

Extracting the Interfacial Electrostatic Features from
Experimentally Determined Antigen and/or
Antibody-Related Structures inside Protein Data Bank
for Machine Learning-Based Antibody Design:
Supplementary Materials

Wei Li*

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*Institute of Special Environment Medicine, Nantong University, No. 9, Seyuan Road, Nantong City, Jiangsu Province, P. R. China

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1825	Interfacial 5U3N-specific side chain and main chain hydrogen bonding analysis	4386
1826	Interfacial 5UCB-specific side chain and main chain hydrogen bonding analysis	4387
1827	Interfacial 5UK0-specific side chain and main chain hydrogen bonding analysis	4388
1828	Interfacial 5VXJ-specific side chain and main chain hydrogen bonding analysis	4389

1829	Interfacial 5VXK-specific side chain and main chain hydrogen bonding analysis	4390
1830	Interfacial 5VXL-specific side chain and main chain hydrogen bonding analysis	4391
1831	Interfacial 5VXM-specific side chain and main chain hydrogen bonding analysis	4392
1832	Interfacial 5VXR-specific side chain and main chain hydrogen bonding analysis	4393
1833	Interfacial 5WKQ-specific side chain and main chain hydrogen bonding analysis	4394
1834	Interfacial 5WN9-specific side chain and main chain hydrogen bonding analysis	4395
1835	1A14-specific interfacial side chain hydrogen bonding analysis	4396
1836	1E6J-specific interfacial side chain hydrogen bonding analysis	4397
1837	1F3R-specific interfacial side chain hydrogen bonding analysis	4398
1838	1HGD-specific interfacial side chain hydrogen bonding analysis	4400
1839	1HGE-specific interfacial side chain hydrogen bonding analysis	4402
1840	1HGF-specific interfacial side chain hydrogen bonding analysis	4404
1841	1HGG-specific interfacial side chain hydrogen bonding analysis	4406
1842	1HGH-specific interfacial side chain hydrogen bonding analysis	4408
1843	1HGI-specific interfacial side chain hydrogen bonding analysis	4410
1844	1HGT-specific interfacial side chain hydrogen bonding analysis	4412
1845	1OSP-specific interfacial side chain hydrogen bonding analysis	4413
1846	1VFB-specific interfacial side chain hydrogen bonding analysis	4414
1847	3SE8-specific interfacial side chain hydrogen bonding analysis	4415
1848	3SE9-specific interfacial side chain hydrogen bonding analysis	4416
1849	3THM-specific interfacial side chain hydrogen bonding analysis	4417
1850	3TJE-specific interfacial side chain hydrogen bonding analysis	4418
1851	3U2S-specific interfacial side chain hydrogen bonding analysis	4419
1852	3UYR-specific interfacial side chain hydrogen bonding analysis	4420
1853	4F33-specific interfacial side chain hydrogen bonding analysis	4421
1854	4F3F-specific interfacial side chain hydrogen bonding analysis	4422
1855	4JAM-specific interfacial side chain hydrogen bonding analysis	4423
1856	4JAN-specific interfacial side chain hydrogen bonding analysis	4424
1857	4KRM-specific interfacial side chain hydrogen bonding analysis	4425
1858	4KRO-specific interfacial side chain hydrogen bonding analysis	4426

1859 4KRP-specific interfacial side chain hydrogen bonding analysis	4427
1860 4NZR-specific interfacial side chain hydrogen bonding analysis	4428
1861 4WUU-specific interfacial side chain hydrogen bonding analysis	4429
1862 4Z0X-specific interfacial side chain hydrogen bonding analysis	4430
1863 5I76-specific interfacial side chain hydrogen bonding analysis	4431
1864 5JO5-specific interfacial side chain hydrogen bonding analysis	4432
1865 5JR1-specific interfacial side chain hydrogen bonding analysis	4433
1866 5JUE-specific interfacial side chain hydrogen bonding analysis	4434
1867 5JXA-specific interfacial side chain hydrogen bonding analysis	4435
1868 5T6P-specific interfacial side chain hydrogen bonding analysis	4436
1869 5T78-specific interfacial side chain hydrogen bonding analysis	4437
1870 5U3J-specific interfacial side chain hydrogen bonding analysis	4438
1871 5U3N-specific interfacial side chain hydrogen bonding analysis	4439
1872 5UCB-specific interfacial side chain hydrogen bonding analysis	4440
1873 5UK0-specific interfacial side chain hydrogen bonding analysis	4441
1874 5VXJ-specific interfacial side chain hydrogen bonding analysis	4442
1875 5VXK-specific interfacial side chain hydrogen bonding analysis	4443
1876 5VXL-specific interfacial side chain hydrogen bonding analysis	4444
1877 5VXM-specific interfacial side chain hydrogen bonding analysis	4445
1878 5VXR-specific interfacial side chain hydrogen bonding analysis	4446
1879 5WKQ-specific interfacial side chain hydrogen bonding analysis	4447
1880 5WN9-specific interfacial side chain hydrogen bonding analysis	4448

Supporting Material

Overall analysis of the interfacial electrostatic features of all experimentally determined antigen-antibody-related structures

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1A14	N_ARG_82	NH1	N_ASP_127	OD2	3.377
1A14	N_ARG_82	NH2	N_ASP_127	OD2	3.103
1A14	N_ARG_118	NH1	N_GLU_119	OE2	3.614
1A14	N_ARG_118	NH2	N_GLU_425	OE1	2.718
1A14	N_ARG_118	NH2	N_GLU_425	OE2	3.457
1A14	N_ARG_130	NH1	N_GLU_128	OE2	3.346
1A14	N_ARG_141	NH1	N_GLU_110	OE2	2.663
1A14	N_ARG_156	NH1	N_GLU_119	OE1	3.576
1A14	N_ARG_156	NH2	N_GLU_119	OE1	3.307
1A14	N_ARG_172	NH1	N_GLU_174	OE1	3.579
1A14	N_ARG_172	NH1	N_GLU_174	OE2	2.688
1A14	N_ARG_189	NH1	N_ASP_125	OD1	2.993
1A14	N_ARG_209	NH2	N_GLU_174	OE1	2.647
1A14	N_ARG_224	NH1	N_GLU_276	OE1	3.468
1A14	N_ARG_224	NH1	N_GLU_276	OE2	2.449
1A14	N_ARG_224	NH2	N_GLU_276	OE2	3.362
1A14	N_HIS_274	ND1	N_GLU_276	OE2	3.981
1A14	N_HIS_274	NE2	N_GLU_276	OE2	3.658
1A14	N_ARG_292	NH2	N_GLU_277	OE1	3.076
1A14	N_ARG_292	NH2	N_GLU_277	OE2	3.834
1A14	N_ARG_300	NH1	N_ASP_324	OD1	3.224
1A14	N_ARG_300	NH2	N_ASP_324	OD1	3.465
1A14	N_ARG_304	NH1	N_GLU_286	OE2	3.487
1A14	N_HIS_312	ND1	N_GLU_266	OE1	3.839
1A14	N_HIS_312	ND1	N_GLU_266	OE2	2.824
1A14	N_ARG_364	NH1	N_ASP_330	OD2	3.955
1A14	N_ARG_364	NH1	N_GLU_375	OE2	2.918
1A14	N_ARG_364	NH2	N_ASP_330	OD1	2.939
1A14	N_ARG_364	NH2	N_ASP_330	OD2	2.852
1A14	N_LYS_387	NZ	N_ASP_386	OD1	2.949
1A14	N_LYS_387	NZ	N_ASP_386	OD2	3.684
1A14	N_ARG_428	NH1	N_ASP_460	OD2	2.670
1A14	N_ARG_428	NH2	N_GLU_433	OE1	3.485
1A14	N_ARG_428	NH2	N_GLU_433	OE2	2.572
1A14	N_LYS_432	NZ	H_ASP_56	OD1	3.071
1A14	H_LYS_38	NZ	H_ASP_86	OD1	3.927
1A14	H_LYS_66	NZ	H_ASP_86	OD1	3.084
1A14	H_LYS_66	NZ	H_ASP_86	OD2	3.096
1A14	H_ARG_94	NH2	H_ASP_101	OD2	2.754
1A14	H_ARG_100	NH1	H_ASP_100B	OD1	2.852
1A14	H_ARG_100	NH1	H_ASP_100B	OD2	3.179
1A14	L_ARG_61	NH1	L_GLU_79	OE1	3.189
1A14	L_ARG_61	NH1	L_GLU_79	OE2	3.942
1A14	L_ARG_61	NH2	L_GLU_79	OE1	3.107
1A14	L_ARG_61	NH2	L_ASP_82	OD1	2.650
1A14	L_ARG_61	NH2	L_ASP_82	OD2	3.122
1A2Y	A_ARG_61	NH2	A_GLU_81	OE2	3.299
1A2Y	A_ARG_61	NH2	A_ASP_82	OD1	2.783
1A2Y	A_ARG_61	NH2	A_ASP_82	OD2	3.405
1A2Y	A_ARG_96	NH1	B_GLU_98	OE1	2.846
1A2Y	A_ARG_96	NH1	B_GLU_98	OE2	3.664
1A2Y	A_ARG_96	NH2	B_GLU_98	OE1	3.545
1A2Y	A_ARG_96	NH2	B_GLU_98	OE2	2.882
1A2Y	B_ARG_38	NH1	B_ASP_89	OD1	3.030
1A2Y	B_ARG_38	NH2	B_GLU_46	OE1	3.122
1A2Y	B_ARG_38	NH2	B_ASP_89	OD1	3.828
1A2Y	B_ARG_66	NH1	B_ASP_89	OD1	3.898

1A2Y	B_ARG.66	NH1	B_ASP.89	OD2	3.063
1A2Y	B_ARG.66	NH2	B_ASP.89	OD1	3.023
1A2Y	B_ARG.66	NH2	B_ASP.89	OD2	3.441
1A2Y	B_ARG.97	NH2	B_ASP.104	OD1	3.891
1A2Y	B_ARG.97	NH2	B_ASP.104	OD2	2.921
1A2Y	B_ARG.102	NH1	B_ASP.100	OD2	3.378
1A2Y	C_ARG.61	NH1	C_ASP.48	OD1	2.641
1A2Y	C_ARG.68	NH1	C_ASP.66	OD2	3.417
1A2Y	C_ARG.125	NH1	C_ASP.119	OD1	3.449
1A2Y	C_ARG.125	NH1	C_ASP.119	OD2	3.142
1A2Y	C_ARG.125	NH2	C_ASP.119	OD2	3.057
1A7L	A_LYS.15	NZ	A_GLU.111	OE1	3.415
1A7L	A_LYS.15	NZ	A_GLU.111	OE2	2.711
1A7L	A_LYS.83	NZ	A_ASP.87	OD1	3.030
1A7L	A_LYS.83	NZ	A_ASP.87	OD2	3.304
1A7L	A_LYS.140	NZ	A_ASP.136	OD1	3.902
1A7L	A_LYS.140	NZ	A_ASP.136	OD2	2.755
1A7L	A_LYS.170	NZ	A_ASP.180	OD2	2.887
1A7L	A_LYS.189	NZ	A_ASP.358	OD2	2.997
1A7L	A_HIS.203	ND1	A_ASP.136	OD2	2.891
1A7L	A_LYS.219	NZ	B_GLU.131	OE1	3.835
1A7L	A_LYS.251	NZ	A_ASP.164	OD2	3.413
1A7L	A_ARG.316	NH1	A_ASP.236	OD2	3.471
1A7L	A_ARG.316	NH2	A_ASP.314	OD2	2.893
1A7L	A_ARG.344	NH2	A_GLU.153	OE1	2.800
1A7L	A_ARG.344	NH2	A_GLU.153	OE2	3.001
1A7L	A_ARG.135E	NH2	A_ASP.133E	OD1	3.683
1A7L	A_ARG.135E	NH2	A_ASP.133E	OD2	3.429
1A7L	B_LYS.15	NZ	B_GLU.111	OE1	3.377
1A7L	B_LYS.15	NZ	B_GLU.111	OE2	3.759
1A7L	B_LYS.42	NZ	B_GLU.44	OE2	3.460
1A7L	B_LYS.42	NZ	B_GLU.45	OE2	3.115
1A7L	B_LYS.140	NZ	B_ASP.136	OD2	3.464
1A7L	B_LYS.170	NZ	B_ASP.180	OD2	3.114
1A7L	B_LYS.189	NZ	B_ASP.358	OD2	3.685
1A7L	B_HIS.203	ND1	B_ASP.136	OD2	2.601
1A7L	B_LYS.251	NZ	B_ASP.164	OD2	3.639
1A7L	B_LYS.277	NZ	B_GLU.281	OE1	3.203
1A7L	B_LYS.277	NZ	B_GLU.281	OE2	2.832
1A7L	B_ARG.316	NH1	B_ASP.236	OD1	3.944
1A7L	B_ARG.316	NH1	B_ASP.236	OD2	3.485
1A7L	B_ARG.316	NH2	B_ASP.314	OD2	3.346
1A7L	B_LYS.326	NZ	B_GLU.322	OE2	3.744
1A7L	B_ARG.344	NH2	B_GLU.153	OE1	2.942
1A7L	B_ARG.344	NH2	B_GLU.153	OE2	3.765
1A7L	C_LYS.29	NZ	C_GLU.28	OE2	3.650
1A7L	C_LYS.83	NZ	C_ASP.87	OD1	3.169
1A7L	C_LYS.83	NZ	C_ASP.87	OD2	3.327
1A7L	C_LYS.102	NZ	C_GLU.78	OE1	3.945
1A7L	C_LYS.140	NZ	C_ASP.136	OD1	2.897
1A7L	C_LYS.140	NZ	C_ASP.136	OD2	3.618
1A7L	C_LYS.170	NZ	C_GLU.172	OE2	3.002
1A7L	C_LYS.189	NZ	C_ASP.184	OD1	3.860
1A7L	C_LYS.189	NZ	C_ASP.358	OD2	3.399
1A7L	C_HIS.203	ND1	C_ASP.136	OD1	2.895
1A7L	C_LYS.219	NZ	C_GLU.221	OE2	3.817
1A7L	C_LYS.277	NZ	C_GLU.281	OE1	3.148
1A7L	C_LYS.277	NZ	C_GLU.281	OE2	3.283

1A7L	C_LYS_295	NZ	C_GLU_291	OE2	3.540
1A7L	C_ARG_316	NH1	C_ASP_236	OD2	3.877
1A7L	C_ARG_316	NH2	C_ASP_314	OD2	3.048
1A7L	C_LYS_326	NZ	C_GLU_322	OE2	3.201
1A7L	C_ARG_344	NH1	C_GLU_153	OE1	3.865
1A7L	C_ARG_344	NH1	C_GLU_153	OE2	2.640
1A7L	C_ARG_344	NH2	C_GLU_153	OE1	2.933
1A7L	C_ARG_344	NH2	C_GLU_153	OE2	3.058
1A7L	C_LYS_362	NZ	C_ASP_363	OD1	3.768
1A7N	L_ARG_61	NH2	L_ASP_81	OD2	3.125
1A7N	L_ARG_61	NH2	L_ASP_82	OD1	2.727
1A7N	L_ARG_61	NH2	L_ASP_82	OD2	3.246
1A7N	L_ARG_96	NH1	H_GLU_298	OE1	2.957
1A7N	L_ARG_96	NH1	H_GLU_298	OE2	3.249
1A7N	L_ARG_96	NH2	H_GLU_298	OE2	3.297
1A7N	L_LYS_107	NZ	L_GLU_17	OE2	2.821
1A7N	H_ARG_238	NH1	H_ASP_289	OD1	2.802
1A7N	H_ARG_238	NH2	H_GLU_246	OE1	3.463
1A7N	H_ARG_238	NH2	H_GLU_246	OE2	3.781
1A7N	H_ARG_238	NH2	H_ASP_289	OD1	3.741
1A7N	H_ARG_266	NH1	H_ASP_289	OD1	3.782
1A7N	H_ARG_266	NH1	H_ASP_289	OD2	2.637
1A7N	H_ARG_266	NH2	H_ASP_289	OD1	3.006
1A7N	H_ARG_266	NH2	H_ASP_289	OD2	3.237
1A7N	H_LYS_275	NZ	H_ASP_272	OD2	3.739
1A7N	H_ARG_297	NH2	H_ASP_304	OD1	3.472
1A7N	H_ARG_297	NH2	H_ASP_304	OD2	2.559
1A7N	H_ARG_302	NH1	H_ASP_300	OD1	2.938
1A7O	L_ARG_61	NH2	L_ASP_81	OD2	3.044
1A7O	L_ARG_61	NH2	L_ASP_82	OD1	2.765
1A7O	L_ARG_61	NH2	L_ASP_82	OD2	3.549
1A7O	L_LYS_107	NZ	L_GLU_17	OE2	3.441
1A7O	H_ARG_238	NH1	H_ASP_289	OD1	2.721
1A7O	H_ARG_238	NH2	H_GLU_246	OE1	3.298
1A7O	H_ARG_238	NH2	H_GLU_246	OE2	3.986
1A7O	H_ARG_238	NH2	H_ASP_289	OD1	3.845
1A7O	H_ARG_266	NH1	H_ASP_289	OD1	3.739
1A7O	H_ARG_266	NH1	H_ASP_289	OD2	2.614
1A7O	H_ARG_266	NH2	H_ASP_289	OD1	2.654
1A7O	H_ARG_266	NH2	H_ASP_289	OD2	2.979
1A7O	H_ARG_297	NH2	H_ASP_304	OD1	3.602
1A7O	H_ARG_297	NH2	H_ASP_304	OD2	2.696
1A7P	L_ARG_61	NH2	L_ASP_81	OD2	3.219
1A7P	L_ARG_61	NH2	L_ASP_82	OD1	2.851
1A7P	L_ARG_61	NH2	L_ASP_82	OD2	3.384
1A7P	L_ARG_96	NH2	H_GLU_298	OE1	3.845
1A7P	L_ARG_96	NH2	H_GLU_298	OE2	2.867
1A7P	L_LYS_107	NZ	L_GLU_17	OE2	2.919
1A7P	H_ARG_238	NH1	H_ASP_289	OD1	2.885
1A7P	H_ARG_238	NH2	H_GLU_246	OE1	3.234
1A7P	H_ARG_238	NH2	H_GLU_246	OE2	3.868
1A7P	H_ARG_238	NH2	H_ASP_289	OD1	3.785
1A7P	H_ARG_266	NH1	H_ASP_289	OD1	3.679
1A7P	H_ARG_266	NH1	H_ASP_289	OD2	2.508
1A7P	H_ARG_266	NH2	H_ASP_289	OD1	2.957
1A7P	H_ARG_266	NH2	H_ASP_289	OD2	3.253
1A7P	H_ARG_297	NH2	H_ASP_304	OD1	3.629
1A7P	H_ARG_297	NH2	H_ASP_304	OD2	2.709

1A7Q	L_ARG_96	NH1	H_GLU_298	OE1	2.615
1A7Q	L_ARG_96	NH1	H_GLU_298	OE2	3.239
1A7Q	L_ARG_96	NH2	H_GLU_298	OE1	3.431
1A7Q	L_ARG_96	NH2	H_GLU_298	OE2	2.621
1A7Q	H_ARG_238	NH1	H_ASP_289	OD1	2.800
1A7Q	H_ARG_238	NH2	H_GLU_246	OE1	3.193
1A7Q	H_ARG_238	NH2	H_GLU_246	OE2	3.915
1A7Q	H_ARG_238	NH2	H_ASP_289	OD1	3.788
1A7Q	H_ARG_266	NH1	H_ASP_289	OD1	3.820
1A7Q	H_ARG_266	NH1	H_ASP_289	OD2	2.595
1A7Q	H_ARG_266	NH2	H_ASP_289	OD1	2.974
1A7Q	H_ARG_266	NH2	H_ASP_289	OD2	3.211
1A7Q	H_ARG_297	NH2	H_ASP_304	OD1	3.728
1A7Q	H_ARG_297	NH2	H_ASP_304	OD2	2.870
1A7Q	H_ARG_299	NH1	H_ASP_304	OD2	3.412
1A7Q	H_ARG_302	NH1	H_ASP_300	OD2	3.990
1A7R	L_ARG_61	NH2	L_ASP_81	OD2	3.198
1A7R	L_ARG_61	NH2	L_ASP_82	OD1	2.615
1A7R	L_ARG_61	NH2	L_ASP_82	OD2	3.098
1A7R	L_ARG_96	NH1	H_GLU_298	OE1	2.658
1A7R	L_ARG_96	NH1	H_GLU_298	OE2	3.535
1A7R	L_ARG_96	NH2	H_GLU_298	OE1	3.614
1A7R	L_ARG_96	NH2	H_GLU_298	OE2	2.905
1A7R	L_LYS_107	NZ	L_GLU_17	OE2	3.377
1A7R	H_ARG_238	NH1	H_ASP_289	OD1	2.846
1A7R	H_ARG_238	NH2	H_GLU_246	OE1	3.349
1A7R	H_ARG_238	NH2	H_GLU_246	OE2	3.834
1A7R	H_ARG_238	NH2	H_ASP_289	OD1	3.880
1A7R	H_ARG_266	NH1	H_ASP_289	OD1	3.623
1A7R	H_ARG_266	NH1	H_ASP_289	OD2	2.578
1A7R	H_ARG_266	NH2	H_ASP_289	OD1	2.893
1A7R	H_ARG_266	NH2	H_ASP_289	OD2	3.226
1A7R	H_LYS_275	NZ	H_ASP_272	OD2	3.976
1A7R	H_ARG_297	NH2	H_ASP_304	OD1	3.559
1A7R	H_ARG_297	NH2	H_ASP_304	OD2	2.633
1ADQ	A_LYS_248	NZ	A_GLU_380	OE2	3.226
1ADQ	A_ARG_255	NH1	A_ASP_249	OD1	3.987
1ADQ	A_ARG_255	NH2	H_ASP_31	OD2	2.929
1ADQ	A_LYS_320	NZ	A_GLU_333	OE1	3.855
1ADQ	A_LYS_320	NZ	A_GLU_333	OE2	3.755
1ADQ	A_LYS_326	NZ	A_ASP_270	OD1	3.273
1ADQ	A_LYS_326	NZ	A_ASP_270	OD2	3.723
1ADQ	A_LYS_338	NZ	A_GLU_430	OE1	3.031
1ADQ	A_LYS_338	NZ	A_GLU_430	OE2	2.803
1ADQ	A_ARG_344	NH1	A_ASP_401	OD2	3.235
1ADQ	A_ARG_416	NH1	A_GLU_388	OE1	3.926
1ADQ	A_ARG_416	NH1	A_GLU_388	OE2	3.113
1ADQ	A_ARG_416	NH2	A_GLU_388	OE1	3.507
1ADQ	A_ARG_416	NH2	A_GLU_388	OE2	2.923
1ADQ	A_HIS_433	NE2	L_ASP_50	OD1	3.394
1ADQ	A_HIS_433	NE2	L_ASP_50	OD2	3.883
1ADQ	L_LYS_31	NZ	L_ASP_92	OD1	3.026
1ADQ	L_ARG_61	NH2	L_GLU_79	OE1	3.104
1ADQ	L_ARG_61	NH2	L_ASP_82	OD1	3.715
1ADQ	L_ARG_61	NH2	L_ASP_82	OD2	3.959
1ADQ	L_HIS_95B	NE2	H_ASP_61	OD2	3.425
1ADQ	L_LYS_149	NZ	L_GLU_206	OE1	3.712
1ADQ	H_ARG_38	NH1	H_ASP_86	OD1	3.336

1ADQ	H_ARG.66	NH1	H_ASP.86	OD1	3.600
1ADQ	H_ARG.66	NH1	H_ASP.86	OD2	2.617
1ADQ	H_ARG.66	NH2	H_ASP.86	OD1	2.939
1ADQ	H_ARG.66	NH2	H_ASP.86	OD2	3.254
1ADQ	H_LYS.158	NZ	H_GLU.220	OE1	3.150
1ADQ	H_LYS.184	NZ	H_ASP.146	OD2	3.128
1ADQ	H_LYS.221	NZ	H_ASP.222	OD2	3.919
1BJ1	L_ARG.61	NH2	L_GLU.81	OE2	3.689
1BJ1	L_ARG.61	NH2	L_ASP.82	OD1	2.770
1BJ1	L_ARG.61	NH2	L_ASP.82	OD2	3.181
1BJ1	L_LYS.103	NZ	L_GLU.165	OE2	3.052
1BJ1	L_ARG.142	NH2	L_GLU.105	OE2	3.352
1BJ1	L_LYS.188	NZ	L_ASP.185	OD1	3.571
1BJ1	H_ARG.38	NH1	H_ASP.90	OD1	3.092
1BJ1	H_ARG.38	NH2	H_GLU.46	OE1	3.575
1BJ1	H_ARG.38	NH2	H_ASP.90	OD1	3.916
1BJ1	H_ARG.67	NH1	H_ASP.90	OD2	2.757
1BJ1	H_ARG.67	NH2	H_ASP.90	OD1	3.333
1BJ1	H_ARG.67	NH2	H_ASP.90	OD2	3.289
1BJ1	H_ARG.87	NH1	H_GLU.89	OE2	3.150
1BJ1	H_LYS.153	NZ	H_ASP.154	OD1	3.946
1BJ1	H_LYS.219	NZ	L_GLU.123	OE1	2.948
1BJ1	H_LYS.220	NZ	H_GLU.222	OE1	3.519
1BJ1	H_LYS.224	NZ	L_ASP.122	OD2	2.691
1BJ1	V_ARG.23	NH1	W_GLU.30	OE1	3.305
1BJ1	V_ARG.56	NH2	V_GLU.38	OE1	3.031
1BJ1	V_ARG.82	NH1	V_GLU.42	OE1	3.483
1BJ1	V_ARG.82	NH2	V_GLU.42	OE1	2.954
1BJ1	V_HIS.99	NE2	V_GLU.73	OE2	3.634
1BJ1	V_LYS.107	NZ	V_GLU.64	OE1	3.520
1BJ1	W_ARG.23	NH1	V_GLU.30	OE1	3.351
1BJ1	W_ARG.56	NH2	W_GLU.38	OE1	3.008
1BJ1	W_ARG.82	NH1	W_GLU.42	OE2	3.753
1BJ1	W_ARG.82	NH2	W_GLU.42	OE2	2.675
1BJ1	W_HIS.99	NE2	W_GLU.73	OE2	3.679
1BJ1	W_ARG.105	NH1	W_GLU.103	OE1	3.917
1BJ1	W_ARG.105	NH2	W_GLU.103	OE1	2.651
1BJ1	W_LYS.107	NZ	W_GLU.64	OE1	3.656
1BJ1	J_ARG.61	NH2	J_GLU.81	OE2	3.502
1BJ1	J_ARG.61	NH2	J_ASP.82	OD1	2.721
1BJ1	J_ARG.61	NH2	J_ASP.82	OD2	3.272
1BJ1	J_LYS.103	NZ	J_GLU.165	OE2	3.042
1BJ1	J_LYS.126	NZ	J_GLU.123	OE2	3.084
1BJ1	J_LYS.145	NZ	J_GLU.195	OE2	3.741
1BJ1	J_LYS.188	NZ	J_ASP.185	OD1	3.653
1BJ1	K_ARG.38	NH1	K_ASP.90	OD1	3.157
1BJ1	K_ARG.38	NH2	K_GLU.46	OE1	3.735
1BJ1	K_ARG.38	NH2	K_ASP.90	OD1	3.789
1BJ1	K_ARG.67	NH1	K_ASP.90	OD2	2.824
1BJ1	K_ARG.67	NH2	K_ASP.90	OD1	3.565
1BJ1	K_ARG.67	NH2	K_ASP.90	OD2	3.500
1BJ1	K_ARG.87	NH1	K_GLU.89	OE2	3.633
1BJ1	K_LYS.127	NZ	K_ASP.154	OD2	3.373
1BJ1	K_LYS.220	NZ	K_GLU.222	OE1	3.843
1BLN	A_ARG.24	NH1	A_ASP.70	OD1	2.713
1BLN	A_LYS.39	NZ	A_GLU.81	OE1	3.030
1BLN	A_LYS.39	NZ	A_GLU.81	OE2	2.665
1BLN	A_ARG.54	NH1	A_ASP.60	OD1	3.451

1BLN	A_ARG_54	NH1	A_ASP_60	OD2	2.737
1BLN	A_ARG_54	NH2	A_ASP_60	OD1	3.686
1BLN	A_ARG_61	NH1	A_GLU_79	OE1	3.238
1BLN	A_ARG_61	NH1	A_GLU_79	OE2	2.929
1BLN	A_ARG_61	NH2	A_GLU_79	OE1	2.868
1BLN	A_ARG_61	NH2	A_ASP_82	OD1	2.719
1BLN	A_ARG_61	NH2	A_ASP_82	OD2	2.933
1BLN	A_LYS_103	NZ	A_ASP_165	OD1	2.680
1BLN	A_LYS_103	NZ	A_ASP_165	OD2	2.779
1BLN	A_LYS_149	NZ	A_GLU_195	OE1	2.904
1BLN	A_LYS_149	NZ	A_GLU_195	OE2	2.718
1BLN	A_LYS_169	NZ	A_ASP_167	OD1	3.151
1BLN	A_LYS_169	NZ	A_ASP_167	OD2	2.577
1BLN	A_LYS_169	NZ	A_ASP_170	OD2	3.534
1BLN	A_LYS_183	NZ	A_ASP_184	OD1	3.490
1BLN	A_LYS_183	NZ	A_ASP_184	OD2	2.917
1BLN	A_ARG_188	NH1	A_GLU_185	OE2	2.624
1BLN	A_ARG_188	NH2	A_GLU_185	OE1	3.741
1BLN	A_ARG_188	NH2	A_GLU_185	OE2	2.727
1BLN	A_HIS_189	ND1	A_ASP_151	OD2	2.822
1BLN	A_HIS_189	NE2	A_GLU_154	OE1	3.457
1BLN	A_HIS_189	NE2	A_GLU_154	OE2	3.510
1BLN	A_ARG_211	NH1	A_GLU_213	OE2	3.546
1BLN	B_ARG_38	NH1	B_GLU_46	OE1	2.899
1BLN	B_ARG_38	NH2	B_ASP_86	OD1	2.861
1BLN	B_LYS_64	NZ	B_ASP_61	OD1	2.441
1BLN	B_ARG_66	NH1	B_ASP_86	OD1	3.791
1BLN	B_ARG_66	NH1	B_ASP_86	OD2	2.687
1BLN	B_ARG_66	NH2	B_GLU_85	OE2	2.818
1BLN	B_ARG_66	NH2	B_ASP_86	OD1	2.906
1BLN	B_ARG_66	NH2	B_ASP_86	OD2	3.348
1BLN	B_LYS_75	NZ	B_ASP_72	OD1	2.753
1BLN	B_LYS_75	NZ	B_ASP_72	OD2	2.989
1BLN	B_ARG_83	NH2	B_GLU_85	OE1	2.930
1BLN	B_ARG_83	NH2	B_GLU_85	OE2	2.872
1BLN	B_LYS_218	NZ	B_ASP_220	OD1	2.783
1BLN	B_LYS_218	NZ	B_ASP_220	OD2	2.601
1BLN	B_LYS_221	NZ	A_GLU_123	OE2	2.688
1BLN	B_LYS_222	NZ	B_GLU_226	OE1	2.622
1BLN	B_LYS_222	NZ	B_GLU_226	OE2	2.602
1BLN	C_ARG_24	NH1	C_ASP_70	OD1	3.436
1BLN	C_ARG_24	NH1	C_ASP_70	OD2	2.560
1BLN	C_LYS_39	NZ	C_GLU_81	OE1	2.548
1BLN	C_LYS_39	NZ	C_GLU_81	OE2	2.754
1BLN	C_ARG_54	NH1	C_ASP_60	OD2	3.393
1BLN	C_ARG_61	NH1	C_GLU_79	OE1	3.333
1BLN	C_ARG_61	NH1	C_GLU_79	OE2	2.726
1BLN	C_ARG_61	NH2	C_GLU_79	OE1	3.200
1BLN	C_ARG_61	NH2	C_ASP_82	OD1	2.668
1BLN	C_ARG_61	NH2	C_ASP_82	OD2	3.423
1BLN	C_LYS_103	NZ	C_GLU_105	OE2	2.790
1BLN	C_LYS_103	NZ	C_ASP_165	OD1	3.363
1BLN	C_LYS_103	NZ	C_ASP_165	OD2	3.568
1BLN	C_LYS_149	NZ	C_GLU_195	OE1	2.899
1BLN	C_LYS_149	NZ	C_GLU_195	OE2	2.725
1BLN	C_LYS_169	NZ	C_ASP_167	OD1	3.137
1BLN	C_LYS_169	NZ	C_ASP_167	OD2	2.563
1BLN	C_LYS_169	NZ	C_ASP_170	OD2	3.533

1BLN	C_LYS_183	NZ	C_ASP_184	OD1	3.499
1BLN	C_LYS_183	NZ	C_ASP_184	OD2	2.904
1BLN	C_ARG_188	NH1	C_GLU_185	OE2	2.652
1BLN	C_ARG_188	NH2	C_GLU_185	OE1	3.758
1BLN	C_ARG_188	NH2	C_GLU_185	OE2	2.730
1BLN	C_HIS_189	ND1	C_ASP_151	OD2	2.783
1BLN	C_HIS_189	NE2	C_GLU_154	OE1	3.449
1BLN	C_HIS_189	NE2	C_GLU_154	OE2	3.510
1BLN	C_ARG_211	NH1	C_GLU_213	OE2	3.540
1BLN	D_ARG_38	NH1	D_ASP_86	OD1	2.873
1BLN	D_ARG_38	NH2	D_GLU_46	OE1	2.870
1BLN	D_ARG_38	NH2	D_ASP_86	OD1	3.962
1BLN	D_LYS_64	NZ	D_ASP_61	OD1	2.496
1BLN	D_ARG_66	NH1	D_ASP_86	OD1	3.322
1BLN	D_ARG_66	NH1	D_ASP_86	OD2	3.365
1BLN	D_ARG_66	NH2	D_ASP_86	OD1	3.949
1BLN	D_ARG_66	NH2	D_ASP_86	OD2	2.588
1BLN	D_LYS_75	NZ	D_ASP_72	OD1	2.846
1BLN	D_LYS_75	NZ	D_ASP_72	OD2	2.946
1BLN	D_ARG_83	NH2	D_GLU_85	OE2	2.754
1BLN	D_LYS_218	NZ	D_ASP_220	OD1	2.806
1BLN	D_LYS_218	NZ	D_ASP_220	OD2	2.614
1BLN	D_LYS_221	NZ	C_GLU_123	OE2	2.694
1BLN	D_LYS_222	NZ	D_GLU_226	OE1	2.616
1BLN	D_LYS_222	NZ	D_GLU_226	OE2	2.583
1BQL	L_LYS_44	NZ	H_ASP_104	OD1	3.995
1BQL	L_ARG_45	NH2	H_ASP_104	OD2	3.212
1BQL	L_ARG_60	NH2	L_ASP_81	OD1	2.877
1BQL	L_ARG_106	NH2	L_ASP_168	OD1	2.775
1BQL	L_ARG_106	NH2	L_ASP_168	OD2	3.565
1BQL	L_LYS_147	NZ	L_GLU_193	OE1	3.381
1BQL	L_LYS_147	NZ	L_GLU_193	OE2	3.056
1BQL	L_LYS_167	NZ	L_ASP_165	OD1	3.577
1BQL	L_ARG_186	NH2	L_ASP_182	OD2	3.759
1BQL	L_HIS_187	ND1	L_ASP_149	OD2	3.204
1BQL	H_LYS_38	NZ	H_GLU_46	OE2	3.708
1BQL	H_LYS_67	NZ	H_ASP_90	OD1	3.576
1BQL	H_LYS_67	NZ	H_ASP_90	OD2	2.891
1BQL	H_LYS_208	NZ	H_ASP_210	OD1	3.394
1BQL	H_LYS_211	NZ	L_GLU_121	OE1	2.714
1BQL	H_LYS_211	NZ	L_GLU_121	OE2	2.963
1BQL	Y_LYS_1	NZ	Y_GLU_7	OE1	2.931
1BQL	Y_LYS_1	NZ	Y_GLU_7	OE2	3.316
1BQL	Y_LYS_13	NZ	Y_ASP_18	OD2	3.337
1BQL	Y_ARG_45	NH1	H_GLU_50	OE1	3.800
1BQL	Y_ARG_45	NH1	H_GLU_50	OE2	2.920
1BQL	Y_LYS_68	NZ	H_GLU_50	OE1	3.561
1BQL	Y_LYS_97	NZ	Y_ASP_101	OD1	2.891
1BQL	Y_ARG_125	NH2	Y_ASP_119	OD2	2.588
1BVK	A_ARG_24	NH1	A_ASP_70	OD1	2.987
1BVK	A_ARG_61	NH2	A_GLU_81	OE1	3.459
1BVK	A_ARG_61	NH2	A_ASP_82	OD1	2.453
1BVK	A_ARG_61	NH2	A_ASP_82	OD2	3.255
1BVK	A_ARG_96	NH2	B_GLU_98	OE1	2.978
1BVK	A_ARG_96	NH2	B_GLU_98	OE2	2.932
1BVK	B_ARG_38	NH1	B_ASP_89	OD1	2.858
1BVK	B_ARG_38	NH2	B_GLU_46	OE1	3.400
1BVK	B_ARG_38	NH2	B_GLU_46	OE2	3.917

1BVK	B_ARG_38	NH2	B_ASP_89	OD1	3.415
1BVK	B_ARG_66	NH1	B_ASP_89	OD1	3.789
1BVK	B_ARG_66	NH1	B_ASP_89	OD2	2.919
1BVK	B_ARG_66	NH2	B_ASP_89	OD1	2.669
1BVK	B_ARG_66	NH2	B_ASP_89	OD2	3.080
1BVK	B_ARG_97	NH2	B_ASP_104	OD1	3.302
1BVK	B_ARG_97	NH2	B_ASP_104	OD2	3.220
1BVK	B_ARG_102	NH1	B_ASP_100	OD2	3.508
1BVK	B_ARG_102	NH2	B_ASP_100	OD2	3.959
1BVK	C_ARG_61	NH1	C_ASP_48	OD2	2.726
1BVK	C_ARG_68	NH1	C_ASP_66	OD2	3.814
1BVK	C_ARG_125	NH1	C_ASP_119	OD2	3.413
1BVK	C_ARG_125	NH2	C_ASP_119	OD2	2.659
1BVK	D_ARG_24	NH1	D_ASP_70	OD1	3.898
1BVK	D_ARG_24	NH1	D_ASP_70	OD2	3.517
1BVK	D_ARG_61	NH1	D_GLU_81	OE1	3.485
1BVK	D_ARG_61	NH1	D_GLU_81	OE2	3.564
1BVK	D_ARG_61	NH2	D_GLU_81	OE1	2.809
1BVK	D_ARG_61	NH2	D_GLU_81	OE2	3.799
1BVK	D_ARG_61	NH2	D_ASP_82	OD1	2.873
1BVK	D_ARG_61	NH2	D_ASP_82	OD2	3.655
1BVK	D_ARG_96	NH2	E_GLU_98	OE1	2.525
1BVK	D_ARG_96	NH2	E_GLU_98	OE2	2.753
1BVK	E_ARG_38	NH1	E_ASP_89	OD1	3.089
1BVK	E_ARG_38	NH2	E_GLU_46	OE1	3.613
1BVK	E_ARG_38	NH2	E_GLU_46	OE2	3.594
1BVK	E_ARG_38	NH2	E_ASP_89	OD1	3.476
1BVK	E_ARG_66	NH1	E_ASP_89	OD1	3.924
1BVK	E_ARG_66	NH1	E_ASP_89	OD2	2.743
1BVK	E_ARG_66	NH2	E_ASP_89	OD1	3.027
1BVK	E_ARG_66	NH2	E_ASP_89	OD2	3.167
1BVK	E_ARG_97	NH2	E_ASP_104	OD1	3.359
1BVK	E_ARG_97	NH2	E_ASP_104	OD2	2.447
1BVK	E_ARG_102	NH1	E_ASP_100	OD2	3.374
1BVK	E_ARG_102	NH2	E_ASP_100	OD2	3.788
1BVK	F_LYS_1	NZ	F_GLU_7	OE2	2.724
1BVK	F_LYS_13	NZ	F_ASP_18	OD2	3.816
1BVK	F_ARG_61	NH1	F_ASP_48	OD2	3.232
1BVK	F_ARG_125	NH1	F_ASP_119	OD1	3.126
1BVK	F_ARG_125	NH1	F_ASP_119	OD2	2.577
1BVK	F_ARG_125	NH2	F_ASP_119	OD2	2.733
1C08	A_ARG_61	NH1	A_GLU_79	OE1	3.359
1C08	A_ARG_61	NH1	A_GLU_79	OE2	3.299
1C08	A_ARG_61	NH2	A_GLU_79	OE1	3.600
1C08	A_ARG_61	NH2	A_GLU_81	OE2	3.058
1C08	A_ARG_61	NH2	A_ASP_82	OD1	2.615
1C08	A_ARG_61	NH2	A_ASP_82	OD2	3.483
1C08	A_LYS_103	NZ	A_GLU_105	OE2	3.843
1C08	B_ARG_38	NH1	B_ASP_89	OD1	2.821
1C08	B_ARG_38	NH2	B_GLU_46	OE1	2.693
1C08	B_ARG_38	NH2	B_ASP_89	OD1	3.615
1C08	B_ARG_66	NH1	B_ASP_89	OD1	3.916
1C08	B_ARG_66	NH1	B_ASP_89	OD2	3.160
1C08	B_ARG_66	NH2	B_ASP_89	OD1	3.080
1C08	B_ARG_66	NH2	B_ASP_89	OD2	3.629
1C08	B_LYS_75	NZ	B_ASP_72	OD2	2.822
1C08	C_LYS_1	NZ	C_GLU_7	OE1	3.861
1C08	C_LYS_1	NZ	C_GLU_7	OE2	2.619

1C08	C_ARG.61	NH1	C_ASP_48	OD2	2.684
1C08	C_ARG.61	NH2	C_ASP_48	OD2	3.901
1C08	C_LYS.97	NZ	B_ASP_32	OD1	2.620
1C08	C_LYS.97	NZ	B_ASP_32	OD2	3.999
1C08	C_LYS.97	NZ	B_ASP_99	OD2	2.365
1C08	C_ARG_125	NH1	C_ASP_119	OD2	3.458
1C08	C_ARG_125	NH2	C_ASP_119	OD1	3.749
1C08	C_ARG_125	NH2	C_ASP_119	OD2	3.808
1C12	A_ARG.61	NH1	A_GLU_79	OE1	3.872
1C12	A_ARG.61	NH1	A_GLU_79	OE2	3.629
1C12	A_ARG.61	NH1	A_GLU_81	OE2	3.588
1C12	A_ARG.61	NH1	A_ASP_82	OD1	3.976
1C12	A_ARG.61	NH2	A_ASP_82	OD1	2.627
1C12	A_ARG.61	NH2	A_ASP_82	OD2	3.162
1C12	A_LYS_103	NZ	A_ASP_85	OD1	2.711
1C12	A_LYS_103	NZ	A_ASP_85	OD2	3.993
1C12	A_LYS_147	NZ	A_GLU_154	OE2	3.218
1C12	A_LYS_149	NZ	A_GLU_154	OE1	3.689
1C12	A_ARG_155	NH1	A_GLU_185	OE1	3.418
1C12	A_ARG_155	NH2	A_GLU_185	OE1	3.302
1C12	A_LYS_169	NZ	A_ASP_167	OD1	3.892
1C12	A_ARG_188	NH1	A_ASP_184	OD1	3.647
1C12	A_ARG_188	NH1	A_ASP_184	OD2	3.352
1C12	A_HIS_189	ND1	A_ASP_151	OD2	3.592
1C12	A_LYS_199	NZ	A_ASP_143	OD2	3.366
1C12	A_ARG_211	NH2	A_GLU_187	OE2	3.347
1C12	B_ARG_338	NH1	B_GLU_346	OE2	2.575
1C12	B_ARG_338	NH2	B_ASP_386	OD1	2.668
1C12	B_ARG_366	NH1	B_ASP_386	OD1	2.858
1C12	B_ARG_366	NH1	B_ASP_386	OD2	3.220
1C12	B_ARG_366	NH2	B_ASP_386	OD1	3.966
1C12	B_ARG_366	NH2	B_ASP_386	OD2	2.872
1C12	B_LYS_508	NZ	A_GLU_123	OE2	3.314
1CE1	L_ARG.61	NH2	L_GLU_81	OE1	3.727
1CE1	L_ARG.61	NH2	L_ASP_82	OD1	2.705
1CE1	L_ARG.61	NH2	L_ASP_82	OD2	3.700
1CE1	L_ARG_94	NH2	H_GLU_61	OE2	3.979
1CE1	L_ARG_96	NH1	H_GLU_101	OE1	2.707
1CE1	L_ARG_96	NH1	H_GLU_101	OE2	3.562
1CE1	L_ARG_96	NH2	H_GLU_101	OE1	3.509
1CE1	L_ARG_96	NH2	H_GLU_101	OE2	2.787
1CE1	L_LYS_103	NZ	L_GLU_105	OE1	3.913
1CE1	L_LYS_149	NZ	L_GLU_195	OE2	3.867
1CE1	L_LYS_188	NZ	L_ASP_185	OD1	3.892
1CE1	H_ARG_38	NH1	H_ASP_92	OD1	2.855
1CE1	H_ARG_38	NH2	H_GLU_46	OE1	2.954
1CE1	H_ARG_38	NH2	H_ASP_92	OD1	3.724
1CE1	H_ARG_52	NH1	H_GLU_61	OE2	3.297
1CE1	H_ARG_52	NH2	H_GLU_61	OE2	2.740
1CE1	H_ARG_52	NH2	P_ASP_7	OD1	3.481
1CE1	H_LYS_56	NZ	P_ASP_7	OD2	2.951
1CE1	H_ARG_69	NH1	H_ASP_92	OD1	3.674
1CE1	H_ARG_69	NH1	H_ASP_92	OD2	2.964
1CE1	H_ARG_69	NH2	H_ASP_92	OD1	2.906
1CE1	H_ARG_69	NH2	H_ASP_92	OD2	3.491
1CE1	H_ARG_100	NH2	H_ASP_109	OD1	3.721
1CE1	H_ARG_100	NH2	H_ASP_109	OD2	2.688
1CE1	H_LYS_218	NZ	H_GLU_220	OE2	3.210

1CFS	A_ARG.61	NH1	A_GLU_79	OE1	3.782
1CFS	A_ARG.61	NH1	A_ASP_82	OD1	2.689
1CFS	A_ARG.61	NH1	A_ASP_82	OD2	2.385
1CFS	A_ARG.61	NH2	A_GLU_79	OE1	3.368
1CFS	A_LYS_147	NZ	A_GLU_154	OE2	3.751
1CFS	A_LYS_149	NZ	A_GLU_195	OE1	3.919
1CFS	A_LYS_149	NZ	A_GLU_195	OE2	2.427
1CFS	A_HIS_189	ND1	A_ASP_151	OD2	3.201
1CFS	A_LYS_199	NZ	A_ASP_110	OD2	2.468
1CFS	A_ARG.211	NH2	A_GLU_187	OE2	3.817
1CFS	B_LYS_19	NZ	B_GLU_82	OE1	2.420
1CFS	B_LYS_19	NZ	B_GLU_82	OE2	3.235
1CFS	B_HIS_35	NE2	B_GLU_33	OE1	3.092
1CFS	B_LYS_38	NZ	B_ASP_90	OD1	3.977
1CFS	B_LYS_63	NZ	B_GLU_46	OE2	2.435
1CFS	B_LYS_67	NZ	B_ASP_90	OD2	3.258
1CFS	B_ARG_98	NH1	B_ASP_100	OD1	3.172
1CFS	B_ARG_98	NH1	B_ASP_100	OD2	2.621
1CFS	B_LYS_99	NZ	B_GLU_33	OE1	3.391
1CFS	B_LYS_207	NZ	A_GLU_123	OE1	3.526
1CFS	B_ARG.212	NH2	B_GLU_210	OE1	3.742
1CFT	A_ARG.61	NH1	A_GLU_79	OE1	3.018
1CFT	A_ARG.61	NH1	A_GLU_79	OE2	2.933
1CFT	A_ARG.61	NH1	A_ASP_82	OD1	3.900
1CFT	A_ARG.61	NH1	A_ASP_82	OD2	3.509
1CFT	A_ARG.61	NH2	A_ASP_82	OD1	3.453
1CFT	A_LYS_103	NZ	A_ASP_105	OD1	3.879
1CFT	A_LYS_103	NZ	A_ASP_105	OD2	3.379
1CFT	A_LYS_149	NZ	A_GLU_195	OE1	3.740
1CFT	A_LYS_149	NZ	A_GLU_195	OE2	2.938
1CFT	A_ARG_155	NH1	A_GLU_185	OE2	3.873
1CFT	A_ARG_155	NH2	A_GLU_185	OE1	3.494
1CFT	A_ARG_155	NH2	A_GLU_185	OE2	2.450
1CFT	A_LYS_183	NZ	A_GLU_187	OE1	3.152
1CFT	A_LYS_183	NZ	A_GLU_187	OE2	3.103
1CFT	A_HIS_189	ND1	A_ASP_151	OD2	2.935
1CFT	B_HIS_35	NE2	B_GLU_33	OE1	2.890
1CFT	B_LYS_38	NZ	B_ASP_90	OD1	3.646
1CFT	B_LYS_63	NZ	B_GLU_46	OE1	3.173
1CFT	B_LYS_63	NZ	B_GLU_46	OE2	3.453
1CFT	B_LYS_67	NZ	B_ASP_90	OD1	3.866
1CFT	B_LYS_67	NZ	B_ASP_90	OD2	2.897
1CFT	B_ARG_98	NH2	B_ASP_100	OD1	3.436
1CFT	B_ARG_98	NH2	B_ASP_100	OD2	2.735
1CFT	B_LYS_99	NZ	B_GLU_33	OE1	2.555
1CFT	B_LYS_204	NZ	B_ASP_206	OD2	3.553
1CFT	B_LYS_207	NZ	A_GLU_123	OE1	2.550
1CFT	B_LYS_208	NZ	B_GLU_210	OE2	2.675
1CFT	C_LYS.2	NZ	A_ASP_92	OD1	2.682
1CG9	A_HIS.3	ND1	A_ASP_29	OD2	2.918
1CG9	A_ARG.6	NH1	A_ASP_102	OD1	3.165
1CG9	A_ARG.6	NH2	A_ASP_102	OD1	2.958
1CG9	A_ARG.6	NH2	A_ASP_102	OD2	3.809
1CG9	A_ARG_14	NH1	A_ASP_39	OD1	3.895
1CG9	A_ARG_14	NH1	A_ASP_39	OD2	3.383
1CG9	A_ARG_14	NH2	A_ASP_39	OD1	2.876
1CG9	A_ARG_14	NH2	A_ASP_39	OD2	3.696
1CG9	A_ARG_17	NH1	B_ASP_35	OD2	3.201

1CG9	A_ARG_17	NH2	B_ASP_35	OD1	3.038
1CG9	A_ARG_17	NH2	B_ASP_35	OD2	3.401
1CG9	A_ARG_21	NH2	A_ASP_37	OD1	3.415
1CG9	A_ARG_21	NH2	A_ASP_37	OD2	2.852
1CG9	A_ARG_35	NH1	A_GLU_46	OE1	3.005
1CG9	A_ARG_35	NH1	A_GLU_46	OE2	3.637
1CG9	A_ARG_35	NH2	A_ASP_37	OD2	3.660
1CG9	A_ARG_44	NH2	A_GLU_46	OE2	3.936
1CG9	A_ARG_48	NH1	A_GLU_46	OE1	3.350
1CG9	A_ARG_48	NH2	A_GLU_46	OE1	3.509
1CG9	A_ARG_48	NH2	B_ASP_54	OD1	3.456
1CG9	A_ARG_48	NH2	B_ASP_54	OD2	3.762
1CG9	A_ARG_82	NH1	A_GLU_89	OE1	2.878
1CG9	A_ARG_82	NH1	A_GLU_89	OE2	2.767
1CG9	A_HIS_93	ND1	A_ASP_119	OD1	3.615
1CG9	A_HIS_93	ND1	A_ASP_119	OD2	2.882
1CG9	A_ARG_111	NH2	A_ASP_102	OD2	3.428
1CG9	A_HIS_113	NE2	A_ASP_102	OD2	2.935
1CG9	A_ARG_151	NH2	A_GLU_154	OE1	3.687
1CG9	A_ARG_151	NH2	A_GLU_154	OE2	3.160
1CG9	A_ARG_169	NH2	A_GLU_166	OE1	3.233
1CG9	A_ARG_170	NH2	A_GLU_166	OE2	3.714
1CG9	A_HIS_191	NE2	A_GLU_254	OE1	3.499
1CG9	A_HIS_191	NE2	A_GLU_254	OE2	3.158
1CG9	A_HIS_192	ND1	B_ASP_99	OD2	3.812
1CG9	A_ARG_256	NH1	A_ASP_220	OD2	2.755
1CG9	A_ARG_256	NH2	A_GLU_253	OE1	2.835
1CG9	B_LYS_7	NZ	A_GLU_232	OE1	3.887
1CG9	B_ARG_46	NH1	B_GLU_48	OE2	3.451
1CG9	B_ARG_82	NH2	B_ASP_39	OD2	3.296
1CLO	L_ARG_61	NH2	L_GLU_81	OE2	3.507
1CLO	L_ARG_61	NH2	L_ASP_82	OD1	2.686
1CLO	L_ARG_61	NH2	L_ASP_82	OD2	3.628
1CLO	L_LYS_107	NZ	L_GLU_17	OE2	3.193
1CLO	L_LYS_147	NZ	L_GLU_154	OE1	2.893
1CLO	L_LYS_149	NZ	L_GLU_195	OE1	2.730
1CLO	L_LYS_183	NZ	L_GLU_187	OE1	3.637
1CLO	L_ARG_188	NH2	L_ASP_184	OD2	3.790
1CLO	L_HIS_189	ND1	L_ASP_151	OD2	3.698
1CLO	L_HIS_189	NE2	L_GLU_185	OE1	3.878
1CLO	L_HIS_189	NE2	L_GLU_185	OE2	3.586
1CLO	L_LYS_199	NZ	L_ASP_110	OD1	3.988
1CLO	H_ARG_38	NH1	H_ASP_86	OD1	2.756
1CLO	H_ARG_38	NH2	H_GLU_46	OE1	3.383
1CLO	H_ARG_38	NH2	H_GLU_46	OE2	3.812
1CLO	H_ARG_38	NH2	H_ASP_86	OD1	3.644
1CLO	H_ARG_66	NH1	H_ASP_86	OD1	3.875
1CLO	H_ARG_66	NH1	H_ASP_86	OD2	3.046
1CLO	H_ARG_66	NH2	H_ASP_86	OD1	2.884
1CLO	H_ARG_66	NH2	H_ASP_86	OD2	3.391
1CLO	H_ARG_94	NH2	H_ASP_101	OD1	3.855
1CLO	H_ARG_94	NH2	H_ASP_101	OD2	2.771
1CLO	H_ARG_99	NH2	H_GLU_58	OE1	2.867
1CLO	H_ARG_99	NH2	H_GLU_58	OE2	3.927
1CLY	L_ARG_24	NH2	L_ASP_70	OD1	3.806
1CLY	L_ARG_24	NH2	L_ASP_70	OD2	2.805
1CLY	L_ARG_54	NH2	L_ASP_60	OD1	3.787
1CLY	L_ARG_61	NH1	L_ASP_82	OD1	2.802

1CLY	L_ARG.61	NH1	L_ASP.82	OD2	3.085
1CLY	L_LYS.188	NZ	L_ASP.185	OD1	3.969
1CLY	L_HIS.189	ND1	L_ASP.151	OD2	3.439
1CLY	H_ARG.38	NH1	H_ASP.86	OD1	2.869
1CLY	H_ARG.38	NH2	H_GLU.46	OE1	3.344
1CLY	H_ARG.38	NH2	H_ASP.86	OD1	3.797
1CLY	H_LYS.64	NZ	H_ASP.58	OD1	2.930
1CLY	H_ARG.66	NH1	H_ASP.86	OD1	3.905
1CLY	H_ARG.66	NH1	H_ASP.86	OD2	2.752
1CLY	H_ARG.66	NH2	H_ASP.86	OD1	2.793
1CLY	H_ARG.66	NH2	H_ASP.86	OD2	3.024
1CLY	H_LYS.83	NZ	H_GLU.85	OE2	3.267
1CLZ	L_ARG.24	NH1	L_ASP.70	OD1	3.101
1CLZ	L_ARG.24	NH1	L_ASP.70	OD2	3.153
1CLZ	L_ARG.54	NH2	L_ASP.60	OD2	3.723
1CLZ	L_ARG.61	NH1	L_GLU.81	OE2	2.935
1CLZ	L_ARG.61	NH1	L_ASP.82	OD1	2.614
1CLZ	L_ARG.61	NH1	L_ASP.82	OD2	2.847
1CLZ	L_ARG.61	NH2	L_GLU.81	OE2	2.838
1CLZ	L_ARG.155	NH1	L_GLU.195	OE1	3.513
1CLZ	L_ARG.155	NH1	L_GLU.195	OE2	2.873
1CLZ	L_ARG.155	NH2	L_GLU.195	OE2	3.852
1CLZ	L_LYS.183	NZ	L_ASP.184	OD1	3.131
1CLZ	L_LYS.183	NZ	L_ASP.184	OD2	3.972
1CLZ	L_LYS.199	NZ	L_ASP.110	OD1	3.811
1CLZ	L_LYS.207	NZ	H_ASP.130	OD1	3.119
1CLZ	L_LYS.207	NZ	H_ASP.130	OD2	3.445
1CLZ	H_ARG.38	NH1	H_GLU.85	OE2	3.982
1CLZ	H_ARG.38	NH1	H_ASP.86	OD1	2.887
1CLZ	H_ARG.38	NH2	H_GLU.46	OE1	2.799
1CLZ	H_ARG.38	NH2	H_GLU.46	OE2	3.386
1CLZ	H_ARG.38	NH2	H_GLU.85	OE2	3.329
1CLZ	H_LYS.64	NZ	H_ASP.61	OD1	3.149
1CLZ	H_ARG.66	NH1	H_ASP.86	OD2	2.828
1CLZ	H_ARG.66	NH2	H_ASP.86	OD1	3.003
1CLZ	H_ARG.66	NH2	H_ASP.86	OD2	2.860
1CLZ	H_LYS.75	NZ	H_ASP.72	OD1	3.567
1CLZ	H_LYS.75	NZ	H_ASP.72	OD2	3.842
1CLZ	H_ARG.172	NH1	L_ASP.170	OD2	3.885
1CLZ	H_ARG.172	NH2	L_ASP.170	OD2	3.384
1CLZ	H_LYS.221	NZ	L_GLU.123	OE1	3.750
1CLZ	H_LYS.221	NZ	L_GLU.123	OE2	2.509
1CS9-1	A_ARG.5	NH1	A_GLU.7	OE1	3.450
1CS9-1	A_ARG.5	NH2	A_GLU.7	OE1	3.678
1CS9-3	A_ARG.5	NH1	A_GLU.7	OE2	3.468
1CS9-3	A_ARG.5	NH2	A_GLU.7	OE1	3.563
1CS9-3	A_ARG.5	NH2	A_GLU.7	OE2	3.412
1CS9-6	A_ARG.5	NH2	A_GLU.7	OE1	3.965
1CS9-6	A_ARG.5	NH2	A_GLU.7	OE2	3.461
1CT6-1	A_ARG.5	NH2	A_GLU.7	OE2	3.406
1CT6-7	A_ARG.5	NH1	A_GLU.7	OE1	3.406
1CT6-7	A_ARG.5	NH2	A_GLU.7	OE1	3.280
1CZ8	V_ARG.23	NH1	W_GLU.30	OE1	3.162
1CZ8	V_ARG.23	NH1	W_GLU.30	OE2	3.558
1CZ8	V_ARG.56	NH1	V_GLU.38	OE1	2.977
1CZ8	V_ARG.56	NH1	V_GLU.38	OE2	3.581
1CZ8	V_ARG.56	NH2	V_GLU.38	OE1	3.435
1CZ8	V_ARG.82	NH1	V_GLU.42	OE1	3.541

1CZ8	V_ARG.82	NH1	V_GLU.42	OE2	3.530
1CZ8	V_ARG.82	NH2	V_GLU.42	OE1	2.378
1CZ8	V_ARG.82	NH2	V_GLU.42	OE2	3.778
1CZ8	V_LYS.84	NZ	V_GLU.44	OE1	3.578
1CZ8	V_HIS.99	NE2	V_GLU.73	OE2	3.799
1CZ8	W_ARG.23	NH1	V_GLU.30	OE1	3.011
1CZ8	W_ARG.23	NH1	V_GLU.30	OE2	3.663
1CZ8	W_ARG.56	NH1	W_GLU.38	OE1	3.539
1CZ8	W_ARG.56	NH2	W_GLU.38	OE1	2.665
1CZ8	W_ARG.82	NH1	W_GLU.42	OE1	3.515
1CZ8	W_ARG.82	NH1	W_GLU.42	OE2	3.352
1CZ8	W_ARG.82	NH2	W_GLU.42	OE1	2.236
1CZ8	W_ARG.82	NH2	W_GLU.42	OE2	3.471
1CZ8	W_LYS.84	NZ	W_GLU.44	OE1	3.728
1CZ8	W_HIS.99	NE2	W_GLU.73	OE2	3.726
1CZ8	W_ARG.105	NH1	W_GLU.103	OE1	3.814
1CZ8	W_ARG.105	NH2	W_GLU.103	OE1	3.500
1CZ8	L_ARG.61	NH2	L_GLU.81	OE1	3.328
1CZ8	L_ARG.61	NH2	L_ASP.82	OD1	3.668
1CZ8	L_ARG.61	NH2	L_ASP.82	OD2	2.923
1CZ8	L_LYS.103	NZ	L_GLU.165	OE1	3.942
1CZ8	L_LYS.103	NZ	L_GLU.165	OE2	3.656
1CZ8	L_ARG.142	NH1	L_GLU.105	OE1	3.981
1CZ8	L_ARG.142	NH2	L_GLU.105	OE1	2.514
1CZ8	L_LYS.188	NZ	L_ASP.185	OD1	3.914
1CZ8	H_HIS.31	NE2	H_ASP.28	OD1	3.613
1CZ8	H_HIS.31	NE2	H_ASP.28	OD2	3.218
1CZ8	H_ARG.38	NH1	H_ASP.90	OD1	2.960
1CZ8	H_ARG.38	NH2	H_GLU.46	OE2	3.234
1CZ8	H_ARG.67	NH1	H_ASP.90	OD1	3.710
1CZ8	H_ARG.67	NH1	H_ASP.90	OD2	2.499
1CZ8	H_ARG.67	NH2	H_ASP.90	OD1	2.930
1CZ8	H_ARG.67	NH2	H_ASP.90	OD2	3.145
1CZ8	H_ARG.87	NH1	H_GLU.89	OE2	3.671
1CZ8	H_LYS.98	NZ	H_ASP.111	OD1	3.604
1CZ8	H_LYS.153	NZ	H_ASP.154	OD1	3.169
1CZ8	H_LYS.153	NZ	H_ASP.154	OD2	3.317
1CZ8	H_LYS.219	NZ	L_GLU.123	OE1	3.027
1CZ8	H_LYS.224	NZ	L_ASP.122	OD1	2.846
1CZ8	H_LYS.224	NZ	L_ASP.122	OD2	3.185
1CZ8	X_ARG.61	NH2	X_GLU.81	OE1	2.956
1CZ8	X_ARG.61	NH2	X_ASP.82	OD1	3.979
1CZ8	X_ARG.61	NH2	X_ASP.82	OD2	3.064
1CZ8	X_LYS.103	NZ	X_GLU.165	OE1	3.796
1CZ8	X_LYS.103	NZ	X_GLU.165	OE2	3.476
1CZ8	X_LYS.183	NZ	X_GLU.187	OE1	3.233
1CZ8	X_HIS.189	ND1	X_ASP.151	OD2	2.531
1CZ8	X_ARG.211	NH1	X_GLU.187	OE2	3.961
1CZ8	X_ARG.211	NH2	X_GLU.187	OE2	3.336
1CZ8	Y_HIS.31	NE2	Y_ASP.28	OD2	2.704
1CZ8	Y_ARG.38	NH1	Y_ASP.90	OD1	2.984
1CZ8	Y_ARG.38	NH2	Y_GLU.46	OE2	3.050
1CZ8	Y_ARG.67	NH1	Y_ASP.90	OD1	3.758
1CZ8	Y_ARG.67	NH1	Y_ASP.90	OD2	2.753
1CZ8	Y_ARG.67	NH2	Y_ASP.90	OD1	3.089
1CZ8	Y_ARG.67	NH2	Y_ASP.90	OD2	3.481
1CZ8	Y_ARG.87	NH1	Y_GLU.89	OE2	3.919
1CZ8	Y_LYS.98	NZ	Y_ASP.111	OD1	3.728

1CZ8	Y_LYS_153	NZ	Y_ASP_154	OD1	3.924
1CZ8	Y_LYS_219	NZ	X_GLU_123	OE2	3.832
1DBJ	L_ARG_61	NH1	L_ASP_82	OD1	2.891
1DBJ	L_ARG_61	NH1	L_ASP_82	OD2	2.924
1DBJ	L_LYS_149	NZ	L_GLU_195	OE2	2.903
1DBJ	L_ARG_155	NH2	L_GLU_185	OE1	3.640
1DBJ	L_LYS_183	NZ	L_GLU_187	OE1	3.039
1DBJ	L_LYS_183	NZ	L_GLU_187	OE2	3.038
1DBJ	L_ARG_188	NH1	L_GLU_185	OE1	2.980
1DBJ	L_ARG_188	NH1	L_GLU_185	OE2	3.840
1DBJ	L_HIS_189	ND1	L_ASP_151	OD1	3.098
1DBJ	L_HIS_189	ND1	L_ASP_151	OD2	3.952
1DBJ	L_HIS_189	NE2	L_GLU_185	OE2	3.171
1DBJ	H_LYS_13	NZ	H_GLU_16	OE1	3.105
1DBJ	H_LYS_46	NZ	H_ASP_62	OD2	3.771
1DBJ	H_ARG_66	NH1	H_ASP_86	OD2	2.961
1DBJ	H_ARG_66	NH2	H_ASP_86	OD1	3.477
1DBJ	H_ARG_66	NH2	H_ASP_86	OD2	3.338
1DBJ	H_LYS_83	NZ	H_GLU_85	OE1	3.571
1DBJ	H_LYS_83	NZ	H_GLU_85	OE2	3.324
1DBJ	H_ARG_94	NH2	H_ASP_101	OD1	3.264
1DBJ	H_ARG_94	NH2	H_ASP_101	OD2	2.951
1DBJ	H_LYS_221	NZ	L_GLU_123	OE1	3.386
1DBJ	H_LYS_221	NZ	L_GLU_123	OE2	2.770
1DBK	L_LYS_39	NZ	L_GLU_81	OE2	2.712
1DBK	L_ARG_61	NH1	L_ASP_82	OD1	2.915
1DBK	L_ARG_61	NH1	L_ASP_82	OD2	2.731
1DBK	L_ARG_61	NH2	L_GLU_79	OE1	3.019
1DBK	L_ARG_61	NH2	L_ASP_82	OD1	2.792
1DBK	L_ARG_61	NH2	L_ASP_82	OD2	3.954
1DBK	L_LYS_149	NZ	L_GLU_195	OE1	3.811
1DBK	L_LYS_149	NZ	L_GLU_195	OE2	3.034
1DBK	L_ARG_155	NH2	L_GLU_185	OE2	2.794
1DBK	L_LYS_169	NZ	L_ASP_167	OD1	2.955
1DBK	L_LYS_169	NZ	L_ASP_167	OD2	3.539
1DBK	L_HIS_189	ND1	L_ASP_151	OD1	3.187
1DBK	L_HIS_189	NE2	L_GLU_185	OE1	3.126
1DBK	L_HIS_189	NE2	L_GLU_185	OE2	3.082
1DBK	H_LYS_12	NZ	H_GLU_16	OE2	3.384
1DBK	H_LYS_46	NZ	H_ASP_62	OD2	3.857
1DBK	H_ARG_66	NH1	H_ASP_86	OD1	3.550
1DBK	H_ARG_66	NH2	H_ASP_86	OD1	3.122
1DBK	H_ARG_66	NH2	H_ASP_86	OD2	2.683
1DBK	H_ARG_94	NH2	H_ASP_101	OD2	3.605
1DBK	H_HIS_172	ND1	L_ASP_167	OD2	3.619
1DBK	H_LYS_221	NZ	L_GLU_123	OE2	3.030
1DBM	L_ARG_61	NH1	L_ASP_82	OD1	2.913
1DBM	L_ARG_61	NH1	L_ASP_82	OD2	3.927
1DBM	L_LYS_103	NZ	L_GLU_105	OE1	2.993
1DBM	L_LYS_142	NZ	L_GLU_105	OE1	2.864
1DBM	L_LYS_147	NZ	L_GLU_154	OE2	3.864
1DBM	L_LYS_149	NZ	L_GLU_195	OE1	3.140
1DBM	L_LYS_149	NZ	L_GLU_195	OE2	3.919
1DBM	L_ARG_155	NH2	L_GLU_185	OE2	2.959
1DBM	L_LYS_183	NZ	L_GLU_187	OE1	3.017
1DBM	L_LYS_183	NZ	L_GLU_187	OE2	2.825
1DBM	L_HIS_189	ND1	L_ASP_151	OD1	3.307
1DBM	L_HIS_189	ND1	L_ASP_151	OD2	3.881

1DBM	L_HIS_189	NE2	L_ASP_151	OD1	3.334
1DBM	L_HIS_189	NE2	L_ASP_151	OD2	2.747
1DBM	L_LYS_199	NZ	L_ASP_110	OD1	3.963
1DBM	L_LYS_199	NZ	L_ASP_110	OD2	3.388
1DBM	H_LYS_12	NZ	H_GLU_16	OE1	3.842
1DBM	H_LYS_46	NZ	H_ASP_62	OD1	3.760
1DBM	H_LYS_46	NZ	H_ASP_62	OD2	2.943
1DBM	H_ARG_66	NH2	H_ASP_86	OD1	2.873
1DBM	H_ARG_66	NH2	H_ASP_86	OD2	2.647
1DBM	H_ARG_94	NH1	H_ASP_101	OD1	3.264
1DBM	H_ARG_94	NH1	H_ASP_101	OD2	2.957
1DBM	H_LYS_218	NZ	H_ASP_220	OD1	2.773
1DBM	H_LYS_218	NZ	H_ASP_220	OD2	3.444
1DBM	H_LYS_221	NZ	L_GLU_123	OE2	3.277
1DEE	A_ARG_24	NH1	D_GLU_1555	OE1	3.510
1DEE	A_ARG_24	NH2	A_ASP_70	OD2	3.825
1DEE	A_ARG_61	NH1	A_GLU_81	OE2	3.998
1DEE	A_ARG_61	NH2	A_GLU_81	OE2	3.015
1DEE	A_ARG_61	NH2	A_ASP_82	OD1	2.929
1DEE	A_ARG_61	NH2	A_ASP_82	OD2	3.738
1DEE	A_ARG_142	NH1	A_GLU_105	OE2	3.645
1DEE	A_ARG_142	NH2	A_GLU_105	OE2	3.806
1DEE	A_LYS_149	NZ	A_GLU_195	OE1	3.119
1DEE	A_LYS_183	NZ	A_GLU_187	OE1	3.333
1DEE	A_LYS_183	NZ	A_GLU_187	OE2	3.384
1DEE	A_HIS_189	ND1	A_ASP_151	OD2	3.212
1DEE	B_ARG_538	NH1	B_ASP_590	OD1	2.876
1DEE	B_ARG_538	NH2	B_GLU_546	OE1	3.449
1DEE	B_ARG_538	NH2	B_ASP_590	OD1	3.533
1DEE	B_ARG_567	NH1	B_ASP_590	OD1	3.757
1DEE	B_ARG_567	NH1	B_ASP_590	OD2	2.653
1DEE	B_ARG_567	NH2	B_ASP_590	OD1	2.770
1DEE	B_ARG_567	NH2	B_ASP_590	OD2	3.245
1DEE	B_ARG_587	NH2	B_GLU_589	OE2	3.287
1DEE	B_ARG_587	NH2	B_ASP_590	OD1	3.980
1DEE	B_LYS_598	NZ	B_ASP_609	OD1	3.328
1DEE	B_LYS_598	NZ	B_ASP_609	OD2	2.849
1DEE	B_LYS_663	NZ	B_ASP_669	OD1	2.882
1DEE	B_LYS_663	NZ	B_ASP_669	OD2	3.035
1DEE	B_LYS_665	NZ	B_GLU_704	OE1	2.806
1DEE	B_LYS_665	NZ	B_GLU_704	OE2	3.764
1DEE	B_ARG_674	NH1	A_ASP_167	OD2	3.579
1DEE	B_LYS_684	NZ	B_ASP_652	OD2	3.529
1DEE	B_HIS_705	NE2	B_ASP_720	OD2	3.635
1DEE	B_LYS_719	NZ	A_GLU_123	OE1	2.730
1DEE	B_LYS_719	NZ	A_GLU_123	OE2	3.113
1DEE	C_ARG_1024	NH1	C_ASP_1070	OD1	3.035
1DEE	C_ARG_1024	NH1	C_ASP_1070	OD2	3.310
1DEE	C_ARG_1061	NH2	C_GLU_1081	OE2	3.124
1DEE	C_ARG_1061	NH2	C_ASP_1082	OD1	2.857
1DEE	C_ARG_1061	NH2	C_ASP_1082	OD2	3.774
1DEE	C_LYS_1103	NZ	C_GLU_1165	OE1	3.566
1DEE	C_LYS_1103	NZ	C_GLU_1165	OE2	2.924
1DEE	C_LYS_1107	NZ	C_ASP_1017	OD2	3.997
1DEE	C_LYS_1149	NZ	C_GLU_1195	OE1	3.072
1DEE	C_LYS_1183	NZ	C_GLU_1187	OE2	3.540
1DEE	C_LYS_1188	NZ	C_ASP_1185	OD2	3.897
1DEE	C_HIS_1189	ND1	C_ASP_1151	OD2	2.785

1DEE	D_ARG_1519	NH1	G_ASP_1834	OD1	3.122
1DEE	D_ARG_1519	NH1	G_ASP_1834	OD2	3.064
1DEE	D_ARG_1519	NH2	G_ASP_1834	OD1	3.684
1DEE	D_ARG_1519	NH2	G_ASP_1834	OD2	2.875
1DEE	D_ARG_1538	NH1	D_ASP_1590	OD1	2.724
1DEE	D_ARG_1538	NH2	D_GLU_1546	OE1	3.584
1DEE	D_ARG_1538	NH2	D_GLU_1546	OE2	3.849
1DEE	D_ARG_1538	NH2	D_ASP_1590	OD1	3.421
1DEE	D_LYS_1565	NZ	D_ASP_1562	OD1	2.918
1DEE	D_ARG_1567	NH1	D_ASP_1590	OD1	3.432
1DEE	D_ARG_1567	NH2	D_ASP_1590	OD1	2.922
1DEE	D_ARG_1567	NH2	D_ASP_1590	OD2	2.448
1DEE	D_LYS_1576	NZ	D_ASP_1573	OD2	3.953
1DEE	D_ARG_1587	NH1	D_GLU_1589	OE2	3.755
1DEE	D_ARG_1587	NH2	D_GLU_1589	OE2	2.965
1DEE	D_LYS_1598	NZ	D_ASP_1609	OD1	3.236
1DEE	D_LYS_1598	NZ	D_ASP_1609	OD2	3.057
1DEE	D_LYS_1663	NZ	D_ASP_1669	OD1	3.393
1DEE	D_LYS_1663	NZ	D_ASP_1669	OD2	3.077
1DEE	D_LYS_1665	NZ	D_GLU_1704	OE1	2.915
1DEE	D_ARG_1674	NH1	C_ASP_1167	OD2	3.619
1DEE	D_HIS_1705	NE2	D_ASP_1720	OD2	3.228
1DEE	D_LYS_1719	NZ	C_GLU_1123	OE1	3.687
1DEE	D_LYS_1719	NZ	C_GLU_1123	OE2	2.890
1DEE	E_ARG_2024	NH1	E_ASP_2070	OD1	3.455
1DEE	E_ARG_2024	NH1	E_ASP_2070	OD2	3.446
1DEE	E_ARG_2024	NH2	E_ASP_2070	OD2	3.331
1DEE	E_ARG_2061	NH2	E_GLU_2081	OE2	3.103
1DEE	E_ARG_2061	NH2	E_ASP_2082	OD1	3.070
1DEE	E_ARG_2061	NH2	E_ASP_2082	OD2	3.805
1DEE	E_ARG_2142	NH1	E_GLU_2165	OE2	3.927
1DEE	E_LYS_2149	NZ	E_GLU_2195	OE1	2.878
1DEE	E_LYS_2149	NZ	E_GLU_2195	OE2	3.165
1DEE	E_LYS_2183	NZ	E_GLU_2187	OE1	2.894
1DEE	E_LYS_2183	NZ	E_GLU_2187	OE2	3.210
1DEE	E_HIS_2189	ND1	E_ASP_2151	OD2	3.099
1DEE	F_ARG_2519	NH1	H_ASP_2834	OD1	3.463
1DEE	F_ARG_2519	NH1	H_ASP_2834	OD2	2.731
1DEE	F_ARG_2519	NH2	H_ASP_2834	OD1	3.523
1DEE	F_ARG_2519	NH2	H_ASP_2834	OD2	3.444
1DEE	F_ARG_2538	NH1	F_ASP_2590	OD1	2.942
1DEE	F_ARG_2538	NH2	F_GLU_2546	OE1	3.386
1DEE	F_ARG_2538	NH2	F_GLU_2546	OE2	3.004
1DEE	F_LYS_2565	NZ	F_ASP_2562	OD1	3.402
1DEE	F_ARG_2567	NH1	F_ASP_2590	OD1	3.677
1DEE	F_ARG_2567	NH2	F_ASP_2590	OD1	2.797
1DEE	F_ARG_2567	NH2	F_ASP_2590	OD2	2.401
1DEE	F_ARG_2587	NH2	F_GLU_2589	OE2	3.479
1DEE	F_LYS_2598	NZ	F_ASP_2609	OD1	3.297
1DEE	F_LYS_2598	NZ	F_ASP_2609	OD2	2.926
1DEE	F_LYS_2663	NZ	F_ASP_2669	OD1	3.683
1DEE	F_LYS_2663	NZ	F_ASP_2669	OD2	2.643
1DEE	F_LYS_2665	NZ	F_GLU_2704	OE1	3.853
1DEE	F_LYS_2665	NZ	F_GLU_2704	OE2	3.766
1DEE	F_ARG_2674	NH1	E_ASP_2167	OD2	3.989
1DEE	F_HIS_2705	ND1	F_ASP_2720	OD2	3.943
1DEE	F_HIS_2705	NE2	F_ASP_2720	OD2	2.896
1DEE	F_LYS_2719	NZ	E_GLU_2123	OE1	2.882

1DEE	F_LYS_2719	NZ	E_GLU_2123	OE2	3.779
1DEE	G_LYS_1848	NZ	G_GLU_1845	OE1	3.421
1DEE	G_LYS_1848	NZ	G_GLU_1845	OE2	3.954
1DEE	H_ARG_2825	NH1	H_GLU_2822	OE2	2.870
1DLF	L_ARG_61	NH1	L_GLU_79	OE2	3.180
1DLF	L_ARG_61	NH1	L_GLU_81	OE2	3.784
1DLF	L_ARG_61	NH2	L_GLU_79	OE1	3.855
1DLF	L_ARG_61	NH2	L_GLU_79	OE2	3.835
1DLF	L_ARG_61	NH2	L_GLU_81	OE2	2.913
1DLF	L_ARG_61	NH2	L_ASP_82	OD1	2.721
1DLF	L_ARG_61	NH2	L_ASP_82	OD2	3.431
1DLF	L_LYS_103	NZ	L_GLU_105	OE1	3.806
1DLF	H_ARG_38	NH1	H_GLU_85	OE2	3.709
1DLF	H_ARG_38	NH1	H_ASP_86	OD1	2.859
1DLF	H_ARG_38	NH2	H_GLU_46	OE2	3.187
1DLF	H_ARG_38	NH2	H_GLU_85	OE2	2.874
1DLF	H_ARG_38	NH2	H_ASP_86	OD1	3.920
1DLF	H_HIS_55	NE2	H_ASP_73	OD2	3.282
1DLF	H_ARG_66	NH1	H_ASP_86	OD1	3.873
1DLF	H_ARG_66	NH1	H_ASP_86	OD2	2.756
1DLF	H_ARG_66	NH2	H_GLU_85	OE2	3.284
1DLF	H_ARG_66	NH2	H_ASP_86	OD1	3.045
1DLF	H_ARG_66	NH2	H_ASP_86	OD2	3.370
1DLF	H_ARG_71	NH2	H_ASP_73	OD1	3.603
1DQD	L_ARG_60	NH2	L_GLU_80	OE1	2.987
1DQD	L_ARG_60	NH2	L_ASP_81	OD1	3.630
1DQD	L_ARG_60	NH2	L_ASP_81	OD2	2.547
1DQD	L_LYS_146	NZ	L_GLU_153	OE2	3.290
1DQD	L_LYS_148	NZ	L_GLU_194	OE1	2.964
1DQD	L_LYS_148	NZ	L_GLU_194	OE2	3.564
1DQD	L_ARG_154	NH2	L_GLU_184	OE1	2.744
1DQD	L_ARG_154	NH2	L_GLU_184	OE2	3.605
1DQD	L_ARG_187	NH1	L_ASP_183	OD1	2.725
1DQD	L_ARG_187	NH2	L_ASP_183	OD1	3.759
1DQD	L_HIS_188	ND1	L_ASP_150	OD2	2.488
1DQD	L_ARG_210	NH2	L_GLU_186	OE1	3.748
1DQD	H_ARG_38	NH1	H_GLU_46	OE2	2.968
1DQD	H_ARG_38	NH1	H_ASP_89	OD2	3.490
1DQD	H_ARG_38	NH2	H_ASP_89	OD2	2.519
1DQD	H_ARG_66	NH1	H_ASP_89	OD1	3.667
1DQD	H_ARG_66	NH1	H_ASP_89	OD2	3.034
1DQD	H_ARG_66	NH2	H_ASP_89	OD1	3.179
1DQD	H_ARG_66	NH2	H_ASP_89	OD2	3.557
1DQD	H_ARG_75	NH1	H_ASP_72	OD2	3.952
1DQD	H_LYS_217	NZ	L_GLU_122	OE2	3.953
1DQJ	A_ARG_24	NH2	A_ASP_70	OD1	3.733
1DQJ	A_ARG_61	NH2	A_GLU_81	OE1	3.324
1DQJ	A_ARG_61	NH2	A_ASP_82	OD1	2.881
1DQJ	A_ARG_61	NH2	A_ASP_82	OD2	3.607
1DQJ	A_ARG_155	NH1	A_GLU_185	OE2	3.740
1DQJ	A_ARG_155	NH2	A_GLU_185	OE2	3.256
1DQJ	A_LYS_199	NZ	A_ASP_110	OD2	3.573
1DQJ	B_ARG_38	NH1	B_GLU_46	OE1	2.669
1DQJ	B_ARG_38	NH1	B_ASP_89	OD1	3.653
1DQJ	B_ARG_38	NH2	B_ASP_89	OD1	2.527
1DQJ	B_ARG_66	NH1	B_ASP_89	OD1	3.044
1DQJ	B_ARG_66	NH1	B_ASP_89	OD2	3.584
1DQJ	B_ARG_66	NH2	B_ASP_89	OD1	3.713

1DQJ	B_ARG_66	NH2	B_ASP_89	OD2	2.977
1DQJ	B_LYS_216	NZ	B_ASP_218	OD2	3.941
1DQJ	B_LYS_219	NZ	A_GLU_123	OE2	2.598
1DQJ	C_LYS_1	NZ	C_GLU_7	OE1	3.940
1DQJ	C_LYS_1	NZ	C_GLU_7	OE2	2.753
1DQJ	C_LYS_97	NZ	B_ASP_32	OD2	2.665
1DQJ	C_ARG_125	NH2	C_ASP_119	OD1	3.333
1DQJ	C_ARG_125	NH2	C_ASP_119	OD2	2.489
1DQM	L_ARG_61	NH1	L_GLU_81	OE2	3.595
1DQM	L_ARG_61	NH1	L_ASP_82	OD1	2.747
1DQM	L_ARG_61	NH1	L_ASP_82	OD2	3.200
1DQM	L_ARG_61	NH2	L_GLU_81	OE2	3.902
1DQM	L_LYS_147	NZ	L_GLU_154	OE1	3.964
1DQM	L_LYS_147	NZ	L_GLU_195	OE2	3.903
1DQM	L_LYS_149	NZ	L_GLU_195	OE1	3.696
1DQM	L_ARG_155	NH1	L_GLU_185	OE2	3.981
1DQM	L_ARG_188	NH2	L_ASP_184	OD1	3.190
1DQM	L_HIS_189	ND1	L_ASP_151	OD2	3.171
1DQM	L_LYS_199	NZ	L_ASP_110	OD2	3.862
1DQM	L_LYS_207	NZ	H_ASP_130	OD1	3.491
1DQM	L_LYS_207	NZ	H_ASP_130	OD2	3.782
1DQM	H_ARG_38	NH1	H_GLU_46	OE1	2.699
1DQM	H_ARG_38	NH1	H_ASP_89	OD1	3.926
1DQM	H_ARG_38	NH2	H_ASP_89	OD1	2.730
1DQM	H_ARG_66	NH1	H_ASP_89	OD1	3.559
1DQM	H_ARG_66	NH1	H_ASP_89	OD2	2.987
1DQM	H_ARG_66	NH2	H_ASP_89	OD1	3.082
1DQM	H_ARG_66	NH2	H_ASP_89	OD2	3.726
1DQQ	A_ARG_24	NH1	A_ASP_70	OD2	3.225
1DQQ	A_LYS_49	NZ	B_ASP_101	OD1	2.957
1DQQ	A_ARG_61	NH1	A_ASP_82	OD1	2.631
1DQQ	A_ARG_61	NH1	A_ASP_82	OD2	2.802
1DQQ	A_ARG_61	NH2	A_GLU_79	OE1	3.923
1DQQ	A_ARG_61	NH2	A_GLU_79	OE2	3.136
1DQQ	A_ARG_61	NH2	A_GLU_81	OE2	3.324
1DQQ	A_ARG_61	NH2	A_ASP_82	OD1	3.627
1DQQ	A_LYS_147	NZ	A_GLU_154	OE1	3.318
1DQQ	A_LYS_147	NZ	A_GLU_154	OE2	3.055
1DQQ	A_LYS_149	NZ	A_GLU_195	OE1	3.522
1DQQ	A_LYS_149	NZ	A_GLU_195	OE2	3.885
1DQQ	A_ARG_155	NH1	A_GLU_185	OE2	3.911
1DQQ	A_ARG_155	NH2	A_GLU_185	OE2	3.794
1DQQ	A_ARG_188	NH2	A_ASP_184	OD1	2.977
1DQQ	A_LYS_199	NZ	A_ASP_110	OD1	3.108
1DQQ	A_LYS_199	NZ	A_ASP_110	OD2	3.095
1DQQ	B_ARG_38	NH1	B_GLU_46	OE1	2.694
1DQQ	B_ARG_38	NH1	B_ASP_89	OD1	3.867
1DQQ	B_ARG_38	NH2	B_ASP_89	OD1	2.625
1DQQ	B_ARG_66	NH1	B_ASP_89	OD1	3.469
1DQQ	B_ARG_66	NH1	B_ASP_89	OD2	2.954
1DQQ	B_ARG_66	NH2	B_ASP_89	OD1	2.959
1DQQ	B_ARG_66	NH2	B_ASP_89	OD2	3.690
1DQQ	B_LYS_216	NZ	D_ASP_218	OD1	2.965
1DQQ	B_LYS_219	NZ	A_GLU_123	OE2	2.763
1DQQ	C_LYS_49	NZ	D_ASP_101	OD1	3.456
1DQQ	C_LYS_49	NZ	D_ASP_101	OD2	3.943
1DQQ	C_LYS_147	NZ	C_GLU_154	OE2	3.726
1DQQ	C_LYS_149	NZ	C_GLU_195	OE1	3.353

1DQQ	C_ARG_155	NH2	C_GLU_185	OE2	3.704
1DQQ	C_ARG_188	NH2	C_ASP_184	OD1	2.882
1DQQ	C_ARG_188	NH2	C_ASP_184	OD2	3.940
1DQQ	C_HIS_189	ND1	C_ASP_151	OD2	2.642
1DQQ	C_LYS_199	NZ	C_ASP_110	OD2	3.094
1DQQ	C_ARG_211	NH2	C_GLU_187	OE2	2.769
1DQQ	D_ARG_38	NH1	D_GLU_46	OE1	2.831
1DQQ	D_ARG_38	NH1	D_ASP_89	OD1	3.780
1DQQ	D_ARG_38	NH2	D_ASP_89	OD1	2.692
1DQQ	D_ARG_66	NH1	D_ASP_89	OD1	3.708
1DQQ	D_ARG_66	NH2	D_ASP_89	OD1	3.416
1DQQ	D_ARG_66	NH2	D_ASP_89	OD2	2.649
1DQQ	D_LYS_216	NZ	D_ASP_218	OD1	2.953
1DQQ	D_LYS_216	NZ	D_ASP_218	OD2	2.618
1DQQ	D_LYS_219	NZ	C_GLU_123	OE1	3.088
1DVF	A_ARG_61	NH2	A_GLU_81	OE2	3.091
1DVF	A_ARG_61	NH2	A_ASP_82	OD1	2.772
1DVF	A_ARG_61	NH2	A_ASP_82	OD2	3.277
1DVF	A_ARG_96	NH1	B_GLU_98	OE1	2.616
1DVF	A_ARG_96	NH1	B_GLU_98	OE2	3.746
1DVF	A_ARG_96	NH2	B_GLU_98	OE1	3.400
1DVF	A_ARG_96	NH2	B_GLU_98	OE2	2.958
1DVF	A_LYS_103	NZ	A_GLU_105	OE2	3.937
1DVF	B_ARG_38	NH1	B_ASP_89	OD1	2.871
1DVF	B_ARG_38	NH2	B_GLU_46	OE1	3.990
1DVF	B_ARG_38	NH2	B_GLU_46	OE2	3.805
1DVF	B_ARG_38	NH2	B_ASP_89	OD1	3.345
1DVF	B_ARG_66	NH1	B_ASP_89	OD1	3.908
1DVF	B_ARG_66	NH1	B_ASP_89	OD2	3.826
1DVF	B_ARG_66	NH2	B_ASP_89	OD1	3.644
1DVF	B_ARG_66	NH2	B_ASP_89	OD2	2.583
1DVF	B_LYS_75	NZ	B_ASP_72	OD2	2.871
1DVF	B_HIS_86	ND1	B_ASP_88	OD2	3.353
1DVF	B_ARG_97	NH2	B_ASP_104	OD1	3.629
1DVF	B_ARG_97	NH2	B_ASP_104	OD2	2.634
1DVF	B_ARG_102	NH1	B_ASP_100	OD2	2.926
1DVF	C_ARG_61	NH1	C_ASP_82	OD1	3.565
1DVF	C_ARG_61	NH1	C_ASP_82	OD2	2.521
1DVF	C_ARG_61	NH2	C_GLU_79	OE2	3.798
1DVF	C_ARG_61	NH2	C_GLU_81	OE2	3.578
1DVF	C_ARG_61	NH2	C_ASP_82	OD1	2.671
1DVF	C_ARG_61	NH2	C_ASP_82	OD2	3.084
1DVF	C_LYS_103	NZ	C_GLU_105	OE2	3.563
1DVF	D_HIS_33	NE2	B_ASP_100	OD1	3.569
1DVF	D_HIS_33	NE2	B_ASP_100	OD2	3.052
1DVF	D_HIS_33	NE2	D_ASP_52	OD2	3.296
1DVF	D_LYS_62	NZ	D_GLU_46	OE1	3.985
1DVF	D_LYS_66	NZ	D_ASP_86	OD1	3.906
1DVF	D_LYS_66	NZ	D_ASP_86	OD2	2.839
1DZB	A_LYS_38	NZ	A_ASP_90	OD1	3.686
1DZB	A_ARG_40	NH2	A_GLU_46	OE1	3.204
1DZB	A_ARG_40	NH2	A_GLU_46	OE2	2.668
1DZB	A_LYS_63	NZ	B_GLU_89	OE1	3.983
1DZB	A_LYS_67	NZ	B_ASP_90	OD2	3.792
1DZB	A_ARG_234	NH2	A_ASP_104	OD1	2.721
1DZB	A_ARG_234	NH2	A_ASP_104	OD2	3.895
1DZB	A_ARG_261	NH1	A_GLU_279	OE1	3.537
1DZB	B_LYS_38	NZ	B_ASP_90	OD1	3.512

1DZB	B_ARG_40	NH2	B_GLU_46	OE1	3.754
1DZB	B_ARG_40	NH2	B_GLU_46	OE2	3.419
1DZB	B_LYS_63	NZ	B_GLU_46	OE1	3.854
1DZB	B_LYS_67	NZ	B_ASP_90	OD1	3.833
1DZB	B_ARG_234	NH2	B_ASP_104	OD1	2.732
1DZB	B_ARG_234	NH2	B_ASP_104	OD2	3.591
1DZB	B_ARG_261	NH1	B_GLU_279	OE2	3.580
1DZB	X_LYS_1	NZ	X_GLU_7	OE1	3.363
1DZB	X_LYS_1	NZ	X_GLU_7	OE2	3.292
1DZB	X_ARG_61	NH2	A_ASP_256	OD2	3.887
1DZB	X_LYS_73	NZ	A_ASP_256	OD1	3.412
1DZB	X_LYS_73	NZ	A_ASP_256	OD2	3.290
1DZB	X_ARG_112	NH2	A_ASP_31	OD2	3.878
1DZB	X_ARG_125	NH2	X_ASP_119	OD2	3.529
1DZB	Y_LYS_73	NZ	B_ASP_256	OD1	3.559
1E4W	H_HIS_35	ND1	H_GLU_50	OE1	3.798
1E4W	H_HIS_35	NE2	H_GLU_50	OE1	3.250
1E4W	H_ARG_40	NH1	H_GLU_85	OE1	2.990
1E4W	H_ARG_40	NH1	H_GLU_85	OE2	3.128
1E4W	H_ARG_40	NH2	H_GLU_85	OE1	3.469
1E4W	H_LYS_62	NZ	H_GLU_46	OE1	2.859
1E4W	H_LYS_62	NZ	H_GLU_46	OE2	3.777
1E4W	H_LYS_64	NZ	H_GLU_61	OE2	3.986
1E4W	H_LYS_66	NZ	H_ASP_86	OD1	3.553
1E4W	H_LYS_66	NZ	H_ASP_86	OD2	2.752
1E4W	H_LYS_205	NZ	L_GLU_123	OE1	3.384
1E4W	H_LYS_205	NZ	L_GLU_123	OE2	3.066
1E4W	L_ARG_24	NH2	L_ASP_70	OD1	2.921
1E4W	L_ARG_24	NH2	L_ASP_70	OD2	2.509
1E4W	L_ARG_61	NH1	L_GLU_79	OE2	3.003
1E4W	L_ARG_61	NH2	L_GLU_79	OE2	3.488
1E4W	L_ARG_61	NH2	L_GLU_81	OE2	2.874
1E4W	L_ARG_61	NH2	L_ASP_82	OD1	2.888
1E4W	L_ARG_61	NH2	L_ASP_82	OD2	3.583
1E4W	L_LYS_103	NZ	L_ASP_165	OD1	3.413
1E4W	L_LYS_147	NZ	L_GLU_154	OE1	3.975
1E4W	L_LYS_149	NZ	L_GLU_195	OE1	3.539
1E4W	L_LYS_149	NZ	L_GLU_195	OE2	2.744
1E4W	L_ARG_155	NH1	L_GLU_185	OE1	3.875
1E4W	L_ARG_155	NH1	L_GLU_185	OE2	2.836
1E4W	L_ARG_155	NH2	L_GLU_185	OE1	3.575
1E4W	L_ARG_155	NH2	L_GLU_185	OE2	3.879
1E4W	L_LYS_183	NZ	L_GLU_187	OE2	2.427
1E4W	P_HIS_2	ND1	P_GLU_5	OE1	3.603
1E4W	P_HIS_2	ND1	P_GLU_5	OE2	2.765
1E4X	H_HIS_35	ND1	H_GLU_50	OE1	3.676
1E4X	H_HIS_35	NE2	H_GLU_50	OE1	3.169
1E4X	H_ARG_40	NH1	H_GLU_85	OE1	3.357
1E4X	H_LYS_62	NZ	H_GLU_46	OE1	2.577
1E4X	H_LYS_62	NZ	H_GLU_46	OE2	3.834
1E4X	H_LYS_64	NZ	H_GLU_61	OE1	2.708
1E4X	H_LYS_64	NZ	H_GLU_61	OE2	3.973
1E4X	H_LYS_66	NZ	H_ASP_86	OD1	3.625
1E4X	H_LYS_66	NZ	H_ASP_86	OD2	3.022
1E4X	I_HIS_35	ND1	I_GLU_50	OE1	3.895
1E4X	I_HIS_35	NE2	I_GLU_50	OE1	3.180
1E4X	I_ARG_40	NH1	I_GLU_85	OE1	2.650
1E4X	I_ARG_40	NH2	I_GLU_46	OE1	3.611

1E4X	L.LYS_62	NZ	L.GLU_46	OE2	2.935
1E4X	L.LYS_64	NZ	L.GLU_61	OE1	2.622
1E4X	L.LYS_66	NZ	L.ASP_86	OD1	3.395
1E4X	L.LYS_66	NZ	L.ASP_86	OD2	2.825
1E4X	L.LYS_205	NZ	M.GLU_123	OE1	2.874
1E4X	L.LYS_205	NZ	M.GLU_123	OE2	3.751
1E4X	L.ARG_24	NH1	L.ASP_70	OD1	2.619
1E4X	L.ARG_24	NH1	L.ASP_70	OD2	3.556
1E4X	L.ARG_24	NH2	L.ASP_70	OD1	3.060
1E4X	L.ARG_24	NH2	L.ASP_70	OD2	2.776
1E4X	L.ARG_61	NH2	L.GLU_81	OE2	3.067
1E4X	L.ARG_61	NH2	L.ASP_82	OD1	2.814
1E4X	L.ARG_61	NH2	L.ASP_82	OD2	3.641
1E4X	L.LYS_147	NZ	L.GLU_154	OE1	3.971
1E4X	L.LYS_149	NZ	L.GLU_195	OE1	3.274
1E4X	L.LYS_149	NZ	L.GLU_195	OE2	2.560
1E4X	L.ARG_155	NH1	L.GLU_185	OE1	3.930
1E4X	L.ARG_155	NH1	L.GLU_185	OE2	2.776
1E4X	L.ARG_155	NH2	L.GLU_185	OE1	3.867
1E4X	L.ARG_155	NH2	L.GLU_185	OE2	3.813
1E4X	L.LYS_183	NZ	L.GLU_187	OE1	2.722
1E4X	L.LYS_183	NZ	L.GLU_187	OE2	2.806
1E4X	L.HIS_189	ND1	L.ASP_151	OD2	2.526
1E4X	L.LYS_199	NZ	L.ASP_110	OD1	3.989
1E4X	L.LYS_199	NZ	L.ASP_110	OD2	2.510
1E4X	M.ARG_24	NH1	M.ASP_70	OD1	2.588
1E4X	M.ARG_24	NH1	M.ASP_70	OD2	3.544
1E4X	M.ARG_61	NH2	M.GLU_81	OE2	2.997
1E4X	M.ARG_61	NH2	M.ASP_82	OD1	2.719
1E4X	M.ARG_61	NH2	M.ASP_82	OD2	3.382
1E4X	M.LYS_147	NZ	M.GLU_195	OE1	3.439
1E4X	M.LYS_149	NZ	M.GLU_195	OE1	3.962
1E4X	M.LYS_149	NZ	M.GLU_195	OE2	3.421
1E4X	M.ARG_155	NH1	M.GLU_185	OE1	3.714
1E4X	M.ARG_155	NH1	M.GLU_185	OE2	2.851
1E4X	M.ARG_155	NH2	M.GLU_185	OE1	3.119
1E4X	M.ARG_155	NH2	M.GLU_185	OE2	3.643
1E4X	M.LYS_183	NZ	M.GLU_187	OE1	3.326
1E4X	M.LYS_183	NZ	M.GLU_187	OE2	2.734
1E4X	M.HIS_189	ND1	M.ASP_151	OD2	2.418
1E4X	M.LYS_199	NZ	M.ASP_110	OD2	3.890
1E4X	P.HIS_4	ND1	P.ASP_7	OD1	3.911
1E4X	P.HIS_4	ND1	P.ASP_7	OD2	2.895
1E4X	Q.HIS_4	ND1	Q.ASP_7	OD1	3.489
1E4X	Q.HIS_4	ND1	Q.ASP_7	OD2	2.725
1E4X	Q.HIS_4	NE2	L.ASP_98	OD2	3.960
1E6J	H.LYS_38	NZ	H.ASP_90	OD1	3.507
1E6J	H.ARG_40	NH2	H.GLU_89	OE1	3.271
1E6J	H.LYS_63	NZ	H.GLU_46	OE1	2.880
1E6J	H.LYS_63	NZ	H.GLU_46	OE2	3.429
1E6J	H.LYS_67	NZ	H.ASP_90	OD1	3.890
1E6J	H.LYS_67	NZ	H.ASP_90	OD2	2.857
1E6J	H.ARG_102	NH1	H.ASP_108	OD1	3.654
1E6J	H.ARG_102	NH1	H.ASP_108	OD2	3.188
1E6J	H.ARG_102	NH2	H.ASP_108	OD2	3.453
1E6J	H.LYS_215	NZ	L.GLU_121	OE1	3.273
1E6J	H.LYS_215	NZ	L.GLU_121	OE2	3.199
1E6J	L.LYS_52	NZ	L.GLU_49	OE1	2.788

1E6J	L_ARG_60	NH1	L_GLU_78	OE1	3.448
1E6J	L_ARG_60	NH1	L_GLU_78	OE2	3.377
1E6J	L_ARG_60	NH2	L_GLU_80	OE1	3.435
1E6J	L_ARG_60	NH2	L_GLU_80	OE2	3.837
1E6J	L_ARG_60	NH2	L_ASP_81	OD1	3.036
1E6J	L_ARG_60	NH2	L_ASP_81	OD2	3.778
1E6J	L_LYS_101	NZ	L_GLU_103	OE2	3.191
1E6J	L_LYS_101	NZ	L_ASP_163	OD1	3.381
1E6J	L_LYS_101	NZ	L_ASP_163	OD2	3.618
1E6J	L_LYS_140	NZ	L_GLU_103	OE1	3.034
1E6J	L_LYS_140	NZ	L_GLU_103	OE2	3.715
1E6J	L_LYS_147	NZ	L_GLU_193	OE1	3.705
1E6J	L_LYS_147	NZ	L_GLU_193	OE2	3.642
1E6J	L_ARG_153	NH2	L_GLU_183	OE2	3.850
1E6J	L_LYS_181	NZ	L_GLU_185	OE1	2.925
1E6J	L_LYS_181	NZ	L_GLU_185	OE2	3.102
1E6J	L_HIS_187	ND1	L_ASP_149	OD2	3.110
1E6J	L_LYS_197	NZ	L_ASP_108	OD1	3.404
1E6J	L_LYS_197	NZ	L_ASP_108	OD2	3.535
1E6J	P_LYS_25	NZ	P_GLU_28	OE1	3.310
1E6J	P_LYS_30	NZ	P_GLU_35	OE1	3.279
1E6J	P_LYS_30	NZ	P_GLU_35	OE2	3.714
1E6J	P_ARG_82	NH2	P_GLU_79	OE1	3.880
1E6J	P_ARG_82	NH2	P_GLU_79	OE2	2.977
1E6J	P_ARG_97	NH1	P_ASP_103	OD1	3.867
1E6J	P_ARG_97	NH1	P_ASP_103	OD2	2.872
1E6J	P_ARG_97	NH2	P_ASP_103	OD2	2.992
1E6J	P_ARG_97	NH2	P_GLU_113	OE1	3.011
1E6J	P_ARG_97	NH2	P_GLU_113	OE2	2.907
1E6J	P_LYS_131	NZ	P_GLU_128	OE2	3.566
1E6J	P_LYS_140	NZ	P_GLU_75	OE1	3.007
1E6J	P_ARG_162	NH2	P_ASP_166	OD1	2.737
1E6J	P_ARG_162	NH2	P_ASP_166	OD2	3.737
1E6J	P_ARG_167	NH2	P_GLU_159	OE1	3.117
1E6J	P_ARG_167	NH2	P_GLU_159	OE2	3.307
1E6O	H_ARG_40	NH1	H_GLU_89	OE1	3.448
1E6O	H_ARG_40	NH2	H_GLU_89	OE1	2.779
1E6O	H_LYS_63	NZ	H_GLU_46	OE1	3.050
1E6O	H_LYS_67	NZ	H_ASP_90	OD1	3.728
1E6O	H_LYS_67	NZ	H_ASP_90	OD2	2.754
1E6O	H_ARG_98	NH2	H_ASP_108	OD1	3.003
1E6O	H_ARG_98	NH2	H_ASP_108	OD2	3.258
1E6O	H_LYS_215	NZ	L_GLU_121	OE1	2.731
1E6O	H_LYS_215	NZ	L_GLU_121	OE2	3.094
1E6O	L_LYS_52	NZ	L_GLU_49	OE1	2.480
1E6O	L_ARG_60	NH1	L_GLU_78	OE1	3.734
1E6O	L_ARG_60	NH1	L_GLU_78	OE2	3.517
1E6O	L_ARG_60	NH2	L_GLU_78	OE1	3.763
1E6O	L_ARG_60	NH2	L_GLU_80	OE1	3.787
1E6O	L_ARG_60	NH2	L_GLU_80	OE2	3.444
1E6O	L_ARG_60	NH2	L_ASP_81	OD1	2.714
1E6O	L_ARG_60	NH2	L_ASP_81	OD2	3.690
1E6O	L_LYS_101	NZ	L_GLU_103	OE2	2.711
1E6O	L_LYS_101	NZ	L_ASP_163	OD1	2.813
1E6O	L_LYS_101	NZ	L_ASP_163	OD2	3.565
1E6O	L_LYS_140	NZ	L_GLU_103	OE1	2.639
1E6O	L_LYS_140	NZ	L_GLU_103	OE2	3.651
1E6O	L_LYS_147	NZ	L_GLU_193	OE1	3.537

1E6O	L_LYS_147	NZ	L_GLU_193	OE2	3.485
1E6O	L_LYS_181	NZ	L_GLU_185	OE1	3.457
1E6O	L_LYS_181	NZ	L_GLU_185	OE2	2.602
1E6O	L_HIS_187	ND1	L_ASP_149	OD2	2.973
1E6O	L_LYS_197	NZ	L_ASP_108	OD1	3.626
1E6O	L_LYS_197	NZ	L_ASP_108	OD2	2.685
1EJO	L_HIS_2038	NE2	H_ASP_2603	OD1	3.217
1EJO	L_ARG_2065	NH1	L_ASP_2085	OD1	3.884
1EJO	L_ARG_2065	NH1	L_ASP_2085	OD2	3.751
1EJO	L_ARG_2065	NH1	L_ASP_2086	OD1	3.789
1EJO	L_ARG_2065	NH1	L_ASP_2086	OD2	2.949
1EJO	L_ARG_2065	NH2	L_GLU_2083	OE2	3.437
1EJO	L_LYS_2107	NZ	L_ASP_2169	OD1	3.608
1EJO	L_LYS_2153	NZ	L_GLU_2199	OE2	3.964
1EJO	L_ARG_2159	NH2	L_GLU_2189	OE1	2.792
1EJO	L_ARG_2159	NH2	L_GLU_2189	OE2	2.939
1EJO	L_LYS_2187	NZ	L_ASP_2188	OD1	3.810
1EJO	H_ARG_2537	NH1	H_ASP_2589	OD1	2.793
1EJO	H_ARG_2537	NH2	H_GLU_2545	OE1	3.422
1EJO	H_ARG_2537	NH2	H_ASP_2589	OD1	3.718
1EJO	H_ARG_2543	NH1	H_GLU_2545	OE1	3.893
1EJO	H_ARG_2543	NH1	H_GLU_2545	OE2	2.876
1EJO	H_ARG_2543	NH2	H_GLU_2541	OE1	3.189
1EJO	H_ARG_2566	NH1	H_ASP_2589	OD2	2.850
1EJO	H_ARG_2566	NH2	H_ASP_2589	OD1	3.228
1EJO	H_ARG_2566	NH2	H_ASP_2589	OD2	3.243
1EJO	H_ARG_2598	NH1	H_ASP_2603	OD1	3.142
1EJO	H_ARG_2598	NH1	H_ASP_2603	OD2	3.978
1EJO	H_ARG_2598	NH2	H_ASP_2603	OD1	3.242
1EJO	H_ARG_2598	NH2	H_ASP_2603	OD2	2.790
1EJO	H_ARG_2598	NH2	P_ASP_3143	OD1	3.795
1EJO	H_ARG_2598	NH2	P_ASP_3143	OD2	2.982
1EJO	H_LYS_2714	NZ	L_GLU_2127	OE1	2.933
1EJO	H_LYS_2714	NZ	L_GLU_2127	OE2	3.046
1EJO	P_ARG_3141	NH1	L_GLU_2027	OE2	3.696
1EJO	P_ARG_3141	NH1	L_GLU_2097	OE1	2.675
1EJO	P_ARG_3141	NH2	L_GLU_2027	OE2	3.441
1EMT	L_LYS_39	NZ	L_GLU_81	OE1	2.666
1EMT	L_LYS_39	NZ	L_GLU_81	OE2	3.409
1EMT	L_ARG_61	NH1	L_ASP_82	OD1	2.890
1EMT	L_ARG_61	NH2	L_ASP_82	OD1	2.955
1EMT	L_ARG_61	NH2	L_ASP_82	OD2	2.766
1EMT	L_LYS_147	NZ	L_GLU_154	OE2	3.689
1EMT	L_LYS_149	NZ	L_GLU_195	OE2	3.241
1EMT	L_LYS_183	NZ	L_GLU_187	OE1	2.782
1EMT	L_LYS_183	NZ	L_GLU_187	OE2	3.826
1EMT	L_ARG_188	NH2	L_GLU_185	OE1	3.057
1EMT	L_ARG_188	NH2	L_GLU_185	OE2	3.248
1EMT	L_HIS_189	ND1	L_GLU_185	OE2	3.669
1EMT	L_HIS_189	NE2	L_GLU_185	OE2	3.443
1EMT	H_LYS_63	NZ	L_ASP_1	OD1	3.310
1EMT	H_LYS_67	NZ	H_ASP_90	OD1	2.648
1EMT	H_LYS_67	NZ	H_ASP_90	OD2	3.672
1EMT	H_LYS_211	NZ	L_GLU_123	OE1	2.945
1EMT	H_LYS_211	NZ	L_GLU_123	OE2	2.554
1ETZ	L_ARG_23	NH2	L_ASP_71	OD2	3.806
1ETZ	L_ARG_63	NH2	L_GLU_83	OE2	3.283
1ETZ	L_ARG_63	NH2	L_ASP_84	OD1	2.986

1ETZ	L_ARG_63	NH2	L_ASP_84	OD2	3.556
1ETZ	L_LYS_113	NZ	L_GLU_201	OE1	3.231
1ETZ	L_ARG_186	NH1	B_GLU_48	OE1	2.771
1ETZ	L_ARG_186	NH1	B_GLU_48	OE2	3.248
1ETZ	L_ARG_190	NH1	L_GLU_189	OE2	3.584
1ETZ	L_ARG_190	NH2	L_GLU_189	OE2	3.089
1ETZ	L_ARG_190	NH2	B_GLU_48	OE2	3.331
1ETZ	H_ARG_40	NH1	H_ASP_91	OD1	2.907
1ETZ	H_ARG_40	NH2	H_GLU_48	OE1	3.221
1ETZ	H_ARG_40	NH2	H_ASP_91	OD1	3.222
1ETZ	H_ARG_68	NH2	H_ASP_91	OD1	3.774
1ETZ	H_ARG_68	NH2	H_ASP_91	OD2	2.733
1ETZ	H_LYS_73	NZ	H_ASP_57	OD1	3.834
1ETZ	H_ARG_99	NH1	H_ASP_114	OD1	2.968
1ETZ	H_ARG_99	NH1	H_ASP_114	OD2	3.185
1ETZ	H_ARG_100	NH1	H_ASP_52	OD1	3.260
1ETZ	H_ARG_100	NH1	H_ASP_52	OD2	2.758
1ETZ	H_LYS_156	NZ	L_GLU_127	OE2	3.377
1ETZ	H_LYS_221	NZ	L_GLU_126	OE1	3.184
1ETZ	A_ARG_23	NH1	A_ASP_71	OD2	2.921
1ETZ	A_ARG_23	NH2	A_ASP_71	OD2	2.821
1ETZ	A_ARG_63	NH2	A_GLU_83	OE2	3.430
1ETZ	A_ARG_63	NH2	A_ASP_84	OD1	2.842
1ETZ	A_ARG_63	NH2	A_ASP_84	OD2	3.406
1ETZ	A_LYS_113	NZ	A_GLU_201	OE1	2.940
1ETZ	A_ARG_186	NH1	H_GLU_45	OE2	3.236
1ETZ	A_ARG_186	NH2	H_GLU_48	OE1	3.518
1ETZ	B_ARG_40	NH1	B_ASP_91	OD1	3.069
1ETZ	B_ARG_40	NH2	B_GLU_48	OE1	3.077
1ETZ	B_ARG_40	NH2	B_ASP_91	OD1	3.733
1ETZ	B_LYS_59	NZ	B_ASP_57	OD1	3.243
1ETZ	B_LYS_59	NZ	B_ASP_57	OD2	3.017
1ETZ	B_ARG_68	NH1	B_ASP_91	OD1	3.924
1ETZ	B_ARG_68	NH2	B_ASP_91	OD1	3.185
1ETZ	B_ARG_68	NH2	B_ASP_91	OD2	2.598
1ETZ	B_LYS_73	NZ	B_ASP_57	OD1	2.975
1ETZ	B_ARG_99	NH1	B_ASP_114	OD1	2.870
1ETZ	B_ARG_99	NH1	B_ASP_114	OD2	3.787
1ETZ	B_ARG_100	NH1	B_ASP_52	OD1	2.947
1ETZ	B_ARG_100	NH1	B_ASP_52	OD2	2.788
1ETZ	B_LYS_156	NZ	A_GLU_127	OE2	2.979
1ETZ	B_LYS_221	NZ	A_GLU_126	OE1	3.572
1ETZ	B_LYS_222	NZ	B_GLU_224	OE1	3.556
1F11	A_ARG_61	NH1	A_GLU_79	OE2	3.870
1F11	A_ARG_61	NH1	A_GLU_81	OE1	3.780
1F11	A_ARG_61	NH2	A_GLU_81	OE1	3.819
1F11	A_ARG_61	NH2	A_ASP_82	OD1	2.589
1F11	A_ARG_61	NH2	A_ASP_82	OD2	2.998
1F11	A_LYS_147	NZ	A_GLU_154	OE1	3.554
1F11	A_LYS_149	NZ	A_GLU_195	OE1	2.800
1F11	A_LYS_149	NZ	A_GLU_195	OE2	3.495
1F11	A_ARG_155	NH2	A_GLU_185	OE2	3.833
1F11	A_LYS_183	NZ	A_ASP_184	OD1	3.227
1F11	A_LYS_183	NZ	A_ASP_184	OD2	3.413
1F11	A_HIS_189	NE2	A_ASP_151	OD2	3.960
1F11	A_ARG_211	NH1	A_GLU_187	OE1	3.379
1F11	B_LYS_35	NZ	B_ASP_50	OD2	2.899
1F11	B_LYS_62	NZ	B_GLU_46	OE1	3.878

1F11	B.LYS.62	NZ	B.GLU.46	OE2	3.017
1F11	B.LYS.66	NZ	B.ASP.86	OD1	3.898
1F11	B.LYS.66	NZ	B.ASP.86	OD2	2.909
1F11	B.LYS.218	NZ	B.ASP.220	OD1	3.293
1F11	B.LYS.221	NZ	A.GLU.123	OE2	3.880
1F11	C.ARG.61	NH1	C.GLU.79	OE2	3.820
1F11	C.ARG.61	NH1	C.GLU.81	OE1	3.765
1F11	C.ARG.61	NH2	C.GLU.81	OE1	3.827
1F11	C.ARG.61	NH2	C.ASP.82	OD1	2.588
1F11	C.ARG.61	NH2	C.ASP.82	OD2	2.920
1F11	C.LYS.147	NZ	C.GLU.154	OE1	3.496
1F11	C.LYS.149	NZ	C.GLU.195	OE1	2.803
1F11	C.LYS.149	NZ	C.GLU.195	OE2	3.539
1F11	C.ARG.155	NH2	C.GLU.185	OE2	3.909
1F11	C.LYS.183	NZ	C.ASP.184	OD1	3.200
1F11	C.LYS.183	NZ	C.ASP.184	OD2	3.469
1F11	C.ARG.211	NH1	C.GLU.187	OE1	3.266
1F11	D.LYS.35	NZ	D.ASP.50	OD2	2.846
1F11	D.LYS.62	NZ	D.GLU.46	OE1	3.912
1F11	D.LYS.62	NZ	D.GLU.46	OE2	3.130
1F11	D.LYS.66	NZ	D.ASP.86	OD1	3.943
1F11	D.LYS.66	NZ	D.ASP.86	OD2	2.885
1F11	D.LYS.218	NZ	D.ASP.220	OD1	3.381
1F11	D.LYS.221	NZ	C.GLU.123	OE2	3.786
1F2X	K.ARG.838	NH1	K.ASP.888	OD1	2.859
1F2X	K.ARG.838	NH2	K.GLU.846	OE2	2.923
1F2X	K.ARG.865	NH1	K.ASP.888	OD1	3.794
1F2X	K.ARG.865	NH1	K.ASP.888	OD2	2.763
1F2X	K.ARG.865	NH2	K.ASP.888	OD1	3.027
1F2X	K.ARG.865	NH2	K.ASP.888	OD2	3.447
1F2X	K.LYS.874	NZ	K.ASP.871	OD1	3.294
1F2X	K.ARG.909	NH2	K.ASP.912	OD1	2.589
1F2X	K.ARG.909	NH2	K.ASP.912	OD2	3.255
1F2X	L.ARG.1038	NH1	L.ASP.1088	OD1	2.834
1F2X	L.ARG.1038	NH2	L.GLU.1046	OE2	3.098
1F2X	L.ARG.1038	NH2	L.ASP.1088	OD1	3.939
1F2X	L.ARG.1065	NH1	L.ASP.1088	OD1	3.834
1F2X	L.ARG.1065	NH1	L.ASP.1088	OD2	2.618
1F2X	L.ARG.1065	NH2	L.ASP.1088	OD1	3.165
1F2X	L.ARG.1065	NH2	L.ASP.1088	OD2	3.405
1F2X	L.ARG.1109	NH2	L.ASP.1112	OD1	3.166
1F2X	L.ARG.1109	NH2	L.ASP.1112	OD2	2.892
1F3R	B.ARG.38	NH1	B.ASP.89	OD2	2.997
1F3R	B.ARG.38	NH2	B.GLU.46	OE1	3.068
1F3R	B.ARG.50	NH1	B.ASP.98	OD1	3.532
1F3R	B.ARG.66	NH1	B.ASP.89	OD1	3.017
1F3R	B.ARG.66	NH2	B.ASP.89	OD1	3.057
1F3R	B.ARG.97	NH1	B.ASP.111	OD1	3.327
1F3R	B.ARG.97	NH1	B.ASP.111	OD2	3.427
1F3R	B.ARG.97	NH2	B.ASP.111	OD1	3.187
1F3R	B.ARG.97	NH2	B.ASP.111	OD2	3.419
1F3R	B.LYS.177	NZ	B.GLU.180	OE1	3.798
1F3R	B.LYS.177	NZ	B.GLU.180	OE2	3.027
1F3R	B.ARG.199	NH1	B.ASP.220	OD1	2.891
1F3R	B.ARG.199	NH1	B.ASP.220	OD2	3.346
1F3R	B.ARG.199	NH2	B.GLU.219	OE1	3.171
1F3R	B.LYS.244	NZ	B.GLU.242	OE2	3.193
1F3R	B.LYS.249	NZ	B.GLU.247	OE1	3.078

1F4W	L_ARG.63	NH2	L_GLU_83	OE2	3.740
1F4W	L_ARG.63	NH2	L_ASP_84	OD1	3.103
1F4W	L_ARG.63	NH2	L_ASP_84	OD2	3.558
1F4W	L_LYS_113	NZ	L_GLU_201	OE1	2.889
1F4W	L_LYS_169	NZ	L_GLU_85	OE2	3.500
1F4W	H_ARG_38	NH1	H_ASP_90	OD1	2.942
1F4W	H_ARG_38	NH2	H_GLU_46	OE1	2.644
1F4W	H_ARG_67	NH1	H_ASP_90	OD1	3.871
1F4W	H_ARG_67	NH1	H_ASP_90	OD2	2.697
1F4W	H_ARG_67	NH2	H_ASP_90	OD1	3.052
1F4W	H_ARG_67	NH2	H_ASP_90	OD2	3.253
1F4W	H_ARG_72	NH2	H_ASP_74	OD1	3.561
1F4W	H_LYS_76	NZ	H_ASP_73	OD2	3.208
1F4W	H_ARG_98	NH1	H_ASP_105	OD1	3.445
1F4W	H_ARG_98	NH1	H_ASP_105	OD2	2.877
1F4W	H_LYS_147	NZ	L_GLU_127	OE2	2.611
1F4W	H_LYS_212	NZ	L_GLU_126	OE1	2.614
1F4W	H_LYS_212	NZ	L_GLU_126	OE2	2.379
1F4X	L_HIS_44	ND1	L_GLU_40	OE2	3.729
1F4X	L_ARG.63	NH2	L_ASP_84	OD1	3.061
1F4X	L_ARG.63	NH2	L_ASP_84	OD2	3.605
1F4X	L_LYS_113	NZ	L_GLU_201	OE1	3.012
1F4X	L_LYS_169	NZ	L_GLU_85	OE2	3.678
1F4X	H_ARG_38	NH1	H_ASP_90	OD1	2.949
1F4X	H_ARG_38	NH2	H_GLU_46	OE1	2.849
1F4X	H_ARG_38	NH2	H_ASP_90	OD1	3.913
1F4X	H_ARG_67	NH1	H_ASP_90	OD1	3.808
1F4X	H_ARG_67	NH1	H_ASP_90	OD2	2.538
1F4X	H_ARG_67	NH2	H_ASP_90	OD1	3.205
1F4X	H_ARG_67	NH2	H_ASP_90	OD2	3.358
1F4X	H_ARG_72	NH2	H_ASP_74	OD1	3.580
1F4X	H_LYS_76	NZ	H_ASP_73	OD2	2.862
1F4X	H_ARG_98	NH1	H_ASP_105	OD1	3.356
1F4X	H_ARG_98	NH1	H_ASP_105	OD2	2.740
1F4X	H_LYS_147	NZ	L_GLU_127	OE2	2.699
1F4X	H_LYS_212	NZ	L_GLU_126	OE1	2.421
1F4X	H_LYS_212	NZ	L_GLU_126	OE2	2.990
1F4Y	L_ARG.63	NH2	L_ASP_84	OD1	3.366
1F4Y	L_LYS_105	NZ	L_GLU_85	OE1	3.158
1F4Y	H_ARG_38	NH1	H_ASP_90	OD1	3.048
1F4Y	H_ARG_38	NH2	H_GLU_46	OE1	2.579
1F4Y	H_LYS_65	NZ	H_ASP_62	OD1	3.084
1F4Y	H_LYS_65	NZ	H_ASP_62	OD2	3.693
1F4Y	H_ARG_67	NH1	H_ASP_90	OD1	3.760
1F4Y	H_ARG_67	NH1	H_ASP_90	OD2	2.465
1F4Y	H_ARG_67	NH2	H_ASP_90	OD1	2.587
1F4Y	H_ARG_67	NH2	H_ASP_90	OD2	2.864
1F4Y	H_ARG_98	NH1	H_ASP_105	OD1	3.675
1F4Y	H_ARG_98	NH1	H_ASP_105	OD2	3.275
1F4Y	H_LYS_212	NZ	L_GLU_126	OE2	3.609
1F8T	L_ARG.46	NH2	L_ASP_55	OD1	2.680
1F8T	L_ARG.46	NH2	L_ASP_55	OD2	3.749
1F8T	L_ARG.61	NH1	L_GLU_79	OE1	3.213
1F8T	L_ARG.61	NH2	L_GLU_79	OE1	3.750
1F8T	L_ARG.61	NH2	L_ASP_82	OD1	2.713
1F8T	L_ARG.61	NH2	L_ASP_82	OD2	3.022
1F8T	L_ARG.77	NH1	L_GLU_79	OE2	2.715
1F8T	L_ARG.77	NH2	L_GLU_79	OE2	3.752

1F8T	L_ARG_96	NH1	H_ASP_97	OD1	3.105
1F8T	L_ARG_96	NH1	H_ASP_97	OD2	3.586
1F8T	L_ARG_96	NH2	H_ASP_97	OD1	3.395
1F8T	L_ARG_96	NH2	H_ASP_97	OD2	2.424
1F8T	L_LYS_	NZ	L_GLU_	OE1	3.476
1F8T	L_LYS_	NZ	L_GLU_	OE1	3.068
1F8T	L_LYS_	NZ	L_GLU_	OE2	3.947
1F8T	L_ARG_	NH2	L_GLU_	OE1	3.027
1F8T	L_ARG_	NH2	L_GLU_	OE2	2.531
1F8T	L_LYS_	NZ	L_GLU_	OE2	3.307
1F8T	L_HIS_	ND1	L_ASP_	OD2	2.855
1F8T	L_LYS_199	NZ	L_ASP_110	OD2	3.253
1F8T	H_ARG_38	NH1	H_ASP_86	OD1	2.940
1F8T	H_ARG_38	NH2	H_GLU_46	OE1	2.881
1F8T	H_ARG_38	NH2	H_ASP_86	OD1	3.828
1F8T	H_ARG_66	NH1	H_ASP_86	OD1	3.709
1F8T	H_ARG_66	NH1	H_ASP_86	OD2	3.187
1F8T	H_ARG_66	NH2	H_ASP_86	OD1	2.923
1F8T	H_ARG_66	NH2	H_ASP_86	OD2	3.622
1F8T	H_LYS_221	NZ	L_GLU_123	OE1	3.087
1F90	L_LYS_30	NZ	E_GLU_4	OE1	2.620
1F90	L_LYS_30	NZ	E_GLU_4	OE2	2.679
1F90	L_ARG_46	NH2	L_ASP_55	OD1	2.495
1F90	L_ARG_46	NH2	L_ASP_55	OD2	3.861
1F90	L_ARG_61	NH1	L_GLU_79	OE2	3.045
1F90	L_ARG_61	NH2	L_GLU_79	OE2	3.948
1F90	L_ARG_61	NH2	L_GLU_81	OE1	3.955
1F90	L_ARG_61	NH2	L_ASP_82	OD1	2.600
1F90	L_ARG_61	NH2	L_ASP_82	OD2	2.843
1F90	L_ARG_77	NH1	L_GLU_79	OE1	2.895
1F90	L_ARG_77	NH1	L_GLU_79	OE2	3.695
1F90	L_ARG_96	NH2	H_ASP_97	OD1	2.720
1F90	L_ARG_96	NH2	H_ASP_97	OD2	2.722
1F90	L_LYS_103	NZ	L_GLU_105	OE1	3.749
1F90	L_LYS_103	NZ	L_ASP_165	OD1	3.843
1F90	L_LYS_149	NZ	L_GLU_195	OE1	3.370
1F90	L_LYS_149	NZ	L_GLU_195	OE2	3.504
1F90	L_ARG_188	NH1	L_GLU_185	OE2	2.963
1F90	L_ARG_188	NH2	L_GLU_185	OE2	3.164
1F90	L_HIS_189	ND1	L_ASP_151	OD2	3.004
1F90	L_HIS_189	NE2	L_GLU_185	OE2	2.903
1F90	H_ARG_38	NH1	H_ASP_86	OD1	3.080
1F90	H_ARG_38	NH2	H_GLU_46	OE1	3.030
1F90	H_ARG_38	NH2	H_ASP_86	OD1	3.543
1F90	H_ARG_66	NH1	H_ASP_86	OD1	3.378
1F90	H_ARG_66	NH1	H_ASP_86	OD2	3.136
1F90	H_ARG_66	NH2	H_ASP_86	OD1	2.890
1F90	H_ARG_66	NH2	H_ASP_86	OD2	3.648
1F90	H_LYS_221	NZ	L_GLU_123	OE2	3.675
1F90	E_LYS_1	NZ	E_GLU_5	OE1	3.986
1F90	E_LYS_1	NZ	E_GLU_5	OE2	3.901
1FBI	L_ARG_61	NH1	L_ASP_82	OD1	3.634
1FBI	L_ARG_61	NH1	L_ASP_82	OD2	2.723
1FBI	L_ARG_61	NH2	L_ASP_82	OD1	3.289
1FBI	L_ARG_61	NH2	L_ASP_82	OD2	3.818
1FBI	L_LYS_147	NZ	L_GLU_195	OE2	3.806
1FBI	L_LYS_149	NZ	L_GLU_195	OE1	2.895
1FBI	L_LYS_149	NZ	L_GLU_195	OE2	3.340

1FBI	L_ARG_155	NH1	L_GLU_185	OE2	3.988
1FBI	L_ARG_155	NH2	L_GLU_185	OE1	3.443
1FBI	L_ARG_155	NH2	L_GLU_185	OE2	3.420
1FBI	L_LYS_183	NZ	L_GLU_187	OE1	3.147
1FBI	L_LYS_183	NZ	L_GLU_187	OE2	3.215
1FBI	L_HIS_189	ND1	L_ASP_151	OD2	3.770
1FBI	L_LYS_199	NZ	L_ASP_110	OD1	2.851
1FBI	L_LYS_199	NZ	L_ASP_110	OD2	3.860
1FBI	H_HIS_35	ND1	H_GLU_50	OE2	3.933
1FBI	H_HIS_35	NE2	H_GLU_50	OE2	3.486
1FBI	H_LYS_38	NZ	H_ASP_90	OD1	3.514
1FBI	H_LYS_38	NZ	H_ASP_90	OD2	3.031
1FBI	H_LYS_63	NZ	L_ASP_1	OD1	2.933
1FBI	H_LYS_63	NZ	L_ASP_1	OD2	2.804
1FBI	H_LYS_65	NZ	H_GLU_62	OE1	2.904
1FBI	H_LYS_67	NZ	H_ASP_90	OD1	3.905
1FBI	H_LYS_217	NZ	L_GLU_123	OE1	3.667
1FBI	X_LYS_1	NZ	X_GLU_7	OE2	3.145
1FBI	X_HIS_15	ND1	H_ASP_55	OD1	3.190
1FBI	X_HIS_15	ND1	H_ASP_55	OD2	3.649
1FBI	X_ARG_61	NH1	X_ASP_48	OD1	3.808
1FBI	X_ARG_61	NH1	X_ASP_48	OD2	3.628
1FBI	X_ARG_61	NH2	X_ASP_48	OD1	3.862
1FBI	X_LYS_96	NZ	H_ASP_52	OD2	2.922
1FBI	X_LYS_97	NZ	H_GLU_50	OE1	3.586
1FBI	X_LYS_97	NZ	H_GLU_50	OE2	2.898
1FBI	X_ARG_121	NH1	X_ASP_119	OD1	3.058
1FBI	P_ARG_24	NH2	P_ASP_70	OD1	3.358
1FBI	P_ARG_61	NH1	P_GLU_79	OE2	3.500
1FBI	P_ARG_61	NH2	P_ASP_82	OD2	2.619
1FBI	P_LYS_149	NZ	P_GLU_195	OE1	3.522
1FBI	P_LYS_149	NZ	P_GLU_195	OE2	3.273
1FBI	P_LYS_183	NZ	P_GLU_187	OE1	3.943
1FBI	P_HIS_189	ND1	P_ASP_151	OD2	3.620
1FBI	P_HIS_189	NE2	P_GLU_185	OE1	3.397
1FBI	P_HIS_189	NE2	P_GLU_185	OE2	3.570
1FBI	P_LYS_199	NZ	P_ASP_110	OD2	3.380
1FBI	P_ARG_211	NH2	P_GLU_187	OE1	3.763
1FBI	Q_HIS_35	NE2	Q_GLU_50	OE2	3.940
1FBI	Q_LYS_63	NZ	P_ASP_1	OD1	3.020
1FBI	Q_LYS_63	NZ	P_ASP_1	OD2	3.850
1FBI	Q_LYS_65	NZ	Q_GLU_62	OE1	2.725
1FBI	Q_LYS_65	NZ	Q_GLU_62	OE2	3.529
1FBI	Y_HIS_15	ND1	Q_ASP_55	OD1	3.335
1FBI	Y_HIS_15	ND1	Q_ASP_55	OD2	3.838
1FBI	Y_LYS_96	NZ	Q_ASP_52	OD2	2.727
1FBI	Y_LYS_97	NZ	Q_GLU_50	OE1	2.828
1FBI	Y_LYS_97	NZ	Q_GLU_50	OE2	3.159
1FCC	A_LYS_248	NZ	A_GLU_380	OE2	2.872
1FCC	A_ARG_255	NH1	A_ASP_249	OD1	3.810
1FCC	A_LYS_317	NZ	A_ASP_280	OD2	3.593
1FCC	A_LYS_320	NZ	A_GLU_333	OE2	2.861
1FCC	A_LYS_322	NZ	A_GLU_333	OE2	3.431
1FCC	A_LYS_338	NZ	A_GLU_430	OE1	3.073
1FCC	A_LYS_338	NZ	A_GLU_430	OE2	2.873
1FCC	A_LYS_370	NZ	B_GLU_357	OE2	2.948
1FCC	A_LYS_409	NZ	B_ASP_399	OD2	2.859
1FCC	A_ARG_416	NH1	A_GLU_388	OE1	2.663

1FCC	A_ARG_416	NH1	A_GLU_388	OE2	2.822
1FCC	A_ARG_416	NH2	A_GLU_388	OE1	3.781
1FCC	A_ARG_416	NH2	A_GLU_388	OE2	2.901
1FCC	A_LYS_439	NZ	B_GLU_356	OE1	3.550
1FCC	A_LYS_439	NZ	B_GLU_356	OE2	3.522
1FCC	C_LYS_4	NZ	C_GLU_15	OE1	3.955
1FCC	C_LYS_4	NZ	C_GLU_15	OE2	3.020
1FCC	C_LYS_28	NZ	A_GLU_380	OE1	2.730
1FCC	C_LYS_28	NZ	A_GLU_380	OE2	3.982
1FCC	C_LYS_28	NZ	A_GLU_382	OE1	3.879
1FCC	C_LYS_28	NZ	A_GLU_382	OE2	2.866
1FCC	C_LYS_31	NZ	C_GLU_27	OE2	2.693
1FCC	B_LYS_248	NZ	B_GLU_380	OE2	2.873
1FCC	B_ARG_255	NH1	B_ASP_249	OD1	3.810
1FCC	B_LYS_317	NZ	B_ASP_280	OD2	3.592
1FCC	B_LYS_320	NZ	B_GLU_333	OE2	2.862
1FCC	B_LYS_322	NZ	B_GLU_333	OE2	3.430
1FCC	B_LYS_338	NZ	B_GLU_430	OE1	3.074
1FCC	B_LYS_338	NZ	B_GLU_430	OE2	2.873
1FCC	B_LYS_370	NZ	A_GLU_357	OE2	2.633
1FCC	B_LYS_409	NZ	A_ASP_399	OD2	3.360
1FCC	B_ARG_416	NH1	B_GLU_388	OE1	2.663
1FCC	B_ARG_416	NH1	B_GLU_388	OE2	2.823
1FCC	B_ARG_416	NH2	B_GLU_388	OE1	3.781
1FCC	B_ARG_416	NH2	B_GLU_388	OE2	2.902
1FCC	B_LYS_439	NZ	A_GLU_356	OE1	3.166
1FCC	B_LYS_439	NZ	A_GLU_356	OE2	3.295
1FCC	D_LYS_4	NZ	D_GLU_15	OE1	3.955
1FCC	D_LYS_4	NZ	D_GLU_15	OE2	3.020
1FCC	D_LYS_28	NZ	B_GLU_380	OE1	2.730
1FCC	D_LYS_28	NZ	B_GLU_380	OE2	3.982
1FCC	D_LYS_28	NZ	B_GLU_382	OE1	3.879
1FCC	D_LYS_28	NZ	B_GLU_382	OE2	2.865
1FCC	D_LYS_31	NZ	D_GLU_27	OE2	2.693
1FDL	L_ARG_61	NH1	L_GLU_81	OE2	3.900
1FDL	L_ARG_61	NH1	L_ASP_82	OD1	2.792
1FDL	L_ARG_61	NH1	L_ASP_82	OD2	2.681
1FDL	L_ARG_61	NH2	L_GLU_81	OE2	3.608
1FDL	L_ARG_96	NH1	H_GLU_98	OE1	3.307
1FDL	L_ARG_96	NH1	H_GLU_98	OE2	2.802
1FDL	L_ARG_96	NH2	H_GLU_98	OE1	2.754
1FDL	L_ARG_96	NH2	H_GLU_98	OE2	3.656
1FDL	L_LYS_107	NZ	L_GLU_17	OE1	3.380
1FDL	L_LYS_149	NZ	L_GLU_195	OE1	3.099
1FDL	L_LYS_149	NZ	L_GLU_195	OE2	3.490
1FDL	L_ARG_155	NH2	L_GLU_185	OE1	3.454
1FDL	L_ARG_155	NH2	L_GLU_185	OE2	3.567
1FDL	L_LYS_183	NZ	L_GLU_187	OE1	2.772
1FDL	L_LYS_183	NZ	L_GLU_187	OE2	2.921
1FDL	L_HIS_189	ND1	L_ASP_151	OD2	3.048
1FDL	L_LYS_199	NZ	L_ASP_110	OD1	2.959
1FDL	L_LYS_199	NZ	L_ASP_110	OD2	3.198
1FDL	H_ARG_38	NH1	H_ASP_89	OD2	3.284
1FDL	H_ARG_38	NH2	H_GLU_46	OE1	3.064
1FDL	H_ARG_38	NH2	H_ASP_89	OD2	3.961
1FDL	H_ARG_66	NH1	H_ASP_89	OD2	3.688
1FDL	H_ARG_66	NH2	H_ASP_89	OD1	2.978
1FDL	H_ARG_66	NH2	H_ASP_89	OD2	3.755

1FDL	H_ARG.97	NH2	H_ASP.104	OD1	2.804
1FDL	H_ARG.97	NH2	H_ASP.104	OD2	2.688
1FDL	H_ARG.102	NH1	H_ASP.100	OD1	3.620
1FDL	H_LYS.211	NZ	L_GLU.123	OE1	2.896
1FDL	H_LYS.211	NZ	L_GLU.123	OE2	3.291
1FDL	Y_LYS.1	NZ	Y_GLU.7	OE2	3.281
1FDL	Y_ARG.61	NH1	Y_ASP.48	OD2	3.796
1FDL	Y_ARG.61	NH2	Y_ASP.48	OD2	3.093
1FDL	Y_ARG.125	NH1	Y_ASP.119	OD1	3.041
1FDL	Y_ARG.125	NH1	Y_ASP.119	OD2	3.285
1FDL	Y_ARG.125	NH2	Y_ASP.119	OD1	3.894
1FDL	Y_ARG.125	NH2	Y_ASP.119	OD2	2.759
1FJ1	A_LYS.24	NZ	A_ASP.70	OD1	3.672
1FJ1	A_LYS.24	NZ	A_ASP.70	OD2	2.846
1FJ1	A_ARG.61	NH2	A_ASP.82	OD1	2.576
1FJ1	A_ARG.61	NH2	A_ASP.82	OD2	2.776
1FJ1	A_LYS.103	NZ	A_GLU.105	OE2	3.775
1FJ1	A_LYS.147	NZ	A_GLU.154	OE2	3.963
1FJ1	A_LYS.149	NZ	A_GLU.195	OE2	2.928
1FJ1	A_ARG.155	NH1	A_GLU.185	OE2	3.662
1FJ1	A_ARG.155	NH2	A_GLU.185	OE1	2.919
1FJ1	A_ARG.155	NH2	A_GLU.185	OE2	3.026
1FJ1	A_ARG.188	NH2	E_GLU.196	OE2	3.475
1FJ1	A_HIS.189	ND1	E_GLU.196	OE1	3.723
1FJ1	A_HIS.189	NE2	E_GLU.196	OE1	3.502
1FJ1	A_LYS.199	NZ	A_ASP.110	OD1	3.803
1FJ1	A_LYS.199	NZ	A_ASP.110	OD2	3.857
1FJ1	B_ARG.47	NH1	A_ASP.1	OD1	3.251
1FJ1	B_ARG.47	NH2	A_ASP.1	OD1	2.492
1FJ1	B_LYS.65	NZ	B_ASP.62	OD1	3.433
1FJ1	B_ARG.67	NH1	B_ASP.90	OD1	2.927
1FJ1	B_ARG.67	NH1	B_ASP.90	OD2	3.891
1FJ1	B_ARG.67	NH2	B_ASP.90	OD1	3.450
1FJ1	B_ARG.67	NH2	B_ASP.90	OD2	3.269
1FJ1	B_ARG.98	NH2	B_ASP.101	OD1	3.026
1FJ1	B_ARG.98	NH2	B_ASP.101	OD2	3.672
1FJ1	B_LYS.209	NZ	B_GLU.211	OE1	3.349
1FJ1	B_LYS.209	NZ	B_GLU.211	OE2	3.845
1FJ1	C_LYS.24	NZ	C_ASP.70	OD1	3.574
1FJ1	C_LYS.24	NZ	C_ASP.70	OD2	2.777
1FJ1	C_ARG.61	NH2	C_ASP.82	OD1	2.572
1FJ1	C_ARG.61	NH2	C_ASP.82	OD2	2.742
1FJ1	C_LYS.103	NZ	C_GLU.105	OE2	3.738
1FJ1	C_LYS.147	NZ	C_GLU.154	OE2	3.995
1FJ1	C_LYS.149	NZ	C_GLU.195	OE2	2.876
1FJ1	C_ARG.155	NH1	C_GLU.185	OE2	3.699
1FJ1	C_ARG.155	NH2	C_GLU.185	OE1	2.898
1FJ1	C_ARG.155	NH2	C_GLU.185	OE2	3.006
1FJ1	C_HIS.189	NE2	F_GLU.196	OE1	3.808
1FJ1	C_LYS.199	NZ	C_ASP.110	OD1	3.817
1FJ1	C_LYS.199	NZ	C_ASP.110	OD2	3.838
1FJ1	D_ARG.47	NH1	C_ASP.1	OD1	3.296
1FJ1	D_ARG.47	NH2	C_ASP.1	OD1	2.800
1FJ1	D_LYS.65	NZ	D_ASP.62	OD1	3.432
1FJ1	D_ARG.67	NH1	D_ASP.90	OD1	2.939
1FJ1	D_ARG.67	NH1	D_ASP.90	OD2	3.923
1FJ1	D_ARG.67	NH2	D_ASP.90	OD1	3.458
1FJ1	D_ARG.67	NH2	D_ASP.90	OD2	3.292

1FJ1	D_ARG_98	NH2	D_ASP_101	OD1	3.012
1FJ1	D_ARG_98	NH2	D_ASP_101	OD2	3.702
1FJ1	D_LYS_209	NZ	D_GLU_211	OE1	3.891
1FJ1	E_LYS_117	NZ	E_ASP_118	OD1	3.779
1FJ1	E_ARG_139	NH1	E_GLU_160	OE2	3.349
1FJ1	E_ARG_139	NH2	E_GLU_160	OE2	3.249
1FJ1	E_ARG_144	NH1	E_GLU_146	OE2	2.339
1FJ1	E_ARG_144	NH2	E_GLU_146	OE2	3.724
1FJ1	E_LYS_157	NZ	E_GLU_168	OE2	3.224
1FJ1	E_LYS_159	NZ	E_GLU_168	OE2	3.688
1FJ1	E_LYS_175	NZ	E_GLU_174	OE1	3.503
1FJ1	E_LYS_189	NZ	E_GLU_160	OE1	2.964
1FJ1	E_LYS_189	NZ	E_GLU_160	OE2	3.493
1FJ1	E_LYS_212	NZ	E_ASP_203	OD2	3.853
1FJ1	F_LYS_117	NZ	F_ASP_118	OD1	3.790
1FJ1	F_ARG_139	NH1	F_GLU_160	OE2	3.340
1FJ1	F_ARG_139	NH2	F_GLU_160	OE2	3.235
1FJ1	F_ARG_144	NH1	F_GLU_146	OE2	2.359
1FJ1	F_ARG_144	NH2	F_GLU_146	OE2	3.733
1FJ1	F_LYS_157	NZ	F_GLU_168	OE2	3.244
1FJ1	F_LYS_159	NZ	F_GLU_168	OE2	3.700
1FJ1	F_LYS_175	NZ	F_GLU_174	OE1	3.506
1FJ1	F_LYS_189	NZ	F_GLU_160	OE1	2.954
1FJ1	F_LYS_189	NZ	F_GLU_160	OE2	3.524
1FJ1	F_LYS_212	NZ	F_ASP_203	OD2	3.830
1FRG	L_LYS_24	NZ	L_ASP_76	OD2	3.234
1FRG	L_ARG_67	NH2	L_GLU_87	OE2	3.036
1FRG	L_ARG_67	NH2	L_ASP_88	OD1	2.765
1FRG	L_ARG_67	NH2	L_ASP_88	OD2	3.277
1FRG	L_LYS_109	NZ	L_ASP_171	OD1	2.782
1FRG	L_LYS_109	NZ	L_ASP_171	OD2	3.487
1FRG	L_LYS_113	NZ	L_GLU_17	OE2	3.158
1FRG	L_LYS_148	NZ	L_GLU_111	OE2	3.465
1FRG	L_LYS_155	NZ	L_GLU_201	OE1	3.359
1FRG	L_LYS_155	NZ	L_GLU_201	OE2	3.552
1FRG	L_ARG_161	NH2	L_GLU_191	OE1	3.188
1FRG	L_ARG_161	NH2	L_GLU_191	OE2	2.743
1FRG	L_LYS_175	NZ	L_ASP_176	OD2	3.335
1FRG	L_ARG_194	NH2	L_ASP_190	OD2	3.738
1FRG	L_LYS_205	NZ	L_ASP_116	OD1	2.961
1FRG	L_LYS_205	NZ	L_ASP_116	OD2	3.132
1FRG	L_LYS_213	NZ	H_ASP_354	OD1	3.324
1FRG	L_ARG_217	NH2	L_GLU_193	OE1	3.045
1FRG	H_ARG_255	NH1	H_GLU_263	OE1	2.874
1FRG	H_ARG_255	NH2	H_ASP_307	OD1	2.867
1FRG	H_LYS_282	NZ	H_ASP_279	OD1	3.750
1FRG	H_LYS_282	NZ	H_ASP_279	OD2	3.157
1FRG	H_ARG_284	NH1	H_ASP_307	OD1	3.863
1FRG	H_ARG_284	NH1	H_ASP_307	OD2	2.813
1FRG	H_ARG_284	NH2	H_ASP_307	OD1	2.826
1FRG	H_ARG_284	NH2	H_ASP_307	OD2	3.114
1FRG	H_LYS_304	NZ	H_GLU_306	OE2	3.614
1FRG	H_ARG_315	NH1	H_GLU_317	OE1	2.677
1FRG	H_ARG_315	NH1	H_GLU_317	OE2	3.312
1FRG	H_ARG_316	NH1	L_ASP_97	OD1	2.879
1FRG	H_ARG_316	NH2	L_ASP_97	OD1	3.078
1FRG	H_ARG_316	NH2	P_ASP_5	OD2	2.959
1FRG	H_LYS_322	NZ	L_GLU_61	OE1	2.861

1FRG	H.LYS_322	NZ	L_GLU_61	OE2	3.997
1FRG	H.LYS_432	NZ	L_GLU_129	OE1	3.086
1FRG	H.LYS_432	NZ	L_GLU_129	OE2	3.769
1FUJ	A_HIS_20	NE2	A_GLU_157	OE2	3.467
1FUJ	A_ARG_27	NH2	A_GLU_157	OE1	3.676
1FUJ	A_ARG_27	NH2	A_GLU_157	OE2	3.673
1FUJ	A_HIS_57	ND1	A_ASP_102	OD1	3.496
1FUJ	A_HIS_57	ND1	A_ASP_102	OD2	2.542
1FUJ	A_HIS_71	NE2	A_GLU_21	OE2	2.398
1FUJ	A_LYS_187	NZ	B_GLU_97	OE1	3.506
1FUJ	B_ARG_27	NH1	B_GLU_157	OE1	2.690
1FUJ	B_ARG_27	NH1	B_GLU_157	OE2	2.783
1FUJ	B_HIS_57	ND1	B_ASP_102	OD1	3.393
1FUJ	B_HIS_57	ND1	B_ASP_102	OD2	2.604
1FUJ	B_HIS_71	NE2	B_GLU_21	OE2	2.397
1FUJ	B_ARG_143	NH1	A_ASP_61	OD2	3.455
1FUJ	B_LYS_187	NZ	A_GLU_97	OE1	3.870
1FUJ	C_HIS_20	ND1	C_GLU_157	OE2	3.974
1FUJ	C_HIS_20	NE2	C_GLU_157	OE2	3.570
1FUJ	C_ARG_27	NH2	C_GLU_157	OE1	2.756
1FUJ	C_ARG_27	NH2	C_GLU_157	OE2	3.280
1FUJ	C_HIS_57	ND1	C_ASP_102	OD1	3.598
1FUJ	C_HIS_57	ND1	C_ASP_102	OD2	2.742
1FUJ	C_ARG_60	NH2	C_ASP_61	OD1	3.164
1FUJ	C_HIS_71	NE2	C_GLU_21	OE2	2.759
1FUJ	C_ARG_143	NH2	D_ASP_61	OD1	3.394
1FUJ	C_ARG_143	NH2	D_ASP_61	OD2	3.428
1FUJ	C_LYS_187	NZ	D_GLU_97	OE2	2.917
1FUJ	D_HIS_20	NE2	D_GLU_157	OE2	3.668
1FUJ	D_ARG_27	NH1	D_GLU_157	OE1	2.572
1FUJ	D_ARG_27	NH1	D_GLU_157	OE2	3.950
1FUJ	D_HIS_57	ND1	D_ASP_102	OD1	3.325
1FUJ	D_HIS_57	ND1	D_ASP_102	OD2	2.459
1FUJ	D_HIS_71	NE2	D_GLU_21	OE2	2.398
1FUJ	D_HIS_147	ND1	C_GLU_97	OE1	3.734
1FUJ	D_LYS_187	NZ	C_GLU_97	OE1	3.930
1FVC	A_ARG_24	NH1	A_ASP_70	OD1	3.629
1FVC	A_ARG_24	NH1	A_ASP_70	OD2	3.125
1FVC	A_ARG_24	NH2	A_ASP_70	OD2	3.258
1FVC	A_ARG_61	NH2	A_GLU_81	OE2	3.238
1FVC	A_ARG_61	NH2	A_ASP_82	OD1	2.827
1FVC	A_ARG_61	NH2	A_ASP_82	OD2	3.397
1FVC	A_LYS_107	NZ	A_ASP_17	OD2	3.723
1FVC	B_LYS_30	NZ	B_ASP_31	OD1	2.864
1FVC	B_ARG_38	NH1	B_ASP_90	OD1	3.106
1FVC	B_ARG_38	NH2	B_GLU_46	OE1	3.355
1FVC	B_ARG_38	NH2	B_ASP_90	OD1	3.972
1FVC	B_ARG_67	NH1	B_ASP_90	OD1	3.826
1FVC	B_ARG_67	NH1	B_ASP_90	OD2	2.865
1FVC	B_ARG_67	NH2	B_ASP_90	OD1	2.815
1FVC	B_ARG_67	NH2	B_ASP_90	OD2	3.370
1FVC	B_LYS_76	NZ	B_ASP_73	OD2	3.296
1FVC	B_ARG_98	NH1	B_ASP_108	OD1	3.172
1FVC	B_ARG_98	NH1	B_ASP_108	OD2	2.880
1FVC	C_ARG_61	NH1	C_GLU_81	OE2	3.955
1FVC	C_ARG_61	NH2	C_GLU_81	OE2	3.336
1FVC	C_ARG_61	NH2	C_ASP_82	OD1	2.944
1FVC	C_ARG_61	NH2	C_ASP_82	OD2	3.489

1FVC	C_ARG_66	NH2	C_ASP_28	OD1	3.198
1FVC	D_ARG_38	NH1	D_ASP_90	OD1	3.684
1FVC	D_ARG_38	NH2	D_GLU_46	OE1	3.562
1FVC	D_ARG_67	NH1	D_ASP_90	OD1	3.498
1FVC	D_ARG_67	NH1	D_ASP_90	OD2	2.863
1FVC	D_ARG_67	NH2	D_ASP_90	OD1	3.039
1FVC	D_ARG_67	NH2	D_ASP_90	OD2	3.182
1FVC	D_ARG_98	NH1	D_ASP_108	OD1	3.384
1FVC	D_ARG_98	NH1	D_ASP_108	OD2	2.939
1FVD	A_ARG_18	NH1	C_ASP_70	OD2	3.361
1FVD	A_ARG_24	NH2	A_ASP_70	OD1	3.049
1FVD	A_ARG_24	NH2	A_ASP_70	OD2	3.841
1FVD	A_ARG_61	NH2	A_GLU_81	OE2	3.219
1FVD	A_ARG_61	NH2	A_ASP_82	OD1	3.298
1FVD	A_ARG_61	NH2	A_ASP_82	OD2	3.528
1FVD	A_ARG_66	NH2	A_ASP_28	OD1	3.272
1FVD	A_LYS_103	NZ	A_GLU_165	OE2	2.750
1FVD	A_ARG_142	NH1	A_GLU_105	OE1	3.252
1FVD	A_ARG_142	NH1	A_GLU_105	OE2	3.136
1FVD	A_ARG_142	NH2	A_GLU_105	OE1	2.987
1FVD	A_ARG_142	NH2	A_GLU_105	OE2	3.986
1FVD	A_LYS_183	NZ	A_GLU_187	OE2	3.983
1FVD	A_LYS_188	NZ	A_ASP_185	OD1	3.689
1FVD	B_ARG_38	NH1	B_ASP_90	OD1	2.959
1FVD	B_ARG_38	NH2	B_GLU_46	OE1	3.651
1FVD	B_ARG_38	NH2	B_ASP_90	OD1	3.403
1FVD	B_LYS_65	NZ	B_ASP_62	OD1	3.297
1FVD	B_ARG_67	NH1	B_ASP_90	OD2	3.358
1FVD	B_ARG_67	NH2	B_ASP_90	OD1	3.444
1FVD	B_ARG_67	NH2	B_ASP_90	OD2	3.537
1FVD	B_LYS_76	NZ	B_ASP_73	OD2	3.292
1FVD	B_ARG_98	NH2	B_ASP_108	OD1	3.885
1FVD	B_ARG_98	NH2	B_ASP_108	OD2	2.828
1FVD	B_LYS_150	NZ	B_ASP_151	OD1	3.971
1FVD	B_LYS_150	NZ	B_ASP_151	OD2	3.685
1FVD	B_LYS_216	NZ	A_GLU_123	OE2	3.426
1FVD	C_ARG_18	NH1	A_ASP_70	OD2	3.065
1FVD	C_ARG_24	NH1	C_ASP_70	OD1	3.877
1FVD	C_ARG_24	NH2	C_ASP_70	OD1	3.499
1FVD	C_ARG_24	NH2	C_ASP_70	OD2	3.062
1FVD	C_ARG_61	NH2	C_GLU_81	OE2	3.791
1FVD	C_ARG_61	NH2	C_ASP_82	OD1	2.871
1FVD	C_ARG_61	NH2	C_ASP_82	OD2	3.205
1FVD	C_ARG_66	NH2	C_ASP_28	OD1	3.599
1FVD	C_LYS_103	NZ	C_GLU_165	OE1	3.456
1FVD	C_ARG_142	NH1	C_GLU_105	OE1	3.866
1FVD	D_ARG_38	NH1	D_ASP_90	OD1	2.804
1FVD	D_ARG_38	NH2	D_GLU_46	OE1	3.405
1FVD	D_ARG_38	NH2	D_ASP_90	OD1	3.854
1FVD	D_ARG_67	NH1	D_ASP_90	OD1	3.794
1FVD	D_ARG_67	NH1	D_ASP_90	OD2	2.754
1FVD	D_ARG_67	NH2	D_ASP_90	OD1	2.991
1FVD	D_ARG_67	NH2	D_ASP_90	OD2	3.196
1FVD	D_LYS_76	NZ	D_ASP_73	OD2	3.310
1FVD	D_ARG_87	NH1	D_GLU_89	OE1	3.906
1FVD	D_ARG_87	NH2	D_GLU_89	OE1	3.896
1FVD	D_ARG_87	NH2	D_ASP_90	OD1	3.754
1FVD	D_ARG_98	NH1	D_ASP_108	OD1	3.545

1FVD	D_ARG_98	NH1	D_ASP_108	OD2	3.091
1FVD	D_LYS_150	NZ	D_ASP_151	OD1	3.457
1FVD	D_LYS_150	NZ	D_ASP_151	OD2	3.794
1FVD	D_LYS_213	NZ	D_ASP_215	OD1	2.673
1FVD	D_LYS_216	NZ	C_GLU_123	OE1	2.737
1FVE	A_ARG_18	NH1	C_ASP_70	OD1	3.613
1FVE	A_ARG_18	NH1	C_ASP_70	OD2	3.316
1FVE	A_ARG_24	NH2	A_ASP_70	OD1	3.581
1FVE	A_ARG_24	NH2	A_ASP_70	OD2	3.679
1FVE	A_ARG_61	NH2	A_GLU_81	OE2	3.047
1FVE	A_ARG_61	NH2	A_ASP_82	OD1	3.215
1FVE	A_ARG_61	NH2	A_ASP_82	OD2	3.538
1FVE	A_ARG_66	NH2	A_ASP_28	OD1	3.900
1FVE	A_LYS_103	NZ	A_GLU_105	OE1	3.573
1FVE	A_LYS_103	NZ	A_GLU_105	OE2	3.185
1FVE	A_LYS_103	NZ	A_GLU_165	OE1	2.869
1FVE	A_LYS_103	NZ	A_GLU_165	OE2	3.988
1FVE	A_ARG_142	NH2	A_GLU_105	OE1	3.848
1FVE	A_ARG_142	NH2	A_GLU_105	OE2	3.667
1FVE	A_ARG_142	NH2	A_GLU_165	OE2	3.452
1FVE	A_LYS_149	NZ	A_GLU_195	OE1	2.902
1FVE	A_LYS_169	NZ	A_ASP_167	OD2	3.928
1FVE	A_LYS_169	NZ	A_ASP_170	OD2	3.977
1FVE	B_ARG_38	NH1	B_ASP_90	OD1	3.055
1FVE	B_ARG_38	NH2	B_GLU_46	OE2	3.767
1FVE	B_ARG_38	NH2	B_ASP_90	OD1	3.522
1FVE	B_ARG_67	NH1	B_ASP_90	OD2	3.077
1FVE	B_ARG_67	NH2	B_ASP_90	OD1	3.046
1FVE	B_ARG_67	NH2	B_ASP_90	OD2	3.273
1FVE	B_LYS_76	NZ	B_ASP_73	OD2	3.045
1FVE	B_ARG_87	NH1	B_GLU_89	OE2	3.292
1FVE	B_ARG_98	NH2	B_ASP_108	OD2	3.050
1FVE	B_LYS_150	NZ	B_ASP_151	OD1	3.911
1FVE	B_LYS_150	NZ	B_ASP_151	OD2	3.600
1FVE	B_LYS_216	NZ	A_GLU_123	OE2	3.328
1FVE	B_LYS_217	NZ	B_GLU_219	OE1	3.280
1FVE	C_ARG_61	NH2	C_GLU_81	OE2	3.092
1FVE	C_ARG_61	NH2	C_ASP_82	OD1	2.991
1FVE	C_ARG_61	NH2	C_ASP_82	OD2	3.500
1FVE	C_LYS_103	NZ	C_GLU_165	OE1	3.377
1FVE	C_LYS_103	NZ	C_GLU_165	OE2	3.755
1FVE	C_ARG_142	NH2	C_GLU_105	OE1	3.256
1FVE	C_HIS_189	ND1	C_ASP_151	OD2	3.275
1FVE	C_LYS_190	NZ	C_ASP_151	OD1	3.284
1FVE	C_LYS_190	NZ	C_ASP_151	OD2	3.663
1FVE	D_ARG_38	NH1	D_GLU_46	OE1	3.179
1FVE	D_ARG_38	NH1	D_GLU_46	OE2	3.488
1FVE	D_ARG_38	NH2	D_ASP_90	OD1	2.634
1FVE	D_ARG_67	NH1	D_ASP_90	OD1	3.960
1FVE	D_ARG_67	NH1	D_ASP_90	OD2	2.712
1FVE	D_ARG_67	NH2	D_ASP_90	OD1	2.924
1FVE	D_ARG_67	NH2	D_ASP_90	OD2	3.109
1FVE	D_LYS_76	NZ	D_ASP_73	OD2	3.266
1FVE	D_ARG_87	NH1	D_GLU_89	OE2	3.190
1FVE	D_ARG_87	NH2	D_ASP_90	OD1	3.371
1FVE	D_ARG_98	NH1	D_ASP_108	OD1	3.433
1FVE	D_ARG_98	NH1	D_ASP_108	OD2	2.999
1FVE	D_LYS_150	NZ	D_ASP_151	OD1	3.818

1FVE	D_LYS_150	NZ	D_ASP_151	OD2	3.688
1G6V	A_HIS_4	NE2	A_ASP_19	OD2	3.118
1G6V	A_HIS_15	NE2	A_GLU_14	OE1	3.258
1G6V	A_ARG_58	NH1	A_GLU_69	OE1	3.110
1G6V	A_ARG_58	NH1	A_GLU_69	OE2	2.848
1G6V	A_LYS_76	NZ	A_ASP_71	OD2	3.042
1G6V	A_ARG_89	NH2	A_ASP_75	OD1	3.650
1G6V	A_ARG_89	NH2	A_ASP_75	OD2	3.835
1G6V	A_HIS_96	ND1	A_GLU_106	OE2	3.452
1G6V	A_HIS_96	NE2	A_GLU_106	OE1	3.503
1G6V	A_HIS_96	NE2	A_GLU_106	OE2	3.870
1G6V	A_HIS_107	ND1	A_GLU_117	OE1	3.817
1G6V	A_HIS_107	ND1	A_GLU_117	OE2	3.100
1G6V	A_HIS_119	NE2	A_GLU_117	OE2	2.477
1G6V	A_LYS_127	NZ	A_ASP_139	OD1	3.129
1G6V	A_LYS_168	NZ	A_GLU_238	OE1	3.560
1G6V	A_ARG_182	NH1	A_ASP_180	OD1	3.589
1G6V	A_ARG_182	NH1	A_ASP_180	OD2	3.216
1G6V	A_ARG_182	NH2	A_ASP_180	OD2	2.890
1G6V	A_LYS_225	NZ	A_ASP_165	OD1	3.680
1G6V	A_LYS_225	NZ	A_ASP_165	OD2	3.357
1G6V	A_ARG_227	NH1	A_ASP_101	OD2	3.543
1G6V	A_ARG_227	NH2	A_ASP_101	OD2	3.620
1G6V	A_LYS_228	NZ	A_GLU_238	OE1	3.937
1G6V	A_LYS_257	NZ	A_ASP_41	OD1	3.993
1G6V	K_ARG_838	NH1	K_GLU_887	OE1	3.646
1G6V	K_ARG_838	NH1	K_ASP_888	OD1	3.042
1G6V	K_ARG_838	NH2	K_GLU_846	OE1	3.505
1G6V	K_ARG_838	NH2	K_GLU_846	OE2	3.350
1G6V	K_ARG_838	NH2	K_GLU_887	OE1	3.576
1G6V	K_ARG_838	NH2	K_GLU_887	OE2	3.967
1G6V	K_ARG_865	NH1	K_ASP_888	OD2	3.258
1G6V	K_ARG_865	NH2	K_ASP_888	OD1	2.941
1G6V	K_ARG_865	NH2	K_ASP_888	OD2	3.106
1G6V	K_LYS_885	NZ	K_GLU_887	OE2	3.937
1G6V	K_ARG_907	NH1	A_GLU_187	OE2	2.962
1G6V	K_ARG_909	NH1	A_GLU_187	OE1	3.909
1G6V	K_ARG_909	NH2	A_GLU_187	OE1	3.477
1G6V	K_ARG_909	NH2	K_ASP_912	OD1	3.915
1G7H	A_ARG_61	NH1	A_GLU_81	OE2	3.037
1G7H	A_ARG_61	NH1	A_ASP_82	OD1	3.527
1G7H	A_ARG_61	NH1	A_ASP_82	OD2	2.782
1G7H	A_ARG_96	NH1	B_GLU_98	OE1	2.788
1G7H	A_ARG_96	NH1	B_GLU_98	OE2	3.317
1G7H	A_ARG_96	NH2	B_GLU_98	OE1	3.736
1G7H	A_ARG_96	NH2	B_GLU_98	OE2	2.819
1G7H	A_LYS_107	NZ	A_GLU_17	OE1	3.055
1G7H	A_LYS_107	NZ	A_GLU_17	OE2	3.162
1G7H	B_ARG_38	NH1	B_GLU_46	OE1	3.731
1G7H	B_ARG_38	NH1	B_GLU_46	OE2	3.064
1G7H	B_ARG_38	NH1	B_ASP_89	OD1	3.653
1G7H	B_ARG_38	NH2	B_ASP_89	OD1	3.025
1G7H	B_ARG_66	NH1	B_ASP_89	OD1	2.763
1G7H	B_ARG_66	NH1	B_ASP_89	OD2	2.968
1G7H	B_ARG_66	NH2	B_ASP_89	OD1	3.934
1G7H	B_ARG_66	NH2	B_ASP_89	OD2	2.612
1G7H	B_LYS_75	NZ	B_ASP_72	OD1	2.977
1G7H	B_ARG_97	NH1	B_ASP_104	OD1	3.709

1G7H	B_ARG_97	NH1	B_ASP_104	OD2	2.680
1G7H	B_ARG_102	NH2	B_ASP_100	OD1	3.012
1G7H	C_LYS_1	NZ	C_GLU_7	OE1	3.565
1G7H	C_ARG_61	NH2	C_ASP_48	OD2	3.173
1G7H	C_ARG_125	NH1	C_ASP_119	OD2	2.772
1G7H	C_ARG_125	NH2	C_ASP_119	OD1	3.386
1G7H	C_ARG_125	NH2	C_ASP_119	OD2	3.194
1G7I	A_ARG_61	NH1	A_GLU_81	OE2	2.718
1G7I	A_ARG_61	NH1	A_ASP_82	OD1	3.562
1G7I	A_ARG_61	NH1	A_ASP_82	OD2	2.822
1G7I	A_ARG_96	NH1	B_GLU_98	OE1	2.881
1G7I	A_ARG_96	NH1	B_GLU_98	OE2	3.589
1G7I	A_ARG_96	NH2	B_GLU_98	OE1	3.599
1G7I	A_ARG_96	NH2	B_GLU_98	OE2	2.841
1G7I	A_LYS_107	NZ	A_GLU_17	OE1	2.870
1G7I	A_LYS_107	NZ	A_GLU_17	OE2	3.799
1G7I	B_ARG_38	NH1	B_GLU_46	OE2	3.033
1G7I	B_ARG_38	NH1	B_ASP_89	OD1	3.781
1G7I	B_ARG_38	NH2	B_ASP_89	OD1	3.005
1G7I	B_ARG_66	NH1	B_ASP_89	OD1	2.745
1G7I	B_ARG_66	NH1	B_ASP_89	OD2	3.417
1G7I	B_ARG_66	NH2	B_ASP_89	OD1	3.758
1G7I	B_ARG_66	NH2	B_ASP_89	OD2	2.954
1G7I	B_ARG_97	NH1	B_ASP_104	OD1	3.710
1G7I	B_ARG_97	NH1	B_ASP_104	OD2	2.883
1G7I	B_ARG_102	NH2	B_ASP_100	OD1	3.310
1G7I	C_LYS_1	NZ	C_GLU_7	OE1	3.016
1G7I	C_LYS_1	NZ	C_GLU_7	OE2	3.596
1G7I	C_ARG_61	NH2	C_ASP_48	OD1	3.373
1G7I	C_ARG_68	NH2	C_ASP_66	OD2	3.145
1G7I	C_ARG_125	NH1	C_ASP_119	OD2	2.952
1G7I	C_ARG_125	NH2	C_ASP_119	OD1	3.392
1G7I	C_ARG_125	NH2	C_ASP_119	OD2	2.970
1G7J	A_ARG_61	NH1	A_GLU_81	OE2	3.122
1G7J	A_ARG_61	NH1	A_ASP_82	OD1	3.459
1G7J	A_ARG_61	NH1	A_ASP_82	OD2	2.826
1G7J	A_ARG_96	NH1	B_GLU_98	OE1	2.834
1G7J	A_ARG_96	NH1	B_GLU_98	OE2	3.535
1G7J	A_ARG_96	NH2	B_GLU_98	OE1	3.524
1G7J	A_ARG_96	NH2	B_GLU_98	OE2	2.694
1G7J	A_LYS_107	NZ	A_GLU_17	OE1	3.323
1G7J	A_LYS_107	NZ	A_GLU_17	OE2	2.601
1G7J	B_ARG_38	NH1	B_GLU_46	OE1	3.932
1G7J	B_ARG_38	NH1	B_GLU_46	OE2	2.970
1G7J	B_ARG_38	NH1	B_ASP_89	OD1	3.769
1G7J	B_ARG_38	NH2	B_ASP_89	OD1	2.824
1G7J	B_ARG_66	NH1	B_ASP_89	OD1	2.871
1G7J	B_ARG_66	NH1	B_ASP_89	OD2	3.276
1G7J	B_ARG_66	NH2	B_ASP_89	OD1	3.824
1G7J	B_ARG_66	NH2	B_ASP_89	OD2	2.793
1G7J	B_HIS_86	NE2	B_ASP_88	OD1	3.358
1G7J	B_HIS_86	NE2	B_ASP_88	OD2	3.564
1G7J	B_ARG_97	NH1	B_ASP_104	OD1	3.791
1G7J	B_ARG_97	NH1	B_ASP_104	OD2	2.737
1G7J	B_ARG_102	NH2	B_ASP_100	OD1	3.301
1G7J	C_LYS_1	NZ	C_GLU_7	OE1	2.740
1G7J	C_ARG_61	NH1	C_ASP_48	OD2	3.771
1G7J	C_ARG_125	NH1	C_ASP_119	OD2	3.004

1G7J	C_ARG.125	NH2	C_ASP.119	OD1	3.354
1G7J	C_ARG.125	NH2	C_ASP.119	OD2	3.147
1G7L	A_ARG.61	NH1	A_GLU.81	OE2	3.595
1G7L	A_ARG.61	NH1	A_ASP.82	OD1	3.389
1G7L	A_ARG.61	NH1	A_ASP.82	OD2	2.780
1G7L	A_ARG.96	NH1	B_GLU.98	OE1	2.744
1G7L	A_ARG.96	NH1	B_GLU.98	OE2	3.483
1G7L	A_ARG.96	NH2	B_GLU.98	OE1	3.535
1G7L	A_ARG.96	NH2	B_GLU.98	OE2	2.761
1G7L	A_LYS.107	NZ	A_GLU.17	OE1	3.286
1G7L	A_LYS.107	NZ	A_GLU.17	OE2	2.822
1G7L	B_ARG.38	NH1	B_GLU.46	OE2	3.105
1G7L	B_ARG.38	NH1	B_ASP.89	OD1	3.832
1G7L	B_ARG.38	NH2	B_ASP.89	OD1	2.874
1G7L	B_ARG.66	NH1	B_ASP.89	OD1	3.004
1G7L	B_ARG.66	NH1	B_ASP.89	OD2	3.786
1G7L	B_ARG.66	NH2	B_ASP.89	OD1	3.392
1G7L	B_ARG.66	NH2	B_ASP.89	OD2	2.877
1G7L	B_ARG.97	NH1	B_ASP.104	OD1	3.584
1G7L	B_ARG.97	NH1	B_ASP.104	OD2	2.551
1G7L	B_ARG.102	NH2	B_ASP.100	OD1	3.204
1G7L	C_LYS.1	NZ	C_GLU.7	OE1	2.763
1G7L	C_HIS.15	NE2	C_ASP.87	OD2	3.997
1G7L	C_ARG.61	NH2	C_ASP.48	OD2	2.882
1G7L	C_ARG.125	NH1	C_ASP.119	OD2	2.762
1G7L	C_ARG.125	NH2	C_ASP.119	OD1	3.327
1G7L	C_ARG.125	NH2	C_ASP.119	OD2	2.838
1G7M	A_ARG.61	NH1	A_GLU.81	OE2	3.936
1G7M	A_ARG.61	NH1	A_ASP.82	OD1	3.601
1G7M	A_ARG.61	NH1	A_ASP.82	OD2	2.851
1G7M	A_ARG.96	NH1	B_GLU.98	OE1	2.792
1G7M	A_ARG.96	NH1	B_GLU.98	OE2	3.493
1G7M	A_ARG.96	NH2	B_GLU.98	OE1	3.544
1G7M	A_ARG.96	NH2	B_GLU.98	OE2	2.732
1G7M	B_ARG.38	NH1	B_GLU.46	OE1	3.743
1G7M	B_ARG.38	NH1	B_GLU.46	OE2	3.134
1G7M	B_ARG.38	NH1	B_ASP.89	OD1	3.885
1G7M	B_ARG.38	NH2	B_ASP.89	OD1	2.901
1G7M	B_ARG.66	NH1	B_ASP.89	OD1	3.117
1G7M	B_ARG.66	NH1	B_ASP.89	OD2	3.721
1G7M	B_ARG.66	NH2	B_ASP.89	OD1	3.761
1G7M	B_ARG.66	NH2	B_ASP.89	OD2	2.897
1G7M	B_LYS.75	NZ	B_ASP.72	OD1	3.993
1G7M	B_ARG.97	NH1	B_ASP.104	OD1	3.720
1G7M	B_ARG.97	NH1	B_ASP.104	OD2	2.732
1G7M	B_ARG.102	NH2	B_ASP.100	OD1	3.308
1G7M	C_LYS.1	NZ	C_GLU.7	OE1	2.835
1G7M	C_ARG.61	NH2	C_ASP.48	OD2	3.861
1G7M	C_ARG.125	NH1	C_ASP.119	OD2	2.991
1G7M	C_ARG.125	NH2	C_ASP.119	OD1	3.407
1G7M	C_ARG.125	NH2	C_ASP.119	OD2	3.048
1G8Q	A_LYS.121	NZ	A_ASP.122	OD1	2.599
1G8Q	A_LYS.121	NZ	A_ASP.122	OD2	3.460
1G8Q	A_LYS.124	NZ	A_ASP.195	OD1	3.016
1G8Q	A_LYS.124	NZ	A_ASP.195	OD2	3.072
1G8Q	A_LYS.187	NZ	A_ASP.155	OD2	2.795
1G8Q	A_HIS.191	NE2	A_ASP.128	OD1	3.354
1G8Q	A_HIS.191	NE2	A_ASP.128	OD2	2.859

1G8Q	A_LYS_193	NZ	A_ASP_155	OD1	3.991
1G8Q	B_LYS_224	NZ	B_ASP_295	OD1	2.542
1G8Q	B_LYS_224	NZ	B_ASP_295	OD2	3.203
1G8Q	B_HIS_291	NE2	B_ASP_228	OD1	2.670
1G8Q	B_HIS_291	NE2	B_ASP_228	OD2	3.342
1G8Q	B_LYS_293	NZ	B_GLU_288	OE2	2.739
1G9M	G_LYS_207	NZ	G_GLU_381	OE1	3.792
1G9M	G_LYS_207	NZ	G_GLU_381	OE2	2.500
1G9M	G_LYS_231	NZ	G_GLU_268	OE2	3.144
1G9M	G_HIS_249	NE2	G_GLU_482	OE1	3.558
1G9M	G_HIS_249	NE2	G_GLU_482	OE2	3.514
1G9M	G_LYS_337	NZ	G_GLU_293	OE2	3.954
1G9M	G_LYS_348	NZ	G_GLU_269	OE2	2.920
1G9M	G_LYS_348	NZ	G_GLU_351	OE2	3.765
1G9M	G_LYS_357	NZ	G_GLU_466	OE1	3.174
1G9M	G_ARG_419	NH1	H_GLU_103	OE2	3.773
1G9M	G_ARG_419	NH2	H_GLU_103	OE2	2.762
1G9M	G_ARG_419	NH2	H_GLU_108	OE2	3.794
1G9M	G_ARG_456	NH2	G_GLU_466	OE1	3.727
1G9M	G_ARG_456	NH2	G_GLU_466	OE2	3.003
1G9M	G_ARG_469	NH2	G_ASP_457	OD1	3.290
1G9M	G_ARG_476	NH1	G_ASP_474	OD1	2.906
1G9M	G_ARG_480	NH1	G_ASP_477	OD1	2.553
1G9M	G_LYS_487	NZ	G_GLU_91	OE1	3.951
1G9M	G_LYS_487	NZ	G_GLU_91	OE2	2.923
1G9M	C_LYS_8	NZ	C_GLU_119	OE1	2.848
1G9M	C_HIS_27	NE2	C_GLU_85	OE1	2.711
1G9M	C_LYS_29	NZ	G_ASP_279	OD2	3.077
1G9M	C_LYS_29	NZ	C_GLU_85	OE1	2.735
1G9M	C_LYS_29	NZ	C_GLU_85	OE2	3.809
1G9M	C_LYS_46	NZ	C_ASP_56	OD1	3.759
1G9M	C_ARG_54	NH1	C_ASP_78	OD1	3.768
1G9M	C_ARG_54	NH1	C_ASP_78	OD2	2.778
1G9M	C_ARG_54	NH2	C_ASP_78	OD1	2.931
1G9M	C_ARG_54	NH2	C_ASP_78	OD2	3.434
1G9M	C_ARG_59	NH1	G_ASP_368	OD1	3.576
1G9M	C_ARG_59	NH1	G_ASP_368	OD2	3.197
1G9M	C_ARG_59	NH2	G_ASP_368	OD1	2.550
1G9M	C_ARG_59	NH2	G_ASP_368	OD2	3.360
1G9M	C_ARG_134	NH2	C_ASP_153	OD1	3.987
1G9M	L_ARG_24	NH2	L_GLU_3	OE2	3.072
1G9M	L_ARG_61	NH2	L_GLU_81	OE2	3.403
1G9M	L_ARG_61	NH2	L_ASP_82	OD1	2.707
1G9M	L_ARG_61	NH2	L_ASP_82	OD2	3.381
1G9M	L_LYS_151	NZ	L_GLU_197	OE1	3.157
1G9M	L_LYS_151	NZ	L_GLU_197	OE2	3.538
1G9M	L_HIS_191	ND1	L_ASP_153	OD2	3.573
1G9M	H_LYS_12	NZ	H_GLU_10	OE1	3.811
1G9M	H_LYS_19	NZ	H_GLU_82	OE2	2.937
1G9M	H_ARG_31	NH2	H_GLU_103	OE1	3.557
1G9M	H_ARG_31	NH2	H_ASP_105	OD1	3.841
1G9M	H_ARG_31	NH2	H_ASP_105	OD2	3.073
1G9M	H_ARG_38	NH1	H_GLU_46	OE1	3.715
1G9M	H_ARG_38	NH1	H_GLU_46	OE2	2.917
1G9M	H_ARG_38	NH2	H_ASP_90	OD2	2.688
1G9M	H_ARG_50	NH2	H_GLU_101	OE2	2.484
1G9M	H_HIS_63	NE2	H_GLU_46	OE1	3.776
1G9M	H_HIS_63	NE2	H_GLU_46	OE2	2.782

1G9M	H_ARG_67	NH1	H_ASP_90	OD1	2.916
1G9M	H_ARG_67	NH1	H_ASP_90	OD2	3.928
1G9M	H_ARG_67	NH2	H_ASP_90	OD1	3.114
1G9M	H_ARG_67	NH2	H_ASP_90	OD2	2.646
1G9M	H_LYS_74	NZ	H_ASP_56	OD1	3.247
1G9M	H_LYS_74	NZ	H_ASP_56	OD2	3.751
1G9M	H_ARG_84	NH2	H_GLU_82	OE1	2.803
1G9M	H_ARG_110	NH2	H_GLU_108	OE1	3.721
1G9M	H_LYS_158	NZ	H_ASP_159	OD1	2.791
1G9M	H_LYS_158	NZ	H_ASP_159	OD2	2.929
1G9N	G_LYS_121	NZ	G_GLU_429	OE1	2.598
1G9N	G_LYS_121	NZ	G_GLU_429	OE2	3.835
1G9N	G_LYS_207	NZ	G_GLU_381	OE1	3.761
1G9N	G_LYS_207	NZ	G_GLU_381	OE2	3.069
1G9N	G_HIS_249	NE2	G_GLU_482	OE1	3.588
1G9N	G_LYS_282	NZ	G_GLU_275	OE1	3.728
1G9N	G_LYS_282	NZ	G_GLU_275	OE2	2.699
1G9N	G_LYS_348	NZ	G_GLU_269	OE2	3.322
1G9N	G_LYS_348	NZ	G_GLU_351	OE1	3.879
1G9N	G_LYS_348	NZ	G_GLU_351	OE2	3.198
1G9N	G_LYS_350	NZ	G_ASP_395	OD1	3.491
1G9N	G_LYS_357	NZ	G_GLU_466	OE1	3.697
1G9N	G_ARG_419	NH1	H_GLU_106	OE1	2.930
1G9N	G_ARG_419	NH1	H_GLU_106	OE2	3.665
1G9N	G_ARG_419	NH2	H_GLU_103	OE1	2.300
1G9N	G_ARG_419	NH2	H_GLU_106	OE2	3.990
1G9N	G_ARG_456	NH2	G_GLU_466	OE1	3.622
1G9N	G_ARG_456	NH2	G_GLU_466	OE2	3.509
1G9N	G_ARG_469	NH2	G_ASP_457	OD1	3.668
1G9N	G_ARG_476	NH1	G_ASP_474	OD1	3.685
1G9N	G_ARG_476	NH2	G_GLU_102	OE1	3.192
1G9N	G_ARG_476	NH2	G_GLU_102	OE2	2.740
1G9N	G_ARG_480	NH1	G_ASP_477	OD1	3.994
1G9N	G_LYS_487	NZ	G_GLU_91	OE2	3.841
1G9N	G_LYS_490	NZ	G_GLU_492	OE1	3.571
1G9N	C_LYS_29	NZ	C_GLU_85	OE1	3.106
1G9N	C_LYS_29	NZ	C_GLU_85	OE2	3.864
1G9N	C_LYS_35	NZ	G_ASP_457	OD2	3.608
1G9N	C_ARG_54	NH1	C_ASP_78	OD1	3.979
1G9N	C_ARG_54	NH1	C_ASP_78	OD2	2.754
1G9N	C_ARG_54	NH2	C_ASP_78	OD1	2.744
1G9N	C_ARG_54	NH2	C_ASP_78	OD2	3.015
1G9N	C_ARG_59	NH1	G_ASP_368	OD1	3.032
1G9N	C_ARG_59	NH1	G_ASP_368	OD2	3.045
1G9N	C_ARG_59	NH2	G_ASP_368	OD1	2.609
1G9N	C_ARG_59	NH2	G_ASP_368	OD2	3.355
1G9N	C_HIS_107	ND1	C_ASP_105	OD1	2.754
1G9N	C_HIS_107	ND1	C_ASP_105	OD2	3.107
1G9N	C_ARG_134	NH2	C_ASP_153	OD1	3.650
1G9N	C_LYS_136	NZ	C_GLU_150	OE2	3.852
1G9N	C_LYS_136	NZ	C_ASP_153	OD1	3.794
1G9N	C_LYS_136	NZ	C_ASP_153	OD2	2.773
1G9N	C_LYS_171	NZ	C_GLU_169	OE1	3.972
1G9N	C_LYS_171	NZ	C_GLU_169	OE2	2.770
1G9N	L_ARG_61	NH2	L_GLU_81	OE1	3.113
1G9N	L_ARG_61	NH2	L_ASP_82	OD1	3.659
1G9N	L_ARG_97	NH2	L_GLU_1	OE1	3.685
1G9N	L_ARG_97	NH2	L_GLU_1	OE2	2.961

1G9N	L_HIS_191	ND1	L_ASP_153	OD2	2.588
1G9N	L_HIS_191	NE2	L_ASP_187	OD2	2.897
1G9N	L_ARG_213	NH1	L_GLU_189	OE1	3.830
1G9N	H_ARG_31	NH2	H_ASP_105	OD1	3.178
1G9N	H_ARG_31	NH2	H_ASP_105	OD2	3.436
1G9N	H_ARG_38	NH1	H_GLU_46	OE1	2.711
1G9N	H_ARG_38	NH1	H_GLU_46	OE2	3.252
1G9N	H_ARG_38	NH2	H_ASP_90	OD2	2.680
1G9N	H_ARG_50	NH2	H_GLU_101	OE2	2.305
1G9N	H_ARG_67	NH1	H_ASP_90	OD1	3.457
1G9N	H_ARG_67	NH2	H_ASP_90	OD1	2.540
1G9N	H_ARG_67	NH2	H_ASP_90	OD2	2.635
1G9N	H_LYS_74	NZ	H_ASP_56	OD2	2.889
1G9N	H_ARG_84	NH2	H_GLU_82	OE1	3.161
1G9N	H_ARG_110	NH1	H_GLU_108	OE1	3.833
1G9N	H_ARG_110	NH2	H_GLU_108	OE1	3.692
1G9N	H_LYS_158	NZ	H_ASP_159	OD1	2.649
1G9N	H_LYS_158	NZ	H_ASP_159	OD2	3.459
1G9N	H_LYS_224	NZ	L_GLU_125	OE1	3.507
1G9N	H_LYS_224	NZ	L_GLU_125	OE2	3.538
1G9N	H_LYS_229	NZ	L_ASP_124	OD2	3.557
1GC1	G_LYS_207	NZ	G_GLU_381	OE1	3.546
1GC1	G_LYS_207	NZ	G_GLU_381	OE2	2.763
1GC1	G_LYS_231	NZ	G_GLU_268	OE1	2.870
1GC1	G_HIS_249	NE2	G_GLU_482	OE1	2.874
1GC1	G_LYS_282	NZ	G_ASP_279	OD2	2.766
1GC1	G_ARG_335	NH1	G_ASP_412	OD1	2.680
1GC1	G_ARG_335	NH1	G_ASP_412	OD2	3.973
1GC1	G_ARG_335	NH2	G_ASP_412	OD1	3.328
1GC1	G_LYS_337	NZ	G_GLU_293	OE1	2.668
1GC1	G_LYS_357	NZ	G_GLU_466	OE2	3.400
1GC1	G_ARG_419	NH1	H_GLU_106	OE1	2.761
1GC1	G_ARG_419	NH2	H_GLU_106	OE1	2.942
1GC1	G_ARG_419	NH2	H_GLU_108	OE1	3.887
1GC1	G_ARG_419	NH2	H_GLU_108	OE2	3.401
1GC1	G_ARG_456	NH2	G_GLU_466	OE1	2.736
1GC1	G_ARG_456	NH2	G_GLU_466	OE2	3.604
1GC1	G_ARG_469	NH2	G_ASP_457	OD1	3.571
1GC1	G_ARG_469	NH2	G_ASP_457	OD2	2.956
1GC1	G_ARG_476	NH1	G_ASP_474	OD1	3.210
1GC1	G_ARG_480	NH1	G_ASP_477	OD1	3.075
1GC1	C_LYS_1	NZ	C_GLU_92	OE1	2.611
1GC1	C_LYS_7	NZ	C_ASP_10	OD1	3.825
1GC1	C_LYS_7	NZ	C_ASP_10	OD2	2.811
1GC1	C_LYS_8	NZ	C_GLU_119	OE1	2.599
1GC1	C_HIS_27	ND1	C_GLU_85	OE1	2.734
1GC1	C_LYS_29	NZ	G_ASP_279	OD1	2.748
1GC1	C_LYS_29	NZ	C_GLU_85	OE1	2.817
1GC1	C_LYS_29	NZ	C_GLU_85	OE2	3.379
1GC1	C_LYS_46	NZ	C_ASP_56	OD2	2.852
1GC1	C_LYS_50	NZ	C_GLU_77	OE1	2.464
1GC1	C_LYS_50	NZ	C_GLU_77	OE2	3.327
1GC1	C_ARG_54	NH1	C_ASP_78	OD1	3.681
1GC1	C_ARG_54	NH1	C_ASP_78	OD2	2.523
1GC1	C_ARG_54	NH2	C_ASP_78	OD1	2.648
1GC1	C_ARG_54	NH2	C_ASP_78	OD2	3.132
1GC1	C_ARG_59	NH1	G_ASP_368	OD1	2.780
1GC1	C_ARG_59	NH1	G_ASP_368	OD2	3.645

1GC1	C_ARG_59	NH2	G_ASP_368	OD1	3.062
1GC1	C_ARG_59	NH2	G_ASP_368	OD2	2.481
1GC1	C_LYS_90	NZ	C_GLU_85	OE2	3.366
1GC1	C_ARG_134	NH2	C_ASP_153	OD1	3.312
1GC1	C_ARG_134	NH2	C_ASP_153	OD2	3.071
1GC1	C_LYS_167	NZ	C_GLU_169	OE1	3.179
1GC1	L_ARG_24	NH1	L_GLU_3	OE1	2.728
1GC1	L_ARG_24	NH2	L_GLU_3	OE1	3.024
1GC1	L_ARG_24	NH2	L_GLU_3	OE2	3.874
1GC1	L_ARG_61	NH1	L_GLU_81	OE2	3.374
1GC1	L_ARG_61	NH1	L_ASP_82	OD1	2.506
1GC1	L_ARG_61	NH1	L_ASP_82	OD2	2.919
1GC1	L_ARG_61	NH2	L_GLU_81	OE2	3.159
1GC1	L_LYS_128	NZ	L_ASP_124	OD1	2.735
1GC1	L_LYS_185	NZ	L_GLU_189	OE1	3.492
1GC1	L_LYS_185	NZ	L_GLU_189	OE2	3.997
1GC1	L_HIS_191	ND1	L_ASP_153	OD2	3.341
1GC1	L_HIS_191	NE2	L_ASP_187	OD1	2.956
1GC1	L_HIS_191	NE2	L_ASP_187	OD2	3.839
1GC1	H_LYS_12	NZ	H_GLU_10	OE1	2.918
1GC1	H_LYS_19	NZ	H_GLU_82	OE1	2.992
1GC1	H_ARG_31	NH1	H_GLU_106	OE2	2.532
1GC1	H_ARG_38	NH1	H_GLU_46	OE2	2.989
1GC1	H_ARG_38	NH1	H_ASP_90	OD1	3.814
1GC1	H_ARG_38	NH2	H_ASP_90	OD1	2.619
1GC1	H_ARG_50	NH2	H_GLU_101	OE2	2.957
1GC1	H_HIS_63	NE2	H_GLU_46	OE1	3.828
1GC1	H_HIS_63	NE2	H_GLU_46	OE2	2.878
1GC1	H_ARG_67	NH1	H_ASP_90	OD1	3.587
1GC1	H_ARG_67	NH1	H_ASP_90	OD2	2.706
1GC1	H_ARG_67	NH2	H_ASP_90	OD1	2.708
1GC1	H_ARG_67	NH2	H_ASP_90	OD2	3.261
1GC1	H_ARG_84	NH2	H_GLU_82	OE2	2.925
1GC1	H_LYS_158	NZ	H_ASP_159	OD1	2.936
1GC1	H_LYS_158	NZ	H_ASP_159	OD2	3.481
1GC1	H_LYS_224	NZ	L_GLU_125	OE1	2.581
1GC1	H_LYS_224	NZ	L_GLU_125	OE2	3.963
1GGB	L_LYS_39	NZ	L_ASP_81	OD1	3.691
1GGB	L_ARG_61	NH2	L_ASP_82	OD1	3.069
1GGB	L_ARG_61	NH2	L_ASP_82	OD2	3.921
1GGB	L_LYS_149	NZ	L_GLU_195	OE1	3.055
1GGB	L_LYS_149	NZ	L_GLU_195	OE2	3.602
1GGB	L_ARG_155	NH1	L_GLU_185	OE1	3.649
1GGB	L_ARG_155	NH2	L_GLU_185	OE1	2.814
1GGB	L_HIS_189	ND1	L_ASP_151	OD2	3.149
1GGB	L_ARG_211	NH2	L_GLU_187	OE2	3.888
1GGB	H_ARG_38	NH1	H_ASP_86	OD1	3.008
1GGB	H_ARG_38	NH2	H_GLU_46	OE1	3.247
1GGB	H_ARG_38	NH2	H_ASP_86	OD1	3.365
1GGB	H_ARG_58	NH1	L_ASP_94	OD1	3.623
1GGB	H_ARG_58	NH2	L_ASP_94	OD1	2.873
1GGB	H_ARG_66	NH1	H_ASP_83	OD1	3.682
1GGB	H_ARG_66	NH1	H_ASP_86	OD1	3.167
1GGB	H_ARG_66	NH1	H_ASP_86	OD2	3.895
1GGB	H_ARG_66	NH2	H_ASP_83	OD1	3.328
1GGB	H_ARG_66	NH2	H_ASP_86	OD1	3.262
1GGB	H_ARG_66	NH2	H_ASP_86	OD2	2.539
1GGB	H_LYS_221	NZ	L_GLU_123	OE1	2.690

1GGB	H.LYS_221	NZ	L.GLU_123	OE2	3.205
1GGB	H.LYS_222	NZ	H.GLU_226	OE2	3.191
1GGC	L.ARG_61	NH1	L.GLU_79	OE2	3.692
1GGC	L.ARG_61	NH1	L.ASP_82	OD1	3.115
1GGC	L.ARG_61	NH1	L.ASP_82	OD2	2.752
1GGC	L.ARG_61	NH2	L.GLU_79	OE1	3.661
1GGC	L.ARG_61	NH2	L.GLU_79	OE2	3.675
1GGC	L.ARG_61	NH2	L.ASP_82	OD1	3.438
1GGC	L.LYS_149	NZ	L.GLU_195	OE2	3.691
1GGC	L.ARG_155	NH2	L.GLU_185	OE2	2.870
1GGC	L.LYS_183	NZ	L.GLU_187	OE1	3.373
1GGC	L.LYS_183	NZ	L.GLU_187	OE2	3.046
1GGC	L.LYS_199	NZ	L.ASP_110	OD1	3.437
1GGC	L.LYS_199	NZ	L.ASP_110	OD2	2.666
1GGC	H.ARG_38	NH1	H.ASP_86	OD1	3.206
1GGC	H.ARG_38	NH2	H.GLU_46	OE1	3.183
1GGC	H.ARG_38	NH2	H.ASP_86	OD1	3.921
1GGC	H.ARG_58	NH2	L.ASP_94	OD1	3.221
1GGC	H.ARG_66	NH1	H.ASP_86	OD1	3.876
1GGC	H.ARG_66	NH2	H.ASP_86	OD1	2.865
1GGC	H.ARG_66	NH2	H.ASP_86	OD2	2.907
1GGC	H.LYS_218	NZ	H.ASP_220	OD1	3.849
1GGC	H.LYS_221	NZ	L.GLU_123	OE1	2.942
1GGI	L.LYS_39	NZ	L.ASP_81	OD2	3.200
1GGI	L.ARG_61	NH2	L.ASP_82	OD1	3.494
1GGI	L.ARG_61	NH2	L.ASP_82	OD2	3.194
1GGI	L.LYS_142	NZ	L.GLU_105	OE1	3.057
1GGI	L.LYS_149	NZ	L.GLU_195	OE1	3.085
1GGI	L.LYS_149	NZ	L.GLU_195	OE2	2.765
1GGI	L.ARG_155	NH2	L.GLU_185	OE1	2.906
1GGI	L.ARG_155	NH2	L.GLU_185	OE2	3.331
1GGI	L.LYS_183	NZ	L.GLU_187	OE1	2.955
1GGI	L.LYS_183	NZ	L.GLU_187	OE2	3.308
1GGI	H.ARG_38	NH1	H.GLU_46	OE1	2.813
1GGI	H.ARG_38	NH2	H.ASP_86	OD1	2.641
1GGI	H.HIS_50	NE2	H.GLU_95	OE1	3.102
1GGI	H.ARG_58	NH1	H.ASP_56	OD1	3.338
1GGI	H.ARG_58	NH1	H.ASP_56	OD2	3.571
1GGI	H.ARG_58	NH2	L.ASP_94	OD2	3.749
1GGI	H.ARG_66	NH1	H.ASP_86	OD1	3.518
1GGI	H.ARG_66	NH1	H.ASP_86	OD2	3.473
1GGI	H.ARG_66	NH2	H.ASP_86	OD1	3.109
1GGI	H.ARG_66	NH2	H.ASP_86	OD2	2.810
1GGI	H.LYS_221	NZ	L.GLU_123	OE2	3.900
1GGI	P.LYS_312	NZ	H.ASP_54	OD1	2.914
1GGI	P.LYS_312	NZ	H.ASP_54	OD2	3.188
1GGI	P.LYS_312	NZ	H.ASP_56	OD1	2.830
1GGI	P.LYS_312	NZ	H.ASP_56	OD2	3.728
1GGI	M.ARG_24	NH1	M.ASP_70	OD1	2.935
1GGI	M.ARG_24	NH1	M.ASP_70	OD2	3.520
1GGI	M.ARG_61	NH1	M.ASP_82	OD1	2.935
1GGI	M.ARG_61	NH1	M.ASP_82	OD2	2.776
1GGI	M.ARG_61	NH2	M.ASP_82	OD1	3.065
1GGI	M.LYS_142	NZ	M.GLU_105	OE1	3.711
1GGI	M.LYS_142	NZ	M.GLU_105	OE2	2.989
1GGI	M.ARG_155	NH1	M.GLU_185	OE2	3.862
1GGI	M.ARG_155	NH2	M.GLU_185	OE1	2.644
1GGI	M.ARG_155	NH2	M.GLU_185	OE2	3.063

1GGI	M.LYS_183	NZ	M_GLU_187	OE1	3.427
1GGI	M.LYS_183	NZ	M_GLU_187	OE2	3.848
1GGI	M.HIS_189	ND1	M.ASP_151	OD2	3.374
1GGI	M.LYS_199	NZ	M.ASP_110	OD1	3.172
1GGI	M.LYS_199	NZ	M.ASP_110	OD2	3.326
1GGI	J.ARG_38	NH1	J.ASP_86	OD1	2.716
1GGI	J.ARG_38	NH2	J.ASP_86	OD1	3.121
1GGI	J.HIS_50	NE2	J_GLU_95	OE1	2.732
1GGI	J.ARG_58	NH1	J.ASP_56	OD2	2.535
1GGI	J.ARG_58	NH2	M.ASP_94	OD2	3.966
1GGI	J.ARG_66	NH1	J.ASP_86	OD1	3.627
1GGI	J.ARG_66	NH2	J.ASP_86	OD1	3.502
1GGI	J.ARG_66	NH2	J.ASP_86	OD2	2.746
1GGI	J.HIS_172	NE2	M.ASP_167	OD2	3.287
1GGI	J.LYS_221	NZ	M_GLU_123	OE1	3.528
1GGI	J.LYS_221	NZ	M_GLU_123	OE2	3.781
1GGI	Q.LYS_312	NZ	J.ASP_54	OD1	3.299
1GGI	Q.LYS_312	NZ	J.ASP_54	OD2	2.967
1GGI	Q.LYS_312	NZ	J.ASP_56	OD1	3.964
1GGI	Q.LYS_312	NZ	J.ASP_56	OD2	3.120
1GPO	L.LYS_54	NZ	H.ASP_101	OD1	2.768
1GPO	L.LYS_54	NZ	H.ASP_101	OD2	3.525
1GPO	L.ARG_66	NH2	L_GLU_86	OE2	3.655
1GPO	L.ARG_66	NH2	L.ASP_87	OD1	2.651
1GPO	L.ARG_66	NH2	L.ASP_87	OD2	3.453
1GPO	L.LYS_147	NZ	L.ASP_148	OD1	3.371
1GPO	L.LYS_152	NZ	L_GLU_159	OE2	2.707
1GPO	L.LYS_154	NZ	L_GLU_200	OE2	3.219
1GPO	L.ARG_160	NH1	L_GLU_190	OE2	3.906
1GPO	L.ARG_193	NH2	L.ASP_189	OD1	3.683
1GPO	L.ARG_193	NH2	L.ASP_189	OD2	2.940
1GPO	L.HIS_194	NE2	L_GLU_190	OE2	3.215
1GPO	L.LYS_204	NZ	L.ASP_115	OD1	3.884
1GPO	L.LYS_204	NZ	L.ASP_115	OD2	2.884
1GPO	H.ARG_38	NH1	H.ASP_89	OD1	3.025
1GPO	H.ARG_38	NH2	H_GLU_46	OE1	2.836
1GPO	H.ARG_38	NH2	H.ASP_89	OD1	3.663
1GPO	H.ARG_66	NH1	H.ASP_89	OD1	3.859
1GPO	H.ARG_66	NH1	H.ASP_89	OD2	3.366
1GPO	H.ARG_66	NH2	H.ASP_89	OD1	3.032
1GPO	H.ARG_66	NH2	H.ASP_89	OD2	3.658
1GPO	H.LYS_208	NZ	L_GLU_128	OE2	3.848
1GPO	M.ARG_24	NH1	M.ASP_75	OD1	3.059
1GPO	M.LYS_44	NZ	M_GLU_86	OE1	3.993
1GPO	M.LYS_54	NZ	L.ASP_101	OD1	3.704
1GPO	M.ARG_66	NH2	M_GLU_86	OE2	3.739
1GPO	M.ARG_66	NH2	M.ASP_87	OD1	2.836
1GPO	M.ARG_66	NH2	M.ASP_87	OD2	3.679
1GPO	M.LYS_108	NZ	M_GLU_110	OE1	2.976
1GPO	M.LYS_108	NZ	M_GLU_110	OE2	3.953
1GPO	M.LYS_154	NZ	M_GLU_200	OE1	3.791
1GPO	M.LYS_154	NZ	M_GLU_200	OE2	3.297
1GPO	M.HIS_194	ND1	M.ASP_156	OD2	3.167
1GPO	M.HIS_194	NE2	M_GLU_190	OE2	3.816
1GPO	L.ARG_38	NH1	L.ASP_89	OD1	2.915
1GPO	L.ARG_38	NH2	L_GLU_46	OE1	3.130
1GPO	L.ARG_38	NH2	L_GLU_46	OE2	3.937
1GPO	L.ARG_38	NH2	L.ASP_89	OD1	3.560

1GPO	L_ARG.66	NH1	L_ASP.89	OD1	3.810
1GPO	L_ARG.66	NH1	L_ASP.89	OD2	3.000
1GPO	L_ARG.66	NH2	L_ASP.89	OD1	3.073
1GPO	L_ARG.66	NH2	L_ASP.89	OD2	3.643
1GPO	L_LYS.208	NZ	M_GLU.128	OE2	3.367
1HCV	A_ARG.38	NH1	A_ASP.86	OD1	2.863
1HCV	A_ARG.38	NH2	A_GLU.46	OE2	3.573
1HCV	A_ARG.38	NH2	A_ASP.86	OD1	3.820
1HCV	A_ARG.66	NH2	A_ASP.86	OD1	3.579
1HCV	A_ARG.66	NH2	A_ASP.86	OD2	2.581
1HEZ	A_ARG.24	NH1	C_ASP.70	OD1	3.567
1HEZ	A_ARG.24	NH1	C_ASP.70	OD2	3.209
1HEZ	A_ARG.24	NH2	A_ASP.70	OD1	3.267
1HEZ	A_ARG.24	NH2	A_ASP.70	OD2	3.046
1HEZ	A_ARG.61	NH2	A_GLU.81	OE1	2.928
1HEZ	A_ARG.61	NH2	A_ASP.82	OD1	2.762
1HEZ	A_ARG.61	NH2	A_ASP.82	OD2	3.538
1HEZ	A_LYS.103	NZ	A_GLU.165	OE2	3.539
1HEZ	A_LYS.145	NZ	A_GLU.143	OE1	3.528
1HEZ	A_LYS.145	NZ	A_GLU.143	OE2	2.903
1HEZ	A_LYS.149	NZ	A_GLU.195	OE1	2.775
1HEZ	B_ARG.38	NH1	B_ASP.90	OD1	3.118
1HEZ	B_ARG.38	NH2	B_GLU.46	OE1	2.692
1HEZ	B_ARG.38	NH2	B_GLU.46	OE2	3.888
1HEZ	B_ARG.67	NH1	B_ASP.90	OD1	3.575
1HEZ	B_ARG.67	NH1	B_ASP.90	OD2	3.985
1HEZ	B_ARG.67	NH2	B_ASP.90	OD1	3.231
1HEZ	B_ARG.67	NH2	B_ASP.90	OD2	2.419
1HEZ	B_LYS.98	NZ	B_ASP.109	OD1	3.274
1HEZ	B_LYS.98	NZ	B_ASP.109	OD2	3.047
1HEZ	B_HIS.205	NE2	B_ASP.220	OD2	3.169
1HEZ	B_LYS.219	NZ	A_GLU.123	OE1	2.923
1HEZ	B_LYS.219	NZ	A_GLU.123	OE2	2.722
1HEZ	C_ARG.24	NH1	E_ASP.855	OD1	2.717
1HEZ	C_ARG.61	NH2	C_GLU.81	OE1	3.663
1HEZ	C_ARG.61	NH2	C_GLU.81	OE2	3.949
1HEZ	C_ARG.61	NH2	C_ASP.82	OD1	2.937
1HEZ	C_ARG.61	NH2	C_ASP.82	OD2	3.542
1HEZ	C_LYS.103	NZ	C_GLU.165	OE1	2.714
1HEZ	C_LYS.107	NZ	E_ASP.867	OD1	2.620
1HEZ	C_LYS.149	NZ	C_GLU.195	OE2	3.147
1HEZ	C_LYS.169	NZ	C_ASP.167	OD1	3.018
1HEZ	C_LYS.169	NZ	C_ASP.167	OD2	3.798
1HEZ	C_LYS.183	NZ	C_GLU.187	OE1	3.073
1HEZ	C_LYS.183	NZ	C_GLU.187	OE2	3.001
1HEZ	C_LYS.190	NZ	C_GLU.213	OE1	3.539
1HEZ	D_ARG.38	NH1	D_ASP.90	OD1	2.991
1HEZ	D_ARG.38	NH2	D_GLU.46	OE1	3.960
1HEZ	D_ARG.38	NH2	D_GLU.46	OE2	3.492
1HEZ	D_ARG.38	NH2	D_ASP.90	OD1	3.798
1HEZ	D_ARG.67	NH1	D_ASP.90	OD1	3.763
1HEZ	D_ARG.67	NH1	D_ASP.90	OD2	2.714
1HEZ	D_ARG.67	NH2	D_ASP.90	OD1	2.942
1HEZ	D_ARG.67	NH2	D_ASP.90	OD2	3.444
1HEZ	D_LYS.76	NZ	D_ASP.73	OD1	3.956
1HEZ	D_LYS.76	NZ	D_ASP.73	OD2	3.200
1HEZ	D_LYS.98	NZ	D_ASP.109	OD1	2.982
1HEZ	D_LYS.98	NZ	D_ASP.109	OD2	3.292

1HEZ	D_LYS_163	NZ	D_ASP_169	OD1	2.707
1HEZ	D_LYS_163	NZ	D_ASP_169	OD2	2.741
1HEZ	D_HIS_205	NE2	D_ASP_220	OD1	3.150
1HEZ	D_HIS_205	NE2	D_ASP_220	OD2	3.664
1HEZ	E_ARG_852	NH1	E_GLU_849	OE1	2.953
1HEZ	E_ARG_852	NH1	E_GLU_849	OE2	2.803
1HEZ	E_ARG_852	NH2	E_GLU_849	OE2	3.099
1HEZ	E_HIS_874	NE2	E_GLU_869	OE2	3.386
1HGD	A_LYS_27	NZ	B_GLU_97	OE1	2.787
1HGD	A_LYS_27	NZ	B_GLU_97	OE2	2.801
1HGD	A_LYS_50	NZ	A_ASP_275	OD1	3.503
1HGD	A_LYS_50	NZ	A_ASP_275	OD2	2.699
1HGD	A_ARG_57	NH2	A_GLU_82	OE1	2.541
1HGD	A_ARG_57	NH2	A_GLU_82	OE2	3.602
1HGD	A_HIS_75	ND1	A_ASP_73	OD1	2.825
1HGD	A_HIS_75	ND1	A_ASP_73	OD2	3.404
1HGD	A_HIS_75	NE2	A_ASP_63	OD1	3.503
1HGD	A_ARG_90	NH2	A_ASP_60	OD1	3.606
1HGD	A_ARG_90	NH2	A_ASP_60	OD2	2.804
1HGD	A_ARG_109	NH1	A_GLU_89	OE1	2.520
1HGD	A_ARG_109	NH1	A_GLU_89	OE2	3.261
1HGD	A_ARG_109	NH2	B_GLU_67	OE1	3.474
1HGD	A_ARG_109	NH2	B_GLU_67	OE2	2.826
1HGD	A_ARG_141	NH2	A_ASP_77	OD1	2.863
1HGD	A_ARG_141	NH2	A_ASP_77	OD2	2.743
1HGD	A_LYS_176	NZ	A_GLU_123	OE2	2.689
1HGD	A_HIS_183	NE2	A_GLU_190	OE2	3.734
1HGD	A_LYS_238	NZ	F_GLU_72	OE1	2.925
1HGD	A_LYS_238	NZ	F_GLU_72	OE2	2.815
1HGD	A_ARG_261	NH1	A_GLU_119	OE2	2.647
1HGD	A_ARG_261	NH2	A_GLU_119	OE1	2.879
1HGD	A_ARG_261	NH2	A_GLU_119	OE2	2.926
1HGD	A_LYS_264	NZ	A_ASP_85	OD1	3.573
1HGD	A_LYS_264	NZ	A_ASP_85	OD2	2.845
1HGD	A_ARG_269	NH1	B_GLU_67	OE1	2.758
1HGD	A_ARG_269	NH2	B_GLU_67	OE1	3.754
1HGD	A_LYS_292	NZ	A_ASP_291	OD1	2.852
1HGD	A_LYS_292	NZ	A_ASP_291	OD2	2.779
1HGD	A_LYS_299	NZ	B_GLU_69	OE2	2.769
1HGD	A_LYS_310	NZ	B_ASP_86	OD1	2.861
1HGD	A_LYS_310	NZ	B_ASP_90	OD1	2.569
1HGD	A_LYS_315	NZ	A_GLU_41	OE1	2.760
1HGD	A_LYS_326	NZ	A_GLU_325	OE1	3.012
1HGD	A_LYS_326	NZ	B_GLU_15	OE1	3.037
1HGD	A_LYS_326	NZ	B_GLU_15	OE2	2.743
1HGD	B_ARG_25	NH1	A_GLU_325	OE2	3.743
1HGD	B_ARG_25	NH2	A_GLU_325	OE2	3.016
1HGD	B_LYS_51	NZ	B_GLU_103	OE1	2.725
1HGD	B_ARG_54	NH1	B_GLU_57	OE1	2.860
1HGD	B_ARG_54	NH1	B_GLU_57	OE2	2.845
1HGD	B_ARG_54	NH1	F_GLU_97	OE2	3.275
1HGD	B_ARG_54	NH2	F_GLU_97	OE2	2.774
1HGD	B_LYS_58	NZ	B_GLU_61	OE2	2.905
1HGD	B_LYS_62	NZ	F_ASP_86	OD1	2.852
1HGD	B_LYS_62	NZ	F_ASP_86	OD2	2.612
1HGD	B_LYS_62	NZ	F_ASP_90	OD1	3.620
1HGD	B_LYS_62	NZ	F_ASP_90	OD2	2.727
1HGD	B_LYS_68	NZ	B_GLU_85	OE1	3.140

1HGD	B_LYS_68	NZ	B_GLU_85	OE2	2.759
1HGD	B_ARG_76	NH1	D_GLU_74	OE1	3.558
1HGD	B_ARG_76	NH1	D_GLU_74	OE2	2.838
1HGD	B_ARG_76	NH2	D_GLU_74	OE1	2.751
1HGD	B_ARG_76	NH2	D_GLU_74	OE2	3.529
1HGD	B_ARG_76	NH2	D_GLU_81	OE1	2.707
1HGD	B_ARG_76	NH2	D_GLU_81	OE2	3.498
1HGD	B_LYS_117	NZ	B_GLU_114	OE1	2.958
1HGD	B_LYS_117	NZ	B_GLU_114	OE2	2.520
1HGD	B_ARG_123	NH1	B_GLU_120	OE1	2.589
1HGD	B_ARG_123	NH1	B_GLU_120	OE2	2.787
1HGD	B_ARG_123	NH2	F_GLU_132	OE1	3.169
1HGD	B_ARG_124	NH1	B_GLU_120	OE1	3.722
1HGD	B_ARG_124	NH2	F_GLU_132	OE1	3.011
1HGD	B_ARG_124	NH2	F_GLU_132	OE2	3.294
1HGD	B_ARG_127	NH1	F_GLU_131	OE1	2.471
1HGD	B_LYS_143	NZ	B_ASP_145	OD2	2.849
1HGD	B_ARG_153	NH1	B_GLU_150	OE1	2.627
1HGD	B_HIS_159	NE2	B_ASP_160	OD2	3.135
1HGD	B_ARG_163	NH2	F_GLU_131	OE1	2.583
1HGD	B_ARG_163	NH2	F_GLU_131	OE2	2.596
1HGD	B_ARG_170	NH1	B_GLU_131	OE2	2.779
1HGD	B_ARG_170	NH1	D_GLU_128	OE1	3.354
1HGD	B_ARG_170	NH1	D_GLU_128	OE2	3.628
1HGD	B_ARG_170	NH2	B_GLU_128	OE2	2.668
1HGD	B_LYS_174	NZ	D_ASP_164	OD1	2.787
1HGD	B_LYS_174	NZ	D_ASP_164	OD2	2.517
1HGD	C_LYS_27	NZ	D_GLU_97	OE1	2.760
1HGD	C_LYS_27	NZ	D_GLU_97	OE2	2.799
1HGD	C_LYS_50	NZ	C_ASP_275	OD1	3.482
1HGD	C_LYS_50	NZ	C_ASP_275	OD2	2.664
1HGD	C_ARG_57	NH2	C_GLU_82	OE1	2.562
1HGD	C_ARG_57	NH2	C_GLU_82	OE2	3.993
1HGD	C_HIS_75	ND1	C_ASP_73	OD1	2.767
1HGD	C_HIS_75	ND1	C_ASP_73	OD2	3.384
1HGD	C_HIS_75	NE2	C_ASP_63	OD1	3.497
1HGD	C_ARG_90	NH2	C_ASP_60	OD1	3.613
1HGD	C_ARG_90	NH2	C_ASP_60	OD2	2.775
1HGD	C_ARG_109	NH1	C_GLU_89	OE1	2.543
1HGD	C_ARG_109	NH1	C_GLU_89	OE2	3.286
1HGD	C_ARG_109	NH2	D_GLU_67	OE1	3.480
1HGD	C_ARG_109	NH2	D_GLU_67	OE2	2.867
1HGD	C_ARG_141	NH2	C_ASP_77	OD1	2.873
1HGD	C_ARG_141	NH2	C_ASP_77	OD2	2.747
1HGD	C_LYS_176	NZ	C_GLU_123	OE2	2.693
1HGD	C_HIS_183	NE2	C_GLU_190	OE2	3.721
1HGD	C_LYS_238	NZ	B_GLU_72	OE1	2.801
1HGD	C_LYS_238	NZ	B_GLU_72	OE2	2.746
1HGD	C_ARG_261	NH1	C_GLU_119	OE2	2.657
1HGD	C_ARG_261	NH2	C_GLU_119	OE1	2.896
1HGD	C_ARG_261	NH2	C_GLU_119	OE2	2.924
1HGD	C_LYS_264	NZ	C_ASP_85	OD1	3.582
1HGD	C_LYS_264	NZ	C_ASP_85	OD2	2.818
1HGD	C_ARG_269	NH1	D_GLU_67	OE1	2.720
1HGD	C_ARG_269	NH2	D_GLU_67	OE1	3.733
1HGD	C_LYS_292	NZ	C_ASP_291	OD1	2.883
1HGD	C_LYS_292	NZ	C_ASP_291	OD2	2.789
1HGD	C_LYS_299	NZ	D_GLU_69	OE2	2.796

1HGD	C_LYS_310	NZ	D_ASP_86	OD1	2.878
1HGD	C_LYS_310	NZ	D_ASP_90	OD1	2.526
1HGD	C_LYS_315	NZ	C_GLU_41	OE1	2.785
1HGD	C_LYS_326	NZ	D_GLU_15	OE1	2.784
1HGD	C_LYS_326	NZ	D_GLU_15	OE2	3.881
1HGD	D_LYS_51	NZ	D_GLU_103	OE1	2.736
1HGD	D_ARG_54	NH1	B_GLU_97	OE2	3.293
1HGD	D_ARG_54	NH1	D_GLU_57	OE1	2.846
1HGD	D_ARG_54	NH1	D_GLU_57	OE2	2.834
1HGD	D_ARG_54	NH2	B_GLU_97	OE2	2.793
1HGD	D_LYS_58	NZ	D_GLU_61	OE2	2.900
1HGD	D_LYS_62	NZ	B_ASP_86	OD1	2.884
1HGD	D_LYS_62	NZ	B_ASP_86	OD2	2.567
1HGD	D_LYS_62	NZ	B_ASP_90	OD1	3.576
1HGD	D_LYS_62	NZ	B_ASP_90	OD2	2.617
1HGD	D_LYS_68	NZ	D_GLU_85	OE1	3.140
1HGD	D_LYS_68	NZ	D_GLU_85	OE2	2.777
1HGD	D_ARG_76	NH1	F_GLU_74	OE1	3.379
1HGD	D_ARG_76	NH1	F_GLU_74	OE2	2.785
1HGD	D_ARG_76	NH2	F_GLU_74	OE1	2.687
1HGD	D_ARG_76	NH2	F_GLU_74	OE2	3.593
1HGD	D_ARG_76	NH2	F_GLU_81	OE1	2.649
1HGD	D_ARG_76	NH2	F_GLU_81	OE2	3.537
1HGD	D_LYS_117	NZ	D_GLU_114	OE1	3.015
1HGD	D_LYS_117	NZ	D_GLU_114	OE2	2.569
1HGD	D_ARG_123	NH1	D_GLU_120	OE1	2.582
1HGD	D_ARG_123	NH1	D_GLU_120	OE2	2.804
1HGD	D_ARG_123	NH2	B_GLU_132	OE1	3.120
1HGD	D_ARG_124	NH1	D_GLU_120	OE1	3.720
1HGD	D_ARG_124	NH2	B_GLU_132	OE1	2.998
1HGD	D_ARG_124	NH2	B_GLU_132	OE2	3.261
1HGD	D_ARG_127	NH1	B_GLU_131	OE1	2.513
1HGD	D_LYS_143	NZ	D_ASP_145	OD2	2.863
1HGD	D_ARG_153	NH1	D_GLU_150	OE1	2.616
1HGD	D_HIS_159	NE2	D_ASP_160	OD2	3.164
1HGD	D_ARG_163	NH2	B_GLU_131	OE1	2.583
1HGD	D_ARG_163	NH2	B_GLU_131	OE2	2.616
1HGD	D_ARG_170	NH1	D_GLU_131	OE2	2.771
1HGD	D_ARG_170	NH1	F_GLU_128	OE1	3.487
1HGD	D_ARG_170	NH1	F_GLU_128	OE2	3.741
1HGD	D_ARG_170	NH2	D_GLU_128	OE2	2.697
1HGD	D_LYS_174	NZ	F_ASP_164	OD1	2.806
1HGD	D_LYS_174	NZ	F_ASP_164	OD2	2.686
1HGD	E_LYS_27	NZ	F_GLU_97	OE1	2.794
1HGD	E_LYS_27	NZ	F_GLU_97	OE2	2.792
1HGD	E_LYS_50	NZ	E_ASP_275	OD1	3.496
1HGD	E_LYS_50	NZ	E_ASP_275	OD2	2.695
1HGD	E_ARG_57	NH2	E_GLU_82	OE1	2.588
1HGD	E_HIS_75	ND1	E_ASP_73	OD1	2.791
1HGD	E_HIS_75	ND1	E_ASP_73	OD2	3.377
1HGD	E_HIS_75	NE2	E_ASP_63	OD1	3.540
1HGD	E_ARG_90	NH2	E_ASP_60	OD1	3.606
1HGD	E_ARG_90	NH2	E_ASP_60	OD2	2.820
1HGD	E_ARG_109	NH1	E_GLU_89	OE1	2.520
1HGD	E_ARG_109	NH1	E_GLU_89	OE2	3.279
1HGD	E_ARG_109	NH2	F_GLU_67	OE1	3.474
1HGD	E_ARG_109	NH2	F_GLU_67	OE2	2.818
1HGD	E_ARG_141	NH2	E_ASP_77	OD1	2.875

1HGD	E_ARG_141	NH2	E_ASP_77	OD2	2.746
1HGD	E_LYS_176	NZ	E_GLU_123	OE2	2.694
1HGD	E_HIS_183	NE2	E_GLU_190	OE2	3.738
1HGD	E_LYS_238	NZ	D_GLU_72	OE1	2.872
1HGD	E_LYS_238	NZ	D_GLU_72	OE2	2.843
1HGD	E_ARG_261	NH1	E_GLU_119	OE2	2.644
1HGD	E_ARG_261	NH2	E_GLU_119	OE1	2.878
1HGD	E_ARG_261	NH2	E_GLU_119	OE2	2.908
1HGD	E_LYS_264	NZ	E_ASP_85	OD1	3.622
1HGD	E_LYS_264	NZ	E_ASP_85	OD2	2.868
1HGD	E_ARG_269	NH1	F_GLU_67	OE1	2.732
1HGD	E_ARG_269	NH2	F_GLU_67	OE1	3.760
1HGD	E_LYS_292	NZ	E_ASP_291	OD1	2.887
1HGD	E_LYS_292	NZ	E_ASP_291	OD2	2.826
1HGD	E_LYS_299	NZ	F_GLU_69	OE2	2.767
1HGD	E_LYS_310	NZ	F_ASP_86	OD1	2.884
1HGD	E_LYS_310	NZ	F_ASP_90	OD1	2.533
1HGD	E_LYS_315	NZ	E_GLU_41	OE1	2.761
1HGD	E_LYS_326	NZ	F_GLU_15	OE1	2.967
1HGD	E_LYS_326	NZ	F_GLU_15	OE2	3.203
1HGD	F_LYS_51	NZ	F_GLU_103	OE1	2.718
1HGD	F_ARG_54	NH1	D_GLU_97	OE2	3.306
1HGD	F_ARG_54	NH1	F_GLU_57	OE1	2.855
1HGD	F_ARG_54	NH1	F_GLU_57	OE2	2.837
1HGD	F_ARG_54	NH2	D_GLU_97	OE2	2.719
1HGD	F_LYS_58	NZ	F_GLU_61	OE2	2.922
1HGD	F_LYS_62	NZ	D_ASP_86	OD1	2.854
1HGD	F_LYS_62	NZ	D_ASP_86	OD2	2.590
1HGD	F_LYS_62	NZ	D_ASP_90	OD1	3.656
1HGD	F_LYS_62	NZ	D_ASP_90	OD2	2.713
1HGD	F_HIS_64	NE2	D_ASP_79	OD2	3.996
1HGD	F_LYS_68	NZ	F_GLU_85	OE1	3.116
1HGD	F_LYS_68	NZ	F_GLU_85	OE2	2.719
1HGD	F_ARG_76	NH1	B_GLU_74	OE1	3.419
1HGD	F_ARG_76	NH1	B_GLU_74	OE2	2.766
1HGD	F_ARG_76	NH2	B_GLU_74	OE1	2.711
1HGD	F_ARG_76	NH2	B_GLU_74	OE2	3.568
1HGD	F_ARG_76	NH2	B_GLU_81	OE1	2.637
1HGD	F_ARG_76	NH2	B_GLU_81	OE2	3.557
1HGD	F_LYS_117	NZ	F_GLU_114	OE1	3.015
1HGD	F_LYS_117	NZ	F_GLU_114	OE2	2.552
1HGD	F_ARG_123	NH1	F_GLU_120	OE1	2.598
1HGD	F_ARG_123	NH1	F_GLU_120	OE2	2.770
1HGD	F_ARG_123	NH2	D_GLU_132	OE1	3.156
1HGD	F_ARG_124	NH1	F_GLU_120	OE1	3.728
1HGD	F_ARG_124	NH2	D_GLU_132	OE1	3.098
1HGD	F_ARG_124	NH2	D_GLU_132	OE2	3.292
1HGD	F_ARG_127	NH1	D_GLU_131	OE1	2.558
1HGD	F_LYS_143	NZ	F_ASP_145	OD2	2.843
1HGD	F_ARG_153	NH1	F_GLU_150	OE2	2.541
1HGD	F_HIS_159	NE2	F_ASP_160	OD2	3.168
1HGD	F_ARG_163	NH2	D_GLU_131	OE1	2.583
1HGD	F_ARG_163	NH2	D_GLU_131	OE2	2.699
1HGD	F_ARG_170	NH1	B_GLU_128	OE1	3.398
1HGD	F_ARG_170	NH1	B_GLU_128	OE2	3.736
1HGD	F_ARG_170	NH1	F_GLU_131	OE2	2.763
1HGD	F_ARG_170	NH2	F_GLU_128	OE2	2.704
1HGD	F_LYS_174	NZ	B_ASP_164	OD1	2.545

1HGD	F_LYS_174	NZ	B_ASP_164	OD2	2.838
1HGE	A_LYS_27	NZ	B_GLU_97	OE1	2.881
1HGE	A_LYS_27	NZ	B_GLU_97	OE2	2.803
1HGE	A_LYS_50	NZ	A_ASP_275	OD1	3.562
1HGE	A_LYS_50	NZ	A_ASP_275	OD2	2.748
1HGE	A_ARG_57	NH2	A_GLU_82	OE1	2.500
1HGE	A_ARG_57	NH2	A_GLU_82	OE2	3.546
1HGE	A_HIS_75	ND1	A_ASP_73	OD1	2.802
1HGE	A_HIS_75	ND1	A_ASP_73	OD2	3.532
1HGE	A_HIS_75	NE2	A_ASP_63	OD1	3.437
1HGE	A_ARG_90	NH2	A_ASP_60	OD1	3.553
1HGE	A_ARG_90	NH2	A_ASP_60	OD2	2.793
1HGE	A_ARG_109	NH1	A_GLU_89	OE1	2.487
1HGE	A_ARG_109	NH1	A_GLU_89	OE2	3.213
1HGE	A_ARG_109	NH2	B_GLU_67	OE1	3.666
1HGE	A_ARG_109	NH2	B_GLU_67	OE2	2.737
1HGE	A_ARG_141	NH2	A_ASP_77	OD1	2.893
1HGE	A_ARG_141	NH2	A_ASP_77	OD2	2.750
1HGE	A_LYS_176	NZ	A_GLU_123	OE2	2.715
1HGE	A_HIS_183	NE2	A_GLU_190	OE2	3.843
1HGE	A_LYS_238	NZ	F_GLU_72	OE1	2.915
1HGE	A_LYS_238	NZ	F_GLU_72	OE2	2.732
1HGE	A_ARG_261	NH1	A_GLU_119	OE2	2.640
1HGE	A_ARG_261	NH2	A_GLU_119	OE1	2.839
1HGE	A_ARG_261	NH2	A_GLU_119	OE2	2.928
1HGE	A_LYS_264	NZ	A_ASP_85	OD1	3.662
1HGE	A_LYS_264	NZ	A_ASP_85	OD2	2.767
1HGE	A_ARG_269	NH1	B_GLU_67	OE1	2.727
1HGE	A_ARG_269	NH2	B_GLU_67	OE1	3.813
1HGE	A_LYS_292	NZ	A_ASP_291	OD1	2.918
1HGE	A_LYS_292	NZ	A_ASP_291	OD2	2.823
1HGE	A_LYS_299	NZ	B_GLU_69	OE2	2.765
1HGE	A_LYS_310	NZ	B_ASP_86	OD1	2.860
1HGE	A_LYS_310	NZ	B_ASP_90	OD1	2.586
1HGE	A_LYS_310	NZ	B_ASP_90	OD2	3.982
1HGE	A_LYS_315	NZ	A_GLU_41	OE1	2.816
1HGE	A_LYS_326	NZ	A_GLU_325	OE1	2.847
1HGE	A_LYS_326	NZ	B_GLU_15	OE1	3.112
1HGE	A_LYS_326	NZ	B_GLU_15	OE2	2.788
1HGE	B_ARG_25	NH1	A_GLU_325	OE2	3.901
1HGE	B_ARG_25	NH2	A_GLU_325	OE2	3.058
1HGE	B_LYS_51	NZ	B_GLU_103	OE1	2.764
1HGE	B_ARG_54	NH1	B_GLU_57	OE1	2.831
1HGE	B_ARG_54	NH1	B_GLU_57	OE2	2.867
1HGE	B_ARG_54	NH1	F_GLU_97	OE2	3.352
1HGE	B_ARG_54	NH2	F_GLU_97	OE2	2.840
1HGE	B_LYS_58	NZ	B_GLU_61	OE2	3.128
1HGE	B_LYS_62	NZ	F_ASP_86	OD1	2.965
1HGE	B_LYS_62	NZ	F_ASP_86	OD2	2.602
1HGE	B_LYS_62	NZ	F_ASP_90	OD1	3.562
1HGE	B_LYS_62	NZ	F_ASP_90	OD2	2.691
1HGE	B_LYS_68	NZ	B_GLU_85	OE1	3.200
1HGE	B_LYS_68	NZ	B_GLU_85	OE2	2.780
1HGE	B_ARG_76	NH1	D_GLU_74	OE1	3.487
1HGE	B_ARG_76	NH1	D_GLU_74	OE2	2.838
1HGE	B_ARG_76	NH2	D_GLU_74	OE1	2.788
1HGE	B_ARG_76	NH2	D_GLU_74	OE2	3.585
1HGE	B_ARG_76	NH2	D_GLU_81	OE1	2.698

1HGE	B_ARG_76	NH2	D_GLU_81	OE2	3.486
1HGE	B_LYS_117	NZ	B_GLU_114	OE1	3.021
1HGE	B_LYS_117	NZ	B_GLU_114	OE2	2.593
1HGE	B_ARG_123	NH1	B_GLU_120	OE1	2.560
1HGE	B_ARG_123	NH1	B_GLU_120	OE2	2.842
1HGE	B_ARG_123	NH2	F_GLU_132	OE1	3.159
1HGE	B_ARG_124	NH1	B_GLU_120	OE1	3.659
1HGE	B_ARG_124	NH2	F_GLU_132	OE1	3.028
1HGE	B_ARG_124	NH2	F_GLU_132	OE2	3.444
1HGE	B_ARG_127	NH1	F_GLU_131	OE1	2.492
1HGE	B_LYS_143	NZ	B_ASP_145	OD2	2.791
1HGE	B_ARG_153	NH1	B_GLU_150	OE1	2.552
1HGE	B_HIS_159	NE2	B_ASP_160	OD2	2.984
1HGE	B_ARG_163	NH2	F_GLU_131	OE1	2.609
1HGE	B_ARG_163	NH2	F_GLU_131	OE2	2.622
1HGE	B_ARG_170	NH1	B_GLU_131	OE2	2.795
1HGE	B_ARG_170	NH1	D_GLU_128	OE1	3.351
1HGE	B_ARG_170	NH1	D_GLU_128	OE2	3.595
1HGE	B_ARG_170	NH2	B_GLU_128	OE2	2.691
1HGE	B_LYS_174	NZ	D_ASP_164	OD1	2.542
1HGE	B_LYS_174	NZ	D_ASP_164	OD2	2.784
1HGE	C_LYS_27	NZ	D_GLU_97	OE1	2.850
1HGE	C_LYS_27	NZ	D_GLU_97	OE2	2.792
1HGE	C_LYS_50	NZ	C_ASP_275	OD1	3.553
1HGE	C_LYS_50	NZ	C_ASP_275	OD2	2.700
1HGE	C_ARG_57	NH2	C_GLU_82	OE1	2.538
1HGE	C_ARG_57	NH2	C_GLU_82	OE2	3.923
1HGE	C_HIS_75	ND1	C_ASP_73	OD1	2.756
1HGE	C_HIS_75	ND1	C_ASP_73	OD2	3.513
1HGE	C_HIS_75	NE2	C_ASP_63	OD1	3.447
1HGE	C_ARG_90	NH2	C_ASP_60	OD1	3.557
1HGE	C_ARG_90	NH2	C_ASP_60	OD2	2.770
1HGE	C_ARG_109	NH1	C_GLU_89	OE1	2.521
1HGE	C_ARG_109	NH1	C_GLU_89	OE2	3.282
1HGE	C_ARG_109	NH2	D_GLU_67	OE1	3.673
1HGE	C_ARG_109	NH2	D_GLU_67	OE2	2.784
1HGE	C_ARG_141	NH2	C_ASP_77	OD1	2.880
1HGE	C_ARG_141	NH2	C_ASP_77	OD2	2.743
1HGE	C_LYS_176	NZ	C_GLU_123	OE2	2.713
1HGE	C_HIS_183	NE2	C_GLU_190	OE2	3.847
1HGE	C_LYS_238	NZ	B_GLU_72	OE1	2.779
1HGE	C_LYS_238	NZ	B_GLU_72	OE2	2.668
1HGE	C_ARG_261	NH1	C_GLU_119	OE2	2.652
1HGE	C_ARG_261	NH2	C_GLU_119	OE1	2.839
1HGE	C_ARG_261	NH2	C_GLU_119	OE2	2.930
1HGE	C_LYS_264	NZ	C_ASP_85	OD1	3.674
1HGE	C_LYS_264	NZ	C_ASP_85	OD2	2.771
1HGE	C_ARG_269	NH1	D_GLU_67	OE1	2.720
1HGE	C_ARG_269	NH2	D_GLU_67	OE1	3.811
1HGE	C_LYS_292	NZ	C_ASP_291	OD1	2.950
1HGE	C_LYS_292	NZ	C_ASP_291	OD2	2.836
1HGE	C_LYS_299	NZ	D_GLU_69	OE2	2.808
1HGE	C_LYS_310	NZ	D_ASP_86	OD1	2.890
1HGE	C_LYS_310	NZ	D_ASP_90	OD1	2.566
1HGE	C_LYS_310	NZ	D_ASP_90	OD2	3.955
1HGE	C_LYS_315	NZ	C_GLU_41	OE1	2.819
1HGE	C_LYS_326	NZ	D_GLU_15	OE1	2.739
1HGE	C_LYS_326	NZ	D_GLU_15	OE2	3.731

1HGE	D_LYS_51	NZ	D_GLU_103	OE1	2.765
1HGE	D_ARG_54	NH1	B_GLU_97	OE2	3.383
1HGE	D_ARG_54	NH1	D_GLU_57	OE1	2.823
1HGE	D_ARG_54	NH1	D_GLU_57	OE2	2.877
1HGE	D_ARG_54	NH2	B_GLU_97	OE2	2.866
1HGE	D_LYS_58	NZ	D_GLU_61	OE2	3.115
1HGE	D_LYS_62	NZ	B_ASP_86	OD1	3.023
1HGE	D_LYS_62	NZ	B_ASP_86	OD2	2.550
1HGE	D_LYS_62	NZ	B_ASP_90	OD1	3.565
1HGE	D_LYS_62	NZ	B_ASP_90	OD2	2.627
1HGE	D_LYS_68	NZ	D_GLU_85	OE1	3.196
1HGE	D_LYS_68	NZ	D_GLU_85	OE2	2.796
1HGE	D_ARG_76	NH1	F_GLU_74	OE1	3.355
1HGE	D_ARG_76	NH1	F_GLU_74	OE2	2.783
1HGE	D_ARG_76	NH2	F_GLU_74	OE1	2.745
1HGE	D_ARG_76	NH2	F_GLU_74	OE2	3.636
1HGE	D_ARG_76	NH2	F_GLU_81	OE1	2.634
1HGE	D_ARG_76	NH2	F_GLU_81	OE2	3.497
1HGE	D_LYS_117	NZ	D_GLU_114	OE1	3.039
1HGE	D_LYS_117	NZ	D_GLU_114	OE2	2.617
1HGE	D_ARG_123	NH1	D_GLU_120	OE1	2.560
1HGE	D_ARG_123	NH1	D_GLU_120	OE2	2.826
1HGE	D_ARG_123	NH2	B_GLU_132	OE1	3.118
1HGE	D_ARG_124	NH1	D_GLU_120	OE1	3.700
1HGE	D_ARG_124	NH2	B_GLU_132	OE1	3.002
1HGE	D_ARG_124	NH2	B_GLU_132	OE2	3.417
1HGE	D_ARG_127	NH1	B_GLU_131	OE1	2.524
1HGE	D_LYS_143	NZ	D_ASP_145	OD2	2.817
1HGE	D_ARG_153	NH1	D_GLU_150	OE2	2.568
1HGE	D_HIS_159	NE2	D_ASP_160	OD2	3.004
1HGE	D_ARG_163	NH2	B_GLU_131	OE1	2.587
1HGE	D_ARG_163	NH2	B_GLU_131	OE2	2.600
1HGE	D_ARG_170	NH1	D_GLU_131	OE2	2.790
1HGE	D_ARG_170	NH1	F_GLU_128	OE1	3.477
1HGE	D_ARG_170	NH1	F_GLU_128	OE2	3.701
1HGE	D_ARG_170	NH2	D_GLU_128	OE2	2.719
1HGE	D_LYS_174	NZ	F_ASP_164	OD1	2.678
1HGE	D_LYS_174	NZ	F_ASP_164	OD2	2.785
1HGE	E_LYS_27	NZ	F_GLU_97	OE1	2.844
1HGE	E_LYS_27	NZ	F_GLU_97	OE2	2.791
1HGE	E_LYS_50	NZ	E_ASP_275	OD1	3.556
1HGE	E_LYS_50	NZ	E_ASP_275	OD2	2.730
1HGE	E_ARG_57	NH2	E_GLU_82	OE1	2.607
1HGE	E_ARG_57	NH2	E_GLU_82	OE2	3.970
1HGE	E_HIS_75	ND1	E_ASP_73	OD1	2.770
1HGE	E_HIS_75	ND1	E_ASP_73	OD2	3.474
1HGE	E_HIS_75	NE2	E_ASP_63	OD1	3.473
1HGE	E_ARG_90	NH2	E_ASP_60	OD1	3.571
1HGE	E_ARG_90	NH2	E_ASP_60	OD2	2.802
1HGE	E_ARG_109	NH1	E_GLU_89	OE1	2.498
1HGE	E_ARG_109	NH1	E_GLU_89	OE2	3.250
1HGE	E_ARG_109	NH2	F_GLU_67	OE1	3.658
1HGE	E_ARG_109	NH2	F_GLU_67	OE2	2.776
1HGE	E_ARG_141	NH2	E_ASP_77	OD1	2.913
1HGE	E_ARG_141	NH2	E_ASP_77	OD2	2.749
1HGE	E_LYS_176	NZ	E_GLU_123	OE2	2.730
1HGE	E_HIS_183	NE2	E_GLU_190	OE2	3.836
1HGE	E_LYS_238	NZ	D_GLU_72	OE1	2.851

1HGE	E_LYS_238	NZ	D_GLU_72	OE2	2.740
1HGE	E_ARG_261	NH1	E_GLU_119	OE2	2.647
1HGE	E_ARG_261	NH2	E_GLU_119	OE1	2.833
1HGE	E_ARG_261	NH2	E_GLU_119	OE2	2.933
1HGE	E_LYS_264	NZ	E_ASP_85	OD1	3.706
1HGE	E_LYS_264	NZ	E_ASP_85	OD2	2.812
1HGE	E_ARG_269	NH1	F_GLU_67	OE1	2.696
1HGE	E_ARG_269	NH2	F_GLU_67	OE1	3.784
1HGE	E_LYS_292	NZ	E_ASP_291	OD1	2.975
1HGE	E_LYS_292	NZ	E_ASP_291	OD2	2.845
1HGE	E_LYS_299	NZ	F_GLU_69	OE2	2.768
1HGE	E_LYS_310	NZ	F_ASP_86	OD1	2.863
1HGE	E_LYS_310	NZ	F_ASP_90	OD1	2.577
1HGE	E_LYS_310	NZ	F_ASP_90	OD2	3.952
1HGE	E_LYS_315	NZ	E_GLU_41	OE1	2.801
1HGE	E_LYS_326	NZ	F_GLU_15	OE1	2.987
1HGE	E_LYS_326	NZ	F_GLU_15	OE2	3.095
1HGE	F_LYS_51	NZ	F_GLU_103	OE1	2.773
1HGE	F_ARG_54	NH1	D_GLU_97	OE2	3.384
1HGE	F_ARG_54	NH1	F_GLU_57	OE1	2.822
1HGE	F_ARG_54	NH1	F_GLU_57	OE2	2.866
1HGE	F_ARG_54	NH2	D_GLU_97	OE2	2.800
1HGE	F_LYS_58	NZ	F_GLU_61	OE2	3.128
1HGE	F_LYS_62	NZ	D_ASP_86	OD1	2.945
1HGE	F_LYS_62	NZ	D_ASP_86	OD2	2.535
1HGE	F_LYS_62	NZ	D_ASP_90	OD1	3.592
1HGE	F_LYS_62	NZ	D_ASP_90	OD2	2.671
1HGE	F_LYS_68	NZ	F_GLU_85	OE1	3.151
1HGE	F_LYS_68	NZ	F_GLU_85	OE2	2.745
1HGE	F_ARG_76	NH1	B_GLU_74	OE1	3.326
1HGE	F_ARG_76	NH1	B_GLU_74	OE2	2.732
1HGE	F_ARG_76	NH2	B_GLU_74	OE1	2.705
1HGE	F_ARG_76	NH2	B_GLU_74	OE2	3.590
1HGE	F_ARG_76	NH2	B_GLU_81	OE1	2.650
1HGE	F_ARG_76	NH2	B_GLU_81	OE2	3.592
1HGE	F_LYS_117	NZ	F_GLU_114	OE1	3.064
1HGE	F_LYS_117	NZ	F_GLU_114	OE2	2.613
1HGE	F_ARG_123	NH1	F_GLU_120	OE1	2.576
1HGE	F_ARG_123	NH1	F_GLU_120	OE2	2.810
1HGE	F_ARG_123	NH2	D_GLU_132	OE1	3.161
1HGE	F_ARG_124	NH1	F_GLU_120	OE1	3.667
1HGE	F_ARG_124	NH2	D_GLU_132	OE1	3.085
1HGE	F_ARG_124	NH2	D_GLU_132	OE2	3.468
1HGE	F_ARG_127	NH1	D_GLU_131	OE1	2.578
1HGE	F_LYS_143	NZ	F_ASP_145	OD2	2.798
1HGE	F_ARG_153	NH1	F_GLU_150	OE2	2.492
1HGE	F_HIS_159	NE2	F_ASP_160	OD2	3.030
1HGE	F_ARG_163	NH2	D_GLU_131	OE1	2.628
1HGE	F_ARG_163	NH2	D_GLU_131	OE2	2.698
1HGE	F_ARG_170	NH1	B_GLU_128	OE1	3.389
1HGE	F_ARG_170	NH1	B_GLU_128	OE2	3.679
1HGE	F_ARG_170	NH1	F_GLU_131	OE2	2.783
1HGE	F_ARG_170	NH2	F_GLU_128	OE2	2.721
1HGE	F_LYS_174	NZ	B_ASP_164	OD1	2.537
1HGE	F_LYS_174	NZ	B_ASP_164	OD2	2.796
1HGF	A_LYS_27	NZ	B_GLU_97	OE1	2.809
1HGF	A_LYS_27	NZ	B_GLU_97	OE2	2.791
1HGF	A_LYS_50	NZ	A_ASP_275	OD2	2.912

1HGF	A_ARG.57	NH2	A_GLU.82	OE1	2.650
1HGF	A_ARG.57	NH2	A_GLU.82	OE2	3.590
1HGF	A_HIS.75	ND1	A_ASP.73	OD1	2.838
1HGF	A_HIS.75	ND1	A_ASP.73	OD2	3.347
1HGF	A_HIS.75	NE2	A_ASP.63	OD1	3.455
1HGF	A_ARG.90	NH2	A_ASP.60	OD1	3.473
1HGF	A_ARG.90	NH2	A_ASP.60	OD2	2.841
1HGF	A_ARG.109	NH1	A_GLU.89	OE1	2.536
1HGF	A_ARG.109	NH1	A_GLU.89	OE2	2.889
1HGF	A_ARG.109	NH2	B_GLU.67	OE1	3.699
1HGF	A_ARG.109	NH2	B_GLU.67	OE2	2.917
1HGF	A_ARG.141	NH2	A_ASP.77	OD1	2.837
1HGF	A_ARG.141	NH2	A_ASP.77	OD2	2.783
1HGF	A_LYS.176	NZ	A_GLU.123	OE2	2.716
1HGF	A_LYS.176	NZ	A_ASP.172	OD1	3.709
1HGF	A_HIS.183	NE2	A_GLU.190	OE2	3.660
1HGF	A_LYS.238	NZ	F_GLU.72	OE1	2.852
1HGF	A_LYS.238	NZ	F_GLU.72	OE2	2.778
1HGF	A_ARG.261	NH1	A_GLU.119	OE1	3.779
1HGF	A_ARG.261	NH1	A_GLU.119	OE2	2.603
1HGF	A_ARG.261	NH2	A_GLU.119	OE1	2.742
1HGF	A_ARG.261	NH2	A_GLU.119	OE2	3.168
1HGF	A_LYS.264	NZ	A_ASP.85	OD2	3.310
1HGF	A_ARG.269	NH1	B_GLU.67	OE1	2.939
1HGF	A_LYS.292	NZ	A_ASP.291	OD1	2.863
1HGF	A_LYS.292	NZ	A_ASP.291	OD2	3.511
1HGF	A_LYS.299	NZ	B_GLU.69	OE2	3.681
1HGF	A_LYS.310	NZ	B_ASP.86	OD1	2.820
1HGF	A_LYS.310	NZ	B_ASP.90	OD1	2.555
1HGF	A_LYS.310	NZ	B_ASP.90	OD2	3.978
1HGF	A_LYS.315	NZ	A_GLU.41	OE1	3.740
1HGF	A_LYS.326	NZ	A_GLU.325	OE1	2.712
1HGF	A_LYS.326	NZ	B_GLU.15	OE1	3.851
1HGF	A_LYS.326	NZ	B_GLU.15	OE2	3.863
1HGF	B_ARG.25	NH1	A_GLU.325	OE2	3.563
1HGF	B_ARG.25	NH2	A_GLU.325	OE2	2.989
1HGF	B_LYS.51	NZ	B_GLU.103	OE1	2.735
1HGF	B_ARG.54	NH1	B_GLU.57	OE1	3.296
1HGF	B_ARG.54	NH1	F_GLU.97	OE2	3.282
1HGF	B_ARG.54	NH2	F_GLU.97	OE2	2.831
1HGF	B_LYS.62	NZ	F_ASP.86	OD1	3.116
1HGF	B_LYS.62	NZ	F_ASP.86	OD2	2.708
1HGF	B_LYS.62	NZ	F_ASP.90	OD1	3.733
1HGF	B_LYS.62	NZ	F_ASP.90	OD2	2.767
1HGF	B_LYS.68	NZ	B_GLU.85	OE1	3.045
1HGF	B_LYS.68	NZ	B_GLU.85	OE2	2.673
1HGF	B_ARG.76	NH1	D_GLU.74	OE1	2.859
1HGF	B_ARG.76	NH1	D_GLU.74	OE2	3.561
1HGF	B_ARG.76	NH2	D_GLU.74	OE1	3.524
1HGF	B_ARG.76	NH2	D_GLU.74	OE2	2.746
1HGF	B_ARG.76	NH2	D_GLU.81	OE1	2.726
1HGF	B_ARG.76	NH2	D_GLU.81	OE2	3.662
1HGF	B_LYS.117	NZ	B_GLU.114	OE1	3.311
1HGF	B_LYS.117	NZ	B_GLU.114	OE2	2.558
1HGF	B_ARG.123	NH1	B_GLU.120	OE1	2.618
1HGF	B_ARG.123	NH1	B_GLU.120	OE2	2.780
1HGF	B_ARG.123	NH2	F_GLU.132	OE1	3.495
1HGF	B_ARG.124	NH2	F_GLU.132	OE1	3.111

1HGF	B_ARG_124	NH2	F_GLU_132	OE2	3.495
1HGF	B_ARG_127	NH1	F_GLU_131	OE1	2.468
1HGF	B_ARG_153	NH1	B_GLU_150	OE1	2.531
1HGF	B_HIS_159	NE2	B_ASP_160	OD2	3.002
1HGF	B_ARG_163	NH2	F_GLU_131	OE1	2.740
1HGF	B_ARG_163	NH2	F_GLU_131	OE2	2.533
1HGF	B_ARG_170	NH1	B_GLU_131	OE2	2.840
1HGF	B_ARG_170	NH1	D_GLU_128	OE1	3.455
1HGF	B_ARG_170	NH1	D_GLU_128	OE2	3.294
1HGF	B_ARG_170	NH2	B_GLU_128	OE2	2.821
1HGF	B_LYS_174	NZ	D_ASP_164	OD2	3.813
1HGF	C_LYS_27	NZ	D_GLU_97	OE1	2.824
1HGF	C_LYS_27	NZ	D_GLU_97	OE2	2.808
1HGF	C_LYS_50	NZ	C_ASP_275	OD2	2.881
1HGF	C_ARG_57	NH2	C_GLU_82	OE1	2.589
1HGF	C_ARG_57	NH2	C_GLU_82	OE2	3.890
1HGF	C_HIS_75	ND1	C_ASP_73	OD1	2.839
1HGF	C_HIS_75	ND1	C_ASP_73	OD2	3.334
1HGF	C_HIS_75	NE2	C_ASP_63	OD1	3.432
1HGF	C_ARG_90	NH2	C_ASP_60	OD1	3.494
1HGF	C_ARG_90	NH2	C_ASP_60	OD2	2.843
1HGF	C_ARG_109	NH1	C_GLU_89	OE1	2.579
1HGF	C_ARG_109	NH1	C_GLU_89	OE2	2.919
1HGF	C_ARG_109	NH2	D_GLU_67	OE1	3.698
1HGF	C_ARG_109	NH2	D_GLU_67	OE2	2.914
1HGF	C_ARG_141	NH2	C_ASP_77	OD1	2.838
1HGF	C_ARG_141	NH2	C_ASP_77	OD2	2.786
1HGF	C_LYS_176	NZ	C_GLU_123	OE2	2.724
1HGF	C_LYS_176	NZ	C_ASP_172	OD1	3.678
1HGF	C_HIS_183	NE2	C_GLU_190	OE2	3.665
1HGF	C_LYS_238	NZ	B_GLU_72	OE1	2.746
1HGF	C_LYS_238	NZ	B_GLU_72	OE2	2.727
1HGF	C_ARG_261	NH1	C_GLU_119	OE1	3.774
1HGF	C_ARG_261	NH1	C_GLU_119	OE2	2.592
1HGF	C_ARG_261	NH2	C_GLU_119	OE1	2.721
1HGF	C_ARG_261	NH2	C_GLU_119	OE2	3.119
1HGF	C_LYS_264	NZ	C_ASP_85	OD2	3.303
1HGF	C_ARG_269	NH1	D_GLU_67	OE1	2.900
1HGF	C_LYS_292	NZ	C_ASP_291	OD1	2.883
1HGF	C_LYS_292	NZ	C_ASP_291	OD2	3.545
1HGF	C_LYS_299	NZ	D_GLU_69	OE2	3.732
1HGF	C_LYS_310	NZ	D_ASP_86	OD1	2.839
1HGF	C_LYS_310	NZ	D_ASP_90	OD1	2.507
1HGF	C_LYS_310	NZ	D_ASP_90	OD2	3.941
1HGF	C_LYS_315	NZ	C_GLU_41	OE1	3.725
1HGF	C_LYS_326	NZ	D_GLU_15	OE1	3.713
1HGF	D_LYS_51	NZ	D_GLU_103	OE1	2.742
1HGF	D_ARG_54	NH1	B_GLU_97	OE2	3.314
1HGF	D_ARG_54	NH1	D_GLU_57	OE1	3.296
1HGF	D_ARG_54	NH2	B_GLU_97	OE2	2.840
1HGF	D_LYS_62	NZ	B_ASP_86	OD1	3.122
1HGF	D_LYS_62	NZ	B_ASP_86	OD2	2.686
1HGF	D_LYS_62	NZ	B_ASP_90	OD1	3.703
1HGF	D_LYS_62	NZ	B_ASP_90	OD2	2.682
1HGF	D_LYS_68	NZ	D_GLU_85	OE1	3.023
1HGF	D_LYS_68	NZ	D_GLU_85	OE2	2.732
1HGF	D_ARG_76	NH1	F_GLU_74	OE1	2.790
1HGF	D_ARG_76	NH1	F_GLU_74	OE2	3.379

1HGF	D_ARG_76	NH2	F_GLU_74	OE1	3.594
1HGF	D_ARG_76	NH2	F_GLU_74	OE2	2.697
1HGF	D_ARG_76	NH2	F_GLU_81	OE1	2.644
1HGF	D_ARG_76	NH2	F_GLU_81	OE2	3.691
1HGF	D_LYS_117	NZ	D_GLU_114	OE1	3.303
1HGF	D_LYS_117	NZ	D_GLU_114	OE2	2.574
1HGF	D_ARG_123	NH1	D_GLU_120	OE1	2.580
1HGF	D_ARG_123	NH1	D_GLU_120	OE2	2.788
1HGF	D_ARG_123	NH2	B_GLU_132	OE1	3.407
1HGF	D_ARG_124	NH2	B_GLU_132	OE1	3.100
1HGF	D_ARG_124	NH2	B_GLU_132	OE2	3.442
1HGF	D_ARG_127	NH1	B_GLU_131	OE1	2.516
1HGF	D_ARG_153	NH1	D_GLU_150	OE1	2.657
1HGF	D_HIS_159	NE2	D_ASP_160	OD2	3.002
1HGF	D_ARG_163	NH2	B_GLU_131	OE1	2.704
1HGF	D_ARG_163	NH2	B_GLU_131	OE2	2.556
1HGF	D_ARG_170	NH1	D_GLU_131	OE2	2.839
1HGF	D_ARG_170	NH1	F_GLU_128	OE1	3.604
1HGF	D_ARG_170	NH1	F_GLU_128	OE2	3.428
1HGF	D_ARG_170	NH2	D_GLU_128	OE2	2.843
1HGF	E_LYS_27	NZ	F_GLU_97	OE1	2.793
1HGF	E_LYS_27	NZ	F_GLU_97	OE2	2.754
1HGF	E_LYS_50	NZ	E_ASP_275	OD2	2.903
1HGF	E_ARG_57	NH2	E_GLU_82	OE1	2.780
1HGF	E_HIS_75	ND1	E_ASP_73	OD1	2.855
1HGF	E_HIS_75	ND1	E_ASP_73	OD2	3.339
1HGF	E_HIS_75	NE2	E_ASP_63	OD1	3.444
1HGF	E_ARG_90	NH2	E_ASP_60	OD1	3.506
1HGF	E_ARG_90	NH2	E_ASP_60	OD2	2.882
1HGF	E_ARG_109	NH1	E_GLU_89	OE1	2.522
1HGF	E_ARG_109	NH1	E_GLU_89	OE2	2.887
1HGF	E_ARG_109	NH2	F_GLU_67	OE1	3.694
1HGF	E_ARG_109	NH2	F_GLU_67	OE2	2.878
1HGF	E_ARG_141	NH2	E_ASP_77	OD1	2.834
1HGF	E_ARG_141	NH2	E_ASP_77	OD2	2.773
1HGF	E_LYS_176	NZ	E_GLU_123	OE2	2.761
1HGF	E_LYS_176	NZ	E_ASP_172	OD1	3.700
1HGF	E_HIS_183	NE2	E_GLU_190	OE2	3.673
1HGF	E_LYS_238	NZ	D_GLU_72	OE1	2.831
1HGF	E_LYS_238	NZ	D_GLU_72	OE2	2.834
1HGF	E_ARG_261	NH1	E_GLU_119	OE1	3.764
1HGF	E_ARG_261	NH1	E_GLU_119	OE2	2.590
1HGF	E_ARG_261	NH2	E_GLU_119	OE1	2.729
1HGF	E_ARG_261	NH2	E_GLU_119	OE2	3.139
1HGF	E_LYS_264	NZ	E_ASP_85	OD2	3.295
1HGF	E_ARG_269	NH1	F_GLU_67	OE1	2.906
1HGF	E_LYS_292	NZ	E_ASP_291	OD1	2.871
1HGF	E_LYS_292	NZ	E_ASP_291	OD2	3.523
1HGF	E_LYS_299	NZ	F_GLU_69	OE2	3.655
1HGF	E_LYS_310	NZ	F_ASP_86	OD1	2.832
1HGF	E_LYS_310	NZ	F_ASP_90	OD1	2.514
1HGF	E_LYS_310	NZ	F_ASP_90	OD2	3.973
1HGF	E_LYS_315	NZ	E_GLU_41	OE1	3.726
1HGF	E_LYS_326	NZ	F_GLU_15	OE1	3.652
1HGF	E_LYS_326	NZ	F_GLU_15	OE2	3.771
1HGF	F_LYS_51	NZ	F_GLU_103	OE1	2.723
1HGF	F_ARG_54	NH1	D_GLU_97	OE2	3.368
1HGF	F_ARG_54	NH1	F_GLU_57	OE1	3.280

1HGF	F_ARG_54	NH2	D_GLU_97	OE2	2.791
1HGF	F_LYS_62	NZ	D_ASP_86	OD1	3.076
1HGF	F_LYS_62	NZ	D_ASP_86	OD2	2.672
1HGF	F_LYS_62	NZ	D_ASP_90	OD1	3.773
1HGF	F_LYS_62	NZ	D_ASP_90	OD2	2.752
1HGF	F_LYS_68	NZ	F_GLU_85	OE1	3.011
1HGF	F_LYS_68	NZ	F_GLU_85	OE2	2.638
1HGF	F_ARG_76	NH1	B_GLU_74	OE1	2.779
1HGF	F_ARG_76	NH1	B_GLU_74	OE2	3.420
1HGF	F_ARG_76	NH2	B_GLU_74	OE1	3.542
1HGF	F_ARG_76	NH2	B_GLU_74	OE2	2.707
1HGF	F_ARG_76	NH2	B_GLU_81	OE1	2.689
1HGF	F_ARG_76	NH2	B_GLU_81	OE2	3.716
1HGF	F_LYS_117	NZ	F_GLU_114	OE1	3.348
1HGF	F_LYS_117	NZ	F_GLU_114	OE2	2.589
1HGF	F_ARG_123	NH1	F_GLU_120	OE1	2.596
1HGF	F_ARG_123	NH1	F_GLU_120	OE2	2.789
1HGF	F_ARG_123	NH2	D_GLU_132	OE1	3.469
1HGF	F_ARG_124	NH2	D_GLU_132	OE1	3.198
1HGF	F_ARG_124	NH2	D_GLU_132	OE2	3.522
1HGF	F_ARG_127	NH1	D_GLU_131	OE1	2.568
1HGF	F_HIS_159	NE2	F_ASP_160	OD2	3.032
1HGF	F_ARG_163	NH2	D_GLU_131	OE1	2.689
1HGF	F_ARG_163	NH2	D_GLU_131	OE2	2.644
1HGF	F_ARG_170	NH1	B_GLU_128	OE1	3.432
1HGF	F_ARG_170	NH1	B_GLU_128	OE2	3.366
1HGF	F_ARG_170	NH1	F_GLU_131	OE2	2.852
1HGF	F_ARG_170	NH2	F_GLU_128	OE2	2.847
1HGF	F_LYS_174	NZ	B_ASP_164	OD2	3.837
1HGG	A_LYS_27	NZ	B_GLU_97	OE1	2.679
1HGG	A_LYS_27	NZ	B_GLU_97	OE2	2.904
1HGG	A_LYS_50	NZ	A_ASP_275	OD1	3.658
1HGG	A_LYS_50	NZ	A_ASP_275	OD2	2.711
1HGG	A_ARG_57	NH2	A_GLU_82	OE1	2.519
1HGG	A_ARG_57	NH2	A_GLU_82	OE2	3.336
1HGG	A_HIS_75	ND1	A_ASP_73	OD1	2.772
1HGG	A_HIS_75	ND1	A_ASP_73	OD2	3.336
1HGG	A_HIS_75	NE2	A_ASP_63	OD1	3.694
1HGG	A_ARG_90	NH2	A_ASP_60	OD1	3.622
1HGG	A_ARG_90	NH2	A_ASP_60	OD2	2.794
1HGG	A_ARG_109	NH1	A_GLU_89	OE1	2.517
1HGG	A_ARG_109	NH1	A_GLU_89	OE2	3.003
1HGG	A_ARG_109	NH2	B_GLU_67	OE1	3.854
1HGG	A_ARG_109	NH2	B_GLU_67	OE2	2.838
1HGG	A_ARG_141	NH2	A_ASP_77	OD1	2.758
1HGG	A_ARG_141	NH2	A_ASP_77	OD2	2.757
1HGG	A_LYS_176	NZ	A_GLU_123	OE2	2.648
1HGG	A_HIS_183	NE2	A_GLU_190	OE2	3.990
1HGG	A_LYS_238	NZ	F_GLU_72	OE1	2.931
1HGG	A_LYS_238	NZ	F_GLU_72	OE2	2.744
1HGG	A_ARG_261	NH1	A_GLU_119	OE1	3.988
1HGG	A_ARG_261	NH1	A_GLU_119	OE2	2.685
1HGG	A_ARG_261	NH2	A_GLU_119	OE1	2.738
1HGG	A_ARG_261	NH2	A_GLU_119	OE2	2.969
1HGG	A_LYS_264	NZ	A_ASP_85	OD1	3.326
1HGG	A_LYS_264	NZ	A_ASP_85	OD2	2.834
1HGG	A_ARG_269	NH1	B_GLU_67	OE1	2.694
1HGG	A_ARG_269	NH2	B_GLU_67	OE1	3.814

1HGG	A_LYS_292	NZ	A_ASP_291	OD1	2.980
1HGG	A_LYS_292	NZ	A_ASP_291	OD2	2.773
1HGG	A_LYS_299	NZ	B_GLU_69	OE2	2.915
1HGG	A_LYS_310	NZ	B_ASP_86	OD1	2.852
1HGG	A_LYS_310	NZ	B_ASP_90	OD1	2.700
1HGG	A_LYS_310	NZ	B_ASP_90	OD2	3.923
1HGG	A_LYS_315	NZ	A_GLU_41	OE1	2.731
1HGG	A_LYS_326	NZ	A_GLU_325	OE1	2.817
1HGG	A_LYS_326	NZ	B_GLU_15	OE1	3.039
1HGG	A_LYS_326	NZ	B_GLU_15	OE2	2.830
1HGG	B_ARG_25	NH1	A_GLU_325	OE2	3.770
1HGG	B_ARG_25	NH2	A_GLU_325	OE2	2.944
1HGG	B_LYS_51	NZ	B_GLU_103	OE1	2.759
1HGG	B_ARG_54	NH1	B_GLU_57	OE1	2.857
1HGG	B_ARG_54	NH1	B_GLU_57	OE2	2.882
1HGG	B_ARG_54	NH1	F_GLU_97	OE2	3.410
1HGG	B_ARG_54	NH2	F_GLU_97	OE2	2.750
1HGG	B_LYS_58	NZ	B_GLU_61	OE2	2.938
1HGG	B_LYS_62	NZ	F_ASP_86	OD1	2.889
1HGG	B_LYS_62	NZ	F_ASP_86	OD2	2.639
1HGG	B_LYS_62	NZ	F_ASP_90	OD1	3.716
1HGG	B_LYS_62	NZ	F_ASP_90	OD2	2.650
1HGG	B_LYS_68	NZ	B_GLU_85	OE1	3.149
1HGG	B_LYS_68	NZ	B_GLU_85	OE2	2.746
1HGG	B_ARG_76	NH1	D_GLU_74	OE1	2.882
1HGG	B_ARG_76	NH1	D_GLU_74	OE2	3.580
1HGG	B_ARG_76	NH2	D_GLU_74	OE1	3.459
1HGG	B_ARG_76	NH2	D_GLU_74	OE2	2.820
1HGG	B_ARG_76	NH2	D_GLU_81	OE1	2.731
1HGG	B_ARG_76	NH2	D_GLU_81	OE2	3.473
1HGG	B_LYS_117	NZ	B_GLU_114	OE1	3.037
1HGG	B_LYS_117	NZ	B_GLU_114	OE2	2.573
1HGG	B_ARG_123	NH1	B_GLU_120	OE1	2.615
1HGG	B_ARG_123	NH1	B_GLU_120	OE2	2.734
1HGG	B_ARG_123	NH2	F_GLU_132	OE1	2.827
1HGG	B_ARG_124	NH1	B_GLU_120	OE1	3.704
1HGG	B_ARG_124	NH2	F_GLU_132	OE1	3.221
1HGG	B_ARG_124	NH2	F_GLU_132	OE2	3.297
1HGG	B_ARG_127	NH1	F_GLU_131	OE1	2.465
1HGG	B_LYS_143	NZ	B_ASP_145	OD2	2.940
1HGG	B_ARG_153	NH1	B_GLU_150	OE1	2.632
1HGG	B_HIS_159	NE2	B_ASP_160	OD2	3.121
1HGG	B_ARG_163	NH2	B_GLU_128	OE1	3.737
1HGG	B_ARG_163	NH2	F_GLU_131	OE1	2.594
1HGG	B_ARG_163	NH2	F_GLU_131	OE2	2.562
1HGG	B_ARG_170	NH1	B_GLU_131	OE2	2.846
1HGG	B_ARG_170	NH1	D_GLU_128	OE1	3.236
1HGG	B_ARG_170	NH1	D_GLU_128	OE2	3.289
1HGG	B_ARG_170	NH2	B_GLU_128	OE2	2.890
1HGG	B_LYS_174	NZ	D_ASP_164	OD1	2.736
1HGG	B_LYS_174	NZ	D_ASP_164	OD2	2.575
1HGG	C_LYS_27	NZ	D_GLU_97	OE1	2.683
1HGG	C_LYS_27	NZ	D_GLU_97	OE2	2.941
1HGG	C_LYS_50	NZ	C_ASP_275	OD1	3.663
1HGG	C_LYS_50	NZ	C_ASP_275	OD2	2.681
1HGG	C_ARG_57	NH2	C_GLU_82	OE1	2.593
1HGG	C_ARG_57	NH2	C_GLU_82	OE2	3.431
1HGG	C_HIS_75	ND1	C_ASP_73	OD1	2.715

1HGG	C_HIS_75	ND1	C_ASP_73	OD2	3.305
1HGG	C_HIS_75	NE2	C_ASP_63	OD1	3.698
1HGG	C_ARG_90	NH2	C_ASP_60	OD1	3.640
1HGG	C_ARG_90	NH2	C_ASP_60	OD2	2.792
1HGG	C_ARG_109	NH1	C_GLU_89	OE1	2.511
1HGG	C_ARG_109	NH1	C_GLU_89	OE2	3.012
1HGG	C_ARG_109	NH2	D_GLU_67	OE1	3.869
1HGG	C_ARG_109	NH2	D_GLU_67	OE2	2.853
1HGG	C_ARG_141	NH2	C_ASP_77	OD1	2.758
1HGG	C_ARG_141	NH2	C_ASP_77	OD2	2.737
1HGG	C_LYS_176	NZ	C_GLU_123	OE2	2.629
1HGG	C_HIS_183	NE2	C_GLU_190	OE2	3.969
1HGG	C_LYS_238	NZ	B_GLU_72	OE1	2.830
1HGG	C_LYS_238	NZ	B_GLU_72	OE2	2.699
1HGG	C_ARG_261	NH1	C_GLU_119	OE1	3.989
1HGG	C_ARG_261	NH1	C_GLU_119	OE2	2.670
1HGG	C_ARG_261	NH2	C_GLU_119	OE1	2.730
1HGG	C_ARG_261	NH2	C_GLU_119	OE2	2.933
1HGG	C_LYS_264	NZ	C_ASP_85	OD1	3.356
1HGG	C_LYS_264	NZ	C_ASP_85	OD2	2.849
1HGG	C_ARG_269	NH1	D_GLU_67	OE1	2.688
1HGG	C_ARG_269	NH2	D_GLU_67	OE1	3.820
1HGG	C_LYS_292	NZ	C_ASP_291	OD1	3.021
1HGG	C_LYS_292	NZ	C_ASP_291	OD2	2.777
1HGG	C_LYS_299	NZ	D_GLU_69	OE2	2.932
1HGG	C_LYS_310	NZ	D_ASP_86	OD1	2.859
1HGG	C_LYS_310	NZ	D_ASP_90	OD1	2.651
1HGG	C_LYS_310	NZ	D_ASP_90	OD2	3.858
1HGG	C_LYS_315	NZ	C_GLU_41	OE1	2.732
1HGG	C_LYS_326	NZ	D_GLU_15	OE1	2.591
1HGG	C_LYS_326	NZ	D_GLU_15	OE2	3.450
1HGG	D_LYS_51	NZ	D_GLU_103	OE1	2.765
1HGG	D_ARG_54	NH1	B_GLU_97	OE2	3.442
1HGG	D_ARG_54	NH1	D_GLU_57	OE1	2.855
1HGG	D_ARG_54	NH1	D_GLU_57	OE2	2.880
1HGG	D_ARG_54	NH2	B_GLU_97	OE2	2.764
1HGG	D_LYS_58	NZ	D_GLU_61	OE2	2.913
1HGG	D_LYS_62	NZ	B_ASP_86	OD1	2.924
1HGG	D_LYS_62	NZ	B_ASP_86	OD2	2.567
1HGG	D_LYS_62	NZ	B_ASP_90	OD1	3.695
1HGG	D_LYS_62	NZ	B_ASP_90	OD2	2.575
1HGG	D_LYS_68	NZ	D_GLU_85	OE1	3.169
1HGG	D_LYS_68	NZ	D_GLU_85	OE2	2.772
1HGG	D_ARG_76	NH1	F_GLU_74	OE1	2.783
1HGG	D_ARG_76	NH1	F_GLU_74	OE2	3.379
1HGG	D_ARG_76	NH2	F_GLU_74	OE1	3.480
1HGG	D_ARG_76	NH2	F_GLU_74	OE2	2.737
1HGG	D_ARG_76	NH2	F_GLU_81	OE1	2.674
1HGG	D_ARG_76	NH2	F_GLU_81	OE2	3.521
1HGG	D_LYS_117	NZ	D_GLU_114	OE1	3.041
1HGG	D_LYS_117	NZ	D_GLU_114	OE2	2.574
1HGG	D_ARG_123	NH1	D_GLU_120	OE1	2.613
1HGG	D_ARG_123	NH1	D_GLU_120	OE2	2.730
1HGG	D_ARG_123	NH2	B_GLU_132	OE1	2.793
1HGG	D_ARG_124	NH1	D_GLU_120	OE1	3.717
1HGG	D_ARG_124	NH2	B_GLU_132	OE1	3.241
1HGG	D_ARG_124	NH2	B_GLU_132	OE2	3.297
1HGG	D_ARG_127	NH1	B_GLU_131	OE1	2.475

1HGG	D_LYS_143	NZ	D_ASP_145	OD2	2.930
1HGG	D_ARG_153	NH1	D_GLU_150	OE1	2.636
1HGG	D_HIS_159	NE2	D_ASP_160	OD2	3.127
1HGG	D_ARG_163	NH2	B_GLU_131	OE1	2.580
1HGG	D_ARG_163	NH2	B_GLU_131	OE2	2.598
1HGG	D_ARG_163	NH2	D_GLU_128	OE1	3.766
1HGG	D_ARG_170	NH1	D_GLU_131	OE2	2.855
1HGG	D_ARG_170	NH1	F_GLU_128	OE1	3.365
1HGG	D_ARG_170	NH1	F_GLU_128	OE2	3.390
1HGG	D_ARG_170	NH2	D_GLU_128	OE2	2.921
1HGG	D_LYS_174	NZ	F_ASP_164	OD1	2.763
1HGG	D_LYS_174	NZ	F_ASP_164	OD2	2.711
1HGG	E_LYS_27	NZ	F_GLU_97	OE1	2.689
1HGG	E_LYS_27	NZ	F_GLU_97	OE2	2.909
1HGG	E_LYS_50	NZ	E_ASP_275	OD1	3.653
1HGG	E_LYS_50	NZ	E_ASP_275	OD2	2.678
1HGG	E_ARG_57	NH2	E_GLU_82	OE1	2.569
1HGG	E_ARG_57	NH2	E_GLU_82	OE2	3.845
1HGG	E_HIS_75	ND1	E_ASP_73	OD1	2.755
1HGG	E_HIS_75	ND1	E_ASP_73	OD2	3.285
1HGG	E_HIS_75	NE2	E_ASP_63	OD1	3.700
1HGG	E_ARG_90	NH2	E_ASP_60	OD1	3.616
1HGG	E_ARG_90	NH2	E_ASP_60	OD2	2.834
1HGG	E_ARG_109	NH1	E_GLU_89	OE1	2.488
1HGG	E_ARG_109	NH1	E_GLU_89	OE2	2.947
1HGG	E_ARG_109	NH2	F_GLU_67	OE1	3.891
1HGG	E_ARG_109	NH2	F_GLU_67	OE2	2.876
1HGG	E_ARG_141	NH2	E_ASP_77	OD1	2.801
1HGG	E_ARG_141	NH2	E_ASP_77	OD2	2.744
1HGG	E_LYS_176	NZ	E_GLU_123	OE2	2.653
1HGG	E_HIS_183	NE2	E_GLU_190	OE2	3.980
1HGG	E_LYS_238	NZ	D_GLU_72	OE1	2.893
1HGG	E_LYS_238	NZ	D_GLU_72	OE2	2.782
1HGG	E_ARG_261	NH1	E_GLU_119	OE1	3.984
1HGG	E_ARG_261	NH1	E_GLU_119	OE2	2.694
1HGG	E_ARG_261	NH2	E_GLU_119	OE1	2.738
1HGG	E_ARG_261	NH2	E_GLU_119	OE2	2.981
1HGG	E_LYS_264	NZ	E_ASP_85	OD1	3.369
1HGG	E_LYS_264	NZ	E_ASP_85	OD2	2.847
1HGG	E_ARG_269	NH1	F_GLU_67	OE1	2.691
1HGG	E_ARG_269	NH2	F_GLU_67	OE1	3.830
1HGG	E_LYS_292	NZ	E_ASP_291	OD1	2.996
1HGG	E_LYS_292	NZ	E_ASP_291	OD2	2.759
1HGG	E_LYS_299	NZ	F_GLU_69	OE2	2.920
1HGG	E_LYS_310	NZ	F_ASP_86	OD1	2.871
1HGG	E_LYS_310	NZ	F_ASP_90	OD1	2.639
1HGG	E_LYS_310	NZ	F_ASP_90	OD2	3.900
1HGG	E_LYS_315	NZ	E_GLU_41	OE1	2.684
1HGG	E_LYS_326	NZ	F_GLU_15	OE1	2.975
1HGG	E_LYS_326	NZ	F_GLU_15	OE2	3.000
1HGG	F_LYS_51	NZ	F_GLU_103	OE1	2.794
1HGG	F_ARG_54	NH1	D_GLU_97	OE2	3.483
1HGG	F_ARG_54	NH1	F_GLU_57	OE1	2.848
1HGG	F_ARG_54	NH1	F_GLU_57	OE2	2.863
1HGG	F_ARG_54	NH2	D_GLU_97	OE2	2.727
1HGG	F_LYS_58	NZ	F_GLU_61	OE2	2.938
1HGG	F_LYS_62	NZ	D_ASP_86	OD1	2.904
1HGG	F_LYS_62	NZ	D_ASP_86	OD2	2.582

1HGG	F_LYS_62	NZ	D_ASP_90	OD1	3.752
1HGG	F_LYS_62	NZ	D_ASP_90	OD2	2.595
1HGG	F_LYS_68	NZ	F_GLU_85	OE1	3.147
1HGG	F_LYS_68	NZ	F_GLU_85	OE2	2.755
1HGG	F_ARG_76	NH1	B_GLU_74	OE1	2.750
1HGG	F_ARG_76	NH1	B_GLU_74	OE2	3.432
1HGG	F_ARG_76	NH2	B_GLU_74	OE1	3.456
1HGG	F_ARG_76	NH2	B_GLU_74	OE2	2.786
1HGG	F_ARG_76	NH2	B_GLU_81	OE1	2.674
1HGG	F_ARG_76	NH2	B_GLU_81	OE2	3.545
1HGG	F_LYS_117	NZ	F_GLU_114	OE1	3.063
1HGG	F_LYS_117	NZ	F_GLU_114	OE2	2.581
1HGG	F_ARG_123	NH1	F_GLU_120	OE1	2.640
1HGG	F_ARG_123	NH1	F_GLU_120	OE2	2.718
1HGG	F_ARG_123	NH2	D_GLU_132	OE1	2.843
1HGG	F_ARG_124	NH1	F_GLU_120	OE1	3.721
1HGG	F_ARG_124	NH2	D_GLU_132	OE1	3.317
1HGG	F_ARG_124	NH2	D_GLU_132	OE2	3.342
1HGG	F_ARG_127	NH1	D_GLU_131	OE1	2.523
1HGG	F_LYS_143	NZ	F_ASP_145	OD2	2.914
1HGG	F_ARG_153	NH1	F_GLU_150	OE2	2.532
1HGG	F_HIS_159	NE2	F_ASP_160	OD2	3.162
1HGG	F_ARG_163	NH2	D_GLU_131	OE1	2.589
1HGG	F_ARG_163	NH2	D_GLU_131	OE2	2.640
1HGG	F_ARG_163	NH2	F_GLU_128	OE1	3.754
1HGG	F_ARG_170	NH1	B_GLU_128	OE1	3.237
1HGG	F_ARG_170	NH1	B_GLU_128	OE2	3.354
1HGG	F_ARG_170	NH1	F_GLU_131	OE2	2.835
1HGG	F_ARG_170	NH2	F_GLU_128	OE2	2.924
1HGG	F_LYS_174	NZ	B_ASP_164	OD1	2.757
1HGG	F_LYS_174	NZ	B_ASP_164	OD2	2.547
1HGH	A_LYS_27	NZ	B_GLU_97	OE1	2.856
1HGH	A_LYS_27	NZ	B_GLU_97	OE2	2.781
1HGH	A_LYS_50	NZ	A_ASP_275	OD1	3.680
1HGH	A_LYS_50	NZ	A_ASP_275	OD2	2.788
1HGH	A_ARG_57	NH2	A_GLU_82	OE1	2.548
1HGH	A_ARG_57	NH2	A_GLU_82	OE2	3.398
1HGH	A_HIS_75	ND1	A_ASP_73	OD1	2.741
1HGH	A_HIS_75	ND1	A_ASP_73	OD2	3.401
1HGH	A_HIS_75	NE2	A_ASP_63	OD1	3.595
1HGH	A_ARG_90	NH2	A_ASP_60	OD1	3.580
1HGH	A_ARG_90	NH2	A_ASP_60	OD2	2.788
1HGH	A_ARG_109	NH1	A_GLU_89	OE1	2.475
1HGH	A_ARG_109	NH1	A_GLU_89	OE2	3.343
1HGH	A_ARG_109	NH2	B_GLU_67	OE1	3.697
1HGH	A_ARG_109	NH2	B_GLU_67	OE2	2.864
1HGH	A_ARG_141	NH2	A_ASP_77	OD1	2.863
1HGH	A_ARG_141	NH2	A_ASP_77	OD2	2.744
1HGH	A_LYS_176	NZ	A_GLU_123	OE2	2.684
1HGH	A_HIS_183	NE2	A_GLU_190	OE2	3.803
1HGH	A_LYS_238	NZ	F_GLU_72	OE1	2.921
1HGH	A_LYS_238	NZ	F_GLU_72	OE2	2.736
1HGH	A_ARG_261	NH1	A_GLU_119	OE2	2.623
1HGH	A_ARG_261	NH2	A_GLU_119	OE1	2.866
1HGH	A_ARG_261	NH2	A_GLU_119	OE2	2.801
1HGH	A_LYS_264	NZ	A_ASP_85	OD1	3.600
1HGH	A_LYS_264	NZ	A_ASP_85	OD2	2.814
1HGH	A_ARG_269	NH1	B_GLU_67	OE1	2.720

1HGH	A_ARG_269	NH2	B_GLU_67	OE1	3.718
1HGH	A_LYS_292	NZ	A_ASP_291	OD1	3.015
1HGH	A_LYS_292	NZ	A_ASP_291	OD2	2.819
1HGH	A_LYS_299	NZ	B_GLU_69	OE2	2.918
1HGH	A_LYS_310	NZ	B_ASP_86	OD1	2.712
1HGH	A_LYS_310	NZ	B_ASP_90	OD1	2.578
1HGH	A_LYS_310	NZ	B_ASP_90	OD2	3.975
1HGH	A_LYS_315	NZ	A_GLU_41	OE1	2.869
1HGH	A_LYS_326	NZ	A_GLU_325	OE1	2.838
1HGH	A_LYS_326	NZ	B_GLU_15	OE1	3.092
1HGH	A_LYS_326	NZ	B_GLU_15	OE2	2.707
1HGH	B_ARG_25	NH1	A_GLU_325	OE2	3.971
1HGH	B_ARG_25	NH2	A_GLU_325	OE2	3.017
1HGH	B_LYS_51	NZ	B_GLU_103	OE1	2.789
1HGH	B_ARG_54	NH1	B_GLU_57	OE1	2.865
1HGH	B_ARG_54	NH1	B_GLU_57	OE2	2.969
1HGH	B_ARG_54	NH1	F_GLU_97	OE2	3.285
1HGH	B_ARG_54	NH2	F_GLU_97	OE2	2.823
1HGH	B_LYS_58	NZ	B_GLU_61	OE2	3.237
1HGH	B_LYS_62	NZ	F_ASP_86	OD1	3.064
1HGH	B_LYS_62	NZ	F_ASP_86	OD2	2.661
1HGH	B_LYS_62	NZ	F_ASP_90	OD1	3.547
1HGH	B_LYS_62	NZ	F_ASP_90	OD2	2.683
1HGH	B_LYS_68	NZ	B_GLU_85	OE1	3.132
1HGH	B_LYS_68	NZ	B_GLU_85	OE2	2.734
1HGH	B_ARG_76	NH1	D_GLU_74	OE1	3.707
1HGH	B_ARG_76	NH1	D_GLU_74	OE2	2.912
1HGH	B_ARG_76	NH2	D_GLU_74	OE1	2.889
1HGH	B_ARG_76	NH2	D_GLU_74	OE2	3.526
1HGH	B_ARG_76	NH2	D_GLU_81	OE1	2.765
1HGH	B_ARG_76	NH2	D_GLU_81	OE2	3.411
1HGH	B_LYS_117	NZ	B_GLU_114	OE1	3.139
1HGH	B_LYS_117	NZ	B_GLU_114	OE2	2.561
1HGH	B_ARG_123	NH1	B_GLU_120	OE1	2.569
1HGH	B_ARG_123	NH1	B_GLU_120	OE2	2.742
1HGH	B_ARG_123	NH2	F_GLU_132	OE1	3.134
1HGH	B_ARG_124	NH1	B_GLU_120	OE1	3.740
1HGH	B_ARG_124	NH2	F_GLU_132	OE1	3.005
1HGH	B_ARG_124	NH2	F_GLU_132	OE2	3.302
1HGH	B_ARG_127	NH1	F_GLU_131	OE1	2.524
1HGH	B_LYS_143	NZ	B_ASP_145	OD2	2.787
1HGH	B_ARG_153	NH1	B_GLU_150	OE1	2.556
1HGH	B_HIS_159	NE2	B_ASP_160	OD2	3.003
1HGH	B_ARG_163	NH2	F_GLU_131	OE1	2.607
1HGH	B_ARG_163	NH2	F_GLU_131	OE2	2.538
1HGH	B_ARG_170	NH1	B_GLU_131	OE2	2.832
1HGH	B_ARG_170	NH1	D_GLU_128	OE1	3.253
1HGH	B_ARG_170	NH1	D_GLU_128	OE2	3.577
1HGH	B_ARG_170	NH2	B_GLU_128	OE2	2.706
1HGH	B_LYS_174	NZ	D_ASP_164	OD1	2.767
1HGH	B_LYS_174	NZ	D_ASP_164	OD2	2.573
1HGH	C_LYS_27	NZ	D_GLU_97	OE1	2.897
1HGH	C_LYS_27	NZ	D_GLU_97	OE2	2.815
1HGH	C_LYS_50	NZ	C_ASP_275	OD1	3.681
1HGH	C_LYS_50	NZ	C_ASP_275	OD2	2.765
1HGH	C_ARG_57	NH2	C_GLU_82	OE1	2.537
1HGH	C_ARG_57	NH2	C_GLU_82	OE2	3.720
1HGH	C_HIS_75	ND1	C_ASP_73	OD1	2.705

1HGH	C_HIS_75	ND1	C_ASP_73	OD2	3.403
1HGH	C_HIS_75	NE2	C_ASP_63	OD1	3.580
1HGH	C_ARG_90	NH2	C_ASP_60	OD1	3.561
1HGH	C_ARG_90	NH2	C_ASP_60	OD2	2.760
1HGH	C_ARG_109	NH1	C_GLU_89	OE1	2.510
1HGH	C_ARG_109	NH1	C_GLU_89	OE2	3.378
1HGH	C_ARG_109	NH2	D_GLU_67	OE1	3.686
1HGH	C_ARG_109	NH2	D_GLU_67	OE2	2.856
1HGH	C_ARG_141	NH2	C_ASP_77	OD1	2.881
1HGH	C_ARG_141	NH2	C_ASP_77	OD2	2.750
1HGH	C_LYS_176	NZ	C_GLU_123	OE2	2.654
1HGH	C_HIS_183	NE2	C_GLU_190	OE2	3.784
1HGH	C_LYS_238	NZ	B_GLU_72	OE1	2.713
1HGH	C_LYS_238	NZ	B_GLU_72	OE2	2.597
1HGH	C_ARG_261	NH1	C_GLU_119	OE2	2.638
1HGH	C_ARG_261	NH2	C_GLU_119	OE1	2.853
1HGH	C_ARG_261	NH2	C_GLU_119	OE2	2.786
1HGH	C_LYS_264	NZ	C_ASP_85	OD1	3.599
1HGH	C_LYS_264	NZ	C_ASP_85	OD2	2.793
1HGH	C_ARG_269	NH1	D_GLU_67	OE1	2.732
1HGH	C_ARG_269	NH2	D_GLU_67	OE1	3.725
1HGH	C_LYS_292	NZ	C_ASP_291	OD1	3.012
1HGH	C_LYS_292	NZ	C_ASP_291	OD2	2.815
1HGH	C_LYS_299	NZ	D_GLU_69	OE2	2.939
1HGH	C_LYS_310	NZ	D_ASP_86	OD1	2.734
1HGH	C_LYS_310	NZ	D_ASP_90	OD1	2.551
1HGH	C_LYS_310	NZ	D_ASP_90	OD2	3.913
1HGH	C_LYS_315	NZ	C_GLU_41	OE1	2.867
1HGH	C_LYS_326	NZ	D_GLU_15	OE1	2.774
1HGH	C_LYS_326	NZ	D_GLU_15	OE2	3.676
1HGH	D_LYS_51	NZ	D_GLU_103	OE1	2.742
1HGH	D_ARG_54	NH1	B_GLU_97	OE2	3.277
1HGH	D_ARG_54	NH1	D_GLU_57	OE1	2.856
1HGH	D_ARG_54	NH1	D_GLU_57	OE2	2.958
1HGH	D_ARG_54	NH2	B_GLU_97	OE2	2.797
1HGH	D_LYS_58	NZ	D_GLU_61	OE2	3.225
1HGH	D_LYS_62	NZ	B_ASP_86	OD1	3.011
1HGH	D_LYS_62	NZ	B_ASP_86	OD2	2.510
1HGH	D_LYS_62	NZ	B_ASP_90	OD1	3.543
1HGH	D_LYS_62	NZ	B_ASP_90	OD2	2.589
1HGH	D_LYS_68	NZ	D_GLU_85	OE1	3.123
1HGH	D_LYS_68	NZ	D_GLU_85	OE2	2.750
1HGH	D_ARG_76	NH1	F_GLU_74	OE1	3.430
1HGH	D_ARG_76	NH1	F_GLU_74	OE2	2.765
1HGH	D_ARG_76	NH2	F_GLU_74	OE1	2.747
1HGH	D_ARG_76	NH2	F_GLU_74	OE2	3.553
1HGH	D_ARG_76	NH2	F_GLU_81	OE1	2.698
1HGH	D_ARG_76	NH2	F_GLU_81	OE2	3.487
1HGH	D_LYS_117	NZ	D_GLU_114	OE1	3.179
1HGH	D_LYS_117	NZ	D_GLU_114	OE2	2.579
1HGH	D_ARG_123	NH1	D_GLU_120	OE1	2.573
1HGH	D_ARG_123	NH1	D_GLU_120	OE2	2.771
1HGH	D_ARG_123	NH2	B_GLU_132	OE1	3.141
1HGH	D_ARG_124	NH1	D_GLU_120	OE1	3.722
1HGH	D_ARG_124	NH2	B_GLU_132	OE1	3.050
1HGH	D_ARG_124	NH2	B_GLU_132	OE2	3.354
1HGH	D_ARG_127	NH1	B_GLU_131	OE1	2.536
1HGH	D_LYS_143	NZ	D_ASP_145	OD2	2.793

1HGH	D_ARG_153	NH1	D_GLU_150	OE2	2.554
1HGH	D_HIS_159	NE2	D_ASP_160	OD2	3.042
1HGH	D_ARG_163	NH2	B_GLU_131	OE1	2.609
1HGH	D_ARG_163	NH2	B_GLU_131	OE2	2.570
1HGH	D_ARG_170	NH1	D_GLU_131	OE2	2.834
1HGH	D_ARG_170	NH1	F_GLU_128	OE1	3.352
1HGH	D_ARG_170	NH1	F_GLU_128	OE2	3.641
1HGH	D_ARG_170	NH2	D_GLU_128	OE2	2.742
1HGH	D_LYS_174	NZ	F_ASP_164	OD1	2.863
1HGH	D_LYS_174	NZ	F_ASP_164	OD2	2.724
1HGH	E_LYS_27	NZ	F_GLU_97	OE1	2.917
1HGH	E_LYS_27	NZ	F_GLU_97	OE2	2.767
1HGH	E_LYS_50	NZ	E_ASP_275	OD1	3.706
1HGH	E_LYS_50	NZ	E_ASP_275	OD2	2.783
1HGH	E_ARG_57	NH2	E_GLU_82	OE1	2.543
1HGH	E_ARG_57	NH2	E_GLU_82	OE2	3.770
1HGH	E_HIS_75	ND1	E_ASP_73	OD1	2.703
1HGH	E_HIS_75	ND1	E_ASP_73	OD2	3.377
1HGH	E_HIS_75	NE2	E_ASP_63	OD1	3.572
1HGH	E_ARG_90	NH2	E_ASP_60	OD1	3.573
1HGH	E_ARG_90	NH2	E_ASP_60	OD2	2.816
1HGH	E_ARG_109	NH1	E_GLU_89	OE1	2.463
1HGH	E_ARG_109	NH1	E_GLU_89	OE2	3.357
1HGH	E_ARG_109	NH2	F_GLU_67	OE1	3.698
1HGH	E_ARG_109	NH2	F_GLU_67	OE2	2.878
1HGH	E_ARG_141	NH2	E_ASP_77	OD1	2.892
1HGH	E_ARG_141	NH2	E_ASP_77	OD2	2.736
1HGH	E_LYS_176	NZ	E_GLU_123	OE2	2.692
1HGH	E_HIS_183	NE2	E_GLU_190	OE2	3.780
1HGH	E_LYS_238	NZ	D_GLU_72	OE1	2.870
1HGH	E_LYS_238	NZ	D_GLU_72	OE2	2.766
1HGH	E_ARG_261	NH1	E_GLU_119	OE2	2.629
1HGH	E_ARG_261	NH2	E_GLU_119	OE1	2.852
1HGH	E_ARG_261	NH2	E_GLU_119	OE2	2.789
1HGH	E_LYS_264	NZ	E_ASP_85	OD1	3.620
1HGH	E_LYS_264	NZ	E_ASP_85	OD2	2.815
1HGH	E_ARG_269	NH1	F_GLU_67	OE1	2.705
1HGH	E_ARG_269	NH2	F_GLU_67	OE1	3.715
1HGH	E_LYS_292	NZ	E_ASP_291	OD1	3.036
1HGH	E_LYS_292	NZ	E_ASP_291	OD2	2.839
1HGH	E_LYS_299	NZ	F_GLU_69	OE2	2.896
1HGH	E_LYS_310	NZ	F_ASP_86	OD1	2.740
1HGH	E_LYS_310	NZ	F_ASP_90	OD1	2.571
1HGH	E_LYS_310	NZ	F_ASP_90	OD2	3.948
1HGH	E_LYS_315	NZ	E_GLU_41	OE1	2.853
1HGH	E_LYS_326	NZ	F_GLU_15	OE1	2.900
1HGH	E_LYS_326	NZ	F_GLU_15	OE2	3.072
1HGH	F_LYS_51	NZ	F_GLU_103	OE1	2.753
1HGH	F_ARG_54	NH1	D_GLU_97	OE2	3.293
1HGH	F_ARG_54	NH1	F_GLU_57	OE1	2.877
1HGH	F_ARG_54	NH1	F_GLU_57	OE2	2.968
1HGH	F_ARG_54	NH2	D_GLU_97	OE2	2.723
1HGH	F_LYS_58	NZ	F_GLU_61	OE2	3.244
1HGH	F_LYS_62	NZ	D_ASP_86	OD1	3.012
1HGH	F_LYS_62	NZ	D_ASP_86	OD2	2.546
1HGH	F_LYS_62	NZ	D_ASP_90	OD1	3.612
1HGH	F_LYS_62	NZ	D_ASP_90	OD2	2.682
1HGH	F_LYS_68	NZ	F_GLU_85	OE1	3.145

1HGH	F_LYS_68	NZ	F_GLU_85	OE2	2.728
1HGH	F_ARG_76	NH1	B_GLU_74	OE1	3.509
1HGH	F_ARG_76	NH1	B_GLU_74	OE2	2.732
1HGH	F_ARG_76	NH2	B_GLU_74	OE1	2.780
1HGH	F_ARG_76	NH2	B_GLU_74	OE2	3.488
1HGH	F_ARG_76	NH2	B_GLU_81	OE1	2.709
1HGH	F_ARG_76	NH2	B_GLU_81	OE2	3.513
1HGH	F_LYS_117	NZ	F_GLU_114	OE1	3.171
1HGH	F_LYS_117	NZ	F_GLU_114	OE2	2.578
1HGH	F_ARG_123	NH1	F_GLU_120	OE1	2.557
1HGH	F_ARG_123	NH1	F_GLU_120	OE2	2.739
1HGH	F_ARG_123	NH2	D_GLU_132	OE1	3.148
1HGH	F_ARG_124	NH1	F_GLU_120	OE1	3.713
1HGH	F_ARG_124	NH2	D_GLU_132	OE1	3.099
1HGH	F_ARG_124	NH2	D_GLU_132	OE2	3.356
1HGH	F_ARG_127	NH1	D_GLU_131	OE1	2.577
1HGH	F_LYS_143	NZ	F_ASP_145	OD2	2.769
1HGH	F_ARG_153	NH1	F_GLU_150	OE2	2.536
1HGH	F_HIS_159	NE2	F_ASP_160	OD2	3.043
1HGH	F_ARG_163	NH2	D_GLU_131	OE1	2.600
1HGH	F_ARG_163	NH2	D_GLU_131	OE2	2.611
1HGH	F_ARG_170	NH1	B_GLU_128	OE1	3.225
1HGH	F_ARG_170	NH1	B_GLU_128	OE2	3.576
1HGH	F_ARG_170	NH1	F_GLU_131	OE2	2.843
1HGH	F_ARG_170	NH2	F_GLU_128	OE2	2.737
1HGH	F_LYS_174	NZ	B_ASP_164	OD1	2.776
1HGH	F_LYS_174	NZ	B_ASP_164	OD2	2.495
1HGI	A_LYS_27	NZ	B_GLU_97	OE1	2.940
1HGI	A_LYS_27	NZ	B_GLU_97	OE2	2.900
1HGI	A_LYS_50	NZ	A_ASP_275	OD1	3.608
1HGI	A_LYS_50	NZ	A_ASP_275	OD2	2.707
1HGI	A_ARG_57	NH2	A_GLU_82	OE1	2.526
1HGI	A_ARG_57	NH2	A_GLU_82	OE2	3.433
1HGI	A_HIS_75	ND1	A_ASP_73	OD1	2.896
1HGI	A_HIS_75	ND1	A_ASP_73	OD2	3.177
1HGI	A_HIS_75	NE2	A_ASP_63	OD1	3.557
1HGI	A_ARG_90	NH2	A_ASP_60	OD1	3.597
1HGI	A_ARG_90	NH2	A_ASP_60	OD2	2.834
1HGI	A_ARG_109	NH1	A_GLU_89	OE1	2.511
1HGI	A_ARG_109	NH1	A_GLU_89	OE2	3.252
1HGI	A_ARG_109	NH2	B_GLU_67	OE1	3.638
1HGI	A_ARG_109	NH2	B_GLU_67	OE2	2.797
1HGI	A_ARG_141	NH2	A_ASP_77	OD1	2.933
1HGI	A_ARG_141	NH2	A_ASP_77	OD2	2.691
1HGI	A_LYS_176	NZ	A_GLU_123	OE2	2.677
1HGI	A_LYS_238	NZ	F_GLU_72	OE1	2.849
1HGI	A_LYS_238	NZ	F_GLU_72	OE2	2.839
1HGI	A_ARG_261	NH1	A_GLU_119	OE2	2.655
1HGI	A_ARG_261	NH2	A_GLU_119	OE1	2.852
1HGI	A_ARG_261	NH2	A_GLU_119	OE2	2.888
1HGI	A_LYS_264	NZ	A_ASP_85	OD1	3.460
1HGI	A_LYS_264	NZ	A_ASP_85	OD2	2.825
1HGI	A_ARG_269	NH1	B_GLU_67	OE1	2.748
1HGI	A_ARG_269	NH2	B_GLU_67	OE1	3.823
1HGI	A_LYS_292	NZ	A_ASP_291	OD1	2.954
1HGI	A_LYS_292	NZ	A_ASP_291	OD2	2.810
1HGI	A_LYS_299	NZ	B_GLU_69	OE2	2.728
1HGI	A_LYS_310	NZ	B_ASP_86	OD1	2.759

1HGI	A_LYS_310	NZ	B_ASP_90	OD1	2.527
1HGI	A_LYS_315	NZ	A_GLU_41	OE1	2.774
1HGI	A_LYS_326	NZ	A_GLU_325	OE1	2.913
1HGI	A_LYS_326	NZ	B_GLU_15	OE1	3.374
1HGI	A_LYS_326	NZ	B_GLU_15	OE2	2.794
1HGI	B_ARG_25	NH1	A_GLU_325	OE2	3.734
1HGI	B_ARG_25	NH2	A_GLU_325	OE2	2.929
1HGI	B_LYS_51	NZ	B_GLU_103	OE1	2.815
1HGI	B_ARG_54	NH1	B_GLU_57	OE1	2.860
1HGI	B_ARG_54	NH1	B_GLU_57	OE2	2.893
1HGI	B_ARG_54	NH1	F_GLU_97	OE2	3.222
1HGI	B_ARG_54	NH2	F_GLU_97	OE2	2.806
1HGI	B_LYS_58	NZ	B_GLU_61	OE2	3.021
1HGI	B_LYS_62	NZ	F_ASP_86	OD1	2.942
1HGI	B_LYS_62	NZ	F_ASP_86	OD2	2.668
1HGI	B_LYS_62	NZ	F_ASP_90	OD1	3.332
1HGI	B_LYS_62	NZ	F_ASP_90	OD2	2.667
1HGI	B_LYS_68	NZ	B_GLU_85	OE1	3.269
1HGI	B_LYS_68	NZ	B_GLU_85	OE2	2.791
1HGI	B_ARG_76	NH1	D_GLU_74	OE1	3.625
1HGI	B_ARG_76	NH1	D_GLU_74	OE2	2.918
1HGI	B_ARG_76	NH2	D_GLU_74	OE1	2.861
1HGI	B_ARG_76	NH2	D_GLU_74	OE2	3.621
1HGI	B_ARG_76	NH2	D_GLU_81	OE1	2.708
1HGI	B_ARG_76	NH2	D_GLU_81	OE2	3.474
1HGI	B_LYS_117	NZ	B_GLU_114	OE1	3.138
1HGI	B_LYS_117	NZ	B_GLU_114	OE2	2.563
1HGI	B_ARG_123	NH1	B_GLU_120	OE1	2.571
1HGI	B_ARG_123	NH1	B_GLU_120	OE2	2.840
1HGI	B_ARG_123	NH2	F_GLU_132	OE1	3.105
1HGI	B_ARG_124	NH1	B_GLU_120	OE1	3.733
1HGI	B_ARG_124	NH2	F_GLU_132	OE1	3.081
1HGI	B_ARG_124	NH2	F_GLU_132	OE2	3.356
1HGI	B_ARG_127	NH1	F_GLU_131	OE1	2.493
1HGI	B_LYS_143	NZ	B_ASP_145	OD2	2.749
1HGI	B_ARG_153	NH1	B_GLU_150	OE1	2.584
1HGI	B_HIS_159	NE2	B_ASP_160	OD2	3.012
1HGI	B_ARG_163	NH2	B_GLU_128	OE1	3.957
1HGI	B_ARG_163	NH2	F_GLU_131	OE1	2.586
1HGI	B_ARG_163	NH2	F_GLU_131	OE2	2.598
1HGI	B_ARG_170	NH1	B_GLU_131	OE2	2.767
1HGI	B_ARG_170	NH1	D_GLU_128	OE1	3.640
1HGI	B_ARG_170	NH1	D_GLU_128	OE2	3.301
1HGI	B_ARG_170	NH2	B_GLU_128	OE2	2.947
1HGI	B_LYS_174	NZ	D_ASP_164	OD1	2.745
1HGI	B_LYS_174	NZ	D_ASP_164	OD2	2.560
1HGI	C_LYS_27	NZ	D_GLU_97	OE1	2.951
1HGI	C_LYS_27	NZ	D_GLU_97	OE2	2.876
1HGI	C_LYS_50	NZ	C_ASP_275	OD1	3.635
1HGI	C_LYS_50	NZ	C_ASP_275	OD2	2.676
1HGI	C_ARG_57	NH2	C_GLU_82	OE1	2.525
1HGI	C_ARG_57	NH2	C_GLU_82	OE2	3.836
1HGI	C_HIS_75	ND1	C_ASP_73	OD1	2.875
1HGI	C_HIS_75	ND1	C_ASP_73	OD2	3.155
1HGI	C_HIS_75	NE2	C_ASP_63	OD1	3.544
1HGI	C_ARG_90	NH2	C_ASP_60	OD1	3.575
1HGI	C_ARG_90	NH2	C_ASP_60	OD2	2.774
1HGI	C_ARG_109	NH1	C_GLU_89	OE1	2.522

1HGI	C_ARG_109	NH1	C_GLU_89	OE2	3.270
1HGI	C_ARG_109	NH2	D_GLU_67	OE1	3.637
1HGI	C_ARG_109	NH2	D_GLU_67	OE2	2.819
1HGI	C_ARG_141	NH2	C_ASP_77	OD1	2.934
1HGI	C_ARG_141	NH2	C_ASP_77	OD2	2.703
1HGI	C_LYS_176	NZ	C_GLU_123	OE2	2.678
1HGI	C_LYS_238	NZ	B_GLU_72	OE1	2.671
1HGI	C_LYS_238	NZ	B_GLU_72	OE2	2.721
1HGI	C_ARG_261	NH1	C_GLU_119	OE2	2.664
1HGI	C_ARG_261	NH2	C_GLU_119	OE1	2.844
1HGI	C_ARG_261	NH2	C_GLU_119	OE2	2.850
1HGI	C_LYS_264	NZ	C_ASP_85	OD1	3.489
1HGI	C_LYS_264	NZ	C_ASP_85	OD2	2.832
1HGI	C_ARG_269	NH1	D_GLU_67	OE1	2.753
1HGI	C_ARG_269	NH2	D_GLU_67	OE1	3.850
1HGI	C_LYS_292	NZ	C_ASP_291	OD1	2.977
1HGI	C_LYS_292	NZ	C_ASP_291	OD2	2.816
1HGI	C_LYS_299	NZ	D_GLU_69	OE2	2.739
1HGI	C_LYS_310	NZ	D_ASP_86	OD1	2.772
1HGI	C_LYS_310	NZ	D_ASP_90	OD1	2.525
1HGI	C_LYS_315	NZ	C_GLU_41	OE1	2.748
1HGI	C_LYS_326	NZ	D_GLU_15	OE1	2.825
1HGI	C_LYS_326	NZ	D_GLU_15	OE2	3.570
1HGI	D_LYS_51	NZ	D_GLU_103	OE1	2.810
1HGI	D_ARG_54	NH1	B_GLU_97	OE2	3.254
1HGI	D_ARG_54	NH1	D_GLU_57	OE1	2.846
1HGI	D_ARG_54	NH1	D_GLU_57	OE2	2.899
1HGI	D_ARG_54	NH2	B_GLU_97	OE2	2.808
1HGI	D_LYS_58	NZ	D_GLU_61	OE2	2.998
1HGI	D_LYS_62	NZ	B_ASP_86	OD1	2.962
1HGI	D_LYS_62	NZ	B_ASP_86	OD2	2.570
1HGI	D_LYS_62	NZ	B_ASP_90	OD1	3.335
1HGI	D_LYS_62	NZ	B_ASP_90	OD2	2.541
1HGI	D_LYS_68	NZ	D_GLU_85	OE1	3.268
1HGI	D_LYS_68	NZ	D_GLU_85	OE2	2.807
1HGI	D_ARG_76	NH1	F_GLU_74	OE1	3.375
1HGI	D_ARG_76	NH1	F_GLU_74	OE2	2.776
1HGI	D_ARG_76	NH2	F_GLU_74	OE1	2.760
1HGI	D_ARG_76	NH2	F_GLU_74	OE2	3.657
1HGI	D_ARG_76	NH2	F_GLU_81	OE1	2.608
1HGI	D_ARG_76	NH2	F_GLU_81	OE2	3.506
1HGI	D_LYS_117	NZ	D_GLU_114	OE1	3.195
1HGI	D_LYS_117	NZ	D_GLU_114	OE2	2.582
1HGI	D_ARG_123	NH1	D_GLU_120	OE1	2.549
1HGI	D_ARG_123	NH1	D_GLU_120	OE2	2.835
1HGI	D_ARG_123	NH2	B_GLU_132	OE1	3.093
1HGI	D_ARG_124	NH1	D_GLU_120	OE1	3.750
1HGI	D_ARG_124	NH2	B_GLU_132	OE1	3.096
1HGI	D_ARG_124	NH2	B_GLU_132	OE2	3.377
1HGI	D_ARG_127	NH1	B_GLU_131	OE1	2.513
1HGI	D_LYS_143	NZ	D_ASP_145	OD2	2.778
1HGI	D_ARG_153	NH1	D_GLU_150	OE2	2.550
1HGI	D_HIS_159	NE2	D_ASP_160	OD2	3.012
1HGI	D_ARG_163	NH2	B_GLU_131	OE1	2.590
1HGI	D_ARG_163	NH2	B_GLU_131	OE2	2.616
1HGI	D_ARG_163	NH2	D_GLU_128	OE1	3.999
1HGI	D_ARG_170	NH1	D_GLU_131	OE2	2.771
1HGI	D_ARG_170	NH1	F_GLU_128	OE1	3.797

1HGI	D_ARG.170	NH1	F_GLU.128	OE2	3.417
1HGI	D_ARG.170	NH2	D_GLU.128	OE2	2.974
1HGI	D_LYS.174	NZ	F_ASP.164	OD1	2.814
1HGI	D_LYS.174	NZ	F_ASP.164	OD2	2.727
1HGI	E_LYS.27	NZ	F_GLU.97	OE1	2.961
1HGI	E_LYS.27	NZ	F_GLU.97	OE2	2.862
1HGI	E_LYS.50	NZ	E_ASP.275	OD1	3.624
1HGI	E_LYS.50	NZ	E_ASP.275	OD2	2.698
1HGI	E_ARG.57	NH2	E_GLU.82	OE1	2.652
1HGI	E_ARG.57	NH2	E_GLU.82	OE2	3.886
1HGI	E_HIS.75	ND1	E_ASP.73	OD1	2.868
1HGI	E_HIS.75	ND1	E_ASP.73	OD2	3.142
1HGI	E_HIS.75	NE2	E_ASP.63	OD1	3.556
1HGI	E_ARG.90	NH2	E_ASP.60	OD1	3.607
1HGI	E_ARG.90	NH2	E_ASP.60	OD2	2.841
1HGI	E_ARG.109	NH1	E_GLU.89	OE1	2.478
1HGI	E_ARG.109	NH1	E_GLU.89	OE2	3.260
1HGI	E_ARG.109	NH2	F_GLU.67	OE1	3.649
1HGI	E_ARG.109	NH2	F_GLU.67	OE2	2.781
1HGI	E_ARG.141	NH2	E_ASP.77	OD1	2.937
1HGI	E_ARG.141	NH2	E_ASP.77	OD2	2.703
1HGI	E_LYS.176	NZ	E_GLU.123	OE2	2.685
1HGI	E_LYS.238	NZ	D_GLU.72	OE1	2.803
1HGI	E_LYS.238	NZ	D_GLU.72	OE2	2.859
1HGI	E_ARG.261	NH1	E_GLU.119	OE2	2.651
1HGI	E_ARG.261	NH2	E_GLU.119	OE1	2.844
1HGI	E_ARG.261	NH2	E_GLU.119	OE2	2.870
1HGI	E_LYS.264	NZ	E_ASP.85	OD1	3.485
1HGI	E_LYS.264	NZ	E_ASP.85	OD2	2.858
1HGI	E_ARG.269	NH1	F_GLU.67	OE1	2.720
1HGI	E_ARG.269	NH2	F_GLU.67	OE1	3.815
1HGI	E_LYS.292	NZ	E_ASP.291	OD1	2.984
1HGI	E_LYS.292	NZ	E_ASP.291	OD2	2.865
1HGI	E_LYS.299	NZ	F_GLU.69	OE2	2.715
1HGI	E_LYS.310	NZ	F_ASP.86	OD1	2.757
1HGI	E_LYS.310	NZ	F_ASP.90	OD1	2.523
1HGI	E_LYS.315	NZ	E_GLU.41	OE1	2.741
1HGI	E_LYS.326	NZ	F_GLU.15	OE1	2.882
1HGI	E_LYS.326	NZ	F_GLU.15	OE2	3.090
1HGI	F_LYS.51	NZ	F_GLU.103	OE1	2.800
1HGI	F_ARG.54	NH1	D_GLU.97	OE2	3.254
1HGI	F_ARG.54	NH1	F_GLU.57	OE1	2.835
1HGI	F_ARG.54	NH1	F_GLU.57	OE2	2.892
1HGI	F_ARG.54	NH2	D_GLU.97	OE2	2.750
1HGI	F_LYS.58	NZ	F_GLU.61	OE2	3.021
1HGI	F_LYS.62	NZ	D_ASP.86	OD1	2.884
1HGI	F_LYS.62	NZ	D_ASP.86	OD2	2.563
1HGI	F_LYS.62	NZ	D_ASP.90	OD1	3.358
1HGI	F_LYS.62	NZ	D_ASP.90	OD2	2.609
1HGI	F_LYS.68	NZ	F_GLU.85	OE1	3.264
1HGI	F_LYS.68	NZ	F_GLU.85	OE2	2.739
1HGI	F_ARG.76	NH1	B_GLU.74	OE1	3.420
1HGI	F_ARG.76	NH1	B_GLU.74	OE2	2.771
1HGI	F_ARG.76	NH2	B_GLU.74	OE1	2.763
1HGI	F_ARG.76	NH2	B_GLU.74	OE2	3.604
1HGI	F_ARG.76	NH2	B_GLU.81	OE1	2.645
1HGI	F_ARG.76	NH2	B_GLU.81	OE2	3.592
1HGI	F_LYS.117	NZ	F_GLU.114	OE1	3.182

1HGI	F_LYS_117	NZ	F_GLU_114	OE2	2.543
1HGI	F_ARG_123	NH1	F_GLU_120	OE1	2.586
1HGI	F_ARG_123	NH1	F_GLU_120	OE2	2.812
1HGI	F_ARG_123	NH2	D_GLU_132	OE1	3.144
1HGI	F_ARG_124	NH1	F_GLU_120	OE1	3.763
1HGI	F_ARG_124	NH2	D_GLU_132	OE1	3.185
1HGI	F_ARG_124	NH2	D_GLU_132	OE2	3.386
1HGI	F_ARG_127	NH1	D_GLU_131	OE1	2.561
1HGI	F_LYS_143	NZ	F_ASP_145	OD2	2.731
1HGI	F_ARG_153	NH1	F_GLU_150	OE2	2.577
1HGI	F_HIS_159	NE2	F_ASP_160	OD2	3.055
1HGI	F_ARG_163	NH2	D_GLU_131	OE1	2.567
1HGI	F_ARG_163	NH2	D_GLU_131	OE2	2.692
1HGI	F_ARG_163	NH2	F_GLU_128	OE1	3.975
1HGI	F_ARG_170	NH1	B_GLU_128	OE1	3.621
1HGI	F_ARG_170	NH1	B_GLU_128	OE2	3.345
1HGI	F_ARG_170	NH1	F_GLU_131	OE2	2.754
1HGI	F_ARG_170	NH2	F_GLU_128	OE2	2.972
1HGI	F_LYS_174	NZ	B_ASP_164	OD1	2.789
1HGI	F_LYS_174	NZ	B_ASP_164	OD2	2.521
1HGJ	A_LYS_27	NZ	B_GLU_97	OE1	2.775
1HGJ	A_LYS_27	NZ	B_GLU_97	OE2	2.807
1HGJ	A_LYS_50	NZ	A_ASP_275	OD1	3.487
1HGJ	A_LYS_50	NZ	A_ASP_275	OD2	2.742
1HGJ	A_ARG_57	NH2	A_GLU_82	OE1	2.521
1HGJ	A_ARG_57	NH2	A_GLU_82	OE2	3.796
1HGJ	A_HIS_75	ND1	A_ASP_73	OD1	2.831
1HGJ	A_HIS_75	ND1	A_ASP_73	OD2	3.407
1HGJ	A_HIS_75	NE2	A_ASP_63	OD1	3.353
1HGJ	A_ARG_90	NH2	A_ASP_60	OD1	3.662
1HGJ	A_ARG_90	NH2	A_ASP_60	OD2	2.811
1HGJ	A_ARG_109	NH1	A_GLU_89	OE1	2.528
1HGJ	A_ARG_109	NH1	A_GLU_89	OE2	3.223
1HGJ	A_ARG_109	NH2	B_GLU_67	OE1	3.648
1HGJ	A_ARG_109	NH2	B_GLU_67	OE2	2.748
1HGJ	A_ARG_141	NH2	A_ASP_77	OD1	2.818
1HGJ	A_ARG_141	NH2	A_ASP_77	OD2	2.748
1HGJ	A_LYS_176	NZ	A_GLU_123	OE2	2.680
1HGJ	A_HIS_183	NE2	A_GLU_190	OE2	3.316
1HGJ	A_LYS_238	NZ	F_GLU_72	OE1	2.903
1HGJ	A_LYS_238	NZ	F_GLU_72	OE2	2.788
1HGJ	A_ARG_261	NH1	A_GLU_119	OE2	2.647
1HGJ	A_ARG_261	NH2	A_GLU_119	OE1	2.898
1HGJ	A_ARG_261	NH2	A_GLU_119	OE2	2.927
1HGJ	A_LYS_264	NZ	A_ASP_85	OD1	3.715
1HGJ	A_LYS_264	NZ	A_ASP_85	OD2	2.840
1HGJ	A_ARG_269	NH1	B_GLU_67	OE1	2.736
1HGJ	A_ARG_269	NH2	B_GLU_67	OE1	3.791
1HGJ	A_LYS_292	NZ	A_ASP_291	OD1	2.856
1HGJ	A_LYS_292	NZ	A_ASP_291	OD2	2.799
1HGJ	A_LYS_299	NZ	B_GLU_69	OE2	2.821
1HGJ	A_LYS_310	NZ	B_ASP_86	OD1	2.922
1HGJ	A_LYS_310	NZ	B_ASP_90	OD1	2.569
1HGJ	A_LYS_315	NZ	A_GLU_41	OE1	2.855
1HGJ	A_LYS_326	NZ	A_GLU_325	OE1	2.919
1HGJ	A_LYS_326	NZ	B_GLU_15	OE1	3.187
1HGJ	A_LYS_326	NZ	B_GLU_15	OE2	2.826
1HGJ	B_ARG_25	NH1	A_GLU_325	OE2	3.775

1HGJ	B_ARG_25	NH2	A_GLU_325	OE2	2.974
1HGJ	B_LYS_51	NZ	B_GLU_103	OE1	2.778
1HGJ	B_ARG_54	NH1	B_GLU_57	OE1	2.874
1HGJ	B_ARG_54	NH1	B_GLU_57	OE2	2.925
1HGJ	B_ARG_54	NH1	F_GLU_97	OE2	3.272
1HGJ	B_ARG_54	NH2	F_GLU_97	OE2	2.774
1HGJ	B_LYS_58	NZ	B_GLU_61	OE2	3.374
1HGJ	B_LYS_62	NZ	F_ASP_86	OD1	2.863
1HGJ	B_LYS_62	NZ	F_ASP_86	OD2	2.651
1HGJ	B_LYS_62	NZ	F_ASP_90	OD1	3.453
1HGJ	B_LYS_62	NZ	F_ASP_90	OD2	2.738
1HGJ	B_LYS_68	NZ	B_GLU_85	OE1	3.167
1HGJ	B_LYS_68	NZ	B_GLU_85	OE2	2.782
1HGJ	B_ARG_76	NH1	D_GLU_74	OE1	3.648
1HGJ	B_ARG_76	NH1	D_GLU_74	OE2	2.885
1HGJ	B_ARG_76	NH2	D_GLU_74	OE1	2.846
1HGJ	B_ARG_76	NH2	D_GLU_74	OE2	3.547
1HGJ	B_ARG_76	NH2	D_GLU_81	OE1	2.721
1HGJ	B_ARG_76	NH2	D_GLU_81	OE2	3.500
1HGJ	B_LYS_117	NZ	B_GLU_114	OE1	3.054
1HGJ	B_LYS_117	NZ	B_GLU_114	OE2	2.578
1HGJ	B_ARG_123	NH1	B_GLU_120	OE1	2.614
1HGJ	B_ARG_123	NH1	B_GLU_120	OE2	2.737
1HGJ	B_ARG_123	NH2	F_GLU_132	OE1	3.120
1HGJ	B_ARG_124	NH1	B_GLU_120	OE1	3.704
1HGJ	B_ARG_124	NH2	F_GLU_132	OE1	3.095
1HGJ	B_ARG_124	NH2	F_GLU_132	OE2	3.375
1HGJ	B_ARG_127	NH1	F_GLU_131	OE1	2.484
1HGJ	B_LYS_143	NZ	B_ASP_145	OD2	2.863
1HGJ	B_ARG_153	NH1	B_GLU_150	OE1	2.677
1HGJ	B_HIS_159	NE2	B_ASP_160	OD2	3.106
1HGJ	B_ARG_163	NH2	F_GLU_131	OE1	2.591
1HGJ	B_ARG_163	NH2	F_GLU_131	OE2	2.571
1HGJ	B_ARG_170	NH1	B_GLU_131	OE2	2.795
1HGJ	B_ARG_170	NH1	D_GLU_128	OE1	3.291
1HGJ	B_ARG_170	NH1	D_GLU_128	OE2	3.706
1HGJ	B_ARG_170	NH2	B_GLU_128	OE2	2.712
1HGJ	B_LYS_174	NZ	D_ASP_164	OD1	2.810
1HGJ	B_LYS_174	NZ	D_ASP_164	OD2	2.550
1HGJ	C_LYS_27	NZ	D_GLU_97	OE1	2.755
1HGJ	C_LYS_27	NZ	D_GLU_97	OE2	2.824
1HGJ	C_LYS_50	NZ	C_ASP_275	OD1	3.494
1HGJ	C_LYS_50	NZ	C_ASP_275	OD2	2.741
1HGJ	C_ARG_57	NH2	C_GLU_82	OE1	2.545
1HGJ	C_ARG_57	NH2	C_GLU_82	OE2	3.939
1HGJ	C_HIS_75	ND1	C_ASP_73	OD1	2.800
1HGJ	C_HIS_75	ND1	C_ASP_73	OD2	3.368
1HGJ	C_HIS_75	NE2	C_ASP_63	OD1	3.332
1HGJ	C_ARG_90	NH2	C_ASP_60	OD1	3.676
1HGJ	C_ARG_90	NH2	C_ASP_60	OD2	2.784
1HGJ	C_ARG_109	NH1	C_GLU_89	OE1	2.558
1HGJ	C_ARG_109	NH1	C_GLU_89	OE2	3.226
1HGJ	C_ARG_109	NH2	D_GLU_67	OE1	3.638
1HGJ	C_ARG_109	NH2	D_GLU_67	OE2	2.758
1HGJ	C_ARG_141	NH2	C_ASP_77	OD1	2.808
1HGJ	C_ARG_141	NH2	C_ASP_77	OD2	2.737
1HGJ	C_LYS_176	NZ	C_GLU_123	OE2	2.691
1HGJ	C_HIS_183	NE2	C_GLU_190	OE2	3.331

1HGJ	C_LYS_238	NZ	B_GLU_72	OE1	2.749
1HGJ	C_LYS_238	NZ	B_GLU_72	OE2	2.713
1HGJ	C_ARG_261	NH1	C_GLU_119	OE2	2.654
1HGJ	C_ARG_261	NH2	C_GLU_119	OE1	2.921
1HGJ	C_ARG_261	NH2	C_GLU_119	OE2	2.914
1HGJ	C_LYS_264	NZ	C_ASP_85	OD1	3.727
1HGJ	C_LYS_264	NZ	C_ASP_85	OD2	2.825
1HGJ	C_ARG_269	NH1	D_GLU_67	OE1	2.708
1HGJ	C_ARG_269	NH2	D_GLU_67	OE1	3.781
1HGJ	C_LYS_292	NZ	C_ASP_291	OD1	2.908
1HGJ	C_LYS_292	NZ	C_ASP_291	OD2	2.818
1HGJ	C_LYS_299	NZ	D_GLU_69	OE2	2.827
1HGJ	C_LYS_310	NZ	D_ASP_86	OD1	2.943
1HGJ	C_LYS_310	NZ	D_ASP_90	OD1	2.532
1HGJ	C_LYS_315	NZ	C_GLU_41	OE1	2.864
1HGJ	C_LYS_326	NZ	D_GLU_15	OE1	2.911
1HGJ	C_LYS_326	NZ	D_GLU_15	OE2	3.904
1HGJ	D_LYS_51	NZ	D_GLU_103	OE1	2.796
1HGJ	D_ARG_54	NH1	B_GLU_97	OE2	3.338
1HGJ	D_ARG_54	NH1	D_GLU_57	OE1	2.865
1HGJ	D_ARG_54	NH1	D_GLU_57	OE2	2.909
1HGJ	D_ARG_54	NH2	B_GLU_97	OE2	2.835
1HGJ	D_LYS_58	NZ	D_GLU_61	OE2	3.356
1HGJ	D_LYS_62	NZ	B_ASP_86	OD1	2.910
1HGJ	D_LYS_62	NZ	B_ASP_86	OD2	2.574
1HGJ	D_LYS_62	NZ	B_ASP_90	OD1	3.419
1HGJ	D_LYS_62	NZ	B_ASP_90	OD2	2.622
1HGJ	D_LYS_68	NZ	D_GLU_85	OE1	3.144
1HGJ	D_LYS_68	NZ	D_GLU_85	OE2	2.820
1HGJ	D_ARG_76	NH1	F_GLU_74	OE1	3.424
1HGJ	D_ARG_76	NH1	F_GLU_74	OE2	2.763
1HGJ	D_ARG_76	NH2	F_GLU_74	OE1	2.714
1HGJ	D_ARG_76	NH2	F_GLU_74	OE2	3.550
1HGJ	D_ARG_76	NH2	F_GLU_81	OE1	2.684
1HGJ	D_ARG_76	NH2	F_GLU_81	OE2	3.574
1HGJ	D_LYS_117	NZ	D_GLU_114	OE1	3.086
1HGJ	D_LYS_117	NZ	D_GLU_114	OE2	2.611
1HGJ	D_ARG_123	NH1	D_GLU_120	OE1	2.598
1HGJ	D_ARG_123	NH1	D_GLU_120	OE2	2.741
1HGJ	D_ARG_123	NH2	B_GLU_132	OE1	3.075
1HGJ	D_ARG_124	NH1	D_GLU_120	OE1	3.708
1HGJ	D_ARG_124	NH2	B_GLU_132	OE1	3.055
1HGJ	D_ARG_124	NH2	B_GLU_132	OE2	3.342
1HGJ	D_ARG_127	NH1	B_GLU_131	OE1	2.514
1HGJ	D_LYS_143	NZ	D_ASP_145	OD2	2.897
1HGJ	D_ARG_153	NH1	D_GLU_150	OE1	2.604
1HGJ	D_HIS_159	NE2	D_ASP_160	OD2	3.102
1HGJ	D_ARG_163	NH2	B_GLU_131	OE1	2.599
1HGJ	D_ARG_163	NH2	B_GLU_131	OE2	2.594
1HGJ	D_ARG_170	NH1	D_GLU_131	OE2	2.793
1HGJ	D_ARG_170	NH1	F_GLU_128	OE1	3.405
1HGJ	D_ARG_170	NH1	F_GLU_128	OE2	3.769
1HGJ	D_ARG_170	NH2	D_GLU_128	OE2	2.726
1HGJ	D_LYS_174	NZ	F_ASP_164	OD1	2.824
1HGJ	D_LYS_174	NZ	F_ASP_164	OD2	2.673
1HGJ	E_LYS_27	NZ	F_GLU_97	OE1	2.779
1HGJ	E_LYS_27	NZ	F_GLU_97	OE2	2.813
1HGJ	E_LYS_50	NZ	E_ASP_275	OD1	3.506

1HGJ	E_LYS_50	NZ	E_ASP_275	OD2	2.739
1HGJ	E_ARG_57	NH2	E_GLU_82	OE1	2.663
1HGJ	E_HIS_75	ND1	E_ASP_73	OD1	2.798
1HGJ	E_HIS_75	ND1	E_ASP_73	OD2	3.347
1HGJ	E_HIS_75	NE2	E_ASP_63	OD1	3.371
1HGJ	E_ARG_90	NH2	E_ASP_60	OD1	3.683
1HGJ	E_ARG_90	NH2	E_ASP_60	OD2	2.826
1HGJ	E_ARG_109	NH1	E_GLU_89	OE1	2.541
1HGJ	E_ARG_109	NH1	E_GLU_89	OE2	3.205
1HGJ	E_ARG_109	NH2	F_GLU_67	OE1	3.635
1HGJ	E_ARG_109	NH2	F_GLU_67	OE2	2.759
1HGJ	E_ARG_141	NH2	E_ASP_77	OD1	2.840
1HGJ	E_ARG_141	NH2	E_ASP_77	OD2	2.747
1HGJ	E_LYS_176	NZ	E_GLU_123	OE2	2.685
1HGJ	E_HIS_183	NE2	E_GLU_190	OE2	3.333
1HGJ	E_LYS_238	NZ	D_GLU_72	OE1	2.865
1HGJ	E_LYS_238	NZ	D_GLU_72	OE2	2.804
1HGJ	E_ARG_261	NH1	E_GLU_119	OE2	2.651
1HGJ	E_ARG_261	NH2	E_GLU_119	OE1	2.905
1HGJ	E_ARG_261	NH2	E_GLU_119	OE2	2.913
1HGJ	E_LYS_264	NZ	E_ASP_85	OD1	3.746
1HGJ	E_LYS_264	NZ	E_ASP_85	OD2	2.856
1HGJ	E_ARG_269	NH1	F_GLU_67	OE1	2.691
1HGJ	E_ARG_269	NH2	F_GLU_67	OE1	3.759
1HGJ	E_LYS_292	NZ	E_ASP_291	OD1	2.893
1HGJ	E_LYS_292	NZ	E_ASP_291	OD2	2.833
1HGJ	E_LYS_299	NZ	F_GLU_69	OE2	2.806
1HGJ	E_LYS_310	NZ	F_ASP_86	OD1	2.930
1HGJ	E_LYS_310	NZ	F_ASP_90	OD1	2.553
1HGJ	E_LYS_315	NZ	E_GLU_41	OE1	2.860
1HGJ	E_LYS_326	NZ	F_GLU_15	OE1	2.874
1HGJ	E_LYS_326	NZ	F_GLU_15	OE2	3.254
1HGJ	F_LYS_51	NZ	F_GLU_103	OE1	2.791
1HGJ	F_ARG_54	NH1	D_GLU_97	OE2	3.349
1HGJ	F_ARG_54	NH1	F_GLU_57	OE1	2.862
1HGJ	F_ARG_54	NH1	F_GLU_57	OE2	2.926
1HGJ	F_ARG_54	NH2	D_GLU_97	OE2	2.771
1HGJ	F_LYS_58	NZ	F_GLU_61	OE2	3.370
1HGJ	F_LYS_62	NZ	D_ASP_86	OD1	2.846
1HGJ	F_LYS_62	NZ	D_ASP_86	OD2	2.568
1HGJ	F_LYS_62	NZ	D_ASP_90	OD1	3.467
1HGJ	F_LYS_62	NZ	D_ASP_90	OD2	2.658
1HGJ	F_LYS_68	NZ	F_GLU_85	OE1	3.136
1HGJ	F_LYS_68	NZ	F_GLU_85	OE2	2.737
1HGJ	F_ARG_76	NH1	B_GLU_74	OE1	3.383
1HGJ	F_ARG_76	NH1	B_GLU_74	OE2	2.704
1HGJ	F_ARG_76	NH2	B_GLU_74	OE1	2.715
1HGJ	F_ARG_76	NH2	B_GLU_74	OE2	3.551
1HGJ	F_ARG_76	NH2	B_GLU_81	OE1	2.654
1HGJ	F_ARG_76	NH2	B_GLU_81	OE2	3.611
1HGJ	F_LYS_117	NZ	F_GLU_114	OE1	3.106
1HGJ	F_LYS_117	NZ	F_GLU_114	OE2	2.590
1HGJ	F_ARG_123	NH1	F_GLU_120	OE1	2.625
1HGJ	F_ARG_123	NH1	F_GLU_120	OE2	2.732
1HGJ	F_ARG_123	NH2	D_GLU_132	OE1	3.110
1HGJ	F_ARG_124	NH1	F_GLU_120	OE1	3.711
1HGJ	F_ARG_124	NH2	D_GLU_132	OE1	3.125
1HGJ	F_ARG_124	NH2	D_GLU_132	OE2	3.360

1HGJ	F_ARG_127	NH1	D_GLU_131	OE1	2.554
1HGJ	F_LYS_143	NZ	F_ASP_145	OD2	2.873
1HGJ	F_ARG_153	NH1	F_GLU_150	OE2	2.597
1HGJ	F_HIS_159	NE2	F_ASP_160	OD2	3.139
1HGJ	F_ARG_163	NH2	D_GLU_131	OE1	2.636
1HGJ	F_ARG_163	NH2	D_GLU_131	OE2	2.696
1HGJ	F_ARG_170	NH1	B_GLU_128	OE1	3.311
1HGJ	F_ARG_170	NH1	B_GLU_128	OE2	3.766
1HGJ	F_ARG_170	NH1	F_GLU_131	OE2	2.790
1HGJ	F_ARG_170	NH2	F_GLU_128	OE2	2.737
1HGJ	F_LYS_174	NZ	B_ASP_164	OD1	2.859
1HGJ	F_LYS_174	NZ	B_ASP_164	OD2	2.554
1HIL	A_LYS_28	NZ	B_ASP_99	OD1	3.388
1HIL	A_LYS_28	NZ	B_ASP_99	OD2	3.371
1HIL	A_LYS_30	NZ	B_ASP_99	OD2	3.991
1HIL	A_ARG_61	NH2	A_GLU_81	OE2	3.453
1HIL	A_ARG_61	NH2	A_ASP_82	OD1	2.803
1HIL	A_ARG_61	NH2	A_ASP_82	OD2	3.572
1HIL	A_LYS_142	NZ	A_GLU_105	OE1	3.449
1HIL	A_LYS_147	NZ	A_GLU_154	OE1	3.856
1HIL	A_LYS_147	NZ	A_GLU_154	OE2	3.602
1HIL	A_LYS_149	NZ	A_GLU_195	OE2	3.175
1HIL	A_ARG_155	NH2	A_GLU_185	OE1	3.376
1HIL	A_ARG_155	NH2	A_GLU_185	OE2	2.897
1HIL	A_LYS_169	NZ	A_ASP_170	OD2	2.962
1HIL	A_LYS_183	NZ	A_GLU_187	OE1	2.919
1HIL	A_LYS_183	NZ	A_GLU_187	OE2	3.001
1HIL	A_ARG_188	NH1	A_ASP_184	OD1	2.997
1HIL	A_ARG_188	NH2	A_ASP_184	OD1	2.719
1HIL	A_HIS_189	ND1	A_ASP_151	OD2	2.887
1HIL	A_HIS_189	NE2	A_GLU_185	OE2	3.281
1HIL	A_LYS_199	NZ	A_ASP_110	OD1	3.849
1HIL	A_LYS_199	NZ	A_ASP_110	OD2	2.611
1HIL	B_ARG_38	NH1	B_ASP_86	OD1	2.872
1HIL	B_ARG_38	NH2	B_GLU_46	OE1	2.814
1HIL	B_ARG_38	NH2	B_ASP_86	OD1	3.831
1HIL	B_ARG_44	NH1	B_ASP_42	OD2	3.962
1HIL	B_ARG_44	NH2	B_ASP_42	OD2	2.795
1HIL	B_ARG_66	NH1	B_ASP_86	OD1	3.878
1HIL	B_ARG_66	NH1	B_ASP_86	OD2	2.766
1HIL	B_ARG_66	NH2	B_ASP_86	OD1	2.971
1HIL	B_ARG_66	NH2	B_ASP_86	OD2	3.323
1HIL	B_ARG_94	NH2	B_GLU_96	OE1	2.937
1HIL	B_ARG_94	NH2	B_GLU_96	OE2	3.442
1HIL	B_ARG_95	NH1	A_ASP_91	OD1	2.828
1HIL	B_ARG_95	NH1	A_ASP_91	OD2	3.804
1HIL	B_ARG_95	NH2	A_ASP_91	OD1	3.160
1HIL	B_ARG_95	NH2	A_ASP_91	OD2	3.904
1HIL	B_HIS_172	NE2	A_ASP_167	OD2	3.701
1HIL	B_LYS_221	NZ	A_GLU_123	OE1	2.980
1HIL	B_LYS_222	NZ	B_GLU_226	OE2	3.471
1HIL	C_LYS_28	NZ	D_ASP_99	OD1	3.565
1HIL	C_LYS_28	NZ	D_ASP_99	OD2	3.509
1HIL	C_ARG_61	NH2	C_GLU_81	OE1	3.959
1HIL	C_ARG_61	NH2	C_GLU_81	OE2	3.333
1HIL	C_ARG_61	NH2	C_ASP_82	OD1	2.824
1HIL	C_ARG_61	NH2	C_ASP_82	OD2	3.820
1HIL	C_LYS_149	NZ	C_GLU_195	OE1	2.867

1HIL	C_LYS_149	NZ	C_GLU_195	OE2	3.545
1HIL	C_ARG_155	NH1	C_GLU_185	OE2	3.376
1HIL	C_LYS_183	NZ	C_GLU_187	OE1	2.913
1HIL	C_LYS_183	NZ	C_GLU_187	OE2	2.922
1HIL	C_ARG_188	NH2	C_ASP_184	OD2	3.681
1HIL	C_HIS_189	ND1	C_ASP_151	OD2	2.657
1HIL	C_LYS_199	NZ	C_ASP_110	OD1	3.869
1HIL	C_LYS_199	NZ	C_ASP_110	OD2	3.718
1HIL	D_ARG_38	NH1	D_GLU_85	OE2	3.765
1HIL	D_ARG_38	NH1	D_ASP_86	OD1	2.811
1HIL	D_ARG_38	NH2	D_GLU_46	OE1	2.914
1HIL	D_ARG_38	NH2	D_GLU_85	OE1	3.376
1HIL	D_ARG_38	NH2	D_GLU_85	OE2	2.939
1HIL	D_ARG_38	NH2	D_ASP_86	OD1	3.843
1HIL	D_LYS_64	NZ	D_ASP_61	OD1	3.347
1HIL	D_ARG_66	NH1	D_ASP_86	OD2	2.825
1HIL	D_ARG_66	NH2	D_GLU_85	OE2	3.393
1HIL	D_ARG_66	NH2	D_ASP_86	OD1	3.008
1HIL	D_ARG_66	NH2	D_ASP_86	OD2	3.234
1HIL	D_ARG_94	NH2	D_GLU_96	OE1	3.117
1HIL	D_ARG_94	NH2	D_GLU_96	OE2	3.597
1HIL	D_ARG_95	NH1	C_ASP_91	OD1	2.906
1HIL	D_ARG_95	NH1	C_ASP_91	OD2	3.993
1HIL	D_ARG_95	NH2	C_ASP_91	OD1	3.045
1HIL	D_ARG_95	NH2	C_ASP_91	OD2	3.822
1HIL	D_LYS_221	NZ	C_GLU_123	OE1	2.896
1HIL	D_LYS_221	NZ	C_GLU_123	OE2	3.091
1HIM	H_ARG_54	NH1	H_ASP_60	OD1	3.270
1HIM	H_ARG_61	NH1	H_ASP_82	OD1	2.766
1HIM	H_ARG_61	NH1	H_ASP_82	OD2	2.580
1HIM	H_ARG_61	NH2	H_GLU_81	OE1	3.629
1HIM	H_ARG_61	NH2	H_GLU_81	OE2	3.486
1HIM	H_LYS_103	NZ	H_GLU_105	OE1	2.947
1HIM	H_LYS_103	NZ	H_GLU_105	OE2	3.074
1HIM	H_LYS_103	NZ	H_ASP_165	OD1	2.840
1HIM	H_LYS_103	NZ	H_ASP_165	OD2	2.960
1HIM	H_ARG_108	NH2	H_ASP_170	OD1	3.527
1HIM	H_LYS_142	NZ	H_GLU_105	OE2	3.186
1HIM	H_LYS_149	NZ	H_GLU_195	OE1	3.565
1HIM	H_ARG_155	NH1	H_GLU_185	OE1	3.606
1HIM	H_ARG_155	NH2	H_GLU_185	OE1	3.185
1HIM	H_LYS_183	NZ	H_GLU_187	OE1	3.388
1HIM	H_ARG_188	NH1	H_ASP_184	OD2	3.229
1HIM	H_ARG_188	NH2	H_ASP_184	OD2	3.788
1HIM	H_ARG_188	NH2	H_GLU_185	OE2	3.216
1HIM	H_HIS_189	ND1	H_ASP_151	OD2	3.238
1HIM	H_HIS_189	NE2	H_GLU_185	OE1	3.139
1HIM	H_HIS_189	NE2	H_GLU_185	OE2	2.919
1HIM	H_LYS_199	NZ	H_ASP_110	OD1	3.999
1HIM	H_LYS_199	NZ	H_ASP_110	OD2	3.600
1HIM	H_ARG_211	NH2	H_GLU_187	OE2	3.728
1HIM	L_ARG_38	NH1	L_GLU_46	OE1	2.537
1HIM	L_ARG_38	NH2	L_ASP_86	OD1	2.913
1HIM	L_ARG_44	NH1	L_ASP_42	OD2	3.518
1HIM	L_ARG_44	NH2	L_ASP_42	OD2	2.772
1HIM	L_LYS_64	NZ	L_ASP_61	OD1	3.754
1HIM	L_ARG_66	NH2	L_ASP_86	OD1	3.439
1HIM	L_ARG_66	NH2	L_ASP_86	OD2	2.636

1HIM	L_ARG_94	NH2	L_GLU_96	OE1	2.855
1HIM	L_ARG_94	NH2	L_GLU_96	OE2	2.784
1HIM	L_ARG_95	NH1	H_ASP_91	OD1	3.100
1HIM	L_ARG_95	NH2	H_ASP_91	OD1	3.427
1HIM	L_ARG_95	NH2	P_ASP_104	OD1	3.909
1HIM	L_ARG_95	NH2	P_ASP_104	OD2	3.079
1HIM	L_LYS_218	NZ	L_ASP_220	OD1	2.947
1HIM	L_LYS_218	NZ	L_ASP_220	OD2	3.790
1HIM	L_LYS_221	NZ	H_GLU_123	OE1	3.486
1HIM	L_LYS_221	NZ	H_GLU_123	OE2	2.924
1HIM	L_LYS_222	NZ	L_GLU_226	OE1	3.594
1HIM	L_LYS_222	NZ	L_GLU_226	OE2	3.507
1HIM	J_LYS_28	NZ	M_GLU_100	OE1	3.991
1HIM	J_LYS_28	NZ	M_GLU_100	OE2	3.433
1HIM	J_ARG_54	NH1	J_ASP_60	OD1	3.053
1HIM	J_ARG_61	NH1	J_GLU_81	OE1	2.794
1HIM	J_ARG_61	NH1	J_ASP_82	OD1	2.566
1HIM	J_ARG_61	NH1	J_ASP_82	OD2	2.940
1HIM	J_ARG_61	NH2	J_GLU_81	OE1	2.977
1HIM	J_ARG_61	NH2	J_GLU_81	OE2	3.767
1HIM	J_LYS_103	NZ	J_GLU_105	OE1	3.363
1HIM	J_LYS_103	NZ	J_GLU_105	OE2	3.574
1HIM	J_LYS_103	NZ	J_ASP_165	OD1	2.834
1HIM	J_LYS_103	NZ	J_ASP_165	OD2	3.265
1HIM	J_ARG_108	NH1	J_ASP_170	OD2	3.737
1HIM	J_LYS_142	NZ	J_GLU_105	OE2	3.350
1HIM	J_LYS_147	NZ	J_GLU_154	OE1	3.824
1HIM	J_LYS_149	NZ	J_GLU_195	OE1	2.922
1HIM	J_ARG_155	NH1	J_GLU_185	OE2	2.780
1HIM	J_ARG_155	NH2	J_GLU_185	OE2	2.860
1HIM	J_LYS_183	NZ	J_GLU_187	OE1	3.132
1HIM	J_LYS_183	NZ	J_GLU_187	OE2	3.144
1HIM	J_ARG_188	NH1	J_GLU_185	OE1	3.001
1HIM	J_ARG_188	NH2	J_GLU_185	OE1	3.202
1HIM	J_HIS_189	ND1	J_ASP_151	OD2	3.228
1HIM	J_HIS_189	NE2	J_GLU_185	OE1	3.040
1HIM	J_HIS_189	NE2	J_GLU_185	OE2	3.204
1HIM	J_LYS_199	NZ	J_ASP_110	OD1	2.949
1HIM	J_LYS_199	NZ	J_ASP_110	OD2	3.017
1HIM	M_ARG_38	NH1	M_ASP_86	OD1	2.851
1HIM	M_ARG_38	NH2	M_GLU_46	OE1	3.834
1HIM	M_ARG_38	NH2	M_ASP_86	OD1	3.546
1HIM	M_LYS_64	NZ	M_ASP_61	OD1	3.375
1HIM	M_LYS_64	NZ	M_ASP_61	OD2	3.721
1HIM	M_ARG_66	NH1	M_ASP_86	OD2	2.851
1HIM	M_ARG_66	NH2	M_ASP_86	OD1	3.649
1HIM	M_ARG_66	NH2	M_ASP_86	OD2	3.020
1HIM	M_LYS_75	NZ	M_ASP_72	OD2	3.415
1HIM	M_LYS_83	NZ	M_GLU_85	OE2	3.803
1HIM	M_LYS_83	NZ	M_ASP_86	OD1	2.818
1HIM	M_LYS_83	NZ	M_ASP_86	OD2	3.385
1HIM	M_ARG_94	NH2	M_GLU_96	OE1	2.883
1HIM	M_ARG_94	NH2	M_GLU_96	OE2	2.984
1HIM	M_ARG_95	NH1	J_ASP_91	OD1	2.854
1HIM	M_ARG_95	NH2	J_ASP_91	OD1	3.712
1HIM	M_ARG_95	NH2	R_ASP_104	OD1	2.834
1HIM	M_ARG_95	NH2	R_ASP_104	OD2	3.540
1HIM	M_LYS_222	NZ	M_GLU_226	OE2	2.900

1HIN	L_LYS_28	NZ	H_GLU_100	OE2	2.975
1HIN	L_ARG_54	NH1	L_ASP_60	OD1	2.976
1HIN	L_ARG_54	NH2	L_ASP_60	OD1	3.006
1HIN	L_ARG_61	NH2	L_ASP_82	OD1	3.350
1HIN	L_LYS_103	NZ	L_GLU_105	OE1	3.163
1HIN	L_LYS_103	NZ	L_GLU_105	OE2	2.963
1HIN	L_LYS_103	NZ	L_ASP_165	OD1	3.325
1HIN	L_LYS_107	NZ	L_GLU_17	OE1	3.860
1HIN	L_LYS_147	NZ	L_GLU_195	OE2	3.604
1HIN	L_LYS_183	NZ	L_GLU_187	OE1	3.063
1HIN	L_LYS_183	NZ	L_GLU_187	OE2	2.809
1HIN	L_ARG_188	NH1	L_GLU_185	OE1	3.655
1HIN	L_HIS_189	ND1	L_ASP_151	OD2	2.920
1HIN	L_HIS_189	NE2	L_GLU_185	OE2	2.966
1HIN	H_ARG_38	NH1	H_ASP_86	OD1	2.756
1HIN	H_ARG_38	NH2	H_GLU_46	OE2	3.346
1HIN	H_ARG_38	NH2	H_ASP_86	OD1	3.928
1HIN	H_ARG_44	NH1	H_ASP_42	OD1	3.927
1HIN	H_ARG_44	NH1	H_ASP_42	OD2	3.226
1HIN	H_ARG_44	NH2	H_ASP_42	OD1	3.335
1HIN	H_ARG_66	NH1	H_ASP_86	OD1	3.830
1HIN	H_ARG_66	NH1	H_ASP_86	OD2	3.068
1HIN	H_ARG_66	NH2	H_ASP_86	OD1	3.938
1HIN	H_LYS_83	NZ	H_ASP_86	OD1	3.978
1HIN	H_ARG_94	NH2	H_GLU_96	OE1	2.995
1HIN	H_ARG_94	NH2	H_GLU_96	OE2	3.965
1HIN	H_ARG_95	NH1	L_ASP_91	OD1	3.169
1HIN	H_ARG_95	NH1	P_ASP_104	OD1	3.889
1HIN	H_ARG_95	NH2	L_ASP_91	OD1	2.746
1I8I	A_ARG_22	NH2	A_ASP_70	OD2	3.152
1I8I	A_ARG_61	NH1	A_GLU_81	OE1	3.598
1I8I	A_ARG_61	NH2	A_GLU_81	OE1	2.756
1I8I	A_ARG_61	NH2	A_ASP_82	OD1	2.774
1I8I	B_ARG_338	NH1	B_ASP_390	OD1	3.395
1I8I	B_ARG_338	NH2	B_GLU_346	OE1	3.519
1I8I	B_ARG_338	NH2	B_GLU_346	OE2	3.077
1I8I	B_LYS_343	NZ	A_ASP_85	OD1	3.777
1I8I	B_ARG_367	NH1	B_ASP_390	OD1	3.777
1I8I	B_ARG_367	NH1	B_ASP_390	OD2	2.803
1I8I	B_ARG_367	NH2	B_ASP_390	OD1	2.832
1I8I	B_ARG_367	NH2	B_ASP_390	OD2	3.335
1I8I	B_ARG_398	NH1	B_ASP_408	OD1	2.704
1I8I	B_ARG_398	NH1	B_ASP_408	OD2	3.295
1I8I	C_LYS_502	NZ	A_GLU_50	OE1	3.673
1I8I	C_LYS_502	NZ	A_GLU_50	OE2	3.232
1I8K	A_ARG_61	NH1	A_GLU_81	OE1	3.901
1I8K	A_ARG_61	NH2	A_GLU_81	OE1	2.704
1I8K	A_ARG_61	NH2	A_ASP_82	OD1	2.775
1I8K	A_ARG_61	NH2	A_ASP_82	OD2	3.582
1I8K	A_LYS_103	NZ	A_GLU_105	OE1	3.849
1I8K	A_LYS_103	NZ	A_GLU_105	OE2	3.265
1I8K	B_ARG_338	NH1	B_ASP_390	OD1	2.955
1I8K	B_ARG_338	NH2	B_GLU_346	OE2	2.897
1I8K	B_LYS_343	NZ	A_ASP_85	OD1	3.688
1I8K	B_LYS_343	NZ	A_ASP_85	OD2	2.833
1I8K	B_LYS_365	NZ	B_ASP_362	OD1	3.025
1I8K	B_ARG_367	NH1	B_ASP_390	OD1	3.793
1I8K	B_ARG_367	NH1	B_ASP_390	OD2	2.806

118K	B_ARG_367	NH2	B_ASP_390	OD1	2.921
118K	B_ARG_367	NH2	B_ASP_390	OD2	3.420
118K	B_ARG_398	NH1	B_ASP_408	OD1	3.548
118K	B_ARG_398	NH1	B_ASP_408	OD2	2.958
118K	C_LYS_502	NZ	A_GLU_50	OE1	3.381
118K	C_LYS_502	NZ	A_GLU_50	OE2	3.653
118M	L_ARG_61	NH2	L_GLU_81	OE2	3.348
118M	L_ARG_61	NH2	L_ASP_82	OD1	2.791
118M	L_ARG_61	NH2	L_ASP_82	OD2	3.473
118M	L_LYS_149	NZ	L_GLU_195	OE1	2.669
118M	L_ARG_155	NH1	L_GLU_185	OE1	3.608
118M	L_ARG_155	NH1	L_GLU_185	OE2	3.044
118M	L_ARG_155	NH2	L_GLU_185	OE1	2.570
118M	L_ARG_155	NH2	L_GLU_185	OE2	3.578
118M	L_ARG_188	NH1	L_GLU_185	OE1	3.999
118M	L_HIS_189	ND1	L_ASP_151	OD2	2.965
118M	L_HIS_189	NE2	L_GLU_185	OE1	3.384
118M	L_ARG_211	NH1	L_GLU_187	OE1	3.084
118M	H_LYS_62	NZ	H_GLU_46	OE2	2.992
118M	H_LYS_66	NZ	H_ASP_86	OD1	2.668
118M	H_LYS_66	NZ	H_ASP_86	OD2	3.680
118M	H_ARG_94	NH2	H_ASP_101	OD1	3.336
118M	H_ARG_94	NH2	H_ASP_101	OD2	3.003
118M	H_LYS_208	NZ	L_GLU_123	OE1	2.918
118M	A_ARG_61	NH1	A_GLU_81	OE2	3.331
118M	A_ARG_61	NH1	A_ASP_82	OD1	2.710
118M	A_ARG_61	NH1	A_ASP_82	OD2	3.466
118M	A_LYS_147	NZ	A_GLU_195	OE1	3.288
118M	A_LYS_149	NZ	A_GLU_195	OE1	3.797
118M	A_LYS_149	NZ	A_GLU_195	OE2	2.770
118M	A_ARG_155	NH1	A_GLU_185	OE1	2.722
118M	A_ARG_155	NH2	A_GLU_185	OE1	3.688
118M	A_LYS_183	NZ	A_GLU_187	OE1	3.381
118M	A_HIS_189	ND1	A_ASP_151	OD2	2.740
118M	A_LYS_199	NZ	A_ASP_110	OD2	3.951
118M	A_ARG_211	NH1	A_GLU_187	OE2	3.834
118M	B_LYS_66	NZ	B_ASP_86	OD1	2.796
118M	B_LYS_66	NZ	B_ASP_86	OD2	3.783
118M	B_ARG_94	NH2	B_ASP_101	OD1	3.715
118M	B_ARG_94	NH2	B_ASP_101	OD2	2.888
118M	B_LYS_208	NZ	A_GLU_123	OE2	2.887
11C4	L_ARG_61	NH1	L_GLU_81	OE1	2.751
11C4	L_ARG_61	NH1	L_ASP_82	OD1	2.563
11C4	L_ARG_61	NH1	L_ASP_82	OD2	3.173
11C4	L_ARG_61	NH2	L_GLU_79	OE1	3.626
11C4	L_ARG_61	NH2	L_GLU_81	OE1	3.608
11C4	H_ARG_38	NH1	H_ASP_89	OD1	2.935
11C4	H_ARG_38	NH2	H_GLU_46	OE1	2.745
11C4	H_ARG_38	NH2	H_ASP_89	OD1	3.350
11C4	H_ARG_66	NH1	H_ASP_89	OD2	3.087
11C4	H_ARG_66	NH2	H_ASP_89	OD1	3.196
11C4	H_ARG_66	NH2	H_ASP_89	OD2	3.495
11C4	H_LYS_75	NZ	H_ASP_72	OD2	2.682
11C4	Y_LYS_1	NZ	Y_GLU_7	OE1	3.619
11C4	Y_LYS_1	NZ	Y_GLU_7	OE2	2.535
11C4	Y_LYS_13	NZ	Y_ASP_18	OD2	3.711
11C4	Y_ARG_61	NH2	Y_ASP_48	OD1	3.871
11C4	Y_ARG_68	NH2	Y_ASP_66	OD2	2.848

1IC4	Y_LYS.97	NZ	H_ASP.99	OD1	2.657
1IC4	Y_LYS.97	NZ	H_ASP.99	OD2	3.938
1IC4	Y_ARG.125	NH1	Y_ASP.119	OD1	3.300
1IC4	Y_ARG.125	NH1	Y_ASP.119	OD2	3.023
1IC4	Y_ARG.125	NH2	Y_ASP.119	OD2	3.490
1IC5	L_LYS.39	NZ	L_GLU.42	OE1	3.119
1IC5	L_ARG.61	NH1	L_GLU.79	OE1	3.450
1IC5	L_ARG.61	NH1	L_GLU.81	OE1	2.953
1IC5	L_ARG.61	NH1	L_ASP.82	OD1	2.717
1IC5	L_ARG.61	NH1	L_ASP.82	OD2	3.546
1IC5	L_ARG.61	NH2	L_GLU.79	OE1	3.079
1IC5	L_ARG.61	NH2	L_GLU.79	OE2	3.755
1IC5	L_LYS.103	NZ	L_GLU.105	OE2	3.954
1IC5	H_ARG.38	NH1	H_ASP.89	OD1	2.839
1IC5	H_ARG.38	NH2	H_GLU.46	OE1	2.758
1IC5	H_ARG.38	NH2	H_ASP.89	OD1	3.693
1IC5	H_ARG.66	NH1	H_ASP.89	OD1	3.998
1IC5	H_ARG.66	NH1	H_ASP.89	OD2	3.250
1IC5	H_ARG.66	NH2	H_ASP.89	OD1	3.110
1IC5	H_ARG.66	NH2	H_ASP.89	OD2	3.644
1IC5	H_LYS.75	NZ	H_ASP.72	OD2	3.897
1IC5	Y_LYS.1	NZ	Y_GLU.7	OE1	3.768
1IC5	Y_LYS.1	NZ	Y_GLU.7	OE2	2.582
1IC5	Y_ARG.61	NH2	Y_ASP.48	OD1	3.930
1IC5	Y_LYS.97	NZ	H_ASP.32	OD1	2.694
1IC5	Y_ARG.125	NH1	Y_ASP.119	OD1	3.569
1IC5	Y_ARG.125	NH1	Y_ASP.119	OD2	3.500
1IC5	Y_ARG.125	NH2	Y_ASP.119	OD1	3.857
1IC5	Y_ARG.125	NH2	Y_ASP.119	OD2	2.635
1IC7	L_ARG.45	NH2	L_GLU.42	OE1	3.451
1IC7	L_ARG.61	NH1	L_GLU.79	OE1	3.604
1IC7	L_ARG.61	NH1	L_GLU.81	OE2	3.867
1IC7	L_ARG.61	NH2	L_GLU.81	OE2	2.625
1IC7	L_ARG.61	NH2	L_ASP.82	OD1	2.810
1IC7	L_ARG.61	NH2	L_ASP.82	OD2	3.484
1IC7	L_LYS.103	NZ	L_GLU.105	OE2	2.664
1IC7	H_ARG.38	NH1	H_ASP.89	OD1	2.659
1IC7	H_ARG.38	NH2	H_GLU.46	OE1	2.814
1IC7	H_ARG.38	NH2	H_ASP.89	OD1	3.507
1IC7	H_ARG.66	NH1	H_ASP.89	OD1	3.777
1IC7	H_ARG.66	NH1	H_ASP.89	OD2	2.821
1IC7	H_ARG.66	NH2	H_ASP.89	OD1	3.054
1IC7	H_ARG.66	NH2	H_ASP.89	OD2	3.478
1IC7	Y_LYS.1	NZ	Y_GLU.7	OE1	3.641
1IC7	Y_LYS.1	NZ	Y_GLU.7	OE2	2.660
1IC7	Y_ARG.125	NH2	Y_ASP.119	OD1	3.644
1IC7	Y_ARG.125	NH2	Y_ASP.119	OD2	2.585
1IFH	L_ARG.54	NH1	L_ASP.60	OD1	3.414
1IFH	L_ARG.54	NH1	L_ASP.60	OD2	3.205
1IFH	L_ARG.61	NH1	L_ASP.82	OD1	2.658
1IFH	L_ARG.61	NH1	L_ASP.82	OD2	3.079
1IFH	L_ARG.61	NH2	L_GLU.81	OE2	3.987
1IFH	L_LYS.149	NZ	L_GLU.195	OE1	3.474
1IFH	L_LYS.149	NZ	L_GLU.195	OE2	3.400
1IFH	L_ARG.155	NH1	L_GLU.185	OE1	3.273
1IFH	L_ARG.155	NH2	L_GLU.185	OE2	3.721
1IFH	L_ARG.188	NH1	L_ASP.184	OD1	3.900
1IFH	L_ARG.188	NH2	L_ASP.184	OD1	3.145

1IFH	L_HIS_189	ND1	L_ASP_151	OD2	3.236
1IFH	L_LYS_199	NZ	L_ASP_110	OD1	3.492
1IFH	L_LYS_199	NZ	L_ASP_110	OD2	3.178
1IFH	H_ARG_38	NH1	H_ASP_86	OD1	3.355
1IFH	H_ARG_38	NH2	H_GLU_46	OE1	3.340
1IFH	H_ARG_38	NH2	H_ASP_86	OD1	3.860
1IFH	H_ARG_66	NH1	H_ASP_86	OD1	3.538
1IFH	H_ARG_66	NH2	H_ASP_86	OD1	3.023
1IFH	H_ARG_66	NH2	H_ASP_86	OD2	2.605
1IFH	H_ARG_94	NH2	H_GLU_96	OE1	2.733
1IFH	H_ARG_95	NH1	L_ASP_91	OD1	2.782
1IFH	H_ARG_95	NH2	P_ASP_104	OD1	2.974
1IFH	H_ARG_95	NH2	P_ASP_104	OD2	2.813
1IFH	H_LYS_221	NZ	L_GLU_123	OE1	3.267
1IFH	H_LYS_221	NZ	L_GLU_123	OE2	2.926
1IFH	H_LYS_222	NZ	H_GLU_226	OE2	3.617
1IGF	L_LYS_50	NZ	H_ASP_98	OD2	3.036
1IGF	L_ARG_61	NH1	L_GLU_79	OE1	3.608
1IGF	L_ARG_61	NH1	L_GLU_79	OE2	3.209
1IGF	L_ARG_61	NH2	L_ASP_82	OD1	2.804
1IGF	L_ARG_61	NH2	L_ASP_82	OD2	2.709
1IGF	L_LYS_142	NZ	L_ASP_143	OD1	3.847
1IGF	L_LYS_142	NZ	L_ASP_143	OD2	3.953
1IGF	L_LYS_149	NZ	L_GLU_195	OE1	3.005
1IGF	L_HIS_189	ND1	L_GLU_185	OE1	3.423
1IGF	L_HIS_189	ND1	L_GLU_185	OE2	3.814
1IGF	L_HIS_189	NE2	L_GLU_154	OE1	3.930
1IGF	L_HIS_189	NE2	L_GLU_154	OE2	2.963
1IGF	L_HIS_189	NE2	L_GLU_185	OE1	3.959
1IGF	L_LYS_199	NZ	L_ASP_110	OD1	2.851
1IGF	L_LYS_199	NZ	L_ASP_110	OD2	3.161
1IGF	H_ARG_38	NH1	H_GLU_46	OE1	2.875
1IGF	H_ARG_38	NH1	H_GLU_46	OE2	3.277
1IGF	H_ARG_38	NH2	H_ASP_86	OD1	2.708
1IGF	H_LYS_64	NZ	H_ASP_61	OD1	3.360
1IGF	H_ARG_66	NH1	H_ASP_86	OD1	3.532
1IGF	H_ARG_66	NH1	H_ASP_86	OD2	2.901
1IGF	H_ARG_66	NH2	H_ASP_86	OD1	3.011
1IGF	H_ARG_66	NH2	H_ASP_86	OD2	3.582
1IGF	H_ARG_83	NH2	H_GLU_85	OE2	3.398
1IGF	H_ARG_94	NH1	H_ASP_101	OD1	2.803
1IGF	H_ARG_94	NH1	H_ASP_101	OD2	2.950
1IGF	H_LYS_221	NZ	L_GLU_123	OE1	3.549
1IGF	M_ARG_61	NH1	M_ASP_82	OD1	3.656
1IGF	M_ARG_61	NH2	M_GLU_79	OE1	3.684
1IGF	M_ARG_61	NH2	M_GLU_79	OE2	3.861
1IGF	M_ARG_61	NH2	M_ASP_82	OD1	3.256
1IGF	M_ARG_61	NH2	M_ASP_82	OD2	2.603
1IGF	M_LYS_149	NZ	M_GLU_195	OE1	3.495
1IGF	M_LYS_183	NZ	M_GLU_187	OE2	2.898
1IGF	M_LYS_199	NZ	M_ASP_110	OD2	3.163
1IGF	J_ARG_38	NH1	J_ASP_86	OD1	3.058
1IGF	J_ARG_38	NH2	J_GLU_46	OE1	2.898
1IGF	J_ARG_38	NH2	J_GLU_85	OE2	3.952
1IGF	J_LYS_64	NZ	J_ASP_61	OD1	3.146
1IGF	J_LYS_64	NZ	J_ASP_61	OD2	3.948
1IGF	J_ARG_66	NH1	J_GLU_85	OE2	3.586
1IGF	J_ARG_66	NH1	J_ASP_86	OD1	3.108

1IGF	J_ARG.66	NH1	J_ASP.86	OD2	3.486
1IGF	J_ARG.66	NH2	J_ASP.86	OD1	3.509
1IGF	J_ARG.66	NH2	J_ASP.86	OD2	2.722
1IGF	J_ARG.83	NH1	J_GLU.85	OE1	3.819
1IGF	J_ARG.83	NH2	J_GLU.85	OE1	3.702
1IGF	J_ARG.83	NH2	J_GLU.85	OE2	3.508
1IGF	J_ARG.94	NH2	J_ASP.101	OD1	2.994
1IGF	J_ARG.94	NH2	J_ASP.101	OD2	2.766
1IGF	J_LYS.218	NZ	J_ASP.220	OD1	3.151
1IGF	J_LYS.221	NZ	M_GLU.123	OE1	3.800
1IGF	J_LYS.221	NZ	M_GLU.123	OE2	3.750
1IND	L_LYS.41	NZ	L_GLU.83	OE1	3.721
1IND	L_ARG.63	NH2	L_GLU.83	OE2	3.365
1IND	L_ARG.63	NH2	L_ASP.84	OD1	2.728
1IND	L_ARG.63	NH2	L_ASP.84	OD2	3.765
1IND	L_LYS.72	NZ	L_ASP.71	OD1	3.764
1IND	L_LYS.113	NZ	L_GLU.201	OE1	3.425
1IND	L_ARG.186	NH2	L_GLU.189	OE1	2.887
1IND	L_ARG.186	NH2	L_GLU.189	OE2	2.679
1IND	L_HIS.191	ND1	L_ASP.154	OD2	3.038
1IND	H_ARG.38	NH1	H_GLU.46	OE1	3.013
1IND	H_ARG.38	NH2	H_ASP.90	OD1	2.950
1IND	H_ARG.67	NH1	H_ASP.90	OD1	3.223
1IND	H_ARG.67	NH2	H_ASP.90	OD1	3.035
1IND	H_ARG.67	NH2	H_ASP.90	OD2	2.402
1IND	H_ARG.87	NH2	H_GLU.89	OE1	2.860
1IND	H_HIS.106	ND1	H_GLU.6	OE1	3.067
1IND	H_LYS.143	NZ	L_GLU.127	OE2	2.765
1IND	H_HIS.164	NE2	L_ASP.141	OD1	3.891
1INE	L_ARG.63	NH1	L_ASP.84	OD1	3.522
1INE	L_ARG.63	NH1	L_ASP.84	OD2	3.841
1INE	L_LYS.113	NZ	L_GLU.201	OE1	3.453
1INE	L_LYS.152	NZ	L_GLU.206	OE1	3.945
1INE	L_ARG.186	NH2	L_GLU.189	OE1	3.738
1INE	L_ARG.186	NH2	L_GLU.189	OE2	2.847
1INE	L_HIS.191	ND1	L_ASP.154	OD2	2.790
1INE	H_ARG.38	NH1	H_GLU.46	OE1	3.495
1INE	H_ARG.38	NH1	H_GLU.46	OE2	3.232
1INE	H_ARG.38	NH2	H_ASP.90	OD1	2.602
1INE	H_ARG.67	NH2	H_ASP.90	OD1	3.249
1INE	H_ARG.67	NH2	H_ASP.90	OD2	2.823
1INE	H_ARG.87	NH2	H_GLU.89	OE1	2.822
1INE	H_LYS.143	NZ	L_GLU.127	OE2	2.920
1INE	H_HIS.164	NE2	L_ASP.141	OD2	3.817
1IQW	L_LYS.24	NZ	L_ASP.74	OD1	3.077
1IQW	L_LYS.24	NZ	L_ASP.74	OD2	3.598
1IQW	L_ARG.65	NH1	L_GLU.83	OE2	3.811
1IQW	L_ARG.65	NH1	L_GLU.85	OE2	3.948
1IQW	L_ARG.65	NH2	L_GLU.85	OE2	2.881
1IQW	L_ARG.65	NH2	L_ASP.86	OD1	2.853
1IQW	L_ARG.65	NH2	L_ASP.86	OD2	3.630
1IQW	L_ARG.100	NH1	L_ASP.98	OD2	3.926
1IQW	L_ARG.100	NH2	L_ASP.98	OD2	3.900
1IQW	L_ARG.100	NH2	H_GLU.50	OE1	2.572
1IQW	L_ARG.100	NH2	H_GLU.50	OE2	2.799
1IQW	L_ARG.112	NH1	L_ASP.174	OD1	3.939
1IQW	L_LYS.146	NZ	L_GLU.109	OE1	3.307
1IQW	L_LYS.151	NZ	L_GLU.158	OE1	3.903

1IQW	L_LYS_151	NZ	L_GLU_158	OE2	3.426
1IQW	L_LYS_153	NZ	L_GLU_199	OE1	2.679
1IQW	L_LYS_153	NZ	L_GLU_199	OE2	3.687
1IQW	L_ARG_159	NH1	L_GLU_189	OE1	2.786
1IQW	L_ARG_159	NH2	L_GLU_189	OE1	3.653
1IQW	L_LYS_187	NZ	L_GLU_191	OE1	3.905
1IQW	L_HIS_193	ND1	L_ASP_155	OD2	3.111
1IQW	L_LYS_203	NZ	L_ASP_114	OD1	2.895
1IQW	L_LYS_203	NZ	L_ASP_114	OD2	3.727
1IQW	H_LYS_67	NZ	H_ASP_90	OD1	3.551
1IQW	H_ARG_98	NH2	H_ASP_109	OD1	2.686
1IQW	H_ARG_98	NH2	H_ASP_109	OD2	3.835
1IQW	H_ARG_100	NH1	H_ASP_109	OD1	3.614
1IQW	H_HIS_172	NE2	L_ASP_171	OD1	3.594
1IT9	L_ARG_65	NH1	L_GLU_85	OE1	3.637
1IT9	L_ARG_65	NH2	L_GLU_85	OE1	2.628
1IT9	L_ARG_65	NH2	L_ASP_86	OD1	2.793
1IT9	L_ARG_65	NH2	L_ASP_86	OD2	3.255
1IT9	L_ARG_100	NH1	L_ASP_98	OD2	3.522
1IT9	L_ARG_100	NH2	L_ASP_98	OD2	3.953
1IT9	L_ARG_100	NH2	H_GLU_50	OE2	3.105
1IT9	L_LYS_153	NZ	L_GLU_199	OE1	3.686
1IT9	L_LYS_187	NZ	L_GLU_191	OE2	3.697
1IT9	L_LYS_192	NZ	L_ASP_189	OD1	3.604
1IT9	H_LYS_63	NZ	H_GLU_46	OE1	3.197
1IT9	H_LYS_67	NZ	H_ASP_90	OD1	3.421
1IT9	H_LYS_67	NZ	H_ASP_90	OD2	2.822
1IT9	H_ARG_98	NH1	H_ASP_109	OD1	3.442
1IT9	H_ARG_98	NH1	H_ASP_109	OD2	2.634
1IT9	H_LYS_217	NZ	L_GLU_127	OE1	3.545
1IT9	H_LYS_217	NZ	L_GLU_127	OE2	3.302
1J05	L_ARG_18	NH1	L_ASP_76	OD2	2.833
1J05	L_LYS_103	NZ	L_GLU_105	OE2	3.967
1J05	H_ARG_40	NH1	H_GLU_85	OE1	3.148
1J05	H_ARG_40	NH2	H_GLU_85	OE1	2.682
1J05	H_LYS_58	NZ	L_ASP_94	OD2	2.663
1J05	H_LYS_62	NZ	H_GLU_46	OE2	2.498
1J05	H_LYS_66	NZ	H_ASP_86	OD1	3.951
1J05	H_LYS_66	NZ	H_ASP_86	OD2	2.776
1J05	A_ARG_18	NH2	A_ASP_76	OD2	3.093
1J05	A_ARG_61	NH2	A_ASP_81	OD1	3.469
1J05	A_ARG_61	NH2	A_ASP_82	OD1	2.736
1J05	A_ARG_61	NH2	A_ASP_82	OD2	3.685
1J05	B_LYS_58	NZ	A_ASP_94	OD2	2.870
1J05	B_LYS_62	NZ	B_GLU_46	OE1	3.609
1J05	B_LYS_66	NZ	B_ASP_86	OD1	3.619
1J05	B_LYS_66	NZ	B_ASP_86	OD2	2.721
1J1O	L_ARG_61	NH2	L_ASP_82	OD1	2.910
1J1O	L_ARG_61	NH2	L_ASP_82	OD2	3.568
1J1O	L_LYS_103	NZ	L_GLU_105	OE2	3.101
1J1O	H_ARG_38	NH1	H_ASP_89	OD1	2.830
1J1O	H_ARG_38	NH2	H_GLU_46	OE1	2.878
1J1O	H_ARG_38	NH2	H_ASP_89	OD1	3.468
1J1O	H_ARG_66	NH1	H_ASP_89	OD1	3.734
1J1O	H_ARG_66	NH1	H_ASP_89	OD2	3.001
1J1O	H_ARG_66	NH2	H_ASP_89	OD1	3.010
1J1O	H_ARG_66	NH2	H_ASP_89	OD2	3.624
1J1O	H_LYS_75	NZ	H_ASP_72	OD1	3.670

1J1O	H_LYS.75	NZ	H_ASP.72	OD2	2.565
1J1O	Y_LYS.1	NZ	Y_GLU.7	OE2	2.858
1J1O	Y_LYS.13	NZ	Y_ASP.18	OD1	3.427
1J1O	Y_LYS.13	NZ	Y_ASP.18	OD2	3.311
1J1O	Y_ARG.61	NH1	Y_ASP.48	OD2	2.936
1J1O	Y_ARG.61	NH2	Y_ASP.48	OD2	3.586
1J1O	Y_ARG.68	NH2	Y_ASP.66	OD2	3.730
1J1O	Y_LYS.97	NZ	H_ASP.32	OD1	2.636
1J1O	Y_LYS.97	NZ	H_ASP.32	OD2	3.985
1J1O	Y_LYS.97	NZ	H_ASP.99	OD1	3.590
1J1O	Y_LYS.97	NZ	H_ASP.99	OD2	2.896
1J1O	Y_ARG.125	NH1	Y_ASP.119	OD2	3.446
1J1O	Y_ARG.125	NH2	Y_ASP.119	OD1	3.689
1J1O	Y_ARG.125	NH2	Y_ASP.119	OD2	3.547
1J1P	L_ARG.61	NH2	L_ASP.82	OD1	2.811
1J1P	L_ARG.61	NH2	L_ASP.82	OD2	3.464
1J1P	L_LYS.103	NZ	L_GLU.105	OE2	2.960
1J1P	H_ARG.38	NH1	H_ASP.89	OD1	2.854
1J1P	H_ARG.38	NH2	H_GLU.46	OE1	2.924
1J1P	H_ARG.38	NH2	H_ASP.89	OD1	3.457
1J1P	H_ARG.66	NH1	H_ASP.89	OD1	3.754
1J1P	H_ARG.66	NH1	H_ASP.89	OD2	3.009
1J1P	H_ARG.66	NH2	H_ASP.89	OD1	2.987
1J1P	H_ARG.66	NH2	H_ASP.89	OD2	3.600
1J1P	H_LYS.75	NZ	H_ASP.72	OD1	3.943
1J1P	H_LYS.75	NZ	H_ASP.72	OD2	2.743
1J1P	Y_LYS.1	NZ	Y_GLU.7	OE2	2.945
1J1P	Y_ARG.61	NH1	Y_ASP.48	OD1	3.659
1J1P	Y_ARG.61	NH1	Y_ASP.48	OD2	2.763
1J1P	Y_ARG.61	NH2	Y_ASP.48	OD2	3.923
1J1P	Y_ARG.68	NH2	Y_ASP.66	OD2	3.805
1J1P	Y_LYS.97	NZ	H_ASP.32	OD1	2.700
1J1P	Y_LYS.97	NZ	H_ASP.99	OD1	3.721
1J1P	Y_LYS.97	NZ	H_ASP.99	OD2	2.595
1J1P	Y_ARG.125	NH1	Y_ASP.119	OD1	3.879
1J1P	Y_ARG.125	NH1	Y_ASP.119	OD2	2.802
1J1P	Y_ARG.125	NH2	Y_ASP.119	OD1	3.068
1J1P	Y_ARG.125	NH2	Y_ASP.119	OD2	3.059
1J1X	L_ARG.61	NH1	L_GLU.81	OE2	3.955
1J1X	L_ARG.61	NH2	L_GLU.81	OE2	2.869
1J1X	L_ARG.61	NH2	L_ASP.82	OD1	2.807
1J1X	L_ARG.61	NH2	L_ASP.82	OD2	3.443
1J1X	L_LYS.103	NZ	L_GLU.105	OE2	3.635
1J1X	H_ARG.38	NH1	H_ASP.89	OD1	2.839
1J1X	H_ARG.38	NH2	H_GLU.46	OE1	2.984
1J1X	H_ARG.38	NH2	H_ASP.89	OD1	3.410
1J1X	H_ARG.66	NH1	H_ASP.89	OD1	3.723
1J1X	H_ARG.66	NH1	H_ASP.89	OD2	3.043
1J1X	H_ARG.66	NH2	H_ASP.89	OD1	3.064
1J1X	H_ARG.66	NH2	H_ASP.89	OD2	3.686
1J1X	Y_LYS.1	NZ	Y_GLU.7	OE2	2.973
1J1X	Y_ARG.61	NH1	Y_ASP.48	OD2	2.934
1J1X	Y_ARG.68	NH2	Y_ASP.66	OD2	3.707
1J1X	Y_LYS.97	NZ	H_ASP.32	OD1	2.655
1J1X	Y_LYS.97	NZ	H_ASP.32	OD2	3.935
1J1X	Y_LYS.97	NZ	H_ASP.99	OD1	3.479
1J1X	Y_LYS.97	NZ	H_ASP.99	OD2	2.956
1J1X	Y_ARG.125	NH1	Y_ASP.119	OD1	3.927

1J1X	Y_ARG_125	NH1	Y_ASP_119	OD2	3.825
1J1X	Y_ARG_125	NH2	Y_ASP_119	OD2	2.717
1JFQ	L_ARG_61	NH2	L_GLU_81	OE2	3.034
1JFQ	L_ARG_61	NH2	L_ASP_82	OD1	2.626
1JFQ	L_ARG_61	NH2	L_ASP_82	OD2	3.469
1JFQ	L_LYS_147	NZ	L_GLU_154	OE2	3.134
1JFQ	L_LYS_149	NZ	L_GLU_195	OE1	3.635
1JFQ	L_LYS_149	NZ	L_GLU_195	OE2	2.808
1JFQ	L_LYS_169	NZ	L_ASP_167	OD1	3.763
1JFQ	L_LYS_169	NZ	L_ASP_167	OD2	3.427
1JFQ	L_LYS_183	NZ	L_GLU_187	OE2	3.965
1JFQ	L_ARG_188	NH1	L_ASP_184	OD1	2.482
1JFQ	L_ARG_188	NH1	L_ASP_184	OD2	3.747
1JFQ	L_ARG_188	NH2	L_GLU_185	OE2	3.747
1JFQ	L_HIS_189	NE2	L_GLU_185	OE2	3.915
1JFQ	L_LYS_199	NZ	L_ASP_110	OD1	3.726
1JFQ	L_LYS_199	NZ	L_ASP_110	OD2	2.782
1JFQ	H_LYS_363	NZ	H_GLU_346	OE1	2.893
1JFQ	H_LYS_367	NZ	H_ASP_390	OD2	3.164
1JFQ	H_ARG_398	NH2	H_ASP_409	OD1	3.741
1JFQ	H_ARG_398	NH2	H_ASP_409	OD2	2.842
1JFQ	H_LYS_516	NZ	L_GLU_123	OE1	3.003
1JFQ	H_LYS_516	NZ	L_GLU_123	OE2	3.095
1JHL	L_ARG_61	NH2	L_ASP_82	OD2	2.857
1JHL	L_LYS_107	NZ	L_GLU_17	OE1	3.758
1JHL	H_LYS_63	NZ	H_GLU_46	OE1	2.911
1JHL	H_LYS_63	NZ	H_GLU_46	OE2	3.457
1JHL	H_ARG_98	NH1	H_ASP_106	OD1	3.193
1JHL	H_ARG_98	NH1	H_ASP_106	OD2	2.879
1JHL	A_LYS_1	NZ	A_GLU_7	OE2	2.890
1JHL	A_ARG_112	NH1	H_ASP_55	OD1	3.828
1JHL	A_ARG_112	NH1	H_ASP_55	OD2	3.112
1JHL	A_LYS_116	NZ	H_ASP_99	OD1	3.763
1JHL	A_LYS_116	NZ	H_ASP_99	OD2	3.232
1JHL	A_ARG_125	NH2	A_ASP_119	OD2	3.005
1JP5	A_ARG_24	NH1	A_ASP_75	OD1	3.622
1JP5	A_ARG_24	NH1	A_ASP_75	OD2	2.930
1JP5	A_ARG_24	NH2	A_ASP_75	OD1	2.789
1JP5	A_ARG_24	NH2	A_ASP_75	OD2	3.224
1JP5	A_ARG_66	NH1	A_GLU_84	OE2	3.961
1JP5	A_ARG_66	NH2	A_GLU_86	OE1	3.649
1JP5	A_ARG_66	NH2	A_ASP_87	OD1	2.642
1JP5	A_ARG_66	NH2	A_ASP_87	OD2	2.495
1JP5	A_ARG_82	NH1	A_GLU_84	OE2	3.359
1JP5	A_HIS_162	NE2	A_ASP_226	OD1	3.329
1JP5	A_HIS_162	NE2	A_ASP_226	OD2	3.666
1JP5	A_LYS_173	NZ	A_ASP_190	OD2	2.916
1JP5	A_LYS_192	NZ	A_ASP_189	OD1	2.549
1JP5	A_ARG_194	NH1	A_GLU_216	OE2	3.691
1JP5	A_ARG_194	NH1	A_ASP_217	OD1	3.483
1JP5	A_ARG_194	NH1	A_ASP_217	OD2	3.993
1JP5	A_ARG_194	NH2	A_ASP_217	OD1	3.125
1JP5	A_ARG_194	NH2	A_ASP_217	OD2	2.288
1JP5	A_ARG_227	NH1	A_GLU_232	OE1	3.878
1JP5	A_ARG_227	NH1	A_GLU_232	OE2	3.876
1JP5	A_HIS_228	ND1	A_ASP_226	OD1	3.183
1JP5	A_HIS_228	ND1	A_ASP_226	OD2	3.924
1JP5	B_ARG_24	NH1	B_ASP_75	OD1	3.589

1JP5	B_ARG_24	NH1	B_ASP_75	OD2	2.884
1JP5	B_ARG_24	NH2	B_ASP_75	OD1	2.786
1JP5	B_ARG_24	NH2	B_ASP_75	OD2	3.283
1JP5	B_ARG_66	NH2	B_GLU_86	OE1	3.667
1JP5	B_ARG_66	NH2	B_ASP_87	OD1	2.594
1JP5	B_ARG_66	NH2	B_ASP_87	OD2	2.543
1JP5	B_ARG_82	NH1	B_GLU_84	OE2	3.388
1JP5	B_LYS_139	NZ	B_GLU_137	OE1	3.932
1JP5	B_HIS_162	NE2	B_ASP_226	OD1	3.248
1JP5	B_HIS_162	NE2	B_ASP_226	OD2	3.774
1JP5	B_LYS_173	NZ	B_ASP_190	OD2	3.014
1JP5	B_LYS_192	NZ	B_ASP_189	OD1	2.617
1JP5	B_ARG_194	NH1	B_GLU_216	OE2	3.383
1JP5	B_ARG_194	NH1	B_ASP_217	OD1	2.811
1JP5	B_ARG_194	NH1	B_ASP_217	OD2	3.494
1JP5	B_ARG_194	NH2	B_ASP_217	OD1	3.744
1JP5	B_ARG_194	NH2	B_ASP_217	OD2	2.928
1JP5	B_ARG_227	NH1	B_GLU_232	OE1	3.968
1JP5	B_ARG_227	NH1	B_GLU_232	OE2	3.830
1JP5	B_HIS_228	ND1	B_ASP_226	OD1	3.260
1JP5	B_HIS_228	ND1	B_ASP_226	OD2	3.862
1JPS	L_ARG_24	NH1	L_ASP_70	OD2	3.616
1JPS	L_ARG_27	NH2	L_GLU_93	OE1	3.147
1JPS	L_ARG_61	NH2	L_GLU_81	OE2	3.693
1JPS	L_ARG_61	NH2	L_ASP_82	OD1	2.870
1JPS	L_ARG_61	NH2	L_ASP_82	OD2	3.637
1JPS	L_LYS_103	NZ	L_GLU_165	OE1	2.915
1JPS	L_LYS_126	NZ	L_GLU_123	OE1	3.492
1JPS	L_ARG_142	NH2	L_GLU_105	OE2	3.364
1JPS	L_LYS_149	NZ	L_GLU_195	OE2	3.272
1JPS	L_LYS_188	NZ	L_ASP_185	OD1	3.281
1JPS	H_LYS_30	NZ	H_GLU_54	OE1	3.726
1JPS	H_HIS_35	NE2	H_ASP_99	OD2	2.904
1JPS	H_ARG_38	NH1	H_ASP_90	OD1	2.795
1JPS	H_ARG_38	NH2	H_GLU_46	OE2	3.099
1JPS	H_ARG_38	NH2	H_ASP_90	OD1	3.661
1JPS	H_LYS_63	NZ	H_ASP_61	OD1	2.512
1JPS	H_LYS_63	NZ	H_ASP_61	OD2	3.231
1JPS	H_ARG_67	NH1	H_ASP_90	OD1	3.087
1JPS	H_ARG_67	NH1	H_ASP_90	OD2	3.639
1JPS	H_ARG_67	NH2	H_ASP_90	OD1	3.450
1JPS	H_ARG_67	NH2	H_ASP_90	OD2	2.676
1JPS	H_ARG_98	NH2	H_ASP_105	OD1	3.651
1JPS	H_ARG_98	NH2	H_ASP_105	OD2	2.801
1JPS	H_LYS_147	NZ	H_ASP_148	OD1	3.289
1JPS	H_LYS_214	NZ	H_GLU_216	OE2	3.681
1JPS	T_LYS_15	NZ	T_GLU_24	OE2	3.265
1JPS	T_LYS_20	NZ	T_ASP_58	OD2	3.975
1JPS	T_LYS_46	NZ	T_GLU_62	OE2	3.654
1JPS	T_LYS_48	NZ	T_GLU_62	OE2	2.510
1JPS	T_LYS_65	NZ	T_GLU_62	OE1	3.161
1JPS	T_LYS_65	NZ	T_GLU_62	OE2	3.595
1JPS	T_LYS_122	NZ	T_ASP_178	OD1	2.673
1JPS	T_LYS_122	NZ	T_ASP_178	OD2	3.856
1JPS	T_LYS_159	NZ	T_ASP_180	OD2	2.746
1JPS	T_LYS_201	NZ	H_ASP_52	OD1	2.781
1JPT	L_ARG_24	NH2	L_ASP_70	OD1	3.381
1JPT	L_ARG_24	NH2	L_ASP_70	OD2	2.823

1JPT	L_ARG_27	NH2	L_GLU_93	OE1	2.552
1JPT	L_ARG_61	NH2	L_GLU_81	OE2	3.592
1JPT	L_ARG_61	NH2	L_ASP_82	OD1	2.733
1JPT	L_ARG_61	NH2	L_ASP_82	OD2	3.583
1JPT	L_LYS_149	NZ	L_GLU_195	OE1	3.445
1JPT	L_HIS_189	ND1	L_ASP_151	OD2	2.609
1JPT	L_ARG_211	NH1	L_GLU_187	OE1	3.952
1JPT	H_LYS_30	NZ	H_GLU_54	OE1	3.750
1JPT	H_HIS_35	NE2	H_ASP_99	OD2	2.901
1JPT	H_ARG_38	NH1	H_ASP_90	OD1	2.806
1JPT	H_ARG_38	NH2	H_GLU_46	OE2	3.279
1JPT	H_ARG_38	NH2	H_ASP_90	OD1	3.559
1JPT	H_LYS_63	NZ	H_GLU_46	OE1	2.705
1JPT	H_LYS_63	NZ	H_ASP_61	OD1	3.701
1JPT	H_ARG_67	NH1	H_ASP_90	OD1	3.340
1JPT	H_ARG_67	NH1	H_ASP_90	OD2	3.607
1JPT	H_ARG_67	NH2	H_ASP_90	OD1	3.600
1JPT	H_ARG_67	NH2	H_ASP_90	OD2	2.497
1JPT	H_ARG_87	NH2	H_GLU_89	OE1	3.851
1JPT	H_ARG_98	NH2	H_ASP_105	OD1	3.572
1JPT	H_ARG_98	NH2	H_ASP_105	OD2	2.539
1JPT	H_LYS_147	NZ	H_ASP_148	OD1	3.107
1JPT	H_LYS_147	NZ	H_ASP_148	OD2	3.168
1JPT	H_LYS_213	NZ	L_GLU_123	OE1	3.226
1JPT	H_LYS_213	NZ	L_GLU_123	OE2	3.740
1JRH	L_ARG_61	NH2	L_ASP_82	OD1	3.229
1JRH	L_ARG_61	NH2	L_ASP_82	OD2	3.948
1JRH	L_LYS_103	NZ	L_ASP_165	OD2	3.995
1JRH	H_ARG_38	NH1	H_GLU_46	OE1	2.881
1JRH	H_ARG_38	NH1	H_GLU_46	OE2	3.879
1JRH	H_ARG_38	NH2	H_ASP_86	OD2	3.530
1JRH	H_LYS_57	NZ	H_ASP_55	OD2	3.070
1JRH	H_ARG_66	NH1	H_ASP_86	OD1	3.819
1JRH	H_ARG_66	NH1	H_ASP_86	OD2	3.178
1JRH	H_ARG_66	NH2	H_ASP_86	OD1	3.486
1JRH	H_ARG_66	NH2	H_ASP_86	OD2	2.963
1JRH	H_LYS_71	NZ	H_ASP_55	OD1	3.729
1JRH	H_ARG_75	NH2	H_ASP_72	OD2	2.739
1JRH	H_ARG_94	NH2	H_ASP_101	OD2	2.863
1JRH	L_LYS_52	NZ	H_ASP_54	OD1	3.471
1JRH	L_LYS_52	NZ	H_ASP_54	OD2	2.819
1JRH	L_LYS_52	NZ	H_ASP_56	OD2	2.824
1JRH	L_HIS_73	NE2	L_ASP_72	OD1	3.994
1JRH	L_HIS_73	NE2	L_ASP_72	OD2	3.992
1JRH	L_ARG_84	NH1	L_GLU_45	OE1	2.869
1JRH	L_ARG_84	NH1	L_GLU_45	OE2	3.093
1JRH	L_ARG_84	NH2	L_GLU_27	OE1	3.652
1JRH	L_ARG_84	NH2	L_GLU_27	OE2	3.984
1JRH	L_LYS_86	NZ	L_GLU_93	OE1	3.237
1JRH	L_LYS_86	NZ	L_GLU_93	OE2	3.629
1JTO	A_ARG_38	NH1	A_ASP_90	OD2	2.989
1JTO	A_ARG_38	NH2	A_GLU_46	OE1	3.765
1JTO	A_ARG_38	NH2	A_GLU_46	OE2	3.163
1JTO	A_ARG_38	NH2	A_ASP_90	OD2	3.961
1JTO	A_ARG_67	NH1	A_ASP_90	OD1	2.656
1JTO	A_ARG_67	NH1	A_ASP_90	OD2	3.690
1JTO	A_ARG_67	NH2	A_ASP_90	OD1	3.432
1JTO	A_ARG_67	NH2	A_ASP_90	OD2	2.929

1JTO	B_ARG_38	NH1	B_ASP_90	OD2	2.804
1JTO	B_ARG_38	NH2	B_GLU_46	OE1	3.744
1JTO	B_ARG_38	NH2	B_ASP_90	OD2	3.904
1JTO	B_LYS_65	NZ	B_ASP_62	OD1	3.988
1JTO	B_ARG_67	NH1	B_ASP_90	OD1	2.582
1JTO	B_ARG_67	NH1	B_ASP_90	OD2	4.000
1JTO	B_ARG_67	NH2	B_ASP_90	OD1	3.081
1JTO	B_ARG_67	NH2	B_ASP_90	OD2	2.986
1JTO	L_LYS_1	NZ	L_GLU_7	OE2	3.834
1JTO	L_LYS_13	NZ	L_ASP_18	OD2	2.997
1JTO	L_ARG_61	NH2	L_ASP_48	OD1	3.510
1JTO	L_LYS_97	NZ	L_ASP_101	OD1	2.937
1JTO	L_ARG_125	NH1	L_ASP_119	OD2	3.230
1JTO	L_ARG_125	NH2	L_ASP_119	OD1	3.769
1JTO	L_ARG_125	NH2	L_ASP_119	OD2	3.012
1JTO	M_LYS_1	NZ	M_GLU_7	OE1	3.717
1JTO	M_LYS_1	NZ	M_GLU_7	OE2	2.519
1JTO	M_ARG_61	NH2	M_ASP_48	OD1	3.874
1JTO	M_ARG_125	NH1	M_ASP_119	OD2	2.938
1JTO	M_ARG_125	NH2	M_ASP_119	OD1	3.078
1JTO	M_ARG_125	NH2	M_ASP_119	OD2	3.152
1JTP	A_ARG_38	NH1	A_ASP_90	OD1	2.844
1JTP	A_ARG_38	NH2	A_GLU_46	OE1	2.990
1JTP	A_ARG_38	NH2	A_ASP_90	OD1	3.872
1JTP	A_LYS_65	NZ	A_ASP_62	OD1	3.073
1JTP	A_ARG_67	NH1	A_GLU_87	OE1	3.833
1JTP	A_ARG_67	NH1	A_ASP_90	OD1	3.796
1JTP	A_ARG_67	NH1	A_ASP_90	OD2	2.836
1JTP	A_ARG_67	NH2	A_GLU_87	OE2	3.971
1JTP	A_ARG_67	NH2	A_ASP_90	OD1	3.167
1JTP	A_ARG_67	NH2	A_ASP_90	OD2	3.669
1JTP	B_ARG_38	NH1	B_ASP_90	OD1	3.088
1JTP	B_ARG_38	NH2	B_GLU_46	OE1	3.231
1JTP	B_ARG_38	NH2	B_GLU_46	OE2	3.901
1JTP	B_LYS_65	NZ	B_ASP_62	OD1	2.767
1JTP	B_ARG_67	NH1	B_ASP_90	OD1	3.639
1JTP	B_ARG_67	NH1	B_ASP_90	OD2	2.730
1JTP	B_ARG_67	NH2	B_ASP_90	OD1	2.941
1JTP	B_ARG_67	NH2	B_ASP_90	OD2	3.599
1JTP	L_LYS_1	NZ	L_GLU_7	OE1	3.651
1JTP	L_LYS_1	NZ	L_GLU_7	OE2	2.871
1JTP	L_LYS_13	NZ	L_ASP_18	OD2	2.822
1JTP	L_ARG_61	NH2	L_ASP_48	OD2	3.676
1JTP	L_ARG_125	NH2	L_ASP_119	OD2	3.456
1JTP	M_LYS_1	NZ	M_GLU_7	OE1	3.807
1JTP	M_LYS_1	NZ	M_GLU_7	OE2	2.795
1JTP	M_LYS_13	NZ	M_ASP_18	OD2	3.184
1JTP	M_ARG_61	NH2	M_ASP_48	OD2	3.928
1JTP	M_ARG_125	NH1	M_ASP_119	OD1	3.405
1JTP	M_ARG_125	NH1	M_ASP_119	OD2	2.529
1JTP	M_ARG_125	NH2	M_ASP_119	OD1	2.657
1JTP	M_ARG_125	NH2	M_ASP_119	OD2	3.292
1JTT	A_ARG_38	NH1	A_ASP_90	OD1	2.882
1JTT	A_ARG_38	NH2	A_GLU_46	OE2	2.917
1JTT	A_LYS_65	NZ	A_ASP_62	OD2	2.806
1JTT	A_ARG_67	NH1	A_ASP_90	OD1	3.707
1JTT	A_ARG_67	NH1	A_ASP_90	OD2	2.718
1JTT	A_ARG_67	NH2	A_ASP_90	OD1	3.006

1JTT	A_ARG.67	NH2	A_ASP.90	OD2	3.559
1JTT	L_LYS.1	NZ	L_GLU.7	OE2	2.871
1JTT	L_ARG.61	NH2	L_ASP.48	OD2	3.382
1JTT	L_ARG.125	NH1	L_ASP.119	OD1	3.528
1JTT	L_ARG.125	NH1	L_ASP.119	OD2	3.412
1JTT	L_ARG.125	NH2	L_ASP.119	OD1	3.866
1JTT	L_ARG.125	NH2	L_ASP.119	OD2	2.346
1JV5	A_ARG.61	NH1	A_GLU.81	OE1	3.715
1JV5	A_ARG.61	NH1	A_ASP.82	OD1	3.734
1JV5	A_ARG.61	NH2	A_ASP.82	OD1	2.672
1JV5	A_ARG.61	NH2	A_ASP.82	OD2	3.335
1JV5	B_LYS.363	NZ	B_GLU.346	OE1	3.710
1JV5	B_LYS.367	NZ	B_ASP.390	OD1	2.564
1JV5	B_LYS.367	NZ	B_ASP.390	OD2	3.314
1K6Q	L_LYS.3	NZ	L_ASP.1	OD1	3.247
1K6Q	L_LYS.3	NZ	L_ASP.1	OD2	3.989
1K6Q	L_ARG.27	NH1	L_GLU.93	OE1	3.087
1K6Q	L_ARG.27	NH2	L_GLU.93	OE1	3.061
1K6Q	L_ARG.27	NH2	L_GLU.93	OE2	3.535
1K6Q	L_ARG.61	NH1	L_GLU.79	OE2	3.467
1K6Q	L_ARG.61	NH2	L_GLU.79	OE1	3.569
1K6Q	L_ARG.61	NH2	L_GLU.79	OE2	3.481
1K6Q	L_ARG.61	NH2	L_ASP.81	OD1	3.557
1K6Q	L_ARG.61	NH2	L_ASP.82	OD1	2.902
1K6Q	L_ARG.61	NH2	L_ASP.82	OD2	3.306
1K6Q	L_LYS.149	NZ	L_GLU.195	OE1	3.892
1K6Q	L_LYS.149	NZ	L_GLU.195	OE2	2.797
1K6Q	L_ARG.188	NH1	L_GLU.185	OE1	3.503
1K6Q	L_ARG.188	NH2	L_GLU.185	OE1	2.593
1K6Q	L_ARG.188	NH2	L_GLU.185	OE2	3.878
1K6Q	L_HIS.189	ND1	L_ASP.151	OD2	2.798
1K6Q	H_LYS.30	NZ	H_GLU.54	OE1	3.652
1K6Q	H_HIS.35	NE2	H_ASP.99	OD2	3.337
1K6Q	H_ARG.40	NH1	H_GLU.89	OE2	2.763
1K6Q	H_ARG.40	NH2	H_GLU.89	OE2	2.831
1K6Q	H_LYS.63	NZ	H_GLU.46	OE1	3.998
1K6Q	H_LYS.67	NZ	H_ASP.90	OD1	3.649
1K6Q	H_LYS.67	NZ	H_ASP.90	OD2	3.070
1K6Q	H_ARG.98	NH2	H_ASP.105	OD1	3.693
1K6Q	H_ARG.98	NH2	H_ASP.105	OD2	2.580
1K6Q	H_HIS.168	NE2	L_ASP.167	OD1	3.896
1KB5	A_ARG.4	NH1	A_GLU.25	OE1	3.756
1KB5	A_ARG.4	NH1	A_GLU.25	OE2	3.640
1KB5	A_ARG.4	NH2	A_GLU.25	OE1	2.650
1KB5	A_ARG.4	NH2	A_GLU.25	OE2	3.717
1KB5	A_ARG.61	NH1	A_ASP.84	OD1	3.434
1KB5	A_ARG.61	NH1	A_ASP.84	OD2	2.899
1KB5	A_ARG.61	NH2	A_ASP.84	OD1	2.515
1KB5	A_ARG.61	NH2	A_ASP.84	OD2	3.185
1KB5	A_LYS.72	NZ	A_GLU.70	OE1	3.823
1KB5	A_ARG.93	NH1	B_GLU.105	OE1	2.975
1KB5	A_ARG.93	NH1	B_GLU.105	OE2	3.412
1KB5	A_ARG.101	NH2	H_ASP.98	OD1	2.690
1KB5	B_ARG.22	NH2	B_GLU.74	OE2	3.622
1KB5	B_LYS.26	NZ	B_GLU.5	OE1	2.619
1KB5	B_ARG.50	NH2	B_ASP.72	OD1	3.832
1KB5	L_LYS.27	NZ	B_ASP.54	OD1	3.460
1KB5	L_ARG.61	NH1	L_ASP.82	OD1	3.130

1KB5	L_ARG_61	NH1	L_ASP_82	OD2	2.318
1KB5	L_ARG_61	NH2	L_GLU_81	OE2	3.530
1KB5	L_ARG_61	NH2	L_ASP_82	OD1	2.659
1KB5	L_ARG_61	NH2	L_ASP_82	OD2	3.409
1KB5	L_LYS_149	NZ	L_GLU_195	OE1	3.078
1KB5	L_ARG_155	NH2	L_GLU_185	OE1	2.951
1KB5	L_ARG_155	NH2	L_GLU_185	OE2	3.151
1KB5	L_ARG_188	NH1	L_GLU_185	OE2	3.844
1KB5	L_ARG_188	NH2	L_ASP_184	OD1	3.621
1KB5	L_HIS_189	NE2	L_ASP_151	OD2	3.476
1KB5	H_LYS_62	NZ	H_GLU_46	OE2	3.773
1KB5	H_ARG_66	NH1	H_ASP_86	OD2	3.354
1KB5	H_ARG_94	NH1	H_ASP_101	OD1	3.952
1KB5	H_ARG_94	NH1	H_ASP_101	OD2	2.472
1KB5	H_ARG_94	NH2	H_ASP_101	OD2	2.694
1KB5	H_ARG_96	NH1	A_ASP_26	OD1	2.599
1KB5	H_ARG_96	NH1	A_ASP_26	OD2	2.834
1KB5	H_ARG_96	NH2	L_GLU_56	OE2	2.981
1KB5	H_ARG_96	NH2	H_ASP_101	OD1	3.517
1KB5	H_ARG_96	NH2	H_ASP_101	OD2	3.239
1KB5	H_LYS_209	NZ	H_GLU_211	OE1	3.539
1KB5	H_LYS_209	NZ	H_GLU_211	OE2	3.472
1KC5	L_ARG_54	NH1	L_ASP_60	OD1	2.682
1KC5	L_ARG_61	NH1	L_ASP_82	OD1	2.395
1KC5	L_ARG_61	NH1	L_ASP_82	OD2	2.703
1KC5	L_ARG_61	NH2	L_ASP_82	OD1	3.920
1KC5	L_LYS_107	NZ	L_GLU_17	OE2	3.192
1KC5	L_LYS_142	NZ	L_GLU_105	OE2	3.861
1KC5	L_LYS_147	NZ	L_GLU_154	OE1	3.049
1KC5	L_LYS_147	NZ	L_GLU_154	OE2	3.591
1KC5	L_LYS_149	NZ	L_GLU_195	OE1	2.716
1KC5	L_LYS_149	NZ	L_GLU_195	OE2	3.100
1KC5	L_ARG_155	NH1	L_GLU_185	OE1	3.442
1KC5	L_LYS_169	NZ	L_ASP_167	OD1	3.457
1KC5	L_LYS_169	NZ	L_ASP_167	OD2	3.411
1KC5	L_ARG_188	NH1	L_GLU_185	OE2	3.469
1KC5	L_HIS_189	ND1	L_ASP_151	OD2	3.918
1KC5	L_HIS_189	NE2	L_GLU_185	OE1	3.880
1KC5	L_LYS_199	NZ	L_ASP_110	OD2	2.858
1KC5	H_ARG_39	NH1	H_ASP_90	OD1	3.033
1KC5	H_ARG_39	NH2	H_GLU_47	OE1	2.994
1KC5	H_ARG_67	NH2	H_ASP_90	OD1	3.361
1KC5	H_ARG_67	NH2	H_ASP_90	OD2	2.772
1KC5	H_ARG_98	NH1	H_ASP_104	OD2	2.421
1KC5	H_LYS_211	NZ	L_GLU_123	OE2	2.759
1KCR	L_ARG_61	NH1	L_ASP_82	OD1	3.167
1KCR	L_ARG_61	NH1	L_ASP_82	OD2	3.442
1KCR	L_LYS_146	NZ	L_GLU_153	OE1	3.602
1KCR	L_LYS_146	NZ	L_GLU_153	OE2	3.503
1KCR	L_LYS_148	NZ	L_GLU_194	OE1	3.325
1KCR	L_ARG_154	NH2	L_GLU_184	OE1	3.047
1KCR	L_ARG_154	NH2	L_GLU_184	OE2	3.767
1KCR	L_HIS_188	ND1	L_ASP_150	OD2	3.289
1KCR	H_ARG_39	NH1	H_ASP_90	OD1	2.787
1KCR	H_ARG_39	NH2	H_GLU_47	OE1	3.186
1KCR	H_ARG_39	NH2	H_ASP_90	OD1	2.864
1KCR	H_ARG_67	NH1	H_ASP_90	OD1	3.439
1KCR	H_ARG_67	NH1	H_ASP_90	OD2	3.339

1KCR	H_ARG.67	NH2	H_ASP_90	OD1	3.781
1KCR	H_ARG.67	NH2	H_ASP_90	OD2	2.578
1KCR	H_LYS.76	NZ	H_ASP_73	OD2	3.906
1KCS	L_LYS.24	NZ	L_ASP_70	OD1	3.278
1KCS	L_ARG.54	NH1	L_ASP_60	OD1	3.351
1KCS	L_ARG.61	NH1	L_ASP_82	OD1	3.132
1KCS	L_ARG.61	NH1	L_ASP_82	OD2	3.710
1KCS	L_LYS_103	NZ	L_ASP_85	OD2	3.830
1KCS	L_LYS_149	NZ	L_GLU_195	OE1	3.249
1KCS	L_LYS_149	NZ	L_GLU_195	OE2	3.257
1KCS	L_HIS_189	ND1	L_ASP_151	OD2	2.813
1KCS	L_LYS_199	NZ	L_ASP_110	OD1	3.476
1KCS	L_LYS_199	NZ	L_ASP_110	OD2	3.643
1KCS	H_ARG.39	NH1	H_ASP_90	OD1	2.811
1KCS	H_ARG.39	NH2	H_GLU_47	OE1	2.833
1KCS	H_ARG.39	NH2	H_ASP_90	OD1	3.463
1KCS	H_ARG.67	NH1	H_ASP_90	OD1	3.415
1KCS	H_ARG.67	NH1	H_ASP_90	OD2	3.871
1KCS	H_ARG.67	NH2	H_ASP_90	OD1	2.423
1KCS	H_ARG.67	NH2	H_ASP_90	OD2	2.528
1KCS	H_LYS_211	NZ	L_GLU_123	OE1	3.340
1KCS	H_LYS_211	NZ	L_GLU_123	OE2	2.904
1KCS	H_LYS_212	NZ	H_GLU_214	OE2	2.957
1KIP	A_ARG.61	NH2	A_GLU_81	OE2	3.479
1KIP	A_ARG.61	NH2	A_ASP_82	OD1	2.597
1KIP	A_ARG.61	NH2	A_ASP_82	OD2	3.338
1KIP	A_ARG.96	NH1	B_GLU_98	OE1	2.773
1KIP	A_ARG.96	NH1	B_GLU_98	OE2	3.817
1KIP	A_ARG.96	NH2	B_GLU_98	OE1	3.280
1KIP	A_ARG.96	NH2	B_GLU_98	OE2	2.802
1KIP	A_LYS_107	NZ	A_GLU_17	OE1	3.197
1KIP	A_LYS_107	NZ	A_GLU_17	OE2	2.849
1KIP	B_ARG.38	NH1	B_ASP_89	OD1	3.191
1KIP	B_ARG.38	NH2	B_GLU_46	OE1	3.093
1KIP	B_ARG.38	NH2	B_GLU_46	OE2	3.933
1KIP	B_ARG.38	NH2	B_ASP_89	OD1	3.743
1KIP	B_ARG.66	NH1	B_ASP_89	OD1	3.854
1KIP	B_ARG.66	NH1	B_ASP_89	OD2	2.776
1KIP	B_ARG.66	NH2	B_ASP_89	OD1	2.725
1KIP	B_ARG.66	NH2	B_ASP_89	OD2	3.126
1KIP	B_ARG.97	NH2	B_ASP_104	OD1	3.837
1KIP	B_ARG.97	NH2	B_ASP_104	OD2	2.804
1KIP	B_ARG_102	NH1	B_ASP_100	OD2	3.276
1KIP	C_LYS.1	NZ	C_GLU.7	OE2	3.468
1KIP	C_ARG.61	NH1	C_ASP_48	OD1	3.721
1KIP	C_ARG.125	NH1	C_ASP_119	OD1	3.514
1KIP	C_ARG.125	NH1	C_ASP_119	OD2	3.062
1KIP	C_ARG.125	NH2	C_ASP_119	OD2	3.245
1KIQ	A_ARG.61	NH2	A_GLU_81	OE2	3.197
1KIQ	A_ARG.61	NH2	A_ASP_82	OD1	2.691
1KIQ	A_ARG.61	NH2	A_ASP_82	OD2	3.415
1KIQ	A_ARG.96	NH1	B_GLU_98	OE1	2.812
1KIQ	A_ARG.96	NH1	B_GLU_98	OE2	3.589
1KIQ	A_ARG.96	NH2	B_GLU_98	OE1	3.677
1KIQ	A_ARG.96	NH2	B_GLU_98	OE2	2.919
1KIQ	A_LYS_103	NZ	A_GLU_105	OE1	2.805
1KIQ	A_LYS_103	NZ	A_GLU_105	OE2	3.912
1KIQ	A_LYS_107	NZ	A_GLU_17	OE1	3.881

1KIQ	A_LYS_107	NZ	A_GLU_17	OE2	2.784
1KIQ	B_ARG_38	NH1	B_ASP_89	OD1	2.893
1KIQ	B_ARG_38	NH2	B_GLU_46	OE1	3.199
1KIQ	B_ARG_38	NH2	B_GLU_46	OE2	3.778
1KIQ	B_ARG_38	NH2	B_ASP_89	OD1	3.733
1KIQ	B_ARG_66	NH1	B_ASP_89	OD1	3.789
1KIQ	B_ARG_66	NH1	B_ASP_89	OD2	2.815
1KIQ	B_ARG_66	NH2	B_ASP_89	OD1	2.856
1KIQ	B_ARG_66	NH2	B_ASP_89	OD2	3.346
1KIQ	B_LYS_75	NZ	B_ASP_72	OD2	3.652
1KIQ	B_ARG_97	NH2	B_ASP_104	OD1	3.671
1KIQ	B_ARG_97	NH2	B_ASP_104	OD2	2.756
1KIQ	B_ARG_102	NH1	B_ASP_100	OD2	3.299
1KIQ	C_LYS_1	NZ	C_GLU_7	OE1	3.271
1KIQ	C_LYS_1	NZ	C_GLU_7	OE2	3.227
1KIQ	C_LYS_13	NZ	C_ASP_18	OD2	3.514
1KIQ	C_ARG_68	NH1	C_ASP_66	OD2	2.812
1KIQ	C_ARG_125	NH1	C_ASP_119	OD1	3.267
1KIQ	C_ARG_125	NH1	C_ASP_119	OD2	3.095
1KIQ	C_ARG_125	NH2	C_ASP_119	OD2	3.062
1KIR	A_ARG_61	NH2	A_GLU_81	OE2	3.612
1KIR	A_ARG_61	NH2	A_ASP_82	OD1	2.646
1KIR	A_ARG_61	NH2	A_ASP_82	OD2	3.502
1KIR	A_ARG_96	NH1	B_GLU_98	OE1	2.757
1KIR	A_ARG_96	NH1	B_GLU_98	OE2	3.582
1KIR	A_ARG_96	NH2	B_GLU_98	OE1	3.625
1KIR	A_ARG_96	NH2	B_GLU_98	OE2	2.980
1KIR	A_LYS_107	NZ	A_GLU_17	OE2	2.685
1KIR	B_ARG_38	NH1	B_ASP_89	OD1	3.082
1KIR	B_ARG_38	NH2	B_GLU_46	OE1	3.138
1KIR	B_ARG_38	NH2	B_GLU_46	OE2	3.860
1KIR	B_ARG_38	NH2	B_ASP_89	OD1	3.771
1KIR	B_ARG_66	NH1	B_ASP_89	OD2	2.949
1KIR	B_ARG_66	NH2	B_ASP_89	OD1	2.669
1KIR	B_ARG_66	NH2	B_ASP_89	OD2	2.955
1KIR	B_LYS_75	NZ	B_ASP_72	OD2	3.972
1KIR	B_ARG_97	NH2	B_ASP_104	OD1	3.914
1KIR	B_ARG_97	NH2	B_ASP_104	OD2	2.816
1KIR	B_ARG_102	NH1	B_ASP_100	OD2	3.339
1KIR	C_LYS_1	NZ	C_GLU_7	OE1	3.936
1KIR	C_LYS_1	NZ	C_GLU_7	OE2	3.274
1KIR	C_ARG_68	NH1	C_ASP_66	OD2	3.347
1KIR	C_ARG_125	NH1	C_ASP_119	OD1	3.220
1KIR	C_ARG_125	NH1	C_ASP_119	OD2	2.967
1KIR	C_ARG_125	NH2	C_ASP_119	OD2	3.129
1KTR	L_ARG_24	NH2	L_ASP_75	OD1	3.305
1KTR	L_ARG_24	NH2	L_ASP_75	OD2	3.234
1KTR	L_ARG_66	NH1	L_ASP_87	OD1	3.908
1KTR	L_ARG_66	NH1	L_ASP_87	OD2	2.898
1KTR	L_ARG_66	NH2	L_GLU_84	OE1	3.858
1KTR	L_ARG_66	NH2	L_GLU_84	OE2	3.876
1KTR	L_ARG_66	NH2	L_ASP_87	OD1	2.818
1KTR	L_ARG_66	NH2	L_ASP_87	OD2	3.123
1KTR	L_LYS_108	NZ	L_GLU_110	OE2	3.290
1KTR	L_ARG_200	NH1	L_ASP_223	OD1	3.461
1KTR	L_ARG_200	NH1	L_ASP_223	OD2	3.017
1KTR	L_ARG_200	NH2	L_ASP_223	OD1	2.813
1KTR	L_ARG_200	NH2	L_ASP_223	OD2	3.629

1KTR	P_HIS_4	NE2	L_ASP_183	OD1	3.445
1KTR	P_HIS_4	NE2	L_ASP_183	OD2	2.673
1KTR	P_HIS_6	ND1	L_GLU_39	OE1	3.223
1KTR	P_HIS_6	ND1	L_GLU_39	OE2	2.811
1KTR	P_HIS_6	NE2	L_GLU_230	OE1	3.040
1KTR	P_HIS_6	NE2	L_GLU_230	OE2	3.199
1L7I	L_LYS_24	NZ	L_ASP_70	OD1	3.450
1L7I	L_LYS_24	NZ	L_ASP_70	OD2	2.756
1L7I	L_ARG_61	NH2	L_GLU_81	OE1	3.159
1L7I	L_ARG_61	NH2	L_ASP_82	OD1	2.832
1L7I	L_ARG_61	NH2	L_ASP_82	OD2	3.810
1L7I	L_LYS_149	NZ	L_GLU_195	OE1	3.108
1L7I	L_LYS_149	NZ	L_GLU_195	OE2	3.606
1L7I	L_HIS_189	ND1	L_ASP_151	OD2	3.427
1L7I	H_ARG_38	NH1	H_ASP_86	OD1	2.914
1L7I	H_ARG_38	NH2	H_GLU_46	OE1	3.005
1L7I	H_ARG_62	NH2	H_GLU_46	OE1	3.101
1L7I	H_ARG_62	NH2	H_GLU_46	OE2	2.791
1L7I	H_ARG_66	NH1	H_ASP_86	OD1	2.927
1L7I	H_ARG_66	NH1	H_ASP_86	OD2	3.600
1L7I	H_ARG_94	NH2	H_ASP_101	OD1	3.112
1L7I	H_LYS_143	NZ	H_ASP_144	OD1	3.173
1L7I	H_LYS_143	NZ	H_ASP_144	OD2	3.234
1L7I	H_LYS_209	NZ	L_GLU_123	OE1	2.718
1L7I	H_LYS_210	NZ	H_GLU_212	OE2	3.013
1LK3	A_ARG_27	NH1	A_GLU_151	OE1	3.162
1LK3	A_ARG_27	NH1	A_GLU_151	OE2	3.248
1LK3	A_ARG_27	NH2	A_GLU_151	OE2	2.810
1LK3	A_LYS_99	NZ	A_GLU_96	OE2	3.379
1LK3	A_LYS_125	NZ	A_GLU_122	OE2	3.974
1LK3	A_LYS_130	NZ	L_ASP_1	OD1	2.906
1LK3	L_ARG_31	NH1	A_GLU_133	OE1	2.703
1LK3	L_ARG_60	NH1	L_GLU_78	OE1	3.757
1LK3	L_ARG_60	NH1	L_ASP_81	OD1	3.577
1LK3	L_ARG_60	NH1	L_ASP_81	OD2	2.703
1LK3	L_ARG_60	NH2	L_GLU_78	OE1	3.450
1LK3	L_ARG_60	NH2	L_GLU_78	OE2	3.792
1LK3	L_ARG_60	NH2	L_ASP_81	OD1	2.902
1LK3	L_ARG_60	NH2	L_ASP_81	OD2	3.590
1LK3	L_LYS_146	NZ	L_GLU_153	OE2	2.870
1LK3	L_LYS_148	NZ	L_GLU_194	OE1	2.968
1LK3	L_LYS_148	NZ	L_GLU_194	OE2	3.177
1LK3	L_ARG_154	NH1	L_ASP_184	OD1	3.134
1LK3	L_ARG_154	NH1	L_ASP_184	OD2	3.607
1LK3	L_ARG_154	NH2	L_ASP_184	OD1	3.715
1LK3	L_ARG_154	NH2	L_ASP_184	OD2	2.806
1LK3	L_ARG_155	NH1	L_GLU_153	OE2	2.979
1LK3	L_LYS_182	NZ	L_GLU_186	OE2	3.604
1LK3	L_HIS_188	ND1	L_ASP_150	OD2	3.740
1LK3	L_HIS_188	NE2	L_ASP_184	OD1	3.222
1LK3	H_LYS_13	NZ	H_GLU_121	OE2	2.581
1LK3	H_LYS_23	NZ	L_GLU_121	OE2	2.800
1LK3	H_LYS_65	NZ	H_GLU_62	OE1	3.360
1LK3	H_LYS_67	NZ	H_ASP_90	OD1	3.589
1LK3	H_LYS_67	NZ	H_ASP_90	OD2	2.874
1LK3	H_LYS_214	NZ	L_GLU_122	OE1	2.517
1LK3	B_ARG_27	NH1	B_GLU_151	OE1	2.917
1LK3	B_ARG_27	NH2	B_GLU_151	OE1	3.090

1LK3	B_ARG_27	NH2	B_GLU_151	OE2	3.902
1LK3	B_LYS_88	NZ	B_GLU_81	OE2	3.290
1LK3	B_LYS_99	NZ	B_GLU_96	OE1	3.193
1LK3	B_LYS_99	NZ	B_GLU_96	OE2	3.913
1LK3	B_LYS_125	NZ	B_GLU_122	OE2	3.816
1LK3	B_LYS_130	NZ	M_ASP_1	OD1	2.851
1LK3	M_LYS_23	NZ	M_ASP_69	OD1	2.916
1LK3	M_LYS_23	NZ	M_ASP_69	OD2	3.739
1LK3	M_ARG_31	NH1	B_GLU_133	OE1	2.693
1LK3	M_LYS_38	NZ	M_ASP_80	OD1	3.251
1LK3	M_LYS_38	NZ	M_ASP_80	OD2	3.163
1LK3	M_ARG_60	NH1	M_ASP_81	OD1	3.524
1LK3	M_ARG_60	NH1	M_ASP_81	OD2	2.748
1LK3	M_ARG_60	NH2	M_GLU_78	OE1	3.446
1LK3	M_ARG_60	NH2	M_GLU_78	OE2	3.705
1LK3	M_ARG_60	NH2	M_ASP_81	OD1	2.992
1LK3	M_ARG_60	NH2	M_ASP_81	OD2	3.699
1LK3	M_LYS_148	NZ	M_GLU_194	OE1	3.154
1LK3	M_LYS_148	NZ	M_GLU_194	OE2	2.891
1LK3	M_ARG_154	NH1	M_ASP_184	OD1	3.102
1LK3	M_ARG_154	NH1	M_ASP_184	OD2	3.559
1LK3	M_ARG_154	NH2	M_ASP_184	OD1	3.772
1LK3	M_ARG_154	NH2	M_ASP_184	OD2	2.866
1LK3	M_ARG_155	NH1	M_GLU_153	OE2	2.799
1LK3	M_LYS_182	NZ	M_GLU_186	OE1	2.894
1LK3	M_LYS_182	NZ	M_GLU_186	OE2	3.921
1LK3	M_HIS_188	ND1	M_ASP_150	OD2	3.800
1LK3	M_HIS_188	NE2	M_ASP_184	OD1	3.004
1LK3	M_LYS_198	NZ	M_ASP_109	OD1	3.702
1LK3	M_LYS_198	NZ	M_ASP_109	OD2	3.602
1LK3	I_LYS_13	NZ	I_GLU_121	OE1	2.774
1LK3	I_LYS_63	NZ	M_ASP_1	OD2	3.881
1LK3	I_LYS_67	NZ	I_ASP_90	OD1	3.913
1LK3	I_LYS_67	NZ	I_ASP_90	OD2	2.939
1LK3	I_LYS_214	NZ	M_GLU_122	OE2	2.753
1M71	A_ARG_14	NH1	A_ASP_17	OD1	3.710
1M71	A_HIS_27D	ND1	A_ASP_28	OD1	3.392
1M71	A_HIS_27D	ND1	A_ASP_28	OD2	2.865
1M71	A_LYS_39	NZ	A_GLU_81	OE1	2.866
1M71	A_ARG_61	NH1	A_GLU_79	OE1	3.543
1M71	A_ARG_61	NH2	A_ASP_82	OD1	2.481
1M71	A_ARG_61	NH2	A_ASP_82	OD2	2.894
1M71	A_LYS_149	NZ	A_GLU_195	OE2	3.376
1M71	A_LYS_183	NZ	A_GLU_187	OE1	2.685
1M71	A_ARG_188	NH1	A_GLU_185	OE1	3.609
1M71	A_ARG_188	NH2	A_ASP_184	OD1	3.517
1M71	A_HIS_189	ND1	A_ASP_151	OD1	3.287
1M71	A_LYS_199	NZ	A_ASP_110	OD1	2.781
1M71	A_LYS_199	NZ	A_ASP_110	OD2	3.508
1M71	B_ARG_38	NH1	B_GLU_46	OE1	2.911
1M71	B_ARG_38	NH1	B_GLU_46	OE2	3.780
1M71	B_ARG_38	NH2	B_ASP_86	OD1	3.068
1M71	B_ARG_52	NH1	B_GLU_50	OE2	2.697
1M71	B_HIS_58	ND1	B_GLU_50	OE2	3.091
1M71	B_ARG_66	NH1	B_ASP_86	OD1	3.230
1M71	B_ARG_66	NH1	B_ASP_86	OD2	3.124
1M71	B_ARG_66	NH2	B_ASP_86	OD1	3.143
1M71	B_ARG_66	NH2	B_ASP_86	OD2	3.298

1M7I	B_ARG_71	NH1	B_ASP_73	OD2	3.433
1M7I	B_LYS_75	NZ	B_ASP_72	OD2	3.881
1M7I	B_ARG_83	NH1	B_GLU_85	OE2	3.022
1M7I	B_ARG_83	NH2	B_GLU_85	OE2	2.413
1M7I	B_ARG_94	NH1	B_ASP_101	OD1	3.346
1M7I	B_ARG_94	NH1	B_ASP_101	OD2	3.346
1M7I	B_ARG_164	NH1	A_ASP_167	OD2	3.246
1M7I	B_ARG_164	NH1	A_ASP_170	OD1	3.912
1M7I	B_ARG_164	NH2	A_ASP_167	OD2	2.886
1M7I	B_LYS_208	NZ	A_GLU_123	OE1	2.546
1M7I	B_LYS_208	NZ	A_GLU_123	OE2	3.594
1M7D	A_ARG_24	NH1	A_ASP_70	OD1	3.427
1M7D	A_HIS_27D	ND1	A_ASP_28	OD1	3.488
1M7D	A_HIS_27D	ND1	A_ASP_28	OD2	3.058
1M7D	A_LYS_39	NZ	A_GLU_81	OE1	2.802
1M7D	A_ARG_61	NH1	A_ASP_82	OD1	2.789
1M7D	A_ARG_61	NH1	A_ASP_82	OD2	3.838
1M7D	A_ARG_61	NH2	A_ASP_82	OD1	3.397
1M7D	A_ARG_61	NH2	A_ASP_82	OD2	2.952
1M7D	A_LYS_103	NZ	A_ASP_165	OD1	3.651
1M7D	A_LYS_149	NZ	A_GLU_195	OE1	2.888
1M7D	A_LYS_149	NZ	A_GLU_195	OE2	3.877
1M7D	A_ARG_188	NH1	A_GLU_185	OE1	2.963
1M7D	A_ARG_188	NH2	A_ASP_184	OD1	3.464
1M7D	A_HIS_189	ND1	A_ASP_151	OD1	2.856
1M7D	A_HIS_189	NE2	A_GLU_185	OE2	2.728
1M7D	A_LYS_199	NZ	A_ASP_110	OD1	3.424
1M7D	B_ARG_38	NH1	B_GLU_46	OE1	3.681
1M7D	B_ARG_38	NH1	B_GLU_46	OE2	3.270
1M7D	B_ARG_38	NH2	B_ASP_86	OD1	3.018
1M7D	B_ARG_52	NH1	B_GLU_50	OE2	3.410
1M7D	B_HIS_58	ND1	B_GLU_50	OE2	3.864
1M7D	B_ARG_66	NH1	B_ASP_86	OD1	3.193
1M7D	B_ARG_66	NH1	B_ASP_86	OD2	3.613
1M7D	B_ARG_66	NH2	B_ASP_86	OD1	3.775
1M7D	B_ARG_66	NH2	B_ASP_86	OD2	2.708
1M7D	B_ARG_71	NH1	B_ASP_73	OD2	2.991
1M7D	B_LYS_75	NZ	B_ASP_72	OD1	3.686
1M7D	B_ARG_94	NH1	B_ASP_101	OD1	3.533
1M7D	B_ARG_94	NH1	B_ASP_101	OD2	2.689
1M7D	B_ARG_164	NH1	A_ASP_167	OD2	3.313
1M7D	B_ARG_164	NH1	A_ASP_170	OD1	3.795
1M7D	B_ARG_164	NH2	A_ASP_167	OD2	3.482
1M7D	B_LYS_208	NZ	A_GLU_123	OE1	2.586
1M7D	B_LYS_208	NZ	A_GLU_123	OE2	3.420
1M7I	A_ARG_14	NH1	A_ASP_17	OD1	3.105
1M7I	A_ARG_14	NH1	A_ASP_17	OD2	3.058
1M7I	A_ARG_24	NH1	A_ASP_70	OD1	3.369
1M7I	A_ARG_24	NH1	A_ASP_70	OD2	3.708
1M7I	A_HIS_27D	ND1	A_ASP_28	OD1	3.271
1M7I	A_HIS_27D	ND1	A_ASP_28	OD2	2.955
1M7I	A_LYS_39	NZ	A_GLU_81	OE1	3.102
1M7I	A_ARG_61	NH1	A_ASP_82	OD1	2.522
1M7I	A_ARG_61	NH1	A_ASP_82	OD2	3.863
1M7I	A_ARG_61	NH2	A_GLU_79	OE2	3.752
1M7I	A_ARG_61	NH2	A_ASP_82	OD1	2.961
1M7I	A_ARG_61	NH2	A_ASP_82	OD2	2.695
1M7I	A_LYS_103	NZ	A_ASP_165	OD1	3.427

1M7I	A_LYS_147	NZ	A_GLU_154	OE1	3.983
1M7I	A_LYS_149	NZ	A_GLU_195	OE1	2.955
1M7I	A_LYS_183	NZ	A_GLU_187	OE1	3.069
1M7I	A_LYS_183	NZ	A_GLU_187	OE2	2.718
1M7I	A_ARG_188	NH1	A_GLU_185	OE1	2.765
1M7I	A_ARG_188	NH1	A_GLU_185	OE2	3.812
1M7I	A_ARG_188	NH2	A_ASP_184	OD1	3.546
1M7I	A_HIS_189	ND1	A_ASP_151	OD1	2.633
1M7I	A_HIS_189	NE2	A_GLU_185	OE2	3.470
1M7I	A_LYS_199	NZ	A_ASP_110	OD1	3.401
1M7I	A_LYS_199	NZ	A_ASP_110	OD2	3.942
1M7I	B_LYS_3	NZ	B_GLU_5	OE1	3.875
1M7I	B_ARG_38	NH1	B_GLU_46	OE1	3.661
1M7I	B_ARG_38	NH1	B_GLU_46	OE2	3.487
1M7I	B_ARG_38	NH2	B_ASP_86	OD1	2.988
1M7I	B_ARG_52	NH1	B_GLU_50	OE2	3.454
1M7I	B_LYS_64	NZ	B_GLU_61	OE1	3.621
1M7I	B_ARG_66	NH1	B_ASP_86	OD1	3.442
1M7I	B_ARG_66	NH2	B_ASP_86	OD1	3.524
1M7I	B_ARG_66	NH2	B_ASP_86	OD2	3.046
1M7I	B_ARG_71	NH1	B_ASP_73	OD2	3.013
1M7I	B_ARG_83	NH2	B_GLU_85	OE2	3.534
1M7I	B_ARG_94	NH1	B_ASP_101	OD1	3.458
1M7I	B_ARG_94	NH1	B_ASP_101	OD2	2.750
1M7I	B_ARG_164	NH1	A_ASP_167	OD2	3.340
1M7I	B_ARG_164	NH1	A_ASP_170	OD1	3.884
1M7I	B_ARG_164	NH2	A_ASP_167	OD2	3.473
1M7I	B_LYS_208	NZ	A_GLU_123	OE1	3.031
1M7I	B_LYS_208	NZ	A_GLU_123	OE2	3.016
1MCO	L_LYS_55	NZ	L_GLU_52	OE1	3.257
1MCO	L_LYS_55	NZ	L_GLU_52	OE2	2.994
1MCO	L_ARG_63	NH1	L_GLU_83	OE1	3.878
1MCO	L_ARG_63	NH1	L_ASP_84	OD1	3.777
1MCO	L_ARG_63	NH1	L_ASP_84	OD2	3.204
1MCO	L_ARG_63	NH2	L_GLU_83	OE1	2.986
1MCO	L_LYS_153	NZ	L_GLU_207	OE1	3.930
1MCO	L_HIS_192	ND1	L_ASP_155	OD1	3.857
1MCO	L_HIS_192	ND1	L_ASP_155	OD2	3.328
1MCO	H_ARG_40	NH1	H_ASP_91	OD2	3.601
1MCO	H_ARG_40	NH2	H_GLU_48	OE1	3.700
1MCO	H_ARG_68	NH1	H_ASP_91	OD2	3.621
1MCO	H_ARG_68	NH2	H_ASP_91	OD2	3.951
1MCO	H_ARG_99	NH1	H_ASP_27	OD1	3.647
1MCO	H_ARG_99	NH1	H_ASP_27	OD2	2.797
1MCO	H_LYS_302	NZ	H_ASP_265	OD1	3.759
1MCO	H_LYS_302	NZ	H_ASP_265	OD2	3.098
1MCO	H_LYS_305	NZ	H_GLU_318	OE1	3.587
1MCO	H_LYS_305	NZ	H_GLU_318	OE2	3.377
1MCO	H_ARG_329	NH1	H_ASP_386	OD1	3.691
1MCO	H_ARG_401	NH1	H_GLU_373	OE1	3.230
1MCO	H_ARG_401	NH1	H_GLU_373	OE2	3.498
1MCO	H_ARG_401	NH2	H_GLU_373	OE1	3.949
1MCO	H_ARG_401	NH2	H_GLU_373	OE2	3.117
1MEL	A_ARG_38	NH1	A_ASP_90	OD1	3.059
1MEL	A_ARG_38	NH2	A_GLU_46	OE1	3.526
1MEL	A_ARG_38	NH2	A_GLU_46	OE2	3.673
1MEL	A_ARG_38	NH2	A_ASP_90	OD1	3.839
1MEL	A_ARG_67	NH1	A_ASP_90	OD1	3.797

1MEL	A_ARG_67	NH1	A_ASP_90	OD2	2.991
1MEL	A_ARG_67	NH2	A_ASP_90	OD1	2.893
1MEL	A_ARG_67	NH2	A_ASP_90	OD2	3.367
1MEL	B_ARG_38	NH1	B_ASP_90	OD1	3.033
1MEL	B_ARG_38	NH2	B_GLU_46	OE2	2.855
1MEL	B_ARG_38	NH2	B_ASP_90	OD1	3.939
1MEL	B_LYS_65	NZ	B_ASP_62	OD1	3.615
1MEL	B_ARG_67	NH1	B_ASP_90	OD2	2.997
1MEL	B_ARG_67	NH2	B_ASP_90	OD1	2.985
1MEL	B_ARG_67	NH2	B_ASP_90	OD2	2.943
1MEL	B_HIS_111	NE2	B_GLU_108	OE1	3.372
1MEL	L_LYS_1	NZ	L_GLU_7	OE1	3.475
1MEL	L_LYS_1	NZ	L_GLU_7	OE2	3.097
1MEL	L_HIS_15	NE2	L_ASP_87	OD1	3.885
1MEL	L_ARG_61	NH2	L_ASP_48	OD2	3.045
1MEL	L_LYS_97	NZ	L_ASP_101	OD2	2.722
1MEL	L_ARG_125	NH2	L_ASP_119	OD1	3.620
1MEL	L_ARG_125	NH2	L_ASP_119	OD2	2.816
1MEL	M_LYS_1	NZ	M_GLU_7	OE1	3.630
1MEL	M_LYS_1	NZ	M_GLU_7	OE2	2.907
1MEL	M_ARG_61	NH2	M_ASP_48	OD2	3.828
1MEL	M_ARG_125	NH1	M_ASP_119	OD2	3.053
1MEL	M_ARG_125	NH2	M_ASP_119	OD1	3.215
1MEL	M_ARG_125	NH2	M_ASP_119	OD2	3.106
1MFA	L_HIS_34	ND1	L_ASP_52	OD1	2.763
1MFA	L_ARG_63	NH2	L_ASP_84	OD1	2.796
1MFA	L_ARG_63	NH2	L_ASP_84	OD2	3.671
1MFA	H_LYS_313	NZ	H_GLU_296	OE1	3.001
1MFA	H_LYS_313	NZ	H_GLU_296	OE2	3.675
1MFA	H_LYS_317	NZ	H_ASP_340	OD1	3.252
1MFA	H_LYS_317	NZ	H_ASP_340	OD2	2.782
1MFA	H_ARG_348	NH2	H_ASP_356	OD1	3.621
1MFA	H_ARG_348	NH2	H_ASP_356	OD2	2.864
1MFB	L_HIS_34	ND1	L_ASP_52	OD1	2.852
1MFB	L_HIS_44	ND1	L_GLU_40	OE2	3.943
1MFB	L_ARG_63	NH2	L_GLU_83	OE2	3.681
1MFB	L_ARG_63	NH2	L_ASP_84	OD1	2.962
1MFB	L_ARG_63	NH2	L_ASP_84	OD2	3.489
1MFB	L_LYS_113	NZ	L_GLU_201	OE1	3.004
1MFB	L_LYS_169	NZ	L_GLU_85	OE2	3.323
1MFB	L_HIS_191	ND1	L_ASP_154	OD2	3.623
1MFB	H_LYS_313	NZ	H_GLU_296	OE1	3.225
1MFB	H_LYS_313	NZ	H_GLU_296	OE2	3.887
1MFB	H_LYS_317	NZ	H_ASP_340	OD1	3.570
1MFB	H_LYS_317	NZ	H_ASP_340	OD2	2.807
1MFB	H_ARG_348	NH1	H_ASP_356	OD1	3.475
1MFB	H_ARG_348	NH1	H_ASP_356	OD2	3.034
1MFB	H_LYS_398	NZ	L_GLU_127	OE2	2.924
1MFB	H_LYS_463	NZ	L_GLU_126	OE1	3.780
1MFC	L_HIS_34	ND1	L_ASP_52	OD1	2.788
1MFC	L_ARG_63	NH2	L_GLU_83	OE2	3.733
1MFC	L_ARG_63	NH2	L_ASP_84	OD1	2.943
1MFC	L_ARG_63	NH2	L_ASP_84	OD2	3.639
1MFC	L_LYS_72	NZ	L_ASP_71	OD1	3.757
1MFC	L_LYS_113	NZ	L_GLU_201	OE1	2.885
1MFC	L_LYS_169	NZ	L_GLU_85	OE2	2.931
1MFC	L_HIS_191	ND1	L_ASP_154	OD2	3.170
1MFC	H_LYS_313	NZ	H_GLU_296	OE1	3.268

1MFC	H.LYS_313	NZ	H.GLU_296	OE2	3.847
1MFC	H.LYS_317	NZ	H.ASP_340	OD1	3.122
1MFC	H.LYS_317	NZ	H.ASP_340	OD2	2.805
1MFC	H.ARG_348	NH1	H.ASP_356	OD1	3.435
1MFC	H.ARG_348	NH1	H.ASP_356	OD2	2.938
1MFC	H.LYS_398	NZ	L.GLU_127	OE2	2.815
1MFC	H.LYS_463	NZ	L.GLU_126	OE1	3.807
1MHH	A.ARG_61	NH1	A.GLU_81	OE1	3.842
1MHH	A.ARG_61	NH2	A.GLU_81	OE1	2.895
1MHH	A.ARG_61	NH2	A.ASP_82	OD1	2.685
1MHH	A.ARG_61	NH2	A.ASP_82	OD2	3.421
1MHH	A.LYS_103	NZ	A.GLU_105	OE1	3.375
1MHH	A.LYS_103	NZ	A.GLU_105	OE2	3.766
1MHH	A.LYS_142	NZ	A.GLU_105	OE1	3.319
1MHH	A.LYS_142	NZ	A.GLU_105	OE2	2.969
1MHH	A.LYS_147	NZ	A.GLU_195	OE2	3.944
1MHH	A.LYS_149	NZ	A.GLU_195	OE1	2.919
1MHH	A.LYS_149	NZ	A.GLU_195	OE2	3.626
1MHH	A.ARG_155	NH2	A.GLU_185	OE2	3.327
1MHH	A.LYS_183	NZ	A.GLU_187	OE1	2.817
1MHH	A.LYS_183	NZ	A.GLU_187	OE2	3.387
1MHH	A.HIS_189	ND1	A.ASP_151	OD2	2.738
1MHH	A.LYS_199	NZ	A.ASP_110	OD2	3.962
1MHH	B.LYS_64	NZ	B.ASP_61	OD1	3.336
1MHH	B.ARG_66	NH1	B.ASP_86	OD1	3.761
1MHH	B.ARG_66	NH1	B.ASP_86	OD2	2.813
1MHH	B.ARG_66	NH2	B.ASP_86	OD1	3.094
1MHH	B.ARG_66	NH2	B.ASP_86	OD2	3.485
1MHH	B.ARG_94	NH2	B.ASP_101	OD1	2.684
1MHH	B.ARG_94	NH2	B.ASP_101	OD2	3.615
1MHH	B.LYS_208	NZ	A.GLU_123	OE2	3.019
1MHH	C.LYS_24	NZ	C.ASP_70	OD1	3.911
1MHH	C.ARG_61	NH1	C.GLU_81	OE2	3.375
1MHH	C.ARG_61	NH1	C.ASP_82	OD1	2.924
1MHH	C.ARG_61	NH1	C.ASP_82	OD2	3.294
1MHH	C.ARG_61	NH2	C.ASP_82	OD1	3.459
1MHH	C.ARG_61	NH2	C.ASP_82	OD2	2.571
1MHH	C.LYS_147	NZ	C.GLU_195	OE1	3.060
1MHH	C.LYS_149	NZ	C.GLU_195	OE2	3.143
1MHH	C.ARG_155	NH1	C.GLU_185	OE1	3.912
1MHH	C.ARG_155	NH1	C.GLU_185	OE2	3.653
1MHH	C.ARG_155	NH2	C.GLU_185	OE1	2.731
1MHH	C.ARG_155	NH2	C.GLU_185	OE2	3.507
1MHH	C.LYS_183	NZ	C.GLU_187	OE1	2.713
1MHH	C.ARG_188	NH1	E.ASP_831	OD2	3.196
1MHH	C.ARG_188	NH2	E.ASP_831	OD2	3.360
1MHH	C.HIS_189	ND1	C.ASP_151	OD1	2.633
1MHH	C.LYS_199	NZ	C.ASP_110	OD2	2.558
1MHH	D.ARG_66	NH1	D.ASP_86	OD1	3.829
1MHH	D.ARG_66	NH1	D.ASP_86	OD2	2.884
1MHH	D.ARG_66	NH2	D.ASP_86	OD1	2.828
1MHH	D.ARG_66	NH2	D.ASP_86	OD2	3.264
1MHH	D.ARG_94	NH2	D.ASP_101	OD1	3.655
1MHH	D.ARG_94	NH2	D.ASP_101	OD2	2.611
1MHH	E.LYS_833	NZ	C.GLU_185	OE2	2.489
1MHH	E.LYS_840	NZ	E.GLU_838	OE1	3.866
1MHH	E.HIS_874	NE2	E.GLU_869	OE2	3.707
1MHH	E.LYS_878	NZ	E.ASP_867	OD2	2.644

1MHH	F_LYS_1833	NZ	C_GLU_17	OE1	3.798
1MLB	A_ARG_61	NH1	A_ASP_82	OD1	2.159
1MLB	A_ARG_61	NH1	A_ASP_82	OD2	2.329
1MLB	A_ARG_61	NH2	A_GLU_79	OE1	3.872
1MLB	A_ARG_61	NH2	A_GLU_81	OE2	3.099
1MLB	A_LYS_147	NZ	A_GLU_154	OE1	3.634
1MLB	A_LYS_147	NZ	A_GLU_154	OE2	2.438
1MLB	A_LYS_149	NZ	A_GLU_195	OE1	3.556
1MLB	A_LYS_149	NZ	A_GLU_195	OE2	3.786
1MLB	A_ARG_155	NH1	A_GLU_185	OE2	2.511
1MLB	A_ARG_155	NH2	A_GLU_185	OE1	3.793
1MLB	A_ARG_155	NH2	A_GLU_185	OE2	2.918
1MLB	A_HIS_189	ND1	A_ASP_151	OD2	2.937
1MLB	A_LYS_199	NZ	A_ASP_110	OD2	2.869
1MLB	B_ARG_40	NH1	B_GLU_89	OE2	3.375
1MLB	B_ARG_40	NH2	B_GLU_89	OE2	3.648
1MLB	B_LYS_63	NZ	B_GLU_46	OE1	3.279
1MLB	B_LYS_67	NZ	B_ASP_90	OD1	2.983
1MLB	B_LYS_67	NZ	B_ASP_90	OD2	2.383
1MLB	B_ARG_98	NH2	B_ASP_100	OD1	3.092
1MLB	B_ARG_98	NH2	B_ASP_100	OD2	2.647
1MLB	B_LYS_211	NZ	A_GLU_123	OE1	3.556
1MLC	A_ARG_61	NH1	A_ASP_82	OD1	2.951
1MLC	A_ARG_61	NH1	A_ASP_82	OD2	2.608
1MLC	A_LYS_149	NZ	A_GLU_195	OE1	3.271
1MLC	A_LYS_149	NZ	A_GLU_195	OE2	2.595
1MLC	A_ARG_155	NH2	A_GLU_185	OE1	2.706
1MLC	A_ARG_155	NH2	A_GLU_185	OE2	3.006
1MLC	A_LYS_183	NZ	A_GLU_187	OE1	2.465
1MLC	A_LYS_183	NZ	A_GLU_187	OE2	2.957
1MLC	A_HIS_189	ND1	A_ASP_151	OD2	3.264
1MLC	A_HIS_189	NE2	A_GLU_185	OE2	3.846
1MLC	A_LYS_199	NZ	A_ASP_110	OD1	3.804
1MLC	A_LYS_199	NZ	A_ASP_110	OD2	2.246
1MLC	B_LYS_38	NZ	B_ASP_90	OD1	3.791
1MLC	B_ARG_40	NH2	B_GLU_89	OE1	3.285
1MLC	B_LYS_63	NZ	B_GLU_46	OE2	3.505
1MLC	B_LYS_67	NZ	B_ASP_90	OD1	3.662
1MLC	B_LYS_67	NZ	B_ASP_90	OD2	2.412
1MLC	B_ARG_98	NH2	B_ASP_100	OD1	2.914
1MLC	B_ARG_98	NH2	B_ASP_100	OD2	3.525
1MLC	C_ARG_61	NH1	C_ASP_82	OD1	3.434
1MLC	C_ARG_61	NH1	C_ASP_82	OD2	2.291
1MLC	C_ARG_61	NH2	C_ASP_82	OD1	2.696
1MLC	C_ARG_61	NH2	C_ASP_82	OD2	3.196
1MLC	C_ARG_155	NH2	C_GLU_185	OE2	3.214
1MLC	C_LYS_183	NZ	C_GLU_187	OE1	2.976
1MLC	C_LYS_183	NZ	C_GLU_187	OE2	3.623
1MLC	C_ARG_188	NH1	C_GLU_185	OE1	3.888
1MLC	C_HIS_189	ND1	C_ASP_151	OD2	3.300
1MLC	C_HIS_189	NE2	C_GLU_185	OE1	2.956
1MLC	C_LYS_199	NZ	C_ASP_110	OD2	3.357
1MLC	D_LYS_63	NZ	D_GLU_46	OE2	2.938
1MLC	D_LYS_67	NZ	D_ASP_90	OD1	3.041
1MLC	D_LYS_67	NZ	D_ASP_90	OD2	2.752
1MLC	D_ARG_98	NH2	D_ASP_100	OD1	3.684
1MLC	D_ARG_98	NH2	D_ASP_100	OD2	2.571
1MLC	E_LYS_1	NZ	E_GLU_7	OE2	3.616

1MLC	E_ARG_45	NH2	B_GLU_50	OE2	3.032
1MLC	E_ARG_68	NH1	B_GLU_50	OE2	3.781
1MLC	E_ARG_68	NH2	B_GLU_35	OE2	2.927
1MLC	E_ARG_68	NH2	B_GLU_50	OE1	2.510
1MLC	E_ARG_68	NH2	B_GLU_50	OE2	3.189
1MLC	F_LYS_1	NZ	F_GLU_7	OE2	3.323
1MLC	F_ARG_45	NH2	D_GLU_50	OE2	2.431
1MLC	F_ARG_68	NH2	D_GLU_35	OE2	3.266
1MLC	F_ARG_68	NH2	D_GLU_50	OE1	2.710
1MLC	F_ARG_68	NH2	D_GLU_50	OE2	3.606
1MLC	F_ARG_125	NH1	F_ASP_119	OD2	3.464
1MLC	F_ARG_125	NH2	F_ASP_119	OD2	2.213
1N64	L_LYS_24	NZ	L_ASP_70	OD2	3.651
1N64	L_ARG_54	NH2	L_ASP_60	OD2	3.449
1N64	L_ARG_61	NH1	L_GLU_81	OE1	3.429
1N64	L_ARG_61	NH1	L_ASP_82	OD1	2.971
1N64	L_ARG_61	NH1	L_ASP_82	OD2	2.992
1N64	L_LYS_142	NZ	L_GLU_105	OE2	3.590
1N64	L_LYS_149	NZ	L_GLU_195	OE1	3.534
1N64	L_ARG_155	NH2	L_GLU_185	OE2	3.243
1N64	L_LYS_183	NZ	L_GLU_187	OE2	2.697
1N64	L_HIS_189	ND1	L_ASP_151	OD2	3.116
1N64	L_ARG_211	NH2	L_GLU_187	OE1	3.018
1N64	H_LYS_12	NZ	H_GLU_16	OE1	3.976
1N64	H_LYS_64	NZ	H_ASP_61	OD1	2.775
1N64	H_ARG_66	NH1	H_ASP_86	OD1	3.467
1N64	H_ARG_66	NH1	H_ASP_86	OD2	3.004
1N64	H_ARG_66	NH2	H_ASP_86	OD1	2.824
1N64	H_ARG_66	NH2	H_ASP_86	OD2	3.196
1N64	H_ARG_94	NH1	H_ASP_101	OD1	2.581
1N64	H_ARG_94	NH1	H_ASP_101	OD2	3.313
1N64	H_LYS_208	NZ	L_GLU_123	OE1	3.752
1NBY	A_ARG_61	NH2	A_GLU_81	OE1	3.423
1NBY	A_ARG_61	NH2	A_ASP_82	OD1	2.821
1NBY	A_ARG_61	NH2	A_ASP_82	OD2	3.549
1NBY	A_LYS_103	NZ	A_GLU_105	OE2	3.768
1NBY	A_LYS_147	NZ	A_GLU_154	OE2	3.844
1NBY	A_LYS_149	NZ	A_GLU_195	OE1	3.898
1NBY	A_LYS_149	NZ	A_GLU_195	OE2	3.414
1NBY	A_ARG_155	NH2	A_GLU_185	OE2	3.438
1NBY	A_LYS_169	NZ	A_ASP_167	OD1	3.633
1NBY	A_LYS_169	NZ	A_ASP_167	OD2	2.995
1NBY	B_ARG_338	NH1	B_ASP_389	OD1	2.811
1NBY	B_ARG_338	NH2	B_GLU_346	OE1	2.861
1NBY	B_ARG_338	NH2	B_ASP_389	OD1	3.519
1NBY	B_ARG_366	NH1	B_ASP_389	OD1	3.031
1NBY	B_ARG_366	NH1	B_ASP_389	OD2	3.595
1NBY	B_ARG_366	NH2	B_ASP_389	OD1	3.673
1NBY	B_ARG_366	NH2	B_ASP_389	OD2	2.895
1NBY	B_LYS_508	NZ	A_GLU_123	OE1	2.458
1NBY	B_LYS_508	NZ	A_GLU_123	OE2	3.274
1NBY	C_LYS_601	NZ	C_GLU_607	OE2	2.838
1NBY	C_LYS_613	NZ	C_ASP_618	OD1	3.678
1NBY	C_LYS_697	NZ	B_ASP_332	OD1	3.949
1NBY	C_LYS_697	NZ	B_ASP_332	OD2	2.515
1NBY	C_ARG_725	NH1	C_ASP_719	OD1	3.590
1NBY	C_ARG_725	NH1	C_ASP_719	OD2	3.913
1NBY	C_ARG_725	NH2	C_ASP_719	OD1	3.444

1NBY	C_ARG_725	NH2	C_ASP_719	OD2	3.368
1NBZ	A_ARG_24	NH2	A_ASP_70	OD1	2.834
1NBZ	A_ARG_61	NH1	A_GLU_79	OE2	3.336
1NBZ	A_ARG_61	NH2	A_GLU_79	OE2	3.126
1NBZ	A_ARG_61	NH2	A_GLU_81	OE1	3.673
1NBZ	A_ARG_61	NH2	A_ASP_82	OD1	2.933
1NBZ	A_ARG_61	NH2	A_ASP_82	OD2	3.530
1NBZ	A_LYS_147	NZ	A_GLU_154	OE1	3.461
1NBZ	A_LYS_149	NZ	A_GLU_195B	OE1	3.640
1NBZ	A_ARG_155	NH1	A_GLU_185	OE2	3.835
1NBZ	A_ARG_155	NH2	A_GLU_185	OE2	3.081
1NBZ	B_ARG_338	NH1	B_GLU_346	OE1	2.666
1NBZ	B_ARG_338	NH1	B_ASP_389	OD1	3.713
1NBZ	B_ARG_338	NH2	B_ASP_389	OD1	2.601
1NBZ	B_ARG_366	NH1	B_ASP_389	OD1	3.099
1NBZ	B_ARG_366	NH1	B_ASP_389	OD2	3.734
1NBZ	B_ARG_366	NH2	B_ASP_389	OD1	3.577
1NBZ	B_ARG_366	NH2	B_ASP_389	OD2	2.894
1NBZ	C_LYS_601	NZ	C_GLU_607	OE2	3.226
1NBZ	C_ARG_661	NH1	C_ASP_648	OD1	3.578
1NBZ	C_ARG_661	NH1	C_ASP_648	OD2	3.756
1NDG	A_ARG_61	NH2	A_GLU_81	OE1	3.007
1NDG	A_ARG_61	NH2	A_ASP_82	OD1	2.723
1NDG	A_ARG_61	NH2	A_ASP_82	OD2	3.409
1NDG	A_LYS_147	NZ	A_GLU_154	OE1	3.627
1NDG	A_LYS_149	NZ	A_GLU_195	OE1	3.917
1NDG	A_LYS_149	NZ	A_GLU_195	OE2	3.737
1NDG	A_ARG_155	NH2	A_GLU_185	OE2	3.269
1NDG	A_LYS_199	NZ	A_ASP_110	OD2	3.863
1NDG	B_ARG_338	NH1	B_GLU_346	OE1	2.782
1NDG	B_ARG_338	NH1	B_ASP_389	OD1	3.738
1NDG	B_ARG_338	NH2	B_ASP_389	OD1	2.639
1NDG	B_HIS_360	NE2	A_ASP_1	OD2	3.716
1NDG	B_ARG_366	NH1	B_ASP_389	OD1	3.027
1NDG	B_ARG_366	NH1	B_ASP_389	OD2	3.618
1NDG	B_ARG_366	NH2	B_ASP_389	OD1	3.672
1NDG	B_ARG_366	NH2	B_ASP_389	OD2	2.903
1NDG	B_LYS_519	NZ	A_GLU_123	OE2	2.645
1NDG	C_LYS_601	NZ	C_GLU_607	OE1	3.948
1NDG	C_LYS_601	NZ	C_GLU_607	OE2	3.018
1NDG	C_LYS_613	NZ	C_ASP_618	OD2	3.695
1NDG	C_ARG_668	NH1	C_ASP_666	OD2	3.998
1NDG	C_LYS_697	NZ	B_ASP_332	OD1	3.996
1NDG	C_LYS_697	NZ	B_ASP_332	OD2	2.706
1NDG	C_LYS_697	NZ	B_ASP_399	OD1	2.922
1NDG	C_LYS_697	NZ	B_ASP_399	OD2	3.579
1NDG	C_ARG_725	NH2	C_ASP_719	OD1	3.484
1NDG	C_ARG_725	NH2	C_ASP_719	OD2	2.665
1NDM	A_ARG_24	NH2	A_ASP_70	OD1	3.107
1NDM	A_ARG_61	NH1	A_GLU_79	OE1	3.684
1NDM	A_ARG_61	NH1	A_GLU_79	OE2	2.866
1NDM	A_ARG_61	NH2	A_GLU_79	OE1	3.477
1NDM	A_ARG_61	NH2	A_GLU_79	OE2	3.744
1NDM	A_ARG_61	NH2	A_GLU_81	OE1	3.172
1NDM	A_ARG_61	NH2	A_ASP_82	OD1	2.876
1NDM	A_ARG_61	NH2	A_ASP_82	OD2	3.578
1NDM	A_LYS_149	NZ	A_GLU_195	OE1	3.953
1NDM	A_LYS_149	NZ	A_GLU_195	OE2	3.016

1NDM	A_ARG_155	NH1	A_GLU_185	OE1	3.939
1NDM	A_ARG_155	NH2	A_GLU_185	OE1	3.970
1NDM	A_ARG_188	NH2	A_ASP_184	OD1	3.023
1NDM	A_LYS_199	NZ	A_ASP_110	OD2	3.562
1NDM	B_ARG_338	NH1	B_GLU_346	OE1	2.753
1NDM	B_ARG_338	NH1	B_ASP_389	OD1	3.746
1NDM	B_ARG_338	NH2	B_ASP_389	OD1	2.687
1NDM	B_ARG_366	NH1	B_ASP_389	OD1	3.863
1NDM	B_ARG_366	NH2	B_ASP_389	OD1	3.499
1NDM	B_ARG_366	NH2	B_ASP_389	OD2	2.806
1NDM	B_ARG_397	NH1	B_ASP_332	OD1	3.700
1NDM	B_ARG_397	NH2	B_ASP_401	OD1	2.798
1NDM	B_ARG_397	NH2	B_ASP_401	OD2	3.696
1NDM	B_LYS_519	NZ	A_GLU_123	OE1	3.184
1NDM	C_LYS_601	NZ	C_GLU_607	OE1	3.751
1NDM	C_LYS_601	NZ	C_GLU_607	OE2	2.713
1NDM	C_ARG_668	NH1	C_ASP_666	OD2	3.599
1NDM	C_LYS_697	NZ	B_ASP_332	OD1	3.954
1NDM	C_LYS_697	NZ	B_ASP_332	OD2	2.468
1NDM	C_LYS_697	NZ	B_GLU_399	OE1	2.743
1NGW	L_LYS_24	NZ	L_ASP_70	OD1	3.381
1NGW	L_ARG_61	NH1	L_ASP_82	OD1	2.889
1NGW	L_ARG_61	NH1	L_ASP_82	OD2	3.061
1NGW	L_LYS_103	NZ	L_GLU_165	OE1	3.834
1NGW	L_LYS_103	NZ	L_GLU_165	OE2	3.110
1NGW	L_LYS_149	NZ	L_GLU_195	OE1	2.871
1NGW	L_LYS_183	NZ	L_GLU_187	OE1	3.850
1NGW	L_LYS_183	NZ	L_GLU_187	OE2	2.603
1NGW	L_LYS_188	NZ	L_ASP_185	OD1	3.745
1NGW	H_LYS_38	NZ	H_GLU_89	OE1	3.916
1NGW	H_LYS_38	NZ	H_GLU_89	OE2	3.046
1NGW	H_ARG_40	NH1	H_GLU_89	OE2	3.692
1NGW	H_LYS_63	NZ	H_GLU_46	OE1	3.487
1NGW	H_LYS_67	NZ	H_GLU_89	OE1	3.643
1NGW	H_LYS_67	NZ	H_ASP_90	OD1	2.985
1NGW	H_LYS_67	NZ	H_ASP_90	OD2	3.338
1NGW	H_ARG_98	NH1	H_ASP_102	OD1	3.333
1NGW	H_ARG_99	NH2	H_ASP_100	OD1	3.884
1NGW	H_ARG_99	NH2	H_ASP_100	OD2	3.152
1NGW	H_LYS_144	NZ	H_ASP_145	OD1	3.933
1NGW	H_LYS_144	NZ	H_ASP_145	OD2	3.556
1NGW	H_HIS_165	NE2	L_ASP_167	OD1	3.771
1NGW	H_LYS_210	NZ	L_GLU_123	OE1	3.544
1NGW	H_LYS_210	NZ	L_GLU_123	OE2	3.092
1NGW	A_LYS_24	NZ	A_ASP_70	OD1	3.412
1NGW	A_ARG_61	NH1	A_ASP_82	OD1	2.833
1NGW	A_ARG_61	NH1	A_ASP_82	OD2	3.020
1NGW	A_LYS_103	NZ	A_GLU_165	OE2	3.226
1NGW	A_LYS_149	NZ	A_GLU_195	OE1	2.874
1NGW	A_LYS_183	NZ	A_GLU_187	OE1	3.842
1NGW	A_LYS_183	NZ	A_GLU_187	OE2	2.592
1NGW	A_LYS_188	NZ	A_ASP_185	OD1	3.777
1NGW	B_LYS_38	NZ	B_GLU_89	OE1	3.908
1NGW	B_LYS_38	NZ	B_GLU_89	OE2	3.066
1NGW	B_ARG_40	NH1	B_GLU_89	OE2	3.715
1NGW	B_LYS_63	NZ	B_GLU_46	OE1	3.549
1NGW	B_LYS_67	NZ	B_GLU_89	OE1	3.643
1NGW	B_LYS_67	NZ	B_ASP_90	OD1	2.988

1NGW	B.LYS.67	NZ	B.ASP.90	OD2	3.345
1NGW	B.ARG.98	NH1	B.ASP.102	OD1	3.321
1NGW	B.ARG.99	NH2	B.ASP.100	OD1	3.865
1NGW	B.ARG.99	NH2	B.ASP.100	OD2	3.174
1NGW	B.LYS.144	NZ	B.ASP.145	OD1	3.893
1NGW	B.LYS.144	NZ	B.ASP.145	OD2	3.494
1NGW	B.HIS.165	NE2	A.ASP.167	OD1	3.804
1NGW	B.LYS.210	NZ	A.GLU.123	OE1	3.662
1NGW	B.LYS.210	NZ	A.GLU.123	OE2	3.240
1NGX	A.LYS.24	NZ	A.ASP.70	OD1	3.081
1NGX	A.LYS.24	NZ	A.ASP.70	OD2	3.994
1NGX	A.ARG.61	NH2	A.ASP.82	OD1	2.985
1NGX	A.ARG.61	NH2	A.ASP.82	OD2	2.969
1NGX	A.LYS.149	NZ	A.GLU.195	OE1	3.396
1NGX	A.LYS.149	NZ	A.GLU.195	OE2	3.345
1NGX	A.LYS.188	NZ	A.ASP.185	OD2	3.626
1NGX	B.ARG.40	NH1	B.GLU.46	OE2	3.949
1NGX	B.ARG.40	NH2	B.GLU.89	OE1	3.668
1NGX	B.ARG.40	NH2	B.GLU.89	OE2	3.900
1NGX	B.LYS.65	NZ	B.GLU.62	OE1	3.589
1NGX	B.LYS.65	NZ	B.GLU.62	OE2	2.814
1NGX	B.ARG.98	NH1	B.GLU.6	OE1	3.105
1NGX	B.ARG.98	NH1	B.GLU.6	OE2	3.939
1NGX	B.ARG.98	NH2	B.GLU.6	OE1	3.343
1NGX	B.ARG.98	NH2	B.GLU.6	OE2	2.833
1NGX	B.LYS.210	NZ	A.GLU.123	OE1	3.994
1NGX	L.LYS.24	NZ	L.ASP.70	OD1	3.096
1NGX	L.LYS.24	NZ	L.ASP.70	OD2	3.994
1NGX	L.LYS.45	NZ	H.ASP.102	OD2	3.800
1NGX	L.ARG.61	NH2	L.ASP.82	OD1	2.986
1NGX	L.ARG.61	NH2	L.ASP.82	OD2	2.973
1NGX	L.LYS.149	NZ	L.GLU.195	OE1	3.398
1NGX	L.LYS.149	NZ	L.GLU.195	OE2	3.336
1NGX	L.LYS.188	NZ	L.ASP.185	OD2	3.617
1NGX	H.ARG.40	NH1	H.GLU.46	OE2	3.939
1NGX	H.ARG.40	NH2	H.GLU.89	OE1	3.665
1NGX	H.ARG.40	NH2	H.GLU.89	OE2	3.888
1NGX	H.LYS.65	NZ	H.GLU.62	OE1	3.585
1NGX	H.LYS.65	NZ	H.GLU.62	OE2	2.810
1NGX	H.ARG.98	NH1	H.GLU.6	OE1	3.117
1NGX	H.ARG.98	NH1	H.GLU.6	OE2	3.962
1NGX	H.ARG.98	NH2	H.GLU.6	OE1	3.326
1NGX	H.ARG.98	NH2	H.GLU.6	OE2	2.854
1NGX	H.LYS.210	NZ	L.GLU.123	OE1	3.804
1NGY	A.ARG.18	NH1	A.ASP.17	OD2	3.594
1NGY	A.LYS.24	NZ	A.ASP.70	OD2	3.919
1NGY	A.ARG.61	NH2	A.ASP.82	OD1	2.968
1NGY	A.ARG.61	NH2	A.ASP.82	OD2	3.529
1NGY	A.LYS.103	NZ	A.ASP.85	OD1	3.853
1NGY	A.LYS.103	NZ	A.ASP.85	OD2	3.272
1NGY	A.LYS.188	NZ	A.ASP.185	OD2	2.771
1NGY	A.HIS.189	ND1	A.ASP.151	OD1	3.054
1NGY	B.LYS.67	NZ	B.ASP.90	OD1	3.731
1NGY	B.LYS.67	NZ	B.ASP.90	OD2	2.958
1NGY	B.ARG.98	NH1	B.ASP.102	OD1	3.607
1NGY	B.ARG.98	NH1	B.ASP.102	OD2	3.510
1NGY	B.ARG.99	NH2	B.ASP.100	OD2	3.858
1NGY	B.LYS.144	NZ	B.ASP.145	OD1	3.371

1NGY	B_LYS_144	NZ	B_ASP_145	OD2	3.636
1NGY	B_LYS_211	NZ	B_GLU_213	OE2	3.805
1NGY	B_LYS_215	NZ	A_ASP_122	OD1	3.713
1NGY	B_LYS_215	NZ	A_ASP_122	OD2	3.325
1NGZ	A_ARG_	NH1	A_ASP_	OD1	3.637
1NGZ	A_ARG_	NH1	A_ASP_	OD2	2.596
1NGZ	A_ARG_	NH2	A_GLU_	OE1	3.959
1NGZ	A_ARG_	NH2	A_ASP_	OD1	3.037
1NGZ	A_ARG_	NH2	A_ASP_	OD2	3.356
1NGZ	A_LYS_	NZ	A_GLU_	OE1	2.828
1NGZ	A_LYS_	NZ	A_GLU_	OE2	3.489
1NGZ	A_LYS_	NZ	A_GLU_	OE1	3.044
1NGZ	A_LYS_	NZ	A_GLU_	OE1	3.604
1NGZ	A_HIS_	ND1	A_ASP_	OD1	3.223
1NGZ	B_LYS_	NZ	B_GLU_	OE1	2.735
1NGZ	B_ARG_	NH2	B_ASP_	OD2	3.084
1NGZ	B_LYS_	NZ	B_ASP_	OD1	3.293
1NGZ	B_LYS_	NZ	A_GLU_	OE2	3.517
1NGZ	B_LYS_	NZ	B_GLU_	OE2	3.319
1NLB	L_ARG_61	NH1	L_GLU_81	OE1	3.945
1NLB	L_ARG_61	NH1	L_ASP_82	OD1	3.512
1NLB	L_ARG_61	NH1	L_ASP_82	OD2	2.842
1NLB	L_ARG_61	NH2	L_ASP_82	OD1	2.825
1NLB	L_ARG_61	NH2	L_ASP_82	OD2	3.519
1NLB	L_LYS_103	NZ	L_GLU_105	OE1	2.975
1NLB	L_LYS_149	NZ	L_GLU_195	OE1	2.997
1NLB	L_LYS_149	NZ	L_GLU_195	OE2	3.428
1NLB	L_ARG_155	NH1	L_GLU_185	OE1	3.426
1NLB	L_ARG_155	NH1	L_GLU_185	OE2	3.047
1NLB	L_HIS_189	ND1	L_ASP_151	OD2	2.936
1NLB	L_LYS_199	NZ	L_ASP_110	OD1	3.501
1NLB	H_LYS_64	NZ	H_ASP_61	OD2	2.732
1NLB	H_ARG_66	NH1	H_ASP_86	OD1	3.711
1NLB	H_ARG_66	NH1	H_ASP_86	OD2	2.788
1NLB	H_ARG_66	NH2	H_ASP_86	OD1	2.985
1NLB	H_ARG_66	NH2	H_ASP_86	OD2	3.410
1NLB	H_ARG_94	NH1	H_ASP_101	OD1	2.645
1NLB	H_ARG_94	NH1	H_ASP_101	OD2	3.679
1NLB	H_LYS_115	NZ	H_ASP_173	OD2	3.346
1NLB	H_LYS_205	NZ	H_ASP_207	OD1	3.946
1NLB	H_LYS_205	NZ	H_ASP_207	OD2	2.901
1NLB	H_LYS_208	NZ	L_GLU_123	OE1	3.572
1NMC	N_ARG_118	NH1	N_GLU_119	OE2	3.499
1NMC	N_ARG_118	NH2	N_GLU_119	OE2	3.987
1NMC	N_ARG_118	NH2	N_GLU_425	OE1	2.873
1NMC	N_ARG_118	NH2	N_GLU_425	OE2	3.183
1NMC	N_ARG_130	NH1	N_GLU_128	OE1	3.693
1NMC	N_ARG_130	NH1	N_GLU_128	OE2	3.810
1NMC	N_ARG_141	NH1	N_GLU_110	OE2	2.793
1NMC	N_ARG_152	NH2	N_ASP_151	OD1	3.884
1NMC	N_ARG_156	NH1	N_GLU_119	OE1	3.978
1NMC	N_ARG_156	NH2	N_GLU_119	OE1	3.322
1NMC	N_ARG_172	NH1	N_GLU_174	OE2	2.630
1NMC	N_ARG_189	NH2	N_ASP_125	OD1	2.838
1NMC	N_ARG_209	NH1	N_GLU_174	OE1	3.221
1NMC	N_ARG_209	NH1	N_GLU_174	OE2	3.350
1NMC	N_ARG_209	NH2	N_GLU_174	OE1	3.641
1NMC	N_ARG_209	NH2	N_GLU_174	OE2	3.567

1NMC	N_ARG_224	NH2	N_GLU_276	OE1	3.973
1NMC	N_ARG_224	NH2	N_GLU_276	OE2	2.790
1NMC	N_LYS_264	NZ	N_GLU_266	OE1	3.220
1NMC	N_LYS_273	NZ	N_ASP_339	OD1	3.418
1NMC	N_HIS_274	NE2	N_GLU_276	OE2	3.907
1NMC	N_ARG_292	NH1	N_GLU_277	OE1	2.656
1NMC	N_ARG_292	NH1	N_GLU_277	OE2	3.466
1NMC	N_ARG_300	NH1	N_ASP_324	OD2	3.693
1NMC	N_ARG_300	NH2	N_ASP_324	OD1	3.980
1NMC	N_ARG_304	NH1	N_GLU_286	OE2	2.662
1NMC	N_HIS_312	ND1	N_GLU_266	OE2	2.860
1NMC	N_ARG_364	NH1	N_GLU_375	OE2	2.972
1NMC	N_ARG_364	NH2	N_ASP_330	OD1	3.061
1NMC	N_ARG_364	NH2	N_ASP_330	OD2	2.772
1NMC	N_ARG_428	NH1	N_ASP_460	OD2	2.607
1NMC	N_ARG_428	NH2	N_GLU_433	OE1	3.420
1NMC	N_ARG_428	NH2	N_GLU_433	OE2	2.884
1NMC	N_LYS_432	NZ	H_ASP_56	OD1	2.750
1NMC	H_LYS_62	NZ	H_GLU_46	OE1	2.874
1NMC	H_LYS_62	NZ	H_GLU_46	OE2	3.520
1NMC	H_LYS_66	NZ	H_ASP_86	OD2	3.403
1NMC	H_ARG_94	NH2	H_ASP_101	OD1	3.582
1NMC	H_ARG_94	NH2	H_ASP_101	OD2	2.789
1NMC	H_ARG_100	NH1	H_ASP_100B	OD1	2.808
1NMC	H_ARG_100	NH1	H_ASP_100B	OD2	2.674
1NMC	H_ARG_100	NH2	H_ASP_100B	OD1	3.142
1NMC	L_ARG_61	NH1	L_GLU_79	OE1	3.308
1NMC	L_ARG_61	NH2	L_GLU_79	OE1	3.314
1NMC	L_ARG_61	NH2	L_ASP_82	OD1	2.650
1NMC	L_ARG_61	NH2	L_ASP_82	OD2	3.093
1NMC	L_ARG_107	NH2	L_ASP_108	OD2	3.871
1NMC	A_ARG_118	NH1	A_GLU_119	OE2	3.500
1NMC	A_ARG_118	NH2	A_GLU_119	OE2	3.987
1NMC	A_ARG_118	NH2	A_GLU_425	OE1	2.872
1NMC	A_ARG_118	NH2	A_GLU_425	OE2	3.182
1NMC	A_ARG_130	NH1	A_GLU_128	OE1	3.693
1NMC	A_ARG_130	NH1	A_GLU_128	OE2	3.809
1NMC	A_ARG_141	NH1	A_GLU_110	OE2	2.794
1NMC	A_ARG_152	NH2	A_ASP_151	OD1	3.884
1NMC	A_ARG_156	NH1	A_GLU_119	OE1	3.979
1NMC	A_ARG_156	NH2	A_GLU_119	OE1	3.323
1NMC	A_ARG_172	NH1	A_GLU_174	OE2	2.630
1NMC	A_ARG_189	NH2	A_ASP_125	OD1	2.839
1NMC	A_ARG_209	NH1	A_GLU_174	OE1	3.221
1NMC	A_ARG_209	NH1	A_GLU_174	OE2	3.350
1NMC	A_ARG_209	NH2	A_GLU_174	OE1	3.641
1NMC	A_ARG_209	NH2	A_GLU_174	OE2	3.567
1NMC	A_ARG_224	NH2	A_GLU_276	OE1	3.973
1NMC	A_ARG_224	NH2	A_GLU_276	OE2	2.791
1NMC	A_LYS_264	NZ	A_GLU_266	OE1	3.220
1NMC	A_LYS_273	NZ	A_ASP_339	OD1	3.419
1NMC	A_HIS_274	NE2	A_GLU_276	OE2	3.907
1NMC	A_ARG_292	NH1	A_GLU_277	OE1	2.655
1NMC	A_ARG_292	NH1	A_GLU_277	OE2	3.465
1NMC	A_ARG_300	NH1	A_ASP_324	OD2	3.694
1NMC	A_ARG_300	NH2	A_ASP_324	OD1	3.980
1NMC	A_ARG_304	NH1	A_GLU_286	OE2	2.663
1NMC	A_HIS_312	ND1	A_GLU_266	OE2	2.860

1NMC	A_ARG_364	NH1	A_GLU_375	OE2	2.972
1NMC	A_ARG_364	NH2	A_ASP_330	OD1	3.062
1NMC	A_ARG_364	NH2	A_ASP_330	OD2	2.772
1NMC	A_ARG_428	NH1	A_ASP_460	OD2	2.606
1NMC	A_ARG_428	NH2	A_GLU_433	OE1	3.421
1NMC	A_ARG_428	NH2	A_GLU_433	OE2	2.883
1NMC	A_LYS_432	NZ	B_ASP_56	OD1	2.750
1NMC	B_LYS_62	NZ	B_GLU_46	OE1	2.874
1NMC	B_LYS_62	NZ	B_GLU_46	OE2	3.520
1NMC	B_LYS_66	NZ	B_ASP_86	OD2	3.404
1NMC	B_ARG_94	NH2	B_ASP_101	OD1	3.582
1NMC	B_ARG_94	NH2	B_ASP_101	OD2	2.789
1NMC	B_ARG_100	NH1	B_ASP_100B	OD1	2.808
1NMC	B_ARG_100	NH1	B_ASP_100B	OD2	2.675
1NMC	B_ARG_100	NH2	B_ASP_100B	OD1	3.142
1NMC	C_ARG_61	NH1	C_GLU_79	OE1	3.308
1NMC	C_ARG_61	NH2	C_GLU_79	OE1	3.313
1NMC	C_ARG_61	NH2	C_ASP_82	OD1	2.649
1NMC	C_ARG_61	NH2	C_ASP_82	OD2	3.094
1NMC	C_ARG_107	NH2	C_ASP_108	OD2	3.871
1OB1	A_ARG_61	NH1	A_GLU_81	OE2	3.808
1OB1	A_ARG_61	NH1	A_ASP_82	OD1	2.619
1OB1	A_ARG_61	NH1	A_ASP_82	OD2	2.877
1OB1	A_ARG_61	NH2	A_GLU_81	OE2	3.763
1OB1	A_ARG_61	NH2	F_ASP_59	OD1	3.421
1OB1	A_ARG_61	NH2	F_ASP_59	OD2	2.223
1OB1	A_LYS_103	NZ	A_GLU_105	OE1	3.763
1OB1	A_ARG_154	NH2	A_GLU_184	OE2	2.981
1OB1	A_LYS_182	NZ	A_ASP_183	OD1	3.727
1OB1	A_LYS_182	NZ	A_GLU_186	OE1	3.077
1OB1	A_HIS_188	NE2	A_GLU_184	OE2	3.652
1OB1	A_ARG_210	NH2	A_GLU_186	OE2	3.268
1OB1	B_LYS_13	NZ	B_GLU_16	OE2	3.100
1OB1	B_ARG_66	NH1	B_ASP_86	OD1	3.867
1OB1	B_ARG_66	NH2	B_ASP_86	OD1	2.818
1OB1	B_ARG_66	NH2	B_ASP_86	OD2	3.197
1OB1	B_ARG_94	NH1	B_ASP_101	OD1	3.340
1OB1	B_ARG_94	NH1	B_ASP_101	OD2	2.759
1OB1	B_HIS_164	NE2	A_ASP_166	OD2	3.671
1OB1	B_LYS_205	NZ	B_ASP_207	OD1	3.102
1OB1	B_LYS_205	NZ	B_ASP_207	OD2	2.900
1OB1	B_LYS_209	NZ	B_GLU_211	OE1	3.918
1OB1	B_LYS_209	NZ	B_GLU_211	OE2	3.120
1OB1	C_LYS_9	NZ	C_GLU_24	OE2	3.557
1OB1	C_LYS_9	NZ	C_GLU_26	OE2	3.148
1OB1	C_LYS_10	NZ	B_ASP_100	OD1	2.437
1OB1	C_ARG_20	NH1	C_GLU_24	OE1	3.737
1OB1	C_ARG_20	NH2	C_GLU_24	OE1	2.454
1OB1	C_ARG_20	NH2	C_GLU_24	OE2	3.232
1OB1	C_HIS_21	NE2	C_GLU_27	OE2	2.879
1OB1	C_LYS_80	NZ	D_GLU_79	OE1	3.373
1OB1	C_LYS_80	NZ	D_GLU_81	OE1	3.553
1OB1	C_LYS_80	NZ	D_GLU_81	OE2	2.714
1OB1	D_ARG_61	NH1	D_GLU_81	OE2	3.991
1OB1	D_ARG_61	NH1	D_ASP_82	OD1	2.474
1OB1	D_ARG_61	NH1	D_ASP_82	OD2	2.804
1OB1	D_ARG_61	NH2	C_ASP_59	OD1	3.599
1OB1	D_ARG_61	NH2	C_ASP_59	OD2	2.460

1OB1	D_ARG_61	NH2	D_GLU_81	OE2	3.779
1OB1	D_LYS_103	NZ	D_GLU_105	OE1	3.861
1OB1	D_ARG_154	NH2	D_GLU_184	OE2	2.971
1OB1	D_LYS_182	NZ	D_ASP_183	OD1	3.753
1OB1	D_LYS_182	NZ	D_GLU_186	OE1	3.086
1OB1	D_HIS_188	NE2	D_GLU_184	OE2	3.651
1OB1	D_ARG_210	NH2	D_GLU_186	OE2	3.229
1OB1	E_LYS_13	NZ	E_GLU_16	OE2	3.102
1OB1	E_LYS_46	NZ	E_ASP_44	OD2	3.971
1OB1	E_ARG_66	NH1	E_ASP_86	OD1	3.843
1OB1	E_ARG_66	NH2	E_ASP_86	OD1	2.795
1OB1	E_ARG_66	NH2	E_ASP_86	OD2	3.186
1OB1	E_ARG_94	NH1	E_ASP_101	OD1	3.270
1OB1	E_ARG_94	NH1	E_ASP_101	OD2	2.697
1OB1	E_ARG_98	NH1	F_ASP_39	OD1	2.706
1OB1	E_HIS_164	NE2	D_ASP_166	OD2	3.790
1OB1	E_LYS_205	NZ	E_ASP_207	OD1	3.032
1OB1	E_LYS_205	NZ	E_ASP_207	OD2	2.849
1OB1	E_LYS_209	NZ	E_GLU_211	OE1	3.962
1OB1	E_LYS_209	NZ	E_GLU_211	OE2	3.194
1OB1	F_LYS_9	NZ	F_GLU_24	OE2	3.571
1OB1	F_LYS_9	NZ	F_GLU_26	OE2	3.085
1OB1	F_LYS_10	NZ	E_ASP_100	OD1	2.524
1OB1	F_ARG_20	NH1	F_GLU_24	OE1	3.734
1OB1	F_ARG_20	NH2	F_GLU_24	OE1	2.432
1OB1	F_ARG_20	NH2	F_GLU_24	OE2	3.245
1OB1	F_HIS_21	NE2	F_GLU_27	OE2	2.859
1OB1	F_LYS_80	NZ	A_GLU_79	OE1	3.743
1OB1	F_LYS_80	NZ	A_GLU_81	OE1	3.454
1OB1	F_LYS_80	NZ	A_GLU_81	OE2	2.796
1OB1	F_HIS_96	NE2	A_GLU_79	OE1	3.773
1OP9	A_ARG_35	NH1	A_ASP_87	OD1	2.983
1OP9	A_ARG_35	NH2	A_GLU_43	OE2	2.955
1OP9	A_ARG_49	NH1	A_ASP_52	OD1	2.941
1OP9	A_ARG_49	NH1	A_ASP_52	OD2	3.907
1OP9	A_ARG_64	NH1	A_ASP_87	OD1	3.965
1OP9	A_ARG_64	NH1	A_ASP_87	OD2	2.867
1OP9	A_ARG_64	NH2	A_ASP_87	OD1	3.040
1OP9	A_ARG_64	NH2	A_ASP_87	OD2	3.424
1OP9	B_LYS_1	NZ	B_GLU_7	OE2	2.875
1OP9	B_LYS_97	NZ	A_GLU_97	OE1	2.570
1OP9	B_ARG_98	NH1	B_ASP_102	OD1	2.828
1OP9	B_ARG_98	NH1	B_ASP_102	OD2	3.807
1OP9	B_ARG_101	NH1	A_ASP_109	OD1	3.213
1OP9	B_ARG_101	NH1	A_ASP_109	OD2	2.829
1OP9	B_ARG_101	NH2	A_ASP_109	OD1	2.793
1OP9	B_ARG_101	NH2	A_ASP_109	OD2	3.765
1OP9	B_ARG_122	NH1	B_ASP_120	OD1	3.408
1OSP	L_ARG_61	NH1	L_GLU_81	OE2	3.794
1OSP	L_ARG_61	NH1	L_ASP_82	OD1	2.742
1OSP	L_ARG_61	NH1	L_ASP_82	OD2	3.281
1OSP	L_LYS_69	NZ	L_ASP_70	OD2	3.957
1OSP	L_LYS_147	NZ	L_GLU_154	OE1	3.795
1OSP	L_LYS_149	NZ	L_GLU_195	OE1	3.168
1OSP	L_LYS_149	NZ	L_GLU_195	OE2	3.070
1OSP	L_ARG_155	NH2	L_GLU_185	OE1	3.054
1OSP	L_ARG_155	NH2	L_GLU_185	OE2	3.470
1OSP	L_ARG_188	NH2	L_GLU_185	OE2	3.854

1OSP	L_LYS_199	NZ	L_ASP_110	OD1	3.945
1OSP	L_LYS_199	NZ	L_ASP_110	OD2	2.639
1OSP	L_ARG_211	NH1	L_GLU_187	OE2	3.387
1OSP	L_ARG_211	NH2	L_GLU_187	OE2	3.391
1OSP	H_ARG_38	NH1	H_GLU_46	OE1	2.774
1OSP	H_ARG_38	NH2	H_ASP_89	OD1	2.825
1OSP	H_ARG_97	NH2	H_GLU_27	OE1	3.273
1OSP	H_ARG_99	NH1	L_GLU_55	OE1	3.970
1OSP	H_ARG_99	NH1	L_GLU_55	OE2	2.686
1OSP	H_ARG_99	NH2	O_ASP_92	OD1	3.355
1OSP	H_ARG_99	NH2	O_ASP_92	OD2	2.514
1OSP	H_LYS_215	NZ	L_GLU_123	OE1	2.783
1OSP	H_LYS_215	NZ	L_GLU_123	OE2	3.079
1OSP	O_LYS_39	NZ	O_ASP_33	OD1	2.809
1OSP	O_LYS_46	NZ	L_ASP_66	OD2	3.087
1OSP	O_LYS_69	NZ	O_ASP_92	OD1	3.769
1OSP	O_LYS_103	NZ	O_GLU_128	OE2	3.115
1OSP	O_LYS_113	NZ	O_GLU_123	OE1	3.755
1OSP	O_LYS_129	NZ	O_GLU_131	OE1	3.327
1OSP	O_ARG_139	NH1	O_GLU_160	OE2	3.268
1OSP	O_ARG_139	NH2	O_GLU_160	OE2	2.962
1OSP	O_ARG_144	NH1	O_GLU_146	OE1	3.930
1OSP	O_ARG_144	NH1	O_GLU_146	OE2	2.637
1OSP	O_LYS_159	NZ	O_GLU_168	OE2	3.915
1OSP	O_LYS_175	NZ	O_GLU_174	OE2	3.895
1OSP	O_LYS_189	NZ	O_GLU_160	OE1	2.949
1OSP	O_LYS_189	NZ	O_GLU_160	OE2	3.302
1OW0	A_ARG_250	NH1	A_ASP_378	OD1	2.566
1OW0	A_ARG_250	NH1	A_ASP_378	OD2	3.422
1OW0	A_ARG_250	NH1	A_GLU_437	OE1	2.982
1OW0	A_ARG_250	NH2	A_ASP_378	OD1	3.947
1OW0	A_ARG_250	NH2	A_GLU_437	OE1	2.644
1OW0	A_ARG_372	NH1	A_GLU_403	OE1	2.406
1OW0	A_ARG_372	NH1	A_GLU_403	OE2	2.605
1OW0	A_ARG_372	NH2	A_GLU_403	OE1	3.805
1OW0	B_ARG_250	NH1	B_ASP_378	OD1	2.587
1OW0	B_ARG_250	NH1	B_ASP_378	OD2	3.428
1OW0	B_ARG_250	NH1	B_GLU_437	OE1	2.993
1OW0	B_ARG_250	NH2	B_ASP_378	OD1	3.931
1OW0	B_ARG_250	NH2	B_GLU_437	OE1	2.615
1OW0	B_ARG_372	NH1	B_GLU_403	OE1	2.384
1OW0	B_ARG_372	NH1	B_GLU_403	OE2	2.617
1OW0	B_ARG_372	NH2	B_GLU_403	OE1	3.789
1OW0	C_LYS_13	NZ	C_GLU_63	OE2	3.686
1OW0	C_ARG_52	NH2	C_GLU_49	OE1	2.995
1OW0	C_ARG_52	NH2	C_GLU_49	OE2	3.667
1OW0	C_LYS_55	NZ	C_GLU_59	OE1	3.649
1OW0	C_LYS_55	NZ	C_GLU_59	OE2	3.759
1OW0	C_HIS_68	ND1	C_ASP_21	OD2	3.825
1OW0	C_HIS_68	NE2	C_ASP_21	OD2	3.915
1OW0	C_LYS_139	NZ	C_GLU_142	OE2	3.692
1OW0	C_ARG_171	NH1	C_GLU_140	OE2	3.418
1OW0	C_ARG_171	NH2	C_GLU_140	OE2	3.168
1OW0	D_LYS_13	NZ	D_GLU_63	OE2	3.662
1OW0	D_ARG_52	NH2	D_GLU_49	OE1	3.006
1OW0	D_ARG_52	NH2	D_GLU_49	OE2	3.670
1OW0	D_LYS_55	NZ	D_GLU_59	OE1	3.602
1OW0	D_LYS_55	NZ	D_GLU_59	OE2	3.741

1OW0	D_HIS_68	ND1	D_ASP_21	OD2	3.833
1OW0	D_HIS_68	NE2	D_ASP_21	OD2	3.920
1OW0	D_LYS_139	NZ	D_GLU_142	OE2	3.692
1OW0	D_ARG_171	NH1	D_GLU_140	OE2	3.423
1OW0	D_ARG_171	NH2	D_GLU_140	OE2	3.181
1P2C	A_ARG_24	NH2	A_ASP_70	OD1	3.561
1P2C	A_ARG_24	NH2	A_ASP_70	OD2	3.968
1P2C	A_ARG_61	NH1	A_GLU_79	OE1	3.212
1P2C	A_ARG_61	NH1	A_ASP_82	OD1	3.355
1P2C	A_ARG_61	NH1	A_ASP_82	OD2	2.848
1P2C	A_ARG_61	NH2	A_GLU_79	OE1	2.589
1P2C	A_ARG_61	NH2	A_GLU_79	OE2	3.654
1P2C	A_LYS_149	NZ	A_GLU_195	OE1	3.222
1P2C	A_LYS_149	NZ	A_GLU_195	OE2	3.909
1P2C	A_ARG_155	NH1	A_GLU_185	OE1	3.712
1P2C	A_ARG_155	NH1	A_GLU_185	OE2	3.813
1P2C	A_ARG_155	NH2	A_GLU_185	OE1	3.966
1P2C	A_ARG_155	NH2	A_GLU_185	OE2	2.811
1P2C	A_LYS_183	NZ	A_GLU_187	OE2	2.959
1P2C	A_ARG_188	NH2	F_ASP_1518	OD1	2.778
1P2C	A_HIS_189	ND1	A_ASP_151	OD2	2.583
1P2C	A_LYS_199	NZ	A_ASP_110	OD1	2.789
1P2C	B_ARG_340	NH1	B_GLU_389	OE1	3.429
1P2C	B_LYS_363	NZ	B_GLU_346	OE1	3.861
1P2C	B_LYS_367	NZ	B_ASP_390	OD1	2.706
1P2C	B_LYS_367	NZ	B_ASP_390	OD2	3.064
1P2C	B_ARG_398	NH2	B_ASP_400	OD1	2.942
1P2C	B_ARG_398	NH2	B_ASP_400	OD2	3.446
1P2C	B_LYS_511	NZ	A_GLU_123	OE1	3.498
1P2C	C_LYS_601	NZ	C_GLU_607	OE1	2.618
1P2C	C_ARG_645	NH2	B_GLU_350	OE1	2.980
1P2C	C_ARG_668	NH1	B_GLU_350	OE1	3.355
1P2C	C_ARG_668	NH1	B_GLU_350	OE2	3.681
1P2C	C_ARG_668	NH2	B_GLU_335	OE2	3.090
1P2C	C_ARG_668	NH2	B_GLU_350	OE1	3.316
1P2C	C_ARG_668	NH2	B_GLU_350	OE2	2.404
1P2C	C_ARG_725	NH2	C_ASP_719	OD1	2.463
1P2C	C_ARG_725	NH2	C_ASP_719	OD2	3.674
1P2C	D_ARG_924	NH2	D_ASP_970	OD2	3.311
1P2C	D_ARG_961	NH1	D_GLU_981	OE2	3.455
1P2C	D_ARG_961	NH1	D_ASP_982	OD1	3.476
1P2C	D_ARG_961	NH1	D_ASP_982	OD2	3.040
1P2C	D_LYS_1049	NZ	D_GLU_1095	OE1	3.108
1P2C	D_ARG_1055	NH1	D_GLU_1085	OE1	3.789
1P2C	D_ARG_1055	NH1	D_GLU_1085	OE2	2.663
1P2C	D_ARG_1055	NH2	D_GLU_1085	OE2	2.728
1P2C	D_HIS_1089	ND1	D_ASP_1051	OD1	2.579
1P2C	D_LYS_1099	NZ	D_ASP_1010	OD2	2.865
1P2C	D_ARG_1111	NH1	D_GLU_1087	OE2	3.738
1P2C	E_LYS_1263	NZ	E_GLU_1246	OE2	3.563
1P2C	E_LYS_1267	NZ	E_ASP_1290	OD2	2.785
1P2C	E_ARG_1298	NH2	E_ASP_1300	OD1	2.640
1P2C	E_ARG_1298	NH2	E_ASP_1300	OD2	3.489
1P2C	E_LYS_1411	NZ	D_GLU_1023	OE1	3.897
1P2C	F_LYS_1501	NZ	F_GLU_1507	OE1	2.851
1P2C	F_ARG_1545	NH2	E_GLU_1250	OE1	2.861
1P2C	F_ARG_1561	NH1	F_ASP_1548	OD2	3.292
1P2C	F_ARG_1568	NH1	E_GLU_1250	OE1	3.580

1P2C	F_ARG_1568	NH1	E_GLU_1250	OE2	3.708
1P2C	F_ARG_1568	NH2	E_GLU_1235	OE2	2.833
1P2C	F_ARG_1568	NH2	E_GLU_1250	OE1	3.551
1P2C	F_ARG_1568	NH2	E_GLU_1250	OE2	2.418
1P2C	F_ARG_1625	NH2	F_ASP_1619	OD1	3.266
1P2C	F_ARG_1625	NH2	F_ASP_1619	OD2	3.611
1P4B	L_ARG_77	NH2	L_GLU_99	OE2	3.709
1P4B	L_ARG_77	NH2	L_ASP_100	OD1	2.914
1P4B	L_ARG_77	NH2	L_ASP_100	OD2	3.654
1P4B	H_ARG_45	NH1	H_ASP_100	OD1	2.724
1P4B	H_ARG_45	NH2	H_GLU_53	OE1	3.936
1P4B	H_ARG_45	NH2	H_GLU_53	OE2	3.140
1P4B	H_ARG_45	NH2	H_ASP_100	OD1	3.840
1P4B	H_ARG_77	NH1	H_ASP_100	OD1	3.338
1P4B	H_ARG_77	NH1	H_ASP_100	OD2	2.557
1P4B	H_ARG_77	NH2	H_ASP_100	OD1	3.920
1P4B	H_LYS_86	NZ	H_ASP_83	OD1	3.623
1P4B	P_HIS_2	NE2	H_ASP_65	OD1	3.248
1P4B	P_HIS_2	NE2	H_ASP_65	OD2	3.747
1P4B	P_ARG_9	NH1	H_ASP_137	OD1	2.804
1P4B	P_ARG_9	NH1	H_ASP_137	OD2	3.838
1P4B	P_ARG_9	NH2	H_ASP_137	OD1	3.399
1P4B	P_ARG_9	NH2	H_ASP_137	OD2	3.080
1P4B	P_ARG_9	NH2	P_GLU_6	OE1	3.138
1P7K	L_ARG_61	NH2	L_GLU_81	OE2	2.946
1P7K	L_ARG_61	NH2	L_ASP_82	OD1	2.757
1P7K	L_ARG_61	NH2	L_ASP_82	OD2	3.505
1P7K	L_LYS_149	NZ	L_GLU_195	OE1	3.555
1P7K	L_LYS_149	NZ	L_GLU_195	OE2	3.346
1P7K	L_ARG_155	NH1	L_GLU_185	OE2	3.215
1P7K	L_ARG_155	NH2	L_GLU_185	OE2	2.646
1P7K	H_LYS_40	NZ	H_GLU_85	OE1	3.931
1P7K	H_LYS_62	NZ	L_GLU_1	OE2	3.723
1P7K	H_LYS_66	NZ	H_ASP_86	OD1	2.877
1P7K	H_LYS_66	NZ	H_ASP_86	OD2	3.789
1P7K	H_ARG_94	NH2	H_ASP_101	OD1	3.280
1P7K	H_ARG_94	NH2	H_ASP_101	OD2	3.021
1P7K	H_LYS_208	NZ	L_GLU_123	OE1	3.517
1P7K	H_LYS_208	NZ	L_GLU_123	OE2	2.802
1P7K	A_ARG_61	NH2	A_ASP_82	OD1	2.829
1P7K	A_ARG_61	NH2	A_ASP_82	OD2	3.548
1P7K	A_LYS_103	NZ	A_ASP_165	OD1	3.013
1P7K	A_LYS_103	NZ	A_ASP_165	OD2	3.850
1P7K	A_LYS_149	NZ	A_GLU_195	OE2	3.766
1P7K	A_ARG_155	NH1	A_GLU_185	OE2	3.343
1P7K	A_ARG_155	NH2	A_GLU_185	OE2	3.044
1P7K	A_HIS_189	ND1	A_ASP_151	OD2	3.542
1P7K	A_LYS_199	NZ	A_ASP_110	OD1	3.716
1P7K	A_LYS_199	NZ	A_ASP_110	OD2	2.490
1P7K	B_LYS_62	NZ	A_GLU_1	OE2	2.848
1P7K	B_LYS_66	NZ	B_ASP_86	OD1	2.903
1P7K	B_LYS_66	NZ	B_ASP_86	OD2	3.739
1P7K	B_ARG_94	NH2	B_ASP_101	OD1	3.555
1P7K	B_ARG_94	NH2	B_ASP_101	OD2	2.792
1PG7	H_HIS_35	NE2	H_ASP_95	OD2	2.988
1PG7	H_ARG_38	NH1	H_ASP_86	OD1	2.891
1PG7	H_ARG_38	NH2	H_GLU_46	OE1	2.886
1PG7	H_ARG_38	NH2	H_GLU_46	OE2	3.488

1PG7	H_ARG_38	NH2	H_ASP_86	OD1	3.755
1PG7	H_LYS_62	NZ	H_GLU_46	OE1	3.013
1PG7	H_LYS_62	NZ	H_ASP_60	OD2	3.697
1PG7	H_ARG_66	NH2	H_ASP_86	OD1	3.366
1PG7	H_ARG_66	NH2	H_ASP_86	OD2	2.811
1PG7	H_ARG_83	NH1	H_GLU_85	OE2	3.159
1PG7	H_ARG_94	NH2	H_ASP_101	OD1	3.671
1PG7	H_ARG_94	NH2	H_ASP_101	OD2	2.700
1PG7	H_LYS_143	NZ	H_ASP_144	OD1	3.667
1PG7	H_LYS_209	NZ	L_GLU_123	OE1	2.828
1PG7	H_LYS_209	NZ	L_GLU_123	OE2	3.697
1PG7	I_HIS_35	NE2	I_ASP_95	OD2	2.860
1PG7	I_ARG_38	NH1	I_ASP_86	OD1	3.016
1PG7	I_ARG_38	NH2	I_GLU_46	OE1	3.146
1PG7	I_ARG_38	NH2	I_GLU_46	OE2	3.649
1PG7	I_ARG_38	NH2	I_GLU_85	OE2	3.601
1PG7	I_ARG_38	NH2	I_ASP_86	OD1	3.900
1PG7	I_ARG_66	NH2	I_ASP_86	OD1	3.391
1PG7	I_ARG_66	NH2	I_ASP_86	OD2	2.626
1PG7	I_ARG_83	NH2	I_GLU_85	OE1	3.938
1PG7	I_ARG_94	NH2	I_ASP_101	OD1	3.654
1PG7	I_ARG_94	NH2	I_ASP_101	OD2	2.818
1PG7	I_LYS_143	NZ	I_ASP_144	OD1	3.370
1PG7	I_LYS_209	NZ	M_GLU_123	OE1	2.829
1PG7	I_LYS_209	NZ	M_GLU_123	OE2	3.963
1PG7	I_LYS_210	NZ	I_GLU_212	OE1	3.335
1PG7	I_LYS_210	NZ	I_GLU_212	OE2	3.997
1PG7	L_LYS_30	NZ	X_GLU_95	OE1	3.476
1PG7	L_LYS_30	NZ	X_GLU_95	OE2	2.795
1PG7	L_ARG_61	NH2	L_ASP_82	OD1	3.019
1PG7	L_ARG_61	NH2	L_ASP_82	OD2	3.567
1PG7	L_LYS_149	NZ	L_GLU_195	OE1	3.477
1PG7	L_LYS_149	NZ	L_GLU_195	OE2	3.023
1PG7	L_LYS_183	NZ	L_GLU_187	OE2	2.996
1PG7	L_HIS_189	ND1	L_ASP_151	OD2	3.757
1PG7	M_ARG_24	NH2	M_ASP_70	OD1	3.617
1PG7	M_ARG_24	NH2	M_ASP_70	OD2	2.951
1PG7	M_ARG_27	NH1	M_GLU_93	OE2	3.544
1PG7	M_LYS_30	NZ	Z_GLU_95	OE2	3.166
1PG7	M_ARG_61	NH2	M_GLU_81	OE2	3.691
1PG7	M_ARG_61	NH2	M_ASP_82	OD1	3.010
1PG7	M_ARG_61	NH2	M_ASP_82	OD2	3.569
1PG7	M_LYS_149	NZ	M_GLU_195	OE1	2.679
1PG7	M_LYS_183	NZ	M_GLU_187	OE1	3.114
1PG7	M_LYS_183	NZ	M_GLU_187	OE2	2.640
1PG7	M_LYS_188	NZ	M_ASP_185	OD1	3.378
1PG7	M_HIS_189	ND1	M_ASP_151	OD2	3.163
1PG7	W_ARG_24	NH2	W_ASP_69	OD1	2.965
1PG7	W_HIS_42	ND1	W_GLU_38	OE2	3.572
1PG7	W_ARG_61	NH2	W_ASP_82	OD1	2.800
1PG7	W_ARG_61	NH2	W_ASP_82	OD2	3.379
1PG7	W_LYS_111	NZ	W_GLU_197	OE1	3.487
1PG7	W_LYS_111	NZ	W_GLU_197	OE2	3.605
1PG7	W_LYS_150	NZ	W_GLU_202	OE1	3.697
1PG7	W_LYS_150	NZ	W_GLU_202	OE2	2.961
1PG7	W_HIS_193	NE2	W_GLU_202	OE1	2.915
1PG7	W_HIS_193	NE2	W_GLU_202	OE2	3.635
1PG7	X_HIS_32	NE2	X_ASP_96	OD1	3.692

1PG7	X.LYS.62	NZ	X.GLU.46	OE2	3.660
1PG7	X.LYS.64	NZ	X.ASP.65	OD2	3.444
1PG7	X.LYS.66	NZ	X.ASP.86	OD1	2.694
1PG7	X.LYS.66	NZ	X.ASP.86	OD2	3.927
1PG7	X_ARG.94	NH1	H.GLU.53	OE1	3.386
1PG7	X_ARG.94	NH1	H.GLU.53	OE2	3.321
1PG7	X_ARG.94	NH2	H.GLU.53	OE1	3.937
1PG7	X_ARG.94	NH2	H.GLU.53	OE2	2.866
1PG7	X_ARG.94	NH2	X.ASP.101	OD1	3.743
1PG7	X_ARG.94	NH2	X.ASP.101	OD2	2.609
1PG7	X_ARG.98	NH2	H.ASP.95	OD1	2.990
1PG7	X_ARG.98	NH2	H.ASP.95	OD2	3.561
1PG7	X.HIS.100	NE2	X.ASP.96	OD1	3.548
1PG7	X.HIS.100	NE2	X.ASP.96	OD2	3.817
1PG7	X.LYS.143	NZ	W.GLU.125	OE2	2.675
1PG7	X.HIS.164	NE2	W.GLU.139	OE2	3.801
1PG7	X.LYS.208	NZ	W.GLU.124	OE2	2.927
1PG7	Y_ARG.24	NH1	Y.ASP.69	OD2	3.633
1PG7	Y.HIS.42	ND1	Y.GLU.38	OE2	2.936
1PG7	Y_ARG.61	NH2	Y.GLU.81	OE1	3.193
1PG7	Y_ARG.61	NH2	Y.ASP.82	OD1	2.746
1PG7	Y_ARG.61	NH2	Y.ASP.82	OD2	3.675
1PG7	Y.LYS.111	NZ	Y.GLU.197	OE1	3.272
1PG7	Y.LYS.111	NZ	Y.GLU.197	OE2	2.744
1PG7	Y.LYS.150	NZ	Y.GLU.202	OE2	3.486
1PG7	Y.LYS.170	NZ	Y.GLU.139	OE1	3.781
1PG7	Y.HIS.193	NE2	Y.GLU.202	OE1	3.285
1PG7	Y.HIS.193	NE2	Y.GLU.202	OE2	3.532
1PG7	Z.LYS.66	NZ	Z.ASP.86	OD2	2.953
1PG7	Z_ARG.94	NH1	I.GLU.53	OE1	3.259
1PG7	Z_ARG.94	NH1	I.GLU.53	OE2	3.931
1PG7	Z_ARG.94	NH1	Z.ASP.101	OD1	3.771
1PG7	Z_ARG.94	NH1	Z.ASP.101	OD2	2.810
1PG7	Z_ARG.94	NH2	I.GLU.53	OE1	2.918
1PG7	Z_ARG.94	NH2	I.GLU.53	OE2	2.525
1PG7	Z_ARG.98	NH2	L.ASP.95	OD1	3.168
1PG7	Z_ARG.98	NH2	L.ASP.95	OD2	3.781
1PG7	Z.HIS.100	NE2	Z.ASP.96	OD1	3.911
1PG7	Z.HIS.100	NE2	Z.ASP.96	OD2	3.774
1PG7	Z.LYS.143	NZ	Y.GLU.125	OE2	2.901
1PG7	Z.LYS.208	NZ	Y.GLU.124	OE2	3.302
1PSK	L_ARG.60	NH1	L.GLU.80	OE1	3.760
1PSK	L_ARG.60	NH1	L.GLU.80	OE2	3.891
1PSK	L_ARG.60	NH1	L.ASP.81	OD2	3.537
1PSK	L_ARG.60	NH2	L.GLU.80	OE1	3.568
1PSK	L_ARG.60	NH2	L.GLU.80	OE2	3.225
1PSK	L_ARG.60	NH2	L.ASP.81	OD1	3.069
1PSK	L_ARG.60	NH2	L.ASP.81	OD2	3.788
1PSK	L.LYS.141	NZ	L.ASP.142	OD2	3.990
1PSK	L.LYS.148	NZ	L.GLU.194	OE2	2.802
1PSK	L_ARG.154	NH2	L.GLU.184	OE1	3.691
1PSK	L.HIS.188	ND1	L.ASP.150	OD2	2.717
1PSK	L.LYS.198	NZ	L.ASP.142	OD2	3.973
1PSK	H.LYS.38	NZ	H.ASP.90	OD1	3.879
1PSK	H_ARG.84	NH1	H.GLU.82	OE1	3.149
1PSK	H_ARG.84	NH2	H.GLU.82	OE1	3.059
1PSK	H_ARG.84	NH2	H.GLU.82	OE2	3.244
1PSK	H.LYS.99	NZ	H.ASP.102	OD2	3.135

1PZ5	A_ARG_24	NH1	A_ASP_70	OD1	3.050
1PZ5	A_ARG_24	NH1	A_ASP_70	OD2	3.589
1PZ5	A_HIS_27D	ND1	A_ASP_28	OD1	3.297
1PZ5	A_HIS_27D	ND1	A_ASP_28	OD2	3.192
1PZ5	A_HIS_27D	NE2	C_ASP_2	OD1	2.720
1PZ5	A_LYS_39	NZ	A_GLU_81	OE1	3.469
1PZ5	A_ARG_61	NH1	A_ASP_82	OD1	2.720
1PZ5	A_ARG_61	NH1	A_ASP_82	OD2	3.796
1PZ5	A_ARG_61	NH2	A_GLU_79	OE1	3.814
1PZ5	A_ARG_61	NH2	A_GLU_79	OE2	3.855
1PZ5	A_ARG_61	NH2	A_ASP_82	OD1	3.374
1PZ5	A_ARG_61	NH2	A_ASP_82	OD2	2.955
1PZ5	A_ARG_77	NH1	A_ASP_60	OD2	3.886
1PZ5	A_LYS_147	NZ	A_GLU_154	OE1	3.998
1PZ5	A_LYS_149	NZ	A_GLU_195	OE1	2.953
1PZ5	A_LYS_149	NZ	A_GLU_195	OE2	3.630
1PZ5	A_LYS_183	NZ	A_GLU_187	OE1	2.839
1PZ5	A_LYS_183	NZ	A_GLU_187	OE2	2.663
1PZ5	A_ARG_188	NH1	A_ASP_184	OD1	3.586
1PZ5	A_ARG_188	NH1	A_GLU_185	OE1	3.143
1PZ5	A_ARG_188	NH2	A_ASP_184	OD1	2.987
1PZ5	A_HIS_189	ND1	A_ASP_151	OD1	3.048
1PZ5	A_HIS_189	NE2	A_GLU_185	OE2	2.825
1PZ5	A_LYS_199	NZ	A_ASP_110	OD1	3.069
1PZ5	A_LYS_199	NZ	A_ASP_110	OD2	3.840
1PZ5	B_ARG_38	NH1	B_GLU_46	OE2	2.914
1PZ5	B_ARG_38	NH1	B_ASP_86	OD1	3.910
1PZ5	B_ARG_38	NH2	B_ASP_86	OD1	2.823
1PZ5	B_ARG_52	NH1	B_GLU_50	OE2	2.848
1PZ5	B_HIS_58	ND1	B_GLU_50	OE2	3.633
1PZ5	B_ARG_66	NH1	B_ASP_86	OD1	3.057
1PZ5	B_ARG_66	NH1	B_ASP_86	OD2	3.525
1PZ5	B_ARG_66	NH2	B_ASP_86	OD1	3.778
1PZ5	B_ARG_66	NH2	B_ASP_86	OD2	2.847
1PZ5	B_ARG_71	NH1	B_ASP_73	OD2	3.288
1PZ5	B_ARG_94	NH1	B_ASP_101	OD1	3.495
1PZ5	B_ARG_94	NH1	B_ASP_101	OD2	2.627
1PZ5	B_ARG_164	NH1	A_ASP_167	OD2	3.218
1PZ5	B_ARG_164	NH2	A_ASP_167	OD2	3.712
1PZ5	B_LYS_208	NZ	A_GLU_123	OE1	2.648
1PZ5	B_LYS_208	NZ	A_GLU_123	OE2	3.713
1Q9K	A_ARG_54	NH2	A_ASP_60	OD2	3.319
1Q9K	A_ARG_61	NH1	A_ASP_82	OD1	2.801
1Q9K	A_ARG_61	NH1	A_ASP_82	OD2	3.363
1Q9K	A_ARG_61	NH2	A_GLU_81	OE1	3.964
1Q9K	A_ARG_95	NH2	B_ASP_95	OD1	3.932
1Q9K	A_ARG_95	NH2	B_ASP_95	OD2	3.226
1Q9K	A_LYS_146	NZ	A_GLU_153	OE1	3.709
1Q9K	A_LYS_148	NZ	A_GLU_194	OE1	3.150
1Q9K	A_LYS_148	NZ	A_GLU_194	OE2	3.820
1Q9K	A_LYS_168	NZ	A_ASP_166	OD1	2.237
1Q9K	A_LYS_168	NZ	A_ASP_166	OD2	3.163
1Q9K	A_HIS_188	ND1	A_ASP_150	OD2	2.831
1Q9K	A_LYS_198	NZ	A_ASP_109	OD1	3.804
1Q9K	A_LYS_198	NZ	A_ASP_109	OD2	3.067
1Q9K	B_ARG_38	NH1	B_ASP_86	OD2	2.774
1Q9K	B_ARG_38	NH2	B_GLU_46	OE1	3.263
1Q9K	B_ARG_38	NH2	B_ASP_86	OD2	3.827

1Q9K	B_ARG_52	NH1	B_GLU_56	OE2	3.179
1Q9K	B_ARG_52	NH2	B_GLU_56	OE2	2.529
1Q9K	B_ARG_64	NH1	B_ASP_86	OD1	2.817
1Q9K	B_ARG_64	NH1	B_ASP_86	OD2	3.706
1Q9K	B_ARG_64	NH2	B_ASP_86	OD1	3.623
1Q9K	B_ARG_64	NH2	B_ASP_86	OD2	3.040
1Q9K	B_HIS_162	NE2	A_ASP_166	OD1	3.847
1Q9L	B_ARG_38	NH1	B_ASP_86	OD2	2.938
1Q9L	B_ARG_38	NH2	B_GLU_46	OE1	3.214
1Q9L	B_ARG_38	NH2	B_GLU_46	OE2	3.981
1Q9L	B_ARG_38	NH2	B_ASP_86	OD2	3.814
1Q9L	B_ARG_52	NH1	B_GLU_56	OE2	3.639
1Q9L	B_ARG_52	NH2	B_GLU_56	OE2	2.657
1Q9L	B_ARG_64	NH1	B_ASP_86	OD1	2.799
1Q9L	B_ARG_64	NH2	B_ASP_86	OD1	3.122
1Q9L	B_ARG_64	NH2	B_ASP_86	OD2	2.942
1Q9L	B_HIS_96	ND1	B_ASP_97	OD2	2.998
1Q9L	B_LYS_113	NZ	B_ASP_171	OD2	3.940
1Q9L	B_LYS_206	NZ	A_GLU_122	OE2	3.242
1Q9L	D_ARG_38	NH1	D_ASP_86	OD2	3.041
1Q9L	D_ARG_38	NH2	D_GLU_46	OE1	2.944
1Q9L	D_ARG_38	NH2	D_GLU_46	OE2	3.965
1Q9L	D_ARG_52	NH1	D_GLU_56	OE2	3.147
1Q9L	D_ARG_52	NH2	D_GLU_56	OE2	2.760
1Q9L	D_ARG_64	NH1	D_ASP_86	OD1	2.602
1Q9L	D_ARG_64	NH1	D_ASP_86	OD2	3.534
1Q9L	D_ARG_64	NH2	D_ASP_86	OD1	3.533
1Q9L	D_ARG_64	NH2	D_ASP_86	OD2	2.877
1Q9L	D_HIS_96	ND1	D_ASP_97	OD2	3.015
1Q9L	D_HIS_96	NE2	D_ASP_97	OD2	3.962
1Q9L	D_ARG_100B	NH1	B_GLU_85	OE1	3.618
1Q9L	D_ARG_100B	NH1	B_GLU_85	OE2	3.115
1Q9L	D_HIS_162	NE2	C_ASP_166	OD1	3.172
1Q9L	A_LYS_24	NZ	A_ASP_70	OD2	3.888
1Q9L	A_LYS_39	NZ	A_GLU_81	OE2	3.778
1Q9L	A_ARG_54	NH2	A_ASP_60	OD2	3.464
1Q9L	A_ARG_61	NH1	A_ASP_82	OD1	3.170
1Q9L	A_ARG_61	NH1	A_ASP_82	OD2	2.681
1Q9L	A_ARG_61	NH2	A_GLU_81	OE1	3.824
1Q9L	A_ARG_95	NH2	B_ASP_95	OD2	3.284
1Q9L	A_LYS_102	NZ	A_GLU_104	OE2	2.656
1Q9L	A_LYS_146	NZ	A_GLU_194	OE2	3.634
1Q9L	A_LYS_148	NZ	A_GLU_194	OE1	3.229
1Q9L	A_LYS_148	NZ	A_GLU_194	OE2	3.316
1Q9L	A_ARG_154	NH2	A_GLU_184	OE1	2.873
1Q9L	A_LYS_168	NZ	A_ASP_166	OD1	3.711
1Q9L	A_LYS_168	NZ	A_ASP_166	OD2	3.118
1Q9L	A_ARG_187	NH1	A_GLU_184	OE2	2.612
1Q9L	A_HIS_188	ND1	A_ASP_150	OD2	2.879
1Q9L	A_HIS_188	NE2	A_GLU_184	OE1	3.087
1Q9L	A_HIS_188	NE2	A_GLU_184	OE2	3.294
1Q9L	A_LYS_198	NZ	A_ASP_109	OD2	3.680
1Q9L	C_LYS_39	NZ	C_GLU_81	OE1	3.843
1Q9L	C_ARG_54	NH2	C_ASP_60	OD2	2.952
1Q9L	C_ARG_61	NH1	C_ASP_82	OD1	2.562
1Q9L	C_ARG_61	NH1	C_ASP_82	OD2	2.760
1Q9L	C_ARG_95	NH2	D_ASP_95	OD2	3.309
1Q9L	C_LYS_102	NZ	C_GLU_104	OE2	3.348

1Q9L	C_LYS_148	NZ	C_GLU_194	OE1	2.541
1Q9L	C_LYS_148	NZ	C_GLU_194	OE2	3.918
1Q9L	C_ARG_154	NH1	C_GLU_184	OE1	3.911
1Q9L	C_LYS_168	NZ	C_ASP_166	OD1	2.581
1Q9L	C_LYS_168	NZ	C_ASP_166	OD2	2.492
1Q9L	C_ARG_187	NH1	C_GLU_184	OE2	2.720
1Q9L	C_HIS_188	ND1	C_ASP_150	OD2	2.739
1Q9L	C_HIS_188	NE2	C_GLU_184	OE1	3.004
1Q9L	C_HIS_188	NE2	C_GLU_184	OE2	3.759
1Q9O	B_ARG_38	NH1	B_GLU_46	OE1	3.016
1Q9O	B_ARG_38	NH1	B_GLU_46	OE2	3.916
1Q9O	B_ARG_38	NH1	B_ASP_86	OD2	3.956
1Q9O	B_ARG_38	NH2	B_ASP_86	OD2	2.860
1Q9O	B_ARG_52	NH1	B_GLU_56	OE2	2.831
1Q9O	B_ARG_52	NH2	B_GLU_56	OE2	3.407
1Q9O	B_ARG_64	NH1	B_ASP_86	OD1	3.248
1Q9O	B_ARG_64	NH1	B_ASP_86	OD2	2.899
1Q9O	B_ARG_64	NH2	B_ASP_86	OD1	2.692
1Q9O	B_ARG_64	NH2	B_ASP_86	OD2	3.771
1Q9O	B_ARG_83	NH2	B_GLU_85	OE1	2.612
1Q9O	B_ARG_94	NH1	B_ASP_100D	OD1	3.613
1Q9O	B_ARG_94	NH1	B_ASP_100D	OD2	2.755
1Q9O	B_ARG_100	NH1	A_GLU_55	OE1	3.447
1Q9O	B_ARG_100	NH1	A_GLU_55	OE2	3.466
1Q9O	B_ARG_100	NH2	A_GLU_55	OE1	3.378
1Q9O	B_ARG_100	NH2	A_GLU_55	OE2	2.999
1Q9O	B_LYS_206	NZ	A_GLU_122	OE2	3.964
1Q9O	D_ARG_38	NH1	D_ASP_86	OD2	2.888
1Q9O	D_ARG_38	NH2	D_GLU_46	OE1	3.098
1Q9O	D_ARG_38	NH2	D_ASP_86	OD2	3.945
1Q9O	D_ARG_52	NH1	D_GLU_56	OE2	3.504
1Q9O	D_ARG_52	NH2	D_GLU_56	OE2	3.047
1Q9O	D_ARG_64	NH1	D_ASP_86	OD1	2.898
1Q9O	D_ARG_64	NH1	D_ASP_86	OD2	3.621
1Q9O	D_ARG_64	NH2	D_ASP_86	OD1	3.767
1Q9O	D_ARG_64	NH2	D_ASP_86	OD2	3.117
1Q9O	D_ARG_83	NH2	D_GLU_85	OE1	3.293
1Q9O	D_ARG_83	NH2	D_GLU_85	OE2	3.082
1Q9O	D_ARG_94	NH2	D_ASP_100D	OD1	2.763
1Q9O	D_ARG_94	NH2	D_ASP_100D	OD2	3.701
1Q9O	D_ARG_100	NH1	C_GLU_55	OE1	3.493
1Q9O	D_ARG_100	NH1	C_GLU_55	OE2	3.040
1Q9O	D_ARG_100	NH2	C_GLU_55	OE1	3.391
1Q9O	D_ARG_100	NH2	C_GLU_55	OE2	3.047
1Q9O	A_ARG_54	NH1	A_ASP_60	OD2	3.439
1Q9O	A_ARG_61	NH1	A_ASP_82	OD1	3.512
1Q9O	A_ARG_61	NH1	A_ASP_82	OD2	2.892
1Q9O	A_ARG_61	NH2	A_GLU_81	OE1	3.882
1Q9O	A_ARG_61	NH2	A_ASP_82	OD1	2.949
1Q9O	A_ARG_61	NH2	A_ASP_82	OD2	3.770
1Q9O	A_ARG_95	NH2	B_ASP_95	OD1	2.958
1Q9O	A_ARG_95	NH2	B_ASP_95	OD2	3.717
1Q9O	A_LYS_102	NZ	A_GLU_104	OE1	2.779
1Q9O	A_LYS_146	NZ	A_GLU_194	OE2	2.676
1Q9O	A_LYS_148	NZ	A_GLU_194	OE1	3.510
1Q9O	A_LYS_182	NZ	A_GLU_186	OE1	2.761
1Q9O	A_LYS_182	NZ	A_GLU_186	OE2	3.253
1Q9O	A_HIS_188	ND1	A_ASP_150	OD2	2.674

1Q9O	A_LYS_198	NZ	A_ASP_109	OD1	3.691
1Q9O	A_LYS_198	NZ	A_ASP_109	OD2	3.683
1Q9O	C_ARG_61	NH1	C_ASP_82	OD1	2.516
1Q9O	C_ARG_61	NH1	C_ASP_82	OD2	3.228
1Q9O	C_ARG_61	NH2	C_GLU_81	OE2	3.883
1Q9O	C_ARG_95	NH2	D_ASP_95	OD1	3.672
1Q9O	C_ARG_95	NH2	D_ASP_95	OD2	2.974
1Q9O	C_LYS_102	NZ	C_GLU_104	OE1	3.839
1Q9O	C_LYS_148	NZ	C_GLU_194	OE1	2.914
1Q9O	C_LYS_148	NZ	C_GLU_194	OE2	3.816
1Q9W	A_ARG_61	NH2	A_ASP_82	OD1	2.327
1Q9W	A_ARG_61	NH2	A_ASP_82	OD2	2.627
1Q9W	A_ARG_95	NH2	B_ASP_95	OD1	2.949
1Q9W	A_ARG_95	NH2	B_ASP_95	OD2	3.845
1Q9W	A_LYS_102	NZ	A_GLU_104	OE1	3.845
1Q9W	A_LYS_146	NZ	A_GLU_153	OE2	3.713
1Q9W	A_LYS_148	NZ	A_GLU_194	OE1	2.859
1Q9W	A_ARG_154	NH1	A_GLU_184	OE1	3.813
1Q9W	A_ARG_154	NH2	A_GLU_184	OE1	3.493
1Q9W	A_ARG_154	NH2	A_GLU_184	OE2	2.753
1Q9W	A_ARG_187	NH1	A_GLU_184	OE2	3.961
1Q9W	A_ARG_187	NH2	A_GLU_184	OE2	2.743
1Q9W	A_HIS_188	ND1	A_ASP_150	OD2	2.924
1Q9W	B_ARG_38	NH1	B_ASP_86	OD2	2.826
1Q9W	B_ARG_38	NH2	B_GLU_46	OE1	3.067
1Q9W	B_ARG_38	NH2	B_ASP_86	OD2	3.866
1Q9W	B_ARG_52	NH1	B_GLU_56	OE2	3.024
1Q9W	B_ARG_52	NH2	B_GLU_56	OE2	3.531
1Q9W	B_ARG_64	NH1	B_ASP_86	OD1	2.680
1Q9W	B_ARG_64	NH1	B_ASP_86	OD2	3.618
1Q9W	B_ARG_64	NH2	B_ASP_86	OD1	3.562
1Q9W	B_ARG_64	NH2	B_ASP_86	OD2	3.048
1Q9W	B_ARG_83	NH2	B_GLU_85	OE1	3.148
1Q9W	B_ARG_83	NH2	B_GLU_85	OE2	3.088
1Q9W	B_ARG_94	NH2	B_ASP_100D	OD1	2.686
1Q9W	B_ARG_94	NH2	B_ASP_100D	OD2	3.453
1Q9W	B_ARG_100	NH1	A_GLU_55	OE1	2.615
1Q9W	B_ARG_100	NH1	A_GLU_55	OE2	3.657
1Q9W	B_ARG_100	NH2	A_GLU_55	OE1	2.891
1Q9W	B_ARG_100	NH2	A_GLU_55	OE2	3.820
1Q9W	C_LYS_24	NZ	C_ASP_70	OD1	3.583
1Q9W	C_ARG_61	NH2	C_ASP_82	OD1	2.769
1Q9W	C_ARG_61	NH2	C_ASP_82	OD2	3.531
1Q9W	C_ARG_95	NH2	D_ASP_95	OD1	2.929
1Q9W	C_ARG_95	NH2	D_ASP_95	OD2	3.831
1Q9W	C_LYS_106	NZ	C_GLU_17	OE1	2.879
1Q9W	C_LYS_148	NZ	C_GLU_194	OE1	2.881
1Q9W	C_LYS_148	NZ	C_GLU_194	OE2	3.569
1Q9W	C_ARG_154	NH2	C_GLU_184	OE1	2.757
1Q9W	C_LYS_168	NZ	C_ASP_166	OD1	3.032
1Q9W	C_LYS_168	NZ	C_ASP_166	OD2	2.758
1Q9W	C_ARG_187	NH1	C_GLU_184	OE2	2.691
1Q9W	C_ARG_187	NH2	C_GLU_184	OE2	2.833
1Q9W	D_ARG_38	NH1	D_ASP_86	OD2	2.855
1Q9W	D_ARG_38	NH2	D_GLU_46	OE1	3.105
1Q9W	D_ARG_38	NH2	D_ASP_86	OD2	3.747
1Q9W	D_ARG_52	NH1	D_GLU_56	OE2	3.012
1Q9W	D_ARG_52	NH2	D_GLU_56	OE2	3.725

1Q9W	D_ARG_64	NH1	D_ASP_86	OD1	3.569
1Q9W	D_ARG_64	NH1	D_ASP_86	OD2	3.180
1Q9W	D_ARG_94	NH2	D_ASP_100D	OD1	2.639
1Q9W	D_ARG_94	NH2	D_ASP_100D	OD2	3.620
1Q9W	D_ARG_100	NH1	C_GLU_55	OE1	3.356
1Q9W	D_ARG_100	NH1	C_GLU_55	OE2	3.002
1Q9W	D_ARG_100	NH2	C_GLU_55	OE1	3.373
1Q9W	D_ARG_100	NH2	C_GLU_55	OE2	3.045
1QBL	L_ARG_61	NH2	L_ASP_82	OD1	2.786
1QBL	L_ARG_61	NH2	L_ASP_82	OD2	3.721
1QBL	L_LYS_147	NZ	L_GLU_154	OE1	3.338
1QBL	L_LYS_149	NZ	L_GLU_195	OE1	3.827
1QBL	L_LYS_149	NZ	L_GLU_195	OE2	2.952
1QBL	L_ARG_155	NH1	L_GLU_185	OE1	3.191
1QBL	L_ARG_155	NH1	L_GLU_185	OE2	3.323
1QBL	L_ARG_155	NH2	L_GLU_185	OE1	3.979
1QBL	L_ARG_155	NH2	L_GLU_185	OE2	2.777
1QBL	L_HIS_189	ND1	L_ASP_151	OD2	2.720
1QBL	L_HIS_189	NE2	L_GLU_185	OE2	3.448
1QBL	L_LYS_199	NZ	L_ASP_110	OD2	3.257
1QBL	H_LYS_63	NZ	H_GLU_46	OE1	3.796
1QBL	H_LYS_67	NZ	H_ASP_90	OD2	3.852
1QBL	H_LYS_212	NZ	L_GLU_123	OE1	3.581
1QBM	L_ARG_61	NH2	L_GLU_81	OE2	2.739
1QBM	L_ARG_61	NH2	L_ASP_82	OD1	2.797
1QBM	L_ARG_61	NH2	L_ASP_82	OD2	3.689
1QBM	L_LYS_107	NZ	L_GLU_17	OE1	3.352
1QBM	L_LYS_107	NZ	L_GLU_17	OE2	3.277
1QBM	L_LYS_142	NZ	L_ASP_143	OD1	3.711
1QBM	L_LYS_147	NZ	L_GLU_154	OE2	2.702
1QBM	L_LYS_149	NZ	L_GLU_195	OE1	3.463
1QBM	L_LYS_149	NZ	L_GLU_195	OE2	3.031
1QBM	L_ARG_155	NH1	L_GLU_185	OE1	3.258
1QBM	L_ARG_155	NH1	L_GLU_185	OE2	2.899
1QBM	L_ARG_155	NH2	L_GLU_185	OE2	2.603
1QBM	L_HIS_189	ND1	L_ASP_151	OD2	2.710
1QBM	H_LYS_63	NZ	H_GLU_46	OE1	3.520
1QBM	H_LYS_67	NZ	H_ASP_90	OD1	3.236
1QBM	H_LYS_67	NZ	H_ASP_90	OD2	3.485
1QBM	H_LYS_212	NZ	L_GLU_123	OE1	2.762
1QBM	H_LYS_212	NZ	L_GLU_123	OE2	3.773
1QGC	1_LYS_41	NZ	1_GLU_175	OE2	3.394
1QGC	1_HIS_57	NE2	1_ASP_59	OD2	3.737
1QGC	1_ARG_114	NH2	1_GLU_77	OE2	2.895
1QGC	1_ARG_124	NH1	2_ASP_41	OD1	3.642
1QGC	1_ARG_124	NH1	2_ASP_41	OD2	2.877
1QGC	1_ARG_124	NH2	2_ASP_41	OD1	3.740
1QGC	1_ARG_179	NH1	1_ASP_37	OD1	3.088
1QGC	1_ARG_179	NH2	1_ASP_37	OD1	3.997
1QGC	1_ARG_179	NH2	1_GLU_77	OE2	3.665
1QGC	1_LYS_181	NZ	1_ASP_37	OD1	3.047
1QGC	1_LYS_181	NZ	1_ASP_37	OD2	3.465
1QGC	1_LYS_181	NZ	1_GLU_77	OE2	3.717
1QGC	2_ARG_54	NH1	2_GLU_59	OE1	3.984
1QGC	2_ARG_54	NH1	2_GLU_59	OE2	3.432
1QGC	2_ARG_54	NH2	2_GLU_59	OE1	3.031
1QGC	2_ARG_54	NH2	2_GLU_59	OE2	3.842
1QGC	2_LYS_88	NZ	2_GLU_86	OE1	3.903

1QGC	2_ARG_102	NH1	2_GLU_40	OE1	2.629
1QGC	2_ARG_102	NH2	2_ASP_41	OD1	2.799
1QGC	2_ARG_102	NH2	2_ASP_41	OD2	3.402
1QGC	2_HIS_157	NE2	2_ASP_106	OD1	2.653
1QGC	2_HIS_157	NE2	2_ASP_106	OD2	3.740
1QGC	2_ARG_167	NH2	3_ASP_166	OD1	2.757
1QGC	2_ARG_167	NH2	3_ASP_166	OD2	2.777
1QGC	2_HIS_174	ND1	2_ASP_169	OD1	3.562
1QGC	2_HIS_174	ND1	2_ASP_169	OD2	2.877
1QGC	2_HIS_174	NE2	2_GLU_128	OE1	2.739
1QGC	2_HIS_174	NE2	2_GLU_128	OE2	3.273
1QGC	2_LYS_198	NZ	2_ASP_68	OD1	3.053
1QGC	2_LYS_198	NZ	2_ASP_68	OD2	3.315
1QGC	3_LYS_20	NZ	3_ASP_18	OD2	2.699
1QGC	3_ARG_120	NH1	3_GLU_146	OE2	2.906
1QGC	3_ARG_120	NH2	3_ASP_148	OD2	2.596
1QGC	3_LYS_193	NZ	3_ASP_116	OD2	3.610
1QGC	3_LYS_207	NZ	3_GLU_49	OE1	3.193
1QGC	4_ARG_18	NH1	4_ASP_80	OD2	2.980
1QGC	4_ARG_18	NH2	4_ASP_80	OD2	3.279
1QGC	4_ARG_24	NH1	4_ASP_74	OD2	3.755
1QGC	4_ARG_24	NH2	4_ASP_74	OD1	3.361
1QGC	4_ARG_24	NH2	4_ASP_74	OD2	2.753
1QGC	4_ARG_65	NH1	4_ASP_86	OD1	3.995
1QGC	4_ARG_65	NH1	4_ASP_86	OD2	2.787
1QGC	4_ARG_65	NH2	4_ASP_85	OD2	3.117
1QGC	4_ARG_65	NH2	4_ASP_86	OD1	3.250
1QGC	4_ARG_65	NH2	4_ASP_86	OD2	3.419
1QGC	4_LYS_107	NZ	4_ASP_109	OD1	3.987
1QGC	4_LYS_107	NZ	4_ASP_169	OD1	3.205
1QGC	4_LYS_153	NZ	4_GLU_199	OE1	3.327
1QGC	4_ARG_159	NH1	4_GLU_189	OE1	3.473
1QGC	4_LYS_173	NZ	4_ASP_171	OD1	3.263
1QGC	4_LYS_173	NZ	4_ASP_171	OD2	3.461
1QGC	4_LYS_187	NZ	4_GLU_191	OE1	2.654
1QGC	4_LYS_203	NZ	4_ASP_114	OD1	3.911
1QGC	4_LYS_203	NZ	4_ASP_114	OD2	3.518
1QGC	A_ARG_38	NH1	A_ASP_90	OD1	3.118
1QGC	A_ARG_38	NH2	A_GLU_46	OE1	3.211
1QGC	A_ARG_38	NH2	A_ASP_90	OD1	3.660
1QGC	A_ARG_67	NH1	A_ASP_90	OD1	3.761
1QGC	A_ARG_67	NH1	A_ASP_90	OD2	2.866
1QGC	A_ARG_67	NH2	A_ASP_90	OD1	3.418
1QGC	A_ARG_67	NH2	A_ASP_90	OD2	3.559
1QGC	A_ARG_98	NH1	A_ASP_101	OD1	3.353
1QGC	A_ARG_98	NH1	A_ASP_101	OD2	3.278
1QGC	A_ARG_98	NH2	A_ASP_101	OD1	3.317
1QGC	A_ARG_98	NH2	A_ASP_101	OD2	3.911
1QGC	A_ARG_99	NH1	A_ASP_104	OD1	2.799
1QGC	A_ARG_99	NH2	A_ASP_104	OD1	2.841
1QGC	A_ARG_99	NH2	A_ASP_104	OD2	3.281
1QGC	A_ARG_99	NH2	5_ASP_143	OD1	3.483
1QGC	A_LYS_215	NZ	4_GLU_127	OE2	3.716
1QKZ	A_LYS_15	NZ	A_GLU_61	OE1	3.616
1QKZ	A_LYS_36	NZ	A_GLU_32	OE2	3.573
1QKZ	H_ARG_38	NH1	H_ASP_86	OD1	2.872
1QKZ	H_ARG_38	NH2	H_GLU_46	OE1	2.843
1QKZ	H_ARG_38	NH2	H_GLU_46	OE2	3.701

1QKZ	H_ARG_38	NH2	H_ASP_86	OD1	3.867
1QKZ	H_LYS_64	NZ	H_ASP_61	OD1	2.866
1QKZ	H_ARG_66	NH2	H_ASP_86	OD1	3.410
1QKZ	H_ARG_66	NH2	H_ASP_86	OD2	2.614
1QKZ	H_LYS_83	NZ	H_GLU_85	OE1	3.867
1QKZ	H_ARG_94	NH2	H_ASP_101	OD1	3.649
1QKZ	H_ARG_94	NH2	H_ASP_101	OD2	2.613
1QKZ	H_LYS_208	NZ	L_GLU_123	OE2	2.582
1QKZ	L_ARG_61	NH1	L_ASP_82	OD1	3.436
1QKZ	L_ARG_61	NH1	L_ASP_82	OD2	2.498
1QKZ	L_ARG_61	NH2	L_GLU_79	OE1	3.597
1QKZ	L_ARG_61	NH2	L_ASP_82	OD1	2.782
1QKZ	L_ARG_61	NH2	L_ASP_82	OD2	3.478
1QKZ	L_ARG_77	NH2	L_GLU_79	OE2	3.903
1QKZ	L_LYS_103	NZ	L_GLU_105	OE1	3.233
1QKZ	L_LYS_147	NZ	L_GLU_154	OE1	3.920
1QKZ	L_LYS_147	NZ	L_GLU_154	OE2	2.870
1QKZ	L_LYS_149	NZ	L_GLU_195	OE1	2.933
1QKZ	L_LYS_149	NZ	L_GLU_195	OE2	3.912
1QKZ	L_ARG_155	NH1	L_GLU_185	OE1	3.847
1QKZ	L_ARG_155	NH1	L_GLU_185	OE2	2.779
1QKZ	L_ARG_155	NH2	L_GLU_185	OE2	3.332
1QKZ	L_LYS_183	NZ	L_GLU_187	OE1	3.886
1QKZ	L_LYS_183	NZ	L_GLU_187	OE2	2.674
1QKZ	L_HIS_189	ND1	L_ASP_151	OD2	2.784
1QKZ	L_LYS_199	NZ	L_ASP_110	OD2	2.613
1QOK	A_ARG_64	NH1	A_GLU_72	OE2	2.857
1QOK	A_ARG_64	NH2	A_ASP_116	OD1	2.731
1QOK	A_LYS_89	NZ	A_GLU_72	OE1	3.015
1QOK	A_LYS_89	NZ	A_GLU_72	OE2	3.466
1QOK	A_LYS_93	NZ	A_ASP_116	OD1	3.171
1QOK	A_LYS_93	NZ	A_ASP_116	OD2	2.764
1QOK	A_ARG_221	NH2	A_GLU_241	OE1	3.500
1QOK	A_ARG_221	NH2	A_GLU_241	OE2	3.768
1QOK	A_ARG_221	NH2	A_ASP_242	OD1	2.782
1QOK	A_ARG_221	NH2	A_ASP_242	OD2	3.516
1QOK	A_LYS_263	NZ	A_GLU_265	OE2	3.711
1QOK	A_LYS_267	NZ	A_GLU_178	OE1	3.144
1QOK	A_LYS_267	NZ	A_GLU_178	OE2	3.767
1R21-1	A_HIS_54	NE2	A_GLU_52	OE2	3.592
1R21-1	A_HIS_61	NE2	A_GLU_52	OE1	3.344
1R21-1	A_ARG_96	NH1	A_ASP_16	OD1	3.366
1R21-1	A_ARG_96	NH2	A_GLU_98	OE2	3.736
1R21-10	A_HIS_54	NE2	A_GLU_52	OE1	3.820
1R21-10	A_HIS_54	NE2	A_GLU_52	OE2	3.819
1R21-10	A_HIS_61	NE2	A_GLU_52	OE1	3.243
1R21-11	A_LYS_50	NZ	A_GLU_52	OE1	3.980
1R21-11	A_HIS_54	NE2	A_GLU_52	OE1	3.682
1R21-11	A_HIS_54	NE2	A_GLU_52	OE2	3.726
1R21-11	A_HIS_61	NE2	A_GLU_52	OE1	3.099
1R21-11	A_ARG_81	NH2	A_GLU_57	OE1	3.622
1R21-11	A_ARG_81	NH2	A_GLU_57	OE2	3.877
1R21-12	A_ARG_6	NH2	A_GLU_98	OE2	3.220
1R21-12	A_LYS_50	NZ	A_GLU_52	OE2	3.513
1R21-12	A_HIS_54	ND1	A_GLU_55	OE1	3.706
1R21-12	A_HIS_61	NE2	A_GLU_52	OE1	3.484
1R21-12	A_HIS_61	NE2	A_GLU_52	OE2	3.957
1R21-12	A_LYS_83	NZ	A_ASP_86	OD1	3.921

1R21-12	A_ARG_96	NH1	A_ASP_16	OD1	2.338
1R21-12	A_ARG_96	NH2	A_ASP_16	OD1	3.435
1R21-13	A_LYS_50	NZ	A_GLU_52	OE2	3.811
1R21-13	A_HIS_61	NE2	A_GLU_52	OE1	3.018
1R21-13	A_HIS_61	NE2	A_GLU_52	OE2	3.663
1R21-13	A_ARG_96	NH1	A_ASP_16	OD1	2.697
1R21-13	A_ARG_96	NH2	A_GLU_98	OE2	3.649
1R21-14	A_HIS_61	ND1	A_GLU_52	OE2	3.472
1R21-14	A_HIS_61	NE2	A_GLU_52	OE1	2.859
1R21-14	A_HIS_61	NE2	A_GLU_52	OE2	3.106
1R21-14	A_ARG_81	NH2	A_GLU_57	OE1	3.503
1R21-14	A_ARG_81	NH2	A_GLU_57	OE2	2.460
1R21-14	A_ARG_96	NH2	A_GLU_98	OE2	2.878
1R21-15	A_ARG_6	NH2	A_GLU_100	OE1	2.871
1R21-15	A_ARG_6	NH2	A_GLU_100	OE2	3.726
1R21-15	A_HIS_54	NE2	A_GLU_52	OE1	3.410
1R21-15	A_HIS_54	NE2	A_GLU_52	OE2	3.502
1R21-15	A_HIS_61	NE2	A_GLU_52	OE1	3.119
1R21-15	A_ARG_81	NH2	A_GLU_57	OE1	3.147
1R21-16	A_HIS_54	NE2	A_GLU_52	OE1	3.412
1R21-16	A_HIS_54	NE2	A_GLU_52	OE2	3.663
1R21-16	A_HIS_61	NE2	A_GLU_52	OE1	2.774
1R21-16	A_ARG_81	NH2	A_GLU_57	OE1	2.662
1R21-16	A_ARG_81	NH2	A_GLU_57	OE2	3.500
1R21-16	A_ARG_96	NH2	A_GLU_98	OE2	3.655
1R21-17	A_HIS_19	NE2	A_ASP_16	OD1	2.979
1R21-17	A_LYS_50	NZ	A_GLU_52	OE1	3.597
1R21-17	A_HIS_54	NE2	A_GLU_52	OE1	3.729
1R21-17	A_HIS_54	NE2	A_GLU_52	OE2	3.299
1R21-17	A_HIS_61	NE2	A_GLU_52	OE1	3.150
1R21-17	A_ARG_96	NH1	A_ASP_16	OD1	3.990
1R21-17	A_ARG_96	NH1	A_ASP_16	OD2	3.847
1R21-18	A_HIS_54	NE2	A_GLU_52	OE2	3.726
1R21-18	A_HIS_61	NE2	A_GLU_52	OE1	3.370
1R21-18	A_HIS_84	NE2	A_GLU_100	OE2	2.435
1R21-18	A_ARG_96	NH2	A_GLU_98	OE2	3.170
1R21-19	A_HIS_54	NE2	A_GLU_52	OE2	3.585
1R21-19	A_HIS_61	NE2	A_GLU_52	OE1	3.355
1R21-19	A_ARG_96	NH2	A_GLU_98	OE2	2.978
1R21-2	A_HIS_54	NE2	A_GLU_52	OE1	3.826
1R21-2	A_HIS_54	NE2	A_GLU_52	OE2	2.948
1R21-2	A_HIS_61	NE2	A_GLU_52	OE1	3.312
1R21-2	A_ARG_96	NH1	A_ASP_16	OD1	2.740
1R21-2	A_ARG_96	NH1	A_ASP_16	OD2	2.714
1R21-2	A_ARG_96	NH2	A_ASP_16	OD1	3.323
1R21-20	A_HIS_54	NE2	A_GLU_52	OE2	3.415
1R21-20	A_HIS_61	NE2	A_GLU_52	OE1	3.170
1R21-20	A_HIS_84	NE2	A_GLU_100	OE2	3.227
1R21-20	A_ARG_96	NH1	A_ASP_16	OD1	3.434
1R21-20	A_ARG_96	NH1	A_ASP_16	OD2	3.592
1R21-21	A_ARG_6	NH2	A_GLU_98	OE1	3.967
1R21-21	A_HIS_19	NE2	A_ASP_16	OD2	3.709
1R21-21	A_HIS_61	NE2	A_GLU_52	OE1	3.030
1R21-22	A_HIS_54	NE2	A_GLU_52	OE1	3.543
1R21-22	A_HIS_54	NE2	A_GLU_52	OE2	3.368
1R21-22	A_HIS_61	NE2	A_GLU_52	OE1	3.436
1R21-22	A_ARG_96	NH1	A_ASP_16	OD1	3.702
1R21-22	A_ARG_96	NH1	A_ASP_16	OD2	3.090

1R21-23	A_ARG_6	NH1	A_GLU_98	OE1	2.790
1R21-23	A_HIS_61	NE2	A_GLU_52	OE1	3.027
1R21-23	A_ARG_81	NH2	A_GLU_57	OE1	3.135
1R21-23	A_ARG_96	NH1	A_ASP_16	OD1	2.357
1R21-23	A_ARG_96	NH1	A_ASP_16	OD2	3.412
1R21-23	A_ARG_96	NH2	A_GLU_98	OE2	3.160
1R21-3	A_HIS_19	NE2	A_ASP_16	OD1	2.708
1R21-3	A_HIS_19	NE2	A_ASP_16	OD2	3.092
1R21-3	A_LYS_50	NZ	A_GLU_52	OE2	3.328
1R21-3	A_HIS_61	NE2	A_GLU_52	OE1	3.178
1R21-3	A_HIS_61	NE2	A_GLU_52	OE2	3.637
1R21-3	A_ARG_81	NH2	A_GLU_57	OE1	3.507
1R21-3	A_ARG_81	NH2	A_GLU_57	OE2	2.346
1R21-3	A_ARG_96	NH1	A_GLU_98	OE1	3.034
1R21-3	A_ARG_96	NH2	A_GLU_98	OE1	3.009
1R21-4	A_HIS_61	ND1	A_GLU_52	OE2	3.789
1R21-4	A_HIS_61	NE2	A_GLU_52	OE1	2.749
1R21-4	A_HIS_61	NE2	A_GLU_52	OE2	3.111
1R21-4	A_ARG_81	NH2	A_GLU_57	OE1	2.933
1R21-4	A_ARG_96	NH1	A_GLU_98	OE1	3.705
1R21-4	A_ARG_96	NH1	A_GLU_98	OE2	3.277
1R21-4	A_ARG_96	NH2	A_GLU_98	OE2	2.612
1R21-5	A_ARG_6	NH1	A_GLU_100	OE2	3.869
1R21-5	A_ARG_6	NH2	A_GLU_100	OE2	2.476
1R21-5	A_HIS_54	NE2	A_GLU_52	OE1	3.312
1R21-5	A_HIS_54	NE2	A_GLU_52	OE2	3.040
1R21-5	A_HIS_61	NE2	A_GLU_52	OE1	2.875
1R21-5	A_ARG_96	NH2	A_GLU_98	OE2	3.021
1R21-6	A_HIS_19	NE2	A_ASP_16	OD2	3.980
1R21-6	A_HIS_54	NE2	A_GLU_52	OE1	3.369
1R21-6	A_HIS_54	NE2	A_GLU_52	OE2	3.405
1R21-6	A_HIS_61	NE2	A_GLU_52	OE1	3.317
1R21-7	A_HIS_19	NE2	A_ASP_16	OD1	3.586
1R21-7	A_HIS_19	NE2	A_ASP_16	OD2	3.080
1R21-7	A_HIS_61	NE2	A_GLU_52	OE1	3.436
1R21-7	A_ARG_81	NH2	A_GLU_57	OE2	3.637
1R21-8	A_ARG_6	NH2	A_GLU_98	OE1	3.720
1R21-8	A_HIS_54	NE2	A_GLU_52	OE1	3.655
1R21-8	A_HIS_54	NE2	A_GLU_52	OE2	3.218
1R21-8	A_HIS_61	NE2	A_GLU_52	OE1	3.063
1R21-8	A_ARG_96	NH2	A_GLU_98	OE2	3.712
1R21-9	A_HIS_54	ND1	A_GLU_55	OE1	2.611
1R21-9	A_HIS_61	NE2	A_GLU_52	OE1	3.068
1R21-9	A_ARG_96	NH2	A_GLU_98	OE2	3.654
1RZJ	G_LYS_207	NZ	G_GLU_381	OE1	3.995
1RZJ	G_LYS_207	NZ	G_GLU_381	OE2	2.764
1RZJ	G_LYS_231	NZ	G_GLU_268	OE2	3.358
1RZJ	G_HIS_249	NE2	G_GLU_482	OE1	3.036
1RZJ	G_LYS_348	NZ	G_GLU_269	OE2	2.716
1RZJ	G_LYS_357	NZ	G_GLU_466	OE1	3.793
1RZJ	G_ARG_419	NH2	H_GLU_99	OE2	2.591
1RZJ	G_ARG_456	NH2	G_GLU_466	OE1	3.427
1RZJ	G_ARG_456	NH2	G_GLU_466	OE2	2.814
1RZJ	G_ARG_469	NH2	G_ASP_457	OD1	2.972
1RZJ	G_ARG_476	NH1	G_ASP_474	OD1	2.853
1RZJ	G_ARG_480	NH1	G_ASP_477	OD1	2.656
1RZJ	G_LYS_487	NZ	G_GLU_91	OE1	3.654
1RZJ	G_LYS_487	NZ	G_GLU_91	OE2	2.711

1RZJ	C_LYS_8	NZ	C_GLU_119	OE1	2.627
1RZJ	C_LYS_8	NZ	C_GLU_119	OE2	3.972
1RZJ	C_HIS_27	NE2	C_GLU_85	OE1	2.626
1RZJ	C_LYS_29	NZ	G_ASP_279	OD2	3.209
1RZJ	C_LYS_29	NZ	C_GLU_85	OE1	3.520
1RZJ	C_LYS_35	NZ	G_ASP_457	OD2	3.838
1RZJ	C_LYS_46	NZ	C_ASP_56	OD1	3.928
1RZJ	C_ARG_54	NH1	C_ASP_78	OD2	3.656
1RZJ	C_ARG_54	NH2	C_ASP_78	OD1	2.906
1RZJ	C_ARG_54	NH2	C_ASP_78	OD2	3.632
1RZJ	C_ARG_58	NH1	C_GLU_13	OE1	2.664
1RZJ	C_ARG_59	NH1	G_ASP_368	OD1	3.788
1RZJ	C_ARG_59	NH1	G_ASP_368	OD2	3.342
1RZJ	C_ARG_59	NH2	G_ASP_368	OD1	2.531
1RZJ	C_ARG_59	NH2	G_ASP_368	OD2	3.174
1RZJ	C_LYS_90	NZ	C_GLU_85	OE2	3.877
1RZJ	C_LYS_171	NZ	C_GLU_169	OE1	3.508
1RZJ	L_ARG_61	NH2	L_GLU_81	OE2	3.350
1RZJ	L_ARG_61	NH2	L_ASP_82	OD1	2.670
1RZJ	L_ARG_61	NH2	L_ASP_82	OD2	3.090
1RZJ	L_LYS_149	NZ	L_GLU_195	OE1	2.951
1RZJ	L_LYS_149	NZ	L_GLU_195	OE2	3.523
1RZJ	L_HIS_189	ND1	L_ASP_151	OD2	3.250
1RZJ	H_LYS_12	NZ	H_GLU_10	OE1	3.962
1RZJ	H_LYS_19	NZ	H_GLU_81	OE2	3.444
1RZJ	H_ARG_31	NH2	H_ASP_100A	OD1	3.714
1RZJ	H_ARG_31	NH2	H_ASP_100A	OD2	2.889
1RZJ	H_ARG_38	NH1	H_GLU_46	OE1	3.693
1RZJ	H_ARG_38	NH1	H_GLU_46	OE2	2.534
1RZJ	H_ARG_38	NH2	H_ASP_86	OD2	2.669
1RZJ	H_ARG_50	NH2	H_GLU_97	OE2	2.721
1RZJ	H_HIS_62	NE2	H_GLU_46	OE1	3.941
1RZJ	H_HIS_62	NE2	H_GLU_46	OE2	3.006
1RZJ	H_ARG_66	NH1	H_ASP_86	OD1	2.823
1RZJ	H_ARG_66	NH1	H_ASP_86	OD2	3.878
1RZJ	H_ARG_66	NH2	H_ASP_86	OD1	3.045
1RZJ	H_ARG_66	NH2	H_ASP_86	OD2	2.664
1RZJ	H_ARG_82A	NH1	H_GLU_81	OE1	2.688
1RZJ	H_LYS_101	NZ	H_GLU_1	OE1	3.982
1RZJ	H_HIS_102	NE2	H_GLU_1	OE1	3.443
1RZJ	H_LYS_143	NZ	H_ASP_144	OD1	3.134
1RZJ	H_LYS_143	NZ	H_ASP_144	OD2	3.259
1RZJ	H_LYS_209	NZ	L_GLU_123	OE1	3.812
1RZK	G_LYS_121	NZ	G_GLU_429	OE1	2.734
1RZK	G_LYS_121	NZ	G_GLU_429	OE2	3.567
1RZK	G_LYS_207	NZ	G_GLU_381	OE1	3.945
1RZK	G_LYS_207	NZ	G_GLU_381	OE2	3.126
1RZK	G_LYS_232	NZ	G_GLU_351	OE1	3.994
1RZK	G_HIS_249	NE2	G_GLU_482	OE1	3.525
1RZK	G_LYS_282	NZ	G_GLU_275	OE1	3.953
1RZK	G_LYS_282	NZ	G_GLU_275	OE2	2.642
1RZK	G_LYS_348	NZ	G_GLU_269	OE2	3.206
1RZK	G_LYS_348	NZ	G_GLU_351	OE1	3.941
1RZK	G_LYS_348	NZ	G_GLU_351	OE2	3.259
1RZK	G_LYS_350	NZ	G_ASP_395	OD1	3.580
1RZK	G_LYS_357	NZ	G_GLU_466	OE1	3.719
1RZK	G_ARG_419	NH1	H_GLU_100B	OE1	2.999
1RZK	G_ARG_419	NH1	H_GLU_100B	OE2	3.674

1RZK	G_ARG_419	NH2	H_GLU_99	OE1	2.292
1RZK	G_ARG_419	NH2	H_GLU_100B	OE2	3.969
1RZK	G_ARG_456	NH2	G_GLU_466	OE1	3.468
1RZK	G_ARG_456	NH2	G_GLU_466	OE2	3.536
1RZK	G_ARG_469	NH2	G_ASP_457	OD1	3.234
1RZK	G_ARG_476	NH1	G_ASP_474	OD1	3.441
1RZK	G_ARG_476	NH2	G_GLU_102	OE1	3.296
1RZK	G_ARG_476	NH2	G_GLU_102	OE2	3.010
1RZK	G_LYS_487	NZ	G_GLU_91	OE2	3.524
1RZK	G_LYS_490	NZ	G_GLU_492	OE1	3.300
1RZK	C_LYS_29	NZ	C_GLU_85	OE1	2.833
1RZK	C_LYS_29	NZ	C_GLU_85	OE2	3.848
1RZK	C_LYS_35	NZ	G_ASP_457	OD2	3.741
1RZK	C_ARG_54	NH1	C_ASP_78	OD1	3.987
1RZK	C_ARG_54	NH1	C_ASP_78	OD2	2.755
1RZK	C_ARG_54	NH2	C_ASP_78	OD1	2.666
1RZK	C_ARG_54	NH2	C_ASP_78	OD2	2.988
1RZK	C_ARG_59	NH1	G_ASP_368	OD1	3.343
1RZK	C_ARG_59	NH1	G_ASP_368	OD2	3.154
1RZK	C_ARG_59	NH2	G_ASP_368	OD1	2.433
1RZK	C_ARG_59	NH2	G_ASP_368	OD2	2.977
1RZK	C_HIS_107	ND1	C_ASP_105	OD1	2.891
1RZK	C_HIS_107	ND1	C_ASP_105	OD2	3.166
1RZK	C_ARG_134	NH2	C_ASP_153	OD1	3.766
1RZK	C_LYS_136	NZ	C_GLU_150	OE2	3.884
1RZK	C_LYS_136	NZ	C_ASP_153	OD1	3.936
1RZK	C_LYS_136	NZ	C_ASP_153	OD2	2.987
1RZK	C_LYS_171	NZ	C_GLU_169	OE2	2.874
1RZK	L_ARG_61	NH2	L_GLU_81	OE1	3.127
1RZK	L_ARG_61	NH2	L_ASP_82	OD1	3.576
1RZK	L_ARG_95B	NH2	L_ASP_1	OD2	2.985
1RZK	L_HIS_189	ND1	L_ASP_151	OD2	2.585
1RZK	L_HIS_189	NE2	L_ASP_185	OD1	3.599
1RZK	L_HIS_189	NE2	L_ASP_185	OD2	2.802
1RZK	L_ARG_211	NH1	L_GLU_187	OE1	3.851
1RZK	H_ARG_31	NH2	H_ASP_100A	OD1	3.070
1RZK	H_ARG_31	NH2	H_ASP_100A	OD2	3.614
1RZK	H_ARG_38	NH1	H_GLU_46	OE1	2.779
1RZK	H_ARG_38	NH1	H_GLU_46	OE2	3.342
1RZK	H_ARG_38	NH2	H_ASP_86	OD2	2.684
1RZK	H_ARG_50	NH2	H_GLU_97	OE2	2.332
1RZK	H_ARG_66	NH1	H_ASP_86	OD1	3.598
1RZK	H_ARG_66	NH2	H_ASP_86	OD1	2.415
1RZK	H_ARG_66	NH2	H_ASP_86	OD2	2.739
1RZK	H_LYS_73	NZ	H_ASP_55	OD2	2.968
1RZK	H_ARG_82A	NH2	H_GLU_81	OE1	3.271
1RZK	H_LYS_143	NZ	H_ASP_144	OD1	2.615
1RZK	H_LYS_143	NZ	H_ASP_144	OD2	3.235
1RZK	H_HIS_164	NE2	L_ASP_167	OD1	3.880
1RZK	H_HIS_164	NE2	L_ASP_167	OD2	2.505
1RZK	H_LYS_206	NZ	H_ASP_208	OD2	3.965
1RZK	H_LYS_209	NZ	L_GLU_123	OE1	3.513
1RZK	H_LYS_209	NZ	L_GLU_123	OE2	3.584
1S3K	L_ARG_66	NH2	L_GLU_86	OE2	3.884
1S3K	L_ARG_66	NH2	L_ASP_87	OD1	2.838
1S3K	L_ARG_66	NH2	L_ASP_87	OD2	3.885
1S3K	L_LYS_108	NZ	L_GLU_170	OE2	3.919
1S3K	L_HIS_194	ND1	L_ASP_156	OD2	2.733

1S3K	H_ARG_38	NH1	H_ASP_90	OD1	2.899
1S3K	H_ARG_38	NH2	H_GLU_46	OE2	3.185
1S3K	H_ARG_38	NH2	H_ASP_90	OD1	3.935
1S3K	H_LYS_65	NZ	H_ASP_59	OD1	3.006
1S3K	H_ARG_67	NH1	H_ASP_90	OD1	3.672
1S3K	H_ARG_67	NH1	H_ASP_90	OD2	2.699
1S3K	H_ARG_67	NH2	H_ASP_90	OD1	2.977
1S3K	H_ARG_67	NH2	H_ASP_90	OD2	3.482
1S3K	H_ARG_101	NH1	H_ASP_31	OD2	3.352
1S3K	H_LYS_149	NZ	H_ASP_150	OD1	3.589
1S5I	L_ARG_46	NH2	L_ASP_55	OD1	2.460
1S5I	L_ARG_46	NH2	L_ASP_55	OD2	3.856
1S5I	L_ARG_61	NH1	L_GLU_79	OE1	3.126
1S5I	L_ARG_61	NH1	L_GLU_81	OE2	3.788
1S5I	L_ARG_61	NH2	L_GLU_79	OE1	3.704
1S5I	L_ARG_61	NH2	L_ASP_82	OD1	2.499
1S5I	L_ARG_61	NH2	L_ASP_82	OD2	2.521
1S5I	L_ARG_77	NH1	L_GLU_79	OE2	3.348
1S5I	L_ARG_96	NH1	H_ASP_97	OD1	3.601
1S5I	L_ARG_96	NH2	H_ASP_97	OD1	2.496
1S5I	L_ARG_96	NH2	H_ASP_97	OD2	2.511
1S5I	L_LYS_147	NZ	L_GLU_154	OE1	3.415
1S5I	L_LYS_149	NZ	L_GLU_195	OE1	2.811
1S5I	L_LYS_149	NZ	L_GLU_195	OE2	3.034
1S5I	L_ARG_155	NH1	L_GLU_185	OE1	2.637
1S5I	L_ARG_155	NH2	L_GLU_185	OE1	3.738
1S5I	L_ARG_188	NH2	L_GLU_185	OE2	2.926
1S5I	L_HIS_189	ND1	L_ASP_151	OD2	2.858
1S5I	L_HIS_189	NE2	L_GLU_185	OE1	2.459
1S5I	L_HIS_189	NE2	L_GLU_185	OE2	3.318
1S5I	H_ARG_38	NH1	H_ASP_86	OD1	2.668
1S5I	H_ARG_38	NH2	H_GLU_46	OE1	2.890
1S5I	H_ARG_38	NH2	H_ASP_86	OD1	3.667
1S5I	H_ARG_66	NH1	H_ASP_86	OD1	3.962
1S5I	H_ARG_66	NH1	H_ASP_86	OD2	3.293
1S5I	H_ARG_66	NH2	H_ASP_86	OD1	3.251
1S5I	H_ARG_66	NH2	H_ASP_86	OD2	3.537
1S5I	H_LYS_75	NZ	H_ASP_72	OD1	3.618
1S5I	H_LYS_75	NZ	H_ASP_72	OD2	2.868
1S5I	H_HIS_172	NE2	L_ASP_167	OD2	3.741
1S5I	H_LYS_218	NZ	H_ASP_220	OD1	3.717
1S5I	H_LYS_221	NZ	L_GLU_123	OE2	3.213
1S78	A_ARG_25	NH2	A_ASP_22	OD2	3.377
1S78	A_HIS_26	NE2	A_ASP_22	OD1	3.860
1S78	A_HIS_26	NE2	A_ASP_22	OD2	3.677
1S78	A_ARG_76	NH1	A_ASP_54	OD1	3.940
1S78	A_ARG_81	NH2	A_GLU_57	OE1	3.403
1S78	A_ARG_81	NH2	A_GLU_57	OE2	3.079
1S78	A_ARG_121	NH1	A_GLU_188	OE1	2.989
1S78	A_ARG_121	NH2	A_GLU_188	OE1	3.618
1S78	A_ARG_121	NH2	A_ASP_189	OD1	3.441
1S78	A_ARG_121	NH2	A_ASP_189	OD2	3.303
1S78	A_ARG_135	NH2	A_ASP_96	OD1	3.677
1S78	A_ARG_135	NH2	A_ASP_96	OD2	3.036
1S78	A_HIS_152	NE2	A_GLU_125	OE1	3.976
1S78	A_ARG_166	NH2	A_ASP_143	OD1	3.122
1S78	A_ARG_204	NH1	A_ASP_149	OD1	3.810
1S78	A_ARG_204	NH2	A_GLU_125	OE2	2.685

1S78	A_LYS_206	NZ	A_ASP_212	OD2	3.591
1S78	A_HIS_238	ND1	A_GLU_243	OE1	3.574
1S78	A_HIS_238	ND1	A_GLU_243	OE2	2.921
1S78	A_ARG_308	NH2	A_GLU_310	OE2	3.285
1S78	A_LYS_311	NZ	A_ASP_285	OD2	3.743
1S78	A_HIS_327	NE2	A_GLU_341	OE1	2.783
1S78	A_HIS_327	NE2	A_GLU_341	OE2	2.983
1S78	A_ARG_332	NH1	A_GLU_357	OE2	3.575
1S78	A_ARG_332	NH2	A_GLU_357	OE1	3.867
1S78	A_ARG_332	NH2	A_GLU_357	OE2	2.955
1S78	A_LYS_347	NZ	A_GLU_299	OE2	2.643
1S78	A_LYS_347	NZ	A_GLU_383	OE1	3.238
1S78	A_ARG_410	NH2	A_GLU_383	OE1	3.550
1S78	A_ARG_410	NH2	A_GLU_383	OE2	3.659
1S78	A_ARG_412	NH1	A_GLU_299	OE1	3.168
1S78	A_ARG_412	NH1	A_GLU_299	OE2	3.462
1S78	A_ARG_412	NH2	A_GLU_299	OE2	3.187
1S78	A_ARG_437	NH1	A_GLU_438	OE1	3.837
1S78	A_ARG_465	NH1	A_GLU_438	OE1	2.796
1S78	A_ARG_465	NH1	A_GLU_438	OE2	3.955
1S78	A_ARG_477	NH1	A_GLU_485	OE1	2.683
1S78	A_ARG_477	NH2	A_GLU_481	OE2	3.214
1S78	A_ARG_477	NH2	A_GLU_485	OE1	3.223
1S78	A_ARG_514	NH1	A_GLU_531	OE2	2.772
1S78	A_ARG_523	NH1	A_GLU_531	OE1	3.483
1S78	A_ARG_523	NH1	A_GLU_531	OE2	3.476
1S78	B_ARG_25	NH2	B_ASP_22	OD2	3.334
1S78	B_HIS_26	NE2	B_ASP_22	OD1	3.990
1S78	B_HIS_26	NE2	B_ASP_22	OD2	3.840
1S78	B_ARG_76	NH1	B_ASP_54	OD1	3.948
1S78	B_ARG_81	NH2	B_GLU_57	OE1	3.380
1S78	B_ARG_81	NH2	B_GLU_57	OE2	3.017
1S78	B_ARG_121	NH1	B_GLU_188	OE1	2.787
1S78	B_ARG_121	NH2	B_GLU_188	OE1	3.424
1S78	B_ARG_121	NH2	B_ASP_189	OD1	3.468
1S78	B_ARG_121	NH2	B_ASP_189	OD2	3.329
1S78	B_ARG_135	NH2	B_ASP_96	OD1	3.610
1S78	B_ARG_135	NH2	B_ASP_96	OD2	2.916
1S78	B_HIS_152	NE2	B_GLU_125	OE1	3.902
1S78	B_ARG_166	NH2	B_ASP_143	OD1	3.128
1S78	B_ARG_204	NH1	B_ASP_149	OD1	3.952
1S78	B_ARG_204	NH2	B_GLU_125	OE2	2.608
1S78	B_LYS_206	NZ	B_ASP_212	OD2	3.574
1S78	B_HIS_238	ND1	B_GLU_243	OE1	3.602
1S78	B_HIS_238	ND1	B_GLU_243	OE2	2.978
1S78	B_ARG_308	NH2	B_GLU_310	OE2	3.284
1S78	B_LYS_311	NZ	B_ASP_285	OD2	3.757
1S78	B_HIS_327	NE2	B_GLU_341	OE1	2.772
1S78	B_HIS_327	NE2	B_GLU_341	OE2	2.972
1S78	B_ARG_332	NH1	B_GLU_357	OE2	3.726
1S78	B_ARG_332	NH2	B_GLU_357	OE1	3.938
1S78	B_ARG_332	NH2	B_GLU_357	OE2	2.990
1S78	B_LYS_347	NZ	B_GLU_299	OE2	2.672
1S78	B_LYS_347	NZ	B_GLU_383	OE1	3.084
1S78	B_LYS_347	NZ	B_GLU_383	OE2	3.934
1S78	B_ARG_410	NH2	B_GLU_383	OE1	3.602
1S78	B_ARG_410	NH2	B_GLU_383	OE2	3.759
1S78	B_ARG_412	NH1	B_GLU_299	OE1	3.217

1S78	B_ARG_412	NH1	B_GLU_299	OE2	3.556
1S78	B_ARG_412	NH2	B_GLU_299	OE2	3.170
1S78	B_ARG_465	NH1	B_GLU_438	OE1	2.881
1S78	B_ARG_477	NH1	B_GLU_485	OE1	2.617
1S78	B_ARG_477	NH1	B_GLU_485	OE2	3.941
1S78	B_ARG_477	NH2	B_GLU_481	OE2	3.169
1S78	B_ARG_477	NH2	B_GLU_485	OE1	3.166
1S78	B_ARG_514	NH1	B_GLU_531	OE1	3.612
1S78	B_ARG_514	NH1	B_GLU_531	OE2	2.336
1S78	B_ARG_523	NH1	B_GLU_531	OE1	3.374
1S78	B_ARG_523	NH1	B_GLU_531	OE2	3.242
1S78	B_HIS_567	ND1	B_GLU_544	OE1	3.248
1S78	B_HIS_567	ND1	B_GLU_544	OE2	3.019
1S78	C_LYS_24	NZ	C_ASP_70	OD1	3.323
1S78	C_ARG_61	NH2	C_ASP_82	OD1	2.646
1S78	C_ARG_61	NH2	C_ASP_82	OD2	3.273
1S78	C_LYS_103	NZ	C_GLU_165	OE1	3.918
1S78	C_LYS_103	NZ	C_GLU_165	OE2	2.759
1S78	C_LYS_149	NZ	C_GLU_195	OE2	3.249
1S78	C_HIS_189	ND1	C_ASP_151	OD2	3.312
1S78	C_ARG_211	NH1	C_GLU_187	OE2	3.367
1S78	D_ARG_38	NH1	D_ASP_86	OD1	3.229
1S78	D_ARG_38	NH2	D_GLU_46	OE1	2.855
1S78	D_ARG_62	NH1	D_GLU_85	OE1	3.019
1S78	D_ARG_62	NH2	D_GLU_46	OE1	3.024
1S78	D_ARG_62	NH2	D_GLU_46	OE2	3.448
1S78	D_ARG_66	NH1	D_ASP_86	OD1	3.283
1S78	D_ARG_66	NH1	D_ASP_86	OD2	2.439
1S78	D_ARG_66	NH2	D_ASP_86	OD1	3.573
1S78	D_ARG_94	NH2	D_ASP_101	OD1	3.501
1S78	D_ARG_94	NH2	D_ASP_101	OD2	2.662
1S78	D_LYS_143	NZ	D_ASP_144	OD2	3.814
1S78	D_HIS_164	NE2	C_ASP_167	OD1	3.839
1S78	D_LYS_209	NZ	C_GLU_123	OE1	3.290
1S78	D_LYS_214	NZ	C_ASP_122	OD1	3.484
1S78	E_LYS_24	NZ	E_ASP_70	OD1	3.695
1S78	E_LYS_24	NZ	E_ASP_70	OD2	3.318
1S78	E_ARG_61	NH2	E_GLU_81	OE1	3.985
1S78	E_ARG_61	NH2	E_GLU_81	OE2	3.655
1S78	E_ARG_61	NH2	E_ASP_82	OD1	2.822
1S78	E_ARG_61	NH2	E_ASP_82	OD2	3.506
1S78	E_LYS_103	NZ	E_GLU_165	OE1	2.948
1S78	E_LYS_103	NZ	E_GLU_165	OE2	3.258
1S78	E_HIS_189	ND1	E_ASP_151	OD2	2.704
1S78	F_ARG_38	NH1	F_ASP_86	OD1	3.191
1S78	F_ARG_38	NH2	F_GLU_46	OE1	2.976
1S78	F_ARG_38	NH2	F_ASP_86	OD1	3.546
1S78	F_ARG_66	NH1	F_ASP_86	OD1	2.849
1S78	F_ARG_66	NH1	F_ASP_86	OD2	2.628
1S78	F_ARG_83	NH1	F_GLU_85	OE1	3.280
1S78	F_ARG_83	NH1	F_GLU_85	OE2	3.676
1S78	F_ARG_94	NH2	F_ASP_101	OD1	3.456
1S78	F_ARG_94	NH2	F_ASP_101	OD2	2.584
1SM3	L_HIS_42	ND1	L_GLU_38	OE2	3.552
1SM3	L_ARG_61	NH2	L_GLU_81	OE2	2.761
1SM3	L_ARG_61	NH2	L_ASP_82	OD1	2.739
1SM3	L_ARG_61	NH2	L_ASP_82	OD2	3.626
1SM3	L_LYS_110	NZ	L_GLU_198	OE2	2.701

1SM3	L_HIS_188	ND1	L_ASP_151	OD2	2.837
1SM3	H_ARG_38	NH1	H_ASP_86	OD1	2.991
1SM3	H_ARG_38	NH2	H_GLU_46	OE1	3.308
1SM3	H_ARG_38	NH2	H_GLU_46	OE2	3.468
1SM3	H_ARG_38	NH2	H_ASP_86	OD1	3.893
1SM3	H_LYS_43	NZ	H_GLU_46	OE1	3.090
1SM3	H_ARG_52	NH1	H_GLU_50	OE2	2.647
1SM3	H_HIS_58	ND1	H_GLU_50	OE2	2.597
1SM3	H_ARG_66	NH1	H_ASP_86	OD1	3.622
1SM3	H_ARG_66	NH2	H_ASP_86	OD1	3.305
1SM3	H_ARG_66	NH2	H_ASP_86	OD2	2.417
1SM3	H_ARG_71	NH2	H_ASP_73	OD1	3.453
1SM3	H_LYS_143	NZ	L_GLU_124	OE2	2.757
1SQ2	L_LYS_1	NZ	L_GLU_7	OE1	3.597
1SQ2	L_LYS_1	NZ	L_GLU_7	OE2	2.720
1SQ2	L_ARG_61	NH1	L_ASP_48	OD2	3.006
1SQ2	L_ARG_73	NH2	N_ASP_93	OD1	3.549
1SQ2	L_ARG_73	NH2	N_ASP_93	OD2	3.002
1SQ2	L_ARG_125	NH1	L_ASP_119	OD2	3.203
1SQ2	L_ARG_125	NH2	L_ASP_119	OD1	3.605
1SQ2	L_ARG_125	NH2	L_ASP_119	OD2	2.909
1SQ2	N_ARG_2	NH1	N_ASP_26	OD2	3.782
1SQ2	N_ARG_2	NH2	N_ASP_4	OD1	3.667
1SQ2	N_ARG_2	NH2	N_ASP_4	OD2	3.350
1SQ2	N_ARG_8	NH1	N_ASP_106	OD1	3.394
1SQ2	N_ARG_38	NH1	N_ASP_77	OD1	3.866
1SQ2	N_LYS_39	NZ	N_GLU_46	OE1	3.723
1SQ2	N_LYS_51	NZ	N_GLU_57	OE1	2.817
1SQ2	N_LYS_51	NZ	N_GLU_57	OE2	3.620
1SQ2	N_ARG_54	NH1	N_ASP_77	OD1	3.089
1SQ2	N_ARG_54	NH1	N_ASP_77	OD2	3.597
1SQ2	N_ARG_54	NH2	N_ASP_77	OD1	3.562
1SQ2	N_ARG_54	NH2	N_ASP_77	OD2	2.591
1SQ2	N_ARG_82	NH1	N_GLU_46	OE2	3.823
1SQ2	N_ARG_100	NH1	L_ASP_52	OD1	3.032
1SQ2	N_ARG_100	NH1	L_ASP_52	OD2	3.454
1SQ2	N_ARG_100	NH2	L_ASP_52	OD1	3.561
1SQ2	N_ARG_100	NH2	L_ASP_52	OD2	3.218
1SVZ	A_ARG_24	NH2	A_ASP_75	OD1	2.929
1SVZ	A_ARG_66	NH1	A_ASP_87	OD1	3.870
1SVZ	A_ARG_66	NH1	A_ASP_87	OD2	2.678
1SVZ	A_ARG_66	NH2	A_GLU_84	OE1	3.931
1SVZ	A_ARG_66	NH2	A_GLU_86	OE2	3.128
1SVZ	A_ARG_66	NH2	A_ASP_87	OD1	3.084
1SVZ	A_ARG_66	NH2	A_ASP_87	OD2	3.325
1SVZ	A_LYS_139	NZ	A_GLU_137	OE1	3.533
1SVZ	A_HIS_162	NE2	A_ASP_226	OD2	2.871
1SVZ	A_LYS_173	NZ	A_ASP_190	OD2	3.311
1SVZ	A_LYS_192	NZ	A_ASP_189	OD1	2.477
1SVZ	A_ARG_194	NH1	A_ASP_217	OD1	3.731
1SVZ	A_ARG_194	NH1	A_ASP_217	OD2	2.724
1SVZ	A_ARG_194	NH2	A_ASP_217	OD1	2.551
1SVZ	A_ARG_194	NH2	A_ASP_217	OD2	2.852
1SVZ	A_ARG_227	NH2	A_GLU_232	OE1	3.187
1SVZ	A_ARG_227	NH2	A_GLU_232	OE2	2.728
1SVZ	A_HIS_228	ND1	A_ASP_226	OD1	2.644
1SVZ	B_ARG_24	NH2	B_ASP_75	OD1	3.400
1SVZ	B_ARG_24	NH2	B_ASP_75	OD2	3.186

1SVZ	B_ARG.66	NH1	B_GLU_84	OE2	3.553
1SVZ	B_ARG.66	NH2	B_GLU_86	OE2	2.747
1SVZ	B_ARG.66	NH2	B_ASP_87	OD1	3.046
1SVZ	B_ARG.66	NH2	B_ASP_87	OD2	3.702
1SVZ	B_LYS_139	NZ	B_GLU_143	OE1	3.577
1SVZ	B_HIS_162	NE2	B_ASP_226	OD2	2.989
1SVZ	B_LYS_165	NZ	B_GLU_216	OE2	2.834
1SVZ	B_LYS_173	NZ	B_ASP_190	OD1	3.857
1SVZ	B_LYS_173	NZ	B_ASP_190	OD2	3.237
1SVZ	B_LYS_192	NZ	B_ASP_189	OD1	3.974
1SVZ	B_ARG_194	NH2	B_ASP_217	OD1	3.693
1SVZ	B_ARG_194	NH2	B_ASP_217	OD2	2.595
1SVZ	B_ARG_227	NH1	B_GLU_232	OE1	3.056
1SVZ	B_ARG_227	NH1	B_GLU_232	OE2	3.538
1SVZ	B_HIS_228	ND1	B_ASP_226	OD1	2.570
1SVZ	B_HIS_228	ND1	B_ASP_226	OD2	3.901
1T2Q	L_ARG.25	NH2	L_ASP_76	OD1	3.792
1T2Q	L_ARG.60	NH2	L_ASP_66	OD1	3.739
1T2Q	L_ARG.67	NH1	L_GLU_85	OE1	3.406
1T2Q	L_ARG.67	NH2	L_GLU_85	OE1	3.629
1T2Q	L_ARG.67	NH2	L_GLU_87	OE2	3.632
1T2Q	L_ARG.67	NH2	L_ASP_88	OD1	2.658
1T2Q	L_ARG.67	NH2	L_ASP_88	OD2	3.450
1T2Q	L_LYS_109	NZ	L_ASP_171	OD1	3.845
1T2Q	L_LYS_148	NZ	L_GLU_111	OE2	3.401
1T2Q	L_LYS_155	NZ	L_GLU_201	OE1	3.097
1T2Q	L_LYS_155	NZ	L_GLU_201	OE2	2.790
1T2Q	L_ARG_194	NH2	L_ASP_190	OD2	2.982
1T2Q	L_HIS_195	ND1	L_ASP_157	OD2	2.589
1T2Q	H_ARG.39	NH1	H_ASP_90	OD1	2.798
1T2Q	H_ARG.39	NH2	H_GLU_47	OE1	2.910
1T2Q	H_ARG.39	NH2	H_GLU_47	OE2	3.823
1T2Q	H_ARG.39	NH2	H_ASP_90	OD1	3.822
1T2Q	H_LYS.44	NZ	H_ASP_89	OD2	3.291
1T2Q	H_ARG.67	NH1	H_ASP_90	OD1	3.874
1T2Q	H_ARG.67	NH1	H_ASP_90	OD2	2.949
1T2Q	H_ARG.67	NH2	H_ASP_90	OD1	2.874
1T2Q	H_ARG.67	NH2	H_ASP_90	OD2	3.246
1T2Q	H_LYS.76	NZ	H_ASP_73	OD2	3.621
1T2Q	H_ARG.98	NH2	H_ASP_107	OD1	3.528
1T2Q	H_ARG.98	NH2	H_ASP_107	OD2	2.637
1T6V	L_LYS.1	NZ	L_GLU_7	OE1	3.814
1T6V	L_LYS.1	NZ	L_GLU_7	OE2	2.661
1T6V	L_ARG.61	NH1	L_ASP_48	OD2	3.269
1T6V	L_ARG.73	NH1	N_ASP_93	OD2	3.564
1T6V	L_ARG.73	NH2	N_ASP_93	OD1	3.874
1T6V	L_ARG.73	NH2	N_ASP_93	OD2	2.603
1T6V	L_ARG_125	NH1	L_ASP_119	OD2	3.001
1T6V	L_ARG_125	NH2	L_ASP_119	OD1	3.584
1T6V	L_ARG_125	NH2	L_ASP_119	OD2	2.767
1T6V	N_ARG.2	NH2	N_ASP.4	OD1	3.696
1T6V	N_ARG.2	NH2	N_ASP.4	OD2	3.005
1T6V	N_ARG.25	NH1	N_ASP.4	OD2	2.946
1T6V	N_ARG.38	NH2	N_GLU_47	OE1	3.551
1T6V	N_LYS.40	NZ	N_GLU_76	OE1	3.049
1T6V	N_LYS.51	NZ	N_GLU_57	OE1	2.788
1T6V	N_LYS.51	NZ	N_GLU_57	OE2	3.528
1T6V	N_ARG.54	NH1	N_ASP_77	OD1	2.809

1T6V	N_ARG_54	NH1	N_ASP_77	OD2	3.785
1T6V	N_ARG_54	NH2	N_ASP_77	OD1	3.326
1T6V	N_ARG_54	NH2	N_ASP_77	OD2	2.873
1T6V	N_ARG_100	NH1	L_ASP_52	OD1	2.973
1T6V	N_ARG_100	NH1	L_ASP_52	OD2	3.510
1T6V	N_ARG_100	NH2	L_ASP_52	OD1	3.501
1T6V	N_ARG_100	NH2	L_ASP_52	OD2	3.094
1T6V	M_LYS_1	NZ	M_GLU_7	OE1	3.728
1T6V	M_LYS_1	NZ	M_GLU_7	OE2	2.757
1T6V	M_ARG_61	NH1	M_ASP_48	OD1	3.656
1T6V	M_ARG_61	NH1	M_ASP_48	OD2	3.383
1T6V	M_ARG_73	NH2	O_ASP_93	OD1	3.734
1T6V	M_ARG_73	NH2	O_ASP_93	OD2	2.904
1T6V	M_LYS_97	NZ	N_ASP_106	OD1	3.749
1T6V	M_LYS_97	NZ	N_ASP_106	OD2	2.853
1T6V	M_ARG_125	NH1	M_ASP_119	OD2	2.764
1T6V	M_ARG_125	NH2	M_ASP_119	OD1	3.456
1T6V	M_ARG_125	NH2	M_ASP_119	OD2	3.061
1T6V	O_ARG_2	NH1	O_ASP_26	OD2	3.626
1T6V	O_ARG_2	NH2	O_ASP_4	OD1	3.686
1T6V	O_ARG_2	NH2	O_ASP_4	OD2	2.970
1T6V	O_ARG_8	NH1	O_ASP_106	OD1	3.002
1T6V	O_ARG_8	NH2	O_ASP_106	OD1	3.850
1T6V	O_LYS_51	NZ	O_GLU_57	OE1	2.819
1T6V	O_LYS_51	NZ	O_GLU_57	OE2	3.551
1T6V	O_ARG_54	NH1	O_ASP_77	OD1	3.107
1T6V	O_ARG_54	NH1	O_ASP_77	OD2	3.912
1T6V	O_ARG_54	NH2	O_ASP_77	OD1	3.448
1T6V	O_ARG_54	NH2	O_ASP_77	OD2	2.988
1T6V	O_ARG_82	NH1	O_GLU_46	OE1	3.614
1T6V	O_ARG_82	NH1	O_GLU_46	OE2	3.761
1T6V	O_ARG_100	NH1	M_ASP_52	OD1	3.232
1T6V	O_ARG_100	NH1	M_ASP_52	OD2	2.872
1T6V	O_ARG_100	NH2	M_ASP_52	OD1	3.920
1T6V	O_ARG_100	NH2	M_ASP_52	OD2	2.990
1TYE	A_HIS_30	ND1	A_GLU_136	OE2	3.797
1TYE	A_HIS_30	ND1	E_ASP_429	OD2	3.896
1TYE	A_HIS_30	NE2	A_GLU_136	OE2	3.547
1TYE	A_ARG_32	NH1	E_ASP_429	OD1	3.657
1TYE	A_ARG_32	NH1	E_ASP_429	OD2	2.825
1TYE	A_ARG_73	NH1	C_ASP_71	OD1	3.528
1TYE	A_ARG_73	NH1	C_ASP_71	OD2	3.396
1TYE	A_ARG_73	NH2	A_ASP_71	OD1	3.946
1TYE	A_ARG_73	NH2	A_ASP_71	OD2	3.781
1TYE	A_ARG_73	NH2	C_ASP_71	OD2	2.714
1TYE	A_ARG_73	NH2	C_GLU_75	OE1	3.907
1TYE	A_LYS_88	NZ	A_ASP_71	OD1	3.924
1TYE	A_LYS_88	NZ	A_GLU_75	OE1	3.696
1TYE	A_ARG_90	NH2	A_GLU_49	OE1	3.556
1TYE	A_ARG_147	NH1	A_GLU_142	OE2	3.894
1TYE	A_ARG_147	NH2	A_GLU_142	OE2	3.182
1TYE	A_ARG_153	NH1	A_GLU_157	OE2	3.772
1TYE	A_ARG_153	NH2	A_GLU_120	OE1	3.065
1TYE	A_ARG_153	NH2	A_GLU_120	OE2	3.052
1TYE	A_ARG_165	NH1	A_ASP_163	OD1	2.964
1TYE	A_ARG_165	NH1	A_ASP_163	OD2	2.782
1TYE	A_ARG_165	NH2	A_GLU_123	OE1	2.740
1TYE	A_ARG_165	NH2	A_GLU_123	OE2	3.080

1TYE	A_ARG_279	NH2	A_GLU_268	OE2	3.715
1TYE	A_ARG_327	NH1	A_GLU_283	OE1	2.906
1TYE	A_ARG_335	NH1	A_ASP_301	OD1	3.950
1TYE	A_ARG_335	NH1	A_ASP_301	OD2	2.979
1TYE	A_ARG_335	NH2	A_ASP_301	OD1	3.045
1TYE	A_ARG_335	NH2	A_ASP_301	OD2	3.119
1TYE	A_ARG_422	NH1	A_ASP_24	OD1	3.230
1TYE	B_ARG_91	NH1	B_GLU_60	OE1	3.253
1TYE	B_ARG_91	NH2	B_ASP_432	OD2	3.964
1TYE	B_ARG_105	NH1	B_ASP_71	OD1	3.549
1TYE	B_LYS_159	NZ	B_ASP_224	OD1	3.816
1TYE	B_LYS_159	NZ	B_ASP_224	OD2	2.677
1TYE	B_LYS_209	NZ	B_GLU_206	OE1	3.537
1TYE	B_LYS_209	NZ	B_GLU_206	OE2	3.891
1TYE	B_ARG_216	NH1	A_GLU_123	OE1	2.702
1TYE	B_ARG_239	NH1	B_ASP_113	OD1	2.627
1TYE	B_LYS_253	NZ	A_ASP_232	OD2	3.290
1TYE	B_HIS_255	ND1	B_ASP_259	OD2	3.030
1TYE	B_HIS_255	NE2	B_ASP_158	OD2	3.791
1TYE	B_HIS_255	NE2	B_ASP_217	OD1	3.796
1TYE	B_HIS_255	NE2	B_ASP_217	OD2	2.660
1TYE	B_HIS_274	NE2	B_ASP_270	OD1	3.163
1TYE	B_HIS_274	NE2	B_ASP_270	OD2	2.921
1TYE	B_HIS_280	ND1	B_ASP_278	OD2	3.747
1TYE	B_LYS_298	NZ	B_GLU_297	OE2	3.673
1TYE	B_LYS_302	NZ	B_ASP_233	OD1	3.013
1TYE	B_LYS_302	NZ	B_ASP_233	OD2	3.373
1TYE	B_LYS_354	NZ	B_GLU_356	OE1	3.389
1TYE	B_LYS_390	NZ	B_ASP_393	OD2	3.994
1TYE	B_ARG_404	NH2	B_GLU_364	OE2	2.885
1TYE	B_LYS_410	NZ	B_ASP_434	OD1	3.437
1TYE	C_ARG_73	NH1	A_ASP_71	OD1	3.491
1TYE	C_ARG_73	NH2	A_ASP_71	OD1	3.688
1TYE	C_ARG_73	NH2	A_ASP_71	OD2	3.197
1TYE	C_ARG_73	NH2	C_ASP_71	OD1	3.681
1TYE	C_ARG_73	NH2	C_ASP_71	OD2	3.705
1TYE	C_LYS_88	NZ	C_ASP_71	OD1	3.778
1TYE	C_LYS_88	NZ	C_GLU_75	OE2	3.812
1TYE	C_ARG_90	NH1	C_GLU_49	OE1	2.673
1TYE	C_ARG_90	NH1	C_GLU_49	OE2	3.918
1TYE	C_LYS_118	NZ	C_GLU_117	OE2	3.898
1TYE	C_ARG_147	NH1	C_GLU_142	OE2	3.614
1TYE	C_ARG_147	NH2	C_GLU_142	OE2	3.566
1TYE	C_ARG_153	NH2	C_GLU_120	OE1	3.220
1TYE	C_ARG_153	NH2	C_GLU_120	OE2	3.597
1TYE	C_ARG_165	NH1	C_ASP_163	OD1	3.313
1TYE	C_ARG_165	NH1	C_ASP_163	OD2	2.716
1TYE	C_ARG_165	NH2	C_GLU_123	OE1	3.193
1TYE	C_ARG_165	NH2	C_GLU_123	OE2	3.129
1TYE	C_ARG_279	NH2	C_GLU_268	OE2	3.615
1TYE	C_ARG_281	NH2	C_GLU_229	OE2	3.746
1TYE	C_ARG_327	NH1	C_GLU_283	OE2	2.647
1TYE	C_ARG_422	NH1	C_ASP_24	OD1	2.911
1TYE	C_ARG_422	NH1	C_ASP_24	OD2	3.921
1TYE	D_LYS_46	NZ	D_ASP_47	OD2	3.909
1TYE	D_ARG_62	NH2	D_GLU_60	OE1	3.320
1TYE	D_ARG_91	NH1	D_ASP_432	OD2	3.976
1TYE	D_ARG_91	NH2	D_ASP_432	OD1	3.669

1TYE	D_ARG_91	NH2	D_ASP_432	OD2	3.225
1TYE	D_ARG_105	NH1	D_ASP_71	OD1	3.673
1TYE	D_LYS_159	NZ	D_ASP_224	OD1	3.999
1TYE	D_LYS_159	NZ	D_ASP_224	OD2	2.881
1TYE	D_LYS_209	NZ	D_GLU_206	OE2	3.266
1TYE	D_ARG_216	NH1	C_GLU_123	OE1	2.914
1TYE	D_ARG_216	NH1	C_GLU_123	OE2	3.969
1TYE	D_ARG_239	NH1	D_ASP_113	OD1	2.677
1TYE	D_HIS_244	NE2	D_ASP_113	OD2	3.772
1TYE	D_LYS_253	NZ	C_ASP_232	OD2	3.400
1TYE	D_HIS_255	ND1	D_ASP_259	OD2	2.788
1TYE	D_HIS_255	NE2	D_ASP_158	OD2	3.582
1TYE	D_HIS_255	NE2	D_ASP_217	OD1	3.881
1TYE	D_HIS_255	NE2	D_ASP_217	OD2	2.918
1TYE	D_HIS_274	NE2	D_ASP_270	OD1	3.141
1TYE	D_HIS_274	NE2	D_ASP_270	OD2	2.980
1TYE	D_HIS_280	ND1	D_ASP_278	OD2	3.600
1TYE	D_LYS_298	NZ	D_GLU_297	OE2	3.766
1TYE	D_LYS_302	NZ	D_ASP_233	OD1	3.683
1TYE	D_LYS_302	NZ	D_ASP_233	OD2	3.005
1TYE	D_LYS_354	NZ	D_GLU_356	OE1	3.054
1TYE	D_LYS_354	NZ	D_GLU_356	OE2	3.182
1TYE	D_ARG_360	NH1	D_GLU_358	OE2	2.869
1TYE	E_HIS_30	NE2	E_GLU_136	OE2	3.296
1TYE	E_ARG_32	NH2	E_ASP_28	OD2	3.193
1TYE	E_ARG_73	NH2	E_ASP_71	OD2	3.212
1TYE	E_LYS_88	NZ	E_GLU_75	OE1	3.717
1TYE	E_ARG_90	NH1	E_GLU_49	OE1	3.580
1TYE	E_ARG_153	NH1	E_GLU_157	OE2	3.995
1TYE	E_ARG_153	NH2	E_GLU_120	OE1	3.767
1TYE	E_ARG_165	NH1	E_ASP_163	OD1	3.534
1TYE	E_ARG_165	NH1	E_ASP_163	OD2	2.834
1TYE	E_ARG_165	NH2	E_GLU_123	OE1	2.970
1TYE	E_ARG_165	NH2	E_GLU_123	OE2	3.167
1TYE	E_ARG_279	NH2	E_GLU_268	OE2	3.525
1TYE	E_ARG_281	NH2	E_GLU_229	OE2	3.697
1TYE	E_ARG_327	NH1	E_GLU_283	OE2	2.691
1TYE	E_ARG_355	NH1	E_GLU_324	OE2	3.503
1TYE	E_ARG_368	NH2	A_ASP_429	OD2	3.921
1TYE	E_ARG_422	NH1	E_ASP_24	OD1	3.604
1TYE	E_ARG_422	NH1	E_ASP_24	OD2	3.672
1TYE	F_ARG_67	NH2	F_GLU_65	OE1	3.259
1TYE	F_ARG_91	NH1	F_GLU_60	OE2	2.911
1TYE	F_ARG_91	NH2	F_ASP_432	OD2	2.722
1TYE	F_LYS_159	NZ	F_ASP_224	OD2	2.976
1TYE	F_LYS_209	NZ	F_GLU_206	OE1	3.424
1TYE	F_ARG_214	NH2	F_ASP_179	OD2	2.925
1TYE	F_ARG_216	NH1	E_GLU_123	OE1	2.938
1TYE	F_ARG_216	NH1	E_GLU_123	OE2	3.244
1TYE	F_ARG_239	NH1	F_ASP_113	OD1	2.831
1TYE	F_ARG_239	NH1	F_ASP_113	OD2	3.398
1TYE	F_HIS_244	NE2	F_ASP_113	OD2	3.408
1TYE	F_LYS_253	NZ	E_ASP_232	OD2	3.394
1TYE	F_HIS_255	ND1	F_ASP_259	OD2	2.813
1TYE	F_HIS_255	NE2	F_ASP_158	OD2	3.756
1TYE	F_HIS_255	NE2	F_ASP_217	OD1	3.834
1TYE	F_HIS_255	NE2	F_ASP_217	OD2	2.822
1TYE	F_HIS_274	NE2	F_ASP_270	OD1	3.189

1TYE	F_HIS_274	NE2	F_ASP_270	OD2	2.810
1TYE	F_HIS_280	ND1	F_ASP_278	OD2	3.328
1TYE	F_LYS_298	NZ	F_GLU_297	OE2	3.779
1TYE	F_LYS_302	NZ	F_ASP_233	OD2	2.915
1TYE	F_LYS_354	NZ	F_GLU_356	OE2	3.665
1TYE	F_ARG_360	NH1	F_GLU_358	OE2	2.965
1TZH	V_ARG_23	NH1	W_GLU_30	OE2	3.100
1TZH	V_ARG_56	NH1	V_GLU_38	OE2	3.313
1TZH	V_ARG_56	NH2	V_GLU_38	OE1	3.086
1TZH	V_ARG_56	NH2	V_GLU_38	OE2	3.428
1TZH	V_ARG_82	NH2	V_GLU_42	OE1	2.933
1TZH	V_LYS_84	NZ	V_GLU_44	OE2	3.642
1TZH	V_HIS_90	NE2	H_ASP_33	OD1	2.826
1TZH	V_HIS_90	NE2	H_ASP_33	OD2	2.524
1TZH	V_ARG_105	NH2	V_GLU_103	OE1	3.855
1TZH	W_ARG_23	NH1	V_GLU_30	OE1	3.346
1TZH	W_ARG_56	NH1	W_GLU_38	OE2	3.335
1TZH	W_ARG_56	NH2	W_GLU_38	OE1	3.077
1TZH	W_ARG_56	NH2	W_GLU_38	OE2	3.382
1TZH	W_ARG_82	NH2	W_GLU_42	OE2	2.977
1TZH	W_HIS_90	NE2	B_ASP_33	OD1	3.121
1TZH	W_HIS_90	NE2	B_ASP_33	OD2	2.585
1TZH	W_HIS_99	NE2	W_GLU_73	OE2	3.842
1TZH	W_ARG_105	NH2	W_GLU_103	OE1	3.129
1TZH	W_LYS_107	NZ	W_GLU_67	OE1	3.188
1TZH	W_LYS_107	NZ	W_GLU_67	OE2	3.161
1TZH	A_ARG_24	NH1	A_ASP_70	OD2	3.886
1TZH	A_ARG_61	NH2	A_GLU_81	OE1	3.363
1TZH	A_ARG_61	NH2	A_ASP_82	OD1	3.162
1TZH	A_ARG_61	NH2	A_ASP_82	OD2	3.912
1TZH	A_LYS_103	NZ	A_GLU_165	OE1	2.800
1TZH	A_LYS_103	NZ	A_GLU_165	OE2	3.540
1TZH	A_LYS_149	NZ	A_GLU_195	OE1	3.634
1TZH	A_LYS_149	NZ	A_GLU_195	OE2	2.910
1TZH	A_LYS_183	NZ	A_GLU_187	OE1	3.287
1TZH	A_LYS_183	NZ	A_GLU_187	OE2	2.651
1TZH	A_LYS_188	NZ	A_ASP_185	OD1	3.831
1TZH	A_HIS_189	ND1	A_ASP_151	OD2	2.992
1TZH	B_ARG_38	NH1	B_ASP_86	OD1	3.008
1TZH	B_ARG_38	NH2	B_GLU_46	OE1	3.146
1TZH	B_ARG_38	NH2	B_GLU_46	OE2	3.677
1TZH	B_ARG_38	NH2	B_ASP_86	OD1	3.681
1TZH	B_ARG_66	NH1	B_ASP_86	OD1	3.515
1TZH	B_ARG_66	NH1	B_ASP_86	OD2	2.745
1TZH	B_ARG_66	NH2	B_ASP_86	OD1	3.270
1TZH	B_ARG_66	NH2	B_ASP_86	OD2	3.900
1TZH	B_ARG_94	NH2	B_ASP_32	OD1	3.304
1TZH	B_ARG_94	NH2	B_ASP_32	OD2	3.875
1TZH	B_LYS_143	NZ	B_ASP_144	OD1	2.731
1TZH	B_LYS_143	NZ	B_ASP_144	OD2	3.209
1TZH	B_LYS_209	NZ	A_GLU_123	OE2	3.903
1TZH	L_ARG_24	NH2	L_ASP_70	OD2	3.428
1TZH	L_ARG_61	NH2	L_GLU_81	OE1	3.330
1TZH	L_ARG_61	NH2	L_ASP_82	OD1	3.040
1TZH	L_ARG_61	NH2	L_ASP_82	OD2	3.443
1TZH	L_LYS_103	NZ	L_GLU_105	OE2	3.246
1TZH	L_LYS_103	NZ	L_GLU_165	OE1	3.341
1TZH	L_LYS_103	NZ	L_GLU_165	OE2	3.547

1TZH	L_ARG_142	NH2	L_GLU_165	OE1	3.821
1TZH	L_LYS_183	NZ	L_GLU_187	OE2	3.055
1TZH	L_ARG_211	NH2	L_GLU_187	OE1	3.313
1TZH	H_ARG_38	NH1	H_ASP_86	OD1	3.223
1TZH	H_ARG_38	NH2	H_GLU_46	OE1	3.456
1TZH	H_ARG_38	NH2	H_ASP_86	OD1	3.593
1TZH	H_ARG_66	NH1	H_ASP_86	OD2	3.197
1TZH	H_ARG_66	NH2	H_ASP_86	OD1	2.884
1TZH	H_ARG_66	NH2	H_ASP_86	OD2	3.307
1TZH	H_ARG_94	NH2	H_ASP_32	OD1	3.594
1TZH	H_ARG_94	NH2	H_ASP_32	OD2	2.870
1TZH	H_LYS_143	NZ	H_ASP_144	OD1	3.985
1TZH	H_LYS_143	NZ	H_ASP_144	OD2	3.661
1TZH	H_HIS_164	NE2	L_ASP_167	OD1	3.495
1TZH	H_LYS_209	NZ	L_GLU_123	OE1	2.754
1TZH	H_LYS_209	NZ	L_GLU_123	OE2	3.404
1TZI	A_ARG_24	NH1	A_ASP_70	OD1	3.345
1TZI	A_ARG_61	NH2	A_GLU_81	OE2	3.484
1TZI	A_ARG_61	NH2	A_ASP_82	OD1	3.184
1TZI	A_LYS_103	NZ	A_GLU_165	OE2	3.341
1TZI	A_LYS_149	NZ	A_GLU_195	OE2	3.678
1TZI	B_HIS_35	NE2	B_ASP_33	OD1	3.655
1TZI	B_HIS_35	NE2	B_ASP_33	OD2	3.046
1TZI	B_HIS_35	NE2	B_ASP_50	OD2	3.907
1TZI	B_ARG_38	NH1	B_ASP_86	OD1	3.155
1TZI	B_ARG_38	NH2	B_GLU_46	OE1	3.042
1TZI	B_ARG_38	NH2	B_GLU_46	OE2	3.847
1TZI	B_ARG_38	NH2	B_ASP_86	OD1	3.843
1TZI	B_LYS_64	NZ	B_ASP_61	OD1	3.600
1TZI	B_LYS_64	NZ	B_ASP_61	OD2	3.744
1TZI	B_ARG_66	NH1	B_ASP_86	OD2	3.093
1TZI	B_ARG_66	NH2	B_ASP_86	OD1	3.082
1TZI	B_ARG_66	NH2	B_ASP_86	OD2	3.244
1TZI	B_ARG_94	NH2	B_ASP_101	OD1	3.674
1TZI	B_ARG_94	NH2	B_ASP_101	OD2	2.631
1TZI	B_LYS_143	NZ	B_ASP_144	OD1	3.643
1TZI	B_LYS_143	NZ	B_ASP_144	OD2	3.293
1TZI	B_LYS_209	NZ	A_GLU_123	OE2	3.786
1TZI	V_ARG_56	NH1	V_GLU_38	OE1	3.287
1TZI	V_ARG_56	NH1	V_GLU_38	OE2	3.396
1TZI	V_ARG_56	NH2	V_GLU_38	OE2	3.863
1TZI	V_HIS_99	NE2	V_GLU_73	OE2	3.539
1U6A	L_ARG_24	NH2	L_ASP_70	OD2	3.902
1U6A	L_ARG_61	NH1	L_GLU_79	OE2	3.901
1U6A	L_ARG_61	NH2	L_GLU_81	OE2	3.590
1U6A	L_ARG_61	NH2	L_ASP_82	OD1	2.937
1U6A	L_ARG_61	NH2	L_ASP_82	OD2	3.603
1U6A	L_LYS_149	NZ	L_GLU_195	OE1	2.946
1U6A	L_LYS_149	NZ	L_GLU_195	OE2	3.367
1U6A	L_LYS_188	NZ	L_ASP_185	OD1	3.941
1U6A	L_HIS_189	ND1	L_ASP_151	OD2	2.371
1U6A	L_ARG_211	NH1	L_GLU_187	OE1	2.862
1U6A	H_ARG_38	NH1	H_ASP_86	OD1	2.883
1U6A	H_ARG_38	NH2	H_ASP_86	OD1	3.710
1U6A	H_ARG_66	NH1	H_ASP_86	OD1	3.475
1U6A	H_ARG_66	NH1	H_ASP_86	OD2	2.761
1U6A	H_ARG_66	NH2	H_ASP_86	OD1	2.683
1U6A	H_ARG_66	NH2	H_ASP_86	OD2	3.375

1U6A	H.LYS_143	NZ	H.ASP_144	OD1	3.705
1U6A	H.LYS_143	NZ	H.ASP_144	OD2	3.600
1U6A	H.HIS_164	NE2	L.ASP_167	OD1	3.994
1U6A	H.LYS_210	NZ	H.GLU_212	OE2	3.157
1UA6	L.ARG_61	NH1	L.GLU_81	OE2	3.789
1UA6	L.ARG_61	NH2	L.GLU_81	OE2	2.779
1UA6	L.ARG_61	NH2	L.ASP_82	OD1	2.629
1UA6	L.ARG_61	NH2	L.ASP_82	OD2	3.362
1UA6	L.LYS_103	NZ	L.GLU_105	OE2	3.651
1UA6	H.ARG_38	NH1	H.ASP_89	OD2	2.881
1UA6	H.ARG_38	NH2	H.GLU_46	OE1	2.829
1UA6	H.ARG_38	NH2	H.ASP_89	OD2	3.526
1UA6	H.ARG_66	NH1	H.ASP_89	OD1	3.005
1UA6	H.ARG_66	NH1	H.ASP_89	OD2	3.836
1UA6	H.ARG_66	NH2	H.ASP_89	OD1	3.531
1UA6	H.ARG_66	NH2	H.ASP_89	OD2	2.947
1UA6	Y.LYS_1	NZ	Y.GLU_7	OE2	3.070
1UA6	Y.LYS_13	NZ	Y.ASP_18	OD2	2.985
1UA6	Y.LYS_97	NZ	H.ASP_32	OD1	2.722
1UA6	Y.LYS_97	NZ	H.ASP_99	OD2	2.674
1UA6	Y.ARG_125	NH1	Y.ASP_119	OD1	3.848
1UA6	Y.ARG_125	NH1	Y.ASP_119	OD2	3.662
1UA6	Y.ARG_125	NH2	Y.ASP_119	OD2	2.731
1UAC	L.ARG_45	NH2	L.GLU_42	OE1	3.506
1UAC	L.ARG_61	NH1	L.GLU_79	OE1	3.446
1UAC	L.ARG_61	NH1	L.GLU_79	OE2	3.988
1UAC	L.ARG_61	NH2	L.GLU_79	OE1	3.597
1UAC	L.ARG_61	NH2	L.GLU_81	OE2	2.939
1UAC	L.ARG_61	NH2	L.ASP_82	OD1	3.382
1UAC	L.ARG_61	NH2	L.ASP_82	OD2	3.786
1UAC	H.ARG_38	NH1	H.ASP_89	OD1	2.495
1UAC	H.ARG_38	NH2	H.GLU_46	OE1	2.848
1UAC	H.ARG_38	NH2	H.ASP_89	OD1	3.590
1UAC	H.ARG_66	NH1	H.ASP_89	OD1	3.633
1UAC	H.ARG_66	NH1	H.ASP_89	OD2	2.604
1UAC	H.ARG_66	NH2	H.ASP_89	OD1	3.226
1UAC	H.ARG_66	NH2	H.ASP_89	OD2	3.547
1UAC	Y.LYS_1	NZ	Y.GLU_7	OE2	3.056
1UAC	Y.LYS_13	NZ	Y.ASP_18	OD2	3.156
1UAC	Y.LYS_97	NZ	H.ASP_32	OD1	2.750
1UAC	Y.LYS_97	NZ	H.ASP_32	OD2	3.845
1UAC	Y.LYS_97	NZ	H.ASP_99	OD2	2.749
1UAC	Y.HIS_121	ND1	Y.ASP_119	OD1	3.781
1UAC	Y.HIS_121	NE2	Y.ASP_119	OD1	3.474
1UAC	Y.ARG_125	NH1	Y.ASP_119	OD1	3.237
1UAC	Y.ARG_125	NH1	Y.ASP_119	OD2	3.553
1UAC	Y.ARG_125	NH2	Y.ASP_119	OD1	3.403
1UAC	Y.ARG_125	NH2	Y.ASP_119	OD2	2.499
1UCB	L.ARG_24	NH1	L.ASP_70	OD1	3.292
1UCB	L.ARG_24	NH1	L.ASP_70	OD2	3.887
1UCB	L.ARG_24	NH2	L.ASP_70	OD1	3.839
1UCB	L.ARG_24	NH2	L.ASP_70	OD2	3.203
1UCB	L.LYS_50	NZ	H.ASP_98	OD1	3.160
1UCB	L.ARG_61	NH1	L.ASP_82	OD2	2.752
1UCB	L.ARG_61	NH2	L.GLU_81	OE2	3.557
1UCB	L.ARG_61	NH2	L.ASP_82	OD1	2.863
1UCB	L.ARG_61	NH2	L.ASP_82	OD2	2.961
1UCB	L.ARG_77	NH2	L.GLU_79	OE1	3.741

1UCB	L_ARG_77	NH2	L_GLU_79	OE2	2.900
1UCB	L_LYS_103	NZ	L_GLU_165	OE1	3.505
1UCB	L_LYS_103	NZ	L_GLU_165	OE2	3.935
1UCB	L_ARG_142	NH2	L_GLU_165	OE1	3.407
1UCB	L_LYS_188	NZ	L_ASP_185	OD2	3.372
1UCB	L_HIS_189	ND1	L_ASP_151	OD2	3.021
1UCB	L_ARG_211	NH2	L_GLU_187	OE1	3.809
1UCB	H_ARG_38	NH1	H_ASP_86	OD1	2.991
1UCB	H_ARG_38	NH2	H_GLU_46	OE1	3.160
1UCB	H_LYS_64	NZ	H_ASP_61	OD1	2.788
1UCB	H_LYS_64	NZ	H_ASP_61	OD2	3.139
1UCB	H_ARG_66	NH1	H_ASP_86	OD1	3.656
1UCB	H_ARG_66	NH1	H_ASP_86	OD2	2.889
1UCB	H_ARG_66	NH2	H_ASP_86	OD1	3.058
1UCB	H_ARG_66	NH2	H_ASP_86	OD2	3.202
1UCB	H_LYS_75	NZ	H_ASP_72	OD2	3.809
1UCB	H_LYS_221	NZ	L_GLU_123	OE1	3.128
1UCB	H_ARG_222	NH1	H_GLU_226	OE1	3.921
1UCB	H_ARG_222	NH1	H_GLU_226	OE2	3.794
1UCB	H_ARG_222	NH2	H_GLU_226	OE2	3.739
1UJ3	A_ARG_61	NH2	A_GLU_81	OE2	3.553
1UJ3	A_ARG_61	NH2	A_ASP_82	OD1	2.902
1UJ3	A_ARG_61	NH2	A_ASP_82	OD2	3.527
1UJ3	A_HIS_91	NE2	B_ASP_399	OD1	3.708
1UJ3	A_HIS_91	NE2	B_ASP_399	OD2	2.884
1UJ3	A_LYS_103	NZ	A_GLU_165	OE1	3.612
1UJ3	A_LYS_103	NZ	A_GLU_165	OE2	3.641
1UJ3	A_LYS_107	NZ	A_ASP_17	OD2	3.650
1UJ3	A_LYS_149	NZ	A_GLU_195	OE1	2.640
1UJ3	A_LYS_149	NZ	A_GLU_195	OE2	3.439
1UJ3	A_LYS_183	NZ	A_GLU_187	OE1	3.625
1UJ3	A_LYS_183	NZ	A_GLU_187	OE2	3.082
1UJ3	A_LYS_188	NZ	A_ASP_185	OD1	3.389
1UJ3	B_HIS_335	NE2	B_ASP_399	OD1	3.715
1UJ3	B_LYS_363	NZ	B_ASP_361	OD1	2.797
1UJ3	B_LYS_363	NZ	B_ASP_361	OD2	3.526
1UJ3	B_ARG_367	NH1	B_ASP_390	OD1	3.568
1UJ3	B_ARG_367	NH1	B_ASP_390	OD2	2.817
1UJ3	B_ARG_367	NH2	B_ASP_390	OD1	2.726
1UJ3	B_ARG_367	NH2	B_ASP_390	OD2	3.364
1UJ3	B_ARG_398	NH2	B_ASP_405	OD1	3.535
1UJ3	B_ARG_398	NH2	B_ASP_405	OD2	2.642
1UJ3	B_ARG_433	NH2	B_GLU_516	OE2	3.825
1UJ3	B_LYS_447	NZ	B_ASP_448	OD1	3.091
1UJ3	B_LYS_447	NZ	B_ASP_448	OD2	2.878
1UJ3	B_LYS_513	NZ	A_GLU_123	OE1	3.554
1UJ3	B_LYS_513	NZ	A_GLU_123	OE2	3.075
1UJ3	B_ARG_514	NH2	B_GLU_516	OE1	3.640
1UJ3	C_LYS_615	NZ	C_GLU_624	OE1	2.927
1UJ3	C_LYS_646	NZ	C_GLU_662	OE2	3.280
1UJ3	C_LYS_648	NZ	C_GLU_662	OE2	3.204
1UJ3	C_LYS_665	NZ	C_GLU_662	OE1	3.069
1UJ3	C_LYS_665	NZ	C_GLU_662	OE2	3.168
1UJ3	C_LYS_722	NZ	C_ASP_778	OD1	2.825
1UJ3	C_LYS_722	NZ	C_ASP_778	OD2	3.467
1UJ3	C_LYS_759	NZ	C_ASP_780	OD2	2.414
1UJ3	C_LYS_766	NZ	A_ASP_1	OD1	3.997
1UJ3	C_LYS_769	NZ	B_ASP_399	OD1	2.791

1UJ3	C.LYS_769	NZ	B.ASP_399	OD2	3.372
1UJ3	C.LYS_801	NZ	B.ASP_352	OD1	2.774
1UJ3	C.LYS_801	NZ	B.ASP_352	OD2	3.632
1UWX	A.LYS_36	NZ	A.GLU_32	OE1	2.824
1UWX	B.LYS_36	NZ	B.GLU_32	OE2	2.807
1UWX	H.LYS_12	NZ	H.GLU_10	OE1	3.100
1UWX	H.LYS_64	NZ	H.ASP_61	OD1	3.798
1UWX	H.ARG_66	NH1	H.ASP_86	OD1	2.454
1UWX	H.ARG_66	NH1	H.ASP_86	OD2	2.896
1UWX	H.ARG_94	NH2	H.ASP_101	OD1	2.904
1UWX	H.ARG_94	NH2	H.ASP_101	OD2	3.891
1UWX	H.HIS_164	NE2	L.ASP_168	OD2	3.899
1UWX	H.LYS_208	NZ	L.GLU_124	OE2	2.744
1UWX	H.LYS_209	NZ	H.GLU_211	OE2	3.816
1UWX	K.ARG_63	NH1	K.ASP_84	OD1	3.154
1UWX	K.ARG_63	NH1	K.ASP_84	OD2	2.158
1UWX	K.ARG_63	NH2	K.ASP_84	OD1	3.226
1UWX	K.ARG_63	NH2	K.ASP_84	OD2	3.623
1UWX	K.LYS_150	NZ	K.GLU_196	OE1	3.737
1UWX	K.LYS_150	NZ	K.GLU_196	OE2	3.159
1UWX	K.ARG_156	NH1	K.GLU_186	OE1	2.610
1UWX	K.ARG_156	NH1	K.GLU_186	OE2	3.937
1UWX	K.ARG_156	NH2	K.GLU_186	OE1	3.178
1UWX	K.ARG_156	NH2	K.GLU_186	OE2	2.975
1UWX	K.LYS_184	NZ	K.GLU_188	OE1	3.993
1UWX	K.HIS_190	ND1	K.ASP_152	OD2	2.933
1UWX	K.LYS_200	NZ	K.ASP_111	OD2	3.114
1UWX	K.ARG_212	NH1	K.GLU_188	OE2	3.245
1UWX	L.ARG_63	NH1	L.ASP_84	OD1	3.321
1UWX	L.ARG_63	NH1	L.ASP_84	OD2	2.266
1UWX	L.ARG_63	NH2	L.ASP_84	OD1	3.278
1UWX	L.ARG_63	NH2	L.ASP_84	OD2	3.625
1UWX	L.LYS_150	NZ	L.GLU_196	OE1	3.639
1UWX	L.LYS_150	NZ	L.GLU_196	OE2	3.224
1UWX	L.ARG_156	NH1	L.GLU_186	OE1	2.635
1UWX	L.ARG_156	NH1	L.GLU_186	OE2	3.963
1UWX	L.ARG_156	NH2	L.GLU_186	OE1	3.120
1UWX	L.ARG_156	NH2	L.GLU_186	OE2	2.947
1UWX	L.LYS_184	NZ	L.GLU_188	OE1	3.917
1UWX	L.HIS_190	ND1	L.ASP_152	OD2	2.931
1UWX	L.LYS_200	NZ	L.ASP_111	OD2	3.029
1UWX	L.ARG_212	NH1	L.GLU_188	OE2	3.191
1UWX	M.LYS_12	NZ	M.GLU_10	OE1	3.235
1UWX	M.LYS_64	NZ	M.ASP_61	OD1	3.798
1UWX	M.ARG_66	NH1	M.ASP_86	OD1	2.526
1UWX	M.ARG_66	NH1	M.ASP_86	OD2	2.861
1UWX	M.ARG_94	NH2	M.ASP_101	OD1	2.895
1UWX	M.ARG_94	NH2	M.ASP_101	OD2	3.832
1UWX	M.LYS_208	NZ	K.GLU_124	OE2	2.705
1UWX	M.LYS_209	NZ	M.GLU_211	OE1	3.750
1UZ6	E.ARG_24	NH1	E.ASP_70	OD2	3.187
1UZ6	E.LYS_39	NZ	E.GLU_81	OE1	3.464
1UZ6	E.ARG_61	NH1	E.ASP_82	OD1	3.736
1UZ6	E.ARG_61	NH1	E.ASP_82	OD2	2.887
1UZ6	E.ARG_61	NH2	E.GLU_79	OE1	3.920
1UZ6	E.ARG_61	NH2	E.GLU_79	OE2	3.989
1UZ6	E.ARG_61	NH2	E.ASP_82	OD1	3.165
1UZ6	E.ARG_61	NH2	E.ASP_82	OD2	3.643

1UZ6	E_LYS_103	NZ	E_ASP_164	OD1	3.599
1UZ6	E_ARG_154	NH2	E_GLU_184	OE1	3.820
1UZ6	E_ARG_154	NH2	E_GLU_184	OE2	3.327
1UZ6	E_LYS_182	NZ	E_ASP_183	OD1	3.722
1UZ6	E_ARG_210	NH1	E_GLU_186	OE1	3.231
1UZ6	F_ARG_38	NH1	F_ASP_86	OD1	2.903
1UZ6	F_ARG_38	NH2	F_GLU_46	OE1	2.942
1UZ6	F_ARG_38	NH2	F_ASP_86	OD1	3.966
1UZ6	F_LYS_66	NZ	F_ASP_86	OD1	3.610
1UZ6	F_LYS_66	NZ	F_ASP_86	OD2	2.606
1UZ6	F_ARG_164	NH1	E_ASP_166	OD1	3.662
1UZ6	F_ARG_164	NH2	E_ASP_166	OD1	3.708
1UZ6	F_ARG_164	NH2	E_ASP_169	OD2	3.554
1UZ6	F_LYS_208	NZ	E_GLU_122	OE1	3.883
1UZ6	F_ARG_209	NH1	E_GLU_122	OE2	3.531
1UZ6	H_ARG_38	NH1	H_ASP_86	OD1	2.872
1UZ6	H_ARG_38	NH2	H_GLU_46	OE1	3.043
1UZ6	H_ARG_38	NH2	H_ASP_86	OD1	3.674
1UZ6	H_LYS_66	NZ	H_GLU_85	OE2	3.660
1UZ6	H_LYS_66	NZ	H_ASP_86	OD1	3.366
1UZ6	H_LYS_66	NZ	H_ASP_86	OD2	2.666
1UZ6	H_ARG_164	NH1	L_ASP_166	OD1	3.603
1UZ6	H_ARG_164	NH2	L_ASP_166	OD1	3.557
1UZ6	H_ARG_164	NH2	L_ASP_169	OD2	3.746
1UZ6	H_LYS_208	NZ	L_GLU_122	OE1	3.795
1UZ6	H_ARG_209	NH1	L_GLU_122	OE2	3.180
1UZ6	L_ARG_24	NH1	L_ASP_70	OD2	3.991
1UZ6	L_LYS_27	NZ	L_GLU_93	OE1	3.534
1UZ6	L_LYS_27	NZ	L_GLU_93	OE2	2.676
1UZ6	L_ARG_61	NH1	L_ASP_82	OD1	3.953
1UZ6	L_ARG_61	NH1	L_ASP_82	OD2	2.962
1UZ6	L_ARG_61	NH2	L_GLU_79	OE1	3.473
1UZ6	L_ARG_61	NH2	L_GLU_79	OE2	3.740
1UZ6	L_ARG_61	NH2	L_ASP_82	OD1	3.090
1UZ6	L_ARG_61	NH2	L_ASP_82	OD2	3.270
1UZ6	L_LYS_103	NZ	L_ASP_164	OD1	3.480
1UZ6	L_LYS_146	NZ	L_GLU_194	OE1	3.535
1UZ6	L_LYS_148	NZ	L_GLU_194	OE1	3.899
1UZ6	L_ARG_154	NH2	L_GLU_184	OE2	3.580
1UZ6	L_LYS_182	NZ	L_ASP_183	OD1	3.739
1UZ6	L_HIS_188	ND1	L_ASP_150	OD2	3.153
1UZ6	L_ARG_210	NH1	L_GLU_186	OE1	3.084
1UZ6	M_ARG_61	NH1	M_ASP_82	OD1	3.933
1UZ6	M_ARG_61	NH1	M_ASP_82	OD2	3.129
1UZ6	M_ARG_61	NH2	M_GLU_79	OE1	3.335
1UZ6	M_ARG_61	NH2	M_GLU_79	OE2	3.866
1UZ6	M_ARG_61	NH2	M_ASP_82	OD1	3.049
1UZ6	M_ARG_61	NH2	M_ASP_82	OD2	3.623
1UZ6	M_LYS_148	NZ	M_GLU_194	OE2	3.095
1UZ6	M_ARG_187	NH2	M_ASP_183	OD2	3.819
1UZ6	M_ARG_210	NH1	M_GLU_186	OE1	3.314
1UZ6	P_ARG_38	NH1	P_ASP_86	OD1	3.091
1UZ6	P_ARG_38	NH2	P_GLU_46	OE1	3.209
1UZ6	P_LYS_66	NZ	P_GLU_85	OE2	3.456
1UZ6	P_LYS_66	NZ	P_ASP_86	OD1	3.180
1UZ6	P_LYS_66	NZ	P_ASP_86	OD2	2.816
1UZ6	P_ARG_164	NH1	M_ASP_166	OD1	3.636
1UZ6	P_ARG_164	NH2	M_ASP_166	OD1	3.666

1UZ6	P_ARG_164	NH2	M_ASP_166	OD2	3.901
1UZ6	P_ARG_164	NH2	M_ASP_169	OD2	3.942
1UZ6	P_LYS_208	NZ	M_GLU_122	OE1	3.361
1UZ6	V_ARG_24	NH1	V_ASP_70	OD1	3.878
1UZ6	V_ARG_61	NH1	V_GLU_79	OE2	3.911
1UZ6	V_ARG_61	NH1	V_ASP_82	OD1	3.899
1UZ6	V_ARG_61	NH1	V_ASP_82	OD2	2.935
1UZ6	V_ARG_61	NH2	V_GLU_79	OE1	3.307
1UZ6	V_ARG_61	NH2	V_GLU_79	OE2	3.400
1UZ6	V_ARG_61	NH2	V_ASP_82	OD1	3.022
1UZ6	V_ARG_61	NH2	V_ASP_82	OD2	3.415
1UZ6	V_ARG_210	NH1	V_GLU_186	OE1	3.469
1UZ6	W_ARG_38	NH1	W_ASP_86	OD1	2.995
1UZ6	W_ARG_38	NH2	W_GLU_46	OE1	3.152
1UZ6	W_ARG_38	NH2	W_ASP_86	OD1	3.942
1UZ6	W_LYS_66	NZ	W_ASP_86	OD1	3.438
1UZ6	W_LYS_66	NZ	W_ASP_86	OD2	2.729
1UZ6	W_ARG_164	NH2	V_ASP_166	OD1	3.892
1UZ6	W_LYS_208	NZ	V_GLU_122	OE1	3.069
1UZ8	A_LYS_27	NZ	A_GLU_93	OE1	3.391
1UZ8	A_LYS_27	NZ	A_GLU_93	OE2	2.682
1UZ8	A_ARG_61	NH1	A_ASP_82	OD1	3.976
1UZ8	A_ARG_61	NH1	A_ASP_82	OD2	2.909
1UZ8	A_ARG_61	NH2	A_GLU_79	OE1	3.289
1UZ8	A_ARG_61	NH2	A_GLU_79	OE2	3.601
1UZ8	A_ARG_61	NH2	A_ASP_82	OD1	3.343
1UZ8	A_ARG_61	NH2	A_ASP_82	OD2	3.539
1UZ8	A_LYS_146	NZ	A_GLU_153	OE1	3.641
1UZ8	A_LYS_148	NZ	A_GLU_194	OE1	3.715
1UZ8	A_LYS_148	NZ	A_GLU_194	OE2	3.109
1UZ8	A_ARG_154	NH2	A_GLU_184	OE2	3.405
1UZ8	A_LYS_198	NZ	A_ASP_109	OD2	3.179
1UZ8	B_ARG_38	NH1	B_ASP_86	OD1	2.828
1UZ8	B_ARG_38	NH2	B_GLU_46	OE1	2.788
1UZ8	B_ARG_38	NH2	B_ASP_86	OD1	3.820
1UZ8	B_ARG_164	NH1	A_ASP_166	OD1	3.299
1UZ8	B_ARG_164	NH2	A_ASP_166	OD1	3.745
1UZ8	B_ARG_164	NH2	A_ASP_169	OD2	3.660
1UZ8	H_ARG_38	NH1	H_ASP_86	OD1	2.763
1UZ8	H_ARG_38	NH2	H_GLU_46	OE1	2.922
1UZ8	H_ARG_38	NH2	H_GLU_46	OE2	3.999
1UZ8	H_ARG_38	NH2	H_ASP_86	OD1	3.765
1UZ8	H_LYS_66	NZ	H_ASP_86	OD1	3.706
1UZ8	H_LYS_66	NZ	H_ASP_86	OD2	2.911
1UZ8	H_ARG_83	NH1	H_GLU_85	OE1	3.092
1UZ8	H_ARG_164	NH1	L_ASP_166	OD1	3.385
1UZ8	H_ARG_164	NH2	L_ASP_166	OD1	3.573
1UZ8	H_ARG_164	NH2	L_ASP_169	OD2	3.234
1UZ8	H_ARG_209	NH1	H_GLU_211	OE2	3.154
1UZ8	L_ARG_24	NH1	L_ASP_70	OD1	2.826
1UZ8	L_ARG_24	NH1	L_ASP_70	OD2	3.113
1UZ8	L_ARG_24	NH2	L_ASP_70	OD1	3.329
1UZ8	L_LYS_27	NZ	L_GLU_93	OE2	2.774
1UZ8	L_ARG_61	NH1	L_ASP_82	OD1	3.829
1UZ8	L_ARG_61	NH1	L_ASP_82	OD2	2.912
1UZ8	L_ARG_61	NH2	L_GLU_79	OE1	3.480
1UZ8	L_ARG_61	NH2	L_GLU_79	OE2	3.414
1UZ8	L_ARG_61	NH2	L_ASP_82	OD1	3.012

1UZ8	L_ARG_61	NH2	L_ASP_82	OD2	3.357
1UZ8	L_LYS_148	NZ	L_GLU_194	OE1	3.195
1UZ8	L_LYS_148	NZ	L_GLU_194	OE2	2.816
1UZ8	L_LYS_168	NZ	L_ASP_169	OD2	3.822
1UZ8	L_ARG_187	NH1	L_ASP_183	OD1	2.762
1UZ8	L_ARG_187	NH1	L_ASP_183	OD2	3.197
1UZ8	L_ARG_187	NH2	L_ASP_183	OD2	3.876
1UZ8	L_HIS_188	ND1	L_ASP_150	OD2	3.610
1UZ8	L_LYS_198	NZ	L_ASP_109	OD2	3.897
1V7M	L_ARG_60	NH1	L_GLU_80	OE2	3.088
1V7M	L_ARG_60	NH1	L_ASP_81	OD1	3.052
1V7M	L_ARG_60	NH1	L_ASP_81	OD2	3.141
1V7M	L_ARG_60	NH2	L_GLU_80	OE2	3.221
1V7M	L_ARG_95	NH1	H_GLU_50	OE1	3.532
1V7M	L_LYS_106	NZ	L_GLU_17	OE1	3.130
1V7M	L_LYS_106	NZ	L_GLU_17	OE2	3.699
1V7M	L_LYS_148	NZ	L_GLU_194	OE2	3.477
1V7M	L_ARG_154	NH1	L_GLU_184	OE1	3.773
1V7M	L_HIS_188	ND1	L_ASP_150	OD2	2.800
1V7M	H_ARG_38	NH1	H_GLU_46	OE1	2.783
1V7M	H_ARG_38	NH1	H_GLU_46	OE2	2.898
1V7M	H_ARG_38	NH2	H_ASP_92	OD1	2.675
1V7M	H_ARG_52	NH1	H_GLU_50	OE2	3.445
1V7M	H_LYS_54	NZ	H_ASP_76	OD2	3.910
1V7M	H_HIS_58	NE2	H_ASP_76	OD2	3.340
1V7M	H_LYS_67	NZ	H_GLU_64	OE2	3.635
1V7M	H_ARG_69	NH1	H_ASP_92	OD1	3.860
1V7M	H_ARG_69	NH2	H_ASP_92	OD1	3.348
1V7M	H_ARG_69	NH2	H_ASP_92	OD2	2.369
1V7M	H_ARG_74	NH2	H_ASP_76	OD1	3.636
1V7M	V_LYS_14	NZ	V_ASP_18	OD1	3.648
1V7M	V_ARG_98	NH2	H_ASP_31	OD1	3.697
1V7M	M_ARG_60	NH1	M_GLU_80	OE2	3.752
1V7M	M_ARG_60	NH1	M_ASP_81	OD1	2.835
1V7M	M_ARG_60	NH1	M_ASP_81	OD2	3.333
1V7M	M_ARG_60	NH2	M_GLU_80	OE2	3.575
1V7M	M_ARG_95	NH1	L_GLU_50	OE1	3.801
1V7M	M_LYS_102	NZ	M_GLU_104	OE1	2.649
1V7M	M_LYS_106	NZ	M_GLU_17	OE1	2.876
1V7M	M_LYS_148	NZ	M_GLU_194	OE2	3.647
1V7M	M_ARG_154	NH1	M_GLU_184	OE1	3.586
1V7M	M_ARG_154	NH1	M_GLU_184	OE2	3.164
1V7M	M_LYS_182	NZ	M_GLU_186	OE1	2.598
1V7M	M_LYS_182	NZ	M_GLU_186	OE2	3.298
1V7M	M_ARG_187	NH2	M_ASP_183	OD1	3.583
1V7M	M_HIS_188	ND1	M_ASP_150	OD2	3.144
1V7M	M_HIS_188	NE2	M_GLU_184	OE1	3.787
1V7M	I_LYS_3	NZ	I_GLU_1	OE1	3.725
1V7M	I_LYS_3	NZ	I_GLU_1	OE2	3.237
1V7M	I_ARG_38	NH1	I_GLU_46	OE1	2.802
1V7M	I_ARG_38	NH1	I_GLU_46	OE2	3.233
1V7M	I_ARG_38	NH2	I_ASP_92	OD1	2.882
1V7M	I_ARG_52	NH1	I_GLU_50	OE2	3.907
1V7M	I_HIS_58	NE2	I_ASP_76	OD2	3.052
1V7M	I_LYS_67	NZ	I_GLU_64	OE2	3.990
1V7M	I_ARG_69	NH1	I_ASP_92	OD1	3.419
1V7M	I_ARG_69	NH2	I_ASP_92	OD1	2.654
1V7M	I_ARG_69	NH2	I_ASP_92	OD2	2.603

1V7M	L_ARG_74	NH2	L_ASP_76	OD1	3.380
1V7M	X_LYS_14	NZ	X_ASP_18	OD1	3.674
1V7M	X_HIS_33	ND1	X_GLU_31	OE2	3.284
1V7M	X_LYS_59	NZ	X_GLU_56	OE2	3.569
1V7M	X_ARG_98	NH2	L_ASP_31	OD1	3.214
1V7M	X_ARG_117	NH1	X_ASP_45	OD1	3.802
1V7M	X_ARG_117	NH1	X_ASP_45	OD2	3.906
1V7N	L_ARG_60	NH1	L_ASP_81	OD1	2.332
1V7N	L_ARG_60	NH1	L_ASP_81	OD2	3.010
1V7N	L_ARG_60	NH2	L_GLU_80	OE2	2.836
1V7N	L_ARG_95	NH1	H_GLU_50	OE1	3.194
1V7N	L_LYS_102	NZ	L_ASP_164	OD1	2.653
1V7N	L_ARG_107	NH1	L_ASP_169	OD2	2.613
1V7N	L_ARG_107	NH1	O_GLU_78	OE2	3.587
1V7N	L_ARG_107	NH2	O_GLU_78	OE1	3.844
1V7N	L_ARG_107	NH2	O_GLU_78	OE2	2.214
1V7N	L_LYS_148	NZ	L_GLU_194	OE2	3.869
1V7N	L_ARG_154	NH2	L_GLU_184	OE1	2.591
1V7N	L_ARG_154	NH2	L_GLU_184	OE2	3.206
1V7N	L_LYS_182	NZ	L_GLU_186	OE2	3.250
1V7N	L_HIS_188	ND1	L_ASP_150	OD2	2.542
1V7N	L_LYS_198	NZ	L_ASP_109	OD2	2.675
1V7N	H_LYS_3	NZ	H_GLU_5	OE1	3.106
1V7N	H_ARG_38	NH1	H_GLU_46	OE1	2.776
1V7N	H_ARG_38	NH1	H_GLU_46	OE2	3.676
1V7N	H_ARG_38	NH1	H_ASP_92	OD1	3.973
1V7N	H_ARG_38	NH2	H_ASP_92	OD1	3.183
1V7N	H_LYS_43	NZ	H_GLU_46	OE2	3.925
1V7N	H_LYS_54	NZ	H_ASP_76	OD2	3.243
1V7N	H_HIS_58	NE2	H_ASP_76	OD1	3.889
1V7N	H_HIS_58	NE2	H_ASP_76	OD2	2.715
1V7N	H_LYS_67	NZ	H_GLU_64	OE2	2.803
1V7N	H_ARG_69	NH1	H_ASP_92	OD1	3.102
1V7N	H_ARG_69	NH1	H_ASP_92	OD2	3.339
1V7N	H_ARG_69	NH2	H_ASP_92	OD1	3.121
1V7N	H_ARG_69	NH2	H_ASP_92	OD2	2.212
1V7N	H_ARG_74	NH2	H_ASP_76	OD1	3.408
1V7N	H_LYS_78	NZ	H_ASP_75	OD2	3.016
1V7N	H_ARG_216	NH1	H_ASP_217	OD2	3.146
1V7N	H_ARG_216	NH2	Z_ASP_123	OD2	3.997
1V7N	M_ARG_60	NH1	M_ASP_81	OD1	2.547
1V7N	M_ARG_60	NH1	M_ASP_81	OD2	2.256
1V7N	M_ARG_60	NH2	M_GLU_80	OE2	3.293
1V7N	M_ARG_60	NH2	M_ASP_81	OD1	3.559
1V7N	M_ARG_95	NH1	L_GLU_50	OE1	2.984
1V7N	M_LYS_102	NZ	M_ASP_164	OD1	3.198
1V7N	M_ARG_107	NH1	M_ASP_169	OD2	3.983
1V7N	M_ARG_107	NH1	N_GLU_78	OE2	3.960
1V7N	M_ARG_107	NH2	N_GLU_78	OE1	3.607
1V7N	M_ARG_107	NH2	N_GLU_78	OE2	2.132
1V7N	M_ARG_154	NH1	M_GLU_184	OE1	3.775
1V7N	M_ARG_154	NH1	M_GLU_184	OE2	3.880
1V7N	M_ARG_154	NH2	M_GLU_184	OE1	2.821
1V7N	M_HIS_188	ND1	M_ASP_150	OD2	2.789
1V7N	M_LYS_198	NZ	M_ASP_109	OD1	2.627
1V7N	M_LYS_198	NZ	M_ASP_109	OD2	3.022
1V7N	L_LYS_3	NZ	L_GLU_5	OE1	2.717
1V7N	L_ARG_38	NH1	L_GLU_46	OE1	2.490

1V7N	L_ARG_38	NH1	L_GLU_46	OE2	3.766
1V7N	L_ARG_38	NH2	L_ASP_92	OD1	2.898
1V7N	L_ARG_52	NH1	L_GLU_50	OE2	3.407
1V7N	L_LYS_54	NZ	L_ASP_76	OD2	3.877
1V7N	L_HIS_58	NE2	L_ASP_76	OD2	3.223
1V7N	L_LYS_67	NZ	L_GLU_64	OE2	2.515
1V7N	L_ARG_69	NH1	L_ASP_92	OD1	3.853
1V7N	L_ARG_69	NH1	L_ASP_92	OD2	3.813
1V7N	L_ARG_69	NH2	L_ASP_92	OD1	3.126
1V7N	L_ARG_69	NH2	L_ASP_92	OD2	2.285
1V7N	L_ARG_74	NH2	L_ASP_76	OD1	3.069
1V7N	L_LYS_78	NZ	L_ASP_75	OD2	3.595
1V7N	L_ARG_216	NH1	L_ASP_217	OD1	3.402
1V7N	N_ARG_60	NH1	N_GLU_80	OE2	3.770
1V7N	N_ARG_60	NH1	N_ASP_81	OD1	3.278
1V7N	N_ARG_60	NH1	N_ASP_81	OD2	2.829
1V7N	N_ARG_60	NH2	N_GLU_80	OE2	3.679
1V7N	N_ARG_95	NH1	J_GLU_50	OE1	3.631
1V7N	N_LYS_102	NZ	N_GLU_104	OE1	3.217
1V7N	N_LYS_102	NZ	N_ASP_164	OD1	2.603
1V7N	N_ARG_107	NH1	N_ASP_169	OD2	2.506
1V7N	N_ARG_107	NH2	M_GLU_78	OE1	2.980
1V7N	N_ARG_107	NH2	M_GLU_78	OE2	2.369
1V7N	N_LYS_148	NZ	N_GLU_194	OE1	3.525
1V7N	N_LYS_148	NZ	N_GLU_194	OE2	3.387
1V7N	N_ARG_154	NH1	N_GLU_184	OE1	3.587
1V7N	N_ARG_154	NH2	N_GLU_184	OE1	2.367
1V7N	N_HIS_188	ND1	N_ASP_150	OD2	2.601
1V7N	N_LYS_198	NZ	N_ASP_109	OD1	3.661
1V7N	N_LYS_198	NZ	N_ASP_109	OD2	2.822
1V7N	J_LYS_3	NZ	J_GLU_5	OE1	2.975
1V7N	J_LYS_3	NZ	J_GLU_5	OE2	2.953
1V7N	J_ARG_38	NH1	J_GLU_46	OE1	2.786
1V7N	J_ARG_38	NH2	J_ASP_92	OD1	2.704
1V7N	J_LYS_43	NZ	J_GLU_46	OE1	2.811
1V7N	J_ARG_52	NH1	J_GLU_50	OE2	3.959
1V7N	J_HIS_61	NE2	J_GLU_50	OE2	3.467
1V7N	J_LYS_67	NZ	J_GLU_64	OE2	2.606
1V7N	J_ARG_69	NH2	J_ASP_92	OD1	2.762
1V7N	J_ARG_69	NH2	J_ASP_92	OD2	3.189
1V7N	J_ARG_74	NH2	J_ASP_76	OD1	2.889
1V7N	J_LYS_78	NZ	J_ASP_75	OD2	3.061
1V7N	J_ARG_216	NH2	J_ASP_217	OD1	3.973
1V7N	J_ARG_216	NH2	X_ASP_123	OD2	3.982
1V7N	O_ARG_60	NH1	O_ASP_81	OD1	2.582
1V7N	O_ARG_60	NH1	O_ASP_81	OD2	2.736
1V7N	O_ARG_95	NH1	K_GLU_50	OE1	2.735
1V7N	O_LYS_102	NZ	O_ASP_164	OD1	3.384
1V7N	O_ARG_107	NH1	L_GLU_78	OE1	3.650
1V7N	O_ARG_107	NH1	L_GLU_78	OE2	3.114
1V7N	O_ARG_107	NH1	O_ASP_169	OD2	3.206
1V7N	O_ARG_107	NH2	L_GLU_78	OE2	2.402
1V7N	O_ARG_154	NH1	O_GLU_184	OE1	2.811
1V7N	O_ARG_154	NH1	O_GLU_184	OE2	2.989
1V7N	O_ARG_154	NH2	O_GLU_184	OE1	2.352
1V7N	O_ARG_154	NH2	O_GLU_184	OE2	3.668
1V7N	O_HIS_188	ND1	O_ASP_150	OD2	2.853
1V7N	O_LYS_198	NZ	O_ASP_109	OD1	3.907

1V7N	O_LYS_198	NZ	O_ASP_109	OD2	2.580
1V7N	K_LYS_3	NZ	K_GLU_5	OE1	3.714
1V7N	K_LYS_3	NZ	K_GLU_5	OE2	3.152
1V7N	K_ARG_38	NH1	K_GLU_46	OE1	2.302
1V7N	K_ARG_38	NH1	K_GLU_46	OE2	3.483
1V7N	K_ARG_38	NH2	K_ASP_92	OD1	3.795
1V7N	K_ARG_38	NH2	K_ASP_92	OD2	3.370
1V7N	K_LYS_43	NZ	K_GLU_46	OE2	2.793
1V7N	K_ARG_52	NH1	K_GLU_50	OE2	3.501
1V7N	K_HIS_58	NE2	K_ASP_76	OD2	3.479
1V7N	K_ARG_69	NH1	K_ASP_92	OD2	3.967
1V7N	K_ARG_69	NH2	K_ASP_92	OD1	3.583
1V7N	K_ARG_69	NH2	K_ASP_92	OD2	2.311
1V7N	K_ARG_74	NH2	K_ASP_76	OD1	3.141
1V7N	K_ARG_74	NH2	K_ASP_76	OD2	3.766
1V7N	K_LYS_78	NZ	K_ASP_75	OD2	2.815
1V7N	K_ARG_216	NH1	K_ASP_217	OD1	2.786
1V7N	V_LYS_59	NZ	V_GLU_56	OE2	3.100
1V7N	V_ARG_98	NH2	H_ASP_31	OD1	3.580
1V7N	V_LYS_138	NZ	V_ASP_62	OD2	2.822
1V7N	X_LYS_59	NZ	X_GLU_56	OE2	2.913
1V7N	X_ARG_98	NH2	L_ASP_31	OD1	3.389
1V7N	X_ARG_117	NH2	X_ASP_45	OD1	3.524
1V7N	X_HIS_121	ND1	J_ASP_217	OD1	2.619
1V7N	X_HIS_121	NE2	J_ASP_217	OD1	3.422
1V7N	X_LYS_138	NZ	X_ASP_62	OD2	3.394
1V7N	Y_HIS_20	ND1	H_ASP_217	OD1	3.368
1V7N	Y_HIS_20	ND1	H_ASP_217	OD2	3.116
1V7N	Y_HIS_20	NE2	H_ASP_217	OD1	3.862
1V7N	Y_HIS_33	NE2	Y_GLU_31	OE1	3.707
1V7N	Y_LYS_59	NZ	Y_GLU_56	OE1	3.270
1V7N	Y_LYS_59	NZ	Y_GLU_56	OE2	2.783
1V7N	Y_HIS_121	ND1	L_ASP_217	OD1	3.108
1V7N	Y_HIS_133	ND1	Y_ASP_45	OD1	3.752
1V7N	Y_LYS_138	NZ	Y_ASP_45	OD2	3.882
1V7N	Z_HIS_33	ND1	Z_GLU_31	OE1	3.839
1V7N	Z_HIS_33	NE2	Z_GLU_31	OE1	3.105
1V7N	Z_LYS_59	NZ	Z_GLU_56	OE1	3.900
1V7N	Z_LYS_59	NZ	Z_GLU_56	OE2	3.150
1V7N	Z_ARG_98	NH2	K_ASP_31	OD1	3.622
1V7N	Z_HIS_133	NE2	Z_ASP_45	OD2	3.937
1V7N	Z_LYS_138	NZ	Z_ASP_45	OD1	2.983
1V7N	Z_ARG_140	NH2	M_GLU_212	OE1	3.768
1VER	A_ARG_25	NH1	A_ASP_4	OD1	3.368
1VER	A_LYS_40	NZ	A_GLU_76	OE2	2.714
1VER	A_ARG_54	NH1	A_ASP_77	OD2	3.441
1VER	A_ARG_54	NH2	A_ASP_77	OD1	3.240
1VER	A_ARG_54	NH2	A_ASP_77	OD2	3.161
1VER	A_ARG_74	NH1	A_ASP_72	OD2	2.935
1VER	A_LYS_102	NZ	A_GLU_46	OE1	3.941
1VER	A_LYS_102	NZ	A_GLU_46	OE2	3.470
1VES	A_ARG_25	NH1	A_ASP_4	OD2	3.079
1VES	A_ARG_25	NH1	B_ASP_4	OD1	3.636
1VES	A_ARG_25	NH1	B_ASP_4	OD2	2.836
1VES	A_ARG_25	NH2	B_ASP_4	OD1	2.879
1VES	A_ARG_25	NH2	B_ASP_4	OD2	3.552
1VES	A_LYS_32	NZ	A_GLU_30	OE2	2.725
1VES	A_ARG_38	NH2	A_ASP_77	OD1	3.118

1VES	A_ARG_54	NH1	A_ASP_77	OD1	3.920
1VES	A_ARG_54	NH1	A_ASP_77	OD2	2.727
1VES	A_ARG_54	NH2	A_ASP_77	OD1	3.109
1VES	A_ARG_54	NH2	A_ASP_77	OD2	3.297
1VES	A_ARG_74	NH1	A_GLU_76	OE2	3.745
1VES	A_LYS_104	NZ	A_GLU_46	OE1	2.629
1VES	A_LYS_104	NZ	A_GLU_46	OE2	3.276
1VES	B_ARG_25	NH1	A_ASP_4	OD1	3.762
1VES	B_ARG_25	NH1	A_ASP_4	OD2	2.782
1VES	B_ARG_25	NH1	B_ASP_4	OD2	3.050
1VES	B_ARG_25	NH2	A_ASP_4	OD1	3.070
1VES	B_ARG_25	NH2	A_ASP_4	OD2	3.548
1VES	B_ARG_38	NH2	B_ASP_77	OD1	3.081
1VES	B_ARG_54	NH1	B_ASP_77	OD2	2.889
1VES	B_ARG_54	NH2	B_ASP_77	OD1	3.186
1VES	B_ARG_54	NH2	B_ASP_77	OD2	3.405
1VES	B_ARG_74	NH1	B_GLU_76	OE1	3.458
1VES	B_ARG_74	NH2	B_GLU_76	OE1	3.401
1VES	B_LYS_104	NZ	B_GLU_46	OE1	2.701
1VES	B_LYS_104	NZ	B_GLU_46	OE2	2.906
1VFA	A_ARG_61	NH2	A_GLU_81	OE2	3.353
1VFA	A_ARG_61	NH2	A_ASP_82	OD1	2.725
1VFA	A_ARG_61	NH2	A_ASP_82	OD2	3.247
1VFA	A_ARG_96	NH1	B_GLU_98	OE1	2.794
1VFA	A_ARG_96	NH1	B_GLU_98	OE2	3.600
1VFA	A_ARG_96	NH2	B_GLU_98	OE1	3.537
1VFA	A_ARG_96	NH2	B_GLU_98	OE2	2.928
1VFA	A_LYS_103	NZ	A_GLU_105	OE1	2.845
1VFA	B_ARG_38	NH1	B_ASP_89	OD1	2.914
1VFA	B_ARG_38	NH2	B_GLU_46	OE1	2.995
1VFA	B_ARG_38	NH2	B_GLU_46	OE2	3.956
1VFA	B_ARG_38	NH2	B_ASP_89	OD1	3.945
1VFA	B_ARG_66	NH1	B_ASP_89	OD1	3.137
1VFA	B_ARG_66	NH1	B_ASP_89	OD2	3.571
1VFA	B_ARG_66	NH2	B_ASP_89	OD1	3.559
1VFA	B_ARG_66	NH2	B_ASP_89	OD2	2.619
1VFA	B_ARG_97	NH2	B_ASP_104	OD1	3.679
1VFA	B_ARG_97	NH2	B_ASP_104	OD2	2.862
1VFA	B_ARG_99	NH1	B_ASP_104	OD2	3.881
1VFA	B_ARG_99	NH2	B_ASP_100	OD2	3.016
1VFB	A_ARG_61	NH2	A_GLU_81	OE2	3.736
1VFB	A_ARG_61	NH2	A_ASP_82	OD1	2.846
1VFB	A_ARG_61	NH2	A_ASP_82	OD2	3.553
1VFB	A_ARG_96	NH1	B_GLU_98	OE1	2.821
1VFB	A_ARG_96	NH1	B_GLU_98	OE2	3.695
1VFB	A_ARG_96	NH2	B_GLU_98	OE1	3.393
1VFB	A_ARG_96	NH2	B_GLU_98	OE2	2.813
1VFB	A_LYS_107	NZ	A_GLU_17	OE2	3.099
1VFB	B_ARG_38	NH1	B_ASP_89	OD1	3.000
1VFB	B_ARG_38	NH2	B_GLU_46	OE1	3.296
1VFB	B_ARG_38	NH2	B_GLU_46	OE2	3.076
1VFB	B_ARG_38	NH2	B_ASP_89	OD1	3.911
1VFB	B_ARG_66	NH1	B_ASP_89	OD1	3.700
1VFB	B_ARG_66	NH1	B_ASP_89	OD2	2.886
1VFB	B_ARG_66	NH2	B_ASP_89	OD1	2.927
1VFB	B_ARG_66	NH2	B_ASP_89	OD2	3.546
1VFB	B_LYS_75	NZ	B_ASP_72	OD2	3.347
1VFB	B_ARG_97	NH2	B_ASP_104	OD1	3.680

1VFB	B_ARG_97	NH2	B_ASP_104	OD2	2.861
1VFB	B_ARG_102	NH1	B_ASP_100	OD2	3.203
1VFB	C_LYS_1	NZ	C_GLU_7	OE2	3.235
1VFB	C_ARG_61	NH1	C_ASP_48	OD2	3.212
1VFB	C_ARG_125	NH1	C_ASP_119	OD1	3.267
1VFB	C_ARG_125	NH1	C_ASP_119	OD2	3.059
1VFB	C_ARG_125	NH2	C_ASP_119	OD2	3.016
1W72	A_HIS_3	ND1	A_ASP_29	OD1	3.652
1W72	A_HIS_3	ND1	A_ASP_29	OD2	2.584
1W72	A_ARG_6	NH1	A_ASP_102	OD1	2.915
1W72	A_ARG_6	NH2	A_ASP_102	OD1	2.976
1W72	A_ARG_6	NH2	A_ASP_102	OD2	3.593
1W72	A_ARG_14	NH1	A_ASP_39	OD1	3.691
1W72	A_ARG_14	NH1	A_ASP_39	OD2	2.979
1W72	A_ARG_14	NH2	A_ASP_39	OD1	3.402
1W72	A_ARG_21	NH1	A_ASP_37	OD1	3.986
1W72	A_ARG_21	NH2	A_ASP_37	OD1	3.181
1W72	A_ARG_21	NH2	A_ASP_37	OD2	2.787
1W72	A_ARG_35	NH1	B_ASP_53	OD1	2.945
1W72	A_ARG_35	NH2	A_GLU_46	OE2	3.408
1W72	A_LYS_44	NZ	A_ASP_61	OD1	3.998
1W72	A_ARG_48	NH1	B_ASP_53	OD2	3.978
1W72	A_ARG_48	NH2	B_ASP_53	OD1	3.455
1W72	A_ARG_48	NH2	B_ASP_53	OD2	2.916
1W72	A_ARG_65	NH1	H_ASP_30	OD1	3.409
1W72	A_ARG_65	NH1	H_ASP_31	OD1	2.977
1W72	A_HIS_70	NE2	A_ASP_74	OD1	3.569
1W72	A_HIS_70	NE2	A_ASP_74	OD2	2.953
1W72	A_ARG_75	NH1	A_GLU_19	OE1	3.767
1W72	A_HIS_93	ND1	A_ASP_119	OD1	3.369
1W72	A_HIS_93	ND1	A_ASP_119	OD2	2.599
1W72	A_ARG_114	NH1	C_ASP_3	OD2	3.999
1W72	A_LYS_144	NZ	A_GLU_148	OE1	3.900
1W72	A_LYS_144	NZ	A_GLU_148	OE2	2.626
1W72	A_LYS_146	NZ	L_ASP_95A	OD1	3.112
1W72	A_LYS_146	NZ	L_ASP_95A	OD2	3.996
1W72	A_ARG_156	NH1	C_ASP_3	OD1	3.704
1W72	A_ARG_156	NH1	C_ASP_3	OD2	2.953
1W72	A_ARG_163	NH1	C_GLU_1	OE1	3.400
1W72	A_ARG_163	NH2	C_GLU_1	OE1	3.293
1W72	A_ARG_163	NH2	C_GLU_1	OE2	3.482
1W72	A_ARG_170	NH1	C_GLU_1	OE2	3.205
1W72	A_ARG_170	NH2	A_GLU_55	OE1	3.864
1W72	A_ARG_170	NH2	A_GLU_55	OE2	3.639
1W72	A_ARG_170	NH2	C_GLU_1	OE2	2.677
1W72	A_LYS_176	NZ	A_GLU_173	OE2	3.940
1W72	A_HIS_191	NE2	A_GLU_254	OE2	3.120
1W72	A_HIS_192	NE2	B_ASP_98	OD1	3.224
1W72	A_HIS_192	NE2	B_ASP_98	OD2	2.823
1W72	A_ARG_202	NH2	A_GLU_229	OE1	3.772
1W72	A_ARG_219	NH1	A_ASP_220	OD2	3.707
1W72	A_ARG_256	NH1	A_GLU_253	OE1	3.148
1W72	A_ARG_256	NH2	A_ASP_220	OD1	3.691
1W72	A_ARG_256	NH2	A_ASP_220	OD2	2.725
1W72	B_LYS_6	NZ	A_GLU_232	OE1	3.881
1W72	B_LYS_41	NZ	B_ASP_76	OD1	3.260
1W72	B_LYS_41	NZ	B_ASP_76	OD2	2.923
1W72	B_ARG_45	NH1	B_GLU_47	OE1	3.217

1W72	B_ARG_45	NH2	B_ASP_38	OD1	3.659
1W72	B_HIS_51	ND1	B_GLU_50	OE2	3.875
1W72	B_ARG_81	NH2	B_ASP_38	OD2	3.262
1W72	D_HIS_3	ND1	D_ASP_29	OD1	3.695
1W72	D_HIS_3	ND1	D_ASP_29	OD2	2.674
1W72	D_ARG_6	NH1	D_ASP_102	OD1	2.917
1W72	D_ARG_6	NH2	D_ASP_102	OD1	2.831
1W72	D_ARG_6	NH2	D_ASP_102	OD2	3.484
1W72	D_ARG_14	NH1	D_ASP_39	OD1	3.609
1W72	D_ARG_14	NH1	D_ASP_39	OD2	3.105
1W72	D_ARG_14	NH2	D_ASP_39	OD1	3.305
1W72	D_ARG_21	NH1	D_ASP_39	OD2	3.364
1W72	D_ARG_21	NH2	D_ASP_37	OD1	3.519
1W72	D_ARG_21	NH2	D_ASP_37	OD2	2.786
1W72	D_ARG_35	NH1	D_GLU_46	OE1	3.132
1W72	D_ARG_35	NH2	D_ASP_37	OD2	3.650
1W72	D_ARG_35	NH2	E_ASP_53	OD1	3.761
1W72	D_ARG_48	NH1	D_GLU_46	OE2	3.543
1W72	D_ARG_65	NH1	L_ASP_30	OD1	2.970
1W72	D_ARG_65	NH1	L_ASP_31	OD1	3.035
1W72	D_HIS_70	NE2	D_ASP_74	OD1	3.533
1W72	D_HIS_70	NE2	D_ASP_74	OD2	3.234
1W72	D_ARG_75	NH1	D_GLU_19	OE1	3.532
1W72	D_ARG_75	NH2	D_GLU_19	OE1	3.186
1W72	D_HIS_93	ND1	D_ASP_119	OD1	3.233
1W72	D_HIS_93	ND1	D_ASP_119	OD2	2.484
1W72	D_LYS_144	NZ	D_GLU_148	OE2	2.839
1W72	D_LYS_146	NZ	M_ASP_95A	OD2	3.397
1W72	D_ARG_156	NH1	F_ASP_3	OD1	3.644
1W72	D_ARG_156	NH1	F_ASP_3	OD2	3.082
1W72	D_ARG_157	NH2	D_GLU_154	OE2	3.289
1W72	D_ARG_163	NH1	F_GLU_1	OE1	3.609
1W72	D_ARG_163	NH1	F_GLU_1	OE2	3.022
1W72	D_ARG_163	NH2	D_ASP_166	OD2	3.278
1W72	D_ARG_170	NH2	D_GLU_55	OE1	3.599
1W72	D_ARG_170	NH2	D_GLU_55	OE2	3.371
1W72	D_HIS_191	NE2	D_GLU_254	OE2	2.873
1W72	D_HIS_192	NE2	E_ASP_98	OD2	3.123
1W72	D_ARG_219	NH1	D_ASP_220	OD2	3.836
1W72	D_ARG_256	NH1	D_ASP_220	OD2	3.881
1W72	D_ARG_256	NH2	D_GLU_253	OE1	3.311
1W72	E_LYS_6	NZ	D_GLU_232	OE2	2.863
1W72	E_LYS_41	NZ	E_ASP_76	OD1	3.809
1W72	E_LYS_41	NZ	E_ASP_76	OD2	3.639
1W72	E_ARG_45	NH1	E_ASP_38	OD1	3.708
1W72	E_ARG_81	NH1	E_ASP_38	OD2	3.844
1W72	H_ARG_38	NH1	H_ASP_86	OD1	3.015
1W72	H_ARG_38	NH2	H_GLU_46	OE1	3.060
1W72	H_ARG_38	NH2	H_GLU_46	OE2	3.921
1W72	H_ARG_38	NH2	H_ASP_86	OD1	3.932
1W72	H_ARG_66	NH1	H_ASP_86	OD1	3.676
1W72	H_ARG_66	NH1	H_ASP_86	OD2	2.720
1W72	H_ARG_66	NH2	H_ASP_86	OD1	3.173
1W72	H_ARG_66	NH2	H_ASP_86	OD2	3.657
1W72	H_ARG_83	NH1	H_GLU_85	OE1	3.964
1W72	H_ARG_94	NH2	H_ASP_101	OD1	3.551
1W72	H_ARG_94	NH2	H_ASP_101	OD2	2.836
1W72	H_LYS_145	NZ	L_GLU_124	OE2	2.720

1W72	H.LYS_221	NZ	L_GLU_123	OE1	2.737
1W72	H.LYS_221	NZ	L_GLU_123	OE2	3.946
1W72	H.LYS_222	NZ	H_GLU_226	OE2	2.721
1W72	L_ARG_38	NH1	L ASP_86	OD1	3.126
1W72	L_ARG_38	NH2	L_GLU_46	OE1	3.128
1W72	L_ARG_38	NH2	L_GLU_46	OE2	3.763
1W72	L_ARG_38	NH2	L ASP_86	OD1	3.826
1W72	L.LYS_64	NZ	L ASP_61	OD1	2.896
1W72	L_ARG_66	NH1	L ASP_86	OD1	3.873
1W72	L_ARG_66	NH1	L ASP_86	OD2	2.731
1W72	L_ARG_66	NH2	L ASP_86	OD1	3.149
1W72	L_ARG_66	NH2	L ASP_86	OD2	3.465
1W72	L_ARG_94	NH2	L ASP_101	OD1	3.478
1W72	L_ARG_94	NH2	L ASP_101	OD2	2.930
1W72	L_ARG_96	NH1	L ASP_101	OD2	3.483
1W72	L.LYS_145	NZ	M_GLU_124	OE2	2.470
1W72	L.LYS_222	NZ	L_GLU_226	OE2	3.445
1W72	L.LYS_228	NZ	M_GLU_123	OE2	3.514
1W72	L_ARG_31	NH2	L ASP_92	OD2	2.894
1W72	L_ARG_61	NH1	L ASP_82	OD1	3.611
1W72	L_ARG_61	NH1	L ASP_82	OD2	2.785
1W72	L_ARG_61	NH2	L_GLU_79	OE1	2.992
1W72	L_ARG_61	NH2	L ASP_82	OD1	3.068
1W72	L_ARG_61	NH2	L ASP_82	OD2	3.602
1W72	L.LYS_166	NZ	L_GLU_83	OE2	2.718
1W72	L.HIS_189	ND1	L ASP_151	OD2	2.787
1W72	M_ARG_31	NH2	M ASP_92	OD2	3.047
1W72	M_ARG_61	NH1	M ASP_82	OD1	3.754
1W72	M_ARG_61	NH1	M ASP_82	OD2	2.671
1W72	M_ARG_61	NH2	M_GLU_79	OE1	3.828
1W72	M_ARG_61	NH2	M_GLU_79	OE2	3.741
1W72	M_ARG_61	NH2	M ASP_82	OD1	2.860
1W72	M_ARG_61	NH2	M ASP_82	OD2	3.245
1W72	M.HIS_95B	NE2	L ASP_61	OD2	3.924
1W72	M.LYS_166	NZ	M_GLU_83	OE2	2.783
1W72	M.HIS_189	ND1	M ASP_151	OD2	2.728
1WEJ	L.HIS_30	ND1	F_GLU_104	OE1	2.984
1WEJ	L.HIS_30	ND1	F_GLU_104	OE2	2.758
1WEJ	L_ARG_61	NH2	L_GLU_81	OE2	3.867
1WEJ	L_ARG_61	NH2	L ASP_82	OD1	2.963
1WEJ	L_ARG_61	NH2	L ASP_82	OD2	3.742
1WEJ	L.LYS_142	NZ	L ASP_143	OD1	3.329
1WEJ	L.LYS_147	NZ	L_GLU_154	OE1	2.866
1WEJ	L.LYS_149	NZ	L_GLU_195	OE1	3.636
1WEJ	L.LYS_149	NZ	L_GLU_195	OE2	3.035
1WEJ	L_ARG_155	NH1	L_GLU_185	OE1	3.455
1WEJ	L_ARG_155	NH1	L_GLU_185	OE2	3.112
1WEJ	L_ARG_155	NH2	L_GLU_185	OE2	2.727
1WEJ	L.HIS_189	ND1	L ASP_151	OD2	3.628
1WEJ	L.HIS_189	NE2	L_GLU_185	OE2	3.295
1WEJ	L.LYS_199	NZ	L ASP_110	OD2	3.451
1WEJ	H_ARG_40	NH2	H_GLU_89	OE2	3.626
1WEJ	H_ARG_50	NH1	F_GLU_62	OE2	3.319
1WEJ	H_ARG_50	NH2	F_GLU_62	OE2	2.823
1WEJ	H.LYS_67	NZ	H ASP_90	OD1	3.685
1WEJ	H.LYS_67	NZ	H ASP_90	OD2	2.798
1WEJ	H.LYS_212	NZ	L_GLU_123	OE2	3.963
1WEJ	F.LYS_60	NZ	H ASP_100	OD2	3.322

1WEJ	F_LYS.87	NZ	F_GLU_90	OE2	3.504
1WEJ	F_LYS.88	NZ	F_GLU_92	OE2	3.066
1WEJ	F_LYS.99	NZ	F_GLU_61	OE2	2.733
1WZ1	L_ARG.24	NH1	L_ASP_75	OD2	3.952
1WZ1	L_ARG.66	NH1	L_GLU_84	OE1	3.457
1WZ1	L_ARG.66	NH1	L_GLU_84	OE2	3.613
1WZ1	L_ARG.66	NH2	L_GLU_84	OE2	3.590
1WZ1	L_ARG.66	NH2	L_GLU_86	OE2	2.822
1WZ1	L_ARG.66	NH2	L_ASP_87	OD1	2.607
1WZ1	L_ARG.66	NH2	L_ASP_87	OD2	3.494
1WZ1	H_ARG.38	NH1	H_GLU_46	OE1	3.212
1WZ1	H_ARG.38	NH1	H_GLU_46	OE2	3.069
1WZ1	H_ARG.38	NH2	H_ASP_92	OD2	2.708
1WZ1	H_ARG.52	NH1	H_GLU_50	OE2	3.191
1WZ1	H_HIS.58	NE2	H_ASP_76	OD2	3.006
1WZ1	H_ARG.69	NH1	H_ASP_92	OD1	3.703
1WZ1	H_ARG.69	NH1	H_ASP_92	OD2	3.712
1WZ1	H_ARG.69	NH2	H_ASP_92	OD1	2.195
1WZ1	H_ARG.69	NH2	H_ASP_92	OD2	3.555
1WZ1	H_ARG.74	NH2	H_ASP_76	OD1	3.331
1XF2	L_ARG.61	NH2	L_GLU_81	OE2	3.419
1XF2	L_ARG.61	NH2	L_ASP_82	OD1	3.006
1XF2	L_ARG.61	NH2	L_ASP_82	OD2	3.455
1XF2	L_LYS.149	NZ	L_GLU_195	OE1	3.344
1XF2	L_ARG.155	NH1	L_GLU_185	OE2	3.754
1XF2	L_ARG.155	NH2	L_GLU_185	OE2	2.954
1XF2	L_ARG.188	NH1	L_GLU_185	OE1	2.837
1XF2	L_HIS.189	ND1	L_ASP_151	OD2	3.000
1XF2	L_HIS.189	NE2	L_GLU_185	OE2	3.246
1XF2	L_ARG.211	NH1	L_GLU_187	OE1	3.085
1XF2	H_LYS.66	NZ	H_ASP_86	OD1	2.700
1XF2	H_LYS.66	NZ	H_ASP_86	OD2	3.586
1XF2	H_ARG.94	NH2	H_ASP_101	OD1	3.923
1XF2	H_ARG.94	NH2	H_ASP_101	OD2	3.252
1XF2	H_LYS.208	NZ	L_GLU_123	OE1	3.369
1XF2	H_LYS.208	NZ	L_GLU_123	OE2	2.577
1XF2	A_ARG.61	NH1	A_GLU_81	OE2	3.119
1XF2	A_ARG.61	NH1	A_ASP_82	OD1	2.988
1XF2	A_ARG.61	NH1	A_ASP_82	OD2	3.665
1XF2	A_LYS.149	NZ	A_GLU_195	OE2	3.121
1XF2	A_ARG.155	NH1	A_GLU_185	OE1	3.880
1XF2	A_ARG.155	NH1	A_GLU_185	OE2	2.861
1XF2	A_ARG.155	NH2	A_GLU_185	OE2	2.971
1XF2	A_ARG.188	NH2	A_GLU_185	OE1	3.702
1XF2	A_HIS.189	ND1	A_ASP_151	OD2	2.794
1XF2	A_LYS.199	NZ	A_ASP_110	OD2	3.768
1XF2	A_ARG.211	NH1	A_GLU_187	OE2	3.554
1XF2	B_LYS.66	NZ	B_ASP_86	OD1	2.668
1XF2	B_LYS.66	NZ	B_ASP_86	OD2	3.588
1XF2	B_ARG.94	NH2	B_ASP_101	OD1	3.898
1XF2	B_ARG.94	NH2	B_ASP_101	OD2	2.974
1XF2	B_LYS.208	NZ	A_GLU_123	OE2	2.913
1XGY	L_LYS.27	NZ	L_GLU_93	OE1	3.138
1XGY	L_LYS.27	NZ	L_GLU_93	OE2	3.725
1XGY	L_ARG.50	NH2	P_GLU_6	OE1	2.621
1XGY	L_ARG.61	NH1	L_ASP_82	OD1	2.794
1XGY	L_ARG.61	NH1	L_ASP_82	OD2	2.267
1XGY	L_ARG.61	NH2	L_GLU_79	OE1	3.265

1XGY	L_ARG.61	NH2	L_GLU_79	OE2	3.639
1XGY	L_ARG.61	NH2	L_GLU_81	OE2	3.975
1XGY	L_ARG.61	NH2	L_ASP_82	OD1	3.476
1XGY	L_ARG.61	NH2	L_ASP_82	OD2	3.700
1XGY	L_LYS_142	NZ	L_GLU_105	OE1	3.607
1XGY	L_LYS_147	NZ	L_GLU_195	OE1	2.404
1XGY	L_LYS_149	NZ	L_GLU_195	OE1	3.987
1XGY	L_LYS_149	NZ	L_GLU_195	OE2	2.719
1XGY	L_ARG.155	NH1	L_GLU_185	OE2	3.616
1XGY	L_ARG.155	NH2	L_GLU_185	OE2	2.613
1XGY	L_HIS_189	ND1	L_ASP_151	OD2	3.191
1XGY	L_LYS_199	NZ	L_ASP_110	OD1	2.374
1XGY	L_LYS_199	NZ	L_ASP_110	OD2	2.995
1XGY	H_ARG.40	NH1	H_GLU_85	OE1	3.102
1XGY	H_LYS.66	NZ	H_ASP_86	OD1	3.962
1XGY	H_LYS.66	NZ	H_ASP_86	OD2	2.962
1XGY	H_LYS_205	NZ	H_ASP_207	OD1	3.695
1XGY	H_LYS_208	NZ	L_GLU_123	OE2	3.768
1XGY	M_LYS.27	NZ	M_GLU_93	OE1	2.941
1XGY	M_LYS.27	NZ	M_GLU_93	OE2	3.832
1XGY	M_ARG.50	NH2	Q_GLU_6	OE1	3.022
1XGY	M_ARG.61	NH1	M_ASP_82	OD1	3.884
1XGY	M_ARG.61	NH1	M_ASP_82	OD2	2.768
1XGY	M_ARG.61	NH2	M_GLU_79	OE1	3.581
1XGY	M_ARG.61	NH2	M_GLU_79	OE2	3.865
1XGY	M_ARG.61	NH2	M_ASP_82	OD1	3.106
1XGY	M_ARG.61	NH2	M_ASP_82	OD2	3.415
1XGY	M_ARG.77	NH1	M_GLU_79	OE2	3.806
1XGY	M_LYS_142	NZ	M_GLU_105	OE1	2.680
1XGY	M_LYS_147	NZ	M_GLU_154	OE1	3.126
1XGY	M_LYS_147	NZ	M_GLU_154	OE2	3.008
1XGY	M_LYS_149	NZ	M_GLU_195	OE1	3.612
1XGY	M_LYS_149	NZ	M_GLU_195	OE2	2.488
1XGY	M_ARG.155	NH1	M_GLU_185	OE2	3.086
1XGY	M_ARG.155	NH2	M_GLU_185	OE1	3.630
1XGY	M_ARG.155	NH2	M_GLU_185	OE2	2.772
1XGY	M_HIS_189	ND1	M_ASP_151	OD2	3.229
1XGY	M_LYS_199	NZ	M_ASP_110	OD1	2.140
1XGY	M_LYS_199	NZ	M_ASP_110	OD2	2.774
1XGY	I_ARG.40	NH1	I_GLU_85	OE2	3.888
1XGY	I_LYS.66	NZ	I_ASP_86	OD1	3.839
1XGY	I_LYS.66	NZ	I_ASP_86	OD2	2.661
1XGY	I_LYS_205	NZ	I_ASP_207	OD1	3.293
1XGY	I_LYS_208	NZ	M_GLU_123	OE2	3.551
1XIW	A_LYS.52	NZ	A_ASP_48	OD1	3.395
1XIW	A_HIS.60	ND1	A_ASP_59	OD1	3.757
1XIW	A_HIS.60	NE2	A_ASP_59	OD1	3.245
1XIW	A_ARG.80	NH1	D_ASP_106	OD2	2.879
1XIW	A_ARG.80	NH2	A_GLU_35	OE1	3.061
1XIW	A_ARG.80	NH2	A_GLU_35	OE2	3.325
1XIW	A_ARG.94	NH1	A_GLU_68	OE2	2.956
1XIW	A_ARG.94	NH2	A_GLU_68	OE2	3.474
1XIW	A_ARG.94	NH2	B_GLU_7	OE1	3.648
1XIW	A_ARG.94	NH2	B_GLU_7	OE2	2.974
1XIW	B_LYS.2	NZ	A_ASP_42	OD1	3.017
1XIW	B_LYS.2	NZ	A_ASP_42	OD2	2.678
1XIW	B_ARG.11	NH1	B_ASP_38	OD1	3.352
1XIW	B_ARG.11	NH1	B_ASP_38	OD2	3.240

1XIW	B_ARG_36	NH2	B_GLU_6	OE1	3.782
1XIW	B_ARG_36	NH2	B_GLU_6	OE2	2.940
1XIW	B_ARG_42	NH1	B_GLU_7	OE2	2.789
1XIW	B_ARG_47	NH2	B_ASP_45	OD2	3.150
1XIW	C_ARG_25	NH1	C_ASP_71	OD1	2.681
1XIW	C_ARG_25	NH1	C_ASP_71	OD2	3.457
1XIW	C_ARG_31	NH1	A_ASP_86	OD1	2.919
1XIW	C_ARG_31	NH1	A_ASP_86	OD2	3.491
1XIW	C_ARG_31	NH2	A_ASP_86	OD1	3.709
1XIW	C_ARG_31	NH2	A_ASP_86	OD2	2.755
1XIW	C_ARG_54	NH1	F_GLU_6	OE1	2.951
1XIW	C_ARG_54	NH2	F_GLU_6	OE1	3.193
1XIW	C_ARG_54	NH2	F_GLU_6	OE2	3.073
1XIW	C_HIS_56	ND1	F_GLU_9	OE1	3.139
1XIW	C_HIS_56	ND1	F_GLU_9	OE2	2.963
1XIW	C_LYS_62	NZ	C_GLU_80	OE1	2.741
1XIW	C_LYS_62	NZ	C_ASP_83	OD1	3.773
1XIW	C_LYS_62	NZ	C_ASP_83	OD2	2.726
1XIW	D_LYS_55	NZ	A_ASP_57	OD1	3.690
1XIW	D_LYS_63	NZ	D_GLU_46	OE1	2.923
1XIW	D_LYS_63	NZ	D_GLU_46	OE2	3.778
1XIW	D_LYS_67	NZ	D_ASP_90	OD1	3.837
1XIW	D_LYS_67	NZ	D_ASP_90	OD2	2.934
1XIW	D_ARG_98	NH2	D_ASP_110	OD1	3.519
1XIW	D_ARG_98	NH2	D_ASP_110	OD2	2.851
1XIW	E_HIS_60	ND1	E_ASP_59	OD1	3.485
1XIW	E_HIS_60	NE2	E_ASP_59	OD1	2.909
1XIW	E_ARG_80	NH1	H_ASP_106	OD2	2.741
1XIW	E_ARG_80	NH2	E_GLU_35	OE1	3.223
1XIW	E_ARG_80	NH2	E_GLU_35	OE2	2.970
1XIW	E_ARG_94	NH1	E_GLU_68	OE2	3.220
1XIW	E_ARG_94	NH2	E_GLU_68	OE2	2.578
1XIW	E_ARG_94	NH2	F_GLU_7	OE2	3.577
1XIW	F_LYS_2	NZ	E_ASP_42	OD1	3.079
1XIW	F_LYS_2	NZ	E_ASP_42	OD2	3.491
1XIW	F_ARG_11	NH1	F_ASP_38	OD1	3.262
1XIW	F_ARG_11	NH1	F_ASP_38	OD2	3.138
1XIW	F_ARG_36	NH2	F_GLU_6	OE1	3.809
1XIW	F_ARG_36	NH2	F_GLU_6	OE2	2.975
1XIW	F_ARG_42	NH2	F_GLU_7	OE2	3.760
1XIW	F_ARG_47	NH2	F_ASP_45	OD2	3.702
1XIW	G_ARG_31	NH1	E_ASP_86	OD1	3.076
1XIW	G_ARG_31	NH1	E_ASP_86	OD2	3.219
1XIW	G_ARG_31	NH2	E_ASP_86	OD2	2.817
1XIW	G_ARG_54	NH1	B_GLU_6	OE1	2.839
1XIW	G_ARG_54	NH2	B_GLU_6	OE1	3.146
1XIW	G_ARG_54	NH2	B_GLU_6	OE2	3.222
1XIW	G_HIS_56	ND1	B_GLU_9	OE1	2.509
1XIW	G_HIS_56	ND1	B_GLU_9	OE2	3.961
1XIW	G_LYS_62	NZ	G_GLU_80	OE1	2.856
1XIW	G_LYS_62	NZ	G_ASP_83	OD1	3.394
1XIW	G_LYS_62	NZ	G_ASP_83	OD2	2.415
1XIW	H_LYS_67	NZ	H_ASP_90	OD1	3.722
1XIW	H_LYS_67	NZ	H_ASP_90	OD2	3.068
1XIW	H_ARG_98	NH2	H_ASP_110	OD1	3.520
1XIW	H_ARG_98	NH2	H_ASP_110	OD2	2.683
1YC7	A_ARG_38	NH1	A_ASP_89	OD1	2.902
1YC7	A_ARG_38	NH2	A_GLU_46	OE2	3.097

1YC7	A_ARG.38	NH2	A_ASP.89	OD1	3.949
1YC7	A_LYS.64	NZ	A_ASP.61	OD1	2.723
1YC7	A_LYS.64	NZ	A_ASP.61	OD2	3.957
1YC7	A_ARG.66	NH1	A_ASP.89	OD1	2.987
1YC7	A_ARG.66	NH1	A_ASP.89	OD2	3.524
1YC7	A_ARG.66	NH2	A_ASP.89	OD1	3.641
1YC7	A_ARG.66	NH2	A_ASP.89	OD2	2.704
1YC7	B_ARG.38	NH1	B_ASP.89	OD1	2.874
1YC7	B_ARG.38	NH2	B_GLU.46	OE2	3.356
1YC7	B_ARG.38	NH2	B_ASP.89	OD1	3.943
1YC7	B_ARG.66	NH1	B_ASP.89	OD1	3.049
1YC7	B_ARG.66	NH1	B_ASP.89	OD2	3.521
1YC7	B_ARG.66	NH2	B_ASP.89	OD1	3.788
1YC7	B_ARG.66	NH2	B_ASP.89	OD2	2.754
1YC8	A_ARG.38	NH1	A_ASP.89	OD1	2.913
1YC8	A_ARG.38	NH2	A_GLU.46	OE1	3.560
1YC8	A_ARG.38	NH2	A_GLU.46	OE2	3.758
1YC8	A_LYS.64	NZ	A_ASP.61	OD1	3.092
1YC8	A_ARG.66	NH1	A_ASP.89	OD1	2.701
1YC8	A_ARG.66	NH1	A_ASP.89	OD2	3.515
1YC8	A_ARG.66	NH2	A_ASP.89	OD1	3.553
1YC8	A_ARG.66	NH2	A_ASP.89	OD2	2.766
1YC8	B_ARG.38	NH1	B_ASP.89	OD1	2.947
1YC8	B_ARG.38	NH2	B_GLU.46	OE1	3.738
1YC8	B_ARG.38	NH2	B_GLU.46	OE2	3.326
1YC8	B_ARG.38	NH2	B_ASP.89	OD1	3.942
1YC8	B_LYS.64	NZ	B_ASP.61	OD1	2.743
1YC8	B_ARG.66	NH1	B_ASP.89	OD1	2.596
1YC8	B_ARG.66	NH1	B_ASP.89	OD2	2.980
1YC8	B_ARG.66	NH2	B_ASP.89	OD1	3.764
1YC8	B_ARG.66	NH2	B_ASP.89	OD2	2.564
1YEI	L_LYS.24	NZ	L_ASP.70	OD1	3.938
1YEI	L_LYS.30	NZ	H_GLU.100B	OE1	2.979
1YEI	L_LYS.45	NZ	H_ASP.101	OD1	2.746
1YEI	L_LYS.45	NZ	H_ASP.101	OD2	3.891
1YEI	L_ARG.46	NH2	L_ASP.55	OD1	3.728
1YEI	L_ARG.46	NH2	L_ASP.55	OD2	2.823
1YEI	L_ARG.46	NH2	H_ASP.101	OD1	3.707
1YEI	L_HIS.49	ND1	L_ASP.55	OD1	2.748
1YEI	L_HIS.49	ND1	L_ASP.55	OD2	3.813
1YEI	L_HIS.49	NE2	H_ASP.100C	OD1	3.542
1YEI	L_ARG.61	NH1	L_ASP.82	OD1	3.376
1YEI	L_ARG.61	NH1	L_ASP.82	OD2	2.794
1YEI	L_ARG.61	NH2	L_ASP.82	OD1	3.026
1YEI	L_ARG.61	NH2	L_ASP.82	OD2	3.859
1YEI	L_ARG.77	NH1	L_GLU.79	OE2	2.773
1YEI	L_LYS.103	NZ	L_ASP.165	OD1	3.211
1YEI	L_LYS.149	NZ	L_GLU.195	OE1	3.290
1YEI	L_LYS.149	NZ	L_GLU.195	OE2	3.378
1YEI	L_ARG.155	NH1	L_GLU.185	OE1	3.467
1YEI	L_ARG.155	NH1	L_GLU.185	OE2	2.801
1YEI	L_ARG.155	NH2	L_GLU.185	OE1	2.921
1YEI	L_ARG.155	NH2	L_GLU.185	OE2	3.794
1YEI	L_LYS.183	NZ	L_GLU.187	OE1	2.856
1YEI	L_LYS.183	NZ	L_GLU.187	OE2	3.649
1YEI	L_HIS.189	ND1	L_ASP.151	OD2	3.711
1YEI	L_HIS.189	NE2	L_GLU.185	OE2	2.707
1YEI	L_LYS.199	NZ	L_ASP.110	OD1	3.088

1YEI	L_LYS_199	NZ	L_ASP_110	OD2	3.565
1YEI	H_LYS_62	NZ	H_GLU_46	OE1	2.847
1YEI	H_LYS_62	NZ	H_GLU_46	OE2	3.937
1YEI	H_LYS_64	NZ	H_GLU_61	OE1	2.773
1YEI	H_LYS_66	NZ	H_ASP_86	OD1	3.924
1YEI	H_LYS_66	NZ	H_ASP_86	OD2	2.870
1YEI	H_LYS_216	NZ	H_ASP_218	OD1	3.297
1YEI	H_LYS_216	NZ	H_ASP_218	OD2	3.256
1YEJ	L_LYS_24	NZ	L_ASP_70	OD1	3.770
1YEJ	L_LYS_45	NZ	H_ASP_101	OD1	2.790
1YEJ	L_LYS_45	NZ	H_ASP_101	OD2	3.988
1YEJ	L_ARG_46	NH2	L_ASP_55	OD1	3.922
1YEJ	L_ARG_46	NH2	L_ASP_55	OD2	2.854
1YEJ	L_ARG_46	NH2	H_ASP_101	OD1	3.745
1YEJ	L_HIS_49	ND1	L_ASP_55	OD1	2.776
1YEJ	L_HIS_49	ND1	L_ASP_55	OD2	3.660
1YEJ	L_HIS_49	NE2	H_ASP_100C	OD1	3.536
1YEJ	L_LYS_53	NZ	H_ASP_100C	OD1	3.377
1YEJ	L_LYS_53	NZ	H_ASP_100C	OD2	3.298
1YEJ	L_ARG_61	NH1	L_ASP_82	OD1	3.561
1YEJ	L_ARG_61	NH1	L_ASP_82	OD2	2.867
1YEJ	L_ARG_61	NH2	L_ASP_82	OD1	3.034
1YEJ	L_ARG_61	NH2	L_ASP_82	OD2	3.799
1YEJ	L_ARG_77	NH1	L_GLU_79	OE2	2.713
1YEJ	L_LYS_103	NZ	L_ASP_165	OD1	3.615
1YEJ	L_LYS_149	NZ	L_GLU_195	OE1	3.131
1YEJ	L_LYS_149	NZ	L_GLU_195	OE2	3.063
1YEJ	L_ARG_155	NH1	L_GLU_185	OE1	3.833
1YEJ	L_ARG_155	NH1	L_GLU_185	OE2	2.788
1YEJ	L_ARG_155	NH2	L_GLU_185	OE1	2.959
1YEJ	L_ARG_155	NH2	L_GLU_185	OE2	3.459
1YEJ	L_LYS_183	NZ	L_ASP_184	OD1	3.622
1YEJ	L_LYS_183	NZ	L_GLU_187	OE1	2.703
1YEJ	L_LYS_183	NZ	L_GLU_187	OE2	3.871
1YEJ	L_HIS_189	ND1	L_ASP_151	OD2	3.584
1YEJ	L_HIS_189	NE2	L_GLU_185	OE2	2.940
1YEJ	L_LYS_199	NZ	L_ASP_110	OD1	3.252
1YEJ	L_LYS_199	NZ	L_ASP_110	OD2	3.582
1YEJ	L_ARG_211	NH2	L_GLU_213	OE2	3.445
1YEJ	H_LYS_62	NZ	H_GLU_46	OE1	3.693
1YEJ	H_LYS_62	NZ	H_GLU_46	OE2	2.771
1YEJ	H_LYS_64	NZ	H_GLU_61	OE1	2.970
1YEJ	H_LYS_66	NZ	H_ASP_86	OD1	3.807
1YEJ	H_LYS_66	NZ	H_ASP_86	OD2	2.899
1YEJ	H_LYS_220	NZ	H_GLU_222	OE2	3.507
1YEK	L_LYS_30	NZ	H_GLU_100B	OE1	2.464
1YEK	L_LYS_45	NZ	H_ASP_101	OD1	2.830
1YEK	L_ARG_46	NH2	L_ASP_55	OD1	3.853
1YEK	L_ARG_46	NH2	L_ASP_55	OD2	2.868
1YEK	L_ARG_46	NH2	H_ASP_101	OD1	3.853
1YEK	L_HIS_49	ND1	L_ASP_55	OD1	2.761
1YEK	L_HIS_49	ND1	L_ASP_55	OD2	3.901
1YEK	L_HIS_49	NE2	H_ASP_100C	OD1	3.610
1YEK	L_ARG_61	NH1	L_ASP_82	OD1	3.781
1YEK	L_ARG_61	NH1	L_ASP_82	OD2	2.826
1YEK	L_ARG_61	NH2	L_ASP_82	OD1	2.807
1YEK	L_ARG_61	NH2	L_ASP_82	OD2	3.333
1YEK	L_ARG_77	NH1	L_GLU_79	OE1	3.282

1YEK	L_ARG_77	NH1	L_GLU_79	OE2	3.016
1YEK	L_LYS_103	NZ	L_ASP_165	OD1	3.840
1YEK	L_LYS_149	NZ	L_GLU_195	OE1	3.270
1YEK	L_LYS_149	NZ	L_GLU_195	OE2	3.257
1YEK	L_ARG_155	NH1	L_GLU_185	OE1	3.905
1YEK	L_ARG_155	NH1	L_GLU_185	OE2	2.816
1YEK	L_ARG_155	NH2	L_GLU_185	OE1	3.007
1YEK	L_ARG_155	NH2	L_GLU_185	OE2	3.425
1YEK	L_LYS_169	NZ	L_ASP_167	OD1	3.838
1YEK	L_LYS_183	NZ	L_ASP_184	OD1	3.851
1YEK	L_LYS_183	NZ	L_GLU_187	OE1	2.883
1YEK	L_HIS_189	ND1	L_ASP_151	OD2	3.477
1YEK	L_HIS_189	NE2	L_GLU_185	OE2	2.892
1YEK	L_LYS_199	NZ	L_ASP_110	OD1	3.770
1YEK	L_LYS_199	NZ	L_ASP_110	OD2	3.854
1YEK	L_ARG_211	NH2	L_GLU_213	OE1	3.144
1YEK	L_ARG_211	NH2	L_GLU_213	OE2	3.561
1YEK	H_LYS_62	NZ	H_GLU_46	OE1	3.791
1YEK	H_LYS_62	NZ	H_GLU_46	OE2	2.855
1YEK	H_LYS_64	NZ	H_GLU_61	OE1	2.862
1YEK	H_LYS_66	NZ	H_ASP_86	OD1	3.789
1YEK	H_LYS_66	NZ	H_ASP_86	OD2	2.810
1YEK	H_LYS_216	NZ	H_ASP_218	OD1	2.879
1YEK	H_LYS_216	NZ	H_ASP_218	OD2	3.161
1YEK	H_LYS_220	NZ	H_GLU_222	OE1	3.196
1YEK	H_LYS_220	NZ	H_GLU_222	OE2	3.085
1YNT	A_ARG_24	NH1	A_ASP_70	OD1	3.062
1YNT	A_ARG_24	NH1	C_ASP_1070	OD2	3.114
1YNT	A_ARG_24	NH2	C_ASP_1070	OD2	3.728
1YNT	A_ARG_61	NH1	A_ASP_82	OD1	3.482
1YNT	A_ARG_61	NH1	A_ASP_82	OD2	2.608
1YNT	A_ARG_61	NH2	A_ASP_82	OD1	2.789
1YNT	A_ARG_61	NH2	A_ASP_82	OD2	2.940
1YNT	A_LYS_142	NZ	A_GLU_105	OE1	3.414
1YNT	A_LYS_142	NZ	A_GLU_105	OE2	3.809
1YNT	A_LYS_149	NZ	A_GLU_195	OE1	3.930
1YNT	A_LYS_149	NZ	A_GLU_195	OE2	3.328
1YNT	A_ARG_155	NH1	A_GLU_185	OE1	3.418
1YNT	A_ARG_155	NH2	A_GLU_185	OE1	2.764
1YNT	A_ARG_155	NH2	A_GLU_185	OE2	3.917
1YNT	A_LYS_183	NZ	A_GLU_187	OE1	3.129
1YNT	A_LYS_183	NZ	A_GLU_187	OE2	2.879
1YNT	A_LYS_199	NZ	A_ASP_110	OD1	3.520
1YNT	A_LYS_199	NZ	A_ASP_110	OD2	2.749
1YNT	B_LYS_538	NZ	B_ASP_590	OD1	3.512
1YNT	B_LYS_563	NZ	A_ASP_1	OD1	2.935
1YNT	B_LYS_563	NZ	A_ASP_1	OD2	3.384
1YNT	B_ARG_598	NH1	B_ASP_606	OD1	3.368
1YNT	B_ARG_598	NH1	B_ASP_606	OD2	3.829
1YNT	B_LYS_713	NZ	A_GLU_123	OE1	3.645
1YNT	B_LYS_714	NZ	B_GLU_716	OE1	2.761
1YNT	B_LYS_714	NZ	B_GLU_716	OE2	3.569
1YNT	C_ARG_1024	NH1	A_ASP_70	OD2	3.173
1YNT	C_ARG_1024	NH1	C_ASP_1070	OD1	3.033
1YNT	C_ARG_1024	NH2	A_ASP_70	OD2	3.802
1YNT	C_ARG_1061	NH1	C_ASP_1082	OD1	3.503
1YNT	C_ARG_1061	NH1	C_ASP_1082	OD2	2.533
1YNT	C_ARG_1061	NH2	C_ASP_1082	OD1	2.790

1YNT	C_ARG_1061	NH2	C_ASP_1082	OD2	2.886
1YNT	C_LYS_1107	NZ	E_GLU_869	OE1	3.719
1YNT	C_LYS_1142	NZ	C_GLU_1105	OE1	3.297
1YNT	C_LYS_1142	NZ	C_GLU_1105	OE2	3.821
1YNT	C_LYS_1149	NZ	C_GLU_1195	OE2	3.387
1YNT	C_ARG_1155	NH1	C_GLU_1185	OE1	3.385
1YNT	C_ARG_1155	NH2	C_GLU_1185	OE1	2.679
1YNT	C_ARG_1155	NH2	C_GLU_1185	OE2	3.830
1YNT	C_LYS_1183	NZ	C_GLU_1187	OE1	3.084
1YNT	C_LYS_1183	NZ	C_GLU_1187	OE2	2.801
1YNT	C_LYS_1199	NZ	C_ASP_1110	OD1	3.564
1YNT	C_LYS_1199	NZ	C_ASP_1110	OD2	2.804
1YNT	D_LYS_1538	NZ	D_ASP_1590	OD1	3.573
1YNT	D_LYS_1563	NZ	C_ASP_1001	OD1	2.913
1YNT	D_LYS_1563	NZ	C_ASP_1001	OD2	3.385
1YNT	D_ARG_1598	NH1	D_ASP_1606	OD1	3.332
1YNT	D_ARG_1598	NH1	D_ASP_1606	OD2	3.789
1YNT	D_LYS_1713	NZ	C_GLU_1123	OE1	3.557
1YNT	D_LYS_1714	NZ	D_GLU_1716	OE1	2.757
1YNT	D_LYS_1714	NZ	D_GLU_1716	OE2	3.550
1YNT	E_LYS_824	NZ	A_ASP_143	OD1	3.012
1YNT	E_LYS_824	NZ	A_ASP_143	OD2	3.238
1YNT	E_LYS_833	NZ	A_ASP_17	OD2	3.941
1YNT	E_ARG_852	NH1	E_GLU_845	OE1	3.602
1YNT	E_ARG_852	NH1	E_GLU_849	OE2	3.768
1YNT	E_LYS_878	NZ	E_ASP_867	OD2	2.972
1YNT	F_LYS_2036	NZ	F_ASP_2089	OD2	3.981
1YNT	F_ARG_2051	NH1	F_ASP_2078	OD1	3.866
1YNT	F_LYS_2115	NZ	F_ASP_2014	OD1	3.292
1YNT	F_ARG_2141	NH2	F_GLU_2100	OE2	3.866
1YNT	F_LYS_2154	NZ	F_GLU_2252	OE1	3.701
1YNT	F_LYS_2154	NZ	F_GLU_2252	OE2	3.571
1YNT	F_LYS_2169	NZ	F_ASP_2214	OD1	3.970
1YNT	F_LYS_2231	NZ	F_GLU_2229	OE2	3.851
1YNT	F_HIS_2245	NE2	F_GLU_2243	OE2	3.227
1YNT	F_HIS_2246	ND1	F_ASP_2147	OD1	3.500
1YNT	G_ARG_3051	NH1	G_ASP_3078	OD1	3.903
1YNT	G_LYS_3115	NZ	G_ASP_3014	OD1	3.279
1YNT	G_ARG_3141	NH2	G_GLU_3100	OE2	3.839
1YNT	G_LYS_3169	NZ	G_ASP_3214	OD1	3.964
1YNT	G_LYS_3231	NZ	G_GLU_3229	OE2	3.832
1YNT	G_HIS_3245	NE2	G_GLU_3243	OE2	3.216
1YNT	G_HIS_3246	ND1	G_ASP_3147	OD1	3.543
1YQV	L_ARG_46	NH2	H_ASP_101	OD2	3.072
1YQV	L_ARG_61	NH2	L_GLU_81	OE2	3.786
1YQV	L_ARG_61	NH2	L_ASP_82	OD1	2.822
1YQV	L_ARG_61	NH2	L_ASP_82	OD2	3.604
1YQV	L_LYS_103	NZ	L_GLU_105	OE2	2.814
1YQV	L_LYS_147	NZ	L_GLU_154	OE1	3.872
1YQV	L_LYS_149	NZ	L_GLU_195	OE1	3.292
1YQV	L_LYS_149	NZ	L_GLU_195	OE2	3.231
1YQV	L_ARG_155	NH1	L_GLU_185	OE2	3.246
1YQV	L_ARG_155	NH2	L_GLU_185	OE1	3.852
1YQV	L_ARG_155	NH2	L_GLU_185	OE2	3.444
1YQV	L_LYS_183	NZ	L_GLU_187	OE1	3.191
1YQV	L_LYS_183	NZ	L_GLU_187	OE2	2.706
1YQV	L_ARG_188	NH2	L_ASP_184	OD2	3.511
1YQV	L_HIS_189	ND1	L_ASP_151	OD2	2.829

1YQV	L_LYS_199	NZ	L_ASP_110	OD2	3.414
1YQV	H_ARG_40	NH1	H_GLU_85	OE1	3.131
1YQV	H_ARG_40	NH2	H_GLU_46	OE1	3.444
1YQV	H_ARG_62	NH1	H_GLU_46	OE2	2.704
1YQV	H_ARG_62	NH2	H_GLU_46	OE1	3.964
1YQV	H_ARG_62	NH2	H_GLU_46	OE2	2.670
1YQV	H_LYS_66	NZ	H_ASP_86	OD1	3.613
1YQV	H_LYS_66	NZ	H_ASP_86	OD2	2.967
1YQV	H_LYS_221	NZ	L_GLU_123	OE1	3.123
1YQV	H_LYS_221	NZ	L_GLU_123	OE2	2.724
1YQV	Y_LYS_1	NZ	Y_GLU_7	OE1	3.896
1YQV	Y_LYS_1	NZ	Y_GLU_7	OE2	2.890
1YQV	Y_LYS_13	NZ	Y_ASP_18	OD2	3.870
1YQV	Y_ARG_45	NH1	H_GLU_50	OE1	3.514
1YQV	Y_ARG_45	NH1	H_GLU_50	OE2	2.957
1YQV	Y_ARG_68	NH1	H_GLU_50	OE1	2.746
1YQV	Y_ARG_68	NH1	H_GLU_50	OE2	3.759
1YQV	Y_ARG_68	NH2	H_GLU_50	OE1	3.492
1YQV	Y_ARG_68	NH2	H_GLU_50	OE2	2.963
1YQV	Y_ARG_125	NH1	Y_ASP_119	OD2	3.693
1YQV	Y_ARG_125	NH2	Y_ASP_119	OD1	3.830
1YQV	Y_ARG_125	NH2	Y_ASP_119	OD2	2.874
1YYL	G_LYS_121	NZ	G_GLU_429	OE2	3.711
1YYL	G_HIS_249	NE2	G_GLU_482	OE1	2.847
1YYL	G_LYS_282	NZ	G_GLU_275	OE1	2.882
1YYL	G_LYS_348	NZ	G_GLU_269	OE1	2.580
1YYL	G_LYS_357	NZ	G_GLU_466	OE2	3.616
1YYL	G_ARG_419	NH1	H_GLU_100D	OE2	3.749
1YYL	G_ARG_419	NH2	H_GLU_99	OE2	2.852
1YYL	G_ARG_419	NH2	H_GLU_100D	OE1	3.510
1YYL	G_ARG_419	NH2	H_GLU_100D	OE2	2.773
1YYL	G_ARG_456	NH1	G_GLU_466	OE1	3.131
1YYL	G_ARG_469	NH2	G_ASP_457	OD1	3.629
1YYL	G_ARG_469	NH2	G_ASP_457	OD2	3.271
1YYL	G_ARG_476	NH1	G_GLU_102	OE1	3.069
1YYL	G_ARG_476	NH1	G_GLU_102	OE2	3.149
1YYL	G_ARG_476	NH2	G_ASP_474	OD1	3.673
1YYL	G_ARG_476	NH2	G_ASP_474	OD2	3.290
1YYL	G_ARG_480	NH1	G_ASP_477	OD1	2.475
1YYL	L_ARG_24	NH1	L_GLU_70	OE2	3.902
1YYL	L_ARG_24	NH2	L_GLU_70	OE2	2.664
1YYL	L_ARG_61	NH2	L_GLU_81	OE1	2.377
1YYL	L_ARG_61	NH2	L_ASP_82	OD1	2.888
1YYL	L_ARG_61	NH2	L_ASP_82	OD2	3.800
1YYL	L_LYS_149	NZ	L_GLU_195	OE1	3.064
1YYL	L_HIS_189	ND1	L_ASP_151	OD2	2.706
1YYL	H_ARG_31	NH2	H_ASP_100A	OD1	2.948
1YYL	H_ARG_31	NH2	H_ASP_100A	OD2	3.167
1YYL	H_ARG_38	NH1	H_GLU_46	OE1	3.897
1YYL	H_ARG_38	NH1	H_GLU_46	OE2	2.772
1YYL	H_ARG_38	NH2	H_ASP_86	OD2	3.486
1YYL	H_ARG_50	NH2	H_GLU_97	OE1	3.557
1YYL	H_ARG_50	NH2	H_GLU_97	OE2	2.825
1YYL	H_ARG_66	NH1	H_ASP_86	OD1	3.071
1YYL	H_ARG_66	NH2	H_ASP_86	OD1	3.527
1YYL	H_ARG_66	NH2	H_ASP_86	OD2	3.411
1YYL	H_ARG_82A	NH2	H_GLU_81	OE1	2.703
1YYL	H_ARG_83	NH2	H_ASP_85	OD1	3.539

1YYL	H_ARG_83	NH2	H_ASP_85	OD2	3.994
1YYL	H_LYS_143	NZ	H_ASP_144	OD1	3.315
1YYL	H_LYS_209	NZ	L_GLU_123	OE1	2.745
1YYL	H_LYS_209	NZ	L_GLU_123	OE2	3.202
1YYL	H_LYS_210	NZ	H_GLU_212	OE2	3.491
1YYL	P_LYS_1121	NZ	P_GLU_1429	OE1	3.348
1YYL	P_LYS_1207	NZ	P_GLU_1381	OE1	3.416
1YYL	P_LYS_1207	NZ	P_GLU_1381	OE2	2.566
1YYL	P_LYS_1232	NZ	P_GLU_1351	OE2	3.532
1YYL	P_HIS_1249	NE2	P_GLU_1482	OE1	3.004
1YYL	P_LYS_1282	NZ	P_GLU_1275	OE1	2.887
1YYL	P_LYS_1348	NZ	P_GLU_1269	OE1	3.461
1YYL	P_LYS_1348	NZ	P_GLU_1351	OE1	3.495
1YYL	P_LYS_1357	NZ	P_GLU_1466	OE1	3.122
1YYL	P_ARG_1419	NH1	R_GLU_1100B	OE1	3.247
1YYL	P_ARG_1419	NH2	R_GLU_1099	OE1	2.456
1YYL	P_ARG_1419	NH2	R_GLU_1100D	OE1	3.853
1YYL	P_ARG_1456	NH1	P_GLU_1466	OE1	3.752
1YYL	P_ARG_1456	NH1	P_GLU_1466	OE2	3.112
1YYL	P_ARG_1469	NH2	P_ASP_1457	OD1	3.096
1YYL	P_ARG_1476	NH1	P_GLU_1102	OE2	2.557
1YYL	P_ARG_1476	NH2	P_ASP_1474	OD2	3.225
1YYL	P_LYS_1487	NZ	P_GLU_1091	OE2	3.909
1YYL	Q_ARG_1061	NH2	Q_GLU_1081	OE1	3.180
1YYL	Q_ARG_1061	NH2	Q_ASP_1082	OD1	3.173
1YYL	Q_ARG_1061	NH2	Q_ASP_1082	OD2	3.802
1YYL	Q_ARG_1095B	NH2	Q_ASP_1001	OD1	3.399
1YYL	Q_ARG_1095B	NH2	Q_ASP_1001	OD2	3.231
1YYL	Q_LYS_1149	NZ	Q_GLU_1195	OE1	2.952
1YYL	Q_LYS_1183	NZ	Q_GLU_1187	OE1	3.809
1YYL	Q_LYS_1183	NZ	Q_GLU_1187	OE2	3.019
1YYL	Q_HIS_1189	ND1	Q_ASP_1151	OD2	3.098
1YYL	R_ARG_1031	NH1	R_GLU_1099	OE2	3.928
1YYL	R_ARG_1031	NH2	R_GLU_1099	OE2	3.597
1YYL	R_ARG_1031	NH2	R_ASP_1100A	OD1	3.501
1YYL	R_ARG_1038	NH1	R_GLU_1046	OE2	3.535
1YYL	R_ARG_1038	NH1	R_ASP_1086	OD2	3.751
1YYL	R_ARG_1038	NH2	R_ASP_1086	OD2	2.896
1YYL	R_ARG_1050	NH2	R_GLU_1097	OE2	3.268
1YYL	R_ARG_1066	NH1	R_ASP_1086	OD1	3.056
1YYL	R_ARG_1066	NH2	R_ASP_1086	OD1	3.383
1YYL	R_ARG_1066	NH2	R_ASP_1086	OD2	3.344
1YYL	R_ARG_1082A	NH2	R_GLU_1081	OE1	2.841
1YYL	R_ARG_1083	NH2	R_ASP_1085	OD1	3.521
1YYL	R_ARG_1083	NH2	R_ASP_1085	OD2	3.389
1YYL	R_LYS_1143	NZ	R_ASP_1144	OD2	3.941
1YYL	R_LYS_1201	NZ	H_GLU_10	OE1	3.633
1YYL	R_LYS_1209	NZ	Q_GLU_1123	OE2	3.934
1YYL	R_LYS_1210	NZ	R_GLU_1212	OE2	3.311
1YYL	S_ARG_1009	NH1	P_ASP_1368	OD2	3.204
1YYL	S_ARG_1009	NH2	P_ASP_1368	OD2	2.930
1YYM	G_LYS_207	NZ	G_GLU_381	OE2	3.762
1YYM	G_HIS_249	NE2	G_GLU_482	OE1	2.851
1YYM	G_LYS_282	NZ	G_GLU_275	OE1	2.507
1YYM	G_LYS_348	NZ	G_GLU_269	OE1	2.728
1YYM	G_LYS_348	NZ	G_GLU_351	OE1	3.554
1YYM	G_LYS_348	NZ	G_GLU_351	OE2	3.474
1YYM	G_LYS_350	NZ	G_ASP_395	OD2	3.297

1YYM	G_ARG.419	NH2	H_GLU_99	OE2	2.868
1YYM	G_ARG.419	NH2	H_GLU_100D	OE1	3.511
1YYM	G_ARG.456	NH1	G_GLU_466	OE1	3.106
1YYM	G_ARG.469	NH2	G_ASP_457	OD2	3.063
1YYM	G_ARG.476	NH1	G_GLU_102	OE1	3.223
1YYM	G_ARG.476	NH1	G_GLU_102	OE2	3.388
1YYM	G_ARG.476	NH2	G_ASP_474	OD1	3.743
1YYM	G_ARG.476	NH2	G_ASP_474	OD2	2.651
1YYM	G_ARG.480	NH1	G_ASP_477	OD1	2.715
1YYM	L_ARG.61	NH2	L_GLU_81	OE1	2.791
1YYM	L_ARG.61	NH2	L_ASP_82	OD1	3.065
1YYM	L_ARG.61	NH2	L_ASP_82	OD2	3.869
1YYM	L_LYS_183	NZ	L_GLU_187	OE1	3.511
1YYM	L_HIS_189	ND1	L_ASP_151	OD2	2.884
1YYM	H_LYS_12	NZ	H_GLU_10	OE1	3.907
1YYM	H_ARG.31	NH2	H_ASP_100A	OD1	3.488
1YYM	H_ARG.31	NH2	H_ASP_100A	OD2	3.551
1YYM	H_ARG.38	NH1	H_GLU_46	OE2	3.168
1YYM	H_ARG.38	NH2	H_ASP_86	OD2	3.293
1YYM	H_ARG.50	NH2	H_GLU_97	OE2	2.832
1YYM	H_ARG.66	NH1	H_ASP_86	OD1	3.105
1YYM	H_ARG.66	NH1	H_ASP_86	OD2	3.982
1YYM	H_ARG.66	NH2	H_ASP_86	OD1	3.852
1YYM	H_ARG.66	NH2	H_ASP_86	OD2	3.349
1YYM	H_ARG.82A	NH2	H_GLU_81	OE1	3.100
1YYM	H_ARG.83	NH2	H_ASP_85	OD1	3.328
1YYM	H_ARG.83	NH2	H_ASP_85	OD2	3.453
1YYM	H_LYS_143	NZ	H_ASP_144	OD1	3.488
1YYM	H_LYS_143	NZ	H_ASP_144	OD2	3.824
1YYM	H_LYS_209	NZ	L_GLU_123	OE1	2.715
1YYM	H_LYS_209	NZ	L_GLU_123	OE2	2.976
1YYM	H_LYS_210	NZ	H_GLU_212	OE2	3.803
1YYM	P_LYS_1097	NZ	P_GLU_1275	OE2	3.820
1YYM	P_LYS_1207	NZ	P_GLU_1381	OE1	3.711
1YYM	P_LYS_1207	NZ	P_GLU_1381	OE2	2.708
1YYM	P_HIS_1249	NE2	P_GLU_1482	OE1	3.026
1YYM	P_LYS_1282	NZ	P_GLU_1275	OE1	3.159
1YYM	P_LYS_1348	NZ	P_GLU_1269	OE1	3.365
1YYM	P_LYS_1348	NZ	P_GLU_1351	OE1	3.721
1YYM	P_LYS_1357	NZ	P_GLU_1466	OE1	3.358
1YYM	P_ARG.1419	NH1	R_GLU_1100B	OE1	2.635
1YYM	P_ARG.1419	NH2	R_GLU_1099	OE1	3.192
1YYM	P_ARG.1456	NH1	P_GLU_1466	OE2	3.024
1YYM	P_ARG.1469	NH2	P_ASP_1457	OD1	3.346
1YYM	P_ARG.1476	NH1	P_GLU_1102	OE2	3.088
1YYM	P_ARG.1476	NH2	P_ASP_1474	OD1	3.920
1YYM	P_ARG.1476	NH2	P_ASP_1474	OD2	3.018
1YYM	P_ARG.1480	NH1	P_ASP_1477	OD1	3.891
1YYM	Q_ARG.1061	NH2	Q_GLU_1081	OE1	3.918
1YYM	Q_ARG.1061	NH2	Q_ASP_1082	OD1	2.770
1YYM	Q_ARG.1061	NH2	Q_ASP_1082	OD2	3.285
1YYM	Q_ARG.1095B	NH2	Q_ASP_1001	OD1	3.276
1YYM	Q_ARG.1095B	NH2	Q_ASP_1001	OD2	3.393
1YYM	Q_LYS_1149	NZ	Q_GLU_1195	OE1	3.456
1YYM	Q_LYS_1183	NZ	Q_GLU_1187	OE1	3.987
1YYM	Q_LYS_1183	NZ	Q_GLU_1187	OE2	2.753
1YYM	Q_HIS_1189	ND1	Q_ASP_1151	OD2	2.971
1YYM	R_ARG.1031	NH2	R_GLU_1099	OE2	2.952

1YYM	R_ARG_1031	NH2	R_ASP_1100A	OD1	3.903
1YYM	R_ARG_1038	NH1	R_GLU_1046	OE2	3.211
1YYM	R_ARG_1038	NH2	R_ASP_1086	OD2	2.820
1YYM	R_ARG_1050	NH2	R_GLU_1097	OE2	2.957
1YYM	R_ARG_1066	NH1	R_ASP_1086	OD1	2.623
1YYM	R_ARG_1066	NH1	R_ASP_1086	OD2	3.373
1YYM	R_ARG_1066	NH2	R_ASP_1086	OD1	3.663
1YYM	R_ARG_1066	NH2	R_ASP_1086	OD2	2.872
1YYM	R_ARG_1082A	NH2	R_GLU_1081	OE1	2.831
1YYM	R_ARG_1083	NH1	R_ASP_1085	OD1	3.896
1YYM	R_ARG_1083	NH1	R_ASP_1085	OD2	3.741
1YYM	R_ARG_1083	NH2	R_ASP_1085	OD1	3.214
1YYM	R_ARG_1083	NH2	R_ASP_1085	OD2	2.624
1YYM	R_LYS_1210	NZ	R_GLU_1212	OE2	3.428
1YYM	S_ARG_1009	NH1	P_ASP_1368	OD2	3.572
1YYM	S_ARG_1009	NH2	P_ASP_1368	OD2	2.725
1YZZ	A_ARG_38	NH1	A_ASP_89	OD1	2.737
1YZZ	A_ARG_38	NH2	A_GLU_46	OE2	3.110
1YZZ	A_ARG_38	NH2	A_ASP_89	OD1	3.687
1YZZ	A_ARG_66	NH1	A_ASP_89	OD1	3.398
1YZZ	A_ARG_66	NH1	A_ASP_89	OD2	3.558
1YZZ	A_ARG_66	NH2	A_ASP_89	OD2	2.939
1YZZ	B_ARG_38	NH1	B_ASP_89	OD1	2.975
1YZZ	B_ARG_38	NH2	B_GLU_46	OE2	3.058
1YZZ	B_LYS_64	NZ	B_ASP_61	OD1	2.623
1YZZ	B_ARG_66	NH1	B_ASP_89	OD1	2.532
1YZZ	B_ARG_66	NH1	B_ASP_89	OD2	3.353
1YZZ	B_ARG_66	NH2	B_ASP_89	OD1	3.279
1YZZ	B_ARG_66	NH2	B_ASP_89	OD2	2.407
1ZEA	L_LYS_24	NZ	L_ASP_70	OD1	2.669
1ZEA	L_LYS_24	NZ	L_ASP_70	OD2	2.887
1ZEA	L_LYS_39	NZ	L_GLU_81	OE1	3.641
1ZEA	L_ARG_61	NH1	L_ASP_82	OD1	3.651
1ZEA	L_ARG_61	NH1	L_ASP_82	OD2	2.744
1ZEA	L_ARG_61	NH2	L_GLU_79	OE1	3.732
1ZEA	L_ARG_61	NH2	L_ASP_82	OD1	3.003
1ZEA	L_ARG_61	NH2	L_ASP_82	OD2	3.574
1ZEA	L_ARG_77	NH2	L_ASP_60	OD2	3.436
1ZEA	L_LYS_149	NZ	L_GLU_195	OE1	2.851
1ZEA	L_LYS_149	NZ	L_GLU_195	OE2	3.548
1ZEA	L_LYS_169	NZ	L_GLU_81	OE2	3.652
1ZEA	L_ARG_188	NH2	L_ASP_184	OD1	2.975
1ZEA	L_HIS_189	ND1	L_ASP_151	OD2	2.735
1ZEA	L_LYS_199	NZ	L_ASP_110	OD2	3.834
1ZEA	H_LYS_46	NZ	H_ASP_62	OD2	2.871
1ZEA	H_LYS_64	NZ	H_ASP_61	OD1	3.284
1ZEA	H_ARG_66	NH1	H_ASP_86	OD1	3.918
1ZEA	H_ARG_66	NH1	H_ASP_86	OD2	2.875
1ZEA	H_ARG_66	NH2	H_ASP_86	OD1	2.957
1ZEA	H_ARG_66	NH2	H_ASP_86	OD2	3.243
1ZEA	H_ARG_94	NH2	H_ASP_101	OD1	3.691
1ZEA	H_ARG_94	NH2	H_ASP_101	OD2	2.853
1ZEA	H_ARG_95	NH1	L_GLU_34	OE1	2.842
1ZEA	H_ARG_95	NH1	L_GLU_34	OE2	3.642
1ZEA	H_ARG_95	NH2	L_GLU_34	OE1	3.613
1ZEA	H_ARG_95	NH2	L_GLU_34	OE2	2.859
1ZEA	H_LYS_143	NZ	H_ASP_173	OD2	3.046
1ZEA	H_LYS_205	NZ	H_ASP_207	OD1	2.729

1ZEA	H.LYS_205	NZ	H.ASP_207	OD2	3.512
1ZEA	H.LYS_208	NZ	L.GLU_123	OE2	2.817
1ZMY	A.ARG_38	NH1	A.ASP_90	OD2	2.840
1ZMY	A.ARG_38	NH2	A.GLU_46	OE2	3.583
1ZMY	A.ARG_38	NH2	A.ASP_90	OD2	3.677
1ZMY	A.LYS_65	NZ	A.ASP_62	OD1	3.540
1ZMY	A.ARG_67	NH1	A.ASP_90	OD1	2.500
1ZMY	A.ARG_67	NH1	A.ASP_90	OD2	3.775
1ZMY	A.ARG_67	NH2	A.ASP_90	OD1	3.202
1ZMY	A.ARG_67	NH2	A.ASP_90	OD2	3.068
1ZMY	L.LYS_1	NZ	L.GLU_7	OE2	2.765
1ZMY	L.LYS_13	NZ	L.ASP_18	OD2	3.088
1ZMY	L.ARG_61	NH2	L.ASP_48	OD2	3.432
1ZMY	M.LYS_1	NZ	M.GLU_7	OE1	3.919
1ZMY	M.LYS_1	NZ	M.GLU_7	OE2	2.657
1ZMY	M.LYS_13	NZ	M.ASP_18	OD2	3.984
2AAB	L.ARG_24	NH1	L.ASP_70	OD1	3.378
2AAB	L.ARG_24	NH1	L.ASP_70	OD2	3.076
2AAB	L.ARG_61	NH1	L.GLU_79	OE1	3.401
2AAB	L.ARG_61	NH1	L.ASP_82	OD1	2.799
2AAB	L.ARG_61	NH1	L.ASP_82	OD2	3.081
2AAB	L.ARG_61	NH2	L.GLU_79	OE1	3.087
2AAB	L.LYS_93	NZ	L.GLU_27	OE1	2.856
2AAB	L.LYS_103	NZ	L.GLU_105	OE2	3.933
2AAB	L.LYS_149	NZ	L.GLU_195	OE1	2.658
2AAB	L.LYS_149	NZ	L.GLU_195	OE2	3.769
2AAB	L.ARG_155	NH1	L.GLU_185	OE1	3.205
2AAB	L.ARG_155	NH2	L.GLU_185	OE1	3.657
2AAB	L.ARG_155	NH2	L.GLU_185	OE2	3.891
2AAB	L.HIS_189	ND1	L.ASP_151	OD2	2.588
2AAB	H.ARG_38	NH1	H.ASP_86	OD1	2.796
2AAB	H.ARG_38	NH2	H.GLU_46	OE1	2.650
2AAB	H.ARG_38	NH2	H.GLU_46	OE2	3.853
2AAB	H.ARG_38	NH2	H.ASP_86	OD1	3.953
2AAB	H.LYS_64	NZ	H.ASP_61	OD2	3.741
2AAB	H.ARG_66	NH1	H.ASP_86	OD1	3.938
2AAB	H.ARG_66	NH1	H.ASP_86	OD2	2.836
2AAB	H.ARG_66	NH2	H.ASP_86	OD1	3.107
2AAB	H.ARG_66	NH2	H.ASP_86	OD2	3.400
2AAB	H.ARG_83	NH1	H.GLU_85	OE1	3.354
2AAB	H.ARG_83	NH2	H.GLU_85	OE1	3.065
2AAB	H.ARG_94	NH2	H.ASP_101	OD1	3.332
2AAB	H.ARG_94	NH2	H.ASP_101	OD2	3.671
2AAB	H.LYS_208	NZ	L.GLU_123	OE1	3.545
2ARJ	L.ARG_61	NH1	L.ASP_82	OD1	2.599
2ARJ	L.ARG_61	NH1	L.ASP_82	OD2	2.529
2ARJ	L.LYS_103	NZ	L.GLU_105	OE2	2.787
2ARJ	L.LYS_147	NZ	L.GLU_154	OE1	3.563
2ARJ	L.LYS_147	NZ	L.GLU_154	OE2	3.021
2ARJ	L.LYS_149	NZ	L.GLU_195	OE1	3.558
2ARJ	L.ARG_156	NH1	L.GLU_154	OE1	3.520
2ARJ	L.ARG_156	NH1	L.GLU_154	OE2	3.250
2ARJ	L.LYS_183	NZ	L.GLU_187	OE1	3.507
2ARJ	L.HIS_189	ND1	L.ASP_151	OD2	3.253
2ARJ	L.HIS_189	NE2	L.GLU_185	OE2	2.888
2ARJ	L.LYS_199	NZ	L.ASP_110	OD1	3.590
2ARJ	L.LYS_199	NZ	L.ASP_110	OD2	2.881
2ARJ	H.ARG_38	NH1	H.ASP_86	OD1	2.915

2ARJ	H_ARG_38	NH2	H_GLU_46	OE2	3.238
2ARJ	H_ARG_38	NH2	H_ASP_86	OD1	3.950
2ARJ	H_ARG_66	NH1	H_ASP_86	OD2	3.425
2ARJ	H_ARG_66	NH2	H_ASP_86	OD1	2.734
2ARJ	H_ARG_66	NH2	H_ASP_86	OD2	2.913
2ARJ	H_HIS_172	NE2	H_ASP_169	OD1	3.945
2ARJ	A_ARG_61	NH1	A_ASP_82	OD1	2.811
2ARJ	A_ARG_61	NH1	A_ASP_82	OD2	2.467
2ARJ	A_ARG_61	NH2	A_ASP_81	OD2	3.853
2ARJ	A_LYS_103	NZ	A_GLU_105	OE2	3.414
2ARJ	A_LYS_147	NZ	A_GLU_154	OE2	2.780
2ARJ	A_LYS_149	NZ	A_GLU_195	OE1	3.948
2ARJ	A_LYS_149	NZ	A_GLU_195	OE2	3.695
2ARJ	A_ARG_156	NH1	A_GLU_154	OE1	2.977
2ARJ	A_ARG_156	NH1	A_GLU_154	OE2	3.024
2ARJ	A_ARG_156	NH2	A_GLU_154	OE1	3.339
2ARJ	A_LYS_183	NZ	A_GLU_187	OE1	3.790
2ARJ	A_HIS_189	ND1	A_ASP_151	OD2	3.869
2ARJ	A_HIS_189	NE2	A_GLU_185	OE2	2.726
2ARJ	A_LYS_199	NZ	A_ASP_110	OD1	3.226
2ARJ	A_LYS_199	NZ	A_ASP_110	OD2	2.734
2ARJ	B_ARG_38	NH1	B_ASP_86	OD1	2.957
2ARJ	B_ARG_38	NH2	B_GLU_46	OE1	3.840
2ARJ	B_ARG_38	NH2	B_GLU_46	OE2	3.335
2ARJ	B_ARG_38	NH2	B_ASP_86	OD1	3.960
2ARJ	B_ARG_66	NH1	B_ASP_86	OD2	3.486
2ARJ	B_ARG_66	NH2	B_ASP_86	OD1	2.770
2ARJ	B_ARG_66	NH2	B_ASP_86	OD2	2.899
2ARJ	R_LYS_21	NZ	R_ASP_23	OD2	3.940
2ARJ	R_LYS_68	NZ	R_ASP_66	OD2	3.453
2ARJ	Q_LYS_21	NZ	Q_ASP_23	OD1	3.938
2ARJ	Q_LYS_21	NZ	Q_ASP_23	OD2	3.026
2ARJ	Q_LYS_68	NZ	Q_ASP_66	OD2	2.542
2ARJ	Q_LYS_121	NZ	Q_GLU_17	OE1	3.957
2ARJ	Q_LYS_121	NZ	Q_GLU_17	OE2	3.774
2B2X	A_LYS_174	NZ	A_ASP_171	OD1	3.646
2B2X	A_ARG_175	NH1	A_ASP_171	OD1	2.653
2B2X	A_ARG_175	NH2	A_ASP_171	OD1	3.756
2B2X	A_HIS_196	NE2	A_GLU_236	OE1	2.662
2B2X	A_ARG_219	NH2	A_GLU_197	OE2	3.539
2B2X	A_ARG_222	NH2	A_GLU_192	OE1	3.578
2B2X	A_ARG_222	NH2	A_GLU_192	OE2	3.205
2B2X	A_ARG_234	NH1	A_ASP_231	OD1	2.877
2B2X	A_ARG_234	NH2	A_ASP_231	OD1	3.527
2B2X	A_ARG_234	NH2	A_ASP_272	OD1	3.389
2B2X	A_LYS_235	NZ	A_ASP_231	OD2	2.623
2B2X	A_ARG_242	NH2	A_GLU_236	OE1	3.815
2B2X	A_ARG_245	NH2	A_ASP_148	OD2	2.857
2B2X	A_ARG_246	NH2	A_GLU_240	OE1	3.473
2B2X	A_LYS_250	NZ	A_GLU_276	OE2	3.894
2B2X	A_HIS_261	NE2	H_ASP_101	OD2	3.121
2B2X	A_ARG_265	NH2	A_ASP_231	OD2	3.021
2B2X	A_ARG_280	NH1	A_GLU_274	OE1	3.434
2B2X	A_ARG_280	NH2	A_GLU_274	OE1	2.884
2B2X	A_HIS_288	NE2	A_ASP_257	OD2	3.303
2B2X	A_LYS_329	NZ	A_GLU_333	OE1	2.878
2B2X	A_LYS_329	NZ	A_GLU_333	OE2	3.222
2B2X	H_ARG_38	NH1	H_GLU_46	OE1	2.704

2B2X	H_ARG_38	NH2	H_ASP_89	OD2	2.877
2B2X	H_ARG_66	NH1	H_ASP_89	OD1	2.835
2B2X	H_ARG_66	NH1	H_ASP_89	OD2	3.848
2B2X	H_ARG_66	NH2	H_ASP_89	OD1	3.615
2B2X	H_ARG_66	NH2	H_ASP_89	OD2	3.196
2B2X	H_ARG_97	NH2	H_ASP_106	OD1	3.043
2B2X	H_ARG_97	NH2	H_ASP_106	OD2	3.052
2B2X	H_HIS_169	NE2	L_ASP_171	OD2	3.832
2B2X	H_LYS_213	NZ	L_GLU_127	OE1	2.709
2B2X	H_LYS_213	NZ	L_GLU_127	OE2	3.416
2B2X	L_HIS_31	NE2	A_GLU_259	OE2	3.821
2B2X	L_ARG_60	NH2	L_ASP_81	OD1	2.811
2B2X	L_ARG_60	NH2	L_ASP_81	OD2	3.437
2B2X	L_LYS_102	NZ	L_ASP_169	OD1	3.045
2B2X	L_LYS_153	NZ	L_GLU_199	OE2	2.862
2B2X	L_ARG_159	NH2	L_GLU_189	OE1	3.544
2B2X	L_LYS_187	NZ	L_GLU_191	OE1	3.187
2B2X	L_LYS_187	NZ	L_GLU_191	OE2	3.179
2B2X	L_HIS_193	ND1	L_ASP_155	OD2	3.401
2B2X	B_LYS_174	NZ	B_ASP_171	OD1	3.653
2B2X	B_LYS_174	NZ	B_ASP_171	OD2	3.858
2B2X	B_HIS_196	NE2	B_GLU_236	OE1	2.785
2B2X	B_ARG_219	NH1	B_GLU_197	OE1	3.424
2B2X	B_ARG_219	NH1	B_GLU_197	OE2	2.578
2B2X	B_ARG_222	NH2	B_GLU_192	OE1	3.396
2B2X	B_ARG_222	NH2	B_GLU_192	OE2	3.088
2B2X	B_ARG_234	NH1	B_ASP_231	OD1	2.739
2B2X	B_ARG_234	NH1	B_ASP_231	OD2	3.550
2B2X	B_ARG_234	NH2	B_ASP_231	OD1	3.736
2B2X	B_ARG_234	NH2	B_ASP_272	OD1	3.791
2B2X	B_LYS_235	NZ	B_ASP_231	OD2	2.860
2B2X	B_ARG_245	NH2	B_ASP_148	OD1	3.373
2B2X	B_HIS_261	NE2	L_ASP_101	OD2	3.107
2B2X	B_ARG_280	NH1	B_GLU_274	OE1	3.062
2B2X	B_ARG_280	NH1	B_GLU_274	OE2	3.945
2B2X	B_ARG_280	NH2	B_GLU_274	OE1	3.114
2B2X	B_HIS_288	ND1	B_ASP_257	OD2	3.336
2B2X	B_LYS_329	NZ	B_GLU_333	OE1	3.450
2B2X	B_LYS_329	NZ	B_GLU_333	OE2	3.053
2B2X	L_ARG_38	NH1	L_GLU_46	OE1	2.780
2B2X	L_ARG_38	NH2	L_ASP_89	OD2	2.859
2B2X	L_ARG_66	NH1	L_ASP_89	OD1	2.954
2B2X	L_ARG_66	NH1	L_ASP_89	OD2	3.737
2B2X	L_ARG_66	NH2	L_ASP_89	OD1	3.772
2B2X	L_ARG_66	NH2	L_ASP_89	OD2	3.121
2B2X	L_ARG_97	NH2	L_ASP_106	OD1	3.823
2B2X	L_ARG_97	NH2	L_ASP_106	OD2	2.979
2B2X	L_HIS_169	NE2	M_ASP_171	OD2	3.874
2B2X	L_LYS_213	NZ	M_GLU_127	OE2	3.245
2B2X	M_HIS_31	NE2	B_GLU_259	OE2	3.848
2B2X	M_ARG_60	NH2	M_GLU_80	OE2	3.305
2B2X	M_ARG_60	NH2	M_ASP_81	OD1	2.985
2B2X	M_ARG_60	NH2	M_ASP_81	OD2	3.811
2B2X	M_LYS_102	NZ	M_ASP_169	OD1	3.157
2B2X	M_LYS_146	NZ	M_GLU_104	OE1	3.183
2B2X	M_LYS_151	NZ	M_GLU_158	OE1	3.453
2B2X	M_LYS_187	NZ	M_GLU_191	OE1	2.648
2B2X	M_LYS_187	NZ	M_GLU_191	OE2	3.145

2B2X	M_HIS_193	ND1	M_ASP_155	OD2	3.516
2B4C	G_LYS_	NZ	G_ASP_	OD1	3.338
2B4C	G_LYS_	NZ	G_ASP_	OD1	3.491
2B4C	G_ARG_	NH1	H_ASP_	OD2	3.237
2B4C	G_ARG_	NH2	H_ASP_	OD2	2.859
2B4C	G_LYS_	NZ	G_GLU_	OE2	3.048
2B4C	G_LYS_	NZ	G_GLU_	OE1	3.552
2B4C	G_LYS_	NZ	G_GLU_	OE2	3.954
2B4C	G_ARG_	NH2	G_GLU_	OE1	3.957
2B4C	G_LYS_	NZ	G_GLU_	OE1	3.503
2B4C	G_ARG_	NH1	G_ASP_	OD1	3.623
2B4C	G_LYS_	NZ	H_ASP_	OD2	2.598
2B4C	G_ARG_	NH1	G_GLU_	OE2	3.070
2B4C	G_ARG_	NH1	G_ASP_	OD1	3.468
2B4C	G_ARG_	NH2	G_GLU_	OE2	3.385
2B4C	C_LYS_	NZ	C_GLU_	OE1	3.632
2B4C	C_LYS_	NZ	C_GLU_	OE1	3.382
2B4C	C_LYS_	NZ	C_GLU_	OE2	3.763
2B4C	C_LYS_	NZ	C_ASP_	OD1	3.946
2B4C	C_ARG_	NH1	C_ASP_	OD2	3.370
2B4C	C_ARG_	NH2	C_ASP_	OD1	2.876
2B4C	C_ARG_	NH2	C_ASP_	OD2	3.161
2B4C	C_ARG_	NH1	H_GLU_	OE2	3.957
2B4C	C_ARG_	NH2	H_GLU_	OE2	3.405
2B4C	C_ARG_	NH1	G_ASP_	OD1	2.937
2B4C	C_ARG_	NH1	G_ASP_	OD2	3.245
2B4C	L_LYS_39	NZ	L_GLU_81	OE1	3.785
2B4C	L_LYS_39	NZ	L_GLU_81	OE2	3.605
2B4C	L_ARG_61	NH1	L_GLU_79	OE1	2.769
2B4C	L_ARG_61	NH1	L_ASP_82	OD1	3.180
2B4C	L_ARG_61	NH2	L_GLU_79	OE1	3.620
2B4C	L_ARG_61	NH2	L_ASP_82	OD1	3.064
2B4C	L_ARG_61	NH2	L_ASP_82	OD2	2.938
2B4C	L_LYS_103	NZ	L_GLU_165	OE1	3.532
2B4C	L_LYS_103	NZ	L_GLU_165	OE2	3.078
2B4C	L_LYS_149	NZ	L_GLU_195	OE1	2.786
2B4C	L_LYS_149	NZ	L_GLU_195	OE2	3.526
2B4C	L_ARG_169	NH2	L_ASP_170	OD2	3.503
2B4C	L_HIS_189	ND1	L_ASP_151	OD1	3.907
2B4C	L_HIS_189	NE2	L_ASP_185	OD2	3.165
2B4C	L_ARG_211	NH1	L_GLU_187	OE1	3.570
2B4C	H_ARG_	NH1	H_ASP_	OD2	3.124
2B4C	H_ARG_	NH2	H_GLU_	OE2	3.384
2B4C	H_LYS_	NZ	L_GLU_	OE1	3.365
2B4C	H_ARG_	NH1	H_ASP_	OD1	2.883
2B4C	H_ARG_	NH1	H_ASP_	OD2	3.887
2B4C	H_ARG_	NH2	H_ASP_	OD1	3.707
2B4C	H_ARG_	NH2	H_ASP_	OD2	3.345
2B4C	H_ARG_	NH1	H_ASP_	OD2	3.458
2B4C	H_ARG_	NH2	H_ASP_	OD2	2.912
2B4C	H_LYS_143	NZ	H_ASP_144	OD2	3.642
2B4C	H_LYS_209	NZ	L_GLU_123	OE2	3.837
2B4C	H_LYS_210	NZ	H_GLU_212	OE2	3.952
2BDN	A_ARG_29	NH2	A_GLU_50	OE1	2.816
2BDN	A_LYS_56	NZ	H_ASP_52	OD1	2.539
2BDN	A_LYS_56	NZ	H_ASP_52	OD2	3.792
2BDN	A_LYS_58	NZ	A_ASP_62	OD1	3.823
2BDN	A_LYS_58	NZ	A_ASP_62	OD2	3.097

2BDN	L_LYS_24	NZ	L_ASP_70	OD1	2.861
2BDN	L_ARG_32	NH1	A_ASP_65	OD1	3.196
2BDN	L_ARG_32	NH1	A_ASP_68	OD1	2.578
2BDN	L_ARG_32	NH2	A_ASP_65	OD1	2.774
2BDN	L_ARG_61	NH2	L_GLU_81	OE2	3.319
2BDN	L_ARG_61	NH2	L_ASP_82	OD1	2.963
2BDN	L_ARG_61	NH2	L_ASP_82	OD2	3.256
2BDN	L_LYS_147	NZ	L_GLU_154	OE1	3.710
2BDN	L_LYS_147	NZ	L_GLU_154	OE2	3.490
2BDN	L_LYS_149	NZ	L_GLU_195	OE1	3.088
2BDN	L_LYS_149	NZ	L_GLU_195	OE2	3.458
2BDN	L_ARG_155	NH1	L_GLU_185	OE2	3.304
2BDN	L_ARG_155	NH2	L_GLU_185	OE2	3.205
2BDN	L_LYS_183	NZ	L_GLU_187	OE1	3.602
2BDN	L_LYS_183	NZ	L_GLU_187	OE2	3.004
2BDN	L_ARG_188	NH1	L_GLU_185	OE1	3.733
2BDN	L_HIS_189	ND1	L_GLU_185	OE1	3.536
2BDN	L_LYS_199	NZ	L_ASP_110	OD1	2.836
2BDN	L_LYS_199	NZ	L_ASP_110	OD2	3.459
2BDN	H_ARG_40	NH1	H_GLU_89	OE1	3.907
2BDN	H_ARG_40	NH2	H_GLU_46	OE2	3.172
2BDN	H_LYS_67	NZ	H_ASP_90	OD1	3.376
2BDN	H_LYS_67	NZ	H_ASP_90	OD2	2.583
2BDN	H_ARG_98	NH1	A_GLU_39	OE2	3.155
2BDN	H_ARG_98	NH2	H_ASP_105	OD1	2.453
2BDN	H_ARG_98	NH2	H_ASP_105	OD2	3.385
2BDN	H_LYS_212	NZ	L_GLU_123	OE2	3.177
2BJM	H_LYS_67	NZ	H_ASP_90	OD2	3.645
2BJM	L_ARG_63	NH2	L_ASP_84	OD1	2.452
2BJM	L_ARG_63	NH2	L_ASP_84	OD2	2.754
2BRR	H_LYS_46	NZ	H_ASP_62	OD2	2.761
2BRR	H_LYS_64	NZ	H_ASP_61	OD1	3.587
2BRR	H_ARG_66	NH1	H_ASP_86	OD1	3.672
2BRR	H_ARG_66	NH1	H_ASP_86	OD2	2.665
2BRR	H_ARG_66	NH2	H_ASP_86	OD1	2.817
2BRR	H_ARG_66	NH2	H_ASP_86	OD2	3.203
2BRR	H_ARG_94	NH2	H_ASP_101	OD1	3.717
2BRR	H_ARG_94	NH2	H_ASP_101	OD2	2.794
2BRR	H_ARG_213	NH1	L_GLU_123	OE1	2.600
2BRR	H_ARG_213	NH1	L_GLU_123	OE2	3.932
2BRR	H_ARG_213	NH2	L_GLU_123	OE1	3.110
2BRR	H_ARG_213	NH2	L_GLU_123	OE2	3.029
2BRR	L_ARG_61	NH1	L_GLU_79	OE1	3.644
2BRR	L_ARG_61	NH1	L_GLU_79	OE2	3.599
2BRR	L_ARG_61	NH1	L_GLU_81	OE2	3.861
2BRR	L_ARG_61	NH2	L_GLU_79	OE1	3.852
2BRR	L_ARG_61	NH2	L_GLU_81	OE2	2.730
2BRR	L_ARG_61	NH2	L_ASP_82	OD1	2.665
2BRR	L_ARG_61	NH2	L_ASP_82	OD2	3.473
2BRR	L_LYS_149	NZ	L_GLU_195	OE1	3.904
2BRR	L_LYS_149	NZ	L_GLU_195	OE2	3.270
2BRR	L_ARG_155	NH2	L_GLU_185	OE1	3.742
2BRR	L_LYS_183	NZ	L_ASP_184	OD1	3.014
2BRR	L_HIS_189	ND1	L_ASP_151	OD2	2.911
2BRR	L_ARG_211	NH2	L_GLU_187	OE1	3.989
2BRR	P_LYS_7	NZ	H_ASP_95	OD1	3.067
2BRR	P_LYS_7	NZ	H_ASP_95	OD2	2.549
2BRR	P_HIS_11	ND1	Y_ASP_95	OD2	2.841

2BRR	X_ARG.61	NH1	X_GLU_79	OE1	3.351
2BRR	X_ARG.61	NH1	X_GLU_79	OE2	3.765
2BRR	X_ARG.61	NH1	X_GLU_81	OE2	3.529
2BRR	X_ARG.61	NH2	X_GLU_79	OE1	3.617
2BRR	X_ARG.61	NH2	X_GLU_81	OE2	2.522
2BRR	X_ARG.61	NH2	X_ASP_82	OD1	2.621
2BRR	X_ARG.61	NH2	X_ASP_82	OD2	3.589
2BRR	X_LYS_103	NZ	X_GLU_105	OE2	3.852
2BRR	X_LYS_149	NZ	X_GLU_195	OE1	3.717
2BRR	X_LYS_149	NZ	X_GLU_195	OE2	3.215
2BRR	X_ARG_155	NH1	X_GLU_185	OE2	2.695
2BRR	X_ARG_155	NH2	X_GLU_185	OE2	3.654
2BRR	X_LYS_183	NZ	X_ASP_184	OD1	3.269
2BRR	Y_LYS_46	NZ	Y_ASP_62	OD2	3.113
2BRR	Y_LYS_64	NZ	Y_ASP_61	OD1	3.329
2BRR	Y_ARG_66	NH1	Y_ASP_86	OD1	3.748
2BRR	Y_ARG_66	NH1	Y_ASP_86	OD2	2.611
2BRR	Y_ARG_66	NH2	Y_GLU_85	OE2	3.661
2BRR	Y_ARG_66	NH2	Y_ASP_86	OD1	2.891
2BRR	Y_ARG_66	NH2	Y_ASP_86	OD2	3.154
2BRR	Y_ARG_94	NH2	Y_ASP_101	OD1	3.703
2BRR	Y_ARG_94	NH2	Y_ASP_101	OD2	2.789
2BRR	Y_LYS_208	NZ	X_GLU_123	OE2	3.359
2BRR	Y_ARG_213	NH1	X_GLU_123	OE1	2.523
2BRR	Y_ARG_213	NH1	X_GLU_123	OE2	3.327
2BRR	Y_ARG_213	NH2	X_GLU_123	OE1	3.468
2BRR	Y_ARG_213	NH2	X_GLU_123	OE2	2.546
2COQ	A_ARG_25	NH1	A_ASP_4	OD1	2.687
2COQ	A_ARG_25	NH1	A_ASP_4	OD2	3.796
2COQ	A_ARG_25	NH2	A_ASP_4	OD1	3.959
2COQ	A_ARG_54	NH1	A_ASP_77	OD1	2.737
2COQ	A_ARG_54	NH1	A_ASP_77	OD2	3.255
2COQ	A_ARG_54	NH2	A_ASP_77	OD1	3.769
2COQ	A_ARG_54	NH2	A_ASP_77	OD2	2.959
2COQ	A_ARG_74	NH1	A_ASP_72	OD2	2.997
2COQ	A_LYS_84	NZ	A_GLU_99	OE1	2.795
2D03	L_ARG_67	NH1	L_GLU_85	OE1	3.502
2D03	L_ARG_67	NH2	L_GLU_85	OE1	3.293
2D03	L_ARG_67	NH2	L_ASP_88	OD1	2.725
2D03	L_ARG_67	NH2	L_ASP_88	OD2	3.706
2D03	L_LYS_148	NZ	L_GLU_111	OE2	3.675
2D03	L_LYS_155	NZ	L_GLU_201	OE1	3.930
2D03	L_LYS_155	NZ	L_GLU_201	OE2	2.490
2D03	L_ARG_194	NH1	L_ASP_190	OD2	3.257
2D03	L_HIS_195	ND1	L_ASP_157	OD2	2.581
2D03	L_ARG_217	NH1	L_GLU_193	OE2	3.351
2D03	H_ARG_39	NH1	H_ASP_90	OD1	2.887
2D03	H_ARG_39	NH2	H_GLU_47	OE1	3.007
2D03	H_ARG_39	NH2	H_ASP_90	OD1	3.668
2D03	H_LYS_44	NZ	H_ASP_89	OD2	2.726
2D03	H_ARG_67	NH1	H_ASP_90	OD1	3.817
2D03	H_ARG_67	NH1	H_ASP_90	OD2	2.856
2D03	H_ARG_67	NH2	H_ASP_90	OD1	2.855
2D03	H_ARG_67	NH2	H_ASP_90	OD2	3.320
2D03	H_ARG_98	NH2	H_ASP_107	OD1	3.817
2D03	H_ARG_98	NH2	H_ASP_107	OD2	2.632
2D03	H_ARG_100	NH1	H_ASP_107	OD2	3.028
2DBL	L_ARG_24	NH1	L_ASP_70	OD1	3.462

2DBL	L_ARG.61	NH1	L_ASP_82	OD1	3.576
2DBL	L_ARG.61	NH1	L_ASP_82	OD2	3.889
2DBL	L_ARG.61	NH2	L_GLU_81	OE2	3.218
2DBL	L_ARG.61	NH2	L_ASP_82	OD1	2.842
2DBL	L_ARG.61	NH2	L_ASP_82	OD2	3.577
2DBL	L_LYS_149	NZ	L_GLU_195	OE1	3.270
2DBL	L_LYS_149	NZ	L_GLU_195	OE2	2.656
2DBL	L_LYS_169	NZ	L_ASP_167	OD1	3.936
2DBL	L_LYS_183	NZ	L_GLU_187	OE2	3.658
2DBL	L_ARG_188	NH1	L_GLU_185	OE1	3.115
2DBL	L_ARG_188	NH1	L_GLU_185	OE2	3.486
2DBL	L_ARG_188	NH2	L_GLU_185	OE1	3.398
2DBL	L_HIS_189	ND1	L_ASP_151	OD2	2.678
2DBL	L_HIS_189	NE2	L_GLU_185	OE2	3.450
2DBL	L_LYS_199	NZ	L_ASP_110	OD2	2.951
2DBL	H_LYS_12	NZ	H_GLU_16	OE1	3.932
2DBL	H_LYS_46	NZ	H_ASP_62	OD2	3.919
2DBL	H_ARG.66	NH2	H_ASP_86	OD1	2.889
2DBL	H_ARG.66	NH2	H_ASP_86	OD2	2.859
2DBL	H_ARG.94	NH1	H_ASP_101	OD1	3.455
2DBL	H_ARG.94	NH1	H_ASP_101	OD2	2.558
2DBL	H_LYS_221	NZ	L_GLU_123	OE2	3.660
2DLF	L_ARG.24	NH1	L_ASP_70	OD1	2.656
2DLF	L_ARG.24	NH2	L_ASP_70	OD1	3.467
2DLF	L_ARG.61	NH1	L_ASP_82	OD1	3.387
2DLF	L_ARG.61	NH1	L_ASP_82	OD2	2.663
2DLF	L_ARG.61	NH2	L_GLU_79	OE1	3.785
2DLF	L_ARG.61	NH2	L_GLU_79	OE2	3.705
2DLF	L_ARG.61	NH2	L_ASP_82	OD1	2.886
2DLF	L_ARG.61	NH2	L_ASP_82	OD2	3.503
2DLF	H_ARG.38	NH1	H_ASP_86	OD2	2.865
2DLF	H_ARG.38	NH2	H_GLU_46	OE2	3.124
2DLF	H_ARG.38	NH2	H_ASP_86	OD2	3.931
2DLF	H_HIS_55	NE2	H_ASP_73	OD1	3.901
2DLF	H_HIS_55	NE2	H_ASP_73	OD2	3.007
2DLF	H_ARG.66	NH1	H_ASP_86	OD1	2.819
2DLF	H_ARG.66	NH1	H_ASP_86	OD2	3.911
2DLF	H_ARG.66	NH2	H_ASP_86	OD1	3.370
2DLF	H_ARG.66	NH2	H_ASP_86	OD2	3.052
2DLF	H_ARG.71	NH2	H_ASP_73	OD1	3.380
2DLF	H_LYS_75	NZ	H_ASP_72	OD1	3.168
2DQC	L_ARG.61	NH2	L_GLU_81	OE2	2.947
2DQC	L_ARG.61	NH2	L_ASP_82	OD1	2.824
2DQC	L_ARG.61	NH2	L_ASP_82	OD2	3.557
2DQC	L_LYS_103	NZ	L_GLU_105	OE1	3.912
2DQC	H_ARG.38	NH1	H_ASP_89	OD1	2.829
2DQC	H_ARG.38	NH2	H_GLU_46	OE1	2.957
2DQC	H_ARG.38	NH2	H_ASP_89	OD1	3.436
2DQC	H_ARG.66	NH1	H_ASP_89	OD1	3.729
2DQC	H_ARG.66	NH1	H_ASP_89	OD2	3.006
2DQC	H_ARG.66	NH2	H_ASP_89	OD1	3.000
2DQC	H_ARG.66	NH2	H_ASP_89	OD2	3.596
2DQC	H_LYS_75	NZ	H_ASP_72	OD1	3.870
2DQC	H_LYS_75	NZ	H_ASP_72	OD2	2.592
2DQC	Y_LYS_1	NZ	Y_GLU_7	OE1	3.856
2DQC	Y_LYS_1	NZ	Y_GLU_7	OE2	2.924
2DQC	Y_LYS_13	NZ	Y_ASP_18	OD2	3.571
2DQC	Y_ARG.61	NH1	Y_ASP_48	OD2	2.731

2DQC	Y_ARG.61	NH2	Y_ASP_48	OD2	3.603
2DQC	Y_ARG.68	NH2	Y_ASP_66	OD2	3.942
2DQC	Y_LYS.97	NZ	H_ASP_32	OD1	2.612
2DQC	Y_LYS.97	NZ	H_ASP_32	OD2	3.998
2DQC	Y_LYS.97	NZ	H_ASP_99	OD1	3.500
2DQC	Y_LYS.97	NZ	H_ASP_99	OD2	2.637
2DQC	Y_ARG.125	NH1	Y_ASP_119	OD2	3.978
2DQC	Y_ARG.125	NH2	Y_ASP_119	OD1	3.933
2DQC	Y_ARG.125	NH2	Y_ASP_119	OD2	2.677
2DQD	L_ARG.61	NH1	L_GLU_79	OE1	3.706
2DQD	L_ARG.61	NH1	L_GLU_79	OE2	2.828
2DQD	L_ARG.61	NH1	L_GLU_81	OE2	3.927
2DQD	L_ARG.61	NH2	L_GLU_79	OE1	3.771
2DQD	L_ARG.61	NH2	L_GLU_79	OE2	3.992
2DQD	L_ARG.61	NH2	L_GLU_81	OE2	2.897
2DQD	L_ARG.61	NH2	L_ASP_82	OD1	2.786
2DQD	L_ARG.61	NH2	L_ASP_82	OD2	3.531
2DQD	H_ARG.38	NH1	H_ASP_89	OD1	2.878
2DQD	H_ARG.38	NH2	H_GLU_46	OE1	2.790
2DQD	H_ARG.38	NH2	H_ASP_89	OD1	3.572
2DQD	H_ARG.66	NH1	H_ASP_89	OD1	3.626
2DQD	H_ARG.66	NH1	H_ASP_89	OD2	2.940
2DQD	H_ARG.66	NH2	H_ASP_89	OD1	2.871
2DQD	H_ARG.66	NH2	H_ASP_89	OD2	3.563
2DQD	H_LYS.75	NZ	H_ASP_72	OD1	3.653
2DQD	H_LYS.75	NZ	H_ASP_72	OD2	2.566
2DQD	Y_LYS.1	NZ	Y_GLU_7	OE1	3.745
2DQD	Y_LYS.1	NZ	Y_GLU_7	OE2	2.721
2DQD	Y_ARG.61	NH2	Y_ASP_48	OD2	3.731
2DQD	Y_LYS.97	NZ	H_ASP_32	OD1	2.767
2DQD	Y_LYS.97	NZ	H_ASP_32	OD2	3.965
2DQD	Y_LYS.97	NZ	H_ASP_99	OD1	3.334
2DQD	Y_LYS.97	NZ	H_ASP_99	OD2	3.048
2DQD	Y_ARG.125	NH1	Y_ASP_119	OD2	3.233
2DQD	Y_ARG.125	NH2	Y_ASP_119	OD1	3.581
2DQD	Y_ARG.125	NH2	Y_ASP_119	OD2	3.417
2DQE	L_ARG.61	NH2	L_GLU_81	OE2	2.959
2DQE	L_ARG.61	NH2	L_ASP_82	OD1	2.845
2DQE	L_ARG.61	NH2	L_ASP_82	OD2	3.487
2DQE	L_LYS.103	NZ	L_GLU_105	OE2	3.264
2DQE	H_ARG.38	NH1	H_ASP_89	OD1	2.861
2DQE	H_ARG.38	NH2	H_GLU_46	OE1	2.782
2DQE	H_ARG.38	NH2	H_ASP_89	OD1	3.510
2DQE	H_ARG.66	NH1	H_ASP_89	OD1	3.735
2DQE	H_ARG.66	NH1	H_ASP_89	OD2	2.920
2DQE	H_ARG.66	NH2	H_ASP_89	OD1	2.982
2DQE	H_ARG.66	NH2	H_ASP_89	OD2	3.570
2DQE	Y_LYS.1	NZ	Y_GLU_7	OE2	2.773
2DQE	Y_ARG.61	NH1	Y_ASP_48	OD2	3.262
2DQE	Y_ARG.61	NH2	Y_ASP_48	OD2	3.792
2DQE	Y_LYS.97	NZ	H_ASP_32	OD1	2.650
2DQE	Y_LYS.97	NZ	H_ASP_99	OD1	3.314
2DQE	Y_LYS.97	NZ	H_ASP_99	OD2	2.899
2DQE	Y_ARG.125	NH1	Y_ASP_119	OD2	3.515
2DQE	Y_ARG.125	NH2	Y_ASP_119	OD1	3.565
2DQE	Y_ARG.125	NH2	Y_ASP_119	OD2	3.316
2DQF	A_ARG.24	NH1	A_ASP_70	OD1	2.550
2DQF	A_ARG.24	NH1	A_ASP_70	OD2	3.744

2DQF	A_LYS_39	NZ	A_GLU_81	OE2	2.959
2DQF	A_ARG_45	NH1	E_ASP_1	OD2	3.511
2DQF	A_LYS_49	NZ	B_ASP_99	OD1	3.470
2DQF	A_ARG_61	NH1	A_GLU_79	OE1	3.872
2DQF	A_ARG_61	NH1	A_GLU_79	OE2	2.799
2DQF	A_ARG_61	NH1	E_ASP_27	OD1	3.814
2DQF	A_ARG_61	NH2	A_GLU_79	OE1	3.614
2DQF	A_ARG_61	NH2	A_GLU_79	OE2	3.760
2DQF	A_ARG_61	NH2	A_ASP_82	OD1	2.799
2DQF	A_ARG_61	NH2	A_ASP_82	OD2	3.265
2DQF	A_LYS_103	NZ	A_GLU_105	OE2	3.654
2DQF	B_ARG_38	NH1	B_ASP_89	OD1	2.770
2DQF	B_ARG_38	NH2	B_GLU_46	OE1	2.742
2DQF	B_ARG_38	NH2	B_ASP_89	OD1	3.406
2DQF	B_ARG_66	NH1	B_ASP_89	OD1	3.473
2DQF	B_ARG_66	NH1	B_ASP_89	OD2	2.668
2DQF	B_ARG_66	NH2	B_ASP_89	OD1	2.704
2DQF	B_ARG_66	NH2	B_ASP_89	OD2	3.223
2DQF	C_LYS_1	NZ	C_GLU_7	OE1	3.699
2DQF	C_LYS_1	NZ	C_GLU_7	OE2	2.773
2DQF	C_LYS_97	NZ	B_ASP_99	OD1	3.543
2DQF	C_LYS_97	NZ	B_ASP_99	OD2	2.851
2DQF	C_ARG_125	NH1	C_ASP_119	OD2	3.803
2DQF	C_ARG_125	NH2	C_ASP_119	OD1	3.819
2DQF	C_ARG_125	NH2	C_ASP_119	OD2	3.276
2DQF	D_LYS_39	NZ	B_ASP_1	OD1	3.005
2DQF	D_LYS_39	NZ	D_GLU_42	OE2	3.387
2DQF	D_LYS_39	NZ	D_GLU_81	OE2	3.094
2DQF	D_ARG_61	NH1	B_ASP_27	OD1	3.581
2DQF	D_ARG_61	NH1	D_GLU_79	OE1	3.632
2DQF	D_ARG_61	NH1	D_GLU_79	OE2	2.878
2DQF	D_ARG_61	NH2	D_GLU_79	OE1	3.547
2DQF	D_ARG_61	NH2	D_GLU_79	OE2	3.942
2DQF	D_ARG_61	NH2	D_ASP_82	OD1	2.591
2DQF	D_ARG_61	NH2	D_ASP_82	OD2	3.479
2DQF	E_ARG_38	NH1	E_ASP_89	OD1	2.707
2DQF	E_ARG_38	NH2	E_GLU_46	OE1	2.703
2DQF	E_ARG_38	NH2	E_ASP_89	OD1	3.576
2DQF	E_ARG_66	NH1	E_ASP_89	OD1	3.354
2DQF	E_ARG_66	NH1	E_ASP_89	OD2	2.779
2DQF	E_ARG_66	NH2	E_ASP_89	OD1	2.920
2DQF	E_ARG_66	NH2	E_ASP_89	OD2	3.732
2DQF	E_LYS_75	NZ	E_ASP_72	OD1	3.480
2DQF	E_LYS_75	NZ	E_ASP_72	OD2	3.040
2DQF	F_LYS_1	NZ	F_GLU_7	OE1	3.776
2DQF	F_LYS_1	NZ	F_GLU_7	OE2	2.553
2DQF	F_ARG_61	NH1	F_ASP_48	OD1	3.965
2DQF	F_ARG_61	NH1	F_ASP_48	OD2	3.568
2DQF	F_LYS_97	NZ	E_ASP_99	OD2	3.165
2DQF	F_ARG_125	NH2	F_ASP_119	OD2	3.151
2DQG	L_ARG_24	NH1	L_ASP_70	OD2	2.455
2DQG	L_ARG_24	NH2	L_ASP_70	OD2	2.946
2DQG	L_ARG_61	NH1	L_GLU_81	OE1	3.776
2DQG	L_ARG_61	NH1	L_GLU_81	OE2	3.040
2DQG	L_ARG_61	NH1	L_ASP_82	OD1	2.735
2DQG	L_ARG_61	NH1	L_ASP_82	OD2	3.392
2DQG	L_ARG_61	NH2	L_GLU_81	OE2	3.998
2DQG	H_ARG_38	NH1	H_ASP_89	OD1	2.997

2DQG	H_ARG_38	NH2	H_GLU_46	OE1	2.883
2DQG	H_ARG_38	NH2	H_ASP_89	OD1	3.559
2DQG	H_ARG_66	NH1	H_ASP_89	OD1	3.739
2DQG	H_ARG_66	NH1	H_ASP_89	OD2	2.946
2DQG	H_ARG_66	NH2	H_ASP_89	OD1	2.769
2DQG	H_ARG_66	NH2	H_ASP_89	OD2	3.415
2DQG	Y_LYS_1	NZ	Y_GLU_7	OE1	2.718
2DQG	Y_ARG_61	NH1	Y_ASP_48	OD1	3.819
2DQG	Y_ARG_61	NH2	Y_ASP_48	OD1	3.754
2DQG	Y_LYS_97	NZ	H_ASP_32	OD1	3.992
2DQG	Y_LYS_97	NZ	H_ASP_32	OD2	2.695
2DQG	Y_LYS_97	NZ	H_ASP_99	OD1	3.156
2DQG	Y_LYS_97	NZ	H_ASP_99	OD2	3.019
2DQG	Y_ARG_125	NH2	Y_ASP_119	OD1	3.345
2DQG	Y_ARG_125	NH2	Y_ASP_119	OD2	2.899
2DQH	L_ARG_61	NH1	L_GLU_81	OE2	3.943
2DQH	L_ARG_61	NH2	L_GLU_81	OE2	2.998
2DQH	L_ARG_61	NH2	L_ASP_82	OD1	2.603
2DQH	L_ARG_61	NH2	L_ASP_82	OD2	3.284
2DQH	L_LYS_103	NZ	L_GLU_105	OE2	3.440
2DQH	H_ARG_38	NH1	H_ASP_89	OD1	3.065
2DQH	H_ARG_38	NH2	H_GLU_46	OE1	2.818
2DQH	H_ARG_38	NH2	H_ASP_89	OD1	3.616
2DQH	H_ARG_66	NH1	H_ASP_89	OD1	3.542
2DQH	H_ARG_66	NH1	H_ASP_89	OD2	2.882
2DQH	H_ARG_66	NH2	H_ASP_89	OD1	2.810
2DQH	H_ARG_66	NH2	H_ASP_89	OD2	3.639
2DQH	Y_LYS_1	NZ	Y_GLU_7	OE1	3.804
2DQH	Y_LYS_1	NZ	Y_GLU_7	OE2	2.722
2DQH	Y_LYS_13	NZ	Y_ASP_18	OD1	3.180
2DQH	Y_ARG_61	NH1	Y_ASP_48	OD2	3.913
2DQH	Y_ARG_68	NH2	Y_ASP_66	OD2	3.732
2DQH	Y_LYS_97	NZ	H_ASP_32	OD1	2.777
2DQH	Y_LYS_97	NZ	H_ASP_99	OD1	3.694
2DQH	Y_LYS_97	NZ	H_ASP_99	OD2	2.635
2DQH	Y_ARG_125	NH1	Y_ASP_119	OD2	3.546
2DQH	Y_ARG_125	NH2	Y_ASP_119	OD1	3.902
2DQH	Y_ARG_125	NH2	Y_ASP_119	OD2	3.500
2DQI	L_LYS_49	NZ	H_ASP_99	OD1	2.843
2DQI	L_LYS_49	NZ	H_ASP_101	OD1	3.541
2DQI	L_LYS_49	NZ	H_ASP_101	OD2	3.285
2DQI	L_ARG_61	NH2	L_GLU_81	OE2	2.840
2DQI	L_ARG_61	NH2	L_ASP_82	OD1	2.897
2DQI	L_ARG_61	NH2	L_ASP_82	OD2	3.427
2DQI	L_LYS_103	NZ	L_GLU_105	OE2	3.837
2DQI	H_ARG_38	NH1	H_ASP_89	OD1	2.893
2DQI	H_ARG_38	NH2	H_GLU_46	OE1	2.861
2DQI	H_ARG_38	NH2	H_ASP_89	OD1	3.612
2DQI	H_ARG_66	NH1	H_ASP_89	OD1	3.831
2DQI	H_ARG_66	NH1	H_ASP_89	OD2	3.064
2DQI	H_ARG_66	NH2	H_ASP_89	OD1	3.099
2DQI	H_ARG_66	NH2	H_ASP_89	OD2	3.699
2DQI	H_LYS_75	NZ	H_ASP_72	OD2	2.738
2DQI	Y_LYS_1	NZ	Y_GLU_7	OE2	3.385
2DQI	Y_LYS_97	NZ	H_ASP_32	OD1	2.729
2DQI	Y_ARG_125	NH1	Y_ASP_119	OD2	3.366
2DQI	Y_ARG_125	NH2	Y_ASP_119	OD1	3.841
2DQI	Y_ARG_125	NH2	Y_ASP_119	OD2	3.842

2DQJ	L_ARG.61	NH2	L_GLU_81	OE2	2.931
2DQJ	L_ARG.61	NH2	L_ASP_82	OD1	2.808
2DQJ	L_ARG.61	NH2	L_ASP_82	OD2	3.434
2DQJ	L_LYS_103	NZ	L_GLU_105	OE2	3.227
2DQJ	H_ARG_38	NH1	H_ASP_89	OD1	2.842
2DQJ	H_ARG_38	NH2	H_GLU_46	OE1	2.847
2DQJ	H_ARG_38	NH2	H_ASP_89	OD1	3.505
2DQJ	H_ARG_66	NH1	H_ASP_89	OD1	3.735
2DQJ	H_ARG_66	NH1	H_ASP_89	OD2	3.036
2DQJ	H_ARG_66	NH2	H_ASP_89	OD1	3.031
2DQJ	H_ARG_66	NH2	H_ASP_89	OD2	3.659
2DQJ	Y_LYS_1	NZ	Y_GLU_7	OE2	2.929
2DQJ	Y_ARG.61	NH1	Y_ASP_48	OD2	3.313
2DQJ	Y_ARG.61	NH2	Y_ASP_48	OD2	3.891
2DQJ	Y_ARG.68	NH2	Y_ASP_66	OD2	3.769
2DQJ	Y_LYS_97	NZ	H_ASP_32	OD1	2.638
2DQJ	Y_LYS_97	NZ	H_ASP_32	OD2	3.939
2DQJ	Y_LYS_97	NZ	H_ASP_99	OD1	3.482
2DQJ	Y_LYS_97	NZ	H_ASP_99	OD2	2.865
2DQJ	Y_ARG.125	NH1	Y_ASP_119	OD2	3.846
2DQJ	Y_ARG.125	NH2	Y_ASP_119	OD1	3.702
2DQJ	Y_ARG.125	NH2	Y_ASP_119	OD2	3.192
2DQT	L_LYS_50	NZ	L_ASP_30	OD2	2.780
2DQT	L_LYS_50	NZ	H_ASP_100C	OD1	3.056
2DQT	L_ARG.61	NH1	L_GLU_79	OE1	3.616
2DQT	L_ARG.61	NH2	L_GLU_81	OE1	3.572
2DQT	L_ARG.61	NH2	L_ASP_82	OD1	2.662
2DQT	L_ARG.61	NH2	L_ASP_82	OD2	3.115
2DQT	L_ARG.77	NH1	L_GLU_79	OE2	3.435
2DQT	L_LYS_103	NZ	L_GLU_105	OE2	3.442
2DQT	L_LYS_149	NZ	L_GLU_195	OE1	3.095
2DQT	L_LYS_149	NZ	L_GLU_195	OE2	3.166
2DQT	L_ARG.155	NH1	L_GLU_185	OE1	3.261
2DQT	L_ARG.155	NH1	L_GLU_185	OE2	3.888
2DQT	L_ARG.155	NH2	L_GLU_185	OE1	3.596
2DQT	L_ARG.155	NH2	L_GLU_185	OE2	2.765
2DQT	L_LYS_183	NZ	L_GLU_187	OE1	3.433
2DQT	L_LYS_183	NZ	L_GLU_187	OE2	2.630
2DQT	L_ARG.188	NH1	L_ASP_184	OD2	2.854
2DQT	L_HIS_189	ND1	L_ASP_151	OD2	2.914
2DQT	L_HIS_189	NE2	L_GLU_185	OE2	3.113
2DQT	L_LYS_199	NZ	L_ASP_110	OD2	3.558
2DQT	H_ARG_38	NH1	H_GLU_46	OE1	2.794
2DQT	H_ARG_38	NH2	H_ASP_86	OD1	2.704
2DQT	H_LYS_64	NZ	H_ASP_61	OD1	2.620
2DQT	H_ARG.66	NH1	H_ASP_86	OD1	3.819
2DQT	H_ARG.66	NH1	H_ASP_86	OD2	2.700
2DQT	H_ARG.66	NH2	H_ASP_86	OD1	2.983
2DQT	H_ARG.66	NH2	H_ASP_86	OD2	3.389
2DQT	H_ARG.83	NH2	H_GLU_85	OE1	3.980
2DQT	H_ARG.83	NH2	H_GLU_85	OE2	3.275
2DQT	H_ARG.94	NH2	H_ASP_101	OD1	3.570
2DQT	H_ARG.94	NH2	H_ASP_101	OD2	2.733
2DQT	H_ARG_100B	NH2	L_ASP_30	OD1	3.486
2DQT	H_ARG_100B	NH2	L_ASP_30	OD2	3.745
2DQU	L_ARG.24	NH1	L_ASP_70	OD1	3.427
2DQU	L_LYS_50	NZ	H_ASP_100C	OD1	2.628
2DQU	L_LYS_50	NZ	H_ASP_100C	OD2	3.616

2DQU	L_ARG_61	NH2	L_GLU_79	OE1	2.958
2DQU	L_LYS_147	NZ	L_GLU_154	OE1	3.676
2DQU	L_LYS_147	NZ	L_GLU_154	OE2	2.961
2DQU	L_LYS_147	NZ	L_GLU_195	OE2	3.938
2DQU	L_LYS_149	NZ	L_GLU_195	OE1	2.875
2DQU	L_LYS_149	NZ	L_GLU_195	OE2	3.568
2DQU	L_LYS_183	NZ	L_GLU_187	OE2	3.122
2DQU	L_HIS_189	ND1	L_ASP_151	OD2	3.386
2DQU	L_HIS_189	NE2	L_GLU_185	OE2	2.712
2DQU	L_LYS_199	NZ	L_ASP_110	OD2	3.230
2DQU	H_ARG_38	NH1	H_GLU_46	OE1	2.604
2DQU	H_ARG_38	NH1	H_ASP_86	OD1	3.950
2DQU	H_ARG_38	NH2	H_ASP_86	OD1	2.687
2DQU	H_ARG_44	NH2	H_GLU_46	OE1	2.549
2DQU	H_ARG_44	NH2	H_GLU_46	OE2	2.851
2DQU	H_ARG_66	NH1	H_ASP_86	OD1	3.787
2DQU	H_ARG_66	NH1	H_ASP_86	OD2	2.695
2DQU	H_ARG_66	NH2	H_ASP_86	OD1	2.995
2DQU	H_ARG_66	NH2	H_ASP_86	OD2	3.363
2DQU	H_ARG_94	NH2	H_ASP_101	OD1	3.556
2DQU	H_ARG_94	NH2	H_ASP_101	OD2	2.729
2DQU	H_ARG_100B	NH2	L_ASP_30	OD2	2.721
2DQU	H_LYS_208	NZ	L_GLU_123	OE2	2.915
2DQU	H_ARG_213	NH1	L_GLU_123	OE1	3.471
2FB4	L_ARG_53	NH1	L_ASP_59	OD2	3.714
2FB4	L_ARG_53	NH2	L_ASP_59	OD1	3.808
2FB4	L_ARG_60	NH1	L_GLU_80	OE2	3.376
2FB4	L_ARG_60	NH2	L_GLU_80	OE2	2.766
2FB4	L_ARG_60	NH2	L_ASP_81	OD1	3.071
2FB4	L_ARG_60	NH2	L_ASP_81	OD2	2.621
2FB4	L_LYS_104	NZ	L_ASP_84	OD1	3.495
2FB4	L_LYS_104	NZ	L_ASP_84	OD2	2.981
2FB4	L_HIS_190	ND1	L_ASP_153	OD1	2.983
2FB4	H_ARG_38	NH1	H_ASP_90	OD1	2.997
2FB4	H_ARG_38	NH2	H_GLU_46	OE1	3.277
2FB4	H_ARG_38	NH2	H_GLU_46	OE2	3.164
2FB4	H_ARG_38	NH2	H_ASP_90	OD1	3.798
2FB4	H_HIS_59	NE2	H_ASP_57	OD1	3.817
2FB4	H_ARG_67	NH1	H_ASP_90	OD1	3.916
2FB4	H_ARG_67	NH1	H_ASP_90	OD2	2.836
2FB4	H_ARG_67	NH2	H_ASP_90	OD1	2.913
2FB4	H_ARG_67	NH2	H_ASP_90	OD2	3.297
2FB4	H_ARG_72	NH2	H_ASP_74	OD2	3.188
2FB4	H_ARG_98	NH2	H_ASP_106	OD1	2.760
2FB4	H_ARG_98	NH2	H_ASP_106	OD2	3.392
2FB4	H_LYS_148	NZ	L_GLU_126	OE2	2.805
2FB4	H_LYS_214	NZ	L_GLU_125	OE1	3.053
2FB4	H_LYS_214	NZ	L_GLU_125	OE2	2.759
2FD6	A_HIS_29	NE2	A_ASP_12	OD1	3.017
2FD6	A_HIS_29	NE2	A_ASP_12	OD2	3.253
2FD6	A_HIS_41	NE2	A_ASP_12	OD1	2.670
2FD6	A_HIS_41	NE2	A_ASP_12	OD2	3.732
2FD6	A_ARG_69	NH2	A_ASP_65	OD2	2.800
2FD6	A_HIS_87	ND1	U_ASP_11	OD2	3.705
2FD6	A_ARG_88	NH1	A_ASP_90	OD1	3.269
2FD6	A_ARG_88	NH1	A_ASP_90	OD2	2.893
2FD6	L_LYS_53	NZ	L_GLU_50	OE1	2.800
2FD6	L_ARG_61	NH1	L_GLU_79	OE1	3.611

2FD6	L_ARG_61	NH1	L_GLU_79	OE2	3.439
2FD6	L_ARG_61	NH2	L_GLU_79	OE1	3.617
2FD6	L_ARG_61	NH2	L_GLU_81	OE2	2.650
2FD6	L_ARG_61	NH2	L_ASP_82	OD1	2.824
2FD6	L_ARG_61	NH2	L_ASP_82	OD2	3.518
2FD6	L_LYS_103	NZ	L_ASP_164	OD1	3.838
2FD6	L_LYS_146	NZ	L_GLU_153	OE1	3.751
2FD6	L_LYS_148	NZ	L_GLU_194	OE1	2.730
2FD6	L_LYS_148	NZ	L_GLU_194	OE2	2.883
2FD6	L_ARG_154	NH1	L_GLU_184	OE1	3.569
2FD6	L_ARG_154	NH1	L_GLU_184	OE2	3.359
2FD6	L_ARG_154	NH2	L_GLU_184	OE1	2.421
2FD6	L_ARG_154	NH2	L_GLU_184	OE2	3.540
2FD6	L_ARG_187	NH1	L_ASP_183	OD1	3.359
2FD6	L_HIS_188	ND1	L_ASP_150	OD2	2.696
2FD6	H_ARG_40	NH1	H_GLU_85	OE1	2.850
2FD6	H_ARG_40	NH2	H_GLU_85	OE1	3.358
2FD6	H_LYS_64	NZ	H_GLU_61	OE1	3.156
2FD6	H_LYS_66	NZ	H_ASP_86	OD1	3.700
2FD6	H_LYS_66	NZ	H_ASP_86	OD2	2.976
2FD6	H_ARG_94	NH2	H_ASP_101	OD1	3.603
2FD6	H_ARG_94	NH2	H_ASP_101	OD2	2.621
2FD6	H_HIS_98	ND1	L_GLU_50	OE1	3.050
2FD6	H_HIS_98	ND1	L_GLU_50	OE2	3.997
2FD6	H_LYS_203	NZ	L_GLU_122	OE2	2.585
2FD6	U_ARG_2	NH2	U_ASP_74	OD1	3.037
2FD6	U_ARG_2	NH2	U_ASP_74	OD2	3.628
2FD6	U_ARG_25	NH1	U_GLU_42	OE2	3.105
2FD6	U_ARG_25	NH2	U_GLU_42	OE2	2.986
2FD6	U_ARG_30	NH2	U_GLU_39	OE1	3.610
2FD6	U_LYS_50	NZ	U_ASP_254	OD1	3.179
2FD6	U_ARG_53	NH1	U_ASP_254	OD1	3.463
2FD6	U_ARG_53	NH1	U_ASP_254	OD2	2.584
2FD6	U_ARG_53	NH2	U_ASP_254	OD2	3.352
2FD6	U_HIS_128	NE2	U_GLU_183	OE1	2.860
2FD6	U_HIS_143	NE2	U_GLU_183	OE1	3.388
2FD6	U_HIS_143	NE2	U_GLU_183	OE2	2.574
2FD6	U_ARG_145	NH2	U_ASP_124	OD2	3.333
2FD6	U_LYS_175	NZ	U_GLU_94	OE2	3.307
2FD6	U_ARG_192	NH1	H_GLU_58	OE2	2.359
2FD6	U_ARG_192	NH2	H_GLU_58	OE2	3.898
2FD6	U_HIS_260	NE2	U_ASP_262	OD1	3.106
2FD6	U_HIS_260	NE2	U_ASP_262	OD2	3.788
2FR4	L_ARG_61	NH2	L_ASP_82	OD1	2.807
2FR4	L_ARG_61	NH2	L_ASP_82	OD2	3.787
2FR4	L_LYS_142	NZ	L_GLU_105	OE1	2.764
2FR4	L_LYS_142	NZ	L_GLU_105	OE2	3.125
2FR4	L_ARG_155	NH2	L_GLU_185	OE1	3.754
2FR4	L_ARG_155	NH2	L_GLU_185	OE2	3.022
2FR4	L_LYS_183	NZ	L_GLU_187	OE1	3.253
2FR4	L_LYS_183	NZ	L_GLU_187	OE2	3.697
2FR4	L_HIS_189	ND1	L_ASP_151	OD2	3.437
2FR4	L_HIS_189	NE2	L_GLU_185	OE1	3.779
2FR4	H_LYS_38	NZ	H_GLU_85	OE1	3.892
2FR4	H_LYS_64	NZ	H_GLU_61	OE1	2.978
2FR4	H_LYS_66	NZ	H_ASP_86	OD1	2.719
2FR4	H_LYS_66	NZ	H_ASP_86	OD2	3.742
2FR4	H_ARG_94	NH2	H_ASP_101	OD1	3.962

2FR4	H_ARG_94	NH2	H_ASP_101	OD2	2.959
2FR4	H_LYS_208	NZ	L_GLU_123	OE2	3.199
2FR4	A_ARG_61	NH2	A_ASP_82	OD1	3.363
2FR4	A_LYS_142	NZ	A_ASP_143	OD1	3.736
2FR4	A_LYS_142	NZ	A_ASP_143	OD2	3.296
2FR4	A_LYS_169	NZ	A_ASP_167	OD1	3.777
2FR4	A_LYS_183	NZ	A_GLU_187	OE1	2.836
2FR4	A_LYS_183	NZ	A_GLU_187	OE2	3.027
2FR4	A_HIS_189	ND1	A_ASP_151	OD2	3.087
2FR4	B_LYS_40	NZ	B_GLU_85	OE1	3.845
2FR4	B_LYS_62	NZ	B_GLU_46	OE2	3.403
2FR4	B_LYS_64	NZ	B_GLU_61	OE2	2.733
2FR4	B_LYS_66	NZ	B_ASP_86	OD1	2.762
2FR4	B_LYS_66	NZ	B_ASP_86	OD2	3.704
2FR4	B_ARG_94	NH2	B_ASP_101	OD1	3.630
2FR4	B_ARG_94	NH2	B_ASP_101	OD2	2.755
2FR4	B_LYS_208	NZ	A_GLU_123	OE1	2.539
2H32	A_ARG_25	NH2	A_ASP_27	OD1	3.505
2H32	A_ARG_25	NH2	A_ASP_27	OD2	3.293
2H32	A_HIS_28	NE2	A_ASP_27	OD2	3.559
2H32	A_ARG_51	NH1	A_ASP_57	OD1	3.175
2H32	A_ARG_51	NH2	A_ASP_57	OD1	2.596
2H32	A_ARG_67	NH1	A_ASP_90	OD1	3.374
2H32	A_ARG_67	NH1	A_ASP_90	OD2	2.396
2H32	A_ARG_67	NH2	A_ASP_90	OD1	2.457
2H32	A_ARG_67	NH2	A_ASP_90	OD2	3.234
2H32	A_ARG_110	NH2	A_GLU_109	OE1	3.763
2H32	B_ARG_153	NH1	B_ASP_115	OD1	3.775
2H32	H_LYS_12	NZ	H_GLU_16	OE1	3.609
2H32	H_LYS_13	NZ	H_GLU_16	OE2	3.581
2H32	H_ARG_38	NH1	H_GLU_46	OE1	3.487
2H32	H_ARG_38	NH1	H_GLU_46	OE2	2.617
2H32	H_ARG_59	NH1	A_GLU_106	OE1	3.937
2H32	H_ARG_59	NH1	A_GLU_106	OE2	3.372
2H32	H_ARG_59	NH2	A_GLU_106	OE2	3.412
2H32	H_ARG_98	NH1	H_ASP_107	OD1	3.509
2H32	H_ARG_98	NH1	H_ASP_107	OD2	3.182
2H32	H_LYS_162	NZ	H_ASP_168	OD1	2.915
2H32	H_LYS_162	NZ	H_ASP_168	OD2	3.888
2H32	H_LYS_183	NZ	H_ASP_151	OD1	3.157
2H32	H_LYS_183	NZ	H_ASP_151	OD2	3.441
2H32	H_HIS_204	ND1	H_GLU_203	OE1	3.406
2H32	H_HIS_204	ND1	H_GLU_203	OE2	2.840
2H9G	A_ARG_24	NH1	A_ASP_70	OD1	3.267
2H9G	A_ARG_61	NH2	A_GLU_81	OE1	3.875
2H9G	A_ARG_61	NH2	A_ASP_82	OD1	3.215
2H9G	A_ARG_61	NH2	A_ASP_82	OD2	3.850
2H9G	A_LYS_103	NZ	A_GLU_105	OE2	3.674
2H9G	A_LYS_103	NZ	A_GLU_165	OE1	2.740
2H9G	A_LYS_103	NZ	A_GLU_165	OE2	3.762
2H9G	A_ARG_142	NH1	A_GLU_105	OE1	3.505
2H9G	A_ARG_142	NH2	A_GLU_105	OE1	3.340
2H9G	A_ARG_142	NH2	A_GLU_105	OE2	3.102
2H9G	A_LYS_149	NZ	A_GLU_195	OE2	3.684
2H9G	A_LYS_183	NZ	A_GLU_187	OE1	2.832
2H9G	A_LYS_183	NZ	A_GLU_187	OE2	3.382
2H9G	B_ARG_38	NH1	B_ASP_86	OD1	2.752
2H9G	B_ARG_38	NH2	B_GLU_46	OE1	3.198

2H9G	B_ARG_38	NH2	B_GLU_46	OE2	3.634
2H9G	B_ARG_38	NH2	B_ASP_86	OD1	3.743
2H9G	B_HIS_53	ND1	R_GLU_36	OE2	3.471
2H9G	B_ARG_66	NH1	B_ASP_86	OD2	2.729
2H9G	B_ARG_66	NH2	B_ASP_86	OD1	3.172
2H9G	B_ARG_66	NH2	B_ASP_86	OD2	3.302
2H9G	B_ARG_94	NH2	B_ASP_101	OD2	3.035
2H9G	B_LYS_143	NZ	B_ASP_144	OD1	3.273
2H9G	B_LYS_143	NZ	B_ASP_144	OD2	3.261
2H9G	B_LYS_209	NZ	A_GLU_123	OE1	2.713
2H9G	R_ARG_39	NH2	R_ASP_37	OD2	2.798
2H9G	R_ARG_104	NH1	R_ASP_122	OD2	3.726
2H9G	L_ARG_24	NH1	L_ASP_70	OD1	2.993
2H9G	L_ARG_24	NH2	L_ASP_70	OD1	3.108
2H9G	L_ARG_24	NH2	L_ASP_70	OD2	3.776
2H9G	L_ARG_61	NH2	L_GLU_81	OE1	3.703
2H9G	L_ARG_61	NH2	L_ASP_82	OD1	3.174
2H9G	L_ARG_61	NH2	L_ASP_82	OD2	3.885
2H9G	L_LYS_103	NZ	L_GLU_165	OE1	2.850
2H9G	L_LYS_103	NZ	L_GLU_165	OE2	3.736
2H9G	L_LYS_149	NZ	L_GLU_195	OE2	3.720
2H9G	L_LYS_183	NZ	L_GLU_187	OE1	2.899
2H9G	L_LYS_183	NZ	L_GLU_187	OE2	2.665
2H9G	H_ARG_38	NH1	H_ASP_86	OD1	2.962
2H9G	H_ARG_38	NH2	H_GLU_46	OE1	3.123
2H9G	H_ARG_38	NH2	H_GLU_46	OE2	3.981
2H9G	H_ARG_38	NH2	H_ASP_86	OD1	3.869
2H9G	H_LYS_64	NZ	H_ASP_61	OD1	3.096
2H9G	H_ARG_66	NH1	H_ASP_86	OD1	3.877
2H9G	H_ARG_66	NH1	H_ASP_86	OD2	2.818
2H9G	H_ARG_66	NH2	H_ASP_86	OD1	3.235
2H9G	H_ARG_66	NH2	H_ASP_86	OD2	3.633
2H9G	H_ARG_94	NH2	H_ASP_101	OD2	3.129
2H9G	H_LYS_143	NZ	H_ASP_144	OD1	3.284
2H9G	H_LYS_143	NZ	H_ASP_144	OD2	3.199
2H9G	H_LYS_209	NZ	L_GLU_123	OE1	2.570
2HFG	L_ARG_61	NH2	L_GLU_81	OE2	3.934
2HFG	L_ARG_61	NH2	L_ASP_82	OD1	2.654
2HFG	L_ARG_61	NH2	L_ASP_82	OD2	3.306
2HFG	L_LYS_148	NZ	L_GLU_194	OE2	2.762
2HFG	L_LYS_168	NZ	L_ASP_166	OD1	2.951
2HFG	L_LYS_168	NZ	L_ASP_166	OD2	3.686
2HFG	L_LYS_182	NZ	L_GLU_186	OE1	3.789
2HFG	H_ARG_38	NH1	H_ASP_86	OD1	3.062
2HFG	H_ARG_38	NH2	H_GLU_46	OE1	2.864
2HFG	H_ARG_38	NH2	H_GLU_46	OE2	3.710
2HFG	H_LYS_64	NZ	H_ASP_61	OD1	3.871
2HFG	H_ARG_66	NH1	H_ASP_86	OD1	3.665
2HFG	H_ARG_66	NH1	H_ASP_86	OD2	2.735
2HFG	H_ARG_66	NH2	H_ASP_86	OD1	3.183
2HFG	H_ARG_66	NH2	H_ASP_86	OD2	3.738
2HFG	H_ARG_83	NH1	H_GLU_85	OE2	3.672
2HFG	H_ARG_94	NH2	H_ASP_101	OD1	3.612
2HFG	H_ARG_94	NH2	H_ASP_101	OD2	2.745
2HFG	H_ARG_95	NH2	R_ASP_26	OD1	2.783
2HFG	H_ARG_95	NH2	R_ASP_26	OD2	3.667
2HFG	H_LYS_143	NZ	H_ASP_144	OD1	3.062
2HFG	H_LYS_143	NZ	H_ASP_144	OD2	2.650

2HFG	H.LYS_209	NZ	L.GLU_122	OE1	3.336
2HFG	H.LYS_209	NZ	L.GLU_122	OE2	2.886
2HKF	L.ARG_24	NH2	L.ASP_75	OD2	3.672
2HKF	L.LYS_44	NZ	L.GLU_86	OE2	3.798
2HKF	L.LYS_55	NZ	P.ASP_6	OD1	2.651
2HKF	L.ARG_66	NH1	L.GLU_84	OE1	2.688
2HKF	L.ARG_66	NH1	L.GLU_84	OE2	3.893
2HKF	L.ARG_66	NH2	L.GLU_84	OE1	3.861
2HKF	L.ARG_66	NH2	L.GLU_84	OE2	3.865
2HKF	L.ARG_66	NH2	L.GLU_86	OE1	3.229
2HKF	L.ARG_66	NH2	L.ASP_87	OD1	2.449
2HKF	L.ARG_66	NH2	L.ASP_87	OD2	3.580
2HKF	L.LYS_152	NZ	L.GLU_159	OE1	3.074
2HKF	L.LYS_152	NZ	L.GLU_159	OE2	3.333
2HKF	L.LYS_154	NZ	L.GLU_200	OE1	3.172
2HKF	L.LYS_154	NZ	L.GLU_200	OE2	3.401
2HKF	L.ARG_160	NH1	L.GLU_190	OE1	2.551
2HKF	L.ARG_160	NH2	L.GLU_190	OE1	2.732
2HKF	L.ARG_160	NH2	L.GLU_190	OE2	3.200
2HKF	L.ARG_193	NH1	L.ASP_189	OD1	2.634
2HKF	L.ARG_193	NH1	L.ASP_189	OD2	3.330
2HKF	L.ARG_193	NH2	L.ASP_189	OD1	3.591
2HKF	L.LYS_204	NZ	L.ASP_115	OD2	3.829
2HKF	H.ARG_38	NH1	H.ASP_92	OD1	2.875
2HKF	H.ARG_38	NH2	H.GLU_46	OE1	3.030
2HKF	H.ARG_38	NH2	H.GLU_46	OE2	3.901
2HKF	H.ARG_38	NH2	H.ASP_92	OD1	3.900
2HKF	H.ARG_50	NH2	P.GLU_5	OE1	3.869
2HKF	H.ARG_50	NH2	P.GLU_5	OE2	2.886
2HKF	H.ARG_52	NH2	P.GLU_5	OE1	3.116
2HKF	H.ARG_69	NH1	H.ASP_92	OD1	3.597
2HKF	H.ARG_69	NH1	H.ASP_92	OD2	2.654
2HKF	H.ARG_69	NH2	H.ASP_92	OD1	2.988
2HKF	H.ARG_69	NH2	H.ASP_92	OD2	3.598
2HKF	H.ARG_74	NH1	H.ASP_76	OD1	3.578
2HKF	H.LYS_214	NZ	L.GLU_128	OE2	2.891
2HMG	A.LYS_27	NZ	B.GLU_97	OE1	2.762
2HMG	A.LYS_27	NZ	B.GLU_97	OE2	3.001
2HMG	A.ARG_57	NH1	A.GLU_82	OE1	2.651
2HMG	A.ARG_57	NH1	A.GLU_82	OE2	3.908
2HMG	A.HIS_75	ND1	A.ASP_73	OD1	3.346
2HMG	A.HIS_75	ND1	A.ASP_73	OD2	2.800
2HMG	A.HIS_75	NE2	A.ASP_63	OD1	3.583
2HMG	A.ARG_90	NH1	A.ASP_60	OD1	2.824
2HMG	A.ARG_90	NH1	A.ASP_60	OD2	3.456
2HMG	A.ARG_109	NH1	B.GLU_67	OE1	3.634
2HMG	A.ARG_109	NH1	B.GLU_67	OE2	2.959
2HMG	A.ARG_109	NH2	A.GLU_89	OE1	3.190
2HMG	A.ARG_109	NH2	A.GLU_89	OE2	2.530
2HMG	A.ARG_141	NH1	A.ASP_77	OD1	3.112
2HMG	A.ARG_141	NH1	A.ASP_77	OD2	2.766
2HMG	A.ARG_141	NH2	A.ASP_146	OD1	2.729
2HMG	A.LYS_176	NZ	A.GLU_123	OE1	2.634
2HMG	A.LYS_176	NZ	A.GLU_123	OE2	3.933
2HMG	A.HIS_183	NE2	A.GLU_190	OE1	3.669
2HMG	A.ARG_208	NH2	A.ASP_241	OD2	2.864
2HMG	A.ARG_261	NH1	A.GLU_119	OE1	2.807
2HMG	A.ARG_261	NH1	A.GLU_119	OE2	2.727

2HMG	A_ARG_261	NH2	A_GLU_119	OE1	2.881
2HMG	A_LYS_264	NZ	A_ASP_85	OD1	3.585
2HMG	A_LYS_264	NZ	A_ASP_85	OD2	2.732
2HMG	A_ARG_269	NH2	B_GLU_67	OE1	2.999
2HMG	A_LYS_292	NZ	A_ASP_291	OD1	3.659
2HMG	A_LYS_299	NZ	B_GLU_69	OE1	3.169
2HMG	B_LYS_51	NZ	B_GLU_103	OE2	3.601
2HMG	B_ARG_54	NH1	F_GLU_97	OE1	2.721
2HMG	B_ARG_54	NH2	B_GLU_57	OE1	2.859
2HMG	B_ARG_54	NH2	B_GLU_57	OE2	3.200
2HMG	B_ARG_54	NH2	F_GLU_97	OE1	3.280
2HMG	B_LYS_62	NZ	F_ASP_86	OD1	3.023
2HMG	B_LYS_62	NZ	F_ASP_86	OD2	2.718
2HMG	B_LYS_62	NZ	F_ASP_90	OD1	3.256
2HMG	B_LYS_62	NZ	F_ASP_90	OD2	2.780
2HMG	B_HIS_64	NE2	F_ASP_79	OD2	3.863
2HMG	B_LYS_68	NZ	B_GLU_85	OE1	3.214
2HMG	B_LYS_68	NZ	B_GLU_85	OE2	2.698
2HMG	B_ARG_76	NH1	D_GLU_74	OE1	3.508
2HMG	B_ARG_76	NH1	D_GLU_74	OE2	2.816
2HMG	B_ARG_76	NH1	D_GLU_81	OE1	2.774
2HMG	B_ARG_76	NH1	D_GLU_81	OE2	3.655
2HMG	B_ARG_76	NH2	D_GLU_74	OE1	2.915
2HMG	B_ARG_76	NH2	D_GLU_74	OE2	3.598
2HMG	B_LYS_88	NZ	B_GLU_85	OE1	3.844
2HMG	B_LYS_117	NZ	B_GLU_114	OE1	2.609
2HMG	B_LYS_117	NZ	B_GLU_114	OE2	3.322
2HMG	B_ARG_123	NH1	F_GLU_132	OE2	3.122
2HMG	B_ARG_123	NH2	B_GLU_120	OE1	2.604
2HMG	B_ARG_123	NH2	B_GLU_120	OE2	2.778
2HMG	B_ARG_124	NH1	F_GLU_132	OE1	3.544
2HMG	B_ARG_124	NH1	F_GLU_132	OE2	3.040
2HMG	B_ARG_127	NH2	F_GLU_131	OE1	2.502
2HMG	B_ARG_153	NH2	B_GLU_150	OE2	2.575
2HMG	B_HIS_159	NE2	B_ASP_160	OD1	3.987
2HMG	B_HIS_159	NE2	B_ASP_160	OD2	3.070
2HMG	B_ARG_163	NH1	F_GLU_131	OE1	2.668
2HMG	B_ARG_163	NH1	F_GLU_131	OE2	2.605
2HMG	B_ARG_170	NH1	B_GLU_128	OE1	3.667
2HMG	B_ARG_170	NH1	D_GLU_128	OE1	3.860
2HMG	B_ARG_170	NH2	B_GLU_131	OE2	2.770
2HMG	B_ARG_170	NH2	D_GLU_128	OE1	2.750
2HMG	B_ARG_170	NH2	D_GLU_128	OE2	3.837
2HMG	C_LYS_27	NZ	D_GLU_97	OE1	2.819
2HMG	C_LYS_27	NZ	D_GLU_97	OE2	3.060
2HMG	C_ARG_57	NH1	C_GLU_82	OE1	2.635
2HMG	C_ARG_57	NH1	C_GLU_82	OE2	3.911
2HMG	C_HIS_75	ND1	C_ASP_73	OD1	3.326
2HMG	C_HIS_75	ND1	C_ASP_73	OD2	2.769
2HMG	C_HIS_75	NE2	C_ASP_63	OD1	3.558
2HMG	C_ARG_90	NH1	C_ASP_60	OD1	2.831
2HMG	C_ARG_90	NH1	C_ASP_60	OD2	3.485
2HMG	C_ARG_109	NH1	D_GLU_67	OE1	3.653
2HMG	C_ARG_109	NH1	D_GLU_67	OE2	2.947
2HMG	C_ARG_109	NH2	C_GLU_89	OE1	3.184
2HMG	C_ARG_109	NH2	C_GLU_89	OE2	2.523
2HMG	C_ARG_141	NH1	C_ASP_77	OD1	3.115
2HMG	C_ARG_141	NH1	C_ASP_77	OD2	2.775

2HMG	C_ARG_141	NH2	C_ASP_146	OD1	2.729
2HMG	C_LYS_176	NZ	C_GLU_123	OE1	2.643
2HMG	C_LYS_176	NZ	C_GLU_123	OE2	3.924
2HMG	C_HIS_183	NE2	C_GLU_190	OE1	3.657
2HMG	C_ARG_208	NH2	C_ASP_241	OD2	2.844
2HMG	C_ARG_261	NH1	C_GLU_119	OE1	2.785
2HMG	C_ARG_261	NH1	C_GLU_119	OE2	2.729
2HMG	C_ARG_261	NH2	C_GLU_119	OE1	2.874
2HMG	C_LYS_264	NZ	C_ASP_85	OD1	3.649
2HMG	C_LYS_264	NZ	C_ASP_85	OD2	2.789
2HMG	C_ARG_269	NH2	D_GLU_67	OE1	2.972
2HMG	C_LYS_292	NZ	C_ASP_291	OD1	3.718
2HMG	C_LYS_299	NZ	D_GLU_69	OE1	3.147
2HMG	D_LYS_51	NZ	D_GLU_103	OE2	3.620
2HMG	D_ARG_54	NH1	B_GLU_97	OE1	2.735
2HMG	D_ARG_54	NH2	B_GLU_97	OE1	3.312
2HMG	D_ARG_54	NH2	D_GLU_57	OE1	2.829
2HMG	D_ARG_54	NH2	D_GLU_57	OE2	3.186
2HMG	D_LYS_62	NZ	B_ASP_86	OD1	3.037
2HMG	D_LYS_62	NZ	B_ASP_86	OD2	2.683
2HMG	D_LYS_62	NZ	B_ASP_90	OD1	3.222
2HMG	D_LYS_62	NZ	B_ASP_90	OD2	2.673
2HMG	D_HIS_64	NE2	B_ASP_79	OD2	3.737
2HMG	D_LYS_68	NZ	D_GLU_85	OE1	3.177
2HMG	D_LYS_68	NZ	D_GLU_85	OE2	2.694
2HMG	D_ARG_76	NH1	F_GLU_74	OE1	3.549
2HMG	D_ARG_76	NH1	F_GLU_74	OE2	2.731
2HMG	D_ARG_76	NH1	F_GLU_81	OE1	2.698
2HMG	D_ARG_76	NH1	F_GLU_81	OE2	3.690
2HMG	D_ARG_76	NH2	F_GLU_74	OE1	2.828
2HMG	D_ARG_76	NH2	F_GLU_74	OE2	3.390
2HMG	D_LYS_88	NZ	D_GLU_85	OE1	3.822
2HMG	D_LYS_117	NZ	D_GLU_114	OE1	2.665
2HMG	D_LYS_117	NZ	D_GLU_114	OE2	3.347
2HMG	D_ARG_123	NH1	B_GLU_132	OE2	3.058
2HMG	D_ARG_123	NH2	D_GLU_120	OE1	2.590
2HMG	D_ARG_123	NH2	D_GLU_120	OE2	2.762
2HMG	D_ARG_124	NH1	B_GLU_132	OE1	3.508
2HMG	D_ARG_124	NH1	B_GLU_132	OE2	3.040
2HMG	D_ARG_127	NH2	B_GLU_131	OE1	2.517
2HMG	D_ARG_153	NH2	D_GLU_150	OE1	2.574
2HMG	D_HIS_159	NE2	D_ASP_160	OD2	3.088
2HMG	D_ARG_163	NH1	B_GLU_131	OE1	2.667
2HMG	D_ARG_163	NH1	B_GLU_131	OE2	2.648
2HMG	D_ARG_170	NH1	D_GLU_128	OE1	3.661
2HMG	D_ARG_170	NH1	F_GLU_128	OE1	3.974
2HMG	D_ARG_170	NH2	D_GLU_131	OE2	2.792
2HMG	D_ARG_170	NH2	F_GLU_128	OE1	2.843
2HMG	E_LYS_27	NZ	F_GLU_97	OE1	2.743
2HMG	E_LYS_27	NZ	F_GLU_97	OE2	3.029
2HMG	E_ARG_57	NH1	E_GLU_82	OE1	2.650
2HMG	E_ARG_57	NH1	E_GLU_82	OE2	3.908
2HMG	E_HIS_75	ND1	E_ASP_73	OD1	3.328
2HMG	E_HIS_75	ND1	E_ASP_73	OD2	2.787
2HMG	E_HIS_75	NE2	E_ASP_63	OD1	3.573
2HMG	E_ARG_90	NH1	E_ASP_60	OD1	2.857
2HMG	E_ARG_90	NH1	E_ASP_60	OD2	3.460
2HMG	E_ARG_109	NH1	F_GLU_67	OE1	3.629

2HMG	E_ARG_109	NH1	F_GLU_67	OE2	2.891
2HMG	E_ARG_109	NH2	E_GLU_89	OE1	3.184
2HMG	E_ARG_109	NH2	E_GLU_89	OE2	2.485
2HMG	E_ARG_141	NH1	E_ASP_77	OD1	3.113
2HMG	E_ARG_141	NH1	E_ASP_77	OD2	2.782
2HMG	E_ARG_141	NH2	E_ASP_146	OD1	2.726
2HMG	E_LYS_176	NZ	E_GLU_123	OE1	2.651
2HMG	E_LYS_176	NZ	E_GLU_123	OE2	3.954
2HMG	E_HIS_183	NE2	E_GLU_190	OE1	3.654
2HMG	E_ARG_208	NH2	E_ASP_241	OD2	2.863
2HMG	E_ARG_261	NH1	E_GLU_119	OE1	2.815
2HMG	E_ARG_261	NH1	E_GLU_119	OE2	2.721
2HMG	E_ARG_261	NH2	E_GLU_119	OE1	2.908
2HMG	E_LYS_264	NZ	E_ASP_85	OD1	3.640
2HMG	E_LYS_264	NZ	E_ASP_85	OD2	2.756
2HMG	E_ARG_269	NH2	F_GLU_67	OE1	2.967
2HMG	E_LYS_292	NZ	E_ASP_291	OD1	3.670
2HMG	E_LYS_299	NZ	F_GLU_69	OE1	3.127
2HMG	F_LYS_51	NZ	F_GLU_103	OE2	3.629
2HMG	F_ARG_54	NH1	D_GLU_97	OE1	2.701
2HMG	F_ARG_54	NH2	D_GLU_97	OE1	3.310
2HMG	F_ARG_54	NH2	F_GLU_57	OE1	2.831
2HMG	F_ARG_54	NH2	F_GLU_57	OE2	3.190
2HMG	F_LYS_62	NZ	D_ASP_86	OD1	2.945
2HMG	F_LYS_62	NZ	D_ASP_86	OD2	2.624
2HMG	F_LYS_62	NZ	D_ASP_90	OD1	3.290
2HMG	F_LYS_62	NZ	D_ASP_90	OD2	2.741
2HMG	F_HIS_64	NE2	D_ASP_79	OD2	3.679
2HMG	F_LYS_68	NZ	F_GLU_85	OE1	3.184
2HMG	F_LYS_68	NZ	F_GLU_85	OE2	2.666
2HMG	F_ARG_76	NH1	B_GLU_74	OE1	3.499
2HMG	F_ARG_76	NH1	B_GLU_74	OE2	2.732
2HMG	F_ARG_76	NH1	B_GLU_81	OE1	2.710
2HMG	F_ARG_76	NH1	B_GLU_81	OE2	3.754
2HMG	F_ARG_76	NH2	B_GLU_74	OE1	2.743
2HMG	F_ARG_76	NH2	B_GLU_74	OE2	3.373
2HMG	F_LYS_88	NZ	F_GLU_85	OE1	3.793
2HMG	F_LYS_117	NZ	F_GLU_114	OE1	2.621
2HMG	F_LYS_117	NZ	F_GLU_114	OE2	3.345
2HMG	F_ARG_123	NH1	D_GLU_132	OE2	3.112
2HMG	F_ARG_123	NH2	F_GLU_120	OE1	2.606
2HMG	F_ARG_123	NH2	F_GLU_120	OE2	2.778
2HMG	F_ARG_124	NH1	D_GLU_132	OE1	3.531
2HMG	F_ARG_124	NH1	D_GLU_132	OE2	3.090
2HMG	F_ARG_127	NH2	D_GLU_131	OE1	2.569
2HMG	F_HIS_159	NE2	F_ASP_160	OD2	3.079
2HMG	F_ARG_163	NH1	D_GLU_131	OE1	2.672
2HMG	F_ARG_163	NH1	D_GLU_131	OE2	2.717
2HMG	F_ARG_170	NH1	B_GLU_128	OE1	3.849
2HMG	F_ARG_170	NH1	F_GLU_128	OE1	3.672
2HMG	F_ARG_170	NH2	B_GLU_128	OE1	2.798
2HMG	F_ARG_170	NH2	B_GLU_128	OE2	3.855
2HMG	F_ARG_170	NH2	F_GLU_131	OE2	2.792
2HQ6	A_LYS_14	NZ	A_ASP_25	OD1	2.679
2HQ6	A_LYS_14	NZ	A_ASP_25	OD2	3.183
2HQ6	A_LYS_14	NZ	A_GLU_27	OE2	3.336
2HQ6	A_LYS_18	NZ	A_GLU_165	OE1	3.585
2HQ6	A_ARG_56	NH2	A_GLU_153	OE1	3.553

2HQ6	A_ARG_95	NH2	A_GLU_8	OE1	3.484
2HQ6	A_ARG_95	NH2	A_GLU_8	OE2	3.029
2HQ6	A_HIS_107	ND1	A_ASP_85	OD2	3.517
2HQ6	A_ARG_119	NH2	A_ASP_121	OD1	2.931
2HQ6	A_ARG_119	NH2	A_ASP_121	OD2	3.815
2HQ6	A_LYS_132	NZ	A_GLU_27	OE1	3.975
2HRP	L_ARG_24	NH1	L_ASP_70	OD1	2.572
2HRP	L_ARG_24	NH1	L_ASP_70	OD2	3.000
2HRP	L_ARG_24	NH2	L_ASP_70	OD1	3.375
2HRP	L_ARG_24	NH2	L_ASP_70	OD2	3.315
2HRP	L_LYS_30	NZ	H_ASP_100B	OD2	3.323
2HRP	L_ARG_61	NH1	L_GLU_79	OE1	3.245
2HRP	L_ARG_61	NH1	L_GLU_79	OE2	3.462
2HRP	L_ARG_61	NH1	M_GLU_79	OE1	2.692
2HRP	L_ARG_61	NH1	M_GLU_79	OE2	2.607
2HRP	L_ARG_61	NH2	L_ASP_82	OD1	2.560
2HRP	L_ARG_61	NH2	L_ASP_82	OD2	3.088
2HRP	L_ARG_108	NH1	N_ASP_1	OD1	3.613
2HRP	L_ARG_108	NH1	N_ASP_1	OD2	2.869
2HRP	L_ARG_108	NH2	N_ASP_1	OD1	3.306
2HRP	L_ARG_108	NH2	N_ASP_1	OD2	3.988
2HRP	L_LYS_149	NZ	L_GLU_195	OE1	3.493
2HRP	L_ARG_155	NH1	L_GLU_185	OE2	3.630
2HRP	L_LYS_183	NZ	L_ASP_184	OD1	3.230
2HRP	L_LYS_183	NZ	L_GLU_187	OE1	3.035
2HRP	L_LYS_183	NZ	L_GLU_187	OE2	3.729
2HRP	L_ARG_188	NH1	L_GLU_185	OE1	2.934
2HRP	L_HIS_189	ND1	L_GLU_185	OE1	3.671
2HRP	L_HIS_189	ND1	L_GLU_185	OE2	3.948
2HRP	L_HIS_189	NE2	L_GLU_185	OE1	3.865
2HRP	L_LYS_199	NZ	L_ASP_110	OD2	2.970
2HRP	H_ARG_38	NH1	H_ASP_86	OD1	2.821
2HRP	H_ARG_38	NH2	H_GLU_46	OE1	3.156
2HRP	H_ARG_38	NH2	H_ASP_86	OD1	3.790
2HRP	H_ARG_66	NH1	H_ASP_86	OD1	3.830
2HRP	H_ARG_66	NH1	H_ASP_86	OD2	2.641
2HRP	H_ARG_66	NH2	H_ASP_86	OD1	2.914
2HRP	H_ARG_66	NH2	H_ASP_86	OD2	3.262
2HRP	H_ARG_83	NH1	H_GLU_85	OE1	2.871
2HRP	H_ARG_83	NH1	H_GLU_85	OE2	3.696
2HRP	H_ARG_94	NH1	H_ASP_101	OD1	3.338
2HRP	H_ARG_94	NH1	H_ASP_101	OD2	2.708
2HRP	H_ARG_100	NH1	H_ASP_100B	OD1	2.631
2HRP	H_ARG_100	NH1	H_ASP_100B	OD2	2.982
2HRP	H_LYS_205	NZ	N_ASP_207	OD2	3.339
2HRP	H_LYS_208	NZ	L_GLU_123	OE1	2.834
2HRP	M_ARG_24	NH1	M_ASP_70	OD2	3.391
2HRP	M_ARG_24	NH2	M_ASP_70	OD2	3.532
2HRP	M_LYS_30	NZ	N_ASP_100B	OD2	3.922
2HRP	M_ARG_61	NH1	L_GLU_79	OE1	2.827
2HRP	M_ARG_61	NH1	L_GLU_79	OE2	2.489
2HRP	M_ARG_61	NH1	M_GLU_79	OE1	3.762
2HRP	M_ARG_61	NH1	M_GLU_79	OE2	3.462
2HRP	M_ARG_61	NH2	L_GLU_79	OE1	3.658
2HRP	M_ARG_61	NH2	M_GLU_79	OE1	3.939
2HRP	M_ARG_61	NH2	M_ASP_82	OD1	2.828
2HRP	M_ARG_61	NH2	M_ASP_82	OD2	3.440
2HRP	M_LYS_92	NZ	M_GLU_93	OE2	2.546

2HRP	M_ARG.108	NH1	H_ASP.1	OD2	3.449
2HRP	M_ARG.108	NH1	M_ASP.170	OD2	3.998
2HRP	M_LYS.149	NZ	M_GLU.195	OE1	3.803
2HRP	M_LYS.149	NZ	M_GLU.195	OE2	2.914
2HRP	M_ARG.155	NH2	M_GLU.185	OE1	2.687
2HRP	M_ARG.155	NH2	M_GLU.185	OE2	3.383
2HRP	N_ARG.38	NH1	N_ASP.86	OD1	2.969
2HRP	N_ARG.38	NH2	N_GLU.46	OE1	3.031
2HRP	N_ARG.38	NH2	N_ASP.86	OD1	3.858
2HRP	N_LYS.43	NZ	N_GLU.46	OE1	3.283
2HRP	N_LYS.64	NZ	N_ASP.61	OD1	3.922
2HRP	N_ARG.66	NH1	N_ASP.86	OD1	3.805
2HRP	N_ARG.66	NH1	N_ASP.86	OD2	2.812
2HRP	N_ARG.66	NH2	N_ASP.86	OD1	2.794
2HRP	N_ARG.66	NH2	N_ASP.86	OD2	3.248
2HRP	N_ARG.83	NH1	N_GLU.85	OE2	3.361
2HRP	N_ARG.94	NH2	N_ASP.101	OD1	3.720
2HRP	N_ARG.94	NH2	N_ASP.101	OD2	2.978
2HRP	N_LYS.208	NZ	M_GLU.123	OE1	2.875
2HRP	N_LYS.208	NZ	M_GLU.123	OE2	3.117
2I24	N_ARG.2	NH1	N_ASP.26	OD2	2.648
2I24	N_ARG.2	NH2	N_ASP.4	OD1	3.932
2I24	N_ARG.2	NH2	N_ASP.4	OD2	2.968
2I24	N_ARG.28	NH2	N_ASP.93	OD1	2.817
2I24	N_ARG.28	NH2	N_ASP.93	OD2	3.512
2I24	N_ARG.54	NH1	N_ASP.77	OD1	3.458
2I24	N_ARG.54	NH1	N_ASP.77	OD2	2.886
2I24	N_ARG.54	NH2	N_ASP.77	OD1	2.870
2I24	N_ARG.54	NH2	N_ASP.77	OD2	3.606
2I24	N_ARG.82	NH2	N_GLU.46	OE1	2.871
2I24	N_ARG.82	NH2	N_GLU.46	OE2	3.583
2I25	N_ARG.2	NH2	N_ASP.4	OD1	2.643
2I25	N_ARG.2	NH2	N_ASP.4	OD2	3.217
2I25	N_ARG.25	NH1	O_ASP.101	OD1	3.459
2I25	N_ARG.25	NH1	O_ASP.101	OD2	3.204
2I25	N_ARG.25	NH2	N_ASP.4	OD2	2.988
2I25	N_ARG.25	NH2	O_ASP.101	OD1	2.762
2I25	N_ARG.25	NH2	O_ASP.101	OD2	3.967
2I25	N_ARG.28	NH2	N_ASP.26	OD1	2.978
2I25	N_ARG.54	NH1	N_ASP.77	OD1	3.557
2I25	N_ARG.54	NH1	N_ASP.77	OD2	2.836
2I25	N_ARG.54	NH2	N_ASP.77	OD1	2.859
2I25	N_ARG.54	NH2	N_ASP.77	OD2	3.514
2I25	N_ARG.82	NH2	N_GLU.46	OE1	3.665
2I25	N_ARG.82	NH2	N_GLU.46	OE2	2.763
2I25	N_ARG.88	NH1	N_GLU.86	OE2	2.745
2I25	N_ARG.88	NH2	L_ASP.101	OD1	2.875
2I25	N_ARG.88	NH2	L_ASP.101	OD2	3.303
2I25	L_LYS.1	NZ	L_GLU.7	OE2	3.014
2I25	L_ARG.61	NH1	L_ASP.48	OD2	3.041
2I25	L_ARG.61	NH2	N_ASP.101	OD2	3.227
2I25	L_ARG.73	NH1	N_GLU.86	OE1	3.764
2I25	L_ARG.73	NH1	N_GLU.86	OE2	2.771
2I25	L_ARG.112	NH2	N_ASP.93	OD1	2.693
2I25	O_ARG.25	NH1	O_ASP.4	OD2	2.746
2I25	O_ARG.28	NH2	O_ASP.26	OD1	3.729
2I25	O_ARG.28	NH2	O_ASP.26	OD2	3.922
2I25	O_ARG.44	NH2	N_GLU.57	OE1	3.011

2I25	O_ARG_54	NH1	O_ASP_77	OD1	3.402
2I25	O_ARG_54	NH1	O_ASP_77	OD2	2.888
2I25	O_ARG_54	NH2	O_ASP_77	OD1	2.865
2I25	O_ARG_54	NH2	O_ASP_77	OD2	3.679
2I25	O_ARG_82	NH2	O_GLU_46	OE1	3.734
2I25	O_ARG_82	NH2	O_GLU_46	OE2	2.820
2I25	O_ARG_88	NH1	O_GLU_86	OE2	2.786
2I25	O_ARG_88	NH2	M_ASP_101	OD1	2.850
2I25	O_ARG_88	NH2	M_ASP_101	OD2	3.440
2I25	M_LYS_1	NZ	M_GLU_7	OE1	3.922
2I25	M_LYS_1	NZ	M_GLU_7	OE2	2.669
2I25	M_ARG_61	NH1	M_ASP_48	OD2	3.015
2I25	M_ARG_61	NH2	O_ASP_101	OD2	2.975
2I25	M_ARG_73	NH1	O_GLU_86	OE1	3.850
2I25	M_ARG_73	NH1	O_GLU_86	OE2	2.851
2I25	M_ARG_112	NH1	O_ASP_93	OD1	3.660
2I25	M_ARG_112	NH2	O_ASP_93	OD1	3.176
2I25	M_ARG_125	NH1	M_ASP_119	OD1	3.683
2I25	M_ARG_125	NH1	M_ASP_119	OD2	2.977
2I25	M_ARG_125	NH2	M_ASP_119	OD1	3.282
2I25	M_ARG_125	NH2	M_ASP_119	OD2	3.843
2I26	N_ARG_2	NH1	N_ASP_4	OD2	3.516
2I26	N_ARG_2	NH2	N_ASP_4	OD1	3.612
2I26	N_ARG_2	NH2	N_ASP_4	OD2	3.274
2I26	N_ARG_38	NH2	N_GLU_47	OE2	3.790
2I26	N_LYS_51	NZ	N_GLU_57	OE1	3.254
2I26	N_LYS_51	NZ	N_GLU_57	OE2	3.781
2I26	N_ARG_54	NH1	N_ASP_77	OD1	3.540
2I26	N_ARG_54	NH1	N_ASP_77	OD2	3.097
2I26	N_ARG_54	NH2	N_ASP_77	OD1	2.953
2I26	N_ARG_54	NH2	N_ASP_77	OD2	3.934
2I26	N_ARG_82	NH2	N_GLU_46	OE1	3.207
2I26	N_ARG_82	NH2	N_GLU_46	OE2	3.809
2I26	N_ARG_88	NH1	N_GLU_86	OE2	2.847
2I26	N_ARG_88	NH2	L_ASP_101	OD1	3.268
2I26	N_ARG_88	NH2	L_ASP_101	OD2	3.652
2I26	L_LYS_1	NZ	L_GLU_7	OE2	3.495
2I26	L_ARG_73	NH1	N_GLU_86	OE2	3.511
2I26	L_ARG_73	NH2	N_GLU_86	OE1	3.590
2I26	L_ARG_73	NH2	N_GLU_86	OE2	3.542
2I26	L_ARG_112	NH1	N_ASP_93	OD2	3.838
2I26	L_ARG_112	NH2	N_ASP_93	OD2	3.391
2I26	O_LYS_12	NZ	O_GLU_16	OE1	2.500
2I26	O_LYS_12	NZ	O_GLU_16	OE2	3.336
2I26	O_ARG_25	NH2	O_ASP_4	OD1	3.978
2I26	O_ARG_38	NH1	O_ASP_77	OD1	3.853
2I26	O_LYS_51	NZ	O_GLU_57	OE1	2.746
2I26	O_LYS_51	NZ	O_GLU_57	OE2	3.677
2I26	O_ARG_54	NH1	O_ASP_77	OD1	3.513
2I26	O_ARG_54	NH1	O_ASP_77	OD2	3.061
2I26	O_ARG_54	NH2	O_ASP_77	OD1	3.014
2I26	O_ARG_82	NH2	O_GLU_46	OE1	3.607
2I26	O_ARG_82	NH2	O_GLU_46	OE2	2.938
2I26	O_ARG_88	NH1	M_ASP_101	OD1	2.648
2I26	O_ARG_88	NH1	M_ASP_101	OD2	2.840
2I26	O_ARG_88	NH2	O_GLU_86	OE2	3.407
2I26	M_LYS_1	NZ	M_GLU_7	OE2	2.378
2I26	M_ARG_61	NH1	M_ASP_48	OD2	3.000

2I26	M_ARG.73	NH1	O_GLU.86	OE1	2.832
2I26	M_ARG.73	NH1	O_GLU.86	OE2	3.677
2I26	M_ARG.112	NH1	O_ASP.93	OD2	3.127
2I26	M_ARG.112	NH2	O_ASP.93	OD2	3.198
2I26	P_ARG.2	NH1	P_ASP.4	OD2	3.455
2I26	P_ARG.25	NH1	P_ASP.4	OD2	3.288
2I26	P_ARG.38	NH1	P_ASP.77	OD1	3.296
2I26	P_ARG.38	NH2	P_GLU.47	OE2	3.357
2I26	P_LYS.51	NZ	P_GLU.57	OE1	2.842
2I26	P_LYS.51	NZ	P_GLU.57	OE2	3.265
2I26	P_ARG.54	NH1	P_ASP.77	OD1	3.557
2I26	P_ARG.54	NH1	P_ASP.77	OD2	3.011
2I26	P_ARG.54	NH2	P_ASP.77	OD1	2.936
2I26	P_ARG.54	NH2	P_ASP.77	OD2	3.842
2I26	P_ARG.82	NH2	P_GLU.46	OE1	3.185
2I26	P_ARG.82	NH2	P_GLU.46	OE2	3.977
2I26	P_ARG.88	NH1	Q_ASP.101	OD1	3.139
2I26	P_ARG.88	NH1	Q_ASP.101	OD2	3.016
2I26	P_ARG.88	NH2	P_GLU.86	OE2	3.489
2I26	Q_LYS.1	NZ	Q_GLU.7	OE1	3.316
2I26	Q_LYS.1	NZ	Q_GLU.7	OE2	2.614
2I26	Q_ARG.61	NH1	Q_ASP.48	OD2	2.954
2I26	Q_ARG.61	NH2	P_ASP.101	OD2	3.115
2I26	Q_ARG.73	NH1	P_GLU.86	OE2	2.623
2I26	Q_ARG.112	NH1	P_ASP.93	OD2	3.805
2I26	Q_ARG.112	NH2	P_ASP.93	OD2	3.685
2I27	N_ARG.2	NH1	N_ASP.26	OD2	2.576
2I27	N_ARG.2	NH2	N_ASP.4	OD1	3.448
2I27	N_ARG.2	NH2	N_ASP.4	OD2	2.863
2I27	N_ARG.2	NH2	N_ASP.26	OD2	3.218
2I27	N_ARG.25	NH1	N_ASP.4	OD2	2.953
2I27	N_ARG.25	NH2	O_GLU.46	OE2	3.350
2I27	N_ARG.38	NH1	N_ASP.77	OD1	3.382
2I27	N_ARG.38	NH2	N_GLU.47	OE2	3.845
2I27	N_LYS.40	NZ	N_GLU.47	OE1	3.628
2I27	N_LYS.40	NZ	N_GLU.47	OE2	3.547
2I27	N_LYS.51	NZ	N_GLU.57	OE1	2.697
2I27	N_LYS.51	NZ	N_GLU.57	OE2	3.720
2I27	N_ARG.54	NH1	N_ASP.77	OD2	3.203
2I27	N_ARG.54	NH2	N_ASP.77	OD1	3.149
2I27	N_ARG.54	NH2	N_ASP.77	OD2	3.554
2I27	N_ARG.82	NH2	N_GLU.46	OE1	3.563
2I27	N_ARG.82	NH2	N_GLU.46	OE2	3.008
2I27	N_LYS.84	NZ	N_GLU.86	OE2	3.122
2I27	O_ARG.2	NH1	O_ASP.4	OD1	3.181
2I27	O_ARG.2	NH1	O_ASP.4	OD2	2.592
2I27	O_ARG.2	NH1	O_ASP.26	OD1	3.779
2I27	O_ARG.25	NH1	O_ASP.4	OD2	2.830
2I27	O_ARG.38	NH1	O_ASP.77	OD1	3.942
2I27	O_ARG.38	NH2	O_GLU.47	OE1	3.232
2I27	O_LYS.51	NZ	O_GLU.57	OE1	2.589
2I27	O_LYS.51	NZ	O_GLU.57	OE2	3.473
2I27	O_ARG.54	NH1	O_ASP.77	OD1	3.892
2I27	O_ARG.54	NH1	O_ASP.77	OD2	2.920
2I27	O_ARG.54	NH2	O_ASP.77	OD1	2.998
2I27	O_ARG.54	NH2	O_ASP.77	OD2	3.435
2I27	O_ARG.82	NH2	O_GLU.46	OE1	3.189
2I27	O_ARG.82	NH2	O_GLU.46	OE2	3.126

2I27	O_LYS_84	NZ	O_GLU_86	OE2	2.951
2I5Y	G_LYS_121	NZ	G_GLU_429	OE2	3.126
2I5Y	G_LYS_207	NZ	G_GLU_381	OE2	3.637
2I5Y	G_HIS_249	NE2	G_GLU_482	OE1	2.873
2I5Y	G_LYS_282	NZ	G_GLU_275	OE1	2.722
2I5Y	G_LYS_348	NZ	G_GLU_269	OE1	2.750
2I5Y	G_LYS_348	NZ	G_GLU_351	OE1	3.311
2I5Y	G_LYS_348	NZ	G_GLU_351	OE2	3.874
2I5Y	G_ARG_419	NH1	H_GLU_100B	OE1	3.248
2I5Y	G_ARG_419	NH2	H_GLU_99	OE2	3.146
2I5Y	G_ARG_419	NH2	H_GLU_100D	OE2	2.601
2I5Y	G_ARG_456	NH1	G_GLU_466	OE1	2.646
2I5Y	G_ARG_469	NH2	G_ASP_457	OD1	3.980
2I5Y	G_ARG_469	NH2	G_ASP_457	OD2	2.626
2I5Y	G_ARG_476	NH1	G_GLU_102	OE2	2.957
2I5Y	G_ARG_476	NH2	G_ASP_474	OD1	3.611
2I5Y	G_ARG_476	NH2	G_ASP_474	OD2	2.800
2I5Y	G_ARG_480	NH2	G_ASP_477	OD1	3.599
2I5Y	L_ARG_24	NH1	L_GLU_70	OE1	3.407
2I5Y	L_ARG_24	NH2	L_GLU_70	OE1	3.609
2I5Y	L_ARG_24	NH2	L_GLU_70	OE2	2.932
2I5Y	L_ARG_61	NH2	L_GLU_81	OE2	2.667
2I5Y	L_ARG_61	NH2	L_ASP_82	OD1	2.958
2I5Y	L_ARG_61	NH2	L_ASP_82	OD2	3.675
2I5Y	L_LYS_149	NZ	L_GLU_195	OE1	3.958
2I5Y	L_LYS_183	NZ	L_GLU_187	OE1	2.546
2I5Y	L_HIS_189	ND1	L_ASP_151	OD2	2.886
2I5Y	H_ARG_31	NH2	H_ASP_100A	OD1	3.028
2I5Y	H_ARG_31	NH2	H_ASP_100A	OD2	3.251
2I5Y	H_ARG_38	NH2	H_ASP_86	OD2	3.623
2I5Y	H_ARG_50	NH2	H_GLU_97	OE1	2.885
2I5Y	H_ARG_66	NH1	H_ASP_86	OD1	2.818
2I5Y	H_ARG_66	NH1	H_ASP_86	OD2	3.645
2I5Y	H_ARG_66	NH2	H_ASP_86	OD1	3.819
2I5Y	H_ARG_66	NH2	H_ASP_86	OD2	3.195
2I5Y	H_LYS_73	NZ	H_ASP_55	OD2	3.789
2I5Y	H_ARG_82A	NH2	H_GLU_81	OE1	3.762
2I5Y	H_ARG_83	NH2	H_ASP_85	OD1	3.770
2I5Y	H_ARG_83	NH2	H_ASP_85	OD2	3.930
2I5Y	H_LYS_143	NZ	H_ASP_144	OD1	3.144
2I5Y	H_LYS_143	NZ	H_ASP_144	OD2	3.616
2I5Y	H_LYS_201	NZ	R_GLU_10	OE2	3.615
2I5Y	H_LYS_209	NZ	L_GLU_123	OE1	2.531
2I5Y	H_LYS_209	NZ	L_GLU_123	OE2	3.403
2I5Y	H_LYS_210	NZ	H_GLU_212	OE2	3.232
2I5Y	P_LYS_117	NZ	P_ASP_113	OD2	3.200
2I5Y	P_LYS_121	NZ	P_GLU_429	OE1	3.512
2I5Y	P_LYS_207	NZ	P_GLU_381	OE1	3.955
2I5Y	P_LYS_207	NZ	P_GLU_381	OE2	2.682
2I5Y	P_LYS_231	NZ	P_GLU_268	OE2	3.227
2I5Y	P_LYS_232	NZ	P_GLU_269	OE2	3.441
2I5Y	P_HIS_249	NE2	P_GLU_482	OE1	2.831
2I5Y	P_LYS_282	NZ	P_GLU_275	OE1	2.851
2I5Y	P_LYS_348	NZ	P_GLU_269	OE2	2.858
2I5Y	P_LYS_357	NZ	P_GLU_466	OE1	3.584
2I5Y	P_ARG_419	NH1	R_GLU_99	OE2	3.800
2I5Y	P_ARG_419	NH1	R_GLU_100D	OE1	2.563
2I5Y	P_ARG_419	NH1	R_GLU_100D	OE2	3.898

2I5Y	P_ARG_456	NH1	P_GLU_466	OE1	3.726
2I5Y	P_ARG_456	NH1	P_GLU_466	OE2	3.233
2I5Y	P_ARG_469	NH2	P_ASP_457	OD1	3.175
2I5Y	P_ARG_476	NH1	P_ASP_474	OD1	3.001
2I5Y	P_ARG_480	NH1	P_ASP_477	OD1	3.430
2I5Y	P_LYS_487	NZ	P_GLU_91	OE2	3.288
2I5Y	Q_ARG_24	NH1	Q_GLU_70	OE2	3.564
2I5Y	Q_ARG_61	NH2	Q_GLU_81	OE1	2.900
2I5Y	Q_ARG_61	NH2	Q_ASP_82	OD1	2.991
2I5Y	Q_ARG_61	NH2	Q_ASP_82	OD2	3.633
2I5Y	Q_ARG_95B	NH2	Q_ASP_1	OD2	3.695
2I5Y	Q_LYS_149	NZ	Q_GLU_195	OE1	3.615
2I5Y	Q_LYS_149	NZ	Q_GLU_195	OE2	3.356
2I5Y	Q_LYS_183	NZ	Q_GLU_187	OE1	3.007
2I5Y	Q_LYS_183	NZ	Q_GLU_187	OE2	3.247
2I5Y	Q_HIS_189	ND1	Q_ASP_151	OD1	2.992
2I5Y	R_LYS_12	NZ	R_GLU_10	OE2	3.536
2I5Y	R_ARG_31	NH2	R_ASP_100A	OD1	3.101
2I5Y	R_ARG_38	NH1	R_GLU_46	OE2	3.641
2I5Y	R_ARG_38	NH2	R_ASP_86	OD2	2.978
2I5Y	R_ARG_50	NH2	R_GLU_97	OE2	2.640
2I5Y	R_ARG_66	NH1	R_ASP_86	OD1	3.507
2I5Y	R_ARG_66	NH2	R_ASP_86	OD1	3.587
2I5Y	R_ARG_66	NH2	R_ASP_86	OD2	3.055
2I5Y	R_ARG_83	NH2	R_ASP_85	OD1	3.357
2I5Y	R_ARG_83	NH2	R_ASP_85	OD2	2.690
2I5Y	R_LYS_209	NZ	Q_GLU_123	OE2	3.373
2I5Y	R_LYS_210	NZ	R_GLU_212	OE1	3.854
2I5Y	S_ARG_9	NH1	P_ASP_368	OD2	2.853
2I5Y	S_ARG_9	NH2	P_ASP_368	OD2	3.453
2I60	G_LYS_85	NZ	G_GLU_87	OE1	2.991
2I60	G_LYS_97	NZ	G_GLU_275	OE2	3.907
2I60	G_LYS_121	NZ	G_GLU_429	OE2	3.453
2I60	G_LYS_207	NZ	G_GLU_381	OE2	3.877
2I60	G_LYS_231	NZ	G_GLU_268	OE1	3.768
2I60	G_HIS_249	NE2	G_GLU_482	OE1	2.855
2I60	G_LYS_282	NZ	G_GLU_275	OE1	2.727
2I60	G_LYS_348	NZ	G_GLU_269	OE1	3.168
2I60	G_LYS_350	NZ	G_ASP_395	OD2	3.640
2I60	G_ARG_419	NH2	H_GLU_99	OE1	3.736
2I60	G_ARG_419	NH2	H_GLU_99	OE2	2.767
2I60	G_ARG_419	NH2	H_GLU_100D	OE2	3.611
2I60	G_ARG_456	NH1	G_GLU_466	OE1	2.710
2I60	G_ARG_456	NH1	G_GLU_466	OE2	3.759
2I60	G_ARG_469	NH2	G_ASP_457	OD1	2.579
2I60	G_ARG_469	NH2	G_ASP_457	OD2	3.789
2I60	G_ARG_476	NH1	G_GLU_102	OE1	3.422
2I60	G_ARG_476	NH2	G_ASP_474	OD1	3.929
2I60	G_ARG_476	NH2	G_ASP_474	OD2	2.677
2I60	G_ARG_480	NH1	G_ASP_477	OD1	3.717
2I60	L_ARG_24	NH1	L_GLU_70	OE2	3.278
2I60	L_ARG_24	NH2	L_GLU_70	OE2	2.910
2I60	L_ARG_61	NH2	L_GLU_81	OE2	2.838
2I60	L_ARG_61	NH2	L_ASP_82	OD1	2.837
2I60	L_ARG_61	NH2	L_ASP_82	OD2	3.354
2I60	L_LYS_149	NZ	L_GLU_195	OE1	3.670
2I60	H_ARG_31	NH2	H_ASP_100A	OD1	3.164
2I60	H_ARG_31	NH2	H_ASP_100A	OD2	3.397

2I60	H_ARG_38	NH1	H_GLU_46	OE2	3.054
2I60	H_ARG_38	NH2	H_ASP_86	OD2	3.336
2I60	H_ARG_50	NH2	H_GLU_97	OE2	3.134
2I60	H_ARG_66	NH1	H_ASP_86	OD1	3.041
2I60	H_ARG_66	NH1	H_ASP_86	OD2	3.960
2I60	H_ARG_66	NH2	H_ASP_86	OD1	3.627
2I60	H_ARG_66	NH2	H_ASP_86	OD2	3.212
2I60	H_ARG_82A	NH2	H_GLU_81	OE2	3.855
2I60	H_ARG_83	NH1	H_ASP_85	OD1	3.248
2I60	H_ARG_83	NH1	H_ASP_85	OD2	3.416
2I60	H_LYS_143	NZ	H_ASP_144	OD1	3.384
2I60	H_LYS_209	NZ	L_GLU_123	OE1	3.997
2I60	H_LYS_210	NZ	H_GLU_212	OE2	3.501
2I60	P_LYS_121	NZ	P_GLU_429	OE1	3.897
2I60	P_LYS_207	NZ	P_GLU_381	OE1	3.463
2I60	P_LYS_207	NZ	P_GLU_381	OE2	2.996
2I60	P_HIS_249	NE2	P_GLU_482	OE1	2.831
2I60	P_LYS_282	NZ	P_GLU_275	OE1	2.805
2I60	P_LYS_348	NZ	P_GLU_269	OE1	2.586
2I60	P_LYS_357	NZ	P_GLU_466	OE2	3.512
2I60	P_ARG_419	NH1	R_GLU_100B	OE1	3.610
2I60	P_ARG_419	NH2	R_GLU_99	OE1	3.892
2I60	P_ARG_456	NH1	P_GLU_466	OE1	2.943
2I60	P_ARG_456	NH1	P_GLU_466	OE2	3.500
2I60	P_ARG_469	NH2	P_ASP_457	OD1	3.419
2I60	P_ARG_476	NH1	P_GLU_102	OE1	3.696
2I60	P_ARG_476	NH1	P_GLU_102	OE2	2.989
2I60	P_ARG_476	NH2	P_ASP_474	OD2	3.307
2I60	P_ARG_480	NH1	P_ASP_477	OD1	3.241
2I60	Q_ARG_24	NH1	Q_GLU_70	OE2	3.297
2I60	Q_ARG_61	NH2	Q_GLU_81	OE1	3.836
2I60	Q_ARG_61	NH2	Q_ASP_82	OD1	3.255
2I60	Q_ARG_61	NH2	Q_ASP_82	OD2	3.646
2I60	Q_LYS_183	NZ	Q_GLU_187	OE1	3.479
2I60	Q_LYS_183	NZ	Q_GLU_187	OE2	3.280
2I60	Q_HIS_189	ND1	Q_ASP_151	OD1	3.866
2I60	R_ARG_31	NH2	R_ASP_100A	OD1	3.967
2I60	R_ARG_31	NH2	R_ASP_100A	OD2	2.823
2I60	R_ARG_38	NH1	R_GLU_46	OE2	2.939
2I60	R_ARG_38	NH2	R_ASP_86	OD2	3.162
2I60	R_ARG_50	NH2	R_GLU_97	OE2	2.924
2I60	R_ARG_66	NH1	R_ASP_86	OD1	3.520
2I60	R_ARG_66	NH1	R_ASP_86	OD2	3.317
2I60	R_ARG_66	NH2	R_ASP_86	OD1	3.743
2I60	R_ARG_66	NH2	R_ASP_86	OD2	3.021
2I60	R_ARG_82A	NH2	R_GLU_81	OE1	3.453
2I60	R_ARG_83	NH2	R_ASP_85	OD1	3.280
2I60	R_LYS_143	NZ	R_ASP_144	OD1	3.244
2I60	R_LYS_143	NZ	R_ASP_144	OD2	3.755
2I60	R_LYS_209	NZ	Q_GLU_123	OE2	3.485
2I60	S_ARG_9	NH1	P_ASP_368	OD2	3.268
2I60	S_ARG_9	NH2	P_ASP_368	OD1	3.938
2I60	S_ARG_9	NH2	P_ASP_368	OD2	2.664
2IFF	L_LYS_44	NZ	H_ASP_104	OD1	2.935
2IFF	L_ARG_45	NH2	H_ASP_104	OD2	3.348
2IFF	L_ARG_60	NH2	L_ASP_81	OD1	2.794
2IFF	L_ARG_60	NH2	L_ASP_81	OD2	3.163
2IFF	L_LYS_101	NZ	L_ASP_163	OD1	3.641

2IFF	L_LYS_105	NZ	L_GLU_17	OE1	3.700
2IFF	L_LYS_105	NZ	L_GLU_17	OE2	3.218
2IFF	L_ARG_106	NH2	L_ASP_168	OD1	2.967
2IFF	L_ARG_106	NH2	L_ASP_168	OD2	3.027
2IFF	L_LYS_147	NZ	L_GLU_193	OE1	3.478
2IFF	L_LYS_147	NZ	L_GLU_193	OE2	3.002
2IFF	L_LYS_181	NZ	L_GLU_185	OE1	2.942
2IFF	L_LYS_181	NZ	L_GLU_185	OE2	3.794
2IFF	L_ARG_186	NH2	L_ASP_182	OD2	3.027
2IFF	L_HIS_187	ND1	L_ASP_149	OD2	3.188
2IFF	L_HIS_196	ND1	L_ASP_141	OD1	3.647
2IFF	H_HIS_43	ND1	H_GLU_46	OE1	3.306
2IFF	H_HIS_43	ND1	H_GLU_46	OE2	3.465
2IFF	H_HIS_43	NE2	H_GLU_46	OE2	3.940
2IFF	H_LYS_65	NZ	H_GLU_62	OE2	3.927
2IFF	H_LYS_67	NZ	H_ASP_90	OD1	3.416
2IFF	H_LYS_67	NZ	H_ASP_90	OD2	3.000
2IFF	H_LYS_208	NZ	H_ASP_210	OD1	3.142
2IFF	H_LYS_208	NZ	H_ASP_210	OD2	3.455
2IFF	H_LYS_211	NZ	L_GLU_121	OE1	3.040
2IFF	H_LYS_211	NZ	L_GLU_121	OE2	2.921
2IFF	Y_LYS_1	NZ	Y_GLU_7	OE1	2.914
2IFF	Y_LYS_1	NZ	Y_GLU_7	OE2	3.893
2IFF	Y_LYS_13	NZ	Y_ASP_18	OD2	3.220
2IFF	Y_ARG_45	NH1	H_GLU_50	OE1	3.425
2IFF	Y_ARG_45	NH1	H_GLU_50	OE2	2.959
2IFF	Y_LYS_97	NZ	Y_ASP_101	OD1	2.879
2IFF	Y_ARG_125	NH1	Y_ASP_119	OD2	3.485
2IFF	Y_ARG_125	NH2	Y_ASP_119	OD1	3.655
2IFF	Y_ARG_125	NH2	Y_ASP_119	OD2	2.761
2IG2	L_ARG_60	NH1	L_GLU_80	OE1	3.431
2IG2	L_ARG_60	NH2	L_GLU_80	OE1	2.806
2IG2	L_ARG_60	NH2	L_ASP_81	OD1	3.509
2IG2	L_ARG_60	NH2	L_ASP_81	OD2	2.584
2IG2	L_LYS_104	NZ	L_ASP_84	OD1	3.314
2IG2	L_LYS_104	NZ	L_ASP_84	OD2	2.687
2IG2	L_LYS_112	NZ	L_GLU_200	OE2	3.492
2IG2	H_ARG_38	NH1	H_ASP_90	OD2	3.025
2IG2	H_ARG_38	NH2	H_GLU_46	OE1	3.194
2IG2	H_ARG_38	NH2	H_GLU_46	OE2	3.026
2IG2	H_ARG_67	NH1	H_ASP_90	OD1	2.773
2IG2	H_ARG_67	NH2	H_ASP_90	OD1	2.946
2IG2	H_ARG_67	NH2	H_ASP_90	OD2	2.843
2IG2	H_ARG_72	NH1	H_ASP_74	OD2	3.016
2IG2	H_ARG_98	NH2	H_ASP_106	OD1	2.603
2IG2	H_ARG_98	NH2	H_ASP_106	OD2	3.320
2IG2	H_LYS_148	NZ	L_GLU_126	OE2	2.854
2IG2	H_LYS_214	NZ	L_GLU_125	OE1	3.816
2IG2	H_LYS_214	NZ	L_GLU_125	OE2	2.866
2IG2	H_ARG_215	NH1	H_GLU_217	OE1	2.857
2IG2	H_ARG_215	NH1	H_GLU_217	OE2	3.431
2IG2	H_HIS_225	ND1	H_ASP_222	OD1	2.822
2IG2	H_HIS_225	ND1	H_ASP_222	OD2	3.302
2IGF	L_LYS_50	NZ	L_ASP_30	OD1	3.055
2IGF	L_LYS_50	NZ	L_ASP_30	OD2	3.465
2IGF	L_ARG_61	NH1	L_GLU_79	OE2	3.565
2IGF	L_ARG_61	NH2	L_ASP_82	OD1	2.974
2IGF	L_ARG_61	NH2	L_ASP_82	OD2	2.588

2IGF	L_LYS_149	NZ	L_GLU_195	OE2	3.389
2IGF	L_HIS_189	ND1	L_ASP_151	OD2	3.248
2IGF	L_ARG_211	NH1	L_GLU_187	OE1	2.780
2IGF	H_ARG_38	NH1	H_GLU_46	OE1	3.128
2IGF	H_ARG_38	NH1	H_GLU_46	OE2	2.803
2IGF	H_ARG_38	NH2	H_GLU_46	OE2	3.695
2IGF	H_ARG_38	NH2	H_ASP_86	OD1	3.966
2IGF	H_ARG_44	NH1	H_GLU_46	OE1	3.519
2IGF	H_ARG_44	NH2	H_GLU_46	OE1	3.195
2IGF	H_ARG_66	NH1	H_ASP_86	OD2	3.364
2IGF	H_ARG_66	NH2	H_ASP_86	OD1	2.723
2IGF	H_ARG_66	NH2	H_ASP_86	OD2	3.057
2IGF	H_ARG_94	NH1	H_ASP_101	OD1	2.615
2IGF	H_ARG_94	NH1	H_ASP_101	OD2	2.615
2IGF	H_LYS_221	NZ	L_GLU_123	OE1	3.203
2IGF	P_LYS_75	NZ	L_ASP_28	OD1	3.253
2IGF	P_LYS_75	NZ	L_ASP_28	OD2	2.849
2IGF	P_LYS_75	NZ	L_ASP_30	OD2	3.458
2IHL	A_LYS_1	NZ	A_GLU_7	OE1	3.817
2IHL	A_LYS_1	NZ	A_GLU_7	OE2	2.767
2IHL	A_LYS_19	NZ	A_ASP_18	OD2	3.871
2IHL	A_ARG_125	NH1	A_ASP_119	OD2	2.708
2IHL	A_ARG_125	NH2	A_ASP_119	OD1	3.281
2IHL	A_ARG_125	NH2	A_ASP_119	OD2	2.935
2J4W	D_LYS_427	NZ	D_GLU_435	OE2	3.034
2J4W	D_LYS_427	NZ	H_ASP_52A	OD1	3.478
2J4W	D_LYS_427	NZ	H_ASP_52A	OD2	2.864
2J4W	H_ARG_38	NH1	H_ASP_86	OD1	2.975
2J4W	H_ARG_38	NH2	H_GLU_46	OE1	3.139
2J4W	H_LYS_64	NZ	H_ASP_61	OD1	3.371
2J4W	H_ARG_66	NH1	H_ASP_86	OD1	3.417
2J4W	H_ARG_66	NH1	H_ASP_86	OD2	3.943
2J4W	H_ARG_66	NH2	H_ASP_86	OD1	3.210
2J4W	H_ARG_66	NH2	H_ASP_86	OD2	2.467
2J4W	H_LYS_221	NZ	L_GLU_123	OE1	3.280
2J4W	H_LYS_221	NZ	L_GLU_123	OE2	3.313
2J4W	L_ARG_61	NH1	L_GLU_79	OE1	3.729
2J4W	L_ARG_61	NH1	L_GLU_79	OE2	3.488
2J4W	L_ARG_61	NH2	L_GLU_79	OE1	3.516
2J4W	L_ARG_61	NH2	L_GLU_81	OE1	2.766
2J4W	L_ARG_61	NH2	L_ASP_82	OD1	2.774
2J4W	L_ARG_61	NH2	L_ASP_82	OD2	3.759
2J4W	L_LYS_142	NZ	L_GLU_105	OE1	3.490
2J4W	L_LYS_142	NZ	L_GLU_105	OE2	3.345
2J4W	L_LYS_149	NZ	L_GLU_195	OE1	3.192
2J4W	L_LYS_149	NZ	L_GLU_195	OE2	3.504
2J4W	L_LYS_183	NZ	L_GLU_187	OE1	3.405
2J4W	L_HIS_189	ND1	L_ASP_151	OD2	3.005
2J4W	L_LYS_199	NZ	L_ASP_110	OD1	3.337
2J4W	L_LYS_199	NZ	L_ASP_110	OD2	2.705
2J5L	A_LYS_485	NZ	A_ASP_493	OD2	3.126
2J5L	A_LYS_485	NZ	C_ASP_52A	OD1	3.476
2J5L	A_LYS_485	NZ	C_ASP_52A	OD2	3.193
2J5L	B_ARG_61	NH1	B_GLU_79	OE1	3.650
2J5L	B_ARG_61	NH1	B_GLU_81	OE1	3.873
2J5L	B_ARG_61	NH2	B_GLU_79	OE1	3.530
2J5L	B_ARG_61	NH2	B_GLU_81	OE1	2.133
2J5L	B_ARG_61	NH2	B_ASP_82	OD1	3.268

2J5L	B_ARG_61	NH2	B_ASP_82	OD2	3.063
2J5L	B_LYS_107	NZ	B_GLU_17	OE1	3.863
2J5L	B_LYS_142	NZ	B_GLU_105	OE2	3.802
2J5L	B_LYS_149	NZ	B_GLU_195	OE1	3.695
2J5L	B_LYS_149	NZ	B_GLU_195	OE2	3.425
2J5L	B_LYS_183	NZ	B_GLU_187	OE1	3.637
2J5L	B_HIS_	ND1	B_ASP_	OD1	3.873
2J5L	B_HIS_	ND1	B_ASP_	OD2	2.683
2J5L	B_LYS_199	NZ	B_ASP_110	OD1	3.371
2J5L	B_LYS_199	NZ	B_ASP_110	OD2	3.451
2J5L	B_ARG_	NH2	B_GLU_187	OE2	3.792
2J5L	C_LYS_13	NZ	C_GLU_113	OE2	3.785
2J5L	C_ARG_38	NH1	C_ASP_86	OD1	3.392
2J5L	C_ARG_38	NH2	C_GLU_46	OE1	3.226
2J5L	C_ARG_38	NH2	C_ASP_86	OD1	3.787
2J5L	C_LYS_64	NZ	C_ASP_61	OD1	2.837
2J5L	C_ARG_66	NH2	C_ASP_86	OD1	3.420
2J5L	C_ARG_66	NH2	C_ASP_86	OD2	2.859
2JB6	A_ARG_63	NH1	A_ASP_84	OD1	3.533
2JB6	A_ARG_63	NH1	A_ASP_84	OD2	2.728
2JB6	A_ARG_63	NH2	A_GLU_83	OE2	3.226
2JB6	A_ARG_63	NH2	A_ASP_84	OD1	2.862
2JB6	A_ARG_63	NH2	A_ASP_84	OD2	3.549
2JB6	A_LYS_115	NZ	A_GLU_203	OE1	3.724
2JB6	A_LYS_115	NZ	A_GLU_203	OE2	2.595
2JB6	A_LYS_171	NZ	A_GLU_85	OE2	2.779
2JB6	A_LYS_176	NZ	A_ASP_143	OD2	3.821
2JB6	B_ARG_38	NH1	B_GLU_46	OE2	3.287
2JB6	B_ARG_38	NH2	B_ASP_90	OD1	2.735
2JB6	B_LYS_63	NZ	B_GLU_46	OE1	3.460
2JB6	B_LYS_63	NZ	B_GLU_46	OE2	2.655
2JB6	B_ARG_67	NH1	B_ASP_90	OD1	2.699
2JB6	B_ARG_67	NH1	B_ASP_90	OD2	3.291
2JB6	B_ARG_67	NH2	B_ASP_90	OD2	3.389
2JB6	B_ARG_87	NH2	B_ASP_90	OD1	3.736
2JB6	B_LYS_150	NZ	B_ASP_151	OD2	3.447
2JB6	B_LYS_216	NZ	A_GLU_128	OE2	3.078
2JB6	H_LYS_19	NZ	H_GLU_82	OE2	3.873
2JB6	H_ARG_38	NH1	H_ASP_90	OD1	3.271
2JB6	H_ARG_38	NH2	H_GLU_46	OE2	3.202
2JB6	H_LYS_63	NZ	H_GLU_46	OE1	3.407
2JB6	H_LYS_63	NZ	H_GLU_46	OE2	3.102
2JB6	H_ARG_67	NH1	H_ASP_90	OD1	2.780
2JB6	H_ARG_67	NH1	H_ASP_90	OD2	2.831
2JB6	H_ARG_67	NH2	H_ASP_90	OD1	3.259
2JB6	H_LYS_150	NZ	H_ASP_151	OD1	3.864
2JB6	L_ARG_63	NH1	L_ASP_84	OD1	3.793
2JB6	L_ARG_63	NH1	L_ASP_84	OD2	2.807
2JB6	L_ARG_63	NH2	L_ASP_84	OD1	2.677
2JB6	L_ARG_63	NH2	L_ASP_84	OD2	3.231
2JB6	L_LYS_115	NZ	L_GLU_203	OE2	3.325
2JB6	L_LYS_154	NZ	L_GLU_208	OE2	3.249
2JB6	L_LYS_171	NZ	L_GLU_85	OE2	2.744
2JEL	L_ARG_24	NH2	L_ASP_70	OD1	3.600
2JEL	L_ARG_24	NH2	L_ASP_70	OD2	3.545
2JEL	L_LYS_50	NZ	H_GLU_98	OE1	2.874
2JEL	L_LYS_50	NZ	P_GLU_66	OE1	3.050
2JEL	L_LYS_50	NZ	P_GLU_66	OE2	3.051

2JEL	L_ARG_54	NH2	L_ASP_60	OD1	2.887
2JEL	L_ARG_61	NH1	L_ASP_82	OD1	3.350
2JEL	L_ARG_61	NH1	L_ASP_82	OD2	2.775
2JEL	L_ARG_61	NH2	L_GLU_81	OE2	3.253
2JEL	L_ARG_61	NH2	L_ASP_82	OD1	3.113
2JEL	L_ARG_61	NH2	L_ASP_82	OD2	3.996
2JEL	L_ARG_77	NH1	L_GLU_79	OE2	3.110
2JEL	L_LYS_103	NZ	L_ASP_165	OD1	2.863
2JEL	L_LYS_142	NZ	L_ASP_143	OD1	3.795
2JEL	L_LYS_142	NZ	L_ASP_143	OD2	3.573
2JEL	L_LYS_149	NZ	L_GLU_195	OE1	3.417
2JEL	L_LYS_149	NZ	L_GLU_195	OE2	3.269
2JEL	L_HIS_189	ND1	L_ASP_152	OD1	3.014
2JEL	L_LYS_199	NZ	L_ASP_110	OD2	2.782
2JEL	H_LYS_62	NZ	H_GLU_46	OE1	3.175
2JEL	H_LYS_62	NZ	H_GLU_46	OE2	3.429
2JEL	H_LYS_66	NZ	H_ASP_86	OD1	3.906
2JEL	H_LYS_66	NZ	H_ASP_86	OD2	2.853
2JEL	H_ARG_94	NH2	H_ASP_101	OD2	2.854
2JEL	H_LYS_218	NZ	H_ASP_220	OD1	3.234
2JEL	P_LYS_79	NZ	P_GLU_75	OE2	2.896
2MCP	L_ARG_67	NH1	L_ASP_88	OD1	3.540
2MCP	L_ARG_67	NH1	L_ASP_88	OD2	2.647
2MCP	L_ARG_67	NH2	L_GLU_87	OE1	3.416
2MCP	L_ARG_67	NH2	L_ASP_88	OD1	2.658
2MCP	L_ARG_67	NH2	L_ASP_88	OD2	3.318
2MCP	L_LYS_109	NZ	L_ASP_171	OD1	3.858
2MCP	L_LYS_148	NZ	L_ASP_149	OD1	3.270
2MCP	L_LYS_148	NZ	L_ASP_149	OD2	2.997
2MCP	L_LYS_155	NZ	L_GLU_201	OE2	2.618
2MCP	L_ARG_194	NH1	L_GLU_191	OE2	3.915
2MCP	L_HIS_195	ND1	L_ASP_157	OD1	3.712
2MCP	L_LYS_205	NZ	L_ASP_116	OD2	3.742
2MCP	H_ARG_38	NH1	H_ASP_92	OD2	3.060
2MCP	H_ARG_38	NH2	H_GLU_46	OE1	3.610
2MCP	H_ARG_38	NH2	H_GLU_46	OE2	2.688
2MCP	H_ARG_52	NH2	H_GLU_61	OE1	2.754
2MCP	H_ARG_69	NH1	H_ASP_92	OD2	3.561
2MCP	H_ARG_69	NH2	H_ASP_92	OD1	2.431
2MCP	H_ARG_69	NH2	H_ASP_92	OD2	2.824
2MCP	H_ARG_89	NH2	H_GLU_91	OE1	3.538
2MCP	H_ARG_89	NH2	H_GLU_91	OE2	3.717
2MCP	H_ARG_100	NH1	H_ASP_110	OD1	2.497
2MCP	H_ARG_100	NH1	H_ASP_110	OD2	2.947
2MCP	H_ARG_126	NH1	H_ASP_152	OD2	3.242
2MCP	H_ARG_184	NH1	H_ASP_152	OD1	2.420
2MCP	H_ARG_184	NH1	H_ASP_152	OD2	2.976
2MCP	H_LYS_205	NZ	H_ASP_219	OD1	3.027
2MCP	H_LYS_205	NZ	H_ASP_219	OD2	3.236
2MKL-1	C_ARG_50	NH1	C_GLU_49	OE2	3.937
2MKL-1	C_ARG_50	NH2	C_GLU_49	OE2	3.687
2MKL-1	C_LYS_52	NZ	C_GLU_55	OE1	2.974
2MKL-1	C_LYS_104	NZ	C_ASP_80	OD1	2.719
2MKL-10	C_LYS_40	NZ	C_GLU_90	OE1	3.590
2MKL-10	C_LYS_40	NZ	C_GLU_90	OE2	2.585
2MKL-10	C_ARG_50	NH2	C_GLU_49	OE2	3.606
2MKL-10	C_LYS_65	NZ	C_ASP_6	OD1	3.508
2MKL-10	C_LYS_71	NZ	C_GLU_55	OE2	3.851

2MKL-10	C_LYS_104	NZ	C_ASP_80	OD1	3.644
2MKL-2	C_ARG_50	NH1	C_GLU_78	OE1	3.157
2MKL-2	C_ARG_50	NH1	C_GLU_78	OE2	2.728
2MKL-2	C_LYS_65	NZ	C_ASP_6	OD2	3.453
2MKL-2	C_LYS_71	NZ	C_GLU_55	OE1	2.717
2MKL-2	C_LYS_104	NZ	C_ASP_80	OD1	3.607
2MKL-3	C_ARG_3	NH1	C_GLU_93	OE1	2.682
2MKL-3	C_ARG_3	NH2	C_GLU_93	OE1	3.724
2MKL-3	C_LYS_65	NZ	C_ASP_6	OD2	3.268
2MKL-3	C_LYS_71	NZ	C_GLU_55	OE2	2.641
2MKL-3	C_LYS_104	NZ	C_ASP_80	OD1	2.606
2MKL-4	C_ARG_50	NH2	C_GLU_78	OE1	2.697
2MKL-4	C_ARG_50	NH2	C_GLU_78	OE2	3.554
2MKL-4	C_LYS_71	NZ	C_GLU_55	OE2	2.650
2MKL-5	C_ARG_50	NH1	C_GLU_78	OE1	3.904
2MKL-5	C_ARG_50	NH2	C_GLU_78	OE1	2.759
2MKL-5	C_LYS_65	NZ	C_ASP_6	OD2	2.680
2MKL-5	C_LYS_104	NZ	C_ASP_80	OD1	2.921
2MKL-6	C_LYS_13	NZ	C_GLU_17	OE1	3.559
2MKL-6	C_LYS_13	NZ	C_GLU_17	OE2	2.627
2MKL-6	C_ARG_50	NH1	C_GLU_78	OE2	3.662
2MKL-6	C_ARG_50	NH2	C_GLU_78	OE2	2.716
2MKL-6	C_LYS_65	NZ	C_ASP_6	OD2	2.594
2MKL-6	C_LYS_71	NZ	C_GLU_55	OE2	2.698
2MKL-6	C_LYS_104	NZ	C_ASP_80	OD1	2.644
2MKL-7	C_ARG_3	NH2	C_ASP_6	OD1	3.888
2MKL-7	C_ARG_3	NH2	C_ASP_6	OD2	2.720
2MKL-7	C_LYS_52	NZ	C_GLU_55	OE1	3.242
2MKL-7	C_LYS_52	NZ	C_GLU_55	OE2	2.760
2MKL-7	C_LYS_65	NZ	C_ASP_6	OD1	2.615
2MKL-8	C_ARG_50	NH1	C_GLU_78	OE1	3.617
2MKL-8	C_ARG_50	NH1	C_GLU_78	OE2	2.634
2MKL-8	C_ARG_50	NH2	C_GLU_78	OE1	3.131
2MKL-8	C_ARG_50	NH2	C_GLU_78	OE2	3.571
2MKL-8	C_LYS_65	NZ	C_ASP_6	OD1	3.884
2MKL-8	C_LYS_65	NZ	C_ASP_6	OD2	2.638
2MKL-8	C_LYS_104	NZ	C_ASP_80	OD1	2.614
2MKL-9	C_ARG_50	NH1	C_GLU_78	OE2	3.771
2MKL-9	C_ARG_50	NH2	C_GLU_78	OE2	2.683
2MKL-9	C_LYS_65	NZ	C_ASP_6	OD1	2.835
2MKL-9	C_LYS_65	NZ	C_ASP_6	OD2	2.746
2MTW	A_LYS_16	NZ	A_ASP_13	OD2	3.436
2NXY	A_LYS_207	NZ	A_GLU_381	OE1	3.502
2NXY	A_LYS_207	NZ	A_GLU_381	OE2	2.666
2NXY	A_LYS_231	NZ	A_GLU_267	OE1	3.733
2NXY	A_HIS_249	NE2	A_GLU_482	OE1	2.788
2NXY	A_LYS_348	NZ	A_GLU_269	OE2	2.765
2NXY	A_LYS_348	NZ	A_GLU_351	OE1	3.417
2NXY	A_LYS_348	NZ	A_GLU_351	OE2	3.879
2NXY	A_LYS_357	NZ	A_GLU_464	OE1	3.655
2NXY	A_LYS_357	NZ	A_GLU_464	OE2	2.914
2NXY	A_ARG_419	NH1	D_GLU_3103	OE2	3.305
2NXY	A_ARG_419	NH2	D_GLU_3103	OE2	2.288
2NXY	A_ARG_456	NH2	A_GLU_466	OE1	3.797
2NXY	A_ARG_456	NH2	A_GLU_466	OE2	3.132
2NXY	A_ARG_469	NH2	A_ASP_457	OD1	2.896
2NXY	A_ARG_469	NH2	A_ASP_457	OD2	3.967
2NXY	A_ARG_476	NH1	A_ASP_474	OD1	2.903

2NXY	A_ARG_476	NH1	A_ASP_474	OD2	3.603
2NXY	A_ARG_480	NH1	A_ASP_477	OD1	2.733
2NXY	A_LYS_487	NZ	A_GLU_91	OE2	2.870
2NXY	B_LYS_1008	NZ	B_GLU_1119	OE1	3.058
2NXY	B_LYS_1029	NZ	A_ASP_279	OD2	2.892
2NXY	B_LYS_1029	NZ	B_GLU_1085	OE1	3.597
2NXY	B_LYS_1029	NZ	B_GLU_1085	OE2	3.802
2NXY	B_ARG_1054	NH1	B_ASP_1078	OD1	3.769
2NXY	B_ARG_1054	NH1	B_ASP_1078	OD2	2.694
2NXY	B_ARG_1054	NH2	B_ASP_1078	OD1	2.766
2NXY	B_ARG_1054	NH2	B_ASP_1078	OD2	3.269
2NXY	B_ARG_1058	NH1	B_GLU_1013	OE1	3.012
2NXY	B_ARG_1058	NH1	B_GLU_1013	OE2	3.108
2NXY	B_ARG_1058	NH2	B_GLU_1013	OE2	2.848
2NXY	B_ARG_1059	NH1	A_ASP_368	OD1	3.350
2NXY	B_ARG_1059	NH1	A_ASP_368	OD2	2.835
2NXY	B_ARG_1059	NH2	A_ASP_368	OD1	2.856
2NXY	B_ARG_1059	NH2	A_ASP_368	OD2	3.647
2NXY	B_LYS_1171	NZ	B_GLU_1169	OE1	3.367
2NXY	C_ARG_2061	NH2	C_GLU_2081	OE2	3.328
2NXY	C_ARG_2061	NH2	C_ASP_2082	OD1	2.675
2NXY	C_ARG_2061	NH2	C_ASP_2082	OD2	3.402
2NXY	C_LYS_2185	NZ	C_GLU_2189	OE2	3.692
2NXY	C_LYS_2190	NZ	C_ASP_2187	OD1	3.154
2NXY	C_HIS_2191	ND1	C_ASP_2153	OD2	3.374
2NXY	D_ARG_3031	NH2	D_GLU_3103	OE1	3.976
2NXY	D_ARG_3031	NH2	D_ASP_3105	OD1	3.526
2NXY	D_ARG_3031	NH2	D_ASP_3105	OD2	3.213
2NXY	D_ARG_3038	NH1	D_ASP_3090	OD2	2.829
2NXY	D_ARG_3038	NH2	D_GLU_3046	OE2	2.946
2NXY	D_ARG_3038	NH2	D_ASP_3090	OD2	3.771
2NXY	D_ARG_3050	NH2	D_GLU_3101	OE2	2.808
2NXY	D_HIS_3063	NE2	D_GLU_3046	OE1	3.857
2NXY	D_HIS_3063	NE2	D_GLU_3046	OE2	2.872
2NXY	D_ARG_3067	NH1	D_ASP_3090	OD1	2.854
2NXY	D_ARG_3067	NH1	D_ASP_3090	OD2	3.874
2NXY	D_ARG_3067	NH2	D_ASP_3090	OD1	3.263
2NXY	D_ARG_3067	NH2	D_ASP_3090	OD2	2.885
2NXY	D_ARG_3084	NH1	D_GLU_3082	OE1	2.798
2NXY	D_LYS_3158	NZ	D_ASP_3159	OD1	3.389
2NXY	D_LYS_3158	NZ	D_ASP_3159	OD2	3.068
2NXY	D_LYS_3224	NZ	C_GLU_2125	OE2	3.113
2NXY	D_LYS_3225	NZ	D_GLU_3227	OE2	3.652
2NXZ	A_LYS_207	NZ	A_GLU_381	OE1	3.614
2NXZ	A_LYS_207	NZ	A_GLU_381	OE2	2.716
2NXZ	A_HIS_249	NE2	A_GLU_482	OE1	3.015
2NXZ	A_LYS_348	NZ	A_GLU_269	OE2	2.534
2NXZ	A_LYS_348	NZ	A_GLU_351	OE2	3.687
2NXZ	A_ARG_419	NH1	D_GLU_3103	OE2	3.647
2NXZ	A_ARG_419	NH2	D_GLU_3103	OE2	2.536
2NXZ	A_ARG_456	NH2	A_GLU_466	OE1	3.919
2NXZ	A_ARG_456	NH2	A_GLU_466	OE2	3.186
2NXZ	A_ARG_469	NH2	A_ASP_457	OD1	2.972
2NXZ	A_ARG_469	NH2	A_ASP_457	OD2	3.979
2NXZ	A_ARG_476	NH1	A_ASP_474	OD1	2.887
2NXZ	A_ARG_476	NH1	A_ASP_474	OD2	3.798
2NXZ	A_ARG_480	NH1	A_ASP_477	OD1	2.702
2NXZ	A_LYS_487	NZ	A_GLU_91	OE2	2.923

2NXZ	B_LYS_1008	NZ	B_GLU_1119	OE1	2.808
2NXZ	B_LYS_1029	NZ	A_ASP_279	OD2	3.046
2NXZ	B_LYS_1029	NZ	B_GLU_1085	OE1	3.780
2NXZ	B_ARG_1054	NH1	B_ASP_1078	OD1	3.891
2NXZ	B_ARG_1054	NH1	B_ASP_1078	OD2	2.802
2NXZ	B_ARG_1054	NH2	B_ASP_1078	OD1	2.919
2NXZ	B_ARG_1054	NH2	B_ASP_1078	OD2	3.323
2NXZ	B_ARG_1058	NH1	B_GLU_1013	OE1	3.851
2NXZ	B_ARG_1058	NH1	B_GLU_1013	OE2	3.822
2NXZ	B_ARG_1058	NH2	B_GLU_1013	OE1	3.720
2NXZ	B_ARG_1058	NH2	B_GLU_1013	OE2	2.745
2NXZ	B_ARG_1059	NH1	A_ASP_368	OD1	3.623
2NXZ	B_ARG_1059	NH1	A_ASP_368	OD2	3.029
2NXZ	B_ARG_1059	NH2	A_ASP_368	OD1	2.916
2NXZ	B_ARG_1059	NH2	A_ASP_368	OD2	3.612
2NXZ	B_LYS_1171	NZ	B_GLU_1169	OE1	2.773
2NXZ	C_ARG_2024	NH2	C_GLU_2070	OE2	3.227
2NXZ	C_ARG_2061	NH2	C_GLU_2081	OE2	3.424
2NXZ	C_ARG_2061	NH2	C_ASP_2082	OD1	2.628
2NXZ	C_ARG_2061	NH2	C_ASP_2082	OD2	3.308
2NXZ	C_LYS_2185	NZ	C_GLU_2189	OE2	3.904
2NXZ	C_LYS_2190	NZ	C_ASP_2187	OD1	3.130
2NXZ	C_HIS_2191	ND1	C_ASP_2153	OD2	3.486
2NXZ	D_ARG_3031	NH2	D_GLU_3103	OE1	3.879
2NXZ	D_ARG_3031	NH2	D_ASP_3105	OD1	3.392
2NXZ	D_ARG_3031	NH2	D_ASP_3105	OD2	3.171
2NXZ	D_ARG_3038	NH1	D_ASP_3090	OD2	2.879
2NXZ	D_ARG_3038	NH2	D_GLU_3046	OE1	3.581
2NXZ	D_ARG_3038	NH2	D_GLU_3046	OE2	3.314
2NXZ	D_ARG_3038	NH2	D_ASP_3090	OD2	3.776
2NXZ	D_ARG_3050	NH2	D_GLU_3101	OE2	2.731
2NXZ	D_ARG_3067	NH1	D_ASP_3090	OD1	2.950
2NXZ	D_ARG_3067	NH1	D_ASP_3090	OD2	3.870
2NXZ	D_ARG_3067	NH2	D_ASP_3090	OD1	3.342
2NXZ	D_ARG_3067	NH2	D_ASP_3090	OD2	2.876
2NXZ	D_ARG_3084	NH1	D_GLU_3082	OE1	2.896
2NXZ	D_ARG_3087	NH2	D_ASP_3089	OD2	3.888
2NXZ	D_HIS_3117	NE2	D_GLU_3001	OE1	3.258
2NXZ	D_LYS_3158	NZ	D_ASP_3159	OD1	3.552
2NXZ	D_LYS_3158	NZ	D_ASP_3159	OD2	3.527
2NXZ	D_HIS_3179	NE2	C_ASP_2169	OD2	3.986
2NXZ	D_LYS_3224	NZ	C_GLU_2125	OE1	3.503
2NXZ	D_LYS_3224	NZ	C_GLU_2125	OE2	2.801
2NXZ	D_LYS_3225	NZ	D_GLU_3227	OE2	3.804
2NY0	A_LYS_207	NZ	A_GLU_381	OE1	3.809
2NY0	A_LYS_207	NZ	A_GLU_381	OE2	2.857
2NY0	A_HIS_249	NE2	A_GLU_482	OE1	2.815
2NY0	A_LYS_337	NZ	A_GLU_293	OE1	3.033
2NY0	A_LYS_337	NZ	A_GLU_293	OE2	3.370
2NY0	A_LYS_348	NZ	A_GLU_269	OE2	2.803
2NY0	A_LYS_348	NZ	A_GLU_351	OE1	3.817
2NY0	A_LYS_348	NZ	A_GLU_351	OE2	3.477
2NY0	A_ARG_419	NH1	D_GLU_3103	OE2	3.320
2NY0	A_ARG_419	NH2	D_GLU_3103	OE2	2.328
2NY0	A_ARG_456	NH2	A_GLU_466	OE1	3.843
2NY0	A_ARG_456	NH2	A_GLU_466	OE2	3.172
2NY0	A_ARG_469	NH2	A_ASP_457	OD1	3.138
2NY0	A_ARG_469	NH2	A_ASP_457	OD2	3.931

2NY0	A_ARG_476	NH1	A_ASP_474	OD1	3.150
2NY0	A_ARG_476	NH1	A_ASP_474	OD2	3.157
2NY0	A_ARG_480	NH1	A_ASP_477	OD1	2.991
2NY0	A_LYS_487	NZ	A_GLU_91	OE2	3.787
2NY0	B_LYS_1008	NZ	B_GLU_1119	OE1	2.749
2NY0	B_LYS_1029	NZ	A_ASP_279	OD2	2.858
2NY0	B_LYS_1029	NZ	B_GLU_1085	OE1	3.146
2NY0	B_LYS_1029	NZ	B_GLU_1085	OE2	3.532
2NY0	B_ARG_1054	NH1	B_ASP_1078	OD1	3.780
2NY0	B_ARG_1054	NH1	B_ASP_1078	OD2	2.599
2NY0	B_ARG_1054	NH2	B_ASP_1078	OD1	2.962
2NY0	B_ARG_1054	NH2	B_ASP_1078	OD2	3.339
2NY0	B_ARG_1058	NH1	B_GLU_1013	OE1	3.138
2NY0	B_ARG_1058	NH1	B_GLU_1013	OE2	3.075
2NY0	B_ARG_1058	NH2	B_GLU_1013	OE2	3.481
2NY0	B_ARG_1059	NH1	A_ASP_368	OD1	3.389
2NY0	B_ARG_1059	NH1	A_ASP_368	OD2	2.874
2NY0	B_ARG_1059	NH2	A_ASP_368	OD1	2.859
2NY0	B_ARG_1059	NH2	A_ASP_368	OD2	3.661
2NY0	B_LYS_1171	NZ	B_GLU_1169	OE1	3.740
2NY0	C_ARG_2024	NH2	C_GLU_2070	OE2	3.845
2NY0	C_ARG_2061	NH2	C_GLU_2081	OE2	3.765
2NY0	C_ARG_2061	NH2	C_ASP_2082	OD1	2.698
2NY0	C_ARG_2061	NH2	C_ASP_2082	OD2	3.430
2NY0	C_LYS_2151	NZ	C_GLU_2197	OE1	3.031
2NY0	C_HIS_2191	ND1	C_ASP_2153	OD2	3.524
2NY0	D_LYS_3012	NZ	D_GLU_3010	OE1	3.853
2NY0	D_ARG_3031	NH2	D_ASP_3105	OD1	3.446
2NY0	D_ARG_3031	NH2	D_ASP_3105	OD2	3.463
2NY0	D_ARG_3038	NH1	D_ASP_3090	OD2	2.827
2NY0	D_ARG_3038	NH2	D_GLU_3046	OE2	2.883
2NY0	D_ARG_3038	NH2	D_ASP_3090	OD2	3.849
2NY0	D_ARG_3050	NH2	D_GLU_3101	OE2	2.918
2NY0	D_HIS_3063	NE2	D_GLU_3046	OE2	3.738
2NY0	D_ARG_3067	NH1	D_ASP_3090	OD1	2.827
2NY0	D_ARG_3067	NH1	D_ASP_3090	OD2	3.838
2NY0	D_ARG_3067	NH2	D_ASP_3090	OD1	3.421
2NY0	D_ARG_3067	NH2	D_ASP_3090	OD2	3.091
2NY0	D_ARG_3084	NH1	D_GLU_3082	OE1	2.595
2NY0	D_ARG_3087	NH2	D_ASP_3089	OD2	3.920
2NY0	D_HIS_3117	NE2	D_GLU_3001	OE1	3.721
2NY0	D_HIS_3117	NE2	D_GLU_3001	OE2	3.707
2NY0	D_LYS_3158	NZ	D_ASP_3159	OD1	3.309
2NY0	D_LYS_3158	NZ	D_ASP_3159	OD2	2.901
2NY0	D_LYS_3224	NZ	C_GLU_2125	OE2	3.518
2NY0	D_LYS_3225	NZ	D_GLU_3227	OE2	3.771
2NY1	A_LYS_207	NZ	A_GLU_381	OE1	3.601
2NY1	A_LYS_207	NZ	A_GLU_381	OE2	2.693
2NY1	A_LYS_231	NZ	A_GLU_268	OE2	3.557
2NY1	A_HIS_249	NE2	A_GLU_482	OE1	2.972
2NY1	A_LYS_348	NZ	A_GLU_269	OE2	2.629
2NY1	A_LYS_348	NZ	A_GLU_351	OE1	3.454
2NY1	A_LYS_348	NZ	A_GLU_351	OE2	3.942
2NY1	A_LYS_357	NZ	A_GLU_466	OE1	2.761
2NY1	A_ARG_419	NH1	D_GLU_3103	OE2	3.396
2NY1	A_ARG_419	NH2	D_GLU_3103	OE1	3.789
2NY1	A_ARG_419	NH2	D_GLU_3103	OE2	2.363
2NY1	A_ARG_456	NH2	A_GLU_466	OE2	3.471

2NY1	A_ARG_469	NH2	A_ASP_457	OD1	3.038
2NY1	A_ARG_476	NH1	A_ASP_474	OD1	2.963
2NY1	A_ARG_476	NH1	A_ASP_474	OD2	3.170
2NY1	A_LYS_487	NZ	A_GLU_91	OE1	2.543
2NY1	B_LYS_1007	NZ	B_ASP_1010	OD2	3.969
2NY1	B_LYS_1008	NZ	B_GLU_1119	OE1	3.276
2NY1	B_LYS_1029	NZ	A_ASP_279	OD2	3.031
2NY1	B_LYS_1029	NZ	B_GLU_1085	OE1	3.492
2NY1	B_LYS_1029	NZ	B_GLU_1085	OE2	3.928
2NY1	B_ARG_1054	NH1	B_ASP_1078	OD1	3.747
2NY1	B_ARG_1054	NH1	B_ASP_1078	OD2	2.698
2NY1	B_ARG_1054	NH2	B_ASP_1078	OD1	2.961
2NY1	B_ARG_1054	NH2	B_ASP_1078	OD2	3.434
2NY1	B_ARG_1058	NH1	B_GLU_1013	OE1	3.860
2NY1	B_ARG_1058	NH1	B_GLU_1013	OE2	3.051
2NY1	B_ARG_1058	NH2	B_GLU_1013	OE2	3.952
2NY1	B_ARG_1059	NH1	A_ASP_368	OD1	3.481
2NY1	B_ARG_1059	NH1	A_ASP_368	OD2	3.131
2NY1	B_ARG_1059	NH2	A_ASP_368	OD1	2.526
2NY1	B_ARG_1059	NH2	A_ASP_368	OD2	3.458
2NY1	B_LYS_1171	NZ	B_GLU_1169	OE1	2.799
2NY1	C_ARG_2024	NH1	C_GLU_2070	OE1	3.232
2NY1	C_ARG_2061	NH2	C_GLU_2081	OE2	3.250
2NY1	C_ARG_2061	NH2	C_ASP_2082	OD1	2.692
2NY1	C_ARG_2061	NH2	C_ASP_2082	OD2	3.384
2NY1	C_LYS_2190	NZ	C_ASP_2187	OD1	3.137
2NY1	C_HIS_2191	ND1	C_ASP_2153	OD2	3.008
2NY1	D_ARG_3031	NH2	D_GLU_3103	OE1	3.623
2NY1	D_ARG_3031	NH2	D_ASP_3105	OD1	3.228
2NY1	D_ARG_3031	NH2	D_ASP_3105	OD2	3.278
2NY1	D_ARG_3038	NH1	D_GLU_3046	OE1	3.615
2NY1	D_ARG_3038	NH1	D_GLU_3046	OE2	3.409
2NY1	D_ARG_3038	NH1	D_ASP_3090	OD2	3.757
2NY1	D_ARG_3038	NH2	D_ASP_3090	OD2	2.650
2NY1	D_ARG_3050	NH2	D_GLU_3101	OE2	2.827
2NY1	D_HIS_3063	ND1	D_GLU_3046	OE2	3.810
2NY1	D_HIS_3063	NE2	D_GLU_3046	OE2	2.146
2NY1	D_ARG_3067	NH1	D_ASP_3090	OD1	2.855
2NY1	D_ARG_3067	NH1	D_ASP_3090	OD2	3.809
2NY1	D_ARG_3067	NH2	D_ASP_3090	OD1	3.381
2NY1	D_ARG_3067	NH2	D_ASP_3090	OD2	3.002
2NY1	D_ARG_3084	NH1	D_GLU_3082	OE1	2.758
2NY1	D_HIS_3117	NE2	D_GLU_3001	OE1	3.822
2NY1	D_LYS_3158	NZ	D_ASP_3159	OD1	3.295
2NY1	D_LYS_3158	NZ	D_ASP_3159	OD2	2.966
2NY1	D_LYS_3224	NZ	C_GLU_2125	OE1	3.100
2NY1	D_LYS_3224	NZ	C_GLU_2125	OE2	3.945
2NY2	A_LYS_207	NZ	A_GLU_381	OE1	3.598
2NY2	A_LYS_207	NZ	A_GLU_381	OE2	2.704
2NY2	A_HIS_249	NE2	A_GLU_482	OE1	3.019
2NY2	A_LYS_337	NZ	A_GLU_293	OE1	2.850
2NY2	A_LYS_337	NZ	A_GLU_293	OE2	3.461
2NY2	A_LYS_348	NZ	A_GLU_269	OE2	2.783
2NY2	A_LYS_348	NZ	A_GLU_351	OE1	3.652
2NY2	A_LYS_348	NZ	A_GLU_351	OE2	3.603
2NY2	A_LYS_357	NZ	A_GLU_466	OE1	3.351
2NY2	A_ARG_419	NH1	D_GLU_3103	OE2	2.325
2NY2	A_ARG_419	NH2	D_GLU_3103	OE2	3.124

2NY2	A_ARG_456	NH2	A_GLU_466	OE1	3.779
2NY2	A_ARG_456	NH2	A_GLU_466	OE2	3.231
2NY2	A_ARG_469	NH2	A_ASP_457	OD1	2.829
2NY2	A_ARG_469	NH2	A_ASP_457	OD2	3.887
2NY2	A_ARG_476	NH2	A_ASP_474	OD1	3.619
2NY2	A_ARG_476	NH2	A_ASP_474	OD2	3.356
2NY2	A_ARG_480	NH2	A_ASP_477	OD1	3.946
2NY2	A_LYS_487	NZ	A_GLU_91	OE2	3.417
2NY2	B_LYS_1008	NZ	B_GLU_1119	OE1	3.204
2NY2	B_LYS_1029	NZ	A_ASP_279	OD2	2.981
2NY2	B_LYS_1029	NZ	B_GLU_1085	OE1	3.198
2NY2	B_LYS_1029	NZ	B_GLU_1085	OE2	3.665
2NY2	B_ARG_1054	NH1	B_ASP_1078	OD1	3.894
2NY2	B_ARG_1054	NH1	B_ASP_1078	OD2	2.718
2NY2	B_ARG_1054	NH2	B_ASP_1078	OD1	2.960
2NY2	B_ARG_1054	NH2	B_ASP_1078	OD2	3.298
2NY2	B_ARG_1058	NH1	B_GLU_1013	OE1	3.281
2NY2	B_ARG_1058	NH1	B_GLU_1013	OE2	2.757
2NY2	B_ARG_1058	NH2	B_GLU_1013	OE2	3.611
2NY2	B_ARG_1059	NH1	A_ASP_368	OD1	3.464
2NY2	B_ARG_1059	NH1	A_ASP_368	OD2	2.895
2NY2	B_ARG_1059	NH2	A_ASP_368	OD1	2.934
2NY2	B_ARG_1059	NH2	A_ASP_368	OD2	3.638
2NY2	B_LYS_1171	NZ	B_GLU_1169	OE1	3.055
2NY2	C_ARG_2024	NH1	C_GLU_2070	OE2	3.499
2NY2	C_ARG_2061	NH2	C_GLU_2081	OE2	3.670
2NY2	C_ARG_2061	NH2	C_ASP_2082	OD1	2.785
2NY2	C_ARG_2061	NH2	C_ASP_2082	OD2	3.417
2NY2	C_LYS_2151	NZ	C_GLU_2197	OE1	3.471
2NY2	C_LYS_2185	NZ	C_GLU_2189	OE2	3.651
2NY2	C_LYS_2190	NZ	C_ASP_2187	OD1	3.182
2NY2	C_HIS_2191	ND1	C_ASP_2153	OD2	3.206
2NY2	D_ARG_3031	NH2	D_GLU_3103	OE1	3.751
2NY2	D_ARG_3031	NH2	D_ASP_3105	OD1	3.389
2NY2	D_ARG_3031	NH2	D_ASP_3105	OD2	3.283
2NY2	D_ARG_3038	NH1	D_ASP_3090	OD2	2.806
2NY2	D_ARG_3038	NH2	D_GLU_3046	OE1	3.191
2NY2	D_ARG_3038	NH2	D_GLU_3046	OE2	3.670
2NY2	D_ARG_3038	NH2	D_ASP_3090	OD2	3.755
2NY2	D_ARG_3050	NH2	D_GLU_3101	OE1	3.994
2NY2	D_ARG_3050	NH2	D_GLU_3101	OE2	2.680
2NY2	D_ARG_3067	NH1	D_ASP_3090	OD1	2.784
2NY2	D_ARG_3067	NH1	D_ASP_3090	OD2	3.789
2NY2	D_ARG_3067	NH2	D_ASP_3090	OD1	3.313
2NY2	D_ARG_3067	NH2	D_ASP_3090	OD2	2.881
2NY2	D_ARG_3084	NH1	D_GLU_3082	OE1	2.941
2NY2	D_LYS_3158	NZ	D_ASP_3159	OD1	3.305
2NY2	D_LYS_3158	NZ	D_ASP_3159	OD2	3.053
2NY2	D_LYS_3224	NZ	C_GLU_2125	OE2	2.721
2NY2	D_LYS_3225	NZ	D_GLU_3227	OE2	3.413
2NY3	A_LYS_207	NZ	A_GLU_381	OE1	3.708
2NY3	A_LYS_207	NZ	A_GLU_381	OE2	2.801
2NY3	A_HIS_249	NE2	A_GLU_482	OE1	3.056
2NY3	A_LYS_348	NZ	A_GLU_269	OE2	2.607
2NY3	A_LYS_348	NZ	A_GLU_351	OE2	3.538
2NY3	A_LYS_357	NZ	A_GLU_466	OE1	3.160
2NY3	A_ARG_419	NH1	D_GLU_3103	OE2	3.671
2NY3	A_ARG_419	NH2	D_GLU_3103	OE1	3.681

2NY3	A_ARG_419	NH2	D_GLU_3103	OE2	2.058
2NY3	A_ARG_456	NH2	A_GLU_466	OE1	3.768
2NY3	A_ARG_456	NH2	A_GLU_466	OE2	3.134
2NY3	A_ARG_469	NH2	A_ASP_457	OD1	2.972
2NY3	A_ARG_476	NH1	A_ASP_474	OD1	2.845
2NY3	A_ARG_476	NH1	A_ASP_474	OD2	3.451
2NY3	A_ARG_480	NH1	A_ASP_477	OD1	2.886
2NY3	A_LYS_487	NZ	A_GLU_91	OE2	3.142
2NY3	B_LYS_1008	NZ	B_GLU_1119	OE1	3.194
2NY3	B_LYS_1029	NZ	A_ASP_279	OD2	3.124
2NY3	B_LYS_1029	NZ	B_GLU_1085	OE1	3.294
2NY3	B_LYS_1029	NZ	B_GLU_1085	OE2	3.406
2NY3	B_ARG_1054	NH1	B_ASP_1078	OD1	3.826
2NY3	B_ARG_1054	NH1	B_ASP_1078	OD2	2.678
2NY3	B_ARG_1054	NH2	B_ASP_1078	OD1	2.943
2NY3	B_ARG_1054	NH2	B_ASP_1078	OD2	3.308
2NY3	B_ARG_1058	NH1	B_GLU_1013	OE1	3.406
2NY3	B_ARG_1058	NH1	B_GLU_1013	OE2	3.310
2NY3	B_ARG_1059	NH1	A_ASP_368	OD1	2.775
2NY3	B_ARG_1059	NH1	A_ASP_368	OD2	3.550
2NY3	B_ARG_1059	NH2	A_ASP_368	OD1	3.449
2NY3	B_ARG_1059	NH2	A_ASP_368	OD2	2.862
2NY3	B_LYS_1171	NZ	B_GLU_1169	OE1	2.751
2NY3	B_LYS_1171	NZ	B_GLU_1169	OE2	3.911
2NY3	C_ARG_2024	NH1	C_GLU_2070	OE2	3.678
2NY3	C_ARG_2061	NH2	C_GLU_2081	OE2	3.396
2NY3	C_ARG_2061	NH2	C_ASP_2082	OD1	2.625
2NY3	C_ARG_2061	NH2	C_ASP_2082	OD2	3.244
2NY3	C_ARG_2097	NH1	C_ASP_2001	OD1	3.924
2NY3	C_ARG_2097	NH1	C_ASP_2001	OD2	3.626
2NY3	C_LYS_2185	NZ	C_GLU_2189	OE2	3.801
2NY3	C_LYS_2190	NZ	C_ASP_2187	OD1	3.285
2NY3	C_HIS_2191	ND1	C_ASP_2153	OD2	3.220
2NY3	D_ARG_3031	NH2	D_GLU_3103	OE1	3.899
2NY3	D_ARG_3031	NH2	D_ASP_3105	OD1	3.267
2NY3	D_ARG_3031	NH2	D_ASP_3105	OD2	3.028
2NY3	D_ARG_3038	NH1	D_GLU_3046	OE1	3.243
2NY3	D_ARG_3038	NH1	D_GLU_3046	OE2	3.575
2NY3	D_ARG_3038	NH1	D_ASP_3090	OD2	3.960
2NY3	D_ARG_3038	NH2	D_ASP_3090	OD2	2.751
2NY3	D_ARG_3050	NH2	D_GLU_3101	OE2	2.844
2NY3	D_ARG_3067	NH1	D_ASP_3090	OD1	2.783
2NY3	D_ARG_3067	NH1	D_ASP_3090	OD2	3.729
2NY3	D_ARG_3067	NH2	D_ASP_3090	OD1	3.344
2NY3	D_ARG_3067	NH2	D_ASP_3090	OD2	2.833
2NY3	D_ARG_3084	NH1	D_GLU_3082	OE1	2.996
2NY3	D_HIS_3117	NE2	D_GLU_3001	OE1	3.405
2NY3	D_LYS_3158	NZ	D_ASP_3159	OD1	3.506
2NY3	D_LYS_3158	NZ	D_ASP_3159	OD2	3.209
2NY3	D_LYS_3224	NZ	C_GLU_2125	OE1	3.624
2NY3	D_LYS_3224	NZ	C_GLU_2125	OE2	2.832
2NY3	D_LYS_3225	NZ	D_GLU_3227	OE2	3.573
2NY4	A_LYS_207	NZ	A_GLU_381	OE1	3.731
2NY4	A_LYS_207	NZ	A_GLU_381	OE2	2.708
2NY4	A_HIS_249	NE2	A_GLU_482	OE1	2.936
2NY4	A_LYS_348	NZ	A_GLU_269	OE2	2.582
2NY4	A_LYS_348	NZ	A_GLU_351	OE2	3.483
2NY4	A_ARG_419	NH1	D_GLU_3103	OE2	3.167

2NY4	A_ARG_419	NH2	D_GLU_3103	OE2	2.562
2NY4	A_ARG_456	NH2	A_GLU_466	OE1	3.845
2NY4	A_ARG_456	NH2	A_GLU_466	OE2	3.077
2NY4	A_ARG_469	NH2	A_ASP_457	OD1	2.967
2NY4	A_ARG_476	NH1	A_ASP_474	OD1	3.082
2NY4	A_ARG_476	NH1	A_ASP_474	OD2	3.721
2NY4	A_ARG_480	NH2	A_ASP_477	OD1	3.706
2NY4	A_LYS_487	NZ	A_GLU_91	OE2	2.555
2NY4	B_LYS_1008	NZ	B_GLU_1119	OE1	3.022
2NY4	B_LYS_1029	NZ	A_ASP_279	OD2	3.126
2NY4	B_LYS_1029	NZ	B_GLU_1085	OE2	3.736
2NY4	B_ARG_1054	NH1	B_ASP_1078	OD1	3.885
2NY4	B_ARG_1054	NH1	B_ASP_1078	OD2	2.724
2NY4	B_ARG_1054	NH2	B_ASP_1078	OD1	2.927
2NY4	B_ARG_1054	NH2	B_ASP_1078	OD2	3.270
2NY4	B_ARG_1058	NH2	B_GLU_1013	OE1	3.510
2NY4	B_ARG_1058	NH2	B_GLU_1013	OE2	2.959
2NY4	B_ARG_1059	NH1	A_ASP_368	OD1	3.376
2NY4	B_ARG_1059	NH1	A_ASP_368	OD2	2.816
2NY4	B_ARG_1059	NH2	A_ASP_368	OD1	2.784
2NY4	B_ARG_1059	NH2	A_ASP_368	OD2	3.537
2NY4	B_LYS_1171	NZ	B_GLU_1169	OE1	2.831
2NY4	C_ARG_2024	NH2	C_GLU_2070	OE2	3.822
2NY4	C_ARG_2061	NH2	C_GLU_2081	OE2	3.356
2NY4	C_ARG_2061	NH2	C_ASP_2082	OD1	2.733
2NY4	C_ARG_2061	NH2	C_ASP_2082	OD2	3.375
2NY4	C_LYS_2151	NZ	C_GLU_2197	OE1	3.803
2NY4	C_LYS_2190	NZ	C_ASP_2187	OD1	3.227
2NY4	C_HIS_2191	ND1	C_ASP_2153	OD2	3.008
2NY4	D_ARG_3031	NH2	D_ASP_3105	OD1	3.479
2NY4	D_ARG_3031	NH2	D_ASP_3105	OD2	2.910
2NY4	D_ARG_3038	NH1	D_ASP_3090	OD2	2.802
2NY4	D_ARG_3038	NH2	D_GLU_3046	OE1	3.197
2NY4	D_ARG_3038	NH2	D_GLU_3046	OE2	3.685
2NY4	D_ARG_3038	NH2	D_ASP_3090	OD2	3.711
2NY4	D_ARG_3050	NH2	D_GLU_3101	OE2	2.802
2NY4	D_HIS_3063	ND1	D_GLU_3046	OE2	2.743
2NY4	D_HIS_3063	NE2	D_GLU_3046	OE2	3.513
2NY4	D_ARG_3067	NH1	D_ASP_3090	OD1	2.775
2NY4	D_ARG_3067	NH1	D_ASP_3090	OD2	3.804
2NY4	D_ARG_3067	NH2	D_ASP_3090	OD1	3.309
2NY4	D_ARG_3067	NH2	D_ASP_3090	OD2	2.883
2NY4	D_ARG_3084	NH1	D_GLU_3082	OE1	3.001
2NY4	D_HIS_3117	NE2	D_GLU_3001	OE2	3.655
2NY4	D_LYS_3158	NZ	D_ASP_3159	OD1	3.252
2NY4	D_LYS_3158	NZ	D_ASP_3159	OD2	2.781
2NY4	D_LYS_3224	NZ	C_GLU_2125	OE1	3.625
2NY4	D_LYS_3224	NZ	C_GLU_2125	OE2	3.179
2NY4	D_LYS_3225	NZ	D_GLU_3227	OE2	3.815
2NY5	G_LYS_207	NZ	G_GLU_381	OE1	3.510
2NY5	G_LYS_207	NZ	G_GLU_381	OE2	2.865
2NY5	G_HIS_249	NE2	G_GLU_482	OE1	2.564
2NY5	G_LYS_348	NZ	G_GLU_269	OE2	2.724
2NY5	G_LYS_348	NZ	G_GLU_351	OE1	3.888
2NY5	G_LYS_357	NZ	G_GLU_466	OE1	3.541
2NY5	G_ARG_419	NH2	H_GLU_3103	OE2	3.818
2NY5	G_ARG_456	NH2	G_GLU_466	OE2	3.080
2NY5	G_ARG_469	NH2	G_ASP_457	OD1	3.091

2NY5	G_ARG_469	NH2	G_ASP_457	OD2	3.726
2NY5	G_ARG_476	NH1	G_ASP_474	OD1	2.768
2NY5	G_ARG_476	NH1	G_ASP_474	OD2	3.024
2NY5	G_ARG_480	NH2	G_ASP_477	OD1	2.981
2NY5	G_LYS_487	NZ	G_GLU_91	OE2	2.768
2NY5	C_LYS_1008	NZ	C_GLU_1119	OE1	3.207
2NY5	C_LYS_1029	NZ	G_ASP_279	OD2	3.358
2NY5	C_LYS_1029	NZ	C_GLU_1085	OE1	3.759
2NY5	C_ARG_1054	NH1	C_ASP_1078	OD1	3.454
2NY5	C_ARG_1054	NH1	C_ASP_1078	OD2	3.024
2NY5	C_ARG_1054	NH2	C_ASP_1078	OD1	2.904
2NY5	C_ARG_1054	NH2	C_ASP_1078	OD2	3.790
2NY5	C_ARG_1058	NH1	C_GLU_1013	OE1	2.971
2NY5	C_ARG_1058	NH1	C_GLU_1013	OE2	3.085
2NY5	C_ARG_1058	NH2	C_GLU_1013	OE2	3.977
2NY5	C_ARG_1059	NH1	G_ASP_368	OD1	3.253
2NY5	C_ARG_1059	NH1	G_ASP_368	OD2	2.656
2NY5	C_ARG_1059	NH2	G_ASP_368	OD1	2.825
2NY5	C_ARG_1059	NH2	G_ASP_368	OD2	3.554
2NY5	L_ARG_2024	NH1	L_GLU_2070	OE2	3.011
2NY5	L_ARG_2061	NH2	L_ASP_2082	OD1	2.513
2NY5	L_ARG_2061	NH2	L_ASP_2082	OD2	3.250
2NY5	L_LYS_2151	NZ	L_GLU_2197	OE1	3.120
2NY5	L_LYS_2151	NZ	L_GLU_2197	OE2	3.898
2NY5	L_LYS_2185	NZ	L_GLU_2189	OE2	3.201
2NY5	L_LYS_2190	NZ	L_ASP_2187	OD1	3.698
2NY5	L_HIS_2191	ND1	L_ASP_2153	OD2	3.806
2NY5	H_LYS_3012	NZ	H_GLU_3010	OE1	3.934
2NY5	H_LYS_3019	NZ	H_GLU_3082	OE2	3.776
2NY5	H_ARG_3031	NH2	H_ASP_3105	OD1	3.319
2NY5	H_ARG_3031	NH2	H_ASP_3105	OD2	3.589
2NY5	H_ARG_3038	NH1	H_ASP_3090	OD2	2.958
2NY5	H_ARG_3038	NH2	H_GLU_3046	OE1	3.774
2NY5	H_ARG_3038	NH2	H_GLU_3046	OE2	3.269
2NY5	H_ARG_3038	NH2	H_ASP_3090	OD2	3.880
2NY5	H_ARG_3050	NH2	H_GLU_3101	OE2	2.904
2NY5	H_HIS_3063	NE2	H_GLU_3046	OE2	2.714
2NY5	H_ARG_3067	NH1	H_ASP_3090	OD1	2.954
2NY5	H_ARG_3067	NH1	H_ASP_3090	OD2	3.690
2NY5	H_ARG_3067	NH2	H_ASP_3090	OD1	3.799
2NY5	H_ARG_3067	NH2	H_ASP_3090	OD2	3.231
2NY5	H_ARG_3084	NH1	H_GLU_3082	OE1	2.806
2NY5	H_ARG_3087	NH2	H_ASP_3089	OD2	3.608
2NY5	H_HIS_3117	NE2	H_GLU_3001	OE2	3.918
2NY5	H_LYS_3158	NZ	H_ASP_3159	OD1	3.923
2NY5	H_LYS_3158	NZ	H_ASP_3159	OD2	3.240
2NY5	H_LYS_3224	NZ	L_GLU_2125	OE1	3.285
2NY5	H_LYS_3224	NZ	L_GLU_2125	OE2	3.364
2NY6	A_LYS_207	NZ	A_GLU_381	OE1	3.730
2NY6	A_LYS_207	NZ	A_GLU_381	OE2	2.822
2NY6	A_HIS_249	NE2	A_GLU_482	OE2	3.456
2NY6	A_LYS_337	NZ	A_GLU_293	OE1	3.079
2NY6	A_LYS_337	NZ	A_GLU_293	OE2	3.670
2NY6	A_LYS_348	NZ	A_GLU_269	OE2	3.288
2NY6	A_LYS_357	NZ	A_GLU_466	OE1	2.793
2NY6	A_ARG_419	NH2	D_GLU_3103	OE1	3.563
2NY6	A_ARG_419	NH2	D_GLU_3103	OE2	2.589
2NY6	A_ARG_456	NH2	A_GLU_466	OE1	3.680

2NY6	A_ARG_456	NH2	A_GLU_466	OE2	3.058
2NY6	A_ARG_469	NH2	A_ASP_457	OD1	2.900
2NY6	A_ARG_469	NH2	A_ASP_457	OD2	3.561
2NY6	A_ARG_476	NH1	A_ASP_474	OD1	2.511
2NY6	A_ARG_476	NH1	A_ASP_474	OD2	2.768
2NY6	A_ARG_480	NH2	A_ASP_477	OD1	2.891
2NY6	A_LYS_487	NZ	A_GLU_91	OE2	3.003
2NY6	B_LYS_1008	NZ	B_GLU_1119	OE1	2.791
2NY6	B_LYS_1029	NZ	A_ASP_279	OD2	3.061
2NY6	B_LYS_1029	NZ	B_GLU_1085	OE1	3.222
2NY6	B_ARG_1054	NH1	B_ASP_1078	OD1	3.684
2NY6	B_ARG_1054	NH1	B_ASP_1078	OD2	3.346
2NY6	B_ARG_1054	NH2	B_ASP_1078	OD1	2.747
2NY6	B_ARG_1054	NH2	B_ASP_1078	OD2	3.402
2NY6	B_ARG_1058	NH1	B_GLU_1013	OE1	3.563
2NY6	B_ARG_1058	NH2	B_GLU_1013	OE1	2.875
2NY6	B_ARG_1058	NH2	B_GLU_1013	OE2	2.875
2NY6	B_ARG_1059	NH1	A_ASP_368	OD1	2.945
2NY6	B_ARG_1059	NH1	A_ASP_368	OD2	2.767
2NY6	B_ARG_1059	NH2	A_ASP_368	OD1	3.097
2NY6	B_LYS_1090	NZ	B_GLU_1085	OE2	3.439
2NY6	B_LYS_1171	NZ	B_GLU_1169	OE1	3.858
2NY6	C_ARG_2024	NH1	C_GLU_2070	OE2	3.729
2NY6	C_ARG_2061	NH2	C_GLU_2081	OE2	3.042
2NY6	C_ARG_2061	NH2	C_ASP_2082	OD1	2.719
2NY6	C_ARG_2061	NH2	C_ASP_2082	OD2	3.011
2NY6	C_ARG_2105	NH1	C_GLU_2107	OE2	3.132
2NY6	C_LYS_2151	NZ	C_GLU_2197	OE1	3.256
2NY6	C_LYS_2151	NZ	C_GLU_2197	OE2	3.632
2NY6	C_LYS_2185	NZ	C_GLU_2189	OE2	3.738
2NY6	C_LYS_2190	NZ	C_ASP_2187	OD1	3.524
2NY6	D_LYS_3012	NZ	D_GLU_3010	OE1	3.730
2NY6	D_ARG_3031	NH2	D_ASP_3105	OD1	3.047
2NY6	D_ARG_3031	NH2	D_ASP_3105	OD2	3.789
2NY6	D_ARG_3038	NH1	D_ASP_3090	OD2	3.061
2NY6	D_ARG_3038	NH2	D_GLU_3046	OE2	3.246
2NY6	D_ARG_3038	NH2	D_ASP_3090	OD2	3.492
2NY6	D_ARG_3050	NH2	D_GLU_3101	OE2	2.217
2NY6	D_HIS_3063	ND1	D_GLU_3046	OE1	3.616
2NY6	D_HIS_3063	NE2	D_GLU_3046	OE1	2.623
2NY6	D_ARG_3067	NH1	D_ASP_3090	OD1	2.710
2NY6	D_ARG_3067	NH2	D_ASP_3090	OD1	3.291
2NY6	D_ARG_3067	NH2	D_ASP_3090	OD2	3.292
2NY6	D_LYS_3074	NZ	D_ASP_3056	OD2	3.513
2NY6	D_ARG_3084	NH1	D_GLU_3082	OE1	2.898
2NY6	D_ARG_3087	NH2	D_ASP_3089	OD2	3.510
2NY6	D_HIS_3117	ND1	D_GLU_3001	OE1	3.967
2NY6	D_HIS_3117	NE2	D_GLU_3001	OE1	3.266
2NY6	D_LYS_3158	NZ	D_ASP_3159	OD1	3.626
2NY6	D_LYS_3158	NZ	D_ASP_3159	OD2	2.711
2NY6	D_LYS_3224	NZ	C_GLU_2125	OE1	3.158
2NY6	D_LYS_3224	NZ	C_GLU_2125	OE2	2.701
2NY7	G_LYS_117	NZ	G_GLU_211	OE1	2.565
2NY7	G_LYS_117	NZ	G_GLU_211	OE2	3.261
2NY7	G_LYS_231	NZ	G_GLU_267	OE1	3.791
2NY7	G_LYS_231	NZ	G_GLU_267	OE2	3.613
2NY7	G_HIS_249	NE2	G_GLU_482	OE2	3.021
2NY7	G_LYS_337	NZ	G_GLU_293	OE1	3.715

2NY7	G_LYS_348	NZ	G_GLU_269	OE1	3.162
2NY7	G_LYS_348	NZ	G_GLU_269	OE2	3.975
2NY7	G_LYS_348	NZ	G_GLU_351	OE1	3.003
2NY7	G_LYS_357	NZ	G_GLU_466	OE1	2.755
2NY7	G_ARG_456	NH1	G_GLU_466	OE1	3.969
2NY7	G_ARG_456	NH1	G_GLU_466	OE2	3.127
2NY7	G_ARG_469	NH2	G_ASP_457	OD2	2.950
2NY7	G_ARG_480	NH1	G_ASP_99	OD2	3.193
2NY7	G_ARG_480	NH1	G_ASP_474	OD1	3.425
2NY7	G_ARG_480	NH2	G_ASP_474	OD1	2.783
2NY7	G_ARG_480	NH2	G_ASP_477	OD2	2.839
2NY7	G_LYS_487	NZ	G_GLU_91	OE2	2.858
2NY7	H_ARG_38	NH1	H_GLU_46	OE1	2.977
2NY7	H_ARG_38	NH2	H_ASP_86	OD1	2.526
2NY7	H_ARG_66	NH1	H_ASP_86	OD1	3.144
2NY7	H_ARG_66	NH1	H_ASP_86	OD2	3.436
2NY7	H_ARG_66	NH2	H_ASP_86	OD1	3.533
2NY7	H_ARG_66	NH2	H_ASP_86	OD2	2.282
2NY7	H_ARG_94	NH2	H_ASP_101	OD2	2.976
2NY7	H_LYS_145	NZ	H_ASP_146	OD1	3.590
2NY7	H_LYS_145	NZ	H_ASP_146	OD2	3.675
2NY7	H_LYS_221	NZ	L_GLU_123	OE1	3.153
2NY7	L_ARG_32	NH1	H_ASP_100F	OD2	2.962
2NY7	L_ARG_61	NH1	L_ASP_82	OD1	3.480
2NY7	L_ARG_61	NH1	L_ASP_82	OD2	2.630
2NY7	L_ARG_61	NH2	L_GLU_81	OE2	3.843
2NY7	L_ARG_61	NH2	L_ASP_82	OD1	3.037
2NY7	L_ARG_61	NH2	L_ASP_82	OD2	3.695
2NY7	L_ARG_77	NH1	L_GLU_79	OE2	3.409
2NY7	L_LYS_149	NZ	L_GLU_195	OE2	2.771
2OR9	L_LYS_39	NZ	L_ASP_81	OD1	2.675
2OR9	L_LYS_39	NZ	L_ASP_81	OD2	2.850
2OR9	L_ARG_61	NH1	L_GLU_79	OE1	3.065
2OR9	L_ARG_61	NH1	L_ASP_82	OD1	3.876
2OR9	L_ARG_61	NH2	L_GLU_79	OE1	3.933
2OR9	L_ARG_61	NH2	L_ASP_82	OD1	2.452
2OR9	L_ARG_61	NH2	L_ASP_82	OD2	2.431
2OR9	L_LYS_103	NZ	L_ASP_165	OD1	3.314
2OR9	L_LYS_147	NZ	L_GLU_154	OE1	3.105
2OR9	L_LYS_149	NZ	L_GLU_195	OE1	2.901
2OR9	L_LYS_149	NZ	L_GLU_195	OE2	3.775
2OR9	L_ARG_155	NH2	L_GLU_185	OE1	2.944
2OR9	L_HIS_189	ND1	L_ASP_151	OD2	3.316
2OR9	L_LYS_199	NZ	L_ASP_110	OD2	2.936
2OR9	H_ARG_38	NH1	H_ASP_86	OD1	2.712
2OR9	H_ARG_38	NH2	H_GLU_46	OE1	2.757
2OR9	H_ARG_38	NH2	H_ASP_86	OD1	3.623
2OR9	H_ARG_53	NH2	P_GLU_8	OE2	3.967
2OR9	H_ARG_66	NH2	H_ASP_86	OD1	2.780
2OR9	H_ARG_66	NH2	H_ASP_86	OD2	2.470
2OR9	H_ARG_94	NH2	H_ASP_101	OD1	3.716
2OR9	H_ARG_94	NH2	H_ASP_101	OD2	2.813
2OR9	H_ARG_95	NH2	H_GLU_97	OE1	3.064
2OR9	H_ARG_95	NH2	H_GLU_97	OE2	2.977
2OR9	M_LYS_39	NZ	M_ASP_81	OD1	2.510
2OR9	M_LYS_39	NZ	M_ASP_81	OD2	2.625
2OR9	M_ARG_61	NH1	M_GLU_79	OE1	3.146
2OR9	M_ARG_61	NH1	M_ASP_82	OD1	3.834

2OR9	M_ARG_61	NH2	M_GLU_79	OE1	3.978
2OR9	M_ARG_61	NH2	M_ASP_82	OD1	2.403
2OR9	M_ARG_61	NH2	M_ASP_82	OD2	2.459
2OR9	M_LYS_92	NZ	M_GLU_93	OE2	3.399
2OR9	M_LYS_147	NZ	M_GLU_154	OE1	3.668
2OR9	M_LYS_149	NZ	M_GLU_195	OE1	3.660
2OR9	M_LYS_149	NZ	M_GLU_195	OE2	3.945
2OR9	M_ARG_155	NH2	M_GLU_185	OE1	2.980
2OR9	M_HIS_189	ND1	M_ASP_151	OD2	2.969
2OR9	M_LYS_199	NZ	M_ASP_110	OD2	2.911
2OR9	I_HIS_3	NE2	I_GLU_1	OE1	2.704
2OR9	I_HIS_3	NE2	I_GLU_1	OE2	3.924
2OR9	I_ARG_38	NH1	I_ASP_86	OD1	2.804
2OR9	I_ARG_38	NH2	I_GLU_46	OE1	2.738
2OR9	I_ARG_38	NH2	I_ASP_86	OD1	3.727
2OR9	I_ARG_66	NH2	I_ASP_86	OD1	2.548
2OR9	I_ARG_66	NH2	I_ASP_86	OD2	2.491
2OR9	I_ARG_94	NH2	I_ASP_101	OD1	3.025
2OR9	I_ARG_94	NH2	I_ASP_101	OD2	2.934
2OR9	I_ARG_95	NH2	I_GLU_97	OE1	3.211
2OR9	I_LYS_208	NZ	M_GLU_123	OE2	3.803
2ORB	L_LYS_39	NZ	L_ASP_81	OD1	3.102
2ORB	L_LYS_39	NZ	L_ASP_81	OD2	2.922
2ORB	L_ARG_61	NH1	L_GLU_79	OE1	3.405
2ORB	L_ARG_61	NH1	L_GLU_79	OE2	3.954
2ORB	L_ARG_61	NH2	L_GLU_79	OE1	3.851
2ORB	L_ARG_61	NH2	L_ASP_82	OD1	2.602
2ORB	L_ARG_61	NH2	L_ASP_82	OD2	3.319
2ORB	L_LYS_92	NZ	L_GLU_93	OE2	2.584
2ORB	L_LYS_103	NZ	L_ASP_165	OD1	3.225
2ORB	L_LYS_149	NZ	L_GLU_195	OE1	3.600
2ORB	L_ARG_155	NH1	L_GLU_185	OE1	3.207
2ORB	L_ARG_155	NH2	L_GLU_185	OE1	2.465
2ORB	L_ARG_155	NH2	L_GLU_185	OE2	3.749
2ORB	L_LYS_183	NZ	L_ASP_184	OD2	3.348
2ORB	L_ARG_211	NH1	L_GLU_187	OE1	3.744
2ORB	H_HIS_3	ND1	H_GLU_1	OE1	3.990
2ORB	H_HIS_3	NE2	H_GLU_1	OE1	3.016
2ORB	H_ARG_38	NH1	H_GLU_46	OE1	3.421
2ORB	H_ARG_38	NH1	H_GLU_46	OE2	2.892
2ORB	H_ARG_38	NH2	H_ASP_86	OD1	2.745
2ORB	H_LYS_64	NZ	H_ASP_61	OD1	2.825
2ORB	H_ARG_66	NH1	H_ASP_86	OD2	2.863
2ORB	H_ARG_66	NH2	H_ASP_86	OD1	3.152
2ORB	H_ARG_66	NH2	H_ASP_86	OD2	3.464
2ORB	H_ARG_94	NH2	H_ASP_101	OD2	2.967
2ORB	M_LYS_39	NZ	M_ASP_81	OD1	3.035
2ORB	M_LYS_39	NZ	M_ASP_81	OD2	2.955
2ORB	M_ARG_61	NH1	M_GLU_79	OE1	3.351
2ORB	M_ARG_61	NH1	M_GLU_79	OE2	3.951
2ORB	M_ARG_61	NH2	M_GLU_79	OE1	3.841
2ORB	M_ARG_61	NH2	M_ASP_82	OD1	2.637
2ORB	M_ARG_61	NH2	M_ASP_82	OD2	3.364
2ORB	M_LYS_103	NZ	M_ASP_165	OD1	3.221
2ORB	M_LYS_149	NZ	M_GLU_195	OE1	3.434
2ORB	M_ARG_155	NH1	M_GLU_185	OE1	3.183
2ORB	M_ARG_155	NH2	M_GLU_185	OE1	2.497
2ORB	M_ARG_155	NH2	M_GLU_185	OE2	3.779

2ORB	M.LYS_183	NZ	M.ASP_184	OD2	3.320
2ORB	M.ARG_211	NH1	M.GLU_187	OE1	3.810
2ORB	L.HIS_3	NE2	L.GLU_1	OE1	2.997
2ORB	L.ARG_38	NH1	L.GLU_46	OE1	3.408
2ORB	L.ARG_38	NH1	L.GLU_46	OE2	2.958
2ORB	L.ARG_38	NH2	L.ASP_86	OD1	2.616
2ORB	L.LYS_64	NZ	L.ASP_61	OD1	2.889
2ORB	L.ARG_66	NH1	L.ASP_86	OD1	3.960
2ORB	L.ARG_66	NH1	L.ASP_86	OD2	2.821
2ORB	L.ARG_66	NH2	L.ASP_86	OD1	2.981
2ORB	L.ARG_66	NH2	L.ASP_86	OD2	3.330
2ORB	L.ARG_94	NH2	L.ASP_101	OD1	3.695
2ORB	L.ARG_94	NH2	L.ASP_101	OD2	3.090
2OSL	L.HIS_33	NE2	H.ASP_105	OD1	3.260
2OSL	L.HIS_33	NE2	H.ASP_105	OD2	2.885
2OSL	L.ARG_60	NH1	L.GLU_78	OE2	2.907
2OSL	L.ARG_60	NH2	L.ASP_81	OD1	2.573
2OSL	L.ARG_60	NH2	L.ASP_81	OD2	2.599
2OSL	L.LYS_102	NZ	L.GLU_164	OE1	3.278
2OSL	L.LYS_102	NZ	L.GLU_164	OE2	3.140
2OSL	L.ARG_107	NH2	B.GLU_194	OE2	3.976
2OSL	L.LYS_187	NZ	L.ASP_184	OD1	2.734
2OSL	L.LYS_187	NZ	L.ASP_184	OD2	3.949
2OSL	L.HIS_188	ND1	L.ASP_150	OD2	2.901
2OSL	H.LYS_63	NZ	H.GLU_46	OE1	3.906
2OSL	H.LYS_63	NZ	H.GLU_46	OE2	2.831
2OSL	H.LYS_67	NZ	H.ASP_90	OD1	3.942
2OSL	H.LYS_67	NZ	H.ASP_90	OD2	2.944
2OSL	H.LYS_151	NZ	H.ASP_152	OD1	3.605
2OSL	H.LYS_151	NZ	H.ASP_152	OD2	2.970
2OSL	B.HIS_33	ND1	A.ASP_105	OD2	3.615
2OSL	B.HIS_33	NE2	A.ASP_105	OD2	3.957
2OSL	B.ARG_60	NH1	B.GLU_78	OE1	3.239
2OSL	B.ARG_60	NH1	B.GLU_78	OE2	3.966
2OSL	B.ARG_60	NH2	B.ASP_81	OD1	2.569
2OSL	B.ARG_60	NH2	B.ASP_81	OD2	3.261
2OSL	B.ARG_76	NH2	B.GLU_78	OE1	3.595
2OSL	B.LYS_102	NZ	B.GLU_104	OE1	3.425
2OSL	B.ARG_141	NH2	B.GLU_160	OE1	3.816
2OSL	B.HIS_188	ND1	B.ASP_150	OD2	3.233
2OSL	A.LYS_63	NZ	A.GLU_46	OE1	2.696
2OSL	A.LYS_67	NZ	A.ASP_90	OD1	2.936
2OSL	A.LYS_67	NZ	A.ASP_90	OD2	2.944
2OSL	A.LYS_151	NZ	A.ASP_152	OD1	3.042
2OSL	A.LYS_151	NZ	A.ASP_152	OD2	3.081
2OSL	A.LYS_217	NZ	B.GLU_122	OE1	2.793
2OTU	A.ARG_65	NH1	A.ASP_86	OD1	3.180
2OTU	A.ARG_65	NH1	A.ASP_86	OD2	2.487
2OTU	A.ARG_65	NH2	A.ASP_86	OD1	3.397
2OTU	A.ARG_65	NH2	A.ASP_86	OD2	3.745
2OTU	B.ARG_38	NH1	B.ASP_90	OD1	2.946
2OTU	B.ARG_38	NH2	B.GLU_46	OE1	2.919
2OTU	B.LYS_65	NZ	B.ASP_62	OD1	3.442
2OTU	B.ARG_67	NH1	B.ASP_90	OD1	3.744
2OTU	B.ARG_67	NH1	B.ASP_90	OD2	2.752
2OTU	B.ARG_67	NH2	B.ASP_90	OD1	2.959
2OTU	B.ARG_67	NH2	B.ASP_90	OD2	3.506
2OTU	B.LYS_87	NZ	F.ASP_31	OD1	3.793

2OTU	B.LYS.87	NZ	F.ASP.31	OD2	2.711
2OTU	C.ARG.65	NH1	C.ASP.86	OD1	3.191
2OTU	C.ARG.65	NH1	C.ASP.86	OD2	2.444
2OTU	C.ARG.65	NH2	C.GLU.85	OE1	3.930
2OTU	C.ARG.65	NH2	C.ASP.86	OD1	3.938
2OTU	C.ARG.65	NH2	C.ASP.86	OD2	3.948
2OTU	D.ARG.38	NH1	D.ASP.90	OD1	2.961
2OTU	D.ARG.38	NH2	D.GLU.46	OE1	2.890
2OTU	D.ARG.38	NH2	D.GLU.46	OE2	3.975
2OTU	D.ARG.38	NH2	D.ASP.90	OD1	3.915
2OTU	D.ARG.67	NH1	D.ASP.90	OD1	3.940
2OTU	D.ARG.67	NH1	D.ASP.90	OD2	2.837
2OTU	D.ARG.67	NH2	D.ASP.90	OD1	2.974
2OTU	D.ARG.67	NH2	D.ASP.90	OD2	3.349
2OTU	E.ARG.65	NH1	E.ASP.86	OD1	3.707
2OTU	E.ARG.65	NH1	E.ASP.86	OD2	2.736
2OTU	E.ARG.65	NH2	E.ASP.86	OD1	3.658
2OTU	E.ARG.65	NH2	E.ASP.86	OD2	3.976
2OTU	F.ARG.38	NH1	F.ASP.90	OD1	2.925
2OTU	F.ARG.38	NH2	F.GLU.46	OE1	2.898
2OTU	F.ARG.38	NH2	F.ASP.90	OD1	3.956
2OTU	F.LYS.65	NZ	F.ASP.62	OD1	3.608
2OTU	F.ARG.67	NH1	F.ASP.90	OD1	3.636
2OTU	F.ARG.67	NH1	F.ASP.90	OD2	2.694
2OTU	F.ARG.67	NH2	F.ASP.90	OD1	2.962
2OTU	F.ARG.67	NH2	F.ASP.90	OD2	3.544
2OTU	F.LYS.76	NZ	F.ASP.73	OD1	3.979
2OTU	F.ARG.100	NH1	E.ASP.60	OD1	3.255
2OTU	F.ARG.100	NH1	E.ASP.60	OD2	3.915
2OTU	G.ARG.65	NH1	G.ASP.86	OD1	3.029
2OTU	G.ARG.65	NH1	G.ASP.86	OD2	2.451
2OTU	G.ARG.65	NH2	G.GLU.85	OE2	3.992
2OTU	G.ARG.65	NH2	G.ASP.86	OD1	2.757
2OTU	G.ARG.65	NH2	G.ASP.86	OD2	3.075
2OTU	H.ARG.38	NH1	H.ASP.90	OD1	2.927
2OTU	H.ARG.38	NH2	H.GLU.46	OE2	3.512
2OTU	H.ARG.44	NH1	C.ASP.60	OD1	3.017
2OTU	H.ARG.44	NH1	C.ASP.60	OD2	3.518
2OTU	H.ARG.44	NH2	C.ASP.60	OD1	3.945
2OTU	H.ARG.44	NH2	C.ASP.60	OD2	3.013
2OTU	H.ARG.67	NH1	H.ASP.90	OD1	3.843
2OTU	H.ARG.67	NH1	H.ASP.90	OD2	2.748
2OTU	H.ARG.67	NH2	H.ASP.90	OD1	3.051
2OTU	H.ARG.67	NH2	H.ASP.90	OD2	3.464
2OTU	H.LYS.87	NZ	D.ASP.31	OD1	3.910
2OTU	H.LYS.87	NZ	D.ASP.31	OD2	2.759
2OTW	A.ARG.65	NH1	A.ASP.86	OD1	2.815
2OTW	A.ARG.65	NH1	A.ASP.86	OD2	2.356
2OTW	A.ARG.65	NH2	A.GLU.85	OE2	3.711
2OTW	A.ARG.65	NH2	A.ASP.86	OD1	2.988
2OTW	A.ARG.65	NH2	A.ASP.86	OD2	3.514
2OTW	B.ARG.38	NH1	B.ASP.90	OD1	3.114
2OTW	B.ARG.38	NH2	B.GLU.46	OE1	3.177
2OTW	B.ARG.38	NH2	B.GLU.46	OE2	3.352
2OTW	B.LYS.65	NZ	B.ASP.62	OD1	3.341
2OTW	B.ARG.67	NH1	B.ASP.90	OD1	3.557
2OTW	B.ARG.67	NH1	B.ASP.90	OD2	2.723
2OTW	B.ARG.67	NH2	B.ASP.90	OD1	3.013

2OTW	B_ARG.67	NH2	B_ASP_90	OD2	3.717
2OTW	B_LYS.87	NZ	D_ASP_31	OD1	3.659
2OTW	B_LYS.87	NZ	D_ASP_31	OD2	2.671
2OTW	B_ARG.100	NH1	A_ASP_60	OD1	3.223
2OTW	B_ARG.100	NH1	A_ASP_60	OD2	3.943
2OTW	C_ARG.65	NH1	C_ASP_86	OD1	2.692
2OTW	C_ARG.65	NH1	C_ASP_86	OD2	2.598
2OTW	D_ARG.38	NH1	D_ASP_90	OD1	2.989
2OTW	D_ARG.38	NH2	D_GLU_46	OE1	2.871
2OTW	D_ARG.38	NH2	D_GLU_46	OE2	3.541
2OTW	D_ARG.44	NH2	D_GLU_42	OE1	3.918
2OTW	D_ARG.67	NH1	D_ASP_90	OD1	3.886
2OTW	D_ARG.67	NH1	D_ASP_90	OD2	2.722
2OTW	D_ARG.67	NH2	D_ASP_90	OD1	2.979
2OTW	D_ARG.67	NH2	D_ASP_90	OD2	3.322
2OTW	D_ARG.100	NH1	C_ASP_60	OD1	3.882
2OTW	D_ARG.100	NH1	C_ASP_60	OD2	3.653
2P8L	A_ARG.24	NH2	A_GLU_70	OE2	3.694
2P8L	A_ARG.37	NH1	A_ASP_82	OD1	2.662
2P8L	A_ARG.61	NH2	A_ASP_82	OD1	3.178
2P8L	A_ARG.61	NH2	A_ASP_82	OD2	3.399
2P8L	A_HIS.96	NE2	C_ASP_5	OD1	2.766
2P8L	A_LYS.149	NZ	A_GLU_195	OE1	3.348
2P8L	A_LYS.149	NZ	A_GLU_195	OE2	2.911
2P8L	A_LYS.183	NZ	A_GLU_187	OE1	3.209
2P8L	A_LYS.183	NZ	A_GLU_187	OE2	3.403
2P8L	B_ARG.38	NH1	B_GLU_46	OE1	2.804
2P8L	B_ARG.38	NH1	B_GLU_46	OE2	3.681
2P8L	B_ARG.38	NH2	B_ASP_86	OD1	2.496
2P8L	B_LYS.57	NZ	B_ASP_55	OD2	3.457
2P8L	B_ARG.58	NH1	C_GLU_3	OE1	1.911
2P8L	B_ARG.58	NH1	C_GLU_3	OE2	3.223
2P8L	B_ARG.58	NH2	B_ASP_56	OD1	3.758
2P8L	B_ARG.58	NH2	B_ASP_56	OD2	3.029
2P8L	B_ARG.58	NH2	C_GLU_3	OE1	3.943
2P8L	B_ARG.66	NH1	B_ASP_86	OD1	3.620
2P8L	B_ARG.66	NH1	B_ASP_86	OD2	3.879
2P8L	B_ARG.66	NH2	B_ASP_86	OD1	3.123
2P8L	B_ARG.66	NH2	B_ASP_86	OD2	2.431
2P8L	B_LYS.71	NZ	B_ASP_55	OD1	3.582
2P8L	B_HIS.94	ND1	B_ASP_101	OD1	2.660
2P8L	B_HIS.94	ND1	B_ASP_101	OD2	3.511
2P8L	B_ARG.95	NH1	C_ASP_5	OD1	2.951
2P8L	B_ARG.95	NH1	C_ASP_5	OD2	3.619
2P8L	B_ARG.95	NH2	C_ASP_5	OD1	3.420
2P8L	B_ARG.95	NH2	C_ASP_5	OD2	2.971
2P8L	B_ARG.96	NH1	A_GLU_55	OE1	3.236
2P8L	B_ARG.96	NH1	A_GLU_55	OE2	3.320
2P8L	B_ARG.96	NH1	B_ASP_101	OD2	3.133
2P8L	B_ARG.96	NH2	A_GLU_55	OE1	3.018
2P8L	B_LYS.143	NZ	B_ASP_144	OD1	3.794
2P8L	B_LYS.209	NZ	A_GLU_123	OE1	3.743
2P8L	B_ARG.210	NH1	B_GLU_212	OE1	2.518
2P8L	B_ARG.210	NH1	B_GLU_212	OE2	2.702
2P8L	B_ARG.210	NH2	B_GLU_212	OE1	2.760
2P8L	C_LYS.6	NZ	B_ASP_54	OD1	3.641
2P8L	C_LYS.6	NZ	B_ASP_54	OD2	3.025
2P8L	C_LYS.6	NZ	B_ASP_56	OD1	2.878

2P8M	A_ARG_37	NH1	A_ASP_82	OD1	2.839
2P8M	A_ARG_61	NH2	A_ASP_82	OD1	2.944
2P8M	A_ARG_61	NH2	A_ASP_82	OD2	3.371
2P8M	A_HIS_96	NE2	C_ASP_3	OD2	2.613
2P8M	A_LYS_149	NZ	A_GLU_193	OE1	3.222
2P8M	A_LYS_149	NZ	A_GLU_195	OE1	3.752
2P8M	A_LYS_183	NZ	A_GLU_187	OE2	2.931
2P8M	A_LYS_190	NZ	A_GLU_213	OE2	3.479
2P8M	B_ARG_1	NH2	A_GLU_55	OE2	3.915
2P8M	B_ARG_38	NH1	B_GLU_46	OE1	2.460
2P8M	B_ARG_38	NH1	B_GLU_46	OE2	3.000
2P8M	B_ARG_38	NH2	B_ASP_86	OD1	2.567
2P8M	B_LYS_57	NZ	B_ASP_55	OD1	3.800
2P8M	B_LYS_57	NZ	B_ASP_55	OD2	3.375
2P8M	B_ARG_58	NH1	B_ASP_56	OD1	2.812
2P8M	B_ARG_58	NH2	C_GLU_1	OE1	2.510
2P8M	B_ARG_66	NH1	B_ASP_86	OD1	3.550
2P8M	B_ARG_66	NH2	B_ASP_86	OD1	3.137
2P8M	B_ARG_66	NH2	B_ASP_86	OD2	2.617
2P8M	B_HIS_94	ND1	B_ASP_101	OD1	2.569
2P8M	B_HIS_94	ND1	B_ASP_101	OD2	3.296
2P8M	B_ARG_95	NH1	C_ASP_3	OD1	2.973
2P8M	B_ARG_95	NH1	C_ASP_3	OD2	3.042
2P8M	B_ARG_95	NH2	C_ASP_3	OD1	3.169
2P8M	B_ARG_96	NH1	A_GLU_55	OE1	3.351
2P8M	B_ARG_96	NH1	A_GLU_55	OE2	3.448
2P8M	B_ARG_96	NH1	B_ASP_101	OD2	3.545
2P8M	B_ARG_96	NH2	A_GLU_55	OE1	3.393
2P8M	B_LYS_143	NZ	B_ASP_144	OD1	3.820
2P8M	B_LYS_143	NZ	B_ASP_144	OD2	3.945
2P8M	B_LYS_209	NZ	A_GLU_123	OE1	3.649
2P8M	B_ARG_210	NH2	B_GLU_212	OE1	2.714
2P8M	B_ARG_210	NH2	B_GLU_212	OE2	3.508
2P8M	C_LYS_4	NZ	B_ASP_54	OD1	2.903
2P8M	C_LYS_4	NZ	B_ASP_54	OD2	2.371
2P8M	C_LYS_4	NZ	B_ASP_56	OD2	3.183
2P8P	A_ARG_24	NH1	A_GLU_70	OE2	3.886
2P8P	A_ARG_24	NH2	A_GLU_70	OE2	2.623
2P8P	A_ARG_37	NH1	A_GLU_81	OE1	3.668
2P8P	A_ARG_37	NH1	A_GLU_81	OE2	3.049
2P8P	A_ARG_37	NH1	A_ASP_82	OD1	3.193
2P8P	A_ARG_37	NH2	A_GLU_81	OE1	3.421
2P8P	A_LYS_39	NZ	A_GLU_81	OE1	3.598
2P8P	A_ARG_61	NH2	A_GLU_81	OE2	2.595
2P8P	A_ARG_61	NH2	A_ASP_82	OD1	3.431
2P8P	A_HIS_96	NE2	C_ASP_3	OD1	3.214
2P8P	A_LYS_149	NZ	A_GLU_195	OE1	3.534
2P8P	A_LYS_183	NZ	A_GLU_187	OE1	2.848
2P8P	A_LYS_183	NZ	A_GLU_187	OE2	3.221
2P8P	A_LYS_188	NZ	A_ASP_185	OD1	2.922
2P8P	B_ARG_38	NH1	B_ASP_86	OD1	2.794
2P8P	B_ARG_38	NH2	B_GLU_46	OE1	3.420
2P8P	B_ARG_38	NH2	B_GLU_46	OE2	3.340
2P8P	B_ARG_38	NH2	B_ASP_86	OD1	3.738
2P8P	B_LYS_57	NZ	B_ASP_55	OD1	3.547
2P8P	B_LYS_57	NZ	B_ASP_55	OD2	2.954
2P8P	B_ARG_58	NH1	B_ASP_56	OD1	2.448
2P8P	B_ARG_58	NH1	B_ASP_56	OD2	3.762

2P8P	B_ARG_58	NH2	B_ASP_56	OD1	3.457
2P8P	B_ARG_58	NH2	B_ASP_56	OD2	3.922
2P8P	B_ARG_58	NH2	C_GLU_1	OE2	3.147
2P8P	B_ARG_66	NH1	B_ASP_86	OD1	3.503
2P8P	B_ARG_66	NH1	B_ASP_86	OD2	3.962
2P8P	B_ARG_66	NH2	B_ASP_86	OD1	3.025
2P8P	B_ARG_66	NH2	B_ASP_86	OD2	2.685
2P8P	B_LYS_71	NZ	B_ASP_55	OD1	3.926
2P8P	B_HIS_94	ND1	B_ASP_101	OD1	2.554
2P8P	B_HIS_94	ND1	B_ASP_101	OD2	3.579
2P8P	B_ARG_95	NH1	C_ASP_3	OD1	2.805
2P8P	B_ARG_95	NH1	C_ASP_3	OD2	3.510
2P8P	B_ARG_95	NH2	C_ASP_3	OD1	3.459
2P8P	B_ARG_95	NH2	C_ASP_3	OD2	2.629
2P8P	B_ARG_96	NH1	A_GLU_55	OE1	3.239
2P8P	B_ARG_96	NH1	A_GLU_55	OE2	3.518
2P8P	B_ARG_96	NH1	B_ASP_101	OD2	2.782
2P8P	B_ARG_96	NH2	A_GLU_55	OE1	3.128
2P8P	B_LYS_144	NZ	B_ASP_145	OD1	3.635
2P8P	B_LYS_144	NZ	B_ASP_145	OD2	3.553
2P8P	B_LYS_210	NZ	A_GLU_123	OE1	3.349
2P8P	B_LYS_210	NZ	A_GLU_123	OE2	3.192
2P8P	B_ARG_211	NH1	B_GLU_213	OE1	3.506
2P8P	B_ARG_211	NH1	B_GLU_213	OE2	3.532
2P8P	B_ARG_211	NH2	B_GLU_213	OE1	2.609
2P8P	B_ARG_211	NH2	B_GLU_213	OE2	3.996
2P8P	C_LYS_4	NZ	B_ASP_54	OD1	3.623
2P8P	C_LYS_4	NZ	B_ASP_54	OD2	3.010
2P8P	C_LYS_4	NZ	B_ASP_56	OD2	2.836
2PR4	L_ARG_37	NH1	L_ASP_82	OD1	3.024
2PR4	L_ARG_61	NH2	L_ASP_82	OD1	2.716
2PR4	L_ARG_61	NH2	L_ASP_82	OD2	3.445
2PR4	L_ARG_108	NH1	L_ASP_170	OD1	3.583
2PR4	L_LYS_149	NZ	L_GLU_195	OE1	3.734
2PR4	L_LYS_183	NZ	L_GLU_187	OE2	2.711
2PR4	L_LYS_190	NZ	L_ASP_151	OD1	3.274
2PR4	H_ARG_40	NH1	H_GLU_48	OE1	3.002
2PR4	H_ARG_40	NH1	H_ASP_91	OD1	3.704
2PR4	H_ARG_40	NH2	H_ASP_91	OD1	2.605
2PR4	H_ARG_60	NH1	H_ASP_58	OD1	3.465
2PR4	H_ARG_60	NH1	H_ASP_58	OD2	3.213
2PR4	H_ARG_68	NH1	H_ASP_91	OD1	3.656
2PR4	H_ARG_68	NH1	H_ASP_91	OD2	3.886
2PR4	H_ARG_68	NH2	H_ASP_91	OD1	3.393
2PR4	H_ARG_68	NH2	H_ASP_91	OD2	2.646
2PR4	H_HIS_99	ND1	H_ASP_120	OD1	2.785
2PR4	H_HIS_99	ND1	H_ASP_120	OD2	3.650
2PR4	H_ARG_101	NH1	L_GLU_55	OE1	3.296
2PR4	H_ARG_101	NH1	L_GLU_55	OE2	3.376
2PR4	H_ARG_101	NH1	H_ASP_120	OD2	3.802
2PR4	H_ARG_101	NH2	L_GLU_55	OE1	3.286
2PR4	H_LYS_162	NZ	H_ASP_163	OD1	3.519
2PR4	H_LYS_228	NZ	L_GLU_123	OE1	3.151
2PR4	H_ARG_229	NH1	H_GLU_231	OE2	3.222
2PR4	H_ARG_229	NH2	H_GLU_231	OE1	3.609
2PR4	H_ARG_229	NH2	H_GLU_231	OE2	2.833
2Q8A	A_ARG_128	NH1	A_GLU_343	OE2	2.727
2Q8A	A_ARG_128	NH2	A_GLU_256	OE1	2.979

2Q8A	A_ARG_128	NH2	A_GLU_256	OE2	2.971
2Q8A	A_LYS_203	NZ	L_ASP_32	OD1	3.044
2Q8A	A_LYS_203	NZ	L_ASP_32	OD2	2.513
2Q8A	A_LYS_245	NZ	A_GLU_213	OE2	3.921
2Q8A	A_LYS_245	NZ	A_ASP_242	OD1	3.383
2Q8A	A_LYS_245	NZ	A_ASP_242	OD2	2.933
2Q8A	A_ARG_270	NH1	A_ASP_178	OD1	2.638
2Q8A	A_ARG_270	NH1	A_ASP_178	OD2	3.624
2Q8A	A_LYS_292	NZ	A_GLU_133	OE2	2.672
2Q8A	A_ARG_304	NH1	A_GLU_436	OE1	3.883
2Q8A	A_ARG_304	NH1	A_GLU_436	OE2	2.055
2Q8A	A_ARG_304	NH2	A_GLU_436	OE1	3.764
2Q8A	A_ARG_304	NH2	A_GLU_436	OE2	3.204
2Q8A	A_LYS_311	NZ	A_ASP_322	OD1	2.775
2Q8A	A_LYS_311	NZ	A_ASP_322	OD2	3.906
2Q8A	A_LYS_339	NZ	A_GLU_336	OE1	3.158
2Q8A	A_LYS_339	NZ	A_GLU_336	OE2	3.923
2Q8A	A_LYS_364	NZ	A_GLU_361	OE1	3.383
2Q8A	A_LYS_364	NZ	A_GLU_361	OE2	3.258
2Q8A	A_LYS_368	NZ	A_ASP_227	OD1	2.672
2Q8A	A_LYS_368	NZ	A_ASP_227	OD2	3.440
2Q8A	A_LYS_391	NZ	A_ASP_134	OD2	2.727
2Q8A	A_HIS_433	NE2	A_GLU_436	OE1	3.631
2Q8A	L_ARG_54	NH1	L_ASP_60	OD1	3.683
2Q8A	L_ARG_61	NH1	L_ASP_82	OD1	2.388
2Q8A	L_ARG_61	NH1	L_ASP_82	OD2	3.063
2Q8A	L_ARG_61	NH2	L_GLU_81	OE2	3.801
2Q8A	L_ARG_96	NH1	A_ASP_204	OD1	2.971
2Q8A	L_ARG_96	NH1	A_ASP_204	OD2	2.580
2Q8A	L_ARG_96	NH2	A_ASP_204	OD1	2.882
2Q8A	L_ARG_96	NH2	A_ASP_204	OD2	3.927
2Q8A	L_ARG_96	NH2	H_GLU_59	OE2	3.755
2Q8A	L_LYS_103	NZ	L_ASP_165	OD1	3.929
2Q8A	L_HIS_189	ND1	L_ASP_151	OD2	2.903
2Q8A	L_LYS_199	NZ	L_ASP_110	OD2	2.695
2Q8A	H_HIS_35	NE2	A_ASP_204	OD2	3.930
2Q8A	H_ARG_50	NH1	H_ASP_52	OD2	3.087
2Q8A	H_ARG_50	NH2	H_GLU_59	OE2	3.157
2Q8A	H_LYS_63	NZ	H_GLU_46	OE1	3.799
2Q8A	H_LYS_67	NZ	H_ASP_90	OD1	3.906
2Q8A	H_LYS_67	NZ	H_ASP_90	OD2	3.028
2Q8B	A_ARG_128	NH1	A_GLU_256	OE1	3.040
2Q8B	A_ARG_128	NH1	A_GLU_256	OE2	3.000
2Q8B	A_ARG_128	NH2	A_GLU_256	OE1	3.059
2Q8B	A_LYS_203	NZ	L_ASP_32	OD1	3.779
2Q8B	A_LYS_203	NZ	L_ASP_32	OD2	2.847
2Q8B	A_LYS_245	NZ	A_GLU_213	OE2	2.777
2Q8B	A_LYS_245	NZ	A_ASP_242	OD2	3.887
2Q8B	A_LYS_292	NZ	A_GLU_133	OE1	3.902
2Q8B	A_LYS_292	NZ	A_GLU_133	OE2	2.733
2Q8B	A_ARG_304	NH1	A_GLU_436	OE1	3.770
2Q8B	A_ARG_304	NH1	A_GLU_436	OE2	2.007
2Q8B	A_ARG_304	NH2	A_GLU_436	OE2	3.545
2Q8B	A_LYS_311	NZ	A_ASP_322	OD1	2.853
2Q8B	A_LYS_311	NZ	A_ASP_322	OD2	3.778
2Q8B	A_LYS_339	NZ	A_GLU_336	OE1	2.983
2Q8B	A_LYS_339	NZ	A_GLU_336	OE2	3.511
2Q8B	A_LYS_351	NZ	A_GLU_343	OE2	2.663

2Q8B	A_LYS_391	NZ	A_ASP_134	OD1	3.749
2Q8B	A_LYS_391	NZ	A_ASP_134	OD2	2.808
2Q8B	A_LYS_391	NZ	A_ASP_388	OD1	3.545
2Q8B	A_HIS_433	NE2	A_GLU_436	OE1	3.672
2Q8B	L_LYS_24	NZ	L_ASP_70	OD1	3.418
2Q8B	L_LYS_24	NZ	L_ASP_70	OD2	3.406
2Q8B	L_ARG_61	NH1	L_ASP_82	OD1	2.518
2Q8B	L_ARG_61	NH1	L_ASP_82	OD2	3.346
2Q8B	L_ARG_96	NH1	A_ASP_204	OD1	3.458
2Q8B	L_ARG_96	NH1	A_ASP_204	OD2	2.952
2Q8B	L_ARG_96	NH2	A_ASP_204	OD1	2.667
2Q8B	L_ARG_96	NH2	A_ASP_204	OD2	3.462
2Q8B	L_ARG_188	NH1	L_GLU_185	OE1	3.851
2Q8B	L_ARG_188	NH1	L_GLU_185	OE2	2.847
2Q8B	L_ARG_188	NH2	L_GLU_185	OE2	3.891
2Q8B	L_HIS_189	ND1	L_GLU_185	OE2	3.560
2Q8B	L_LYS_199	NZ	L_ASP_110	OD2	3.181
2Q8B	H_ARG_40	NH1	H_GLU_89	OE2	2.969
2Q8B	H_ARG_40	NH2	H_GLU_89	OE2	3.558
2Q8B	H_ARG_50	NH2	H_GLU_59	OE2	2.874
2Q8B	H_LYS_63	NZ	H_GLU_46	OE1	2.715
2Q8B	H_LYS_67	NZ	H_ASP_90	OD1	3.762
2Q8B	H_LYS_67	NZ	H_ASP_90	OD2	3.011
2QAD	A_LYS_207	NZ	A_GLU_381	OE1	3.156
2QAD	A_LYS_207	NZ	A_GLU_381	OE2	2.751
2QAD	A_LYS_231	NZ	A_GLU_268	OE2	3.310
2QAD	A_LYS_232	NZ	A_GLU_269	OE2	3.594
2QAD	A_LYS_282	NZ	A_GLU_275	OE2	3.989
2QAD	A_LYS_348	NZ	A_GLU_269	OE1	3.722
2QAD	A_LYS_348	NZ	A_GLU_269	OE2	3.126
2QAD	A_ARG_419	NH1	A_ASP_325	OD2	2.671
2QAD	A_ARG_419	NH2	A_ASP_325	OD2	3.673
2QAD	A_ARG_456	NH2	A_GLU_466	OE2	3.254
2QAD	A_ARG_469	NH2	A_ASP_457	OD2	3.733
2QAD	A_ARG_476	NH1	A_ASP_474	OD1	2.798
2QAD	A_ARG_476	NH2	A_GLU_102	OE2	3.950
2QAD	A_ARG_480	NH2	A_ASP_477	OD1	3.412
2QAD	A_LYS_487	NZ	A_GLU_91	OE1	3.356
2QAD	A_LYS_487	NZ	A_GLU_91	OE2	3.914
2QAD	A_LYS_490	NZ	A_GLU_492	OE2	3.426
2QAD	B_ARG_54	NH1	B_ASP_78	OD2	3.526
2QAD	B_ARG_54	NH2	B_GLU_77	OE2	3.474
2QAD	B_ARG_54	NH2	B_ASP_78	OD2	3.454
2QAD	B_ARG_59	NH1	A_ASP_368	OD1	3.394
2QAD	B_ARG_59	NH1	A_ASP_368	OD2	2.749
2QAD	B_ARG_59	NH2	A_ASP_368	OD1	3.764
2QAD	B_LYS_72	NZ	B_ASP_56	OD2	3.172
2QAD	B_HIS_107	ND1	B_ASP_105	OD2	3.915
2QAD	C_LYS_39	NZ	C_ASP_81	OD1	3.751
2QAD	C_LYS_50	NZ	D_GLU_100F	OE2	2.989
2QAD	C_LYS_55	NZ	D_ASP_101	OD1	3.312
2QAD	C_LYS_55	NZ	D_ASP_101	OD2	3.736
2QAD	C_ARG_61	NH2	C_ASP_82	OD1	3.983
2QAD	C_ARG_61	NH2	C_ASP_82	OD2	3.945
2QAD	C_LYS_103	NZ	C_GLU_165	OE1	3.299
2QAD	C_LYS_103	NZ	C_GLU_165	OE2	3.201
2QAD	C_LYS_183	NZ	C_GLU_187	OE2	3.769
2QAD	C_LYS_188	NZ	C_ASP_185	OD1	3.463

2QAD	C_HIS_189	ND1	C_ASP_151	OD1	3.214
2QAD	C_HIS_189	ND1	C_ASP_151	OD2	3.260
2QAD	D_ARG_38	NH1	D_GLU_46	OE1	3.492
2QAD	D_ARG_38	NH1	D_GLU_46	OE2	3.474
2QAD	D_ARG_62	NH1	D_GLU_46	OE1	2.887
2QAD	D_ARG_62	NH1	D_GLU_46	OE2	2.924
2QAD	D_ARG_62	NH2	D_GLU_46	OE2	3.357
2QAD	D_LYS_143	NZ	D_ASP_144	OD1	2.885
2QAD	D_LYS_143	NZ	D_ASP_144	OD2	3.634
2QAD	D_LYS_206	NZ	D_ASP_208	OD1	3.117
2QAD	D_LYS_209	NZ	D_GLU_212	OE1	3.727
2QAD	D_LYS_210	NZ	D_GLU_212	OE2	3.492
2QAD	E_LYS_207	NZ	E_GLU_381	OE1	3.059
2QAD	E_LYS_207	NZ	E_GLU_381	OE2	2.916
2QAD	E_LYS_231	NZ	E_GLU_268	OE2	3.647
2QAD	E_LYS_282	NZ	E_GLU_275	OE1	3.736
2QAD	E_LYS_282	NZ	E_GLU_275	OE2	3.761
2QAD	E_LYS_348	NZ	E_GLU_269	OE1	3.968
2QAD	E_LYS_348	NZ	E_GLU_269	OE2	3.504
2QAD	E_ARG_419	NH1	E_ASP_325	OD2	2.690
2QAD	E_ARG_419	NH2	E_ASP_325	OD2	3.727
2QAD	E_ARG_456	NH2	E_GLU_466	OE2	3.894
2QAD	E_ARG_476	NH1	E_ASP_474	OD1	3.116
2QAD	E_ARG_476	NH2	E_GLU_102	OE1	3.845
2QAD	E_ARG_476	NH2	E_GLU_102	OE2	3.739
2QAD	E_ARG_480	NH2	E_ASP_477	OD1	3.576
2QAD	E_LYS_487	NZ	E_GLU_91	OE1	3.899
2QAD	E_LYS_487	NZ	E_GLU_91	OE2	3.462
2QAD	E_LYS_490	NZ	E_GLU_492	OE2	3.971
2QAD	F_LYS_1	NZ	F_GLU_92	OE1	3.829
2QAD	F_LYS_29	NZ	F_GLU_85	OE1	3.902
2QAD	F_ARG_54	NH1	F_ASP_78	OD2	3.625
2QAD	F_ARG_54	NH2	F_GLU_77	OE2	3.363
2QAD	F_ARG_54	NH2	F_ASP_78	OD2	3.440
2QAD	F_ARG_59	NH1	E_ASP_368	OD1	2.855
2QAD	F_ARG_59	NH1	E_ASP_368	OD2	2.624
2QAD	F_ARG_59	NH2	E_ASP_368	OD1	3.681
2QAD	F_LYS_72	NZ	F_ASP_56	OD2	3.168
2QAD	F_LYS_90	NZ	F_GLU_85	OE2	3.437
2QAD	F_ARG_134	NH1	F_GLU_150	OE1	3.188
2QAD	F_ARG_134	NH2	F_GLU_150	OE1	2.761
2QAD	F_ARG_134	NH2	F_ASP_153	OD1	2.906
2QAD	G_LYS_39	NZ	G_ASP_81	OD1	3.605
2QAD	G_LYS_50	NZ	H_GLU_100F	OE2	3.151
2QAD	G_LYS_55	NZ	H_ASP_101	OD1	3.191
2QAD	G_LYS_55	NZ	H_ASP_101	OD2	3.496
2QAD	G_ARG_61	NH2	G_ASP_82	OD1	3.464
2QAD	G_ARG_61	NH2	G_ASP_82	OD2	3.576
2QAD	G_LYS_103	NZ	G_GLU_165	OE1	3.223
2QAD	G_LYS_103	NZ	G_GLU_165	OE2	3.176
2QAD	G_LYS_183	NZ	G_GLU_187	OE2	2.926
2QAD	G_LYS_188	NZ	G_ASP_185	OD1	3.437
2QAD	G_HIS_189	ND1	G_ASP_151	OD1	3.455
2QAD	G_HIS_189	ND1	G_ASP_151	OD2	2.830
2QAD	H_ARG_62	NH1	H_GLU_46	OE1	2.833
2QAD	H_ARG_62	NH1	H_GLU_46	OE2	2.981
2QAD	H_ARG_62	NH2	H_GLU_46	OE1	3.733
2QAD	H_ARG_62	NH2	H_GLU_46	OE2	3.274

2QAD	H_ARG_83	NH2	H_ASP_86	OD1	3.458
2QAD	H_ARG_83	NH2	H_ASP_86	OD2	2.513
2QAD	H_LYS_143	NZ	H_ASP_144	OD1	2.852
2QAD	H_LYS_143	NZ	H_ASP_144	OD2	3.707
2QAD	H_LYS_206	NZ	H_ASP_208	OD1	2.954
2QAD	H_LYS_209	NZ	H_GLU_212	OE1	3.668
2QQI	A_ARG_305	NH1	A_GLU_312	OE2	3.025
2QQI	A_ARG_305	NH2	A_GLU_312	OE2	3.597
2QQI	A_LYS_347	NZ	A_GLU_312	OE1	3.337
2QQI	A_ARG_402	NH2	A_ASP_329	OD1	3.538
2QQI	A_ARG_402	NH2	A_ASP_329	OD2	2.925
2QQI	A_LYS_407	NZ	A_ASP_361	OD1	3.110
2QQI	A_LYS_407	NZ	A_ASP_361	OD2	2.901
2QQI	A_ARG_463	NH2	A_ASP_444	OD1	2.807
2QQI	A_ARG_513	NH2	A_GLU_483	OE1	3.254
2QQI	A_LYS_527	NZ	A_ASP_525	OD1	2.652
2QQI	A_LYS_527	NZ	A_ASP_525	OD2	3.292
2QQI	A_ARG_552	NH1	A_GLU_550	OE1	3.271
2QQI	A_ARG_552	NH2	A_GLU_550	OE1	2.899
2QQI	A_ARG_560	NH2	A_ASP_488	OD1	3.697
2QQI	A_ARG_560	NH2	A_ASP_488	OD2	3.358
2QQM	A_ARG_207	NH2	A_ASP_197	OD1	2.822
2QQM	A_ARG_207	NH2	A_ASP_197	OD2	3.844
2QQM	A_HIS_223	NE2	A_GLU_212	OE1	2.681
2QQM	A_ARG_236	NH2	A_GLU_212	OE2	3.329
2QQM	A_ARG_235	NH2	A_GLU_188	OE2	3.062
2QQM	A_ARG_237	NH1	A_GLU_285	OE2	2.734
2QQM	A_ARG_237	NH2	A_GLU_184	OE2	3.025
2QQM	A_ARG_237	NH2	A_GLU_285	OE2	3.428
2QQM	A_HIS_287	ND1	A_ASP_289	OD1	3.807
2QQM	A_HIS_287	ND1	A_ASP_289	OD2	3.593
2QQM	A_ARG_305	NH1	A_GLU_312	OE1	2.993
2QQM	A_ARG_305	NH2	A_GLU_312	OE1	3.753
2QQM	A_ARG_334	NH1	A_GLU_184	OE1	2.860
2QQM	A_ARG_334	NH2	A_GLU_184	OE1	3.414
2QQM	A_ARG_334	NH2	A_GLU_184	OE2	3.144
2QQM	A_LYS_347	NZ	A_GLU_312	OE2	3.827
2QQM	A_LYS_356	NZ	A_GLU_412	OE1	3.925
2QQM	A_ARG_402	NH2	A_ASP_329	OD1	3.702
2QQM	A_ARG_402	NH2	A_ASP_329	OD2	3.069
2QQM	A_LYS_407	NZ	A_ASP_361	OD1	2.925
2QQM	A_LYS_407	NZ	A_ASP_361	OD2	3.013
2QQM	A_ARG_463	NH2	A_ASP_444	OD1	2.977
2QQM	A_LYS_504	NZ	A_ASP_368	OD2	3.089
2QQM	A_ARG_513	NH1	A_GLU_541	OE1	3.868
2QQM	A_ARG_513	NH2	A_GLU_541	OE1	3.920
2QQM	A_LYS_514	NZ	A_GLU_541	OE1	3.415
2QQM	A_LYS_514	NZ	A_GLU_541	OE2	3.311
2QQM	A_LYS_536	NZ	A_ASP_531	OD2	3.748
2QQM	A_ARG_552	NH1	A_GLU_550	OE1	3.256
2QQM	A_ARG_552	NH2	A_GLU_550	OE1	3.455
2QQM	A_ARG_560	NH2	A_ASP_488	OD1	3.975
2QQM	A_ARG_560	NH2	A_ASP_488	OD2	3.187
2QQN	A_ARG_305	NH1	A_GLU_312	OE1	3.596
2QQN	A_LYS_347	NZ	A_GLU_312	OE1	3.909
2QQN	A_LYS_356	NZ	A_GLU_412	OE1	3.215
2QQN	A_ARG_402	NH2	A_ASP_329	OD1	3.587
2QQN	A_ARG_402	NH2	A_ASP_329	OD2	3.150

2QQN	A.LYS_407	NZ	A_ASP_361	OD1	3.212
2QQN	A.LYS_407	NZ	A_ASP_361	OD2	2.958
2QQN	H_ARG_38	NH1	H_ASP_86	OD1	2.933
2QQN	H_ARG_38	NH2	H_GLU_46	OE1	3.167
2QQN	H_ARG_38	NH2	H_ASP_86	OD1	3.865
2QQN	H_ARG_66	NH1	H_ASP_86	OD1	3.782
2QQN	H_ARG_66	NH1	H_ASP_86	OD2	2.772
2QQN	H_ARG_66	NH2	H_ASP_86	OD1	3.232
2QQN	H_ARG_66	NH2	H_ASP_86	OD2	3.638
2QQN	H.LYS_75	NZ	H_ASP_72	OD2	3.885
2QQN	H_ARG_94	NH2	H_ASP_101	OD1	3.705
2QQN	H_ARG_94	NH2	H_ASP_101	OD2	2.999
2QQN	H.LYS_143	NZ	H_ASP_144	OD1	3.148
2QQN	H.LYS_143	NZ	H_ASP_144	OD2	2.751
2QQN	H.LYS_206	NZ	H_ASP_208	OD1	3.934
2QQN	H.LYS_209	NZ	L_GLU_123	OE1	2.782
2QQN	H.LYS_209	NZ	L_GLU_123	OE2	3.506
2QQN	H.LYS_210	NZ	H_GLU_212	OE1	3.071
2QQN	H.LYS_210	NZ	H_GLU_212	OE2	3.673
2QQN	H.LYS_214	NZ	L_ASP_122	OD1	3.854
2QQN	L_ARG_61	NH2	L_GLU_81	OE2	3.892
2QQN	L_ARG_61	NH2	L_ASP_82	OD1	2.963
2QQN	L_ARG_61	NH2	L_ASP_82	OD2	3.635
2QQN	L.LYS_103	NZ	L_GLU_105	OE2	3.304
2QQN	L.LYS_103	NZ	L_GLU_165	OE1	2.460
2QQN	L.LYS_103	NZ	L_GLU_165	OE2	3.133
2QQN	L_ARG_142	NH1	L_GLU_105	OE2	2.892
2QQN	L_ARG_142	NH2	L_GLU_165	OE2	3.206
2QQN	L.LYS_149	NZ	L_GLU_195	OE1	2.720
2QQN	L.LYS_183	NZ	L_GLU_187	OE1	3.367
2QQN	L.LYS_183	NZ	L_GLU_187	OE2	3.373
2QQN	L.LYS_188	NZ	L_ASP_185	OD1	3.017
2R29	A.LYS_307	NZ	A_GLU_327	OE2	3.953
2R29	A.LYS_307	NZ	H_ASP_99	OD1	2.956
2R29	A.LYS_307	NZ	L_GLU_59	OE1	3.335
2R29	A.LYS_310	NZ	H_ASP_52	OD1	3.449
2R29	A.LYS_310	NZ	H_ASP_52	OD2	2.764
2R29	A_ARG_323	NH2	A_GLU_311	OE2	3.982
2R29	A_ARG_350	NH1	A_GLU_370	OE1	2.411
2R29	H_ARG_40	NH2	H_GLU_46	OE2	3.642
2R29	H.LYS_59	NZ	L_ASP_98	OD2	3.485
2R29	H.LYS_67	NZ	H_ASP_90	OD1	3.208
2R29	H.LYS_67	NZ	H_ASP_90	OD2	3.049
2R29	L_ARG_54	NH2	H_GLU_101	OE1	3.814
2R29	L_ARG_54	NH2	H_GLU_101	OE2	3.270
2R29	L.LYS_107	NZ	H_GLU_42	OE1	3.937
2R29	L.LYS_151	NZ	L_GLU_199	OE1	2.854
2R29	L.LYS_151	NZ	L_GLU_199	OE2	3.268
2R29	L_ARG_159	NH2	L_GLU_189	OE1	3.854
2R29	L.HIS_193	ND1	L_ASP_155	OD2	2.763
2R29	L.HIS_193	NE2	L_GLU_189	OE1	3.126
2R69	A.LYS_307	NZ	H_ASP_99	OD2	3.631
2R69	A_HIS_317	NE2	A_GLU_368	OE2	3.012
2R69	A.LYS_344	NZ	A_GLU_338	OE1	3.172
2R69	A_ARG_345	NH1	A_ASP_341	OD2	3.802
2R69	H.LYS_38	NZ	H_ASP_90	OD1	2.910
2R69	H.LYS_38	NZ	H_ASP_90	OD2	2.994
2R69	H_ARG_40	NH2	H_GLU_46	OE2	3.388

2R69	H.LYS.59	NZ	L.ASP.98	OD2	3.723
2R69	H.LYS.67	NZ	H.ASP.90	OD1	3.247
2R69	H.LYS.67	NZ	H.ASP.90	OD2	3.994
2R69	H.LYS.211	NZ	L.GLU.127	OE1	3.695
2R69	H.LYS.211	NZ	L.GLU.127	OE2	3.159
2R69	L.ARG.31	NH2	A.GLU.311	OE2	3.151
2R69	L.LYS.43	NZ	L.ASP.85	OD1	2.285
2R69	L.LYS.43	NZ	L.ASP.85	OD2	3.990
2R69	L.ARG.54	NH2	H.GLU.101	OE1	2.992
2R69	L.ARG.54	NH2	H.GLU.101	OE2	2.911
2R69	L.ARG.72	NH2	L.ASP.74	OD2	3.950
2R69	L.ARG.112	NH2	L.ASP.174	OD1	3.901
2R69	L.LYS.151	NZ	L.GLU.158	OE1	2.692
2R69	L.LYS.151	NZ	L.GLU.158	OE2	3.692
2R69	L.LYS.153	NZ	L.GLU.199	OE1	2.500
2R69	L.LYS.153	NZ	L.GLU.199	OE2	3.634
2R69	L.ARG.159	NH2	L.GLU.189	OE1	3.888
2R69	L.ARG.159	NH2	L.GLU.189	OE2	3.776
2R69	L.HIS.193	NE2	L.GLU.189	OE1	3.028
2UYL	A.ARG.24	NH2	A.ASP.75	OD2	3.541
2UYL	A.LYS.44	NZ	A.GLU.86	OE1	3.928
2UYL	A.LYS.55	NZ	A.ASP.35	OD1	3.890
2UYL	A.ARG.66	NH1	A.GLU.84	OE2	3.593
2UYL	A.ARG.66	NH2	A.GLU.84	OE2	3.108
2UYL	A.ARG.66	NH2	A.GLU.86	OE2	3.573
2UYL	A.ARG.66	NH2	A.ASP.87	OD1	2.859
2UYL	A.ARG.66	NH2	A.ASP.87	OD2	3.807
2UYL	A.ARG.101	NH1	B.GLU.99	OE1	3.183
2UYL	A.ARG.101	NH1	B.GLU.99	OE2	3.530
2UYL	A.ARG.101	NH2	B.GLU.99	OE2	3.803
2UYL	A.LYS.152	NZ	A.GLU.159	OE2	3.364
2UYL	A.LYS.154	NZ	A.GLU.200	OE1	3.299
2UYL	A.ARG.160	NH2	A.GLU.190	OE1	2.667
2UYL	A.ARG.160	NH2	A.GLU.190	OE2	3.767
2UYL	A.LYS.188	NZ	A.GLU.192	OE1	3.100
2UYL	A.HIS.194	ND1	A.ASP.156	OD2	3.217
2UYL	B.ARG.40	NH1	B.GLU.46	OE2	3.963
2UYL	B.ARG.40	NH2	B.ASP.89	OD1	3.905
2UYL	B.LYS.63	NZ	B.GLU.46	OE1	2.751
2UYL	B.LYS.63	NZ	B.GLU.46	OE2	3.738
2UYL	B.LYS.67	NZ	B.ASP.90	OD1	2.822
2UYL	B.LYS.67	NZ	B.ASP.90	OD2	3.465
2UYL	B.ARG.98	NH2	B.GLU.100	OE2	3.144
2UYL	M.ARG.24	NH1	M.ASP.75	OD1	3.039
2UYL	M.ARG.24	NH1	M.ASP.75	OD2	2.784
2UYL	M.ARG.24	NH2	M.ASP.75	OD2	3.872
2UYL	M.ARG.66	NH1	M.GLU.84	OE1	3.248
2UYL	M.ARG.66	NH1	M.GLU.84	OE2	3.722
2UYL	M.ARG.66	NH2	M.GLU.84	OE2	3.790
2UYL	M.ARG.66	NH2	M.GLU.86	OE1	3.569
2UYL	M.ARG.66	NH2	M.GLU.86	OE2	3.070
2UYL	M.ARG.66	NH2	M.ASP.87	OD1	3.037
2UYL	M.ARG.66	NH2	M.ASP.87	OD2	3.967
2UYL	M.ARG.101	NH1	N.GLU.99	OE1	3.058
2UYL	M.ARG.101	NH1	N.GLU.99	OE2	3.775
2UYL	M.ARG.101	NH2	N.GLU.99	OE2	3.923
2UYL	M.LYS.108	NZ	M.GLU.110	OE1	3.809
2UYL	M.LYS.152	NZ	M.GLU.159	OE2	3.798

2UYL	M_LYS_154	NZ	M_GLU_200	OE1	2.830
2UYL	M_ARG_160	NH1	M_GLU_190	OE1	3.456
2UYL	M_ARG_160	NH2	M_GLU_190	OE1	2.573
2UYL	M_ARG_160	NH2	M_GLU_190	OE2	3.199
2UYL	M_LYS_188	NZ	M_GLU_192	OE2	3.865
2UYL	M_HIS_194	ND1	M_ASP_156	OD2	2.773
2UYL	N_LYS_63	NZ	N_GLU_46	OE1	2.897
2UYL	N_LYS_67	NZ	N_ASP_90	OD1	2.827
2UYL	N_LYS_67	NZ	N_ASP_90	OD2	3.442
2UYL	N_ARG_98	NH2	N_GLU_100	OE1	2.786
2UYL	N_ARG_98	NH2	N_GLU_100	OE2	3.617
2UYL	N_HIS_170	NE2	M_ASP_172	OD1	3.811
2UYL	V_ARG_24	NH1	V_ASP_75	OD1	3.803
2UYL	V_ARG_24	NH2	V_ASP_75	OD1	2.930
2UYL	V_ARG_24	NH2	V_ASP_75	OD2	3.669
2UYL	V_LYS_44	NZ	V_GLU_86	OE1	2.905
2UYL	V_LYS_55	NZ	V_ASP_35	OD2	3.201
2UYL	V_ARG_66	NH1	V_GLU_84	OE1	3.900
2UYL	V_ARG_66	NH2	V_GLU_84	OE2	3.992
2UYL	V_ARG_66	NH2	V_GLU_86	OE2	3.799
2UYL	V_ARG_66	NH2	V_ASP_87	OD1	2.834
2UYL	V_ARG_66	NH2	V_ASP_87	OD2	3.258
2UYL	V_ARG_101	NH1	W_GLU_99	OE1	2.958
2UYL	V_ARG_101	NH1	W_GLU_99	OE2	3.417
2UYL	V_ARG_101	NH2	W_GLU_99	OE2	3.369
2UYL	V_LYS_108	NZ	V_ASP_170	OD1	3.736
2UYL	V_LYS_154	NZ	V_GLU_200	OE1	2.621
2UYL	V_LYS_154	NZ	V_GLU_200	OE2	3.889
2UYL	V_ARG_160	NH1	V_GLU_190	OE1	3.166
2UYL	V_ARG_160	NH2	V_GLU_190	OE1	3.294
2UYL	V_ARG_160	NH2	V_GLU_190	OE2	3.839
2UYL	V_HIS_194	ND1	V_ASP_156	OD2	2.891
2UYL	V_LYS_204	NZ	V_ASP_115	OD1	3.190
2UYL	W_LYS_63	NZ	W_GLU_46	OE1	2.810
2UYL	W_LYS_63	NZ	W_GLU_46	OE2	3.935
2UYL	W_LYS_67	NZ	W_ASP_90	OD1	3.006
2UYL	W_LYS_67	NZ	W_ASP_90	OD2	3.683
2UYL	W_ARG_98	NH2	W_GLU_100	OE2	3.033
2UYL	X_ARG_24	NH1	X_ASP_75	OD1	3.584
2UYL	X_ARG_24	NH2	X_ASP_75	OD1	3.267
2UYL	X_LYS_55	NZ	X_ASP_35	OD2	3.064
2UYL	X_ARG_66	NH1	X_GLU_84	OE1	3.245
2UYL	X_ARG_66	NH1	X_GLU_84	OE2	3.798
2UYL	X_ARG_66	NH2	X_GLU_84	OE1	3.726
2UYL	X_ARG_66	NH2	X_GLU_84	OE2	3.244
2UYL	X_ARG_66	NH2	X_GLU_86	OE1	3.815
2UYL	X_ARG_66	NH2	X_GLU_86	OE2	2.779
2UYL	X_ARG_101	NH1	Y_GLU_99	OE1	2.789
2UYL	X_ARG_101	NH1	Y_GLU_99	OE2	3.483
2UYL	X_ARG_101	NH2	Y_GLU_99	OE2	3.405
2UYL	X_LYS_152	NZ	X_GLU_200	OE2	3.544
2UYL	X_LYS_154	NZ	X_GLU_200	OE1	3.293
2UYL	X_LYS_188	NZ	X_GLU_192	OE1	3.104
2UYL	X_LYS_188	NZ	X_GLU_192	OE2	3.213
2UYL	X_HIS_194	ND1	X_ASP_156	OD2	3.029
2UYL	X_LYS_204	NZ	X_ASP_115	OD1	2.823
2UYL	X_LYS_204	NZ	X_ASP_115	OD2	3.875
2UYL	Y_LYS_63	NZ	Y_GLU_46	OE1	3.237

2UYL	Y_LYS_63	NZ	Y_GLU_46	OE2	3.539
2UYL	Y_LYS_67	NZ	Y_ASP_90	OD1	2.881
2UYL	Y_LYS_67	NZ	Y_ASP_90	OD2	3.582
2UYL	Y_ARG_98	NH2	Y_GLU_100	OE1	2.856
2UYL	Y_ARG_98	NH2	Y_GLU_100	OE2	3.603
2VC2	A_HIS_30	ND1	A_GLU_136	OE1	3.993
2VC2	A_ARG_77	NH1	H_ASP_102	OD1	3.536
2VC2	A_ARG_77	NH1	H_ASP_102	OD2	3.007
2VC2	A_ARG_77	NH2	H_ASP_102	OD1	2.794
2VC2	A_ARG_77	NH2	H_ASP_102	OD2	3.630
2VC2	A_LYS_88	NZ	A_ASP_71	OD2	3.044
2VC2	A_LYS_88	NZ	A_GLU_75	OE2	3.709
2VC2	A_ARG_153	NH1	A_GLU_157	OE1	3.976
2VC2	A_ARG_153	NH1	A_GLU_157	OE2	3.374
2VC2	A_ARG_153	NH2	A_GLU_120	OE1	3.288
2VC2	A_ARG_153	NH2	A_GLU_120	OE2	3.798
2VC2	A_ARG_165	NH1	A_GLU_123	OE2	3.067
2VC2	A_ARG_165	NH2	A_ASP_163	OD1	2.956
2VC2	A_ARG_165	NH2	A_ASP_163	OD2	3.881
2VC2	A_ARG_279	NH2	A_GLU_268	OE2	3.656
2VC2	A_ARG_303	NH2	A_ASP_301	OD2	3.119
2VC2	A_ARG_327	NH1	A_GLU_283	OE1	3.141
2VC2	A_ARG_327	NH1	A_GLU_283	OE2	3.525
2VC2	A_ARG_422	NH1	A_ASP_24	OD1	2.995
2VC2	A_ARG_422	NH1	A_ASP_24	OD2	3.442
2VC2	B_ARG_67	NH1	B_GLU_65	OE1	3.348
2VC2	B_LYS_72	NZ	B_ASP_109	OD1	2.615
2VC2	B_LYS_72	NZ	B_ASP_109	OD2	3.592
2VC2	B_ARG_87	NH2	B_GLU_65	OE2	3.439
2VC2	B_ARG_105	NH1	B_ASP_71	OD1	3.409
2VC2	B_LYS_159	NZ	B_ASP_224	OD1	3.836
2VC2	B_LYS_159	NZ	B_ASP_224	OD2	2.792
2VC2	B_LYS_209	NZ	B_GLU_206	OE2	3.718
2VC2	B_ARG_214	NH1	B_ASP_179	OD1	3.968
2VC2	B_ARG_214	NH1	B_ASP_179	OD2	2.988
2VC2	B_ARG_214	NH2	B_ASP_179	OD1	3.866
2VC2	B_ARG_214	NH2	B_ASP_179	OD2	3.629
2VC2	B_ARG_216	NH2	A_GLU_123	OE2	3.081
2VC2	B_ARG_239	NH2	B_ASP_113	OD2	3.274
2VC2	B_HIS_244	NE2	B_ASP_113	OD1	3.820
2VC2	B_LYS_253	NZ	A_ASP_232	OD2	2.805
2VC2	B_HIS_255	ND1	B_ASP_259	OD2	2.957
2VC2	B_HIS_255	NE2	B_ASP_158	OD2	3.335
2VC2	B_HIS_255	NE2	B_ASP_217	OD1	3.717
2VC2	B_HIS_255	NE2	B_ASP_217	OD2	2.761
2VC2	B_HIS_274	NE2	B_ASP_270	OD1	2.976
2VC2	B_HIS_274	NE2	B_ASP_270	OD2	2.687
2VC2	B_LYS_298	NZ	B_GLU_297	OE2	3.182
2VC2	B_LYS_302	NZ	B_ASP_233	OD1	3.549
2VC2	B_LYS_302	NZ	B_ASP_233	OD2	3.146
2VC2	B_LYS_354	NZ	B_GLU_356	OE1	3.116
2VC2	B_ARG_360	NH2	B_GLU_358	OE2	3.412
2VC2	B_ARG_404	NH1	B_GLU_364	OE2	3.062
2VC2	B_ARG_404	NH2	B_GLU_364	OE2	3.029
2VC2	B_LYS_412	NZ	B_GLU_365	OE1	2.695
2VC2	B_LYS_412	NZ	B_GLU_365	OE2	3.221
2VC2	H_LYS_38	NZ	H_ASP_90	OD1	3.582
2VC2	H_ARG_40	NH2	H_GLU_46	OE1	3.291

2VC2	H_ARG_40	NH2	H_GLU_46	OE2	3.920
2VC2	H_LYS_67	NZ	H_ASP_90	OD2	2.912
2VC2	H_LYS_214	NZ	L_GLU_123	OE2	3.240
2VC2	H_LYS_215	NZ	H_GLU_217	OE1	3.925
2VC2	L_HIS_24	ND1	L_ASP_70	OD1	2.720
2VC2	L_HIS_24	ND1	L_ASP_70	OD2	3.328
2VC2	L_LYS_39	NZ	L_GLU_81	OE2	3.318
2VC2	L_ARG_61	NH2	L_ASP_82	OD1	3.251
2VC2	L_ARG_61	NH2	L_ASP_82	OD2	3.737
2VC2	L_LYS_103	NZ	L_ASP_85	OD1	2.978
2VC2	L_LYS_103	NZ	L_ASP_85	OD2	2.787
2VC2	L_LYS_149	NZ	L_GLU_195	OE1	2.774
2VC2	L_LYS_149	NZ	L_GLU_195	OE2	3.388
2VC2	L_ARG_155	NH1	L_GLU_185	OE1	3.167
2VC2	L_ARG_155	NH1	L_GLU_185	OE2	3.736
2VC2	L_ARG_155	NH2	L_GLU_185	OE2	3.256
2VC2	L_HIS_189	ND1	L_ASP_151	OD1	2.726
2VC2	L_LYS_199	NZ	L_ASP_110	OD2	3.011
2VDK	A_HIS_30	ND1	A_GLU_136	OE1	3.867
2VDK	A_ARG_77	NH1	H_ASP_102	OD1	3.535
2VDK	A_ARG_77	NH1	H_ASP_102	OD2	3.168
2VDK	A_ARG_77	NH2	H_ASP_102	OD1	2.738
2VDK	A_ARG_77	NH2	H_ASP_102	OD2	3.673
2VDK	A_LYS_88	NZ	A_ASP_71	OD1	3.934
2VDK	A_LYS_88	NZ	A_GLU_75	OE2	3.775
2VDK	A_ARG_153	NH1	A_GLU_157	OE1	3.920
2VDK	A_ARG_153	NH1	A_GLU_157	OE2	3.540
2VDK	A_ARG_153	NH2	A_GLU_120	OE1	3.575
2VDK	A_ARG_153	NH2	A_GLU_120	OE2	3.437
2VDK	A_ARG_165	NH1	A_GLU_123	OE1	3.551
2VDK	A_ARG_165	NH1	A_GLU_123	OE2	3.025
2VDK	A_ARG_165	NH2	A_ASP_163	OD1	2.867
2VDK	A_ARG_165	NH2	A_ASP_163	OD2	3.841
2VDK	A_ARG_279	NH2	A_GLU_268	OE2	3.830
2VDK	A_ARG_317	NH2	A_GLU_315	OE1	3.703
2VDK	A_ARG_327	NH1	A_GLU_283	OE1	2.969
2VDK	A_ARG_327	NH1	A_GLU_283	OE2	3.151
2VDK	A_ARG_422	NH1	A_ASP_24	OD1	2.982
2VDK	A_ARG_422	NH1	A_ASP_24	OD2	3.550
2VDK	B_ARG_62	NH2	B_GLU_60	OE2	3.869
2VDK	B_ARG_67	NH1	B_GLU_65	OE1	3.128
2VDK	B_LYS_72	NZ	B_ASP_109	OD1	2.883
2VDK	B_LYS_72	NZ	B_ASP_109	OD2	3.231
2VDK	B_ARG_87	NH2	B_GLU_65	OE2	3.747
2VDK	B_ARG_105	NH1	B_ASP_71	OD1	3.501
2VDK	B_LYS_159	NZ	B_ASP_224	OD1	3.871
2VDK	B_LYS_159	NZ	B_ASP_224	OD2	2.724
2VDK	B_LYS_209	NZ	B_GLU_206	OE2	3.427
2VDK	B_ARG_214	NH1	B_ASP_179	OD1	2.883
2VDK	B_ARG_214	NH1	B_ASP_179	OD2	3.837
2VDK	B_ARG_214	NH2	B_ASP_179	OD1	3.373
2VDK	B_ARG_214	NH2	B_ASP_179	OD2	3.883
2VDK	B_ARG_216	NH2	A_GLU_123	OE2	3.072
2VDK	B_ARG_239	NH2	B_ASP_113	OD2	2.945
2VDK	B_HIS_244	NE2	B_ASP_113	OD1	3.799
2VDK	B_LYS_253	NZ	A_ASP_232	OD2	2.921
2VDK	B_HIS_255	ND1	B_ASP_259	OD2	2.885
2VDK	B_HIS_255	NE2	B_ASP_158	OD2	3.290

2VDK	B_HIS_255	NE2	B_ASP_217	OD1	3.718
2VDK	B_HIS_255	NE2	B_ASP_217	OD2	2.719
2VDK	B_HIS_274	NE2	B_ASP_270	OD1	3.028
2VDK	B_HIS_274	NE2	B_ASP_270	OD2	2.677
2VDK	B_LYS_298	NZ	B_GLU_297	OE2	3.464
2VDK	B_LYS_302	NZ	B_ASP_233	OD1	3.247
2VDK	B_LYS_302	NZ	B_ASP_233	OD2	2.825
2VDK	B_LYS_354	NZ	B_GLU_356	OE1	2.748
2VDK	B_LYS_354	NZ	B_GLU_356	OE2	3.777
2VDK	B_ARG_360	NH2	B_GLU_358	OE1	3.701
2VDK	B_ARG_360	NH2	B_GLU_358	OE2	3.427
2VDK	B_ARG_404	NH1	B_GLU_364	OE2	3.192
2VDK	B_ARG_404	NH2	B_GLU_364	OE2	3.127
2VDK	B_LYS_412	NZ	B_GLU_365	OE1	2.671
2VDK	B_LYS_412	NZ	B_GLU_365	OE2	3.186
2VDK	H_LYS_38	NZ	H_GLU_46	OE1	3.930
2VDK	H_ARG_40	NH2	H_GLU_46	OE1	3.206
2VDK	H_ARG_40	NH2	H_GLU_46	OE2	3.861
2VDK	H_LYS_67	NZ	H_ASP_90	OD1	3.807
2VDK	H_LYS_67	NZ	H_ASP_90	OD2	2.831
2VDK	H_LYS_214	NZ	L_GLU_123	OE2	3.461
2VDK	H_LYS_215	NZ	H_GLU_217	OE1	3.919
2VDK	L_HIS_24	ND1	L_ASP_70	OD1	2.714
2VDK	L_HIS_24	ND1	L_ASP_70	OD2	3.907
2VDK	L_LYS_39	NZ	L_GLU_81	OE2	3.076
2VDK	L_ARG_61	NH2	L_ASP_82	OD1	3.150
2VDK	L_ARG_61	NH2	L_ASP_82	OD2	3.695
2VDK	L_LYS_103	NZ	L_ASP_85	OD1	3.316
2VDK	L_LYS_103	NZ	L_ASP_85	OD2	3.639
2VDK	L_LYS_147	NZ	L_GLU_154	OE1	3.768
2VDK	L_LYS_147	NZ	L_GLU_154	OE2	3.469
2VDK	L_LYS_149	NZ	L_GLU_195	OE1	3.051
2VDK	L_LYS_149	NZ	L_GLU_195	OE2	3.550
2VDK	L_ARG_155	NH1	L_GLU_185	OE1	3.070
2VDK	L_ARG_155	NH1	L_GLU_185	OE2	3.757
2VDK	L_ARG_155	NH2	L_GLU_185	OE1	3.874
2VDK	L_ARG_155	NH2	L_GLU_185	OE2	3.166
2VDK	L_HIS_189	ND1	L_ASP_151	OD1	2.842
2VDK	L_LYS_199	NZ	L_ASP_110	OD2	3.918
2VDL	A_HIS_30	ND1	A_GLU_136	OE1	3.983
2VDL	A_ARG_77	NH1	H_ASP_102	OD1	3.566
2VDL	A_ARG_77	NH1	H_ASP_102	OD2	3.106
2VDL	A_ARG_77	NH2	H_ASP_102	OD1	2.722
2VDL	A_ARG_77	NH2	H_ASP_102	OD2	3.538
2VDL	A_LYS_88	NZ	A_ASP_71	OD2	3.901
2VDL	A_LYS_88	NZ	A_GLU_75	OE2	3.727
2VDL	A_ARG_153	NH2	A_GLU_120	OE1	3.211
2VDL	A_ARG_153	NH2	A_GLU_120	OE2	3.450
2VDL	A_ARG_165	NH1	A_GLU_123	OE1	3.959
2VDL	A_ARG_165	NH1	A_GLU_123	OE2	2.984
2VDL	A_ARG_165	NH2	A_ASP_163	OD1	2.925
2VDL	A_ARG_165	NH2	A_ASP_163	OD2	3.806
2VDL	A_ARG_279	NH2	A_GLU_268	OE2	3.603
2VDL	A_ARG_317	NH2	A_GLU_315	OE1	3.612
2VDL	A_ARG_327	NH1	A_GLU_283	OE1	2.900
2VDL	A_ARG_327	NH1	A_GLU_283	OE2	3.367
2VDL	A_ARG_422	NH1	A_ASP_24	OD1	2.923
2VDL	A_ARG_422	NH1	A_ASP_24	OD2	3.362

2VDL	B_ARG_62	NH2	B_GLU_60	OE2	3.680
2VDL	B_ARG_67	NH1	B_GLU_65	OE1	3.332
2VDL	B_LYS_72	NZ	B_ASP_109	OD1	2.951
2VDL	B_LYS_72	NZ	B_ASP_109	OD2	3.006
2VDL	B_ARG_105	NH1	B_ASP_71	OD1	3.378
2VDL	B_LYS_159	NZ	B_ASP_224	OD1	3.910
2VDL	B_LYS_159	NZ	B_ASP_224	OD2	2.697
2VDL	B_ARG_214	NH1	B_ASP_179	OD1	3.402
2VDL	B_ARG_214	NH1	B_ASP_179	OD2	3.426
2VDL	B_ARG_214	NH2	B_ASP_179	OD1	3.763
2VDL	B_ARG_214	NH2	B_ASP_179	OD2	3.522
2VDL	B_ARG_216	NH2	A_GLU_123	OE2	3.160
2VDL	B_ARG_239	NH2	B_ASP_113	OD2	2.965
2VDL	B_HIS_244	NE2	B_ASP_113	OD1	3.758
2VDL	B_LYS_253	NZ	A_ASP_232	OD2	2.886
2VDL	B_HIS_255	ND1	B_ASP_259	OD2	2.838
2VDL	B_HIS_255	NE2	B_ASP_158	OD2	3.301
2VDL	B_HIS_255	NE2	B_ASP_217	OD1	3.748
2VDL	B_HIS_255	NE2	B_ASP_217	OD2	2.696
2VDL	B_HIS_274	NE2	B_ASP_270	OD1	3.004
2VDL	B_HIS_274	NE2	B_ASP_270	OD2	2.721
2VDL	B_LYS_298	NZ	B_GLU_297	OE2	3.472
2VDL	B_LYS_302	NZ	B_ASP_233	OD1	3.054
2VDL	B_LYS_302	NZ	B_ASP_233	OD2	3.066
2VDL	B_LYS_354	NZ	B_GLU_356	OE1	2.717
2VDL	B_ARG_360	NH2	B_GLU_358	OE1	3.910
2VDL	B_ARG_360	NH2	B_GLU_358	OE2	3.469
2VDL	B_ARG_404	NH1	B_GLU_364	OE2	3.049
2VDL	B_ARG_404	NH2	B_GLU_364	OE2	3.073
2VDL	B_LYS_417	NZ	B_GLU_358	OE2	3.933
2VDL	H_ARG_40	NH2	H_GLU_46	OE1	3.013
2VDL	H_ARG_40	NH2	H_GLU_46	OE2	3.976
2VDL	H_LYS_59	NZ	A_GLU_117	OE2	3.964
2VDL	H_LYS_67	NZ	H_ASP_90	OD1	3.729
2VDL	H_LYS_67	NZ	H_ASP_90	OD2	2.693
2VDL	H_LYS_214	NZ	L_GLU_123	OE2	3.400
2VDL	L_HIS_24	ND1	L_ASP_70	OD1	2.670
2VDL	L_HIS_24	ND1	L_ASP_70	OD2	3.843
2VDL	L_ARG_61	NH2	L_ASP_82	OD1	3.133
2VDL	L_ARG_61	NH2	L_ASP_82	OD2	3.618
2VDL	L_LYS_103	NZ	L_ASP_85	OD1	3.222
2VDL	L_LYS_103	NZ	L_ASP_85	OD2	3.662
2VDL	L_LYS_147	NZ	L_GLU_154	OE1	3.870
2VDL	L_LYS_149	NZ	L_GLU_195	OE1	3.028
2VDL	L_LYS_149	NZ	L_GLU_195	OE2	3.950
2VDL	L_ARG_155	NH1	L_GLU_185	OE1	3.118
2VDL	L_ARG_155	NH1	L_GLU_185	OE2	3.879
2VDL	L_ARG_155	NH2	L_GLU_185	OE1	3.756
2VDL	L_ARG_155	NH2	L_GLU_185	OE2	3.072
2VDL	L_HIS_189	ND1	L_ASP_151	OD1	2.876
2VDL	L_LYS_199	NZ	L_ASP_110	OD2	3.382
2VDM	A_HIS_30	ND1	A_GLU_136	OE1	3.623
2VDM	A_ARG_77	NH1	H_ASP_102	OD1	3.512
2VDM	A_ARG_77	NH1	H_ASP_102	OD2	3.196
2VDM	A_ARG_77	NH2	H_ASP_102	OD1	2.762
2VDM	A_ARG_77	NH2	H_ASP_102	OD2	3.757
2VDM	A_LYS_88	NZ	A_ASP_71	OD1	3.506
2VDM	A_LYS_88	NZ	A_GLU_75	OE2	3.717

2VDM	A_ARG_153	NH1	A_GLU_157	OE2	3.526
2VDM	A_ARG_153	NH2	A_GLU_120	OE1	3.629
2VDM	A_ARG_153	NH2	A_GLU_120	OE2	3.472
2VDM	A_ARG_165	NH1	A_GLU_123	OE1	3.954
2VDM	A_ARG_165	NH1	A_GLU_123	OE2	2.915
2VDM	A_ARG_165	NH2	A_ASP_163	OD1	2.984
2VDM	A_ARG_279	NH2	A_GLU_268	OE2	3.711
2VDM	A_ARG_317	NH2	A_GLU_315	OE1	3.553
2VDM	A_ARG_327	NH1	A_GLU_283	OE1	3.196
2VDM	A_ARG_327	NH1	A_GLU_283	OE2	3.335
2VDM	A_ARG_422	NH1	A_ASP_24	OD1	2.877
2VDM	A_ARG_422	NH1	A_ASP_24	OD2	3.314
2VDM	B_ARG_62	NH2	B_GLU_60	OE2	3.866
2VDM	B_LYS_72	NZ	B_ASP_109	OD1	2.865
2VDM	B_LYS_72	NZ	B_ASP_109	OD2	3.109
2VDM	B_ARG_91	NH2	B_GLU_60	OE1	3.150
2VDM	B_ARG_105	NH1	B_ASP_71	OD1	3.646
2VDM	B_LYS_159	NZ	B_ASP_224	OD1	3.821
2VDM	B_LYS_159	NZ	B_ASP_224	OD2	2.737
2VDM	B_LYS_209	NZ	B_GLU_206	OE2	3.484
2VDM	B_ARG_214	NH1	B_ASP_179	OD2	3.120
2VDM	B_ARG_216	NH2	A_GLU_123	OE2	2.982
2VDM	B_ARG_239	NH2	B_ASP_113	OD2	3.117
2VDM	B_HIS_244	NE2	B_ASP_113	OD1	3.810
2VDM	B_LYS_253	NZ	A_ASP_232	OD2	3.306
2VDM	B_HIS_255	ND1	B_ASP_259	OD2	2.883
2VDM	B_HIS_255	NE2	B_ASP_158	OD2	3.162
2VDM	B_HIS_255	NE2	B_ASP_217	OD1	3.723
2VDM	B_HIS_255	NE2	B_ASP_217	OD2	2.768
2VDM	B_HIS_274	NE2	B_ASP_270	OD1	3.033
2VDM	B_HIS_274	NE2	B_ASP_270	OD2	2.759
2VDM	B_HIS_280	ND1	B_ASP_278	OD2	3.990
2VDM	B_LYS_298	NZ	B_GLU_297	OE2	3.783
2VDM	B_LYS_302	NZ	B_ASP_233	OD1	3.512
2VDM	B_LYS_302	NZ	B_ASP_233	OD2	3.089
2VDM	B_LYS_354	NZ	B_GLU_356	OE1	2.934
2VDM	B_LYS_354	NZ	B_GLU_356	OE2	3.448
2VDM	B_ARG_360	NH2	B_GLU_358	OE2	3.602
2VDM	B_LYS_390	NZ	B_ASP_393	OD1	3.190
2VDM	B_ARG_404	NH1	B_GLU_364	OE2	3.379
2VDM	B_ARG_404	NH2	B_GLU_364	OE2	3.556
2VDM	B_LYS_412	NZ	B_GLU_365	OE1	2.778
2VDM	B_LYS_412	NZ	B_GLU_365	OE2	3.744
2VDM	B_LYS_417	NZ	B_GLU_358	OE2	3.687
2VDM	H_ARG_40	NH2	H_GLU_46	OE1	3.139
2VDM	H_LYS_67	NZ	H_ASP_90	OD1	3.953
2VDM	H_LYS_67	NZ	H_ASP_90	OD2	2.810
2VDM	H_LYS_214	NZ	L_GLU_123	OE2	3.334
2VDM	H_LYS_215	NZ	H_GLU_217	OE1	3.652
2VDM	L_HIS_24	ND1	L_ASP_70	OD1	2.661
2VDM	L_HIS_24	ND1	L_ASP_70	OD2	3.812
2VDM	L_LYS_39	NZ	L_GLU_81	OE2	3.325
2VDM	L_ARG_61	NH2	L_ASP_79	OD1	3.812
2VDM	L_ARG_61	NH2	L_ASP_82	OD1	3.292
2VDM	L_ARG_61	NH2	L_ASP_82	OD2	3.719
2VDM	L_LYS_103	NZ	L_ASP_85	OD1	2.836
2VDM	L_LYS_103	NZ	L_ASP_85	OD2	3.351
2VDM	L_LYS_147	NZ	L_GLU_154	OE1	3.824

2VDM	L_LYS_147	NZ	L_GLU_154	OE2	3.630
2VDM	L_LYS_149	NZ	L_GLU_195	OE1	3.194
2VDM	L_LYS_149	NZ	L_GLU_195	OE2	3.563
2VDM	L_ARG_155	NH1	L_GLU_185	OE1	3.186
2VDM	L_ARG_155	NH2	L_GLU_185	OE1	3.687
2VDM	L_ARG_155	NH2	L_GLU_185	OE2	3.288
2VDM	L_HIS_189	ND1	L_ASP_151	OD1	2.728
2VDM	L_LYS_199	NZ	L_ASP_110	OD2	3.757
2VDN	A_HIS_30	ND1	A_GLU_136	OE1	3.948
2VDN	A_ARG_77	NH1	H_ASP_102	OD1	3.491
2VDN	A_ARG_77	NH1	H_ASP_102	OD2	3.169
2VDN	A_ARG_77	NH2	H_ASP_102	OD1	2.808
2VDN	A_ARG_77	NH2	H_ASP_102	OD2	3.762
2VDN	A_LYS_88	NZ	A_ASP_71	OD1	3.146
2VDN	A_LYS_88	NZ	A_GLU_75	OE2	3.755
2VDN	A_ARG_153	NH1	A_GLU_157	OE2	3.732
2VDN	A_ARG_153	NH2	A_GLU_120	OE1	3.385
2VDN	A_ARG_153	NH2	A_GLU_120	OE2	3.434
2VDN	A_ARG_165	NH1	A_GLU_123	OE1	3.564
2VDN	A_ARG_165	NH1	A_GLU_123	OE2	3.322
2VDN	A_ARG_165	NH2	A_ASP_163	OD1	2.897
2VDN	A_ARG_165	NH2	A_ASP_163	OD2	3.963
2VDN	A_ARG_317	NH2	A_GLU_315	OE1	3.869
2VDN	A_ARG_327	NH1	A_GLU_283	OE1	3.115
2VDN	A_ARG_327	NH1	A_GLU_283	OE2	3.543
2VDN	A_ARG_422	NH1	A_ASP_24	OD1	2.918
2VDN	A_ARG_422	NH1	A_ASP_24	OD2	3.024
2VDN	A_ARG_422	NH2	A_ASP_24	OD2	3.873
2VDN	B_ARG_62	NH2	B_GLU_60	OE1	3.892
2VDN	B_ARG_62	NH2	B_GLU_60	OE2	3.874
2VDN	B_ARG_67	NH1	B_GLU_65	OE1	3.311
2VDN	B_LYS_72	NZ	B_ASP_109	OD1	2.643
2VDN	B_LYS_72	NZ	B_ASP_109	OD2	3.617
2VDN	B_ARG_87	NH2	B_GLU_65	OE2	3.986
2VDN	B_ARG_91	NH1	B_GLU_60	OE2	3.487
2VDN	B_ARG_91	NH2	B_GLU_60	OE2	3.817
2VDN	B_ARG_105	NH1	B_ASP_71	OD1	3.631
2VDN	B_LYS_159	NZ	B_ASP_224	OD1	3.745
2VDN	B_LYS_159	NZ	B_ASP_224	OD2	2.600
2VDN	B_LYS_209	NZ	B_GLU_206	OE2	3.458
2VDN	B_ARG_214	NH1	B_ASP_179	OD2	2.971
2VDN	B_ARG_214	NH2	B_ASP_179	OD2	3.917
2VDN	B_ARG_216	NH2	A_GLU_123	OE2	2.995
2VDN	B_ARG_239	NH2	B_ASP_113	OD2	3.167
2VDN	B_HIS_244	NE2	B_ASP_113	OD1	3.751
2VDN	B_HIS_255	ND1	B_ASP_259	OD2	2.831
2VDN	B_HIS_255	NE2	B_ASP_158	OD2	3.236
2VDN	B_HIS_255	NE2	B_ASP_217	OD1	3.761
2VDN	B_HIS_255	NE2	B_ASP_217	OD2	2.725
2VDN	B_HIS_274	NE2	B_ASP_270	OD1	3.136
2VDN	B_HIS_274	NE2	B_ASP_270	OD2	2.767
2VDN	B_HIS_280	ND1	B_ASP_278	OD2	3.961
2VDN	B_LYS_302	NZ	B_ASP_233	OD1	3.616
2VDN	B_LYS_302	NZ	B_ASP_233	OD2	3.020
2VDN	B_LYS_354	NZ	B_GLU_356	OE1	2.617
2VDN	B_ARG_360	NH2	B_GLU_358	OE2	3.301
2VDN	B_LYS_390	NZ	B_ASP_393	OD1	3.452
2VDN	B_ARG_404	NH1	B_GLU_364	OE2	3.371

2VDN	B_ARG_404	NH2	B_GLU_364	OE2	2.851
2VDN	B_LYS_412	NZ	B_GLU_365	OE1	2.766
2VDN	B_LYS_412	NZ	B_GLU_365	OE2	3.273
2VDN	B_LYS_412	NZ	B_GLU_409	OE2	3.840
2VDN	B_LYS_417	NZ	B_GLU_358	OE2	3.820
2VDN	H_ARG_40	NH2	H_GLU_46	OE1	3.092
2VDN	H_LYS_67	NZ	H_ASP_90	OD1	3.750
2VDN	H_LYS_67	NZ	H_ASP_90	OD2	2.688
2VDN	H_LYS_214	NZ	L_GLU_123	OE2	3.685
2VDN	H_LYS_215	NZ	H_GLU_217	OE1	3.744
2VDN	L_HIS_24	ND1	L_ASP_70	OD1	2.783
2VDN	L_LYS_39	NZ	L_GLU_81	OE2	3.138
2VDN	L_ARG_61	NH2	L_ASP_82	OD1	3.159
2VDN	L_ARG_61	NH2	L_ASP_82	OD2	3.820
2VDN	L_LYS_103	NZ	L_ASP_85	OD1	3.058
2VDN	L_LYS_103	NZ	L_ASP_85	OD2	3.355
2VDN	L_LYS_147	NZ	L_GLU_154	OE1	3.309
2VDN	L_LYS_147	NZ	L_GLU_154	OE2	3.600
2VDN	L_LYS_149	NZ	L_GLU_195	OE1	3.164
2VDN	L_LYS_149	NZ	L_GLU_195	OE2	3.705
2VDN	L_ARG_155	NH1	L_GLU_185	OE1	3.044
2VDN	L_ARG_155	NH1	L_GLU_185	OE2	3.873
2VDN	L_ARG_155	NH2	L_GLU_185	OE1	3.640
2VDN	L_ARG_155	NH2	L_GLU_185	OE2	3.207
2VDN	L_LYS_199	NZ	L_ASP_110	OD2	3.394
2VDO	A_HIS_30	ND1	A_GLU_136	OE1	3.920
2VDO	A_ARG_77	NH1	H_ASP_102	OD1	3.703
2VDO	A_ARG_77	NH1	H_ASP_102	OD2	3.042
2VDO	A_ARG_77	NH2	H_ASP_102	OD1	2.789
2VDO	A_ARG_77	NH2	H_ASP_102	OD2	3.375
2VDO	A_LYS_88	NZ	A_GLU_75	OE2	3.810
2VDO	A_ARG_153	NH1	A_GLU_157	OE2	3.784
2VDO	A_ARG_153	NH2	A_GLU_120	OE1	3.533
2VDO	A_ARG_153	NH2	A_GLU_120	OE2	3.754
2VDO	A_ARG_165	NH1	A_GLU_123	OE1	3.613
2VDO	A_ARG_165	NH1	A_GLU_123	OE2	3.354
2VDO	A_ARG_165	NH2	A_ASP_163	OD1	2.853
2VDO	A_ARG_165	NH2	A_ASP_163	OD2	3.749
2VDO	A_ARG_279	NH2	A_GLU_268	OE2	3.621
2VDO	A_ARG_303	NH2	A_ASP_301	OD2	3.328
2VDO	A_ARG_317	NH2	A_GLU_315	OE1	3.691
2VDO	A_ARG_327	NH1	A_GLU_283	OE1	3.064
2VDO	A_ARG_327	NH1	A_GLU_283	OE2	3.315
2VDO	A_ARG_422	NH1	A_ASP_24	OD1	3.045
2VDO	A_ARG_422	NH1	A_ASP_24	OD2	3.220
2VDO	A_ARG_422	NH2	A_ASP_24	OD2	3.964
2VDO	B_LYS_72	NZ	B_ASP_109	OD1	2.524
2VDO	B_LYS_72	NZ	B_ASP_109	OD2	3.663
2VDO	B_ARG_91	NH1	B_GLU_60	OE1	3.543
2VDO	B_ARG_105	NH1	B_ASP_71	OD1	3.285
2VDO	B_LYS_159	NZ	B_ASP_224	OD1	3.842
2VDO	B_LYS_159	NZ	B_ASP_224	OD2	2.647
2VDO	B_LYS_209	NZ	B_GLU_206	OE2	3.221
2VDO	B_ARG_214	NH1	B_ASP_179	OD1	3.754
2VDO	B_ARG_214	NH1	B_ASP_179	OD2	2.724
2VDO	B_ARG_216	NH2	A_GLU_123	OE2	3.092
2VDO	B_ARG_239	NH2	B_ASP_113	OD2	2.947
2VDO	B_HIS_244	NE2	B_ASP_113	OD1	3.778

2VDO	B_LYS_253	NZ	A_ASP_232	OD2	2.836
2VDO	B_HIS_255	ND1	B_ASP_259	OD2	2.644
2VDO	B_HIS_255	NE2	B_ASP_158	OD2	3.337
2VDO	B_HIS_255	NE2	B_ASP_217	OD1	3.680
2VDO	B_HIS_255	NE2	B_ASP_217	OD2	2.699
2VDO	B_HIS_274	NE2	B_ASP_270	OD1	3.105
2VDO	B_HIS_274	NE2	B_ASP_270	OD2	2.754
2VDO	B_HIS_280	ND1	B_ASP_278	OD2	3.796
2VDO	B_LYS_298	NZ	B_GLU_297	OE2	3.249
2VDO	B_LYS_302	NZ	B_ASP_233	OD1	3.475
2VDO	B_LYS_302	NZ	B_ASP_233	OD2	3.319
2VDO	B_LYS_354	NZ	B_GLU_356	OE1	2.694
2VDO	B_LYS_390	NZ	B_ASP_393	OD1	2.830
2VDO	B_LYS_390	NZ	B_ASP_393	OD2	3.993
2VDO	B_ARG_404	NH1	B_GLU_364	OE2	3.382
2VDO	B_ARG_404	NH2	B_GLU_364	OE2	2.912
2VDO	C_LYS_406	NZ	A_ASP_224	OD1	2.673
2VDO	C_LYS_406	NZ	A_ASP_224	OD2	3.263
2VDO	H_ARG_40	NH2	H_GLU_46	OE1	3.274
2VDO	H_LYS_67	NZ	H_ASP_90	OD1	3.624
2VDO	H_LYS_67	NZ	H_ASP_90	OD2	2.582
2VDO	L_HIS_24	ND1	L_ASP_70	OD1	2.820
2VDO	L_HIS_24	ND1	L_ASP_70	OD2	3.898
2VDO	L_LYS_39	NZ	L_GLU_81	OE1	3.127
2VDO	L_ARG_61	NH2	L_ASP_82	OD1	3.036
2VDO	L_ARG_61	NH2	L_ASP_82	OD2	3.553
2VDO	L_LYS_103	NZ	L_ASP_85	OD1	3.186
2VDO	L_LYS_103	NZ	L_ASP_85	OD2	3.792
2VDO	L_LYS_147	NZ	L_GLU_154	OE1	3.276
2VDO	L_LYS_147	NZ	L_GLU_154	OE2	3.435
2VDO	L_LYS_149	NZ	L_GLU_195	OE1	3.199
2VDO	L_LYS_149	NZ	L_GLU_195	OE2	3.780
2VDO	L_HIS_189	ND1	L_ASP_151	OD1	2.775
2VDO	L_LYS_199	NZ	L_ASP_110	OD2	3.339
2VDP	A_HIS_30	ND1	A_GLU_136	OE1	3.660
2VDP	A_ARG_77	NH1	H_ASP_102	OD1	3.519
2VDP	A_ARG_77	NH1	H_ASP_102	OD2	3.089
2VDP	A_ARG_77	NH2	H_ASP_102	OD1	2.733
2VDP	A_ARG_77	NH2	H_ASP_102	OD2	3.585
2VDP	A_LYS_88	NZ	A_ASP_71	OD1	3.039
2VDP	A_LYS_88	NZ	A_GLU_75	OE2	3.920
2VDP	A_ARG_153	NH1	A_GLU_157	OE1	3.962
2VDP	A_ARG_153	NH1	A_GLU_157	OE2	3.572
2VDP	A_ARG_153	NH2	A_GLU_120	OE1	3.448
2VDP	A_ARG_153	NH2	A_GLU_120	OE2	3.842
2VDP	A_ARG_165	NH1	A_GLU_123	OE2	2.955
2VDP	A_ARG_165	NH2	A_ASP_163	OD1	2.890
2VDP	A_ARG_165	NH2	A_ASP_163	OD2	3.894
2VDP	A_ARG_279	NH2	A_GLU_268	OE2	3.568
2VDP	A_ARG_303	NH2	A_ASP_301	OD2	3.133
2VDP	A_ARG_317	NH2	A_GLU_315	OE1	3.662
2VDP	A_ARG_327	NH1	A_GLU_283	OE1	3.008
2VDP	A_ARG_327	NH1	A_GLU_283	OE2	3.186
2VDP	A_ARG_422	NH1	A_ASP_24	OD1	3.204
2VDP	A_ARG_422	NH1	A_ASP_24	OD2	3.337
2VDP	B_LYS_72	NZ	B_ASP_109	OD1	2.827
2VDP	B_LYS_72	NZ	B_ASP_109	OD2	3.031
2VDP	B_ARG_105	NH1	B_ASP_71	OD1	3.982

2VDP	B.LYS_159	NZ	B.ASP_224	OD1	3.737
2VDP	B.LYS_159	NZ	B.ASP_224	OD2	2.652
2VDP	B.ARG_214	NH1	B.ASP_179	OD1	3.890
2VDP	B.ARG_214	NH1	B.ASP_179	OD2	2.793
2VDP	B.ARG_214	NH2	B.ASP_179	OD1	3.782
2VDP	B.ARG_214	NH2	B.ASP_179	OD2	3.940
2VDP	B.ARG_216	NH2	A.GLU_123	OE2	3.038
2VDP	B.ARG_239	NH2	B.ASP_113	OD2	3.143
2VDP	B.HIS_244	NE2	B.ASP_113	OD1	3.933
2VDP	B.LYS_253	NZ	A.ASP_232	OD2	2.914
2VDP	B.HIS_255	ND1	B.ASP_259	OD2	2.924
2VDP	B.HIS_255	NE2	B.ASP_158	OD2	3.261
2VDP	B.HIS_255	NE2	B.ASP_217	OD1	3.670
2VDP	B.HIS_255	NE2	B.ASP_217	OD2	2.811
2VDP	B.HIS_274	NE2	B.ASP_270	OD1	2.909
2VDP	B.HIS_274	NE2	B.ASP_270	OD2	2.812
2VDP	B.HIS_280	ND1	B.ASP_278	OD2	3.653
2VDP	B.LYS_298	NZ	B.GLU_297	OE2	3.585
2VDP	B.LYS_302	NZ	B.ASP_233	OD1	3.588
2VDP	B.LYS_302	NZ	B.ASP_233	OD2	3.086
2VDP	B.LYS_354	NZ	B.GLU_356	OE1	2.651
2VDP	B.ARG_360	NH2	B.GLU_358	OE2	3.559
2VDP	B.LYS_390	NZ	B.ASP_393	OD1	2.846
2VDP	B.LYS_412	NZ	B.GLU_365	OE1	2.691
2VDP	B.LYS_412	NZ	B.GLU_365	OE2	3.358
2VDP	C.LYS_406	NZ	A.ASP_224	OD1	2.604
2VDP	C.LYS_406	NZ	A.ASP_224	OD2	3.297
2VDP	H.ARG_40	NH2	H.GLU_46	OE1	3.121
2VDP	H.LYS_67	NZ	H.ASP_90	OD1	3.700
2VDP	H.LYS_67	NZ	H.ASP_90	OD2	2.763
2VDP	H.LYS_214	NZ	L.GLU_123	OE2	3.425
2VDP	L.HIS_24	ND1	L.ASP_70	OD1	2.731
2VDP	L.HIS_24	ND1	L.ASP_70	OD2	3.759
2VDP	L.LYS_39	NZ	L.GLU_81	OE1	3.012
2VDP	L.ARG_61	NH2	L.ASP_82	OD1	3.212
2VDP	L.ARG_61	NH2	L.ASP_82	OD2	3.647
2VDP	L.LYS_103	NZ	L.ASP_85	OD1	3.404
2VDP	L.LYS_103	NZ	L.ASP_85	OD2	3.147
2VDP	L.LYS_147	NZ	L.GLU_154	OE1	3.927
2VDP	L.LYS_147	NZ	L.GLU_154	OE2	3.984
2VDP	L.LYS_149	NZ	L.GLU_195	OE1	3.337
2VDP	L.LYS_149	NZ	L.GLU_195	OE2	3.651
2VDP	L.ARG_155	NH1	L.GLU_185	OE1	3.124
2VDP	L.ARG_155	NH1	L.GLU_185	OE2	3.854
2VDP	L.ARG_155	NH2	L.GLU_185	OE1	3.803
2VDP	L.ARG_155	NH2	L.GLU_185	OE2	3.129
2VDP	L.HIS_189	ND1	L.ASP_151	OD1	3.064
2VDP	L.LYS_199	NZ	L.ASP_110	OD2	3.415
2VDQ	A.ARG_77	NH1	H.ASP_102	OD1	3.603
2VDQ	A.ARG_77	NH1	H.ASP_102	OD2	3.057
2VDQ	A.ARG_77	NH2	H.ASP_102	OD1	2.765
2VDQ	A.ARG_77	NH2	H.ASP_102	OD2	3.398
2VDQ	A.LYS_88	NZ	A.GLU_75	OE2	3.857
2VDQ	A.ARG_153	NH1	A.GLU_157	OE2	3.540
2VDQ	A.ARG_153	NH2	A.GLU_120	OE1	3.469
2VDQ	A.ARG_153	NH2	A.GLU_120	OE2	3.910
2VDQ	A.ARG_165	NH1	A.GLU_123	OE1	3.775
2VDQ	A.ARG_165	NH1	A.GLU_123	OE2	3.560

2VDQ	A_ARG_165	NH2	A_ASP_163	OD1	2.874
2VDQ	A_ARG_165	NH2	A_ASP_163	OD2	3.776
2VDQ	A_ARG_279	NH2	A_GLU_268	OE2	3.474
2VDQ	A_ARG_317	NH2	A_GLU_315	OE1	3.631
2VDQ	A_ARG_327	NH1	A_GLU_283	OE1	3.069
2VDQ	A_ARG_327	NH1	A_GLU_283	OE2	3.317
2VDQ	A_ARG_422	NH1	A_ASP_24	OD1	2.959
2VDQ	A_ARG_422	NH1	A_ASP_24	OD2	3.217
2VDQ	B_ARG_67	NH1	B_GLU_65	OE1	3.626
2VDQ	B_LYS_72	NZ	B_ASP_109	OD1	2.465
2VDQ	B_LYS_72	NZ	B_ASP_109	OD2	3.694
2VDQ	B_ARG_91	NH1	B_GLU_60	OE1	3.580
2VDQ	B_ARG_91	NH2	B_GLU_60	OE1	2.967
2VDQ	B_ARG_105	NH1	B_ASP_71	OD1	3.573
2VDQ	B_LYS_159	NZ	B_ASP_224	OD1	3.868
2VDQ	B_LYS_159	NZ	B_ASP_224	OD2	2.786
2VDQ	B_LYS_209	NZ	B_GLU_206	OE2	3.302
2VDQ	B_ARG_214	NH1	B_ASP_179	OD1	3.942
2VDQ	B_ARG_214	NH1	B_ASP_179	OD2	2.723
2VDQ	B_ARG_216	NH2	A_GLU_123	OE2	2.900
2VDQ	B_ARG_239	NH2	B_ASP_113	OD2	2.900
2VDQ	B_HIS_244	NE2	B_ASP_113	OD1	3.769
2VDQ	B_LYS_253	NZ	A_ASP_232	OD2	3.522
2VDQ	B_HIS_255	ND1	B_ASP_259	OD2	2.795
2VDQ	B_HIS_255	NE2	B_ASP_158	OD2	3.253
2VDQ	B_HIS_255	NE2	B_ASP_217	OD1	3.618
2VDQ	B_HIS_255	NE2	B_ASP_217	OD2	2.719
2VDQ	B_HIS_274	NE2	B_ASP_270	OD1	3.015
2VDQ	B_HIS_274	NE2	B_ASP_270	OD2	2.786
2VDQ	B_HIS_280	ND1	B_ASP_278	OD2	3.936
2VDQ	B_LYS_298	NZ	B_GLU_297	OE2	3.339
2VDQ	B_LYS_302	NZ	B_ASP_233	OD1	3.182
2VDQ	B_LYS_302	NZ	B_ASP_233	OD2	3.177
2VDQ	B_LYS_354	NZ	B_GLU_356	OE1	2.632
2VDQ	B_ARG_360	NH2	B_GLU_358	OE2	3.805
2VDQ	B_LYS_390	NZ	B_ASP_393	OD1	2.810
2VDQ	B_LYS_390	NZ	B_ASP_393	OD2	3.977
2VDQ	B_ARG_404	NH1	B_GLU_364	OE2	3.193
2VDQ	B_ARG_404	NH2	B_GLU_364	OE2	3.023
2VDQ	B_ARG_447	NH2	B_GLU_442	OE1	3.552
2VDQ	C_ARG_408	NH1	A_ASP_224	OD1	3.059
2VDQ	C_ARG_408	NH1	A_ASP_224	OD2	3.490
2VDQ	C_ARG_408	NH2	A_ASP_224	OD1	3.054
2VDQ	C_ARG_408	NH2	A_ASP_224	OD2	3.761
2VDQ	H_ARG_40	NH2	H_GLU_46	OE1	3.061
2VDQ	H_LYS_59	NZ	A_GLU_117	OE2	3.921
2VDQ	H_LYS_67	NZ	H_ASP_90	OD1	3.616
2VDQ	H_LYS_67	NZ	H_ASP_90	OD2	2.592
2VDQ	H_LYS_214	NZ	L_GLU_123	OE2	3.223
2VDQ	L_HIS_24	ND1	L_ASP_70	OD1	2.751
2VDQ	L_HIS_24	ND1	L_ASP_70	OD2	3.828
2VDQ	L_LYS_39	NZ	L_GLU_81	OE2	3.151
2VDQ	L_ARG_61	NH2	L_ASP_82	OD1	2.929
2VDQ	L_ARG_61	NH2	L_ASP_82	OD2	3.560
2VDQ	L_LYS_103	NZ	L_ASP_85	OD1	3.020
2VDQ	L_LYS_103	NZ	L_ASP_85	OD2	3.466
2VDQ	L_LYS_149	NZ	L_GLU_195	OE1	3.063
2VDQ	L_LYS_149	NZ	L_GLU_195	OE2	3.588

2VDQ	L_HIS_189	ND1	L_ASP_151	OD1	2.754
2VDQ	L_LYS_199	NZ	L_ASP_110	OD2	3.557
2VDR	A_HIS_30	ND1	A_GLU_136	OE1	3.834
2VDR	A_ARG_77	NH1	H_ASP_102	OD1	3.703
2VDR	A_ARG_77	NH1	H_ASP_102	OD2	3.091
2VDR	A_ARG_77	NH2	H_ASP_102	OD1	2.791
2VDR	A_ARG_77	NH2	H_ASP_102	OD2	3.414
2VDR	A_LYS_88	NZ	A_GLU_75	OE2	3.555
2VDR	A_ARG_153	NH1	A_GLU_157	OE2	3.722
2VDR	A_ARG_153	NH2	A_GLU_120	OE1	3.592
2VDR	A_ARG_153	NH2	A_GLU_120	OE2	3.473
2VDR	A_ARG_165	NH1	A_GLU_123	OE1	3.684
2VDR	A_ARG_165	NH1	A_GLU_123	OE2	3.385
2VDR	A_ARG_165	NH2	A_ASP_163	OD1	2.924
2VDR	A_ARG_165	NH2	A_ASP_163	OD2	3.830
2VDR	A_ARG_279	NH2	A_GLU_268	OE2	3.601
2VDR	A_ARG_303	NH2	A_ASP_301	OD2	3.138
2VDR	A_ARG_317	NH2	A_GLU_315	OE1	3.881
2VDR	A_ARG_327	NH1	A_GLU_283	OE1	2.937
2VDR	A_ARG_327	NH1	A_GLU_283	OE2	3.446
2VDR	A_ARG_422	NH1	A_ASP_24	OD1	3.228
2VDR	A_ARG_422	NH1	A_ASP_24	OD2	3.380
2VDR	A_ARG_422	NH2	A_ASP_24	OD1	3.926
2VDR	A_ARG_422	NH2	A_ASP_24	OD2	3.754
2VDR	B_LYS_72	NZ	B_ASP_109	OD1	2.563
2VDR	B_ARG_91	NH1	B_GLU_60	OE1	3.916
2VDR	B_ARG_91	NH2	B_GLU_60	OE1	2.976
2VDR	B_ARG_105	NH1	B_ASP_71	OD1	3.494
2VDR	B_LYS_159	NZ	B_ASP_224	OD1	3.854
2VDR	B_LYS_159	NZ	B_ASP_224	OD2	2.660
2VDR	B_LYS_209	NZ	B_GLU_206	OE2	3.062
2VDR	B_ARG_214	NH1	B_ASP_179	OD2	2.701
2VDR	B_ARG_216	NH2	A_GLU_123	OE2	2.956
2VDR	B_ARG_239	NH2	B_ASP_113	OD2	2.921
2VDR	B_HIS_244	NE2	B_ASP_113	OD1	3.852
2VDR	B_LYS_253	NZ	A_ASP_232	OD2	3.191
2VDR	B_HIS_255	ND1	B_ASP_259	OD2	2.853
2VDR	B_HIS_255	NE2	B_ASP_158	OD2	3.204
2VDR	B_HIS_255	NE2	B_ASP_217	OD1	3.553
2VDR	B_HIS_255	NE2	B_ASP_217	OD2	2.706
2VDR	B_HIS_274	NE2	B_ASP_270	OD1	3.093
2VDR	B_HIS_274	NE2	B_ASP_270	OD2	2.677
2VDR	B_HIS_280	ND1	B_ASP_278	OD2	3.699
2VDR	B_LYS_298	NZ	B_GLU_297	OE2	3.371
2VDR	B_LYS_302	NZ	B_ASP_233	OD1	3.473
2VDR	B_LYS_302	NZ	B_ASP_233	OD2	2.921
2VDR	B_LYS_354	NZ	B_GLU_356	OE1	2.603
2VDR	B_ARG_360	NH2	B_GLU_358	OE2	3.500
2VDR	B_LYS_390	NZ	B_ASP_393	OD1	2.719
2VDR	B_ARG_404	NH1	B_GLU_364	OE2	3.173
2VDR	B_ARG_404	NH2	B_GLU_364	OE2	3.177
2VDR	C_ARG_408	NH1	A_ASP_224	OD1	3.062
2VDR	C_ARG_408	NH1	A_ASP_224	OD2	3.850
2VDR	C_ARG_408	NH2	A_ASP_224	OD1	3.028
2VDR	C_ARG_408	NH2	A_ASP_224	OD2	3.839
2VDR	H_ARG_40	NH2	H_GLU_46	OE1	3.176
2VDR	H_LYS_67	NZ	H_ASP_90	OD1	3.584
2VDR	H_LYS_67	NZ	H_ASP_90	OD2	2.527

2VDR	H.LYS_214	NZ	L.GLU_123	OE2	3.860
2VDR	L.HIS_24	ND1	L.ASP_70	OD1	2.825
2VDR	L.HIS_24	ND1	L.ASP_70	OD2	3.852
2VDR	L.ARG_61	NH2	L.ASP_82	OD1	2.979
2VDR	L.ARG_61	NH2	L.ASP_82	OD2	3.650
2VDR	L.LYS_103	NZ	L.ASP_85	OD1	3.110
2VDR	L.LYS_103	NZ	L.ASP_85	OD2	3.591
2VDR	L.LYS_149	NZ	L.GLU_195	OE1	2.973
2VDR	L.LYS_149	NZ	L.GLU_195	OE2	3.700
2VDR	L.ARG_155	NH1	L.GLU_185	OE1	3.211
2VDR	L.ARG_155	NH1	L.GLU_185	OE2	3.858
2VDR	L.ARG_155	NH2	L.GLU_185	OE1	3.840
2VDR	L.ARG_155	NH2	L.GLU_185	OE2	3.062
2VDR	L.HIS_189	ND1	L.ASP_151	OD1	2.610
2VDR	L.LYS_199	NZ	L.ASP_110	OD2	3.796
2VIR	A.ARG_	NH2	A.GLU_	OE2	3.607
2VIR	A.ARG_	NH2	A.ASP_	OD1	3.333
2VIR	A.ARG_	NH2	A.ASP_	OD2	3.123
2VIR	A.LYS_152	NZ	A.GLU_206	OE1	3.754
2VIR	A.HIS_191	ND1	A.ASP_154	OD2	2.799
2VIR	B.HIS_	NE2	B.ASP_	OD1	3.115
2VIR	B.ARG_	NH1	B.GLU_	OE1	2.667
2VIR	B.ARG_	NH2	B.ASP_	OD1	2.935
2VIR	B.ARG_	NH1	B.ASP_	OD1	3.962
2VIR	B.ARG_	NH2	B.ASP_	OD1	3.249
2VIR	B.ARG_	NH2	B.ASP_	OD2	2.668
2VIR	B.LYS_	NZ	B.ASP_	OD1	3.397
2VIR	B.LYS_	NZ	B.ASP_	OD2	3.134
2VIR	B.ARG_	NH2	B.ASP_	OD1	3.596
2VIR	B.ARG_	NH2	B.ASP_	OD2	2.875
2VIR	B.LYS_	NZ	A.GLU_127	OE2	3.017
2VIR	B.HIS_173	NE2	A.ASP_141	OD1	3.726
2VIR	B.HIS_173	NE2	A.ASP_141	OD2	3.076
2VIR	B.LYS_217	NZ	A.GLU_126	OE2	3.903
2VIR	C.LYS_	NZ	C.ASP_	OD1	3.597
2VIR	C.LYS_	NZ	C.ASP_	OD2	3.554
2VIR	C.HIS_	NE2	C.GLU_	OE1	3.437
2VIR	C.HIS_	NE2	C.GLU_	OE2	2.908
2VIR	C.ARG_	NH1	C.GLU_	OE2	3.901
2VIR	C.ARG_	NH2	C.GLU_	OE2	2.550
2VIR	C.HIS_	ND1	C.ASP_	OD1	2.834
2VIR	C.HIS_	NE2	C.ASP_	OD1	3.558
2VIR	C.ARG_	NH2	C.ASP_	OD1	3.792
2VIR	C.ARG_	NH2	C.ASP_	OD2	2.918
2VIR	C.LYS_	NZ	C.ASP_	OD1	2.776
2VIR	C.ARG_	NH1	C.GLU_	OE1	2.706
2VIR	C.ARG_	NH1	C.GLU_	OE2	2.891
2VIR	C.ARG_	NH2	C.GLU_	OE1	3.747
2VIR	C.ARG_	NH2	C.ASP_	OD1	2.621
2VIR	C.ARG_	NH2	C.ASP_	OD2	3.048
2VIR	C.LYS_	NZ	C.GLU_	OE2	3.095
2VIR	C.LYS_	NZ	C.ASP_	OD1	3.929
2VIR	C.ARG_	NH2	C.ASP_	OD2	3.709
2VIR	C.LYS_	NZ	C.ASP_	OD1	3.380
2VIR	C.LYS_	NZ	C.ASP_	OD2	2.593
2VIR	C.ARG_	NH1	C.GLU_	OE1	3.911
2VIR	C.ARG_	NH2	C.GLU_	OE1	3.735
2VIR	C.LYS_	NZ	C.ASP_	OD1	3.157

2VIS	A_ARG_	NH2	A_GLU_	OE2	3.528
2VIS	A_ARG_	NH2	A_ASP_	OD1	3.225
2VIS	A_ARG_	NH2	A_ASP_	OD2	3.101
2VIS	A_LYS_152	NZ	A_GLU_206	OE1	3.762
2VIS	A_HIS_191	ND1	A_ASP_154	OD2	2.830
2VIS	B_HIS_	NE2	B_ASP_	OD1	3.059
2VIS	B_ARG_	NH1	B_GLU_	OE1	2.654
2VIS	B_ARG_	NH2	B_ASP_	OD1	3.129
2VIS	B_ARG_	NH1	B_ASP_	OD1	3.798
2VIS	B_ARG_	NH2	B_ASP_	OD1	3.126
2VIS	B_ARG_	NH2	B_ASP_	OD2	2.566
2VIS	B_LYS_	NZ	B_ASP_	OD1	3.701
2VIS	B_LYS_	NZ	B_ASP_	OD2	3.019
2VIS	B_ARG_	NH2	B_ASP_	OD1	3.616
2VIS	B_ARG_	NH2	B_ASP_	OD2	2.750
2VIS	B_LYS_	NZ	A_GLU_127	OE2	2.999
2VIS	B_HIS_173	NE2	A_ASP_141	OD1	3.763
2VIS	B_HIS_173	NE2	A_ASP_141	OD2	3.158
2VIS	B_LYS_217	NZ	A_GLU_126	OE2	3.709
2VIS	C_LYS_	NZ	C_ASP_	OD1	3.551
2VIS	C_LYS_	NZ	C_ASP_	OD2	3.585
2VIS	C_HIS_	NE2	C_GLU_	OE1	3.359
2VIS	C_HIS_	NE2	C_GLU_	OE2	2.830
2VIS	C_ARG_	NH1	C_GLU_	OE2	3.968
2VIS	C_ARG_	NH2	C_GLU_	OE2	2.722
2VIS	C_HIS_	ND1	C_ASP_	OD1	2.788
2VIS	C_HIS_	NE2	C_ASP_	OD1	3.544
2VIS	C_ARG_	NH2	C_ASP_	OD1	3.769
2VIS	C_ARG_	NH2	C_ASP_	OD2	2.897
2VIS	C_LYS_	NZ	C_ASP_	OD1	2.890
2VIS	C_ARG_	NH1	C_GLU_	OE1	2.736
2VIS	C_ARG_	NH1	C_GLU_	OE2	2.823
2VIS	C_ARG_	NH2	C_GLU_	OE1	3.753
2VIS	C_ARG_	NH2	C_ASP_	OD1	2.729
2VIS	C_ARG_	NH2	C_ASP_	OD2	2.980
2VIS	C_LYS_	NZ	C_GLU_	OE2	3.175
2VIS	C_LYS_	NZ	C_ASP_	OD1	3.910
2VIS	C_HIS_	NE2	C_GLU_	OE2	3.842
2VIS	C_ARG_	NH2	C_ASP_	OD2	3.593
2VIS	C_LYS_	NZ	C_ASP_	OD1	3.401
2VIS	C_LYS_	NZ	C_ASP_	OD2	2.618
2VIS	C_LYS_	NZ	C_ASP_	OD1	3.801
2VIS	C_ARG_	NH1	C_GLU_	OE1	3.717
2VIS	C_ARG_	NH2	C_GLU_	OE1	3.508
2VIS	C_LYS_	NZ	C_ASP_	OD1	3.060
2VIS	C_LYS_	NZ	C_ASP_	OD2	3.941
2VIT	A_ARG_	NH1	A_ASP_	OD2	3.967
2VIT	A_ARG_	NH2	A_GLU_	OE2	3.548
2VIT	A_ARG_	NH2	A_ASP_	OD1	3.241
2VIT	A_ARG_	NH2	A_ASP_	OD2	3.098
2VIT	A_LYS_152	NZ	A_GLU_206	OE1	3.712
2VIT	A_HIS_191	ND1	A_ASP_154	OD2	2.838
2VIT	B_HIS_	NE2	B_ASP_	OD1	2.907
2VIT	B_ARG_	NH1	B_GLU_	OE1	2.629
2VIT	B_ARG_	NH2	B_ASP_	OD1	2.987
2VIT	B_ARG_	NH1	B_ASP_	OD1	3.943
2VIT	B_ARG_	NH2	B_ASP_	OD1	3.230
2VIT	B_ARG_	NH2	B_ASP_	OD2	2.635

2VIT	B_LYS_	NZ	B_ASP_	OD1	3.471
2VIT	B_LYS_	NZ	B_ASP_	OD2	3.207
2VIT	B_ARG_	NH2	B_ASP_	OD1	3.554
2VIT	B_ARG_	NH2	B_ASP_	OD2	2.686
2VIT	B_LYS_	NZ	A_GLU_127	OE2	2.939
2VIT	B_HIS_173	NE2	A_ASP_141	OD1	3.614
2VIT	B_HIS_173	NE2	A_ASP_141	OD2	3.333
2VIT	B_LYS_217	NZ	A_GLU_126	OE2	3.872
2VIT	C_LYS_	NZ	C_ASP_	OD1	3.503
2VIT	C_LYS_	NZ	C_ASP_	OD2	3.623
2VIT	C_HIS_	NE2	C_GLU_	OE1	3.344
2VIT	C_HIS_	NE2	C_GLU_	OE2	2.697
2VIT	C_ARG_	NH2	C_GLU_	OE2	2.611
2VIT	C_HIS_	ND1	C_ASP_	OD1	2.743
2VIT	C_HIS_	ND1	C_ASP_	OD2	3.981
2VIT	C_HIS_	NE2	C_ASP_	OD1	3.636
2VIT	C_ARG_	NH2	C_ASP_	OD1	3.818
2VIT	C_ARG_	NH2	C_ASP_	OD2	2.935
2VIT	C_LYS_	NZ	C_ASP_	OD1	2.814
2VIT	C_ARG_	NH1	C_GLU_	OE1	2.724
2VIT	C_ARG_	NH1	C_GLU_	OE2	3.066
2VIT	C_ARG_	NH2	C_GLU_	OE1	3.650
2VIT	C_ARG_	NH2	C_ASP_	OD1	2.732
2VIT	C_ARG_	NH2	C_ASP_	OD2	2.999
2VIT	C_LYS_	NZ	C_GLU_	OE2	3.169
2VIT	C_LYS_	NZ	C_ASP_	OD1	3.896
2VIT	C_ARG_	NH2	C_ASP_	OD2	3.650
2VIT	C_LYS_	NZ	C_ASP_	OD1	3.387
2VIT	C_LYS_	NZ	C_ASP_	OD2	2.696
2VIT	C_ARG_	NH2	C_GLU_	OE1	3.981
2VIT	C_LYS_	NZ	C_ASP_	OD1	3.143
2VIU	A_LYS_27	NZ	B_GLU_97	OE1	3.686
2VIU	A_LYS_27	NZ	B_GLU_97	OE2	2.721
2VIU	A_ARG_57	NH1	A_GLU_82	OE1	3.419
2VIU	A_ARG_57	NH2	A_GLU_82	OE1	2.696
2VIU	A_ARG_57	NH2	A_GLU_82	OE2	3.793
2VIU	A_HIS_75	ND1	A_ASP_73	OD1	2.756
2VIU	A_HIS_75	ND1	A_ASP_73	OD2	3.587
2VIU	A_HIS_75	NE2	A_ASP_63	OD1	3.916
2VIU	A_ARG_90	NH2	A_ASP_60	OD1	3.851
2VIU	A_ARG_90	NH2	A_ASP_60	OD2	3.197
2VIU	A_ARG_109	NH1	B_GLU_67	OE1	3.978
2VIU	A_ARG_109	NH1	B_GLU_67	OE2	3.053
2VIU	A_ARG_109	NH2	A_GLU_89	OE1	2.928
2VIU	A_ARG_141	NH2	A_ASP_77	OD1	2.769
2VIU	A_ARG_141	NH2	A_ASP_77	OD2	2.741
2VIU	A_LYS_176	NZ	A_GLU_123	OE2	2.681
2VIU	A_HIS_183	NE2	A_GLU_190	OE2	3.745
2VIU	A_ARG_207	NH1	A_ASP_241	OD1	3.937
2VIU	A_ARG_208	NH1	A_ASP_241	OD2	3.116
2VIU	A_LYS_238	NZ	A_ASP_175	OD2	3.292
2VIU	A_ARG_261	NH2	A_GLU_119	OE1	3.027
2VIU	A_ARG_261	NH2	A_GLU_119	OE2	2.600
2VIU	A_LYS_264	NZ	A_ASP_85	OD1	3.975
2VIU	A_LYS_264	NZ	A_ASP_85	OD2	3.658
2VIU	A_ARG_269	NH1	B_GLU_67	OE1	2.986
2VIU	A_LYS_292	NZ	A_ASP_291	OD2	3.041
2VIU	A_LYS_310	NZ	B_ASP_90	OD1	2.868

2VIU	A_LYS_315	NZ	A_GLU_41	OE1	3.081
2VIU	B_LYS_51	NZ	B_GLU_103	OE1	2.786
2VIU	B_LYS_68	NZ	B_GLU_85	OE1	3.467
2VIU	B_LYS_68	NZ	B_GLU_85	OE2	2.818
2VIU	B_LYS_117	NZ	B_GLU_114	OE1	3.690
2VIU	B_LYS_117	NZ	B_GLU_114	OE2	2.769
2VIU	B_ARG_123	NH1	B_GLU_120	OE1	2.873
2VIU	B_ARG_123	NH1	B_GLU_120	OE2	3.282
2VIU	B_ARG_153	NH2	B_GLU_150	OE1	2.715
2VIU	B_HIS_159	NE2	B_ASP_160	OD1	3.760
2VIU	B_HIS_159	NE2	B_ASP_160	OD2	3.318
2VIU	B_ARG_170	NH1	B_GLU_128	OE1	2.843
2VIU	B_ARG_170	NH2	B_GLU_128	OE1	3.875
2VIU	B_ARG_170	NH2	B_GLU_131	OE2	3.472
2VXS	A_ARG_55	NH2	A_GLU_57	OE2	3.745
2VXS	A_HIS_86	ND1	A_ASP_84	OD1	2.794
2VXS	A_HIS_86	ND1	A_ASP_84	OD2	3.861
2VXS	B_ARG_46	NH1	B_ASP_42	OD2	2.944
2VXS	B_ARG_55	NH2	B_GLU_57	OE2	2.792
2VXS	B_HIS_86	ND1	B_ASP_84	OD1	3.029
2VXS	B_HIS_86	ND1	B_ASP_84	OD2	3.887
2VXS	C_HIS_86	ND1	C_ASP_84	OD1	2.647
2VXS	C_HIS_86	ND1	C_ASP_84	OD2	3.590
2VXS	C_LYS_114	NZ	C_GLU_95	OE2	3.592
2VXS	D_ARG_46	NH1	D_ASP_42	OD2	3.642
2VXS	D_ARG_55	NH2	D_GLU_57	OE2	3.715
2VXS	D_ARG_61	NH1	D_ASP_58	OD2	3.553
2VXS	D_ARG_61	NH2	D_ASP_58	OD2	2.803
2VXS	D_HIS_86	ND1	D_ASP_84	OD1	2.787
2VXS	D_HIS_86	ND1	D_ASP_84	OD2	3.565
2VXS	H_ARG_38	NH1	H_ASP_86	OD1	3.009
2VXS	H_ARG_38	NH2	H_GLU_46	OE1	3.046
2VXS	H_ARG_38	NH2	H_GLU_46	OE2	3.669
2VXS	H_ARG_38	NH2	H_ASP_86	OD1	3.964
2VXS	H_LYS_64	NZ	H_ASP_61	OD1	3.737
2VXS	H_ARG_66	NH1	H_ASP_86	OD1	3.951
2VXS	H_ARG_66	NH1	H_ASP_86	OD2	2.759
2VXS	H_ARG_66	NH2	H_ASP_86	OD1	3.290
2VXS	H_ARG_66	NH2	H_ASP_86	OD2	3.569
2VXS	H_LYS_143	NZ	L_GLU_125	OE2	2.772
2VXS	L_ARG_38	NH1	L_ASP_86	OD1	3.106
2VXS	L_ARG_38	NH2	L_GLU_46	OE1	3.024
2VXS	L_ARG_38	NH2	L_GLU_46	OE2	3.297
2VXS	L_ARG_38	NH2	L_ASP_86	OD1	3.845
2VXS	L_LYS_64	NZ	L_ASP_61	OD1	3.015
2VXS	L_ARG_66	NH1	L_ASP_86	OD1	3.881
2VXS	L_ARG_66	NH1	L_ASP_86	OD2	2.775
2VXS	L_ARG_66	NH2	L_ASP_86	OD1	2.818
2VXS	L_ARG_66	NH2	L_ASP_86	OD2	3.215
2VXS	L_LYS_143	NZ	L_ASP_144	OD1	3.889
2VXS	L_LYS_210	NZ	L_GLU_212	OE1	2.766
2VXS	L_LYS_214	NZ	M_GLU_124	OE1	3.186
2VXS	J_ARG_	NH1	J_ASP_	OD1	2.755
2VXS	J_ARG_	NH2	J_GLU_	OE1	3.312
2VXS	J_ARG_	NH2	J_GLU_	OE2	3.407
2VXS	J_ARG_	NH2	J_ASP_	OD1	3.826
2VXS	J_LYS_64	NZ	J_ASP_	OD1	3.275
2VXS	J_ARG_	NH1	J_ASP_	OD1	3.912

2VXS	J_ARG_	NH1	J_ASP_	OD2	2.751
2VXS	J_ARG_	NH2	J_ASP_	OD1	3.250
2VXS	J_ARG_	NH2	J_ASP_	OD2	3.560
2VXS	J_LYS_	NZ	J_ASP_	OD1	3.641
2VXS	J_LYS_206	NZ	J_ASP_208	OD1	3.503
2VXS	J_LYS_	NZ	N_GLU_	OE1	2.922
2VXS	K_ARG_38	NH1	K_ASP_86	OD1	3.239
2VXS	K_ARG_38	NH2	K_GLU_46	OE1	3.227
2VXS	K_ARG_38	NH2	K_GLU_46	OE2	3.826
2VXS	K_ARG_38	NH2	K_ASP_86	OD1	3.916
2VXS	K_LYS_64	NZ	K_ASP_61	OD1	3.799
2VXS	K_ARG_66	NH1	K_ASP_86	OD1	3.713
2VXS	K_ARG_66	NH1	K_ASP_86	OD2	2.833
2VXS	K_ARG_66	NH2	K_ASP_86	OD1	2.845
2VXS	K_ARG_66	NH2	K_ASP_86	OD2	3.489
2VXS	K_LYS_210	NZ	K_GLU_212	OE1	3.930
2VXS	K_LYS_214	NZ	O_GLU_124	OE1	3.391
2VXS	L_ARG_54	NH1	L_ASP_60	OD1	3.471
2VXS	L_ARG_61	NH2	L_ASP_82	OD1	2.601
2VXS	L_ARG_61	NH2	L_ASP_82	OD2	2.642
2VXS	L_LYS_103	NZ	L_ASP_85	OD1	3.412
2VXS	L_LYS_167	NZ	L_GLU_83	OE1	3.289
2VXS	L_LYS_172	NZ	L_ASP_139	OD1	3.795
2VXS	L_HIS_189	ND1	L_ASP_152	OD2	2.849
2VXS	M_ARG_61	NH1	M_ASP_82	OD1	3.983
2VXS	M_ARG_61	NH2	M_ASP_82	OD1	2.482
2VXS	M_ARG_61	NH2	M_ASP_82	OD2	2.420
2VXS	M_LYS_103	NZ	M_ASP_85	OD1	3.469
2VXS	M_LYS_167	NZ	M_GLU_83	OE1	2.810
2VXS	M_HIS_189	ND1	M_ASP_152	OD2	3.666
2VXS	M_HIS_198	NE2	M_GLU_199	OE2	3.892
2VXS	N_ARG_61	NH2	N_ASP_	OD1	2.670
2VXS	N_ARG_61	NH2	N_ASP_	OD2	2.989
2VXS	N_LYS_	NZ	N_ASP_	OD1	3.427
2VXS	N_LYS_	NZ	J_ASP_	OD2	3.949
2VXS	N_LYS_	NZ	N_GLU_	OE1	2.677
2VXS	N_HIS_	ND1	N_ASP_	OD2	3.568
2VXS	O_ARG_61	NH2	O_ASP_82	OD1	2.574
2VXS	O_ARG_61	NH2	O_ASP_82	OD2	2.733
2VXS	O_LYS_103	NZ	O_ASP_85	OD1	2.839
2VXS	O_LYS_103	NZ	O_ASP_85	OD2	3.719
2VXS	O_LYS_167	NZ	O_GLU_83	OE1	3.622
2VXS	O_LYS_167	NZ	O_GLU_83	OE2	3.743
2VXS	O_HIS_189	ND1	O_ASP_152	OD2	3.412
2VXS	O_HIS_198	NE2	O_GLU_199	OE2	3.877
2VXT	H_LYS_62	NZ	H_GLU_46	OE1	3.909
2VXT	H_LYS_62	NZ	H_GLU_46	OE2	2.756
2VXT	H_LYS_66	NZ	H_ASP_86	OD1	3.652
2VXT	H_LYS_66	NZ	H_ASP_86	OD2	2.674
2VXT	H_ARG_94	NH2	I_GLU_179	OE1	2.816
2VXT	H_ARG_94	NH2	I_GLU_179	OE2	3.466
2VXT	H_ARG_101	NH1	I_GLU_179	OE1	2.914
2VXT	H_LYS_208	NZ	L_GLU_123	OE2	2.940
2VXT	I_LYS_44	NZ	I_GLU_42	OE1	3.741
2VXT	I_ARG_49	NH2	I_ASP_71	OD1	3.048
2VXT	I_LYS_106	NZ	I_GLU_121	OE1	3.321
2VXT	I_HIS_145	NE2	H_ASP_50	OD1	2.753
2VXT	I_LYS_148	NZ	H_ASP_56	OD2	2.664

2VXT	L.LYS_175	NZ	L.ASP_182	OD1	3.559
2VXT	L.LYS_175	NZ	L.ASP_182	OD2	2.678
2VXT	L.ARG_46	NH2	L.ASP_55	OD1	2.847
2VXT	L.ARG_46	NH2	L.ASP_55	OD2	3.641
2VXT	L.ARG_61	NH1	L.GLU_79	OE2	3.449
2VXT	L.ARG_61	NH2	L.GLU_81	OE2	3.316
2VXT	L.ARG_61	NH2	L.ASP_82	OD1	2.855
2VXT	L.ARG_61	NH2	L.ASP_82	OD2	3.570
2VXT	L.ARG_66	NH2	L.ASP_28	OD1	3.957
2VXT	L.ARG_155	NH1	L.GLU_185	OE1	3.695
2VXT	L.ARG_155	NH1	L.GLU_185	OE2	2.926
2VXT	L.ARG_155	NH2	L.GLU_185	OE1	3.294
2VXT	L.ARG_155	NH2	L.GLU_185	OE2	3.952
2VXT	L.LYS_199	NZ	L.ASP_110	OD1	3.760
2VXT	L.LYS_199	NZ	L.ASP_110	OD2	2.706
2VXU	H.LYS_43	NZ	L.ASP_85	OD1	3.097
2VXU	H.LYS_62	NZ	H.GLU_46	OE1	3.879
2VXU	H.LYS_62	NZ	H.GLU_46	OE2	2.639
2VXU	H.LYS_66	NZ	H.ASP_86	OD2	3.095
2VXU	L.LYS_62	NZ	L.GLU_46	OE1	3.778
2VXU	L.LYS_62	NZ	L.GLU_46	OE2	2.481
2VXU	L.LYS_66	NZ	L.ASP_86	OD1	3.703
2VXU	L.LYS_66	NZ	L.ASP_86	OD2	2.733
2VXU	L.LYS_208	NZ	M.GLU_123	OE1	2.734
2VXU	L.LYS_208	NZ	M.GLU_123	OE2	2.893
2VXU	L.ARG_24	NH2	L.ASP_70	OD1	3.272
2VXU	L.ARG_24	NH2	L.ASP_70	OD2	2.791
2VXU	L.ARG_46	NH2	L.ASP_55	OD1	2.844
2VXU	L.ARG_46	NH2	L.ASP_55	OD2	3.772
2VXU	L.ARG_61	NH2	L.GLU_81	OE2	3.219
2VXU	L.ARG_61	NH2	L.ASP_82	OD1	3.151
2VXU	L.ARG_61	NH2	L.ASP_82	OD2	3.745
2VXU	L.ARG_66	NH2	L.ASP_28	OD1	3.861
2VXU	L.LYS_142	NZ	L.ASP_143	OD1	3.748
2VXU	L.LYS_199	NZ	L.ASP_110	OD2	3.400
2VXU	M.ARG_24	NH2	M.ASP_70	OD1	3.639
2VXU	M.ARG_24	NH2	M.ASP_70	OD2	3.054
2VXU	M.ARG_46	NH2	M.ASP_55	OD1	2.799
2VXU	M.ARG_46	NH2	M.ASP_55	OD2	3.746
2VXU	M.ARG_61	NH1	M.GLU_79	OE2	3.549
2VXU	M.ARG_61	NH2	M.GLU_81	OE2	3.079
2VXU	M.ARG_61	NH2	M.ASP_82	OD1	2.801
2VXU	M.ARG_61	NH2	M.ASP_82	OD2	3.460
2VXU	M.ARG_66	NH2	M.ASP_28	OD1	3.960
2VXU	M.LYS_107	NZ	M.GLU_17	OE1	3.246
2VXU	M.LYS_107	NZ	M.GLU_17	OE2	2.558
2VXU	M.LYS_142	NZ	M.ASP_143	OD1	3.635
2VXU	M.ARG_155	NH1	M.GLU_185	OE1	3.951
2VXU	M.ARG_155	NH1	M.GLU_185	OE2	2.762
2VXU	M.ARG_155	NH2	M.GLU_185	OE1	3.497
2VXU	M.ARG_155	NH2	M.GLU_185	OE2	3.662
2VXU	M.HIS_189	ND1	M.ASP_151	OD2	2.958
2VXV	H.ARG_38	NH2	H.GLU_46	OE1	2.913
2VXV	H.ARG_38	NH2	H.GLU_46	OE2	3.297
2VXV	H.ARG_58	NH2	H.GLU_56	OE2	2.796
2VXV	H.ARG_94	NH2	H.ASP_101	OD1	3.566
2VXV	H.ARG_94	NH2	H.ASP_101	OD2	2.867
2VXV	H.LYS_143	NZ	H.ASP_144	OD1	3.484

2VXV	H_LYS_214	NZ	L_ASP_122	OD1	3.721
2VXV	H_LYS_214	NZ	L_ASP_122	OD2	2.868
2VXV	L_ARG_61	NH2	L_GLU_81	OE2	3.747
2VXV	L_ARG_61	NH2	L_ASP_82	OD1	2.862
2VXV	L_ARG_61	NH2	L_ASP_82	OD2	3.507
2VXV	L_HIS_189	ND1	L_ASP_151	OD2	2.974
2XEF	A_HIS_56	NE2	A_GLU_408	OE2	2.799
2XEF	A_LYS_59	NZ	A_ASP_63	OD1	3.841
2XEF	A_LYS_59	NZ	A_ASP_63	OD2	3.009
2XEF	A_ARG_181	NH1	A_GLU_183	OE2	3.625
2XEF	A_ARG_181	NH2	A_ASP_184	OD1	2.949
2XEF	A_ARG_181	NH2	A_ASP_184	OD2	3.602
2XEF	A_ARG_190	NH1	A_ASP_714	OD1	2.918
2XEF	A_ARG_190	NH1	A_ASP_714	OD2	3.597
2XEF	A_ARG_190	NH2	A_ASP_714	OD1	3.579
2XEF	A_ARG_190	NH2	A_ASP_714	OD2	2.730
2XEF	A_ARG_204	NH1	A_ASP_233	OD2	3.163
2XEF	A_ARG_255	NH1	A_GLU_145	OE1	2.685
2XEF	A_ARG_255	NH2	A_GLU_145	OE1	2.757
2XEF	A_LYS_341	NZ	A_ASP_173	OD1	3.395
2XEF	A_LYS_341	NZ	A_ASP_173	OD2	3.841
2XEF	A_LYS_343	NZ	A_GLU_171	OE1	2.875
2XEF	A_HIS_345	ND1	A_GLU_137	OE2	3.926
2XEF	A_HIS_345	NE2	A_GLU_137	OE1	3.980
2XEF	A_HIS_345	NE2	A_GLU_137	OE2	3.120
2XEF	A_ARG_354	NH2	A_ASP_114	OD1	3.536
2XEF	A_ARG_354	NH2	A_ASP_114	OD2	2.909
2XEF	A_ARG_363	NH2	A_ASP_106	OD1	3.752
2XEF	A_ARG_370	NH1	A_ASP_369	OD1	3.987
2XEF	A_ARG_370	NH1	A_ASP_369	OD2	3.614
2XEF	A_ARG_370	NH2	A_ASP_666	OD1	2.894
2XEF	A_ARG_370	NH2	A_ASP_666	OD2	3.631
2XEF	A_HIS_377	ND1	A_ASP_379	OD1	2.940
2XEF	A_HIS_377	ND1	A_GLU_424	OE1	3.983
2XEF	A_HIS_377	NE2	A_ASP_387	OD1	3.185
2XEF	A_HIS_377	NE2	A_GLU_424	OE1	3.244
2XEF	A_HIS_377	NE2	A_GLU_425	OE2	3.914
2XEF	A_HIS_377	NE2	A_ASP_453	OD1	3.247
2XEF	A_HIS_377	NE2	A_ASP_453	OD2	3.086
2XEF	A_ARG_378	NH2	A_ASP_422	OD1	3.926
2XEF	A_ARG_378	NH2	A_ASP_422	OD2	3.342
2XEF	A_ARG_400	NH1	A_GLU_64	OE2	3.095
2XEF	A_ARG_400	NH1	A_GLU_397	OE1	3.701
2XEF	A_ARG_400	NH1	A_GLU_397	OE2	2.838
2XEF	A_ARG_400	NH2	A_GLU_64	OE2	2.882
2XEF	A_LYS_406	NZ	A_ASP_106	OD1	3.218
2XEF	A_ARG_411	NH1	A_ASP_106	OD1	3.513
2XEF	A_ARG_411	NH1	A_ASP_106	OD2	2.703
2XEF	A_ARG_411	NH2	A_ASP_106	OD1	2.830
2XEF	A_ARG_411	NH2	A_ASP_106	OD2	3.623
2XEF	A_ARG_413	NH2	A_GLU_367	OE2	3.405
2XEF	A_ARG_414	NH2	A_GLU_367	OE2	3.182
2XEF	A_ARG_463	NH1	A_GLU_457	OE1	3.344
2XEF	A_ARG_463	NH1	A_GLU_457	OE2	3.045
2XEF	A_ARG_463	NH2	A_ASP_465	OD2	2.862
2XEF	A_LYS_491	NZ	A_GLU_495	OE2	3.112
2XEF	A_LYS_500	NZ	A_ASP_485	OD2	2.872
2XEF	A_ARG_527	NH1	A_GLU_436	OE1	2.777

2XEF	A_ARG_527	NH2	A_GLU_436	OE1	2.984
2XEF	A_ARG_536	NH1	A_GLU_457	OE1	2.900
2XEF	A_HIS_553	NE2	A_ASP_387	OD2	2.946
2XEF	A_HIS_553	NE2	A_GLU_425	OE1	3.142
2XEF	A_HIS_553	NE2	A_GLU_425	OE2	3.233
2XEF	A_HIS_573	ND1	A_ASP_567	OD2	2.719
2XEF	A_ARG_598	NH2	A_ASP_596	OD1	3.762
2XEF	A_ARG_598	NH2	A_ASP_596	OD2	2.978
2XEF	A_LYS_606	NZ	A_GLU_505	OE1	3.281
2XEF	A_LYS_606	NZ	A_GLU_505	OE2	3.681
2XEF	A_LYS_610	NZ	A_GLU_703	OE2	2.847
2XEF	A_HIS_618	NE2	A_GLU_716	OE1	3.725
2XEF	A_LYS_637	NZ	A_GLU_641	OE1	3.067
2XEF	A_LYS_637	NZ	A_GLU_641	OE2	3.880
2XEF	A_ARG_684	NH2	A_ASP_710	OD2	3.381
2XEF	A_HIS_689	NE2	A_GLU_672	OE2	2.802
2XEF	A_ARG_730	NH2	A_GLU_727	OE1	3.848
2XEF	A_ARG_730	NH2	A_GLU_727	OE2	3.085
2XEG	A_HIS_56	ND1	A_GLU_408	OE2	3.766
2XEG	A_HIS_56	NE2	A_GLU_408	OE2	3.847
2XEG	A_LYS_59	NZ	A_ASP_63	OD1	3.760
2XEG	A_LYS_59	NZ	A_ASP_63	OD2	2.920
2XEG	A_ARG_181	NH1	A_GLU_183	OE2	3.616
2XEG	A_ARG_181	NH2	A_ASP_184	OD1	2.935
2XEG	A_ARG_181	NH2	A_ASP_184	OD2	3.536
2XEG	A_ARG_190	NH1	A_ASP_714	OD1	2.995
2XEG	A_ARG_190	NH1	A_ASP_714	OD2	3.628
2XEG	A_ARG_190	NH2	A_ASP_714	OD1	3.604
2XEG	A_ARG_190	NH2	A_ASP_714	OD2	2.717
2XEG	A_ARG_204	NH1	A_ASP_233	OD1	3.945
2XEG	A_ARG_204	NH1	A_ASP_233	OD2	3.115
2XEG	A_ARG_255	NH1	A_GLU_145	OE1	2.705
2XEG	A_ARG_255	NH2	A_GLU_145	OE1	2.760
2XEG	A_LYS_341	NZ	A_ASP_173	OD1	3.295
2XEG	A_LYS_341	NZ	A_ASP_173	OD2	3.942
2XEG	A_HIS_345	ND1	A_GLU_137	OE2	3.875
2XEG	A_HIS_345	NE2	A_GLU_137	OE2	3.207
2XEG	A_ARG_354	NH2	A_ASP_114	OD1	3.519
2XEG	A_ARG_354	NH2	A_ASP_114	OD2	2.914
2XEG	A_ARG_363	NH2	A_ASP_106	OD1	3.705
2XEG	A_ARG_370	NH1	A_ASP_369	OD1	3.956
2XEG	A_ARG_370	NH1	A_ASP_369	OD2	3.628
2XEG	A_ARG_370	NH2	A_ASP_666	OD1	2.842
2XEG	A_ARG_370	NH2	A_ASP_666	OD2	3.618
2XEG	A_HIS_377	ND1	A_ASP_379	OD1	2.925
2XEG	A_HIS_377	NE2	A_ASP_387	OD1	3.241
2XEG	A_HIS_377	NE2	A_GLU_424	OE1	3.209
2XEG	A_HIS_377	NE2	A_GLU_425	OE2	3.926
2XEG	A_HIS_377	NE2	A_ASP_453	OD1	3.264
2XEG	A_HIS_377	NE2	A_ASP_453	OD2	3.104
2XEG	A_ARG_378	NH2	A_ASP_422	OD1	3.876
2XEG	A_ARG_378	NH2	A_ASP_422	OD2	3.238
2XEG	A_ARG_400	NH1	A_GLU_64	OE2	3.039
2XEG	A_ARG_400	NH1	A_GLU_397	OE1	3.703
2XEG	A_ARG_400	NH1	A_GLU_397	OE2	2.812
2XEG	A_ARG_400	NH2	A_GLU_64	OE2	2.850
2XEG	A_LYS_406	NZ	A_ASP_106	OD1	3.308
2XEG	A_ARG_411	NH1	A_ASP_106	OD1	3.560

2XEG	A_ARG_411	NH1	A_ASP_106	OD2	2.790
2XEG	A_ARG_411	NH2	A_ASP_106	OD1	2.807
2XEG	A_ARG_411	NH2	A_ASP_106	OD2	3.629
2XEG	A_ARG_413	NH2	A_GLU_367	OE2	3.344
2XEG	A_ARG_414	NH2	A_GLU_367	OE2	3.206
2XEG	A_LYS_491	NZ	A_GLU_495	OE2	3.175
2XEG	A_LYS_500	NZ	A_ASP_485	OD2	2.873
2XEG	A_ARG_527	NH1	A_GLU_436	OE1	2.787
2XEG	A_ARG_527	NH2	A_GLU_436	OE1	2.964
2XEG	A_ARG_536	NH1	A_GLU_457	OE1	2.897
2XEG	A_HIS_553	NE2	A_ASP_387	OD2	2.992
2XEG	A_HIS_553	NE2	A_GLU_425	OE1	3.084
2XEG	A_HIS_553	NE2	A_GLU_425	OE2	3.216
2XEG	A_HIS_573	ND1	A_ASP_567	OD2	2.723
2XEG	A_ARG_598	NH2	A_ASP_596	OD1	3.731
2XEG	A_ARG_598	NH2	A_ASP_596	OD2	2.927
2XEG	A_LYS_606	NZ	A_GLU_505	OE1	3.338
2XEG	A_LYS_606	NZ	A_GLU_505	OE2	3.829
2XEG	A_HIS_618	NE2	A_GLU_716	OE1	3.759
2XEG	A_LYS_637	NZ	A_GLU_641	OE1	2.943
2XEG	A_LYS_637	NZ	A_GLU_641	OE2	3.902
2XEG	A_ARG_684	NH2	A_ASP_710	OD2	3.396
2XEG	A_HIS_689	NE2	A_GLU_672	OE2	2.814
2XEI	A_HIS_56	NE2	A_GLU_408	OE2	2.969
2XEI	A_LYS_59	NZ	A_ASP_63	OD2	2.953
2XEI	A_ARG_181	NH1	A_GLU_183	OE2	3.722
2XEI	A_ARG_181	NH2	A_ASP_184	OD1	2.939
2XEI	A_ARG_181	NH2	A_ASP_184	OD2	3.606
2XEI	A_LYS_187	NZ	A_ASP_316	OD2	3.720
2XEI	A_ARG_190	NH1	A_ASP_714	OD1	2.931
2XEI	A_ARG_190	NH1	A_ASP_714	OD2	3.551
2XEI	A_ARG_190	NH2	A_ASP_714	OD1	3.589
2XEI	A_ARG_190	NH2	A_ASP_714	OD2	2.720
2XEI	A_ARG_204	NH1	A_ASP_233	OD1	3.976
2XEI	A_ARG_204	NH1	A_ASP_233	OD2	3.187
2XEI	A_ARG_255	NH1	A_GLU_145	OE1	2.647
2XEI	A_ARG_255	NH2	A_GLU_145	OE1	2.713
2XEI	A_LYS_304	NZ	A_GLU_307	OE2	3.381
2XEI	A_LYS_341	NZ	A_ASP_173	OD1	3.842
2XEI	A_LYS_343	NZ	A_GLU_171	OE1	3.105
2XEI	A_HIS_345	NE2	A_GLU_137	OE1	3.939
2XEI	A_HIS_345	NE2	A_GLU_137	OE2	2.664
2XEI	A_ARG_354	NH2	A_ASP_114	OD1	3.459
2XEI	A_ARG_354	NH2	A_ASP_114	OD2	2.831
2XEI	A_ARG_363	NH2	A_ASP_106	OD1	3.622
2XEI	A_ARG_370	NH1	A_ASP_369	OD2	3.552
2XEI	A_ARG_370	NH2	A_ASP_666	OD1	2.830
2XEI	A_ARG_370	NH2	A_ASP_666	OD2	3.553
2XEI	A_HIS_377	ND1	A_ASP_379	OD1	2.915
2XEI	A_HIS_377	ND1	A_GLU_424	OE1	3.971
2XEI	A_HIS_377	NE2	A_ASP_387	OD1	3.175
2XEI	A_HIS_377	NE2	A_GLU_424	OE1	3.231
2XEI	A_HIS_377	NE2	A_GLU_425	OE2	3.821
2XEI	A_HIS_377	NE2	A_ASP_453	OD1	3.238
2XEI	A_HIS_377	NE2	A_ASP_453	OD2	3.140
2XEI	A_ARG_378	NH2	A_ASP_422	OD1	3.870
2XEI	A_ARG_378	NH2	A_ASP_422	OD2	3.255
2XEI	A_ARG_400	NH1	A_GLU_64	OE2	2.965

2XEI	A_ARG_400	NH1	A_GLU_397	OE1	3.705
2XEI	A_ARG_400	NH1	A_GLU_397	OE2	2.906
2XEI	A_ARG_400	NH2	A_GLU_64	OE2	2.816
2XEI	A_LYS_406	NZ	A_ASP_106	OD1	3.048
2XEI	A_ARG_411	NH1	A_ASP_106	OD1	3.535
2XEI	A_ARG_411	NH1	A_ASP_106	OD2	2.723
2XEI	A_ARG_411	NH2	A_ASP_106	OD1	2.835
2XEI	A_ARG_411	NH2	A_ASP_106	OD2	3.617
2XEI	A_ARG_413	NH2	A_GLU_367	OE2	3.221
2XEI	A_ARG_414	NH2	A_GLU_367	OE2	3.265
2XEI	A_ARG_463	NH1	A_GLU_457	OE1	3.475
2XEI	A_ARG_463	NH1	A_GLU_457	OE2	3.028
2XEI	A_ARG_463	NH2	A_ASP_465	OD1	3.828
2XEI	A_ARG_463	NH2	A_ASP_465	OD2	2.781
2XEI	A_LYS_491	NZ	A_GLU_495	OE2	3.533
2XEI	A_LYS_500	NZ	A_ASP_485	OD2	2.834
2XEI	A_ARG_527	NH1	A_GLU_436	OE1	2.782
2XEI	A_ARG_527	NH2	A_GLU_436	OE1	2.914
2XEI	A_ARG_536	NH2	A_GLU_457	OE1	2.981
2XEI	A_HIS_553	NE2	A_ASP_387	OD2	2.945
2XEI	A_HIS_553	NE2	A_GLU_425	OE1	3.184
2XEI	A_HIS_553	NE2	A_GLU_425	OE2	3.250
2XEI	A_HIS_573	ND1	A_ASP_567	OD2	2.635
2XEI	A_ARG_598	NH2	A_ASP_596	OD1	3.686
2XEI	A_ARG_598	NH2	A_ASP_596	OD2	2.928
2XEI	A_LYS_606	NZ	A_GLU_505	OE2	2.921
2XEI	A_LYS_610	NZ	A_GLU_703	OE2	2.865
2XEI	A_LYS_637	NZ	A_GLU_641	OE1	2.954
2XEI	A_LYS_637	NZ	A_GLU_641	OE2	3.988
2XEI	A_ARG_684	NH2	A_ASP_710	OD2	3.374
2XEI	A_HIS_689	NE2	A_GLU_672	OE2	2.779
2XEI	A_ARG_730	NH2	A_GLU_727	OE1	3.881
2XEI	A_ARG_730	NH2	A_GLU_727	OE2	3.068
2XEJ	A_HIS_56	ND1	A_GLU_408	OE2	3.595
2XEJ	A_HIS_56	NE2	A_GLU_408	OE2	3.649
2XEJ	A_LYS_59	NZ	A_ASP_63	OD1	3.833
2XEJ	A_LYS_59	NZ	A_ASP_63	OD2	3.161
2XEJ	A_ARG_181	NH1	A_GLU_183	OE2	3.636
2XEJ	A_ARG_181	NH2	A_ASP_184	OD1	3.044
2XEJ	A_ARG_181	NH2	A_ASP_184	OD2	3.609
2XEJ	A_ARG_190	NH1	A_ASP_714	OD1	2.993
2XEJ	A_ARG_190	NH1	A_ASP_714	OD2	3.604
2XEJ	A_ARG_190	NH2	A_ASP_714	OD1	3.611
2XEJ	A_ARG_190	NH2	A_ASP_714	OD2	2.731
2XEJ	A_ARG_204	NH1	A_ASP_233	OD1	3.963
2XEJ	A_ARG_204	NH1	A_ASP_233	OD2	3.162
2XEJ	A_ARG_255	NH1	A_GLU_145	OE1	2.709
2XEJ	A_ARG_255	NH2	A_GLU_145	OE1	2.779
2XEJ	A_LYS_304	NZ	A_GLU_307	OE2	3.882
2XEJ	A_LYS_341	NZ	A_ASP_173	OD1	3.630
2XEJ	A_HIS_345	NE2	A_GLU_137	OE1	3.939
2XEJ	A_HIS_345	NE2	A_GLU_137	OE2	3.101
2XEJ	A_ARG_354	NH2	A_ASP_114	OD1	3.439
2XEJ	A_ARG_354	NH2	A_ASP_114	OD2	2.884
2XEJ	A_ARG_363	NH2	A_ASP_106	OD1	3.838
2XEJ	A_ARG_370	NH1	A_ASP_369	OD1	3.947
2XEJ	A_ARG_370	NH1	A_ASP_369	OD2	3.540
2XEJ	A_ARG_370	NH2	A_ASP_666	OD1	2.915

2XEJ	A_ARG_370	NH2	A_ASP_666	OD2	3.607
2XEJ	A_HIS_377	ND1	A_ASP_379	OD1	2.947
2XEJ	A_HIS_377	ND1	A_GLU_424	OE1	3.959
2XEJ	A_HIS_377	NE2	A_ASP_387	OD1	3.198
2XEJ	A_HIS_377	NE2	A_GLU_424	OE1	3.200
2XEJ	A_HIS_377	NE2	A_GLU_425	OE2	3.909
2XEJ	A_HIS_377	NE2	A_ASP_453	OD1	3.288
2XEJ	A_HIS_377	NE2	A_ASP_453	OD2	3.106
2XEJ	A_ARG_378	NH2	A_ASP_422	OD1	3.906
2XEJ	A_ARG_378	NH2	A_ASP_422	OD2	3.305
2XEJ	A_ARG_400	NH1	A_GLU_64	OE2	3.030
2XEJ	A_ARG_400	NH1	A_GLU_397	OE1	3.701
2XEJ	A_ARG_400	NH1	A_GLU_397	OE2	2.808
2XEJ	A_ARG_400	NH2	A_GLU_64	OE2	2.879
2XEJ	A_LYS_406	NZ	A_ASP_106	OD1	3.327
2XEJ	A_ARG_411	NH1	A_ASP_106	OD1	3.525
2XEJ	A_ARG_411	NH1	A_ASP_106	OD2	2.766
2XEJ	A_ARG_411	NH2	A_ASP_106	OD1	2.901
2XEJ	A_ARG_411	NH2	A_ASP_106	OD2	3.711
2XEJ	A_ARG_413	NH2	A_GLU_367	OE2	3.406
2XEJ	A_ARG_414	NH2	A_GLU_367	OE2	3.157
2XEJ	A_ARG_463	NH1	A_GLU_457	OE1	3.276
2XEJ	A_ARG_463	NH1	A_GLU_457	OE2	3.003
2XEJ	A_ARG_463	NH2	A_ASP_465	OD1	3.986
2XEJ	A_ARG_463	NH2	A_ASP_465	OD2	2.863
2XEJ	A_LYS_491	NZ	A_GLU_495	OE2	3.392
2XEJ	A_LYS_500	NZ	A_ASP_485	OD2	2.873
2XEJ	A_ARG_527	NH1	A_GLU_436	OE1	2.804
2XEJ	A_ARG_527	NH2	A_GLU_436	OE1	3.018
2XEJ	A_ARG_536	NH1	A_GLU_457	OE1	2.942
2XEJ	A_HIS_553	NE2	A_ASP_387	OD2	2.982
2XEJ	A_HIS_553	NE2	A_GLU_425	OE1	3.077
2XEJ	A_HIS_553	NE2	A_GLU_425	OE2	3.221
2XEJ	A_HIS_573	ND1	A_ASP_567	OD2	2.723
2XEJ	A_ARG_598	NH2	A_ASP_596	OD1	3.718
2XEJ	A_ARG_598	NH2	A_ASP_596	OD2	2.988
2XEJ	A_LYS_606	NZ	A_GLU_505	OE1	3.097
2XEJ	A_LYS_606	NZ	A_GLU_505	OE2	3.795
2XEJ	A_LYS_610	NZ	A_GLU_703	OE2	2.940
2XEJ	A_HIS_618	NE2	A_GLU_716	OE1	3.742
2XEJ	A_LYS_637	NZ	A_GLU_641	OE1	2.900
2XEJ	A_LYS_637	NZ	A_GLU_641	OE2	3.785
2XEJ	A_ARG_684	NH2	A_ASP_710	OD2	3.390
2XEJ	A_HIS_689	NE2	A_GLU_672	OE2	2.745
2XZQ	H_ARG_40	NH1	H_GLU_89	OE2	3.454
2XZQ	H_ARG_40	NH2	H_GLU_89	OE2	2.650
2XZQ	H_LYS_65	NZ	H_GLU_62	OE1	2.508
2XZQ	H_LYS_65	NZ	H_GLU_62	OE2	3.892
2XZQ	H_LYS_67	NZ	H_ASP_90	OD1	3.800
2XZQ	H_LYS_67	NZ	H_ASP_90	OD2	3.016
2XZQ	H_ARG_98	NH1	H_ASP_108	OD1	3.377
2XZQ	H_ARG_98	NH1	H_ASP_108	OD2	2.748
2XZQ	H_LYS_150	NZ	L_GLU_127	OE2	3.822
2XZQ	H_LYS_212	NZ	H_ASP_214	OD1	3.314
2XZQ	H_LYS_215	NZ	L_GLU_126	OE2	2.689
2XZQ	L_ARG_23	NH1	L_ASP_71	OD1	3.290
2XZQ	L_ARG_23	NH1	L_ASP_71	OD2	3.939
2XZQ	L_ARG_23	NH2	L_ASP_71	OD1	2.856

2XZQ	L_ARG_23	NH2	L_ASP_71	OD2	3.986
2XZQ	L_HIS_44	ND1	L_GLU_40	OE2	3.471
2XZQ	L_ARG_63	NH2	L_ASP_84	OD1	2.551
2XZQ	L_ARG_63	NH2	L_ASP_84	OD2	3.490
2XZQ	L_LYS_105	NZ	L_GLU_85	OE2	3.885
2XZQ	L_LYS_113	NZ	L_GLU_201	OE1	2.868
2Y06	H_LYS_63	NZ	H_GLU_46	OE1	3.321
2Y06	H_LYS_63	NZ	H_GLU_46	OE2	2.855
2Y06	H_LYS_67	NZ	H_ASP_90	OD2	3.290
2Y06	H_ARG_98	NH1	H_ASP_108	OD1	3.019
2Y06	H_ARG_98	NH1	H_ASP_108	OD2	3.194
2Y06	H_LYS_215	NZ	L_GLU_126	OE2	2.373
2Y06	L_ARG_23	NH1	L_ASP_71	OD1	3.453
2Y06	L_ARG_23	NH2	L_ASP_71	OD1	2.764
2Y06	L_ARG_63	NH2	L_ASP_84	OD1	2.907
2Y06	L_ARG_63	NH2	L_ASP_84	OD2	3.632
2Y06	L_LYS_113	NZ	L_GLU_201	OE1	3.332
2Y06	L_LYS_169	NZ	L_GLU_85	OE2	3.628
2Y07	H_LYS_67	NZ	H_ASP_90	OD1	3.687
2Y07	H_LYS_67	NZ	H_ASP_90	OD2	2.861
2Y07	H_ARG_98	NH1	H_ASP_108	OD1	3.962
2Y07	H_ARG_98	NH1	H_ASP_108	OD2	2.823
2Y07	H_LYS_215	NZ	L_GLU_126	OE2	2.390
2Y07	L_ARG_23	NH1	L_ASP_71	OD1	3.698
2Y07	L_ARG_23	NH1	L_ASP_71	OD2	3.356
2Y07	L_ARG_23	NH2	L_ASP_71	OD1	2.962
2Y07	L_ARG_23	NH2	L_ASP_71	OD2	2.784
2Y07	L_ARG_63	NH2	L_GLU_82	OE2	3.307
2Y07	L_ARG_63	NH2	L_ASP_83	OD1	2.727
2Y07	L_ARG_63	NH2	L_ASP_83	OD2	3.778
2Y07	L_LYS_113	NZ	L_GLU_201	OE1	3.255
2Y07	L_LYS_113	NZ	L_GLU_201	OE2	3.532
2Y07	L_HIS_200	NE2	L_GLU_201	OE1	3.946
2Y07	L_ARG_211	NH1	L_GLU_189	OE1	3.826
2Y36	H_ARG_40	NH1	H_GLU_89	OE1	3.909
2Y36	H_ARG_40	NH1	H_GLU_89	OE2	3.356
2Y36	H_ARG_40	NH2	H_GLU_89	OE2	2.875
2Y36	H_LYS_65	NZ	H_GLU_62	OE1	2.983
2Y36	H_LYS_67	NZ	H_ASP_90	OD2	3.261
2Y36	H_ARG_98	NH1	H_ASP_108	OD1	3.408
2Y36	H_ARG_98	NH1	H_ASP_108	OD2	2.494
2Y36	H_LYS_150	NZ	L_GLU_127	OE2	3.849
2Y36	H_LYS_215	NZ	L_GLU_126	OE2	2.707
2Y36	L_ARG_23	NH1	L_ASP_71	OD2	3.674
2Y36	L_ARG_23	NH2	L_ASP_71	OD1	3.148
2Y36	L_ARG_23	NH2	L_ASP_71	OD2	3.652
2Y36	L_ARG_63	NH2	L_GLU_83	OE2	3.566
2Y36	L_ARG_63	NH2	L_ASP_84	OD1	2.616
2Y36	L_ARG_63	NH2	L_ASP_84	OD2	3.443
2Y36	L_LYS_113	NZ	L_GLU_201	OE1	3.248
2Y36	L_HIS_191	NE2	L_ASP_154	OD2	3.845
2Y7S	A_LYS_27	NZ	A_ASP_25	OD2	3.076
2Y7S	A_LYS_45	NZ	A_GLU_83	OE1	2.864
2Y7S	A_LYS_47	NZ	A_GLU_54	OE1	3.042
2Y7S	A_LYS_67	NZ	A_ASP_28	OD1	3.289
2Y7S	A_LYS_67	NZ	A_ASP_28	OD2	2.809
2Y7S	A_ARG_75	NH1	A_GLU_95	OE1	2.862
2Y7S	A_ARG_75	NH1	A_GLU_95	OE2	3.954

2Y7S	A_ARG_80	NH1	A_GLU_44	OE1	2.923
2Y7S	A_ARG_80	NH1	A_GLU_44	OE2	3.022
2Y7S	A_ARG_80	NH2	A_GLU_92	OE1	3.248
2Y7S	A_ARG_127	NH1	A_ASP_159	OD1	3.706
2Y7S	A_ARG_127	NH1	A_ASP_159	OD2	2.895
2Y7S	A_ARG_127	NH1	B_GLU_118	OE1	3.457
2Y7S	A_ARG_127	NH2	A_GLU_112	OE1	3.963
2Y7S	A_ARG_127	NH2	A_GLU_112	OE2	2.936
2Y7S	A_ARG_127	NH2	A_ASP_159	OD1	2.847
2Y7S	A_ARG_127	NH2	A_ASP_159	OD2	3.582
2Y7S	A_ARG_130	NH1	A_GLU_92	OE1	3.851
2Y7S	A_ARG_130	NH1	A_GLU_92	OE2	3.019
2Y7S	A_ARG_130	NH2	A_GLU_92	OE1	3.136
2Y7S	A_ARG_130	NH2	A_GLU_92	OE2	3.650
2Y7S	A_ARG_152	NH1	A_GLU_150	OE1	3.228
2Y7S	A_ARG_152	NH2	A_GLU_150	OE1	3.600
2Y7S	A_LYS_179	NZ	A_GLU_181	OE1	3.798
2Y7S	A_LYS_179	NZ	A_GLU_181	OE2	3.366
2Y7S	A_LYS_218	NZ	A_GLU_216	OE1	3.816
2Y7S	A_LYS_218	NZ	B_ASP_85	OD1	3.014
2Y7S	A_LYS_240	NZ	A_GLU_217	OE1	3.163
2Y7S	A_LYS_240	NZ	A_GLU_217	OE2	3.626
2Y7S	A_LYS_253	NZ	A_ASP_71	OD1	3.458
2Y7S	A_LYS_253	NZ	A_ASP_71	OD2	2.809
2Y7S	B_ARG_41	NH2	A_GLU_238	OE2	2.757
2Y7S	B_LYS_42	NZ	B_ASP_37	OD1	3.966
2Y7S	B_LYS_47	NZ	B_GLU_54	OE1	3.576
2Y7S	B_LYS_47	NZ	B_GLU_54	OE2	3.620
2Y7S	B_LYS_67	NZ	B_ASP_28	OD1	3.186
2Y7S	B_LYS_67	NZ	B_ASP_28	OD2	3.425
2Y7S	B_ARG_75	NH1	B_GLU_95	OE2	2.817
2Y7S	B_ARG_80	NH1	B_GLU_44	OE1	3.002
2Y7S	B_ARG_80	NH1	B_GLU_44	OE2	3.573
2Y7S	B_ARG_80	NH2	B_GLU_92	OE1	2.824
2Y7S	B_HIS_103	ND1	B_GLU_137	OE1	2.807
2Y7S	B_HIS_119	NE2	B_ASP_116	OD2	3.821
2Y7S	B_LYS_122	NZ	B_ASP_116	OD2	3.879
2Y7S	B_ARG_127	NH1	B_ASP_159	OD1	3.795
2Y7S	B_ARG_127	NH1	B_ASP_159	OD2	2.884
2Y7S	B_ARG_127	NH2	B_GLU_112	OE1	3.910
2Y7S	B_ARG_127	NH2	B_GLU_112	OE2	2.774
2Y7S	B_ARG_127	NH2	B_ASP_159	OD1	2.931
2Y7S	B_ARG_127	NH2	B_ASP_159	OD2	3.540
2Y7S	B_ARG_130	NH1	B_GLU_92	OE1	3.502
2Y7S	B_ARG_130	NH1	B_GLU_92	OE2	2.814
2Y7S	B_ARG_130	NH2	B_GLU_92	OE1	3.119
2Y7S	B_ARG_130	NH2	B_GLU_92	OE2	3.783
2Y7S	B_LYS_148	NZ	B_ASP_170	OD2	3.415
2Y7S	B_ARG_152	NH1	B_GLU_150	OE1	2.822
2Y7S	B_ARG_152	NH2	B_GLU_150	OE1	3.268
2Y7S	B_LYS_173	NZ	B_ASP_170	OD2	3.896
2Y7S	B_LYS_179	NZ	B_GLU_181	OE1	3.992
2Y7S	B_LYS_179	NZ	B_GLU_181	OE2	3.341
2Y7S	B_LYS_198	NZ	B_GLU_196	OE1	3.898
2Y7S	B_HIS_204	ND1	B_ASP_200	OD2	3.949
2Y7S	B_ARG_212	NH2	B_ASP_210	OD2	3.869
2Y7S	B_LYS_218	NZ	B_GLU_187	OE1	3.745
2Y7S	B_LYS_218	NZ	B_GLU_216	OE2	3.499

2Y7S	B.LYS_253	NZ	B.ASP_71	OD1	3.851
2Y7S	B.LYS_253	NZ	B.ASP_71	OD2	3.059
2YPV	A.HIS_26	ND1	A.ASP_25	OD1	3.615
2YPV	A.LYS_47	NZ	A.GLU_54	OE2	3.265
2YPV	A.LYS_67	NZ	A.ASP_28	OD1	3.119
2YPV	A.LYS_67	NZ	A.ASP_28	OD2	2.907
2YPV	A.ARG_80	NH1	A.GLU_44	OE1	3.085
2YPV	A.ARG_80	NH1	A.GLU_44	OE2	3.642
2YPV	A.ARG_80	NH2	A.GLU_92	OE2	3.509
2YPV	A.HIS_103	ND1	A.GLU_137	OE1	2.799
2YPV	A.HIS_103	ND1	A.GLU_137	OE2	3.510
2YPV	A.ARG_127	NH1	A.ASP_160	OD1	3.664
2YPV	A.ARG_127	NH1	A.ASP_160	OD2	2.748
2YPV	A.ARG_127	NH2	A.GLU_112	OE1	3.713
2YPV	A.ARG_127	NH2	A.GLU_112	OE2	2.780
2YPV	A.ARG_127	NH2	A.ASP_160	OD1	2.809
2YPV	A.ARG_127	NH2	A.ASP_160	OD2	3.468
2YPV	A.ARG_130	NH2	L.ASP_92	OD1	2.916
2YPV	A.ARG_149	NH2	A.ASP_171	OD2	2.711
2YPV	A.LYS_180	NZ	A.GLU_182	OE1	3.802
2YPV	A.LYS_180	NZ	A.GLU_182	OE2	3.312
2YPV	A.ARG_204	NH2	A.ASP_142	OD1	2.851
2YPV	A.ARG_204	NH2	A.ASP_142	OD2	3.577
2YPV	A.HIS_205	ND1	A.ASP_201	OD2	3.920
2YPV	A.LYS_219	NZ	H.ASP_52	OD2	3.469
2YPV	A.LYS_241	NZ	H.ASP_99	OD2	2.741
2YPV	A.ARG_247	NH1	A.GLU_188	OE2	3.707
2YPV	A.LYS_254	NZ	A.ASP_71	OD1	3.594
2YPV	A.LYS_254	NZ	A.ASP_71	OD2	2.807
2YPV	H.LYS_54	NZ	H.ASP_31	OD1	2.744
2YPV	H.LYS_67	NZ	H.ASP_90	OD1	3.738
2YPV	H.LYS_67	NZ	H.ASP_90	OD2	2.816
2YPV	H.LYS_214	NZ	L.GLU_123	OE1	2.788
2YPV	H.LYS_214	NZ	L.GLU_123	OE2	2.975
2YPV	L.HIS_30	ND1	L.ASP_28	OD1	3.934
2YPV	L.HIS_30	ND1	L.ASP_92	OD1	3.607
2YPV	L.HIS_30	ND1	L.ASP_92	OD2	2.797
2YPV	L.HIS_30	NE2	L.ASP_28	OD2	3.772
2YPV	L.ARG_50	NH2	A.GLU_239	OE1	3.110
2YPV	L.ARG_50	NH2	A.GLU_239	OE2	3.975
2YPV	L.ARG_61	NH1	L.GLU_79	OE1	3.426
2YPV	L.ARG_61	NH1	L.GLU_81	OE2	3.737
2YPV	L.ARG_61	NH1	L.ASP_82	OD1	2.772
2YPV	L.ARG_61	NH1	L.ASP_82	OD2	3.085
2YPV	L.ARG_61	NH2	L.GLU_79	OE1	2.918
2YPV	L.ARG_61	NH2	L.GLU_79	OE2	3.335
2YPV	L.ARG_61	NH2	L.GLU_81	OE2	3.973
2YPV	L.LYS_149	NZ	L.GLU_195	OE1	2.918
2YPV	L.LYS_149	NZ	L.GLU_195	OE2	3.889
2YPV	L.HIS_189	ND1	L.ASP_151	OD2	2.963
2YPV	L.LYS_199	NZ	L.ASP_110	OD2	3.962
2YWY	A.ARG_33	NH2	A.ASP_35	OD1	3.217
2YWY	A.LYS_48	NZ	A.ASP_35	OD1	3.576
2YWY	A.LYS_48	NZ	A.ASP_35	OD2	2.413
2YWY	A.LYS_48	NZ	B.GLU_32	OE1	3.306
2YWY	A.LYS_48	NZ	B.GLU_32	OE2	2.998
2YWY	A.ARG_54	NH1	A.ASP_77	OD1	3.047
2YWY	A.ARG_54	NH1	A.ASP_77	OD2	3.216

2YWY	A_ARG_54	NH2	A_ASP_77	OD1	3.942
2YWY	A_ARG_54	NH2	A_ASP_77	OD2	2.619
2YWY	A_LYS_61	NZ	B_GLU_57	OE1	2.550
2YWY	A_LYS_61	NZ	B_GLU_57	OE2	3.211
2YWY	A_LYS_82	NZ	C_ASP_89	OD1	3.260
2YWY	A_LYS_102	NZ	A_GLU_46	OE1	2.844
2YWY	A_LYS_102	NZ	A_GLU_46	OE2	2.777
2YWY	B_LYS_25	NZ	B_ASP_4	OD1	3.823
2YWY	B_ARG_33	NH2	A_GLU_32	OE1	3.506
2YWY	B_ARG_33	NH2	B_ASP_35	OD1	3.061
2YWY	B_ARG_33	NH2	B_ASP_35	OD2	3.585
2YWY	B_ARG_38	NH2	B_ASP_77	OD1	2.791
2YWY	B_LYS_48	NZ	A_GLU_32	OE1	3.520
2YWY	B_LYS_48	NZ	A_GLU_32	OE2	2.757
2YWY	B_ARG_54	NH1	B_ASP_77	OD2	3.038
2YWY	B_ARG_54	NH2	B_ASP_77	OD1	2.760
2YWY	B_ARG_54	NH2	B_ASP_77	OD2	2.618
2YWY	B_LYS_61	NZ	A_GLU_57	OE1	3.086
2YWY	B_LYS_102	NZ	B_GLU_46	OE1	3.457
2YWY	C_LYS_12	NZ	C_GLU_16	OE2	3.484
2YWY	C_ARG_33	NH2	C_ASP_35	OD1	3.627
2YWY	C_LYS_48	NZ	C_ASP_35	OD2	3.144
2YWY	C_LYS_48	NZ	D_GLU_32	OE1	2.723
2YWY	C_LYS_48	NZ	D_GLU_32	OE2	3.404
2YWY	C_ARG_54	NH1	C_ASP_77	OD1	2.958
2YWY	C_ARG_54	NH1	C_ASP_77	OD2	3.216
2YWY	C_ARG_54	NH2	C_ASP_77	OD1	3.555
2YWY	C_ARG_54	NH2	C_ASP_77	OD2	2.224
2YWY	C_LYS_61	NZ	D_GLU_57	OE1	2.801
2YWY	C_LYS_61	NZ	D_GLU_57	OE2	3.948
2YWY	C_ARG_74	NH1	C_ASP_77	OD2	3.935
2YWY	C_LYS_102	NZ	C_GLU_46	OE1	3.626
2YWY	D_ARG_33	NH2	D_ASP_35	OD1	3.658
2YWY	D_ARG_38	NH2	D_ASP_77	OD1	2.919
2YWY	D_LYS_48	NZ	C_GLU_32	OE1	3.239
2YWY	D_LYS_48	NZ	C_GLU_32	OE2	2.447
2YWY	D_ARG_54	NH1	D_ASP_77	OD1	3.877
2YWY	D_ARG_54	NH1	D_ASP_77	OD2	2.884
2YWY	D_ARG_54	NH2	D_ASP_77	OD1	2.689
2YWY	D_ARG_54	NH2	D_ASP_77	OD2	3.195
2YWY	D_LYS_61	NZ	C_GLU_57	OE1	2.837
2YWY	D_LYS_61	NZ	C_GLU_57	OE2	3.637
2YWY	D_ARG_71	NH1	D_ASP_72	OD1	2.537
2YWY	D_ARG_71	NH1	D_ASP_72	OD2	3.727
2YWY	D_ARG_71	NH2	D_ASP_72	OD1	3.924
2YWY	D_LYS_102	NZ	D_GLU_46	OE1	3.940
2YWZ	A_ARG_8	NH1	A_ASP_4	OD2	3.114
2YWZ	A_LYS_25	NZ	A_ASP_4	OD1	3.407
2YWZ	A_ARG_54	NH1	A_ASP_77	OD1	3.632
2YWZ	A_ARG_54	NH1	A_ASP_77	OD2	2.888
2YWZ	A_ARG_54	NH2	A_ASP_77	OD1	3.024
2YWZ	A_ARG_54	NH2	A_ASP_77	OD2	3.599
2YWZ	A_ARG_74	NH1	A_ASP_72	OD2	2.842
2YWZ	A_LYS_82	NZ	A_GLU_46	OE1	3.217
2YWZ	A_LYS_82	NZ	A_GLU_46	OE2	3.322
2YWZ	A_LYS_82	NZ	A_GLU_102	OE1	3.820
2YWZ	A_LYS_82	NZ	A_GLU_102	OE2	3.005
2ZCH	P_HIS_57	ND1	P_ASP_102	OD1	3.188

2ZCH	P_HIS_57	ND1	P_ASP_102	OD2	2.701
2ZCH	P_HIS_70	NE2	P_GLU_21	OE1	3.047
2ZCH	P_LYS_119	NZ	P_ASP_116	OD1	3.130
2ZCH	P_LYS_178	NZ	H_ASP_96	OD1	3.502
2ZCH	P_LYS_178	NZ	H_ASP_96	OD2	3.400
2ZCH	P_ARG_185	NH2	P_ASP_159	OD1	3.236
2ZCH	P_ARG_185	NH2	P_ASP_159	OD2	3.391
2ZCH	P_LYS_188	NZ	P_ASP_159	OD2	3.769
2ZCH	P_LYS_230	NZ	P_GLU_129	OE1	3.520
2ZCH	P_LYS_230	NZ	P_GLU_129	OE2	2.924
2ZCH	P_ARG_235	NH1	L_ASP_28	OD2	2.443
2ZCH	P_ARG_235	NH2	L_ASP_28	OD2	3.166
2ZCH	P_LYS_236	NZ	H_GLU_100C	OE2	3.089
2ZCH	P_LYS_239	NZ	P_ASP_240	OD1	3.042
2ZCH	L_LYS_24	NZ	L_ASP_70	OD1	3.285
2ZCH	L_LYS_24	NZ	L_ASP_70	OD2	3.649
2ZCH	L_ARG_61	NH1	L_ASP_82	OD2	2.822
2ZCH	L_ARG_61	NH2	L_GLU_79	OE1	3.619
2ZCH	L_ARG_61	NH2	L_GLU_81	OE2	3.092
2ZCH	L_ARG_61	NH2	L_ASP_82	OD1	3.377
2ZCH	L_ARG_61	NH2	L_ASP_82	OD2	3.215
2ZCH	L_LYS_103	NZ	L_ASP_165	OD1	2.730
2ZCH	L_LYS_147	NZ	L_GLU_195	OE1	3.268
2ZCH	L_ARG_155	NH1	L_GLU_185	OE2	3.338
2ZCH	L_HIS_189	ND1	L_GLU_185	OE1	3.822
2ZCH	L_LYS_199	NZ	L_ASP_110	OD1	3.298
2ZCH	L_ARG_211	NH2	L_GLU_187	OE2	2.494
2ZCH	H_ARG_38	NH1	H_GLU_46	OE1	3.046
2ZCH	H_ARG_38	NH2	H_ASP_86	OD1	3.480
2ZCH	H_ARG_40	NH1	H_GLU_85	OE2	3.170
2ZCH	H_ARG_40	NH2	H_GLU_85	OE2	3.818
2ZCH	H_ARG_50	NH1	H_GLU_100C	OE1	3.902
2ZCH	H_ARG_50	NH2	L_ASP_94	OD1	2.658
2ZCH	H_ARG_50	NH2	L_ASP_94	OD2	2.887
2ZCH	H_LYS_66	NZ	H_ASP_86	OD1	3.386
2ZCH	H_ARG_94	NH2	H_ASP_101	OD1	3.421
2ZCH	H_ARG_94	NH2	H_ASP_101	OD2	2.694
2ZCH	H_LYS_208	NZ	L_GLU_123	OE1	3.921
2ZCH	H_LYS_208	NZ	L_GLU_123	OE2	3.396
2ZCK	P_HIS_25	NE2	P_GLU_77	OE2	3.078
2ZCK	P_HIS_57	ND1	P_ASP_102	OD1	3.235
2ZCK	P_HIS_57	ND1	P_ASP_102	OD2	2.810
2ZCK	P_ARG_69	NH2	P_GLU_77	OE1	3.765
2ZCK	P_HIS_70	NE2	P_GLU_21	OE1	3.922
2ZCK	P_ARG_95G	NH2	P_GLU_218	OE2	2.834
2ZCK	P_LYS_178	NZ	H_ASP_96	OD1	3.892
2ZCK	P_LYS_178	NZ	H_ASP_96	OD2	3.060
2ZCK	P_ARG_185	NH2	P_ASP_159	OD1	2.897
2ZCK	P_ARG_185	NH2	P_ASP_159	OD2	3.599
2ZCK	P_LYS_188	NZ	P_ASP_159	OD2	3.306
2ZCK	P_LYS_231	NZ	P_GLU_129	OE1	3.939
2ZCK	P_ARG_236	NH2	L_ASP_28	OD1	3.496
2ZCK	P_LYS_240	NZ	P_ASP_241	OD1	3.131
2ZCK	L_ARG_61	NH1	L_ASP_82	OD1	3.643
2ZCK	L_ARG_61	NH1	L_ASP_82	OD2	2.898
2ZCK	L_ARG_61	NH2	L_GLU_79	OE1	3.648
2ZCK	L_ARG_61	NH2	L_GLU_81	OE2	3.878
2ZCK	L_ARG_61	NH2	L_ASP_82	OD1	3.492

2ZCK	L_LYS_103	NZ	L_ASP_165	OD1	3.500
2ZCK	L_LYS_183	NZ	L_GLU_187	OE1	3.434
2ZCK	L_LYS_183	NZ	L_GLU_187	OE2	3.899
2ZCK	L_ARG_188	NH1	L_GLU_185	OE2	3.774
2ZCK	L_ARG_188	NH2	L_ASP_184	OD1	3.893
2ZCK	L_HIS_189	ND1	L_GLU_185	OE1	3.762
2ZCK	L_HIS_189	ND1	L_GLU_185	OE2	3.555
2ZCK	H_ARG_38	NH1	H_GLU_46	OE1	3.860
2ZCK	H_ARG_38	NH1	H_GLU_46	OE2	3.777
2ZCK	H_ARG_38	NH2	H_ASP_86	OD1	2.988
2ZCK	H_ARG_50	NH2	L_ASP_94	OD1	3.095
2ZCK	H_ARG_50	NH2	L_ASP_94	OD2	2.679
2ZCK	H_ARG_94	NH2	H_ASP_101	OD1	3.492
2ZCK	H_ARG_94	NH2	H_ASP_101	OD2	2.952
2ZCK	H_LYS_208	NZ	L_GLU_123	OE2	2.731
2ZCK	H_ARG_213	NH1	H_ASP_214	OD2	3.175
2ZCK	H_ARG_213	NH2	H_ASP_214	OD2	2.814
2ZCL	P_HIS_57	ND1	P_ASP_102	OD1	3.443
2ZCL	P_HIS_57	ND1	P_ASP_102	OD2	2.832
2ZCL	P_HIS_70	ND1	P_GLU_77	OE2	3.941
2ZCL	P_HIS_70	NE2	P_GLU_21	OE2	3.315
2ZCL	P_LYS_175	NZ	P_ASP_98	OD1	2.885
2ZCL	P_LYS_178	NZ	H_ASP_96	OD1	3.272
2ZCL	P_LYS_178	NZ	H_ASP_96	OD2	2.771
2ZCL	P_ARG_185	NH1	P_ASP_159	OD1	3.520
2ZCL	P_ARG_185	NH1	P_ASP_159	OD2	3.828
2ZCL	P_ARG_235	NH2	L_ASP_28	OD1	3.392
2ZCL	P_LYS_239	NZ	P_ASP_240	OD1	3.379
2ZCL	L_LYS_24	NZ	L_ASP_70	OD1	3.131
2ZCL	L_LYS_24	NZ	L_ASP_70	OD2	3.129
2ZCL	L_ARG_61	NH1	L_ASP_82	OD2	2.822
2ZCL	L_ARG_61	NH2	L_GLU_79	OE1	3.403
2ZCL	L_ARG_61	NH2	L_GLU_81	OE2	3.290
2ZCL	L_ARG_61	NH2	L_ASP_82	OD1	3.751
2ZCL	L_ARG_61	NH2	L_ASP_82	OD2	3.541
2ZCL	L_LYS_103	NZ	L_ASP_165	OD1	3.980
2ZCL	L_ARG_108	NH1	L_ASP_170	OD2	3.834
2ZCL	L_HIS_189	ND1	L_GLU_185	OE1	2.939
2ZCL	L_LYS_199	NZ	L_ASP_110	OD2	3.830
2ZCL	L_ARG_211	NH1	L_GLU_187	OE1	2.851
2ZCL	H_ARG_38	NH2	H_ASP_86	OD2	3.902
2ZCL	H_ARG_50	NH2	L_ASP_94	OD1	3.155
2ZCL	H_ARG_50	NH2	L_ASP_94	OD2	2.864
2ZCL	H_LYS_64	NZ	H_GLU_61	OE1	3.636
2ZCL	H_ARG_94	NH2	H_ASP_101	OD1	3.425
2ZCL	H_ARG_94	NH2	H_ASP_101	OD2	2.661
2ZNW	A_ARG_61	NH1	A_GLU_81	OE2	3.724
2ZNW	A_ARG_61	NH2	A_GLU_81	OE1	3.857
2ZNW	A_ARG_61	NH2	A_GLU_81	OE2	2.689
2ZNW	A_ARG_61	NH2	A_ASP_82	OD1	2.714
2ZNW	A_ARG_61	NH2	A_ASP_82	OD2	3.434
2ZNW	A_LYS_103	NZ	A_GLU_105	OE1	2.950
2ZNW	A_LYS_103	NZ	A_GLU_105	OE2	3.174
2ZNW	A_ARG_160	NH1	A_ASP_211	OD1	2.916
2ZNW	A_ARG_160	NH2	A_GLU_168	OE1	2.840
2ZNW	A_ARG_160	NH2	A_ASP_211	OD1	3.551
2ZNW	A_ARG_188	NH1	A_ASP_211	OD1	3.826
2ZNW	A_ARG_188	NH1	A_ASP_211	OD2	3.091

2ZWN	A_ARG_188	NH2	A_ASP_211	OD1	3.128
2ZWN	A_ARG_188	NH2	A_ASP_211	OD2	3.623
2ZWN	A_LYS_197	NZ	A_ASP_194	OD2	3.664
2ZWN	Y_LYS_1	NZ	Y_GLU_7	OE2	2.868
2ZWN	Y_ARG_61	NH2	Y_ASP_48	OD2	3.340
2ZWN	Y_LYS_97	NZ	A_ASP_154	OD1	2.612
2ZWN	Y_LYS_97	NZ	A_ASP_154	OD2	3.786
2ZWN	Y_LYS_97	NZ	A_ASP_221	OD1	3.143
2ZWN	Y_LYS_97	NZ	A_ASP_221	OD2	3.719
2ZWN	Y_LYS_116	NZ	B_ASP_203	OD1	2.664
2ZWN	Y_ARG_125	NH1	Y_ASP_119	OD2	2.994
2ZWN	Y_ARG_125	NH2	Y_ASP_119	OD1	3.200
2ZWN	Y_ARG_125	NH2	Y_ASP_119	OD2	3.148
2ZWN	B_LYS_39	NZ	B_GLU_81	OE1	2.664
2ZWN	B_ARG_45	NH2	B_GLU_42	OE1	3.967
2ZWN	B_ARG_61	NH1	B_GLU_79	OE1	2.886
2ZWN	B_ARG_61	NH1	B_GLU_81	OE2	3.684
2ZWN	B_ARG_61	NH2	B_GLU_79	OE1	3.980
2ZWN	B_ARG_61	NH2	B_GLU_81	OE2	2.740
2ZWN	B_ARG_61	NH2	B_ASP_82	OD1	2.575
2ZWN	B_ARG_61	NH2	B_ASP_82	OD2	3.124
2ZWN	B_LYS_103	NZ	B_GLU_105	OE2	3.056
2ZWN	B_ARG_160	NH1	B_ASP_211	OD1	2.739
2ZWN	B_ARG_160	NH2	B_GLU_168	OE1	2.827
2ZWN	B_ARG_160	NH2	B_ASP_211	OD1	3.579
2ZWN	B_ARG_188	NH1	B_ASP_211	OD2	3.191
2ZWN	B_ARG_188	NH2	B_ASP_211	OD1	3.246
2ZWN	B_ARG_188	NH2	B_ASP_211	OD2	3.554
2ZWN	Z_LYS_1	NZ	Z_GLU_7	OE2	2.784
2ZWN	Z_ARG_61	NH1	Z_ASP_48	OD2	2.495
2ZWN	Z_ARG_61	NH2	Z_ASP_48	OD2	3.711
2ZWN	Z_ARG_68	NH2	Z_ASP_66	OD2	2.978
2ZWN	Z_LYS_97	NZ	B_ASP_154	OD1	3.042
2ZWN	Z_LYS_97	NZ	B_ASP_221	OD1	2.782
2ZWN	Z_LYS_97	NZ	B_ASP_221	OD2	3.319
2ZWN	Z_LYS_116	NZ	A_ASP_203	OD1	2.989
2ZWN	Z_ARG_125	NH1	Z_ASP_119	OD2	3.101
2ZWN	Z_ARG_125	NH2	Z_ASP_119	OD1	3.435
2ZWN	Z_ARG_125	NH2	Z_ASP_119	OD2	3.343
2ZNX	A_ARG_61	NH2	A_GLU_81	OE1	3.274
2ZNX	A_ARG_61	NH2	A_GLU_81	OE2	3.380
2ZNX	A_ARG_61	NH2	A_ASP_82	OD1	2.710
2ZNX	A_ARG_61	NH2	A_ASP_82	OD2	3.576
2ZNX	A_ARG_160	NH1	A_ASP_211	OD1	2.745
2ZNX	A_ARG_160	NH2	A_GLU_168	OE1	2.794
2ZNX	A_ARG_160	NH2	A_ASP_211	OD1	3.557
2ZNX	A_ARG_188	NH1	A_ASP_211	OD1	3.903
2ZNX	A_ARG_188	NH1	A_ASP_211	OD2	3.003
2ZNX	A_ARG_188	NH2	A_ASP_211	OD1	3.102
2ZNX	A_ARG_188	NH2	A_ASP_211	OD2	3.513
2ZNX	A_LYS_197	NZ	A_ASP_194	OD2	3.759
2ZNX	Y_LYS_1	NZ	Y_GLU_7	OE2	2.738
2ZNX	Y_ARG_61	NH2	Y_ASP_48	OD2	3.990
2ZNX	Y_LYS_97	NZ	A_ASP_154	OD1	2.701
2ZNX	Y_LYS_97	NZ	A_ASP_221	OD1	2.716
2ZNX	Y_LYS_97	NZ	A_ASP_221	OD2	3.355
2ZNX	Y_LYS_116	NZ	B_ASP_203	OD1	3.871
2ZNX	Y_LYS_116	NZ	B_ASP_203	OD2	2.956

2ZNX	Y_ARG_125	NH1	Y_ASP_119	OD2	3.017
2ZNX	Y_ARG_125	NH2	Y_ASP_119	OD1	3.028
2ZNX	Y_ARG_125	NH2	Y_ASP_119	OD2	3.017
2ZNX	B_LYS_39	NZ	B_GLU_81	OE1	3.694
2ZNX	B_LYS_39	NZ	B_GLU_81	OE2	3.627
2ZNX	B_ARG_61	NH1	B_GLU_79	OE1	3.548
2ZNX	B_ARG_61	NH1	B_GLU_79	OE2	3.265
2ZNX	B_ARG_61	NH2	B_GLU_81	OE1	3.903
2ZNX	B_ARG_61	NH2	B_GLU_81	OE2	3.625
2ZNX	B_ARG_61	NH2	B_ASP_82	OD1	2.303
2ZNX	B_ARG_61	NH2	B_ASP_82	OD2	3.001
2ZNX	B_LYS_103	NZ	B_GLU_105	OE1	3.986
2ZNX	B_LYS_103	NZ	B_GLU_105	OE2	2.781
2ZNX	B_LYS_135	NZ	Y_ASP_119	OD2	3.744
2ZNX	B_ARG_160	NH1	B_ASP_211	OD1	2.901
2ZNX	B_ARG_160	NH2	B_GLU_168	OE1	2.918
2ZNX	B_ARG_160	NH2	B_ASP_211	OD1	3.424
2ZNX	B_ARG_188	NH1	B_ASP_211	OD1	3.668
2ZNX	B_ARG_188	NH1	B_ASP_211	OD2	2.960
2ZNX	B_ARG_188	NH2	B_ASP_211	OD1	2.965
2ZNX	B_ARG_188	NH2	B_ASP_211	OD2	3.589
2ZNX	Z_LYS_1	NZ	Z_GLU_7	OE2	2.717
2ZNX	Z_ARG_68	NH2	Z_ASP_66	OD2	2.870
2ZNX	Z_LYS_97	NZ	B_ASP_154	OD1	2.804
2ZNX	Z_LYS_97	NZ	B_ASP_221	OD1	3.005
2ZNX	Z_LYS_97	NZ	B_ASP_221	OD2	3.520
2ZNX	Z_LYS_116	NZ	A_ASP_203	OD1	3.699
2ZNX	Z_LYS_116	NZ	A_ASP_203	OD2	3.427
2ZNX	Z_ARG_125	NH1	Z_ASP_119	OD2	3.079
2ZNX	Z_ARG_125	NH2	Z_ASP_119	OD1	3.710
2ZNX	Z_ARG_125	NH2	Z_ASP_119	OD2	3.679
2ZPK	L_ARG_61	NH2	L_GLU_81	OE2	3.597
2ZPK	L_ARG_61	NH2	L_ASP_82	OD1	2.750
2ZPK	L_ARG_61	NH2	L_ASP_82	OD2	3.576
2ZPK	L_HIS_95	NE2	H_ASP_62	OD1	3.977
2ZPK	L_LYS_111	NZ	L_GLU_199	OE1	3.322
2ZPK	L_HIS_189	ND1	L_ASP_152	OD2	2.821
2ZPK	H_LYS_64	NZ	H_GLU_61	OE1	2.974
2ZPK	H_ARG_66	NH1	H_ASP_86	OD1	3.749
2ZPK	H_ARG_66	NH1	H_ASP_86	OD2	2.760
2ZPK	H_ARG_66	NH2	H_ASP_86	OD1	2.842
2ZPK	H_ARG_66	NH2	H_ASP_86	OD2	3.335
2ZPK	H_LYS_143	NZ	L_GLU_125	OE2	2.882
2ZPK	H_LYS_208	NZ	L_GLU_124	OE2	3.548
2ZPK	M_LYS_39	NZ	M_GLU_81	OE2	3.913
2ZPK	M_HIS_42	ND1	M_GLU_38	OE2	3.014
2ZPK	M_ARG_61	NH2	M_GLU_81	OE1	3.031
2ZPK	M_ARG_61	NH2	M_ASP_82	OD1	2.872
2ZPK	M_ARG_61	NH2	M_ASP_82	OD2	3.561
2ZPK	I_LYS_46	NZ	I_ASP_62	OD1	3.734
2ZPK	I_ARG_66	NH1	I_ASP_86	OD1	3.902
2ZPK	I_ARG_66	NH1	I_ASP_86	OD2	2.665
2ZPK	I_ARG_66	NH2	I_ASP_86	OD1	2.915
2ZPK	I_ARG_66	NH2	I_ASP_86	OD2	3.188
2ZPK	I_LYS_143	NZ	M_GLU_125	OE2	2.672
2ZPK	I_LYS_208	NZ	M_GLU_124	OE2	3.137
32C2	A_ARG_24	NH1	A_ASP_74	OD2	3.409
32C2	A_ARG_65	NH1	A_GLU_83	OE1	3.875

32C2	A_ARG.65	NH1	A_ASP.86	OD1	3.841
32C2	A_ARG.65	NH1	A_ASP.86	OD2	3.487
32C2	A_ARG.65	NH2	A_GLU.83	OE1	2.370
32C2	A_ARG.65	NH2	A_GLU.83	OE2	3.913
32C2	A_ARG.65	NH2	A_ASP.86	OD1	3.622
32C2	A_LYS.106	NZ	A_GLU.108	OE2	3.990
32C2	A_LYS.152	NZ	A_GLU.198	OE1	2.795
32C2	A_LYS.152	NZ	A_GLU.198	OE2	3.245
32C2	A_ARG.158	NH2	A_GLU.188	OE2	2.691
32C2	A_LYS.186	NZ	A_GLU.190	OE1	3.548
32C2	A_HIS.192	NE2	A_ASP.154	OD2	3.916
32C2	A_LYS.202	NZ	A_ASP.113	OD1	3.644
32C2	A_LYS.202	NZ	A_ASP.113	OD2	3.444
32C2	B_ARG.39	NH1	B_ASP.90	OD1	2.671
32C2	B_ARG.39	NH2	B_GLU.47	OE1	3.125
32C2	B_ARG.39	NH2	B_ASP.90	OD1	3.482
32C2	B_ARG.67	NH1	B_ASP.90	OD1	3.556
32C2	B_ARG.67	NH1	B_ASP.90	OD2	3.694
32C2	B_ARG.67	NH2	B_ASP.90	OD1	3.933
32C2	B_ARG.67	NH2	B_ASP.90	OD2	2.676
32C2	B_LYS.76	NZ	B_ASP.73	OD1	3.680
32C2	B_LYS.76	NZ	B_ASP.73	OD2	2.879
32C2	B_LYS.214	NZ	A_GLU.126	OE1	3.056
32C2	B_LYS.214	NZ	A_GLU.126	OE2	3.702
3A67	L_ARG.61	NH2	L_GLU.81	OE2	2.941
3A67	L_ARG.61	NH2	L_ASP.82	OD1	2.851
3A67	L_ARG.61	NH2	L_ASP.82	OD2	3.509
3A67	L_LYS.103	NZ	L_GLU.105	OE2	3.056
3A67	H_ARG.38	NH1	H_ASP.89	OD1	2.872
3A67	H_ARG.38	NH2	H_GLU.46	OE1	2.908
3A67	H_ARG.38	NH2	H_ASP.89	OD1	3.548
3A67	H_ARG.66	NH1	H_ASP.89	OD1	3.735
3A67	H_ARG.66	NH1	H_ASP.89	OD2	3.043
3A67	H_ARG.66	NH2	H_ASP.89	OD1	2.999
3A67	H_ARG.66	NH2	H_ASP.89	OD2	3.634
3A67	Y_LYS.1	NZ	Y_GLU.7	OE2	3.083
3A67	Y_ARG.61	NH2	Y_ASP.48	OD2	3.340
3A67	Y_ARG.68	NH2	Y_ASP.66	OD2	3.751
3A67	Y_LYS.96	NZ	L_ASP.31	OD1	2.774
3A67	Y_LYS.96	NZ	L_ASP.31	OD2	3.727
3A67	Y_LYS.97	NZ	H_ASP.32	OD1	2.657
3A67	Y_LYS.97	NZ	H_ASP.99	OD1	3.291
3A67	Y_LYS.97	NZ	H_ASP.99	OD2	2.885
3A67	Y_ARG.125	NH1	Y_ASP.119	OD2	2.827
3A67	Y_ARG.125	NH2	Y_ASP.119	OD1	3.106
3A67	Y_ARG.125	NH2	Y_ASP.119	OD2	3.044
3A6B	L_ARG.61	NH2	L_GLU.81	OE2	2.699
3A6B	L_ARG.61	NH2	L_ASP.82	OD1	2.827
3A6B	L_ARG.61	NH2	L_ASP.82	OD2	3.489
3A6B	L_LYS.103	NZ	L_GLU.105	OE2	2.854
3A6B	H_ARG.38	NH1	H_ASP.89	OD1	2.881
3A6B	H_ARG.38	NH2	H_GLU.46	OE1	2.870
3A6B	H_ARG.38	NH2	H_ASP.89	OD1	3.597
3A6B	H_ARG.66	NH1	H_ASP.89	OD1	3.690
3A6B	H_ARG.66	NH1	H_ASP.89	OD2	3.008
3A6B	H_ARG.66	NH2	H_ASP.89	OD1	2.915
3A6B	H_ARG.66	NH2	H_ASP.89	OD2	3.568
3A6B	Y_LYS.1	NZ	Y_GLU.7	OE2	3.049

3A6B	Y_ARG_61	NH1	Y_ASP_48	OD1	3.308
3A6B	Y_ARG_61	NH1	Y_ASP_48	OD2	2.807
3A6B	Y_ARG_61	NH2	Y_ASP_48	OD2	3.969
3A6B	Y_LYS_96	NZ	L_ASP_32	OD1	2.734
3A6B	Y_LYS_97	NZ	H_ASP_32	OD1	2.700
3A6B	Y_LYS_97	NZ	H_ASP_32	OD2	3.941
3A6B	Y_LYS_97	NZ	H_ASP_99	OD1	2.956
3A6B	Y_LYS_97	NZ	H_ASP_99	OD2	3.259
3A6B	Y_ARG_125	NH1	Y_ASP_119	OD2	3.668
3A6B	Y_ARG_125	NH2	Y_ASP_119	OD1	3.613
3A6B	Y_ARG_125	NH2	Y_ASP_119	OD2	3.218
3A6C	L_ARG_61	NH1	L_GLU_81	OE2	3.920
3A6C	L_ARG_61	NH2	L_GLU_81	OE2	2.707
3A6C	L_ARG_61	NH2	L_ASP_82	OD1	2.812
3A6C	L_ARG_61	NH2	L_ASP_82	OD2	3.543
3A6C	L_LYS_103	NZ	L_GLU_105	OE2	3.380
3A6C	H_ARG_38	NH1	H_ASP_89	OD1	2.907
3A6C	H_ARG_38	NH2	H_GLU_46	OE1	2.827
3A6C	H_ARG_38	NH2	H_ASP_89	OD1	3.601
3A6C	H_ARG_66	NH1	H_ASP_89	OD1	3.604
3A6C	H_ARG_66	NH1	H_ASP_89	OD2	2.873
3A6C	H_ARG_66	NH2	H_ASP_89	OD1	2.870
3A6C	H_ARG_66	NH2	H_ASP_89	OD2	3.526
3A6C	Y_LYS_1	NZ	Y_GLU_7	OE1	3.880
3A6C	Y_LYS_1	NZ	Y_GLU_7	OE2	2.870
3A6C	Y_ARG_61	NH1	Y_ASP_48	OD2	2.954
3A6C	Y_ARG_61	NH2	Y_ASP_48	OD2	3.848
3A6C	Y_ARG_68	NH2	Y_ASP_66	OD2	3.805
3A6C	Y_LYS_97	NZ	H_ASP_32	OD1	2.672
3A6C	Y_LYS_97	NZ	H_ASP_32	OD2	3.916
3A6C	Y_LYS_97	NZ	H_ASP_99	OD1	2.965
3A6C	Y_LYS_97	NZ	H_ASP_99	OD2	3.291
3A6C	Y_ARG_125	NH1	Y_ASP_119	OD2	3.478
3A6C	Y_ARG_125	NH2	Y_ASP_119	OD1	3.773
3A6C	Y_ARG_125	NH2	Y_ASP_119	OD2	3.566
3AUV	A_ARG_72	NH2	A_GLU_92	OE2	3.439
3AUV	A_ARG_72	NH2	A_ASP_93	OD1	2.723
3AUV	A_ARG_72	NH2	A_ASP_93	OD2	3.631
3AUV	A_LYS_114	NZ	A_GLU_116	OE1	3.774
3AUV	A_LYS_114	NZ	A_GLU_116	OE2	3.679
3AUV	A_ARG_172	NH1	A_ASP_224	OD2	2.750
3AUV	A_ARG_172	NH2	A_GLU_180	OE1	2.793
3AUV	A_ARG_172	NH2	A_GLU_180	OE2	3.594
3AUV	A_ARG_172	NH2	A_ASP_224	OD2	3.992
3AUV	A_ARG_201	NH1	A_ASP_224	OD1	2.699
3AUV	A_ARG_201	NH1	A_ASP_224	OD2	3.899
3AUV	A_ARG_201	NH2	A_ASP_224	OD1	3.500
3AUV	A_ARG_201	NH2	A_ASP_224	OD2	3.246
3AUV	A_ARG_232	NH2	A_ASP_242	OD1	2.869
3AUV	A_ARG_232	NH2	A_ASP_242	OD2	3.766
3AUV	B_ARG_72	NH2	B_GLU_92	OE2	3.579
3AUV	B_ARG_72	NH2	B_ASP_93	OD1	2.590
3AUV	B_ARG_72	NH2	B_ASP_93	OD2	3.569
3AUV	B_LYS_114	NZ	B_GLU_116	OE1	3.722
3AUV	B_LYS_114	NZ	B_GLU_116	OE2	3.387
3AUV	B_ARG_172	NH1	B_ASP_224	OD2	2.806
3AUV	B_ARG_172	NH2	B_GLU_180	OE1	2.717
3AUV	B_ARG_172	NH2	B_GLU_180	OE2	3.567

3AUV	B_ARG_201	NH1	B_ASP_224	OD1	2.684
3AUV	B_ARG_201	NH1	B_ASP_224	OD2	3.823
3AUV	B_ARG_201	NH2	B_ASP_224	OD1	3.593
3AUV	B_ARG_201	NH2	B_ASP_224	OD2	3.291
3AUV	B_LYS_210	NZ	B_ASP_207	OD1	3.963
3AUV	B_ARG_232	NH2	B_ASP_242	OD1	2.862
3AUV	B_ARG_232	NH2	B_ASP_242	OD2	3.702
3AUV	C_ARG_72	NH2	C_GLU_92	OE2	3.470
3AUV	C_ARG_72	NH2	C_ASP_93	OD1	2.695
3AUV	C_ARG_72	NH2	C_ASP_93	OD2	3.642
3AUV	C_LYS_114	NZ	C_GLU_116	OE1	3.676
3AUV	C_LYS_114	NZ	C_GLU_116	OE2	3.581
3AUV	C_ARG_172	NH1	C_ASP_224	OD2	2.837
3AUV	C_ARG_172	NH2	C_GLU_180	OE1	2.666
3AUV	C_ARG_172	NH2	C_GLU_180	OE2	3.575
3AUV	C_ARG_201	NH1	C_ASP_224	OD1	2.642
3AUV	C_ARG_201	NH1	C_ASP_224	OD2	3.881
3AUV	C_ARG_201	NH2	C_ASP_224	OD1	3.488
3AUV	C_ARG_201	NH2	C_ASP_224	OD2	3.269
3AUV	C_ARG_232	NH2	C_ASP_242	OD1	2.909
3AUV	C_ARG_232	NH2	C_ASP_242	OD2	3.643
3AUV	D_ARG_72	NH2	D_GLU_92	OE2	3.526
3AUV	D_ARG_72	NH2	D_ASP_93	OD1	2.640
3AUV	D_ARG_72	NH2	D_ASP_93	OD2	3.608
3AUV	D_LYS_114	NZ	D_GLU_116	OE1	3.727
3AUV	D_LYS_114	NZ	D_GLU_116	OE2	3.600
3AUV	D_ARG_172	NH1	D_ASP_224	OD2	2.810
3AUV	D_ARG_172	NH2	D_GLU_180	OE1	2.707
3AUV	D_ARG_172	NH2	D_GLU_180	OE2	3.528
3AUV	D_ARG_201	NH1	D_ASP_224	OD1	2.734
3AUV	D_ARG_201	NH1	D_ASP_224	OD2	3.954
3AUV	D_ARG_201	NH2	D_ASP_224	OD1	3.560
3AUV	D_ARG_201	NH2	D_ASP_224	OD2	3.357
3AUV	D_ARG_232	NH2	D_ASP_242	OD1	2.882
3AUV	D_ARG_232	NH2	D_ASP_242	OD2	3.743
3AUV	E_ARG_72	NH2	E_GLU_92	OE2	3.531
3AUV	E_ARG_72	NH2	E_ASP_93	OD1	2.643
3AUV	E_ARG_72	NH2	E_ASP_93	OD2	3.543
3AUV	E_LYS_114	NZ	E_GLU_116	OE1	3.794
3AUV	E_LYS_114	NZ	E_GLU_116	OE2	3.627
3AUV	E_ARG_172	NH1	E_ASP_224	OD2	2.874
3AUV	E_ARG_172	NH2	E_GLU_180	OE1	2.698
3AUV	E_ARG_172	NH2	E_GLU_180	OE2	3.466
3AUV	E_ARG_201	NH1	E_ASP_224	OD1	2.747
3AUV	E_ARG_201	NH1	E_ASP_224	OD2	3.871
3AUV	E_ARG_201	NH2	E_ASP_224	OD1	3.622
3AUV	E_ARG_201	NH2	E_ASP_224	OD2	3.262
3AUV	E_ARG_232	NH2	E_ASP_242	OD1	2.876
3AUV	E_ARG_232	NH2	E_ASP_242	OD2	3.697
3AUV	F_ARG_72	NH2	F_GLU_92	OE2	3.450
3AUV	F_ARG_72	NH2	F_ASP_93	OD1	2.646
3AUV	F_ARG_72	NH2	F_ASP_93	OD2	3.561
3AUV	F_LYS_114	NZ	F_GLU_116	OE1	3.643
3AUV	F_LYS_114	NZ	F_GLU_116	OE2	3.465
3AUV	F_ARG_172	NH1	F_ASP_224	OD2	2.862
3AUV	F_ARG_172	NH2	F_GLU_180	OE1	2.639
3AUV	F_ARG_172	NH2	F_GLU_180	OE2	3.493
3AUV	F_ARG_201	NH1	F_ASP_224	OD1	2.716

3AUV	F_ARG_201	NH2	F_ASP_224	OD1	3.519
3AUV	F_ARG_201	NH2	F_ASP_224	OD2	3.349
3AUV	F_LYS_210	NZ	F_ASP_207	OD1	3.959
3AUV	F_ARG_232	NH2	F_ASP_242	OD1	2.985
3AUV	F_ARG_232	NH2	F_ASP_242	OD2	3.837
3B9K	L_ARG_61	NH1	L_GLU_81	OE2	3.453
3B9K	L_ARG_61	NH1	L_ASP_82	OD1	2.335
3B9K	L_ARG_61	NH1	L_ASP_82	OD2	3.046
3B9K	L_ARG_61	NH2	L_GLU_81	OE2	2.771
3B9K	L_LYS_149	NZ	L_GLU_195	OE1	3.690
3B9K	L_LYS_149	NZ	L_GLU_195	OE2	2.757
3B9K	L_HIS_189	ND1	L_ASP_151	OD2	2.589
3B9K	L_LYS_199	NZ	L_ASP_110	OD1	3.618
3B9K	H_ARG_38	NH1	H_ASP_86	OD1	2.944
3B9K	H_ARG_38	NH2	H_GLU_46	OE1	3.373
3B9K	H_ARG_38	NH2	H_ASP_86	OD1	3.659
3B9K	H_ARG_66	NH1	H_ASP_86	OD1	3.550
3B9K	H_ARG_66	NH2	H_ASP_86	OD1	3.185
3B9K	H_ARG_66	NH2	H_ASP_86	OD2	2.639
3B9K	H_HIS_172	NE2	H_ASP_167	OD1	3.568
3B9K	H_LYS_221	NZ	L_GLU_123	OE1	2.886
3B9K	A_ARG_8	NH1	A_GLU_6	OE2	3.916
3B9K	A_LYS_13	NZ	B_ASP_42	OD2	3.894
3B9K	B_LYS_17	NZ	B_GLU_72	OE1	3.264
3B9K	B_LYS_27	NZ	H_ASP_32	OD1	2.409
3B9K	B_ARG_35	NH2	B_ASP_92	OD2	2.954
3B9K	B_ARG_37	NH1	B_ASP_39	OD1	3.890
3B9K	B_ARG_37	NH2	B_GLU_46	OE1	3.384
3B9K	B_ARG_37	NH2	B_GLU_46	OE2	3.762
3B9K	B_ARG_37	NH2	B_ASP_64	OD1	3.954
3B9K	B_ARG_37	NH2	B_ASP_64	OD2	3.329
3B9K	B_LYS_43	NZ	B_GLU_36	OE2	3.566
3B9K	B_ARG_77	NH1	B_GLU_21	OE2	3.466
3B9K	B_ARG_77	NH2	L_ASP_92	OD1	3.184
3B9K	B_ARG_77	NH2	B_GLU_21	OE2	3.014
3B9K	B_ARG_78	NH2	L_ASP_92	OD1	2.834
3B9K	B_LYS_103	NZ	A_ASP_66	OD1	3.058
3B9K	C_ARG_	NH1	C_GLU_81	OE2	3.400
3B9K	C_ARG_	NH1	C_ASP_82	OD1	2.519
3B9K	C_ARG_	NH1	C_ASP_	OD2	2.958
3B9K	C_ARG_	NH2	C_GLU_81	OE2	2.927
3B9K	C_LYS_149	NZ	C_GLU_195	OE2	3.057
3B9K	C_LYS_183	NZ	C_GLU_187	OE1	2.738
3B9K	C_HIS_189	ND1	C_ASP_151	OD1	3.967
3B9K	C_HIS_189	ND1	C_ASP_151	OD2	2.217
3B9K	C_LYS_	NZ	C_ASP_	OD1	3.537
3B9K	C_LYS_	NZ	C_ASP_	OD2	2.778
3B9K	D_ARG_38	NH1	D_ASP_86	OD1	2.985
3B9K	D_ARG_38	NH2	D_GLU_46	OE1	3.027
3B9K	D_ARG_38	NH2	D_ASP_86	OD1	3.686
3B9K	D_ARG_66	NH1	D_ASP_86	OD1	3.146
3B9K	D_ARG_66	NH1	D_ASP_86	OD2	3.512
3B9K	D_ARG_66	NH2	D_ASP_86	OD1	3.576
3B9K	D_ARG_66	NH2	D_ASP_86	OD2	2.412
3B9K	D_ARG_96	NH1	D_GLU_97	OE2	2.918
3B9K	D_ARG_96	NH2	D_GLU_97	OE2	3.934
3B9K	D_HIS_172	NE2	D_ASP_167	OD1	2.867
3B9K	D_LYS_221	NZ	C_GLU_123	OE1	3.178

3B9K	E_ARG_8	NH1	E_GLU_27	OE1	3.719
3B9K	E_ARG_8	NH2	E_GLU_27	OE1	3.635
3B9K	E_LYS_	NZ	E_ASP_23	OD1	3.889
3B9K	F_LYS_27	NZ	D_ASP_32	OD1	2.318
3B9K	F_ARG_35	NH2	F_ASP_39	OD2	3.634
3B9K	F_ARG_35	NH2	F_ASP_92	OD2	2.801
3B9K	F_ARG_37	NH1	F_ASP_39	OD2	3.691
3B9K	F_ARG_37	NH2	F_GLU_46	OE1	3.350
3B9K	F_ARG_77	NH1	F_GLU_21	OE2	3.321
3B9K	F_ARG_77	NH2	C_ASP_92	OD1	2.984
3B9K	F_ARG_77	NH2	F_GLU_21	OE2	3.185
3B9K	F_ARG_78	NH2	C_ASP_92	OD1	3.141
3B9K	F_ARG_78	NH2	C_ASP_92	OD2	3.951
3B9K	F_LYS_103	NZ	E_ASP_	OD1	3.044
3BDY	H_ARG_38	NH1	H_ASP_86	OD1	2.999
3BDY	H_ARG_38	NH2	H_GLU_46	OE1	2.808
3BDY	H_ARG_38	NH2	H_GLU_46	OE2	3.622
3BDY	H_ARG_66	NH1	H_ASP_86	OD1	3.951
3BDY	H_ARG_66	NH1	H_ASP_86	OD2	3.006
3BDY	H_ARG_66	NH2	H_ASP_86	OD1	3.023
3BDY	H_ARG_66	NH2	H_ASP_86	OD2	3.512
3BDY	H_ARG_94	NH2	H_ASP_103	OD1	3.777
3BDY	H_ARG_94	NH2	H_ASP_103	OD2	3.008
3BDY	H_LYS_145	NZ	H_ASP_146	OD1	3.125
3BDY	H_LYS_145	NZ	H_ASP_146	OD2	3.665
3BDY	H_LYS_211	NZ	L_GLU_123	OE2	2.706
3BDY	L_ARG_24	NH1	L_ASP_70	OD1	2.932
3BDY	L_ARG_24	NH1	L_ASP_70	OD2	3.729
3BDY	L_ARG_27D	NH2	L_ASP_70	OD2	3.711
3BDY	L_ARG_61	NH2	L_GLU_81	OE1	3.501
3BDY	L_ARG_61	NH2	L_ASP_82	OD1	2.848
3BDY	L_ARG_61	NH2	L_ASP_82	OD2	3.523
3BDY	L_HIS_189	ND1	L_ASP_151	OD2	2.958
3BDY	V_ARG_56	NH1	V_GLU_38	OE1	3.008
3BDY	V_ARG_56	NH1	V_GLU_38	OE2	3.618
3BDY	V_ARG_56	NH2	V_GLU_38	OE1	3.690
3BDY	V_ARG_82	NH2	V_GLU_42	OE1	3.019
3BDY	V_ARG_82	NH2	V_GLU_42	OE2	3.920
3BDY	V_LYS_84	NZ	V_GLU_44	OE2	3.490
3BDY	V_LYS_	NZ	V_GLU_	OE1	2.740
3BDY	V_ARG_	NH1	V_GLU_	OE1	3.312
3BDY	V_ARG_	NH1	V_GLU_	OE2	3.557
3BE1	A_ARG_25	NH2	A_ASP_22	OD1	3.635
3BE1	A_ARG_25	NH2	A_ASP_22	OD2	3.334
3BE1	A_HIS_66	NE2	A_ASP_96	OD2	3.628
3BE1	A_ARG_81	NH2	A_GLU_57	OE1	3.307
3BE1	A_ARG_121	NH1	A_ASP_189	OD1	2.843
3BE1	A_ARG_121	NH1	A_ASP_189	OD2	3.507
3BE1	A_ARG_135	NH2	A_ASP_96	OD1	3.481
3BE1	A_ARG_135	NH2	A_ASP_96	OD2	3.295
3BE1	A_ARG_166	NH1	A_ASP_143	OD2	3.604
3BE1	A_ARG_166	NH2	A_ASP_143	OD1	3.395
3BE1	A_ARG_166	NH2	A_ASP_143	OD2	3.597
3BE1	A_HIS_171	ND1	A_GLU_185	OE1	2.686
3BE1	A_ARG_204	NH1	A_ASP_149	OD2	3.810
3BE1	A_ARG_204	NH2	A_GLU_125	OE1	3.119
3BE1	A_ARG_204	NH2	A_GLU_125	OE2	3.480
3BE1	A_HIS_215	ND1	A_GLU_216	OE2	3.902

3BE1	A_HIS_238	ND1	A_GLU_243	OE1	2.848
3BE1	A_HIS_238	ND1	A_GLU_243	OE2	3.970
3BE1	A_ARG_308	NH2	A_ASP_285	OD1	3.913
3BE1	A_HIS_327	NE2	A_GLU_341	OE2	3.469
3BE1	A_ARG_332	NH2	A_GLU_357	OE2	2.835
3BE1	A_LYS_346	NZ	A_GLU_382	OE1	3.395
3BE1	A_LYS_346	NZ	A_GLU_382	OE2	3.325
3BE1	A_LYS_347	NZ	A_GLU_299	OE1	3.844
3BE1	A_LYS_347	NZ	A_GLU_383	OE1	2.990
3BE1	A_LYS_347	NZ	A_GLU_383	OE2	3.026
3BE1	A_ARG_410	NH1	A_GLU_438	OE2	3.687
3BE1	A_ARG_410	NH2	A_GLU_383	OE1	3.367
3BE1	A_ARG_410	NH2	A_GLU_383	OE2	3.274
3BE1	A_ARG_412	NH1	A_GLU_299	OE1	3.591
3BE1	A_ARG_412	NH1	A_GLU_299	OE2	3.484
3BE1	A_ARG_437	NH1	A_GLU_438	OE1	3.301
3BE1	A_ARG_465	NH2	A_GLU_438	OE1	3.503
3BE1	A_ARG_477	NH1	A_GLU_485	OE1	3.451
3BE1	A_ARG_477	NH2	A_GLU_481	OE1	3.986
3BE1	A_ARG_477	NH2	A_GLU_485	OE1	3.615
3BE1	A_ARG_477	NH2	A_GLU_485	OE2	3.180
3BE1	A_ARG_514	NH2	A_GLU_531	OE1	3.183
3BE1	A_ARG_523	NH1	A_GLU_531	OE1	3.371
3BE1	A_ARG_523	NH1	A_GLU_531	OE2	3.636
3BE1	A_LYS_593	NZ	A_ASP_570	OD1	2.769
3BE1	A_LYS_593	NZ	A_ASP_570	OD2	2.849
3BE1	H_ARG_38	NH1	H_ASP_86	OD1	3.053
3BE1	H_ARG_38	NH2	H_GLU_46	OE1	3.297
3BE1	H_ARG_38	NH2	H_ASP_86	OD1	3.486
3BE1	H_ARG_50	NH1	A_ASP_560	OD2	3.215
3BE1	H_ARG_50	NH2	A_GLU_558	OE1	3.092
3BE1	H_ARG_50	NH2	A_GLU_558	OE2	3.263
3BE1	H_ARG_50	NH2	A_ASP_560	OD1	3.492
3BE1	H_ARG_50	NH2	A_ASP_560	OD2	3.175
3BE1	H_ARG_66	NH1	H_ASP_86	OD2	3.082
3BE1	H_ARG_66	NH2	H_ASP_86	OD1	3.252
3BE1	H_ARG_66	NH2	H_ASP_86	OD2	3.284
3BE1	H_ARG_94	NH2	H_ASP_103	OD1	3.969
3BE1	H_ARG_94	NH2	H_ASP_103	OD2	3.289
3BE1	L_ARG_24	NH1	L_ASP_70	OD1	3.044
3BE1	L_ARG_61	NH2	L_GLU_81	OE1	3.206
3BE1	L_ARG_61	NH2	L_ASP_82	OD1	2.979
3BE1	L_ARG_61	NH2	L_ASP_82	OD2	3.663
3BE1	L_LYS_149	NZ	L_GLU_195	OE2	2.739
3BE1	L_LYS_183	NZ	L_GLU_187	OE2	3.540
3BE1	L_LYS_188	NZ	L_ASP_185	OD1	3.780
3BE1	L_HIS_189	ND1	L_ASP_151	OD1	3.324
3BE1	L_HIS_189	ND1	L_ASP_151	OD2	2.626
3BE1	L_ARG_211	NH2	L_GLU_187	OE1	3.516
3BGF	S_ARG_342	NH2	S_ASP_385	OD1	3.676
3BGF	S_ARG_342	NH2	S_ASP_385	OD2	3.162
3BGF	S_ARG_426	NH1	H_ASP_56	OD1	3.504
3BGF	S_ARG_426	NH1	H_ASP_56	OD2	2.403
3BGF	S_LYS_439	NZ	S_ASP_480	OD1	3.797
3BGF	S_LYS_439	NZ	A_ASP_480	OD2	3.161
3BGF	S_ARG_441	NH2	S_ASP_454	OD1	2.963
3BGF	S_ARG_444	NH2	S_GLU_452	OE2	3.267
3BGF	S_ARG_444	NH2	S_ASP_454	OD2	3.815

3BGF	S_LYS_447	NZ	S_ASP_407	OD1	3.987
3BGF	S_LYS_447	NZ	S_ASP_407	OD2	3.876
3BGF	S_ARG_449	NH2	S_GLU_452	OE1	3.535
3BGF	S_ARG_495	NH2	S_ASP_429	OD1	3.362
3BGF	S_ARG_495	NH2	S_ASP_429	OD2	3.615
3BGF	A_ARG_342	NH2	A_ASP_385	OD1	3.423
3BGF	A_ARG_342	NH2	A_ASP_385	OD2	2.961
3BGF	A_LYS_390	NZ	A_ASP_393	OD1	3.583
3BGF	A_LYS_390	NZ	A_ASP_393	OD2	3.966
3BGF	A_LYS_439	NZ	S_ASP_480	OD2	2.520
3BGF	A_LYS_439	NZ	A_ASP_480	OD1	3.180
3BGF	A_ARG_441	NH2	A_ASP_454	OD1	3.440
3BGF	A_ARG_444	NH2	A_GLU_452	OE2	3.371
3BGF	A_ARG_444	NH2	A_ASP_454	OD2	3.730
3BGF	A_LYS_447	NZ	A_ASP_407	OD1	2.877
3BGF	A_LYS_447	NZ	A_ASP_407	OD2	2.805
3BGF	A_ARG_495	NH2	A_ASP_429	OD1	3.108
3BGF	A_ARG_495	NH2	A_ASP_429	OD2	2.922
3BGF	L_ARG_24	NH2	L_ASP_70	OD1	3.258
3BGF	L_ARG_24	NH2	L_ASP_70	OD2	2.893
3BGF	L_ARG_46	NH1	L_ASP_55	OD1	3.016
3BGF	L_ARG_46	NH1	L_ASP_55	OD2	3.557
3BGF	L_ARG_61	NH1	L_GLU_79	OE1	3.984
3BGF	L_ARG_61	NH1	L_GLU_79	OE2	3.405
3BGF	L_ARG_61	NH2	L_ASP_82	OD1	2.650
3BGF	L_ARG_61	NH2	L_ASP_82	OD2	2.907
3BGF	L_ARG_66	NH2	L_GLU_28	OE2	2.738
3BGF	L_LYS_149	NZ	L_GLU_195	OE1	3.683
3BGF	L_LYS_149	NZ	L_GLU_195	OE2	3.129
3BGF	L_HIS_189	ND1	L_ASP_151	OD1	2.696
3BGF	H_ARG_33	NH1	H_ASP_56	OD2	3.848
3BGF	H_HIS_35	NE2	H_GLU_95	OE1	2.884
3BGF	H_LYS_38	NZ	H_ASP_86	OD1	3.661
3BGF	H_LYS_62	NZ	H_GLU_46	OE1	2.635
3BGF	H_LYS_62	NZ	H_GLU_46	OE2	3.712
3BGF	H_LYS_66	NZ	H_ASP_86	OD1	3.553
3BGF	H_LYS_66	NZ	H_ASP_86	OD2	2.671
3BGF	H_ARG_94	NH1	H_ASP_101	OD1	2.347
3BGF	H_ARG_94	NH1	H_ASP_101	OD2	3.381
3BGF	H_LYS_210	NZ	L_GLU_123	OE1	3.997
3BGF	H_LYS_211	NZ	H_GLU_213	OE2	3.764
3BGF	C_ARG_24	NH2	C_ASP_70	OD1	3.766
3BGF	C_ARG_46	NH1	C_ASP_55	OD1	2.965
3BGF	C_ARG_61	NH1	C_GLU_79	OE1	3.352
3BGF	C_ARG_61	NH1	C_GLU_79	OE2	3.278
3BGF	C_ARG_61	NH2	C_GLU_81	OE2	3.045
3BGF	C_ARG_61	NH2	C_ASP_82	OD1	2.379
3BGF	C_ARG_61	NH2	C_ASP_82	OD2	2.905
3BGF	C_ARG_66	NH2	C_GLU_28	OE1	3.607
3BGF	C_ARG_66	NH2	C_GLU_28	OE2	2.938
3BGF	C_LYS_142	NZ	C_GLU_105	OE1	3.341
3BGF	C_LYS_149	NZ	C_GLU_195	OE1	3.352
3BGF	C_LYS_149	NZ	C_GLU_195	OE2	3.898
3BGF	C_ARG_155	NH2	C_GLU_185	OE2	3.481
3BGF	C_LYS_199	NZ	C_ASP_110	OD2	3.825
3BGF	B_HIS_35	NE2	B_GLU_95	OE1	2.642
3BGF	B_LYS_38	NZ	B_ASP_86	OD1	3.591
3BGF	B_LYS_62	NZ	B_GLU_46	OE1	2.547

3BGF	B.LYS.62	NZ	B.GLU.46	OE2	3.280
3BGF	B.LYS.66	NZ	B.ASP.86	OD1	3.814
3BGF	B.LYS.66	NZ	B.ASP.86	OD2	2.805
3BGF	B.ARG.94	NH1	B.ASP.101	OD1	2.357
3BGF	B.ARG.94	NH1	B.ASP.101	OD2	2.930
3BGF	B.ARG.100B	NH1	B.ASP.101	OD1	3.816
3BIK	A.ARG.84	NH1	A.ASP.108	OD1	2.911
3BIK	A.ARG.84	NH1	A.ASP.108	OD2	3.517
3BIK	A.ARG.84	NH2	A.ASP.108	OD1	3.587
3BIK	A.ARG.84	NH2	A.ASP.108	OD2	2.826
3BIK	A.LYS.105	NZ	A.ASP.103	OD2	3.863
3BIK	A.ARG.113	NH2	B.GLU.136	OE2	3.149
3BIK	A.LYS.124	NZ	A.ASP.122	OD1	3.019
3BIK	A.LYS.124	NZ	A.ASP.122	OD2	3.912
3BIK	A.ARG.125	NH2	B.GLU.136	OE1	3.033
3BIK	A.ARG.125	NH2	B.GLU.136	OE2	3.001
3BIK	A.ARG.198	NH1	A.GLU.152	OE1	3.772
3BIK	A.ARG.198	NH2	A.GLU.152	OE1	3.590
3BIK	A.ARG.213	NH1	A.GLU.218	OE2	3.954
3BIK	A.ARG.213	NH2	A.GLU.218	OE1	3.723
3BIK	A.ARG.213	NH2	A.GLU.218	OE2	3.505
3BIK	A.HIS.220	NE2	A.GLU.218	OE1	3.627
3BIK	A.HIS.220	NE2	A.GLU.218	OE2	3.391
3BIK	B.ARG.33	NH1	B.GLU.135	OE2	3.354
3BIK	B.ARG.94	NH1	B.ASP.117	OD1	3.896
3BIK	B.ARG.94	NH1	B.ASP.117	OD2	2.841
3BIK	B.ARG.94	NH2	B.ASP.92	OD2	2.969
3BIK	B.ARG.94	NH2	B.ASP.117	OD1	3.201
3BIK	B.ARG.94	NH2	B.ASP.117	OD2	3.582
3BIK	B.ARG.103	NH2	B.GLU.61	OE1	3.685
3BIK	B.HIS.104	NE2	B.ASP.105	OD1	3.734
3BIK	C.ARG.33	NH2	C.GLU.135	OE2	3.450
3BIK	C.ARG.94	NH1	C.ASP.117	OD1	3.747
3BIK	C.ARG.94	NH1	C.ASP.117	OD2	2.682
3BIK	C.ARG.94	NH2	C.ASP.92	OD2	3.003
3BIK	C.ARG.94	NH2	C.ASP.117	OD1	2.982
3BIK	C.ARG.94	NH2	C.ASP.117	OD2	3.409
3BIK	C.HIS.104	ND1	C.ASP.105	OD1	2.573
3BIK	C.HIS.104	ND1	C.ASP.105	OD2	3.992
3BIK	C.ARG.114	NH1	C.ASP.92	OD2	3.856
3BIK	C.ARG.115	NH1	C.GLU.146	OE1	3.596
3BIK	C.HIS.129	NE2	C.ASP.62	OD1	3.754
3BIS	A.ARG.84	NH1	A.ASP.108	OD1	2.733
3BIS	A.ARG.84	NH1	A.ASP.108	OD2	3.411
3BIS	A.ARG.84	NH2	A.ASP.108	OD1	3.339
3BIS	A.ARG.84	NH2	A.ASP.108	OD2	2.608
3BIS	A.LYS.105	NZ	A.GLU.187	OE1	3.664
3BIS	A.LYS.124	NZ	A.ASP.122	OD1	3.773
3BIS	A.ARG.140	NH2	A.GLU.152	OE1	3.939
3BIS	A.ARG.186	NH1	A.GLU.158	OE1	2.989
3BIS	A.ARG.186	NH1	A.GLU.158	OE2	3.114
3BIS	A.LYS.189	NZ	A.GLU.188	OE1	3.362
3BIS	A.ARG.198	NH1	A.GLU.150	OE1	3.697
3BIS	A.ARG.198	NH1	A.GLU.150	OE2	2.793
3BIS	A.ARG.198	NH2	A.GLU.152	OE2	2.965
3BIS	A.ARG.212	NH2	A.GLU.217	OE1	3.792
3BIS	A.HIS.220	NE2	A.GLU.218	OE1	2.735
3BIS	B.ARG.84	NH1	B.ASP.108	OD1	3.434

3BIS	B_ARG_84	NH1	B_ASP_108	OD2	3.455
3BIS	B_ARG_84	NH2	B_ASP_108	OD2	2.983
3BIS	B_LYS_105	NZ	B_GLU_188	OE2	3.684
3BIS	B_ARG_113	NH2	B_GLU_58	OE1	3.749
3BIS	B_LYS_124	NZ	B_ASP_122	OD1	3.846
3BIS	B_ARG_140	NH2	B_GLU_152	OE2	3.790
3BIS	B_ARG_198	NH1	B_GLU_150	OE1	2.555
3BIS	B_ARG_212	NH2	B_GLU_164	OE1	3.367
3BIS	B_ARG_213	NH2	B_GLU_218	OE2	3.315
3BKY	H_LYS_38	NZ	H_ASP_90	OD1	3.615
3BKY	H_LYS_63	NZ	H_GLU_46	OE1	3.943
3BKY	H_LYS_63	NZ	H_GLU_46	OE2	3.735
3BKY	H_LYS_67	NZ	H_ASP_90	OD2	2.780
3BKY	H_ARG_98	NH1	H_ASP_110	OD1	3.350
3BKY	H_ARG_98	NH2	H_ASP_110	OD1	3.826
3BKY	H_LYS_138	NZ	L_GLU_212	OE2	2.743
3BKY	H_LYS_152	NZ	H_ASP_153	OD1	3.472
3BKY	H_LYS_152	NZ	H_ASP_153	OD2	3.466
3BKY	L_ARG_60	NH2	L_GLU_80	OE2	3.597
3BKY	L_ARG_60	NH2	L_ASP_81	OD1	2.516
3BKY	L_ARG_60	NH2	L_ASP_81	OD2	3.432
3BKY	L_ARG_76	NH1	L_GLU_78	OE1	2.817
3BKY	L_LYS_102	NZ	L_GLU_164	OE1	3.978
3BKY	L_LYS_182	NZ	L_GLU_186	OE1	3.284
3BKY	L_LYS_187	NZ	L_ASP_184	OD1	3.336
3BKY	L_HIS_188	ND1	L_ASP_150	OD2	2.994
3BO8	A_HIS_3	ND1	A_ASP_29	OD1	3.478
3BO8	A_HIS_3	ND1	A_ASP_29	OD2	2.703
3BO8	A_ARG_6	NH1	A_ASP_102	OD1	2.861
3BO8	A_ARG_6	NH2	A_ASP_102	OD1	2.772
3BO8	A_ARG_6	NH2	A_ASP_102	OD2	3.556
3BO8	A_ARG_14	NH1	A_ASP_39	OD1	3.690
3BO8	A_ARG_14	NH1	A_ASP_39	OD2	2.892
3BO8	A_ARG_14	NH2	A_ASP_39	OD1	3.076
3BO8	A_ARG_14	NH2	A_ASP_39	OD2	3.735
3BO8	A_ARG_21	NH1	A_ASP_39	OD2	3.805
3BO8	A_ARG_21	NH2	A_ASP_37	OD1	3.686
3BO8	A_ARG_21	NH2	A_ASP_37	OD2	2.860
3BO8	A_ARG_35	NH1	A_ASP_37	OD2	3.901
3BO8	A_ARG_35	NH1	B_ASP_53	OD1	3.541
3BO8	A_ARG_35	NH2	A_GLU_46	OE2	3.239
3BO8	A_ARG_48	NH1	B_ASP_53	OD1	3.101
3BO8	A_ARG_48	NH1	B_ASP_53	OD2	3.041
3BO8	A_ARG_48	NH2	B_ASP_53	OD1	3.771
3BO8	A_ARG_48	NH2	B_ASP_53	OD2	3.368
3BO8	A_HIS_70	NE2	A_ASP_74	OD1	3.486
3BO8	A_HIS_70	NE2	A_ASP_74	OD2	3.411
3BO8	A_ARG_75	NH1	A_GLU_19	OE1	2.819
3BO8	A_HIS_93	ND1	A_ASP_119	OD1	3.501
3BO8	A_HIS_93	ND1	A_ASP_119	OD2	2.724
3BO8	A_ARG_111	NH2	A_GLU_128	OE1	3.927
3BO8	A_ARG_114	NH2	A_ASP_116	OD1	3.531
3BO8	A_ARG_114	NH2	A_ASP_116	OD2	3.063
3BO8	A_LYS_144	NZ	A_GLU_148	OE1	3.974
3BO8	A_LYS_144	NZ	A_GLU_148	OE2	2.691
3BO8	A_ARG_156	NH1	C_ASP_3	OD1	3.842
3BO8	A_ARG_156	NH1	C_ASP_3	OD2	2.711
3BO8	A_ARG_163	NH1	A_ASP_166	OD2	3.922

3BO8	A_ARG_163	NH2	C_GLU_1	OE1	3.484
3BO8	A_ARG_163	NH2	C_GLU_1	OE2	2.848
3BO8	A_ARG_170	NH1	C_GLU_1	OE2	2.801
3BO8	A_ARG_170	NH2	A_GLU_55	OE1	3.555
3BO8	A_ARG_170	NH2	A_GLU_55	OE2	3.453
3BO8	A_ARG_170	NH2	C_GLU_1	OE2	3.023
3BO8	A_LYS_176	NZ	A_GLU_173	OE2	3.954
3BO8	A_HIS_191	NE2	A_GLU_254	OE2	2.780
3BO8	A_HIS_192	NE2	B_ASP_98	OD1	3.566
3BO8	A_HIS_192	NE2	B_ASP_98	OD2	3.950
3BO8	A_ARG_256	NH1	A_GLU_253	OE1	2.918
3BO8	A_ARG_256	NH2	A_ASP_220	OD1	3.803
3BO8	A_ARG_256	NH2	A_ASP_220	OD2	2.636
3BO8	B_LYS_75	NZ	B_GLU_74	OE1	3.603
3BO8	B_ARG_81	NH2	B_ASP_38	OD2	2.762
3BT2	A_HIS_29	NE2	A_ASP_12	OD1	2.667
3BT2	A_HIS_29	NE2	A_ASP_12	OD2	2.134
3BT2	A_HIS_41	NE2	A_ASP_12	OD1	3.088
3BT2	A_HIS_41	NE2	A_ASP_12	OD2	2.030
3BT2	A_ARG_69	NH2	A_ASP_65	OD2	3.423
3BT2	A_HIS_87	ND1	U_ASP_11	OD2	3.629
3BT2	A_ARG_88	NH1	A_ASP_90	OD1	3.618
3BT2	A_ARG_88	NH1	A_ASP_90	OD2	3.108
3BT2	A_ARG_108	NH1	A_ASP_106	OD1	3.445
3BT2	A_ARG_108	NH1	A_ASP_106	OD2	2.718
3BT2	A_ARG_108	NH2	A_ASP_106	OD2	3.817
3BT2	A_ARG_110	NH2	A_GLU_125	OE1	3.432
3BT2	L_LYS_53	NZ	L_GLU_50	OE1	2.553
3BT2	L_ARG_61	NH1	L_GLU_79	OE1	2.871
3BT2	L_ARG_61	NH1	L_GLU_79	OE2	3.194
3BT2	L_ARG_61	NH2	L_GLU_79	OE1	3.460
3BT2	L_ARG_61	NH2	L_GLU_81	OE2	3.022
3BT2	L_ARG_61	NH2	L_ASP_82	OD1	3.009
3BT2	L_ARG_61	NH2	L_ASP_82	OD2	3.824
3BT2	L_LYS_103	NZ	L_ASP_164	OD1	3.404
3BT2	L_LYS_148	NZ	L_GLU_194	OE1	3.204
3BT2	L_LYS_148	NZ	L_GLU_194	OE2	3.996
3BT2	L_ARG_154	NH1	L_GLU_184	OE1	3.573
3BT2	L_ARG_154	NH1	L_GLU_184	OE2	2.970
3BT2	L_ARG_154	NH2	L_GLU_184	OE1	2.853
3BT2	L_ARG_154	NH2	L_GLU_184	OE2	3.786
3BT2	L_ARG_187	NH1	L_ASP_183	OD1	3.352
3BT2	L_HIS_188	ND1	L_ASP_150	OD2	2.836
3BT2	H_ARG_40	NH1	H_GLU_85	OE1	3.704
3BT2	H_ARG_40	NH2	H_GLU_85	OE2	3.856
3BT2	H_LYS_64	NZ	H_GLU_61	OE1	2.698
3BT2	H_LYS_64	NZ	H_GLU_61	OE2	3.977
3BT2	H_LYS_66	NZ	H_ASP_86	OD1	3.311
3BT2	H_LYS_66	NZ	H_ASP_86	OD2	2.587
3BT2	H_ARG_94	NH2	H_ASP_101	OD1	3.593
3BT2	H_ARG_94	NH2	H_ASP_101	OD2	2.737
3BT2	H_HIS_98	ND1	L_GLU_50	OE1	2.845
3BT2	H_HIS_98	ND1	L_GLU_50	OE2	2.191
3BT2	H_HIS_98	NE2	L_GLU_50	OE1	3.301
3BT2	H_HIS_98	NE2	L_GLU_50	OE2	3.904
3BT2	H_LYS_203	NZ	L_GLU_122	OE2	3.715
3BT2	U_ARG_2	NH2	U_ASP_74	OD2	3.379
3BT2	U_LYS_7	NZ	U_ASP_11	OD1	3.738

3BT2	U_ARG_25	NH1	U_GLU_42	OE2	3.052
3BT2	U_ARG_25	NH2	U_GLU_42	OE2	3.321
3BT2	U_LYS_50	NZ	U_ASP_254	OD2	2.962
3BT2	U_ARG_53	NH1	U_ASP_254	OD2	3.811
3BT2	U_ARG_91	NH1	B_ASP_22	OD1	3.502
3BT2	U_ARG_91	NH1	B_ASP_22	OD2	3.574
3BT2	U_ARG_91	NH2	B_ASP_22	OD1	3.066
3BT2	U_HIS_128	ND1	U_GLU_183	OE1	3.844
3BT2	U_HIS_128	ND1	U_GLU_183	OE2	3.947
3BT2	U_HIS_128	NE2	U_GLU_183	OE1	2.249
3BT2	U_HIS_128	NE2	U_GLU_183	OE2	1.923
3BT2	U_HIS_143	NE2	U_GLU_183	OE1	3.609
3BT2	U_HIS_143	NE2	U_GLU_183	OE2	1.958
3BT2	U_ARG_145	NH2	U_ASP_124	OD2	3.397
3BT2	U_LYS_175	NZ	U_GLU_94	OE1	3.795
3BT2	U_ARG_192	NH1	H_GLU_58	OE2	2.836
3BT2	U_HIS_260	ND1	U_ASP_262	OD1	3.731
3BZ4	A_LYS_27	NZ	E_ASP_1	OD1	3.348
3BZ4	A_LYS_27	NZ	E_ASP_1	OD2	3.551
3BZ4	A_HIS_27D	ND1	A_ASP_28	OD1	3.339
3BZ4	A_HIS_27D	ND1	A_ASP_28	OD2	3.472
3BZ4	A_ARG_61	NH1	A_ASP_82	OD1	3.791
3BZ4	A_ARG_61	NH1	A_ASP_82	OD2	2.748
3BZ4	A_ARG_61	NH2	A_GLU_79	OE1	3.444
3BZ4	A_ARG_61	NH2	A_GLU_81	OE2	3.683
3BZ4	A_ARG_61	NH2	A_ASP_82	OD1	2.925
3BZ4	A_ARG_61	NH2	A_ASP_82	OD2	3.346
3BZ4	A_ARG_96	NH2	B_GLU_50	OE1	3.591
3BZ4	A_ARG_96	NH2	B_GLU_50	OE2	2.914
3BZ4	A_LYS_147	NZ	A_GLU_154	OE1	3.729
3BZ4	A_LYS_149	NZ	A_GLU_195	OE1	3.803
3BZ4	A_LYS_149	NZ	A_GLU_195	OE2	2.957
3BZ4	A_ARG_155	NH1	A_GLU_185	OE1	3.022
3BZ4	A_ARG_188	NH2	A_ASP_184	OD1	2.966
3BZ4	A_ARG_188	NH2	A_ASP_184	OD2	3.794
3BZ4	A_HIS_189	ND1	A_ASP_151	OD2	3.568
3BZ4	B_ARG_38	NH1	B_ASP_86	OD1	2.836
3BZ4	B_ARG_38	NH2	B_GLU_46	OE1	3.315
3BZ4	B_ARG_38	NH2	B_GLU_46	OE2	3.392
3BZ4	B_ARG_38	NH2	B_ASP_86	OD1	3.736
3BZ4	B_ARG_52	NH2	B_GLU_50	OE2	2.961
3BZ4	B_LYS_64	NZ	B_GLU_61	OE1	2.578
3BZ4	B_LYS_64	NZ	B_GLU_61	OE2	3.962
3BZ4	B_LYS_66	NZ	B_ASP_86	OD1	3.832
3BZ4	B_LYS_66	NZ	B_ASP_86	OD2	2.772
3BZ4	B_ARG_71	NH2	B_ASP_73	OD1	3.536
3BZ4	B_LYS_75	NZ	B_ASP_72	OD2	3.736
3BZ4	B_LYS_210	NZ	A_GLU_123	OE2	2.839
3BZ4	C_LYS_27	NZ	C_GLU_93	OE1	2.862
3BZ4	C_LYS_27	NZ	C_GLU_93	OE2	3.387
3BZ4	C_HIS_27D	ND1	C_ASP_28	OD1	3.351
3BZ4	C_HIS_27D	ND1	C_ASP_28	OD2	3.496
3BZ4	C_LYS_39	NZ	C_GLU_81	OE2	3.178
3BZ4	C_ARG_61	NH1	C_ASP_82	OD1	3.875
3BZ4	C_ARG_61	NH1	C_ASP_82	OD2	2.759
3BZ4	C_ARG_61	NH2	C_GLU_79	OE1	3.734
3BZ4	C_ARG_61	NH2	C_GLU_79	OE2	3.949
3BZ4	C_ARG_61	NH2	C_ASP_82	OD1	3.042

3BZ4	C_ARG_61	NH2	C_ASP_82	OD2	3.345
3BZ4	C_ARG_96	NH2	D_GLU_50	OE1	3.615
3BZ4	C_ARG_96	NH2	D_GLU_50	OE2	2.938
3BZ4	C_LYS_103	NZ	C_ASP_165	OD1	3.993
3BZ4	C_LYS_147	NZ	C_GLU_195	OE1	3.076
3BZ4	C_LYS_149	NZ	C_GLU_195	OE2	2.853
3BZ4	C_ARG_155	NH1	C_GLU_185	OE2	3.198
3BZ4	C_ARG_155	NH2	C_GLU_185	OE1	2.972
3BZ4	C_ARG_155	NH2	C_GLU_185	OE2	3.144
3BZ4	C_HIS_189	ND1	C_ASP_151	OD2	3.072
3BZ4	D_LYS_3	NZ	D_GLU_5	OE1	3.731
3BZ4	D_ARG_38	NH1	D_ASP_86	OD1	2.733
3BZ4	D_ARG_38	NH2	D_GLU_46	OE1	3.389
3BZ4	D_ARG_38	NH2	D_GLU_46	OE2	3.315
3BZ4	D_ARG_38	NH2	D_ASP_86	OD1	3.699
3BZ4	D_ARG_52	NH2	D_GLU_50	OE2	2.968
3BZ4	D_ARG_71	NH2	D_ASP_73	OD1	3.463
3BZ4	D_ARG_83	NH1	D_GLU_85	OE2	3.445
3BZ4	D_ARG_83	NH2	D_GLU_85	OE2	3.957
3BZ4	D_ARG_83	NH2	D_ASP_86	OD1	2.967
3BZ4	D_ARG_83	NH2	D_ASP_86	OD2	3.511
3BZ4	D_LYS_210	NZ	C_GLU_123	OE2	2.929
3BZ4	E_LYS_27	NZ	E_GLU_93	OE1	2.598
3BZ4	E_LYS_27	NZ	E_GLU_93	OE2	3.386
3BZ4	E_HIS_27D	ND1	E_ASP_28	OD1	3.329
3BZ4	E_HIS_27D	ND1	E_ASP_28	OD2	3.369
3BZ4	E_ARG_61	NH1	E_ASP_82	OD1	3.767
3BZ4	E_ARG_61	NH1	E_ASP_82	OD2	2.681
3BZ4	E_ARG_61	NH2	E_GLU_79	OE1	3.679
3BZ4	E_ARG_61	NH2	E_GLU_79	OE2	3.909
3BZ4	E_ARG_61	NH2	E_ASP_82	OD1	2.988
3BZ4	E_ARG_61	NH2	E_ASP_82	OD2	3.375
3BZ4	E_ARG_96	NH2	F_GLU_50	OE1	3.659
3BZ4	E_ARG_96	NH2	F_GLU_50	OE2	3.062
3BZ4	E_LYS_103	NZ	E_ASP_165	OD1	3.694
3BZ4	E_LYS_142	NZ	E_GLU_105	OE1	2.683
3BZ4	E_LYS_147	NZ	E_GLU_154	OE1	3.191
3BZ4	E_LYS_149	NZ	E_GLU_195	OE2	3.492
3BZ4	E_ARG_155	NH1	E_GLU_185	OE2	2.852
3BZ4	E_ARG_155	NH2	E_GLU_185	OE1	3.247
3BZ4	E_ARG_155	NH2	E_GLU_185	OE2	3.385
3BZ4	E_LYS_183	NZ	E_GLU_187	OE1	3.938
3BZ4	E_ARG_188	NH1	E_ASP_184	OD1	2.897
3BZ4	E_HIS_189	ND1	E_ASP_151	OD2	2.915
3BZ4	E_LYS_199	NZ	E_ASP_110	OD2	3.617
3BZ4	F_ARG_38	NH1	F_ASP_86	OD1	2.816
3BZ4	F_ARG_38	NH2	F_GLU_46	OE1	3.339
3BZ4	F_ARG_38	NH2	F_GLU_46	OE2	3.116
3BZ4	F_ARG_38	NH2	F_ASP_86	OD1	3.767
3BZ4	F_ARG_52	NH2	F_GLU_50	OE2	2.956
3BZ4	F_LYS_66	NZ	F_ASP_86	OD1	3.548
3BZ4	F_LYS_66	NZ	F_ASP_86	OD2	2.726
3BZ4	F_ARG_71	NH2	F_ASP_73	OD1	3.320
3BZ4	F_LYS_75	NZ	F_ASP_72	OD2	3.820
3BZ4	F_LYS_210	NZ	E_GLU_123	OE2	2.855
3BZ4	G_LYS_27	NZ	G_GLU_93	OE1	3.193
3BZ4	G_LYS_27	NZ	G_GLU_93	OE2	3.324
3BZ4	G_HIS_27D	ND1	G_ASP_28	OD1	3.438

3BZ4	G_HIS_27D	ND1	G_ASP_28	OD2	3.691
3BZ4	G_LYS_39	NZ	G_GLU_81	OE2	3.982
3BZ4	G_ARG_61	NH1	G_ASP_82	OD1	3.687
3BZ4	G_ARG_61	NH1	G_ASP_82	OD2	2.777
3BZ4	G_ARG_61	NH2	G_GLU_79	OE1	3.890
3BZ4	G_ARG_61	NH2	G_GLU_81	OE2	3.793
3BZ4	G_ARG_61	NH2	G_ASP_82	OD1	3.189
3BZ4	G_ARG_61	NH2	G_ASP_82	OD2	3.680
3BZ4	G_ARG_96	NH2	H_GLU_50	OE1	3.659
3BZ4	G_ARG_96	NH2	H_GLU_50	OE2	3.021
3BZ4	G_LYS_147	NZ	C_GLU_154	OE1	3.559
3BZ4	G_LYS_149	NZ	G_GLU_195	OE1	3.699
3BZ4	G_LYS_149	NZ	G_GLU_195	OE2	3.854
3BZ4	G_ARG_188	NH1	G_ASP_184	OD1	3.650
3BZ4	G_HIS_189	ND1	G_ASP_151	OD2	3.087
3BZ4	G_LYS_199	NZ	G_ASP_110	OD2	3.816
3BZ4	H_ARG_38	NH1	H_ASP_86	OD1	2.822
3BZ4	H_ARG_38	NH2	H_GLU_46	OE1	3.285
3BZ4	H_ARG_38	NH2	H_GLU_46	OE2	3.289
3BZ4	H_ARG_38	NH2	H_ASP_86	OD1	3.691
3BZ4	H_ARG_52	NH2	H_GLU_50	OE2	3.000
3BZ4	H_LYS_66	NZ	H_ASP_86	OD1	3.582
3BZ4	H_LYS_66	NZ	H_ASP_86	OD2	2.709
3BZ4	H_ARG_71	NH2	H_ASP_73	OD1	3.418
3C09	L_ARG_60	NH2	L_ASP_81	OD1	3.198
3C09	L_ARG_60	NH2	L_ASP_81	OD2	3.773
3C09	L_HIS_93	NE2	D_ASP_434	OD1	2.739
3C09	L_HIS_93	NE2	D_ASP_434	OD2	3.466
3C09	L_HIS_188	ND1	L_ASP_150	OD1	3.925
3C09	H_HIS_32	NE2	H_ASP_100	OD2	3.604
3C09	H_HIS_32	NE2	H_ASP_102	OD1	3.701
3C09	H_ARG_38	NH2	H_GLU_46	OE1	2.766
3C09	H_ARG_38	NH2	H_GLU_46	OE2	3.957
3C09	H_ARG_57	NH2	D_GLU_431	OE1	3.682
3C09	H_LYS_151	NZ	H_ASP_152	OD2	3.689
3C09	A_HIS_346	NE2	A_ASP_344	OD2	3.992
3C09	A_HIS_394	NE2	A_ASP_369	OD1	3.580
3C09	A_ARG_403	NH1	A_GLU_376	OE1	2.815
3C09	A_ARG_403	NH1	A_GLU_376	OE2	3.396
3C09	A_LYS_407	NZ	A_ASP_434	OD2	3.026
3C09	A_ARG_427	NH1	A_GLU_397	OE1	3.943
3C09	A_ARG_427	NH2	A_ASP_392	OD2	3.700
3C09	A_ARG_427	NH2	A_ASP_498	OD1	3.376
3C09	A_LYS_454	NZ	C_ASP_100	OD1	2.467
3C09	A_LYS_463	NZ	B_ASP_49	OD2	2.856
3C09	B_ARG_60	NH2	B_ASP_81	OD1	2.668
3C09	B_ARG_60	NH2	B_ASP_81	OD2	3.698
3C09	B_HIS_93	NE2	A_ASP_434	OD1	2.346
3C09	C_LYS_12	NZ	C_GLU_10	OE1	3.298
3C09	C_HIS_32	NE2	C_ASP_102	OD1	3.417
3C09	C_HIS_35	ND1	C_GLU_50	OE2	3.377
3C09	C_HIS_35	NE2	C_GLU_50	OE2	3.892
3C09	C_ARG_38	NH1	C_ASP_90	OD1	3.955
3C09	C_ARG_38	NH2	C_GLU_46	OE1	2.986
3C09	C_ARG_38	NH2	C_GLU_46	OE2	3.298
3C09	D_HIS_394	ND1	D_ASP_369	OD1	3.451
3C09	D_ARG_403	NH2	D_GLU_376	OE1	3.699
3C09	D_ARG_403	NH2	D_GLU_376	OE2	3.471

3C09	D_LYS_407	NZ	D_ASP_434	OD1	3.698
3C09	D_LYS_407	NZ	D_ASP_434	OD2	2.480
3C09	D_LYS_454	NZ	H_ASP_100	OD2	3.482
3C09	D_LYS_463	NZ	L_ASP_49	OD2	3.418
3C5S	A_ARG_61	NH1	A_ASP_82	OD2	3.030
3C5S	A_ARG_61	NH2	A_GLU_79	OE2	3.851
3C5S	A_ARG_61	NH2	A_ASP_82	OD1	3.184
3C5S	A_ARG_61	NH2	A_ASP_82	OD2	3.437
3C5S	A_ARG_96	NH2	B_GLU_50	OE1	3.517
3C5S	A_ARG_96	NH2	B_GLU_50	OE2	2.932
3C5S	A_LYS_103	NZ	A_ASP_165	OD1	3.305
3C5S	A_LYS_147	NZ	A_GLU_154	OE1	2.905
3C5S	A_LYS_149	NZ	A_GLU_195	OE1	2.670
3C5S	A_ARG_188	NH1	A_ASP_184	OD1	2.405
3C5S	A_LYS_199	NZ	A_ASP_110	OD1	3.889
3C5S	A_LYS_199	NZ	A_ASP_110	OD2	2.335
3C5S	B_LYS_3	NZ	B_GLU_5	OE1	3.341
3C5S	B_ARG_38	NH1	B_ASP_86	OD1	2.908
3C5S	B_ARG_38	NH2	B_GLU_46	OE1	3.058
3C5S	B_ARG_38	NH2	B_ASP_86	OD1	3.943
3C5S	B_LYS_43	NZ	B_GLU_46	OE2	2.800
3C5S	B_ARG_52	NH2	B_GLU_50	OE2	2.999
3C5S	B_LYS_64	NZ	B_GLU_61	OE1	2.552
3C5S	B_LYS_64	NZ	B_GLU_61	OE2	3.116
3C5S	B_ARG_71	NH2	B_ASP_73	OD1	3.320
3C5S	B_LYS_75	NZ	B_ASP_72	OD2	3.056
3C5S	B_ARG_83	NH2	B_ASP_86	OD1	3.087
3C5S	B_ARG_83	NH2	B_ASP_86	OD2	3.434
3C5S	B_LYS_210	NZ	A_GLU_123	OE2	3.553
3C5S	C_ARG_61	NH1	C_ASP_82	OD1	3.085
3C5S	C_ARG_61	NH2	C_GLU_79	OE1	3.892
3C5S	C_ARG_61	NH2	C_GLU_79	OE2	3.694
3C5S	C_ARG_61	NH2	C_GLU_81	OE2	2.868
3C5S	C_ARG_61	NH2	C_ASP_82	OD1	3.573
3C5S	C_ARG_61	NH2	C_ASP_82	OD2	3.274
3C5S	C_ARG_96	NH2	D_GLU_50	OE1	3.571
3C5S	C_ARG_96	NH2	D_GLU_50	OE2	2.973
3C5S	C_LYS_103	NZ	C_ASP_165	OD1	3.149
3C5S	C_LYS_142	NZ	C_GLU_105	OE2	3.286
3C5S	C_LYS_147	NZ	C_GLU_154	OE1	2.994
3C5S	C_LYS_149	NZ	C_GLU_195	OE1	2.716
3C5S	C_LYS_149	NZ	C_GLU_195	OE2	3.839
3C5S	C_ARG_155	NH1	C_GLU_185	OE1	3.904
3C5S	C_ARG_155	NH2	C_GLU_185	OE1	3.268
3C5S	C_ARG_188	NH2	C_ASP_184	OD2	3.258
3C5S	C_HIS_189	ND1	C_ASP_151	OD2	2.806
3C5S	C_LYS_199	NZ	C_ASP_110	OD2	2.615
3C5S	C_ARG_211	NH1	C_GLU_187	OE1	3.163
3C5S	D_LYS_3	NZ	D_GLU_5	OE2	3.300
3C5S	D_ARG_38	NH1	D_ASP_86	OD1	2.823
3C5S	D_ARG_38	NH2	D_GLU_46	OE1	3.094
3C5S	D_ARG_38	NH2	D_GLU_46	OE2	3.865
3C5S	D_ARG_38	NH2	D_ASP_86	OD1	3.695
3C5S	D_ARG_52	NH2	D_GLU_50	OE2	2.971
3C5S	D_LYS_66	NZ	D_ASP_86	OD1	3.839
3C5S	D_LYS_66	NZ	D_ASP_86	OD2	2.657
3C5S	D_ARG_71	NH2	D_ASP_73	OD1	3.461
3C6S	A_LYS_27	NZ	F_GLU_61	OE1	2.945

3C6S	A_HIS_27D	NE2	A_ASP_28	OD2	3.782
3C6S	A_ARG_61	NH1	A_ASP_82	OD1	3.871
3C6S	A_ARG_61	NH1	A_ASP_82	OD2	2.772
3C6S	A_ARG_61	NH2	A_GLU_79	OE1	3.467
3C6S	A_ARG_61	NH2	A_GLU_81	OE2	3.840
3C6S	A_ARG_61	NH2	A_ASP_82	OD1	3.008
3C6S	A_ARG_61	NH2	A_ASP_82	OD2	3.321
3C6S	A_ARG_96	NH2	B_GLU_50	OE1	3.551
3C6S	A_ARG_96	NH2	B_GLU_50	OE2	2.936
3C6S	A_LYS_103	NZ	A_ASP_165	OD1	3.865
3C6S	A_LYS_147	NZ	A_GLU_154	OE1	3.762
3C6S	A_LYS_149	NZ	A_GLU_195	OE1	3.629
3C6S	A_LYS_149	NZ	A_GLU_195	OE2	3.115
3C6S	A_ARG_155	NH1	A_GLU_185	OE1	2.818
3C6S	A_ARG_155	NH1	A_GLU_185	OE2	3.763
3C6S	A_ARG_155	NH2	A_GLU_185	OE1	3.570
3C6S	A_ARG_155	NH2	A_GLU_185	OE2	3.121
3C6S	A_HIS_189	ND1	A_ASP_151	OD2	3.710
3C6S	B_LYS_3	NZ	B_GLU_5	OE1	3.976
3C6S	B_ARG_38	NH1	B_ASP_86	OD1	2.860
3C6S	B_ARG_38	NH2	B_GLU_46	OE1	3.287
3C6S	B_ARG_38	NH2	B_GLU_46	OE2	3.192
3C6S	B_ARG_38	NH2	B_ASP_86	OD1	3.858
3C6S	B_ARG_52	NH2	B_GLU_50	OE2	3.018
3C6S	B_LYS_64	NZ	B_GLU_61	OE1	3.776
3C6S	B_LYS_66	NZ	B_ASP_86	OD1	3.351
3C6S	B_LYS_66	NZ	B_ASP_86	OD2	2.603
3C6S	B_ARG_71	NH2	B_ASP_73	OD1	3.493
3C6S	B_ARG_83	NH2	B_GLU_85	OE2	3.633
3C6S	B_LYS_207	NZ	B_ASP_209	OD2	3.344
3C6S	B_LYS_210	NZ	A_GLU_123	OE2	2.871
3C6S	C_HIS_27D	NE2	C_ASP_28	OD2	3.911
3C6S	C_LYS_39	NZ	C_GLU_81	OE2	2.611
3C6S	C_ARG_61	NH1	C_ASP_82	OD1	3.977
3C6S	C_ARG_61	NH1	C_ASP_82	OD2	2.797
3C6S	C_ARG_61	NH2	C_GLU_79	OE1	3.899
3C6S	C_ARG_61	NH2	C_ASP_82	OD1	3.285
3C6S	C_ARG_61	NH2	C_ASP_82	OD2	3.465
3C6S	C_ARG_96	NH2	D_GLU_50	OE1	3.699
3C6S	C_ARG_96	NH2	D_GLU_50	OE2	2.915
3C6S	C_LYS_149	NZ	C_GLU_195	OE2	3.377
3C6S	C_ARG_155	NH1	C_GLU_185	OE1	2.919
3C6S	C_ARG_155	NH2	C_GLU_185	OE1	3.617
3C6S	C_ARG_155	NH2	C_GLU_185	OE2	3.372
3C6S	C_LYS_183	NZ	C_GLU_187	OE1	3.948
3C6S	C_ARG_188	NH1	C_ASP_184	OD1	3.896
3C6S	C_ARG_188	NH1	C_ASP_184	OD2	3.104
3C6S	C_ARG_188	NH2	C_GLU_185	OE1	3.688
3C6S	C_HIS_189	ND1	C_ASP_151	OD2	2.779
3C6S	C_LYS_199	NZ	C_ASP_110	OD2	3.859
3C6S	D_LYS_3	NZ	D_GLU_5	OE1	2.880
3C6S	D_LYS_3	NZ	D_GLU_5	OE2	3.546
3C6S	D_ARG_38	NH1	D_ASP_86	OD1	2.816
3C6S	D_ARG_38	NH2	D_GLU_46	OE1	3.293
3C6S	D_ARG_38	NH2	D_GLU_46	OE2	3.209
3C6S	D_ARG_38	NH2	D_ASP_86	OD1	3.686
3C6S	D_ARG_52	NH2	D_GLU_50	OE2	2.953
3C6S	D_LYS_64	NZ	D_GLU_61	OE1	2.522

3C6S	D_LYS_66	NZ	D_ASP_86	OD1	3.557
3C6S	D_LYS_66	NZ	D_ASP_86	OD2	2.620
3C6S	D_ARG_71	NH2	D_ASP_73	OD1	3.499
3C6S	D_LYS_115	NZ	H_GLU_85	OE1	3.000
3C6S	D_LYS_115	NZ	H_GLU_85	OE2	3.884
3C6S	D_LYS_210	NZ	C_GLU_123	OE2	2.801
3C6S	E_LYS_27	NZ	A_ASP_1	OD1	3.387
3C6S	E_LYS_27	NZ	A_ASP_1	OD2	3.431
3C6S	E_HIS_27D	NE2	E_ASP_28	OD2	3.987
3C6S	E_ARG_61	NH1	E_ASP_82	OD1	3.693
3C6S	E_ARG_61	NH1	E_ASP_82	OD2	2.790
3C6S	E_ARG_61	NH2	E_GLU_79	OE1	3.369
3C6S	E_ARG_61	NH2	E_GLU_81	OE2	3.772
3C6S	E_ARG_61	NH2	E_ASP_82	OD1	2.890
3C6S	E_ARG_61	NH2	E_ASP_82	OD2	3.360
3C6S	E_ARG_96	NH2	F_GLU_50	OE1	3.703
3C6S	E_ARG_96	NH2	F_GLU_50	OE2	3.164
3C6S	E_LYS_149	NZ	E_GLU_195	OE1	3.276
3C6S	E_LYS_149	NZ	E_GLU_195	OE2	3.217
3C6S	E_ARG_155	NH1	E_GLU_185	OE2	3.054
3C6S	E_ARG_155	NH2	E_GLU_185	OE1	3.295
3C6S	E_ARG_155	NH2	E_GLU_185	OE2	3.558
3C6S	E_LYS_183	NZ	E_GLU_187	OE1	3.890
3C6S	E_ARG_188	NH1	E_ASP_184	OD1	3.999
3C6S	E_ARG_188	NH1	E_ASP_184	OD2	2.649
3C6S	E_ARG_188	NH2	E_GLU_185	OE2	3.771
3C6S	E_HIS_189	ND1	E_ASP_151	OD2	2.858
3C6S	E_LYS_199	NZ	E_ASP_110	OD2	3.786
3C6S	F_ARG_38	NH1	F_ASP_86	OD1	2.884
3C6S	F_ARG_38	NH2	F_GLU_46	OE1	3.272
3C6S	F_ARG_38	NH2	F_GLU_46	OE2	3.427
3C6S	F_ARG_38	NH2	F_ASP_86	OD1	3.691
3C6S	F_ARG_52	NH2	F_GLU_50	OE2	2.936
3C6S	F_LYS_64	NZ	F_GLU_61	OE1	3.674
3C6S	F_LYS_64	NZ	F_GLU_61	OE2	3.896
3C6S	F_LYS_66	NZ	F_ASP_86	OD1	3.774
3C6S	F_LYS_66	NZ	F_ASP_86	OD2	2.770
3C6S	F_ARG_71	NH2	F_ASP_73	OD1	3.453
3C6S	F_LYS_207	NZ	F_ASP_209	OD1	2.611
3C6S	F_LYS_207	NZ	F_ASP_209	OD2	3.473
3C6S	F_LYS_210	NZ	E_GLU_123	OE2	3.016
3C6S	G_LYS_27	NZ	G_GLU_93	OE1	2.636
3C6S	G_LYS_27	NZ	G_GLU_93	OE2	3.112
3C6S	G_HIS_27D	NE2	G_ASP_28	OD2	3.978
3C6S	G_ARG_61	NH1	G_ASP_82	OD2	2.808
3C6S	G_ARG_61	NH2	G_GLU_79	OE1	3.851
3C6S	G_ARG_61	NH2	G_ASP_82	OD1	3.155
3C6S	G_ARG_61	NH2	G_ASP_82	OD2	3.092
3C6S	G_ARG_96	NH2	H_GLU_50	OE1	3.733
3C6S	G_ARG_96	NH2	H_GLU_50	OE2	2.958
3C6S	G_LYS_147	NZ	G_GLU_154	OE2	3.966
3C6S	G_LYS_149	NZ	G_GLU_195	OE1	3.546
3C6S	G_LYS_149	NZ	G_GLU_195	OE2	3.011
3C6S	G_ARG_155	NH1	G_GLU_185	OE2	3.226
3C6S	G_LYS_169	NZ	G_GLU_81	OE1	2.347
3C6S	G_LYS_169	NZ	G_GLU_81	OE2	3.920
3C6S	G_ARG_188	NH2	G_GLU_185	OE1	2.920
3C6S	G_HIS_189	ND1	G_ASP_151	OD2	3.004

3C6S	G_HIS_189	NE2	G_GLU_185	OE1	3.998
3C6S	G_LYS_199	NZ	G_ASP_110	OD2	3.920
3C6S	H_LYS_3	NZ	H_GLU_5	OE1	2.755
3C6S	H_ARG_38	NH1	H_ASP_86	OD1	2.900
3C6S	H_ARG_38	NH2	H_GLU_46	OE1	3.369
3C6S	H_ARG_38	NH2	H_GLU_46	OE2	3.273
3C6S	H_ARG_38	NH2	H_ASP_86	OD1	3.683
3C6S	H_ARG_52	NH2	H_GLU_50	OE2	3.044
3C6S	H_ARG_71	NH2	H_ASP_73	OD1	3.344
3C6S	H_LYS_75	NZ	H_ASP_72	OD2	3.808
3C6S	H_ARG_83	NH1	H_GLU_85	OE2	3.502
3C6S	H_ARG_83	NH2	H_ASP_86	OD1	2.979
3C6S	H_ARG_83	NH2	H_ASP_86	OD2	3.571
3C6S	H_LYS_210	NZ	G_GLU_123	OE2	2.402
3CVH	A_HIS_3	ND1	A_ASP_29	OD1	3.340
3CVH	A_HIS_3	ND1	A_ASP_29	OD2	3.186
3CVH	A_ARG_6	NH2	A_ASP_30	OD1	3.294
3CVH	A_ARG_14	NH1	A_ASP_39	OD2	2.927
3CVH	A_ARG_14	NH2	A_ASP_39	OD1	3.777
3CVH	A_ARG_14	NH2	A_ASP_39	OD2	2.767
3CVH	A_ARG_21	NH2	A_ASP_37	OD1	3.377
3CVH	A_ARG_21	NH2	A_ASP_37	OD2	2.615
3CVH	A_ARG_35	NH1	A_GLU_32	OE1	2.677
3CVH	A_ARG_35	NH1	A_GLU_32	OE2	2.491
3CVH	A_ARG_44	NH2	A_GLU_61	OE1	2.791
3CVH	A_ARG_48	NH1	B_ASP_53	OD2	3.820
3CVH	A_ARG_48	NH2	A_GLU_32	OE2	3.651
3CVH	A_ARG_48	NH2	B_ASP_53	OD2	2.637
3CVH	A_ARG_62	NH1	L_GLU_26	OE1	3.514
3CVH	A_ARG_62	NH1	L_GLU_26	OE2	3.458
3CVH	A_ARG_62	NH2	L_GLU_26	OE1	3.664
3CVH	A_LYS_66	NZ	A_GLU_63	OE1	2.982
3CVH	A_LYS_66	NZ	A_GLU_63	OE2	3.930
3CVH	A_ARG_75	NH1	A_GLU_19	OE1	2.649
3CVH	A_ARG_75	NH1	A_GLU_71	OE1	3.442
3CVH	A_ARG_75	NH2	A_GLU_19	OE1	3.819
3CVH	A_ARG_75	NH2	A_GLU_71	OE1	3.726
3CVH	A_HIS_93	ND1	A_ASP_119	OD1	3.615
3CVH	A_HIS_93	ND1	A_ASP_119	OD2	2.743
3CVH	A_ARG_108	NH2	M_GLU_223	OE2	3.938
3CVH	A_ARG_155	NH2	A_GLU_152	OE1	3.097
3CVH	A_ARG_155	NH2	A_GLU_152	OE2	2.655
3CVH	A_ARG_157	NH2	A_GLU_161	OE2	3.326
3CVH	A_ARG_170	NH2	A_GLU_55	OE1	2.438
3CVH	A_ARG_170	NH2	A_GLU_55	OE2	3.042
3CVH	A_ARG_181	NH2	A_ASP_183	OD2	3.102
3CVH	A_HIS_192	ND1	B_ASP_98	OD2	3.410
3CVH	B_LYS_3	NZ	B_ASP_59	OD2	3.798
3CVH	B_LYS_19	NZ	B_GLU_16	OE1	3.984
3CVH	B_LYS_83	NZ	B_GLU_36	OE1	3.948
3CVH	C_LYS_7	NZ	H_ASP_49	OD1	3.577
3CVH	C_LYS_7	NZ	H_ASP_49	OD2	3.552
3CVH	H_LYS_37	NZ	H_ASP_89	OD1	4.000
3CVH	H_LYS_66	NZ	H_ASP_89	OD1	3.905
3CVH	H_LYS_66	NZ	H_ASP_89	OD2	2.944
3CVH	H_LYS_98	NZ	H_ASP_34	OD1	3.326
3CVH	H_LYS_98	NZ	H_ASP_34	OD2	3.016
3CVH	H_LYS_98	NZ	H_ASP_49	OD2	3.605

3CVH	H.LYS_215	NZ	L_GLU_122	OE2	2.643
3CVH	L.LYS_23	NZ	L_ASP_69	OD1	2.944
3CVH	L.LYS_23	NZ	L_ASP_69	OD2	3.859
3CVH	L_ARG_60	NH1	L_GLU_80	OE1	3.977
3CVH	L_ARG_60	NH2	L_GLU_80	OE1	3.053
3CVH	L_ARG_60	NH2	L_ASP_81	OD1	3.208
3CVH	L_ARG_60	NH2	L_ASP_81	OD2	2.613
3CVH	L_ARG_67	NH2	L_ASP_27	OD1	3.678
3CVH	L_ARG_67	NH2	L_ASP_27	OD2	2.811
3CVH	L.LYS_146	NZ	L_GLU_153	OE1	3.893
3CVH	L.LYS_146	NZ	L_GLU_153	OE2	3.978
3CVH	L.LYS_148	NZ	L_GLU_194	OE1	3.826
3CVH	L_ARG_154	NH1	L_GLU_184	OE1	3.751
3CVH	L.LYS_182	NZ	L_GLU_186	OE1	3.005
3CVH	L.LYS_182	NZ	L_GLU_186	OE2	3.813
3CVH	L_ARG_187	NH2	L_ASP_183	OD1	3.139
3CVH	L_ARG_187	NH2	L_ASP_183	OD2	2.810
3CVH	L.LYS_198	NZ	L_ASP_109	OD2	3.543
3CVH	M.HIS_3	ND1	M_ASP_29	OD1	2.963
3CVH	M.HIS_3	ND1	M_ASP_29	OD2	2.771
3CVH	M_ARG_14	NH1	M_ASP_39	OD1	3.573
3CVH	M_ARG_14	NH2	M_ASP_39	OD1	2.587
3CVH	M_ARG_21	NH1	M_ASP_39	OD2	3.455
3CVH	M_ARG_21	NH2	M_ASP_37	OD1	3.446
3CVH	M_ARG_21	NH2	M_ASP_37	OD2	2.717
3CVH	M_ARG_21	NH2	M_ASP_39	OD2	3.712
3CVH	M_ARG_35	NH2	M_GLU_32	OE1	3.151
3CVH	M_ARG_35	NH2	M_GLU_32	OE2	3.351
3CVH	M_ARG_48	NH1	M_GLU_46	OE1	3.444
3CVH	M_ARG_48	NH1	M_GLU_46	OE2	3.832
3CVH	M_ARG_48	NH1	N_ASP_53	OD2	3.601
3CVH	M_ARG_48	NH2	M_GLU_32	OE2	3.692
3CVH	M_ARG_48	NH2	N_ASP_53	OD2	2.621
3CVH	M_ARG_50	NH2	M_GLU_53	OE2	3.272
3CVH	M_ARG_62	NH1	R_GLU_26	OE1	3.418
3CVH	M_ARG_62	NH2	R_GLU_26	OE1	3.162
3CVH	M_ARG_62	NH2	R_GLU_26	OE2	2.706
3CVH	M.LYS_66	NZ	M_GLU_63	OE1	3.245
3CVH	M_ARG_75	NH1	M_GLU_19	OE1	3.628
3CVH	M_ARG_75	NH2	M_GLU_71	OE1	3.921
3CVH	M_ARG_75	NH2	M_GLU_71	OE2	2.545
3CVH	M.HIS_93	ND1	M_ASP_119	OD1	3.830
3CVH	M.HIS_93	ND1	M_ASP_119	OD2	2.828
3CVH	M_ARG_108	NH2	A_GLU_223	OE1	3.207
3CVH	M_ARG_108	NH2	A_GLU_223	OE2	3.250
3CVH	M_ARG_111	NH1	M_GLU_128	OE2	3.369
3CVH	M_ARG_111	NH2	M_GLU_128	OE2	2.639
3CVH	M.HIS_145	ND1	M_GLU_148	OE1	3.811
3CVH	M_ARG_155	NH2	M_GLU_152	OE1	3.335
3CVH	M_ARG_155	NH2	M_GLU_152	OE2	2.756
3CVH	M_ARG_157	NH2	M_GLU_161	OE1	2.814
3CVH	M_ARG_157	NH2	M_GLU_161	OE2	3.333
3CVH	M_ARG_169	NH1	A_GLU_268	OE2	3.364
3CVH	M_ARG_170	NH2	M_GLU_55	OE1	2.487
3CVH	M_ARG_170	NH2	M_GLU_55	OE2	3.462
3CVH	M_ARG_181	NH2	M_ASP_183	OD2	3.222
3CVH	N.LYS_83	NZ	N_GLU_36	OE1	2.685
3CVH	N.LYS_83	NZ	N_GLU_36	OE2	3.981

3CVH	O_LYS_7	NZ	Q_ASP_49	OD1	3.648
3CVH	O_LYS_7	NZ	Q_ASP_49	OD2	3.052
3CVH	Q_LYS_37	NZ	Q_ASP_89	OD1	3.997
3CVH	Q_LYS_98	NZ	Q_ASP_34	OD1	3.064
3CVH	Q_LYS_98	NZ	Q_ASP_34	OD2	2.433
3CVH	Q_LYS_98	NZ	Q_ASP_49	OD2	3.431
3CVH	Q_LYS_215	NZ	R_GLU_122	OE1	3.557
3CVH	R_ARG_60	NH1	R_ASP_81	OD1	3.125
3CVH	R_ARG_60	NH1	R_ASP_81	OD2	2.738
3CVH	R_ARG_60	NH2	R_GLU_80	OE1	3.793
3CVH	R_LYS_102	NZ	R_ASP_164	OD1	3.388
3CVH	R_LYS_141	NZ	R_GLU_104	OE1	3.136
3CVH	R_LYS_148	NZ	R_GLU_194	OE1	3.875
3CVH	R_ARG_154	NH2	R_GLU_184	OE1	3.709
3CVH	R_HIS_188	ND1	R_ASP_150	OD2	3.342
3CVH	R_HIS_188	NE2	R_GLU_184	OE2	3.904
3CXD	L_ARG_61	NH2	L_GLU_81	OE2	3.336
3CXD	L_ARG_61	NH2	L_ASP_82	OD1	3.305
3CXD	L_ARG_61	NH2	L_ASP_82	OD2	2.791
3CXD	L_LYS_147	NZ	L_GLU_154	OE2	3.401
3CXD	L_LYS_149	NZ	L_GLU_195	OE2	2.939
3CXD	L_ARG_155	NH1	L_GLU_185	OE1	3.386
3CXD	L_ARG_155	NH2	L_GLU_185	OE1	3.845
3CXD	L_ARG_155	NH2	L_GLU_185	OE2	3.314
3CXD	L_ARG_188	NH2	L_ASP_184	OD1	3.219
3CXD	L_HIS_189	ND1	L_ASP_151	OD2	2.794
3CXD	L_LYS_199	NZ	L_ASP_110	OD1	3.656
3CXD	L_LYS_199	NZ	L_ASP_110	OD2	3.337
3CXD	H_ARG_38	NH1	H_GLU_46	OE1	3.619
3CXD	H_ARG_38	NH1	H_GLU_46	OE2	2.600
3CXD	H_ARG_38	NH2	H_ASP_92	OD1	2.807
3CXD	H_ARG_52	NH1	P_ASP_47	OD1	3.830
3CXD	H_ARG_52	NH1	P_ASP_47	OD2	3.528
3CXD	H_LYS_67	NZ	H_ASP_64	OD1	2.806
3CXD	H_ARG_69	NH1	H_ASP_92	OD2	2.720
3CXD	H_ARG_69	NH2	H_ASP_92	OD1	3.121
3CXD	H_ARG_69	NH2	H_ASP_92	OD2	2.861
3CXD	H_ARG_74	NH2	H_ASP_76	OD1	3.600
3CXD	H_ARG_100	NH2	H_ASP_104	OD1	3.226
3CXD	H_ARG_100	NH2	H_ASP_104	OD2	2.671
3D0L	A_ARG_37	NH1	A_GLU_81	OE2	3.366
3D0L	A_ARG_37	NH1	A_ASP_82	OD1	2.929
3D0L	A_ARG_37	NH2	A_GLU_81	OE2	3.080
3D0L	A_ARG_61	NH2	A_GLU_81	OE1	3.374
3D0L	A_ARG_61	NH2	A_ASP_82	OD1	2.776
3D0L	A_ARG_61	NH2	A_ASP_82	OD2	3.420
3D0L	A_HIS_96	NE2	C_ASP_5	OD1	3.014
3D0L	A_LYS_149	NZ	A_GLU_195	OE1	3.487
3D0L	A_LYS_183	NZ	A_GLU_187	OE2	3.124
3D0L	A_LYS_190	NZ	A_GLU_213	OE2	3.283
3D0L	B_ARG_38	NH1	B_GLU_46	OE1	2.512
3D0L	B_ARG_38	NH1	B_GLU_46	OE2	3.477
3D0L	B_ARG_38	NH2	B_ASP_86	OD1	2.546
3D0L	B_LYS_57	NZ	B_ASP_55	OD2	3.516
3D0L	B_ARG_58	NH1	B_ASP_56	OD1	2.533
3D0L	B_ARG_58	NH1	B_ASP_56	OD2	3.774
3D0L	B_ARG_58	NH2	B_ASP_56	OD1	3.951
3D0L	B_ARG_58	NH2	C_GLU_3	OE1	3.473

3D0L	B_ARG_58	NH2	C_GLU_3	OE2	3.109
3D0L	B_ARG_66	NH1	B_ASP_86	OD1	3.615
3D0L	B_ARG_66	NH2	B_ASP_86	OD1	3.276
3D0L	B_ARG_66	NH2	B_ASP_86	OD2	2.898
3D0L	B_HIS_94	ND1	B_ASP_101	OD1	2.602
3D0L	B_HIS_94	ND1	B_ASP_101	OD2	3.437
3D0L	B_ARG_95	NH1	C_ASP_5	OD1	2.695
3D0L	B_ARG_95	NH1	C_ASP_5	OD2	3.449
3D0L	B_ARG_95	NH2	C_ASP_5	OD1	3.596
3D0L	B_ARG_95	NH2	C_ASP_5	OD2	3.078
3D0L	B_ARG_96	NH1	A_GLU_55	OE1	3.284
3D0L	B_ARG_96	NH1	A_GLU_55	OE2	3.522
3D0L	B_ARG_96	NH1	B_ASP_101	OD2	3.433
3D0L	B_ARG_96	NH2	A_GLU_55	OE1	3.455
3D0L	B_LYS_143	NZ	B_ASP_144	OD1	3.418
3D0L	B_LYS_143	NZ	B_ASP_144	OD2	3.784
3D0L	B_ARG_210	NH2	B_GLU_212	OE1	2.865
3D0L	C_LYS_6	NZ	B_ASP_54	OD1	2.251
3D0L	C_LYS_6	NZ	B_ASP_54	OD2	2.930
3D0L	C_LYS_6	NZ	B_ASP_56	OD2	3.751
3D0V	A_ARG_37	NH1	A_ASP_82	OD1	2.771
3D0V	A_ARG_61	NH2	A_GLU_81	OE2	3.952
3D0V	A_ARG_61	NH2	A_ASP_82	OD1	2.926
3D0V	A_ARG_61	NH2	A_ASP_82	OD2	3.288
3D0V	A_ARG_79	NH1	A_GLU_81	OE2	3.015
3D0V	A_ARG_79	NH2	A_GLU_81	OE2	2.700
3D0V	A_HIS_96	NE2	C_ASP_5	OD1	2.775
3D0V	A_LYS_149	NZ	A_GLU_195	OE1	3.493
3D0V	A_LYS_149	NZ	A_GLU_195	OE2	3.064
3D0V	A_LYS_183	NZ	A_GLU_187	OE2	3.032
3D0V	A_ARG_211	NH1	A_GLU_187	OE1	3.976
3D0V	B_ARG_38	NH1	B_GLU_46	OE1	2.804
3D0V	B_ARG_38	NH1	B_GLU_46	OE2	3.705
3D0V	B_ARG_38	NH2	B_ASP_86	OD1	2.434
3D0V	B_LYS_57	NZ	B_ASP_55	OD1	3.625
3D0V	B_LYS_57	NZ	B_ASP_55	OD2	3.392
3D0V	B_ARG_58	NH1	B_ASP_56	OD1	3.726
3D0V	B_ARG_58	NH1	B_ASP_56	OD2	2.549
3D0V	B_ARG_58	NH2	B_ASP_56	OD2	3.911
3D0V	B_ARG_58	NH2	C_GLU_3	OE1	2.733
3D0V	B_ARG_66	NH1	B_ASP_86	OD1	3.446
3D0V	B_ARG_66	NH1	B_ASP_86	OD2	3.728
3D0V	B_ARG_66	NH2	B_ASP_86	OD1	3.289
3D0V	B_ARG_66	NH2	B_ASP_86	OD2	2.373
3D0V	B_HIS_94	ND1	B_ASP_101	OD1	2.627
3D0V	B_HIS_94	ND1	B_ASP_101	OD2	3.607
3D0V	B_ARG_95	NH1	C_ASP_5	OD1	2.808
3D0V	B_ARG_95	NH1	C_ASP_5	OD2	3.484
3D0V	B_ARG_95	NH2	C_ASP_5	OD1	3.359
3D0V	B_ARG_95	NH2	C_ASP_5	OD2	2.831
3D0V	B_ARG_96	NH1	A_GLU_55	OE1	3.250
3D0V	B_ARG_96	NH1	A_GLU_55	OE2	3.216
3D0V	B_ARG_96	NH1	B_ASP_101	OD2	3.014
3D0V	B_ARG_96	NH2	A_GLU_55	OE1	3.184
3D0V	B_LYS_143	NZ	B_ASP_144	OD1	3.460
3D0V	B_LYS_143	NZ	B_ASP_144	OD2	3.988
3D0V	B_LYS_209	NZ	A_GLU_123	OE1	3.487
3D0V	B_ARG_210	NH1	B_GLU_212	OE1	2.267

3D0V	B_ARG_210	NH2	B_GLU_212	OE1	3.360
3D0V	C_LYS_6	NZ	B_ASP_54	OD1	3.609
3D0V	C_LYS_6	NZ	B_ASP_54	OD2	2.826
3D0V	C_LYS_6	NZ	B_ASP_56	OD1	3.006
3D9A	C_LYS_601	NZ	C_GLU_607	OE2	3.151
3D9A	C_LYS_697	NZ	H_ASP_332	OD2	2.741
3D9A	C_LYS_697	NZ	H_ASP_399	OD1	2.864
3D9A	C_LYS_697	NZ	H_ASP_399	OD2	3.300
3D9A	L_ARG_24	NH2	L_ASP_70	OD1	3.000
3D9A	L_ARG_24	NH2	L_ASP_70	OD2	3.752
3D9A	L_ARG_61	NH1	L_GLU_79	OE1	3.658
3D9A	L_ARG_61	NH1	L_GLU_79	OE2	3.448
3D9A	L_ARG_61	NH2	L_GLU_79	OE1	3.298
3D9A	L_ARG_61	NH2	L_ASP_82	OD1	2.829
3D9A	L_ARG_61	NH2	L_ASP_82	OD2	3.674
3D9A	L_LYS_147	NZ	L_GLU_154	OE1	3.943
3D9A	L_LYS_149	NZ	L_GLU_195	OE2	3.477
3D9A	L_LYS_169	NZ	L_ASP_167	OD2	3.989
3D9A	L_LYS_199	NZ	L_ASP_110	OD1	3.878
3D9A	L_LYS_199	NZ	L_ASP_110	OD2	3.357
3D9A	H_ARG_338	NH1	H_ASP_389	OD1	2.834
3D9A	H_ARG_338	NH2	H_GLU_346	OE1	2.922
3D9A	H_ARG_338	NH2	H_ASP_389	OD1	3.583
3D9A	H_ARG_366	NH1	H_ASP_389	OD1	2.956
3D9A	H_ARG_366	NH1	H_ASP_389	OD2	3.486
3D9A	H_ARG_366	NH2	H_ASP_389	OD1	3.662
3D9A	H_ARG_366	NH2	H_ASP_389	OD2	2.925
3D9A	H_LYS_508	NZ	L_GLU_123	OE1	3.029
3D9A	H_LYS_508	NZ	L_GLU_123	OE2	3.809
3DRO	A_ARG_37	NH1	A_ASP_82	OD1	2.782
3DRO	A_ARG_61	NH2	A_ASP_82	OD1	2.866
3DRO	A_ARG_61	NH2	A_ASP_82	OD2	3.498
3DRO	A_ARG_107	NH1	A_ASP_17	OD2	3.044
3DRO	A_ARG_107	NH2	A_ASP_17	OD2	3.360
3DRO	A_LYS_149	NZ	A_GLU_195	OE2	3.983
3DRO	A_LYS_183	NZ	A_GLU_187	OE1	3.983
3DRO	A_LYS_183	NZ	A_GLU_187	OE2	3.458
3DRO	A_LYS_188	NZ	A_ASP_185	OD1	3.977
3DRO	A_LYS_190	NZ	A_GLU_213	OE2	3.164
3DRO	B_ARG_1	NH1	B_ASP_101	OD2	3.834
3DRO	B_ARG_38	NH1	B_GLU_46	OE1	2.549
3DRO	B_ARG_38	NH1	B_GLU_46	OE2	3.279
3DRO	B_ARG_38	NH2	B_GLU_46	OE1	3.448
3DRO	B_ARG_38	NH2	B_ASP_86	OD1	3.555
3DRO	B_ARG_58	NH1	B_ASP_56	OD2	3.804
3DRO	B_ARG_66	NH1	B_ASP_86	OD1	3.732
3DRO	B_ARG_66	NH2	B_ASP_86	OD1	3.385
3DRO	B_ARG_66	NH2	B_ASP_86	OD2	2.816
3DRO	B_HIS_94	ND1	B_ASP_101	OD1	2.877
3DRO	B_HIS_94	ND1	B_ASP_101	OD2	3.841
3DRO	B_ARG_95	NH1	P_ASP_5	OD1	3.590
3DRO	B_ARG_95	NH1	P_ASP_5	OD2	3.370
3DRO	B_ARG_95	NH2	P_ASP_5	OD2	3.007
3DRO	B_ARG_96	NH1	B_ASP_101	OD2	2.827
3DRO	B_ARG_96	NH2	A_GLU_55	OE1	2.727
3DRO	B_ARG_96	NH2	A_GLU_55	OE2	3.426
3DRO	B_ARG_96	NH2	B_ASP_101	OD2	3.688
3DRO	B_LYS_143	NZ	B_ASP_144	OD1	3.378

3DRO	B_LYS_143	NZ	B_ASP_144	OD2	3.463
3DRO	B_LYS_209	NZ	A_GLU_123	OE1	3.782
3DRO	B_ARG_210	NH2	B_GLU_212	OE1	3.532
3DRO	P_LYS_6	NZ	B_ASP_54	OD1	2.913
3DRO	P_LYS_6	NZ	B_ASP_54	OD2	3.775
3DRO	P_LYS_6	NZ	B_ASP_56	OD1	3.330
3DRO	P_LYS_6	NZ	B_ASP_56	OD2	3.868
3DRQ	A_ARG_37	NH1	A_ASP_82	OD1	2.863
3DRQ	A_LYS_39	NZ	A_GLU_81	OE1	2.913
3DRQ	A_ARG_61	NH2	A_ASP_82	OD1	2.860
3DRQ	A_ARG_61	NH2	A_ASP_82	OD2	3.418
3DRQ	A_HIS_96	NE2	C_ASP_5	OD1	2.866
3DRQ	A_ARG_107	NH1	A_ASP_17	OD2	3.572
3DRQ	A_LYS_149	NZ	A_GLU_195	OE1	3.681
3DRQ	A_LYS_183	NZ	A_GLU_187	OE2	3.873
3DRQ	A_LYS_190	NZ	A_GLU_213	OE2	3.586
3DRQ	B_ARG_1	NH1	B_ASP_101	OD2	3.864
3DRQ	B_ARG_38	NH1	B_GLU_46	OE1	2.536
3DRQ	B_ARG_38	NH1	B_GLU_46	OE2	3.423
3DRQ	B_ARG_38	NH2	B_ASP_86	OD1	2.585
3DRQ	B_LYS_57	NZ	B_ASP_55	OD2	3.992
3DRQ	B_ARG_58	NH1	B_ASP_56	OD2	3.411
3DRQ	B_ARG_58	NH2	C_GLU_3	OE1	3.516
3DRQ	B_ARG_66	NH1	B_ASP_86	OD1	3.694
3DRQ	B_ARG_66	NH2	B_ASP_86	OD1	3.360
3DRQ	B_ARG_66	NH2	B_ASP_86	OD2	2.903
3DRQ	B_HIS_94	ND1	B_ASP_101	OD1	2.538
3DRQ	B_HIS_94	ND1	B_ASP_101	OD2	3.527
3DRQ	B_ARG_95	NH1	C_ASP_5	OD1	2.806
3DRQ	B_ARG_95	NH1	C_ASP_5	OD2	3.209
3DRQ	B_ARG_95	NH2	C_ASP_5	OD1	3.572
3DRQ	B_ARG_95	NH2	C_ASP_5	OD2	2.688
3DRQ	B_ARG_96	NH1	A_GLU_55	OE1	2.721
3DRQ	B_ARG_96	NH1	A_GLU_55	OE2	2.397
3DRQ	B_ARG_96	NH1	B_ASP_101	OD2	3.478
3DRQ	B_ARG_96	NH2	A_GLU_55	OE1	3.293
3DRQ	B_LYS_143	NZ	B_ASP_144	OD1	3.320
3DRQ	B_LYS_143	NZ	B_ASP_144	OD2	3.881
3DRQ	B_LYS_209	NZ	A_GLU_123	OE1	3.837
3DRQ	C_LYS_6	NZ	B_ASP_54	OD1	2.921
3DRQ	C_LYS_6	NZ	B_ASP_54	OD2	2.342
3DRQ	C_LYS_6	NZ	B_ASP_56	OD1	3.006
3DSF	L_ARG_61	NH1	L_GLU_81	OE2	3.610
3DSF	L_ARG_61	NH2	L_GLU_81	OE2	2.775
3DSF	L_ARG_61	NH2	L_ASP_82	OD1	3.453
3DSF	L_ARG_61	NH2	L_ASP_82	OD2	2.517
3DSF	L_LYS_147	NZ	L_GLU_154	OE2	3.411
3DSF	L_LYS_149	NZ	L_GLU_195	OE2	3.065
3DSF	L_ARG_155	NH1	L_GLU_185	OE1	3.133
3DSF	L_ARG_155	NH2	L_GLU_185	OE1	3.886
3DSF	L_ARG_155	NH2	L_GLU_185	OE2	3.560
3DSF	L_ARG_188	NH2	L_ASP_184	OD1	3.232
3DSF	L_HIS_189	ND1	L_ASP_151	OD2	2.709
3DSF	L_LYS_199	NZ	L_ASP_110	OD1	3.100
3DSF	L_LYS_199	NZ	L_ASP_110	OD2	2.808
3DSF	H_ARG_38	NH1	H_GLU_46	OE1	3.258
3DSF	H_ARG_38	NH1	H_GLU_46	OE2	2.451
3DSF	H_ARG_38	NH2	H_ASP_92	OD1	2.841

3DSF	H_ARG_52	NH1	P_ASP_47	OD2	3.172
3DSF	H_LYS_67	NZ	H_ASP_64	OD1	3.269
3DSF	H_ARG_69	NH1	H_ASP_92	OD2	2.681
3DSF	H_ARG_69	NH2	H_ASP_92	OD1	3.011
3DSF	H_ARG_69	NH2	H_ASP_92	OD2	3.022
3DSF	H_ARG_74	NH2	H_ASP_76	OD1	3.842
3DSF	H_ARG_100	NH2	H_ASP_104	OD1	3.055
3DSF	H_ARG_100	NH2	H_ASP_104	OD2	2.952
3EBA	A_ARG_49	NH1	A_ASP_52	OD1	3.900
3EBA	A_ARG_64	NH1	A_ASP_87	OD1	3.739
3EBA	A_ARG_64	NH1	A_ASP_87	OD2	2.820
3EBA	A_ARG_64	NH2	A_ASP_87	OD1	2.913
3EBA	A_ARG_64	NH2	A_ASP_87	OD2	3.515
3EBA	A_LYS_84	NZ	A_GLU_86	OE1	3.206
3EBA	B_LYS_69	NZ	B_ASP_67	OD2	3.295
3EBA	B_LYS_97	NZ	A_GLU_97	OE2	3.240
3EBA	B_ARG_101	NH1	A_ASP_109	OD1	3.083
3EBA	B_ARG_101	NH1	A_ASP_109	OD2	2.691
3EBA	B_ARG_101	NH2	A_ASP_109	OD1	3.308
3EBA	B_ARG_101	NH2	A_ASP_109	OD2	3.134
3EOA	L_ARG_24	NH2	L_ASP_70	OD1	3.574
3EOA	L_ARG_24	NH2	L_ASP_70	OD2	2.606
3EOA	L_ARG_61	NH1	L_GLU_81	OE2	3.484
3EOA	L_ARG_61	NH1	L_ASP_82	OD1	3.804
3EOA	L_LYS_149	NZ	L_GLU_195	OE1	2.415
3EOA	H_ARG_38	NH1	H_ASP_90	OD1	2.905
3EOA	H_ARG_38	NH2	H_GLU_46	OE2	3.821
3EOA	H_ARG_38	NH2	H_ASP_90	OD1	3.860
3EOA	H_ARG_67	NH1	H_ASP_90	OD2	2.949
3EOA	H_ARG_67	NH2	H_ASP_90	OD1	3.556
3EOA	H_ARG_67	NH2	H_ASP_90	OD2	3.648
3EOA	H_ARG_87	NH1	H_GLU_89	OE1	2.782
3EOA	H_ARG_98	NH1	H_ASP_109	OD2	2.755
3EOA	H_LYS_151	NZ	H_ASP_152	OD1	3.488
3EOA	H_LYS_151	NZ	H_ASP_152	OD2	3.869
3EOA	H_LYS_217	NZ	L_GLU_123	OE2	3.037
3EOA	I_LYS_149	NZ	I_ASP_145	OD1	2.783
3EOA	I_LYS_149	NZ	I_ASP_145	OD2	2.826
3EOA	I_LYS_155	NZ	I_ASP_152	OD1	3.581
3EOA	I_LYS_155	NZ	I_ASP_193	OD1	2.723
3EOA	I_LYS_159	NZ	I_ASP_156	OD1	3.990
3EOA	I_LYS_159	NZ	I_ASP_193	OD2	3.917
3EOA	I_LYS_178	NZ	I_GLU_180	OE1	3.466
3EOA	I_LYS_197	NZ	H_ASP_55	OD1	3.170
3EOA	I_LYS_197	NZ	H_GLU_57	OE1	2.719
3EOA	I_HIS_198	NE2	H_GLU_57	OE1	3.638
3EOA	I_HIS_198	NE2	H_GLU_57	OE2	3.098
3EOA	I_ARG_221	NH1	I_GLU_223	OE2	3.700
3EOA	I_ARG_227	NH2	I_ASP_131	OD2	2.628
3EOA	I_LYS_252	NZ	I_ASP_249	OD2	3.806
3EOA	A_ARG_61	NH1	A_GLU_81	OE2	3.839
3EOA	A_ARG_61	NH1	A_ASP_82	OD1	2.580
3EOA	A_ARG_61	NH1	A_ASP_82	OD2	3.564
3EOA	A_LYS_103	NZ	A_GLU_165	OE1	3.460
3EOA	A_LYS_103	NZ	A_GLU_165	OE2	3.931
3EOA	A_LYS_	NZ	A_GLU_	OE1	3.399
3EOA	A_LYS_	NZ	A_GLU_	OE2	3.445
3EOA	A_LYS_	NZ	A_GLU_	OE2	3.194

3EOA	A_ARG_	NH2	A_GLU_	OE2	3.408
3EOA	B_ARG_38	NH1	B_ASP_90	OD1	2.938
3EOA	B_ARG_38	NH2	B_GLU_46	OE2	3.688
3EOA	B_ARG_38	NH2	B_ASP_90	OD1	3.785
3EOA	B_ARG_67	NH1	B_ASP_90	OD1	3.358
3EOA	B_ARG_67	NH1	B_ASP_90	OD2	2.533
3EOA	B_ARG_67	NH2	B_ASP_90	OD1	3.191
3EOA	B_ARG_67	NH2	B_ASP_90	OD2	3.831
3EOA	B_ARG_98	NH1	B_ASP_109	OD1	3.621
3EOA	B_ARG_98	NH1	B_ASP_109	OD2	2.877
3EOA	B_LYS_	NZ	A_GLU_	OE2	3.673
3EOA	J_LYS_149	NZ	J_ASP_145	OD1	3.029
3EOA	J_LYS_149	NZ	J_GLU_293	OE2	2.826
3EOA	J_LYS_155	NZ	J_ASP_193	OD1	2.719
3EOA	J_LYS_159	NZ	J_ASP_193	OD2	3.556
3EOA	J_LYS_178	NZ	J_GLU_180	OE1	3.070
3EOA	J_LYS_178	NZ	J_GLU_180	OE2	3.956
3EOA	J_LYS_197	NZ	B_ASP_55	OD1	2.626
3EOA	J_LYS_197	NZ	B_ASP_55	OD2	2.997
3EOA	J_LYS_197	NZ	B_GLU_57	OE1	2.784
3EOA	J_HIS_198	NE2	B_GLU_57	OE1	3.322
3EOA	J_HIS_198	NE2	B_GLU_57	OE2	2.793
3EOA	J_ARG_221	NH1	J_GLU_223	OE1	3.385
3EOA	J_ARG_221	NH2	J_GLU_218	OE1	3.711
3EOA	J_ARG_227	NH2	J_ASP_131	OD2	3.169
3EOA	J_LYS_232	NZ	J_ASP_253	OD1	3.326
3EOB	L_ARG_24	NH2	L_ASP_70	OD2	3.407
3EOB	L_ARG_61	NH1	L_ASP_82	OD1	3.432
3EOB	L_ARG_108	NH2	L_ASP_170	OD1	2.979
3EOB	L_LYS_149	NZ	L_GLU_195	OE1	3.677
3EOB	H_ARG_38	NH1	H_ASP_90	OD1	3.001
3EOB	H_ARG_38	NH2	H_GLU_46	OE2	3.103
3EOB	H_ARG_38	NH2	H_ASP_90	OD1	3.672
3EOB	H_LYS_63	NZ	H_GLU_46	OE1	3.646
3EOB	H_ARG_67	NH1	H_ASP_90	OD1	3.982
3EOB	H_ARG_67	NH1	H_ASP_90	OD2	2.820
3EOB	H_ARG_67	NH2	H_ASP_90	OD1	3.369
3EOB	H_ARG_67	NH2	H_ASP_90	OD2	3.450
3EOB	H_ARG_87	NH1	H_GLU_89	OE1	3.348
3EOB	H_ARG_98	NH1	H_ASP_109	OD2	2.860
3EOB	H_LYS_217	NZ	L_GLU_123	OE2	3.176
3EOB	I_LYS_149	NZ	I_ASP_145	OD1	3.604
3EOB	I_LYS_149	NZ	I_ASP_145	OD2	2.585
3EOB	I_LYS_155	NZ	I_ASP_193	OD1	3.215
3EOB	I_LYS_159	NZ	I_ASP_193	OD2	3.529
3EOB	I_LYS_178	NZ	I_GLU_180	OE1	3.871
3EOB	I_LYS_197	NZ	H_GLU_57	OE1	2.792
3EOB	I_LYS_197	NZ	H_GLU_57	OE2	3.051
3EOB	I_HIS_198	ND1	H_GLU_57	OE2	3.691
3EOB	I_HIS_198	NE2	H_GLU_57	OE1	2.182
3EOB	I_HIS_198	NE2	H_GLU_57	OE2	2.522
3EOB	I_ARG_221	NH1	I_GLU_223	OE1	2.856
3EOB	I_ARG_227	NH2	I_ASP_131	OD2	2.963
3EOB	I_LYS_232	NZ	I_ASP_253	OD1	3.583
3EOB	I_HIS_264	NE2	J_GLU_241	OE1	2.369
3EOB	I_HIS_264	NE2	J_GLU_241	OE2	2.595
3EOB	I_HIS_275	ND1	I_GLU_272	OE2	3.714
3EOB	A_ARG_24	NH2	A_ASP_70	OD1	3.782

3EOB	A_ARG_24	NH2	A_ASP_70	OD2	3.414
3EOB	A_ARG_61	NH1	A_GLU_81	OE2	3.358
3EOB	A_ARG_61	NH1	A_ASP_82	OD1	2.901
3EOB	A_ARG_61	NH1	A_ASP_82	OD2	3.391
3EOB	A_ARG_108	NH2	A_ASP_170	OD1	3.529
3EOB	A_LYS_	NZ	A_GLU_	OE1	3.265
3EOB	B_ARG_38	NH1	B_ASP_90	OD1	3.354
3EOB	B_ARG_38	NH2	B_GLU_46	OE2	3.502
3EOB	B_ARG_38	NH2	B_ASP_90	OD1	3.996
3EOB	B_LYS_63	NZ	B_GLU_46	OE1	3.294
3EOB	B_ARG_67	NH1	B_ASP_90	OD2	2.904
3EOB	B_ARG_67	NH2	B_ASP_90	OD1	3.362
3EOB	B_ARG_67	NH2	B_ASP_90	OD2	3.179
3EOB	B_ARG_87	NH1	B_GLU_89	OE1	2.946
3EOB	B_ARG_98	NH1	B_ASP_109	OD2	3.051
3EOB	B_LYS_	NZ	A_GLU_	OE1	3.788
3EOB	B_LYS_	NZ	A_GLU_	OE2	3.219
3EOB	J_LYS_149	NZ	J_ASP_145	OD1	2.827
3EOB	J_LYS_149	NZ	J_ASP_145	OD2	3.169
3EOB	J_LYS_155	NZ	J_ASP_193	OD1	3.290
3EOB	J_LYS_159	NZ	J_ASP_193	OD1	3.983
3EOB	J_LYS_159	NZ	J_ASP_193	OD2	2.888
3EOB	J_LYS_197	NZ	B_ASP_55	OD1	3.833
3EOB	J_LYS_197	NZ	B_GLU_57	OE1	2.107
3EOB	J_LYS_197	NZ	B_GLU_57	OE2	3.802
3EOB	J_HIS_198	ND1	B_GLU_57	OE2	3.839
3EOB	J_HIS_198	NE2	B_GLU_57	OE1	2.356
3EOB	J_HIS_198	NE2	B_GLU_57	OE2	2.609
3EOB	J_ARG_221	NH1	J_GLU_223	OE1	3.220
3EOB	J_ARG_227	NH2	J_ASP_131	OD2	2.997
3EOB	J_LYS_232	NZ	J_ASP_253	OD1	3.217
3EOB	J_HIS_264	NE2	I_GLU_241	OE1	2.434
3EOB	J_HIS_264	NE2	I_GLU_241	OE2	2.722
3EOB	J_LYS_294	NZ	J_ASP_290	OD2	3.936
3ESU	F_ARG_61	NH2	F_GLU_81	OE2	3.099
3ESU	F_ARG_61	NH2	F_ASP_82	OD1	2.818
3ESU	F_ARG_61	NH2	F_ASP_82	OD2	3.481
3ESU	F_LYS_103	NZ	F_GLU_105	OE2	3.657
3ESU	F_LYS_1038	NZ	F_ASP_1086	OD1	3.978
3ESU	F_LYS_1062	NZ	F_GLU_1046	OE1	2.626
3ESU	F_LYS_1062	NZ	F_GLU_1046	OE2	3.804
3ESU	F_LYS_1066	NZ	F_ASP_1086	OD1	3.810
3ESU	F_LYS_1066	NZ	F_ASP_1086	OD2	2.823
3ESU	F_ARG_1094	NH1	F_ASP_1024	OD2	2.978
3ESV	F_LYS_0	NZ	G_ASP_1054	OD1	3.499
3ESV	F_LYS_0	NZ	G_ASP_1054	OD2	2.774
3ESV	F_LYS_0	NZ	G_ASP_1056	OD2	3.090
3ESV	F_ARG_61	NH1	F_GLU_79	OE1	3.359
3ESV	F_ARG_61	NH2	F_GLU_79	OE1	3.662
3ESV	F_ARG_61	NH2	F_GLU_81	OE2	3.198
3ESV	F_ARG_61	NH2	F_ASP_82	OD1	2.780
3ESV	F_ARG_61	NH2	F_ASP_82	OD2	3.438
3ESV	F_LYS_1066	NZ	F_ASP_1086	OD1	3.900
3ESV	F_LYS_1066	NZ	F_ASP_1086	OD2	2.918
3ESV	F_ARG_1094	NH1	F_ASP_1101	OD2	3.844
3ESV	F_ARG_1094	NH2	F_ASP_1101	OD2	3.978
3ESV	F_ARG_1099	NH2	F_ASP_1101	OD2	3.038
3ESV	G_ARG_53	NH1	F_ASP_1056	OD1	2.802

3ESV	G_ARG_53	NH2	F_ASP_1056	OD1	3.489
3ESV	G_ARG_61	NH1	G_GLU_79	OE1	2.958
3ESV	G_ARG_61	NH2	G_GLU_79	OE1	3.174
3ESV	G_ARG_61	NH2	G_GLU_81	OE1	2.849
3ESV	G_ARG_61	NH2	G_ASP_82	OD1	2.663
3ESV	G_ARG_61	NH2	G_ASP_82	OD2	3.554
3ESV	G_LYS_103	NZ	G_GLU_105	OE1	3.664
3ESV	G_LYS_1066	NZ	G_ASP_1086	OD1	3.520
3ESV	G_LYS_1066	NZ	G_ASP_1086	OD2	2.664
3ESV	G_ARG_1099	NH2	G_ASP_1101	OD2	3.345
3ET9	F_ARG_61	NH2	F_GLU_81	OE2	3.021
3ET9	F_ARG_61	NH2	F_ASP_82	OD1	2.714
3ET9	F_ARG_61	NH2	F_ASP_82	OD2	3.090
3ET9	F_LYS_103	NZ	F_GLU_105	OE1	3.734
3ET9	F_LYS_1038	NZ	F_ASP_1086	OD1	3.668
3ET9	F_LYS_1062	NZ	F_GLU_1046	OE1	3.916
3ET9	F_LYS_1066	NZ	F_ASP_1086	OD2	3.146
3ET9	F_ARG_1094	NH1	F_ASP_1024	OD1	3.640
3ET9	F_ARG_1094	NH1	F_ASP_1024	OD2	2.893
3ETB	F_ARG_24	NH1	G_ASP_70	OD1	3.579
3ETB	F_ARG_24	NH1	G_ASP_70	OD2	3.034
3ETB	F_ARG_24	NH2	G_ASP_70	OD1	3.608
3ETB	F_ARG_24	NH2	G_ASP_70	OD2	3.774
3ETB	F_ARG_30	NH1	J_ASP_658	OD2	3.129
3ETB	F_ARG_53	NH1	J_GLU_654	OE1	3.838
3ETB	F_ARG_53	NH2	J_GLU_654	OE1	3.771
3ETB	F_ARG_61	NH1	F_GLU_79	OE2	3.574
3ETB	F_ARG_61	NH2	F_GLU_79	OE1	3.945
3ETB	F_ARG_61	NH2	F_ASP_82	OD1	2.649
3ETB	F_ARG_61	NH2	F_ASP_82	OD2	2.469
3ETB	F_ARG_1050	NH2	J_ASP_683	OD2	3.114
3ETB	F_LYS_1062	NZ	F_GLU_1046	OE1	3.184
3ETB	F_LYS_1062	NZ	F_GLU_1046	OE2	3.847
3ETB	F_LYS_1066	NZ	F_ASP_1086	OD2	3.203
3ETB	F_ARG_1094	NH1	F_ASP_1101	OD1	2.832
3ETB	G_ARG_24	NH1	F_ASP_70	OD1	3.633
3ETB	G_ARG_24	NH1	F_ASP_70	OD2	3.127
3ETB	G_ARG_24	NH2	F_ASP_70	OD1	3.702
3ETB	G_ARG_24	NH2	F_ASP_70	OD2	3.878
3ETB	G_ARG_30	NH1	K_ASP_658	OD2	3.266
3ETB	G_ARG_53	NH2	K_ASP_648	OD2	3.972
3ETB	G_ARG_53	NH2	K_GLU_654	OE1	3.990
3ETB	G_ARG_61	NH1	G_GLU_79	OE2	3.534
3ETB	G_ARG_61	NH2	G_GLU_79	OE1	3.999
3ETB	G_ARG_61	NH2	G_ASP_82	OD1	2.660
3ETB	G_ARG_61	NH2	G_ASP_82	OD2	2.433
3ETB	G_ARG_1050	NH2	K_ASP_683	OD1	3.853
3ETB	G_ARG_1050	NH2	K_ASP_683	OD2	2.796
3ETB	G_LYS_1062	NZ	G_GLU_1046	OE1	3.161
3ETB	G_LYS_1062	NZ	G_GLU_1046	OE2	3.812
3ETB	G_LYS_1066	NZ	G_ASP_1086	OD2	3.138
3ETB	G_ARG_1094	NH1	G_ASP_1101	OD1	2.918
3ETB	H_ARG_24	NH1	I_ASP_70	OD1	3.544
3ETB	H_ARG_24	NH1	I_ASP_70	OD2	3.118
3ETB	H_ARG_24	NH2	I_ASP_70	OD1	3.662
3ETB	H_ARG_24	NH2	I_ASP_70	OD2	3.905
3ETB	H_ARG_30	NH1	L_ASP_658	OD1	3.824
3ETB	H_ARG_30	NH1	L_ASP_658	OD2	2.913

3ETB	H_ARG_53	NH1	L_GLU_654	OE1	3.771
3ETB	H_ARG_53	NH2	L_GLU_654	OE1	3.669
3ETB	H_ARG_61	NH1	H_GLU_79	OE2	3.579
3ETB	H_ARG_61	NH2	H_GLU_79	OE1	3.984
3ETB	H_ARG_61	NH2	H_ASP_82	OD1	2.635
3ETB	H_ARG_61	NH2	H_ASP_82	OD2	2.472
3ETB	H_ARG_1050	NH2	L_ASP_683	OD2	3.159
3ETB	H_LYS_1062	NZ	H_GLU_1046	OE1	3.123
3ETB	H_LYS_1062	NZ	H_GLU_1046	OE2	3.731
3ETB	H_LYS_1066	NZ	H_ASP_1086	OD1	3.989
3ETB	H_LYS_1066	NZ	H_ASP_1086	OD2	3.171
3ETB	H_ARG_1094	NH1	H_ASP_1101	OD1	2.766
3ETB	I_ARG_24	NH1	H_ASP_70	OD1	3.448
3ETB	I_ARG_24	NH1	H_ASP_70	OD2	2.998
3ETB	I_ARG_24	NH2	H_ASP_70	OD1	3.537
3ETB	I_ARG_24	NH2	H_ASP_70	OD2	3.789
3ETB	I_ARG_30	NH1	M_ASP_658	OD2	3.315
3ETB	I_ARG_53	NH1	M_GLU_654	OE1	3.885
3ETB	I_ARG_53	NH2	M_GLU_654	OE1	3.890
3ETB	I_ARG_61	NH1	I_GLU_79	OE2	3.590
3ETB	I_ARG_61	NH2	I_ASP_82	OD1	2.608
3ETB	I_ARG_61	NH2	I_ASP_82	OD2	2.422
3ETB	I_ARG_1050	NH2	M_ASP_683	OD2	3.093
3ETB	I_LYS_1062	NZ	I_GLU_1046	OE1	3.276
3ETB	I_LYS_1062	NZ	I_GLU_1046	OE2	3.841
3ETB	I_LYS_1066	NZ	I_ASP_1086	OD1	3.951
3ETB	I_LYS_1066	NZ	I_ASP_1086	OD2	3.038
3ETB	I_ARG_1094	NH1	I_ASP_1101	OD1	2.853
3ETB	J_HIS_597	ND1	J_GLU_704	OE2	3.548
3ETB	J_HIS_597	NE2	J_ASP_608	OD1	2.727
3ETB	J_LYS_613	NZ	J_GLU_609	OE1	3.973
3ETB	J_LYS_633	NZ	J_ASP_634	OD1	3.253
3ETB	J_LYS_653	NZ	G_ASP_17	OD1	2.972
3ETB	J_ARG_659	NH1	J_ASP_661	OD1	3.263
3ETB	J_ARG_659	NH1	J_ASP_661	OD2	3.124
3ETB	J_ARG_659	NH2	J_ASP_661	OD1	3.589
3ETB	J_ARG_669	NH2	J_ASP_671	OD1	3.245
3ETB	J_ARG_669	NH2	J_ASP_671	OD2	3.457
3ETB	J_LYS_679	NZ	J_GLU_625	OE1	3.523
3ETB	J_LYS_684	NZ	F_ASP_1054	OD1	3.728
3ETB	J_LYS_684	NZ	F_ASP_1054	OD2	3.401
3ETB	J_LYS_684	NZ	F_ASP_1056	OD1	3.220
3ETB	J_LYS_684	NZ	F_ASP_1056	OD2	3.481
3ETB	K_HIS_597	ND1	K_GLU_704	OE2	3.588
3ETB	K_HIS_597	NE2	K_ASP_608	OD1	2.693
3ETB	K_HIS_597	NE2	K_ASP_608	OD2	3.992
3ETB	K_LYS_613	NZ	K_GLU_609	OE1	3.913
3ETB	K_LYS_633	NZ	K_ASP_634	OD1	3.167
3ETB	K_LYS_653	NZ	F_ASP_17	OD1	3.083
3ETB	K_ARG_659	NH1	K_ASP_661	OD1	3.380
3ETB	K_ARG_659	NH1	K_ASP_661	OD2	3.241
3ETB	K_ARG_659	NH2	K_ASP_661	OD1	3.692
3ETB	K_ARG_669	NH2	K_ASP_671	OD1	3.263
3ETB	K_ARG_669	NH2	K_ASP_671	OD2	3.367
3ETB	K_LYS_679	NZ	K_GLU_625	OE1	3.601
3ETB	K_LYS_684	NZ	G_ASP_1054	OD1	3.379
3ETB	K_LYS_684	NZ	G_ASP_1054	OD2	3.075
3ETB	K_LYS_684	NZ	G_ASP_1056	OD1	3.162

3ETB	K_LYS_684	NZ	G_ASP_1056	OD2	3.578
3ETB	L_HIS_597	ND1	L_GLU_704	OE2	3.614
3ETB	L_HIS_597	NE2	L_ASP_608	OD1	2.704
3ETB	L_LYS_613	NZ	L_GLU_609	OE1	3.941
3ETB	L_LYS_633	NZ	L_ASP_634	OD1	3.041
3ETB	L_LYS_653	NZ	L_ASP_17	OD1	2.978
3ETB	L_ARG_659	NH1	L_ASP_661	OD1	3.373
3ETB	L_ARG_659	NH1	L_ASP_661	OD2	3.245
3ETB	L_ARG_659	NH2	L_ASP_661	OD1	3.600
3ETB	L_ARG_669	NH2	L_ASP_671	OD1	3.400
3ETB	L_ARG_669	NH2	L_ASP_671	OD2	3.495
3ETB	L_LYS_679	NZ	L_GLU_625	OE1	3.532
3ETB	L_LYS_684	NZ	H_ASP_1056	OD1	3.616
3ETB	L_LYS_684	NZ	H_ASP_1056	OD2	3.187
3ETB	M_HIS_597	ND1	M_GLU_704	OE2	3.644
3ETB	M_HIS_597	NE2	M_ASP_608	OD1	2.880
3ETB	M_LYS_613	NZ	M_GLU_609	OE1	3.907
3ETB	M_LYS_633	NZ	M_ASP_634	OD1	3.141
3ETB	M_LYS_653	NZ	H_ASP_17	OD1	3.060
3ETB	M_ARG_659	NH1	M_ASP_661	OD1	3.383
3ETB	M_ARG_659	NH1	M_ASP_661	OD2	3.234
3ETB	M_ARG_659	NH2	M_ASP_661	OD1	3.730
3ETB	M_ARG_669	NH2	M_ASP_671	OD1	3.256
3ETB	M_ARG_669	NH2	M_ASP_671	OD2	3.369
3ETB	M_LYS_679	NZ	M_GLU_625	OE1	3.500
3ETB	M_LYS_684	NZ	L_ASP_1054	OD1	3.625
3ETB	M_LYS_684	NZ	L_ASP_1054	OD2	3.167
3ETB	M_LYS_684	NZ	L_ASP_1056	OD1	3.241
3ETB	M_LYS_684	NZ	L_ASP_1056	OD2	3.478
3EYV	L_LYS_55	NZ	H_ASP_102	OD2	3.565
3EYV	L_ARG_66	NH2	L_GLU_86	OE2	3.710
3EYV	L_ARG_66	NH2	L_ASP_87	OD1	2.915
3EYV	L_ARG_66	NH2	L_ASP_87	OD2	3.931
3EYV	L_LYS_108	NZ	L_GLU_170	OE1	3.179
3EYV	L_LYS_154	NZ	L_GLU_200	OE2	3.356
3EYV	L_LYS_188	NZ	L_GLU_192	OE1	3.296
3EYV	L_LYS_188	NZ	L_GLU_192	OE2	2.586
3EYV	L_HIS_194	ND1	L_ASP_156	OD2	2.824
3EYV	L_HIS_194	NE2	L_ASP_190	OD1	3.486
3EYV	H_ARG_38	NH1	H_ASP_90	OD1	2.819
3EYV	H_ARG_38	NH2	H_GLU_46	OE1	3.776
3EYV	H_ARG_38	NH2	H_GLU_46	OE2	3.233
3EYV	H_ARG_38	NH2	H_ASP_90	OD1	3.948
3EYV	H_LYS_65	NZ	H_ASP_59	OD1	2.876
3EYV	H_ARG_67	NH1	H_ASP_90	OD1	3.779
3EYV	H_ARG_67	NH1	H_ASP_90	OD2	2.779
3EYV	H_ARG_67	NH2	H_ASP_90	OD1	3.386
3EYV	H_ARG_67	NH2	H_ASP_90	OD2	3.752
3EYV	H_ARG_101	NH1	H_ASP_31	OD2	3.262
3EYV	H_ARG_101	NH2	H_ASP_31	OD2	3.521
3EYV	H_LYS_149	NZ	H_ASP_150	OD1	3.279
3EYV	H_LYS_149	NZ	H_ASP_150	OD2	3.718
3EYV	H_LYS_212	NZ	H_ASP_214	OD1	3.958
3EYV	H_LYS_212	NZ	H_ASP_214	OD2	2.546
3EYV	H_LYS_215	NZ	L_GLU_128	OE2	3.627
3EYV	H_LYS_216	NZ	H_GLU_218	OE2	3.932
3EYV	A_LYS_55	NZ	B_ASP_102	OD2	3.151
3EYV	A_ARG_66	NH2	A_GLU_86	OE2	3.631

3EYV	A_ARG_66	NH2	A_ASP_87	OD1	3.103
3EYV	A_ARG_66	NH2	A_ASP_87	OD2	3.416
3EYV	A_LYS_108	NZ	A_GLU_170	OE1	3.086
3EYV	A_LYS_108	NZ	A_GLU_170	OE2	3.645
3EYV	A_LYS_154	NZ	A_GLU_200	OE1	3.963
3EYV	A_LYS_154	NZ	A_GLU_200	OE2	2.945
3EYV	A_LYS_193	NZ	A_ASP_190	OD1	3.557
3EYV	A_HIS_194	ND1	A_ASP_156	OD1	2.892
3EYV	B_ARG_38	NH1	B_ASP_90	OD1	2.718
3EYV	B_ARG_38	NH2	B_GLU_46	OE1	3.428
3EYV	B_ARG_38	NH2	B_GLU_46	OE2	3.023
3EYV	B_ARG_38	NH2	B_ASP_90	OD1	3.972
3EYV	B_LYS_65	NZ	B_ASP_59	OD1	2.790
3EYV	B_ARG_67	NH1	B_ASP_90	OD1	3.866
3EYV	B_ARG_67	NH1	B_ASP_90	OD2	2.720
3EYV	B_ARG_67	NH2	B_ASP_90	OD1	3.285
3EYV	B_ARG_67	NH2	B_ASP_90	OD2	3.497
3EYV	B_ARG_87	NH1	B_GLU_89	OE1	3.883
3EYV	B_ARG_101	NH1	B_ASP_31	OD2	3.502
3EYV	B_LYS_220	NZ	A_ASP_127	OD2	3.402
3FMG	L_LYS_50	NZ	H_ASP_106	OD1	3.132
3FMG	L_ARG_61	NH1	L_ASP_82	OD1	3.084
3FMG	L_ARG_61	NH1	L_ASP_82	OD2	2.397
3FMG	L_ARG_61	NH2	L_GLU_81	OE2	3.990
3FMG	L_ARG_61	NH2	L_ASP_82	OD2	3.861
3FMG	L_LYS_103	NZ	L_GLU_105	OE2	2.781
3FMG	L_LYS_103	NZ	L_ASP_165	OD1	3.422
3FMG	L_LYS_103	NZ	L_ASP_165	OD2	3.673
3FMG	L_LYS_147	NZ	L_GLU_154	OE1	3.671
3FMG	L_LYS_149	NZ	L_GLU_195	OE1	2.879
3FMG	L_LYS_149	NZ	L_GLU_195	OE2	3.536
3FMG	L_ARG_155	NH1	L_GLU_185	OE2	3.733
3FMG	L_ARG_155	NH2	L_GLU_185	OE2	3.838
3FMG	L_LYS_169	NZ	L_ASP_167	OD1	3.814
3FMG	L_LYS_183	NZ	L_GLU_187	OE1	3.890
3FMG	L_LYS_183	NZ	L_GLU_187	OE2	3.515
3FMG	L_HIS_189	ND1	L_ASP_151	OD2	3.000
3FMG	L_HIS_189	NE2	L_GLU_185	OE1	3.777
3FMG	L_LYS_199	NZ	L_ASP_110	OD1	3.137
3FMG	L_LYS_199	NZ	L_ASP_110	OD2	3.503
3FMG	H_LYS_19	NZ	H_GLU_10	OE1	2.764
3FMG	H_LYS_19	NZ	H_GLU_10	OE2	2.857
3FMG	H_LYS_38	NZ	H_ASP_92	OD1	3.712
3FMG	H_LYS_64	NZ	L_ASP_1	OD2	3.241
3FMG	H_LYS_68	NZ	H_ASP_92	OD1	3.504
3FMG	H_LYS_68	NZ	H_ASP_92	OD2	2.490
3FMG	H_ARG_100	NH1	H_ASP_111	OD1	2.791
3FMG	H_ARG_100	NH1	H_ASP_111	OD2	3.868
3FMG	H_ARG_100	NH2	H_ASP_111	OD1	3.539
3FMG	H_ARG_100	NH2	H_ASP_111	OD2	3.163
3FMG	H_HIS_102	ND1	H_ASP_111	OD2	2.692
3FMG	H_HIS_108	ND1	H_GLU_35	OE1	3.839
3FMG	H_HIS_108	ND1	H_GLU_50	OE1	3.875
3FMG	H_HIS_108	ND1	H_GLU_50	OE2	3.683
3FMG	H_HIS_108	NE2	H_GLU_50	OE1	3.647
3FMG	H_LYS_125	NZ	H_ASP_193	OD2	3.410
3FMG	H_LYS_228	NZ	H_ASP_230	OD1	2.777
3FMG	A_LYS_143	NZ	A_GLU_88	OE1	3.153

3FMG	A_LYS_183	NZ	A_ASP_228	OD2	3.491
3FMG	A_LYS_194	NZ	A_GLU_217	OE2	2.678
3FMG	A_LYS_250	NZ	A_ASP_179	OD1	3.375
3FMG	A_LYS_251	NZ	A_ASP_157	OD1	2.865
3FMG	A_LYS_251	NZ	A_ASP_157	OD2	3.990
3FMG	A_ARG_255	NH1	A_GLU_162	OE1	3.900
3FMG	A_ARG_255	NH1	A_GLU_162	OE2	3.506
3FMG	A_ARG_255	NH2	A_GLU_162	OE1	3.265
3FMG	A_ARG_283	NH1	A_GLU_256	OE1	2.718
3FMG	A_ARG_283	NH1	A_GLU_256	OE2	3.791
3FMG	A_ARG_283	NH2	A_GLU_256	OE1	3.447
3FMG	A_ARG_283	NH2	A_GLU_256	OE2	2.994
3FMG	A_LYS_312	NZ	A_GLU_282	OE1	3.755
3FMG	A_LYS_312	NZ	A_GLU_282	OE2	3.300
3G39	A_ARG_57	NH2	A_ASP_59	OD1	3.706
3G39	A_ARG_57	NH2	A_ASP_59	OD2	2.784
3G39	A_ARG_125	NH2	A_GLU_159	OE1	3.701
3G39	A_ARG_125	NH2	A_GLU_159	OE2	2.699
3G39	A_ARG_155	NH2	A_ASP_143	OD1	3.190
3G39	A_ARG_155	NH2	A_ASP_143	OD2	3.105
3G3A	A_ARG_57	NH2	A_ASP_59	OD2	3.133
3G3A	A_ARG_155	NH1	A_ASP_143	OD1	3.039
3G3A	A_ARG_155	NH1	A_ASP_143	OD2	3.682
3G3A	B_LYS_1	NZ	B_GLU_7	OE2	2.851
3G3A	B_ARG_61	NH2	A_ASP_59	OD2	3.447
3G3A	B_ARG_73	NH1	A_ASP_61	OD1	2.630
3G3A	B_ARG_73	NH1	A_ASP_61	OD2	3.494
3G3A	B_ARG_73	NH2	A_ASP_59	OD2	3.260
3G3A	B_ARG_73	NH2	A_ASP_61	OD1	3.287
3G3A	B_ARG_73	NH2	A_ASP_61	OD2	2.479
3G3A	B_LYS_97	NZ	B_ASP_101	OD1	3.864
3G3A	B_LYS_97	NZ	B_ASP_101	OD2	3.365
3G3A	B_ARG_112	NH1	A_ASP_141	OD1	3.611
3G3A	B_ARG_112	NH1	A_ASP_141	OD2	2.906
3G3A	B_ARG_112	NH2	A_ASP_141	OD1	2.901
3G3A	B_ARG_112	NH2	A_ASP_141	OD2	3.689
3G3A	B_ARG_112	NH2	A_ASP_143	OD2	3.389
3G3A	C_LYS_43	NZ	C_GLU_45	OE2	3.006
3G3A	C_ARG_57	NH2	C_ASP_59	OD1	3.619
3G3A	C_ARG_57	NH2	C_ASP_59	OD2	2.899
3G3A	C_ARG_94	NH2	C_ASP_119	OD1	3.786
3G3A	C_ARG_155	NH1	C_ASP_143	OD1	2.753
3G3A	C_ARG_155	NH1	C_ASP_143	OD2	3.605
3G3A	D_LYS_1	NZ	D_GLU_7	OE1	3.499
3G3A	D_LYS_1	NZ	D_GLU_7	OE2	2.566
3G3A	D_ARG_61	NH1	C_ASP_59	OD2	3.676
3G3A	D_ARG_61	NH2	C_ASP_59	OD1	3.900
3G3A	D_ARG_61	NH2	C_ASP_59	OD2	3.137
3G3A	D_ARG_73	NH1	C_ASP_61	OD1	3.720
3G3A	D_ARG_73	NH1	C_ASP_61	OD2	2.705
3G3A	D_ARG_73	NH2	C_ASP_59	OD2	2.913
3G3A	D_ARG_73	NH2	C_ASP_61	OD1	2.638
3G3A	D_ARG_73	NH2	C_ASP_61	OD2	3.209
3G3A	D_LYS_97	NZ	D_ASP_101	OD1	3.653
3G3A	D_LYS_97	NZ	D_ASP_101	OD2	2.889
3G3A	D_ARG_112	NH1	C_ASP_141	OD1	3.483
3G3A	D_ARG_112	NH1	C_ASP_141	OD2	2.837
3G3A	D_ARG_112	NH2	C_ASP_141	OD1	2.752

3G3A	D_ARG.112	NH2	C_ASP.141	OD2	3.622
3G3A	D_ARG.112	NH2	C_ASP.143	OD2	3.602
3G3A	E_ARG.57	NH2	E_ASP.59	OD1	3.565
3G3A	E_ARG.57	NH2	E_ASP.59	OD2	3.054
3G3A	E_ARG.155	NH1	E_ASP.143	OD1	2.889
3G3A	F_LYS.1	NZ	F_GLU.7	OE2	2.598
3G3A	F_ARG.61	NH1	E_ASP.59	OD2	3.922
3G3A	F_ARG.61	NH2	E_ASP.59	OD1	3.681
3G3A	F_ARG.61	NH2	E_ASP.59	OD2	2.804
3G3A	F_ARG.73	NH1	E_ASP.61	OD1	3.367
3G3A	F_ARG.73	NH1	E_ASP.61	OD2	2.915
3G3A	F_ARG.73	NH2	E_ASP.59	OD2	2.686
3G3A	F_ARG.73	NH2	E_ASP.61	OD1	2.874
3G3A	F_ARG.73	NH2	E_ASP.61	OD2	3.960
3G3A	F_LYS.97	NZ	F_ASP.101	OD1	3.077
3G3A	F_LYS.97	NZ	F_ASP.101	OD2	2.523
3G3A	F_ARG.112	NH1	E_ASP.141	OD1	3.733
3G3A	F_ARG.112	NH1	E_ASP.141	OD2	3.195
3G3A	F_ARG.112	NH2	E_ASP.141	OD1	3.001
3G3A	F_ARG.112	NH2	E_ASP.141	OD2	3.839
3G3A	F_ARG.112	NH2	E_ASP.143	OD2	3.491
3G3A	G_ARG.57	NH2	G_ASP.59	OD1	3.304
3G3A	G_ARG.57	NH2	G_ASP.59	OD2	2.668
3G3A	G_ARG.125	NH2	G_GLU.159	OE1	3.890
3G3A	G_ARG.125	NH2	G_GLU.159	OE2	3.239
3G3A	G_ARG.155	NH1	G_ASP.143	OD1	3.004
3G3A	G_ARG.155	NH1	G_ASP.143	OD2	3.791
3G3A	H_LYS.1	NZ	H_GLU.7	OE2	2.729
3G3A	H_LYS.13	NZ	H_ASP.18	OD2	3.987
3G3A	H_ARG.61	NH2	G_ASP.59	OD2	3.367
3G3A	H_ARG.73	NH1	G_ASP.59	OD2	3.259
3G3A	H_ARG.73	NH2	G_ASP.59	OD2	3.473
3G3A	H_ARG.73	NH2	G_ASP.61	OD1	2.486
3G3A	H_ARG.73	NH2	G_ASP.61	OD2	2.698
3G3A	H_ARG.112	NH1	G_ASP.141	OD1	3.280
3G3A	H_ARG.112	NH1	G_ASP.143	OD2	3.578
3G3A	H_ARG.112	NH2	G_ASP.141	OD1	3.102
3G3A	H_ARG.112	NH2	G_ASP.141	OD2	2.609
3G3B	A_LYS.43	NZ	A_GLU.45	OE1	2.858
3G3B	A_LYS.43	NZ	A_GLU.45	OE2	2.415
3G3B	A_ARG.57	NH2	A_ASP.59	OD1	3.729
3G3B	A_ARG.57	NH2	A_ASP.59	OD2	2.852
3G3B	A_HIS.142	ND1	A_ASP.143	OD1	3.605
3G3B	A_ARG.155	NH1	A_ASP.143	OD1	2.852
3G3B	B_LYS.1	NZ	B_GLU.7	OE1	3.921
3G3B	B_LYS.1	NZ	B_GLU.7	OE2	2.875
3G3B	B_ARG.61	NH2	A_ASP.59	OD1	3.551
3G3B	B_ARG.61	NH2	A_ASP.59	OD2	3.590
3G3B	B_ARG.73	NH1	A_ASP.61	OD1	2.527
3G3B	B_ARG.73	NH1	A_ASP.61	OD2	3.439
3G3B	B_ARG.73	NH2	A_ASP.59	OD2	2.967
3G3B	B_ARG.73	NH2	A_ASP.61	OD1	3.469
3G3B	B_ARG.73	NH2	A_ASP.61	OD2	2.765
3G3B	B_ARG.112	NH1	A_ASP.141	OD1	3.569
3G3B	B_ARG.112	NH1	A_ASP.141	OD2	2.625
3G3B	B_ARG.112	NH2	A_ASP.141	OD1	2.926
3G3B	B_ARG.112	NH2	A_ASP.141	OD2	3.538
3G3B	B_ARG.112	NH2	A_ASP.143	OD2	3.804

3G3B	B_ARG_125	NH1	B_ASP_119	OD1	3.478
3G3B	B_ARG_125	NH1	B_ASP_119	OD2	3.346
3G3B	C_LYS_43	NZ	C_GLU_45	OE1	3.803
3G3B	C_LYS_43	NZ	C_GLU_45	OE2	3.490
3G3B	C_ARG_57	NH2	C_ASP_59	OD1	3.660
3G3B	C_ARG_57	NH2	C_ASP_59	OD2	2.836
3G3B	C_HIS_142	NE2	C_ASP_143	OD1	3.850
3G3B	C_ARG_155	NH2	C_ASP_143	OD1	2.863
3G3B	C_ARG_155	NH2	C_ASP_143	OD2	3.947
3G3B	D_LYS_1	NZ	D_GLU_7	OE2	2.651
3G3B	D_LYS_13	NZ	D_ASP_18	OD2	3.185
3G3B	D_ARG_61	NH2	C_ASP_59	OD1	3.954
3G3B	D_ARG_73	NH1	C_ASP_61	OD1	2.753
3G3B	D_ARG_73	NH1	C_ASP_61	OD2	3.824
3G3B	D_ARG_73	NH2	C_ASP_59	OD2	3.136
3G3B	D_ARG_73	NH2	C_ASP_61	OD1	3.224
3G3B	D_ARG_73	NH2	C_ASP_61	OD2	2.702
3G3B	D_ARG_112	NH1	C_ASP_141	OD1	3.812
3G3B	D_ARG_112	NH1	C_ASP_141	OD2	2.690
3G3B	D_ARG_112	NH2	C_ASP_141	OD1	2.826
3G3B	D_ARG_112	NH2	C_ASP_141	OD2	3.301
3G3B	D_ARG_112	NH2	C_ASP_143	OD2	3.656
3G3B	D_ARG_125	NH2	D_ASP_119	OD1	2.448
3G3B	D_ARG_125	NH2	D_ASP_119	OD2	3.449
3G3B	E_ARG_57	NH2	E_ASP_59	OD1	3.602
3G3B	E_ARG_57	NH2	E_ASP_59	OD2	2.890
3G3B	E_HIS_142	ND1	E_ASP_143	OD1	3.479
3G3B	E_ARG_155	NH2	E_ASP_143	OD1	3.325
3G3B	F_LYS_1	NZ	F_GLU_7	OE1	3.789
3G3B	F_LYS_1	NZ	F_GLU_7	OE2	2.690
3G3B	F_ARG_61	NH2	E_ASP_59	OD2	3.820
3G3B	F_ARG_73	NH1	E_ASP_61	OD1	2.535
3G3B	F_ARG_73	NH1	E_ASP_61	OD2	3.949
3G3B	F_ARG_73	NH2	E_ASP_59	OD2	2.812
3G3B	F_ARG_73	NH2	E_ASP_61	OD1	3.056
3G3B	F_ARG_73	NH2	E_ASP_61	OD2	2.934
3G3B	F_ARG_112	NH1	E_ASP_141	OD2	2.714
3G3B	F_ARG_112	NH2	E_ASP_141	OD1	3.020
3G3B	F_ARG_112	NH2	E_ASP_141	OD2	3.176
3G3B	F_ARG_112	NH2	E_ASP_143	OD2	3.737
3G3B	G_ARG_57	NH2	G_ASP_59	OD1	3.515
3G3B	G_ARG_57	NH2	G_ASP_59	OD2	3.110
3G3B	G_HIS_142	NE2	G_ASP_143	OD1	3.761
3G3B	G_ARG_155	NH2	G_ASP_143	OD1	2.619
3G3B	G_ARG_155	NH2	G_ASP_143	OD2	3.786
3G3B	H_LYS_1	NZ	H_GLU_7	OE1	3.238
3G3B	H_LYS_1	NZ	H_GLU_7	OE2	2.526
3G3B	H_ARG_61	NH1	H_ASP_48	OD2	3.554
3G3B	H_ARG_73	NH1	G_ASP_61	OD1	2.839
3G3B	H_ARG_73	NH1	G_ASP_61	OD2	3.791
3G3B	H_ARG_73	NH2	G_ASP_59	OD2	2.431
3G3B	H_ARG_73	NH2	G_ASP_61	OD1	3.464
3G3B	H_ARG_73	NH2	G_ASP_61	OD2	2.896
3G3B	H_ARG_112	NH1	G_ASP_141	OD1	3.676
3G3B	H_ARG_112	NH1	G_ASP_141	OD2	2.564
3G3B	H_ARG_112	NH2	G_ASP_141	OD1	2.813
3G3B	H_ARG_112	NH2	G_ASP_141	OD2	3.280
3G3B	H_ARG_112	NH2	G_ASP_143	OD2	3.506

3GGW	A_LYS_27	NZ	A_GLU_93	OE1	3.004
3GGW	A_LYS_27	NZ	A_GLU_93	OE2	3.494
3GGW	A_HIS_27D	ND1	A_ASP_28	OD1	3.397
3GGW	A_HIS_27D	ND1	A_ASP_28	OD2	3.638
3GGW	A_ARG_61	NH1	A_ASP_82	OD1	3.619
3GGW	A_ARG_61	NH1	A_ASP_82	OD2	2.849
3GGW	A_ARG_61	NH2	A_GLU_79	OE1	3.759
3GGW	A_ARG_61	NH2	A_ASP_82	OD1	2.856
3GGW	A_ARG_61	NH2	A_ASP_82	OD2	3.530
3GGW	A_ARG_96	NH2	B_GLU_50	OE1	3.590
3GGW	A_ARG_96	NH2	B_GLU_50	OE2	2.762
3GGW	A_ARG_155	NH1	A_GLU_185	OE1	3.605
3GGW	A_ARG_188	NH2	A_GLU_185	OE2	2.743
3GGW	A_HIS_189	ND1	A_GLU_185	OE1	3.933
3GGW	A_LYS_199	NZ	A_ASP_110	OD2	3.552
3GGW	B_ARG_38	NH1	B_ASP_86	OD1	2.900
3GGW	B_ARG_38	NH2	B_GLU_46	OE1	3.283
3GGW	B_ARG_38	NH2	B_GLU_46	OE2	3.311
3GGW	B_ARG_38	NH2	B_ASP_86	OD1	3.834
3GGW	B_LYS_43	NZ	B_GLU_42	OE2	3.946
3GGW	B_ARG_52	NH1	E_ASP_4	OD2	3.092
3GGW	B_LYS_64	NZ	B_GLU_61	OE1	3.190
3GGW	B_LYS_66	NZ	B_ASP_86	OD1	3.381
3GGW	B_LYS_66	NZ	B_ASP_86	OD2	2.679
3GGW	B_ARG_71	NH2	B_ASP_73	OD1	3.573
3GGW	B_ARG_83	NH1	B_GLU_85	OE1	3.507
3GGW	B_LYS_207	NZ	B_ASP_209	OD1	3.783
3GGW	B_LYS_207	NZ	B_ASP_209	OD2	2.712
3GGW	B_LYS_210	NZ	A_GLU_123	OE2	3.208
3GGW	C_ARG_24	NH2	C_ASP_70	OD2	3.799
3GGW	C_LYS_27	NZ	C_GLU_93	OE1	2.551
3GGW	C_HIS_27D	ND1	C_ASP_28	OD1	3.282
3GGW	C_HIS_27D	ND1	C_ASP_28	OD2	3.541
3GGW	C_LYS_39	NZ	C_GLU_81	OE2	2.827
3GGW	C_ARG_61	NH1	C_ASP_82	OD1	3.646
3GGW	C_ARG_61	NH1	C_ASP_82	OD2	2.827
3GGW	C_ARG_61	NH2	C_GLU_79	OE1	3.494
3GGW	C_ARG_61	NH2	C_GLU_79	OE2	3.557
3GGW	C_ARG_61	NH2	C_ASP_82	OD1	2.827
3GGW	C_ARG_61	NH2	C_ASP_82	OD2	3.383
3GGW	C_ARG_96	NH2	D_GLU_50	OE1	3.555
3GGW	C_ARG_96	NH2	D_GLU_50	OE2	2.962
3GGW	C_LYS_142	NZ	C_GLU_105	OE1	3.612
3GGW	C_ARG_155	NH1	C_GLU_185	OE1	2.976
3GGW	C_ARG_155	NH1	C_GLU_185	OE2	3.624
3GGW	C_ARG_155	NH2	C_GLU_185	OE1	3.679
3GGW	C_ARG_155	NH2	C_GLU_185	OE2	2.798
3GGW	C_LYS_183	NZ	C_GLU_187	OE1	2.937
3GGW	C_LYS_183	NZ	C_GLU_187	OE2	3.524
3GGW	C_ARG_188	NH2	C_ASP_184	OD1	3.157
3GGW	C_ARG_188	NH2	C_ASP_184	OD2	3.938
3GGW	C_LYS_199	NZ	C_ASP_110	OD2	3.525
3GGW	D_ARG_38	NH1	D_ASP_86	OD1	2.856
3GGW	D_ARG_38	NH2	D_GLU_46	OE1	3.438
3GGW	D_ARG_38	NH2	D_GLU_46	OE2	3.122
3GGW	D_ARG_38	NH2	D_ASP_86	OD1	3.653
3GGW	D_ARG_52	NH1	F_ASP_4	OD2	3.127
3GGW	D_LYS_64	NZ	D_GLU_61	OE1	2.566

3GGW	D_LYS_64	NZ	D_GLU_61	OE2	3.883
3GGW	D_LYS_66	NZ	D_ASP_86	OD1	3.597
3GGW	D_LYS_66	NZ	D_ASP_86	OD2	2.711
3GGW	D_ARG_71	NH2	D_ASP_73	OD1	3.666
3GGW	D_LYS_210	NZ	C_GLU_123	OE2	2.871
3GGW	D_ARG_215	NH2	C_GLU_213	OE1	3.834
3GGW	D_ARG_215	NH2	C_GLU_213	OE2	2.618
3GHB	L_ARG_61	NH1	L_ASP_82	OD1	3.774
3GHB	L_ARG_61	NH1	L_ASP_82	OD2	2.845
3GHB	L_ARG_61	NH2	L_ASP_82	OD1	2.959
3GHB	L_ARG_61	NH2	L_ASP_82	OD2	3.458
3GHB	L_LYS_110	NZ	L_GLU_198	OE1	2.584
3GHB	L_HIS_188	NE2	L_ASP_151	OD2	3.966
3GHB	H_ARG_38	NH1	H_ASP_86	OD1	2.865
3GHB	H_ARG_38	NH2	H_GLU_46	OE1	2.815
3GHB	H_ARG_38	NH2	H_GLU_46	OE2	3.771
3GHB	H_ARG_50	NH1	H_ASP_58	OD2	3.042
3GHB	H_ARG_66	NH1	H_ASP_86	OD1	3.838
3GHB	H_ARG_66	NH1	H_ASP_86	OD2	2.797
3GHB	H_ARG_66	NH2	H_ASP_86	OD1	3.183
3GHB	H_ARG_66	NH2	H_ASP_86	OD2	3.533
3GHB	H_ARG_71	NH2	H_ASP_73	OD1	3.367
3GHB	H_LYS_83	NZ	H_GLU_85	OE2	3.603
3GHB	H_LYS_143	NZ	L_GLU_124	OE2	2.614
3GHB	H_LYS_209	NZ	L_GLU_123	OE1	2.751
3GHB	H_LYS_209	NZ	L_GLU_123	OE2	3.411
3GHB	P_LYS_305	NZ	H_GLU_100E	OE1	3.508
3GHB	P_LYS_305	NZ	H_ASP_100F	OD2	3.835
3GHB	M_ARG_61	NH1	M_ASP_82	OD1	3.907
3GHB	M_ARG_61	NH1	M_ASP_82	OD2	3.095
3GHB	M_ARG_61	NH2	M_ASP_82	OD1	2.973
3GHB	M_ARG_61	NH2	M_ASP_82	OD2	3.466
3GHB	M_LYS_110	NZ	M_GLU_198	OE1	2.627
3GHB	L_ARG_38	NH1	L_ASP_86	OD1	2.974
3GHB	L_ARG_38	NH2	L_GLU_46	OE1	2.852
3GHB	L_ARG_38	NH2	L_GLU_46	OE2	3.761
3GHB	L_ARG_38	NH2	L_ASP_86	OD1	3.952
3GHB	L_ARG_50	NH1	L_ASP_58	OD2	2.747
3GHB	L_ARG_66	NH1	L_ASP_86	OD1	3.695
3GHB	L_ARG_66	NH1	L_ASP_86	OD2	2.620
3GHB	L_ARG_66	NH2	L_ASP_86	OD1	3.166
3GHB	L_ARG_66	NH2	L_ASP_86	OD2	3.599
3GHB	L_ARG_71	NH2	L_ASP_73	OD1	3.399
3GHB	L_LYS_75	NZ	L_ASP_72	OD2	3.232
3GHB	L_LYS_143	NZ	M_GLU_124	OE2	2.607
3GHB	L_LYS_209	NZ	M_GLU_123	OE1	2.988
3GHB	L_LYS_209	NZ	M_GLU_123	OE2	3.773
3GHB	L_ARG_210	NH1	L_GLU_212	OE2	3.691
3GHB	Q_LYS_305	NZ	L_ASP_100F	OD1	3.174
3GHE	L_LYS_53	NZ	L_ASP_50	OD2	3.235
3GHE	L_ARG_61	NH1	L_ASP_82	OD1	2.784
3GHE	L_ARG_61	NH1	L_ASP_82	OD2	3.800
3GHE	L_ARG_61	NH2	L_ASP_82	OD1	3.483
3GHE	L_ARG_61	NH2	L_ASP_82	OD2	3.001
3GHE	L_LYS_149	NZ	L_GLU_203	OE2	2.932
3GHE	H_ARG_38	NH1	H_ASP_86	OD1	3.169
3GHE	H_ARG_38	NH2	H_GLU_46	OE1	2.908
3GHE	H_LYS_64	NZ	H_ASP_61	OD2	2.560

3GHE	H_ARG_66	NH1	H_ASP_86	OD2	2.889
3GHE	H_ARG_66	NH2	H_ASP_86	OD1	2.967
3GHE	H_ARG_66	NH2	H_ASP_86	OD2	3.314
3GHE	H_ARG_94	NH2	H_ASP_101	OD1	2.641
3GHE	H_ARG_94	NH2	H_ASP_101	OD2	3.324
3GHE	H_LYS_143	NZ	L_GLU_124	OE2	2.684
3GHE	H_LYS_209	NZ	L_GLU_123	OE1	2.541
3GHE	H_LYS_209	NZ	L_GLU_123	OE2	3.149
3GHE	H_ARG_210	NH1	H_GLU_212	OE2	2.984
3GHE	H_ARG_210	NH2	H_GLU_212	OE2	3.330
3GHE	P_ARG_304	NH1	H_ASP_100A	OD1	3.397
3GHE	P_ARG_304	NH2	H_ASP_100A	OD1	3.243
3GHE	P_ARG_304	NH2	H_ASP_100A	OD2	3.833
3GHE	P_HIS_308	ND1	H_ASP_100H	OD2	3.415
3GHE	P_ARG_315	NH1	H_GLU_95	OE1	3.518
3GHE	P_ARG_315	NH1	H_GLU_95	OE2	2.720
3GHE	P_ARG_315	NH2	H_GLU_95	OE2	3.104
3GJF	A_HIS_3	NE2	A_ASP_29	OD2	3.680
3GJF	A_ARG_6	NH1	A_ASP_102	OD1	3.006
3GJF	A_ARG_14	NH1	A_ASP_39	OD1	3.408
3GJF	A_ARG_14	NH1	A_ASP_39	OD2	2.727
3GJF	A_ARG_14	NH2	A_ASP_39	OD1	2.801
3GJF	A_ARG_14	NH2	A_ASP_39	OD2	3.691
3GJF	A_ARG_17	NH1	A_ASP_39	OD2	3.993
3GJF	A_ARG_21	NH1	A_ASP_39	OD2	3.840
3GJF	A_ARG_21	NH2	A_ASP_37	OD1	3.518
3GJF	A_ARG_21	NH2	A_ASP_37	OD2	2.869
3GJF	A_ARG_35	NH1	A_GLU_46	OE2	3.379
3GJF	A_ARG_35	NH2	A_GLU_46	OE2	2.626
3GJF	A_ARG_44	NH1	A_ASP_61	OD1	3.185
3GJF	A_ARG_44	NH2	A_ASP_61	OD1	2.672
3GJF	A_ARG_48	NH2	B_ASP_53	OD2	3.786
3GJF	A_ARG_65	NH1	L_ASP_52	OD1	3.134
3GJF	A_ARG_65	NH1	L_ASP_52	OD2	3.382
3GJF	A_ARG_65	NH2	L_ASP_52	OD1	2.989
3GJF	A_ARG_65	NH2	L_ASP_52	OD2	3.338
3GJF	A_LYS_66	NZ	A_GLU_63	OE2	2.881
3GJF	A_ARG_75	NH1	A_GLU_19	OE1	2.951
3GJF	A_ARG_75	NH1	A_GLU_19	OE2	2.915
3GJF	A_HIS_93	ND1	A_ASP_119	OD1	3.615
3GJF	A_HIS_93	ND1	A_ASP_119	OD2	2.772
3GJF	A_ARG_97	NH2	A_ASP_77	OD2	3.819
3GJF	A_ARG_111	NH1	A_GLU_128	OE1	3.014
3GJF	A_ARG_111	NH1	A_GLU_128	OE2	3.991
3GJF	A_LYS_121	NZ	A_ASP_137	OD1	2.725
3GJF	A_LYS_144	NZ	A_GLU_148	OE2	2.717
3GJF	A_HIS_151	ND1	A_GLU_154	OE1	3.544
3GJF	A_ARG_170	NH2	A_GLU_55	OE1	2.781
3GJF	A_ARG_170	NH2	A_GLU_55	OE2	3.295
3GJF	A_LYS_176	NZ	A_GLU_177	OE2	2.868
3GJF	A_ARG_181	NH2	A_ASP_183	OD2	3.746
3GJF	A_HIS_191	ND1	A_GLU_254	OE2	3.677
3GJF	A_HIS_191	NE2	A_GLU_254	OE2	3.660
3GJF	A_ARG_219	NH1	A_GLU_222	OE2	3.609
3GJF	B_ARG_45	NH1	B_ASP_38	OD1	3.417
3GJF	B_ARG_81	NH1	B_ASP_38	OD2	3.146
3GJF	D_HIS_3	NE2	D_ASP_29	OD2	3.680
3GJF	D_ARG_6	NH1	D_ASP_102	OD1	2.883

3GJF	D_ARG_14	NH1	D_ASP_39	OD1	3.632
3GJF	D_ARG_14	NH1	D_ASP_39	OD2	2.832
3GJF	D_ARG_14	NH2	D_ASP_39	OD1	2.791
3GJF	D_ARG_14	NH2	D_ASP_39	OD2	3.560
3GJF	D_ARG_21	NH2	D_ASP_37	OD1	3.457
3GJF	D_ARG_21	NH2	D_ASP_37	OD2	2.717
3GJF	D_ARG_35	NH1	D_GLU_46	OE1	2.983
3GJF	D_ARG_35	NH2	E_ASP_53	OD1	3.050
3GJF	D_ARG_35	NH2	E_ASP_53	OD2	3.940
3GJF	D_ARG_44	NH1	D_ASP_61	OD1	3.254
3GJF	D_ARG_44	NH2	D_ASP_61	OD1	2.599
3GJF	D_ARG_48	NH2	E_ASP_53	OD1	3.764
3GJF	D_ARG_48	NH2	E_ASP_53	OD2	3.452
3GJF	D_ARG_65	NH1	K_ASP_52	OD1	3.173
3GJF	D_ARG_65	NH1	K_ASP_52	OD2	3.530
3GJF	D_ARG_65	NH2	K_ASP_52	OD1	3.166
3GJF	D_ARG_65	NH2	K_ASP_52	OD2	2.445
3GJF	D_LYS_66	NZ	D_GLU_63	OE1	3.919
3GJF	D_LYS_66	NZ	D_GLU_63	OE2	2.898
3GJF	D_ARG_82	NH1	D_GLU_89	OE1	3.854
3GJF	D_ARG_82	NH1	D_GLU_89	OE2	3.318
3GJF	D_ARG_82	NH2	D_GLU_89	OE2	3.224
3GJF	D_HIS_93	ND1	D_ASP_119	OD1	3.533
3GJF	D_HIS_93	ND1	D_ASP_119	OD2	2.640
3GJF	D_ARG_97	NH2	D_ASP_77	OD2	3.677
3GJF	D_LYS_144	NZ	D_GLU_148	OE1	3.748
3GJF	D_LYS_144	NZ	D_GLU_148	OE2	2.769
3GJF	D_ARG_170	NH2	D_GLU_55	OE1	2.756
3GJF	D_ARG_170	NH2	D_GLU_55	OE2	3.140
3GJF	D_LYS_176	NZ	D_GLU_177	OE1	2.829
3GJF	D_ARG_181	NH2	D_ASP_183	OD2	3.518
3GJF	D_HIS_191	NE2	D_GLU_254	OE2	3.719
3GJF	E_LYS_6	NZ	D_GLU_232	OE1	3.774
3GJF	E_LYS_6	NZ	D_GLU_232	OE2	2.502
3GJF	E_ARG_45	NH1	E_ASP_38	OD1	3.925
3GJF	E_ARG_81	NH1	E_ASP_38	OD2	3.008
3GJF	L_HIS_51	ND1	L_ASP_52	OD2	2.609
3GJF	L_ARG_56	NH1	L_ASP_62	OD1	3.571
3GJF	L_ARG_63	NH1	L_ASP_84	OD1	2.750
3GJF	L_ARG_63	NH1	L_ASP_84	OD2	3.305
3GJF	L_ARG_63	NH2	L_ASP_84	OD1	3.570
3GJF	L_ARG_63	NH2	L_ASP_84	OD2	2.571
3GJF	K_HIS_51	ND1	K_ASP_52	OD2	2.643
3GJF	K_ARG_56	NH1	K_ASP_62	OD1	3.501
3GJF	K_ARG_63	NH2	K_GLU_83	OE1	3.808
3GJF	K_ARG_63	NH2	K_ASP_84	OD1	2.545
3GJF	K_ARG_63	NH2	K_ASP_84	OD2	3.209
3GJF	K_LYS_169	NZ	K_GLU_85	OE1	2.843
3GJF	H_ARG_38	NH1	H_ASP_90	OD1	2.830
3GJF	H_ARG_38	NH2	H_GLU_46	OE1	3.081
3GJF	H_ARG_38	NH2	H_GLU_46	OE2	3.817
3GJF	H_ARG_38	NH2	H_ASP_90	OD1	3.756
3GJF	H_ARG_67	NH1	H_ASP_90	OD1	3.830
3GJF	H_ARG_67	NH1	H_ASP_90	OD2	2.795
3GJF	H_ARG_67	NH2	H_ASP_90	OD1	3.041
3GJF	H_ARG_67	NH2	H_ASP_90	OD2	3.477
3GJF	H_LYS_216	NZ	H_GLU_218	OE2	2.600
3GJF	M_ARG_38	NH1	M_ASP_90	OD1	2.821

3GJF	M_ARG_38	NH2	M_GLU_46	OE1	3.436
3GJF	M_ARG_38	NH2	M_GLU_46	OE2	2.897
3GJF	M_ARG_38	NH2	M_ASP_90	OD1	3.855
3GJF	M_LYS_65	NZ	M_ASP_62	OD1	3.858
3GJF	M_ARG_67	NH1	M_ASP_90	OD1	3.892
3GJF	M_ARG_67	NH1	M_ASP_90	OD2	2.801
3GJF	M_ARG_67	NH2	M_ASP_90	OD1	3.068
3GJF	M_ARG_67	NH2	M_ASP_90	OD2	3.441
3GJF	M_LYS_215	NZ	K_GLU_126	OE1	3.244
3GJF	M_LYS_215	NZ	K_GLU_126	OE2	2.553
3GNM	L_ARG_66	NH1	L_ASP_87	OD1	3.577
3GNM	L_ARG_66	NH1	L_ASP_87	OD2	2.682
3GNM	L_ARG_66	NH2	L_GLU_84	OE1	3.405
3GNM	L_ARG_66	NH2	L_ASP_87	OD1	2.573
3GNM	L_ARG_66	NH2	L_ASP_87	OD2	3.204
3GNM	L_LYS_152	NZ	L_GLU_159	OE1	3.752
3GNM	L_LYS_154	NZ	L_GLU_200	OE1	2.730
3GNM	L_ARG_160	NH1	L_GLU_190	OE2	3.689
3GNM	L_ARG_160	NH2	L_GLU_190	OE2	2.931
3GNM	L_LYS_188	NZ	L_GLU_192	OE1	3.327
3GNM	L_LYS_188	NZ	L_GLU_192	OE2	3.845
3GNM	L_LYS_204	NZ	L_ASP_115	OD2	2.734
3GNM	H_ARG_40	NH2	H_GLU_89	OE1	3.735
3GNM	H_ARG_65	NH2	H_ASP_66	OD1	3.349
3GNM	H_ARG_65	NH2	H_ASP_66	OD2	3.203
3GNM	H_LYS_67	NZ	H_ASP_90	OD1	3.628
3GNM	H_LYS_67	NZ	H_ASP_90	OD2	2.714
3GNM	H_ARG_98	NH2	H_ASP_106	OD1	3.662
3GNM	H_ARG_98	NH2	H_ASP_106	OD2	2.562
3GNM	H_ARG_169	NH1	L_ASP_172	OD1	3.348
3GNM	H_ARG_169	NH2	L_ASP_172	OD1	3.542
3GNM	H_ARG_169	NH2	L_ASP_175	OD1	3.297
3GNM	H_LYS_213	NZ	L_GLU_128	OE1	2.721
3GNM	H_LYS_213	NZ	L_GLU_128	OE2	3.840
3GO1	L_ARG_61	NH1	L_ASP_82	OD1	3.138
3GO1	L_ARG_61	NH1	L_ASP_82	OD2	3.572
3GO1	L_ARG_61	NH2	L_ASP_82	OD1	3.465
3GO1	L_ARG_61	NH2	L_ASP_82	OD2	2.449
3GO1	L_LYS_166	NZ	L_GLU_83	OE2	2.723
3GO1	L_HIS_188	ND1	L_ASP_151	OD2	3.200
3GO1	H_ARG_38	NH1	H_ASP_86	OD1	2.757
3GO1	H_ARG_38	NH2	H_GLU_46	OE1	3.013
3GO1	H_ARG_38	NH2	H_ASP_86	OD1	3.570
3GO1	H_ARG_66	NH1	H_ASP_86	OD1	3.680
3GO1	H_ARG_66	NH1	H_ASP_86	OD2	3.112
3GO1	H_ARG_66	NH2	H_ASP_86	OD1	2.980
3GO1	H_ARG_66	NH2	H_ASP_86	OD2	3.607
3GO1	H_LYS_143	NZ	H_ASP_144	OD1	3.162
3GO1	H_LYS_143	NZ	H_ASP_144	OD2	3.468
3GO1	H_LYS_209	NZ	L_GLU_123	OE1	2.728
3GO1	H_LYS_209	NZ	L_GLU_123	OE2	3.471
3GO1	P_LYS_305	NZ	L_ASP_51	OD1	2.931
3GO1	P_ARG_315	NH1	H_GLU_95	OE2	3.127
3GO1	P_ARG_315	NH2	H_GLU_95	OE2	2.921
3GO1	P_ARG_315	NH2	H_ASP_100A	OD2	3.393
3HAE	A_HIS_3	NE2	A_ASP_29	OD2	3.587
3HAE	A_ARG_6	NH1	A_ASP_102	OD1	2.847
3HAE	A_ARG_6	NH2	A_ASP_102	OD1	3.019

3HAE	A_ARG_6	NH2	A_ASP_102	OD2	3.923
3HAE	A_ARG_14	NH1	A_ASP_39	OD1	3.472
3HAE	A_ARG_14	NH1	A_ASP_39	OD2	3.188
3HAE	A_ARG_14	NH2	A_ASP_39	OD1	2.664
3HAE	A_ARG_14	NH2	A_ASP_39	OD2	3.862
3HAE	A_ARG_21	NH2	A_ASP_37	OD1	3.621
3HAE	A_ARG_21	NH2	A_ASP_37	OD2	2.935
3HAE	A_ARG_35	NH1	B_ASP_53	OD1	3.527
3HAE	A_ARG_35	NH1	B_ASP_53	OD2	2.844
3HAE	A_ARG_35	NH2	A_GLU_46	OE2	3.050
3HAE	A_ARG_44	NH1	A_ASP_61	OD1	3.254
3HAE	A_ARG_44	NH2	A_ASP_61	OD1	3.535
3HAE	A_ARG_48	NH2	B_ASP_53	OD2	3.583
3HAE	A_ARG_65	NH1	L_ASP_52	OD1	3.495
3HAE	A_ARG_65	NH1	L_ASP_52	OD2	2.908
3HAE	A_ARG_65	NH2	L_ASP_52	OD1	3.452
3HAE	A_ARG_65	NH2	L_ASP_52	OD2	3.099
3HAE	A_LYS_66	NZ	A_GLU_63	OE1	3.753
3HAE	A_LYS_66	NZ	A_GLU_63	OE2	2.237
3HAE	A_HIS_93	ND1	A_ASP_119	OD1	3.412
3HAE	A_HIS_93	ND1	A_ASP_119	OD2	2.765
3HAE	A_ARG_97	NH2	A_ASP_77	OD2	3.602
3HAE	A_ARG_111	NH1	A_GLU_128	OE1	2.647
3HAE	A_LYS_121	NZ	A_ASP_137	OD1	3.114
3HAE	A_LYS_144	NZ	A_GLU_148	OE1	3.429
3HAE	A_LYS_144	NZ	A_GLU_148	OE2	3.081
3HAE	A_HIS_151	ND1	A_GLU_154	OE1	3.731
3HAE	A_ARG_170	NH2	A_GLU_55	OE1	3.140
3HAE	A_ARG_170	NH2	A_GLU_55	OE2	3.964
3HAE	A_ARG_266	NH2	A_ASP_220	OD1	2.688
3HAE	B_LYS_6	NZ	A_GLU_232	OE2	2.622
3HAE	B_ARG_81	NH1	B_ASP_38	OD2	2.783
3HAE	D_ARG_6	NH2	D_ASP_102	OD1	2.556
3HAE	D_ARG_6	NH2	D_ASP_102	OD2	2.949
3HAE	D_ARG_14	NH1	D_ASP_39	OD2	3.857
3HAE	D_ARG_14	NH2	D_ASP_39	OD1	2.936
3HAE	D_ARG_14	NH2	D_ASP_39	OD2	3.916
3HAE	D_ARG_21	NH1	D_ASP_37	OD2	3.671
3HAE	D_ARG_21	NH2	D_ASP_37	OD2	3.722
3HAE	D_ARG_21	NH2	D_ASP_39	OD2	3.808
3HAE	D_ARG_35	NH1	D_GLU_46	OE2	3.262
3HAE	D_ARG_35	NH1	E_ASP_53	OD1	3.949
3HAE	D_ARG_35	NH1	E_ASP_53	OD2	3.963
3HAE	D_ARG_35	NH2	E_ASP_53	OD1	3.106
3HAE	D_ARG_44	NH1	D_ASP_61	OD1	3.859
3HAE	D_ARG_44	NH2	D_ASP_61	OD1	2.693
3HAE	D_ARG_48	NH2	E_ASP_53	OD2	3.593
3HAE	D_ARG_65	NH1	G_ASP_52	OD1	3.201
3HAE	D_ARG_65	NH2	G_ASP_52	OD1	2.885
3HAE	D_ARG_65	NH2	G_ASP_52	OD2	3.031
3HAE	D_LYS_66	NZ	D_GLU_63	OE2	2.605
3HAE	D_ARG_75	NH1	D_GLU_19	OE1	3.280
3HAE	D_ARG_75	NH1	D_GLU_19	OE2	3.330
3HAE	D_ARG_75	NH2	D_GLU_19	OE2	2.623
3HAE	D_ARG_82	NH1	D_GLU_89	OE2	3.821
3HAE	D_ARG_82	NH2	D_GLU_89	OE2	2.676
3HAE	D_HIS_93	ND1	D_ASP_119	OD1	3.379
3HAE	D_HIS_93	ND1	D_ASP_119	OD2	3.104

3HAE	D_ARG_97	NH2	D_ASP_77	OD2	3.161
3HAE	D_ARG_108	NH2	D_ASP_106	OD2	3.619
3HAE	D_ARG_111	NH1	D_GLU_128	OE1	3.567
3HAE	D_ARG_111	NH2	D_GLU_128	OE1	3.292
3HAE	D_LYS_144	NZ	D_GLU_148	OE2	3.433
3HAE	D_HIS_151	ND1	D_GLU_154	OE1	3.330
3HAE	D_ARG_170	NH2	D_GLU_55	OE1	2.334
3HAE	D_ARG_170	NH2	D_GLU_55	OE2	3.072
3HAE	D_LYS_176	NZ	D_GLU_177	OE2	3.306
3HAE	D_ARG_181	NH2	D_ASP_183	OD2	3.347
3HAE	D_ARG_256	NH2	D_ASP_220	OD1	2.715
3HAE	E_LYS_41	NZ	E_ASP_76	OD2	3.802
3HAE	E_ARG_81	NH1	E_ASP_38	OD2	3.706
3HAE	J_HIS_3	NE2	J_ASP_29	OD2	3.809
3HAE	J_ARG_6	NH1	J_ASP_102	OD1	2.906
3HAE	J_ARG_6	NH1	J_ASP_102	OD2	3.945
3HAE	J_ARG_6	NH2	J_ASP_102	OD1	2.506
3HAE	J_ARG_14	NH1	J_ASP_39	OD1	3.669
3HAE	J_ARG_14	NH1	J_ASP_39	OD2	2.840
3HAE	J_ARG_14	NH2	J_ASP_39	OD1	2.935
3HAE	J_ARG_14	NH2	J_ASP_39	OD2	3.651
3HAE	J_ARG_21	NH2	J_ASP_37	OD1	3.222
3HAE	J_ARG_21	NH2	J_ASP_37	OD2	2.441
3HAE	J_ARG_35	NH1	J_GLU_46	OE1	3.957
3HAE	J_ARG_35	NH1	J_GLU_46	OE2	2.953
3HAE	J_ARG_35	NH2	K_ASP_53	OD1	3.520
3HAE	J_ARG_44	NH1	J_ASP_61	OD1	3.422
3HAE	J_ARG_44	NH2	J_ASP_61	OD1	3.290
3HAE	J_ARG_48	NH2	K_ASP_53	OD1	3.945
3HAE	J_ARG_48	NH2	K_ASP_53	OD2	3.051
3HAE	J_ARG_65	NH1	N_ASP_52	OD1	3.749
3HAE	J_ARG_65	NH2	N_ASP_52	OD1	2.440
3HAE	J_ARG_65	NH2	N_ASP_52	OD2	2.989
3HAE	J_LYS_66	NZ	J_GLU_63	OE1	2.982
3HAE	J_LYS_66	NZ	J_GLU_63	OE2	2.809
3HAE	J_HIS_93	ND1	J_ASP_119	OD1	3.377
3HAE	J_HIS_93	ND1	J_ASP_119	OD2	2.805
3HAE	J_ARG_108	NH2	J_ASP_106	OD1	3.482
3HAE	J_ARG_108	NH2	J_ASP_106	OD2	3.608
3HAE	J_LYS_121	NZ	J_ASP_137	OD1	3.426
3HAE	J_HIS_151	ND1	J_GLU_154	OE1	3.986
3HAE	J_ARG_170	NH2	J_GLU_55	OE1	2.482
3HAE	J_ARG_170	NH2	J_GLU_55	OE2	3.313
3HAE	J_ARG_181	NH2	J_ASP_183	OD2	3.327
3HAE	J_HIS_191	ND1	J_GLU_254	OE2	3.434
3HAE	J_ARG_256	NH2	J_ASP_220	OD1	3.258
3HAE	K_ARG_81	NH1	K_ASP_38	OD2	2.492
3HAE	P_HIS_3	NE2	P_ASP_29	OD2	3.769
3HAE	P_ARG_6	NH1	P_ASP_102	OD1	2.755
3HAE	P_ARG_6	NH2	P_ASP_102	OD1	3.424
3HAE	P_ARG_14	NH1	P_ASP_39	OD1	3.423
3HAE	P_ARG_14	NH1	P_ASP_39	OD2	3.000
3HAE	P_ARG_14	NH2	P_ASP_39	OD1	2.960
3HAE	P_ARG_14	NH2	P_ASP_39	OD2	3.984
3HAE	P_ARG_21	NH2	P_ASP_37	OD1	3.733
3HAE	P_ARG_21	NH2	P_ASP_37	OD2	3.125
3HAE	P_ARG_35	NH1	P_GLU_46	OE2	3.659
3HAE	P_ARG_35	NH1	Q_ASP_53	OD2	3.921

3HAE	P_ARG_35	NH2	P_GLU_46	OE2	2.679
3HAE	P_ARG_44	NH1	P_ASP_61	OD1	3.128
3HAE	P_ARG_44	NH2	P_ASP_61	OD1	3.068
3HAE	P_ARG_48	NH2	Q_ASP_53	OD1	3.566
3HAE	P_ARG_48	NH2	Q_ASP_53	OD2	2.872
3HAE	P_ARG_65	NH1	S_ASP_52	OD1	3.579
3HAE	P_ARG_65	NH1	S_ASP_52	OD2	3.466
3HAE	P_ARG_65	NH2	S_ASP_52	OD1	3.120
3HAE	P_ARG_65	NH2	S_ASP_52	OD2	2.826
3HAE	P_LYS_66	NZ	P_GLU_63	OE1	3.514
3HAE	P_LYS_66	NZ	P_GLU_63	OE2	3.135
3HAE	P_HIS_93	ND1	P_ASP_119	OD1	3.199
3HAE	P_HIS_93	ND1	P_ASP_119	OD2	2.626
3HAE	P_ARG_97	NH2	P_ASP_77	OD2	3.656
3HAE	P_ARG_108	NH2	P_ASP_106	OD1	3.268
3HAE	P_ARG_108	NH2	P_ASP_106	OD2	2.709
3HAE	P_ARG_111	NH1	P_GLU_128	OE1	3.578
3HAE	P_LYS_144	NZ	P_GLU_148	OE1	3.286
3HAE	P_HIS_151	ND1	P_GLU_154	OE1	3.029
3HAE	P_ARG_157	NH2	P_GLU_161	OE1	3.353
3HAE	P_ARG_157	NH2	P_GLU_161	OE2	3.284
3HAE	P_ARG_170	NH1	P_GLU_55	OE1	3.443
3HAE	P_ARG_170	NH1	P_GLU_55	OE2	3.001
3HAE	P_ARG_170	NH2	P_GLU_55	OE1	3.201
3HAE	P_ARG_170	NH2	P_GLU_55	OE2	3.200
3HAE	P_ARG_181	NH2	P_ASP_183	OD2	3.944
3HAE	P_HIS_191	ND1	P_GLU_254	OE2	3.652
3HAE	P_HIS_191	NE2	P_GLU_254	OE2	3.983
3HAE	P_ARG_256	NH2	P_ASP_220	OD2	2.906
3HAE	Q_LYS_6	NZ	P_GLU_232	OE2	3.965
3HAE	Q_ARG_45	NH1	Q_ASP_38	OD1	3.784
3HAE	Q_ARG_45	NH2	Q_GLU_47	OE1	3.894
3HAE	Q_LYS_75	NZ	Q_GLU_74	OE2	3.176
3HAE	L_HIS_51	ND1	L_ASP_52	OD2	3.196
3HAE	L_ARG_63	NH1	L_GLU_83	OE1	3.861
3HAE	L_ARG_63	NH1	L_ASP_84	OD1	3.672
3HAE	L_ARG_63	NH1	L_ASP_84	OD2	3.946
3HAE	L_ARG_63	NH2	L_ASP_84	OD1	2.766
3HAE	L_ARG_63	NH2	L_ASP_84	OD2	2.158
3HAE	L_HIS_87	ND1	L_ASP_105	OD1	3.871
3HAE	L_HIS_87	NE2	L_ASP_105	OD1	3.639
3HAE	L_LYS_169	NZ	L_GLU_85	OE1	2.871
3HAE	G_HIS_51	ND1	G_ASP_52	OD2	2.400
3HAE	G_ARG_63	NH1	G_ASP_84	OD1	3.142
3HAE	G_ARG_63	NH1	G_ASP_84	OD2	3.199
3HAE	G_ARG_63	NH2	G_ASP_84	OD1	3.746
3HAE	G_ARG_63	NH2	G_ASP_84	OD2	2.857
3HAE	G_LYS_169	NZ	G_GLU_85	OE1	2.988
3HAE	N_HIS_51	ND1	N_ASP_52	OD2	2.806
3HAE	N_ARG_63	NH1	N_ASP_84	OD1	3.108
3HAE	N_ARG_63	NH1	N_ASP_84	OD2	3.603
3HAE	N_ARG_63	NH2	N_ASP_84	OD1	3.712
3HAE	N_ARG_63	NH2	N_ASP_84	OD2	2.760
3HAE	N_HIS_87	ND1	N_ASP_105	OD1	3.966
3HAE	N_HIS_87	NE2	N_ASP_105	OD1	3.798
3HAE	N_LYS_132	NZ	O_ASP_150	OD2	3.615
3HAE	N_LYS_169	NZ	N_GLU_85	OE1	3.035
3HAE	N_LYS_169	NZ	N_GLU_85	OE2	3.916

3HAE	S_HIS_51	ND1	S_ASP_52	OD2	2.614
3HAE	S_ARG_63	NH1	S_ASP_84	OD1	3.147
3HAE	S_ARG_63	NH1	S_ASP_84	OD2	3.129
3HAE	S_ARG_63	NH2	S_ASP_84	OD1	3.845
3HAE	S_ARG_63	NH2	S_ASP_84	OD2	2.474
3HAE	S_HIS_87	ND1	S_ASP_105	OD1	3.612
3HAE	S_HIS_87	NE2	S_ASP_105	OD1	3.221
3HAE	S_LYS_169	NZ	S_GLU_85	OE2	3.086
3HAE	S_LYS_174	NZ	S_ASP_141	OD2	3.360
3HAE	H_ARG_38	NH1	H_ASP_90	OD1	3.222
3HAE	H_ARG_38	NH2	H_GLU_46	OE1	3.510
3HAE	H_ARG_38	NH2	H_GLU_46	OE2	2.712
3HAE	H_ARG_38	NH2	H_ASP_90	OD1	4.000
3HAE	H_LYS_65	NZ	H_ASP_62	OD1	3.122
3HAE	H_ARG_67	NH1	H_ASP_90	OD1	3.984
3HAE	H_ARG_67	NH1	H_ASP_90	OD2	2.555
3HAE	H_ARG_67	NH2	H_ASP_90	OD1	2.773
3HAE	H_ARG_67	NH2	H_ASP_90	OD2	2.913
3HAE	H_LYS_76	NZ	H_ASP_73	OD1	3.678
3HAE	H_LYS_215	NZ	L_GLU_126	OE1	3.537
3HAE	H_LYS_215	NZ	L_GLU_126	OE2	3.674
3HAE	L_ARG_38	NH1	L_ASP_90	OD1	3.105
3HAE	L_ARG_38	NH2	L_GLU_46	OE1	3.780
3HAE	L_ARG_38	NH2	L_GLU_46	OE2	2.913
3HAE	L_ARG_38	NH2	L_ASP_90	OD1	3.959
3HAE	L_LYS_65	NZ	L_ASP_62	OD1	2.989
3HAE	L_ARG_67	NH1	L_ASP_90	OD2	2.847
3HAE	L_ARG_67	NH2	L_ASP_90	OD1	2.911
3HAE	L_ARG_67	NH2	L_ASP_90	OD2	3.060
3HAE	L_LYS_76	NZ	L_ASP_73	OD1	3.921
3HAE	L_LYS_149	NZ	L_ASP_150	OD1	3.830
3HAE	L_LYS_212	NZ	L_ASP_214	OD1	2.825
3HAE	L_LYS_212	NZ	L_ASP_214	OD2	3.108
3HAE	L_LYS_215	NZ	G_GLU_126	OE1	3.678
3HAE	L_LYS_216	NZ	L_GLU_218	OE2	3.121
3HAE	O_ARG_38	NH1	O_ASP_90	OD1	2.713
3HAE	O_ARG_38	NH2	O_GLU_46	OE1	3.369
3HAE	O_ARG_38	NH2	O_GLU_46	OE2	3.065
3HAE	O_ARG_38	NH2	O_ASP_90	OD1	3.703
3HAE	O_ARG_67	NH1	O_ASP_90	OD2	2.733
3HAE	O_ARG_67	NH2	O_ASP_90	OD1	3.178
3HAE	O_ARG_67	NH2	O_ASP_90	OD2	3.173
3HAE	O_LYS_215	NZ	N_GLU_126	OE2	3.736
3HAE	O_LYS_216	NZ	O_GLU_218	OE2	3.610
3HAE	T_ARG_38	NH1	T_ASP_90	OD1	3.080
3HAE	T_ARG_38	NH2	T_GLU_46	OE1	3.373
3HAE	T_ARG_38	NH2	T_GLU_46	OE2	2.779
3HAE	T_ARG_38	NH2	T_ASP_90	OD1	3.979
3HAE	T_ARG_67	NH1	T_ASP_90	OD2	2.923
3HAE	T_ARG_67	NH2	T_ASP_90	OD1	3.524
3HAE	T_ARG_67	NH2	T_ASP_90	OD2	3.612
3HAE	T_LYS_212	NZ	T_ASP_214	OD1	3.968
3HAE	T_LYS_215	NZ	S_GLU_126	OE1	2.660
3HAE	T_LYS_215	NZ	S_GLU_126	OE2	3.779
3HAE	T_LYS_216	NZ	T_GLU_218	OE2	3.675
3HFM	L_HIS_34	ND1	H_ASP_99	OD1	3.756
3HFM	L_HIS_34	ND1	H_ASP_99	OD2	3.698
3HFM	L_LYS_49	NZ	H_ASP_99	OD1	3.423

3HFM	L_ARG_61	NH1	L_ASP_82	OD1	2.585
3HFM	L_ARG_61	NH1	L_ASP_82	OD2	2.332
3HFM	L_ARG_61	NH2	L_GLU_79	OE1	3.732
3HFM	L_ARG_108	NH1	L_ASP_170	OD1	3.833
3HFM	L_LYS_142	NZ	L_GLU_105	OE2	3.995
3HFM	L_LYS_147	NZ	L_GLU_154	OE2	3.463
3HFM	L_LYS_149	NZ	L_GLU_195	OE1	3.304
3HFM	L_LYS_149	NZ	L_GLU_195	OE2	3.873
3HFM	L_HIS_189	ND1	L_ASP_151	OD1	2.425
3HFM	L_LYS_199	NZ	L_ASP_110	OD2	3.937
3HFM	H_ARG_38	NH1	H_ASP_89	OD2	3.586
3HFM	H_ARG_38	NH2	H_GLU_46	OE1	3.434
3HFM	H_ARG_38	NH2	H_GLU_46	OE2	2.361
3HFM	H_ARG_66	NH1	H_ASP_89	OD1	2.908
3HFM	H_ARG_66	NH1	H_ASP_89	OD2	3.682
3HFM	H_ARG_66	NH2	H_ASP_89	OD1	3.356
3HFM	H_ARG_66	NH2	H_ASP_89	OD2	2.574
3HFM	H_LYS_209	NZ	L_GLU_123	OE1	2.622
3HFM	H_ARG_213	NH2	L_GLU_123	OE1	3.991
3HFM	Y_LYS_1	NZ	Y_GLU_7	OE1	2.881
3HFM	Y_LYS_1	NZ	Y_GLU_7	OE2	2.663
3HFM	Y_LYS_97	NZ	H_ASP_32	OD1	3.609
3HFM	Y_ARG_125	NH1	Y_ASP_119	OD2	3.874
3HI6	A_LYS_155	NZ	A_ASP_193	OD1	2.768
3HI6	A_LYS_178	NZ	A_GLU_180	OE1	3.586
3HI6	A_ARG_221	NH1	A_GLU_218	OE1	3.057
3HI6	A_ARG_227	NH2	A_ASP_131	OD1	2.862
3HI6	A_LYS_252	NZ	A_ASP_249	OD2	3.996
3HI6	A_LYS_287	NZ	A_GLU_301	OE1	3.340
3HI6	A_LYS_287	NZ	A_GLU_301	OE2	2.773
3HI6	A_LYS_304	NZ	A_GLU_301	OE2	2.760
3HI6	B_LYS_155	NZ	B_ASP_193	OD1	3.786
3HI6	B_LYS_159	NZ	B_ASP_193	OD1	3.099
3HI6	B_LYS_159	NZ	B_ASP_193	OD2	3.154
3HI6	B_LYS_178	NZ	B_GLU_180	OE1	2.889
3HI6	B_ARG_221	NH1	B_GLU_223	OE2	2.829
3HI6	B_ARG_221	NH2	B_GLU_218	OE1	3.646
3HI6	B_ARG_227	NH2	B_ASP_131	OD1	2.921
3HI6	B_LYS_304	NZ	B_GLU_301	OE2	3.130
3HI6	H_ARG_38	NH1	H_ASP_90	OD1	3.103
3HI6	H_ARG_38	NH2	H_GLU_46	OE1	3.371
3HI6	H_ARG_38	NH2	H_GLU_46	OE2	3.628
3HI6	H_LYS_65	NZ	H_ASP_62	OD1	3.388
3HI6	H_ARG_67	NH1	H_ASP_90	OD1	3.897
3HI6	H_ARG_67	NH1	H_ASP_90	OD2	2.936
3HI6	H_ARG_67	NH2	H_ASP_90	OD1	3.035
3HI6	H_ARG_67	NH2	H_ASP_90	OD2	3.561
3HI6	H_LYS_150	NZ	H_ASP_151	OD1	3.237
3HI6	H_LYS_150	NZ	H_ASP_151	OD2	3.331
3HI6	H_LYS_216	NZ	L_GLU_122	OE1	2.896
3HI6	H_LYS_216	NZ	L_GLU_122	OE2	3.887
3HI6	H_ARG_217	NH2	H_GLU_219	OE1	3.060
3HI6	L_ARG_61	NH2	L_ASP_82	OD1	2.928
3HI6	L_ARG_61	NH2	L_ASP_82	OD2	3.639
3HI6	L_LYS_102	NZ	L_GLU_164	OE1	3.006
3HI6	L_LYS_102	NZ	L_GLU_164	OE2	3.181
3HI6	L_LYS_106	NZ	L_ASP_17	OD2	3.521
3HI6	L_ARG_141	NH1	L_GLU_164	OE2	3.935

3HI6	L_HIS_188	ND1	L_ASP_150	OD2	2.681
3HI6	X_ARG_38	NH1	X_ASP_90	OD1	2.944
3HI6	X_ARG_38	NH2	X_GLU_46	OE1	3.305
3HI6	X_ARG_38	NH2	X_GLU_46	OE2	3.929
3HI6	X_ARG_38	NH2	X_ASP_90	OD1	3.837
3HI6	X_ARG_67	NH1	X_ASP_90	OD2	3.146
3HI6	X_ARG_67	NH2	X_ASP_90	OD1	3.168
3HI6	X_ARG_67	NH2	X_ASP_90	OD2	3.554
3HI6	X_LYS_150	NZ	X_ASP_151	OD2	3.620
3HI6	X_LYS_216	NZ	Y_GLU_122	OE1	3.212
3HI6	Y_ARG_	NH1	Y_ASP_70	OD1	2.911
3HI6	Y_ARG_	NH1	Y_ASP_70	OD2	3.450
3HI6	Y_ARG_	NH2	Y_ASP_70	OD1	3.656
3HI6	Y_ARG_61	NH2	Y_GLU_81	OE1	3.524
3HI6	Y_ARG_61	NH2	Y_ASP_82	OD1	2.775
3HI6	Y_ARG_61	NH2	Y_ASP_82	OD2	3.667
3HI6	Y_HIS_188	ND1	Y_ASP_150	OD2	3.043
3HMG	A_LYS_27	NZ	A_ASP_32	OD2	2.671
3HMG	A_HIS_56	ND1	A_ASP_85	OD2	3.968
3HMG	A_ARG_57	NH1	A_GLU_82	OE1	2.607
3HMG	A_ARG_57	NH1	A_GLU_82	OE2	3.527
3HMG	A_HIS_75	ND1	A_ASP_73	OD1	3.517
3HMG	A_HIS_75	ND1	A_ASP_73	OD2	2.768
3HMG	A_HIS_75	NE2	A_ASP_63	OD1	3.581
3HMG	A_ARG_90	NH1	A_ASP_60	OD1	2.768
3HMG	A_ARG_90	NH1	A_ASP_60	OD2	3.650
3HMG	A_LYS_92	NZ	A_ASP_271	OD2	3.725
3HMG	A_ARG_109	NH1	B_GLU_67	OE1	3.372
3HMG	A_ARG_109	NH1	B_GLU_67	OE2	2.849
3HMG	A_ARG_109	NH2	A_GLU_89	OE1	3.268
3HMG	A_ARG_109	NH2	A_GLU_89	OE2	2.513
3HMG	A_ARG_141	NH1	A_ASP_77	OD1	2.813
3HMG	A_ARG_141	NH1	A_ASP_77	OD2	3.101
3HMG	A_LYS_176	NZ	A_GLU_123	OE1	2.594
3HMG	A_LYS_176	NZ	A_GLU_123	OE2	3.871
3HMG	A_HIS_183	NE2	A_GLU_190	OE1	3.525
3HMG	A_ARG_208	NH2	A_ASP_241	OD2	2.755
3HMG	A_LYS_238	NZ	A_ASP_175	OD1	2.646
3HMG	A_LYS_238	NZ	A_ASP_175	OD2	3.452
3HMG	A_LYS_238	NZ	F_GLU_72	OE2	2.747
3HMG	A_ARG_261	NH1	A_GLU_119	OE1	2.789
3HMG	A_ARG_261	NH1	A_GLU_119	OE2	2.604
3HMG	A_ARG_261	NH2	A_GLU_119	OE1	3.241
3HMG	A_LYS_264	NZ	A_ASP_85	OD1	3.861
3HMG	A_LYS_264	NZ	A_ASP_85	OD2	2.924
3HMG	A_ARG_269	NH2	B_GLU_67	OE1	2.883
3HMG	A_LYS_292	NZ	A_ASP_291	OD1	2.917
3HMG	A_LYS_299	NZ	B_GLU_69	OE1	3.233
3HMG	A_LYS_310	NZ	B_ASP_90	OD1	2.577
3HMG	A_LYS_315	NZ	A_GLU_41	OE2	3.626
3HMG	B_ARG_25	NH1	A_GLU_325	OE1	3.777
3HMG	B_LYS_51	NZ	B_GLU_103	OE2	2.839
3HMG	B_ARG_54	NH1	F_GLU_97	OE1	2.798
3HMG	B_ARG_54	NH2	B_GLU_57	OE1	2.910
3HMG	B_ARG_54	NH2	B_GLU_57	OE2	3.325
3HMG	B_ARG_54	NH2	F_GLU_97	OE1	3.127
3HMG	B_LYS_62	NZ	F_ASP_86	OD1	2.986
3HMG	B_LYS_62	NZ	F_ASP_86	OD2	2.761

3HMG	B_LYS_62	NZ	F_ASP_90	OD1	3.490
3HMG	B_LYS_62	NZ	F_ASP_90	OD2	2.774
3HMG	B_HIS_64	NE2	F_ASP_79	OD1	3.991
3HMG	B_HIS_64	NE2	F_ASP_79	OD2	3.618
3HMG	B_LYS_68	NZ	B_GLU_85	OE1	3.186
3HMG	B_LYS_68	NZ	B_GLU_85	OE2	2.686
3HMG	B_ARG_76	NH1	D_GLU_74	OE1	3.445
3HMG	B_ARG_76	NH1	D_GLU_74	OE2	2.823
3HMG	B_ARG_76	NH1	D_GLU_81	OE1	2.738
3HMG	B_ARG_76	NH1	D_GLU_81	OE2	3.615
3HMG	B_ARG_76	NH2	D_GLU_74	OE1	2.830
3HMG	B_ARG_76	NH2	D_GLU_74	OE2	3.630
3HMG	B_LYS_117	NZ	B_GLU_114	OE1	2.569
3HMG	B_LYS_117	NZ	B_GLU_114	OE2	3.024
3HMG	B_ARG_123	NH1	F_GLU_132	OE2	3.281
3HMG	B_ARG_123	NH2	B_GLU_120	OE1	2.630
3HMG	B_ARG_123	NH2	B_GLU_120	OE2	3.334
3HMG	B_ARG_124	NH1	F_GLU_132	OE1	3.422
3HMG	B_ARG_124	NH1	F_GLU_132	OE2	3.128
3HMG	B_ARG_124	NH2	B_GLU_120	OE1	3.713
3HMG	B_ARG_127	NH2	F_GLU_131	OE1	2.404
3HMG	B_ARG_153	NH2	B_GLU_150	OE2	2.579
3HMG	B_HIS_159	NE2	B_ASP_160	OD2	3.179
3HMG	B_ARG_163	NH1	F_GLU_131	OE1	2.713
3HMG	B_ARG_163	NH1	F_GLU_131	OE2	2.661
3HMG	B_ARG_170	NH1	B_GLU_128	OE1	2.573
3HMG	B_ARG_170	NH2	B_GLU_131	OE2	2.707
3HMG	B_ARG_170	NH2	D_GLU_128	OE1	3.667
3HMG	B_ARG_170	NH2	D_GLU_128	OE2	3.704
3HMG	C_LYS_27	NZ	C_ASP_32	OD2	2.666
3HMG	C_HIS_56	ND1	C_ASP_85	OD2	3.933
3HMG	C_ARG_57	NH1	C_GLU_82	OE1	2.582
3HMG	C_ARG_57	NH1	C_GLU_82	OE2	3.551
3HMG	C_HIS_75	ND1	C_ASP_73	OD1	3.511
3HMG	C_HIS_75	ND1	C_ASP_73	OD2	2.757
3HMG	C_HIS_75	NE2	C_ASP_63	OD1	3.577
3HMG	C_ARG_90	NH1	C_ASP_60	OD1	2.751
3HMG	C_ARG_90	NH1	C_ASP_60	OD2	3.640
3HMG	C_LYS_92	NZ	C_ASP_271	OD2	3.710
3HMG	C_ARG_109	NH1	D_GLU_67	OE1	3.376
3HMG	C_ARG_109	NH1	D_GLU_67	OE2	2.842
3HMG	C_ARG_109	NH2	C_GLU_89	OE1	3.278
3HMG	C_ARG_109	NH2	C_GLU_89	OE2	2.563
3HMG	C_ARG_141	NH1	C_ASP_77	OD1	2.813
3HMG	C_ARG_141	NH1	C_ASP_77	OD2	3.109
3HMG	C_LYS_176	NZ	C_GLU_123	OE1	2.579
3HMG	C_LYS_176	NZ	C_GLU_123	OE2	3.881
3HMG	C_HIS_183	NE2	C_GLU_190	OE1	3.534
3HMG	C_ARG_208	NH2	C_ASP_241	OD2	2.719
3HMG	C_LYS_238	NZ	B_GLU_72	OE2	2.625
3HMG	C_LYS_238	NZ	C_ASP_175	OD1	2.646
3HMG	C_LYS_238	NZ	C_ASP_175	OD2	3.428
3HMG	C_ARG_261	NH1	C_GLU_119	OE1	2.776
3HMG	C_ARG_261	NH1	C_GLU_119	OE2	2.620
3HMG	C_ARG_261	NH2	C_GLU_119	OE1	3.254
3HMG	C_LYS_264	NZ	C_ASP_85	OD1	3.851
3HMG	C_LYS_264	NZ	C_ASP_85	OD2	2.872
3HMG	C_ARG_269	NH2	D_GLU_67	OE1	2.813

3HMG	C_LYS_292	NZ	C_ASP_291	OD1	2.970
3HMG	C_LYS_299	NZ	D_GLU_69	OE1	3.251
3HMG	C_LYS_310	NZ	D_ASP_90	OD1	2.544
3HMG	C_LYS_315	NZ	C_GLU_41	OE2	3.625
3HMG	D_LYS_51	NZ	D_GLU_103	OE2	2.876
3HMG	D_ARG_54	NH1	B_GLU_97	OE1	2.804
3HMG	D_ARG_54	NH2	B_GLU_97	OE1	3.138
3HMG	D_ARG_54	NH2	D_GLU_57	OE1	2.911
3HMG	D_ARG_54	NH2	D_GLU_57	OE2	3.348
3HMG	D_LYS_62	NZ	B_ASP_86	OD1	2.985
3HMG	D_LYS_62	NZ	B_ASP_86	OD2	2.721
3HMG	D_LYS_62	NZ	B_ASP_90	OD1	3.453
3HMG	D_LYS_62	NZ	B_ASP_90	OD2	2.701
3HMG	D_HIS_64	NE2	B_ASP_79	OD1	3.960
3HMG	D_HIS_64	NE2	B_ASP_79	OD2	3.444
3HMG	D_LYS_68	NZ	D_GLU_85	OE1	3.145
3HMG	D_LYS_68	NZ	D_GLU_85	OE2	2.743
3HMG	D_ARG_76	NH1	F_GLU_74	OE1	3.513
3HMG	D_ARG_76	NH1	F_GLU_74	OE2	2.767
3HMG	D_ARG_76	NH1	F_GLU_81	OE1	2.643
3HMG	D_ARG_76	NH1	F_GLU_81	OE2	3.636
3HMG	D_ARG_76	NH2	F_GLU_74	OE1	2.766
3HMG	D_ARG_76	NH2	F_GLU_74	OE2	3.449
3HMG	D_LYS_117	NZ	D_GLU_114	OE1	2.579
3HMG	D_LYS_117	NZ	D_GLU_114	OE2	3.024
3HMG	D_ARG_123	NH1	B_GLU_132	OE2	3.299
3HMG	D_ARG_123	NH2	D_GLU_120	OE1	2.630
3HMG	D_ARG_123	NH2	D_GLU_120	OE2	3.353
3HMG	D_ARG_124	NH1	B_GLU_132	OE1	3.459
3HMG	D_ARG_124	NH1	B_GLU_132	OE2	3.169
3HMG	D_ARG_124	NH2	D_GLU_120	OE1	3.725
3HMG	D_ARG_127	NH2	B_GLU_131	OE1	2.449
3HMG	D_ARG_153	NH2	D_GLU_150	OE1	2.831
3HMG	D_HIS_159	NE2	D_ASP_160	OD2	3.206
3HMG	D_ARG_163	NH1	B_GLU_131	OE1	2.694
3HMG	D_ARG_163	NH1	B_GLU_131	OE2	2.707
3HMG	D_ARG_170	NH1	D_GLU_128	OE1	2.604
3HMG	D_ARG_170	NH2	D_GLU_131	OE2	2.731
3HMG	D_ARG_170	NH2	F_GLU_128	OE1	3.716
3HMG	D_ARG_170	NH2	F_GLU_128	OE2	3.859
3HMG	E_LYS_27	NZ	E_ASP_32	OD2	2.652
3HMG	E_HIS_56	ND1	E_ASP_85	OD2	3.934
3HMG	E_ARG_57	NH1	E_GLU_82	OE1	2.626
3HMG	E_ARG_57	NH1	E_GLU_82	OE2	3.570
3HMG	E_HIS_75	ND1	E_ASP_73	OD1	3.497
3HMG	E_HIS_75	ND1	E_ASP_73	OD2	2.783
3HMG	E_HIS_75	NE2	E_ASP_63	OD1	3.565
3HMG	E_ARG_90	NH1	E_ASP_60	OD1	2.760
3HMG	E_ARG_90	NH1	E_ASP_60	OD2	3.651
3HMG	E_LYS_92	NZ	E_ASP_271	OD2	3.691
3HMG	E_ARG_109	NH1	F_GLU_67	OE1	3.402
3HMG	E_ARG_109	NH1	F_GLU_67	OE2	2.841
3HMG	E_ARG_109	NH2	E_GLU_89	OE1	3.254
3HMG	E_ARG_109	NH2	E_GLU_89	OE2	2.493
3HMG	E_ARG_141	NH1	E_ASP_77	OD1	2.813
3HMG	E_ARG_141	NH1	E_ASP_77	OD2	3.105
3HMG	E_LYS_176	NZ	E_GLU_123	OE1	2.615
3HMG	E_LYS_176	NZ	E_GLU_123	OE2	3.893

3HMG	E_HIS_183	NE2	E_GLU_190	OE1	3.535
3HMG	E_ARG_208	NH2	E_ASP_241	OD2	2.774
3HMG	E_LYS_238	NZ	D_GLU_72	OE2	2.745
3HMG	E_LYS_238	NZ	E_ASP_175	OD1	2.643
3HMG	E_LYS_238	NZ	E_ASP_175	OD2	3.469
3HMG	E_ARG_261	NH1	E_GLU_119	OE1	2.788
3HMG	E_ARG_261	NH1	E_GLU_119	OE2	2.617
3HMG	E_ARG_261	NH2	E_GLU_119	OE1	3.257
3HMG	E_LYS_264	NZ	E_ASP_85	OD1	3.857
3HMG	E_LYS_264	NZ	E_ASP_85	OD2	2.875
3HMG	E_ARG_269	NH2	F_GLU_67	OE1	2.840
3HMG	E_LYS_292	NZ	E_ASP_291	OD1	2.926
3HMG	E_LYS_299	NZ	F_GLU_69	OE1	3.192
3HMG	E_LYS_310	NZ	F_ASP_90	OD1	2.563
3HMG	E_LYS_315	NZ	E_GLU_41	OE2	3.619
3HMG	F_ARG_25	NH1	E_GLU_325	OE2	3.879
3HMG	F_ARG_25	NH2	E_GLU_325	OE2	3.668
3HMG	F_LYS_51	NZ	F_GLU_103	OE2	2.823
3HMG	F_ARG_54	NH1	D_GLU_97	OE1	2.700
3HMG	F_ARG_54	NH2	D_GLU_97	OE1	3.155
3HMG	F_ARG_54	NH2	F_GLU_57	OE1	2.900
3HMG	F_ARG_54	NH2	F_GLU_57	OE2	3.295
3HMG	F_LYS_62	NZ	D_ASP_86	OD1	2.928
3HMG	F_LYS_62	NZ	D_ASP_86	OD2	2.697
3HMG	F_LYS_62	NZ	D_ASP_90	OD1	3.563
3HMG	F_LYS_62	NZ	D_ASP_90	OD2	2.800
3HMG	F_HIS_64	NE2	D_ASP_79	OD1	3.875
3HMG	F_HIS_64	NE2	D_ASP_79	OD2	3.441
3HMG	F_LYS_68	NZ	F_GLU_85	OE1	3.194
3HMG	F_LYS_68	NZ	F_GLU_85	OE2	2.724
3HMG	F_ARG_76	NH1	B_GLU_74	OE1	3.414
3HMG	F_ARG_76	NH1	B_GLU_74	OE2	2.793
3HMG	F_ARG_76	NH1	B_GLU_81	OE1	2.687
3HMG	F_ARG_76	NH1	B_GLU_81	OE2	3.711
3HMG	F_ARG_76	NH2	B_GLU_74	OE1	2.734
3HMG	F_ARG_76	NH2	B_GLU_74	OE2	3.548
3HMG	F_LYS_117	NZ	F_GLU_114	OE1	2.569
3HMG	F_LYS_117	NZ	F_GLU_114	OE2	3.073
3HMG	F_ARG_123	NH1	D_GLU_132	OE2	3.319
3HMG	F_ARG_123	NH2	F_GLU_120	OE1	2.637
3HMG	F_ARG_123	NH2	F_GLU_120	OE2	3.351
3HMG	F_ARG_124	NH1	D_GLU_132	OE1	3.517
3HMG	F_ARG_124	NH1	D_GLU_132	OE2	3.294
3HMG	F_ARG_124	NH1	F_GLU_120	OE1	3.989
3HMG	F_ARG_124	NH2	F_GLU_120	OE1	3.690
3HMG	F_ARG_127	NH2	D_GLU_131	OE1	2.559
3HMG	F_HIS_159	NE2	F_ASP_160	OD2	3.217
3HMG	F_ARG_163	NH1	D_GLU_131	OE1	2.673
3HMG	F_ARG_163	NH1	D_GLU_131	OE2	2.666
3HMG	F_ARG_170	NH1	F_GLU_128	OE1	2.616
3HMG	F_ARG_170	NH2	B_GLU_128	OE1	3.705
3HMG	F_ARG_170	NH2	B_GLU_128	OE2	3.753
3HMG	F_ARG_170	NH2	F_GLU_131	OE2	2.717
3HZK	A_LYS_24	NZ	A_ASP_70	OD1	3.032
3HZK	A_LYS_24	NZ	A_ASP_70	OD2	3.302
3HZK	A_ARG_61	NH1	A_ASP_82	OD1	2.826
3HZK	A_ARG_61	NH1	A_ASP_82	OD2	3.622
3HZK	A_ARG_95	NH2	B_ASP_95	OD1	3.611

3HZK	A_ARG_95	NH2	B_ASP_95	OD2	2.795
3HZK	A_LYS_102	NZ	A_GLU_104	OE1	3.918
3HZK	A_LYS_148	NZ	A_GLU_194	OE1	3.895
3HZK	A_LYS_148	NZ	A_GLU_194	OE2	3.185
3HZK	A_ARG_154	NH1	A_GLU_184	OE1	3.701
3HZK	A_ARG_154	NH2	A_GLU_184	OE1	3.490
3HZK	A_LYS_182	NZ	A_GLU_186	OE1	2.645
3HZK	A_LYS_182	NZ	A_GLU_186	OE2	3.525
3HZK	A_HIS_188	ND1	A_ASP_150	OD2	3.092
3HZK	A_LYS_198	NZ	A_ASP_109	OD2	3.722
3HZK	B_ARG_38	NH1	B_ASP_86	OD2	2.994
3HZK	B_ARG_38	NH2	B_GLU_46	OE1	3.036
3HZK	B_ARG_38	NH2	B_GLU_46	OE2	3.939
3HZK	B_ARG_38	NH2	B_ASP_86	OD2	3.973
3HZK	B_ARG_52	NH1	B_GLU_58	OE2	2.780
3HZK	B_ARG_52	NH2	B_GLU_58	OE2	3.087
3HZK	B_ARG_66	NH1	B_ASP_86	OD1	2.850
3HZK	B_ARG_66	NH1	B_ASP_86	OD2	3.686
3HZK	B_ARG_66	NH2	B_ASP_86	OD1	3.613
3HZK	B_ARG_66	NH2	B_ASP_86	OD2	2.940
3HZK	B_ARG_94	NH2	B_ASP_101	OD1	3.902
3HZK	B_ARG_94	NH2	B_ASP_101	OD2	2.967
3HZK	B_LYS_207	NZ	A_GLU_122	OE2	3.993
3HZM	A_LYS_24	NZ	A_ASP_70	OD1	2.853
3HZM	A_LYS_24	NZ	A_ASP_70	OD2	3.528
3HZM	A_LYS_39	NZ	A_GLU_81	OE2	3.193
3HZM	A_ARG_61	NH1	A_GLU_81	OE1	3.361
3HZM	A_ARG_61	NH1	A_ASP_82	OD1	2.891
3HZM	A_ARG_61	NH1	A_ASP_82	OD2	3.592
3HZM	A_ARG_95	NH2	B_ASP_95	OD1	3.493
3HZM	A_ARG_95	NH2	B_ASP_95	OD2	2.771
3HZM	A_ARG_95	NH2	B_ASP_100E	OD1	3.831
3HZM	A_LYS_146	NZ	A_GLU_153	OE2	3.706
3HZM	A_LYS_148	NZ	A_GLU_194	OE1	3.173
3HZM	A_LYS_148	NZ	A_GLU_194	OE2	2.785
3HZM	A_ARG_154	NH1	A_GLU_184	OE2	3.270
3HZM	A_LYS_182	NZ	A_GLU_186	OE1	3.833
3HZM	A_LYS_182	NZ	A_GLU_186	OE2	3.992
3HZM	A_ARG_187	NH2	A_GLU_184	OE1	3.077
3HZM	A_HIS_188	ND1	A_ASP_150	OD2	3.055
3HZM	A_HIS_188	NE2	A_GLU_184	OE1	3.680
3HZM	A_HIS_188	NE2	A_GLU_184	OE2	3.167
3HZM	A_LYS_198	NZ	A_ASP_109	OD2	3.763
3HZM	B_ARG_38	NH1	B_ASP_86	OD2	2.747
3HZM	B_ARG_38	NH2	B_GLU_46	OE1	2.957
3HZM	B_ARG_38	NH2	B_GLU_46	OE2	3.921
3HZM	B_ARG_38	NH2	B_ASP_86	OD2	3.860
3HZM	B_ARG_52	NH1	B_GLU_58	OE2	2.944
3HZM	B_ARG_52	NH2	B_GLU_58	OE2	2.835
3HZM	B_ARG_66	NH1	B_ASP_86	OD1	2.764
3HZM	B_ARG_66	NH1	B_ASP_86	OD2	3.758
3HZM	B_ARG_66	NH2	B_ASP_86	OD1	3.543
3HZM	B_ARG_66	NH2	B_ASP_86	OD2	3.021
3HZM	B_ARG_94	NH2	B_ASP_101	OD1	3.649
3HZM	B_ARG_94	NH2	B_ASP_101	OD2	2.613
3HZM	B_LYS_207	NZ	A_GLU_122	OE2	3.353
3HZV	A_LYS_24	NZ	A_ASP_70	OD1	3.175
3HZV	A_LYS_24	NZ	A_ASP_70	OD2	3.513

3HZV	A_LYS_39	NZ	A_GLU_81	OE2	2.855
3HZV	A_ARG_61	NH1	A_GLU_81	OE1	3.565
3HZV	A_ARG_61	NH1	A_ASP_82	OD1	2.789
3HZV	A_ARG_61	NH1	A_ASP_82	OD2	3.461
3HZV	A_ARG_95	NH2	B_ASP_95	OD1	3.498
3HZV	A_ARG_95	NH2	B_ASP_95	OD2	2.821
3HZV	A_ARG_95	NH2	B_ASP_100E	OD1	3.905
3HZV	A_LYS_148	NZ	A_GLU_194	OE1	3.263
3HZV	A_LYS_148	NZ	A_GLU_194	OE2	3.225
3HZV	A_LYS_182	NZ	A_GLU_186	OE1	3.453
3HZV	A_ARG_187	NH2	A_GLU_184	OE1	2.816
3HZV	A_HIS_188	ND1	A_ASP_150	OD2	2.755
3HZV	A_HIS_188	NE2	A_GLU_184	OE1	3.971
3HZV	A_HIS_188	NE2	A_GLU_184	OE2	3.358
3HZV	A_LYS_198	NZ	A_ASP_109	OD2	3.800
3HZV	B_ARG_38	NH1	B_ASP_86	OD2	2.840
3HZV	B_ARG_38	NH2	B_GLU_46	OE1	3.130
3HZV	B_ARG_38	NH2	B_ASP_86	OD2	3.863
3HZV	B_ARG_52	NH1	B_GLU_58	OE2	2.906
3HZV	B_ARG_52	NH2	B_GLU_58	OE2	2.746
3HZV	B_ARG_66	NH1	B_ASP_86	OD1	2.687
3HZV	B_ARG_66	NH1	B_ASP_86	OD2	3.671
3HZV	B_ARG_66	NH2	B_ASP_86	OD1	3.381
3HZV	B_ARG_66	NH2	B_ASP_86	OD2	2.850
3HZV	B_ARG_94	NH2	B_ASP_101	OD1	3.676
3HZV	B_ARG_94	NH2	B_ASP_101	OD2	2.608
3HZV	B_LYS_207	NZ	A_GLU_122	OE2	3.521
3HZY	A_LYS_24	NZ	A_ASP_70	OD1	2.966
3HZY	A_LYS_24	NZ	A_ASP_70	OD2	3.808
3HZY	A_LYS_39	NZ	A_GLU_81	OE2	3.561
3HZY	A_ARG_54	NH2	A_ASP_60	OD2	3.979
3HZY	A_ARG_61	NH1	A_ASP_82	OD1	2.810
3HZY	A_ARG_61	NH1	A_ASP_82	OD2	3.525
3HZY	A_ARG_95	NH2	B_ASP_95	OD1	3.688
3HZY	A_ARG_95	NH2	B_ASP_95	OD2	3.045
3HZY	A_ARG_95	NH2	B_ASP_100E	OD1	3.820
3HZY	A_LYS_146	NZ	A_GLU_153	OE2	3.963
3HZY	A_LYS_148	NZ	A_GLU_194	OE1	2.878
3HZY	A_LYS_148	NZ	A_GLU_194	OE2	3.571
3HZY	A_ARG_154	NH1	A_GLU_184	OE2	3.171
3HZY	A_ARG_187	NH2	A_GLU_184	OE1	2.952
3HZY	A_HIS_188	ND1	A_ASP_150	OD2	3.206
3HZY	A_HIS_188	NE2	A_GLU_184	OE2	3.220
3HZY	A_LYS_198	NZ	A_ASP_109	OD2	3.836
3HZY	B_LYS_3	NZ	B_GLU_1	OE2	3.921
3HZY	B_ARG_38	NH1	B_ASP_86	OD2	2.721
3HZY	B_ARG_38	NH2	B_ASP_86	OD2	3.756
3HZY	B_ARG_52	NH1	B_GLU_58	OE2	2.797
3HZY	B_ARG_52	NH2	B_GLU_58	OE2	2.569
3HZY	B_ARG_66	NH1	B_ASP_86	OD1	2.833
3HZY	B_ARG_66	NH1	B_ASP_86	OD2	3.703
3HZY	B_ARG_66	NH2	B_ASP_86	OD1	3.472
3HZY	B_ARG_66	NH2	B_ASP_86	OD2	2.924
3HZY	B_ARG_94	NH2	B_ASP_101	OD1	3.400
3HZY	B_ARG_94	NH2	B_ASP_101	OD2	2.530
3HZY	B_LYS_207	NZ	A_GLU_122	OE2	3.902
3I02	A_ARG_61	NH1	A_ASP_82	OD1	3.000
3I02	A_ARG_61	NH1	A_ASP_82	OD2	3.958

3I02	A_ARG_95	NH2	B_ASP_95	OD2	3.028
3I02	A_LYS_102	NZ	A_GLU_104	OE2	2.902
3I02	A_LYS_146	NZ	A_GLU_194	OE2	2.628
3I02	A_LYS_148	NZ	A_GLU_194	OE2	3.134
3I02	A_ARG_154	NH1	A_GLU_184	OE2	3.155
3I02	A_LYS_182	NZ	A_ASP_183	OD1	3.921
3I02	A_LYS_182	NZ	A_GLU_186	OE2	2.799
3I02	A_ARG_187	NH2	A_GLU_184	OE1	2.793
3I02	A_HIS_188	ND1	A_ASP_150	OD2	3.259
3I02	A_LYS_198	NZ	A_ASP_109	OD1	3.541
3I02	A_LYS_198	NZ	A_ASP_109	OD2	3.982
3I02	B_ARG_38	NH1	B_ASP_86	OD2	2.730
3I02	B_ARG_38	NH2	B_GLU_46	OE1	3.082
3I02	B_ARG_38	NH2	B_GLU_46	OE2	3.832
3I02	B_ARG_38	NH2	B_ASP_86	OD2	3.854
3I02	B_ARG_52	NH1	B_ASP_58	OD2	3.947
3I02	B_ARG_52	NH2	B_ASP_58	OD2	3.567
3I02	B_ARG_66	NH1	B_ASP_86	OD1	2.819
3I02	B_ARG_66	NH1	B_ASP_86	OD2	3.716
3I02	B_ARG_66	NH2	B_ASP_86	OD1	3.582
3I02	B_ARG_66	NH2	B_ASP_86	OD2	3.033
3I02	B_ARG_94	NH2	B_ASP_101	OD2	2.982
3I02	B_ARG_98	NH1	B_ASP_100	OD2	3.749
3I02	B_ARG_98	NH2	B_ASP_100	OD2	3.470
3I02	B_ARG_98	NH2	B_ASP_100A	OD1	3.832
3I02	B_ARG_98	NH2	B_ASP_100A	OD2	3.991
3I02	C_LYS_24	NZ	C_ASP_70	OD2	3.426
3I02	C_ARG_61	NH1	C_ASP_82	OD1	2.423
3I02	C_ARG_61	NH1	C_ASP_82	OD2	3.328
3I02	C_ARG_95	NH2	D_ASP_95	OD1	3.601
3I02	C_ARG_95	NH2	D_ASP_95	OD2	2.826
3I02	C_LYS_102	NZ	C_GLU_104	OE2	3.372
3I02	C_ARG_187	NH2	C_GLU_184	OE1	2.763
3I02	C_HIS_188	NE2	C_GLU_184	OE2	3.413
3I02	C_LYS_198	NZ	C_ASP_109	OD1	3.870
3I02	C_LYS_198	NZ	C_ASP_109	OD2	2.949
3I02	D_ARG_38	NH1	D_ASP_86	OD2	2.646
3I02	D_ARG_38	NH2	D_GLU_46	OE1	2.952
3I02	D_ARG_38	NH2	D_GLU_46	OE2	3.936
3I02	D_ARG_38	NH2	D_ASP_86	OD2	3.805
3I02	D_ARG_52	NH1	D_ASP_58	OD2	3.197
3I02	D_ARG_52	NH2	D_ASP_58	OD2	2.792
3I02	D_ARG_66	NH1	D_ASP_86	OD1	2.833
3I02	D_ARG_66	NH1	D_ASP_86	OD2	3.584
3I02	D_ARG_66	NH2	D_ASP_86	OD1	3.662
3I02	D_ARG_66	NH2	D_ASP_86	OD2	2.930
3I02	D_ARG_94	NH2	D_ASP_101	OD2	2.660
3I02	D_ARG_97	NH2	D_ASP_100A	OD2	3.024
3I02	D_LYS_208	NZ	C_GLU_122	OE2	3.585
3I9G	H_ARG_38	NH2	H_GLU_46	OE1	2.845
3I9G	H_ARG_38	NH2	H_GLU_46	OE2	3.261
3I9G	H_ARG_53	NH2	H_ASP_31	OD1	2.786
3I9G	H_ARG_94	NH1	H_ASP_101	OD1	3.167
3I9G	H_ARG_94	NH1	H_ASP_101	OD2	3.902
3I9G	H_LYS_143	NZ	H_ASP_144	OD1	3.018
3I9G	H_LYS_143	NZ	H_ASP_144	OD2	2.935
3I9G	H_ARG_210	NH2	H_GLU_212	OE2	2.989
3I9G	L_LYS_42	NZ	L_GLU_39	OE1	2.937

3I9G	L_ARG_61	NH2	L_GLU_81	OE1	3.841
3I9G	L_ARG_61	NH2	L_ASP_82	OD1	2.775
3I9G	L_ARG_61	NH2	L_ASP_82	OD2	3.368
3I9G	L_LYS_149	NZ	L_GLU_195	OE1	3.806
3I9G	L_LYS_149	NZ	L_GLU_195	OE2	3.005
3I9G	L_LYS_183	NZ	L_GLU_187	OE1	3.717
3I9G	L_LYS_183	NZ	L_GLU_187	OE2	3.176
3IET	A_LYS_50	NZ	X_GLU_8	OE1	3.701
3IET	A_LYS_50	NZ	X_GLU_8	OE2	3.403
3IET	A_ARG_61	NH1	A_GLU_79	OE1	3.211
3IET	A_ARG_61	NH1	A_GLU_79	OE2	3.820
3IET	A_ARG_61	NH2	A_ASP_82	OD1	3.553
3IET	A_ARG_61	NH2	A_ASP_82	OD2	2.781
3IET	A_LYS_149	NZ	A_GLU_195	OE1	2.884
3IET	A_LYS_149	NZ	A_GLU_195	OE2	3.548
3IET	A_ARG_155	NH1	A_GLU_185	OE2	3.262
3IET	A_LYS_183	NZ	A_GLU_187	OE1	3.582
3IET	A_LYS_183	NZ	A_GLU_187	OE2	3.667
3IET	A_ARG_188	NH1	A_GLU_185	OE1	3.150
3IET	A_HIS_189	ND1	A_ASP_151	OD1	2.682
3IET	A_HIS_189	NE2	A_GLU_185	OE1	3.596
3IET	A_HIS_189	NE2	A_GLU_185	OE2	3.220
3IET	A_LYS_199	NZ	A_ASP_110	OD1	3.761
3IET	A_LYS_199	NZ	A_ASP_110	OD2	3.765
3IET	B_ARG_38	NH1	B_GLU_46	OE1	3.404
3IET	B_ARG_38	NH1	B_GLU_46	OE2	3.350
3IET	B_ARG_38	NH2	B_ASP_86	OD1	2.967
3IET	B_LYS_43	NZ	B_GLU_46	OE1	3.606
3IET	B_LYS_43	NZ	B_GLU_46	OE2	2.694
3IET	B_ARG_52	NH1	B_GLU_50	OE1	3.452
3IET	B_HIS_55	NE2	B_ASP_73	OD1	2.597
3IET	B_HIS_55	NE2	B_ASP_73	OD2	3.551
3IET	B_LYS_64	NZ	B_GLU_61	OE1	2.971
3IET	B_ARG_66	NH1	B_ASP_86	OD1	2.974
3IET	B_ARG_66	NH1	B_ASP_86	OD2	3.464
3IET	B_ARG_66	NH2	B_ASP_86	OD1	3.752
3IET	B_ARG_66	NH2	B_ASP_86	OD2	2.865
3IET	B_ARG_71	NH1	B_ASP_73	OD2	3.338
3IET	B_ARG_83	NH2	B_GLU_85	OE2	3.927
3IET	B_LYS_96	NZ	B_ASP_31	OD2	3.537
3IET	B_ARG_98	NH1	B_ASP_35	OD1	2.639
3IET	B_ARG_98	NH1	B_ASP_35	OD2	3.020
3IET	B_ARG_98	NH1	B_GLU_50	OE2	3.794
3IET	B_LYS_208	NZ	A_GLU_123	OE1	3.818
3IET	C_ARG_54	NH2	C_ASP_60	OD2	3.637
3IET	C_ARG_61	NH1	C_GLU_79	OE1	3.085
3IET	C_ARG_61	NH2	C_GLU_79	OE1	3.940
3IET	C_ARG_61	NH2	C_ASP_82	OD1	2.938
3IET	C_ARG_61	NH2	C_ASP_82	OD2	3.003
3IET	C_LYS_147	NZ	C_GLU_154	OE1	3.272
3IET	C_LYS_149	NZ	C_GLU_195	OE2	3.728
3IET	C_ARG_188	NH1	C_GLU_185	OE1	3.678
3IET	C_HIS_189	ND1	C_ASP_151	OD1	2.372
3IET	C_HIS_189	NE2	C_GLU_185	OE1	3.376
3IET	C_HIS_189	NE2	C_GLU_185	OE2	2.388
3IET	C_LYS_199	NZ	C_ASP_110	OD1	3.614
3IET	D_ARG_38	NH1	D_GLU_46	OE1	3.769
3IET	D_ARG_38	NH1	D_GLU_46	OE2	3.554

3IET	D_ARG_38	NH2	D_ASP_86	OD1	3.017
3IET	D_ARG_52	NH1	D_GLU_50	OE1	3.520
3IET	D_HIS_55	ND1	A_ASP_143	OD1	3.412
3IET	D_HIS_55	ND1	A_ASP_143	OD2	3.385
3IET	D_HIS_55	NE2	D_ASP_73	OD1	2.773
3IET	D_HIS_55	NE2	D_ASP_73	OD2	3.630
3IET	D_LYS_64	NZ	D_GLU_61	OE1	2.801
3IET	D_LYS_64	NZ	D_GLU_61	OE2	3.652
3IET	D_ARG_66	NH1	D_ASP_86	OD1	2.949
3IET	D_ARG_66	NH1	D_ASP_86	OD2	3.534
3IET	D_ARG_66	NH2	D_ASP_86	OD1	3.686
3IET	D_ARG_66	NH2	D_ASP_86	OD2	2.898
3IET	D_ARG_71	NH1	D_ASP_73	OD2	3.179
3IET	D_LYS_75	NZ	D_ASP_72	OD1	3.887
3IET	D_LYS_75	NZ	D_ASP_72	OD2	3.840
3IET	D_LYS_96	NZ	D_ASP_31	OD2	3.952
3IET	D_ARG_98	NH1	D_ASP_35	OD1	2.733
3IET	D_ARG_98	NH1	D_ASP_35	OD2	2.840
3IET	D_LYS_114	NZ	D_ASP_173	OD2	3.662
3IET	D_LYS_208	NZ	C_GLU_123	OE2	3.321
3IET	D_LYS_209	NZ	D_GLU_211	OE1	3.547
3IF1	A_ARG_24	NH1	A_ASP_70	OD2	3.644
3IF1	A_ARG_24	NH2	A_ASP_70	OD2	3.131
3IF1	A_ARG_61	NH1	A_GLU_79	OE1	3.948
3IF1	A_ARG_61	NH1	A_GLU_79	OE2	3.315
3IF1	A_ARG_61	NH2	A_ASP_82	OD1	2.825
3IF1	A_ARG_61	NH2	A_ASP_82	OD2	2.702
3IF1	A_LYS_142	NZ	A_GLU_105	OE2	3.983
3IF1	A_LYS_147	NZ	A_GLU_154	OE1	3.522
3IF1	A_LYS_149	NZ	A_GLU_195	OE1	2.902
3IF1	A_ARG_155	NH1	A_GLU_185	OE2	2.578
3IF1	A_ARG_188	NH1	A_GLU_185	OE1	3.024
3IF1	A_HIS_189	ND1	A_ASP_151	OD1	2.587
3IF1	A_HIS_189	NE2	A_GLU_185	OE1	3.887
3IF1	A_HIS_189	NE2	A_GLU_185	OE2	3.017
3IF1	A_LYS_199	NZ	A_ASP_110	OD1	2.811
3IF1	A_LYS_199	NZ	A_ASP_110	OD2	3.664
3IF1	B_ARG_38	NH1	B_GLU_46	OE1	3.546
3IF1	B_ARG_38	NH1	B_GLU_46	OE2	3.505
3IF1	B_ARG_38	NH1	B_ASP_86	OD1	3.939
3IF1	B_ARG_38	NH2	B_ASP_86	OD1	3.024
3IF1	B_LYS_43	NZ	B_GLU_46	OE1	3.786
3IF1	B_LYS_43	NZ	B_GLU_46	OE2	2.709
3IF1	B_ARG_52	NH1	B_GLU_50	OE1	3.600
3IF1	B_HIS_55	NE2	B_ASP_73	OD1	2.678
3IF1	B_HIS_55	NE2	B_ASP_73	OD2	3.590
3IF1	B_LYS_64	NZ	B_GLU_61	OE1	3.313
3IF1	B_ARG_66	NH1	B_ASP_86	OD1	3.142
3IF1	B_ARG_66	NH1	B_ASP_86	OD2	3.480
3IF1	B_ARG_66	NH2	B_ASP_86	OD1	3.813
3IF1	B_ARG_66	NH2	B_ASP_86	OD2	2.708
3IF1	B_ARG_71	NH1	B_ASP_73	OD2	3.261
3IF1	B_LYS_96	NZ	B_ASP_31	OD2	3.416
3IF1	B_ARG_98	NH1	B_ASP_35	OD1	2.801
3IF1	B_ARG_98	NH1	B_ASP_35	OD2	2.999
3IF1	B_ARG_98	NH1	B_GLU_50	OE1	3.809
3IF1	B_ARG_98	NH1	B_GLU_50	OE2	3.524
3IF1	B_ARG_98	NH2	B_GLU_50	OE1	3.792

3IF1	B_ARG_98	NH2	B_GLU_50	OE2	3.692
3IF1	C_ARG_24	NH1	C_ASP_70	OD2	3.431
3IF1	C_ARG_24	NH2	C_ASP_70	OD2	2.995
3IF1	C_ARG_61	NH1	C_GLU_79	OE2	3.277
3IF1	C_ARG_61	NH2	C_ASP_82	OD1	2.778
3IF1	C_ARG_61	NH2	C_ASP_82	OD2	2.710
3IF1	C_LYS_147	NZ	C_GLU_154	OE1	3.247
3IF1	C_LYS_149	NZ	C_GLU_195	OE1	3.400
3IF1	C_ARG_155	NH1	C_GLU_185	OE2	2.578
3IF1	C_ARG_188	NH1	C_GLU_185	OE1	2.910
3IF1	C_HIS_189	ND1	C_ASP_151	OD1	2.543
3IF1	C_HIS_189	NE2	C_GLU_185	OE2	2.831
3IF1	C_LYS_199	NZ	C_ASP_110	OD1	2.846
3IF1	C_LYS_199	NZ	C_ASP_110	OD2	3.766
3IF1	D_ARG_38	NH1	D_GLU_46	OE1	3.513
3IF1	D_ARG_38	NH1	D_GLU_46	OE2	3.484
3IF1	D_ARG_38	NH2	D_ASP_86	OD1	3.055
3IF1	D_LYS_43	NZ	D_GLU_46	OE1	3.762
3IF1	D_LYS_43	NZ	D_GLU_46	OE2	3.359
3IF1	D_ARG_52	NH1	D_GLU_50	OE1	3.903
3IF1	D_LYS_52B	NZ	A_ASP_143	OD2	3.658
3IF1	D_HIS_55	ND1	A_ASP_143	OD1	3.559
3IF1	D_HIS_55	ND1	A_ASP_143	OD2	3.251
3IF1	D_HIS_55	NE2	D_ASP_73	OD1	2.642
3IF1	D_HIS_55	NE2	D_ASP_73	OD2	3.393
3IF1	D_LYS_64	NZ	D_GLU_61	OE1	3.366
3IF1	D_ARG_66	NH1	D_ASP_86	OD1	2.982
3IF1	D_ARG_66	NH1	D_ASP_86	OD2	3.435
3IF1	D_ARG_66	NH2	D_ASP_86	OD1	3.897
3IF1	D_ARG_66	NH2	D_ASP_86	OD2	2.982
3IF1	D_ARG_71	NH1	D_ASP_73	OD2	3.435
3IF1	D_ARG_98	NH1	D_ASP_35	OD1	2.797
3IF1	D_ARG_98	NH1	D_ASP_35	OD2	2.984
3IF1	D_ARG_98	NH1	D_GLU_50	OE1	3.619
3IF1	D_ARG_98	NH1	D_GLU_50	OE2	3.743
3IF1	D_ARG_98	NH2	D_GLU_50	OE1	3.809
3IF1	D_ARG_98	NH2	D_GLU_50	OE2	3.688
3IF1	D_LYS_209	NZ	D_GLU_211	OE1	3.626
3IF1	D_LYS_209	NZ	D_GLU_211	OE2	3.891
3IJH	A_ARG_54	NH1	A_ASP_60	OD1	3.984
3IJH	A_ARG_61	NH1	A_ASP_82	OD1	3.244
3IJH	A_ARG_61	NH1	A_ASP_82	OD2	2.314
3IJH	A_ARG_61	NH2	A_ASP_82	OD1	3.682
3IJH	A_ARG_95	NH2	B_ASP_95	OD1	3.392
3IJH	A_ARG_95	NH2	B_ASP_95	OD2	2.832
3IJH	A_ARG_95	NH2	B_GLU_100E	OE1	3.920
3IJH	A_LYS_148	NZ	A_GLU_194	OE1	3.527
3IJH	A_LYS_148	NZ	A_GLU_194	OE2	2.720
3IJH	A_ARG_154	NH2	A_GLU_184	OE2	3.756
3IJH	A_HIS_188	ND1	A_ASP_150	OD2	2.926
3IJH	A_LYS_198	NZ	A_ASP_109	OD2	3.088
3IJH	B_ARG_38	NH1	B_ASP_86	OD2	2.842
3IJH	B_ARG_38	NH2	B_GLU_46	OE1	3.209
3IJH	B_ARG_38	NH2	B_ASP_86	OD2	3.896
3IJH	B_ARG_52	NH1	B_GLU_58	OE2	2.824
3IJH	B_ARG_52	NH2	B_GLU_58	OE2	3.202
3IJH	B_ARG_66	NH1	B_ASP_86	OD1	2.813
3IJH	B_ARG_66	NH1	B_ASP_86	OD2	3.750

3IJH	B_ARG_66	NH2	B_ASP_86	OD1	3.334
3IJH	B_ARG_66	NH2	B_ASP_86	OD2	2.758
3IJH	B_ARG_83	NH1	B_ASP_86	OD2	3.914
3IJH	B_ARG_164	NH1	A_ASP_166	OD1	3.428
3IJH	B_ARG_164	NH2	A_ASP_166	OD1	3.938
3IJH	B_LYS_208	NZ	A_GLU_122	OE1	2.744
3IJH	C_LYS_24	NZ	C_ASP_70	OD2	3.835
3IJH	C_ARG_54	NH1	C_ASP_60	OD1	3.972
3IJH	C_ARG_61	NH1	C_ASP_82	OD1	2.606
3IJH	C_ARG_61	NH1	C_ASP_82	OD2	2.580
3IJH	C_ARG_95	NH2	D_ASP_95	OD1	3.394
3IJH	C_ARG_95	NH2	D_ASP_95	OD2	2.734
3IJH	C_LYS_102	NZ	C_GLU_104	OE2	3.655
3IJH	C_LYS_146	NZ	C_GLU_153	OE2	3.796
3IJH	C_LYS_148	NZ	C_GLU_194	OE1	3.503
3IJH	C_LYS_148	NZ	C_GLU_194	OE2	3.158
3IJH	C_LYS_198	NZ	C_ASP_109	OD2	3.332
3IJH	D_ARG_38	NH1	D_ASP_86	OD2	2.796
3IJH	D_ARG_38	NH2	D_GLU_46	OE1	3.273
3IJH	D_ARG_38	NH2	D_ASP_86	OD2	3.880
3IJH	D_ARG_52	NH1	D_GLU_58	OE2	2.836
3IJH	D_ARG_52	NH2	D_GLU_58	OE2	3.043
3IJH	D_ARG_66	NH1	D_ASP_86	OD1	2.773
3IJH	D_ARG_66	NH1	D_ASP_86	OD2	3.767
3IJH	D_ARG_66	NH2	D_ASP_86	OD1	3.326
3IJH	D_ARG_66	NH2	D_ASP_86	OD2	2.861
3IJH	D_ARG_83	NH1	D_GLU_85	OE2	2.756
3IJH	D_ARG_164	NH1	C_ASP_166	OD1	3.593
3IJH	D_ARG_164	NH2	C_ASP_166	OD1	3.440
3IJH	D_ARG_209	NH1	D_GLU_211	OE2	3.993
3IJH	D_ARG_209	NH2	D_GLU_211	OE1	3.933
3IJS	A_ARG_61	NH1	A_ASP_82	OD1	2.832
3IJS	A_ARG_61	NH1	A_ASP_82	OD2	2.527
3IJS	A_ARG_61	NH2	A_GLU_81	OE1	3.669
3IJS	A_ARG_61	NH2	A_ASP_82	OD1	3.818
3IJS	A_ARG_95	NH2	B_ASP_95	OD1	3.603
3IJS	A_ARG_95	NH2	B_ASP_95	OD2	3.018
3IJS	A_ARG_95	NH2	B_GLU_100E	OE1	3.734
3IJS	A_LYS_102	NZ	A_GLU_104	OE2	3.940
3IJS	A_LYS_146	NZ	A_GLU_153	OE2	3.777
3IJS	A_LYS_148	NZ	A_GLU_194	OE1	3.285
3IJS	A_LYS_148	NZ	A_GLU_194	OE2	2.974
3IJS	A_LYS_182	NZ	A_GLU_186	OE1	2.825
3IJS	A_LYS_182	NZ	A_GLU_186	OE2	2.949
3IJS	A_HIS_188	ND1	A_ASP_150	OD2	2.814
3IJS	A_LYS_198	NZ	A_ASP_109	OD2	3.057
3IJS	B_ARG_38	NH1	B_ASP_86	OD2	2.852
3IJS	B_ARG_38	NH2	B_GLU_46	OE1	3.406
3IJS	B_ARG_38	NH2	B_ASP_86	OD2	3.872
3IJS	B_ARG_52	NH1	B_GLU_58	OE2	2.821
3IJS	B_ARG_52	NH2	B_GLU_58	OE2	2.883
3IJS	B_ARG_66	NH1	B_ASP_86	OD1	2.838
3IJS	B_ARG_66	NH1	B_ASP_86	OD2	3.824
3IJS	B_ARG_66	NH2	B_ASP_86	OD1	3.278
3IJS	B_ARG_66	NH2	B_ASP_86	OD2	2.729
3IJS	B_ARG_83	NH1	B_GLU_85	OE2	3.989
3IJS	B_ARG_164	NH1	A_ASP_166	OD1	3.855
3IJS	B_LYS_208	NZ	A_GLU_122	OE1	2.963

3IJS	C_ARG_54	NH1	C_ASP_60	OD2	3.567
3IJS	C_ARG_61	NH1	C_ASP_82	OD1	2.893
3IJS	C_ARG_61	NH1	C_ASP_82	OD2	3.574
3IJS	C_ARG_95	NH2	D_ASP_95	OD1	3.466
3IJS	C_ARG_95	NH2	D_ASP_95	OD2	2.795
3IJS	C_ARG_95	NH2	D_GLU_100E	OE1	3.752
3IJS	C_LYS_102	NZ	C_GLU_104	OE2	3.639
3IJS	C_LYS_146	NZ	C_GLU_153	OE1	3.935
3IJS	C_LYS_148	NZ	C_GLU_194	OE2	3.029
3IJS	C_ARG_154	NH2	C_GLU_184	OE2	3.755
3IJS	C_HIS_188	ND1	C_ASP_150	OD2	3.093
3IJS	C_LYS_198	NZ	C_ASP_109	OD2	3.489
3IJS	D_ARG_38	NH1	D_ASP_86	OD2	2.884
3IJS	D_ARG_38	NH2	D_GLU_46	OE1	3.237
3IJS	D_ARG_38	NH2	D_GLU_46	OE2	3.977
3IJS	D_ARG_52	NH1	D_GLU_58	OE2	3.033
3IJS	D_ARG_52	NH2	D_GLU_58	OE2	3.006
3IJS	D_ARG_66	NH1	D_ASP_86	OD1	2.827
3IJS	D_ARG_66	NH1	D_ASP_86	OD2	3.633
3IJS	D_ARG_66	NH2	D_ASP_86	OD1	3.506
3IJS	D_ARG_66	NH2	D_ASP_86	OD2	2.897
3IJS	D_ARG_164	NH1	C_ASP_166	OD1	3.815
3IJS	D_ARG_164	NH2	C_ASP_166	OD1	3.576
3IJS	D_LYS_208	NZ	C_GLU_122	OE1	3.219
3IJS	D_LYS_208	NZ	C_GLU_122	OE2	2.679
3IJS	D_ARG_209	NH1	D_GLU_211	OE2	2.704
3IJY	A_LYS_24	NZ	A_ASP_70	OD2	3.532
3IJY	A_ARG_54	NH1	A_ASP_60	OD1	3.326
3IJY	A_ARG_54	NH2	A_ASP_60	OD1	3.494
3IJY	A_ARG_61	NH1	A_ASP_82	OD1	2.847
3IJY	A_ARG_61	NH1	A_ASP_82	OD2	2.458
3IJY	A_ARG_61	NH2	A_GLU_81	OE1	3.326
3IJY	A_ARG_61	NH2	A_ASP_82	OD1	3.959
3IJY	A_ARG_95	NH2	B_ASP_95	OD1	3.420
3IJY	A_ARG_95	NH2	B_ASP_95	OD2	2.800
3IJY	A_ARG_95	NH2	B_GLU_100E	OE1	3.751
3IJY	A_LYS_148	NZ	A_GLU_194	OE1	3.793
3IJY	A_LYS_148	NZ	A_GLU_194	OE2	3.098
3IJY	A_HIS_188	ND1	A_ASP_150	OD2	3.295
3IJY	A_LYS_198	NZ	A_ASP_109	OD1	3.840
3IJY	A_LYS_198	NZ	A_ASP_109	OD2	3.869
3IJY	B_ARG_38	NH1	B_ASP_86	OD2	2.847
3IJY	B_ARG_38	NH2	B_GLU_46	OE1	3.463
3IJY	B_ARG_38	NH2	B_ASP_86	OD2	3.755
3IJY	B_ARG_52	NH1	B_GLU_58	OE2	3.349
3IJY	B_ARG_52	NH2	B_GLU_58	OE2	3.866
3IJY	B_ARG_66	NH1	B_ASP_86	OD1	3.730
3IJY	B_ARG_66	NH2	B_ASP_86	OD1	2.942
3IJY	B_ARG_66	NH2	B_ASP_86	OD2	2.730
3IJY	B_ARG_83	NH1	B_GLU_85	OE2	3.920
3IJY	B_ARG_83	NH1	B_ASP_86	OD2	3.633
3IJY	B_ARG_164	NH2	A_ASP_166	OD1	3.730
3IJY	B_ARG_164	NH2	A_ASP_166	OD2	3.693
3IJY	B_LYS_208	NZ	A_GLU_122	OE1	2.748
3IJY	B_ARG_209	NH2	B_GLU_211	OE2	3.922
3IJY	C_ARG_54	NH1	C_ASP_60	OD1	3.685
3IJY	C_ARG_61	NH1	C_ASP_82	OD1	2.672
3IJY	C_ARG_61	NH1	C_ASP_82	OD2	2.698

3IJY	C_ARG_95	NH2	D_ASP_95	OD1	2.992
3IJY	C_ARG_95	NH2	D_ASP_95	OD2	2.767
3IJY	C_ARG_95	NH2	D_GLU_100E	OE1	3.905
3IJY	C_LYS_102	NZ	C_GLU_104	OE2	3.111
3IJY	C_LYS_148	NZ	C_GLU_194	OE1	3.624
3IJY	C_LYS_148	NZ	C_GLU_194	OE2	2.838
3IJY	C_ARG_154	NH1	C_GLU_184	OE2	3.667
3IJY	D_ARG_38	NH1	D_ASP_86	OD2	3.093
3IJY	D_ARG_38	NH2	D_GLU_46	OE1	3.401
3IJY	D_ARG_52	NH1	D_GLU_58	OE2	3.273
3IJY	D_ARG_52	NH2	D_GLU_58	OE2	3.154
3IJY	D_ARG_66	NH1	D_ASP_86	OD1	2.831
3IJY	D_ARG_66	NH1	D_ASP_86	OD2	3.858
3IJY	D_ARG_66	NH2	D_ASP_86	OD1	3.574
3IJY	D_ARG_66	NH2	D_ASP_86	OD2	3.130
3IJY	D_ARG_83	NH1	D_GLU_85	OE2	2.929
3IJY	D_ARG_164	NH2	C_ASP_166	OD1	3.199
3IJY	D_ARG_209	NH1	D_GLU_211	OE2	2.725
3IKC	A_ARG_54	NH1	A_ASP_60	OD1	3.615
3IKC	A_ARG_54	NH2	A_ASP_60	OD1	3.863
3IKC	A_ARG_61	NH1	A_ASP_82	OD1	2.899
3IKC	A_ARG_61	NH1	A_ASP_82	OD2	2.400
3IKC	A_ARG_61	NH2	A_GLU_81	OE1	3.912
3IKC	A_ARG_61	NH2	A_ASP_82	OD1	3.699
3IKC	A_ARG_95	NH2	B_ASP_95	OD1	3.326
3IKC	A_ARG_95	NH2	B_ASP_95	OD2	2.867
3IKC	A_ARG_95	NH2	B_GLU_100E	OE1	3.865
3IKC	A_LYS_148	NZ	A_GLU_194	OE1	3.579
3IKC	A_LYS_148	NZ	A_GLU_194	OE2	2.692
3IKC	A_ARG_154	NH2	A_GLU_184	OE2	3.624
3IKC	A_HIS_188	ND1	A_ASP_150	OD2	2.784
3IKC	A_LYS_198	NZ	A_ASP_109	OD2	3.594
3IKC	B_ARG_38	NH1	B_ASP_86	OD2	2.851
3IKC	B_ARG_38	NH2	B_GLU_46	OE1	3.629
3IKC	B_ARG_38	NH2	B_GLU_46	OE2	3.974
3IKC	B_ARG_38	NH2	B_ASP_86	OD2	3.641
3IKC	B_ARG_52	NH1	B_GLU_58	OE2	2.895
3IKC	B_ARG_52	NH2	B_GLU_58	OE2	3.215
3IKC	B_ARG_66	NH1	B_ASP_86	OD1	3.007
3IKC	B_ARG_66	NH2	B_ASP_86	OD1	3.019
3IKC	B_ARG_66	NH2	B_ASP_86	OD2	2.604
3IKC	B_ARG_83	NH1	B_ASP_86	OD2	3.982
3IKC	B_LYS_208	NZ	A_GLU_122	OE1	3.042
3IKC	C_LYS_24	NZ	C_ASP_70	OD2	3.866
3IKC	C_ARG_54	NH1	C_ASP_60	OD1	3.727
3IKC	C_ARG_61	NH1	C_ASP_82	OD1	2.574
3IKC	C_ARG_61	NH1	C_ASP_82	OD2	2.683
3IKC	C_ARG_95	NH2	D_ASP_95	OD1	3.250
3IKC	C_ARG_95	NH2	D_ASP_95	OD2	2.670
3IKC	C_LYS_102	NZ	C_GLU_104	OE2	3.309
3IKC	C_LYS_148	NZ	C_GLU_194	OE1	3.402
3IKC	C_LYS_148	NZ	C_GLU_194	OE2	2.783
3IKC	C_ARG_154	NH1	C_GLU_184	OE2	3.991
3IKC	C_LYS_198	NZ	C_ASP_109	OD2	3.716
3IKC	D_ARG_38	NH1	D_ASP_86	OD2	2.796
3IKC	D_ARG_38	NH2	D_GLU_46	OE1	3.035
3IKC	D_ARG_38	NH2	D_GLU_46	OE2	3.845
3IKC	D_ARG_52	NH1	D_GLU_58	OE2	2.859

3IKC	D_ARG_52	NH2	D_GLU_58	OE2	3.107
3IKC	D_ARG_66	NH1	D_ASP_86	OD1	2.890
3IKC	D_ARG_66	NH1	D_ASP_86	OD2	3.713
3IKC	D_ARG_66	NH2	D_ASP_86	OD1	3.634
3IKC	D_ARG_66	NH2	D_ASP_86	OD2	3.025
3IKC	D_ARG_83	NH1	D_GLU_85	OE2	2.787
3IKC	D_ARG_164	NH1	C_ASP_166	OD1	3.903
3IKC	D_ARG_164	NH2	C_ASP_166	OD1	3.107
3IKC	D_ARG_209	NH1	D_GLU_211	OE2	3.689
3IKC	D_ARG_209	NH2	D_GLU_211	OE1	3.739
3IU3	A_ARG_29	NH2	K_ASP_6	OD1	2.779
3IU3	A_HIS_33	ND1	A_ASP_97	OD1	3.722
3IU3	A_HIS_33	NE2	A_ASP_97	OD1	3.462
3IU3	A_LYS_36	NZ	A_ASP_88	OD1	3.600
3IU3	A_ARG_96	NH2	A_ASP_103	OD1	3.718
3IU3	A_ARG_96	NH2	A_ASP_103	OD2	2.602
3IU3	A_LYS_211	NZ	B_GLU_120	OE1	2.457
3IU3	B_LYS_52	NZ	B_ASP_49	OD2	3.235
3IU3	B_ARG_60	NH1	B_GLU_80	OE2	3.898
3IU3	B_ARG_60	NH1	B_ASP_81	OD1	2.333
3IU3	B_ARG_60	NH1	B_ASP_81	OD2	2.901
3IU3	B_ARG_60	NH2	B_GLU_78	OE1	3.558
3IU3	B_ARG_60	NH2	B_GLU_78	OE2	3.050
3IU3	B_ARG_90	NH1	B_ASP_49	OD1	2.801
3IU3	B_ARG_90	NH1	K_ASP_56	OD2	3.059
3IU3	B_ARG_90	NH2	B_ASP_49	OD1	2.779
3IU3	B_LYS_100	NZ	B_GLU_162	OE1	3.331
3IU3	B_LYS_100	NZ	B_GLU_162	OE2	3.171
3IU3	B_LYS_146	NZ	B_GLU_192	OE1	3.006
3IU3	B_LYS_146	NZ	B_GLU_192	OE2	3.977
3IU3	B_HIS_186	ND1	B_ASP_148	OD2	3.079
3IU3	C_ARG_29	NH1	J_ASP_6	OD1	3.038
3IU3	C_ARG_29	NH1	J_ASP_6	OD2	3.788
3IU3	C_ARG_29	NH2	J_ASP_6	OD1	3.464
3IU3	C_HIS_33	ND1	C_ASP_97	OD2	3.423
3IU3	C_HIS_33	NE2	C_ASP_97	OD2	3.493
3IU3	C_ARG_38	NH2	C_GLU_87	OE2	3.961
3IU3	C_LYS_61	NZ	C_GLU_44	OE2	2.894
3IU3	C_LYS_65	NZ	C_ASP_88	OD2	3.093
3IU3	C_LYS_67	NZ	C_GLU_80	OE2	3.813
3IU3	C_ARG_96	NH1	C_ASP_103	OD1	3.896
3IU3	C_ARG_96	NH1	C_ASP_103	OD2	2.604
3IU3	C_LYS_145	NZ	C_ASP_146	OD1	3.489
3IU3	C_LYS_145	NZ	C_ASP_146	OD2	3.988
3IU3	C_LYS_211	NZ	D_GLU_120	OE2	3.231
3IU3	C_ARG_212	NH1	C_GLU_214	OE1	3.436
3IU3	C_ARG_212	NH1	C_GLU_214	OE2	3.171
3IU3	D_LYS_52	NZ	D_ASP_49	OD2	2.969
3IU3	D_ARG_60	NH1	D_GLU_78	OE1	3.425
3IU3	D_ARG_60	NH1	D_GLU_78	OE2	3.777
3IU3	D_ARG_60	NH2	D_GLU_78	OE1	3.729
3IU3	D_ARG_60	NH2	D_ASP_81	OD1	2.613
3IU3	D_ARG_60	NH2	D_ASP_81	OD2	3.360
3IU3	D_ARG_90	NH1	D_ASP_49	OD1	2.486
3IU3	D_ARG_90	NH1	D_ASP_49	OD2	3.966
3IU3	D_ARG_90	NH2	D_ASP_49	OD1	2.791
3IU3	D_ARG_90	NH2	J_ASP_56	OD2	3.101
3IU3	D_LYS_100	NZ	D_GLU_162	OE1	3.352

3IU3	D_LYS_100	NZ	D_GLU_162	OE2	3.241
3IU3	D_ARG_139	NH2	D_GLU_102	OE1	3.961
3IU3	D_ARG_139	NH2	D_GLU_102	OE2	2.898
3IU3	D_LYS_146	NZ	D_GLU_192	OE1	3.339
3IU3	D_HIS_186	ND1	D_ASP_148	OD2	3.055
3IU3	H_ARG_29	NH1	L_ASP_6	OD1	3.964
3IU3	H_ARG_29	NH1	L_ASP_6	OD2	3.865
3IU3	H_ARG_29	NH2	L_ASP_6	OD1	2.749
3IU3	H_ARG_29	NH2	L_ASP_6	OD2	3.378
3IU3	H_HIS_33	ND1	H_ASP_97	OD2	3.649
3IU3	H_HIS_33	NE2	H_ASP_97	OD2	3.672
3IU3	H_ARG_38	NH2	H_GLU_87	OE2	3.294
3IU3	H_LYS_65	NZ	H_ASP_88	OD1	3.023
3IU3	H_LYS_65	NZ	H_ASP_88	OD2	2.754
3IU3	H_ARG_96	NH2	H_ASP_103	OD1	3.935
3IU3	H_ARG_96	NH2	H_ASP_103	OD2	2.794
3IU3	H_HIS_166	NE2	L_ASP_164	OD1	3.898
3IU3	H_LYS_211	NZ	L_GLU_120	OE2	3.694
3IU3	L_ARG_29	NH2	L_ASP_56	OD2	3.164
3IU3	L_LYS_52	NZ	L_ASP_49	OD2	2.964
3IU3	L_ARG_60	NH1	L_GLU_78	OE1	3.113
3IU3	L_ARG_60	NH1	L_GLU_78	OE2	3.592
3IU3	L_ARG_60	NH2	L_GLU_78	OE1	3.507
3IU3	L_ARG_60	NH2	L_GLU_80	OE1	3.605
3IU3	L_ARG_60	NH2	L_ASP_81	OD1	2.623
3IU3	L_ARG_60	NH2	L_ASP_81	OD2	3.232
3IU3	L_ARG_90	NH1	L_ASP_49	OD1	2.693
3IU3	L_ARG_90	NH2	L_ASP_49	OD1	2.879
3IU3	L_ARG_90	NH2	L_ASP_56	OD1	2.806
3IU3	L_LYS_100	NZ	L_GLU_102	OE2	3.519
3IU3	L_LYS_100	NZ	L_GLU_162	OE1	3.094
3IU3	L_LYS_100	NZ	L_GLU_162	OE2	3.091
3IU3	L_ARG_139	NH1	L_GLU_102	OE2	3.791
3IU3	L_ARG_139	NH2	L_GLU_102	OE1	3.338
3IU3	L_ARG_139	NH2	L_GLU_102	OE2	2.994
3IU3	L_LYS_185	NZ	L_ASP_182	OD1	3.411
3IU3	L_HIS_186	ND1	L_ASP_148	OD2	2.793
3IU3	L_ARG_36	NH1	H_ASP_55	OD1	3.819
3IU3	L_ARG_36	NH2	H_ASP_55	OD1	3.008
3IU3	L_ARG_36	NH2	H_ASP_55	OD2	2.747
3IU3	L_ARG_117	NH2	L_GLU_106	OE2	3.361
3IU3	L_HIS_120	NE2	L_ASP_4	OD2	3.993
3IU3	J_ARG_117	NH2	J_GLU_113	OE1	3.255
3IU3	J_ARG_117	NH2	J_GLU_113	OE2	3.394
3IU3	K_LYS_16	NZ	K_GLU_116	OE1	3.890
3IU3	K_ARG_117	NH2	K_GLU_113	OE1	3.765
3IU3	K_ARG_117	NH2	K_GLU_113	OE2	3.085
3IU3	K_HIS_120	NE2	K_ASP_4	OD1	3.824
3IU4	H_ARG_38	NH1	H_ASP_86	OD1	2.694
3IU4	H_ARG_38	NH2	H_GLU_46	OE1	2.936
3IU4	H_ARG_38	NH2	H_GLU_46	OE2	3.977
3IU4	H_ARG_38	NH2	H_ASP_86	OD1	3.682
3IU4	H_ARG_66	NH1	H_ASP_86	OD1	3.618
3IU4	H_ARG_66	NH1	H_ASP_86	OD2	2.904
3IU4	H_ARG_66	NH2	H_ASP_86	OD1	2.858
3IU4	H_ARG_66	NH2	H_ASP_86	OD2	3.468
3IU4	H_LYS_143	NZ	H_ASP_144	OD1	3.173
3IU4	H_LYS_143	NZ	H_ASP_144	OD2	3.097

3IU4	H.LYS_210	NZ	H.GLU_212	OE2	3.515
3IU4	L.ARG_54	NH2	L.ASP_60	OD1	3.494
3IU4	L.ARG_61	NH2	L.ASP_82	OD1	2.721
3IU4	L.ARG_61	NH2	L.ASP_82	OD2	3.542
3IU4	L.LYS_103	NZ	L.GLU_165	OE1	2.777
3IU4	L.LYS_103	NZ	L.GLU_165	OE2	3.441
3IU4	L.LYS_149	NZ	L.GLU_195	OE2	3.735
3IU4	L.LYS_190	NZ	L.GLU_213	OE2	2.585
3IVK	L.ARG_25	NH2	L.ASP_71	OD1	3.565
3IVK	L.ARG_25	NH2	L.ASP_71	OD2	3.118
3IVK	L.ARG_62	NH2	L.GLU_82	OE1	3.240
3IVK	L.ARG_62	NH2	L.ASP_83	OD1	3.041
3IVK	L.ARG_62	NH2	L.ASP_83	OD2	3.362
3IVK	L.LYS_104	NZ	L.GLU_106	OE2	2.881
3IVK	L.ARG_143	NH1	L.GLU_106	OE2	2.980
3IVK	L.LYS_150	NZ	L.GLU_196	OE2	2.646
3IVK	H.ARG_41	NH1	H.ASP_93	OD1	2.697
3IVK	H.ARG_41	NH2	H.GLU_49	OE1	3.359
3IVK	H.ARG_41	NH2	H.GLU_49	OE2	3.688
3IVK	H.ARG_41	NH2	H.ASP_93	OD1	3.849
3IVK	H.ARG_70	NH1	H.ASP_93	OD2	2.963
3IVK	H.ARG_70	NH2	H.ASP_93	OD1	2.795
3IVK	H.ARG_70	NH2	H.ASP_93	OD2	2.668
3IVK	H.LYS_79	NZ	H.ASP_76	OD2	3.978
3IVK	H.ARG_101	NH2	H.ASP_113	OD2	3.051
3IVK	H.ARG_107	NH1	H.ASP_113	OD2	3.782
3IVK	H.LYS_155	NZ	H.ASP_156	OD1	3.783
3IVK	H.LYS_155	NZ	H.ASP_156	OD2	3.283
3IVK	H.LYS_218	NZ	H.ASP_220	OD1	3.490
3IVK	H.LYS_218	NZ	H.ASP_220	OD2	3.548
3IVK	H.LYS_222	NZ	H.GLU_224	OE1	3.186
3IVK	H.LYS_222	NZ	H.GLU_224	OE2	3.235
3IVK	B.ARG_25	NH2	B.ASP_71	OD1	3.579
3IVK	B.ARG_25	NH2	B.ASP_71	OD2	3.085
3IVK	B.ARG_62	NH2	B.GLU_82	OE1	3.276
3IVK	B.ARG_62	NH2	B.ASP_83	OD1	3.056
3IVK	B.ARG_62	NH2	B.ASP_83	OD2	3.370
3IVK	B.LYS_104	NZ	B.GLU_106	OE2	2.879
3IVK	B.ARG_143	NH1	B.GLU_106	OE2	2.970
3IVK	B.LYS_150	NZ	B.GLU_196	OE2	2.638
3IVK	A.ARG_41	NH1	A.ASP_93	OD1	2.649
3IVK	A.ARG_41	NH2	A.GLU_49	OE1	3.405
3IVK	A.ARG_41	NH2	A.GLU_49	OE2	3.702
3IVK	A.ARG_41	NH2	A.ASP_93	OD1	3.815
3IVK	A.ARG_70	NH1	A.ASP_93	OD2	2.973
3IVK	A.ARG_70	NH2	A.ASP_93	OD1	2.836
3IVK	A.ARG_70	NH2	A.ASP_93	OD2	2.675
3IVK	A.LYS_79	NZ	A.ASP_76	OD2	3.988
3IVK	A.ARG_101	NH2	A.ASP_113	OD2	3.070
3IVK	A.ARG_107	NH1	A.ASP_113	OD2	3.837
3IVK	A.LYS_155	NZ	A.ASP_156	OD1	3.802
3IVK	A.LYS_155	NZ	A.ASP_156	OD2	3.283
3IVK	A.LYS_218	NZ	A.ASP_220	OD1	3.505
3IVK	A.LYS_218	NZ	A.ASP_220	OD2	3.577
3IVK	A.LYS_222	NZ	A.GLU_224	OE1	3.213
3IVK	A.LYS_222	NZ	A.GLU_224	OE2	3.240
3J5M	A.LYS_46	NZ	A.GLU_492	OE1	3.718
3J5M	A.LYS_46	NZ	A.GLU_492	OE2	2.915

3J5M	A_HIS_66	ND1	A_GLU_64	OE2	3.151
3J5M	A_ARG_143	NH2	A_GLU_145	OE1	2.805
3J5M	A_ARG_143	NH2	A_GLU_145	OE2	3.445
3J5M	A_LYS_229	NZ	A_GLU_83	OE1	2.907
3J5M	A_LYS_231	NZ	A_GLU_268	OE2	2.874
3J5M	A_HIS_249	NE2	A_GLU_482	OE1	3.482
3J5M	A_LYS_282	NZ	A_GLU_275	OE1	2.857
3J5M	A_LYS_282	NZ	A_GLU_275	OE2	3.935
3J5M	A_LYS_344	NZ	A_GLU_340	OE2	3.897
3J5M	A_LYS_421	NZ	A_GLU_145	OE2	3.812
3J5M	A_ARG_429	NH2	D_ASP_74	OD1	3.207
3J5M	A_ARG_429	NH2	D_ASP_74	OD2	3.203
3J5M	A_ARG_456	NH1	A_GLU_466	OE1	2.968
3J5M	A_ARG_476	NH2	A_ASP_474	OD1	3.858
3J5M	A_ARG_480	NH1	A_ASP_477	OD1	2.834
3J5M	A_LYS_487	NZ	A_GLU_91	OE2	2.895
3J5M	C_ARG_54	NH2	C_ASP_60	OD1	2.987
3J5M	C_ARG_61	NH1	C_GLU_79	OE2	3.926
3J5M	C_ARG_61	NH2	C_GLU_79	OE1	3.624
3J5M	C_ARG_61	NH2	C_ASP_82	OD1	3.040
3J5M	C_ARG_61	NH2	C_ASP_82	OD2	3.088
3J5M	C_ARG_103	NH2	C_GLU_165	OE1	2.814
3J5M	C_ARG_142	NH1	C_GLU_165	OE1	3.243
3J5M	C_ARG_142	NH2	C_GLU_105	OE2	3.198
3J5M	C_LYS_149	NZ	C_GLU_195	OE1	3.376
3J5M	C_LYS_149	NZ	C_GLU_195	OE2	2.944
3J5M	C_HIS_189	ND1	C_ASP_151	OD2	2.803
3J5M	D_ARG_19	NH1	D_ASP_81	OD2	3.870
3J5M	D_ARG_19	NH2	D_ASP_81	OD2	3.177
3J5M	D_ARG_31	NH2	D_ASP_27	OD2	3.998
3J5M	D_ARG_38	NH1	D_ASP_86	OD1	2.857
3J5M	D_ARG_38	NH2	D_GLU_46	OE2	2.922
3J5M	D_LYS_52	NZ	A_ASP_474	OD2	2.827
3J5M	D_LYS_52	NZ	D_GLU_33	OE2	3.615
3J5M	D_ARG_64	NH2	A_ASP_457	OD2	3.079
3J5M	D_ARG_73	NH2	D_GLU_30	OE1	2.847
3J5M	D_ARG_73	NH2	D_GLU_30	OE2	3.839
3J5M	D_LYS_209	NZ	C_GLU_123	OE1	3.480
3J5M	D_LYS_209	NZ	C_GLU_123	OE2	2.844
3J5M	D_LYS_214	NZ	C_ASP_122	OD2	2.841
3J5M	E_LYS_46	NZ	E_GLU_492	OE1	3.718
3J5M	E_LYS_46	NZ	E_GLU_492	OE2	2.915
3J5M	E_HIS_66	ND1	E_GLU_64	OE2	3.151
3J5M	E_ARG_143	NH2	E_GLU_145	OE1	2.804
3J5M	E_ARG_143	NH2	E_GLU_145	OE2	3.444
3J5M	E_LYS_229	NZ	E_GLU_83	OE1	2.907
3J5M	E_LYS_231	NZ	E_GLU_268	OE2	2.874
3J5M	E_HIS_249	NE2	E_GLU_482	OE1	3.482
3J5M	E_LYS_282	NZ	E_GLU_275	OE1	2.858
3J5M	E_LYS_282	NZ	E_GLU_275	OE2	3.935
3J5M	E_LYS_344	NZ	E_GLU_340	OE2	3.897
3J5M	E_LYS_421	NZ	E_GLU_145	OE2	3.812
3J5M	E_ARG_429	NH2	H_ASP_74	OD1	3.207
3J5M	E_ARG_429	NH2	H_ASP_74	OD2	3.202
3J5M	E_ARG_456	NH1	E_GLU_466	OE1	2.967
3J5M	E_ARG_476	NH2	E_ASP_474	OD1	3.859
3J5M	E_ARG_480	NH1	E_ASP_477	OD1	2.834
3J5M	E_LYS_487	NZ	E_GLU_91	OE2	2.894

3J5M	G_ARG_54	NH2	G_ASP_60	OD1	2.988
3J5M	G_ARG_61	NH1	G_GLU_79	OE2	3.925
3J5M	G_ARG_61	NH2	G_GLU_79	OE1	3.624
3J5M	G_ARG_61	NH2	G_ASP_82	OD1	3.040
3J5M	G_ARG_61	NH2	G_ASP_82	OD2	3.087
3J5M	G_ARG_103	NH2	G_GLU_165	OE1	2.814
3J5M	G_ARG_142	NH1	G_GLU_165	OE1	3.243
3J5M	G_ARG_142	NH2	G_GLU_105	OE2	3.199
3J5M	G_LYS_149	NZ	G_GLU_195	OE1	3.376
3J5M	G_LYS_149	NZ	G_GLU_195	OE2	2.944
3J5M	G_HIS_189	ND1	G_ASP_151	OD2	2.802
3J5M	H_ARG_19	NH1	H_ASP_81	OD2	3.869
3J5M	H_ARG_19	NH2	H_ASP_81	OD2	3.177
3J5M	H_ARG_31	NH2	H_ASP_27	OD2	3.998
3J5M	H_ARG_38	NH1	H_ASP_86	OD1	2.857
3J5M	H_ARG_38	NH2	H_GLU_46	OE2	2.922
3J5M	H_LYS_52	NZ	E_ASP_474	OD2	2.827
3J5M	H_LYS_52	NZ	H_GLU_33	OE2	3.614
3J5M	H_ARG_64	NH2	E_ASP_457	OD2	3.078
3J5M	H_ARG_73	NH2	H_GLU_30	OE1	2.847
3J5M	H_ARG_73	NH2	H_GLU_30	OE2	3.840
3J5M	H_LYS_209	NZ	G_GLU_123	OE1	3.479
3J5M	H_LYS_209	NZ	G_GLU_123	OE2	2.843
3J5M	H_LYS_214	NZ	G_ASP_122	OD2	2.842
3J5M	I_LYS_46	NZ	I_GLU_492	OE1	3.718
3J5M	I_LYS_46	NZ	I_GLU_492	OE2	2.915
3J5M	I_HIS_66	ND1	I_GLU_64	OE2	3.151
3J5M	I_ARG_143	NH2	I_GLU_145	OE1	2.805
3J5M	I_ARG_143	NH2	I_GLU_145	OE2	3.445
3J5M	I_LYS_229	NZ	I_GLU_83	OE1	2.907
3J5M	I_LYS_231	NZ	I_GLU_268	OE2	2.875
3J5M	I_HIS_249	NE2	I_GLU_482	OE1	3.482
3J5M	I_LYS_282	NZ	I_GLU_275	OE1	2.857
3J5M	I_LYS_282	NZ	I_GLU_275	OE2	3.934
3J5M	I_LYS_344	NZ	I_GLU_340	OE2	3.896
3J5M	I_LYS_421	NZ	I_GLU_145	OE2	3.811
3J5M	I_ARG_429	NH2	L_ASP_74	OD1	3.207
3J5M	I_ARG_429	NH2	L_ASP_74	OD2	3.202
3J5M	I_ARG_456	NH1	I_GLU_466	OE1	2.967
3J5M	I_ARG_476	NH2	I_ASP_474	OD1	3.859
3J5M	I_ARG_480	NH1	I_ASP_477	OD1	2.834
3J5M	I_LYS_487	NZ	I_GLU_91	OE2	2.895
3J5M	K_ARG_54	NH2	K_ASP_60	OD1	2.987
3J5M	K_ARG_61	NH1	K_GLU_79	OE2	3.926
3J5M	K_ARG_61	NH2	K_GLU_79	OE1	3.624
3J5M	K_ARG_61	NH2	K_ASP_82	OD1	3.041
3J5M	K_ARG_61	NH2	K_ASP_82	OD2	3.088
3J5M	K_ARG_103	NH2	K_GLU_165	OE1	2.814
3J5M	K_ARG_142	NH1	K_GLU_165	OE1	3.243
3J5M	K_ARG_142	NH2	K_GLU_105	OE2	3.198
3J5M	K_LYS_149	NZ	K_GLU_195	OE1	3.376
3J5M	K_LYS_149	NZ	K_GLU_195	OE2	2.944
3J5M	K_HIS_189	ND1	K_ASP_151	OD2	2.803
3J5M	L_ARG_19	NH1	L_ASP_81	OD2	3.870
3J5M	L_ARG_19	NH2	L_ASP_81	OD2	3.177
3J5M	L_ARG_31	NH2	L_ASP_27	OD2	3.998
3J5M	L_ARG_38	NH1	L_ASP_86	OD1	2.857
3J5M	L_ARG_38	NH2	L_GLU_46	OE2	2.922

3J5M	L_LYS_52	NZ	I_ASP_474	OD2	2.827
3J5M	L_LYS_52	NZ	L_GLU_33	OE2	3.615
3J5M	L_ARG_64	NH2	I_ASP_457	OD2	3.078
3J5M	L_ARG_73	NH2	L_GLU_30	OE1	2.847
3J5M	L_ARG_73	NH2	L_GLU_30	OE2	3.839
3J5M	L_LYS_209	NZ	K_GLU_123	OE1	3.480
3J5M	L_LYS_209	NZ	K_GLU_123	OE2	2.844
3J5M	L_LYS_214	NZ	K_ASP_122	OD2	2.841
3J70	A_ARG_38	NH1	A_ASP_86	OD1	3.866
3J70	A_ARG_38	NH2	A_GLU_46	OE1	2.795
3J70	A_ARG_38	NH2	A_ASP_86	OD1	2.823
3J70	A_LYS_62	NZ	A_GLU_46	OE2	2.813
3J70	A_ARG_64	NH2	B_ASP_1	OD1	2.676
3J70	A_ARG_66	NH2	A_ASP_86	OD2	2.896
3J70	A_ARG_83	NH2	A_GLU_85	OE2	3.748
3J70	A_LYS_209	NZ	B_GLU_123	OE1	3.744
3J70	A_LYS_209	NZ	B_GLU_123	OE2	2.604
3J70	A_LYS_210	NZ	A_GLU_212	OE1	3.567
3J70	A_LYS_214	NZ	A_GLU_212	OE1	3.762
3J70	A_LYS_214	NZ	A_GLU_212	OE2	3.583
3J70	B_ARG_61	NH2	B_ASP_82	OD1	2.797
3J70	B_ARG_61	NH2	B_ASP_82	OD2	2.800
3J70	B_LYS_103	NZ	B_GLU_165	OE1	2.848
3J70	B_LYS_103	NZ	B_GLU_165	OE2	3.750
3J70	B_ARG_108	NH1	B_ASP_170	OD2	3.189
3J70	B_LYS_149	NZ	B_GLU_195	OE1	3.334
3J70	B_LYS_149	NZ	B_GLU_195	OE2	2.862
3J70	C_LYS_8	NZ	C_GLU_119	OE1	2.764
3J70	C_HIS_27	ND1	C_GLU_85	OE1	3.187
3J70	C_LYS_29	NZ	C_GLU_85	OE1	3.965
3J70	C_LYS_29	NZ	D_ASP_279	OD2	2.704
3J70	C_LYS_46	NZ	C_ASP_56	OD1	2.811
3J70	C_LYS_50	NZ	C_GLU_77	OE1	2.765
3J70	C_LYS_50	NZ	C_GLU_77	OE2	3.345
3J70	C_ARG_54	NH1	C_ASP_78	OD2	2.875
3J70	C_ARG_54	NH2	C_ASP_78	OD1	2.822
3J70	C_ARG_54	NH2	C_ASP_78	OD2	2.827
3J70	C_ARG_59	NH1	D_ASP_368	OD1	3.842
3J70	C_ARG_59	NH1	D_ASP_368	OD2	2.986
3J70	C_ARG_59	NH2	D_ASP_368	OD1	2.621
3J70	C_ARG_59	NH2	D_ASP_368	OD2	3.173
3J70	C_LYS_72	NZ	C_ASP_56	OD2	2.565
3J70	C_LYS_90	NZ	C_GLU_85	OE2	2.709
3J70	C_HIS_107	ND1	C_ASP_105	OD2	3.850
3J70	C_ARG_134	NH2	C_ASP_153	OD1	3.650
3J70	C_ARG_134	NH2	C_ASP_153	OD2	3.960
3J70	D_LYS_46	NZ	D_GLU_492	OE1	2.843
3J70	D_LYS_46	NZ	D_GLU_492	OE2	2.835
3J70	D_LYS_130	NZ	D_GLU_150	OE2	2.774
3J70	D_ARG_146	NH1	C_GLU_169	OE1	2.841
3J70	D_ARG_146	NH1	C_GLU_169	OE2	2.796
3J70	D_ARG_146	NH2	C_GLU_169	OE1	3.599
3J70	D_LYS_171	NZ	C_GLU_13	OE1	3.949
3J70	D_LYS_192	NZ	D_ASP_137	OD2	2.718
3J70	D_LYS_207	NZ	D_GLU_381	OE2	2.776
3J70	D_HIS_249	NE2	D_GLU_482	OE1	2.775
3J70	D_LYS_282	NZ	D_ASP_279	OD1	2.794
3J70	D_LYS_322	NZ	A_ASP_95	OD2	2.908

3J70	D_ARG_327	NH2	A_ASP_52	OD2	3.286
3J70	D_LYS_337	NZ	D_GLU_293	OE2	2.865
3J70	D_LYS_348	NZ	D_GLU_269	OE1	2.779
3J70	D_LYS_348	NZ	D_GLU_269	OE2	3.998
3J70	D_ARG_419	NH1	A_ASP_54	OD1	3.985
3J70	D_ARG_456	NH1	D_GLU_466	OE1	2.870
3J70	D_ARG_456	NH1	D_GLU_466	OE2	2.877
3J70	D_ARG_469	NH1	D_ASP_457	OD1	2.823
3J70	D_ARG_469	NH1	D_ASP_457	OD2	3.449
3J70	D_ARG_469	NH2	D_ASP_457	OD2	3.357
3J70	D_ARG_476	NH1	D_ASP_474	OD1	2.860
3J70	D_ARG_480	NH1	D_ASP_474	OD2	2.862
3J70	D_ARG_480	NH1	D_ASP_477	OD1	2.641
3J70	D_ARG_480	NH1	D_ASP_477	OD2	3.954
3J70	D_ARG_480	NH2	D_ASP_474	OD2	3.415
3J70	D_LYS_487	NZ	D_GLU_47	OE2	3.606
3J70	D_LYS_487	NZ	D_GLU_91	OE2	2.796
3J70	M_ARG_38	NH1	M_ASP_86	OD1	3.866
3J70	M_ARG_38	NH2	M_GLU_46	OE1	2.795
3J70	M_ARG_38	NH2	M_ASP_86	OD1	2.824
3J70	M_LYS_62	NZ	M_GLU_46	OE2	2.814
3J70	M_ARG_64	NH2	N_ASP_1	OD1	2.677
3J70	M_ARG_66	NH2	M_ASP_86	OD2	2.896
3J70	M_ARG_83	NH2	M_GLU_85	OE2	3.748
3J70	M_LYS_209	NZ	N_GLU_123	OE1	3.744
3J70	M_LYS_209	NZ	N_GLU_123	OE2	2.604
3J70	M_LYS_210	NZ	M_GLU_212	OE1	3.567
3J70	M_LYS_214	NZ	M_GLU_212	OE1	3.762
3J70	M_LYS_214	NZ	M_GLU_212	OE2	3.583
3J70	N_ARG_61	NH2	N_ASP_82	OD1	2.798
3J70	N_ARG_61	NH2	N_ASP_82	OD2	2.800
3J70	N_LYS_103	NZ	N_GLU_165	OE1	2.848
3J70	N_LYS_103	NZ	N_GLU_165	OE2	3.750
3J70	N_ARG_108	NH1	N_ASP_170	OD2	3.190
3J70	N_LYS_149	NZ	N_GLU_195	OE1	3.334
3J70	N_LYS_149	NZ	N_GLU_195	OE2	2.861
3J70	O_LYS_8	NZ	O_GLU_119	OE1	2.765
3J70	O_HIS_27	ND1	O_GLU_85	OE1	3.187
3J70	O_LYS_29	NZ	O_GLU_85	OE1	3.964
3J70	O_LYS_29	NZ	P_ASP_279	OD2	2.704
3J70	O_LYS_46	NZ	O_ASP_56	OD1	2.811
3J70	O_LYS_50	NZ	O_GLU_77	OE1	2.765
3J70	O_LYS_50	NZ	O_GLU_77	OE2	3.346
3J70	O_ARG_54	NH1	O_ASP_78	OD2	2.875
3J70	O_ARG_54	NH2	O_ASP_78	OD1	2.822
3J70	O_ARG_54	NH2	O_ASP_78	OD2	2.827
3J70	O_ARG_59	NH1	P_ASP_368	OD1	3.842
3J70	O_ARG_59	NH1	P_ASP_368	OD2	2.986
3J70	O_ARG_59	NH2	P_ASP_368	OD1	2.620
3J70	O_ARG_59	NH2	P_ASP_368	OD2	3.173
3J70	O_LYS_72	NZ	O_ASP_56	OD2	2.565
3J70	O_LYS_90	NZ	O_GLU_85	OE2	2.709
3J70	O_HIS_107	ND1	O_ASP_105	OD2	3.851
3J70	O_ARG_134	NH2	O_ASP_153	OD1	3.650
3J70	O_ARG_134	NH2	O_ASP_153	OD2	3.960
3J70	P_LYS_46	NZ	P_GLU_492	OE1	2.843
3J70	P_LYS_46	NZ	P_GLU_492	OE2	2.835
3J70	P_LYS_130	NZ	P_GLU_150	OE2	2.774

3J70	P_ARG_146	NH1	O_GLU_169	OE1	2.841
3J70	P_ARG_146	NH1	O_GLU_169	OE2	2.796
3J70	P_ARG_146	NH2	O_GLU_169	OE1	3.599
3J70	P_LYS_171	NZ	O_GLU_13	OE1	3.948
3J70	P_LYS_192	NZ	P_ASP_137	OD2	2.718
3J70	P_LYS_207	NZ	P_GLU_381	OE2	2.776
3J70	P_HIS_249	NE2	P_GLU_482	OE1	2.775
3J70	P_LYS_282	NZ	P_ASP_279	OD1	2.794
3J70	P_LYS_322	NZ	M_ASP_95	OD2	2.909
3J70	P_ARG_327	NH2	M_ASP_52	OD2	3.286
3J70	P_LYS_337	NZ	P_GLU_293	OE2	2.865
3J70	P_LYS_348	NZ	P_GLU_269	OE1	2.779
3J70	P_LYS_348	NZ	P_GLU_269	OE2	3.999
3J70	P_ARG_419	NH1	M_ASP_54	OD1	3.985
3J70	P_ARG_456	NH1	P_GLU_466	OE1	2.870
3J70	P_ARG_456	NH1	P_GLU_466	OE2	2.877
3J70	P_ARG_469	NH1	P_ASP_457	OD1	2.823
3J70	P_ARG_469	NH1	P_ASP_457	OD2	3.450
3J70	P_ARG_469	NH2	P_ASP_457	OD2	3.357
3J70	P_ARG_476	NH1	P_ASP_474	OD1	2.859
3J70	P_ARG_480	NH1	P_ASP_474	OD2	2.862
3J70	P_ARG_480	NH1	P_ASP_477	OD1	2.642
3J70	P_ARG_480	NH1	P_ASP_477	OD2	3.954
3J70	P_ARG_480	NH2	P_ASP_474	OD2	3.415
3J70	P_LYS_487	NZ	P_GLU_47	OE2	3.605
3J70	P_LYS_487	NZ	P_GLU_91	OE2	2.797
3J70	R_ARG_38	NH1	R_ASP_86	OD1	3.866
3J70	R_ARG_38	NH2	R_GLU_46	OE1	2.795
3J70	R_ARG_38	NH2	R_ASP_86	OD1	2.824
3J70	R_LYS_62	NZ	R_GLU_46	OE2	2.814
3J70	R_ARG_64	NH2	S_ASP_1	OD1	2.677
3J70	R_ARG_66	NH2	R_ASP_86	OD2	2.896
3J70	R_ARG_83	NH2	R_GLU_85	OE2	3.748
3J70	R_LYS_209	NZ	S_GLU_123	OE1	3.743
3J70	R_LYS_209	NZ	S_GLU_123	OE2	2.603
3J70	R_LYS_210	NZ	R_GLU_212	OE1	3.567
3J70	R_LYS_214	NZ	R_GLU_212	OE1	3.762
3J70	R_LYS_214	NZ	R_GLU_212	OE2	3.584
3J70	S_ARG_61	NH2	S_ASP_82	OD1	2.798
3J70	S_ARG_61	NH2	S_ASP_82	OD2	2.800
3J70	S_LYS_103	NZ	S_GLU_165	OE1	2.848
3J70	S_LYS_103	NZ	S_GLU_165	OE2	3.750
3J70	S_ARG_108	NH1	S_ASP_170	OD2	3.190
3J70	S_LYS_149	NZ	S_GLU_195	OE1	3.334
3J70	S_LYS_149	NZ	S_GLU_195	OE2	2.862
3J70	T_LYS_8	NZ	T_GLU_119	OE1	2.764
3J70	T_HIS_27	ND1	T_GLU_85	OE1	3.187
3J70	T_LYS_29	NZ	T_GLU_85	OE1	3.965
3J70	T_LYS_29	NZ	U_ASP_279	OD2	2.704
3J70	T_LYS_46	NZ	T_ASP_56	OD1	2.811
3J70	T_LYS_50	NZ	T_GLU_77	OE1	2.766
3J70	T_LYS_50	NZ	T_GLU_77	OE2	3.346
3J70	T_ARG_54	NH1	T_ASP_78	OD2	2.876
3J70	T_ARG_54	NH2	T_ASP_78	OD1	2.822
3J70	T_ARG_54	NH2	T_ASP_78	OD2	2.826
3J70	T_ARG_59	NH1	U_ASP_368	OD1	3.842
3J70	T_ARG_59	NH1	U_ASP_368	OD2	2.986
3J70	T_ARG_59	NH2	U_ASP_368	OD1	2.621

3J70	T_ARG_59	NH2	U_ASP_368	OD2	3.174
3J70	T_LYS_72	NZ	T_ASP_56	OD2	2.565
3J70	T_LYS_90	NZ	T_GLU_85	OE2	2.710
3J70	T_HIS_107	ND1	T_ASP_105	OD2	3.850
3J70	T_ARG_134	NH2	T_ASP_153	OD1	3.650
3J70	T_ARG_134	NH2	T_ASP_153	OD2	3.960
3J70	U_LYS_46	NZ	U_GLU_492	OE1	2.842
3J70	U_LYS_46	NZ	U_GLU_492	OE2	2.835
3J70	U_LYS_130	NZ	U_GLU_150	OE2	2.774
3J70	U_ARG_146	NH1	T_GLU_169	OE1	2.840
3J70	U_ARG_146	NH1	T_GLU_169	OE2	2.796
3J70	U_ARG_146	NH2	T_GLU_169	OE1	3.599
3J70	U_LYS_171	NZ	T_GLU_13	OE1	3.949
3J70	U_LYS_192	NZ	U_ASP_137	OD2	2.718
3J70	U_LYS_207	NZ	U_GLU_381	OE2	2.777
3J70	U_HIS_249	NE2	U_GLU_482	OE1	2.776
3J70	U_LYS_282	NZ	U_ASP_279	OD1	2.794
3J70	U_LYS_322	NZ	R_ASP_95	OD2	2.909
3J70	U_ARG_327	NH2	R_ASP_52	OD2	3.287
3J70	U_LYS_337	NZ	U_GLU_293	OE2	2.865
3J70	U_LYS_348	NZ	U_GLU_269	OE1	2.778
3J70	U_LYS_348	NZ	U_GLU_269	OE2	3.998
3J70	U_ARG_419	NH1	R_ASP_54	OD1	3.985
3J70	U_ARG_456	NH1	U_GLU_466	OE1	2.869
3J70	U_ARG_456	NH1	U_GLU_466	OE2	2.877
3J70	U_ARG_469	NH1	U_ASP_457	OD1	2.823
3J70	U_ARG_469	NH1	U_ASP_457	OD2	3.449
3J70	U_ARG_469	NH2	U_ASP_457	OD2	3.356
3J70	U_ARG_476	NH1	U_ASP_474	OD1	2.860
3J70	U_ARG_480	NH1	U_ASP_474	OD2	2.861
3J70	U_ARG_480	NH1	U_ASP_477	OD1	2.641
3J70	U_ARG_480	NH1	U_ASP_477	OD2	3.954
3J70	U_ARG_480	NH2	U_ASP_474	OD2	3.415
3J70	U_LYS_487	NZ	U_GLU_47	OE2	3.606
3J70	U_LYS_487	NZ	U_GLU_91	OE2	2.796
3JCC	A_LYS_46	NZ	A_GLU_492	OE1	3.517
3JCC	A_LYS_227	NZ	A_GLU_83	OE2	3.448
3JCC	A_ARG_429	NH2	D_ASP_63	OD2	3.854
3JCC	A_ARG_456	NH2	A_GLU_466	OE1	3.660
3JCC	A_ARG_456	NH2	A_GLU_466	OE2	3.547
3JCC	A_ARG_469	NH2	A_ASP_457	OD2	3.023
3JCC	A_ARG_476	NH1	A_ASP_474	OD1	3.399
3JCC	A_ARG_476	NH1	A_ASP_474	OD2	2.964
3JCC	A_ARG_480	NH2	A_ASP_477	OD1	2.803
3JCC	A_LYS_485	NZ	A_GLU_267	OE2	3.722
3JCC	A_LYS_487	NZ	A_ASP_47	OD2	3.970
3JCC	B_ARG_61	NH1	B_ASP_82	OD2	2.931
3JCC	B_ARG_61	NH2	B_ASP_82	OD1	3.215
3JCC	B_ARG_61	NH2	B_ASP_82	OD2	3.003
3JCC	B_HIS_189	ND1	B_ASP_152	OD2	2.901
3JCC	C_ARG_38	NH1	C_ASP_86	OD1	2.894
3JCC	C_ARG_38	NH2	C_GLU_46	OE1	2.884
3JCC	C_ARG_38	NH2	C_ASP_86	OD1	3.828
3JCC	C_ARG_66	NH1	C_ASP_86	OD1	3.699
3JCC	C_ARG_66	NH1	C_ASP_86	OD2	2.932
3JCC	C_ARG_66	NH2	C_ASP_86	OD1	3.002
3JCC	C_ARG_66	NH2	C_ASP_86	OD2	3.413
3JCC	C_LYS_73	NZ	C_ASP_53	OD1	3.190

3JCC	C_LYS_73	NZ	C_ASP_53	OD2	3.723
3JCC	C_LYS_207	NZ	B_GLU_124	OE1	3.629
3JCC	D_LYS_8	NZ	D_GLU_119	OE1	3.039
3JCC	D_LYS_8	NZ	D_GLU_119	OE2	3.886
3JCC	D_LYS_29	NZ	D_GLU_85	OE1	2.956
3JCC	D_LYS_29	NZ	D_GLU_85	OE2	3.072
3JCC	D_ARG_54	NH1	D_ASP_78	OD2	2.902
3JCC	D_ARG_54	NH2	D_ASP_78	OD1	3.053
3JCC	D_ARG_54	NH2	D_ASP_78	OD2	2.965
3JCC	D_ARG_58	NH1	D_GLU_13	OE1	3.576
3JCC	D_ARG_58	NH1	D_GLU_13	OE2	3.174
3JCC	D_ARG_58	NH2	D_GLU_13	OE1	2.940
3JCC	D_ARG_58	NH2	D_GLU_13	OE2	3.860
3JCC	D_ARG_59	NH2	A_ASP_368	OD1	2.961
3JCC	D_ARG_59	NH2	A_ASP_368	OD2	3.986
3JCC	E_LYS_46	NZ	E_GLU_492	OE1	3.569
3JCC	E_LYS_46	NZ	E_GLU_492	OE2	3.703
3JCC	E_LYS_97	NZ	E_GLU_275	OE2	3.827
3JCC	E_LYS_227	NZ	E_GLU_83	OE1	3.969
3JCC	E_LYS_227	NZ	E_GLU_83	OE2	3.697
3JCC	E_LYS_282	NZ	E_GLU_275	OE1	3.981
3JCC	E_ARG_298	NH2	E_GLU_381	OE1	3.660
3JCC	E_ARG_298	NH2	E_GLU_381	OE2	3.777
3JCC	E_LYS_305	NZ	E_ASP_321	OD2	3.131
3JCC	E_ARG_456	NH1	E_GLU_466	OE1	3.660
3JCC	E_ARG_456	NH1	E_GLU_466	OE2	3.969
3JCC	E_ARG_456	NH2	E_GLU_466	OE1	3.908
3JCC	E_ARG_456	NH2	E_GLU_466	OE2	3.604
3JCC	E_ARG_469	NH1	E_ASP_457	OD1	3.767
3JCC	E_ARG_480	NH1	E_ASP_477	OD1	3.074
3JCC	E_LYS_485	NZ	E_GLU_267	OE2	3.897
3JCC	E_LYS_487	NZ	E_ASP_47	OD2	3.681
3JCC	E_LYS_490	NZ	E_GLU_49	OE2	2.934
3JCC	I_LYS_46	NZ	I_GLU_492	OE1	3.919
3JCC	I_ARG_166	NH2	I_ASP_167	OD2	3.510
3JCC	I_LYS_227	NZ	I_GLU_83	OE2	3.974
3JCC	I_LYS_305	NZ	I_ASP_321	OD2	3.762
3JCC	I_ARG_456	NH2	I_GLU_466	OE1	3.385
3JCC	I_ARG_456	NH2	I_GLU_466	OE2	3.431
3JCC	I_ARG_476	NH1	I_ASP_474	OD2	3.645
3JCC	I_ARG_480	NH1	I_ASP_477	OD1	3.186
3JCC	I_LYS_490	NZ	I_GLU_49	OE2	3.753
3KS0	L_ARG_63	NH2	L_GLU_83	OE2	3.743
3KS0	L_ARG_63	NH2	L_ASP_84	OD1	3.432
3KS0	L_ARG_63	NH2	L_ASP_84	OD2	3.922
3KS0	L_LYS_113	NZ	L_GLU_201	OE1	3.009
3KS0	H_ARG_38	NH1	H_ASP_89	OD1	2.927
3KS0	H_ARG_38	NH2	H_GLU_46	OE1	2.737
3KS0	H_LYS_39	NZ	L_GLU_40	OE1	3.686
3KS0	H_LYS_39	NZ	L_GLU_40	OE2	2.843
3KS0	H_ARG_66	NH1	H_ASP_89	OD1	2.901
3KS0	H_ARG_66	NH1	H_ASP_89	OD2	3.003
3KS0	H_ARG_66	NH2	H_ASP_89	OD1	3.781
3KS0	H_ARG_97	NH2	H_ASP_105	OD1	3.237
3KS0	H_ARG_97	NH2	H_ASP_105	OD2	2.854
3KS0	H_LYS_147	NZ	L_GLU_127	OE2	3.112
3KS0	H_LYS_212	NZ	L_GLU_126	OE1	3.920
3KS0	H_LYS_212	NZ	L_GLU_126	OE2	3.042

3KS0	A_LYS_18	NZ	A_GLU_15	OE2	3.032
3KS0	A_HIS_19	ND1	A_GLU_15	OE1	3.858
3KS0	A_HIS_19	NE2	A_GLU_15	OE1	3.591
3KS0	A_HIS_19	NE2	A_ASP_24	OD1	3.901
3KS0	A_HIS_19	NE2	A_ASP_24	OD2	3.803
3KS0	A_LYS_79	NZ	A_ASP_35	OD2	3.088
3KS0	A_LYS_80	NZ	A_ASP_72	OD1	2.255
3KS0	A_LYS_80	NZ	A_ASP_72	OD2	3.580
3KS0	J_ARG_63	NH2	J_GLU_83	OE2	3.774
3KS0	J_ARG_63	NH2	J_ASP_84	OD1	2.968
3KS0	J_ARG_63	NH2	J_ASP_84	OD2	3.838
3KS0	J_LYS_113	NZ	J_GLU_201	OE1	3.035
3KS0	J_HIS_191	NE2	J_ASP_154	OD2	3.977
3KS0	K_ARG_38	NH1	K_ASP_89	OD1	2.723
3KS0	K_ARG_38	NH2	K_GLU_46	OE1	2.728
3KS0	K_ARG_38	NH2	K_GLU_46	OE2	3.919
3KS0	K_LYS_39	NZ	J_GLU_40	OE1	3.754
3KS0	K_LYS_39	NZ	J_GLU_40	OE2	2.934
3KS0	K_ARG_66	NH1	K_ASP_89	OD1	3.466
3KS0	K_ARG_66	NH1	K_ASP_89	OD2	2.993
3KS0	K_ARG_66	NH2	K_ASP_89	OD1	3.246
3KS0	K_ARG_97	NH1	K_ASP_27	OD2	3.899
3KS0	K_ARG_97	NH2	K_ASP_105	OD1	3.477
3KS0	K_ARG_97	NH2	K_ASP_105	OD2	3.126
3KS0	K_LYS_147	NZ	J_GLU_127	OE2	3.169
3KS0	K_LYS_212	NZ	J_GLU_126	OE1	3.344
3KS0	K_LYS_212	NZ	J_GLU_126	OE2	2.562
3KS0	B_LYS_18	NZ	B_GLU_15	OE2	3.407
3KS0	B_HIS_19	NE2	B_GLU_15	OE1	3.733
3KS0	B_HIS_19	NE2	B_ASP_24	OD1	3.929
3KS0	B_LYS_79	NZ	B_ASP_35	OD2	3.032
3KS0	B_LYS_80	NZ	B_ASP_72	OD1	2.482
3KS0	B_LYS_80	NZ	B_ASP_72	OD2	3.798
3L7E	L_ARG_61	NH1	L_ASP_82	OD1	3.610
3L7E	L_ARG_61	NH1	L_ASP_82	OD2	2.820
3L7E	L_ARG_61	NH2	L_GLU_79	OE1	3.380
3L7E	L_ARG_61	NH2	L_GLU_79	OE2	3.052
3L7E	L_ARG_61	NH2	L_ASP_82	OD1	3.146
3L7E	L_ARG_61	NH2	L_ASP_82	OD2	3.585
3L7E	L_LYS_103	NZ	L_GLU_165	OE1	2.700
3L7E	L_LYS_145	NZ	L_GLU_161	OE1	3.739
3L7E	L_LYS_145	NZ	L_GLU_161	OE2	2.941
3L7E	L_LYS_149	NZ	L_GLU_195	OE2	3.782
3L7E	H_ARG_40	NH1	H_ASP_91	OD1	2.619
3L7E	H_ARG_40	NH2	H_GLU_48	OE1	3.221
3L7E	H_ARG_40	NH2	H_ASP_91	OD1	3.670
3L7E	H_ARG_68	NH1	H_ASP_91	OD1	3.997
3L7E	H_ARG_68	NH1	H_ASP_91	OD2	3.070
3L7E	H_ARG_68	NH2	H_ASP_91	OD1	3.385
3L7E	H_ARG_68	NH2	H_ASP_91	OD2	3.481
3L7E	H_ARG_99	NH2	H_ASP_109	OD1	3.758
3L7E	H_ARG_99	NH2	H_ASP_109	OD2	2.966
3L7E	H_LYS_151	NZ	H_ASP_152	OD1	3.202
3L7E	H_LYS_151	NZ	H_ASP_152	OD2	3.603
3L7E	H_LYS_214	NZ	H_ASP_216	OD2	3.774
3L7E	H_LYS_217	NZ	L_GLU_123	OE1	3.175
3L7E	H_LYS_218	NZ	H_GLU_220	OE2	2.784
3L7E	A_ARG_61	NH1	A_ASP_82	OD1	3.894

3L7E	A_ARG_61	NH1	A_ASP_82	OD2	2.738
3L7E	A_ARG_61	NH2	A_GLU_79	OE1	3.630
3L7E	A_ARG_61	NH2	A_GLU_79	OE2	3.597
3L7E	A_ARG_61	NH2	A_ASP_82	OD1	2.858
3L7E	A_ARG_61	NH2	A_ASP_82	OD2	3.208
3L7E	A_LYS_103	NZ	A_GLU_165	OE1	2.858
3L7E	A_LYS_103	NZ	A_GLU_165	OE2	3.136
3L7E	A_LYS_149	NZ	A_GLU_195	OE1	2.753
3L7E	A_ARG_211	NH2	A_GLU_187	OE2	3.405
3L7E	B_ARG_40	NH1	B_ASP_91	OD1	2.997
3L7E	B_ARG_40	NH2	B_GLU_48	OE1	3.270
3L7E	B_ARG_40	NH2	B_GLU_48	OE2	3.888
3L7E	B_ARG_40	NH2	B_ASP_91	OD1	3.815
3L7E	B_LYS_59	NZ	B_ASP_57	OD1	3.071
3L7E	B_LYS_59	NZ	B_ASP_57	OD2	3.376
3L7E	B_ARG_68	NH1	B_ASP_91	OD2	3.159
3L7E	B_ARG_68	NH2	B_ASP_91	OD1	2.945
3L7E	B_ARG_68	NH2	B_ASP_91	OD2	2.970
3L7E	B_ARG_99	NH2	B_ASP_109	OD1	3.495
3L7E	B_ARG_99	NH2	B_ASP_109	OD2	2.485
3L7E	B_LYS_151	NZ	B_ASP_152	OD1	3.115
3L7E	B_LYS_151	NZ	B_ASP_152	OD2	3.672
3L7E	B_LYS_217	NZ	A_GLU_123	OE1	2.697
3L7E	B_LYS_217	NZ	A_GLU_123	OE2	3.970
3L7E	B_LYS_218	NZ	B_GLU_220	OE2	3.907
3LZF	A_LYS_53	NZ	A_ASP_276	OD1	3.007
3LZF	A_LYS_63	NZ	A_GLU_75	OE1	3.244
3LZF	A_ARG_109	NH1	A_GLU_89	OE1	2.815
3LZF	A_ARG_109	NH1	A_GLU_89	OE2	3.490
3LZF	A_ARG_109	NH2	A_GLU_89	OE1	3.694
3LZF	A_ARG_109	NH2	A_GLU_89	OE2	3.025
3LZF	A_ARG_109	NH2	B_GLU_69	OE1	3.970
3LZF	A_ARG_109	NH2	B_GLU_69	OE2	2.555
3LZF	A_LYS_133A	NZ	A_GLU_131	OE1	3.911
3LZF	A_ARG_149	NH2	A_ASP_77	OD1	3.274
3LZF	A_ARG_149	NH2	A_ASP_77	OD2	2.737
3LZF	A_LYS_157	NZ	H_ASP_52	OD1	3.712
3LZF	A_LYS_157	NZ	H_ASP_52	OD2	3.952
3LZF	A_LYS_157	NZ	H_ASP_54	OD2	2.960
3LZF	A_LYS_163	NZ	A_GLU_246	OE1	3.633
3LZF	A_LYS_166	NZ	L_ASP_93	OD1	2.890
3LZF	A_LYS_166	NZ	L_ASP_93	OD2	2.667
3LZF	A_LYS_174	NZ	A_GLU_119	OE1	2.507
3LZF	A_LYS_174	NZ	A_GLU_119	OE2	3.039
3LZF	A_HIS_184	ND1	A_GLU_216	OE1	3.917
3LZF	A_LYS_208	NZ	A_GLU_238	OE2	3.278
3LZF	A_ARG_262	NH2	A_GLU_175	OE1	3.039
3LZF	A_ARG_262	NH2	A_GLU_175	OE2	3.035
3LZF	A_ARG_310	NH1	B_ASP_90	OD1	2.412
3LZF	A_ARG_310	NH2	B_ASP_90	OD1	3.228
3LZF	A_ARG_315	NH1	A_ASP_24	OD2	3.770
3LZF	A_ARG_321	NH1	A_GLU_31	OE1	3.446
3LZF	A_ARG_321	NH1	A_GLU_31	OE2	3.361
3LZF	B_LYS_51	NZ	B_GLU_103	OE1	2.812
3LZF	B_LYS_68	NZ	A_GLU_110	OE1	3.290
3LZF	B_LYS_68	NZ	A_GLU_110	OE2	2.778
3LZF	B_LYS_82	NZ	B_ASP_86	OD2	3.052
3LZF	B_ARG_116	NH2	B_GLU_120	OE1	3.732

3LZF	B_ARG_116	NH2	B_GLU_120	OE2	3.831
3LZF	B_LYS_123	NZ	B_GLU_132	OE2	2.843
3LZF	B_LYS_143	NZ	B_GLU_29	OE1	3.843
3LZF	B_LYS_143	NZ	B_GLU_29	OE2	3.948
3LZF	B_ARG_153	NH2	B_GLU_150	OE2	3.778
3LZF	H_ARG_38	NH1	H_ASP_86	OD1	2.752
3LZF	H_ARG_38	NH2	H_GLU_46	OE1	2.805
3LZF	H_ARG_38	NH2	H_ASP_86	OD1	3.834
3LZF	H_ARG_66	NH1	H_ASP_86	OD2	3.179
3LZF	H_ARG_66	NH2	H_ASP_86	OD1	3.026
3LZF	H_ARG_66	NH2	H_ASP_86	OD2	3.038
3LZF	H_LYS_71	NZ	H_ASP_55	OD1	2.502
3LZF	H_ARG_94	NH2	H_ASP_101	OD2	2.420
3LZF	H_ARG_97	NH1	H_ASP_52	OD1	2.811
3LZF	H_ARG_97	NH1	H_ASP_52	OD2	3.899
3LZF	H_ARG_97	NH2	H_ASP_52	OD1	2.854
3LZF	H_ARG_97	NH2	H_ASP_52	OD2	2.731
3LZF	H_ARG_97	NH2	H_ASP_53	OD1	2.942
3LZF	H_ARG_100D	NH2	H_ASP_100A	OD2	2.691
3LZF	H_LYS_145	NZ	H_ASP_146	OD1	3.565
3LZF	H_LYS_221	NZ	L_GLU_123	OE2	3.483
3LZF	L_ARG_61	NH2	L_ASP_82	OD1	3.298
3LZF	L_ARG_61	NH2	L_ASP_82	OD2	3.277
3LZF	L_LYS_103	NZ	L_ASP_85	OD1	3.336
3LZF	L_LYS_166	NZ	L_GLU_83	OE1	2.813
3LZF	L_HIS_189	ND1	L_ASP_	OD2	3.741
3M18	A_ARG_55	NH1	A_ASP_80	OD1	3.709
3M18	A_ARG_136	NH2	A_GLU_134	OE2	2.915
3M18	A_LYS_232	NZ	A_ASP_230	OD1	3.832
3M18	A_LYS_232	NZ	A_ASP_230	OD2	2.770
3M18	A_ARG_235	NH2	A_ASP_224	OD1	3.588
3M18	A_ARG_235	NH2	A_ASP_224	OD2	3.213
3M18	B_LYS_1	NZ	B_GLU_7	OE2	2.569
3M18	B_LYS_13	NZ	B_ASP_18	OD2	3.673
3M18	B_ARG_61	NH1	B_ASP_48	OD2	3.299
3M18	B_ARG_125	NH1	B_ASP_119	OD2	3.044
3M18	B_ARG_125	NH2	B_ASP_119	OD1	3.195
3M18	B_ARG_125	NH2	B_ASP_119	OD2	3.443
3M19	A_LYS_59	NZ	A_GLU_37	OE2	3.221
3M19	A_HIS_104	ND1	A_ASP_79	OD1	3.554
3M19	A_HIS_104	NE2	A_ASP_79	OD1	3.514
3M19	A_HIS_104	NE2	A_ASP_79	OD2	3.839
3M19	A_ARG_128	NH1	A_ASP_103	OD2	3.998
3M19	A_ARG_128	NH2	A_ASP_103	OD2	3.816
3M19	A_ARG_136	NH2	A_GLU_134	OE2	2.501
3M19	A_LYS_243	NZ	A_GLU_245	OE2	3.905
3M19	B_HIS_104	ND1	B_ASP_79	OD1	3.606
3M19	B_HIS_104	NE2	B_ASP_79	OD1	3.640
3M19	B_HIS_104	NE2	B_ASP_79	OD2	3.894
3M19	B_ARG_128	NH1	B_ASP_103	OD2	3.698
3M19	B_ARG_128	NH2	B_ASP_103	OD2	3.517
3M19	B_ARG_136	NH2	B_GLU_134	OE1	2.918
3M19	B_ARG_136	NH2	B_GLU_134	OE2	3.574
3M19	B_LYS_152	NZ	B_ASP_127	OD1	3.986
3M19	B_LYS_152	NZ	B_ASP_127	OD2	3.666
3M19	B_ARG_194	NH2	B_ASP_191	OD2	3.254
3MLR	L_LYS_27	NZ	L_ASP_92	OD1	2.852
3MLR	L_LYS_31	NZ	L_ASP_30	OD1	3.628

3MLR	L_LYS_31	NZ	L_ASP_30	OD2	3.071
3MLR	L_ARG_61	NH1	L_ASP_82	OD1	3.647
3MLR	L_ARG_61	NH1	L_ASP_82	OD2	2.892
3MLR	L_ARG_61	NH2	L_ASP_82	OD1	2.845
3MLR	L_ARG_61	NH2	L_ASP_82	OD2	3.527
3MLR	L_LYS_66	NZ	L_ASP_51	OD1	3.042
3MLR	L_LYS_66	NZ	L_ASP_51	OD2	3.142
3MLR	L_ARG_106A	NH2	L_ASP_85	OD1	3.458
3MLR	L_ARG_106A	NH2	L_ASP_85	OD2	3.111
3MLR	L_LYS_153	NZ	L_GLU_207	OE2	3.546
3MLR	H_ARG_38	NH2	H_GLU_46	OE1	2.819
3MLR	H_ARG_94	NH2	H_ASP_101	OD1	3.334
3MLR	H_ARG_94	NH2	H_ASP_101	OD2	2.709
3MLR	H_LYS_129	NZ	L_ASP_142	OD2	3.806
3MLR	H_LYS_209	NZ	L_GLU_127	OE2	3.182
3MLR	P_LYS_304	NZ	H_ASP_31	OD1	3.470
3MLR	P_LYS_305	NZ	H_ASP_54	OD1	2.683
3MLR	P_LYS_305	NZ	H_ASP_54	OD2	3.624
3MLR	P_LYS_305	NZ	H_ASP_56	OD2	3.011
3MLS	L_LYS_27	NZ	L_ASP_92	OD1	3.433
3MLS	L_LYS_27	NZ	L_ASP_92	OD2	3.469
3MLS	L_LYS_31	NZ	L_ASP_30	OD1	3.032
3MLS	L_LYS_31	NZ	L_ASP_30	OD2	2.898
3MLS	L_ARG_61	NH1	L_ASP_82	OD1	3.401
3MLS	L_ARG_61	NH2	L_ASP_82	OD1	3.515
3MLS	L_ARG_61	NH2	L_ASP_82	OD2	3.451
3MLS	L_LYS_66	NZ	L_ASP_51	OD1	3.260
3MLS	L_LYS_66	NZ	L_ASP_51	OD2	3.251
3MLS	L_LYS_69	NZ	L_ASP_29	OD1	3.080
3MLS	L_ARG_106A	NH2	L_ASP_85	OD1	3.981
3MLS	L_ARG_106A	NH2	L_ASP_85	OD2	3.840
3MLS	H_ARG_38	NH1	H_ASP_86	OD1	3.821
3MLS	H_ARG_38	NH2	H_GLU_46	OE1	3.613
3MLS	H_ARG_38	NH2	H_GLU_46	OE2	3.084
3MLS	H_LYS_73	NZ	H_ASP_53	OD1	3.435
3MLS	H_LYS_73	NZ	L_ASP_31	OD1	3.962
3MLS	H_LYS_73	NZ	L_ASP_31	OD2	2.716
3MLS	H_LYS_73	NZ	L_ASP_53	OD1	3.242
3MLS	H_LYS_73	NZ	L_ASP_53	OD2	3.339
3MLS	H_ARG_94	NH2	H_ASP_101	OD1	2.712
3MLS	H_ARG_94	NH2	H_ASP_101	OD2	2.782
3MLS	H_LYS_117	NZ	J_GLU_10	OE1	3.515
3MLS	H_LYS_143	NZ	L_GLU_128	OE2	2.664
3MLS	H_LYS_209	NZ	L_GLU_127	OE1	2.677
3MLS	H_LYS_210	NZ	H_GLU_212	OE2	2.981
3MLS	P_ARG_11	NH1	H_GLU_99	OE1	3.690
3MLS	P_ARG_11	NH1	H_GLU_99	OE2	3.548
3MLS	P_ARG_11	NH2	H_GLU_99	OE1	3.097
3MLS	P_ARG_11	NH2	H_GLU_99	OE2	3.355
3MLS	P_LYS_12	NZ	H_ASP_54	OD1	3.420
3MLS	P_LYS_12	NZ	H_ASP_54	OD2	2.807
3MLS	P_LYS_12	NZ	H_ASP_56	OD1	3.833
3MLS	P_LYS_12	NZ	H_ASP_56	OD2	3.175
3MLS	M_LYS_27	NZ	M_ASP_92	OD1	2.791
3MLS	M_LYS_27	NZ	M_ASP_92	OD2	3.981
3MLS	M_LYS_31	NZ	M_ASP_30	OD1	2.980
3MLS	M_LYS_31	NZ	M_ASP_30	OD2	3.022
3MLS	M_ARG_61	NH1	M_ASP_82	OD2	2.881

3MLS	M_ARG_61	NH2	M_ASP_82	OD1	3.067
3MLS	M_ARG_61	NH2	M_ASP_82	OD2	3.143
3MLS	M_LYS_66	NZ	M_ASP_51	OD1	3.245
3MLS	M_LYS_66	NZ	M_ASP_51	OD2	3.348
3MLS	M_LYS_69	NZ	M_ASP_29	OD1	3.369
3MLS	M_ARG_106A	NH2	M_ASP_85	OD1	3.977
3MLS	M_ARG_106A	NH2	M_ASP_85	OD2	3.547
3MLS	M_LYS_170	NZ	M_GLU_83	OE1	3.910
3MLS	I_ARG_38	NH2	I_GLU_46	OE1	2.757
3MLS	I_ARG_38	NH2	I_GLU_46	OE2	3.394
3MLS	I_ARG_94	NH2	I_ASP_101	OD1	3.196
3MLS	I_ARG_94	NH2	I_ASP_101	OD2	2.556
3MLS	I_LYS_143	NZ	M_GLU_128	OE2	2.744
3MLS	I_LYS_210	NZ	I_GLU_212	OE2	3.234
3MLS	Q_LYS_12	NZ	I_ASP_54	OD1	2.683
3MLS	Q_LYS_12	NZ	I_ASP_54	OD2	3.484
3MLS	Q_LYS_12	NZ	I_ASP_56	OD1	3.650
3MLS	N_LYS_27	NZ	N_ASP_92	OD1	2.638
3MLS	N_LYS_27	NZ	N_ASP_92	OD2	3.279
3MLS	N_LYS_31	NZ	N_ASP_92	OD1	3.789
3MLS	N_ARG_61	NH1	N_ASP_82	OD1	3.670
3MLS	N_ARG_61	NH1	N_ASP_82	OD2	2.886
3MLS	N_ARG_61	NH2	N_ASP_82	OD1	2.936
3MLS	N_ARG_61	NH2	N_ASP_82	OD2	3.467
3MLS	N_LYS_66	NZ	N_ASP_51	OD1	2.940
3MLS	N_LYS_66	NZ	N_ASP_51	OD2	2.905
3MLS	N_LYS_69	NZ	N_ASP_26	OD2	3.361
3MLS	N_LYS_97	NZ	J_GLU_64	OE2	3.402
3MLS	N_ARG_106A	NH1	N_ASP_85	OD1	3.854
3MLS	N_ARG_106A	NH2	N_ASP_85	OD1	3.571
3MLS	N_ARG_106A	NH2	N_ASP_85	OD2	3.057
3MLS	N_LYS_153	NZ	N_GLU_207	OE2	2.702
3MLS	N_HIS_192	ND1	N_ASP_155	OD1	2.942
3MLS	N_LYS_193	NZ	N_ASP_155	OD1	3.885
3MLS	N_LYS_193	NZ	N_ASP_155	OD2	3.535
3MLS	J_ARG_38	NH2	J_GLU_46	OE1	3.096
3MLS	J_ARG_38	NH2	J_GLU_46	OE2	3.226
3MLS	J_ARG_94	NH2	J_ASP_101	OD1	3.116
3MLS	J_ARG_94	NH2	J_ASP_101	OD2	2.667
3MLS	J_LYS_117	NZ	H_GLU_10	OE1	3.984
3MLS	J_LYS_209	NZ	N_GLU_127	OE2	3.428
3MLS	J_LYS_210	NZ	J_GLU_212	OE1	2.956
3MLS	J_LYS_210	NZ	J_GLU_212	OE2	3.284
3MLS	R_LYS_12	NZ	J_ASP_54	OD1	2.569
3MLS	R_LYS_12	NZ	J_ASP_54	OD2	3.629
3MLS	R_LYS_12	NZ	J_ASP_56	OD2	2.975
3MLS	O_LYS_27	NZ	O_ASP_92	OD1	3.055
3MLS	O_LYS_27	NZ	O_ASP_92	OD2	3.636
3MLS	O_LYS_31	NZ	O_ASP_30	OD1	3.500
3MLS	O_LYS_31	NZ	O_ASP_30	OD2	3.178
3MLS	O_ARG_61	NH1	O_ASP_82	OD1	3.846
3MLS	O_ARG_61	NH1	O_ASP_82	OD2	3.018
3MLS	O_ARG_61	NH2	O_ASP_82	OD1	2.964
3MLS	O_ARG_61	NH2	O_ASP_82	OD2	3.525
3MLS	O_LYS_66	NZ	O_ASP_51	OD1	3.127
3MLS	O_LYS_66	NZ	O_ASP_51	OD2	3.042
3MLS	O_LYS_69	NZ	O_ASP_26	OD1	3.632
3MLS	O_LYS_69	NZ	O_ASP_29	OD2	3.396

3MLS	O_ARG_106A	NH2	O_ASP_85	OD1	3.674
3MLS	O_ARG_106A	NH2	O_ASP_85	OD2	3.358
3MLS	O_LYS_153	NZ	O_GLU_207	OE1	2.594
3MLS	O_HIS_192	NE2	O_ASP_155	OD2	3.869
3MLS	K_ARG_38	NH2	K_GLU_46	OE1	2.675
3MLS	K_ARG_38	NH2	K_GLU_46	OE2	3.386
3MLS	K_ARG_94	NH1	K_ASP_101	OD1	2.987
3MLS	K_ARG_94	NH1	K_ASP_101	OD2	2.783
3MLS	K_LYS_117	NZ	L_GLU_10	OE1	3.985
3MLS	K_LYS_210	NZ	K_GLU_212	OE1	3.047
3MLS	S_LYS_12	NZ	K_ASP_54	OD1	2.573
3MLS	S_LYS_12	NZ	K_ASP_54	OD2	3.736
3MLS	S_LYS_12	NZ	K_ASP_56	OD2	3.122
3MLT	L_LYS_27	NZ	L_ASP_26	OD1	2.656
3MLT	L_LYS_31	NZ	L_ASP_92	OD1	3.056
3MLT	L_ARG_61	NH1	L_ASP_82	OD1	3.939
3MLT	L_ARG_61	NH1	L_ASP_82	OD2	2.821
3MLT	L_ARG_61	NH2	L_ASP_82	OD1	2.818
3MLT	L_ARG_61	NH2	L_ASP_82	OD2	3.100
3MLT	L_LYS_66	NZ	L_ASP_51	OD1	2.985
3MLT	L_ARG_106A	NH2	L_ASP_85	OD1	3.829
3MLT	L_ARG_106A	NH2	L_ASP_85	OD2	3.125
3MLT	H_ARG_38	NH2	H_GLU_46	OE1	3.303
3MLT	H_ARG_38	NH2	H_GLU_46	OE2	2.941
3MLT	H_ARG_94	NH2	H_ASP_101	OD1	3.578
3MLT	H_ARG_94	NH2	H_ASP_101	OD2	2.428
3MLT	P_ARG_304	NH1	H_ASP_31	OD1	2.766
3MLT	P_LYS_305	NZ	H_ASP_54	OD1	2.503
3MLT	P_LYS_305	NZ	H_ASP_54	OD2	3.276
3MLT	P_LYS_305	NZ	H_ASP_56	OD2	2.482
3MLT	A_ARG_61	NH1	A_ASP_82	OD1	3.737
3MLT	A_ARG_61	NH1	A_ASP_82	OD2	2.967
3MLT	A_ARG_61	NH2	A_ASP_82	OD1	2.371
3MLT	A_ARG_61	NH2	A_ASP_82	OD2	3.018
3MLT	A_LYS_66	NZ	A_ASP_51	OD1	2.928
3MLT	A_LYS_66	NZ	A_ASP_51	OD2	3.040
3MLT	A_LYS_69	NZ	A_ASP_26	OD2	2.462
3MLT	A_ARG_106A	NH2	A_ASP_85	OD1	3.818
3MLT	A_ARG_106A	NH2	A_ASP_85	OD2	2.999
3MLT	A_LYS_114	NZ	A_GLU_202	OE2	3.077
3MLT	B_ARG_38	NH2	B_GLU_46	OE1	3.094
3MLT	B_ARG_38	NH2	B_GLU_46	OE2	3.367
3MLT	B_ARG_94	NH2	B_ASP_101	OD1	3.119
3MLT	B_ARG_94	NH2	B_ASP_101	OD2	2.679
3MLT	B_LYS_209	NZ	A_GLU_127	OE2	3.807
3MLT	C_LYS_305	NZ	B_ASP_54	OD1	3.099
3MLT	C_LYS_305	NZ	B_ASP_54	OD2	3.737
3MLT	C_LYS_305	NZ	B_ASP_56	OD2	3.095
3MLT	D_LYS_27	NZ	D_ASP_92	OD1	3.259
3MLT	D_LYS_27	NZ	D_ASP_92	OD2	3.970
3MLT	D_ARG_61	NH1	D_ASP_82	OD1	3.697
3MLT	D_ARG_61	NH1	D_ASP_82	OD2	3.252
3MLT	D_ARG_61	NH2	D_ASP_82	OD1	2.341
3MLT	D_ARG_61	NH2	D_ASP_82	OD2	3.303
3MLT	D_LYS_66	NZ	D_ASP_51	OD1	3.307
3MLT	D_ARG_106A	NH1	D_ASP_85	OD1	3.298
3MLT	D_ARG_106A	NH1	D_ASP_85	OD2	2.670
3MLT	E_ARG_38	NH2	E_GLU_46	OE1	2.985

3MLT	E_ARG_38	NH2	E_GLU_46	OE2	2.979
3MLT	E_LYS_73	NZ	E_ASP_53	OD1	3.727
3MLT	E_ARG_94	NH2	E_ASP_101	OD1	3.644
3MLT	E_ARG_94	NH2	E_ASP_101	OD2	2.588
3MLT	E_LYS_143	NZ	E_ASP_144	OD1	3.787
3MLT	E_LYS_209	NZ	D_GLU_127	OE2	3.591
3MLT	E_LYS_210	NZ	E_GLU_212	OE2	3.760
3MLT	G_LYS_27	NZ	G_ASP_92	OD2	2.642
3MLT	G_ARG_61	NH1	G_ASP_82	OD1	3.714
3MLT	G_ARG_61	NH1	G_ASP_82	OD2	2.758
3MLT	G_ARG_61	NH2	G_ASP_82	OD1	2.637
3MLT	G_ARG_61	NH2	G_ASP_82	OD2	2.852
3MLT	G_LYS_66	NZ	G_ASP_51	OD1	3.206
3MLT	G_LYS_66	NZ	G_ASP_51	OD2	2.686
3MLT	G_LYS_69	NZ	G_ASP_26	OD2	3.323
3MLT	G_ARG_106A	NH2	G_ASP_85	OD1	3.421
3MLT	G_ARG_106A	NH2	G_ASP_85	OD2	2.884
3MLT	G_LYS_153	NZ	G_GLU_207	OE2	2.787
3MLT	L_ARG_38	NH2	L_GLU_46	OE1	3.057
3MLT	L_ARG_38	NH2	L_GLU_46	OE2	3.429
3MLT	L_LYS_73	NZ	L_ASP_53	OD1	3.113
3MLT	L_ARG_94	NH2	L_ASP_101	OD1	3.494
3MLT	L_ARG_94	NH2	L_ASP_101	OD2	2.793
3MLT	L_LYS_209	NZ	G_GLU_127	OE2	3.669
3MLT	L_LYS_210	NZ	L_GLU_212	OE2	3.480
3MLU	L_LYS_27	NZ	L_ASP_92	OD1	2.977
3MLU	L_LYS_27	NZ	L_ASP_92	OD2	3.686
3MLU	L_LYS_31	NZ	L_ASP_30	OD1	2.935
3MLU	L_ARG_61	NH1	L_ASP_82	OD1	3.030
3MLU	L_ARG_61	NH1	L_ASP_82	OD2	2.397
3MLU	L_ARG_61	NH2	L_ASP_82	OD1	3.188
3MLU	L_ARG_61	NH2	L_ASP_82	OD2	3.941
3MLU	L_LYS_66	NZ	L_ASP_51	OD1	3.330
3MLU	L_LYS_66	NZ	L_ASP_51	OD2	3.601
3MLU	L_LYS_69	NZ	L_ASP_29	OD1	3.656
3MLU	L_ARG_106A	NH1	L_ASP_85	OD1	2.728
3MLU	L_ARG_106A	NH1	L_ASP_85	OD2	2.846
3MLU	L_ARG_106A	NH2	L_ASP_85	OD2	3.672
3MLU	L_LYS_133	NZ	H_ASP_144	OD2	3.641
3MLU	H_ARG_38	NH2	H_GLU_46	OE1	2.684
3MLU	H_ARG_38	NH2	H_GLU_46	OE2	3.582
3MLU	H_ARG_94	NH2	H_ASP_101	OD1	3.350
3MLU	H_ARG_94	NH2	H_ASP_101	OD2	2.802
3MLU	H_LYS_143	NZ	H_ASP_144	OD1	3.930
3MLU	P_LYS_305	NZ	H_ASP_54	OD1	2.586
3MLU	P_LYS_305	NZ	H_ASP_54	OD2	3.496
3MLU	P_LYS_305	NZ	H_ASP_56	OD2	3.684
3MLV	L_LYS_27	NZ	L_ASP_92	OD1	2.732
3MLV	L_LYS_27	NZ	L_ASP_92	OD2	3.328
3MLV	L_LYS_31	NZ	L_ASP_30	OD1	3.535
3MLV	L_LYS_31	NZ	L_ASP_30	OD2	3.503
3MLV	L_ARG_61	NH1	L_ASP_82	OD1	3.622
3MLV	L_ARG_61	NH1	L_ASP_82	OD2	2.916
3MLV	L_ARG_61	NH2	L_ASP_82	OD1	2.553
3MLV	L_ARG_61	NH2	L_ASP_82	OD2	3.370
3MLV	L_LYS_66	NZ	L_ASP_51	OD1	3.119
3MLV	L_LYS_66	NZ	L_ASP_51	OD2	3.196
3MLV	L_LYS_69	NZ	L_ASP_26	OD1	3.247

3MLV	L_ARG_106A	NH2	L_ASP_85	OD2	3.095
3MLV	L_LYS_153	NZ	L_GLU_207	OE2	3.705
3MLV	H_ARG_38	NH2	H_GLU_46	OE1	2.542
3MLV	H_LYS_73	NZ	H_ASP_53	OD1	3.402
3MLV	H_ARG_94	NH2	H_ASP_101	OD1	2.930
3MLV	H_ARG_94	NH2	H_ASP_101	OD2	2.968
3MLV	P_ARG_304	NH1	H_ASP_31	OD1	3.750
3MLV	P_LYS_305	NZ	H_ASP_54	OD1	2.508
3MLV	P_LYS_305	NZ	H_ASP_54	OD2	3.477
3MLV	P_LYS_305	NZ	H_ASP_56	OD2	2.918
3MLV	M_LYS_27	NZ	M_ASP_92	OD1	3.721
3MLV	M_LYS_27	NZ	M_ASP_92	OD2	3.379
3MLV	M_LYS_31	NZ	M_ASP_30	OD1	3.507
3MLV	M_LYS_31	NZ	M_ASP_30	OD2	3.277
3MLV	M_ARG_54	NH1	M_GLU_60	OE1	3.723
3MLV	M_ARG_61	NH1	M_ASP_82	OD2	2.841
3MLV	M_ARG_61	NH2	M_ASP_82	OD1	2.635
3MLV	M_ARG_61	NH2	M_ASP_82	OD2	2.881
3MLV	M_LYS_66	NZ	M_ASP_51	OD1	2.909
3MLV	M_LYS_66	NZ	M_ASP_51	OD2	3.135
3MLV	M_LYS_97	NZ	N_GLU_64	OE1	2.901
3MLV	M_ARG_106A	NH1	M_ASP_85	OD1	3.025
3MLV	M_ARG_106A	NH1	M_ASP_85	OD2	3.882
3MLV	M_LYS_133	NZ	M_GLU_128	OE2	3.108
3MLV	M_LYS_153	NZ	M_GLU_207	OE1	3.506
3MLV	M_LYS_153	NZ	M_GLU_207	OE2	2.957
3MLV	N_ARG_38	NH2	N_GLU_46	OE1	3.294
3MLV	N_ARG_38	NH2	N_GLU_46	OE2	3.518
3MLV	N_HIS_58	NE2	N_ASP_56	OD1	3.956
3MLV	N_ARG_94	NH2	N_ASP_101	OD1	2.759
3MLV	N_ARG_94	NH2	N_ASP_101	OD2	2.721
3MLV	N_LYS_117	NZ	N_ASP_144	OD2	3.293
3MLV	N_LYS_210	NZ	N_GLU_212	OE1	3.364
3MLV	Q_ARG_304	NH1	N_GLU_99	OE2	3.900
3MLV	Q_ARG_304	NH2	N_GLU_99	OE2	3.849
3MLV	Q_LYS_305	NZ	N_ASP_54	OD1	3.154
3MLV	Q_LYS_305	NZ	N_ASP_54	OD2	3.686
3MLV	Q_LYS_305	NZ	N_ASP_56	OD2	2.702
3MLW	L_ARG_50	NH1	H_ASP_100G	OD1	2.178
3MLW	L_ARG_50	NH1	H_ASP_100G	OD2	3.432
3MLW	L_ARG_61	NH1	L_ASP_82	OD1	3.181
3MLW	L_ARG_61	NH1	L_ASP_82	OD2	2.655
3MLW	L_ARG_61	NH2	L_ASP_82	OD1	3.279
3MLW	L_ARG_61	NH2	L_ASP_82	OD2	3.991
3MLW	L_LYS_66	NZ	L_ASP_51	OD1	3.270
3MLW	L_LYS_66	NZ	L_ASP_51	OD2	3.246
3MLW	L_ARG_95	NH2	L_ASP_95D	OD1	3.851
3MLW	L_ARG_95	NH2	L_ASP_95D	OD2	3.710
3MLW	L_LYS_129	NZ	H_ASP_144	OD2	3.472
3MLW	L_HIS_188	ND1	L_ASP_151	OD1	3.480
3MLW	H_LYS_12	NZ	H_GLU_10	OE2	3.873
3MLW	H_ARG_38	NH2	H_GLU_46	OE2	2.598
3MLW	H_ARG_58	NH1	L_ASP_95D	OD1	3.535
3MLW	H_ARG_58	NH1	L_ASP_95D	OD2	2.585
3MLW	H_ARG_66	NH1	H_GLU_83	OE1	3.904
3MLW	H_ARG_66	NH1	H_ASP_86	OD1	3.710
3MLW	H_ARG_66	NH1	H_ASP_86	OD2	3.995
3MLW	H_ARG_66	NH2	H_GLU_83	OE1	3.901

3MLW	H_ARG.66	NH2	H_ASP.86	OD1	3.540
3MLW	H_ARG.66	NH2	H_ASP.86	OD2	2.479
3MLW	H_LYS.143	NZ	H_ASP.144	OD1	3.302
3MLW	H_LYS.210	NZ	H_GLU.212	OE2	3.365
3MLW	P_LYS.303	NZ	H_ASP.31	OD2	3.075
3MLW	P_ARG.304	NH1	H_ASP.31	OD1	3.646
3MLW	P_LYS.305	NZ	H_ASP.54	OD1	3.646
3MLW	P_LYS.305	NZ	H_ASP.54	OD2	2.863
3MLW	P_LYS.305	NZ	H_ASP.56	OD1	3.537
3MLW	P_ARG.315	NH1	L_ASP.93	OD1	2.718
3MLW	P_ARG.315	NH1	L_ASP.93	OD2	3.239
3MLW	M_ARG.50	NH2	L_ASP.100G	OD1	2.708
3MLW	M_ARG.50	NH2	L_ASP.100G	OD2	3.923
3MLW	M_ARG.54	NH2	M_ASP.60	OD2	3.038
3MLW	M_ARG.61	NH1	M_ASP.82	OD1	3.703
3MLW	M_ARG.61	NH1	M_ASP.82	OD2	2.485
3MLW	M_ARG.61	NH2	M_ASP.82	OD1	3.327
3MLW	M_ARG.61	NH2	M_ASP.82	OD2	3.484
3MLW	M_LYS.66	NZ	M_ASP.51	OD1	3.422
3MLW	M_LYS.66	NZ	M_ASP.51	OD2	3.571
3MLW	M_ARG.95	NH2	M_ASP.95D	OD1	3.135
3MLW	M_ARG.95	NH2	M_ASP.95D	OD2	3.399
3MLW	M_LYS.149	NZ	M_GLU.203	OE1	3.625
3MLW	L_LYS.12	NZ	L_GLU.10	OE2	3.682
3MLW	L_ARG.58	NH1	M_ASP.95D	OD1	2.653
3MLW	L_ARG.58	NH1	M_ASP.95D	OD2	3.643
3MLW	L_ARG.66	NH1	L_ASP.86	OD1	3.246
3MLW	L_ARG.66	NH1	L_ASP.86	OD2	3.692
3MLW	L_ARG.66	NH2	L_ASP.86	OD1	3.577
3MLW	L_ARG.66	NH2	L_ASP.86	OD2	2.544
3MLW	L_LYS.143	NZ	L_ASP.144	OD1	3.053
3MLW	L_LYS.209	NZ	M_GLU.123	OE1	2.581
3MLW	L_LYS.209	NZ	M_GLU.123	OE2	3.213
3MLW	L_LYS.210	NZ	L_GLU.212	OE1	3.364
3MLW	Q_LYS.305	NZ	L_ASP.54	OD2	3.005
3MLW	Q_LYS.305	NZ	L_ASP.56	OD1	2.747
3MLW	Q_ARG.315	NH1	M_ASP.93	OD1	3.021
3MLX	L_LYS.53	NZ	L_GLU.50	OE1	2.558
3MLX	L_ARG.61	NH1	L_ASP.82	OD1	3.582
3MLX	L_ARG.61	NH1	L_ASP.82	OD2	2.890
3MLX	L_ARG.61	NH2	L_ASP.82	OD1	2.629
3MLX	L_ARG.61	NH2	L_ASP.82	OD2	3.257
3MLX	L_LYS.110	NZ	L_GLU.198	OE1	3.541
3MLX	L_LYS.110	NZ	L_GLU.198	OE2	2.823
3MLX	L_ARG.189	NH1	L_ASP.151	OD2	3.869
3MLX	H_ARG.38	NH1	H_ASP.86	OD1	2.668
3MLX	H_ARG.38	NH2	H_GLU.46	OE1	2.979
3MLX	H_ARG.38	NH2	H_ASP.86	OD1	3.494
3MLX	H_ARG.66	NH1	H_ASP.86	OD1	3.775
3MLX	H_ARG.66	NH1	H_ASP.86	OD2	3.101
3MLX	H_ARG.66	NH2	H_ASP.86	OD1	3.040
3MLX	H_ARG.66	NH2	H_ASP.86	OD2	3.650
3MLX	H_ARG.94	NH2	H_ASP.101	OD1	3.962
3MLX	H_ARG.94	NH2	H_ASP.101	OD2	2.675
3MLX	H_HIS.100	NE2	H_GLU.98	OE1	3.039
3MLX	H_ARG.100D	NH1	H_ASP.100B	OD1	3.189
3MLX	H_ARG.100D	NH1	H_ASP.100B	OD2	2.525
3MLX	H_ARG.100D	NH2	H_ASP.100B	OD2	3.445

3MLX	H_LYS_143	NZ	L_GLU_124	OE2	3.021
3MLX	H_LYS_143	NZ	H_ASP_144	OD2	3.971
3MLX	H_LYS_210	NZ	H_GLU_212	OE1	3.310
3MLX	P_HIS_308	ND1	H_GLU_98	OE2	3.800
3MLX	P_HIS_308	NE2	H_GLU_98	OE2	3.892
3MLX	M_LYS_53	NZ	M_GLU_50	OE1	2.998
3MLX	M_ARG_61	NH1	M_ASP_82	OD1	3.548
3MLX	M_ARG_61	NH1	M_ASP_82	OD2	2.848
3MLX	M_ARG_61	NH2	M_ASP_82	OD1	2.885
3MLX	M_ARG_61	NH2	M_ASP_82	OD2	3.369
3MLX	M_LYS_110	NZ	M_GLU_198	OE1	3.722
3MLX	M_LYS_110	NZ	M_GLU_198	OE2	2.779
3MLX	L_ARG_38	NH1	L_ASP_86	OD1	2.800
3MLX	L_ARG_38	NH2	L_GLU_46	OE1	2.963
3MLX	L_ARG_38	NH2	L_ASP_86	OD1	3.764
3MLX	L_ARG_66	NH1	L_ASP_86	OD1	3.651
3MLX	L_ARG_66	NH1	L_ASP_86	OD2	3.063
3MLX	L_ARG_66	NH2	L_ASP_86	OD1	2.826
3MLX	L_ARG_66	NH2	L_ASP_86	OD2	3.585
3MLX	L_ARG_94	NH2	L_ASP_101	OD1	3.940
3MLX	L_ARG_94	NH2	L_ASP_101	OD2	2.619
3MLX	L_ARG_100D	NH2	L_ASP_100B	OD1	3.500
3MLX	L_LYS_143	NZ	M_GLU_124	OE2	2.608
3MLX	L_LYS_214	NZ	M_GLU_123	OE1	3.588
3MLX	Q_HIS_308	ND1	L_GLU_98	OE1	3.280
3MLY	L_LYS_53	NZ	L_GLU_50	OE1	2.642
3MLY	L_ARG_61	NH1	L_ASP_82	OD1	3.644
3MLY	L_ARG_61	NH1	L_ASP_82	OD2	2.899
3MLY	L_ARG_61	NH2	L_ASP_82	OD1	2.860
3MLY	L_ARG_61	NH2	L_ASP_82	OD2	3.465
3MLY	L_LYS_110	NZ	L_GLU_198	OE2	2.940
3MLY	L_ARG_189	NH1	L_ASP_151	OD2	3.794
3MLY	L_ARG_189	NH2	L_ASP_151	OD1	3.939
3MLY	L_ARG_189	NH2	L_ASP_151	OD2	3.922
3MLY	H_ARG_38	NH1	H_ASP_86	OD1	2.772
3MLY	H_ARG_38	NH2	H_GLU_46	OE1	3.019
3MLY	H_ARG_38	NH2	H_ASP_86	OD1	3.609
3MLY	H_ARG_66	NH1	H_ASP_86	OD1	3.669
3MLY	H_ARG_66	NH1	H_ASP_86	OD2	3.034
3MLY	H_ARG_66	NH2	H_ASP_86	OD1	2.918
3MLY	H_ARG_66	NH2	H_ASP_86	OD2	3.605
3MLY	H_ARG_94	NH2	H_ASP_101	OD1	3.843
3MLY	H_ARG_94	NH2	H_ASP_101	OD2	2.725
3MLY	H_ARG_100D	NH1	H_ASP_100B	OD1	3.662
3MLY	H_ARG_100D	NH1	H_ASP_100B	OD2	2.984
3MLY	H_ARG_100D	NH2	H_ASP_100B	OD2	3.444
3MLY	H_LYS_143	NZ	L_GLU_124	OE2	3.991
3MLY	H_LYS_143	NZ	H_ASP_144	OD1	3.690
3MLY	H_LYS_143	NZ	H_ASP_144	OD2	3.304
3MLY	H_LYS_210	NZ	H_GLU_212	OE1	3.480
3MLY	H_LYS_214	NZ	L_GLU_123	OE1	3.745
3MLY	P_LYS_308	NZ	L_GLU_50	OE1	3.397
3MLY	P_LYS_308	NZ	L_GLU_50	OE2	3.390
3MLY	M_LYS_53	NZ	M_GLU_50	OE1	3.091
3MLY	M_ARG_61	NH1	M_ASP_82	OD1	3.807
3MLY	M_ARG_61	NH1	M_ASP_82	OD2	2.828
3MLY	M_ARG_61	NH2	M_ASP_82	OD1	2.920
3MLY	M_ARG_61	NH2	M_ASP_82	OD2	3.357

3MLY	M.LYS_110	NZ	M_GLU_198	OE1	3.945
3MLY	M.LYS_110	NZ	M_GLU_198	OE2	2.680
3MLY	L.ARG_38	NH1	L.ASP_86	OD1	2.750
3MLY	L.ARG_38	NH2	L_GLU_46	OE1	3.018
3MLY	L.ARG_38	NH2	L.ASP_86	OD1	3.672
3MLY	L.ARG_66	NH1	L.ASP_86	OD1	3.657
3MLY	L.ARG_66	NH1	L.ASP_86	OD2	2.961
3MLY	L.ARG_66	NH2	L.ASP_86	OD1	2.888
3MLY	L.ARG_66	NH2	L.ASP_86	OD2	3.536
3MLY	L.ARG_94	NH2	L.ASP_101	OD1	3.875
3MLY	L.ARG_94	NH2	L.ASP_101	OD2	2.678
3MLY	L.ARG_100D	NH2	L.ASP_100B	OD1	3.986
3MLY	L.ARG_100D	NH2	L.ASP_100B	OD2	3.120
3MLY	L.LYS_143	NZ	M_GLU_124	OE2	2.661
3MLY	L.LYS_214	NZ	M_GLU_123	OE1	3.594
3MLZ	L.LYS_	NZ	L_GLU_	OE1	2.997
3MLZ	L.ARG_	NH1	L.ASP_	OD1	3.594
3MLZ	L.ARG_	NH1	L.ASP_	OD2	2.458
3MLZ	L.ARG_	NH2	L.ASP_	OD1	3.627
3MLZ	L.ARG_	NH2	L.ASP_	OD2	3.688
3MLZ	H.ARG_	NH1	H.ASP_	OD1	2.831
3MLZ	H.ARG_	NH2	H_GLU_	OE1	2.975
3MLZ	H.ARG_	NH2	H_GLU_	OE2	3.939
3MLZ	H.ARG_	NH2	H.ASP_	OD1	3.724
3MLZ	H.ARG_	NH1	H.ASP_	OD1	3.168
3MLZ	H.ARG_	NH1	H.ASP_	OD2	2.769
3MLZ	H.ARG_	NH2	H.ASP_	OD1	2.975
3MLZ	H.ARG_	NH2	H.ASP_	OD2	3.884
3MLZ	H.ARG_	NH2	H.ASP_	OD1	3.878
3MLZ	H.ARG_	NH2	H.ASP_	OD2	3.028
3MLZ	H.HIS_	ND1	H.ASP_	OD2	3.791
3MLZ	H.HIS_	NE2	H_GLU_	OE1	3.406
3MLZ	H.HIS_	NE2	H_GLU_	OE2	3.681
3MLZ	H.ARG_	NH2	H.ASP_	OD2	2.582
3MLZ	H.LYS_	NZ	L_GLU_	OE1	3.724
3MLZ	H.LYS_	NZ	L_GLU_	OE2	3.184
3MLZ	H.LYS_	NZ	L_GLU_	OE2	2.805
3MLZ	H.LYS_	NZ	L_GLU_	OE1	3.039
3MLZ	H.LYS_	NZ	L_GLU_	OE2	3.262
3NFP	A.ARG_33	NH1	K.ASP_4	OD1	3.227
3NFP	A.ARG_33	NH2	K.ASP_6	OD1	3.995
3NFP	A.ARG_33	NH2	K.ASP_6	OD2	2.804
3NFP	A.HIS_35	NE2	K.ASP_4	OD1	3.568
3NFP	A.HIS_35	NE2	K.ASP_4	OD2	3.384
3NFP	A.ARG_38	NH1	A_GLU_46	OE1	3.521
3NFP	A.ARG_38	NH1	A_GLU_46	OE2	2.606
3NFP	A.ARG_38	NH2	A_GLU_46	OE1	3.385
3NFP	A.ARG_38	NH2	A_GLU_46	OE2	3.747
3NFP	A.LYS_63	NZ	A_GLU_46	OE1	3.380
3NFP	A.LYS_67	NZ	A.ASP_90	OD2	3.506
3NFP	A.LYS_146	NZ	A.ASP_147	OD1	3.848
3NFP	A.LYS_146	NZ	A.ASP_147	OD2	3.462
3NFP	B.LYS_38	NZ	B.ASP_80	OD1	3.548
3NFP	B.LYS_38	NZ	B.ASP_80	OD2	3.365
3NFP	B.ARG_60	NH2	B.ASP_81	OD1	2.805
3NFP	B.ARG_60	NH2	B.ASP_81	OD2	3.684
3NFP	B.LYS_125	NZ	B_GLU_122	OE1	3.467
3NFP	B.LYS_148	NZ	B_GLU_194	OE1	2.803

3NFP	B_LYS_148	NZ	B_GLU_194	OE2	3.777
3NFP	B_HIS_188	ND1	B_ASP_150	OD2	2.700
3NFP	H_ARG_33	NH1	I_ASP_4	OD2	2.868
3NFP	H_ARG_33	NH2	I_ASP_6	OD2	3.531
3NFP	H_HIS_35	NE2	I_ASP_4	OD1	3.314
3NFP	H_HIS_35	NE2	I_ASP_4	OD2	3.660
3NFP	H_ARG_38	NH2	H_GLU_46	OE1	3.221
3NFP	H_ARG_38	NH2	H_GLU_46	OE2	2.659
3NFP	H_LYS_67	NZ	H_ASP_90	OD2	3.005
3NFP	H_LYS_212	NZ	L_GLU_122	OE1	3.767
3NFP	L_LYS_38	NZ	L_ASP_80	OD1	3.309
3NFP	L_ARG_60	NH2	L_ASP_81	OD1	2.888
3NFP	L_ARG_60	NH2	L_ASP_81	OD2	3.365
3NFP	L_LYS_148	NZ	L_GLU_194	OE1	3.812
3NFP	L_LYS_148	NZ	L_GLU_194	OE2	2.763
3NFP	L_LYS_182	NZ	L_GLU_186	OE2	3.310
3NFP	L_HIS_188	ND1	L_ASP_150	OD2	3.342
3NFP	L_ARG_117	NH2	I_GLU_113	OE1	3.200
3NFP	L_ARG_117	NH2	I_GLU_113	OE2	2.798
3NFP	I_HIS_120	NE2	H_GLU_59	OE1	3.799
3NFP	I_HIS_120	NE2	H_GLU_59	OE2	3.285
3NFP	K_ARG_117	NH1	K_GLU_106	OE2	2.607
3NFP	K_ARG_117	NH2	K_GLU_113	OE1	3.049
3NFP	K_ARG_117	NH2	K_GLU_113	OE2	2.896
3NFP	K_HIS_120	NE2	A_GLU_59	OE2	3.393
3NGB	G_LYS_46	NZ	G_GLU_492	OE1	3.975
3NGB	G_LYS_	NZ	G_GLU_	OE1	3.767
3NGB	G_HIS_	NE2	G_GLU_	OE1	3.641
3NGB	G_HIS_	ND1	G_GLU_	OE2	2.917
3NGB	G_LYS_97	NZ	G_GLU_275	OE2	3.810
3NGB	G_LYS_97	NZ	H_ASP_99	OD2	3.903
3NGB	G_LYS_	NZ	G_GLU_	OE1	3.983
3NGB	G_LYS_	NZ	G_GLU_	OE2	3.483
3NGB	G_HIS_	NE2	G_GLU_	OE1	3.355
3NGB	G_LYS_282	NZ	G_GLU_275	OE1	3.701
3NGB	G_ARG_456	NH1	G_GLU_466	OE2	3.510
3NGB	G_ARG_469	NH2	G_ASP_457	OD1	2.956
3NGB	G_LYS_476	NZ	G_GLU_102	OE1	2.614
3NGB	G_ARG_480	NH1	G_ASP_477	OD1	2.964
3NGB	G_ARG_480	NH2	G_GLU_102	OE2	3.814
3NGB	G_LYS_487	NZ	G_ASP_47	OD1	2.938
3NGB	G_LYS_487	NZ	G_ASP_47	OD2	3.396
3NGB	G_LYS_487	NZ	G_GLU_91	OE1	2.798
3NGB	H_LYS_12	NZ	H_GLU_16	OE2	3.621
3NGB	H_ARG_38	NH1	H_GLU_46	OE1	3.003
3NGB	H_ARG_38	NH2	H_ASP_86	OD1	2.813
3NGB	H_ARG_66	NH1	H_ASP_86	OD1	3.475
3NGB	H_ARG_66	NH2	H_ASP_86	OD1	2.969
3NGB	H_ARG_66	NH2	H_ASP_86	OD2	2.693
3NGB	H_ARG_71	NH1	G_ASP_368	OD1	3.623
3NGB	H_ARG_71	NH1	G_ASP_368	OD2	3.004
3NGB	H_ARG_71	NH2	G_ASP_368	OD1	2.815
3NGB	H_ARG_71	NH2	G_ASP_368	OD2	3.723
3NGB	H_ARG_82A	NH1	H_GLU_81	OE2	3.784
3NGB	H_LYS_209	NZ	L_GLU_125	OE1	3.421
3NGB	H_LYS_209	NZ	L_GLU_125	OE2	3.841
3NGB	H_LYS_210	NZ	H_GLU_212	OE2	3.426
3NGB	L_ARG_61	NH1	L_ASP_82	OD2	2.817

3NGB	L_ARG_61	NH2	L_ASP_82	OD1	3.422
3NGB	L_ARG_61	NH2	L_ASP_82	OD2	2.949
3NGB	L_LYS_109	NZ	L_GLU_17	OE1	3.534
3NGB	L_LYS_151	NZ	L_GLU_197	OE2	3.936
3NGB	L_HIS_191	ND1	L_ASP_153	OD2	2.883
3NGB	L_HIS_191	NE2	L_ASP_187	OD2	3.579
3NGB	L_ARG_213	NH2	L_GLU_189	OE1	2.766
3NGB	A_LYS_46	NZ	A_GLU_492	OE1	3.410
3NGB	A_HIS_66	ND1	A_GLU_64	OE2	2.775
3NGB	A_LYS_97	NZ	B_ASP_99	OD2	3.768
3NGB	A_LYS_207	NZ	A_GLU_381	OE1	3.837
3NGB	A_LYS_207	NZ	A_GLU_381	OE2	2.908
3NGB	A_LYS_231	NZ	A_GLU_267	OE2	3.487
3NGB	A_HIS_249	NE2	A_GLU_482	OE1	3.108
3NGB	A_LYS_282	NZ	A_GLU_275	OE1	3.363
3NGB	A_LYS_343	NZ	A_GLU_405	OE2	2.857
3NGB	A_LYS_348	NZ	A_GLU_269	OE1	3.929
3NGB	A_LYS_348	NZ	A_GLU_269	OE2	3.717
3NGB	A_ARG_456	NH1	A_GLU_466	OE1	3.489
3NGB	A_ARG_469	NH2	A_ASP_457	OD1	2.818
3NGB	A_LYS_476	NZ	A_GLU_102	OE1	2.746
3NGB	A_ARG_480	NH1	A_ASP_477	OD1	3.036
3NGB	A_ARG_480	NH2	A_GLU_102	OE2	3.823
3NGB	A_LYS_487	NZ	A_ASP_47	OD1	3.201
3NGB	A_LYS_487	NZ	A_ASP_47	OD2	3.287
3NGB	A_LYS_487	NZ	A_GLU_91	OE1	2.776
3NGB	B_LYS_12	NZ	B_GLU_16	OE2	3.669
3NGB	B_ARG_38	NH1	B_ASP_86	OD1	3.017
3NGB	B_ARG_38	NH2	B_GLU_46	OE1	3.330
3NGB	B_ARG_38	NH2	B_GLU_46	OE2	3.608
3NGB	B_ARG_38	NH2	B_ASP_86	OD1	3.928
3NGB	B_ARG_66	NH1	B_ASP_86	OD1	3.986
3NGB	B_ARG_66	NH2	B_ASP_86	OD1	3.009
3NGB	B_ARG_66	NH2	B_ASP_86	OD2	2.581
3NGB	B_ARG_71	NH1	A_ASP_368	OD1	3.647
3NGB	B_ARG_71	NH1	A_ASP_368	OD2	2.944
3NGB	B_ARG_71	NH2	A_ASP_368	OD1	2.895
3NGB	B_ARG_71	NH2	A_ASP_368	OD2	3.718
3NGB	B_ARG_82A	NH1	B_GLU_81	OE2	3.349
3NGB	B_HIS_102	NE2	B_GLU_101	OE1	3.498
3NGB	B_LYS_209	NZ	C_GLU_125	OE1	2.774
3NGB	B_LYS_209	NZ	C_GLU_125	OE2	2.799
3NGB	C_ARG_61	NH1	C_ASP_82	OD2	2.721
3NGB	C_ARG_61	NH2	C_GLU_79	OE1	3.703
3NGB	C_ARG_61	NH2	C_ASP_82	OD1	3.248
3NGB	C_ARG_61	NH2	C_ASP_82	OD2	2.976
3NGB	C_LYS_109	NZ	C_GLU_17	OE1	3.524
3NGB	C_LYS_151	NZ	C_GLU_197	OE2	3.960
3NGB	C_LYS_185	NZ	C_GLU_189	OE2	3.711
3NGB	C_HIS_191	ND1	C_ASP_153	OD2	2.841
3NGB	C_ARG_213	NH2	C_GLU_189	OE1	2.808
3NGB	D_LYS_46	NZ	D_GLU_492	OE1	2.932
3NGB	D_HIS_66	ND1	D_GLU_64	OE2	2.933
3NGB	D_LYS_97	NZ	D_GLU_275	OE2	3.702
3NGB	D_LYS_97	NZ	E_ASP_99	OD1	3.709
3NGB	D_LYS_207	NZ	D_GLU_381	OE1	3.872
3NGB	D_LYS_207	NZ	D_GLU_381	OE2	3.299
3NGB	D_LYS_231	NZ	D_GLU_267	OE2	3.490

3NGB	D_HIS_249	NE2	D_GLU_482	OE1	3.177
3NGB	D_LYS_282	NZ	D_GLU_275	OE1	2.984
3NGB	D_LYS_282	NZ	D_GLU_275	OE2	3.901
3NGB	D_ARG_327	NH1	D_ASP_325	OD1	3.823
3NGB	D_LYS_348	NZ	D_GLU_269	OE2	3.794
3NGB	D_LYS_348	NZ	D_GLU_351	OE1	3.701
3NGB	D_ARG_456	NH1	D_GLU_466	OE2	3.539
3NGB	D_ARG_469	NH2	D_ASP_457	OD1	2.868
3NGB	D_LYS_476	NZ	D_GLU_102	OE1	2.805
3NGB	D_LYS_476	NZ	D_GLU_102	OE2	3.737
3NGB	D_ARG_480	NH1	D_ASP_477	OD1	2.794
3NGB	D_LYS_487	NZ	D_ASP_47	OD1	3.083
3NGB	D_LYS_487	NZ	D_ASP_47	OD2	3.202
3NGB	D_LYS_487	NZ	D_GLU_91	OE1	2.774
3NGB	E_LYS_12	NZ	E_GLU_16	OE2	3.601
3NGB	E_ARG_38	NH1	E_GLU_46	OE1	2.881
3NGB	E_ARG_38	NH2	E_ASP_86	OD1	2.976
3NGB	E_ARG_53	NH2	E_ASP_31	OD1	3.658
3NGB	E_ARG_66	NH2	E_ASP_86	OD1	2.908
3NGB	E_ARG_66	NH2	E_ASP_86	OD2	2.859
3NGB	E_ARG_71	NH1	D_ASP_368	OD1	3.715
3NGB	E_ARG_71	NH1	D_ASP_368	OD2	3.074
3NGB	E_ARG_71	NH2	D_ASP_368	OD1	3.026
3NGB	E_ARG_71	NH2	D_ASP_368	OD2	3.848
3NGB	E_ARG_82A	NH1	E_GLU_81	OE2	3.296
3NGB	E_LYS_	NZ	E_ASP_	OD1	3.774
3NGB	E_HIS_164	ND1	F_ASP_169	OD1	3.984
3NGB	E_LYS_	NZ	F_GLU_	OE1	3.345
3NGB	E_LYS_	NZ	F_GLU_	OE2	2.927
3NGB	F_ARG_61	NH1	F_ASP_82	OD2	3.066
3NGB	F_ARG_61	NH2	F_ASP_82	OD1	3.415
3NGB	F_ARG_61	NH2	F_ASP_82	OD2	2.796
3NGB	F_LYS_109	NZ	F_GLU_17	OE1	3.447
3NGB	F_HIS_	ND1	F_ASP_	OD2	2.855
3NGB	F_ARG_	NH1	F_GLU_	OE1	3.426
3NGB	I_LYS_46	NZ	I_GLU_492	OE1	3.345
3NGB	I_LYS_97	NZ	J_ASP_99	OD1	3.443
3NGB	I_LYS_207	NZ	I_GLU_381	OE1	3.684
3NGB	I_LYS_207	NZ	I_GLU_381	OE2	3.363
3NGB	I_HIS_249	NE2	I_GLU_482	OE1	3.245
3NGB	I_LYS_282	NZ	I_GLU_275	OE1	3.040
3NGB	I_LYS_348	NZ	I_GLU_269	OE2	3.888
3NGB	I_LYS_348	NZ	I_GLU_351	OE1	3.585
3NGB	I_ARG_456	NH1	I_GLU_466	OE1	3.750
3NGB	I_ARG_456	NH1	I_GLU_466	OE2	3.932
3NGB	I_ARG_469	NH2	I_ASP_457	OD1	3.266
3NGB	I_LYS_476	NZ	I_GLU_102	OE1	2.886
3NGB	I_LYS_476	NZ	I_GLU_102	OE2	3.914
3NGB	I_ARG_480	NH1	I_ASP_477	OD1	2.955
3NGB	I_LYS_487	NZ	I_ASP_47	OD1	2.972
3NGB	I_LYS_487	NZ	I_ASP_47	OD2	3.331
3NGB	I_LYS_487	NZ	I_GLU_91	OE1	3.195
3NGB	J_LYS_12	NZ	J_GLU_16	OE2	3.692
3NGB	J_ARG_19	NH1	J_GLU_81	OE1	3.898
3NGB	J_ARG_38	NH1	J_GLU_46	OE1	3.036
3NGB	J_ARG_38	NH1	J_GLU_46	OE2	3.958
3NGB	J_ARG_38	NH2	J_ASP_86	OD1	3.148
3NGB	J_ARG_53	NH2	J_ASP_31	OD1	3.422

3NGB	J_ARG_66	NH2	J_ASP_86	OD1	2.966
3NGB	J_ARG_66	NH2	J_ASP_86	OD2	2.680
3NGB	J_ARG_71	NH1	L_ASP_368	OD1	3.645
3NGB	J_ARG_71	NH1	L_ASP_368	OD2	3.125
3NGB	J_ARG_71	NH2	L_ASP_368	OD1	3.120
3NGB	J_ARG_82A	NH1	J_GLU_81	OE2	3.471
3NGB	J_HIS_102	NE2	J_GLU_101	OE1	3.491
3NGB	J_LYS_143	NZ	J_ASP_144	OD1	3.698
3NGB	J_LYS_209	NZ	K_GLU_125	OE1	2.929
3NGB	J_LYS_209	NZ	K_GLU_125	OE2	3.060
3NGB	J_LYS_210	NZ	J_GLU_212	OE2	3.040
3NGB	J_LYS_214	NZ	K_ASP_124	OD1	3.305
3NGB	K_ARG_24	NH1	K_ASP_70	OD1	3.807
3NGB	K_ARG_24	NH2	K_ASP_70	OD1	3.052
3NGB	K_ARG_61	NH1	K_ASP_82	OD2	2.794
3NGB	K_ARG_61	NH2	K_GLU_79	OE2	3.644
3NGB	K_ARG_61	NH2	K_ASP_82	OD1	3.448
3NGB	K_ARG_61	NH2	K_ASP_82	OD2	3.147
3NGB	K_LYS_109	NZ	K_GLU_17	OE1	3.600
3NGB	K_LYS_151	NZ	K_GLU_197	OE2	2.833
3NGB	K_LYS_185	NZ	K_GLU_189	OE2	3.051
3NH7	H_ARG_38	NH1	H_ASP_90	OD1	3.170
3NH7	H_ARG_38	NH2	H_GLU_46	OE1	2.648
3NH7	H_ARG_38	NH2	H_GLU_46	OE2	3.155
3NH7	H_LYS_65	NZ	H_ASP_62	OD1	3.429
3NH7	H_ARG_67	NH1	H_ASP_90	OD1	3.942
3NH7	H_ARG_67	NH1	H_ASP_90	OD2	3.259
3NH7	H_ARG_67	NH2	H_ASP_90	OD1	3.009
3NH7	H_ARG_67	NH2	H_ASP_90	OD2	3.648
3NH7	H_ARG_98	NH1	H_ASP_108	OD1	3.173
3NH7	H_ARG_98	NH1	H_ASP_108	OD2	2.691
3NH7	H_ARG_98	NH1	A_ASP_67	OD2	3.819
3NH7	H_ARG_98	NH2	A_ASP_67	OD1	2.850
3NH7	H_ARG_98	NH2	A_ASP_67	OD2	2.389
3NH7	H_ARG_100	NH2	A_GLU_64	OE2	3.004
3NH7	H_HIS_102	ND1	A_GLU_64	OE1	2.378
3NH7	H_ARG_104	NH2	A_GLU_81	OE1	3.515
3NH7	H_ARG_104	NH2	A_GLU_81	OE2	2.462
3NH7	H_HIS_109	ND1	H_ASP_108	OD1	3.252
3NH7	H_HIS_109	ND1	H_ASP_108	OD2	3.832
3NH7	H_LYS_216	NZ	L_GLU_125	OE2	3.557
3NH7	H_LYS_217	NZ	H_GLU_219	OE2	2.342
3NH7	L_ARG_60	NH1	L_ASP_81	OD1	2.484
3NH7	L_ARG_60	NH1	L_ASP_81	OD2	2.037
3NH7	L_ARG_60	NH2	L_GLU_80	OE2	3.016
3NH7	L_ARG_60	NH2	L_ASP_81	OD1	3.954
3NH7	L_LYS_112	NZ	L_GLU_200	OE1	3.379
3NH7	L_HIS_190	ND1	L_ASP_153	OD2	3.719
3NH7	A_LYS_79	NZ	L_ASP_50	OD1	3.333
3NH7	A_LYS_79	NZ	L_ASP_50	OD2	3.058
3NH7	A_LYS_92	NZ	H_GLU_99	OE1	3.975
3NH7	A_LYS_92	NZ	H_GLU_99	OE2	3.561
3NH7	A_ARG_96	NH1	A_GLU_65	OE1	3.606
3NH7	A_ARG_96	NH1	A_GLU_65	OE2	2.868
3NH7	L_ARG_38	NH1	L_ASP_90	OD1	2.985
3NH7	L_ARG_38	NH2	L_GLU_46	OE1	2.998
3NH7	L_ARG_38	NH2	L_GLU_46	OE2	3.375
3NH7	L_LYS_65	NZ	L_ASP_62	OD1	3.472

3NH7	L_ARG_67	NH1	L_ASP_90	OD1	3.848
3NH7	L_ARG_67	NH1	L_ASP_90	OD2	2.660
3NH7	L_ARG_67	NH2	L_ASP_90	OD1	2.985
3NH7	L_ARG_67	NH2	L_ASP_90	OD2	3.250
3NH7	L_ARG_98	NH1	L_ASP_108	OD1	3.301
3NH7	L_ARG_98	NH1	L_ASP_108	OD2	2.609
3NH7	L_ARG_98	NH1	B_ASP_67	OD2	3.924
3NH7	L_ARG_98	NH2	B_ASP_67	OD1	3.388
3NH7	L_ARG_98	NH2	B_ASP_67	OD2	2.296
3NH7	L_ARG_100	NH2	B_GLU_64	OE2	2.996
3NH7	L_HIS_102	ND1	B_GLU_64	OE1	2.707
3NH7	L_ARG_104	NH2	B_GLU_81	OE1	3.637
3NH7	L_ARG_104	NH2	B_GLU_81	OE2	2.502
3NH7	L_HIS_109	ND1	L_ASP_108	OD1	3.553
3NH7	L_HIS_109	ND1	L_ASP_108	OD2	3.821
3NH7	L_LYS_216	NZ	M_GLU_125	OE1	3.301
3NH7	L_LYS_216	NZ	M_GLU_125	OE2	3.320
3NH7	L_LYS_217	NZ	L_GLU_219	OE2	3.028
3NH7	M_ARG_60	NH1	M_ASP_81	OD1	2.461
3NH7	M_ARG_60	NH1	M_ASP_81	OD2	1.882
3NH7	M_ARG_60	NH2	M_GLU_80	OE2	3.159
3NH7	M_ARG_60	NH2	M_ASP_81	OD1	3.816
3NH7	M_LYS_112	NZ	M_GLU_200	OE1	3.202
3NH7	M_HIS_190	ND1	M_ASP_153	OD2	3.749
3NH7	B_LYS_79	NZ	M_ASP_50	OD1	3.625
3NH7	B_LYS_79	NZ	M_ASP_50	OD2	2.953
3NH7	B_LYS_92	NZ	L_GLU_99	OE1	3.831
3NH7	B_LYS_92	NZ	L_GLU_99	OE2	3.683
3NH7	B_ARG_96	NH1	B_GLU_65	OE1	3.695
3NH7	B_ARG_96	NH1	B_GLU_65	OE2	2.714
3NH7	J_ARG_38	NH1	J_ASP_90	OD1	2.984
3NH7	J_ARG_38	NH2	J_GLU_46	OE1	2.989
3NH7	J_ARG_38	NH2	J_GLU_46	OE2	3.443
3NH7	J_LYS_65	NZ	J_ASP_62	OD1	3.599
3NH7	J_ARG_67	NH1	J_ASP_90	OD1	3.748
3NH7	J_ARG_67	NH1	J_ASP_90	OD2	2.498
3NH7	J_ARG_67	NH2	J_ASP_90	OD1	3.051
3NH7	J_ARG_67	NH2	J_ASP_90	OD2	3.237
3NH7	J_ARG_98	NH1	J_ASP_108	OD1	3.197
3NH7	J_ARG_98	NH1	J_ASP_108	OD2	2.669
3NH7	J_ARG_98	NH1	C_ASP_67	OD2	3.893
3NH7	J_ARG_98	NH2	C_ASP_67	OD1	3.313
3NH7	J_ARG_98	NH2	C_ASP_67	OD2	2.401
3NH7	J_ARG_100	NH2	C_GLU_64	OE2	3.173
3NH7	J_HIS_102	ND1	C_GLU_64	OE1	2.668
3NH7	J_ARG_104	NH2	C_GLU_81	OE1	3.595
3NH7	J_ARG_104	NH2	C_GLU_81	OE2	2.634
3NH7	J_HIS_109	ND1	J_ASP_108	OD1	3.604
3NH7	J_HIS_109	ND1	J_ASP_108	OD2	3.993
3NH7	J_LYS_216	NZ	N_GLU_125	OE1	2.816
3NH7	J_LYS_216	NZ	N_GLU_125	OE2	3.044
3NH7	J_LYS_217	NZ	J_GLU_219	OE2	3.134
3NH7	N_ARG_60	NH1	N_ASP_81	OD1	2.494
3NH7	N_ARG_60	NH1	N_ASP_81	OD2	2.049
3NH7	N_ARG_60	NH2	N_GLU_80	OE2	3.067
3NH7	N_ARG_60	NH2	N_ASP_81	OD1	3.767
3NH7	N_LYS_112	NZ	N_GLU_200	OE1	3.295
3NH7	N_HIS_190	ND1	N_ASP_153	OD2	3.738

3NH7	C.LYS.79	NZ	N.ASP.50	OD1	3.064
3NH7	C.LYS.79	NZ	N.ASP.50	OD2	3.315
3NH7	C.LYS.92	NZ	J.GLU.99	OE1	3.721
3NH7	C.LYS.92	NZ	J.GLU.99	OE2	3.806
3NH7	C.ARG.96	NH1	C.GLU.65	OE1	3.714
3NH7	C.ARG.96	NH1	C.GLU.65	OE2	2.792
3NH7	K.ARG.38	NH1	K.ASP.90	OD1	2.979
3NH7	K.ARG.38	NH2	K.GLU.46	OE1	2.902
3NH7	K.ARG.38	NH2	K.GLU.46	OE2	3.544
3NH7	K.LYS.65	NZ	K.ASP.62	OD1	3.572
3NH7	K.ARG.67	NH1	K.ASP.90	OD1	3.729
3NH7	K.ARG.67	NH1	K.ASP.90	OD2	2.672
3NH7	K.ARG.67	NH2	K.ASP.90	OD1	2.973
3NH7	K.ARG.67	NH2	K.ASP.90	OD2	3.433
3NH7	K.ARG.98	NH1	K.ASP.108	OD1	3.399
3NH7	K.ARG.98	NH1	K.ASP.108	OD2	2.677
3NH7	K.ARG.98	NH1	D.ASP.67	OD2	3.348
3NH7	K.ARG.98	NH2	D.ASP.67	OD1	3.350
3NH7	K.ARG.98	NH2	D.ASP.67	OD2	2.647
3NH7	K.ARG.100	NH2	D.GLU.64	OE2	3.101
3NH7	K.HIS.102	ND1	D.GLU.64	OE1	2.313
3NH7	K.ARG.104	NH2	D.GLU.81	OE1	3.830
3NH7	K.ARG.104	NH2	D.GLU.81	OE2	2.800
3NH7	K.HIS.109	ND1	K.ASP.108	OD1	3.611
3NH7	K.HIS.109	ND1	K.ASP.108	OD2	3.969
3NH7	K.LYS.216	NZ	O.GLU.125	OE1	3.159
3NH7	K.LYS.216	NZ	O.GLU.125	OE2	3.376
3NH7	K.LYS.217	NZ	K.GLU.219	OE2	3.149
3NH7	O.ARG.60	NH1	O.ASP.81	OD1	2.503
3NH7	O.ARG.60	NH1	O.ASP.81	OD2	2.023
3NH7	O.ARG.60	NH2	O.GLU.80	OE2	3.060
3NH7	O.LYS.112	NZ	O.GLU.200	OE1	3.202
3NH7	O.HIS.190	ND1	O.ASP.153	OD2	3.736
3NH7	D.LYS.79	NZ	O.ASP.50	OD1	3.661
3NH7	D.LYS.79	NZ	O.ASP.50	OD2	3.355
3NH7	D.LYS.92	NZ	K.GLU.99	OE1	3.766
3NH7	D.LYS.92	NZ	K.GLU.99	OE2	3.832
3NH7	D.ARG.96	NH1	D.GLU.65	OE1	3.668
3NH7	D.ARG.96	NH1	D.GLU.65	OE2	2.730
3NZ8	A.LYS.62	NZ	A.GLU.46	OE2	3.140
3NZ8	A.LYS.64	NZ	A.GLU.61	OE2	2.792
3NZ8	A.ARG.94	NH2	A.ASP.101	OD1	3.538
3NZ8	A.ARG.94	NH2	A.ASP.101	OD2	2.636
3NZ8	A.HIS.164	NE2	B.ASP.167	OD1	3.115
3NZ8	A.LYS.208	NZ	B.GLU.123	OE2	3.283
3NZ8	B.ARG.24	NH2	B.ASP.70	OD1	3.560
3NZ8	B.LYS.39	NZ	B.GLU.81	OE1	3.652
3NZ8	B.ARG.61	NH1	B.ASP.82	OD1	3.498
3NZ8	B.ARG.61	NH1	B.ASP.82	OD2	3.472
3NZ8	B.ARG.61	NH2	B.GLU.79	OE1	3.670
3NZ8	B.ARG.61	NH2	B.ASP.82	OD1	3.552
3NZ8	B.ARG.61	NH2	B.ASP.82	OD2	2.363
3NZ8	B.HIS.189	ND1	B.ASP.151	OD2	2.708
3NZ8	B.LYS.199	NZ	B.ASP.110	OD2	2.820
3NZ8	H.LYS.62	NZ	H.GLU.46	OE1	3.871
3NZ8	H.LYS.62	NZ	H.GLU.46	OE2	3.041
3NZ8	H.LYS.64	NZ	H.GLU.61	OE1	2.981
3NZ8	H.ARG.94	NH2	H.ASP.101	OD1	2.752

3NZ8	H_ARG_94	NH2	H_ASP_101	OD2	3.572
3NZ8	H_LYS_208	NZ	L_GLU_123	OE2	3.808
3NZ8	L_ARG_61	NH1	L_GLU_79	OE1	3.401
3NZ8	L_ARG_61	NH2	L_GLU_79	OE1	3.938
3NZ8	L_ARG_61	NH2	L_ASP_82	OD1	2.739
3NZ8	L_ARG_61	NH2	L_ASP_82	OD2	2.929
3NZ8	L_LYS_103	NZ	L_ASP_165	OD1	2.546
3NZ8	L_LYS_147	NZ	L_GLU_154	OE2	3.916
3NZ8	L_LYS_149	NZ	L_GLU_195	OE2	3.208
3NZ8	L_ARG_155	NH1	L_GLU_185	OE1	3.404
3NZ8	L_ARG_155	NH2	L_GLU_185	OE1	2.909
3NZ8	L_ARG_155	NH2	L_GLU_185	OE2	2.942
3NZ8	L_LYS_183	NZ	L_GLU_187	OE1	3.631
3NZ8	L_LYS_183	NZ	L_GLU_187	OE2	3.993
3NZ8	L_HIS_189	ND1	L_ASP_151	OD2	2.961
3NZ8	L_HIS_189	NE2	L_GLU_185	OE2	3.576
3O2D	L_ARG_61	NH1	L_GLU_81	OE2	3.060
3O2D	L_ARG_61	NH1	L_ASP_82	OD1	2.620
3O2D	L_ARG_61	NH1	L_ASP_82	OD2	3.291
3O2D	L_ARG_61	NH2	L_GLU_81	OE2	3.508
3O2D	L_ARG_95	NH1	H_GLU_95	OE2	2.847
3O2D	L_ARG_95	NH2	H_GLU_95	OE2	3.717
3O2D	L_LYS_102	NZ	L_GLU_164	OE1	3.911
3O2D	L_LYS_148	NZ	L_GLU_194	OE1	2.853
3O2D	L_HIS_188	ND1	L_ASP_150	OD2	3.198
3O2D	L_HIS_188	NE2	L_ASP_184	OD1	3.050
3O2D	L_ARG_210	NH2	L_GLU_186	OE1	3.119
3O2D	H_HIS_35	NE2	H_GLU_95	OE2	2.861
3O2D	H_ARG_38	NH2	H_ASP_46	OD2	3.124
3O2D	H_LYS_66	NZ	H_ASP_86	OD1	2.870
3O2D	H_LYS_66	NZ	H_ASP_86	OD2	2.859
3O2D	H_ARG_83	NH1	H_GLU_85	OE2	3.005
3O2D	H_ARG_83	NH2	H_ASP_86	OD1	3.533
3O2D	H_LYS_143	NZ	H_ASP_144	OD1	3.677
3O2D	H_LYS_209	NZ	L_GLU_122	OE1	2.503
3O2D	H_LYS_209	NZ	L_GLU_122	OE2	3.547
3O2D	H_ARG_210	NH1	H_GLU_212	OE2	3.400
3O2D	A_LYS_8	NZ	A_GLU_119	OE1	3.898
3O2D	A_LYS_8	NZ	A_GLU_119	OE2	2.918
3O2D	A_HIS_27	NE2	A_GLU_85	OE1	3.858
3O2D	A_LYS_29	NZ	A_GLU_85	OE1	3.824
3O2D	A_ARG_54	NH1	A_ASP_78	OD1	3.603
3O2D	A_ARG_54	NH1	A_ASP_78	OD2	2.872
3O2D	A_ARG_54	NH2	A_ASP_78	OD1	3.001
3O2D	A_ARG_54	NH2	A_ASP_78	OD2	3.706
3O2D	A_LYS_90	NZ	A_GLU_92	OE1	3.860
3O2D	A_ARG_134	NH1	A_GLU_150	OE1	3.461
3O2D	A_LYS_171	NZ	A_GLU_169	OE1	3.959
3O41	L_LYS_39	NZ	L_GLU_81	OE1	3.974
3O41	L_ARG_61	NH1	L_GLU_79	OE1	3.261
3O41	L_ARG_61	NH1	L_GLU_79	OE2	3.697
3O41	L_ARG_61	NH1	L_GLU_81	OE2	3.860
3O41	L_ARG_61	NH2	L_GLU_79	OE2	3.810
3O41	L_ARG_61	NH2	L_GLU_81	OE2	2.759
3O41	L_ARG_61	NH2	L_ASP_82	OD1	2.918
3O41	L_ARG_61	NH2	L_ASP_82	OD2	3.904
3O41	L_LYS_149	NZ	L_GLU_195	OE1	2.951
3O41	L_LYS_149	NZ	L_GLU_195	OE2	3.097

3O41	L_ARG_155	NH2	L_GLU_185	OE2	3.569
3O41	L_HIS_189	ND1	L_ASP_151	OD2	3.090
3O41	L_LYS_199	NZ	L_ASP_110	OD2	3.725
3O41	H_ARG_38	NH1	H_ASP_86	OD1	2.779
3O41	H_ARG_38	NH2	H_GLU_46	OE1	3.126
3O41	H_ARG_38	NH2	H_ASP_86	OD1	3.703
3O41	H_LYS_57	NZ	H_ASP_55	OD1	3.135
3O41	H_LYS_57	NZ	H_ASP_55	OD2	3.981
3O41	H_ARG_58	NH1	H_ASP_56	OD1	2.885
3O41	H_ARG_58	NH1	H_ASP_56	OD2	2.978
3O41	H_ARG_58	NH2	H_ASP_56	OD2	2.836
3O41	H_ARG_66	NH1	H_ASP_86	OD1	3.749
3O41	H_ARG_66	NH1	H_ASP_86	OD2	2.911
3O41	H_ARG_66	NH2	H_ASP_86	OD1	2.994
3O41	H_ARG_66	NH2	H_ASP_86	OD2	3.466
3O41	H_ARG_94	NH1	A_GLU_191	OE1	2.970
3O41	H_ARG_94	NH1	A_GLU_191	OE2	3.394
3O41	H_ARG_94	NH2	A_GLU_191	OE1	3.744
3O41	H_ARG_94	NH2	A_GLU_191	OE2	2.660
3O41	H_LYS_208	NZ	L_GLU_123	OE2	3.054
3O41	A_ARG_38	NH1	A_ASP_86	OD1	2.874
3O41	A_ARG_38	NH2	A_GLU_46	OE1	2.942
3O41	A_ARG_38	NH2	A_ASP_86	OD1	3.757
3O41	A_LYS_57	NZ	A_ASP_55	OD1	3.432
3O41	A_LYS_57	NZ	A_ASP_55	OD2	3.491
3O41	A_ARG_58	NH1	A_ASP_56	OD1	2.791
3O41	A_ARG_58	NH1	A_ASP_56	OD2	3.222
3O41	A_ARG_58	NH2	A_ASP_56	OD1	3.748
3O41	A_ARG_58	NH2	A_ASP_56	OD2	2.672
3O41	A_ARG_66	NH1	A_ASP_86	OD1	3.581
3O41	A_ARG_66	NH1	A_ASP_86	OD2	2.922
3O41	A_ARG_66	NH2	A_ASP_86	OD1	2.880
3O41	A_ARG_66	NH2	A_ASP_86	OD2	3.514
3O41	A_ARG_75	NH1	A_ASP_72	OD2	2.827
3O41	A_LYS_208	NZ	B_GLU_123	OE2	2.651
3O41	B_ARG_24	NH1	B_ASP_70	OD1	3.055
3O41	B_ARG_24	NH1	B_ASP_70	OD2	2.756
3O41	B_LYS_39	NZ	B_GLU_81	OE1	3.471
3O41	B_ARG_61	NH1	B_GLU_79	OE1	3.277
3O41	B_ARG_61	NH1	B_GLU_79	OE2	3.207
3O41	B_ARG_61	NH2	B_GLU_79	OE2	3.637
3O41	B_ARG_61	NH2	B_GLU_81	OE2	3.110
3O41	B_ARG_61	NH2	B_ASP_82	OD1	2.801
3O41	B_ARG_61	NH2	B_ASP_82	OD2	3.822
3O41	B_LYS_149	NZ	B_GLU_195	OE2	3.553
3O41	B_ARG_155	NH2	B_GLU_185	OE1	3.463
3O41	B_ARG_155	NH2	B_GLU_185	OE2	2.863
3O41	B_HIS_189	ND1	B_ASP_151	OD2	3.087
3O41	B_LYS_199	NZ	B_ASP_110	OD2	3.995
3O41	P_LYS_433	NZ	H_ASP_54	OD1	3.659
3O41	P_LYS_433	NZ	H_ASP_54	OD2	2.887
3O41	P_LYS_433	NZ	H_ASP_56	OD2	2.760
3O41	C_LYS_433	NZ	A_ASP_54	OD1	3.503
3O41	C_LYS_433	NZ	A_ASP_54	OD2	2.671
3O41	C_LYS_433	NZ	A_ASP_56	OD2	2.936
3O45	L_LYS_39	NZ	L_GLU_81	OE1	3.955
3O45	L_ARG_61	NH1	L_GLU_79	OE1	3.563
3O45	L_ARG_61	NH1	L_GLU_79	OE2	3.651

3O45	L_ARG_61	NH2	L_GLU_79	OE2	3.980
3O45	L_ARG_61	NH2	L_GLU_81	OE2	2.981
3O45	L_ARG_61	NH2	L_ASP_82	OD1	2.891
3O45	L_LYS_149	NZ	L_GLU_195	OE1	3.064
3O45	L_LYS_149	NZ	L_GLU_195	OE2	2.826
3O45	L_ARG_155	NH2	L_GLU_185	OE2	2.881
3O45	L_HIS_189	ND1	L_ASP_151	OD2	3.388
3O45	L_LYS_199	NZ	L_ASP_110	OD2	3.915
3O45	H_ARG_38	NH1	H_ASP_86	OD1	2.834
3O45	H_ARG_38	NH2	H_GLU_46	OE1	3.512
3O45	H_ARG_38	NH2	H_ASP_86	OD1	3.614
3O45	H_LYS_57	NZ	H_ASP_55	OD1	2.960
3O45	H_LYS_57	NZ	H_ASP_55	OD2	3.684
3O45	H_ARG_58	NH1	H_ASP_56	OD1	2.872
3O45	H_ARG_58	NH1	H_ASP_56	OD2	2.820
3O45	H_ARG_58	NH2	H_ASP_56	OD2	3.333
3O45	H_ARG_66	NH1	H_ASP_86	OD2	2.963
3O45	H_ARG_66	NH2	H_ASP_86	OD1	3.158
3O45	H_ARG_66	NH2	H_ASP_86	OD2	3.218
3O45	H_LYS_71	NZ	H_ASP_55	OD1	3.837
3O45	H_ARG_94	NH1	A_GLU_191	OE1	3.085
3O45	H_ARG_94	NH1	A_GLU_191	OE2	3.621
3O45	H_ARG_94	NH2	A_GLU_191	OE1	3.709
3O45	H_ARG_94	NH2	A_GLU_191	OE2	2.802
3O45	H_LYS_208	NZ	L_GLU_123	OE2	3.033
3O45	A_ARG_38	NH1	A_ASP_86	OD1	2.784
3O45	A_ARG_38	NH2	A_GLU_46	OE1	3.151
3O45	A_ARG_38	NH2	A_ASP_86	OD1	3.920
3O45	A_LYS_57	NZ	A_ASP_55	OD1	3.779
3O45	A_LYS_57	NZ	A_ASP_55	OD2	3.231
3O45	A_ARG_58	NH1	A_ASP_56	OD1	2.824
3O45	A_ARG_58	NH1	A_ASP_56	OD2	3.062
3O45	A_ARG_58	NH2	A_ASP_56	OD2	2.817
3O45	A_ARG_66	NH1	A_ASP_86	OD2	2.985
3O45	A_ARG_66	NH2	A_ASP_86	OD1	2.861
3O45	A_ARG_66	NH2	A_ASP_86	OD2	3.279
3O45	A_LYS_71	NZ	A_ASP_55	OD1	3.913
3O45	A_ARG_75	NH1	A_ASP_72	OD2	3.016
3O45	A_LYS_208	NZ	B_GLU_123	OE2	2.878
3O45	B_ARG_24	NH1	B_ASP_70	OD1	2.848
3O45	B_ARG_24	NH1	B_ASP_70	OD2	2.930
3O45	B_LYS_39	NZ	B_GLU_81	OE1	3.627
3O45	B_ARG_61	NH1	B_GLU_79	OE1	3.550
3O45	B_ARG_61	NH1	B_GLU_79	OE2	3.481
3O45	B_ARG_61	NH2	B_GLU_79	OE2	3.674
3O45	B_ARG_61	NH2	B_GLU_81	OE2	3.283
3O45	B_ARG_61	NH2	B_ASP_82	OD1	2.929
3O45	B_ARG_61	NH2	B_ASP_82	OD2	3.946
3O45	B_LYS_149	NZ	B_GLU_195	OE2	3.399
3O45	B_ARG_155	NH2	B_GLU_185	OE1	3.860
3O45	B_ARG_155	NH2	B_GLU_185	OE2	2.997
3O45	B_HIS_189	ND1	B_ASP_151	OD2	3.113
3O45	B_LYS_199	NZ	B_ASP_110	OD2	3.896
3O45	P_LYS_433	NZ	H_ASP_54	OD1	3.518
3O45	P_LYS_433	NZ	H_ASP_54	OD2	2.818
3O45	P_LYS_433	NZ	H_ASP_56	OD2	2.927
3O45	C_LYS_433	NZ	A_ASP_54	OD1	3.297
3O45	C_LYS_433	NZ	A_ASP_54	OD2	2.723

3O45	C_LYS_433	NZ	A_ASP_56	OD2	2.899
3OJD	A_ARG_61	NH2	A_GLU_81	OE1	3.519
3OJD	A_ARG_61	NH2	A_ASP_82	OD1	2.711
3OJD	A_ARG_61	NH2	A_ASP_82	OD2	3.501
3OJD	A_LYS_149	NZ	A_GLU_195	OE1	3.123
3OJD	A_LYS_149	NZ	A_GLU_195	OE2	3.726
3OJD	A_ARG_155	NH2	A_GLU_185	OE2	2.919
3OJD	A_LYS_183	NZ	A_GLU_187	OE2	3.320
3OJD	A_HIS_189	ND1	A_ASP_151	OD2	2.920
3OJD	A_HIS_189	NE2	A_GLU_185	OE1	3.630
3OJD	B_LYS_13	NZ	B_GLU_16	OE2	2.846
3OJD	B_LYS_64	NZ	B_ASP_61	OD1	3.166
3OJD	B_ARG_66	NH1	B_ASP_86	OD1	3.558
3OJD	B_ARG_66	NH1	B_ASP_86	OD2	2.686
3OJD	B_ARG_66	NH2	B_ASP_86	OD1	2.934
3OJD	B_ARG_66	NH2	B_ASP_86	OD2	3.558
3OJD	B_LYS_83	NZ	B_GLU_85	OE1	3.736
3OJD	B_LYS_83	NZ	B_GLU_85	OE2	2.635
3OJD	B_ARG_94	NH2	B_ASP_101	OD1	2.661
3OJD	B_ARG_94	NH2	B_ASP_101	OD2	3.562
3OJD	B_LYS_205	NZ	B_ASP_207	OD1	3.219
3OJD	B_LYS_205	NZ	B_ASP_207	OD2	3.147
3OJD	B_LYS_208	NZ	A_GLU_123	OE2	3.588
3OJD	B_ARG_213	NH1	A_GLU_213	OE2	3.118
3OJD	B_ARG_213	NH2	A_GLU_213	OE2	3.609
3P0V	L_ARG_61	NH2	L_GLU_81	OE2	3.980
3P0V	L_ARG_61	NH2	L_ASP_82	OD1	2.725
3P0V	L_ARG_61	NH2	L_ASP_82	OD2	3.097
3P0V	L_LYS_103	NZ	L_GLU_165	OE2	2.532
3P0V	L_LYS_149	NZ	L_GLU_195	OE1	3.890
3P0V	L_LYS_149	NZ	L_GLU_195	OE2	2.540
3P0V	L_LYS_188	NZ	L_ASP_185	OD1	3.371
3P0V	H_HIS_35	NE2	H_GLU_50	OE1	3.401
3P0V	H_HIS_35	NE2	H_GLU_95	OE2	3.628
3P0V	H_ARG_38	NH1	H_ASP_86	OD1	2.715
3P0V	H_ARG_38	NH2	H_GLU_46	OE1	3.599
3P0V	H_ARG_38	NH2	H_ASP_86	OD1	3.530
3P0V	H_LYS_64	NZ	H_ASP_58	OD1	3.681
3P0V	H_ARG_66	NH1	H_ASP_86	OD1	3.613
3P0V	H_ARG_66	NH1	H_ASP_86	OD2	3.306
3P0V	H_ARG_66	NH2	H_ASP_86	OD1	3.888
3P0V	H_ARG_83	NH1	H_GLU_85	OE2	3.227
3P0V	H_ARG_94	NH2	H_ASP_32	OD2	3.649
3P0V	H_ARG_97	NH1	H_ASP_32	OD1	3.877
3P0V	H_ARG_97	NH1	H_ASP_32	OD2	3.520
3P0V	H_LYS_143	NZ	H_ASP_144	OD2	3.455
3P0V	M_ARG_24	NH1	M_ASP_70	OD1	2.624
3P0V	M_ARG_61	NH2	M_GLU_81	OE2	3.977
3P0V	M_ARG_61	NH2	M_ASP_82	OD1	2.677
3P0V	M_ARG_61	NH2	M_ASP_82	OD2	3.250
3P0V	M_LYS_103	NZ	M_GLU_165	OE2	2.754
3P0V	M_LYS_149	NZ	M_GLU_195	OE2	2.947
3P0V	M_LYS_188	NZ	M_ASP_185	OD1	3.655
3P0V	I_HIS_35	NE2	I_GLU_50	OE1	3.344
3P0V	I_HIS_35	NE2	I_GLU_95	OE2	3.386
3P0V	I_ARG_38	NH1	I_ASP_86	OD1	2.831
3P0V	I_ARG_38	NH2	I_GLU_46	OE1	3.289
3P0V	I_ARG_38	NH2	I_GLU_46	OE2	3.805

3P0V	L_ARG_38	NH2	L_ASP_86	OD1	3.779
3P0V	L_LYS_64	NZ	L_ASP_58	OD1	3.535
3P0V	L_ARG_66	NH1	L_ASP_86	OD1	3.463
3P0V	L_ARG_66	NH1	L_ASP_86	OD2	3.181
3P0V	L_ARG_66	NH2	L_ASP_86	OD1	3.209
3P0V	L_ARG_66	NH2	L_ASP_86	OD2	3.655
3P0V	L_ARG_83	NH1	L_GLU_85	OE2	2.465
3P0V	L_ARG_94	NH2	L_ASP_32	OD1	3.895
3P0V	L_ARG_94	NH2	L_ASP_32	OD2	3.368
3P0V	L_LYS_143	NZ	L_ASP_144	OD2	3.595
3P0Y	A_LYS_322	NZ	A_ASP_323	OD1	3.929
3P0Y	A_LYS_372	NZ	A_ASP_369	OD1	3.817
3P0Y	A_LYS_372	NZ	A_GLU_397	OE2	3.911
3P0Y	A_HIS_394	NE2	A_ASP_369	OD1	3.176
3P0Y	A_ARG_403	NH2	A_GLU_376	OE2	3.071
3P0Y	A_LYS_407	NZ	A_ASP_434	OD2	2.888
3P0Y	A_ARG_427	NH1	A_ASP_392	OD2	3.627
3P0Y	A_ARG_427	NH1	A_ASP_498	OD1	3.045
3P0Y	A_ARG_427	NH2	A_GLU_397	OE1	3.220
3P0Y	A_LYS_455	NZ	A_GLU_489	OE1	3.791
3P0Y	A_LYS_455	NZ	A_GLU_489	OE2	3.520
3P0Y	A_LYS_463	NZ	H_GLU_95	OE2	2.859
3P0Y	A_LYS_465	NZ	H_GLU_50	OE1	2.656
3P0Y	A_LYS_465	NZ	H_GLU_50	OE2	3.845
3P0Y	A_LYS_465	NZ	H_GLU_95	OE1	2.777
3P0Y	A_LYS_465	NZ	H_GLU_95	OE2	3.671
3P0Y	H_HIS_35	NE2	H_GLU_50	OE1	3.331
3P0Y	H_HIS_35	NE2	H_GLU_95	OE1	3.467
3P0Y	H_ARG_38	NH1	H_ASP_86	OD1	2.814
3P0Y	H_ARG_38	NH2	H_GLU_46	OE1	3.115
3P0Y	H_ARG_38	NH2	H_GLU_46	OE2	3.997
3P0Y	H_ARG_38	NH2	H_ASP_86	OD1	3.796
3P0Y	H_LYS_64	NZ	H_ASP_61	OD1	3.749
3P0Y	H_ARG_66	NH1	H_ASP_86	OD1	3.756
3P0Y	H_ARG_66	NH1	H_ASP_86	OD2	2.816
3P0Y	H_ARG_66	NH2	H_ASP_86	OD1	3.074
3P0Y	H_ARG_66	NH2	H_ASP_86	OD2	3.530
3P0Y	H_LYS_75	NZ	H_ASP_72	OD2	3.063
3P0Y	H_ARG_94	NH2	H_ASP_101	OD1	3.544
3P0Y	H_ARG_94	NH2	H_ASP_101	OD2	2.757
3P0Y	H_ARG_97	NH1	A_ASP_436	OD1	2.876
3P0Y	H_ARG_97	NH1	A_ASP_436	OD2	3.533
3P0Y	H_ARG_97	NH2	A_ASP_436	OD1	3.647
3P0Y	H_ARG_97	NH2	A_ASP_436	OD2	2.823
3P0Y	H_LYS_143	NZ	H_ASP_144	OD1	3.090
3P0Y	H_LYS_143	NZ	H_ASP_144	OD2	3.144
3P0Y	H_LYS_209	NZ	L_GLU_123	OE1	2.674
3P0Y	H_LYS_209	NZ	L_GLU_123	OE2	3.317
3P0Y	H_LYS_210	NZ	H_GLU_212	OE1	3.756
3P0Y	L_ARG_61	NH2	L_GLU_81	OE2	3.697
3P0Y	L_ARG_61	NH2	L_ASP_82	OD1	2.833
3P0Y	L_ARG_61	NH2	L_ASP_82	OD2	3.670
3P0Y	L_LYS_149	NZ	L_GLU_195	OE1	2.821
3P0Y	L_HIS_189	ND1	L_ASP_151	OD2	3.174
3P0Y	L_LYS_190	NZ	L_GLU_213	OE2	3.914
3P11	H_HIS_35	NE2	H_GLU_50	OE1	3.507
3P11	H_HIS_35	NE2	H_GLU_95	OE2	3.809
3P11	H_ARG_38	NH1	H_ASP_86	OD1	3.036

3P11	H_ARG_38	NH2	H_GLU_46	OE1	2.678
3P11	H_ARG_38	NH2	H_GLU_46	OE2	3.985
3P11	H_LYS_64	NZ	H_ASP_58	OD1	3.516
3P11	H_ARG_66	NH1	H_ASP_86	OD2	3.567
3P11	H_ARG_66	NH2	H_ASP_86	OD1	3.699
3P11	H_ARG_94	NH1	H_ASP_101	OD1	3.477
3P11	H_ARG_94	NH1	H_ASP_101	OD2	3.282
3P11	H_ARG_94	NH2	H_ASP_32	OD2	3.500
3P11	H_ARG_97	NH1	H_ASP_32	OD1	3.837
3P11	L_ARG_24	NH1	L_ASP_70	OD2	3.972
3P11	L_ARG_61	NH1	L_GLU_81	OE2	3.937
3P11	L_ARG_61	NH2	L_GLU_81	OE2	3.076
3P11	L_ARG_61	NH2	L_ASP_82	OD1	2.965
3P11	L_ARG_61	NH2	L_ASP_82	OD2	3.758
3P11	L_LYS_103	NZ	L_GLU_105	OE1	3.365
3P11	L_LYS_103	NZ	L_GLU_165	OE2	2.876
3P11	L_LYS_183	NZ	L_GLU_187	OE1	2.907
3P11	A_HIS_51	ND1	A_GLU_74	OE1	3.956
3P11	A_ARG_62	NH1	A_GLU_38	OE1	3.231
3P11	A_ARG_62	NH2	A_GLU_63	OE2	3.811
3P11	A_ARG_87	NH1	A_GLU_63	OE1	3.389
3P11	A_ARG_116	NH1	A_ASP_182	OD1	3.330
3P11	A_ARG_116	NH1	A_ASP_182	OD2	2.794
3P11	A_LYS_	NZ	A_GLU_131	OE1	3.633
3P11	A_ARG_	NH2	A_ASP_134	OD2	3.573
3P11	A_HIS_209	NE2	A_ASP_221	OD1	3.391
3P11	A_LYS_260	NZ	A_ASP_232	OD1	3.022
3P11	A_LYS_290	NZ	A_ASP_278	OD1	2.957
3P11	A_ARG_402	NH1	A_GLU_373	OE1	3.428
3P11	A_ARG_441	NH1	H_ASP_58	OD2	3.356
3P11	A_ARG_441	NH1	L_GLU_94	OE1	2.859
3P11	A_ARG_441	NH1	L_GLU_94	OE2	3.310
3P11	A_ARG_441	NH2	L_GLU_94	OE2	3.075
3P11	A_ARG_456	NH1	A_GLU_429	OE1	3.324
3P11	A_ARG_456	NH2	A_GLU_429	OE1	3.225
3P11	A_LYS_466	NZ	H_GLU_95	OE1	2.568
3P11	A_LYS_466	NZ	H_GLU_95	OE2	3.227
3P11	A_HIS_467	ND1	H_GLU_50	OE2	3.466
3P11	A_HIS_467	ND1	L_GLU_94	OE2	3.926
3P11	A_HIS_467	NE2	H_GLU_50	OE1	3.754
3P11	A_HIS_467	NE2	H_GLU_50	OE2	3.679
3P11	A_HIS_467	NE2	H_GLU_95	OE2	3.533
3P11	A_ARG_469	NH1	A_GLU_477	OE1	3.032
3P11	A_ARG_469	NH2	A_ASP_473	OD2	3.365
3P11	A_ARG_469	NH2	A_GLU_477	OE1	3.595
3P11	A_ARG_469	NH2	A_GLU_477	OE2	3.199
3PGF	A_LYS_15	NZ	A_ASP_14	OD1	2.931
3PGF	A_LYS_15	NZ	A_GLU_111	OE2	3.982
3PGF	A_LYS_26	NZ	A_ASP_30	OD2	2.898
3PGF	A_LYS_83	NZ	A_ASP_87	OD1	3.179
3PGF	A_ARG_98	NH1	A_ASP_95	OD1	2.849
3PGF	A_LYS_140	NZ	A_ASP_136	OD1	3.415
3PGF	A_LYS_140	NZ	A_ASP_136	OD2	2.764
3PGF	A_HIS_203	ND1	A_ASP_136	OD2	2.718
3PGF	A_LYS_251	NZ	A_ASP_164	OD1	3.745
3PGF	A_LYS_251	NZ	A_ASP_164	OD2	2.761
3PGF	A_ARG_316	NH1	A_ASP_236	OD1	3.984
3PGF	A_ARG_316	NH1	A_ASP_236	OD2	3.954

3PGF	A_ARG_316	NH2	A_ASP_314	OD2	2.795
3PGF	A_LYS_326	NZ	A_GLU_322	OE2	2.961
3PGF	H_ARG_38	NH1	H_ASP_86	OD1	3.038
3PGF	H_ARG_38	NH2	H_GLU_46	OE1	2.948
3PGF	H_ARG_66	NH1	H_ASP_86	OD1	3.643
3PGF	H_ARG_66	NH1	H_ASP_86	OD2	2.938
3PGF	H_ARG_66	NH2	H_ASP_86	OD1	3.135
3PGF	H_ARG_66	NH2	H_ASP_86	OD2	3.904
3PGF	H_ARG_94	NH2	H_ASP_101	OD1	3.471
3PGF	H_ARG_94	NH2	H_ASP_101	OD2	2.638
3PGF	L_ARG_24	NH1	L_ASP_70	OD1	3.567
3PGF	L_ARG_24	NH1	L_ASP_70	OD2	3.066
3PGF	L_ARG_61	NH2	L_GLU_81	OE2	3.869
3PGF	L_ARG_61	NH2	L_ASP_82	OD1	2.691
3PGF	L_ARG_61	NH2	L_ASP_82	OD2	3.502
3PGF	L_ARG_66	NH1	A_GLU_309	OE2	3.045
3PGF	L_ARG_66	NH2	A_GLU_309	OE2	2.501
3PGF	L_LYS_149	NZ	L_GLU_195	OE2	3.143
3PGF	L_LYS_190	NZ	L_GLU_213	OE2	3.299
3PNW	A_ARG_62	NH2	A_GLU_82	OE2	2.760
3PNW	A_ARG_62	NH2	A_ASP_83	OD1	3.251
3PNW	A_LYS_106	NZ	A_GLU_168	OE1	3.588
3PNW	A_LYS_106	NZ	A_GLU_168	OE2	3.143
3PNW	A_LYS_152	NZ	A_GLU_198	OE1	3.462
3PNW	A_HIS_192	ND1	A_ASP_154	OD2	2.766
3PNW	B_ARG_41	NH1	B_GLU_49	OE1	3.120
3PNW	B_ARG_41	NH1	B_GLU_49	OE2	3.686
3PNW	B_ARG_41	NH1	B_ASP_93	OD1	3.860
3PNW	B_ARG_41	NH2	B_ASP_93	OD1	2.838
3PNW	B_ARG_70	NH1	B_ASP_93	OD1	3.254
3PNW	B_ARG_70	NH1	B_ASP_93	OD2	3.946
3PNW	B_ARG_70	NH2	B_ASP_93	OD1	3.639
3PNW	B_ARG_70	NH2	B_ASP_93	OD2	2.902
3PNW	B_LYS_79	NZ	B_ASP_76	OD2	2.841
3PNW	B_ARG_90	NH1	B_GLU_92	OE1	3.741
3PNW	B_ARG_101	NH2	B_ASP_117	OD2	3.317
3PNW	B_ARG_104	NH1	C_GLU_599	OE1	3.048
3PNW	B_LYS_159	NZ	B_ASP_160	OD1	3.439
3PNW	C_LYS_557	NZ	C_ASP_560	OD1	3.049
3PNW	C_LYS_557	NZ	C_ASP_560	OD2	3.693
3PNW	C_LYS_590	NZ	C_GLU_576	OE1	3.383
3PNW	D_ARG_25	NH1	J_GLU_82	OE1	2.858
3PNW	D_ARG_25	NH1	J_GLU_82	OE2	3.430
3PNW	D_ARG_25	NH2	J_GLU_82	OE1	3.626
3PNW	D_ARG_25	NH2	J_GLU_82	OE2	3.034
3PNW	D_ARG_62	NH2	D_GLU_82	OE2	3.353
3PNW	D_ARG_62	NH2	D_ASP_83	OD1	3.192
3PNW	D_ARG_62	NH2	D_ASP_83	OD2	3.678
3PNW	D_ARG_145	NH1	D_GLU_108	OE2	3.475
3PNW	D_ARG_145	NH2	D_GLU_108	OE1	3.526
3PNW	D_ARG_145	NH2	D_GLU_108	OE2	3.197
3PNW	D_LYS_152	NZ	D_GLU_198	OE1	3.454
3PNW	D_LYS_152	NZ	D_GLU_198	OE2	3.452
3PNW	D_LYS_186	NZ	D_GLU_190	OE1	3.419
3PNW	D_LYS_186	NZ	D_GLU_190	OE2	2.925
3PNW	D_HIS_192	ND1	D_ASP_154	OD2	2.749
3PNW	E_ARG_41	NH1	E_GLU_49	OE1	3.072
3PNW	E_ARG_41	NH1	E_GLU_49	OE2	3.615

3PNW	E_ARG_41	NH1	E_ASP_93	OD1	3.772
3PNW	E_ARG_41	NH2	E_ASP_93	OD1	2.776
3PNW	E_LYS_68	NZ	E_ASP_65	OD1	2.738
3PNW	E_ARG_70	NH1	E_ASP_93	OD1	3.047
3PNW	E_ARG_70	NH1	E_ASP_93	OD2	3.582
3PNW	E_ARG_70	NH2	E_ASP_93	OD1	3.597
3PNW	E_ARG_70	NH2	E_ASP_93	OD2	2.576
3PNW	E_LYS_79	NZ	E_ASP_76	OD2	2.902
3PNW	E_ARG_101	NH2	E_ASP_117	OD2	3.400
3PNW	E_ARG_104	NH1	F_GLU_599	OE2	2.653
3PNW	E_LYS_159	NZ	E_ASP_160	OD1	3.050
3PNW	E_LYS_159	NZ	E_ASP_160	OD2	2.633
3PNW	F_LYS_590	NZ	F_GLU_576	OE2	3.831
3PNW	G_ARG_25	NH1	G_ASP_71	OD1	3.445
3PNW	G_ARG_25	NH1	G_ASP_71	OD2	2.863
3PNW	G_ARG_62	NH2	G_GLU_82	OE2	3.208
3PNW	G_ARG_62	NH2	G_ASP_83	OD1	2.937
3PNW	G_ARG_62	NH2	G_ASP_83	OD2	3.584
3PNW	G_LYS_106	NZ	G_GLU_168	OE1	2.721
3PNW	G_LYS_106	NZ	G_GLU_168	OE2	3.243
3PNW	G_LYS_152	NZ	G_GLU_198	OE2	3.706
3PNW	G_LYS_186	NZ	G_GLU_190	OE2	3.219
3PNW	G_HIS_192	ND1	G_ASP_154	OD2	3.161
3PNW	G_HIS_192	NE2	G_ASP_188	OD1	3.976
3PNW	H_ARG_41	NH1	H_GLU_49	OE1	3.103
3PNW	H_ARG_41	NH1	H_GLU_49	OE2	3.667
3PNW	H_ARG_41	NH1	H_ASP_93	OD1	3.761
3PNW	H_ARG_41	NH2	H_ASP_93	OD1	2.861
3PNW	H_LYS_68	NZ	H_ASP_65	OD1	2.900
3PNW	H_ARG_70	NH1	H_ASP_93	OD1	3.098
3PNW	H_ARG_70	NH1	H_ASP_93	OD2	3.479
3PNW	H_ARG_70	NH2	H_ASP_93	OD1	3.791
3PNW	H_ARG_70	NH2	H_ASP_93	OD2	2.662
3PNW	H_LYS_79	NZ	H_ASP_76	OD2	3.008
3PNW	H_ARG_90	NH1	H_GLU_92	OE2	3.922
3PNW	H_ARG_101	NH2	H_ASP_117	OD2	3.291
3PNW	H_ARG_104	NH1	I_GLU_599	OE1	3.020
3PNW	H_LYS_159	NZ	H_ASP_160	OD1	3.348
3PNW	H_LYS_159	NZ	H_ASP_160	OD2	3.221
3PNW	I_LYS_590	NZ	I_GLU_576	OE1	3.342
3PNW	J_ARG_25	NH2	J_ASP_71	OD1	3.699
3PNW	J_ARG_62	NH2	J_GLU_82	OE2	3.268
3PNW	J_ARG_62	NH2	J_ASP_83	OD1	3.032
3PNW	J_ARG_62	NH2	J_ASP_83	OD2	3.641
3PNW	J_LYS_106	NZ	J_GLU_168	OE1	2.693
3PNW	J_LYS_106	NZ	J_GLU_168	OE2	3.468
3PNW	J_ARG_145	NH1	J_GLU_108	OE1	3.314
3PNW	J_ARG_145	NH1	J_GLU_108	OE2	2.910
3PNW	J_ARG_145	NH2	J_GLU_108	OE1	3.149
3PNW	J_LYS_152	NZ	J_GLU_198	OE2	2.718
3PNW	J_HIS_192	ND1	J_ASP_154	OD2	2.849
3PNW	J_ARG_214	NH2	J_GLU_190	OE1	3.561
3PNW	K_ARG_41	NH1	K_GLU_49	OE1	3.097
3PNW	K_ARG_41	NH1	K_GLU_49	OE2	3.636
3PNW	K_ARG_41	NH1	K_ASP_93	OD1	3.969
3PNW	K_ARG_41	NH2	K_ASP_93	OD1	2.946
3PNW	K_LYS_68	NZ	K_ASP_65	OD1	2.902
3PNW	K_ARG_70	NH1	K_ASP_93	OD1	3.172

3PNW	K_ARG_70	NH1	K_ASP_93	OD2	3.777
3PNW	K_ARG_70	NH2	K_ASP_93	OD1	3.650
3PNW	K_ARG_70	NH2	K_ASP_93	OD2	2.817
3PNW	K_LYS_79	NZ	K_ASP_76	OD2	3.145
3PNW	K_ARG_101	NH2	K_ASP_117	OD2	3.216
3PNW	K_ARG_104	NH1	L_GLU_599	OE1	2.888
3PNW	K_ARG_104	NH1	L_GLU_599	OE2	2.772
3PNW	K_ARG_104	NH2	L_GLU_599	OE2	3.083
3PNW	K_LYS_159	NZ	K_ASP_160	OD1	3.020
3PNW	K_LYS_159	NZ	K_ASP_160	OD2	2.839
3PNW	M_ARG_62	NH2	M_GLU_82	OE2	2.988
3PNW	M_ARG_62	NH2	M_ASP_83	OD1	2.932
3PNW	M_ARG_62	NH2	M_ASP_83	OD2	3.718
3PNW	M_LYS_106	NZ	M_GLU_168	OE1	3.752
3PNW	M_LYS_106	NZ	M_GLU_168	OE2	2.837
3PNW	M_LYS_152	NZ	M_GLU_198	OE1	3.636
3PNW	M_LYS_152	NZ	M_GLU_198	OE2	3.599
3PNW	M_LYS_191	NZ	M_ASP_188	OD1	2.912
3PNW	M_HIS_192	ND1	M_ASP_154	OD2	3.108
3PNW	N_ARG_41	NH1	N_GLU_49	OE1	3.141
3PNW	N_ARG_41	NH1	N_GLU_49	OE2	3.699
3PNW	N_ARG_41	NH1	N_ASP_93	OD1	3.824
3PNW	N_ARG_41	NH2	N_ASP_93	OD1	2.841
3PNW	N_ARG_70	NH1	N_ASP_93	OD1	3.199
3PNW	N_ARG_70	NH1	N_ASP_93	OD2	3.846
3PNW	N_ARG_70	NH2	N_ASP_93	OD1	3.653
3PNW	N_ARG_70	NH2	N_ASP_93	OD2	2.921
3PNW	N_LYS_79	NZ	N_ASP_76	OD2	2.793
3PNW	N_ARG_101	NH2	N_ASP_117	OD2	3.225
3PNW	N_LYS_159	NZ	N_ASP_160	OD1	3.030
3PNW	N_LYS_159	NZ	N_ASP_160	OD2	3.040
3PNW	O_LYS_557	NZ	O_ASP_560	OD1	3.174
3PNW	O_LYS_557	NZ	O_ASP_560	OD2	3.756
3PNW	P_ARG_25	NH2	P_ASP_71	OD1	3.282
3PNW	P_ARG_25	NH2	P_ASP_71	OD2	3.069
3PNW	P_ARG_62	NH2	P_GLU_82	OE2	3.510
3PNW	P_ARG_62	NH2	P_ASP_83	OD1	2.765
3PNW	P_ARG_62	NH2	P_ASP_83	OD2	3.484
3PNW	P_LYS_106	NZ	P_GLU_108	OE2	3.990
3PNW	P_LYS_106	NZ	P_GLU_168	OE1	2.957
3PNW	P_LYS_106	NZ	P_GLU_168	OE2	2.919
3PNW	P_LYS_152	NZ	P_GLU_198	OE1	3.282
3PNW	P_LYS_186	NZ	P_GLU_190	OE1	3.349
3PNW	P_LYS_186	NZ	P_GLU_190	OE2	3.801
3PNW	Q_ARG_41	NH1	Q_GLU_49	OE1	2.971
3PNW	Q_ARG_41	NH1	Q_GLU_49	OE2	3.698
3PNW	Q_ARG_41	NH1	Q_ASP_93	OD1	3.890
3PNW	Q_ARG_41	NH2	Q_ASP_93	OD1	2.813
3PNW	Q_LYS_68	NZ	Q_ASP_65	OD1	2.792
3PNW	Q_ARG_70	NH1	Q_ASP_93	OD1	3.070
3PNW	Q_ARG_70	NH1	Q_ASP_93	OD2	3.435
3PNW	Q_ARG_70	NH2	Q_ASP_93	OD1	3.828
3PNW	Q_ARG_70	NH2	Q_ASP_93	OD2	2.681
3PNW	Q_LYS_79	NZ	Q_ASP_76	OD2	3.067
3PNW	Q_ARG_101	NH2	Q_ASP_117	OD2	3.288
3PNW	Q_ARG_104	NH1	R_GLU_599	OE1	3.284
3PNW	Q_LYS_159	NZ	Q_ASP_160	OD1	2.929
3PNW	Q_LYS_159	NZ	Q_ASP_160	OD2	2.916

3PNW	R_LYS_590	NZ	R_GLU_576	OE1	3.429
3PNW	S_ARG_62	NH2	S_GLU_82	OE2	3.335
3PNW	S_ARG_62	NH2	S_ASP_83	OD1	3.032
3PNW	S_LYS_106	NZ	S_GLU_168	OE1	2.994
3PNW	S_LYS_106	NZ	S_GLU_168	OE2	3.350
3PNW	S_LYS_186	NZ	S_GLU_190	OE2	3.826
3PNW	S_HIS_192	ND1	S_ASP_154	OD2	2.873
3PNW	S_ARG_214	NH2	S_GLU_190	OE1	3.425
3PNW	T_ARG_41	NH1	T_GLU_49	OE1	3.208
3PNW	T_ARG_41	NH1	T_GLU_49	OE2	3.692
3PNW	T_ARG_41	NH1	T_ASP_93	OD1	3.888
3PNW	T_ARG_41	NH2	T_ASP_93	OD1	2.764
3PNW	T_ARG_70	NH1	T_ASP_93	OD1	2.873
3PNW	T_ARG_70	NH1	T_ASP_93	OD2	3.677
3PNW	T_ARG_70	NH2	T_ASP_93	OD1	3.433
3PNW	T_ARG_70	NH2	T_ASP_93	OD2	2.704
3PNW	T_LYS_79	NZ	T_ASP_76	OD2	2.965
3PNW	T_ARG_101	NH2	T_ASP_117	OD2	3.568
3PNW	T_ARG_104	NH1	U_GLU_599	OE2	2.955
3PNW	T_LYS_159	NZ	T_ASP_160	OD1	2.985
3PNW	T_LYS_159	NZ	T_ASP_160	OD2	2.572
3PNW	U_LYS_590	NZ	U_GLU_576	OE1	3.326
3PNW	V_ARG_62	NH2	V_GLU_82	OE2	3.071
3PNW	V_ARG_62	NH2	V_ASP_83	OD1	3.114
3PNW	V_ARG_62	NH2	V_ASP_83	OD2	3.749
3PNW	V_LYS_106	NZ	V_GLU_168	OE1	3.033
3PNW	V_LYS_106	NZ	V_GLU_168	OE2	2.809
3PNW	V_LYS_152	NZ	V_GLU_198	OE1	3.564
3PNW	V_LYS_152	NZ	V_GLU_198	OE2	3.540
3PNW	V_LYS_186	NZ	V_GLU_190	OE1	3.466
3PNW	V_HIS_192	ND1	V_ASP_154	OD2	2.830
3PNW	W_ARG_41	NH1	W_GLU_49	OE1	3.191
3PNW	W_ARG_41	NH1	W_GLU_49	OE2	3.754
3PNW	W_ARG_41	NH1	W_ASP_93	OD1	3.797
3PNW	W_ARG_41	NH2	W_ASP_93	OD1	2.759
3PNW	W_ARG_70	NH1	W_ASP_93	OD1	3.055
3PNW	W_ARG_70	NH1	W_ASP_93	OD2	3.508
3PNW	W_ARG_70	NH2	W_ASP_93	OD1	3.808
3PNW	W_ARG_70	NH2	W_ASP_93	OD2	2.825
3PNW	W_LYS_79	NZ	W_ASP_76	OD2	3.031
3PNW	W_ARG_101	NH2	W_ASP_117	OD2	3.265
3PNW	W_ARG_104	NH2	X_GLU_599	OE2	3.113
3PNW	W_LYS_159	NZ	W_ASP_160	OD1	3.077
3PNW	W_LYS_159	NZ	W_ASP_160	OD2	3.386
3PNW	X_LYS_590	NZ	X_GLU_576	OE1	3.570
3PP4	H_ARG_38	NH1	H_ASP_90	OD1	2.857
3PP4	H_ARG_38	NH2	H_ASP_90	OD1	3.876
3PP4	H_ARG_50	NH2	H_ASP_59	OD2	3.031
3PP4	H_LYS_63	NZ	H_GLU_46	OE1	3.948
3PP4	H_ARG_67	NH1	H_ASP_90	OD1	3.622
3PP4	H_ARG_67	NH1	H_ASP_90	OD2	2.862
3PP4	H_ARG_67	NH2	H_ASP_90	OD1	2.967
3PP4	H_ARG_67	NH2	H_ASP_90	OD2	3.587
3PP4	H_ARG_87	NH2	H_GLU_89	OE2	3.547
3PP4	H_LYS_149	NZ	H_ASP_150	OD1	3.507
3PP4	H_LYS_215	NZ	L_GLU_128	OE1	3.038
3PP4	H_LYS_215	NZ	L_GLU_128	OE2	2.948
3PP4	L_LYS_27	NZ	L_GLU_98	OE1	2.607

3PP4	L_LYS_27	NZ	L_GLU_98	OE2	3.934
3PP4	L_ARG_66	NH2	L_ASP_87	OD1	2.843
3PP4	L_ARG_66	NH2	L_ASP_87	OD2	3.715
3PP4	L_LYS_108	NZ	L_GLU_170	OE1	2.761
3PP4	L_LYS_108	NZ	L_GLU_170	OE2	3.634
3PP4	L_ARG_147	NH1	L_GLU_110	OE1	3.275
3PP4	L_ARG_147	NH1	L_GLU_110	OE2	3.845
3PP4	L_ARG_147	NH2	L_GLU_110	OE1	3.278
3PP4	L_ARG_147	NH2	L_GLU_110	OE2	2.614
3PP4	L_LYS_154	NZ	L_GLU_200	OE1	2.680
3PP4	L_LYS_188	NZ	L_GLU_192	OE2	3.037
3PP4	L_HIS_194	ND1	L_ASP_156	OD2	3.533
3PP4	P_LYS_175	NZ	H_ASP_57	OD2	3.518
3Q3G	C_ARG_67	NH1	C_GLU_87	OE2	3.777
3Q3G	C_ARG_67	NH1	C_ASP_88	OD1	2.749
3Q3G	C_ARG_67	NH1	C_ASP_88	OD2	3.177
3Q3G	C_ARG_67	NH2	C_GLU_87	OE2	3.999
3Q3G	C_LYS_109	NZ	D_GLU_44	OE1	3.620
3Q3G	C_LYS_113	NZ	C_GLU_17	OE1	3.434
3Q3G	C_LYS_113	NZ	C_GLU_17	OE2	3.287
3Q3G	C_LYS_153	NZ	C_GLU_160	OE2	3.996
3Q3G	C_LYS_153	NZ	C_GLU_201	OE1	3.776
3Q3G	C_LYS_155	NZ	C_GLU_201	OE2	3.559
3Q3G	C_ARG_161	NH2	C_GLU_191	OE2	3.538
3Q3G	C_LYS_205	NZ	C_ASP_116	OD1	3.501
3Q3G	C_LYS_205	NZ	C_ASP_116	OD2	3.005
3Q3G	D_LYS_21	NZ	H_GLU_202	OE2	2.633
3Q3G	D_ARG_42	NH1	D_GLU_48	OE1	3.596
3Q3G	D_ARG_52	NH1	G_GLU_179	OE2	3.405
3Q3G	D_ARG_52	NH2	G_GLU_178	OE1	2.845
3Q3G	D_ARG_52	NH2	G_GLU_179	OE2	2.628
3Q3G	D_LYS_69	NZ	D_ASP_92	OD1	3.860
3Q3G	D_LYS_69	NZ	D_ASP_92	OD2	2.915
3Q3G	D_LYS_219	NZ	C_GLU_129	OE2	3.237
3Q3G	G_ARG_152	NH1	G_ASP_149	OD1	2.824
3Q3G	G_LYS_166	NZ	G_GLU_320	OE1	3.506
3Q3G	G_ARG_196	NH1	G_GLU_155	OE1	2.640
3Q3G	G_ARG_196	NH1	G_GLU_155	OE2	3.732
3Q3G	G_ARG_196	NH2	G_GLU_155	OE1	3.730
3Q3G	G_ARG_196	NH2	G_GLU_155	OE2	3.858
3Q3G	G_ARG_196	NH2	G_GLU_162	OE1	2.809
3Q3G	G_ARG_208	NH1	D_GLU_101	OE1	3.693
3Q3G	G_ARG_208	NH1	D_GLU_101	OE2	2.792
3Q3G	G_ARG_208	NH1	G_GLU_178	OE2	2.763
3Q3G	G_ARG_208	NH2	D_GLU_101	OE1	2.994
3Q3G	G_ARG_208	NH2	D_GLU_101	OE2	3.045
3Q3G	G_LYS_217	NZ	G_GLU_221	OE2	3.531
3Q3G	G_ARG_220	NH2	G_GLU_258	OE1	3.606
3Q3G	G_ARG_220	NH2	G_GLU_258	OE2	3.754
3Q3G	G_ARG_230	NH1	G_ASP_132	OD1	3.893
3Q3G	G_ARG_230	NH1	G_ASP_134	OD1	2.660
3Q3G	G_ARG_230	NH2	G_ASP_132	OD1	3.914
3Q3G	G_LYS_235	NZ	G_GLU_262	OE1	3.889
3Q3G	G_ARG_266	NH1	G_ASP_260	OD1	2.915
3Q3G	G_ARG_266	NH2	G_ASP_260	OD1	3.197
3Q3G	G_LYS_279	NZ	G_GLU_244	OE2	3.345
3Q3G	G_LYS_306	NZ	G_GLU_303	OE2	2.592
3Q3G	G_ARG_313	NH2	G_GLU_314	OE2	2.833

3Q3G	A_ARG.67	NH1	A_GLU.87	OE2	3.721
3Q3G	A_ARG.67	NH1	A_ASP.88	OD1	2.647
3Q3G	A_ARG.67	NH1	A_ASP.88	OD2	3.126
3Q3G	A_ARG.67	NH2	A_GLU.87	OE2	3.644
3Q3G	A_LYS.113	NZ	A_GLU.17	OE1	3.382
3Q3G	A_LYS.113	NZ	A_GLU.17	OE2	3.288
3Q3G	A_LYS.153	NZ	A_GLU.201	OE1	3.786
3Q3G	A_ARG.161	NH1	A_GLU.191	OE2	3.907
3Q3G	A_ARG.161	NH2	A_GLU.191	OE2	2.992
3Q3G	A_LYS.205	NZ	A_ASP.116	OD1	3.527
3Q3G	A_LYS.205	NZ	A_ASP.116	OD2	2.946
3Q3G	B_LYS.21	NZ	K_GLU.202	OE2	2.668
3Q3G	B_ARG.42	NH2	B_GLU.91	OE2	2.813
3Q3G	B_ARG.52	NH1	E_GLU.179	OE2	3.409
3Q3G	B_ARG.52	NH2	E_GLU.178	OE1	2.858
3Q3G	B_ARG.52	NH2	E_GLU.179	OE2	2.617
3Q3G	B_LYS.69	NZ	B_ASP.92	OD1	3.850
3Q3G	B_LYS.69	NZ	B_ASP.92	OD2	2.909
3Q3G	B_LYS.219	NZ	A_GLU.129	OE2	3.294
3Q3G	E_ARG.152	NH1	E_ASP.149	OD1	2.849
3Q3G	E_ARG.196	NH1	E_GLU.155	OE2	3.730
3Q3G	E_ARG.196	NH2	E_GLU.162	OE1	2.828
3Q3G	E_ARG.208	NH1	B_GLU.101	OE1	3.701
3Q3G	E_ARG.208	NH1	B_GLU.101	OE2	2.888
3Q3G	E_ARG.208	NH1	E_GLU.178	OE2	2.758
3Q3G	E_ARG.208	NH2	B_GLU.101	OE1	3.046
3Q3G	E_ARG.208	NH2	B_GLU.101	OE2	3.227
3Q3G	E_LYS.217	NZ	E_GLU.221	OE2	3.514
3Q3G	E_ARG.220	NH2	E_GLU.258	OE1	3.606
3Q3G	E_ARG.220	NH2	E_GLU.258	OE2	3.748
3Q3G	E_ARG.230	NH1	E_ASP.132	OD1	3.896
3Q3G	E_ARG.230	NH1	E_ASP.134	OD1	2.958
3Q3G	E_ARG.230	NH2	E_ASP.132	OD1	3.948
3Q3G	E_LYS.235	NZ	E_GLU.262	OE1	3.891
3Q3G	E_ARG.266	NH1	E_ASP.260	OD1	2.728
3Q3G	E_ARG.266	NH2	E_ASP.260	OD1	3.401
3Q3G	E_ARG.276	NH1	E_ASP.273	OD1	3.848
3Q3G	E_LYS.306	NZ	E_GLU.303	OE1	3.875
3Q3G	E_LYS.306	NZ	E_GLU.303	OE2	2.953
3Q3G	E_ARG.313	NH2	E_GLU.314	OE2	2.838
3Q3G	F_ARG.67	NH1	F_GLU.87	OE2	3.457
3Q3G	F_ARG.67	NH1	F_ASP.88	OD1	2.936
3Q3G	F_ARG.67	NH1	F_ASP.88	OD2	3.406
3Q3G	F_ARG.67	NH2	F_GLU.87	OE2	3.930
3Q3G	F_LYS.113	NZ	F_GLU.17	OE1	3.384
3Q3G	F_LYS.113	NZ	F_GLU.17	OE2	3.304
3Q3G	F_LYS.153	NZ	F_GLU.201	OE1	3.790
3Q3G	F_LYS.155	NZ	F_GLU.160	OE2	3.570
3Q3G	F_ARG.161	NH1	F_GLU.191	OE2	3.911
3Q3G	F_ARG.161	NH2	F_GLU.191	OE2	3.286
3Q3G	F_LYS.205	NZ	F_ASP.116	OD1	3.529
3Q3G	F_LYS.205	NZ	F_ASP.116	OD2	2.950
3Q3G	H_LYS.40	NZ	H_ASP.92	OD1	3.981
3Q3G	H_ARG.42	NH2	H_GLU.91	OE2	3.153
3Q3G	H_ARG.52	NH1	I_GLU.179	OE2	3.532
3Q3G	H_ARG.52	NH2	I_GLU.178	OE1	2.972
3Q3G	H_ARG.52	NH2	I_GLU.179	OE2	2.629
3Q3G	H_LYS.61	NZ	I_GLU.179	OE2	3.923

3Q3G	H.LYS.69	NZ	H.ASP.92	OD1	3.838
3Q3G	H.LYS.69	NZ	H.ASP.92	OD2	2.905
3Q3G	H.LYS.219	NZ	F.GLU.129	OE2	3.319
3Q3G	I.ARG.152	NH1	I.ASP.149	OD1	2.842
3Q3G	I.ARG.196	NH1	I.GLU.155	OE1	2.643
3Q3G	I.ARG.196	NH1	I.GLU.155	OE2	3.755
3Q3G	I.ARG.196	NH2	I.GLU.155	OE1	3.725
3Q3G	I.ARG.196	NH2	I.GLU.155	OE2	3.863
3Q3G	I.ARG.196	NH2	I.GLU.162	OE1	2.829
3Q3G	I.ARG.208	NH1	H.GLU.101	OE1	3.704
3Q3G	I.ARG.208	NH1	H.GLU.101	OE2	2.809
3Q3G	I.ARG.208	NH1	I.GLU.178	OE2	2.759
3Q3G	I.ARG.208	NH2	H.GLU.101	OE1	3.098
3Q3G	I.ARG.208	NH2	H.GLU.101	OE2	3.125
3Q3G	I.LYS.217	NZ	I.GLU.221	OE2	3.508
3Q3G	I.ARG.220	NH2	I.GLU.258	OE1	3.602
3Q3G	I.ARG.220	NH2	I.GLU.258	OE2	3.748
3Q3G	I.ARG.230	NH1	I.ASP.132	OD1	3.884
3Q3G	I.ARG.230	NH1	I.ASP.134	OD1	2.627
3Q3G	I.ARG.230	NH2	I.ASP.132	OD1	3.901
3Q3G	I.LYS.235	NZ	I.GLU.262	OE1	3.888
3Q3G	I.ARG.266	NH1	I.ASP.260	OD1	2.847
3Q3G	I.ARG.266	NH2	I.ASP.260	OD1	3.632
3Q3G	I.ARG.276	NH1	I.ASP.273	OD1	3.306
3Q3G	I.ARG.293	NH1	I.ASP.294	OD1	2.569
3Q3G	I.ARG.293	NH1	I.ASP.294	OD2	3.199
3Q3G	I.ARG.293	NH2	I.ASP.294	OD2	3.674
3Q3G	I.LYS.306	NZ	I.GLU.303	OE2	2.953
3Q3G	I.ARG.313	NH2	I.GLU.314	OE2	2.841
3Q3G	J.ARG.67	NH1	J.GLU.87	OE2	3.904
3Q3G	J.ARG.67	NH1	J.ASP.88	OD1	2.685
3Q3G	J.ARG.67	NH1	J.ASP.88	OD2	2.963
3Q3G	J.ARG.67	NH2	J.GLU.87	OE2	3.860
3Q3G	J.LYS.109	NZ	K.GLU.44	OE1	3.972
3Q3G	J.LYS.113	NZ	J.GLU.17	OE1	3.413
3Q3G	J.LYS.113	NZ	J.GLU.17	OE2	3.281
3Q3G	J.LYS.153	NZ	J.GLU.201	OE1	3.780
3Q3G	J.LYS.155	NZ	J.GLU.201	OE2	2.804
3Q3G	J.ARG.161	NH1	J.GLU.191	OE2	3.912
3Q3G	J.ARG.161	NH2	J.GLU.191	OE2	3.262
3Q3G	J.LYS.205	NZ	J.ASP.116	OD1	3.511
3Q3G	J.LYS.205	NZ	J.ASP.116	OD2	2.982
3Q3G	K.LYS.40	NZ	K.ASP.92	OD1	3.980
3Q3G	K.ARG.52	NH1	L.GLU.179	OE2	3.394
3Q3G	K.ARG.52	NH2	L.GLU.178	OE1	2.871
3Q3G	K.ARG.52	NH2	L.GLU.179	OE2	2.626
3Q3G	K.LYS.69	NZ	K.ASP.92	OD1	3.854
3Q3G	K.LYS.69	NZ	K.ASP.92	OD2	2.911
3Q3G	K.LYS.219	NZ	J.GLU.129	OE2	3.216
3Q3G	L.ARG.152	NH1	L.ASP.149	OD1	2.835
3Q3G	L.ARG.196	NH1	L.GLU.155	OE1	2.611
3Q3G	L.ARG.196	NH1	L.GLU.155	OE2	3.736
3Q3G	L.ARG.196	NH2	L.GLU.155	OE1	3.784
3Q3G	L.ARG.196	NH2	L.GLU.162	OE1	2.844
3Q3G	L.ARG.208	NH1	K.GLU.101	OE1	3.706
3Q3G	L.ARG.208	NH1	K.GLU.101	OE2	2.777
3Q3G	L.ARG.208	NH1	L.GLU.178	OE2	2.802
3Q3G	L.ARG.208	NH2	K.GLU.101	OE1	3.099

3Q3G	L_ARG_208	NH2	K_GLU_101	OE2	3.162
3Q3G	L_LYS_217	NZ	L_GLU_221	OE2	3.517
3Q3G	L_ARG_220	NH2	L_GLU_258	OE1	3.603
3Q3G	L_ARG_220	NH2	L_GLU_258	OE2	3.763
3Q3G	L_ARG_230	NH1	L_ASP_132	OD1	3.881
3Q3G	L_ARG_230	NH1	L_ASP_134	OD1	2.707
3Q3G	L_ARG_230	NH1	L_ASP_134	OD2	3.460
3Q3G	L_ARG_230	NH2	L_ASP_132	OD1	3.905
3Q3G	L_LYS_235	NZ	L_GLU_262	OE1	3.906
3Q3G	L_ARG_266	NH1	L_ASP_260	OD1	2.751
3Q3G	L_ARG_266	NH2	L_ASP_260	OD1	2.771
3Q3G	L_ARG_266	NH2	L_ASP_260	OD2	3.493
3Q3G	L_ARG_276	NH2	L_ASP_273	OD1	3.904
3Q3G	L_ARG_276	NH2	L_ASP_273	OD2	3.992
3Q3G	L_ARG_281	NH1	L_GLU_278	OE2	3.655
3Q3G	L_LYS_306	NZ	L_GLU_303	OE2	3.422
3Q3G	L_ARG_313	NH2	L_GLU_314	OE2	2.844
3QA3	C_LYS_24	NZ	C_ASP_76	OD2	3.522
3QA3	C_ARG_67	NH1	C_GLU_87	OE2	3.269
3QA3	C_ARG_67	NH1	C_ASP_88	OD1	2.660
3QA3	C_ARG_67	NH1	C_ASP_88	OD2	2.924
3QA3	C_ARG_67	NH2	C_GLU_87	OE2	3.168
3QA3	C_LYS_109	NZ	C_ASP_171	OD1	3.926
3QA3	C_LYS_109	NZ	D_GLU_44	OE1	3.919
3QA3	C_LYS_113	NZ	C_GLU_17	OE1	3.598
3QA3	C_LYS_113	NZ	C_GLU_17	OE2	3.105
3QA3	C_LYS_155	NZ	C_GLU_201	OE2	3.611
3QA3	C_ARG_161	NH2	C_GLU_191	OE2	3.603
3QA3	C_LYS_189	NZ	C_GLU_193	OE1	3.703
3QA3	C_LYS_205	NZ	C_ASP_116	OD1	3.367
3QA3	C_LYS_205	NZ	C_ASP_116	OD2	2.961
3QA3	C_ARG_217	NH1	C_GLU_193	OE2	3.785
3QA3	D_LYS_21	NZ	B_GLU_202	OE2	2.710
3QA3	D_LYS_40	NZ	D_ASP_92	OD1	3.621
3QA3	D_ARG_42	NH2	D_GLU_91	OE1	3.456
3QA3	D_ARG_52	NH1	G_GLU_179	OE2	3.492
3QA3	D_ARG_52	NH2	G_GLU_178	OE1	3.012
3QA3	D_ARG_52	NH2	G_GLU_179	OE2	2.776
3QA3	D_LYS_61	NZ	G_GLU_179	OE1	3.896
3QA3	D_LYS_61	NZ	G_GLU_179	OE2	3.867
3QA3	D_LYS_69	NZ	D_ASP_92	OD2	3.339
3QA3	D_LYS_219	NZ	C_GLU_129	OE2	3.586
3QA3	G_ARG_151	NH1	G_GLU_155	OE1	3.186
3QA3	G_ARG_151	NH1	G_GLU_155	OE2	3.465
3QA3	G_ARG_152	NH1	G_ASP_149	OD1	3.120
3QA3	G_ARG_196	NH2	G_GLU_162	OE1	3.407
3QA3	G_ARG_208	NH1	D_GLU_101	OE1	3.094
3QA3	G_ARG_208	NH1	D_GLU_101	OE2	3.755
3QA3	G_ARG_208	NH1	G_GLU_178	OE2	2.905
3QA3	G_ARG_208	NH2	D_GLU_101	OE1	2.802
3QA3	G_LYS_217	NZ	G_GLU_221	OE1	3.238
3QA3	G_LYS_217	NZ	G_GLU_221	OE2	3.591
3QA3	G_ARG_220	NH2	G_GLU_258	OE1	3.098
3QA3	G_ARG_220	NH2	G_GLU_258	OE2	3.589
3QA3	G_ARG_230	NH1	G_ASP_134	OD1	2.776
3QA3	G_LYS_235	NZ	G_GLU_262	OE1	3.322
3QA3	G_ARG_266	NH1	G_ASP_260	OD1	3.130
3QA3	G_ARG_266	NH2	G_ASP_260	OD1	3.273

3QA3	G_ARG_266	NH2	G_ASP_260	OD2	3.917
3QA3	G_ARG_281	NH1	G_GLU_278	OE2	3.336
3QA3	G_ARG_293	NH2	G_ASP_294	OD2	3.535
3QA3	G_LYS_306	NZ	F_GLU_61	OE1	2.676
3QA3	G_LYS_306	NZ	F_GLU_61	OE2	3.962
3QA3	G_ARG_313	NH2	G_GLU_314	OE2	3.236
3QA3	A_LYS_24	NZ	A_ASP_76	OD2	3.526
3QA3	A_ARG_67	NH1	A_GLU_87	OE2	3.266
3QA3	A_ARG_67	NH1	A_ASP_88	OD1	2.659
3QA3	A_ARG_67	NH1	A_ASP_88	OD2	2.926
3QA3	A_ARG_67	NH2	A_GLU_87	OE2	3.154
3QA3	A_LYS_109	NZ	A_ASP_171	OD1	3.971
3QA3	A_LYS_113	NZ	A_GLU_17	OE1	3.580
3QA3	A_LYS_113	NZ	A_GLU_17	OE2	3.100
3QA3	A_LYS_155	NZ	A_GLU_201	OE2	2.971
3QA3	A_LYS_205	NZ	A_ASP_116	OD1	3.377
3QA3	A_LYS_205	NZ	A_ASP_116	OD2	2.963
3QA3	B_LYS_40	NZ	B_ASP_92	OD1	3.602
3QA3	B_ARG_52	NH1	E_GLU_179	OE2	3.674
3QA3	B_ARG_52	NH2	E_GLU_178	OE1	3.139
3QA3	B_ARG_52	NH2	E_GLU_179	OE2	2.772
3QA3	B_LYS_61	NZ	E_GLU_179	OE1	3.626
3QA3	B_LYS_61	NZ	E_GLU_179	OE2	3.531
3QA3	B_LYS_69	NZ	B_ASP_92	OD2	3.326
3QA3	B_LYS_219	NZ	A_GLU_129	OE2	3.689
3QA3	E_ARG_152	NH1	E_ASP_149	OD1	3.421
3QA3	E_ARG_152	NH1	E_GLU_303	OE2	3.891
3QA3	E_ARG_196	NH1	E_GLU_155	OE2	2.779
3QA3	E_ARG_196	NH1	E_GLU_162	OE1	3.631
3QA3	E_ARG_196	NH2	E_GLU_155	OE1	3.951
3QA3	E_ARG_196	NH2	E_GLU_155	OE2	3.547
3QA3	E_ARG_196	NH2	E_GLU_162	OE1	3.609
3QA3	E_ARG_208	NH1	B_GLU_101	OE1	3.112
3QA3	E_ARG_208	NH1	B_GLU_101	OE2	3.639
3QA3	E_ARG_208	NH1	E_GLU_178	OE1	3.992
3QA3	E_ARG_208	NH1	E_GLU_178	OE2	2.905
3QA3	E_ARG_208	NH2	B_GLU_101	OE1	2.913
3QA3	E_ARG_208	NH2	B_GLU_101	OE2	3.978
3QA3	E_LYS_217	NZ	E_GLU_221	OE1	3.240
3QA3	E_LYS_217	NZ	E_GLU_221	OE2	3.588
3QA3	E_ARG_220	NH2	E_GLU_258	OE1	3.091
3QA3	E_ARG_220	NH2	E_GLU_258	OE2	3.588
3QA3	E_ARG_230	NH1	E_ASP_134	OD1	2.769
3QA3	E_LYS_235	NZ	E_GLU_262	OE1	3.320
3QA3	E_ARG_266	NH1	E_ASP_260	OD1	3.181
3QA3	E_ARG_266	NH2	E_ASP_260	OD1	3.305
3QA3	E_ARG_281	NH1	E_GLU_278	OE2	2.753
3QA3	F_LYS_24	NZ	F_ASP_76	OD2	3.520
3QA3	F_ARG_67	NH1	F_GLU_87	OE2	3.259
3QA3	F_ARG_67	NH1	F_ASP_88	OD1	2.663
3QA3	F_ARG_67	NH1	F_ASP_88	OD2	2.926
3QA3	F_ARG_67	NH2	F_GLU_87	OE2	3.150
3QA3	F_LYS_113	NZ	F_GLU_17	OE1	3.577
3QA3	F_LYS_113	NZ	F_GLU_17	OE2	3.091
3QA3	F_LYS_153	NZ	F_GLU_201	OE1	3.153
3QA3	F_LYS_155	NZ	F_GLU_201	OE1	3.670
3QA3	F_LYS_155	NZ	F_GLU_201	OE2	3.187
3QA3	F_HIS_195	ND1	F_ASP_157	OD2	2.743

3QA3	F_LYS_205	NZ	F_ASP_116	OD1	3.352
3QA3	F_LYS_205	NZ	F_ASP_116	OD2	2.987
3QA3	F_ARG_217	NH1	F_GLU_193	OE2	3.646
3QA3	H_LYS_21	NZ	K_GLU_202	OE1	2.630
3QA3	H_LYS_40	NZ	H_ASP_92	OD1	3.607
3QA3	H_ARG_52	NH1	I_GLU_179	OE2	3.536
3QA3	H_ARG_52	NH2	I_GLU_178	OE1	3.079
3QA3	H_ARG_52	NH2	I_GLU_179	OE2	2.753
3QA3	H_LYS_61	NZ	I_GLU_179	OE1	3.833
3QA3	H_LYS_61	NZ	I_GLU_179	OE2	3.714
3QA3	H_LYS_69	NZ	H_ASP_92	OD2	3.333
3QA3	H_LYS_219	NZ	F_GLU_129	OE2	3.683
3QA3	I_ARG_151	NH1	I_GLU_155	OE1	3.176
3QA3	I_ARG_151	NH1	I_GLU_155	OE2	3.423
3QA3	I_ARG_152	NH1	I_ASP_149	OD1	3.295
3QA3	I_ARG_208	NH1	H_GLU_101	OE1	2.952
3QA3	I_ARG_208	NH1	H_GLU_101	OE2	3.280
3QA3	I_ARG_208	NH1	I_GLU_178	OE2	2.910
3QA3	I_ARG_208	NH2	H_GLU_101	OE1	2.858
3QA3	I_ARG_208	NH2	H_GLU_101	OE2	3.749
3QA3	I_LYS_217	NZ	I_GLU_221	OE1	3.237
3QA3	I_LYS_217	NZ	I_GLU_221	OE2	3.599
3QA3	I_ARG_220	NH2	I_GLU_258	OE1	3.094
3QA3	I_ARG_220	NH2	I_GLU_258	OE2	3.593
3QA3	I_ARG_230	NH1	I_ASP_134	OD1	2.778
3QA3	I_LYS_235	NZ	I_GLU_262	OE1	3.330
3QA3	I_ARG_266	NH1	I_ASP_260	OD1	2.823
3QA3	I_ARG_266	NH2	I_ASP_260	OD1	2.813
3QA3	I_ARG_266	NH2	I_ASP_260	OD2	3.696
3QA3	I_ARG_293	NH2	I_ASP_294	OD2	3.520
3QA3	I_LYS_306	NZ	C_GLU_61	OE1	3.836
3QA3	J_LYS_24	NZ	J_ASP_76	OD2	3.532
3QA3	J_ARG_67	NH1	J_GLU_87	OE2	3.263
3QA3	J_ARG_67	NH1	J_ASP_88	OD1	2.670
3QA3	J_ARG_67	NH1	J_ASP_88	OD2	2.921
3QA3	J_ARG_67	NH2	J_GLU_87	OE2	3.148
3QA3	J_LYS_109	NZ	K_GLU_44	OE1	3.982
3QA3	J_LYS_113	NZ	J_GLU_17	OE1	3.620
3QA3	J_LYS_113	NZ	J_GLU_17	OE2	3.124
3QA3	J_LYS_205	NZ	J_ASP_116	OD1	3.342
3QA3	J_LYS_205	NZ	J_ASP_116	OD2	2.981
3QA3	K_LYS_40	NZ	K_ASP_92	OD1	3.624
3QA3	K_ARG_52	NH1	L_GLU_179	OE2	3.477
3QA3	K_ARG_52	NH2	L_GLU_178	OE1	3.052
3QA3	K_ARG_52	NH2	L_GLU_179	OE2	2.734
3QA3	K_LYS_61	NZ	L_GLU_179	OE1	3.839
3QA3	K_LYS_61	NZ	L_GLU_179	OE2	3.819
3QA3	K_LYS_69	NZ	K_ASP_92	OD2	3.339
3QA3	K_LYS_219	NZ	J_GLU_129	OE2	3.538
3QA3	L_ARG_152	NH1	L_ASP_149	OD1	3.084
3QA3	L_LYS_165	NZ	L_GLU_162	OE2	3.035
3QA3	L_ARG_196	NH2	L_GLU_162	OE1	3.491
3QA3	L_ARG_208	NH1	K_GLU_101	OE1	3.296
3QA3	L_ARG_208	NH1	K_GLU_101	OE2	3.152
3QA3	L_ARG_208	NH1	L_GLU_178	OE1	3.993
3QA3	L_ARG_208	NH1	L_GLU_178	OE2	2.907
3QA3	L_ARG_208	NH2	K_GLU_101	OE1	3.120
3QA3	L_ARG_208	NH2	K_GLU_101	OE2	3.548

3QA3	L_LYS_217	NZ	L_GLU_221	OE1	3.242
3QA3	L_LYS_217	NZ	L_GLU_221	OE2	3.595
3QA3	L_ARG_220	NH2	L_GLU_258	OE1	3.097
3QA3	L_ARG_220	NH2	L_GLU_258	OE2	3.600
3QA3	L_ARG_230	NH1	L_ASP_134	OD1	2.780
3QA3	L_LYS_235	NZ	L_GLU_262	OE1	3.332
3QA3	L_ARG_266	NH1	L_ASP_260	OD1	2.676
3QA3	L_ARG_266	NH2	L_ASP_260	OD1	3.599
3QA3	L_LYS_279	NZ	L_GLU_244	OE1	3.218
3QA3	L_LYS_279	NZ	L_GLU_244	OE2	3.599
3QA3	L_ARG_281	NH1	L_GLU_278	OE2	2.973
3QA3	L_ARG_293	NH2	L_ASP_294	OD2	3.523
3QG6	A_ARG_61	NH1	A_ASP_82	OD1	3.432
3QG6	A_ARG_61	NH1	A_ASP_82	OD2	2.717
3QG6	A_ARG_61	NH2	A_GLU_79	OE1	3.943
3QG6	A_ARG_61	NH2	A_ASP_82	OD1	3.288
3QG6	A_ARG_61	NH2	A_ASP_82	OD2	3.964
3QG6	A_LYS_142	NZ	A_GLU_105	OE1	3.461
3QG6	A_LYS_142	NZ	A_GLU_105	OE2	3.669
3QG6	A_LYS_147	NZ	A_GLU_154	OE1	3.545
3QG6	A_LYS_149	NZ	A_GLU_195	OE1	2.687
3QG6	A_LYS_149	NZ	A_GLU_195	OE2	3.955
3QG6	A_ARG_155	NH1	A_GLU_185	OE1	3.832
3QG6	A_ARG_155	NH1	A_GLU_185	OE2	3.376
3QG6	A_ARG_155	NH2	A_GLU_185	OE1	3.065
3QG6	A_ARG_155	NH2	A_GLU_185	OE2	3.907
3QG6	A_LYS_183	NZ	A_GLU_187	OE1	3.106
3QG6	A_LYS_183	NZ	A_GLU_187	OE2	3.334
3QG6	A_ARG_188	NH1	H_ASP_86	OD2	3.997
3QG6	A_ARG_188	NH2	H_ASP_86	OD1	3.422
3QG6	A_HIS_189	ND1	A_ASP_151	OD2	2.899
3QG6	A_HIS_189	NE2	A_GLU_185	OE2	3.272
3QG6	A_HIS_189	NE2	H_GLU_85	OE1	3.361
3QG6	A_HIS_189	NE2	H_GLU_85	OE2	3.215
3QG6	A_LYS_199	NZ	A_ASP_110	OD2	3.955
3QG6	B_ARG_38	NH1	B_ASP_86	OD1	2.928
3QG6	B_ARG_38	NH2	B_GLU_46	OE1	2.323
3QG6	B_LYS_44	NZ	B_GLU_46	OE2	3.659
3QG6	B_LYS_44	NZ	L_ASP_151	OD2	2.912
3QG6	B_LYS_64	NZ	L_GLU_187	OE1	3.778
3QG6	B_LYS_75	NZ	B_ASP_72	OD2	3.646
3QG6	B_ARG_94	NH2	B_ASP_101	OD2	2.932
3QG6	B_LYS_221	NZ	A_GLU_123	OE1	2.433
3QG6	H_ARG_38	NH1	H_ASP_86	OD1	2.717
3QG6	H_ARG_38	NH2	H_GLU_46	OE1	2.691
3QG6	H_ARG_38	NH2	H_ASP_86	OD1	3.824
3QG6	H_LYS_44	NZ	A_ASP_151	OD2	2.924
3QG6	H_LYS_44	NZ	H_GLU_46	OE2	3.702
3QG6	H_LYS_64	NZ	A_GLU_187	OE1	3.924
3QG6	H_LYS_75	NZ	H_ASP_72	OD2	3.688
3QG6	H_ARG_94	NH1	H_ASP_101	OD2	2.954
3QG6	H_LYS_221	NZ	L_GLU_123	OE1	2.733
3QG6	L_ARG_61	NH1	L_ASP_82	OD1	2.705
3QG6	L_ARG_61	NH1	L_ASP_82	OD2	2.689
3QG6	L_ARG_61	NH2	L_GLU_79	OE1	3.908
3QG6	L_ARG_61	NH2	L_GLU_79	OE2	3.936
3QG6	L_LYS_142	NZ	L_GLU_105	OE1	3.323
3QG6	L_LYS_142	NZ	L_GLU_105	OE2	3.219

3QG6	L_LYS_147	NZ	L_GLU_154	OE1	3.582
3QG6	L_LYS_149	NZ	L_GLU_195	OE1	2.845
3QG6	L_ARG_155	NH1	L_GLU_185	OE1	3.862
3QG6	L_ARG_155	NH1	L_GLU_185	OE2	3.392
3QG6	L_ARG_155	NH2	L_GLU_185	OE1	3.092
3QG6	L_ARG_155	NH2	L_GLU_185	OE2	3.899
3QG6	L_LYS_183	NZ	L_GLU_187	OE1	3.324
3QG6	L_LYS_183	NZ	L_GLU_187	OE2	3.444
3QG6	L_HIS_189	ND1	L_ASP_151	OD2	2.895
3QG6	L_HIS_189	NE2	B_GLU_85	OE1	3.320
3QG6	L_HIS_189	NE2	B_GLU_85	OE2	3.623
3QG6	L_HIS_189	NE2	L_GLU_185	OE2	3.346
3QG6	L_LYS_199	NZ	L_ASP_110	OD2	3.663
3QG7	H_ARG_38	NH1	H_ASP_86	OD1	2.959
3QG7	H_ARG_38	NH2	H_GLU_46	OE1	2.726
3QG7	H_ARG_94	NH2	H_ASP_101	OD2	3.399
3QG7	H_LYS_221	NZ	L_GLU_123	OE2	2.769
3QG7	H_LYS_222	NZ	H_GLU_226	OE2	3.925
3QG7	L_ARG_61	NH1	L_ASP_82	OD2	3.032
3QG7	L_ARG_61	NH2	L_GLU_79	OE1	3.794
3QG7	L_ARG_61	NH2	L_ASP_82	OD1	3.231
3QG7	L_ARG_61	NH2	L_ASP_82	OD2	3.013
3QG7	L_LYS_103	NZ	L_ASP_165	OD1	3.787
3QG7	L_LYS_147	NZ	L_GLU_195	OE1	3.261
3QG7	L_LYS_149	NZ	L_GLU_195	OE1	3.464
3QG7	L_LYS_149	NZ	L_GLU_195	OE2	2.727
3QG7	L_ARG_155	NH1	L_GLU_185	OE1	2.977
3QG7	L_LYS_183	NZ	L_GLU_187	OE1	2.941
3QG7	L_LYS_183	NZ	L_GLU_187	OE2	2.894
3QG7	L_LYS_199	NZ	L_ASP_110	OD2	3.998
3QO1	A_ARG_24	NH1	A_ASP_75	OD1	3.412
3QO1	A_ARG_24	NH2	A_ASP_75	OD1	2.963
3QO1	A_ARG_31	NH1	A_ASP_37	OD1	3.003
3QO1	A_ARG_31	NH2	A_ASP_33	OD1	3.693
3QO1	A_ARG_31	NH2	A_ASP_33	OD2	3.104
3QO1	A_HIS_35	ND1	A_ASP_33	OD1	3.949
3QO1	A_HIS_35	ND1	A_ASP_33	OD2	3.517
3QO1	A_LYS_44	NZ	A_GLU_86	OE1	3.342
3QO1	A_ARG_59	NH2	A_ASP_65	OD1	3.479
3QO1	A_ARG_66	NH2	A_ASP_87	OD1	2.560
3QO1	A_ARG_66	NH2	A_ASP_87	OD2	2.753
3QO1	B_ARG_38	NH1	B_GLU_46	OE1	3.400
3QO1	B_ARG_38	NH1	B_ASP_92	OD1	3.707
3QO1	B_ARG_38	NH2	B_ASP_92	OD1	2.890
3QO1	B_LYS_52	NZ	B_GLU_56	OE2	2.709
3QO1	B_ARG_53	NH1	B_GLU_56	OE1	3.115
3QO1	B_ARG_69	NH1	B_ASP_92	OD1	3.910
3QO1	B_ARG_69	NH1	B_ASP_92	OD2	2.658
3QO1	B_ARG_69	NH2	B_ASP_92	OD1	3.220
3QO1	B_ARG_69	NH2	B_ASP_92	OD2	3.334
3QO1	B_ARG_74	NH1	B_ASP_58	OD1	2.936
3QO1	B_ARG_74	NH2	B_ASP_58	OD1	3.003
3QO1	B_ARG_74	NH2	B_ASP_58	OD2	3.404
3QO1	B_ARG_74	NH2	B_ASP_76	OD1	3.459
3QO1	B_ARG_74	NH2	B_ASP_76	OD2	2.806
3QO1	B_ARG_101	NH1	A_GLU_39	OE1	3.830
3QO1	B_ARG_101	NH1	A_GLU_39	OE2	2.711
3QO1	B_ARG_101	NH2	A_GLU_39	OE1	2.782

3QO1	B_ARG_101	NH2	A_GLU_39	OE2	3.238
3QO1	B_LYS_149	NZ	B_ASP_150	OD1	3.291
3QO1	B_LYS_149	NZ	B_ASP_150	OD2	3.610
3QO1	B_LYS_215	NZ	A_GLU_128	OE1	3.939
3QO1	B_ARG_216	NH2	B_GLU_218	OE2	3.982
3QUM	P_ARG_36	NH1	A_ASP_94	OD2	3.603
3QUM	P_ARG_36	NH1	B_GLU_58	OE1	3.234
3QUM	P_ARG_36	NH1	B_GLU_58	OE2	3.373
3QUM	P_ARG_36	NH2	B_GLU_58	OE1	3.423
3QUM	P_HIS_57	ND1	P_ASP_102	OD1	3.257
3QUM	P_HIS_57	ND1	P_ASP_102	OD2	2.714
3QUM	P_LYS_62	NZ	B_GLU_58	OE2	3.762
3QUM	P_LYS_119	NZ	H_ASP_54	OD1	2.788
3QUM	P_LYS_119	NZ	H_ASP_54	OD2	3.700
3QUM	P_LYS_119	NZ	H_ASP_56	OD2	3.000
3QUM	P_LYS_230	NZ	P_GLU_129	OE1	3.910
3QUM	P_LYS_236	NZ	P_ASP_240	OD1	3.355
3QUM	P_LYS_236	NZ	P_ASP_240	OD2	3.879
3QUM	L_ARG_24	NH2	L_ASP_70	OD2	3.454
3QUM	L_LYS_27	NZ	L_GLU_93	OE2	2.631
3QUM	L_ARG_50	NH2	P_GLU_23	OE1	2.715
3QUM	L_ARG_61	NH1	L_ASP_82	OD1	3.063
3QUM	L_ARG_61	NH1	L_ASP_82	OD2	2.700
3QUM	L_ARG_61	NH2	L_GLU_79	OE1	3.466
3QUM	L_LYS_149	NZ	L_GLU_195	OE1	3.180
3QUM	L_LYS_149	NZ	L_GLU_195	OE2	2.848
3QUM	L_HIS_189	ND1	L_ASP_151	OD1	3.513
3QUM	L_HIS_189	ND1	L_ASP_151	OD2	3.827
3QUM	H_ARG_50	NH1	H_ASP_95	OD2	2.461
3QUM	H_LYS_62	NZ	H_GLU_46	OE1	2.726
3QUM	H_LYS_66	NZ	H_ASP_86	OD1	3.700
3QUM	H_LYS_66	NZ	H_ASP_86	OD2	2.890
3QUM	H_ARG_94	NH2	H_ASP_101	OD1	3.980
3QUM	H_ARG_94	NH2	H_ASP_101	OD2	2.778
3QUM	H_ARG_98	NH2	P_ASP_159	OD1	3.868
3QUM	H_ARG_98	NH2	P_ASP_159	OD2	3.474
3QUM	H_HIS_164	NE2	L_ASP_167	OD1	3.746
3QUM	H_LYS_208	NZ	L_GLU_123	OE1	3.317
3QUM	A_ARG_61	NH1	A_ASP_82	OD2	2.784
3QUM	A_ARG_61	NH2	A_ASP_82	OD2	3.879
3QUM	A_ARG_68	NH2	A_ASP_27C	OD2	3.611
3QUM	A_ARG_188	NH1	A_GLU_185	OE1	3.541
3QUM	A_ARG_188	NH1	A_GLU_185	OE2	2.650
3QUM	A_HIS_189	ND1	A_ASP_151	OD2	3.524
3QUM	A_HIS_189	NE2	A_GLU_185	OE1	3.506
3QUM	A_LYS_207	NZ	M_ASP_70	OD2	3.646
3QUM	B_ARG_40	NH1	B_GLU_85	OE2	3.723
3QUM	B_LYS_62	NZ	A_ASP_1	OD1	3.967
3QUM	B_LYS_62	NZ	A_ASP_1	OD2	3.654
3QUM	B_LYS_64	NZ	B_ASP_65	OD1	3.709
3QUM	B_LYS_64	NZ	B_ASP_65	OD2	3.188
3QUM	B_ARG_94	NH2	B_ASP_102	OD1	3.002
3QUM	B_ARG_94	NH2	B_ASP_102	OD2	3.802
3QUM	B_LYS_209	NZ	A_GLU_123	OE1	3.994
3QUM	B_LYS_209	NZ	A_GLU_123	OE2	2.553
3QUM	Q_HIS_57	ND1	Q_ASP_102	OD2	3.489
3QUM	Q_ARG_69	NH1	Q_GLU_77	OE1	2.522
3QUM	Q_ARG_69	NH2	Q_GLU_77	OE1	2.832

3QUM	Q_LYS_119	NZ	K_ASP_54	OD1	3.579
3QUM	Q_LYS_119	NZ	K_ASP_54	OD2	2.557
3QUM	Q_LYS_119	NZ	K_ASP_56	OD2	3.138
3QUM	Q_LYS_230	NZ	Q_GLU_129	OE2	2.982
3QUM	M_ARG_24	NH2	B_ASP_131	OD1	2.867
3QUM	M_ARG_24	NH2	B_ASP_131	OD2	3.402
3QUM	M_ARG_50	NH1	Q_GLU_21	OE2	3.456
3QUM	M_ARG_50	NH2	Q_GLU_21	OE2	3.792
3QUM	M_ARG_61	NH1	M_GLU_79	OE1	2.865
3QUM	M_ARG_61	NH1	M_GLU_79	OE2	3.959
3QUM	M_ARG_61	NH2	M_GLU_79	OE1	3.169
3QUM	M_ARG_61	NH2	M_ASP_82	OD1	2.669
3QUM	M_ARG_61	NH2	M_ASP_82	OD2	2.826
3QUM	M_LYS_183	NZ	M_GLU_187	OE1	3.466
3QUM	K_ARG_50	NH1	K_ASP_95	OD2	2.549
3QUM	K_LYS_58	NZ	Q_ASP_116	OD2	3.811
3QUM	K_LYS_58	NZ	K_ASP_56	OD1	3.915
3QUM	K_LYS_58	NZ	K_ASP_56	OD2	3.991
3QUM	K_LYS_62	NZ	M_ASP_1	OD1	2.803
3QUM	K_LYS_66	NZ	K_ASP_86	OD1	3.473
3QUM	K_LYS_66	NZ	K_ASP_86	OD2	3.448
3QUM	K_ARG_94	NH2	K_ASP_101	OD1	2.367
3QUM	K_ARG_94	NH2	K_ASP_101	OD2	2.940
3QUM	K_ARG_98	NH2	Q_ASP_159	OD2	3.098
3QUM	K_LYS_208	NZ	M_GLU_123	OE1	3.358
3QUM	K_ARG_213	NH2	K_ASP_214	OD2	3.796
3QUM	C_ARG_24	NH1	C_ASP_70	OD1	3.778
3QUM	C_ARG_24	NH1	C_ASP_70	OD2	2.622
3QUM	C_ARG_24	NH2	C_ASP_70	OD1	2.926
3QUM	C_ARG_24	NH2	C_ASP_70	OD2	3.340
3QUM	C_LYS_39	NZ	C_ASP_81	OD1	2.883
3QUM	C_ARG_61	NH1	C_GLU_79	OE1	2.943
3QUM	C_ARG_61	NH1	C_ASP_82	OD2	3.848
3QUM	C_ARG_61	NH2	C_ASP_82	OD1	3.376
3QUM	C_ARG_61	NH2	C_ASP_82	OD2	3.578
3QUM	C_LYS_142	NZ	C_GLU_105	OE1	2.648
3QUM	C_LYS_142	NZ	C_GLU_105	OE2	3.163
3QUM	C_LYS_147	NZ	C_GLU_195	OE2	3.770
3QUM	C_LYS_149	NZ	C_GLU_195	OE1	2.711
3QUM	C_LYS_149	NZ	C_GLU_195	OE2	3.595
3QUM	C_ARG_188	NH1	C_GLU_185	OE1	3.368
3QUM	D_LYS_38	NZ	D_GLU_46	OE2	3.663
3QUM	D_ARG_40	NH1	D_GLU_85	OE1	2.968
3QUM	D_LYS_66	NZ	D_ASP_86	OD1	3.445
3QUM	D_ARG_94	NH2	D_ASP_102	OD2	2.430
3QUM	D_ARG_97	NH1	C_GLU_55	OE1	3.578
3QUM	D_ARG_97	NH1	C_GLU_55	OE2	3.784
3QUM	D_ARG_97	NH2	Q_GLU_110	OE2	3.547
3R08	L_ARG_61	NH1	L_GLU_79	OE1	3.254
3R08	L_ARG_61	NH1	L_GLU_79	OE2	3.378
3R08	L_ARG_61	NH2	L_GLU_79	OE1	2.676
3R08	L_ARG_61	NH2	L_GLU_81	OE2	3.468
3R08	L_ARG_61	NH2	L_ASP_82	OD1	3.777
3R08	L_ARG_61	NH2	L_ASP_82	OD2	3.454
3R08	L_LYS_103	NZ	L_ASP_165	OD1	3.486
3R08	L_LYS_142	NZ	L_GLU_105	OE1	3.662
3R08	L_LYS_147	NZ	L_GLU_195	OE1	2.773
3R08	L_LYS_155	NZ	L_ASP_185	OD2	3.988

3R08	L_ARG_156	NH1	L_GLU_154	OE2	3.311
3R08	L_LYS_183	NZ	L_GLU_187	OE2	3.914
3R08	L_ARG_188	NH1	L_ASP_185	OD1	3.352
3R08	L_HIS_189	ND1	L_ASP_151	OD2	3.760
3R08	L_HIS_189	NE2	L_ASP_185	OD1	3.852
3R08	L_LYS_199	NZ	L_ASP_110	OD2	3.241
3R08	L_LYS_207	NZ	H_ASP_129	OD1	3.653
3R08	L_LYS_207	NZ	H_ASP_129	OD2	2.868
3R08	L_ARG_211	NH1	L_GLU_187	OE1	3.899
3R08	L_ARG_211	NH2	L_GLU_187	OE1	3.052
3R08	H_ARG_38	NH1	H_ASP_86	OD1	3.285
3R08	H_ARG_38	NH2	H_GLU_46	OE1	3.027
3R08	H_ARG_43	NH1	H_GLU_46	OE1	3.166
3R08	H_ARG_43	NH1	H_GLU_46	OE2	2.679
3R08	H_ARG_43	NH2	H_GLU_46	OE1	3.767
3R08	H_ARG_43	NH2	H_GLU_46	OE2	3.517
3R08	H_LYS_58	NZ	E_GLU_4	OE2	3.175
3R08	H_ARG_66	NH1	H_ASP_86	OD1	3.453
3R08	H_ARG_66	NH1	H_ASP_86	OD2	3.405
3R08	H_LYS_83	NZ	H_GLU_85	OE2	3.138
3R08	H_ARG_94	NH2	H_ASP_96	OD1	3.331
3R08	H_ARG_94	NH2	H_ASP_96	OD2	3.042
3R08	H_LYS_99	NZ	L_ASP_56	OD2	3.746
3R08	E_HIS_45	ND1	E_ASP_43	OD2	3.535
3R08	E_LYS_69	NZ	E_GLU_4	OE1	2.708
3R08	E_LYS_76	NZ	E_GLU_53	OE2	3.300
3SE8	G_HIS_66	ND1	G_GLU_64	OE2	2.819
3SE8	G_LYS_207	NZ	G_GLU_381	OE1	3.451
3SE8	G_LYS_207	NZ	G_GLU_381	OE2	2.740
3SE8	G_LYS_231	NZ	G_GLU_267	OE1	3.718
3SE8	G_HIS_249	NE2	G_GLU_482	OE1	2.997
3SE8	G_LYS_282	NZ	G_GLU_275	OE1	2.928
3SE8	G_LYS_282	NZ	H_ASP_100C	OD2	3.668
3SE8	G_LYS_343	NZ	G_GLU_347	OE1	3.295
3SE8	G_LYS_348	NZ	G_GLU_269	OE2	2.902
3SE8	G_LYS_348	NZ	G_GLU_351	OE1	2.955
3SE8	G_LYS_348	NZ	G_GLU_351	OE2	3.971
3SE8	G_LYS_350	NZ	G_GLU_347	OE1	3.922
3SE8	G_LYS_357	NZ	G_GLU_466	OE2	3.935
3SE8	G_ARG_379	NH2	G_ASP_211	OD1	3.636
3SE8	G_ARG_379	NH2	G_ASP_211	OD2	3.899
3SE8	G_ARG_456	NH1	G_GLU_466	OE1	3.921
3SE8	G_ARG_469	NH2	G_ASP_457	OD1	2.926
3SE8	G_ARG_469	NH2	G_ASP_457	OD2	3.898
3SE8	G_LYS_476	NZ	G_GLU_102	OE1	2.540
3SE8	G_ARG_480	NH1	G_ASP_477	OD1	2.656
3SE8	G_LYS_487	NZ	G_ASP_47	OD1	2.902
3SE8	G_LYS_487	NZ	G_GLU_91	OE1	2.578
3SE8	H_LYS_19	NZ	H_GLU_81	OE1	3.800
3SE8	H_ARG_38	NH1	H_GLU_46	OE1	2.640
3SE8	H_ARG_38	NH1	H_ASP_86	OD1	3.748
3SE8	H_ARG_38	NH2	H_ASP_86	OD1	2.672
3SE8	H_ARG_66	NH1	H_ASP_86	OD1	3.543
3SE8	H_ARG_66	NH1	H_ASP_86	OD2	3.893
3SE8	H_ARG_66	NH2	H_ASP_86	OD1	3.365
3SE8	H_ARG_66	NH2	H_ASP_86	OD2	2.596
3SE8	H_ARG_71	NH1	G_ASP_368	OD1	3.115
3SE8	H_ARG_71	NH1	G_ASP_368	OD2	3.763

3SE8	H_ARG_71	NH2	G_ASP_368	OD1	3.733
3SE8	H_ARG_71	NH2	G_ASP_368	OD2	2.907
3SE8	H_LYS_143	NZ	H_ASP_144	OD1	3.313
3SE8	H_LYS_143	NZ	H_ASP_144	OD2	3.811
3SE8	H_LYS_209	NZ	L_GLU_123	OE1	3.768
3SE8	H_LYS_210	NZ	H_GLU_212	OE1	2.816
3SE8	H_LYS_210	NZ	H_GLU_212	OE2	3.024
3SE8	L_LYS_24	NZ	L_ASP_70	OD1	2.618
3SE8	L_LYS_24	NZ	L_ASP_70	OD2	3.708
3SE8	L_ARG_39	NH1	L_GLU_81	OE1	3.909
3SE8	L_ARG_53	NH1	L_ASP_50	OD2	3.743
3SE8	L_ARG_61	NH2	L_ASP_82	OD1	2.770
3SE8	L_ARG_61	NH2	L_ASP_82	OD2	3.437
3SE8	L_ARG_142	NH1	L_GLU_103	OE1	3.000
3SE8	L_ARG_142	NH1	L_GLU_103	OE2	3.759
3SE8	L_ARG_142	NH2	L_GLU_103	OE1	3.192
3SE8	L_ARG_142	NH2	L_GLU_103	OE2	2.840
3SE8	L_ARG_142	NH2	L_GLU_105	OE2	3.734
3SE8	L_LYS_188	NZ	L_ASP_185	OD2	3.776
3SE9	G_HIS_66	ND1	G_GLU_64	OE2	2.728
3SE9	G_LYS_207	NZ	G_GLU_381	OE1	3.396
3SE9	G_LYS_207	NZ	G_GLU_381	OE2	3.043
3SE9	G_HIS_249	NE2	G_GLU_482	OE1	3.086
3SE9	G_LYS_282	NZ	G_GLU_275	OE1	3.135
3SE9	G_LYS_343	NZ	G_GLU_347	OE2	2.995
3SE9	G_LYS_348	NZ	G_GLU_269	OE2	3.584
3SE9	G_LYS_348	NZ	G_GLU_351	OE1	3.691
3SE9	G_LYS_357	NZ	G_GLU_466	OE1	3.212
3SE9	G_ARG_456	NH1	G_GLU_466	OE2	2.713
3SE9	G_ARG_469	NH1	G_ASP_457	OD1	2.966
3SE9	G_ARG_469	NH1	G_ASP_457	OD2	3.436
3SE9	G_LYS_476	NZ	G_GLU_102	OE1	2.755
3SE9	G_LYS_476	NZ	G_GLU_102	OE2	3.946
3SE9	G_ARG_480	NH1	G_ASP_477	OD1	3.009
3SE9	G_ARG_480	NH2	G_GLU_102	OE2	3.763
3SE9	G_LYS_487	NZ	G_ASP_47	OD1	2.626
3SE9	G_LYS_487	NZ	G_ASP_47	OD2	3.721
3SE9	G_LYS_487	NZ	G_GLU_91	OE1	2.626
3SE9	H_ARG_19	NH2	H_ASP_81	OD1	3.575
3SE9	H_ARG_19	NH2	H_ASP_81	OD2	3.127
3SE9	H_ARG_31	NH2	H_GLU_30	OE2	3.962
3SE9	H_ARG_38	NH1	H_ASP_86	OD1	2.864
3SE9	H_ARG_38	NH2	H_GLU_46	OE1	3.505
3SE9	H_ARG_64	NH1	G_ASP_457	OD2	3.853
3SE9	H_ARG_64	NH2	G_ASP_457	OD1	3.358
3SE9	H_ARG_64	NH2	G_ASP_457	OD2	3.280
3SE9	H_ARG_66	NH1	H_ASP_62	OD1	3.472
3SE9	H_ARG_66	NH1	H_ASP_62	OD2	2.990
3SE9	H_ARG_66	NH1	H_ASP_86	OD1	3.657
3SE9	H_ARG_66	NH1	H_ASP_86	OD2	3.617
3SE9	H_ARG_66	NH2	H_ASP_86	OD1	3.675
3SE9	H_ARG_66	NH2	H_ASP_86	OD2	2.373
3SE9	H_ARG_71	NH1	G_ASP_368	OD1	3.515
3SE9	H_ARG_71	NH1	G_ASP_368	OD2	2.768
3SE9	H_ARG_71	NH2	G_ASP_368	OD1	3.012
3SE9	H_ARG_71	NH2	G_ASP_368	OD2	3.769
3SE9	H_ARG_94	NH2	H_ASP_101	OD1	2.737
3SE9	H_ARG_94	NH2	H_ASP_101	OD2	3.906

3SE9	H.LYS_143	NZ	H.ASP_144	OD1	3.511
3SE9	H.LYS_209	NZ	L.GLU_123	OE1	3.388
3SE9	H.LYS_214	NZ	L.ASP_122	OD1	3.332
3SE9	L.ARG_61	NH1	L.ASP_82	OD1	2.919
3SE9	L.ARG_61	NH1	L.ASP_82	OD2	3.116
3SE9	L.LYS_183	NZ	L.GLU_187	OE1	2.818
3SE9	L.HIS_189	ND1	L.ASP_151	OD2	2.887
3SGD	L.LYS_24	NZ	L.ASP_75	OD1	2.783
3SGD	L.ARG_51	NH2	L.ASP_60	OD1	3.495
3SGD	L.ARG_51	NH2	L.ASP_60	OD2	3.021
3SGD	L.ARG_66	NH1	L.ASP_87	OD1	3.680
3SGD	L.ARG_66	NH1	L.ASP_87	OD2	2.782
3SGD	L.ARG_66	NH2	L.GLU_84	OE1	3.767
3SGD	L.ARG_66	NH2	L.ASP_87	OD1	2.989
3SGD	L.ARG_66	NH2	L.ASP_87	OD2	3.564
3SGD	L.HIS_98	ND1	L.ASP_31	OD2	3.644
3SGD	L.LYS_152	NZ	L.GLU_159	OE1	3.644
3SGD	L.LYS_152	NZ	L.GLU_159	OE2	3.885
3SGD	L.LYS_154	NZ	L.GLU_200	OE1	3.346
3SGD	L.LYS_154	NZ	L.GLU_200	OE2	3.354
3SGD	L.ARG_160	NH2	L.GLU_190	OE1	2.808
3SGD	L.ARG_160	NH2	L.GLU_190	OE2	2.668
3SGD	L.ARG_193	NH1	L.ASP_189	OD2	2.692
3SGD	L.ARG_193	NH2	L.GLU_190	OE2	3.962
3SGD	L.HIS_194	ND1	L.ASP_156	OD2	2.735
3SGD	L.HIS_194	NE2	L.GLU_190	OE2	3.628
3SGD	L.LYS_204	NZ	L.ASP_115	OD2	3.348
3SGD	L.LYS_204	NZ	J.ASP_75	OD1	3.665
3SGD	L.LYS_204	NZ	J.ASP_75	OD2	3.246
3SGD	H.ARG_38	NH1	H.ASP_92	OD2	2.803
3SGD	H.ARG_38	NH2	H.GLU_46	OE2	3.026
3SGD	H.ARG_38	NH2	H.ASP_92	OD2	3.826
3SGD	H.LYS_43	NZ	J.ASP_68	OD1	3.910
3SGD	H.ARG_69	NH1	H.ASP_92	OD1	2.725
3SGD	H.ARG_69	NH1	H.ASP_92	OD2	3.812
3SGD	H.ARG_69	NH2	H.ASP_92	OD1	3.411
3SGD	H.ARG_69	NH2	H.ASP_92	OD2	3.054
3SGD	H.ARG_74	NH2	H.ASP_76	OD1	3.619
3SGD	H.LYS_210	NZ	L.GLU_128	OE1	3.898
3SGD	L.LYS_24	NZ	L.ASP_75	OD1	3.796
3SGD	L.LYS_24	NZ	L.ASP_75	OD2	2.962
3SGD	L.ARG_44	NH2	L.GLU_86	OE2	3.752
3SGD	L.ARG_51	NH2	L.ASP_60	OD1	2.717
3SGD	L.ARG_51	NH2	L.ASP_60	OD2	3.541
3SGD	L.ARG_66	NH1	L.ASP_87	OD1	3.518
3SGD	L.ARG_66	NH1	L.ASP_87	OD2	2.585
3SGD	L.ARG_66	NH2	L.GLU_84	OE1	3.635
3SGD	L.ARG_66	NH2	L.GLU_86	OE1	3.914
3SGD	L.ARG_66	NH2	L.GLU_86	OE2	3.879
3SGD	L.ARG_66	NH2	L.ASP_87	OD1	2.899
3SGD	L.ARG_66	NH2	L.ASP_87	OD2	3.479
3SGD	L.ARG_82	NH1	L.GLU_84	OE2	2.800
3SGD	L.ARG_82	NH2	L.GLU_84	OE2	3.178
3SGD	L.LYS_154	NZ	L.GLU_200	OE1	3.141
3SGD	L.LYS_154	NZ	L.GLU_200	OE2	2.988
3SGD	L.LYS_174	NZ	L.ASP_172	OD1	3.706
3SGD	L.LYS_174	NZ	L.ASP_172	OD2	3.091
3SGD	L.LYS_174	NZ	L.ASP_175	OD1	3.919

3SGD	L_ARG_193	NH2	L_ASP_189	OD2	2.737
3SGD	L_HIS_194	ND1	L_ASP_156	OD2	2.901
3SGD	L_LYS_204	NZ	L_ASP_115	OD2	3.676
3SGD	J_LYS_19	NZ	L_ASP_148	OD1	3.248
3SGD	J_LYS_19	NZ	L_ASP_148	OD2	2.952
3SGD	J_ARG_38	NH1	J_ASP_92	OD2	2.794
3SGD	J_ARG_38	NH2	J_GLU_46	OE1	3.737
3SGD	J_ARG_38	NH2	J_GLU_46	OE2	2.952
3SGD	J_ARG_38	NH2	J_ASP_92	OD2	3.905
3SGD	J_ARG_69	NH1	J_ASP_92	OD1	2.689
3SGD	J_ARG_69	NH1	J_ASP_92	OD2	3.808
3SGD	J_ARG_69	NH2	J_ASP_92	OD1	3.488
3SGD	J_ARG_69	NH2	J_ASP_92	OD2	3.217
3SGD	J_ARG_74	NH2	J_ASP_76	OD1	3.467
3SKJ	L_ARG_24	NH1	L_GLU_70	OE1	3.770
3SKJ	L_ARG_61	NH2	L_ASP_82	OD1	2.965
3SKJ	L_ARG_61	NH2	L_ASP_82	OD2	3.776
3SKJ	L_ARG_96	NH1	H_GLU_100I	OE1	2.505
3SKJ	L_ARG_96	NH1	H_GLU_100I	OE2	2.799
3SKJ	L_LYS_103	NZ	L_GLU_165	OE1	2.601
3SKJ	L_LYS_103	NZ	L_GLU_165	OE2	3.499
3SKJ	L_HIS_189	ND1	L_ASP_151	OD2	3.871
3SKJ	L_ARG_211	NH2	L_GLU_187	OE2	3.617
3SKJ	H_HIS_31	ND1	H_ASP_96	OD2	2.640
3SKJ	H_HIS_31	NE2	E_GLU_133	OE2	3.297
3SKJ	H_ARG_38	NH1	H_ASP_86	OD1	2.911
3SKJ	H_ARG_38	NH2	H_GLU_46	OE1	3.116
3SKJ	H_ARG_38	NH2	H_GLU_46	OE2	3.301
3SKJ	H_ARG_38	NH2	H_ASP_86	OD1	3.993
3SKJ	H_ARG_50	NH1	H_GLU_100I	OE1	3.128
3SKJ	H_LYS_64	NZ	H_ASP_61	OD2	3.941
3SKJ	H_ARG_66	NH1	H_ASP_86	OD1	3.677
3SKJ	H_ARG_66	NH2	H_ASP_86	OD1	3.495
3SKJ	H_ARG_66	NH2	H_ASP_86	OD2	2.568
3SKJ	H_HIS_161	NE2	L_ASP_167	OD2	3.763
3SKJ	H_LYS_206	NZ	L_GLU_123	OE1	2.501
3SKJ	H_LYS_206	NZ	L_GLU_123	OE2	3.323
3SKJ	H_ARG_207	NH1	H_GLU_209	OE2	3.580
3SKJ	M_ARG_24	NH1	M_GLU_70	OE1	3.068
3SKJ	M_ARG_24	NH1	M_GLU_70	OE2	3.024
3SKJ	M_ARG_24	NH2	M_GLU_70	OE1	3.407
3SKJ	M_LYS_39	NZ	M_ASP_81	OD1	2.568
3SKJ	M_ARG_61	NH2	M_ASP_82	OD1	2.991
3SKJ	M_ARG_61	NH2	M_ASP_82	OD2	2.909
3SKJ	M_ARG_96	NH2	L_GLU_100I	OE1	3.081
3SKJ	M_ARG_96	NH2	L_GLU_100I	OE2	3.831
3SKJ	M_LYS_103	NZ	M_GLU_165	OE2	3.149
3SKJ	M_LYS_149	NZ	M_GLU_195	OE2	3.240
3SKJ	M_LYS_188	NZ	M_ASP_185	OD2	3.381
3SKJ	L_ARG_38	NH1	L_ASP_86	OD1	2.866
3SKJ	L_ARG_38	NH2	L_GLU_46	OE1	3.262
3SKJ	L_ARG_38	NH2	L_GLU_46	OE2	3.203
3SKJ	L_LYS_43	NZ	L_ASP_1	OD1	3.862
3SKJ	L_ARG_50	NH1	L_GLU_100I	OE1	3.217
3SKJ	L_ARG_50	NH1	L_GLU_100I	OE2	3.198
3SKJ	L_ARG_66	NH1	L_ASP_86	OD1	3.975
3SKJ	L_ARG_66	NH1	L_ASP_86	OD2	2.891
3SKJ	L_ARG_66	NH2	L_ASP_86	OD1	3.263

3SKJ	L_ARG.66	NH2	L_ASP.86	OD2	3.539
3SKJ	L_ARG.83	NH1	L_GLU.85	OE1	3.307
3SKJ	L_ARG.83	NH1	L_GLU.85	OE2	3.711
3SKJ	L_LYS.140	NZ	L_ASP.141	OD1	2.912
3SKJ	L_LYS.140	NZ	L_ASP.141	OD2	3.281
3SKJ	L_LYS.211	NZ	M_ASP.122	OD2	3.816
3SKJ	L_LYS.211	NZ	M_GLU.123	OE1	3.612
3SKJ	E_LYS.112	NZ	E_ASP.54	OD1	3.156
3SKJ	E_ARG.144	NH1	E_GLU.142	OE1	3.346
3SKJ	E_ARG.144	NH2	E_ASP.119	OD1	3.475
3SKJ	E_ARG.144	NH2	E_GLU.142	OE1	3.494
3SKJ	E_ARG.171	NH1	E_GLU.73	OE1	3.665
3SKJ	E_ARG.171	NH1	E_GLU.73	OE2	3.183
3SKJ	E_ARG.171	NH2	E_GLU.4	OE1	2.631
3SKJ	E_LYS.176	NZ	E_GLU.66	OE2	2.522
3SY0	A_LYS.24	NZ	A_ASP.70	OD1	2.683
3SY0	A_LYS.24	NZ	A_ASP.70	OD2	3.488
3SY0	A_LYS.39	NZ	A_GLU.81	OE1	2.857
3SY0	A_ARG.61	NH1	A_GLU.81	OE2	3.627
3SY0	A_ARG.61	NH1	A_ASP.82	OD1	2.753
3SY0	A_ARG.61	NH1	A_ASP.82	OD2	3.623
3SY0	A_ARG.95	NH2	B_ASP.95	OD1	3.609
3SY0	A_ARG.95	NH2	B_ASP.95	OD2	2.821
3SY0	A_LYS.146	NZ	A_GLU.194	OE2	3.742
3SY0	A_LYS.148	NZ	A_GLU.194	OE1	2.676
3SY0	A_LYS.148	NZ	A_GLU.194	OE2	2.913
3SY0	A_LYS.182	NZ	A_GLU.186	OE1	2.287
3SY0	A_LYS.182	NZ	A_GLU.186	OE2	3.835
3SY0	A_ARG.187	NH2	A_GLU.184	OE1	2.876
3SY0	A_HIS.188	ND1	A_ASP.150	OD2	2.895
3SY0	A_HIS.188	NE2	A_GLU.184	OE2	2.965
3SY0	A_LYS.198	NZ	A_ASP.109	OD2	3.892
3SY0	B_ARG.38	NH1	B_ASP.86	OD2	2.779
3SY0	B_ARG.38	NH2	B_GLU.46	OE1	3.151
3SY0	B_ARG.38	NH2	B_GLU.46	OE2	4.000
3SY0	B_ARG.38	NH2	B_ASP.86	OD2	3.804
3SY0	B_ARG.52	NH1	B_GLU.56	OE2	2.894
3SY0	B_ARG.52	NH2	B_GLU.56	OE2	3.121
3SY0	B_ARG.64	NH1	B_ASP.86	OD1	2.875
3SY0	B_ARG.64	NH1	B_ASP.86	OD2	3.721
3SY0	B_ARG.64	NH2	B_ASP.86	OD1	3.464
3SY0	B_ARG.64	NH2	B_ASP.86	OD2	2.919
3SY0	B_HIS.96	ND1	B_GLU.100A	OE2	3.230
3SY0	B_HIS.96	NE2	B_GLU.100A	OE2	3.820
3SY0	B_ARG.100B	NH1	A_GLU.55	OE1	2.843
3SY0	B_ARG.100B	NH1	A_GLU.55	OE2	3.786
3SY0	B_LYS.206	NZ	A_GLU.122	OE1	3.980
3T4Y	A_LYS.24	NZ	A_ASP.70	OD1	2.903
3T4Y	A_LYS.24	NZ	A_ASP.70	OD2	3.502
3T4Y	A_LYS.39	NZ	A_GLU.81	OE2	3.124
3T4Y	A_ARG.61	NH1	A_GLU.81	OE1	3.284
3T4Y	A_ARG.61	NH1	A_ASP.82	OD1	2.653
3T4Y	A_ARG.61	NH1	A_ASP.82	OD2	3.419
3T4Y	A_ARG.95	NH2	B_ASP.95	OD1	3.796
3T4Y	A_ARG.95	NH2	B_ASP.95	OD2	2.951
3T4Y	A_LYS.148	NZ	A_GLU.194	OE1	2.908
3T4Y	A_LYS.148	NZ	A_GLU.194	OE2	3.013
3T4Y	A_ARG.187	NH2	A_GLU.184	OE1	2.855

3T4Y	A_HIS_188	ND1	A_ASP_150	OD2	2.865
3T4Y	A_HIS_188	NE2	A_GLU_184	OE2	2.755
3T4Y	B_ARG_38	NH1	B_ASP_86	OD2	2.806
3T4Y	B_ARG_38	NH2	B_GLU_46	OE1	3.203
3T4Y	B_ARG_38	NH2	B_GLU_85	OE2	3.852
3T4Y	B_ARG_38	NH2	B_ASP_86	OD2	3.884
3T4Y	B_ARG_52	NH1	B_GLU_56	OE2	2.817
3T4Y	B_ARG_52	NH2	B_GLU_56	OE2	2.987
3T4Y	B_ARG_64	NH1	B_ASP_86	OD1	2.822
3T4Y	B_ARG_64	NH1	B_ASP_86	OD2	3.726
3T4Y	B_ARG_64	NH2	B_ASP_86	OD1	3.460
3T4Y	B_ARG_64	NH2	B_ASP_86	OD2	2.866
3T4Y	B_HIS_96	ND1	B_GLU_100A	OE2	3.510
3T4Y	B_HIS_96	NE2	B_GLU_100A	OE2	3.981
3T4Y	B_ARG_100B	NH1	A_GLU_55	OE1	3.824
3T4Y	B_ARG_100B	NH1	A_GLU_55	OE2	2.840
3T4Y	B_LYS_206	NZ	A_GLU_122	OE2	2.652
3T65	B_ARG_38	NH1	B_ASP_86	OD2	2.756
3T65	B_ARG_38	NH2	B_GLU_46	OE1	3.099
3T65	B_ARG_38	NH2	B_GLU_85	OE1	3.408
3T65	B_ARG_38	NH2	B_ASP_86	OD2	3.896
3T65	B_ARG_52	NH1	B_GLU_56	OE2	2.912
3T65	B_ARG_52	NH2	B_GLU_56	OE2	3.090
3T65	B_ARG_64	NH1	B_ASP_86	OD1	2.927
3T65	B_ARG_64	NH1	B_ASP_86	OD2	3.734
3T65	B_ARG_64	NH2	B_ASP_86	OD1	3.486
3T65	B_ARG_64	NH2	B_ASP_86	OD2	2.925
3T65	B_HIS_96	ND1	B_GLU_100A	OE2	3.351
3T65	B_HIS_96	NE2	B_GLU_100A	OE2	3.804
3T65	B_ARG_100B	NH1	A_GLU_55	OE1	3.841
3T65	B_ARG_100B	NH1	A_GLU_55	OE2	2.883
3T65	A_LYS_24	NZ	A_ASP_70	OD1	2.811
3T65	A_LYS_24	NZ	A_ASP_70	OD2	3.571
3T65	A_LYS_39	NZ	A_GLU_81	OE2	3.467
3T65	A_ARG_54	NH2	A_ASP_60	OD1	3.593
3T65	A_ARG_61	NH1	A_GLU_81	OE1	3.085
3T65	A_ARG_61	NH1	A_ASP_82	OD1	2.841
3T65	A_ARG_61	NH1	A_ASP_82	OD2	3.657
3T65	A_ARG_95	NH2	B_ASP_95	OD1	3.666
3T65	A_ARG_95	NH2	B_ASP_95	OD2	2.866
3T65	A_LYS_146	NZ	A_GLU_153	OE2	3.733
3T65	A_LYS_148	NZ	A_GLU_194	OE1	2.726
3T65	A_LYS_148	NZ	A_GLU_194	OE2	3.149
3T65	A_LYS_182	NZ	A_GLU_186	OE1	3.601
3T65	A_LYS_182	NZ	A_GLU_186	OE2	3.775
3T65	A_ARG_187	NH2	A_GLU_184	OE1	2.825
3T65	A_HIS_188	ND1	A_ASP_150	OD2	2.935
3T65	A_HIS_188	NE2	A_GLU_184	OE2	2.940
3T65	A_LYS_198	NZ	A_ASP_109	OD2	3.914
3T77	A_LYS_24	NZ	A_ASP_70	OD1	2.759
3T77	A_LYS_24	NZ	A_ASP_70	OD2	3.590
3T77	A_LYS_39	NZ	A_GLU_81	OE1	3.726
3T77	A_ARG_61	NH2	A_GLU_81	OE2	3.966
3T77	A_ARG_61	NH2	A_ASP_82	OD1	2.868
3T77	A_ARG_61	NH2	A_ASP_82	OD2	3.521
3T77	A_ARG_95	NH2	B_ASP_95	OD1	3.723
3T77	A_ARG_95	NH2	B_ASP_95	OD2	2.997
3T77	A_LYS_102	NZ	A_GLU_104	OE1	3.775

3T77	A_LYS_102	NZ	A_GLU_104	OE2	3.007
3T77	A_LYS_148	NZ	A_GLU_194	OE1	3.783
3T77	A_LYS_148	NZ	A_GLU_194	OE2	2.306
3T77	A_LYS_182	NZ	A_GLU_186	OE1	3.731
3T77	A_ARG_187	NH2	A_GLU_184	OE1	2.585
3T77	A_HIS_188	ND1	A_ASP_150	OD2	3.031
3T77	A_HIS_188	NE2	A_GLU_184	OE2	2.771
3T77	A_LYS_198	NZ	A_ASP_109	OD1	3.952
3T77	B_ARG_38	NH1	B_ASP_86	OD2	2.829
3T77	B_ARG_38	NH2	B_GLU_46	OE1	3.138
3T77	B_ARG_38	NH2	B_ASP_86	OD2	3.744
3T77	B_ARG_52	NH1	B_GLU_56	OE2	2.717
3T77	B_ARG_52	NH2	B_GLU_56	OE2	3.056
3T77	B_ARG_64	NH1	B_ASP_86	OD1	2.807
3T77	B_ARG_64	NH1	B_ASP_86	OD2	3.626
3T77	B_ARG_64	NH2	B_ASP_86	OD1	3.476
3T77	B_ARG_64	NH2	B_ASP_86	OD2	2.870
3T77	B_HIS_96	ND1	B_GLU_100A	OE1	3.974
3T77	B_HIS_96	NE2	B_GLU_100A	OE1	2.416
3T77	B_ARG_100B	NH1	A_GLU_55	OE1	3.125
3T77	B_ARG_100B	NH1	A_GLU_55	OE2	2.687
3T77	B_LYS_206	NZ	A_GLU_122	OE2	3.917
3THM	L_ARG_31	NH1	L_ASP_94	OD1	2.844
3THM	L_ARG_31	NH1	L_ASP_94	OD2	2.885
3THM	L_ARG_55	NH1	L_ASP_61	OD2	3.667
3THM	L_ARG_62	NH2	L_ASP_83	OD1	3.471
3THM	L_ARG_62	NH2	L_ASP_83	OD2	2.633
3THM	L_ARG_77	NH1	L_ASP_78	OD2	2.791
3THM	L_HIS_192	ND1	L_ASP_155	OD1	2.840
3THM	L_ARG_193	NH1	L_ASP_155	OD2	3.695
3THM	L_ARG_193	NH2	L_ASP_155	OD1	3.787
3THM	H_ARG_40	NH1	H_ASP_96	OD1	2.763
3THM	H_ARG_40	NH2	H_GLU_48	OE1	3.112
3THM	H_ARG_40	NH2	H_ASP_96	OD1	3.732
3THM	H_ARG_73	NH1	H_ASP_96	OD1	3.781
3THM	H_ARG_73	NH1	H_ASP_96	OD2	3.095
3THM	H_ARG_73	NH2	H_ASP_96	OD1	2.910
3THM	H_ARG_73	NH2	H_ASP_96	OD2	3.508
3THM	H_LYS_82	NZ	H_ASP_79	OD2	3.975
3THM	H_ARG_104	NH2	H_ASP_120	OD1	3.520
3THM	H_ARG_104	NH2	H_ASP_120	OD2	2.748
3THM	H_LYS_225	NZ	H_ASP_227	OD2	3.663
3THM	H_LYS_229	NZ	H_GLU_231	OE1	3.584
3THM	F_HIS_38	ND1	F_ASP_56	OD1	3.082
3THM	F_HIS_38	ND1	F_ASP_56	OD2	2.768
3THM	F_LYS_45	NZ	L_GLU_97	OE2	3.172
3THM	F_LYS_53	NZ	F_GLU_63	OE1	2.774
3THM	F_LYS_78	NZ	L_ASP_52	OD1	3.702
3THM	F_ARG_112	NH2	F_GLU_98	OE1	3.774
3TJE	L_ARG_31	NH1	L_ASP_94	OD1	2.809
3TJE	L_ARG_62	NH1	L_ASP_83	OD1	3.626
3TJE	L_ARG_62	NH1	L_ASP_83	OD2	2.774
3TJE	L_ARG_62	NH2	L_ASP_83	OD1	2.866
3TJE	L_ARG_62	NH2	L_ASP_83	OD2	3.498
3TJE	L_ARG_77	NH1	L_ASP_78	OD2	2.738
3TJE	L_ARG_77	NH2	L_ASP_61	OD2	3.491
3TJE	L_LYS_114	NZ	L_GLU_202	OE2	3.788
3TJE	H_ARG_40	NH1	H_ASP_96	OD1	2.839

3TJE	H_ARG_40	NH2	H_GLU_48	OE1	3.044
3TJE	H_ARG_40	NH2	H_ASP_96	OD1	3.722
3TJE	H_ARG_73	NH1	H_ASP_96	OD1	3.710
3TJE	H_ARG_73	NH1	H_ASP_96	OD2	2.838
3TJE	H_ARG_73	NH2	H_ASP_96	OD1	2.943
3TJE	H_ARG_73	NH2	H_ASP_96	OD2	3.439
3TJE	H_ARG_104	NH2	H_ASP_120	OD1	3.469
3TJE	H_ARG_104	NH2	H_ASP_120	OD2	2.676
3TJE	H_LYS_225	NZ	H_ASP_227	OD2	3.295
3TJE	H_LYS_229	NZ	H_GLU_231	OE1	3.568
3TJE	F_LYS_53	NZ	F_GLU_63	OE1	2.653
3TJE	F_HIS_95	ND1	F_ASP_92	OD2	3.202
3TJE	F_ARG_105	NH1	F_GLU_71	OE1	3.450
3TJE	F_ARG_105	NH1	F_GLU_71	OE2	3.955
3TJE	F_ARG_105	NH2	F_GLU_71	OE2	3.995
3TJE	F_LYS_110	NZ	F_GLU_100	OE1	2.868
3TJE	F_LYS_110	NZ	F_GLU_100	OE2	3.645
3TJE	F_ARG_112	NH2	F_GLU_98	OE2	3.462
3TJE	F_LYS_114	NZ	F_GLU_93	OE2	3.047
3TJE	F_HIS_126	NE2	F_ASP_128	OD1	3.055
3TJE	F_HIS_126	NE2	F_ASP_128	OD2	3.467
3U1S	L_LYS_24	NZ	L_ASP_70	OD2	3.165
3U1S	L_HIS_27D	NE2	H_ASP_100B	OD2	2.859
3U1S	L_ARG_61	NH1	L_ASP_82	OD1	3.331
3U1S	L_ARG_61	NH1	L_ASP_82	OD2	2.471
3U1S	L_ARG_61	NH2	L_GLU_79	OE1	3.597
3U1S	L_ARG_61	NH2	L_GLU_79	OE2	3.692
3U1S	L_ARG_61	NH2	L_ASP_82	OD1	2.705
3U1S	L_ARG_61	NH2	L_ASP_82	OD2	3.338
3U1S	L_LYS_149	NZ	L_GLU_195	OE2	2.775
3U1S	L_HIS_189	ND1	L_ASP_151	OD2	3.043
3U1S	H_LYS_12	NZ	H_GLU_10	OE2	3.798
3U1S	H_ARG_38	NH1	H_ASP_86	OD1	2.812
3U1S	H_ARG_38	NH2	H_GLU_46	OE1	3.161
3U1S	H_ARG_38	NH2	H_ASP_86	OD1	3.811
3U1S	H_HIS_52A	ND1	H_GLU_52B	OE1	3.637
3U1S	H_HIS_52A	NE2	H_ASP_33	OD1	3.943
3U1S	H_HIS_52A	NE2	H_GLU_52B	OE1	3.544
3U1S	H_HIS_52A	NE2	H_GLU_52B	OE2	3.663
3U1S	H_LYS_60	NZ	H_GLU_46	OE1	3.515
3U1S	H_LYS_60	NZ	H_GLU_46	OE2	2.683
3U1S	H_ARG_64	NH1	H_ASP_86	OD1	3.631
3U1S	H_ARG_64	NH1	H_ASP_86	OD2	3.169
3U1S	H_ARG_64	NH2	H_ASP_86	OD1	2.578
3U1S	H_ARG_64	NH2	H_ASP_86	OD2	3.420
3U1S	H_LYS_97	NZ	H_ASP_33	OD1	2.873
3U1S	H_LYS_97	NZ	H_ASP_33	OD2	3.430
3U1S	H_LYS_97	NZ	H_GLU_52B	OE1	2.747
3U1S	H_LYS_97	NZ	H_GLU_52B	OE2	3.729
3U1S	H_ARG_99	NH1	H_GLU_52B	OE1	3.885
3U1S	H_ARG_99	NH1	H_GLU_52B	OE2	3.932
3U1S	H_ARG_99	NH1	H_ASP_53	OD1	2.841
3U1S	H_ARG_99	NH1	H_ASP_53	OD2	3.415
3U1S	H_ARG_99	NH2	H_ASP_53	OD1	3.710
3U1S	H_ARG_99	NH2	H_ASP_53	OD2	2.972
3U1S	H_ARG_99	NH2	H_ASP_100R	OD1	3.526
3U1S	H_ARG_99	NH2	H_ASP_100R	OD2	2.851
3U1S	H_ARG_100A	NH1	H_GLU_100N	OE2	3.328

3U1S	H.LYS_211	NZ	H.ASP_213	OD1	2.712
3U1S	H.LYS_211	NZ	H.ASP_213	OD2	3.729
3U1S	H.LYS_214	NZ	L.GLU_123	OE1	3.475
3U1S	H.LYS_215	NZ	H.GLU_217	OE2	3.772
3U2S	H.ARG_31	NH1	H.ASP_100L	OD2	3.978
3U2S	H.ARG_31	NH2	H.ASP_100L	OD1	3.963
3U2S	H.ARG_31	NH2	H.ASP_100L	OD2	2.965
3U2S	H.HIS_35	NE2	H.GLU_95	OE1	2.640
3U2S	H.ARG_38	NH1	H.ASP_86	OD1	2.839
3U2S	H.ARG_38	NH2	H.GLU_46	OE1	3.925
3U2S	H.ARG_38	NH2	H.GLU_46	OE2	2.923
3U2S	H.ARG_38	NH2	H.ASP_86	OD1	3.911
3U2S	H.LYS_52	NZ	H.ASP_100I	OD2	3.366
3U2S	H.ARG_66	NH1	H.ASP_86	OD1	3.572
3U2S	H.ARG_66	NH1	H.ASP_86	OD2	2.527
3U2S	H.ARG_66	NH2	H.ASP_86	OD1	2.931
3U2S	H.ARG_66	NH2	H.ASP_86	OD2	3.433
3U2S	H.ARG_94	NH2	H.ASP_101	OD1	3.597
3U2S	H.ARG_94	NH2	H.ASP_101	OD2	2.850
3U2S	L.LYS_53	NZ	L.ASP_50	OD2	2.841
3U2S	L.ARG_54	NH2	C.ASP_167	OD1	3.525
3U2S	L.ARG_54	NH2	C.ASP_167	OD2	3.282
3U2S	L.ARG_61	NH1	L.ASP_82	OD1	3.649
3U2S	L.ARG_61	NH1	L.ASP_82	OD2	2.861
3U2S	L.ARG_61	NH2	L.ASP_82	OD1	2.965
3U2S	L.ARG_61	NH2	L.ASP_82	OD2	3.572
3U2S	L.LYS_66	NZ	L.GLU_31	OE2	2.988
3U2S	L.ARG_95A	NH1	H.ASP_61	OD1	2.794
3U2S	L.ARG_95A	NH1	H.ASP_61	OD2	3.373
3U2S	L.ARG_95A	NH2	H.ASP_61	OD1	2.338
3U2S	L.ARG_96	NH2	H.GLU_95	OE1	3.743
3U2S	L.ARG_96	NH2	H.GLU_95	OE2	2.869
3U2S	L.LYS_129	NZ	H.ASP_144	OD1	3.881
3U2S	L.HIS_188	ND1	L.ASP_151	OD2	3.681
3U2S	G.ARG_168	NH2	H.ASP_100L	OD1	3.358
3U2S	G.ARG_168	NH2	H.ASP_100L	OD2	3.104
3U2S	G.LYS_171	NZ	H.ASP_100I	OD1	3.178
3U2S	A.ARG_31	NH2	A.ASP_100L	OD1	3.437
3U2S	A.ARG_31	NH2	A.ASP_100L	OD2	3.464
3U2S	A.HIS_35	NE2	A.GLU_95	OE1	2.700
3U2S	A.ARG_38	NH1	A.ASP_86	OD1	2.886
3U2S	A.ARG_38	NH2	A.GLU_46	OE1	3.872
3U2S	A.ARG_38	NH2	A.GLU_46	OE2	2.898
3U2S	A.ARG_38	NH2	A.ASP_86	OD1	3.831
3U2S	A.LYS_52	NZ	A.ASP_100I	OD2	3.513
3U2S	A.ARG_66	NH1	A.ASP_86	OD1	3.554
3U2S	A.ARG_66	NH1	A.ASP_86	OD2	2.481
3U2S	A.ARG_66	NH2	A.ASP_86	OD1	3.013
3U2S	A.ARG_66	NH2	A.ASP_86	OD2	3.477
3U2S	A.ARG_83	NH1	A.GLU_85	OE1	2.914
3U2S	A.ARG_94	NH2	A.ASP_101	OD1	3.528
3U2S	A.ARG_94	NH2	A.ASP_101	OD2	2.897
3U2S	A.LYS_143	NZ	B.GLU_124	OE2	3.550
3U2S	B.LYS_53	NZ	B.ASP_50	OD2	2.754
3U2S	B.ARG_61	NH1	B.ASP_82	OD1	3.698
3U2S	B.ARG_61	NH1	B.ASP_82	OD2	2.775
3U2S	B.ARG_61	NH2	B.ASP_82	OD1	2.930
3U2S	B.ARG_61	NH2	B.ASP_82	OD2	3.413

3U2S	B_LYS_66	NZ	B_GLU_31	OE2	3.053
3U2S	B_ARG_95A	NH1	A_ASP_61	OD1	2.632
3U2S	B_ARG_95A	NH1	A_ASP_61	OD2	3.483
3U2S	B_ARG_95A	NH2	A_ASP_61	OD1	3.270
3U2S	B_ARG_96	NH2	A_GLU_95	OE1	3.738
3U2S	B_ARG_96	NH2	A_GLU_95	OE2	2.983
3U2S	C_ARG_168	NH2	A_ASP_100L	OD1	2.424
3U2S	C_ARG_168	NH2	A_ASP_100L	OD2	3.228
3U2S	C_LYS_169	NZ	C_ASP_223	OD1	3.001
3U2S	C_LYS_169	NZ	C_ASP_223	OD2	3.464
3U2S	C_LYS_169	NZ	C_GLU_239	OE2	2.484
3U2S	C_LYS_171	NZ	A_ASP_100I	OD1	3.279
3U36	H_HIS_35	NE2	H_GLU_95	OE1	2.791
3U36	H_ARG_38	NH1	H_ASP_86	OD1	3.091
3U36	H_ARG_38	NH2	H_GLU_46	OE2	3.256
3U36	H_ARG_66	NH1	H_ASP_86	OD1	3.636
3U36	H_ARG_66	NH1	H_ASP_86	OD2	2.875
3U36	H_ARG_66	NH2	H_ASP_86	OD1	3.304
3U36	H_ARG_66	NH2	H_ASP_86	OD2	3.804
3U36	H_ARG_83	NH1	H_GLU_85	OE2	3.153
3U36	H_ARG_94	NH2	H_ASP_101	OD1	3.359
3U36	H_ARG_94	NH2	H_ASP_101	OD2	2.948
3U36	H_LYS_210	NZ	H_GLU_212	OE1	3.728
3U36	L_LYS_53	NZ	L_ASP_50	OD2	3.306
3U36	L_ARG_61	NH1	L_ASP_82	OD1	3.774
3U36	L_ARG_61	NH1	L_ASP_82	OD2	2.558
3U36	L_ARG_61	NH2	L_ASP_82	OD1	2.956
3U36	L_ARG_61	NH2	L_ASP_82	OD2	3.131
3U36	L_LYS_66	NZ	L_GLU_31	OE1	3.601
3U36	L_LYS_66	NZ	L_GLU_31	OE2	3.328
3U36	L_LYS_89	NZ	H_GLU_95	OE1	3.857
3U36	L_ARG_95A	NH1	H_ASP_61	OD1	3.290
3U36	L_ARG_95A	NH1	H_ASP_61	OD2	1.959
3U36	L_ARG_95A	NH2	H_ASP_61	OD1	3.530
3U36	L_ARG_95A	NH2	H_ASP_61	OD2	3.624
3U36	L_ARG_96	NH2	H_GLU_95	OE2	3.606
3U36	L_HIS_188	ND1	L_ASP_151	OD2	3.797
3U36	A_HIS_35	NE2	A_GLU_95	OE1	2.797
3U36	A_ARG_38	NH1	A_ASP_86	OD1	3.094
3U36	A_ARG_38	NH2	A_GLU_46	OE1	3.989
3U36	A_ARG_38	NH2	A_GLU_46	OE2	3.229
3U36	A_ARG_66	NH1	A_ASP_86	OD1	3.636
3U36	A_ARG_66	NH1	A_ASP_86	OD2	2.878
3U36	A_ARG_66	NH2	A_ASP_86	OD1	3.312
3U36	A_ARG_66	NH2	A_ASP_86	OD2	3.805
3U36	A_ARG_83	NH1	A_GLU_85	OE2	3.159
3U36	A_ARG_94	NH2	A_ASP_101	OD1	3.386
3U36	A_ARG_94	NH2	A_ASP_101	OD2	2.941
3U36	A_LYS_210	NZ	A_GLU_212	OE1	3.743
3U36	B_LYS_53	NZ	B_ASP_50	OD2	3.349
3U36	B_ARG_61	NH1	B_ASP_82	OD1	3.756
3U36	B_ARG_61	NH1	B_ASP_82	OD2	2.547
3U36	B_ARG_61	NH2	B_ASP_82	OD1	2.945
3U36	B_ARG_61	NH2	B_ASP_82	OD2	3.139
3U36	B_LYS_66	NZ	B_GLU_31	OE1	3.580
3U36	B_LYS_66	NZ	B_GLU_31	OE2	3.318
3U36	B_LYS_89	NZ	A_GLU_95	OE1	3.772
3U36	B_ARG_95A	NH1	A_ASP_61	OD1	3.519

3U36	B_ARG_95A	NH1	A_ASP_61	OD2	2.198
3U36	B_ARG_95A	NH2	A_ASP_61	OD1	3.831
3U36	B_ARG_95A	NH2	A_ASP_61	OD2	3.817
3U36	B_ARG_96	NH2	A_GLU_95	OE2	3.395
3U36	B_LYS_129	NZ	A_ASP_144	OD1	3.769
3U36	B_HIS_188	ND1	B_ASP_151	OD2	3.839
3U36	C_HIS_35	NE2	C_GLU_95	OE1	2.789
3U36	C_ARG_38	NH1	C_ASP_86	OD1	3.079
3U36	C_ARG_38	NH2	C_GLU_46	OE2	3.262
3U36	C_ARG_38	NH2	C_ASP_86	OD1	3.997
3U36	C_ARG_66	NH1	C_ASP_86	OD1	3.625
3U36	C_ARG_66	NH1	C_ASP_86	OD2	2.865
3U36	C_ARG_66	NH2	C_ASP_86	OD1	3.335
3U36	C_ARG_66	NH2	C_ASP_86	OD2	3.835
3U36	C_ARG_83	NH1	C_GLU_85	OE2	3.161
3U36	C_ARG_94	NH2	C_ASP_101	OD1	3.358
3U36	C_ARG_94	NH2	C_ASP_101	OD2	2.963
3U36	C_LYS_210	NZ	C_GLU_212	OE1	3.726
3U36	D_LYS_53	NZ	D_ASP_50	OD2	3.331
3U36	D_ARG_61	NH1	D_ASP_82	OD1	3.763
3U36	D_ARG_61	NH1	D_ASP_82	OD2	2.558
3U36	D_ARG_61	NH2	D_ASP_82	OD1	2.940
3U36	D_ARG_61	NH2	D_ASP_82	OD2	3.134
3U36	D_LYS_66	NZ	D_GLU_31	OE1	3.617
3U36	D_LYS_66	NZ	D_GLU_31	OE2	3.349
3U36	D_LYS_89	NZ	C_GLU_95	OE1	3.877
3U36	D_ARG_95A	NH1	C_ASP_61	OD1	3.266
3U36	D_ARG_95A	NH1	C_ASP_61	OD2	2.045
3U36	D_ARG_95A	NH2	C_ASP_61	OD1	3.629
3U36	D_ARG_95A	NH2	C_ASP_61	OD2	3.782
3U36	D_ARG_96	NH2	C_GLU_95	OE2	3.569
3U36	D_HIS_188	ND1	D_ASP_151	OD2	3.779
3U36	E_HIS_35	NE2	E_GLU_95	OE1	2.788
3U36	E_ARG_38	NH1	E_ASP_86	OD1	3.110
3U36	E_ARG_38	NH2	E_GLU_46	OE2	3.229
3U36	E_ARG_66	NH1	E_ASP_86	OD1	3.638
3U36	E_ARG_66	NH1	E_ASP_86	OD2	2.884
3U36	E_ARG_66	NH2	E_ASP_86	OD1	3.328
3U36	E_ARG_66	NH2	E_ASP_86	OD2	3.837
3U36	E_ARG_83	NH1	E_GLU_85	OE2	3.161
3U36	E_ARG_94	NH2	E_ASP_101	OD1	3.373
3U36	E_ARG_94	NH2	E_ASP_101	OD2	2.982
3U36	E_LYS_210	NZ	E_GLU_212	OE1	3.712
3U36	F_LYS_53	NZ	F_ASP_50	OD2	3.348
3U36	F_ARG_61	NH1	F_ASP_82	OD1	3.756
3U36	F_ARG_61	NH1	F_ASP_82	OD2	2.549
3U36	F_ARG_61	NH2	F_ASP_82	OD1	2.945
3U36	F_ARG_61	NH2	F_ASP_82	OD2	3.125
3U36	F_LYS_66	NZ	F_GLU_31	OE1	3.599
3U36	F_LYS_66	NZ	F_GLU_31	OE2	3.326
3U36	F_ARG_95A	NH1	E_ASP_61	OD1	3.076
3U36	F_ARG_95A	NH1	E_ASP_61	OD2	1.876
3U36	F_ARG_95A	NH2	E_ASP_61	OD1	3.424
3U36	F_ARG_95A	NH2	E_ASP_61	OD2	3.670
3U36	F_ARG_96	NH2	E_GLU_95	OE2	3.739
3U36	F_HIS_188	ND1	F_ASP_151	OD2	3.814
3UBX	A_ARG_21	NH2	A_GLU_92	OE1	3.225
3UBX	A_ARG_21	NH2	A_GLU_92	OE2	2.650

3UBX	A_ARG_25	NH2	A_ASP_27	OD1	3.138
3UBX	A_ARG_25	NH2	A_ASP_27	OD2	3.670
3UBX	A_ARG_25	NH2	A_ASP_43	OD2	3.995
3UBX	A_ARG_39	NH2	B_ASP_53	OD2	3.336
3UBX	A_LYS_51	NZ	A_GLU_243	OE1	2.918
3UBX	A_LYS_51	NZ	A_GLU_243	OE2	3.104
3UBX	A_HIS_203	ND1	A_ASP_252	OD1	3.478
3UBX	A_ARG_204	NH1	A_GLU_258	OE2	2.763
3UBX	A_ARG_204	NH2	A_GLU_258	OE2	2.916
3UBX	A_ARG_264	NH2	A_ASP_274	OD2	3.397
3UBX	A_LYS_266	NZ	A_ASP_274	OD2	2.636
3UBX	A_HIS_282	NE2	B_ASP_98	OD1	3.815
3UBX	A_HIS_282	NE2	B_ASP_98	OD2	3.128
3UBX	B_ARG_12	NH2	A_ASP_242	OD1	3.715
3UBX	B_ARG_12	NH2	A_ASP_242	OD2	3.324
3UBX	B_LYS_19	NZ	B_GLU_16	OE1	3.108
3UBX	B_LYS_19	NZ	B_GLU_16	OE2	3.855
3UBX	B_LYS_	NZ	B_ASP_76	OD2	3.469
3UBX	B_HIS_67	NE2	B_GLU_50	OE1	3.182
3UBX	D_ARG_21	NH2	D_GLU_92	OE1	3.198
3UBX	D_ARG_21	NH2	D_GLU_92	OE2	2.624
3UBX	D_ARG_	NH2	D_ASP_	OD1	3.097
3UBX	D_ARG_	NH2	D_ASP_	OD2	3.631
3UBX	D_ARG_	NH2	E_ASP_	OD2	3.464
3UBX	D_LYS_	NZ	D_GLU_	OE1	2.938
3UBX	D_LYS_	NZ	D_GLU_	OE2	3.121
3UBX	D_HIS_	ND1	D_ASP_	OD1	3.543
3UBX	D_ARG_	NH1	D_GLU_	OE2	2.718
3UBX	D_ARG_	NH2	D_GLU_	OE2	2.872
3UBX	D_ARG_	NH2	D_ASP_	OD2	3.382
3UBX	D_LYS_	NZ	D_ASP_	OD2	2.644
3UBX	D_HIS_	NE2	E_ASP_	OD1	3.963
3UBX	D_HIS_	NE2	E_ASP_	OD2	3.193
3UBX	E_ARG_	NH2	D_ASP_	OD1	3.594
3UBX	E_ARG_	NH2	D_ASP_	OD2	3.257
3UBX	E_LYS_	NZ	E_GLU_	OE1	3.157
3UBX	E_LYS_	NZ	E_GLU_	OE2	3.909
3UBX	E_HIS_	ND1	D_GLU_97	OE1	3.846
3UBX	E_LYS_	NZ	E_ASP_	OD2	3.547
3UBX	E_HIS_	NE2	E_GLU_	OE1	3.185
3UBX	L_ARG_32	NH2	A_ASP_80	OD1	3.479
3UBX	L_ARG_32	NH2	A_ASP_80	OD2	3.348
3UBX	L_ARG_32	NH2	A_ASP_153	OD2	3.795
3UBX	L_ARG_61	NH2	L_ASP_82	OD1	2.895
3UBX	L_ARG_61	NH2	L_ASP_82	OD2	3.241
3UBX	L_LYS_103	NZ	L_ASP_165	OD1	3.380
3UBX	L_LYS_142	NZ	L_GLU_105	OE1	2.881
3UBX	L_LYS_142	NZ	L_GLU_105	OE2	3.829
3UBX	L_LYS_	NZ	L_GLU_	OE1	3.629
3UBX	L_LYS_	NZ	L_GLU_	OE2	3.666
3UBX	L_ARG_	NH1	L_GLU_	OE2	3.855
3UBX	L_LYS_169	NZ	L_GLU_81	OE1	3.852
3UBX	L_LYS_169	NZ	L_GLU_81	OE2	3.096
3UBX	L_HIS_	NE2	L_GLU_	OE2	3.994
3UBX	L_LYS_	NZ	L_ASP_	OD2	3.189
3UBX	H_LYS_12	NZ	H_GLU_10	OE2	3.934
3UBX	H_LYS_65	NZ	H_ASP_62	OD1	3.945
3UBX	H_ARG_67	NH2	H_ASP_90	OD1	2.984

3UBX	H_ARG_67	NH2	H_ASP_90	OD2	2.362
3UBX	H_ARG_103	NH2	A_ASP_80	OD1	2.578
3UBX	H_LYS_215	NZ	L_GLU_123	OE1	3.082
3UBX	H_LYS_215	NZ	L_GLU_123	OE2	3.481
3UBX	L_ARG_32	NH2	D_ASP_80	OD1	3.383
3UBX	L_ARG_32	NH2	D_ASP_80	OD2	3.294
3UBX	L_ARG_32	NH2	D_ASP_153	OD2	3.950
3UBX	L_ARG_61	NH2	L_ASP_82	OD1	2.893
3UBX	L_ARG_61	NH2	L_ASP_82	OD2	3.343
3UBX	L_LYS_103	NZ	L_ASP_165	OD1	3.385
3UBX	L_LYS_142	NZ	L_GLU_105	OE1	2.848
3UBX	L_LYS_142	NZ	L_GLU_105	OE2	3.795
3UBX	L_LYS_149	NZ	L_GLU_195	OE1	3.611
3UBX	L_LYS_149	NZ	L_GLU_195	OE2	3.678
3UBX	L_ARG_155	NH1	L_GLU_185	OE2	3.804
3UBX	L_LYS_169	NZ	L_GLU_81	OE1	3.837
3UBX	L_LYS_169	NZ	L_GLU_81	OE2	3.130
3UBX	L_LYS_199	NZ	L_ASP_110	OD2	3.216
3UBX	G_LYS_12	NZ	G_GLU_10	OE2	3.983
3UBX	G_ARG_67	NH2	G_ASP_90	OD1	3.006
3UBX	G_ARG_67	NH2	G_ASP_90	OD2	2.366
3UBX	G_ARG_103	NH2	D_ASP_80	OD1	2.614
3UBX	G_LYS_215	NZ	L_GLU_123	OE1	3.204
3UBX	G_LYS_215	NZ	L_GLU_123	OE2	3.514
3UJI	L_LYS_53	NZ	L_GLU_50	OE1	2.671
3UJI	L_ARG_61	NH2	L_ASP_82	OD1	2.783
3UJI	L_ARG_61	NH2	L_ASP_82	OD2	3.833
3UJI	L_LYS_66	NZ	L_ASP_51	OD1	2.934
3UJI	L_LYS_66	NZ	L_ASP_51	OD2	3.132
3UJI	L_LYS_103	NZ	L_ASP_85	OD1	2.947
3UJI	L_LYS_103	NZ	L_ASP_85	OD2	3.475
3UJI	L_LYS_110	NZ	L_GLU_198	OE1	2.866
3UJI	L_LYS_110	NZ	L_GLU_198	OE2	3.915
3UJI	L_HIS_188	ND1	L_ASP_151	OD2	3.040
3UJI	L_LYS_189	NZ	L_ASP_151	OD1	3.884
3UJI	H_LYS_12	NZ	H_GLU_16	OE1	3.975
3UJI	H_LYS_73	NZ	H_ASP_53	OD2	3.330
3UJI	H_ARG_94	NH2	H_ASP_101	OD1	3.451
3UJI	H_ARG_94	NH2	H_ASP_101	OD2	2.842
3UJI	H_LYS_143	NZ	L_GLU_124	OE2	2.632
3UJI	H_LYS_206	NZ	H_ASP_208	OD1	3.500
3UJI	H_LYS_209	NZ	L_GLU_123	OE1	3.097
3UJI	H_LYS_209	NZ	L_GLU_123	OE2	2.701
3UJI	H_LYS_210	NZ	H_GLU_212	OE1	3.946
3UJI	H_LYS_210	NZ	H_GLU_212	OE2	3.699
3UJI	P_LYS_305	NZ	H_ASP_54	OD1	2.722
3UJI	P_LYS_305	NZ	H_ASP_54	OD2	3.687
3UJI	P_LYS_305	NZ	H_ASP_56	OD2	2.744
3UJI	P_HIS_308	ND1	H_GLU_98	OE1	2.731
3UJI	P_HIS_308	ND1	H_GLU_98	OE2	3.371
3UJJ	L_LYS_39	NZ	L_ASP_81	OD2	3.776
3UJJ	L_ARG_61	NH1	L_ASP_81	OD1	3.440
3UJJ	L_ARG_61	NH1	L_ASP_82	OD1	2.656
3UJJ	L_ARG_61	NH1	L_ASP_82	OD2	3.380
3UJJ	L_ARG_66	NH2	L_ASP_51	OD1	3.920
3UJJ	L_ARG_66	NH2	L_ASP_51	OD2	2.951
3UJJ	H_ARG_38	NH2	H_GLU_46	OE1	3.170
3UJJ	H_ARG_38	NH2	H_GLU_46	OE2	3.073

3UJJ	H_ARG_58	NH2	H_ASP_56	OD1	3.555
3UJJ	H_ARG_58	NH2	H_ASP_56	OD2	2.847
3UJJ	H_LYS_143	NZ	H_ASP_144	OD1	2.864
3UJJ	H_LYS_143	NZ	H_ASP_144	OD2	2.969
3UJJ	H_LYS_209	NZ	L_GLU_123	OE1	2.859
3UJJ	H_LYS_209	NZ	L_GLU_123	OE2	2.771
3UJJ	H_LYS_210	NZ	H_GLU_212	OE2	2.981
3UJJ	P_LYS_305	NZ	H_ASP_54	OD1	3.600
3UJJ	P_LYS_305	NZ	H_ASP_54	OD2	2.628
3UJJ	P_LYS_305	NZ	H_ASP_56	OD2	2.857
3UJJ	P_ARG_308	NH2	L_GLU_50	OE2	2.898
3UJT	H_LYS_19	NZ	H_ASP_78	OD1	2.829
3UJT	H_HIS_35	ND1	H_GLU_50	OE1	3.828
3UJT	H_HIS_35	NE2	H_GLU_50	OE1	3.223
3UJT	H_ARG_40	NH1	H_GLU_85	OE2	3.140
3UJT	H_LYS_64	NZ	H_GLU_61	OE1	2.811
3UJT	H_LYS_66	NZ	H_ASP_86	OD1	3.766
3UJT	H_LYS_66	NZ	H_ASP_86	OD2	2.865
3UJT	H_LYS_143	NZ	M_ASP_60	OD2	3.914
3UJT	H_LYS_208	NZ	L_GLU_123	OE2	2.966
3UJT	H_LYS_209	NZ	H_GLU_211	OE2	3.384
3UJT	L_ARG_61	NH2	L_ASP_82	OD1	2.769
3UJT	L_ARG_61	NH2	L_ASP_82	OD2	3.414
3UJT	L_LYS_103	NZ	L_ASP_85	OD1	3.942
3UJT	L_LYS_149	NZ	L_GLU_195	OE2	3.036
3UJT	L_ARG_155	NH1	L_GLU_185	OE1	2.986
3UJT	L_ARG_155	NH2	L_GLU_185	OE1	3.804
3UJT	L_LYS_183	NZ	L_GLU_187	OE1	3.131
3UJT	L_LYS_183	NZ	L_GLU_187	OE2	3.169
3UJT	L_HIS_189	ND1	L_ASP_151	OD2	3.929
3UJT	L_HIS_35	ND1	L_GLU_50	OE1	3.921
3UJT	L_HIS_35	NE2	L_GLU_50	OE1	3.458
3UJT	L_ARG_40	NH1	L_GLU_85	OE1	3.716
3UJT	L_LYS_66	NZ	L_ASP_86	OD1	3.625
3UJT	L_LYS_66	NZ	L_ASP_86	OD2	2.830
3UJT	L_HIS_164	NE2	M_ASP_167	OD1	3.917
3UJT	L_LYS_208	NZ	M_GLU_123	OE2	3.024
3UJT	L_LYS_209	NZ	L_GLU_211	OE2	3.830
3UJT	M_LYS_39	NZ	M_GLU_81	OE2	3.196
3UJT	M_ARG_61	NH2	M_GLU_81	OE1	3.337
3UJT	M_ARG_61	NH2	M_ASP_82	OD1	2.863
3UJT	M_ARG_61	NH2	M_ASP_82	OD2	3.614
3UJT	M_LYS_103	NZ	M_GLU_105	OE2	3.799
3UJT	M_LYS_147	NZ	M_GLU_154	OE1	3.066
3UJT	M_LYS_149	NZ	M_GLU_195	OE2	3.255
3UJT	M_LYS_183	NZ	M_GLU_187	OE1	3.301
3UJT	M_HIS_189	ND1	M_ASP_151	OD2	2.746
3UJT	M_LYS_199	NZ	M_ASP_110	OD2	3.794
3UO1	H_ARG_38	NH1	H_ASP_90	OD1	3.119
3UO1	H_ARG_38	NH2	H_GLU_46	OE1	3.165
3UO1	H_ARG_67	NH1	H_ASP_90	OD2	2.918
3UO1	H_ARG_67	NH2	H_ASP_90	OD1	3.039
3UO1	H_ARG_67	NH2	H_ASP_90	OD2	3.214
3UO1	H_ARG_87	NH1	H_GLU_89	OE2	3.676
3UO1	H_ARG_98	NH2	H_ASP_105	OD1	3.545
3UO1	H_ARG_98	NH2	H_ASP_105	OD2	2.915
3UO1	H_LYS_147	NZ	H_GLU_175	OE2	3.203
3UO1	H_LYS_212	NZ	L_GLU_127	OE2	2.634

3UO1	L_ARG_24	NH2	L_ASP_75	OD1	3.866
3UO1	L_ARG_66	NH1	L_ASP_87	OD1	3.885
3UO1	L_ARG_66	NH1	L_ASP_87	OD2	2.800
3UO1	L_ARG_66	NH2	L_GLU_84	OE1	3.875
3UO1	L_ARG_66	NH2	L_GLU_84	OE2	3.880
3UO1	L_ARG_66	NH2	L_ASP_87	OD1	3.014
3UO1	L_ARG_66	NH2	L_ASP_87	OD2	3.371
3UO1	L_LYS_153	NZ	L_GLU_199	OE1	3.850
3UO1	L_LYS_153	NZ	L_GLU_199	OE2	3.003
3UO1	L_ARG_159	NH1	L_GLU_189	OE1	3.609
3UO1	L_ARG_159	NH2	L_GLU_189	OE1	3.559
3UO1	L_ARG_192	NH2	L_ASP_188	OD1	3.033
3UO1	L_HIS_193	ND1	L_ASP_155	OD2	2.858
3UO1	L_LYS_203	NZ	L_ASP_114	OD2	3.912
3UYR	H_ARG_38	NH1	H_ASP_90	OD1	3.056
3UYR	H_ARG_38	NH2	H_GLU_46	OE1	3.014
3UYR	H_ARG_67	NH1	H_ASP_90	OD2	3.083
3UYR	H_ARG_67	NH2	H_ASP_90	OD1	3.206
3UYR	H_ARG_67	NH2	H_ASP_90	OD2	3.238
3UYR	H_ARG_98	NH2	H_ASP_105	OD1	3.584
3UYR	H_ARG_98	NH2	H_ASP_105	OD2	2.920
3UYR	H_LYS_212	NZ	L_GLU_127	OE2	2.869
3UYR	H_LYS_213	NZ	H_GLU_215	OE2	3.848
3UYR	L_ARG_24	NH1	L_ASP_75	OD1	3.439
3UYR	L_ARG_59	NH1	L_ASP_65	OD1	3.730
3UYR	L_ARG_66	NH1	L_ASP_87	OD1	3.905
3UYR	L_ARG_66	NH1	L_ASP_87	OD2	2.920
3UYR	L_ARG_66	NH2	L_GLU_84	OE1	3.701
3UYR	L_ARG_66	NH2	L_GLU_84	OE2	3.783
3UYR	L_ARG_66	NH2	L_ASP_87	OD1	3.182
3UYR	L_ARG_66	NH2	L_ASP_87	OD2	3.579
3UYR	L_LYS_153	NZ	L_GLU_199	OE2	3.046
3UYR	L_ARG_192	NH2	L_ASP_188	OD1	3.145
3UYR	L_HIS_193	ND1	L_ASP_155	OD2	2.932
3UYR	L_LYS_203	NZ	L_ASP_114	OD2	3.650
3V4P	A_HIS_28	NE2	A_ASP_138	OD1	3.437
3V4P	A_ARG_57	NH2	A_GLU_69	OE1	3.613
3V4P	A_ARG_57	NH2	A_GLU_69	OE2	3.235
3V4P	A_LYS_126	NZ	A_GLU_88	OE1	3.906
3V4P	A_LYS_126	NZ	A_GLU_88	OE2	3.280
3V4P	A_LYS_157	NZ	A_GLU_160	OE1	3.915
3V4P	A_LYS_203	NZ	A_GLU_255	OE2	3.829
3V4P	A_ARG_228	NH1	A_GLU_234	OE2	3.256
3V4P	A_ARG_228	NH2	A_GLU_234	OE2	3.842
3V4P	A_HIS_242	NE2	A_GLU_243	OE1	3.925
3V4P	A_LYS_247	NZ	A_GLU_263	OE2	2.474
3V4P	A_LYS_265	NZ	A_GLU_243	OE2	3.624
3V4P	A_ARG_305	NH1	A_ASP_329	OD1	2.732
3V4P	A_ARG_305	NH2	A_ASP_329	OD1	2.778
3V4P	A_ARG_305	NH2	A_ASP_329	OD2	3.464
3V4P	A_LYS_330	NZ	A_GLU_360	OE1	3.537
3V4P	A_LYS_330	NZ	A_ASP_361	OD1	3.264
3V4P	A_LYS_330	NZ	A_ASP_361	OD2	3.668
3V4P	A_ARG_334	NH1	A_GLU_337	OE1	3.017
3V4P	A_ARG_334	NH1	A_GLU_337	OE2	2.987
3V4P	A_ARG_334	NH2	A_GLU_302	OE2	3.593
3V4P	A_ARG_384	NH1	A_GLU_386	OE1	3.396
3V4P	A_ARG_384	NH2	A_GLU_360	OE1	2.505

3V4P	A_ARG_384	NH2	A_ASP_361	OD2	3.166
3V4P	A_ARG_384	NH2	A_GLU_386	OE1	3.325
3V4P	A_ARG_429	NH2	A_ASP_408	OD2	3.082
3V4P	A_ARG_499	NH1	A_ASP_489	OD2	3.923
3V4P	A_ARG_499	NH1	A_ASP_537	OD2	3.979
3V4P	A_ARG_532	NH1	A_ASP_534	OD2	3.421
3V4P	A_LYS_533	NZ	A_GLU_455	OE1	3.724
3V4P	A_LYS_533	NZ	A_GLU_455	OE2	3.681
3V4P	A_ARG_536	NH2	A_ASP_534	OD1	3.784
3V4P	A_LYS_574	NZ	A_ASP_375	OD1	2.978
3V4P	B_ARG_108	NH2	B_GLU_450	OE1	2.652
3V4P	B_ARG_110	NH1	B_GLU_85	OE1	3.635
3V4P	B_ARG_110	NH2	B_GLU_450	OE2	3.758
3V4P	B_ARG_124	NH2	B_ASP_89	OD1	3.110
3V4P	B_ARG_124	NH2	B_ASP_89	OD2	3.634
3V4P	B_LYS_146	NZ	B_GLU_202	OE2	2.939
3V4P	B_LYS_180	NZ	B_ASP_244	OD1	3.554
3V4P	B_LYS_180	NZ	B_ASP_244	OD2	2.740
3V4P	B_ARG_194	NH1	H_ASP_102	OD1	2.860
3V4P	B_ARG_194	NH1	H_ASP_102	OD2	2.764
3V4P	B_ARG_200	NH2	H_ASP_102	OD1	3.172
3V4P	B_ARG_259	NH2	B_ASP_134	OD1	2.676
3V4P	B_HIS_274	ND1	B_ASP_278	OD2	2.831
3V4P	B_HIS_274	NE2	B_ASP_179	OD2	3.371
3V4P	B_HIS_274	NE2	B_ASP_237	OD2	2.863
3V4P	B_HIS_293	NE2	B_ASP_289	OD1	2.750
3V4P	B_HIS_293	NE2	B_ASP_289	OD2	2.939
3V4P	B_ARG_302	NH2	B_GLU_305	OE1	3.376
3V4P	B_ARG_399	NH1	B_GLU_390	OE1	3.166
3V4P	B_ARG_399	NH1	B_GLU_390	OE2	2.988
3V4P	B_ARG_399	NH2	B_GLU_390	OE2	3.915
3V4P	B_LYS_402	NZ	B_GLU_404	OE2	3.864
3V4P	B_HIS_434	NE2	B_GLU_432	OE1	3.790
3V4P	B_ARG_439	NH2	B_GLU_377	OE1	3.416
3V4P	B_HIS_452	ND1	B_GLU_450	OE2	3.943
3V4P	C_HIS_28	NE2	C_ASP_138	OD1	3.435
3V4P	C_ARG_57	NH2	C_GLU_69	OE1	3.610
3V4P	C_ARG_57	NH2	C_GLU_69	OE2	3.231
3V4P	C_LYS_126	NZ	C_GLU_88	OE1	3.915
3V4P	C_LYS_126	NZ	C_GLU_88	OE2	3.295
3V4P	C_LYS_157	NZ	C_GLU_160	OE1	3.917
3V4P	C_LYS_203	NZ	C_GLU_255	OE2	3.826
3V4P	C_ARG_228	NH1	C_GLU_234	OE2	3.252
3V4P	C_ARG_228	NH2	C_GLU_234	OE2	3.840
3V4P	C_HIS_242	NE2	C_GLU_243	OE1	3.935
3V4P	C_LYS_247	NZ	C_GLU_263	OE2	2.476
3V4P	C_LYS_265	NZ	C_GLU_243	OE2	3.624
3V4P	C_ARG_305	NH1	C_ASP_329	OD1	2.736
3V4P	C_ARG_305	NH2	C_ASP_329	OD1	2.777
3V4P	C_ARG_305	NH2	C_ASP_329	OD2	3.462
3V4P	C_LYS_330	NZ	C_GLU_360	OE1	3.551
3V4P	C_LYS_330	NZ	C_ASP_361	OD1	3.262
3V4P	C_LYS_330	NZ	C_ASP_361	OD2	3.668
3V4P	C_ARG_334	NH1	C_GLU_337	OE1	3.021
3V4P	C_ARG_334	NH1	C_GLU_337	OE2	2.997
3V4P	C_ARG_334	NH2	C_GLU_302	OE2	3.598
3V4P	C_ARG_384	NH1	C_GLU_386	OE1	3.393
3V4P	C_ARG_384	NH2	C_GLU_360	OE1	2.506

3V4P	C_ARG_384	NH2	C_ASP_361	OD2	3.170
3V4P	C_ARG_384	NH2	C_GLU_386	OE1	3.316
3V4P	C_ARG_429	NH2	C_ASP_408	OD2	3.082
3V4P	C_ARG_499	NH1	C_ASP_489	OD2	3.928
3V4P	C_ARG_499	NH1	C_ASP_537	OD2	3.667
3V4P	C_ARG_532	NH1	C_ASP_534	OD2	3.504
3V4P	C_LYS_533	NZ	C_GLU_455	OE1	3.658
3V4P	C_ARG_536	NH2	C_ASP_534	OD1	3.773
3V4P	C_LYS_574	NZ	C_ASP_375	OD1	3.893
3V4P	D_ARG_108	NH2	D_GLU_450	OE1	2.653
3V4P	D_ARG_110	NH1	D_GLU_85	OE1	3.633
3V4P	D_ARG_110	NH2	D_GLU_450	OE2	3.756
3V4P	D_ARG_124	NH2	D_ASP_89	OD1	3.117
3V4P	D_ARG_124	NH2	D_ASP_89	OD2	3.640
3V4P	D_LYS_146	NZ	D_GLU_202	OE2	2.944
3V4P	D_LYS_180	NZ	D_ASP_244	OD1	3.559
3V4P	D_LYS_180	NZ	D_ASP_244	OD2	2.747
3V4P	D_ARG_194	NH1	M_ASP_102	OD1	2.738
3V4P	D_ARG_194	NH1	M_ASP_102	OD2	2.760
3V4P	D_ARG_200	NH2	M_ASP_102	OD1	3.233
3V4P	D_ARG_259	NH2	D_ASP_134	OD1	2.676
3V4P	D_HIS_274	ND1	D_ASP_278	OD2	2.837
3V4P	D_HIS_274	NE2	D_ASP_179	OD2	3.371
3V4P	D_HIS_274	NE2	D_ASP_237	OD2	2.865
3V4P	D_HIS_293	NE2	D_ASP_289	OD1	2.751
3V4P	D_HIS_293	NE2	D_ASP_289	OD2	2.938
3V4P	D_ARG_302	NH2	D_GLU_305	OE1	3.367
3V4P	D_ARG_399	NH1	D_GLU_390	OE1	3.160
3V4P	D_ARG_399	NH1	D_GLU_390	OE2	2.983
3V4P	D_ARG_399	NH2	D_GLU_390	OE2	3.909
3V4P	D_LYS_402	NZ	D_GLU_404	OE2	3.866
3V4P	D_HIS_434	NE2	D_GLU_432	OE1	3.794
3V4P	D_ARG_439	NH2	D_GLU_377	OE1	3.413
3V4P	D_HIS_452	ND1	D_GLU_450	OE2	3.942
3V4P	H_HIS_35	ND1	H_GLU_50	OE1	3.827
3V4P	H_ARG_40	NH1	H_GLU_46	OE2	3.925
3V4P	H_ARG_40	NH2	H_GLU_46	OE2	3.891
3V4P	H_LYS_63	NZ	H_GLU_46	OE1	3.617
3V4P	H_LYS_67	NZ	H_ASP_90	OD1	3.016
3V4P	H_LYS_67	NZ	H_ASP_90	OD2	2.785
3V4P	H_ARG_98	NH2	H_ASP_109	OD1	3.538
3V4P	H_ARG_98	NH2	H_ASP_109	OD2	2.869
3V4P	H_LYS_151	NZ	H_GLU_179	OE1	3.924
3V4P	H_LYS_151	NZ	H_GLU_179	OE2	3.342
3V4P	H_HIS_172	ND1	L_ASP_172	OD2	3.780
3V4P	H_LYS_216	NZ	L_GLU_128	OE2	3.270
3V4P	L_ARG_24	NH2	L_ASP_75	OD2	3.872
3V4P	L_ARG_66	NH2	L_GLU_86	OE1	3.540
3V4P	L_ARG_66	NH2	L_ASP_87	OD1	2.923
3V4P	L_ARG_66	NH2	L_ASP_87	OD2	3.479
3V4P	L_HIS_194	ND1	L_ASP_156	OD1	3.668
3V4P	L_HIS_194	ND1	L_ASP_156	OD2	3.022
3V4P	M_HIS_35	ND1	M_GLU_50	OE1	3.826
3V4P	M_ARG_40	NH1	M_GLU_46	OE2	3.929
3V4P	M_ARG_40	NH2	M_GLU_46	OE2	3.895
3V4P	M_LYS_63	NZ	M_GLU_46	OE1	3.628
3V4P	M_LYS_67	NZ	M_ASP_90	OD1	3.021
3V4P	M_LYS_67	NZ	M_ASP_90	OD2	2.783

3V4P	M_ARG_98	NH2	M_ASP_109	OD1	3.527
3V4P	M_ARG_98	NH2	M_ASP_109	OD2	2.863
3V4P	M_LYS_151	NZ	M_GLU_179	OE1	3.922
3V4P	M_LYS_151	NZ	M_GLU_179	OE2	3.343
3V4P	M_HIS_172	ND1	N_ASP_172	OD2	3.600
3V4P	M_LYS_216	NZ	N_GLU_128	OE2	3.408
3V4P	N_ARG_24	NH2	N_ASP_75	OD2	3.878
3V4P	N_ARG_66	NH2	N_GLU_86	OE1	3.541
3V4P	N_ARG_66	NH2	N_ASP_87	OD1	2.925
3V4P	N_ARG_66	NH2	N_ASP_87	OD2	3.479
3V4P	N_HIS_194	ND1	N_ASP_156	OD1	3.669
3V4P	N_HIS_194	ND1	N_ASP_156	OD2	3.021
3V4U	H_ARG_38	NH1	H_ASP_90	OD1	3.026
3V4U	H_ARG_38	NH2	H_GLU_46	OE1	2.923
3V4U	H_ARG_38	NH2	H_ASP_90	OD1	3.942
3V4U	H_ARG_67	NH1	H_ASP_90	OD2	3.062
3V4U	H_ARG_67	NH2	H_ASP_90	OD1	3.515
3V4U	H_ARG_67	NH2	H_ASP_90	OD2	3.172
3V4U	H_ARG_98	NH2	H_ASP_105	OD1	3.657
3V4U	H_ARG_98	NH2	H_ASP_105	OD2	3.151
3V4U	H_LYS_147	NZ	H_GLU_175	OE2	2.827
3V4U	H_LYS_212	NZ	L_GLU_127	OE2	2.667
3V4U	L_ARG_24	NH2	L_ASP_75	OD1	3.756
3V4U	L_ARG_66	NH1	L_ASP_87	OD1	3.777
3V4U	L_ARG_66	NH1	L_ASP_87	OD2	2.819
3V4U	L_ARG_66	NH2	L_GLU_84	OE1	3.720
3V4U	L_ARG_66	NH2	L_GLU_84	OE2	3.860
3V4U	L_ARG_66	NH2	L_ASP_87	OD1	2.775
3V4U	L_ARG_66	NH2	L_ASP_87	OD2	3.243
3V4U	L_LYS_153	NZ	L_GLU_199	OE1	3.350
3V4U	L_LYS_153	NZ	L_GLU_199	OE2	2.923
3V4U	L_ARG_159	NH1	L_GLU_189	OE1	2.754
3V4U	L_ARG_159	NH2	L_GLU_189	OE1	3.366
3V4U	L_LYS_187	NZ	L_GLU_191	OE2	3.065
3V4U	L_ARG_192	NH2	L_ASP_188	OD1	3.394
3V4V	A_HIS_28	NE2	A_ASP_138	OD1	3.625
3V4V	A_ARG_57	NH2	A_GLU_69	OE2	3.446
3V4V	A_LYS_126	NZ	A_GLU_88	OE1	3.984
3V4V	A_LYS_126	NZ	A_GLU_88	OE2	3.844
3V4V	A_LYS_157	NZ	A_GLU_160	OE1	3.707
3V4V	A_LYS_203	NZ	A_GLU_255	OE2	4.000
3V4V	A_ARG_228	NH2	A_GLU_234	OE2	3.810
3V4V	A_HIS_242	NE2	A_GLU_243	OE1	3.962
3V4V	A_LYS_247	NZ	A_GLU_263	OE2	2.864
3V4V	A_ARG_301	NH2	A_GLU_302	OE1	3.852
3V4V	A_ARG_305	NH1	A_ASP_329	OD1	2.728
3V4V	A_ARG_305	NH2	A_ASP_329	OD1	2.929
3V4V	A_ARG_305	NH2	A_ASP_329	OD2	3.468
3V4V	A_LYS_330	NZ	A_GLU_360	OE1	3.937
3V4V	A_LYS_330	NZ	A_ASP_361	OD1	3.025
3V4V	A_LYS_330	NZ	A_ASP_361	OD2	3.585
3V4V	A_ARG_334	NH1	A_GLU_337	OE1	3.450
3V4V	A_ARG_334	NH1	A_GLU_337	OE2	3.152
3V4V	A_ARG_334	NH2	A_GLU_302	OE2	3.584
3V4V	A_ARG_384	NH1	A_GLU_386	OE1	3.340
3V4V	A_ARG_384	NH2	A_GLU_360	OE1	2.718
3V4V	A_ARG_384	NH2	A_ASP_361	OD2	3.178
3V4V	A_ARG_384	NH2	A_GLU_386	OE1	2.970

3V4V	A_ARG_429	NH2	A_ASP_408	OD2	2.821
3V4V	A_ARG_499	NH1	A_ASP_489	OD2	3.736
3V4V	A_ARG_499	NH1	A_ASP_537	OD2	3.000
3V4V	A_ARG_499	NH2	A_ASP_537	OD2	3.346
3V4V	A_ARG_532	NH1	A_ASP_534	OD2	3.643
3V4V	A_LYS_533	NZ	A_GLU_455	OE1	3.618
3V4V	A_ARG_536	NH2	A_ASP_534	OD1	3.812
3V4V	A_LYS_574	NZ	A_ASP_375	OD1	3.230
3V4V	A_LYS_574	NZ	A_ASP_375	OD2	3.530
3V4V	B_ARG_108	NH2	B_GLU_450	OE1	2.540
3V4V	B_ARG_110	NH1	B_GLU_85	OE1	3.653
3V4V	B_ARG_110	NH2	B_GLU_450	OE2	3.788
3V4V	B_ARG_124	NH2	B_ASP_89	OD1	3.503
3V4V	B_LYS_180	NZ	B_ASP_244	OD1	3.343
3V4V	B_LYS_180	NZ	B_ASP_244	OD2	2.615
3V4V	B_ARG_194	NH1	H_ASP_102	OD1	2.874
3V4V	B_ARG_194	NH1	H_ASP_102	OD2	3.211
3V4V	B_ARG_200	NH2	H_ASP_102	OD1	3.237
3V4V	B_ARG_259	NH2	B_ASP_134	OD1	2.874
3V4V	B_HIS_274	ND1	B_ASP_278	OD2	3.045
3V4V	B_HIS_274	NE2	B_ASP_179	OD2	3.250
3V4V	B_HIS_274	NE2	B_ASP_237	OD2	3.128
3V4V	B_HIS_293	NE2	B_ASP_289	OD1	2.625
3V4V	B_HIS_293	NE2	B_ASP_289	OD2	2.924
3V4V	B_ARG_302	NH2	B_GLU_305	OE1	3.474
3V4V	B_ARG_399	NH1	B_GLU_390	OE1	2.982
3V4V	B_ARG_399	NH1	B_GLU_390	OE2	2.814
3V4V	B_ARG_399	NH2	B_GLU_390	OE2	3.187
3V4V	B_LYS_402	NZ	B_GLU_404	OE2	3.543
3V4V	B_HIS_434	NE2	B_GLU_432	OE1	3.549
3V4V	B_ARG_439	NH2	B_GLU_377	OE1	3.529
3V4V	B_HIS_452	ND1	B_GLU_450	OE2	3.839
3V4V	H_HIS_35	ND1	H_GLU_50	OE1	3.868
3V4V	H_HIS_35	NE2	H_GLU_50	OE1	3.873
3V4V	H_ARG_40	NH2	H_GLU_89	OE1	3.118
3V4V	H_LYS_63	NZ	H_GLU_46	OE1	3.657
3V4V	H_LYS_67	NZ	H_ASP_90	OD1	2.996
3V4V	H_LYS_67	NZ	H_ASP_90	OD2	2.684
3V4V	H_ARG_98	NH2	H_ASP_109	OD1	3.554
3V4V	H_ARG_98	NH2	H_ASP_109	OD2	2.682
3V4V	H_LYS_151	NZ	H_GLU_179	OE2	3.864
3V4V	H_HIS_172	ND1	L_ASP_172	OD1	3.644
3V4V	H_LYS_216	NZ	L_GLU_128	OE2	3.607
3V4V	L_ARG_66	NH2	L_GLU_86	OE1	3.477
3V4V	L_ARG_66	NH2	L_ASP_87	OD1	3.326
3V4V	L_ARG_66	NH2	L_ASP_87	OD2	3.224
3V4V	L_LYS_152	NZ	L_GLU_200	OE2	3.741
3V4V	L_HIS_194	ND1	L_ASP_156	OD1	3.854
3V4V	L_HIS_194	ND1	L_ASP_156	OD2	2.969
3V4V	C_HIS_28	NE2	C_ASP_138	OD1	3.619
3V4V	C_ARG_57	NH2	C_GLU_69	OE2	3.454
3V4V	C_LYS_126	NZ	C_GLU_88	OE1	3.966
3V4V	C_LYS_126	NZ	C_GLU_88	OE2	3.832
3V4V	C_LYS_157	NZ	C_GLU_160	OE1	3.712
3V4V	C_ARG_228	NH2	C_GLU_234	OE2	3.809
3V4V	C_HIS_242	NE2	C_GLU_243	OE1	3.957
3V4V	C_LYS_247	NZ	C_GLU_263	OE2	2.858
3V4V	C_ARG_301	NH2	C_GLU_302	OE1	3.856

3V4V	C_ARG_305	NH1	C_ASP_329	OD1	2.717
3V4V	C_ARG_305	NH2	C_ASP_329	OD1	2.917
3V4V	C_ARG_305	NH2	C_ASP_329	OD2	3.457
3V4V	C_LYS_330	NZ	C_GLU_360	OE1	3.928
3V4V	C_LYS_330	NZ	C_ASP_361	OD1	3.024
3V4V	C_LYS_330	NZ	C_ASP_361	OD2	3.579
3V4V	C_ARG_334	NH1	C_GLU_337	OE1	3.446
3V4V	C_ARG_334	NH1	C_GLU_337	OE2	3.179
3V4V	C_ARG_334	NH2	C_GLU_302	OE2	3.589
3V4V	C_ARG_373	NH2	C_GLU_575	OE2	3.832
3V4V	C_ARG_384	NH1	C_GLU_386	OE1	3.331
3V4V	C_ARG_384	NH2	C_GLU_360	OE1	2.721
3V4V	C_ARG_384	NH2	C_ASP_361	OD2	3.178
3V4V	C_ARG_384	NH2	C_GLU_386	OE1	2.966
3V4V	C_ARG_429	NH2	C_ASP_408	OD2	2.836
3V4V	C_ARG_499	NH1	C_ASP_489	OD2	3.733
3V4V	C_ARG_499	NH1	C_ASP_537	OD2	3.002
3V4V	C_ARG_499	NH2	C_ASP_537	OD2	3.340
3V4V	C_ARG_532	NH1	C_ASP_534	OD2	3.655
3V4V	C_LYS_533	NZ	C_GLU_455	OE1	3.182
3V4V	C_LYS_533	NZ	C_GLU_455	OE2	3.301
3V4V	C_ARG_536	NH2	C_ASP_534	OD1	3.809
3V4V	C_LYS_573	NZ	C_ASP_577	OD1	3.849
3V4V	C_LYS_574	NZ	C_ASP_346	OD2	3.367
3V4V	C_LYS_574	NZ	C_ASP_348	OD2	3.730
3V4V	D_ARG_108	NH2	D_GLU_450	OE1	2.539
3V4V	D_ARG_110	NH1	D_GLU_85	OE1	3.659
3V4V	D_ARG_110	NH2	D_GLU_450	OE2	3.785
3V4V	D_ARG_124	NH2	D_ASP_89	OD1	3.506
3V4V	D_LYS_146	NZ	D_GLU_202	OE2	3.999
3V4V	D_LYS_180	NZ	D_ASP_244	OD1	3.344
3V4V	D_LYS_180	NZ	D_ASP_244	OD2	2.642
3V4V	D_ARG_194	NH1	M_ASP_102	OD1	2.657
3V4V	D_ARG_194	NH1	M_ASP_102	OD2	2.923
3V4V	D_ARG_200	NH2	M_ASP_102	OD1	3.070
3V4V	D_ARG_259	NH2	D_ASP_134	OD1	2.871
3V4V	D_HIS_274	ND1	D_ASP_278	OD2	3.033
3V4V	D_HIS_274	NE2	D_ASP_179	OD2	3.229
3V4V	D_HIS_274	NE2	D_ASP_237	OD2	3.108
3V4V	D_HIS_293	NE2	D_ASP_289	OD1	2.628
3V4V	D_HIS_293	NE2	D_ASP_289	OD2	2.920
3V4V	D_ARG_302	NH2	D_GLU_305	OE1	3.475
3V4V	D_ARG_399	NH1	D_GLU_390	OE1	2.981
3V4V	D_ARG_399	NH1	D_GLU_390	OE2	2.805
3V4V	D_ARG_399	NH2	D_GLU_390	OE2	3.180
3V4V	D_LYS_402	NZ	D_GLU_404	OE2	3.526
3V4V	D_HIS_434	NE2	D_GLU_432	OE1	3.565
3V4V	D_ARG_439	NH2	D_GLU_377	OE1	3.517
3V4V	D_HIS_452	ND1	D_GLU_450	OE2	3.844
3V4V	M_HIS_35	ND1	M_GLU_50	OE1	3.871
3V4V	M_HIS_35	NE2	M_GLU_50	OE1	3.860
3V4V	M_ARG_40	NH2	M_GLU_89	OE1	3.456
3V4V	M_LYS_63	NZ	M_GLU_46	OE1	3.661
3V4V	M_LYS_67	NZ	M_ASP_90	OD1	2.998
3V4V	M_LYS_67	NZ	M_ASP_90	OD2	2.683
3V4V	M_ARG_98	NH2	M_ASP_109	OD1	3.565
3V4V	M_ARG_98	NH2	M_ASP_109	OD2	2.672
3V4V	M_LYS_151	NZ	M_GLU_179	OE2	3.863

3V4V	M_HIS_172	ND1	N_ASP_172	OD1	3.594
3V4V	M_LYS_216	NZ	N_GLU_128	OE2	3.217
3V4V	N_ARG_66	NH2	N_GLU_86	OE1	3.488
3V4V	N_ARG_66	NH2	N_ASP_87	OD1	3.328
3V4V	N_ARG_66	NH2	N_ASP_87	OD2	3.226
3V4V	N_LYS_152	NZ	N_GLU_200	OE2	3.759
3V4V	N_HIS_194	ND1	N_ASP_156	OD1	3.862
3V4V	N_HIS_194	ND1	N_ASP_156	OD2	2.969
3V52	H_ARG_38	NH1	H_ASP_90	OD1	3.011
3V52	H_ARG_38	NH2	H_GLU_46	OE1	2.934
3V52	H_ARG_67	NH1	H_ASP_90	OD2	3.055
3V52	H_ARG_67	NH2	H_ASP_90	OD1	3.178
3V52	H_ARG_67	NH2	H_ASP_90	OD2	3.296
3V52	H_ARG_98	NH2	H_ASP_105	OD1	3.591
3V52	H_ARG_98	NH2	H_ASP_105	OD2	2.829
3V52	H_LYS_212	NZ	L_GLU_127	OE2	2.929
3V52	H_LYS_213	NZ	H_GLU_215	OE2	3.959
3V52	L_ARG_66	NH1	L_ASP_87	OD1	3.858
3V52	L_ARG_66	NH1	L_ASP_87	OD2	2.692
3V52	L_ARG_66	NH2	L_GLU_84	OE1	3.797
3V52	L_ARG_66	NH2	L_GLU_84	OE2	3.912
3V52	L_ARG_66	NH2	L_ASP_87	OD1	3.033
3V52	L_ARG_66	NH2	L_ASP_87	OD2	3.323
3V52	L_LYS_153	NZ	L_GLU_199	OE2	2.980
3V52	L_ARG_159	NH1	L_GLU_189	OE1	3.150
3V52	L_ARG_159	NH2	L_GLU_189	OE1	2.854
3V52	L_ARG_192	NH2	L_ASP_188	OD1	3.092
3V52	L_ARG_192	NH2	L_ASP_188	OD2	3.931
3V52	L_HIS_193	ND1	L_ASP_155	OD2	2.916
3V52	L_LYS_203	NZ	L_ASP_114	OD2	2.574
3V6F	A_ARG_38	NH1	A_ASP_86	OD1	2.911
3V6F	A_ARG_38	NH2	A_GLU_46	OE1	3.291
3V6F	A_ARG_38	NH2	A_GLU_46	OE2	3.661
3V6F	A_ARG_38	NH2	A_ASP_86	OD1	3.667
3V6F	A_LYS_64	NZ	A_ASP_61	OD1	2.842
3V6F	A_ARG_66	NH1	A_ASP_86	OD1	3.978
3V6F	A_ARG_66	NH1	A_ASP_86	OD2	2.845
3V6F	A_ARG_66	NH2	A_ASP_86	OD1	3.048
3V6F	A_ARG_66	NH2	A_ASP_86	OD2	3.388
3V6F	A_LYS_75	NZ	A_ASP_72	OD2	3.618
3V6F	A_ARG_94	NH1	A_ASP_106	OD1	3.312
3V6F	A_ARG_94	NH1	A_ASP_106	OD2	3.358
3V6F	A_LYS_213	NZ	B_GLU_130	OE1	3.799
3V6F	B_ARG_60	NH1	B_ASP_66	OD1	3.189
3V6F	B_ARG_60	NH2	B_ASP_66	OD1	3.662
3V6F	B_ARG_67	NH2	B_ASP_88	OD1	2.925
3V6F	B_ARG_67	NH2	B_ASP_88	OD2	3.716
3V6F	B_ARG_162	NH1	B_GLU_192	OE2	3.473
3V6F	B_ARG_195	NH1	B_GLU_192	OE1	3.435
3V6F	B_ARG_195	NH1	B_GLU_192	OE2	2.954
3V6F	B_HIS_196	ND1	B_GLU_192	OE2	3.778
3V6F	C_ARG_38	NH1	C_ASP_86	OD1	2.982
3V6F	C_ARG_38	NH2	C_GLU_46	OE1	3.377
3V6F	C_ARG_38	NH2	C_GLU_46	OE2	3.714
3V6F	C_ARG_38	NH2	C_ASP_86	OD1	3.729
3V6F	C_LYS_64	NZ	C_ASP_61	OD1	2.824
3V6F	C_ARG_66	NH1	C_ASP_86	OD1	3.704
3V6F	C_ARG_66	NH1	C_ASP_86	OD2	2.748

3V6F	C_ARG.66	NH2	C_ASP.86	OD1	3.318
3V6F	C_ARG.66	NH2	C_ASP.86	OD2	3.791
3V6F	C_LYS.75	NZ	C_ASP.72	OD2	3.653
3V6F	C_ARG.94	NH1	C_ASP.106	OD1	3.027
3V6F	C_ARG.94	NH1	C_ASP.106	OD2	2.907
3V6F	C_LYS.213	NZ	D_GLU.130	OE1	3.956
3V6F	D_ARG.60	NH1	D_ASP.66	OD1	3.192
3V6F	D_ARG.60	NH2	D_ASP.66	OD1	3.669
3V6F	D_ARG.67	NH2	D_ASP.88	OD1	2.880
3V6F	D_ARG.67	NH2	D_ASP.88	OD2	3.702
3V6F	D_ARG.162	NH1	D_GLU.192	OE2	3.490
3V6F	D_ARG.195	NH1	D_GLU.192	OE1	3.464
3V6F	D_ARG.195	NH1	D_GLU.192	OE2	2.977
3V6F	D_HIS.196	ND1	D_GLU.192	OE2	3.829
3V6F	E_ARG.38	NH1	E_ASP.86	OD1	2.938
3V6F	E_ARG.38	NH2	E_GLU.46	OE1	3.288
3V6F	E_ARG.38	NH2	E_GLU.46	OE2	3.689
3V6F	E_ARG.38	NH2	E_ASP.86	OD1	3.691
3V6F	E_LYS.64	NZ	E_ASP.61	OD1	3.118
3V6F	E_ARG.66	NH1	E_ASP.86	OD1	3.831
3V6F	E_ARG.66	NH1	E_ASP.86	OD2	2.617
3V6F	E_ARG.66	NH2	E_ASP.86	OD1	2.929
3V6F	E_ARG.66	NH2	E_ASP.86	OD2	3.284
3V6F	E_LYS.75	NZ	E_ASP.72	OD2	3.617
3V6F	E_ARG.94	NH1	E_ASP.106	OD1	3.312
3V6F	E_ARG.94	NH1	E_ASP.106	OD2	3.177
3V6F	E_LYS.213	NZ	F_GLU.130	OE1	3.763
3V6F	F_ARG.60	NH1	F_ASP.66	OD1	3.236
3V6F	F_ARG.60	NH2	F_ASP.66	OD1	3.718
3V6F	F_ARG.67	NH2	F_ASP.88	OD1	2.889
3V6F	F_ARG.67	NH2	F_ASP.88	OD2	3.693
3V6F	F_LYS.114	NZ	F_GLU.17	OE1	3.958
3V6F	F_ARG.162	NH1	F_GLU.192	OE2	3.447
3V6F	F_ARG.195	NH1	F_GLU.192	OE1	3.438
3V6F	F_ARG.195	NH1	F_GLU.192	OE2	2.943
3V6F	F_HIS.196	ND1	F_GLU.192	OE2	3.828
3V6F	H_ARG.38	NH1	H_ASP.86	OD1	2.929
3V6F	H_ARG.38	NH2	H_GLU.46	OE1	3.278
3V6F	H_ARG.38	NH2	H_GLU.46	OE2	3.715
3V6F	H_ARG.38	NH2	H_ASP.86	OD1	3.746
3V6F	H_LYS.64	NZ	H_ASP.61	OD1	2.949
3V6F	H_ARG.66	NH1	H_ASP.86	OD1	3.602
3V6F	H_ARG.66	NH1	H_ASP.86	OD2	2.554
3V6F	H_ARG.66	NH2	H_ASP.86	OD1	2.925
3V6F	H_ARG.66	NH2	H_ASP.86	OD2	3.444
3V6F	H_LYS.75	NZ	H_ASP.72	OD2	3.633
3V6F	H_ARG.94	NH1	H_ASP.106	OD1	3.513
3V6F	H_ARG.94	NH1	H_ASP.106	OD2	2.779
3V6F	H_HIS.169	NE2	L_ASP.174	OD1	3.656
3V6F	L_ARG.60	NH1	L_ASP.66	OD1	3.201
3V6F	L_ARG.60	NH2	L_ASP.66	OD1	3.668
3V6F	L_ARG.67	NH2	L_ASP.88	OD1	2.904
3V6F	L_ARG.67	NH2	L_ASP.88	OD2	3.773
3V6F	L_ARG.162	NH1	L_GLU.192	OE2	3.508
3V6F	L_ARG.195	NH1	L_GLU.192	OE1	3.445
3V6F	L_ARG.195	NH1	L_GLU.192	OE2	2.967
3V6F	L_HIS.196	ND1	L_GLU.192	OE2	3.834
3WIH	L_ARG.24	NH1	L_ASP.70	OD1	3.918

3WIH	L_ARG_24	NH1	L_ASP_70	OD2	2.824
3WIH	L_ARG_61	NH1	L_GLU_81	OE1	3.206
3WIH	L_ARG_61	NH1	L_ASP_82	OD1	2.733
3WIH	L_ARG_61	NH1	L_ASP_82	OD2	3.500
3WIH	L_LYS_103	NZ	L_GLU_105	OE2	3.849
3WIH	L_LYS_149	NZ	L_GLU_195	OE1	3.529
3WIH	L_LYS_149	NZ	L_GLU_195	OE2	2.994
3WIH	L_ARG_155	NH1	L_GLU_185	OE2	3.108
3WIH	L_ARG_155	NH2	L_GLU_185	OE1	3.573
3WIH	L_ARG_155	NH2	L_GLU_185	OE2	3.738
3WIH	L_LYS_183	NZ	L_GLU_187	OE1	2.854
3WIH	L_LYS_183	NZ	L_GLU_187	OE2	2.954
3WIH	L_HIS_189	ND1	L_ASP_151	OD2	2.633
3WIH	L_LYS_199	NZ	L_GLU_110	OE2	3.646
3WIH	H_LYS_67	NZ	H_ASP_90	OD1	3.761
3WIH	H_LYS_67	NZ	H_ASP_90	OD2	2.892
3WIH	H_ARG_98	NH2	H_ASP_107	OD1	3.653
3WIH	H_ARG_98	NH2	H_ASP_107	OD2	2.796
3WIH	H_LYS_214	NZ	L_GLU_123	OE2	3.755
3WIH	H_LYS_215	NZ	H_GLU_217	OE2	3.819
3WIH	M_ARG_61	NH1	M_GLU_81	OE1	3.086
3WIH	M_ARG_61	NH1	M_ASP_82	OD1	2.841
3WIH	M_ARG_61	NH1	M_ASP_82	OD2	3.629
3WIH	M_LYS_103	NZ	M_GLU_105	OE2	3.685
3WIH	M_LYS_147	NZ	M_GLU_154	OE1	3.932
3WIH	M_LYS_149	NZ	M_GLU_195	OE1	3.414
3WIH	M_LYS_149	NZ	M_GLU_195	OE2	2.992
3WIH	M_ARG_155	NH1	M_GLU_185	OE2	3.084
3WIH	M_ARG_155	NH2	M_GLU_185	OE1	3.729
3WIH	M_ARG_155	NH2	M_GLU_185	OE2	3.794
3WIH	M_HIS_189	ND1	M_ASP_151	OD2	2.674
3WIH	I_LYS_67	NZ	I_ASP_90	OD1	3.687
3WIH	I_LYS_67	NZ	I_ASP_90	OD2	2.807
3WIH	I_ARG_98	NH2	I_ASP_107	OD1	3.645
3WIH	I_ARG_98	NH2	I_ASP_107	OD2	2.793
3WIH	I_LYS_214	NZ	M_GLU_123	OE1	2.678
3WIH	I_LYS_214	NZ	M_GLU_123	OE2	3.619
3WIH	I_LYS_215	NZ	I_GLU_217	OE2	3.670
3WN5	A_ARG_255	NH1	A_ASP_249	OD1	2.832
3WN5	A_HIS_285	NE2	A_GLU_283	OE2	3.642
3WN5	A_LYS_317	NZ	A_ASP_312	OD1	2.941
3WN5	A_LYS_320	NZ	A_GLU_333	OE1	3.207
3WN5	A_LYS_338	NZ	A_GLU_430	OE1	3.924
3WN5	A_LYS_338	NZ	A_GLU_430	OE2	3.222
3WN5	A_LYS_370	NZ	B_GLU_357	OE2	3.815
3WN5	A_LYS_409	NZ	B_ASP_399	OD2	3.327
3WN5	A_ARG_416	NH1	A_GLU_388	OE1	3.624
3WN5	A_ARG_416	NH1	A_GLU_388	OE2	3.234
3WN5	A_ARG_416	NH2	A_GLU_388	OE1	2.983
3WN5	A_ARG_416	NH2	A_GLU_388	OE2	3.949
3WN5	B_LYS_248	NZ	B_GLU_380	OE1	2.957
3WN5	B_LYS_248	NZ	B_GLU_380	OE2	3.881
3WN5	B_ARG_255	NH1	B_ASP_249	OD1	2.667
3WN5	B_HIS_285	NE2	B_GLU_283	OE2	2.816
3WN5	B_LYS_317	NZ	B_ASP_312	OD1	3.123
3WN5	B_LYS_320	NZ	B_GLU_333	OE1	3.014
3WN5	B_LYS_338	NZ	B_GLU_430	OE1	3.374
3WN5	B_LYS_370	NZ	A_GLU_357	OE1	3.801

3WN5	B_LYS_409	NZ	A_ASP_399	OD1	3.830
3WN5	B_LYS_409	NZ	A_ASP_399	OD2	3.511
3WN5	B_ARG_416	NH1	B_GLU_388	OE1	2.996
3WN5	B_ARG_416	NH1	B_GLU_388	OE2	3.505
3WN5	B_ARG_416	NH2	B_GLU_388	OE1	3.528
3WN5	B_ARG_416	NH2	B_GLU_388	OE2	2.698
3WN5	C_LYS_4	NZ	C_ASP_77	OD1	3.098
3WN5	C_LYS_4	NZ	C_ASP_77	OD2	2.841
3WN5	C_ARG_67	NH1	C_GLU_65	OE1	3.514
3WN5	C_HIS_84	ND1	C_GLU_163	OE1	3.890
3WN5	C_HIS_84	NE2	C_GLU_82	OE1	2.954
3WN5	C_HIS_104	NE2	C_ASP_135	OD2	2.827
3WN5	C_HIS_108	ND1	C_ASP_20	OD2	3.561
3WN5	C_HIS_108	NE2	C_ASP_20	OD1	3.787
3WN5	C_LYS_117	NZ	B_ASP_265	OD2	2.853
3WN5	C_ARG_127	NH1	C_ASP_145	OD1	3.210
3WN5	C_ARG_127	NH2	C_ASP_145	OD1	3.171
3WN5	C_HIS_131	NE2	B_ASP_270	OD1	3.342
3WN5	C_HIS_131	NE2	B_ASP_270	OD2	2.619
3WN5	D_LYS_248	NZ	D_GLU_380	OE1	2.793
3WN5	D_LYS_248	NZ	D_GLU_380	OE2	3.908
3WN5	D_HIS_268	NE2	D_GLU_294	OE2	3.025
3WN5	D_HIS_285	NE2	D_GLU_283	OE2	3.554
3WN5	D_LYS_317	NZ	D_ASP_312	OD1	2.899
3WN5	D_LYS_320	NZ	D_GLU_333	OE1	3.733
3WN5	D_LYS_338	NZ	D_GLU_430	OE1	3.660
3WN5	D_LYS_338	NZ	D_GLU_430	OE2	3.172
3WN5	D_ARG_344	NH1	D_ASP_401	OD2	3.301
3WN5	D_LYS_370	NZ	E_GLU_357	OE2	3.279
3WN5	D_LYS_409	NZ	E_ASP_399	OD2	3.246
3WN5	D_ARG_416	NH2	D_GLU_388	OE1	2.919
3WN5	D_ARG_416	NH2	D_GLU_388	OE2	3.802
3WN5	E_LYS_248	NZ	E_GLU_380	OE1	2.911
3WN5	E_ARG_255	NH1	E_ASP_249	OD1	3.513
3WN5	E_HIS_285	NE2	E_GLU_283	OE2	3.997
3WN5	E_LYS_320	NZ	E_GLU_333	OE1	3.266
3WN5	E_LYS_338	NZ	E_GLU_430	OE1	3.039
3WN5	E_LYS_338	NZ	E_GLU_430	OE2	3.495
3WN5	E_ARG_344	NH1	E_ASP_401	OD2	3.679
3WN5	E_LYS_370	NZ	D_GLU_357	OE1	3.843
3WN5	E_LYS_409	NZ	D_ASP_399	OD2	2.789
3WN5	E_ARG_416	NH1	E_GLU_388	OE1	2.774
3WN5	E_ARG_416	NH2	E_GLU_388	OE1	3.165
3WN5	E_ARG_416	NH2	E_GLU_388	OE2	3.510
3WN5	F_HIS_84	ND1	F_GLU_163	OE1	3.205
3WN5	F_HIS_84	NE2	F_GLU_82	OE1	3.100
3WN5	F_HIS_104	NE2	F_ASP_135	OD2	2.820
3WN5	F_HIS_108	ND1	F_ASP_20	OD2	3.674
3WN5	F_HIS_108	NE2	F_ASP_20	OD1	3.365
3WN5	F_HIS_108	NE2	F_ASP_20	OD2	3.881
3WN5	F_LYS_117	NZ	E_ASP_265	OD2	3.157
3WN5	F_ARG_127	NH1	F_ASP_145	OD1	3.151
3WN5	F_ARG_127	NH2	F_ASP_145	OD1	3.144
3WN5	F_HIS_131	NE2	E_ASP_270	OD2	2.923
3WN5	F_LYS_140	NZ	F_GLU_100	OE1	3.841
3X0E	A_LYS_124	NZ	A_ASP_195	OD1	3.186
3X0E	A_LYS_124	NZ	A_ASP_195	OD2	2.999
3X0E	A_LYS_187	NZ	A_ASP_155	OD1	2.836

3X0E	A_LYS_187	NZ	A_ASP_155	OD2	3.800
3X0E	A_HIS_191	NE2	A_ASP_128	OD1	2.835
3X0E	A_HIS_191	NE2	A_ASP_128	OD2	3.342
3X0E	B_LYS_124	NZ	B_ASP_195	OD1	2.748
3X0E	B_LYS_124	NZ	B_ASP_195	OD2	3.043
3X0E	B_LYS_144	NZ	B_ASP_138	OD2	3.823
3X0E	B_HIS_191	NE2	B_ASP_128	OD1	2.682
3X0E	B_HIS_191	NE2	B_ASP_128	OD2	3.448
3X0F	A_LYS_124	NZ	A_ASP_195	OD1	2.914
3X0F	A_LYS_124	NZ	A_ASP_195	OD2	3.712
3X0F	A_LYS_148	NZ	A_GLU_152	OE2	2.835
3X0F	A_ARG_171	NH2	A_ASP_138	OD1	3.978
3X0F	A_ARG_171	NH2	A_ASP_138	OD2	3.900
3X0F	A_HIS_191	NE2	A_ASP_128	OD1	2.650
3X0F	A_HIS_191	NE2	A_ASP_128	OD2	3.274
3X0F	B_LYS_124	NZ	B_ASP_195	OD2	3.594
3X0F	B_ARG_171	NH2	B_ASP_138	OD1	2.531
3X0F	B_HIS_191	NE2	B_ASP_128	OD1	2.685
3X0F	B_HIS_191	NE2	B_ASP_128	OD2	3.306
4A6Y	A_ARG_23	NH1	A_ASP_71	OD1	3.205
4A6Y	A_ARG_23	NH1	A_ASP_71	OD2	3.345
4A6Y	A_ARG_23	NH2	A_ASP_71	OD2	3.364
4A6Y	A_ARG_63	NH2	A_GLU_83	OE2	2.831
4A6Y	A_ARG_63	NH2	A_ASP_84	OD1	3.057
4A6Y	A_ARG_63	NH2	A_ASP_84	OD2	3.695
4A6Y	A_LYS_72	NZ	A_ASP_71	OD1	3.673
4A6Y	A_ARG_186	NH2	H_ASP_180	OD2	3.656
4A6Y	A_ARG_190	NH1	H_GLU_89	OE2	3.969
4A6Y	A_HIS_191	ND1	A_ASP_154	OD2	3.123
4A6Y	A_ARG_211	NH2	A_GLU_189	OE1	3.962
4A6Y	A_ARG_211	NH2	A_GLU_189	OE2	2.597
4A6Y	B_ARG_40	NH1	B_GLU_89	OE1	2.984
4A6Y	B_ARG_40	NH1	B_GLU_89	OE2	3.972
4A6Y	B_ARG_40	NH2	B_GLU_89	OE1	3.630
4A6Y	B_LYS_65	NZ	B_GLU_62	OE1	3.475
4A6Y	B_LYS_67	NZ	B_ASP_90	OD1	3.299
4A6Y	B_LYS_67	NZ	B_ASP_90	OD2	3.248
4A6Y	B_ARG_98	NH2	B_ASP_108	OD1	3.444
4A6Y	B_ARG_98	NH2	B_ASP_108	OD2	3.726
4A6Y	B_LYS_150	NZ	A_GLU_127	OE2	3.258
4A6Y	H_LYS_38	NZ	H_ASP_90	OD1	3.850
4A6Y	H_ARG_40	NH2	H_GLU_89	OE1	2.546
4A6Y	H_ARG_40	NH2	H_GLU_89	OE2	3.778
4A6Y	H_LYS_67	NZ	H_ASP_90	OD1	3.781
4A6Y	H_LYS_67	NZ	H_ASP_90	OD2	3.430
4A6Y	H_ARG_98	NH2	H_ASP_108	OD1	3.889
4A6Y	H_ARG_98	NH2	H_ASP_108	OD2	2.725
4A6Y	H_LYS_150	NZ	L_GLU_127	OE2	3.131
4A6Y	H_HIS_171	NE2	L_ASP_141	OD1	3.968
4A6Y	L_ARG_63	NH2	L_ASP_84	OD1	3.284
4A6Y	L_LYS_113	NZ	L_GLU_201	OE2	3.880
4A6Y	L_ARG_190	NH2	B_GLU_89	OE2	3.440
4A6Y	L_HIS_191	ND1	L_ASP_154	OD2	2.878
4AG4	A_ARG_40	NH1	A_ASP_68	OD2	3.311
4AG4	A_ARG_40	NH2	A_ASP_68	OD1	3.723
4AG4	A_ARG_40	NH2	A_ASP_68	OD2	3.146
4AG4	A_ARG_60	NH1	A_ASP_55	OD1	3.893
4AG4	A_ARG_60	NH2	A_ASP_55	OD1	2.714

4AG4	A_ARG_60	NH2	A_ASP_55	OD2	2.648
4AG4	A_ARG_63	NH2	A_ASP_44	OD1	3.060
4AG4	A_ARG_105	NH2	A_GLU_113	OE1	2.869
4AG4	A_ARG_105	NH2	A_GLU_113	OE2	2.817
4AG4	A_ARG_119	NH1	A_GLU_83	OE1	3.220
4AG4	A_ARG_119	NH1	A_GLU_83	OE2	3.262
4AG4	A_ARG_119	NH2	A_GLU_83	OE1	3.601
4AG4	A_ARG_124	NH1	A_ASP_216	OD2	3.269
4AG4	A_ARG_124	NH2	A_ASP_216	OD1	3.026
4AG4	A_ARG_124	NH2	A_ASP_216	OD2	2.840
4AG4	A_ARG_162	NH1	A_ASP_90	OD1	2.607
4AG4	A_ARG_162	NH1	A_ASP_90	OD2	3.377
4AG4	A_ARG_162	NH2	A_ASP_90	OD1	3.110
4AG4	A_ARG_162	NH2	A_ASP_90	OD2	2.698
4AG4	A_ARG_242	NH2	A_ASP_240	OD1	3.701
4AG4	A_ARG_242	NH2	A_ASP_240	OD2	3.113
4AG4	A_ARG_278	NH2	A_ASP_275	OD1	3.438
4AG4	A_ARG_278	NH2	A_ASP_275	OD2	3.642
4AG4	A_ARG_304	NH2	A_GLU_302	OE1	3.291
4AG4	A_ARG_307	NH2	A_GLU_314	OE2	3.264
4AG4	A_ARG_330	NH2	A_ASP_328	OD2	3.952
4AG4	A_ARG_332	NH1	A_ASP_328	OD2	3.874
4AG4	A_ARG_349	NH1	A_GLU_269	OE2	2.534
4AG4	H_LYS_62	NZ	H_GLU_46	OE1	3.542
4AG4	H_LYS_62	NZ	H_GLU_46	OE2	3.611
4AG4	H_ARG_94	NH2	H_ASP_101	OD1	3.424
4AG4	H_ARG_94	NH2	H_ASP_101	OD2	2.703
4AG4	H_LYS_208	NZ	L_GLU_123	OE2	2.708
4AG4	L_ARG_61	NH1	L_GLU_81	OE2	3.821
4AG4	L_ARG_61	NH2	L_GLU_81	OE2	3.157
4AG4	L_ARG_61	NH2	L_ASP_82	OD1	2.518
4AG4	L_ARG_61	NH2	L_ASP_82	OD2	3.022
4AG4	L_LYS_103	NZ	L_GLU_105	OE2	3.708
4AG4	L_LYS_103	NZ	L_ASP_165	OD1	3.872
4AG4	L_LYS_103	NZ	L_ASP_165	OD2	3.264
4AG4	L_LYS_147	NZ	L_GLU_154	OE1	3.276
4AG4	L_ARG_155	NH2	L_GLU_185	OE1	3.301
4AG4	L_HIS_189	ND1	L_ASP_151	OD2	2.672
4AG4	L_LYS_199	NZ	L_ASP_110	OD2	3.556
4B50	A_ARG_38	NH1	A_ASP_86	OD1	2.836
4B50	A_ARG_38	NH2	A_GLU_46	OE1	3.561
4B50	A_ARG_38	NH2	A_ASP_86	OD1	3.779
4B50	A_ARG_66	NH1	A_ASP_86	OD1	3.976
4B50	A_ARG_66	NH1	A_ASP_86	OD2	2.773
4B50	A_ARG_66	NH2	A_ASP_86	OD1	3.265
4B50	A_ARG_66	NH2	A_ASP_86	OD2	3.358
4B50	A_ARG_93	NH1	A_GLU_95	OE2	3.608
4B50	A_ARG_93	NH2	A_GLU_95	OE2	3.523
4B50	A_ARG_93	NH2	A_ASP_101	OD1	3.368
4B50	A_ARG_93	NH2	A_ASP_101	OD2	2.912
4BH7	A_ARG_24	NH1	A_ASP_70	OD1	3.258
4BH7	A_ARG_24	NH1	A_ASP_70	OD2	3.469
4BH7	A_ARG_24	NH2	A_ASP_70	OD2	3.985
4BH7	A_ARG_61	NH1	A_GLU_79	OE1	2.456
4BH7	A_ARG_61	NH1	A_GLU_79	OE2	3.328
4BH7	A_ARG_61	NH2	A_GLU_79	OE1	3.232
4BH7	A_ARG_61	NH2	A_GLU_81	OE1	3.871
4BH7	A_ARG_61	NH2	A_ASP_82	OD1	3.092

4BH7	A_ARG_61	NH2	A_ASP_82	OD2	3.325
4BH7	A_LYS_103	NZ	A_ASP_165	OD1	3.734
4BH7	A_LYS_147	NZ	A_GLU_154	OE2	3.502
4BH7	A_LYS_149	NZ	A_GLU_195	OE1	3.693
4BH7	A_LYS_149	NZ	A_GLU_195	OE2	2.842
4BH7	A_ARG_155	NH1	A_GLU_185	OE1	3.587
4BH7	A_ARG_155	NH1	A_GLU_185	OE2	2.731
4BH7	A_ARG_155	NH2	A_GLU_185	OE1	3.886
4BH7	A_LYS_183	NZ	A_GLU_187	OE2	3.868
4BH7	A_LYS_199	NZ	A_ASP_110	OD1	3.983
4BH7	A_LYS_199	NZ	A_ASP_110	OD2	3.698
4BH7	B_LYS_38	NZ	B_ASP_90	OD1	3.793
4BH7	B_ARG_40	NH2	B_GLU_89	OE1	3.542
4BH7	B_ARG_40	NH2	B_GLU_89	OE2	2.796
4BH7	B_LYS_63	NZ	B_GLU_46	OE1	3.614
4BH7	B_LYS_63	NZ	B_GLU_46	OE2	2.841
4BH7	B_ARG_98	NH2	B_ASP_109	OD1	3.844
4BH7	B_ARG_98	NH2	B_ASP_109	OD2	2.412
4BH8	A_ARG_24	NH2	A_ASP_70	OD2	3.331
4BH8	A_ARG_61	NH1	A_GLU_79	OE1	3.277
4BH8	A_ARG_61	NH2	A_GLU_79	OE1	3.420
4BH8	A_ARG_61	NH2	A_GLU_81	OE2	3.313
4BH8	A_ARG_61	NH2	A_ASP_82	OD1	2.737
4BH8	A_ARG_61	NH2	A_ASP_82	OD2	3.137
4BH8	A_LYS_103	NZ	A_ASP_165	OD1	3.847
4BH8	A_LYS_142	NZ	A_ASP_143	OD1	3.850
4BH8	A_LYS_147	NZ	A_GLU_154	OE1	3.754
4BH8	A_LYS_149	NZ	A_GLU_195	OE1	3.565
4BH8	A_LYS_149	NZ	A_GLU_195	OE2	2.762
4BH8	A_ARG_155	NH1	A_GLU_185	OE2	2.660
4BH8	A_ARG_155	NH2	A_GLU_185	OE1	3.812
4BH8	A_ARG_155	NH2	A_GLU_185	OE2	3.243
4BH8	A_LYS_183	NZ	A_GLU_187	OE1	2.950
4BH8	A_LYS_183	NZ	A_GLU_187	OE2	3.305
4BH8	A_LYS_199	NZ	A_ASP_110	OD1	3.983
4BH8	A_LYS_199	NZ	A_ASP_110	OD2	3.388
4BH8	B_ARG_40	NH1	B_GLU_89	OE1	3.007
4BH8	B_ARG_40	NH2	B_GLU_46	OE1	3.740
4BH8	B_LYS_63	NZ	B_GLU_46	OE1	3.869
4BH8	B_LYS_63	NZ	B_GLU_46	OE2	2.693
4BH8	B_ARG_98	NH2	B_ASP_109	OD1	3.876
4BH8	B_ARG_98	NH2	B_ASP_109	OD2	2.532
4C83	A_HIS_35	NE2	A_ASP_95	OD1	2.464
4C83	A_ARG_38	NH1	A_ASP_86	OD1	3.261
4C83	A_ARG_38	NH2	A_GLU_46	OE1	3.691
4C83	A_ARG_38	NH2	A_GLU_46	OE2	3.824
4C83	A_ARG_66	NH1	A_ASP_86	OD1	3.704
4C83	A_ARG_66	NH1	A_ASP_86	OD2	2.349
4C83	A_ARG_66	NH2	A_ASP_86	OD1	3.078
4C83	A_ARG_66	NH2	A_ASP_86	OD2	3.279
4C83	A_ARG_83	NH2	A_GLU_85	OE2	3.570
4C83	A_ARG_94	NH1	A_GLU_96	OE1	2.827
4C83	A_ARG_94	NH1	A_GLU_96	OE2	2.141
4C83	B_LYS_53	NZ	B_ASP_50	OD1	3.953
4C83	B_LYS_53	NZ	B_ASP_50	OD2	3.875
4C83	B_ARG_61	NH1	B_GLU_79	OE1	3.356
4C83	B_ARG_61	NH1	B_ASP_82	OD1	3.496
4C83	B_ARG_61	NH1	B_ASP_82	OD2	2.349

4C83	B_ARG_61	NH2	B_GLU_79	OE1	3.840
4C83	B_ARG_61	NH2	B_ASP_82	OD1	2.878
4C83	B_ARG_61	NH2	B_ASP_82	OD2	3.259
4C83	B_LYS_103	NZ	B_GLU_105	OE1	3.618
4C83	B_LYS_103	NZ	B_GLU_105	OE2	3.871
4C83	B_LYS_147	NZ	B_GLU_154	OE2	3.593
4C83	B_LYS_149	NZ	B_GLU_195	OE1	2.933
4C83	B_LYS_149	NZ	B_GLU_195	OE2	2.669
4C83	B_ARG_155	NH2	B_GLU_185	OE2	3.551
4C83	B_ARG_188	NH1	B_GLU_185	OE1	3.402
4C83	C_HIS_35	NE2	C_ASP_95	OD1	2.757
4C83	C_ARG_38	NH1	C_ASP_86	OD1	3.096
4C83	C_ARG_38	NH2	C_GLU_46	OE1	3.335
4C83	C_ARG_38	NH2	C_ASP_86	OD1	3.866
4C83	C_ARG_66	NH1	C_ASP_86	OD2	3.260
4C83	C_ARG_66	NH2	C_ASP_86	OD1	2.653
4C83	C_ARG_66	NH2	C_ASP_86	OD2	1.985
4C83	C_ARG_94	NH1	C_GLU_96	OE1	3.930
4C83	C_ARG_94	NH1	C_GLU_96	OE2	1.996
4C83	C_ARG_94	NH2	C_GLU_96	OE2	3.476
4C83	C_LYS_208	NZ	D_GLU_123	OE1	2.304
4C83	C_LYS_208	NZ	D_GLU_123	OE2	2.598
4C83	D_LYS_53	NZ	D_ASP_50	OD2	3.324
4C83	D_ARG_61	NH1	D_GLU_79	OE1	3.777
4C83	D_ARG_61	NH1	D_ASP_82	OD1	2.299
4C83	D_ARG_61	NH1	D_ASP_82	OD2	2.134
4C83	D_ARG_61	NH2	D_GLU_79	OE1	3.916
4C83	D_ARG_61	NH2	D_ASP_82	OD1	3.608
4C83	D_LYS_103	NZ	D_GLU_105	OE2	3.442
4C83	D_LYS_103	NZ	D_ASP_165	OD1	3.353
4C83	D_LYS_147	NZ	D_GLU_154	OE2	3.595
4C83	D_LYS_149	NZ	D_GLU_195	OE1	3.533
4C83	D_LYS_149	NZ	D_GLU_195	OE2	2.856
4C83	D_ARG_155	NH2	D_GLU_185	OE2	3.932
4C83	D_LYS_183	NZ	D_ASP_184	OD1	3.344
4C83	D_HIS_189	ND1	D_ASP_151	OD2	2.752
4C83	D_LYS_199	NZ	D_ASP_110	OD1	3.795
4CJD	A_LYS_35	NZ	A_ASP_31	OD1	3.731
4CJD	A_LYS_35	NZ	A_ASP_31	OD2	2.727
4CJD	A_LYS_52	NZ	A_ASP_55	OD1	2.992
4CJD	A_ARG_68	NH1	A_ASP_74	OD1	3.693
4CJD	A_ARG_68	NH1	A_ASP_74	OD2	3.009
4CJD	A_ARG_68	NH2	A_ASP_74	OD1	2.966
4CJD	A_ARG_68	NH2	A_ASP_74	OD2	3.665
4CJD	A_LYS_76	NZ	A_GLU_72	OE2	3.775
4DAG	A_ARG_40	NH2	A_ASP_336	OD1	2.596
4DAG	A_ARG_40	NH2	A_ASP_336	OD2	3.693
4DAG	A_ARG_91	NH1	A_GLU_92	OE1	3.086
4DAG	A_ARG_248	NH1	A_ASP_224	OD2	2.986
4DAG	A_ARG_252	NH2	A_ASP_224	OD1	2.791
4DAG	A_ARG_304	NH2	A_ASP_306	OD2	3.086
4DAG	A_LYS_312	NZ	A_GLU_345	OE1	3.422
4DAG	A_HIS_332	NE2	A_ASP_280	OD1	3.787
4DAG	H_ARG_38	NH1	H_GLU_46	OE2	3.364
4DAG	H_ARG_38	NH2	H_ASP_89	OD1	3.055
4DAG	H_ARG_66	NH1	H_ASP_89	OD1	3.443
4DAG	H_ARG_66	NH1	H_ASP_89	OD2	3.823
4DAG	H_ARG_66	NH2	H_ASP_89	OD1	3.179

4DAG	H_ARG.66	NH2	H_ASP.89	OD2	2.772
4DAG	H_LYS.75	NZ	H_ASP.72	OD2	3.891
4DAG	H_ARG.97	NH2	H_ASP.110	OD2	2.600
4DAG	H_ARG.101	NH2	A_GLU.33	OE1	3.620
4DAG	H_ARG.101	NH2	A_GLU.33	OE2	2.107
4DAG	H_LYS.152	NZ	H_ASP.153	OD2	3.881
4DAG	L_LYS.46	NZ	A_ASP.414	OD1	3.558
4DAG	L_LYS.46	NZ	A_ASP.414	OD2	3.550
4DAG	L_LYS.50	NZ	L_ASP.111	OD1	3.845
4DAG	L_ARG.80	NH2	L_ASP.101	OD1	3.368
4DAG	L_ARG.80	NH2	L_ASP.101	OD2	3.445
4DAG	L_LYS.186	NZ	L_GLU.102	OE1	3.649
4DAG	L_LYS.186	NZ	L_GLU.102	OE2	2.377
4DGV	H_HIS.35	NE2	H_ASP.95	OD2	2.670
4DGV	H_ARG.38	NH1	H_ASP.86	OD1	2.801
4DGV	H_ARG.38	NH2	H_GLU.46	OE1	3.005
4DGV	H_ARG.38	NH2	H_GLU.46	OE2	3.829
4DGV	H_ARG.38	NH2	H_ASP.86	OD1	3.806
4DGV	H_ARG.64	NH1	H_ASP.61	OD1	2.727
4DGV	H_ARG.64	NH2	H_ASP.61	OD1	2.493
4DGV	H_ARG.66	NH1	H_ASP.86	OD1	3.757
4DGV	H_ARG.66	NH1	H_ASP.86	OD2	2.704
4DGV	H_ARG.66	NH2	H_ASP.86	OD1	3.075
4DGV	H_ARG.66	NH2	H_ASP.86	OD2	3.481
4DGV	H_ARG.94	NH2	H_ASP.101	OD1	3.600
4DGV	H_ARG.94	NH2	H_ASP.101	OD2	2.840
4DGV	H_LYS.143	NZ	H_ASP.144	OD1	3.303
4DGV	H_LYS.143	NZ	H_ASP.144	OD2	3.171
4DGV	H_LYS.209	NZ	L_GLU.123	OE1	2.915
4DGV	H_LYS.209	NZ	L_GLU.123	OE2	3.422
4DGV	H_LYS.210	NZ	H_GLU.212	OE2	3.411
4DGV	L_ARG.61	NH1	L_ASP.82	OD2	2.699
4DGV	L_ARG.61	NH2	L_GLU.79	OE1	3.439
4DGV	L_ARG.61	NH2	L_GLU.79	OE2	3.431
4DGV	L_ARG.61	NH2	L_ASP.82	OD1	3.032
4DGV	L_ARG.61	NH2	L_ASP.82	OD2	3.080
4DGV	L_LYS.149	NZ	L_GLU.195	OE1	3.591
4DGV	L_LYS.149	NZ	L_GLU.195	OE2	3.604
4DGV	L_HIS.189	ND1	L_ASP.151	OD2	3.493
4DGY	H_HIS.35	NE2	H_ASP.95	OD2	2.790
4DGY	H_ARG.38	NH1	H_ASP.86	OD1	2.922
4DGY	H_ARG.38	NH2	H_GLU.46	OE1	2.965
4DGY	H_ARG.38	NH2	H_GLU.46	OE2	3.707
4DGY	H_LYS.43	NZ	H_GLU.85	OE1	3.738
4DGY	H_ARG.64	NH1	H_ASP.61	OD1	2.545
4DGY	H_ARG.64	NH2	H_ASP.61	OD1	3.007
4DGY	H_ARG.66	NH1	H_ASP.86	OD1	3.675
4DGY	H_ARG.66	NH1	H_ASP.86	OD2	2.708
4DGY	H_ARG.66	NH2	H_ASP.86	OD1	3.089
4DGY	H_ARG.66	NH2	H_ASP.86	OD2	3.611
4DGY	H_LYS.83	NZ	H_GLU.85	OE2	2.758
4DGY	H_ARG.94	NH2	H_ASP.101	OD1	3.594
4DGY	H_ARG.94	NH2	H_ASP.101	OD2	2.861
4DGY	H_LYS.143	NZ	H_ASP.144	OD1	3.074
4DGY	H_LYS.143	NZ	H_ASP.144	OD2	3.615
4DGY	H_LYS.210	NZ	H_GLU.212	OE1	3.786
4DGY	H_LYS.214	NZ	L_ASP.122	OD1	3.699
4DGY	H_LYS.214	NZ	L_ASP.122	OD2	2.517

4DGY	L_ARG.61	NH2	L_ASP_82	OD1	2.957
4DGY	L_ARG.61	NH2	L_ASP_82	OD2	3.558
4DGY	L_LYS_149	NZ	L_GLU_195	OE1	2.631
4DGY	L_HIS_189	ND1	L_ASP_185	OD1	2.991
4DGY	L_ARG.211	NH1	L_GLU_187	OE1	3.660
4E9O	X_LYS_13	NZ	X_ASP_83	OD1	2.596
4E9O	X_LYS_13	NZ	X_ASP_83	OD2	3.399
4E9O	X_HIS_80	ND1	X_GLU_90	OE1	3.847
4E9O	X_HIS_80	ND1	X_GLU_90	OE2	3.037
4E9O	X_LYS_100	NZ	X_ASP_112	OD2	2.817
4E9O	X_HIS_110	NE2	X_GLU_106	OE2	2.743
4E9O	X_HIS_192	ND1	X_ASP_194	OD1	3.800
4E9O	X_HIS_192	ND1	X_ASP_194	OD2	3.793
4E9O	X_HIS_192	NE2	X_ASP_125	OD1	3.109
4E9O	X_ARG.200	NH1	X_ASP_74	OD1	3.919
4E9O	X_ARG.200	NH2	X_ASP_74	OD1	3.092
4EBQ	H_ARG.41	NH2	H_GLU_90	OE2	3.943
4EBQ	H_LYS.64	NZ	H_GLU_47	OE1	3.182
4EBQ	H_LYS.68	NZ	H_ASP_91	OD1	3.801
4EBQ	H_LYS.68	NZ	H_ASP_91	OD2	2.849
4EBQ	H_ARG.99	NH2	H_ASP_108	OD1	3.551
4EBQ	H_ARG.99	NH2	H_ASP_108	OD2	2.902
4EBQ	H_LYS_215	NZ	L_GLU_123	OE2	2.960
4EBQ	H_LYS_216	NZ	H_GLU_218	OE2	3.694
4EBQ	L_ARG.61	NH1	L_GLU_79	OE1	3.472
4EBQ	L_ARG.61	NH1	L_GLU_79	OE2	3.398
4EBQ	L_ARG.61	NH2	L_GLU_79	OE1	3.555
4EBQ	L_ARG.61	NH2	L_GLU_81	OE2	2.928
4EBQ	L_ARG.61	NH2	L_ASP_82	OD1	2.828
4EBQ	L_ARG.61	NH2	L_ASP_82	OD2	3.746
4EBQ	L_LYS_149	NZ	L_GLU_195	OE1	3.126
4EBQ	L_HIS_189	ND1	L_ASP_151	OD2	2.598
4EBQ	L_HIS_198	NE2	L_ASP_143	OD1	3.201
4EBQ	L_HIS_198	NE2	L_ASP_143	OD2	3.999
4EBQ	L_ARG.211	NH1	L_GLU_187	OE1	3.580
4EDW	V_LYS.25	NZ	V_GLU_55	OE2	2.812
4EDW	V_ARG.59	NH1	V_ASP_16	OD2	3.820
4EDW	V_ARG.69	NH1	V_ASP_16	OD2	3.587
4EDW	V_ARG.69	NH1	V_ASP_65	OD2	3.446
4EDW	V_ARG.69	NH2	V_ASP_16	OD1	2.627
4EDW	V_ARG.69	NH2	V_ASP_16	OD2	3.468
4EDW	V_HIS_75	ND1	V_ASP_72	OD2	3.959
4EDW	V_HIS_84	NE2	V_ASP_105	OD1	3.310
4EDW	V_ARG.100	NH2	V_ASP_93	OD2	3.018
4EDW	L_ARG.61	NH2	L_GLU_81	OE2	3.755
4EDW	L_ARG.61	NH2	L_ASP_82	OD1	3.001
4EDW	L_LYS_149	NZ	L_GLU_195	OE1	3.988
4EDW	L_LYS_149	NZ	L_GLU_195	OE2	3.571
4EDW	H_ARG.38	NH1	H_ASP_86	OD1	2.786
4EDW	H_ARG.38	NH2	H_GLU_46	OE1	3.202
4EDW	H_ARG.38	NH2	H_GLU_46	OE2	3.836
4EDW	H_ARG.38	NH2	H_ASP_86	OD1	3.735
4EDW	H_LYS.64	NZ	H_ASP_58	OD1	3.460
4EDW	H_ARG.66	NH1	H_ASP_86	OD1	3.705
4EDW	H_ARG.66	NH1	H_ASP_86	OD2	3.011
4EDW	H_ARG.66	NH2	H_ASP_86	OD1	3.297
4EDW	H_ARG.66	NH2	H_ASP_86	OD2	3.810
4EDW	H_ARG.94	NH1	H_ASP_101	OD1	3.531

4EDW	H_ARG_94	NH1	H_ASP_101	OD2	3.123
4EDW	H_LYS_143	NZ	H_ASP_144	OD1	3.362
4EDW	H_LYS_143	NZ	H_ASP_144	OD2	3.438
4EDW	H_LYS_206	NZ	H_ASP_199	OD1	3.486
4EDW	H_LYS_206	NZ	H_ASP_199	OD2	3.672
4EDW	H_LYS_209	NZ	L_GLU_123	OE2	2.707
4EDX	W_LYS_25	NZ	W_GLU_55	OE1	3.801
4EDX	W_LYS_25	NZ	W_GLU_55	OE2	2.552
4EDX	W_LYS_32	NZ	H_ASP_58	OD1	2.886
4EDX	W_LYS_32	NZ	H_ASP_58	OD2	2.677
4EDX	W_LYS_34	NZ	W_ASP_93	OD1	3.065
4EDX	W_LYS_34	NZ	W_ASP_93	OD2	3.190
4EDX	W_ARG_69	NH1	W_ASP_16	OD1	3.423
4EDX	W_ARG_69	NH1	W_ASP_16	OD2	3.292
4EDX	W_ARG_69	NH2	W_ASP_16	OD1	3.501
4EDX	W_ARG_69	NH2	W_ASP_16	OD2	3.076
4EDX	W_HIS_75	ND1	W_ASP_72	OD1	2.972
4EDX	W_HIS_75	ND1	W_ASP_72	OD2	2.422
4EDX	W_HIS_75	NE2	W_ASP_72	OD1	3.095
4EDX	W_HIS_75	NE2	W_ASP_72	OD2	3.906
4EDX	W_HIS_84	NE2	W_ASP_105	OD1	3.552
4EDX	A_ARG_24	NH1	A_ASP_70	OD1	2.849
4EDX	A_ARG_24	NH1	A_ASP_70	OD2	3.069
4EDX	A_ARG_53	NH1	W_GLU_11	OE1	2.795
4EDX	A_ARG_61	NH1	A_GLU_79	OE1	3.710
4EDX	A_ARG_61	NH1	A_GLU_79	OE2	3.737
4EDX	A_ARG_61	NH2	A_GLU_81	OE2	3.420
4EDX	A_ARG_61	NH2	A_ASP_82	OD1	2.960
4EDX	A_ARG_61	NH2	A_ASP_82	OD2	3.581
4EDX	A_LYS_142	NZ	A_ASP_143	OD2	3.962
4EDX	A_LYS_149	NZ	A_GLU_195	OE1	3.345
4EDX	A_ARG_155	NH1	A_GLU_185	OE2	3.186
4EDX	A_ARG_155	NH2	A_GLU_185	OE1	3.161
4EDX	A_ARG_155	NH2	A_GLU_185	OE2	3.235
4EDX	A_HIS_189	ND1	A_ASP_151	OD2	2.695
4EDX	A_LYS_199	NZ	A_ASP_110	OD2	3.513
4EDX	B_ARG_38	NH1	B_ASP_86	OD1	2.727
4EDX	B_ARG_38	NH2	B_GLU_46	OE1	3.309
4EDX	B_ARG_38	NH2	B_GLU_46	OE2	3.547
4EDX	B_ARG_38	NH2	B_ASP_86	OD1	3.872
4EDX	B_ARG_66	NH1	B_ASP_86	OD1	3.949
4EDX	B_ARG_66	NH2	B_ASP_86	OD1	3.356
4EDX	B_ARG_66	NH2	B_ASP_86	OD2	2.590
4EDX	B_ARG_83	NH1	B_ASP_85	OD2	3.918
4EDX	B_ARG_94	NH2	B_ASP_101	OD1	3.751
4EDX	B_ARG_94	NH2	B_ASP_101	OD2	2.789
4EDX	B_LYS_221	NZ	A_GLU_123	OE2	3.878
4EDX	V_LYS_25	NZ	V_GLU_55	OE2	2.718
4EDX	V_LYS_32	NZ	B_ASP_58	OD1	3.117
4EDX	V_LYS_32	NZ	B_ASP_58	OD2	2.681
4EDX	V_LYS_34	NZ	V_ASP_93	OD1	2.694
4EDX	V_LYS_34	NZ	V_ASP_93	OD2	3.572
4EDX	V_ARG_69	NH1	V_ASP_16	OD1	3.521
4EDX	V_HIS_75	ND1	V_ASP_72	OD2	2.859
4EDX	V_HIS_84	NE2	V_ASP_105	OD1	3.612
4EDX	V_LYS_88	NZ	B_ASP_54	OD2	3.805
4EDX	V_ARG_100	NH1	V_ASP_30	OD2	3.837
4EDX	L_ARG_24	NH1	L_ASP_70	OD1	2.767

4EDX	L_ARG_24	NH1	L_ASP_70	OD2	3.056
4EDX	L_ARG_53	NH1	V_GLU_11	OE1	3.269
4EDX	L_ARG_61	NH1	L_GLU_79	OE1	3.421
4EDX	L_ARG_61	NH1	L_GLU_79	OE2	3.637
4EDX	L_ARG_61	NH2	L_GLU_79	OE1	3.585
4EDX	L_ARG_61	NH2	L_GLU_81	OE1	3.985
4EDX	L_ARG_61	NH2	L_GLU_81	OE2	3.833
4EDX	L_ARG_61	NH2	L_ASP_82	OD1	3.225
4EDX	L_LYS_149	NZ	L_GLU_195	OE1	3.431
4EDX	L_LYS_149	NZ	L_GLU_195	OE2	2.686
4EDX	L_ARG_155	NH1	L_GLU_185	OE1	3.892
4EDX	L_ARG_155	NH1	L_GLU_185	OE2	3.334
4EDX	L_ARG_155	NH2	L_GLU_185	OE1	3.107
4EDX	L_ARG_155	NH2	L_GLU_185	OE2	3.593
4EDX	L_LYS_199	NZ	L_ASP_110	OD2	2.658
4EDX	L_ARG_211	NH1	L_GLU_187	OE1	3.902
4EDX	H_ARG_38	NH1	H_ASP_86	OD1	2.944
4EDX	H_ARG_38	NH2	H_GLU_46	OE1	3.536
4EDX	H_ARG_38	NH2	H_GLU_46	OE2	3.204
4EDX	H_ARG_66	NH2	H_ASP_86	OD1	3.277
4EDX	H_ARG_66	NH2	H_ASP_86	OD2	2.900
4EDX	H_ARG_94	NH2	H_ASP_101	OD1	3.827
4EDX	H_ARG_94	NH2	H_ASP_101	OD2	3.037
4EDX	H_LYS_221	NZ	L_GLU_123	OE2	3.893
4EDX	H_LYS_222	NZ	H_GLU_226	OE2	3.370
4ETQ	H_ARG_41	NH1	H_GLU_90	OE1	3.867
4ETQ	H_ARG_41	NH2	H_GLU_90	OE1	3.122
4ETQ	H_ARG_60	NH1	C_ASP_179	OD1	3.609
4ETQ	H_ARG_60	NH2	C_ASP_179	OD1	3.375
4ETQ	H_LYS_68	NZ	H_ASP_91	OD2	3.125
4ETQ	H_ARG_99	NH2	H_ASP_108	OD1	3.442
4ETQ	H_ARG_99	NH2	H_ASP_108	OD2	2.818
4ETQ	H_ARG_103	NH1	C_GLU_217	OE1	3.862
4ETQ	H_ARG_103	NH1	C_GLU_217	OE2	2.754
4ETQ	H_ARG_103	NH2	C_GLU_217	OE2	2.933
4ETQ	H_LYS_215	NZ	L_GLU_123	OE2	3.075
4ETQ	L_ARG_61	NH1	L_GLU_79	OE1	3.879
4ETQ	L_ARG_61	NH1	L_GLU_79	OE2	3.227
4ETQ	L_ARG_61	NH2	L_GLU_81	OE1	3.581
4ETQ	L_ARG_61	NH2	L_ASP_82	OD1	2.731
4ETQ	L_ARG_61	NH2	L_ASP_82	OD2	3.292
4ETQ	L_LYS_142	NZ	L_GLU_105	OE2	3.174
4ETQ	L_LYS_147	NZ	L_GLU_195	OE2	3.710
4ETQ	L_LYS_149	NZ	L_GLU_195	OE1	3.106
4ETQ	L_ARG_155	NH2	L_GLU_185	OE1	3.585
4ETQ	L_ARG_155	NH2	L_GLU_185	OE2	2.828
4ETQ	L_LYS_183	NZ	L_GLU_187	OE1	3.169
4ETQ	L_LYS_183	NZ	L_GLU_187	OE2	2.853
4ETQ	L_HIS_189	ND1	L_ASP_151	OD2	2.872
4ETQ	L_LYS_199	NZ	L_ASP_110	OD2	3.675
4ETQ	A_LYS_39	NZ	A_GLU_90	OE1	3.180
4ETQ	A_LYS_39	NZ	A_GLU_90	OE2	3.761
4ETQ	A_LYS_68	NZ	A_ASP_91	OD1	3.615
4ETQ	A_LYS_68	NZ	A_ASP_91	OD2	2.627
4ETQ	A_ARG_99	NH2	A_ASP_108	OD1	3.812
4ETQ	A_ARG_99	NH2	A_ASP_108	OD2	2.756
4ETQ	A_ARG_103	NH1	X_GLU_217	OE1	2.753
4ETQ	A_ARG_103	NH1	X_GLU_217	OE2	3.565

4ETQ	A_ARG_103	NH2	X_GLU_217	OE1	2.983
4ETQ	A_ARG_103	NH2	X_GLU_217	OE2	3.995
4ETQ	A_LYS_215	NZ	B_GLU_123	OE2	3.774
4ETQ	B_ARG_61	NH1	B_GLU_79	OE1	3.950
4ETQ	B_ARG_61	NH1	B_GLU_79	OE2	3.355
4ETQ	B_ARG_61	NH2	B_GLU_81	OE2	3.928
4ETQ	B_ARG_61	NH2	B_ASP_82	OD1	2.543
4ETQ	B_ARG_61	NH2	B_ASP_82	OD2	3.461
4ETQ	B_LYS_149	NZ	B_GLU_195	OE1	3.167
4ETQ	B_ARG_155	NH1	B_GLU_185	OE1	3.157
4ETQ	B_ARG_155	NH1	B_GLU_185	OE2	3.489
4ETQ	B_ARG_155	NH2	B_GLU_185	OE2	3.114
4ETQ	B_LYS_183	NZ	B_GLU_187	OE1	3.261
4ETQ	B_LYS_183	NZ	B_GLU_187	OE2	2.751
4ETQ	B_HIS_189	ND1	B_ASP_151	OD2	2.691
4ETQ	B_LYS_199	NZ	B_ASP_110	OD2	3.415
4ETQ	X_LYS_14	NZ	X_GLU_11	OE1	2.773
4ETQ	X_LYS_14	NZ	X_GLU_11	OE2	3.470
4ETQ	X_HIS_27	NE2	X_ASP_25	OD1	3.152
4ETQ	X_HIS_27	NE2	X_ASP_25	OD2	2.861
4ETQ	X_ARG_44	NH1	A_GLU_56	OE1	3.611
4ETQ	X_ARG_44	NH1	A_GLU_56	OE2	3.023
4ETQ	X_HIS_80	ND1	X_GLU_90	OE1	3.588
4ETQ	X_HIS_80	ND1	X_GLU_90	OE2	2.761
4ETQ	X_LYS_100	NZ	X_ASP_112	OD2	2.820
4ETQ	X_LYS_108	NZ	A_GLU_58	OE2	3.014
4ETQ	X_LYS_108	NZ	X_GLU_105	OE2	3.377
4ETQ	X_LYS_109	NZ	X_GLU_106	OE1	3.662
4ETQ	X_HIS_110	NE2	X_GLU_106	OE2	3.990
4ETQ	X_HIS_192	ND1	X_ASP_194	OD1	3.490
4ETQ	X_HIS_192	NE2	X_ASP_125	OD2	3.701
4ETQ	X_ARG_200	NH1	X_ASP_74	OD1	3.672
4ETQ	X_ARG_200	NH2	X_ASP_74	OD1	3.193
4ETQ	X_ARG_220	NH1	A_ASP_105	OD1	3.937
4ETQ	X_ARG_220	NH2	A_ASP_105	OD1	2.929
4ETQ	C_HIS_27	NE2	C_ASP_25	OD2	2.566
4ETQ	C_ARG_44	NH1	H_GLU_56	OE1	2.601
4ETQ	C_HIS_80	ND1	C_GLU_90	OE1	3.837
4ETQ	C_HIS_80	ND1	C_GLU_90	OE2	2.937
4ETQ	C_LYS_100	NZ	C_ASP_112	OD1	3.753
4ETQ	C_LYS_100	NZ	C_ASP_112	OD2	2.909
4ETQ	C_LYS_109	NZ	C_GLU_106	OE1	3.550
4ETQ	C_HIS_110	ND1	C_GLU_106	OE2	3.980
4ETQ	C_HIS_192	ND1	C_ASP_194	OD2	3.346
4ETQ	C_HIS_192	NE2	C_ASP_125	OD1	3.763
4ETQ	C_ARG_200	NH1	C_ASP_74	OD1	3.594
4ETQ	C_ARG_200	NH2	C_ASP_74	OD1	3.106
4ETQ	C_ARG_220	NH1	H_ASP_105	OD1	3.872
4ETQ	C_ARG_220	NH2	H_ASP_105	OD1	3.103
4F33	A_LYS_39	NZ	A_ASP_83	OD1	2.996
4F33	A_LYS_53	NZ	A_ASP_50	OD2	3.806
4F33	A_ARG_61	NH1	A_GLU_79	OE1	3.342
4F33	A_ARG_61	NH1	A_GLU_79	OE2	3.490
4F33	A_ARG_61	NH2	A_GLU_79	OE1	3.654
4F33	A_ARG_61	NH2	A_GLU_81	OE2	3.050
4F33	A_ARG_61	NH2	A_ASP_82	OD1	2.710
4F33	A_ARG_61	NH2	A_ASP_82	OD2	3.535
4F33	A_LYS_103	NZ	A_GLU_165	OE1	3.608

4F33	A_LYS_103	NZ	A_GLU_165	OE2	2.863
4F33	A_LYS_149	NZ	A_GLU_195	OE1	2.590
4F33	A_LYS_149	NZ	A_GLU_195	OE2	3.755
4F33	A_LYS_183	NZ	A_GLU_187	OE1	2.975
4F33	A_LYS_183	NZ	A_GLU_187	OE2	2.979
4F33	A_LYS_188	NZ	A_ASP_185	OD1	3.192
4F33	A_HIS_189	ND1	A_ASP_151	OD2	3.095
4F33	B_LYS_19	NZ	B_ASP_82	OD1	2.810
4F33	B_LYS_19	NZ	B_ASP_82	OD2	3.855
4F33	B_LYS_63	NZ	B_GLU_46	OE1	3.902
4F33	B_LYS_63	NZ	B_GLU_46	OE2	2.703
4F33	B_LYS_67	NZ	B_ASP_90	OD1	3.672
4F33	B_LYS_67	NZ	B_ASP_90	OD2	2.735
4F33	B_ARG_98	NH2	B_ASP_107	OD1	3.642
4F33	B_ARG_98	NH2	B_ASP_107	OD2	2.737
4F33	B_ARG_104	NH1	B_ASP_107	OD2	2.783
4F33	B_ARG_104	NH2	B_ASP_102	OD1	3.769
4F33	B_ARG_104	NH2	B_ASP_102	OD2	2.871
4F33	B_LYS_149	NZ	B_ASP_150	OD1	3.476
4F33	B_LYS_212	NZ	B_ASP_214	OD1	2.935
4F33	B_LYS_212	NZ	B_ASP_214	OD2	3.480
4F33	B_LYS_215	NZ	A_GLU_123	OE1	2.676
4F33	B_LYS_215	NZ	A_GLU_123	OE2	3.528
4F33	B_LYS_216	NZ	B_GLU_218	OE2	3.538
4F33	C_LYS_39	NZ	C_ASP_83	OD1	3.023
4F33	C_ARG_61	NH1	C_GLU_79	OE1	3.546
4F33	C_ARG_61	NH1	C_GLU_79	OE2	3.480
4F33	C_ARG_61	NH2	C_GLU_79	OE1	3.378
4F33	C_ARG_61	NH2	C_GLU_81	OE2	3.030
4F33	C_ARG_61	NH2	C_ASP_82	OD1	2.905
4F33	C_ARG_61	NH2	C_ASP_82	OD2	3.629
4F33	C_LYS_103	NZ	C_GLU_165	OE1	3.632
4F33	C_LYS_103	NZ	C_GLU_165	OE2	2.738
4F33	C_LYS_149	NZ	C_GLU_195	OE1	2.670
4F33	C_LYS_149	NZ	C_GLU_195	OE2	3.770
4F33	C_LYS_183	NZ	C_GLU_187	OE1	2.957
4F33	C_LYS_183	NZ	C_GLU_187	OE2	3.355
4F33	C_HIS_189	ND1	C_ASP_151	OD2	3.653
4F33	D_LYS_19	NZ	D_ASP_82	OD1	2.919
4F33	D_LYS_19	NZ	D_ASP_82	OD2	3.318
4F33	D_LYS_63	NZ	D_GLU_46	OE1	3.665
4F33	D_LYS_63	NZ	D_GLU_46	OE2	2.603
4F33	D_LYS_67	NZ	D_ASP_90	OD1	3.611
4F33	D_LYS_67	NZ	D_ASP_90	OD2	2.762
4F33	D_ARG_98	NH2	D_ASP_107	OD1	3.663
4F33	D_ARG_98	NH2	D_ASP_107	OD2	2.741
4F33	D_ARG_104	NH1	D_ASP_107	OD2	2.826
4F33	D_ARG_104	NH2	D_ASP_102	OD1	3.818
4F33	D_ARG_104	NH2	D_ASP_102	OD2	2.913
4F33	D_LYS_149	NZ	D_ASP_150	OD1	3.466
4F33	D_LYS_149	NZ	D_ASP_150	OD2	3.828
4F33	D_LYS_212	NZ	D_ASP_214	OD1	2.938
4F33	D_LYS_212	NZ	D_ASP_214	OD2	3.473
4F33	D_LYS_215	NZ	C_GLU_123	OE1	2.787
4F33	D_LYS_215	NZ	C_GLU_123	OE2	3.695
4F33	D_LYS_216	NZ	D_GLU_218	OE2	3.391
4F33	E_LYS_39	NZ	E_ASP_83	OD1	2.874
4F33	E_LYS_53	NZ	E_ASP_50	OD2	3.486

4F33	E_ARG.61	NH1	E_GLU_79	OE1	3.890
4F33	E_ARG.61	NH1	E_GLU_79	OE2	3.753
4F33	E_ARG.61	NH2	E_GLU_79	OE1	3.703
4F33	E_ARG.61	NH2	E_GLU_81	OE2	3.201
4F33	E_ARG.61	NH2	E_ASP_82	OD1	2.824
4F33	E_ARG.61	NH2	E_ASP_82	OD2	3.545
4F33	E_LYS_103	NZ	E_GLU_165	OE1	3.553
4F33	E_LYS_103	NZ	E_GLU_165	OE2	3.041
4F33	E_LYS_149	NZ	E_GLU_195	OE1	2.766
4F33	E_LYS_149	NZ	E_GLU_195	OE2	3.971
4F33	E_LYS_183	NZ	E_GLU_187	OE1	3.278
4F33	E_LYS_183	NZ	E_GLU_187	OE2	2.769
4F33	E_LYS_188	NZ	E_ASP_185	OD1	3.409
4F33	E_HIS_189	ND1	E_ASP_151	OD2	3.133
4F33	F_LYS_19	NZ	F_ASP_82	OD1	3.043
4F33	F_LYS_63	NZ	F_GLU_46	OE1	3.844
4F33	F_LYS_63	NZ	F_GLU_46	OE2	2.677
4F33	F_LYS_67	NZ	F_ASP_90	OD1	3.822
4F33	F_LYS_67	NZ	F_ASP_90	OD2	2.975
4F33	F_ARG_98	NH2	F_ASP_107	OD1	3.603
4F33	F_ARG_98	NH2	F_ASP_107	OD2	2.766
4F33	F_ARG_104	NH1	F_ASP_107	OD2	2.837
4F33	F_ARG_104	NH2	F_ASP_102	OD1	3.766
4F33	F_ARG_104	NH2	F_ASP_102	OD2	2.901
4F33	F_LYS_149	NZ	F_ASP_150	OD1	3.004
4F33	F_LYS_149	NZ	F_ASP_150	OD2	3.043
4F33	F_LYS_212	NZ	D_ASP_214	OD2	3.519
4F33	F_LYS_212	NZ	F_ASP_214	OD1	3.366
4F33	F_LYS_212	NZ	F_ASP_214	OD2	3.190
4F33	F_LYS_215	NZ	E_GLU_123	OE1	2.609
4F33	F_LYS_215	NZ	E_GLU_123	OE2	3.626
4F33	G_LYS_39	NZ	G_ASP_83	OD1	2.914
4F33	G_LYS_53	NZ	G_ASP_50	OD2	3.491
4F33	G_ARG.61	NH1	G_GLU_79	OE1	3.696
4F33	G_ARG.61	NH1	G_GLU_79	OE2	3.825
4F33	G_ARG.61	NH2	G_GLU_79	OE1	3.720
4F33	G_ARG.61	NH2	G_GLU_81	OE2	2.958
4F33	G_ARG.61	NH2	G_ASP_82	OD1	2.734
4F33	G_ARG.61	NH2	G_ASP_82	OD2	3.619
4F33	G_LYS_103	NZ	G_GLU_165	OE1	3.422
4F33	G_LYS_103	NZ	G_GLU_165	OE2	2.954
4F33	G_LYS_149	NZ	G_GLU_195	OE1	3.155
4F33	G_LYS_183	NZ	G_GLU_187	OE1	3.171
4F33	G_LYS_183	NZ	G_GLU_187	OE2	3.240
4F33	G_HIS_189	ND1	G_ASP_151	OD2	2.855
4F33	H_LYS_19	NZ	H_ASP_82	OD1	2.977
4F33	H_LYS_19	NZ	H_ASP_82	OD2	3.331
4F33	H_LYS_63	NZ	H_GLU_46	OE1	3.962
4F33	H_LYS_63	NZ	H_GLU_46	OE2	2.721
4F33	H_LYS_67	NZ	H_ASP_90	OD1	3.773
4F33	H_LYS_67	NZ	H_ASP_90	OD2	2.822
4F33	H_ARG_98	NH2	H_ASP_107	OD1	3.660
4F33	H_ARG_98	NH2	H_ASP_107	OD2	2.794
4F33	H_ARG_104	NH1	H_ASP_107	OD2	2.850
4F33	H_ARG_104	NH2	H_ASP_102	OD1	3.752
4F33	H_ARG_104	NH2	H_ASP_102	OD2	2.926
4F33	H_LYS_149	NZ	H_ASP_150	OD1	3.202
4F33	H_LYS_149	NZ	H_ASP_150	OD2	3.778

4F33	H.LYS_212	NZ	H.ASP_214	OD1	3.294
4F33	H.LYS_212	NZ	H.ASP_214	OD2	3.751
4F33	H.LYS_215	NZ	G.GLU_123	OE1	2.968
4F33	H.LYS_215	NZ	G.GLU_123	OE2	3.966
4F3F	A.LYS_39	NZ	A.ASP_83	OD1	3.139
4F3F	A.LYS_53	NZ	A.ASP_50	OD2	3.180
4F3F	A.ARG_61	NH1	A.GLU_79	OE1	3.186
4F3F	A.ARG_61	NH2	A.GLU_79	OE1	3.636
4F3F	A.ARG_61	NH2	A.GLU_81	OE2	2.949
4F3F	A.ARG_61	NH2	A.ASP_82	OD1	2.598
4F3F	A.ARG_61	NH2	A.ASP_82	OD2	3.459
4F3F	A.HIS_94	NE2	C.GLU_18	OE1	3.664
4F3F	A.HIS_94	NE2	C.GLU_18	OE2	3.880
4F3F	A.LYS_103	NZ	A.GLU_165	OE1	2.677
4F3F	A.LYS_103	NZ	A.GLU_165	OE2	3.463
4F3F	A.LYS_126	NZ	A.ASP_122	OD2	3.488
4F3F	A.LYS_149	NZ	A.GLU_195	OE1	3.346
4F3F	A.LYS_149	NZ	A.GLU_195	OE2	3.599
4F3F	A.LYS_188	NZ	A.ASP_185	OD1	3.466
4F3F	A.HIS_189	ND1	A.ASP_151	OD2	2.913
4F3F	B.LYS_67	NZ	B.ASP_90	OD1	3.515
4F3F	B.LYS_67	NZ	B.ASP_90	OD2	2.923
4F3F	B.ARG_98	NH2	B.ASP_107	OD1	3.433
4F3F	B.ARG_98	NH2	B.ASP_107	OD2	2.792
4F3F	B.LYS_149	NZ	B.ASP_150	OD1	3.423
4F3F	B.LYS_149	NZ	B.ASP_150	OD2	3.482
4F3F	C.LYS_11	NZ	C.GLU_27	OE1	3.675
4F3F	C.LYS_11	NZ	C.GLU_27	OE2	2.987
4F3F	C.LYS_24	NZ	A.ASP_50	OD1	2.832
4F3F	C.LYS_24	NZ	A.ASP_50	OD2	3.865
4F3F	C.ARG_43	NH2	C.GLU_15	OE2	2.883
4F3F	C.LYS_60	NZ	C.GLU_29	OE1	3.765
4F3F	C.LYS_60	NZ	C.GLU_29	OE2	3.687
4FFV	A.ARG_39	NH1	A.ASP_45	OD1	3.963
4FFV	A.ARG_39	NH1	A.ASP_45	OD2	2.719
4FFV	A.ARG_39	NH2	A.ASP_45	OD1	3.080
4FFV	A.ARG_39	NH2	A.ASP_45	OD2	3.080
4FFV	A.ARG_59	NH2	A.ASP_102	OD1	3.051
4FFV	A.ARG_109	NH1	A.GLU_65	OE1	3.268
4FFV	A.ARG_109	NH1	A.GLU_65	OE2	3.741
4FFV	A.ARG_109	NH2	A.GLU_65	OE1	2.989
4FFV	A.LYS_120	NZ	A.ASP_740	OD2	3.330
4FFV	A.ARG_123	NH2	A.GLU_203	OE1	3.682
4FFV	A.ARG_123	NH2	A.GLU_203	OE2	2.712
4FFV	A.HIS_160	ND1	A.ASP_108	OD2	2.635
4FFV	A.HIS_160	NE2	A.GLU_175	OE1	3.358
4FFV	A.HIS_160	NE2	A.GLU_175	OE2	2.796
4FFV	A.LYS_161	NZ	A.ASP_272	OD1	2.746
4FFV	A.LYS_161	NZ	A.ASP_272	OD2	3.688
4FFV	A.ARG_182	NH1	A.ASP_169	OD1	3.856
4FFV	A.ARG_182	NH1	A.ASP_169	OD2	2.767
4FFV	A.ARG_182	NH2	A.ASP_169	OD2	3.302
4FFV	A.ARG_308	NH2	A.ASP_327	OD2	3.552
4FFV	A.ARG_316	NH1	A.ASP_295	OD2	3.083
4FFV	A.ARG_316	NH2	A.GLU_669	OE1	3.538
4FFV	A.ARG_316	NH2	A.GLU_669	OE2	2.880
4FFV	A.ARG_354	NH2	A.GLU_404	OE1	2.806
4FFV	A.HIS_361	NE2	A.GLU_359	OE2	3.865

4FFV	A_LYS_371	NZ	A_GLU_345	OE1	3.266
4FFV	A_LYS_380	NZ	A_ASP_589	OD1	3.110
4FFV	A_LYS_380	NZ	A_ASP_589	OD2	3.542
4FFV	A_HIS_381	NE2	A_ASP_375	OD2	3.813
4FFV	A_LYS_443	NZ	A_GLU_422	OE1	2.784
4FFV	A_LYS_443	NZ	A_GLU_422	OE2	3.590
4FFV	A_LYS_513	NZ	A_ASP_557	OD1	3.202
4FFV	A_LYS_514	NZ	A_ASP_516	OD2	3.647
4FFV	A_ARG_524	NH1	A_GLU_425	OE1	3.869
4FFV	A_LYS_555	NZ	A_ASP_546	OD1	3.412
4FFV	A_LYS_555	NZ	A_ASP_546	OD2	3.059
4FFV	A_ARG_561	NH1	A_ASP_557	OD1	2.919
4FFV	A_ARG_561	NH1	A_ASP_557	OD2	3.499
4FFV	A_ARG_561	NH2	A_ASP_557	OD1	3.437
4FFV	A_ARG_561	NH2	A_ASP_557	OD2	2.894
4FFV	A_ARG_582	NH2	A_GLU_605	OE2	3.235
4FFV	A_ARG_582	NH2	A_ASP_606	OD1	2.825
4FFV	A_ARG_582	NH2	A_ASP_606	OD2	3.726
4FFV	A_LYS_597	NZ	A_ASP_679	OD1	2.818
4FFV	A_LYS_597	NZ	A_ASP_679	OD2	3.476
4FFV	A_ARG_624	NH2	A_ASP_621	OD2	3.551
4FFV	A_LYS_649	NZ	A_GLU_700	OE2	3.425
4FFV	A_ARG_659	NH1	A_GLU_661	OE1	2.918
4FFV	A_ARG_659	NH1	A_GLU_661	OE2	3.900
4FFV	A_ARG_659	NH2	B_GLU_242	OE2	2.683
4FFV	A_LYS_697	NZ	A_GLU_694	OE1	2.696
4FFV	A_HIS_705	NE2	A_ASP_709	OD2	3.369
4FFV	A_HIS_741	ND1	A_ASP_709	OD1	3.395
4FFV	A_HIS_741	ND1	A_ASP_709	OD2	2.789
4FFV	A_HIS_755	ND1	B_ASP_730	OD1	2.996
4FFV	B_ARG_39	NH1	B_ASP_45	OD1	2.616
4FFV	B_ARG_39	NH1	B_ASP_45	OD2	3.948
4FFV	B_ARG_39	NH2	B_ASP_45	OD1	3.428
4FFV	B_ARG_39	NH2	B_ASP_45	OD2	3.350
4FFV	B_ARG_59	NH2	B_ASP_102	OD1	2.946
4FFV	B_ARG_109	NH2	B_GLU_65	OE1	2.873
4FFV	B_ARG_109	NH2	B_GLU_65	OE2	3.587
4FFV	B_ARG_123	NH2	B_GLU_203	OE1	3.775
4FFV	B_ARG_123	NH2	B_GLU_203	OE2	2.935
4FFV	B_HIS_160	ND1	B_ASP_108	OD2	2.803
4FFV	B_HIS_160	NE2	B_GLU_175	OE1	2.723
4FFV	B_HIS_160	NE2	B_GLU_175	OE2	3.449
4FFV	B_LYS_161	NZ	B_ASP_272	OD1	2.924
4FFV	B_ARG_182	NH2	B_ASP_169	OD1	2.817
4FFV	B_ARG_308	NH1	B_ASP_327	OD1	2.983
4FFV	B_ARG_308	NH1	B_ASP_327	OD2	2.869
4FFV	B_ARG_316	NH1	B_GLU_669	OE1	3.104
4FFV	B_ARG_316	NH1	B_GLU_669	OE2	3.019
4FFV	B_ARG_316	NH2	B_ASP_295	OD2	3.354
4FFV	B_ARG_354	NH2	B_GLU_404	OE1	2.935
4FFV	B_LYS_371	NZ	B_GLU_345	OE1	2.807
4FFV	B_LYS_467	NZ	B_GLU_80	OE2	3.637
4FFV	B_ARG_485	NH2	B_ASP_488	OD1	2.633
4FFV	B_LYS_513	NZ	B_ASP_557	OD1	3.220
4FFV	B_ARG_524	NH1	B_GLU_425	OE1	3.953
4FFV	B_ARG_524	NH2	B_GLU_425	OE1	3.954
4FFV	B_LYS_555	NZ	B_ASP_546	OD1	3.219
4FFV	B_LYS_555	NZ	B_ASP_546	OD2	3.109

4FFV	B_ARG_561	NH1	B_ASP_557	OD1	2.961
4FFV	B_ARG_561	NH1	B_ASP_557	OD2	3.596
4FFV	B_ARG_561	NH2	B_ASP_557	OD1	3.466
4FFV	B_ARG_561	NH2	B_ASP_557	OD2	2.798
4FFV	B_ARG_582	NH2	B_ASP_606	OD1	2.846
4FFV	B_ARG_582	NH2	B_ASP_606	OD2	3.802
4FFV	B_ARG_612	NH1	B_GLU_609	OE2	3.858
4FFV	B_LYS_623	NZ	B_ASP_621	OD1	3.779
4FFV	B_ARG_624	NH1	B_ASP_621	OD2	2.973
4FFV	B_ARG_659	NH1	B_GLU_661	OE1	3.697
4FFV	B_ARG_659	NH1	B_GLU_661	OE2	2.842
4FFV	B_ARG_659	NH2	A_GLU_242	OE2	2.592
4FFV	B_LYS_697	NZ	B_GLU_694	OE2	3.213
4FFV	B_HIS_705	NE2	B_ASP_709	OD2	3.391
4FFV	B_HIS_741	ND1	B_ASP_709	OD1	3.377
4FFV	B_HIS_741	ND1	B_ASP_709	OD2	2.794
4FFV	B_HIS_755	ND1	A_ASP_730	OD1	2.989
4FFV	B_HIS_755	ND1	A_ASP_730	OD2	3.942
4FFV	C_ARG_60	NH2	C_GLU_78	OE2	2.738
4FFV	C_LYS_146	NZ	C_GLU_153	OE2	3.897
4FFV	D_LYS_54	NZ	B_GLU_89	OE1	3.460
4FFV	D_LYS_54	NZ	B_GLU_89	OE2	3.556
4FFV	D_LYS_54	NZ	D_ASP_31	OD1	3.816
4FFV	D_LYS_63	NZ	D_GLU_46	OE2	3.471
4FFV	D_LYS_67	NZ	D_ASP_90	OD2	2.846
4FFV	D_ARG_98	NH2	D_ASP_105	OD1	3.968
4FFV	D_ARG_98	NH2	D_ASP_105	OD2	2.804
4FFV	D_LYS_209	NZ	D_ASP_211	OD1	3.459
4FFV	L_ARG_60	NH1	L_GLU_78	OE2	3.980
4FFV	L_ARG_60	NH2	L_GLU_80	OE2	2.908
4FFV	L_ARG_76	NH1	L_GLU_78	OE2	3.920
4FFV	L_ARG_76	NH2	L_GLU_78	OE2	3.454
4FFV	L_LYS_146	NZ	L_GLU_153	OE2	3.863
4FFV	L_LYS_148	NZ	L_GLU_194	OE1	3.895
4FFV	L_LYS_168	NZ	L_ASP_169	OD2	3.641
4FFV	H_LYS_54	NZ	A_GLU_89	OE1	3.584
4FFV	H_LYS_54	NZ	A_GLU_89	OE2	3.871
4FFV	H_LYS_63	NZ	H_GLU_46	OE2	3.768
4FFV	H_LYS_67	NZ	H_ASP_90	OD1	2.976
4FFV	H_LYS_67	NZ	H_ASP_90	OD2	3.578
4FFV	H_ARG_98	NH1	H_ASP_105	OD1	3.804
4FFV	H_ARG_98	NH1	H_ASP_105	OD2	3.268
4FFV	H_ARG_98	NH2	H_ASP_105	OD2	3.823
4FFV	H_HIS_168	NE2	L_ASP_166	OD1	3.178
4FFV	H_HIS_168	NE2	L_ASP_166	OD2	3.870
4FFV	H_LYS_209	NZ	H_ASP_211	OD1	3.064
4FFW	A_ARG_39	NH2	A_ASP_45	OD1	3.225
4FFW	A_ARG_39	NH2	A_ASP_45	OD2	2.703
4FFW	A_ARG_109	NH1	A_GLU_65	OE1	3.415
4FFW	A_ARG_109	NH1	A_GLU_65	OE2	3.525
4FFW	A_ARG_109	NH2	A_GLU_65	OE1	3.203
4FFW	A_LYS_120	NZ	A_ASP_740	OD2	3.434
4FFW	A_ARG_123	NH2	A_GLU_203	OE2	3.187
4FFW	A_HIS_160	NE2	A_ASP_108	OD2	3.962
4FFW	A_LYS_161	NZ	A_ASP_272	OD1	2.704
4FFW	A_ARG_182	NH1	A_ASP_169	OD2	2.886
4FFW	A_ARG_308	NH2	A_ASP_327	OD2	3.670
4FFW	A_ARG_316	NH1	A_ASP_295	OD2	3.273

4FFW	A_ARG_316	NH2	A_GLU_669	OE1	3.641
4FFW	A_ARG_316	NH2	A_GLU_669	OE2	2.963
4FFW	A_ARG_354	NH2	A_GLU_404	OE1	3.227
4FFW	A_HIS_361	NE2	A_GLU_359	OE2	3.514
4FFW	A_LYS_371	NZ	A_GLU_345	OE1	2.680
4FFW	A_LYS_380	NZ	A_ASP_589	OD1	3.098
4FFW	A_LYS_380	NZ	A_ASP_589	OD2	2.829
4FFW	A_LYS_443	NZ	A_GLU_422	OE1	2.937
4FFW	A_LYS_513	NZ	A_ASP_557	OD1	3.106
4FFW	A_ARG_524	NH1	A_GLU_425	OE1	2.739
4FFW	A_LYS_555	NZ	A_ASP_546	OD1	3.312
4FFW	A_ARG_561	NH1	A_ASP_557	OD1	2.928
4FFW	A_ARG_561	NH1	A_ASP_557	OD2	3.570
4FFW	A_ARG_561	NH2	A_ASP_557	OD1	3.591
4FFW	A_ARG_561	NH2	A_ASP_557	OD2	3.082
4FFW	A_ARG_582	NH2	A_GLU_605	OE2	3.554
4FFW	A_ARG_582	NH2	A_ASP_606	OD1	3.161
4FFW	A_ARG_582	NH2	A_ASP_606	OD2	3.803
4FFW	A_LYS_597	NZ	A_ASP_679	OD1	2.982
4FFW	A_ARG_624	NH2	A_ASP_621	OD2	3.236
4FFW	A_LYS_649	NZ	A_GLU_700	OE2	3.883
4FFW	A_ARG_659	NH1	A_GLU_661	OE1	3.045
4FFW	A_ARG_659	NH2	B_GLU_242	OE2	3.187
4FFW	A_LYS_697	NZ	A_GLU_694	OE1	3.166
4FFW	A_HIS_705	NE2	A_ASP_709	OD2	3.560
4FFW	A_HIS_741	ND1	A_ASP_709	OD1	3.680
4FFW	A_HIS_741	ND1	A_ASP_709	OD2	2.834
4FFW	A_HIS_755	ND1	B_ASP_730	OD1	3.111
4FFW	B_ARG_39	NH1	B_ASP_45	OD1	3.148
4FFW	B_ARG_39	NH2	B_ASP_45	OD1	3.305
4FFW	B_ARG_39	NH2	B_ASP_45	OD2	3.479
4FFW	B_ARG_59	NH2	B_ASP_102	OD1	3.000
4FFW	B_ARG_109	NH2	B_GLU_65	OE1	3.413
4FFW	B_ARG_109	NH2	B_GLU_65	OE2	3.745
4FFW	B_LYS_120	NZ	B_ASP_740	OD2	3.578
4FFW	B_ARG_123	NH2	B_GLU_203	OE2	2.505
4FFW	B_HIS_160	ND1	B_ASP_108	OD2	3.785
4FFW	B_HIS_160	NE2	B_GLU_175	OE1	2.698
4FFW	B_HIS_160	NE2	B_GLU_175	OE2	3.643
4FFW	B_LYS_161	NZ	B_ASP_272	OD1	3.156
4FFW	B_ARG_182	NH2	B_ASP_169	OD1	2.942
4FFW	B_ARG_308	NH1	B_ASP_327	OD1	3.218
4FFW	B_ARG_308	NH1	B_ASP_327	OD2	2.634
4FFW	B_ARG_316	NH1	B_GLU_669	OE1	2.973
4FFW	B_ARG_316	NH1	B_GLU_669	OE2	3.097
4FFW	B_ARG_316	NH2	B_ASP_295	OD2	3.399
4FFW	B_LYS_330	NZ	B_ASP_307	OD2	3.516
4FFW	B_ARG_354	NH2	B_GLU_404	OE1	2.920
4FFW	B_ARG_356	NH2	B_ASP_300	OD2	3.885
4FFW	B_LYS_371	NZ	B_GLU_345	OE1	2.782
4FFW	B_LYS_371	NZ	B_GLU_345	OE2	3.778
4FFW	B_LYS_380	NZ	B_ASP_589	OD2	3.568
4FFW	B_ARG_485	NH2	B_ASP_488	OD1	3.387
4FFW	B_LYS_513	NZ	B_ASP_557	OD1	3.212
4FFW	B_LYS_514	NZ	B_ASP_516	OD1	3.257
4FFW	B_ARG_524	NH1	B_GLU_425	OE1	3.639
4FFW	B_LYS_555	NZ	B_ASP_546	OD1	3.368
4FFW	B_ARG_561	NH1	B_ASP_557	OD1	3.049

4FFW	B_ARG_561	NH1	B_ASP_557	OD2	3.722
4FFW	B_ARG_561	NH2	B_ASP_557	OD1	3.485
4FFW	B_ARG_561	NH2	B_ASP_557	OD2	3.243
4FFW	B_ARG_582	NH2	B_ASP_606	OD1	3.041
4FFW	B_LYS_597	NZ	B_ASP_679	OD1	3.641
4FFW	B_LYS_623	NZ	B_ASP_621	OD1	3.750
4FFW	B_ARG_624	NH1	B_ASP_621	OD2	3.247
4FFW	B_ARG_659	NH1	B_GLU_661	OE2	2.930
4FFW	B_ARG_659	NH2	A_GLU_242	OE2	3.068
4FFW	B_ARG_670	NH2	B_GLU_204	OE1	3.913
4FFW	B_HIS_705	NE2	B_ASP_709	OD2	3.534
4FFW	B_HIS_741	ND1	B_ASP_709	OD1	3.671
4FFW	B_HIS_741	ND1	B_ASP_709	OD2	2.858
4FFW	C_ARG_60	NH2	C_GLU_80	OE2	3.345
4FFW	C_LYS_146	NZ	C_GLU_153	OE1	3.486
4FFW	C_LYS_146	NZ	C_GLU_153	OE2	3.680
4FFW	C_ARG_154	NH1	C_GLU_184	OE2	3.454
4FFW	C_ARG_154	NH2	C_GLU_184	OE2	3.842
4FFW	C_LYS_182	NZ	C_GLU_186	OE2	2.882
4FFW	D_LYS_54	NZ	B_GLU_89	OE1	3.085
4FFW	D_LYS_54	NZ	B_GLU_89	OE2	3.381
4FFW	D_LYS_63	NZ	D_GLU_46	OE2	3.795
4FFW	D_LYS_67	NZ	D_ASP_90	OD2	2.893
4FFW	D_ARG_98	NH2	D_ASP_105	OD1	3.888
4FFW	D_ARG_98	NH2	D_ASP_105	OD2	3.038
4FFW	H_LYS_54	NZ	A_GLU_89	OE1	3.517
4FFW	H_LYS_54	NZ	A_GLU_89	OE2	3.666
4FFW	H_LYS_63	NZ	H_GLU_46	OE2	3.928
4FFW	H_ARG_98	NH2	H_ASP_105	OD1	3.858
4FFW	H_ARG_98	NH2	H_ASP_105	OD2	3.152
4FFW	H_HIS_168	NE2	L_ASP_166	OD1	3.737
4FFW	L_ARG_60	NH1	L_GLU_78	OE2	3.910
4FFW	L_ARG_60	NH2	L_GLU_80	OE2	3.325
4FFW	L_ARG_60	NH2	L_ASP_81	OD1	2.865
4FFW	L_ARG_60	NH2	L_ASP_81	OD2	3.727
4FFW	L_LYS_	NZ	L_GLU_	OE2	3.349
4FQH	H_ARG_38	NH1	H_ASP_86	OD1	2.793
4FQH	H_ARG_38	NH2	H_ASP_86	OD1	3.878
4FQH	H_LYS_62	NZ	H_ASP_46	OD2	3.060
4FQH	H_ARG_66	NH1	H_ASP_86	OD1	3.673
4FQH	H_ARG_66	NH1	H_ASP_86	OD2	2.888
4FQH	H_ARG_66	NH2	H_ASP_86	OD1	2.891
4FQH	H_ARG_66	NH2	H_ASP_86	OD2	3.511
4FQH	H_ARG_94	NH1	H_ASP_101	OD1	3.949
4FQH	H_ARG_94	NH1	H_ASP_101	OD2	3.141
4FQH	H_ARG_94	NH2	H_ASP_101	OD1	3.729
4FQH	H_ARG_94	NH2	H_ASP_101	OD2	3.721
4FQH	H_LYS_143	NZ	L_GLU_124	OE2	2.906
4FQH	H_LYS_214	NZ	L_GLU_123	OE1	3.752
4FQH	H_LYS_214	NZ	L_GLU_123	OE2	2.217
4FQH	L_ARG_30	NH1	L_ASP_93	OD2	3.341
4FQH	L_ARG_31	NH1	L_ASP_93	OD1	2.902
4FQH	L_ARG_31	NH1	L_ASP_93	OD2	3.963
4FQH	L_ARG_61	NH2	L_ASP_82	OD1	2.708
4FQH	L_ARG_61	NH2	L_ASP_82	OD2	3.349
4FQH	L_HIS_188	ND1	L_ASP_151	OD1	2.726
4FQH	A_ARG_38	NH1	A_ASP_86	OD1	2.939
4FQH	A_LYS_62	NZ	A_ASP_46	OD1	3.347

4FQH	A_LYS_62	NZ	A_ASP_46	OD2	2.737
4FQH	A_ARG_66	NH1	A_ASP_86	OD1	3.497
4FQH	A_ARG_66	NH1	A_ASP_86	OD2	2.905
4FQH	A_ARG_66	NH2	A_ASP_86	OD1	2.643
4FQH	A_ARG_66	NH2	A_ASP_86	OD2	3.511
4FQH	A_LYS_143	NZ	A_ASP_144	OD2	3.998
4FQH	A_LYS_143	NZ	B_GLU_124	OE2	3.049
4FQH	A_LYS_214	NZ	B_GLU_123	OE1	3.132
4FQH	B_ARG_31	NH2	B_ASP_93	OD1	2.853
4FQH	B_ARG_61	NH2	B_ASP_82	OD1	2.666
4FQH	B_ARG_61	NH2	B_ASP_82	OD2	3.538
4FQI	A_LYS_45	NZ	A_ASP_41	OD1	3.116
4FQI	A_LYS_45	NZ	A_ASP_41	OD2	2.607
4FQI	A_LYS_46	NZ	A_GLU_44	OE1	2.647
4FQI	A_LYS_46	NZ	A_GLU_44	OE2	3.567
4FQI	A_ARG_62	NH1	A_GLU_78	OE1	3.913
4FQI	A_ARG_62	NH1	A_GLU_78	OE2	3.007
4FQI	A_LYS_90	NZ	A_GLU_273	OE1	2.798
4FQI	A_LYS_109	NZ	A_GLU_89	OE1	2.835
4FQI	A_LYS_109	NZ	A_GLU_89	OE2	3.759
4FQI	A_LYS_109	NZ	B_GLU_69	OE1	2.615
4FQI	A_LYS_109	NZ	B_GLU_69	OE2	3.205
4FQI	A_ARG_149	NH2	A_ASP_77	OD1	3.711
4FQI	A_ARG_149	NH2	A_ASP_77	OD2	2.863
4FQI	A_HIS_184	NE2	A_GLU_231	OE1	2.822
4FQI	A_ARG_216	NH1	A_GLU_231	OE1	3.982
4FQI	A_ARG_216	NH2	A_GLU_231	OE1	3.265
4FQI	A_LYS_259	NZ	A_GLU_119	OE1	3.578
4FQI	A_LYS_261	NZ	A_GLU_83A	OE1	3.943
4FQI	A_LYS_261	NZ	A_GLU_83A	OE2	2.598
4FQI	A_LYS_262	NZ	A_ASP_175	OD2	3.224
4FQI	A_LYS_269	NZ	A_GLU_89	OE1	2.759
4FQI	A_LYS_307	NZ	B_GLU_64	OE2	3.371
4FQI	A_LYS_310	NZ	B_ASP_90	OD1	2.687
4FQI	A_LYS_310	NZ	B_ASP_90	OD2	3.739
4FQI	B_LYS_51	NZ	B_GLU_103	OE1	2.743
4FQI	B_ARG_68	NH1	B_GLU_85	OE2	3.042
4FQI	B_LYS_82	NZ	B_ASP_86	OD2	2.769
4FQI	B_ARG_123	NH2	B_ASP_120	OD1	3.250
4FQI	B_ARG_153	NH2	B_GLU_150	OE2	2.775
4FQI	B_ARG_167	NH2	B_GLU_164	OE1	3.918
4FQI	B_ARG_167	NH2	B_GLU_164	OE2	2.444
4FQI	B_ARG_170	NH1	B_ASP_128	OD1	3.871
4FQI	B_ARG_170	NH1	B_ASP_128	OD2	3.616
4FQI	B_ARG_170	NH2	B_ASP_128	OD2	3.649
4FQI	H_ARG_38	NH1	H_ASP_86	OD1	2.837
4FQI	H_ARG_38	NH2	H_ASP_86	OD1	3.841
4FQI	H_LYS_62	NZ	H_ASP_46	OD1	3.985
4FQI	H_LYS_62	NZ	H_ASP_46	OD2	2.950
4FQI	H_ARG_66	NH1	H_ASP_86	OD1	3.456
4FQI	H_ARG_66	NH1	H_ASP_86	OD2	2.873
4FQI	H_ARG_66	NH2	H_ASP_86	OD1	2.889
4FQI	H_ARG_66	NH2	H_ASP_86	OD2	3.655
4FQI	H_LYS_143	NZ	L_GLU_124	OE2	2.947
4FQI	H_LYS_206	NZ	H_ASP_208	OD1	2.657
4FQI	H_LYS_206	NZ	H_ASP_208	OD2	3.897
4FQI	L_ARG_30	NH1	L_ASP_93	OD2	2.748
4FQI	L_ARG_30	NH2	L_ASP_93	OD2	3.772

4FQI	L_ARG_31	NH2	L_ASP_93	OD1	2.914
4FQI	L_ARG_31	NH2	L_ASP_93	OD2	3.671
4FQI	L_ARG_61	NH2	L_GLU_81	OE2	3.854
4FQI	L_ARG_61	NH2	L_ASP_82	OD1	2.818
4FQI	L_ARG_61	NH2	L_ASP_82	OD2	3.558
4G6A	C_ARG_38	NH1	C_ASP_86	OD1	2.901
4G6A	C_ARG_38	NH2	C_GLU_46	OE1	2.973
4G6A	C_ARG_38	NH2	C_ASP_86	OD1	3.508
4G6A	C_ARG_64	NH1	D_ASP_94	OD1	3.792
4G6A	C_ARG_64	NH1	D_ASP_94	OD2	3.701
4G6A	C_ARG_66	NH1	C_ASP_86	OD1	3.401
4G6A	C_ARG_66	NH1	C_ASP_86	OD2	2.759
4G6A	C_ARG_66	NH2	C_ASP_86	OD1	2.824
4G6A	C_ARG_66	NH2	C_ASP_86	OD2	3.567
4G6A	C_LYS_143	NZ	C_ASP_144	OD1	3.200
4G6A	C_LYS_143	NZ	C_ASP_144	OD2	3.786
4G6A	C_LYS_209	NZ	D_GLU_123	OE1	2.784
4G6A	C_LYS_209	NZ	D_GLU_123	OE2	3.529
4G6A	C_LYS_210	NZ	C_GLU_212	OE2	3.247
4G6A	D_ARG_18	NH2	D_ASP_76	OD2	2.934
4G6A	D_ARG_18	NH2	L_GLU_27	OE2	3.721
4G6A	D_LYS_39	NZ	D_ASP_81	OD1	2.823
4G6A	D_ARG_61	NH1	D_ASP_82	OD1	3.328
4G6A	D_ARG_61	NH1	D_ASP_82	OD2	2.369
4G6A	D_ARG_61	NH2	D_ASP_82	OD1	2.953
4G6A	D_ARG_61	NH2	D_ASP_82	OD2	3.506
4G6A	D_LYS_149	NZ	D_GLU_195	OE1	3.087
4G6A	D_LYS_183	NZ	D_GLU_187	OE1	3.747
4G6A	D_LYS_183	NZ	D_GLU_187	OE2	3.452
4G6A	D_LYS_188	NZ	D_ASP_185	OD1	3.129
4G6A	D_HIS_189	ND1	D_ASP_151	OD2	3.322
4G6A	D_LYS_190	NZ	D_GLU_213	OE2	2.978
4G6A	H_ARG_38	NH1	H_ASP_86	OD1	3.081
4G6A	H_ARG_38	NH2	H_GLU_46	OE1	3.078
4G6A	H_ARG_38	NH2	H_ASP_86	OD1	3.738
4G6A	H_ARG_64	NH2	L_ASP_94	OD1	3.443
4G6A	H_ARG_64	NH2	L_ASP_94	OD2	3.275
4G6A	H_ARG_66	NH1	H_ASP_86	OD1	3.684
4G6A	H_ARG_66	NH1	H_ASP_86	OD2	3.528
4G6A	H_ARG_66	NH2	H_ASP_86	OD1	2.640
4G6A	H_ARG_66	NH2	H_ASP_86	OD2	3.507
4G6A	H_LYS_143	NZ	H_ASP_144	OD1	3.327
4G6A	H_LYS_143	NZ	H_ASP_144	OD2	3.934
4G6A	H_LYS_206	NZ	H_ASP_208	OD1	2.915
4G6A	H_LYS_206	NZ	H_ASP_208	OD2	3.666
4G6A	H_LYS_209	NZ	L_GLU_123	OE1	2.940
4G6A	H_LYS_209	NZ	L_GLU_123	OE2	3.622
4G6A	H_LYS_210	NZ	H_GLU_212	OE2	3.489
4G6A	L_ARG_18	NH2	L_ASP_76	OD2	3.695
4G6A	L_LYS_39	NZ	L_ASP_81	OD1	2.869
4G6A	L_LYS_39	NZ	L_ASP_81	OD2	3.930
4G6A	L_ARG_61	NH1	L_ASP_82	OD1	3.564
4G6A	L_ARG_61	NH1	L_ASP_82	OD2	2.948
4G6A	L_ARG_61	NH2	L_ASP_82	OD1	3.384
4G6A	L_LYS_149	NZ	L_GLU_195	OE2	3.404
4G6A	L_LYS_183	NZ	L_GLU_187	OE1	3.001
4G6A	L_LYS_183	NZ	L_GLU_187	OE2	3.388
4G6A	L_LYS_190	NZ	L_GLU_213	OE2	3.611

4G6F	H_ARG_38	NH1	H_ASP_86	OD1	2.906
4G6F	H_ARG_38	NH2	H_GLU_46	OE1	3.116
4G6F	H_ARG_38	NH2	H_GLU_46	OE2	3.531
4G6F	H_ARG_38	NH2	H_ASP_86	OD1	3.904
4G6F	H_ARG_50	NH1	H_ASP_58	OD2	3.658
4G6F	H_ARG_50	NH1	H_GLU_100J	OE1	3.226
4G6F	H_ARG_50	NH1	H_GLU_100J	OE2	2.985
4G6F	H_ARG_50	NH2	H_ASP_58	OD2	2.110
4G6F	H_ARG_66	NH1	H_ASP_86	OD1	3.936
4G6F	H_ARG_66	NH1	H_ASP_86	OD2	2.633
4G6F	H_ARG_66	NH2	H_ASP_86	OD1	3.136
4G6F	H_ARG_66	NH2	H_ASP_86	OD2	3.299
4G6F	H_ARG_83	NH2	H_GLU_85	OE1	3.916
4G6F	H_ARG_94	NH2	H_ASP_102	OD2	3.304
4G6F	H_LYS_143	NZ	H_ASP_144	OD2	3.573
4G6F	H_LYS_143	NZ	L_GLU_125	OE2	3.341
4G6F	H_LYS_209	NZ	L_GLU_124	OE1	3.080
4G6F	H_LYS_209	NZ	L_GLU_124	OE2	2.558
4G6F	H_ARG_210	NH1	H_GLU_212	OE2	3.716
4G6F	B_ARG_38	NH1	B_ASP_86	OD1	3.151
4G6F	B_ARG_38	NH2	B_GLU_46	OE1	3.414
4G6F	B_ARG_38	NH2	B_GLU_46	OE2	3.922
4G6F	B_ARG_50	NH1	B_ASP_58	OD2	3.630
4G6F	B_ARG_50	NH1	B_GLU_100J	OE1	3.222
4G6F	B_ARG_50	NH1	B_GLU_100J	OE2	2.975
4G6F	B_ARG_50	NH2	B_ASP_58	OD2	2.343
4G6F	B_ARG_66	NH1	B_ASP_86	OD1	3.598
4G6F	B_ARG_66	NH1	B_ASP_86	OD2	2.769
4G6F	B_ARG_66	NH2	B_ASP_86	OD1	2.916
4G6F	B_ARG_66	NH2	B_ASP_86	OD2	3.570
4G6F	B_ARG_83	NH2	B_GLU_85	OE1	3.938
4G6F	B_ARG_94	NH2	B_ASP_102	OD2	3.253
4G6F	B_LYS_143	NZ	D_GLU_125	OE2	2.735
4G6F	B_LYS_209	NZ	D_GLU_124	OE1	3.470
4G6F	B_LYS_209	NZ	D_GLU_124	OE2	2.107
4G6F	L_ARG_29	NH1	L_ASP_26	OD1	3.314
4G6F	L_HIS_31	ND1	H_GLU_100I	OE2	2.912
4G6F	L_ARG_54	NH1	L_ASP_60	OD1	3.621
4G6F	L_ARG_61	NH2	L_GLU_81	OE1	3.555
4G6F	L_ARG_61	NH2	L_ASP_82	OD1	2.760
4G6F	L_ARG_61	NH2	L_ASP_82	OD2	3.527
4G6F	L_ARG_91	NH1	H_GLU_100J	OE2	2.715
4G6F	L_ARG_91	NH2	H_GLU_100J	OE2	2.951
4G6F	L_LYS_103	NZ	L_ASP_83	OD1	2.500
4G6F	L_LYS_111	NZ	L_GLU_199	OE1	3.003
4G6F	L_LYS_150	NZ	L_GLU_204	OE2	2.904
4G6F	D_HIS_31	ND1	B_GLU_100I	OE2	2.954
4G6F	D_ARG_54	NH1	D_ASP_60	OD1	3.426
4G6F	D_ARG_61	NH2	D_ASP_82	OD1	2.776
4G6F	D_ARG_61	NH2	D_ASP_82	OD2	3.304
4G6F	D_ARG_91	NH1	B_GLU_100J	OE2	2.854
4G6F	D_ARG_91	NH2	B_GLU_100J	OE2	2.880
4G6F	D_ARG_95B	NH2	B_ASP_58	OD1	3.343
4G6F	D_LYS_103	NZ	D_ASP_83	OD1	2.777
4G6F	D_LYS_111	NZ	D_GLU_199	OE1	3.031
4G6F	D_LYS_150	NZ	D_GLU_204	OE1	3.970
4G6F	D_LYS_150	NZ	D_GLU_204	OE2	2.492
4G6F	D_LYS_167	NZ	D_ASP_83	OD2	3.935

4G6F	D_LYS_172	NZ	D_ASP_139	OD2	3.592
4G6F	D_ARG_190	NH2	D_ASP_152	OD2	3.898
4G6F	P_LYS_665	NZ	P_GLU_662	OE2	3.965
4G6F	F_LYS_665	NZ	F_GLU_662	OE1	3.301
4G6F	F_LYS_665	NZ	F_GLU_662	OE2	2.956
4GMT	L_LYS_24	NZ	L_ASP_70	OD1	3.260
4GMT	L_LYS_24	NZ	L_ASP_70	OD2	3.149
4GMT	L_ARG_61	NH2	L_GLU_81	OE2	3.799
4GMT	L_ARG_61	NH2	L_ASP_82	OD1	3.260
4GMT	L_ARG_61	NH2	L_ASP_82	OD2	2.628
4GMT	L_ARG_108	NH1	L_ASP_170	OD1	3.942
4GMT	L_LYS_142	NZ	L_ASP_143	OD1	3.297
4GMT	L_LYS_142	NZ	L_ASP_143	OD2	2.972
4GMT	L_LYS_147	NZ	L_GLU_195	OE1	3.733
4GMT	L_LYS_149	NZ	L_GLU_195	OE2	3.437
4GMT	L_ARG_155	NH1	L_GLU_185	OE2	3.030
4GMT	L_ARG_155	NH2	L_GLU_185	OE1	3.075
4GMT	L_ARG_155	NH2	L_GLU_185	OE2	2.988
4GMT	L_HIS_189	ND1	L_ASP_151	OD2	3.653
4GMT	L_LYS_199	NZ	L_ASP_110	OD2	2.866
4GMT	L_ARG_211	NH1	L_GLU_187	OE2	3.717
4GMT	H_LYS_12	NZ	H_GLU_10	OE1	3.698
4GMT	H_ARG_40	NH1	H_GLU_85	OE1	3.459
4GMT	H_ARG_40	NH2	H_GLU_85	OE1	3.548
4GMT	H_LYS_64	NZ	H_GLU_61	OE1	3.355
4GMT	H_LYS_64	NZ	H_GLU_61	OE2	3.496
4GMT	H_LYS_66	NZ	H_ASP_86	OD2	3.279
4GMT	H_HIS_164	NE2	L_ASP_167	OD2	3.650
4GMT	H_LYS_205	NZ	H_ASP_207	OD1	2.972
4GMT	H_LYS_205	NZ	H_ASP_207	OD2	3.617
4GMT	M_ARG_61	NH1	M_GLU_81	OE2	3.800
4GMT	M_ARG_61	NH2	M_GLU_81	OE2	3.404
4GMT	M_ARG_61	NH2	M_ASP_82	OD1	3.417
4GMT	M_ARG_61	NH2	M_ASP_82	OD2	2.761
4GMT	M_LYS_103	NZ	M_GLU_85	OE1	3.664
4GMT	M_LYS_107	NZ	M_ASP_17	OD2	3.878
4GMT	M_LYS_142	NZ	M_ASP_143	OD1	2.867
4GMT	M_ARG_155	NH1	M_GLU_185	OE1	3.423
4GMT	M_ARG_188	NH2	M_GLU_185	OE2	2.544
4GMT	M_LYS_199	NZ	M_ASP_110	OD2	3.054
4GMT	I_LYS_38	NZ	I_GLU_46	OE1	3.821
4GMT	I_ARG_40	NH1	I_GLU_85	OE1	2.810
4GMT	I_ARG_40	NH2	I_GLU_85	OE1	3.101
4GMT	I_ARG_40	NH2	I_GLU_85	OE2	3.496
4GMT	I_LYS_64	NZ	I_GLU_61	OE1	2.992
4GMT	I_LYS_66	NZ	I_ASP_86	OD1	3.775
4GMT	I_LYS_66	NZ	I_ASP_86	OD2	3.105
4GMT	I_LYS_205	NZ	I_ASP_207	OD1	3.730
4GXU	A_LYS_	NZ	F_GLU_	OE1	3.529
4GXU	A_LYS_	NZ	F_GLU_	OE2	3.469
4GXU	A_LYS_53	NZ	A_ASP_276	OD1	3.005
4GXU	A_LYS_	NZ	A_GLU_75	OE1	2.922
4GXU	A_ARG_109	NH1	A_GLU_89	OE1	2.638
4GXU	A_ARG_109	NH1	A_GLU_89	OE2	3.793
4GXU	A_ARG_109	NH2	A_GLU_89	OE1	3.235
4GXU	A_ARG_109	NH2	A_GLU_89	OE2	3.010
4GXU	A_ARG_109	NH2	B_GLU_69	OE1	3.987
4GXU	A_ARG_109	NH2	B_GLU_69	OE2	3.286

4GXU	A_ARG_149	NH2	A_ASP_77	OD1	3.644
4GXU	A_ARG_149	NH2	A_ASP_77	OD2	2.613
4GXU	A_LYS_163	NZ	A_GLU_246	OE1	2.988
4GXU	A_LYS_163	NZ	A_GLU_246	OE2	3.949
4GXU	A_LYS_174	NZ	A_GLU_119	OE1	2.547
4GXU	A_LYS_174	NZ	A_GLU_119	OE2	3.226
4GXU	A_LYS_208	NZ	A_GLU_238	OE1	3.242
4GXU	A_LYS_208	NZ	A_GLU_238	OE2	3.214
4GXU	A_ARG_262	NH2	A_GLU_175	OE1	3.438
4GXU	A_ARG_262	NH2	A_GLU_175	OE2	2.905
4GXU	A_ARG_	NH1	B_ASP_	OD1	2.648
4GXU	A_ARG_	NH2	B_ASP_	OD1	2.545
4GXU	A_ARG_	NH1	A_GLU_	OE2	3.223
4GXU	A_ARG_	NH2	A_GLU_	OE2	3.931
4GXU	B_LYS_	NZ	B_GLU_	OE1	2.602
4GXU	B_LYS_58	NZ	B_GLU_57	OE1	3.935
4GXU	B_LYS_58	NZ	D_GLU_97	OE1	3.748
4GXU	B_LYS_68	NZ	A_GLU_110	OE2	3.492
4GXU	B_ARG_76	NH1	F_GLU_74	OE1	3.015
4GXU	B_ARG_76	NH1	F_GLU_74	OE2	2.935
4GXU	B_ARG_76	NH2	E_GLU_107	OE2	3.559
4GXU	B_ARG_76	NH2	F_GLU_74	OE2	2.547
4GXU	B_LYS_83	NZ	F_ASP_85	OD1	3.431
4GXU	B_LYS_83	NZ	F_ASP_85	OD2	3.614
4GXU	B_ARG_	NH2	D_ASP_	OD2	3.432
4GXU	B_ARG_	NH1	F_GLU_	OE1	3.168
4GXU	B_ARG_	NH2	F_GLU_	OE1	3.085
4GXU	B_ARG_	NH2	F_GLU_	OE2	3.110
4GXU	B_LYS_	NZ	B_GLU_	OE1	3.038
4GXU	B_LYS_	NZ	B_GLU_	OE2	3.952
4GXU	B_ARG_	NH1	B_GLU_	OE2	2.823
4GXU	B_LYS_	NZ	B_GLU_	OE1	3.999
4GXU	C_LYS_32	NZ	B_GLU_57	OE1	3.823
4GXU	C_LYS_32	NZ	B_GLU_57	OE2	3.681
4GXU	C_LYS_	NZ	C_ASP_276	OD1	3.258
4GXU	C_LYS_63	NZ	C_GLU_75	OE1	3.089
4GXU	C_ARG_109	NH1	C_GLU_89	OE1	2.661
4GXU	C_ARG_109	NH1	C_GLU_89	OE2	3.514
4GXU	C_ARG_109	NH2	C_GLU_89	OE1	3.287
4GXU	C_ARG_109	NH2	C_GLU_89	OE2	2.852
4GXU	C_ARG_109	NH2	D_GLU_69	OE1	3.507
4GXU	C_ARG_109	NH2	D_GLU_69	OE2	3.205
4GXU	C_ARG_149	NH2	C_ASP_77	OD1	3.970
4GXU	C_ARG_149	NH2	C_ASP_77	OD2	3.229
4GXU	C_LYS_163	NZ	C_GLU_246	OE1	3.356
4GXU	C_LYS_	NZ	C_GLU_119	OE1	2.755
4GXU	C_LYS_	NZ	C_GLU_119	OE2	2.730
4GXU	C_LYS_208	NZ	C_GLU_238	OE1	3.337
4GXU	C_LYS_208	NZ	C_GLU_238	OE2	3.528
4GXU	C_LYS_	NZ	C_GLU_	OE2	3.454
4GXU	C_ARG_310	NH1	D_ASP_90	OD1	3.385
4GXU	C_ARG_310	NH2	D_ASP_90	OD1	3.336
4GXU	C_ARG_321	NH1	C_GLU_31	OE2	3.152
4GXU	C_ARG_321	NH2	C_GLU_31	OE2	3.675
4GXU	D_HIS_	NE2	D_ASP_	OD1	3.647
4GXU	D_LYS_	NZ	D_GLU_	OE1	2.571
4GXU	D_LYS_	NZ	D_GLU_	OE1	3.860
4GXU	D_LYS_68	NZ	C_GLU_110	OE2	3.981

4GXU	D_ARG_76	NH1	B_GLU_74	OE1	2.948
4GXU	D_ARG_76	NH1	B_GLU_74	OE2	3.453
4GXU	D_ARG_76	NH2	A_GLU_107	OE2	3.465
4GXU	D_ARG_76	NH2	B_GLU_74	OE1	3.835
4GXU	D_ARG_76	NH2	B_GLU_74	OE2	2.916
4GXU	D_LYS_83	NZ	B_ASP_85	OD1	3.057
4GXU	D_LYS_83	NZ	B_ASP_85	OD2	3.527
4GXU	D_ARG_	NH2	F_ASP_	OD2	3.392
4GXU	D_ARG_	NH1	B_GLU_	OE1	2.743
4GXU	D_ARG_	NH1	B_GLU_	OE2	3.931
4GXU	D_ARG_	NH2	B_GLU_	OE1	2.897
4GXU	D_ARG_	NH2	B_GLU_	OE2	2.579
4GXU	D_ARG_	NH2	D_GLU_	OE2	3.558
4GXU	D_LYS_	NZ	D_GLU_	OE1	3.191
4GXU	D_LYS_	NZ	D_GLU_	OE2	3.786
4GXU	D_ARG_	NH1	D_GLU_	OE2	2.518
4GXU	D_LYS_	NZ	D_GLU_	OE1	3.949
4GXU	E_LYS_	NZ	D_GLU_	OE1	3.848
4GXU	E_LYS_	NZ	D_GLU_	OE2	3.549
4GXU	E_LYS_	NZ	E_ASP_	OD1	3.280
4GXU	E_LYS_	NZ	E_GLU_	OE1	3.829
4GXU	E_LYS_	NZ	E_GLU_	OE1	2.868
4GXU	E_ARG_109	NH1	E_GLU_89	OE1	2.836
4GXU	E_ARG_109	NH1	E_GLU_89	OE2	3.830
4GXU	E_ARG_109	NH2	E_GLU_89	OE1	3.271
4GXU	E_ARG_109	NH2	E_GLU_89	OE2	2.995
4GXU	E_ARG_109	NH2	F_GLU_69	OE1	3.819
4GXU	E_ARG_109	NH2	F_GLU_69	OE2	3.459
4GXU	E_ARG_149	NH2	E_ASP_77	OD2	3.169
4GXU	E_LYS_163	NZ	E_GLU_246	OE1	3.757
4GXU	E_LYS_	NZ	E_GLU_	OE1	2.406
4GXU	E_LYS_	NZ	E_GLU_	OE2	3.375
4GXU	E_LYS_208	NZ	E_GLU_	OE1	3.387
4GXU	E_LYS_208	NZ	E_GLU_238	OE2	3.285
4GXU	E_ARG_262	NH2	E_GLU_	OE1	3.936
4GXU	E_ARG_262	NH2	E_GLU_	OE2	3.458
4GXU	E_LYS_	NZ	E_GLU_	OE2	3.797
4GXU	E_ARG_310	NH1	F_ASP_90	OD1	2.704
4GXU	E_ARG_310	NH2	F_ASP_90	OD1	2.770
4GXU	E_ARG_	NH1	E_GLU_	OE1	3.512
4GXU	E_ARG_	NH1	E_GLU_	OE2	2.851
4GXU	E_ARG_	NH2	E_GLU_	OE2	3.048
4GXU	F_LYS_	NZ	F_GLU_	OE1	2.531
4GXU	F_LYS_	NZ	B_GLU_	OE1	3.893
4GXU	F_LYS_68	NZ	E_GLU_110	OE2	3.968
4GXU	F_ARG_76	NH1	D_GLU_74	OE1	2.787
4GXU	F_ARG_76	NH1	D_GLU_74	OE2	3.366
4GXU	F_ARG_76	NH2	C_GLU_107	OE2	3.548
4GXU	F_ARG_76	NH2	D_GLU_74	OE1	3.616
4GXU	F_ARG_76	NH2	D_GLU_74	OE2	2.732
4GXU	F_LYS_83	NZ	D_ASP_85	OD1	3.339
4GXU	F_LYS_83	NZ	D_ASP_85	OD2	3.717
4GXU	F_ARG_	NH2	B_ASP_	OD2	3.670
4GXU	F_ARG_	NH1	D_GLU_	OE1	3.077
4GXU	F_ARG_	NH2	D_GLU_	OE1	2.952
4GXU	F_ARG_	NH2	D_GLU_	OE2	3.074
4GXU	F_ARG_	NH2	F_GLU_	OE2	3.328
4GXU	F_LYS_	NZ	F_GLU_	OE1	3.535

4GXU	F_LYS_	NZ	F_GLU_	OE2	3.712
4GXU	F_ARG_	NH1	F_GLU_	OE2	2.854
4GXU	G_LYS_	NZ	J_GLU_	OE1	3.601
4GXU	G_LYS_	NZ	J_GLU_	OE2	3.403
4GXU	G_LYS_	NZ	G_ASP_	OD1	3.005
4GXU	G_LYS_	NZ	G_GLU_	OE1	2.980
4GXU	G_ARG_	NH1	G_GLU_	OE1	2.812
4GXU	G_ARG_	NH1	G_GLU_	OE2	3.396
4GXU	G_ARG_	NH2	G_GLU_	OE1	3.672
4GXU	G_ARG_	NH2	G_GLU_	OE2	2.896
4GXU	G_ARG_	NH2	H_GLU_	OE2	3.183
4GXU	G_ARG_	NH2	G_ASP_	OD1	3.470
4GXU	G_ARG_	NH2	G_ASP_	OD2	2.671
4GXU	G_LYS_	NZ	G_GLU_	OE1	3.089
4GXU	G_LYS_	NZ	G_GLU_	OE2	3.833
4GXU	G_LYS_	NZ	G_GLU_	OE1	2.593
4GXU	G_LYS_	NZ	G_GLU_	OE2	3.863
4GXU	G_LYS_	NZ	G_GLU_	OE1	3.478
4GXU	G_ARG_	NH2	G_GLU_	OE1	3.819
4GXU	G_ARG_	NH2	G_GLU_	OE2	3.300
4GXU	G_ARG_	NH1	H_ASP_	OD1	2.337
4GXU	G_ARG_	NH2	H_ASP_	OD1	2.900
4GXU	G_ARG_	NH1	G_ASP_	OD1	3.664
4GXU	G_ARG_	NH1	G_GLU_	OE1	3.532
4GXU	G_ARG_	NH1	G_GLU_	OE2	3.002
4GXU	G_ARG_	NH2	G_GLU_	OE2	3.072
4GXU	H_HIS_	NE2	H_ASP_	OD1	3.881
4GXU	H_LYS_	NZ	H_GLU_	OE1	2.920
4GXU	H_LYS_	NZ	L_GLU_	OE1	3.639
4GXU	H_LYS_	NZ	G_GLU_	OE2	3.438
4GXU	H_ARG_	NH1	J_GLU_	OE1	2.612
4GXU	H_ARG_	NH1	J_GLU_	OE2	3.374
4GXU	H_ARG_	NH2	L_GLU_	OE2	3.506
4GXU	H_ARG_	NH2	J_GLU_	OE1	3.326
4GXU	H_ARG_	NH2	J_GLU_	OE2	2.517
4GXU	H_LYS_	NZ	J_ASP_	OD1	2.938
4GXU	H_LYS_	NZ	J_ASP_	OD2	3.368
4GXU	H_ARG_	NH2	L_ASP_	OD2	3.212
4GXU	H_ARG_	NH1	J_GLU_	OE1	3.044
4GXU	H_ARG_	NH2	J_GLU_	OE1	2.714
4GXU	H_ARG_	NH2	J_GLU_	OE2	3.067
4GXU	H_LYS_	NZ	H_GLU_	OE1	3.090
4GXU	H_ARG_	NH1	H_GLU_	OE2	2.508
4GXU	H_LYS_	NZ	H_GLU_	OE1	3.808
4GXU	H_LYS_	NZ	H_GLU_	OE2	3.001
4GXU	L_LYS_	NZ	L_GLU_	OE1	3.747
4GXU	L_LYS_	NZ	L_GLU_	OE2	3.353
4GXU	L_LYS_	NZ	L_ASP_	OD1	3.170
4GXU	L_LYS_	NZ	L_GLU_	OE1	2.809
4GXU	L_ARG_	NH1	L_GLU_	OE1	2.622
4GXU	L_ARG_	NH1	L_GLU_	OE2	3.326
4GXU	L_ARG_	NH2	L_GLU_	OE1	3.446
4GXU	L_ARG_	NH2	L_GLU_	OE2	2.752
4GXU	L_ARG_	NH2	J_GLU_	OE1	3.762
4GXU	L_ARG_	NH2	J_GLU_	OE2	2.924
4GXU	L_ARG_	NH2	L_ASP_	OD1	3.969
4GXU	L_ARG_	NH2	L_ASP_	OD2	2.932
4GXU	L_LYS_	NZ	L_GLU_	OE1	3.315

4GXU	LLYS_	NZ	L_GLU_	OE2	3.981
4GXU	LLYS_	NZ	L_GLU_	OE1	2.410
4GXU	LLYS_	NZ	L_GLU_	OE2	3.536
4GXU	LLYS_	NZ	L_GLU_	OE1	3.215
4GXU	L_ARG_	NH2	L_GLU_	OE2	3.984
4GXU	LLYS_	NZ	L_GLU_	OE1	3.949
4GXU	LLYS_	NZ	L_GLU_	OE2	3.673
4GXU	L_ARG_	NH1	J_ASP_	OD1	2.388
4GXU	L_ARG_	NH2	J_ASP_	OD1	2.649
4GXU	L_ARG_	NH1	L_GLU_	OE1	3.395
4GXU	L_ARG_	NH1	L_GLU_	OE2	2.991
4GXU	L_ARG_	NH2	L_GLU_	OE2	3.022
4GXU	J_HIS_	NE2	J_ASP_	OD1	3.723
4GXU	J_LYS_	NZ	J_GLU_	OE1	2.696
4GXU	J_LYS_	NZ	H_GLU_	OE1	3.949
4GXU	J_LYS_	NZ	L_GLU_	OE2	3.674
4GXU	J_ARG_	NH1	L_GLU_	OE1	2.912
4GXU	J_ARG_	NH1	L_GLU_	OE2	3.322
4GXU	J_ARG_	NH2	K_GLU_	OE2	3.542
4GXU	J_ARG_	NH2	L_GLU_	OE1	3.621
4GXU	J_ARG_	NH2	L_GLU_	OE2	2.520
4GXU	J_LYS_	NZ	L_ASP_	OD1	3.139
4GXU	J_LYS_	NZ	L_ASP_	OD2	3.566
4GXU	J_ARG_	NH2	H_ASP_	OD2	3.270
4GXU	J_ARG_	NH1	L_GLU_	OE1	3.377
4GXU	J_ARG_	NH2	J_GLU_	OE2	3.805
4GXU	J_ARG_	NH2	L_GLU_	OE1	2.504
4GXU	J_ARG_	NH2	L_GLU_	OE2	3.208
4GXU	J_LYS_	NZ	J_GLU_	OE1	3.200
4GXU	J_LYS_	NZ	J_GLU_	OE2	3.922
4GXU	J_ARG_	NH1	J_GLU_	OE2	2.706
4GXU	J_LYS_	NZ	J_GLU_	OE1	3.514
4GXU	J_LYS_	NZ	J_GLU_	OE2	3.322
4GXU	K_LYS_	NZ	H_GLU_	OE2	3.068
4GXU	K_LYS_	NZ	K_ASP_	OD1	3.466
4GXU	K_LYS_	NZ	K_GLU_	OE1	2.616
4GXU	K_ARG_	NH1	K_GLU_	OE1	2.847
4GXU	K_ARG_	NH1	K_GLU_	OE2	3.789
4GXU	K_ARG_	NH2	K_GLU_	OE1	3.337
4GXU	K_ARG_	NH2	K_GLU_	OE2	2.934
4GXU	K_ARG_	NH2	L_GLU_	OE1	3.835
4GXU	K_ARG_	NH2	L_GLU_	OE2	3.159
4GXU	K_ARG_	NH2	K_ASP_	OD1	3.461
4GXU	K_ARG_	NH2	K_ASP_	OD2	2.584
4GXU	K_LYS_	NZ	K_GLU_	OE1	2.688
4GXU	K_LYS_	NZ	K_GLU_	OE2	3.997
4GXU	K_LYS_	NZ	K_GLU_	OE1	3.262
4GXU	K_LYS_	NZ	K_GLU_	OE2	2.919
4GXU	K_ARG_	NH2	K_GLU_	OE1	3.557
4GXU	K_ARG_	NH2	K_GLU_	OE2	3.243
4GXU	K_ARG_	NH1	L_ASP_	OD1	2.447
4GXU	K_ARG_	NH2	L_ASP_	OD1	2.754
4GXU	K_ARG_	NH1	K_GLU_	OE1	3.546
4GXU	K_ARG_	NH1	K_GLU_	OE2	2.807
4GXU	K_ARG_	NH2	K_GLU_	OE2	3.397
4GXU	L_LYS_	NZ	L_GLU_	OE1	2.769
4GXU	L_LYS_	NZ	J_GLU_	OE1	3.674
4GXU	L_LYS_	NZ	L_GLU_	OE1	3.962

4GXU	L_LYS_	NZ	K_GLU_	OE2	3.305
4GXU	L_ARG_	NH1	H_GLU_	OE1	2.958
4GXU	L_ARG_	NH1	H_GLU_	OE2	3.138
4GXU	L_ARG_	NH2	G_GLU_	OE2	3.886
4GXU	L_ARG_	NH2	H_GLU_	OE1	3.887
4GXU	L_ARG_	NH2	H_GLU_	OE2	2.595
4GXU	L_LYS_	NZ	H_ASP_	OD1	2.732
4GXU	L_LYS_	NZ	H_ASP_	OD2	3.190
4GXU	L_ARG_	NH2	J_ASP_	OD2	3.583
4GXU	L_ARG_	NH1	H_GLU_	OE1	3.044
4GXU	L_ARG_	NH2	H_GLU_	OE1	2.477
4GXU	L_ARG_	NH2	H_GLU_	OE2	3.036
4GXU	L_ARG_	NH2	L_GLU_	OE2	3.856
4GXU	L_LYS_	NZ	L_GLU_	OE1	2.914
4GXU	L_LYS_	NZ	L_GLU_	OE2	3.773
4GXU	L_LYS_	NZ	L_GLU_	OE2	3.996
4GXU	L_LYS_	NZ	L_GLU_	OE1	3.816
4GXU	L_ARG_	NH1	L_GLU_	OE1	3.472
4GXU	L_LYS_	NZ	L_GLU_	OE1	3.566
4GXU	M_ARG_	NH2	H_GLU_	OE2	3.356
4GXU	M_HIS_35	NE2	M_GLU_95	OE1	2.618
4GXU	M_ARG_	NH1	M_ASP_	OD1	2.787
4GXU	M_ARG_	NH2	M_GLU_46	OE1	3.155
4GXU	M_ARG_	NH2	M_GLU_46	OE2	3.384
4GXU	M_ARG_	NH2	M_ASP_	OD1	3.807
4GXU	M_ARG_	NH1	M_ASP_	OD1	2.866
4GXU	M_ARG_	NH1	M_ASP_	OD1	3.767
4GXU	M_ARG_	NH1	M_ASP_	OD2	2.685
4GXU	M_ARG_	NH2	M_ASP_	OD1	3.010
4GXU	M_ARG_	NH2	M_ASP_	OD2	3.446
4GXU	M_LYS_	NZ	N_GLU_	OE2	2.851
4GXU	M_LYS_	NZ	N_GLU_	OE1	3.371
4GXU	M_ARG_210	NH1	M_GLU_212	OE2	3.375
4GXU	N_ARG_61	NH1	N_ASP_82	OD1	3.079
4GXU	N_ARG_61	NH1	N_ASP_82	OD2	3.905
4GXU	N_ARG_61	NH2	N_ASP_82	OD1	3.806
4GXU	N_ARG_61	NH2	N_ASP_82	OD2	3.473
4GXU	N_HIS_95C	NE2	N_ASP_92	OD2	3.978
4GXU	N_LYS_149	NZ	N_GLU_203	OE1	3.458
4GXU	N_LYS_149	NZ	N_GLU_203	OE2	3.365
4GXU	N_LYS_	NZ	N_GLU_	OE2	3.800
4GXU	N_ARG_189	NH2	N_ASP_151	OD2	3.992
4GXU	O_HIS_35	NE2	O_GLU_95	OE1	2.632
4GXU	O_ARG_38	NH1	O_ASP_86	OD1	2.799
4GXU	O_ARG_38	NH2	O_GLU_46	OE1	3.065
4GXU	O_ARG_38	NH2	O_GLU_46	OE2	3.637
4GXU	O_ARG_38	NH2	O_ASP_86	OD1	3.453
4GXU	O_ARG_55	NH1	O_ASP_53	OD1	3.043
4GXU	O_ARG_66	NH1	O_ASP_86	OD2	2.898
4GXU	O_ARG_66	NH2	O_ASP_86	OD1	3.023
4GXU	O_ARG_66	NH2	O_ASP_86	OD2	2.955
4GXU	P_ARG_61	NH1	P_ASP_82	OD1	2.845
4GXU	P_ARG_61	NH2	P_ASP_82	OD1	3.213
4GXU	P_ARG_61	NH2	P_ASP_82	OD2	3.256
4GXU	P_HIS_95C	NE2	P_ASP_92	OD2	3.801
4GXU	Q_HIS_35	NE2	Q_GLU_95	OE1	2.629
4GXU	Q_ARG_38	NH1	Q_ASP_	OD1	2.771
4GXU	Q_ARG_38	NH2	Q_GLU_46	OE1	3.023

4GXU	Q_ARG_38	NH2	Q_GLU_46	OE2	3.310
4GXU	Q_ARG_38	NH2	Q_ASP_	OD1	3.767
4GXU	Q_ARG_	NH1	Q_ASP_53	OD1	2.937
4GXU	Q_ARG_	NH1	Q_ASP_	OD2	3.290
4GXU	Q_ARG_	NH2	Q_ASP_	OD1	3.283
4GXU	Q_ARG_	NH2	Q_ASP_	OD2	3.512
4GXU	Q_LYS_143	NZ	R_GLU_124	OE2	3.025
4GXU	Q_LYS_209	NZ	R_GLU_123	OE1	3.619
4GXU	Q_LYS_209	NZ	R_GLU_123	OE2	3.564
4GXU	Q_ARG_210	NH1	Q_GLU_212	OE2	3.790
4GXU	R_ARG_61	NH1	R_ASP_82	OD1	3.111
4GXU	R_ARG_61	NH2	R_ASP_82	OD1	3.457
4GXU	R_ARG_61	NH2	R_ASP_82	OD2	3.282
4GXU	R_HIS_95C	NE2	R_ASP_92	OD2	3.471
4GXU	R_LYS_103	NZ	R_GLU_83	OE1	3.281
4GXU	R_LYS_149	NZ	R_GLU_203	OE1	3.940
4GXU	R_LYS_149	NZ	R_GLU_203	OE2	3.587
4GXU	R_LYS_166	NZ	R_GLU_83	OE1	3.059
4GXU	R_ARG_189	NH2	R_ASP_151	OD2	3.874
4GXU	S_HIS_	NE2	S_GLU_	OE1	2.529
4GXU	S_ARG_	NH1	S_ASP_	OD1	2.740
4GXU	S_ARG_	NH2	S_GLU_	OE1	3.285
4GXU	S_ARG_	NH2	S_GLU_	OE2	3.746
4GXU	S_ARG_	NH2	S_ASP_	OD1	2.949
4GXU	S_ARG_	NH1	S_ASP_	OD1	3.061
4GXU	S_ARG_	NH1	S_ASP_	OD2	3.313
4GXU	S_ARG_	NH2	S_ASP_	OD1	3.673
4GXU	S_ARG_	NH2	S_ASP_	OD2	3.715
4GXU	T_ARG_	NH1	T_ASP_	OD1	3.011
4GXU	T_ARG_	NH1	T_ASP_	OD2	3.957
4GXU	T_ARG_	NH2	T_GLU_	OE2	3.945
4GXU	T_ARG_	NH2	T_ASP_	OD1	3.986
4GXU	T_ARG_	NH2	T_ASP_	OD2	3.749
4GXU	T_HIS_	NE2	T_ASP_	OD1	3.982
4GXU	T_HIS_	NE2	T_ASP_	OD2	3.480
4GXU	U_HIS_	NE2	U_GLU_	OE1	2.653
4GXU	U_ARG_	NH1	U_ASP_	OD1	2.802
4GXU	U_ARG_	NH2	U_GLU_	OE1	3.190
4GXU	U_ARG_	NH2	U_GLU_	OE2	3.845
4GXU	U_ARG_	NH2	U_ASP_	OD1	3.446
4GXU	U_ARG_	NH1	U_ASP_	OD1	2.649
4GXU	U_ARG_	NH1	U_ASP_	OD1	3.706
4GXU	U_ARG_	NH1	U_ASP_	OD2	2.832
4GXU	U_ARG_	NH2	U_ASP_	OD1	3.260
4GXU	U_ARG_	NH2	U_ASP_	OD2	3.829
4GXU	V_ARG_	NH1	V_ASP_	OD1	2.994
4GXU	V_ARG_	NH1	V_ASP_	OD2	3.811
4GXU	V_ARG_	NH2	V_GLU_	OE2	3.535
4GXU	V_ARG_	NH2	V_ASP_	OD1	3.986
4GXU	V_ARG_	NH2	V_ASP_	OD2	3.677
4GXU	V_HIS_	NE2	V_ASP_	OD2	3.617
4GXU	V_LYS_	NZ	V_GLU_	OE1	3.869
4GXU	W_HIS_	NE2	W_GLU_	OE1	2.707
4GXU	W_ARG_	NH1	W_ASP_	OD1	3.050
4GXU	W_ARG_	NH2	W_GLU_	OE1	2.832
4GXU	W_ARG_	NH2	W_GLU_	OE2	3.553
4GXU	W_ARG_	NH2	W_ASP_	OD1	3.987
4GXU	W_ARG_	NH1	W_ASP_	OD1	3.089

4GXU	W_ARG_	NH1	W_ASP_	OD2	3.168
4GXU	W_ARG_	NH2	W_ASP_	OD1	3.409
4GXU	W_ARG_	NH2	W_ASP_	OD2	3.720
4GXU	X_ARG_	NH1	X_ASP_	OD1	2.797
4GXU	X_ARG_	NH1	X_ASP_	OD2	3.814
4GXU	X_ARG_	NH2	X_GLU_	OE2	3.994
4GXU	X_ARG_	NH2	X_ASP_	OD1	3.445
4GXU	X_ARG_	NH2	X_ASP_	OD2	3.232
4GXU	X_HIS_	NE2	X_ASP_	OD2	3.599
4GXU	X_LYS_	NZ	X_GLU_	OE1	3.798
4GXV	H_HIS_35	NE2	H_GLU_95	OE1	2.785
4GXV	H_ARG_38	NH1	H_ASP_86	OD1	3.019
4GXV	H_ARG_38	NH2	H_GLU_46	OE1	2.905
4GXV	H_LYS_64	NZ	H_ASP_61	OD2	3.173
4GXV	H_ARG_66	NH1	H_ASP_86	OD1	3.703
4GXV	H_ARG_66	NH1	H_ASP_86	OD2	2.746
4GXV	H_ARG_66	NH2	H_ASP_86	OD1	2.952
4GXV	H_ARG_66	NH2	H_ASP_86	OD2	3.509
4GXV	H_ARG_83	NH2	H_GLU_85	OE2	3.727
4GXV	H_HIS_100C	ND1	H_ASP_100B	OD1	3.205
4GXV	H_LYS_143	NZ	L_GLU_124	OE2	2.866
4GXV	H_LYS_209	NZ	L_GLU_123	OE1	3.472
4GXV	H_LYS_209	NZ	L_GLU_123	OE2	2.731
4GXV	L_ARG_61	NH2	L_GLU_81	OE2	3.689
4GXV	L_ARG_61	NH2	L_ASP_82	OD1	3.502
4GXV	L_ARG_61	NH2	L_ASP_82	OD2	2.802
4GXV	L_HIS_35	NE2	L_GLU_95	OE1	2.829
4GXV	L_ARG_38	NH1	L_ASP_86	OD1	2.848
4GXV	L_ARG_38	NH2	L_GLU_46	OE1	2.855
4GXV	L_ARG_38	NH2	L_GLU_46	OE2	3.582
4GXV	L_ARG_38	NH2	L_ASP_86	OD1	3.824
4GXV	L_ARG_55	NH1	L_ASP_53	OD1	3.307
4GXV	L_ARG_66	NH1	L_ASP_86	OD1	3.857
4GXV	L_ARG_66	NH1	L_ASP_86	OD2	2.776
4GXV	L_ARG_66	NH2	L_ASP_86	OD1	2.973
4GXV	L_ARG_66	NH2	L_ASP_86	OD2	3.413
4GXV	L_LYS_143	NZ	M_GLU_124	OE2	2.455
4GXV	L_LYS_209	NZ	M_GLU_123	OE1	2.930
4GXV	L_LYS_209	NZ	M_GLU_123	OE2	3.487
4GXV	L_ARG_210	NH1	L_GLU_212	OE2	3.879
4GXV	M_ARG_61	NH1	M_ASP_82	OD1	2.653
4GXV	M_ARG_61	NH1	M_ASP_82	OD2	3.622
4GXV	M_ARG_61	NH2	M_ASP_82	OD1	3.282
4GXV	M_ARG_61	NH2	M_ASP_82	OD2	2.922
4GXV	M_HIS_95C	NE2	M_ASP_92	OD2	3.598
4GXV	M_LYS_149	NZ	M_GLU_203	OE1	2.967
4GXV	M_LYS_149	NZ	M_GLU_203	OE2	3.317
4GXV	M_LYS_186	NZ	M_GLU_183	OE2	3.984
4GXX	A_LYS_32	NZ	D_GLU_57	OE1	3.386
4GXX	A_LYS_53	NZ	A_ASP_276	OD1	2.754
4GXX	A_LYS_63	NZ	A_GLU_75	OE1	2.652
4GXX	A_ARG_109	NH1	A_GLU_89	OE1	2.892
4GXX	A_ARG_109	NH1	A_GLU_89	OE2	3.475
4GXX	A_ARG_109	NH2	A_GLU_89	OE1	3.797
4GXX	A_ARG_109	NH2	A_GLU_89	OE2	3.059
4GXX	A_ARG_109	NH2	B_GLU_69	OE2	3.594
4GXX	A_ARG_149	NH2	A_ASP_77	OD1	3.790
4GXX	A_ARG_149	NH2	A_ASP_77	OD2	2.838

4GXX	A_LYS_163	NZ	A_GLU_246	OE1	3.535
4GXX	A_LYS_163	NZ	A_GLU_246	OE2	2.771
4GXX	A_LYS_174	NZ	A_GLU_119	OE1	2.872
4GXX	A_LYS_174	NZ	A_GLU_119	OE2	3.399
4GXX	A_HIS_183	NE2	A_GLU_190	OE2	3.881
4GXX	A_ARG_262	NH2	A_GLU_175	OE1	2.990
4GXX	A_ARG_262	NH2	A_GLU_175	OE2	3.463
4GXX	A_LYS_280	NZ	A_GLU_304	OE2	3.580
4GXX	A_ARG_310	NH1	B_ASP_90	OD1	2.488
4GXX	A_ARG_310	NH2	B_ASP_90	OD1	2.951
4GXX	A_ARG_315	NH1	A_ASP_24	OD1	3.593
4GXX	A_ARG_315	NH1	A_ASP_24	OD2	3.965
4GXX	A_ARG_321	NH1	A_GLU_31	OE1	3.882
4GXX	A_ARG_321	NH1	A_GLU_31	OE2	3.177
4GXX	A_ARG_321	NH2	A_GLU_31	OE2	3.764
4GXX	B_LYS_51	NZ	B_GLU_103	OE1	3.113
4GXX	B_LYS_58	NZ	B_GLU_57	OE1	3.239
4GXX	B_LYS_58	NZ	F_GLU_97	OE1	3.721
4GXX	B_LYS_68	NZ	A_GLU_110	OE2	2.734
4GXX	B_ARG_76	NH1	D_GLU_74	OE1	2.782
4GXX	B_ARG_76	NH1	D_GLU_74	OE2	3.511
4GXX	B_ARG_76	NH2	C_GLU_107	OE2	3.651
4GXX	B_ARG_76	NH2	D_GLU_74	OE1	3.625
4GXX	B_ARG_76	NH2	D_GLU_74	OE2	2.818
4GXX	B_LYS_82	NZ	B_ASP_86	OD1	3.639
4GXX	B_LYS_82	NZ	B_ASP_86	OD2	2.969
4GXX	B_LYS_83	NZ	D_ASP_85	OD1	2.661
4GXX	B_LYS_83	NZ	D_ASP_85	OD2	3.421
4GXX	B_ARG_106	NH2	F_ASP_109	OD2	3.780
4GXX	B_ARG_116	NH2	B_GLU_120	OE2	3.845
4GXX	B_ARG_116	NH2	D_GLU_120	OE1	2.669
4GXX	B_LYS_123	NZ	B_GLU_132	OE1	2.906
4GXX	B_LYS_123	NZ	B_GLU_132	OE2	3.252
4GXX	B_LYS_	NZ	B_GLU_	OE1	3.764
4GXX	B_LYS_	NZ	B_GLU_139	OE2	3.010
4GXX	B_LYS_	NZ	B_GLU_	OE1	3.439
4GXX	B_ARG_153	NH1	B_GLU_150	OE2	2.852
4GXX	C_LYS_32	NZ	F_GLU_57	OE2	3.165
4GXX	C_LYS_53	NZ	C_ASP_276	OD1	3.539
4GXX	C_LYS_63	NZ	C_GLU_75	OE2	3.863
4GXX	C_ARG_109	NH1	C_GLU_89	OE1	2.866
4GXX	C_ARG_109	NH1	C_GLU_89	OE2	3.437
4GXX	C_ARG_109	NH2	C_GLU_89	OE1	3.601
4GXX	C_ARG_109	NH2	C_GLU_89	OE2	2.826
4GXX	C_ARG_109	NH2	D_GLU_69	OE1	3.802
4GXX	C_ARG_109	NH2	D_GLU_69	OE2	3.427
4GXX	C_ARG_149	NH2	C_ASP_77	OD1	3.699
4GXX	C_ARG_149	NH2	C_ASP_77	OD2	2.803
4GXX	C_LYS_174	NZ	C_GLU_119	OE1	3.067
4GXX	C_LYS_174	NZ	C_GLU_119	OE2	3.650
4GXX	C_LYS_208	NZ	C_GLU_238	OE1	3.321
4GXX	C_LYS_208	NZ	C_GLU_238	OE2	3.002
4GXX	C_ARG_262	NH2	C_GLU_175	OE1	3.519
4GXX	C_ARG_262	NH2	C_GLU_175	OE2	2.926
4GXX	C_LYS_280	NZ	C_GLU_304	OE1	3.956
4GXX	C_ARG_310	NH1	D_ASP_90	OD1	2.336
4GXX	C_ARG_310	NH2	D_ASP_86	OD1	3.727
4GXX	C_ARG_310	NH2	D_ASP_90	OD1	3.012

4GXX	C_ARG.315	NH1	C_ASP.24	OD2	3.922
4GXX	D_LYS.51	NZ	D_GLU.103	OE1	2.595
4GXX	D_LYS.58	NZ	B_GLU.97	OE1	3.529
4GXX	D_LYS.68	NZ	C_GLU.110	OE2	2.872
4GXX	D_ARG.76	NH1	F_GLU.74	OE1	2.910
4GXX	D_ARG.76	NH1	F_GLU.74	OE2	3.571
4GXX	D_ARG.76	NH2	E_GLU.107	OE2	3.622
4GXX	D_ARG.76	NH2	F_GLU.74	OE1	3.615
4GXX	D_ARG.76	NH2	F_GLU.74	OE2	2.803
4GXX	D_LYS.83	NZ	F_ASP.85	OD1	2.774
4GXX	D_LYS.83	NZ	F_ASP.85	OD2	3.514
4GXX	D_ARG.106	NH2	B_ASP.109	OD2	3.920
4GXX	D_ARG.116	NH1	F_GLU.120	OE1	3.357
4GXX	D_ARG.116	NH2	D_GLU.120	OE1	3.858
4GXX	D_ARG.116	NH2	F_GLU.120	OE1	3.225
4GXX	D_ARG.116	NH2	F_GLU.120	OE2	3.007
4GXX	D_LYS.123	NZ	D_GLU.132	OE1	3.074
4GXX	D_LYS.123	NZ	D_GLU.132	OE2	3.639
4GXX	D_LYS.131	NZ	D_GLU.139	OE2	3.654
4GXX	D_ARG.153	NH1	D_GLU.150	OE2	2.580
4GXX	E_LYS.32	NZ	B_GLU.57	OE2	3.237
4GXX	E_LYS.53	NZ	E_ASP.276	OD1	3.134
4GXX	E_LYS.63	NZ	E_GLU.75	OE1	2.624
4GXX	E_ARG.109	NH1	E_GLU.89	OE1	2.778
4GXX	E_ARG.109	NH1	E_GLU.89	OE2	3.312
4GXX	E_ARG.109	NH2	E_GLU.89	OE1	3.734
4GXX	E_ARG.109	NH2	E_GLU.89	OE2	2.889
4GXX	E_ARG.109	NH2	F_GLU.69	OE1	3.858
4GXX	E_ARG.109	NH2	F_GLU.69	OE2	2.773
4GXX	E_ARG.149	NH2	E_ASP.77	OD1	3.759
4GXX	E_ARG.149	NH2	E_ASP.77	OD2	2.793
4GXX	E_LYS.163	NZ	E_GLU.246	OE1	3.415
4GXX	E_LYS.174	NZ	E_GLU.119	OE1	2.751
4GXX	E_LYS.174	NZ	E_GLU.119	OE2	3.791
4GXX	E_LYS.208	NZ	E_GLU.238	OE1	3.310
4GXX	E_LYS.208	NZ	E_GLU.238	OE2	3.144
4GXX	E_ARG.262	NH2	E_GLU.175	OE1	3.412
4GXX	E_ARG.262	NH2	E_GLU.175	OE2	3.052
4GXX	E_ARG.310	NH1	F_ASP.90	OD1	2.470
4GXX	E_ARG.310	NH2	F_ASP.90	OD1	2.925
4GXX	E_ARG.315	NH1	E_ASP.24	OD1	3.908
4GXX	E_ARG.321	NH1	E_GLU.31	OE1	3.912
4GXX	E_ARG.321	NH1	E_GLU.31	OE2	2.977
4GXX	E_ARG.321	NH2	E_GLU.31	OE2	3.461
4GXX	F_HIS.26	NE2	F_ASP.146	OD1	3.842
4GXX	F_LYS.51	NZ	F_GLU.103	OE1	2.680
4GXX	F_LYS.58	NZ	D_GLU.97	OE1	3.142
4GXX	F_LYS.68	NZ	E_GLU.110	OE2	2.982
4GXX	F_ARG.76	NH1	B_GLU.74	OE1	2.798
4GXX	F_ARG.76	NH1	B_GLU.74	OE2	3.572
4GXX	F_ARG.76	NH2	A_GLU.107	OE2	3.644
4GXX	F_ARG.76	NH2	B_GLU.74	OE1	3.566
4GXX	F_ARG.76	NH2	B_GLU.74	OE2	2.823
4GXX	F_LYS.83	NZ	B_ASP.85	OD1	2.859
4GXX	F_LYS.83	NZ	B_ASP.85	OD2	3.462
4GXX	F_ARG.106	NH2	D_ASP.109	OD2	3.576
4GXX	F_ARG.116	NH1	B_GLU.120	OE1	2.775
4GXX	F_ARG.116	NH1	B_GLU.120	OE2	3.643

4GXX	F_ARG.116	NH2	B_GLU.120	OE1	3.285
4GXX	F_ARG.116	NH2	B_GLU.120	OE2	2.552
4GXX	F_ARG.116	NH2	F_GLU.120	OE2	3.662
4GXX	F_LYS.123	NZ	F_GLU.132	OE1	2.969
4GXX	F_LYS.123	NZ	F_GLU.132	OE2	3.560
4GXX	F_LYS.	NZ	F_GLU.139	OE2	3.889
4GXX	F_ARG.153	NH1	F_GLU.150	OE2	2.818
4GXX	F_LYS.	NZ	F_GLU.	OE1	3.562
4GXX	F_LYS.	NZ	F_GLU.	OE2	3.737
4H0G	A_LYS.64	NZ	A_GLU.47	OE1	3.762
4H0G	A_LYS.64	NZ	A_GLU.47	OE2	3.209
4H0G	A_LYS.68	NZ	A_ASP.91	OD1	2.637
4H0G	A_LYS.68	NZ	A_ASP.91	OD2	2.768
4H0G	A_ARG.99	NH2	A_ASP.108	OD1	3.595
4H0G	A_ARG.99	NH2	A_ASP.108	OD2	3.122
4H0G	A_ARG.205	NH2	A_ASP.226	OD1	2.570
4H0G	A_ARG.205	NH2	A_ASP.226	OD2	3.224
4H0G	A_LYS.247	NZ	A_GLU.249	OE1	2.645
4H0H	B_LYS.64	NZ	B_GLU.47	OE2	2.501
4H0H	B_LYS.68	NZ	B_ASP.91	OD1	3.545
4H0H	B_LYS.68	NZ	B_ASP.91	OD2	2.692
4H0H	B_ARG.99	NH2	B_ASP.108	OD1	3.511
4H0H	B_ARG.99	NH2	B_ASP.108	OD2	2.749
4H0H	B_ARG.163	NH1	B_ASP.214	OD1	3.546
4H0H	B_ARG.163	NH2	B_ASP.214	OD1	3.756
4H0H	B_ARG.205	NH1	B_GLU.223	OE2	3.240
4H0H	B_ARG.205	NH2	B_GLU.223	OE1	3.635
4H0H	B_ARG.205	NH2	B_GLU.223	OE2	3.897
4H0H	B_ARG.205	NH2	B_GLU.225	OE1	2.872
4H0H	B_ARG.205	NH2	B_ASP.226	OD1	2.832
4H0H	B_ARG.205	NH2	B_ASP.226	OD2	3.613
4H0H	B_ARG.221	NH2	B_GLU.223	OE2	2.851
4H0I	A_LYS.68	NZ	A_ASP.91	OD1	3.664
4H0I	A_LYS.68	NZ	A_ASP.91	OD2	2.815
4H0I	A_ARG.99	NH2	A_ASP.108	OD1	3.509
4H0I	A_ARG.99	NH2	A_ASP.108	OD2	2.911
4H0I	A_ARG.163	NH2	A_ASP.214	OD1	2.763
4H0I	A_ARG.205	NH1	A_GLU.223	OE2	3.851
4H0I	A_ARG.205	NH2	A_GLU.225	OE2	2.757
4H0I	A_ARG.205	NH2	A_ASP.226	OD1	3.005
4H0I	A_ARG.205	NH2	A_ASP.226	OD2	3.508
4H0I	A_ARG.221	NH2	A_GLU.223	OE2	3.683
4H0I	A_LYS.247	NZ	A_GLU.249	OE1	3.405
4H0I	A_LYS.247	NZ	A_GLU.249	OE2	3.892
4H8W	G_HIS.66	ND1	G_GLU.64	OE2	2.743
4H8W	G_LYS.207	NZ	G_GLU.381	OE1	3.361
4H8W	G_LYS.207	NZ	G_GLU.381	OE2	2.825
4H8W	G_LYS.227	NZ	G_GLU.83	OE1	3.758
4H8W	G_LYS.231	NZ	G_GLU.267	OE1	2.924
4H8W	G_HIS.249	NE2	G_GLU.482	OE1	2.960
4H8W	G_LYS.282	NZ	G_GLU.275	OE1	2.895
4H8W	G_LYS.343	NZ	G_GLU.347	OE2	3.998
4H8W	G_LYS.348	NZ	G_GLU.269	OE1	3.647
4H8W	G_LYS.348	NZ	G_GLU.269	OE2	3.325
4H8W	G_LYS.348	NZ	G_GLU.351	OE2	2.761
4H8W	G_ARG.379	NH1	G_ASP.211	OD2	3.811
4H8W	G_ARG.456	NH1	G_GLU.466	OE1	2.922
4H8W	G_ARG.456	NH1	G_GLU.466	OE2	3.660

4H8W	G_ARG_469	NH2	G_ASP_457	OD1	3.748
4H8W	G_ARG_469	NH2	G_ASP_457	OD2	2.810
4H8W	G_LYS_476	NZ	G_GLU_102	OE1	3.752
4H8W	G_ARG_480	NH1	G_ASP_477	OD1	2.732
4H8W	G_LYS_485	NZ	G_GLU_267	OE2	3.866
4H8W	G_LYS_487	NZ	G_ASP_47	OD1	2.663
4H8W	G_LYS_487	NZ	G_ASP_47	OD2	3.551
4H8W	G_LYS_487	NZ	G_GLU_91	OE1	3.873
4H8W	G_LYS_487	NZ	G_GLU_91	OE2	3.127
4H8W	H_ARG_38	NH1	H_ASP_86	OD2	2.753
4H8W	H_ARG_38	NH2	H_GLU_46	OE1	2.942
4H8W	H_ARG_38	NH2	H_GLU_46	OE2	3.785
4H8W	H_ARG_38	NH2	H_ASP_86	OD2	3.820
4H8W	H_ARG_55	NH1	G_ASP_107	OD1	3.623
4H8W	H_ARG_55	NH1	G_ASP_107	OD2	3.025
4H8W	H_ARG_66	NH1	H_ASP_86	OD1	3.602
4H8W	H_ARG_66	NH1	H_ASP_86	OD2	3.242
4H8W	H_ARG_66	NH2	H_ASP_86	OD1	2.663
4H8W	H_ARG_66	NH2	H_ASP_86	OD2	3.744
4H8W	H_LYS_94	NZ	H_ASP_101	OD1	3.932
4H8W	H_LYS_94	NZ	H_ASP_101	OD2	3.783
4H8W	H_LYS_209	NZ	L_GLU_124	OE1	2.673
4H8W	H_LYS_209	NZ	L_GLU_124	OE2	2.808
4H8W	H_ARG_210	NH2	H_GLU_212	OE2	3.750
4H8W	L_ARG_61	NH1	L_ASP_82	OD1	3.642
4H8W	L_ARG_61	NH1	L_ASP_82	OD2	2.727
4H8W	L_ARG_61	NH2	L_ASP_82	OD1	2.875
4H8W	L_ARG_61	NH2	L_ASP_82	OD2	3.419
4H8W	L_LYS_167	NZ	L_GLU_83	OE1	3.479
4H8W	L_LYS_167	NZ	L_GLU_83	OE2	2.659
4H8W	L_ARG_190	NH1	L_ASP_152	OD1	3.209
4H8W	L_ARG_190	NH1	L_ASP_152	OD2	3.525
4H8W	C_LYS_8	NZ	C_GLU_119	OE1	2.938
4H8W	C_LYS_29	NZ	C_GLU_85	OE1	3.161
4H8W	C_LYS_29	NZ	C_GLU_85	OE2	3.156
4H8W	C_ARG_54	NH1	C_ASP_78	OD1	3.760
4H8W	C_ARG_54	NH1	C_ASP_78	OD2	2.826
4H8W	C_ARG_54	NH2	C_ASP_78	OD1	2.862
4H8W	C_ARG_54	NH2	C_ASP_78	OD2	3.438
4H8W	C_ARG_58	NH2	C_GLU_13	OE1	3.422
4H8W	C_ARG_58	NH2	C_GLU_13	OE2	2.940
4H8W	C_ARG_59	NH1	G_ASP_368	OD1	2.952
4H8W	C_ARG_59	NH1	G_ASP_368	OD2	3.318
4H8W	C_ARG_59	NH2	G_ASP_368	OD1	3.741
4H8W	C_ARG_59	NH2	G_ASP_368	OD2	2.611
4H8W	C_ARG_134	NH1	C_GLU_150	OE2	3.466
4H8W	C_ARG_134	NH2	C_GLU_150	OE2	2.720
4H8W	C_ARG_134	NH2	C_ASP_153	OD1	2.923
4H8W	C_ARG_134	NH2	C_ASP_153	OD2	3.632
4HF5	A_LYS_45	NZ	A_ASP_41	OD1	3.023
4HF5	A_LYS_45	NZ	A_ASP_41	OD2	2.738
4HF5	A_LYS_50	NZ	A_GLU_275	OE1	3.846
4HF5	A_LYS_109	NZ	A_GLU_89	OE1	3.835
4HF5	A_LYS_109	NZ	B_GLU_69	OE1	3.017
4HF5	A_LYS_119	NZ	A_GLU_255	OE2	3.751
4HF5	A_LYS_123	NZ	A_GLU_255	OE1	3.191
4HF5	A_ARG_137	NH1	H_ASP_97	OD2	2.969
4HF5	A_ARG_137	NH2	H_ASP_97	OD1	3.008

4HF5	A_ARG_137	NH2	H_ASP_97	OD2	2.797
4HF5	A_HIS_183	NE2	A_GLU_190	OE2	3.373
4HF5	A_HIS_184	NE2	A_GLU_231	OE1	3.723
4HF5	A_LYS_262	NZ	A_GLU_83	OE1	3.426
4HF5	A_LYS_262	NZ	A_GLU_83	OE2	2.633
4HF5	A_ARG_263	NH1	A_GLU_174	OE2	3.471
4HF5	A_ARG_263	NH2	A_GLU_174	OE2	2.803
4HF5	A_LYS_269	NZ	A_GLU_89	OE1	3.758
4HF5	A_LYS_269	NZ	B_GLU_69	OE1	2.931
4HF5	A_LYS_269	NZ	B_GLU_69	OE2	3.200
4HF5	A_LYS_280	NZ	A_GLU_278	OE2	2.927
4HF5	A_LYS_307	NZ	B_GLU_64	OE2	3.558
4HF5	A_LYS_310	NZ	B_ASP_90	OD1	2.877
4HF5	A_ARG_321	NH1	A_GLU_31	OE1	2.994
4HF5	A_ARG_321	NH1	A_GLU_31	OE2	2.844
4HF5	A_ARG_321	NH2	A_GLU_31	OE1	3.793
4HF5	B_LYS_51	NZ	B_GLU_103	OE1	3.501
4HF5	B_ARG_75	NH1	B_GLU_78	OE1	2.803
4HF5	B_ARG_75	NH1	B_GLU_78	OE2	3.443
4HF5	B_ARG_75	NH2	B_GLU_78	OE1	2.681
4HF5	B_LYS_82	NZ	B_ASP_86	OD1	3.014
4HF5	B_ARG_123	NH1	B_ASP_120	OD2	3.836
4HF5	B_LYS_143	NZ	A_ASP_11	OD2	3.934
4HF5	B_ARG_170	NH2	B_ASP_128	OD2	3.090
4HF5	H_ARG_38	NH1	H_ASP_86	OD1	3.397
4HF5	H_ARG_38	NH2	H_GLU_46	OE1	3.432
4HF5	H_ARG_38	NH2	H_GLU_46	OE2	3.377
4HF5	H_ARG_64	NH1	H_ASP_61	OD1	3.700
4HF5	H_ARG_64	NH2	H_ASP_61	OD1	3.901
4HF5	H_ARG_66	NH1	H_ASP_86	OD1	3.656
4HF5	H_ARG_66	NH2	H_ASP_86	OD1	2.847
4HF5	H_ARG_66	NH2	H_ASP_86	OD2	2.651
4HF5	H_LYS_75	NZ	H_ASP_72	OD1	3.287
4HF5	H_ARG_94	NH2	H_ASP_101	OD1	3.485
4HF5	H_ARG_94	NH2	H_ASP_101	OD2	2.891
4HF5	H_LYS_143	NZ	H_ASP_144	OD1	2.973
4HF5	H_LYS_143	NZ	H_ASP_144	OD2	2.934
4HF5	L_HIS_53	ND1	L_GLU_52	OE1	3.652
4HF5	L_HIS_53	NE2	L_GLU_52	OE1	3.847
4HF5	L_ARG_54	NH2	L_ASP_60	OD1	2.781
4HF5	L_ARG_61	NH2	L_ASP_82	OD1	3.562
4HF5	L_LYS_66	NZ	L_ASP_51	OD1	3.019
4HF5	L_LYS_66	NZ	L_ASP_51	OD2	3.023
4HF5	L_LYS_103	NZ	L_ASP_85	OD1	3.547
4HF5	L_LYS_103	NZ	L_ASP_85	OD2	2.955
4HGK	A_HIS_9	ND1	A_GLU_6	OE2	3.257
4HGK	A_HIS_9	ND1	A_ASP_13	OD2	3.915
4HGK	A_HIS_9	NE2	A_ASP_13	OD1	3.802
4HGK	A_HIS_9	NE2	A_ASP_13	OD2	2.774
4HGK	A_ARG_10	NH1	A_ASP_255	OD2	2.741
4HGK	A_ARG_10	NH2	A_GLU_6	OE2	3.561
4HGK	A_LYS_12	NZ	A_GLU_57	OE2	2.562
4HGK	A_LYS_51	NZ	A_GLU_16	OE1	2.813
4HGK	A_HIS_67	ND1	A_ASP_249	OD1	3.864
4HGK	A_HIS_67	NE2	A_ASP_249	OD1	2.767
4HGK	A_HIS_67	NE2	A_ASP_249	OD2	3.220
4HGK	A_LYS_73	NZ	A_GLU_45	OE1	3.064
4HGK	A_ARG_98	NH1	A_ASP_72	OD1	2.860

4HGK	A_ARG_98	NH2	A_ASP_72	OD1	3.120
4HGK	A_ARG_98	NH2	A_GLU_95	OE2	2.998
4HGK	A_HIS_105	NE2	A_GLU_86	OE1	3.472
4HGK	A_ARG_117	NH2	A_ASP_183	OD1	3.422
4HGK	A_ARG_117	NH2	A_ASP_183	OD2	3.534
4HGK	A_ARG_144	NH1	A_GLU_141	OE1	3.085
4HGK	A_ARG_145	NH2	A_GLU_141	OE1	2.935
4HGK	A_ARG_160	NH1	A_GLU_285	OE2	3.710
4HGK	A_LYS_162	NZ	A_GLU_131	OE2	3.380
4HGK	A_LYS_174	NZ	A_ASP_121	OD1	3.589
4HGK	A_LYS_181	NZ	A_GLU_167	OE1	2.954
4HGK	A_LYS_181	NZ	A_GLU_167	OE2	3.073
4HGK	A_ARG_186	NH1	A_ASP_187	OD1	3.404
4HGK	A_LYS_190	NZ	A_GLU_425	OE1	3.698
4HGK	A_LYS_190	NZ	A_GLU_425	OE2	3.906
4HGK	A_ARG_209	NH1	A_ASP_324	OD1	3.792
4HGK	A_ARG_209	NH2	A_ASP_324	OD1	3.124
4HGK	A_ARG_209	NH2	A_GLU_354	OE1	3.847
4HGK	A_ARG_209	NH2	A_GLU_354	OE2	3.387
4HGK	A_LYS_212	NZ	A_GLU_208	OE2	3.796
4HGK	A_LYS_225	NZ	A_ASP_296	OD1	3.782
4HGK	A_LYS_225	NZ	A_ASP_296	OD2	3.781
4HGK	A_LYS_233	NZ	A_ASP_237	OD1	3.352
4HGK	A_LYS_233	NZ	A_ASP_237	OD2	2.652
4HGK	A_LYS_240	NZ	A_ASP_256	OD2	3.517
4HGK	A_ARG_257	NH1	A_GLU_153	OE2	3.027
4HGK	A_ARG_257	NH2	A_GLU_153	OE2	2.860
4HGK	A_LYS_274	NZ	A_GLU_294	OE1	3.878
4HGK	A_LYS_274	NZ	A_GLU_294	OE2	3.129
4HGK	A_HIS_288	ND1	A_GLU_153	OE1	2.949
4HGK	A_HIS_288	ND1	A_GLU_153	OE2	3.659
4HGK	A_LYS_323	NZ	A_GLU_358	OE1	2.748
4HGK	A_LYS_323	NZ	A_GLU_358	OE2	3.753
4HGK	A_ARG_336	NH1	A_GLU_333	OE1	2.887
4HGK	A_ARG_336	NH1	A_GLU_333	OE2	3.968
4HGK	A_ARG_337	NH1	A_GLU_333	OE1	2.815
4HGK	A_ARG_337	NH2	A_GLU_333	OE1	3.771
4HGK	A_ARG_348	NH1	A_GLU_450	OE2	3.559
4HGK	A_ARG_348	NH2	A_GLU_450	OE2	2.854
4HGK	A_LYS_378	NZ	A_ASP_375	OD1	3.797
4HGK	A_ARG_428	NH2	A_GLU_425	OE2	3.049
4HGK	A_ARG_485	NH1	A_GLU_383	OE2	3.444
4HGK	A_ARG_485	NH2	A_GLU_383	OE1	2.699
4HGK	A_ARG_485	NH2	A_GLU_383	OE2	3.000
4HGK	A_ARG_485	NH2	A_GLU_450	OE2	3.657
4HGK	B_LYS_4	NZ	B_GLU_57	OE1	3.991
4HGK	B_HIS_9	ND1	B_GLU_6	OE2	3.774
4HGK	B_HIS_9	NE2	B_ASP_13	OD2	2.894
4HGK	B_ARG_10	NH1	B_ASP_255	OD2	2.787
4HGK	B_ARG_10	NH2	B_GLU_6	OE2	3.189
4HGK	B_LYS_12	NZ	B_GLU_57	OE1	3.527
4HGK	B_LYS_12	NZ	B_GLU_57	OE2	3.163
4HGK	B_LYS_51	NZ	B_GLU_16	OE1	2.848
4HGK	B_HIS_67	ND1	B_ASP_249	OD1	3.381
4HGK	B_HIS_67	NE2	B_ASP_249	OD1	2.384
4HGK	B_HIS_67	NE2	B_ASP_249	OD2	2.929
4HGK	B_LYS_73	NZ	B_GLU_45	OE1	3.090
4HGK	B_ARG_98	NH1	B_ASP_72	OD1	2.872

4HGK	B_ARG_98	NH2	B_ASP_72	OD1	3.149
4HGK	B_ARG_98	NH2	B_GLU_95	OE2	3.021
4HGK	B_HIS_105	NE2	B_GLU_86	OE1	3.473
4HGK	B_ARG_117	NH1	B_ASP_183	OD1	3.152
4HGK	B_ARG_117	NH2	B_ASP_183	OD1	2.607
4HGK	B_ARG_117	NH2	B_ASP_183	OD2	3.783
4HGK	B_ARG_144	NH1	B_GLU_141	OE1	3.094
4HGK	B_ARG_145	NH2	B_GLU_141	OE1	2.948
4HGK	B_ARG_160	NH1	B_GLU_285	OE2	3.974
4HGK	B_LYS_162	NZ	B_GLU_131	OE2	3.359
4HGK	B_LYS_181	NZ	B_GLU_167	OE1	2.749
4HGK	B_LYS_181	NZ	B_GLU_167	OE2	2.805
4HGK	B_LYS_205	NZ	B_GLU_465	OE2	3.218
4HGK	B_ARG_209	NH2	B_ASP_324	OD1	3.305
4HGK	B_ARG_209	NH2	B_GLU_354	OE2	3.723
4HGK	B_LYS_225	NZ	B_ASP_296	OD1	3.981
4HGK	B_LYS_233	NZ	B_ASP_237	OD1	3.425
4HGK	B_LYS_233	NZ	B_ASP_237	OD2	2.618
4HGK	B_LYS_240	NZ	B_ASP_256	OD2	3.510
4HGK	B_HIS_247	NE2	B_ASP_249	OD2	3.558
4HGK	B_ARG_257	NH1	B_GLU_153	OE1	3.383
4HGK	B_ARG_257	NH2	B_GLU_153	OE1	2.959
4HGK	B_LYS_262	NZ	B_GLU_266	OE1	3.407
4HGK	B_LYS_262	NZ	B_GLU_266	OE2	3.772
4HGK	B_LYS_274	NZ	B_GLU_294	OE1	3.883
4HGK	B_LYS_274	NZ	B_GLU_294	OE2	3.144
4HGK	B_HIS_288	ND1	B_GLU_153	OE1	3.601
4HGK	B_HIS_288	ND1	B_GLU_153	OE2	2.554
4HGK	B_LYS_317	NZ	B_ASP_314	OD2	3.790
4HGK	B_LYS_323	NZ	B_GLU_358	OE1	2.750
4HGK	B_LYS_323	NZ	B_GLU_358	OE2	3.753
4HGK	B_ARG_336	NH1	B_GLU_333	OE1	2.876
4HGK	B_ARG_336	NH1	B_GLU_333	OE2	3.980
4HGK	B_ARG_337	NH1	B_GLU_333	OE1	2.817
4HGK	B_ARG_337	NH2	B_GLU_333	OE1	3.764
4HGK	B_ARG_348	NH1	B_GLU_450	OE2	3.585
4HGK	B_ARG_348	NH2	B_GLU_450	OE2	2.871
4HGK	B_LYS_378	NZ	B_ASP_375	OD1	3.753
4HGK	B_LYS_389	NZ	B_GLU_393	OE1	3.466
4HGK	B_ARG_445	NH1	B_GLU_442	OE2	3.842
4HGK	B_ARG_445	NH2	B_GLU_442	OE2	3.028
4HGK	B_ARG_485	NH1	B_GLU_383	OE2	3.455
4HGK	B_ARG_485	NH2	B_GLU_383	OE1	2.708
4HGK	B_ARG_485	NH2	B_GLU_383	OE2	3.008
4HGK	B_ARG_485	NH2	B_GLU_450	OE2	3.644
4HGK	C_ARG_21	NH1	C_ASP_45	OD2	2.805
4HGK	C_ARG_21	NH2	C_ASP_23	OD2	3.642
4HGK	C_ARG_21	NH2	C_ASP_45	OD2	3.962
4HGK	C_LYS_65	NZ	B_GLU_230	OE1	3.917
4HGK	C_LYS_65	NZ	C_ASP_113	OD2	3.638
4HGK	C_ARG_73	NH2	C_ASP_96	OD1	2.911
4HGK	C_ARG_73	NH2	C_ASP_96	OD2	3.688
4HGK	C_ARG_103	NH1	B_GLU_230	OE1	3.099
4HGK	C_ARG_103	NH2	B_GLU_230	OE1	3.263
4HGK	C_ARG_103	NH2	B_GLU_230	OE2	3.968
4HGK	C_ARG_103	NH2	C_ASP_113	OD1	3.388
4HGK	C_ARG_103	NH2	C_ASP_113	OD2	2.979
4HGK	D_ARG_21	NH1	D_ASP_45	OD2	2.813

4HGK	D_ARG_21	NH2	D_ASP_45	OD2	3.945
4HGK	D_ARG_27	NH1	D_ASP_23	OD1	3.814
4HGK	D_ARG_57	NH2	D_ASP_96	OD1	3.778
4HGK	D_LYS_65	NZ	A_GLU_230	OE1	3.741
4HGK	D_LYS_65	NZ	D_ASP_113	OD2	3.664
4HGK	D_ARG_73	NH2	D_ASP_96	OD1	3.000
4HGK	D_ARG_73	NH2	D_ASP_96	OD2	3.124
4HGK	D_ARG_103	NH1	A_GLU_230	OE1	3.115
4HGK	D_ARG_103	NH2	A_GLU_230	OE1	3.112
4HGK	D_ARG_103	NH2	A_GLU_230	OE2	3.907
4HGK	D_ARG_103	NH2	D_ASP_113	OD1	3.384
4HGK	D_ARG_103	NH2	D_ASP_113	OD2	2.984
4HH9	A_ARG_54	NH1	C_ASP_50	OD2	3.238
4HH9	A_ARG_54	NH2	C_ASP_50	OD2	3.183
4HH9	A_ARG_61	NH1	A_GLU_79	OE1	3.519
4HH9	A_ARG_61	NH1	A_GLU_79	OE2	3.676
4HH9	A_ARG_61	NH2	A_GLU_79	OE1	3.286
4HH9	A_ARG_61	NH2	A_GLU_81	OE1	3.129
4HH9	A_ARG_61	NH2	A_ASP_82	OD1	3.001
4HH9	A_ARG_61	NH2	A_ASP_82	OD2	3.679
4HH9	A_ARG_91	NH2	A_ASP_50	OD1	2.827
4HH9	A_LYS_149	NZ	A_GLU_195	OE1	3.346
4HH9	A_LYS_183	NZ	A_GLU_187	OE2	3.477
4HH9	B_HIS_35	NE2	B_GLU_95	OE2	2.800
4HH9	B_ARG_38	NH1	B_ASP_86	OD1	2.849
4HH9	B_ARG_38	NH2	B_ASP_86	OD1	3.956
4HH9	B_LYS_64	NZ	B_ASP_61	OD1	2.675
4HH9	B_ARG_66	NH1	B_ASP_86	OD1	3.513
4HH9	B_ARG_66	NH1	B_ASP_86	OD2	3.921
4HH9	B_ARG_66	NH2	B_ASP_86	OD1	3.293
4HH9	B_ARG_66	NH2	B_ASP_86	OD2	2.337
4HH9	B_LYS_75	NZ	B_ASP_72	OD2	2.839
4HH9	B_ARG_94	NH2	B_ASP_101	OD1	3.522
4HH9	B_ARG_94	NH2	B_ASP_101	OD2	2.685
4HH9	B_LYS_143	NZ	B_ASP_144	OD1	3.830
4HH9	B_LYS_209	NZ	A_GLU_123	OE1	3.274
4HH9	B_LYS_209	NZ	A_GLU_123	OE2	3.488
4HH9	B_LYS_214	NZ	A_ASP_122	OD1	3.788
4HH9	C_ARG_24	NH2	C_ASP_70	OD2	3.842
4HH9	C_ARG_54	NH1	A_ASP_50	OD2	2.782
4HH9	C_ARG_54	NH2	A_ASP_50	OD2	3.752
4HH9	C_ARG_61	NH1	C_GLU_79	OE1	3.726
4HH9	C_ARG_61	NH1	C_GLU_79	OE2	3.687
4HH9	C_ARG_61	NH2	C_GLU_79	OE1	3.548
4HH9	C_ARG_61	NH2	C_GLU_81	OE1	3.056
4HH9	C_ARG_61	NH2	C_ASP_82	OD1	2.727
4HH9	C_ARG_61	NH2	C_ASP_82	OD2	3.346
4HH9	C_ARG_91	NH2	C_ASP_50	OD1	2.719
4HH9	C_LYS_149	NZ	C_GLU_195	OE1	3.641
4HH9	C_LYS_149	NZ	C_GLU_195	OE2	3.059
4HH9	C_HIS_189	NE2	C_ASP_151	OD2	3.983
4HH9	C_ARG_211	NH1	C_GLU_187	OE1	3.912
4HH9	D_HIS_35	NE2	D_GLU_95	OE2	2.710
4HH9	D_ARG_38	NH1	D_ASP_86	OD1	2.846
4HH9	D_ARG_38	NH2	D_ASP_86	OD1	3.935
4HH9	D_ARG_66	NH1	D_ASP_86	OD1	3.013
4HH9	D_ARG_66	NH1	D_ASP_86	OD2	3.359
4HH9	D_ARG_66	NH2	D_ASP_86	OD1	3.871

4HH9	D_ARG_66	NH2	D_ASP_86	OD2	2.760
4HH9	D_ARG_94	NH2	D_ASP_101	OD1	3.831
4HH9	D_ARG_94	NH2	D_ASP_101	OD2	2.965
4HH9	D_LYS_129	NZ	C_GLU_213	OE1	3.401
4HH9	D_LYS_129	NZ	C_GLU_213	OE2	3.163
4HH9	D_LYS_143	NZ	D_ASP_144	OD1	3.474
4HH9	D_LYS_143	NZ	D_ASP_144	OD2	3.679
4HH9	D_LYS_209	NZ	C_GLU_123	OE2	3.057
4HH9	D_LYS_210	NZ	D_GLU_212	OE1	3.242
4HH9	D_LYS_214	NZ	C_ASP_122	OD2	3.367
4HHA	A_ARG_61	NH1	A_GLU_79	OE1	3.133
4HHA	A_ARG_61	NH2	A_GLU_79	OE1	3.839
4HHA	A_ARG_61	NH2	A_ASP_82	OD1	2.950
4HHA	A_ARG_61	NH2	A_ASP_82	OD2	3.472
4HHA	A_ARG_91	NH2	A_ASP_50	OD1	2.826
4HHA	A_ARG_103	NH1	A_GLU_105	OE1	3.652
4HHA	A_ARG_103	NH2	A_GLU_105	OE1	3.992
4HHA	A_LYS_107	NZ	A_GLU_17	OE1	3.316
4HHA	A_LYS_107	NZ	A_GLU_17	OE2	3.376
4HHA	A_LYS_149	NZ	A_GLU_195	OE2	2.569
4HHA	A_ARG_211	NH1	A_GLU_187	OE1	2.769
4HHA	B_HIS_32	ND1	P_GLU_1	OE1	4.000
4HHA	B_HIS_32	NE2	P_GLU_1	OE1	3.076
4HHA	B_HIS_32	NE2	P_GLU_1	OE2	2.639
4HHA	B_HIS_35	NE2	B_GLU_95	OE2	2.765
4HHA	B_ARG_38	NH1	B_ASP_86	OD1	2.958
4HHA	B_ARG_66	NH1	B_ASP_86	OD1	3.061
4HHA	B_ARG_66	NH1	B_ASP_86	OD2	3.374
4HHA	B_ARG_66	NH2	B_ASP_86	OD1	3.930
4HHA	B_ARG_66	NH2	B_ASP_86	OD2	2.793
4HHA	B_ARG_87	NH2	B_GLU_148	OE1	3.817
4HHA	B_ARG_87	NH2	B_GLU_148	OE2	3.007
4HHA	B_ARG_94	NH1	P_GLU_1	OE2	3.723
4HHA	B_ARG_94	NH2	B_ASP_101	OD1	3.771
4HHA	B_ARG_94	NH2	B_ASP_101	OD2	2.779
4HHA	B_ARG_94	NH2	P_GLU_1	OE2	3.026
4HHA	B_LYS_143	NZ	B_ASP_144	OD1	3.788
4HHA	B_HIS_164	NE2	A_ASP_167	OD1	3.917
4HHA	B_LYS_209	NZ	A_GLU_123	OE2	2.754
4HHA	B_LYS_210	NZ	B_GLU_212	OE1	3.348
4HIE	A_ARG_24	NH1	A_ASP_70	OD2	2.822
4HIE	A_ARG_61	NH2	A_GLU_81	OE1	3.581
4HIE	A_ARG_61	NH2	A_ASP_82	OD1	2.932
4HIE	A_ARG_61	NH2	A_ASP_82	OD2	3.691
4HIE	A_ARG_91	NH2	B_GLU_95	OE1	3.457
4HIE	A_ARG_91	NH2	B_GLU_95	OE2	3.317
4HIE	A_LYS_188	NZ	A_ASP_185	OD1	3.766
4HIE	B_HIS_35	NE2	B_GLU_95	OE2	2.692
4HIE	B_ARG_38	NH2	B_GLU_46	OE1	3.053
4HIE	B_ARG_38	NH2	B_GLU_46	OE2	3.761
4HIE	B_ARG_66	NH1	B_ASP_86	OD1	2.947
4HIE	B_ARG_66	NH1	B_ASP_86	OD2	3.482
4HIE	B_ARG_66	NH2	B_ASP_86	OD1	3.793
4HIE	B_ARG_66	NH2	B_ASP_86	OD2	2.815
4HIE	B_LYS_94	NZ	B_ASP_101	OD1	3.259
4HIE	B_LYS_94	NZ	B_ASP_101	OD2	2.919
4HIE	B_LYS_143	NZ	B_ASP_144	OD1	3.226
4HIE	B_LYS_143	NZ	B_ASP_144	OD2	3.341

4HIE	B.LYS_201	NZ	B.ASP_199	OD2	3.632
4HIH	A.ARG_24	NH1	A.ASP_70	OD1	3.074
4HIH	A.ARG_24	NH1	A.ASP_70	OD2	2.888
4HIH	A.ARG_61	NH2	A.GLU_81	OE1	3.240
4HIH	A.ARG_61	NH2	A.ASP_82	OD1	2.810
4HIH	A.ARG_61	NH2	A.ASP_82	OD2	3.489
4HIH	A.ARG_91	NH2	B.GLU_95	OE1	3.470
4HIH	A.ARG_91	NH2	B.GLU_95	OE2	3.314
4HIH	A.LYS_107	NZ	A.GLU_17	OE1	3.699
4HIH	A.LYS_149	NZ	A.GLU_195	OE1	3.559
4HIH	A.LYS_169	NZ	A.ASP_170	OD2	3.069
4HIH	A.LYS_188	NZ	A.ASP_185	OD1	3.565
4HIH	A.ARG_211	NH1	A.GLU_187	OE1	3.810
4HIH	B.HIS_35	NE2	B.GLU_95	OE2	2.814
4HIH	B.ARG_38	NH2	B.GLU_46	OE1	3.181
4HIH	B.ARG_38	NH2	B.GLU_46	OE2	3.797
4HIH	B.ARG_55	NH1	B.ASP_53	OD1	3.769
4HIH	B.ARG_55	NH1	B.ASP_53	OD2	3.363
4HIH	B.ARG_66	NH1	B.ASP_86	OD1	3.461
4HIH	B.ARG_66	NH2	B.ASP_86	OD1	3.186
4HIH	B.ARG_66	NH2	B.ASP_86	OD2	2.400
4HIH	B.LYS_94	NZ	B.ASP_101	OD1	3.233
4HIH	B.LYS_94	NZ	B.ASP_101	OD2	2.906
4HIH	B.LYS_143	NZ	B.ASP_144	OD1	3.210
4HIH	B.LYS_143	NZ	B.ASP_144	OD2	3.587
4HIH	B.LYS_209	NZ	A.GLU_123	OE1	2.853
4HIH	B.LYS_209	NZ	A.GLU_123	OE2	3.685
4HIH	C.ARG_24	NH1	C.ASP_70	OD2	2.725
4HIH	C.ARG_24	NH2	C.ASP_70	OD2	2.940
4HIH	C.ARG_61	NH2	C.ASP_82	OD1	3.061
4HIH	C.ARG_61	NH2	C.ASP_82	OD2	3.666
4HIH	C.ARG_91	NH2	D.GLU_95	OE1	3.527
4HIH	C.ARG_91	NH2	D.GLU_95	OE2	3.339
4HIH	C.LYS_169	NZ	C.ASP_167	OD1	3.850
4HIH	C.LYS_169	NZ	C.ASP_170	OD2	3.306
4HIH	C.LYS_183	NZ	C.GLU_187	OE2	3.644
4HIH	C.LYS_188	NZ	C.ASP_185	OD1	3.956
4HIH	C.ARG_211	NH1	C.GLU_187	OE1	3.874
4HIH	D.HIS_35	NE2	D.GLU_95	OE2	2.717
4HIH	D.ARG_38	NH2	D.GLU_46	OE1	2.906
4HIH	D.ARG_38	NH2	D.GLU_46	OE2	3.704
4HIH	D.ARG_55	NH1	D.ASP_53	OD2	3.143
4HIH	D.LYS_64	NZ	D.ASP_61	OD1	3.074
4HIH	D.ARG_66	NH1	D.ASP_86	OD1	3.418
4HIH	D.ARG_66	NH1	D.ASP_86	OD2	3.903
4HIH	D.ARG_66	NH2	D.ASP_86	OD1	3.186
4HIH	D.ARG_66	NH2	D.ASP_86	OD2	2.280
4HIH	D.LYS_94	NZ	D.ASP_101	OD1	3.190
4HIH	D.LYS_94	NZ	D.ASP_101	OD2	2.845
4HIH	D.LYS_143	NZ	D.ASP_144	OD1	2.994
4HIH	D.LYS_143	NZ	D.ASP_144	OD2	3.430
4HIH	D.LYS_209	NZ	C.GLU_123	OE1	2.616
4HIH	D.LYS_209	NZ	C.GLU_123	OE2	2.820
4HII	A.ARG_24	NH1	A.ASP_70	OD1	2.503
4HII	A.ARG_24	NH1	A.ASP_70	OD2	2.815
4HII	A.ARG_61	NH2	A.GLU_81	OE1	2.820
4HII	A.ARG_61	NH2	A.ASP_82	OD1	3.181
4HII	A.ARG_61	NH2	A.ASP_82	OD2	3.709

4HII	A_ARG_91	NH2	B_GLU_95	OE1	3.439
4HII	A_ARG_91	NH2	B_GLU_95	OE2	3.542
4HII	A_LYS_107	NZ	A_GLU_17	OE1	3.144
4HII	A_LYS_107	NZ	A_GLU_17	OE2	3.461
4HII	A_LYS_183	NZ	A_GLU_187	OE2	3.590
4HII	B_HIS_35	NE2	B_GLU_95	OE2	2.635
4HII	B_ARG_38	NH2	B_GLU_46	OE1	3.115
4HII	B_ARG_38	NH2	B_GLU_46	OE2	3.676
4HII	B_ARG_55	NH1	B_ASP_53	OD2	2.693
4HII	B_LYS_64	NZ	B_ASP_61	OD1	3.295
4HII	B_ARG_66	NH1	B_ASP_86	OD1	3.781
4HII	B_ARG_66	NH2	B_ASP_86	OD1	3.392
4HII	B_ARG_66	NH2	B_ASP_86	OD2	2.480
4HII	B_LYS_94	NZ	B_ASP_101	OD1	3.440
4HII	B_LYS_94	NZ	B_ASP_101	OD2	3.082
4HII	B_LYS_143	NZ	B_ASP_144	OD1	3.286
4HII	B_LYS_143	NZ	B_ASP_144	OD2	3.429
4HII	B_LYS_201	NZ	B_ASP_199	OD2	3.171
4HII	B_LYS_209	NZ	A_GLU_123	OE1	2.845
4HII	B_LYS_209	NZ	A_GLU_123	OE2	2.723
4HII	C_ARG_24	NH1	C_ASP_70	OD2	2.819
4HII	C_ARG_24	NH2	C_ASP_70	OD2	3.355
4HII	C_ARG_61	NH2	C_ASP_82	OD1	3.075
4HII	C_ARG_61	NH2	C_ASP_82	OD2	3.678
4HII	C_ARG_91	NH1	D_GLU_95	OE2	3.915
4HII	C_ARG_91	NH2	D_GLU_95	OE1	3.687
4HII	C_ARG_91	NH2	D_GLU_95	OE2	3.380
4HII	C_ARG_211	NH1	C_GLU_187	OE1	3.789
4HII	D_HIS_35	NE2	D_GLU_95	OE2	2.645
4HII	D_ARG_38	NH2	D_GLU_46	OE1	2.570
4HII	D_ARG_38	NH2	D_GLU_46	OE2	3.392
4HII	D_ARG_55	NH1	D_ASP_53	OD2	3.825
4HII	D_LYS_64	NZ	D_ASP_61	OD1	2.713
4HII	D_ARG_66	NH1	D_ASP_86	OD1	3.823
4HII	D_ARG_66	NH2	D_ASP_86	OD1	2.954
4HII	D_ARG_66	NH2	D_ASP_86	OD2	2.357
4HII	D_LYS_94	NZ	D_ASP_101	OD1	3.250
4HII	D_LYS_94	NZ	D_ASP_101	OD2	2.971
4HII	D_LYS_143	NZ	D_ASP_144	OD1	3.120
4HII	D_LYS_143	NZ	D_ASP_144	OD2	3.351
4HII	D_LYS_201	NZ	D_ASP_199	OD2	3.563
4HIJ	A_ARG_24	NH1	A_ASP_70	OD2	2.299
4HIJ	A_ARG_24	NH2	A_ASP_70	OD2	3.791
4HIJ	A_ARG_61	NH2	A_GLU_81	OE1	2.950
4HIJ	A_ARG_61	NH2	A_ASP_82	OD1	3.410
4HIJ	A_ARG_61	NH2	A_ASP_82	OD2	3.898
4HIJ	A_ARG_91	NH1	B_GLU_95	OE2	3.962
4HIJ	A_ARG_91	NH2	B_GLU_95	OE1	3.390
4HIJ	A_ARG_91	NH2	B_GLU_95	OE2	3.274
4HIJ	A_LYS_107	NZ	A_GLU_17	OE1	3.611
4HIJ	B_HIS_35	NE2	B_GLU_95	OE2	2.959
4HIJ	B_ARG_38	NH1	B_ASP_86	OD1	3.073
4HIJ	B_ARG_38	NH2	B_GLU_46	OE1	3.833
4HIJ	B_ARG_66	NH2	B_ASP_86	OD1	3.357
4HIJ	B_ARG_66	NH2	B_ASP_86	OD2	2.483
4HIJ	B_LYS_94	NZ	B_ASP_101	OD1	3.665
4HIJ	B_LYS_94	NZ	B_ASP_101	OD2	3.228
4HIJ	B_LYS_143	NZ	B_ASP_144	OD1	3.068

4HIJ	B.LYS_143	NZ	B.ASP_144	OD2	3.410
4HIJ	B.LYS_201	NZ	B.ASP_199	OD2	3.924
4HIJ	C.ARG_24	NH1	C.ASP_70	OD1	2.906
4HIJ	C.ARG_24	NH1	C.ASP_70	OD2	2.387
4HIJ	C.ARG_24	NH2	C.ASP_70	OD2	3.911
4HIJ	C.ARG_61	NH2	C.ASP_82	OD1	3.100
4HIJ	C.ARG_61	NH2	C.ASP_82	OD2	3.911
4HIJ	C.ARG_91	NH2	D.GLU_95	OE1	3.772
4HIJ	C.ARG_91	NH2	D.GLU_95	OE2	3.260
4HIJ	C.ARG_211	NH1	C.GLU_187	OE1	3.642
4HIJ	D.HIS_35	NE2	D.GLU_95	OE2	3.142
4HIJ	D.ARG_38	NH1	D.GLU_46	OE1	2.836
4HIJ	D.ARG_38	NH1	D.GLU_46	OE2	3.204
4HIJ	D.ARG_38	NH2	D.GLU_46	OE1	2.304
4HIJ	D.ARG_38	NH2	D.GLU_46	OE2	3.866
4HIJ	D.ARG_66	NH1	D.ASP_86	OD1	3.893
4HIJ	D.ARG_66	NH2	D.ASP_86	OD1	3.106
4HIJ	D.ARG_66	NH2	D.ASP_86	OD2	2.216
4HIJ	D.ARG_83	NH1	D.GLU_85	OE1	3.248
4HIJ	D.LYS_94	NZ	D.ASP_101	OD1	3.449
4HIJ	D.LYS_94	NZ	D.ASP_101	OD2	2.903
4HIJ	D.LYS_143	NZ	D.ASP_144	OD1	3.444
4HIJ	D.LYS_201	NZ	D.ASP_199	OD2	3.897
4HIJ	D.LYS_209	NZ	C.GLU_123	OE2	3.644
4HK0	A.ARG_38	NH1	A.ASP_90	OD1	3.774
4HK0	A.ARG_38	NH2	A.GLU_46	OE1	3.385
4HK0	A.LYS_63	NZ	A.GLU_46	OE1	3.620
4HK0	A.LYS_63	NZ	A.GLU_46	OE2	2.816
4HK0	A.ARG_98	NH1	A.ASP_114	OD1	2.925
4HK0	A.ARG_98	NH1	A.ASP_114	OD2	2.908
4HK0	A.LYS_156	NZ	A.ASP_157	OD2	3.983
4HK0	A.LYS_222	NZ	B.GLU_125	OE2	2.735
4HK0	B.HIS_33	ND1	B.ASP_49	OD1	3.937
4HK0	B.ARG_53	NH2	B.GLU_59	OE1	3.235
4HK0	B.ARG_60	NH1	B.ASP_81	OD1	3.686
4HK0	B.ARG_60	NH1	B.ASP_81	OD2	2.420
4HK0	B.ARG_60	NH2	B.GLU_78	OE1	3.881
4HK0	B.ARG_60	NH2	B.GLU_78	OE2	3.957
4HK0	B.ARG_60	NH2	B.ASP_81	OD1	2.791
4HK0	B.ARG_60	NH2	B.ASP_81	OD2	3.073
4HK0	B.LYS_168	NZ	B.GLU_82	OE1	2.997
4HK0	C.LYS_12	NZ	C.GLU_10	OE1	3.899
4HK0	C.ARG_38	NH1	C.ASP_90	OD1	3.244
4HK0	C.ARG_38	NH2	C.GLU_46	OE1	3.777
4HK0	C.LYS_63	NZ	C.GLU_46	OE1	3.276
4HK0	C.LYS_63	NZ	C.GLU_46	OE2	3.058
4HK0	C.ARG_98	NH1	C.ASP_114	OD1	3.138
4HK0	C.ARG_98	NH1	C.ASP_114	OD2	3.046
4HK0	C.ARG_104	NH2	D.ASP_95	OD2	3.573
4HK0	C.ARG_223	NH1	C.GLU_225	OE2	2.198
4HK0	D.HIS_33	ND1	D.ASP_49	OD1	3.742
4HK0	D.ARG_60	NH1	D.ASP_81	OD1	3.821
4HK0	D.ARG_60	NH1	D.ASP_81	OD2	2.677
4HK0	D.ARG_60	NH2	D.GLU_78	OE1	3.974
4HK0	D.ARG_60	NH2	D.GLU_78	OE2	3.744
4HK0	D.ARG_60	NH2	D.ASP_81	OD1	2.869
4HK0	D.ARG_60	NH2	D.ASP_81	OD2	3.194
4HK0	D.LYS_104	NZ	B.ASP_50	OD1	3.601

4HK0	D_LYS_104	NZ	B_ASP_50	OD2	2.755
4HK0	D_LYS_168	NZ	D_GLU_82	OE1	2.591
4HK0	D_LYS_168	NZ	D_GLU_82	OE2	3.531
4HK3	J_LYS_12	NZ	J_GLU_10	OE1	3.915
4HK3	J_ARG_38	NH2	J_GLU_46	OE1	2.769
4HK3	J_ARG_38	NH2	J_GLU_46	OE2	3.282
4HK3	J_LYS_63	NZ	J_GLU_46	OE2	2.332
4HK3	J_ARG_87	NH1	J_ASP_89	OD2	2.971
4HK3	J_ARG_87	NH2	J_ASP_89	OD2	3.577
4HK3	J_ARG_98	NH2	J_ASP_114	OD2	3.696
4HK3	J_LYS_222	NZ	N_GLU_125	OE2	3.801
4HK3	N_ARG_60	NH1	N_ASP_81	OD1	3.992
4HK3	N_ARG_60	NH1	N_ASP_81	OD2	2.782
4HK3	N_ARG_60	NH2	N_GLU_78	OE1	3.386
4HK3	N_ARG_60	NH2	N_ASP_81	OD1	3.085
4HK3	N_ARG_60	NH2	N_ASP_81	OD2	3.312
4HK3	N_LYS_168	NZ	N_GLU_82	OE1	3.394
4HK3	N_HIS_190	ND1	N_ASP_153	OD2	3.547
4HK3	N_ARG_191	NH2	N_ASP_153	OD1	3.900
4HKB	J_ARG_12	NH2	J_GLU_10	OE1	3.239
4HKB	J_ARG_12	NH2	J_GLU_10	OE2	3.220
4HKB	J_LYS_19	NZ	J_GLU_82	OE1	3.848
4HKB	J_LYS_23	NZ	C_ASP_73	OD1	3.505
4HKB	J_ARG_38	NH1	J_ASP_90	OD1	3.980
4HKB	J_ARG_38	NH2	J_GLU_46	OE1	3.646
4HKB	J_LYS_63	NZ	J_GLU_46	OE1	3.117
4HKB	J_LYS_63	NZ	J_GLU_46	OE2	3.110
4HKB	J_ARG_72	NH2	A_GLU_10	OE1	3.065
4HKB	J_ARG_72	NH2	A_GLU_10	OE2	2.664
4HKB	J_ARG_87	NH1	J_ASP_89	OD2	3.926
4HKB	J_ARG_87	NH2	J_ASP_89	OD2	2.996
4HKB	J_ARG_98	NH2	J_ASP_114	OD2	3.564
4HKB	J_LYS_222	NZ	N_GLU_125	OE1	3.188
4HKB	J_LYS_222	NZ	N_GLU_125	OE2	3.564
4HKB	A_ARG_12	NH2	A_GLU_10	OE1	3.493
4HKB	A_ARG_12	NH2	A_GLU_10	OE2	3.910
4HKB	A_LYS_19	NZ	A_GLU_82	OE2	2.857
4HKB	A_LYS_63	NZ	A_GLU_46	OE1	2.508
4HKB	A_LYS_63	NZ	A_GLU_46	OE2	3.155
4HKB	A_ARG_72	NH2	C_GLU_10	OE1	3.154
4HKB	A_ARG_72	NH2	C_GLU_10	OE2	2.755
4HKB	A_ARG_87	NH2	A_ASP_90	OD1	3.948
4HKB	A_ARG_98	NH1	A_ASP_114	OD2	3.306
4HKB	A_LYS_156	NZ	B_GLU_126	OE2	3.919
4HKB	A_LYS_222	NZ	B_GLU_125	OE1	3.019
4HKB	A_LYS_222	NZ	B_GLU_125	OE2	3.903
4HKB	C_LYS_63	NZ	E_ASP_89	OD1	3.939
4HKB	C_LYS_63	NZ	E_ASP_89	OD2	3.374
4HKB	C_ARG_87	NH2	E_ASP_90	OD1	3.045
4HKB	C_ARG_87	NH2	E_ASP_90	OD2	2.962
4HKB	C_ARG_98	NH2	C_ASP_114	OD2	3.961
4HKB	C_LYS_222	NZ	D_GLU_125	OE1	3.332
4HKB	C_LYS_222	NZ	D_GLU_125	OE2	3.836
4HKB	E_LYS_23	NZ	G_ASP_73	OD1	2.630
4HKB	E_ARG_38	NH2	E_GLU_46	OE1	2.965
4HKB	E_LYS_63	NZ	C_ASP_89	OD1	3.625
4HKB	E_LYS_63	NZ	C_ASP_89	OD2	3.095
4HKB	E_ARG_72	NH1	I_GLU_10	OE1	2.874

4HKB	E_ARG_72	NH1	L_GLU_10	OE2	2.849
4HKB	E_ARG_87	NH1	C_ASP_90	OD1	3.489
4HKB	E_ARG_87	NH1	C_ASP_90	OD2	3.954
4HKB	E_ARG_87	NH2	C_ASP_90	OD1	3.930
4HKB	E_ARG_87	NH2	C_ASP_90	OD2	3.219
4HKB	E_ARG_98	NH1	E_ASP_114	OD1	3.817
4HKB	E_ARG_98	NH2	E_ASP_114	OD1	3.776
4HKB	E_ARG_98	NH2	E_ASP_114	OD2	3.131
4HKB	E_LYS_222	NZ	F_GLU_125	OE2	3.327
4HKB	G_ARG_12	NH2	G_GLU_10	OE1	3.730
4HKB	G_LYS_63	NZ	G_GLU_46	OE1	3.337
4HKB	G_LYS_63	NZ	G_GLU_46	OE2	2.386
4HKB	G_ARG_87	NH1	J_ASP_90	OD1	3.108
4HKB	G_ARG_87	NH1	J_ASP_90	OD2	3.912
4HKB	G_ARG_87	NH2	J_ASP_90	OD2	3.607
4HKB	G_ARG_98	NH1	G_ASP_114	OD1	3.184
4HKB	G_ARG_98	NH1	G_ASP_114	OD2	2.840
4HKB	I_ARG_12	NH1	I_GLU_10	OE2	3.852
4HKB	I_ARG_12	NH2	I_GLU_10	OE1	2.937
4HKB	I_ARG_12	NH2	I_GLU_10	OE2	2.684
4HKB	I_LYS_63	NZ	I_GLU_46	OE1	3.642
4HKB	I_LYS_63	NZ	I_GLU_46	OE2	2.727
4HKB	I_ARG_72	NH2	G_GLU_10	OE1	3.560
4HKB	I_ARG_72	NH2	G_GLU_10	OE2	2.553
4HKB	I_ARG_87	NH2	I_ASP_90	OD1	3.524
4HKB	I_ARG_98	NH1	I_ASP_114	OD1	2.891
4HKB	I_ARG_98	NH1	I_ASP_114	OD2	2.660
4HKB	I_LYS_222	NZ	K_GLU_125	OE2	3.211
4HKB	N_ARG_29	NH1	J_ASP_107	OD1	3.664
4HKB	N_ARG_29	NH1	J_ASP_107	OD2	2.469
4HKB	N_ARG_31	NH1	N_ASP_33	OD2	3.836
4HKB	N_ARG_31	NH2	N_ASP_33	OD1	2.568
4HKB	N_ARG_31	NH2	N_ASP_33	OD2	3.159
4HKB	N_ARG_60	NH1	N_GLU_78	OE1	3.549
4HKB	N_ARG_60	NH2	N_GLU_78	OE1	3.300
4HKB	N_ARG_60	NH2	N_GLU_78	OE2	3.943
4HKB	N_ARG_60	NH2	N_ASP_81	OD1	3.653
4HKB	N_ARG_60	NH2	N_ASP_81	OD2	3.144
4HKB	N_ARG_76	NH2	N_GLU_59	OE1	3.931
4HKB	N_LYS_104	NZ	N_ASP_84	OD1	3.498
4HKB	N_LYS_131	NZ	J_ASP_157	OD2	3.951
4HKB	B_ARG_29	NH1	A_ASP_107	OD2	3.659
4HKB	B_LYS_30	NZ	B_ASP_91	OD1	3.949
4HKB	B_ARG_31	NH2	B_ASP_33	OD1	3.960
4HKB	B_ARG_31	NH2	B_ASP_33	OD2	3.759
4HKB	B_ARG_60	NH1	B_GLU_78	OE2	3.613
4HKB	B_ARG_60	NH2	B_ASP_81	OD1	3.250
4HKB	B_ARG_60	NH2	B_ASP_81	OD2	3.168
4HKB	D_ARG_29	NH1	C_ASP_107	OD2	3.254
4HKB	D_LYS_30	NZ	D_ASP_91	OD1	2.419
4HKB	D_ARG_60	NH1	D_ASP_81	OD2	3.419
4HKB	D_ARG_60	NH2	D_ASP_81	OD1	2.947
4HKB	D_ARG_60	NH2	D_ASP_81	OD2	2.756
4HKB	D_LYS_173	NZ	D_ASP_140	OD1	3.957
4HKB	F_ARG_60	NH1	F_GLU_78	OE2	3.243
4HKB	F_ARG_60	NH1	F_ASP_81	OD2	3.702
4HKB	F_ARG_60	NH2	F_GLU_78	OE2	3.760
4HKB	F_ARG_60	NH2	F_ASP_81	OD1	3.084

4HKB	F_ARG_60	NH2	F_ASP_81	OD2	2.449
4HKB	H_ARG_29	NH1	G_ASP_107	OD2	3.325
4HKB	H_ARG_29	NH2	G_ASP_107	OD2	3.189
4HKB	H_LYS_30	NZ	H_ASP_91	OD1	3.082
4HKB	H_ARG_31	NH1	H_ASP_33	OD1	3.793
4HKB	H_ARG_31	NH1	H_ASP_33	OD2	3.908
4HKB	H_ARG_31	NH2	H_ASP_33	OD1	2.388
4HKB	H_ARG_31	NH2	H_ASP_33	OD2	3.779
4HKB	H_ARG_60	NH1	H_GLU_78	OE1	3.666
4HKB	H_ARG_60	NH2	H_GLU_78	OE1	3.977
4HKB	H_ARG_60	NH2	H_ASP_81	OD1	2.952
4HKB	H_ARG_60	NH2	H_ASP_81	OD2	3.391
4HKB	K_ARG_31	NH1	I_ASP_107	OD2	3.242
4HKB	K_ARG_60	NH1	K_GLU_78	OE1	2.918
4HKB	K_ARG_60	NH1	K_ASP_81	OD2	3.967
4HKB	K_ARG_60	NH2	K_GLU_78	OE1	3.867
4HKB	K_ARG_60	NH2	K_ASP_81	OD1	3.109
4HKB	K_ARG_60	NH2	K_ASP_81	OD2	3.013
4HKB	K_LYS_168	NZ	K_GLU_82	OE1	3.989
4HKX	E_LYS_86	NZ	E_GLU_90	OE2	3.670
4HKX	E_ARG_106	NH1	E_GLU_85	OE1	2.849
4HKX	E_ARG_106	NH1	E_GLU_85	OE2	3.341
4HKX	E_ARG_117	NH2	E_GLU_72	OE1	2.670
4HKX	E_ARG_117	NH2	E_GLU_72	OE2	3.532
4HKX	E_ARG_192	NH1	B_ASP_95	OD2	3.293
4HKX	E_ARG_192	NH2	E_GLU_198	OE1	3.620
4HKX	E_ARG_192	NH2	E_GLU_198	OE2	3.387
4HKX	E_HIS_208	NE2	E_GLU_238	OE2	2.261
4HKX	E_LYS_219	NZ	E_GLU_227	OE1	3.854
4HKX	E_LYS_219	NZ	B_ASP_93	OD1	2.877
4HKX	E_LYS_219	NZ	B_ASP_93	OD2	3.792
4HKX	E_LYS_222	NZ	E_ASP_225	OD1	3.665
4HKX	E_ARG_255	NH2	E_GLU_119	OE2	3.522
4HKX	E_ARG_262	NH1	E_GLU_175	OE2	3.705
4HKX	E_ARG_262	NH2	E_GLU_175	OE1	3.350
4HKX	E_ARG_262	NH2	E_GLU_175	OE2	2.626
4HKX	A_ARG_12	NH1	A_GLU_10	OE1	2.383
4HKX	A_ARG_12	NH2	A_GLU_10	OE1	3.758
4HKX	A_ARG_38	NH1	A_ASP_90	OD1	3.193
4HKX	A_ARG_38	NH2	A_GLU_46	OE1	3.363
4HKX	A_LYS_63	NZ	A_GLU_46	OE1	3.731
4HKX	A_LYS_63	NZ	A_GLU_46	OE2	3.103
4HKX	A_ARG_87	NH2	A_ASP_89	OD2	3.799
4HKX	A_ARG_98	NH1	A_ASP_114	OD1	3.449
4HKX	A_ARG_98	NH1	A_ASP_114	OD2	2.980
4HKX	A_LYS_222	NZ	B_GLU_125	OE1	3.981
4HKX	B_ARG_29	NH2	A_ASP_107	OD2	3.853
4HKX	B_ARG_31	NH1	B_ASP_33	OD1	2.677
4HKX	B_ARG_31	NH1	B_ASP_33	OD2	2.578
4HKX	B_ARG_60	NH1	B_ASP_81	OD1	3.864
4HKX	B_ARG_60	NH1	B_ASP_81	OD2	2.652
4HKX	B_ARG_60	NH2	B_GLU_78	OE1	3.882
4HKX	B_ARG_60	NH2	B_GLU_78	OE2	3.841
4HKX	B_ARG_60	NH2	B_ASP_81	OD1	3.111
4HKX	B_ARG_60	NH2	B_ASP_81	OD2	3.335
4HKX	B_LYS_104	NZ	B_ASP_84	OD1	2.803
4HKX	B_LYS_104	NZ	B_ASP_84	OD2	3.287
4HKX	B_LYS_112	NZ	B_GLU_200	OE1	2.796

4HKX	B.LYS_131	NZ	A.ASP_157	OD2	3.310
4HKX	B.HIS_190	ND1	B.ASP_153	OD2	3.199
4HLZ	A.LYS_45	NZ	A.ASP_41	OD1	3.467
4HLZ	A.LYS_45	NZ	A.ASP_41	OD2	2.740
4HLZ	A.LYS_50	NZ	A.GLU_275	OE1	3.453
4HLZ	A.ARG_94	NH1	A.ASP_63	OD1	3.722
4HLZ	A.ARG_94	NH1	A.ASP_63	OD2	2.940
4HLZ	A.LYS_109	NZ	A.GLU_89	OE1	2.563
4HLZ	A.LYS_109	NZ	A.GLU_89	OE2	3.402
4HLZ	A.LYS_109	NZ	B.GLU_69	OE1	3.478
4HLZ	A.LYS_109	NZ	B.GLU_69	OE2	2.999
4HLZ	A.LYS_119	NZ	A.GLU_255	OE2	3.868
4HLZ	A.LYS_123	NZ	A.GLU_255	OE1	3.335
4HLZ	A.LYS_123	NZ	A.GLU_255	OE2	2.676
4HLZ	A.ARG_149	NH1	A.ASP_77	OD2	3.932
4HLZ	A.ARG_149	NH2	A.ASP_77	OD1	3.367
4HLZ	A.ARG_149	NH2	A.ASP_77	OD2	2.770
4HLZ	A.LYS_165	NZ	A.GLU_246	OE1	3.809
4HLZ	A.HIS_184	NE2	A.GLU_231	OE1	3.401
4HLZ	A.ARG_263	NH2	A.GLU_174	OE1	3.264
4HLZ	A.LYS_269	NZ	A.GLU_89	OE1	3.398
4HLZ	A.LYS_310	NZ	B.ASP_90	OD1	2.429
4HLZ	A.LYS_310	NZ	B.ASP_90	OD2	3.948
4HLZ	A.LYS_313	NZ	A.ASP_27	OD2	3.590
4HLZ	A.ARG_321	NH1	A.GLU_31	OE1	3.534
4HLZ	A.ARG_321	NH1	A.GLU_31	OE2	3.033
4HLZ	A.ARG_321	NH2	A.GLU_31	OE1	2.812
4HLZ	A.ARG_321	NH2	A.GLU_31	OE2	3.752
4HLZ	B.LYS_51	NZ	B.GLU_103	OE1	2.548
4HLZ	B.LYS_58	NZ	F.GLU_97	OE1	3.865
4HLZ	B.LYS_58	NZ	F.GLU_97	OE2	3.885
4HLZ	B.ARG_75	NH1	B.GLU_78	OE1	2.253
4HLZ	B.ARG_75	NH1	B.GLU_78	OE2	3.633
4HLZ	B.ARG_76	NH1	D.GLU_74	OE1	2.838
4HLZ	B.ARG_76	NH1	D.GLU_74	OE2	3.993
4HLZ	B.ARG_76	NH2	D.GLU_74	OE1	3.145
4HLZ	B.ARG_76	NH2	D.GLU_74	OE2	2.917
4HLZ	B.LYS_82	NZ	B.ASP_86	OD1	3.774
4HLZ	B.LYS_82	NZ	B.ASP_86	OD2	2.458
4HLZ	B.LYS_83	NZ	D.GLU_85	OE2	2.459
4HLZ	B.ARG_106	NH2	F.ASP_109	OD2	3.278
4HLZ	B.ARG_123	NH2	B.ASP_120	OD1	3.032
4HLZ	B.LYS_131	NZ	B.GLU_139	OE2	3.861
4HLZ	B.LYS_143	NZ	A.ASP_11	OD1	3.527
4HLZ	B.LYS_143	NZ	A.ASP_11	OD2	3.714
4HLZ	B.LYS_143	NZ	B.ASP_29	OD1	3.825
4HLZ	B.LYS_143	NZ	B.ASP_29	OD2	2.836
4HLZ	B.ARG_170	NH1	B.ASP_128	OD2	3.529
4HLZ	B.ARG_170	NH2	B.ASP_128	OD2	3.130
4HLZ	C.ARG_32	NH1	F.GLU_57	OE1	3.413
4HLZ	C.LYS_45	NZ	C.ASP_41	OD1	3.408
4HLZ	C.LYS_45	NZ	C.ASP_41	OD2	2.813
4HLZ	C.LYS_90	NZ	C.ASP_63	OD1	3.022
4HLZ	C.LYS_90	NZ	C.ASP_63	OD2	3.647
4HLZ	C.ARG_94	NH1	C.GLU_75	OE1	3.383
4HLZ	C.ARG_94	NH1	C.ASP_95	OD1	3.179
4HLZ	C.ARG_94	NH1	C.ASP_95	OD2	3.935
4HLZ	C.LYS_109	NZ	C.GLU_89	OE1	2.906

4HLZ	C_LYS_109	NZ	C_GLU_89	OE2	3.287
4HLZ	C_LYS_109	NZ	D_GLU_69	OE1	2.904
4HLZ	C_LYS_109	NZ	D_GLU_69	OE2	3.394
4HLZ	C_ARG_126	NH2	C_ASP_125	OD2	3.430
4HLZ	C_ARG_149	NH1	C_ASP_77	OD2	3.631
4HLZ	C_ARG_149	NH2	C_ASP_77	OD1	3.636
4HLZ	C_ARG_149	NH2	C_ASP_77	OD2	2.529
4HLZ	C_HIS_184	NE2	C_GLU_231	OE1	3.054
4HLZ	C_ARG_263	NH2	C_GLU_174	OE1	2.955
4HLZ	C_ARG_263	NH2	C_GLU_174	OE2	3.891
4HLZ	C_LYS_269	NZ	C_GLU_89	OE1	2.769
4HLZ	C_LYS_310	NZ	D_ASP_86	OD2	2.827
4HLZ	C_LYS_310	NZ	D_ASP_90	OD1	2.357
4HLZ	C_LYS_310	NZ	D_ASP_90	OD2	3.459
4HLZ	C_LYS_313	NZ	C_ASP_27	OD2	2.972
4HLZ	C_ARG_321	NH1	C_GLU_31	OE1	3.468
4HLZ	C_ARG_321	NH1	C_GLU_31	OE2	3.239
4HLZ	C_ARG_321	NH2	C_GLU_31	OE1	3.056
4HLZ	C_ARG_321	NH2	C_GLU_31	OE2	3.827
4HLZ	D_LYS_51	NZ	D_GLU_103	OE1	2.956
4HLZ	D_LYS_58	NZ	B_GLU_97	OE1	2.796
4HLZ	D_LYS_58	NZ	D_GLU_57	OE2	3.744
4HLZ	D_ARG_75	NH1	D_GLU_78	OE1	3.640
4HLZ	D_ARG_75	NH1	D_GLU_78	OE2	2.859
4HLZ	D_ARG_76	NH1	F_GLU_74	OE1	3.279
4HLZ	D_ARG_76	NH1	F_GLU_74	OE2	2.976
4HLZ	D_ARG_76	NH2	E_GLU_107	OE2	3.277
4HLZ	D_ARG_76	NH2	F_GLU_74	OE2	2.480
4HLZ	D_LYS_83	NZ	F_GLU_85	OE2	2.714
4HLZ	D_ARG_106	NH2	B_ASP_109	OD2	3.865
4HLZ	D_LYS_116	NZ	D_ASP_120	OD2	3.998
4HLZ	D_ARG_123	NH2	D_ASP_120	OD1	2.808
4HLZ	D_LYS_131	NZ	F_ASP_128	OD1	3.317
4HLZ	D_LYS_167	NZ	D_GLU_164	OE1	2.593
4HLZ	E_LYS_45	NZ	E_ASP_41	OD1	3.643
4HLZ	E_LYS_45	NZ	E_ASP_41	OD2	2.964
4HLZ	E_LYS_90	NZ	E_ASP_63	OD1	3.784
4HLZ	E_LYS_109	NZ	E_GLU_89	OE1	3.198
4HLZ	E_LYS_109	NZ	E_GLU_89	OE2	3.420
4HLZ	E_LYS_109	NZ	F_GLU_69	OE1	2.572
4HLZ	E_LYS_109	NZ	F_GLU_69	OE2	3.930
4HLZ	E_LYS_123	NZ	E_GLU_255	OE1	3.027
4HLZ	E_ARG_149	NH2	E_ASP_77	OD1	3.597
4HLZ	E_ARG_149	NH2	E_ASP_77	OD2	3.190
4HLZ	E_HIS_183	NE2	E_GLU_190	OE2	3.927
4HLZ	E_LYS_259	NZ	E_GLU_116C	OE1	3.783
4HLZ	E_LYS_259	NZ	E_GLU_116C	OE2	3.326
4HLZ	E_LYS_269	NZ	E_GLU_89	OE1	3.197
4HLZ	E_LYS_280	NZ	E_GLU_304	OE1	3.278
4HLZ	E_LYS_310	NZ	F_ASP_86	OD1	3.890
4HLZ	E_LYS_310	NZ	F_ASP_90	OD1	3.800
4HLZ	E_ARG_321	NH1	E_GLU_31	OE1	3.413
4HLZ	E_ARG_321	NH1	E_GLU_31	OE2	2.743
4HLZ	E_ARG_321	NH2	E_GLU_31	OE1	3.001
4HLZ	E_ARG_321	NH2	E_GLU_31	OE2	3.732
4HLZ	F_LYS_51	NZ	F_GLU_103	OE1	2.737
4HLZ	F_LYS_58	NZ	D_GLU_97	OE1	3.641
4HLZ	F_ARG_75	NH1	F_GLU_78	OE1	2.620

4HLZ	F_ARG_75	NH2	F_GLU_78	OE1	3.832
4HLZ	F_ARG_76	NH1	B_GLU_74	OE1	3.514
4HLZ	F_ARG_76	NH1	B_GLU_74	OE2	3.227
4HLZ	F_ARG_76	NH2	B_GLU_74	OE1	3.962
4HLZ	F_ARG_76	NH2	B_GLU_74	OE2	2.467
4HLZ	F_ARG_106	NH1	F_GLU_103	OE2	3.652
4HLZ	F_LYS_116	NZ	F_ASP_120	OD2	2.737
4HLZ	F_ARG_123	NH2	F_ASP_120	OD1	2.964
4HLZ	F_LYS_131	NZ	F_GLU_139	OE1	3.361
4HLZ	F_LYS_131	NZ	F_GLU_139	OE2	3.419
4HLZ	F_LYS_143	NZ	F_ASP_29	OD1	2.830
4HLZ	F_ARG_170	NH1	F_ASP_128	OD2	3.604
4HLZ	F_ARG_170	NH2	F_ASP_128	OD2	3.330
4HLZ	G_ARG_38	NH1	G_ASP_86	OD1	3.271
4HLZ	G_ARG_38	NH2	G_GLU_46	OE1	3.356
4HLZ	G_ARG_38	NH2	G_GLU_46	OE2	3.777
4HLZ	G_ARG_38	NH2	G_ASP_86	OD1	3.890
4HLZ	G_ARG_52	NH2	G_ASP_32	OD1	2.343
4HLZ	G_ARG_52	NH2	G_ASP_32	OD2	3.536
4HLZ	G_ARG_66	NH1	G_ASP_86	OD1	3.326
4HLZ	G_ARG_66	NH1	G_ASP_86	OD2	2.639
4HLZ	G_ARG_66	NH2	G_ASP_86	OD1	3.814
4HLZ	G_ARG_83	NH1	G_GLU_85	OE1	3.950
4HLZ	H_ARG_63	NH2	H_ASP_84	OD1	2.596
4HLZ	H_ARG_63	NH2	H_ASP_84	OD2	2.745
4HLZ	H_LYS_144	NZ	H_GLU_107	OE1	3.903
4HLZ	H_LYS_144	NZ	H_GLU_107	OE2	3.652
4HLZ	H_LYS_151	NZ	H_GLU_197	OE1	3.384
4HLZ	H_LYS_151	NZ	H_GLU_197	OE2	3.081
4HLZ	H_LYS_201	NZ	H_ASP_112	OD2	3.156
4HLZ	H_ARG_213	NH2	H_GLU_189	OE1	2.950
4HLZ	I_ARG_38	NH1	I_ASP_86	OD2	2.915
4HLZ	I_ARG_38	NH2	I_GLU_46	OE1	3.111
4HLZ	I_ARG_38	NH2	I_GLU_46	OE2	3.673
4HLZ	I_ARG_38	NH2	I_ASP_86	OD2	3.591
4HLZ	I_ARG_52	NH2	I_ASP_32	OD1	2.561
4HLZ	I_ARG_52	NH2	I_ASP_32	OD2	3.549
4HLZ	I_ARG_66	NH1	I_ASP_86	OD1	2.650
4HLZ	I_ARG_66	NH1	I_ASP_86	OD2	3.900
4HLZ	I_ARG_66	NH2	I_ASP_86	OD1	3.129
4HLZ	I_ARG_66	NH2	I_ASP_86	OD2	2.801
4HLZ	I_ARG_71	NH2	I_ASP_31	OD2	3.990
4HLZ	I_ARG_83	NH2	I_GLU_85	OE1	3.778
4HLZ	I_LYS_96	NZ	D_ASP_46	OD1	2.912
4HLZ	I_LYS_96	NZ	D_ASP_46	OD2	3.655
4HLZ	I_LYS_205	NZ	I_ASP_207	OD1	2.427
4HLZ	I_LYS_208	NZ	J_GLU_125	OE2	3.495
4HLZ	I_ARG_213	NH2	J_GLU_125	OE1	3.227
4HLZ	I_ARG_213	NH2	J_GLU_125	OE2	3.829
4HLZ	J_ARG_63	NH2	J_ASP_84	OD2	2.740
4HLZ	J_LYS_149	NZ	J_GLU_156	OE2	3.758
4HLZ	J_LYS_151	NZ	J_GLU_197	OE2	2.583
4HLZ	J_ARG_157	NH2	J_GLU_187	OE1	3.252
4HLZ	J_ARG_190	NH1	J_ASP_186	OD2	3.881
4HLZ	J_ARG_190	NH2	J_ASP_186	OD2	3.287
4HLZ	J_LYS_201	NZ	J_ASP_112	OD1	3.693
4HLZ	J_LYS_201	NZ	J_ASP_112	OD2	2.715
4HLZ	K_ARG_38	NH1	K_ASP_86	OD2	2.904

4HLZ	K_ARG_38	NH2	K_GLU_46	OE1	3.825
4HLZ	K_ARG_38	NH2	K_GLU_46	OE2	3.374
4HLZ	K_ARG_38	NH2	K_ASP_86	OD2	3.795
4HLZ	K_ARG_52	NH2	K_ASP_32	OD2	3.514
4HLZ	K_ARG_66	NH1	K_ASP_86	OD1	2.524
4HLZ	K_ARG_66	NH2	K_ASP_86	OD1	2.641
4HLZ	K_ARG_66	NH2	K_ASP_86	OD2	2.778
4HLZ	L_ARG_63	NH2	L_ASP_84	OD1	3.511
4HLZ	L_ARG_63	NH2	L_ASP_84	OD2	3.426
4HLZ	L_LYS_151	NZ	L_GLU_197	OE2	3.915
4HMG	A_LYS_27	NZ	B_GLU_97	OE1	2.795
4HMG	A_LYS_27	NZ	B_GLU_97	OE2	3.247
4HMG	A_LYS_50	NZ	A_ASP_275	OD1	2.738
4HMG	A_HIS_56	NE2	A_GLU_280	OE2	3.458
4HMG	A_ARG_57	NH1	A_GLU_82	OE1	2.930
4HMG	A_ARG_57	NH1	A_GLU_82	OE2	3.739
4HMG	A_ARG_57	NH2	A_GLU_82	OE1	3.316
4HMG	A_HIS_75	ND1	A_ASP_73	OD1	2.731
4HMG	A_HIS_75	ND1	A_ASP_73	OD2	3.421
4HMG	A_HIS_75	NE2	A_ASP_63	OD1	3.435
4HMG	A_ARG_90	NH1	A_ASP_60	OD1	2.846
4HMG	A_ARG_90	NH1	A_ASP_60	OD2	3.713
4HMG	A_ARG_109	NH1	B_GLU_67	OE1	3.584
4HMG	A_ARG_109	NH1	B_GLU_67	OE2	2.773
4HMG	A_ARG_109	NH2	A_GLU_89	OE1	3.290
4HMG	A_ARG_109	NH2	A_GLU_89	OE2	2.543
4HMG	A_ARG_141	NH1	A_ASP_77	OD1	2.714
4HMG	A_ARG_141	NH1	A_ASP_77	OD2	3.370
4HMG	A_ARG_141	NH2	A_ASP_77	OD1	2.707
4HMG	A_LYS_176	NZ	A_GLU_123	OE1	2.555
4HMG	A_LYS_176	NZ	A_GLU_123	OE2	3.715
4HMG	A_HIS_183	NE2	A_GLU_190	OE1	3.735
4HMG	A_ARG_207	NH2	A_ASP_241	OD1	3.612
4HMG	A_ARG_208	NH2	A_ASP_241	OD1	3.591
4HMG	A_ARG_208	NH2	A_ASP_241	OD2	2.706
4HMG	A_LYS_238	NZ	A_ASP_175	OD1	2.945
4HMG	A_LYS_238	NZ	A_ASP_175	OD2	2.559
4HMG	A_LYS_238	NZ	F_GLU_72	OE2	2.782
4HMG	A_ARG_261	NH1	A_GLU_119	OE1	3.272
4HMG	A_ARG_261	NH1	A_GLU_119	OE2	3.090
4HMG	A_ARG_261	NH2	A_GLU_119	OE1	2.807
4HMG	A_ARG_261	NH2	A_GLU_119	OE2	2.795
4HMG	A_LYS_264	NZ	A_ASP_85	OD1	3.254
4HMG	A_LYS_264	NZ	A_ASP_85	OD2	2.704
4HMG	A_ARG_269	NH2	B_GLU_67	OE1	2.783
4HMG	A_LYS_292	NZ	A_ASP_291	OD1	2.976
4HMG	A_LYS_292	NZ	A_ASP_291	OD2	2.795
4HMG	A_LYS_310	NZ	B_ASP_90	OD1	3.350
4HMG	A_LYS_310	NZ	B_ASP_90	OD2	2.711
4HMG	A_LYS_315	NZ	A_GLU_41	OE2	3.691
4HMG	B_LYS_51	NZ	B_GLU_103	OE2	2.574
4HMG	B_ARG_54	NH1	F_GLU_97	OE1	3.078
4HMG	B_ARG_54	NH2	B_GLU_57	OE1	2.870
4HMG	B_ARG_54	NH2	B_GLU_57	OE2	3.339
4HMG	B_ARG_54	NH2	E_ASP_32	OD2	3.863
4HMG	B_ARG_54	NH2	F_GLU_97	OE1	3.088
4HMG	B_LYS_62	NZ	F_ASP_86	OD1	2.890
4HMG	B_LYS_62	NZ	F_ASP_86	OD2	2.630

4HMG	B.LYS.62	NZ	F.ASP.90	OD1	3.620
4HMG	B.LYS.62	NZ	F.ASP.90	OD2	3.931
4HMG	B.HIS.64	NE2	F.ASP.79	OD2	3.785
4HMG	B.LYS.68	NZ	B.GLU.85	OE1	2.990
4HMG	B.LYS.68	NZ	B.GLU.85	OE2	2.568
4HMG	B.ARG.76	NH1	D.GLU.74	OE1	2.796
4HMG	B.ARG.76	NH1	D.GLU.74	OE2	3.711
4HMG	B.ARG.76	NH1	D.GLU.81	OE1	2.672
4HMG	B.ARG.76	NH1	D.GLU.81	OE2	3.308
4HMG	B.ARG.76	NH2	D.GLU.74	OE1	3.404
4HMG	B.ARG.76	NH2	D.GLU.74	OE2	2.827
4HMG	B.LYS.117	NZ	B.GLU.114	OE1	2.600
4HMG	B.LYS.117	NZ	B.GLU.114	OE2	3.394
4HMG	B.ARG.123	NH1	F.GLU.132	OE2	3.178
4HMG	B.ARG.123	NH2	B.GLU.120	OE1	2.819
4HMG	B.ARG.123	NH2	B.GLU.120	OE2	2.567
4HMG	B.ARG.124	NH1	F.GLU.132	OE1	3.359
4HMG	B.ARG.124	NH1	F.GLU.132	OE2	3.102
4HMG	B.ARG.124	NH2	B.GLU.120	OE2	3.559
4HMG	B.ARG.127	NH2	F.GLU.131	OE1	2.525
4HMG	B.LYS.143	NZ	B.ASP.145	OD2	3.353
4HMG	B.HIS.159	NE2	B.ASP.160	OD1	3.910
4HMG	B.HIS.159	NE2	B.ASP.160	OD2	3.133
4HMG	B.ARG.163	NH1	F.GLU.131	OE1	3.338
4HMG	B.ARG.163	NH1	F.GLU.131	OE2	2.796
4HMG	B.ARG.163	NH2	F.GLU.131	OE1	2.694
4HMG	B.ARG.163	NH2	F.GLU.131	OE2	3.492
4HMG	B.ARG.170	NH1	B.GLU.128	OE1	2.770
4HMG	B.ARG.170	NH2	B.GLU.131	OE2	2.764
4HMG	B.ARG.170	NH2	D.GLU.128	OE1	3.784
4HMG	B.ARG.170	NH2	D.GLU.128	OE2	3.698
4HMG	C.LYS.27	NZ	D.GLU.97	OE1	2.789
4HMG	C.LYS.27	NZ	D.GLU.97	OE2	3.246
4HMG	C.LYS.50	NZ	C.ASP.275	OD1	2.725
4HMG	C.HIS.56	NE2	C.GLU.280	OE2	3.428
4HMG	C.ARG.57	NH1	C.GLU.82	OE1	2.906
4HMG	C.ARG.57	NH1	C.GLU.82	OE2	3.723
4HMG	C.ARG.57	NH2	C.GLU.82	OE1	3.281
4HMG	C.HIS.75	ND1	C.ASP.73	OD1	2.703
4HMG	C.HIS.75	ND1	C.ASP.73	OD2	3.384
4HMG	C.HIS.75	NE2	C.ASP.63	OD1	3.436
4HMG	C.ARG.90	NH1	C.ASP.60	OD1	2.839
4HMG	C.ARG.90	NH1	C.ASP.60	OD2	3.741
4HMG	C.ARG.109	NH1	D.GLU.67	OE1	3.616
4HMG	C.ARG.109	NH1	D.GLU.67	OE2	2.791
4HMG	C.ARG.109	NH2	C.GLU.89	OE1	3.304
4HMG	C.ARG.109	NH2	C.GLU.89	OE2	2.531
4HMG	C.ARG.141	NH1	C.ASP.77	OD1	2.711
4HMG	C.ARG.141	NH1	C.ASP.77	OD2	3.370
4HMG	C.ARG.141	NH2	C.ASP.77	OD1	2.681
4HMG	C.LYS.176	NZ	C.GLU.123	OE1	2.557
4HMG	C.LYS.176	NZ	C.GLU.123	OE2	3.685
4HMG	C.HIS.183	NE2	C.GLU.190	OE1	3.742
4HMG	C.ARG.207	NH2	C.ASP.241	OD1	3.569
4HMG	C.ARG.208	NH2	C.ASP.241	OD1	3.571
4HMG	C.ARG.208	NH2	C.ASP.241	OD2	2.695
4HMG	C.LYS.238	NZ	B.GLU.72	OE2	2.606
4HMG	C.LYS.238	NZ	C.ASP.175	OD1	2.940

4HMG	C_LYS_238	NZ	C_ASP_175	OD2	2.570
4HMG	C_ARG_261	NH1	C_GLU_119	OE1	3.250
4HMG	C_ARG_261	NH1	C_GLU_119	OE2	3.087
4HMG	C_ARG_261	NH2	C_GLU_119	OE1	2.811
4HMG	C_ARG_261	NH2	C_GLU_119	OE2	2.823
4HMG	C_LYS_264	NZ	C_ASP_85	OD1	3.271
4HMG	C_LYS_264	NZ	C_ASP_85	OD2	2.729
4HMG	C_ARG_269	NH2	D_GLU_67	OE1	2.764
4HMG	C_LYS_292	NZ	C_ASP_291	OD1	2.981
4HMG	C_LYS_292	NZ	C_ASP_291	OD2	2.812
4HMG	C_LYS_310	NZ	D_ASP_90	OD1	3.321
4HMG	C_LYS_310	NZ	D_ASP_90	OD2	2.697
4HMG	C_LYS_315	NZ	C_GLU_41	OE2	3.694
4HMG	C_LYS_326	NZ	D_GLU_15	OE1	3.836
4HMG	C_LYS_326	NZ	D_GLU_15	OE2	2.684
4HMG	D_LYS_51	NZ	D_GLU_103	OE2	2.595
4HMG	D_ARG_54	NH1	B_GLU_97	OE1	3.076
4HMG	D_ARG_54	NH2	A_ASP_32	OD2	3.995
4HMG	D_ARG_54	NH2	B_GLU_97	OE1	3.112
4HMG	D_ARG_54	NH2	D_GLU_57	OE1	2.847
4HMG	D_ARG_54	NH2	D_GLU_57	OE2	3.364
4HMG	D_LYS_62	NZ	B_ASP_86	OD1	2.940
4HMG	D_LYS_62	NZ	B_ASP_86	OD2	2.591
4HMG	D_LYS_62	NZ	B_ASP_90	OD1	3.586
4HMG	D_LYS_62	NZ	B_ASP_90	OD2	3.891
4HMG	D_HIS_64	NE2	B_ASP_79	OD2	3.731
4HMG	D_LYS_68	NZ	D_GLU_85	OE1	2.969
4HMG	D_LYS_68	NZ	D_GLU_85	OE2	2.606
4HMG	D_ARG_76	NH1	F_GLU_74	OE1	2.745
4HMG	D_ARG_76	NH1	F_GLU_74	OE2	3.756
4HMG	D_ARG_76	NH1	F_GLU_81	OE1	2.644
4HMG	D_ARG_76	NH1	F_GLU_81	OE2	3.314
4HMG	D_ARG_76	NH2	F_GLU_74	OE1	3.255
4HMG	D_ARG_76	NH2	F_GLU_74	OE2	2.777
4HMG	D_LYS_117	NZ	D_GLU_114	OE1	2.606
4HMG	D_LYS_117	NZ	D_GLU_114	OE2	3.387
4HMG	D_ARG_123	NH1	B_GLU_132	OE2	3.157
4HMG	D_ARG_123	NH2	D_GLU_120	OE1	2.828
4HMG	D_ARG_123	NH2	D_GLU_120	OE2	2.538
4HMG	D_ARG_124	NH1	B_GLU_132	OE1	3.347
4HMG	D_ARG_124	NH1	B_GLU_132	OE2	3.074
4HMG	D_ARG_124	NH2	D_GLU_120	OE2	3.592
4HMG	D_ARG_127	NH2	B_GLU_131	OE1	2.541
4HMG	D_LYS_143	NZ	D_ASP_145	OD2	3.357
4HMG	D_HIS_159	NE2	D_ASP_160	OD1	3.925
4HMG	D_HIS_159	NE2	D_ASP_160	OD2	3.140
4HMG	D_ARG_163	NH1	B_GLU_131	OE1	3.321
4HMG	D_ARG_163	NH1	B_GLU_131	OE2	2.801
4HMG	D_ARG_163	NH2	B_GLU_131	OE1	2.729
4HMG	D_ARG_163	NH2	B_GLU_131	OE2	3.526
4HMG	D_ARG_170	NH1	D_GLU_128	OE1	2.798
4HMG	D_ARG_170	NH2	D_GLU_131	OE2	2.778
4HMG	D_ARG_170	NH2	F_GLU_128	OE1	3.859
4HMG	D_ARG_170	NH2	F_GLU_128	OE2	3.829
4HMG	E_LYS_27	NZ	F_GLU_97	OE1	2.764
4HMG	E_LYS_27	NZ	F_GLU_97	OE2	3.247
4HMG	E_LYS_50	NZ	E_ASP_275	OD1	2.749
4HMG	E_HIS_56	NE2	E_GLU_280	OE2	3.460

4HMG	E_ARG_57	NH1	E_GLU_82	OE1	2.908
4HMG	E_ARG_57	NH1	E_GLU_82	OE2	3.750
4HMG	E_ARG_57	NH2	E_GLU_82	OE1	3.320
4HMG	E_HIS_75	ND1	E_ASP_73	OD1	2.714
4HMG	E_HIS_75	ND1	E_ASP_73	OD2	3.391
4HMG	E_HIS_75	NE2	E_ASP_63	OD1	3.445
4HMG	E_ARG_90	NH1	E_ASP_60	OD1	2.880
4HMG	E_ARG_90	NH1	E_ASP_60	OD2	3.726
4HMG	E_ARG_109	NH1	F_GLU_67	OE1	3.614
4HMG	E_ARG_109	NH1	F_GLU_67	OE2	2.773
4HMG	E_ARG_109	NH2	E_GLU_89	OE1	3.299
4HMG	E_ARG_109	NH2	E_GLU_89	OE2	2.546
4HMG	E_ARG_141	NH1	E_ASP_77	OD1	2.709
4HMG	E_ARG_141	NH1	E_ASP_77	OD2	3.383
4HMG	E_ARG_141	NH2	E_ASP_77	OD1	2.687
4HMG	E_LYS_176	NZ	E_GLU_123	OE1	2.598
4HMG	E_LYS_176	NZ	E_GLU_123	OE2	3.726
4HMG	E_HIS_183	NE2	E_GLU_190	OE1	3.747
4HMG	E_ARG_207	NH2	E_ASP_241	OD1	3.575
4HMG	E_ARG_208	NH2	E_ASP_241	OD1	3.603
4HMG	E_ARG_208	NH2	E_ASP_241	OD2	2.770
4HMG	E_LYS_238	NZ	D_GLU_72	OE2	2.707
4HMG	E_LYS_238	NZ	E_ASP_175	OD1	2.946
4HMG	E_LYS_238	NZ	E_ASP_175	OD2	2.555
4HMG	E_ARG_261	NH1	E_GLU_119	OE1	3.244
4HMG	E_ARG_261	NH1	E_GLU_119	OE2	3.073
4HMG	E_ARG_261	NH2	E_GLU_119	OE1	2.813
4HMG	E_ARG_261	NH2	E_GLU_119	OE2	2.815
4HMG	E_LYS_264	NZ	E_ASP_85	OD1	3.266
4HMG	E_LYS_264	NZ	E_ASP_85	OD2	2.734
4HMG	E_ARG_269	NH2	F_GLU_67	OE1	2.739
4HMG	E_LYS_292	NZ	E_ASP_291	OD1	3.009
4HMG	E_LYS_292	NZ	E_ASP_291	OD2	2.847
4HMG	E_LYS_310	NZ	F_ASP_90	OD1	3.300
4HMG	E_LYS_310	NZ	F_ASP_90	OD2	2.685
4HMG	E_LYS_315	NZ	E_GLU_41	OE2	3.689
4HMG	F_ARG_25	NH1	E_GLU_325	OE1	3.853
4HMG	F_LYS_51	NZ	F_GLU_103	OE2	2.620
4HMG	F_ARG_54	NH1	D_GLU_97	OE1	3.052
4HMG	F_ARG_54	NH2	C_ASP_32	OD2	3.923
4HMG	F_ARG_54	NH2	D_GLU_97	OE1	3.130
4HMG	F_ARG_54	NH2	F_GLU_57	OE1	2.861
4HMG	F_ARG_54	NH2	F_GLU_57	OE2	3.350
4HMG	F_LYS_62	NZ	D_ASP_86	OD1	2.900
4HMG	F_LYS_62	NZ	D_ASP_86	OD2	2.597
4HMG	F_LYS_62	NZ	D_ASP_90	OD1	3.664
4HMG	F_LYS_62	NZ	D_ASP_90	OD2	3.951
4HMG	F_HIS_64	NE2	D_ASP_79	OD2	3.646
4HMG	F_LYS_68	NZ	F_GLU_85	OE1	3.007
4HMG	F_LYS_68	NZ	F_GLU_85	OE2	2.563
4HMG	F_ARG_76	NH1	B_GLU_74	OE1	2.714
4HMG	F_ARG_76	NH1	B_GLU_74	OE2	3.687
4HMG	F_ARG_76	NH1	B_GLU_81	OE1	2.651
4HMG	F_ARG_76	NH1	B_GLU_81	OE2	3.434
4HMG	F_ARG_76	NH2	B_GLU_74	OE1	3.281
4HMG	F_ARG_76	NH2	B_GLU_74	OE2	2.711
4HMG	F_LYS_117	NZ	F_GLU_114	OE1	2.613
4HMG	F_LYS_117	NZ	F_GLU_114	OE2	3.409

4HMG	F_ARG_123	NH1	D_GLU_132	OE2	3.178
4HMG	F_ARG_123	NH2	F_GLU_120	OE1	2.836
4HMG	F_ARG_123	NH2	F_GLU_120	OE2	2.539
4HMG	F_ARG_124	NH1	D_GLU_132	OE1	3.402
4HMG	F_ARG_124	NH1	D_GLU_132	OE2	3.132
4HMG	F_ARG_124	NH2	F_GLU_120	OE2	3.562
4HMG	F_ARG_127	NH2	D_GLU_131	OE1	2.579
4HMG	F_LYS_143	NZ	F_ASP_145	OD2	3.346
4HMG	F_ARG_153	NH2	F_GLU_150	OE1	2.613
4HMG	F_HIS_159	NE2	F_ASP_160	OD1	3.932
4HMG	F_HIS_159	NE2	F_ASP_160	OD2	3.131
4HMG	F_ARG_163	NH1	D_GLU_131	OE1	3.299
4HMG	F_ARG_163	NH1	D_GLU_131	OE2	2.816
4HMG	F_ARG_163	NH2	D_GLU_131	OE1	2.752
4HMG	F_ARG_163	NH2	D_GLU_131	OE2	3.575
4HMG	F_ARG_170	NH1	F_GLU_128	OE1	2.781
4HMG	F_ARG_170	NH2	B_GLU_128	OE1	3.815
4HMG	F_ARG_170	NH2	B_GLU_128	OE2	3.719
4HMG	F_ARG_170	NH2	F_GLU_131	OE2	2.764
4HWB	A_ARG_230	NH2	H_ASP_56	OD2	3.246
4HWB	A_ARG_285	NH2	A_GLU_237	OE1	2.762
4HWB	A_ARG_285	NH2	A_GLU_237	OE2	3.252
4HWB	A_ARG_287	NH2	A_GLU_235	OE1	2.730
4HWB	A_ARG_287	NH2	A_GLU_235	OE2	3.307
4HWB	H_ARG_39	NH2	H_GLU_47	OE2	3.027
4HWB	H_ARG_99	NH2	H_ASP_107	OD1	3.362
4HWB	H_ARG_99	NH2	H_ASP_107	OD2	2.612
4HWB	H_LYS_149	NZ	H_ASP_150	OD1	3.433
4HWB	H_LYS_149	NZ	H_ASP_150	OD2	3.050
4HWB	H_LYS_215	NZ	L_GLU_120	OE2	3.469
4HWB	L_ARG_24	NH1	L_ASP_71	OD2	3.912
4HWB	L_ARG_62	NH2	L_GLU_82	OE1	3.563
4HWB	L_ARG_62	NH2	L_ASP_83	OD1	3.123
4HWB	L_ARG_62	NH2	L_ASP_83	OD2	3.996
4HWB	L_LYS_146	NZ	L_GLU_192	OE2	2.824
4HWB	L_LYS_180	NZ	L_GLU_184	OE2	3.810
4HWB	L_HIS_186	ND1	L_ASP_148	OD2	3.236
4HXA	L_HIS_34	ND1	L_ASP_50	OD2	3.892
4HXA	L_ARG_61	NH1	L_GLU_79	OE1	3.572
4HXA	L_ARG_61	NH1	L_GLU_79	OE2	3.959
4HXA	L_ARG_61	NH2	L_GLU_79	OE1	3.712
4HXA	L_ARG_61	NH2	L_GLU_81	OE2	2.919
4HXA	L_ARG_61	NH2	L_ASP_82	OD1	2.910
4HXA	L_ARG_61	NH2	L_ASP_82	OD2	3.687
4HXA	L_LYS_103	NZ	L_ASP_165	OD1	3.306
4HXA	L_LYS_142	NZ	L_GLU_105	OE1	2.359
4HXA	L_LYS_142	NZ	L_GLU_105	OE2	3.217
4HXA	L_LYS_147	NZ	L_GLU_154	OE2	3.699
4HXA	L_LYS_183	NZ	L_GLU_187	OE1	2.855
4HXA	L_LYS_183	NZ	L_GLU_187	OE2	3.206
4HXA	L_HIS_189	ND1	L_ASP_151	OD1	2.656
4HXA	L_LYS_199	NZ	L_ASP_110	OD1	2.782
4HXA	H_ARG_33	NH2	H_ASP_53	OD2	3.146
4HXA	H_ARG_38	NH1	H_ASP_86	OD1	2.911
4HXA	H_ARG_38	NH2	H_GLU_46	OE1	3.220
4HXA	H_ARG_38	NH2	H_GLU_46	OE2	3.961
4HXA	H_ARG_38	NH2	H_ASP_86	OD1	3.758
4HXA	H_ARG_66	NH1	H_ASP_86	OD1	3.213

4HXA	H_ARG.66	NH1	H_ASP.86	OD2	3.541
4HXA	H_ARG.66	NH2	H_ASP.86	OD1	3.547
4HXA	H_ARG.66	NH2	H_ASP.86	OD2	2.335
4HXA	H_ARG.71	NH2	H_ASP.73	OD2	3.421
4HXA	H_LYS.75	NZ	H_ASP.72	OD1	2.706
4HXA	H_ARG.94	NH2	H_ASP.101	OD1	2.566
4HXA	H_ARG.94	NH2	H_ASP.101	OD2	3.802
4HXA	H_ARG.98	NH1	L_ASP.50	OD1	2.959
4HXA	H_ARG.98	NH1	L_ASP.50	OD2	3.607
4HXA	H_HIS.164	NE2	L_ASP.167	OD1	3.601
4HXA	H_LYS.205	NZ	H_ASP.207	OD1	3.339
4HXA	H_LYS.205	NZ	H_ASP.207	OD2	2.614
4HXB	L_ARG.61	NH1	L_ASP.82	OD1	3.754
4HXB	L_ARG.61	NH1	L_ASP.82	OD2	2.851
4HXB	L_ARG.61	NH2	L_GLU.79	OE2	3.892
4HXB	L_ARG.61	NH2	L_GLU.81	OE2	3.579
4HXB	L_ARG.61	NH2	L_ASP.82	OD1	2.893
4HXB	L_ARG.61	NH2	L_ASP.82	OD2	3.275
4HXB	L_LYS.147	NZ	L_GLU.195	OE2	2.100
4HXB	L_LYS.149	NZ	L_GLU.195	OE1	2.509
4HXB	L_LYS.149	NZ	L_GLU.195	OE2	3.644
4HXB	L_ARG.155	NH1	L_GLU.185	OE2	3.650
4HXB	L_ARG.155	NH2	L_GLU.185	OE1	2.787
4HXB	L_ARG.155	NH2	L_GLU.185	OE2	2.877
4HXB	L_LYS.183	NZ	L_GLU.187	OE1	3.719
4HXB	L_HIS.189	ND1	L_ASP.151	OD2	2.591
4HXB	L_HIS.189	NE2	L_GLU.185	OE2	3.681
4HXB	L_LYS.199	NZ	L_ASP.110	OD2	3.163
4HXB	H_LYS.12	NZ	H_GLU.10	OE2	3.536
4HXB	H_LYS.46	NZ	H_ASP.62	OD2	2.395
4HXB	H_LYS.64	NZ	H_GLU.61	OE1	2.630
4HXB	H_LYS.64	NZ	H_GLU.61	OE2	2.953
4HXB	H_ARG.66	NH1	H_ASP.86	OD1	3.620
4HXB	H_ARG.66	NH1	H_ASP.86	OD2	2.850
4HXB	H_ARG.66	NH2	H_ASP.86	OD1	2.767
4HXB	H_ARG.66	NH2	H_ASP.86	OD2	3.484
4HXB	H_LYS.83	NZ	H_GLU.85	OE1	2.634
4HXB	H_ARG.94	NH1	H_ASP.101	OD1	3.226
4HXB	H_ARG.94	NH1	H_ASP.101	OD2	2.767
4HXB	H_ARG.96	NH1	L_ASP.94	OD1	3.212
4HXB	H_ARG.96	NH1	L_ASP.94	OD2	2.665
4HXB	H_ARG.96	NH2	L_ASP.94	OD1	2.669
4HXB	H_ARG.96	NH2	L_ASP.94	OD2	3.708
4I2X	A_LYS.24	NZ	A_ASP.70	OD1	3.809
4I2X	A_ARG.61	NH2	A_ASP.82	OD1	2.612
4I2X	A_ARG.61	NH2	A_ASP.82	OD2	3.075
4I2X	A_LYS.147	NZ	A_GLU.154	OE2	3.876
4I2X	A_LYS.149	NZ	A_GLU.195	OE2	3.016
4I2X	A_ARG.155	NH2	A_GLU.185	OE1	2.492
4I2X	A_LYS.199	NZ	A_ASP.110	OD2	3.998
4I2X	A_ARG.211	NH1	A_GLU.187	OE1	2.914
4I2X	B_LYS.38	NZ	B_ASP.90	OD1	3.997
4I2X	B_LYS.59	NZ	E_GLU.10	OE2	3.418
4I2X	B_LYS.65	NZ	E_ASP.208	OD1	3.256
4I2X	B_LYS.67	NZ	B_ASP.90	OD1	3.836
4I2X	B_LYS.67	NZ	B_ASP.90	OD2	2.957
4I2X	B_LYS.214	NZ	A_GLU.123	OE2	3.742
4I2X	C_ARG.61	NH2	C_GLU.81	OE2	3.536

4I2X	C_ARG_61	NH2	C_ASP_82	OD1	2.611
4I2X	C_ARG_61	NH2	C_ASP_82	OD2	3.223
4I2X	C_LYS_147	NZ	C_GLU_154	OE2	3.881
4I2X	C_LYS_147	NZ	C_GLU_195	OE1	3.855
4I2X	C_LYS_149	NZ	C_GLU_195	OE2	3.745
4I2X	C_ARG_155	NH1	C_GLU_185	OE1	3.098
4I2X	C_ARG_155	NH2	C_GLU_185	OE1	2.928
4I2X	C_LYS_183	NZ	C_GLU_187	OE2	3.224
4I2X	C_LYS_199	NZ	C_ASP_110	OD1	3.402
4I2X	C_LYS_199	NZ	C_ASP_110	OD2	3.168
4I2X	C_ARG_211	NH1	C_GLU_187	OE1	3.303
4I2X	D_ARG_40	NH1	D_GLU_89	OE1	3.368
4I2X	D_ARG_40	NH2	D_GLU_89	OE1	3.617
4I2X	D_LYS_63	NZ	C_ASP_1	OD2	3.656
4I2X	D_LYS_65	NZ	F_ASP_208	OD1	3.848
4I2X	D_LYS_67	NZ	D_ASP_90	OD1	3.613
4I2X	D_LYS_67	NZ	D_ASP_90	OD2	3.084
4I2X	D_HIS_170	ND1	C_ASP_167	OD2	3.958
4I2X	D_LYS_211	NZ	D_ASP_213	OD1	3.197
4I2X	D_LYS_214	NZ	C_GLU_123	OE2	3.815
4I2X	E_HIS_24	ND1	E_GLU_10	OE1	3.035
4I2X	E_ARG_40	NH2	E_GLU_47	OE1	3.242
4I2X	E_ARG_40	NH2	E_GLU_47	OE2	3.478
4I2X	E_ARG_46	NH1	E_GLU_103	OE1	2.979
4I2X	E_ARG_46	NH2	E_GLU_103	OE1	3.021
4I2X	E_ARG_59	NH1	E_ASP_85	OD1	2.932
4I2X	E_ARG_59	NH1	E_ASP_85	OD2	3.555
4I2X	E_ARG_59	NH2	E_ASP_85	OD1	3.558
4I2X	E_ARG_59	NH2	E_ASP_85	OD2	2.755
4I2X	E_HIS_143	ND1	E_GLU_141	OE1	3.000
4I2X	E_HIS_143	ND1	E_GLU_141	OE2	3.158
4I2X	E_LYS_153	NZ	E_GLU_160	OE1	3.145
4I2X	E_LYS_153	NZ	E_GLU_160	OE2	3.307
4I2X	E_LYS_156	NZ	E_ASP_188	OD2	3.753
4I2X	E_LYS_156	NZ	E_ASP_191	OD1	3.430
4I2X	E_LYS_156	NZ	E_ASP_191	OD2	2.599
4I2X	E_ARG_180	NH2	E_ASP_169	OD2	3.719
4I2X	E_ARG_193	NH1	E_GLU_274	OE2	3.753
4I2X	E_ARG_193	NH2	E_GLU_274	OE2	2.935
4I2X	E_ARG_211	NH2	E_GLU_199	OE2	2.968
4I2X	E_ARG_221	NH1	E_ASP_306	OD2	2.386
4I2X	E_ARG_246	NH1	E_GLU_227	OE1	3.432
4I2X	E_ARG_266	NH1	E_GLU_259	OE2	2.959
4I2X	F_HIS_24	ND1	F_GLU_10	OE1	3.383
4I2X	F_ARG_40	NH2	F_GLU_47	OE1	2.707
4I2X	F_ARG_40	NH2	F_GLU_47	OE2	3.337
4I2X	F_ARG_46	NH1	F_GLU_103	OE1	3.160
4I2X	F_ARG_46	NH1	F_GLU_103	OE2	3.864
4I2X	F_ARG_46	NH2	F_GLU_103	OE1	3.013
4I2X	F_ARG_59	NH1	F_ASP_85	OD1	2.871
4I2X	F_ARG_59	NH1	F_ASP_85	OD2	2.922
4I2X	F_ARG_59	NH2	F_ASP_85	OD1	3.943
4I2X	F_ARG_59	NH2	F_ASP_85	OD2	2.928
4I2X	F_HIS_143	ND1	F_GLU_141	OE1	2.771
4I2X	F_HIS_143	ND1	F_GLU_141	OE2	3.495
4I2X	F_LYS_156	NZ	F_ASP_188	OD2	3.315
4I2X	F_LYS_156	NZ	F_ASP_191	OD2	3.515
4I2X	F_ARG_180	NH1	E_GLU_47	OE1	3.834

4I2X	F_ARG_211	NH2	F_GLU_199	OE2	2.770
4I2X	F_ARG_221	NH1	F_ASP_306	OD2	2.711
4I2X	F_ARG_246	NH1	F_GLU_227	OE1	2.969
4I2X	F_ARG_266	NH1	F_GLU_259	OE2	3.157
4I3R	G_LYS_282	NZ	H_GLU_33	OE1	3.996
4I3R	G_LYS_282	NZ	H_GLU_33	OE2	2.684
4I3R	G_LYS_351	NZ	G_GLU_269	OE1	3.563
4I3R	G_ARG_456	NH1	G_GLU_466	OE1	3.067
4I3R	G_ARG_469	NH2	G_ASP_457	OD1	3.936
4I3R	G_ARG_469	NH2	G_ASP_457	OD2	2.877
4I3R	H_ARG_19	NH1	H_ASP_81	OD1	3.627
4I3R	H_ARG_19	NH1	H_ASP_81	OD2	3.350
4I3R	H_ARG_38	NH1	H_ASP_86	OD1	3.177
4I3R	H_ARG_38	NH2	H_GLU_46	OE1	3.721
4I3R	H_ARG_38	NH2	H_ASP_86	OD1	3.995
4I3R	H_LYS_52	NZ	H_GLU_33	OE2	3.671
4I3R	H_ARG_64	NH2	G_ASP_457	OD1	3.551
4I3R	H_ARG_64	NH2	G_ASP_457	OD2	3.482
4I3R	H_ARG_66	NH1	H_ASP_62	OD1	3.277
4I3R	H_ARG_66	NH1	H_ASP_62	OD2	3.049
4I3R	H_ARG_66	NH1	H_ASP_86	OD1	3.545
4I3R	H_ARG_66	NH1	H_ASP_86	OD2	3.903
4I3R	H_ARG_66	NH2	H_ASP_86	OD1	3.310
4I3R	H_ARG_66	NH2	H_ASP_86	OD2	2.449
4I3R	H_ARG_71	NH1	G_ASP_368	OD1	3.996
4I3R	H_ARG_71	NH1	G_ASP_368	OD2	2.319
4I3R	H_ARG_71	NH2	G_ASP_368	OD1	3.997
4I3R	H_ARG_71	NH2	G_ASP_368	OD2	3.530
4I3R	H_ARG_94	NH1	H_ASP_101	OD1	2.785
4I3R	H_ARG_94	NH1	H_ASP_101	OD2	2.504
4I3R	H_LYS_96	NZ	H_ASP_101	OD2	3.693
4I3R	H_LYS_143	NZ	H_ASP_144	OD1	3.690
4I3R	H_LYS_143	NZ	H_ASP_144	OD2	3.274
4I3R	H_LYS_206	NZ	H_ASP_208	OD1	3.805
4I3R	H_LYS_209	NZ	L_GLU_123	OE2	2.484
4I3R	L_LYS_39	NZ	L_GLU_81	OE1	3.444
4I3R	L_ARG_54	NH2	L_ASP_60	OD1	2.979
4I3R	L_ARG_61	NH1	L_ASP_82	OD1	2.605
4I3R	L_ARG_61	NH1	L_ASP_82	OD2	2.581
4I3R	L_ARG_61	NH2	L_GLU_79	OE1	3.506
4I3R	L_ARG_61	NH2	L_GLU_79	OE2	3.423
4I3R	L_ARG_103	NH1	L_GLU_105	OE2	3.685
4I3R	L_ARG_107	NH2	L_GLU_17	OE1	3.953
4I3R	L_ARG_107	NH2	L_GLU_17	OE2	3.600
4I3R	L_LYS_149	NZ	L_GLU_195	OE2	3.690
4I3R	L_LYS_183	NZ	L_GLU_187	OE2	3.197
4I3S	G_LYS_282	NZ	G_GLU_275	OE1	3.977
4I3S	G_LYS_282	NZ	H_GLU_33	OE1	3.669
4I3S	G_LYS_282	NZ	H_GLU_33	OE2	3.690
4I3S	G_ARG_456	NH1	G_GLU_466	OE2	3.826
4I3S	G_ARG_469	NH2	G_ASP_457	OD2	3.288
4I3S	H_ARG_19	NH1	H_ASP_81	OD2	3.959
4I3S	H_ARG_31	NH1	H_ASP_27	OD2	3.996
4I3S	H_ARG_31	NH2	H_ASP_27	OD2	3.298
4I3S	H_ARG_38	NH1	H_ASP_86	OD1	2.791
4I3S	H_ARG_38	NH2	H_GLU_46	OE1	3.972
4I3S	H_ARG_38	NH2	H_ASP_86	OD1	3.641
4I3S	H_ARG_64	NH2	G_ASP_457	OD1	3.430

4I3S	H_ARG_64	NH2	G_ASP_457	OD2	3.082
4I3S	H_ARG_66	NH1	H_ASP_86	OD1	3.764
4I3S	H_ARG_66	NH1	H_ASP_86	OD2	3.474
4I3S	H_ARG_66	NH2	H_ASP_62	OD2	3.970
4I3S	H_ARG_66	NH2	H_ASP_86	OD1	2.906
4I3S	H_ARG_66	NH2	H_ASP_86	OD2	3.336
4I3S	H_ARG_71	NH1	G_ASP_368	OD1	3.370
4I3S	H_ARG_71	NH1	G_ASP_368	OD2	3.053
4I3S	H_ARG_71	NH2	G_ASP_368	OD1	3.484
4I3S	H_ARG_94	NH1	H_ASP_101	OD1	3.080
4I3S	H_ARG_94	NH1	H_ASP_101	OD2	2.812
4I3S	H_LYS_209	NZ	L_GLU_123	OE1	2.882
4I3S	L_ARG_54	NH1	L_ASP_60	OD1	3.742
4I3S	L_ARG_54	NH2	L_ASP_60	OD1	3.363
4I3S	L_ARG_61	NH1	L_GLU_79	OE2	2.892
4I3S	L_ARG_61	NH2	L_ASP_82	OD1	3.478
4I3S	L_ARG_103	NH1	L_GLU_105	OE1	3.837
4I3S	L_ARG_211	NH1	L_GLU_187	OE1	3.303
4I3S	L_ARG_211	NH2	L_GLU_187	OE1	3.109
4JAM	H_LYS_13	NZ	H_GLU_16	OE2	3.105
4JAM	H_ARG_38	NH1	H_ASP_86	OD1	2.909
4JAM	H_ARG_38	NH2	H_GLU_46	OE2	3.439
4JAM	H_ARG_38	NH2	H_ASP_86	OD1	3.603
4JAM	H_ARG_66	NH1	H_ASP_86	OD1	3.959
4JAM	H_ARG_66	NH1	H_ASP_86	OD2	3.260
4JAM	H_ARG_66	NH2	H_ASP_86	OD1	2.963
4JAM	H_ARG_66	NH2	H_ASP_86	OD2	3.519
4JAM	H_LYS_143	NZ	H_ASP_144	OD1	2.996
4JAM	H_LYS_143	NZ	H_ASP_144	OD2	3.461
4JAM	H_LYS_209	NZ	L_GLU_123	OE2	3.865
4JAM	H_LYS_210	NZ	H_GLU_212	OE2	3.818
4JAM	L_LYS_53	NZ	L_GLU_50	OE1	2.810
4JAM	L_ARG_54	NH1	L_ASP_60	OD1	3.496
4JAM	L_ARG_54	NH2	L_ASP_60	OD1	3.753
4JAM	L_ARG_61	NH2	L_ASP_82	OD1	2.928
4JAM	L_ARG_61	NH2	L_ASP_82	OD2	3.591
4JAM	L_LYS_110	NZ	L_GLU_198	OE1	2.600
4JAM	L_LYS_110	NZ	L_GLU_198	OE2	3.111
4JAM	L_LYS_149	NZ	L_GLU_203	OE1	2.760
4JAM	A_ARG_38	NH1	A_ASP_86	OD1	2.792
4JAM	A_ARG_38	NH2	A_GLU_46	OE1	3.309
4JAM	A_ARG_38	NH2	A_ASP_86	OD1	3.667
4JAM	A_ARG_66	NH1	A_ASP_86	OD1	3.551
4JAM	A_ARG_66	NH1	A_ASP_86	OD2	3.941
4JAM	A_ARG_66	NH2	A_ASP_86	OD1	3.154
4JAM	A_ARG_66	NH2	A_ASP_86	OD2	2.339
4JAM	A_LYS_143	NZ	A_ASP_144	OD1	3.127
4JAM	A_LYS_143	NZ	A_ASP_144	OD2	3.610
4JAM	A_LYS_206	NZ	A_ASP_208	OD1	2.503
4JAM	A_LYS_206	NZ	A_ASP_208	OD2	3.012
4JAM	A_LYS_209	NZ	B_GLU_123	OE2	3.814
4JAM	A_LYS_210	NZ	A_GLU_212	OE2	3.874
4JAM	B_LYS_53	NZ	B_GLU_50	OE1	2.752
4JAM	B_ARG_61	NH2	B_ASP_82	OD1	2.903
4JAM	B_ARG_61	NH2	B_ASP_82	OD2	3.571
4JAM	B_LYS_110	NZ	B_GLU_198	OE2	3.885
4JAM	B_LYS_149	NZ	B_GLU_203	OE1	3.006
4JAM	B_ARG_189	NH1	B_ASP_151	OD1	3.987

4JAM	B_ARG_189	NH1	B_ASP_151	OD2	3.937
4JAN	G_LYS_282	NZ	G_GLU_275	OE1	3.474
4JAN	G_LYS_360	NZ	G_GLU_362	OE1	3.523
4JAN	G_ARG_456	NH1	G_GLU_466	OE1	3.351
4JAN	G_ARG_456	NH1	G_GLU_466	OE2	3.176
4JAN	G_ARG_469	NH2	G_GLU_362	OE2	3.387
4JAN	H_ARG_38	NH1	H_ASP_86	OD1	3.352
4JAN	H_ARG_38	NH2	H_GLU_46	OE1	3.075
4JAN	H_ARG_66	NH1	H_ASP_86	OD1	3.928
4JAN	H_ARG_66	NH1	H_ASP_86	OD2	3.649
4JAN	H_ARG_66	NH2	H_ASP_86	OD1	2.680
4JAN	H_ARG_66	NH2	H_ASP_86	OD2	3.194
4JAN	H_ARG_97	NH2	G_ASP_368	OD2	2.609
4JAN	H_ARG_97	NH2	G_GLU_370	OE1	2.554
4JAN	H_LYS_143	NZ	H_ASP_144	OD2	3.820
4JAN	H_LYS_143	NZ	L_GLU_124	OE2	3.811
4JAN	H_LYS_209	NZ	L_GLU_123	OE1	2.888
4JAN	L_LYS_53	NZ	L_GLU_50	OE1	2.884
4JAN	L_ARG_61	NH2	L_ASP_82	OD1	2.695
4JAN	L_ARG_61	NH2	L_ASP_82	OD2	3.778
4JAN	L_ARG_107	NH1	L_GLU_83	OE1	3.896
4JAN	L_LYS_110	NZ	L_GLU_198	OE1	2.837
4JAN	L_LYS_129	NZ	H_ASP_144	OD2	3.458
4JAN	L_LYS_344	NZ	L_GLU_290	OE1	3.334
4JAN	L_LYS_357	NZ	L_ASP_464	OD1	2.885
4JAN	L_LYS_360	NZ	L_GLU_362	OE1	3.054
4JAN	L_ARG_456	NH1	L_GLU_466	OE1	3.190
4JAN	L_ARG_456	NH1	L_GLU_466	OE2	3.591
4JAN	L_ARG_469	NH1	L_GLU_362	OE2	3.886
4JAN	L_ARG_469	NH2	L_GLU_362	OE2	3.292
4JAN	L_ARG_469	NH2	L_ASP_457	OD2	3.746
4JAN	A_ARG_38	NH1	A_ASP_86	OD1	3.100
4JAN	A_ARG_38	NH2	A_GLU_46	OE1	2.957
4JAN	A_ARG_38	NH2	A_ASP_86	OD1	3.991
4JAN	A_LYS_43	NZ	A_ASP_86	OD1	3.939
4JAN	A_ARG_66	NH1	A_ASP_86	OD2	3.380
4JAN	A_ARG_66	NH2	A_ASP_86	OD1	3.178
4JAN	A_ARG_66	NH2	A_ASP_86	OD2	3.385
4JAN	A_ARG_97	NH2	L_ASP_368	OD1	2.825
4JAN	A_ARG_97	NH2	L_ASP_368	OD2	3.792
4JAN	A_ARG_97	NH2	L_GLU_370	OE1	3.106
4JAN	A_LYS_143	NZ	A_ASP_144	OD1	3.191
4JAN	A_LYS_143	NZ	A_ASP_144	OD2	3.150
4JAN	A_LYS_209	NZ	B_GLU_123	OE1	3.788
4JAN	A_LYS_209	NZ	B_GLU_123	OE2	3.189
4JAN	A_LYS_210	NZ	A_GLU_212	OE2	3.659
4JAN	B_LYS_53	NZ	B_GLU_50	OE1	2.587
4JAN	B_ARG_61	NH2	B_ASP_82	OD1	2.736
4JAN	B_ARG_61	NH2	B_ASP_82	OD2	3.458
4JAN	B_HIS_188	NE2	B_ASP_151	OD2	3.951
4JHA	H_ARG_30	NH2	H_GLU_73	OE1	2.826
4JHA	H_ARG_30	NH2	H_GLU_73	OE2	3.416
4JHA	H_ARG_38	NH1	H_ASP_86	OD1	2.732
4JHA	H_ARG_38	NH2	H_GLU_85	OE1	3.002
4JHA	H_ARG_38	NH2	H_ASP_86	OD1	3.574
4JHA	H_LYS_62	NZ	H_GLU_46	OE1	3.088
4JHA	H_LYS_62	NZ	H_GLU_46	OE2	3.359
4JHA	H_LYS_62	NZ	H_GLU_85	OE1	3.798

4JHA	H_ARG_66	NH1	H_ASP_86	OD1	3.556
4JHA	H_ARG_66	NH1	H_ASP_86	OD2	2.912
4JHA	H_ARG_66	NH2	H_GLU_85	OE1	3.941
4JHA	H_ARG_66	NH2	H_GLU_85	OE2	3.694
4JHA	H_ARG_66	NH2	H_ASP_86	OD1	2.845
4JHA	H_ARG_66	NH2	H_ASP_86	OD2	3.591
4JHA	H_ARG_83	NH1	H_GLU_85	OE2	3.452
4JHA	H_HIS_100G	ND1	H_GLU_95	OE1	2.690
4JHA	H_HIS_100G	ND1	H_GLU_95	OE2	3.485
4JHA	H_LYS_143	NZ	H_ASP_144	OD1	3.717
4JHA	L_ARG_61	NH2	L_GLU_81	OE2	3.203
4JHA	L_ARG_61	NH2	L_ASP_82	OD1	2.990
4JHA	L_ARG_61	NH2	L_ASP_82	OD2	3.835
4JHA	L_LYS_103	NZ	L_GLU_165	OE1	3.560
4JHA	L_HIS_189	ND1	L_ASP_151	OD1	3.067
4JHA	L_HIS_189	ND1	L_ASP_151	OD2	2.332
4JHW	H_LYS_12	NZ	H_GLU_10	OE1	3.774
4JHW	H_LYS_12	NZ	H_GLU_10	OE2	3.410
4JHW	H_ARG_30	NH2	H_GLU_73	OE1	3.253
4JHW	H_ARG_30	NH2	H_GLU_73	OE2	3.595
4JHW	H_ARG_38	NH1	H_ASP_86	OD1	2.933
4JHW	H_ARG_38	NH2	H_GLU_85	OE1	3.397
4JHW	H_LYS_62	NZ	H_GLU_46	OE1	3.508
4JHW	H_LYS_62	NZ	H_GLU_46	OE2	3.235
4JHW	H_ARG_66	NH1	H_ASP_86	OD1	3.796
4JHW	H_ARG_66	NH1	H_ASP_86	OD2	3.522
4JHW	H_ARG_66	NH2	H_ASP_86	OD1	3.083
4JHW	H_ARG_83	NH1	H_GLU_85	OE2	3.470
4JHW	H_HIS_100G	ND1	H_GLU_95	OE1	2.582
4JHW	H_HIS_100G	ND1	H_GLU_95	OE2	3.471
4JHW	H_LYS_143	NZ	H_ASP_144	OD1	3.702
4JHW	L_ARG_61	NH2	L_GLU_81	OE2	2.896
4JHW	L_ARG_61	NH2	L_ASP_82	OD1	3.273
4JHW	L_ARG_61	NH2	L_ASP_82	OD2	3.811
4JHW	L_LYS_103	NZ	L_GLU_165	OE1	3.410
4JHW	L_LYS_103	NZ	L_GLU_165	OE2	3.764
4JHW	L_HIS_189	ND1	L_ASP_151	OD1	3.229
4JHW	L_HIS_189	ND1	L_ASP_151	OD2	2.338
4JHW	F_ARG_49	NH2	F_ASP_368	OD1	3.536
4JHW	F_LYS_85	NZ	F_GLU_82	OE1	3.836
4JHW	F_LYS_166	NZ	F_GLU_163	OE2	3.574
4JHW	F_LYS_168	NZ	F_GLU_294	OE1	3.244
4JHW	F_LYS_176	NZ	F_ASP_263	OD2	3.508
4JHW	F_LYS_191	NZ	F_GLU_60	OE2	3.607
4JHW	F_LYS_191	NZ	F_ASP_194	OD2	3.605
4JHW	F_LYS_196	NZ	F_GLU_60	OE1	2.692
4JHW	F_LYS_209	NZ	H_ASP_101	OD2	3.535
4JHW	F_LYS_209	NZ	L_GLU_55	OE1	2.845
4JHW	F_LYS_209	NZ	L_GLU_55	OE2	3.356
4JHW	F_ARG_229	NH1	F_GLU_256	OE1	3.739
4JHW	F_ARG_229	NH1	F_GLU_256	OE2	3.024
4JHW	F_ARG_229	NH2	F_GLU_256	OE1	2.796
4JHW	F_ARG_229	NH2	F_GLU_256	OE2	3.605
4JHW	F_ARG_235	NH2	F_GLU_236	OE2	3.517
4JHW	F_ARG_336	NH2	F_ASP_338	OD1	3.908
4JHW	F_ARG_336	NH2	F_ASP_338	OD2	3.114
4JHW	F_ARG_364	NH1	F_ASP_310	OD1	2.617
4JHW	F_ARG_364	NH2	F_ASP_310	OD1	2.621

4JHW	F_LYS_433	NZ	F_ASP_440	OD2	3.857
4JHW	F_LYS_461	NZ	F_ASP_448	OD1	2.628
4JHW	F_LYS_498	NZ	F_GLU_487	OE1	3.211
4JHW	F_LYS_498	NZ	F_GLU_487	OE2	3.707
4JHW	F_ARG_507	NH1	F_GLU_511	OE2	3.100
4JO1	L_LYS_39	NZ	L_ASP_81	OD2	2.927
4JO1	L_LYS_53	NZ	L_ASP_50	OD1	2.687
4JO1	L_ARG_61	NH1	L_ASP_82	OD1	2.727
4JO1	L_ARG_61	NH1	L_ASP_82	OD2	3.457
4JO1	L_ARG_61	NH2	L_ASP_82	OD1	3.476
4JO1	L_ARG_61	NH2	L_ASP_82	OD2	2.757
4JO1	L_LYS_138	NZ	L_ASP_169	OD1	2.582
4JO1	L_LYS_162	NZ	L_ASP_142	OD1	2.686
4JO1	L_LYS_162	NZ	L_ASP_142	OD2	3.695
4JO1	H_ARG_38	NH1	H_ASP_86	OD2	2.789
4JO1	H_ARG_38	NH2	H_GLU_46	OE1	3.151
4JO1	H_ARG_38	NH2	H_ASP_86	OD2	3.780
4JO1	H_ARG_66	NH1	H_ASP_86	OD1	2.959
4JO1	H_ARG_66	NH1	H_ASP_86	OD2	3.751
4JO1	H_ARG_66	NH2	H_ASP_86	OD1	3.523
4JO1	H_ARG_66	NH2	H_ASP_86	OD2	3.003
4JO1	P_ARG_304	NH1	H_ASP_34	OD1	3.045
4JO1	P_ARG_304	NH1	H_ASP_34	OD2	3.346
4JO1	P_ARG_304	NH2	H_ASP_34	OD2	2.892
4JO1	M_LYS_39	NZ	M_ASP_81	OD2	2.924
4JO1	M_LYS_53	NZ	M_ASP_50	OD1	2.678
4JO1	M_ARG_61	NH1	M_ASP_82	OD1	2.722
4JO1	M_ARG_61	NH1	M_ASP_82	OD2	3.406
4JO1	M_ARG_61	NH2	M_ASP_82	OD1	3.488
4JO1	M_ARG_61	NH2	M_ASP_82	OD2	2.707
4JO1	M_LYS_138	NZ	M_ASP_169	OD1	2.539
4JO1	M_LYS_162	NZ	M_ASP_142	OD1	2.679
4JO1	M_LYS_162	NZ	M_ASP_142	OD2	3.651
4JO1	L_ARG_38	NH1	L_ASP_86	OD2	2.786
4JO1	L_ARG_38	NH2	L_GLU_46	OE1	3.154
4JO1	L_ARG_38	NH2	L_ASP_86	OD2	3.771
4JO1	L_ARG_66	NH1	L_ASP_86	OD1	3.031
4JO1	L_ARG_66	NH1	L_ASP_86	OD2	3.805
4JO1	L_ARG_66	NH2	L_ASP_86	OD1	3.492
4JO1	L_ARG_66	NH2	L_ASP_86	OD2	2.959
4JO1	Q_ARG_304	NH1	L_ASP_34	OD1	2.949
4JO1	Q_ARG_304	NH1	L_ASP_34	OD2	3.344
4JO1	Q_ARG_304	NH2	L_ASP_34	OD1	3.946
4JO1	Q_ARG_304	NH2	L_ASP_34	OD2	2.878
4JO2	L_LYS_39	NZ	L_ASP_81	OD2	2.922
4JO2	L_LYS_53	NZ	L_ASP_50	OD1	3.017
4JO2	L_ARG_61	NH1	L_ASP_82	OD1	3.605
4JO2	L_ARG_61	NH1	L_ASP_82	OD2	2.772
4JO2	L_ARG_61	NH2	L_ASP_82	OD1	3.007
4JO2	L_ARG_61	NH2	L_ASP_82	OD2	3.330
4JO2	L_LYS_138	NZ	L_ASP_169	OD2	3.573
4JO2	L_LYS_162	NZ	L_ASP_142	OD2	3.171
4JO2	H_ARG_38	NH1	H_ASP_86	OD2	2.606
4JO2	H_ARG_38	NH2	H_GLU_46	OE1	2.897
4JO2	H_ARG_38	NH2	H_ASP_86	OD2	3.987
4JO2	H_ARG_66	NH1	H_ASP_86	OD1	2.938
4JO2	H_ARG_66	NH1	H_ASP_86	OD2	3.840
4JO2	H_ARG_66	NH2	H_ASP_86	OD1	3.186

4JO2	H_ARG_66	NH2	H_ASP_86	OD2	2.917
4JO2	P_ARG_304	NH1	H_ASP_34	OD1	2.726
4JO2	P_ARG_304	NH1	H_ASP_34	OD2	3.333
4JO2	P_ARG_304	NH2	H_ASP_34	OD1	3.721
4JO2	P_ARG_304	NH2	H_ASP_34	OD2	2.854
4JO2	M_LYS_39	NZ	M_ASP_81	OD1	3.476
4JO2	M_LYS_39	NZ	M_ASP_81	OD2	3.290
4JO2	M_LYS_53	NZ	M_ASP_50	OD2	3.292
4JO2	M_ARG_61	NH1	M_ASP_82	OD1	3.140
4JO2	M_ARG_61	NH1	M_ASP_82	OD2	3.618
4JO2	M_ARG_61	NH2	M_ASP_82	OD1	3.726
4JO2	M_ARG_61	NH2	M_ASP_82	OD2	2.780
4JO2	M_LYS_138	NZ	M_ASP_169	OD2	2.742
4JO2	M_LYS_162	NZ	M_ASP_142	OD1	3.921
4JO2	M_LYS_162	NZ	M_ASP_142	OD2	3.385
4JO2	L_ARG_38	NH1	L_ASP_86	OD2	2.900
4JO2	L_ARG_38	NH2	L_GLU_46	OE1	3.086
4JO2	L_ARG_38	NH2	L_ASP_86	OD2	3.924
4JO2	L_ARG_66	NH1	L_ASP_86	OD1	2.929
4JO2	L_ARG_66	NH1	L_ASP_86	OD2	3.643
4JO2	L_ARG_66	NH2	L_ASP_86	OD1	3.202
4JO2	L_ARG_66	NH2	L_ASP_86	OD2	2.584
4JO2	L_LYS_199	NZ	L_ASP_201	OD1	3.625
4JO2	L_LYS_199	NZ	L_ASP_201	OD2	3.197
4JO2	Q_ARG_304	NH1	L_ASP_34	OD1	2.965
4JO2	Q_ARG_304	NH1	L_ASP_34	OD2	3.252
4JO2	Q_ARG_304	NH2	L_ASP_34	OD2	3.328
4JO3	L_LYS_39	NZ	L_ASP_81	OD1	3.210
4JO3	L_LYS_39	NZ	L_ASP_81	OD2	3.108
4JO3	L_ARG_61	NH1	L_ASP_82	OD1	3.683
4JO3	L_ARG_61	NH1	L_ASP_82	OD2	2.743
4JO3	L_ARG_61	NH2	L_ASP_82	OD1	2.826
4JO3	L_ARG_61	NH2	L_ASP_82	OD2	3.482
4JO3	L_LYS_162	NZ	L_ASP_142	OD1	2.811
4JO3	L_LYS_162	NZ	L_ASP_142	OD2	3.312
4JO3	H_ARG_38	NH1	H_ASP_86	OD2	2.684
4JO3	H_ARG_38	NH2	H_GLU_46	OE1	3.692
4JO3	H_ARG_38	NH2	H_ASP_86	OD2	3.553
4JO3	H_ARG_54	NH1	P_GLU_321	OE1	3.970
4JO3	H_ARG_66	NH1	H_ASP_86	OD1	2.860
4JO3	H_ARG_66	NH1	H_ASP_86	OD2	3.702
4JO3	H_ARG_66	NH2	H_ASP_86	OD1	3.555
4JO3	H_ARG_66	NH2	H_ASP_86	OD2	3.007
4JO3	H_ARG_94	NH1	H_ASP_101	OD1	2.669
4JO3	H_ARG_94	NH1	H_ASP_101	OD2	3.152
4JO3	P_ARG_327	NH1	L_ASP_1	OD1	2.994
4JO3	P_ARG_327	NH2	L_ASP_1	OD1	2.732
4JO3	P_ARG_327	NH2	L_GLU_27	OE1	3.272
4JO3	P_ARG_327	NH2	L_GLU_27	OE2	3.099
4JO3	M_LYS_39	NZ	M_ASP_81	OD1	3.363
4JO3	M_LYS_39	NZ	M_ASP_81	OD2	3.485
4JO3	M_ARG_61	NH1	M_ASP_82	OD1	3.977
4JO3	M_ARG_61	NH1	M_ASP_82	OD2	2.819
4JO3	M_ARG_61	NH2	M_ASP_82	OD1	2.923
4JO3	M_ARG_61	NH2	M_ASP_82	OD2	3.229
4JO3	M_LYS_162	NZ	M_ASP_142	OD1	3.056
4JO3	M_LYS_162	NZ	M_ASP_142	OD2	3.799
4JO3	L_ARG_38	NH1	L_ASP_86	OD2	2.673

4JO3	L_ARG_38	NH2	L_GLU_46	OE1	3.528
4JO3	L_ARG_38	NH2	L_GLU_46	OE2	3.898
4JO3	L_ARG_38	NH2	L_ASP_86	OD2	3.887
4JO3	L_ARG_66	NH1	L_ASP_86	OD1	3.159
4JO3	L_ARG_66	NH1	L_ASP_86	OD2	3.577
4JO3	L_ARG_66	NH2	L_ASP_86	OD1	3.570
4JO3	L_ARG_66	NH2	L_ASP_86	OD2	2.893
4JO3	L_ARG_94	NH1	L_ASP_101	OD1	2.954
4JO3	L_ARG_94	NH1	L_ASP_101	OD2	3.750
4JO3	Q_ARG_327	NH1	M_ASP_1	OD1	3.248
4JO3	Q_ARG_327	NH2	M_ASP_1	OD1	2.447
4JO3	Q_ARG_327	NH2	M_ASP_1	OD2	3.524
4JO3	Q_ARG_327	NH2	M_GLU_27	OE1	3.837
4JO3	Q_ARG_327	NH2	M_GLU_27	OE2	3.723
4JO4	L_LYS_39	NZ	L_ASP_81	OD1	3.937
4JO4	L_LYS_39	NZ	L_ASP_81	OD2	3.155
4JO4	L_ARG_61	NH1	L_ASP_82	OD1	3.796
4JO4	L_ARG_61	NH1	L_ASP_82	OD2	2.750
4JO4	L_ARG_61	NH2	L_ASP_82	OD1	3.079
4JO4	L_ARG_61	NH2	L_ASP_82	OD2	3.445
4JO4	L_LYS_162	NZ	L_ASP_142	OD1	2.940
4JO4	L_LYS_162	NZ	L_ASP_142	OD2	3.881
4JO4	H_ARG_38	NH1	H_ASP_86	OD2	2.736
4JO4	H_ARG_38	NH2	H_GLU_46	OE1	3.500
4JO4	H_ARG_38	NH2	H_GLU_46	OE2	3.857
4JO4	H_ARG_38	NH2	H_ASP_86	OD2	3.761
4JO4	H_ARG_66	NH1	H_ASP_86	OD1	2.970
4JO4	H_ARG_66	NH1	H_ASP_86	OD2	3.623
4JO4	H_ARG_66	NH2	H_ASP_86	OD1	3.534
4JO4	H_ARG_66	NH2	H_ASP_86	OD2	2.909
4JO4	H_ARG_94	NH1	H_ASP_101	OD1	2.897
4JO4	H_ARG_94	NH1	H_ASP_101	OD2	3.447
4JO4	M_LYS_39	NZ	M_ASP_81	OD1	2.860
4JO4	M_LYS_39	NZ	M_ASP_81	OD2	3.880
4JO4	M_ARG_61	NH1	M_ASP_82	OD1	3.524
4JO4	M_ARG_61	NH1	M_ASP_82	OD2	2.695
4JO4	M_ARG_61	NH2	M_ASP_82	OD1	2.799
4JO4	M_ARG_61	NH2	M_ASP_82	OD2	3.460
4JO4	M_LYS_162	NZ	M_ASP_142	OD1	2.860
4JO4	M_LYS_162	NZ	M_ASP_142	OD2	3.801
4JO4	L_ARG_38	NH1	L_ASP_86	OD2	2.762
4JO4	L_ARG_38	NH2	L_GLU_46	OE1	3.585
4JO4	L_ARG_38	NH2	L_GLU_46	OE2	3.974
4JO4	L_ARG_38	NH2	L_ASP_86	OD2	3.717
4JO4	L_ARG_66	NH1	L_ASP_86	OD1	2.993
4JO4	L_ARG_66	NH1	L_ASP_86	OD2	3.710
4JO4	L_ARG_66	NH2	L_ASP_86	OD1	3.487
4JO4	L_ARG_66	NH2	L_ASP_86	OD2	2.841
4JO4	L_ARG_94	NH1	L_ASP_101	OD1	3.375
4JO4	L_ARG_94	NH1	L_ASP_101	OD2	2.907
4K24	A_LYS_46	NZ	U_GLU_33	OE2	3.632
4K24	A_LYS_46	NZ	U_GLU_36	OE2	2.856
4K24	A_ARG_69	NH1	A_ASP_65	OD2	2.685
4K24	A_HIS_87	ND1	U_ASP_11	OD1	3.994
4K24	A_ARG_88	NH1	A_ASP_90	OD1	2.450
4K24	A_ARG_88	NH1	A_ASP_90	OD2	2.041
4K24	A_ARG_88	NH2	A_ASP_90	OD2	3.515
4K24	A_ARG_108	NH2	A_ASP_106	OD1	3.775

4K24	A_ARG_109	NH2	A_GLU_125	OE1	3.204
4K24	A_ARG_109	NH2	A_GLU_125	OE2	3.379
4K24	A_ARG_110	NH2	A_GLU_125	OE1	3.434
4K24	B_LYS_6	NZ	B_GLU_38	OE1	3.295
4K24	B_LYS_6	NZ	B_GLU_38	OE2	3.051
4K24	H_LYS_62	NZ	L_ASP_1	OD1	3.610
4K24	H_ARG_66	NH2	H_ASP_86	OD1	3.579
4K24	H_ARG_66	NH2	H_ASP_86	OD2	3.959
4K24	H_ARG_94	NH2	H_ASP_101	OD2	3.501
4K24	H_LYS_205	NZ	H_ASP_207	OD1	3.964
4K24	H_LYS_208	NZ	L_GLU_123	OE1	2.286
4K24	H_LYS_208	NZ	L_GLU_123	OE2	3.345
4K24	L_ARG_46	NH2	L_ASP_55	OD1	2.623
4K24	L_ARG_46	NH2	L_ASP_55	OD2	2.874
4K24	L_ARG_61	NH1	L_GLU_79	OE1	3.659
4K24	L_ARG_61	NH1	L_ASP_82	OD2	3.380
4K24	L_ARG_61	NH2	L_GLU_79	OE1	2.490
4K24	L_ARG_61	NH2	L_GLU_79	OE2	3.979
4K24	L_ARG_61	NH2	L_ASP_82	OD1	3.491
4K24	L_ARG_61	NH2	L_ASP_82	OD2	3.569
4K24	L_LYS_142	NZ	L_ASP_143	OD1	3.088
4K24	L_LYS_147	NZ	L_GLU_154	OE1	3.964
4K24	L_LYS_147	NZ	L_GLU_154	OE2	3.385
4K24	L_LYS_147	NZ	L_GLU_195	OE2	3.600
4K24	L_HIS_189	ND1	L_GLU_185	OE2	3.464
4K24	L_HIS_189	NE2	L_ASP_151	OD2	3.905
4K24	L_ARG_211	NH1	L_GLU_187	OE1	3.878
4K24	L_ARG_211	NH2	L_GLU_187	OE1	2.437
4K24	U_ARG_25	NH1	U_GLU_42	OE2	3.583
4K24	U_ARG_25	NH1	U_GLU_68	OE1	3.761
4K24	U_ARG_25	NH2	U_GLU_42	OE2	3.008
4K24	U_ARG_30	NH1	U_GLU_37	OE2	3.811
4K24	U_ARG_30	NH2	U_GLU_37	OE1	3.105
4K24	U_ARG_30	NH2	U_GLU_37	OE2	2.352
4K24	U_LYS_50	NZ	U_GLU_68	OE2	3.702
4K24	U_LYS_50	NZ	U_ASP_254	OD1	3.827
4K24	U_ARG_53	NH1	U_ASP_254	OD1	3.567
4K24	U_ARG_53	NH1	U_ASP_254	OD2	3.288
4K24	U_ARG_53	NH2	U_ASP_254	OD1	3.503
4K24	U_ARG_53	NH2	U_ASP_254	OD2	3.622
4K24	U_LYS_62	NZ	U_GLU_33	OE1	3.765
4K24	U_ARG_91	NH1	B_ASP_22	OD2	3.233
4K24	U_ARG_91	NH2	B_ASP_22	OD1	3.988
4K24	U_ARG_91	NH2	B_ASP_22	OD2	3.635
4K24	U_HIS_143	ND1	U_GLU_106	OE2	3.213
4K24	U_ARG_145	NH1	U_ASP_124	OD1	3.705
4K24	U_ARG_145	NH2	U_ASP_124	OD1	2.588
4K24	U_ARG_145	NH2	U_ASP_124	OD2	3.556
4K24	U_LYS_175	NZ	U_GLU_178	OE2	3.964
4K2U	A_LYS_	NZ	A_GLU_	OE1	3.768
4K2U	A_LYS_	NZ	A_GLU_	OE2	2.609
4K2U	A_ARG_	NH1	A_ASP_	OD1	2.573
4K2U	A_ARG_	NH1	A_ASP_	OD2	3.255
4K2U	A_LYS_	NZ	A_ASP_	OD1	2.738
4K2U	A_LYS_	NZ	A_ASP_	OD1	3.468
4K2U	A_ARG_	NH1	A_ASP_	OD2	2.783
4K2U	A_ARG_	NH2	A_ASP_	OD2	2.667
4K2U	A_ARG_	NH2	A_GLU_	OE1	3.027

4K2U	A_ARG_	NH2	A_GLU_	OE2	3.639
4K2U	A_ARG_	NH1	A_ASP_	OD2	3.283
4K2U	A_ARG_	NH2	A_ASP_	OD1	3.700
4K2U	A_ARG_	NH2	A_ASP_	OD2	2.890
4K2U	A_ARG_	NH2	A_ASP_	OD2	3.924
4K2U	A_LYS_	NZ	A_GLU_	OE1	3.682
4K2U	A_LYS_	NZ	A_GLU_	OE2	3.521
4K2U	A_LYS_	NZ	A_ASP_	OD2	3.301
4K2U	A_LYS_	NZ	A_ASP_	OD2	3.690
4K2U	A_ARG_	NH1	A_GLU_	OE1	3.492
4K2U	A_ARG_	NH1	A_GLU_	OE2	3.531
4K2U	A_ARG_	NH2	A_GLU_	OE1	3.963
4K2U	A_ARG_	NH2	A_GLU_	OE2	2.886
4K2U	A_HIS_	NE2	A_GLU_	OE1	3.170
4K2U	A_LYS_	NZ	A_GLU_	OE1	3.297
4K2U	A_LYS_	NZ	A_GLU_	OE2	3.450
4K2U	A_ARG_	NH1	A_ASP_	OD1	3.497
4K2U	A_ARG_	NH2	A_ASP_	OD1	3.758
4K2U	B_LYS_	NZ	B_GLU_	OE1	3.571
4K2U	B_LYS_	NZ	B_GLU_	OE2	2.646
4K2U	B_ARG_	NH1	B_ASP_	OD1	2.642
4K2U	B_ARG_	NH1	B_ASP_	OD2	3.466
4K2U	B_LYS_	NZ	B_ASP_	OD1	2.561
4K2U	B_ARG_	NH1	B_ASP_	OD2	2.664
4K2U	B_ARG_	NH2	B_ASP_	OD2	2.621
4K2U	B_ARG_	NH2	B_GLU_	OE1	3.057
4K2U	B_ARG_	NH2	B_GLU_	OE2	3.570
4K2U	B_ARG_	NH1	B_ASP_	OD2	3.462
4K2U	B_ARG_	NH2	B_ASP_	OD1	3.706
4K2U	B_ARG_	NH2	B_ASP_	OD2	3.043
4K2U	B_ARG_	NH2	B_ASP_	OD2	3.804
4K2U	B_LYS_	NZ	B_GLU_	OE1	3.474
4K2U	B_LYS_	NZ	B_GLU_	OE2	3.437
4K2U	B_LYS_	NZ	B_GLU_	OE2	3.372
4K2U	B_LYS_	NZ	B_ASP_	OD2	3.125
4K2U	B_ARG_	NH1	B_GLU_	OE2	2.841
4K2U	B_ARG_	NH2	B_GLU_	OE1	3.192
4K2U	B_ARG_	NH2	B_GLU_	OE2	3.341
4K2U	B_LYS_	NZ	B_GLU_	OE1	3.826
4K2U	B_HIS_	NE2	B_GLU_	OE1	3.714
4K2U	B_LYS_	NZ	B_GLU_	OE1	3.312
4K2U	B_LYS_	NZ	B_GLU_	OE2	3.705
4K2U	B_ARG_	NH1	B_ASP_	OD1	3.090
4K2U	B_ARG_	NH2	B_ASP_	OD1	3.461
4K2U	B_LYS_	NZ	B_GLU_	OE2	3.384
4K2U	B_LYS_	NZ	B_ASP_	OD1	3.229
4K2U	B_LYS_	NZ	B_ASP_	OD2	2.796
4K2U	H_ARG_	NH1	H_GLU_	OE1	3.927
4K2U	H_LYS_	NZ	H_ASP_	OD1	3.481
4K2U	H_LYS_	NZ	H_ASP_	OD2	3.636
4K2U	H_LYS_	NZ	L_ASP_	OD2	2.646
4K2U	H_LYS_	NZ	H_ASP_	OD1	3.694
4K2U	H_LYS_	NZ	H_ASP_	OD2	2.669
4K2U	H_ARG_	NH2	H_ASP_	OD1	3.475
4K2U	H_ARG_	NH2	H_GLU_	OE1	2.820
4K2U	H_LYS_	NZ	L_GLU_	OE2	3.160
4K2U	I_ARG_	NH1	I_GLU_	OE1	3.521
4K2U	I_ARG_	NH2	I_GLU_	OE1	2.623

4K2U	L_LYS_	NZ	I_ASP_	OD1	3.612
4K2U	L_LYS_	NZ	I_ASP_	OD2	3.457
4K2U	L_LYS_	NZ	M_ASP_	OD2	2.895
4K2U	L_LYS_	NZ	I_ASP_	OD1	3.839
4K2U	L_LYS_	NZ	I_ASP_	OD2	2.840
4K2U	L_ARG_	NH2	I_ASP_	OD1	3.888
4K2U	L_ARG_	NH2	I_GLU_	OE1	2.738
4K2U	L_ARG_	NH1	L_ASP_	OD1	2.627
4K2U	L_ARG_	NH1	L_ASP_	OD2	2.684
4K2U	L_ARG_	NH1	A_GLU_	OE1	2.808
4K2U	L_ARG_	NH1	A_GLU_	OE2	3.439
4K2U	L_ARG_	NH2	A_GLU_	OE1	3.591
4K2U	L_ARG_	NH2	A_GLU_	OE2	2.619
4K2U	L_ARG_	NH1	L_GLU_	OE1	3.276
4K2U	L_ARG_	NH1	L_GLU_	OE2	3.602
4K2U	L_ARG_	NH2	L_GLU_	OE2	3.191
4K2U	L_ARG_	NH2	L_GLU_	OE1	3.486
4K2U	L_ARG_	NH2	L_ASP_	OD1	3.236
4K2U	L_ARG_	NH2	L_ASP_	OD2	3.657
4K2U	L_LYS_	NZ	L_GLU_	OE1	3.754
4K2U	L_LYS_	NZ	L_GLU_	OE2	2.528
4K2U	L_ARG_	NH1	L_GLU_	OE2	3.762
4K2U	L_ARG_	NH2	L_GLU_	OE1	3.990
4K2U	L_ARG_	NH2	L_GLU_	OE2	2.325
4K2U	L_HIS_	ND1	L_ASP_	OD2	2.555
4K2U	M_ARG_	NH1	M_ASP_	OD1	2.384
4K2U	M_ARG_	NH1	M_ASP_	OD2	3.237
4K2U	M_ARG_	NH1	B_GLU_	OE1	2.744
4K2U	M_ARG_	NH1	B_GLU_	OE2	3.321
4K2U	M_ARG_	NH2	B_GLU_	OE1	3.489
4K2U	M_ARG_	NH2	B_GLU_	OE2	2.673
4K2U	M_HIS_	ND1	I_GLU_	OE2	3.997
4K2U	M_ARG_	NH1	M_GLU_	OE2	3.472
4K2U	M_ARG_	NH2	M_GLU_	OE2	3.787
4K2U	M_ARG_	NH2	M_GLU_	OE1	3.410
4K2U	M_ARG_	NH2	M_ASP_	OD1	3.140
4K2U	M_ARG_	NH2	M_ASP_	OD1	3.175
4K2U	M_LYS_	NZ	M_GLU_	OE1	3.487
4K2U	M_LYS_	NZ	M_GLU_	OE2	2.899
4K2U	M_HIS_	ND1	M_ASP_	OD2	2.547
4KI5	C_HIS_35	NE2	C_GLU_99	OE1	2.952
4KI5	C_LYS_46	NZ	C_ASP_63	OD2	2.850
4KI5	C_LYS_65	NZ	C_ASP_62	OD1	3.382
4KI5	C_ARG_67	NH1	C_ASP_90	OD1	3.757
4KI5	C_ARG_67	NH1	C_ASP_90	OD2	2.867
4KI5	C_ARG_67	NH2	C_ASP_90	OD1	3.010
4KI5	C_ARG_67	NH2	C_ASP_90	OD2	3.538
4KI5	C_ARG_98	NH1	C_ASP_100	OD1	3.340
4KI5	C_LYS_211	NZ	D_GLU_122	OE2	2.907
4KI5	C_ARG_216	NH2	C_GLU_214	OE1	3.340
4KI5	D_ARG_60	NH2	D_GLU_80	OE2	3.447
4KI5	D_ARG_60	NH2	D_ASP_81	OD1	2.653
4KI5	D_ARG_60	NH2	D_ASP_81	OD2	3.443
4KI5	D_LYS_102	NZ	D_ASP_164	OD1	3.660
4KI5	D_LYS_102	NZ	D_ASP_164	OD2	3.125
4KI5	D_LYS_146	NZ	D_GLU_153	OE1	3.729
4KI5	D_LYS_148	NZ	D_GLU_194	OE1	2.836
4KI5	D_ARG_154	NH1	D_GLU_184	OE1	3.010

4KI5	D_ARG_154	NH2	D_GLU_184	OE1	3.600
4KI5	D_LYS_182	NZ	D_GLU_186	OE2	3.376
4KI5	D_HIS_188	ND1	D_ASP_150	OD2	2.808
4KI5	D_HIS_197	ND1	D_ASP_142	OD1	2.559
4KI5	D_HIS_197	ND1	D_ASP_142	OD2	3.147
4KI5	E_ARG_40	NH2	E_GLU_89	OE2	3.648
4KI5	E_ARG_63	NH1	E_GLU_46	OE2	2.566
4KI5	E_LYS_65	NZ	E_GLU_62	OE1	3.306
4KI5	E_LYS_65	NZ	E_GLU_62	OE2	3.510
4KI5	E_LYS_67	NZ	E_ASP_90	OD1	3.938
4KI5	E_LYS_67	NZ	E_ASP_90	OD2	2.897
4KI5	E_ARG_98	NH2	E_ASP_110	OD1	3.380
4KI5	E_ARG_98	NH2	E_ASP_110	OD2	2.498
4KI5	E_LYS_217	NZ	F_GLU_123	OE2	3.401
4KI5	E_LYS_218	NZ	E_GLU_220	OE2	3.129
4KI5	E_ARG_222	NH1	F_GLU_123	OE1	3.106
4KI5	E_ARG_222	NH1	F_GLU_123	OE2	3.925
4KI5	E_ARG_222	NH2	F_GLU_123	OE1	3.823
4KI5	E_ARG_222	NH2	F_GLU_123	OE2	3.234
4KI5	F_ARG_24	NH2	F_ASP_70	OD1	3.045
4KI5	F_ARG_24	NH2	F_ASP_70	OD2	2.870
4KI5	F_ARG_46	NH2	F_ASP_55	OD2	3.256
4KI5	F_ARG_61	NH1	F_ASP_79	OD2	3.671
4KI5	F_ARG_61	NH2	F_ASP_79	OD2	3.651
4KI5	F_ARG_61	NH2	F_ASP_82	OD1	2.633
4KI5	F_ARG_61	NH2	F_ASP_82	OD2	3.268
4KI5	F_ARG_66	NH1	F_GLU_28	OE2	3.847
4KI5	F_ARG_66	NH2	F_GLU_28	OE2	3.615
4KI5	F_LYS_103	NZ	F_ASP_165	OD1	3.937
4KI5	F_LYS_103	NZ	F_ASP_165	OD2	3.643
4KI5	F_LYS_149	NZ	F_GLU_195	OE1	2.911
4KI5	F_ARG_155	NH1	F_GLU_185	OE2	3.880
4KI5	F_ARG_155	NH2	F_GLU_185	OE2	2.938
4KI5	F_LYS_169	NZ	F_GLU_81	OE2	3.864
4KI5	F_LYS_183	NZ	F_ASP_184	OD1	2.750
4KI5	F_HIS_189	ND1	F_ASP_151	OD2	2.998
4KI5	F_ARG_211	NH2	F_GLU_187	OE1	3.825
4KI5	M_ARG_2209	NH2	M_ASP_2187	OD2	2.570
4KI5	M_ARG_2215	NH1	C_ASP_100	OD1	2.868
4KI5	M_ARG_2215	NH1	C_ASP_100	OD2	3.241
4KI5	M_ARG_2215	NH2	C_ASP_100	OD1	3.324
4KI5	M_ARG_2215	NH2	C_ASP_100	OD2	2.939
4KI5	M_ARG_2215	NH2	C_ASP_101	OD2	3.819
4KI5	M_LYS_2227	NZ	E_GLU_50	OE1	3.493
4KI5	M_ARG_2304	NH2	M_ASP_2233	OD1	3.696
4KI5	M_ARG_2304	NH2	M_ASP_2233	OD2	3.280
4KJY	A_LYS_39	NZ	B_ASP_100	OD1	2.809
4KJY	A_LYS_41	NZ	A_GLU_97	OE2	2.999
4KJY	A_LYS_41	NZ	A_GLU_106	OE1	2.835
4KJY	A_ARG_45	NH1	A_ASP_62	OD1	3.701
4KJY	A_ARG_45	NH1	A_ASP_62	OD2	2.667
4KJY	A_ARG_45	NH2	A_ASP_62	OD2	2.900
4KJY	A_HIS_90	NE2	A_ASP_62	OD2	3.464
4KJY	A_ARG_103	NH2	A_GLU_100	OE1	3.259
4KJY	A_ARG_103	NH2	A_GLU_100	OE2	3.050
4KJY	B_ARG_46	NH1	B_GLU_102	OE1	3.091
4KJY	B_ARG_46	NH2	B_GLU_102	OE1	3.045
4KJY	B_ARG_53	NH1	A_GLU_97	OE2	3.571

4KJY	B_ARG_53	NH1	A_GLU_106	OE1	3.135
4KJY	B_ARG_59	NH1	B_ASP_85	OD1	3.565
4KJY	B_ARG_59	NH2	B_ASP_85	OD1	3.099
4KJY	B_ARG_59	NH2	B_ASP_85	OD2	2.288
4KJY	B_ARG_68	NH1	B_GLU_65	OE1	3.402
4KJY	B_ARG_68	NH2	B_GLU_65	OE1	3.828
4KJY	B_ARG_69	NH1	A_GLU_35	OE1	2.737
4KJY	B_ARG_69	NH1	A_GLU_35	OE2	3.607
4KJY	B_ARG_69	NH1	A_GLU_100	OE2	2.961
4KJY	B_ARG_69	NH2	A_GLU_35	OE1	3.476
4KJY	B_ARG_69	NH2	A_GLU_35	OE2	2.813
4KJY	B_LYS_96	NZ	A_GLU_97	OE1	2.567
4KJY	B_LYS_96	NZ	B_ASP_100	OD1	3.158
4KJY	B_LYS_96	NZ	B_ASP_100	OD2	2.571
4KJY	B_LYS_104	NZ	B_GLU_3	OE1	3.935
4KJY	B_LYS_104	NZ	B_GLU_3	OE2	3.416
4KJY	C_LYS_41	NZ	C_GLU_97	OE2	2.660
4KJY	C_LYS_41	NZ	C_GLU_106	OE1	2.848
4KJY	C_ARG_45	NH1	C_ASP_62	OD2	3.404
4KJY	C_ARG_45	NH2	C_ASP_62	OD1	3.143
4KJY	C_ARG_45	NH2	C_ASP_62	OD2	3.381
4KJY	C_LYS_67	NZ	C_GLU_69	OE1	3.854
4KJY	C_LYS_67	NZ	C_GLU_69	OE2	2.799
4KJY	C_LYS_81	NZ	C_GLU_69	OE2	2.680
4KJY	C_HIS_90	NE2	C_ASP_62	OD2	3.141
4KJY	C_ARG_103	NH2	C_GLU_100	OE1	3.185
4KJY	C_ARG_103	NH2	C_GLU_100	OE2	3.021
4KJY	D_ARG_40	NH1	A_GLU_29	OE1	3.310
4KJY	D_ARG_40	NH2	A_GLU_29	OE1	3.253
4KJY	D_ARG_40	NH2	A_GLU_29	OE2	2.999
4KJY	D_ARG_40	NH2	B_GLU_70	OE1	3.440
4KJY	D_ARG_46	NH1	D_GLU_102	OE1	3.026
4KJY	D_ARG_46	NH2	D_GLU_102	OE1	2.981
4KJY	D_ARG_53	NH1	C_GLU_97	OE2	3.949
4KJY	D_ARG_53	NH2	C_GLU_104	OE1	3.112
4KJY	D_ARG_53	NH2	C_GLU_104	OE2	3.607
4KJY	D_ARG_59	NH1	D_ASP_85	OD1	3.248
4KJY	D_ARG_59	NH2	D_ASP_85	OD1	3.278
4KJY	D_ARG_59	NH2	D_ASP_85	OD2	2.654
4KJY	D_ARG_68	NH2	D_GLU_65	OE1	2.908
4KJY	D_ARG_69	NH1	C_GLU_35	OE1	2.786
4KJY	D_ARG_69	NH1	C_GLU_35	OE2	3.903
4KJY	D_ARG_69	NH1	C_GLU_100	OE2	3.005
4KJY	D_ARG_69	NH2	C_GLU_35	OE1	3.286
4KJY	D_ARG_69	NH2	C_GLU_35	OE2	2.868
4KJY	D_LYS_96	NZ	C_GLU_97	OE1	2.747
4KJY	D_LYS_96	NZ	D_ASP_100	OD1	3.105
4KJY	D_LYS_96	NZ	D_ASP_100	OD2	2.750
4KJY	D_LYS_104	NZ	D_GLU_3	OE1	2.954
4KPH	L_LYS_39	NZ	L_GLU_81	OE1	3.604
4KPH	L_ARG_61	NH1	L_ASP_82	OD1	3.220
4KPH	L_ARG_61	NH1	L_ASP_82	OD2	2.394
4KPH	L_ARG_61	NH2	L_GLU_79	OE1	3.711
4KPH	L_ARG_61	NH2	L_GLU_79	OE2	3.781
4KPH	L_ARG_61	NH2	L_ASP_82	OD1	2.574
4KPH	L_ARG_61	NH2	L_ASP_82	OD2	3.380
4KPH	L_ARG_61	NH2	L_GLU_85	OE2	3.345
4KPH	L_LYS_103	NZ	L_ASP_85	OD1	2.968

4KPH	L_LYS_103	NZ	L_ASP_85	OD2	3.649
4KPH	L_LYS_147	NZ	L_GLU_154	OE2	3.845
4KPH	L_LYS_149	NZ	L_GLU_195	OE1	3.580
4KPH	L_LYS_149	NZ	L_GLU_195	OE2	2.888
4KPH	L_ARG_155	NH1	L_GLU_185	OE2	3.834
4KPH	L_LYS_169	NZ	L_GLU_81	OE2	3.946
4KPH	L_ARG_188	NH1	L_GLU_185	OE1	2.941
4KPH	L_ARG_188	NH2	L_GLU_185	OE1	3.830
4KPH	L_HIS_189	ND1	L_ASP_151	OD2	3.425
4KPH	L_HIS_189	NE2	L_GLU_185	OE2	3.271
4KPH	L_LYS_199	NZ	L_ASP_110	OD2	3.817
4KPH	H_ARG_38	NH1	H_ASP_86	OD1	2.609
4KPH	H_ARG_38	NH2	H_GLU_46	OE2	2.879
4KPH	H_ARG_38	NH2	H_ASP_86	OD1	3.494
4KPH	H_ARG_66	NH1	H_ASP_86	OD1	3.691
4KPH	H_ARG_66	NH1	H_ASP_86	OD2	3.301
4KPH	H_ARG_66	NH2	H_ASP_86	OD1	2.689
4KPH	H_ARG_66	NH2	H_ASP_86	OD2	2.980
4KPH	H_LYS_75	NZ	H_ASP_72	OD2	2.680
4KPH	H_LYS_208	NZ	L_GLU_123	OE2	2.903
4KPH	M_LYS_39	NZ	M_GLU_81	OE1	3.784
4KPH	M_ARG_61	NH1	M_ASP_82	OD1	3.526
4KPH	M_ARG_61	NH1	M_ASP_82	OD2	2.643
4KPH	M_ARG_61	NH2	M_GLU_79	OE1	3.955
4KPH	M_ARG_61	NH2	M_GLU_79	OE2	3.623
4KPH	M_ARG_61	NH2	M_ASP_82	OD1	2.593
4KPH	M_ARG_61	NH2	M_ASP_82	OD2	3.290
4KPH	L_ARG_38	NH1	L_ASP_86	OD1	2.756
4KPH	L_ARG_38	NH2	L_GLU_46	OE1	2.881
4KPH	L_ARG_38	NH2	L_ASP_86	OD1	3.615
4KPH	L_ARG_66	NH1	L_ASP_86	OD1	3.166
4KPH	L_ARG_66	NH1	L_ASP_86	OD2	2.662
4KPH	L_ARG_66	NH2	L_ASP_86	OD1	3.175
4KPH	L_ARG_66	NH2	L_ASP_86	OD2	3.816
4KPH	L_LYS_75	NZ	L_ASP_72	OD2	2.592
4KPH	L_LYS_208	NZ	M_GLU_123	OE2	2.312
4KRL	B_ARG_19	NH2	B_ASP_80	OD2	3.165
4KRL	B_ARG_30	NH1	A_ASP_355	OD1	3.258
4KRL	B_ARG_30	NH1	A_ASP_355	OD2	2.275
4KRL	B_ARG_30	NH2	A_ASP_355	OD1	3.549
4KRL	B_ARG_30	NH2	A_ASP_355	OD2	3.938
4KRL	B_ARG_38	NH1	B_ASP_90	OD2	3.344
4KRL	B_ARG_38	NH2	B_GLU_46	OE1	2.859
4KRL	B_ARG_38	NH2	B_ASP_90	OD2	3.931
4KRL	B_ARG_67	NH1	B_ASP_90	OD1	2.738
4KRL	B_ARG_67	NH1	B_ASP_90	OD2	3.832
4KRL	B_ARG_67	NH2	B_ASP_90	OD1	3.067
4KRL	B_ARG_67	NH2	B_ASP_90	OD2	2.979
4KRL	A_ARG_353	NH1	B_GLU_110	OE1	2.654
4KRL	A_ARG_353	NH2	B_ASP_112	OD1	3.873
4KRL	A_ARG_353	NH2	B_ASP_112	OD2	2.978
4KRL	A_LYS_372	NZ	A_GLU_397	OE2	2.311
4KRL	A_HIS_394	NE2	A_ASP_369	OD1	3.965
4KRL	A_ARG_403	NH1	A_GLU_376	OE1	2.323
4KRL	A_ARG_403	NH1	A_GLU_376	OE2	3.739
4KRL	A_LYS_407	NZ	A_ASP_434	OD1	3.147
4KRL	A_LYS_407	NZ	A_ASP_434	OD2	3.510
4KRL	A_ARG_427	NH1	A_GLU_397	OE1	3.352

4KRL	A_ARG_427	NH2	A_GLU_495	OE1	3.797
4KRL	A_ARG_427	NH2	A_ASP_498	OD1	2.739
4KRL	A_ARG_427	NH2	A_ASP_498	OD2	3.969
4KRL	A_LYS_455	NZ	A_GLU_489	OE2	3.930
4KRL	A_LYS_463	NZ	A_ASP_436	OD2	3.876
4KRM	A_HIS_334	ND1	A_GLU_320	OE1	3.977
4KRM	A_HIS_334	ND1	A_GLU_320	OE2	2.370
4KRM	A_HIS_334	NE2	A_GLU_320	OE2	3.990
4KRM	A_ARG_353	NH1	B_GLU_110	OE1	2.811
4KRM	A_ARG_353	NH2	B_ASP_112	OD1	3.965
4KRM	A_ARG_353	NH2	B_ASP_112	OD2	2.932
4KRM	A_LYS_372	NZ	A_GLU_397	OE2	3.950
4KRM	A_ARG_390	NH1	A_ASP_369	OD1	3.291
4KRM	A_ARG_390	NH2	A_ASP_369	OD1	3.166
4KRM	A_ARG_390	NH2	A_ASP_369	OD2	3.036
4KRM	A_HIS_394	ND1	A_ASP_392	OD1	3.439
4KRM	A_HIS_394	ND1	A_ASP_392	OD2	3.192
4KRM	A_HIS_394	ND1	A_GLU_397	OE1	3.878
4KRM	A_HIS_394	NE2	A_ASP_392	OD2	2.923
4KRM	A_ARG_403	NH2	A_GLU_376	OE1	2.698
4KRM	A_LYS_407	NZ	A_ASP_434	OD1	2.923
4KRM	A_LYS_407	NZ	H_GLU_5	OE1	3.498
4KRM	A_LYS_407	NZ	H_GLU_5	OE2	3.022
4KRM	A_LYS_463	NZ	A_ASP_436	OD2	3.346
4KRM	B_ARG_19	NH2	B_ASP_80	OD1	2.971
4KRM	B_ARG_30	NH1	A_ASP_355	OD1	3.162
4KRM	B_ARG_30	NH1	A_ASP_355	OD2	2.423
4KRM	B_ARG_30	NH2	A_ASP_355	OD1	3.525
4KRM	B_ARG_38	NH1	B_ASP_90	OD2	2.849
4KRM	B_ARG_38	NH2	B_GLU_46	OE1	3.190
4KRM	B_ARG_38	NH2	B_ASP_90	OD2	3.870
4KRM	B_ARG_67	NH1	B_ASP_90	OD1	2.285
4KRM	B_ARG_67	NH1	B_ASP_90	OD2	3.184
4KRM	B_ARG_67	NH2	B_ASP_90	OD2	3.620
4KRM	C_LYS_310	NZ	C_GLU_308	OE2	3.505
4KRM	C_HIS_334	ND1	C_GLU_320	OE1	3.487
4KRM	C_ARG_353	NH1	D_GLU_110	OE1	2.866
4KRM	C_ARG_353	NH2	D_ASP_112	OD2	3.218
4KRM	C_LYS_372	NZ	C_GLU_397	OE2	3.670
4KRM	C_HIS_394	NE2	C_GLU_397	OE1	2.760
4KRM	C_HIS_394	NE2	C_GLU_397	OE2	3.646
4KRM	C_ARG_403	NH1	C_GLU_376	OE1	2.996
4KRM	C_ARG_403	NH2	C_GLU_431	OE2	3.962
4KRM	C_LYS_407	NZ	C_ASP_434	OD1	2.908
4KRM	C_ARG_427	NH1	C_GLU_397	OE1	3.430
4KRM	C_ARG_427	NH2	C_ASP_498	OD1	2.428
4KRM	C_ARG_427	NH2	C_ASP_498	OD2	3.809
4KRM	C_LYS_455	NZ	C_GLU_489	OE1	2.730
4KRM	C_LYS_455	NZ	C_GLU_489	OE2	3.273
4KRM	C_LYS_463	NZ	C_ASP_436	OD2	3.365
4KRM	D_ARG_19	NH2	D_ASP_80	OD1	3.355
4KRM	D_ARG_19	NH2	D_ASP_80	OD2	3.916
4KRM	D_ARG_30	NH1	C_ASP_355	OD1	3.295
4KRM	D_ARG_30	NH1	C_ASP_355	OD2	2.452
4KRM	D_ARG_30	NH2	C_ASP_355	OD1	3.096
4KRM	D_ARG_30	NH2	C_ASP_355	OD2	3.699
4KRM	D_ARG_38	NH1	D_ASP_90	OD2	3.036
4KRM	D_ARG_38	NH2	D_GLU_46	OE1	3.135

4KRM	D_ARG_67	NH2	D_ASP_90	OD1	2.355
4KRM	D_ARG_67	NH2	D_ASP_90	OD2	3.277
4KRM	E_HIS_334	ND1	E_GLU_320	OE2	2.610
4KRM	E_ARG_353	NH1	F_GLU_110	OE1	2.855
4KRM	E_ARG_353	NH2	F_ASP_112	OD2	2.965
4KRM	E_LYS_372	NZ	E_GLU_397	OE2	3.677
4KRM	E_LYS_375	NZ	E_GLU_308	OE2	3.450
4KRM	E_ARG_390	NH1	E_ASP_369	OD1	3.281
4KRM	E_HIS_394	ND1	E_GLU_397	OE1	3.143
4KRM	E_HIS_394	ND1	E_GLU_397	OE2	3.895
4KRM	E_HIS_394	NE2	E_GLU_397	OE1	3.783
4KRM	E_HIS_394	NE2	E_GLU_397	OE2	3.447
4KRM	E_ARG_403	NH1	E_GLU_376	OE1	2.574
4KRM	E_ARG_403	NH1	E_GLU_376	OE2	3.773
4KRM	E_LYS_407	NZ	E_ASP_434	OD1	2.654
4KRM	E_LYS_407	NZ	E_ASP_434	OD2	3.337
4KRM	E_LYS_407	NZ	L_GLU_5	OE1	3.054
4KRM	E_LYS_407	NZ	L_GLU_5	OE2	2.995
4KRM	E_ARG_427	NH1	E_GLU_495	OE1	3.905
4KRM	E_ARG_427	NH1	E_ASP_498	OD1	3.791
4KRM	E_ARG_427	NH2	E_ASP_498	OD1	2.763
4KRM	E_ARG_427	NH2	E_ASP_498	OD2	3.959
4KRM	F_ARG_19	NH2	F_ASP_80	OD1	2.815
4KRM	F_ARG_30	NH1	E_ASP_355	OD1	3.119
4KRM	F_ARG_30	NH1	E_ASP_355	OD2	2.396
4KRM	F_ARG_30	NH2	E_ASP_355	OD1	3.504
4KRM	F_ARG_38	NH1	F_ASP_90	OD2	2.948
4KRM	F_ARG_38	NH2	F_GLU_46	OE1	2.970
4KRM	F_ARG_38	NH2	F_ASP_90	OD2	3.609
4KRM	F_ARG_67	NH1	F_ASP_90	OD1	3.689
4KRM	F_ARG_67	NH1	F_ASP_90	OD2	3.954
4KRM	F_ARG_67	NH2	F_ASP_90	OD1	2.190
4KRM	F_ARG_67	NH2	F_ASP_90	OD2	3.534
4KRM	G_LYS_310	NZ	G_GLU_376	OE2	3.271
4KRM	G_ARG_353	NH1	H_GLU_110	OE1	3.021
4KRM	G_ARG_353	NH2	H_ASP_112	OD2	3.118
4KRM	G_LYS_372	NZ	G_GLU_397	OE1	3.892
4KRM	G_LYS_372	NZ	G_GLU_397	OE2	2.517
4KRM	G_LYS_375	NZ	G_GLU_308	OE2	2.881
4KRM	G_HIS_394	ND1	G_GLU_397	OE1	3.232
4KRM	G_ARG_403	NH1	G_GLU_376	OE1	2.469
4KRM	G_LYS_407	NZ	B_GLU_5	OE1	3.493
4KRM	G_LYS_407	NZ	B_GLU_5	OE2	2.984
4KRM	G_LYS_407	NZ	G_ASP_434	OD1	2.773
4KRM	G_ARG_427	NH1	G_GLU_397	OE1	2.912
4KRM	G_ARG_427	NH2	G_ASP_392	OD2	3.305
4KRM	G_ARG_427	NH2	G_ASP_498	OD1	3.141
4KRM	G_LYS_463	NZ	G_ASP_436	OD2	2.681
4KRM	G_ARG_497	NH2	G_GLU_495	OE1	3.599
4KRM	H_ARG_19	NH2	H_ASP_80	OD1	3.560
4KRM	H_ARG_19	NH2	H_ASP_80	OD2	3.970
4KRM	H_ARG_27	NH1	G_ASP_323	OD1	2.688
4KRM	H_ARG_27	NH2	G_ASP_323	OD1	3.952
4KRM	H_ARG_30	NH1	G_ASP_355	OD1	3.358
4KRM	H_ARG_30	NH1	G_ASP_355	OD2	2.448
4KRM	H_ARG_30	NH2	G_ASP_355	OD1	3.423
4KRM	H_ARG_30	NH2	G_ASP_355	OD2	3.935
4KRM	H_ARG_38	NH1	H_ASP_90	OD2	2.777

4KRM	H_ARG_38	NH2	H_GLU_46	OE1	3.420
4KRM	H_ARG_38	NH2	H_ASP_90	OD2	3.551
4KRM	H_ARG_67	NH1	H_ASP_90	OD2	3.818
4KRM	H_ARG_67	NH2	H_ASP_90	OD1	2.298
4KRM	H_ARG_67	NH2	H_ASP_90	OD2	3.171
4KRM	L_ARG_353	NH1	J_GLU_110	OE1	2.862
4KRM	L_ARG_353	NH2	J_ASP_112	OD2	2.998
4KRM	L_ARG_390	NH2	L_ASP_369	OD1	2.686
4KRM	L_ARG_390	NH2	L_ASP_369	OD2	3.689
4KRM	L_ARG_403	NH1	L_GLU_376	OE1	2.441
4KRM	L_LYS_407	NZ	L_ASP_434	OD2	3.279
4KRM	L_ARG_427	NH1	L_GLU_397	OE1	3.054
4KRM	L_ARG_427	NH2	L_ASP_498	OD1	3.187
4KRM	L_LYS_463	NZ	L_ASP_436	OD2	3.450
4KRM	J_ARG_19	NH2	J_ASP_80	OD1	3.277
4KRM	J_ARG_30	NH1	L_ASP_355	OD1	3.164
4KRM	J_ARG_30	NH1	L_ASP_355	OD2	2.382
4KRM	J_ARG_30	NH2	L_ASP_355	OD1	3.707
4KRM	J_ARG_38	NH1	J_ASP_90	OD2	2.970
4KRM	J_ARG_38	NH2	J_GLU_46	OE1	3.503
4KRM	J_ARG_38	NH2	J_ASP_90	OD2	3.921
4KRM	J_ARG_54	NH1	J_ASP_56	OD1	3.183
4KRM	J_ARG_54	NH1	J_ASP_56	OD2	2.886
4KRM	J_ARG_54	NH2	J_ASP_56	OD2	3.668
4KRM	J_ARG_67	NH1	J_ASP_90	OD1	3.429
4KRM	J_ARG_67	NH1	J_ASP_90	OD2	3.042
4KRM	J_ARG_67	NH2	J_ASP_90	OD1	2.611
4KRM	J_ARG_67	NH2	J_ASP_90	OD2	3.747
4KRM	K_HIS_334	ND1	K_GLU_320	OE2	3.444
4KRM	K_ARG_353	NH1	L_GLU_110	OE1	2.887
4KRM	K_ARG_353	NH1	L_ASP_112	OD2	3.973
4KRM	K_ARG_353	NH2	L_ASP_112	OD2	2.890
4KRM	K_LYS_375	NZ	K_GLU_400	OE2	3.857
4KRM	K_HIS_394	ND1	K_GLU_397	OE1	3.459
4KRM	K_HIS_394	NE2	K_GLU_397	OE1	3.631
4KRM	K_HIS_394	NE2	K_GLU_397	OE2	3.863
4KRM	K_ARG_403	NH1	K_GLU_376	OE1	3.745
4KRM	K_ARG_403	NH1	K_GLU_376	OE2	2.249
4KRM	K_LYS_407	NZ	K_ASP_434	OD1	3.042
4KRM	K_LYS_407	NZ	K_ASP_434	OD2	3.679
4KRM	K_ARG_427	NH2	K_ASP_498	OD1	3.193
4KRM	L_ARG_19	NH2	L_ASP_80	OD1	3.556
4KRM	L_ARG_30	NH1	K_ASP_355	OD1	3.487
4KRM	L_ARG_30	NH1	K_ASP_355	OD2	2.441
4KRM	L_ARG_30	NH2	K_ASP_355	OD1	3.452
4KRM	L_ARG_30	NH2	K_ASP_355	OD2	3.835
4KRM	L_ARG_38	NH1	L_ASP_90	OD2	3.094
4KRM	L_ARG_38	NH2	L_GLU_46	OE1	3.277
4KRM	L_ARG_67	NH1	L_ASP_90	OD1	3.933
4KRM	L_ARG_67	NH1	L_ASP_90	OD2	3.289
4KRM	L_ARG_67	NH2	L_ASP_90	OD1	2.604
4KRM	L_ARG_67	NH2	L_ASP_90	OD2	3.420
4KRO	A_ARG_310	NH2	A_GLU_376	OE2	2.978
4KRO	A_HIS_394	NE2	A_ASP_369	OD1	3.673
4KRO	A_ARG_403	NH1	A_GLU_376	OE1	2.481
4KRO	A_ARG_403	NH1	A_GLU_376	OE2	3.999
4KRO	A_ARG_403	NH2	B_ASP_118	OD2	3.168
4KRO	A_ARG_405	NH2	B_ASP_118	OD1	3.123

4KRO	A_ARG_405	NH2	B_ASP_118	OD2	3.849
4KRO	A_LYS_407	NZ	A_ASP_434	OD1	3.794
4KRO	A_LYS_407	NZ	A_ASP_434	OD2	2.246
4KRO	A_ARG_427	NH1	A_GLU_397	OE1	3.467
4KRO	A_ARG_427	NH2	A_ASP_498	OD1	2.615
4KRO	A_LYS_443	NZ	D_ASP_58	OD1	2.597
4KRO	A_LYS_443	NZ	D_ASP_58	OD2	3.457
4KRO	A_LYS_465	NZ	D_ASP_103	OD2	2.400
4KRO	A_LYS_476	NZ	A_GLU_472	OE1	3.768
4KRO	A_ARG_503	NH1	A_ASP_513	OD1	3.566
4KRO	A_ARG_507	NH2	A_GLU_524	OE1	3.712
4KRO	A_HIS_594	NE2	A_ASP_588	OD1	2.943
4KRO	B_ARG_27	NH1	A_GLU_431	OE1	3.073
4KRO	B_ARG_27	NH2	A_GLU_431	OE1	3.933
4KRO	B_ARG_113	NH1	B_ASP_116	OD2	3.449
4KRO	B_ARG_113	NH2	B_ASP_116	OD1	2.666
4KRO	B_ARG_113	NH2	B_ASP_116	OD2	3.479
4KRO	C_LYS_49	NZ	D_GLU_105	OE2	3.247
4KRO	C_ARG_61	NH1	C_GLU_79	OE2	3.404
4KRO	C_ARG_61	NH2	C_GLU_81	OE2	3.298
4KRO	C_ARG_61	NH2	C_ASP_82	OD1	2.644
4KRO	C_ARG_61	NH2	C_ASP_82	OD2	3.807
4KRO	C_LYS_103	NZ	C_GLU_165	OE1	3.774
4KRO	C_LYS_103	NZ	C_GLU_165	OE2	3.693
4KRO	D_ARG_38	NH1	D_ASP_89	OD1	3.529
4KRO	D_ARG_38	NH2	D_GLU_46	OE1	2.983
4KRO	D_ARG_38	NH2	D_GLU_46	OE2	3.441
4KRO	D_ARG_66	NH1	D_ASP_89	OD2	3.598
4KRO	D_ARG_66	NH2	D_ASP_89	OD1	2.749
4KRO	D_ARG_66	NH2	D_ASP_89	OD2	3.332
4KRO	D_LYS_149	NZ	D_ASP_150	OD1	3.048
4KRO	D_LYS_149	NZ	D_ASP_150	OD2	2.797
4KRP	A_ARG_310	NH2	A_GLU_376	OE1	3.735
4KRP	A_ARG_310	NH2	A_GLU_376	OE2	2.935
4KRP	A_HIS_394	NE2	A_ASP_369	OD1	3.309
4KRP	A_ARG_403	NH1	A_GLU_376	OE1	2.285
4KRP	A_ARG_403	NH2	B_ASP_115	OD2	3.818
4KRP	A_ARG_405	NH1	B_GLU_113	OE1	2.923
4KRP	A_ARG_405	NH2	B_GLU_113	OE1	3.376
4KRP	A_ARG_405	NH2	B_ASP_115	OD1	2.626
4KRP	A_LYS_407	NZ	A_ASP_434	OD2	2.386
4KRP	A_ARG_427	NH2	A_ASP_392	OD2	3.997
4KRP	A_ARG_427	NH2	A_ASP_498	OD1	2.593
4KRP	A_ARG_427	NH2	A_ASP_498	OD2	3.626
4KRP	A_LYS_443	NZ	D_ASP_58	OD1	2.649
4KRP	A_LYS_443	NZ	D_ASP_58	OD2	3.951
4KRP	A_LYS_455	NZ	A_GLU_489	OE1	2.953
4KRP	A_LYS_455	NZ	A_GLU_489	OE2	2.814
4KRP	A_LYS_463	NZ	A_ASP_436	OD2	3.639
4KRP	A_LYS_465	NZ	D_ASP_103	OD2	2.931
4KRP	A_ARG_497	NH2	A_GLU_495	OE1	3.513
4KRP	A_ARG_507	NH2	A_GLU_524	OE1	3.179
4KRP	A_ARG_550	NH1	A_GLU_527	OE2	2.828
4KRP	A_ARG_550	NH2	A_GLU_527	OE1	3.298
4KRP	A_ARG_550	NH2	A_GLU_527	OE2	2.540
4KRP	A_HIS_560	NE2	A_GLU_537	OE1	3.908
4KRP	A_LYS_585	NZ	A_ASP_563	OD1	2.533
4KRP	C_LYS_49	NZ	C_GLU_53	OE1	2.808

4KRP	C_ARG.61	NH1	C_GLU_79	OE2	3.577
4KRP	C_ARG.61	NH2	C_GLU_79	OE1	3.975
4KRP	C_ARG.61	NH2	C_GLU_81	OE1	3.909
4KRP	C_ARG.61	NH2	C_GLU_81	OE2	3.782
4KRP	C_ARG.61	NH2	C_ASP_82	OD1	2.795
4KRP	C_ARG.61	NH2	C_ASP_82	OD2	3.835
4KRP	C_LYS_103	NZ	C_GLU_105	OE2	2.819
4KRP	C_LYS_149	NZ	C_GLU_195	OE1	2.866
4KRP	D_ARG.38	NH1	D_ASP_89	OD1	2.914
4KRP	D_ARG.38	NH2	D_GLU_46	OE1	3.258
4KRP	D_ARG.38	NH2	D_ASP_89	OD1	3.860
4KRP	D_ARG.66	NH1	D_ASP_89	OD1	3.718
4KRP	D_ARG.66	NH1	D_ASP_89	OD2	3.786
4KRP	D_ARG.66	NH2	D_ASP_89	OD1	2.586
4KRP	D_ARG.66	NH2	D_ASP_89	OD2	3.503
4KRP	D_LYS_149	NZ	D_ASP_150	OD1	3.078
4KRP	D_LYS_149	NZ	D_ASP_150	OD2	2.845
4KRP	B_ARG.27	NH1	A_GLU_431	OE1	3.144
4KRP	B_ARG.27	NH2	B_GLU_1	OE2	3.797
4KV5	C_LYS.26	NZ	C_ASP_23	OD2	3.341
4KV5	C_LYS.60	NZ	G_ASP_56	OD2	3.911
4KV5	C_LYS.60	NZ	G_GLU_74	OE2	3.252
4KV5	C_ARG.94	NH1	E_ASP_231	OD2	3.776
4KV5	C_ARG.107	NH1	C_GLU_84	OE1	2.912
4KV5	D_LYS.26	NZ	D_ASP_23	OD2	3.617
4KV5	D_LYS.60	NZ	E_GLU_74	OE2	3.237
4KV5	D_ARG.107	NH1	D_GLU_84	OE1	2.427
4KV5	D_ARG.107	NH1	D_GLU_84	OE2	3.699
4KV5	A_LYS.26	NZ	A_ASP_23	OD1	3.905
4KV5	A_LYS.26	NZ	A_ASP_23	OD2	3.181
4KV5	A_ARG.94	NH1	H_ASP_231	OD2	3.628
4KV5	A_ARG.107	NH1	A_GLU_84	OE1	2.439
4KV5	A_ARG.107	NH1	A_GLU_84	OE2	3.529
4KV5	B_LYS.26	NZ	B_ASP_23	OD2	3.176
4KV5	B_LYS.60	NZ	H_ASP_56	OD2	3.938
4KV5	B_LYS.60	NZ	H_GLU_74	OE2	3.524
4KV5	B_ARG.107	NH1	B_GLU_84	OE1	2.808
4KV5	B_ARG.107	NH1	B_GLU_84	OE2	3.463
4KV5	J_LYS.12	NZ	J_GLU_10	OE1	3.764
4KV5	J_ARG.38	NH1	J_ASP_90	OD1	3.233
4KV5	J_ARG.38	NH2	J_GLU_46	OE1	3.110
4KV5	J_ARG.38	NH2	J_ASP_90	OD1	3.659
4KV5	J_ARG.63	NH1	J_GLU_138	OE2	3.309
4KV5	J_ARG.63	NH2	J_GLU_46	OE1	3.549
4KV5	J_ARG.63	NH2	J_GLU_46	OE2	2.611
4KV5	J_ARG.67	NH1	J_ASP_90	OD2	3.363
4KV5	J_ARG.67	NH2	J_ASP_90	OD1	3.304
4KV5	J_ARG.67	NH2	J_ASP_90	OD2	3.334
4KV5	J_ARG.161	NH1	J_ASP_208	OD2	3.042
4KV5	J_ARG.199	NH1	J_GLU_217	OE2	3.577
4KV5	J_ARG.199	NH1	J_GLU_219	OE1	3.495
4KV5	J_ARG.199	NH1	J_ASP_220	OD1	2.798
4KV5	J_ARG.199	NH1	J_ASP_220	OD2	3.031
4KV5	J_ARG.199	NH2	J_GLU_217	OE1	3.655
4KV5	H_LYS.12	NZ	H_GLU_10	OE1	3.355
4KV5	H_ARG.38	NH1	H_ASP_90	OD1	3.401
4KV5	H_ARG.38	NH2	H_GLU_46	OE1	3.103
4KV5	H_ARG.38	NH2	H_ASP_90	OD1	3.880

4KV5	H_ARG.63	NH1	H_GLU_138	OE2	3.222
4KV5	H_ARG.63	NH2	H_GLU_46	OE1	3.904
4KV5	H_ARG.63	NH2	H_GLU_46	OE2	3.081
4KV5	H_ARG.67	NH1	H_ASP_90	OD2	3.586
4KV5	H_ARG.67	NH2	H_ASP_90	OD1	3.193
4KV5	H_ARG.67	NH2	H_ASP_90	OD2	3.057
4KV5	H_ARG.161	NH1	H_ASP_208	OD1	3.304
4KV5	H_ARG.161	NH1	H_ASP_208	OD2	2.542
4KV5	H_LYS_177	NZ	H_GLU_219	OE2	3.873
4KV5	H_ARG.199	NH1	H_GLU_219	OE1	3.591
4KV5	H_ARG.199	NH1	H_ASP_220	OD1	2.535
4KV5	H_ARG.199	NH1	H_ASP_220	OD2	2.810
4KV5	H_ARG.199	NH2	H_GLU_217	OE1	3.657
4KV5	E_LYS.12	NZ	E_GLU_10	OE1	3.582
4KV5	E_ARG.38	NH1	E_ASP_90	OD1	3.243
4KV5	E_ARG.38	NH2	E_GLU_46	OE1	3.194
4KV5	E_ARG.38	NH2	E_ASP_90	OD1	3.863
4KV5	E_ARG.63	NH1	E_GLU_138	OE2	3.426
4KV5	E_ARG.63	NH2	E_GLU_46	OE1	3.563
4KV5	E_ARG.63	NH2	E_GLU_46	OE2	3.213
4KV5	E_ARG.67	NH1	E_ASP_90	OD2	3.666
4KV5	E_ARG.67	NH2	E_ASP_90	OD1	2.990
4KV5	E_ARG.67	NH2	E_ASP_90	OD2	3.041
4KV5	E_ARG.161	NH1	E_ASP_208	OD1	3.920
4KV5	E_ARG.161	NH1	E_ASP_208	OD2	2.895
4KV5	E_LYS_177	NZ	E_GLU_219	OE2	3.890
4KV5	E_ARG.199	NH1	E_GLU_217	OE2	3.831
4KV5	E_ARG.199	NH1	E_GLU_219	OE1	3.226
4KV5	E_ARG.199	NH1	E_ASP_220	OD1	3.288
4KV5	E_ARG.199	NH1	E_ASP_220	OD2	3.702
4KV5	E_ARG.199	NH2	E_GLU_217	OE1	3.523
4KV5	G_LYS.12	NZ	G_GLU_10	OE1	3.677
4KV5	G_ARG.38	NH1	G_ASP_90	OD1	3.460
4KV5	G_ARG.38	NH2	G_GLU_46	OE1	2.859
4KV5	G_ARG.38	NH2	G_ASP_90	OD1	3.976
4KV5	G_ARG.63	NH1	G_GLU_138	OE2	3.087
4KV5	G_ARG.63	NH2	G_GLU_46	OE1	3.637
4KV5	G_ARG.63	NH2	G_GLU_46	OE2	2.834
4KV5	G_ARG.67	NH1	G_ASP_90	OD2	3.423
4KV5	G_ARG.67	NH2	G_ASP_90	OD1	3.401
4KV5	G_ARG.67	NH2	G_ASP_90	OD2	3.441
4KV5	G_ARG.161	NH1	G_ASP_208	OD1	3.631
4KV5	G_ARG.161	NH1	G_ASP_208	OD2	2.851
4KV5	G_ARG.199	NH1	G_GLU_217	OE2	3.903
4KV5	G_ARG.199	NH1	G_GLU_219	OE1	3.208
4KV5	G_ARG.199	NH1	G_GLU_219	OE2	3.799
4KV5	G_ARG.199	NH1	G_ASP_220	OD1	3.065
4KV5	G_ARG.199	NH1	G_ASP_220	OD2	3.673
4KV5	G_ARG.199	NH2	G_GLU_217	OE1	3.544
4KXZ	A_ARG.26	NH1	A_ASP_27	OD1	3.110
4KXZ	A_ARG.26	NH1	A_ASP_27	OD2	2.701
4KXZ	A_ARG.60	NH2	J_GLU_74	OE1	3.804
4KXZ	A_LYS_107	NZ	A_GLU_84	OE1	2.831
4KXZ	A_LYS_110	NZ	A_ASP_55	OD1	3.869
4KXZ	A_LYS_110	NZ	A_ASP_55	OD2	3.509
4KXZ	B_ARG.26	NH1	B_ASP_27	OD1	3.225
4KXZ	B_ARG.26	NH1	B_ASP_27	OD2	2.899
4KXZ	B_LYS_37	NZ	B_GLU_35	OE2	3.695

4KXZ	B_ARG_60	NH2	H_ASP_56	OD1	3.585
4KXZ	B_ARG_60	NH2	H_GLU_74	OE1	3.374
4KXZ	B_ARG_60	NH2	H_GLU_74	OE2	3.199
4KXZ	B_LYS_107	NZ	B_GLU_84	OE1	2.748
4KXZ	D_ARG_26	NH1	D_ASP_27	OD1	3.954
4KXZ	D_ARG_26	NH1	D_ASP_27	OD2	3.663
4KXZ	D_LYS_37	NZ	D_GLU_35	OE1	2.767
4KXZ	D_LYS_37	NZ	D_GLU_35	OE2	3.981
4KXZ	D_ARG_60	NH1	N_GLU_74	OE2	3.775
4KXZ	D_ARG_60	NH2	N_GLU_74	OE2	2.746
4KXZ	D_LYS_110	NZ	D_ASP_55	OD1	3.900
4KXZ	D_LYS_110	NZ	D_ASP_55	OD2	3.944
4KXZ	E_ARG_26	NH1	E_ASP_27	OD1	3.052
4KXZ	E_ARG_26	NH1	E_ASP_27	OD2	2.752
4KXZ	E_LYS_37	NZ	E_GLU_35	OE1	2.815
4KXZ	E_ARG_60	NH1	Q_GLU_74	OE1	3.619
4KXZ	E_LYS_107	NZ	E_GLU_84	OE1	2.833
4KXZ	E_LYS_110	NZ	E_ASP_55	OD1	3.262
4KXZ	E_LYS_110	NZ	E_ASP_55	OD2	3.430
4KXZ	H_LYS_12	NZ	H_GLU_10	OE1	3.843
4KXZ	H_ARG_38	NH1	H_ASP_90	OD1	2.815
4KXZ	H_ARG_38	NH2	H_GLU_46	OE2	3.360
4KXZ	H_ARG_38	NH2	H_ASP_90	OD1	3.535
4KXZ	H_ARG_63	NH1	H_GLU_46	OE2	2.772
4KXZ	H_ARG_67	NH1	H_ASP_90	OD1	3.629
4KXZ	H_ARG_67	NH1	H_ASP_90	OD2	2.716
4KXZ	H_ARG_67	NH2	H_ASP_90	OD1	3.064
4KXZ	H_ARG_67	NH2	H_ASP_90	OD2	3.651
4KXZ	H_LYS_150	NZ	H_ASP_151	OD1	3.357
4KXZ	H_LYS_150	NZ	H_ASP_151	OD2	3.542
4KXZ	H_LYS_208	NZ	H_ASP_206	OD2	3.838
4KXZ	H_HIS_219	NE2	Q_ASP_56	OD2	3.789
4KXZ	H_HIS_223	ND1	Q_GLU_82	OE1	3.688
4KXZ	H_HIS_223	ND1	Q_GLU_82	OE2	3.984
4KXZ	H_HIS_223	ND1	L_ASP_123	OD1	3.085
4KXZ	H_HIS_223	NE2	Q_GLU_82	OE2	3.368
4KXZ	H_HIS_223	NE2	L_ASP_123	OD1	3.457
4KXZ	J_LYS_12	NZ	J_GLU_10	OE1	3.778
4KXZ	J_ARG_38	NH1	J_ASP_90	OD1	3.085
4KXZ	J_ARG_38	NH2	J_GLU_46	OE1	3.558
4KXZ	J_ARG_38	NH2	J_ASP_90	OD1	3.950
4KXZ	J_ARG_63	NH1	J_GLU_46	OE2	2.664
4KXZ	J_ARG_67	NH1	J_ASP_90	OD1	3.719
4KXZ	J_ARG_67	NH1	J_ASP_90	OD2	2.552
4KXZ	J_ARG_67	NH2	J_ASP_90	OD1	2.776
4KXZ	J_ARG_67	NH2	J_ASP_90	OD2	3.166
4KXZ	J_LYS_150	NZ	J_ASP_151	OD1	3.358
4KXZ	J_LYS_150	NZ	J_ASP_151	OD2	3.511
4KXZ	J_LYS_208	NZ	J_ASP_206	OD2	3.900
4KXZ	J_LYS_216	NZ	I_GLU_124	OE1	2.736
4KXZ	J_LYS_216	NZ	I_GLU_124	OE2	3.105
4KXZ	N_LYS_12	NZ	N_GLU_10	OE1	3.790
4KXZ	N_ARG_38	NH1	N_ASP_90	OD1	3.020
4KXZ	N_ARG_38	NH2	N_GLU_46	OE1	3.356
4KXZ	N_ARG_38	NH2	N_ASP_90	OD1	3.762
4KXZ	N_ARG_63	NH1	N_GLU_46	OE2	2.704
4KXZ	N_ARG_67	NH1	N_ASP_90	OD1	3.612
4KXZ	N_ARG_67	NH1	N_ASP_90	OD2	2.733

4KXZ	N_ARG.67	NH2	N_ASP_90	OD1	3.034
4KXZ	N_ARG.67	NH2	N_ASP_90	OD2	3.633
4KXZ	N_ARG.87	NH2	N_GLU_89	OE1	3.697
4KXZ	N_LYS_150	NZ	N_ASP_151	OD1	3.348
4KXZ	N_LYS_150	NZ	N_ASP_151	OD2	3.490
4KXZ	N_LYS_208	NZ	N_ASP_206	OD2	3.916
4KXZ	N_HIS_219	NE2	J_ASP_56	OD2	3.889
4KXZ	N_HIS_223	ND1	J_GLU_82	OE1	3.240
4KXZ	N_HIS_223	ND1	M_ASP_123	OD1	3.197
4KXZ	N_HIS_223	NE2	J_GLU_82	OE1	3.650
4KXZ	N_HIS_223	NE2	J_GLU_82	OE2	3.394
4KXZ	N_HIS_223	NE2	M_ASP_123	OD1	3.310
4KXZ	Q_LYS_12	NZ	Q_GLU_10	OE1	3.907
4KXZ	Q_ARG.38	NH1	Q_ASP_90	OD1	3.058
4KXZ	Q_ARG.38	NH2	Q_GLU_46	OE1	3.407
4KXZ	Q_ARG.38	NH2	Q_ASP_90	OD1	3.856
4KXZ	Q_ARG.63	NH1	Q_GLU_46	OE2	2.707
4KXZ	Q_ARG.67	NH1	Q_ASP_90	OD1	3.587
4KXZ	Q_ARG.67	NH1	Q_ASP_90	OD2	2.735
4KXZ	Q_ARG.67	NH2	Q_ASP_90	OD1	3.009
4KXZ	Q_ARG.67	NH2	Q_ASP_90	OD2	3.660
4KXZ	Q_LYS_150	NZ	Q_ASP_151	OD1	3.335
4KXZ	Q_LYS_150	NZ	Q_ASP_151	OD2	3.512
4KXZ	Q_LYS_208	NZ	Q_ASP_206	OD2	3.889
4KXZ	L_ARG.24	NH1	L_ASP_71	OD1	3.813
4KXZ	L_ARG.24	NH2	L_ASP_71	OD1	3.864
4KXZ	L_ARG.24	NH2	L_ASP_71	OD2	3.073
4KXZ	L_ARG.55	NH1	L_ASP_61	OD1	3.473
4KXZ	L_ARG.62	NH1	L_GLU_82	OE1	3.700
4KXZ	L_ARG.62	NH1	L_ASP_83	OD1	3.621
4KXZ	L_ARG.62	NH1	L_ASP_83	OD2	2.958
4KXZ	L_LYS_108	NZ	L_GLU_17	OE2	3.073
4KXZ	L_LYS_150	NZ	L_GLU_196	OE1	2.905
4KXZ	L_HIS_190	ND1	L_ASP_152	OD1	2.847
4KXZ	L_HIS_190	NE2	L_ASP_186	OD1	3.845
4KXZ	L_ARG.24	NH1	L_ASP_71	OD1	3.783
4KXZ	L_ARG.24	NH2	L_ASP_71	OD1	3.857
4KXZ	L_ARG.24	NH2	L_ASP_71	OD2	3.080
4KXZ	L_ARG.62	NH1	L_GLU_82	OE1	3.794
4KXZ	L_ARG.62	NH1	L_ASP_83	OD1	3.459
4KXZ	L_ARG.62	NH1	L_ASP_83	OD2	2.664
4KXZ	L_ARG.78	NH2	L_ASP_61	OD1	3.145
4KXZ	L_ARG.104	NH1	L_GLU_166	OE1	3.969
4KXZ	L_LYS_127	NZ	L_GLU_124	OE1	3.662
4KXZ	L_LYS_127	NZ	L_GLU_124	OE2	3.133
4KXZ	L_LYS_150	NZ	L_GLU_196	OE1	2.895
4KXZ	L_HIS_190	ND1	L_ASP_152	OD1	3.069
4KXZ	L_HIS_190	NE2	L_ASP_186	OD1	3.912
4KXZ	M_ARG.24	NH1	M_ASP_71	OD1	3.817
4KXZ	M_ARG.24	NH2	M_ASP_71	OD1	3.870
4KXZ	M_ARG.24	NH2	M_ASP_71	OD2	3.074
4KXZ	M_ARG.62	NH1	M_GLU_82	OE1	3.945
4KXZ	M_ARG.62	NH1	M_ASP_83	OD1	2.966
4KXZ	M_ARG.62	NH1	M_ASP_83	OD2	2.505
4KXZ	M_ARG.104	NH1	M_GLU_166	OE1	3.774
4KXZ	M_LYS_127	NZ	M_GLU_124	OE1	3.654
4KXZ	M_LYS_127	NZ	M_GLU_124	OE2	3.133
4KXZ	M_LYS_150	NZ	M_GLU_196	OE1	2.934

4KXZ	M_HIS_190	ND1	M_ASP_152	OD1	2.804
4KXZ	M_HIS_190	NE2	M_ASP_186	OD1	3.796
4KXZ	P_ARG_24	NH1	P_ASP_71	OD1	3.864
4KXZ	P_ARG_24	NH2	P_ASP_71	OD1	3.911
4KXZ	P_ARG_24	NH2	P_ASP_71	OD2	3.105
4KXZ	P_ARG_62	NH1	P_GLU_82	OE1	3.797
4KXZ	P_ARG_62	NH1	P_ASP_83	OD1	3.211
4KXZ	P_ARG_62	NH1	P_ASP_83	OD2	2.770
4KXZ	P_ARG_104	NH1	P_GLU_166	OE1	3.937
4KXZ	P_LYS_127	NZ	P_GLU_124	OE1	3.704
4KXZ	P_LYS_127	NZ	P_GLU_124	OE2	3.171
4KXZ	P_LYS_150	NZ	P_GLU_196	OE1	2.899
4KXZ	P_HIS_190	ND1	P_ASP_186	OD1	3.702
4LQF	A_HIS_113	NE2	A_GLU_129	OE1	3.149
4LQF	A_HIS_113	NE2	A_GLU_129	OE2	3.669
4LQF	A_ARG_176	NH1	A_GLU_174	OE1	2.869
4LQF	A_ARG_176	NH2	A_GLU_174	OE1	2.927
4LQF	H_ARG_38	NH1	H_ASP_90	OD1	2.938
4LQF	H_ARG_38	NH2	H_GLU_46	OE1	3.480
4LQF	H_ARG_38	NH2	H_GLU_46	OE2	3.018
4LQF	H_ARG_38	NH2	H_ASP_90	OD1	3.987
4LQF	H_LYS_65	NZ	H_ASP_62	OD1	3.431
4LQF	H_ARG_67	NH1	H_ASP_90	OD1	3.786
4LQF	H_ARG_67	NH1	H_ASP_90	OD2	2.716
4LQF	H_ARG_67	NH2	H_ASP_90	OD1	2.856
4LQF	H_ARG_67	NH2	H_ASP_90	OD2	3.328
4LQF	H_ARG_98	NH2	H_ASP_105	OD1	3.789
4LQF	H_ARG_98	NH2	H_ASP_105	OD2	2.616
4LQF	H_LYS_212	NZ	L_GLU_129	OE1	2.714
4LQF	H_LYS_212	NZ	L_GLU_129	OE2	3.879
4LQF	H_LYS_213	NZ	H_GLU_215	OE2	3.811
4LQF	L_ARG_24	NH2	L_ASP_75	OD1	3.452
4LQF	L_LYS_55	NZ	A_ASP_170	OD2	2.731
4LQF	L_ARG_59	NH2	L_ASP_65	OD1	3.368
4LQF	L_ARG_66	NH1	L_GLU_84	OE1	3.227
4LQF	L_ARG_66	NH2	L_GLU_84	OE1	3.232
4LQF	L_ARG_66	NH2	L_GLU_86	OE1	3.495
4LQF	L_ARG_66	NH2	L_ASP_87	OD1	2.884
4LQF	L_ARG_66	NH2	L_ASP_87	OD2	3.750
4LQF	L_LYS_109	NZ	L_ASP_171	OD1	3.085
4LQF	L_LYS_153	NZ	L_GLU_201	OE2	3.416
4LQF	L_LYS_155	NZ	L_GLU_201	OE1	2.827
4LQF	L_LYS_155	NZ	L_GLU_201	OE2	3.989
4LQF	L_ARG_161	NH1	L_GLU_191	OE2	2.916
4LQF	L_ARG_161	NH2	L_GLU_191	OE2	3.407
4LQF	L_LYS_189	NZ	L_ASP_190	OD1	2.644
4LQF	L_HIS_195	ND1	L_ASP_157	OD2	2.742
4LQF	L_HIS_195	NE2	L_GLU_191	OE2	3.503
4LQF	L_LYS_205	NZ	L_ASP_116	OD1	3.781
4LQF	L_LYS_205	NZ	L_ASP_116	OD2	2.661
4LSS	G_LYS_46	NZ	G_GLU_492	OE2	3.983
4LSS	G_LYS_59	NZ	G_ASP_57	OD1	3.236
4LSS	G_LYS_59	NZ	G_ASP_57	OD2	3.806
4LSS	G_HIS_66	ND1	G_GLU_64	OE2	2.739
4LSS	G_LYS_97	NZ	G_GLU_275	OE2	2.397
4LSS	G_LYS_97	NZ	H_ASP_99	OD2	3.791
4LSS	G_LYS_207	NZ	G_GLU_381	OE1	3.905
4LSS	G_LYS_207	NZ	G_GLU_381	OE2	3.089

4LSS	G_LYS_229	NZ	G_GLU_83	OE2	3.491
4LSS	G_HIS_249	NE2	G_GLU_482	OE1	3.577
4LSS	G_LYS_282	NZ	G_GLU_275	OE1	3.241
4LSS	G_ARG_335	NH2	G_ASP_412	OD2	3.767
4LSS	G_LYS_351	NZ	G_GLU_269	OE2	3.712
4LSS	G_ARG_419	NH2	G_ASP_325	OD1	3.444
4LSS	G_ARG_419	NH2	G_ASP_325	OD2	2.969
4LSS	G_ARG_429	NH1	G_ASP_113	OD1	3.219
4LSS	G_ARG_429	NH1	G_ASP_113	OD2	3.237
4LSS	G_ARG_429	NH2	G_ASP_113	OD2	2.924
4LSS	G_ARG_456	NH1	G_GLU_466	OE1	3.330
4LSS	G_ARG_469	NH2	G_ASP_457	OD2	2.938
4LSS	G_ARG_476	NH1	G_GLU_102	OE1	3.477
4LSS	G_ARG_476	NH1	G_GLU_102	OE2	3.366
4LSS	G_ARG_476	NH2	G_ASP_474	OD2	3.933
4LSS	G_ARG_476	NH2	H_ASP_31	OD1	3.839
4LSS	G_ARG_480	NH1	G_ASP_477	OD1	2.752
4LSS	G_LYS_485	NZ	G_GLU_267	OE2	3.906
4LSS	G_LYS_487	NZ	G_GLU_91	OE1	2.643
4LSS	H_ARG_19	NH2	H_GLU_81	OE1	3.566
4LSS	H_ARG_38	NH1	H_ASP_86	OD1	3.014
4LSS	H_ARG_38	NH2	H_GLU_46	OE1	3.219
4LSS	H_ARG_38	NH2	H_ASP_86	OD1	3.812
4LSS	H_ARG_53	NH2	H_ASP_31	OD1	3.384
4LSS	H_ARG_61	NH2	G_GLU_466	OE1	3.951
4LSS	H_ARG_66	NH1	H_ASP_86	OD1	3.855
4LSS	H_ARG_66	NH2	H_ASP_86	OD1	2.799
4LSS	H_ARG_66	NH2	H_ASP_86	OD2	2.736
4LSS	H_ARG_71	NH1	G_ASP_368	OD1	3.719
4LSS	H_ARG_71	NH1	G_ASP_368	OD2	3.126
4LSS	H_ARG_71	NH2	G_ASP_368	OD1	3.278
4LSS	H_ARG_82A	NH1	H_GLU_81	OE2	3.430
4LSS	H_LYS_209	NZ	L_GLU_125	OE1	3.429
4LSS	H_LYS_209	NZ	L_GLU_125	OE2	3.562
4LSS	H_LYS_210	NZ	H_GLU_212	OE2	3.090
4LSS	L_ARG_24	NH2	L_ASP_70	OD1	3.687
4LSS	L_ARG_24	NH2	L_ASP_70	OD2	3.435
4LSS	L_ARG_54	NH1	L_ASP_60	OD2	3.825
4LSS	L_ARG_61	NH1	L_ASP_82	OD1	3.979
4LSS	L_ARG_61	NH1	L_ASP_82	OD2	2.997
4LSS	L_ARG_61	NH2	L_GLU_79	OE1	3.337
4LSS	L_ARG_61	NH2	L_ASP_82	OD1	3.196
4LSS	L_ARG_61	NH2	L_ASP_82	OD2	3.376
4LSS	L_LYS_109	NZ	L_GLU_17	OE1	3.541
4LSS	L_LYS_109	NZ	L_GLU_17	OE2	3.227
4LSS	L_LYS_109	NZ	L_ASP_107	OD1	3.475
4LSS	L_LYS_151	NZ	L_GLU_197	OE2	3.341
4LST	G_HIS_66	ND1	G_GLU_64	OE1	3.932
4LST	G_HIS_66	ND1	G_GLU_64	OE2	2.793
4LST	G_LYS_207	NZ	G_GLU_381	OE1	2.992
4LST	G_LYS_207	NZ	G_GLU_381	OE2	2.424
4LST	G_HIS_249	NE2	G_GLU_482	OE1	3.272
4LST	G_LYS_282	NZ	G_GLU_275	OE1	2.940
4LST	G_LYS_357	NZ	G_ASP_461	OD2	3.749
4LST	G_LYS_357	NZ	G_ASP_464	OD1	3.358
4LST	G_LYS_357	NZ	L_GLU_1	OE1	2.783
4LST	G_LYS_360	NZ	G_GLU_362	OE1	3.583
4LST	G_ARG_419	NH2	G_ASP_325	OD1	3.855

4LST	G_ARG_419	NH2	G_ASP_325	OD2	3.169
4LST	G_ARG_456	NH1	G_GLU_466	OE1	3.211
4LST	G_ARG_469	NH1	G_GLU_362	OE2	3.557
4LST	G_ARG_469	NH2	G_GLU_362	OE2	3.437
4LST	G_ARG_469	NH2	G_ASP_457	OD2	3.388
4LST	G_ARG_476	NH1	G_ASP_474	OD1	3.272
4LST	G_ARG_476	NH1	G_ASP_474	OD2	2.826
4LST	G_ARG_480	NH1	G_ASP_477	OD1	3.383
4LST	H_LYS_12	NZ	H_GLU_16	OE2	3.461
4LST	H_ARG_38	NH1	H_ASP_86	OD1	2.980
4LST	H_ARG_38	NH2	H_GLU_46	OE1	3.044
4LST	H_ARG_38	NH2	H_ASP_86	OD1	3.692
4LST	H_LYS_43	NZ	H_ASP_85	OD1	3.823
4LST	H_ARG_53	NH1	H_ASP_31	OD1	3.186
4LST	H_ARG_53	NH2	H_ASP_31	OD1	3.110
4LST	H_ARG_61	NH1	G_GLU_466	OE1	3.812
4LST	H_ARG_61	NH2	G_ASP_461	OD1	2.947
4LST	H_ARG_66	NH1	H_ASP_86	OD1	3.435
4LST	H_ARG_66	NH2	H_ASP_86	OD1	2.875
4LST	H_ARG_66	NH2	H_ASP_86	OD2	2.791
4LST	H_ARG_71	NH1	G_ASP_368	OD1	3.527
4LST	H_ARG_71	NH1	G_ASP_368	OD2	2.632
4LST	H_ARG_71	NH2	G_ASP_368	OD1	2.939
4LST	H_ARG_71	NH2	G_ASP_368	OD2	3.624
4LST	H_ARG_82A	NH1	H_GLU_81	OE2	3.069
4LST	H_HIS_102	NE2	H_GLU_101	OE1	3.589
4LST	H_LYS_143	NZ	H_ASP_144	OD2	3.387
4LST	H_LYS_209	NZ	L_GLU_125	OE2	3.921
4LST	H_LYS_214	NZ	L_ASP_124	OD1	3.010
4LST	H_LYS_214	NZ	L_ASP_124	OD2	3.020
4LST	L_ARG_24	NH1	L_ASP_70	OD1	3.104
4LST	L_ARG_24	NH1	L_ASP_70	OD2	3.678
4LST	L_ARG_61	NH1	L_ASP_82	OD1	3.975
4LST	L_ARG_61	NH1	L_ASP_82	OD2	2.621
4LST	L_ARG_61	NH2	L_GLU_79	OE1	3.426
4LST	L_ARG_61	NH2	L_ASP_82	OD1	3.303
4LST	L_ARG_61	NH2	L_ASP_82	OD2	3.231
4LST	L_LYS_109	NZ	L_GLU_17	OE1	2.684
4LST	L_LYS_185	NZ	L_GLU_189	OE2	3.865
4LU5	A_HIS_113	NE2	A_GLU_129	OE2	3.983
4LU5	A_LYS_161	NZ	A_ASP_146	OD1	3.296
4LU5	A_LYS_161	NZ	A_GLU_149	OE1	3.749
4LU5	A_LYS_161	NZ	A_GLU_149	OE2	3.934
4LU5	A_ARG_176	NH1	A_ASP_150	OD1	2.940
4LU5	A_ARG_176	NH2	A_GLU_174	OE1	2.726
4LU5	B_HIS_113	ND1	B_ASP_115	OD1	3.948
4LU5	B_LYS_161	NZ	B_ASP_146	OD1	3.334
4LU5	B_LYS_161	NZ	B_GLU_149	OE2	3.499
4LU5	B_ARG_176	NH1	B_ASP_150	OD2	3.286
4LU5	B_ARG_176	NH2	B_GLU_174	OE1	3.070
4LU5	H_ARG_38	NH1	H_ASP_90	OD1	2.792
4LU5	H_ARG_38	NH2	H_GLU_46	OE1	3.705
4LU5	H_ARG_38	NH2	H_ASP_90	OD1	3.789
4LU5	H_ARG_44	NH1	H_GLU_42	OE2	3.479
4LU5	H_ARG_44	NH2	H_GLU_46	OE2	3.762
4LU5	H_LYS_65	NZ	H_ASP_62	OD1	3.768
4LU5	H_ARG_67	NH1	H_ASP_90	OD1	3.815
4LU5	H_ARG_67	NH1	H_ASP_90	OD2	2.768

4LU5	H_ARG_67	NH2	H_ASP_90	OD1	2.850
4LU5	H_ARG_67	NH2	H_ASP_90	OD2	3.112
4LU5	H_ARG_98	NH2	B_ASP_168	OD2	3.392
4LU5	H_LYS_208	NZ	L_GLU_128	OE1	3.058
4LU5	H_LYS_208	NZ	L_GLU_128	OE2	3.445
4LU5	H_LYS_209	NZ	H_GLU_211	OE1	2.959
4LU5	L_ARG_51	NH1	H_ASP_101	OD1	3.227
4LU5	L_ARG_51	NH2	H_ASP_101	OD1	2.925
4LU5	L_ARG_51	NH2	L_ASP_60	OD1	2.906
4LU5	L_ARG_51	NH2	L_ASP_60	OD2	3.008
4LU5	L_ARG_66	NH1	L_GLU_84	OE1	3.197
4LU5	L_ARG_66	NH1	L_GLU_84	OE2	3.353
4LU5	L_ARG_66	NH2	L_ASP_87	OD1	2.665
4LU5	L_ARG_66	NH2	L_ASP_87	OD2	2.880
4LU5	L_ARG_82	NH2	L_GLU_84	OE2	3.688
4LU5	L_LYS_108	NZ	L_GLU_110	OE2	3.434
4LU5	L_LYS_154	NZ	L_GLU_200	OE1	3.567
4LU5	L_ARG_160	NH2	L_GLU_190	OE1	3.714
4LU5	L_ARG_160	NH2	L_GLU_190	OE2	2.875
4LU5	L_LYS_174	NZ	L_GLU_86	OE2	3.749
4LU5	L_LYS_188	NZ	L_GLU_192	OE1	2.486
4LU5	L_HIS_194	ND1	L_ASP_156	OD2	2.594
4LU5	L_LYS_204	NZ	L_ASP_115	OD2	3.897
4LU5	L_ARG_38	NH1	L_ASP_90	OD1	2.773
4LU5	L_ARG_38	NH2	L_GLU_46	OE1	3.420
4LU5	L_ARG_38	NH2	L_ASP_90	OD1	3.756
4LU5	L_ARG_44	NH1	L_GLU_42	OE1	3.393
4LU5	L_ARG_44	NH1	L_GLU_42	OE2	2.926
4LU5	L_ARG_44	NH2	L_GLU_42	OE2	3.842
4LU5	L_ARG_44	NH2	L_GLU_46	OE2	3.631
4LU5	L_LYS_65	NZ	L_ASP_62	OD1	3.327
4LU5	L_ARG_67	NH1	L_ASP_90	OD1	3.710
4LU5	L_ARG_67	NH1	L_ASP_90	OD2	2.762
4LU5	L_ARG_67	NH2	L_ASP_90	OD1	2.979
4LU5	L_ARG_67	NH2	L_ASP_90	OD2	3.184
4LU5	L_ARG_98	NH2	A_ASP_168	OD2	3.317
4LU5	L_LYS_209	NZ	L_GLU_211	OE2	3.549
4LU5	M_LYS_24	NZ	M_ASP_75	OD1	3.847
4LU5	M_ARG_51	NH1	L_ASP_101	OD2	3.086
4LU5	M_ARG_51	NH2	L_ASP_101	OD1	3.927
4LU5	M_ARG_51	NH2	L_ASP_101	OD2	2.770
4LU5	M_ARG_51	NH2	M_ASP_60	OD1	3.599
4LU5	M_ARG_51	NH2	M_ASP_60	OD2	3.102
4LU5	M_ARG_66	NH1	M_GLU_84	OE1	3.699
4LU5	M_ARG_66	NH1	M_GLU_84	OE2	3.904
4LU5	M_ARG_66	NH2	M_ASP_87	OD1	2.686
4LU5	M_ARG_66	NH2	M_ASP_87	OD2	3.050
4LU5	M_ARG_82	NH1	M_GLU_84	OE2	2.836
4LU5	M_LYS_152	NZ	M_GLU_200	OE2	3.478
4LU5	M_LYS_154	NZ	M_GLU_200	OE1	3.458
4LU5	M_LYS_154	NZ	M_GLU_200	OE2	3.926
4LU5	M_ARG_160	NH1	M_GLU_190	OE2	3.887
4LU5	M_ARG_160	NH2	M_GLU_190	OE2	2.853
4LU5	M_LYS_188	NZ	M_GLU_192	OE1	3.556
4LU5	M_ARG_193	NH1	M_ASP_189	OD2	3.951
4LU5	M_HIS_194	ND1	M_ASP_156	OD2	2.781
4LU5	M_LYS_204	NZ	M_ASP_115	OD2	3.771
4M1D	L_ARG_61	NH1	L_ASP_82	OD1	3.859

4M1D	L_ARG_61	NH1	L_ASP_82	OD2	2.922
4M1D	L_ARG_61	NH2	L_ASP_82	OD1	2.932
4M1D	L_ARG_61	NH2	L_ASP_82	OD2	3.341
4M1D	L_LYS_103	NZ	L_GLU_83	OE2	3.169
4M1D	L_LYS_110	NZ	L_GLU_198	OE1	2.670
4M1D	L_LYS_129	NZ	H_ASP_144	OD2	3.436
4M1D	L_LYS_149	NZ	L_GLU_203	OE2	3.944
4M1D	H_ARG_38	NH1	H_ASP_86	OD1	2.929
4M1D	H_ARG_38	NH2	H_GLU_46	OE1	3.018
4M1D	H_ARG_38	NH2	H_GLU_46	OE2	3.822
4M1D	H_ARG_38	NH2	H_ASP_86	OD1	3.988
4M1D	H_ARG_50	NH1	H_ASP_58	OD2	2.819
4M1D	H_ARG_66	NH1	H_ASP_86	OD1	3.809
4M1D	H_ARG_66	NH1	H_ASP_86	OD2	2.702
4M1D	H_ARG_66	NH2	H_ASP_86	OD1	3.069
4M1D	H_ARG_66	NH2	H_ASP_86	OD2	3.476
4M1D	H_ARG_71	NH2	H_ASP_73	OD1	3.470
4M1D	H_LYS_143	NZ	L_GLU_124	OE2	2.547
4M1D	H_LYS_209	NZ	L_GLU_123	OE1	2.798
4M1D	H_LYS_209	NZ	L_GLU_123	OE2	2.782
4M1D	P_ARG_315	NH2	H_ASP_95	OD2	3.175
4M1D	M_ARG_61	NH1	M_ASP_82	OD1	3.820
4M1D	M_ARG_61	NH1	M_ASP_82	OD2	2.675
4M1D	M_ARG_61	NH2	M_ASP_82	OD1	2.789
4M1D	M_ARG_61	NH2	M_ASP_82	OD2	3.154
4M1D	M_LYS_149	NZ	M_GLU_203	OE2	3.156
4M1D	L_ARG_38	NH1	L_ASP_86	OD1	2.903
4M1D	L_ARG_38	NH2	L_GLU_46	OE1	3.115
4M1D	L_ARG_38	NH2	L_GLU_46	OE2	3.904
4M1D	L_ARG_38	NH2	L_ASP_86	OD1	3.856
4M1D	L_ARG_50	NH1	L_ASP_58	OD2	2.888
4M1D	L_ARG_66	NH1	L_ASP_86	OD1	3.904
4M1D	L_ARG_66	NH1	L_ASP_86	OD2	2.765
4M1D	L_ARG_66	NH2	L_ASP_86	OD1	3.096
4M1D	L_ARG_66	NH2	L_ASP_86	OD2	3.440
4M1D	L_ARG_71	NH2	L_ASP_73	OD1	3.398
4M1D	L_LYS_209	NZ	M_GLU_123	OE1	3.060
4M1D	L_LYS_209	NZ	M_GLU_123	OE2	2.485
4M1D	L_ARG_210	NH1	L_GLU_212	OE2	3.506
4M1D	Q_ARG_315	NH2	L_ASP_95	OD2	3.051
4M1G	L_ARG_62	NH2	L_GLU_82	OE2	3.764
4M1G	L_ARG_62	NH2	L_ASP_83	OD1	2.800
4M1G	L_ARG_62	NH2	L_ASP_83	OD2	3.468
4M1G	L_LYS_104	NZ	L_ASP_166	OD1	2.839
4M1G	L_LYS_143	NZ	L_GLU_106	OE1	2.794
4M1G	L_LYS_143	NZ	L_GLU_106	OE2	3.443
4M1G	L_LYS_150	NZ	L_GLU_196	OE1	3.090
4M1G	L_LYS_150	NZ	L_GLU_196	OE2	3.774
4M1G	L_ARG_156	NH1	L_GLU_186	OE2	2.941
4M1G	L_ARG_189	NH2	L_ASP_185	OD2	3.981
4M1G	L_HIS_190	ND1	L_ASP_152	OD2	2.973
4M1G	L_LYS_200	NZ	L_ASP_111	OD2	3.784
4M1G	H_ARG_38	NH1	H_GLU_46	OE1	3.046
4M1G	H_ARG_38	NH1	H_ASP_89	OD1	3.832
4M1G	H_ARG_38	NH2	H_ASP_89	OD1	2.835
4M1G	H_ARG_66	NH1	H_ASP_89	OD1	3.787
4M1G	H_ARG_66	NH1	H_ASP_89	OD2	2.752
4M1G	H_ARG_66	NH2	H_ASP_89	OD1	2.894

4M1G	H_ARG_66	NH2	H_ASP_89	OD2	3.336
4M1G	H_LYS_97	NZ	H_ASP_106	OD1	3.138
4M1G	H_LYS_97	NZ	H_ASP_106	OD2	2.944
4M1G	H_LYS_210	NZ	H_ASP_212	OD2	3.380
4M1G	H_LYS_213	NZ	L_GLU_124	OE2	2.837
4M1G	H_ARG_218	NH2	L_GLU_124	OE1	2.657
4M1G	H_ARG_218	NH2	L_GLU_124	OE2	3.648
4M1G	A_LYS_161	NZ	H_ASP_31	OD1	3.895
4M1G	A_LYS_161	NZ	A_ASP_146	OD1	2.636
4M1G	A_ARG_176	NH2	A_GLU_174	OE2	2.901
4M1G	B_LYS_161	NZ	B_ASP_146	OD1	3.297
4M1G	B_ARG_176	NH1	B_GLU_174	OE1	3.072
4M1G	B_ARG_176	NH2	B_ASP_150	OD1	3.937
4M1G	B_ARG_176	NH2	B_GLU_174	OE1	3.174
4M3J	A_ARG_66	NH1	A_ASP_89	OD1	2.995
4M3J	A_ARG_66	NH1	A_ASP_89	OD2	3.290
4M3J	A_ARG_66	NH2	A_ASP_89	OD1	3.827
4M3J	A_ARG_66	NH2	A_ASP_89	OD2	2.608
4M3J	B_ARG_19	NH2	B_GLU_81	OE2	4.000
4M3J	B_ARG_38	NH1	B_ASP_89	OD1	2.933
4M3J	B_ARG_38	NH2	B_GLU_46	OE2	3.526
4M3J	B_ARG_66	NH1	B_ASP_89	OD1	2.977
4M3J	B_ARG_66	NH1	B_ASP_89	OD2	3.346
4M3J	B_ARG_66	NH2	B_ASP_89	OD1	3.861
4M3J	B_ARG_66	NH2	B_ASP_89	OD2	2.734
4M3K	A_LYS_43	NZ	A_GLU_64	OE1	3.810
4M3K	A_LYS_43	NZ	A_GLU_64	OE2	3.952
4M3K	A_ARG_61	NH2	A_GLU_37	OE1	2.874
4M3K	A_ARG_61	NH2	A_GLU_37	OE2	2.937
4M3K	A_LYS_73	NZ	A_GLU_166	OE2	3.458
4M3K	A_ARG_128	NH2	A_ASP_124	OD1	2.865
4M3K	A_ARG_128	NH2	A_ASP_124	OD2	3.740
4M3K	A_LYS_149	NZ	A_GLU_163	OE2	2.784
4M3K	A_LYS_154	NZ	A_GLU_151	OE1	3.231
4M3K	A_ARG_164	NH2	A_ASP_179	OD2	2.865
4M3K	A_ARG_184	NH2	A_ASP_63	OD1	3.681
4M3K	A_ARG_184	NH2	A_ASP_63	OD2	2.944
4M3K	A_ARG_204	NH1	A_GLU_196	OE2	2.953
4M3K	A_ARG_204	NH2	A_GLU_196	OE2	3.454
4M3K	A_LYS_212	NZ	A_GLU_230	OE2	3.176
4M3K	A_ARG_213	NH2	A_ASP_124	OD2	3.388
4M3K	A_ARG_213	NH2	A_ASP_209	OD2	3.177
4M3K	A_ARG_244	NH2	A_ASP_276	OD1	3.324
4M3K	A_ARG_244	NH2	A_ASP_276	OD2	3.717
4M3K	A_ARG_267	NH2	A_ASP_41	OD2	2.755
4M3K	A_LYS_277	NZ	A_GLU_281	OE2	3.368
4M3K	A_LYS_284	NZ	A_GLU_281	OE2	3.066
4M3K	A_LYS_288	NZ	A_ASP_32	OD1	3.999
4M3K	B_ARG_38	NH1	B_ASP_89	OD1	2.927
4M3K	B_ARG_38	NH2	B_GLU_46	OE2	3.059
4M3K	B_ARG_66	NH1	B_ASP_89	OD1	3.228
4M3K	B_ARG_66	NH1	B_ASP_89	OD2	3.507
4M3K	B_ARG_66	NH2	B_ASP_89	OD1	3.903
4M3K	B_ARG_66	NH2	B_ASP_89	OD2	2.748
4M5Y	H_ARG_38	NH1	H_ASP_86	OD1	2.740
4M5Y	H_ARG_38	NH2	H_GLU_46	OE1	3.005
4M5Y	H_ARG_38	NH2	H_GLU_46	OE2	3.867
4M5Y	H_ARG_38	NH2	H_ASP_86	OD1	3.427

4M5Y	H.LYS_60	NZ	H.GLU_46	OE2	3.961
4M5Y	H.ARG_66	NH1	H.ASP_86	OD1	3.597
4M5Y	H.ARG_66	NH1	H.ASP_86	OD2	3.103
4M5Y	H.ARG_66	NH2	H.ASP_86	OD1	3.032
4M5Y	H.ARG_66	NH2	H.ASP_86	OD2	3.612
4M5Y	H.ARG_94	NH2	H.ASP_101	OD1	3.590
4M5Y	H.ARG_94	NH2	H.ASP_101	OD2	2.687
4M5Y	H.LYS_143	NZ	L.GLU_124	OE2	2.602
4M5Y	H.ARG_210	NH1	H.GLU_212	OE2	3.298
4M5Y	L.ARG_61	NH1	L.ASP_82	OD1	3.807
4M5Y	L.ARG_61	NH1	L.ASP_82	OD2	2.837
4M5Y	L.ARG_61	NH2	L.GLU_79	OE1	3.774
4M5Y	L.ARG_61	NH2	L.GLU_79	OE2	3.834
4M5Y	L.ARG_61	NH2	L.ASP_82	OD1	2.987
4M5Y	L.ARG_61	NH2	L.ASP_82	OD2	3.453
4M5Y	L.LYS_103	NZ	L.ASP_85	OD1	2.950
4M5Y	L.LYS_103	NZ	L.ASP_85	OD2	3.655
4M5Y	L.LYS_166	NZ	L.GLU_83	OE1	3.021
4M5Y	L.ARG_38	NH1	L.ASP_86	OD1	2.800
4M5Y	L.ARG_38	NH2	L.GLU_46	OE1	3.015
4M5Y	L.ARG_38	NH2	L.GLU_46	OE2	3.972
4M5Y	L.ARG_38	NH2	L.ASP_86	OD1	3.483
4M5Y	L.LYS_60	NZ	L.GLU_46	OE2	3.961
4M5Y	L.ARG_66	NH1	L.ASP_86	OD1	3.585
4M5Y	L.ARG_66	NH1	L.ASP_86	OD2	3.054
4M5Y	L.ARG_66	NH2	L.ASP_86	OD1	3.004
4M5Y	L.ARG_66	NH2	L.ASP_86	OD2	3.622
4M5Y	L.ARG_94	NH2	L.ASP_101	OD1	3.599
4M5Y	L.ARG_94	NH2	L.ASP_101	OD2	2.713
4M5Y	L.LYS_143	NZ	M.GLU_124	OE2	2.668
4M5Y	L.ARG_210	NH2	L.GLU_212	OE1	3.354
4M5Y	L.ARG_210	NH2	L.GLU_212	OE2	2.881
4M5Y	M.ARG_61	NH1	M.ASP_82	OD1	3.838
4M5Y	M.ARG_61	NH1	M.ASP_82	OD2	2.829
4M5Y	M.ARG_61	NH2	M.GLU_79	OE1	3.888
4M5Y	M.ARG_61	NH2	M.GLU_79	OE2	3.912
4M5Y	M.ARG_61	NH2	M.ASP_82	OD1	2.982
4M5Y	M.ARG_61	NH2	M.ASP_82	OD2	3.418
4M5Y	M.LYS_103	NZ	M.ASP_85	OD1	2.936
4M5Y	M.LYS_103	NZ	M.ASP_85	OD2	3.698
4M5Y	M.LYS_166	NZ	M.GLU_83	OE1	2.838
4M7J	H.ARG_38	NH1	H.ASP_86	OD1	2.851
4M7J	H.ARG_38	NH2	H.GLU_46	OE1	2.998
4M7J	H.ARG_38	NH2	H.GLU_46	OE2	3.979
4M7J	H.ARG_38	NH2	H.ASP_86	OD1	3.844
4M7J	H.ARG_66	NH1	H.ASP_86	OD1	3.723
4M7J	H.ARG_66	NH1	H.ASP_86	OD2	2.912
4M7J	H.ARG_66	NH2	H.ASP_86	OD1	2.833
4M7J	H.ARG_66	NH2	H.ASP_86	OD2	3.435
4M7J	H.ARG_94	NH2	H.ASP_100	OD1	2.757
4M7J	H.ARG_94	NH2	H.ASP_100	OD2	3.594
4M7J	H.LYS_208	NZ	L.GLU_123	OE1	3.727
4M7J	H.LYS_208	NZ	L.GLU_123	OE2	3.593
4M7J	L.ARG_24	NH2	L.ASP_70	OD1	2.939
4M7J	L.ARG_24	NH2	L.ASP_70	OD2	3.255
4M7J	L.ARG_61	NH1	L.GLU_79	OE1	3.494
4M7J	L.ARG_61	NH1	L.GLU_79	OE2	3.711
4M7J	L.ARG_61	NH1	L.GLU_81	OE2	3.788

4M7J	L_ARG_61	NH2	L_GLU_79	OE1	3.751
4M7J	L_ARG_61	NH2	L_GLU_81	OE2	3.003
4M7J	L_ARG_61	NH2	L_ASP_82	OD1	2.487
4M7J	L_ARG_61	NH2	L_ASP_82	OD2	3.268
4M7J	L_LYS_103	NZ	L_GLU_105	OE1	3.663
4M7J	L_LYS_142	NZ	L_GLU_105	OE1	3.970
4M7J	L_LYS_149	NZ	L_GLU_195	OE2	3.349
4M7J	L_ARG_155	NH1	L_GLU_185	OE1	3.230
4M7J	L_ARG_155	NH1	L_GLU_185	OE2	3.937
4M7J	L_ARG_155	NH2	L_GLU_185	OE1	3.656
4M7J	L_ARG_155	NH2	L_GLU_185	OE2	2.916
4M7J	L_HIS_189	ND1	L_ASP_151	OD2	3.046
4M7J	L_LYS_199	NZ	L_ASP_110	OD1	3.848
4M7J	L_LYS_199	NZ	L_ASP_110	OD2	2.665
4M7Z	B_ARG_38	NH1	B_ASP_86	OD1	2.932
4M7Z	B_ARG_38	NH2	B_ASP_86	OD1	3.472
4M7Z	B_ARG_66	NH1	B_ASP_86	OD2	3.153
4M7Z	B_ARG_66	NH2	B_ASP_86	OD1	2.921
4M7Z	B_ARG_66	NH2	B_ASP_86	OD2	2.946
4M7Z	B_LYS_208	NZ	C_GLU_123	OE1	3.318
4M7Z	B_LYS_208	NZ	C_GLU_123	OE2	3.881
4M7Z	H_ARG_38	NH1	H_ASP_86	OD1	2.917
4M7Z	H_ARG_38	NH2	H_ASP_86	OD1	3.458
4M7Z	H_ARG_66	NH1	H_ASP_86	OD2	3.181
4M7Z	H_ARG_66	NH2	H_ASP_86	OD1	2.909
4M7Z	H_ARG_66	NH2	H_ASP_86	OD2	2.975
4M7Z	H_LYS_208	NZ	L_GLU_123	OE1	3.192
4M7Z	C_ARG_54	NH2	C_ASP_60	OD1	3.316
4M7Z	C_ARG_61	NH1	C_GLU_79	OE1	3.863
4M7Z	C_ARG_61	NH2	C_GLU_79	OE1	3.870
4M7Z	C_ARG_61	NH2	C_ASP_82	OD1	2.761
4M7Z	C_ARG_61	NH2	C_ASP_82	OD2	3.263
4M7Z	C_LYS_103	NZ	C_ASP_165	OD1	2.648
4M7Z	C_LYS_103	NZ	C_ASP_165	OD2	3.360
4M7Z	C_LYS_142	NZ	C_GLU_105	OE2	2.662
4M7Z	C_LYS_149	NZ	C_GLU_195	OE2	3.957
4M7Z	C_ARG_155	NH2	C_GLU_185	OE1	3.931
4M7Z	C_LYS_183	NZ	C_GLU_187	OE1	3.956
4M7Z	C_LYS_183	NZ	C_GLU_187	OE2	2.784
4M7Z	C_ARG_188	NH2	C_GLU_185	OE2	2.653
4M7Z	C_HIS_189	ND1	C_ASP_151	OD2	2.788
4M7Z	C_HIS_189	NE2	C_GLU_185	OE1	2.917
4M7Z	C_LYS_199	NZ	C_ASP_110	OD1	3.655
4M7Z	C_LYS_199	NZ	C_ASP_110	OD2	3.049
4M7Z	L_ARG_24	NH2	L_ASP_70	OD1	3.791
4M7Z	L_ARG_54	NH2	L_ASP_60	OD1	3.293
4M7Z	L_ARG_61	NH1	L_GLU_79	OE1	3.704
4M7Z	L_ARG_61	NH1	L_GLU_79	OE2	3.709
4M7Z	L_ARG_61	NH2	L_ASP_82	OD1	2.705
4M7Z	L_ARG_61	NH2	L_ASP_82	OD2	2.341
4M7Z	L_LYS_103	NZ	L_ASP_165	OD1	2.672
4M7Z	L_LYS_103	NZ	L_ASP_165	OD2	3.377
4M7Z	L_LYS_142	NZ	L_GLU_105	OE1	3.125
4M7Z	L_LYS_147	NZ	L_GLU_195	OE1	3.579
4M7Z	L_LYS_149	NZ	L_GLU_195	OE2	3.946
4M7Z	L_ARG_155	NH1	L_GLU_185	OE2	3.594
4M7Z	L_ARG_155	NH2	L_GLU_185	OE2	2.584
4M7Z	L_LYS_183	NZ	L_GLU_187	OE1	3.987

4M7Z	L_LYS_183	NZ	L_GLU_187	OE2	2.788
4M7Z	L_HIS_189	ND1	L_ASP_151	OD2	2.804
4M7Z	L_LYS_199	NZ	L_ASP_110	OD1	3.668
4M7Z	L_LYS_199	NZ	L_ASP_110	OD2	3.056
4M93	L_ARG_24	NH1	L_ASP_70	OD1	3.616
4M93	L_ARG_24	NH2	L_ASP_70	OD1	3.168
4M93	L_ARG_24	NH2	L_ASP_70	OD2	3.984
4M93	L_ARG_61	NH1	L_GLU_79	OE1	2.878
4M93	L_ARG_61	NH1	L_GLU_79	OE2	3.335
4M93	L_ARG_61	NH2	L_GLU_79	OE1	2.843
4M93	L_ARG_61	NH2	L_GLU_81	OE1	3.821
4M93	L_ARG_61	NH2	L_ASP_82	OD1	2.762
4M93	L_ARG_61	NH2	L_ASP_82	OD2	3.319
4M93	L_LYS_103	NZ	L_GLU_105	OE1	3.651
4M93	L_LYS_142	NZ	L_GLU_105	OE2	3.741
4M93	L_LYS_147	NZ	L_GLU_154	OE2	3.291
4M93	L_LYS_149	NZ	L_GLU_195	OE1	3.825
4M93	L_LYS_149	NZ	L_GLU_195	OE2	2.937
4M93	L_ARG_155	NH1	L_GLU_185	OE1	3.047
4M93	L_ARG_155	NH2	L_GLU_185	OE1	3.711
4M93	L_ARG_155	NH2	L_GLU_185	OE2	3.785
4M93	L_HIS_189	ND1	L_ASP_151	OD2	3.324
4M93	H_ARG_38	NH1	H_ASP_86	OD1	2.784
4M93	H_ARG_38	NH2	H_GLU_46	OE1	2.935
4M93	H_ARG_38	NH2	H_GLU_46	OE2	3.934
4M93	H_ARG_38	NH2	H_ASP_86	OD1	3.972
4M93	H_ARG_66	NH1	H_ASP_86	OD1	3.479
4M93	H_ARG_66	NH1	H_ASP_86	OD2	2.918
4M93	H_ARG_66	NH2	H_ASP_86	OD1	2.693
4M93	H_ARG_66	NH2	H_ASP_86	OD2	3.421
4M93	H_LYS_208	NZ	L_GLU_123	OE1	3.795
4M93	C_ARG_24	NH1	C_ASP_70	OD1	3.167
4M93	C_ARG_61	NH1	C_GLU_79	OE1	3.833
4M93	C_ARG_61	NH1	C_GLU_79	OE2	3.475
4M93	C_ARG_61	NH2	C_GLU_79	OE1	3.979
4M93	C_ARG_61	NH2	C_GLU_81	OE1	3.225
4M93	C_ARG_61	NH2	C_ASP_82	OD1	2.620
4M93	C_ARG_61	NH2	C_ASP_82	OD2	3.543
4M93	C_LYS_149	NZ	C_GLU_195	OE2	3.911
4M93	C_ARG_155	NH1	C_GLU_185	OE1	2.917
4M93	C_LYS_169	NZ	C_ASP_170	OD1	2.606
4M93	C_LYS_183	NZ	C_GLU_187	OE2	3.968
4M93	C_HIS_189	ND1	C_ASP_151	OD2	2.956
4M93	C_LYS_199	NZ	C_ASP_110	OD2	3.011
4M93	B_ARG_38	NH1	B_ASP_86	OD1	2.720
4M93	B_ARG_38	NH2	B_GLU_46	OE1	3.263
4M93	B_ARG_38	NH2	B_ASP_86	OD1	3.854
4M93	B_ARG_66	NH1	B_ASP_86	OD1	3.675
4M93	B_ARG_66	NH1	B_ASP_86	OD2	3.114
4M93	B_ARG_66	NH2	B_ASP_86	OD1	2.983
4M93	B_ARG_66	NH2	B_ASP_86	OD2	3.452
4M93	B_LYS_208	NZ	C_GLU_123	OE1	3.203
4MA1	B_LYS_5	NZ	F_GLU_187	OE1	3.315
4MA1	B_ARG_38	NH1	B_ASP_86	OD1	2.969
4MA1	B_ARG_38	NH2	B_GLU_46	OE1	3.713
4MA1	B_ARG_66	NH1	B_ASP_86	OD1	3.588
4MA1	B_ARG_66	NH1	B_ASP_86	OD2	2.940
4MA1	B_ARG_66	NH2	B_ASP_86	OD1	2.611

4MA1	B_ARG_66	NH2	B_ASP_86	OD2	3.400
4MA1	B_LYS_208	NZ	C_GLU_123	OE1	3.857
4MA1	E_ARG_38	NH1	E_ASP_86	OD1	3.045
4MA1	E_ARG_38	NH2	E_GLU_46	OE1	3.606
4MA1	E_ARG_38	NH2	E_ASP_86	OD1	3.907
4MA1	E_ARG_66	NH1	E_ASP_86	OD2	3.475
4MA1	E_ARG_66	NH2	E_ASP_86	OD1	2.678
4MA1	E_ARG_66	NH2	E_ASP_86	OD2	3.064
4MA1	H_ARG_38	NH1	H_ASP_86	OD1	2.748
4MA1	H_ARG_38	NH2	H_GLU_46	OE1	3.316
4MA1	H_ARG_38	NH2	H_GLU_46	OE2	3.996
4MA1	H_ARG_38	NH2	H_ASP_86	OD1	3.832
4MA1	H_ARG_66	NH1	H_ASP_86	OD1	3.691
4MA1	H_ARG_66	NH1	H_ASP_86	OD2	2.891
4MA1	H_ARG_66	NH2	H_ASP_86	OD1	2.643
4MA1	H_ARG_66	NH2	H_ASP_86	OD2	3.187
4MA1	H_LYS_208	NZ	L_GLU_123	OE1	3.752
4MA1	C_ARG_61	NH1	C_GLU_79	OE1	3.057
4MA1	C_ARG_61	NH2	C_GLU_79	OE1	3.843
4MA1	C_ARG_61	NH2	C_GLU_81	OE1	3.130
4MA1	C_ARG_61	NH2	C_ASP_82	OD1	2.795
4MA1	C_ARG_61	NH2	C_ASP_82	OD2	3.615
4MA1	C_LYS_103	NZ	C_GLU_105	OE1	2.684
4MA1	C_LYS_142	NZ	C_GLU_105	OE1	3.393
4MA1	C_LYS_142	NZ	C_GLU_105	OE2	3.621
4MA1	C_LYS_149	NZ	C_GLU_195	OE1	2.926
4MA1	C_ARG_155	NH1	C_GLU_185	OE1	3.289
4MA1	C_ARG_155	NH1	C_GLU_185	OE2	3.515
4MA1	C_ARG_155	NH2	C_GLU_185	OE2	3.110
4MA1	C_LYS_183	NZ	C_GLU_187	OE2	3.186
4MA1	C_HIS_189	ND1	C_ASP_151	OD2	3.088
4MA1	C_LYS_199	NZ	C_ASP_110	OD2	3.151
4MA1	F_ARG_24	NH2	F_ASP_70	OD2	2.964
4MA1	F_ARG_61	NH1	F_GLU_79	OE1	3.869
4MA1	F_ARG_61	NH1	F_GLU_79	OE2	3.320
4MA1	F_ARG_61	NH2	F_GLU_79	OE1	3.924
4MA1	F_ARG_61	NH2	F_GLU_81	OE2	3.033
4MA1	F_ARG_61	NH2	F_ASP_82	OD1	2.712
4MA1	F_ARG_61	NH2	F_ASP_82	OD2	3.811
4MA1	F_ARG_77	NH2	F_GLU_79	OE2	3.716
4MA1	F_LYS_103	NZ	F_GLU_105	OE2	2.828
4MA1	F_LYS_142	NZ	F_GLU_105	OE1	3.726
4MA1	F_LYS_142	NZ	F_GLU_105	OE2	3.145
4MA1	F_LYS_149	NZ	F_GLU_195	OE2	2.884
4MA1	F_ARG_155	NH1	F_GLU_185	OE1	3.214
4MA1	F_ARG_155	NH1	F_GLU_185	OE2	3.510
4MA1	F_ARG_155	NH2	F_GLU_185	OE2	2.964
4MA1	F_LYS_183	NZ	F_GLU_187	OE2	3.006
4MA1	F_HIS_189	ND1	F_ASP_151	OD2	2.997
4MA1	F_LYS_199	NZ	F_ASP_110	OD2	3.201
4MA1	L_ARG_61	NH1	L_GLU_79	OE2	3.784
4MA1	L_ARG_61	NH2	L_GLU_79	OE2	3.895
4MA1	L_ARG_61	NH2	L_GLU_81	OE1	3.533
4MA1	L_ARG_61	NH2	L_ASP_82	OD1	2.756
4MA1	L_ARG_61	NH2	L_ASP_82	OD2	3.629
4MA1	L_LYS_142	NZ	L_GLU_105	OE1	2.731
4MA1	L_LYS_142	NZ	L_GLU_105	OE2	3.970
4MA1	L_LYS_149	NZ	L_GLU_195	OE1	3.692

4MA1	L_LYS_149	NZ	L_GLU_195	OE2	2.968
4MA1	L_ARG_155	NH1	L_GLU_185	OE1	3.117
4MA1	L_ARG_155	NH1	L_GLU_185	OE2	3.471
4MA1	L_ARG_155	NH2	L_GLU_185	OE2	3.260
4MA1	L_LYS_183	NZ	L_GLU_187	OE2	3.272
4MA1	L_HIS_189	ND1	L_ASP_151	OD2	2.941
4MA1	L_LYS_199	NZ	L_ASP_110	OD2	3.106
4N0Y	H_LYS_12	NZ	H_GLU_10	OE1	3.602
4N0Y	H_HIS_35	NE2	H_ASP_95	OD2	2.820
4N0Y	H_ARG_38	NH1	H_ASP_86	OD1	2.849
4N0Y	H_ARG_38	NH2	H_ASP_86	OD1	3.733
4N0Y	H_ARG_62	NH1	H_GLU_46	OE1	3.633
4N0Y	H_ARG_62	NH1	H_GLU_46	OE2	2.564
4N0Y	H_ARG_66	NH1	H_ASP_86	OD1	3.587
4N0Y	H_ARG_66	NH1	H_ASP_86	OD2	2.986
4N0Y	H_ARG_66	NH2	H_ASP_86	OD1	2.907
4N0Y	H_ARG_66	NH2	H_ASP_86	OD2	3.646
4N0Y	H_LYS_143	NZ	H_ASP_144	OD1	3.625
4N0Y	H_LYS_143	NZ	H_ASP_144	OD2	3.475
4N0Y	H_LYS_209	NZ	L_GLU_123	OE1	2.939
4N0Y	H_LYS_210	NZ	H_GLU_212	OE1	3.922
4N0Y	L_ARG_61	NH2	L_GLU_81	OE2	3.404
4N0Y	L_ARG_61	NH2	L_ASP_82	OD1	2.584
4N0Y	L_ARG_61	NH2	L_ASP_82	OD2	3.315
4N0Y	L_LYS_110	NZ	L_GLU_198	OE1	3.860
4N1H	A_LYS_35	NZ	A_ASP_32	OD1	2.685
4N1H	A_ARG_61	NH2	A_GLU_37	OE1	3.246
4N1H	A_ARG_61	NH2	A_GLU_37	OE2	3.574
4N1H	A_LYS_73	NZ	A_GLU_166	OE1	3.851
4N1H	A_LYS_111	NZ	C_GLU_202	OE1	3.097
4N1H	A_LYS_111	NZ	C_GLU_202	OE2	2.712
4N1H	A_HIS_112	ND1	C_GLU_205	OE2	3.407
4N1H	A_HIS_112	NE2	C_GLU_202	OE1	2.950
4N1H	A_HIS_112	NE2	C_GLU_205	OE2	3.971
4N1H	A_ARG_128	NH1	C_GLU_89	OE1	3.101
4N1H	A_ARG_128	NH2	A_ASP_124	OD1	3.594
4N1H	A_ARG_128	NH2	A_ASP_124	OD2	3.398
4N1H	A_LYS_149	NZ	A_GLU_163	OE1	3.271
4N1H	A_LYS_150	NZ	B_ASP_115	OD2	2.748
4N1H	A_ARG_153	NH2	B_ASP_106	OD1	3.262
4N1H	A_ARG_153	NH2	B_ASP_106	OD2	3.262
4N1H	A_LYS_154	NZ	A_GLU_151	OE1	3.414
4N1H	A_LYS_154	NZ	A_GLU_151	OE2	2.635
4N1H	A_ARG_164	NH2	A_ASP_179	OD2	2.730
4N1H	A_ARG_184	NH2	A_ASP_63	OD1	3.800
4N1H	A_ARG_184	NH2	A_ASP_63	OD2	3.087
4N1H	A_ARG_204	NH2	A_GLU_196	OE2	3.365
4N1H	A_LYS_212	NZ	A_GLU_230	OE2	3.115
4N1H	A_ARG_213	NH2	A_ASP_209	OD1	2.990
4N1H	A_ARG_213	NH2	A_ASP_209	OD2	2.705
4N1H	A_ARG_222	NH2	A_ASP_233	OD1	3.305
4N1H	A_ARG_244	NH2	A_ASP_276	OD1	3.949
4N1H	A_ARG_244	NH2	A_ASP_276	OD2	3.570
4N1H	A_ARG_267	NH2	A_ASP_41	OD2	3.599
4N1H	A_LYS_284	NZ	A_GLU_281	OE1	3.697
4N1H	A_LYS_284	NZ	A_GLU_281	OE2	2.598
4N1H	B_ARG_38	NH1	B_ASP_90	OD1	3.247
4N1H	B_ARG_38	NH2	B_GLU_46	OE2	3.382

4N1H	B_ARG_38	NH2	B_ASP_90	OD1	3.865
4N1H	B_ARG_67	NH2	B_ASP_90	OD1	2.723
4N1H	B_ARG_67	NH2	B_ASP_90	OD2	2.861
4N1H	C_LYS_43	NZ	C_GLU_64	OE2	2.688
4N1H	C_ARG_61	NH2	C_GLU_37	OE1	2.807
4N1H	C_ARG_61	NH2	C_GLU_37	OE2	3.294
4N1H	C_LYS_73	NZ	C_GLU_166	OE2	3.581
4N1H	C_LYS_149	NZ	C_GLU_163	OE1	3.581
4N1H	C_LYS_149	NZ	C_GLU_163	OE2	3.310
4N1H	C_LYS_149	NZ	D_ASP_106	OD1	3.587
4N1H	C_LYS_149	NZ	D_ASP_106	OD2	3.735
4N1H	C_LYS_150	NZ	D_ASP_115	OD1	3.157
4N1H	C_ARG_153	NH2	D_ASP_106	OD1	2.772
4N1H	C_LYS_154	NZ	C_GLU_151	OE1	3.966
4N1H	C_LYS_154	NZ	C_GLU_151	OE2	3.090
4N1H	C_ARG_164	NH2	C_ASP_179	OD2	2.708
4N1H	C_ARG_204	NH2	A_GLU_121	OE2	3.425
4N1H	C_LYS_212	NZ	C_GLU_230	OE2	3.370
4N1H	C_ARG_213	NH2	C_ASP_209	OD2	2.965
4N1H	C_ARG_222	NH2	C_ASP_233	OD1	3.546
4N1H	C_ARG_244	NH2	C_ASP_276	OD1	3.134
4N1H	C_ARG_267	NH2	C_ASP_41	OD2	2.979
4N1H	C_LYS_277	NZ	C_GLU_281	OE2	3.711
4N1H	C_LYS_284	NZ	C_GLU_281	OE1	3.788
4N1H	C_LYS_284	NZ	C_GLU_281	OE2	2.689
4N1H	D_ARG_38	NH1	D_ASP_90	OD1	2.942
4N1H	D_ARG_38	NH2	D_ASP_90	OD1	3.612
4N1H	D_ARG_45	NH1	D_GLU_111	OE1	3.652
4N1H	D_ARG_45	NH1	D_GLU_111	OE2	3.043
4N1H	D_LYS_65	NZ	D_ASP_62	OD1	2.639
4N1H	D_LYS_65	NZ	D_ASP_62	OD2	3.577
4N1H	D_ARG_67	NH1	D_ASP_90	OD1	2.750
4N1H	D_ARG_67	NH1	D_ASP_90	OD2	3.293
4N1H	D_ARG_67	NH2	D_ASP_90	OD1	3.769
4N1H	D_ARG_67	NH2	D_ASP_90	OD2	2.732
4NBX	A_LYS_31	NZ	A_GLU_20	OE1	3.754
4NBX	A_LYS_31	NZ	A_GLU_20	OE2	2.760
4NBX	A_ARG_75	NH2	A_ASP_65	OD1	3.378
4NBX	B_ARG_34	NH1	B_ASP_39	OD2	2.728
4NBX	B_ARG_34	NH2	B_ASP_39	OD2	3.692
4NBX	B_ARG_45	NH1	B_ASP_97	OD1	3.021
4NBX	B_ARG_45	NH2	B_GLU_53	OE2	3.422
4NBX	B_ARG_52	NH2	B_ASP_115	OD1	3.103
4NBX	B_ARG_52	NH2	B_ASP_115	OD2	3.478
4NBX	B_ARG_74	NH1	B_ASP_97	OD1	3.854
4NBX	B_ARG_74	NH1	B_ASP_97	OD2	2.776
4NBX	B_ARG_74	NH2	B_ASP_97	OD1	2.873
4NBX	B_ARG_74	NH2	B_ASP_97	OD2	3.326
4NBX	B_LYS_83	NZ	B_ASP_80	OD2	3.208
4NBX	B_ARG_114	NH2	B_GLU_116	OE1	3.887
4NBY	A_LYS_42	NZ	A_GLU_97	OE1	2.799
4NBY	A_LYS_149	NZ	A_GLU_138	OE1	2.480
4NBY	A_LYS_149	NZ	A_GLU_138	OE2	3.061
4NBY	A_ARG_193	NH2	A_ASP_183	OD1	3.347
4NBY	B_ARG_34	NH1	B_ASP_39	OD1	2.677
4NBY	B_ARG_34	NH2	B_ASP_39	OD1	3.790
4NBY	B_ARG_45	NH1	B_ASP_97	OD1	2.996
4NBY	B_ARG_45	NH2	B_GLU_53	OE2	3.496

4NBY	B_ARG_52	NH2	B_ASP_115	OD2	3.092
4NBY	B_ARG_74	NH1	B_ASP_97	OD1	3.798
4NBY	B_ARG_74	NH1	B_ASP_97	OD2	2.779
4NBY	B_ARG_74	NH2	B_ASP_97	OD1	2.996
4NBY	B_ARG_74	NH2	B_ASP_97	OD2	3.496
4NBY	C_ARG_34	NH1	C_ASP_39	OD1	2.785
4NBY	C_ARG_34	NH2	C_ASP_39	OD1	3.629
4NBY	C_ARG_45	NH1	C_ASP_97	OD1	2.914
4NBY	C_ARG_45	NH2	C_GLU_53	OE2	3.403
4NBY	C_ARG_45	NH2	C_ASP_97	OD1	3.956
4NBY	C_LYS_72	NZ	C_ASP_69	OD1	3.359
4NBY	C_ARG_74	NH1	C_ASP_97	OD1	3.947
4NBY	C_ARG_74	NH1	C_ASP_97	OD2	2.935
4NBY	C_ARG_74	NH2	C_ASP_97	OD1	2.957
4NBY	C_ARG_74	NH2	C_ASP_97	OD2	3.430
4NBY	C_LYS_83	NZ	C_ASP_80	OD2	3.758
4NBZ	A_LYS_31	NZ	A_GLU_20	OE2	2.992
4NBZ	A_ARG_75	NH2	A_ASP_65	OD2	3.115
4NBZ	B_ARG_38	NH1	B_ASP_90	OD1	2.831
4NBZ	B_ARG_38	NH2	B_GLU_46	OE2	3.420
4NBZ	B_ARG_38	NH2	B_ASP_90	OD1	3.761
4NBZ	B_ARG_67	NH1	B_ASP_90	OD1	3.836
4NBZ	B_ARG_67	NH1	B_ASP_90	OD2	2.796
4NBZ	B_ARG_67	NH2	B_ASP_90	OD1	3.068
4NBZ	B_ARG_67	NH2	B_ASP_90	OD2	3.514
4NBZ	B_ARG_104	NH1	B_ASP_107	OD2	2.788
4NBZ	B_ARG_104	NH1	B_GLU_110	OE2	2.708
4NBZ	B_ARG_104	NH2	B_ASP_107	OD2	3.003
4NBZ	C_LYS_31	NZ	C_GLU_20	OE2	3.958
4NBZ	C_ARG_75	NH2	C_ASP_65	OD2	3.050
4NBZ	D_ARG_38	NH1	D_ASP_90	OD1	2.888
4NBZ	D_ARG_38	NH2	D_ASP_90	OD1	3.800
4NBZ	D_ARG_67	NH1	D_ASP_90	OD1	3.887
4NBZ	D_ARG_67	NH1	D_ASP_90	OD2	2.770
4NBZ	D_ARG_67	NH2	D_ASP_90	OD1	3.220
4NBZ	D_ARG_67	NH2	D_ASP_90	OD2	3.516
4NBZ	D_ARG_104	NH1	D_ASP_107	OD2	3.039
4NBZ	D_ARG_104	NH2	D_ASP_107	OD2	2.649
4NBZ	D_ARG_104	NH2	D_GLU_110	OE2	2.846
4NC0	A_LYS_20	NZ	A_ASP_18	OD2	3.612
4NC0	A_LYS_21	NZ	A_ASP_69	OD2	3.571
4NC0	A_ARG_102	NH2	A_ASP_92	OD1	3.131
4NC0	A_LYS_149	NZ	A_GLU_138	OE1	3.144
4NC0	A_LYS_149	NZ	A_GLU_138	OE2	3.032
4NC0	B_ARG_38	NH1	B_ASP_90	OD1	2.856
4NC0	B_ARG_38	NH2	B_GLU_46	OE2	3.008
4NC0	B_ARG_38	NH2	B_ASP_90	OD1	3.917
4NC0	B_ARG_67	NH1	B_ASP_90	OD1	3.847
4NC0	B_ARG_67	NH1	B_ASP_90	OD2	2.731
4NC0	B_ARG_67	NH2	B_ASP_90	OD1	3.092
4NC0	B_ARG_67	NH2	B_ASP_90	OD2	3.455
4NC0	B_ARG_104	NH2	B_GLU_110	OE2	3.883
4NC1	A_LYS_122	NZ	A_GLU_84	OE1	3.788
4NC1	A_ARG_133	NH1	D_ASP_115	OD2	3.145
4NC1	A_LYS_149	NZ	A_GLU_138	OE2	3.865
4NC1	C_ARG_34	NH1	C_ASP_39	OD1	2.542
4NC1	C_ARG_34	NH2	C_ASP_39	OD1	3.596
4NC1	C_ARG_45	NH1	C_ASP_97	OD1	3.313

4NC1	C_ARG_45	NH2	C_GLU_53	OE2	3.315
4NC1	C_ARG_52	NH2	C_ASP_115	OD2	3.087
4NC1	C_LYS_72	NZ	C_ASP_69	OD1	2.940
4NC1	C_ARG_74	NH1	C_ASP_97	OD2	3.393
4NC1	C_ARG_74	NH2	C_ASP_97	OD1	3.034
4NC1	C_ARG_74	NH2	C_ASP_97	OD2	3.018
4NC1	C_ARG_114	NH1	D_ASP_115	OD1	3.051
4NC1	C_ARG_114	NH1	D_ASP_115	OD2	3.046
4NC1	C_ARG_114	NH2	D_ASP_115	OD1	2.896
4NC1	E_ARG_38	NH1	E_ASP_90	OD1	3.159
4NC1	E_ARG_38	NH2	E_GLU_46	OE2	3.512
4NC1	E_ARG_38	NH2	E_ASP_90	OD1	3.704
4NC1	E_ARG_67	NH1	E_ASP_90	OD1	3.858
4NC1	E_ARG_67	NH1	E_ASP_90	OD2	2.770
4NC1	E_ARG_67	NH2	E_ASP_90	OD1	2.972
4NC1	E_ARG_67	NH2	E_ASP_90	OD2	3.415
4NC1	E_LYS_87	NZ	E_GLU_89	OE2	3.782
4NC1	E_ARG_104	NH1	E_ASP_107	OD1	2.648
4NC1	E_ARG_104	NH1	E_GLU_110	OE2	3.366
4NC1	E_ARG_104	NH2	E_ASP_107	OD1	3.918
4NC1	B_HIS_63	ND1	B_GLU_84	OE1	3.153
4NC1	B_HIS_63	ND1	B_GLU_84	OE2	3.732
4NC1	B_ARG_102	NH1	B_ASP_92	OD1	3.669
4NC1	B_ARG_102	NH1	B_ASP_92	OD2	3.606
4NC1	B_ARG_102	NH2	B_ASP_92	OD1	3.288
4NC1	B_ARG_133	NH2	C_ASP_115	OD2	3.404
4NC1	B_LYS_149	NZ	B_GLU_138	OE1	3.187
4NC1	B_LYS_149	NZ	B_GLU_138	OE2	3.383
4NC1	B_LYS_154	NZ	B_ASP_152	OD2	3.007
4NC1	D_ARG_34	NH1	D_ASP_39	OD1	2.692
4NC1	D_ARG_34	NH2	D_ASP_39	OD1	3.446
4NC1	D_ARG_45	NH1	D_ASP_97	OD1	3.007
4NC1	D_ARG_45	NH2	D_GLU_53	OE2	3.250
4NC1	D_ARG_52	NH2	D_ASP_115	OD2	2.993
4NC1	D_ARG_63	NH1	B_ASP_112	OD2	3.125
4NC1	D_LYS_72	NZ	D_ASP_69	OD1	2.783
4NC1	D_ARG_74	NH1	D_ASP_97	OD1	3.561
4NC1	D_ARG_74	NH1	D_ASP_97	OD2	2.537
4NC1	D_ARG_74	NH2	D_ASP_97	OD1	2.939
4NC1	D_ARG_74	NH2	D_ASP_97	OD2	3.487
4NC1	D_ARG_114	NH1	C_ASP_115	OD1	2.908
4NC1	D_ARG_114	NH2	C_ASP_115	OD1	2.942
4NC1	F_ARG_38	NH1	F_ASP_90	OD1	2.906
4NC1	F_ARG_38	NH2	F_GLU_46	OE2	3.353
4NC1	F_LYS_65	NZ	F_ASP_62	OD1	3.606
4NC1	F_ARG_67	NH1	F_ASP_90	OD1	3.956
4NC1	F_ARG_67	NH1	F_ASP_90	OD2	2.763
4NC1	F_ARG_67	NH2	F_ASP_90	OD1	2.876
4NC1	F_ARG_67	NH2	F_ASP_90	OD2	3.144
4NC1	F_ARG_104	NH2	F_ASP_107	OD1	2.987
4NC2	A_LYS_41	NZ	A_GLU_78	OE1	2.781
4NC2	A_LYS_41	NZ	A_GLU_78	OE2	3.286
4NC2	A_HIS_67	ND1	A_GLU_76	OE1	3.371
4NC2	A_HIS_67	ND1	A_GLU_76	OE2	3.155
4NC2	A_ARG_92	NH2	A_ASP_87	OD1	3.549
4NC2	A_ARG_92	NH2	A_ASP_87	OD2	3.725
4NC2	B_ARG_38	NH1	B_ASP_89	OD1	2.682
4NC2	B_ARG_38	NH2	B_GLU_46	OE2	3.122

4NC2	B_ARG_38	NH2	B_ASP_89	OD1	3.705
4NC2	B_ARG_66	NH1	B_ASP_89	OD2	2.844
4NC2	B_ARG_66	NH2	B_ASP_89	OD1	3.155
4NC2	B_ARG_66	NH2	B_ASP_89	OD2	3.294
4NC2	B_LYS_86	NZ	B_GLU_88	OE1	3.812
4NC2	B_ARG_104	NH2	B_ASP_102	OD1	3.825
4NC2	B_ARG_104	NH2	B_ASP_102	OD2	2.662
4NGH	L_ARG_54	NH2	L_ASP_60	OD1	3.463
4NGH	L_ARG_61	NH1	L_GLU_79	OE1	3.684
4NGH	L_ARG_61	NH2	L_GLU_81	OE2	3.634
4NGH	L_ARG_61	NH2	L_ASP_82	OD1	2.877
4NGH	L_ARG_61	NH2	L_ASP_82	OD2	3.482
4NGH	L_LYS_188	NZ	L_ASP_185	OD2	3.961
4NGH	L_HIS_189	ND1	L_ASP_151	OD2	3.057
4NGH	H_ARG_38	NH1	H_ASP_86	OD1	3.532
4NGH	H_ARG_38	NH2	H_ASP_86	OD1	2.824
4NGH	H_ARG_62	NH2	H_GLU_46	OE1	2.983
4NGH	H_ARG_66	NH1	H_ASP_86	OD1	3.419
4NGH	H_ARG_66	NH1	H_ASP_86	OD2	2.324
4NGH	H_ARG_66	NH2	H_ASP_86	OD1	3.466
4NGH	H_ARG_66	NH2	H_ASP_86	OD2	3.699
4NGH	H_LYS_145	NZ	H_ASP_146	OD1	3.519
4NGH	H_LYS_145	NZ	H_ASP_146	OD2	3.560
4NGH	H_LYS_228	NZ	L_ASP_122	OD1	3.887
4NHC	L_ARG_24	NH1	L_ASP_70	OD2	3.488
4NHC	L_ARG_24	NH2	L_ASP_70	OD1	2.813
4NHC	L_ARG_24	NH2	L_ASP_70	OD2	3.633
4NHC	L_ARG_61	NH1	L_GLU_81	OE2	3.514
4NHC	L_ARG_61	NH2	L_GLU_81	OE2	3.347
4NHC	L_ARG_61	NH2	L_ASP_82	OD1	2.882
4NHC	L_ARG_61	NH2	L_ASP_82	OD2	3.443
4NHC	L_LYS_103	NZ	L_GLU_165	OE1	3.841
4NHC	L_HIS_189	ND1	L_ASP_151	OD2	3.138
4NHC	H_ARG_38	NH1	H_GLU_46	OE2	3.463
4NHC	H_ARG_38	NH1	H_ASP_86	OD1	3.758
4NHC	H_ARG_38	NH2	H_ASP_86	OD1	2.917
4NHC	H_ARG_62	NH1	H_GLU_46	OE1	2.931
4NHC	H_ARG_62	NH1	H_GLU_46	OE2	3.111
4NHC	H_ARG_66	NH1	H_ASP_86	OD1	2.881
4NHC	H_ARG_66	NH1	H_ASP_86	OD2	2.433
4NHC	H_LYS_145	NZ	H_ASP_146	OD1	3.579
4NHC	H_LYS_145	NZ	H_ASP_146	OD2	3.804
4NHC	H_LYS_222	NZ	H_GLU_226	OE1	3.793
4NIK	A_ARG_35	NH2	A_ASP_29	OD2	3.085
4NIK	A_ARG_41	NH2	A_ASP_70	OD2	3.597
4NIK	A_ARG_145	NH1	A_ASP_136	OD2	2.773
4NIK	A_LYS_153	NZ	B_ASP_104	OD1	3.730
4NIK	A_LYS_153	NZ	B_ASP_104	OD2	2.794
4NIK	A_LYS_153	NZ	B_GLU_186	OE2	2.639
4NIK	A_LYS_189	NZ	A_GLU_186	OE2	3.854
4NIK	A_LYS_206	NZ	A_GLU_204	OE1	3.160
4NIK	A_LYS_213	NZ	A_ASP_181	OD1	3.738
4NIK	A_LYS_221	NZ	A_GLU_225	OE1	3.992
4NIK	B_ARG_40	NH1	B_ASP_92	OD1	3.000
4NIK	B_ARG_40	NH2	B_GLU_48	OE1	3.129
4NIK	B_ARG_40	NH2	B_ASP_92	OD1	3.930
4NIK	B_ARG_69	NH1	B_ASP_92	OD2	3.600
4NIK	B_ARG_69	NH2	B_ASP_92	OD1	3.146

4NIK	B_ARG_69	NH2	B_ASP_92	OD2	2.929
4NIK	B_ARG_100	NH2	B_ASP_107	OD2	2.770
4NIK	B_ARG_197	NH1	B_ASP_218	OD1	2.833
4NIK	B_ARG_197	NH1	B_ASP_218	OD2	3.035
4NIK	B_LYS_202	NZ	B_ASP_187	OD1	2.979
4NIK	B_LYS_202	NZ	B_ASP_187	OD2	3.172
4NZR	H_ARG_38	NH1	H_ASP_86	OD1	2.731
4NZR	H_ARG_38	NH2	H_GLU_46	OE1	2.782
4NZR	H_ARG_38	NH2	H_ASP_86	OD1	3.585
4NZR	H_LYS_43	NZ	H_GLU_46	OE1	3.101
4NZR	H_HIS_52	NE2	H_ASP_31G	OD1	2.604
4NZR	H_LYS_60	NZ	H_GLU_46	OE2	3.047
4NZR	H_LYS_60	NZ	L_GLU_1	OE1	3.647
4NZR	H_ARG_66	NH1	H_ASP_86	OD1	3.620
4NZR	H_ARG_66	NH1	H_ASP_86	OD2	2.979
4NZR	H_ARG_66	NH2	H_ASP_86	OD1	3.027
4NZR	H_ARG_66	NH2	H_ASP_86	OD2	3.661
4NZR	H_ARG_94	NH2	H_ASP_101	OD1	3.578
4NZR	H_ARG_94	NH2	H_ASP_101	OD2	2.728
4NZR	H_ARG_96	NH2	H_ASP_101	OD2	2.950
4NZR	H_HIS_97	NE2	L_GLU_50	OE2	3.635
4NZR	H_HIS_98	NE2	L_GLU_50	OE1	2.875
4NZR	H_HIS_172	NE2	L_ASP_167	OD2	3.398
4NZR	H_LYS_221	NZ	L_GLU_123	OE2	2.989
4NZR	H_ARG_222	NH2	H_GLU_226	OE1	3.956
4NZR	H_ARG_222	NH2	H_GLU_226	OE2	3.389
4NZR	L_ARG_24	NH2	L_GLU_70	OE1	3.307
4NZR	L_ARG_61	NH1	L_ASP_82	OD1	3.803
4NZR	L_ARG_61	NH1	L_ASP_82	OD2	2.705
4NZR	L_ARG_61	NH2	L_ASP_82	OD1	2.855
4NZR	L_ARG_61	NH2	L_ASP_82	OD2	3.226
4NZR	L_LYS_103	NZ	L_GLU_165	OE1	3.228
4NZR	L_LYS_183	NZ	L_GLU_187	OE1	3.271
4NZR	L_LYS_183	NZ	L_GLU_187	OE2	3.181
4NZR	L_LYS_188	NZ	L_ASP_185	OD1	3.734
4NZR	L_HIS_189	ND1	L_ASP_151	OD2	2.848
4NZR	M_LYS_114	NZ	L_GLU_17	OE1	3.119
4NZR	M_LYS_130	NZ	M_ASP_87	OD2	3.899
4NZR	M_LYS_141	NZ	M_GLU_124	OE1	3.708
4NZR	M_LYS_141	NZ	M_GLU_124	OE2	2.958
4NZR	M_ARG_167	NH2	M_ASP_339	OD1	2.843
4NZR	M_LYS_218	NZ	M_GLU_261	OE1	3.674
4NZR	M_LYS_218	NZ	M_GLU_261	OE2	3.033
4NZR	M_LYS_242	NZ	M_GLU_261	OE1	2.962
4NZR	M_LYS_249	NZ	M_ASP_250	OD1	2.926
4NZR	M_LYS_249	NZ	M_ASP_250	OD2	3.476
4NZR	M_ARG_269	NH1	M_ASP_217	OD2	2.818
4NZR	M_ARG_269	NH2	M_ASP_217	OD2	3.169
4NZR	M_LYS_289	NZ	M_GLU_311	OE1	2.888
4NZR	M_LYS_289	NZ	M_GLU_313	OE1	3.192
4NZR	M_LYS_289	NZ	M_GLU_313	OE2	2.704
4NZR	M_LYS_370	NZ	M_GLU_420	OE1	2.609
4NZR	M_ARG_380	NH1	M_GLU_383	OE1	2.654
4NZR	M_ARG_380	NH1	M_GLU_383	OE2	3.072
4NZR	M_ARG_381	NH2	M_GLU_162	OE1	2.997
4NZR	M_ARG_384	NH2	L_GLU_81	OE1	3.444
4NZR	M_ARG_384	NH2	L_GLU_81	OE2	3.239
4NZR	M_LYS_397	NZ	M_ASP_396	OD1	2.896

4NZR	M_LYS_397	NZ	M_ASP_396	OD2	3.739
4NZR	M_ARG_416	NH1	M_GLU_464	OE1	3.487
4NZR	M_ARG_416	NH1	M_GLU_464	OE2	2.684
4NZR	M_ARG_416	NH2	M_ASP_412	OD1	3.736
4NZR	M_ARG_416	NH2	M_GLU_464	OE1	2.883
4NZR	M_ARG_416	NH2	M_GLU_464	OE2	3.634
4NZR	M_LYS_419	NZ	M_GLU_451	OE2	3.987
4NZR	M_ARG_430	NH1	M_ASP_411	OD1	2.838
4NZR	M_ARG_430	NH1	M_ASP_411	OD2	3.179
4NZR	M_ARG_430	NH2	M_ASP_408	OD1	3.554
4NZR	M_ARG_430	NH2	M_ASP_411	OD1	3.944
4NZR	M_ARG_430	NH2	M_ASP_411	OD2	2.828
4NZR	M_ARG_438	NH2	M_ASP_396	OD2	3.613
4NZR	M_ARG_454	NH1	M_ASP_412	OD1	2.790
4NZR	M_ARG_454	NH2	M_ASP_412	OD1	3.325
4NZR	M_ARG_457	NH1	H_ASP_31E	OD1	2.958
4NZR	M_ARG_457	NH1	H_ASP_31E	OD2	3.096
4NZR	M_ARG_457	NH2	H_ASP_31E	OD1	3.746
4NZR	M_ARG_457	NH2	H_ASP_31E	OD2	2.554
4NZT	M_ARG_99	NH1	M_GLU_162	OE1	3.515
4NZT	M_ARG_99	NH1	M_GLU_162	OE2	2.816
4NZT	M_ARG_99	NH2	M_GLU_162	OE1	2.782
4NZT	M_ARG_99	NH2	M_GLU_162	OE2	3.647
4NZT	M_ARG_99	NH2	L_ASP_60	OD1	3.096
4NZT	M_LYS_130	NZ	M_GLU_85	OE2	3.790
4NZT	M_LYS_141	NZ	M_GLU_124	OE1	3.986
4NZT	M_LYS_141	NZ	M_GLU_124	OE2	3.262
4NZT	M_ARG_167	NH2	M_ASP_339	OD1	3.102
4NZT	M_ARG_185	NH2	M_GLU_313	OE2	3.948
4NZT	M_ARG_192	NH2	M_ASP_189	OD1	3.955
4NZT	M_LYS_218	NZ	M_GLU_261	OE1	3.101
4NZT	M_LYS_218	NZ	M_GLU_261	OE2	2.614
4NZT	M_LYS_242	NZ	M_GLU_261	OE1	2.807
4NZT	M_LYS_249	NZ	M_ASP_250	OD1	3.040
4NZT	M_LYS_249	NZ	M_ASP_250	OD2	3.872
4NZT	M_LYS_255	NZ	M_ASP_259	OD1	3.504
4NZT	M_LYS_255	NZ	M_ASP_259	OD2	2.413
4NZT	M_LYS_289	NZ	M_GLU_311	OE1	2.933
4NZT	M_LYS_289	NZ	M_GLU_313	OE1	3.576
4NZT	M_LYS_289	NZ	M_GLU_313	OE2	2.891
4NZT	M_LYS_370	NZ	M_GLU_420	OE1	2.990
4NZT	M_ARG_380	NH1	M_GLU_383	OE1	2.676
4NZT	M_ARG_380	NH1	M_GLU_383	OE2	2.970
4NZT	M_ARG_381	NH2	M_GLU_162	OE1	3.002
4NZT	M_ARG_384	NH2	L_GLU_81	OE1	3.193
4NZT	M_ARG_384	NH2	L_GLU_81	OE2	3.684
4NZT	M_LYS_397	NZ	M_ASP_396	OD1	2.602
4NZT	M_LYS_397	NZ	M_ASP_396	OD2	3.737
4NZT	M_ARG_416	NH2	M_ASP_412	OD2	3.317
4NZT	M_LYS_419	NZ	M_GLU_451	OE2	3.820
4NZT	M_ARG_430	NH1	M_ASP_408	OD1	3.883
4NZT	M_ARG_430	NH2	M_ASP_408	OD1	2.461
4NZT	M_ARG_430	NH2	M_ASP_411	OD2	3.064
4NZT	M_ARG_438	NH1	M_GLU_426	OE1	2.584
4NZT	M_ARG_438	NH2	M_GLU_426	OE1	3.586
4NZT	M_ARG_438	NH2	M_GLU_427	OE1	3.398
4NZT	M_ARG_454	NH2	M_ASP_408	OD1	3.446
4NZT	M_ARG_454	NH2	M_ASP_411	OD2	3.646

4NZT	H.LYS.19	NZ	H.GLU.81	OE1	3.595
4NZT	H.ARG.38	NH1	H.ASP.86	OD1	2.816
4NZT	H.ARG.38	NH2	H.ASP.86	OD1	3.377
4NZT	H.LYS.62	NZ	H.ASP.46	OD1	3.175
4NZT	H.LYS.62	NZ	H.ASP.46	OD2	3.992
4NZT	H.ARG.66	NH1	H.ASP.86	OD2	3.140
4NZT	H.ARG.66	NH2	H.ASP.86	OD1	2.815
4NZT	H.ARG.66	NH2	H.ASP.86	OD2	3.193
4NZT	H.LYS.145	NZ	L.GLU.124	OE2	2.541
4NZT	H.LYS.218	NZ	H.ASP.220	OD2	3.664
4NZT	L.ARG.31	NH1	L.ASP.93	OD1	3.320
4NZT	L.ARG.31	NH1	L.ASP.93	OD2	2.823
4NZT	L.ARG.61	NH1	L.ASP.82	OD1	3.965
4NZT	L.ARG.61	NH1	L.ASP.82	OD2	2.961
4NZT	L.ARG.61	NH2	L.ASP.82	OD1	2.857
4NZT	L.ARG.61	NH2	L.ASP.82	OD2	3.259
4NZT	L.LYS.149	NZ	L.GLU.206	OE1	3.814
4NZT	L.LYS.166	NZ	L.GLU.83	OE2	3.236
4NZU	L.ARG.61	NH2	L.GLU.81	OE2	3.339
4NZU	L.ARG.61	NH2	L.ASP.82	OD1	2.846
4NZU	L.ARG.61	NH2	L.ASP.82	OD2	3.553
4NZU	L.HIS.90	NE2	L.ASP.93	OD1	3.539
4NZU	L.LYS.149	NZ	L.GLU.195	OE1	2.806
4NZU	L.LYS.169	NZ	L.ASP.170	OD2	3.815
4NZU	L.HIS.189	ND1	L.ASP.151	OD2	3.001
4NZU	L.HIS.189	NE2	L.ASP.185	OD1	3.093
4NZU	L.ARG.211	NH1	L.GLU.187	OE1	3.760
4NZU	H.ARG.38	NH1	H.ASP.86	OD1	2.872
4NZU	H.ARG.38	NH2	H.GLU.46	OE2	3.007
4NZU	H.ARG.38	NH2	H.ASP.86	OD1	3.843
4NZU	H.ARG.66	NH1	H.ASP.86	OD1	3.832
4NZU	H.ARG.66	NH1	H.ASP.86	OD2	2.798
4NZU	H.ARG.66	NH2	H.ASP.86	OD1	3.266
4NZU	H.ARG.66	NH2	H.ASP.86	OD2	3.679
4NZU	H.ARG.94	NH2	H.ASP.97	OD1	2.847
4NZU	H.LYS.100E	NZ	L.ASP.50	OD1	3.991
4NZU	H.LYS.100E	NZ	L.ASP.50	OD2	2.752
4NZU	H.LYS.145	NZ	H.ASP.146	OD1	3.213
4NZU	H.LYS.145	NZ	H.ASP.146	OD2	3.743
4NZU	H.LYS.218	NZ	H.ASP.220	OD1	3.972
4NZU	H.LYS.218	NZ	H.ASP.220	OD2	3.728
4NZU	H.LYS.221	NZ	L.GLU.123	OE2	2.899
4O5L	L.ARG.61	NH1	L.ASP.82	OD1	3.592
4O5L	L.ARG.61	NH1	L.ASP.82	OD2	2.774
4O5L	L.ARG.61	NH2	L.ASP.82	OD1	2.915
4O5L	L.ARG.61	NH2	L.ASP.82	OD2	3.469
4O5L	H.LYS.12	NZ	H.GLU.10	OE2	3.928
4O5L	H.ARG.38	NH1	H.ASP.86	OD1	2.874
4O5L	H.ARG.38	NH2	H.GLU.46	OE1	3.001
4O5L	H.ARG.38	NH2	H.ASP.86	OD1	3.839
4O5L	H.LYS.62	NZ	H.GLU.46	OE1	3.697
4O5L	H.LYS.62	NZ	H.GLU.46	OE2	2.608
4O5L	H.ARG.66	NH1	H.ASP.86	OD1	3.710
4O5L	H.ARG.66	NH1	H.ASP.86	OD2	2.867
4O5L	H.ARG.66	NH2	H.ASP.86	OD1	2.964
4O5L	H.ARG.66	NH2	H.ASP.86	OD2	3.444
4O5L	H.LYS.100I	NZ	L.ASP.93	OD1	2.723
4O5L	H.LYS.100I	NZ	L.ASP.93	OD2	3.455

4O5L	H.LYS_210	NZ	H.GLU_212	OE2	3.158
4OLU	G.HIS_66	ND1	G.GLU_64	OE1	3.959
4OLU	G.HIS_66	ND1	G.GLU_64	OE2	2.779
4OLU	G.LYS_97	NZ	G.GLU_275	OE2	3.740
4OLU	G.LYS_97	NZ	H.ASP_100B	OD1	3.513
4OLU	G.LYS_97	NZ	H.ASP_100B	OD2	2.385
4OLU	G.LYS_207	NZ	G.GLU_381	OE1	3.549
4OLU	G.LYS_207	NZ	G.GLU_381	OE2	2.955
4OLU	G.HIS_249	NE2	G.GLU_482	OE1	2.876
4OLU	G.LYS_282	NZ	G.GLU_275	OE1	3.870
4OLU	G.LYS_343	NZ	G.GLU_347	OE2	2.649
4OLU	G.LYS_348	NZ	G.GLU_269	OE2	3.261
4OLU	G.LYS_350	NZ	G.GLU_347	OE2	3.965
4OLU	G.LYS_357	NZ	G.GLU_466	OE2	3.506
4OLU	G.ARG_379	NH2	G.ASP_211	OD1	3.811
4OLU	G.ARG_456	NH1	G.GLU_466	OE1	3.682
4OLU	G.ARG_469	NH2	G.ASP_457	OD1	3.894
4OLU	G.ARG_469	NH2	G.ASP_457	OD2	2.873
4OLU	G.LYS_476	NZ	G.GLU_102	OE1	2.812
4OLU	G.LYS_476	NZ	G.GLU_102	OE2	3.887
4OLU	G.ARG_480	NH1	G.ASP_477	OD1	2.835
4OLU	G.LYS_487	NZ	G.ASP_47	OD1	2.977
4OLU	G.LYS_487	NZ	G.ASP_47	OD2	3.556
4OLU	G.LYS_487	NZ	G.GLU_91	OE1	2.775
4OLU	H.ARG_19	NH2	H.GLU_81	OE1	3.190
4OLU	H.ARG_38	NH1	H.ASP_86	OD1	2.943
4OLU	H.ARG_38	NH2	H.GLU_46	OE1	2.821
4OLU	H.ARG_38	NH2	H.GLU_46	OE2	3.765
4OLU	H.ARG_38	NH2	H.ASP_86	OD1	3.966
4OLU	H.ARG_61	NH1	G.GLU_466	OE1	2.734
4OLU	H.ARG_66	NH2	H.ASP_86	OD1	3.375
4OLU	H.ARG_66	NH2	H.ASP_86	OD2	3.135
4OLU	H.ARG_71	NH1	G.ASP_368	OD1	3.753
4OLU	H.ARG_71	NH1	G.ASP_368	OD2	2.863
4OLU	H.ARG_71	NH2	G.ASP_368	OD1	3.092
4OLU	H.ARG_71	NH2	G.ASP_368	OD2	3.692
4OLU	H.ARG_82A	NH1	H.GLU_81	OE2	3.267
4OLU	H.HIS_102	NE2	H.GLU_101	OE1	3.618
4OLU	H.LYS_143	NZ	H.ASP_144	OD1	3.446
4OLU	H.LYS_209	NZ	L.GLU_125	OE1	3.927
4OLU	H.LYS_209	NZ	L.GLU_125	OE2	3.166
4OLU	H.LYS_210	NZ	H.GLU_212	OE1	3.680
4OLU	L.ARG_24	NH1	L.ASP_70	OD1	3.438
4OLU	L.ARG_24	NH1	L.ASP_70	OD2	3.910
4OLU	L.ARG_24	NH2	L.ASP_70	OD1	3.381
4OLU	L.ARG_24	NH2	L.ASP_70	OD2	3.367
4OLU	L.ARG_61	NH1	L.ASP_82	OD1	3.876
4OLU	L.ARG_61	NH1	L.ASP_82	OD2	2.552
4OLU	L.ARG_61	NH2	L.GLU_79	OE1	3.652
4OLU	L.ARG_61	NH2	L.GLU_79	OE2	3.968
4OLU	L.ARG_61	NH2	L.ASP_82	OD1	3.189
4OLU	L.ARG_61	NH2	L.ASP_82	OD2	3.276
4OLU	L.LYS_109	NZ	L.GLU_17	OE2	3.752
4OLU	L.LYS_151	NZ	L.GLU_197	OE1	3.524
4OLV	G.HIS_66	ND1	G.GLU_64	OE1	3.978
4OLV	G.HIS_66	ND1	G.GLU_64	OE2	2.916
4OLV	G.LYS_97	NZ	G.GLU_275	OE1	3.722
4OLV	G.LYS_97	NZ	G.GLU_275	OE2	2.587

4OLV	G.LYS_97	NZ	H.ASP_100B	OD1	3.067
4OLV	G.LYS_97	NZ	H.ASP_100B	OD2	2.942
4OLV	G.LYS_207	NZ	G.GLU_381	OE1	3.681
4OLV	G.LYS_207	NZ	G.GLU_381	OE2	2.814
4OLV	G.HIS_249	NE2	G.GLU_482	OE1	2.670
4OLV	G.LYS_282	NZ	G.GLU_275	OE1	3.553
4OLV	G.LYS_343	NZ	G.GLU_347	OE2	2.439
4OLV	G.LYS_348	NZ	G.GLU_269	OE2	3.240
4OLV	G.LYS_357	NZ	G.GLU_466	OE2	3.394
4OLV	G.ARG_456	NH1	G.GLU_466	OE1	3.770
4OLV	G.ARG_469	NH2	G.ASP_457	OD2	3.028
4OLV	G.LYS_476	NZ	G.GLU_102	OE1	2.934
4OLV	G.LYS_476	NZ	G.GLU_102	OE2	3.534
4OLV	G.ARG_480	NH1	G.ASP_477	OD1	2.701
4OLV	G.ARG_480	NH2	G.GLU_102	OE2	3.998
4OLV	G.LYS_487	NZ	G.ASP_47	OD1	3.089
4OLV	G.LYS_487	NZ	G.ASP_47	OD2	3.641
4OLV	G.LYS_487	NZ	G.GLU_91	OE1	2.653
4OLV	H.ARG_19	NH2	H.GLU_81	OE1	3.551
4OLV	H.ARG_38	NH1	H.ASP_86	OD1	2.917
4OLV	H.ARG_38	NH2	H.GLU_46	OE1	2.756
4OLV	H.ARG_38	NH2	H.GLU_46	OE2	3.739
4OLV	H.ARG_38	NH2	H.ASP_86	OD1	3.920
4OLV	H.ARG_61	NH1	G.GLU_466	OE1	2.769
4OLV	H.ARG_66	NH1	H.ASP_86	OD1	3.961
4OLV	H.ARG_66	NH2	H.ASP_86	OD1	3.054
4OLV	H.ARG_66	NH2	H.ASP_86	OD2	2.735
4OLV	H.ARG_71	NH1	G.ASP_368	OD1	3.700
4OLV	H.ARG_71	NH1	G.ASP_368	OD2	2.815
4OLV	H.ARG_71	NH2	G.ASP_368	OD1	3.136
4OLV	H.ARG_71	NH2	G.ASP_368	OD2	3.717
4OLV	H.ARG_82A	NH1	H.GLU_81	OE1	3.993
4OLV	H.ARG_82A	NH1	H.GLU_81	OE2	3.151
4OLV	H.HIS_102	NE2	H.GLU_101	OE1	3.357
4OLV	H.LYS_209	NZ	L.GLU_125	OE1	3.978
4OLV	H.LYS_209	NZ	L.GLU_125	OE2	3.214
4OLV	H.LYS_210	NZ	H.GLU_212	OE1	2.484
4OLV	L.ARG_24	NH2	L.ASP_70	OD1	3.226
4OLV	L.ARG_24	NH2	L.ASP_70	OD2	2.875
4OLV	L.ARG_61	NH1	L.ASP_82	OD1	3.700
4OLV	L.ARG_61	NH1	L.ASP_82	OD2	2.636
4OLV	L.ARG_61	NH2	L.GLU_79	OE1	3.645
4OLV	L.ARG_61	NH2	L.GLU_79	OE2	3.982
4OLV	L.ARG_61	NH2	L.ASP_82	OD1	3.217
4OLV	L.ARG_61	NH2	L.ASP_82	OD2	3.476
4OLV	L.LYS_109	NZ	L.GLU_17	OE2	2.752
4OLV	L.LYS_151	NZ	L.GLU_197	OE1	3.476
4OLV	L.LYS_151	NZ	L.GLU_197	OE2	3.958
4OLW	G.HIS_66	ND1	G.GLU_64	OE2	2.882
4OLW	G.LYS_97	NZ	G.GLU_275	OE1	3.783
4OLW	G.LYS_97	NZ	G.GLU_275	OE2	2.873
4OLW	G.LYS_97	NZ	H.ASP_100B	OD1	3.637
4OLW	G.LYS_97	NZ	H.ASP_100B	OD2	3.575
4OLW	G.LYS_207	NZ	G.GLU_381	OE1	3.441
4OLW	G.LYS_207	NZ	G.GLU_381	OE2	3.248
4OLW	G.HIS_249	NE2	G.GLU_482	OE1	2.947
4OLW	G.LYS_343	NZ	G.GLU_347	OE2	2.661
4OLW	G.LYS_348	NZ	G.GLU_269	OE2	2.637

4OLW	G_LYS_348	NZ	G_GLU_351	OE1	2.952
4OLW	G_LYS_357	NZ	G_GLU_466	OE2	3.143
4OLW	G_ARG_379	NH2	G_ASP_211	OD2	3.654
4OLW	G_ARG_469	NH2	G_ASP_457	OD2	3.245
4OLW	G_LYS_476	NZ	G_GLU_102	OE1	2.987
4OLW	G_LYS_476	NZ	G_GLU_102	OE2	3.972
4OLW	G_ARG_480	NH1	G_ASP_477	OD1	2.768
4OLW	G_ARG_480	NH2	G_GLU_102	OE2	3.752
4OLW	G_LYS_487	NZ	G_ASP_47	OD1	3.005
4OLW	G_LYS_487	NZ	G_ASP_47	OD2	3.475
4OLW	G_LYS_487	NZ	G_GLU_91	OE1	2.972
4OLW	H_ARG_19	NH2	H_GLU_81	OE1	3.633
4OLW	H_ARG_38	NH1	H_ASP_86	OD1	2.849
4OLW	H_ARG_38	NH2	H_GLU_46	OE1	3.103
4OLW	H_ARG_38	NH2	H_GLU_46	OE2	3.816
4OLW	H_ARG_38	NH2	H_ASP_86	OD1	3.655
4OLW	H_ARG_61	NH1	G_GLU_466	OE1	2.598
4OLW	H_ARG_61	NH2	G_GLU_466	OE1	3.969
4OLW	H_ARG_66	NH2	H_ASP_86	OD1	2.804
4OLW	H_ARG_66	NH2	H_ASP_86	OD2	2.718
4OLW	H_ARG_71	NH1	G_ASP_368	OD1	3.570
4OLW	H_ARG_71	NH1	G_ASP_368	OD2	2.966
4OLW	H_ARG_71	NH2	G_ASP_368	OD1	3.028
4OLW	H_ARG_71	NH2	G_ASP_368	OD2	3.898
4OLW	H_ARG_82A	NH1	H_GLU_81	OE2	3.263
4OLW	H_ARG_100A	NH2	G_GLU_106	OE1	3.908
4OLW	H_HIS_102	NE2	H_GLU_101	OE1	3.698
4OLW	H_LYS_209	NZ	L_GLU_125	OE1	2.861
4OLW	H_LYS_209	NZ	L_GLU_125	OE2	2.764
4OLW	H_LYS_210	NZ	H_GLU_212	OE1	3.770
4OLW	H_LYS_214	NZ	L_ASP_124	OD1	3.031
4OLW	H_LYS_214	NZ	L_ASP_124	OD2	3.691
4OLW	L_ARG_24	NH1	L_ASP_70	OD1	3.761
4OLW	L_ARG_24	NH1	L_ASP_70	OD2	3.911
4OLW	L_ARG_24	NH2	L_ASP_70	OD1	3.614
4OLW	L_ARG_24	NH2	L_ASP_70	OD2	3.428
4OLW	L_ARG_61	NH1	L_ASP_82	OD2	2.747
4OLW	L_ARG_61	NH2	L_GLU_79	OE1	3.693
4OLW	L_ARG_61	NH2	L_GLU_79	OE2	3.864
4OLW	L_ARG_61	NH2	L_ASP_82	OD1	3.396
4OLW	L_ARG_61	NH2	L_ASP_82	OD2	2.990
4OLW	L_LYS_109	NZ	L_GLU_17	OE2	2.961
4OLX	G_HIS_66	ND1	G_GLU_64	OE1	3.879
4OLX	G_HIS_66	ND1	G_GLU_64	OE2	2.717
4OLX	G_LYS_97	NZ	G_GLU_275	OE2	3.052
4OLX	G_LYS_97	NZ	H_ASP_100B	OD1	3.339
4OLX	G_LYS_97	NZ	H_ASP_100B	OD2	2.904
4OLX	G_LYS_121	NZ	G_ASP_113	OD1	3.856
4OLX	G_LYS_207	NZ	G_GLU_381	OE1	3.451
4OLX	G_LYS_207	NZ	G_GLU_381	OE2	3.129
4OLX	G_HIS_249	NE2	G_GLU_482	OE1	3.186
4OLX	G_LYS_282	NZ	G_GLU_275	OE1	3.971
4OLX	G_LYS_343	NZ	G_GLU_347	OE2	2.614
4OLX	G_LYS_348	NZ	G_GLU_269	OE2	2.682
4OLX	G_LYS_348	NZ	G_GLU_351	OE1	3.091
4OLX	G_ARG_379	NH2	G_ASP_211	OD2	3.162
4OLX	G_ARG_456	NH1	G_GLU_466	OE1	3.738
4OLX	G_ARG_469	NH2	G_ASP_457	OD2	3.011

4OLX	G_LYS_476	NZ	G_GLU_102	OE1	2.845
4OLX	G_LYS_476	NZ	G_GLU_102	OE2	3.693
4OLX	G_ARG_480	NH1	G_ASP_477	OD1	2.869
4OLX	G_LYS_487	NZ	G_ASP_47	OD1	2.956
4OLX	G_LYS_487	NZ	G_ASP_47	OD2	3.569
4OLX	G_LYS_487	NZ	G_GLU_91	OE1	2.836
4OLX	H_ARG_19	NH2	H_GLU_81	OE1	3.130
4OLX	H_ARG_38	NH1	H_ASP_86	OD1	2.798
4OLX	H_ARG_38	NH2	H_GLU_46	OE1	2.957
4OLX	H_ARG_38	NH2	H_GLU_46	OE2	3.969
4OLX	H_ARG_38	NH2	H_ASP_86	OD1	3.641
4OLX	H_ARG_61	NH1	G_GLU_466	OE1	2.655
4OLX	H_ARG_66	NH1	H_ASP_86	OD1	3.694
4OLX	H_ARG_66	NH2	H_ASP_86	OD1	2.980
4OLX	H_ARG_66	NH2	H_ASP_86	OD2	2.792
4OLX	H_ARG_71	NH1	G_ASP_368	OD1	3.883
4OLX	H_ARG_71	NH1	G_ASP_368	OD2	2.896
4OLX	H_ARG_71	NH2	G_ASP_368	OD1	3.066
4OLX	H_ARG_71	NH2	G_ASP_368	OD2	3.572
4OLX	H_ARG_82A	NH1	H_GLU_81	OE2	3.153
4OLX	H_ARG_100A	NH2	G_GLU_106	OE1	3.646
4OLX	H_HIS_102	NE2	H_GLU_101	OE1	3.407
4OLX	H_LYS_209	NZ	L_GLU_125	OE2	3.132
4OLX	H_LYS_210	NZ	H_GLU_212	OE1	3.806
4OLX	L_ARG_24	NH1	L_ASP_70	OD1	3.727
4OLX	L_ARG_24	NH1	L_ASP_70	OD2	3.694
4OLX	L_ARG_24	NH2	L_ASP_70	OD1	3.311
4OLX	L_ARG_24	NH2	L_ASP_70	OD2	3.200
4OLX	L_ARG_61	NH1	L_ASP_82	OD1	3.778
4OLX	L_ARG_61	NH1	L_ASP_82	OD2	2.580
4OLX	L_ARG_61	NH2	L_GLU_79	OE1	3.684
4OLX	L_ARG_61	NH2	L_GLU_79	OE2	3.925
4OLX	L_ARG_61	NH2	L_ASP_82	OD1	3.428
4OLX	L_ARG_61	NH2	L_ASP_82	OD2	3.600
4OLX	L_LYS_109	NZ	L_GLU_17	OE2	3.701
4OLY	G_HIS_66	ND1	G_GLU_64	OE1	3.788
4OLY	G_HIS_66	ND1	G_GLU_64	OE2	2.753
4OLY	G_LYS_97	NZ	G_GLU_275	OE2	3.627
4OLY	G_LYS_97	NZ	H_ASP_100B	OD1	3.240
4OLY	G_LYS_97	NZ	H_ASP_100B	OD2	2.829
4OLY	G_LYS_207	NZ	G_GLU_381	OE1	3.205
4OLY	G_LYS_207	NZ	G_GLU_381	OE2	2.631
4OLY	G_HIS_249	NE2	G_GLU_482	OE1	3.173
4OLY	G_LYS_343	NZ	G_GLU_347	OE2	2.662
4OLY	G_LYS_348	NZ	G_GLU_269	OE2	3.719
4OLY	G_LYS_350	NZ	G_GLU_347	OE2	3.790
4OLY	G_LYS_357	NZ	G_GLU_466	OE2	3.515
4OLY	G_ARG_379	NH1	G_ASP_211	OD2	3.852
4OLY	G_ARG_379	NH2	G_ASP_211	OD2	2.543
4OLY	G_ARG_456	NH1	G_GLU_466	OE1	3.658
4OLY	G_ARG_469	NH2	G_ASP_457	OD1	3.982
4OLY	G_ARG_469	NH2	G_ASP_457	OD2	2.914
4OLY	G_LYS_476	NZ	G_GLU_102	OE1	2.927
4OLY	G_LYS_476	NZ	G_GLU_102	OE2	3.744
4OLY	G_ARG_480	NH1	G_ASP_477	OD1	2.751
4OLY	G_LYS_487	NZ	G_ASP_47	OD1	3.049
4OLY	G_LYS_487	NZ	G_ASP_47	OD2	3.763
4OLY	G_LYS_487	NZ	G_GLU_91	OE1	2.756

4OLY	H_ARG_19	NH2	H_GLU_81	OE1	3.423
4OLY	H_ARG_38	NH1	H_ASP_86	OD1	2.745
4OLY	H_ARG_38	NH2	H_GLU_46	OE1	2.979
4OLY	H_ARG_38	NH2	H_GLU_46	OE2	3.847
4OLY	H_ARG_38	NH2	H_ASP_86	OD1	3.687
4OLY	H_ARG_61	NH1	G_GLU_466	OE1	2.641
4OLY	H_ARG_66	NH1	H_ASP_86	OD1	3.641
4OLY	H_ARG_66	NH2	H_ASP_86	OD1	3.013
4OLY	H_ARG_66	NH2	H_ASP_86	OD2	2.555
4OLY	H_ARG_71	NH1	G_ASP_368	OD1	3.538
4OLY	H_ARG_71	NH1	G_ASP_368	OD2	2.816
4OLY	H_ARG_71	NH2	G_ASP_368	OD1	3.002
4OLY	H_ARG_71	NH2	G_ASP_368	OD2	3.765
4OLY	H_ARG_82A	NH1	H_GLU_81	OE2	3.546
4OLY	H_HIS_102	NE2	H_GLU_101	OE1	3.748
4OLY	H_LYS_209	NZ	L_GLU_125	OE1	3.888
4OLY	H_LYS_209	NZ	L_GLU_125	OE2	3.336
4OLY	H_LYS_210	NZ	H_GLU_212	OE1	3.837
4OLY	L_ARG_24	NH1	L_ASP_70	OD1	3.758
4OLY	L_ARG_24	NH1	L_ASP_70	OD2	3.814
4OLY	L_ARG_24	NH2	L_ASP_70	OD1	3.375
4OLY	L_ARG_24	NH2	L_ASP_70	OD2	3.161
4OLY	L_ARG_61	NH1	L_ASP_82	OD2	2.658
4OLY	L_ARG_61	NH2	L_GLU_79	OE1	3.938
4OLY	L_ARG_61	NH2	L_ASP_82	OD1	3.043
4OLY	L_ARG_61	NH2	L_ASP_82	OD2	2.970
4OLZ	G_HIS_66	ND1	G_GLU_64	OE1	3.923
4OLZ	G_HIS_66	ND1	G_GLU_64	OE2	2.689
4OLZ	G_LYS_97	NZ	G_GLU_275	OE1	3.801
4OLZ	G_LYS_97	NZ	G_GLU_275	OE2	2.401
4OLZ	G_LYS_97	NZ	H_ASP_100B	OD1	3.552
4OLZ	G_LYS_97	NZ	H_ASP_100B	OD2	3.545
4OLZ	G_LYS_207	NZ	G_GLU_381	OE1	3.397
4OLZ	G_LYS_207	NZ	G_GLU_381	OE2	3.037
4OLZ	G_HIS_249	NE2	G_GLU_482	OE1	2.924
4OLZ	G_LYS_282	NZ	G_GLU_275	OE1	3.959
4OLZ	G_LYS_343	NZ	G_GLU_347	OE2	2.767
4OLZ	G_LYS_348	NZ	G_GLU_269	OE2	2.968
4OLZ	G_LYS_348	NZ	G_GLU_351	OE1	3.207
4OLZ	G_ARG_379	NH2	G_ASP_211	OD2	3.935
4OLZ	G_ARG_469	NH2	G_ASP_457	OD1	3.787
4OLZ	G_ARG_469	NH2	G_ASP_457	OD2	2.835
4OLZ	G_LYS_476	NZ	G_GLU_102	OE1	2.783
4OLZ	G_LYS_476	NZ	G_GLU_102	OE2	3.635
4OLZ	G_ARG_480	NH1	G_ASP_477	OD1	2.745
4OLZ	G_LYS_487	NZ	G_ASP_47	OD1	2.885
4OLZ	G_LYS_487	NZ	G_ASP_47	OD2	3.377
4OLZ	G_LYS_487	NZ	G_GLU_91	OE1	2.760
4OLZ	H_ARG_19	NH2	H_GLU_81	OE1	3.284
4OLZ	H_ARG_38	NH1	H_ASP_86	OD1	2.920
4OLZ	H_ARG_38	NH2	H_GLU_46	OE1	3.145
4OLZ	H_ARG_38	NH2	H_ASP_86	OD1	3.640
4OLZ	H_ARG_61	NH1	G_GLU_466	OE1	2.620
4OLZ	H_ARG_66	NH2	H_ASP_86	OD1	2.412
4OLZ	H_ARG_66	NH2	H_ASP_86	OD2	3.005
4OLZ	H_ARG_71	NH1	G_ASP_368	OD1	3.472
4OLZ	H_ARG_71	NH1	G_ASP_368	OD2	2.715
4OLZ	H_ARG_71	NH2	G_ASP_368	OD1	2.877

4OLZ	H_ARG_71	NH2	G_ASP_368	OD2	3.685
4OLZ	H_ARG_82A	NH1	H_GLU_81	OE2	3.365
4OLZ	H_HIS_102	NE2	H_GLU_101	OE1	3.537
4OLZ	H_LYS_143	NZ	H_ASP_144	OD1	3.616
4OLZ	H_LYS_209	NZ	L_GLU_125	OE1	3.703
4OLZ	H_LYS_209	NZ	L_GLU_125	OE2	3.063
4OLZ	H_LYS_210	NZ	H_GLU_212	OE1	3.813
4OLZ	H_LYS_214	NZ	L_ASP_124	OD1	3.528
4OLZ	H_LYS_214	NZ	L_ASP_124	OD2	3.896
4OLZ	L_ARG_24	NH2	L_ASP_70	OD1	3.107
4OLZ	L_ARG_24	NH2	L_ASP_70	OD2	2.518
4OLZ	L_ARG_61	NH1	L_ASP_82	OD1	3.951
4OLZ	L_ARG_61	NH1	L_ASP_82	OD2	2.771
4OLZ	L_ARG_61	NH2	L_GLU_79	OE1	3.245
4OLZ	L_ARG_61	NH2	L_GLU_79	OE2	3.953
4OLZ	L_ARG_61	NH2	L_ASP_82	OD1	3.377
4OLZ	L_ARG_61	NH2	L_ASP_82	OD2	3.458
4OLZ	L_LYS_109	NZ	L_GLU_17	OE2	2.896
4OM0	G_HIS_66	ND1	G_GLU_64	OE1	3.833
4OM0	G_HIS_66	ND1	G_GLU_64	OE2	2.725
4OM0	G_LYS_97	NZ	G_GLU_275	OE1	3.804
4OM0	G_LYS_97	NZ	G_GLU_275	OE2	2.555
4OM0	G_LYS_97	NZ	H_ASP_100B	OD1	3.843
4OM0	G_LYS_97	NZ	H_ASP_100B	OD2	3.296
4OM0	G_LYS_207	NZ	G_GLU_381	OE1	3.664
4OM0	G_LYS_207	NZ	G_GLU_381	OE2	3.001
4OM0	G_HIS_249	NE2	G_GLU_482	OE1	3.206
4OM0	G_LYS_282	NZ	G_GLU_275	OE1	3.687
4OM0	G_LYS_343	NZ	G_GLU_347	OE2	2.544
4OM0	G_LYS_348	NZ	G_GLU_269	OE2	2.992
4OM0	G_LYS_348	NZ	G_GLU_351	OE1	3.079
4OM0	G_ARG_379	NH2	G_ASP_211	OD1	3.805
4OM0	G_ARG_469	NH2	G_ASP_457	OD1	3.868
4OM0	G_ARG_469	NH2	G_ASP_457	OD2	2.885
4OM0	G_LYS_476	NZ	G_GLU_102	OE1	2.824
4OM0	G_ARG_480	NH1	G_ASP_477	OD1	2.762
4OM0	G_ARG_480	NH2	G_GLU_102	OE2	3.978
4OM0	G_LYS_487	NZ	G_ASP_47	OD1	2.993
4OM0	G_LYS_487	NZ	G_ASP_47	OD2	3.296
4OM0	G_LYS_487	NZ	G_GLU_91	OE1	2.866
4OM0	H_ARG_19	NH2	H_GLU_81	OE1	3.635
4OM0	H_ARG_38	NH1	H_ASP_86	OD1	2.891
4OM0	H_ARG_38	NH2	H_GLU_46	OE1	3.152
4OM0	H_ARG_38	NH2	H_GLU_46	OE2	3.952
4OM0	H_ARG_38	NH2	H_ASP_86	OD1	3.799
4OM0	H_ARG_61	NH1	G_GLU_466	OE1	2.871
4OM0	H_ARG_66	NH1	H_ASP_86	OD1	3.542
4OM0	H_ARG_66	NH2	H_ASP_86	OD1	3.067
4OM0	H_ARG_66	NH2	H_ASP_86	OD2	2.679
4OM0	H_ARG_71	NH1	G_ASP_368	OD1	3.724
4OM0	H_ARG_71	NH1	G_ASP_368	OD2	2.771
4OM0	H_ARG_71	NH2	G_ASP_368	OD1	3.189
4OM0	H_ARG_71	NH2	G_ASP_368	OD2	3.713
4OM0	H_ARG_82A	NH1	H_GLU_81	OE2	3.957
4OM0	H_HIS_102	NE2	H_GLU_101	OE1	3.389
4OM0	H_LYS_143	NZ	H_ASP_144	OD1	3.715
4OM0	H_LYS_209	NZ	L_GLU_125	OE2	3.121
4OM0	H_LYS_210	NZ	H_GLU_212	OE1	3.995

4OM0	L_ARG_24	NH1	L_ASP_70	OD1	3.645
4OM0	L_ARG_24	NH1	L_ASP_70	OD2	3.913
4OM0	L_ARG_24	NH2	L_ASP_70	OD1	3.504
4OM0	L_ARG_24	NH2	L_ASP_70	OD2	3.395
4OM0	L_ARG_61	NH1	L_ASP_82	OD1	3.878
4OM0	L_ARG_61	NH1	L_ASP_82	OD2	2.597
4OM0	L_ARG_61	NH2	L_GLU_79	OE1	3.542
4OM0	L_ARG_61	NH2	L_GLU_79	OE2	3.993
4OM0	L_ARG_61	NH2	L_ASP_82	OD1	3.348
4OM0	L_ARG_61	NH2	L_ASP_82	OD2	3.442
4OM1	G_HIS_66	ND1	G_GLU_64	OE1	3.968
4OM1	G_HIS_66	ND1	G_GLU_64	OE2	2.708
4OM1	G_LYS_97	NZ	G_GLU_275	OE1	3.600
4OM1	G_LYS_97	NZ	G_GLU_275	OE2	2.568
4OM1	G_LYS_97	NZ	H_ASP_100B	OD1	3.927
4OM1	G_LYS_97	NZ	H_ASP_100B	OD2	3.635
4OM1	G_LYS_207	NZ	G_GLU_381	OE1	3.308
4OM1	G_LYS_207	NZ	G_GLU_381	OE2	2.686
4OM1	G_HIS_249	NE2	G_GLU_482	OE1	3.036
4OM1	G_LYS_282	NZ	G_GLU_275	OE1	3.818
4OM1	G_LYS_343	NZ	G_GLU_347	OE2	2.690
4OM1	G_LYS_348	NZ	G_GLU_351	OE1	3.702
4OM1	G_LYS_357	NZ	G_GLU_466	OE2	2.685
4OM1	G_LYS_357	NZ	L_GLU_1	OE2	3.763
4OM1	G_ARG_379	NH2	G_ASP_211	OD2	3.954
4OM1	G_ARG_456	NH1	G_GLU_466	OE1	3.023
4OM1	G_ARG_469	NH2	G_ASP_457	OD1	3.972
4OM1	G_ARG_469	NH2	G_ASP_457	OD2	2.755
4OM1	G_LYS_476	NZ	G_GLU_102	OE1	2.848
4OM1	G_LYS_476	NZ	G_GLU_102	OE2	3.744
4OM1	G_ARG_480	NH1	G_ASP_477	OD1	2.846
4OM1	G_LYS_487	NZ	G_ASP_47	OD1	2.990
4OM1	G_LYS_487	NZ	G_ASP_47	OD2	3.195
4OM1	G_LYS_487	NZ	G_GLU_91	OE1	2.549
4OM1	H_ARG_19	NH2	H_GLU_81	OE1	3.387
4OM1	H_ARG_38	NH1	H_ASP_86	OD1	2.946
4OM1	H_ARG_38	NH2	H_GLU_46	OE1	2.854
4OM1	H_ARG_38	NH2	H_GLU_46	OE2	3.922
4OM1	H_ARG_38	NH2	H_ASP_86	OD1	3.859
4OM1	H_ARG_66	NH1	H_ASP_86	OD1	3.431
4OM1	H_ARG_66	NH2	H_ASP_86	OD1	2.947
4OM1	H_ARG_66	NH2	H_ASP_86	OD2	2.686
4OM1	H_ARG_71	NH1	G_ASP_368	OD1	3.565
4OM1	H_ARG_71	NH1	G_ASP_368	OD2	2.752
4OM1	H_ARG_71	NH2	G_ASP_368	OD1	3.031
4OM1	H_ARG_71	NH2	G_ASP_368	OD2	3.734
4OM1	H_ARG_82A	NH1	H_GLU_81	OE2	3.380
4OM1	H_LYS_96	NZ	H_GLU_101	OE1	3.890
4OM1	H_LYS_96	NZ	H_GLU_101	OE2	3.816
4OM1	H_HIS_102	NE2	H_GLU_101	OE1	3.730
4OM1	H_LYS_209	NZ	L_GLU_125	OE1	3.639
4OM1	H_LYS_209	NZ	L_GLU_125	OE2	3.008
4OM1	H_LYS_210	NZ	H_GLU_212	OE1	3.752
4OM1	L_ARG_24	NH2	L_ASP_70	OD1	3.182
4OM1	L_ARG_24	NH2	L_ASP_70	OD2	2.699
4OM1	L_ARG_61	NH1	L_ASP_82	OD1	3.829
4OM1	L_ARG_61	NH1	L_ASP_82	OD2	2.671
4OM1	L_ARG_61	NH2	L_GLU_79	OE1	3.602

4OM1	L_ARG_61	NH2	L_GLU_79	OE2	3.954
4OM1	L_ARG_61	NH2	L_ASP_82	OD1	3.243
4OM1	L_ARG_61	NH2	L_ASP_82	OD2	3.379
4OM1	L_LYS_109	NZ	L_GLU_17	OE1	3.450
4OM1	L_LYS_109	NZ	L_GLU_17	OE2	2.771
4OM1	L_HIS_191	ND1	L_ASP_153	OD2	2.919
4OT1	A_ARG_131	NH1	A_GLU_422	OE2	3.994
4OT1	A_ARG_357	NH2	A_ASP_122	OD2	2.900
4OT1	A_LYS_378	NZ	A_ASP_362	OD1	3.505
4OT1	A_LYS_378	NZ	A_ASP_362	OD2	3.358
4OT1	A_LYS_379	NZ	A_GLU_359	OE2	2.737
4OT1	A_ARG_393	NH1	A_ASP_390	OD1	2.905
4OT1	A_ARG_393	NH2	A_ASP_390	OD1	2.768
4OT1	A_LYS_435	NZ	A_GLU_413	OE2	2.567
4OT1	H_ARG_12	NH1	H_GLU_10	OE1	3.166
4OT1	H_ARG_12	NH2	H_GLU_10	OE1	3.283
4OT1	H_LYS_30	NZ	H_ASP_31	OD1	3.047
4OT1	H_ARG_38	NH1	H_ASP_90	OD1	2.615
4OT1	H_ARG_38	NH2	H_GLU_46	OE1	3.314
4OT1	H_ARG_38	NH2	H_ASP_90	OD1	3.679
4OT1	H_LYS_63	NZ	H_GLU_46	OE1	3.385
4OT1	H_LYS_63	NZ	H_GLU_46	OE2	2.667
4OT1	H_ARG_67	NH1	H_ASP_90	OD1	3.883
4OT1	H_ARG_67	NH1	H_ASP_90	OD2	3.033
4OT1	H_ARG_67	NH2	H_ASP_90	OD1	3.016
4OT1	H_ARG_67	NH2	H_ASP_90	OD2	3.552
4OT1	H_ARG_87	NH2	H_ASP_89	OD1	3.432
4OT1	H_ARG_87	NH2	H_ASP_89	OD2	2.704
4OT1	H_ARG_98	NH2	H_ASP_119	OD1	3.496
4OT1	H_ARG_98	NH2	H_ASP_119	OD2	2.884
4OT1	H_HIS_115	ND1	H_ASP_99	OD1	2.738
4OT1	H_HIS_115	ND1	H_ASP_99	OD2	3.714
4OT1	H_LYS_161	NZ	L_GLU_127	OE2	2.572
4OT1	H_LYS_227	NZ	L_GLU_126	OE1	2.521
4OT1	H_LYS_227	NZ	L_GLU_126	OE2	3.241
4OT1	L_LYS_54	NZ	L_ASP_51	OD2	3.014
4OT1	L_ARG_55	NH1	L_ASP_61	OD1	3.917
4OT1	L_ARG_62	NH1	L_ASP_83	OD1	2.721
4OT1	L_ARG_62	NH1	L_ASP_83	OD2	3.462
4OT1	L_ARG_62	NH2	L_ASP_83	OD1	3.562
4OT1	L_ARG_62	NH2	L_ASP_83	OD2	2.996
4OT1	L_LYS_67	NZ	A_GLU_361	OE2	3.026
4OT1	L_LYS_152	NZ	L_GLU_206	OE1	3.999
4OT1	L_LYS_152	NZ	L_GLU_206	OE2	2.900
4OTX	L_ARG_54	NH1	L_ASP_60	OD1	3.335
4OTX	L_ARG_54	NH2	L_ASP_60	OD1	2.587
4OTX	L_ARG_61	NH2	L_GLU_81	OE1	3.052
4OTX	L_ARG_61	NH2	L_ASP_82	OD1	2.662
4OTX	L_ARG_61	NH2	L_ASP_82	OD2	3.622
4OTX	L_LYS_149	NZ	L_GLU_195	OE1	3.784
4OTX	L_HIS_189	ND1	L_ASP_151	OD2	2.906
4OTX	H_LYS_62	NZ	H_GLU_46	OE1	3.813
4OTX	H_LYS_62	NZ	H_GLU_46	OE2	2.843
4OTX	H_LYS_66	NZ	H_ASP_86	OD1	3.726
4OTX	H_LYS_66	NZ	H_ASP_86	OD2	2.772
4OTX	M_LYS_24	NZ	M_ASP_70	OD1	3.831
4OTX	M_ARG_54	NH2	M_ASP_60	OD1	3.076
4OTX	M_ARG_61	NH2	M_GLU_81	OE2	2.931

4OTX	M_ARG_61	NH2	M_ASP_82	OD1	2.705
4OTX	M_ARG_61	NH2	M_ASP_82	OD2	3.780
4OTX	M_ARG_155	NH1	M_GLU_185	OE2	2.645
4OTX	M_ARG_155	NH2	M_GLU_185	OE1	3.700
4OTX	M_ARG_155	NH2	M_GLU_185	OE2	3.518
4OTX	M_HIS_189	ND1	M_ASP_151	OD2	2.662
4OTX	M_ARG_211	NH1	M_GLU_187	OE2	3.522
4OTX	I_LYS_62	NZ	I_GLU_46	OE2	2.424
4OTX	I_LYS_66	NZ	I_ASP_86	OD2	2.972
4OTX	I_ARG_94	NH2	I_ASP_101	OD2	3.905
4OTX	I_LYS_209	NZ	I_GLU_211	OE1	3.618
4P49	A_LYS_33	NZ	A_GLU_76	OE2	3.764
4P49	A_ARG_56	NH2	A_GLU_76	OE1	3.151
4P49	A_ARG_56	NH2	A_ASP_77	OD1	2.851
4P49	A_ARG_56	NH2	A_ASP_77	OD2	3.564
4P49	A_ARG_158	NH1	A_ASP_211	OD1	2.929
4P49	A_ARG_158	NH2	A_GLU_166	OE1	3.049
4P49	A_ARG_158	NH2	A_ASP_211	OD1	3.847
4P49	A_ARG_188	NH1	A_ASP_211	OD1	3.709
4P49	A_ARG_188	NH1	A_ASP_211	OD2	2.796
4P49	A_ARG_188	NH2	A_ASP_211	OD1	2.980
4P49	A_ARG_188	NH2	A_ASP_211	OD2	3.547
4P49	A_ARG_219	NH2	A_ASP_232	OD1	3.462
4P49	A_ARG_219	NH2	A_ASP_232	OD2	2.815
4P49	A_HIS_221	ND1	A_ASP_232	OD2	2.753
4P49	A_HIS_236	ND1	A_GLU_126	OE1	3.338
4P49	A_HIS_236	NE2	A_ASP_125	OD1	2.678
4P49	A_HIS_236	NE2	A_GLU_126	OE1	3.576
4P9H	C_LYS_7	NZ	C_ASP_10	OD2	3.690
4P9H	C_LYS_8	NZ	C_GLU_119	OE1	3.955
4P9H	C_LYS_8	NZ	C_GLU_119	OE2	2.953
4P9H	C_LYS_29	NZ	C_GLU_85	OE1	3.562
4P9H	C_LYS_29	NZ	C_GLU_85	OE2	3.697
4P9H	C_ARG_54	NH1	C_ASP_78	OD2	2.976
4P9H	C_ARG_54	NH2	C_ASP_78	OD1	3.086
4P9H	C_ARG_54	NH2	C_ASP_78	OD2	2.930
4P9H	C_ARG_58	NH1	C_GLU_13	OE1	2.881
4P9H	C_ARG_58	NH1	C_GLU_13	OE2	2.882
4P9H	C_ARG_58	NH2	C_GLU_13	OE2	3.671
4P9H	C_ARG_59	NH1	G_ASP_368	OD1	2.832
4P9H	C_ARG_59	NH1	G_ASP_368	OD2	3.395
4P9H	C_ARG_59	NH2	G_ASP_368	OD1	3.561
4P9H	C_ARG_59	NH2	G_ASP_368	OD2	2.514
4P9H	C_LYS_171	NZ	C_GLU_169	OE2	3.618
4P9H	G_HIS_66	ND1	G_GLU_64	OE1	3.936
4P9H	G_HIS_66	ND1	G_GLU_64	OE2	2.459
4P9H	G_LYS_227	NZ	G_GLU_83	OE2	3.669
4P9H	G_HIS_249	NE2	G_GLU_482	OE1	2.955
4P9H	G_LYS_282	NZ	G_GLU_275	OE1	3.022
4P9H	G_LYS_282	NZ	G_GLU_275	OE2	3.961
4P9H	G_LYS_348	NZ	G_GLU_269	OE1	2.726
4P9H	G_LYS_348	NZ	G_GLU_351	OE1	3.154
4P9H	G_LYS_348	NZ	G_GLU_351	OE2	3.034
4P9H	G_LYS_357	NZ	G_GLU_466	OE2	2.986
4P9H	G_ARG_456	NH1	G_GLU_466	OE1	3.795
4P9H	G_ARG_456	NH1	G_GLU_466	OE2	3.185
4P9H	G_ARG_469	NH2	G_ASP_457	OD2	3.218
4P9H	G_LYS_476	NZ	G_GLU_102	OE1	2.706

4P9H	G_ARG_480	NH1	G_ASP_477	OD1	3.014
4P9H	G_ARG_480	NH2	G_GLU_102	OE2	3.549
4P9H	G_LYS_487	NZ	G_ASP_47	OD1	3.793
4P9H	G_LYS_487	NZ	G_ASP_47	OD2	2.540
4P9H	G_LYS_487	NZ	G_GLU_91	OE2	2.794
4P9H	H_ARG_38	NH1	H_ASP_86	OD1	2.679
4P9H	H_ARG_38	NH2	H_GLU_46	OE1	3.970
4P9H	H_ARG_38	NH2	H_ASP_86	OD1	3.498
4P9H	H_HIS_61	NE2	L_ASP_1	OD2	3.817
4P9H	H_ARG_66	NH2	H_ASP_86	OD1	2.897
4P9H	H_ARG_66	NH2	H_ASP_86	OD2	2.412
4P9H	H_LYS_143	NZ	H_ASP_144	OD1	3.073
4P9H	H_LYS_143	NZ	H_ASP_144	OD2	2.969
4P9H	L_ARG_24	NH2	L_ASP_70	OD1	3.255
4P9H	L_ARG_61	NH1	L_GLU_81	OE2	3.724
4P9H	L_ARG_61	NH1	L_ASP_82	OD1	3.931
4P9H	L_ARG_61	NH1	L_ASP_82	OD2	2.983
4P9H	L_ARG_61	NH2	L_GLU_81	OE2	2.893
4P9H	L_ARG_61	NH2	L_ASP_82	OD1	3.839
4PTT	A_ARG_24	NH1	A_ASP_70	OD1	3.965
4PTT	A_ARG_24	NH1	A_ASP_70	OD2	3.009
4PTT	A_ARG_53	NH1	A_ASP_50	OD2	3.791
4PTT	A_ARG_53	NH2	A_ASP_50	OD2	2.752
4PTT	A_ARG_61	NH1	A_GLU_79	OE1	3.274
4PTT	A_ARG_61	NH2	A_GLU_79	OE1	3.194
4PTT	A_ARG_61	NH2	A_GLU_81	OE1	3.963
4PTT	A_ARG_61	NH2	A_ASP_82	OD1	2.721
4PTT	A_ARG_61	NH2	A_ASP_82	OD2	3.451
4PTT	A_ARG_91	NH2	B_GLU_95	OE1	3.477
4PTT	A_ARG_91	NH2	B_GLU_95	OE2	3.208
4PTT	A_LYS_107	NZ	A_GLU_17	OE1	3.991
4PTT	A_LYS_107	NZ	A_GLU_17	OE2	3.451
4PTT	A_LYS_149	NZ	A_GLU_195	OE1	2.707
4PTT	A_LYS_149	NZ	A_GLU_195	OE2	2.811
4PTT	A_LYS_188	NZ	A_ASP_185	OD1	3.692
4PTT	A_ARG_211	NH1	A_GLU_187	OE1	3.911
4PTT	B_HIS_32	ND1	B_ASP_97	OD1	3.351
4PTT	B_HIS_32	NE2	B_ASP_97	OD1	3.881
4PTT	B_HIS_35	NE2	B_GLU_95	OE2	2.791
4PTT	B_ARG_38	NH1	B_ASP_86	OD1	2.956
4PTT	B_ARG_38	NH2	B_GLU_46	OE1	3.058
4PTT	B_ARG_38	NH2	B_GLU_46	OE2	3.774
4PTT	B_ARG_66	NH1	B_ASP_86	OD1	3.031
4PTT	B_ARG_66	NH1	B_ASP_86	OD2	3.456
4PTT	B_ARG_66	NH2	B_ASP_86	OD1	3.848
4PTT	B_ARG_66	NH2	B_ASP_86	OD2	2.768
4PTT	B_LYS_94	NZ	B_ASP_97	OD1	2.735
4PTT	B_LYS_94	NZ	B_ASP_97	OD2	3.827
4PTT	B_LYS_94	NZ	B_ASP_101	OD1	3.084
4PTT	B_LYS_94	NZ	B_ASP_101	OD2	2.853
4PTT	B_LYS_143	NZ	B_ASP_144	OD1	3.257
4PTT	B_LYS_143	NZ	B_ASP_144	OD2	3.722
4PTT	B_LYS_209	NZ	A_GLU_123	OE2	3.476
4PTT	B_ARG_210	NH1	B_GLU_212	OE2	3.500
4PTT	B_ARG_210	NH2	B_GLU_212	OE2	2.861
4PTU	A_ARG_24	NH1	A_ASP_70	OD2	3.705
4PTU	A_ARG_53	NH1	A_ASP_50	OD2	3.480
4PTU	A_ARG_53	NH2	A_ASP_50	OD2	2.718

4PTU	A_ARG_61	NH1	A_GLU_79	OE1	3.172
4PTU	A_ARG_61	NH2	A_GLU_79	OE1	3.200
4PTU	A_ARG_61	NH2	A_ASP_82	OD1	2.746
4PTU	A_ARG_61	NH2	A_ASP_82	OD2	3.514
4PTU	A_ARG_91	NH2	B_GLU_95	OE1	3.438
4PTU	A_ARG_91	NH2	B_GLU_95	OE2	3.334
4PTU	A_LYS_107	NZ	A_GLU_17	OE1	3.740
4PTU	A_LYS_107	NZ	A_GLU_17	OE2	3.243
4PTU	A_LYS_149	NZ	A_GLU_195	OE1	3.016
4PTU	A_LYS_149	NZ	A_GLU_195	OE2	3.379
4PTU	A_LYS_183	NZ	A_GLU_187	OE1	2.720
4PTU	A_LYS_188	NZ	A_ASP_185	OD1	3.765
4PTU	A_HIS_189	ND1	A_ASP_151	OD2	3.327
4PTU	B_HIS_32	ND1	B_ASP_97	OD1	3.387
4PTU	B_HIS_32	NE2	B_ASP_97	OD1	3.899
4PTU	B_HIS_35	NE2	B_GLU_95	OE2	2.750
4PTU	B_ARG_38	NH1	B_ASP_86	OD1	2.924
4PTU	B_ARG_38	NH2	B_GLU_46	OE1	3.021
4PTU	B_ARG_38	NH2	B_GLU_46	OE2	3.729
4PTU	B_ARG_38	NH2	B_ASP_86	OD1	3.966
4PTU	B_ARG_66	NH1	B_ASP_86	OD1	3.085
4PTU	B_ARG_66	NH1	B_ASP_86	OD2	3.410
4PTU	B_ARG_66	NH2	B_ASP_86	OD1	3.877
4PTU	B_ARG_66	NH2	B_ASP_86	OD2	2.723
4PTU	B_LYS_94	NZ	B_ASP_97	OD1	2.781
4PTU	B_LYS_94	NZ	B_ASP_97	OD2	3.846
4PTU	B_LYS_94	NZ	B_ASP_101	OD1	3.172
4PTU	B_LYS_94	NZ	B_ASP_101	OD2	2.801
4PTU	B_LYS_143	NZ	B_ASP_144	OD1	3.236
4PTU	B_LYS_143	NZ	B_ASP_144	OD2	3.531
4PTU	B_LYS_209	NZ	A_GLU_123	OE1	3.628
4PTU	B_ARG_210	NH1	B_GLU_212	OE2	3.352
4Q6I	A_ARG_24	NH2	A_ASP_70	OD1	3.547
4Q6I	A_LYS_49	NZ	A_GLU_55	OE1	3.733
4Q6I	A_LYS_49	NZ	B_ASP_100A	OD1	2.964
4Q6I	A_ARG_61	NH1	A_GLU_79	OE1	3.355
4Q6I	A_ARG_61	NH1	A_GLU_79	OE2	3.338
4Q6I	A_ARG_61	NH1	A_GLU_81	OE2	3.926
4Q6I	A_ARG_61	NH2	A_GLU_79	OE2	3.547
4Q6I	A_ARG_61	NH2	A_GLU_81	OE2	3.022
4Q6I	A_ARG_61	NH2	A_ASP_82	OD1	2.927
4Q6I	A_ARG_61	NH2	A_ASP_82	OD2	3.845
4Q6I	A_LYS_103	NZ	A_GLU_105	OE2	3.808
4Q6I	A_LYS_142	NZ	A_GLU_105	OE1	3.421
4Q6I	A_LYS_142	NZ	A_GLU_105	OE2	2.841
4Q6I	A_LYS_147	NZ	A_GLU_154	OE1	3.796
4Q6I	A_LYS_149	NZ	A_GLU_195	OE1	3.162
4Q6I	A_LYS_149	NZ	A_GLU_195	OE2	3.016
4Q6I	A_ARG_155	NH1	A_GLU_185	OE2	3.506
4Q6I	A_HIS_189	ND1	A_ASP_151	OD2	2.954
4Q6I	B_HIS_66	ND1	B_ASP_61	OD1	3.699
4Q6I	B_HIS_66	ND1	B_ASP_61	OD2	3.085
4Q6I	B_HIS_66	NE2	B_ASP_86	OD1	3.906
4Q6I	B_HIS_66	NE2	B_ASP_86	OD2	2.658
4Q6I	B_ARG_94	NH2	B_ASP_101	OD1	3.897
4Q6I	B_ARG_94	NH2	B_ASP_101	OD2	2.713
4Q6I	B_LYS_208	NZ	A_GLU_123	OE2	2.822
4Q6I	C_LYS_8	NZ	C_GLU_119	OE1	2.805

4Q6I	C_HIS_27	NE2	C_GLU_85	OE1	3.053
4Q6I	C_LYS_50	NZ	C_GLU_77	OE2	3.944
4Q6I	C_LYS_50	NZ	L_GLU_93	OE2	2.549
4Q6I	C_ARG_54	NH1	C_ASP_78	OD2	2.778
4Q6I	C_ARG_54	NH2	C_ASP_78	OD1	3.552
4Q6I	C_ARG_54	NH2	C_ASP_78	OD2	3.385
4Q6I	C_ARG_134	NH1	C_GLU_150	OE1	2.907
4Q6I	C_ARG_134	NH1	C_GLU_150	OE2	3.926
4Q6I	C_LYS_136	NZ	C_ASP_153	OD1	3.102
4Q6I	C_LYS_136	NZ	C_ASP_153	OD2	3.702
4Q6I	C_LYS_167	NZ	C_GLU_169	OE2	3.766
4Q6I	C_LYS_181	NZ	G_GLU_56	OE1	2.499
4Q6I	D_ARG_24	NH2	D_ASP_70	OD1	3.494
4Q6I	D_LYS_49	NZ	D_GLU_55	OE1	3.186
4Q6I	D_LYS_49	NZ	D_GLU_55	OE2	3.674
4Q6I	D_LYS_49	NZ	E_ASP_100A	OD1	3.008
4Q6I	D_ARG_61	NH1	D_GLU_79	OE1	3.297
4Q6I	D_ARG_61	NH1	D_GLU_79	OE2	3.483
4Q6I	D_ARG_61	NH2	D_GLU_79	OE2	3.497
4Q6I	D_ARG_61	NH2	D_GLU_81	OE2	3.188
4Q6I	D_ARG_61	NH2	D_ASP_82	OD1	3.128
4Q6I	D_ARG_61	NH2	D_ASP_82	OD2	3.997
4Q6I	D_LYS_142	NZ	D_GLU_105	OE1	3.699
4Q6I	D_LYS_142	NZ	D_GLU_105	OE2	2.690
4Q6I	D_LYS_147	NZ	D_GLU_154	OE1	3.636
4Q6I	D_LYS_149	NZ	D_GLU_195	OE1	3.195
4Q6I	D_LYS_149	NZ	D_GLU_195	OE2	2.990
4Q6I	D_ARG_155	NH1	D_GLU_185	OE2	3.476
4Q6I	D_ARG_155	NH2	D_GLU_185	OE2	3.858
4Q6I	D_HIS_189	ND1	D_ASP_151	OD2	2.792
4Q6I	E_HIS_66	ND1	E_ASP_61	OD1	3.611
4Q6I	E_HIS_66	ND1	E_ASP_61	OD2	3.049
4Q6I	E_HIS_66	NE2	E_ASP_86	OD1	3.914
4Q6I	E_HIS_66	NE2	E_ASP_86	OD2	2.560
4Q6I	E_ARG_94	NH2	E_ASP_101	OD1	3.957
4Q6I	E_ARG_94	NH2	E_ASP_101	OD2	2.680
4Q6I	E_LYS_208	NZ	D_GLU_123	OE2	3.047
4Q6I	F_ARG_24	NH2	F_ASP_70	OD1	3.340
4Q6I	F_ARG_24	NH2	F_ASP_70	OD2	3.665
4Q6I	F_LYS_49	NZ	F_GLU_55	OE1	3.518
4Q6I	F_LYS_49	NZ	G_ASP_100A	OD1	3.146
4Q6I	F_ARG_61	NH1	F_GLU_79	OE1	3.116
4Q6I	F_ARG_61	NH1	F_GLU_79	OE2	3.200
4Q6I	F_ARG_61	NH2	F_GLU_79	OE2	3.435
4Q6I	F_ARG_61	NH2	F_GLU_81	OE2	3.194
4Q6I	F_ARG_61	NH2	F_ASP_82	OD1	2.864
4Q6I	F_ARG_61	NH2	F_ASP_82	OD2	3.691
4Q6I	F_LYS_103	NZ	F_GLU_105	OE2	3.989
4Q6I	F_LYS_142	NZ	F_GLU_105	OE1	3.572
4Q6I	F_LYS_142	NZ	F_GLU_105	OE2	2.671
4Q6I	F_LYS_147	NZ	F_GLU_154	OE1	3.784
4Q6I	F_LYS_149	NZ	F_GLU_195	OE1	3.282
4Q6I	F_LYS_149	NZ	F_GLU_195	OE2	2.913
4Q6I	F_ARG_155	NH1	F_GLU_185	OE2	3.619
4Q6I	F_ARG_155	NH2	F_GLU_185	OE2	3.997
4Q6I	F_HIS_189	ND1	F_ASP_151	OD2	2.927
4Q6I	G_HIS_66	ND1	G_ASP_61	OD1	3.622
4Q6I	G_HIS_66	ND1	G_ASP_61	OD2	3.038

4Q6I	G_HIS_66	NE2	G_ASP_86	OD1	3.886
4Q6I	G_HIS_66	NE2	G_ASP_86	OD2	2.589
4Q6I	G_ARG_94	NH2	G_ASP_101	OD1	3.834
4Q6I	G_ARG_94	NH2	G_ASP_101	OD2	2.611
4Q6I	G_LYS_208	NZ	F_GLU_123	OE2	3.409
4Q6I	H_HIS_66	ND1	H_ASP_61	OD1	3.559
4Q6I	H_HIS_66	ND1	H_ASP_61	OD2	2.808
4Q6I	H_HIS_66	NE2	H_ASP_86	OD1	3.762
4Q6I	H_HIS_66	NE2	H_ASP_86	OD2	2.594
4Q6I	H_ARG_94	NH2	H_ASP_101	OD1	3.987
4Q6I	H_ARG_94	NH2	H_ASP_101	OD2	2.731
4Q6I	H_LYS_208	NZ	L_GLU_123	OE2	3.045
4Q6I	I_LYS_8	NZ	I_GLU_119	OE1	2.686
4Q6I	I_LYS_8	NZ	I_GLU_119	OE2	3.813
4Q6I	I_HIS_27	NE2	I_GLU_85	OE1	3.108
4Q6I	I_LYS_50	NZ	F_GLU_93	OE2	2.473
4Q6I	I_LYS_50	NZ	I_GLU_77	OE2	3.955
4Q6I	I_ARG_54	NH1	I_ASP_78	OD2	2.649
4Q6I	I_ARG_54	NH2	I_ASP_78	OD1	3.358
4Q6I	I_ARG_54	NH2	I_ASP_78	OD2	3.298
4Q6I	I_ARG_134	NH1	I_GLU_150	OE1	2.570
4Q6I	I_ARG_134	NH1	I_GLU_150	OE2	3.190
4Q6I	I_LYS_136	NZ	I_ASP_153	OD1	2.871
4Q6I	I_LYS_136	NZ	I_ASP_153	OD2	3.533
4Q6I	I_LYS_167	NZ	I_GLU_169	OE2	3.738
4Q6I	I_LYS_181	NZ	H_GLU_56	OE1	3.345
4Q6I	J_LYS_8	NZ	J_GLU_119	OE1	2.575
4Q6I	J_LYS_8	NZ	J_GLU_119	OE2	3.660
4Q6I	J_HIS_27	NE2	J_GLU_85	OE1	3.112
4Q6I	J_LYS_50	NZ	D_GLU_93	OE2	2.666
4Q6I	J_LYS_50	NZ	J_GLU_77	OE2	3.985
4Q6I	J_ARG_54	NH1	J_ASP_78	OD2	2.642
4Q6I	J_ARG_54	NH2	J_ASP_78	OD1	3.414
4Q6I	J_ARG_54	NH2	J_ASP_78	OD2	3.086
4Q6I	J_ARG_134	NH1	J_GLU_150	OE1	3.114
4Q6I	J_LYS_136	NZ	J_ASP_153	OD1	2.951
4Q6I	J_LYS_136	NZ	J_ASP_153	OD2	3.722
4Q6I	J_LYS_167	NZ	J_GLU_169	OE2	3.737
4Q6I	K_LYS_8	NZ	K_GLU_119	OE1	2.674
4Q6I	K_LYS_8	NZ	K_GLU_119	OE2	3.835
4Q6I	K_HIS_27	NE2	K_GLU_85	OE1	2.922
4Q6I	K_LYS_50	NZ	A_GLU_93	OE2	2.835
4Q6I	K_LYS_50	NZ	K_GLU_77	OE2	3.766
4Q6I	K_ARG_54	NH1	K_ASP_78	OD2	2.757
4Q6I	K_ARG_54	NH2	K_ASP_78	OD1	3.522
4Q6I	K_ARG_54	NH2	K_ASP_78	OD2	3.092
4Q6I	K_ARG_134	NH1	K_GLU_150	OE1	2.737
4Q6I	K_ARG_134	NH1	K_GLU_150	OE2	2.516
4Q6I	K_LYS_136	NZ	K_ASP_153	OD1	3.074
4Q6I	K_LYS_136	NZ	K_ASP_153	OD2	3.548
4Q6I	L_ARG_24	NH2	L_ASP_70	OD1	3.386
4Q6I	L_ARG_24	NH2	L_ASP_70	OD2	3.804
4Q6I	L_LYS_49	NZ	H_ASP_100A	OD1	3.063
4Q6I	L_LYS_49	NZ	L_GLU_55	OE1	3.608
4Q6I	L_ARG_61	NH1	L_GLU_79	OE1	3.293
4Q6I	L_ARG_61	NH1	L_GLU_79	OE2	3.453
4Q6I	L_ARG_61	NH2	L_GLU_79	OE2	3.533
4Q6I	L_ARG_61	NH2	L_GLU_81	OE2	3.058

4Q6I	L_ARG_61	NH2	L_ASP_82	OD1	3.103
4Q6I	L_LYS_142	NZ	L_GLU_105	OE1	3.663
4Q6I	L_LYS_142	NZ	L_GLU_105	OE2	2.645
4Q6I	L_LYS_147	NZ	L_GLU_154	OE1	3.681
4Q6I	L_LYS_149	NZ	L_GLU_195	OE1	3.252
4Q6I	L_LYS_149	NZ	L_GLU_195	OE2	2.874
4Q6I	L_ARG_155	NH1	L_GLU_185	OE2	3.717
4Q6I	L_ARG_155	NH2	L_GLU_185	OE2	3.978
4Q6I	L_HIS_189	ND1	L_ASP_151	OD2	2.862
4Q97	A_LYS_181	NZ	A_GLU_215	OE1	3.508
4Q97	A_LYS_181	NZ	A_GLU_215	OE2	2.452
4Q97	A_ARG_218	NH2	A_GLU_215	OE1	3.903
4Q97	A_ARG_240	NH2	A_GLU_238	OE1	2.864
4Q97	A_ARG_240	NH2	A_GLU_238	OE2	3.199
4Q97	B_LYS_181	NZ	B_GLU_215	OE1	3.498
4Q97	B_LYS_181	NZ	B_GLU_215	OE2	2.431
4Q97	B_ARG_218	NH2	B_GLU_215	OE1	3.910
4Q97	B_ARG_240	NH2	B_GLU_238	OE1	2.853
4Q97	B_ARG_240	NH2	B_GLU_238	OE2	3.203
4Q9B	A_ARG_250	NH1	A_GLU_268	OE2	2.895
4Q9B	A_ARG_288	NH1	A_GLU_316	OE1	3.608
4Q9B	A_ARG_288	NH1	A_GLU_316	OE2	2.926
4Q9B	A_ARG_288	NH2	A_GLU_316	OE1	2.765
4Q9B	A_ARG_288	NH2	A_GLU_316	OE2	3.617
4Q9B	A_ARG_309	NH1	A_GLU_295	OE1	2.883
4Q9B	A_ARG_309	NH1	A_GLU_295	OE2	3.399
4Q9B	A_ARG_309	NH1	B_GLU_255	OE1	3.484
4Q9B	A_ARG_309	NH1	B_GLU_255	OE2	2.912
4Q9B	A_ARG_309	NH2	B_GLU_255	OE2	3.212
4Q9B	A_ARG_339	NH2	A_GLU_322	OE1	3.788
4Q9B	A_ARG_339	NH2	A_GLU_322	OE2	2.973
4Q9B	A_ARG_341	NH1	A_GLU_322	OE2	3.129
4Q9B	B_ARG_250	NH1	B_GLU_268	OE2	2.773
4Q9B	B_ARG_288	NH1	B_GLU_316	OE1	3.649
4Q9B	B_ARG_288	NH1	B_GLU_316	OE2	2.767
4Q9B	B_ARG_288	NH2	B_GLU_316	OE1	2.902
4Q9B	B_ARG_288	NH2	B_GLU_316	OE2	3.570
4Q9B	B_ARG_309	NH1	A_GLU_255	OE1	3.145
4Q9B	B_ARG_309	NH1	A_GLU_255	OE2	2.858
4Q9B	B_ARG_309	NH1	B_GLU_295	OE1	3.156
4Q9B	B_ARG_309	NH1	B_GLU_295	OE2	3.958
4Q9B	B_ARG_309	NH2	B_GLU_295	OE1	2.549
4Q9B	B_ARG_339	NH2	B_GLU_322	OE1	2.438
4Q9B	B_ARG_339	NH2	B_GLU_322	OE2	3.097
4Q9B	B_ARG_341	NH2	B_GLU_322	OE2	2.672
4Q9C	A_LYS_388	NZ	A_GLU_422	OE1	3.305
4Q9C	A_LYS_428	NZ	A_ASP_390	OD2	3.566
4QEX	A_LYS_17	NZ	A_GLU_71	OE1	3.725
4QEX	A_LYS_17	NZ	A_GLU_71	OE2	2.956
4QEX	A_ARG_18	NH1	A_ASP_39	OD1	2.342
4QEX	A_ARG_18	NH1	A_ASP_39	OD2	2.888
4QEX	A_ARG_18	NH2	A_ASP_39	OD1	3.858
4QEX	A_LYS_19	NZ	A_ASP_80	OD1	2.818
4QEX	A_LYS_19	NZ	A_ASP_80	OD2	3.469
4QEX	A_LYS_26	NZ	A_ASP_108	OD1	3.934
4QEX	A_ARG_40	NH1	A_ASP_97	OD2	2.989
4QEX	A_ARG_40	NH2	A_ASP_97	OD2	2.794
4QEX	A_ARG_40	NH2	A_GLU_182	OE1	3.072

4QEX	A_ARG_40	NH2	A_GLU_182	OE2	3.122
4QEX	A_ARG_41	NH1	A_ASP_108	OD2	2.767
4QEX	A_ARG_41	NH2	A_ASP_106	OD1	3.672
4QEX	A_ARG_41	NH2	A_ASP_106	OD2	2.658
4QEX	A_ARG_41	NH2	A_ASP_108	OD2	3.573
4QEX	A_LYS_61	NZ	A_GLU_146	OE2	3.762
4QEX	A_LYS_78	NZ	A_ASP_90	OD1	3.235
4QEX	A_ARG_140	NH1	A_GLU_117	OE2	3.439
4QEX	A_LYS_141	NZ	A_GLU_172	OE1	3.378
4QEX	A_HIS_159	NE2	A_GLU_158	OE2	3.794
4QEX	A_LYS_181	NZ	A_GLU_173	OE1	3.704
4QEX	A_LYS_181	NZ	A_GLU_173	OE2	3.359
4QEX	A_ARG_191	NH2	A_ASP_263	OD2	3.924
4QEX	A_ARG_194	NH2	A_GLU_190	OE2	3.371
4QEX	A_LYS_199	NZ	A_GLU_276	OE2	3.126
4QEX	A_LYS_230	NZ	A_ASP_274	OD1	3.711
4QEX	A_LYS_230	NZ	A_ASP_274	OD2	3.195
4QEX	A_LYS_284	NZ	A_ASP_309	OD2	3.762
4QEX	A_LYS_284	NZ	A_ASP_312	OD1	3.824
4QEX	A_LYS_284	NZ	A_ASP_312	OD2	2.849
4QEX	A_LYS_320	NZ	A_ASP_311	OD1	3.730
4QEX	A_LYS_333	NZ	A_GLU_331	OE1	2.647
4QEX	A_LYS_341	NZ	A_GLU_545	OE1	3.181
4QEX	A_LYS_341	NZ	A_GLU_545	OE2	2.966
4QEX	A_LYS_341	NZ	H_ASP_53	OD1	3.875
4QEX	A_ARG_348	NH1	A_ASP_405	OD2	3.055
4QEX	A_ARG_348	NH2	A_ASP_405	OD2	2.876
4QEX	A_ARG_348	NH2	A_GLU_488	OE1	3.045
4QEX	A_ARG_348	NH2	A_GLU_488	OE2	3.938
4QEX	A_ARG_349	NH2	A_ASP_414	OD1	3.531
4QEX	A_ARG_349	NH2	A_ASP_414	OD2	2.996
4QEX	A_LYS_384	NZ	A_GLU_306	OE1	3.997
4QEX	A_LYS_384	NZ	A_GLU_306	OE2	3.752
4QEX	A_ARG_385	NH2	A_ASP_324	OD1	3.155
4QEX	A_LYS_386	NZ	A_GLU_351	OE1	3.481
4QEX	A_LYS_386	NZ	A_GLU_351	OE2	3.992
4QEX	A_ARG_422	NH2	H_ASP_97	OD2	3.116
4QEX	A_LYS_423	NZ	A_ASP_358	OD1	3.415
4QEX	A_LYS_423	NZ	A_ASP_358	OD2	3.036
4QEX	A_LYS_427	NZ	A_ASP_362	OD1	2.843
4QEX	A_ARG_437	NH2	A_ASP_442	OD2	3.346
4QEX	A_LYS_443	NZ	A_ASP_447	OD1	3.941
4QEX	A_LYS_443	NZ	A_ASP_447	OD2	2.889
4QEX	A_ARG_484	NH1	A_ASP_408	OD2	3.149
4QEX	A_ARG_484	NH2	A_ASP_405	OD1	3.156
4QEX	A_ARG_484	NH2	A_ASP_405	OD2	3.109
4QEX	A_ARG_484	NH2	A_ASP_408	OD2	3.711
4QEX	A_LYS_497	NZ	A_GLU_582	OE1	2.757
4QEX	A_LYS_531	NZ	A_GLU_535	OE2	3.270
4QEX	A_LYS_532	NZ	A_GLU_535	OE1	3.348
4QEX	A_LYS_532	NZ	A_GLU_535	OE2	3.847
4QEX	A_LYS_573	NZ	A_GLU_394	OE2	3.110
4QEX	L_ARG_18	NH2	L_ASP_76	OD1	3.851
4QEX	L_ARG_24	NH2	L_ASP_70	OD2	3.377
4QEX	L_LYS_27	NZ	L_GLU_93	OE1	3.354
4QEX	L_ARG_39	NH1	L_ASP_81	OD1	3.904
4QEX	L_ARG_61	NH1	L_ASP_82	OD1	2.872
4QEX	L_ARG_61	NH1	L_ASP_82	OD2	2.775

4QEX	L_ARG_61	NH2	L_GLU_79	OE1	3.798
4QEX	L_ARG_61	NH2	L_ASP_82	OD1	2.840
4QEX	L_ARG_61	NH2	L_ASP_82	OD2	3.147
4QEX	L_LYS_149	NZ	L_GLU_154	OE1	3.545
4QEX	L_ARG_155	NH2	L_GLU_185	OE2	3.880
4QEX	L_HIS_189	ND1	L_ASP_151	OD2	3.464
4QEX	L_LYS_199	NZ	L_ASP_110	OD2	3.727
4QEX	H_LYS_38	NZ	H_ASP_86	OD1	3.545
4QEX	H_LYS_62	NZ	H_ASP_46	OD1	3.147
4QEX	H_LYS_62	NZ	H_ASP_46	OD2	3.315
4QEX	H_LYS_66	NZ	H_ASP_86	OD2	3.686
4QEX	H_ARG_82A	NH2	H_GLU_81	OE1	3.257
4QEX	B_LYS_17	NZ	B_GLU_71	OE1	3.723
4QEX	B_LYS_17	NZ	B_GLU_71	OE2	2.955
4QEX	B_ARG_18	NH1	B_ASP_39	OD1	2.348
4QEX	B_ARG_18	NH1	B_ASP_39	OD2	2.891
4QEX	B_ARG_18	NH2	B_ASP_39	OD1	3.859
4QEX	B_LYS_19	NZ	B_ASP_80	OD1	2.821
4QEX	B_LYS_19	NZ	B_ASP_80	OD2	3.471
4QEX	B_LYS_26	NZ	B_ASP_108	OD1	3.946
4QEX	B_ARG_40	NH1	B_ASP_97	OD2	2.987
4QEX	B_ARG_40	NH2	B_ASP_97	OD2	2.795
4QEX	B_ARG_40	NH2	B_GLU_182	OE1	3.067
4QEX	B_ARG_40	NH2	B_GLU_182	OE2	3.120
4QEX	B_ARG_41	NH1	B_ASP_108	OD2	2.740
4QEX	B_ARG_41	NH2	B_ASP_106	OD1	3.677
4QEX	B_ARG_41	NH2	B_ASP_106	OD2	2.651
4QEX	B_ARG_41	NH2	B_ASP_108	OD2	3.554
4QEX	B_LYS_61	NZ	B_GLU_146	OE2	3.752
4QEX	B_LYS_78	NZ	B_ASP_90	OD1	3.242
4QEX	B_LYS_125	NZ	B_GLU_130	OE1	3.909
4QEX	B_ARG_140	NH1	B_GLU_117	OE2	3.438
4QEX	B_LYS_141	NZ	B_GLU_172	OE1	3.375
4QEX	B_HIS_159	NE2	B_GLU_158	OE2	3.791
4QEX	B_LYS_181	NZ	B_GLU_173	OE1	3.691
4QEX	B_LYS_181	NZ	B_GLU_173	OE2	3.345
4QEX	B_ARG_191	NH2	B_ASP_263	OD2	3.920
4QEX	B_ARG_194	NH2	B_GLU_190	OE2	3.366
4QEX	B_LYS_199	NZ	B_GLU_276	OE2	3.126
4QEX	B_LYS_230	NZ	B_ASP_274	OD1	3.714
4QEX	B_LYS_230	NZ	B_ASP_274	OD2	3.188
4QEX	B_LYS_284	NZ	B_ASP_309	OD2	3.751
4QEX	B_LYS_284	NZ	B_ASP_312	OD1	3.816
4QEX	B_LYS_284	NZ	B_ASP_312	OD2	2.842
4QEX	B_LYS_320	NZ	B_ASP_311	OD1	3.720
4QEX	B_LYS_333	NZ	B_GLU_331	OE1	2.649
4QEX	B_LYS_341	NZ	B_GLU_545	OE1	3.179
4QEX	B_LYS_341	NZ	B_GLU_545	OE2	2.971
4QEX	B_ARG_348	NH1	B_ASP_405	OD2	3.038
4QEX	B_ARG_348	NH2	B_ASP_405	OD2	2.871
4QEX	B_ARG_348	NH2	B_GLU_488	OE1	3.051
4QEX	B_ARG_348	NH2	B_GLU_488	OE2	3.938
4QEX	B_ARG_349	NH2	B_ASP_414	OD1	3.521
4QEX	B_ARG_349	NH2	B_ASP_414	OD2	2.994
4QEX	B_LYS_384	NZ	B_GLU_306	OE2	3.763
4QEX	B_ARG_385	NH2	B_ASP_324	OD1	3.156
4QEX	B_LYS_386	NZ	B_GLU_351	OE1	3.485
4QEX	B_LYS_386	NZ	B_GLU_351	OE2	3.984

4QEX	B_LYS_423	NZ	B_ASP_358	OD1	3.425
4QEX	B_LYS_423	NZ	B_ASP_358	OD2	3.036
4QEX	B_LYS_427	NZ	B_ASP_362	OD1	2.827
4QEX	B_ARG_437	NH2	B_ASP_442	OD2	3.351
4QEX	B_LYS_443	NZ	B_ASP_447	OD1	3.938
4QEX	B_LYS_443	NZ	B_ASP_447	OD2	2.877
4QEX	B_ARG_484	NH1	B_ASP_408	OD2	3.150
4QEX	B_ARG_484	NH2	B_ASP_405	OD1	3.172
4QEX	B_ARG_484	NH2	B_ASP_405	OD2	3.124
4QEX	B_ARG_484	NH2	B_ASP_408	OD2	3.702
4QEX	B_LYS_497	NZ	B_GLU_582	OE1	2.759
4QEX	B_LYS_531	NZ	B_GLU_535	OE2	3.281
4QEX	B_LYS_532	NZ	B_GLU_535	OE1	3.369
4QEX	B_LYS_532	NZ	B_GLU_535	OE2	3.868
4QEX	B_LYS_573	NZ	B_GLU_394	OE2	3.119
4QEX	M_ARG_18	NH2	M_ASP_76	OD1	3.849
4QEX	M_ARG_24	NH2	M_ASP_70	OD2	3.380
4QEX	M_LYS_27	NZ	M_GLU_93	OE1	3.352
4QEX	M_ARG_39	NH1	M_ASP_81	OD1	3.900
4QEX	M_ARG_61	NH1	M_ASP_82	OD1	2.873
4QEX	M_ARG_61	NH1	M_ASP_82	OD2	2.791
4QEX	M_ARG_61	NH2	M_GLU_79	OE1	3.795
4QEX	M_ARG_61	NH2	M_ASP_82	OD1	2.843
4QEX	M_ARG_61	NH2	M_ASP_82	OD2	3.151
4QEX	M_LYS_149	NZ	M_GLU_154	OE1	3.545
4QEX	M_ARG_155	NH2	M_GLU_185	OE2	3.873
4QEX	M_HIS_189	ND1	M_ASP_151	OD2	3.467
4QEX	M_LYS_199	NZ	M_ASP_110	OD2	3.724
4QEX	L_LYS_38	NZ	L_ASP_86	OD1	3.550
4QEX	L_LYS_62	NZ	L_ASP_46	OD1	3.149
4QEX	L_LYS_62	NZ	L_ASP_46	OD2	3.316
4QEX	L_LYS_66	NZ	L_ASP_86	OD2	3.689
4QEX	L_ARG_82A	NH2	L_GLU_81	OE1	3.265
4QHU	L_LYS_30	NZ	L_ASP_29	OD1	3.579
4QHU	L_LYS_30	NZ	L_ASP_91	OD2	3.632
4QHU	L_ARG_60	NH2	L_GLU_80	OE2	3.111
4QHU	L_ARG_60	NH2	L_ASP_81	OD1	2.567
4QHU	L_ARG_60	NH2	L_ASP_81	OD2	3.488
4QHU	L_LYS_104	NZ	L_ASP_84	OD1	3.091
4QHU	L_LYS_104	NZ	L_ASP_84	OD2	3.639
4QHU	L_LYS_151	NZ	L_GLU_205	OE1	3.904
4QHU	L_LYS_151	NZ	L_GLU_205	OE2	3.118
4QHU	L_LYS_168	NZ	L_GLU_82	OE2	2.712
4QHU	L_ARG_191	NH2	L_ASP_153	OD1	3.474
4QHU	L_ARG_191	NH2	L_ASP_153	OD2	3.847
4QHU	H_ARG_38	NH1	H_ASP_90	OD1	2.949
4QHU	H_ARG_38	NH2	H_GLU_46	OE1	3.628
4QHU	H_ARG_38	NH2	H_GLU_46	OE2	3.083
4QHU	H_ARG_38	NH2	H_ASP_90	OD1	3.976
4QHU	H_LYS_65	NZ	H_ASP_62	OD1	2.679
4QHU	H_ARG_67	NH1	H_ASP_90	OD1	3.783
4QHU	H_ARG_67	NH1	H_ASP_90	OD2	2.761
4QHU	H_ARG_67	NH2	H_ASP_90	OD1	3.192
4QHU	H_ARG_67	NH2	H_ASP_90	OD2	3.606
4QHU	H_LYS_76	NZ	H_ASP_73	OD2	3.381
4QHU	H_ARG_98	NH1	H_ASP_103	OD1	3.756
4QHU	H_ARG_98	NH1	H_ASP_103	OD2	2.704
4QHU	H_LYS_208	NZ	H_ASP_210	OD1	3.995

4QHU	A_LYS_30	NZ	A_ASP_91	OD2	4.000
4QHU	A_ARG_60	NH1	A_GLU_80	OE2	3.278
4QHU	A_ARG_60	NH1	A_ASP_81	OD1	2.573
4QHU	A_ARG_60	NH1	A_ASP_81	OD2	3.449
4QHU	A_LYS_104	NZ	A_ASP_84	OD1	3.029
4QHU	A_LYS_104	NZ	A_ASP_84	OD2	3.813
4QHU	A_LYS_168	NZ	A_GLU_82	OE1	3.026
4QHU	A_HIS_190	ND1	A_ASP_153	OD2	2.727
4QHU	A_ARG_191	NH1	A_ASP_153	OD1	3.616
4QHU	A_ARG_191	NH2	A_ASP_153	OD1	3.771
4QHU	A_ARG_191	NH2	A_ASP_153	OD2	3.954
4QHU	B_ARG_38	NH1	B_ASP_90	OD1	2.780
4QHU	B_ARG_38	NH2	B_GLU_46	OE1	3.193
4QHU	B_ARG_38	NH2	B_GLU_46	OE2	3.721
4QHU	B_ARG_38	NH2	B_ASP_90	OD1	3.946
4QHU	B_LYS_65	NZ	B_ASP_62	OD1	3.086
4QHU	B_ARG_67	NH1	B_ASP_90	OD1	3.968
4QHU	B_ARG_67	NH1	B_ASP_90	OD2	2.779
4QHU	B_ARG_67	NH2	B_ASP_90	OD1	3.132
4QHU	B_ARG_67	NH2	B_ASP_90	OD2	3.380
4QHU	B_ARG_98	NH2	B_ASP_103	OD1	3.608
4QHU	B_ARG_98	NH2	B_ASP_103	OD2	2.836
4QHU	B_LYS_145	NZ	A_GLU_126	OE2	2.821
4QHU	B_LYS_212	NZ	B_GLU_214	OE2	3.019
4QHU	C_ARG_20	NH2	C_ASP_15	OD1	3.523
4QHU	C_HIS_29	ND1	D_GLU_113	OE1	3.672
4QHU	C_ARG_31	NH1	D_GLU_113	OE2	3.297
4QHU	C_ARG_31	NH2	D_GLU_113	OE1	3.241
4QHU	C_ARG_31	NH2	D_GLU_113	OE2	3.844
4QHU	C_ARG_39	NH1	L_ASP_52	OD1	3.835
4QHU	C_ARG_39	NH1	L_ASP_52	OD2	2.646
4QHU	C_ARG_46	NH1	C_ASP_42	OD1	3.319
4QHU	C_ARG_55	NH1	L_ASP_49	OD1	2.860
4QHU	C_ARG_55	NH1	L_ASP_49	OD2	3.543
4QHU	C_ARG_55	NH1	C_GLU_57	OE2	3.286
4QHU	C_ARG_55	NH2	C_GLU_57	OE2	2.950
4QHU	C_HIS_86	ND1	C_ASP_84	OD1	2.680
4QHU	C_ARG_100	NH1	C_ASP_58	OD2	2.953
4QHU	C_ARG_100	NH2	C_ASP_58	OD1	3.928
4QHU	C_ARG_100	NH2	C_ASP_58	OD2	3.080
4QHU	C_ARG_111	NH1	C_GLU_102	OE2	2.856
4QHU	D_ARG_46	NH1	D_ASP_42	OD1	3.904
4QHU	D_ARG_55	NH1	D_GLU_57	OE1	2.360
4QHU	D_ARG_55	NH2	D_GLU_57	OE1	3.394
4QHU	D_HIS_86	ND1	D_ASP_84	OD1	2.832
4QHU	D_ARG_100	NH1	D_ASP_58	OD1	3.905
4QHU	D_ARG_100	NH1	D_ASP_58	OD2	3.109
4QHU	D_ARG_100	NH2	D_ASP_58	OD2	3.081
4QHU	D_ARG_100	NH2	D_GLU_113	OE2	3.668
4QHU	D_LYS_114	NZ	D_GLU_95	OE2	2.739
4QTI	H_ARG_38	NH2	H_GLU_46	OE1	3.681
4QTI	H_ARG_38	NH2	H_GLU_46	OE2	2.663
4QTI	H_LYS_67	NZ	H_ASP_90	OD1	3.556
4QTI	H_LYS_67	NZ	H_ASP_90	OD2	2.827
4QTI	H_ARG_98	NH2	H_ASP_110	OD2	3.023
4QTI	H_LYS_217	NZ	L_GLU_123	OE2	2.684
4QTI	L_ARG_24	NH1	L_ASP_70	OD1	3.175
4QTI	L_ARG_24	NH1	L_ASP_70	OD2	2.707

4QTI	L_ARG_24	NH2	L_ASP_70	OD1	3.394
4QTI	L_ARG_24	NH2	L_ASP_70	OD2	3.619
4QTI	L_ARG_46	NH2	L_ASP_55	OD1	2.886
4QTI	L_ARG_46	NH2	L_ASP_55	OD2	3.715
4QTI	L_ARG_61	NH2	L_ASP_82	OD1	2.723
4QTI	L_ARG_61	NH2	L_ASP_82	OD2	3.112
4QTI	L_ARG_66	NH1	L_ASP_28	OD2	3.786
4QTI	L_LYS_103	NZ	L_GLU_105	OE1	2.889
4QTI	L_LYS_103	NZ	L_GLU_105	OE2	3.497
4QTI	L_LYS_147	NZ	L_GLU_154	OE1	3.641
4QTI	L_LYS_149	NZ	L_GLU_195	OE1	2.748
4QTI	L_ARG_188	NH2	L_ASP_184	OD1	3.219
4QTI	L_HIS_189	ND1	L_ASP_151	OD2	3.900
4QTI	L_LYS_199	NZ	L_ASP_110	OD2	3.524
4QTI	L_ARG_211	NH2	L_GLU_187	OE2	2.655
4QTI	U_ARG_2	NH1	U_GLU_16	OE1	3.772
4QTI	U_ARG_2	NH1	U_GLU_16	OE2	3.501
4QTI	U_ARG_25	NH2	U_GLU_42	OE2	3.368
4QTI	U_LYS_50	NZ	U_GLU_230	OE2	3.973
4QTI	U_ARG_53	NH1	U_ASP_254	OD2	3.882
4QTI	U_ARG_53	NH2	U_ASP_254	OD1	3.258
4QTI	U_ARG_58	NH2	H_ASP_103	OD2	2.819
4QTI	U_ARG_89	NH1	H_ASP_99	OD2	3.048
4QTI	U_ARG_91	NH1	H_ASP_99	OD1	2.759
4QTI	U_ARG_91	NH1	H_ASP_99	OD2	2.751
4QTI	U_ARG_91	NH2	H_ASP_99	OD2	3.786
4QTI	U_ARG_116	NH1	H_ASP_103	OD2	3.777
4QTI	U_ARG_116	NH2	H_ASP_103	OD1	3.889
4QTI	U_HIS_143	NE2	U_GLU_183	OE2	3.484
4QTI	U_LYS_175	NZ	U_GLU_94	OE2	2.662
4QTI	U_LYS_198	NZ	U_ASP_163	OD1	2.860
4QTI	U_LYS_198	NZ	U_ASP_163	OD2	3.382
4QTI	U_ARG_239	NH1	U_ASP_277	OD1	2.952
4QTI	U_ARG_239	NH1	U_ASP_277	OD2	3.438
4QTI	U_ARG_239	NH2	U_ASP_277	OD1	3.749
4QTI	U_ARG_239	NH2	U_ASP_277	OD2	2.737
4QTI	U_HIS_273	ND1	U_ASP_275	OD1	3.694
4QTI	U_HIS_273	ND1	U_ASP_275	OD2	3.712
4QXG	H_ARG_38	NH1	H_GLU_46	OE1	3.582
4QXG	H_ARG_38	NH1	H_GLU_46	OE2	3.109
4QXG	H_ARG_38	NH2	H_ASP_90	OD1	3.835
4QXG	H_LYS_87	NZ	H_ASP_90	OD1	2.584
4QXG	H_LYS_87	NZ	H_ASP_90	OD2	3.997
4QXG	H_ARG_98	NH2	H_ASP_100	OD2	3.302
4QXG	H_ARG_98	NH2	H_ASP_105	OD1	3.741
4QXG	H_ARG_98	NH2	H_ASP_105	OD2	2.750
4QXG	H_LYS_147	NZ	H_ASP_148	OD1	3.049
4QXG	H_LYS_147	NZ	H_ASP_148	OD2	3.141
4QXG	H_LYS_213	NZ	L_GLU_124	OE2	3.477
4QXG	L_ARG_24	NH2	L_ASP_71	OD2	3.349
4QXG	L_ARG_55	NH1	L_ASP_61	OD1	3.811
4QXG	L_ARG_55	NH2	L_ASP_61	OD1	3.150
4QXG	L_ARG_62	NH2	L_GLU_82	OE2	3.622
4QXG	L_ARG_62	NH2	L_ASP_83	OD1	2.986
4QXG	L_ARG_62	NH2	L_ASP_83	OD2	3.699
4QXG	L_LYS_150	NZ	L_GLU_196	OE1	2.605
4QXG	L_HIS_190	ND1	L_ASP_152	OD2	2.741
4QXG	L_LYS_191	NZ	L_GLU_214	OE1	3.615

4QXG	L_LYS_191	NZ	L_GLU_214	OE2	3.288
4R2G	E_LYS_121	NZ	E_GLU_429	OE2	2.858
4R2G	E_LYS_236	NZ	E_ASP_275	OD1	2.708
4R2G	E_HIS_249	NE2	E_GLU_482	OE1	3.748
4R2G	E_LYS_269	NZ	E_GLU_347	OE1	3.075
4R2G	E_ARG_298	NH1	E_GLU_381	OE1	3.375
4R2G	E_ARG_298	NH1	E_GLU_381	OE2	2.613
4R2G	E_LYS_348	NZ	E_GLU_351	OE1	3.563
4R2G	E_LYS_357	NZ	E_GLU_466	OE1	3.854
4R2G	E_ARG_456	NH1	E_GLU_466	OE1	3.060
4R2G	E_ARG_456	NH1	E_GLU_466	OE2	3.336
4R2G	E_ARG_469	NH2	E_ASP_457	OD2	2.761
4R2G	E_ARG_476	NH1	E_GLU_102	OE1	3.512
4R2G	E_ARG_476	NH1	E_GLU_102	OE2	3.993
4R2G	E_ARG_476	NH2	E_ASP_474	OD1	3.762
4R2G	E_ARG_476	NH2	E_ASP_474	OD2	3.245
4R2G	E_ARG_480	NH1	E_ASP_477	OD1	2.966
4R2G	F_LYS_8	NZ	F_GLU_119	OE1	2.961
4R2G	F_LYS_8	NZ	F_GLU_119	OE2	3.833
4R2G	F_LYS_29	NZ	E_ASP_279	OD2	2.979
4R2G	F_LYS_29	NZ	F_GLU_85	OE1	3.831
4R2G	F_ARG_54	NH1	F_ASP_78	OD1	3.678
4R2G	F_ARG_54	NH1	F_ASP_78	OD2	2.955
4R2G	F_ARG_54	NH2	F_ASP_78	OD1	3.395
4R2G	F_ARG_54	NH2	F_ASP_78	OD2	3.824
4R2G	F_ARG_58	NH1	F_GLU_13	OE1	3.679
4R2G	F_ARG_58	NH1	F_GLU_13	OE2	2.912
4R2G	F_ARG_58	NH2	F_GLU_13	OE2	3.429
4R2G	F_ARG_59	NH1	E_ASP_368	OD1	2.950
4R2G	F_ARG_59	NH1	E_ASP_368	OD2	2.577
4R2G	F_ARG_59	NH2	E_ASP_368	OD2	3.352
4R2G	F_LYS_90	NZ	F_GLU_85	OE2	3.878
4R2G	P_ARG_31	NH2	P_ASP_66A	OD1	3.703
4R2G	P_ARG_61	NH1	P_GLU_79	OE1	3.610
4R2G	P_ARG_61	NH1	P_ASP_82	OD1	2.724
4R2G	P_ARG_61	NH1	P_ASP_82	OD2	2.827
4R2G	P_ARG_61	NH2	P_ASP_82	OD2	2.747
4R2G	P_ARG_103	NH2	P_ASP_85	OD1	3.554
4R2G	P_ARG_103	NH2	P_ASP_85	OD2	3.072
4R2G	P_LYS_167	NZ	P_GLU_83	OE2	2.375
4R2G	Q_ARG_38	NH1	Q_ASP_86	OD1	2.531
4R2G	Q_ARG_38	NH2	Q_GLU_46	OE2	3.197
4R2G	Q_ARG_38	NH2	Q_ASP_86	OD1	3.417
4R2G	Q_ARG_66	NH1	Q_ASP_86	OD2	3.138
4R2G	Q_ARG_66	NH2	Q_ASP_86	OD1	3.109
4R2G	Q_ARG_66	NH2	Q_ASP_86	OD2	3.353
4R2G	Q_ARG_71	NH2	Q_GLU_55	OE1	2.657
4R2G	Q_ARG_96	NH1	Q_ASP_101	OD2	2.840
4R2G	Q_ARG_96	NH2	Q_ASP_101	OD1	3.076
4R2G	Q_ARG_96	NH2	Q_ASP_101	OD2	2.587
4R2G	Q_ARG_100	NH2	P_ASP_66A	OD2	2.815
4R2G	Q_LYS_227	NZ	P_GLU_124	OE2	3.083
4R2G	B_LYS_29	NZ	O_ASP_279	OD2	3.448
4R2G	B_ARG_54	NH1	B_ASP_78	OD1	2.279
4R2G	B_ARG_54	NH1	B_ASP_78	OD2	2.720
4R2G	B_ARG_54	NH2	B_ASP_78	OD1	3.403
4R2G	B_ARG_54	NH2	B_ASP_78	OD2	1.961
4R2G	B_ARG_58	NH1	B_GLU_13	OE2	3.274

4R2G	B_ARG_58	NH2	B_GLU_13	OE2	3.415
4R2G	B_ARG_59	NH1	O_ASP_368	OD1	2.838
4R2G	B_ARG_59	NH1	O_ASP_368	OD2	3.428
4R2G	B_ARG_59	NH2	O_ASP_368	OD1	3.471
4R2G	B_ARG_59	NH2	O_ASP_368	OD2	2.776
4R2G	B_ARG_134	NH1	B_ASP_153	OD1	3.163
4R2G	B_ARG_134	NH2	B_ASP_153	OD1	3.693
4R2G	C_ARG_31	NH1	C_ASP_66A	OD1	3.082
4R2G	C_ARG_54	NH1	C_GLU_60	OE2	3.362
4R2G	C_ARG_61	NH1	C_GLU_79	OE1	3.445
4R2G	C_ARG_61	NH1	C_ASP_82	OD1	3.443
4R2G	C_ARG_61	NH1	C_ASP_82	OD2	2.957
4R2G	C_ARG_61	NH2	C_ASP_82	OD2	3.224
4R2G	C_ARG_103	NH1	C_ASP_85	OD1	3.613
4R2G	C_ARG_103	NH2	C_ASP_85	OD2	3.803
4R2G	C_LYS_167	NZ	C_GLU_83	OE2	3.124
4R2G	C_HIS_189	ND1	C_ASP_152	OD1	3.916
4R2G	C_HIS_189	ND1	C_ASP_152	OD2	2.449
4R2G	D_ARG_13	NH2	D_GLU_16	OE1	3.234
4R2G	D_ARG_13	NH2	D_GLU_16	OE2	2.237
4R2G	D_ARG_38	NH1	D_ASP_86	OD1	2.671
4R2G	D_ARG_38	NH2	D_GLU_46	OE1	3.784
4R2G	D_ARG_38	NH2	D_GLU_46	OE2	3.013
4R2G	D_ARG_38	NH2	D_ASP_86	OD1	3.766
4R2G	D_ARG_66	NH1	D_ASP_86	OD1	3.577
4R2G	D_ARG_66	NH1	D_ASP_86	OD2	3.981
4R2G	D_ARG_66	NH2	D_ASP_86	OD1	3.085
4R2G	D_ARG_66	NH2	D_ASP_86	OD2	3.712
4R2G	D_ARG_71	NH2	D_GLU_55	OE1	2.726
4R2G	D_ARG_71	NH2	D_GLU_55	OE2	3.442
4R2G	D_ARG_96	NH1	D_ASP_101	OD2	3.369
4R2G	D_ARG_100	NH2	C_ASP_66A	OD2	3.131
4R2G	D_LYS_227	NZ	C_GLU_124	OE1	3.473
4R2G	D_LYS_227	NZ	C_GLU_124	OE2	3.405
4R2G	H_LYS_8	NZ	H_GLU_119	OE1	2.920
4R2G	H_LYS_8	NZ	H_GLU_119	OE2	3.405
4R2G	H_LYS_29	NZ	H_GLU_85	OE1	3.621
4R2G	H_LYS_29	NZ	H_GLU_85	OE2	3.077
4R2G	H_LYS_29	NZ	K_ASP_279	OD1	2.934
4R2G	H_LYS_46	NZ	H_ASP_56	OD2	3.403
4R2G	H_ARG_54	NH1	H_ASP_78	OD1	3.987
4R2G	H_ARG_54	NH1	H_ASP_78	OD2	2.782
4R2G	H_ARG_54	NH2	H_ASP_78	OD1	2.816
4R2G	H_ARG_54	NH2	H_ASP_78	OD2	3.143
4R2G	H_ARG_59	NH1	K_ASP_368	OD1	2.502
4R2G	H_ARG_59	NH1	K_ASP_368	OD2	3.259
4R2G	H_LYS_90	NZ	H_GLU_85	OE2	3.434
4R2G	H_LYS_171	NZ	H_GLU_169	OE1	3.154
4R2G	I_ARG_31	NH1	I_ASP_66A	OD1	3.172
4R2G	I_ARG_61	NH1	I_ASP_82	OD1	2.991
4R2G	I_ARG_61	NH1	I_ASP_82	OD2	3.035
4R2G	I_ARG_61	NH2	I_ASP_82	OD2	2.782
4R2G	I_ARG_103	NH1	I_ASP_85	OD1	2.492
4R2G	I_ARG_103	NH1	I_ASP_85	OD2	3.056
4R2G	I_ARG_103	NH2	I_ASP_85	OD1	3.464
4R2G	I_ARG_103	NH2	I_ASP_85	OD2	3.445
4R2G	I_LYS_167	NZ	I_GLU_83	OE1	3.520
4R2G	I_LYS_167	NZ	I_GLU_83	OE2	3.546

4R2G	L_HIS_189	ND1	L_ASP_152	OD2	3.243
4R2G	J_ARG_38	NH1	J_ASP_86	OD1	2.814
4R2G	J_ARG_38	NH2	J_GLU_46	OE1	3.964
4R2G	J_ARG_38	NH2	J_GLU_46	OE2	3.167
4R2G	J_ARG_38	NH2	J_ASP_86	OD1	3.659
4R2G	J_ARG_66	NH1	J_ASP_86	OD1	3.625
4R2G	J_ARG_66	NH1	J_ASP_86	OD2	3.378
4R2G	J_ARG_66	NH2	J_ASP_86	OD1	2.765
4R2G	J_ARG_66	NH2	J_ASP_86	OD2	3.353
4R2G	J_ARG_71	NH1	J_GLU_55	OE1	3.851
4R2G	J_ARG_96	NH2	J_ASP_101	OD1	3.956
4R2G	J_ARG_96	NH2	J_ASP_101	OD2	3.793
4R2G	J_ARG_100	NH2	L_ASP_66A	OD2	3.189
4R2G	J_LYS_161	NZ	L_GLU_125	OE2	3.537
4R2G	L_LYS_8	NZ	L_GLU_119	OE1	3.207
4R2G	L_LYS_29	NZ	L_GLU_85	OE2	3.720
4R2G	L_LYS_29	NZ	A_ASP_279	OD1	3.450
4R2G	L_ARG_54	NH1	L_ASP_78	OD1	3.725
4R2G	L_ARG_54	NH1	L_ASP_78	OD2	2.856
4R2G	L_ARG_54	NH2	L_ASP_78	OD1	3.320
4R2G	L_ARG_54	NH2	L_ASP_78	OD2	3.657
4R2G	L_ARG_59	NH1	A_ASP_368	OD1	2.642
4R2G	L_ARG_59	NH1	A_ASP_368	OD2	2.825
4R2G	L_ARG_59	NH2	A_ASP_368	OD1	3.793
4R2G	L_ARG_59	NH2	A_ASP_368	OD2	2.422
4R2G	L_LYS_90	NZ	L_GLU_85	OE1	3.363
4R2G	M_ARG_31	NH1	M_ASP_66A	OD1	2.301
4R2G	M_ARG_31	NH2	M_ASP_66A	OD1	3.968
4R2G	M_ARG_61	NH1	M_GLU_79	OE1	3.516
4R2G	M_ARG_61	NH1	M_ASP_82	OD1	3.186
4R2G	M_ARG_61	NH1	M_ASP_82	OD2	3.220
4R2G	M_ARG_61	NH2	M_ASP_82	OD1	3.607
4R2G	M_ARG_61	NH2	M_ASP_82	OD2	2.287
4R2G	M_ARG_103	NH2	M_ASP_85	OD1	3.750
4R2G	M_ARG_103	NH2	M_ASP_85	OD2	2.638
4R2G	M_LYS_167	NZ	M_GLU_83	OE2	3.138
4R2G	M_HIS_189	ND1	M_ASP_152	OD2	3.175
4R2G	M_LYS_190	NZ	M_ASP_152	OD1	3.703
4R2G	M_LYS_190	NZ	M_ASP_152	OD2	3.996
4R2G	N_ARG_38	NH1	N_ASP_86	OD1	2.735
4R2G	N_ARG_38	NH2	N_GLU_46	OE2	2.998
4R2G	N_ARG_38	NH2	N_ASP_86	OD1	3.645
4R2G	N_ARG_66	NH1	N_ASP_86	OD1	3.424
4R2G	N_ARG_66	NH1	N_ASP_86	OD2	3.369
4R2G	N_ARG_66	NH2	N_ASP_86	OD1	3.057
4R2G	N_ARG_66	NH2	N_ASP_86	OD2	3.652
4R2G	N_ARG_71	NH2	N_GLU_55	OE1	3.590
4R2G	N_ARG_71	NH2	N_GLU_55	OE2	2.787
4R2G	N_ARG_96	NH2	N_ASP_101	OD2	3.284
4R2G	N_ARG_100	NH2	M_ASP_66A	OD2	3.592
4R2G	N_LYS_161	NZ	M_GLU_125	OE2	2.706
4R2G	N_LYS_228	NZ	N_GLU_230	OE2	3.127
4R2G	O_LYS_121	NZ	O_ASP_113	OD1	3.734
4R2G	O_LYS_121	NZ	O_GLU_429	OE2	2.953
4R2G	O_LYS_231	NZ	O_GLU_267	OE1	3.348
4R2G	O_LYS_236	NZ	O_ASP_275	OD1	3.482
4R2G	O_HIS_249	NE2	O_GLU_482	OE1	3.152
4R2G	O_LYS_282	NZ	O_ASP_275	OD2	3.470

4R2G	O_ARG_298	NH1	O_GLU_381	OE1	3.809
4R2G	O_ARG_327	NH1	D_GLU_100I	OE2	3.858
4R2G	O_LYS_348	NZ	O_GLU_351	OE1	3.344
4R2G	O_LYS_348	NZ	O_GLU_351	OE2	3.244
4R2G	O_LYS_357	NZ	O_GLU_466	OE1	3.349
4R2G	O_LYS_400	NZ	O_ASP_397	OD2	3.952
4R2G	O_ARG_456	NH2	O_GLU_466	OE2	3.589
4R2G	O_ARG_469	NH2	O_ASP_457	OD1	3.913
4R2G	O_ARG_469	NH2	O_ASP_457	OD2	2.731
4R2G	O_ARG_476	NH1	O_ASP_474	OD1	3.974
4R2G	O_ARG_476	NH2	O_ASP_474	OD1	3.817
4R2G	O_ARG_476	NH2	O_ASP_474	OD2	3.016
4R2G	O_ARG_480	NH1	O_ASP_477	OD1	3.400
4R2G	A_LYS_121	NZ	A_ASP_113	OD1	3.373
4R2G	A_LYS_236	NZ	A_ASP_275	OD1	3.935
4R2G	A_LYS_236	NZ	A_ASP_275	OD2	3.895
4R2G	A_ARG_298	NH2	A_GLU_381	OE2	3.354
4R2G	A_ARG_327	NH1	N_GLU_100I	OE1	3.235
4R2G	A_LYS_348	NZ	A_GLU_351	OE1	3.114
4R2G	A_LYS_348	NZ	A_GLU_351	OE2	3.018
4R2G	A_LYS_357	NZ	A_GLU_466	OE1	3.762
4R2G	A_ARG_456	NH2	A_GLU_466	OE1	3.604
4R2G	A_ARG_456	NH2	A_GLU_466	OE2	3.481
4R2G	A_ARG_469	NH2	A_ASP_457	OD2	3.008
4R2G	A_ARG_476	NH2	A_ASP_474	OD2	3.246
4R2G	A_ARG_480	NH1	A_ASP_477	OD1	3.318
4R2G	K_LYS_121	NZ	K_GLU_429	OE2	2.599
4R2G	K_LYS_236	NZ	K_ASP_275	OD1	3.419
4R2G	K_HIS_249	NE2	K_GLU_482	OE1	3.520
4R2G	K_ARG_298	NH1	K_GLU_381	OE2	3.970
4R2G	K_ARG_298	NH2	K_GLU_381	OE2	3.778
4R2G	K_LYS_348	NZ	K_GLU_351	OE1	3.371
4R2G	K_LYS_348	NZ	K_GLU_351	OE2	3.265
4R2G	K_ARG_350	NH2	K_ASP_397	OD1	3.693
4R2G	K_LYS_357	NZ	K_GLU_466	OE2	3.015
4R2G	K_ARG_469	NH2	K_ASP_457	OD2	3.592
4R2G	K_ARG_476	NH1	K_ASP_474	OD2	3.916
4R2G	K_ARG_476	NH2	K_ASP_474	OD2	3.188
4R2G	K_ARG_480	NH1	K_ASP_477	OD1	2.647
4R2G	K_LYS_487	NZ	K_ASP_92	OD1	3.177
4R4H	A_HIS_66	ND1	A_GLU_64	OE1	3.252
4R4H	A_LYS_207	NZ	A_GLU_380	OE1	3.742
4R4H	A_LYS_207	NZ	A_GLU_380	OE2	3.215
4R4H	A_HIS_249	NE2	A_GLU_482	OE1	2.873
4R4H	A_LYS_348	NZ	A_ASP_269	OD2	3.101
4R4H	A_LYS_348	NZ	A_GLU_351	OE1	3.859
4R4H	A_LYS_356	NZ	A_GLU_466	OE2	2.887
4R4H	A_ARG_455	NH1	A_GLU_466	OE1	3.185
4R4H	A_ARG_455	NH1	A_GLU_466	OE2	3.399
4R4H	A_ARG_469	NH2	A_ASP_456	OD2	3.413
4R4H	A_ARG_476	NH1	A_ASP_474	OD1	3.458
4R4H	A_ARG_480	NH1	A_ASP_477	OD1	2.787
4R4H	A_LYS_487	NZ	A_GLU_47	OE2	3.588
4R4H	A_LYS_487	NZ	A_GLU_91	OE2	2.837
4R4H	B_LYS_7	NZ	B_ASP_10	OD2	3.666
4R4H	B_LYS_29	NZ	A_ASP_279	OD1	2.795
4R4H	B_LYS_29	NZ	B_GLU_85	OE1	3.423
4R4H	B_LYS_29	NZ	B_GLU_85	OE2	3.572

4R4H	B_ARG_54	NH1	B_ASP_78	OD2	2.980
4R4H	B_ARG_54	NH2	B_ASP_78	OD1	3.209
4R4H	B_ARG_54	NH2	B_ASP_78	OD2	3.205
4R4H	B_ARG_58	NH1	B_GLU_13	OE1	3.001
4R4H	B_ARG_58	NH1	B_GLU_13	OE2	3.359
4R4H	B_ARG_58	NH2	B_GLU_13	OE2	3.123
4R4H	B_ARG_59	NH1	A_ASP_367	OD1	3.294
4R4H	B_ARG_59	NH1	A_ASP_367	OD2	3.409
4R4H	B_ARG_59	NH2	A_ASP_367	OD2	3.834
4R4H	B_LYS_171	NZ	B_GLU_169	OE1	3.963
4R4H	B_LYS_171	NZ	B_GLU_169	OE2	3.179
4R4H	L_ARG_61	NH2	L_GLU_81	OE2	2.783
4R4H	L_ARG_61	NH2	L_ASP_82	OD1	3.470
4R4H	L_LYS_	NZ	L_GLU_	OE1	2.933
4R4H	L_HIS_	ND1	L_ASP_	OD2	2.805
4R4H	L_HIS_	NE2	L_ASP_	OD1	3.352
4R4H	H_HIS_32	ND1	H_GLU_27	OE2	3.036
4R4H	H_HIS_32	NE2	H_GLU_27	OE2	3.485
4R4H	H_ARG_38	NH1	H_ASP_89	OD1	3.491
4R4H	H_ARG_38	NH2	H_GLU_46	OE1	3.502
4R4H	H_ARG_38	NH2	H_GLU_46	OE2	3.452
4R4H	H_LYS_52	NZ	A_ASP_78	OD1	3.615
4R4H	H_ARG_66	NH1	H_ASP_89	OD2	3.497
4R4H	H_ARG_66	NH2	H_ASP_89	OD1	3.408
4R4H	H_ARG_66	NH2	H_ASP_89	OD2	3.604
4R4H	H_LYS_75	NZ	H_ASP_72	OD2	3.924
4R4H	H_ARG_97	NH1	H_GLU_27	OE1	2.972
4R4H	H_ARG_97	NH1	H_GLU_27	OE2	2.769
4R4H	H_ARG_98	NH1	H_GLU_50	OE1	3.064
4R4H	H_ARG_98	NH1	H_GLU_50	OE2	3.007
4R4H	H_LYS_	NZ	H_ASP_	OD1	2.850
4R4H	H_LYS_	NZ	H_ASP_	OD2	3.439
4R4H	H_LYS_	NZ	H_GLU_	OE2	3.585
4R4H	H_LYS_	NZ	L_ASP_	OD2	3.470
4R7D	A_ARG_39	NH1	A_ASP_90	OD1	2.757
4R7D	A_ARG_39	NH2	A_GLU_47	OE1	3.609
4R7D	A_ARG_39	NH2	A_GLU_47	OE2	3.143
4R7D	A_ARG_39	NH2	A_ASP_90	OD1	3.533
4R7D	A_LYS_65	NZ	A_ASP_59	OD1	3.382
4R7D	A_ARG_67	NH1	A_ASP_90	OD2	3.363
4R7D	A_ARG_67	NH2	A_ASP_90	OD1	3.104
4R7D	A_ARG_67	NH2	A_ASP_90	OD2	3.445
4R7D	A_LYS_76	NZ	A_ASP_73	OD2	3.850
4R7D	A_LYS_148	NZ	A_ASP_149	OD1	3.326
4R7D	A_LYS_148	NZ	A_ASP_149	OD2	3.734
4R7D	A_LYS_214	NZ	B_GLU_123	OE1	3.736
4R7D	B_ARG_61	NH1	B_GLU_81	OE1	3.280
4R7D	B_ARG_61	NH1	B_ASP_82	OD1	2.669
4R7D	B_ARG_61	NH1	B_ASP_82	OD2	3.082
4R7D	B_ARG_61	NH2	B_GLU_81	OE1	3.146
4R7D	B_LYS_107	NZ	D_ASP_9	OD2	3.947
4R7D	B_LYS_126	NZ	B_ASP_122	OD1	2.338
4R7D	B_ARG_142	NH1	B_GLU_143	OE1	3.636
4R7D	B_ARG_142	NH2	B_GLU_105	OE1	3.989
4R7D	B_LYS_149	NZ	B_GLU_195	OE1	3.373
4R7D	B_LYS_149	NZ	B_GLU_195	OE2	3.135
4R7D	B_HIS_189	ND1	B_ASP_151	OD2	2.870
4R7D	C_ARG_39	NH1	C_ASP_90	OD1	2.627

4R7D	C_ARG_39	NH2	C_GLU_47	OE2	3.405
4R7D	C_ARG_39	NH2	C_ASP_90	OD1	3.918
4R7D	C_ARG_67	NH1	C_ASP_90	OD1	3.705
4R7D	C_ARG_67	NH1	C_ASP_90	OD2	3.301
4R7D	C_ARG_67	NH2	C_ASP_90	OD1	3.685
4R7D	C_LYS_99	NZ	C_ASP_103	OD2	3.216
4R7D	C_LYS_148	NZ	C_ASP_149	OD1	3.368
4R7D	C_LYS_211	NZ	C_ASP_213	OD1	2.945
4R7D	D_LYS_18	NZ	B_ASP_70	OD2	3.792
4R7D	D_HIS_32	NE2	D_ASP_31	OD1	3.817
4R7D	D_ARG_61	NH2	D_ASP_82	OD1	2.539
4R7D	D_ARG_61	NH2	D_ASP_82	OD2	3.670
4R7D	D_LYS_103	NZ	D_GLU_165	OE1	3.985
4R7D	D_LYS_107	NZ	B_ASP_9	OD2	3.503
4R7D	D_HIS_189	ND1	D_ASP_151	OD2	2.473
4R7D	E_ARG_39	NH1	E_ASP_90	OD1	2.896
4R7D	E_ARG_39	NH2	E_GLU_47	OE1	3.759
4R7D	E_ARG_39	NH2	E_GLU_47	OE2	3.092
4R7D	E_ARG_67	NH1	E_ASP_90	OD1	3.553
4R7D	E_ARG_67	NH1	E_ASP_90	OD2	3.603
4R7D	E_ARG_67	NH2	E_ASP_90	OD1	3.329
4R7D	E_ARG_67	NH2	E_ASP_90	OD2	3.799
4R7D	E_LYS_76	NZ	E_ASP_73	OD2	3.684
4R7D	E_LYS_148	NZ	E_ASP_149	OD2	2.850
4R7D	E_LYS_214	NZ	F_GLU_123	OE1	3.862
4R7D	E_LYS_214	NZ	F_GLU_123	OE2	3.571
4R7D	E_ARG_215	NH1	E_GLU_217	OE1	3.936
4R7D	E_ARG_215	NH1	E_GLU_217	OE2	3.249
4R7D	E_ARG_215	NH2	E_GLU_217	OE1	2.728
4R7D	E_ARG_215	NH2	E_GLU_217	OE2	3.501
4R7D	F_LYS_16	NZ	F_GLU_79	OE2	3.230
4R7D	F_HIS_32	NE2	F_ASP_31	OD1	3.921
4R7D	F_ARG_61	NH2	F_ASP_82	OD1	2.326
4R7D	F_ARG_61	NH2	F_ASP_82	OD2	2.732
4R7D	F_LYS_103	NZ	F_GLU_165	OE1	3.918
4R7D	F_LYS_103	NZ	F_GLU_165	OE2	3.931
4R7D	F_LYS_149	NZ	F_GLU_195	OE1	3.595
4R7D	F_LYS_149	NZ	F_GLU_195	OE2	3.164
4R7D	F_LYS_169	NZ	F_GLU_81	OE2	3.685
4R7D	G_ARG_39	NH1	G_ASP_90	OD1	2.853
4R7D	G_ARG_39	NH2	G_GLU_47	OE2	2.958
4R7D	G_ARG_39	NH2	G_ASP_90	OD1	3.467
4R7D	G_LYS_65	NZ	G_ASP_59	OD1	3.423
4R7D	G_ARG_67	NH1	G_ASP_90	OD1	3.986
4R7D	G_ARG_67	NH1	G_ASP_90	OD2	3.243
4R7D	G_ARG_67	NH2	G_ASP_90	OD1	2.698
4R7D	G_ARG_67	NH2	G_ASP_90	OD2	3.350
4R7D	G_LYS_99	NZ	G_ASP_103	OD2	3.638
4R7D	G_LYS_148	NZ	G_ASP_149	OD2	2.977
4R7D	H_HIS_32	NE2	H_ASP_31	OD1	3.837
4R7D	H_ARG_61	NH1	H_GLU_79	OE1	3.684
4R7D	H_ARG_61	NH2	H_GLU_81	OE1	3.325
4R7D	H_ARG_61	NH2	H_ASP_82	OD1	2.892
4R7D	H_ARG_61	NH2	H_ASP_82	OD2	3.435
4R7D	H_LYS_126	NZ	H_ASP_122	OD2	3.954
4R7D	H_ARG_142	NH1	H_GLU_143	OE1	3.953
4R7D	H_ARG_142	NH2	H_GLU_105	OE2	3.620
4R7D	H_LYS_149	NZ	H_GLU_195	OE2	2.396

4R7D	H_LYS_183	NZ	H_GLU_187	OE2	3.853
4R7D	H_LYS_188	NZ	H_ASP_185	OD1	3.959
4R7D	H_HIS_189	ND1	H_ASP_151	OD2	2.743
4R7D	L_ARG_39	NH1	L_ASP_90	OD1	2.779
4R7D	L_ARG_39	NH2	L_GLU_47	OE2	3.308
4R7D	L_ARG_39	NH2	L_ASP_90	OD1	3.305
4R7D	L_LYS_65	NZ	L_ASP_59	OD1	3.650
4R7D	L_ARG_67	NH1	L_ASP_90	OD2	3.228
4R7D	L_ARG_67	NH2	L_ASP_90	OD1	2.929
4R7D	L_ARG_67	NH2	L_ASP_90	OD2	3.207
4R7D	L_HIS_169	NE2	J_ASP_167	OD1	3.970
4R7D	L_LYS_211	NZ	L_ASP_213	OD1	3.549
4R7D	J_LYS_16	NZ	J_GLU_79	OE2	3.737
4R7D	J_LYS_18	NZ	N_ASP_70	OD1	3.913
4R7D	J_ARG_24	NH2	N_GLU_17	OE1	3.275
4R7D	J_ARG_24	NH2	N_GLU_17	OE2	2.135
4R7D	J_ARG_61	NH1	J_GLU_79	OE1	3.344
4R7D	J_ARG_61	NH1	J_GLU_79	OE2	3.871
4R7D	J_ARG_61	NH2	J_GLU_81	OE1	3.710
4R7D	J_ARG_61	NH2	J_ASP_82	OD1	3.792
4R7D	J_HIS_189	ND1	J_ASP_151	OD2	3.674
4R7D	K_ARG_39	NH1	K_ASP_90	OD1	3.019
4R7D	K_ARG_39	NH2	K_GLU_47	OE1	3.928
4R7D	K_ARG_39	NH2	K_GLU_47	OE2	3.206
4R7D	K_ARG_39	NH2	K_ASP_90	OD1	3.749
4R7D	K_ARG_67	NH1	K_ASP_90	OD1	3.223
4R7D	K_ARG_67	NH1	K_ASP_90	OD2	3.237
4R7D	K_ARG_67	NH2	K_ASP_90	OD1	3.233
4R7D	K_LYS_76	NZ	K_ASP_73	OD2	3.794
4R7D	K_LYS_99	NZ	K_ASP_103	OD1	2.821
4R7D	K_LYS_148	NZ	K_ASP_149	OD2	3.160
4R7D	K_HIS_169	NE2	L_ASP_167	OD2	3.666
4R7D	K_LYS_214	NZ	L_GLU_123	OE1	3.074
4R7D	L_HIS_32	NE2	L_ASP_31	OD1	3.658
4R7D	L_LYS_49	NZ	K_ASP_100	OD2	3.591
4R7D	L_ARG_61	NH2	L_GLU_79	OE1	3.885
4R7D	L_ARG_61	NH2	L_GLU_79	OE2	3.873
4R7D	L_LYS_149	NZ	L_GLU_195	OE1	3.728
4R7D	L_LYS_149	NZ	L_GLU_195	OE2	3.660
4R7D	L_LYS_188	NZ	L_ASP_185	OD1	3.757
4R7D	L_HIS_189	ND1	L_ASP_151	OD2	2.882
4R7D	M_ARG_39	NH1	M_ASP_90	OD1	2.741
4R7D	M_ARG_39	NH2	M_GLU_47	OE2	3.151
4R7D	M_ARG_39	NH2	M_ASP_90	OD1	3.559
4R7D	M_LYS_65	NZ	M_ASP_59	OD1	3.528
4R7D	M_ARG_67	NH1	M_ASP_90	OD2	3.446
4R7D	M_ARG_67	NH2	M_ASP_90	OD1	3.853
4R7D	M_LYS_76	NZ	M_ASP_73	OD2	3.604
4R7D	M_LYS_99	NZ	M_ASP_103	OD2	2.528
4R7D	M_LYS_148	NZ	M_ASP_149	OD1	3.371
4R7D	M_LYS_211	NZ	M_ASP_213	OD1	3.991
4R7D	M_LYS_214	NZ	N_GLU_123	OE1	3.058
4R7D	M_LYS_214	NZ	N_GLU_123	OE2	2.866
4R7D	M_ARG_215	NH2	M_GLU_217	OE1	3.754
4R7D	N_ARG_61	NH1	N_GLU_79	OE1	3.461
4R7D	N_LYS_103	NZ	N_GLU_165	OE1	3.691
4R7D	N_LYS_107	NZ	J_ASP_9	OD2	3.244
4R7D	N_LYS_149	NZ	N_GLU_195	OE1	3.733

4R7D	N_LYS_149	NZ	N_GLU_195	OE2	3.015
4R7D	N_HIS_189	ND1	N_ASP_151	OD2	2.626
4R7D	O_ARG_39	NH1	O_ASP_90	OD1	2.621
4R7D	O_ARG_39	NH2	O_GLU_47	OE2	2.902
4R7D	O_ARG_39	NH2	O_ASP_90	OD1	3.952
4R7D	O_ARG_67	NH1	O_ASP_90	OD2	3.648
4R7D	O_ARG_67	NH2	O_ASP_90	OD1	2.490
4R7D	O_ARG_67	NH2	O_ASP_90	OD2	2.748
4R7D	O_LYS_76	NZ	O_ASP_73	OD2	3.837
4R7D	O_LYS_214	NZ	P_GLU_123	OE1	2.454
4R7D	O_LYS_214	NZ	P_GLU_123	OE2	3.167
4R7D	O_ARG_215	NH1	O_GLU_217	OE1	2.819
4R7D	O_ARG_215	NH1	O_GLU_217	OE2	2.975
4R7D	O_ARG_215	NH2	O_GLU_217	OE1	3.432
4R7D	P_LYS_16	NZ	P_GLU_79	OE2	3.343
4R7D	P_ARG_61	NH2	P_ASP_82	OD1	2.934
4R7D	P_ARG_61	NH2	P_ASP_82	OD2	3.314
4R7D	P_ARG_142	NH1	P_GLU_143	OE1	3.551
4R7D	P_ARG_142	NH2	P_GLU_105	OE1	3.275
4R7D	P_ARG_142	NH2	P_GLU_105	OE2	3.523
4R7D	P_LYS_149	NZ	P_GLU_195	OE1	3.907
4R7D	P_LYS_149	NZ	P_GLU_195	OE2	2.589
4R7D	P_HIS_189	ND1	P_ASP_151	OD2	3.283
4R7N	A_ARG_39	NH1	A_ASP_90	OD1	2.825
4R7N	A_ARG_39	NH2	A_GLU_47	OE2	3.023
4R7N	A_ARG_39	NH2	A_ASP_90	OD1	3.603
4R7N	A_ARG_67	NH1	A_ASP_90	OD1	3.650
4R7N	A_ARG_67	NH1	A_ASP_90	OD2	2.898
4R7N	A_ARG_67	NH2	A_ASP_90	OD1	3.091
4R7N	A_ARG_67	NH2	A_ASP_90	OD2	3.794
4R7N	A_ARG_98	NH1	A_ASP_100	OD2	3.775
4R7N	A_ARG_98	NH2	A_ASP_100	OD2	2.512
4R7N	A_LYS_148	NZ	A_ASP_149	OD1	2.897
4R7N	A_LYS_148	NZ	A_ASP_149	OD2	2.755
4R7N	A_LYS_214	NZ	B_GLU_123	OE1	3.674
4R7N	A_LYS_214	NZ	B_GLU_123	OE2	3.683
4R7N	B_LYS_16	NZ	B_GLU_79	OE1	3.765
4R7N	B_LYS_16	NZ	B_GLU_79	OE2	3.236
4R7N	B_ARG_24	NH2	J_GLU_17	OE1	3.625
4R7N	B_ARG_24	NH2	J_GLU_17	OE2	2.355
4R7N	B_ARG_61	NH1	B_GLU_81	OE1	3.359
4R7N	B_ARG_61	NH2	B_GLU_81	OE1	3.738
4R7N	B_ARG_61	NH2	B_ASP_82	OD1	2.397
4R7N	B_ARG_61	NH2	B_ASP_82	OD2	3.170
4R7N	B_LYS_103	NZ	B_GLU_165	OE1	3.820
4R7N	B_LYS_107	NZ	J_ASP_9	OD2	3.605
4R7N	B_LYS_149	NZ	B_GLU_195	OE2	2.745
4R7N	C_ARG_39	NH1	C_ASP_90	OD1	2.845
4R7N	C_ARG_39	NH2	C_GLU_47	OE2	2.963
4R7N	C_ARG_39	NH2	C_ASP_90	OD1	3.701
4R7N	C_ARG_67	NH1	C_ASP_90	OD1	3.078
4R7N	C_ARG_67	NH1	C_ASP_90	OD2	2.222
4R7N	C_ARG_67	NH2	C_ASP_90	OD1	2.771
4R7N	C_ARG_67	NH2	C_ASP_90	OD2	3.580
4R7N	C_LYS_76	NZ	C_ASP_73	OD2	2.761
4R7N	C_ARG_98	NH2	C_ASP_100	OD2	3.773
4R7N	C_LYS_211	NZ	C_ASP_213	OD1	3.637
4R7N	C_LYS_214	NZ	D_GLU_123	OE1	2.537

4R7N	C_LYS_214	NZ	D_GLU_123	OE2	3.321
4R7N	C_ARG_215	NH1	C_GLU_217	OE2	3.613
4R7N	C_ARG_215	NH2	C_GLU_217	OE1	3.821
4R7N	C_ARG_215	NH2	C_GLU_217	OE2	3.518
4R7N	D_ARG_24	NH2	F_GLU_17	OE1	3.787
4R7N	D_ARG_24	NH2	F_GLU_17	OE2	2.414
4R7N	D_ARG_61	NH1	D_GLU_81	OE1	3.464
4R7N	D_ARG_61	NH1	D_ASP_82	OD1	2.853
4R7N	D_ARG_61	NH1	D_ASP_82	OD2	3.611
4R7N	D_ARG_61	NH2	D_GLU_81	OE1	3.128
4R7N	D_LYS_103	NZ	D_GLU_165	OE1	3.770
4R7N	D_LYS_107	NZ	F_ASP_9	OD2	3.633
4R7N	D_LYS_149	NZ	D_GLU_195	OE2	3.176
4R7N	D_HIS_189	ND1	D_ASP_151	OD2	3.153
4R7N	E_ARG_39	NH1	E_ASP_90	OD1	2.803
4R7N	E_ARG_39	NH2	E_GLU_47	OE1	3.978
4R7N	E_ARG_39	NH2	E_GLU_47	OE2	3.076
4R7N	E_ARG_39	NH2	E_ASP_90	OD1	3.735
4R7N	E_LYS_65	NZ	E_ASP_59	OD1	3.735
4R7N	E_ARG_67	NH1	E_ASP_90	OD1	3.124
4R7N	E_ARG_67	NH1	E_ASP_90	OD2	3.240
4R7N	E_ARG_98	NH1	E_ASP_100	OD2	3.090
4R7N	E_ARG_98	NH2	E_ASP_100	OD2	2.869
4R7N	E_HIS_169	NE2	F_ASP_167	OD1	3.616
4R7N	E_HIS_169	NE2	F_ASP_167	OD2	3.474
4R7N	E_LYS_214	NZ	F_GLU_123	OE2	3.072
4R7N	F_LYS_16	NZ	F_GLU_79	OE1	3.193
4R7N	F_LYS_16	NZ	F_GLU_79	OE2	2.766
4R7N	F_ARG_24	NH2	D_GLU_17	OE1	3.696
4R7N	F_ARG_24	NH2	D_GLU_17	OE2	2.325
4R7N	F_ARG_61	NH2	F_GLU_81	OE2	3.726
4R7N	F_ARG_61	NH2	F_ASP_82	OD1	2.275
4R7N	F_ARG_61	NH2	F_ASP_82	OD2	3.114
4R7N	F_LYS_103	NZ	F_GLU_165	OE1	3.429
4R7N	F_LYS_107	NZ	D_ASP_9	OD2	3.641
4R7N	F_ARG_142	NH1	F_GLU_143	OE1	3.991
4R7N	F_ARG_142	NH2	F_GLU_105	OE1	3.315
4R7N	F_LYS_149	NZ	F_GLU_195	OE1	3.479
4R7N	F_LYS_149	NZ	F_GLU_195	OE2	2.946
4R7N	G_ARG_39	NH1	G_ASP_90	OD1	2.781
4R7N	G_ARG_39	NH2	G_GLU_47	OE1	3.904
4R7N	G_ARG_39	NH2	G_GLU_47	OE2	2.981
4R7N	G_ARG_39	NH2	G_ASP_90	OD1	3.571
4R7N	G_LYS_65	NZ	G_ASP_59	OD1	3.786
4R7N	G_ARG_67	NH1	G_ASP_90	OD1	3.700
4R7N	G_ARG_67	NH1	G_ASP_90	OD2	2.751
4R7N	G_ARG_67	NH2	G_ASP_90	OD1	3.048
4R7N	G_ARG_67	NH2	G_ASP_90	OD2	3.620
4R7N	G_ARG_98	NH1	G_ASP_100	OD1	3.954
4R7N	G_ARG_98	NH1	G_ASP_100	OD2	2.296
4R7N	G_ARG_98	NH2	G_ASP_100	OD2	3.918
4R7N	G_LYS_214	NZ	H_GLU_123	OE1	2.389
4R7N	G_LYS_214	NZ	H_GLU_123	OE2	3.440
4R7N	G_ARG_215	NH2	G_GLU_217	OE2	3.692
4R7N	H_LYS_16	NZ	H_GLU_79	OE1	3.784
4R7N	H_LYS_16	NZ	H_GLU_79	OE2	3.778
4R7N	H_ARG_24	NH2	L_GLU_17	OE1	3.413
4R7N	H_ARG_24	NH2	L_GLU_17	OE2	2.312

4R7N	H_ARG_61	NH1	H_GLU_81	OE1	3.674
4R7N	H_ARG_61	NH1	H_ASP_82	OD1	2.998
4R7N	H_ARG_61	NH1	H_ASP_82	OD2	3.659
4R7N	H_ARG_61	NH2	H_GLU_81	OE1	3.398
4R7N	H_LYS_103	NZ	H_GLU_165	OE1	3.531
4R7N	H_LYS_149	NZ	H_GLU_195	OE2	2.677
4R7N	I_ARG_39	NH1	I_ASP_90	OD1	2.559
4R7N	I_ARG_39	NH2	I_GLU_47	OE2	3.220
4R7N	I_ARG_39	NH2	I_ASP_90	OD1	3.236
4R7N	I_ARG_67	NH1	I_ASP_90	OD1	3.787
4R7N	I_ARG_67	NH1	I_ASP_90	OD2	2.994
4R7N	I_ARG_67	NH2	I_ASP_90	OD1	2.852
4R7N	I_ARG_67	NH2	I_ASP_90	OD2	3.576
4R7N	I_ARG_98	NH1	I_ASP_100	OD2	3.172
4R7N	I_ARG_98	NH2	I_ASP_100	OD2	3.171
4R7N	I_LYS_214	NZ	J_GLU_123	OE1	3.635
4R7N	I_LYS_214	NZ	J_GLU_123	OE2	2.942
4R7N	J_ARG_24	NH2	B_GLU_17	OE1	3.555
4R7N	J_ARG_24	NH2	B_GLU_17	OE2	2.304
4R7N	J_ARG_61	NH1	J_ASP_82	OD1	2.881
4R7N	J_ARG_61	NH1	J_ASP_82	OD2	2.940
4R7N	J_ARG_142	NH2	J_GLU_105	OE1	3.516
4R7N	J_LYS_149	NZ	J_GLU_195	OE1	2.936
4R7N	K_ARG_39	NH1	K_ASP_90	OD1	2.585
4R7N	K_ARG_39	NH2	K_GLU_47	OE2	3.296
4R7N	K_ARG_39	NH2	K_ASP_90	OD1	3.354
4R7N	K_ARG_67	NH1	K_ASP_90	OD1	3.756
4R7N	K_ARG_67	NH1	K_ASP_90	OD2	2.865
4R7N	K_ARG_67	NH2	K_ASP_90	OD1	3.074
4R7N	K_ARG_67	NH2	K_ASP_90	OD2	3.668
4R7N	K_ARG_98	NH2	K_ASP_100	OD2	3.706
4R7N	K_LYS_148	NZ	K_ASP_149	OD1	2.955
4R7N	K_LYS_148	NZ	K_ASP_149	OD2	2.836
4R7N	K_LYS_214	NZ	L_GLU_123	OE2	3.794
4R7N	K_ARG_215	NH2	K_GLU_217	OE2	2.789
4R7N	L_LYS_16	NZ	L_GLU_79	OE1	3.348
4R7N	L_LYS_16	NZ	L_GLU_79	OE2	3.110
4R7N	L_ARG_24	NH2	H_GLU_17	OE1	3.531
4R7N	L_ARG_24	NH2	H_GLU_17	OE2	2.313
4R7N	L_ARG_61	NH1	L_ASP_82	OD1	3.398
4R7N	L_ARG_61	NH1	L_ASP_82	OD2	2.327
4R7N	L_ARG_61	NH2	L_ASP_82	OD1	2.642
4R7N	L_ARG_61	NH2	L_ASP_82	OD2	3.265
4R7N	L_LYS_103	NZ	L_GLU_165	OE1	3.773
4R7N	L_LYS_149	NZ	L_GLU_195	OE1	3.879
4R7N	L_LYS_149	NZ	L_GLU_195	OE2	3.013
4R7N	M_ARG_39	NH1	M_ASP_90	OD1	2.831
4R7N	M_ARG_39	NH2	M_GLU_47	OE2	3.008
4R7N	M_ARG_39	NH2	M_ASP_90	OD1	3.609
4R7N	M_ARG_67	NH1	M_ASP_90	OD2	3.507
4R7N	M_ARG_67	NH2	M_ASP_90	OD1	3.326
4R7N	M_ARG_67	NH2	M_ASP_90	OD2	3.775
4R7N	M_LYS_76	NZ	M_ASP_73	OD1	3.417
4R7N	M_LYS_76	NZ	M_ASP_73	OD2	3.788
4R7N	M_ARG_98	NH1	M_ASP_100	OD2	2.760
4R7N	M_ARG_98	NH2	M_ASP_100	OD2	2.685
4R7N	M_LYS_148	NZ	M_ASP_149	OD1	2.958
4R7N	M_LYS_148	NZ	M_ASP_149	OD2	2.802

4R7N	N_ARG_24	NH2	P_GLU_17	OE1	3.814
4R7N	N_ARG_24	NH2	P_GLU_17	OE2	2.289
4R7N	N_ARG_61	NH1	N_GLU_79	OE1	2.882
4R7N	N_ARG_61	NH1	N_ASP_82	OD1	2.547
4R7N	N_ARG_61	NH1	N_ASP_82	OD2	3.212
4R7N	N_ARG_61	NH2	N_GLU_79	OE1	3.252
4R7N	N_LYS_103	NZ	N_GLU_165	OE1	3.332
4R7N	N_LYS_107	NZ	P_ASP_9	OD2	3.591
4R7N	N_LYS_149	NZ	N_GLU_195	OE1	2.916
4R7N	N_HIS_189	ND1	N_ASP_151	OD2	2.809
4R7N	N_LYS_190	NZ	N_GLU_187	OE1	3.890
4R7N	O_ARG_39	NH1	O_ASP_90	OD1	2.710
4R7N	O_ARG_39	NH2	O_GLU_47	OE1	3.778
4R7N	O_ARG_39	NH2	O_GLU_47	OE2	2.955
4R7N	O_ARG_39	NH2	O_ASP_90	OD1	3.975
4R7N	O_ARG_67	NH1	O_ASP_90	OD1	3.623
4R7N	O_ARG_67	NH1	O_ASP_90	OD2	2.994
4R7N	O_ARG_67	NH2	O_ASP_90	OD1	3.294
4R7N	O_ARG_98	NH2	O_ASP_100	OD2	3.721
4R7N	O_HIS_169	NE2	P_ASP_167	OD2	3.725
4R7N	P_ARG_24	NH2	N_GLU_17	OE1	3.525
4R7N	P_ARG_24	NH2	N_GLU_17	OE2	2.277
4R7N	P_ARG_61	NH1	P_GLU_79	OE1	2.179
4R7N	P_ARG_61	NH1	P_GLU_79	OE2	3.956
4R7N	P_ARG_61	NH2	P_GLU_79	OE1	3.623
4R7N	P_LYS_103	NZ	P_GLU_165	OE1	3.040
4R7N	P_ARG_108	NH1	P_GLU_105	OE2	2.550
4R7N	P_ARG_108	NH2	P_GLU_105	OE2	3.860
4R7N	P_LYS_149	NZ	P_GLU_195	OE1	3.164
4R7N	P_LYS_149	NZ	P_GLU_195	OE2	3.343
4R7N	P_LYS_188	NZ	P_ASP_185	OD1	3.703
4R7N	P_HIS_189	ND1	P_ASP_151	OD2	2.247
4R7N	Q_ARG_39	NH1	Q_ASP_90	OD1	2.764
4R7N	Q_ARG_39	NH2	Q_GLU_47	OE1	3.665
4R7N	Q_ARG_39	NH2	Q_GLU_47	OE2	2.481
4R7N	Q_ARG_67	NH2	Q_ASP_90	OD1	3.614
4R7N	Q_ARG_67	NH2	Q_ASP_90	OD2	2.212
4R7N	Q_ARG_98	NH1	Q_ASP_100	OD2	2.913
4R7N	Q_ARG_98	NH2	Q_ASP_100	OD2	2.616
4R7N	Q_LYS_148	NZ	Q_ASP_149	OD1	3.127
4R7N	Q_LYS_148	NZ	Q_ASP_149	OD2	2.663
4R7N	Q_LYS_211	NZ	G_ASP_213	OD2	3.009
4R7N	Q_LYS_214	NZ	R_GLU_123	OE1	3.438
4R7N	Q_LYS_214	NZ	R_GLU_123	OE2	3.002
4R7N	Q_ARG_215	NH2	Q_GLU_217	OE2	3.165
4R7N	R_ARG_61	NH2	R_ASP_82	OD1	3.978
4R7N	R_LYS_103	NZ	R_GLU_165	OE1	2.945
4R7N	R_LYS_103	NZ	R_GLU_165	OE2	3.633
4R7N	R_LYS_145	NZ	F_ASP_93	OD2	3.627
4R7N	R_LYS_149	NZ	R_GLU_195	OE1	3.543
4R7N	R_LYS_149	NZ	R_GLU_195	OE2	2.531
4R7N	R_LYS_188	NZ	R_ASP_185	OD1	2.716
4R7N	R_LYS_188	NZ	R_ASP_185	OD2	3.719
4R7N	S_ARG_39	NH1	S_ASP_90	OD1	2.779
4R7N	S_ARG_39	NH2	S_GLU_47	OE2	3.044
4R7N	S_ARG_39	NH2	S_ASP_90	OD1	3.585
4R7N	S_ARG_67	NH1	S_ASP_90	OD1	3.352
4R7N	S_ARG_67	NH1	S_ASP_90	OD2	2.290

4R7N	S_ARG_67	NH2	S_ASP_90	OD1	2.345
4R7N	S_ARG_67	NH2	S_ASP_90	OD2	3.063
4R7N	S_ARG_98	NH1	S_ASP_100	OD2	2.688
4R7N	S_ARG_98	NH2	S_ASP_100	OD2	2.786
4R7N	S_LYS_148	NZ	S_ASP_149	OD1	3.013
4R7N	S_LYS_148	NZ	S_ASP_149	OD2	2.778
4R7N	S_LYS_214	NZ	T_GLU_123	OE1	3.934
4R7N	S_LYS_214	NZ	T_GLU_123	OE2	3.931
4R7N	T_LYS_16	NZ	T_GLU_79	OE1	3.838
4R7N	T_LYS_16	NZ	T_GLU_79	OE2	3.370
4R7N	T_ARG_61	NH1	T_GLU_81	OE1	3.260
4R7N	T_ARG_61	NH2	T_GLU_81	OE1	3.615
4R7N	T_ARG_61	NH2	T_ASP_82	OD1	2.440
4R7N	T_ARG_61	NH2	T_ASP_82	OD2	3.240
4R7N	T_LYS_103	NZ	T_GLU_165	OE1	3.688
4R7N	T_LYS_149	NZ	T_GLU_195	OE2	2.601
4R9Y	L_ARG_86	NH2	L_ASP_107	OD1	3.056
4R9Y	L_ARG_86	NH2	L_ASP_107	OD2	2.747
4R9Y	L_LYS_128	NZ	L_ASP_190	OD2	3.847
4R9Y	L_LYS_174	NZ	L_GLU_220	OE1	2.876
4R9Y	L_ARG_180	NH2	L_GLU_210	OE2	3.355
4R9Y	L_HIS_214	ND1	L_GLU_210	OE1	3.897
4R9Y	H_LYS_37	NZ	H_GLU_45	OE1	2.976
4R9Y	H_ARG_66	NH1	H_GLU_88	OE2	2.888
4R9Y	H_ARG_66	NH2	H_GLU_88	OE2	3.617
4R9Y	H_LYS_214	NZ	L_GLU_148	OE2	2.745
4R9Y	B_LYS_50	NZ	B_GLU_28	OE2	3.071
4R9Y	A_LYS_50	NZ	A_GLU_28	OE2	2.662
4R9Y	M_ARG_79	NH2	M_ASP_85	OD1	3.700
4R9Y	M_ARG_86	NH2	M_ASP_107	OD1	2.946
4R9Y	M_ARG_86	NH2	M_ASP_107	OD2	2.694
4R9Y	M_LYS_128	NZ	M_ASP_190	OD1	3.808
4R9Y	M_LYS_128	NZ	M_ASP_190	OD2	3.124
4R9Y	M_LYS_	NZ	M_GLU_	OE1	3.152
4R9Y	M_ARG_	NH2	M_GLU_	OE2	3.203
4R9Y	M_HIS_	ND1	M_GLU_	OE1	3.630
4R9Y	M_LYS_	NZ	M_ASP_	OD1	3.535
4R9Y	M_LYS_	NZ	M_ASP_	OD2	3.766
4R9Y	N_LYS_37	NZ	N_GLU_45	OE1	2.708
4R9Y	N_ARG_66	NH1	N_GLU_88	OE2	3.382
4R9Y	N_ARG_66	NH2	N_GLU_88	OE2	3.864
4R9Y	N_LYS_	NZ	M_GLU_	OE2	3.272
4RAU	A_ARG_39	NH1	A_ASP_84	OD1	3.918
4RAU	A_ARG_63	NH1	A_ASP_84	OD1	3.252
4RAU	A_ARG_63	NH1	A_ASP_84	OD2	2.474
4RAU	A_ARG_63	NH2	A_GLU_81	OE1	3.641
4RAU	A_LYS_95	NZ	C_ASP_7	OD1	3.997
4RAU	A_LYS_95	NZ	C_ASP_7	OD2	3.077
4RAU	A_LYS_105	NZ	A_ASP_167	OD1	3.803
4RAU	A_LYS_144	NZ	A_GLU_107	OE1	3.648
4RAU	A_LYS_149	NZ	A_GLU_156	OE1	3.640
4RAU	A_LYS_149	NZ	A_GLU_156	OE2	3.515
4RAU	A_LYS_151	NZ	A_GLU_197	OE1	3.640
4RAU	A_LYS_151	NZ	A_GLU_197	OE2	2.823
4RAU	A_LYS_185	NZ	A_GLU_189	OE1	3.707
4RAU	A_LYS_185	NZ	A_GLU_189	OE2	3.597
4RAU	A_HIS_191	ND1	A_ASP_153	OD2	2.734
4RAU	A_LYS_201	NZ	A_ASP_112	OD2	3.033

4RAU	B_ARG_40	NH1	B_ASP_92	OD1	3.503
4RAU	B_ARG_40	NH2	B_GLU_48	OE1	3.720
4RAU	B_ARG_40	NH2	B_GLU_48	OE2	3.277
4RAU	B_ARG_46	NH1	B_GLU_44	OE1	3.716
4RAU	B_ARG_69	NH1	B_ASP_92	OD2	2.694
4RAU	B_ARG_69	NH2	B_ASP_92	OD1	3.312
4RAU	B_ARG_69	NH2	B_ASP_92	OD2	3.295
4RAU	B_ARG_89	NH1	B_GLU_91	OE1	3.989
4RAU	B_ARG_100	NH2	B_ASP_109	OD1	3.691
4RAU	B_ARG_100	NH2	B_ASP_109	OD2	2.652
4RAU	D_ARG_39	NH1	D_ASP_84	OD1	3.919
4RAU	D_ARG_63	NH1	D_ASP_84	OD1	3.251
4RAU	D_ARG_63	NH1	D_ASP_84	OD2	2.476
4RAU	D_ARG_63	NH2	D_GLU_81	OE1	3.630
4RAU	D_LYS_95	NZ	F_ASP_7	OD1	3.860
4RAU	D_LYS_105	NZ	D_ASP_167	OD1	3.863
4RAU	D_LYS_144	NZ	D_GLU_107	OE1	3.652
4RAU	D_LYS_149	NZ	D_GLU_156	OE1	3.639
4RAU	D_LYS_149	NZ	D_GLU_156	OE2	3.516
4RAU	D_LYS_151	NZ	D_GLU_197	OE1	3.630
4RAU	D_LYS_151	NZ	D_GLU_197	OE2	2.814
4RAU	D_LYS_185	NZ	D_GLU_189	OE1	3.707
4RAU	D_LYS_185	NZ	D_GLU_189	OE2	3.596
4RAU	D_HIS_191	ND1	D_ASP_153	OD2	2.728
4RAU	D_LYS_201	NZ	D_ASP_112	OD2	3.033
4RAU	E_ARG_40	NH1	E_ASP_92	OD1	3.503
4RAU	E_ARG_40	NH2	E_GLU_48	OE1	3.725
4RAU	E_ARG_40	NH2	E_GLU_48	OE2	3.283
4RAU	E_ARG_46	NH1	E_GLU_44	OE1	3.723
4RAU	E_ARG_69	NH1	E_ASP_92	OD2	2.692
4RAU	E_ARG_69	NH2	E_ASP_92	OD1	3.311
4RAU	E_ARG_69	NH2	E_ASP_92	OD2	3.296
4RAU	E_ARG_89	NH1	E_GLU_91	OE1	3.988
4RAU	E_ARG_100	NH2	E_ASP_109	OD1	3.682
4RAU	E_ARG_100	NH2	E_ASP_109	OD2	2.642
4RAU	G_ARG_39	NH1	G_ASP_84	OD1	3.926
4RAU	G_LYS_41	NZ	G_GLU_83	OE2	3.332
4RAU	G_ARG_63	NH1	G_ASP_84	OD1	3.251
4RAU	G_ARG_63	NH1	G_ASP_84	OD2	2.480
4RAU	G_ARG_63	NH2	G_GLU_81	OE1	3.649
4RAU	G_LYS_95	NZ	I_ASP_7	OD1	3.805
4RAU	G_LYS_95	NZ	I_ASP_7	OD2	2.755
4RAU	G_LYS_105	NZ	G_ASP_167	OD1	3.810
4RAU	G_LYS_144	NZ	G_GLU_107	OE1	3.652
4RAU	G_LYS_149	NZ	G_GLU_156	OE1	3.643
4RAU	G_LYS_149	NZ	G_GLU_156	OE2	3.517
4RAU	G_LYS_151	NZ	G_GLU_197	OE1	3.632
4RAU	G_LYS_151	NZ	G_GLU_197	OE2	2.815
4RAU	G_LYS_185	NZ	G_GLU_189	OE1	3.707
4RAU	G_LYS_185	NZ	G_GLU_189	OE2	3.598
4RAU	G_HIS_191	ND1	G_ASP_153	OD2	2.730
4RAU	G_LYS_201	NZ	G_ASP_112	OD2	3.033
4RAU	H_ARG_40	NH1	H_ASP_92	OD1	3.494
4RAU	H_ARG_40	NH2	H_GLU_48	OE1	3.724
4RAU	H_ARG_40	NH2	H_GLU_48	OE2	3.281
4RAU	H_ARG_46	NH1	H_GLU_44	OE1	3.700
4RAU	H_ARG_69	NH1	H_ASP_92	OD2	2.699
4RAU	H_ARG_69	NH2	H_ASP_92	OD1	3.317

4RAU	H_ARG_69	NH2	H_ASP_92	OD2	3.297
4RAU	H_ARG_89	NH1	H_GLU_91	OE1	3.985
4RAU	H_ARG_100	NH2	H_ASP_109	OD1	3.685
4RAU	H_ARG_100	NH2	H_ASP_109	OD2	2.644
4RAU	J_ARG_39	NH1	J_ASP_84	OD1	3.913
4RAU	J_ARG_63	NH1	J_ASP_84	OD1	3.253
4RAU	J_ARG_63	NH1	J_ASP_84	OD2	2.480
4RAU	J_ARG_63	NH2	J_GLU_81	OE1	3.649
4RAU	J_LYS_105	NZ	J_ASP_167	OD1	3.805
4RAU	J_LYS_144	NZ	J_GLU_107	OE1	3.646
4RAU	J_LYS_149	NZ	J_GLU_156	OE1	3.641
4RAU	J_LYS_149	NZ	J_GLU_156	OE2	3.516
4RAU	J_LYS_151	NZ	J_GLU_197	OE1	3.631
4RAU	J_LYS_151	NZ	J_GLU_197	OE2	2.814
4RAU	J_LYS_171	NZ	J_ASP_169	OD2	3.647
4RAU	J_LYS_185	NZ	J_GLU_189	OE1	3.708
4RAU	J_LYS_185	NZ	J_GLU_189	OE2	3.602
4RAU	J_HIS_191	ND1	J_ASP_153	OD2	2.728
4RAU	J_LYS_201	NZ	J_ASP_112	OD2	3.034
4RAU	K_ARG_40	NH1	K_ASP_92	OD1	3.498
4RAU	K_ARG_40	NH2	K_GLU_48	OE1	3.722
4RAU	K_ARG_40	NH2	K_GLU_48	OE2	3.276
4RAU	K_ARG_46	NH1	K_GLU_44	OE1	3.698
4RAU	K_ARG_69	NH1	K_ASP_92	OD2	2.699
4RAU	K_ARG_69	NH2	K_ASP_92	OD1	3.319
4RAU	K_ARG_69	NH2	K_ASP_92	OD2	3.299
4RAU	K_ARG_89	NH1	K_GLU_91	OE1	3.987
4RAU	K_ARG_100	NH2	K_ASP_109	OD1	3.690
4RAU	K_ARG_100	NH2	K_ASP_109	OD2	2.645
4RAU	K_LYS_216	NZ	J_GLU_125	OE2	3.935
4RAU	M_ARG_39	NH1	M_ASP_84	OD1	3.922
4RAU	M_ARG_63	NH1	M_ASP_84	OD1	3.250
4RAU	M_ARG_63	NH1	M_ASP_84	OD2	2.472
4RAU	M_ARG_63	NH2	M_GLU_81	OE1	3.646
4RAU	M_LYS_105	NZ	M_ASP_167	OD1	3.861
4RAU	M_LYS_149	NZ	M_GLU_156	OE1	3.646
4RAU	M_LYS_149	NZ	M_GLU_156	OE2	3.522
4RAU	M_LYS_151	NZ	M_GLU_197	OE1	3.627
4RAU	M_LYS_151	NZ	M_GLU_197	OE2	2.809
4RAU	M_LYS_185	NZ	M_GLU_189	OE1	3.710
4RAU	M_LYS_185	NZ	M_GLU_189	OE2	3.598
4RAU	M_HIS_191	ND1	M_ASP_153	OD2	2.731
4RAU	M_LYS_201	NZ	M_ASP_112	OD2	3.028
4RAU	N_ARG_40	NH1	N_ASP_92	OD1	3.508
4RAU	N_ARG_40	NH2	N_GLU_48	OE1	3.718
4RAU	N_ARG_40	NH2	N_GLU_48	OE2	3.273
4RAU	N_ARG_46	NH2	N_GLU_44	OE1	2.944
4RAU	N_ARG_69	NH1	N_ASP_92	OD2	2.695
4RAU	N_ARG_69	NH2	N_ASP_92	OD1	3.318
4RAU	N_ARG_69	NH2	N_ASP_92	OD2	3.302
4RAU	N_ARG_89	NH1	N_GLU_91	OE1	3.987
4RAU	N_ARG_100	NH2	N_ASP_109	OD1	3.684
4RAU	N_ARG_100	NH2	N_ASP_109	OD2	2.647
4RAU	O_ARG_49	NH2	X_ASP_7	OD1	2.993
4RAU	O_ARG_49	NH2	X_ASP_7	OD2	3.647
4RAU	P_ARG_39	NH1	P_ASP_84	OD1	3.913
4RAU	P_ARG_63	NH1	P_ASP_84	OD1	3.257
4RAU	P_ARG_63	NH1	P_ASP_84	OD2	2.479

4RAU	P_ARG_63	NH2	P_GLU_81	OE1	3.679
4RAU	P_LYS_	NZ	R_ASP_	OD1	3.104
4RAU	P_LYS_105	NZ	P_ASP_167	OD1	3.844
4RAU	P_LYS_144	NZ	P_GLU_107	OE1	3.654
4RAU	P_LYS_149	NZ	P_GLU_156	OE1	3.641
4RAU	P_LYS_149	NZ	P_GLU_156	OE2	3.516
4RAU	P_LYS_151	NZ	P_GLU_197	OE1	3.629
4RAU	P_LYS_151	NZ	P_GLU_197	OE2	2.811
4RAU	P_LYS_185	NZ	P_GLU_189	OE1	3.705
4RAU	P_LYS_185	NZ	P_GLU_189	OE2	3.595
4RAU	P_HIS_191	ND1	P_ASP_153	OD2	2.722
4RAU	P_LYS_201	NZ	P_ASP_112	OD2	3.034
4RAU	Q_ARG_40	NH1	Q_ASP_92	OD1	3.502
4RAU	Q_ARG_40	NH2	Q_GLU_48	OE1	3.727
4RAU	Q_ARG_40	NH2	Q_GLU_48	OE2	3.276
4RAU	Q_ARG_46	NH1	Q_GLU_44	OE1	3.700
4RAU	Q_ARG_69	NH1	Q_ASP_92	OD2	2.695
4RAU	Q_ARG_69	NH2	Q_ASP_92	OD1	3.314
4RAU	Q_ARG_69	NH2	Q_ASP_92	OD2	3.297
4RAU	Q_ARG_89	NH1	Q_GLU_91	OE1	3.990
4RAU	Q_ARG_100	NH2	Q_ASP_109	OD1	3.684
4RAU	Q_ARG_100	NH2	Q_ASP_109	OD2	2.645
4RAU	S_ARG_39	NH2	S_ASP_84	OD1	2.426
4RAU	S_ARG_63	NH1	S_ASP_84	OD1	3.257
4RAU	S_ARG_63	NH1	S_ASP_84	OD2	2.480
4RAU	S_ARG_63	NH2	S_GLU_81	OE1	3.645
4RAU	S_LYS_105	NZ	S_ASP_167	OD1	3.810
4RAU	S_LYS_144	NZ	S_GLU_107	OE1	3.627
4RAU	S_LYS_149	NZ	S_GLU_156	OE1	3.640
4RAU	S_LYS_149	NZ	S_GLU_156	OE2	3.514
4RAU	S_LYS_151	NZ	S_GLU_197	OE1	3.630
4RAU	S_LYS_151	NZ	S_GLU_197	OE2	2.813
4RAU	S_LYS_185	NZ	S_GLU_189	OE1	3.708
4RAU	S_LYS_185	NZ	S_GLU_189	OE2	3.598
4RAU	S_HIS_191	ND1	S_ASP_153	OD2	2.725
4RAU	S_LYS_201	NZ	S_ASP_112	OD2	3.035
4RAU	T_ARG_40	NH1	T_ASP_92	OD1	3.503
4RAU	T_ARG_40	NH2	T_GLU_48	OE1	3.728
4RAU	T_ARG_40	NH2	T_GLU_48	OE2	3.283
4RAU	T_ARG_46	NH1	T_GLU_44	OE1	3.699
4RAU	T_ARG_69	NH1	T_ASP_92	OD2	2.696
4RAU	T_ARG_69	NH2	T_ASP_92	OD1	3.316
4RAU	T_ARG_69	NH2	T_ASP_92	OD2	3.295
4RAU	T_ARG_89	NH1	T_GLU_91	OE1	3.989
4RAU	T_ARG_100	NH2	T_ASP_109	OD1	3.693
4RAU	T_ARG_100	NH2	T_ASP_109	OD2	2.653
4RAU	V_ARG_39	NH1	V_ASP_84	OD1	3.915
4RAU	V_ARG_63	NH1	V_ASP_84	OD1	3.255
4RAU	V_ARG_63	NH1	V_ASP_84	OD2	2.479
4RAU	V_ARG_63	NH2	V_GLU_81	OE1	3.648
4RAU	V_LYS_95	NZ	X_ASP_7	OD1	3.972
4RAU	V_LYS_95	NZ	X_ASP_7	OD2	3.050
4RAU	V_LYS_105	NZ	V_ASP_167	OD1	3.821
4RAU	V_LYS_144	NZ	V_GLU_107	OE1	3.639
4RAU	V_LYS_149	NZ	V_GLU_156	OE1	3.641
4RAU	V_LYS_149	NZ	V_GLU_156	OE2	3.514
4RAU	V_LYS_151	NZ	V_GLU_197	OE1	3.631
4RAU	V_LYS_151	NZ	V_GLU_197	OE2	2.814

4RAU	V_LYS_185	NZ	V_GLU_189	OE1	3.708
4RAU	V_LYS_185	NZ	V_GLU_189	OE2	3.599
4RAU	V_HIS_191	ND1	V_ASP_153	OD2	2.732
4RAU	V_LYS_201	NZ	V_ASP_112	OD2	3.032
4RAU	W_ARG_40	NH1	W_ASP_92	OD1	3.502
4RAU	W_ARG_40	NH2	W_GLU_48	OE1	3.718
4RAU	W_ARG_40	NH2	W_GLU_48	OE2	3.275
4RAU	W_ARG_46	NH1	W_GLU_44	OE1	3.702
4RAU	W_ARG_69	NH1	W_ASP_92	OD2	2.696
4RAU	W_ARG_69	NH2	W_ASP_92	OD1	3.317
4RAU	W_ARG_69	NH2	W_ASP_92	OD2	3.298
4RAU	W_ARG_89	NH1	W_GLU_91	OE1	3.988
4RAU	W_ARG_100	NH2	W_ASP_109	OD1	3.693
4RAU	W_ARG_100	NH2	W_ASP_109	OD2	2.652
4RAU	X_ARG_49	NH2	O_ASP_7	OD1	2.791
4RAU	X_ARG_49	NH2	O_ASP_7	OD2	3.699
4RRP	A_ARG_24	NH2	A_ASP_70	OD1	3.536
4RRP	A_ARG_24	NH2	A_ASP_70	OD2	3.877
4RRP	A_ARG_61	NH2	A_GLU_81	OE2	3.090
4RRP	A_ARG_61	NH2	A_ASP_82	OD1	2.844
4RRP	A_ARG_61	NH2	A_ASP_82	OD2	3.386
4RRP	A_LYS_149	NZ	A_GLU_195	OE1	2.796
4RRP	A_LYS_149	NZ	A_GLU_195	OE2	3.574
4RRP	A_LYS_169	NZ	A_ASP_167	OD1	3.364
4RRP	A_LYS_169	NZ	A_ASP_167	OD2	3.265
4RRP	A_LYS_183	NZ	A_GLU_187	OE1	3.356
4RRP	A_LYS_183	NZ	A_GLU_187	OE2	2.482
4RRP	A_LYS_188	NZ	A_ASP_185	OD1	3.338
4RRP	G_ARG_38	NH1	G_ASP_86	OD1	3.090
4RRP	G_ARG_38	NH2	G_GLU_46	OE1	3.292
4RRP	G_ARG_38	NH2	G_GLU_46	OE2	3.713
4RRP	G_ARG_38	NH2	G_ASP_86	OD1	3.929
4RRP	G_LYS_64	NZ	G_ASP_61	OD1	3.718
4RRP	G_ARG_66	NH1	G_ASP_86	OD1	3.753
4RRP	G_ARG_66	NH1	G_ASP_86	OD2	2.642
4RRP	G_ARG_66	NH2	G_ASP_86	OD1	3.093
4RRP	G_ARG_66	NH2	G_ASP_86	OD2	3.474
4RRP	G_LYS_75	NZ	G_ASP_72	OD2	3.613
4RRP	G_ARG_94	NH1	G_ASP_101	OD2	2.572
4RRP	G_LYS_143	NZ	G_ASP_144	OD1	3.513
4RRP	G_LYS_143	NZ	G_ASP_144	OD2	3.377
4RRP	G_LYS_214	NZ	A_ASP_122	OD1	3.271
4RRP	G_LYS_214	NZ	A_ASP_122	OD2	3.253
4RRP	B_ARG_24	NH1	B_ASP_70	OD1	2.974
4RRP	B_ARG_24	NH2	B_ASP_70	OD1	3.509
4RRP	B_ARG_24	NH2	B_ASP_70	OD2	3.520
4RRP	B_ARG_61	NH1	Q_GLU_32	OE1	3.055
4RRP	B_ARG_61	NH1	Q_GLU_32	OE2	3.683
4RRP	B_ARG_61	NH2	B_GLU_81	OE2	3.319
4RRP	B_ARG_61	NH2	B_ASP_82	OD1	2.867
4RRP	B_ARG_61	NH2	B_ASP_82	OD2	3.594
4RRP	B_ARG_61	NH2	Q_GLU_32	OE2	3.637
4RRP	B_LYS_103	NZ	B_GLU_165	OE1	2.902
4RRP	B_LYS_103	NZ	B_GLU_165	OE2	2.974
4RRP	B_LYS_149	NZ	B_GLU_195	OE2	2.877
4RRP	B_LYS_188	NZ	B_ASP_185	OD1	3.756
4RRP	B_HIS_189	ND1	B_ASP_151	OD2	3.126
4RRP	H_ARG_38	NH1	H_ASP_86	OD1	2.743

4RRP	H_ARG_38	NH2	H_GLU_46	OE1	3.267
4RRP	H_ARG_38	NH2	H_GLU_46	OE2	3.655
4RRP	H_ARG_38	NH2	H_ASP_86	OD1	3.792
4RRP	H_ARG_66	NH1	H_ASP_86	OD2	2.961
4RRP	H_ARG_66	NH2	H_ASP_86	OD1	3.400
4RRP	H_ARG_66	NH2	H_ASP_86	OD2	3.201
4RRP	H_ARG_94	NH2	H_ASP_101	OD1	3.922
4RRP	H_ARG_94	NH2	H_ASP_101	OD2	2.800
4RRP	H_LYS_143	NZ	H_ASP_144	OD1	3.372
4RRP	H_LYS_143	NZ	H_ASP_144	OD2	3.115
4RRP	H_LYS_210	NZ	H_GLU_212	OE2	3.908
4RRP	C_ARG_24	NH1	C_ASP_70	OD1	3.210
4RRP	C_ARG_24	NH1	C_ASP_70	OD2	3.811
4RRP	C_ARG_24	NH2	C_ASP_70	OD1	3.266
4RRP	C_ARG_24	NH2	C_ASP_70	OD2	3.021
4RRP	C_ARG_61	NH2	C_GLU_81	OE2	3.872
4RRP	C_ARG_61	NH2	C_ASP_82	OD1	2.499
4RRP	C_ARG_61	NH2	C_ASP_82	OD2	3.003
4RRP	C_LYS_103	NZ	C_GLU_105	OE1	2.759
4RRP	C_LYS_103	NZ	C_GLU_165	OE1	3.916
4RRP	C_LYS_188	NZ	C_ASP_185	OD1	3.719
4RRP	L_ARG_38	NH1	L_ASP_86	OD1	3.037
4RRP	L_ARG_38	NH2	L_GLU_46	OE1	3.102
4RRP	L_ARG_38	NH2	L_GLU_46	OE2	3.753
4RRP	L_LYS_64	NZ	L_ASP_61	OD1	2.958
4RRP	L_ARG_66	NH1	L_ASP_86	OD1	3.306
4RRP	L_ARG_66	NH1	L_ASP_86	OD2	3.894
4RRP	L_ARG_66	NH2	L_ASP_86	OD1	3.160
4RRP	L_ARG_66	NH2	L_ASP_86	OD2	2.282
4RRP	L_ARG_94	NH1	L_ASP_101	OD2	2.705
4RRP	L_LYS_143	NZ	L_ASP_144	OD1	3.710
4RRP	D_ARG_24	NH2	D_ASP_70	OD1	3.941
4RRP	D_ARG_61	NH2	D_GLU_81	OE2	3.108
4RRP	D_ARG_61	NH2	D_ASP_82	OD1	2.819
4RRP	D_ARG_61	NH2	D_ASP_82	OD2	3.344
4RRP	D_LYS_103	NZ	D_GLU_165	OE1	3.545
4RRP	D_LYS_103	NZ	D_GLU_165	OE2	3.420
4RRP	D_LYS_149	NZ	D_GLU_195	OE2	2.585
4RRP	D_LYS_188	NZ	D_ASP_185	OD1	2.752
4RRP	D_HIS_189	ND1	D_ASP_151	OD2	3.191
4RRP	J_ARG_38	NH1	J_ASP_86	OD1	3.091
4RRP	J_ARG_38	NH2	J_GLU_46	OE1	3.176
4RRP	J_ARG_38	NH2	J_ASP_86	OD1	3.697
4RRP	J_ARG_66	NH1	J_ASP_86	OD1	3.907
4RRP	J_ARG_66	NH1	J_ASP_86	OD2	2.891
4RRP	J_ARG_66	NH2	J_ASP_86	OD1	2.922
4RRP	J_ARG_66	NH2	J_ASP_86	OD2	3.426
4RRP	J_ARG_83	NH1	J_GLU_85	OE2	3.812
4RRP	J_ARG_94	NH2	J_ASP_101	OD1	3.162
4RRP	J_LYS_143	NZ	J_ASP_144	OD1	3.206
4RRP	J_LYS_143	NZ	J_ASP_144	OD2	3.279
4RRP	J_LYS_210	NZ	J_GLU_212	OE2	3.248
4RRP	J_LYS_214	NZ	D_ASP_122	OD1	3.176
4RRP	J_LYS_214	NZ	D_ASP_122	OD2	2.924
4RRP	E_ARG_24	NH1	E_ASP_70	OD1	3.504
4RRP	E_ARG_24	NH1	E_ASP_70	OD2	2.757
4RRP	E_ARG_24	NH2	E_ASP_70	OD1	3.612
4RRP	E_ARG_24	NH2	E_ASP_70	OD2	3.877

4RRP	E_ARG.61	NH2	E_GLU_81	OE2	3.265
4RRP	E_ARG.61	NH2	E_ASP_82	OD1	2.971
4RRP	E_ARG.61	NH2	E_ASP_82	OD2	3.278
4RRP	E_LYS_103	NZ	E_GLU_165	OE1	3.997
4RRP	E_ARG_108	NH1	E_ASP_170	OD1	3.279
4RRP	E_LYS_188	NZ	E_ASP_185	OD1	3.369
4RRP	E_HIS_189	ND1	E_ASP_151	OD2	3.342
4RRP	K_ARG_38	NH1	K_ASP_86	OD1	3.316
4RRP	K_ARG_38	NH2	K_GLU_46	OE1	3.348
4RRP	K_ARG_38	NH2	K_GLU_46	OE2	3.150
4RRP	K_ARG_38	NH2	K_ASP_86	OD1	3.806
4RRP	K_ARG_66	NH1	K_ASP_86	OD1	3.794
4RRP	K_ARG_66	NH1	K_ASP_86	OD2	2.585
4RRP	K_ARG_94	NH2	K_ASP_101	OD2	3.065
4RRP	K_LYS_143	NZ	K_ASP_144	OD1	3.052
4RRP	K_LYS_143	NZ	K_ASP_144	OD2	3.747
4RRP	K_LYS_210	NZ	K_GLU_212	OE2	3.209
4RRP	F_ARG_24	NH1	F_ASP_70	OD1	3.513
4RRP	F_ARG_24	NH2	F_ASP_70	OD1	3.347
4RRP	F_ARG_24	NH2	F_ASP_70	OD2	3.453
4RRP	F_ARG_61	NH2	F_GLU_81	OE2	3.201
4RRP	F_ARG_61	NH2	F_ASP_82	OD1	3.111
4RRP	F_ARG_61	NH2	F_ASP_82	OD2	2.880
4RRP	F_LYS_183	NZ	F_GLU_187	OE2	3.854
4RRP	F_HIS_189	ND1	F_ASP_151	OD2	3.499
4RRP	L_ARG_38	NH1	L_ASP_86	OD1	2.782
4RRP	L_ARG_38	NH2	L_GLU_46	OE1	2.958
4RRP	L_ARG_38	NH2	L_GLU_46	OE2	3.099
4RRP	L_ARG_38	NH2	L_ASP_86	OD1	3.809
4RRP	L_ARG_66	NH1	L_ASP_86	OD2	3.387
4RRP	L_ARG_66	NH2	L_ASP_86	OD1	3.433
4RRP	L_ARG_66	NH2	L_ASP_86	OD2	3.328
4RRP	L_ARG_94	NH1	L_ASP_101	OD1	2.541
4RRP	L_ARG_94	NH2	L_ASP_101	OD1	3.963
4RRP	L_HIS_164	NE2	F_ASP_167	OD1	3.853
4RRP	L_LYS_214	NZ	F_ASP_122	OD2	3.247
4RRP	M_LYS_10	NZ	M_GLU_25	OE2	2.815
4RRP	M_LYS_10	NZ	N_GLU_29	OE1	3.876
4RRP	M_LYS_10	NZ	N_GLU_29	OE2	3.237
4RRP	M_LYS_41	NZ	M_GLU_39	OE1	3.872
4RRP	M_ARG_104	NH1	M_ASP_102	OD2	2.905
4RRP	M_ARG_104	NH2	M_ASP_102	OD2	3.495
4RRP	M_ARG_108	NH2	M_GLU_105	OE1	3.086
4RRP	M_ARG_108	NH2	M_GLU_105	OE2	3.305
4RRP	M_ARG_123	NH1	M_GLU_120	OE1	3.669
4RRP	M_ARG_123	NH1	M_GLU_120	OE2	3.750
4RRP	M_HIS_134	ND1	M_ASP_118	OD2	2.756
4RRP	M_HIS_134	ND1	M_GLU_119	OE1	3.923
4RRP	N_LYS_10	NZ	M_GLU_29	OE1	3.319
4RRP	N_LYS_10	NZ	M_GLU_29	OE2	2.389
4RRP	N_LYS_10	NZ	N_GLU_25	OE1	2.628
4RRP	N_HIS_36	ND1	N_ASP_102	OD1	3.589
4RRP	N_HIS_36	ND1	N_ASP_102	OD2	3.342
4RRP	N_ARG_104	NH1	N_ASP_102	OD2	2.932
4RRP	N_ARG_104	NH2	N_ASP_102	OD2	3.308
4RRP	N_ARG_108	NH2	N_GLU_105	OE1	3.337
4RRP	N_ARG_108	NH2	N_GLU_105	OE2	2.984
4RRP	O_LYS_10	NZ	O_GLU_25	OE2	3.092

4RRP	O_LYS_35	NZ	O_GLU_156	OE2	3.793
4RRP	O_LYS_41	NZ	O_GLU_56	OE1	3.628
4RRP	O_LYS_71	NZ	O_GLU_25	OE2	3.721
4RRP	O_ARG_104	NH1	O_ASP_102	OD2	3.187
4RRP	O_ARG_104	NH2	O_ASP_102	OD2	2.791
4RRP	O_ARG_108	NH2	O_GLU_105	OE2	3.068
4RRP	O_ARG_123	NH1	Q_ASP_54	OD1	3.356
4RRP	O_ARG_123	NH1	Q_ASP_54	OD2	3.533
4RRP	O_ARG_123	NH2	O_GLU_120	OE1	3.551
4RRP	O_ARG_123	NH2	Q_ASP_54	OD2	3.134
4RRP	O_HIS_134	ND1	O_ASP_118	OD1	3.804
4RRP	O_HIS_134	ND1	O_ASP_118	OD2	2.643
4RRP	O_HIS_134	NE2	N_GLU_121	OE1	3.780
4RRP	O_HIS_134	NE2	N_GLU_121	OE2	3.192
4RRP	O_ARG_145	NH2	Q_GLU_116	OE1	3.921
4RRP	O_ARG_145	NH2	Q_GLU_116	OE2	3.324
4RRP	P_LYS_10	NZ	P_GLU_25	OE2	2.613
4RRP	P_HIS_36	ND1	P_ASP_102	OD1	3.540
4RRP	P_HIS_36	NE2	P_ASP_102	OD2	3.863
4RRP	P_ARG_49	NH1	P_GLU_88	OE2	3.737
4RRP	P_HIS_53	ND1	P_ASP_54	OD1	3.310
4RRP	P_ARG_104	NH1	P_ASP_102	OD2	2.923
4RRP	P_ARG_104	NH2	P_ASP_102	OD2	3.980
4RRP	P_ARG_108	NH2	P_GLU_105	OE1	2.888
4RRP	P_ARG_108	NH2	P_GLU_105	OE2	3.217
4RRP	P_ARG_123	NH2	P_GLU_120	OE1	2.430
4RRP	P_HIS_134	ND1	P_ASP_118	OD1	3.512
4RRP	P_HIS_134	ND1	P_ASP_118	OD2	2.998
4RRP	P_HIS_134	ND1	P_GLU_119	OE2	3.490
4RRP	P_HIS_134	NE2	P_ASP_133	OD2	3.140
4RRP	Q_LYS_10	NZ	Q_GLU_25	OE2	2.946
4RRP	Q_HIS_36	NE2	Q_ASP_102	OD2	3.552
4RRP	Q_LYS_41	NZ	Q_GLU_56	OE1	3.618
4RRP	Q_HIS_53	ND1	Q_GLU_88	OE2	3.194
4RRP	Q_ARG_104	NH1	Q_ASP_102	OD1	3.295
4RRP	Q_ARG_108	NH2	Q_GLU_105	OE1	3.208
4RRP	Q_ARG_108	NH2	Q_GLU_105	OE2	3.290
4RRP	Q_ARG_123	NH1	Q_GLU_120	OE1	3.019
4RRP	Q_HIS_134	ND1	Q_ASP_118	OD1	3.096
4RRP	Q_HIS_134	ND1	Q_ASP_118	OD2	3.045
4RRP	Q_ARG_145	NH1	O_GLU_116	OE2	3.050
4RRP	Q_ARG_145	NH2	O_GLU_116	OE2	3.244
4RRP	R_LYS_10	NZ	R_GLU_25	OE2	2.771
4RRP	R_LYS_41	NZ	R_GLU_56	OE2	3.957
4RRP	R_LYS_71	NZ	R_GLU_25	OE1	3.947
4RRP	R_LYS_71	NZ	R_GLU_25	OE2	3.610
4RRP	R_ARG_104	NH1	R_ASP_102	OD2	3.150
4RRP	R_ARG_104	NH2	R_ASP_102	OD2	3.913
4RRP	R_ARG_108	NH2	R_GLU_105	OE1	3.360
4RRP	R_ARG_108	NH2	R_GLU_105	OE2	3.892
4RRP	R_HIS_134	NE2	R_GLU_119	OE2	3.581
4TRP	H_LYS_63	NZ	H_GLU_46	OE1	3.694
4TRP	H_LYS_63	NZ	H_GLU_46	OE2	2.776
4TRP	H_ARG_67	NH1	H_ASP_90	OD1	3.592
4TRP	H_ARG_67	NH1	H_ASP_90	OD2	2.874
4TRP	H_ARG_67	NH2	H_ASP_90	OD1	2.862
4TRP	H_ARG_67	NH2	H_ASP_90	OD2	3.539
4TRP	H_LYS_208	NZ	L_GLU_129	OE2	3.281

4TRP	H.LYS_209	NZ	H.GLU_211	OE1	3.661
4TRP	H.LYS_209	NZ	H.GLU_211	OE2	3.286
4TRP	L.ARG_66	NH2	L.GLU_86	OE1	3.076
4TRP	L.ARG_66	NH2	L.ASP_87	OD1	2.816
4TRP	L.ARG_66	NH2	L.ASP_87	OD2	3.551
4TRP	L.LYS_153	NZ	L.GLU_160	OE1	2.821
4TRP	L.LYS_153	NZ	L.GLU_160	OE2	3.459
4TRP	L.LYS_155	NZ	L.GLU_201	OE1	2.685
4TRP	L.LYS_155	NZ	L.GLU_201	OE2	3.225
4TRP	L.ARG_161	NH1	L.GLU_191	OE1	3.775
4TRP	L.ARG_161	NH1	L.GLU_191	OE2	2.926
4TRP	L.ARG_161	NH2	L.GLU_191	OE1	3.592
4TRP	L.ARG_161	NH2	L.GLU_191	OE2	3.079
4TRP	L.ARG_194	NH1	L.ASP_190	OD2	2.875
4TRP	L.HIS_195	ND1	L.ASP_157	OD2	2.604
4TRP	L.LYS_205	NZ	L.ASP_116	OD1	3.811
4TRP	L.LYS_205	NZ	L.ASP_116	OD2	3.031
4TUJ	A.ARG_38	NH1	A.ASP_90	OD1	2.738
4TUJ	A.ARG_38	NH2	A.GLU_46	OE1	3.121
4TUJ	A.ARG_38	NH2	A.ASP_90	OD1	3.886
4TUJ	A.ARG_67	NH1	A.ASP_90	OD1	3.524
4TUJ	A.ARG_67	NH1	A.ASP_90	OD2	2.860
4TUJ	A.ARG_67	NH2	A.ASP_90	OD1	3.074
4TUJ	A.ARG_67	NH2	A.ASP_90	OD2	3.761
4TUJ	B.ARG_59	NH1	B.ASP_65	OD1	3.932
4TUJ	B.ARG_66	NH1	B.GLU_84	OE1	3.650
4TUJ	B.ARG_66	NH1	B.GLU_84	OE2	3.183
4TUJ	B.ARG_66	NH2	B.GLU_84	OE1	3.557
4TUJ	B.ARG_66	NH2	B.GLU_86	OE1	2.800
4TUJ	B.ARG_66	NH2	B.ASP_87	OD1	2.741
4TUJ	B.ARG_66	NH2	B.ASP_87	OD2	3.500
4TUJ	B.LYS_153	NZ	B.GLU_160	OE1	2.671
4TUJ	B.LYS_153	NZ	B.GLU_160	OE2	2.941
4TUJ	B.LYS_155	NZ	B.GLU_201	OE1	2.816
4TUJ	B.LYS_155	NZ	B.GLU_201	OE2	3.174
4TUJ	B.HIS_195	ND1	B.ASP_157	OD2	3.098
4TUJ	B.LYS_205	NZ	B.ASP_116	OD1	3.715
4TUJ	B.LYS_205	NZ	B.ASP_116	OD2	2.602
4TUJ	C.ARG_38	NH1	C.ASP_90	OD1	2.708
4TUJ	C.ARG_38	NH2	C.GLU_46	OE1	3.153
4TUJ	C.ARG_38	NH2	C.ASP_90	OD1	3.791
4TUJ	C.ARG_67	NH1	C.ASP_90	OD1	3.571
4TUJ	C.ARG_67	NH1	C.ASP_90	OD2	2.878
4TUJ	C.ARG_67	NH2	C.ASP_90	OD1	2.853
4TUJ	C.ARG_67	NH2	C.ASP_90	OD2	3.465
4TUJ	D.ARG_66	NH1	D.GLU_84	OE1	3.649
4TUJ	D.ARG_66	NH1	D.GLU_84	OE2	3.433
4TUJ	D.ARG_66	NH2	D.GLU_84	OE1	3.528
4TUJ	D.ARG_66	NH2	D.ASP_87	OD1	2.665
4TUJ	D.ARG_66	NH2	D.ASP_87	OD2	3.342
4TUJ	D.LYS_148	NZ	D.GLU_111	OE1	2.802
4TUJ	D.LYS_148	NZ	D.GLU_111	OE2	3.509
4TUJ	D.LYS_155	NZ	D.GLU_201	OE1	2.443
4TUJ	D.LYS_155	NZ	D.GLU_201	OE2	3.654
4TUK	H.ARG_38	NH1	H.ASP_90	OD1	2.774
4TUK	H.ARG_38	NH2	H.GLU_46	OE1	2.957
4TUK	H.ARG_38	NH2	H.ASP_90	OD1	3.936
4TUK	H.LYS_63	NZ	H.GLU_46	OE1	3.702

4TUK	H.LYS.63	NZ	H.GLU.46	OE2	2.804
4TUK	H.ARG.67	NH1	H.ASP.90	OD1	3.628
4TUK	H.ARG.67	NH1	H.ASP.90	OD2	2.878
4TUK	H.ARG.67	NH2	H.ASP.90	OD1	2.889
4TUK	H.ARG.67	NH2	H.ASP.90	OD2	3.540
4TUK	H.LYS.208	NZ	L.GLU.129	OE2	3.061
4TUK	L.ARG.24	NH2	L.ASP.75	OD2	3.142
4TUK	L.ARG.66	NH2	L.GLU.86	OE1	3.710
4TUK	L.ARG.66	NH2	L.GLU.86	OE2	3.717
4TUK	L.ARG.66	NH2	L.ASP.87	OD1	2.787
4TUK	L.ARG.66	NH2	L.ASP.87	OD2	3.636
4TUK	L.LYS.148	NZ	L.GLU.111	OE1	3.533
4TUK	L.LYS.148	NZ	L.GLU.111	OE2	2.823
4TUK	L.LYS.153	NZ	L.GLU.160	OE1	2.835
4TUK	L.LYS.153	NZ	L.GLU.160	OE2	3.347
4TUK	L.LYS.155	NZ	L.GLU.201	OE1	2.857
4TUK	L.LYS.155	NZ	L.GLU.201	OE2	3.381
4TUK	L.HIS.195	ND1	L.ASP.157	OD2	2.878
4TUK	L.LYS.205	NZ	L.ASP.116	OD1	3.635
4TUK	L.LYS.205	NZ	L.ASP.116	OD2	3.012
4TUL	H.ARG.38	NH1	H.ASP.90	OD1	2.759
4TUL	H.ARG.38	NH2	H.GLU.46	OE1	2.795
4TUL	H.ARG.38	NH2	H.GLU.46	OE2	3.616
4TUL	H.LYS.63	NZ	H.GLU.46	OE1	3.726
4TUL	H.LYS.63	NZ	H.GLU.46	OE2	2.751
4TUL	H.ARG.67	NH1	H.ASP.90	OD1	3.442
4TUL	H.ARG.67	NH1	H.ASP.90	OD2	2.779
4TUL	H.ARG.67	NH2	H.ASP.90	OD1	2.973
4TUL	H.ARG.67	NH2	H.ASP.90	OD2	3.614
4TUL	H.LYS.205	NZ	H.ASP.207	OD2	3.859
4TUL	H.LYS.208	NZ	L.GLU.129	OE1	3.059
4TUL	H.LYS.208	NZ	L.GLU.129	OE2	2.741
4TUL	H.LYS.209	NZ	H.GLU.211	OE2	3.869
4TUL	L.ARG.66	NH1	L.GLU.84	OE1	3.630
4TUL	L.ARG.66	NH2	L.GLU.84	OE1	3.505
4TUL	L.ARG.66	NH2	L.GLU.84	OE2	3.947
4TUL	L.ARG.66	NH2	L.ASP.87	OD1	2.922
4TUL	L.ARG.66	NH2	L.ASP.87	OD2	3.565
4TUL	L.LYS.148	NZ	L.GLU.111	OE1	2.732
4TUL	L.LYS.148	NZ	L.GLU.111	OE2	3.835
4TUL	L.LYS.153	NZ	L.GLU.160	OE1	2.798
4TUL	L.LYS.153	NZ	L.GLU.160	OE2	3.593
4TUL	L.LYS.155	NZ	L.GLU.201	OE1	2.684
4TUL	L.LYS.155	NZ	L.GLU.201	OE2	3.268
4TUL	L.HIS.195	ND1	L.ASP.157	OD2	2.731
4TUL	L.LYS.205	NZ	L.ASP.116	OD1	3.657
4TUL	L.LYS.205	NZ	L.ASP.116	OD2	2.664
4TUO	A.ARG.38	NH1	A.ASP.90	OD1	2.863
4TUO	A.ARG.38	NH2	A.GLU.46	OE1	3.170
4TUO	A.ARG.38	NH2	A.ASP.90	OD1	3.978
4TUO	A.LYS.63	NZ	A.GLU.46	OE1	3.760
4TUO	A.LYS.63	NZ	A.GLU.46	OE2	2.759
4TUO	A.ARG.67	NH1	A.ASP.90	OD1	3.571
4TUO	A.ARG.67	NH1	A.ASP.90	OD2	2.889
4TUO	A.ARG.67	NH2	A.ASP.90	OD1	3.053
4TUO	A.ARG.67	NH2	A.ASP.90	OD2	3.693
4TUO	A.LYS.208	NZ	B.GLU.129	OE1	3.043
4TUO	B.ARG.66	NH1	B.GLU.84	OE2	3.371

4TUO	B_ARG_66	NH2	B_GLU_84	OE1	3.783
4TUO	B_ARG_66	NH2	B_GLU_86	OE1	2.770
4TUO	B_ARG_66	NH2	B_ASP_87	OD1	2.806
4TUO	B_ARG_66	NH2	B_ASP_87	OD2	3.596
4TUO	B_ARG_82	NH1	B_GLU_84	OE2	3.609
4TUO	B_LYS_153	NZ	B_GLU_160	OE1	3.151
4TUO	B_LYS_153	NZ	C_GLU_10	OE2	3.051
4TUO	B_LYS_155	NZ	B_GLU_201	OE1	2.809
4TUO	B_LYS_155	NZ	B_GLU_201	OE2	3.457
4TUO	B_ARG_161	NH1	B_GLU_191	OE1	3.847
4TUO	B_ARG_161	NH1	B_GLU_191	OE2	3.170
4TUO	B_ARG_161	NH2	B_GLU_191	OE1	3.069
4TUO	B_ARG_161	NH2	B_GLU_191	OE2	3.668
4TUO	B_HIS_195	ND1	B_ASP_157	OD2	3.859
4TUO	B_LYS_205	NZ	B_ASP_116	OD1	3.307
4TUO	B_LYS_205	NZ	B_ASP_116	OD2	3.070
4TUO	C_ARG_38	NH1	C_ASP_90	OD1	2.853
4TUO	C_ARG_38	NH2	C_GLU_46	OE1	3.152
4TUO	C_LYS_63	NZ	C_GLU_46	OE1	3.805
4TUO	C_LYS_63	NZ	C_GLU_46	OE2	2.709
4TUO	C_ARG_67	NH1	C_ASP_90	OD1	3.699
4TUO	C_ARG_67	NH1	C_ASP_90	OD2	2.901
4TUO	C_ARG_67	NH2	C_ASP_90	OD1	3.051
4TUO	C_ARG_67	NH2	C_ASP_90	OD2	3.598
4TUO	C_LYS_208	NZ	D_GLU_129	OE1	2.720
4TUO	C_LYS_208	NZ	D_GLU_129	OE2	3.136
4TUO	C_LYS_209	NZ	C_GLU_211	OE2	2.713
4TUO	D_ARG_66	NH1	D_GLU_84	OE1	3.352
4TUO	D_ARG_66	NH1	D_GLU_84	OE2	3.741
4TUO	D_ARG_66	NH2	D_GLU_84	OE2	3.775
4TUO	D_ARG_66	NH2	D_GLU_86	OE2	3.297
4TUO	D_ARG_66	NH2	D_ASP_87	OD1	2.690
4TUO	D_ARG_66	NH2	D_ASP_87	OD2	3.681
4TUO	D_LYS_148	NZ	D_GLU_111	OE1	3.722
4TUO	D_LYS_148	NZ	D_GLU_111	OE2	2.538
4TUO	D_LYS_153	NZ	D_GLU_160	OE1	3.774
4TUO	D_LYS_155	NZ	D_GLU_201	OE1	3.955
4TUO	D_ARG_161	NH1	D_GLU_191	OE1	3.866
4TUO	D_ARG_194	NH1	D_ASP_190	OD1	3.370
4TUO	D_ARG_194	NH1	D_ASP_190	OD2	2.866
4TUO	D_HIS_195	ND1	D_ASP_157	OD2	3.872
4TUO	D_HIS_195	NE2	D_GLU_191	OE1	2.622
4TUO	D_LYS_205	NZ	D_ASP_116	OD1	3.469
4TUO	D_LYS_205	NZ	D_ASP_116	OD2	2.762
4U0Q	A_HIS_187	NE2	A_ASP_183	OD1	2.822
4U0Q	A_HIS_187	NE2	A_ASP_183	OD2	3.914
4U0Q	A_LYS_211	NZ	A_GLU_215	OE2	3.825
4U0Q	A_LYS_221	NZ	A_ASP_172	OD1	3.037
4U0Q	A_HIS_240	NE2	A_GLU_168	OE1	2.387
4U0Q	A_HIS_240	NE2	A_GLU_168	OE2	3.627
4U0Q	A_LYS_302	NZ	A_ASP_305	OD1	3.987
4U0Q	A_LYS_302	NZ	A_ASP_305	OD2	2.715
4U0Q	A_LYS_310	NZ	A_ASP_230	OD2	2.731
4U0Q	A_LYS_366	NZ	A_GLU_362	OE1	3.983
4U0Q	A_HIS_414	NE2	A_GLU_391	OE1	2.780
4U0Q	A_HIS_414	NE2	A_GLU_391	OE2	3.302
4U0Q	A_ARG_423	NH2	A_ASP_162	OD2	3.272
4U0Q	A_HIS_427	NE2	A_ASP_162	OD1	3.792

4U0Q	A_LYS_434	NZ	A_GLU_465	OE2	2.539
4U0Q	A_LYS_436	NZ	A_ASP_440	OD1	3.388
4U0Q	A_LYS_436	NZ	A_ASP_440	OD2	3.258
4U0Q	A_LYS_441	NZ	A_ASP_461	OD1	2.915
4U0Q	A_LYS_441	NZ	A_ASP_461	OD2	3.189
4U0Q	A_LYS_441	NZ	A_GLU_465	OE1	3.453
4U0Q	A_ARG_458	NH2	A_GLU_454	OE1	3.364
4U0Q	A_ARG_476	NH1	A_ASP_473	OD1	3.385
4U0Q	A_LYS_486	NZ	A_GLU_239	OE1	3.379
4U0Q	A_LYS_486	NZ	A_GLU_239	OE2	2.794
4U0Q	A_HIS_489	NE2	A_GLU_168	OE1	2.333
4U0Q	A_HIS_489	NE2	A_GLU_239	OE1	3.275
4U0Q	A_HIS_495	NE2	D_GLU_31	OE1	3.802
4U0Q	A_HIS_495	NE2	D_GLU_31	OE2	2.620
4U0Q	A_HIS_496	ND1	D_GLU_31	OE1	3.680
4U0Q	B_HIS_53	ND1	B_GLU_64	OE1	2.648
4U0Q	B_HIS_53	ND1	B_GLU_64	OE2	3.336
4U0Q	B_ARG_54	NH2	B_GLU_92	OE1	2.778
4U0Q	B_ARG_54	NH2	B_GLU_92	OE2	3.437
4U0Q	B_LYS_148	NZ	B_GLU_155	OE2	3.304
4U0Q	B_ARG_157	NH1	B_ASP_179	OD2	3.570
4U0Q	B_ARG_157	NH2	B_ASP_179	OD1	2.730
4U0Q	B_ARG_157	NH2	B_ASP_179	OD2	2.748
4U0Q	B_HIS_170	ND1	D_GLU_172	OE1	2.788
4U0Q	B_HIS_170	NE2	B_GLU_168	OE1	3.394
4U0Q	B_ARG_184	NH2	B_ASP_147	OD2	3.560
4U0Q	C_HIS_187	NE2	C_ASP_183	OD1	2.825
4U0Q	C_HIS_187	NE2	C_ASP_183	OD2	3.905
4U0Q	C_LYS_211	NZ	C_GLU_215	OE2	3.781
4U0Q	C_LYS_221	NZ	C_ASP_172	OD1	3.043
4U0Q	C_HIS_240	NE2	C_GLU_168	OE1	2.360
4U0Q	C_HIS_240	NE2	C_GLU_168	OE2	3.605
4U0Q	C_LYS_310	NZ	C_ASP_230	OD2	2.754
4U0Q	C_LYS_327	NZ	C_ASP_331	OD1	3.020
4U0Q	C_LYS_327	NZ	C_ASP_331	OD2	3.351
4U0Q	C_LYS_411	NZ	C_ASP_408	OD1	3.493
4U0Q	C_HIS_414	NE2	C_GLU_391	OE2	3.600
4U0Q	C_ARG_423	NH2	C_ASP_162	OD2	3.190
4U0Q	C_HIS_427	NE2	C_ASP_162	OD1	3.751
4U0Q	C_LYS_434	NZ	C_GLU_465	OE2	2.762
4U0Q	C_LYS_436	NZ	C_ASP_440	OD1	3.394
4U0Q	C_LYS_436	NZ	C_ASP_440	OD2	3.260
4U0Q	C_LYS_441	NZ	C_ASP_461	OD1	3.208
4U0Q	C_LYS_441	NZ	C_ASP_461	OD2	2.815
4U0Q	C_LYS_441	NZ	C_GLU_465	OE1	3.460
4U0Q	C_ARG_476	NH2	C_ASP_473	OD1	2.770
4U0Q	C_LYS_486	NZ	C_GLU_239	OE1	3.354
4U0Q	C_LYS_486	NZ	C_GLU_239	OE2	2.814
4U0Q	C_HIS_489	NE2	C_GLU_168	OE1	2.335
4U0Q	C_HIS_489	NE2	C_GLU_239	OE1	3.280
4U0Q	C_HIS_495	ND1	B_ASP_32	OD2	3.411
4U0Q	D_HIS_53	ND1	D_GLU_64	OE1	2.807
4U0Q	D_HIS_53	ND1	D_GLU_64	OE2	3.881
4U0Q	D_ARG_54	NH2	D_GLU_92	OE1	2.781
4U0Q	D_ARG_54	NH2	D_GLU_92	OE2	3.453
4U0Q	D_LYS_63	NZ	D_ASP_65	OD1	3.005
4U0Q	D_LYS_63	NZ	D_ASP_65	OD2	3.008
4U0Q	D_ARG_106	NH1	D_GLU_129	OE1	2.747

4U0Q	D_ARG_106	NH1	D_GLU_129	OE2	3.871
4U0Q	D_LYS_148	NZ	D_GLU_155	OE2	3.319
4U0Q	D_ARG_157	NH1	D_ASP_179	OD1	3.344
4U0Q	D_ARG_157	NH1	D_ASP_179	OD2	2.708
4U0Q	D_ARG_157	NH2	D_GLU_155	OE1	3.810
4U0Q	D_ARG_157	NH2	D_ASP_179	OD1	2.790
4U0Q	D_ARG_157	NH2	D_ASP_179	OD2	3.368
4U0Q	D_HIS_170	ND1	B_GLU_172	OE1	2.879
4U0Q	D_HIS_170	ND1	B_GLU_172	OE2	2.959
4U0Q	D_HIS_170	NE2	D_GLU_168	OE1	3.465
4U0Q	D_ARG_184	NH2	D_ASP_147	OD2	3.553
4U0Q	D_LYS_191	NZ	C_GLU_362	OE2	3.108
4U3X	A_ARG_38	NH1	A_ASP_90	OD1	2.898
4U3X	A_ARG_67	NH1	A_ASP_90	OD1	3.886
4U3X	A_ARG_67	NH1	A_ASP_90	OD2	2.695
4U3X	A_ARG_67	NH2	A_ASP_90	OD1	3.163
4U3X	A_ARG_67	NH2	A_ASP_90	OD2	3.392
4U3X	A_LYS_98	NZ	A_GLU_32	OE2	3.316
4U3X	A_HIS_106	NE2	B_GLU_35	OE1	2.597
4U3X	A_HIS_106	NE2	B_GLU_35	OE2	3.650
4U3X	B_LYS_1	NZ	B_GLU_7	OE1	2.763
4U3X	B_LYS_1	NZ	B_GLU_7	OE2	3.987
4U3X	B_ARG_61	NH1	A_ASP_33	OD2	2.723
4U3X	B_ARG_61	NH2	A_ASP_33	OD2	2.983
4U3X	B_ARG_112	NH2	A_ASP_109	OD1	3.763
4U3X	B_ARG_112	NH2	A_ASP_109	OD2	3.035
4U3X	B_ARG_125	NH1	B_ASP_119	OD2	3.378
4U3X	B_ARG_125	NH2	B_ASP_119	OD1	3.266
4U3X	B_ARG_125	NH2	B_ASP_119	OD2	3.781
4U3X	C_ARG_38	NH1	C_ASP_90	OD1	3.008
4U3X	C_ARG_38	NH2	C_ASP_90	OD1	3.918
4U3X	C_ARG_67	NH1	C_ASP_90	OD1	3.636
4U3X	C_ARG_67	NH1	C_ASP_90	OD2	3.951
4U3X	C_ARG_67	NH2	C_ASP_90	OD1	3.430
4U3X	C_ARG_67	NH2	C_ASP_90	OD2	2.349
4U3X	C_LYS_98	NZ	C_GLU_32	OE1	3.558
4U3X	C_LYS_98	NZ	C_GLU_32	OE2	2.950
4U3X	C_HIS_106	NE2	D_GLU_35	OE1	2.720
4U3X	C_HIS_106	NE2	D_GLU_35	OE2	3.669
4U3X	D_LYS_1	NZ	D_GLU_7	OE1	3.339
4U3X	D_LYS_1	NZ	D_GLU_7	OE2	2.952
4U3X	D_LYS_13	NZ	D_ASP_18	OD2	3.704
4U3X	D_ARG_61	NH1	C_ASP_33	OD2	3.116
4U3X	D_ARG_61	NH2	C_ASP_33	OD2	3.400
4U3X	D_ARG_112	NH2	C_ASP_109	OD2	3.567
4U3X	D_ARG_125	NH1	D_ASP_119	OD1	3.983
4U3X	D_ARG_125	NH1	D_ASP_119	OD2	3.205
4U3X	D_ARG_125	NH2	D_ASP_119	OD1	3.233
4U3X	D_ARG_125	NH2	D_ASP_119	OD2	3.715
4U6G	H_ARG_38	NH1	H_ASP_86	OD1	3.182
4U6G	H_ARG_38	NH2	H_GLU_46	OE1	3.518
4U6G	H_ARG_38	NH2	H_GLU_46	OE2	3.054
4U6G	H_ARG_50	NH1	H_ASP_58	OD2	3.942
4U6G	H_ARG_50	NH1	H_GLU_100J	OE1	3.369
4U6G	H_ARG_50	NH1	H_GLU_100J	OE2	2.951
4U6G	H_ARG_50	NH2	H_ASP_58	OD2	2.415
4U6G	H_ARG_66	NH1	H_ASP_86	OD2	3.486
4U6G	H_ARG_66	NH2	H_ASP_86	OD1	3.579

4U6G	H_ARG_66	NH2	H_ASP_86	OD2	3.807
4U6G	H_ARG_94	NH2	H_ASP_102	OD1	2.954
4U6G	H_LYS_143	NZ	L_GLU_125	OE2	3.603
4U6G	H_LYS_209	NZ	L_GLU_124	OE1	2.829
4U6G	H_LYS_209	NZ	L_GLU_124	OE2	2.866
4U6G	H_ARG_210	NH1	H_GLU_212	OE2	3.692
4U6G	H_ARG_210	NH2	H_GLU_212	OE2	3.652
4U6G	L_ARG_29	NH1	L_ASP_26	OD1	3.440
4U6G	L_HIS_31	ND1	H_GLU_100I	OE2	3.196
4U6G	L_ARG_54	NH1	L_ASP_60	OD1	3.819
4U6G	L_ARG_61	NH1	B_GLU_81	OE1	3.298
4U6G	L_ARG_61	NH2	L_ASP_82	OD1	3.284
4U6G	L_ARG_61	NH2	L_ASP_82	OD2	3.928
4U6G	L_ARG_91	NH1	H_GLU_100J	OE1	3.679
4U6G	L_ARG_91	NH1	H_GLU_100J	OE2	3.478
4U6G	L_ARG_91	NH2	H_GLU_100J	OE2	3.428
4U6G	L_LYS_93	NZ	L_GLU_3	OE2	3.425
4U6G	L_LYS_103	NZ	L_ASP_83	OD1	2.775
4U6G	L_LYS_150	NZ	L_GLU_204	OE2	3.294
4U6G	A_ARG_38	NH1	A_ASP_86	OD1	3.130
4U6G	A_ARG_38	NH2	A_GLU_46	OE2	3.390
4U6G	A_ARG_50	NH1	A_GLU_100J	OE1	2.748
4U6G	A_ARG_50	NH1	A_GLU_100J	OE2	2.961
4U6G	A_ARG_50	NH2	A_ASP_58	OD2	2.646
4U6G	A_ARG_50	NH2	A_GLU_100J	OE2	3.684
4U6G	A_ARG_66	NH1	A_ASP_86	OD2	3.552
4U6G	A_ARG_66	NH2	A_ASP_86	OD1	3.394
4U6G	A_ARG_66	NH2	A_ASP_86	OD2	3.979
4U6G	A_ARG_94	NH2	A_ASP_102	OD1	2.808
4U6G	A_LYS_143	NZ	B_GLU_125	OE2	3.217
4U6G	A_LYS_201	NZ	H_ASP_30	OD1	3.983
4U6G	A_LYS_209	NZ	B_GLU_124	OE1	2.769
4U6G	A_LYS_209	NZ	B_GLU_124	OE2	3.063
4U6G	B_ARG_29	NH1	B_ASP_26	OD1	3.536
4U6G	B_HIS_31	ND1	A_GLU_100I	OE2	3.102
4U6G	B_ARG_54	NH1	B_ASP_60	OD1	3.700
4U6G	B_ARG_61	NH2	B_GLU_81	OE1	3.869
4U6G	B_ARG_61	NH2	B_ASP_82	OD1	3.159
4U6G	B_ARG_61	NH2	B_ASP_82	OD2	3.682
4U6G	B_ARG_91	NH1	A_GLU_100J	OE1	3.587
4U6G	B_ARG_91	NH1	A_GLU_100J	OE2	3.310
4U6G	B_ARG_91	NH2	A_GLU_100J	OE2	3.407
4U6G	B_LYS_103	NZ	B_ASP_83	OD1	2.873
4U6G	B_LYS_111	NZ	B_GLU_199	OE1	3.272
4U6G	B_LYS_150	NZ	B_GLU_204	OE1	3.711
4U6G	B_LYS_150	NZ	B_GLU_204	OE2	3.254
4U6V	H_HIS_35	NE2	H_ASP_98	OD1	3.305
4U6V	H_HIS_35	NE2	H_ASP_98	OD2	2.654
4U6V	H_ARG_38	NH1	H_ASP_89	OD2	2.858
4U6V	H_ARG_38	NH2	H_GLU_46	OE1	3.188
4U6V	H_ARG_38	NH2	H_GLU_46	OE2	3.968
4U6V	H_ARG_38	NH2	H_ASP_89	OD2	3.604
4U6V	H_ARG_66	NH1	H_ASP_89	OD1	2.752
4U6V	H_ARG_66	NH1	H_ASP_89	OD2	3.786
4U6V	H_ARG_66	NH2	H_ASP_89	OD1	3.455
4U6V	H_ARG_66	NH2	H_ASP_89	OD2	2.979
4U6V	H_ARG_97	NH2	H_ASP_110	OD2	2.478
4U6V	H_ARG_99	NH2	H_ASP_110	OD1	3.312

4U6V	H_ARG_99	NH2	L_GLU_55	OE1	2.660
4U6V	H_ARG_99	NH2	L_GLU_55	OE2	2.823
4U6V	H_HIS_105	NE2	A_ASP_183	OD1	3.150
4U6V	H_HIS_105	NE2	A_ASP_183	OD2	3.236
4U6V	H_LYS_152	NZ	H_ASP_153	OD1	3.594
4U6V	H_LYS_152	NZ	H_ASP_153	OD2	3.480
4U6V	H_LYS_215	NZ	H_ASP_217	OD1	3.333
4U6V	H_LYS_215	NZ	H_ASP_217	OD2	3.285
4U6V	H_LYS_218	NZ	L_GLU_122	OE1	2.258
4U6V	H_LYS_218	NZ	L_GLU_122	OE2	3.923
4U6V	H_ARG_219	NH1	H_GLU_221	OE1	3.555
4U6V	L_ARG_24	NH2	L_GLU_70	OE1	3.373
4U6V	L_LYS_39	NZ	L_ASP_81	OD1	3.062
4U6V	L_LYS_39	NZ	L_ASP_81	OD2	3.255
4U6V	L_ARG_61	NH2	L_ASP_82	OD1	2.876
4U6V	L_ARG_61	NH2	L_ASP_82	OD2	3.235
4U6V	L_ARG_141	NH1	L_GLU_164	OE2	3.480
4U6V	L_ARG_141	NH2	L_GLU_104	OE1	3.162
4U6V	L_ARG_141	NH2	L_GLU_104	OE2	3.384
4U6V	L_ARG_141	NH2	L_GLU_164	OE1	3.915
4U6V	L_ARG_141	NH2	L_GLU_164	OE2	3.880
4U6V	L_LYS_148	NZ	L_GLU_194	OE2	3.817
4U6V	L_LYS_187	NZ	L_ASP_184	OD1	3.136
4U6V	A_LYS_36	NZ	A_GLU_280	OE1	3.134
4U6V	A_LYS_46	NZ	A_ASP_44	OD2	3.954
4U6V	A_LYS_51	NZ	A_ASP_44	OD2	3.960
4U6V	A_LYS_51	NZ	A_GLU_289	OE2	3.066
4U6V	A_ARG_56	NH2	A_ASP_227	OD1	3.348
4U6V	A_ARG_56	NH2	A_ASP_227	OD2	2.841
4U6V	A_LYS_85	NZ	A_GLU_250	OE2	3.967
4U6V	A_ARG_104	NH2	A_ASP_100	OD1	3.350
4U6V	A_ARG_104	NH2	A_ASP_100	OD2	2.842
4U6V	A_LYS_147	NZ	A_GLU_111	OE1	3.728
4U6V	A_LYS_163	NZ	A_ASP_162	OD2	3.943
4U6V	A_LYS_164	NZ	A_GLU_158	OE1	3.750
4U6V	A_ARG_184	NH2	A_ASP_254	OD1	2.848
4U6V	A_ARG_184	NH2	A_ASP_254	OD2	2.966
4U6V	A_ARG_184	NH2	A_ASP_272	OD1	2.573
4U6V	A_ARG_200	NH1	H_ASP_56	OD1	3.722
4U6V	A_ARG_200	NH1	H_ASP_56	OD2	3.481
4U6V	A_LYS_205	NZ	A_GLU_70	OE1	3.668
4U6V	A_LYS_205	NZ	A_GLU_70	OE2	3.472
4U6V	A_ARG_236	NH1	A_ASP_44	OD1	3.407
4U6V	A_ARG_236	NH2	A_ASP_44	OD1	3.125
4U6V	A_ARG_251	NH2	A_ASP_276	OD2	3.363
4U6V	A_ARG_253	NH2	A_ASP_276	OD1	2.926
4U6V	A_ARG_253	NH2	A_ASP_276	OD2	3.227
4U6V	A_LYS_266	NZ	L_ASP_93	OD1	2.981
4U6V	A_LYS_271	NZ	A_ASP_185	OD1	2.718
4U6V	A_LYS_273	NZ	A_ASP_255	OD2	3.278
4U6V	A_ARG_277	NH2	A_GLU_250	OE1	2.466
4U6V	A_ARG_281	NH2	A_ASP_246	OD1	2.738
4U6V	K_HIS_35	NE2	K_ASP_98	OD1	3.310
4U6V	K_HIS_35	NE2	K_ASP_98	OD2	2.683
4U6V	K_ARG_38	NH1	K_ASP_89	OD2	2.844
4U6V	K_ARG_38	NH2	K_GLU_46	OE1	3.203
4U6V	K_ARG_38	NH2	K_GLU_46	OE2	3.978
4U6V	K_ARG_38	NH2	K_ASP_89	OD2	3.616

4U6V	K_ARG_66	NH1	K_ASP_89	OD1	2.744
4U6V	K_ARG_66	NH1	K_ASP_89	OD2	3.770
4U6V	K_ARG_66	NH2	K_ASP_89	OD1	3.441
4U6V	K_ARG_66	NH2	K_ASP_89	OD2	2.968
4U6V	K_ARG_97	NH2	K_ASP_110	OD2	2.501
4U6V	K_ARG_99	NH2	K_ASP_110	OD1	3.302
4U6V	K_ARG_99	NH2	M_GLU_55	OE1	2.606
4U6V	K_ARG_99	NH2	M_GLU_55	OE2	2.857
4U6V	K_HIS_105	NE2	B_ASP_183	OD1	2.992
4U6V	K_HIS_105	NE2	B_ASP_183	OD2	3.142
4U6V	K_LYS_152	NZ	K_ASP_153	OD1	3.584
4U6V	K_LYS_152	NZ	K_ASP_153	OD2	3.467
4U6V	K_LYS_215	NZ	K_ASP_217	OD1	3.339
4U6V	K_LYS_215	NZ	K_ASP_217	OD2	3.278
4U6V	K_LYS_218	NZ	M_GLU_122	OE1	2.653
4U6V	K_ARG_219	NH1	K_GLU_221	OE1	3.551
4U6V	M_ARG_24	NH2	M_GLU_70	OE1	3.369
4U6V	M_LYS_39	NZ	M_ASP_81	OD1	3.066
4U6V	M_LYS_39	NZ	M_ASP_81	OD2	3.241
4U6V	M_ARG_61	NH2	M_ASP_82	OD1	2.871
4U6V	M_ARG_61	NH2	M_ASP_82	OD2	3.232
4U6V	M_ARG_141	NH1	M_GLU_164	OE2	3.486
4U6V	M_ARG_141	NH2	M_GLU_104	OE1	3.180
4U6V	M_ARG_141	NH2	M_GLU_104	OE2	3.454
4U6V	M_ARG_141	NH2	M_GLU_164	OE1	3.895
4U6V	M_ARG_141	NH2	M_GLU_164	OE2	3.876
4U6V	M_LYS_148	NZ	M_GLU_194	OE1	3.300
4U6V	M_LYS_168	NZ	M_ASP_166	OD1	3.534
4U6V	M_LYS_168	NZ	M_ASP_169	OD2	3.988
4U6V	M_LYS_187	NZ	M_ASP_184	OD1	3.129
4U6V	M_HIS_188	ND1	M_ASP_150	OD2	3.072
4U6V	B_LYS_36	NZ	B_GLU_280	OE1	3.143
4U6V	B_LYS_46	NZ	B_ASP_44	OD2	3.962
4U6V	B_LYS_51	NZ	B_ASP_44	OD2	3.959
4U6V	B_LYS_51	NZ	B_GLU_289	OE2	3.068
4U6V	B_ARG_56	NH2	B_ASP_227	OD1	3.358
4U6V	B_ARG_56	NH2	B_ASP_227	OD2	2.849
4U6V	B_LYS_85	NZ	B_GLU_250	OE2	3.970
4U6V	B_ARG_104	NH2	B_ASP_100	OD1	3.340
4U6V	B_ARG_104	NH2	B_ASP_100	OD2	2.845
4U6V	B_LYS_147	NZ	B_GLU_111	OE1	3.726
4U6V	B_LYS_163	NZ	B_ASP_162	OD2	3.942
4U6V	B_LYS_164	NZ	B_GLU_158	OE1	3.594
4U6V	B_ARG_184	NH2	B_ASP_254	OD1	2.852
4U6V	B_ARG_184	NH2	B_ASP_254	OD2	2.960
4U6V	B_ARG_184	NH2	B_ASP_272	OD1	2.585
4U6V	B_ARG_200	NH1	K_ASP_56	OD1	3.809
4U6V	B_ARG_200	NH1	K_ASP_56	OD2	3.557
4U6V	B_LYS_205	NZ	B_GLU_70	OE1	3.673
4U6V	B_LYS_205	NZ	B_GLU_70	OE2	3.473
4U6V	B_ARG_236	NH1	B_ASP_44	OD1	3.418
4U6V	B_ARG_236	NH2	B_ASP_44	OD1	3.133
4U6V	B_ARG_251	NH2	B_ASP_276	OD2	3.376
4U6V	B_ARG_253	NH2	B_ASP_276	OD1	2.931
4U6V	B_ARG_253	NH2	B_ASP_276	OD2	3.222
4U6V	B_LYS_266	NZ	M_ASP_93	OD1	3.145
4U6V	B_LYS_271	NZ	B_ASP_185	OD1	2.724
4U6V	B_LYS_273	NZ	B_ASP_255	OD2	3.277

4U6V	B_ARG_277	NH2	B_GLU_250	OE1	2.460
4U6V	B_ARG_281	NH2	B_ASP_246	OD1	2.737
4UAO	A_ARG_73	NH2	A_GLU_201	OE1	3.924
4UAO	A_ARG_73	NH2	A_GLU_201	OE2	3.498
4UAO	A_ARG_120	NH1	A_GLU_123	OE1	3.546
4UAO	A_ARG_120	NH1	A_ASP_216	OD2	3.693
4UAO	A_ARG_120	NH2	A_GLU_123	OE1	3.780
4UAO	A_LYS_122	NZ	A_ASP_216	OD2	2.797
4UAO	A_LYS_190	NZ	A_ASP_158	OD2	3.237
4UAO	A_LYS_190	NZ	A_GLU_187	OE2	3.980
4UAO	A_LYS_237	NZ	A_GLU_78	OE1	3.297
4UAO	A_ARG_249	NH1	A_GLU_187	OE1	3.415
4UAO	A_ARG_249	NH1	A_GLU_381	OE1	3.557
4UAO	A_ARG_249	NH1	A_GLU_381	OE2	3.345
4UAO	A_ARG_249	NH2	A_GLU_187	OE1	3.981
4UAO	A_LYS_250	NZ	A_GLU_381	OE2	3.404
4UAO	A_LYS_256	NZ	A_GLU_267	OE1	2.830
4UAO	A_LYS_256	NZ	A_GLU_267	OE2	3.541
4UAO	A_ARG_277	NH1	A_GLU_275	OE1	2.891
4UAO	A_ARG_280	NH1	A_ASP_230	OD1	2.845
4UAO	A_ARG_280	NH1	A_ASP_230	OD2	3.123
4UAO	A_ARG_280	NH2	A_ASP_230	OD2	3.328
4UAO	A_ARG_284	NH2	A_ASP_224	OD1	3.788
4UAO	A_ARG_284	NH2	A_ASP_224	OD2	3.066
4UAO	A_ARG_296	NH2	A_GLU_288	OE1	2.772
4UAO	A_ARG_317	NH1	C_GLU_100B	OE2	3.537
4UAO	A_ARG_317	NH2	C_GLU_100B	OE1	3.794
4UAO	A_ARG_317	NH2	C_GLU_100B	OE2	2.800
4UAO	A_LYS_336	NZ	A_ASP_79	OD1	2.775
4UAO	A_LYS_336	NZ	A_ASP_79	OD2	3.272
4UAO	A_LYS_353	NZ	A_GLU_273	OE1	3.628
4UAO	A_LYS_360	NZ	A_ASP_63	OD1	3.580
4UAO	A_LYS_360	NZ	A_ASP_63	OD2	3.421
4UAO	B_ARG_61	NH2	B_ASP_82	OD1	3.532
4UAO	B_ARG_66	NH2	B_ASP_28	OD1	3.432
4UAO	B_LYS_92	NZ	B_ASP_28	OD2	3.374
4UAO	B_ARG_103	NH2	B_ASP_165	OD1	2.738
4UAO	B_ARG_108	NH1	B_ASP_170	OD2	3.952
4UAO	B_LYS_149	NZ	B_GLU_195	OE2	3.010
4UAO	B_ARG_155	NH1	B_ASP_157	OD1	3.116
4UAO	B_ARG_155	NH1	B_ASP_185	OD2	3.521
4UAO	B_ARG_155	NH2	B_ASP_185	OD1	3.054
4UAO	B_ARG_155	NH2	B_ASP_185	OD2	3.232
4UAO	B_HIS_189	ND1	B_ASP_185	OD1	3.890
4UAO	B_LYS_199	NZ	B_ASP_110	OD1	3.495
4UAO	B_LYS_199	NZ	B_ASP_110	OD2	3.079
4UAO	C_ARG_38	NH1	C_ASP_86	OD1	3.163
4UAO	C_ARG_38	NH2	C_GLU_46	OE1	3.888
4UAO	C_ARG_38	NH2	C_GLU_46	OE2	3.064
4UAO	C_ARG_38	NH2	C_ASP_86	OD1	3.804
4UAO	C_ARG_56	NH1	A_GLU_81	OE2	2.819
4UAO	C_ARG_56	NH2	A_ASP_174	OD1	3.129
4UAO	C_ARG_56	NH2	A_ASP_174	OD2	2.857
4UAO	C_ARG_66	NH1	C_GLU_83	OE1	3.463
4UAO	C_ARG_66	NH1	C_ASP_86	OD1	2.970
4UAO	C_ARG_66	NH1	C_ASP_86	OD2	2.789
4UAO	C_ARG_66	NH2	C_GLU_83	OE1	3.731
4UAO	C_ARG_94	NH1	C_GLU_100B	OE1	2.986

4UAO	C_ARG_94	NH1	C_ASP_101	OD1	3.545
4UAO	C_ARG_94	NH1	C_ASP_101	OD2	3.032
4UAO	C_ARG_95	NH1	C_ASP_100C	OD2	2.956
4UAO	C_ARG_95	NH2	A_GLU_173	OE2	3.027
4UV6	A_ARG_73	NH1	A_GLU_201	OE1	2.994
4UV6	A_ARG_73	NH1	A_GLU_201	OE2	3.932
4UV6	A_ARG_73	NH2	A_GLU_201	OE1	3.217
4UV6	A_ARG_73	NH2	A_GLU_201	OE2	2.666
4UV6	A_ARG_73	NH2	A_GLU_288	OE2	3.591
4UV6	A_ARG_120	NH1	A_GLU_123	OE2	3.707
4UV6	A_ARG_120	NH2	A_ASP_216	OD1	3.645
4UV6	A_LYS_122	NZ	A_ASP_216	OD1	3.360
4UV6	A_ARG_146	NH2	A_ASP_133	OD2	3.248
4UV6	A_LYS_148	NZ	A_GLU_145	OE2	3.128
4UV6	A_LYS_190	NZ	A_ASP_158	OD2	3.666
4UV6	A_LYS_222	NZ	A_GLU_104	OE2	2.916
4UV6	A_LYS_237	NZ	A_GLU_78	OE1	2.996
4UV6	A_LYS_237	NZ	A_GLU_78	OE2	3.806
4UV6	A_LYS_246	NZ	A_ASP_242	OD2	3.993
4UV6	A_ARG_249	NH1	A_GLU_187	OE1	3.777
4UV6	A_ARG_249	NH1	A_GLU_187	OE2	2.741
4UV6	A_ARG_249	NH2	A_GLU_187	OE1	2.790
4UV6	A_ARG_249	NH2	A_GLU_187	OE2	3.285
4UV6	A_ARG_249	NH2	A_GLU_381	OE1	3.049
4UV6	A_ARG_249	NH2	A_GLU_381	OE2	2.841
4UV6	A_LYS_256	NZ	A_GLU_267	OE1	3.465
4UV6	A_LYS_256	NZ	A_GLU_267	OE2	3.209
4UV6	A_LYS_256	NZ	A_ASP_367	OD2	3.488
4UV6	A_ARG_277	NH2	A_GLU_275	OE2	3.331
4UV6	A_ARG_280	NH1	A_ASP_230	OD1	2.732
4UV6	A_ARG_280	NH1	A_ASP_230	OD2	3.546
4UV6	A_ARG_280	NH2	A_GLU_227	OE1	3.879
4UV6	A_ARG_280	NH2	A_ASP_230	OD1	3.530
4UV6	A_ARG_280	NH2	A_ASP_230	OD2	2.776
4UV6	A_ARG_284	NH2	A_ASP_224	OD1	3.612
4UV6	A_ARG_284	NH2	A_ASP_224	OD2	3.190
4UV6	A_ARG_296	NH2	A_GLU_288	OE2	3.629
4UV6	A_ARG_313	NH1	A_GLU_310	OE1	2.851
4UV6	A_ARG_313	NH1	A_GLU_310	OE2	3.172
4UV6	A_LYS_321	NZ	A_ASP_318	OD1	3.965
4UV6	A_LYS_336	NZ	A_ASP_79	OD1	3.453
4UV6	A_LYS_336	NZ	A_ASP_79	OD2	3.112
4UV6	A_LYS_336	NZ	A_ASP_333	OD1	3.782
4UV6	A_HIS_378	NE2	A_GLU_381	OE2	3.710
4UV6	B_ARG_73	NH1	B_GLU_201	OE1	3.228
4UV6	B_ARG_73	NH2	B_GLU_201	OE1	3.286
4UV6	B_ARG_73	NH2	B_GLU_201	OE2	2.695
4UV6	B_ARG_73	NH2	B_GLU_288	OE2	3.736
4UV6	B_LYS_148	NZ	B_GLU_145	OE2	3.156
4UV6	B_ARG_180	NH2	A_GLU_396	OE2	2.784
4UV6	B_LYS_190	NZ	B_ASP_158	OD2	3.677
4UV6	B_LYS_222	NZ	B_GLU_104	OE2	2.924
4UV6	B_LYS_237	NZ	B_GLU_78	OE1	2.994
4UV6	B_LYS_237	NZ	B_GLU_78	OE2	3.805
4UV6	B_LYS_246	NZ	B_ASP_242	OD2	3.993
4UV6	B_ARG_249	NH1	B_GLU_187	OE1	3.799
4UV6	B_ARG_249	NH1	B_GLU_187	OE2	2.742
4UV6	B_ARG_249	NH2	B_GLU_187	OE1	2.790

4UV6	B_ARG_249	NH2	B_GLU_187	OE2	3.296
4UV6	B_ARG_249	NH2	B_GLU_381	OE1	3.038
4UV6	B_ARG_249	NH2	B_GLU_381	OE2	2.812
4UV6	B_LYS_256	NZ	B_GLU_267	OE1	3.476
4UV6	B_LYS_256	NZ	B_GLU_267	OE2	3.242
4UV6	B_LYS_256	NZ	B_ASP_367	OD2	3.465
4UV6	B_ARG_277	NH2	B_GLU_275	OE2	3.309
4UV6	B_ARG_280	NH1	B_ASP_230	OD1	2.709
4UV6	B_ARG_280	NH1	B_ASP_230	OD2	3.518
4UV6	B_ARG_280	NH2	B_GLU_227	OE2	3.911
4UV6	B_ARG_280	NH2	B_ASP_230	OD1	3.525
4UV6	B_ARG_280	NH2	B_ASP_230	OD2	2.745
4UV6	B_ARG_284	NH2	B_ASP_224	OD1	3.584
4UV6	B_ARG_284	NH2	B_ASP_224	OD2	3.156
4UV6	B_ARG_313	NH1	B_GLU_310	OE1	2.951
4UV6	B_ARG_313	NH1	B_GLU_310	OE2	2.848
4UV6	B_ARG_313	NH2	A_GLU_60	OE1	2.768
4UV6	B_LYS_321	NZ	B_ASP_318	OD1	3.922
4UV6	B_LYS_336	NZ	B_ASP_79	OD2	3.702
4UV6	B_LYS_336	NZ	B_ASP_333	OD1	3.823
4UV6	B_HIS_378	NE2	B_GLU_381	OE2	3.739
4WEU	D_ARG_838	NH1	D_ASP_890	OD1	3.018
4WEU	D_ARG_838	NH2	D_GLU_846	OE1	2.933
4WEU	D_ARG_838	NH2	D_GLU_846	OE2	3.823
4WEU	D_ARG_867	NH1	D_ASP_890	OD1	3.567
4WEU	D_ARG_867	NH1	D_ASP_890	OD2	2.686
4WEU	D_ARG_867	NH2	D_ASP_890	OD1	2.946
4WEU	D_ARG_867	NH2	D_ASP_890	OD2	3.615
4WEU	D_LYS_887	NZ	A_GLU_145	OE1	3.143
4WEU	A_LYS_49	NZ	A_GLU_240	OE2	2.906
4WEU	A_ARG_64	NH1	A_GLU_26	OE2	3.571
4WEU	A_LYS_66	NZ	A_GLU_26	OE1	3.929
4WEU	A_ARG_96	NH1	A_GLU_94	OE2	3.701
4WEU	A_ARG_96	NH1	B_GLU_94	OE1	3.636
4WEU	A_ARG_96	NH1	B_GLU_94	OE2	3.058
4WEU	A_ARG_96	NH2	B_GLU_94	OE1	2.949
4WEU	A_ARG_96	NH2	B_GLU_94	OE2	3.852
4WEU	A_LYS_104	NZ	A_GLU_101	OE1	3.418
4WEU	A_LYS_120	NZ	A_GLU_89	OE1	2.914
4WEU	A_ARG_136	NH1	D_GLU_889	OE1	2.898
4WEU	A_ARG_136	NH2	A_GLU_145	OE1	3.553
4WEU	A_HIS_155	NE2	A_GLU_152	OE2	2.869
4WEU	A_LYS_172	NZ	A_GLU_170	OE2	3.445
4WEU	B_LYS_49	NZ	B_GLU_240	OE1	3.611
4WEU	B_LYS_49	NZ	B_GLU_240	OE2	3.160
4WEU	B_ARG_64	NH1	B_GLU_26	OE2	3.559
4WEU	B_LYS_66	NZ	B_GLU_26	OE1	3.923
4WEU	B_ARG_96	NH1	A_GLU_94	OE1	3.754
4WEU	B_ARG_96	NH1	A_GLU_94	OE2	2.795
4WEU	B_ARG_96	NH1	B_GLU_94	OE2	3.704
4WEU	B_ARG_96	NH2	A_GLU_94	OE1	2.707
4WEU	B_ARG_96	NH2	A_GLU_94	OE2	3.344
4WEU	B_LYS_120	NZ	B_GLU_89	OE1	2.742
4WEU	B_ARG_136	NH2	B_GLU_145	OE1	3.533
4WEU	B_HIS_155	NE2	B_GLU_152	OE1	3.472
4WEU	B_HIS_155	NE2	B_GLU_152	OE2	2.880
4WEU	B_LYS_172	NZ	B_GLU_170	OE2	3.468
4WEU	B_ARG_198	NH1	B_GLU_67	OE2	2.375

4WEU	B_ARG_198	NH2	B_GLU_67	OE2	3.911
4WEU	E_ARG_838	NH1	E_ASP_890	OD1	3.012
4WEU	E_ARG_838	NH2	E_GLU_846	OE1	2.950
4WEU	E_ARG_838	NH2	E_GLU_846	OE2	3.817
4WEU	E_ARG_867	NH1	E_ASP_890	OD1	3.574
4WEU	E_ARG_867	NH1	E_ASP_890	OD2	2.661
4WEU	E_ARG_867	NH2	E_ASP_890	OD1	2.927
4WEU	E_ARG_867	NH2	E_ASP_890	OD2	3.566
4WHT	A_ARG_38	NH1	A_ASP_90	OD1	2.990
4WHT	A_ARG_38	NH2	A_GLU_46	OE1	2.993
4WHT	A_ARG_38	NH2	A_GLU_89	OE1	3.403
4WHT	A_ARG_61	NH2	A_GLU_46	OE2	3.778
4WHT	A_LYS_65	NZ	A_ASP_62	OD1	3.169
4WHT	A_ARG_67	NH1	A_ASP_90	OD1	3.859
4WHT	A_ARG_67	NH1	A_ASP_90	OD2	2.717
4WHT	A_ARG_67	NH2	A_GLU_89	OE1	3.463
4WHT	A_ARG_67	NH2	A_ASP_90	OD1	3.102
4WHT	A_ARG_67	NH2	A_ASP_90	OD2	3.428
4WHT	A_ARG_98	NH1	A_ASP_100	OD1	3.573
4WHT	A_ARG_98	NH1	A_ASP_100	OD2	2.704
4WHT	A_LYS_207	NZ	B_GLU_127	OE1	2.607
4WHT	A_LYS_207	NZ	B_GLU_127	OE2	3.670
4WHT	C_ARG_38	NH1	C_ASP_90	OD1	2.946
4WHT	C_ARG_38	NH2	C_GLU_46	OE1	2.996
4WHT	C_ARG_38	NH2	C_GLU_89	OE1	3.393
4WHT	C_ARG_61	NH2	C_GLU_46	OE2	3.777
4WHT	C_LYS_65	NZ	C_ASP_62	OD1	3.197
4WHT	C_ARG_67	NH1	C_ASP_90	OD1	3.881
4WHT	C_ARG_67	NH1	C_ASP_90	OD2	2.676
4WHT	C_ARG_67	NH2	C_GLU_89	OE1	3.528
4WHT	C_ARG_67	NH2	C_ASP_90	OD1	3.088
4WHT	C_ARG_67	NH2	C_ASP_90	OD2	3.360
4WHT	C_ARG_98	NH2	C_ASP_100	OD1	3.559
4WHT	C_ARG_98	NH2	C_ASP_100	OD2	2.716
4WHT	C_LYS_204	NZ	C_ASP_206	OD1	2.994
4WHT	C_LYS_204	NZ	C_ASP_206	OD2	3.710
4WHT	C_LYS_207	NZ	D_GLU_127	OE1	3.293
4WHT	E_ARG_38	NH1	E_ASP_90	OD1	2.955
4WHT	E_ARG_38	NH2	E_GLU_46	OE1	2.986
4WHT	E_ARG_38	NH2	E_GLU_89	OE1	3.434
4WHT	E_ARG_61	NH2	E_GLU_46	OE2	3.795
4WHT	E_LYS_65	NZ	E_ASP_62	OD1	3.160
4WHT	E_ARG_67	NH1	E_ASP_90	OD1	3.902
4WHT	E_ARG_67	NH1	E_ASP_90	OD2	2.757
4WHT	E_ARG_67	NH2	E_GLU_89	OE1	3.512
4WHT	E_ARG_67	NH2	E_ASP_90	OD1	3.132
4WHT	E_ARG_67	NH2	E_ASP_90	OD2	3.444
4WHT	E_ARG_98	NH2	E_ASP_100	OD1	3.535
4WHT	E_ARG_98	NH2	E_ASP_100	OD2	2.656
4WHT	E_LYS_204	NZ	E_ASP_206	OD1	2.987
4WHT	E_LYS_204	NZ	E_ASP_206	OD2	3.777
4WHT	E_LYS_207	NZ	F_GLU_127	OE1	3.118
4WHT	G_ARG_38	NH1	G_ASP_90	OD1	2.947
4WHT	G_ARG_38	NH2	G_GLU_46	OE1	2.995
4WHT	G_ARG_61	NH2	G_GLU_46	OE2	3.807
4WHT	G_LYS_65	NZ	G_ASP_62	OD1	3.270
4WHT	G_ARG_67	NH1	G_ASP_90	OD1	3.770
4WHT	G_ARG_67	NH1	G_ASP_90	OD2	2.706

4WHT	G_ARG_67	NH2	G_ASP_90	OD1	3.124
4WHT	G_ARG_67	NH2	G_ASP_90	OD2	3.413
4WHT	G_ARG_98	NH2	G_ASP_100	OD1	3.568
4WHT	G_ARG_98	NH2	G_ASP_100	OD2	2.686
4WHT	G_LYS_204	NZ	G_ASP_206	OD1	2.980
4WHT	G_LYS_204	NZ	G_ASP_206	OD2	3.681
4WHT	G_LYS_204	NZ	U_ASP_206	OD2	3.854
4WHT	I_ARG_38	NH1	I_ASP_90	OD1	2.871
4WHT	I_ARG_38	NH2	I_GLU_46	OE1	3.011
4WHT	I_ARG_38	NH2	I_ASP_90	OD1	3.937
4WHT	I_ARG_61	NH2	I_GLU_46	OE2	3.804
4WHT	I_LYS_65	NZ	I_ASP_62	OD1	3.703
4WHT	I_LYS_65	NZ	R_GLU_84	OE2	3.044
4WHT	I_ARG_67	NH1	I_ASP_90	OD1	3.990
4WHT	I_ARG_67	NH1	I_ASP_90	OD2	2.725
4WHT	I_ARG_67	NH2	I_ASP_90	OD1	3.173
4WHT	I_ARG_67	NH2	I_ASP_90	OD2	3.289
4WHT	I_ARG_98	NH2	I_ASP_100	OD1	3.524
4WHT	I_ARG_98	NH2	I_ASP_100	OD2	2.670
4WHT	I_LYS_207	NZ	J_GLU_127	OE1	2.774
4WHT	I_LYS_207	NZ	J_GLU_127	OE2	3.846
4WHT	J_ARG_24	NH1	J_ASP_75	OD1	2.778
4WHT	J_ARG_24	NH1	J_ASP_75	OD2	3.695
4WHT	J_ARG_66	NH2	J_ASP_87	OD1	2.769
4WHT	J_ARG_66	NH2	J_ASP_87	OD2	3.342
4WHT	J_LYS_153	NZ	J_GLU_199	OE1	3.137
4WHT	J_LYS_153	NZ	J_GLU_199	OE2	3.249
4WHT	J_ARG_159	NH1	J_ASP_189	OD1	3.763
4WHT	J_ARG_159	NH1	J_ASP_189	OD2	2.878
4WHT	J_ARG_159	NH2	J_ASP_189	OD1	2.936
4WHT	J_ARG_159	NH2	J_ASP_189	OD2	3.572
4WHT	J_LYS_187	NZ	J_GLU_191	OE1	2.768
4WHT	J_HIS_193	ND1	J_ASP_189	OD1	3.761
4WHT	J_LYS_203	NZ	J_ASP_114	OD2	2.967
4WHT	K_ARG_38	NH1	K_GLU_89	OE1	3.948
4WHT	K_ARG_38	NH1	K_ASP_90	OD1	2.761
4WHT	K_ARG_38	NH2	K_GLU_46	OE1	2.930
4WHT	K_ARG_38	NH2	K_GLU_89	OE1	3.349
4WHT	K_LYS_65	NZ	K_ASP_62	OD1	3.187
4WHT	K_ARG_67	NH1	K_ASP_90	OD1	3.739
4WHT	K_ARG_67	NH1	K_ASP_90	OD2	2.796
4WHT	K_ARG_67	NH2	K_GLU_89	OE1	3.552
4WHT	K_ARG_67	NH2	K_ASP_90	OD1	3.403
4WHT	K_ARG_67	NH2	K_ASP_90	OD2	3.608
4WHT	K_ARG_98	NH2	K_ASP_100	OD1	3.517
4WHT	K_ARG_98	NH2	K_ASP_100	OD2	2.664
4WHT	K_LYS_204	NZ	K_ASP_206	OD1	2.984
4WHT	K_LYS_204	NZ	K_ASP_206	OD2	3.680
4WHT	K_LYS_207	NZ	L_GLU_127	OE1	2.813
4WHT	M_ARG_38	NH1	M_ASP_90	OD1	2.959
4WHT	M_ARG_38	NH2	M_GLU_46	OE1	2.979
4WHT	M_ARG_38	NH2	M_GLU_89	OE1	3.377
4WHT	M_ARG_61	NH2	M_GLU_46	OE2	3.777
4WHT	M_LYS_65	NZ	M_ASP_62	OD1	3.185
4WHT	M_ARG_67	NH1	M_ASP_90	OD1	3.861
4WHT	M_ARG_67	NH1	M_ASP_90	OD2	2.742
4WHT	M_ARG_67	NH2	M_GLU_89	OE1	3.527
4WHT	M_ARG_67	NH2	M_ASP_90	OD1	3.102

4WHT	M_ARG_67	NH2	M_ASP_90	OD2	3.458
4WHT	M_ARG_98	NH2	M_ASP_100	OD1	3.946
4WHT	M_ARG_98	NH2	M_ASP_100	OD2	3.534
4WHT	M_LYS_204	NZ	K_ASP_206	OD2	2.701
4WHT	M_LYS_207	NZ	N_GLU_127	OE1	3.186
4WHT	O_ARG_38	NH1	O_ASP_90	OD1	2.964
4WHT	O_ARG_38	NH2	O_GLU_46	OE1	3.022
4WHT	O_ARG_38	NH2	O_GLU_89	OE1	3.336
4WHT	O_ARG_61	NH2	O_GLU_46	OE2	3.788
4WHT	O_LYS_65	NZ	O_ASP_62	OD1	3.252
4WHT	O_ARG_67	NH1	O_ASP_90	OD1	3.841
4WHT	O_ARG_67	NH1	O_ASP_90	OD2	2.724
4WHT	O_ARG_67	NH2	O_GLU_89	OE1	3.541
4WHT	O_ARG_67	NH2	O_ASP_90	OD1	3.068
4WHT	O_ARG_67	NH2	O_ASP_90	OD2	3.434
4WHT	O_ARG_98	NH2	O_ASP_100	OD1	3.531
4WHT	O_ARG_98	NH2	O_ASP_100	OD2	2.711
4WHT	O_LYS_204	NZ	O_ASP_206	OD1	2.964
4WHT	O_LYS_204	NZ	O_ASP_206	OD2	3.737
4WHT	O_LYS_207	NZ	P_GLU_127	OE1	3.812
4WHT	O_LYS_207	NZ	P_GLU_127	OE2	2.822
4WHT	Q_ARG_38	NH1	Q_ASP_90	OD1	2.935
4WHT	Q_ARG_38	NH2	Q_GLU_46	OE1	3.059
4WHT	Q_ARG_38	NH2	Q_ASP_90	OD1	3.866
4WHT	Q_ARG_61	NH2	Q_GLU_46	OE2	3.813
4WHT	Q_LYS_65	NZ	Q_ASP_62	OD1	3.159
4WHT	Q_ARG_67	NH1	Q_ASP_90	OD1	3.892
4WHT	Q_ARG_67	NH1	Q_ASP_90	OD2	2.790
4WHT	Q_ARG_67	NH2	Q_ASP_90	OD1	3.108
4WHT	Q_ARG_67	NH2	Q_ASP_90	OD2	3.473
4WHT	Q_ARG_98	NH2	Q_ASP_100	OD1	3.545
4WHT	Q_ARG_98	NH2	Q_ASP_100	OD2	2.754
4WHT	Q_LYS_207	NZ	R_GLU_127	OE1	2.572
4WHT	Q_LYS_207	NZ	R_GLU_127	OE2	3.627
4WHT	S_ARG_38	NH1	S_ASP_90	OD1	2.866
4WHT	S_ARG_38	NH2	S_GLU_46	OE1	2.984
4WHT	S_ARG_38	NH2	S_GLU_89	OE1	3.382
4WHT	S_ARG_38	NH2	S_ASP_90	OD1	3.993
4WHT	S_ARG_61	NH2	S_GLU_46	OE1	3.723
4WHT	S_ARG_61	NH2	S_GLU_46	OE2	3.200
4WHT	S_ARG_67	NH1	S_ASP_90	OD2	2.809
4WHT	S_ARG_67	NH2	S_GLU_89	OE1	3.479
4WHT	S_ARG_67	NH2	S_ASP_90	OD1	3.317
4WHT	S_ARG_67	NH2	S_ASP_90	OD2	3.452
4WHT	S_LYS_76	NZ	S_ASP_73	OD2	2.618
4WHT	S_ARG_98	NH2	S_ASP_100	OD1	3.534
4WHT	S_ARG_98	NH2	S_ASP_100	OD2	2.742
4WHT	S_LYS_204	NZ	S_ASP_206	OD1	3.164
4WHT	S_LYS_207	NZ	T_GLU_127	OE1	3.197
4WHT	U_ARG_38	NH1	U_ASP_90	OD1	2.992
4WHT	U_ARG_38	NH2	U_GLU_46	OE1	3.032
4WHT	U_ARG_38	NH2	U_GLU_89	OE1	3.377
4WHT	U_ARG_61	NH2	U_GLU_46	OE2	3.808
4WHT	U_LYS_65	NZ	U_ASP_62	OD1	3.172
4WHT	U_ARG_67	NH1	U_ASP_90	OD1	3.855
4WHT	U_ARG_67	NH1	U_ASP_90	OD2	2.721
4WHT	U_ARG_67	NH2	U_GLU_89	OE1	3.526
4WHT	U_ARG_67	NH2	U_ASP_90	OD1	3.080

4WHT	U_ARG_67	NH2	U_ASP_90	OD2	3.418
4WHT	U_ARG_98	NH2	U_ASP_100	OD1	3.455
4WHT	U_ARG_98	NH2	U_ASP_100	OD2	2.628
4WHT	U_LYS_204	NZ	G_ASP_206	OD2	3.954
4WHT	U_LYS_204	NZ	U_ASP_206	OD1	2.956
4WHT	U_LYS_204	NZ	U_ASP_206	OD2	3.682
4WHT	U_LYS_207	NZ	V_GLU_127	OE1	3.622
4WHT	X_ARG_38	NH1	X_ASP_90	OD1	2.631
4WHT	X_ARG_38	NH2	X_GLU_46	OE1	3.058
4WHT	X_ARG_38	NH2	X_GLU_46	OE2	3.652
4WHT	X_ARG_38	NH2	X_ASP_90	OD1	3.918
4WHT	X_ARG_61	NH2	X_GLU_46	OE2	3.153
4WHT	X_LYS_65	NZ	X_ASP_62	OD1	3.157
4WHT	X_ARG_67	NH1	X_ASP_90	OD1	3.978
4WHT	X_ARG_67	NH1	X_ASP_90	OD2	2.777
4WHT	X_ARG_67	NH2	X_ASP_90	OD1	3.272
4WHT	X_ARG_67	NH2	X_ASP_90	OD2	3.480
4WHT	X_ARG_98	NH2	X_ASP_100	OD1	3.516
4WHT	X_ARG_98	NH2	X_ASP_100	OD2	2.709
4WHT	X_LYS_207	NZ	Y_GLU_127	OE2	2.718
4WHT	B_ARG_24	NH1	B_ASP_75	OD1	2.804
4WHT	B_ARG_24	NH1	B_ASP_75	OD2	3.712
4WHT	B_ARG_66	NH2	B_ASP_87	OD1	2.784
4WHT	B_ARG_66	NH2	B_ASP_87	OD2	3.450
4WHT	B_LYS_111	NZ	J_GLU_73	OE2	3.842
4WHT	B_LYS_153	NZ	B_GLU_199	OE1	3.076
4WHT	B_LYS_153	NZ	B_GLU_199	OE2	3.271
4WHT	B_ARG_159	NH1	B_ASP_189	OD1	3.800
4WHT	B_ARG_159	NH1	B_ASP_189	OD2	2.909
4WHT	B_ARG_159	NH2	B_ASP_189	OD1	2.972
4WHT	B_ARG_159	NH2	B_ASP_189	OD2	3.584
4WHT	B_LYS_	NZ	B_GLU_	OE1	2.805
4WHT	B_HIS_193	ND1	B_ASP_155	OD2	3.362
4WHT	B_HIS_193	NE2	B_ASP_189	OD1	3.524
4WHT	B_LYS_203	NZ	B_ASP_114	OD2	2.836
4WHT	D_ARG_24	NH1	D_ASP_75	OD1	2.773
4WHT	D_ARG_24	NH1	D_ASP_75	OD2	3.816
4WHT	D_ARG_44	NH1	D_GLU_86	OE2	3.678
4WHT	D_ARG_44	NH2	D_GLU_86	OE2	2.752
4WHT	D_ARG_66	NH2	D_ASP_87	OD1	2.868
4WHT	D_ARG_66	NH2	D_ASP_87	OD2	3.621
4WHT	D_LYS_151	NZ	D_GLU_199	OE2	3.961
4WHT	D_LYS_151	NZ	L_GLU_191	OE2	3.259
4WHT	D_LYS_153	NZ	D_GLU_199	OE1	3.094
4WHT	D_LYS_153	NZ	D_GLU_199	OE2	3.252
4WHT	D_ARG_159	NH1	D_ASP_189	OD1	3.780
4WHT	D_ARG_159	NH1	D_ASP_189	OD2	2.927
4WHT	D_ARG_159	NH2	D_ASP_189	OD1	2.960
4WHT	D_ARG_159	NH2	D_ASP_189	OD2	3.602
4WHT	D_LYS_187	NZ	I_GLU_114	OE1	3.576
4WHT	D_LYS_187	NZ	I_GLU_114	OE2	3.498
4WHT	D_LYS_187	NZ	D_GLU_191	OE1	2.796
4WHT	D_HIS_193	ND1	D_ASP_189	OD1	3.687
4WHT	D_LYS_203	NZ	D_ASP_114	OD2	2.798
4WHT	F_ARG_24	NH1	F_ASP_75	OD1	2.809
4WHT	F_ARG_24	NH1	F_ASP_75	OD2	3.755
4WHT	F_ARG_66	NH2	F_GLU_86	OE1	3.638
4WHT	F_ARG_66	NH2	F_GLU_86	OE2	3.286

4WHT	F_ARG_66	NH2	F_ASP_87	OD1	2.757
4WHT	F_ARG_66	NH2	F_ASP_87	OD2	3.450
4WHT	F_LYS_151	NZ	F_GLU_199	OE2	3.084
4WHT	F_LYS_153	NZ	F_GLU_199	OE1	3.224
4WHT	F_LYS_153	NZ	F_GLU_199	OE2	3.396
4WHT	F_ARG_159	NH1	F_ASP_189	OD1	3.759
4WHT	F_ARG_159	NH1	F_ASP_189	OD2	2.800
4WHT	F_ARG_159	NH2	F_ASP_189	OD1	2.952
4WHT	F_ARG_159	NH2	F_ASP_189	OD2	3.529
4WHT	F_ARG_160	NH2	F_GLU_158	OE2	3.114
4WHT	F_LYS_187	NZ	F_GLU_191	OE1	2.776
4WHT	F_HIS_193	ND1	F_ASP_155	OD2	3.338
4WHT	F_HIS_193	NE2	F_ASP_189	OD1	3.541
4WHT	H_ARG_24	NH1	H_ASP_75	OD1	2.789
4WHT	H_ARG_24	NH1	H_ASP_75	OD2	3.775
4WHT	H_ARG_66	NH1	Q_ASP_62	OD2	3.949
4WHT	H_ARG_66	NH2	H_ASP_87	OD1	2.787
4WHT	H_ARG_66	NH2	H_ASP_87	OD2	3.453
4WHT	H_LYS_151	NZ	H_GLU_199	OE2	3.589
4WHT	H_LYS_153	NZ	H_GLU_199	OE1	3.108
4WHT	H_LYS_153	NZ	H_GLU_199	OE2	3.315
4WHT	H_ARG_159	NH1	H_ASP_189	OD1	3.818
4WHT	H_ARG_159	NH1	H_ASP_189	OD2	2.990
4WHT	H_ARG_159	NH2	H_ASP_189	OD1	2.984
4WHT	H_ARG_159	NH2	H_ASP_189	OD2	3.636
4WHT	H_LYS_187	NZ	H_GLU_191	OE1	2.806
4WHT	H_HIS_193	ND1	H_ASP_155	OD2	3.385
4WHT	H_HIS_193	NE2	H_ASP_189	OD1	3.584
4WHT	H_LYS_203	NZ	H_ASP_114	OD2	2.843
4WHT	L_ARG_24	NH1	L_ASP_75	OD1	2.813
4WHT	L_ARG_24	NH1	L_ASP_75	OD2	3.652
4WHT	L_ARG_66	NH2	L_ASP_87	OD1	2.659
4WHT	L_ARG_66	NH2	L_ASP_87	OD2	3.387
4WHT	L_LYS_151	NZ	L_GLU_158	OE1	3.149
4WHT	L_LYS_151	NZ	L_GLU_158	OE2	3.351
4WHT	L_LYS_153	NZ	L_GLU_199	OE1	3.106
4WHT	L_LYS_153	NZ	L_GLU_199	OE2	3.200
4WHT	L_ARG_159	NH1	L_ASP_189	OD1	3.780
4WHT	L_ARG_159	NH1	L_ASP_189	OD2	2.946
4WHT	L_ARG_159	NH2	L_ASP_189	OD1	2.925
4WHT	L_ARG_159	NH2	L_ASP_189	OD2	3.602
4WHT	L_LYS_187	NZ	L_GLU_191	OE1	2.795
4WHT	L_HIS_193	ND1	L_ASP_155	OD2	3.400
4WHT	L_HIS_193	NE2	L_ASP_189	OD1	3.590
4WHT	L_LYS_203	NZ	L_ASP_114	OD2	2.774
4WHT	N_ARG_24	NH1	N_ASP_75	OD1	3.802
4WHT	N_ARG_24	NH1	N_ASP_75	OD2	3.728
4WHT	N_ARG_66	NH2	N_ASP_87	OD1	2.772
4WHT	N_ARG_66	NH2	N_ASP_87	OD2	3.477
4WHT	N_LYS_151	NZ	N_GLU_199	OE2	3.991
4WHT	N_LYS_153	NZ	N_GLU_199	OE1	3.073
4WHT	N_LYS_153	NZ	N_GLU_199	OE2	3.236
4WHT	N_ARG_159	NH1	N_ASP_189	OD2	3.146
4WHT	N_ARG_159	NH2	N_ASP_189	OD1	2.954
4WHT	N_ARG_159	NH2	N_ASP_189	OD2	3.533
4WHT	N_ARG_160	NH2	N_GLU_158	OE1	2.762
4WHT	N_LYS_187	NZ	K_GLU_114	OE1	3.270
4WHT	N_LYS_187	NZ	K_GLU_114	OE2	3.221

4WHT	N_LYS_187	NZ	N_GLU_191	OE1	2.851
4WHT	N_HIS_193	ND1	N_ASP_189	OD1	3.702
4WHT	N_LYS_203	NZ	N_ASP_147	OD2	3.088
4WHT	P_ARG_24	NH1	P_ASP_75	OD1	2.762
4WHT	P_ARG_24	NH1	P_ASP_75	OD2	3.651
4WHT	P_ARG_66	NH2	P_ASP_87	OD1	2.759
4WHT	P_ARG_66	NH2	P_ASP_87	OD2	3.423
4WHT	P_LYS_151	NZ	P_GLU_199	OE1	3.866
4WHT	P_LYS_153	NZ	P_GLU_199	OE1	3.110
4WHT	P_LYS_153	NZ	P_GLU_199	OE2	3.243
4WHT	P_ARG_159	NH1	P_ASP_189	OD1	3.789
4WHT	P_ARG_159	NH1	P_ASP_189	OD2	2.890
4WHT	P_ARG_159	NH2	P_ASP_189	OD1	2.989
4WHT	P_ARG_159	NH2	P_ASP_189	OD2	3.601
4WHT	P_LYS_187	NZ	P_GLU_191	OE1	2.785
4WHT	P_HIS_193	ND1	P_ASP_155	OD2	3.395
4WHT	P_HIS_193	NE2	P_ASP_189	OD1	3.524
4WHT	R_ARG_24	NH1	R_ASP_75	OD1	2.839
4WHT	R_ARG_24	NH1	R_ASP_75	OD2	3.562
4WHT	R_ARG_66	NH2	R_ASP_87	OD1	2.765
4WHT	R_ARG_66	NH2	R_ASP_87	OD2	3.213
4WHT	R_LYS_153	NZ	R_GLU_199	OE1	3.156
4WHT	R_LYS_153	NZ	R_GLU_199	OE2	3.439
4WHT	R_ARG_159	NH1	R_ASP_189	OD1	3.788
4WHT	R_ARG_159	NH1	R_ASP_189	OD2	2.882
4WHT	R_ARG_159	NH2	R_ASP_189	OD1	2.978
4WHT	R_ARG_159	NH2	R_ASP_189	OD2	3.578
4WHT	R_LYS_187	NZ	R_GLU_191	OE1	2.817
4WHT	R_HIS_193	ND1	R_ASP_189	OD1	3.674
4WHT	R_LYS_203	NZ	R_ASP_114	OD2	2.819
4WHT	T_ARG_24	NH1	T_ASP_75	OD1	2.790
4WHT	T_ARG_24	NH1	T_ASP_75	OD2	3.795
4WHT	T_ARG_66	NH2	T_ASP_87	OD1	2.749
4WHT	T_ARG_66	NH2	T_ASP_87	OD2	3.461
4WHT	T_LYS_153	NZ	T_GLU_199	OE1	3.110
4WHT	T_LYS_153	NZ	T_GLU_199	OE2	3.186
4WHT	T_ARG_159	NH1	T_ASP_189	OD1	3.798
4WHT	T_ARG_159	NH1	T_ASP_189	OD2	2.872
4WHT	T_ARG_159	NH2	T_ASP_189	OD1	3.018
4WHT	T_ARG_159	NH2	T_ASP_189	OD2	3.596
4WHT	T_LYS_187	NZ	T_GLU_191	OE1	3.436
4WHT	T_LYS_187	NZ	T_GLU_191	OE2	3.114
4WHT	T_HIS_193	ND1	T_ASP_155	OD2	2.632
4WHT	T_HIS_193	NE2	T_ASP_189	OD1	3.485
4WHT	T_LYS_203	NZ	T_ASP_114	OD2	2.869
4WHT	V_ARG_66	NH2	V_ASP_87	OD1	2.798
4WHT	V_ARG_66	NH2	V_ASP_87	OD2	3.518
4WHT	V_LYS_151	NZ	V_GLU_199	OE2	2.908
4WHT	V_LYS_153	NZ	V_GLU_199	OE1	3.090
4WHT	V_LYS_153	NZ	V_GLU_199	OE2	3.267
4WHT	V_ARG_159	NH1	V_ASP_189	OD1	3.784
4WHT	V_ARG_159	NH1	V_ASP_189	OD2	2.899
4WHT	V_ARG_159	NH2	V_ASP_189	OD1	2.972
4WHT	V_ARG_159	NH2	V_ASP_189	OD2	3.593
4WHT	V_LYS_187	NZ	G_GLU_114	OE1	3.353
4WHT	V_LYS_187	NZ	G_GLU_114	OE2	3.189
4WHT	V_LYS_187	NZ	V_GLU_191	OE1	2.841
4WHT	V_HIS_193	NE2	V_ASP_189	OD1	3.541

4WHT	Y_ARG_24	NH1	Y_ASP_75	OD1	3.206
4WHT	Y_ARG_24	NH1	Y_ASP_75	OD2	2.692
4WHT	Y_ARG_66	NH2	Y_GLU_86	OE2	3.955
4WHT	Y_ARG_66	NH2	Y_ASP_87	OD1	2.832
4WHT	Y_ARG_66	NH2	Y_ASP_87	OD2	3.932
4WHT	Y_LYS_153	NZ	Y_GLU_199	OE1	3.170
4WHT	Y_LYS_153	NZ	Y_GLU_199	OE2	2.813
4WHT	Y_ARG_159	NH1	Y_GLU_158	OE1	3.340
4WHT	Y_ARG_160	NH1	Y_ASP_165	OD2	3.538
4WHT	Y_ARG_160	NH2	Y_ASP_165	OD2	3.332
4WHT	Y_HIS_193	ND1	Y_ASP_155	OD2	3.964
4WHT	Y_LYS_203	NZ	Y_ASP_114	OD2	2.871
4WHY	G_ARG_38	NH1	G_ASP_90	OD1	3.796
4WHY	G_ARG_38	NH2	G_GLU_46	OE1	3.426
4WHY	G_ARG_38	NH2	G_GLU_89	OE1	3.357
4WHY	G_ARG_61	NH2	G_GLU_46	OE2	3.723
4WHY	G_LYS_65	NZ	G_ASP_62	OD1	2.662
4WHY	G_ARG_67	NH1	G_ASP_90	OD1	3.682
4WHY	G_ARG_67	NH1	G_ASP_90	OD2	2.803
4WHY	G_ARG_67	NH2	G_GLU_89	OE1	3.560
4WHY	G_ARG_67	NH2	G_ASP_90	OD1	3.140
4WHY	G_ARG_67	NH2	G_ASP_90	OD2	3.738
4WHY	G_ARG_98	NH2	G_ASP_100	OD1	3.694
4WHY	G_ARG_98	NH2	G_ASP_100	OD2	2.760
4WHY	H_ARG_24	NH1	H_ASP_75	OD1	3.176
4WHY	H_ARG_24	NH1	H_ASP_75	OD2	3.772
4WHY	H_ARG_24	NH2	H_ASP_75	OD1	3.589
4WHY	H_ARG_66	NH2	H_GLU_86	OE2	3.670
4WHY	H_ARG_66	NH2	H_ASP_87	OD1	2.742
4WHY	H_ARG_66	NH2	H_ASP_87	OD2	3.368
4WHY	H_LYS_153	NZ	H_GLU_199	OE1	2.781
4WHY	H_ARG_159	NH1	H_ASP_161	OD2	3.986
4WHY	H_ARG_159	NH2	H_ASP_189	OD2	3.516
4WHY	H_LYS_187	NZ	H_GLU_191	OE1	3.190
4WHY	H_HIS_193	NE2	H_ASP_189	OD1	2.905
4WHY	H_LYS_203	NZ	H_ASP_114	OD2	2.769
4WHY	L_ARG_38	NH1	L_ASP_90	OD1	2.978
4WHY	L_ARG_38	NH2	L_GLU_46	OE1	3.414
4WHY	L_ARG_38	NH2	L_GLU_89	OE1	3.357
4WHY	L_ARG_38	NH2	L_ASP_90	OD1	3.749
4WHY	L_ARG_61	NH2	L_GLU_46	OE2	3.662
4WHY	L_LYS_65	NZ	L_ASP_62	OD1	2.662
4WHY	L_ARG_67	NH1	L_ASP_90	OD1	3.785
4WHY	L_ARG_67	NH1	L_ASP_90	OD2	2.958
4WHY	L_ARG_67	NH2	L_GLU_89	OE1	3.554
4WHY	L_ARG_67	NH2	L_ASP_90	OD1	3.099
4WHY	L_ARG_67	NH2	L_ASP_90	OD2	3.665
4WHY	L_ARG_98	NH2	L_ASP_100	OD1	3.706
4WHY	L_ARG_98	NH2	L_ASP_100	OD2	2.729
4WHY	L_LYS_204	NZ	L_ASP_206	OD1	3.011
4WHY	L_LYS_204	NZ	L_ASP_206	OD2	3.199
4WHY	J_ARG_24	NH1	J_ASP_75	OD1	3.069
4WHY	J_ARG_24	NH2	J_ASP_75	OD1	3.630
4WHY	J_ARG_66	NH1	J_GLU_84	OE1	3.874
4WHY	J_ARG_66	NH2	J_GLU_86	OE2	3.624
4WHY	J_ARG_66	NH2	J_ASP_87	OD1	2.726
4WHY	J_ARG_66	NH2	J_ASP_87	OD2	3.349
4WHY	J_LYS_153	NZ	J_GLU_199	OE1	3.490

4WHY	J_LYS_153	NZ	J_GLU_199	OE2	3.292
4WHY	J_ARG_159	NH1	J_ASP_189	OD2	3.515
4WHY	J_ARG_159	NH2	J_ASP_189	OD1	3.310
4WHY	J_ARG_159	NH2	J_ASP_189	OD2	3.228
4WHY	J_LYS_187	NZ	J_GLU_191	OE1	3.198
4WHY	J_HIS_193	NE2	J_ASP_189	OD1	2.893
4WHY	J_LYS_203	NZ	J_ASP_114	OD2	2.763
4WHY	K_ARG_38	NH1	K_ASP_90	OD1	2.916
4WHY	K_ARG_38	NH2	K_GLU_46	OE1	3.411
4WHY	K_ARG_38	NH2	K_GLU_89	OE1	3.357
4WHY	K_ARG_38	NH2	K_ASP_90	OD1	3.663
4WHY	K_LYS_43	NZ	K_GLU_46	OE2	3.479
4WHY	K_ARG_61	NH2	K_GLU_46	OE1	3.975
4WHY	K_ARG_61	NH2	K_GLU_46	OE2	3.699
4WHY	K_LYS_65	NZ	K_ASP_62	OD1	2.646
4WHY	K_ARG_67	NH1	K_ASP_90	OD2	3.001
4WHY	K_ARG_67	NH2	K_GLU_89	OE1	3.597
4WHY	K_ARG_67	NH2	K_ASP_90	OD1	3.410
4WHY	K_ARG_67	NH2	K_ASP_90	OD2	3.539
4WHY	K_ARG_98	NH2	K_ASP_100	OD1	3.492
4WHY	K_ARG_98	NH2	K_ASP_100	OD2	2.572
4WHY	K_LYS_204	NZ	G_ASP_206	OD2	3.182
4WHY	K_LYS_204	NZ	K_ASP_206	OD1	3.046
4WHY	K_LYS_204	NZ	K_ASP_206	OD2	3.729
4WHY	K_LYS_207	NZ	L_GLU_127	OE1	3.798
4WHY	L_ARG_66	NH1	L_GLU_84	OE2	3.906
4WHY	L_ARG_66	NH2	L_GLU_86	OE2	3.615
4WHY	L_ARG_66	NH2	L_ASP_87	OD1	2.731
4WHY	L_ARG_66	NH2	L_ASP_87	OD2	3.360
4WHY	L_LYS_153	NZ	L_GLU_199	OE1	3.524
4WHY	L_LYS_153	NZ	L_GLU_199	OE2	3.214
4WHY	L_ARG_159	NH1	L_ASP_189	OD1	3.322
4WHY	L_ARG_159	NH1	L_ASP_189	OD2	2.478
4WHY	L_ARG_159	NH2	L_ASP_189	OD1	3.410
4WHY	L_ARG_159	NH2	L_ASP_189	OD2	3.993
4WHY	L_LYS_187	NZ	G_GLU_114	OE1	3.275
4WHY	L_LYS_187	NZ	G_GLU_114	OE2	3.634
4WHY	L_LYS_187	NZ	L_GLU_191	OE1	3.202
4WHY	L_HIS_193	NE2	L_ASP_189	OD1	2.644
4WHY	M_ARG_38	NH1	M_ASP_90	OD1	3.063
4WHY	M_ARG_38	NH2	M_GLU_46	OE1	3.415
4WHY	M_ARG_38	NH2	M_GLU_89	OE1	3.380
4WHY	M_ARG_61	NH2	M_GLU_46	OE2	3.734
4WHY	M_LYS_65	NZ	M_ASP_62	OD1	2.631
4WHY	M_ARG_67	NH1	M_ASP_90	OD1	3.787
4WHY	M_ARG_67	NH1	M_ASP_90	OD2	2.862
4WHY	M_ARG_67	NH2	M_GLU_89	OE1	3.563
4WHY	M_ARG_67	NH2	M_ASP_90	OD1	3.288
4WHY	M_ARG_67	NH2	M_ASP_90	OD2	3.753
4WHY	M_ARG_87	NH1	M_GLU_89	OE1	3.642
4WHY	M_ARG_87	NH1	M_GLU_89	OE2	2.644
4WHY	M_ARG_98	NH2	M_ASP_100	OD1	3.669
4WHY	M_ARG_98	NH2	M_ASP_100	OD2	2.644
4WHY	M_LYS_207	NZ	N_GLU_127	OE1	3.795
4WHY	N_ARG_24	NH1	N_ASP_75	OD1	3.064
4WHY	N_ARG_24	NH2	N_ASP_75	OD1	3.627
4WHY	N_ARG_66	NH1	N_GLU_84	OE1	3.806
4WHY	N_ARG_66	NH2	N_GLU_86	OE2	3.626

4WHY	N_ARG.66	NH2	N_ASP.87	OD1	2.746
4WHY	N_ARG.66	NH2	N_ASP.87	OD2	3.352
4WHY	N_LYS.153	NZ	N_GLU.199	OE1	3.388
4WHY	N_LYS.153	NZ	N_GLU.199	OE2	3.311
4WHY	N_ARG.159	NH1	N_ASP.189	OD1	3.704
4WHY	N_ARG.159	NH1	N_ASP.189	OD2	2.785
4WHY	N_ARG.159	NH2	N_ASP.189	OD2	3.806
4WHY	N_LYS.187	NZ	I_GLU.114	OE1	2.397
4WHY	N_LYS.187	NZ	I_GLU.114	OE2	3.551
4WHY	N_LYS.187	NZ	N_GLU.191	OE1	3.175
4WHY	N_HIS.193	NE2	N_ASP.189	OD1	2.893
4WHY	N_LYS.203	NZ	N_ASP.114	OD2	2.778
4WUU	A_HIS.3	ND1	A_ASP.29	OD1	3.341
4WUU	A_HIS.3	ND1	A_ASP.29	OD2	2.929
4WUU	A_ARG.6	NH2	A_ASP.102	OD1	3.941
4WUU	A_ARG.6	NH2	A_ASP.102	OD2	3.738
4WUU	A_ARG.14	NH2	A_ASP.39	OD1	3.219
4WUU	A_ARG.14	NH2	A_ASP.39	OD2	2.950
4WUU	A_ARG.21	NH1	A_ASP.39	OD2	2.675
4WUU	A_ARG.21	NH2	A_ASP.37	OD2	3.480
4WUU	A_ARG.35	NH1	B_ASP.53	OD1	3.025
4WUU	A_ARG.35	NH1	B_ASP.53	OD2	3.278
4WUU	A_ARG.35	NH2	A_GLU.46	OE1	3.105
4WUU	A_ARG.44	NH1	A_ASP.61	OD1	3.882
4WUU	A_ARG.44	NH2	A_ASP.61	OD1	3.159
4WUU	A_ARG.48	NH2	B_ASP.53	OD1	3.607
4WUU	A_ARG.48	NH2	B_ASP.53	OD2	3.368
4WUU	A_HIS.74	ND1	A_ASP.77	OD2	3.868
4WUU	A_ARG.75	NH1	A_GLU.19	OE2	3.917
4WUU	A_ARG.82	NH1	A_GLU.89	OE2	3.819
4WUU	A_ARG.82	NH2	A_GLU.89	OE2	3.766
4WUU	A_HIS.93	ND1	A_ASP.119	OD1	3.903
4WUU	A_HIS.93	ND1	A_ASP.119	OD2	3.323
4WUU	A_ARG.111	NH2	A_ASP.102	OD2	3.306
4WUU	A_ARG.157	NH1	A_GLU.161	OE1	3.446
4WUU	A_ARG.157	NH1	A_GLU.161	OE2	3.465
4WUU	A_ARG.157	NH2	A_GLU.161	OE1	3.936
4WUU	A_ARG.170	NH2	A_GLU.55	OE1	3.101
4WUU	A_ARG.170	NH2	A_GLU.55	OE2	3.506
4WUU	A_ARG.181	NH1	A_ASP.183	OD2	3.977
4WUU	A_HIS.191	NE2	A_GLU.254	OE2	3.880
4WUU	A_HIS.197	ND1	A_GLU.198	OE1	3.876
4WUU	B_ARG.3	NH2	B_ASP.59	OD1	3.704
4WUU	B_LYS.19	NZ	B_GLU.16	OE1	3.969
4WUU	B_LYS.19	NZ	B_GLU.16	OE2	3.703
4WUU	B_ARG.45	NH2	B_GLU.47	OE2	2.936
4WUU	B_LYS.94	NZ	B_GLU.77	OE2	3.352
4WUU	D_ARG.62	NH2	D_GLU.82	OE2	3.196
4WUU	D_ARG.62	NH2	D_ASP.83	OD1	2.858
4WUU	D_ARG.62	NH2	D_ASP.83	OD2	3.260
4WUU	D_LYS.114	NZ	D_GLU.202	OE1	2.842
4WUU	E_LYS.12	NZ	E_GLU.16	OE2	3.576
4WUU	E_ARG.38	NH2	E_GLU.46	OE1	2.721
4WUU	E_ARG.38	NH2	E_GLU.46	OE2	3.649
4WUU	E_ARG.50	NH1	A_GLU.166	OE2	3.181
4WUU	E_ARG.50	NH2	A_GLU.166	OE1	3.839
4WUU	E_ARG.50	NH2	A_GLU.166	OE2	2.671
4WUU	E_LYS.87	NZ	E_ASP.90	OD1	3.097

4WUU	E_ARG_98	NH2	E_ASP_109	OD2	3.982
4WUU	E_ARG_218	NH1	E_GLU_220	OE1	3.981
4WUU	E_ARG_218	NH2	E_GLU_220	OE1	3.055
4XVJ	A_ARG_1	NH2	L_ASP_51	OD1	3.482
4XVJ	H_ARG_38	NH1	H_ASP_90	OD2	3.020
4XVJ	H_ARG_38	NH2	H_GLU_46	OE1	2.936
4XVJ	H_LYS_65	NZ	H_ASP_62	OD1	3.256
4XVJ	H_ARG_67	NH1	H_ASP_90	OD1	2.560
4XVJ	H_ARG_67	NH1	H_ASP_90	OD2	3.768
4XVJ	H_ARG_67	NH2	H_ASP_90	OD1	3.378
4XVJ	H_ARG_67	NH2	H_ASP_90	OD2	3.034
4XVJ	H_ARG_98	NH2	H_ASP_115	OD1	3.741
4XVJ	H_ARG_98	NH2	H_ASP_115	OD2	2.973
4XVJ	L_LYS_17	NZ	L_ASP_75	OD2	3.177
4XVJ	L_ARG_62	NH1	L_ASP_83	OD1	3.002
4XVJ	L_ARG_62	NH1	L_ASP_83	OD2	3.479
4XVJ	L_ARG_62	NH2	L_ASP_83	OD1	3.793
4XVJ	L_ARG_62	NH2	L_ASP_83	OD2	2.894
4YHP	P_LYS_4	NZ	H_ASP_62	OD1	3.318
4YHP	A_ARG_38	NH1	A_ASP_90	OD1	2.967
4YHP	A_ARG_38	NH2	A_GLU_46	OE1	2.987
4YHP	A_ARG_67	NH1	A_ASP_90	OD1	3.983
4YHP	A_ARG_67	NH1	A_ASP_90	OD2	2.902
4YHP	A_ARG_67	NH2	A_ASP_90	OD1	2.805
4YHP	A_ARG_67	NH2	A_ASP_90	OD2	3.034
4YHP	A_LYS_76	NZ	A_ASP_73	OD1	3.954
4YHP	A_LYS_76	NZ	A_ASP_73	OD2	3.046
4YHP	A_ARG_98	NH2	A_ASP_109	OD1	3.450
4YHP	A_ARG_98	NH2	A_ASP_109	OD2	2.693
4YHP	A_LYS_151	NZ	A_ASP_152	OD1	3.053
4YHP	A_LYS_151	NZ	A_ASP_152	OD2	3.629
4YHP	A_LYS_214	NZ	A_ASP_216	OD1	3.351
4YHP	A_LYS_218	NZ	A_GLU_220	OE2	2.671
4YHP	A_LYS_222	NZ	B_ASP_123	OD2	3.677
4YHP	B_ARG_53	NH2	B_GLU_59	OE1	3.593
4YHP	B_ARG_60	NH1	B_ASP_81	OD1	3.610
4YHP	B_ARG_60	NH1	B_ASP_81	OD2	2.819
4YHP	B_ARG_60	NH2	B_GLU_78	OE2	3.931
4YHP	B_ARG_60	NH2	B_ASP_81	OD1	3.172
4YHP	B_ARG_60	NH2	B_ASP_81	OD2	3.721
4YHP	B_LYS_104	NZ	B_ASP_84	OD1	3.453
4YHP	B_LYS_104	NZ	B_GLU_166	OE2	3.500
4YHP	B_LYS_150	NZ	B_GLU_196	OE1	3.634
4YHP	B_LYS_150	NZ	B_GLU_196	OE2	3.240
4YHP	B_LYS_184	NZ	B_GLU_188	OE1	3.665
4YHP	B_LYS_184	NZ	B_GLU_188	OE2	2.296
4YHP	Q_LYS_4	NZ	C_ASP_62	OD1	3.313
4YHP	C_ARG_38	NH1	C_ASP_90	OD1	2.918
4YHP	C_ARG_38	NH2	C_GLU_46	OE1	2.810
4YHP	C_ARG_38	NH2	C_ASP_90	OD1	3.983
4YHP	C_ARG_67	NH1	C_ASP_90	OD1	3.935
4YHP	C_ARG_67	NH1	C_ASP_90	OD2	2.912
4YHP	C_ARG_67	NH2	C_ASP_90	OD1	3.223
4YHP	C_ARG_67	NH2	C_ASP_90	OD2	3.530
4YHP	C_ARG_98	NH2	C_ASP_109	OD1	3.729
4YHP	C_ARG_98	NH2	C_ASP_109	OD2	2.531
4YHP	C_LYS_151	NZ	C_ASP_152	OD1	3.396
4YHP	C_LYS_151	NZ	C_ASP_152	OD2	3.552

4YHP	C_LYS_218	NZ	C_GLU_220	OE2	3.718
4YHP	C_LYS_222	NZ	D_ASP_123	OD1	3.776
4YHP	C_LYS_222	NZ	D_ASP_123	OD2	3.442
4YHP	D_ARG_60	NH1	D_ASP_81	OD1	3.548
4YHP	D_ARG_60	NH1	D_ASP_81	OD2	2.563
4YHP	D_ARG_60	NH2	D_GLU_78	OE1	3.956
4YHP	D_ARG_60	NH2	D_ASP_81	OD1	3.366
4YHP	D_ARG_60	NH2	D_ASP_81	OD2	3.671
4YHP	D_LYS_104	NZ	D_ASP_84	OD1	3.616
4YHP	D_LYS_104	NZ	D_ASP_84	OD2	3.921
4YHP	D_LYS_104	NZ	D_GLU_166	OE1	3.541
4YHP	D_LYS_104	NZ	D_GLU_166	OE2	2.873
4YHP	D_LYS_150	NZ	D_GLU_196	OE1	3.981
4YHP	D_LYS_150	NZ	D_GLU_196	OE2	2.313
4YHP	D_LYS_189	NZ	D_ASP_186	OD1	2.853
4YHP	D_HIS_190	ND1	D_ASP_152	OD2	2.771
4YHP	D_HIS_190	NE2	L_GLU_59	OE2	2.478
4YHP	E_ARG_38	NH1	E_ASP_90	OD1	3.131
4YHP	E_ARG_38	NH2	E_GLU_46	OE1	2.855
4YHP	E_ARG_67	NH1	E_ASP_90	OD1	3.715
4YHP	E_ARG_67	NH1	E_ASP_90	OD2	2.746
4YHP	E_ARG_67	NH2	E_ASP_90	OD1	3.053
4YHP	E_ARG_67	NH2	E_ASP_90	OD2	3.561
4YHP	E_ARG_98	NH2	E_ASP_109	OD1	3.385
4YHP	E_ARG_98	NH2	E_ASP_109	OD2	2.631
4YHP	E_LYS_151	NZ	E_ASP_152	OD1	3.289
4YHP	E_LYS_151	NZ	E_ASP_152	OD2	3.442
4YHP	E_LYS_222	NZ	F_ASP_123	OD1	3.304
4YHP	E_LYS_222	NZ	F_ASP_123	OD2	2.842
4YHP	H_ARG_38	NH1	H_ASP_90	OD1	2.947
4YHP	H_ARG_38	NH2	H_GLU_46	OE1	2.947
4YHP	H_ARG_38	NH2	H_ASP_90	OD1	3.968
4YHP	H_ARG_67	NH1	H_ASP_90	OD1	3.789
4YHP	H_ARG_67	NH1	H_ASP_90	OD2	2.848
4YHP	H_ARG_67	NH2	H_ASP_90	OD1	3.026
4YHP	H_ARG_67	NH2	H_ASP_90	OD2	3.449
4YHP	H_LYS_76	NZ	H_ASP_73	OD2	3.599
4YHP	H_ARG_98	NH2	H_ASP_109	OD1	3.571
4YHP	H_ARG_98	NH2	H_ASP_109	OD2	2.451
4YHP	H_LYS_151	NZ	H_ASP_152	OD1	3.964
4YHP	H_LYS_151	NZ	H_ASP_152	OD2	3.805
4YHP	H_LYS_218	NZ	H_GLU_220	OE1	3.935
4YHP	L_ARG_60	NH1	L_ASP_81	OD1	3.435
4YHP	L_ARG_60	NH1	L_ASP_81	OD2	2.451
4YHP	L_ARG_60	NH2	L_GLU_78	OE2	3.891
4YHP	L_ARG_60	NH2	L_ASP_81	OD1	3.204
4YHP	L_ARG_60	NH2	L_ASP_81	OD2	3.593
4YHP	L_LYS_104	NZ	L_ASP_84	OD1	2.935
4YHP	L_LYS_104	NZ	L_ASP_84	OD2	3.845
4YHP	L_LYS_104	NZ	L_GLU_166	OE2	3.174
4YHP	L_LYS_150	NZ	L_GLU_196	OE2	2.309
4YHP	L_LYS_189	NZ	L_ASP_186	OD1	2.837
4YHP	L_HIS_190	ND1	L_ASP_152	OD2	2.727
4YHP	F_HIS_33	ND1	F_ASP_49	OD1	3.954
4YHP	F_ARG_60	NH1	F_ASP_81	OD1	3.515
4YHP	F_ARG_60	NH1	F_ASP_81	OD2	2.794
4YHP	F_ARG_60	NH2	F_GLU_78	OE2	3.996
4YHP	F_ARG_60	NH2	F_ASP_81	OD1	3.303

4YHP	F_ARG_60	NH2	F_ASP_81	OD2	3.936
4YHP	F_LYS_104	NZ	F_ASP_84	OD1	3.436
4YHP	F_LYS_104	NZ	F_GLU_166	OE2	3.438
4YHP	F_HIS_190	ND1	F_ASP_152	OD2	3.922
4YHY	C_HIS_33	ND1	C_ASP_49	OD1	3.834
4YHY	C_ARG_60	NH1	C_ASP_81	OD1	3.547
4YHY	C_ARG_60	NH1	C_ASP_81	OD2	2.684
4YHY	C_ARG_60	NH2	C_GLU_78	OE1	3.841
4YHY	C_ARG_60	NH2	C_ASP_81	OD1	2.796
4YHY	C_ARG_60	NH2	C_ASP_81	OD2	3.359
4YHY	C_LYS_104	NZ	C_ASP_84	OD1	3.080
4YHY	C_LYS_104	NZ	C_ASP_84	OD2	3.747
4YHY	C_LYS_104	NZ	C_GLU_166	OE1	3.855
4YHY	C_LYS_104	NZ	C_GLU_166	OE2	3.371
4YHY	C_LYS_184	NZ	C_GLU_188	OE1	2.479
4YHY	C_LYS_184	NZ	C_GLU_188	OE2	3.850
4YHY	C_LYS_189	NZ	C_ASP_186	OD1	3.979
4YHY	C_HIS_190	ND1	C_ASP_152	OD2	3.638
4YHY	B_ARG_38	NH1	B_ASP_90	OD1	2.962
4YHY	B_ARG_38	NH2	B_GLU_46	OE1	3.075
4YHY	B_ARG_38	NH2	B_ASP_90	OD1	3.920
4YHY	B_ARG_67	NH1	B_ASP_90	OD1	3.667
4YHY	B_ARG_67	NH1	B_ASP_90	OD2	2.922
4YHY	B_ARG_67	NH2	B_ASP_90	OD1	2.906
4YHY	B_ARG_67	NH2	B_ASP_90	OD2	3.527
4YHY	B_ARG_98	NH2	B_ASP_109	OD1	3.412
4YHY	B_ARG_98	NH2	B_ASP_109	OD2	2.741
4YHY	B_LYS_151	NZ	B_ASP_152	OD1	3.708
4YHY	B_LYS_151	NZ	B_ASP_152	OD2	3.789
4YHY	B_LYS_218	NZ	B_GLU_220	OE2	3.937
4YHY	H_ARG_38	NH1	H_ASP_90	OD1	2.943
4YHY	H_ARG_38	NH2	H_GLU_46	OE1	3.065
4YHY	H_ARG_38	NH2	H_ASP_90	OD1	3.927
4YHY	H_ARG_67	NH1	H_ASP_90	OD1	3.683
4YHY	H_ARG_67	NH1	H_ASP_90	OD2	2.873
4YHY	H_ARG_67	NH2	H_ASP_90	OD1	2.953
4YHY	H_ARG_67	NH2	H_ASP_90	OD2	3.520
4YHY	H_ARG_98	NH2	H_ASP_109	OD1	3.446
4YHY	H_ARG_98	NH2	H_ASP_109	OD2	2.805
4YHY	H_LYS_151	NZ	H_ASP_152	OD1	3.926
4YHY	L_HIS_33	ND1	L_ASP_49	OD1	3.834
4YHY	L_ARG_60	NH1	L_ASP_81	OD1	3.514
4YHY	L_ARG_60	NH1	L_ASP_81	OD2	2.687
4YHY	L_ARG_60	NH2	L_GLU_78	OE1	3.800
4YHY	L_ARG_60	NH2	L_ASP_81	OD1	2.830
4YHY	L_ARG_60	NH2	L_ASP_81	OD2	3.411
4YHY	L_LYS_104	NZ	L_ASP_84	OD1	3.118
4YHY	L_LYS_104	NZ	L_ASP_84	OD2	3.782
4YHY	L_LYS_104	NZ	L_GLU_166	OE1	3.846
4YHY	L_LYS_104	NZ	L_GLU_166	OE2	3.435
4YHY	L_LYS_184	NZ	L_GLU_188	OE1	2.816
4YHY	L_LYS_189	NZ	L_ASP_186	OD1	3.965
4YHY	L_HIS_190	ND1	L_ASP_152	OD2	3.667
4YHZ	H_ARG_38	NH1	H_ASP_90	OD1	3.041
4YHZ	H_ARG_38	NH2	H_GLU_46	OE1	2.993
4YHZ	H_ARG_67	NH1	H_ASP_90	OD1	3.565
4YHZ	H_ARG_67	NH1	H_ASP_90	OD2	2.787
4YHZ	H_ARG_67	NH2	H_ASP_90	OD1	3.041

4YHZ	H_ARG_67	NH2	H_ASP_90	OD2	3.647
4YHZ	H_ARG_98	NH2	H_ASP_109	OD1	3.319
4YHZ	H_ARG_98	NH2	H_ASP_109	OD2	2.731
4YHZ	H_ARG_102	NH1	L_ASP_52	OD2	3.952
4YHZ	H_LYS_151	NZ	H_ASP_152	OD1	3.146
4YHZ	H_LYS_151	NZ	H_ASP_152	OD2	3.730
4YHZ	H_LYS_218	NZ	H_GLU_220	OE2	2.294
4YHZ	L_ARG_60	NH1	L_ASP_81	OD1	3.699
4YHZ	L_ARG_60	NH1	L_ASP_81	OD2	2.763
4YHZ	L_ARG_60	NH2	L_GLU_78	OE2	3.725
4YHZ	L_ARG_60	NH2	L_ASP_81	OD1	2.809
4YHZ	L_ARG_60	NH2	L_ASP_81	OD2	3.312
4YHZ	L_LYS_104	NZ	L_ASP_84	OD1	2.930
4YHZ	L_LYS_104	NZ	L_ASP_84	OD2	3.859
4YHZ	L_LYS_104	NZ	L_GLU_166	OE2	3.711
4YHZ	L_LYS_150	NZ	L_GLU_196	OE1	3.382
4YHZ	L_LYS_150	NZ	L_GLU_196	OE2	3.096
4YHZ	L_LYS_189	NZ	L_ASP_186	OD1	3.342
4YNY	A_ARG_57	NH1	A_ASP_109	OD1	2.933
4YNY	A_ARG_57	NH2	A_GLU_65	OE1	3.525
4YNY	A_ARG_57	NH2	A_GLU_65	OE2	3.243
4YNY	A_ARG_57	NH2	A_ASP_109	OD1	3.948
4YNY	A_ARG_86	NH1	A_ASP_109	OD1	3.716
4YNY	A_ARG_86	NH1	A_ASP_109	OD2	2.746
4YNY	A_ARG_86	NH2	A_ASP_109	OD1	3.047
4YNY	A_ARG_86	NH2	A_ASP_109	OD2	3.560
4YNY	A_ARG_106	NH2	A_GLU_108	OE1	3.999
4YNY	A_LYS_117	NZ	A_ASP_124	OD1	3.494
4YNY	A_LYS_117	NZ	A_ASP_124	OD2	2.864
4YNY	A_LYS_166	NZ	B_GLU_146	OE2	2.702
4YNY	B_LYS_73	NZ	B_ASP_72	OD2	3.025
4YNY	B_ARG_81	NH1	B_ASP_104	OD1	3.819
4YNY	B_ARG_81	NH1	B_ASP_104	OD2	2.603
4YNY	B_ARG_81	NH2	B_ASP_104	OD1	2.915
4YNY	B_ARG_81	NH2	B_ASP_104	OD2	3.187
4YNY	B_LYS_132	NZ	B_GLU_219	OE2	3.320
4YNY	B_LYS_188	NZ	B_GLU_105	OE1	3.576
4YNY	B_LYS_188	NZ	B_GLU_105	OE2	2.488
4YNY	B_LYS_192	NZ	B_ASP_160	OD1	3.032
4YNY	B_ARG_200	NH2	B_ASP_182	OD1	3.555
4YNY	B_ARG_200	NH2	B_ASP_182	OD2	2.866
4YNY	C_ARG_57	NH1	C_ASP_109	OD1	2.834
4YNY	C_ARG_57	NH2	C_GLU_65	OE1	3.680
4YNY	C_ARG_57	NH2	C_GLU_65	OE2	3.119
4YNY	C_ARG_57	NH2	C_ASP_109	OD1	3.921
4YNY	C_ARG_86	NH1	C_ASP_109	OD1	3.790
4YNY	C_ARG_86	NH1	C_ASP_109	OD2	2.710
4YNY	C_ARG_86	NH2	C_ASP_109	OD1	3.106
4YNY	C_ARG_86	NH2	C_ASP_109	OD2	3.542
4YNY	C_LYS_117	NZ	C_ASP_124	OD1	3.354
4YNY	C_LYS_117	NZ	C_ASP_124	OD2	2.744
4YNY	C_LYS_166	NZ	D_GLU_146	OE2	2.776
4YNY	D_LYS_73	NZ	D_ASP_72	OD1	3.416
4YNY	D_ARG_81	NH1	D_ASP_104	OD1	3.697
4YNY	D_ARG_81	NH1	D_ASP_104	OD2	2.693
4YNY	D_ARG_81	NH2	D_ASP_104	OD1	2.906
4YNY	D_ARG_81	NH2	D_ASP_104	OD2	3.380
4YNY	D_LYS_188	NZ	D_GLU_105	OE1	3.077

4YNY	D_LYS_192	NZ	D_ASP_160	OD2	3.867
4YNY	D_ARG_200	NH2	D_ASP_182	OD1	3.317
4YNY	D_ARG_200	NH2	D_ASP_182	OD2	3.323
4YO0	A_ARG_57	NH1	A_ASP_109	OD1	3.022
4YO0	A_ARG_57	NH2	A_GLU_65	OE1	3.398
4YO0	A_LYS_76	NZ	E_ASP_11	OD1	3.807
4YO0	A_LYS_76	NZ	E_ASP_11	OD2	3.094
4YO0	A_ARG_86	NH1	A_ASP_109	OD1	3.794
4YO0	A_ARG_86	NH1	A_ASP_109	OD2	2.742
4YO0	A_ARG_86	NH2	A_ASP_109	OD1	2.929
4YO0	A_ARG_86	NH2	A_ASP_109	OD2	3.356
4YO0	A_LYS_95	NZ	A_ASP_92	OD2	3.971
4YO0	A_LYS_117	NZ	A_ASP_124	OD1	3.329
4YO0	A_LYS_117	NZ	A_ASP_124	OD2	2.540
4YO0	A_LYS_166	NZ	B_GLU_146	OE2	2.816
4YO0	B_ARG_81	NH2	B_ASP_104	OD1	2.781
4YO0	B_ARG_81	NH2	B_ASP_104	OD2	3.330
4YO0	B_LYS_188	NZ	B_GLU_105	OE2	2.712
4YO0	B_LYS_192	NZ	B_ASP_160	OD1	3.003
4YO0	B_ARG_200	NH1	B_ASP_182	OD1	3.660
4YO0	B_ARG_200	NH1	B_ASP_182	OD2	2.289
4YO0	C_ARG_57	NH1	C_ASP_109	OD1	2.959
4YO0	C_ARG_57	NH2	C_GLU_65	OE1	3.257
4YO0	C_ARG_57	NH2	C_ASP_109	OD1	3.982
4YO0	C_LYS_76	NZ	F_GLU_10	OE2	3.111
4YO0	C_LYS_76	NZ	F_ASP_11	OD1	3.515
4YO0	C_LYS_76	NZ	F_ASP_11	OD2	2.782
4YO0	C_ARG_86	NH1	C_ASP_109	OD1	3.789
4YO0	C_ARG_86	NH1	C_ASP_109	OD2	2.778
4YO0	C_ARG_86	NH2	C_ASP_109	OD1	2.949
4YO0	C_ARG_86	NH2	C_ASP_109	OD2	3.459
4YO0	C_LYS_117	NZ	C_ASP_124	OD1	3.359
4YO0	C_LYS_117	NZ	C_ASP_124	OD2	2.756
4YO0	C_LYS_166	NZ	D_GLU_146	OE2	2.660
4YO0	C_LYS_231	NZ	D_GLU_145	OE1	3.828
4YO0	C_LYS_231	NZ	D_GLU_145	OE2	3.815
4YO0	D_LYS_188	NZ	D_GLU_105	OE1	2.881
4YO0	D_LYS_192	NZ	D_ASP_160	OD1	2.854
4YO0	D_ARG_200	NH1	D_ASP_182	OD2	2.726
4Z0X	A_LYS_30	NZ	A_ASP_91	OD1	2.897
4Z0X	A_ARG_60	NH1	A_ASP_81	OD1	3.753
4Z0X	A_ARG_60	NH1	A_ASP_81	OD2	2.721
4Z0X	A_ARG_60	NH2	A_ASP_81	OD1	3.000
4Z0X	A_ARG_60	NH2	A_ASP_81	OD2	3.078
4Z0X	B_LYS_37	NZ	B_GLU_35	OE1	3.057
4Z0X	B_ARG_63	NH1	B_ASP_115	OD1	2.995
4Z0X	B_ARG_63	NH2	B_GLU_71	OE2	3.549
4Z0X	B_ARG_63	NH2	B_ASP_115	OD1	3.828
4Z0X	B_ARG_92	NH1	B_ASP_115	OD1	3.502
4Z0X	B_ARG_92	NH1	B_ASP_115	OD2	2.905
4Z0X	B_ARG_92	NH2	B_ASP_115	OD1	2.679
4Z0X	B_ARG_92	NH2	B_ASP_115	OD2	3.355
4Z0X	B_ARG_123	NH1	B_ASP_132	OD1	3.837
4Z0X	C_LYS_446	NZ	A_ASP_50	OD1	3.873
4Z0X	C_LYS_446	NZ	A_ASP_50	OD2	2.440
4ZD3	H_ARG_43	NH2	H_GLU_51	OE1	2.895
4ZD3	H_ARG_43	NH2	H_GLU_51	OE2	3.597
4ZD3	H_ARG_66	NH2	H_ASP_64	OD1	3.286

4ZD3	H_ARG_66	NH2	H_ASP_64	OD2	2.638
4ZD3	H_ARG_106	NH2	H_ASP_116	OD1	3.450
4ZD3	H_ARG_106	NH2	H_ASP_116	OD2	3.904
4ZD3	H_HIS_108	ND1	H_ASP_116	OD1	3.941
4ZD3	H_HIS_108	ND1	H_ASP_116	OD2	2.771
4ZD3	H_HIS_108	NE2	L_GLU_68	OE1	2.549
4ZD3	H_HIS_108	NE2	L_GLU_68	OE2	3.986
4ZD3	H_LYS_158	NZ	H_ASP_159	OD1	3.455
4ZD3	H_LYS_158	NZ	H_ASP_159	OD2	3.407
4ZD3	H_LYS_224	NZ	L_GLU_143	OE2	2.997
4ZD3	L_ARG_75	NH2	L_ASP_98	OD1	2.930
4ZD3	L_ARG_75	NH2	L_ASP_98	OD2	3.672
4ZD3	L_LYS_123	NZ	L_GLU_185	OE2	3.206
4ZD3	L_ARG_128	NH2	L_ASP_190	OD1	3.816
4ZD3	L_LYS_169	NZ	L_GLU_215	OE1	2.511
4ZFF	A_ARG_38	NH1	A_ASP_86	OD1	2.818
4ZFF	A_ARG_38	NH2	A_GLU_46	OE2	2.795
4ZFF	A_ARG_66	NH1	A_ASP_86	OD1	3.744
4ZFF	A_ARG_66	NH1	A_ASP_86	OD2	2.802
4ZFF	A_ARG_66	NH2	A_ASP_86	OD1	2.833
4ZFF	A_ARG_66	NH2	A_ASP_86	OD2	3.432
4ZFF	A_LYS_75	NZ	A_ASP_72	OD2	3.517
4ZFF	A_ARG_94	NH2	A_ASP_101	OD1	2.782
4ZFF	A_ARG_94	NH2	A_ASP_101	OD2	3.644
4ZFF	A_LYS_143	NZ	A_ASP_144	OD2	3.566
4ZFF	A_LYS_209	NZ	B_GLU_123	OE1	3.193
4ZFF	B_ARG_61	NH1	B_GLU_81	OE2	3.817
4ZFF	B_ARG_61	NH1	B_ASP_82	OD1	2.656
4ZFF	B_ARG_61	NH1	B_ASP_82	OD2	3.672
4ZFF	B_LYS_149	NZ	B_GLU_195	OE2	2.800
4ZFF	B_HIS_189	ND1	B_ASP_151	OD1	3.097
4ZFF	B_HIS_189	ND1	B_ASP_151	OD2	3.583
4ZFF	C_ARG_23	NH1	D_GLU_30	OE1	3.414
4ZFF	C_ARG_56	NH1	C_GLU_38	OE2	3.486
4ZFF	C_ARG_56	NH2	C_GLU_38	OE1	2.778
4ZFF	C_ARG_56	NH2	C_GLU_38	OE2	3.528
4ZFF	C_ARG_82	NH2	C_GLU_42	OE1	3.647
4ZFF	C_ARG_82	NH2	C_GLU_42	OE2	2.877
4ZFF	C_HIS_99	NE2	C_GLU_73	OE2	3.973
4ZFF	C_ARG_105	NH2	C_GLU_103	OE1	3.895
4ZFF	C_ARG_105	NH2	C_GLU_103	OE2	2.902
4ZFF	C_LYS_107	NZ	C_GLU_64	OE1	3.791
4ZFF	C_LYS_107	NZ	C_GLU_64	OE2	3.768
4ZFF	D_ARG_23	NH2	D_ASP_19	OD2	3.386
4ZFF	D_ARG_56	NH1	D_GLU_38	OE2	3.530
4ZFF	D_ARG_56	NH2	D_GLU_38	OE1	2.807
4ZFF	D_ARG_56	NH2	D_GLU_38	OE2	3.533
4ZFF	D_ARG_82	NH1	D_GLU_42	OE1	2.977
4ZFF	D_ARG_82	NH1	D_GLU_42	OE2	3.475
4ZFF	D_LYS_84	NZ	D_GLU_44	OE1	2.813
4ZFF	D_LYS_84	NZ	D_GLU_44	OE2	3.787
4ZFF	D_HIS_99	NE2	D_GLU_73	OE2	3.971
4ZFF	D_ARG_105	NH2	D_GLU_103	OE1	3.892
4ZFF	D_ARG_105	NH2	D_GLU_103	OE2	2.901
4ZFF	D_LYS_107	NZ	D_GLU_64	OE1	3.795
4ZFF	D_LYS_107	NZ	D_GLU_64	OE2	3.756
4ZFF	H_ARG_38	NH1	H_ASP_86	OD1	3.173
4ZFF	H_ARG_38	NH2	H_GLU_46	OE2	3.109

4ZFF	H_ARG_66	NH1	H_ASP_86	OD1	3.724
4ZFF	H_ARG_66	NH1	H_ASP_86	OD2	2.802
4ZFF	H_ARG_66	NH2	H_ASP_86	OD1	2.829
4ZFF	H_ARG_66	NH2	H_ASP_86	OD2	3.437
4ZFF	H_LYS_75	NZ	H_ASP_72	OD2	3.526
4ZFF	H_ARG_94	NH2	H_ASP_101	OD1	2.747
4ZFF	H_ARG_94	NH2	H_ASP_101	OD2	3.634
4ZFF	H_LYS_143	NZ	H_ASP_144	OD2	3.565
4ZFF	H_LYS_209	NZ	L_GLU_123	OE1	3.731
4ZFF	L_ARG_61	NH1	L_GLU_81	OE2	3.489
4ZFF	L_ARG_61	NH1	L_ASP_82	OD1	2.794
4ZFF	L_ARG_61	NH1	L_ASP_82	OD2	3.847
4ZFF	L_LYS_	NZ	L_GLU_195	OE1	3.785
4ZFF	L_LYS_	NZ	L_GLU_195	OE2	2.790
4ZFF	L_LYS_	NZ	L_ASP_	OD1	3.960
4ZFF	L_HIS_	ND1	L_ASP_	OD1	3.345
4ZFG	A_ARG_282	NH1	A_GLU_286	OE2	2.789
4ZFG	A_ARG_337	NH2	A_GLU_341	OE2	3.147
4ZFG	A_LYS_343	NZ	A_GLU_395	OE1	3.481
4ZFG	A_LYS_343	NZ	A_GLU_395	OE2	2.744
4ZFG	A_ARG_400	NH2	A_ASP_422	OD1	3.271
4ZFG	A_LYS_478	NZ	A_ASP_377	OD1	2.811
4ZFG	H_ARG_38	NH1	H_ASP_86	OD1	2.945
4ZFG	H_ARG_38	NH2	H_GLU_46	OE1	3.779
4ZFG	H_ARG_38	NH2	H_GLU_46	OE2	2.970
4ZFG	H_ARG_38	NH2	H_ASP_86	OD1	3.795
4ZFG	H_ARG_66	NH1	H_ASP_86	OD1	3.748
4ZFG	H_ARG_66	NH1	H_ASP_86	OD2	2.697
4ZFG	H_ARG_66	NH2	H_ASP_86	OD1	3.191
4ZFG	H_ARG_66	NH2	H_ASP_86	OD2	3.631
4ZFG	H_ARG_94	NH2	H_ASP_101	OD1	2.815
4ZFG	H_ARG_94	NH2	H_ASP_101	OD2	3.685
4ZFG	H_LYS_143	NZ	H_ASP_144	OD1	3.369
4ZFG	H_LYS_143	NZ	H_ASP_144	OD2	3.092
4ZFG	H_LYS_209	NZ	L_GLU_123	OE1	2.808
4ZFG	H_LYS_210	NZ	H_GLU_212	OE1	3.187
4ZFG	H_LYS_210	NZ	H_GLU_212	OE2	3.341
4ZFG	L_ARG_61	NH2	L_GLU_81	OE2	3.382
4ZFG	L_ARG_61	NH2	L_ASP_82	OD1	2.847
4ZFG	L_ARG_61	NH2	L_ASP_82	OD2	3.547
4ZFG	L_LYS_149	NZ	L_GLU_195	OE1	2.802
4ZFG	L_HIS_189	ND1	L_ASP_151	OD2	3.313
4ZFO	F_HIS_19	NE2	A_GLU_50	OE1	2.994
4ZFO	F_HIS_19	NE2	A_GLU_50	OE2	3.320
4ZFO	L_LYS_24	NZ	L_ASP_70	OD1	2.843
4ZFO	L_LYS_24	NZ	L_ASP_70	OD2	3.681
4ZFO	L_ARG_41	NH1	L_GLU_165	OE1	2.854
4ZFO	L_ARG_41	NH1	L_GLU_165	OE2	3.771
4ZFO	L_ARG_41	NH2	L_GLU_165	OE1	3.602
4ZFO	L_ARG_41	NH2	L_GLU_165	OE2	3.007
4ZFO	L_ARG_61	NH1	L_GLU_81	OE2	3.554
4ZFO	L_ARG_61	NH1	L_ASP_82	OD1	2.833
4ZFO	L_ARG_61	NH1	L_ASP_82	OD2	3.587
4ZFO	L_LYS_149	NZ	L_GLU_195	OE2	3.249
4ZFO	L_HIS_189	ND1	L_ASP_151	OD2	2.754
4ZFO	H_ARG_38	NH1	H_ASP_90	OD1	2.859
4ZFO	H_ARG_38	NH2	H_GLU_46	OE2	3.054
4ZFO	H_ARG_38	NH2	H_ASP_90	OD1	3.757

4ZFO	H_ARG_39	NH1	L_GLU_85	OE2	3.425
4ZFO	H_ARG_39	NH2	L_GLU_85	OE1	3.703
4ZFO	H_ARG_39	NH2	L_GLU_85	OE2	2.644
4ZFO	H_LYS_67	NZ	H_ASP_90	OD1	3.687
4ZFO	H_LYS_67	NZ	H_ASP_90	OD2	2.794
4ZFO	H_LYS_150	NZ	H_ASP_151	OD1	3.394
4ZFO	H_LYS_216	NZ	L_GLU_123	OE2	3.666
4ZFO	H_ARG_217	NH2	H_GLU_219	OE1	3.524
4ZFO	B_LYS_24	NZ	B_ASP_70	OD1	2.732
4ZFO	B_LYS_24	NZ	B_ASP_70	OD2	3.699
4ZFO	B_ARG_61	NH1	B_GLU_81	OE1	3.604
4ZFO	B_ARG_61	NH1	B_ASP_82	OD1	2.928
4ZFO	B_ARG_61	NH1	B_ASP_82	OD2	3.562
4ZFO	B_LYS_103	NZ	B_GLU_165	OE1	3.091
4ZFO	B_LYS_103	NZ	B_GLU_165	OE2	2.652
4ZFO	B_LYS_149	NZ	B_GLU_195	OE1	2.655
4ZFO	B_LYS_149	NZ	B_GLU_195	OE2	3.647
4ZFO	B_LYS_183	NZ	B_GLU_187	OE2	3.657
4ZFO	B_LYS_188	NZ	B_ASP_185	OD1	2.524
4ZFO	B_HIS_189	ND1	B_ASP_151	OD2	2.980
4ZFO	A_ARG_31	NH1	A_ASP_102	OD1	3.536
4ZFO	A_ARG_31	NH1	A_ASP_102	OD2	2.769
4ZFO	A_ARG_38	NH1	A_ASP_90	OD1	2.884
4ZFO	A_ARG_38	NH2	A_GLU_46	OE1	3.650
4ZFO	A_ARG_38	NH2	A_GLU_46	OE2	2.886
4ZFO	A_ARG_38	NH2	A_ASP_90	OD1	3.988
4ZFO	A_ARG_39	NH1	B_GLU_85	OE1	3.845
4ZFO	A_ARG_39	NH2	B_GLU_85	OE1	2.855
4ZFO	A_ARG_39	NH2	B_GLU_85	OE2	3.746
4ZFO	A_LYS_67	NZ	A_ASP_90	OD1	3.473
4ZFO	A_LYS_67	NZ	A_ASP_90	OD2	2.764
4ZFO	A_LYS_150	NZ	A_ASP_151	OD1	3.442
4ZFO	K_HIS_19	NE2	H_GLU_50	OE1	2.755
4ZFO	K_HIS_19	NE2	H_GLU_50	OE2	3.392
4ZH7	A_ARG_32	NH1	A_ASP_28	OD1	2.616
4ZH7	A_ARG_32	NH1	A_ASP_28	OD2	2.970
4ZH7	A_LYS_155	NZ	A_GLU_151	OE2	3.235
4ZH7	A_ARG_169	NH2	A_ASP_257	OD2	3.147
4ZH7	A_LYS_175	NZ	A_GLU_176	OE2	3.803
4ZH7	A_LYS_251	NZ	A_GLU_253	OE1	3.001
4ZH7	A_LYS_251	NZ	A_GLU_253	OE2	3.952
4ZH7	A_LYS_313	NZ	A_ASP_317	OD2	2.913
4ZH7	A_LYS_343	NZ	A_ASP_350	OD1	3.604
4ZH7	A_LYS_343	NZ	A_ASP_350	OD2	2.780
4ZH7	A_LYS_366	NZ	A_GLU_320	OE2	2.717
4ZH7	A_LYS_437	NZ	A_GLU_381	OE1	3.484
4ZH7	A_LYS_437	NZ	A_GLU_381	OE2	3.811
4ZH7	A_ARG_466	NH2	A_ASP_458	OD1	2.975
4ZH7	A_ARG_466	NH2	A_ASP_458	OD2	3.143
5A2I	H_ARG_38	NH1	H_ASP_86	OD1	2.884
5A2I	H_ARG_38	NH2	H_GLU_46	OE1	3.128
5A2I	H_ARG_38	NH2	H_GLU_46	OE2	3.996
5A2I	H_ARG_38	NH2	H_ASP_86	OD1	3.809
5A2I	H_ARG_52	NH1	H_GLU_50	OE2	2.458
5A2I	H_HIS_58	ND1	H_GLU_50	OE2	2.942
5A2I	H_ARG_66	NH1	H_ASP_86	OD1	3.097
5A2I	H_ARG_66	NH1	H_ASP_86	OD2	3.703
5A2I	H_ARG_66	NH2	H_ASP_86	OD1	3.277

5A2I	H_ARG_66	NH2	H_ASP_86	OD2	2.349
5A2I	H_ARG_71	NH2	H_ASP_73	OD1	3.396
5A2I	H_ARG_1024	NH1	H_ASP_1069	OD2	3.870
5A2I	H_ARG_1024	NH2	H_ASP_1069	OD1	2.961
5A2I	H_ARG_1024	NH2	H_ASP_1069	OD2	3.137
5A2I	H_HIS_1042	ND1	H_GLU_1038	OE2	3.431
5A2I	H_HIS_1042	ND1	H_ASP_1041	OD1	3.140
5A2I	H_HIS_1042	NE2	H_ASP_1041	OD1	2.854
5A2I	H_ARG_1061	NH2	H_GLU_1081	OE2	3.967
5A2I	H_ARG_1061	NH2	H_ASP_1082	OD1	2.886
5A2I	H_ARG_1061	NH2	H_ASP_1082	OD2	3.803
5A2J	H_ARG_38	NH1	H_ASP_86	OD1	2.875
5A2J	H_ARG_38	NH2	H_GLU_46	OE1	3.145
5A2J	H_ARG_38	NH2	H_GLU_46	OE2	3.372
5A2J	H_ARG_38	NH2	H_ASP_86	OD1	3.987
5A2J	H_LYS_43	NZ	H_GLU_46	OE1	3.646
5A2J	H_LYS_43	NZ	H_GLU_85	OE1	2.765
5A2J	H_ARG_52	NH2	H_GLU_50	OE2	2.945
5A2J	H_ARG_66	NH1	H_ASP_86	OD1	3.341
5A2J	H_ARG_66	NH1	H_ASP_86	OD2	3.539
5A2J	H_ARG_66	NH2	H_ASP_86	OD1	3.626
5A2J	H_ARG_66	NH2	H_ASP_86	OD2	2.364
5A2J	H_ARG_71	NH2	H_ASP_73	OD1	3.334
5A2J	H_LYS_75	NZ	H_ASP_72	OD2	3.979
5A2J	H_ARG_83	NH1	H_GLU_85	OE2	3.360
5A2J	H_ARG_1024	NH1	H_ASP_1069	OD1	3.811
5A2J	H_ARG_1024	NH1	H_ASP_1069	OD2	2.838
5A2J	H_ARG_1024	NH2	H_ASP_1069	OD1	3.142
5A2J	H_ARG_1024	NH2	H_ASP_1069	OD2	3.430
5A2J	H_HIS_1042	ND1	H_GLU_1038	OE2	3.360
5A2J	H_ARG_1061	NH2	H_GLU_1081	OE2	3.894
5A2J	H_ARG_1061	NH2	H_ASP_1082	OD1	2.853
5A2J	H_ARG_1061	NH2	H_ASP_1082	OD2	3.674
5A2K	H_ARG_38	NH1	H_ASP_86	OD1	2.875
5A2K	H_ARG_38	NH2	H_GLU_46	OE1	2.994
5A2K	H_ARG_38	NH2	H_GLU_46	OE2	3.664
5A2K	H_ARG_38	NH2	H_ASP_86	OD1	3.944
5A2K	H_LYS_43	NZ	H_GLU_46	OE1	3.807
5A2K	H_LYS_43	NZ	H_GLU_85	OE1	3.399
5A2K	H_ARG_52	NH1	H_GLU_50	OE1	3.946
5A2K	H_ARG_52	NH1	H_GLU_50	OE2	2.653
5A2K	H_HIS_58	ND1	H_GLU_50	OE2	2.712
5A2K	H_ARG_66	NH1	H_ASP_86	OD1	3.221
5A2K	H_ARG_66	NH1	H_ASP_86	OD2	3.625
5A2K	H_ARG_66	NH2	H_ASP_86	OD1	3.474
5A2K	H_ARG_66	NH2	H_ASP_86	OD2	2.358
5A2K	H_ARG_71	NH2	H_ASP_73	OD1	3.340
5A2K	H_ARG_83	NH1	H_GLU_85	OE2	3.612
5A2K	H_HIS_1042	ND1	H_GLU_1038	OE2	3.466
5A2K	H_HIS_1042	NE2	H_ASP_1041	OD1	3.782
5A2K	H_ARG_1061	NH2	H_GLU_1081	OE2	3.980
5A2K	H_ARG_1061	NH2	H_ASP_1082	OD1	2.834
5A2K	H_ARG_1061	NH2	H_ASP_1082	OD2	3.700
5A2L	H_ARG_38	NH1	H_ASP_86	OD1	2.857
5A2L	H_ARG_38	NH2	H_GLU_46	OE1	3.272
5A2L	H_ARG_38	NH2	H_GLU_46	OE2	3.166
5A2L	H_ARG_38	NH2	H_ASP_86	OD1	3.882
5A2L	H_LYS_43	NZ	H_GLU_46	OE1	2.594

5A2L	H.LYS_43	NZ	H.GLU_46	OE2	3.749
5A2L	H.LYS_43	NZ	H.GLU_85	OE1	3.820
5A2L	H.ARG_52	NH1	H.GLU_50	OE2	2.656
5A2L	H.HIS_58	ND1	H.GLU_50	OE2	2.623
5A2L	H.ARG_66	NH1	H.ASP_86	OD1	3.373
5A2L	H.ARG_66	NH1	H.ASP_86	OD2	3.769
5A2L	H.ARG_66	NH2	H.ASP_86	OD1	3.135
5A2L	H.ARG_66	NH2	H.ASP_86	OD2	2.092
5A2L	H.ARG_71	NH2	H.ASP_73	OD1	3.516
5A2L	H.ARG_83	NH1	H.GLU_85	OE2	3.111
5A2L	H.ARG_1024	NH1	H.ASP_1069	OD2	3.824
5A2L	H.ARG_1024	NH2	H.ASP_1069	OD1	3.107
5A2L	H.ARG_1024	NH2	H.ASP_1069	OD2	2.735
5A2L	H.HIS_1042	ND1	H.GLU_1038	OE2	3.532
5A2L	H.ARG_1061	NH2	H.GLU_1081	OE2	3.627
5A2L	H.ARG_1061	NH2	H.ASP_1082	OD1	2.860
5A2L	H.ARG_1061	NH2	H.ASP_1082	OD2	3.701
5A2L	H.LYS_1103	NZ	H.GLU_1083	OE2	3.909
5A7X	A.LYS_121	NZ	A.GLU_429	OE1	3.568
5A7X	A.LYS_121	NZ	A.GLU_429	OE2	2.734
5A7X	A.LYS_207	NZ	A.GLU_381	OE1	3.945
5A7X	A.LYS_207	NZ	A.GLU_381	OE2	3.126
5A7X	A.LYS_232	NZ	A.GLU_351	OE1	3.994
5A7X	A.HIS_249	NE2	A.GLU_482	OE1	3.525
5A7X	A.LYS_282	NZ	A.GLU_275	OE1	3.953
5A7X	A.LYS_282	NZ	A.GLU_275	OE2	2.643
5A7X	A.LYS_348	NZ	A.GLU_269	OE1	3.207
5A7X	A.LYS_348	NZ	A.GLU_351	OE1	3.940
5A7X	A.LYS_348	NZ	A.GLU_351	OE2	3.259
5A7X	A.LYS_350	NZ	A.ASP_395	OD2	3.580
5A7X	A.LYS_357	NZ	A.GLU_466	OE2	3.719
5A7X	A.ARG_419	NH1	D.GLU_100B	OE1	3.000
5A7X	A.ARG_419	NH1	D.GLU_100B	OE2	3.675
5A7X	A.ARG_419	NH2	D.GLU_99	OE1	2.292
5A7X	A.ARG_419	NH2	D.GLU_100B	OE2	3.969
5A7X	A.ARG_456	NH2	A.GLU_466	OE1	3.535
5A7X	A.ARG_456	NH2	A.GLU_466	OE2	3.469
5A7X	A.ARG_469	NH2	A.ASP_457	OD2	3.234
5A7X	A.ARG_476	NH1	A.ASP_474	OD1	3.441
5A7X	A.ARG_476	NH2	A.GLU_102	OE1	3.296
5A7X	A.ARG_476	NH2	A.GLU_102	OE2	3.010
5A7X	A.LYS_487	NZ	A.GLU_91	OE1	3.525
5A7X	A.LYS_490	NZ	A.GLU_492	OE1	3.300
5A7X	B.LYS_29	NZ	B.GLU_85	OE1	2.833
5A7X	B.LYS_29	NZ	B.GLU_85	OE2	3.848
5A7X	B.LYS_35	NZ	A.ASP_457	OD1	3.741
5A7X	B.ARG_54	NH1	B.ASP_78	OD1	3.987
5A7X	B.ARG_54	NH1	B.ASP_78	OD2	2.755
5A7X	B.ARG_54	NH2	B.ASP_78	OD1	2.666
5A7X	B.ARG_54	NH2	B.ASP_78	OD2	2.988
5A7X	B.ARG_59	NH1	A.ASP_368	OD1	3.154
5A7X	B.ARG_59	NH1	A.ASP_368	OD2	3.344
5A7X	B.ARG_59	NH2	A.ASP_368	OD1	2.976
5A7X	B.ARG_59	NH2	A.ASP_368	OD2	2.433
5A7X	B.HIS_107	ND1	B.ASP_105	OD1	3.166
5A7X	B.HIS_107	ND1	B.ASP_105	OD2	2.892
5A7X	B.ARG_134	NH2	B.ASP_153	OD1	3.765
5A7X	B.LYS_136	NZ	B.GLU_150	OE2	3.886

5A7X	B_LYS_136	NZ	B_ASP_153	OD1	3.937
5A7X	B_LYS_136	NZ	B_ASP_153	OD2	2.987
5A7X	B_LYS_171	NZ	B_GLU_169	OE2	2.874
5A7X	C_ARG_61	NH2	C_GLU_81	OE2	3.127
5A7X	C_ARG_61	NH2	C_ASP_82	OD1	3.575
5A7X	C_ARG_95B	NH2	C_ASP_1	OD2	2.985
5A7X	C_HIS_189	ND1	C_ASP_151	OD2	2.584
5A7X	C_HIS_189	NE2	C_ASP_185	OD1	2.801
5A7X	C_HIS_189	NE2	C_ASP_185	OD2	3.600
5A7X	C_ARG_211	NH1	C_GLU_187	OE1	3.852
5A7X	D_ARG_31	NH2	D_ASP_100A	OD1	3.069
5A7X	D_ARG_31	NH2	D_ASP_100A	OD2	3.614
5A7X	D_ARG_38	NH1	D_GLU_46	OE1	2.778
5A7X	D_ARG_38	NH1	D_GLU_46	OE2	3.341
5A7X	D_ARG_38	NH2	D_ASP_86	OD1	2.685
5A7X	D_ARG_50	NH2	D_GLU_97	OE2	2.331
5A7X	D_ARG_66	NH1	D_ASP_86	OD2	3.597
5A7X	D_ARG_66	NH2	D_ASP_86	OD1	2.740
5A7X	D_ARG_66	NH2	D_ASP_86	OD2	2.415
5A7X	D_LYS_73	NZ	D_ASP_55	OD1	2.968
5A7X	D_ARG_82A	NH2	D_GLU_81	OE1	3.271
5A7X	D_LYS_143	NZ	D_ASP_144	OD1	2.614
5A7X	D_LYS_143	NZ	D_ASP_144	OD2	3.235
5A7X	D_HIS_164	NE2	C_ASP_167	OD1	3.880
5A7X	D_HIS_164	NE2	C_ASP_167	OD2	2.506
5A7X	D_LYS_206	NZ	D_ASP_208	OD1	3.965
5A7X	D_LYS_209	NZ	C_GLU_123	OE1	3.513
5A7X	D_LYS_209	NZ	C_GLU_123	OE2	3.583
5A7X	E_LYS_121	NZ	E_GLU_429	OE1	3.567
5A7X	E_LYS_121	NZ	E_GLU_429	OE2	2.734
5A7X	E_LYS_207	NZ	E_GLU_381	OE1	3.946
5A7X	E_LYS_207	NZ	E_GLU_381	OE2	3.125
5A7X	E_LYS_232	NZ	E_GLU_351	OE1	3.995
5A7X	E_HIS_249	NE2	E_GLU_482	OE1	3.525
5A7X	E_LYS_282	NZ	E_GLU_275	OE1	3.954
5A7X	E_LYS_282	NZ	E_GLU_275	OE2	2.642
5A7X	E_LYS_348	NZ	E_GLU_269	OE1	3.207
5A7X	E_LYS_348	NZ	E_GLU_351	OE1	3.941
5A7X	E_LYS_348	NZ	E_GLU_351	OE2	3.259
5A7X	E_LYS_350	NZ	E_ASP_395	OD2	3.580
5A7X	E_LYS_357	NZ	E_GLU_466	OE2	3.719
5A7X	E_ARG_419	NH1	H_GLU_100B	OE1	2.998
5A7X	E_ARG_419	NH1	H_GLU_100B	OE2	3.674
5A7X	E_ARG_419	NH2	H_GLU_99	OE1	2.293
5A7X	E_ARG_419	NH2	H_GLU_100B	OE2	3.968
5A7X	E_ARG_456	NH2	E_GLU_466	OE1	3.536
5A7X	E_ARG_456	NH2	E_GLU_466	OE2	3.468
5A7X	E_ARG_469	NH2	E_ASP_457	OD2	3.234
5A7X	E_ARG_476	NH1	E_ASP_474	OD1	3.440
5A7X	E_ARG_476	NH2	E_GLU_102	OE1	3.296
5A7X	E_ARG_476	NH2	E_GLU_102	OE2	3.010
5A7X	E_LYS_487	NZ	E_GLU_91	OE1	3.524
5A7X	E_LYS_490	NZ	E_GLU_492	OE1	3.301
5A7X	F_LYS_29	NZ	F_GLU_85	OE1	2.832
5A7X	F_LYS_29	NZ	F_GLU_85	OE2	3.847
5A7X	F_LYS_35	NZ	E_ASP_457	OD1	3.741
5A7X	F_ARG_54	NH1	F_ASP_78	OD1	3.987
5A7X	F_ARG_54	NH1	F_ASP_78	OD2	2.755

5A7X	F_ARG_54	NH2	F_ASP_78	OD1	2.666
5A7X	F_ARG_54	NH2	F_ASP_78	OD2	2.988
5A7X	F_ARG_59	NH1	E_ASP_368	OD1	3.154
5A7X	F_ARG_59	NH1	E_ASP_368	OD2	3.343
5A7X	F_ARG_59	NH2	E_ASP_368	OD1	2.977
5A7X	F_ARG_59	NH2	E_ASP_368	OD2	2.434
5A7X	F_HIS_107	ND1	F_ASP_105	OD1	3.166
5A7X	F_HIS_107	ND1	F_ASP_105	OD2	2.891
5A7X	F_ARG_134	NH2	F_ASP_153	OD1	3.765
5A7X	F_LYS_136	NZ	F_GLU_150	OE2	3.883
5A7X	F_LYS_136	NZ	F_ASP_153	OD1	3.936
5A7X	F_LYS_136	NZ	F_ASP_153	OD2	2.987
5A7X	F_LYS_171	NZ	F_GLU_169	OE2	2.875
5A7X	G_ARG_61	NH2	G_GLU_81	OE2	3.126
5A7X	G_ARG_61	NH2	G_ASP_82	OD1	3.576
5A7X	G_ARG_95B	NH2	G_ASP_1	OD2	2.984
5A7X	G_HIS_189	ND1	G_ASP_151	OD2	2.584
5A7X	G_HIS_189	NE2	G_ASP_185	OD1	2.802
5A7X	G_HIS_189	NE2	G_ASP_185	OD2	3.599
5A7X	G_ARG_211	NH1	G_GLU_187	OE1	3.852
5A7X	H_ARG_31	NH2	H_ASP_100A	OD1	3.070
5A7X	H_ARG_31	NH2	H_ASP_100A	OD2	3.615
5A7X	H_ARG_38	NH1	H_GLU_46	OE1	2.780
5A7X	H_ARG_38	NH1	H_GLU_46	OE2	3.343
5A7X	H_ARG_38	NH2	H_ASP_86	OD1	2.684
5A7X	H_ARG_50	NH2	H_GLU_97	OE2	2.333
5A7X	H_ARG_66	NH1	H_ASP_86	OD2	3.598
5A7X	H_ARG_66	NH2	H_ASP_86	OD1	2.739
5A7X	H_ARG_66	NH2	H_ASP_86	OD2	2.416
5A7X	H_LYS_73	NZ	H_ASP_55	OD1	2.968
5A7X	H_ARG_82A	NH2	H_GLU_81	OE1	3.271
5A7X	H_LYS_143	NZ	H_ASP_144	OD1	2.614
5A7X	H_LYS_143	NZ	H_ASP_144	OD2	3.234
5A7X	H_HIS_164	NE2	G_ASP_167	OD1	3.880
5A7X	H_HIS_164	NE2	G_ASP_167	OD2	2.505
5A7X	H_LYS_206	NZ	H_ASP_208	OD1	3.966
5A7X	H_LYS_209	NZ	G_GLU_123	OE1	3.512
5A7X	H_LYS_209	NZ	G_GLU_123	OE2	3.584
5A7X	LLYS_121	NZ	I_GLU_429	OE1	3.568
5A7X	LLYS_121	NZ	I_GLU_429	OE2	2.736
5A7X	LLYS_207	NZ	I_GLU_381	OE1	3.945
5A7X	LLYS_207	NZ	I_GLU_381	OE2	3.127
5A7X	LLYS_232	NZ	I_GLU_351	OE1	3.995
5A7X	I_HIS_249	NE2	I_GLU_482	OE1	3.525
5A7X	LLYS_282	NZ	I_GLU_275	OE1	3.953
5A7X	LLYS_282	NZ	I_GLU_275	OE2	2.643
5A7X	LLYS_348	NZ	I_GLU_269	OE1	3.206
5A7X	LLYS_348	NZ	I_GLU_351	OE1	3.941
5A7X	LLYS_348	NZ	I_GLU_351	OE2	3.259
5A7X	LLYS_350	NZ	I_ASP_395	OD2	3.579
5A7X	LLYS_357	NZ	I_GLU_466	OE2	3.720
5A7X	I_ARG_419	NH1	L_GLU_100B	OE1	2.999
5A7X	I_ARG_419	NH1	L_GLU_100B	OE2	3.675
5A7X	I_ARG_419	NH2	L_GLU_99	OE1	2.293
5A7X	I_ARG_419	NH2	L_GLU_100B	OE2	3.968
5A7X	I_ARG_456	NH2	I_GLU_466	OE1	3.536
5A7X	I_ARG_456	NH2	I_GLU_466	OE2	3.468
5A7X	I_ARG_469	NH2	I_ASP_457	OD2	3.234

5A7X	L_ARG_476	NH1	L_ASP_474	OD1	3.441
5A7X	L_ARG_476	NH2	L_GLU_102	OE1	3.297
5A7X	L_ARG_476	NH2	L_GLU_102	OE2	3.009
5A7X	L_LYS_487	NZ	L_GLU_91	OE1	3.523
5A7X	L_LYS_490	NZ	L_GLU_492	OE1	3.300
5A7X	J_LYS_29	NZ	J_GLU_85	OE1	2.833
5A7X	J_LYS_29	NZ	J_GLU_85	OE2	3.848
5A7X	J_LYS_35	NZ	L_ASP_457	OD1	3.740
5A7X	J_ARG_54	NH1	J_ASP_78	OD1	3.987
5A7X	J_ARG_54	NH1	J_ASP_78	OD2	2.755
5A7X	J_ARG_54	NH2	J_ASP_78	OD1	2.665
5A7X	J_ARG_54	NH2	J_ASP_78	OD2	2.989
5A7X	J_ARG_59	NH1	L_ASP_368	OD1	3.154
5A7X	J_ARG_59	NH1	L_ASP_368	OD2	3.344
5A7X	J_ARG_59	NH2	L_ASP_368	OD1	2.976
5A7X	J_ARG_59	NH2	L_ASP_368	OD2	2.433
5A7X	J_HIS_107	ND1	J_ASP_105	OD1	3.166
5A7X	J_HIS_107	ND1	J_ASP_105	OD2	2.892
5A7X	J_ARG_134	NH2	J_ASP_153	OD1	3.765
5A7X	J_LYS_136	NZ	J_GLU_150	OE2	3.885
5A7X	J_LYS_136	NZ	J_ASP_153	OD1	3.936
5A7X	J_LYS_136	NZ	J_ASP_153	OD2	2.987
5A7X	J_LYS_171	NZ	J_GLU_169	OE2	2.873
5A7X	K_ARG_61	NH2	K_GLU_81	OE2	3.128
5A7X	K_ARG_61	NH2	K_ASP_82	OD1	3.577
5A7X	K_ARG_95B	NH2	K_ASP_1	OD2	2.985
5A7X	K_HIS_189	ND1	K_ASP_151	OD2	2.584
5A7X	K_HIS_189	NE2	K_ASP_185	OD1	2.801
5A7X	K_HIS_189	NE2	K_ASP_185	OD2	3.597
5A7X	K_ARG_211	NH1	K_GLU_187	OE1	3.851
5A7X	L_ARG_31	NH2	L_ASP_100A	OD1	3.070
5A7X	L_ARG_31	NH2	L_ASP_100A	OD2	3.615
5A7X	L_ARG_38	NH1	L_GLU_46	OE1	2.779
5A7X	L_ARG_38	NH1	L_GLU_46	OE2	3.342
5A7X	L_ARG_38	NH2	L_ASP_86	OD1	2.685
5A7X	L_ARG_50	NH2	L_GLU_97	OE2	2.332
5A7X	L_ARG_66	NH1	L_ASP_86	OD2	3.598
5A7X	L_ARG_66	NH2	L_ASP_86	OD1	2.739
5A7X	L_ARG_66	NH2	L_ASP_86	OD2	2.415
5A7X	L_LYS_73	NZ	L_ASP_55	OD1	2.968
5A7X	L_ARG_82A	NH2	L_GLU_81	OE1	3.271
5A7X	L_LYS_143	NZ	L_ASP_144	OD1	2.615
5A7X	L_LYS_143	NZ	L_ASP_144	OD2	3.236
5A7X	L_HIS_164	NE2	K_ASP_167	OD1	3.880
5A7X	L_HIS_164	NE2	K_ASP_167	OD2	2.504
5A7X	L_LYS_206	NZ	L_ASP_208	OD1	3.966
5A7X	L_LYS_209	NZ	K_GLU_123	OE1	3.514
5A7X	L_LYS_209	NZ	K_GLU_123	OE2	3.585
5A7X	M_ARG_24	NH2	M_ASP_70	OD1	3.351
5A7X	M_ARG_24	NH2	M_ASP_70	OD2	2.877
5A7X	M_ARG_61	NH1	M_ASP_82	OD1	3.079
5A7X	M_ARG_61	NH1	M_ASP_82	OD2	3.077
5A7X	M_ARG_61	NH2	M_GLU_81	OE2	3.862
5A7X	M_LYS_103	NZ	M_GLU_165	OE1	3.804
5A7X	M_LYS_149	NZ	M_GLU_195	OE1	2.746
5A7X	M_LYS_149	NZ	M_GLU_195	OE2	3.963
5A7X	M_LYS_183	NZ	M_GLU_187	OE2	2.699
5A7X	M_HIS_189	ND1	M_ASP_151	OD1	3.975

5A7X	M_HIS_189	ND1	M_ASP_151	OD2	2.261
5A7X	N_ARG_38	NH1	N_ASP_86	OD1	3.024
5A7X	N_ARG_38	NH2	N_GLU_46	OE1	3.886
5A7X	N_ARG_66	NH1	N_ASP_86	OD1	3.550
5A7X	N_ARG_66	NH1	N_ASP_86	OD2	2.799
5A7X	N_ARG_66	NH2	N_ASP_86	OD1	2.933
5A7X	N_ARG_66	NH2	N_ASP_86	OD2	3.625
5A7X	N_LYS_82A	NZ	N_GLU_81	OE2	2.705
5A7X	N_HIS_100F	ND1	N_ASP_100G	OD2	3.940
5A7X	N_LYS_143	NZ	N_ASP_144	OD1	3.370
5A7X	N_LYS_143	NZ	N_ASP_144	OD2	3.506
5A7X	N_LYS_206	NZ	N_ASP_208	OD2	3.418
5A7X	O_ARG_24	NH2	O_ASP_70	OD1	3.351
5A7X	O_ARG_24	NH2	O_ASP_70	OD2	2.877
5A7X	O_ARG_61	NH1	O_ASP_82	OD1	3.079
5A7X	O_ARG_61	NH1	O_ASP_82	OD2	3.077
5A7X	O_ARG_61	NH2	O_GLU_81	OE2	3.862
5A7X	O_LYS_103	NZ	O_GLU_165	OE1	3.804
5A7X	O_LYS_149	NZ	O_GLU_195	OE1	2.747
5A7X	O_LYS_149	NZ	O_GLU_195	OE2	3.963
5A7X	O_LYS_183	NZ	O_GLU_187	OE2	2.699
5A7X	O_HIS_189	ND1	O_ASP_151	OD1	3.974
5A7X	O_HIS_189	ND1	O_ASP_151	OD2	2.260
5A7X	P_ARG_38	NH1	P_ASP_86	OD1	3.023
5A7X	P_ARG_38	NH2	P_GLU_46	OE1	3.886
5A7X	P_ARG_66	NH1	P_ASP_86	OD1	3.549
5A7X	P_ARG_66	NH1	P_ASP_86	OD2	2.799
5A7X	P_ARG_66	NH2	P_ASP_86	OD1	2.932
5A7X	P_ARG_66	NH2	P_ASP_86	OD2	3.625
5A7X	P_LYS_82A	NZ	P_GLU_81	OE2	2.706
5A7X	P_HIS_100F	ND1	P_ASP_100G	OD2	3.938
5A7X	P_LYS_143	NZ	P_ASP_144	OD1	3.371
5A7X	P_LYS_143	NZ	P_ASP_144	OD2	3.506
5A7X	P_LYS_206	NZ	P_ASP_208	OD2	3.418
5A7X	Q_ARG_24	NH2	Q_ASP_70	OD1	3.350
5A7X	Q_ARG_24	NH2	Q_ASP_70	OD2	2.876
5A7X	Q_ARG_61	NH1	Q_ASP_82	OD1	3.081
5A7X	Q_ARG_61	NH1	Q_ASP_82	OD2	3.078
5A7X	Q_ARG_61	NH2	Q_GLU_81	OE2	3.863
5A7X	Q_LYS_103	NZ	Q_GLU_165	OE1	3.804
5A7X	Q_LYS_149	NZ	Q_GLU_195	OE1	2.747
5A7X	Q_LYS_149	NZ	Q_GLU_195	OE2	3.963
5A7X	Q_LYS_183	NZ	Q_GLU_187	OE2	2.698
5A7X	Q_HIS_189	ND1	Q_ASP_151	OD1	3.974
5A7X	Q_HIS_189	ND1	Q_ASP_151	OD2	2.260
5A7X	R_ARG_38	NH1	R_ASP_86	OD1	3.024
5A7X	R_ARG_38	NH2	R_GLU_46	OE1	3.886
5A7X	R_ARG_66	NH1	R_ASP_86	OD1	3.548
5A7X	R_ARG_66	NH1	R_ASP_86	OD2	2.798
5A7X	R_ARG_66	NH2	R_ASP_86	OD1	2.932
5A7X	R_ARG_66	NH2	R_ASP_86	OD2	3.625
5A7X	R_LYS_82A	NZ	R_GLU_81	OE2	2.705
5A7X	R_HIS_100F	ND1	R_ASP_100G	OD2	3.938
5A7X	R_LYS_143	NZ	R_ASP_144	OD1	3.370
5A7X	R_LYS_143	NZ	R_ASP_144	OD2	3.506
5A7X	R_LYS_206	NZ	R_ASP_208	OD2	3.419
5A8H	A_LYS_121	NZ	A_GLU_429	OE1	3.567
5A8H	A_LYS_121	NZ	A_GLU_429	OE2	2.735

5A8H	A_LYS_207	NZ	A_GLU_381	OE1	3.945
5A8H	A_LYS_207	NZ	A_GLU_381	OE2	3.126
5A8H	A_LYS_232	NZ	A_GLU_351	OE1	3.995
5A8H	A_HIS_249	NE2	A_GLU_482	OE1	3.525
5A8H	A_LYS_282	NZ	A_GLU_275	OE1	3.954
5A8H	A_LYS_282	NZ	A_GLU_275	OE2	2.643
5A8H	A_LYS_348	NZ	A_GLU_269	OE1	3.206
5A8H	A_LYS_348	NZ	A_GLU_351	OE1	3.941
5A8H	A_LYS_348	NZ	A_GLU_351	OE2	3.259
5A8H	A_LYS_350	NZ	A_ASP_395	OD2	3.579
5A8H	A_LYS_357	NZ	A_GLU_466	OE2	3.720
5A8H	A_ARG_419	NH1	D_GLU_100B	OE1	2.999
5A8H	A_ARG_419	NH1	D_GLU_100B	OE2	3.674
5A8H	A_ARG_419	NH2	D_GLU_99	OE1	2.292
5A8H	A_ARG_419	NH2	D_GLU_100B	OE2	3.968
5A8H	A_ARG_456	NH2	A_GLU_466	OE1	3.537
5A8H	A_ARG_456	NH2	A_GLU_466	OE2	3.468
5A8H	A_ARG_469	NH2	A_ASP_457	OD2	3.234
5A8H	A_ARG_476	NH1	A_ASP_474	OD1	3.441
5A8H	A_ARG_476	NH2	A_GLU_102	OE1	3.296
5A8H	A_ARG_476	NH2	A_GLU_102	OE2	3.009
5A8H	A_LYS_487	NZ	A_GLU_91	OE1	3.523
5A8H	A_LYS_490	NZ	A_GLU_492	OE1	3.301
5A8H	B_LYS_29	NZ	B_GLU_85	OE1	2.833
5A8H	B_LYS_29	NZ	B_GLU_85	OE2	3.848
5A8H	B_LYS_35	NZ	A_ASP_457	OD1	3.740
5A8H	B_ARG_54	NH1	B_ASP_78	OD1	3.987
5A8H	B_ARG_54	NH1	B_ASP_78	OD2	2.755
5A8H	B_ARG_54	NH2	B_ASP_78	OD1	2.665
5A8H	B_ARG_54	NH2	B_ASP_78	OD2	2.988
5A8H	B_ARG_59	NH1	A_ASP_368	OD1	3.154
5A8H	B_ARG_59	NH1	A_ASP_368	OD2	3.342
5A8H	B_ARG_59	NH2	A_ASP_368	OD1	2.977
5A8H	B_ARG_59	NH2	A_ASP_368	OD2	2.433
5A8H	B_HIS_107	ND1	B_ASP_105	OD1	3.166
5A8H	B_HIS_107	ND1	B_ASP_105	OD2	2.891
5A8H	B_ARG_134	NH2	B_ASP_153	OD1	3.766
5A8H	B_LYS_136	NZ	B_GLU_150	OE2	3.884
5A8H	B_LYS_136	NZ	B_ASP_153	OD1	3.937
5A8H	B_LYS_136	NZ	B_ASP_153	OD2	2.986
5A8H	B_LYS_171	NZ	B_GLU_169	OE2	2.874
5A8H	C_ARG_61	NH2	C_GLU_81	OE2	3.127
5A8H	C_ARG_61	NH2	C_ASP_82	OD1	3.576
5A8H	C_ARG_95B	NH2	C_ASP_1	OD2	2.985
5A8H	C_HIS_189	ND1	C_ASP_151	OD2	2.585
5A8H	C_HIS_189	NE2	C_ASP_185	OD1	2.803
5A8H	C_HIS_189	NE2	C_ASP_185	OD2	3.599
5A8H	C_ARG_211	NH1	C_GLU_187	OE1	3.851
5A8H	D_ARG_31	NH2	D_ASP_100A	OD1	3.070
5A8H	D_ARG_31	NH2	D_ASP_100A	OD2	3.615
5A8H	D_ARG_38	NH1	D_GLU_46	OE1	2.779
5A8H	D_ARG_38	NH1	D_GLU_46	OE2	3.342
5A8H	D_ARG_38	NH2	D_ASP_86	OD1	2.684
5A8H	D_ARG_50	NH2	D_GLU_97	OE2	2.333
5A8H	D_ARG_66	NH1	D_ASP_86	OD2	3.597
5A8H	D_ARG_66	NH2	D_ASP_86	OD1	2.739
5A8H	D_ARG_66	NH2	D_ASP_86	OD2	2.414
5A8H	D_LYS_73	NZ	D_ASP_55	OD1	2.968

5A8H	D_ARG_82A	NH2	D_GLU_81	OE1	3.271
5A8H	D_LYS_143	NZ	D_ASP_144	OD1	2.615
5A8H	D_LYS_143	NZ	D_ASP_144	OD2	3.235
5A8H	D_HIS_164	NE2	C_ASP_167	OD1	3.880
5A8H	D_HIS_164	NE2	C_ASP_167	OD2	2.505
5A8H	D_LYS_206	NZ	D_ASP_208	OD1	3.966
5A8H	D_LYS_209	NZ	C_GLU_123	OE1	3.514
5A8H	D_LYS_209	NZ	C_GLU_123	OE2	3.584
5A8H	E_ARG_24	NH2	E_ASP_70	OD1	3.351
5A8H	E_ARG_24	NH2	E_ASP_70	OD2	2.876
5A8H	E_ARG_61	NH1	E_ASP_82	OD1	3.079
5A8H	E_ARG_61	NH1	E_ASP_82	OD2	3.077
5A8H	E_ARG_61	NH2	E_GLU_81	OE2	3.862
5A8H	E_LYS_103	NZ	E_GLU_165	OE1	3.805
5A8H	E_LYS_149	NZ	E_GLU_195	OE1	2.746
5A8H	E_LYS_149	NZ	E_GLU_195	OE2	3.963
5A8H	E_LYS_183	NZ	E_GLU_187	OE2	2.699
5A8H	E_HIS_189	ND1	E_ASP_151	OD1	3.975
5A8H	E_HIS_189	ND1	E_ASP_151	OD2	2.260
5A8H	F_ARG_38	NH1	F_ASP_86	OD1	3.024
5A8H	F_ARG_38	NH2	F_GLU_46	OE1	3.885
5A8H	F_ARG_66	NH1	F_ASP_86	OD1	3.548
5A8H	F_ARG_66	NH1	F_ASP_86	OD2	2.798
5A8H	F_ARG_66	NH2	F_ASP_86	OD1	2.933
5A8H	F_ARG_66	NH2	F_ASP_86	OD2	3.625
5A8H	F_LYS_82A	NZ	F_GLU_81	OE2	2.706
5A8H	F_LYS_100	NZ	A_GLU_91	OE1	3.015
5A8H	F_LYS_100	NZ	A_GLU_91	OE2	3.536
5A8H	F_HIS_100F	ND1	F_ASP_100G	OD2	3.939
5A8H	F_LYS_143	NZ	F_ASP_144	OD1	3.370
5A8H	F_LYS_143	NZ	F_ASP_144	OD2	3.507
5A8H	F_LYS_206	NZ	F_ASP_208	OD2	3.418
5A8H	G_LYS_121	NZ	G_GLU_429	OE1	3.567
5A8H	G_LYS_121	NZ	G_GLU_429	OE2	2.734
5A8H	G_LYS_207	NZ	G_GLU_381	OE1	3.945
5A8H	G_LYS_207	NZ	G_GLU_381	OE2	3.127
5A8H	G_LYS_232	NZ	G_GLU_351	OE1	3.995
5A8H	G_HIS_249	NE2	G_GLU_482	OE1	3.524
5A8H	G_LYS_282	NZ	G_GLU_275	OE1	3.953
5A8H	G_LYS_282	NZ	G_GLU_275	OE2	2.642
5A8H	G_LYS_348	NZ	G_GLU_269	OE1	3.206
5A8H	G_LYS_348	NZ	G_GLU_351	OE1	3.942
5A8H	G_LYS_348	NZ	G_GLU_351	OE2	3.260
5A8H	G_LYS_350	NZ	G_ASP_395	OD2	3.580
5A8H	G_LYS_357	NZ	G_GLU_466	OE2	3.719
5A8H	G_ARG_419	NH1	J_GLU_100B	OE1	2.998
5A8H	G_ARG_419	NH1	J_GLU_100B	OE2	3.675
5A8H	G_ARG_419	NH2	J_GLU_99	OE1	2.292
5A8H	G_ARG_419	NH2	J_GLU_100B	OE2	3.969
5A8H	G_ARG_456	NH2	G_GLU_466	OE1	3.536
5A8H	G_ARG_456	NH2	G_GLU_466	OE2	3.469
5A8H	G_ARG_469	NH2	G_ASP_457	OD2	3.234
5A8H	G_ARG_476	NH1	G_ASP_474	OD1	3.441
5A8H	G_ARG_476	NH2	G_GLU_102	OE1	3.297
5A8H	G_ARG_476	NH2	G_GLU_102	OE2	3.010
5A8H	G_LYS_487	NZ	G_GLU_91	OE1	3.524
5A8H	G_LYS_490	NZ	G_GLU_492	OE1	3.300
5A8H	H_LYS_29	NZ	H_GLU_85	OE1	2.833

5A8H	H.LYS_29	NZ	H.GLU_85	OE2	3.847
5A8H	H.LYS_35	NZ	G.ASP_457	OD1	3.741
5A8H	H.ARG_54	NH1	H.ASP_78	OD1	3.987
5A8H	H.ARG_54	NH1	H.ASP_78	OD2	2.755
5A8H	H.ARG_54	NH2	H.ASP_78	OD1	2.666
5A8H	H.ARG_54	NH2	H.ASP_78	OD2	2.989
5A8H	H.ARG_59	NH1	G.ASP_368	OD1	3.154
5A8H	H.ARG_59	NH1	G.ASP_368	OD2	3.343
5A8H	H.ARG_59	NH2	G.ASP_368	OD1	2.977
5A8H	H.ARG_59	NH2	G.ASP_368	OD2	2.433
5A8H	H.HIS_107	ND1	H.ASP_105	OD1	3.165
5A8H	H.HIS_107	ND1	H.ASP_105	OD2	2.890
5A8H	H.ARG_134	NH2	H.ASP_153	OD1	3.766
5A8H	H.LYS_136	NZ	H.GLU_150	OE2	3.885
5A8H	H.LYS_136	NZ	H.ASP_153	OD1	3.936
5A8H	H.LYS_136	NZ	H.ASP_153	OD2	2.987
5A8H	H.LYS_171	NZ	H.GLU_169	OE2	2.874
5A8H	I.ARG_61	NH2	I.GLU_81	OE2	3.127
5A8H	I.ARG_61	NH2	I.ASP_82	OD1	3.576
5A8H	I.ARG_95B	NH2	I.ASP_1	OD2	2.985
5A8H	I.HIS_189	ND1	I.ASP_151	OD2	2.585
5A8H	I.HIS_189	NE2	I.ASP_185	OD1	2.802
5A8H	I.HIS_189	NE2	I.ASP_185	OD2	3.598
5A8H	I.ARG_211	NH1	I.GLU_187	OE1	3.851
5A8H	J.ARG_31	NH2	J.ASP_100A	OD1	3.070
5A8H	J.ARG_31	NH2	J.ASP_100A	OD2	3.615
5A8H	J.ARG_38	NH1	J.GLU_46	OE1	2.778
5A8H	J.ARG_38	NH1	J.GLU_46	OE2	3.342
5A8H	J.ARG_38	NH2	J.ASP_86	OD1	2.685
5A8H	J.ARG_50	NH2	J.GLU_97	OE2	2.333
5A8H	J.ARG_66	NH1	J.ASP_86	OD2	3.597
5A8H	J.ARG_66	NH2	J.ASP_86	OD1	2.739
5A8H	J.ARG_66	NH2	J.ASP_86	OD2	2.414
5A8H	J.LYS_73	NZ	J.ASP_55	OD1	2.968
5A8H	J.ARG_82A	NH2	J.GLU_81	OE1	3.271
5A8H	J.LYS_143	NZ	J.ASP_144	OD1	2.615
5A8H	J.LYS_143	NZ	J.ASP_144	OD2	3.235
5A8H	J.HIS_164	NE2	I.ASP_167	OD1	3.881
5A8H	J.HIS_164	NE2	I.ASP_167	OD2	2.505
5A8H	J.LYS_206	NZ	J.ASP_208	OD1	3.966
5A8H	J.LYS_209	NZ	I.GLU_123	OE1	3.513
5A8H	J.LYS_209	NZ	I.GLU_123	OE2	3.584
5A8H	K.ARG_24	NH2	K.ASP_70	OD1	3.351
5A8H	K.ARG_24	NH2	K.ASP_70	OD2	2.876
5A8H	K.ARG_61	NH1	K.ASP_82	OD1	3.079
5A8H	K.ARG_61	NH1	K.ASP_82	OD2	3.077
5A8H	K.ARG_61	NH2	K.GLU_81	OE2	3.862
5A8H	K.LYS_103	NZ	K.GLU_165	OE1	3.804
5A8H	K.LYS_149	NZ	K.GLU_195	OE1	2.745
5A8H	K.LYS_149	NZ	K.GLU_195	OE2	3.962
5A8H	K.LYS_183	NZ	K.GLU_187	OE2	2.699
5A8H	K.HIS_189	ND1	K.ASP_151	OD1	3.974
5A8H	K.HIS_189	ND1	K.ASP_151	OD2	2.260
5A8H	L.ARG_38	NH1	L.ASP_86	OD1	3.025
5A8H	L.ARG_38	NH2	L.GLU_46	OE1	3.886
5A8H	L.ARG_66	NH1	L.ASP_86	OD1	3.549
5A8H	L.ARG_66	NH1	L.ASP_86	OD2	2.799
5A8H	L.ARG_66	NH2	L.ASP_86	OD1	2.933

5A8H	L_ARG_66	NH2	L_ASP_86	OD2	3.625
5A8H	L_LYS_82A	NZ	L_GLU_81	OE2	2.706
5A8H	L_LYS_100	NZ	G_GLU_87	OE1	2.922
5A8H	L_LYS_100	NZ	G_GLU_87	OE2	3.552
5A8H	L_HIS_100E	NE2	G_GLU_91	OE2	3.049
5A8H	L_HIS_100F	ND1	L_ASP_100G	OD2	3.939
5A8H	L_LYS_143	NZ	L_ASP_144	OD1	3.369
5A8H	L_LYS_143	NZ	L_ASP_144	OD2	3.505
5A8H	L_LYS_206	NZ	L_ASP_208	OD2	3.418
5A8H	M_LYS_121	NZ	M_GLU_429	OE1	3.568
5A8H	M_LYS_121	NZ	M_GLU_429	OE2	2.734
5A8H	M_LYS_207	NZ	M_GLU_381	OE1	3.945
5A8H	M_LYS_207	NZ	M_GLU_381	OE2	3.127
5A8H	M_LYS_232	NZ	M_GLU_351	OE1	3.995
5A8H	M_HIS_249	NE2	M_GLU_482	OE1	3.525
5A8H	M_LYS_282	NZ	M_GLU_275	OE1	3.953
5A8H	M_LYS_282	NZ	M_GLU_275	OE2	2.642
5A8H	M_LYS_348	NZ	M_GLU_269	OE1	3.206
5A8H	M_LYS_348	NZ	M_GLU_351	OE1	3.941
5A8H	M_LYS_348	NZ	M_GLU_351	OE2	3.259
5A8H	M_LYS_350	NZ	M_ASP_395	OD2	3.579
5A8H	M_LYS_357	NZ	M_GLU_466	OE2	3.719
5A8H	M_ARG_419	NH1	P_GLU_100B	OE1	2.999
5A8H	M_ARG_419	NH1	P_GLU_100B	OE2	3.675
5A8H	M_ARG_419	NH2	P_GLU_99	OE1	2.292
5A8H	M_ARG_419	NH2	P_GLU_100B	OE2	3.969
5A8H	M_ARG_456	NH2	M_GLU_466	OE1	3.537
5A8H	M_ARG_456	NH2	M_GLU_466	OE2	3.469
5A8H	M_ARG_469	NH2	M_ASP_457	OD2	3.235
5A8H	M_ARG_476	NH1	M_ASP_474	OD1	3.441
5A8H	M_ARG_476	NH2	M_GLU_102	OE1	3.296
5A8H	M_ARG_476	NH2	M_GLU_102	OE2	3.009
5A8H	M_LYS_487	NZ	M_GLU_91	OE1	3.525
5A8H	M_LYS_490	NZ	M_GLU_492	OE1	3.300
5A8H	N_LYS_29	NZ	N_GLU_85	OE1	2.833
5A8H	N_LYS_29	NZ	N_GLU_85	OE2	3.848
5A8H	N_LYS_35	NZ	M_ASP_457	OD1	3.741
5A8H	N_ARG_54	NH1	N_ASP_78	OD1	3.987
5A8H	N_ARG_54	NH1	N_ASP_78	OD2	2.755
5A8H	N_ARG_54	NH2	N_ASP_78	OD1	2.666
5A8H	N_ARG_54	NH2	N_ASP_78	OD2	2.989
5A8H	N_ARG_59	NH1	M_ASP_368	OD1	3.154
5A8H	N_ARG_59	NH1	M_ASP_368	OD2	3.343
5A8H	N_ARG_59	NH2	M_ASP_368	OD1	2.977
5A8H	N_ARG_59	NH2	M_ASP_368	OD2	2.433
5A8H	N_HIS_107	ND1	N_ASP_105	OD1	3.166
5A8H	N_HIS_107	ND1	N_ASP_105	OD2	2.891
5A8H	N_ARG_134	NH2	N_ASP_153	OD1	3.765
5A8H	N_LYS_136	NZ	N_GLU_150	OE2	3.885
5A8H	N_LYS_136	NZ	N_ASP_153	OD1	3.936
5A8H	N_LYS_136	NZ	N_ASP_153	OD2	2.986
5A8H	N_LYS_171	NZ	N_GLU_169	OE2	2.873
5A8H	O_ARG_61	NH2	O_GLU_81	OE2	3.127
5A8H	O_ARG_61	NH2	O_ASP_82	OD1	3.576
5A8H	O_ARG_95B	NH2	O_ASP_1	OD2	2.985
5A8H	O_LYS_145	NZ	C_GLU_17	OE1	3.474
5A8H	O_LYS_145	NZ	C_GLU_17	OE2	2.123
5A8H	O_HIS_189	ND1	O_ASP_151	OD2	2.585

5A8H	O_HIS_189	NE2	O_ASP_185	OD1	2.802
5A8H	O_HIS_189	NE2	O_ASP_185	OD2	3.598
5A8H	O_ARG_211	NH1	O_GLU_187	OE1	3.851
5A8H	P_ARG_31	NH2	P_ASP_100A	OD1	3.070
5A8H	P_ARG_31	NH2	P_ASP_100A	OD2	3.615
5A8H	P_ARG_38	NH1	P_GLU_46	OE1	2.780
5A8H	P_ARG_38	NH1	P_GLU_46	OE2	3.342
5A8H	P_ARG_38	NH2	P_ASP_86	OD1	2.685
5A8H	P_ARG_50	NH2	P_GLU_97	OE2	2.332
5A8H	P_ARG_66	NH1	P_ASP_86	OD2	3.598
5A8H	P_ARG_66	NH2	P_ASP_86	OD1	2.740
5A8H	P_ARG_66	NH2	P_ASP_86	OD2	2.415
5A8H	P_LYS_73	NZ	P_ASP_55	OD1	2.967
5A8H	P_ARG_82A	NH2	P_GLU_81	OE1	3.272
5A8H	P_LYS_143	NZ	P_ASP_144	OD1	2.615
5A8H	P_LYS_143	NZ	P_ASP_144	OD2	3.235
5A8H	P_HIS_164	NE2	O_ASP_167	OD1	3.881
5A8H	P_HIS_164	NE2	O_ASP_167	OD2	2.505
5A8H	P_LYS_206	NZ	P_ASP_208	OD1	3.966
5A8H	P_LYS_209	NZ	O_GLU_123	OE1	3.514
5A8H	P_LYS_209	NZ	O_GLU_123	OE2	3.584
5A8H	Q_ARG_24	NH2	Q_ASP_70	OD1	3.351
5A8H	Q_ARG_24	NH2	Q_ASP_70	OD2	2.877
5A8H	Q_ARG_61	NH1	Q_ASP_82	OD1	3.079
5A8H	Q_ARG_61	NH1	Q_ASP_82	OD2	3.077
5A8H	Q_ARG_61	NH2	Q_GLU_81	OE2	3.861
5A8H	Q_LYS_103	NZ	Q_GLU_165	OE1	3.805
5A8H	Q_LYS_149	NZ	Q_GLU_195	OE1	2.746
5A8H	Q_LYS_149	NZ	Q_GLU_195	OE2	3.963
5A8H	Q_LYS_183	NZ	Q_GLU_187	OE2	2.700
5A8H	Q_HIS_189	ND1	Q_ASP_151	OD1	3.975
5A8H	Q_HIS_189	ND1	Q_ASP_151	OD2	2.261
5A8H	R_ARG_38	NH1	R_ASP_86	OD1	3.024
5A8H	R_ARG_38	NH2	R_GLU_46	OE1	3.885
5A8H	R_ARG_66	NH1	R_ASP_86	OD1	3.548
5A8H	R_ARG_66	NH1	R_ASP_86	OD2	2.798
5A8H	R_ARG_66	NH2	R_ASP_86	OD1	2.932
5A8H	R_ARG_66	NH2	R_ASP_86	OD2	3.625
5A8H	R_LYS_82A	NZ	R_GLU_81	OE2	2.706
5A8H	R_HIS_100E	ND1	M_GLU_87	OE2	2.709
5A8H	R_HIS_100E	NE2	M_GLU_87	OE2	3.097
5A8H	R_HIS_100F	ND1	R_ASP_100G	OD2	3.938
5A8H	R_LYS_143	NZ	R_ASP_144	OD1	3.369
5A8H	R_LYS_143	NZ	R_ASP_144	OD2	3.506
5A8H	R_LYS_206	NZ	R_ASP_208	OD2	3.418
5AZE	L_HIS_36	NE2	H_GLU_105	OE2	2.756
5AZE	L_ARG_63	NH2	L_GLU_83	OE1	3.980
5AZE	L_ARG_63	NH2	L_GLU_83	OE2	3.863
5AZE	L_ARG_63	NH2	L_ASP_84	OD1	2.738
5AZE	L_ARG_63	NH2	L_ASP_84	OD2	3.659
5AZE	L_LYS_154	NZ	L_GLU_208	OE1	3.064
5AZE	L_LYS_154	NZ	L_GLU_208	OE2	3.679
5AZE	L_HIS_193	ND1	L_ASP_156	OD2	2.884
5AZE	H_LYS_12	NZ	H_GLU_10	OE1	3.838
5AZE	H_HIS_35	NE2	H_ASP_99	OD1	3.262
5AZE	H_ARG_38	NH1	H_GLU_46	OE1	2.776
5AZE	H_ARG_38	NH2	H_ASP_90	OD1	2.628
5AZE	H_ARG_67	NH1	H_ASP_90	OD1	3.423

5AZE	H_ARG_67	NH1	H_ASP_90	OD2	3.983
5AZE	H_ARG_67	NH2	H_ASP_90	OD1	3.299
5AZE	H_ARG_67	NH2	H_ASP_90	OD2	2.559
5AZE	H_ARG_98	NH2	H_ASP_109	OD1	3.795
5AZE	H_ARG_98	NH2	H_ASP_109	OD2	3.043
5AZE	H_LYS_137	NZ	L_ASP_143	OD2	2.939
5AZE	H_LYS_214	NZ	H_ASP_216	OD1	3.542
5AZE	H_LYS_214	NZ	H_ASP_216	OD2	3.113
5AZE	H_LYS_217	NZ	L_GLU_128	OE2	2.701
5BW7	A_LYS_248	NZ	A_GLU_380	OE1	3.595
5BW7	A_LYS_248	NZ	A_GLU_380	OE2	2.687
5BW7	A_ARG_255	NH2	A_ASP_249	OD2	3.416
5BW7	A_HIS_285	NE2	A_GLU_283	OE2	3.140
5BW7	A_ARG_292	NH2	A_GLU_272	OE1	3.982
5BW7	A_ARG_292	NH2	A_GLU_272	OE2	2.655
5BW7	A_LYS_317	NZ	A_ASP_312	OD1	3.705
5BW7	A_LYS_320	NZ	A_GLU_333	OE2	3.392
5BW7	A_LYS_338	NZ	A_GLU_430	OE1	3.180
5BW7	A_LYS_338	NZ	A_GLU_430	OE2	3.249
5BW7	A_LYS_370	NZ	B_GLU_357	OE2	3.993
5BW7	A_LYS_409	NZ	B_ASP_399	OD1	3.864
5BW7	A_LYS_409	NZ	B_ASP_399	OD2	2.990
5BW7	A_ARG_416	NH1	A_GLU_388	OE1	2.970
5BW7	A_ARG_416	NH1	A_GLU_388	OE2	3.913
5BW7	A_ARG_416	NH2	A_GLU_388	OE1	3.370
5BW7	A_ARG_416	NH2	A_GLU_388	OE2	2.800
5BW7	B_LYS_248	NZ	B_GLU_380	OE1	3.958
5BW7	B_LYS_248	NZ	B_GLU_380	OE2	2.755
5BW7	B_ARG_255	NH2	B_ASP_249	OD1	2.907
5BW7	B_HIS_268	NE2	B_GLU_294	OE1	3.100
5BW7	B_HIS_268	NE2	B_GLU_294	OE2	3.206
5BW7	B_ARG_301	NH1	B_GLU_293	OE1	3.024
5BW7	B_LYS_317	NZ	B_ASP_312	OD1	3.532
5BW7	B_LYS_320	NZ	B_GLU_333	OE1	2.787
5BW7	B_LYS_320	NZ	B_GLU_333	OE2	3.803
5BW7	B_LYS_338	NZ	B_GLU_430	OE1	3.215
5BW7	B_LYS_338	NZ	B_GLU_430	OE2	3.370
5BW7	B_ARG_344	NH1	B_ASP_401	OD2	3.270
5BW7	B_LYS_370	NZ	A_GLU_357	OE2	3.748
5BW7	B_LYS_409	NZ	A_ASP_399	OD1	3.328
5BW7	B_LYS_409	NZ	A_ASP_399	OD2	2.988
5BW7	B_ARG_416	NH1	B_GLU_388	OE1	3.138
5BW7	B_ARG_416	NH1	B_GLU_388	OE2	3.904
5BW7	B_ARG_416	NH2	B_GLU_388	OE1	3.540
5BW7	B_ARG_416	NH2	B_GLU_388	OE2	2.872
5BW7	C_ARG_18	NH1	C_GLU_85	OE1	3.505
5BW7	C_HIS_87	NE2	C_GLU_85	OE1	2.748
5BW7	C_ARG_97	NH2	C_ASP_104	OD2	2.992
5BW7	C_HIS_107	NE2	C_ASP_138	OD2	2.660
5BW7	C_HIS_111	NE2	C_ASP_23	OD1	2.716
5BW7	C_HIS_111	NE2	C_ASP_23	OD2	3.022
5BW7	C_LYS_120	NZ	A_ASP_265	OD2	2.730
5BW7	C_ARG_130	NH1	C_ASP_148	OD1	3.404
5BW7	C_ARG_130	NH2	C_ASP_148	OD1	3.221
5BW7	C_LYS_131	NZ	A_GLU_269	OE1	3.414
5BW7	C_LYS_131	NZ	A_GLU_269	OE2	2.642
5CMA	A_ARG_45	NH2	A_GLU_42	OE2	3.432
5CMA	A_ARG_61	NH1	A_ASP_82	OD1	3.594

5CMA	A_ARG_61	NH1	A_ASP_82	OD2	2.573
5CMA	A_LYS_149	NZ	A_GLU_195	OE1	3.918
5CMA	A_LYS_149	NZ	A_GLU_195	OE2	3.051
5CMA	A_LYS_183	NZ	A_GLU_187	OE1	2.559
5CMA	A_LYS_183	NZ	A_GLU_187	OE2	3.255
5CMA	A_HIS_189	ND1	A_ASP_151	OD2	2.867
5CMA	B_ARG_38	NH1	B_ASP_90	OD1	3.651
5CMA	B_ARG_38	NH2	B_GLU_46	OE2	3.149
5CMA	B_ARG_40	NH1	B_GLU_89	OE2	3.793
5CMA	B_LYS_67	NZ	B_ASP_90	OD1	3.746
5CMA	B_LYS_67	NZ	B_ASP_90	OD2	3.140
5CMA	B_LYS_148	NZ	B_ASP_149	OD1	2.890
5CMA	B_LYS_148	NZ	B_ASP_149	OD2	3.271
5CMA	B_LYS_214	NZ	A_GLU_123	OE1	2.706
5CMA	B_LYS_214	NZ	A_GLU_123	OE2	3.531
5CMA	B_ARG_215	NH2	B_GLU_217	OE2	3.910
5CP3	A_LYS_24	NZ	A_ASP_75	OD1	2.942
5CP3	A_ARG_51	NH2	A_ASP_60	OD2	3.029
5CP3	A_ARG_62	NH2	A_ASP_60	OD1	3.616
5CP3	A_ARG_62	NH2	A_ASP_60	OD2	2.822
5CP3	A_ARG_66	NH1	A_ASP_87	OD1	3.163
5CP3	A_ARG_66	NH1	A_ASP_87	OD2	2.516
5CP3	A_ARG_66	NH2	A_ASP_87	OD1	2.966
5CP3	A_ARG_66	NH2	A_ASP_87	OD2	3.742
5CP3	A_LYS_154	NZ	A_GLU_200	OE1	3.304
5CP3	A_LYS_154	NZ	A_GLU_200	OE2	3.326
5CP3	A_ARG_160	NH2	A_GLU_190	OE1	3.660
5CP3	A_HIS_194	ND1	A_ASP_156	OD2	3.197
5CP3	A_LYS_204	NZ	A_GLU_115	OE2	2.402
5CP3	H_ARG_39	NH1	H_ASP_90	OD1	2.626
5CP3	H_ARG_39	NH2	H_GLU_47	OE1	2.850
5CP3	H_ARG_39	NH2	H_ASP_90	OD1	3.448
5CP3	H_ARG_67	NH1	H_ASP_90	OD1	3.807
5CP3	H_ARG_67	NH1	H_ASP_90	OD2	2.888
5CP3	H_ARG_67	NH2	H_ASP_90	OD1	3.094
5CP3	H_ARG_67	NH2	H_ASP_90	OD2	3.526
5CP3	H_LYS_207	NZ	A_GLU_128	OE2	2.762
5CP7	A_LYS_24	NZ	A_ASP_75	OD1	3.319
5CP7	A_LYS_24	NZ	A_ASP_75	OD2	2.961
5CP7	A_ARG_51	NH2	A_ASP_60	OD1	2.851
5CP7	A_ARG_62	NH1	A_ASP_60	OD1	3.820
5CP7	A_ARG_62	NH1	A_ASP_60	OD2	3.151
5CP7	A_ARG_62	NH2	A_ASP_60	OD2	3.961
5CP7	A_ARG_66	NH1	A_ASP_87	OD1	3.341
5CP7	A_ARG_66	NH1	A_ASP_87	OD2	2.576
5CP7	A_ARG_66	NH2	A_ASP_87	OD1	2.858
5CP7	A_ARG_66	NH2	A_ASP_87	OD2	3.668
5CP7	A_LYS_154	NZ	A_GLU_200	OE1	3.247
5CP7	A_LYS_154	NZ	A_GLU_200	OE2	3.620
5CP7	A_ARG_160	NH2	A_GLU_190	OE1	3.902
5CP7	A_HIS_194	ND1	A_ASP_156	OD1	2.879
5CP7	A_LYS_204	NZ	A_ASP_115	OD2	3.110
5CP7	B_ARG_39	NH1	B_ASP_90	OD1	2.860
5CP7	B_ARG_39	NH2	B_GLU_47	OE1	2.798
5CP7	B_ARG_39	NH2	B_ASP_90	OD1	3.702
5CP7	B_ARG_67	NH1	B_ASP_90	OD1	3.401
5CP7	B_ARG_67	NH1	B_ASP_90	OD2	3.152
5CP7	B_ARG_67	NH2	B_ASP_90	OD1	2.884

5CP7	B_ARG_67	NH2	B_ASP_90	OD2	3.459
5CP7	B_LYS_76	NZ	B_ASP_73	OD1	3.357
5CP7	B_LYS_76	NZ	B_ASP_73	OD2	2.651
5CP7	B_LYS_204	NZ	B_ASP_206	OD1	2.613
5CP7	B_LYS_204	NZ	B_ASP_206	OD2	3.566
5CP7	B_LYS_207	NZ	C_GLU_128	OE2	3.335
5CP7	C_LYS_24	NZ	C_ASP_75	OD1	2.777
5CP7	C_ARG_51	NH2	C_ASP_60	OD1	2.666
5CP7	C_LYS_58	NZ	H_ASP_1	OD1	3.663
5CP7	C_LYS_58	NZ	H_ASP_1	OD2	3.316
5CP7	C_ARG_62	NH1	C_ASP_60	OD1	3.272
5CP7	C_ARG_62	NH1	C_ASP_60	OD2	2.754
5CP7	C_ARG_66	NH1	C_GLU_84	OE2	3.677
5CP7	C_ARG_66	NH2	C_GLU_86	OE1	3.796
5CP7	C_ARG_66	NH2	C_ASP_87	OD1	3.282
5CP7	C_ARG_66	NH2	C_ASP_87	OD2	3.388
5CP7	C_LYS_154	NZ	C_GLU_200	OE1	3.236
5CP7	C_LYS_154	NZ	C_GLU_200	OE2	3.406
5CP7	C_HIS_194	ND1	C_ASP_156	OD1	3.216
5CP7	D_ARG_39	NH1	D_ASP_90	OD1	3.144
5CP7	D_ARG_39	NH2	D_GLU_47	OE1	2.804
5CP7	D_ARG_39	NH2	D_ASP_90	OD1	3.507
5CP7	D_ARG_67	NH1	D_ASP_90	OD1	3.613
5CP7	D_ARG_67	NH1	D_ASP_90	OD2	2.972
5CP7	D_ARG_67	NH2	D_ASP_90	OD1	2.843
5CP7	D_ARG_67	NH2	D_ASP_90	OD2	3.447
5CP7	D_LYS_207	NZ	E_GLU_128	OE2	2.825
5CP7	E_LYS_24	NZ	E_ASP_75	OD1	2.820
5CP7	E_LYS_24	NZ	E_ASP_75	OD2	3.689
5CP7	E_ARG_44	NH1	E_ASP_87	OD1	3.971
5CP7	E_LYS_50	NZ	E_ASP_60	OD2	2.506
5CP7	E_ARG_51	NH2	E_ASP_60	OD1	2.623
5CP7	E_ARG_66	NH2	E_GLU_84	OE1	2.942
5CP7	E_ARG_66	NH2	E_ASP_87	OD1	3.262
5CP7	E_ARG_66	NH2	E_ASP_87	OD2	2.428
5CP7	E_ARG_193	NH2	E_GLU_190	OE1	3.878
5CP7	E_HIS_194	ND1	E_ASP_156	OD1	3.868
5CP7	E_LYS_204	NZ	E_ASP_115	OD2	2.617
5CP7	F_ARG_39	NH1	F_ASP_90	OD1	3.469
5CP7	F_ARG_39	NH2	F_GLU_47	OE1	2.925
5CP7	F_ARG_67	NH1	F_ASP_90	OD1	3.818
5CP7	F_ARG_67	NH1	F_ASP_90	OD2	2.761
5CP7	F_ARG_67	NH2	F_ASP_90	OD1	2.929
5CP7	F_ARG_67	NH2	F_ASP_90	OD2	3.414
5CP7	F_LYS_76	NZ	F_ASP_73	OD2	2.874
5CP7	F_HIS_163	ND1	G_ASP_172	OD2	3.652
5CP7	F_LYS_207	NZ	G_GLU_128	OE2	3.951
5CP7	G_ARG_44	NH1	G_GLU_86	OE2	3.392
5CP7	G_ARG_51	NH2	G_ASP_60	OD1	3.311
5CP7	G_ARG_66	NH1	G_GLU_84	OE1	3.858
5CP7	G_ARG_66	NH1	G_GLU_84	OE2	3.754
5CP7	G_ARG_66	NH2	G_GLU_84	OE2	3.523
5CP7	G_ARG_66	NH2	G_ASP_87	OD1	3.495
5CP7	G_ARG_66	NH2	G_ASP_87	OD2	3.175
5CP7	G_ARG_82	NH2	G_ASP_65	OD1	3.926
5CP7	G_LYS_152	NZ	G_GLU_159	OE1	3.709
5CP7	G_ARG_160	NH1	G_GLU_190	OE1	3.944
5CP7	G_LYS_204	NZ	G_ASP_115	OD2	3.779

5CP7	H_ARG_39	NH1	H_ASP_90	OD1	2.809
5CP7	H_ARG_39	NH2	H_GLU_47	OE1	3.145
5CP7	H_ARG_39	NH2	H_ASP_90	OD1	3.745
5CP7	H_ARG_67	NH1	H_ASP_90	OD1	3.710
5CP7	H_ARG_67	NH1	H_ASP_90	OD2	3.464
5CP7	H_ARG_67	NH2	H_ASP_90	OD1	2.784
5CP7	H_ARG_67	NH2	H_ASP_90	OD2	3.529
5CP7	H_LYS_207	NZ	A_GLU_128	OE2	3.290
5DFV	A_LYS_116	NZ	A_ASP_117	OD2	3.422
5DFV	A_LYS_124	NZ	A_ASP_195	OD1	3.196
5DFV	A_LYS_124	NZ	A_ASP_195	OD2	2.771
5DFV	A_LYS_171	NZ	C_ASP_288	OD1	3.582
5DFV	A_LYS_171	NZ	C_ASP_288	OD2	2.737
5DFV	A_LYS_171	NZ	C_ASP_290	OD2	2.874
5DFV	A_HIS_191	NE2	A_ASP_128	OD1	3.031
5DFV	A_HIS_191	NE2	A_ASP_128	OD2	2.615
5DFV	B_LYS_124	NZ	B_ASP_195	OD1	2.682
5DFV	B_LYS_124	NZ	B_ASP_195	OD2	3.204
5DFV	B_LYS_171	NZ	E_ASP_288	OD1	3.695
5DFV	B_LYS_171	NZ	E_ASP_288	OD2	3.653
5DFV	B_LYS_171	NZ	E_ASP_290	OD2	2.646
5DFV	B_HIS_191	NE2	B_ASP_128	OD1	2.625
5DFV	B_HIS_191	NE2	B_ASP_128	OD2	3.194
5DFV	C_LYS_203	NZ	C_ASP_324	OD1	3.802
5DFV	C_ARG_251	NH2	C_GLU_351	OE1	2.978
5DFV	C_ARG_251	NH2	C_GLU_351	OE2	3.038
5DFV	C_LYS_301	NZ	C_ASP_324	OD1	3.240
5DFV	C_LYS_301	NZ	C_ASP_324	OD2	2.740
5DFV	C_ARG_398	NH1	C_ASP_394	OD1	2.945
5DFV	C_ARG_398	NH1	C_ASP_394	OD2	3.790
5DFV	C_ARG_398	NH2	D_GLU_698	OE1	3.277
5DFV	C_LYS_1095	NZ	C_GLU_1097	OE1	3.280
5DFV	C_ARG_1099	NH1	C_GLU_1097	OE1	3.200
5DFV	C_ARG_1099	NH2	C_GLU_1097	OE1	3.340
5DFV	C_ARG_1099	NH2	C_GLU_1097	OE2	3.202
5DFV	D_ARG_551	NH1	D_ASP_716	OD1	3.170
5DFV	D_ARG_551	NH1	D_ASP_716	OD2	3.766
5DFV	D_ARG_551	NH2	D_ASP_716	OD1	3.082
5DFV	D_ARG_551	NH2	D_ASP_716	OD2	3.372
5DFV	D_LYS_556	NZ	D_GLU_755	OE1	3.326
5DFV	D_ARG_705	NH1	D_GLU_725	OE2	3.117
5DFV	D_ARG_705	NH1	D_GLU_727	OE2	3.146
5DFV	D_ARG_705	NH1	D_ASP_728	OD2	3.659
5DFV	D_ARG_705	NH2	D_GLU_725	OE1	3.510
5DFV	D_ARG_705	NH2	D_GLU_725	OE2	3.133
5DFV	D_LYS_2039	NZ	D_GLU_2087	OE1	3.958
5DFV	D_LYS_2041	NZ	D_GLU_2087	OE1	3.712
5DFV	D_LYS_2041	NZ	D_GLU_2087	OE2	2.836
5DFV	D_LYS_2091	NZ	D_ASP_2002	OD1	3.903
5DFV	D_ARG_2103	NH1	D_GLU_2079	OE1	3.925
5DFV	E_ARG_251	NH2	E_GLU_351	OE1	2.986
5DFV	E_ARG_251	NH2	E_GLU_351	OE2	2.952
5DFV	E_LYS_301	NZ	E_ASP_324	OD2	2.835
5DFV	E_ARG_398	NH1	F_GLU_698	OE2	3.319
5DFV	E_ARG_398	NH2	E_ASP_394	OD1	3.919
5DFV	E_ARG_398	NH2	E_ASP_394	OD2	2.696
5DFV	E_LYS_1094	NZ	F_GLU_2015	OE1	3.713
5DFV	E_LYS_1095	NZ	E_GLU_1097	OE1	2.895

5DFV	E_ARG_1099	NH1	F_GLU_2105	OE2	3.679
5DFV	F_ARG_551	NH1	F_ASP_716	OD2	3.150
5DFV	F_LYS_556	NZ	F_GLU_755	OE1	2.676
5DFV	F_LYS_556	NZ	F_GLU_755	OE2	3.758
5DFV	F_LYS_615	NZ	F_GLU_698	OE2	3.399
5DFV	F_ARG_705	NH1	F_GLU_727	OE2	3.693
5DFV	F_ARG_705	NH1	F_ASP_728	OD1	3.492
5DFV	F_ARG_705	NH1	F_ASP_728	OD2	3.045
5DFV	F_LYS_2041	NZ	F_GLU_2087	OE1	3.680
5DFV	F_LYS_2041	NZ	F_GLU_2087	OE2	2.777
5DFV	F_LYS_2091	NZ	F_ASP_2002	OD1	2.898
5DFV	F_LYS_2091	NZ	F_ASP_2002	OD2	2.887
5DFW	A_LYS_124	NZ	A_ASP_195	OD1	3.150
5DFW	A_LYS_124	NZ	A_ASP_195	OD2	3.337
5DFW	A_LYS_171	NZ	H_ASP_156	OD2	2.691
5DFW	A_LYS_171	NZ	H_ASP_253	OD1	2.751
5DFW	A_LYS_171	NZ	H_ASP_253	OD2	3.799
5DFW	A_LYS_187	NZ	A_ASP_155	OD2	3.976
5DFW	A_HIS_191	NE2	A_ASP_128	OD1	3.407
5DFW	A_HIS_191	NE2	A_ASP_128	OD2	2.578
5DFW	A_LYS_193	NZ	A_ASP_155	OD1	3.885
5DFW	H_LYS_203	NZ	H_ASP_324	OD1	3.276
5DFW	H_ARG_251	NH2	A_ASP_138	OD1	3.392
5DFW	H_ARG_251	NH2	A_ASP_138	OD2	2.698
5DFW	H_LYS_292	NZ	A_ASP_138	OD1	3.884
5DFW	H_LYS_292	NZ	A_ASP_138	OD2	2.950
5DFW	H_LYS_292	NZ	A_ASP_139	OD1	3.019
5DFW	H_LYS_296	NZ	H_ASP_294	OD1	3.151
5DFW	H_LYS_301	NZ	H_ASP_324	OD1	3.890
5DFW	H_LYS_301	NZ	H_ASP_324	OD2	3.833
5DFW	H_ARG_705	NH1	H_GLU_727	OE2	3.307
5DFW	H_ARG_705	NH2	H_ASP_728	OD2	2.557
5DFW	H_LYS_806	NZ	H_GLU_808	OE2	3.023
5DMI	A_LYS_46	NZ	L_ASP_31	OD1	2.761
5DMI	A_LYS_46	NZ	L_ASP_31	OD2	3.234
5DMI	A_HIS_76	ND1	H_ASP_100A	OD2	3.977
5DMI	A_HIS_78	ND1	A_GLU_74	OE1	3.991
5DMI	A_HIS_78	NE2	A_GLU_74	OE2	3.806
5DMI	H_ARG_66	NH1	H_ASP_86	OD1	3.834
5DMI	H_ARG_66	NH1	H_ASP_86	OD2	2.698
5DMI	H_ARG_66	NH2	H_ASP_86	OD1	3.014
5DMI	H_ARG_66	NH2	H_ASP_86	OD2	2.861
5DMI	H_LYS_221	NZ	L_GLU_123	OE2	3.105
5DMI	L_ARG_45	NH1	L_GLU_42	OE1	2.998
5DMI	L_ARG_45	NH1	L_GLU_42	OE2	3.354
5DMI	L_ARG_45	NH2	L_GLU_42	OE1	2.809
5DMI	L_ARG_61	NH1	L_GLU_81	OE1	3.011
5DMI	L_ARG_61	NH1	L_ASP_82	OD1	2.794
5DMI	L_ARG_61	NH1	L_ASP_82	OD2	3.657
5DMI	L_ARG_61	NH2	L_GLU_79	OE1	3.312
5DMI	L_ARG_61	NH2	L_GLU_79	OE2	3.348
5DMI	L_LYS_103	NZ	L_GLU_105	OE1	3.441
5DMI	L_LYS_103	NZ	L_GLU_165	OE2	3.954
5DMI	L_LYS_149	NZ	L_GLU_195	OE2	2.814
5DMI	L_LYS_183	NZ	L_GLU_187	OE1	2.795
5DMI	L_LYS_188	NZ	L_ASP_185	OD1	2.852
5DMI	L_ARG_211	NH1	L_GLU_187	OE2	3.522
5DMJ	A_HIS_78	NE2	A_GLU_74	OE2	3.682

5DMJ	A_HIS_162	NE2	A_GLU_159	OE1	3.307
5DMJ	B_ARG_38	NH1	B_GLU_46	OE1	3.733
5DMJ	B_ARG_38	NH1	B_GLU_46	OE2	3.183
5DMJ	B_ARG_38	NH1	B_ASP_86	OD1	3.833
5DMJ	B_ARG_38	NH2	B_ASP_86	OD1	2.916
5DMJ	B_ARG_66	NH1	B_ASP_86	OD1	3.274
5DMJ	B_ARG_66	NH1	B_ASP_86	OD2	2.599
5DMJ	B_ARG_66	NH2	B_ASP_86	OD1	3.293
5DMJ	B_ARG_83	NH2	G_ASP_72	OD1	3.449
5DMJ	B_LYS_94	NZ	B_ASP_102	OD1	3.363
5DMJ	D_HIS_78	NE2	D_GLU_74	OE2	3.689
5DMJ	D_ARG_123	NH1	D_ASP_140	OD2	3.071
5DMJ	D_HIS_162	NE2	D_GLU_159	OE1	3.282
5DMJ	D_LYS_181	NZ	D_ASP_180	OD2	3.498
5DMJ	E_ARG_38	NH1	E_GLU_46	OE1	3.747
5DMJ	E_ARG_38	NH1	E_GLU_46	OE2	3.182
5DMJ	E_ARG_38	NH1	E_ASP_86	OD1	3.846
5DMJ	E_ARG_38	NH2	E_ASP_86	OD1	2.939
5DMJ	E_ARG_66	NH1	E_ASP_86	OD1	3.321
5DMJ	E_ARG_66	NH1	E_ASP_86	OD2	2.623
5DMJ	E_ARG_66	NH2	E_ASP_86	OD1	3.325
5DMJ	E_LYS_75	NZ	E_ASP_72	OD2	3.917
5DMJ	E_LYS_94	NZ	E_ASP_102	OD1	3.533
5DMJ	F_HIS_78	NE2	F_GLU_74	OE2	3.703
5DMJ	F_HIS_162	NE2	F_GLU_159	OE1	3.306
5DMJ	G_ARG_38	NH1	G_GLU_46	OE1	3.769
5DMJ	G_ARG_38	NH1	G_GLU_46	OE2	3.178
5DMJ	G_ARG_38	NH1	G_ASP_86	OD1	3.862
5DMJ	G_ARG_38	NH2	G_ASP_86	OD1	2.937
5DMJ	G_ARG_66	NH1	G_ASP_86	OD1	3.324
5DMJ	G_ARG_66	NH1	G_ASP_86	OD2	2.634
5DMJ	G_ARG_66	NH2	G_ASP_86	OD1	3.327
5DMJ	G_LYS_75	NZ	B_GLU_85	OE1	3.187
5DMJ	G_LYS_94	NZ	G_ASP_102	OD1	3.775
5DWU	B_ARG_377	NH2	B_ASP_379	OD1	3.390
5DWU	B_ARG_407	NH1	B_ASP_435	OD1	2.835
5DWU	B_ARG_407	NH2	B_ASP_435	OD1	3.962
5DWU	H_ARG_38	NH1	H_ASP_90	OD1	2.590
5DWU	H_ARG_38	NH2	H_GLU_46	OE1	2.502
5DWU	H_ARG_52	NH1	A_ASP_107	OD1	3.435
5DWU	H_ARG_52	NH1	A_ASP_107	OD2	2.568
5DWU	H_ARG_52	NH2	A_ASP_107	OD1	2.685
5DWU	H_ARG_52	NH2	A_ASP_107	OD2	3.250
5DWU	H_ARG_98	NH2	H_ASP_105	OD2	3.961
5DWU	L_ARG_61	NH1	L_ASP_82	OD1	3.900
5DWU	L_ARG_61	NH2	L_ASP_82	OD1	2.608
5DWU	L_ARG_61	NH2	L_ASP_82	OD2	2.917
5DWU	L_HIS_189	ND1	L_ASP_151	OD2	3.598
5ERW	A_LYS_12	NZ	A_GLU_10	OE1	2.949
5ERW	A_ARG_38	NH1	A_ASP_90	OD1	2.885
5ERW	A_ARG_38	NH2	A_GLU_46	OE1	3.486
5ERW	A_ARG_38	NH2	A_GLU_46	OE2	3.818
5ERW	A_ARG_38	NH2	A_ASP_90	OD1	3.778
5ERW	A_ARG_67	NH1	A_ASP_90	OD2	2.657
5ERW	A_ARG_67	NH2	A_ASP_90	OD1	3.007
5ERW	A_ARG_67	NH2	A_ASP_90	OD2	3.030
5ERW	A_ARG_87	NH1	A_GLU_89	OE2	3.913
5ERW	A_ARG_103	NH1	B_ASP_49	OD2	2.990

5ERW	A_LYS_214	NZ	B_GLU_122	OE1	2.490
5ERW	B_LYS_30	NZ	B_ASP_91	OD1	2.653
5ERW	B_HIS_33	ND1	B_ASP_49	OD1	3.753
5ERW	B_ARG_60	NH2	B_ASP_81	OD1	2.998
5ERW	B_ARG_60	NH2	B_ASP_81	OD2	2.524
5ERW	B_LYS_102	NZ	B_ASP_84	OD1	3.442
5ERW	B_LYS_102	NZ	B_ASP_84	OD2	3.632
5ERW	B_LYS_102	NZ	B_ASP_164	OD1	3.634
5ERW	B_LYS_146	NZ	B_GLU_153	OE1	2.547
5ERW	B_LYS_146	NZ	B_GLU_153	OE2	3.654
5ERW	B_LYS_148	NZ	B_GLU_194	OE1	3.651
5ERW	B_LYS_148	NZ	B_GLU_194	OE2	2.963
5ERW	B_ARG_154	NH1	B_GLU_184	OE1	3.549
5ERW	B_LYS_168	NZ	B_ASP_166	OD2	3.760
5ERW	B_LYS_182	NZ	B_GLU_186	OE1	3.952
5ERW	B_LYS_182	NZ	B_GLU_186	OE2	2.341
5ERW	B_HIS_188	ND1	B_ASP_150	OD2	2.455
5ERW	B_LYS_198	NZ	B_ASP_109	OD1	3.278
5ERW	B_LYS_198	NZ	B_ASP_109	OD2	2.412
5ERW	C_LYS_446	NZ	B_ASP_50	OD1	3.926
5ERW	C_LYS_446	NZ	B_ASP_50	OD2	2.398
5EZI	H_ARG_45	NH2	H_ASP_42	OD2	3.860
5EZI	H_ARG_52	NH1	H_GLU_60	OE1	3.045
5EZI	H_ARG_52	NH1	H_ASP_104	OD1	3.782
5EZI	H_ARG_52	NH2	H_ASP_104	OD1	2.793
5EZI	H_LYS_79	NZ	H_ASP_80	OD1	3.553
5EZI	H_LYS_79	NZ	H_ASP_80	OD2	3.228
5EZI	H_LYS_81	NZ	H_ASP_104	OD1	3.557
5EZI	H_LYS_81	NZ	H_ASP_104	OD2	2.766
5EZI	H_ARG_112	NH2	H_ASP_121	OD1	3.513
5EZI	H_ARG_112	NH2	H_ASP_121	OD2	2.756
5EZI	L_ARG_54	NH1	L_ASP_56	OD2	3.800
5EZI	L_ARG_54	NH2	L_ASP_56	OD1	3.697
5EZI	L_ARG_54	NH2	L_ASP_56	OD2	2.546
5EZI	L_ARG_78	NH2	L_ASP_84	OD1	3.854
5EZI	L_ARG_85	NH2	L_GLU_105	OE2	3.655
5EZI	L_ARG_85	NH2	L_ASP_106	OD1	2.746
5EZI	L_ARG_85	NH2	L_ASP_106	OD2	3.689
5EZI	L_ARG_120	NH1	H_GLU_64	OE1	3.561
5EZI	L_ARG_120	NH1	H_GLU_64	OE2	2.826
5EZI	L_LYS_166	NZ	L_GLU_129	OE2	3.752
5EZI	L_LYS_173	NZ	L_GLU_219	OE1	3.356
5EZI	L_LYS_173	NZ	L_GLU_219	OE2	2.974
5EZI	L_ARG_179	NH1	L_GLU_209	OE1	3.490
5EZI	L_ARG_179	NH1	L_GLU_209	OE2	3.054
5EZI	L_ARG_179	NH2	L_GLU_209	OE1	3.322
5EZI	L_HIS_213	ND1	L_ASP_175	OD2	3.083
5EZI	L_LYS_223	NZ	L_ASP_134	OD2	3.368
5EZJ	A_ARG_52	NH1	A_GLU_60	OE1	2.978
5EZJ	A_ARG_52	NH1	A_ASP_104	OD1	3.803
5EZJ	A_ARG_52	NH2	A_ASP_104	OD1	2.735
5EZJ	A_LYS_79	NZ	A_ASP_80	OD1	3.518
5EZJ	A_LYS_79	NZ	A_ASP_80	OD2	2.915
5EZJ	A_LYS_81	NZ	A_ASP_104	OD1	3.567
5EZJ	A_LYS_81	NZ	A_ASP_104	OD2	2.848
5EZJ	A_ARG_112	NH2	A_ASP_121	OD1	2.747
5EZJ	A_ARG_112	NH2	A_ASP_121	OD2	3.431
5EZJ	A_LYS_228	NZ	B_GLU_147	OE1	3.274

5EZJ	A_LYS_229	NZ	A_GLU_231	OE2	3.771
5EZJ	B_LYS_48	NZ	B_ASP_94	OD1	3.784
5EZJ	B_LYS_48	NZ	B_ASP_94	OD2	2.891
5EZJ	B_ARG_54	NH2	B_ASP_56	OD1	3.856
5EZJ	B_ARG_54	NH2	B_ASP_56	OD2	2.671
5EZJ	B_ARG_78	NH2	B_ASP_84	OD1	3.656
5EZJ	B_ARG_85	NH1	B_ASP_106	OD1	2.928
5EZJ	B_ARG_85	NH1	B_ASP_106	OD2	3.850
5EZJ	B_ARG_120	NH1	A_GLU_64	OE1	3.637
5EZJ	B_ARG_120	NH1	A_GLU_64	OE2	2.843
5EZJ	B_LYS_127	NZ	B_GLU_129	OE1	3.869
5EZJ	B_LYS_173	NZ	B_GLU_219	OE1	3.389
5EZJ	B_LYS_173	NZ	B_GLU_219	OE2	2.427
5EZJ	B_ARG_179	NH1	B_GLU_209	OE1	3.217
5EZJ	B_ARG_179	NH1	B_GLU_209	OE2	3.402
5EZJ	B_ARG_179	NH2	B_GLU_209	OE1	3.880
5EZJ	B_ARG_179	NH2	B_GLU_209	OE2	2.776
5EZJ	B_HIS_213	ND1	B_ASP_175	OD2	3.143
5EZL	A_ARG_45	NH2	A_ASP_42	OD2	3.885
5EZL	A_ARG_52	NH1	A_GLU_60	OE1	3.345
5EZL	A_ARG_52	NH1	A_ASP_104	OD1	3.820
5EZL	A_ARG_52	NH2	A_ASP_104	OD1	2.908
5EZL	A_LYS_81	NZ	A_ASP_104	OD1	3.524
5EZL	A_LYS_81	NZ	A_ASP_104	OD2	2.698
5EZL	A_ARG_112	NH1	A_ASP_121	OD2	2.196
5EZL	A_LYS_228	NZ	B_GLU_147	OE1	3.314
5EZL	A_LYS_229	NZ	A_GLU_231	OE2	2.784
5EZL	B_ARG_54	NH2	B_ASP_56	OD1	3.684
5EZL	B_ARG_54	NH2	B_ASP_56	OD2	2.960
5EZL	B_ARG_78	NH2	B_ASP_84	OD1	3.876
5EZL	B_ARG_85	NH1	B_ASP_106	OD1	2.623
5EZL	B_ARG_85	NH1	B_ASP_106	OD2	2.985
5EZL	B_ARG_120	NH1	A_GLU_64	OE1	3.901
5EZL	B_ARG_120	NH1	A_GLU_64	OE2	2.804
5EZL	B_LYS_127	NZ	B_GLU_129	OE2	3.626
5EZL	B_LYS_173	NZ	B_GLU_219	OE1	3.456
5EZL	B_LYS_173	NZ	B_GLU_219	OE2	2.709
5EZL	B_LYS_223	NZ	B_ASP_134	OD2	3.131
5EZL	H_ARG_52	NH1	H_GLU_60	OE1	3.219
5EZL	H_ARG_52	NH1	H_GLU_60	OE2	3.769
5EZL	H_ARG_52	NH1	H_ASP_104	OD1	3.785
5EZL	H_ARG_52	NH2	H_ASP_104	OD1	3.045
5EZL	H_LYS_81	NZ	H_ASP_104	OD1	3.442
5EZL	H_LYS_81	NZ	H_ASP_104	OD2	2.623
5EZL	H_ARG_112	NH1	H_ASP_121	OD1	3.400
5EZL	H_ARG_112	NH1	H_ASP_121	OD2	2.409
5EZL	H_LYS_228	NZ	L_GLU_147	OE2	3.445
5EZL	H_LYS_229	NZ	H_GLU_231	OE2	2.742
5EZL	L_ARG_54	NH2	L_ASP_56	OD1	3.764
5EZL	L_ARG_54	NH2	L_ASP_56	OD2	2.783
5EZL	L_LYS_63	NZ	L_GLU_105	OE1	3.769
5EZL	L_ARG_78	NH1	L_ASP_84	OD1	3.894
5EZL	L_ARG_78	NH2	L_ASP_84	OD1	3.679
5EZL	L_ARG_85	NH2	L_GLU_105	OE1	3.813
5EZL	L_ARG_85	NH2	L_GLU_105	OE2	3.287
5EZL	L_ARG_85	NH2	L_ASP_106	OD1	3.191
5EZL	L_ARG_85	NH2	L_ASP_106	OD2	3.915
5EZL	L_ARG_120	NH1	H_GLU_64	OE1	3.668

5EZL	L_ARG_120	NH1	H_GLU_64	OE2	2.626
5EZL	L_LYS_127	NZ	L_ASP_189	OD1	3.123
5EZL	L_LYS_173	NZ	L_GLU_219	OE2	2.984
5EZL	L_LYS_223	NZ	L_ASP_134	OD2	3.564
5EZN	A_ARG_58	NH1	E_ASP_336	OD2	3.940
5EZN	A_ARG_58	NH2	E_ASP_336	OD2	2.479
5EZN	A_HIS_76	ND1	A_ASP_92	OD2	3.010
5EZN	A_HIS_76	NE2	A_GLU_74	OE2	3.795
5EZN	A_LYS_81	NZ	A_GLU_59	OE1	3.642
5EZN	A_LYS_95	NZ	A_ASP_92	OD2	2.550
5EZN	A_ARG_102	NH2	A_ASP_67	OD2	3.108
5EZN	A_HIS_104	NE2	A_ASP_121	OD1	3.856
5EZN	A_HIS_134	NE2	A_ASP_98	OD2	3.544
5EZN	A_LYS_188	NZ	A_GLU_123	OE1	3.017
5EZN	E_LYS_204	NZ	A_GLU_113	OE1	2.243
5EZN	E_LYS_204	NZ	A_GLU_113	OE2	3.142
5EZN	E_LYS_215	NZ	E_GLU_265	OE2	3.398
5EZN	E_LYS_220	NZ	E_ASP_245	OD2	3.852
5EZN	E_ARG_229	NH2	E_ASP_282	OD1	2.680
5EZN	E_ARG_229	NH2	E_ASP_282	OD2	3.870
5EZN	E_HIS_240	NE2	E_ASP_282	OD1	3.980
5EZN	E_LYS_251	NZ	B_GLU_72	OE2	3.130
5EZN	E_ARG_271	NH1	E_GLU_257	OE2	3.148
5EZN	E_LYS_334	NZ	E_GLU_337	OE1	3.441
5EZN	E_LYS_334	NZ	E_GLU_337	OE2	3.486
5EZN	B_ARG_36	NH1	B_GLU_38	OE2	3.346
5EZN	B_LYS_69	NZ	B_GLU_72	OE1	2.194
5EZN	B_LYS_69	NZ	B_GLU_74	OE1	3.478
5EZN	B_HIS_76	ND1	B_ASP_92	OD2	3.694
5EZN	B_LYS_81	NZ	B_GLU_59	OE2	2.979
5EZN	B_ARG_102	NH2	B_ASP_67	OD2	3.883
5EZN	B_HIS_134	ND1	B_GLU_148	OE1	3.830
5EZN	B_HIS_134	NE2	B_GLU_148	OE1	3.515
5EZN	B_ARG_135	NH1	G_GLU_206	OE2	3.927
5EZN	B_ARG_135	NH2	G_GLU_206	OE2	3.596
5EZN	G_LYS_204	NZ	B_GLU_112	OE1	2.749
5EZN	G_LYS_204	NZ	B_GLU_112	OE2	3.972
5EZN	G_LYS_204	NZ	B_GLU_113	OE2	3.260
5EZN	G_LYS_215	NZ	G_ASP_194	OD1	3.377
5EZN	G_LYS_215	NZ	G_ASP_194	OD2	2.294
5EZN	G_ARG_229	NH1	G_ASP_282	OD1	3.051
5EZN	G_ARG_229	NH2	G_ASP_282	OD1	3.739
5EZN	G_HIS_240	NE2	G_ASP_282	OD1	3.769
5EZN	G_LYS_262	NZ	G_GLU_265	OE1	3.917
5EZN	G_LYS_316	NZ	G_GLU_302	OE2	2.834
5EZN	G_LYS_334	NZ	G_GLU_337	OE1	3.582
5EZN	G_LYS_334	NZ	G_GLU_337	OE2	2.552
5EZN	G_ARG_339	NH2	G_ASP_336	OD2	3.484
5EZO	H_ARG_56	NH1	H_GLU_64	OE1	3.259
5EZO	H_ARG_56	NH1	H_ASP_108	OD1	3.756
5EZO	H_ARG_56	NH2	H_ASP_108	OD1	2.964
5EZO	H_LYS_85	NZ	H_ASP_108	OD1	3.343
5EZO	H_LYS_85	NZ	H_ASP_108	OD2	3.101
5EZO	H_ARG_116	NH1	H_ASP_125	OD1	3.598
5EZO	H_ARG_116	NH1	H_ASP_125	OD2	2.331
5EZO	H_LYS_232	NZ	L_GLU_143	OE1	3.314
5EZO	H_LYS_232	NZ	L_GLU_143	OE2	2.456
5EZO	H_LYS_233	NZ	H_GLU_235	OE2	3.779

5EZO	L_ARG_50	NH1	A_ASP_66	OD1	3.943
5EZO	L_ARG_50	NH1	A_ASP_66	OD2	3.721
5EZO	L_LYS_59	NZ	L_GLU_101	OE1	3.526
5EZO	L_ARG_74	NH1	L_ASP_80	OD1	3.915
5EZO	L_ARG_81	NH1	L_GLU_101	OE2	3.291
5EZO	L_ARG_81	NH1	L_ASP_102	OD1	3.399
5EZO	L_ARG_81	NH1	L_ASP_102	OD2	3.360
5EZO	L_ARG_81	NH2	L_GLU_101	OE2	3.105
5EZO	L_ARG_116	NH1	H_GLU_68	OE1	3.718
5EZO	L_ARG_116	NH1	H_GLU_68	OE2	2.774
5EZO	L_LYS_123	NZ	L_ASP_185	OD1	3.241
5EZO	L_LYS_123	NZ	L_ASP_185	OD2	3.353
5EZO	L_LYS_219	NZ	L_ASP_130	OD2	3.420
5EZO	A_ARG_36	NH1	A_GLU_38	OE2	2.554
5EZO	A_LYS_43	NZ	A_ASP_85	OD2	3.209
5EZO	A_HIS_76	ND1	A_ASP_92	OD2	2.596
5EZO	A_LYS_81	NZ	A_GLU_59	OE2	2.928
5EZO	A_ARG_102	NH2	A_ASP_67	OD2	2.790
5EZO	A_LYS_129	NZ	A_GLU_122	OE2	3.798
5EZO	A_HIS_134	ND1	A_GLU_148	OE1	3.764
5EZO	A_ARG_135	NH1	A_GLU_206	OE2	3.876
5EZO	A_ARG_135	NH2	A_GLU_206	OE2	3.659
5EZO	A_LYS_186	NZ	A_ASP_195	OD1	2.722
5EZO	A_LYS_192	NZ	A_ASP_217	OD2	3.683
5EZO	A_LYS_204	NZ	A_GLU_112	OE1	3.269
5EZO	A_LYS_204	NZ	A_GLU_113	OE2	3.314
5EZO	A_ARG_229	NH2	A_ASP_282	OD1	2.774
5EZO	A_ARG_229	NH2	A_ASP_282	OD2	3.510
5EZO	A_HIS_240	NE2	A_ASP_282	OD1	3.983
5EZO	A_ARG_271	NH1	A_GLU_257	OE1	3.813
5EZO	A_LYS_316	NZ	A_GLU_302	OE2	3.408
5EZO	A_LYS_334	NZ	A_GLU_337	OE1	3.354
5EZO	A_LYS_334	NZ	A_GLU_337	OE2	2.671
5EZO	A_ARG_339	NH2	A_ASP_336	OD2	3.220
5GGV	L_ARG_24	NH1	L_ASP_70	OD1	2.800
5GGV	L_ARG_24	NH1	L_ASP_70	OD2	3.234
5GGV	L_ARG_24	NH2	L_ASP_70	OD1	3.597
5GGV	L_ARG_61	NH2	L_GLU_81	OE2	3.323
5GGV	L_ARG_61	NH2	L_ASP_82	OD1	2.670
5GGV	L_ARG_61	NH2	L_ASP_82	OD2	3.226
5GGV	L_LYS_149	NZ	L_GLU_195	OE1	3.933
5GGV	L_LYS_183	NZ	L_GLU_187	OE2	3.997
5GGV	L_HIS_189	ND1	L_ASP_151	OD2	2.820
5GGV	L_LYS_190	NZ	L_GLU_213	OE2	2.696
5GGV	H_HIS_35	NE2	H_ASP_99	OD2	2.983
5GGV	H_ARG_38	NH1	H_ASP_90	OD1	2.864
5GGV	H_ARG_38	NH2	H_GLU_46	OE1	3.166
5GGV	H_ARG_38	NH2	H_ASP_90	OD1	3.783
5GGV	H_ARG_67	NH1	H_ASP_90	OD1	3.548
5GGV	H_ARG_67	NH1	H_ASP_90	OD2	3.804
5GGV	H_ARG_67	NH2	H_ASP_90	OD1	3.503
5GGV	H_ARG_67	NH2	H_ASP_90	OD2	2.364
5GGV	H_LYS_76	NZ	H_ASP_73	OD2	3.976
5GGV	H_ARG_98	NH2	H_ASP_113	OD1	3.862
5GGV	H_ARG_98	NH2	H_ASP_113	OD2	2.927
5GGV	H_ARG_101	NH1	Y_GLU_97	OE2	3.572
5GGV	H_LYS_155	NZ	H_ASP_156	OD1	3.101
5GGV	H_LYS_155	NZ	H_ASP_156	OD2	3.435

5GGV	H.LYS_221	NZ	L.GLU_123	OE1	2.304
5GGV	H.LYS_221	NZ	L.GLU_123	OE2	3.975
5GKR	A.ARG_38	NH1	A.ASP_86	OD1	2.742
5GKR	A.ARG_38	NH2	A.GLU_46	OE1	2.810
5GKR	A.ARG_38	NH2	A.ASP_86	OD1	3.641
5GKR	A.ARG_66	NH1	A.ASP_86	OD1	3.332
5GKR	A.ARG_66	NH1	A.ASP_86	OD2	3.801
5GKR	A.ARG_66	NH2	A.ASP_86	OD1	3.354
5GKR	A.ARG_66	NH2	A.ASP_86	OD2	2.729
5GKR	A.ARG_94	NH1	A.ASP_101	OD1	3.700
5GKR	A.ARG_94	NH1	A.ASP_101	OD2	2.566
5GKR	A.LYS_143	NZ	B.GLU_125	OE2	2.806
5GKR	A.LYS_201	NZ	A.ASP_199	OD2	2.935
5GKR	A.LYS_206	NZ	A.ASP_199	OD1	3.198
5GKR	A.LYS_209	NZ	B.GLU_124	OE1	2.825
5GKR	A.LYS_209	NZ	B.GLU_124	OE2	3.325
5GKR	B.LYS_53	NZ	B.ASP_50	OD2	3.716
5GKR	B.ARG_61	NH2	B.GLU_81	OE2	3.803
5GKR	B.ARG_61	NH2	B.ASP_82	OD1	2.896
5GKR	B.ARG_61	NH2	B.ASP_82	OD2	3.817
5GKR	B.LYS_130	NZ	A.ASP_144	OD2	3.639
5GKR	B.LYS_164	NZ	B.ASP_85	OD2	2.873
5GKR	B.HIS_189	ND1	B.ASP_152	OD2	3.078
5GKR	C.ARG_38	NH1	C.ASP_86	OD1	2.720
5GKR	C.ARG_38	NH2	C.GLU_46	OE2	2.991
5GKR	C.ARG_38	NH2	C.ASP_86	OD1	3.638
5GKR	C.ARG_66	NH1	C.ASP_86	OD1	3.317
5GKR	C.ARG_66	NH1	C.ASP_86	OD2	3.769
5GKR	C.ARG_66	NH2	C.ASP_86	OD1	3.362
5GKR	C.ARG_66	NH2	C.ASP_86	OD2	2.717
5GKR	C.ARG_94	NH2	C.ASP_101	OD1	3.797
5GKR	C.ARG_94	NH2	C.ASP_101	OD2	2.747
5GKR	C.LYS_143	NZ	D.GLU_125	OE2	2.591
5GKR	C.LYS_206	NZ	C.ASP_199	OD1	3.203
5GKR	C.LYS_209	NZ	D.GLU_124	OE1	2.486
5GKR	C.LYS_209	NZ	D.GLU_124	OE2	2.893
5GKR	D.LYS_53	NZ	D.ASP_50	OD2	3.715
5GKR	D.ARG_61	NH1	D.ASP_82	OD1	3.020
5GKR	D.ARG_61	NH1	D.ASP_82	OD2	3.903
5GKR	D.LYS_130	NZ	C.ASP_144	OD2	3.574
5GKR	D.LYS_164	NZ	D.ASP_85	OD2	2.940
5GKR	D.ARG_190	NH2	D.ASP_152	OD1	3.635
5GKS	A.ARG_38	NH1	A.ASP_86	OD1	2.822
5GKS	A.ARG_38	NH2	A.GLU_46	OE1	2.937
5GKS	A.ARG_38	NH2	A.ASP_86	OD1	3.692
5GKS	A.ARG_66	NH1	A.ASP_86	OD1	3.105
5GKS	A.ARG_66	NH1	A.ASP_86	OD2	3.788
5GKS	A.ARG_66	NH2	A.ASP_86	OD1	3.456
5GKS	A.ARG_66	NH2	A.ASP_86	OD2	2.799
5GKS	A.ARG_94	NH1	A.ASP_101	OD1	3.889
5GKS	A.ARG_94	NH1	A.ASP_101	OD2	2.710
5GKS	A.ARG_96	NH2	A.ASP_101	OD2	3.709
5GKS	A.LYS_143	NZ	A.ASP_144	OD1	3.345
5GKS	A.LYS_143	NZ	A.ASP_144	OD2	3.710
5GKS	A.LYS_	NZ	A.ASP_	OD2	3.919
5GKS	A.LYS_	NZ	B.GLU_124	OE1	3.518
5GKS	A.LYS_	NZ	B.GLU_124	OE2	2.790
5GKS	B.LYS_53	NZ	B.ASP_50	OD2	3.623

5GKS	B_ARG_	NH1	B_ASP_	OD1	2.870
5GKS	B_ARG_	NH1	B_ASP_82	OD2	3.493
5GKS	B_LYS_111	NZ	B_GLU_199	OE1	3.161
5GKS	B_LYS_130	NZ	A_ASP_144	OD2	3.783
5GKS	B_LYS_150	NZ	B_GLU_204	OE2	3.960
5GKS	B_LYS_164	NZ	B_ASP_85	OD2	3.552
5GKS	B_HIS_189	ND1	B_ASP_152	OD2	3.043
5GKS	C_ARG_	NH1	C_ASP_	OD1	2.746
5GKS	C_ARG_	NH2	C_GLU_	OE1	3.164
5GKS	C_ARG_	NH2	C_ASP_	OD1	3.556
5GKS	C_ARG_66	NH1	C_ASP_	OD1	3.136
5GKS	C_ARG_66	NH1	C_ASP_	OD2	3.770
5GKS	C_ARG_66	NH2	C_ASP_	OD1	3.522
5GKS	C_ARG_66	NH2	C_ASP_	OD2	2.841
5GKS	C_ARG_	NH1	C_ASP_	OD1	3.682
5GKS	C_ARG_	NH1	C_ASP_	OD2	2.656
5GKS	C_ARG_	NH2	C_ASP_	OD2	3.498
5GKS	C_LYS_	NZ	C_ASP_	OD1	3.276
5GKS	C_LYS_	NZ	C_ASP_	OD2	3.251
5GKS	C_LYS_	NZ	C_ASP_	OD2	3.224
5GKS	C_LYS_	NZ	C_ASP_	OD1	3.903
5GKS	C_LYS_	NZ	C_ASP_	OD2	3.334
5GKS	C_LYS_	NZ	D_GLU_	OE1	3.455
5GKS	C_LYS_	NZ	D_GLU_	OE2	2.665
5GKS	D_LYS_	NZ	D_ASP_	OD2	3.974
5GKS	D_ARG_	NH1	D_ASP_	OD1	2.964
5GKS	D_ARG_	NH1	D_GLU_	OE2	3.512
5GKS	D_ARG_	NH1	D_ASP_	OD1	2.891
5GKS	D_ARG_	NH1	D_ASP_	OD2	3.896
5GKS	D_LYS_	NZ	D_GLU_	OE1	2.751
5GKS	D_LYS_	NZ	D_GLU_	OE2	3.899
5GKS	D_HIS_189	ND1	D_ASP_152	OD2	3.002
5HDQ	A_HIS_40	NE2	A_ASP_58	OD1	2.837
5HDQ	A_HIS_50	NE2	A_GLU_189	OE2	3.103
5HDQ	A_HIS_50	NE2	A_ASP_264	OD1	3.865
5HDQ	A_HIS_50	NE2	A_ASP_264	OD2	3.335
5HDQ	A_HIS_123	ND1	A_ASP_121	OD2	2.936
5HDQ	A_HIS_123	NE2	A_GLU_189	OE1	3.291
5HDQ	A_HIS_123	NE2	A_GLU_189	OE2	3.492
5HDQ	A_HIS_123	NE2	A_ASP_264	OD1	2.880
5HDQ	A_HIS_123	NE2	A_ASP_264	OD2	3.860
5HDQ	A_HIS_149	ND1	A_ASP_146	OD1	3.055
5HDQ	A_HIS_149	ND1	A_ASP_146	OD2	2.834
5HDQ	A_LYS_172	NZ	A_ASP_129	OD1	3.820
5HDQ	A_LYS_193	NZ	A_GLU_208	OE2	3.325
5HDQ	A_HIS_230	ND1	A_GLU_181	OE1	3.289
5HDQ	A_HIS_234	ND1	H_ASP_97	OD2	3.865
5HDQ	A_LYS_243	NZ	A_GLU_260	OE2	3.481
5HDQ	A_LYS_254	NZ	A_GLU_251	OE1	3.552
5HDQ	A_LYS_278	NZ	A_ASP_274	OD1	2.808
5HDQ	A_HIS_288	NE2	A_ASP_177	OD1	3.242
5HDQ	A_HIS_288	NE2	A_ASP_177	OD2	3.881
5HDQ	H_LYS_62	NZ	H_GLU_46	OE1	3.737
5HDQ	H_LYS_62	NZ	H_GLU_46	OE2	2.605
5HDQ	H_LYS_66	NZ	H_ASP_86	OD1	3.893
5HDQ	H_LYS_66	NZ	H_ASP_86	OD2	2.747
5HDQ	H_ARG_94	NH1	H_ASP_101	OD1	3.466
5HDQ	H_ARG_94	NH1	H_ASP_101	OD2	2.979

5HDQ	H.LYS_95	NZ	A_ASP_256	OD2	3.739
5HDQ	H.LYS_208	NZ	L_GLU_123	OE1	2.947
5HDQ	L.LYS_24	NZ	L_ASP_70	OD2	2.740
5HDQ	L_ARG_54	NH1	L_ASP_60	OD1	3.546
5HDQ	L_ARG_61	NH1	L_GLU_81	OE1	3.772
5HDQ	L_ARG_61	NH1	L_ASP_82	OD1	2.690
5HDQ	L_ARG_61	NH1	L_ASP_82	OD2	3.697
5HDQ	L.LYS_103	NZ	L_GLU_105	OE2	3.387
5HDQ	L.LYS_142	NZ	L_GLU_105	OE1	3.286
5HDQ	L.LYS_142	NZ	L_GLU_105	OE2	2.974
5HDQ	L.LYS_149	NZ	L_GLU_195	OE2	3.652
5HDQ	L.LYS_183	NZ	L_GLU_187	OE1	2.880
5HDQ	L.LYS_183	NZ	L_GLU_187	OE2	3.085
5HDQ	L.HIS_189	ND1	L_ASP_151	OD2	2.925
5HDQ	L.HIS_189	NE2	L_GLU_185	OE1	3.931
5HDQ	L.HIS_189	NE2	L_GLU_185	OE2	3.287
5HMG	A.LYS_27	NZ	B_GLU_97	OE1	2.931
5HMG	A.LYS_27	NZ	B_GLU_97	OE2	3.005
5HMG	A.HIS_56	ND1	A_ASP_85	OD2	3.602
5HMG	A_ARG_57	NH1	A_GLU_82	OE1	2.653
5HMG	A_ARG_57	NH1	A_GLU_82	OE2	3.746
5HMG	A.HIS_75	ND1	A_ASP_73	OD1	3.505
5HMG	A.HIS_75	ND1	A_ASP_73	OD2	2.667
5HMG	A.HIS_75	NE2	A_ASP_63	OD1	3.736
5HMG	A_ARG_90	NH1	A_ASP_60	OD1	2.782
5HMG	A_ARG_90	NH1	A_ASP_60	OD2	3.490
5HMG	A_ARG_109	NH1	B_GLU_67	OE1	2.841
5HMG	A_ARG_109	NH1	B_GLU_67	OE2	3.185
5HMG	A_ARG_109	NH2	A_GLU_89	OE1	2.955
5HMG	A_ARG_109	NH2	A_GLU_89	OE2	2.579
5HMG	A_ARG_141	NH1	A_ASP_77	OD1	3.382
5HMG	A_ARG_141	NH1	A_ASP_77	OD2	3.145
5HMG	A_ARG_141	NH2	A_ASP_77	OD1	2.618
5HMG	A_ARG_141	NH2	A_ASP_77	OD2	2.942
5HMG	A.LYS_176	NZ	A_GLU_123	OE1	2.608
5HMG	A.LYS_176	NZ	A_GLU_123	OE2	3.621
5HMG	A.HIS_183	NE2	A_GLU_190	OE1	3.761
5HMG	A_ARG_207	NH2	A_ASP_241	OD1	3.512
5HMG	A_ARG_261	NH1	A_GLU_119	OE1	3.028
5HMG	A_ARG_261	NH1	A_GLU_119	OE2	3.069
5HMG	A_ARG_261	NH2	A_GLU_119	OE1	2.801
5HMG	A_ARG_261	NH2	A_GLU_119	OE2	2.923
5HMG	A.LYS_264	NZ	A_ASP_85	OD1	3.963
5HMG	A.LYS_264	NZ	A_ASP_85	OD2	2.713
5HMG	A_ARG_269	NH1	B_GLU_67	OE1	3.577
5HMG	A_ARG_269	NH2	B_GLU_67	OE1	3.220
5HMG	A.LYS_292	NZ	A_ASP_291	OD1	2.545
5HMG	A.LYS_299	NZ	B_GLU_69	OE1	3.343
5HMG	A.LYS_310	NZ	B_ASP_86	OD1	3.434
5HMG	A.LYS_310	NZ	B_ASP_90	OD1	2.661
5HMG	A.LYS_315	NZ	A_GLU_41	OE2	2.757
5HMG	B.LYS_51	NZ	B_GLU_103	OE2	2.773
5HMG	B_ARG_54	NH1	F_GLU_97	OE1	2.843
5HMG	B_ARG_54	NH2	B_GLU_57	OE2	3.728
5HMG	B_ARG_54	NH2	F_GLU_97	OE1	2.937
5HMG	B.LYS_58	NZ	B_GLU_57	OE1	3.084
5HMG	B.LYS_58	NZ	B_GLU_57	OE2	3.561
5HMG	B.LYS_58	NZ	F_GLU_97	OE1	3.606

5HMG	B.LYS_58	NZ	F_GLU_97	OE2	3.524
5HMG	B.LYS_62	NZ	F_ASP_86	OD1	3.085
5HMG	B.LYS_62	NZ	F_ASP_86	OD2	2.792
5HMG	B.LYS_62	NZ	F_ASP_90	OD1	3.679
5HMG	B.LYS_62	NZ	F_ASP_90	OD2	2.748
5HMG	B_HIS_64	NE2	F_ASP_79	OD2	3.617
5HMG	B.LYS_68	NZ	B_GLU_85	OE1	3.409
5HMG	B.LYS_68	NZ	B_GLU_85	OE2	2.733
5HMG	B_ARG_76	NH1	D_GLU_74	OE1	3.275
5HMG	B_ARG_76	NH1	D_GLU_74	OE2	2.882
5HMG	B_ARG_76	NH1	D_GLU_81	OE1	2.781
5HMG	B_ARG_76	NH1	D_GLU_81	OE2	3.484
5HMG	B_ARG_76	NH2	D_GLU_74	OE1	2.814
5HMG	B_ARG_76	NH2	D_GLU_74	OE2	3.691
5HMG	B.LYS_117	NZ	B_GLU_114	OE1	2.674
5HMG	B.LYS_117	NZ	B_GLU_114	OE2	3.512
5HMG	B_ARG_123	NH1	B_GLU_120	OE1	3.893
5HMG	B_ARG_123	NH1	F_GLU_132	OE2	3.002
5HMG	B_ARG_123	NH2	B_GLU_120	OE1	2.612
5HMG	B_ARG_123	NH2	B_GLU_120	OE2	3.339
5HMG	B_ARG_124	NH1	B_GLU_120	OE1	3.640
5HMG	B_ARG_124	NH1	F_GLU_132	OE1	3.424
5HMG	B_ARG_124	NH1	F_GLU_132	OE2	3.265
5HMG	B_ARG_124	NH2	B_GLU_120	OE1	3.919
5HMG	B_ARG_127	NH2	F_GLU_131	OE1	2.537
5HMG	B.LYS_143	NZ	B_ASP_145	OD1	2.698
5HMG	B_ARG_153	NH2	B_GLU_150	OE1	3.021
5HMG	B_HIS_159	NE2	B_ASP_160	OD2	3.062
5HMG	B_ARG_163	NH1	F_GLU_131	OE1	2.770
5HMG	B_ARG_163	NH1	F_GLU_131	OE2	2.532
5HMG	B_ARG_170	NH1	B_GLU_128	OE1	3.922
5HMG	B_ARG_170	NH1	B_GLU_131	OE2	3.597
5HMG	B_ARG_170	NH1	D_GLU_128	OE1	3.169
5HMG	B_ARG_170	NH1	D_GLU_128	OE2	3.597
5HMG	B_ARG_170	NH2	B_GLU_128	OE1	3.011
5HMG	C.LYS_27	NZ	D_GLU_97	OE1	2.934
5HMG	C.LYS_27	NZ	D_GLU_97	OE2	2.988
5HMG	C_HIS_56	ND1	C_ASP_85	OD2	3.578
5HMG	C_ARG_57	NH1	C_GLU_82	OE1	2.634
5HMG	C_ARG_57	NH1	C_GLU_82	OE2	3.752
5HMG	C_HIS_75	ND1	C_ASP_73	OD1	3.515
5HMG	C_HIS_75	ND1	C_ASP_73	OD2	2.678
5HMG	C_HIS_75	NE2	C_ASP_63	OD1	3.699
5HMG	C_ARG_90	NH1	C_ASP_60	OD1	2.783
5HMG	C_ARG_90	NH1	C_ASP_60	OD2	3.521
5HMG	C_ARG_109	NH1	D_GLU_67	OE1	2.853
5HMG	C_ARG_109	NH1	D_GLU_67	OE2	3.184
5HMG	C_ARG_109	NH2	C_GLU_89	OE1	2.925
5HMG	C_ARG_109	NH2	C_GLU_89	OE2	2.571
5HMG	C_ARG_141	NH1	C_ASP_77	OD1	3.417
5HMG	C_ARG_141	NH1	C_ASP_77	OD2	3.195
5HMG	C_ARG_141	NH2	C_ASP_77	OD1	2.635
5HMG	C_ARG_141	NH2	C_ASP_77	OD2	2.953
5HMG	C.LYS_176	NZ	C_GLU_123	OE1	2.578
5HMG	C.LYS_176	NZ	C_GLU_123	OE2	3.604
5HMG	C_HIS_183	NE2	C_GLU_190	OE1	3.762
5HMG	C_ARG_207	NH2	C_ASP_241	OD1	3.485
5HMG	C_ARG_261	NH1	C_GLU_119	OE1	3.007

5HMG	C_ARG_261	NH1	C_GLU_119	OE2	3.058
5HMG	C_ARG_261	NH2	C_GLU_119	OE1	2.812
5HMG	C_ARG_261	NH2	C_GLU_119	OE2	2.915
5HMG	C_LYS_264	NZ	C_ASP_85	OD1	3.974
5HMG	C_LYS_264	NZ	C_ASP_85	OD2	2.709
5HMG	C_ARG_269	NH1	D_GLU_67	OE1	3.552
5HMG	C_ARG_269	NH2	D_GLU_67	OE1	3.173
5HMG	C_LYS_292	NZ	C_ASP_291	OD1	2.561
5HMG	C_LYS_299	NZ	D_GLU_69	OE1	3.348
5HMG	C_LYS_310	NZ	D_ASP_86	OD1	3.449
5HMG	C_LYS_310	NZ	D_ASP_90	OD1	2.638
5HMG	C_LYS_315	NZ	C_GLU_41	OE2	2.755
5HMG	D_LYS_51	NZ	D_GLU_103	OE2	2.776
5HMG	D_ARG_54	NH1	B_GLU_97	OE1	2.819
5HMG	D_ARG_54	NH2	B_GLU_97	OE1	2.943
5HMG	D_ARG_54	NH2	D_GLU_57	OE2	3.747
5HMG	D_LYS_58	NZ	B_GLU_97	OE1	3.646
5HMG	D_LYS_58	NZ	B_GLU_97	OE2	3.528
5HMG	D_LYS_58	NZ	D_GLU_57	OE1	3.109
5HMG	D_LYS_58	NZ	D_GLU_57	OE2	3.568
5HMG	D_LYS_62	NZ	B_ASP_86	OD1	3.110
5HMG	D_LYS_62	NZ	B_ASP_86	OD2	2.718
5HMG	D_LYS_62	NZ	B_ASP_90	OD1	3.686
5HMG	D_LYS_62	NZ	B_ASP_90	OD2	2.685
5HMG	D_HIS_64	NE2	B_ASP_79	OD2	3.446
5HMG	D_LYS_68	NZ	D_GLU_85	OE1	3.418
5HMG	D_LYS_68	NZ	D_GLU_85	OE2	2.785
5HMG	D_ARG_76	NH1	F_GLU_74	OE1	3.349
5HMG	D_ARG_76	NH1	F_GLU_74	OE2	2.805
5HMG	D_ARG_76	NH1	F_GLU_81	OE1	2.685
5HMG	D_ARG_76	NH1	F_GLU_81	OE2	3.513
5HMG	D_ARG_76	NH2	F_GLU_74	OE1	2.710
5HMG	D_ARG_76	NH2	F_GLU_74	OE2	3.478
5HMG	D_LYS_117	NZ	D_GLU_114	OE1	2.687
5HMG	D_LYS_117	NZ	D_GLU_114	OE2	3.495
5HMG	D_ARG_123	NH1	B_GLU_132	OE2	2.981
5HMG	D_ARG_123	NH1	D_GLU_120	OE1	3.874
5HMG	D_ARG_123	NH2	D_GLU_120	OE1	2.616
5HMG	D_ARG_123	NH2	D_GLU_120	OE2	3.345
5HMG	D_ARG_124	NH1	B_GLU_132	OE1	3.466
5HMG	D_ARG_124	NH1	B_GLU_132	OE2	3.303
5HMG	D_ARG_124	NH1	D_GLU_120	OE1	3.636
5HMG	D_ARG_124	NH2	D_GLU_120	OE1	3.931
5HMG	D_ARG_127	NH2	B_GLU_131	OE1	2.578
5HMG	D_LYS_143	NZ	D_ASP_145	OD1	2.713
5HMG	D_ARG_153	NH2	D_GLU_150	OE1	2.620
5HMG	D_HIS_159	NE2	D_ASP_160	OD2	3.088
5HMG	D_ARG_163	NH1	B_GLU_131	OE1	2.694
5HMG	D_ARG_163	NH1	B_GLU_131	OE2	2.571
5HMG	D_ARG_170	NH1	D_GLU_128	OE1	3.949
5HMG	D_ARG_170	NH1	D_GLU_131	OE2	3.612
5HMG	D_ARG_170	NH1	F_GLU_128	OE1	3.252
5HMG	D_ARG_170	NH1	F_GLU_128	OE2	3.705
5HMG	D_ARG_170	NH2	D_GLU_128	OE1	3.068
5HMG	E_LYS_27	NZ	F_GLU_97	OE1	2.935
5HMG	E_LYS_27	NZ	F_GLU_97	OE2	3.012
5HMG	E_HIS_56	ND1	E_ASP_85	OD2	3.574
5HMG	E_ARG_57	NH1	E_GLU_82	OE1	2.672

5HMG	E_ARG_57	NH1	E_GLU_82	OE2	3.760
5HMG	E_HIS_75	ND1	E_ASP_73	OD1	3.480
5HMG	E_HIS_75	ND1	E_ASP_73	OD2	2.665
5HMG	E_HIS_75	NE2	E_ASP_63	OD1	3.721
5HMG	E_ARG_90	NH1	E_ASP_60	OD1	2.808
5HMG	E_ARG_90	NH1	E_ASP_60	OD2	3.495
5HMG	E_ARG_109	NH1	F_GLU_67	OE1	2.825
5HMG	E_ARG_109	NH1	F_GLU_67	OE2	3.180
5HMG	E_ARG_109	NH2	E_GLU_89	OE1	2.931
5HMG	E_ARG_109	NH2	E_GLU_89	OE2	2.544
5HMG	E_ARG_141	NH1	E_ASP_77	OD1	3.401
5HMG	E_ARG_141	NH1	E_ASP_77	OD2	3.198
5HMG	E_ARG_141	NH2	E_ASP_77	OD1	2.626
5HMG	E_ARG_141	NH2	E_ASP_77	OD2	2.960
5HMG	E_LYS_176	NZ	E_GLU_123	OE1	2.587
5HMG	E_LYS_176	NZ	E_GLU_123	OE2	3.609
5HMG	E_HIS_183	NE2	E_GLU_190	OE1	3.758
5HMG	E_ARG_207	NH2	E_ASP_241	OD1	3.508
5HMG	E_ARG_261	NH1	E_GLU_119	OE1	2.998
5HMG	E_ARG_261	NH1	E_GLU_119	OE2	3.065
5HMG	E_ARG_261	NH2	E_GLU_119	OE1	2.789
5HMG	E_ARG_261	NH2	E_GLU_119	OE2	2.904
5HMG	E_LYS_264	NZ	E_ASP_85	OD1	3.978
5HMG	E_LYS_264	NZ	E_ASP_85	OD2	2.713
5HMG	E_ARG_269	NH1	F_GLU_67	OE1	3.584
5HMG	E_ARG_269	NH2	F_GLU_67	OE1	3.233
5HMG	E_LYS_292	NZ	E_ASP_291	OD1	2.537
5HMG	E_LYS_299	NZ	F_GLU_69	OE1	3.318
5HMG	E_LYS_310	NZ	F_ASP_86	OD1	3.440
5HMG	E_LYS_310	NZ	F_ASP_90	OD1	2.621
5HMG	E_LYS_315	NZ	E_GLU_41	OE2	2.747
5HMG	F_LYS_51	NZ	F_GLU_103	OE2	2.774
5HMG	F_ARG_54	NH1	D_GLU_97	OE1	2.726
5HMG	F_ARG_54	NH2	D_GLU_97	OE1	2.912
5HMG	F_ARG_54	NH2	F_GLU_57	OE2	3.744
5HMG	F_LYS_58	NZ	D_GLU_97	OE1	3.765
5HMG	F_LYS_58	NZ	D_GLU_97	OE2	3.593
5HMG	F_LYS_58	NZ	F_GLU_57	OE1	3.108
5HMG	F_LYS_58	NZ	F_GLU_57	OE2	3.569
5HMG	F_LYS_62	NZ	D_ASP_86	OD1	3.013
5HMG	F_LYS_62	NZ	D_ASP_86	OD2	2.694
5HMG	F_LYS_62	NZ	D_ASP_90	OD1	3.718
5HMG	F_LYS_62	NZ	D_ASP_90	OD2	2.750
5HMG	F_HIS_64	NE2	D_ASP_79	OD1	3.885
5HMG	F_HIS_64	NE2	D_ASP_79	OD2	3.364
5HMG	F_LYS_68	NZ	F_GLU_85	OE1	3.382
5HMG	F_LYS_68	NZ	F_GLU_85	OE2	2.722
5HMG	F_ARG_76	NH1	B_GLU_74	OE1	3.251
5HMG	F_ARG_76	NH1	B_GLU_74	OE2	2.826
5HMG	F_ARG_76	NH1	B_GLU_81	OE1	2.735
5HMG	F_ARG_76	NH1	B_GLU_81	OE2	3.601
5HMG	F_ARG_76	NH2	B_GLU_74	OE1	2.649
5HMG	F_ARG_76	NH2	B_GLU_74	OE2	3.569
5HMG	F_LYS_117	NZ	F_GLU_114	OE1	2.666
5HMG	F_LYS_117	NZ	F_GLU_114	OE2	3.516
5HMG	F_ARG_123	NH1	D_GLU_132	OE2	2.992
5HMG	F_ARG_123	NH1	F_GLU_120	OE1	3.906
5HMG	F_ARG_123	NH2	F_GLU_120	OE1	2.639

5HMG	F_ARG.123	NH2	F_GLU.120	OE2	3.377
5HMG	F_ARG.124	NH1	D_GLU.132	OE1	3.514
5HMG	F_ARG.124	NH1	D_GLU.132	OE2	3.395
5HMG	F_ARG.124	NH1	F_GLU.120	OE1	3.630
5HMG	F_ARG.124	NH2	F_GLU.120	OE1	3.883
5HMG	F_ARG.127	NH2	D_GLU.131	OE1	2.609
5HMG	F_LYS.143	NZ	F_ASP.145	OD1	2.695
5HMG	F_HIS.159	NE2	F_ASP.160	OD2	3.088
5HMG	F_ARG.163	NH1	D_GLU.131	OE1	2.712
5HMG	F_ARG.163	NH1	D_GLU.131	OE2	2.596
5HMG	F_ARG.170	NH1	B_GLU.128	OE1	3.210
5HMG	F_ARG.170	NH1	B_GLU.128	OE2	3.530
5HMG	F_ARG.170	NH1	F_GLU.128	OE1	3.950
5HMG	F_ARG.170	NH1	F_GLU.131	OE2	3.600
5HMG	F_ARG.170	NH2	F_GLU.128	OE1	3.064
5I4F	A_LYS.64	NZ	A_GLU.47	OE2	2.666
5I4F	A_LYS.68	NZ	A_ASP.91	OD1	3.548
5I4F	A_LYS.68	NZ	A_ASP.91	OD2	2.948
5I4F	A_ARG.99	NH2	A_ASP.108	OD1	3.501
5I4F	A_ARG.99	NH2	A_ASP.108	OD2	2.781
5I4F	A_ARG.198	NH2	A_ASP.204	OD1	3.850
5I4F	A_ARG.205	NH1	A_GLU.223	OE2	3.321
5I4F	A_ARG.205	NH2	A_GLU.223	OE1	3.768
5I4F	A_ARG.205	NH2	A_GLU.223	OE2	3.756
5I4F	A_ARG.205	NH2	A_GLU.225	OE2	2.829
5I4F	A_ARG.205	NH2	A_ASP.226	OD1	2.710
5I4F	A_ARG.205	NH2	A_ASP.226	OD2	3.577
5I76	A_ARG.24	NH1	A_ASP.70	OD2	3.774
5I76	A_LYS.49	NZ	A_GLU.53	OE1	2.941
5I76	A_LYS.49	NZ	B_GLU.105	OE1	3.995
5I76	A_ARG.61	NH1	A_GLU.79	OE2	3.393
5I76	A_ARG.61	NH1	A_GLU.81	OE2	3.803
5I76	A_ARG.61	NH2	A_GLU.79	OE2	3.760
5I76	A_ARG.61	NH2	A_GLU.81	OE2	2.766
5I76	A_ARG.61	NH2	A_ASP.82	OD1	2.773
5I76	A_ARG.61	NH2	A_ASP.82	OD2	3.589
5I76	A_LYS.103	NZ	A_GLU.165	OE1	3.841
5I76	A_LYS.145	NZ	A_GLU.143	OE1	3.548
5I76	A_LYS.145	NZ	A_GLU.143	OE2	2.870
5I76	A_LYS.149	NZ	A_GLU.195	OE1	2.637
5I76	A_HIS.189	ND1	A_ASP.151	OD2	3.111
5I76	A_HIS.189	NE2	A_ASP.185	OD1	3.124
5I76	B_ARG.38	NH1	B_ASP.89	OD1	2.810
5I76	B_ARG.38	NH2	B_GLU.46	OE1	3.124
5I76	B_ARG.38	NH2	B_ASP.89	OD1	3.773
5I76	B_ARG.66	NH1	B_ASP.89	OD1	3.709
5I76	B_ARG.66	NH1	B_ASP.89	OD2	2.960
5I76	B_ARG.66	NH2	B_ASP.89	OD1	2.836
5I76	B_ARG.66	NH2	B_ASP.89	OD2	3.415
5I76	B_LYS.149	NZ	B_ASP.150	OD1	3.571
5I76	B_LYS.215	NZ	A_GLU.123	OE1	2.731
5I76	B_LYS.215	NZ	A_GLU.123	OE2	2.888
5I76	B_ARG.216	NH2	B_GLU.218	OE1	2.687
5I76	B_LYS.220	NZ	A_ASP.122	OD2	3.474
5I76	C_ARG.24	NH1	A_ASP.70	OD1	3.725
5I76	C_ARG.24	NH1	A_ASP.70	OD2	2.949
5I76	C_ARG.24	NH1	C_ASP.70	OD1	3.422
5I76	C_ARG.24	NH2	A_ASP.70	OD1	3.138

5I76	C_ARG_24	NH2	A_ASP_70	OD2	3.394
5I76	C_LYS_49	NZ	C_GLU_53	OE1	2.642
5I76	C_ARG_61	NH1	C_GLU_79	OE2	3.544
5I76	C_ARG_61	NH1	C_GLU_81	OE2	3.961
5I76	C_ARG_61	NH2	C_GLU_79	OE2	3.781
5I76	C_ARG_61	NH2	C_GLU_81	OE2	2.825
5I76	C_ARG_61	NH2	C_ASP_82	OD1	2.761
5I76	C_ARG_61	NH2	C_ASP_82	OD2	3.560
5I76	C_LYS_103	NZ	C_ASP_85	OD1	3.711
5I76	C_LYS_103	NZ	C_ASP_85	OD2	3.969
5I76	C_LYS_103	NZ	C_GLU_165	OE1	3.241
5I76	C_LYS_103	NZ	C_GLU_165	OE2	3.658
5I76	C_LYS_149	NZ	C_GLU_195	OE1	2.493
5I76	C_LYS_183	NZ	C_GLU_187	OE1	3.091
5I76	C_LYS_183	NZ	C_GLU_187	OE2	3.350
5I76	C_HIS_189	ND1	C_ASP_151	OD2	2.352
5I76	D_ARG_38	NH1	D_ASP_89	OD1	2.883
5I76	D_ARG_38	NH2	D_GLU_46	OE1	3.400
5I76	D_ARG_38	NH2	D_ASP_89	OD1	3.880
5I76	D_ARG_66	NH1	D_ASP_89	OD1	3.587
5I76	D_ARG_66	NH1	D_ASP_89	OD2	2.851
5I76	D_ARG_66	NH2	D_ASP_89	OD1	2.736
5I76	D_ARG_66	NH2	D_ASP_89	OD2	3.459
5I76	D_LYS_149	NZ	D_ASP_150	OD1	2.862
5I76	D_LYS_149	NZ	D_ASP_150	OD2	2.853
5I76	D_LYS_215	NZ	C_GLU_123	OE1	2.596
5I76	D_LYS_215	NZ	C_GLU_123	OE2	3.738
5IHL	A_HIS_78	NE2	A_ASP_69	OD1	3.151
5IHL	A_HIS_78	NE2	A_GLU_74	OE1	3.112
5IHL	A_HIS_78	NE2	A_GLU_74	OE2	3.476
5IHL	A_LYS_81	NZ	A_ASP_100	OD2	3.844
5IHL	A_ARG_123	NH1	A_ASP_140	OD2	3.023
5IHL	A_ARG_123	NH2	A_ASP_140	OD2	3.466
5IHL	A_LYS_132	NZ	A_GLU_144	OE2	3.445
5IHL	B_ARG_38	NH1	B_GLU_46	OE2	3.444
5IHL	B_ARG_38	NH1	B_ASP_86	OD1	3.975
5IHL	B_ARG_38	NH2	B_ASP_86	OD1	3.323
5IHL	B_ARG_66	NH1	B_ASP_86	OD1	3.298
5IHL	B_ARG_66	NH1	B_ASP_86	OD2	2.656
5IHL	B_ARG_66	NH2	B_ASP_86	OD1	3.517
5IHL	D_HIS_78	NE2	D_ASP_69	OD1	3.189
5IHL	D_HIS_78	NE2	D_GLU_74	OE1	3.120
5IHL	D_HIS_78	NE2	D_GLU_74	OE2	3.496
5IHL	D_ARG_123	NH2	D_ASP_140	OD2	3.433
5IHL	D_HIS_162	NE2	D_GLU_159	OE1	3.297
5IHL	E_ARG_38	NH1	E_ASP_86	OD1	3.969
5IHL	E_ARG_38	NH2	E_ASP_86	OD1	3.308
5IHL	E_ARG_66	NH1	E_ASP_86	OD1	3.287
5IHL	E_ARG_66	NH1	E_ASP_86	OD2	2.657
5IHL	E_ARG_66	NH2	E_ASP_86	OD1	3.504
5IHL	F_HIS_78	ND1	F_ASP_69	OD1	3.127
5IHL	F_HIS_78	NE2	F_GLU_74	OE1	3.224
5IHL	F_HIS_110	ND1	F_ASP_140	OD1	3.789
5IHL	F_HIS_110	ND1	F_ASP_140	OD2	2.873
5IHL	F_ARG_123	NH1	F_ASP_140	OD2	3.408
5IHL	F_HIS_162	NE2	F_GLU_159	OE1	2.954
5IHL	G_ARG_38	NH1	G_GLU_46	OE1	3.917
5IHL	G_ARG_38	NH1	G_GLU_46	OE2	3.596

5IHL	G_ARG_38	NH1	G_ASP_86	OD1	3.962
5IHL	G_ARG_38	NH2	G_ASP_86	OD1	3.314
5IHL	G_ARG_66	NH1	G_ASP_86	OD1	3.297
5IHL	G_ARG_66	NH1	G_ASP_86	OD2	2.675
5IHL	G_ARG_66	NH2	G_ASP_86	OD1	3.505
5IHL	H_LYS_29	NZ	H_GLU_28	OE1	3.389
5IHL	H_HIS_78	NE2	H_ASP_69	OD1	3.188
5IHL	H_HIS_78	NE2	H_GLU_74	OE1	3.148
5IHL	H_HIS_78	NE2	H_GLU_74	OE2	3.496
5IHL	L_ARG_38	NH1	L_GLU_46	OE1	3.944
5IHL	L_ARG_38	NH1	L_GLU_46	OE2	3.555
5IHL	L_ARG_38	NH1	L_ASP_86	OD1	3.950
5IHL	L_ARG_38	NH2	L_ASP_86	OD1	3.321
5IHL	L_ARG_66	NH1	L_ASP_86	OD1	3.272
5IHL	L_ARG_66	NH1	L_ASP_86	OD2	2.644
5IHL	L_ARG_66	NH2	L_ASP_86	OD1	3.520
5ITB	H_ARG_43	NH1	H_ASP_98	OD1	2.808
5ITB	H_ARG_43	NH2	H_GLU_51	OE1	2.922
5ITB	H_ARG_43	NH2	H_GLU_51	OE2	3.615
5ITB	H_ARG_43	NH2	H_ASP_98	OD1	3.996
5ITB	H_ARG_75	NH1	H_ASP_98	OD1	3.710
5ITB	H_ARG_75	NH1	H_ASP_98	OD2	2.943
5ITB	H_ARG_75	NH2	H_ASP_98	OD1	3.077
5ITB	H_ARG_75	NH2	H_ASP_98	OD2	3.700
5ITB	H_ARG_107	NH1	H_ASP_114	OD1	3.122
5ITB	H_ARG_111	NH1	L_GLU_68	OE1	3.426
5ITB	H_ARG_111	NH2	H_ASP_114	OD2	2.687
5ITB	H_ARG_111	NH2	H_ASP_116	OD2	3.548
5ITB	H_ARG_111	NH2	L_GLU_68	OE1	2.856
5ITB	H_LYS_224	NZ	L_GLU_143	OE1	3.323
5ITB	H_LYS_224	NZ	L_GLU_143	OE2	2.099
5ITB	H_ARG_225	NH2	H_GLU_227	OE2	3.950
5ITB	L_LYS_45	NZ	L_ASP_97	OD1	3.221
5ITB	L_LYS_45	NZ	L_ASP_97	OD2	3.180
5ITB	L_ARG_75	NH2	L_ASP_98	OD1	2.991
5ITB	L_ARG_75	NH2	L_ASP_98	OD2	3.652
5ITB	L_LYS_203	NZ	L_GLU_207	OE1	3.111
5ITB	L_LYS_203	NZ	L_GLU_207	OE2	2.934
5ITB	L_HIS_209	ND1	L_ASP_171	OD2	3.207
5ITB	L_HIS_209	NE2	L_ASP_205	OD1	2.812
5ITB	L_HIS_209	NE2	L_ASP_205	OD2	3.009
5J3D	A_ARG_43	NH1	A_ASP_98	OD1	2.896
5J3D	A_ARG_43	NH2	A_GLU_51	OE1	2.997
5J3D	A_ARG_43	NH2	A_GLU_51	OE2	2.988
5J3D	A_ARG_75	NH1	A_ASP_98	OD1	3.601
5J3D	A_ARG_75	NH1	A_ASP_98	OD2	3.013
5J3D	A_ARG_75	NH2	A_ASP_98	OD1	3.254
5J3D	A_ARG_95	NH2	A_GLU_97	OE2	3.552
5J3D	A_ARG_107	NH1	A_ASP_114	OD1	3.567
5J3D	A_ARG_111	NH2	A_ASP_114	OD2	3.401
5J3D	A_ARG_111	NH2	B_GLU_68	OE1	3.664
5J3D	A_LYS_158	NZ	A_ASP_159	OD1	3.439
5J3D	A_LYS_158	NZ	A_ASP_159	OD2	3.508
5J3D	A_LYS_224	NZ	B_GLU_143	OE1	3.390
5J3D	A_LYS_229	NZ	B_ASP_142	OD1	3.902
5J3D	A_LYS_229	NZ	B_ASP_142	OD2	3.196
5J3D	B_LYS_45	NZ	B_ASP_97	OD1	3.783
5J3D	B_ARG_75	NH2	B_ASP_97	OD2	3.805

5J3D	B_LYS_123	NZ	B_GLU_185	OE2	3.379
5J3D	B_LYS_169	NZ	B_GLU_215	OE2	3.640
5J3D	B_LYS_203	NZ	B_GLU_207	OE2	2.374
5J3D	B_HIS_209	ND1	B_ASP_171	OD1	3.892
5J3D	B_HIS_209	ND1	B_ASP_171	OD2	2.212
5J3D	C_ARG_	NH1	C_ASP_	OD1	3.000
5J3D	C_ARG_	NH2	C_GLU_	OE1	3.686
5J3D	C_ARG_	NH2	C_ASP_	OD1	3.849
5J3D	C_ARG_	NH1	C_ASP_	OD1	3.639
5J3D	C_ARG_	NH1	C_ASP_	OD2	3.007
5J3D	C_ARG_	NH2	C_ASP_	OD1	3.160
5J3D	C_ARG_	NH2	C_ASP_	OD2	3.889
5J3D	C_ARG_107	NH1	C_ASP_114	OD1	2.971
5J3D	C_ARG_107	NH1	C_ASP_114	OD2	3.218
5J3D	C_ARG_111	NH2	C_ASP_114	OD2	3.073
5J3D	C_ARG_111	NH2	D_GLU_68	OE1	3.489
5J3D	C_LYS_	NZ	C_ASP_	OD1	3.508
5J3D	C_LYS_	NZ	C_ASP_	OD2	3.782
5J3D	C_LYS_	NZ	D_GLU_	OE1	3.377
5J3D	C_LYS_	NZ	D_ASP_	OD1	2.847
5J3D	C_LYS_	NZ	D_ASP_	OD2	2.791
5J3D	D_ARG_75	NH2	D_ASP_97	OD1	3.325
5J3D	D_LYS_	NZ	D_GLU_	OE1	3.275
5J3D	D_LYS_	NZ	D_GLU_	OE2	2.521
5J3D	D_LYS_	NZ	D_GLU_	OE1	3.944
5J3D	D_LYS_	NZ	D_GLU_	OE2	3.225
5J3D	D_HIS_	ND1	D_ASP_	OD2	2.270
5J3D	E_ARG_49	NH2	F_ASP_368	OD1	2.801
5J3D	E_ARG_49	NH2	F_ASP_368	OD2	3.628
5J3D	E_LYS_80	NZ	E_ASP_84	OD2	2.975
5J3D	E_LYS_85	NZ	E_GLU_82	OE1	3.904
5J3D	E_LYS_85	NZ	E_GLU_82	OE2	3.954
5J3D	F_LYS_	NZ	I_GLU_	OE2	3.850
5J3D	F_HIS_	NE2	F_GLU_	OE1	3.357
5J3D	F_LYS_191	NZ	F_ASP_194	OD2	3.179
5J3D	F_LYS_196	NZ	I_ASP_489	OD1	2.634
5J3D	F_LYS_196	NZ	I_ASP_489	OD2	3.067
5J3D	F_LYS_201	NZ	F_ASP_200	OD2	3.113
5J3D	F_ARG_229	NH1	F_GLU_256	OE1	3.268
5J3D	F_ARG_229	NH1	F_GLU_256	OE2	2.433
5J3D	F_ARG_229	NH2	F_GLU_256	OE1	2.288
5J3D	F_ARG_229	NH2	F_GLU_256	OE2	3.196
5J3D	F_ARG_235	NH1	I_GLU_232	OE1	3.071
5J3D	F_ARG_235	NH1	I_GLU_232	OE2	2.514
5J3D	F_ARG_235	NH2	F_GLU_232	OE2	3.966
5J3D	F_LYS_272	NZ	B_ASP_56	OD2	3.606
5J3D	F_LYS_293	NZ	F_GLU_295	OE2	3.714
5J3D	F_ARG_336	NH2	F_ASP_338	OD1	2.882
5J3D	F_ARG_336	NH2	F_ASP_338	OD2	3.428
5J3D	F_ARG_364	NH1	F_ASP_310	OD1	3.194
5J3D	F_ARG_364	NH2	F_ASP_310	OD1	2.918
5J3D	F_LYS_399	NZ	K_ASP_392	OD1	3.567
5J3D	F_LYS_470	NZ	J_GLU_60	OE1	3.190
5J3D	F_LYS_470	NZ	J_GLU_60	OE2	3.891
5J3D	G_ARG_49	NH2	I_ASP_368	OD1	3.151
5J3D	G_LYS_80	NZ	G_ASP_84	OD2	2.927
5J3D	G_LYS_85	NZ	G_GLU_82	OE2	3.889
5J3D	H_ARG_43	NH1	H_ASP_98	OD1	2.849

5J3D	H_ARG_43	NH2	H_GLU_51	OE1	3.608
5J3D	H_ARG_43	NH2	H_GLU_51	OE2	3.183
5J3D	H_ARG_43	NH2	H_ASP_98	OD1	3.954
5J3D	H_ARG_75	NH1	H_ASP_98	OD2	3.150
5J3D	H_ARG_75	NH2	H_ASP_98	OD1	3.434
5J3D	H_ARG_75	NH2	H_ASP_98	OD2	3.495
5J3D	H_ARG_107	NH1	H_ASP_114	OD1	3.119
5J3D	H_ARG_107	NH1	H_ASP_114	OD2	3.930
5J3D	H_ARG_111	NH2	H_ASP_114	OD2	2.954
5J3D	H_ARG_111	NH2	L_GLU_68	OE1	3.466
5J3D	H_LYS_158	NZ	H_ASP_159	OD1	3.555
5J3D	H_LYS_158	NZ	H_ASP_159	OD2	3.908
5J3D	H_LYS_224	NZ	L_GLU_143	OE1	3.364
5J3D	H_LYS_	NZ	L_ASP_	OD1	3.352
5J3D	H_LYS_	NZ	L_ASP_	OD2	3.692
5J3D	I_LYS_	NZ	K_GLU_	OE1	3.226
5J3D	I_LYS_	NZ	K_GLU_	OE2	3.914
5J3D	I_LYS_	NZ	L_GLU_	OE1	3.318
5J3D	I_LYS_191	NZ	L_ASP_194	OD2	3.257
5J3D	I_LYS_196	NZ	K_ASP_489	OD1	2.833
5J3D	I_LYS_196	NZ	K_ASP_489	OD2	3.027
5J3D	I_LYS_201	NZ	L_ASP_200	OD2	3.213
5J3D	I_ARG_229	NH1	L_GLU_256	OE1	3.887
5J3D	I_ARG_229	NH1	L_GLU_256	OE2	2.592
5J3D	I_ARG_229	NH2	L_GLU_256	OE1	2.607
5J3D	I_ARG_229	NH2	L_GLU_256	OE2	2.843
5J3D	I_ARG_235	NH1	K_GLU_232	OE1	3.110
5J3D	I_ARG_235	NH1	K_GLU_232	OE2	2.664
5J3D	I_LYS_272	NZ	D_ASP_56	OD2	3.795
5J3D	I_LYS_293	NZ	L_GLU_295	OE2	3.743
5J3D	I_ARG_336	NH2	L_ASP_338	OD1	3.080
5J3D	I_ARG_336	NH2	L_ASP_338	OD2	3.543
5J3D	I_ARG_364	NH1	L_ASP_310	OD1	3.192
5J3D	I_ARG_364	NH2	L_ASP_310	OD1	2.780
5J3D	I_LYS_399	NZ	F_ASP_392	OD1	3.746
5J3D	I_LYS_470	NZ	E_GLU_60	OE1	3.634
5J3D	I_LYS_470	NZ	E_GLU_60	OE2	3.872
5J3D	J_ARG_49	NH2	K_ASP_368	OD1	3.049
5J3D	J_ARG_49	NH2	K_ASP_368	OD2	3.898
5J3D	J_LYS_80	NZ	J_ASP_84	OD2	3.423
5J3D	J_LYS_85	NZ	J_GLU_82	OE1	3.982
5J3D	J_LYS_85	NZ	J_GLU_82	OE2	3.902
5J3D	J_LYS_87	NZ	K_GLU_294	OE1	3.791
5J3D	K_LYS_	NZ	F_GLU_	OE1	2.905
5J3D	K_LYS_	NZ	K_GLU_	OE1	3.429
5J3D	K_LYS_191	NZ	K_ASP_194	OD2	3.194
5J3D	K_LYS_196	NZ	F_ASP_489	OD1	2.822
5J3D	K_LYS_196	NZ	F_ASP_489	OD2	3.022
5J3D	K_LYS_201	NZ	K_ASP_200	OD2	2.845
5J3D	K_ARG_229	NH1	K_GLU_256	OE1	3.743
5J3D	K_ARG_229	NH1	K_GLU_256	OE2	2.813
5J3D	K_ARG_229	NH2	K_GLU_256	OE1	2.714
5J3D	K_ARG_229	NH2	K_GLU_256	OE2	3.345
5J3D	K_ARG_235	NH1	F_GLU_232	OE1	2.445
5J3D	K_ARG_235	NH1	F_GLU_232	OE2	2.683
5J3D	K_ARG_235	NH2	F_GLU_232	OE2	3.814
5J3D	K_ARG_235	NH2	K_GLU_232	OE2	3.561
5J3D	K_LYS_293	NZ	K_GLU_295	OE2	3.880

5J3D	K_ARG_336	NH2	K_ASP_338	OD1	2.871
5J3D	K_ARG_336	NH2	K_ASP_338	OD2	3.213
5J3D	K_LYS_359	NZ	K_GLU_356	OE2	3.629
5J3D	K_ARG_364	NH1	K_ASP_310	OD1	3.298
5J3D	K_ARG_364	NH2	K_ASP_310	OD1	2.637
5J3D	K_ARG_364	NH2	K_ASP_310	OD2	3.766
5J3D	K_LYS_399	NZ	L_ASP_392	OD1	3.598
5J3D	K_LYS_470	NZ	G_GLU_60	OE1	3.953
5J3D	L_ARG_75	NH2	L_ASP_97	OD2	3.011
5J3D	L_LYS_123	NZ	L_GLU_185	OE2	3.382
5J3D	L_LYS_169	NZ	L_GLU_215	OE2	3.052
5J3D	L_LYS_203	NZ	L_GLU_207	OE1	3.556
5J3D	L_LYS_203	NZ	L_GLU_207	OE2	2.397
5J3D	L_HIS_209	ND1	L_ASP_171	OD2	2.293
5JO5	H_ARG_38	NH1	H_ASP_86	OD1	2.872
5JO5	H_ARG_38	NH2	H_GLU_46	OE1	3.137
5JO5	H_ARG_38	NH2	H_ASP_86	OD1	3.899
5JO5	H_ARG_50	NH1	H_ASP_58	OD2	3.272
5JO5	H_ARG_50	NH1	H_GLU_100J	OE1	3.655
5JO5	H_ARG_50	NH1	H_GLU_100J	OE2	3.015
5JO5	H_ARG_50	NH2	H_ASP_58	OD2	2.837
5JO5	H_ARG_66	NH1	H_ASP_86	OD1	3.782
5JO5	H_ARG_66	NH1	H_ASP_86	OD2	2.781
5JO5	H_ARG_66	NH2	H_ASP_86	OD1	3.036
5JO5	H_ARG_66	NH2	H_ASP_86	OD2	3.534
5JO5	H_ARG_71	NH2	H_ASP_73	OD1	3.590
5JO5	H_LYS_75	NZ	H_ASP_72	OD2	3.855
5JO5	H_ARG_94	NH1	H_ASP_102	OD2	2.698
5JO5	H_LYS_143	NZ	L_GLU_124	OE2	2.459
5JO5	H_LYS_206	NZ	H_ASP_208	OD1	3.914
5JO5	H_LYS_206	NZ	H_ASP_208	OD2	3.240
5JO5	H_LYS_209	NZ	L_GLU_	OE2	2.531
5JO5	L_ARG_61	NH2	L_GLU_81	OE2	2.979
5JO5	L_ARG_61	NH2	L_ASP_82	OD1	2.750
5JO5	L_ARG_61	NH2	L_ASP_82	OD2	3.466
5JO5	L_ARG_91	NH1	H_GLU_100J	OE2	3.301
5JO5	L_ARG_91	NH2	H_GLU_100J	OE2	2.691
5JO5	L_ARG_95B	NH2	H_ASP_58	OD1	3.439
5JO5	L_LYS_110	NZ	L_GLU_198	OE1	2.940
5JO5	L_LYS_149	NZ	L_GLU_203	OE2	3.049
5JO5	A_ARG_38	NH1	A_ASP_86	OD1	2.834
5JO5	A_ARG_38	NH2	A_GLU_46	OE1	3.010
5JO5	A_ARG_38	NH2	A_ASP_86	OD1	3.868
5JO5	A_ARG_50	NH1	A_ASP_58	OD2	3.242
5JO5	A_ARG_50	NH1	A_GLU_100J	OE1	3.684
5JO5	A_ARG_50	NH1	A_GLU_100J	OE2	2.906
5JO5	A_ARG_50	NH2	A_ASP_58	OD2	2.882
5JO5	A_ARG_66	NH1	A_ASP_86	OD1	3.892
5JO5	A_ARG_66	NH1	A_ASP_86	OD2	2.803
5JO5	A_ARG_66	NH2	A_ASP_86	OD1	3.001
5JO5	A_ARG_66	NH2	A_ASP_86	OD2	3.402
5JO5	A_ARG_71	NH2	A_ASP_73	OD1	3.562
5JO5	A_ARG_94	NH1	A_ASP_102	OD2	2.584
5JO5	A_LYS_143	NZ	B_GLU_124	OE2	2.618
5JO5	A_LYS_209	NZ	B_GLU_123	OE2	2.545
5JO5	A_ARG_210	NH1	A_GLU_212	OE2	3.723
5JO5	A_ARG_210	NH2	A_GLU_212	OE2	3.222
5JO5	B_ARG_61	NH2	B_GLU_81	OE2	3.302

5JO5	B_ARG_61	NH2	B_ASP_82	OD1	2.664
5JO5	B_ARG_61	NH2	B_ASP_82	OD2	3.454
5JO5	B_ARG_91	NH1	A_GLU_100J	OE2	3.353
5JO5	B_ARG_91	NH2	A_GLU_100J	OE2	3.038
5JO5	C_ARG_38	NH1	C_ASP_86	OD1	2.847
5JO5	C_ARG_38	NH2	C_GLU_46	OE1	3.028
5JO5	C_ARG_38	NH2	C_ASP_86	OD1	3.875
5JO5	C_ARG_50	NH1	C_ASP_58	OD2	2.775
5JO5	C_ARG_50	NH2	C_ASP_58	OD2	3.216
5JO5	C_ARG_50	NH2	C_GLU_100J	OE1	3.640
5JO5	C_ARG_50	NH2	C_GLU_100J	OE2	2.862
5JO5	C_ARG_66	NH1	C_ASP_86	OD1	3.889
5JO5	C_ARG_66	NH1	C_ASP_86	OD2	2.829
5JO5	C_ARG_66	NH2	C_ASP_86	OD1	3.094
5JO5	C_ARG_66	NH2	C_ASP_86	OD2	3.488
5JO5	C_ARG_71	NH2	C_ASP_73	OD1	3.622
5JO5	C_ARG_94	NH1	C_ASP_102	OD2	2.554
5JO5	C_LYS_143	NZ	D_GLU_124	OE2	2.788
5JO5	C_LYS_209	NZ	D_GLU_123	OE2	2.583
5JO5	C_ARG_	NH1	C_GLU_	OE2	2.988
5JO5	D_ARG_61	NH2	D_ASP_82	OD1	2.885
5JO5	D_ARG_61	NH2	D_ASP_82	OD2	3.652
5JO5	D_ARG_91	NH1	C_GLU_100J	OE2	3.302
5JO5	D_ARG_91	NH2	C_GLU_100J	OE2	3.077
5JO5	D_LYS_93	NZ	D_GLU_3	OE2	3.062
5JO5	D_ARG_95B	NH2	C_ASP_58	OD1	3.978
5JO5	D_LYS_149	NZ	D_GLU_203	OE2	2.721
5JO5	D_HIS_188	ND1	D_ASP_151	OD2	2.674
5JO5	E_ARG_38	NH1	E_ASP_86	OD1	2.821
5JO5	E_ARG_38	NH2	E_GLU_46	OE1	3.015
5JO5	E_ARG_38	NH2	E_GLU_46	OE2	3.976
5JO5	E_ARG_38	NH2	E_ASP_86	OD1	3.922
5JO5	E_ARG_50	NH1	E_ASP_58	OD2	2.782
5JO5	E_ARG_50	NH2	E_ASP_58	OD2	3.264
5JO5	E_ARG_50	NH2	E_GLU_100J	OE1	3.626
5JO5	E_ARG_50	NH2	E_GLU_100J	OE2	2.982
5JO5	E_ARG_66	NH1	E_ASP_86	OD1	3.801
5JO5	E_ARG_66	NH1	E_ASP_86	OD2	2.750
5JO5	E_ARG_66	NH2	E_ASP_86	OD1	3.037
5JO5	E_ARG_66	NH2	E_ASP_86	OD2	3.493
5JO5	E_ARG_71	NH2	E_ASP_73	OD1	3.535
5JO5	E_LYS_75	NZ	E_ASP_72	OD2	3.717
5JO5	E_ARG_94	NH2	E_ASP_102	OD2	2.730
5JO5	E_LYS_143	NZ	F_GLU_124	OE2	2.545
5JO5	E_LYS_209	NZ	F_GLU_123	OE2	2.567
5JO5	E_ARG_210	NH1	E_GLU_212	OE2	3.744
5JO5	E_ARG_210	NH2	E_GLU_212	OE2	3.125
5JO5	F_ARG_54	NH1	F_ASP_60	OD1	2.423
5JO5	F_ARG_61	NH2	F_GLU_81	OE2	3.010
5JO5	F_ARG_61	NH2	F_ASP_82	OD1	2.807
5JO5	F_ARG_61	NH2	F_ASP_82	OD2	3.560
5JO5	F_ARG_91	NH1	E_GLU_100J	OE2	3.369
5JO5	F_ARG_91	NH2	E_GLU_100J	OE2	2.722
5JO5	F_ARG_95B	NH2	E_ASP_58	OD1	3.518
5JO5	F_LYS_110	NZ	F_GLU_198	OE1	2.973
5JOF	H_LYS_12	NZ	H_GLU_10	OE1	3.976
5JOF	H_ARG_38	NH1	H_ASP_86	OD1	2.816
5JOF	H_ARG_38	NH2	H_GLU_46	OE1	2.389

5JOF	H_ARG_38	NH2	H_GLU_46	OE2	3.859
5JOF	H_LYS_62	NZ	H_GLU_46	OE2	2.776
5JOF	H_ARG_66	NH1	H_ASP_86	OD2	2.820
5JOF	H_ARG_66	NH2	H_ASP_86	OD1	3.127
5JOF	H_ARG_66	NH2	H_ASP_86	OD2	3.314
5JOF	H_LYS_212	NZ	L_GLU_123	OE2	3.883
5JOF	H_LYS_213	NZ	H_GLU_215	OE1	3.500
5JOF	H_LYS_217	NZ	L_ASP_122	OD2	3.165
5JOF	L_ARG_54	NH1	L_ASP_60	OD1	3.764
5JOF	L_ARG_61	NH2	L_GLU_81	OE2	3.643
5JOF	L_ARG_61	NH2	L_ASP_82	OD1	3.848
5JOF	L_ARG_61	NH2	L_ASP_82	OD2	3.642
5JOF	L_ARG_142	NH1	L_GLU_103	OE1	3.845
5JOF	L_ARG_142	NH1	L_GLU_105	OE2	3.937
5JOF	L_ARG_142	NH2	L_GLU_103	OE1	3.654
5JOF	L_ARG_142	NH2	L_GLU_103	OE2	2.697
5JOF	L_ARG_142	NH2	L_GLU_105	OE2	3.736
5JOF	L_LYS_149	NZ	L_GLU_195	OE1	3.071
5JOF	A_LYS_12	NZ	A_GLU_10	OE1	3.516
5JOF	A_HIS_35	NE2	A_ASP_100C	OD1	2.627
5JOF	A_ARG_38	NH1	A_GLU_46	OE1	3.912
5JOF	A_ARG_38	NH1	A_ASP_86	OD1	3.722
5JOF	A_ARG_38	NH2	A_ASP_86	OD1	2.667
5JOF	A_ARG_66	NH1	A_ASP_86	OD1	2.903
5JOF	A_ARG_66	NH1	A_ASP_86	OD2	2.899
5JOF	A_ARG_83	NH2	A_ASP_85	OD2	3.607
5JOF	A_LYS_143	NZ	A_ASP_144	OD1	3.485
5JOF	A_LYS_209	NZ	B_GLU_123	OE1	3.449
5JOF	A_LYS_209	NZ	B_GLU_123	OE2	3.809
5JOF	B_ARG_24	NH1	C_ASP_99	OD1	2.692
5JOF	B_ARG_24	NH1	C_ASP_99	OD2	3.960
5JOF	B_ARG_61	NH2	B_GLU_81	OE2	3.500
5JOF	B_ARG_61	NH2	B_ASP_82	OD1	3.535
5JOF	B_ARG_61	NH2	B_ASP_82	OD2	3.507
5JOF	B_ARG_77	NH1	B_GLU_79	OE1	3.191
5JOF	B_ARG_77	NH1	B_GLU_79	OE2	3.717
5JOF	B_HIS_189	ND1	B_ASP_151	OD2	2.926
5JOF	C_LYS_12	NZ	C_GLU_10	OE1	3.233
5JOF	C_HIS_35	NE2	C_ASP_100C	OD1	2.684
5JOF	C_ARG_38	NH1	C_ASP_86	OD1	3.621
5JOF	C_ARG_38	NH2	C_GLU_46	OE1	3.694
5JOF	C_ARG_38	NH2	C_ASP_86	OD1	3.344
5JOF	C_LYS_62	NZ	C_GLU_46	OE1	3.985
5JOF	C_LYS_62	NZ	C_GLU_46	OE2	3.097
5JOF	C_ARG_66	NH1	C_ASP_86	OD1	3.730
5JOF	C_ARG_66	NH1	C_ASP_86	OD2	2.579
5JOF	C_ARG_94	NH1	B_GLU_1	OE2	2.653
5JOF	C_ARG_94	NH2	B_GLU_1	OE2	3.195
5JOF	C_LYS_210	NZ	C_GLU_212	OE1	3.967
5JOF	C_LYS_214	NZ	D_ASP_122	OD2	3.772
5JOF	C_LYS_214	NZ	D_GLU_123	OE1	2.987
5JOF	C_LYS_214	NZ	D_GLU_123	OE2	3.631
5JOF	D_ARG_24	NH2	D_ASP_70	OD2	3.929
5JOF	D_LYS_39	NZ	D_GLU_81	OE2	3.210
5JOF	D_ARG_54	NH1	D_ASP_60	OD1	3.417
5JOF	D_ARG_54	NH2	D_ASP_60	OD1	2.714
5JOF	D_ARG_61	NH1	D_GLU_79	OE1	3.968
5JOF	D_ARG_61	NH2	D_GLU_79	OE1	3.623

5JOF	D_ARG_61	NH2	D_ASP_82	OD1	3.619
5JOF	D_LYS_149	NZ	D_GLU_195	OE1	3.879
5JOF	D_LYS_183	NZ	D_GLU_187	OE1	3.559
5JOF	D_ARG_211	NH2	D_GLU_187	OE2	3.871
5JOF	E_HIS_35	NE2	E_ASP_100C	OD1	3.045
5JOF	E_ARG_38	NH1	E_ASP_86	OD1	2.429
5JOF	E_ARG_38	NH2	E_GLU_46	OE1	3.439
5JOF	E_ARG_38	NH2	E_ASP_86	OD1	3.968
5JOF	E_LYS_62	NZ	E_GLU_46	OE1	3.849
5JOF	E_LYS_62	NZ	E_GLU_46	OE2	3.146
5JOF	E_ARG_66	NH1	E_ASP_86	OD1	3.702
5JOF	E_ARG_66	NH1	E_ASP_86	OD2	2.671
5JOF	E_LYS_209	NZ	F_GLU_123	OE1	2.331
5JOF	E_LYS_209	NZ	F_GLU_123	OE2	3.588
5JOF	E_LYS_214	NZ	F_ASP_122	OD2	3.802
5JOF	F_ARG_54	NH1	F_ASP_60	OD1	2.591
5JOF	F_ARG_61	NH1	F_ASP_82	OD1	2.348
5JOF	F_ARG_61	NH1	F_ASP_82	OD2	1.974
5JOF	F_ARG_61	NH2	F_ASP_82	OD1	3.989
5JOF	F_LYS_149	NZ	F_GLU_195	OE1	2.606
5JOF	F_LYS_183	NZ	F_GLU_187	OE1	3.917
5JOF	F_LYS_183	NZ	F_GLU_187	OE2	3.217
5JR1	H_ARG_38	NH1	H_ASP_86	OD1	2.944
5JR1	H_ARG_38	NH2	H_GLU_46	OE2	2.675
5JR1	H_ARG_38	NH2	H_ASP_86	OD1	3.952
5JR1	H_ARG_50	NH1	H_GLU_100J	OE1	3.342
5JR1	H_ARG_50	NH1	H_GLU_100J	OE2	3.375
5JR1	H_ARG_50	NH2	H_GLU_100J	OE1	3.986
5JR1	H_LYS_52	NZ	H_ASP_53	OD1	2.855
5JR1	H_ARG_66	NH1	H_ASP_86	OD1	3.760
5JR1	H_ARG_66	NH1	H_ASP_86	OD2	2.716
5JR1	H_ARG_66	NH2	H_ASP_86	OD1	3.157
5JR1	H_ARG_66	NH2	H_ASP_86	OD2	3.593
5JR1	H_ARG_71	NH2	H_ASP_73	OD1	3.546
5JR1	H_ARG_94	NH1	H_ASP_102	OD2	2.955
5JR1	H_LYS_143	NZ	H_ASP_144	OD1	3.485
5JR1	H_LYS_143	NZ	H_ASP_144	OD2	2.637
5JR1	H_HIS_164	NE2	L_ASP_139	OD1	3.232
5JR1	H_HIS_164	NE2	L_ASP_139	OD2	3.168
5JR1	H_LYS_206	NZ	H_ASP_208	OD1	2.690
5JR1	L_HIS_31	ND1	H_ASP_100	OD2	3.496
5JR1	L_HIS_31	ND1	H_GLU_100I	OE2	3.149
5JR1	L_ARG_61	NH2	L_GLU_81	OE2	3.044
5JR1	L_ARG_61	NH2	L_ASP_82	OD1	2.738
5JR1	L_ARG_61	NH2	L_ASP_82	OD2	3.536
5JR1	L_ARG_95B	NH1	H_ASP_58	OD1	3.367
5JR1	L_ARG_95B	NH1	H_ASP_58	OD2	3.787
5JR1	L_ARG_95B	NH2	H_ASP_58	OD1	3.502
5JR1	L_ARG_95B	NH2	H_ASP_58	OD2	2.474
5JR1	L_LYS_110	NZ	L_GLU_199	OE1	2.769
5JR1	L_HIS_189	ND1	L_ASP_152	OD2	3.281
5JUE	L_ARG_61	NH1	L_ASP_82	OD1	2.841
5JUE	L_ARG_61	NH1	L_ASP_82	OD2	3.261
5JUE	L_ARG_61	NH2	L_ASP_82	OD1	3.675
5JUE	L_ARG_61	NH2	L_ASP_82	OD2	2.578
5JUE	L_LYS_103	NZ	L_ASP_165	OD1	3.155
5JUE	L_LYS_147	NZ	L_GLU_154	OE1	3.955
5JUE	L_LYS_149	NZ	L_GLU_195	OE1	3.435

5JUE	L_LYS_149	NZ	L_GLU_195	OE2	2.940
5JUE	L_ARG_155	NH1	L_GLU_185	OE1	2.977
5JUE	L_ARG_155	NH1	L_GLU_185	OE2	3.732
5JUE	L_ARG_155	NH2	L_GLU_185	OE1	3.822
5JUE	L_ARG_155	NH2	L_GLU_185	OE2	3.203
5JUE	L_ARG_188	NH2	L_ASP_184	OD1	3.007
5JUE	L_ARG_188	NH2	L_ASP_184	OD2	3.926
5JUE	L_HIS_189	ND1	L_ASP_151	OD2	2.628
5JUE	L_LYS_199	NZ	L_ASP_110	OD1	3.968
5JUE	L_LYS_199	NZ	L_ASP_110	OD2	3.647
5JUE	H_LYS_66	NZ	H_ASP_86	OD1	3.729
5JUE	H_LYS_66	NZ	H_ASP_86	OD2	2.761
5JUE	H_ARG_94	NH2	H_ASP_101	OD1	3.685
5JUE	H_ARG_94	NH2	H_ASP_101	OD2	2.851
5JUE	H_LYS_208	NZ	L_GLU_123	OE1	2.809
5JUE	H_LYS_208	NZ	L_GLU_123	OE2	2.812
5JUE	H_LYS_209	NZ	H_GLU_211	OE1	3.891
5JXA	H_ARG_38	NH1	H_ASP_86	OD1	2.740
5JXA	H_ARG_38	NH2	H_GLU_46	OE1	2.757
5JXA	H_ARG_38	NH2	H_ASP_86	OD1	3.580
5JXA	H_ARG_66	NH1	H_ASP_86	OD1	3.702
5JXA	H_ARG_66	NH1	H_ASP_86	OD2	3.100
5JXA	H_ARG_66	NH2	H_ASP_86	OD1	2.964
5JXA	H_ARG_66	NH2	H_ASP_86	OD2	3.681
5JXA	H_ARG_95	NH1	H_ASP_99	OD1	3.572
5JXA	H_ARG_95	NH2	H_ASP_99	OD1	2.948
5JXA	H_LYS_143	NZ	H_ASP_144	OD1	2.917
5JXA	H_LYS_143	NZ	H_ASP_144	OD2	3.163
5JXA	H_LYS_209	NZ	L_GLU_123	OE1	3.277
5JXA	H_LYS_210	NZ	H_GLU_212	OE1	2.675
5JXA	H_LYS_210	NZ	H_GLU_212	OE2	3.292
5JXA	H_LYS_214	NZ	L_ASP_122	OD1	2.755
5JXA	H_LYS_214	NZ	L_ASP_122	OD2	3.275
5JXA	L_LYS_24	NZ	L_ASP_70	OD1	2.561
5JXA	L_LYS_24	NZ	L_ASP_70	OD2	3.785
5JXA	L_ARG_39	NH2	L_GLU_81	OE1	3.801
5JXA	L_ARG_61	NH2	L_ASP_82	OD1	2.836
5JXA	L_ARG_61	NH2	L_ASP_82	OD2	3.523
5JXA	L_ARG_142	NH1	L_GLU_103	OE1	2.871
5JXA	L_ARG_142	NH1	L_GLU_103	OE2	3.755
5JXA	L_ARG_142	NH2	L_GLU_103	OE1	3.345
5JXA	L_ARG_142	NH2	L_GLU_103	OE2	2.786
5JXA	L_ARG_142	NH2	L_GLU_105	OE2	3.779
5JXA	L_LYS_149	NZ	L_GLU_195	OE2	3.064
5JXA	L_LYS_188	NZ	L_ASP_185	OD1	2.848
5JXA	L_HIS_189	ND1	L_ASP_151	OD2	3.368
5KZP	H_HIS_35	NE2	H_ASP_99	OD2	2.522
5KZP	H_ARG_38	NH1	H_ASP_90	OD1	2.873
5KZP	H_ARG_38	NH2	H_GLU_46	OE1	3.219
5KZP	H_ARG_38	NH2	H_GLU_46	OE2	3.666
5KZP	H_ARG_38	NH2	H_ASP_90	OD1	3.689
5KZP	H_ARG_65	NH1	H_ASP_62	OD1	2.911
5KZP	H_ARG_65	NH2	H_ASP_62	OD1	2.885
5KZP	H_ARG_67	NH1	H_ASP_90	OD1	3.700
5KZP	H_ARG_67	NH1	H_ASP_90	OD2	2.484
5KZP	H_ARG_67	NH2	H_ASP_90	OD1	2.918
5KZP	H_ARG_67	NH2	H_ASP_90	OD2	3.301
5KZP	H_ARG_98	NH2	H_ASP_111	OD1	3.703

5KZP	H_ARG_98	NH2	H_ASP_111	OD2	2.809
5KZP	H_LYS_153	NZ	H_ASP_154	OD1	3.314
5KZP	H_LYS_153	NZ	H_ASP_154	OD2	3.555
5KZP	H_LYS_224	NZ	L_ASP_122	OD2	3.852
5KZP	L_ARG_61	NH1	L_GLU_79	OE1	3.104
5KZP	L_ARG_61	NH1	L_GLU_79	OE2	3.279
5KZP	L_ARG_61	NH2	L_GLU_79	OE2	3.588
5KZP	L_ARG_61	NH2	L_GLU_81	OE1	3.551
5KZP	L_ARG_61	NH2	L_ASP_82	OD1	2.835
5KZP	L_ARG_61	NH2	L_ASP_82	OD2	3.395
5KZP	L_ARG_103	NH1	L_GLU_105	OE1	3.734
5KZP	L_ARG_103	NH2	L_GLU_105	OE1	3.962
5KZP	L_LYS_149	NZ	L_GLU_195	OE1	3.543
5KZP	L_LYS_183	NZ	L_GLU_187	OE2	3.769
5KZP	E_HIS_35	NE2	E_ASP_99	OD2	2.563
5KZP	E_ARG_38	NH1	E_ASP_90	OD1	3.683
5KZP	E_ARG_65	NH1	E_ASP_62	OD1	2.341
5KZP	E_ARG_65	NH2	E_ASP_62	OD1	2.619
5KZP	E_ARG_65	NH2	K_GLU_1	OE2	3.580
5KZP	E_ARG_98	NH2	E_ASP_111	OD1	3.416
5KZP	E_ARG_98	NH2	E_ASP_111	OD2	2.790
5KZP	E_LYS_153	NZ	E_ASP_154	OD1	2.756
5KZP	E_LYS_153	NZ	E_ASP_154	OD2	2.951
5KZP	E_LYS_219	NZ	L_GLU_123	OE1	2.944
5KZP	E_LYS_219	NZ	L_GLU_123	OE2	2.510
5KZP	L_ARG_24	NH1	L_ASP_70	OD1	3.891
5KZP	L_ARG_24	NH1	L_ASP_70	OD2	3.598
5KZP	L_ARG_61	NH2	L_GLU_81	OE1	3.907
5KZP	L_ARG_61	NH2	L_ASP_82	OD1	2.991
5KZP	L_ARG_61	NH2	L_ASP_82	OD2	3.614
5KZP	L_HIS_189	ND1	L_ASP_185	OD1	3.770
5KZP	F_HIS_35	NE2	F_ASP_99	OD2	2.631
5KZP	F_ARG_38	NH1	F_ASP_90	OD1	2.940
5KZP	F_ARG_38	NH2	F_GLU_46	OE1	2.834
5KZP	F_ARG_38	NH2	F_GLU_46	OE2	3.617
5KZP	F_ARG_65	NH1	F_ASP_62	OD1	2.904
5KZP	F_ARG_65	NH2	F_ASP_62	OD1	2.941
5KZP	F_ARG_67	NH1	F_ASP_90	OD1	3.792
5KZP	F_ARG_67	NH1	F_ASP_90	OD2	2.747
5KZP	F_ARG_67	NH2	F_ASP_90	OD1	3.178
5KZP	F_ARG_67	NH2	F_ASP_90	OD2	3.633
5KZP	F_ARG_98	NH2	F_ASP_111	OD1	3.568
5KZP	F_ARG_98	NH2	F_ASP_111	OD2	2.783
5KZP	F_LYS_139	NZ	J_GLU_213	OE2	2.615
5KZP	F_LYS_153	NZ	F_ASP_154	OD2	3.275
5KZP	J_ARG_61	NH2	J_GLU_81	OE1	3.789
5KZP	J_ARG_61	NH2	J_ASP_82	OD1	2.791
5KZP	J_ARG_61	NH2	J_ASP_82	OD2	3.369
5KZP	J_ARG_211	NH1	J_GLU_187	OE1	3.757
5KZP	J_ARG_211	NH2	J_GLU_187	OE1	3.382
5KZP	G_HIS_35	NE2	G_ASP_99	OD2	3.393
5KZP	G_ARG_38	NH1	G_ASP_90	OD1	3.839
5KZP	G_ARG_38	NH2	G_GLU_46	OE1	3.198
5KZP	G_ARG_38	NH2	G_GLU_46	OE2	3.193
5KZP	G_ARG_65	NH2	G_ASP_62	OD1	3.015
5KZP	G_ARG_67	NH1	G_ASP_90	OD2	3.513
5KZP	G_LYS_87	NZ	G_GLU_89	OE1	2.242
5KZP	G_LYS_87	NZ	G_GLU_89	OE2	3.284

5KZP	G_ARG_98	NH2	G_ASP_111	OD1	3.923
5KZP	G_ARG_98	NH2	G_ASP_111	OD2	3.052
5KZP	G_LYS_153	NZ	G_ASP_154	OD1	2.784
5KZP	G_LYS_153	NZ	G_ASP_154	OD2	3.265
5KZP	G_LYS_219	NZ	K_GLU_123	OE2	3.381
5KZP	G_LYS_220	NZ	G_GLU_222	OE1	3.746
5KZP	G_LYS_220	NZ	G_GLU_222	OE2	2.332
5KZP	K_ARG_24	NH2	K_ASP_70	OD1	2.089
5KZP	K_ARG_24	NH2	K_ASP_70	OD2	3.470
5KZP	K_ARG_61	NH2	K_GLU_81	OE1	3.540
5KZP	K_ARG_61	NH2	K_ASP_82	OD1	2.863
5KZP	K_ARG_61	NH2	K_ASP_82	OD2	3.407
5KZP	K_ARG_103	NH1	K_GLU_105	OE2	3.064
5KZP	K_HIS_189	ND1	K_ASP_185	OD1	3.899
5KZP	K_ARG_211	NH1	K_GLU_187	OE2	3.000
5KZP	K_ARG_211	NH2	K_GLU_187	OE2	3.195
5LDN	A_ARG_72	NH2	A_ASP_74	OD1	3.403
5LDN	A_ARG_72	NH2	A_ASP_74	OD2	3.634
5LDN	A_LYS_80	NZ	A_ASP_71	OD2	3.125
5LDN	A_LYS_80	NZ	A_GLU_73	OE1	3.933
5LDN	A_LYS_80	NZ	A_GLU_73	OE2	2.939
5LDN	A_LYS_80	NZ	A_GLU_581	OE1	2.882
5LDN	A_ARG_82	NH1	A_ASP_71	OD2	3.811
5LDN	A_ARG_82	NH1	A_GLU_581	OE1	2.442
5LDN	A_ARG_82	NH2	A_GLU_581	OE1	3.951
5LDN	A_LYS_193	NZ	A_GLU_188	OE2	3.913
5LDN	A_ARG_221	NH2	A_GLU_288	OE1	2.862
5LDN	A_ARG_221	NH2	A_GLU_288	OE2	3.399
5LDN	A_LYS_225	NZ	A_ASP_135	OD1	3.401
5LDN	A_LYS_225	NZ	A_ASP_135	OD2	3.221
5LDN	A_LYS_238	NZ	A_ASP_291	OD2	3.266
5LDN	A_LYS_238	NZ	A_GLU_293	OE2	3.311
5LDN	A_ARG_311	NH2	A_GLU_136	OE1	3.150
5LDN	A_ARG_311	NH2	A_GLU_136	OE2	3.587
5LDN	A_ARG_363	NH1	A_ASP_359	OD1	3.274
5LDN	A_ARG_363	NH2	A_ASP_923	OD1	2.881
5LDN	A_ARG_363	NH2	A_ASP_923	OD2	3.367
5LDN	A_ARG_379	NH1	A_ASP_330	OD1	3.918
5LDN	A_ARG_379	NH1	A_ASP_330	OD2	3.115
5LDN	A_ARG_379	NH2	A_ASP_330	OD1	2.861
5LDN	A_ARG_379	NH2	A_ASP_330	OD2	3.485
5LDN	A_ARG_398	NH2	A_ASP_866	OD1	2.806
5LDN	A_ARG_398	NH2	A_ASP_866	OD2	3.196
5LDN	A_HIS_403	NE2	A_GLU_401	OE1	3.143
5LDN	A_LYS_440	NZ	A_ASP_447	OD2	3.777
5LDN	A_LYS_483	NZ	A_ASP_910	OD2	3.275
5LDN	A_LYS_505	NZ	A_ASP_501	OD1	3.131
5LDN	A_LYS_505	NZ	A_ASP_501	OD2	3.450
5LDN	A_ARG_506	NH2	A_ASP_482	OD1	3.756
5LDN	A_ARG_506	NH2	A_ASP_482	OD2	3.168
5LDN	A_ARG_522	NH2	A_GLU_401	OE2	3.872
5LDN	A_ARG_538	NH1	A_ASP_394	OD2	3.250
5LDN	A_ARG_545	NH2	A_ASP_391	OD1	2.660
5LDN	A_ARG_545	NH2	A_ASP_391	OD2	3.895
5LDN	A_ARG_553	NH1	A_ASP_107	OD1	3.270
5LDN	A_ARG_553	NH1	A_ASP_107	OD2	3.176
5LDN	A_HIS_558	NE2	A_ASP_101	OD1	3.369
5LDN	A_HIS_558	NE2	A_ASP_101	OD2	2.749

5LDN	A_LYS_564	NZ	A_GLU_366	OE1	2.705
5LDN	A_LYS_586	NZ	A_ASP_74	OD2	3.049
5LDN	A_ARG_601	NH1	A_ASP_587	OD1	3.101
5LDN	A_ARG_601	NH1	A_ASP_587	OD2	2.666
5LDN	A_ARG_634	NH2	A_GLU_630	OE2	3.382
5LDN	A_ARG_675	NH1	A_GLU_920	OE2	3.980
5LDN	A_ARG_675	NH2	A_GLU_920	OE2	3.771
5LDN	A_LYS_683	NZ	A_GLU_911	OE1	2.897
5LDN	A_LYS_719	NZ	A_GLU_741	OE1	3.754
5LDN	A_LYS_719	NZ	A_GLU_741	OE2	3.492
5LDN	A_LYS_745	NZ	A_ASP_907	OD1	3.711
5LDN	A_LYS_745	NZ	A_ASP_907	OD2	2.722
5LDN	A_ARG_746	NH1	A_GLU_743	OE1	2.687
5LDN	A_ARG_746	NH1	A_GLU_743	OE2	2.969
5LDN	A_ARG_802	NH1	A_ASP_526	OD2	3.579
5LDN	A_LYS_862	NZ	A_ASP_526	OD1	2.598
5LDN	A_LYS_862	NZ	A_ASP_529	OD1	3.751
5LDN	A_LYS_862	NZ	A_ASP_529	OD2	2.683
5LDN	A_ARG_871	NH1	A_GLU_920	OE2	3.400
5LDN	A_HIS_898	ND1	A_ASP_725	OD1	3.639
5LDN	A_HIS_898	ND1	A_ASP_725	OD2	2.775
5LDN	A_ARG_926	NH2	A_ASP_639	OD2	3.350
5LDN	A_HIS_928	ND1	A_ASP_639	OD1	2.832
5LDN	A_HIS_928	ND1	A_ASP_639	OD2	3.728
5LDN	A_HIS_928	NE2	A_ASP_636	OD2	3.490
5LDN	A_ARG_932	NH1	A_ASP_89	OD2	3.407
5LDN	A_ARG_932	NH2	A_ASP_89	OD1	3.679
5LDN	A_ARG_932	NH2	A_ASP_89	OD2	2.766
5LDN	A_ARG_932	NH2	A_GLU_630	OE1	3.434
5LDN	A_ARG_932	NH2	A_GLU_630	OE2	3.081
5LDN	A_ARG_941	NH1	A_ASP_362	OD1	3.367
5LDN	A_ARG_941	NH1	A_ASP_362	OD2	3.176
5LDN	A_ARG_941	NH2	A_ASP_362	OD1	3.000
5LDN	A_ARG_941	NH2	A_ASP_362	OD2	3.971
5LDN	L_LYS_44	NZ	L_ASP_90	OD1	2.996
5LDN	L_ARG_81	NH1	L_ASP_102	OD1	3.268
5LDN	L_ARG_81	NH1	L_ASP_102	OD2	2.452
5LDN	L_ARG_81	NH2	L_ASP_102	OD1	3.517
5LDN	L_ARG_	NH1	L_GLU_	OE1	3.301
5LDN	L_ARG_	NH2	L_GLU_	OE1	3.915
5LDN	L_ARG_	NH1	L_GLU_	OE2	3.234
5LDN	L_HIS_	ND1	L_ASP_	OD1	3.989
5LDN	L_HIS_	ND1	L_ASP_	OD2	2.838
5LDN	H_ARG_37	NH1	H_ASP_88	OD1	2.969
5LDN	H_ARG_37	NH2	H_GLU_45	OE2	3.151
5LDN	H_ARG_65	NH1	H_ASP_88	OD1	3.733
5LDN	H_ARG_65	NH1	H_ASP_	OD2	3.243
5LDN	H_ARG_65	NH2	H_ASP_88	OD1	2.798
5LDN	H_ARG_65	NH2	H_ASP_	OD2	3.381
5LDN	H_LYS_70	NZ	H_ASP_72	OD2	3.198
5LDN	H_ARG_	NH1	H_ASP_	OD1	3.345
5LDN	H_ARG_	NH2	H_ASP_	OD1	3.435
5LDN	H_LYS_	NZ	L_GLU_	OE1	3.019
5M2C	A_LYS_124	NZ	A_ASP_195	OD1	2.994
5M2C	A_LYS_124	NZ	A_ASP_195	OD2	3.852
5M2C	A_LYS_144	NZ	A_ASP_138	OD1	2.840
5M2C	A_LYS_171	NZ	A_ASP_138	OD1	3.119
5M2C	A_LYS_187	NZ	A_ASP_155	OD1	3.762

5M2C	A_LYS_187	NZ	A_ASP_155	OD2	3.179
5M2C	A_HIS_191	NE2	A_ASP_128	OD1	3.269
5M2C	A_HIS_191	NE2	A_ASP_128	OD2	2.695
5M2C	B_LYS_124	NZ	B_ASP_195	OD1	3.117
5M2C	B_LYS_124	NZ	B_ASP_195	OD2	3.775
5M2C	B_LYS_144	NZ	B_ASP_138	OD1	2.798
5M2C	B_LYS_171	NZ	B_ASP_138	OD1	3.131
5M2C	B_LYS_187	NZ	B_ASP_155	OD1	3.683
5M2C	B_LYS_187	NZ	B_ASP_155	OD2	3.174
5M2C	B_HIS_191	NE2	B_ASP_128	OD1	3.220
5M2C	B_HIS_191	NE2	B_ASP_128	OD2	2.713
5M33	A_LYS_124	NZ	A_ASP_195	OD1	2.806
5M33	A_LYS_124	NZ	A_ASP_195	OD2	3.061
5M33	A_LYS_187	NZ	A_ASP_155	OD1	2.820
5M33	A_HIS_191	NE2	A_ASP_128	OD1	3.390
5M33	A_HIS_191	NE2	A_ASP_128	OD2	2.760
5M33	A_LYS_193	NZ	A_GLU_188	OE1	2.934
5M33	B_LYS_124	NZ	B_ASP_195	OD1	3.243
5M33	B_LYS_124	NZ	B_ASP_195	OD2	2.646
5M33	B_HIS_191	NE2	B_ASP_128	OD1	3.361
5M33	B_HIS_191	NE2	B_ASP_128	OD2	2.690
5M3D	A_LYS_116	NZ	A_ASP_117	OD1	3.826
5M3D	A_LYS_124	NZ	A_ASP_195	OD1	3.095
5M3D	A_LYS_124	NZ	A_ASP_195	OD2	2.681
5M3D	A_LYS_144	NZ	A_ASP_138	OD1	3.722
5M3D	A_LYS_148	NZ	A_GLU_152	OE2	2.745
5M3D	A_LYS_187	NZ	A_ASP_155	OD2	2.929
5M3D	A_HIS_191	NE2	A_ASP_128	OD1	3.275
5M3D	A_HIS_191	NE2	A_ASP_128	OD2	2.681
5M3D	A_LYS_201	NZ	A_ASP_196	OD1	3.448
5M3D	B_LYS_116	NZ	B_ASP_117	OD1	3.148
5M3D	B_LYS_124	NZ	B_ASP_195	OD1	2.979
5M3D	B_LYS_124	NZ	B_ASP_195	OD2	2.591
5M3D	B_LYS_144	NZ	B_ASP_138	OD1	3.668
5M3D	B_LYS_148	NZ	B_GLU_152	OE2	2.496
5M3D	B_LYS_187	NZ	B_ASP_155	OD2	3.090
5M3D	B_HIS_191	NE2	B_ASP_128	OD1	3.349
5M3D	B_HIS_191	NE2	B_ASP_128	OD2	2.596
5M3D	C_LYS_124	NZ	C_ASP_195	OD1	2.934
5M3D	C_LYS_124	NZ	C_ASP_195	OD2	3.127
5M3D	C_LYS_148	NZ	C_GLU_152	OE2	2.588
5M3D	C_LYS_171	NZ	C_ASP_137	OD1	3.243
5M3D	C_LYS_171	NZ	C_ASP_137	OD2	3.458
5M3D	C_LYS_187	NZ	C_ASP_155	OD2	3.290
5M3D	C_HIS_191	NE2	C_ASP_128	OD1	3.231
5M3D	C_HIS_191	NE2	C_ASP_128	OD2	2.539
5M3D	D_LYS_124	NZ	D_ASP_195	OD1	3.141
5M3D	D_LYS_124	NZ	D_ASP_195	OD2	3.445
5M3D	D_LYS_148	NZ	D_GLU_152	OE1	3.259
5M3D	D_LYS_171	NZ	D_ASP_137	OD1	2.423
5M3D	D_LYS_171	NZ	D_ASP_137	OD2	3.425
5M3D	D_LYS_187	NZ	D_ASP_155	OD2	3.128
5M3D	D_HIS_191	NE2	D_ASP_128	OD1	3.228
5M3D	D_HIS_191	NE2	D_ASP_128	OD2	2.528
5M3T	A_LYS_124	NZ	A_ASP_195	OD1	3.045
5M3T	A_LYS_124	NZ	A_ASP_195	OD2	3.381
5M3T	A_LYS_144	NZ	A_ASP_137	OD1	3.126
5M3T	A_HIS_191	NE2	A_ASP_128	OD1	2.701

5M3T	A_HIS_191	NE2	A_ASP_128	OD2	3.351
5M3T	B_LYS_116	NZ	B_ASP_117	OD1	3.281
5M3T	B_LYS_124	NZ	B_ASP_195	OD1	2.763
5M3T	B_LYS_124	NZ	B_ASP_195	OD2	2.942
5M3T	B_LYS_144	NZ	B_ASP_138	OD1	2.688
5M3T	B_LYS_144	NZ	B_ASP_138	OD2	3.938
5M3T	B_LYS_148	NZ	B_GLU_152	OE2	3.571
5M3T	B_LYS_187	NZ	B_ASP_155	OD1	3.212
5M3T	B_HIS_191	NE2	B_ASP_128	OD1	2.761
5M3T	B_HIS_191	NE2	B_ASP_128	OD2	3.127
5M4R	A_LYS_124	NZ	A_ASP_195	OD1	3.169
5M4R	A_LYS_124	NZ	A_ASP_195	OD2	3.633
5M4R	A_LYS_171	NZ	A_ASP_138	OD1	2.609
5M4R	A_LYS_187	NZ	A_ASP_155	OD2	3.101
5M4R	A_HIS_191	NE2	A_ASP_128	OD1	3.374
5M4R	A_HIS_191	NE2	A_ASP_128	OD2	2.535
5M4R	B_LYS_124	NZ	B_ASP_195	OD1	3.161
5M4R	B_LYS_124	NZ	B_ASP_195	OD2	3.629
5M4R	B_LYS_144	NZ	B_ASP_138	OD1	2.408
5M4R	B_LYS_187	NZ	B_ASP_155	OD1	3.374
5M4R	B_HIS_191	NE2	B_ASP_128	OD1	3.385
5M4R	B_HIS_191	NE2	B_ASP_128	OD2	2.546
5M4R	C_LYS_124	NZ	C_ASP_195	OD1	3.153
5M4R	C_LYS_124	NZ	C_ASP_195	OD2	3.571
5M4R	C_LYS_171	NZ	C_ASP_138	OD1	3.210
5M4R	C_LYS_187	NZ	C_ASP_155	OD1	3.818
5M4R	C_HIS_191	NE2	C_ASP_128	OD1	3.374
5M4R	C_HIS_191	NE2	C_ASP_128	OD2	2.549
5M4R	D_LYS_124	NZ	D_ASP_195	OD1	3.169
5M4R	D_LYS_124	NZ	D_ASP_195	OD2	3.626
5M4R	D_LYS_187	NZ	D_ASP_155	OD1	3.733
5M4R	D_LYS_187	NZ	D_ASP_155	OD2	3.658
5M4R	D_HIS_191	NE2	D_ASP_128	OD1	3.367
5M4R	D_HIS_191	NE2	D_ASP_128	OD2	2.515
5M4R	E_LYS_124	NZ	E_ASP_195	OD1	3.158
5M4R	E_LYS_124	NZ	E_ASP_195	OD2	3.599
5M4R	E_LYS_144	NZ	E_ASP_137	OD2	3.235
5M4R	E_LYS_187	NZ	E_ASP_155	OD1	3.706
5M4R	E_HIS_191	NE2	E_ASP_128	OD1	3.375
5M4R	E_HIS_191	NE2	E_ASP_128	OD2	2.532
5M4R	E_LYS_201	NZ	E_ASP_196	OD1	3.587
5MO9	H_HIS_35	NE2	H_GLU_33	OE1	3.220
5MO9	H_HIS_43	NE2	H_GLU_89	OE1	3.753
5MO9	H_LYS_63	NZ	H_GLU_46	OE1	3.930
5MO9	H_LYS_63	NZ	H_GLU_46	OE2	3.238
5MO9	H_LYS_67	NZ	H_ASP_90	OD1	3.821
5MO9	H_LYS_67	NZ	H_ASP_90	OD2	2.804
5MO9	H_ARG_84	NH1	H_GLU_82	OE1	3.999
5MO9	H_ARG_84	NH1	H_GLU_82	OE2	3.132
5MO9	H_LYS_146	NZ	H_ASP_147	OD1	3.365
5MO9	H_LYS_146	NZ	H_ASP_147	OD2	3.626
5MO9	H_LYS_212	NZ	L_GLU_128	OE2	3.509
5MO9	H_LYS_213	NZ	H_GLU_215	OE2	3.368
5MO9	L_LYS_44	NZ	L_GLU_86	OE2	3.853
5MO9	L_LYS_55	NZ	X_GLU_371	OE2	2.811
5MO9	L_ARG_59	NH1	L_ASP_65	OD1	3.142
5MO9	L_ARG_66	NH1	L_ASP_87	OD1	3.324
5MO9	L_ARG_66	NH1	L_ASP_87	OD2	2.775

5MO9	L_ARG.66	NH2	L_ASP.87	OD1	2.980
5MO9	L_ARG.66	NH2	L_ASP.87	OD2	3.846
5MO9	L_LYS.108	NZ	L_GLU.170	OE2	3.379
5MO9	L_LYS.154	NZ	L_GLU.200	OE2	3.767
5MO9	X_HIS.343	NE2	X_GLU.341	OE2	3.960
5MO9	X_LYS.364	NZ	H_GLU.33	OE2	2.799
5MO9	X_LYS.364	NZ	H_ASP.52	OD1	3.966
5MO9	X_LYS.369	NZ	X_GLU.371	OE1	3.611
5MO9	X_LYS.372	NZ	X_ASP.370	OD1	3.437
5N2B	A_LYS.82	NZ	A_ASP.144	OD1	3.469
5N4J	L_ARG.38	NH1	H_ASP.100	OD1	2.794
5N4J	L_ARG.38	NH1	H_ASP.100	OD2	3.589
5N4J	L_ARG.60	NH2	L_ASP.66	OD1	3.938
5N4J	L_ARG.67	NH2	L_GLU.87	OE2	2.853
5N4J	L_ARG.67	NH2	L_ASP.88	OD1	2.770
5N4J	L_ARG.67	NH2	L_ASP.88	OD2	3.658
5N4J	L_LYS.174	NZ	L_GLU.89	OE2	2.818
5N4J	H_LYS.11	NZ	H_GLU.9	OE1	3.995
5N4J	H_ARG.37	NH1	H_ASP.89	OD1	2.887
5N4J	H_ARG.37	NH2	H_GLU.45	OE1	3.779
5N4J	H_ARG.37	NH2	H_GLU.45	OE2	3.178
5N4J	H_ARG.37	NH2	H_ASP.89	OD1	3.973
5N4J	H_LYS.62	NZ	H_GLU.45	OE1	2.843
5N4J	H_LYS.62	NZ	H_GLU.45	OE2	3.909
5N4J	H_ARG.66	NH1	H_ASP.89	OD1	3.808
5N4J	H_ARG.66	NH1	H_ASP.89	OD2	2.928
5N4J	H_ARG.66	NH2	H_ASP.89	OD1	2.878
5N4J	H_ARG.66	NH2	H_ASP.89	OD2	3.415
5N4J	H_ARG.83	NH1	H_GLU.81	OE1	2.921
5N4J	H_ARG.86	NH2	H_ASP.88	OD1	3.231
5N4J	H_ARG.86	NH2	H_ASP.88	OD2	2.601
5N4J	H_ARG.97	NH2	H_ASP.102	OD1	3.488
5N4J	H_ARG.97	NH2	H_ASP.102	OD2	2.852
5N4J	H_LYS.210	NZ	L_GLU.131	OE1	2.936
5N4J	H_LYS.210	NZ	L_GLU.131	OE2	3.282
5N4J	H_ARG.211	NH1	H_GLU.213	OE2	3.986
5N7B	H_ARG.38	NH1	H_ASP.92	OD1	2.899
5N7B	H_ARG.38	NH2	H_GLU.46	OE1	3.245
5N7B	H_ARG.38	NH2	H_GLU.46	OE2	3.600
5N7B	H_ARG.38	NH2	H_ASP.92	OD1	3.935
5N7B	H_LYS.43	NZ	H_GLU.46	OE1	3.841
5N7B	H_LYS.43	NZ	H_GLU.91	OE1	3.761
5N7B	H_ARG.52	NH1	H_GLU.50	OE2	2.676
5N7B	H_ARG.69	NH1	H_ASP.92	OD1	3.313
5N7B	H_ARG.69	NH1	H_ASP.92	OD2	3.638
5N7B	H_ARG.69	NH2	H_ASP.92	OD1	3.498
5N7B	H_ARG.69	NH2	H_ASP.92	OD2	2.337
5N7B	H_ARG.74	NH2	H_ASP.76	OD1	3.523
5N7B	H_ARG.89	NH1	H_GLU.91	OE2	3.715
5N7B	H_HIS.1051	ND1	H_GLU.1047	OE2	2.925
5N7B	H_HIS.1051	NE2	H_ASP.1050	OD1	3.871
5N7B	H_ARG.1070	NH2	H_GLU.1090	OE2	3.894
5N7B	H_ARG.1070	NH2	H_ASP.1091	OD1	2.787
5N7B	H_ARG.1070	NH2	H_ASP.1091	OD2	3.671
5N7W	A_LYS.12	NZ	A_GLU.10	OE1	3.956
5N7W	A_ARG.38	NH1	A_ASP.90	OD1	2.843
5N7W	A_ARG.38	NH2	A_GLU.46	OE1	3.305
5N7W	A_ARG.38	NH2	A_ASP.90	OD1	3.827

5N7W	A_LYS.63	NZ	A_GLU_46	OE1	3.619
5N7W	A_LYS.63	NZ	A_GLU_46	OE2	2.845
5N7W	A_ARG.67	NH1	A_ASP_90	OD1	3.584
5N7W	A_ARG.67	NH1	A_ASP_90	OD2	2.765
5N7W	A_ARG.67	NH2	A_ASP_90	OD1	2.880
5N7W	A_ARG.67	NH2	A_ASP_90	OD2	3.520
5N7W	A_ARG.98	NH2	A_ASP_107	OD1	3.757
5N7W	A_ARG.98	NH2	A_ASP_107	OD2	2.848
5N7W	A_LYS.149	NZ	B_GLU_126	OE2	2.961
5N7W	A_LYS.215	NZ	B_GLU_125	OE1	2.755
5N7W	A_LYS.215	NZ	B_GLU_125	OE2	3.335
5N7W	B_LYS.39	NZ	B_GLU_81	OE2	3.652
5N7W	B_ARG.61	NH2	B_ASP_82	OD1	2.909
5N7W	B_ARG.61	NH2	B_ASP_82	OD2	3.717
5N7W	B_HIS.190	ND1	B_ASP_153	OD2	2.856
5N7W	H_LYS.12	NZ	H_GLU_10	OE1	3.973
5N7W	H_ARG.38	NH1	H_ASP_90	OD1	2.822
5N7W	H_ARG.38	NH2	H_GLU_46	OE1	3.307
5N7W	H_ARG.38	NH2	H_ASP_90	OD1	3.828
5N7W	H_LYS.63	NZ	H_GLU_46	OE1	3.613
5N7W	H_LYS.63	NZ	H_GLU_46	OE2	2.860
5N7W	H_ARG.67	NH1	H_ASP_90	OD1	3.649
5N7W	H_ARG.67	NH1	H_ASP_90	OD2	2.788
5N7W	H_ARG.67	NH2	H_ASP_90	OD1	2.914
5N7W	H_ARG.67	NH2	H_ASP_90	OD2	3.510
5N7W	H_ARG.98	NH2	H_ASP_107	OD1	3.723
5N7W	H_ARG.98	NH2	H_ASP_107	OD2	2.808
5N7W	H_LYS.149	NZ	L_GLU_126	OE2	2.605
5N7W	H_ARG.216	NH2	H_GLU_218	OE2	2.838
5N7W	L_LYS.39	NZ	L_GLU_81	OE1	3.895
5N7W	L_ARG.61	NH1	L_GLU_81	OE2	3.879
5N7W	L_ARG.61	NH2	L_GLU_81	OE2	3.018
5N7W	L_ARG.61	NH2	L_ASP_82	OD1	2.869
5N7W	L_ARG.61	NH2	L_ASP_82	OD2	3.688
5N7W	X_HIS.54	NE2	X_GLU_68	OE1	3.783
5N7W	X_ARG.55	NH1	X_GLU_57	OE2	2.811
5N7W	X_ARG.55	NH2	X_GLU_57	OE2	2.683
5N7W	X_ARG.100	NH1	X_ASP_58	OD1	3.676
5N7W	X_ARG.100	NH1	X_ASP_58	OD2	3.093
5N7W	X_ARG.100	NH2	X_ASP_58	OD2	2.743
5N7W	X_ARG.100	NH2	X_GLU_113	OE2	3.977
5N7W	X_ARG.101	NH2	X_GLU_60	OE1	3.293
5N7W	X_ARG.101	NH2	X_GLU_60	OE2	3.261
5N7W	X_HIS.105	NE2	X_GLU_60	OE1	3.956
5N7W	X_HIS.105	NE2	X_GLU_60	OE2	4.000
5N7W	X_ARG.111	NH2	X_GLU_102	OE1	3.583
5N7W	Y_ARG.46	NH1	Y_ASP_42	OD2	2.678
5N7W	Y_ARG.55	NH2	Y_GLU_57	OE2	2.650
5N7W	Y_ARG.100	NH1	Y_ASP_58	OD1	3.688
5N7W	Y_ARG.100	NH1	Y_ASP_58	OD2	3.136
5N7W	Y_ARG.100	NH2	Y_ASP_58	OD2	2.751
5N7W	Y_ARG.100	NH2	Y_GLU_113	OE1	3.830
5N7W	Y_ARG.101	NH2	Y_GLU_60	OE1	3.497
5N7W	Y_ARG.101	NH2	Y_GLU_60	OE2	3.078
5N7W	Y_HIS.105	NE2	Y_GLU_60	OE1	3.784
5N7W	Y_HIS.105	NE2	Y_GLU_60	OE2	3.473
5N7W	Y_ARG.111	NH2	Y_GLU_102	OE1	3.366
5N88	H_ARG.38	NH1	H_ASP_90	OD1	2.861

5N88	H_ARG_38	NH2	H_GLU_46	OE1	2.966
5N88	H_ARG_38	NH2	H_GLU_46	OE2	3.874
5N88	H_ARG_38	NH2	H_ASP_90	OD1	3.775
5N88	H_ARG_53	NH2	H_ASP_105	OD1	3.754
5N88	H_ARG_53	NH2	H_ASP_105	OD2	2.841
5N88	H_LYS_65	NZ	H_ASP_62	OD1	2.674
5N88	H_ARG_67	NH1	H_ASP_90	OD1	3.790
5N88	H_ARG_67	NH1	H_ASP_90	OD2	2.789
5N88	H_ARG_67	NH2	H_ASP_90	OD1	3.111
5N88	H_ARG_67	NH2	H_ASP_90	OD2	3.597
5N88	H_ARG_98	NH2	H_ASP_115	OD1	3.514
5N88	H_ARG_98	NH2	H_ASP_115	OD2	2.816
5N88	D_ARG_351	NH2	D_GLU_379	OE1	2.947
5N88	D_ARG_354	NH1	D_GLU_379	OE1	3.813
5N88	D_ARG_354	NH2	D_GLU_358	OE1	3.788
5N88	D_ARG_354	NH2	D_GLU_358	OE2	3.296
5N88	D_ARG_354	NH2	D_GLU_379	OE1	3.408
5N88	D_ARG_354	NH2	D_GLU_379	OE2	2.654
5N88	D_ARG_372	NH1	D_ASP_369	OD2	3.104
5N88	D_LYS_392	NZ	D_ASP_349	OD1	3.585
5N88	D_LYS_392	NZ	D_ASP_349	OD2	3.429
5N88	D_HIS_393	NE2	D_ASP_349	OD1	2.893
5N88	D_LYS_415	NZ	D_ASP_378	OD1	2.913
5N88	A_ARG_38	NH1	A_ASP_90	OD1	2.946
5N88	A_ARG_38	NH2	A_GLU_46	OE1	2.784
5N88	A_ARG_38	NH2	A_ASP_90	OD1	3.960
5N88	A_LYS_65	NZ	A_ASP_62	OD1	2.935
5N88	A_ARG_67	NH1	A_ASP_90	OD1	3.771
5N88	A_ARG_67	NH1	A_ASP_90	OD2	2.724
5N88	A_ARG_67	NH2	A_ASP_90	OD1	3.229
5N88	A_ARG_67	NH2	A_ASP_90	OD2	3.677
5N88	A_LYS_76	NZ	A_ASP_73	OD2	3.426
5N88	A_ARG_87	NH1	A_GLU_89	OE1	3.467
5N88	A_ARG_87	NH2	A_GLU_89	OE1	3.356
5N88	A_ARG_98	NH2	A_ASP_115	OD1	3.457
5N88	A_ARG_98	NH2	A_ASP_115	OD2	3.121
5N88	E_ARG_372	NH2	E_GLU_358	OE1	2.751
5N88	E_ARG_372	NH2	E_GLU_358	OE2	3.550
5N88	E_LYS_392	NZ	E_ASP_349	OD1	2.862
5N88	E_LYS_392	NZ	E_ASP_349	OD2	3.023
5N88	E_HIS_393	NE2	E_ASP_349	OD1	3.833
5N88	E_LYS_415	NZ	E_ASP_378	OD1	2.913
5N88	E_LYS_415	NZ	E_ASP_378	OD2	3.971
5NPH	H_LYS_63	NZ	H_GLU_46	OE1	2.774
5NPH	H_LYS_63	NZ	H_GLU_46	OE2	3.824
5NPH	H_LYS_67	NZ	H_ASP_90	OD1	3.768
5NPH	H_LYS_67	NZ	H_ASP_90	OD2	2.830
5NPH	H_ARG_84	NH2	H_GLU_82	OE2	2.962
5NPH	H_ARG_98	NH2	H_ASP_108	OD1	3.726
5NPH	H_ARG_98	NH2	H_ASP_108	OD2	2.829
5NPH	H_LYS_215	NZ	L_GLU_123	OE2	2.787
5NPH	L_ARG_61	NH2	L_GLU_81	OE1	2.810
5NPH	L_ARG_61	NH2	L_ASP_82	OD1	2.818
5NPH	L_ARG_61	NH2	L_ASP_82	OD2	3.582
5NPH	L_LYS_93	NZ	A_GLU_533	OE1	3.679
5NPH	L_LYS_149	NZ	L_GLU_195	OE1	3.660
5NPH	L_HIS_189	ND1	L_ASP_151	OD2	3.036
5NPH	L_LYS_199	NZ	L_ASP_110	OD2	2.799

5NPI	A_LYS_63	NZ	A_GLU_46	OE1	2.778
5NPI	A_LYS_63	NZ	A_GLU_46	OE2	3.947
5NPI	A_LYS_67	NZ	A_ASP_90	OD1	3.854
5NPI	A_LYS_67	NZ	A_ASP_90	OD2	2.867
5NPI	A_ARG_98	NH2	A_ASP_108	OD1	3.690
5NPI	A_ARG_98	NH2	A_ASP_108	OD2	2.811
5NPI	A_HIS_181	NE2	B_GLU_10	OE1	3.570
5NPI	A_HIS_181	NE2	B_GLU_10	OE2	3.750
5NPI	A_ARG_201	NH2	A_GLU_221	OE1	2.818
5NPI	A_ARG_201	NH2	A_ASP_222	OD1	2.795
5NPI	A_ARG_201	NH2	A_ASP_222	OD2	3.637
5NPI	A_LYS_243	NZ	A_GLU_245	OE1	3.089
5NPI	B_LYS_63	NZ	B_GLU_46	OE1	2.773
5NPI	B_LYS_63	NZ	B_GLU_46	OE2	3.955
5NPI	B_LYS_67	NZ	B_ASP_90	OD1	3.936
5NPI	B_LYS_67	NZ	B_ASP_90	OD2	2.892
5NPI	B_ARG_98	NH2	B_ASP_108	OD1	3.701
5NPI	B_ARG_98	NH2	B_ASP_108	OD2	2.749
5NPI	B_HIS_181	NE2	A_GLU_10	OE1	3.757
5NPI	B_HIS_181	NE2	A_GLU_10	OE2	3.882
5NPI	B_ARG_201	NH2	B_GLU_221	OE1	2.813
5NPI	B_ARG_201	NH2	B_ASP_222	OD1	2.796
5NPI	B_ARG_201	NH2	B_ASP_222	OD2	3.658
5NPI	B_LYS_233	NZ	E_GLU_533	OE1	3.924
5NPI	B_LYS_243	NZ	B_GLU_245	OE1	3.090
5NPJ	A_LYS_63	NZ	A_GLU_46	OE1	2.799
5NPJ	A_LYS_67	NZ	A_ASP_90	OD1	3.867
5NPJ	A_LYS_67	NZ	A_ASP_90	OD2	2.954
5NPJ	A_ARG_98	NH2	A_ASP_108	OD1	3.695
5NPJ	A_ARG_98	NH2	A_ASP_108	OD2	2.771
5NPJ	A_HIS_181	NE2	B_GLU_10	OE1	3.540
5NPJ	A_HIS_181	NE2	B_GLU_10	OE2	3.793
5NPJ	A_ARG_201	NH2	A_GLU_221	OE1	2.812
5NPJ	A_ARG_201	NH2	A_ASP_222	OD1	2.769
5NPJ	A_ARG_201	NH2	A_ASP_222	OD2	3.614
5NPJ	A_LYS_243	NZ	A_GLU_245	OE1	2.814
5NPJ	B_LYS_63	NZ	B_GLU_46	OE1	2.797
5NPJ	B_LYS_67	NZ	B_ASP_90	OD1	3.887
5NPJ	B_LYS_67	NZ	B_ASP_90	OD2	2.961
5NPJ	B_ARG_98	NH2	B_ASP_108	OD1	3.704
5NPJ	B_ARG_98	NH2	B_ASP_108	OD2	2.768
5NPJ	B_HIS_181	NE2	A_GLU_10	OE1	3.734
5NPJ	B_HIS_181	NE2	A_GLU_10	OE2	3.967
5NPJ	B_ARG_201	NH2	B_GLU_221	OE1	2.825
5NPJ	B_ARG_201	NH2	B_ASP_222	OD1	2.760
5NPJ	B_ARG_201	NH2	B_ASP_222	OD2	3.648
5NPJ	B_LYS_243	NZ	B_GLU_245	OE1	2.926
5NST	A_ARG_39	NH1	C_GLU_81	OE1	3.260
5NST	A_ARG_39	NH1	C_GLU_81	OE2	3.263
5NST	A_ARG_39	NH2	C_GLU_81	OE1	3.038
5NST	A_ARG_61	NH1	A_ASP_82	OD1	3.453
5NST	A_ARG_61	NH1	A_ASP_82	OD2	2.620
5NST	A_ARG_61	NH2	A_ASP_82	OD1	3.456
5NST	A_ARG_61	NH2	A_ASP_82	OD2	3.977
5NST	A_LYS_147	NZ	A_GLU_195	OE2	3.805
5NST	A_LYS_149	NZ	A_GLU_195	OE1	3.194
5NST	A_LYS_149	NZ	A_GLU_195	OE2	3.752
5NST	A_ARG_155	NH1	A_GLU_185	OE2	3.200

5NST	A_ARG_155	NH2	A_GLU_185	OE2	2.920
5NST	A_HIS_189	ND1	A_ASP_151	OD2	3.206
5NST	A_LYS_199	NZ	A_ASP_110	OD1	3.008
5NST	A_LYS_199	NZ	A_ASP_110	OD2	3.591
5NST	B_ARG_33	NH2	B_ASP_27	OD1	3.734
5NST	B_ARG_33	NH2	B_ASP_27	OD2	3.892
5NST	B_ARG_39	NH1	B_ASP_90	OD1	3.041
5NST	B_ARG_39	NH2	B_GLU_47	OE1	3.114
5NST	B_ARG_39	NH2	B_ASP_90	OD1	3.726
5NST	B_HIS_53	NE2	B_GLU_51	OE2	3.083
5NST	B_ARG_67	NH1	B_ASP_90	OD1	3.015
5NST	B_ARG_67	NH1	B_ASP_90	OD2	2.796
5NST	B_ARG_67	NH2	B_ASP_90	OD1	3.245
5NST	B_LYS_76	NZ	B_ASP_73	OD2	2.807
5NST	B_ARG_98	NH1	B_ASP_27	OD2	2.918
5NST	B_ARG_98	NH2	B_ASP_238	OD1	3.501
5NST	B_ARG_98	NH2	B_ASP_238	OD2	2.970
5NST	B_LYS_103	NZ	B_ASP_233	OD1	2.837
5NST	B_ARG_112	NH1	B_ASP_198	OD1	3.483
5NST	B_ARG_112	NH1	B_ASP_198	OD2	3.324
5NST	B_ARG_112	NH2	B_ASP_198	OD1	3.105
5NST	B_ARG_134	NH1	B_GLU_167	OE1	3.225
5NST	B_ARG_143	NH2	B_ASP_154	OD1	3.483
5NST	B_ARG_143	NH2	B_ASP_154	OD2	3.145
5NST	B_ARG_169	NH1	B_GLU_118	OE1	3.192
5NST	B_ARG_169	NH2	B_GLU_167	OE2	3.020
5NST	B_ARG_171	NH1	B_ASP_173	OD1	2.814
5NST	B_ARG_171	NH2	B_ASP_173	OD1	3.985
5NST	B_ARG_184	NH2	B_GLU_145	OE1	3.999
5NST	B_LYS_345	NZ	A_GLU_123	OE1	3.069
5NST	C_ARG_24	NH2	C_ASP_70	OD2	2.795
5NST	C_ARG_39	NH1	A_GLU_81	OE1	3.247
5NST	C_ARG_39	NH1	A_GLU_81	OE2	3.139
5NST	C_ARG_39	NH2	A_GLU_81	OE1	3.004
5NST	C_ARG_61	NH2	C_GLU_81	OE2	3.339
5NST	C_ARG_61	NH2	C_ASP_82	OD1	2.949
5NST	C_ARG_61	NH2	C_ASP_82	OD2	3.501
5NST	C_ARG_103	NH1	C_ASP_165	OD1	3.414
5NST	C_LYS_147	NZ	C_GLU_195	OE2	3.756
5NST	C_LYS_149	NZ	C_GLU_195	OE1	3.043
5NST	C_LYS_149	NZ	C_GLU_195	OE2	3.450
5NST	C_ARG_188	NH1	C_ASP_151	OD2	2.746
5NST	C_ARG_188	NH2	C_GLU_187	OE1	2.814
5NST	C_LYS_199	NZ	C_ASP_110	OD1	3.560
5NST	C_LYS_199	NZ	C_ASP_110	OD2	3.855
5NST	D_ARG_33	NH2	D_ASP_27	OD2	3.973
5NST	D_ARG_39	NH1	D_ASP_90	OD1	3.042
5NST	D_ARG_39	NH2	D_GLU_47	OE1	3.103
5NST	D_ARG_39	NH2	D_ASP_90	OD1	3.721
5NST	D_HIS_53	NE2	D_GLU_51	OE2	2.781
5NST	D_ARG_67	NH1	D_ASP_90	OD1	2.697
5NST	D_ARG_67	NH1	D_ASP_90	OD2	3.158
5NST	D_LYS_76	NZ	D_ASP_73	OD2	2.790
5NST	D_LYS_82	NZ	D_ASP_84	OD2	3.904
5NST	D_ARG_98	NH1	D_ASP_27	OD2	2.885
5NST	D_ARG_98	NH2	D_ASP_238	OD1	3.522
5NST	D_ARG_98	NH2	D_ASP_238	OD2	2.972
5NST	D_LYS_103	NZ	D_ASP_233	OD1	3.094

5NST	D_LYS_103	NZ	D_ASP_233	OD2	3.059
5NST	D_ARG_112	NH1	D_ASP_198	OD1	3.172
5NST	D_ARG_112	NH1	D_ASP_198	OD2	3.063
5NST	D_ARG_112	NH2	D_ASP_198	OD1	2.909
5NST	D_ARG_134	NH1	D_GLU_165	OE1	3.890
5NST	D_ARG_134	NH1	D_GLU_167	OE1	3.201
5NST	D_ARG_143	NH2	D_ASP_154	OD1	3.487
5NST	D_ARG_143	NH2	D_ASP_154	OD2	3.164
5NST	D_ARG_169	NH1	D_GLU_118	OE1	3.163
5NST	D_ARG_169	NH2	D_GLU_167	OE2	3.007
5NST	D_ARG_171	NH1	D_ASP_173	OD1	2.813
5NST	D_ARG_171	NH2	D_ASP_173	OD1	3.989
5NST	D_LYS_345	NZ	C_GLU_123	OE2	3.272
5NUZ	A_LYS_66	NZ	A_ASP_86	OD1	3.693
5NUZ	A_LYS_66	NZ	A_ASP_86	OD2	2.849
5NUZ	A_ARG_94	NH2	A_ASP_101	OD1	3.574
5NUZ	A_ARG_94	NH2	A_ASP_101	OD2	2.713
5NUZ	A_ARG_95	NH1	C_ASP_114	OD1	3.502
5NUZ	A_ARG_95	NH1	C_ASP_114	OD2	2.701
5NUZ	A_ARG_95	NH2	A_ASP_100A	OD2	3.027
5NUZ	A_ARG_95	NH2	C_ASP_114	OD1	2.822
5NUZ	A_ARG_95	NH2	C_ASP_114	OD2	3.585
5NUZ	A_LYS_208	NZ	B_GLU_123	OE1	3.889
5NUZ	A_LYS_208	NZ	B_GLU_123	OE2	2.684
5NUZ	H_LYS_66	NZ	H_ASP_86	OD1	3.692
5NUZ	H_LYS_66	NZ	H_ASP_86	OD2	2.845
5NUZ	H_ARG_94	NH2	H_ASP_101	OD1	3.585
5NUZ	H_ARG_94	NH2	H_ASP_101	OD2	2.715
5NUZ	H_ARG_95	NH1	D_ASP_114	OD1	3.679
5NUZ	H_ARG_95	NH1	D_ASP_114	OD2	2.753
5NUZ	H_ARG_95	NH2	H_ASP_100A	OD2	3.002
5NUZ	H_ARG_95	NH2	D_ASP_114	OD1	2.850
5NUZ	H_ARG_95	NH2	D_ASP_114	OD2	3.470
5NUZ	H_LYS_208	NZ	L_GLU_123	OE2	2.982
5NUZ	B_ARG_24	NH1	B_ASP_70	OD1	3.493
5NUZ	B_ARG_24	NH1	B_ASP_70	OD2	3.358
5NUZ	B_ARG_61	NH1	B_ASP_81	OD1	3.247
5NUZ	B_ARG_61	NH1	B_ASP_82	OD1	2.766
5NUZ	B_ARG_61	NH1	B_ASP_82	OD2	3.636
5NUZ	B_ARG_61	NH2	L_GLU_79	OE1	3.072
5NUZ	B_ARG_61	NH2	L_GLU_79	OE2	3.676
5NUZ	B_LYS_92	NZ	B_GLU_93	OE2	2.758
5NUZ	B_LYS_103	NZ	B_GLU_105	OE2	3.588
5NUZ	B_LYS_142	NZ	B_GLU_105	OE1	3.907
5NUZ	B_LYS_142	NZ	B_GLU_105	OE2	2.608
5NUZ	B_LYS_147	NZ	B_GLU_195	OE1	3.572
5NUZ	B_LYS_149	NZ	B_GLU_195	OE2	3.615
5NUZ	B_ARG_155	NH1	B_GLU_185	OE1	3.558
5NUZ	B_ARG_155	NH1	B_GLU_185	OE2	3.557
5NUZ	B_ARG_155	NH2	B_GLU_185	OE2	2.757
5NUZ	B_ARG_188	NH1	B_GLU_185	OE1	3.922
5NUZ	B_HIS_189	ND1	B_ASP_151	OD2	3.016
5NUZ	B_LYS_199	NZ	B_ASP_110	OD2	3.082
5NUZ	C_LYS_181	NZ	C_GLU_186	OE1	3.275
5NUZ	C_LYS_191	NZ	C_ASP_159	OD1	3.275
5NUZ	C_LYS_191	NZ	C_ASP_159	OD2	2.624
5NUZ	C_LYS_193	NZ	C_ASP_205	OD2	3.554
5NUZ	C_LYS_211	NZ	A_ASP_54	OD1	3.758

5NUZ	C.LYS_211	NZ	A.ASP_54	OD2	3.058
5NUZ	C.LYS_211	NZ	A.ASP_56	OD2	2.861
5NUZ	C.LYS_216	NZ	C.ASP_113	OD1	2.638
5NUZ	L.ARG_61	NH1	L.ASP_82	OD1	2.773
5NUZ	L.ARG_61	NH1	L.ASP_82	OD2	3.655
5NUZ	L.ARG_61	NH2	B.GLU_79	OE1	3.765
5NUZ	L.ARG_61	NH2	B.GLU_79	OE2	2.966
5NUZ	L.LYS_92	NZ	L.GLU_93	OE2	2.743
5NUZ	L.LYS_103	NZ	L.GLU_105	OE2	3.583
5NUZ	L.LYS_142	NZ	L.GLU_105	OE1	3.968
5NUZ	L.LYS_142	NZ	L.GLU_105	OE2	2.583
5NUZ	L.LYS_149	NZ	L.GLU_195	OE2	3.652
5NUZ	L.ARG_155	NH1	L.GLU_185	OE1	3.502
5NUZ	L.ARG_155	NH1	L.GLU_185	OE2	3.552
5NUZ	L.ARG_155	NH2	L.GLU_185	OE2	2.742
5NUZ	L.LYS_183	NZ	L.GLU_187	OE2	3.902
5NUZ	L.HIS_189	ND1	L.ASP_151	OD2	3.012
5NUZ	L.LYS_199	NZ	L.ASP_110	OD2	3.059
5NUZ	D.LYS_169	NZ	D.GLU_171	OE1	3.996
5NUZ	D.LYS_181	NZ	D.ASP_205	OD2	3.184
5NUZ	D.LYS_190	NZ	D.GLU_186	OE2	3.856
5NUZ	D.LYS_191	NZ	D.ASP_159	OD1	3.278
5NUZ	D.LYS_191	NZ	D.ASP_159	OD2	2.625
5NUZ	D.LYS_193	NZ	D.ASP_205	OD2	3.551
5NUZ	D.LYS_211	NZ	H.ASP_54	OD1	3.910
5NUZ	D.LYS_211	NZ	H.ASP_54	OD2	3.105
5NUZ	D.LYS_211	NZ	H.ASP_56	OD2	2.803
5NUZ	D.LYS_216	NZ	D.ASP_113	OD1	2.650
5O14	A.LYS_67	NZ	A.ASP_28	OD1	3.407
5O14	A.LYS_67	NZ	A.ASP_28	OD2	3.007
5O14	A.ARG_75	NH2	A.GLU_95	OE2	3.608
5O14	A.ARG_80	NH1	A.GLU_44	OE1	2.660
5O14	A.ARG_80	NH1	A.GLU_44	OE2	2.889
5O14	A.ARG_80	NH2	A.GLU_92	OE2	3.706
5O14	A.HIS_103	ND1	A.GLU_137	OE1	2.640
5O14	A.HIS_103	ND1	A.GLU_137	OE2	3.720
5O14	A.ARG_127	NH1	A.GLU_112	OE1	2.708
5O14	A.ARG_127	NH1	A.GLU_112	OE2	3.026
5O14	A.ARG_127	NH1	A.ASP_160	OD1	3.772
5O14	A.ARG_127	NH2	A.ASP_160	OD1	2.801
5O14	A.ARG_127	NH2	A.ASP_160	OD2	2.429
5O14	A.ARG_130	NH1	A.GLU_92	OE1	2.377
5O14	A.ARG_130	NH1	A.GLU_92	OE2	3.180
5O14	A.ARG_130	NH2	A.GLU_92	OE2	3.816
5O14	A.ARG_149	NH1	A.ASP_171	OD2	3.921
5O14	A.LYS_180	NZ	A.GLU_182	OE1	3.683
5O14	A.LYS_180	NZ	A.GLU_182	OE2	3.327
5O14	A.LYS_185	NZ	H.ASP_55	OD1	3.249
5O14	A.LYS_185	NZ	H.ASP_55	OD2	2.764
5O14	A.LYS_185	NZ	H.ASP_57	OD2	2.802
5O14	A.ARG_204	NH1	A.ASP_142	OD1	3.025
5O14	A.ARG_204	NH1	A.ASP_142	OD2	3.586
5O14	A.ARG_204	NH1	B.GLU_218	OE1	3.625
5O14	A.LYS_254	NZ	A.ASP_71	OD1	3.427
5O14	A.LYS_254	NZ	A.ASP_71	OD2	2.831
5O14	B.LYS_67	NZ	B.ASP_28	OD1	3.290
5O14	B.LYS_67	NZ	B.ASP_28	OD2	3.377
5O14	B.ARG_75	NH2	B.GLU_95	OE2	3.639

5O14	B_ARG_80	NH1	B_GLU_92	OE1	2.081
5O14	B_ARG_80	NH1	B_GLU_92	OE2	3.936
5O14	B_HIS_103	ND1	B_GLU_137	OE1	2.779
5O14	B_ARG_127	NH1	B_GLU_112	OE1	3.567
5O14	B_ARG_127	NH1	B_GLU_112	OE2	3.007
5O14	B_ARG_127	NH1	B_ASP_160	OD1	3.642
5O14	B_ARG_127	NH1	B_ASP_160	OD2	3.977
5O14	B_ARG_127	NH2	B_ASP_160	OD1	3.089
5O14	B_ARG_127	NH2	B_ASP_160	OD2	2.271
5O14	B_ARG_130	NH1	B_GLU_92	OE1	3.575
5O14	B_ARG_130	NH2	B_GLU_92	OE1	3.187
5O14	B_ARG_130	NH2	B_GLU_92	OE2	2.572
5O14	B_LYS_180	NZ	B_GLU_182	OE1	3.557
5O14	B_LYS_180	NZ	B_GLU_182	OE2	3.069
5O14	B_LYS_185	NZ	C_ASP_55	OD1	3.234
5O14	B_LYS_185	NZ	C_ASP_55	OD2	2.720
5O14	B_LYS_185	NZ	C_ASP_57	OD2	2.736
5O14	B_ARG_204	NH2	B_ASP_142	OD1	2.625
5O14	B_ARG_204	NH2	B_ASP_142	OD2	3.290
5O14	B_HIS_248	ND1	B_GLU_239	OE2	3.868
5O14	B_LYS_254	NZ	B_ASP_71	OD1	3.441
5O14	B_LYS_254	NZ	B_ASP_71	OD2	2.876
5O14	C_ARG_38	NH2	C_GLU_46	OE1	3.250
5O14	C_ARG_38	NH2	C_GLU_46	OE2	3.275
5O14	C_ARG_54	NH2	B_ASP_161	OD1	2.870
5O14	C_ARG_54	NH2	B_ASP_161	OD2	3.505
5O14	C_ARG_59	NH2	C_ASP_57	OD1	3.868
5O14	C_ARG_59	NH2	C_ASP_57	OD2	2.946
5O14	C_ARG_67	NH1	C_ASP_90	OD1	3.547
5O14	C_ARG_67	NH1	C_ASP_90	OD2	2.749
5O14	C_ARG_67	NH2	C_ASP_90	OD1	2.849
5O14	C_ARG_67	NH2	C_ASP_90	OD2	3.598
5O14	C_LYS_152	NZ	C_ASP_153	OD1	3.378
5O14	C_LYS_152	NZ	C_ASP_153	OD2	3.892
5O14	C_LYS_218	NZ	D_GLU_124	OE1	3.107
5O14	C_LYS_219	NZ	C_GLU_221	OE2	3.134
5O14	D_ARG_18	NH1	A_GLU_218	OE1	3.301
5O14	D_ARG_61	NH2	D_GLU_81	OE1	3.945
5O14	D_ARG_61	NH2	D_ASP_82	OD1	2.914
5O14	D_ARG_61	NH2	D_ASP_82	OD2	3.547
5O14	D_LYS_104	NZ	D_GLU_166	OE1	3.330
5O14	D_HIS_190	ND1	D_ASP_152	OD2	2.554
5O14	L_ARG_61	NH2	L_GLU_81	OE2	3.920
5O14	L_ARG_61	NH2	L_ASP_82	OD1	2.835
5O14	L_ARG_61	NH2	L_ASP_82	OD2	3.469
5O14	L_HIS_190	ND1	L_ASP_152	OD2	2.475
5O14	H_ARG_38	NH2	H_GLU_46	OE1	3.594
5O14	H_ARG_38	NH2	H_GLU_46	OE2	3.310
5O14	H_ARG_54	NH1	A_ASP_161	OD1	2.861
5O14	H_ARG_54	NH1	A_ASP_161	OD2	3.283
5O14	H_ARG_59	NH1	L_ASP_94	OD1	3.733
5O14	H_ARG_59	NH1	L_ASP_94	OD2	3.698
5O14	H_ARG_59	NH2	H_ASP_57	OD2	3.228
5O14	H_ARG_67	NH1	H_ASP_90	OD1	2.800
5O14	H_ARG_67	NH1	H_ASP_90	OD2	3.115
5O14	H_ARG_67	NH2	H_ASP_90	OD1	3.984
5O14	H_ARG_67	NH2	H_ASP_90	OD2	2.770
5O14	H_LYS_152	NZ	H_ASP_153	OD1	3.488

5O14	H_LYS_152	NZ	H_ASP_153	OD2	3.902
5O1R	A_HIS_325	NE2	A_ASP_359	OD2	3.546
5O1R	A_ARG_339	NH1	H_ASP_100	OD1	3.968
5O1R	A_ARG_339	NH1	H_ASP_100	OD2	3.203
5O1R	A_ARG_339	NH2	A_ASP_356	OD2	3.370
5O1R	A_HIS_362	ND1	A_ASP_359	OD1	3.211
5O1R	A_HIS_362	ND1	A_ASP_359	OD2	3.253
5O1R	B_HIS_325	NE2	B_ASP_359	OD2	3.534
5O1R	B_HIS_327	ND1	B_ASP_359	OD2	3.365
5O1R	B_HIS_327	NE2	B_GLU_329	OE1	3.540
5O1R	B_ARG_339	NH1	L_ASP_100	OD1	3.595
5O1R	B_ARG_339	NH1	L_ASP_100	OD2	2.991
5O1R	B_ARG_339	NH2	B_ASP_356	OD2	3.328
5O1R	B_HIS_362	ND1	B_ASP_359	OD1	3.462
5O1R	B_HIS_362	ND1	B_ASP_359	OD2	3.359
5O1R	B_LYS_369	NZ	B_ASP_352	OD1	3.251
5O1R	B_LYS_369	NZ	B_ASP_352	OD2	3.231
5O1R	B_LYS_414	NZ	B_GLU_329	OE1	2.817
5O1R	H_ARG_40	NH1	H_ASP_91	OD1	2.787
5O1R	H_ARG_40	NH2	H_GLU_48	OE1	3.205
5O1R	H_ARG_40	NH2	H_ASP_91	OD1	3.587
5O1R	H_ARG_68	NH1	H_ASP_91	OD1	3.869
5O1R	H_ARG_68	NH1	H_ASP_91	OD2	2.814
5O1R	H_ARG_68	NH2	H_ASP_91	OD1	2.730
5O1R	H_ARG_68	NH2	H_ASP_91	OD2	3.072
5O1R	H_LYS_77	NZ	H_ASP_74	OD2	3.598
5O1R	H_ARG_99	NH1	H_ASP_111	OD2	2.787
5O1R	H_ARG_99	NH2	H_ASP_111	OD2	3.771
5O1R	H_ARG_101	NH1	H_ASP_111	OD1	3.295
5O1R	H_LYS_153	NZ	H_ASP_154	OD1	3.367
5O1R	H_LYS_153	NZ	H_ASP_154	OD2	3.373
5O1R	H_LYS_216	NZ	H_ASP_218	OD1	2.810
5O1R	H_LYS_216	NZ	H_ASP_218	OD2	3.814
5O1R	L_ARG_40	NH1	L_ASP_91	OD1	2.950
5O1R	L_ARG_40	NH2	L_GLU_48	OE1	3.324
5O1R	L_ARG_40	NH2	L_ASP_91	OD1	3.459
5O1R	L_ARG_68	NH1	L_ASP_91	OD1	3.823
5O1R	L_ARG_68	NH1	L_ASP_91	OD2	2.796
5O1R	L_ARG_68	NH2	L_ASP_91	OD1	2.735
5O1R	L_ARG_68	NH2	L_ASP_91	OD2	3.137
5O1R	L_ARG_99	NH1	L_ASP_111	OD2	2.797
5O1R	L_ARG_99	NH2	L_ASP_111	OD2	3.787
5O1R	L_ARG_101	NH1	L_ASP_111	OD1	3.285
5O1R	L_LYS_153	NZ	L_ASP_154	OD1	3.364
5O1R	L_LYS_153	NZ	L_ASP_154	OD2	3.368
5O1R	L_ARG_61	NH2	L_ASP_82	OD1	2.771
5O1R	L_ARG_61	NH2	L_ASP_82	OD2	3.474
5O1R	L_ARG_106	NH2	L_ASP_17	OD2	3.826
5O1R	L_LYS_148	NZ	L_GLU_194	OE1	3.986
5O1R	L_LYS_148	NZ	L_GLU_194	OE2	3.121
5O1R	L_LYS_187	NZ	L_ASP_184	OD2	2.794
5O1R	L_ARG_210	NH1	L_GLU_186	OE1	3.088
5O1R	M_ARG_61	NH2	M_ASP_82	OD1	2.703
5O1R	M_ARG_61	NH2	M_ASP_82	OD2	3.538
5O1R	M_ARG_106	NH2	M_ASP_17	OD2	3.805
5O1R	M_LYS_148	NZ	M_GLU_194	OE1	3.979
5O1R	M_LYS_148	NZ	M_GLU_194	OE2	3.088
5O1R	M_LYS_168	NZ	M_ASP_166	OD2	3.194

5O1R	M.LYS_168	NZ	M.ASP_169	OD1	3.618
5O1R	M.LYS_187	NZ	M.ASP_184	OD2	2.800
5O1R	M.HIS_188	ND1	M.ASP_150	OD2	3.718
5OLM	A.HIS_0	NE2	B.GLU_97	OE1	2.769
5OLM	A.HIS_0	NE2	B.GLU_97	OE2	2.598
5OLM	A.ARG_6	NH2	B.GLU_82	OE1	3.071
5OLM	A.ARG_67	NH1	A.GLU_25	OE1	3.750
5OLM	A.ARG_67	NH1	A.GLU_25	OE2	3.549
5OLM	A.ARG_118	NH2	A.GLU_12	OE1	3.821
5OLM	A.ARG_118	NH2	A.GLU_12	OE2	2.560
5OLM	A.LYS_119	NZ	A.ASP_21	OD1	2.937
5OLM	A.LYS_119	NZ	A.ASP_21	OD2	3.505
5OLM	A.HIS_120	ND1	A.ASP_106	OD2	2.406
5OLM	A.HIS_120	NE2	A.ASP_106	OD2	3.755
5OLM	A.HIS_123	ND1	A.ASP_106	OD1	3.485
5OLM	A.HIS_123	ND1	A.ASP_106	OD2	3.274
5OLM	B.HIS_0	NE2	A.GLU_97	OE1	2.741
5OLM	B.HIS_0	NE2	A.GLU_97	OE2	3.001
5OLM	B.ARG_6	NH2	A.GLU_82	OE2	2.559
5OLM	B.ARG_67	NH1	B.GLU_25	OE1	3.574
5OLM	B.ARG_118	NH1	B.GLU_12	OE1	2.892
5OLM	B.ARG_118	NH1	B.GLU_12	OE2	3.281
5OLM	B.LYS_119	NZ	B.ASP_21	OD1	2.647
5OLM	B.LYS_119	NZ	B.ASP_21	OD2	3.211
5OLM	B.HIS_120	ND1	B.ASP_106	OD2	2.889
5OLM	B.HIS_123	ND1	B.ASP_106	OD2	2.910
5OPY	H.ARG_38	NH1	H.ASP_90	OD1	3.516
5OPY	H.ARG_38	NH2	H.GLU_46	OE1	3.707
5OPY	H.ARG_38	NH2	H.GLU_46	OE2	3.605
5OPY	H.ARG_67	NH1	H.ASP_90	OD1	3.928
5OPY	H.ARG_67	NH1	H.ASP_90	OD2	2.808
5OPY	H.ARG_67	NH2	H.ASP_90	OD1	3.025
5OPY	H.ARG_67	NH2	H.ASP_90	OD2	3.394
5OPY	H.LYS_212	NZ	L.GLU_123	OE2	3.578
5OPY	L.ARG_61	NH1	L.ASP_82	OD1	3.825
5OPY	L.ARG_61	NH1	L.ASP_82	OD2	2.771
5OPY	L.ARG_61	NH2	L.GLU_79	OE1	3.579
5OPY	L.ARG_61	NH2	L.GLU_79	OE2	3.640
5OPY	L.ARG_61	NH2	L.ASP_82	OD1	3.036
5OPY	L.ARG_61	NH2	L.ASP_82	OD2	3.486
5OPY	L.LYS_147	NZ	L.GLU_154	OE2	3.483
5OPY	L.LYS_149	NZ	L.GLU_195	OE1	3.661
5OPY	L.LYS_149	NZ	L.GLU_195	OE2	3.217
5OPY	L.ARG_155	NH2	L.GLU_185	OE1	3.459
5OPY	L.LYS_183	NZ	L.GLU_187	OE1	3.576
5OPY	L.LYS_183	NZ	L.GLU_187	OE2	2.833
5OPY	L.HIS_189	ND1	L.ASP_151	OD2	3.278
5OPY	L.HIS_189	NE2	L.GLU_185	OE1	2.982
5OPY	L.HIS_189	NE2	L.GLU_185	OE2	3.936
5OPY	L.LYS_199	NZ	L.ASP_143	OD1	3.965
5OWP	H.ARG_38	NH1	H.ASP_92	OD1	2.637
5OWP	H.ARG_38	NH2	H.GLU_46	OE1	3.304
5OWP	H.ARG_38	NH2	H.GLU_46	OE2	3.626
5OWP	H.ARG_38	NH2	H.ASP_92	OD1	3.777
5OWP	H.ARG_52	NH1	H.GLU_50	OE1	3.856
5OWP	H.ARG_52	NH1	H.GLU_50	OE2	2.567
5OWP	H.HIS_61	ND1	H.GLU_50	OE2	2.863
5OWP	H.ARG_69	NH1	H.ASP_92	OD1	3.470

5OWP	H_ARG_69	NH1	H_ASP_92	OD2	3.501
5OWP	H_ARG_69	NH2	H_ASP_92	OD1	3.595
5OWP	H_ARG_69	NH2	H_ASP_92	OD2	2.233
5OWP	H_ARG_74	NH2	H_ASP_76	OD1	3.541
5OWP	H_ARG_89	NH1	H_GLU_91	OE1	3.703
5OWP	H_HIS_1051	ND1	H_GLU_1047	OE2	3.012
5OWP	H_HIS_1051	NE2	H_ASP_1050	OD1	3.919
5OWP	H_ARG_1070	NH2	H_GLU_1090	OE2	3.696
5OWP	H_ARG_1070	NH2	H_ASP_1091	OD1	2.948
5OWP	H_ARG_1070	NH2	H_ASP_1091	OD2	3.682
5SV3	A_ARG_38	NH1	A_ASP_90	OD1	2.898
5SV3	A_ARG_38	NH2	A_GLU_46	OE1	3.409
5SV3	A_ARG_38	NH2	A_GLU_46	OE2	3.843
5SV3	A_ARG_53	NH2	A_ASP_31	OD1	3.179
5SV3	A_ARG_67	NH1	A_ASP_90	OD1	3.708
5SV3	A_ARG_67	NH1	A_ASP_90	OD2	2.739
5SV3	A_ARG_67	NH2	A_ASP_90	OD1	3.001
5SV3	A_ARG_67	NH2	A_ASP_90	OD2	3.495
5SV3	A_ARG_108	NH2	A_ASP_59	OD1	2.902
5SV3	A_ARG_108	NH2	A_ASP_59	OD2	3.573
5SV3	B_ARG_56	NH2	B_GLU_99	OE2	2.640
5SV3	B_ARG_85	NH1	B_ASP_110	OD1	3.300
5SV3	B_ARG_85	NH2	B_ASP_110	OD1	3.843
5SV3	B_HIS_106	NE2	B_GLU_102	OE1	3.940
5SV3	B_HIS_106	NE2	B_GLU_102	OE2	3.110
5SV3	B_ARG_134	NH2	B_GLU_127	OE2	3.441
5SV3	C_ARG_38	NH1	C_ASP_90	OD1	2.882
5SV3	C_ARG_38	NH2	C_GLU_46	OE1	3.359
5SV3	C_ARG_53	NH2	C_ASP_31	OD1	3.440
5SV3	C_ARG_65	NH1	C_ASP_59	OD1	3.685
5SV3	C_ARG_67	NH1	C_ASP_90	OD1	3.690
5SV3	C_ARG_67	NH1	C_ASP_90	OD2	2.685
5SV3	C_ARG_67	NH2	C_ASP_90	OD1	3.040
5SV3	C_ARG_67	NH2	C_ASP_90	OD2	3.474
5SV3	C_ARG_108	NH2	C_ASP_59	OD1	2.968
5SV3	C_ARG_108	NH2	C_ASP_59	OD2	3.652
5SV3	D_ARG_56	NH1	D_ASP_75	OD1	2.619
5SV3	D_ARG_56	NH1	D_ASP_75	OD2	3.392
5SV3	D_ARG_56	NH2	D_ASP_75	OD1	3.670
5SV3	D_ARG_56	NH2	D_ASP_75	OD2	2.993
5SV3	D_ARG_56	NH2	D_ASP_100	OD1	3.462
5SV3	D_ARG_85	NH2	D_GLU_61	OE2	3.968
5SV3	D_HIS_106	NE2	D_GLU_102	OE2	2.939
5SV3	D_ARG_134	NH2	D_GLU_127	OE2	3.653
5SV4	A_ARG_38	NH1	A_ASP_90	OD1	2.712
5SV4	A_ARG_38	NH2	A_ASP_90	OD1	3.862
5SV4	A_ARG_53	NH2	A_ASP_31	OD1	3.931
5SV4	A_ARG_65	NH1	A_ASP_62	OD1	3.431
5SV4	A_ARG_65	NH2	A_ASP_59	OD1	3.543
5SV4	A_ARG_67	NH1	A_ASP_90	OD1	3.932
5SV4	A_ARG_67	NH1	A_ASP_90	OD2	2.726
5SV4	A_ARG_67	NH2	A_ASP_90	OD1	2.988
5SV4	A_ARG_67	NH2	A_ASP_90	OD2	3.261
5SV4	A_LYS_76	NZ	A_ASP_73	OD2	3.315
5SV4	A_ARG_108	NH2	A_ASP_59	OD1	3.667
5SV4	A_ARG_108	NH2	A_ASP_59	OD2	3.318
5SV4	A_HIS_115	ND1	A_GLU_1	OE1	3.848
5SV4	B_ARG_38	NH1	B_ASP_90	OD1	2.707

5SV4	B_ARG_38	NH2	B_GLU_46	OE2	3.766
5SV4	B_ARG_38	NH2	B_ASP_90	OD1	3.824
5SV4	B_ARG_65	NH2	B_ASP_59	OD1	2.826
5SV4	B_ARG_67	NH1	B_ASP_90	OD1	3.935
5SV4	B_ARG_67	NH1	B_ASP_90	OD2	2.734
5SV4	B_ARG_67	NH2	B_ASP_90	OD1	2.973
5SV4	B_ARG_67	NH2	B_ASP_90	OD2	3.240
5SV4	B_LYS_76	NZ	B_ASP_73	OD2	2.871
5SV4	B_ARG_108	NH2	B_ASP_59	OD2	3.154
5SV4	B_HIS_115	NE2	B_GLU_1	OE1	3.463
5T6P	A_ARG_24	NH2	A_ASP_75	OD1	3.082
5T6P	A_ARG_24	NH2	A_ASP_75	OD2	3.476
5T6P	A_LYS_58	NZ	F_ASP_3	OD2	1.997
5T6P	A_ARG_66	NH1	A_ASP_87	OD1	3.333
5T6P	A_ARG_66	NH1	A_ASP_87	OD2	2.414
5T6P	A_ARG_66	NH2	A_GLU_84	OE1	3.740
5T6P	A_ARG_66	NH2	A_ASP_87	OD1	2.866
5T6P	A_ARG_66	NH2	A_ASP_87	OD2	3.216
5T6P	A_LYS_152	NZ	A_GLU_200	OE2	3.883
5T6P	A_LYS_154	NZ	A_GLU_200	OE1	3.251
5T6P	A_LYS_154	NZ	A_GLU_200	OE2	3.726
5T6P	A_ARG_160	NH1	A_GLU_190	OE2	3.359
5T6P	A_ARG_160	NH2	A_GLU_190	OE1	3.571
5T6P	A_ARG_160	NH2	A_GLU_190	OE2	3.087
5T6P	A_LYS_174	NZ	C_GLU_128	OE2	3.605
5T6P	A_LYS_188	NZ	A_GLU_192	OE1	3.265
5T6P	A_LYS_188	NZ	A_GLU_192	OE2	2.843
5T6P	A_HIS_194	ND1	A_ASP_156	OD2	2.597
5T6P	A_LYS_204	NZ	A_ASP_115	OD2	3.286
5T6P	B_ARG_38	NH1	B_ASP_90	OD1	3.096
5T6P	B_ARG_38	NH2	B_GLU_46	OE1	3.132
5T6P	B_ARG_38	NH2	B_ASP_90	OD1	3.992
5T6P	B_ARG_44	NH1	B_GLU_42	OE1	3.832
5T6P	B_ARG_44	NH2	B_GLU_42	OE1	3.154
5T6P	B_LYS_65	NZ	B_ASP_62	OD1	3.614
5T6P	B_ARG_67	NH2	B_ASP_90	OD1	3.026
5T6P	B_ARG_67	NH2	B_ASP_90	OD2	2.391
5T6P	C_ARG_24	NH2	C_ASP_75	OD1	2.942
5T6P	C_ARG_24	NH2	C_ASP_75	OD2	3.165
5T6P	C_ARG_55	NH1	E_ASP_3	OD2	3.191
5T6P	C_LYS_58	NZ	E_ASP_3	OD2	2.925
5T6P	C_ARG_59	NH2	C_ASP_65	OD1	3.527
5T6P	C_ARG_66	NH1	C_ASP_87	OD1	3.426
5T6P	C_ARG_66	NH1	C_ASP_87	OD2	2.481
5T6P	C_ARG_66	NH2	C_GLU_84	OE1	3.835
5T6P	C_ARG_66	NH2	C_GLU_84	OE2	3.800
5T6P	C_ARG_66	NH2	C_ASP_87	OD1	3.132
5T6P	C_ARG_66	NH2	C_ASP_87	OD2	3.431
5T6P	C_LYS_154	NZ	C_GLU_200	OE1	3.347
5T6P	C_ARG_160	NH1	C_GLU_190	OE2	3.251
5T6P	C_ARG_160	NH2	C_GLU_190	OE1	3.781
5T6P	C_ARG_160	NH2	C_GLU_190	OE2	3.563
5T6P	C_LYS_188	NZ	C_GLU_192	OE1	3.328
5T6P	C_LYS_188	NZ	C_GLU_192	OE2	3.157
5T6P	C_HIS_194	ND1	C_ASP_156	OD2	2.748
5T6P	C_LYS_204	NZ	C_ASP_115	OD2	3.242
5T6P	D_ARG_38	NH1	D_ASP_90	OD1	2.948
5T6P	D_ARG_38	NH2	D_GLU_46	OE1	3.287

5T6P	D_ARG_44	NH2	D_GLU_42	OE1	3.539
5T6P	D_LYS_65	NZ	D_ASP_62	OD1	3.833
5T6P	D_ARG_67	NH2	D_ASP_90	OD1	2.581
5T6P	D_ARG_67	NH2	D_ASP_90	OD2	2.532
5T6P	E_ARG_5	NH2	C_GLU_39	OE1	3.351
5T6P	E_ARG_5	NH2	C_GLU_39	OE2	2.626
5T6P	F_ARG_5	NH2	A_GLU_39	OE1	3.661
5T6P	F_ARG_5	NH2	A_GLU_39	OE2	2.718
5T78	A_ARG_24	NH2	A_ASP_75	OD1	3.292
5T78	A_ARG_24	NH2	A_ASP_75	OD2	3.506
5T78	A_LYS_44	NZ	A_GLU_86	OE2	3.456
5T78	A_LYS_58	NZ	F_ASP_3	OD1	2.579
5T78	A_LYS_58	NZ	F_ASP_3	OD2	3.334
5T78	A_ARG_66	NH1	A_ASP_87	OD1	3.316
5T78	A_ARG_66	NH1	A_ASP_87	OD2	2.549
5T78	A_ARG_66	NH2	A_GLU_84	OE1	3.229
5T78	A_ARG_66	NH2	A_GLU_84	OE2	3.938
5T78	A_ARG_66	NH2	A_ASP_87	OD1	2.866
5T78	A_ARG_66	NH2	A_ASP_87	OD2	3.475
5T78	A_LYS_152	NZ	A_GLU_200	OE2	3.993
5T78	A_LYS_154	NZ	A_GLU_200	OE1	3.160
5T78	A_LYS_154	NZ	A_GLU_200	OE2	3.631
5T78	A_ARG_160	NH1	A_GLU_190	OE2	2.874
5T78	A_ARG_160	NH2	A_GLU_190	OE1	3.635
5T78	A_ARG_160	NH2	A_GLU_190	OE2	3.190
5T78	A_LYS_188	NZ	A_GLU_192	OE1	3.158
5T78	A_LYS_188	NZ	A_GLU_192	OE2	2.974
5T78	A_HIS_194	ND1	A_ASP_156	OD2	2.728
5T78	A_LYS_204	NZ	A_ASP_115	OD1	3.976
5T78	A_LYS_204	NZ	A_ASP_115	OD2	3.220
5T78	B_LYS_3	NZ	B_GLU_1	OE2	3.096
5T78	B_ARG_38	NH1	B_ASP_90	OD1	2.890
5T78	B_ARG_38	NH2	B_GLU_46	OE1	3.379
5T78	B_ARG_38	NH2	B_ASP_90	OD1	3.918
5T78	B_ARG_44	NH2	B_GLU_42	OE1	2.944
5T78	B_ARG_67	NH2	B_ASP_90	OD1	2.740
5T78	B_ARG_67	NH2	B_ASP_90	OD2	2.732
5T78	F_ARG_5	NH1	A_GLU_39	OE1	2.678
5T78	F_ARG_5	NH1	A_GLU_39	OE2	2.480
5T78	C_ARG_24	NH2	C_ASP_75	OD1	3.347
5T78	C_ARG_24	NH2	C_ASP_75	OD2	3.277
5T78	C_ARG_55	NH2	E_ASP_3	OD1	3.685
5T78	C_LYS_58	NZ	E_ASP_3	OD1	2.753
5T78	C_LYS_58	NZ	E_ASP_3	OD2	2.872
5T78	C_ARG_59	NH1	C_ASP_65	OD1	2.623
5T78	C_ARG_66	NH1	C_ASP_87	OD1	3.605
5T78	C_ARG_66	NH1	C_ASP_87	OD2	2.346
5T78	C_ARG_66	NH2	C_GLU_84	OE1	3.346
5T78	C_ARG_66	NH2	C_GLU_84	OE2	3.846
5T78	C_ARG_66	NH2	C_GLU_86	OE2	3.475
5T78	C_ARG_66	NH2	C_ASP_87	OD1	3.004
5T78	C_ARG_66	NH2	C_ASP_87	OD2	3.187
5T78	C_LYS_154	NZ	C_GLU_200	OE1	3.236
5T78	C_ARG_160	NH1	C_GLU_190	OE1	3.681
5T78	C_ARG_160	NH1	C_GLU_190	OE2	2.945
5T78	C_ARG_160	NH2	C_GLU_190	OE1	3.366
5T78	C_ARG_160	NH2	C_GLU_190	OE2	3.933
5T78	C_LYS_188	NZ	C_GLU_192	OE1	3.411

5T78	C_LYS_188	NZ	C_GLU_192	OE2	3.168
5T78	C_HIS_194	ND1	C_ASP_156	OD2	2.579
5T78	C_LYS_204	NZ	C_ASP_115	OD2	3.148
5T78	D_ARG_38	NH1	D_ASP_90	OD1	2.853
5T78	D_ARG_38	NH2	D_GLU_46	OE1	3.156
5T78	D_ARG_38	NH2	D_ASP_90	OD1	3.962
5T78	D_ARG_67	NH2	D_ASP_90	OD1	2.642
5T78	D_ARG_67	NH2	D_ASP_90	OD2	2.478
5T78	D_LYS_211	NZ	C_GLU_128	OE1	3.376
5T78	E_ARG_5	NH1	C_GLU_39	OE1	2.693
5T78	E_ARG_5	NH1	C_GLU_39	OE2	2.664
5TCX	A_LYS_124	NZ	A_ASP_195	OD1	3.385
5TCX	A_LYS_124	NZ	A_ASP_195	OD2	2.891
5TCX	A_LYS_144	NZ	A_ASP_138	OD1	2.296
5TCX	A_LYS_171	NZ	A_ASP_138	OD1	3.371
5TCX	A_LYS_187	NZ	A_ASP_155	OD1	3.854
5TCX	A_LYS_187	NZ	A_ASP_155	OD2	3.942
5TCX	A_HIS_191	NE2	A_ASP_128	OD1	2.502
5TCX	A_HIS_191	NE2	A_ASP_128	OD2	3.422
5TCX	A_LYS_193	NZ	A_GLU_188	OE2	2.937
5TCX	A_LYS_201	NZ	A_ASP_196	OD2	3.323
5TIH	A_HIS_3	ND1	A_GLU_333	OE1	3.713
5TIH	A_LYS_28	NZ	A_GLU_83	OE1	3.102
5TIH	A_ARG_29	NH2	A_ASP_307	OD2	2.694
5TIH	A_LYS_40	NZ	A_ASP_38	OD1	3.409
5TIH	A_LYS_40	NZ	A_ASP_38	OD2	3.673
5TIH	A_HIS_47	ND1	A_ASP_63	OD2	2.822
5TIH	A_LYS_52	NZ	A_GLU_30	OE1	2.433
5TIH	A_LYS_52	NZ	A_GLU_30	OE2	3.751
5TIH	A_LYS_66	NZ	L_ASP_92	OD1	3.482
5TIH	A_ARG_73	NH2	A_ASP_38	OD2	3.662
5TIH	A_HIS_75	NE2	A_ASP_92	OD1	3.360
5TIH	A_LYS_100	NZ	A_ASP_124	OD1	3.619
5TIH	A_ARG_106	NH1	A_GLU_177	OE2	3.261
5TIH	A_LYS_130	NZ	A_ASP_165	OD1	3.418
5TIH	A_LYS_130	NZ	A_ASP_165	OD2	3.868
5TIH	A_LYS_157	NZ	A_ASP_160	OD1	3.149
5TIH	A_LYS_157	NZ	A_ASP_166	OD1	2.621
5TIH	A_LYS_164	NZ	A_GLU_236	OE1	3.487
5TIH	A_LYS_164	NZ	A_GLU_236	OE2	2.956
5TIH	A_LYS_175	NZ	A_GLU_84	OE1	2.559
5TIH	A_LYS_175	NZ	A_GLU_84	OE2	3.472
5TIH	A_LYS_186	NZ	A_ASP_188	OD2	3.836
5TIH	A_LYS_205	NZ	A_ASP_259	OD1	3.347
5TIH	A_LYS_205	NZ	A_GLU_308	OE1	3.703
5TIH	A_LYS_205	NZ	A_GLU_308	OE2	3.973
5TIH	A_HIS_211	NE2	A_ASP_253	OD1	3.623
5TIH	A_LYS_305	NZ	A_GLU_308	OE1	2.934
5TIH	A_LYS_305	NZ	A_GLU_308	OE2	3.911
5TIH	H_HIS_35	NE2	A_ASP_69	OD1	2.973
5TIH	H_HIS_35	NE2	A_ASP_69	OD2	3.535
5TIH	H_ARG_67	NH2	H_ASP_90	OD1	3.399
5TIH	H_ARG_67	NH2	H_ASP_90	OD2	3.193
5TIH	H_ARG_100	NH2	A_ASP_69	OD1	3.080
5TIH	H_ARG_101	NH2	A_GLU_119	OE1	3.357
5TIH	H_ARG_101	NH2	A_GLU_119	OE2	3.359
5TIH	L_ARG_24	NH1	L_ASP_70	OD1	2.418
5TIH	L_ARG_24	NH1	L_ASP_70	OD2	3.060

5TIH	L_ARG_24	NH2	L_ASP_70	OD2	3.324
5TIH	L_LYS_39	NZ	L_GLU_81	OE2	3.732
5TIH	L_LYS_45	NZ	L_GLU_81	OE2	3.780
5TIH	L_ARG_46	NH2	L_ASP_55	OD1	3.597
5TIH	L_ARG_46	NH2	L_ASP_55	OD2	2.892
5TIH	L_ARG_61	NH2	L_GLU_81	OE1	3.907
5TIH	L_ARG_61	NH2	L_ASP_82	OD1	3.126
5TIH	L_ARG_61	NH2	L_ASP_82	OD2	3.816
5TIH	L_ARG_66	NH2	L_GLU_28	OE1	2.831
5TIH	L_ARG_66	NH2	L_GLU_28	OE2	3.769
5TIH	L_LYS_103	NZ	L_ASP_85	OD2	3.969
5TIH	L_LYS_142	NZ	L_GLU_105	OE1	3.302
5TIH	L_LYS_142	NZ	L_GLU_105	OE2	3.271
5TIH	L_LYS_147	NZ	L_GLU_195	OE2	3.679
5TIH	L_LYS_149	NZ	L_GLU_195	OE1	3.506
5TIH	L_LYS_149	NZ	L_GLU_195	OE2	3.625
5TIH	L_ARG_155	NH1	L_GLU_185	OE1	3.848
5TIH	L_ARG_155	NH2	L_GLU_185	OE1	3.868
5TIH	L_HIS_189	ND1	L_ASP_151	OD2	3.122
5TIH	L_ARG_211	NH1	L_GLU_187	OE2	3.061
5TIK	A_HIS_3	ND1	D_GLU_9	OE2	3.832
5TIK	A_HIS_3	NE2	B_GLU_9	OE2	3.597
5TIK	A_LYS_28	NZ	A_GLU_83	OE1	3.971
5TIK	A_HIS_47	NE2	A_GLU_45	OE1	3.808
5TIK	A_HIS_47	NE2	A_GLU_45	OE2	2.915
5TIK	A_HIS_47	NE2	A_ASP_63	OD2	3.962
5TIK	A_LYS_52	NZ	A_GLU_30	OE1	3.759
5TIK	A_LYS_52	NZ	A_GLU_30	OE2	2.781
5TIK	A_HIS_75	NE2	A_ASP_92	OD1	3.609
5TIK	A_HIS_75	NE2	A_ASP_92	OD2	3.079
5TIK	A_ARG_145	NH1	A_ASP_234	OD2	3.502
5TIK	A_ARG_145	NH2	A_ASP_234	OD1	2.795
5TIK	A_ARG_145	NH2	A_ASP_234	OD2	3.031
5TIK	A_LYS_157	NZ	A_ASP_160	OD1	3.965
5TIK	A_LYS_157	NZ	A_ASP_161	OD1	3.943
5TIK	A_LYS_157	NZ	A_ASP_166	OD1	3.100
5TIK	A_LYS_164	NZ	A_ASP_160	OD1	3.523
5TIK	A_LYS_175	NZ	A_ASP_81	OD2	2.307
5TIK	A_LYS_175	NZ	A_GLU_84	OE2	2.899
5TIK	A_LYS_182	NZ	A_ASP_165	OD2	3.588
5TIK	A_LYS_205	NZ	A_GLU_308	OE1	3.830
5TIK	A_LYS_205	NZ	A_GLU_308	OE2	3.734
5TIK	A_HIS_211	NE2	A_ASP_253	OD1	3.988
5TIK	A_LYS_287	NZ	A_GLU_273	OE2	3.653
5TIK	A_LYS_305	NZ	A_GLU_308	OE1	3.281
5TIK	A_LYS_305	NZ	A_GLU_308	OE2	3.263
5TIK	B_HIS_3	NE2	A_GLU_9	OE1	3.627
5TIK	B_HIS_3	NE2	A_GLU_9	OE2	3.175
5TIK	B_HIS_3	NE2	C_GLU_9	OE1	3.296
5TIK	B_HIS_3	NE2	C_GLU_9	OE2	3.823
5TIK	B_LYS_28	NZ	B_GLU_83	OE1	3.175
5TIK	B_LYS_28	NZ	B_GLU_83	OE2	3.839
5TIK	B_HIS_47	ND1	B_ASP_63	OD2	3.018
5TIK	B_LYS_52	NZ	B_GLU_30	OE1	3.671
5TIK	B_HIS_75	NE2	B_ASP_92	OD2	2.903
5TIK	B_LYS_100	NZ	B_ASP_124	OD1	3.470
5TIK	B_LYS_100	NZ	B_ASP_124	OD2	2.292
5TIK	B_ARG_106	NH2	B_GLU_177	OE2	3.673

5TIK	B_LYS_157	NZ	B_ASP_161	OD1	3.470
5TIK	B_LYS_157	NZ	B_ASP_166	OD1	2.331
5TIK	B_LYS_157	NZ	B_ASP_166	OD2	3.739
5TIK	B_LYS_175	NZ	B_GLU_84	OE1	3.721
5TIK	B_LYS_175	NZ	B_GLU_84	OE2	3.186
5TIK	B_LYS_182	NZ	B_ASP_165	OD1	3.333
5TIK	B_LYS_186	NZ	B_GLU_236	OE1	2.882
5TIK	B_LYS_186	NZ	B_GLU_236	OE2	3.887
5TIK	B_LYS_205	NZ	B_ASP_259	OD2	3.092
5TIK	B_HIS_211	NE2	B_ASP_253	OD1	3.835
5TIK	B_ARG_242	NH2	B_GLU_228	OE2	3.300
5TIK	B_LYS_290	NZ	A_GLU_281	OE1	3.703
5TIK	B_LYS_305	NZ	B_GLU_308	OE1	2.748
5TIK	B_ARG_310	NH2	B_ASP_307	OD2	3.708
5TIK	C_HIS_3	NE2	B_GLU_9	OE1	2.908
5TIK	C_ARG_29	NH2	B_ASP_259	OD2	3.311
5TIK	C_HIS_47	ND1	C_ASP_63	OD2	3.231
5TIK	C_LYS_52	NZ	C_GLU_30	OE1	3.235
5TIK	C_LYS_52	NZ	C_GLU_30	OE2	3.319
5TIK	C_LYS_66	NZ	C_ASP_63	OD2	3.918
5TIK	C_LYS_99	NZ	C_GLU_93	OE2	2.385
5TIK	C_ARG_106	NH2	C_GLU_177	OE2	3.784
5TIK	C_LYS_157	NZ	C_ASP_161	OD1	3.341
5TIK	C_LYS_157	NZ	C_ASP_161	OD2	3.707
5TIK	C_LYS_157	NZ	C_ASP_166	OD1	2.361
5TIK	C_HIS_173	ND1	C_ASP_174	OD2	3.723
5TIK	C_LYS_175	NZ	C_GLU_84	OE1	3.431
5TIK	C_LYS_175	NZ	C_GLU_84	OE2	2.598
5TIK	C_LYS_182	NZ	C_ASP_165	OD2	3.481
5TIK	C_LYS_186	NZ	C_GLU_232	OE1	3.373
5TIK	C_LYS_205	NZ	C_ASP_259	OD1	2.434
5TIK	C_LYS_205	NZ	C_ASP_259	OD2	3.747
5TIK	C_LYS_205	NZ	C_GLU_308	OE1	3.839
5TIK	C_LYS_205	NZ	C_GLU_308	OE2	3.684
5TIK	C_LYS_287	NZ	C_GLU_273	OE1	3.786
5TIK	C_LYS_305	NZ	C_GLU_308	OE1	3.517
5TIK	C_LYS_305	NZ	C_GLU_308	OE2	3.437
5TIK	C_ARG_310	NH1	C_ASP_307	OD2	3.297
5TIK	D_HIS_3	NE2	A_GLU_9	OE1	2.950
5TIK	D_HIS_3	NE2	A_GLU_9	OE2	2.918
5TIK	D_ARG_7	NH1	D_GLU_9	OE1	3.447
5TIK	D_LYS_28	NZ	D_GLU_83	OE1	3.595
5TIK	D_LYS_28	NZ	D_GLU_83	OE2	2.506
5TIK	D_HIS_47	ND1	D_ASP_63	OD2	2.503
5TIK	D_LYS_52	NZ	D_GLU_30	OE1	2.944
5TIK	D_LYS_52	NZ	D_GLU_30	OE2	3.601
5TIK	D_HIS_75	NE2	D_ASP_92	OD1	3.926
5TIK	D_LYS_99	NZ	D_GLU_91	OE1	3.765
5TIK	D_ARG_106	NH1	D_GLU_177	OE1	3.872
5TIK	D_ARG_106	NH1	D_GLU_177	OE2	3.044
5TIK	D_ARG_106	NH2	D_GLU_177	OE2	3.983
5TIK	D_LYS_157	NZ	D_ASP_161	OD1	2.995
5TIK	D_LYS_157	NZ	D_ASP_166	OD1	2.612
5TIK	D_LYS_157	NZ	D_ASP_166	OD2	3.577
5TIK	D_LYS_175	NZ	D_GLU_146	OE1	3.788
5TIK	D_LYS_205	NZ	D_GLU_308	OE2	3.635
5TIK	D_LYS_287	NZ	D_GLU_273	OE1	3.724
5TIK	D_LYS_305	NZ	D_GLU_308	OE1	3.354

5TIK	D_LYS_305	NZ	D_GLU_308	OE2	2.963
5TL5	L_LYS_24	NZ	L_ASP_74	OD1	3.254
5TL5	L_LYS_24	NZ	L_ASP_74	OD2	3.141
5TL5	L_ARG_65	NH1	L_ASP_86	OD1	3.543
5TL5	L_ARG_65	NH1	L_ASP_86	OD2	2.755
5TL5	L_ARG_65	NH2	L_GLU_85	OE2	3.698
5TL5	L_ARG_65	NH2	L_ASP_86	OD1	2.948
5TL5	L_ARG_65	NH2	L_ASP_86	OD2	3.662
5TL5	L_LYS_153	NZ	L_GLU_199	OE1	2.824
5TL5	L_HIS_193	ND1	L_ASP_189	OD1	3.571
5TL5	L_ARG_215	NH1	L_GLU_191	OE1	3.322
5TL5	H_ARG_40	NH1	H_GLU_89	OE1	3.264
5TL5	H_ARG_40	NH2	H_GLU_89	OE1	3.195
5TL5	H_ARG_40	NH2	H_GLU_89	OE2	3.409
5TL5	H_ARG_50	NH1	L_ASP_98	OD1	2.887
5TL5	H_ARG_50	NH1	L_ASP_98	OD2	3.532
5TL5	H_ARG_50	NH2	L_ASP_98	OD1	3.785
5TL5	H_ARG_50	NH2	L_ASP_98	OD2	2.933
5TL5	H_LYS_67	NZ	H_ASP_90	OD1	3.648
5TL5	H_LYS_67	NZ	H_ASP_90	OD2	2.769
5TL5	H_ARG_98	NH2	H_ASP_100	OD1	3.835
5TL5	H_LYS_150	NZ	H_ASP_151	OD1	3.624
5TL5	H_LYS_150	NZ	H_ASP_151	OD2	3.145
5TL5	H_LYS_216	NZ	L_GLU_127	OE1	3.027
5TL5	H_LYS_216	NZ	L_GLU_127	OE2	3.571
5TL5	A_LYS_17	NZ	H_ASP_55	OD1	3.610
5TL5	A_LYS_17	NZ	H_ASP_55	OD2	2.637
5TL5	A_LYS_17	NZ	H_ASP_57	OD1	2.990
5TL5	A_HIS_36	NE2	H_ASP_104	OD1	3.017
5TL5	A_HIS_36	NE2	H_ASP_104	OD2	2.947
5TL5	A_ARG_37	NH2	H_ASP_104	OD2	2.895
5TL5	A_ARG_58	NH1	A_ASP_54	OD1	3.167
5TL5	A_ARG_58	NH1	A_ASP_54	OD2	3.803
5TL5	A_ARG_58	NH1	A_GLU_62	OE2	3.990
5TL5	A_ARG_58	NH2	A_ASP_54	OD1	2.943
5TL5	A_ARG_58	NH2	A_GLU_62	OE2	3.654
5TL5	A_ARG_65	NH1	A_GLU_96	OE2	3.447
5TL5	A_ARG_65	NH2	A_GLU_96	OE2	3.907
5TL5	A_ARG_74	NH1	A_GLU_83	OE1	3.799
5TL5	A_ARG_74	NH2	A_GLU_83	OE1	3.360
5TLJ	A_ARG_65	NH1	A_GLU_83	OE2	2.851
5TLJ	A_ARG_65	NH1	A_GLU_85	OE2	3.561
5TLJ	A_ARG_65	NH2	A_ASP_86	OD1	2.756
5TLJ	A_ARG_65	NH2	A_ASP_86	OD2	2.866
5TLJ	A_LYS_153	NZ	A_GLU_199	OE1	3.517
5TLJ	A_LYS_153	NZ	A_GLU_199	OE2	2.835
5TLJ	A_ARG_215	NH1	A_GLU_191	OE1	2.713
5TLJ	B_LYS_38	NZ	B_GLU_46	OE1	3.196
5TLJ	B_LYS_38	NZ	B_ASP_90	OD1	3.704
5TLJ	B_ARG_40	NH1	B_GLU_89	OE2	2.861
5TLJ	B_ARG_50	NH1	A_ASP_98	OD1	2.672
5TLJ	B_ARG_50	NH1	A_ASP_98	OD2	3.926
5TLJ	B_LYS_63	NZ	B_GLU_46	OE1	3.698
5TLJ	B_LYS_63	NZ	B_GLU_89	OE1	3.182
5TLJ	B_LYS_63	NZ	B_GLU_89	OE2	3.310
5TLJ	B_LYS_67	NZ	B_ASP_90	OD2	3.121
5TLJ	B_LYS_150	NZ	B_ASP_151	OD1	3.569
5TLJ	B_LYS_150	NZ	B_ASP_151	OD2	3.604

5TLJ	B_LYS_213	NZ	B_ASP_215	OD2	3.942
5TLJ	C_ARG_65	NH1	C_ASP_86	OD1	2.756
5TLJ	C_ARG_65	NH1	C_ASP_86	OD2	2.971
5TLJ	C_ARG_65	NH2	C_GLU_83	OE1	3.613
5TLJ	C_ARG_65	NH2	C_ASP_86	OD1	3.864
5TLJ	C_LYS_153	NZ	C_GLU_199	OE1	3.775
5TLJ	C_LYS_153	NZ	C_GLU_199	OE2	3.308
5TLJ	C_HIS_193	ND1	C_ASP_189	OD1	3.530
5TLJ	C_ARG_215	NH1	C_GLU_191	OE2	3.808
5TLJ	C_ARG_215	NH2	C_GLU_191	OE2	3.846
5TLJ	D_ARG_38	NH1	D_ASP_90	OD1	3.566
5TLJ	D_ARG_38	NH2	D_GLU_46	OE1	2.710
5TLJ	D_ARG_38	NH2	D_GLU_46	OE2	3.743
5TLJ	D_ARG_38	NH2	D_ASP_90	OD1	3.868
5TLJ	D_ARG_67	NH1	D_ASP_90	OD2	3.824
5TLJ	D_ARG_67	NH2	D_ASP_90	OD1	3.650
5TLJ	D_ARG_100	NH1	X_ASP_43	OD2	3.396
5TLJ	D_ARG_100	NH2	C_GLU_59	OE1	2.703
5TLJ	D_ARG_100	NH2	C_GLU_59	OE2	3.403
5TLJ	D_ARG_100	NH2	X_ASP_43	OD2	3.844
5TLJ	D_LYS_147	NZ	D_ASP_148	OD1	3.264
5TLJ	D_LYS_147	NZ	D_ASP_148	OD2	2.806
5TLJ	E_LYS_24	NZ	E_ASP_74	OD1	3.563
5TLJ	E_ARG_65	NH1	E_GLU_83	OE2	3.709
5TLJ	E_ARG_65	NH2	E_GLU_85	OE1	3.881
5TLJ	E_ARG_65	NH2	E_ASP_86	OD1	2.674
5TLJ	E_ARG_65	NH2	E_ASP_86	OD2	3.332
5TLJ	E_ARG_146	NH2	E_GLU_169	OE1	3.285
5TLJ	E_ARG_215	NH1	E_GLU_191	OE2	3.303
5TLJ	F_LYS_38	NZ	F_GLU_46	OE1	3.804
5TLJ	F_ARG_50	NH1	E_ASP_98	OD1	3.689
5TLJ	F_ARG_50	NH1	E_ASP_98	OD2	2.897
5TLJ	F_ARG_50	NH2	E_ASP_98	OD1	3.671
5TLJ	F_ARG_50	NH2	E_ASP_98	OD2	3.575
5TLJ	F_LYS_63	NZ	F_GLU_89	OE1	3.558
5TLJ	F_LYS_67	NZ	F_ASP_90	OD1	3.830
5TLJ	F_LYS_67	NZ	F_ASP_90	OD2	3.115
5TLJ	F_ARG_98	NH1	F_ASP_100	OD1	3.189
5TLJ	F_ARG_98	NH1	F_ASP_100	OD2	3.943
5TLJ	F_LYS_150	NZ	F_ASP_151	OD1	3.468
5TLJ	F_HIS_171	ND1	E_ASP_171	OD1	3.892
5TLJ	F_HIS_171	NE2	E_ASP_171	OD2	3.411
5TLJ	F_LYS_217	NZ	F_GLU_219	OE2	2.788
5TLJ	G_ARG_24	NH2	G_ASP_74	OD1	3.512
5TLJ	G_ARG_65	NH1	G_GLU_83	OE1	3.877
5TLJ	G_ARG_65	NH1	G_ASP_86	OD1	3.552
5TLJ	G_ARG_65	NH1	G_ASP_86	OD2	2.689
5TLJ	G_ARG_65	NH2	G_GLU_83	OE1	3.030
5TLJ	G_LYS_187	NZ	G_GLU_191	OE2	3.996
5TLJ	H_ARG_38	NH1	H_GLU_46	OE1	3.968
5TLJ	H_ARG_38	NH1	H_ASP_90	OD1	3.590
5TLJ	H_ARG_38	NH2	H_GLU_46	OE1	2.850
5TLJ	H_ARG_38	NH2	H_GLU_46	OE2	3.149
5TLJ	H_ARG_38	NH2	H_ASP_90	OD1	3.501
5TLJ	H_ARG_67	NH1	H_ASP_90	OD1	3.809
5TLJ	H_ARG_67	NH1	H_ASP_90	OD2	2.805
5TLJ	H_ARG_67	NH2	H_ASP_90	OD1	3.038
5TLJ	H_ARG_67	NH2	H_ASP_90	OD2	3.316

5TLJ	H_ARG_76	NH2	H_ASP_73	OD2	3.334
5TLJ	H_ARG_98	NH2	H_ASP_105	OD2	3.277
5TLJ	H_ARG_100	NH2	G_GLU_59	OE1	2.761
5TLJ	H_LYS_147	NZ	H_ASP_148	OD1	3.556
5TLJ	H_LYS_147	NZ	H_ASP_148	OD2	2.892
5TLJ	X_LYS_17	NZ	B_ASP_57	OD2	3.053
5TLJ	X_HIS_36	NE2	B_ASP_104	OD1	3.121
5TLJ	X_HIS_36	NE2	B_ASP_104	OD2	2.886
5TLJ	X_ARG_58	NH1	X_GLU_62	OE2	2.792
5TLJ	X_ARG_58	NH2	X_ASP_54	OD1	3.157
5TLJ	X_ARG_58	NH2	X_GLU_62	OE2	3.987
5TLJ	X_ARG_65	NH2	X_GLU_83	OE2	3.778
5TLK	A_LYS_24	NZ	A_ASP_74	OD1	3.675
5TLK	A_ARG_65	NH1	A_ASP_86	OD1	3.826
5TLK	A_ARG_65	NH1	A_ASP_86	OD2	2.689
5TLK	A_ARG_65	NH2	A_GLU_83	OE2	3.993
5TLK	A_ARG_65	NH2	A_ASP_86	OD1	3.142
5TLK	A_ARG_65	NH2	A_ASP_86	OD2	3.459
5TLK	A_LYS_107	NZ	A_GLU_169	OE2	3.867
5TLK	A_LYS_153	NZ	A_GLU_199	OE1	2.764
5TLK	B_ARG_50	NH1	A_ASP_98	OD1	3.277
5TLK	B_ARG_50	NH1	A_ASP_98	OD2	2.898
5TLK	B_ARG_50	NH2	A_ASP_98	OD1	2.923
5TLK	B_LYS_63	NZ	B_GLU_46	OE1	3.471
5TLK	B_LYS_63	NZ	B_GLU_46	OE2	3.192
5TLK	B_LYS_67	NZ	B_ASP_90	OD1	3.881
5TLK	B_LYS_67	NZ	B_ASP_90	OD2	2.993
5TLK	B_LYS_150	NZ	B_ASP_151	OD1	3.046
5TLK	B_LYS_150	NZ	B_ASP_151	OD2	2.798
5TLK	B_LYS_216	NZ	A_GLU_127	OE1	3.067
5TLK	B_LYS_216	NZ	A_GLU_127	OE2	3.588
5TLK	C_ARG_24	NH1	C_ASP_74	OD1	3.109
5TLK	C_ARG_24	NH1	C_ASP_74	OD2	2.746
5TLK	C_LYS_27	NZ	C_GLU_97	OE1	3.042
5TLK	C_ARG_57	NH2	X_ASP_43	OD1	3.384
5TLK	C_ARG_65	NH1	C_ASP_86	OD1	3.594
5TLK	C_ARG_65	NH1	C_ASP_86	OD2	2.481
5TLK	C_ARG_65	NH2	C_ASP_86	OD1	2.770
5TLK	C_ARG_65	NH2	C_ASP_86	OD2	3.157
5TLK	C_LYS_107	NZ	C_GLU_169	OE2	2.732
5TLK	C_LYS_153	NZ	C_GLU_199	OE1	2.786
5TLK	C_LYS_153	NZ	C_GLU_199	OE2	3.954
5TLK	C_LYS_187	NZ	C_GLU_191	OE2	3.768
5TLK	C_ARG_215	NH1	C_GLU_191	OE1	3.277
5TLK	D_ARG_38	NH1	D_ASP_90	OD1	2.987
5TLK	D_ARG_38	NH2	D_GLU_46	OE1	2.875
5TLK	D_ARG_38	NH2	D_GLU_46	OE2	3.558
5TLK	D_ARG_38	NH2	D_ASP_90	OD1	3.987
5TLK	D_LYS_65	NZ	D_ASP_62	OD1	2.814
5TLK	D_ARG_67	NH1	D_ASP_90	OD2	2.614
5TLK	D_ARG_67	NH2	D_ASP_90	OD1	3.114
5TLK	D_ARG_67	NH2	D_ASP_90	OD2	3.161
5TLK	D_ARG_98	NH2	D_ASP_105	OD1	3.927
5TLK	D_ARG_98	NH2	D_ASP_105	OD2	2.700
5TLK	D_ARG_100	NH1	X_ASP_43	OD2	2.904
5TLK	D_ARG_100	NH2	C_GLU_59	OE1	2.708
5TLK	D_ARG_100	NH2	C_GLU_59	OE2	3.299
5TLK	D_ARG_100	NH2	X_ASP_43	OD2	3.882

5TLK	D_LYS_147	NZ	D_ASP_148	OD1	3.173
5TLK	D_LYS_147	NZ	D_ASP_148	OD2	3.344
5TLK	E_ARG_65	NH1	E_ASP_86	OD1	3.727
5TLK	E_ARG_65	NH1	E_ASP_86	OD2	2.581
5TLK	E_ARG_65	NH2	E_GLU_83	OE1	3.517
5TLK	E_ARG_65	NH2	E_ASP_86	OD1	2.787
5TLK	E_ARG_65	NH2	E_ASP_86	OD2	3.198
5TLK	E_LYS_153	NZ	E_GLU_199	OE1	2.662
5TLK	E_LYS_187	NZ	E_GLU_191	OE1	3.794
5TLK	F_LYS_38	NZ	F_ASP_90	OD1	3.722
5TLK	F_ARG_40	NH1	F_GLU_89	OE1	3.871
5TLK	F_ARG_40	NH2	F_GLU_89	OE1	3.823
5TLK	F_ARG_40	NH2	F_GLU_89	OE2	2.772
5TLK	F_ARG_50	NH1	E_ASP_98	OD1	3.086
5TLK	F_ARG_50	NH1	E_ASP_98	OD2	3.224
5TLK	F_ARG_50	NH2	E_ASP_98	OD1	2.767
5TLK	F_ARG_50	NH2	E_ASP_98	OD2	3.943
5TLK	F_LYS_67	NZ	F_ASP_90	OD2	3.364
5TLK	F_ARG_98	NH1	F_ASP_100	OD1	3.582
5TLK	F_LYS_150	NZ	F_ASP_151	OD1	3.689
5TLK	G_ARG_24	NH1	G_ASP_74	OD2	2.978
5TLK	G_ARG_24	NH2	G_ASP_74	OD1	3.856
5TLK	G_ARG_24	NH2	G_ASP_74	OD2	3.656
5TLK	G_LYS_27	NZ	G_GLU_97	OE1	3.620
5TLK	G_ARG_33	NH1	Y_GLU_24	OE2	3.993
5TLK	G_ARG_33	NH2	Y_GLU_24	OE2	3.475
5TLK	G_ARG_65	NH1	G_ASP_86	OD1	3.101
5TLK	G_ARG_65	NH1	G_ASP_86	OD2	2.770
5TLK	G_ARG_65	NH2	G_GLU_85	OE2	3.596
5TLK	G_LYS_107	NZ	G_GLU_169	OE2	3.886
5TLK	G_LYS_153	NZ	G_GLU_199	OE1	2.760
5TLK	G_LYS_187	NZ	G_GLU_191	OE2	2.938
5TLK	G_HIS_193	ND1	G_ASP_189	OD1	3.813
5TLK	G_ARG_215	NH1	G_GLU_191	OE1	3.873
5TLK	H_ARG_38	NH1	H_ASP_90	OD1	2.755
5TLK	H_ARG_38	NH2	H_GLU_46	OE1	3.268
5TLK	H_ARG_38	NH2	H_GLU_46	OE2	3.476
5TLK	H_ARG_38	NH2	H_ASP_90	OD1	3.679
5TLK	H_LYS_65	NZ	H_ASP_62	OD1	3.982
5TLK	H_ARG_67	NH1	H_ASP_90	OD2	2.783
5TLK	H_ARG_67	NH2	H_ASP_90	OD1	2.925
5TLK	H_ARG_67	NH2	H_ASP_90	OD2	2.986
5TLK	H_ARG_98	NH2	H_ASP_105	OD1	3.818
5TLK	H_ARG_98	NH2	H_ASP_105	OD2	2.712
5TLK	H_ARG_100	NH1	G_GLU_59	OE1	3.531
5TLK	H_ARG_100	NH1	Y_ASP_43	OD2	3.423
5TLK	H_ARG_100	NH2	G_GLU_59	OE1	2.787
5TLK	H_ARG_100	NH2	G_GLU_59	OE2	3.306
5TLK	H_LYS_147	NZ	H_ASP_148	OD1	3.296
5TLK	H_LYS_147	NZ	H_ASP_148	OD2	3.127
5TLK	H_LYS_213	NZ	G_GLU_127	OE1	3.569
5TLK	X_LYS_17	NZ	B_ASP_55	OD1	3.914
5TLK	X_LYS_17	NZ	B_ASP_55	OD2	3.018
5TLK	X_LYS_17	NZ	B_ASP_57	OD2	3.114
5TLK	X_HIS_36	NE2	B_ASP_104	OD1	3.010
5TLK	X_HIS_36	NE2	B_ASP_104	OD2	2.891
5TLK	X_ARG_37	NH2	B_ASP_104	OD1	2.703
5TLK	X_HIS_56	ND1	X_ASP_54	OD1	3.625

5TLK	X_ARG_58	NH2	X_ASP_54	OD1	2.720
5TLK	X_ARG_58	NH2	X_ASP_54	OD2	3.583
5TLK	X_ARG_74	NH1	X_GLU_83	OE2	3.772
5TLK	X_ARG_74	NH2	X_GLU_83	OE2	3.777
5TLK	Y_LYS_17	NZ	F_ASP_55	OD1	3.581
5TLK	Y_LYS_17	NZ	F_ASP_55	OD2	3.170
5TLK	Y_LYS_17	NZ	F_ASP_57	OD2	3.380
5TLK	Y_HIS_36	NE2	F_ASP_104	OD1	3.198
5TLK	Y_HIS_36	NE2	F_ASP_104	OD2	2.793
5TLK	Y_ARG_37	NH2	F_ASP_104	OD1	3.616
5TLK	Y_ARG_58	NH2	Y_ASP_54	OD1	3.024
5TLK	Y_ARG_74	NH1	Y_GLU_83	OE2	3.804
5TLK	Y_ARG_74	NH2	Y_GLU_83	OE2	3.441
5TRU	L_ARG_24	NH1	L_ASP_71	OD2	3.954
5TRU	L_ARG_55	NH2	L_ASP_61	OD1	3.408
5TRU	L_ARG_62	NH2	L_ASP_83	OD1	2.775
5TRU	L_ARG_62	NH2	L_ASP_83	OD2	3.715
5TRU	L_LYS_150	NZ	L_GLU_196	OE1	3.945
5TRU	L_HIS_190	ND1	L_ASP_152	OD2	3.931
5TRU	H_ARG_38	NH1	H_ASP_90	OD1	2.859
5TRU	H_ARG_38	NH2	H_GLU_46	OE1	3.419
5TRU	H_ARG_38	NH2	H_ASP_90	OD1	3.391
5TRU	H_ARG_67	NH1	H_ASP_90	OD1	3.755
5TRU	H_ARG_67	NH1	H_ASP_90	OD2	2.634
5TRU	H_ARG_67	NH2	H_ASP_90	OD1	2.978
5TRU	H_ARG_67	NH2	H_ASP_90	OD2	3.388
5TRU	H_ARG_98	NH2	H_ASP_106	OD1	3.783
5TRU	H_ARG_98	NH2	H_ASP_106	OD2	2.740
5TRU	H_LYS_148	NZ	H_ASP_149	OD1	3.967
5TRU	H_LYS_148	NZ	H_ASP_149	OD2	3.741
5TRU	L_ARG_55	NH2	L_ASP_61	OD1	2.796
5TRU	L_ARG_62	NH2	L_ASP_83	OD1	2.608
5TRU	L_ARG_62	NH2	L_ASP_83	OD2	3.126
5TRU	L_ARG_78	NH1	L_GLU_80	OE2	2.858
5TRU	L_LYS_104	NZ	L_GLU_166	OE2	3.131
5TRU	L_LYS_127	NZ	L_ASP_123	OD2	3.360
5TRU	h_ARG_38	NH1	h_ASP_90	OD1	2.730
5TRU	h_ARG_38	NH2	h_GLU_46	OE1	3.334
5TRU	h_ARG_38	NH2	h_ASP_90	OD1	3.607
5TRU	h_ARG_67	NH1	h_ASP_90	OD1	3.906
5TRU	h_ARG_67	NH1	h_ASP_90	OD2	2.771
5TRU	h_ARG_67	NH2	h_ASP_90	OD1	3.264
5TRU	h_ARG_67	NH2	h_ASP_90	OD2	3.554
5TRU	h_ARG_98	NH2	h_ASP_106	OD2	3.484
5TRU	h_HIS_169	NE2	L_ASP_168	OD2	3.995
5TZ2	H_LYS_12	NZ	H_GLU_16	OE1	3.837
5TZ2	H_ARG_38	NH2	H_GLU_46	OE1	3.145
5TZ2	H_ARG_38	NH2	H_GLU_46	OE2	3.092
5TZ2	H_ARG_59	NH2	H_ASP_57	OD1	3.404
5TZ2	H_ARG_59	NH2	H_ASP_57	OD2	2.670
5TZ2	H_ARG_98	NH2	H_ASP_108	OD1	3.872
5TZ2	H_ARG_98	NH2	H_ASP_108	OD2	2.930
5TZ2	H_ARG_101	NH1	C_ASP_46	OD2	3.182
5TZ2	H_HIS_105	NE2	C_ASP_51	OD1	2.798
5TZ2	H_HIS_105	NE2	C_ASP_51	OD2	2.654
5TZ2	H_LYS_150	NZ	H_ASP_151	OD1	3.764
5TZ2	L_ARG_61	NH2	L_ASP_82	OD1	3.176
5TZ2	L_ARG_61	NH2	L_ASP_82	OD2	3.586

5TZ2	C_LYS_41	NZ	C_ASP_46	OD1	2.641
5TZ2	C_ARG_45	NH1	C_ASP_62	OD2	3.329
5TZ2	C_ARG_45	NH2	C_ASP_62	OD1	3.717
5TZ2	C_ARG_45	NH2	C_ASP_62	OD2	3.722
5TZ2	C_LYS_56	NZ	H_ASP_55	OD1	3.222
5TZ2	C_LYS_56	NZ	H_ASP_55	OD2	2.489
5TZ2	C_LYS_56	NZ	H_ASP_57	OD2	3.354
5TZ2	C_HIS_90	NE2	C_ASP_62	OD2	3.559
5TZ2	C_ARG_103	NH2	C_GLU_29	OE2	3.947
5TZ2	C_ARG_103	NH2	C_GLU_100	OE1	2.920
5TZ2	C_ARG_103	NH2	C_GLU_100	OE2	3.895
5TZT	B_ARG_82	NH2	H_ASP_31	OD1	2.783
5TZT	B_ARG_82	NH2	H_ASP_31	OD2	3.806
5TZT	B_LYS_108	NZ	B_GLU_110	OE2	3.764
5TZT	B_HIS_194	ND1	B_ASP_156	OD2	2.786
5TZT	A_LYS_19	NZ	A_GLU_82	OE1	3.806
5TZT	A_ARG_38	NH1	A_ASP_90	OD2	3.536
5TZT	A_ARG_38	NH2	A_GLU_46	OE1	3.836
5TZT	A_ARG_38	NH2	A_GLU_46	OE2	2.074
5TZT	A_LYS_63	NZ	A_GLU_46	OE1	3.429
5TZT	A_LYS_63	NZ	A_GLU_46	OE2	3.935
5TZT	A_ARG_67	NH1	A_ASP_90	OD1	3.187
5TZT	A_ARG_67	NH1	A_ASP_90	OD2	3.312
5TZT	A_ARG_67	NH2	A_ASP_90	OD1	2.897
5TZT	A_ARG_87	NH1	A_GLU_89	OE1	3.756
5TZT	A_ARG_98	NH1	A_ASP_105	OD1	3.423
5TZT	A_ARG_98	NH1	A_ASP_105	OD2	2.447
5TZT	A_HIS_102	ND1	D_GLU_104	OE2	3.803
5TZT	L_LYS_55	NZ	C_GLU_104	OE1	3.704
5TZT	L_LYS_55	NZ	C_GLU_104	OE2	2.899
5TZT	L_ARG_66	NH1	L_ASP_87	OD1	3.313
5TZT	L_ARG_66	NH1	L_ASP_87	OD2	2.679
5TZT	L_ARG_66	NH2	L_GLU_84	OE1	2.654
5TZT	L_ARG_66	NH2	L_GLU_84	OE2	3.502
5TZT	L_HIS_194	ND1	L_ASP_156	OD2	3.224
5TZT	H_ARG_38	NH2	H_GLU_46	OE1	3.226
5TZT	H_LYS_63	NZ	H_GLU_46	OE2	3.670
5TZT	H_ARG_67	NH2	H_ASP_90	OD2	3.363
5TZT	H_ARG_98	NH1	H_ASP_105	OD1	3.531
5TZT	H_ARG_98	NH1	H_ASP_105	OD2	2.846
5TZT	H_ARG_98	NH2	H_ASP_105	OD1	3.738
5TZT	H_HIS_102	ND1	C_GLU_104	OE1	2.856
5TZT	C_ARG_45	NH1	C_ASP_62	OD1	2.637
5TZT	C_ARG_45	NH1	C_ASP_62	OD2	2.581
5TZT	C_ARG_45	NH2	C_ASP_62	OD1	3.454
5TZT	C_HIS_90	NE2	C_ASP_62	OD1	3.571
5TZT	D_HIS_90	NE2	D_ASP_62	OD1	3.274
5TZT	D_ARG_103	NH2	D_GLU_100	OE1	2.563
5TZT	D_ARG_114	NH1	D_GLU_11	OE1	3.807
5TZT	D_ARG_114	NH1	D_GLU_11	OE2	3.964
5TZU	L_LYS_49	NZ	C_ASP_51	OD1	3.523
5TZU	L_LYS_49	NZ	C_ASP_51	OD2	2.772
5TZU	L_ARG_61	NH1	L_GLU_79	OE1	3.734
5TZU	L_ARG_61	NH1	L_GLU_81	OE2	3.054
5TZU	L_ARG_61	NH1	L_ASP_82	OD1	2.764
5TZU	L_ARG_61	NH1	L_ASP_82	OD2	3.551
5TZU	L_ARG_61	NH2	L_GLU_79	OE1	3.680
5TZU	L_ARG_96	NH1	C_GLU_104	OE1	3.230

5TZU	L_ARG_96	NH1	C_GLU_104	OE2	3.808
5TZU	L_ARG_96	NH2	C_GLU_104	OE1	2.901
5TZU	L_LYS_103	NZ	L_GLU_165	OE1	3.822
5TZU	L_LYS_103	NZ	L_GLU_165	OE2	3.206
5TZU	L_ARG_211	NH1	L_GLU_187	OE1	3.562
5TZU	H_ARG_38	NH1	H_ASP_90	OD2	2.785
5TZU	H_ARG_38	NH2	H_GLU_46	OE1	2.862
5TZU	H_ARG_38	NH2	H_GLU_46	OE2	3.976
5TZU	H_ARG_38	NH2	H_ASP_90	OD2	3.917
5TZU	H_ARG_67	NH1	H_ASP_90	OD1	2.777
5TZU	H_ARG_67	NH1	H_ASP_90	OD2	3.488
5TZU	H_ARG_67	NH2	H_ASP_90	OD1	3.415
5TZU	H_ARG_67	NH2	H_ASP_90	OD2	3.088
5TZU	H_ARG_98	NH2	H_ASP_106	OD1	3.900
5TZU	H_ARG_98	NH2	H_ASP_106	OD2	2.795
5TZU	H_LYS_214	NZ	L_GLU_123	OE1	2.584
5TZU	H_LYS_214	NZ	L_GLU_123	OE2	3.416
5TZU	C_LYS_39	NZ	L_ASP_31	OD1	3.076
5TZU	C_LYS_39	NZ	L_ASP_31	OD2	2.978
5TZU	C_LYS_39	NZ	C_ASP_46	OD1	3.593
5TZU	C_LYS_39	NZ	C_GLU_97	OE2	3.431
5TZU	C_LYS_41	NZ	C_ASP_46	OD2	2.556
5TZU	C_ARG_45	NH1	C_ASP_62	OD2	3.407
5TZU	C_ARG_45	NH2	C_ASP_62	OD1	3.389
5TZU	C_ARG_45	NH2	C_ASP_62	OD2	3.679
5TZU	C_HIS_90	NE2	C_ASP_62	OD2	3.453
5TZU	C_ARG_103	NH1	C_GLU_29	OE2	3.912
5TZU	C_ARG_103	NH2	C_GLU_29	OE1	3.883
5TZU	C_ARG_103	NH2	C_GLU_100	OE1	3.920
5TZU	C_ARG_103	NH2	C_GLU_100	OE2	3.101
5U3J	H_ARG_38	NH1	H_ASP_86	OD1	2.854
5U3J	H_ARG_38	NH2	H_GLU_46	OE1	3.279
5U3J	H_ARG_38	NH2	H_GLU_46	OE2	3.381
5U3J	H_ARG_50	NH2	H_GLU_58	OE1	2.789
5U3J	H_ARG_52A	NH1	H_ASP_53	OD1	3.274
5U3J	H_ARG_52A	NH1	H_ASP_53	OD2	3.547
5U3J	H_ARG_52A	NH1	A_ASP_674	OD1	3.805
5U3J	H_ARG_52A	NH1	A_ASP_674	OD2	3.646
5U3J	H_ARG_52A	NH2	A_ASP_674	OD2	3.216
5U3J	H_LYS_52C	NZ	A_ASP_674	OD1	3.151
5U3J	H_LYS_52C	NZ	A_ASP_674	OD2	3.836
5U3J	H_ARG_66	NH1	H_ASP_86	OD1	3.711
5U3J	H_ARG_66	NH1	H_ASP_86	OD2	2.572
5U3J	H_ARG_66	NH2	H_ASP_86	OD1	2.894
5U3J	H_ARG_66	NH2	H_ASP_86	OD2	3.336
5U3J	H_ARG_71	NH2	H_ASP_73	OD1	3.654
5U3J	H_LYS_143	NZ	H_ASP_144	OD1	3.689
5U3J	H_LYS_209	NZ	L_GLU_123	OE1	3.171
5U3J	H_LYS_209	NZ	L_GLU_123	OE2	2.412
5U3J	L_ARG_24	NH1	L_ASP_70	OD1	3.454
5U3J	L_ARG_24	NH1	L_ASP_70	OD2	3.616
5U3J	L_LYS_39	NZ	L_GLU_81	OE1	2.718
5U3J	L_ARG_61	NH2	L_ASP_82	OD2	3.220
5U3J	L_LYS_149	NZ	L_GLU_195	OE1	2.981
5U3J	L_LYS_188	NZ	L_ASP_185	OD1	3.489
5U3J	L_ARG_211	NH1	L_GLU_187	OE2	3.588
5U3N	H_ARG_38	NH1	H_ASP_86	OD1	3.106
5U3N	H_ARG_38	NH2	H_GLU_46	OE1	3.388

5U3N	H_ARG_38	NH2	H_GLU_46	OE2	3.678
5U3N	H_ARG_50	NH2	H_ASP_58	OD2	3.019
5U3N	H_ARG_52A	NH1	A_ASP_674	OD2	2.997
5U3N	H_ARG_52A	NH2	H_ASP_53	OD1	2.927
5U3N	H_ARG_52A	NH2	H_ASP_53	OD2	3.679
5U3N	H_ARG_52A	NH2	A_ASP_674	OD1	3.173
5U3N	H_ARG_52A	NH2	A_ASP_674	OD2	3.047
5U3N	H_ARG_66	NH1	H_ASP_86	OD1	3.888
5U3N	H_ARG_66	NH1	H_ASP_86	OD2	2.734
5U3N	H_ARG_66	NH2	H_ASP_86	OD1	3.118
5U3N	H_ARG_66	NH2	H_ASP_86	OD2	3.431
5U3N	H_ARG_71	NH2	H_ASP_73	OD1	3.283
5U3N	H_ARG_100B	NH1	L_ASP_31	OD1	3.593
5U3N	H_ARG_100B	NH1	L_ASP_31	OD2	2.967
5U3N	H_ARG_100B	NH2	H_GLU_100E	OE1	3.425
5U3N	H_ARG_100B	NH2	H_GLU_100E	OE2	2.907
5U3N	H_ARG_100B	NH2	L_ASP_31	OD1	2.974
5U3N	H_ARG_100B	NH2	L_ASP_31	OD2	3.816
5U3N	H_LYS_143	NZ	H_ASP_144	OD1	3.337
5U3N	H_LYS_209	NZ	L_GLU_123	OE1	3.254
5U3N	H_ARG_210	NH1	H_GLU_212	OE2	3.469
5U3N	H_ARG_210	NH2	H_GLU_212	OE2	3.206
5U3N	L_LYS_30	NZ	H_GLU_100E	OE1	3.899
5U3N	L_ARG_55	NH2	H_ASP_101	OD1	3.682
5U3N	L_ARG_55	NH2	H_ASP_101	OD2	2.901
5U3N	L_ARG_61	NH1	L_ASP_82	OD1	3.771
5U3N	L_ARG_61	NH1	L_ASP_82	OD2	2.649
5U3N	L_ARG_61	NH2	L_ASP_82	OD1	3.486
5U3N	L_ARG_61	NH2	L_ASP_82	OD2	3.672
5U3N	L_LYS_149	NZ	L_GLU_195	OE1	2.891
5U3N	L_LYS_190	NZ	L_GLU_213	OE1	3.468
5U3N	L_ARG_211	NH1	L_GLU_187	OE2	3.281
5UCB	H_ARG_38	NH1	H_ASP_86	OD1	2.881
5UCB	H_ARG_38	NH2	H_GLU_46	OE1	3.076
5UCB	H_ARG_38	NH2	H_GLU_46	OE2	3.531
5UCB	H_ARG_38	NH2	H_ASP_86	OD1	3.930
5UCB	H_ARG_66	NH1	H_ASP_86	OD1	3.749
5UCB	H_ARG_66	NH1	H_ASP_86	OD2	2.753
5UCB	H_ARG_66	NH2	H_ASP_86	OD1	3.062
5UCB	H_ARG_66	NH2	H_ASP_86	OD2	3.559
5UCB	H_ARG_94	NH2	H_ASP_101	OD2	3.041
5UCB	H_LYS_143	NZ	H_ASP_144	OD1	3.312
5UCB	H_LYS_143	NZ	H_ASP_144	OD2	3.791
5UCB	L_ARG_24	NH1	L_ASP_70	OD1	3.024
5UCB	L_ARG_24	NH1	L_ASP_70	OD2	3.164
5UCB	L_ARG_61	NH2	L_GLU_81	OE2	3.626
5UCB	L_ARG_61	NH2	L_ASP_82	OD1	2.851
5UCB	L_ARG_61	NH2	L_ASP_82	OD2	3.578
5UCB	L_ARG_66	NH2	B_ASP_51	OD1	2.894
5UCB	L_LYS_103	NZ	L_GLU_165	OE1	2.767
5UCB	L_LYS_103	NZ	L_GLU_165	OE2	3.262
5UCB	L_LYS_149	NZ	L_GLU_195	OE1	3.236
5UCB	L_LYS_149	NZ	L_GLU_195	OE2	2.876
5UCB	L_LYS_188	NZ	L_ASP_185	OD1	3.509
5UCB	B_LYS_16	NZ	B_ASP_132	OD1	2.899
5UCB	B_LYS_40	NZ	B_GLU_55	OE1	3.387
5UCB	B_HIS_52	NE2	B_GLU_87	OE1	3.757
5UCB	B_ARG_103	NH1	B_ASP_101	OD2	2.895

5UCB	B_ARG_103	NH2	B_ASP_101	OD2	3.593
5UCB	B_ARG_107	NH2	B_GLU_104	OE1	3.008
5UCB	B_ARG_107	NH2	B_GLU_104	OE2	3.594
5UCB	B_ARG_122	NH2	B_GLU_119	OE1	3.126
5UCB	B_HIS_133	ND1	B_ASP_117	OD1	2.951
5UCB	B_HIS_133	ND1	B_ASP_117	OD2	3.612
5UCB	B_HIS_133	ND1	B_GLU_118	OE2	3.928
5UCB	B_ARG_144	NH2	L_ASP_91	OD1	2.844
5UCB	B_ARG_144	NH2	L_ASP_91	OD2	3.495
5UEA	A_ARG_38	NH1	A_ASP_86	OD1	2.925
5UEA	A_ARG_38	NH2	A_GLU_46	OE1	3.053
5UEA	A_ARG_38	NH2	A_GLU_46	OE2	3.718
5UEA	A_ARG_38	NH2	A_ASP_86	OD1	3.982
5UEA	A_LYS_64	NZ	A_ASP_61	OD1	3.564
5UEA	A_ARG_66	NH1	A_ASP_86	OD1	3.801
5UEA	A_ARG_66	NH1	A_ASP_86	OD2	2.753
5UEA	A_ARG_66	NH2	A_ASP_86	OD1	3.014
5UEA	A_ARG_66	NH2	A_ASP_86	OD2	3.470
5UEA	A_LYS_75	NZ	A_ASP_72	OD2	2.831
5UEA	A_ARG_83	NH1	A_GLU_85	OE2	3.478
5UEA	A_ARG_94	NH1	A_ASP_101	OD2	3.648
5UEA	A_LYS_143	NZ	A_ASP_144	OD1	3.213
5UEA	A_LYS_143	NZ	A_ASP_144	OD2	3.068
5UEA	A_LYS_210	NZ	A_GLU_212	OE2	3.717
5UEA	X_LYS_10	NZ	X_GLU_25	OE1	2.830
5UEA	X_LYS_10	NZ	X_GLU_25	OE2	3.963
5UEA	X_LYS_10	NZ	D_GLU_29	OE1	3.740
5UEA	X_LYS_10	NZ	D_GLU_29	OE2	2.855
5UEA	X_HIS_36	ND1	X_ASP_102	OD1	3.747
5UEA	X_HIS_53	ND1	X_ASP_54	OD1	3.697
5UEA	X_HIS_53	NE2	X_ASP_54	OD1	3.655
5UEA	X_LYS_71	NZ	D_GLU_29	OE2	3.320
5UEA	X_ARG_104	NH1	X_ASP_102	OD2	3.117
5UEA	X_ARG_104	NH2	X_ASP_102	OD2	3.925
5UEA	X_ARG_108	NH2	X_GLU_105	OE1	2.916
5UEA	X_ARG_108	NH2	X_GLU_105	OE2	3.333
5UEA	X_ARG_123	NH2	X_GLU_120	OE1	3.394
5UEA	X_HIS_134	ND1	X_ASP_118	OD2	2.696
5UEA	X_HIS_134	ND1	X_GLU_119	OE1	3.900
5UEA	X_HIS_134	NE2	X_ASP_133	OD2	3.951
5UEA	H_ARG_38	NH1	H_ASP_86	OD1	2.893
5UEA	H_ARG_38	NH2	H_GLU_46	OE1	3.038
5UEA	H_ARG_38	NH2	H_GLU_46	OE2	3.945
5UEA	H_ARG_38	NH2	H_ASP_86	OD1	3.946
5UEA	H_ARG_66	NH1	H_ASP_86	OD1	3.977
5UEA	H_ARG_66	NH1	H_ASP_86	OD2	2.837
5UEA	H_ARG_66	NH2	H_ASP_86	OD1	3.030
5UEA	H_ARG_66	NH2	H_ASP_86	OD2	3.367
5UEA	H_LYS_75	NZ	H_ASP_72	OD2	3.470
5UEA	H_ARG_94	NH1	H_ASP_101	OD2	3.608
5UEA	H_LYS_143	NZ	H_ASP_144	OD1	3.356
5UEA	H_LYS_143	NZ	H_ASP_144	OD2	3.506
5UEA	D_LYS_10	NZ	X_GLU_29	OE1	3.485
5UEA	D_LYS_10	NZ	X_GLU_29	OE2	2.490
5UEA	D_LYS_10	NZ	D_GLU_25	OE1	2.206
5UEA	D_LYS_10	NZ	D_GLU_25	OE2	3.753
5UEA	D_HIS_36	NE2	D_ASP_102	OD2	3.900
5UEA	D_LYS_70	NZ	X_GLU_29	OE2	3.861

5UEA	D_ARG_104	NH1	D_ASP_102	OD2	3.466
5UEA	D_ARG_108	NH2	D_GLU_105	OE1	2.929
5UEA	D_ARG_108	NH2	D_GLU_105	OE2	3.455
5UEA	D_HIS_134	ND1	D_ASP_118	OD2	2.708
5UEA	L_ARG_24	NH2	L_ASP_70	OD1	3.498
5UEA	L_ARG_24	NH2	L_ASP_70	OD2	2.931
5UEA	L_ARG_61	NH2	L_GLU_81	OE2	3.429
5UEA	L_ARG_61	NH2	L_ASP_82	OD1	2.822
5UEA	L_ARG_61	NH2	L_ASP_82	OD2	3.535
5UEA	L_LYS_103	NZ	L_GLU_165	OE1	2.845
5UEA	L_LYS_103	NZ	L_GLU_165	OE2	3.041
5UEA	L_LYS_149	NZ	L_GLU_195	OE1	3.248
5UEA	L_LYS_183	NZ	L_GLU_187	OE1	3.535
5UEA	L_LYS_183	NZ	L_GLU_187	OE2	2.491
5UEA	B_ARG_24	NH1	B_ASP_70	OD1	2.938
5UEA	B_ARG_24	NH1	B_ASP_70	OD2	3.769
5UEA	B_ARG_61	NH2	B_GLU_81	OE2	3.252
5UEA	B_ARG_61	NH2	B_ASP_82	OD1	2.947
5UEA	B_ARG_61	NH2	B_ASP_82	OD2	3.541
5UEA	B_LYS_103	NZ	B_GLU_165	OE1	3.082
5UEA	B_LYS_103	NZ	B_GLU_165	OE2	2.513
5UEA	B_LYS_107	NZ	B_ASP_17	OD2	3.363
5UEA	B_ARG_142	NH1	B_GLU_105	OE1	2.937
5UEA	B_ARG_142	NH1	B_GLU_105	OE2	2.716
5UEA	B_ARG_142	NH2	B_GLU_105	OE1	2.783
5UEA	B_LYS_149	NZ	B_GLU_195	OE1	3.063
5UEA	B_LYS_183	NZ	B_GLU_187	OE2	3.815
5UEA	B_ARG_211	NH1	B_GLU_187	OE1	3.735
5UEK	A_LYS_10	NZ	A_GLU_25	OE1	3.987
5UEK	A_HIS_36	ND1	A_ASP_154	OD1	3.867
5UEK	A_HIS_36	NE2	A_ASP_102	OD1	3.958
5UEK	A_LYS_41	NZ	A_GLU_39	OE1	3.964
5UEK	A_LYS_41	NZ	A_GLU_56	OE1	2.739
5UEK	A_ARG_49	NH1	A_GLU_88	OE1	3.431
5UEK	A_ARG_104	NH1	A_ASP_102	OD2	2.895
5UEK	A_ARG_104	NH2	A_ASP_102	OD2	3.461
5UEK	A_ARG_108	NH2	A_GLU_105	OE1	2.914
5UEK	A_ARG_108	NH2	A_GLU_105	OE2	3.466
5UEK	A_ARG_123	NH1	A_GLU_116	OE1	3.682
5UEK	A_HIS_134	ND1	A_ASP_133	OD1	2.831
5UEK	A_HIS_134	NE2	A_GLU_119	OE1	3.693
5UEK	A_ARG_145	NH2	L_ASP_91	OD1	2.787
5UEK	A_ARG_145	NH2	L_ASP_91	OD2	3.426
5UEK	H_ARG_38	NH1	H_ASP_86	OD2	2.930
5UEK	H_ARG_38	NH2	H_GLU_46	OE1	3.662
5UEK	H_ARG_38	NH2	H_GLU_46	OE2	3.239
5UEK	H_ARG_38	NH2	H_GLU_85	OE1	2.889
5UEK	H_ARG_38	NH2	H_ASP_86	OD2	3.876
5UEK	H_ARG_66	NH1	H_ASP_86	OD1	2.840
5UEK	H_ARG_66	NH1	H_ASP_86	OD2	3.752
5UEK	H_ARG_66	NH2	H_GLU_85	OE1	3.536
5UEK	H_ARG_66	NH2	H_ASP_86	OD1	3.599
5UEK	H_ARG_66	NH2	H_ASP_86	OD2	3.048
5UEK	H_ARG_83	NH1	H_GLU_85	OE2	3.252
5UEK	H_ARG_94	NH2	H_ASP_101	OD1	3.975
5UEK	H_ARG_94	NH2	H_ASP_101	OD2	2.845
5UEK	H_LYS_143	NZ	H_ASP_144	OD1	3.123
5UEK	H_LYS_143	NZ	H_ASP_144	OD2	3.057

5UEK	H.LYS_210	NZ	H.GLU_212	OE1	3.851
5UEK	H.LYS_210	NZ	H.GLU_212	OE2	2.516
5UEK	L.ARG_24	NH1	L.ASP_70	OD1	3.080
5UEK	L.ARG_24	NH1	L.ASP_70	OD2	2.941
5UEK	L.ARG_61	NH2	L.GLU_81	OE1	3.355
5UEK	L.ARG_61	NH2	L.ASP_82	OD1	2.825
5UEK	L.ARG_61	NH2	L.ASP_82	OD2	3.599
5UEK	L.ARG_66	NH2	A.ASP_52	OD1	2.873
5UEK	L.LYS_103	NZ	L.GLU_105	OE2	2.640
5UEK	L.LYS_103	NZ	L.GLU_165	OE1	3.290
5UEK	L.LYS_149	NZ	L.GLU_195	OE2	3.692
5UEK	L.LYS_183	NZ	L.GLU_187	OE1	2.986
5UG0	A.LYS_44	NZ	A.ASP_276	OD1	3.145
5UG0	A.ARG_106	NH1	A.GLU_85	OE1	3.304
5UG0	A.ARG_106	NH1	B.GLU_69	OE1	3.096
5UG0	A.ARG_106	NH1	B.GLU_69	OE2	3.964
5UG0	A.ARG_106	NH2	A.GLU_85	OE1	2.806
5UG0	A.ARG_106	NH2	A.GLU_85	OE2	3.674
5UG0	A.ARG_106	NH2	B.GLU_69	OE1	3.415
5UG0	A.ARG_106	NH2	B.GLU_69	OE2	3.059
5UG0	A.HIS_141	ND1	A.GLU_70	OE2	2.794
5UG0	A.LYS_149	NZ	A.GLU_72	OE1	3.216
5UG0	A.LYS_149	NZ	A.GLU_72	OE2	2.794
5UG0	A.LYS_172	NZ	A.GLU_116	OE2	3.654
5UG0	A.ARG_192	NH1	A.GLU_198	OE1	3.844
5UG0	A.ARG_192	NH1	A.GLU_198	OE2	3.866
5UG0	A.LYS_222	NZ	A.ASP_225	OD1	3.696
5UG0	A.LYS_222	NZ	A.GLU_227	OE2	3.476
5UG0	A.LYS_222	NZ	D.ASP_107	OD2	3.472
5UG0	A.ARG_255	NH2	A.GLU_119	OE2	3.754
5UG0	A.ARG_255	NH2	A.GLU_124	OE2	3.685
5UG0	A.ARG_262	NH1	A.GLU_175	OE1	3.614
5UG0	A.ARG_262	NH1	A.GLU_175	OE2	2.850
5UG0	A.ARG_311	NH1	B.ASP_90	OD1	2.840
5UG0	A.ARG_311	NH2	B.ASP_86	OD1	2.770
5UG0	A.ARG_311	NH2	B.ASP_90	OD1	3.313
5UG0	A.ARG_322	NH2	A.GLU_25	OE2	3.810
5UG0	B.LYS_68	NZ	A.GLU_107	OE2	3.009
5UG0	B.ARG_75	NH1	B.GLU_78	OE2	3.343
5UG0	B.LYS_116	NZ	B.GLU_120	OE2	3.389
5UG0	B.LYS_123	NZ	B.GLU_120	OE1	3.342
5UG0	B.LYS_123	NZ	B.GLU_120	OE2	3.653
5UG0	B.LYS_131	NZ	B.GLU_139	OE1	3.933
5UG0	B.LYS_153	NZ	B.GLU_150	OE1	3.568
5UG0	B.LYS_153	NZ	B.GLU_150	OE2	2.976
5UG0	B.LYS_161	NZ	B.GLU_165	OE1	3.465
5UG0	C.ARG_55	NH1	C.ASP_61	OD1	3.504
5UG0	C.ARG_62	NH2	C.GLU_82	OE1	3.126
5UG0	C.ARG_62	NH2	C.GLU_82	OE2	3.930
5UG0	C.ARG_62	NH2	C.ASP_83	OD1	2.816
5UG0	C.ARG_62	NH2	C.ASP_83	OD2	3.378
5UG0	C.LYS_109	NZ	C.GLU_107	OE1	3.664
5UG0	C.ARG_144	NH1	C.GLU_107	OE1	3.309
5UG0	C.ARG_144	NH1	C.GLU_107	OE2	3.710
5UG0	C.ARG_144	NH1	C.GLU_167	OE1	3.879
5UG0	C.ARG_144	NH2	C.GLU_167	OE1	3.902
5UG0	C.ARG_144	NH2	C.GLU_167	OE2	3.194
5UG0	C.LYS_147	NZ	C.GLU_145	OE2	2.927

5UG0	C_LYS_151	NZ	C_GLU_197	OE1	3.587
5UG0	C_LYS_151	NZ	C_GLU_197	OE2	3.166
5UG0	C_HIS_191	ND1	C_ASP_153	OD2	3.193
5UG0	D_ARG_38	NH1	D_ASP_89	OD1	3.285
5UG0	D_ARG_38	NH2	D_GLU_46	OE1	3.648
5UG0	D_ARG_38	NH2	D_ASP_89	OD1	3.488
5UG0	D_ARG_86	NH2	D_ASP_89	OD1	3.223
5UG0	D_ARG_100	NH1	A_ASP_190	OD1	3.522
5UG0	D_ARG_100	NH1	A_ASP_190	OD2	3.877
5UG0	D_HIS_178	NE2	C_ASP_169	OD2	3.490
5UG0	D_LYS_223	NZ	C_GLU_125	OE2	3.392
5UJZ	A_LYS_86	NZ	A_GLU_90	OE2	3.056
5UJZ	A_ARG_106	NH1	A_GLU_85	OE1	3.777
5UJZ	A_ARG_106	NH1	A_GLU_85	OE2	2.785
5UJZ	A_ARG_106	NH1	B_GLU_569	OE2	3.797
5UJZ	A_ARG_106	NH2	A_GLU_85	OE1	3.157
5UJZ	A_ARG_106	NH2	A_GLU_85	OE2	3.125
5UJZ	A_ARG_106	NH2	B_GLU_569	OE1	3.958
5UJZ	A_ARG_106	NH2	B_GLU_569	OE2	3.070
5UJZ	A_HIS_141	ND1	A_GLU_70	OE2	3.820
5UJZ	A_LYS_174	NZ	A_GLU_116	OE2	3.728
5UJZ	A_ARG_192	NH2	A_GLU_198	OE2	2.656
5UJZ	A_HIS_208	ND1	A_GLU_238	OE2	3.816
5UJZ	A_LYS_219	NZ	A_GLU_227	OE2	3.960
5UJZ	A_ARG_262	NH1	A_GLU_175	OE1	2.805
5UJZ	A_ARG_262	NH1	A_GLU_175	OE2	3.687
5UJZ	A_ARG_311	NH1	B_ASP_586	OD1	3.689
5UJZ	A_ARG_311	NH1	B_ASP_590	OD1	3.217
5UJZ	A_ARG_311	NH1	B_ASP_590	OD2	3.955
5UJZ	A_ARG_311	NH2	B_ASP_586	OD1	2.782
5UJZ	B_LYS_551	NZ	B_GLU_603	OE1	3.842
5UJZ	B_LYS_558	NZ	F_GLU_597	OE1	3.688
5UJZ	B_LYS_558	NZ	F_GLU_597	OE2	3.874
5UJZ	B_ARG_576	NH1	D_GLU_574	OE1	3.986
5UJZ	B_ARG_576	NH1	D_GLU_574	OE2	3.042
5UJZ	B_ARG_576	NH2	C_GLU_104	OE2	3.168
5UJZ	B_LYS_582	NZ	B_ASP_586	OD2	3.643
5UJZ	B_LYS_583	NZ	D_ASP_585	OD1	3.717
5UJZ	B_ARG_606	NH2	F_ASP_609	OD2	2.744
5UJZ	B_LYS_623	NZ	B_GLU_632	OE2	3.820
5UJZ	B_LYS_631	NZ	B_GLU_639	OE1	3.976
5UJZ	B_LYS_643	NZ	A_GLU_4	OE1	2.954
5UJZ	B_LYS_643	NZ	A_ASP_5	OD1	2.763
5UJZ	B_LYS_643	NZ	A_ASP_5	OD2	3.863
5UJZ	B_LYS_643	NZ	B_GLU_529	OE2	3.375
5UJZ	B_LYS_653	NZ	B_GLU_650	OE1	3.647
5UJZ	B_LYS_661	NZ	B_GLU_647	OE1	3.374
5UJZ	B_ARG_670	NH2	B_GLU_671	OE2	2.839
5UJZ	C_LYS_86	NZ	C_GLU_90	OE2	3.056
5UJZ	C_ARG_106	NH1	C_GLU_85	OE1	3.777
5UJZ	C_ARG_106	NH1	C_GLU_85	OE2	2.784
5UJZ	C_ARG_106	NH1	D_GLU_569	OE2	3.872
5UJZ	C_ARG_106	NH2	C_GLU_85	OE1	3.158
5UJZ	C_ARG_106	NH2	C_GLU_85	OE2	3.125
5UJZ	C_ARG_106	NH2	D_GLU_569	OE2	3.260
5UJZ	C_HIS_141	ND1	C_GLU_70	OE2	3.819
5UJZ	C_LYS_174	NZ	C_GLU_116	OE2	3.728
5UJZ	C_ARG_192	NH2	C_GLU_198	OE2	2.657

5UJZ	C_HIS_208	ND1	C_GLU_238	OE2	3.817
5UJZ	C_LYS_219	NZ	C_GLU_227	OE2	3.960
5UJZ	C_ARG_262	NH1	C_GLU_175	OE1	2.805
5UJZ	C_ARG_262	NH1	C_GLU_175	OE2	3.686
5UJZ	C_ARG_311	NH1	D_ASP_586	OD1	3.865
5UJZ	C_ARG_311	NH1	D_ASP_590	OD1	3.148
5UJZ	C_ARG_311	NH1	D_ASP_590	OD2	3.998
5UJZ	C_ARG_311	NH2	D_ASP_586	OD1	2.921
5UJZ	D_LYS_551	NZ	D_GLU_603	OE1	3.842
5UJZ	D_LYS_558	NZ	B_GLU_597	OE1	3.772
5UJZ	D_LYS_572	NZ	E_GLU_238	OE1	3.910
5UJZ	D_ARG_576	NH1	F_GLU_574	OE1	3.863
5UJZ	D_ARG_576	NH1	F_GLU_574	OE2	2.716
5UJZ	D_ARG_576	NH2	E_GLU_104	OE2	3.170
5UJZ	D_LYS_582	NZ	D_ASP_586	OD2	3.642
5UJZ	D_LYS_583	NZ	F_ASP_585	OD1	3.807
5UJZ	D_ARG_606	NH2	B_ASP_609	OD2	2.766
5UJZ	D_LYS_623	NZ	D_GLU_632	OE2	3.820
5UJZ	D_LYS_631	NZ	D_GLU_639	OE1	3.976
5UJZ	D_LYS_643	NZ	C_GLU_4	OE1	3.185
5UJZ	D_LYS_643	NZ	C_ASP_5	OD1	2.519
5UJZ	D_LYS_643	NZ	C_ASP_5	OD2	3.642
5UJZ	D_LYS_643	NZ	D_GLU_529	OE2	3.375
5UJZ	D_LYS_653	NZ	D_GLU_650	OE1	3.648
5UJZ	D_LYS_661	NZ	D_GLU_647	OE1	3.376
5UJZ	D_ARG_670	NH2	D_GLU_671	OE2	2.839
5UJZ	E_LYS_86	NZ	E_GLU_90	OE2	3.056
5UJZ	E_ARG_106	NH1	E_GLU_85	OE1	3.777
5UJZ	E_ARG_106	NH1	E_GLU_85	OE2	2.784
5UJZ	E_ARG_106	NH2	E_GLU_85	OE1	3.158
5UJZ	E_ARG_106	NH2	E_GLU_85	OE2	3.126
5UJZ	E_ARG_106	NH2	F_GLU_569	OE2	3.361
5UJZ	E_HIS_141	ND1	E_GLU_70	OE2	3.819
5UJZ	E_LYS_174	NZ	E_GLU_116	OE2	3.728
5UJZ	E_ARG_192	NH2	E_GLU_198	OE2	2.656
5UJZ	E_HIS_208	ND1	E_GLU_238	OE2	3.816
5UJZ	E_LYS_219	NZ	E_GLU_227	OE2	3.960
5UJZ	E_ARG_262	NH1	E_GLU_175	OE1	2.805
5UJZ	E_ARG_262	NH1	E_GLU_175	OE2	3.687
5UJZ	E_ARG_311	NH1	F_ASP_586	OD1	3.477
5UJZ	E_ARG_311	NH1	F_ASP_590	OD1	3.629
5UJZ	E_ARG_311	NH2	F_ASP_586	OD1	2.793
5UJZ	F_LYS_551	NZ	F_GLU_603	OE1	3.843
5UJZ	F_ARG_576	NH1	B_GLU_574	OE1	3.655
5UJZ	F_ARG_576	NH1	B_GLU_574	OE2	2.847
5UJZ	F_ARG_576	NH2	A_GLU_104	OE2	3.211
5UJZ	F_LYS_582	NZ	F_ASP_586	OD2	3.643
5UJZ	F_LYS_583	NZ	B_ASP_585	OD1	3.548
5UJZ	F_ARG_606	NH2	D_ASP_609	OD2	2.609
5UJZ	F_LYS_623	NZ	F_GLU_632	OE2	3.821
5UJZ	F_LYS_631	NZ	F_GLU_639	OE1	3.976
5UJZ	F_LYS_643	NZ	E_GLU_4	OE1	3.009
5UJZ	F_LYS_643	NZ	E_ASP_5	OD1	2.882
5UJZ	F_LYS_643	NZ	E_ASP_5	OD2	3.935
5UJZ	F_LYS_643	NZ	F_GLU_529	OE2	3.375
5UJZ	F_LYS_653	NZ	F_GLU_650	OE1	3.646
5UJZ	F_LYS_661	NZ	F_GLU_647	OE1	3.375
5UJZ	F_ARG_670	NH2	F_GLU_671	OE2	2.839

5UJZ	G_HIS_160	NE2	G_ASP_158	OD1	3.708
5UJZ	G_ARG_163	NH1	G_ASP_214	OD1	3.087
5UJZ	G_ARG_163	NH2	G_GLU_171	OE1	2.822
5UJZ	G_ARG_163	NH2	G_GLU_171	OE2	3.867
5UJZ	G_ARG_191	NH1	G_ASP_214	OD2	3.584
5UJZ	G_ARG_225	NH1	A_ASP_190	OD1	3.090
5UJZ	G_ARG_225	NH1	A_ASP_190	OD2	3.996
5UJZ	G_ARG_225	NH2	A_ASP_190	OD1	3.715
5UJZ	G_ARG_225	NH2	A_ASP_190	OD2	3.410
5UJZ	H_HIS_160	NE2	H_ASP_158	OD1	3.708
5UJZ	H_ARG_163	NH1	H_ASP_214	OD1	3.088
5UJZ	H_ARG_163	NH2	H_GLU_171	OE1	2.821
5UJZ	H_ARG_163	NH2	H_GLU_171	OE2	3.867
5UJZ	H_ARG_191	NH1	H_ASP_214	OD2	3.583
5UJZ	H_ARG_225	NH1	C_ASP_190	OD1	3.041
5UJZ	H_ARG_225	NH2	C_ASP_190	OD1	3.552
5UJZ	H_ARG_225	NH2	C_ASP_190	OD2	3.366
5UJZ	I_HIS_160	NE2	I_ASP_158	OD1	3.708
5UJZ	I_ARG_163	NH1	I_ASP_214	OD1	3.088
5UJZ	I_ARG_163	NH2	I_GLU_171	OE1	2.823
5UJZ	I_ARG_163	NH2	I_GLU_171	OE2	3.868
5UJZ	I_ARG_191	NH1	I_ASP_214	OD2	3.584
5UJZ	I_ARG_225	NH1	E_ASP_190	OD1	3.119
5UJZ	I_ARG_225	NH1	E_ASP_190	OD2	3.970
5UJZ	I_ARG_225	NH2	E_ASP_190	OD1	3.713
5UJZ	I_ARG_225	NH2	E_ASP_190	OD2	3.347
5UK0	A_LYS_86	NZ	A_GLU_90	OE2	3.309
5UK0	A_ARG_106	NH1	A_GLU_85	OE1	3.645
5UK0	A_ARG_106	NH1	A_GLU_85	OE2	3.045
5UK0	A_ARG_106	NH1	B_GLU_569	OE2	3.967
5UK0	A_ARG_106	NH2	A_GLU_85	OE1	3.291
5UK0	A_ARG_106	NH2	A_GLU_85	OE2	3.562
5UK0	A_ARG_106	NH2	B_GLU_569	OE2	3.244
5UK0	A_LYS_174	NZ	A_GLU_116	OE2	3.452
5UK0	A_ARG_192	NH2	A_GLU_198	OE2	2.543
5UK0	A_HIS_208	ND1	A_GLU_238	OE2	3.818
5UK0	A_HIS_208	NE2	A_GLU_238	OE2	3.885
5UK0	A_ARG_220	NH2	C_ASP_241	OD1	3.711
5UK0	A_ARG_220	NH2	C_ASP_241	OD2	3.819
5UK0	A_ARG_262	NH1	A_GLU_175	OE1	3.069
5UK0	A_ARG_311	NH1	B_ASP_590	OD1	3.139
5UK0	A_ARG_311	NH1	B_ASP_590	OD2	3.961
5UK0	A_ARG_311	NH2	B_ASP_586	OD1	3.197
5UK0	B_LYS_551	NZ	B_GLU_603	OE1	3.035
5UK0	B_LYS_558	NZ	F_GLU_597	OE1	3.717
5UK0	B_LYS_568	NZ	A_GLU_107	OE2	3.962
5UK0	B_ARG_576	NH1	D_GLU_574	OE1	2.500
5UK0	B_ARG_576	NH1	D_GLU_574	OE2	3.431
5UK0	B_ARG_576	NH2	C_GLU_104	OE2	3.446
5UK0	B_ARG_576	NH2	D_GLU_574	OE1	3.430
5UK0	B_ARG_576	NH2	D_GLU_574	OE2	3.016
5UK0	B_LYS_582	NZ	B_ASP_586	OD2	3.693
5UK0	B_ARG_606	NH2	F_ASP_609	OD2	2.765
5UK0	B_LYS_623	NZ	B_GLU_632	OE2	3.579
5UK0	B_LYS_643	NZ	A_GLU_4	OE1	2.724
5UK0	B_LYS_643	NZ	A_ASP_5	OD1	2.705
5UK0	B_LYS_643	NZ	A_ASP_5	OD2	3.831
5UK0	B_LYS_643	NZ	B_GLU_529	OE2	3.437

5UK0	B_LYS_661	NZ	B_GLU_647	OE1	3.387
5UK0	B_ARG_670	NH2	B_GLU_671	OE2	2.699
5UK0	C_LYS_86	NZ	C_GLU_90	OE2	3.309
5UK0	C_ARG_106	NH1	C_GLU_85	OE1	3.646
5UK0	C_ARG_106	NH1	C_GLU_85	OE2	3.045
5UK0	C_ARG_106	NH1	D_GLU_569	OE2	3.998
5UK0	C_ARG_106	NH2	C_GLU_85	OE1	3.291
5UK0	C_ARG_106	NH2	C_GLU_85	OE2	3.562
5UK0	C_ARG_106	NH2	D_GLU_569	OE2	3.213
5UK0	C_LYS_174	NZ	C_GLU_116	OE2	3.452
5UK0	C_ARG_192	NH2	C_GLU_198	OE2	2.542
5UK0	C_HIS_208	ND1	C_GLU_238	OE2	3.819
5UK0	C_HIS_208	NE2	C_GLU_238	OE2	3.885
5UK0	C_ARG_220	NH2	E_ASP_241	OD1	3.755
5UK0	C_ARG_220	NH2	E_ASP_241	OD2	3.891
5UK0	C_ARG_262	NH1	C_GLU_175	OE1	3.069
5UK0	C_ARG_311	NH1	D_ASP_586	OD1	3.901
5UK0	C_ARG_311	NH1	D_ASP_590	OD1	3.110
5UK0	C_ARG_311	NH1	D_ASP_590	OD2	3.851
5UK0	C_ARG_311	NH2	D_ASP_586	OD1	2.981
5UK0	D_LYS_551	NZ	D_GLU_603	OE1	3.035
5UK0	D_LYS_558	NZ	B_GLU_597	OE1	3.800
5UK0	D_LYS_572	NZ	E_GLU_238	OE1	3.723
5UK0	D_ARG_576	NH1	F_GLU_574	OE1	2.823
5UK0	D_ARG_576	NH1	F_GLU_574	OE2	3.743
5UK0	D_ARG_576	NH2	E_GLU_104	OE2	3.003
5UK0	D_ARG_576	NH2	F_GLU_574	OE1	3.596
5UK0	D_ARG_576	NH2	F_GLU_574	OE2	3.278
5UK0	D_LYS_582	NZ	D_ASP_586	OD2	3.695
5UK0	D_ARG_606	NH2	B_ASP_609	OD2	2.683
5UK0	D_LYS_623	NZ	D_GLU_632	OE2	3.578
5UK0	D_LYS_643	NZ	C_GLU_4	OE1	2.844
5UK0	D_LYS_643	NZ	C_ASP_5	OD1	2.693
5UK0	D_LYS_643	NZ	C_ASP_5	OD2	3.673
5UK0	D_LYS_643	NZ	D_GLU_529	OE2	3.436
5UK0	D_LYS_661	NZ	D_GLU_647	OE1	3.387
5UK0	D_ARG_670	NH2	D_GLU_671	OE2	2.700
5UK0	E_LYS_86	NZ	E_GLU_90	OE2	3.309
5UK0	E_ARG_106	NH1	E_GLU_85	OE1	3.645
5UK0	E_ARG_106	NH1	E_GLU_85	OE2	3.045
5UK0	E_ARG_106	NH1	F_GLU_569	OE2	3.924
5UK0	E_ARG_106	NH2	E_GLU_85	OE1	3.291
5UK0	E_ARG_106	NH2	E_GLU_85	OE2	3.563
5UK0	E_ARG_106	NH2	F_GLU_569	OE2	3.130
5UK0	E_LYS_174	NZ	E_GLU_116	OE2	3.453
5UK0	E_ARG_192	NH2	E_GLU_198	OE2	2.543
5UK0	E_HIS_208	ND1	E_GLU_238	OE2	3.818
5UK0	E_HIS_208	NE2	E_GLU_238	OE2	3.885
5UK0	E_ARG_220	NH2	A_ASP_241	OD1	3.703
5UK0	E_ARG_220	NH2	A_ASP_241	OD2	3.860
5UK0	E_ARG_262	NH1	E_GLU_175	OE1	3.069
5UK0	E_ARG_311	NH1	F_ASP_586	OD1	3.927
5UK0	E_ARG_311	NH1	F_ASP_590	OD1	3.174
5UK0	E_ARG_311	NH1	F_ASP_590	OD2	3.882
5UK0	E_ARG_311	NH2	F_ASP_586	OD1	3.095
5UK0	F_LYS_551	NZ	F_GLU_603	OE1	3.034
5UK0	F_LYS_558	NZ	D_GLU_597	OE1	3.758
5UK0	F_LYS_568	NZ	E_GLU_107	OE2	3.989

5UK0	F_LYS_572	NZ	A_GLU_238	OE1	3.995
5UK0	F_ARG_576	NH1	B_GLU_574	OE1	2.515
5UK0	F_ARG_576	NH1	B_GLU_574	OE2	3.607
5UK0	F_ARG_576	NH2	A_GLU_104	OE2	3.281
5UK0	F_ARG_576	NH2	B_GLU_574	OE1	3.248
5UK0	F_ARG_576	NH2	B_GLU_574	OE2	3.003
5UK0	F_LYS_582	NZ	F_ASP_586	OD2	3.694
5UK0	F_ARG_606	NH2	D_ASP_609	OD2	2.740
5UK0	F_LYS_623	NZ	F_GLU_632	OE2	3.578
5UK0	F_LYS_643	NZ	E_GLU_4	OE1	2.987
5UK0	F_LYS_643	NZ	E_ASP_5	OD1	2.694
5UK0	F_LYS_643	NZ	E_ASP_5	OD2	3.721
5UK0	F_LYS_643	NZ	F_GLU_529	OE2	3.437
5UK0	F_LYS_661	NZ	F_GLU_647	OE1	3.387
5UK0	F_ARG_670	NH2	F_GLU_671	OE2	2.698
5UK0	G_ARG_163	NH1	G_ASP_214	OD1	2.891
5UK0	G_ARG_163	NH2	G_GLU_171	OE1	2.986
5UK0	G_ARG_163	NH2	G_GLU_171	OE2	3.691
5UK0	G_ARG_191	NH1	G_ASP_214	OD2	3.874
5UK0	G_ARG_225	NH1	A_ASP_190	OD1	3.056
5UK0	G_ARG_225	NH1	A_ASP_190	OD2	3.844
5UK0	G_ARG_225	NH1	G_ASP_233	OD1	3.964
5UK0	G_ARG_225	NH2	A_ASP_190	OD1	3.909
5UK0	G_ARG_225	NH2	A_ASP_190	OD2	3.442
5UK0	H_ARG_163	NH1	H_ASP_214	OD1	2.890
5UK0	H_ARG_163	NH2	H_GLU_171	OE1	2.986
5UK0	H_ARG_163	NH2	H_GLU_171	OE2	3.690
5UK0	H_ARG_191	NH1	H_ASP_214	OD2	3.874
5UK0	H_ARG_225	NH1	C_ASP_190	OD1	3.008
5UK0	H_ARG_225	NH1	C_ASP_190	OD2	3.873
5UK0	H_ARG_225	NH1	H_ASP_233	OD1	3.965
5UK0	H_ARG_225	NH2	C_ASP_190	OD1	3.782
5UK0	H_ARG_225	NH2	C_ASP_190	OD2	3.377
5UK0	I_ARG_163	NH1	I_ASP_214	OD1	2.890
5UK0	I_ARG_163	NH2	I_GLU_171	OE1	2.985
5UK0	I_ARG_163	NH2	I_GLU_171	OE2	3.690
5UK0	I_ARG_191	NH1	I_ASP_214	OD2	3.873
5UK0	I_ARG_225	NH1	E_ASP_190	OD1	3.078
5UK0	I_ARG_225	NH1	E_ASP_190	OD2	3.875
5UK0	I_ARG_225	NH1	I_ASP_233	OD1	3.965
5UK0	I_ARG_225	NH2	E_ASP_190	OD1	3.886
5UK0	I_ARG_225	NH2	E_ASP_190	OD2	3.433
5UK1	A_LYS_44	NZ	A_ASP_276	OD2	3.906
5UK1	A_LYS_86	NZ	A_GLU_90	OE2	3.504
5UK1	A_ARG_106	NH1	A_GLU_85	OE1	3.701
5UK1	A_ARG_106	NH1	A_GLU_85	OE2	3.090
5UK1	A_ARG_106	NH1	B_GLU_569	OE2	3.892
5UK1	A_ARG_106	NH2	A_GLU_85	OE1	3.008
5UK1	A_ARG_106	NH2	A_GLU_85	OE2	3.228
5UK1	A_ARG_106	NH2	B_GLU_569	OE2	2.755
5UK1	A_LYS_174	NZ	A_GLU_116	OE2	3.687
5UK1	A_ARG_192	NH2	A_GLU_198	OE2	2.985
5UK1	A_ARG_262	NH1	A_GLU_175	OE1	3.086
5UK1	A_ARG_311	NH1	B_ASP_590	OD1	2.545
5UK1	A_ARG_311	NH1	B_ASP_590	OD2	3.367
5UK1	A_ARG_311	NH2	B_ASP_586	OD1	3.117
5UK1	A_ARG_322	NH2	A_GLU_25	OE1	3.980
5UK1	B_LYS_558	NZ	F_GLU_597	OE1	3.470

5UK1	B_ARG_576	NH1	D_GLU_574	OE1	3.845
5UK1	B_ARG_576	NH1	D_GLU_574	OE2	3.273
5UK1	B_ARG_576	NH2	C_GLU_104	OE2	2.839
5UK1	B_LYS_582	NZ	B_ASP_586	OD2	3.755
5UK1	B_ARG_606	NH2	F_ASP_609	OD2	3.320
5UK1	B_LYS_623	NZ	B_GLU_632	OE2	3.460
5UK1	B_LYS_631	NZ	B_GLU_639	OE1	3.968
5UK1	B_LYS_643	NZ	A_GLU_4	OE1	2.898
5UK1	B_LYS_643	NZ	A_ASP_5	OD1	2.632
5UK1	B_LYS_643	NZ	A_ASP_5	OD2	3.703
5UK1	B_LYS_643	NZ	B_GLU_529	OE2	3.727
5UK1	B_LYS_653	NZ	B_GLU_650	OE1	3.697
5UK1	B_LYS_661	NZ	B_GLU_647	OE1	3.063
5UK1	B_ARG_670	NH2	B_GLU_671	OE2	2.925
5UK1	C_LYS_44	NZ	C_ASP_276	OD2	3.906
5UK1	C_LYS_86	NZ	C_GLU_90	OE2	3.504
5UK1	C_ARG_106	NH1	C_GLU_85	OE1	3.701
5UK1	C_ARG_106	NH1	C_GLU_85	OE2	3.090
5UK1	C_ARG_106	NH2	C_GLU_85	OE1	3.009
5UK1	C_ARG_106	NH2	C_GLU_85	OE2	3.227
5UK1	C_ARG_106	NH2	D_GLU_569	OE2	3.108
5UK1	C_LYS_174	NZ	C_GLU_116	OE2	3.686
5UK1	C_ARG_192	NH2	C_GLU_198	OE2	2.984
5UK1	C_ARG_262	NH1	C_GLU_175	OE1	3.087
5UK1	C_ARG_311	NH1	D_ASP_590	OD1	2.901
5UK1	C_ARG_311	NH1	D_ASP_590	OD2	3.798
5UK1	C_ARG_311	NH2	D_ASP_586	OD1	3.261
5UK1	C_ARG_322	NH2	C_GLU_25	OE1	3.979
5UK1	D_LYS_558	NZ	B_GLU_597	OE1	3.543
5UK1	D_ARG_576	NH1	F_GLU_574	OE1	3.490
5UK1	D_ARG_576	NH1	F_GLU_574	OE2	3.058
5UK1	D_ARG_576	NH2	E_GLU_104	OE2	3.186
5UK1	D_LYS_582	NZ	D_ASP_586	OD2	3.755
5UK1	D_ARG_606	NH2	B_ASP_609	OD2	3.177
5UK1	D_LYS_623	NZ	D_GLU_632	OE2	3.460
5UK1	D_LYS_631	NZ	D_GLU_639	OE1	3.968
5UK1	D_LYS_643	NZ	C_GLU_4	OE1	3.015
5UK1	D_LYS_643	NZ	C_ASP_5	OD1	2.615
5UK1	D_LYS_643	NZ	C_ASP_5	OD2	3.806
5UK1	D_LYS_643	NZ	D_GLU_529	OE2	3.727
5UK1	D_LYS_653	NZ	D_GLU_650	OE1	3.695
5UK1	D_LYS_661	NZ	D_GLU_647	OE1	3.063
5UK1	D_ARG_670	NH2	D_GLU_671	OE2	2.927
5UK1	E_LYS_44	NZ	E_ASP_276	OD2	3.905
5UK1	E_LYS_86	NZ	E_GLU_90	OE2	3.505
5UK1	E_ARG_106	NH1	E_GLU_85	OE1	3.700
5UK1	E_ARG_106	NH1	E_GLU_85	OE2	3.089
5UK1	E_ARG_106	NH2	E_GLU_85	OE1	3.009
5UK1	E_ARG_106	NH2	E_GLU_85	OE2	3.227
5UK1	E_ARG_106	NH2	F_GLU_569	OE2	2.991
5UK1	E_LYS_174	NZ	E_GLU_116	OE2	3.687
5UK1	E_ARG_192	NH2	E_GLU_198	OE2	2.984
5UK1	E_ARG_262	NH1	E_GLU_175	OE1	3.086
5UK1	E_ARG_311	NH1	F_ASP_590	OD1	2.696
5UK1	E_ARG_311	NH1	F_ASP_590	OD2	3.637
5UK1	E_ARG_311	NH2	F_ASP_586	OD1	3.291
5UK1	E_ARG_322	NH2	E_GLU_25	OE1	3.980
5UK1	F_LYS_558	NZ	D_GLU_597	OE1	3.566

5UK1	F_ARG_576	NH1	B_GLU_574	OE1	3.570
5UK1	F_ARG_576	NH1	B_GLU_574	OE2	3.065
5UK1	F_ARG_576	NH2	A_GLU_104	OE2	3.295
5UK1	F_LYS_582	NZ	F_ASP_586	OD2	3.755
5UK1	F_ARG_606	NH2	D_ASP_609	OD2	3.182
5UK1	F_LYS_623	NZ	F_GLU_632	OE2	3.459
5UK1	F_LYS_631	NZ	F_GLU_639	OE1	3.967
5UK1	F_LYS_643	NZ	E_GLU_4	OE1	3.024
5UK1	F_LYS_643	NZ	E_ASP_5	OD1	2.503
5UK1	F_LYS_643	NZ	E_ASP_5	OD2	3.650
5UK1	F_LYS_643	NZ	F_GLU_529	OE2	3.727
5UK1	F_LYS_653	NZ	F_GLU_650	OE1	3.696
5UK1	F_LYS_661	NZ	F_GLU_647	OE1	3.063
5UK1	F_ARG_670	NH2	F_GLU_671	OE2	2.926
5UK1	G_HIS_160	NE2	G_ASP_158	OD1	3.432
5UK1	G_ARG_163	NH1	G_ASP_214	OD1	2.991
5UK1	G_ARG_163	NH2	G_GLU_171	OE1	2.756
5UK1	G_ARG_163	NH2	G_GLU_171	OE2	3.832
5UK1	G_ARG_225	NH1	A_ASP_190	OD1	2.887
5UK1	G_ARG_225	NH1	A_ASP_190	OD2	3.709
5UK1	G_ARG_225	NH2	A_ASP_190	OD1	3.956
5UK1	G_ARG_225	NH2	A_ASP_190	OD2	3.555
5UK1	H_HIS_160	NE2	H_ASP_158	OD1	3.431
5UK1	H_ARG_163	NH1	H_ASP_214	OD1	2.991
5UK1	H_ARG_163	NH2	H_GLU_171	OE1	2.756
5UK1	H_ARG_163	NH2	H_GLU_171	OE2	3.832
5UK1	H_ARG_225	NH1	C_ASP_190	OD1	2.683
5UK1	H_ARG_225	NH1	C_ASP_190	OD2	3.511
5UK1	H_ARG_225	NH2	C_ASP_190	OD1	3.809
5UK1	H_ARG_225	NH2	C_ASP_190	OD2	3.346
5UK1	I_HIS_160	NE2	I_ASP_158	OD1	3.432
5UK1	I_ARG_163	NH1	I_ASP_214	OD1	2.991
5UK1	I_ARG_163	NH2	I_GLU_171	OE1	2.756
5UK1	I_ARG_163	NH2	I_GLU_171	OE2	3.832
5UK1	I_ARG_225	NH1	E_ASP_190	OD1	2.885
5UK1	I_ARG_225	NH1	E_ASP_190	OD2	3.789
5UK1	I_ARG_225	NH2	E_ASP_190	OD1	3.888
5UK1	I_ARG_225	NH2	E_ASP_190	OD2	3.567
5UK2	A_LYS_86	NZ	A_GLU_90	OE2	3.657
5UK2	A_ARG_106	NH1	A_GLU_85	OE2	2.898
5UK2	A_ARG_106	NH1	B_GLU_569	OE2	3.935
5UK2	A_ARG_106	NH2	A_GLU_85	OE1	3.401
5UK2	A_ARG_106	NH2	A_GLU_85	OE2	3.141
5UK2	A_ARG_106	NH2	B_GLU_569	OE2	2.216
5UK2	A_HIS_141	ND1	A_GLU_70	OE2	3.497
5UK2	A_LYS_174	NZ	A_GLU_116	OE2	3.324
5UK2	A_ARG_192	NH2	A_GLU_198	OE2	3.178
5UK2	A_HIS_208	ND1	A_GLU_238	OE2	3.989
5UK2	A_LYS_219	NZ	A_GLU_227	OE2	3.929
5UK2	A_ARG_262	NH1	A_GLU_175	OE1	3.101
5UK2	A_ARG_311	NH1	B_ASP_586	OD1	3.877
5UK2	A_ARG_311	NH1	B_ASP_590	OD1	2.946
5UK2	A_ARG_311	NH1	B_ASP_590	OD2	3.729
5UK2	A_ARG_311	NH2	B_ASP_586	OD1	3.044
5UK2	B_LYS_551	NZ	B_GLU_603	OE1	3.663
5UK2	B_LYS_558	NZ	F_GLU_597	OE1	3.672
5UK2	B_LYS_568	NZ	A_GLU_107	OE1	3.896
5UK2	B_ARG_576	NH1	D_GLU_574	OE1	3.949

5UK2	B_ARG_576	NH1	D_GLU_574	OE2	2.806
5UK2	B_ARG_576	NH2	C_GLU_104	OE2	3.501
5UK2	B_LYS_582	NZ	B_ASP_586	OD2	3.917
5UK2	B_LYS_583	NZ	D_ASP_585	OD1	3.241
5UK2	B_LYS_583	NZ	D_ASP_585	OD2	3.954
5UK2	B_ARG_606	NH2	F_ASP_609	OD2	2.779
5UK2	B_LYS_623	NZ	B_GLU_632	OE2	3.089
5UK2	B_LYS_643	NZ	A_GLU_4	OE1	3.076
5UK2	B_LYS_643	NZ	A_ASP_5	OD1	2.565
5UK2	B_LYS_643	NZ	A_ASP_5	OD2	3.717
5UK2	B_LYS_643	NZ	B_GLU_529	OE2	3.623
5UK2	B_LYS_661	NZ	B_GLU_647	OE1	3.251
5UK2	B_ARG_670	NH2	B_GLU_671	OE2	2.809
5UK2	C_LYS_86	NZ	C_GLU_90	OE2	3.657
5UK2	C_ARG_106	NH1	C_GLU_85	OE2	2.898
5UK2	C_ARG_106	NH1	D_GLU_569	OE2	3.977
5UK2	C_ARG_106	NH2	C_GLU_85	OE1	3.401
5UK2	C_ARG_106	NH2	C_GLU_85	OE2	3.141
5UK2	C_ARG_106	NH2	D_GLU_569	OE2	2.287
5UK2	C_HIS_141	ND1	C_GLU_70	OE2	3.498
5UK2	C_LYS_174	NZ	C_GLU_116	OE2	3.326
5UK2	C_ARG_192	NH2	C_GLU_198	OE2	3.177
5UK2	C_HIS_208	ND1	C_GLU_238	OE2	3.990
5UK2	C_LYS_219	NZ	C_GLU_227	OE2	3.929
5UK2	C_ARG_262	NH1	C_GLU_175	OE1	3.100
5UK2	C_ARG_311	NH1	D_ASP_586	OD1	3.894
5UK2	C_ARG_311	NH1	D_ASP_590	OD1	2.932
5UK2	C_ARG_311	NH1	D_ASP_590	OD2	3.727
5UK2	C_ARG_311	NH2	D_ASP_586	OD1	3.043
5UK2	D_LYS_551	NZ	D_GLU_603	OE1	3.662
5UK2	D_LYS_558	NZ	B_GLU_597	OE1	3.518
5UK2	D_LYS_558	NZ	B_GLU_597	OE2	3.929
5UK2	D_LYS_568	NZ	C_GLU_107	OE1	3.830
5UK2	D_ARG_576	NH1	F_GLU_574	OE1	3.823
5UK2	D_ARG_576	NH1	F_GLU_574	OE2	2.724
5UK2	D_ARG_576	NH2	E_GLU_104	OE2	3.539
5UK2	D_LYS_582	NZ	D_ASP_586	OD2	3.917
5UK2	D_LYS_583	NZ	F_ASP_585	OD1	3.067
5UK2	D_LYS_583	NZ	F_ASP_585	OD2	3.783
5UK2	D_ARG_606	NH2	B_ASP_609	OD2	2.604
5UK2	D_LYS_623	NZ	D_GLU_632	OE2	3.089
5UK2	D_LYS_643	NZ	C_GLU_4	OE1	3.112
5UK2	D_LYS_643	NZ	C_ASP_5	OD1	2.525
5UK2	D_LYS_643	NZ	C_ASP_5	OD2	3.631
5UK2	D_LYS_643	NZ	D_GLU_529	OE2	3.624
5UK2	D_LYS_661	NZ	D_GLU_647	OE1	3.251
5UK2	D_ARG_670	NH2	D_GLU_671	OE2	2.809
5UK2	E_LYS_86	NZ	E_GLU_90	OE2	3.657
5UK2	E_ARG_106	NH1	E_GLU_85	OE2	2.898
5UK2	E_ARG_106	NH1	F_GLU_569	OE2	3.948
5UK2	E_ARG_106	NH2	E_GLU_85	OE1	3.401
5UK2	E_ARG_106	NH2	E_GLU_85	OE2	3.140
5UK2	E_ARG_106	NH2	F_GLU_569	OE2	2.300
5UK2	E_HIS_141	ND1	E_GLU_70	OE2	3.497
5UK2	E_LYS_174	NZ	E_GLU_116	OE2	3.326
5UK2	E_ARG_192	NH2	E_GLU_198	OE2	3.179
5UK2	E_HIS_208	ND1	E_GLU_238	OE2	3.988
5UK2	E_LYS_219	NZ	E_GLU_227	OE2	3.928

5UK2	E_ARG_262	NH1	E_GLU_175	OE1	3.100
5UK2	E_ARG_311	NH1	F_ASP_586	OD1	3.963
5UK2	E_ARG_311	NH1	F_ASP_590	OD1	2.962
5UK2	E_ARG_311	NH1	F_ASP_590	OD2	3.800
5UK2	E_ARG_311	NH2	F_ASP_586	OD1	3.154
5UK2	F_LYS_551	NZ	F_GLU_603	OE1	3.663
5UK2	F_LYS_558	NZ	D_GLU_597	OE1	3.583
5UK2	F_LYS_558	NZ	D_GLU_597	OE2	3.900
5UK2	F_LYS_568	NZ	E_GLU_107	OE1	3.789
5UK2	F_ARG_576	NH1	B_GLU_574	OE1	3.881
5UK2	F_ARG_576	NH1	B_GLU_574	OE2	2.699
5UK2	F_ARG_576	NH2	A_GLU_104	OE2	3.688
5UK2	F_LYS_582	NZ	F_ASP_586	OD2	3.917
5UK2	F_LYS_583	NZ	B_ASP_585	OD1	3.058
5UK2	F_LYS_583	NZ	B_ASP_585	OD2	3.745
5UK2	F_ARG_606	NH2	D_ASP_609	OD2	2.605
5UK2	F_LYS_623	NZ	F_GLU_632	OE2	3.089
5UK2	F_LYS_643	NZ	E_GLU_4	OE1	3.293
5UK2	F_LYS_643	NZ	E_ASP_5	OD1	2.450
5UK2	F_LYS_643	NZ	E_ASP_5	OD2	3.677
5UK2	F_LYS_643	NZ	F_GLU_529	OE2	3.624
5UK2	F_LYS_661	NZ	F_GLU_647	OE1	3.251
5UK2	F_ARG_670	NH2	F_GLU_671	OE2	2.809
5UK2	G_HIS_160	NE2	G_ASP_158	OD1	3.898
5UK2	G_ARG_163	NH1	G_ASP_214	OD1	2.808
5UK2	G_ARG_163	NH2	G_GLU_171	OE1	3.032
5UK2	G_ARG_163	NH2	G_GLU_171	OE2	3.708
5UK2	G_ARG_225	NH1	A_ASP_190	OD1	2.979
5UK2	G_ARG_225	NH1	A_ASP_190	OD2	3.894
5UK2	G_ARG_225	NH2	A_ASP_190	OD1	3.206
5UK2	G_ARG_225	NH2	A_ASP_190	OD2	2.785
5UK2	H_HIS_160	NE2	H_ASP_158	OD1	3.898
5UK2	H_ARG_163	NH1	H_ASP_214	OD1	2.808
5UK2	H_ARG_163	NH2	H_GLU_171	OE1	3.032
5UK2	H_ARG_163	NH2	H_GLU_171	OE2	3.708
5UK2	H_ARG_225	NH1	C_ASP_190	OD1	3.085
5UK2	H_ARG_225	NH2	C_ASP_190	OD1	3.195
5UK2	H_ARG_225	NH2	C_ASP_190	OD2	2.865
5UK2	L_HIS_160	NE2	L_ASP_158	OD1	3.898
5UK2	L_ARG_163	NH1	L_ASP_214	OD1	2.807
5UK2	L_ARG_163	NH2	L_GLU_171	OE1	3.032
5UK2	L_ARG_163	NH2	L_GLU_171	OE2	3.708
5UK2	L_ARG_225	NH1	E_ASP_190	OD1	2.888
5UK2	L_ARG_225	NH1	E_ASP_190	OD2	3.869
5UK2	L_ARG_225	NH2	E_ASP_190	OD1	3.014
5UK2	L_ARG_225	NH2	E_ASP_190	OD2	2.625
5UR8	A_ARG_38	NH2	A_GLU_46	OE1	3.406
5UR8	A_ARG_38	NH2	A_GLU_46	OE2	2.842
5UR8	A_ARG_59	NH1	B_ASP_95	OD1	3.084
5UR8	A_ARG_59	NH1	B_ASP_95	OD2	3.357
5UR8	A_ARG_59	NH2	A_ASP_57	OD1	2.972
5UR8	A_ARG_59	NH2	A_ASP_57	OD2	3.995
5UR8	A_ARG_67	NH1	A_ASP_90	OD1	2.756
5UR8	A_ARG_67	NH1	A_ASP_90	OD2	3.331
5UR8	A_ARG_67	NH2	A_ASP_90	OD1	3.669
5UR8	A_ARG_67	NH2	A_ASP_90	OD2	2.616
5UR8	A_LYS_138	NZ	B_GLU_215	OE2	2.961
5UR8	A_LYS_152	NZ	A_ASP_153	OD1	3.501

5UR8	A_LYS_152	NZ	A_ASP_153	OD2	3.066
5UR8	B_ARG_62	NH2	B_GLU_82	OE2	3.548
5UR8	B_ARG_62	NH2	B_ASP_83	OD1	2.828
5UR8	B_ARG_62	NH2	B_ASP_83	OD2	3.632
5UR8	B_LYS_105	NZ	B_GLU_167	OE1	2.973
5UR8	B_LYS_105	NZ	B_GLU_167	OE2	3.906
5UR8	B_LYS_151	NZ	B_GLU_197	OE1	2.809
5UR8	B_LYS_151	NZ	B_GLU_197	OE2	3.414
5UR8	B_LYS_190	NZ	B_ASP_187	OD1	3.286
5UR8	B_HIS_191	ND1	B_ASP_153	OD1	3.243
5VF2	A_LYS_64	NZ	A_GLU_47	OE2	2.716
5VF2	A_LYS_68	NZ	A_ASP_91	OD1	3.611
5VF2	A_LYS_68	NZ	A_ASP_91	OD2	2.737
5VF2	A_ARG_99	NH2	A_ASP_108	OD1	3.519
5VF2	A_ARG_99	NH2	A_ASP_108	OD2	2.783
5VL3	Q_HIS_28	NE2	Q_GLU_130	OE2	3.358
5VL3	Q_ARG_75	NH1	Q_GLU_78	OE2	3.350
5VL3	Q_ARG_91	NH1	Q_ASP_113	OD1	3.515
5VL3	Q_ARG_91	NH1	Q_ASP_113	OD2	2.674
5VL3	Q_ARG_91	NH2	Q_ASP_113	OD1	3.050
5VL3	Q_ARG_91	NH2	Q_ASP_113	OD2	3.746
5VL3	Q_HIS_110	ND1	Q_GLU_36	OE1	3.316
5VL3	Q_HIS_110	ND1	Q_GLU_36	OE2	2.335
5VL3	Q_HIS_213	NE2	H_GLU_58	OE2	3.352
5VL3	Q_LYS_239	NZ	Q_GLU_150	OE1	3.878
5VL3	Q_LYS_239	NZ	Q_GLU_150	OE2	3.128
5VL3	Q_LYS_243	NZ	Q_GLU_153	OE1	2.660
5VL3	Q_LYS_243	NZ	Q_GLU_153	OE2	2.886
5VL3	Q_LYS_281	NZ	Q_ASP_282	OD2	3.077
5VL3	Q_LYS_306	NZ	Q_GLU_322	OE1	3.813
5VL3	R_HIS_28	NE2	R_GLU_130	OE2	3.389
5VL3	R_LYS_70	NZ	R_ASP_72	OD1	3.096
5VL3	R_ARG_91	NH1	R_ASP_113	OD1	3.738
5VL3	R_ARG_91	NH1	R_ASP_113	OD2	2.609
5VL3	R_ARG_91	NH2	R_ASP_113	OD1	2.934
5VL3	R_ARG_91	NH2	R_ASP_113	OD2	3.371
5VL3	R_HIS_110	ND1	R_GLU_36	OE1	3.943
5VL3	R_HIS_110	ND1	R_GLU_36	OE2	2.329
5VL3	R_ARG_120	NH2	T_GLU_54	OE2	3.782
5VL3	R_LYS_127	NZ	R_GLU_122	OE2	3.799
5VL3	R_LYS_127	NZ	T_GLU_54	OE1	2.927
5VL3	R_LYS_127	NZ	T_GLU_122	OE1	2.999
5VL3	R_HIS_213	NE2	A_GLU_58	OE2	3.157
5VL3	R_LYS_239	NZ	R_GLU_150	OE1	3.277
5VL3	R_LYS_247	NZ	R_GLU_266	OE2	3.438
5VL3	R_LYS_281	NZ	R_ASP_282	OD2	3.188
5VL3	R_LYS_306	NZ	R_GLU_322	OE1	3.817
5VL3	R_ARG_319	NH2	R_GLU_322	OE2	3.267
5VL3	S_LYS_23	NZ	S_ASP_50	OD2	3.917
5VL3	S_HIS_28	NE2	S_GLU_130	OE2	3.287
5VL3	S_ARG_75	NH1	S_GLU_78	OE2	2.970
5VL3	S_LYS_100	NZ	S_ASP_97	OD2	2.933
5VL3	S_LYS_205	NZ	S_GLU_156	OE2	3.382
5VL3	S_HIS_213	NE2	C_GLU_58	OE2	3.140
5VL3	S_LYS_227	NZ	S_ASP_225	OD1	3.967
5VL3	S_LYS_239	NZ	S_GLU_150	OE2	3.417
5VL3	S_LYS_243	NZ	S_GLU_153	OE1	2.988
5VL3	S_LYS_243	NZ	S_GLU_153	OE2	2.544

5VL3	S_LYS_281	NZ	S_ASP_282	OD2	3.330
5VL3	S_LYS_306	NZ	S_GLU_322	OE1	3.934
5VL3	T_HIS_28	NE2	T_GLU_130	OE2	3.482
5VL3	T_ARG_75	NH1	T_GLU_78	OE2	2.965
5VL3	T_ARG_91	NH2	T_ASP_113	OD1	2.973
5VL3	T_ARG_91	NH2	T_ASP_113	OD2	2.700
5VL3	T_LYS_98	NZ	T_ASP_52	OD2	3.823
5VL3	T_HIS_110	ND1	T_GLU_36	OE1	3.602
5VL3	T_HIS_110	ND1	T_GLU_36	OE2	2.613
5VL3	T_LYS_127	NZ	R_GLU_54	OE1	3.658
5VL3	T_LYS_127	NZ	R_GLU_122	OE1	3.863
5VL3	T_LYS_205	NZ	T_GLU_156	OE1	3.981
5VL3	T_HIS_213	NE2	E_GLU_58	OE2	3.636
5VL3	T_LYS_239	NZ	T_GLU_150	OE2	3.518
5VL3	T_LYS_243	NZ	T_GLU_153	OE1	3.300
5VL3	T_LYS_243	NZ	T_GLU_153	OE2	2.403
5VL3	T_LYS_247	NZ	T_GLU_266	OE2	3.696
5VL3	T_LYS_281	NZ	T_ASP_282	OD2	3.114
5VL3	T_ARG_319	NH2	T_GLU_322	OE2	3.136
5VL3	A_ARG_38	NH1	A_GLU_46	OE2	3.328
5VL3	A_ARG_53	NH2	R_ASP_232	OD1	3.883
5VL3	A_ARG_53	NH2	R_ASP_232	OD2	3.340
5VL3	A_LYS_66	NZ	A_ASP_86	OD1	3.151
5VL3	A_LYS_66	NZ	A_ASP_86	OD2	3.194
5VL3	A_ARG_83	NH2	A_GLU_85	OE1	2.855
5VL3	A_ARG_83	NH2	A_GLU_85	OE2	3.048
5VL3	A_ARG_95	NH1	R_GLU_179	OE1	3.121
5VL3	A_ARG_95	NH1	R_GLU_179	OE2	3.607
5VL3	A_ARG_95	NH2	R_GLU_179	OE2	3.046
5VL3	A_LYS_210	NZ	B_GLU_124	OE2	3.976
5VL3	A_LYS_215	NZ	A_GLU_213	OE1	2.311
5VL3	C_ARG_38	NH1	C_GLU_46	OE2	3.106
5VL3	C_ARG_53	NH2	S_ASP_232	OD2	3.370
5VL3	C_ARG_94	NH1	C_ASP_96	OD1	3.364
5VL3	C_ARG_94	NH2	C_ASP_96	OD1	3.938
5VL3	C_ARG_95	NH1	S_GLU_179	OE1	3.505
5VL3	C_ARG_95	NH1	S_GLU_179	OE2	3.184
5VL3	C_ARG_95	NH2	S_GLU_179	OE2	3.815
5VL3	C_LYS_144	NZ	C_ASP_145	OD1	3.207
5VL3	C_LYS_144	NZ	C_ASP_145	OD2	2.725
5VL3	E_ARG_38	NH1	E_GLU_46	OE2	3.258
5VL3	E_ARG_53	NH2	T_ASP_232	OD1	3.852
5VL3	E_ARG_53	NH2	T_ASP_232	OD2	3.470
5VL3	E_ARG_83	NH1	E_ASP_86	OD1	3.861
5VL3	E_ARG_94	NH1	E_ASP_96	OD1	2.513
5VL3	E_ARG_95	NH1	T_GLU_179	OE1	2.688
5VL3	E_ARG_95	NH1	T_GLU_179	OE2	2.993
5VL3	E_ARG_95	NH2	T_GLU_179	OE2	3.079
5VL3	E_LYS_144	NZ	E_ASP_145	OD1	2.943
5VL3	E_LYS_144	NZ	E_ASP_145	OD2	2.901
5VL3	E_LYS_210	NZ	F_GLU_	OE2	3.778
5VL3	E_LYS_	NZ	F_ASP_	OD2	3.984
5VL3	H_ARG_38	NH1	H_GLU_46	OE2	2.851
5VL3	H_ARG_53	NH2	Q_ASP_232	OD1	3.950
5VL3	H_ARG_53	NH2	Q_ASP_232	OD2	3.411
5VL3	H_LYS_66	NZ	H_ASP_86	OD1	3.327
5VL3	H_LYS_66	NZ	H_ASP_86	OD2	2.190
5VL3	H_ARG_83	NH2	H_GLU_85	OE1	3.339

5VL3	H_ARG_83	NH2	H_GLU_85	OE2	3.382
5VL3	H_ARG_94	NH1	H_ASP_96	OD1	3.684
5VL3	H_ARG_95	NH1	Q_GLU_179	OE1	3.431
5VL3	H_ARG_95	NH1	Q_GLU_179	OE2	3.819
5VL3	H_ARG_95	NH2	Q_GLU_179	OE2	3.149
5VL3	H_LYS_144	NZ	H_ASP_145	OD1	2.853
5VL3	H_LYS_144	NZ	H_ASP_145	OD2	2.951
5VL3	B_ARG_61	NH2	B_GLU_81	OE1	3.497
5VL3	B_ARG_61	NH2	B_ASP_82	OD1	2.798
5VL3	B_ARG_61	NH2	B_ASP_82	OD2	3.720
5VL3	D_ARG_61	NH2	D_GLU_81	OE1	3.609
5VL3	D_ARG_61	NH2	D_ASP_82	OD1	3.084
5VL3	D_ARG_61	NH2	D_ASP_82	OD2	3.921
5VL3	D_LYS_150	NZ	D_GLU_196	OE1	3.872
5VL3	D_LYS_150	NZ	D_GLU_196	OE2	3.186
5VL3	D_LYS_189	NZ	D_ASP_186	OD1	3.734
5VL3	F_ARG_61	NH1	F_GLU_81	OE2	3.708
5VL3	F_ARG_61	NH2	F_GLU_81	OE2	2.960
5VL3	F_ARG_61	NH2	F_ASP_82	OD1	2.834
5VL3	F_ARG_61	NH2	F_ASP_82	OD2	3.453
5VL3	F_LYS_150	NZ	F_GLU_196	OE1	3.617
5VL3	F_LYS_150	NZ	F_GLU_196	OE2	3.530
5VL3	L_ARG_18	NH2	R_GLU_36	OE2	3.892
5VL3	L_ARG_61	NH2	L_GLU_81	OE1	3.403
5VL3	L_ARG_61	NH2	L_ASP_82	OD1	2.637
5VL3	L_ARG_61	NH2	L_ASP_82	OD2	3.407
5VL3	L_LYS_150	NZ	L_GLU_196	OE1	3.651
5VL3	L_LYS_150	NZ	L_GLU_196	OE2	3.240
5VN8	G_LYS_34	NZ	A_ASP_612	OD1	3.263
5VN8	G_LYS_46	NZ	A_GLU_632	OE1	3.416
5VN8	G_LYS_46	NZ	A_GLU_632	OE2	2.866
5VN8	G_LYS_282	NZ	G_GLU_275	OE1	3.041
5VN8	G_ARG_337	NH1	G_GLU_290	OE1	3.439
5VN8	G_ARG_337	NH1	G_GLU_290	OE2	3.645
5VN8	G_ARG_337	NH1	G_GLU_340	OE1	3.059
5VN8	G_LYS_348	NZ	G_GLU_269	OE2	2.496
5VN8	G_LYS_348	NZ	G_GLU_351	OE1	3.775
5VN8	G_LYS_356	NZ	G_GLU_466	OE2	2.685
5VN8	G_ARG_456	NH1	G_GLU_466	OE2	3.971
5VN8	G_ARG_469	NH2	G_ASP_457	OD2	3.488
5VN8	G_ARG_476	NH2	G_GLU_102	OE1	2.991
5VN8	G_ARG_476	NH2	G_GLU_102	OE2	3.449
5VN8	G_LYS_487	NZ	G_GLU_47	OE1	3.496
5VN8	G_LYS_487	NZ	G_GLU_91	OE2	3.186
5VN8	A_ARG_542	NH2	C_GLU_647	OE2	2.749
5VN8	A_ARG_579	NH1	C_GLU_584	OE1	3.931
5VN8	H_LYS_12	NZ	H_GLU_10	OE2	2.532
5VN8	H_ARG_28	NH1	G_ASP_457	OD1	2.893
5VN8	H_ARG_38	NH1	H_ASP_86	OD1	2.826
5VN8	H_ARG_38	NH2	H_GLU_46	OE1	3.729
5VN8	H_ARG_38	NH2	H_GLU_46	OE2	2.857
5VN8	H_LYS_62	NZ	H_GLU_46	OE1	3.455
5VN8	H_ARG_66	NH2	H_ASP_86	OD1	3.206
5VN8	H_ARG_66	NH2	H_ASP_86	OD2	2.433
5VN8	H_ARG_82A	NH1	H_ASP_65	OD1	3.493
5VN8	H_ARG_94	NH2	H_ASP_101	OD2	3.929
5VN8	L_HIS_27	NE2	L_GLU_1	OE2	2.752
5VN8	L_HIS_49	ND1	H_ASP_101	OD1	3.097

5VN8	L_ARG_61	NH1	L_ASP_82	OD2	2.660
5VN8	L_ARG_61	NH2	L_GLU_81	OE2	3.818
5VN8	L_ARG_61	NH2	L_ASP_82	OD1	3.890
5VN8	L_ARG_61	NH2	L_ASP_82	OD2	2.783
5VN8	L_LYS_103	NZ	L_GLU_105	OE1	3.506
5VN8	D_LYS_34	NZ	B_ASP_612	OD1	3.397
5VN8	D_LYS_46	NZ	B_GLU_632	OE1	3.407
5VN8	D_LYS_46	NZ	B_GLU_632	OE2	2.853
5VN8	D_LYS_282	NZ	D_GLU_275	OE1	3.041
5VN8	D_ARG_337	NH1	D_GLU_290	OE1	3.439
5VN8	D_ARG_337	NH1	D_GLU_290	OE2	3.644
5VN8	D_ARG_337	NH1	D_GLU_340	OE1	3.058
5VN8	D_LYS_348	NZ	D_GLU_269	OE2	2.495
5VN8	D_LYS_348	NZ	D_GLU_351	OE1	3.775
5VN8	D_LYS_356	NZ	D_GLU_466	OE2	2.685
5VN8	D_ARG_456	NH1	D_GLU_466	OE2	3.971
5VN8	D_ARG_469	NH2	D_ASP_457	OD2	3.488
5VN8	D_ARG_476	NH2	D_GLU_102	OE1	2.992
5VN8	D_ARG_476	NH2	D_GLU_102	OE2	3.449
5VN8	D_LYS_487	NZ	D_GLU_47	OE1	3.496
5VN8	D_LYS_487	NZ	D_GLU_91	OE2	3.186
5VN8	B_ARG_542	NH2	A_GLU_647	OE1	3.985
5VN8	B_ARG_542	NH2	A_GLU_647	OE2	2.712
5VN8	B_ARG_579	NH1	A_GLU_584	OE1	3.986
5VN8	F_LYS_12	NZ	F_GLU_10	OE2	2.532
5VN8	F_ARG_28	NH1	D_ASP_457	OD1	2.808
5VN8	F_ARG_38	NH1	F_ASP_86	OD1	2.826
5VN8	F_ARG_38	NH2	F_GLU_46	OE1	3.728
5VN8	F_ARG_38	NH2	F_GLU_46	OE2	2.856
5VN8	F_LYS_62	NZ	F_GLU_46	OE1	3.454
5VN8	F_ARG_66	NH2	F_ASP_86	OD1	3.206
5VN8	F_ARG_66	NH2	F_ASP_86	OD2	2.433
5VN8	F_ARG_82A	NH1	F_ASP_65	OD1	3.494
5VN8	F_ARG_94	NH2	F_ASP_101	OD2	3.929
5VN8	J_HIS_27	NE2	J_GLU_1	OE2	2.753
5VN8	J_HIS_49	ND1	F_ASP_101	OD1	3.213
5VN8	J_ARG_61	NH1	J_ASP_82	OD2	2.661
5VN8	J_ARG_61	NH2	J_GLU_81	OE2	3.818
5VN8	J_ARG_61	NH2	J_ASP_82	OD1	3.889
5VN8	J_ARG_61	NH2	J_ASP_82	OD2	2.783
5VN8	J_LYS_103	NZ	J_GLU_105	OE1	3.505
5VN8	E_LYS_34	NZ	C_ASP_612	OD1	3.266
5VN8	E_LYS_46	NZ	C_GLU_632	OE1	3.380
5VN8	E_LYS_46	NZ	C_GLU_632	OE2	2.776
5VN8	E_LYS_282	NZ	E_GLU_275	OE1	3.041
5VN8	E_ARG_337	NH1	E_GLU_290	OE1	3.439
5VN8	E_ARG_337	NH1	E_GLU_290	OE2	3.643
5VN8	E_ARG_337	NH1	E_GLU_340	OE1	3.057
5VN8	E_LYS_348	NZ	E_GLU_269	OE2	2.495
5VN8	E_LYS_348	NZ	E_GLU_351	OE1	3.775
5VN8	E_LYS_356	NZ	E_GLU_466	OE2	2.685
5VN8	E_ARG_456	NH1	E_GLU_466	OE2	3.971
5VN8	E_ARG_469	NH2	E_ASP_457	OD2	3.488
5VN8	E_ARG_476	NH2	E_GLU_102	OE1	2.991
5VN8	E_ARG_476	NH2	E_GLU_102	OE2	3.449
5VN8	E_LYS_487	NZ	E_GLU_47	OE1	3.496
5VN8	E_LYS_487	NZ	E_GLU_91	OE2	3.186
5VN8	C_ARG_542	NH2	B_GLU_647	OE2	2.738

5VN8	C_ARG_579	NH1	B_GLU_584	OE1	3.772
5VN8	L_LYS_12	NZ	L_GLU_10	OE2	2.532
5VN8	L_ARG_28	NH1	E_ASP_457	OD1	3.234
5VN8	L_ARG_38	NH1	L_ASP_86	OD1	2.826
5VN8	L_ARG_38	NH2	L_GLU_46	OE1	3.728
5VN8	L_ARG_38	NH2	L_GLU_46	OE2	2.857
5VN8	L_LYS_62	NZ	L_GLU_46	OE1	3.455
5VN8	L_ARG_66	NH2	L_ASP_86	OD1	3.206
5VN8	L_ARG_66	NH2	L_ASP_86	OD2	2.435
5VN8	L_ARG_82A	NH1	L_ASP_65	OD1	3.494
5VN8	L_ARG_94	NH2	L_ASP_101	OD2	3.929
5VN8	K_HIS_27	NE2	K_GLU_1	OE2	2.754
5VN8	K_HIS_49	ND1	L_ASP_101	OD1	3.072
5VN8	K_HIS_49	NE2	L_ASP_101	OD1	3.981
5VN8	K_ARG_61	NH1	K_ASP_82	OD2	2.660
5VN8	K_ARG_61	NH2	K_GLU_81	OE2	3.818
5VN8	K_ARG_61	NH2	K_ASP_82	OD1	3.890
5VN8	K_ARG_61	NH2	K_ASP_82	OD2	2.783
5VN8	K_LYS_103	NZ	K_GLU_105	OE1	3.505
5VXJ	A_ARG_55	NH2	A_ASP_309	OD2	2.897
5VXJ	A_LYS_63	NZ	A_GLU_64	OE1	2.911
5VXJ	A_ARG_101	NH2	A_ASP_97	OD2	3.249
5VXJ	A_LYS_151	NZ	A_GLU_147	OE1	3.093
5VXJ	A_LYS_151	NZ	A_GLU_147	OE2	3.176
5VXJ	A_LYS_196	NZ	A_ASP_261	OD1	2.840
5VXJ	A_LYS_197	NZ	A_GLU_201	OE1	3.559
5VXJ	A_LYS_197	NZ	A_GLU_201	OE2	2.683
5VXJ	A_LYS_203	NZ	A_ASP_254	OD1	2.485
5VXJ	A_LYS_203	NZ	A_ASP_254	OD2	3.995
5VXJ	A_LYS_205	NZ	A_ASP_166	OD2	2.597
5VXJ	A_LYS_207	NZ	A_GLU_204	OE2	3.657
5VXJ	A_LYS_207	NZ	A_ASP_208	OD2	3.848
5VXJ	A_LYS_291	NZ	A_ASP_287	OD2	2.858
5VXJ	A_LYS_300	NZ	A_GLU_229	OE2	3.809
5VXJ	B_ARG_19	NH2	A_ASP_97	OD1	2.652
5VXJ	B_ARG_38	NH1	B_ASP_90	OD1	2.762
5VXJ	B_ARG_38	NH2	B_GLU_46	OE2	3.072
5VXJ	B_ARG_38	NH2	B_ASP_90	OD1	3.724
5VXJ	B_ARG_50	NH1	L_GLU_200	OE1	2.921
5VXJ	B_ARG_50	NH2	L_GLU_200	OE1	3.757
5VXJ	B_ARG_67	NH1	B_ASP_90	OD2	2.822
5VXJ	B_ARG_67	NH2	B_ASP_90	OD1	2.956
5VXJ	B_ARG_67	NH2	B_ASP_90	OD2	3.171
5VXJ	B_LYS_76	NZ	A_GLU_122	OE1	2.874
5VXJ	B_HIS_80	NE2	A_ASP_144	OD1	3.165
5VXJ	B_HIS_80	NE2	A_ASP_144	OD2	3.364
5VXJ	C_ARG_55	NH2	C_ASP_309	OD1	3.860
5VXJ	C_ARG_55	NH2	C_ASP_309	OD2	2.973
5VXJ	C_LYS_72	NZ	C_GLU_76	OE2	3.986
5VXJ	C_HIS_81	NE2	C_GLU_77	OE1	3.864
5VXJ	C_ARG_101	NH2	C_ASP_97	OD2	3.028
5VXJ	C_ARG_111	NH1	C_ASP_126	OD1	3.446
5VXJ	C_LYS_137	NZ	C_ASP_124	OD1	3.580
5VXJ	C_LYS_137	NZ	C_ASP_124	OD2	3.859
5VXJ	C_LYS_151	NZ	C_GLU_147	OE1	3.347
5VXJ	C_LYS_151	NZ	C_GLU_147	OE2	3.417
5VXJ	C_LYS_189	NZ	C_GLU_268	OE1	3.664
5VXJ	C_LYS_196	NZ	C_ASP_261	OD1	2.639

5VXJ	C_LYS_196	NZ	C_ASP_261	OD2	3.513
5VXJ	C_LYS_197	NZ	C_GLU_201	OE1	2.594
5VXJ	C_LYS_197	NZ	C_GLU_201	OE2	3.519
5VXJ	C_LYS_203	NZ	C_ASP_254	OD1	2.687
5VXJ	C_LYS_205	NZ	C_ASP_166	OD2	2.854
5VXJ	C_LYS_207	NZ	C_GLU_204	OE1	3.423
5VXJ	C_LYS_207	NZ	C_GLU_204	OE2	2.767
5VXJ	C_LYS_275	NZ	C_ASP_272	OD2	3.447
5VXJ	D_ARG_19	NH1	C_ASP_97	OD1	3.252
5VXJ	D_ARG_31	NH1	D_ASP_102	OD1	3.380
5VXJ	D_ARG_38	NH1	D_ASP_90	OD1	2.860
5VXJ	D_ARG_38	NH2	D_GLU_46	OE2	2.886
5VXJ	D_ARG_50	NH1	E_GLU_200	OE1	3.721
5VXJ	D_ARG_50	NH2	E_GLU_200	OE1	3.781
5VXJ	D_ARG_67	NH1	D_ASP_90	OD1	3.893
5VXJ	D_ARG_67	NH1	D_ASP_90	OD2	2.756
5VXJ	D_ARG_67	NH2	D_ASP_90	OD1	2.919
5VXJ	D_ARG_67	NH2	D_ASP_90	OD2	3.254
5VXJ	D_LYS_76	NZ	C_GLU_122	OE1	3.854
5VXJ	D_HIS_80	NE2	C_ASP_144	OD1	3.067
5VXJ	D_HIS_80	NE2	C_ASP_144	OD2	3.196
5VXJ	E_ARG_55	NH2	E_ASP_309	OD1	3.935
5VXJ	E_ARG_55	NH2	E_ASP_309	OD2	2.817
5VXJ	E_ARG_101	NH1	E_ASP_97	OD2	2.865
5VXJ	E_LYS_119	NZ	E_GLU_120	OE2	3.261
5VXJ	E_LYS_137	NZ	F_ASP_73	OD1	3.543
5VXJ	E_LYS_137	NZ	F_ASP_73	OD2	2.771
5VXJ	E_LYS_151	NZ	E_GLU_154	OE1	3.893
5VXJ	E_LYS_196	NZ	E_ASP_261	OD1	3.147
5VXJ	E_LYS_196	NZ	E_ASP_261	OD2	3.896
5VXJ	E_LYS_197	NZ	E_GLU_201	OE1	3.410
5VXJ	E_LYS_197	NZ	E_GLU_201	OE2	2.471
5VXJ	E_LYS_203	NZ	E_ASP_254	OD1	2.551
5VXJ	E_LYS_203	NZ	E_ASP_254	OD2	3.950
5VXJ	E_LYS_205	NZ	E_ASP_166	OD2	2.795
5VXJ	E_LYS_207	NZ	E_GLU_204	OE2	3.844
5VXJ	E_LYS_207	NZ	E_ASP_208	OD1	3.647
5VXJ	E_LYS_207	NZ	E_ASP_208	OD2	3.353
5VXJ	E_LYS_275	NZ	E_ASP_272	OD1	3.514
5VXJ	E_LYS_275	NZ	E_ASP_272	OD2	3.831
5VXJ	E_LYS_291	NZ	E_ASP_287	OD2	3.845
5VXJ	E_LYS_291	NZ	E_GLU_288	OE2	3.598
5VXJ	F_ARG_19	NH2	E_ASP_97	OD1	2.921
5VXJ	F_ARG_38	NH1	F_ASP_90	OD1	2.919
5VXJ	F_ARG_38	NH2	F_GLU_46	OE2	2.728
5VXJ	F_ARG_50	NH1	G_GLU_200	OE1	3.576
5VXJ	F_ARG_50	NH2	G_GLU_200	OE1	2.702
5VXJ	F_ARG_67	NH1	F_ASP_90	OD1	3.836
5VXJ	F_ARG_67	NH1	F_ASP_90	OD2	2.827
5VXJ	F_ARG_67	NH2	F_ASP_90	OD1	3.120
5VXJ	F_ARG_67	NH2	F_ASP_90	OD2	3.574
5VXJ	F_LYS_76	NZ	E_GLU_122	OE1	3.693
5VXJ	F_HIS_80	NE2	E_ASP_144	OD1	3.009
5VXJ	F_HIS_80	NE2	E_ASP_144	OD2	3.134
5VXJ	F_ARG_106	NH2	F_ASP_102	OD1	3.541
5VXJ	G_ARG_55	NH2	G_ASP_309	OD1	3.852
5VXJ	G_ARG_55	NH2	G_ASP_309	OD2	3.242
5VXJ	G_ARG_101	NH2	G_ASP_97	OD2	3.466

5VXJ	G_HIS_115	ND1	G_GLU_112	OE1	3.174
5VXJ	G_LYS_119	NZ	G_GLU_120	OE2	3.684
5VXJ	G_LYS_137	NZ	G_ASP_124	OD2	3.625
5VXJ	G_LYS_137	NZ	H_ASP_73	OD1	3.131
5VXJ	G_LYS_137	NZ	H_ASP_73	OD2	2.336
5VXJ	G_LYS_151	NZ	G_GLU_147	OE1	3.540
5VXJ	G_LYS_151	NZ	G_GLU_147	OE2	3.043
5VXJ	G_LYS_196	NZ	G_ASP_261	OD1	2.809
5VXJ	G_LYS_197	NZ	G_GLU_201	OE1	3.460
5VXJ	G_LYS_197	NZ	G_GLU_201	OE2	2.587
5VXJ	G_LYS_203	NZ	G_ASP_254	OD1	2.489
5VXJ	G_LYS_203	NZ	G_ASP_254	OD2	3.948
5VXJ	G_LYS_205	NZ	G_ASP_166	OD2	2.817
5VXJ	G_LYS_207	NZ	G_GLU_204	OE2	3.639
5VXJ	G_LYS_207	NZ	G_ASP_208	OD1	3.592
5VXJ	G_LYS_207	NZ	G_ASP_208	OD2	3.456
5VXJ	G_LYS_291	NZ	G_GLU_288	OE1	3.119
5VXJ	H_ARG_19	NH2	G_ASP_97	OD1	2.467
5VXJ	H_ARG_31	NH1	H_ASP_102	OD1	3.947
5VXJ	H_ARG_31	NH2	H_ASP_102	OD1	3.898
5VXJ	H_ARG_38	NH1	H_ASP_90	OD1	2.996
5VXJ	H_ARG_38	NH2	H_GLU_46	OE1	3.400
5VXJ	H_LYS_65	NZ	H_ASP_62	OD1	3.343
5VXJ	H_ARG_67	NH1	H_ASP_90	OD1	3.939
5VXJ	H_ARG_67	NH1	H_ASP_90	OD2	2.890
5VXJ	H_ARG_67	NH2	H_ASP_90	OD1	3.245
5VXJ	H_ARG_67	NH2	H_ASP_90	OD2	3.633
5VXJ	H_LYS_76	NZ	G_ASP_124	OD2	3.951
5VXJ	H_HIS_80	NE2	G_ASP_144	OD1	3.186
5VXJ	H_HIS_80	NE2	G_ASP_144	OD2	3.321
5VXJ	H_ARG_106	NH2	H_ASP_102	OD2	2.976
5VXJ	L_ARG_55	NH2	L_ASP_309	OD2	3.083
5VXJ	L_HIS_81	NE2	L_GLU_77	OE1	3.831
5VXJ	L_ARG_101	NH2	L_ASP_97	OD2	3.365
5VXJ	L_LYS_137	NZ	J_ASP_73	OD1	3.804
5VXJ	L_LYS_137	NZ	J_ASP_73	OD2	2.902
5VXJ	L_LYS_151	NZ	L_GLU_147	OE1	3.728
5VXJ	L_LYS_151	NZ	L_GLU_147	OE2	3.585
5VXJ	L_LYS_196	NZ	L_ASP_261	OD1	2.688
5VXJ	L_LYS_196	NZ	L_ASP_261	OD2	3.785
5VXJ	L_LYS_197	NZ	L_GLU_201	OE1	3.642
5VXJ	L_LYS_197	NZ	L_GLU_201	OE2	2.731
5VXJ	L_LYS_203	NZ	L_ASP_254	OD1	2.602
5VXJ	L_LYS_205	NZ	L_ASP_166	OD2	2.773
5VXJ	L_LYS_207	NZ	L_GLU_204	OE1	3.025
5VXJ	L_LYS_207	NZ	L_GLU_204	OE2	3.929
5VXJ	L_LYS_275	NZ	L_ASP_272	OD1	3.295
5VXJ	L_LYS_275	NZ	L_ASP_272	OD2	2.777
5VXJ	L_LYS_300	NZ	L_GLU_229	OE1	3.150
5VXJ	J_ARG_19	NH2	L_ASP_97	OD1	2.772
5VXJ	J_ARG_31	NH1	J_ASP_102	OD1	3.834
5VXJ	J_ARG_38	NH1	J_ASP_90	OD1	2.886
5VXJ	J_ARG_38	NH2	J_GLU_46	OE2	2.770
5VXJ	J_LYS_65	NZ	J_ASP_62	OD1	2.928
5VXJ	J_ARG_67	NH1	J_ASP_90	OD1	3.756
5VXJ	J_ARG_67	NH1	J_ASP_90	OD2	2.548
5VXJ	J_ARG_67	NH2	J_ASP_90	OD1	2.840
5VXJ	J_ARG_67	NH2	J_ASP_90	OD2	3.177

5VXJ	J_LYS_76	NZ	I_GLU_122	OE2	2.338
5VXJ	J_HIS_80	NE2	I_ASP_144	OD1	3.036
5VXJ	J_HIS_80	NE2	I_ASP_144	OD2	3.151
5VXK	B_ARG_38	NH1	B_ASP_90	OD1	3.007
5VXK	B_ARG_38	NH2	B_GLU_46	OE1	3.833
5VXK	B_ARG_38	NH2	B_GLU_89	OE2	3.179
5VXK	B_ARG_67	NH1	B_ASP_90	OD1	3.692
5VXK	B_ARG_67	NH1	B_ASP_90	OD2	3.910
5VXK	B_ARG_67	NH2	B_ASP_90	OD1	3.395
5VXK	B_ARG_67	NH2	B_ASP_90	OD2	2.274
5VXK	B_HIS_80	NE2	B_ASP_73	OD2	3.665
5VXK	B_ARG_100	NH2	B_ASP_31	OD2	3.630
5VXK	A_LYS_151	NZ	A_GLU_147	OE1	2.685
5VXK	A_LYS_151	NZ	A_GLU_147	OE2	3.996
5VXK	A_LYS_196	NZ	A_ASP_261	OD2	2.739
5VXK	A_LYS_203	NZ	A_ASP_254	OD1	2.600
5VXK	A_LYS_203	NZ	A_ASP_254	OD2	3.429
5VXK	A_LYS_205	NZ	A_ASP_166	OD1	3.632
5VXK	A_LYS_225	NZ	A_GLU_229	OE1	3.736
5VXK	A_LYS_291	NZ	A_ASP_287	OD1	3.331
5VXK	A_LYS_291	NZ	A_GLU_288	OE1	3.331
5VXK	A_LYS_291	NZ	A_GLU_288	OE2	2.840
5VXK	A_LYS_313	NZ	A_ASP_309	OD2	3.376
5VXL	A_ARG_55	NH1	A_ASP_309	OD1	3.335
5VXL	A_ARG_55	NH1	A_ASP_309	OD2	2.392
5VXL	A_ARG_101	NH1	A_ASP_97	OD1	3.775
5VXL	A_ARG_101	NH1	A_ASP_97	OD2	3.730
5VXL	A_ARG_101	NH2	A_ASP_97	OD1	3.151
5VXL	A_ARG_101	NH2	A_ASP_97	OD2	2.610
5VXL	A_LYS_151	NZ	A_GLU_147	OE1	2.946
5VXL	A_LYS_151	NZ	A_GLU_147	OE2	3.503
5VXL	A_LYS_189	NZ	A_GLU_268	OE1	3.767
5VXL	A_LYS_196	NZ	A_ASP_261	OD1	2.987
5VXL	A_LYS_197	NZ	A_GLU_201	OE2	2.961
5VXL	A_LYS_203	NZ	A_ASP_254	OD1	2.551
5VXL	A_LYS_203	NZ	A_ASP_254	OD2	3.633
5VXL	A_LYS_205	NZ	A_ASP_166	OD1	3.841
5VXL	A_LYS_205	NZ	A_ASP_166	OD2	2.867
5VXL	A_LYS_205	NZ	B_ASP_52	OD2	2.998
5VXL	A_LYS_291	NZ	A_ASP_287	OD2	3.686
5VXL	B_ARG_19	NH2	B_GLU_83	OE1	3.609
5VXL	B_ARG_38	NH1	B_ASP_91	OD1	2.974
5VXL	B_ARG_38	NH2	B_GLU_46	OE1	3.298
5VXL	B_ARG_38	NH2	B_GLU_46	OE2	3.686
5VXL	B_LYS_66	NZ	B_ASP_63	OD1	2.473
5VXL	B_ARG_68	NH1	B_ASP_91	OD2	2.829
5VXL	B_ARG_68	NH2	B_ASP_91	OD1	3.190
5VXL	B_ARG_68	NH2	B_ASP_91	OD2	3.203
5VXL	B_ARG_79	NH1	B_GLU_77	OE1	3.438
5VXL	B_ARG_102	NH1	A_GLU_201	OE1	3.097
5VXL	B_ARG_102	NH2	A_GLU_201	OE1	3.202
5VXL	B_ARG_102	NH2	A_GLU_201	OE2	2.871
5VXM	A_ARG_55	NH2	A_ASP_309	OD2	2.709
5VXM	A_HIS_81	ND1	A_GLU_64	OE1	2.699
5VXM	A_HIS_81	ND1	A_GLU_64	OE2	3.443
5VXM	A_LYS_203	NZ	A_ASP_254	OD1	3.048
5VXM	A_LYS_205	NZ	A_ASP_166	OD2	2.794
5VXM	A_LYS_205	NZ	B_ASP_53	OD1	3.221

5VXM	A.LYS_205	NZ	B.ASP_53	OD2	3.090
5VXM	A.LYS_240	NZ	A.ASP_208	OD2	3.009
5VXM	A.LYS_291	NZ	A.ASP_287	OD1	3.603
5VXM	A.LYS_291	NZ	A.ASP_287	OD2	3.020
5VXM	A.LYS_291	NZ	A.GLU_288	OE2	2.698
5VXM	B.ARG_38	NH1	B.ASP_90	OD1	2.771
5VXM	B.ARG_38	NH2	B.GLU_46	OE1	3.784
5VXM	B.ARG_38	NH2	B.GLU_46	OE2	3.779
5VXM	B.ARG_38	NH2	B.ASP_90	OD1	3.793
5VXM	B.ARG_59	NH2	A.GLU_201	OE1	3.364
5VXM	B.LYS_65	NZ	B.ASP_62	OD1	2.888
5VXM	B.ARG_67	NH1	B.ASP_90	OD1	3.808
5VXM	B.ARG_67	NH1	B.ASP_90	OD2	2.755
5VXM	B.ARG_67	NH2	B.ASP_90	OD1	3.073
5VXM	B.ARG_67	NH2	B.ASP_90	OD2	3.515
5VXR	H.ARG_38	NH1	H.ASP_89	OD1	2.812
5VXR	H.ARG_38	NH2	H.GLU_46	OE1	2.830
5VXR	H.ARG_38	NH2	H.ASP_89	OD1	3.607
5VXR	H.ARG_66	NH1	H.ASP_89	OD1	3.628
5VXR	H.ARG_66	NH1	H.ASP_89	OD2	3.027
5VXR	H.ARG_66	NH2	H.ASP_89	OD1	2.986
5VXR	H.ARG_66	NH2	H.ASP_89	OD2	3.606
5VXR	H.ARG_97	NH2	H.ASP_27	OD2	3.982
5VXR	H.LYS_214	NZ	L.GLU_123	OE2	2.932
5VXR	H.LYS_215	NZ	H.GLU_217	OE1	3.858
5VXR	L.ARG_24	NH1	L.ASP_70	OD1	3.927
5VXR	L.LYS_39	NZ	L.ASP_81	OD1	2.793
5VXR	L.LYS_39	NZ	L.ASP_81	OD2	3.461
5VXR	L.ARG_61	NH1	L.ASP_82	OD1	3.414
5VXR	L.ARG_61	NH1	L.ASP_82	OD2	2.748
5VXR	L.ARG_61	NH2	L.GLU_79	OE1	3.909
5VXR	L.ARG_61	NH2	L.ASP_82	OD1	2.825
5VXR	L.ARG_61	NH2	L.ASP_82	OD2	3.695
5VXR	L.LYS_147	NZ	L.GLU_154	OE2	3.969
5VXR	L.LYS_149	NZ	L.GLU_195	OE1	3.427
5VXR	L.LYS_149	NZ	L.GLU_195	OE2	3.261
5VXR	L.ARG_155	NH2	L.GLU_185	OE1	3.900
5VXR	L.HIS_189	ND1	L.ASP_151	OD2	2.731
5VXR	L.LYS_199	NZ	L.ASP_110	OD2	3.874
5VZR	H.HIS_35	NE2	H.ASP_100C	OD1	2.839
5VZR	H.HIS_35	NE2	H.ASP_100C	OD2	3.345
5VZR	H.ARG_66	NH1	H.ASP_86	OD1	3.315
5VZR	H.ARG_66	NH1	H.ASP_86	OD2	2.889
5VZR	H.ARG_66	NH2	H.ASP_86	OD1	2.686
5VZR	H.ARG_66	NH2	H.ASP_86	OD2	3.653
5VZR	H.ARG_94	NH2	H.ASP_101	OD1	3.645
5VZR	H.ARG_94	NH2	H.ASP_101	OD2	2.665
5VZR	H.LYS_219	NZ	L.GLU_123	OE2	3.208
5VZR	L.LYS_39	NZ	L.ASP_81	OD1	3.338
5VZR	L.LYS_39	NZ	L.ASP_81	OD2	2.831
5VZR	L.ARG_61	NH1	L.ASP_82	OD1	3.560
5VZR	L.ARG_61	NH1	L.ASP_82	OD2	2.794
5VZR	L.ARG_61	NH2	L.GLU_79	OE2	3.432
5VZR	L.ARG_61	NH2	L.ASP_82	OD1	2.758
5VZR	L.ARG_61	NH2	L.ASP_82	OD2	3.575
5VZR	L.ARG_96	NH2	H.ASP_100C	OD2	3.042
5VZR	L.LYS_147	NZ	L.GLU_195	OE2	3.957
5VZR	L.LYS_149	NZ	L.GLU_195	OE1	3.473

5VZR	L_LYS_149	NZ	L_GLU_195	OE2	3.623
5VZR	L_ARG_155	NH1	L_GLU_185	OE1	3.298
5VZR	L_ARG_155	NH2	L_GLU_185	OE1	3.461
5VZR	L_LYS_183	NZ	L_GLU_187	OE1	3.869
5VZR	L_HIS_189	ND1	L_ASP_151	OD2	2.938
5VZR	L_LYS_199	NZ	L_ASP_110	OD1	3.115
5VZR	L_LYS_199	NZ	L_ASP_110	OD2	3.180
5VZR	A_HIS_35	NE2	A_ASP_100C	OD1	2.841
5VZR	A_HIS_35	NE2	A_ASP_100C	OD2	3.362
5VZR	A_ARG_66	NH1	A_ASP_86	OD1	3.497
5VZR	A_ARG_66	NH1	A_ASP_86	OD2	2.943
5VZR	A_ARG_66	NH2	A_ASP_86	OD1	2.855
5VZR	A_ARG_66	NH2	A_ASP_86	OD2	3.669
5VZR	A_ARG_94	NH2	A_ASP_101	OD1	3.759
5VZR	A_ARG_94	NH2	A_ASP_101	OD2	2.688
5VZR	A_LYS_219	NZ	B_GLU_123	OE1	3.381
5VZR	B_ARG_24	NH1	B_ASP_70	OD1	3.001
5VZR	B_ARG_24	NH1	B_ASP_70	OD2	3.957
5VZR	B_LYS_39	NZ	B_ASP_81	OD1	3.456
5VZR	B_LYS_39	NZ	B_ASP_81	OD2	2.971
5VZR	B_ARG_61	NH1	B_ASP_82	OD1	3.543
5VZR	B_ARG_61	NH1	B_ASP_82	OD2	2.682
5VZR	B_ARG_61	NH2	B_GLU_79	OE2	3.666
5VZR	B_ARG_61	NH2	B_ASP_82	OD1	2.894
5VZR	B_ARG_61	NH2	B_ASP_82	OD2	3.609
5VZR	B_ARG_96	NH2	A_ASP_100C	OD2	2.983
5VZR	B_LYS_147	NZ	B_GLU_154	OE1	3.313
5VZR	B_LYS_147	NZ	B_GLU_154	OE2	3.668
5VZR	B_LYS_149	NZ	B_GLU_195	OE1	2.858
5VZR	B_LYS_149	NZ	B_GLU_195	OE2	3.431
5VZR	B_ARG_155	NH2	B_GLU_185	OE2	3.691
5VZR	B_LYS_183	NZ	B_GLU_187	OE1	3.084
5VZR	B_LYS_183	NZ	B_GLU_187	OE2	3.264
5VZR	B_ARG_188	NH2	B_GLU_185	OE1	2.762
5VZR	B_HIS_189	ND1	B_ASP_151	OD2	3.256
5VZR	B_HIS_189	NE2	B_GLU_185	OE2	2.898
5W2B	H_ARG_41	NH1	H_ASP_93	OD1	2.811
5W2B	H_ARG_41	NH2	H_GLU_49	OE1	3.026
5W2B	H_ARG_41	NH2	H_GLU_49	OE2	3.821
5W2B	H_ARG_41	NH2	H_ASP_93	OD1	3.696
5W2B	H_LYS_68	NZ	H_ASP_65	OD1	3.641
5W2B	H_ARG_70	NH1	H_ASP_93	OD2	3.880
5W2B	H_ARG_70	NH2	H_ASP_93	OD1	3.178
5W2B	H_ARG_70	NH2	H_ASP_93	OD2	3.275
5W2B	H_ARG_90	NH1	H_GLU_92	OE2	3.439
5W2B	H_ARG_101	NH2	H_ASP_116	OD1	3.885
5W2B	H_ARG_101	NH2	H_ASP_116	OD2	2.522
5W2B	H_LYS_158	NZ	H_ASP_159	OD1	3.610
5W2B	H_LYS_158	NZ	H_ASP_159	OD2	3.126
5W2B	H_LYS_225	NZ	H_GLU_227	OE2	3.518
5W2B	L_ARG_25	NH1	L_ASP_71	OD2	3.833
5W2B	L_ARG_25	NH2	L_ASP_71	OD2	3.096
5W2B	L_ARG_62	NH1	L_GLU_82	OE2	3.995
5W2B	L_ARG_62	NH2	L_GLU_82	OE2	2.777
5W2B	L_ARG_62	NH2	L_ASP_83	OD1	2.811
5W2B	L_ARG_62	NH2	L_ASP_83	OD2	3.485
5W2B	L_LYS_104	NZ	L_GLU_166	OE1	2.996
5W2B	L_LYS_104	NZ	L_GLU_166	OE2	3.194

5W2B	L_LYS_127	NZ	L_ASP_123	OD1	2.992
5W2B	L_LYS_127	NZ	L_ASP_123	OD2	3.947
5W2B	L_ARG_143	NH1	L_GLU_106	OE1	3.368
5W2B	L_ARG_143	NH1	L_GLU_106	OE2	3.850
5W2B	L_ARG_143	NH2	L_GLU_106	OE1	3.513
5W2B	L_ARG_143	NH2	L_GLU_106	OE2	2.678
5W2B	L_LYS_150	NZ	L_GLU_196	OE1	3.463
5W2B	L_HIS_190	ND1	L_ASP_152	OD2	3.239
5W2B	A_HIS_653	NE2	A_GLU_649	OE1	3.647
5W2B	A_LYS_672	NZ	A_GLU_674	OE2	3.333
5W2B	A_ARG_728	NH1	A_ASP_729	OD1	3.255
5W2B	A_HIS_738	ND1	A_ASP_682	OD1	3.266
5W2B	A_HIS_738	ND1	A_ASP_682	OD2	2.866
5W9H	A_ARG_758	NH1	p_ASP_740	OD1	3.106
5W9H	A_LYS_779	NZ	A_GLU_1148	OE1	2.900
5W9H	A_LYS_801	NZ	A_ASP_843	OD1	2.837
5W9H	A_LYS_801	NZ	A_ASP_843	OD2	3.404
5W9H	A_LYS_807	NZ	A_GLU_818	OE2	3.090
5W9H	A_ARG_841	NH2	A_ASP_844	OD2	2.768
5W9H	A_ARG_847	NH2	A_ASP_844	OD1	2.690
5W9H	A_ARG_887	NH2	A_ASP_892	OD1	2.869
5W9H	A_ARG_887	NH2	A_ASP_892	OD2	3.887
5W9H	A_HIS_1020	NE2	A_ASP_1024	OD2	2.968
5W9H	A_ARG_1057	NH1	A_ASP_1053	OD2	3.477
5W9H	A_ARG_1057	NH2	A_ASP_1053	OD1	3.268
5W9H	A_ARG_1057	NH2	A_ASP_1053	OD2	3.305
5W9H	A_LYS_1102	NZ	A_GLU_793	OE1	2.898
5W9H	A_LYS_1102	NZ	A_GLU_793	OE2	3.271
5W9H	A_ARG_1113	NH1	A_GLU_1105	OE1	3.282
5W9H	A_ARG_1113	NH1	A_GLU_1105	OE2	3.829
5W9H	A_ARG_1113	NH2	D_GLU_1105	OE1	3.583
5W9H	A_HIS_1138	NE2	A_GLU_793	OE1	3.148
5W9H	A_LYS_1174	NZ	A_GLU_1183	OE1	2.609
5W9H	A_ARG_1179	NH2	B_ASP_31	OD1	2.752
5W9H	B_LYS_19	NZ	B_GLU_81	OE1	3.976
5W9H	B_LYS_38	NZ	B_ASP_86	OD1	3.271
5W9H	B_LYS_62	NZ	B_GLU_46	OE1	2.834
5W9H	B_LYS_62	NZ	B_GLU_46	OE2	3.973
5W9H	B_ARG_66	NH2	B_ASP_86	OD1	2.870
5W9H	B_ARG_66	NH2	B_ASP_86	OD2	3.022
5W9H	B_ARG_94	NH2	B_ASP_101	OD2	2.758
5W9H	B_LYS_95	NZ	B_ASP_100C	OD2	3.768
5W9H	C_ARG_24	NH1	C_ASP_70	OD1	2.971
5W9H	C_ARG_24	NH1	C_ASP_70	OD2	3.712
5W9H	C_ARG_61	NH1	C_ASP_82	OD1	3.151
5W9H	C_ARG_61	NH1	C_ASP_82	OD2	3.358
5W9H	C_LYS_92	NZ	C_GLU_93	OE1	3.334
5W9H	C_ARG_96	NH1	B_ASP_100C	OD2	2.859
5W9H	C_ARG_96	NH2	A_GLU_1183	OE1	3.871
5W9H	C_ARG_96	NH2	A_GLU_1183	OE2	2.827
5W9H	C_ARG_96	NH2	B_ASP_100C	OD2	2.885
5W9H	C_LYS_103	NZ	C_GLU_105	OE1	3.465
5W9H	D_LYS_779	NZ	D_ASP_771	OD2	3.242
5W9H	D_LYS_779	NZ	D_GLU_1148	OE1	3.666
5W9H	D_LYS_801	NZ	D_ASP_843	OD1	2.844
5W9H	D_LYS_801	NZ	D_ASP_843	OD2	3.387
5W9H	D_LYS_816	NZ	D_ASP_1064	OD1	3.505
5W9H	D_LYS_816	NZ	D_ASP_1064	OD2	2.929

5W9H	D_ARG.841	NH1	D_GLU.1090	OE1	2.843
5W9H	D_ARG.841	NH2	D_GLU.1090	OE1	2.754
5W9H	D_ARG.847	NH2	D_ASP.844	OD1	2.671
5W9H	D_ARG.887	NH2	D_ASP.892	OD1	2.891
5W9H	D_ARG.887	NH2	D_ASP.892	OD2	3.987
5W9H	D_HIS.1020	NE2	D_ASP.1024	OD1	3.700
5W9H	D_HIS.1020	NE2	D_ASP.1024	OD2	3.194
5W9H	D_ARG.1057	NH1	D_ASP.1053	OD1	3.487
5W9H	D_LYS.1102	NZ	D_GLU.793	OE1	2.907
5W9H	D_LYS.1102	NZ	D_GLU.793	OE2	3.062
5W9H	D_ARG.1113	NH1	G_GLU.1105	OE1	3.247
5W9H	D_ARG.1113	NH2	D_GLU.1105	OE1	3.897
5W9H	D_ARG.1113	NH2	D_GLU.1105	OE2	3.876
5W9H	D_HIS.1138	NE2	D_GLU.793	OE1	2.876
5W9H	D_LYS.1174	NZ	D_GLU.1183	OE2	2.738
5W9H	E_LYS.38	NZ	E_ASP.86	OD1	3.906
5W9H	E_LYS.62	NZ	E_GLU.46	OE1	2.861
5W9H	E_LYS.62	NZ	E_GLU.46	OE2	3.757
5W9H	E_ARG.66	NH1	E_ASP.86	OD1	2.947
5W9H	E_ARG.66	NH1	E_ASP.86	OD2	3.381
5W9H	E_ARG.94	NH2	E_ASP.101	OD2	3.822
5W9H	E_LYS.95	NZ	E_ASP.100C	OD1	3.733
5W9H	F_ARG.61	NH1	F_ASP.82	OD1	3.217
5W9H	F_ARG.61	NH1	F_ASP.82	OD2	3.689
5W9H	F_ARG.61	NH2	F_ASP.82	OD1	3.660
5W9H	F_ARG.61	NH2	F_ASP.82	OD2	2.716
5W9H	F_ARG.96	NH1	E_ASP.100C	OD2	2.830
5W9H	F_ARG.96	NH2	E_ASP.100C	OD2	2.948
5W9H	G_ARG.758	NH1	r_ASP.740	OD1	2.922
5W9H	G_LYS.779	NZ	G_ASP.771	OD2	2.887
5W9H	G_LYS.779	NZ	G_GLU.1148	OE1	3.575
5W9H	G_LYS.801	NZ	G_ASP.843	OD1	2.852
5W9H	G_LYS.801	NZ	G_ASP.843	OD2	3.379
5W9H	G_LYS.807	NZ	G_GLU.818	OE1	2.858
5W9H	G_LYS.807	NZ	G_GLU.818	OE2	3.782
5W9H	G_LYS.816	NZ	G_ASP.1064	OD1	3.397
5W9H	G_LYS.816	NZ	G_ASP.1064	OD2	2.986
5W9H	G_ARG.841	NH2	G_ASP.844	OD2	2.751
5W9H	G_ARG.847	NH2	G_ASP.844	OD1	2.677
5W9H	G_ARG.887	NH2	G_ASP.892	OD1	2.871
5W9H	G_ARG.887	NH2	G_ASP.892	OD2	3.986
5W9H	G_HIS.1020	NE2	G_ASP.1024	OD2	2.969
5W9H	G_LYS.1102	NZ	G_GLU.793	OE1	3.868
5W9H	G_LYS.1102	NZ	G_GLU.793	OE2	3.570
5W9H	G_ARG.1113	NH2	A_GLU.1105	OE1	3.110
5W9H	G_HIS.1138	NE2	G_GLU.793	OE2	2.825
5W9H	G_LYS.1174	NZ	G_GLU.1183	OE1	2.701
5W9H	G_ARG.1179	NH2	H_ASP.31	OD1	2.809
5W9H	H_LYS.38	NZ	H_ASP.86	OD1	3.793
5W9H	H_LYS.62	NZ	H_GLU.46	OE1	3.235
5W9H	H_LYS.62	NZ	H_GLU.46	OE2	2.887
5W9H	H_ARG.66	NH1	H_ASP.86	OD1	3.910
5W9H	H_ARG.66	NH1	H_ASP.86	OD2	3.798
5W9H	H_ARG.66	NH2	H_ASP.86	OD1	3.900
5W9H	H_ARG.66	NH2	H_ASP.86	OD2	2.887
5W9H	H_ARG.94	NH2	H_ASP.101	OD2	2.744
5W9H	H_LYS.95	NZ	H_ASP.100C	OD1	3.649
5W9H	L_ARG.24	NH1	L_ASP.70	OD1	2.956

5W9H	L_ARG_24	NH1	L_ASP_70	OD2	3.606
5W9H	L_ARG_24	NH2	L_ASP_70	OD1	3.918
5W9H	L_ARG_61	NH1	L_GLU_79	OE2	2.865
5W9H	L_ARG_61	NH1	L_ASP_82	OD1	3.820
5W9H	L_ARG_61	NH1	L_ASP_82	OD2	3.014
5W9H	L_ARG_61	NH2	L_GLU_79	OE2	2.954
5W9H	L_ARG_96	NH1	H_ASP_100C	OD2	2.791
5W9H	L_ARG_96	NH2	G_GLU_1183	OE2	2.911
5W9H	L_ARG_96	NH2	H_ASP_100C	OD2	2.950
5W9H	p_HIS_81	ND1	p_ASP_80	OD1	3.485
5W9H	p_LYS_99	NZ	p_GLU_32	OE1	2.779
5W9H	p_LYS_110	NZ	p_ASP_83	OD2	2.727
5W9H	p_ARG_119	NH2	p_ASP_54	OD2	3.407
5W9H	p_LYS_142	NZ	p_GLU_252	OE1	3.739
5W9H	p_LYS_142	NZ	p_GLU_252	OE2	3.528
5W9H	p_ARG_190	NH1	p_ASP_24	OD2	3.182
5W9H	p_ARG_190	NH2	p_ASP_24	OD2	3.492
5W9H	p_HIS_194	NE2	p_GLU_32	OE1	3.741
5W9H	p_ARG_235	NH2	p_GLU_188	OE1	2.810
5W9H	p_ARG_235	NH2	p_GLU_188	OE2	3.752
5W9H	p_ARG_269	NH1	p_GLU_252	OE1	3.003
5W9H	p_ARG_334	NH2	p_ASP_330	OD1	3.952
5W9H	p_ARG_334	NH2	p_ASP_330	OD2	3.020
5W9H	p_ARG_335	NH2	p_ASP_326	OD2	2.866
5W9H	p_ARG_401	NH2	p_ASP_444	OD1	3.583
5W9H	p_ARG_401	NH2	p_ASP_444	OD2	2.889
5W9H	p_LYS_496	NZ	p_GLU_536	OE1	3.232
5W9H	p_LYS_496	NZ	p_GLU_536	OE2	3.655
5W9H	p_LYS_502	NZ	p_GLU_513	OE2	2.865
5W9H	p_ARG_614	NH2	p_GLU_605	OE2	2.933
5W9H	p_ARG_629	NH1	p_GLU_376	OE1	3.493
5W9H	p_ARG_629	NH1	p_ASP_644	OD1	2.871
5W9H	p_ARG_629	NH1	p_ASP_644	OD2	3.990
5W9H	p_ARG_629	NH2	p_ASP_644	OD1	2.880
5W9H	p_ARG_629	NH2	p_ASP_644	OD2	3.886
5W9H	p_LYS_665	NZ	p_ASP_355	OD2	3.928
5W9H	p_HIS_681	NE2	D_ASP_910	OD1	2.819
5W9H	p_HIS_681	NE2	D_ASP_910	OD2	3.760
5W9H	p_ARG_694	NH1	p_ASP_343	OD1	3.986
5W9H	p_ARG_694	NH1	p_ASP_343	OD2	2.926
5W9H	p_ARG_694	NH2	p_ASP_343	OD1	3.403
5W9H	p_ARG_694	NH2	p_ASP_343	OD2	3.427
5W9H	p_LYS_728	NZ	p_ASP_726	OD2	2.881
5W9H	q_LYS_99	NZ	q_GLU_32	OE1	2.764
5W9H	q_LYS_110	NZ	q_ASP_83	OD2	2.762
5W9H	q_LYS_110	NZ	q_ASP_108	OD2	3.795
5W9H	q_ARG_119	NH2	q_ASP_54	OD2	3.096
5W9H	q_LYS_142	NZ	q_GLU_252	OE1	2.907
5W9H	q_LYS_142	NZ	q_GLU_252	OE2	3.991
5W9H	q_ARG_181	NH1	q_ASP_174	OD2	3.114
5W9H	q_HIS_194	NE2	q_GLU_32	OE1	3.504
5W9H	q_HIS_208	ND1	q_ASP_213	OD2	3.767
5W9H	q_ARG_235	NH1	q_ASP_24	OD1	3.943
5W9H	q_ARG_235	NH1	q_ASP_24	OD2	3.081
5W9H	q_ARG_235	NH2	q_ASP_24	OD2	2.878
5W9H	q_ARG_235	NH2	q_GLU_188	OE1	2.783
5W9H	q_ARG_235	NH2	q_GLU_188	OE2	3.707
5W9H	q_ARG_269	NH1	q_GLU_252	OE2	3.153

5W9H	q_ARG_335	NH2	q_ASP_326	OD2	2.856
5W9H	q_ARG_401	NH2	q_ASP_444	OD1	3.945
5W9H	q_ARG_401	NH2	q_ASP_444	OD2	3.807
5W9H	q_LYS_502	NZ	q_GLU_513	OE2	2.769
5W9H	q_LYS_543	NZ	q_GLU_549	OE1	3.143
5W9H	q_LYS_543	NZ	q_GLU_549	OE2	2.917
5W9H	q_LYS_587	NZ	q_GLU_382	OE2	2.893
5W9H	q_ARG_614	NH1	q_GLU_605	OE2	3.381
5W9H	q_ARG_629	NH1	q_ASP_644	OD1	3.524
5W9H	q_ARG_629	NH1	q_ASP_644	OD2	3.882
5W9H	q_LYS_668	NZ	q_ASP_355	OD1	3.851
5W9H	q_HIS_681	ND1	q_GLU_680	OE2	3.860
5W9H	q_LYS_728	NZ	q_ASP_726	OD2	2.831
5W9H	r_LYS_27	NZ	r_GLU_230	OE2	2.686
5W9H	r_LYS_52	NZ	r_ASP_49	OD2	3.239
5W9H	r_LYS_99	NZ	r_GLU_32	OE1	2.778
5W9H	r_LYS_110	NZ	r_ASP_83	OD2	3.861
5W9H	r_LYS_110	NZ	r_ASP_108	OD1	3.126
5W9H	r_LYS_110	NZ	r_ASP_108	OD2	3.630
5W9H	r_ARG_119	NH2	r_ASP_54	OD2	3.338
5W9H	r_LYS_142	NZ	r_GLU_252	OE2	3.806
5W9H	r_ARG_181	NH1	r_ASP_174	OD2	3.239
5W9H	r_ARG_190	NH1	r_ASP_24	OD1	3.106
5W9H	r_ARG_190	NH1	r_ASP_24	OD2	3.916
5W9H	r_ARG_190	NH2	r_ASP_24	OD1	2.743
5W9H	r_HIS_194	NE2	r_GLU_32	OE1	3.751
5W9H	r_ARG_235	NH2	r_GLU_188	OE1	3.176
5W9H	r_ARG_269	NH1	r_GLU_252	OE1	3.002
5W9H	r_ARG_335	NH2	r_ASP_326	OD2	2.830
5W9H	r_ARG_401	NH2	r_ASP_444	OD1	3.679
5W9H	r_ARG_401	NH2	r_ASP_444	OD2	3.146
5W9H	r_LYS_413	NZ	r_GLU_382	OE1	3.858
5W9H	r_LYS_413	NZ	r_GLU_382	OE2	2.731
5W9H	r_LYS_502	NZ	r_GLU_513	OE1	3.965
5W9H	r_LYS_502	NZ	r_GLU_513	OE2	2.807
5W9H	r_ARG_511	NH2	r_ASP_509	OD2	3.938
5W9H	r_ARG_614	NH1	r_GLU_605	OE2	3.430
5W9H	r_ARG_629	NH2	r_ASP_644	OD1	3.737
5W9H	r_LYS_665	NZ	r_GLU_666	OE2	2.722
5W9H	r_HIS_681	NE2	A_ASP_910	OD1	2.850
5W9H	r_HIS_681	NE2	A_ASP_910	OD2	3.840
5W9H	r_LYS_728	NZ	r_ASP_726	OD2	2.800
5W9I	A_ARG_758	NH1	B_ASP_740	OD1	2.830
5W9I	A_LYS_779	NZ	A_ASP_771	OD2	2.920
5W9I	A_LYS_779	NZ	A_GLU_1148	OE1	3.679
5W9I	A_LYS_801	NZ	A_ASP_843	OD1	2.853
5W9I	A_LYS_801	NZ	A_ASP_843	OD2	3.508
5W9I	A_LYS_807	NZ	A_GLU_818	OE1	3.679
5W9I	A_LYS_807	NZ	A_GLU_818	OE2	2.901
5W9I	A_LYS_816	NZ	A_ASP_1064	OD1	3.819
5W9I	A_LYS_816	NZ	A_ASP_1064	OD2	3.674
5W9I	A_ARG_841	NH1	A_GLU_1090	OE1	2.870
5W9I	A_ARG_841	NH2	A_GLU_1090	OE1	2.843
5W9I	A_ARG_847	NH1	F_ASP_726	OD1	3.733
5W9I	A_ARG_847	NH1	F_ASP_726	OD2	2.884
5W9I	A_ARG_847	NH2	A_ASP_844	OD1	2.784
5W9I	A_ARG_887	NH2	A_ASP_892	OD1	2.922
5W9I	A_HIS_1020	NE2	A_ASP_1024	OD2	3.009

5W9I	A_LYS_1021	NZ	A_GLU_1017	OE2	3.419
5W9I	A_LYS_1102	NZ	A_GLU_793	OE1	2.923
5W9I	A_LYS_1102	NZ	A_GLU_793	OE2	2.903
5W9I	A_ARG_1113	NH1	A_GLU_1105	OE1	2.902
5W9I	A_ARG_1113	NH1	A_GLU_1105	OE2	3.646
5W9I	A_ARG_1113	NH2	I_GLU_1105	OE2	2.773
5W9I	A_HIS_1138	NE2	A_GLU_793	OE2	2.945
5W9I	A_LYS_1174	NZ	A_GLU_1183	OE1	2.820
5W9I	A_ARG_1179	NH2	C_ASP_31	OD1	2.834
5W9I	B_LYS_99	NZ	B_GLU_32	OE1	2.800
5W9I	B_LYS_110	NZ	B_ASP_83	OD2	2.763
5W9I	B_ARG_119	NH2	B_ASP_54	OD2	3.186
5W9I	B_LYS_142	NZ	B_GLU_252	OE1	2.883
5W9I	B_HIS_194	NE2	B_GLU_32	OE1	3.646
5W9I	B_ARG_235	NH1	B_ASP_24	OD1	3.781
5W9I	B_ARG_235	NH1	B_ASP_24	OD2	3.330
5W9I	B_ARG_235	NH2	B_ASP_24	OD2	2.925
5W9I	B_ARG_235	NH2	B_GLU_188	OE1	2.886
5W9I	B_ARG_235	NH2	B_GLU_188	OE2	3.821
5W9I	B_ARG_335	NH2	B_ASP_326	OD2	2.866
5W9I	B_ARG_614	NH1	B_GLU_367	OE2	2.904
5W9I	B_ARG_614	NH2	B_GLU_367	OE2	2.914
5W9I	B_ARG_629	NH1	B_GLU_376	OE1	3.454
5W9I	B_ARG_629	NH1	B_ASP_644	OD1	2.966
5W9I	B_ARG_629	NH1	B_ASP_644	OD2	3.812
5W9I	B_ARG_629	NH2	B_ASP_644	OD1	2.995
5W9I	B_LYS_665	NZ	B_GLU_357	OE1	2.866
5W9I	B_LYS_665	NZ	B_GLU_357	OE2	3.798
5W9I	B_LYS_668	NZ	B_ASP_355	OD1	2.986
5W9I	B_HIS_681	NE2	I_ASP_910	OD1	2.801
5W9I	B_HIS_681	NE2	I_ASP_910	OD2	3.893
5W9I	B_LYS_728	NZ	B_ASP_726	OD2	2.881
5W9I	C_LYS_38	NZ	C_ASP_86	OD1	3.889
5W9I	C_LYS_62	NZ	C_GLU_46	OE1	3.450
5W9I	C_LYS_62	NZ	C_GLU_46	OE2	2.930
5W9I	C_ARG_66	NH1	C_ASP_86	OD1	3.145
5W9I	C_ARG_66	NH1	C_ASP_86	OD2	3.495
5W9I	C_ARG_66	NH2	C_ASP_86	OD1	3.789
5W9I	C_ARG_66	NH2	C_ASP_86	OD2	2.783
5W9I	C_ARG_94	NH2	C_ASP_101	OD1	2.867
5W9I	C_ARG_94	NH2	C_ASP_101	OD2	3.643
5W9I	C_LYS_95	NZ	C_ASP_100C	OD1	3.543
5W9I	C_LYS_95	NZ	C_ASP_100C	OD2	3.727
5W9I	D_ARG_24	NH2	D_ASP_70	OD1	2.945
5W9I	D_ARG_24	NH2	D_ASP_70	OD2	3.831
5W9I	D_ARG_61	NH1	D_ASP_82	OD1	3.202
5W9I	D_ARG_61	NH1	D_ASP_82	OD2	3.681
5W9I	D_ARG_61	NH2	D_ASP_82	OD1	3.712
5W9I	D_ARG_61	NH2	D_ASP_82	OD2	2.777
5W9I	D_ARG_96	NH1	C_ASP_100C	OD2	2.837
5W9I	D_ARG_96	NH2	A_GLU_1183	OE2	2.862
5W9I	D_ARG_96	NH2	C_ASP_100C	OD2	2.920
5W9I	D_LYS_103	NZ	D_GLU_105	OE2	3.345
5W9I	E_ARG_758	NH1	F_ASP_740	OD1	2.820
5W9I	E_LYS_779	NZ	E_ASP_771	OD2	2.924
5W9I	E_LYS_779	NZ	E_GLU_1148	OE1	3.718
5W9I	E_LYS_801	NZ	E_ASP_843	OD1	2.850
5W9I	E_LYS_801	NZ	E_ASP_843	OD2	3.507

5W9I	E_LYS_807	NZ	E_GLU_818	OE1	3.745
5W9I	E_LYS_807	NZ	E_GLU_818	OE2	3.005
5W9I	E_LYS_816	NZ	E_ASP_1064	OD1	3.825
5W9I	E_LYS_816	NZ	E_ASP_1064	OD2	3.707
5W9I	E_ARG_841	NH1	E_GLU_1090	OE1	2.868
5W9I	E_ARG_841	NH2	E_GLU_1090	OE1	2.843
5W9I	E_ARG_847	NH1	J_ASP_726	OD1	3.709
5W9I	E_ARG_847	NH1	J_ASP_726	OD2	2.881
5W9I	E_ARG_847	NH2	E_ASP_844	OD1	2.801
5W9I	E_ARG_887	NH2	E_ASP_892	OD1	2.928
5W9I	E_HIS_1020	NE2	E_ASP_1024	OD2	2.999
5W9I	E_LYS_1021	NZ	E_GLU_1017	OE2	3.409
5W9I	E_LYS_1102	NZ	E_GLU_793	OE1	2.968
5W9I	E_LYS_1102	NZ	E_GLU_793	OE2	2.898
5W9I	E_ARG_1113	NH1	E_GLU_1105	OE1	2.970
5W9I	E_ARG_1113	NH2	E_GLU_1105	OE1	3.046
5W9I	E_ARG_1113	NH2	E_GLU_1105	OE2	3.856
5W9I	E_HIS_1138	NE2	E_GLU_793	OE2	2.952
5W9I	E_LYS_1174	NZ	E_GLU_1183	OE1	2.800
5W9I	E_ARG_1179	NH2	G_ASP_31	OD1	2.831
5W9I	F_LYS_99	NZ	F_GLU_32	OE1	2.800
5W9I	F_LYS_110	NZ	F_ASP_83	OD2	2.755
5W9I	F_ARG_119	NH2	F_ASP_54	OD2	3.152
5W9I	F_LYS_142	NZ	F_GLU_252	OE1	2.880
5W9I	F_HIS_194	NE2	F_GLU_32	OE1	3.655
5W9I	F_ARG_235	NH1	F_ASP_24	OD1	3.849
5W9I	F_ARG_235	NH1	F_ASP_24	OD2	3.358
5W9I	F_ARG_235	NH2	F_ASP_24	OD2	2.934
5W9I	F_ARG_235	NH2	F_GLU_188	OE1	2.870
5W9I	F_ARG_235	NH2	F_GLU_188	OE2	3.760
5W9I	F_ARG_335	NH2	F_ASP_326	OD2	2.868
5W9I	F_ARG_614	NH1	F_GLU_367	OE2	3.306
5W9I	F_ARG_614	NH2	F_GLU_367	OE2	3.411
5W9I	F_ARG_629	NH1	F_GLU_376	OE1	3.445
5W9I	F_ARG_629	NH1	F_ASP_644	OD1	2.966
5W9I	F_ARG_629	NH1	F_ASP_644	OD2	3.809
5W9I	F_ARG_629	NH2	F_ASP_644	OD1	2.990
5W9I	F_LYS_665	NZ	F_GLU_357	OE1	2.866
5W9I	F_LYS_665	NZ	F_GLU_357	OE2	3.810
5W9I	F_HIS_681	NE2	A_ASP_910	OD1	2.878
5W9I	F_HIS_681	NE2	A_ASP_910	OD2	3.982
5W9I	F_HIS_681	NE2	F_GLU_680	OE2	3.229
5W9I	F_LYS_728	NZ	F_ASP_726	OD2	2.885
5W9I	G_LYS_38	NZ	G_ASP_86	OD1	3.902
5W9I	G_LYS_62	NZ	G_GLU_46	OE1	3.433
5W9I	G_LYS_62	NZ	G_GLU_46	OE2	2.934
5W9I	G_ARG_66	NH1	G_ASP_86	OD1	3.147
5W9I	G_ARG_66	NH1	G_ASP_86	OD2	3.501
5W9I	G_ARG_66	NH2	G_ASP_86	OD1	3.792
5W9I	G_ARG_66	NH2	G_ASP_86	OD2	2.779
5W9I	G_ARG_94	NH2	G_ASP_101	OD1	3.649
5W9I	G_ARG_94	NH2	G_ASP_101	OD2	2.843
5W9I	G_LYS_95	NZ	G_ASP_100C	OD1	3.513
5W9I	G_LYS_95	NZ	G_ASP_100C	OD2	3.725
5W9I	H_ARG_24	NH2	H_ASP_70	OD1	2.942
5W9I	H_ARG_24	NH2	H_ASP_70	OD2	3.817
5W9I	H_ARG_61	NH1	H_ASP_82	OD1	3.183
5W9I	H_ARG_61	NH1	H_ASP_82	OD2	3.671

5W9I	H_ARG_61	NH2	H_ASP_82	OD1	3.703
5W9I	H_ARG_61	NH2	H_ASP_82	OD2	2.773
5W9I	H_LYS_92	NZ	H_GLU_93	OE1	3.454
5W9I	H_ARG_96	NH1	G_ASP_100C	OD2	2.856
5W9I	H_ARG_96	NH2	E_GLU_1183	OE2	2.871
5W9I	H_ARG_96	NH2	G_ASP_100C	OD2	2.925
5W9I	H_LYS_103	NZ	H_GLU_105	OE2	3.616
5W9I	I_ARG_758	NH1	J_ASP_740	OD1	2.804
5W9I	I_LYS_779	NZ	I_ASP_771	OD2	2.925
5W9I	I_LYS_779	NZ	I_GLU_1148	OE1	3.696
5W9I	I_LYS_801	NZ	I_ASP_843	OD1	2.847
5W9I	I_LYS_801	NZ	I_ASP_843	OD2	3.503
5W9I	I_LYS_807	NZ	I_GLU_818	OE1	3.621
5W9I	I_LYS_807	NZ	I_GLU_818	OE2	2.894
5W9I	I_LYS_816	NZ	I_ASP_1064	OD1	3.871
5W9I	I_LYS_816	NZ	I_ASP_1064	OD2	3.720
5W9I	I_ARG_841	NH1	I_GLU_1090	OE1	2.860
5W9I	I_ARG_841	NH2	I_GLU_1090	OE1	2.839
5W9I	I_ARG_847	NH1	B_ASP_726	OD1	3.716
5W9I	I_ARG_847	NH1	B_ASP_726	OD2	2.881
5W9I	I_ARG_847	NH2	I_ASP_844	OD1	2.793
5W9I	I_ARG_887	NH2	I_ASP_892	OD1	2.930
5W9I	I_HIS_1020	NE2	I_ASP_1024	OD2	3.008
5W9I	I_LYS_1021	NZ	I_GLU_1017	OE2	3.414
5W9I	I_LYS_1102	NZ	I_GLU_793	OE1	2.931
5W9I	I_LYS_1102	NZ	I_GLU_793	OE2	2.910
5W9I	I_ARG_1113	NH1	I_GLU_1105	OE1	2.967
5W9I	I_ARG_1113	NH1	I_GLU_1105	OE2	3.647
5W9I	I_ARG_1113	NH2	E_GLU_1105	OE2	2.821
5W9I	I_HIS_1138	NE2	I_GLU_793	OE2	2.948
5W9I	I_LYS_1174	NZ	I_GLU_1183	OE1	2.809
5W9I	I_ARG_1179	NH2	K_ASP_31	OD1	2.785
5W9I	J_LYS_99	NZ	J_GLU_32	OE1	2.800
5W9I	J_LYS_110	NZ	J_ASP_83	OD2	2.766
5W9I	J_ARG_119	NH2	J_ASP_54	OD2	3.206
5W9I	J_LYS_142	NZ	J_GLU_252	OE1	2.986
5W9I	J_HIS_194	NE2	J_GLU_32	OE1	3.656
5W9I	J_ARG_235	NH1	J_ASP_24	OD1	3.840
5W9I	J_ARG_235	NH1	J_ASP_24	OD2	3.366
5W9I	J_ARG_235	NH2	J_ASP_24	OD2	2.931
5W9I	J_ARG_235	NH2	J_GLU_188	OE1	2.868
5W9I	J_ARG_235	NH2	J_GLU_188	OE2	3.758
5W9I	J_ARG_335	NH2	J_ASP_326	OD2	2.865
5W9I	J_ARG_614	NH1	J_GLU_367	OE2	3.042
5W9I	J_ARG_614	NH2	J_GLU_367	OE2	3.261
5W9I	J_ARG_629	NH1	J_ASP_644	OD1	2.970
5W9I	J_ARG_629	NH1	J_ASP_644	OD2	3.960
5W9I	J_ARG_629	NH2	J_ASP_644	OD1	3.193
5W9I	J_LYS_665	NZ	J_GLU_357	OE1	2.867
5W9I	J_LYS_665	NZ	J_GLU_357	OE2	3.780
5W9I	J_LYS_668	NZ	J_ASP_355	OD1	3.043
5W9I	J_HIS_681	NE2	E_ASP_910	OD1	2.832
5W9I	J_HIS_681	NE2	J_GLU_680	OE2	3.209
5W9I	J_LYS_728	NZ	J_ASP_726	OD2	2.883
5W9I	K_LYS_38	NZ	K_ASP_86	OD1	3.899
5W9I	K_LYS_62	NZ	K_GLU_46	OE1	3.395
5W9I	K_LYS_62	NZ	K_GLU_46	OE2	2.930
5W9I	K_ARG_66	NH1	K_ASP_86	OD1	3.149

5W9I	K_ARG.66	NH1	K_ASP.86	OD2	3.507
5W9I	K_ARG.66	NH2	K_ASP.86	OD1	3.795
5W9I	K_ARG.66	NH2	K_ASP.86	OD2	2.786
5W9I	K_ARG.94	NH2	K_ASP.101	OD1	2.859
5W9I	K_ARG.94	NH2	K_ASP.101	OD2	3.615
5W9I	K_LYS.95	NZ	K_ASP.100C	OD1	3.504
5W9I	K_LYS.95	NZ	K_ASP.100C	OD2	3.759
5W9I	L_ARG.24	NH1	L_ASP.70	OD1	2.947
5W9I	L_ARG.24	NH1	L_ASP.70	OD2	3.851
5W9I	L_ARG.61	NH1	L_ASP.82	OD1	3.190
5W9I	L_ARG.61	NH1	L_ASP.82	OD2	3.680
5W9I	L_ARG.61	NH2	L_ASP.82	OD1	3.703
5W9I	L_ARG.61	NH2	L_ASP.82	OD2	2.775
5W9I	L_LYS.92	NZ	L_GLU.93	OE1	3.397
5W9I	L_ARG.96	NH1	K_ASP.100C	OD2	2.856
5W9I	L_ARG.96	NH2	L_GLU.1183	OE2	2.872
5W9I	L_ARG.96	NH2	K_ASP.100C	OD2	2.922
5W9I	L_LYS.103	NZ	L_GLU.105	OE2	3.808
5W9J	D_LYS.779	NZ	D_GLU.1148	OE1	2.939
5W9J	D_LYS.801	NZ	D_ASP.843	OD1	3.375
5W9J	D_LYS.807	NZ	D_GLU.818	OE1	2.817
5W9J	D_LYS.807	NZ	D_GLU.818	OE2	3.422
5W9J	D_LYS.816	NZ	D_ASP.1064	OD1	3.520
5W9J	D_LYS.816	NZ	D_ASP.1064	OD2	3.973
5W9J	D_ARG.841	NH2	D_ASP.844	OD2	2.773
5W9J	D_ARG.847	NH2	D_ASP.844	OD1	2.691
5W9J	D_ARG.887	NH1	D_ASP.892	OD1	2.879
5W9J	D_HIS.1020	NE2	D_ASP.1024	OD1	3.785
5W9J	D_HIS.1020	NE2	D_ASP.1024	OD2	2.892
5W9J	D_ARG.1057	NH2	D_ASP.1053	OD1	3.921
5W9J	D_LYS.1102	NZ	D_GLU.793	OE1	2.814
5W9J	D_LYS.1102	NZ	D_GLU.793	OE2	3.963
5W9J	D_ARG.1113	NH1	D_GLU.1105	OE1	3.016
5W9J	D_ARG.1113	NH2	G_GLU.1105	OE1	3.627
5W9J	D_ARG.1113	NH2	G_GLU.1105	OE2	2.779
5W9J	D_HIS.1138	NE2	D_GLU.793	OE2	2.844
5W9J	E_HIS.35	NE2	E_ASP.100C	OD2	3.981
5W9J	E_LYS.38	NZ	E_GLU.46	OE1	3.833
5W9J	E_LYS.38	NZ	E_ASP.86	OD1	2.905
5W9J	E_LYS.62	NZ	E_GLU.46	OE2	2.796
5W9J	E_ARG.94	NH1	E_ASP.101	OD2	3.268
5W9J	E_LYS.95	NZ	E_ASP.100C	OD2	2.845
5W9J	F_ARG.61	NH1	F_ASP.82	OD1	3.198
5W9J	F_ARG.61	NH1	F_ASP.82	OD2	3.745
5W9J	F_ARG.61	NH2	F_GLU.79	OE1	3.635
5W9J	F_ARG.61	NH2	F_ASP.82	OD1	3.645
5W9J	F_ARG.61	NH2	F_ASP.82	OD2	2.778
5W9J	F_ARG.96	NH1	E_ASP.100C	OD1	3.873
5W9J	F_ARG.96	NH1	E_ASP.100C	OD2	3.469
5W9J	A_LYS.779	NZ	A_GLU.1148	OE1	2.940
5W9J	A_LYS.801	NZ	A_ASP.843	OD1	3.375
5W9J	A_LYS.807	NZ	A_GLU.818	OE1	2.817
5W9J	A_LYS.807	NZ	A_GLU.818	OE2	3.422
5W9J	A_LYS.816	NZ	A_ASP.1064	OD1	3.520
5W9J	A_LYS.816	NZ	A_ASP.1064	OD2	3.973
5W9J	A_ARG.841	NH2	A_ASP.844	OD2	2.773
5W9J	A_ARG.847	NH2	A_ASP.844	OD1	2.691
5W9J	A_ARG.887	NH1	A_ASP.892	OD1	2.879

5W9J	A_HIS_1020	NE2	A_ASP_1024	OD1	3.785
5W9J	A_HIS_1020	NE2	A_ASP_1024	OD2	2.892
5W9J	A_ARG_1057	NH2	A_ASP_1053	OD1	3.921
5W9J	A_LYS_1102	NZ	A_GLU_793	OE1	2.814
5W9J	A_LYS_1102	NZ	A_GLU_793	OE2	3.964
5W9J	A_ARG_1113	NH1	A_GLU_1105	OE1	3.016
5W9J	A_ARG_1113	NH2	D_GLU_1105	OE1	3.626
5W9J	A_ARG_1113	NH2	D_GLU_1105	OE2	2.778
5W9J	A_HIS_1138	NE2	A_GLU_793	OE2	2.844
5W9J	B_HIS_35	NE2	B_ASP_100C	OD2	3.981
5W9J	B_LYS_38	NZ	B_GLU_46	OE1	3.833
5W9J	B_LYS_38	NZ	B_ASP_86	OD1	2.905
5W9J	B_LYS_62	NZ	B_GLU_46	OE2	2.796
5W9J	B_ARG_94	NH1	B_ASP_101	OD2	3.270
5W9J	B_LYS_95	NZ	B_ASP_100C	OD2	2.844
5W9J	C_ARG_61	NH1	C_ASP_82	OD1	3.196
5W9J	C_ARG_61	NH1	C_ASP_82	OD2	3.745
5W9J	C_ARG_61	NH2	C_GLU_79	OE1	3.636
5W9J	C_ARG_61	NH2	C_ASP_82	OD1	3.644
5W9J	C_ARG_61	NH2	C_ASP_82	OD2	2.779
5W9J	C_ARG_96	NH1	B_ASP_100C	OD1	3.873
5W9J	C_ARG_96	NH1	B_ASP_100C	OD2	3.470
5W9J	G_LYS_779	NZ	G_GLU_1148	OE1	2.940
5W9J	G_LYS_801	NZ	G_ASP_843	OD1	3.374
5W9J	G_LYS_807	NZ	G_GLU_818	OE1	2.817
5W9J	G_LYS_807	NZ	G_GLU_818	OE2	3.421
5W9J	G_LYS_816	NZ	G_ASP_1064	OD1	3.521
5W9J	G_LYS_816	NZ	G_ASP_1064	OD2	3.973
5W9J	G_ARG_841	NH2	G_ASP_844	OD2	2.773
5W9J	G_ARG_847	NH2	G_ASP_844	OD1	2.691
5W9J	G_ARG_887	NH1	G_ASP_892	OD1	2.880
5W9J	G_HIS_1020	NE2	G_ASP_1024	OD1	3.785
5W9J	G_HIS_1020	NE2	G_ASP_1024	OD2	2.892
5W9J	G_ARG_1057	NH2	G_ASP_1053	OD1	3.921
5W9J	G_LYS_1102	NZ	G_GLU_793	OE1	2.813
5W9J	G_LYS_1102	NZ	G_GLU_793	OE2	3.963
5W9J	G_ARG_1113	NH1	G_GLU_1105	OE1	3.016
5W9J	G_ARG_1113	NH2	A_GLU_1105	OE1	3.626
5W9J	G_ARG_1113	NH2	A_GLU_1105	OE2	2.777
5W9J	G_HIS_1138	NE2	G_GLU_793	OE2	2.844
5W9J	H_HIS_35	NE2	H_ASP_100C	OD2	3.981
5W9J	H_LYS_38	NZ	H_GLU_46	OE1	3.832
5W9J	H_LYS_38	NZ	H_ASP_86	OD1	2.905
5W9J	H_LYS_62	NZ	H_GLU_46	OE2	2.795
5W9J	H_ARG_94	NH1	H_ASP_101	OD2	3.269
5W9J	H_LYS_95	NZ	H_ASP_100C	OD2	2.844
5W9J	I_ARG_61	NH1	I_ASP_82	OD1	3.197
5W9J	I_ARG_61	NH1	I_ASP_82	OD2	3.745
5W9J	I_ARG_61	NH2	I_GLU_79	OE1	3.636
5W9J	I_ARG_61	NH2	I_ASP_82	OD1	3.644
5W9J	I_ARG_61	NH2	I_ASP_82	OD2	2.779
5W9J	I_ARG_96	NH1	H_ASP_100C	OD1	3.873
5W9J	I_ARG_96	NH1	H_ASP_100C	OD2	3.470
5W9J	J_LYS_52	NZ	J_ASP_49	OD2	2.757
5W9J	J_HIS_81	ND1	J_ASP_80	OD1	3.851
5W9J	J_LYS_99	NZ	J_ASP_34	OD2	2.722
5W9J	J_LYS_110	NZ	J_ASP_108	OD1	3.409
5W9J	J_LYS_110	NZ	J_ASP_108	OD2	3.230

5W9J	J_ARG_119	NH1	J_ASP_54	OD2	3.696
5W9J	J_ARG_119	NH2	J_ASP_54	OD2	3.009
5W9J	J_ARG_181	NH1	J_ASP_174	OD2	3.331
5W9J	J_ARG_190	NH1	J_ASP_24	OD1	3.612
5W9J	J_ARG_190	NH1	J_ASP_24	OD2	3.889
5W9J	J_ARG_190	NH2	J_ASP_24	OD1	2.692
5W9J	J_ARG_235	NH2	J_GLU_188	OE1	2.796
5W9J	J_ARG_334	NH2	J_ASP_330	OD2	3.710
5W9J	J_ARG_335	NH2	J_ASP_326	OD2	3.031
5W9J	J_ARG_401	NH2	J_ASP_444	OD1	3.639
5W9J	J_ARG_401	NH2	J_ASP_444	OD2	3.140
5W9J	J_LYS_502	NZ	J_GLU_513	OE2	2.796
5W9J	J_LYS_543	NZ	J_GLU_549	OE2	3.291
5W9J	J_LYS_587	NZ	J_GLU_382	OE2	2.820
5W9J	J_ARG_614	NH2	J_GLU_605	OE2	2.932
5W9J	J_LYS_665	NZ	J_GLU_666	OE2	2.774
5W9J	J_LYS_728	NZ	J_ASP_726	OD2	2.840
5W9J	K_LYS_52	NZ	K_ASP_49	OD2	2.756
5W9J	K_HIS_81	ND1	K_ASP_80	OD1	3.851
5W9J	K_LYS_99	NZ	K_ASP_34	OD2	2.723
5W9J	K_LYS_110	NZ	K_ASP_108	OD1	3.410
5W9J	K_LYS_110	NZ	K_ASP_108	OD2	3.231
5W9J	K_ARG_119	NH1	K_ASP_54	OD2	3.694
5W9J	K_ARG_119	NH2	K_ASP_54	OD2	3.008
5W9J	K_ARG_181	NH1	K_ASP_174	OD2	3.331
5W9J	K_ARG_190	NH1	K_ASP_24	OD1	3.611
5W9J	K_ARG_190	NH1	K_ASP_24	OD2	3.890
5W9J	K_ARG_190	NH2	K_ASP_24	OD1	2.691
5W9J	K_ARG_235	NH2	K_GLU_188	OE1	2.796
5W9J	K_ARG_334	NH2	K_ASP_330	OD2	3.710
5W9J	K_ARG_335	NH2	K_ASP_326	OD2	3.030
5W9J	K_ARG_401	NH2	K_ASP_444	OD1	3.638
5W9J	K_ARG_401	NH2	K_ASP_444	OD2	3.140
5W9J	K_LYS_502	NZ	K_GLU_513	OE2	2.796
5W9J	K_LYS_543	NZ	K_GLU_549	OE2	3.291
5W9J	K_LYS_587	NZ	K_GLU_382	OE2	2.819
5W9J	K_ARG_614	NH2	K_GLU_605	OE2	2.931
5W9J	K_LYS_665	NZ	K_GLU_666	OE2	2.774
5W9J	K_LYS_728	NZ	K_ASP_726	OD2	2.839
5W9J	L_LYS_52	NZ	L_ASP_49	OD2	2.756
5W9J	L_HIS_81	ND1	L_ASP_80	OD1	3.851
5W9J	L_LYS_99	NZ	L_ASP_34	OD2	2.724
5W9J	L_LYS_110	NZ	L_ASP_108	OD1	3.409
5W9J	L_LYS_110	NZ	L_ASP_108	OD2	3.231
5W9J	L_ARG_119	NH1	L_ASP_54	OD2	3.695
5W9J	L_ARG_119	NH2	L_ASP_54	OD2	3.009
5W9J	L_ARG_181	NH1	L_ASP_174	OD2	3.331
5W9J	L_ARG_190	NH1	L_ASP_24	OD1	3.612
5W9J	L_ARG_190	NH1	L_ASP_24	OD2	3.889
5W9J	L_ARG_190	NH2	L_ASP_24	OD1	2.692
5W9J	L_ARG_235	NH2	L_GLU_188	OE1	2.796
5W9J	L_ARG_334	NH2	L_ASP_330	OD2	3.710
5W9J	L_ARG_335	NH2	L_ASP_326	OD2	3.031
5W9J	L_ARG_401	NH2	L_ASP_444	OD1	3.638
5W9J	L_ARG_401	NH2	L_ASP_444	OD2	3.140
5W9J	L_LYS_502	NZ	L_GLU_513	OE2	2.796
5W9J	L_LYS_543	NZ	L_GLU_549	OE2	3.291
5W9J	L_LYS_587	NZ	L_GLU_382	OE2	2.820

5W9J	L_ARG.614	NH2	L_GLU.605	OE2	2.931
5W9J	L_LYS.665	NZ	L_GLU.666	OE2	2.773
5W9J	L_LYS.728	NZ	L_ASP.726	OD2	2.839
5W9K	A_ARG.758	NH1	J_ASP.740	OD1	3.054
5W9K	A_LYS.801	NZ	A_ASP.843	OD1	2.794
5W9K	A_LYS.801	NZ	A_ASP.843	OD2	3.729
5W9K	A_LYS.807	NZ	A_GLU.818	OE2	3.490
5W9K	A_ARG.841	NH2	A_ASP.844	OD2	2.781
5W9K	A_ARG.847	NH2	A_ASP.844	OD1	2.722
5W9K	A_ARG.887	NH2	A_ASP.892	OD1	2.945
5W9K	A_LYS.995	NZ	A_ASP.868	OD1	3.265
5W9K	A_LYS.995	NZ	A_ASP.868	OD2	1.942
5W9K	A_HIS.1020	NE2	A_ASP.1024	OD2	2.878
5W9K	A_LYS.1102	NZ	A_GLU.793	OE1	2.948
5W9K	A_LYS.1102	NZ	A_GLU.793	OE2	3.271
5W9K	A_ARG.1113	NH1	A_GLU.1105	OE1	3.481
5W9K	A_ARG.1113	NH1	A_GLU.1105	OE2	2.966
5W9K	A_ARG.1113	NH2	D_GLU.1105	OE1	3.698
5W9K	A_HIS.1138	NE2	A_GLU.793	OE1	2.957
5W9K	A_LYS.1174	NZ	A_GLU.1183	OE2	3.009
5W9K	B_LYS.62	NZ	B_GLU.46	OE1	2.956
5W9K	B_LYS.62	NZ	B_GLU.46	OE2	3.368
5W9K	B_ARG.66	NH2	B_ASP.86	OD2	3.716
5W9K	B_ARG.94	NH2	B_ASP.101	OD2	2.759
5W9K	B_LYS.95	NZ	B_ASP.100C	OD2	3.608
5W9K	C_ARG.61	NH1	C_GLU.79	OE1	3.492
5W9K	C_LYS.92	NZ	C_GLU.93	OE1	2.823
5W9K	C_ARG.96	NH1	B_ASP.100C	OD2	2.822
5W9K	C_ARG.96	NH2	A_GLU.1183	OE1	3.683
5W9K	C_ARG.96	NH2	B_ASP.100C	OD2	3.420
5W9K	C_LYS.103	NZ	C_GLU.105	OE1	3.546
5W9K	D_LYS.779	NZ	D_ASP.771	OD2	2.911
5W9K	D_LYS.779	NZ	D_GLU.1148	OE1	3.847
5W9K	D_LYS.801	NZ	D_ASP.843	OD1	3.006
5W9K	D_LYS.807	NZ	D_GLU.818	OE1	2.844
5W9K	D_LYS.807	NZ	D_GLU.818	OE2	3.659
5W9K	D_ARG.841	NH2	D_GLU.1090	OE1	3.013
5W9K	D_ARG.841	NH2	D_GLU.1090	OE2	3.315
5W9K	D_ARG.847	NH1	D_ASP.844	OD1	2.982
5W9K	D_ARG.847	NH2	A_GLU.1017	OE2	3.108
5W9K	D_ARG.847	NH2	D_ASP.844	OD1	2.962
5W9K	D_ARG.887	NH2	D_ASP.892	OD1	2.947
5W9K	D_HIS.1020	NE2	D_ASP.1024	OD1	3.582
5W9K	D_HIS.1020	NE2	D_ASP.1024	OD2	3.188
5W9K	D_ARG.1057	NH1	D_ASP.1053	OD1	3.444
5W9K	D_LYS.1102	NZ	D_GLU.793	OE1	2.980
5W9K	D_LYS.1102	NZ	D_GLU.793	OE2	3.212
5W9K	D_ARG.1113	NH1	G_GLU.1105	OE2	3.336
5W9K	D_ARG.1113	NH2	D_GLU.1105	OE1	3.680
5W9K	D_ARG.1113	NH2	D_GLU.1105	OE2	3.676
5W9K	D_HIS.1138	NE2	D_GLU.793	OE1	3.055
5W9K	E_LYS.62	NZ	E_GLU.46	OE1	2.864
5W9K	E_LYS.62	NZ	E_GLU.46	OE2	3.729
5W9K	E_ARG.66	NH1	E_ASP.86	OD1	2.957
5W9K	E_ARG.66	NH1	E_ASP.86	OD2	3.366
5W9K	E_ARG.94	NH1	E_ASP.101	OD2	3.378
5W9K	E_ARG.94	NH2	E_ASP.101	OD2	2.893
5W9K	E_LYS.95	NZ	E_ASP.100C	OD1	3.994

5W9K	F_ARG_24	NH1	F_ASP_70	OD1	2.969
5W9K	F_ARG_24	NH1	F_ASP_70	OD2	3.751
5W9K	F_ARG_61	NH1	F_GLU_79	OE1	3.263
5W9K	F_ARG_61	NH1	F_GLU_79	OE2	3.365
5W9K	F_ARG_61	NH2	F_GLU_79	OE2	3.136
5W9K	F_ARG_96	NH1	E_ASP_100C	OD2	2.856
5W9K	F_ARG_96	NH2	D_GLU_1183	OE2	3.059
5W9K	F_ARG_96	NH2	E_ASP_100C	OD2	3.317
5W9K	G_ARG_758	NH1	L_ASP_740	OD1	3.028
5W9K	G_ARG_758	NH2	L_ASP_740	OD1	3.483
5W9K	G_LYS_801	NZ	G_ASP_843	OD1	2.854
5W9K	G_LYS_801	NZ	G_ASP_843	OD2	3.469
5W9K	G_LYS_816	NZ	G_ASP_1064	OD2	3.838
5W9K	G_ARG_847	NH1	K_ASP_726	OD2	3.336
5W9K	G_ARG_847	NH2	G_ASP_844	OD1	2.739
5W9K	G_ARG_887	NH2	G_ASP_892	OD1	2.989
5W9K	G_ARG_887	NH2	G_ASP_892	OD2	3.967
5W9K	G_HIS_1020	NE2	G_ASP_1024	OD2	2.997
5W9K	G_LYS_1035	NZ	G_GLU_1039	OE2	2.927
5W9K	G_ARG_1057	NH1	G_ASP_1053	OD2	3.710
5W9K	G_ARG_1057	NH2	G_ASP_1053	OD1	3.602
5W9K	G_ARG_1057	NH2	G_ASP_1053	OD2	3.839
5W9K	G_LYS_1102	NZ	G_GLU_793	OE1	2.948
5W9K	G_LYS_1102	NZ	G_GLU_793	OE2	3.330
5W9K	G_ARG_1113	NH1	G_GLU_1105	OE1	3.508
5W9K	G_ARG_1113	NH1	G_GLU_1105	OE2	2.905
5W9K	G_ARG_1113	NH2	A_GLU_1105	OE2	3.565
5W9K	G_HIS_1138	NE2	G_GLU_793	OE1	3.027
5W9K	G_LYS_1174	NZ	G_GLU_1183	OE1	3.901
5W9K	H_LYS_62	NZ	H_GLU_46	OE1	3.402
5W9K	H_LYS_62	NZ	H_GLU_46	OE2	2.946
5W9K	H_ARG_66	NH2	H_ASP_86	OD2	2.876
5W9K	H_ARG_94	NH2	H_ASP_101	OD2	2.768
5W9K	H_LYS_95	NZ	H_ASP_100C	OD2	3.668
5W9K	I_ARG_24	NH1	I_ASP_70	OD1	3.017
5W9K	I_ARG_24	NH2	I_ASP_70	OD1	3.829
5W9K	I_LYS_92	NZ	I_GLU_93	OE1	2.854
5W9K	I_ARG_96	NH1	H_ASP_100C	OD2	2.828
5W9K	I_ARG_96	NH2	G_GLU_1183	OE2	3.651
5W9K	I_ARG_96	NH2	H_ASP_100C	OD2	3.553
5W9K	I_LYS_103	NZ	I_GLU_105	OE1	3.522
5W9K	J_HIS_81	ND1	J_ASP_80	OD1	3.968
5W9K	J_LYS_99	NZ	J_GLU_32	OE1	2.810
5W9K	J_LYS_110	NZ	J_ASP_83	OD2	2.940
5W9K	J_LYS_142	NZ	J_GLU_247	OE1	3.288
5W9K	J_LYS_142	NZ	J_GLU_249	OE2	2.849
5W9K	J_ARG_190	NH1	J_ASP_24	OD1	3.560
5W9K	J_ARG_190	NH1	J_ASP_24	OD2	3.246
5W9K	J_ARG_190	NH2	J_ASP_24	OD1	2.727
5W9K	J_ARG_190	NH2	J_ASP_24	OD2	3.757
5W9K	J_HIS_194	NE2	J_GLU_32	OE1	3.514
5W9K	J_ARG_235	NH1	J_GLU_188	OE1	2.902
5W9K	J_ARG_235	NH1	J_GLU_188	OE2	3.519
5W9K	J_ARG_334	NH2	J_ASP_330	OD1	3.961
5W9K	J_ARG_334	NH2	J_ASP_330	OD2	3.087
5W9K	J_ARG_335	NH2	J_ASP_326	OD2	2.876
5W9K	J_ARG_401	NH2	J_ASP_444	OD1	3.806
5W9K	J_ARG_401	NH2	J_ASP_444	OD2	3.280

5W9K	J_LYS_502	NZ	J_GLU_513	OE2	3.504
5W9K	J_ARG_505	NH1	J_GLU_549	OE1	3.692
5W9K	J_ARG_629	NH1	J_GLU_376	OE2	3.955
5W9K	J_LYS_665	NZ	J_ASP_355	OD2	3.949
5W9K	J_HIS_681	NE2	D_ASP_910	OD1	2.963
5W9K	J_ARG_694	NH1	J_ASP_343	OD2	3.085
5W9K	J_ARG_694	NH2	J_ASP_343	OD2	2.916
5W9K	J_ARG_700	NH2	A_GLU_756	OE2	2.841
5W9K	J_LYS_728	NZ	J_GLU_666	OE1	3.931
5W9K	J_LYS_728	NZ	J_GLU_666	OE2	3.368
5W9K	K_HIS_81	ND1	K_ASP_80	OD1	3.713
5W9K	K_LYS_99	NZ	K_GLU_32	OE1	2.842
5W9K	K_LYS_142	NZ	K_GLU_252	OE2	3.341
5W9K	K_ARG_190	NH1	K_GLU_188	OE1	2.901
5W9K	K_HIS_194	NE2	K_GLU_32	OE1	3.703
5W9K	K_ARG_235	NH1	K_GLU_188	OE2	3.498
5W9K	K_ARG_335	NH2	K_ASP_326	OD2	2.914
5W9K	K_ARG_401	NH2	K_ASP_444	OD1	3.980
5W9K	K_ARG_401	NH2	K_ASP_444	OD2	3.862
5W9K	K_LYS_502	NZ	K_GLU_513	OE1	2.884
5W9K	K_LYS_502	NZ	K_GLU_513	OE2	3.989
5W9K	K_LYS_543	NZ	K_GLU_549	OE1	3.288
5W9K	K_LYS_543	NZ	K_GLU_549	OE2	3.352
5W9K	K_LYS_587	NZ	K_GLU_382	OE2	2.948
5W9K	K_LYS_665	NZ	K_GLU_666	OE2	2.821
5W9K	K_LYS_668	NZ	K_ASP_355	OD1	3.287
5W9K	K_LYS_668	NZ	K_ASP_355	OD2	3.232
5W9K	K_LYS_728	NZ	K_ASP_726	OD2	2.912
5W9K	L_LYS_27	NZ	L_GLU_230	OE2	3.262
5W9K	L_HIS_81	ND1	L_ASP_80	OD1	3.835
5W9K	L_LYS_99	NZ	L_GLU_32	OE2	3.537
5W9K	L_LYS_99	NZ	L_ASP_34	OD2	3.570
5W9K	L_LYS_110	NZ	L_ASP_83	OD2	2.905
5W9K	L_ARG_119	NH1	L_ASP_54	OD2	3.602
5W9K	L_LYS_142	NZ	L_GLU_252	OE2	3.115
5W9K	L_ARG_190	NH1	L_ASP_24	OD2	3.340
5W9K	L_ARG_190	NH2	L_GLU_188	OE2	3.335
5W9K	L_HIS_194	NE2	L_GLU_32	OE1	3.901
5W9K	L_ARG_235	NH1	L_GLU_188	OE1	2.872
5W9K	L_ARG_269	NH1	L_GLU_252	OE1	2.853
5W9K	L_ARG_334	NH2	L_ASP_330	OD1	3.920
5W9K	L_ARG_334	NH2	L_ASP_330	OD2	3.026
5W9K	L_ARG_335	NH2	L_ASP_326	OD2	2.940
5W9K	L_ARG_401	NH2	L_ASP_444	OD1	3.708
5W9K	L_ARG_401	NH2	L_ASP_444	OD2	3.216
5W9K	L_LYS_496	NZ	L_GLU_536	OE1	2.998
5W9K	L_LYS_496	NZ	L_GLU_536	OE2	3.594
5W9K	L_LYS_502	NZ	L_GLU_513	OE2	3.474
5W9K	L_ARG_505	NH1	L_GLU_549	OE1	2.874
5W9K	L_ARG_629	NH1	L_GLU_376	OE2	3.648
5W9K	L_ARG_629	NH1	L_ASP_644	OD1	2.887
5W9K	L_ARG_629	NH1	L_ASP_644	OD2	3.878
5W9K	L_ARG_629	NH2	L_ASP_644	OD1	2.829
5W9K	L_ARG_629	NH2	L_ASP_644	OD2	3.918
5W9K	L_HIS_681	NE2	A_ASP_910	OD1	3.027
5W9K	L_HIS_681	NE2	A_ASP_910	OD2	3.875
5W9K	L_ARG_691	NH2	L_ASP_343	OD1	3.689
5W9K	L_ARG_694	NH1	L_ASP_343	OD2	3.049

5W9K	L_ARG.694	NH2	L_ASP.343	OD2	2.912
5W9K	L_ARG.700	NH2	G_GLU.756	OE2	2.893
5W9K	L_LYS.728	NZ	L_ASP.726	OD2	2.874
5W9L	A_ARG.758	NH1	B_ASP.740	OD1	2.964
5W9L	A_ARG.758	NH2	B_ASP.740	OD1	3.858
5W9L	A_LYS.801	NZ	A_ASP.843	OD1	2.802
5W9L	A_LYS.801	NZ	A_ASP.843	OD2	3.510
5W9L	A_LYS.807	NZ	A_GLU.818	OE1	2.932
5W9L	A_LYS.807	NZ	A_GLU.818	OE2	3.202
5W9L	A_ARG.841	NH1	A_ASP.844	OD2	3.517
5W9L	A_ARG.847	NH2	A_ASP.844	OD1	2.713
5W9L	A_ARG.887	NH2	A_ASP.892	OD1	2.862
5W9L	A_ARG.887	NH2	A_ASP.892	OD2	3.937
5W9L	A_HIS.1020	NE2	A_ASP.1024	OD2	2.890
5W9L	A_LYS.1021	NZ	A_GLU.793	OE1	3.715
5W9L	A_LYS.1021	NZ	A_GLU.793	OE2	2.898
5W9L	A_ARG.1057	NH2	A_ASP.1053	OD1	3.565
5W9L	A_ARG.1057	NH2	A_ASP.1053	OD2	2.794
5W9L	A_ARG.1113	NH1	A_GLU.1105	OE1	3.356
5W9L	A_ARG.1113	NH1	A_GLU.1105	OE2	2.777
5W9L	A_ARG.1113	NH2	D_GLU.1105	OE1	3.448
5W9L	A_ARG.1113	NH2	D_GLU.1105	OE2	2.879
5W9L	D_LYS.779	NZ	D_ASP.771	OD2	2.899
5W9L	D_LYS.801	NZ	D_ASP.843	OD1	2.808
5W9L	D_LYS.801	NZ	D_ASP.843	OD2	3.150
5W9L	D_LYS.807	NZ	D_GLU.818	OE1	3.544
5W9L	D_LYS.807	NZ	D_GLU.818	OE2	2.846
5W9L	D_ARG.841	NH1	D_GLU.1090	OE1	2.693
5W9L	D_ARG.841	NH1	D_GLU.1090	OE2	3.687
5W9L	D_ARG.841	NH2	D_GLU.1090	OE1	3.508
5W9L	D_ARG.841	NH2	D_GLU.1090	OE2	3.018
5W9L	D_ARG.847	NH1	D_ASP.844	OD1	3.540
5W9L	D_ARG.847	NH2	D_ASP.844	OD1	2.650
5W9L	D_ARG.887	NH2	D_ASP.892	OD1	2.968
5W9L	D_HIS.1020	NE2	D_ASP.1024	OD1	3.581
5W9L	D_HIS.1020	NE2	D_ASP.1024	OD2	2.693
5W9L	D_LYS.1102	NZ	D_GLU.793	OE1	2.889
5W9L	D_LYS.1102	NZ	D_GLU.793	OE2	3.224
5W9L	D_LYS.1174	NZ	D_GLU.1183	OE1	2.743
5W9L	E_LYS.62	NZ	E_GLU.46	OE2	2.839
5W9L	E_ARG.66	NH1	E_ASP.86	OD1	2.896
5W9L	E_ARG.66	NH1	E_ASP.86	OD2	3.239
5W9L	E_ARG.66	NH2	E_ASP.86	OD1	3.963
5W9L	E_ARG.94	NH1	E_ASP.101	OD2	2.725
5W9L	E_LYS.95	NZ	E_ASP.100C	OD1	3.912
5W9L	F_ARG.61	NH1	F_ASP.82	OD1	3.203
5W9L	F_ARG.61	NH1	F_ASP.82	OD2	3.638
5W9L	F_ARG.61	NH2	F_GLU.79	OE2	3.934
5W9L	F_ARG.61	NH2	F_ASP.82	OD1	3.694
5W9L	F_ARG.61	NH2	F_ASP.82	OD2	2.714
5W9L	F_LYS.92	NZ	F_GLU.93	OE1	2.893
5W9L	F_ARG.96	NH1	E_ASP.100C	OD2	3.246
5W9L	F_ARG.96	NH2	D_GLU.1183	OE2	2.643
5W9L	F_ARG.96	NH2	E_ASP.100C	OD2	3.370
5W9L	G_ARG.758	NH1	J_ASP.740	OD1	2.859
5W9L	G_ARG.758	NH2	J_ASP.740	OD1	3.792
5W9L	G_LYS.801	NZ	G_ASP.843	OD1	2.779
5W9L	G_LYS.801	NZ	G_ASP.843	OD2	2.846

5W9L	G_LYS_807	NZ	G_GLU_818	OE1	2.853
5W9L	G_LYS_807	NZ	G_GLU_818	OE2	3.467
5W9L	G_ARG_841	NH1	G_GLU_1090	OE1	3.667
5W9L	G_ARG_841	NH1	G_GLU_1090	OE2	2.809
5W9L	G_ARG_841	NH2	G_GLU_1090	OE1	2.982
5W9L	G_ARG_841	NH2	G_GLU_1090	OE2	3.598
5W9L	G_ARG_847	NH1	G_ASP_844	OD1	3.281
5W9L	G_ARG_847	NH2	G_ASP_844	OD1	2.692
5W9L	G_ARG_887	NH2	G_ASP_892	OD1	2.920
5W9L	G_HIS_1020	NE2	G_ASP_1024	OD1	3.996
5W9L	G_HIS_1020	NE2	G_ASP_1024	OD2	2.966
5W9L	G_LYS_1021	NZ	G_GLU_793	OE1	3.707
5W9L	G_LYS_1021	NZ	G_GLU_793	OE2	2.887
5W9L	G_LYS_1035	NZ	G_GLU_1039	OE2	2.763
5W9L	G_LYS_1174	NZ	G_GLU_1183	OE2	2.797
5W9L	G_ARG_1179	NH2	H_ASP_31	OD1	2.753
5W9L	H_LYS_19	NZ	H_GLU_81	OE1	3.889
5W9L	H_LYS_38	NZ	H_GLU_46	OE1	2.832
5W9L	H_LYS_62	NZ	H_GLU_46	OE2	3.395
5W9L	H_ARG_66	NH1	H_ASP_86	OD1	3.754
5W9L	H_ARG_66	NH1	H_ASP_86	OD2	3.742
5W9L	H_ARG_66	NH2	H_ASP_86	OD1	3.914
5W9L	H_ARG_66	NH2	H_ASP_86	OD2	2.831
5W9L	H_ARG_94	NH2	H_ASP_101	OD2	2.725
5W9L	H_LYS_95	NZ	H_ASP_100C	OD1	3.863
5W9L	L_ARG_24	NH1	L_ASP_70	OD1	2.847
5W9L	L_ARG_24	NH1	L_ASP_70	OD2	3.591
5W9L	L_ARG_61	NH1	L_GLU_79	OE2	2.866
5W9L	L_ARG_61	NH1	L_ASP_82	OD1	3.906
5W9L	L_ARG_61	NH1	L_ASP_82	OD2	2.956
5W9L	L_ARG_61	NH2	L_GLU_79	OE2	2.901
5W9L	L_LYS_92	NZ	L_GLU_93	OE1	2.785
5W9L	L_ARG_96	NH1	H_ASP_100C	OD2	2.945
5W9L	L_ARG_96	NH2	H_ASP_100C	OD2	2.982
5W9L	B_LYS_27	NZ	B_GLU_230	OE2	3.782
5W9L	B_LYS_99	NZ	B_GLU_32	OE1	2.878
5W9L	B_LYS_110	NZ	B_ASP_83	OD2	2.826
5W9L	B_ARG_119	NH2	B_ASP_54	OD2	3.988
5W9L	B_LYS_142	NZ	B_GLU_252	OE1	2.955
5W9L	B_HIS_194	NE2	B_GLU_32	OE1	3.596
5W9L	B_ARG_235	NH1	B_ASP_24	OD1	3.631
5W9L	B_ARG_235	NH1	B_ASP_24	OD2	2.911
5W9L	B_ARG_235	NH2	B_ASP_24	OD2	3.191
5W9L	B_ARG_235	NH2	B_GLU_188	OE1	3.770
5W9L	B_ARG_235	NH2	B_GLU_188	OE2	2.915
5W9L	B_ARG_335	NH2	B_ASP_326	OD2	2.950
5W9L	B_ARG_401	NH2	B_ASP_444	OD1	3.583
5W9L	B_ARG_401	NH2	B_ASP_444	OD2	2.888
5W9L	B_LYS_496	NZ	B_GLU_536	OE1	3.232
5W9L	B_LYS_496	NZ	B_GLU_536	OE2	3.655
5W9L	B_LYS_502	NZ	B_GLU_513	OE2	2.865
5W9L	B_ARG_614	NH2	B_GLU_605	OE2	2.923
5W9L	B_ARG_629	NH1	B_GLU_376	OE1	3.464
5W9L	B_ARG_629	NH1	B_ASP_644	OD1	2.816
5W9L	B_ARG_629	NH2	B_ASP_644	OD1	2.786
5W9L	B_HIS_681	NE2	D_ASP_910	OD1	2.803
5W9L	B_HIS_681	NE2	D_ASP_910	OD2	3.795
5W9L	B_ARG_691	NH1	B_ASP_343	OD2	3.571

5W9L	B_ARG_700	NH1	A_GLU_756	OE2	2.893
5W9L	B_LYS_728	NZ	B_ASP_726	OD2	2.978
5W9L	C_HIS_81	ND1	C_ASP_80	OD1	3.849
5W9L	C_LYS_99	NZ	C_GLU_32	OE1	2.902
5W9L	C_LYS_99	NZ	C_GLU_32	OE2	3.891
5W9L	C_LYS_110	NZ	C_ASP_83	OD2	2.851
5W9L	C_LYS_142	NZ	C_GLU_252	OE1	2.960
5W9L	C_ARG_181	NH1	C_ASP_174	OD2	3.375
5W9L	C_HIS_208	ND1	C_ASP_213	OD2	3.867
5W9L	C_ARG_235	NH1	C_ASP_24	OD1	3.815
5W9L	C_ARG_235	NH1	C_ASP_24	OD2	3.367
5W9L	C_ARG_235	NH2	C_ASP_24	OD2	2.948
5W9L	C_ARG_235	NH2	C_GLU_188	OE1	3.081
5W9L	C_ARG_235	NH2	C_GLU_188	OE2	3.858
5W9L	C_ARG_269	NH1	C_GLU_252	OE2	3.121
5W9L	C_ARG_334	NH2	C_ASP_330	OD2	3.055
5W9L	C_ARG_335	NH2	C_ASP_326	OD2	2.939
5W9L	C_ARG_401	NH2	C_ASP_444	OD1	3.945
5W9L	C_ARG_401	NH2	C_ASP_444	OD2	3.806
5W9L	C_LYS_502	NZ	C_GLU_513	OE2	2.769
5W9L	C_LYS_543	NZ	C_GLU_549	OE1	3.142
5W9L	C_LYS_543	NZ	C_GLU_549	OE2	2.917
5W9L	C_LYS_587	NZ	C_GLU_382	OE2	2.765
5W9L	C_ARG_614	NH2	C_GLU_605	OE2	2.923
5W9L	C_ARG_691	NH2	C_ASP_343	OD1	3.440
5W9L	C_LYS_728	NZ	C_ASP_726	OD2	2.825
5W9L	J_LYS_99	NZ	J_GLU_32	OE1	2.885
5W9L	J_LYS_110	NZ	J_ASP_83	OD2	2.834
5W9L	J_LYS_110	NZ	J_ASP_108	OD2	3.969
5W9L	J_ARG_119	NH2	J_ASP_54	OD2	3.754
5W9L	J_LYS_142	NZ	J_GLU_252	OE1	3.881
5W9L	J_ARG_181	NH1	J_ASP_174	OD2	3.154
5W9L	J_ARG_190	NH1	J_ASP_24	OD1	3.142
5W9L	J_ARG_190	NH2	J_ASP_24	OD1	2.772
5W9L	J_HIS_194	NE2	J_GLU_32	OE1	3.916
5W9L	J_ARG_235	NH2	J_GLU_188	OE1	3.860
5W9L	J_ARG_235	NH2	J_GLU_188	OE2	2.919
5W9L	J_ARG_334	NH2	J_ASP_330	OD2	3.039
5W9L	J_ARG_335	NH2	J_ASP_326	OD2	2.959
5W9L	J_ARG_401	NH2	J_ASP_444	OD1	3.680
5W9L	J_ARG_401	NH2	J_ASP_444	OD2	3.147
5W9L	J_LYS_413	NZ	J_GLU_382	OE1	3.990
5W9L	J_LYS_413	NZ	J_GLU_382	OE2	2.824
5W9L	J_LYS_502	NZ	J_GLU_513	OE1	3.965
5W9L	J_LYS_502	NZ	J_GLU_513	OE2	2.807
5W9L	J_ARG_511	NH2	J_ASP_509	OD2	3.938
5W9L	J_ARG_614	NH2	J_GLU_605	OE1	2.958
5W9L	J_ARG_614	NH2	J_GLU_605	OE2	3.605
5W9L	J_ARG_629	NH1	J_GLU_376	OE1	3.967
5W9L	J_ARG_629	NH1	J_ASP_644	OD1	2.719
5W9L	J_ARG_629	NH2	J_ASP_644	OD1	2.638
5W9L	J_ARG_629	NH2	J_ASP_644	OD2	3.881
5W9L	J_LYS_665	NZ	J_GLU_666	OE2	2.675
5W9L	J_HIS_681	NE2	A_ASP_910	OD1	2.810
5W9L	J_HIS_681	NE2	A_ASP_910	OD2	3.815
5W9L	J_LYS_728	NZ	J_ASP_726	OD2	2.753
5W9M	A_ARG_758	NH1	E_ASP_740	OD1	2.862
5W9M	A_ARG_758	NH2	E_ASP_740	OD1	2.970

5W9M	A_LYS_801	NZ	A_ASP_843	OD1	2.883
5W9M	A_LYS_801	NZ	A_ASP_843	OD2	3.678
5W9M	A_ARG_841	NH1	A_GLU_1090	OE1	3.685
5W9M	A_ARG_841	NH1	A_GLU_1090	OE2	2.836
5W9M	A_ARG_841	NH2	A_GLU_1090	OE1	2.984
5W9M	A_ARG_841	NH2	A_GLU_1090	OE2	3.616
5W9M	A_ARG_847	NH1	J_ASP_726	OD2	3.850
5W9M	A_ARG_847	NH2	A_ASP_844	OD1	2.786
5W9M	A_ARG_887	NH2	A_ASP_892	OD1	2.933
5W9M	A_HIS_1020	NE2	A_ASP_1024	OD2	3.018
5W9M	A_LYS_1035	NZ	A_GLU_1039	OE2	2.904
5W9M	A_ARG_1057	NH2	A_ASP_1053	OD1	2.900
5W9M	A_ARG_1057	NH2	A_ASP_1053	OD2	3.314
5W9M	A_LYS_1102	NZ	A_GLU_793	OE1	2.817
5W9M	A_LYS_1102	NZ	A_GLU_793	OE2	3.330
5W9M	A_ARG_1113	NH1	A_GLU_1105	OE1	2.883
5W9M	A_ARG_1113	NH1	A_GLU_1105	OE2	3.760
5W9M	A_ARG_1113	NH2	A_GLU_1105	OE1	2.893
5W9M	A_HIS_1138	NE2	A_GLU_793	OE2	2.874
5W9M	A_LYS_1174	NZ	A_GLU_1183	OE1	2.780
5W9M	B_LYS_38	NZ	B_GLU_46	OE2	3.812
5W9M	B_LYS_62	NZ	B_GLU_46	OE1	2.808
5W9M	B_LYS_62	NZ	B_GLU_46	OE2	3.864
5W9M	B_ARG_66	NH2	B_ASP_86	OD1	2.831
5W9M	B_ARG_66	NH2	B_ASP_86	OD2	3.198
5W9M	C_ARG_61	NH1	C_GLU_79	OE1	2.869
5W9M	C_ARG_96	NH1	B_ASP_100C	OD2	2.894
5W9M	C_ARG_96	NH2	A_GLU_1183	OE2	2.938
5W9M	C_ARG_96	NH2	B_ASP_100C	OD2	2.940
5W9M	C_LYS_103	NZ	C_GLU_105	OE1	3.072
5W9M	D_LYS_779	NZ	D_GLU_1148	OE1	2.693
5W9M	D_LYS_801	NZ	D_ASP_843	OD1	2.885
5W9M	D_LYS_801	NZ	D_ASP_843	OD2	3.585
5W9M	D_LYS_816	NZ	D_ASP_1064	OD1	3.628
5W9M	D_LYS_816	NZ	D_ASP_1064	OD2	3.861
5W9M	D_ARG_841	NH2	D_GLU_1090	OE1	3.446
5W9M	D_ARG_841	NH2	D_GLU_1090	OE2	2.981
5W9M	D_ARG_847	NH1	A_GLU_1017	OE2	3.300
5W9M	D_ARG_847	NH2	A_GLU_1017	OE2	3.532
5W9M	D_ARG_847	NH2	D_ASP_844	OD1	2.832
5W9M	D_ARG_887	NH2	D_ASP_892	OD1	2.922
5W9M	D_LYS_995	NZ	D_ASP_868	OD1	3.932
5W9M	D_LYS_995	NZ	D_ASP_868	OD2	2.628
5W9M	D_HIS_1020	NE2	D_ASP_1024	OD1	3.644
5W9M	D_HIS_1020	NE2	D_ASP_1024	OD2	3.049
5W9M	D_LYS_1102	NZ	D_GLU_793	OE1	3.825
5W9M	D_ARG_1113	NH1	D_GLU_1105	OE1	2.819
5W9M	D_ARG_1113	NH1	D_GLU_1105	OE2	3.747
5W9M	D_ARG_1113	NH2	D_GLU_1105	OE1	3.533
5W9M	D_ARG_1113	NH2	D_GLU_1105	OE2	2.987
5W9M	D_HIS_1138	NE2	D_GLU_793	OE2	2.837
5W9M	D_LYS_1174	NZ	D_GLU_1183	OE2	2.795
5W9M	G_ARG_758	NH1	J_ASP_740	OD1	2.816
5W9M	G_ARG_758	NH2	J_ASP_740	OD1	3.407
5W9M	G_LYS_779	NZ	G_ASP_771	OD2	2.927
5W9M	G_LYS_779	NZ	G_GLU_1148	OE1	3.707
5W9M	G_LYS_801	NZ	G_ASP_843	OD1	2.888
5W9M	G_LYS_801	NZ	G_ASP_843	OD2	3.840

5W9M	G_LYS_807	NZ	G_GLU_818	OE2	3.982
5W9M	G_ARG_841	NH1	G_GLU_1090	OE1	3.659
5W9M	G_ARG_841	NH1	G_GLU_1090	OE2	2.832
5W9M	G_ARG_841	NH2	G_GLU_1090	OE1	2.944
5W9M	G_ARG_841	NH2	G_GLU_1090	OE2	3.615
5W9M	G_ARG_847	NH2	G_ASP_844	OD1	2.704
5W9M	G_ARG_887	NH2	G_ASP_892	OD1	2.967
5W9M	G_HIS_1020	NE2	G_ASP_1024	OD1	3.635
5W9M	G_HIS_1020	NE2	G_ASP_1024	OD2	3.025
5W9M	G_LYS_1100	NZ	G_ASP_1101	OD1	2.964
5W9M	G_LYS_1102	NZ	G_GLU_793	OE2	3.845
5W9M	G_ARG_1113	NH1	G_GLU_1105	OE1	2.863
5W9M	G_ARG_1113	NH1	G_GLU_1105	OE2	3.297
5W9M	G_ARG_1113	NH2	A_GLU_1105	OE1	3.823
5W9M	G_ARG_1113	NH2	A_GLU_1105	OE2	2.800
5W9M	G_HIS_1138	NE2	G_GLU_793	OE2	2.857
5W9M	G_LYS_1174	NZ	G_GLU_1183	OE1	2.907
5W9M	G_ARG_1179	NH1	H_ASP_31	OD1	3.713
5W9M	H_LYS_62	NZ	H_GLU_46	OE1	3.377
5W9M	H_LYS_62	NZ	H_GLU_46	OE2	2.872
5W9M	H_ARG_66	NH1	H_ASP_86	OD1	3.768
5W9M	H_ARG_66	NH1	H_ASP_86	OD2	3.866
5W9M	H_ARG_66	NH2	H_ASP_86	OD1	3.905
5W9M	H_ARG_66	NH2	H_ASP_86	OD2	2.981
5W9M	H_ARG_94	NH1	H_ASP_101	OD2	3.814
5W9M	H_ARG_94	NH2	H_ASP_101	OD2	2.908
5W9M	H_LYS_95	NZ	H_ASP_100C	OD1	3.555
5W9M	H_LYS_95	NZ	H_ASP_100C	OD2	2.929
5W9M	L_ARG_61	NH1	L_GLU_79	OE1	2.897
5W9M	L_ARG_61	NH1	L_ASP_82	OD1	3.868
5W9M	L_ARG_61	NH1	L_ASP_82	OD2	2.952
5W9M	L_ARG_61	NH2	L_GLU_79	OE1	2.900
5W9M	L_ARG_96	NH1	H_ASP_100C	OD2	2.840
5W9M	L_ARG_96	NH2	G_GLU_1183	OE2	2.957
5W9M	L_ARG_96	NH2	H_ASP_100C	OD2	3.363
5W9M	L_LYS_103	NZ	L_GLU_105	OE2	3.254
5W9M	E_LYS_27	NZ	E_GLU_230	OE2	3.877
5W9M	E_LYS_52	NZ	E_ASP_49	OD2	3.990
5W9M	E_HIS_81	ND1	E_ASP_80	OD1	3.823
5W9M	E_LYS_99	NZ	E_GLU_32	OE1	2.847
5W9M	E_LYS_110	NZ	E_ASP_83	OD2	2.742
5W9M	E_LYS_142	NZ	E_GLU_252	OE1	3.416
5W9M	E_LYS_142	NZ	E_GLU_252	OE2	3.425
5W9M	E_ARG_181	NH1	E_ASP_174	OD2	3.814
5W9M	E_HIS_194	NE2	E_GLU_32	OE1	3.141
5W9M	E_ARG_235	NH1	E_GLU_188	OE1	3.017
5W9M	E_ARG_335	NH2	E_ASP_326	OD2	2.919
5W9M	E_ARG_401	NH2	E_ASP_444	OD1	3.595
5W9M	E_ARG_401	NH2	E_ASP_444	OD2	2.975
5W9M	E_LYS_496	NZ	E_GLU_536	OE1	2.925
5W9M	E_LYS_496	NZ	E_GLU_536	OE2	3.563
5W9M	E_LYS_502	NZ	E_GLU_513	OE2	2.857
5W9M	E_ARG_505	NH1	E_GLU_549	OE1	2.887
5W9M	E_ARG_505	NH2	E_GLU_549	OE1	3.647
5W9M	E_ARG_629	NH1	E_GLU_376	OE2	3.561
5W9M	E_ARG_629	NH1	E_ASP_644	OD1	2.850
5W9M	E_ARG_629	NH2	E_ASP_644	OD1	2.751
5W9M	E_ARG_629	NH2	E_ASP_644	OD2	3.949

5W9M	E_LYS_665	NZ	E_GLU_666	OE2	2.766
5W9M	E_HIS_681	NE2	D_ASP_910	OD1	2.869
5W9M	E_HIS_681	NE2	D_ASP_910	OD2	3.974
5W9M	E_ARG_691	NH2	E_ASP_343	OD1	3.021
5W9M	E_ARG_700	NH2	A_GLU_756	OE1	3.024
5W9M	E_ARG_700	NH2	A_GLU_756	OE2	3.469
5W9M	E_LYS_728	NZ	E_ASP_726	OD2	2.871
5W9M	F_HIS_81	ND1	F_ASP_80	OD1	3.780
5W9M	F_LYS_99	NZ	F_GLU_32	OE1	3.190
5W9M	F_LYS_99	NZ	F_GLU_32	OE2	3.555
5W9M	F_LYS_110	NZ	F_ASP_83	OD2	3.405
5W9M	F_LYS_110	NZ	F_ASP_108	OD1	3.183
5W9M	F_LYS_110	NZ	F_ASP_108	OD2	3.399
5W9M	F_ARG_119	NH1	F_ASP_54	OD2	3.785
5W9M	F_ARG_119	NH2	F_ASP_54	OD2	3.047
5W9M	F_LYS_142	NZ	F_GLU_252	OE1	2.921
5W9M	F_HIS_194	NE2	F_GLU_32	OE1	3.759
5W9M	F_ARG_235	NH1	F_GLU_188	OE2	3.596
5W9M	F_ARG_334	NH2	F_ASP_330	OD1	3.977
5W9M	F_ARG_334	NH2	F_ASP_330	OD2	3.003
5W9M	F_ARG_335	NH2	F_ASP_326	OD2	2.919
5W9M	F_ARG_401	NH2	F_ASP_444	OD1	3.837
5W9M	F_ARG_401	NH2	F_ASP_444	OD2	3.316
5W9M	F_LYS_502	NZ	F_GLU_513	OE1	2.889
5W9M	F_LYS_543	NZ	F_GLU_549	OE2	3.751
5W9M	F_LYS_587	NZ	F_GLU_382	OE2	2.825
5W9M	F_ARG_614	NH2	F_GLU_605	OE1	2.961
5W9M	F_HIS_681	NE2	G_ASP_910	OD1	2.934
5W9M	F_HIS_681	NE2	G_ASP_910	OD2	3.892
5W9M	F_ARG_691	NH2	F_ASP_343	OD1	2.990
5W9M	F_LYS_728	NZ	F_ASP_726	OD1	3.991
5W9M	F_LYS_728	NZ	F_ASP_726	OD2	2.816
5W9M	J_HIS_81	ND1	J_ASP_80	OD1	3.900
5W9M	J_LYS_99	NZ	J_ASP_34	OD2	2.828
5W9M	J_ARG_119	NH2	J_ASP_54	OD2	3.814
5W9M	J_LYS_142	NZ	J_GLU_252	OE1	3.757
5W9M	J_LYS_142	NZ	J_GLU_252	OE2	3.691
5W9M	J_HIS_194	NE2	J_GLU_32	OE1	3.474
5W9M	J_ARG_235	NH2	J_GLU_188	OE1	3.932
5W9M	J_ARG_235	NH2	J_GLU_188	OE2	2.863
5W9M	J_ARG_334	NH2	J_ASP_330	OD1	3.986
5W9M	J_ARG_334	NH2	J_ASP_330	OD2	2.914
5W9M	J_ARG_335	NH2	J_ASP_326	OD2	2.924
5W9M	J_ARG_401	NH2	J_ASP_444	OD1	3.669
5W9M	J_ARG_401	NH2	J_ASP_444	OD2	3.110
5W9M	J_LYS_413	NZ	J_GLU_382	OE1	3.999
5W9M	J_LYS_413	NZ	J_GLU_382	OE2	2.963
5W9M	J_HIS_486	NE2	J_GLU_565	OE2	3.789
5W9M	J_LYS_496	NZ	J_GLU_536	OE2	3.687
5W9M	J_LYS_502	NZ	J_GLU_513	OE1	2.953
5W9M	J_LYS_502	NZ	J_GLU_513	OE2	3.624
5W9M	J_ARG_511	NH2	J_ASP_509	OD2	3.887
5W9M	J_ARG_629	NH1	J_ASP_644	OD1	2.859
5W9M	J_ARG_629	NH2	J_ASP_644	OD1	2.744
5W9M	J_ARG_629	NH2	J_ASP_644	OD2	3.852
5W9M	J_HIS_681	NE2	A_ASP_910	OD1	3.021
5W9M	J_LYS_728	NZ	J_ASP_726	OD2	2.879
5W9M	A_ARG_758	NH1	H_ASP_740	OD1	3.061

5W9N	A_ARG_758	NH2	H_ASP_740	OD1	3.534
5W9N	A_LYS_801	NZ	A_ASP_843	OD1	2.885
5W9N	A_LYS_801	NZ	A_ASP_843	OD2	3.553
5W9N	A_LYS_816	NZ	A_ASP_1064	OD2	3.955
5W9N	A_ARG_841	NH2	A_ASP_844	OD2	2.840
5W9N	A_ARG_847	NH2	A_ASP_844	OD1	2.793
5W9N	A_ARG_887	NH2	A_ASP_892	OD1	2.922
5W9N	A_ARG_887	NH2	A_ASP_892	OD2	3.858
5W9N	A_HIS_1020	NE2	A_ASP_1024	OD2	2.929
5W9N	A_ARG_1057	NH1	A_ASP_1053	OD1	3.524
5W9N	A_LYS_1102	NZ	A_GLU_793	OE1	2.942
5W9N	A_LYS_1102	NZ	A_GLU_793	OE2	3.253
5W9N	A_HIS_1138	NE2	A_GLU_793	OE1	2.975
5W9N	B_LYS_62	NZ	B_GLU_46	OE1	3.336
5W9N	B_LYS_62	NZ	B_GLU_46	OE2	2.950
5W9N	B_ARG_66	NH2	B_ASP_86	OD1	2.875
5W9N	B_ARG_66	NH2	B_ASP_86	OD2	3.096
5W9N	B_ARG_94	NH2	B_ASP_101	OD2	2.805
5W9N	B_LYS_95	NZ	B_ASP_100C	OD2	3.671
5W9N	C_ARG_24	NH1	C_ASP_70	OD1	2.929
5W9N	C_ARG_24	NH1	C_ASP_70	OD2	3.584
5W9N	C_ARG_24	NH2	C_ASP_70	OD1	3.992
5W9N	C_LYS_92	NZ	C_GLU_93	OE1	2.776
5W9N	C_ARG_96	NH1	B_ASP_100C	OD2	2.860
5W9N	C_ARG_96	NH2	A_GLU_1183	OE2	2.942
5W9N	C_ARG_96	NH2	B_ASP_100C	OD2	3.629
5W9N	C_LYS_103	NZ	C_GLU_105	OE1	3.535
5W9N	D_LYS_779	NZ	D_ASP_771	OD2	2.906
5W9N	D_LYS_779	NZ	D_GLU_1148	OE1	3.841
5W9N	D_LYS_801	NZ	D_ASP_843	OD1	2.866
5W9N	D_LYS_801	NZ	D_ASP_843	OD2	3.784
5W9N	D_LYS_807	NZ	D_GLU_818	OE1	2.846
5W9N	D_LYS_807	NZ	D_GLU_818	OE2	3.746
5W9N	D_LYS_816	NZ	D_ASP_1064	OD1	3.551
5W9N	D_LYS_816	NZ	D_ASP_1064	OD2	2.989
5W9N	D_ARG_841	NH2	D_ASP_844	OD2	2.860
5W9N	D_ARG_847	NH2	D_ASP_844	OD1	2.752
5W9N	D_ARG_887	NH2	D_ASP_892	OD1	2.921
5W9N	D_HIS_1020	NE2	D_ASP_1024	OD1	3.511
5W9N	D_HIS_1020	NE2	D_ASP_1024	OD2	3.177
5W9N	D_LYS_1102	NZ	D_GLU_793	OE1	2.862
5W9N	D_LYS_1102	NZ	D_GLU_793	OE2	3.547
5W9N	D_ARG_1113	NH1	D_GLU_1105	OE1	2.833
5W9N	D_ARG_1113	NH1	D_GLU_1105	OE2	3.606
5W9N	D_ARG_1113	NH2	D_GLU_1105	OE1	3.657
5W9N	D_ARG_1113	NH2	D_GLU_1105	OE2	2.979
5W9N	D_HIS_1138	NE2	D_GLU_793	OE1	3.682
5W9N	E_LYS_62	NZ	E_GLU_46	OE1	2.853
5W9N	E_LYS_62	NZ	E_GLU_46	OE2	3.766
5W9N	E_ARG_94	NH1	E_ASP_101	OD2	3.322
5W9N	E_ARG_94	NH2	E_ASP_101	OD2	2.876
5W9N	F_ARG_61	NH1	F_GLU_79	OE1	3.387
5W9N	F_ARG_61	NH1	F_GLU_79	OE2	3.250
5W9N	F_ARG_61	NH2	F_GLU_79	OE2	3.109
5W9N	F_ARG_96	NH1	E_ASP_100C	OD2	2.898
5W9N	F_ARG_96	NH2	D_GLU_1183	OE2	3.465
5W9N	F_ARG_96	NH2	E_ASP_100C	OD2	3.359
5W9N	F_LYS_103	NZ	F_GLU_105	OE2	3.523

5W9N	G_ARG.758	NH1	J_ASP.740	OD1	2.883
5W9N	G_ARG.758	NH2	J_ASP.740	OD1	3.992
5W9N	G_LYS.779	NZ	G_GLU.1148	OE1	3.821
5W9N	G_LYS.801	NZ	G_ASP.843	OD1	3.095
5W9N	G_LYS.807	NZ	G_GLU.818	OE1	2.848
5W9N	G_LYS.807	NZ	G_GLU.818	OE2	3.640
5W9N	G_ARG.841	NH2	G_ASP.844	OD2	2.821
5W9N	G_ARG.847	NH2	G_ASP.844	OD1	2.784
5W9N	G_ARG.887	NH2	G_ASP.892	OD1	2.977
5W9N	G_ARG.887	NH2	G_ASP.892	OD2	3.996
5W9N	G_HIS.1020	NE2	G_ASP.1024	OD1	3.933
5W9N	G_HIS.1020	NE2	G_ASP.1024	OD2	2.877
5W9N	G_ARG.1057	NH2	G_ASP.1053	OD1	2.973
5W9N	G_ARG.1057	NH2	G_ASP.1053	OD2	3.603
5W9N	G_LYS.1102	NZ	G_GLU.793	OE1	3.542
5W9N	G_LYS.1102	NZ	G_GLU.793	OE2	3.374
5W9N	G_ARG.1113	NH1	G_GLU.1105	OE1	3.319
5W9N	G_ARG.1113	NH2	A_GLU.1105	OE1	3.089
5W9N	G_HIS.1138	NE2	G_GLU.793	OE2	2.888
5W9N	H_LYS.99	NZ	H_GLU.32	OE1	2.795
5W9N	H_LYS.110	NZ	H_ASP.83	OD2	2.820
5W9N	H_ARG.119	NH2	H_ASP.54	OD2	3.318
5W9N	H_LYS.142	NZ	H_GLU.252	OE1	3.837
5W9N	H_LYS.142	NZ	H_GLU.252	OE2	3.110
5W9N	H_ARG.181	NH1	H_ASP.174	OD2	2.922
5W9N	H_HIS.194	NE2	H_GLU.32	OE1	3.891
5W9N	H_ARG.334	NH2	H_ASP.330	OD1	3.972
5W9N	H_ARG.334	NH2	H_ASP.330	OD2	3.030
5W9N	H_ARG.335	NH2	H_ASP.326	OD2	2.979
5W9N	H_ARG.401	NH2	H_ASP.444	OD1	3.754
5W9N	H_ARG.401	NH2	H_ASP.444	OD2	3.247
5W9N	H_LYS.496	NZ	H_GLU.536	OE1	3.049
5W9N	H_LYS.496	NZ	H_GLU.536	OE2	3.699
5W9N	H_LYS.502	NZ	H_GLU.513	OE2	3.408
5W9N	H_ARG.505	NH1	H_GLU.549	OE1	2.896
5W9N	H_ARG.505	NH2	H_GLU.549	OE1	3.946
5W9N	H_ARG.629	NH1	H_GLU.376	OE2	3.417
5W9N	H_ARG.629	NH1	H_ASP.644	OD1	2.873
5W9N	H_ARG.629	NH1	H_ASP.644	OD2	3.992
5W9N	H_ARG.629	NH2	H_ASP.644	OD1	2.928
5W9N	H_ARG.629	NH2	H_ASP.644	OD2	3.862
5W9N	H_HIS.681	NE2	D_ASP.910	OD1	2.909
5W9N	H_HIS.681	NE2	D_ASP.910	OD2	3.885
5W9N	H_ARG.691	NH2	H_ASP.343	OD1	3.539
5W9N	H_ARG.694	NH1	H_ASP.343	OD2	3.042
5W9N	H_ARG.694	NH2	H_ASP.343	OD2	2.913
5W9N	H_LYS.728	NZ	H_ASP.726	OD2	2.885
5W9N	I_LYS.99	NZ	I_GLU.32	OE1	2.834
5W9N	I_LYS.110	NZ	I_ASP.108	OD1	3.843
5W9N	I_LYS.110	NZ	I_ASP.108	OD2	3.078
5W9N	I_ARG.119	NH1	I_ASP.54	OD2	3.752
5W9N	I_ARG.119	NH2	I_ASP.54	OD2	3.062
5W9N	I_LYS.142	NZ	I_GLU.247	OE1	2.823
5W9N	I_LYS.142	NZ	I_GLU.249	OE2	2.931
5W9N	I_ARG.181	NH1	I_ASP.174	OD2	3.305
5W9N	I_ARG.190	NH1	I_GLU.188	OE2	2.866
5W9N	I_ARG.334	NH2	I_ASP.330	OD1	3.946
5W9N	I_ARG.334	NH2	I_ASP.330	OD2	3.014

5W9N	I_ARG_335	NH2	I_ASP_326	OD2	2.875
5W9N	I_ARG_401	NH2	I_ASP_444	OD1	3.778
5W9N	I_ARG_401	NH2	I_ASP_444	OD2	3.214
5W9N	I_LYS_502	NZ	I_GLU_513	OE2	2.781
5W9N	I_LYS_587	NZ	I_GLU_382	OE2	2.936
5W9N	I_ARG_614	NH1	I_GLU_605	OE2	3.987
5W9N	I_LYS_668	NZ	I_ASP_355	OD1	3.243
5W9N	I_LYS_668	NZ	I_ASP_355	OD2	3.427
5W9N	I_HIS_681	ND1	I_GLU_680	OE2	3.948
5W9N	I_LYS_728	NZ	I_ASP_726	OD2	2.845
5W9N	J_LYS_52	NZ	J_ASP_49	OD2	3.577
5W9N	J_HIS_81	ND1	J_ASP_80	OD1	3.829
5W9N	J_LYS_99	NZ	J_GLU_32	OE1	2.844
5W9N	J_ARG_119	NH1	J_ASP_54	OD2	3.500
5W9N	J_LYS_142	NZ	J_GLU_252	OE1	3.608
5W9N	J_LYS_142	NZ	J_GLU_252	OE2	3.253
5W9N	J_ARG_190	NH1	J_ASP_24	OD1	3.620
5W9N	J_ARG_190	NH1	J_ASP_24	OD2	3.407
5W9N	J_ARG_190	NH2	J_ASP_24	OD1	2.694
5W9N	J_ARG_190	NH2	J_ASP_24	OD2	3.854
5W9N	J_ARG_235	NH2	J_GLU_188	OE1	2.960
5W9N	J_ARG_235	NH2	J_GLU_188	OE2	3.595
5W9N	J_ARG_334	NH2	J_ASP_330	OD1	3.929
5W9N	J_ARG_334	NH2	J_ASP_330	OD2	2.885
5W9N	J_ARG_335	NH2	J_ASP_326	OD2	2.940
5W9N	J_ARG_401	NH2	J_ASP_444	OD1	3.745
5W9N	J_ARG_401	NH2	J_ASP_444	OD2	3.113
5W9N	J_LYS_413	NZ	J_GLU_382	OE1	3.770
5W9N	J_LYS_413	NZ	J_GLU_382	OE2	2.885
5W9N	J_LYS_502	NZ	J_GLU_513	OE1	3.403
5W9N	J_LYS_502	NZ	J_GLU_513	OE2	3.488
5W9N	J_ARG_511	NH2	J_ASP_509	OD2	3.316
5W9N	J_ARG_614	NH1	J_GLU_605	OE2	3.946
5W9N	J_ARG_629	NH1	J_ASP_644	OD1	2.925
5W9N	J_ARG_629	NH2	J_ASP_644	OD1	2.748
5W9N	J_ARG_629	NH2	J_ASP_644	OD2	3.827
5W9N	J_LYS_665	NZ	J_GLU_666	OE2	2.737
5W9N	J_HIS_681	NE2	A_ASP_910	OD1	2.923
5W9N	J_HIS_681	NE2	A_ASP_910	OD2	3.770
5W9N	J_LYS_728	NZ	J_ASP_726	OD1	3.992
5W9N	J_LYS_728	NZ	J_ASP_726	OD2	2.808
5W9O	A_ARG_758	NH1	J_ASP_740	OD1	2.989
5W9O	A_LYS_779	NZ	A_ASP_771	OD2	3.308
5W9O	A_LYS_779	NZ	A_GLU_1148	OE1	3.756
5W9O	A_LYS_801	NZ	A_ASP_843	OD1	2.906
5W9O	A_LYS_801	NZ	A_ASP_843	OD2	3.361
5W9O	A_LYS_807	NZ	A_GLU_818	OE1	3.592
5W9O	A_LYS_807	NZ	A_GLU_818	OE2	2.924
5W9O	A_ARG_841	NH2	A_ASP_844	OD2	2.838
5W9O	A_ARG_847	NH1	A_ASP_844	OD1	3.667
5W9O	A_ARG_847	NH2	A_ASP_844	OD1	2.759
5W9O	A_ARG_887	NH2	A_ASP_892	OD1	3.046
5W9O	A_ARG_887	NH2	A_ASP_892	OD2	3.709
5W9O	A_HIS_1020	NE2	A_ASP_1024	OD2	2.966
5W9O	A_LYS_1021	NZ	A_GLU_793	OE1	3.937
5W9O	A_LYS_1021	NZ	A_GLU_793	OE2	2.905
5W9O	A_ARG_1057	NH1	A_ASP_1053	OD1	2.779
5W9O	A_ARG_1113	NH1	A_GLU_1105	OE1	3.499

5W9O	A_ARG_1113	NH1	A_GLU_1105	OE2	2.983
5W9O	A_ARG_1113	NH2	D_GLU_1105	OE1	3.178
5W9O	A_ARG_1179	NH2	B_ASP_31	OD1	2.796
5W9O	B_LYS_38	NZ	B_GLU_46	OE1	2.988
5W9O	B_LYS_62	NZ	B_GLU_46	OE1	3.057
5W9O	B_LYS_62	NZ	B_GLU_46	OE2	3.242
5W9O	B_ARG_94	NH2	B_ASP_101	OD2	2.810
5W9O	B_LYS_95	NZ	B_ASP_100C	OD1	3.658
5W9O	C_ARG_24	NH2	C_ASP_70	OD1	3.533
5W9O	C_ARG_24	NH2	C_ASP_70	OD2	2.999
5W9O	C_ARG_61	NH1	C_GLU_79	OE2	2.984
5W9O	C_ARG_61	NH2	C_GLU_79	OE2	3.885
5W9O	C_LYS_92	NZ	C_GLU_93	OE1	2.863
5W9O	C_ARG_96	NH1	B_ASP_100C	OD2	3.180
5W9O	C_ARG_96	NH2	B_ASP_100C	OD2	2.879
5W9O	C_LYS_103	NZ	C_GLU_105	OE1	3.349
5W9O	D_LYS_779	NZ	D_ASP_771	OD2	2.942
5W9O	D_LYS_779	NZ	D_GLU_1148	OE1	3.819
5W9O	D_LYS_801	NZ	D_ASP_843	OD1	2.899
5W9O	D_LYS_801	NZ	D_ASP_843	OD2	3.628
5W9O	D_LYS_807	NZ	D_GLU_818	OE1	2.864
5W9O	D_LYS_807	NZ	D_GLU_818	OE2	3.460
5W9O	D_LYS_816	NZ	D_ASP_1064	OD1	3.778
5W9O	D_LYS_816	NZ	D_ASP_1064	OD2	2.905
5W9O	D_ARG_841	NH2	D_ASP_844	OD2	2.807
5W9O	D_ARG_847	NH1	J_ASP_726	OD2	2.979
5W9O	D_ARG_847	NH2	D_ASP_844	OD1	2.817
5W9O	D_ARG_887	NH2	D_ASP_892	OD1	3.050
5W9O	D_ARG_887	NH2	D_ASP_892	OD2	3.816
5W9O	D_HIS_1020	NE2	D_ASP_1024	OD1	3.793
5W9O	D_HIS_1020	NE2	D_ASP_1024	OD2	3.047
5W9O	D_ARG_1057	NH1	D_ASP_1053	OD1	3.689
5W9O	D_LYS_1102	NZ	D_GLU_793	OE1	2.930
5W9O	D_LYS_1102	NZ	D_GLU_793	OE2	3.237
5W9O	D_ARG_1113	NH1	G_GLU_1105	OE1	3.664
5W9O	D_ARG_1113	NH2	D_GLU_1105	OE1	3.068
5W9O	D_ARG_1113	NH2	D_GLU_1105	OE2	3.628
5W9O	D_HIS_1138	NE2	D_GLU_793	OE1	2.926
5W9O	E_LYS_38	NZ	E_ASP_86	OD1	3.864
5W9O	E_LYS_62	NZ	E_GLU_46	OE1	2.853
5W9O	E_LYS_62	NZ	E_GLU_46	OE2	3.614
5W9O	E_LYS_95	NZ	E_ASP_100C	OD1	3.641
5W9O	E_LYS_95	NZ	E_ASP_100C	OD2	3.940
5W9O	F_ARG_61	NH1	F_GLU_79	OE1	3.425
5W9O	F_ARG_61	NH1	F_GLU_79	OE2	3.162
5W9O	F_ARG_61	NH2	F_GLU_79	OE2	3.303
5W9O	F_ARG_96	NH1	E_ASP_100C	OD2	2.799
5W9O	F_ARG_96	NH2	D_GLU_1183	OE2	3.799
5W9O	F_ARG_96	NH2	E_ASP_100C	OD2	3.255
5W9O	G_ARG_758	NH1	L_ASP_740	OD1	2.934
5W9O	G_LYS_779	NZ	G_ASP_771	OD2	2.924
5W9O	G_LYS_779	NZ	G_GLU_1148	OE1	3.649
5W9O	G_LYS_801	NZ	G_ASP_843	OD1	2.865
5W9O	G_LYS_801	NZ	G_ASP_843	OD2	3.439
5W9O	G_LYS_807	NZ	G_GLU_818	OE1	2.891
5W9O	G_LYS_807	NZ	G_GLU_818	OE2	3.530
5W9O	G_LYS_816	NZ	G_ASP_1064	OD1	3.715
5W9O	G_LYS_816	NZ	G_ASP_1064	OD2	3.538

5W9O	G_ARG_841	NH1	G_GLU_1090	OE2	3.058
5W9O	G_ARG_847	NH1	K_ASP_726	OD2	3.097
5W9O	G_ARG_847	NH2	G_ASP_844	OD1	2.809
5W9O	G_ARG_887	NH2	G_ASP_892	OD1	2.982
5W9O	G_HIS_1020	NE2	G_ASP_1024	OD2	3.021
5W9O	G_LYS_1102	NZ	G_GLU_793	OE1	3.370
5W9O	G_LYS_1102	NZ	G_GLU_793	OE2	2.830
5W9O	G_ARG_1113	NH1	G_GLU_1105	OE1	3.501
5W9O	G_ARG_1113	NH1	G_GLU_1105	OE2	2.926
5W9O	G_HIS_1138	NE2	G_GLU_793	OE1	3.125
5W9O	G_LYS_1174	NZ	G_GLU_1183	OE1	2.745
5W9O	G_ARG_1179	NH2	H_ASP_31	OD1	2.843
5W9O	H_HIS_35	NE2	H_ASP_100C	OD1	3.649
5W9O	H_HIS_35	NE2	H_ASP_100C	OD2	3.605
5W9O	H_LYS_38	NZ	H_ASP_86	OD1	3.619
5W9O	H_LYS_62	NZ	H_GLU_46	OE1	2.840
5W9O	H_LYS_62	NZ	H_GLU_46	OE2	3.755
5W9O	H_ARG_66	NH2	H_ASP_86	OD2	3.025
5W9O	H_ARG_94	NH2	H_ASP_101	OD1	3.987
5W9O	H_ARG_94	NH2	H_ASP_101	OD2	2.829
5W9O	L_ARG_61	NH1	L_GLU_79	OE2	2.913
5W9O	L_ARG_61	NH1	L_ASP_82	OD1	3.774
5W9O	L_ARG_61	NH1	L_ASP_82	OD2	2.961
5W9O	L_ARG_61	NH2	L_GLU_79	OE2	3.003
5W9O	L_LYS_92	NZ	L_GLU_93	OE1	3.065
5W9O	L_ARG_96	NH1	H_ASP_100C	OD2	3.979
5W9O	L_ARG_96	NH2	G_GLU_1183	OE2	2.715
5W9O	L_ARG_96	NH2	H_ASP_100C	OD2	3.993
5W9O	J_LYS_27	NZ	J_GLU_230	OE2	3.475
5W9O	J_LYS_52	NZ	J_ASP_49	OD2	3.987
5W9O	J_LYS_99	NZ	J_GLU_32	OE1	3.930
5W9O	J_LYS_99	NZ	J_GLU_32	OE2	3.469
5W9O	J_LYS_99	NZ	J_ASP_34	OD2	3.652
5W9O	J_LYS_110	NZ	J_ASP_83	OD2	3.502
5W9O	J_LYS_110	NZ	J_ASP_108	OD1	3.336
5W9O	J_LYS_110	NZ	J_ASP_108	OD2	3.601
5W9O	J_ARG_119	NH2	J_ASP_54	OD2	3.505
5W9O	J_LYS_142	NZ	J_GLU_252	OE2	3.340
5W9O	J_HIS_194	NE2	J_GLU_32	OE1	2.883
5W9O	J_HIS_208	ND1	J_ASP_213	OD2	3.923
5W9O	J_HIS_208	NE2	J_ASP_213	OD2	3.787
5W9O	J_ARG_335	NH2	J_ASP_326	OD2	2.668
5W9O	J_ARG_401	NH2	J_ASP_444	OD2	3.561
5W9O	J_LYS_496	NZ	J_GLU_536	OE1	3.601
5W9O	J_LYS_502	NZ	J_GLU_513	OE2	2.998
5W9O	J_ARG_505	NH1	J_GLU_549	OE1	3.551
5W9O	J_ARG_614	NH2	J_GLU_605	OE2	3.078
5W9O	J_LYS_665	NZ	J_GLU_357	OE1	3.881
5W9O	J_LYS_665	NZ	J_GLU_357	OE2	2.936
5W9O	J_LYS_665	NZ	J_GLU_666	OE2	3.739
5W9O	J_HIS_681	NE2	D_ASP_910	OD1	2.932
5W9O	J_ARG_694	NH1	J_ASP_343	OD2	3.143
5W9O	J_ARG_694	NH2	J_ASP_343	OD2	2.962
5W9O	J_ARG_700	NH2	A_GLU_756	OE1	3.931
5W9O	J_ARG_700	NH2	A_GLU_756	OE2	2.914
5W9O	K_LYS_52	NZ	K_ASP_49	OD2	2.630
5W9O	K_LYS_99	NZ	K_GLU_32	OE1	2.833
5W9O	K_LYS_99	NZ	K_GLU_32	OE2	3.941

5W9O	K_LYS_110	NZ	K_ASP_83	OD2	3.249
5W9O	K_LYS_110	NZ	K_ASP_108	OD1	3.411
5W9O	K_LYS_110	NZ	K_ASP_108	OD2	3.722
5W9O	K_ARG_119	NH1	K_ASP_54	OD1	3.012
5W9O	K_ARG_119	NH1	K_ASP_54	OD2	3.524
5W9O	K_LYS_142	NZ	K_GLU_247	OE1	3.485
5W9O	K_LYS_142	NZ	K_GLU_249	OE2	2.994
5W9O	K_ARG_190	NH1	K_GLU_188	OE1	3.568
5W9O	K_HIS_194	NE2	K_GLU_32	OE1	3.387
5W9O	K_HIS_194	NE2	K_GLU_32	OE2	3.889
5W9O	K_HIS_208	NE2	K_ASP_213	OD2	3.790
5W9O	K_ARG_335	NH2	K_ASP_326	OD2	2.949
5W9O	K_ARG_401	NH2	K_ASP_444	OD1	3.796
5W9O	K_ARG_401	NH2	K_ASP_444	OD2	3.928
5W9O	K_LYS_502	NZ	K_GLU_513	OE2	2.673
5W9O	K_LYS_587	NZ	K_GLU_382	OE2	2.796
5W9O	K_ARG_629	NH1	K_ASP_644	OD1	2.889
5W9O	K_ARG_629	NH1	K_ASP_644	OD2	3.817
5W9O	K_LYS_665	NZ	K_ASP_355	OD1	3.037
5W9O	K_LYS_665	NZ	K_ASP_355	OD2	3.492
5W9O	K_ARG_694	NH1	K_ASP_343	OD2	3.613
5W9O	K_ARG_694	NH2	K_ASP_343	OD2	3.571
5W9O	L_LYS_27	NZ	L_GLU_230	OE2	3.874
5W9O	L_LYS_99	NZ	L_ASP_34	OD2	3.209
5W9O	L_ARG_119	NH2	L_ASP_54	OD2	3.705
5W9O	L_LYS_142	NZ	L_GLU_252	OE2	2.676
5W9O	L_HIS_194	NE2	L_GLU_32	OE1	3.367
5W9O	L_HIS_194	NE2	L_GLU_32	OE2	3.603
5W9O	L_HIS_208	NE2	L_ASP_213	OD2	3.918
5W9O	L_ARG_235	NH2	L_GLU_188	OE1	2.895
5W9O	L_ARG_235	NH2	L_GLU_188	OE2	3.955
5W9O	L_ARG_335	NH2	L_ASP_326	OD2	2.658
5W9O	L_ARG_401	NH2	L_ASP_444	OD1	3.946
5W9O	L_LYS_413	NZ	L_GLU_382	OE2	2.929
5W9O	L_LYS_502	NZ	L_GLU_513	OE1	3.607
5W9O	L_LYS_502	NZ	L_GLU_513	OE2	3.762
5W9O	L_ARG_614	NH2	L_GLU_605	OE1	3.049
5W9O	L_ARG_614	NH2	L_GLU_605	OE2	3.623
5W9O	L_ARG_629	NH1	L_ASP_644	OD1	2.908
5W9O	L_ARG_629	NH2	L_ASP_644	OD1	2.789
5W9O	L_ARG_629	NH2	L_ASP_644	OD2	3.634
5W9O	L_LYS_665	NZ	L_GLU_666	OE2	2.768
5W9O	L_HIS_681	NE2	A_ASP_910	OD1	3.028
5W9O	L_HIS_681	NE2	A_ASP_910	OD2	3.886
5W9O	L_HIS_681	NE2	L_GLU_680	OE2	3.236
5W9O	L_ARG_694	NH1	L_ASP_343	OD2	2.925
5W9O	L_ARG_694	NH2	L_ASP_343	OD2	3.698
5W9P	J_ARG_758	NH2	A_ASP_740	OD1	2.970
5W9P	J_LYS_779	NZ	J_ASP_771	OD2	2.978
5W9P	J_LYS_779	NZ	J_GLU_1148	OE1	2.979
5W9P	J_LYS_779	NZ	J_GLU_1148	OE2	3.840
5W9P	J_LYS_801	NZ	J_ASP_843	OD1	2.959
5W9P	J_LYS_801	NZ	J_ASP_843	OD2	3.857
5W9P	J_LYS_807	NZ	J_GLU_818	OE1	3.681
5W9P	J_LYS_807	NZ	J_GLU_818	OE2	2.920
5W9P	J_LYS_816	NZ	J_ASP_1064	OD1	3.615
5W9P	J_LYS_816	NZ	J_ASP_1064	OD2	2.986
5W9P	J_ARG_841	NH2	J_GLU_1090	OE1	2.927

5W9P	J_ARG_841	NH2	J_GLU_1090	OE2	3.745
5W9P	J_ARG_847	NH1	C_ASP_726	OD1	3.573
5W9P	J_ARG_847	NH1	C_ASP_726	OD2	2.973
5W9P	J_ARG_847	NH2	J_ASP_844	OD1	2.813
5W9P	J_ARG_887	NH2	J_ASP_892	OD1	2.929
5W9P	J_HIS_1020	NE2	J_ASP_1024	OD2	3.009
5W9P	J_LYS_1021	NZ	J_GLU_793	OE1	2.955
5W9P	J_LYS_1021	NZ	J_GLU_793	OE2	3.659
5W9P	J_ARG_1113	NH1	J_GLU_1105	OE1	3.033
5W9P	J_ARG_1113	NH2	H_GLU_1105	OE1	3.990
5W9P	J_ARG_1113	NH2	H_GLU_1105	OE2	2.796
5W9P	J_LYS_1174	NZ	J_GLU_1183	OE1	2.861
5W9P	J_ARG_1179	NH2	F_ASP_31	OD1	2.888
5W9P	A_LYS_52	NZ	A_ASP_49	OD2	2.805
5W9P	A_LYS_99	NZ	A_GLU_32	OE1	2.801
5W9P	A_LYS_110	NZ	A_ASP_83	OD2	2.816
5W9P	A_ARG_119	NH2	A_ASP_54	OD1	3.835
5W9P	A_ARG_119	NH2	A_ASP_54	OD2	3.031
5W9P	A_LYS_142	NZ	A_GLU_252	OE1	2.862
5W9P	A_HIS_194	NE2	A_GLU_32	OE1	3.536
5W9P	A_ARG_235	NH1	A_GLU_188	OE1	2.967
5W9P	A_ARG_235	NH1	A_GLU_188	OE2	3.856
5W9P	A_ARG_269	NH1	A_GLU_252	OE1	3.898
5W9P	A_ARG_269	NH1	A_GLU_252	OE2	2.880
5W9P	A_ARG_335	NH2	A_ASP_326	OD2	2.878
5W9P	A_ARG_614	NH1	A_GLU_367	OE2	2.943
5W9P	A_ARG_614	NH2	A_GLU_367	OE2	2.985
5W9P	A_ARG_629	NH1	A_GLU_376	OE1	3.647
5W9P	A_ARG_629	NH1	A_ASP_644	OD1	2.978
5W9P	A_ARG_629	NH2	A_ASP_644	OD1	2.931
5W9P	A_LYS_665	NZ	A_GLU_357	OE1	3.670
5W9P	A_LYS_665	NZ	A_GLU_357	OE2	2.942
5W9P	A_HIS_681	NE2	H_ASP_910	OD1	3.149
5W9P	A_HIS_681	NE2	H_ASP_910	OD2	3.352
5W9P	A_ARG_691	NH2	H_GLU_818	OE2	2.969
5W9P	A_ARG_694	NH2	A_ASP_343	OD1	2.962
5W9P	A_ARG_694	NH2	A_ASP_343	OD2	3.657
5W9P	A_ARG_700	NH2	J_GLU_756	OE2	2.978
5W9P	A_LYS_728	NZ	A_ASP_726	OD2	2.889
5W9P	F_LYS_62	NZ	F_GLU_46	OE1	2.994
5W9P	F_LYS_62	NZ	F_GLU_46	OE2	3.429
5W9P	F_ARG_66	NH1	F_ASP_86	OD1	3.067
5W9P	F_ARG_66	NH1	F_ASP_86	OD2	3.588
5W9P	F_ARG_66	NH2	F_ASP_86	OD1	3.743
5W9P	F_ARG_66	NH2	F_ASP_86	OD2	2.861
5W9P	F_ARG_94	NH2	F_ASP_101	OD1	3.927
5W9P	F_ARG_94	NH2	F_ASP_101	OD2	2.913
5W9P	F_LYS_95	NZ	F_ASP_100C	OD1	2.870
5W9P	F_LYS_95	NZ	F_ASP_100C	OD2	3.708
5W9P	G_ARG_1177	NH1	G_ASP_1198	OD1	3.165
5W9P	G_ARG_1177	NH1	G_ASP_1198	OD2	3.744
5W9P	G_ARG_1177	NH2	G_ASP_1198	OD1	3.713
5W9P	G_ARG_1177	NH2	G_ASP_1198	OD2	2.872
5W9P	G_ARG_1212	NH1	J_GLU_1183	OE2	3.421
5W9P	G_ARG_1212	NH2	J_GLU_1183	OE2	2.921
5W9P	G_ARG_1212	NH2	F_ASP_100C	OD2	2.848
5W9P	G_LYS_1219	NZ	G_GLU_1221	OE2	2.894
5W9P	B_ARG_758	NH2	C_ASP_740	OD1	2.971

5W9P	B_LYS_779	NZ	B_ASP_771	OD2	2.978
5W9P	B_LYS_779	NZ	B_GLU_1148	OE1	2.979
5W9P	B_LYS_779	NZ	B_GLU_1148	OE2	3.841
5W9P	B_LYS_801	NZ	B_ASP_843	OD1	2.958
5W9P	B_LYS_801	NZ	B_ASP_843	OD2	3.857
5W9P	B_LYS_807	NZ	B_GLU_818	OE1	3.681
5W9P	B_LYS_807	NZ	B_GLU_818	OE2	2.920
5W9P	B_LYS_816	NZ	B_ASP_1064	OD1	3.616
5W9P	B_LYS_816	NZ	B_ASP_1064	OD2	2.986
5W9P	B_ARG_841	NH2	B_GLU_1090	OE1	2.927
5W9P	B_ARG_841	NH2	B_GLU_1090	OE2	3.745
5W9P	B_ARG_847	NH1	I_ASP_726	OD1	3.572
5W9P	B_ARG_847	NH1	I_ASP_726	OD2	2.973
5W9P	B_ARG_847	NH2	B_ASP_844	OD1	2.813
5W9P	B_ARG_887	NH2	B_ASP_892	OD1	2.929
5W9P	B_HIS_1020	NE2	B_ASP_1024	OD2	3.009
5W9P	B_LYS_1021	NZ	B_GLU_793	OE1	2.955
5W9P	B_LYS_1021	NZ	B_GLU_793	OE2	3.659
5W9P	B_ARG_1113	NH1	B_GLU_1105	OE1	3.033
5W9P	B_ARG_1113	NH2	J_GLU_1105	OE1	3.989
5W9P	B_ARG_1113	NH2	J_GLU_1105	OE2	2.795
5W9P	B_LYS_1174	NZ	B_GLU_1183	OE1	2.862
5W9P	B_ARG_1179	NH2	D_ASP_31	OD1	2.887
5W9P	C_LYS_52	NZ	C_ASP_49	OD2	2.805
5W9P	C_LYS_99	NZ	C_GLU_32	OE1	2.802
5W9P	C_LYS_110	NZ	C_ASP_83	OD2	2.816
5W9P	C_ARG_119	NH2	C_ASP_54	OD1	3.834
5W9P	C_ARG_119	NH2	C_ASP_54	OD2	3.030
5W9P	C_LYS_142	NZ	C_GLU_252	OE1	2.862
5W9P	C_HIS_194	NE2	C_GLU_32	OE1	3.534
5W9P	C_ARG_235	NH1	C_GLU_188	OE1	2.966
5W9P	C_ARG_235	NH1	C_GLU_188	OE2	3.856
5W9P	C_ARG_269	NH1	C_GLU_252	OE1	3.899
5W9P	C_ARG_269	NH1	C_GLU_252	OE2	2.881
5W9P	C_ARG_335	NH2	C_ASP_326	OD2	2.876
5W9P	C_ARG_614	NH1	C_GLU_367	OE2	2.943
5W9P	C_ARG_614	NH2	C_GLU_367	OE2	2.984
5W9P	C_ARG_629	NH1	C_GLU_376	OE1	3.647
5W9P	C_ARG_629	NH1	C_ASP_644	OD1	2.978
5W9P	C_ARG_629	NH1	C_ASP_644	OD2	4.000
5W9P	C_ARG_629	NH2	C_ASP_644	OD1	2.931
5W9P	C_LYS_665	NZ	C_GLU_357	OE1	3.671
5W9P	C_LYS_665	NZ	C_GLU_357	OE2	2.942
5W9P	C_HIS_681	NE2	J_ASP_910	OD1	3.149
5W9P	C_HIS_681	NE2	J_ASP_910	OD2	3.352
5W9P	C_ARG_691	NH2	J_GLU_818	OE2	2.970
5W9P	C_ARG_694	NH2	C_ASP_343	OD1	2.962
5W9P	C_ARG_694	NH2	C_ASP_343	OD2	3.658
5W9P	C_ARG_700	NH2	B_GLU_756	OE2	2.978
5W9P	C_LYS_728	NZ	C_ASP_726	OD2	2.889
5W9P	D_LYS_62	NZ	D_GLU_46	OE1	2.993
5W9P	D_LYS_62	NZ	D_GLU_46	OE2	3.428
5W9P	D_ARG_66	NH1	D_ASP_86	OD1	3.067
5W9P	D_ARG_66	NH1	D_ASP_86	OD2	3.588
5W9P	D_ARG_66	NH2	D_ASP_86	OD1	3.743
5W9P	D_ARG_66	NH2	D_ASP_86	OD2	2.862
5W9P	D_ARG_94	NH2	D_ASP_101	OD1	3.928
5W9P	D_ARG_94	NH2	D_ASP_101	OD2	2.914

5W9P	D_LYS_95	NZ	D_ASP_100C	OD1	2.871
5W9P	D_LYS_95	NZ	D_ASP_100C	OD2	3.708
5W9P	E_ARG_1177	NH1	E_ASP_1198	OD1	3.165
5W9P	E_ARG_1177	NH1	E_ASP_1198	OD2	3.743
5W9P	E_ARG_1177	NH2	E_ASP_1198	OD1	3.713
5W9P	E_ARG_1177	NH2	E_ASP_1198	OD2	2.872
5W9P	E_ARG_1212	NH1	B_GLU_1183	OE2	3.420
5W9P	E_ARG_1212	NH2	B_GLU_1183	OE2	2.920
5W9P	E_ARG_1212	NH2	D_ASP_100C	OD2	2.848
5W9P	E_LYS_1219	NZ	E_GLU_1221	OE2	2.894
5W9P	H_ARG_758	NH2	I_ASP_740	OD1	2.969
5W9P	H_LYS_779	NZ	H_ASP_771	OD2	2.978
5W9P	H_LYS_779	NZ	H_GLU_1148	OE1	2.978
5W9P	H_LYS_779	NZ	H_GLU_1148	OE2	3.840
5W9P	H_LYS_801	NZ	H_ASP_843	OD1	2.959
5W9P	H_LYS_801	NZ	H_ASP_843	OD2	3.857
5W9P	H_LYS_807	NZ	H_GLU_818	OE1	3.681
5W9P	H_LYS_807	NZ	H_GLU_818	OE2	2.919
5W9P	H_LYS_816	NZ	H_ASP_1064	OD1	3.616
5W9P	H_LYS_816	NZ	H_ASP_1064	OD2	2.986
5W9P	H_ARG_841	NH2	H_GLU_1090	OE1	2.927
5W9P	H_ARG_841	NH2	H_GLU_1090	OE2	3.745
5W9P	H_ARG_847	NH1	A_ASP_726	OD1	3.572
5W9P	H_ARG_847	NH1	A_ASP_726	OD2	2.973
5W9P	H_ARG_847	NH2	H_ASP_844	OD1	2.813
5W9P	H_ARG_887	NH2	H_ASP_892	OD1	2.929
5W9P	H_HIS_1020	NE2	H_ASP_1024	OD2	3.010
5W9P	H_LYS_1021	NZ	H_GLU_793	OE1	2.954
5W9P	H_LYS_1021	NZ	H_GLU_793	OE2	3.659
5W9P	H_ARG_1113	NH1	H_GLU_1105	OE1	3.032
5W9P	H_ARG_1113	NH2	B_GLU_1105	OE1	3.989
5W9P	H_ARG_1113	NH2	B_GLU_1105	OE2	2.795
5W9P	H_LYS_1174	NZ	H_GLU_1183	OE1	2.861
5W9P	H_ARG_1179	NH2	K_ASP_31	OD1	2.888
5W9P	I_LYS_52	NZ	I_ASP_49	OD2	2.805
5W9P	I_LYS_99	NZ	I_GLU_32	OE1	2.802
5W9P	I_LYS_110	NZ	I_ASP_83	OD2	2.816
5W9P	I_ARG_119	NH2	I_ASP_54	OD1	3.835
5W9P	I_ARG_119	NH2	I_ASP_54	OD2	3.031
5W9P	I_LYS_142	NZ	I_GLU_252	OE1	2.862
5W9P	I_HIS_194	NE2	I_GLU_32	OE1	3.534
5W9P	I_ARG_235	NH1	I_GLU_188	OE1	2.967
5W9P	I_ARG_235	NH1	I_GLU_188	OE2	3.856
5W9P	I_ARG_269	NH1	I_GLU_252	OE1	3.899
5W9P	I_ARG_269	NH1	I_GLU_252	OE2	2.881
5W9P	I_ARG_335	NH2	I_ASP_326	OD2	2.877
5W9P	I_ARG_614	NH1	I_GLU_367	OE2	2.944
5W9P	I_ARG_614	NH2	I_GLU_367	OE2	2.985
5W9P	I_ARG_629	NH1	I_GLU_376	OE1	3.647
5W9P	I_ARG_629	NH1	I_ASP_644	OD1	2.978
5W9P	I_ARG_629	NH1	I_ASP_644	OD2	4.000
5W9P	I_ARG_629	NH2	I_ASP_644	OD1	2.931
5W9P	I_LYS_665	NZ	I_GLU_357	OE1	3.671
5W9P	I_LYS_665	NZ	I_GLU_357	OE2	2.942
5W9P	I_HIS_681	NE2	B_ASP_910	OD1	3.149
5W9P	I_HIS_681	NE2	B_ASP_910	OD2	3.352
5W9P	I_ARG_691	NH2	B_GLU_818	OE2	2.970
5W9P	I_ARG_694	NH2	I_ASP_343	OD1	2.962

5W9P	L_ARG_694	NH2	L_ASP_343	OD2	3.657
5W9P	L_ARG_700	NH2	H_GLU_756	OE2	2.977
5W9P	L_LYS_728	NZ	L_ASP_726	OD2	2.890
5W9P	K_LYS_62	NZ	K_GLU_46	OE1	2.994
5W9P	K_LYS_62	NZ	K_GLU_46	OE2	3.429
5W9P	K_ARG_66	NH1	K_ASP_86	OD1	3.067
5W9P	K_ARG_66	NH1	K_ASP_86	OD2	3.588
5W9P	K_ARG_66	NH2	K_ASP_86	OD1	3.743
5W9P	K_ARG_66	NH2	K_ASP_86	OD2	2.862
5W9P	K_ARG_94	NH2	K_ASP_101	OD1	3.928
5W9P	K_ARG_94	NH2	K_ASP_101	OD2	2.914
5W9P	K_LYS_95	NZ	K_ASP_100C	OD1	2.870
5W9P	K_LYS_95	NZ	K_ASP_100C	OD2	3.709
5W9P	L_ARG_1177	NH1	L_ASP_1198	OD1	3.165
5W9P	L_ARG_1177	NH1	L_ASP_1198	OD2	3.743
5W9P	L_ARG_1177	NH2	L_ASP_1198	OD1	3.713
5W9P	L_ARG_1177	NH2	L_ASP_1198	OD2	2.871
5W9P	L_ARG_1212	NH1	H_GLU_1183	OE2	3.420
5W9P	L_ARG_1212	NH2	H_GLU_1183	OE2	2.921
5W9P	L_ARG_1212	NH2	K_ASP_100C	OD2	2.848
5W9P	L_LYS_1219	NZ	L_GLU_1221	OE2	2.893
5WK4	D_ARG_29	NH2	E_ASP_36	OD1	3.168
5WK4	D_ARG_29	NH2	E_ASP_36	OD2	3.056
5WK4	D_ARG_38	NH1	D_ASP_36	OD1	3.446
5WK4	D_ARG_51	NH1	D_ASP_50	OD1	3.642
5WK4	D_ARG_51	NH1	D_ASP_50	OD2	3.657
5WK4	D_ARG_101	NH2	E_ASP_50	OD2	3.021
5WK4	D_ARG_199	NH1	D_ASP_187	OD1	3.481
5WK4	A_ARG_38	NH1	A_ASP_36	OD1	3.370
5WK4	A_ARG_51	NH2	A_ASP_50	OD1	3.057
5WK4	A_ARG_51	NH2	A_ASP_50	OD2	3.306
5WK4	A_HIS_174	NE2	D_GLU_65	OE2	2.738
5WK4	A_ARG_199	NH1	A_ASP_187	OD1	3.560
5WK4	B_ARG_29	NH2	C_ASP_36	OD1	3.257
5WK4	B_ARG_29	NH2	C_ASP_36	OD2	2.944
5WK4	B_ARG_38	NH1	B_ASP_36	OD1	3.452
5WK4	B_ARG_101	NH1	C_ASP_50	OD2	3.997
5WK4	B_ARG_101	NH2	C_ASP_50	OD2	2.811
5WK4	B_ARG_199	NH1	B_ASP_187	OD1	3.746
5WK4	B_ARG_199	NH1	B_ASP_187	OD2	3.724
5WK4	C_ARG_29	NH2	B_ASP_36	OD1	3.196
5WK4	C_ARG_29	NH2	B_ASP_36	OD2	3.146
5WK4	C_ARG_38	NH1	C_ASP_36	OD1	3.439
5WK4	C_ARG_51	NH2	C_ASP_50	OD1	3.405
5WK4	C_ARG_51	NH2	C_ASP_50	OD2	3.912
5WK4	C_ARG_101	NH1	B_ASP_50	OD2	3.840
5WK4	C_ARG_101	NH2	B_ASP_50	OD2	2.874
5WK4	C_ARG_199	NH1	C_ASP_187	OD1	3.232
5WK4	C_ARG_199	NH1	C_ASP_187	OD2	3.963
5WK4	C_LYS_210	NZ	C_GLU_160	OE1	3.001
5WK4	E_ARG_29	NH2	D_ASP_36	OD1	3.889
5WK4	E_ARG_38	NH1	E_ASP_36	OD1	3.587
5WK4	E_ARG_101	NH2	D_ASP_50	OD2	2.922
5WK4	E_ARG_199	NH1	E_ASP_187	OD1	3.573
5WK4	E_ARG_199	NH1	E_ASP_187	OD2	3.380
5WK4	E_LYS_210	NZ	E_GLU_160	OE1	3.540
5WK4	F_ARG_38	NH1	F_ASP_36	OD1	3.514
5WK4	F_ARG_51	NH1	F_ASP_50	OD1	3.360

5WK4	F_ARG_51	NH1	F_ASP_50	OD2	3.476
5WKQ	A_LYS_122	NZ	A_GLU_220	OE1	3.888
5WKQ	A_ARG_135	NH1	B_ASP_212	OD1	3.924
5WKQ	A_ARG_135	NH2	B_ASP_212	OD1	3.057
5WKQ	A_LYS_157	NZ	A_ASP_153	OD1	3.684
5WKQ	A_LYS_157	NZ	A_ASP_153	OD2	2.658
5WKQ	A_ARG_164	NH2	A_GLU_174	OE2	3.301
5WKQ	A_LYS_189	NZ	A_ASP_190	OD1	3.185
5WKQ	B_LYS_115	NZ	B_GLU_220	OE2	3.947
5WKQ	B_LYS_157	NZ	B_ASP_153	OD1	3.490
5WKQ	B_LYS_157	NZ	B_ASP_153	OD2	3.167
5WKQ	B_LYS_189	NZ	B_GLU_155	OE2	3.558
5WKQ	B_ARG_196	NH1	B_ASP_148	OD1	2.868
5WKQ	B_HIS_207	ND1	A_GLU_131	OE1	3.383
5WKQ	B_HIS_207	ND1	A_GLU_131	OE2	2.652
5WKQ	B_LYS_213	NZ	B_GLU_129	OE1	3.323
5WN9	H_ARG_38	NH1	H_GLU_46	OE1	3.227
5WN9	H_ARG_38	NH1	H_GLU_46	OE2	3.503
5WN9	H_ARG_38	NH1	H_ASP_90	OD1	3.902
5WN9	H_ARG_38	NH2	H_ASP_90	OD1	2.913
5WN9	H_LYS_63	NZ	H_GLU_46	OE1	3.637
5WN9	H_LYS_63	NZ	H_GLU_46	OE2	3.106
5WN9	H_ARG_67	NH1	H_ASP_90	OD1	3.282
5WN9	H_ARG_67	NH1	H_ASP_90	OD2	2.270
5WN9	H_ARG_67	NH2	H_ASP_90	OD1	3.376
5WN9	H_ARG_67	NH2	H_ASP_90	OD2	3.700
5WN9	H_ARG_84	NH1	H_GLU_82	OE1	3.057
5WN9	H_ARG_98	NH1	H_ASP_112	OD1	3.399
5WN9	H_ARG_98	NH1	H_ASP_112	OD2	2.841
5WN9	H_ARG_168	NH2	H_ASP_214	OD1	2.927
5WN9	H_ARG_168	NH2	H_ASP_214	OD2	3.594
5WN9	H_ARG_205	NH1	H_GLU_225	OE2	3.482
5WN9	H_ARG_205	NH1	H_ASP_226	OD1	2.888
5WN9	H_ARG_205	NH1	H_ASP_226	OD2	3.550
5WNA	H_ARG_28	NH2	H_GLU_31	OE2	3.703
5WNA	H_ARG_38	NH1	H_ASP_90	OD2	2.959
5WNA	H_ARG_38	NH2	H_GLU_46	OE1	3.180
5WNA	H_LYS_65	NZ	H_ASP_62	OD1	2.520
5WNA	H_ARG_67	NH1	H_ASP_90	OD1	3.443
5WNA	H_ARG_67	NH1	H_ASP_90	OD2	3.943
5WNA	H_ARG_67	NH2	H_ASP_90	OD1	3.917
5WNA	H_ARG_67	NH2	H_ASP_90	OD2	3.253
5WNA	H_LYS_111	NZ	H_GLU_2	OE1	2.349
5WNA	H_LYS_111	NZ	H_GLU_2	OE2	2.999
5WNA	H_LYS_154	NZ	H_ASP_155	OD2	3.921
5WNA	H_LYS_220	NZ	L_GLU_122	OE2	3.667
5WNA	H_LYS_221	NZ	H_GLU_223	OE2	2.498
5WNA	H_LYS_225	NZ	L_ASP_121	OD1	3.706
5WNA	L_HIS_32	ND1	L_GLU_50	OE1	2.885
5WNA	L_HIS_32	ND1	L_GLU_50	OE2	3.439
5WNA	L_LYS_39	NZ	D_GLU_81	OE1	2.898
5WNA	L_LYS_39	NZ	D_GLU_81	OE2	2.887
5WNA	L_ARG_61	NH2	L_GLU_81	OE2	2.586
5WNA	L_ARG_61	NH2	L_ASP_82	OD1	3.471
5WNA	L_ARG_61	NH2	L_ASP_82	OD2	2.813
5WNA	L_LYS_148	NZ	L_GLU_194	OE1	2.468
5WNA	L_LYS_148	NZ	L_GLU_194	OE2	3.864
5WNA	L_LYS_182	NZ	L_GLU_186	OE1	3.903

5WNA	L_LYS_182	NZ	L_GLU_186	OE2	3.646
5WNA	C_ARG_28	NH2	C_GLU_31	OE1	3.185
5WNA	C_ARG_38	NH1	C_ASP_90	OD1	2.822
5WNA	C_ARG_38	NH2	C_GLU_46	OE1	3.169
5WNA	C_ARG_38	NH2	C_GLU_46	OE2	3.973
5WNA	C_ARG_38	NH2	C_ASP_90	OD1	3.613
5WNA	C_LYS_65	NZ	C_ASP_62	OD2	2.607
5WNA	C_ARG_67	NH1	C_ASP_90	OD1	3.948
5WNA	C_ARG_67	NH1	C_ASP_90	OD2	3.192
5WNA	C_ARG_67	NH2	C_ASP_90	OD1	3.187
5WNA	C_ARG_67	NH2	C_ASP_90	OD2	3.777
5WNA	C_LYS_76	NZ	C_ASP_73	OD2	3.522
5WNA	C_LYS_111	NZ	C_GLU_2	OE1	3.732
5WNA	C_LYS_111	NZ	C_GLU_2	OE2	2.480
5WNA	C_LYS_154	NZ	C_ASP_155	OD1	3.662
5WNA	C_LYS_220	NZ	D_GLU_122	OE2	3.567
5WNA	C_LYS_221	NZ	C_GLU_223	OE1	3.081
5WNA	D_ARG_24	NH1	D_ASP_70	OD1	2.370
5WNA	D_ARG_24	NH1	D_ASP_70	OD2	2.529
5WNA	D_ARG_24	NH2	D_ASP_70	OD1	3.649
5WNA	D_HIS_32	ND1	D_GLU_50	OE1	3.272
5WNA	D_HIS_32	ND1	D_GLU_50	OE2	2.966
5WNA	D_LYS_39	NZ	L_GLU_81	OE1	3.744
5WNA	D_ARG_61	NH2	D_GLU_81	OE1	3.776
5WNA	D_ARG_61	NH2	D_ASP_82	OD1	3.311
5WNA	D_ARG_61	NH2	D_ASP_82	OD2	2.738
5WNA	D_LYS_148	NZ	D_GLU_194	OE2	3.083
5WNA	D_LYS_182	NZ	D_GLU_186	OE1	3.810
5WNA	D_LYS_182	NZ	D_GLU_186	OE2	3.086
5WNA	D_LYS_187	NZ	D_ASP_184	OD1	3.142
5WNB	H_ARG_19	NH1	H_GLU_82	OE1	2.506
5WNB	H_ARG_38	NH1	H_ASP_90	OD1	3.116
5WNB	H_ARG_38	NH2	H_GLU_46	OE1	3.477
5WNB	H_ARG_38	NH2	H_GLU_46	OE2	2.945
5WNB	H_ARG_38	NH2	H_ASP_90	OD1	3.843
5WNB	H_LYS_65	NZ	H_ASP_62	OD1	3.127
5WNB	H_ARG_67	NH1	H_ASP_90	OD2	3.008
5WNB	H_ARG_67	NH2	H_ASP_90	OD1	3.462
5WNB	H_ARG_67	NH2	H_ASP_90	OD2	3.519
5WNB	H_ARG_72	NH2	H_ASP_77	OD2	3.365
5WNB	H_LYS_76	NZ	H_ASP_73	OD2	3.433
5WNB	H_HIS_108	ND1	H_ASP_106	OD2	3.787
5WNB	H_HIS_108	NE2	H_ASP_106	OD2	2.649
5WNB	H_LYS_140	NZ	L_GLU_212	OE1	3.467
5WNB	H_LYS_140	NZ	L_GLU_212	OE2	3.708
5WNB	H_LYS_154	NZ	H_ASP_155	OD1	3.075
5WNB	H_LYS_154	NZ	H_ASP_155	OD2	2.337
5WNB	L_HIS_32	ND1	L_GLU_50	OE1	3.927
5WNB	L_HIS_32	ND1	L_GLU_50	OE2	3.082
5WNB	L_ARG_61	NH1	M_GLU_79	OE2	3.612
5WNB	L_ARG_61	NH2	L_GLU_81	OE1	3.333
5WNB	L_ARG_61	NH2	L_ASP_82	OD1	3.537
5WNB	L_ARG_61	NH2	L_ASP_82	OD2	2.770
5WNB	L_LYS_148	NZ	L_GLU_194	OE1	2.500
5WNB	L_LYS_187	NZ	L_ASP_184	OD2	3.098
5WNB	L_HIS_188	ND1	L_ASP_150	OD1	3.403
5WNB	L_ARG_38	NH1	L_ASP_90	OD2	3.224
5WNB	L_ARG_38	NH2	L_GLU_46	OE1	2.966

5WNB	L_ARG_38	NH2	L_GLU_46	OE2	3.754
5WNB	L_ARG_67	NH2	L_ASP_90	OD1	2.682
5WNB	L_ARG_67	NH2	L_ASP_90	OD2	3.569
5WNB	L_HIS_108	NE2	L_ASP_106	OD2	3.548
5WNB	L_LYS_154	NZ	L_ASP_155	OD1	2.470
5WNB	L_LYS_154	NZ	L_ASP_155	OD2	2.919
5WNB	M_HIS_32	ND1	M_GLU_50	OE1	2.976
5WNB	M_HIS_32	ND1	M_GLU_50	OE2	3.054
5WNB	M_ARG_61	NH2	M_GLU_81	OE1	3.769
5WNB	M_ARG_61	NH2	M_ASP_82	OD1	2.298
5WNB	M_ARG_61	NH2	M_ASP_82	OD2	3.245
5WNB	M_LYS_168	NZ	M_ASP_166	OD1	3.331
5WNB	M_LYS_168	NZ	M_ASP_166	OD2	3.217
5WNB	A_HIS_164	ND1	A_GLU_166	OE1	3.440
5WNB	A_HIS_164	NE2	A_ASP_162	OD1	3.262
5WNB	A_HIS_164	NE2	A_ASP_162	OD2	3.502
5WNB	B_HIS_164	ND1	B_GLU_166	OE1	3.999
5WNB	B_HIS_164	ND1	B_GLU_166	OE2	3.280
5WNB	B_HIS_164	NE2	B_ASP_162	OD1	3.381
5XBM	A_ARG_59	NH2	A_GLU_79	OE1	3.378
5XBM	A_ARG_59	NH2	A_ASP_80	OD2	3.511
5XBM	A_LYS_140	NZ	A_GLU_103	OE2	3.814
5XBM	A_LYS_145	NZ	A_GLU_193	OE1	3.556
5XBM	A_LYS_145	NZ	A_GLU_193	OE2	2.956
5XBM	A_ARG_153	NH1	A_GLU_183	OE1	2.925
5XBM	A_ARG_153	NH2	A_GLU_183	OE1	3.437
5XBM	A_LYS_181	NZ	A_GLU_185	OE2	3.524
5XBM	A_LYS_205	NZ	B_ASP_139	OD1	3.654
5XBM	B_LYS_67	NZ	B_ASP_90	OD1	3.066
5XBM	B_LYS_67	NZ	B_ASP_90	OD2	2.464
5XBM	B_ARG_98	NH2	B_ASP_110	OD2	3.054
5XBM	B_LYS_217	NZ	A_GLU_121	OE1	2.614
5XBM	B_LYS_217	NZ	A_GLU_121	OE2	3.625
5XBM	C_ARG_77	NH1	C_GLU_79	OE1	3.381
5XBM	C_ARG_77	NH2	C_GLU_79	OE1	2.852
5XBM	C_ARG_95	NH1	C_ASP_254	OD2	2.603
5XBM	C_ARG_95	NH2	C_GLU_93	OE2	3.851
5XBM	C_ARG_95	NH2	C_GLU_413	OE1	3.677
5XBM	C_ARG_95	NH2	C_GLU_413	OE2	3.452
5XBM	C_LYS_97	NZ	C_ASP_252	OD2	3.959
5XBM	C_HIS_171	ND1	C_GLU_175	OE2	3.888
5XBM	C_ARG_192	NH2	C_ASP_194	OD2	3.106
5XBM	C_HIS_257	NE2	C_GLU_264	OE2	3.860
5XBM	C_ARG_294	NH1	C_GLU_361	OE2	3.640
5XBM	C_ARG_294	NH2	C_ASP_368	OD2	3.362
5XBM	C_LYS_296	NZ	C_GLU_364	OE1	3.065
5XBM	C_LYS_296	NZ	C_GLU_364	OE2	3.891
5XBM	C_HIS_341	NE2	C_GLU_85	OE2	2.443
5XBM	C_LYS_381	NZ	C_ASP_254	OD1	2.330
5XBM	C_LYS_391	NZ	C_ASP_393	OD2	3.425
5XBM	C_LYS_419	NZ	C_GLU_420	OE2	2.764
5XBM	D_ARG_59	NH1	D_ASP_80	OD2	3.136
5XBM	D_LYS_145	NZ	D_GLU_152	OE2	2.597
5XBM	D_ARG_153	NH2	D_GLU_183	OE2	3.712
5XBM	D_LYS_181	NZ	D_GLU_185	OE2	2.414
5XBM	D_ARG_209	NH1	D_GLU_185	OE1	3.438
5XBM	E_LYS_67	NZ	E_ASP_90	OD2	3.658
5XBM	E_ARG_98	NH1	E_ASP_110	OD1	3.749

5XBM	E_ARG_98	NH2	E_ASP_110	OD1	3.811
5XBM	E_LYS_217	NZ	D_GLU_121	OE2	3.463
5XBM	F_ARG_77	NH1	D_ASP_31	OD1	3.188
5XBM	F_ARG_77	NH1	F_GLU_79	OE1	3.586
5XBM	F_ARG_77	NH1	F_GLU_79	OE2	3.933
5XBM	F_ARG_77	NH2	D_ASP_31	OD1	3.156
5XBM	F_ARG_77	NH2	D_ASP_31	OD2	3.938
5XBM	F_ARG_77	NH2	F_GLU_73	OE1	3.951
5XBM	F_ARG_82	NH1	F_GLU_354	OE2	3.586
5XBM	F_ARG_95	NH2	F_GLU_93	OE1	3.848
5XBM	F_ARG_95	NH2	F_GLU_413	OE2	2.568
5XBM	F_LYS_129	NZ	F_ASP_127	OD1	3.700
5XBM	F_LYS_161	NZ	C_GLU_154	OE2	3.149
5XBM	F_HIS_171	ND1	F_GLU_175	OE1	3.652
5XBM	F_HIS_257	NE2	F_GLU_264	OE1	3.279
5XBM	F_HIS_257	NE2	F_GLU_264	OE2	3.085
5XBM	F_ARG_294	NH1	F_GLU_285	OE1	3.934
5XBM	F_ARG_294	NH2	F_GLU_285	OE1	2.990
5XBM	F_ARG_294	NH2	F_GLU_285	OE2	3.166
5XBM	F_ARG_294	NH2	F_ASP_368	OD1	3.670
5XBM	F_LYS_296	NZ	F_GLU_364	OE1	3.766
5XBM	F_LYS_296	NZ	F_GLU_364	OE2	3.585
5XBM	F_HIS_341	NE2	F_GLU_85	OE2	2.413
5XBM	F_LYS_391	NZ	F_ASP_393	OD2	3.195
5XCQ	A_LYS_13	NZ	B_ASP_154	OD1	3.910
5XCQ	A_ARG_66	NH1	A_ASP_86	OD1	3.789
5XCQ	A_ARG_66	NH1	A_ASP_86	OD2	2.772
5XCQ	A_ARG_66	NH2	A_ASP_86	OD1	2.957
5XCQ	A_ARG_66	NH2	A_ASP_86	OD2	3.362
5XCQ	A_LYS_121	NZ	A_GLU_118	OE2	2.790
5XCQ	B_HIS_42	NE2	B_ASP_41	OD1	3.768
5XCQ	B_HIS_42	NE2	B_ASP_41	OD2	3.647
5XCQ	B_HIS_42	NE2	B_GLU_140	OE1	3.727
5XCQ	B_HIS_42	NE2	B_GLU_140	OE2	2.593
5XCQ	B_ARG_61	NH2	B_ASP_82	OD1	2.863
5XCQ	B_ARG_61	NH2	B_ASP_82	OD2	3.535
5XCQ	B_LYS_116	NZ	B_GLU_113	OE1	3.934
5XCQ	B_LYS_116	NZ	B_GLU_113	OE2	2.845
5XCQ	B_LYS_144	NZ	A_GLU_142	OE1	3.005
5XCQ	B_LYS_144	NZ	A_GLU_142	OE2	2.931
5XCR	A_LYS_13	NZ	B_ASP_154	OD1	3.316
5XCR	A_LYS_13	NZ	B_ASP_154	OD2	2.938
5XCR	A_ARG_66	NH1	A_ASP_86	OD1	3.686
5XCR	A_ARG_66	NH1	A_ASP_86	OD2	2.734
5XCR	A_ARG_66	NH2	A_ASP_86	OD1	2.875
5XCR	A_ARG_66	NH2	A_ASP_86	OD2	3.410
5XCR	A_LYS_121	NZ	A_GLU_118	OE2	2.719
5XCR	A_ARG_147	NH2	B_GLU_135	OE2	3.104
5XCR	A_LYS_149	NZ	B_ASP_41	OD1	2.692
5XCR	A_LYS_149	NZ	B_ASP_41	OD2	3.682
5XCR	A_LYS_153	NZ	B_ASP_41	OD1	3.567
5XCR	A_LYS_153	NZ	B_ASP_41	OD2	3.385
5XCR	B_ARG_61	NH2	B_GLU_81	OE2	3.905
5XCR	B_ARG_61	NH2	B_ASP_82	OD1	2.794
5XCR	B_ARG_61	NH2	B_ASP_82	OD2	3.586
5XCR	B_ARG_142	NH1	B_GLU_139	OE1	3.167
5XCR	B_LYS_144	NZ	A_GLU_142	OE1	2.665
5XCR	B_LYS_144	NZ	A_GLU_142	OE2	3.686

5XCR	D_LYS_13	NZ	D_GLU_16	OE2	3.937
5XCR	D_LYS_64	NZ	D_GLU_61	OE2	3.102
5XCR	D_ARG_66	NH1	D_ASP_86	OD1	3.572
5XCR	D_ARG_66	NH1	D_ASP_86	OD2	2.754
5XCR	D_ARG_66	NH2	D_ASP_86	OD1	2.764
5XCR	D_ARG_66	NH2	D_ASP_86	OD2	3.427
5XCR	D_LYS_149	NZ	E_ASP_41	OD1	2.596
5XCR	D_LYS_149	NZ	E_ASP_41	OD2	3.537
5XCR	D_LYS_149	NZ	E_GLU_137	OE1	2.552
5XCR	D_LYS_149	NZ	E_GLU_137	OE2	3.483
5XCR	D_ARG_154	NH2	E_ASP_131	OD1	2.972
5XCR	E_LYS_39	NZ	E_GLU_81	OE2	3.722
5XCR	E_ARG_61	NH2	E_GLU_81	OE1	3.056
5XCR	E_ARG_61	NH2	E_ASP_82	OD1	2.787
5XCR	E_ARG_61	NH2	E_ASP_82	OD2	3.509
5XCR	E_LYS_116	NZ	E_GLU_113	OE1	3.303
5XCR	E_LYS_116	NZ	E_GLU_113	OE2	3.987
5XCR	E_ARG_126	NH1	E_GLU_81	OE2	3.465
5XCR	E_LYS_144	NZ	D_GLU_142	OE1	2.644
5XCR	E_LYS_144	NZ	D_GLU_142	OE2	3.385
5XCS	A_ARG_38	NH1	A_ASP_86	OD1	2.824
5XCS	A_ARG_38	NH2	A_GLU_46	OE1	3.945
5XCS	A_ARG_38	NH2	A_GLU_46	OE2	3.011
5XCS	A_ARG_38	NH2	A_ASP_86	OD1	3.632
5XCS	A_LYS_43	NZ	B_GLU_140	OE2	2.517
5XCS	A_ARG_66	NH1	A_ASP_86	OD1	3.282
5XCS	A_ARG_66	NH1	A_ASP_86	OD2	2.652
5XCS	A_ARG_66	NH2	A_ASP_86	OD1	3.265
5XCS	A_ARG_66	NH2	A_ASP_86	OD2	3.877
5XCS	A_LYS_75	NZ	A_ASP_72	OD2	3.471
5XCS	A_ARG_94	NH2	A_GLU_96	OE1	2.939
5XCS	A_ARG_94	NH2	A_GLU_96	OE2	3.439
5XCS	A_ARG_95	NH1	B_ASP_91	OD1	2.738
5XCS	A_ARG_95	NH1	B_ASP_91	OD2	3.741
5XCS	A_ARG_95	NH2	B_ASP_91	OD1	3.421
5XCS	A_ARG_95	NH2	C_ASP_7	OD1	3.700
5XCS	A_ARG_95	NH2	C_ASP_7	OD2	2.872
5XCS	A_LYS_100A	NZ	B_GLU_55	OE1	2.609
5XCS	A_LYS_100A	NZ	B_GLU_55	OE2	3.239
5XCS	A_ARG_147	NH1	A_GLU_144	OE1	3.227
5XCS	A_LYS_149	NZ	B_GLU_137	OE1	3.069
5XCS	A_LYS_149	NZ	B_GLU_137	OE2	3.874
5XCS	B_ARG_61	NH2	B_GLU_81	OE2	3.146
5XCS	B_ARG_61	NH2	B_ASP_82	OD1	2.765
5XCS	B_ARG_61	NH2	B_ASP_82	OD2	3.342
5XCS	B_HIS_94	NE2	C_ASP_7	OD2	3.772
5XCS	B_LYS_103	NZ	B_GLU_105	OE2	3.336
5XCS	B_LYS_125	NZ	B_GLU_121	OE2	3.175
5XCS	B_ARG_142	NH2	B_GLU_139	OE1	3.838
5XCS	B_LYS_144	NZ	A_GLU_142	OE1	3.111
5XCS	B_LYS_144	NZ	A_GLU_142	OE2	3.511
5XCS	B_ARG_149	NH1	A_ASP_136	OD1	2.816
5XCT	A_ARG_66	NH1	A_ASP_86	OD1	3.743
5XCT	A_ARG_66	NH1	A_ASP_86	OD2	2.753
5XCT	A_ARG_66	NH2	A_ASP_86	OD1	2.868
5XCT	A_ARG_66	NH2	A_ASP_86	OD2	3.322
5XCT	A_ARG_131	NH2	A_ASP_116	OD2	3.928
5XCT	B_HIS_42	NE2	B_ASP_41	OD2	3.182

5XCT	B_HIS_42	NE2	B_GLU_140	OE1	3.857
5XCT	B_HIS_42	NE2	B_GLU_140	OE2	3.342
5XCT	B_ARG_61	NH2	B_ASP_82	OD1	2.811
5XCT	B_ARG_61	NH2	B_ASP_82	OD2	3.636
5XCT	B_LYS_144	NZ	A_GLU_142	OE1	2.822
5XCT	B_LYS_144	NZ	A_GLU_142	OE2	3.117
5XCU	A_LYS_13	NZ	B_ASP_154	OD2	3.098
5XCU	A_ARG_38	NH1	A_GLU_46	OE1	2.812
5XCU	A_ARG_38	NH1	A_GLU_46	OE2	3.498
5XCU	A_ARG_38	NH1	A_ASP_86	OD1	3.796
5XCU	A_ARG_38	NH2	A_ASP_86	OD1	2.904
5XCU	A_ARG_66	NH1	A_ASP_86	OD1	2.877
5XCU	A_ARG_66	NH1	A_ASP_86	OD2	3.351
5XCU	A_ARG_66	NH2	A_ASP_86	OD1	3.756
5XCU	A_ARG_66	NH2	A_ASP_86	OD2	2.690
5XCU	A_ARG_94	NH2	A_GLU_96	OE1	3.021
5XCU	A_ARG_94	NH2	A_GLU_96	OE2	3.420
5XCU	A_ARG_95	NH1	B_ASP_91	OD1	2.822
5XCU	A_ARG_95	NH1	B_ASP_91	OD2	3.880
5XCU	A_ARG_95	NH2	B_ASP_91	OD1	3.668
5XCU	A_ARG_95	NH2	C_ASP_7	OD1	3.592
5XCU	A_ARG_95	NH2	C_ASP_7	OD2	2.664
5XCU	A_LYS_100A	NZ	A_ASP_99	OD2	3.553
5XCU	A_LYS_100A	NZ	B_GLU_55	OE1	3.292
5XCU	A_LYS_100A	NZ	B_GLU_55	OE2	3.457
5XCU	A_LYS_121	NZ	A_GLU_118	OE1	2.230
5XCU	A_LYS_149	NZ	B_GLU_137	OE1	3.142
5XCU	A_LYS_149	NZ	B_GLU_137	OE2	3.674
5XCU	B_LYS_24	NZ	B_ASP_70	OD1	2.759
5XCU	B_LYS_24	NZ	B_ASP_70	OD2	2.992
5XCU	B_ARG_61	NH2	B_GLU_81	OE2	3.746
5XCU	B_ARG_61	NH2	B_ASP_82	OD1	2.826
5XCU	B_ARG_61	NH2	B_ASP_82	OD2	3.416
5XCU	B_HIS_94	NE2	C_ASP_7	OD2	3.530
5XCU	B_LYS_103	NZ	B_GLU_105	OE1	2.119
5XCU	B_LYS_116	NZ	B_GLU_113	OE2	2.757
5XCU	B_ARG_142	NH1	B_GLU_139	OE1	3.141
5XCU	B_ARG_142	NH2	D_GLU_100	OE1	3.626
5XCU	B_ARG_142	NH2	D_GLU_100	OE2	3.496
5XCU	B_LYS_144	NZ	A_GLU_142	OE1	2.843
5XCU	B_LYS_144	NZ	A_GLU_142	OE2	2.719
5XCU	B_ARG_149	NH2	A_ASP_136	OD1	3.520
5XCU	D_LYS_13	NZ	E_ASP_154	OD2	2.965
5XCU	D_ARG_38	NH1	D_ASP_86	OD1	2.931
5XCU	D_ARG_38	NH2	D_GLU_46	OE1	2.982
5XCU	D_ARG_52A	NH1	A_GLU_144	OE1	3.014
5XCU	D_ARG_52A	NH1	A_GLU_144	OE2	3.323
5XCU	D_ARG_52A	NH2	A_GLU_144	OE2	3.086
5XCU	D_ARG_66	NH1	D_ASP_86	OD1	3.903
5XCU	D_ARG_66	NH1	D_ASP_86	OD2	2.901
5XCU	D_ARG_66	NH2	D_ASP_86	OD1	3.158
5XCU	D_ARG_66	NH2	D_ASP_86	OD2	3.501
5XCU	D_ARG_94	NH2	D_GLU_96	OE1	3.413
5XCU	D_ARG_94	NH2	D_GLU_96	OE2	3.168
5XCU	D_ARG_95	NH1	E_ASP_91	OD1	2.736
5XCU	D_ARG_95	NH1	E_ASP_91	OD2	3.660
5XCU	D_ARG_95	NH2	E_ASP_91	OD1	3.272
5XCU	D_ARG_95	NH2	F_ASP_7	OD1	3.878

5XCU	D_ARG_95	NH2	F_ASP_7	OD2	3.169
5XCU	D_LYS_100A	NZ	D_ASP_99	OD2	3.711
5XCU	D_LYS_100A	NZ	E_GLU_55	OE1	3.852
5XCU	D_LYS_100A	NZ	E_GLU_55	OE2	2.994
5XCU	D_ARG_147	NH2	D_GLU_144	OE1	3.695
5XCU	D_LYS_149	NZ	E_GLU_137	OE1	2.785
5XCU	D_LYS_149	NZ	E_GLU_137	OE2	3.293
5XCU	E_LYS_24	NZ	E_ASP_70	OD1	3.892
5XCU	E_LYS_30F	NZ	B_GLU_139	OE1	2.662
5XCU	E_LYS_30F	NZ	B_GLU_139	OE2	3.287
5XCU	E_ARG_61	NH1	E_GLU_81	OE1	3.712
5XCU	E_ARG_61	NH1	E_ASP_82	OD1	3.146
5XCU	E_ARG_61	NH1	E_ASP_82	OD2	3.543
5XCU	E_HIS_94	NE2	F_ASP_7	OD2	3.551
5XCU	E_LYS_103	NZ	E_GLU_105	OE2	3.303
5XCU	E_ARG_142	NH1	E_GLU_139	OE2	3.171
5XCU	E_ARG_142	NH2	D_GLU_140	OE2	3.967
5XCU	E_LYS_144	NZ	D_GLU_142	OE1	3.438
5XCU	E_LYS_144	NZ	D_GLU_142	OE2	2.648
5XCV	A_ARG_38	NH1	A_GLU_46	OE1	3.020
5XCV	A_ARG_38	NH1	A_ASP_86	OD1	3.966
5XCV	A_ARG_38	NH2	A_ASP_86	OD1	2.867
5XCV	A_LYS_56	NZ	C_GLU_10	OE2	3.165
5XCV	A_LYS_56	NZ	C_ASP_11	OD1	3.842
5XCV	A_LYS_56	NZ	C_ASP_11	OD2	2.877
5XCV	A_ARG_66	NH1	A_ASP_86	OD1	3.207
5XCV	A_ARG_66	NH1	A_ASP_86	OD2	3.568
5XCV	A_ARG_66	NH2	A_ASP_86	OD1	3.873
5XCV	A_ARG_66	NH2	A_ASP_86	OD2	2.785
5XCV	A_LYS_75	NZ	A_ASP_72	OD2	3.989
5XCV	A_ARG_83	NH2	A_GLU_85	OE2	3.625
5XCV	A_LYS_94	NZ	A_ASP_101	OD2	3.427
5XCV	A_LYS_121	NZ	A_GLU_118	OE1	2.490
5XCV	A_LYS_121	NZ	A_GLU_118	OE2	3.921
5XCV	A_ARG_131	NH1	D_GLU_142	OE2	2.857
5XCV	A_ARG_131	NH2	D_GLU_142	OE2	3.651
5XCV	A_LYS_149	NZ	B_GLU_137	OE1	3.135
5XCV	A_LYS_149	NZ	B_GLU_137	OE2	2.706
5XCV	A_ARG_154	NH2	B_ASP_131	OD1	2.532
5XCV	B_LYS_53	NZ	B_ASP_52	OD1	2.531
5XCV	B_LYS_53	NZ	B_ASP_52	OD2	3.942
5XCV	B_ARG_61	NH1	B_GLU_81	OE2	2.626
5XCV	B_ARG_61	NH1	B_ASP_82	OD1	3.375
5XCV	B_ARG_61	NH1	B_ASP_82	OD2	3.966
5XCV	B_ARG_61	NH2	B_ASP_82	OD1	2.920
5XCV	B_ARG_61	NH2	B_ASP_82	OD2	2.592
5XCV	B_ARG_142	NH1	B_GLU_135	OE2	3.241
5XCV	B_ARG_142	NH1	B_GLU_139	OE1	2.828
5XCV	B_ARG_142	NH2	B_GLU_135	OE1	3.178
5XCV	B_ARG_142	NH2	B_GLU_135	OE2	3.502
5XCV	B_LYS_144	NZ	A_GLU_142	OE1	2.798
5XCV	B_LYS_144	NZ	A_GLU_142	OE2	3.295
5XCV	B_ARG_149	NH2	A_ASP_136	OD1	3.863
5XCV	B_ARG_149	NH2	A_ASP_136	OD2	3.941
5XCV	D_ARG_38	NH1	D_GLU_46	OE1	3.023
5XCV	D_ARG_38	NH1	D_ASP_86	OD1	3.942
5XCV	D_ARG_38	NH2	D_ASP_86	OD1	2.784
5XCV	D_ARG_66	NH1	D_ASP_86	OD1	3.694

5XCV	D_ARG_66	NH1	D_ASP_86	OD2	2.840
5XCV	D_ARG_66	NH2	D_ASP_86	OD1	3.151
5XCV	D_ARG_66	NH2	D_ASP_86	OD2	3.768
5XCV	D_LYS_94	NZ	D_ASP_101	OD2	3.401
5XCV	D_LYS_121	NZ	D_GLU_118	OE1	3.518
5XCV	D_LYS_121	NZ	D_GLU_118	OE2	3.547
5XCV	D_ARG_131	NH1	A_GLU_142	OE2	2.791
5XCV	D_ARG_131	NH2	A_GLU_142	OE2	3.693
5XCV	D_LYS_149	NZ	E_GLU_137	OE1	2.622
5XCV	D_LYS_149	NZ	E_GLU_137	OE2	3.565
5XCV	D_LYS_153	NZ	E_GLU_40	OE2	3.944
5XCV	E_LYS_53	NZ	E_ASP_52	OD1	2.875
5XCV	E_ARG_61	NH2	E_ASP_82	OD1	3.461
5XCV	E_ARG_61	NH2	E_ASP_82	OD2	3.413
5XCV	E_LYS_116	NZ	E_GLU_113	OE2	3.173
5XCV	E_LYS_144	NZ	D_GLU_142	OE1	2.798
5XCV	E_LYS_144	NZ	D_GLU_142	OE2	3.738
5XJ3	A_ARG_38	NH1	A_ASP_90	OD1	3.056
5XJ3	A_ARG_38	NH2	A_GLU_46	OE1	3.585
5XJ3	A_ARG_38	NH2	A_GLU_46	OE2	3.163
5XJ3	A_ARG_38	NH2	A_GLU_89	OE1	3.576
5XJ3	A_ARG_67	NH1	A_GLU_89	OE2	3.733
5XJ3	A_ARG_67	NH2	A_ASP_90	OD1	2.978
5XJ3	A_ARG_67	NH2	A_ASP_90	OD2	2.554
5XJ3	A_ARG_87	NH1	A_GLU_89	OE2	3.859
5XJ3	A_ARG_98	NH1	A_ASP_106	OD2	3.164
5XJ3	B_ARG_55	NH1	B_ASP_61	OD1	2.406
5XJ3	B_ARG_62	NH2	B_GLU_82	OE2	2.865
5XJ3	B_ARG_62	NH2	B_ASP_83	OD1	3.259
5XJ3	B_LYS_104	NZ	B_GLU_106	OE1	3.023
5XJ3	C_ARG_75	NH1	C_ASP_123	OD1	3.835
5XJ3	C_LYS_130	NZ	C_GLU_132	OE1	3.977
5XJ3	D_ARG_38	NH1	D_ASP_90	OD1	3.121
5XJ3	D_ARG_38	NH2	D_GLU_46	OE2	3.650
5XJ3	D_ARG_38	NH2	D_GLU_89	OE1	3.831
5XJ3	D_ARG_38	NH2	D_ASP_90	OD1	4.000
5XJ3	D_ARG_67	NH1	D_GLU_89	OE2	3.568
5XJ3	D_ARG_67	NH2	D_ASP_90	OD1	2.936
5XJ3	D_ARG_67	NH2	D_ASP_90	OD2	2.379
5XJ3	D_ARG_87	NH1	D_GLU_89	OE2	3.625
5XJ3	D_ARG_98	NH1	D_ASP_106	OD2	3.382
5XJ3	E_ARG_55	NH1	E_ASP_61	OD1	2.462
5XJ3	E_ARG_62	NH2	E_GLU_82	OE2	2.848
5XJ3	E_ARG_62	NH2	E_ASP_83	OD1	3.444
5XJ3	E_LYS_104	NZ	E_GLU_106	OE1	2.817
5XJ3	G_ARG_38	NH1	G_ASP_90	OD1	3.040
5XJ3	G_ARG_38	NH2	G_GLU_46	OE1	3.607
5XJ3	G_ARG_38	NH2	G_GLU_46	OE2	3.241
5XJ3	G_ARG_38	NH2	G_GLU_89	OE1	3.847
5XJ3	G_ARG_67	NH1	G_GLU_89	OE2	3.528
5XJ3	G_ARG_67	NH2	G_ASP_90	OD1	2.953
5XJ3	G_ARG_67	NH2	G_ASP_90	OD2	2.607
5XJ3	G_ARG_87	NH1	G_GLU_89	OE2	3.758
5XJ3	G_ARG_98	NH1	G_ASP_106	OD2	3.240
5XJ3	H_ARG_55	NH1	H_ASP_61	OD1	2.456
5XJ3	H_ARG_62	NH2	H_GLU_82	OE2	3.013
5XJ3	H_ARG_62	NH2	H_ASP_83	OD1	3.165
5XJ3	H_LYS_104	NZ	H_GLU_106	OE1	3.016

5XJ3	I_LYS_130	NZ	I_GLU_132	OE1	3.959
5XJ3	J_ARG_38	NH1	J_ASP_90	OD1	3.001
5XJ3	J_ARG_38	NH2	J_GLU_46	OE1	3.663
5XJ3	J_ARG_38	NH2	J_GLU_46	OE2	3.259
5XJ3	J_ARG_38	NH2	J_GLU_89	OE1	3.925
5XJ3	J_ARG_67	NH1	J_GLU_89	OE2	3.761
5XJ3	J_ARG_67	NH2	J_ASP_90	OD1	3.129
5XJ3	J_ARG_67	NH2	J_ASP_90	OD2	2.474
5XJ3	J_ARG_87	NH1	J_GLU_89	OE2	3.928
5XJ3	J_ARG_98	NH1	J_ASP_106	OD2	3.259
5XJ3	K_ARG_55	NH1	K_ASP_61	OD1	2.399
5XJ3	K_ARG_55	NH2	K_ASP_61	OD1	3.996
5XJ3	K_ARG_62	NH2	K_GLU_82	OE2	2.984
5XJ3	K_ARG_62	NH2	K_ASP_83	OD1	3.334
5XJ3	K_LYS_104	NZ	K_GLU_106	OE1	2.971
5XJ3	L_LYS_130	NZ	L_GLU_132	OE1	3.881
5XRT	A_LYS_27	NZ	B_GLU_97	OE2	3.178
5XRT	A_ARG_50	NH1	A_ASP_275	OD1	3.489
5XRT	A_HIS_75	ND1	A_ASP_73	OD1	2.934
5XRT	A_HIS_75	ND1	A_ASP_73	OD2	3.817
5XRT	A_ARG_90	NH2	A_ASP_60	OD1	3.541
5XRT	A_ARG_90	NH2	A_ASP_60	OD2	3.101
5XRT	A_ARG_109	NH1	B_GLU_67	OE2	3.059
5XRT	A_ARG_109	NH2	A_GLU_89	OE1	3.449
5XRT	A_ARG_109	NH2	B_GLU_67	OE2	3.511
5XRT	A_ARG_141	NH1	A_ASP_77	OD1	3.404
5XRT	A_ARG_141	NH1	A_ASP_77	OD2	2.369
5XRT	A_LYS_176	NZ	A_GLU_123	OE1	3.717
5XRT	A_LYS_176	NZ	A_GLU_123	OE2	2.851
5XRT	A_LYS_238	NZ	F_GLU_72	OE1	3.452
5XRT	A_LYS_238	NZ	F_GLU_72	OE2	2.683
5XRT	A_ARG_255	NH1	A_ASP_133	OD2	3.443
5XRT	A_ARG_255	NH2	A_ASP_133	OD2	3.614
5XRT	A_ARG_269	NH1	B_GLU_67	OE1	3.465
5XRT	A_LYS_292	NZ	A_ASP_291	OD2	3.086
5XRT	A_ARG_307	NH1	F_ASP_90	OD2	3.867
5XRT	A_ARG_307	NH2	F_ASP_90	OD2	3.590
5XRT	A_LYS_310	NZ	B_ASP_90	OD1	2.844
5XRT	A_LYS_315	NZ	A_GLU_41	OE1	3.734
5XRT	A_LYS_326	NZ	B_GLU_11	OE1	2.808
5XRT	A_LYS_326	NZ	B_GLU_11	OE2	2.925
5XRT	B_LYS_51	NZ	B_GLU_103	OE1	3.416
5XRT	B_ARG_54	NH1	F_GLU_97	OE2	3.836
5XRT	B_ARG_54	NH2	F_GLU_97	OE2	2.767
5XRT	B_LYS_62	NZ	F_ASP_86	OD1	3.336
5XRT	B_LYS_62	NZ	F_ASP_86	OD2	2.617
5XRT	B_LYS_62	NZ	F_ASP_90	OD1	3.654
5XRT	B_LYS_62	NZ	F_ASP_90	OD2	2.589
5XRT	B_HIS_64	NE2	F_ASP_79	OD2	3.582
5XRT	B_LYS_68	NZ	B_GLU_85	OE1	3.082
5XRT	B_LYS_68	NZ	B_GLU_85	OE2	2.799
5XRT	B_ARG_76	NH1	D_GLU_74	OE1	3.704
5XRT	B_ARG_76	NH1	D_GLU_74	OE2	3.032
5XRT	B_ARG_76	NH2	D_GLU_74	OE1	2.984
5XRT	B_ARG_76	NH2	D_GLU_74	OE2	3.801
5XRT	B_ARG_76	NH2	D_GLU_81	OE1	2.864
5XRT	B_ARG_76	NH2	D_GLU_81	OE2	3.722
5XRT	B_LYS_117	NZ	B_GLU_114	OE2	3.280

5XRT	B_ARG_121	NH2	B_ASP_37	OD2	3.079
5XRT	B_ARG_123	NH1	B_GLU_120	OE1	2.622
5XRT	B_ARG_123	NH1	B_GLU_120	OE2	3.886
5XRT	B_ARG_123	NH2	B_GLU_120	OE1	3.456
5XRT	B_ARG_123	NH2	F_ASP_132	OD2	3.663
5XRT	B_ARG_124	NH1	F_ASP_132	OD2	2.812
5XRT	B_ARG_127	NH2	F_GLU_131	OE1	3.103
5XRT	B_ARG_163	NH1	F_GLU_131	OE1	3.194
5XRT	B_ARG_163	NH1	F_GLU_131	OE2	3.563
5XRT	B_ARG_163	NH2	F_GLU_131	OE1	3.596
5XRT	B_ARG_163	NH2	F_GLU_131	OE2	2.598
5XRT	B_ARG_170	NH1	B_GLU_128	OE2	3.435
5XRT	B_ARG_170	NH2	B_GLU_131	OE2	3.245
5XRT	B_ARG_170	NH2	D_GLU_128	OE1	3.449
5XRT	B_ARG_170	NH2	D_GLU_128	OE2	3.578
5XRT	C_LYS_27	NZ	D_GLU_97	OE1	3.926
5XRT	C_LYS_27	NZ	D_GLU_97	OE2	3.340
5XRT	C_HIS_56	NE2	C_GLU_280	OE1	3.939
5XRT	C_HIS_75	ND1	C_ASP_73	OD1	2.939
5XRT	C_HIS_75	ND1	C_ASP_73	OD2	3.672
5XRT	C_ARG_90	NH2	C_ASP_60	OD1	3.078
5XRT	C_ARG_90	NH2	C_ASP_60	OD2	2.971
5XRT	C_ARG_109	NH1	D_GLU_67	OE2	2.932
5XRT	C_ARG_109	NH2	C_GLU_89	OE1	3.101
5XRT	C_ARG_141	NH2	C_ASP_77	OD1	3.277
5XRT	C_ARG_141	NH2	C_ASP_77	OD2	3.129
5XRT	C_LYS_176	NZ	C_GLU_123	OE2	3.009
5XRT	C_LYS_238	NZ	B_GLU_72	OE2	3.031
5XRT	C_ARG_255	NH1	C_ASP_133	OD1	3.530
5XRT	C_ARG_255	NH2	C_ASP_133	OD1	3.274
5XRT	C_ARG_269	NH1	D_GLU_67	OE1	3.251
5XRT	C_LYS_292	NZ	C_ASP_291	OD1	3.150
5XRT	C_ARG_307	NH2	B_ASP_90	OD2	3.134
5XRT	C_LYS_310	NZ	D_ASP_90	OD1	3.206
5XRT	C_LYS_310	NZ	D_ASP_90	OD2	3.892
5XRT	D_LYS_51	NZ	D_GLU_103	OE1	3.086
5XRT	D_ARG_54	NH2	B_GLU_97	OE2	3.066
5XRT	D_LYS_62	NZ	B_ASP_86	OD1	3.579
5XRT	D_LYS_62	NZ	B_ASP_86	OD2	3.058
5XRT	D_LYS_62	NZ	B_ASP_90	OD1	3.574
5XRT	D_LYS_62	NZ	B_ASP_90	OD2	2.797
5XRT	D_HIS_64	NE2	B_ASP_79	OD2	3.856
5XRT	D_LYS_68	NZ	D_GLU_85	OE1	3.229
5XRT	D_LYS_68	NZ	D_GLU_85	OE2	3.297
5XRT	D_ARG_76	NH1	F_GLU_74	OE1	3.338
5XRT	D_ARG_76	NH1	F_GLU_74	OE2	2.885
5XRT	D_ARG_76	NH2	F_GLU_74	OE1	2.652
5XRT	D_ARG_76	NH2	F_GLU_74	OE2	3.749
5XRT	D_ARG_76	NH2	F_GLU_81	OE1	2.506
5XRT	D_ARG_76	NH2	F_GLU_81	OE2	3.677
5XRT	D_LYS_117	NZ	D_GLU_114	OE2	2.877
5XRT	D_ARG_121	NH1	D_ASP_37	OD2	3.944
5XRT	D_ARG_121	NH2	D_ASP_37	OD1	3.995
5XRT	D_ARG_121	NH2	D_ASP_37	OD2	3.020
5XRT	D_ARG_123	NH1	D_GLU_120	OE1	2.708
5XRT	D_ARG_123	NH1	D_GLU_120	OE2	3.830
5XRT	D_ARG_123	NH2	B_ASP_132	OD2	3.975
5XRT	D_ARG_123	NH2	D_GLU_120	OE1	3.166

5XRT	D_ARG.124	NH1	B_ASP.132	OD1	3.986
5XRT	D_ARG.124	NH1	B_ASP.132	OD2	2.717
5XRT	D_ARG.127	NH2	B_GLU.131	OE1	2.649
5XRT	D_HIS.159	NE2	D_ASP.160	OD1	3.798
5XRT	D_HIS.159	NE2	D_ASP.160	OD2	3.813
5XRT	D_ARG.163	NH1	B_GLU.131	OE1	3.152
5XRT	D_ARG.163	NH1	B_GLU.131	OE2	3.070
5XRT	D_ARG.163	NH2	B_GLU.131	OE1	3.267
5XRT	D_ARG.163	NH2	B_GLU.131	OE2	2.951
5XRT	D_ARG.170	NH1	D_GLU.128	OE2	3.582
5XRT	D_ARG.170	NH2	D_GLU.131	OE2	3.591
5XRT	D_ARG.170	NH2	F_GLU.128	OE1	2.950
5XRT	D_ARG.170	NH2	F_GLU.128	OE2	3.791
5XRT	E_LYS.27	NZ	F_GLU.97	OE1	3.896
5XRT	E_LYS.27	NZ	F_GLU.97	OE2	3.675
5XRT	E_ARG.50	NH1	E_ASP.275	OD1	3.578
5XRT	E_HIS.56	NE2	E_GLU.280	OE1	3.346
5XRT	E_HIS.75	ND1	E_ASP.73	OD1	2.764
5XRT	E_ARG.90	NH2	E_ASP.60	OD1	3.458
5XRT	E_ARG.90	NH2	E_ASP.60	OD2	2.922
5XRT	E_ARG.109	NH1	F_GLU.67	OE2	2.719
5XRT	E_ARG.109	NH2	E_GLU.89	OE1	3.357
5XRT	E_ARG.109	NH2	F_GLU.67	OE2	3.732
5XRT	E_ARG.141	NH2	E_ASP.77	OD1	3.300
5XRT	E_ARG.141	NH2	E_ASP.77	OD2	3.765
5XRT	E_LYS.176	NZ	E_GLU.123	OE2	3.077
5XRT	E_LYS.238	NZ	D_GLU.72	OE2	3.742
5XRT	E_LYS.238	NZ	E_ASP.175	OD2	3.711
5XRT	E_ARG.255	NH1	E_ASP.133	OD1	2.710
5XRT	E_ARG.269	NH1	F_GLU.67	OE1	2.954
5XRT	E_ARG.269	NH1	F_GLU.67	OE2	3.996
5XRT	E_LYS.292	NZ	E_ASP.291	OD1	3.378
5XRT	E_ARG.307	NH1	D_ASP.90	OD2	3.580
5XRT	E_ARG.307	NH2	D_ASP.90	OD2	3.837
5XRT	E_LYS.310	NZ	F_ASP.90	OD1	3.115
5XRT	E_LYS.326	NZ	F_GLU.11	OE1	3.300
5XRT	F_LYS.51	NZ	F_GLU.103	OE1	3.279
5XRT	F_ARG.54	NH2	D_GLU.97	OE2	3.005
5XRT	F_LYS.62	NZ	D_ASP.86	OD1	3.549
5XRT	F_LYS.62	NZ	D_ASP.86	OD2	2.499
5XRT	F_LYS.62	NZ	D_ASP.90	OD1	3.666
5XRT	F_LYS.62	NZ	D_ASP.90	OD2	2.972
5XRT	F_HIS.64	NE2	D_ASP.79	OD2	3.194
5XRT	F_LYS.68	NZ	F_GLU.85	OE1	3.860
5XRT	F_LYS.68	NZ	F_GLU.85	OE2	3.605
5XRT	F_ARG.76	NH1	B_GLU.74	OE1	3.311
5XRT	F_ARG.76	NH1	B_GLU.74	OE2	3.105
5XRT	F_ARG.76	NH2	B_GLU.74	OE1	2.768
5XRT	F_ARG.76	NH2	B_GLU.74	OE2	3.989
5XRT	F_ARG.76	NH2	B_GLU.81	OE1	2.869
5XRT	F_ARG.76	NH2	B_GLU.81	OE2	3.812
5XRT	F_LYS.117	NZ	F_GLU.114	OE2	3.321
5XRT	F_ARG.121	NH2	F_ASP.37	OD2	3.444
5XRT	F_ARG.123	NH1	F_GLU.120	OE1	2.902
5XRT	F_ARG.123	NH1	F_GLU.120	OE2	2.669
5XRT	F_ARG.123	NH2	F_GLU.120	OE1	2.949
5XRT	F_ARG.124	NH1	D_ASP.132	OD2	3.024
5XRT	F_ARG.127	NH2	D_GLU.131	OE1	2.415

5XRT	F_HIS_159	ND1	F_ASP_160	OD1	3.993
5XRT	F_HIS_159	NE2	F_ASP_160	OD1	2.911
5XRT	F_ARG_163	NH1	D_GLU_131	OE1	3.516
5XRT	F_ARG_163	NH2	D_GLU_131	OE1	3.296
5XRT	F_ARG_163	NH2	D_GLU_131	OE2	2.611
5XRT	F_ARG_170	NH1	F_GLU_128	OE2	3.390
5XRT	F_ARG_170	NH2	B_GLU_128	OE1	3.475
5XRT	F_ARG_170	NH2	B_GLU_128	OE2	3.657
5XRT	F_ARG_170	NH2	F_GLU_128	OE2	3.860
5XRT	F_ARG_170	NH2	F_GLU_131	OE2	3.345
5XRT	F_LYS_174	NZ	B_ASP_160	OD1	3.902
5XRT	G_LYS_27	NZ	H_GLU_97	OE2	3.228
5XRT	G_ARG_50	NH1	G_ASP_275	OD1	3.487
5XRT	G_HIS_56	NE2	G_GLU_280	OE1	3.893
5XRT	G_HIS_75	ND1	G_ASP_73	OD1	2.567
5XRT	G_HIS_75	ND1	G_ASP_73	OD2	3.814
5XRT	G_LYS_82	NZ	E_GLU_119	OE1	3.805
5XRT	G_ARG_90	NH2	G_ASP_60	OD1	3.337
5XRT	G_ARG_90	NH2	G_ASP_60	OD2	3.035
5XRT	G_ARG_109	NH1	H_GLU_67	OE1	3.826
5XRT	G_ARG_109	NH1	H_GLU_67	OE2	2.804
5XRT	G_ARG_109	NH2	G_GLU_89	OE1	2.924
5XRT	G_ARG_141	NH2	G_ASP_77	OD1	3.443
5XRT	G_ARG_141	NH2	G_ASP_77	OD2	3.249
5XRT	G_LYS_176	NZ	G_GLU_123	OE2	3.413
5XRT	G_LYS_176	NZ	G_ASP_172	OD2	3.797
5XRT	G_LYS_238	NZ	G_ASP_175	OD1	3.036
5XRT	G_LYS_238	NZ	G_ASP_175	OD2	3.186
5XRT	G_ARG_255	NH1	G_ASP_133	OD2	3.599
5XRT	G_ARG_255	NH2	G_ASP_133	OD2	3.335
5XRT	G_ARG_269	NH1	H_GLU_67	OE1	3.306
5XRT	G_LYS_292	NZ	G_ASP_291	OD1	3.807
5XRT	G_LYS_292	NZ	G_ASP_291	OD2	3.964
5XRT	G_LYS_299	NZ	H_GLU_69	OE2	3.918
5XRT	G_LYS_310	NZ	H_ASP_90	OD1	2.955
5XRT	H_LYS_51	NZ	H_GLU_103	OE1	3.120
5XRT	H_LYS_68	NZ	H_GLU_85	OE1	3.706
5XRT	H_LYS_68	NZ	H_GLU_85	OE2	3.564
5XRT	H_LYS_117	NZ	H_GLU_114	OE2	3.149
5XRT	H_ARG_121	NH2	H_ASP_37	OD2	3.626
5XRT	H_ARG_123	NH1	H_GLU_120	OE1	3.412
5XRT	H_ARG_170	NH2	H_GLU_131	OE2	3.622
5XWD	A_ARG_48	NH1	A_GLU_73	OE2	3.630
5XWD	A_ARG_74	NH1	A_GLU_110	OE1	2.554
5XWD	A_ARG_74	NH1	A_GLU_110	OE2	3.566
5XWD	A_ARG_74	NH2	A_GLU_78	OE2	2.523
5XWD	A_ARG_84	NH2	A_GLU_60	OE1	3.684
5XWD	A_ARG_84	NH2	A_GLU_60	OE2	3.617
5XWD	A_ARG_114	NH1	A_GLU_78	OE1	3.452
5XWD	A_ARG_114	NH2	A_GLU_78	OE1	2.694
5XWD	A_ARG_198	NH1	A_ASP_142	OD2	3.491
5XWD	A_ARG_198	NH2	A_GLU_118	OE2	3.197
5XWD	A_ARG_220	NH1	A_GLU_221	OE1	3.463
5XWD	A_ARG_220	NH1	A_GLU_221	OE2	2.447
5XWD	A_ARG_220	NH2	A_GLU_221	OE2	3.674
5XWD	A_ARG_228	NH1	A_GLU_118	OE2	3.743
5XWD	A_ARG_228	NH2	A_GLU_118	OE2	3.666
5XWD	A_LYS_237	NZ	A_ASP_232	OD2	2.616

5XWD	A_LYS_260	NZ	A_ASP_232	OD1	2.521
5XWD	A_LYS_260	NZ	A_ASP_232	OD2	3.550
5XWD	A_LYS_260	NZ	A_GLU_233	OE2	3.396
5XWD	A_LYS_301	NZ	A_GLU_296	OE1	3.844
5XWD	A_LYS_303	NZ	A_GLU_296	OE2	3.546
5XWD	A_LYS_333	NZ	A_GLU_367	OE2	3.373
5XWD	A_ARG_353	NH2	D_ASP_96	OD2	3.335
5XWD	A_LYS_372	NZ	A_GLU_397	OE2	3.502
5XWD	A_ARG_390	NH1	A_ASP_369	OD1	3.207
5XWD	A_HIS_394	ND1	A_ASP_369	OD1	3.398
5XWD	A_HIS_394	NE2	A_GLU_397	OE2	3.209
5XWD	A_ARG_403	NH2	A_GLU_376	OE2	3.449
5XWD	A_LYS_407	NZ	A_ASP_434	OD2	3.832
5XWD	A_HIS_409	NE2	H_ASP_108	OD2	2.707
5XWD	A_ARG_427	NH1	A_ASP_498	OD1	2.268
5XWD	A_ARG_427	NH1	A_ASP_498	OD2	3.446
5XWD	A_ARG_427	NH2	A_ASP_392	OD2	3.547
5XWD	A_LYS_443	NZ	D_ASP_51	OD2	2.907
5XWD	A_LYS_455	NZ	A_GLU_489	OE1	2.906
5XWD	A_LYS_463	NZ	A_ASP_436	OD2	2.868
5XWD	A_LYS_465	NZ	D_ASP_53	OD2	3.314
5XWD	A_ARG_497	NH2	A_GLU_510	OE1	3.595
5XWD	A_ARG_507	NH1	A_GLU_524	OE1	3.565
5XWD	A_ARG_507	NH1	A_GLU_524	OE2	2.365
5XWD	A_ARG_550	NH2	A_GLU_527	OE2	2.299
5XWD	A_HIS_560	ND1	A_GLU_537	OE1	2.920
5XWD	A_HIS_560	ND1	A_GLU_537	OE2	3.490
5XWD	A_HIS_566	NE2	A_ASP_553	OD1	3.274
5XWD	A_HIS_566	NE2	A_ASP_553	OD2	3.788
5XWD	A_LYS_585	NZ	A_ASP_563	OD1	2.730
5XWD	A_LYS_585	NZ	A_ASP_563	OD2	3.880
5XWD	H_ARG_40	NH1	H_ASP_91	OD1	2.811
5XWD	H_ARG_40	NH2	H_GLU_48	OE1	3.427
5XWD	H_ARG_40	NH2	H_GLU_48	OE2	3.173
5XWD	H_ARG_40	NH2	H_ASP_91	OD1	3.631
5XWD	H_ARG_68	NH1	H_ASP_91	OD1	3.454
5XWD	H_ARG_68	NH1	H_ASP_91	OD2	3.334
5XWD	H_ARG_68	NH2	H_ASP_91	OD2	3.355
5XWD	H_ARG_99	NH1	H_ASP_108	OD2	3.765
5XWD	D_ARG_54	NH2	D_GLU_60	OE2	3.951
5XWD	D_ARG_61	NH1	D_GLU_79	OE2	3.685
5XWD	D_ARG_61	NH2	D_ASP_82	OD1	3.092
5XWD	D_ARG_61	NH2	D_ASP_82	OD2	2.961
5YC5	A_LYS_248	NZ	A_GLU_380	OE1	3.797
5YC5	A_LYS_248	NZ	A_GLU_380	OE2	2.893
5YC5	A_ARG_255	NH2	A_ASP_249	OD2	2.780
5YC5	A_HIS_268	NE2	A_GLU_294	OE1	3.378
5YC5	A_LYS_317	NZ	A_ASP_312	OD1	3.804
5YC5	A_LYS_320	NZ	A_GLU_333	OE1	3.131
5YC5	A_LYS_320	NZ	A_GLU_333	OE2	3.746
5YC5	A_LYS_322	NZ	A_GLU_333	OE2	3.405
5YC5	A_LYS_338	NZ	A_GLU_430	OE1	3.617
5YC5	A_LYS_338	NZ	A_GLU_430	OE2	3.041
5YC5	A_LYS_340	NZ	A_GLU_318	OE2	3.537
5YC5	A_ARG_344	NH2	A_ASP_401	OD1	3.750
5YC5	A_ARG_344	NH2	A_ASP_401	OD2	3.122
5YC5	A_LYS_409	NZ	B_ASP_399	OD1	3.635
5YC5	A_LYS_409	NZ	B_ASP_399	OD2	2.875

5YC5	A_ARG_416	NH1	A_GLU_388	OE1	3.188
5YC5	A_ARG_416	NH1	A_GLU_388	OE2	3.570
5YC5	A_ARG_416	NH2	A_GLU_388	OE2	2.991
5YC5	A_LYS_439	NZ	B_ASP_356	OD1	3.309
5YC5	B_LYS_248	NZ	B_GLU_380	OE1	3.889
5YC5	B_LYS_248	NZ	B_GLU_380	OE2	2.644
5YC5	B_ARG_255	NH2	B_ASP_249	OD1	3.838
5YC5	B_HIS_268	NE2	B_GLU_294	OE1	2.811
5YC5	B_HIS_268	NE2	B_GLU_294	OE2	3.075
5YC5	B_HIS_285	ND1	B_GLU_283	OE2	3.786
5YC5	B_LYS_317	NZ	B_ASP_312	OD1	3.231
5YC5	B_LYS_320	NZ	B_GLU_333	OE1	3.707
5YC5	B_LYS_338	NZ	B_GLU_430	OE1	3.390
5YC5	B_LYS_338	NZ	B_GLU_430	OE2	3.171
5YC5	B_LYS_340	NZ	B_GLU_318	OE2	3.467
5YC5	B_ARG_344	NH2	B_ASP_401	OD1	3.756
5YC5	B_ARG_344	NH2	B_ASP_401	OD2	2.965
5YC5	B_LYS_409	NZ	A_ASP_399	OD1	3.731
5YC5	B_LYS_409	NZ	A_ASP_399	OD2	2.920
5YC5	B_ARG_416	NH1	B_GLU_388	OE1	2.764
5YC5	B_ARG_416	NH1	B_GLU_388	OE2	3.921
5YC5	B_ARG_416	NH2	B_GLU_388	OE1	3.687
5YC5	C_LYS_7	NZ	C_ASP_80	OD1	3.624
5YC5	C_LYS_7	NZ	C_ASP_80	OD2	3.128
5YC5	C_ARG_18	NH1	C_GLU_85	OE1	3.674
5YC5	C_HIS_87	ND1	C_GLU_166	OE1	3.687
5YC5	C_HIS_87	ND1	C_GLU_166	OE2	2.703
5YC5	C_HIS_87	NE2	C_GLU_85	OE1	3.071
5YC5	C_ARG_97	NH2	C_ASP_104	OD2	3.100
5YC5	C_HIS_107	NE2	C_ASP_138	OD2	2.605
5YC5	C_HIS_111	NE2	C_ASP_23	OD1	2.779
5YC5	C_HIS_111	NE2	C_ASP_23	OD2	2.823
5YC5	C_LYS_120	NZ	A_ASP_265	OD2	2.563
5YC5	C_ARG_130	NH1	C_ASP_148	OD1	3.773
5YC5	C_ARG_130	NH2	C_ASP_148	OD1	3.062
5YC5	C_LYS_131	NZ	A_GLU_269	OE1	3.549
5YC5	C_LYS_131	NZ	A_GLU_269	OE2	2.940
5ZV3	A_LYS_67	NZ	H_ASP_54	OD1	3.656
5ZV3	A_LYS_67	NZ	H_ASP_54	OD2	2.636
5ZV3	A_LYS_67	NZ	H_ASP_56	OD2	3.213
5ZV3	H_LYS_12	NZ	H_GLU_16	OE1	3.523
5ZV3	H_ARG_38	NH2	H_GLU_46	OE1	3.368
5ZV3	H_ARG_38	NH2	H_GLU_46	OE2	2.729
5ZV3	H_ARG_58	NH1	H_ASP_56	OD1	3.153
5ZV3	H_ARG_58	NH1	H_ASP_56	OD2	2.840
5ZV3	H_ARG_58	NH2	A_ASP_65	OD1	3.187
5ZV3	H_ARG_58	NH2	H_ASP_56	OD2	3.078
5ZV3	H_ARG_97	NH1	A_GLU_62	OE2	3.412
5ZV3	H_ARG_97	NH2	A_GLU_62	OE1	3.676
5ZV3	H_ARG_97	NH2	A_GLU_62	OE2	3.134
5ZV3	H_LYS_100	NZ	A_GLU_62	OE1	2.715
5ZV3	H_LYS_143	NZ	H_ASP_144	OD1	3.086
5ZV3	H_LYS_143	NZ	H_ASP_144	OD2	2.913
5ZV3	H_LYS_206	NZ	H_ASP_208	OD1	2.838
5ZV3	H_LYS_206	NZ	H_ASP_208	OD2	3.804
5ZV3	H_LYS_209	NZ	L_GLU_123	OE1	3.860
5ZV3	L_ARG_61	NH2	L_GLU_81	OE1	3.640
5ZV3	L_ARG_61	NH2	L_GLU_81	OE2	2.887

5ZV3	L_ARG_61	NH2	L_ASP_82	OD1	2.840
5ZV3	L_ARG_61	NH2	L_ASP_82	OD2	3.594
5ZV3	L_LYS_149	NZ	L_GLU_195	OE1	3.451
5ZV3	L_LYS_149	NZ	L_GLU_195	OE2	3.726
5ZV3	L_LYS_169	NZ	L_ASP_167	OD1	3.271
5ZV3	L_LYS_169	NZ	L_ASP_167	OD2	2.906
5ZV3	L_LYS_169	NZ	L_ASP_170	OD2	3.903
5ZV3	L_LYS_183	NZ	L_GLU_187	OE1	3.966
5ZV3	L_LYS_183	NZ	L_GLU_187	OE2	3.971
5ZV3	L_LYS_188	NZ	L_ASP_185	OD1	3.915
6A3V	A_ARG_211	NH1	A_GLU_132	OE1	3.731
6A3V	A_HIS_217	ND1	A_ASP_104	OD2	2.707
6A3V	A_HIS_217	NE2	A_GLU_219	OE2	3.407
6A3V	A_ARG_223	NH1	A_ASP_104	OD1	3.394
6A3V	B_ARG_41	NH2	B_ASP_38	OD2	2.943
6A3V	B_ARG_75	NH2	B_ASP_87	OD2	2.598
6A3V	B_HIS_93	ND1	B_ASP_105	OD1	3.013
6A3V	B_HIS_93	NE2	B_GLU_103	OE1	3.252
6A3V	B_ARG_130	NH1	B_ASP_105	OD2	2.750
6A3V	B_ARG_130	NH2	B_ASP_105	OD2	3.837
6A3V	C_ARG_223	NH1	C_ASP_104	OD2	3.845
6A3V	C_ARG_223	NH2	C_ASP_104	OD2	3.259
6A3V	C_HIS_224	NE2	C_GLU_156	OE1	3.858
6A3V	D_ARG_41	NH2	D_ASP_38	OD2	3.204
6A3V	D_ARG_73	NH1	D_ASP_87	OD1	3.159
6A3V	D_ARG_73	NH2	D_ASP_87	OD1	3.076
6A3V	D_LYS_76	NZ	D_GLU_85	OE2	3.594
6A3V	D_HIS_93	NE2	D_GLU_103	OE1	3.727
6A3V	D_LYS_129	NZ	D_ASP_105	OD2	3.162
6A3V	D_ARG_130	NH1	D_ASP_105	OD2	3.228
6A3V	D_LYS_152	NZ	D_ASP_119	OD2	3.272
6A3V	E_ARG_193	NH1	C_ASP_184	OD1	3.333
6A3V	E_ARG_211	NH1	E_GLU_132	OE1	3.556
6A3V	E_HIS_217	ND1	E_ASP_104	OD2	3.184
6A3V	E_HIS_217	NE2	E_GLU_219	OE2	3.906
6A3V	E_HIS_224	NE2	E_GLU_156	OE1	3.569
6A3V	F_ARG_75	NH2	F_ASP_87	OD2	2.816
6A3V	F_HIS_93	NE2	F_GLU_103	OE1	3.902
6A3V	F_LYS_118	NZ	F_GLU_111	OE2	3.173
6A3V	F_ARG_130	NH1	F_ASP_105	OD2	3.184
6A3V	F_ARG_130	NH2	F_ASP_105	OD2	3.490
6A3V	F_LYS_152	NZ	F_ASP_119	OD2	3.307
6A3V	G_ARG_211	NH1	G_GLU_132	OE1	3.434
6A3V	G_HIS_217	ND1	G_ASP_104	OD2	2.526
6A3V	G_ARG_223	NH1	G_ASP_104	OD1	3.210
6A3V	G_ARG_223	NH2	G_ASP_104	OD1	3.429
6A3V	G_ARG_239	NH2	G_GLU_243	OE1	3.944
6A3V	H_ARG_75	NH2	H_ASP_87	OD1	3.886
6A3V	H_ARG_75	NH2	H_ASP_87	OD2	3.340
6A3V	H_HIS_93	NE2	H_ASP_105	OD1	4.000
6A3V	I_ARG_193	NH1	K_ASP_184	OD1	3.791
6A3V	I_ARG_211	NH1	I_GLU_132	OE1	3.418
6A3V	I_ARG_211	NH2	I_GLU_132	OE1	3.588
6A3V	I_HIS_217	ND1	I_ASP_104	OD2	3.427
6A3V	I_ARG_223	NH1	I_ASP_104	OD1	3.086
6A3V	I_ARG_223	NH2	I_ASP_104	OD1	3.348
6A3V	I_ARG_223	NH2	I_ASP_104	OD2	3.799
6A3V	I_HIS_224	ND1	I_GLU_156	OE1	3.995

6A3V	J_ARG_73	NH1	J_ASP_87	OD2	3.305
6A3V	J_ARG_75	NH1	J_GLU_85	OE1	2.939
6A3V	J_ARG_75	NH1	J_GLU_85	OE2	3.776
6A3V	J_HIS_93	NE2	J_GLU_103	OE1	3.602
6A3V	J_LYS_129	NZ	J_ASP_105	OD2	3.649
6A3V	J_LYS_152	NZ	J_ASP_119	OD2	3.759
6A3V	K_ARG_211	NH1	K_GLU_132	OE1	3.841
6A3V	K_ARG_211	NH2	K_GLU_132	OE1	3.828
6A3V	K_HIS_217	ND1	K_ASP_104	OD2	3.054
6A3V	K_HIS_217	NE2	K_GLU_219	OE2	3.795
6A3V	K_ARG_223	NH1	K_ASP_104	OD1	3.294
6A3V	K_ARG_223	NH2	K_ASP_104	OD1	2.971
6A3V	K_ARG_223	NH2	K_ASP_104	OD2	3.952
6A3V	K_HIS_224	NE2	K_GLU_156	OE1	2.347
6A3V	K_ARG_239	NH1	K_GLU_243	OE1	3.687
6A3V	K_ARG_239	NH2	K_GLU_243	OE1	3.100
6A3V	L_ARG_41	NH2	L_ASP_38	OD2	2.939
6A3V	L_ARG_75	NH2	L_ASP_87	OD1	3.204
6A3V	L_ARG_75	NH2	L_ASP_87	OD2	2.988
6A3V	L_HIS_93	ND1	L_ASP_105	OD1	3.521
6A3V	L_LYS_118	NZ	L_GLU_111	OE1	3.470
6A3V	L_ARG_130	NH1	L_ASP_105	OD2	2.982
6A3V	M_ARG_211	NH1	M_GLU_132	OE1	3.246
6A3V	M_ARG_211	NH2	M_GLU_132	OE1	3.377
6A3V	M_HIS_217	ND1	M_ASP_104	OD2	3.857
6A3V	M_HIS_217	NE2	M_GLU_219	OE2	3.798
6A3V	M_ARG_223	NH2	M_ASP_104	OD1	3.607
6A3V	M_HIS_224	NE2	M_GLU_156	OE1	2.966
6A3V	N_ARG_41	NH1	N_ASP_38	OD2	3.719
6A3V	N_ARG_41	NH2	N_ASP_38	OD2	3.742
6A3V	N_ARG_73	NH1	N_ASP_87	OD2	3.095
6A3V	N_ARG_73	NH2	N_ASP_87	OD2	3.858
6A3V	N_HIS_93	NE2	N_GLU_103	OE1	3.849
6A3V	N_ARG_130	NH1	N_ASP_105	OD2	3.648
6A3V	N_LYS_144	NZ	N_ASP_142	OD2	3.634
6A3V	O_ARG_211	NH1	O_GLU_132	OE1	3.603
6A3V	O_HIS_217	NE2	O_ASP_104	OD2	3.976
6A3V	O_ARG_223	NH2	O_ASP_104	OD1	3.679
6A3V	P_ARG_41	NH1	P_ASP_38	OD2	3.282
6A3V	P_ARG_75	NH2	P_ASP_87	OD2	3.792
6A3V	P_LYS_118	NZ	P_GLU_111	OE1	3.659
6A3V	Q_ARG_211	NH1	Q_GLU_132	OE1	3.475
6A3V	Q_HIS_217	ND1	Q_ASP_104	OD2	2.963
6A3V	Q_ARG_223	NH1	Q_ASP_104	OD1	2.976
6A3V	Q_HIS_224	NE2	Q_GLU_156	OE1	3.942
6A3V	R_HIS_93	NE2	R_GLU_103	OE1	3.672
6A3V	R_LYS_118	NZ	R_GLU_111	OE1	3.192
6A3V	R_ARG_130	NH1	R_ASP_105	OD2	3.502
6A3V	S_ARG_211	NH2	S_GLU_132	OE1	3.631
6A3V	S_HIS_217	ND1	S_ASP_104	OD2	2.703
6A3V	S_HIS_217	NE2	S_GLU_219	OE2	3.257
6A3V	S_ARG_223	NH1	S_ASP_104	OD1	3.253
6A3V	S_HIS_224	NE2	S_GLU_156	OE1	3.213
6A3V	T_ARG_73	NH1	T_ASP_87	OD2	2.770
6A3V	T_ARG_73	NH2	T_ASP_87	OD2	3.434
6A3V	T_ARG_75	NH2	T_ASP_87	OD2	3.502
6A3V	T_ARG_130	NH1	T_ASP_105	OD2	3.621
6A3V	T_LYS_152	NZ	T_ASP_119	OD2	3.864

6A3V	U_ARG_193	NH1	W_ASP_184	OD1	2.218
6A3V	U_ARG_193	NH1	W_ASP_184	OD2	3.282
6A3V	U_ARG_193	NH2	W_ASP_184	OD1	3.966
6A3V	U_ARG_193	NH2	W_ASP_184	OD2	3.892
6A3V	U_HIS_217	ND1	U_ASP_104	OD2	2.618
6A3V	U_HIS_217	NE2	U_GLU_219	OE2	3.783
6A3V	U_ARG_223	NH1	U_ASP_104	OD1	2.826
6A3V	U_ARG_223	NH2	U_ASP_104	OD1	3.610
6A3V	U_ARG_223	NH2	U_ASP_104	OD2	3.971
6A3V	U_ARG_239	NH2	U_GLU_243	OE1	3.949
6A3V	V_ARG_41	NH1	V_ASP_38	OD2	3.081
6A3V	V_ARG_41	NH2	V_ASP_38	OD2	3.046
6A3V	V_ARG_73	NH2	V_ASP_87	OD2	3.990
6A3V	V_ARG_75	NH1	V_GLU_85	OE1	3.013
6A3V	V_LYS_152	NZ	V_ASP_119	OD2	3.972
6A3V	W_ARG_211	NH1	W_GLU_132	OE1	3.268
6A3V	W_ARG_211	NH2	W_GLU_132	OE1	3.360
6A3V	W_HIS_217	ND1	W_ASP_104	OD2	3.170
6A3V	W_ARG_223	NH1	W_ASP_104	OD1	2.419
6A3V	W_ARG_223	NH2	W_ASP_104	OD1	3.222
6A3V	W_ARG_223	NH2	W_ASP_104	OD2	3.772
6A3V	W_HIS_224	NE2	W_GLU_156	OE1	3.235
6A3V	W_ARG_239	NH1	W_GLU_243	OE1	3.294
6A3V	W_ARG_239	NH2	W_GLU_243	OE1	3.255
6A3V	X_ARG_41	NH1	X_ASP_38	OD2	3.260
6A3V	X_ARG_75	NH2	X_ASP_87	OD1	3.736
6A3V	X_ARG_75	NH2	X_ASP_87	OD2	2.379
6A3V	X_HIS_93	NE2	X_GLU_103	OE2	3.466
6A3V	X_LYS_152	NZ	X_ASP_119	OD2	3.649
6A3W	A_LYS_12	NZ	A_GLU_16	OE1	3.967
6A3W	A_ARG_38	NH2	A_GLU_46	OE1	3.186
6A3W	A_ARG_38	NH2	A_GLU_46	OE2	3.290
6A3W	A_ARG_98	NH1	A_ASP_104	OD1	3.876
6A3W	A_ARG_98	NH1	A_ASP_104	OD2	2.660
6A3W	B_ARG_61	NH1	B_ASP_82	OD1	2.815
6A3W	B_ARG_61	NH1	B_ASP_82	OD2	3.460
6A3W	C_ARG_73	NH1	C_ASP_87	OD1	3.716
6A3W	C_ARG_73	NH1	C_ASP_87	OD2	2.737
6A3W	C_ARG_75	NH1	C_ASP_87	OD2	3.237
6A3W	C_LYS_76	NZ	C_GLU_85	OE2	3.299
6A3W	C_HIS_93	ND1	C_ASP_105	OD1	2.579
6A3W	C_HIS_93	NE2	C_GLU_103	OE1	2.951
6A3W	C_LYS_107	NZ	E_ASP_30	OD2	3.465
6A3W	C_LYS_114	NZ	B_ASP_51	OD2	2.835
6A3W	C_ARG_134	NH1	C_ASP_127	OD1	3.596
6A3W	C_ARG_134	NH2	A_ASP_55	OD2	3.122
6A3W	C_ARG_134	NH2	C_ASP_127	OD2	3.828
6A3W	C_LYS_152	NZ	C_ASP_119	OD2	3.915
6A3W	D_ARG_38	NH2	D_GLU_46	OE1	3.287
6A3W	D_ARG_38	NH2	D_GLU_46	OE2	3.072
6A3W	D_LYS_43	NZ	K_ASP_26	OD1	2.407
6A3W	D_LYS_43	NZ	K_ASP_26	OD2	3.696
6A3W	D_ARG_98	NH1	D_ASP_104	OD1	3.875
6A3W	D_ARG_98	NH1	D_ASP_104	OD2	2.630
6A3W	E_ARG_61	NH1	E_ASP_82	OD1	2.951
6A3W	E_ARG_61	NH1	E_ASP_82	OD2	3.557
6A3W	F_ARG_73	NH1	F_ASP_87	OD1	3.885
6A3W	F_ARG_75	NH1	F_GLU_85	OE2	2.970

6A3W	F_ARG_75	NH2	F_GLU_85	OE1	3.905
6A3W	F_ARG_75	NH2	F_GLU_85	OE2	2.751
6A3W	F_LYS_76	NZ	F_GLU_85	OE2	3.766
6A3W	F_HIS_93	ND1	F_ASP_105	OD1	2.524
6A3W	F_HIS_93	NE2	F_GLU_103	OE1	2.635
6A3W	F_LYS_114	NZ	E_ASP_51	OD2	2.834
6A3W	F_ARG_134	NH1	F_ASP_127	OD1	3.399
6A3W	F_ARG_134	NH1	F_ASP_127	OD2	3.721
6A3W	F_ARG_134	NH2	D_ASP_55	OD1	3.962
6A3W	F_ARG_134	NH2	D_ASP_55	OD2	2.895
6A3W	F_LYS_152	NZ	F_ASP_119	OD2	3.783
6A3W	G_ARG_38	NH2	G_GLU_46	OE1	3.389
6A3W	G_ARG_38	NH2	G_GLU_46	OE2	3.208
6A3W	G_ARG_98	NH1	G_ASP_104	OD1	3.869
6A3W	G_ARG_98	NH1	G_ASP_104	OD2	2.668
6A3W	H_ARG_61	NH1	H_ASP_82	OD1	2.906
6A3W	H_ARG_61	NH1	H_ASP_82	OD2	3.552
6A3W	L_ARG_73	NH1	L_ASP_87	OD1	2.942
6A3W	L_ARG_73	NH1	L_ASP_87	OD2	3.979
6A3W	L_ARG_75	NH1	L_GLU_85	OE1	2.824
6A3W	L_ARG_75	NH2	L_GLU_85	OE1	2.900
6A3W	L_HIS_93	ND1	L_ASP_105	OD1	2.434
6A3W	L_HIS_93	NE2	L_GLU_103	OE1	3.040
6A3W	L_LYS_114	NZ	H_ASP_51	OD2	2.757
6A3W	L_LYS_115	NZ	L_ASP_119	OD1	3.708
6A3W	L_LYS_115	NZ	L_ASP_119	OD2	3.946
6A3W	L_ARG_134	NH1	L_ASP_127	OD1	2.960
6A3W	L_ARG_134	NH1	L_ASP_127	OD2	3.787
6A3W	L_ARG_134	NH2	G_ASP_55	OD1	3.740
6A3W	L_ARG_134	NH2	G_ASP_55	OD2	2.630
6A3W	L_ARG_154	NH1	E_ASP_26	OD1	2.965
6A3W	L_ARG_154	NH2	E_ASP_26	OD1	3.042
6A3W	J_ARG_38	NH2	J_GLU_46	OE1	3.258
6A3W	J_ARG_38	NH2	J_GLU_46	OE2	2.995
6A3W	J_ARG_98	NH1	J_ASP_104	OD1	3.897
6A3W	J_ARG_98	NH1	J_ASP_104	OD2	2.584
6A3W	K_ARG_61	NH1	K_ASP_82	OD1	2.841
6A3W	K_ARG_61	NH1	K_ASP_82	OD2	3.357
6A3W	K_LYS_105	NZ	K_GLU_83	OE2	3.649
6A3W	L_ARG_73	NH1	L_ASP_87	OD1	2.207
6A3W	L_ARG_73	NH1	L_ASP_87	OD2	3.450
6A3W	L_ARG_75	NH1	L_GLU_85	OE1	2.429
6A3W	L_ARG_75	NH2	L_GLU_85	OE1	3.919
6A3W	L_HIS_93	ND1	L_ASP_105	OD1	2.405
6A3W	L_HIS_93	NE2	L_GLU_103	OE1	2.765
6A3W	L_LYS_107	NZ	H_ASP_30	OD1	3.282
6A3W	L_LYS_107	NZ	H_ASP_30	OD2	2.525
6A3W	L_LYS_114	NZ	K_ASP_51	OD2	2.893
6A3W	L_ARG_134	NH1	L_ASP_127	OD1	3.199
6A3W	L_ARG_134	NH1	L_ASP_127	OD2	3.994
6A3W	L_ARG_134	NH2	J_ASP_55	OD1	3.749
6A3W	L_ARG_134	NH2	J_ASP_55	OD2	2.496
6A3W	L_LYS_152	NZ	L_GLU_153	OE1	2.608
6A76	L_ARG_61	NH1	L_ASP_82	OD1	3.683
6A76	L_ARG_61	NH1	L_ASP_82	OD2	2.680
6A76	L_ARG_61	NH2	L_ASP_82	OD1	3.015
6A76	L_ARG_61	NH2	L_ASP_82	OD2	3.572
6A76	L_LYS_103	NZ	L_ASP_165	OD1	3.109

6A76	L_LYS_142	NZ	L_GLU_105	OE2	3.334
6A76	L_LYS_149	NZ	L_GLU_195	OE1	3.105
6A76	L_LYS_149	NZ	L_GLU_195	OE2	3.126
6A76	L_ARG_155	NH1	L_GLU_185	OE1	3.296
6A76	L_ARG_155	NH1	L_GLU_185	OE2	3.384
6A76	L_LYS_183	NZ	L_GLU_187	OE1	3.631
6A76	L_LYS_183	NZ	L_GLU_187	OE2	3.456
6A76	L_ARG_188	NH1	L_ASP_184	OD1	3.485
6A76	L_HIS_189	ND1	L_ASP_151	OD2	3.115
6A76	L_HIS_189	NE2	L_GLU_185	OE2	3.849
6A76	L_LYS_199	NZ	L_ASP_110	OD1	3.384
6A76	H_ARG_36	NH1	H_GLU_44	OE1	2.863
6A76	H_ARG_36	NH1	H_ASP_88	OD2	3.886
6A76	H_ARG_36	NH2	H_ASP_88	OD2	2.856
6A76	H_ARG_42	NH1	H_ASP_40	OD1	3.023
6A76	H_ARG_65	NH1	H_ASP_88	OD1	2.744
6A76	H_ARG_65	NH1	H_ASP_88	OD2	3.775
6A76	H_ARG_65	NH2	H_ASP_88	OD1	3.457
6A76	H_ARG_65	NH2	H_ASP_88	OD2	2.986
6A76	H_LYS_74	NZ	H_ASP_71	OD2	3.113
6A76	H_ARG_96	NH1	H_ASP_108	OD1	3.592
6A76	H_ARG_96	NH1	H_ASP_108	OD2	2.860
6A76	H_LYS_213	NZ	L_GLU_123	OE1	3.460
6A77	A_LYS_44	NZ	A_ASP_45	OD2	3.622
6A77	A_ARG_55	NH1	A_ASP_73	OD1	3.618
6A77	A_ARG_55	NH1	A_ASP_73	OD2	2.774
6A77	A_ARG_55	NH2	A_ASP_53	OD2	3.164
6A77	A_ARG_55	NH2	A_ASP_73	OD1	2.879
6A77	A_ARG_55	NH2	A_ASP_73	OD2	3.609
6A77	A_ARG_67	NH1	H_GLU_97	OE1	2.680
6A77	A_ARG_67	NH2	H_GLU_97	OE1	3.115
6A77	A_ARG_67	NH2	H_GLU_97	OE2	3.032
6A77	L_LYS_39	NZ	L_ASP_81	OD1	2.939
6A77	L_LYS_39	NZ	L_ASP_81	OD2	3.685
6A77	L_LYS_58	NZ	L_ASP_57	OD2	3.665
6A77	L_ARG_61	NH1	L_ASP_82	OD1	3.988
6A77	L_ARG_61	NH1	L_ASP_82	OD2	2.871
6A77	L_ARG_61	NH2	L_ASP_82	OD1	3.242
6A77	L_ARG_61	NH2	L_ASP_82	OD2	3.518
6A77	L_LYS_103	NZ	L_ASP_165	OD1	2.895
6A77	L_LYS_149	NZ	L_GLU_195	OE2	3.578
6A77	L_ARG_155	NH1	L_GLU_185	OE1	3.397
6A77	L_ARG_155	NH1	L_GLU_185	OE2	3.437
6A77	L_HIS_189	ND1	L_ASP_151	OD2	2.718
6A77	L_LYS_199	NZ	L_ASP_110	OD1	3.833
6A77	H_ARG_36	NH1	H_GLU_44	OE1	2.723
6A77	H_ARG_36	NH1	H_ASP_88	OD2	3.780
6A77	H_ARG_36	NH2	H_ASP_88	OD2	2.740
6A77	H_ARG_42	NH1	H_ASP_40	OD1	3.854
6A77	H_ARG_65	NH1	H_ASP_88	OD1	2.999
6A77	H_ARG_65	NH1	H_ASP_88	OD2	3.898
6A77	H_ARG_65	NH2	H_ASP_88	OD1	3.615
6A77	H_ARG_65	NH2	H_ASP_88	OD2	3.124
6A77	H_LYS_74	NZ	H_ASP_71	OD2	3.837
6A77	H_ARG_96	NH1	H_ASP_108	OD1	3.281
6A77	H_ARG_96	NH1	H_ASP_108	OD2	2.697
6A78	A_LYS_44	NZ	A_ASP_45	OD2	2.854
6A78	A_ARG_55	NH1	A_ASP_73	OD1	3.832

6A78	A_ARG.55	NH1	A_ASP.73	OD2	2.833
6A78	A_ARG.55	NH2	A_ASP.73	OD1	2.906
6A78	A_ARG.55	NH2	A_ASP.73	OD2	3.320
6A78	A_LYS.57	NZ	H_GLU.97	OE1	3.795
6A78	L_ARG.61	NH1	L_ASP.82	OD1	3.686
6A78	L_ARG.61	NH1	L_ASP.82	OD2	2.718
6A78	L_ARG.61	NH2	L_ASP.82	OD1	2.728
6A78	L_ARG.61	NH2	L_ASP.82	OD2	3.282
6A78	L_HIS.79	NE2	L_ASP.81	OD1	3.422
6A78	L_HIS.79	NE2	L_ASP.81	OD2	3.962
6A78	L_LYS.103	NZ	L_GLU.105	OE1	3.231
6A78	H_ARG.36	NH1	H_GLU.44	OE1	2.888
6A78	H_ARG.36	NH1	H_ASP.88	OD2	3.771
6A78	H_ARG.36	NH2	H_ASP.88	OD2	2.790
6A78	H_ARG.42	NH1	H_ASP.40	OD1	2.849
6A78	H_ARG.42	NH2	H_ASP.40	OD1	3.906
6A78	H_ARG.65	NH1	H_ASP.88	OD1	2.758
6A78	H_ARG.65	NH1	H_ASP.88	OD2	3.837
6A78	H_ARG.65	NH2	H_ASP.88	OD1	3.387
6A78	H_ARG.65	NH2	H_ASP.88	OD2	2.998
6A78	H_LYS.85	NZ	H_GLU.87	OE1	2.690
6A78	H_LYS.85	NZ	H_GLU.87	OE2	2.968
6A78	H_ARG.96	NH1	H_ASP.108	OD1	3.531
6A78	H_ARG.96	NH1	H_ASP.108	OD2	2.835
6A78	B_LYS.44	NZ	B_ASP.45	OD2	2.857
6A78	B_ARG.55	NH1	B_ASP.73	OD1	3.872
6A78	B_ARG.55	NH1	B_ASP.73	OD2	2.818
6A78	B_ARG.55	NH2	B_ASP.73	OD1	2.889
6A78	B_ARG.55	NH2	B_ASP.73	OD2	3.230
6A78	M_ARG.61	NH1	M_ASP.82	OD1	3.726
6A78	M_ARG.61	NH1	M_ASP.82	OD2	2.765
6A78	M_ARG.61	NH2	M_ASP.82	OD1	2.709
6A78	M_ARG.61	NH2	M_ASP.82	OD2	3.204
6A78	M_HIS.79	NE2	M_ASP.81	OD1	3.457
6A78	M_LYS.103	NZ	M_GLU.105	OE1	2.516
6A78	L_ARG.36	NH1	L_GLU.44	OE1	2.879
6A78	L_ARG.36	NH1	L_ASP.88	OD2	3.824
6A78	L_ARG.36	NH2	L_ASP.88	OD2	2.775
6A78	L_ARG.42	NH1	L_ASP.40	OD1	3.724
6A78	L_LYS.63	NZ	B_ASP.23	OD1	3.699
6A78	L_ARG.65	NH1	L_ASP.88	OD1	2.785
6A78	L_ARG.65	NH1	L_ASP.88	OD2	3.893
6A78	L_ARG.65	NH2	L_ASP.88	OD1	3.383
6A78	L_ARG.65	NH2	L_ASP.88	OD2	3.054
6A78	L_LYS.85	NZ	L_GLU.87	OE1	3.246
6A78	L_LYS.85	NZ	L_GLU.87	OE2	3.483
6A78	L_ARG.96	NH1	L_ASP.108	OD1	3.557
6A78	L_ARG.96	NH1	L_ASP.108	OD2	2.895
6A79	A_LYS.44	NZ	A_ASP.45	OD2	2.831
6A79	A_ARG.55	NH1	A_ASP.73	OD1	3.891
6A79	A_ARG.55	NH1	A_ASP.73	OD2	2.680
6A79	A_ARG.55	NH2	A_ASP.73	OD1	3.082
6A79	A_ARG.55	NH2	A_ASP.73	OD2	3.256
6A79	L_ARG.61	NH1	L_ASP.82	OD1	3.024
6A79	L_ARG.61	NH1	L_ASP.82	OD2	2.736
6A79	L_ARG.61	NH2	L_ASP.82	OD1	2.726
6A79	L_ARG.61	NH2	L_ASP.82	OD2	3.768
6A79	L_HIS.79	NE2	L_ASP.81	OD1	3.224

6A79	L_HIS_79	NE2	L_ASP_81	OD2	3.424
6A79	L_LYS_103	NZ	L_GLU_105	OE1	2.597
6A79	H_ARG_36	NH1	H_GLU_44	OE1	3.267
6A79	H_ARG_36	NH1	H_GLU_44	OE2	3.458
6A79	H_ARG_36	NH1	H_ASP_88	OD1	3.347
6A79	H_ARG_36	NH2	H_ASP_88	OD1	2.770
6A79	H_ARG_42	NH1	H_ASP_40	OD2	3.039
6A79	H_ARG_42	NH2	H_ASP_40	OD2	3.868
6A79	H_ARG_65	NH1	H_ASP_88	OD2	3.054
6A79	H_ARG_65	NH2	H_ASP_88	OD1	3.293
6A79	H_ARG_65	NH2	H_ASP_88	OD2	3.419
6A79	H_LYS_85	NZ	H_GLU_87	OE1	3.696
6A79	H_LYS_85	NZ	H_GLU_87	OE2	2.564
6A79	H_ARG_96	NH1	H_ASP_108	OD1	3.338
6A79	H_ARG_96	NH1	H_ASP_108	OD2	2.871
6A79	B_LYS_44	NZ	B_ASP_45	OD2	2.762
6A79	B_ARG_55	NH1	B_ASP_73	OD1	3.944
6A79	B_ARG_55	NH1	B_ASP_73	OD2	2.685
6A79	B_ARG_55	NH2	B_ASP_73	OD1	3.213
6A79	B_ARG_55	NH2	B_ASP_73	OD2	3.130
6A79	B_ARG_67	NH1	L_GLU_97	OE2	3.582
6A79	M_ARG_61	NH1	M_ASP_82	OD1	3.110
6A79	M_ARG_61	NH1	M_ASP_82	OD2	2.870
6A79	M_ARG_61	NH2	M_ASP_82	OD1	2.772
6A79	M_ARG_61	NH2	M_ASP_82	OD2	3.856
6A79	M_HIS_79	NE2	M_ASP_81	OD1	3.808
6A79	M_HIS_79	NE2	M_ASP_81	OD2	3.655
6A79	M_LYS_103	NZ	M_GLU_105	OE1	2.465
6A79	L_ARG_36	NH1	L_GLU_44	OE1	3.040
6A79	L_ARG_36	NH1	L_GLU_44	OE2	3.647
6A79	L_ARG_36	NH1	L_ASP_88	OD1	3.777
6A79	L_ARG_36	NH2	L_ASP_88	OD1	2.864
6A79	L_ARG_42	NH1	L_ASP_40	OD2	3.303
6A79	L_ARG_42	NH2	L_ASP_40	OD2	3.939
6A79	L_ARG_65	NH1	L_ASP_88	OD2	2.883
6A79	L_ARG_65	NH2	L_ASP_88	OD1	3.193
6A79	L_ARG_65	NH2	L_ASP_88	OD2	3.477
6A79	L_LYS_85	NZ	L_GLU_87	OE1	3.709
6A79	L_LYS_85	NZ	L_GLU_87	OE2	2.725
6A79	L_ARG_96	NH1	L_ASP_108	OD1	3.351
6A79	L_ARG_96	NH1	L_ASP_108	OD2	2.910
6AL5	A_LYS_155	NZ	H_GLU_74	OE1	3.542
6AL5	A_ARG_163	NH1	A_ASP_162	OD1	3.779
6AL5	A_ARG_163	NH1	A_ASP_162	OD2	2.756
6AL5	A_ARG_163	NH2	A_ASP_162	OD2	3.912
6AL5	A_HIS_218	NE2	A_GLU_120	OE1	3.847
6AL5	A_HIS_218	NE2	A_GLU_120	OE2	3.910
6AL5	A_LYS_220	NZ	H_ASP_55	OD1	3.389
6AL5	A_LYS_220	NZ	H_ASP_55	OD2	2.832
6AL5	A_LYS_220	NZ	H_ASP_57	OD2	3.301
6AL5	A_ARG_237	NH1	A_ASP_255	OD1	3.153
6AL5	A_ARG_237	NH1	A_ASP_255	OD2	2.798
6AL5	A_ARG_277	NH2	A_ASP_32	OD1	2.744
6AL5	L_ARG_65	NH2	L_ASP_86	OD1	3.023
6AL5	L_ARG_65	NH2	L_ASP_86	OD2	3.003
6AL5	L_LYS_107	NZ	L_GLU_109	OE1	3.519
6AL5	L_LYS_107	NZ	L_GLU_169	OE1	3.283
6AL5	L_LYS_107	NZ	L_GLU_169	OE2	3.574

6AL5	L_ARG_146	NH1	L_GLU_109	OE1	2.818
6AL5	L_LYS_153	NZ	L_GLU_199	OE2	3.184
6AL5	L_LYS_187	NZ	L_GLU_191	OE2	3.556
6AL5	L_HIS_193	ND1	L_ASP_189	OD1	3.737
6AL5	H_ARG_38	NH1	H_ASP_90	OD1	3.791
6AL5	H_ARG_38	NH2	H_GLU_46	OE1	3.814
6AL5	H_ARG_67	NH1	H_ASP_90	OD1	3.408
6AL5	H_ARG_67	NH1	H_ASP_90	OD2	3.019
6AL5	H_ARG_67	NH2	H_ASP_90	OD1	3.382
6AL5	H_ARG_98	NH2	H_ASP_112	OD1	3.627
6AL5	H_ARG_98	NH2	H_ASP_112	OD2	2.814
6AL5	H_ARG_106	NH1	H_GLU_100	OE1	3.206
6AL5	H_ARG_106	NH1	H_GLU_100	OE2	2.772
6AL5	H_ARG_106	NH2	L_ASP_54	OD1	3.142
6AL5	H_ARG_106	NH2	L_ASP_54	OD2	3.298
6AL5	H_ARG_106	NH2	H_GLU_100	OE2	3.102
6AL5	H_LYS_154	NZ	H_ASP_155	OD1	3.510
6AL5	H_LYS_154	NZ	H_ASP_155	OD2	3.733
6AL5	H_LYS_220	NZ	L_GLU_127	OE1	3.220
6AL5	H_LYS_221	NZ	H_GLU_223	OE2	3.651
6ANA	H_LYS_64	NZ	H_ASP_65	OD1	3.910
6ANA	H_LYS_64	NZ	H_ASP_65	OD2	2.779
6ANA	H_LYS_66	NZ	H_ASP_86	OD1	3.581
6ANA	H_LYS_66	NZ	H_ASP_86	OD2	2.714
6ANA	H_ARG_94	NH2	H_ASP_96	OD1	3.718
6ANA	H_ARG_94	NH2	H_ASP_96	OD2	3.967
6ANA	H_LYS_142	NZ	H_ASP_143	OD1	3.131
6ANA	H_LYS_142	NZ	H_ASP_143	OD2	2.790
6ANA	H_ARG_209	NH1	H_GLU_211	OE1	3.669
6ANA	L_ARG_61	NH2	L_ASP_82	OD1	2.820
6ANA	L_ARG_61	NH2	L_ASP_82	OD2	3.661
6ANA	L_LYS_102	NZ	L_GLU_104	OE2	2.841
6ANA	L_LYS_148	NZ	L_GLU_194	OE2	2.623
6ANA	L_LYS_182	NZ	L_GLU_186	OE1	2.943
6ANA	L_LYS_182	NZ	L_GLU_186	OE2	3.303
6ANA	L_LYS_187	NZ	L_ASP_184	OD1	2.815
6ANA	L_LYS_189	NZ	L_GLU_212	OE2	2.496
6AND	H_ARG_38	NH1	H_GLU_46	OE2	2.978
6AND	H_ARG_38	NH1	H_ASP_86	OD1	3.864
6AND	H_ARG_38	NH2	H_ASP_86	OD1	2.906
6AND	H_ARG_50	NH2	H_ASP_95	OD1	3.873
6AND	H_ARG_50	NH2	H_ASP_95	OD2	3.421
6AND	H_LYS_62	NZ	H_GLU_46	OE1	2.841
6AND	H_LYS_62	NZ	H_GLU_46	OE2	3.776
6AND	H_ARG_66	NH1	H_ASP_86	OD1	3.755
6AND	H_ARG_66	NH1	H_ASP_86	OD2	2.814
6AND	H_ARG_66	NH2	H_ASP_86	OD1	2.852
6AND	H_ARG_66	NH2	H_ASP_86	OD2	3.248
6AND	H_ARG_94	NH2	H_ASP_101	OD1	3.615
6AND	H_ARG_94	NH2	H_ASP_101	OD2	2.990
6AND	H_LYS_143	NZ	H_ASP_144	OD1	3.840
6AND	H_LYS_209	NZ	L_GLU_123	OE1	2.684
6AND	H_LYS_209	NZ	L_GLU_123	OE2	3.876
6AND	L_LYS_50	NZ	H_ASP_100	OD1	3.188
6AND	L_ARG_61	NH2	L_GLU_81	OE2	3.449
6AND	L_ARG_61	NH2	L_ASP_82	OD1	2.730
6AND	L_ARG_61	NH2	L_ASP_82	OD2	3.513
6AND	L_LYS_103	NZ	L_GLU_165	OE1	3.616

6AND	L_LYS_103	NZ	L_GLU_165	OE2	3.146
6AND	L_LYS_149	NZ	L_GLU_195	OE2	2.858
6AND	L_LYS_188	NZ	L_ASP_185	OD1	3.465
6AND	L_HIS_189	ND1	L_ASP_151	OD2	3.034
6ANI	H_HIS_35	ND1	H_GLU_50	OE1	3.692
6ANI	H_HIS_35	NE2	H_GLU_50	OE1	3.990
6ANI	H_LYS_66	NZ	H_ASP_86	OD1	3.842
6ANI	H_LYS_66	NZ	H_ASP_86	OD2	3.014
6ANI	H_ARG_83	NH2	H_ASP_85	OD2	3.086
6ANI	H_ARG_94	NH2	H_ASP_101	OD1	3.640
6ANI	H_ARG_94	NH2	H_ASP_101	OD2	2.660
6ANI	H_LYS_143	NZ	H_ASP_144	OD1	3.153
6ANI	H_LYS_143	NZ	H_ASP_144	OD2	2.622
6ANI	H_LYS_209	NZ	L_GLU_123	OE1	2.397
6ANI	H_LYS_210	NZ	H_GLU_212	OE1	2.867
6ANI	L_LYS_53	NZ	L_ASP_50	OD2	2.769
6ANI	L_ARG_61	NH1	L_GLU_81	OE2	3.915
6ANI	L_ARG_61	NH2	L_GLU_81	OE2	3.089
6ANI	L_ARG_61	NH2	L_ASP_82	OD1	2.623
6ANI	L_ARG_61	NH2	L_ASP_82	OD2	3.423
6ANI	L_LYS_149	NZ	L_GLU_195	OE1	3.748
6ANI	L_LYS_188	NZ	L_ASP_185	OD1	3.446
6ANI	I_HIS_35	ND1	I_GLU_50	OE1	3.825
6ANI	I_HIS_35	NE2	I_GLU_50	OE1	3.743
6ANI	I_LYS_66	NZ	I_ASP_86	OD1	3.950
6ANI	I_LYS_66	NZ	I_ASP_86	OD2	2.953
6ANI	I_ARG_83	NH2	I_ASP_85	OD2	2.907
6ANI	I_ARG_94	NH2	I_ASP_101	OD1	3.760
6ANI	I_ARG_94	NH2	I_ASP_101	OD2	2.654
6ANI	I_LYS_143	NZ	I_ASP_144	OD1	3.006
6ANI	I_LYS_143	NZ	I_ASP_144	OD2	2.878
6ANI	I_LYS_209	NZ	M_GLU_123	OE2	3.950
6ANI	I_LYS_210	NZ	I_GLU_212	OE2	3.076
6ANI	M_LYS_53	NZ	M_ASP_50	OD2	2.878
6ANI	M_ARG_61	NH2	M_ASP_82	OD1	2.930
6ANI	M_ARG_61	NH2	M_ASP_82	OD2	3.730
6ANI	M_HIS_189	ND1	M_ASP_151	OD2	3.008
6AQ7	A_ARG_155	NH1	A_GLU_195	OE1	2.727
6AQ7	A_ARG_155	NH1	A_GLU_195	OE2	3.462
6AQ7	A_ARG_155	NH2	A_ASP_201	OD1	3.324
6AQ7	A_ARG_155	NH2	A_ASP_201	OD2	3.430
6AQ7	A_ARG_163	NH2	A_ASP_177	OD2	2.708
6AQ7	A_LYS_203	NZ	A_GLU_206	OE1	2.779
6AQ7	A_LYS_203	NZ	A_GLU_206	OE2	3.528
6AQ7	H_HIS_34	NE2	A_GLU_199	OE1	3.934
6AQ7	H_HIS_34	NE2	A_GLU_199	OE2	2.717
6AQ7	H_ARG_37	NH1	H_ASP_89	OD1	2.941
6AQ7	H_ARG_37	NH2	H_GLU_45	OE1	2.823
6AQ7	H_ARG_37	NH2	H_ASP_89	OD1	3.962
6AQ7	H_ARG_49	NH1	A_GLU_199	OE2	2.744
6AQ7	H_LYS_66	NZ	H_ASP_89	OD1	3.144
6AQ7	H_LYS_66	NZ	H_ASP_89	OD2	2.568
6AQ7	H_ARG_97	NH2	H_ASP_103	OD1	3.527
6AQ7	H_ARG_97	NH2	H_ASP_103	OD2	2.817
6AQ7	H_LYS_209	NZ	L_GLU_127	OE2	2.651
6AQ7	L_LYS_24	NZ	L_ASP_74	OD1	3.475
6AQ7	L_LYS_24	NZ	L_ASP_74	OD2	3.224
6AQ7	L_LYS_53	NZ	L_GLU_59	OE1	3.832

6AQ7	L_ARG_65	NH2	L_GLU_85	OE2	3.459
6AQ7	L_ARG_65	NH2	L_ASP_86	OD1	2.720
6AQ7	L_ARG_65	NH2	L_ASP_86	OD2	3.600
6AQ7	L_LYS_146	NZ	L_GLU_109	OE1	3.899
6AQ7	L_LYS_151	NZ	L_GLU_158	OE2	3.172
6AQ7	L_LYS_153	NZ	L_GLU_199	OE1	3.387
6AQ7	L_LYS_153	NZ	L_GLU_199	OE2	2.997
6AQ7	L_ARG_159	NH1	L_GLU_189	OE2	3.035
6AQ7	L_ARG_159	NH2	L_GLU_189	OE2	3.333
6AQ7	L_HIS_193	ND1	L_ASP_155	OD2	2.747
6AQ7	L_LYS_203	NZ	L_ASP_114	OD1	3.000
6AQ7	L_LYS_203	NZ	L_ASP_114	OD2	2.913
6ATT	A_ARG_25	NH2	A_ASP_22	OD1	3.000
6ATT	A_HIS_26	NE2	A_ASP_22	OD1	3.343
6ATT	A_ARG_76	NH1	A_ASP_54	OD1	2.778
6ATT	A_ARG_81	NH2	A_GLU_57	OE1	3.490
6ATT	A_ARG_81	NH2	A_GLU_57	OE2	3.603
6ATT	A_ARG_121	NH1	A_GLU_188	OE1	3.331
6ATT	A_ARG_121	NH1	A_ASP_189	OD1	3.785
6ATT	A_ARG_121	NH2	A_ASP_189	OD1	3.820
6ATT	A_ARG_135	NH1	A_ASP_96	OD1	3.753
6ATT	A_ARG_135	NH1	A_ASP_96	OD2	3.334
6ATT	A_ARG_135	NH2	A_ASP_96	OD2	3.651
6ATT	A_HIS_152	ND1	A_GLU_125	OE2	3.074
6ATT	A_ARG_166	NH1	A_ASP_143	OD2	3.858
6ATT	A_HIS_171	ND1	A_GLU_185	OE1	3.239
6ATT	A_ARG_204	NH1	A_GLU_125	OE1	3.451
6ATT	A_ARG_204	NH2	A_GLU_125	OE1	3.326
6ATT	A_ARG_204	NH2	A_GLU_125	OE2	3.886
6ATT	A_HIS_238	ND1	A_GLU_243	OE1	3.002
6ATT	A_HIS_238	ND1	A_GLU_243	OE2	3.743
6ATT	A_ARG_266	NH2	A_GLU_264	OE1	3.983
6ATT	A_ARG_308	NH1	A_ASP_304	OD2	3.570
6ATT	A_ARG_308	NH2	A_ASP_304	OD2	2.743
6ATT	A_HIS_	NE2	A_GLU_	OE1	2.757
6ATT	A_HIS_	NE2	A_GLU_	OE2	3.385
6ATT	A_ARG_329	NH1	A_GLU_330	OE1	3.614
6ATT	A_ARG_329	NH2	A_GLU_330	OE2	3.989
6ATT	A_ARG_	NH1	A_GLU_	OE1	2.988
6ATT	A_ARG_	NH1	A_GLU_357	OE2	3.696
6ATT	A_ARG_332	NH2	A_GLU_357	OE2	3.986
6ATT	A_LYS_	NZ	A_GLU_	OE1	3.919
6ATT	A_LYS_347	NZ	A_GLU_299	OE2	3.462
6ATT	A_LYS_347	NZ	A_GLU_383	OE2	3.837
6ATT	A_ARG_410	NH1	A_GLU_438	OE2	3.785
6ATT	A_ARG_410	NH2	A_GLU_383	OE1	3.874
6ATT	A_ARG_410	NH2	A_GLU_383	OE2	3.055
6ATT	A_ARG_412	NH1	A_GLU_299	OE1	3.365
6ATT	A_ARG_412	NH1	A_GLU_299	OE2	3.033
6ATT	A_ARG_412	NH2	A_GLU_299	OE2	3.491
6ATT	A_ARG_465	NH1	A_GLU_438	OE1	3.352
6ATT	A_ARG_477	NH1	A_GLU_485	OE1	3.071
6ATT	A_ARG_477	NH2	A_GLU_481	OE2	3.926
6ATT	A_ARG_477	NH2	A_GLU_485	OE1	3.540
6ATT	A_ARG_	NH1	A_GLU_	OE1	2.803
6ATT	A_ARG_	NH1	A_GLU_	OE2	3.745
6ATT	A_ARG_	NH1	A_GLU_	OE1	3.574
6ATT	A_ARG_	NH1	A_GLU_	OE2	2.811

6ATT	A_HIS_	ND1	A_GLU_	OE1	3.143
6ATT	A_HIS_	ND1	A_GLU_	OE2	3.018
6ATT	H_ARG_38	NH1	H_ASP_90	OD1	2.909
6ATT	H_ARG_38	NH2	H_GLU_46	OE1	3.113
6ATT	H_ARG_38	NH2	H_ASP_90	OD1	3.490
6ATT	H_ARG_67	NH1	H_ASP_90	OD1	3.630
6ATT	H_ARG_67	NH1	H_ASP_90	OD2	2.692
6ATT	H_ARG_67	NH2	H_ASP_90	OD1	3.064
6ATT	H_ARG_67	NH2	H_ASP_90	OD2	3.552
6ATT	H_ARG_98	NH2	H_ASP_109	OD2	3.700
6ATT	H_LYS_151	NZ	H_ASP_152	OD1	3.592
6ATT	H_LYS_151	NZ	H_ASP_152	OD2	3.811
6ATT	H_LYS_217	NZ	L_GLU_129	OE1	3.069
6ATT	H_ARG_218	NH1	H_GLU_220	OE2	2.838
6ATT	H_LYS_222	NZ	L_ASP_128	OD1	2.688
6ATT	L_ARG_32	NH1	A_GLU_216	OE1	2.742
6ATT	L_LYS_45	NZ	L_GLU_87	OE1	2.487
6ATT	L_ARG_67	NH1	L_GLU_85	OE1	3.360
6ATT	L_ARG_67	NH1	L_GLU_85	OE2	3.299
6ATT	L_ARG_67	NH2	L_ASP_88	OD1	2.767
6ATT	L_LYS_155	NZ	L_GLU_201	OE1	3.534
6ATT	L_LYS_155	NZ	L_GLU_201	OE2	3.250
6ATT	L_LYS_189	NZ	L_GLU_193	OE1	3.627
6ATT	L_LYS_189	NZ	L_GLU_193	OE2	3.286
6ATT	L_HIS_195	ND1	L_ASP_157	OD2	2.711
6AZZ	F_HIS_35	NE2	F_ASP_95	OD1	2.684
6AZZ	F_HIS_35	NE2	F_ASP_95	OD2	3.272
6AZZ	F_LYS_62	NZ	F_GLU_46	OE1	3.990
6AZZ	F_LYS_62	NZ	F_GLU_46	OE2	2.597
6AZZ	F_ARG_94	NH2	F_ASP_101	OD1	3.814
6AZZ	F_ARG_94	NH2	F_ASP_101	OD2	2.728
6AZZ	F_LYS_209	NZ	E_GLU_124	OE2	3.461
6AZZ	F_LYS_210	NZ	F_GLU_212	OE1	2.660
6AZZ	E_ARG_61	NH1	E_ASP_82	OD1	3.472
6AZZ	E_ARG_61	NH1	E_ASP_82	OD2	2.388
6AZZ	E_ARG_61	NH2	E_GLU_79	OE1	3.246
6AZZ	E_ARG_61	NH2	E_GLU_79	OE2	3.544
6AZZ	E_ARG_61	NH2	E_ASP_82	OD1	2.711
6AZZ	E_ARG_61	NH2	E_ASP_82	OD2	2.961
6AZZ	E_ARG_77	NH1	B_GLU_79	OE2	3.685
6AZZ	E_ARG_77	NH2	B_GLU_79	OE1	3.407
6AZZ	E_ARG_77	NH2	B_GLU_79	OE2	3.489
6AZZ	E_LYS_111	NZ	E_GLU_199	OE1	3.404
6AZZ	E_LYS_130	NZ	F_ASP_144	OD2	3.330
6AZZ	C_HIS_35	NE2	C_ASP_95	OD1	2.700
6AZZ	C_HIS_35	NE2	C_ASP_95	OD2	3.324
6AZZ	C_LYS_62	NZ	C_GLU_46	OE1	3.744
6AZZ	C_LYS_62	NZ	C_GLU_46	OE2	2.907
6AZZ	C_ARG_94	NH2	C_ASP_101	OD1	3.926
6AZZ	C_ARG_94	NH2	C_ASP_101	OD2	2.919
6AZZ	C_LYS_209	NZ	B_GLU_124	OE1	3.784
6AZZ	C_LYS_209	NZ	B_GLU_124	OE2	2.655
6AZZ	C_LYS_210	NZ	C_GLU_212	OE1	2.801
6AZZ	B_LYS_31	NZ	B_ASP_92	OD1	3.992
6AZZ	B_ARG_61	NH1	B_GLU_79	OE2	3.665
6AZZ	B_ARG_61	NH2	B_GLU_79	OE1	3.459
6AZZ	B_ARG_61	NH2	B_GLU_79	OE2	3.381
6AZZ	B_ARG_61	NH2	B_ASP_82	OD1	2.944

6AZZ	B_ARG_61	NH2	B_ASP_82	OD2	3.568
6AZZ	B_LYS_111	NZ	B_GLU_199	OE1	3.484
6AZZ	B_LYS_130	NZ	C_ASP_144	OD2	3.121
6AZZ	A_HIS_20	NE2	A_GLU_22	OE1	2.799
6AZZ	A_LYS_90	NZ	B_ASP_51	OD1	3.552
6AZZ	A_LYS_90	NZ	B_ASP_51	OD2	2.501
6AZZ	A_LYS_98	NZ	A_GLU_22	OE1	2.677
6AZZ	A_LYS_98	NZ	A_GLU_22	OE2	3.134
6AZZ	A_LYS_108	NZ	B_ASP_53	OD2	3.868
6AZZ	A_LYS_108	NZ	A_GLU_88	OE2	3.991
6AZZ	A_LYS_118	NZ	A_ASP_131	OD1	2.501
6AZZ	A_LYS_139	NZ	A_ASP_6	OD1	2.975
6AZZ	D_LYS_10	NZ	D_GLU_35	OE2	3.455
6AZZ	D_ARG_11	NH1	D_GLU_26	OE1	3.991
6AZZ	D_HIS_20	NE2	D_GLU_22	OE1	2.833
6AZZ	D_LYS_90	NZ	E_ASP_51	OD1	3.639
6AZZ	D_LYS_90	NZ	E_ASP_51	OD2	2.901
6AZZ	D_LYS_98	NZ	D_GLU_22	OE1	2.924
6AZZ	D_LYS_98	NZ	D_GLU_22	OE2	3.312
6AZZ	D_LYS_118	NZ	D_ASP_131	OD1	2.526
6AZZ	D_LYS_139	NZ	D_ASP_6	OD1	3.014
6AZZ	D_LYS_139	NZ	D_ASP_6	OD2	3.993
6B08	C_HIS_35	NE2	C_ASP_95	OD1	2.543
6B08	C_HIS_35	NE2	C_ASP_95	OD2	3.235
6B08	C_ARG_38	NH2	C_GLU_46	OE1	3.451
6B08	C_ARG_94	NH2	C_ASP_101	OD1	3.885
6B08	C_ARG_94	NH2	C_ASP_101	OD2	2.821
6B08	C_LYS_143	NZ	B_GLU_125	OE2	2.599
6B08	B_LYS_31	NZ	B_ASP_92	OD2	3.730
6B08	B_ARG_61	NH1	B_GLU_79	OE2	3.112
6B08	B_ARG_61	NH2	B_ASP_82	OD1	2.963
6B08	B_ARG_61	NH2	B_ASP_82	OD2	2.912
6B08	B_LYS_167	NZ	B_GLU_83	OE2	3.572
6B08	A_LYS_10	NZ	A_GLU_35	OE2	3.550
6B08	A_HIS_20	NE2	A_GLU_22	OE2	2.721
6B08	A_LYS_90	NZ	B_ASP_51	OD1	2.529
6B08	A_LYS_90	NZ	B_ASP_51	OD2	3.708
6B08	A_LYS_98	NZ	A_GLU_22	OE1	3.424
6B08	A_LYS_98	NZ	A_GLU_22	OE2	2.846
6B08	A_LYS_118	NZ	A_ASP_131	OD1	3.348
6B08	A_LYS_142	NZ	A_GLU_145	OE1	2.917
6B08	A_LYS_142	NZ	A_GLU_145	OE2	3.424
6B0A	H_ARG_38	NH1	H_ASP_90	OD1	3.014
6B0A	H_ARG_38	NH2	H_GLU_46	OE2	3.036
6B0A	H_ARG_38	NH2	H_ASP_90	OD1	3.967
6B0A	H_LYS_65	NZ	H_ASP_62	OD1	3.558
6B0A	H_ARG_67	NH1	H_ASP_90	OD1	3.030
6B0A	H_ARG_67	NH1	H_ASP_90	OD2	2.551
6B0A	H_ARG_67	NH2	H_ASP_90	OD1	3.040
6B0A	H_ARG_67	NH2	H_ASP_90	OD2	3.966
6B0A	H_LYS_98	NZ	H_ASP_100	OD1	3.067
6B0A	H_LYS_98	NZ	H_ASP_113	OD1	3.416
6B0A	H_LYS_98	NZ	H_ASP_113	OD2	3.062
6B0A	H_LYS_218	NZ	H_ASP_220	OD1	3.753
6B0A	L_ARG_62	NH1	L_GLU_80	OE1	3.743
6B0A	L_ARG_62	NH1	L_GLU_80	OE2	3.406
6B0A	L_ARG_62	NH2	L_GLU_80	OE2	3.228
6B0A	L_ARG_62	NH2	L_GLU_82	OE1	3.824

6B0A	L_ARG_62	NH2	L_ASP_83	OD1	2.621
6B0A	L_ARG_62	NH2	L_ASP_83	OD2	3.165
6B0A	L_ARG_101	NH1	L_GLU_103	OE1	3.058
6B0A	L_HIS_187	ND1	L_ASP_149	OD2	2.488
6B0A	A_HIS_20	NE2	A_GLU_22	OE1	3.003
6B0A	A_LYS_90	NZ	A_ASP_78	OD2	3.536
6B0A	A_LYS_98	NZ	A_GLU_22	OE1	3.288
6B0A	A_LYS_98	NZ	A_GLU_22	OE2	2.898
6B0A	A_LYS_118	NZ	A_ASP_131	OD1	2.522
6B0E	A_ARG_46	NH2	A_ASP_55	OD1	3.681
6B0E	A_ARG_46	NH2	A_ASP_55	OD2	2.616
6B0E	A_ARG_54	NH2	A_ASP_60	OD1	3.407
6B0E	A_ARG_61	NH1	A_GLU_81	OE2	2.864
6B0E	A_ARG_61	NH1	A_ASP_82	OD1	2.718
6B0E	A_ARG_61	NH1	A_ASP_82	OD2	3.652
6B0E	A_ARG_61	NH2	A_GLU_79	OE1	3.681
6B0E	A_ARG_61	NH2	A_GLU_79	OE2	3.517
6B0E	A_ARG_61	NH2	A_GLU_81	OE2	3.930
6B0E	A_HIS_189	ND1	A_ASP_151	OD2	2.935
6B0E	B_ARG_38	NH1	B_ASP_86	OD1	3.019
6B0E	B_ARG_38	NH2	B_GLU_46	OE2	3.029
6B0E	B_ARG_38	NH2	B_ASP_86	OD1	3.941
6B0E	B_ARG_94	NH2	B_ASP_101	OD1	3.699
6B0E	B_ARG_94	NH2	B_ASP_101	OD2	2.508
6B0E	B_LYS_143	NZ	B_ASP_144	OD1	2.734
6B0E	B_LYS_143	NZ	B_ASP_144	OD2	3.061
6B0E	B_HIS_164	ND1	A_ASP_167	OD2	3.677
6B0E	E_HIS_20	NE2	E_GLU_22	OE1	2.862
6B0E	E_LYS_118	NZ	E_ASP_131	OD1	2.359
6B0E	E_LYS_142	NZ	E_GLU_145	OE1	3.928
6B0E	E_LYS_155	NZ	B_ASP_98	OD2	3.864
6B0G	C_ARG_24	NH1	C_ASP_70	OD1	3.644
6B0G	C_ARG_24	NH2	C_ASP_70	OD1	3.217
6B0G	C_ARG_46	NH2	C_ASP_55	OD1	3.667
6B0G	C_ARG_46	NH2	C_ASP_55	OD2	2.584
6B0G	C_ARG_54	NH2	C_ASP_60	OD1	2.717
6B0G	C_ARG_61	NH1	C_GLU_79	OE1	3.756
6B0G	C_ARG_61	NH1	C_GLU_79	OE2	3.832
6B0G	C_ARG_61	NH2	C_GLU_79	OE1	3.846
6B0G	C_ARG_61	NH2	C_ASP_82	OD1	2.542
6B0G	C_ARG_61	NH2	C_ASP_82	OD2	3.446
6B0G	C_LYS_103	NZ	C_GLU_165	OE1	3.504
6B0G	C_LYS_103	NZ	C_GLU_165	OE2	3.698
6B0G	C_LYS_149	NZ	C_GLU_195	OE1	3.121
6B0G	C_LYS_188	NZ	C_ASP_185	OD1	2.887
6B0G	C_HIS_189	ND1	C_ASP_151	OD2	3.287
6B0G	C_ARG_211	NH1	C_GLU_187	OE1	3.151
6B0G	D_ARG_38	NH1	D_ASP_86	OD1	2.889
6B0G	D_ARG_38	NH2	D_ASP_86	OD1	3.880
6B0G	D_LYS_62	NZ	D_GLU_46	OE1	3.387
6B0G	D_LYS_62	NZ	D_GLU_46	OE2	3.344
6B0G	D_ARG_66	NH1	D_ASP_86	OD1	3.686
6B0G	D_ARG_66	NH1	D_ASP_86	OD2	2.815
6B0G	D_ARG_66	NH2	D_ASP_86	OD1	2.895
6B0G	D_ARG_66	NH2	D_ASP_86	OD2	3.345
6B0G	D_ARG_82A	NH2	D_GLU_81	OE1	3.967
6B0G	D_LYS_94	NZ	D_ASP_101	OD1	3.857
6B0G	D_LYS_94	NZ	D_ASP_101	OD2	2.849

6B0G	D_ARG_100B	NH1	C_ASP_91	OD2	3.003
6B0G	D_ARG_100B	NH2	C_ASP_91	OD2	3.130
6B0G	D_LYS_148	NZ	D_ASP_149	OD1	3.128
6B0G	D_LYS_148	NZ	D_ASP_149	OD2	3.390
6B0G	D_LYS_214	NZ	C_GLU_123	OE2	3.176
6B0G	D_LYS_215	NZ	D_GLU_217	OE2	3.125
6B0G	E_ARG_11	NH1	E_GLU_39	OE2	3.696
6B0G	E_HIS_20	NE2	E_GLU_22	OE1	2.725
6B0G	E_LYS_90	NZ	E_ASP_78	OD2	3.931
6B0G	E_LYS_98	NZ	E_GLU_22	OE1	2.876
6B0G	E_LYS_98	NZ	E_GLU_22	OE2	3.660
6B0G	E_LYS_118	NZ	E_ASP_131	OD1	2.414
6B0G	E_LYS_139	NZ	E_ASP_6	OD1	2.804
6B0G	E_LYS_139	NZ	E_ASP_6	OD2	3.888
6B0G	E_LYS_155	NZ	D_ASP_98	OD2	2.837
6B0G	E_LYS_155	NZ	E_ASP_157	OD2	3.894
6B0H	I_ARG_11	NH1	I_GLU_39	OE1	2.905
6B0H	I_ARG_11	NH1	I_GLU_39	OE2	3.603
6B0H	I_ARG_11	NH2	I_GLU_39	OE1	3.421
6B0H	I_ARG_11	NH2	I_GLU_39	OE2	2.810
6B0H	I_HIS_20	NE2	I_GLU_22	OE1	2.759
6B0H	I_LYS_24	NZ	I_GLU_22	OE2	3.743
6B0H	I_LYS_90	NZ	I_ASP_78	OD2	2.698
6B0H	I_LYS_118	NZ	I_ASP_131	OD1	2.468
6B0H	I_LYS_127	NZ	I_ASP_124	OD2	3.708
6B0H	I_LYS_139	NZ	I_ASP_6	OD1	2.845
6B0H	I_LYS_139	NZ	I_ASP_6	OD2	3.883
6B0H	I_LYS_142	NZ	I_GLU_145	OE2	3.701
6B0H	I_LYS_155	NZ	I_ASP_157	OD2	3.811
6B0H	J_ARG_11	NH1	J_GLU_39	OE1	3.153
6B0H	J_ARG_11	NH1	J_GLU_39	OE2	3.697
6B0H	J_ARG_11	NH2	J_GLU_39	OE1	3.428
6B0H	J_ARG_11	NH2	J_GLU_39	OE2	2.670
6B0H	J_HIS_20	NE2	J_GLU_22	OE1	2.670
6B0H	J_LYS_24	NZ	J_GLU_22	OE2	3.866
6B0H	J_LYS_90	NZ	J_ASP_78	OD2	3.917
6B0H	J_LYS_98	NZ	J_GLU_22	OE2	3.958
6B0H	J_LYS_118	NZ	J_ASP_131	OD1	2.439
6B0H	J_LYS_127	NZ	J_ASP_124	OD1	3.354
6B0H	J_LYS_127	NZ	J_ASP_124	OD2	3.839
6B0H	J_LYS_139	NZ	J_ASP_6	OD1	3.036
6B0H	B_ARG_38	NH1	B_ASP_86	OD1	2.831
6B0H	B_ARG_38	NH2	B_GLU_46	OE1	3.367
6B0H	B_ARG_38	NH2	B_ASP_86	OD1	3.809
6B0H	B_LYS_43	NZ	B_GLU_46	OE2	3.945
6B0H	B_HIS_58	ND1	B_GLU_50	OE2	3.817
6B0H	B_ARG_66	NH1	B_ASP_86	OD1	3.737
6B0H	B_ARG_66	NH2	B_ASP_86	OD1	3.093
6B0H	B_ARG_66	NH2	B_ASP_86	OD2	2.466
6B0H	B_ARG_94	NH2	B_ASP_101	OD1	3.827
6B0H	B_ARG_94	NH2	B_ASP_101	OD2	2.750
6B0H	B_ARG_97	NH2	B_GLU_50	OE1	2.771
6B0H	B_ARG_97	NH2	B_GLU_50	OE2	3.459
6B0H	B_ARG_97	NH2	B_GLU_95	OE2	2.917
6B0H	B_LYS_144	NZ	B_ASP_145	OD1	3.326
6B0H	B_LYS_144	NZ	B_ASP_145	OD2	3.603
6B0H	D_ARG_38	NH1	D_ASP_86	OD1	2.588
6B0H	D_ARG_38	NH2	D_GLU_46	OE1	3.399

6B0H	D_ARG_38	NH2	D_ASP_86	OD1	3.688
6B0H	D_LYS_43	NZ	D_GLU_46	OE2	3.764
6B0H	D_HIS_58	ND1	D_GLU_50	OE1	3.722
6B0H	D_ARG_66	NH1	D_ASP_86	OD1	3.850
6B0H	D_ARG_66	NH1	D_ASP_86	OD2	3.946
6B0H	D_ARG_66	NH2	D_ASP_86	OD1	3.173
6B0H	D_ARG_66	NH2	D_ASP_86	OD2	2.383
6B0H	D_ARG_94	NH2	D_ASP_101	OD1	3.853
6B0H	D_ARG_94	NH2	D_ASP_101	OD2	2.885
6B0H	D_ARG_97	NH2	D_GLU_50	OE1	3.508
6B0H	D_ARG_97	NH2	D_GLU_50	OE2	2.823
6B0H	D_ARG_97	NH2	D_GLU_95	OE2	2.857
6B0H	D_LYS_144	NZ	D_ASP_145	OD1	3.294
6B0H	D_LYS_144	NZ	D_ASP_145	OD2	3.795
6B0H	D_LYS_207	NZ	D_ASP_209	OD1	3.527
6B0H	D_LYS_207	NZ	D_ASP_209	OD2	2.851
6B0H	A_ARG_61	NH1	A_GLU_81	OE2	3.989
6B0H	A_ARG_61	NH2	A_GLU_81	OE2	2.801
6B0H	A_ARG_61	NH2	A_ASP_82	OD1	2.591
6B0H	A_ARG_61	NH2	A_ASP_82	OD2	3.548
6B0H	A_LYS_149	NZ	A_GLU_195	OE1	2.772
6B0H	A_LYS_183	NZ	A_GLU_187	OE1	2.500
6B0H	A_LYS_183	NZ	A_GLU_187	OE2	3.165
6B0H	C_ARG_61	NH2	C_GLU_81	OE2	3.031
6B0H	C_ARG_61	NH2	C_ASP_82	OD1	2.583
6B0H	C_ARG_61	NH2	C_ASP_82	OD2	3.415
6B0H	C_LYS_149	NZ	C_GLU_195	OE1	2.730
6BE2	H_ARG_38	NH1	H_ASP_89	OD1	2.773
6BE2	H_ARG_38	NH2	H_GLU_46	OE1	3.073
6BE2	H_ARG_38	NH2	H_ASP_89	OD1	3.711
6BE2	H_ARG_66	NH1	H_ASP_89	OD1	3.581
6BE2	H_ARG_66	NH1	H_ASP_89	OD2	2.936
6BE2	H_ARG_66	NH2	H_ASP_89	OD1	2.937
6BE2	H_ARG_66	NH2	H_ASP_89	OD2	3.585
6BE2	H_ARG_97	NH2	H_ASP_112	OD1	3.701
6BE2	H_ARG_97	NH2	H_ASP_112	OD2	2.907
6BE2	H_LYS_154	NZ	L_GLU_129	OE2	2.747
6BE2	L_LYS_49	NZ	H_GLU_108	OE2	2.828
6BE2	L_ARG_65	NH1	L_ASP_86	OD1	3.600
6BE2	L_ARG_65	NH1	L_ASP_86	OD2	2.741
6BE2	L_ARG_65	NH2	L_ASP_86	OD1	2.925
6BE2	L_ARG_65	NH2	L_ASP_86	OD2	3.429
6BE2	L_ARG_100	NH2	H_ASP_98	OD1	2.914
6BE2	L_LYS_107	NZ	L_ASP_89	OD1	2.799
6BE2	L_LYS_107	NZ	L_ASP_89	OD2	3.237
6BE2	L_LYS_171	NZ	L_GLU_87	OE1	2.671
6BE3	H_ARG_38	NH1	H_ASP_89	OD1	2.759
6BE3	H_ARG_38	NH2	H_GLU_46	OE1	3.050
6BE3	H_ARG_38	NH2	H_ASP_89	OD1	3.706
6BE3	H_ARG_66	NH1	H_ASP_89	OD1	3.702
6BE3	H_ARG_66	NH1	H_ASP_89	OD2	3.027
6BE3	H_ARG_66	NH2	H_ASP_89	OD1	2.994
6BE3	H_ARG_66	NH2	H_ASP_89	OD2	3.609
6BE3	H_ARG_97	NH2	H_ASP_112	OD1	3.602
6BE3	H_ARG_97	NH2	H_ASP_112	OD2	2.963
6BE3	H_LYS_154	NZ	L_GLU_129	OE2	2.742
6BE3	H_LYS_220	NZ	L_GLU_128	OE1	3.265
6BE3	H_LYS_220	NZ	L_GLU_128	OE2	2.896

6BE3	L_LYS_49	NZ	H_GLU_108	OE2	2.860
6BE3	L_ARG_65	NH1	L_ASP_86	OD1	3.594
6BE3	L_ARG_65	NH1	L_ASP_86	OD2	2.669
6BE3	L_ARG_65	NH2	L_ASP_86	OD1	2.920
6BE3	L_ARG_65	NH2	L_ASP_86	OD2	3.411
6BE3	L_ARG_100	NH2	H_ASP_98	OD1	3.147
6BE3	L_ARG_100	NH2	H_ASP_109	OD1	3.865
6BE3	L_LYS_171	NZ	L_GLU_87	OE2	2.868
6BE4	H_ARG_38	NH1	H_ASP_89	OD2	2.649
6BE4	H_ARG_38	NH2	H_GLU_46	OE1	3.034
6BE4	H_ARG_38	NH2	H_ASP_89	OD2	3.562
6BE4	H_ARG_66	NH1	H_ASP_89	OD1	2.856
6BE4	H_ARG_66	NH1	H_ASP_89	OD2	3.787
6BE4	H_ARG_66	NH2	H_ASP_89	OD1	3.571
6BE4	H_ARG_66	NH2	H_ASP_89	OD2	3.108
6BE4	H_ARG_97	NH2	H_ASP_112	OD1	3.623
6BE4	H_ARG_97	NH2	H_ASP_112	OD2	3.151
6BE4	H_LYS_154	NZ	L_GLU_129	OE1	2.824
6BE4	H_LYS_221	NZ	H_GLU_223	OE2	2.728
6BE4	L_ARG_65	NH1	L_ASP_86	OD1	3.135
6BE4	L_ARG_65	NH2	L_ASP_86	OD1	3.000
6BE4	L_ARG_65	NH2	L_ASP_86	OD2	2.628
6BE4	L_ARG_100	NH2	H_ASP_98	OD1	3.253
6BE4	L_ARG_100	NH2	H_ASP_109	OD1	3.926
6BE4	L_LYS_171	NZ	L_GLU_87	OE1	3.243
6BE4	L_ARG_194	NH1	L_ASP_156	OD2	3.672
6BE4	L_ARG_194	NH2	L_ASP_156	OD1	3.622
6BE4	L_ARG_194	NH2	L_ASP_156	OD2	3.634
6BIT	L_HIS_35	NE2	H_GLU_54	OE1	3.340
6BIT	L_ARG_40	NH2	L_GLU_46	OE1	2.891
6BIT	L_ARG_50	NH1	L_GLU_57	OE1	3.032
6BIT	L_ARG_50	NH2	L_GLU_57	OE1	3.316
6BIT	L_ARG_50	NH2	H_ASP_100	OD1	3.331
6BIT	L_ARG_50	NH2	H_ASP_101	OD1	3.135
6BIT	L_ARG_50	NH2	H_ASP_101	OD2	3.871
6BIT	L_LYS_59	NZ	L_GLU_57	OE2	3.249
6BIT	L_LYS_59	NZ	H_ASP_100	OD1	3.680
6BIT	L_LYS_63	NZ	L_GLU_46	OE1	3.651
6BIT	L_LYS_63	NZ	L_GLU_46	OE2	2.777
6BIT	L_LYS_67	NZ	L_ASP_90	OD1	3.668
6BIT	L_LYS_67	NZ	L_ASP_90	OD2	3.222
6BIT	L_LYS_208	NZ	K_GLU_123	OE2	3.567
6BIT	L_ARG_213	NH1	L_ASP_143	OD1	3.423
6BIT	K_ARG_61	NH1	K_GLU_81	OE2	3.581
6BIT	K_ARG_61	NH1	K_ASP_82	OD1	2.603
6BIT	K_ARG_61	NH1	K_ASP_82	OD2	3.046
6BIT	K_ARG_61	NH2	K_GLU_81	OE2	3.311
6BIT	K_ARG_96	NH1	H_GLU_54	OE1	3.223
6BIT	K_ARG_96	NH2	H_GLU_54	OE1	2.904
6BIT	K_ARG_96	NH2	H_GLU_54	OE2	3.687
6BIT	K_LYS_103	NZ	K_ASP_165	OD1	3.785
6BIT	K_LYS_149	NZ	K_GLU_195	OE1	3.128
6BIT	K_LYS_149	NZ	K_GLU_195	OE2	3.026
6BIT	K_LYS_183	NZ	K_GLU_187	OE2	3.925
6BIT	K_LYS_199	NZ	K_ASP_110	OD1	3.991
6BIT	K_LYS_199	NZ	K_ASP_110	OD2	3.333
6BIT	H_ARG_24	NH1	H_ASP_10	OD1	2.961
6BIT	H_ARG_24	NH1	H_ASP_10	OD2	3.571

6BIT	H_ARG_40	NH2	H_GLU_47	OE1	2.715
6BIT	H_ARG_40	NH2	H_GLU_47	OE2	3.722
6BIT	H_ARG_46	NH1	H_GLU_103	OE1	2.965
6BIT	H_ARG_46	NH2	H_GLU_103	OE1	2.785
6BIT	H_LYS_53	NZ	I_ASP_52	OD1	3.518
6BIT	H_LYS_53	NZ	I_GLU_54	OE1	2.817
6BIT	H_ARG_59	NH1	H_ASP_85	OD1	2.707
6BIT	H_ARG_59	NH1	H_ASP_85	OD2	3.494
6BIT	H_ARG_59	NH2	H_ASP_85	OD1	3.485
6BIT	H_ARG_59	NH2	H_ASP_85	OD2	2.872
6BIT	H_LYS_96	NZ	I_ASP_52	OD2	2.786
6BIT	H_LYS_96	NZ	I_ASP_55	OD1	3.426
6BIT	H_LYS_96	NZ	I_ASP_55	OD2	2.655
6BIT	H_LYS_96	NZ	I_GLU_57	OE1	2.771
6BIT	H_LYS_105	NZ	H_GLU_3	OE2	2.864
6BIT	J_HIS_35	NE2	G_GLU_54	OE1	3.221
6BIT	J_ARG_40	NH1	J_GLU_89	OE1	3.452
6BIT	J_ARG_50	NH1	J_GLU_57	OE2	2.730
6BIT	J_ARG_50	NH2	J_GLU_57	OE2	3.003
6BIT	J_ARG_50	NH2	G_ASP_100	OD1	3.724
6BIT	J_ARG_50	NH2	G_ASP_101	OD1	3.330
6BIT	J_LYS_59	NZ	J_GLU_57	OE1	3.468
6BIT	J_LYS_67	NZ	J_ASP_90	OD1	3.323
6BIT	J_LYS_208	NZ	L_GLU_123	OE2	3.539
6BIT	L_ARG_61	NH1	L_GLU_81	OE2	3.351
6BIT	L_ARG_61	NH1	L_ASP_82	OD1	2.686
6BIT	L_ARG_61	NH1	L_ASP_82	OD2	3.128
6BIT	L_ARG_61	NH2	L_GLU_81	OE2	3.264
6BIT	L_ARG_96	NH1	G_GLU_54	OE1	3.007
6BIT	L_ARG_96	NH2	G_GLU_54	OE1	2.768
6BIT	L_ARG_96	NH2	G_GLU_54	OE2	3.419
6BIT	L_LYS_103	NZ	L_ASP_165	OD1	3.780
6BIT	L_LYS_169	NZ	L_ASP_167	OD1	3.582
6BIT	L_LYS_169	NZ	L_ASP_167	OD2	3.848
6BIT	L_LYS_183	NZ	L_GLU_187	OE2	3.386
6BIT	L_HIS_189	ND1	L_ASP_151	OD2	2.866
6BIT	G_ARG_24	NH2	G_ASP_10	OD1	2.805
6BIT	G_ARG_24	NH2	G_ASP_10	OD2	3.462
6BIT	G_ARG_40	NH2	G_GLU_47	OE1	2.503
6BIT	G_ARG_40	NH2	G_GLU_47	OE2	3.922
6BIT	G_ARG_46	NH1	G_GLU_103	OE1	3.088
6BIT	G_ARG_46	NH1	G_GLU_103	OE2	3.993
6BIT	G_ARG_46	NH2	G_GLU_103	OE1	2.832
6BIT	G_LYS_53	NZ	J_ASP_52	OD1	2.843
6BIT	G_LYS_53	NZ	J_ASP_52	OD2	3.656
6BIT	G_LYS_53	NZ	J_GLU_54	OE1	2.681
6BIT	G_ARG_59	NH1	G_ASP_85	OD1	3.056
6BIT	G_ARG_59	NH1	G_ASP_85	OD2	3.619
6BIT	G_ARG_59	NH2	G_ASP_85	OD1	3.597
6BIT	G_ARG_59	NH2	G_ASP_85	OD2	2.677
6BIT	G_LYS_96	NZ	J_ASP_52	OD2	2.719
6BIT	G_LYS_96	NZ	J_ASP_55	OD1	3.165
6BIT	G_LYS_96	NZ	J_ASP_55	OD2	2.701
6BIT	G_LYS_96	NZ	J_GLU_57	OE2	2.943
6BIT	G_LYS_105	NZ	G_GLU_3	OE1	3.650
6BRB	D_LYS_5	NZ	D_GLU_3	OE1	2.959
6BRB	D_LYS_5	NZ	D_GLU_3	OE2	3.636
6BRB	D_LYS_33	NZ	D_GLU_63	OE1	3.743

6BRB	D_ARG.69	NH2	D_GLU.27	OE1	3.803
6BRB	D_ARG.69	NH2	D_GLU.27	OE2	3.492
6BXA	A_ARG.37	NH1	C_GLU.101	OE1	3.957
6BXA	A_ARG.37	NH1	C_GLU.101	OE2	3.920
6BXA	A_ARG.37	NH2	C_GLU.101	OE1	3.689
6BXA	A_ARG.37	NH2	C_GLU.101	OE2	2.525
6BXA	A_LYS.77	NZ	A_ASP.53	OD2	3.745
6BXA	A_LYS.77	NZ	A_GLU.79	OE2	3.822
6BXA	A_LYS.77	NZ	C_ASP.34	OD2	2.860
6BXA	A_ARG.88	NH1	A_GLU.112	OE2	2.776
6BXA	A_ARG.88	NH2	A_GLU.61	OE1	3.314
6BXA	A_LYS.102	NZ	C_ASP.34	OD1	2.955
6BXA	A_ARG.154	NH1	A_ASP.177	OD1	3.604
6BXA	A_ARG.154	NH1	A_ASP.177	OD2	2.924
6BXA	A_ARG.172	NH2	A_GLU.149	OE2	3.243
6BXA	A_LYS.184	NZ	A_ASP.211	OD2	2.992
6BXA	A_LYS.184	NZ	B_ASP.133	OD2	2.709
6BXA	A_ARG.203	NH1	A_ASP.177	OD2	3.223
6BXA	A_LYS.221	NZ	A_GLU.189	OE1	2.737
6BXA	A_LYS.221	NZ	A_GLU.189	OE2	3.962
6BXA	A_LYS.227	NZ	A_GLU.188	OE2	3.721
6BXA	A_LYS.242	NZ	A_GLU.214	OE1	2.824
6BXA	A_LYS.247	NZ	A_ASP.251	OD2	3.024
6BXA	A_LYS.287	NZ	A_GLU.290	OE1	3.206
6BXA	A_LYS.287	NZ	A_GLU.290	OE2	3.365
6BXA	A_LYS.365	NZ	A_ASP.364	OD2	2.586
6BXA	A_ARG.430	NH1	A_ASP.425	OD2	2.739
6BXA	A_ARG.436	NH1	A_ASP.432	OD1	3.991
6BXA	A_ARG.436	NH1	A_ASP.432	OD2	3.281
6BXA	A_ARG.436	NH2	A_ASP.432	OD1	3.255
6BXA	A_ARG.436	NH2	A_ASP.432	OD2	3.091
6BXA	A_ARG.459	NH2	A_GLU.445	OE1	3.182
6BXA	B_ARG.37	NH2	D_GLU.101	OE1	3.840
6BXA	B_ARG.37	NH2	D_GLU.101	OE2	2.839
6BXA	B_LYS.77	NZ	B_ASP.53	OD2	3.863
6BXA	B_LYS.77	NZ	B_GLU.79	OE1	3.945
6BXA	B_LYS.77	NZ	B_GLU.79	OE2	3.546
6BXA	B_LYS.77	NZ	D_ASP.34	OD1	2.907
6BXA	B_ARG.88	NH1	B_GLU.112	OE2	2.748
6BXA	B_ARG.88	NH2	B_GLU.61	OE1	3.185
6BXA	B_ARG.93	NH2	B_GLU.64	OE1	2.917
6BXA	B_ARG.93	NH2	B_GLU.64	OE2	2.657
6BXA	B_LYS.102	NZ	D_ASP.34	OD2	3.845
6BXA	B_ARG.154	NH2	B_ASP.177	OD2	4.000
6BXA	B_LYS.184	NZ	A_ASP.133	OD2	2.771
6BXA	B_LYS.184	NZ	B_ASP.211	OD2	2.792
6BXA	B_ARG.203	NH1	B_ASP.177	OD2	3.054
6BXA	B_LYS.242	NZ	B_GLU.214	OE2	3.352
6BXA	B_LYS.247	NZ	B_ASP.251	OD2	2.934
6BXA	C_ARG.125	NH1	C_GLU.127	OE1	2.840
6BXA	C_ARG.199	NH2	C_ASP.187	OD1	3.576
6BXA	C_ARG.199	NH2	C_ASP.187	OD2	3.048
6BXA	C_LYS.210	NZ	C_GLU.160	OE1	3.673
6BXA	D_ARG.125	NH1	D_GLU.127	OE1	2.909
6BXA	D_ARG.199	NH2	D_ASP.187	OD1	2.818
6BXA	D_ARG.199	NH2	D_ASP.187	OD2	3.045
6BXC	A_ARG.88	NH1	A_GLU.112	OE2	3.484
6BXC	A_LYS.102	NZ	A_GLU.79	OE2	2.891

6BXC	A_LYS_102	NZ	A_ASP_104	OD2	2.667
6BXC	A_ARG_154	NH1	A_ASP_177	OD1	3.409
6BXC	A_ARG_154	NH1	A_ASP_177	OD2	2.660
6BXC	A_ARG_172	NH2	A_GLU_149	OE2	2.307
6BXC	A_LYS_184	NZ	C_ASP_34	OD2	3.851
6BXC	A_HIS_198	NE2	D_GLU_65	OE2	3.317
6BXC	A_ARG_203	NH2	A_ASP_235	OD2	3.882
6BXC	A_LYS_247	NZ	A_ASP_251	OD2	3.104
6BXC	A_HIS_314	ND1	A_GLU_290	OE2	3.791
6BXC	A_ARG_358	NH2	A_ASP_333	OD1	3.683
6BXC	A_ARG_358	NH2	A_ASP_333	OD2	2.263
6BXC	B_LYS_77	NZ	B_ASP_53	OD2	3.559
6BXC	B_LYS_77	NZ	B_GLU_79	OE1	3.681
6BXC	B_LYS_77	NZ	B_GLU_79	OE2	3.867
6BXC	B_ARG_88	NH1	B_GLU_112	OE2	2.734
6BXC	B_ARG_88	NH2	B_GLU_61	OE1	3.021
6BXC	B_ARG_154	NH1	B_ASP_177	OD1	3.602
6BXC	B_ARG_154	NH1	B_ASP_177	OD2	2.827
6BXC	B_LYS_159	NZ	D_ASP_34	OD2	3.891
6BXC	B_ARG_172	NH1	B_GLU_123	OE2	3.880
6BXC	B_ARG_172	NH2	B_GLU_123	OE1	3.923
6BXC	B_ARG_172	NH2	B_GLU_123	OE2	3.236
6BXC	B_ARG_172	NH2	B_GLU_149	OE2	2.392
6BXC	B_LYS_182	NZ	D_GLU_81	OE2	3.361
6BXC	B_LYS_184	NZ	D_ASP_34	OD2	3.547
6BXC	B_ARG_203	NH1	B_ASP_177	OD2	3.785
6BXC	B_LYS_221	NZ	B_GLU_189	OE1	2.699
6BXC	B_LYS_227	NZ	B_GLU_188	OE1	3.703
6BXC	B_LYS_227	NZ	B_GLU_188	OE2	2.986
6BXC	B_LYS_247	NZ	B_ASP_251	OD2	2.562
6BXC	B_LYS_287	NZ	B_GLU_290	OE1	3.663
6BXC	B_HIS_314	ND1	B_GLU_290	OE2	3.748
6BXC	B_ARG_358	NH1	B_ASP_333	OD2	2.973
6BXC	B_ARG_358	NH2	B_ASP_333	OD2	3.373
6BXC	B_HIS_420	NE2	B_ASP_396	OD2	3.947
6BXD	A_ARG_125	NH1	A_GLU_101	OE2	3.973
6BXD	A_ARG_199	NH2	A_ASP_187	OD1	3.406
6BXD	A_LYS_210	NZ	A_GLU_160	OE1	3.837
6BXE	A_LYS_63	NZ	A_GLU_65	OE2	3.493
6BXE	A_HIS_125	NE2	B_GLU_81	OE2	2.552
6BXE	B_LYS_63	NZ	B_GLU_65	OE2	3.400
6BXE	B_HIS_125	NE2	A_GLU_81	OE2	3.833
6BXE	B_ARG_168	NH1	B_GLU_154	OE1	2.963
6BZU	A_ARG_38	NH1	A_ASP_86	OD1	2.830
6BZU	A_ARG_38	NH2	A_GLU_46	OE1	2.706
6BZU	A_ARG_38	NH2	A_GLU_46	OE2	3.949
6BZU	A_ARG_38	NH2	A_ASP_86	OD1	3.655
6BZU	A_ARG_64	NH2	B_ASP_94	OD1	3.703
6BZU	A_ARG_66	NH1	A_ASP_86	OD1	3.455
6BZU	A_ARG_66	NH1	A_ASP_86	OD2	2.992
6BZU	A_ARG_66	NH2	A_ASP_86	OD1	2.772
6BZU	A_ARG_66	NH2	A_ASP_86	OD2	3.274
6BZU	A_ARG_94	NH1	A_ASP_27	OD1	3.748
6BZU	A_ARG_94	NH1	A_ASP_27	OD2	3.345
6BZU	A_ARG_94	NH2	A_ASP_101	OD1	3.362
6BZU	A_ARG_94	NH2	A_ASP_101	OD2	2.575
6BZU	A_LYS_143	NZ	A_ASP_144	OD1	3.544
6BZU	A_LYS_206	NZ	A_ASP_208	OD1	3.589

6BZU	A_LYS_206	NZ	A_ASP_208	OD2	3.931
6BZU	A_LYS_209	NZ	B_GLU_123	OE2	3.980
6BZU	B_ARG_18	NH1	B_ASP_76	OD2	3.621
6BZU	B_ARG_18	NH2	B_ASP_76	OD2	3.174
6BZU	B_ARG_18	NH2	F_ASP_70	OD2	2.642
6BZU	B_ARG_24	NH1	B_ASP_70	OD1	3.347
6BZU	B_ARG_24	NH1	F_ASP_76	OD1	3.597
6BZU	B_ARG_24	NH1	F_ASP_76	OD2	2.861
6BZU	B_LYS_39	NZ	B_ASP_81	OD1	2.891
6BZU	B_LYS_39	NZ	B_ASP_81	OD2	2.853
6BZU	B_ARG_61	NH1	B_ASP_82	OD1	3.370
6BZU	B_ARG_61	NH1	B_ASP_82	OD2	2.618
6BZU	B_ARG_61	NH2	B_ASP_82	OD1	3.228
6BZU	B_ARG_61	NH2	B_ASP_82	OD2	3.877
6BZU	B_LYS_149	NZ	B_GLU_195	OE2	3.153
6BZU	B_LYS_183	NZ	B_GLU_187	OE1	3.079
6BZU	B_LYS_183	NZ	B_GLU_187	OE2	2.953
6BZU	B_HIS_189	ND1	B_ASP_151	OD1	3.911
6BZU	B_HIS_189	ND1	B_ASP_151	OD2	2.360
6BZU	C_ARG_38	NH1	C_ASP_86	OD1	2.726
6BZU	C_ARG_38	NH2	C_GLU_46	OE1	2.726
6BZU	C_ARG_38	NH2	C_GLU_46	OE2	3.930
6BZU	C_ARG_38	NH2	C_ASP_86	OD1	3.517
6BZU	C_ARG_64	NH2	D_ASP_94	OD1	3.618
6BZU	C_ARG_66	NH1	C_ASP_86	OD1	3.539
6BZU	C_ARG_66	NH1	C_ASP_86	OD2	2.951
6BZU	C_ARG_66	NH2	C_ASP_86	OD1	2.783
6BZU	C_ARG_66	NH2	C_ASP_86	OD2	3.152
6BZU	C_ARG_94	NH1	C_ASP_27	OD2	3.167
6BZU	C_ARG_94	NH2	C_ASP_101	OD1	3.308
6BZU	C_ARG_94	NH2	C_ASP_101	OD2	2.595
6BZU	C_LYS_143	NZ	C_ASP_144	OD1	3.728
6BZU	C_LYS_206	NZ	C_ASP_208	OD1	3.579
6BZU	C_LYS_206	NZ	C_ASP_208	OD2	3.842
6BZU	C_LYS_210	NZ	C_GLU_212	OE2	3.412
6BZU	D_ARG_18	NH1	D_ASP_76	OD2	3.756
6BZU	D_ARG_18	NH2	D_ASP_76	OD2	3.639
6BZU	D_ARG_24	NH2	D_ASP_70	OD1	2.824
6BZU	D_ARG_24	NH2	D_ASP_70	OD2	3.740
6BZU	D_LYS_39	NZ	D_ASP_81	OD1	2.752
6BZU	D_LYS_39	NZ	D_ASP_81	OD2	2.990
6BZU	D_ARG_61	NH1	D_ASP_82	OD1	3.166
6BZU	D_ARG_61	NH1	D_ASP_82	OD2	2.739
6BZU	D_ARG_61	NH2	D_ASP_82	OD1	3.480
6BZU	D_LYS_183	NZ	D_GLU_187	OE1	2.974
6BZU	D_LYS_183	NZ	D_GLU_187	OE2	3.283
6BZU	D_HIS_189	ND1	D_ASP_151	OD2	3.151
6BZU	E_ARG_38	NH1	E_ASP_86	OD1	2.631
6BZU	E_ARG_38	NH2	E_GLU_46	OE1	2.648
6BZU	E_ARG_38	NH2	E_GLU_46	OE2	3.839
6BZU	E_ARG_38	NH2	E_ASP_86	OD1	3.682
6BZU	E_ARG_64	NH2	F_ASP_94	OD1	3.701
6BZU	E_ARG_66	NH1	E_ASP_86	OD1	3.600
6BZU	E_ARG_66	NH1	E_ASP_86	OD2	3.079
6BZU	E_ARG_66	NH2	E_ASP_86	OD1	3.151
6BZU	E_ARG_66	NH2	E_ASP_86	OD2	3.506
6BZU	E_ARG_94	NH1	E_ASP_27	OD1	3.760
6BZU	E_ARG_94	NH1	E_ASP_27	OD2	3.069

6BZU	E_ARG_94	NH2	E_ASP_101	OD1	3.575
6BZU	E_ARG_94	NH2	E_ASP_101	OD2	3.123
6BZU	E_LYS_143	NZ	E_ASP_144	OD1	3.596
6BZU	E_LYS_206	NZ	E_ASP_208	OD1	3.535
6BZU	E_LYS_206	NZ	E_ASP_208	OD2	3.797
6BZU	F_ARG_18	NH1	F_ASP_76	OD2	3.679
6BZU	F_ARG_18	NH2	F_ASP_76	OD2	3.069
6BZU	F_ARG_24	NH1	B_ASP_76	OD1	3.333
6BZU	F_ARG_24	NH1	B_ASP_76	OD2	3.080
6BZU	F_LYS_39	NZ	F_ASP_81	OD1	2.757
6BZU	F_LYS_39	NZ	F_ASP_81	OD2	3.575
6BZU	F_ARG_61	NH1	F_ASP_82	OD1	3.022
6BZU	F_ARG_61	NH1	F_ASP_82	OD2	2.655
6BZU	F_ARG_61	NH2	F_ASP_82	OD1	3.315
6BZU	F_LYS_149	NZ	F_GLU_195	OE2	3.477
6BZU	F_LYS_183	NZ	F_GLU_187	OE1	3.247
6BZU	F_LYS_183	NZ	F_GLU_187	OE2	3.817
6BZU	F_HIS_189	ND1	F_ASP_151	OD2	2.440
6BZU	G_ARG_38	NH1	G_ASP_86	OD1	2.471
6BZU	G_ARG_38	NH2	G_GLU_46	OE1	2.713
6BZU	G_ARG_38	NH2	G_GLU_46	OE2	3.875
6BZU	G_ARG_38	NH2	G_ASP_86	OD1	3.468
6BZU	G_ARG_64	NH2	H_ASP_94	OD1	3.197
6BZU	G_ARG_64	NH2	H_ASP_94	OD2	3.837
6BZU	G_ARG_66	NH1	G_ASP_86	OD1	3.947
6BZU	G_ARG_66	NH1	G_ASP_86	OD2	3.042
6BZU	G_ARG_66	NH2	G_ASP_86	OD1	2.869
6BZU	G_ARG_66	NH2	G_ASP_86	OD2	2.950
6BZU	G_ARG_94	NH1	G_ASP_27	OD2	3.484
6BZU	G_ARG_94	NH2	G_ASP_101	OD1	3.468
6BZU	G_ARG_94	NH2	G_ASP_101	OD2	2.612
6BZU	G_LYS_143	NZ	G_ASP_144	OD1	3.677
6BZU	G_LYS_206	NZ	G_ASP_208	OD1	3.523
6BZU	G_LYS_206	NZ	G_ASP_208	OD2	3.779
6BZU	G_LYS_209	NZ	H_GLU_123	OE1	2.734
6BZU	G_LYS_209	NZ	H_GLU_123	OE2	3.547
6BZU	G_LYS_210	NZ	G_GLU_212	OE2	3.397
6BZU	H_ARG_18	NH1	H_ASP_76	OD2	3.879
6BZU	H_ARG_18	NH2	H_ASP_76	OD2	3.299
6BZU	H_LYS_39	NZ	H_ASP_81	OD1	2.621
6BZU	H_LYS_39	NZ	H_ASP_81	OD2	3.478
6BZU	H_ARG_61	NH1	H_ASP_82	OD1	3.357
6BZU	H_ARG_61	NH1	H_ASP_82	OD2	2.854
6BZU	H_ARG_61	NH2	H_ASP_82	OD1	3.381
6BZU	H_LYS_149	NZ	H_GLU_195	OE2	3.735
6BZU	H_LYS_183	NZ	H_GLU_187	OE1	3.364
6BZU	H_LYS_183	NZ	H_GLU_187	OE2	3.961
6BZU	H_LYS_188	NZ	H_ASP_185	OD1	3.876
6BZV	E_ARG_38	NH1	E_ASP_86	OD1	2.844
6BZV	E_ARG_38	NH2	E_GLU_46	OE1	2.762
6BZV	E_ARG_38	NH2	E_ASP_86	OD1	3.884
6BZV	E_ARG_66	NH1	E_ASP_86	OD2	3.252
6BZV	E_ARG_66	NH1	C_GLU_85	OE2	3.540
6BZV	E_ARG_66	NH2	E_ASP_86	OD1	3.097
6BZV	E_ARG_66	NH2	E_ASP_86	OD2	3.221
6BZV	E_ARG_66	NH2	C_GLU_85	OE2	3.482
6BZV	E_ARG_94	NH1	E_ASP_27	OD2	2.862
6BZV	E_ARG_94	NH2	E_ASP_101	OD1	3.797

6BZV	E_ARG_94	NH2	E_ASP_101	OD2	2.904
6BZV	E_LYS_143	NZ	E_ASP_144	OD1	3.856
6BZV	E_LYS_206	NZ	G_ASP_208	OD2	3.271
6BZV	E_LYS_209	NZ	F_GLU_123	OE1	3.953
6BZV	E_LYS_209	NZ	F_GLU_123	OE2	2.713
6BZV	E_LYS_210	NZ	E_GLU_212	OE2	2.831
6BZV	F_ARG_18	NH2	F_ASP_76	OD2	3.890
6BZV	F_LYS_39	NZ	F_ASP_81	OD1	3.137
6BZV	F_LYS_39	NZ	F_ASP_81	OD2	3.795
6BZV	F_ARG_61	NH1	F_ASP_82	OD1	3.530
6BZV	F_ARG_61	NH1	F_ASP_82	OD2	2.932
6BZV	F_ARG_61	NH2	F_ASP_82	OD1	3.252
6BZV	F_LYS_188	NZ	F_ASP_185	OD1	3.910
6BZV	A_ARG_38	NH1	A_ASP_86	OD1	2.647
6BZV	A_ARG_38	NH2	A_GLU_46	OE1	3.008
6BZV	A_ARG_38	NH2	A_ASP_86	OD1	3.189
6BZV	A_ARG_66	NH1	A_ASP_86	OD2	3.345
6BZV	A_ARG_66	NH2	A_ASP_86	OD1	3.206
6BZV	A_ARG_66	NH2	A_ASP_86	OD2	3.333
6BZV	A_ARG_94	NH1	A_ASP_27	OD2	2.749
6BZV	A_ARG_94	NH2	A_ASP_101	OD1	3.799
6BZV	A_ARG_94	NH2	A_ASP_101	OD2	2.974
6BZV	A_LYS_143	NZ	A_ASP_144	OD1	3.960
6BZV	A_LYS_206	NZ	A_ASP_208	OD1	3.297
6BZV	A_LYS_206	NZ	A_ASP_208	OD2	3.789
6BZV	A_LYS_209	NZ	B_GLU_123	OE1	2.709
6BZV	A_LYS_209	NZ	B_GLU_123	OE2	3.439
6BZV	A_LYS_210	NZ	A_GLU_212	OE2	2.656
6BZV	B_ARG_18	NH2	B_ASP_76	OD2	3.495
6BZV	B_ARG_24	NH2	B_ASP_70	OD1	3.551
6BZV	B_ARG_24	NH2	B_ASP_70	OD2	3.558
6BZV	B_LYS_39	NZ	B_ASP_81	OD1	2.943
6BZV	B_LYS_39	NZ	B_ASP_81	OD2	3.840
6BZV	B_ARG_61	NH1	B_ASP_82	OD1	2.943
6BZV	B_ARG_61	NH1	B_ASP_82	OD2	2.669
6BZV	B_ARG_61	NH2	B_ASP_82	OD1	3.350
6BZV	B_LYS_149	NZ	B_GLU_195	OE2	3.685
6BZV	B_LYS_183	NZ	B_GLU_187	OE1	3.842
6BZV	C_ARG_38	NH1	C_ASP_86	OD1	2.657
6BZV	C_ARG_38	NH2	C_GLU_46	OE1	3.551
6BZV	C_ARG_38	NH2	C_ASP_86	OD1	3.055
6BZV	C_ARG_66	NH1	C_ASP_86	OD2	3.524
6BZV	C_ARG_66	NH2	C_ASP_86	OD1	3.405
6BZV	C_ARG_66	NH2	C_ASP_86	OD2	3.206
6BZV	C_ARG_94	NH1	C_ASP_27	OD2	2.994
6BZV	C_ARG_94	NH2	C_ASP_101	OD1	3.607
6BZV	C_ARG_94	NH2	C_ASP_101	OD2	3.021
6BZV	C_LYS_143	NZ	C_ASP_144	OD1	3.671
6BZV	C_LYS_206	NZ	C_ASP_208	OD1	2.715
6BZV	C_LYS_206	NZ	C_ASP_208	OD2	3.362
6BZV	C_LYS_209	NZ	D_GLU_123	OE1	2.619
6BZV	C_LYS_209	NZ	D_GLU_123	OE2	2.945
6BZV	C_LYS_210	NZ	C_GLU_212	OE2	2.891
6BZV	D_ARG_18	NH2	D_ASP_76	OD2	3.172
6BZV	D_ARG_24	NH2	D_ASP_70	OD1	2.988
6BZV	D_ARG_24	NH2	D_ASP_70	OD2	3.384
6BZV	D_LYS_39	NZ	D_ASP_81	OD1	2.720
6BZV	D_LYS_39	NZ	D_ASP_81	OD2	3.480

6BZV	D_ARG_61	NH1	D_ASP_82	OD1	2.908
6BZV	D_ARG_61	NH1	D_ASP_82	OD2	2.744
6BZV	D_ARG_61	NH2	D_GLU_79	OE1	3.805
6BZV	D_ARG_61	NH2	D_ASP_82	OD1	3.651
6BZV	D_LYS_183	NZ	D_GLU_187	OE1	3.827
6BZV	D_LYS_183	NZ	D_GLU_187	OE2	3.971
6BZV	G_ARG_38	NH1	G_ASP_86	OD1	2.748
6BZV	G_ARG_38	NH2	G_GLU_46	OE1	3.230
6BZV	G_ARG_38	NH2	G_ASP_86	OD1	3.248
6BZV	G_ARG_66	NH1	G_ASP_86	OD2	3.499
6BZV	G_ARG_66	NH2	G_ASP_86	OD1	3.475
6BZV	G_ARG_66	NH2	G_ASP_86	OD2	3.645
6BZV	G_ARG_94	NH1	G_ASP_27	OD1	2.468
6BZV	G_ARG_94	NH2	G_ASP_101	OD1	3.530
6BZV	G_ARG_94	NH2	G_ASP_101	OD2	3.139
6BZV	G_LYS_143	NZ	G_ASP_144	OD1	3.706
6BZV	G_HIS_164	NE2	H_ASP_167	OD1	3.817
6BZV	G_LYS_209	NZ	H_GLU_123	OE1	3.054
6BZV	G_LYS_209	NZ	H_GLU_123	OE2	3.192
6BZV	G_LYS_210	NZ	G_GLU_212	OE2	2.995
6BZV	H_ARG_18	NH2	H_ASP_76	OD2	3.078
6BZV	H_LYS_39	NZ	H_ASP_81	OD1	2.837
6BZV	H_LYS_39	NZ	H_ASP_81	OD2	3.626
6BZV	H_ARG_61	NH1	H_ASP_82	OD1	3.084
6BZV	H_ARG_61	NH1	H_ASP_82	OD2	2.483
6BZV	H_ARG_61	NH2	H_ASP_82	OD1	2.797
6BZV	H_ARG_61	NH2	H_ASP_82	OD2	3.746
6BZV	H_LYS_103	NZ	H_GLU_165	OE1	3.239
6BZV	H_LYS_103	NZ	H_GLU_165	OE2	2.963
6BZV	H_LYS_149	NZ	H_GLU_195	OE2	3.595
6BZV	H_LYS_183	NZ	H_GLU_187	OE1	3.837
6BZV	H_LYS_183	NZ	H_GLU_187	OE2	3.903
6BZW	C_ARG_38	NH1	C_ASP_86	OD1	2.855
6BZW	C_ARG_38	NH2	C_GLU_46	OE1	2.761
6BZW	C_ARG_38	NH2	C_GLU_46	OE2	3.900
6BZW	C_ARG_38	NH2	C_ASP_86	OD1	3.525
6BZW	C_ARG_66	NH1	C_ASP_86	OD1	3.684
6BZW	C_ARG_66	NH1	C_ASP_86	OD2	2.944
6BZW	C_ARG_66	NH2	C_ASP_86	OD1	2.982
6BZW	C_ARG_66	NH2	C_ASP_86	OD2	3.451
6BZW	C_ARG_94	NH1	C_ASP_27	OD2	3.411
6BZW	C_ARG_94	NH2	C_ASP_101	OD1	3.817
6BZW	C_ARG_94	NH2	C_ASP_101	OD2	2.574
6BZW	C_LYS_143	NZ	C_ASP_144	OD1	3.327
6BZW	C_LYS_143	NZ	C_ASP_144	OD2	2.941
6BZW	C_LYS_209	NZ	D_GLU_123	OE1	2.857
6BZW	C_LYS_209	NZ	D_GLU_123	OE2	3.990
6BZW	C_LYS_210	NZ	C_GLU_212	OE2	3.580
6BZW	D_ARG_18	NH2	H_GLU_93	OE1	3.070
6BZW	D_LYS_39	NZ	D_ASP_81	OD1	2.338
6BZW	D_LYS_39	NZ	D_ASP_81	OD2	3.833
6BZW	D_ARG_61	NH1	D_ASP_82	OD1	3.630
6BZW	D_ARG_61	NH1	D_ASP_82	OD2	2.695
6BZW	D_ARG_61	NH2	D_ASP_82	OD1	3.497
6BZW	D_ARG_61	NH2	D_ASP_82	OD2	3.898
6BZW	D_LYS_149	NZ	D_GLU_195	OE1	3.578
6BZW	D_LYS_188	NZ	D_ASP_185	OD1	3.347
6BZW	D_HIS_189	ND1	D_ASP_151	OD2	2.863

6BZW	D_ARG_211	NH2	D_GLU_187	OE1	2.961
6BZW	A_ARG_38	NH1	A_ASP_86	OD1	2.806
6BZW	A_ARG_38	NH2	A_GLU_46	OE1	2.810
6BZW	A_ARG_38	NH2	A_ASP_86	OD1	3.534
6BZW	A_ARG_66	NH1	A_ASP_86	OD1	3.766
6BZW	A_ARG_66	NH1	A_ASP_86	OD2	3.088
6BZW	A_ARG_66	NH2	A_ASP_86	OD1	2.975
6BZW	A_ARG_66	NH2	A_ASP_86	OD2	3.224
6BZW	A_ARG_94	NH1	A_ASP_27	OD2	3.062
6BZW	A_ARG_94	NH2	A_ASP_101	OD1	3.805
6BZW	A_ARG_94	NH2	A_ASP_101	OD2	2.322
6BZW	A_LYS_143	NZ	A_ASP_144	OD1	3.396
6BZW	A_LYS_143	NZ	A_ASP_144	OD2	2.710
6BZW	A_LYS_209	NZ	B_GLU_123	OE1	2.988
6BZW	A_LYS_210	NZ	A_GLU_212	OE2	3.336
6BZW	B_ARG_18	NH2	B_ASP_76	OD2	3.990
6BZW	B_LYS_39	NZ	B_ASP_81	OD1	2.457
6BZW	B_LYS_39	NZ	B_ASP_81	OD2	3.775
6BZW	B_ARG_61	NH1	B_ASP_82	OD1	3.435
6BZW	B_ARG_61	NH1	B_ASP_82	OD2	2.481
6BZW	B_ARG_61	NH2	B_ASP_82	OD1	2.977
6BZW	B_ARG_61	NH2	B_ASP_82	OD2	3.551
6BZW	B_ARG_68	NH1	B_ASP_27C	OD2	3.000
6BZW	B_LYS_149	NZ	B_GLU_195	OE1	3.533
6BZW	B_LYS_188	NZ	B_ASP_185	OD1	3.312
6BZW	B_HIS_189	ND1	B_ASP_151	OD2	2.735
6BZW	B_LYS_190	NZ	B_GLU_213	OE2	3.979
6BZW	B_ARG_211	NH2	B_GLU_187	OE1	3.195
6BZW	E_ARG_38	NH1	E_ASP_86	OD1	2.836
6BZW	E_ARG_38	NH2	E_GLU_46	OE1	2.758
6BZW	E_ARG_38	NH2	E_GLU_46	OE2	3.957
6BZW	E_ARG_38	NH2	E_ASP_86	OD1	3.594
6BZW	E_ARG_66	NH1	E_ASP_86	OD1	3.616
6BZW	E_ARG_66	NH1	E_ASP_86	OD2	2.872
6BZW	E_ARG_66	NH2	E_ASP_86	OD1	2.980
6BZW	E_ARG_66	NH2	E_ASP_86	OD2	3.348
6BZW	E_ARG_94	NH1	E_ASP_27	OD2	3.258
6BZW	E_ARG_94	NH2	E_ASP_101	OD1	3.737
6BZW	E_ARG_94	NH2	E_ASP_101	OD2	2.526
6BZW	E_LYS_143	NZ	E_ASP_144	OD1	2.783
6BZW	E_LYS_143	NZ	E_ASP_144	OD2	3.427
6BZW	E_LYS_209	NZ	F_GLU_123	OE1	2.583
6BZW	E_LYS_209	NZ	F_GLU_123	OE2	3.254
6BZW	E_LYS_210	NZ	E_GLU_212	OE2	3.361
6BZW	F_ARG_18	NH2	F_ASP_76	OD2	3.915
6BZW	F_LYS_39	NZ	F_ASP_81	OD1	2.665
6BZW	F_ARG_61	NH2	F_ASP_82	OD1	2.596
6BZW	F_ARG_61	NH2	F_ASP_82	OD2	3.915
6BZW	F_LYS_149	NZ	F_GLU_195	OE1	3.703
6BZW	F_LYS_188	NZ	F_ASP_185	OD1	3.561
6BZW	F_ARG_211	NH2	F_GLU_187	OE1	3.709
6BZW	G_ARG_38	NH1	G_ASP_86	OD1	2.636
6BZW	G_ARG_38	NH2	G_GLU_46	OE1	3.016
6BZW	G_ARG_38	NH2	G_ASP_86	OD1	3.345
6BZW	G_ARG_66	NH1	G_ASP_86	OD1	3.851
6BZW	G_ARG_66	NH1	G_ASP_86	OD2	3.048
6BZW	G_ARG_66	NH2	G_ASP_86	OD1	2.949
6BZW	G_ARG_66	NH2	G_ASP_86	OD2	3.330

6BZW	G_ARG_94	NH1	G_ASP_27	OD2	3.098
6BZW	G_ARG_94	NH2	G_ASP_101	OD1	3.595
6BZW	G_ARG_94	NH2	G_ASP_101	OD2	2.509
6BZW	G_LYS_143	NZ	G_ASP_144	OD1	2.922
6BZW	G_LYS_143	NZ	G_ASP_144	OD2	2.656
6BZW	G_LYS_209	NZ	H_GLU_123	OE1	2.709
6BZW	G_LYS_209	NZ	H_GLU_123	OE2	2.569
6BZW	H_LYS_39	NZ	H_ASP_81	OD1	2.836
6BZW	H_ARG_61	NH1	H_GLU_79	OE1	3.176
6BZW	H_ARG_61	NH2	H_GLU_79	OE1	3.932
6BZW	H_ARG_61	NH2	H_ASP_82	OD1	2.618
6BZW	H_ARG_61	NH2	H_ASP_82	OD2	3.730
6BZW	H_LYS_149	NZ	H_GLU_195	OE1	3.312
6BZW	H_LYS_188	NZ	H_ASP_185	OD1	3.591
6BZW	H_LYS_190	NZ	H_GLU_213	OE2	3.965
6BZW	H_ARG_211	NH2	H_GLU_187	OE1	2.787
6BZY	H_ARG_38	NH1	H_ASP_86	OD1	2.808
6BZY	H_ARG_38	NH2	H_GLU_46	OE1	3.237
6BZY	H_ARG_38	NH2	H_ASP_86	OD1	3.627
6BZY	H_ARG_66	NH1	H_ASP_86	OD1	3.726
6BZY	H_ARG_66	NH1	H_ASP_86	OD2	3.046
6BZY	H_ARG_66	NH2	H_ASP_86	OD1	3.005
6BZY	H_ARG_66	NH2	H_ASP_86	OD2	3.522
6BZY	L_LYS_39	NZ	L_ASP_81	OD1	3.422
6BZY	L_LYS_39	NZ	L_ASP_81	OD2	3.246
6BZY	L_ARG_61	NH1	L_GLU_79	OE1	3.883
6BZY	L_ARG_61	NH1	L_GLU_79	OE2	3.484
6BZY	L_ARG_61	NH2	L_GLU_79	OE2	3.709
6BZY	L_ARG_61	NH2	L_ASP_82	OD1	2.811
6BZY	L_ARG_61	NH2	L_ASP_82	OD2	3.630
6BZY	L_LYS_92	NZ	L_GLU_93	OE1	2.944
6BZY	L_LYS_149	NZ	L_GLU_195	OE1	3.863
6BZY	L_LYS_149	NZ	L_GLU_195	OE2	3.027
6BZY	L_ARG_155	NH1	L_GLU_185	OE2	3.136
6BZY	L_ARG_155	NH2	L_GLU_185	OE1	2.999
6BZY	L_ARG_155	NH2	L_GLU_185	OE2	3.270
6BZY	L_LYS_183	NZ	L_GLU_187	OE1	3.043
6BZY	L_LYS_183	NZ	L_GLU_187	OE2	3.003
6BZY	L_HIS_189	ND1	L_ASP_151	OD2	2.978
6BZY	L_LYS_199	NZ	L_ASP_110	OD1	3.404
6BZY	L_LYS_199	NZ	L_ASP_110	OD2	3.217
6C5H	H_ARG_38	NH1	H_ASP_86	OD1	2.721
6C5H	H_ARG_38	NH2	H_GLU_46	OE1	2.994
6C5H	H_ARG_38	NH2	H_ASP_86	OD1	3.747
6C5H	H_ARG_66	NH1	H_ASP_86	OD1	3.644
6C5H	H_ARG_66	NH1	H_ASP_86	OD2	2.991
6C5H	H_ARG_66	NH2	H_ASP_86	OD1	2.973
6C5H	H_ARG_66	NH2	H_ASP_86	OD2	3.516
6C5H	H_LYS_75	NZ	H_ASP_72	OD2	3.835
6C5H	H_ARG_94	NH2	H_ASP_100	OD1	2.833
6C5H	H_ARG_94	NH2	H_ASP_100	OD2	3.662
6C5H	H_LYS_208	NZ	L_GLU_123	OE1	3.569
6C5H	L_ARG_61	NH1	L_GLU_79	OE1	3.434
6C5H	L_ARG_61	NH1	L_GLU_79	OE2	3.291
6C5H	L_ARG_61	NH2	L_GLU_79	OE1	3.399
6C5H	L_ARG_61	NH2	L_GLU_81	OE1	2.979
6C5H	L_ARG_61	NH2	L_GLU_81	OE2	3.883
6C5H	L_ARG_61	NH2	L_ASP_82	OD1	2.822

6C5H	L_ARG_61	NH2	L_ASP_82	OD2	3.827
6C5H	L_LYS_142	NZ	L_GLU_105	OE1	3.070
6C5H	L_ARG_155	NH1	L_GLU_185	OE1	2.690
6C5H	L_ARG_155	NH1	L_GLU_185	OE2	3.698
6C5H	L_ARG_155	NH2	L_GLU_185	OE1	3.395
6C5H	L_ARG_155	NH2	L_GLU_185	OE2	2.806
6C5H	L_HIS_189	ND1	L_ASP_151	OD2	2.883
6C5H	L_LYS_199	NZ	L_ASP_110	OD1	3.394
6C5H	L_LYS_199	NZ	L_ASP_110	OD2	3.049
6C5H	L_ARG_211	NH1	L_GLU_187	OE2	3.775
6C5I	H_ARG_38	NH1	H_ASP_86	OD1	2.831
6C5I	H_ARG_38	NH2	H_ASP_86	OD1	3.788
6C5I	H_ARG_66	NH1	H_ASP_86	OD1	3.709
6C5I	H_ARG_66	NH1	H_ASP_86	OD2	3.027
6C5I	H_ARG_66	NH2	H_ASP_86	OD1	2.746
6C5I	H_ARG_66	NH2	H_ASP_86	OD2	3.384
6C5I	H_ARG_94	NH2	H_ASP_100	OD1	3.126
6C5I	H_ARG_94	NH2	H_ASP_100	OD2	3.618
6C5I	H_HIS_164	NE2	L_ASP_167	OD2	3.802
6C5I	H_LYS_208	NZ	L_GLU_123	OE1	3.192
6C5I	L_ARG_24	NH2	L_ASP_70	OD2	3.159
6C5I	L_ARG_61	NH1	L_GLU_79	OE2	3.233
6C5I	L_ARG_61	NH2	L_GLU_79	OE1	3.749
6C5I	L_ARG_61	NH2	L_GLU_79	OE2	3.995
6C5I	L_ARG_61	NH2	L_GLU_81	OE1	2.811
6C5I	L_ARG_61	NH2	L_ASP_82	OD1	2.855
6C5I	L_ARG_61	NH2	L_ASP_82	OD2	3.717
6C5I	L_LYS_147	NZ	L_GLU_154	OE1	2.837
6C5I	L_LYS_147	NZ	L_GLU_154	OE2	3.916
6C5I	L_LYS_149	NZ	L_GLU_195	OE2	3.136
6C5I	L_LYS_199	NZ	L_ASP_110	OD1	3.935
6C5I	L_LYS_199	NZ	L_ASP_110	OD2	3.250
6C5J	H_ARG_38	NH1	H_ASP_86	OD1	2.836
6C5J	H_ARG_38	NH2	H_GLU_46	OE1	3.113
6C5J	H_ARG_38	NH2	H_ASP_86	OD1	3.867
6C5J	H_ARG_66	NH1	H_ASP_86	OD1	3.634
6C5J	H_ARG_66	NH1	H_ASP_86	OD2	2.729
6C5J	H_ARG_66	NH2	H_ASP_86	OD1	2.996
6C5J	H_ARG_66	NH2	H_ASP_86	OD2	3.388
6C5J	H_ARG_94	NH2	H_ASP_100	OD1	2.849
6C5J	H_ARG_94	NH2	H_ASP_100	OD2	3.422
6C5J	H_HIS_164	ND1	L_ASP_167	OD1	3.598
6C5J	L_ARG_24	NH1	L_ASP_70	OD1	3.086
6C5J	L_ARG_24	NH2	L_ASP_70	OD1	3.332
6C5J	L_ARG_54	NH1	L_ASP_60	OD1	3.010
6C5J	L_ARG_54	NH2	L_ASP_60	OD1	3.261
6C5J	L_ARG_61	NH1	L_GLU_79	OE2	3.828
6C5J	L_ARG_61	NH1	L_ASP_82	OD1	3.025
6C5J	L_ARG_61	NH1	L_ASP_82	OD2	3.858
6C5J	L_ARG_61	NH2	L_ASP_82	OD1	3.240
6C5J	L_ARG_61	NH2	L_ASP_82	OD2	2.681
6C5J	L_LYS_103	NZ	L_ASP_165	OD1	2.761
6C5J	L_LYS_103	NZ	L_ASP_165	OD2	3.775
6C5J	L_LYS_147	NZ	L_GLU_195	OE1	4.000
6C5J	L_LYS_149	NZ	L_GLU_195	OE1	3.633
6C5J	L_LYS_149	NZ	L_GLU_195	OE2	3.074
6C5J	L_ARG_155	NH1	L_GLU_185	OE1	3.663
6C5J	L_ARG_155	NH2	L_GLU_185	OE1	3.950

6C5J	L_HIS_189	ND1	L_ASP_151	OD2	3.348
6C5J	L_HIS_189	NE2	L_GLU_185	OE2	3.487
6C5K	H_ARG_38	NH1	H_ASP_86	OD1	2.795
6C5K	H_ARG_38	NH2	H_GLU_46	OE1	3.031
6C5K	H_ARG_38	NH2	H_ASP_86	OD1	3.813
6C5K	H_ARG_66	NH1	H_ASP_86	OD1	3.655
6C5K	H_ARG_66	NH1	H_ASP_86	OD2	2.836
6C5K	H_ARG_66	NH2	H_ASP_86	OD1	2.955
6C5K	H_ARG_66	NH2	H_ASP_86	OD2	3.481
6C5K	H_LYS_75	NZ	H_ASP_72	OD2	2.938
6C5K	H_ARG_94	NH2	H_ASP_100	OD1	2.779
6C5K	H_ARG_94	NH2	H_ASP_100	OD2	3.677
6C5K	A_ARG_38	NH1	A_ASP_86	OD1	2.763
6C5K	A_ARG_38	NH2	A_GLU_46	OE1	3.011
6C5K	A_ARG_38	NH2	A_ASP_86	OD1	3.834
6C5K	A_LYS_43	NZ	A_GLU_46	OE2	3.601
6C5K	A_ARG_66	NH1	A_ASP_86	OD1	3.702
6C5K	A_ARG_66	NH1	A_ASP_86	OD2	2.833
6C5K	A_ARG_66	NH2	A_ASP_86	OD1	2.960
6C5K	A_ARG_66	NH2	A_ASP_86	OD2	3.480
6C5K	A_LYS_75	NZ	A_ASP_72	OD2	3.839
6C5K	A_ARG_94	NH2	A_ASP_100	OD1	2.772
6C5K	A_ARG_94	NH2	A_ASP_100	OD2	3.672
6C5K	L_ARG_61	NH1	L_GLU_79	OE2	3.364
6C5K	L_ARG_61	NH2	L_GLU_79	OE1	3.895
6C5K	L_ARG_61	NH2	L_ASP_82	OD1	2.830
6C5K	L_ARG_61	NH2	L_ASP_82	OD2	3.538
6C5K	L_LYS_142	NZ	L_GLU_105	OE1	3.073
6C5K	L_LYS_142	NZ	L_GLU_105	OE2	3.102
6C5K	L_ARG_155	NH1	L_GLU_185	OE2	3.793
6C5K	L_ARG_155	NH2	L_GLU_185	OE2	3.452
6C5K	L_HIS_189	ND1	L_ASP_151	OD2	3.191
6C5K	L_LYS_199	NZ	L_ASP_110	OD2	3.559
6C5K	B_ARG_61	NH1	B_ASP_82	OD1	3.628
6C5K	B_ARG_61	NH1	B_ASP_82	OD2	2.598
6C5K	B_ARG_61	NH2	B_GLU_79	OE1	3.919
6C5K	B_ARG_61	NH2	B_ASP_82	OD1	2.914
6C5K	B_ARG_61	NH2	B_ASP_82	OD2	3.428
6C5K	B_ARG_77	NH1	B_ASP_60	OD1	3.873
6C5K	B_ARG_77	NH2	B_ASP_60	OD1	3.181
6C5K	B_ARG_77	NH2	B_ASP_60	OD2	3.837
6C5K	B_LYS_142	NZ	B_GLU_105	OE1	2.957
6C5K	B_LYS_142	NZ	B_GLU_105	OE2	3.105
6C5K	B_LYS_147	NZ	B_GLU_154	OE1	3.468
6C5K	B_LYS_149	NZ	B_GLU_195	OE1	3.461
6C5K	B_LYS_149	NZ	B_GLU_195	OE2	3.022
6C5K	B_LYS_183	NZ	B_GLU_187	OE1	3.352
6C5K	B_LYS_183	NZ	B_GLU_187	OE2	3.700
6C5K	B_HIS_189	ND1	B_ASP_151	OD2	3.184
6C5K	B_LYS_199	NZ	B_ASP_110	OD2	3.547
6C6X	A_ARG_38	NH1	A_ASP_86	OD1	2.916
6C6X	A_ARG_38	NH2	A_GLU_46	OE1	3.235
6C6X	A_ARG_38	NH2	A_ASP_86	OD1	3.654
6C6X	A_ARG_66	NH1	A_ASP_86	OD1	3.723
6C6X	A_ARG_66	NH1	A_ASP_86	OD2	3.099
6C6X	A_ARG_66	NH2	A_ASP_86	OD1	2.823
6C6X	A_ARG_66	NH2	A_ASP_86	OD2	3.594
6C6X	A_LYS_75	NZ	A_ASP_72	OD2	3.085

6C6X	A_LYS_94	NZ	A_ASP_27	OD1	3.369
6C6X	A_LYS_94	NZ	A_ASP_27	OD2	3.236
6C6X	A_LYS_143	NZ	A_ASP_144	OD1	3.316
6C6X	A_LYS_143	NZ	A_ASP_144	OD2	3.281
6C6X	B_ARG_24	NH2	B_ASP_70	OD2	3.520
6C6X	B_ARG_61	NH1	B_GLU_81	OE2	3.777
6C6X	B_ARG_61	NH2	B_GLU_81	OE2	2.736
6C6X	B_ARG_61	NH2	B_ASP_82	OD1	2.804
6C6X	B_ARG_61	NH2	B_ASP_82	OD2	3.688
6C6X	B_ARG_66	NH1	B_ASP_28	OD1	3.798
6C6X	B_LYS_103	NZ	B_GLU_105	OE1	3.590
6C6X	B_LYS_103	NZ	B_GLU_165	OE2	3.918
6C6X	B_LYS_147	NZ	B_GLU_195	OE2	3.987
6C6X	B_LYS_155	NZ	B_GLU_185	OE2	2.799
6C6X	B_HIS_189	ND1	B_ASP_151	OD2	3.308
6C6X	B_LYS_207	NZ	A_GLU_133	OE1	3.861
6C6X	C_ARG_38	NH1	C_ASP_86	OD1	2.686
6C6X	C_ARG_38	NH2	C_GLU_46	OE1	3.038
6C6X	C_ARG_38	NH2	C_ASP_86	OD1	3.600
6C6X	C_ARG_66	NH1	C_ASP_86	OD1	3.306
6C6X	C_ARG_66	NH1	C_ASP_86	OD2	3.758
6C6X	C_ARG_66	NH2	C_ASP_86	OD1	3.273
6C6X	C_ARG_66	NH2	C_ASP_86	OD2	2.552
6C6X	C_LYS_75	NZ	C_ASP_72	OD2	3.346
6C6X	C_LYS_94	NZ	C_ASP_27	OD1	3.722
6C6X	C_LYS_94	NZ	C_ASP_27	OD2	2.313
6C6X	C_LYS_143	NZ	C_ASP_144	OD1	3.560
6C6X	C_LYS_143	NZ	C_ASP_144	OD2	3.637
6C6X	D_ARG_61	NH2	D_GLU_81	OE2	3.760
6C6X	D_ARG_61	NH2	D_ASP_82	OD1	2.628
6C6X	D_ARG_61	NH2	D_ASP_82	OD2	3.448
6C6X	D_ARG_66	NH1	D_ASP_28	OD1	3.243
6C6X	D_ARG_66	NH1	D_ASP_28	OD2	3.729
6C6X	D_LYS_149	NZ	D_GLU_195	OE1	2.932
6C6X	D_LYS_155	NZ	D_GLU_185	OE2	3.201
6C6X	D_HIS_189	ND1	D_GLU_185	OE1	3.992
6C6X	E_ARG_38	NH1	E_ASP_86	OD1	2.787
6C6X	E_ARG_38	NH2	E_GLU_46	OE2	3.116
6C6X	E_ARG_38	NH2	E_ASP_86	OD1	3.697
6C6X	E_ARG_66	NH1	E_ASP_86	OD1	3.910
6C6X	E_ARG_66	NH1	E_ASP_86	OD2	3.139
6C6X	E_ARG_66	NH2	E_ASP_86	OD1	2.977
6C6X	E_ARG_66	NH2	E_ASP_86	OD2	3.550
6C6X	E_LYS_75	NZ	E_ASP_72	OD2	3.750
6C6X	E_LYS_94	NZ	E_ASP_27	OD1	3.779
6C6X	E_LYS_94	NZ	E_ASP_27	OD2	2.090
6C6X	E_LYS_143	NZ	E_ASP_144	OD1	3.540
6C6X	E_LYS_143	NZ	E_ASP_144	OD2	3.461
6C6X	F_ARG_24	NH1	F_ASP_70	OD1	3.452
6C6X	F_ARG_24	NH1	F_ASP_70	OD2	3.656
6C6X	F_ARG_24	NH2	F_ASP_70	OD2	3.468
6C6X	F_ARG_61	NH2	F_GLU_81	OE1	3.978
6C6X	F_ARG_61	NH2	F_ASP_82	OD1	2.486
6C6X	F_ARG_61	NH2	F_ASP_82	OD2	3.255
6C6X	F_ARG_66	NH1	F_ASP_28	OD1	3.527
6C6X	F_LYS_149	NZ	F_GLU_195	OE2	3.170
6C6X	F_LYS_169	NZ	F_ASP_167	OD1	3.680
6C6X	F_LYS_169	NZ	F_ASP_167	OD2	3.672

6C6X	F_LYS_169	NZ	F_ASP_170	OD2	2.920
6C6X	F_HIS_189	ND1	F_ASP_151	OD2	3.007
6C6X	H_ARG_38	NH1	H_ASP_86	OD1	2.791
6C6X	H_ARG_38	NH2	H_GLU_46	OE1	3.334
6C6X	H_ARG_38	NH2	H_ASP_86	OD1	3.541
6C6X	H_ARG_50	NH2	H_ASP_58	OD2	3.546
6C6X	H_LYS_64	NZ	H_ASP_58	OD1	3.715
6C6X	H_ARG_66	NH1	H_ASP_86	OD1	3.732
6C6X	H_ARG_66	NH1	H_ASP_86	OD2	3.107
6C6X	H_ARG_66	NH2	H_ASP_86	OD1	2.991
6C6X	H_ARG_66	NH2	H_ASP_86	OD2	3.632
6C6X	H_LYS_75	NZ	H_ASP_72	OD2	2.419
6C6X	H_LYS_143	NZ	H_ASP_144	OD1	3.420
6C6X	H_LYS_143	NZ	H_ASP_144	OD2	3.402
6C6X	H_ARG_210	NH1	H_GLU_212	OE2	2.704
6C6X	H_ARG_210	NH2	H_GLU_212	OE2	3.451
6C6X	L_ARG_24	NH2	L_ASP_70	OD1	3.667
6C6X	L_ARG_24	NH2	L_ASP_70	OD2	3.530
6C6X	L_ARG_61	NH2	L_GLU_81	OE1	3.682
6C6X	L_ARG_61	NH2	L_ASP_82	OD1	2.742
6C6X	L_ARG_61	NH2	L_ASP_82	OD2	3.507
6C6X	L_ARG_66	NH2	L_ASP_28	OD1	3.147
6C6X	L_ARG_66	NH2	L_ASP_28	OD2	3.848
6C6X	L_LYS_103	NZ	L_GLU_165	OE1	2.822
6C6X	L_LYS_103	NZ	L_GLU_165	OE2	3.323
6C6X	L_ARG_142	NH1	L_GLU_105	OE1	3.994
6C6X	L_LYS_149	NZ	L_GLU_195	OE1	3.966
6C6X	L_LYS_149	NZ	L_GLU_195	OE2	2.484
6C6X	L_HIS_189	ND1	L_ASP_151	OD2	3.012
6C6Y	A_ARG_38	NH1	A_ASP_86	OD1	3.064
6C6Y	A_ARG_38	NH2	A_GLU_46	OE2	3.198
6C6Y	A_ARG_66	NH1	A_ASP_86	OD2	3.498
6C6Y	A_ARG_66	NH2	A_ASP_86	OD1	3.146
6C6Y	A_ARG_66	NH2	A_ASP_86	OD2	3.520
6C6Y	A_LYS_94	NZ	A_ASP_27	OD2	3.819
6C6Y	A_LYS_143	NZ	A_ASP_144	OD1	3.805
6C6Y	B_ARG_24	NH1	B_ASP_70	OD1	3.301
6C6Y	B_ARG_24	NH2	B_ASP_70	OD1	3.031
6C6Y	B_ARG_24	NH2	B_ASP_70	OD2	3.357
6C6Y	B_ARG_61	NH1	B_GLU_81	OE1	3.827
6C6Y	B_ARG_61	NH2	B_GLU_81	OE1	3.995
6C6Y	B_ARG_61	NH2	B_ASP_82	OD1	2.452
6C6Y	B_ARG_61	NH2	B_ASP_82	OD2	3.063
6C6Y	B_ARG_66	NH1	B_ASP_28	OD1	2.856
6C6Y	B_LYS_103	NZ	B_GLU_165	OE1	2.786
6C6Y	B_LYS_103	NZ	B_GLU_165	OE2	3.365
6C6Y	B_ARG_142	NH1	B_GLU_165	OE2	3.444
6C6Y	B_LYS_149	NZ	B_GLU_195	OE1	3.173
6C6Y	B_LYS_149	NZ	B_GLU_195	OE2	3.288
6C6Y	B_LYS_155	NZ	B_GLU_185	OE1	3.980
6C6Y	B_LYS_155	NZ	B_GLU_185	OE2	2.781
6C6Y	H_ARG_38	NH1	H_ASP_86	OD1	3.029
6C6Y	H_ARG_38	NH2	H_GLU_46	OE2	2.521
6C6Y	H_ARG_38	NH2	H_ASP_86	OD1	3.913
6C6Y	H_ARG_50	NH2	H_ASP_58	OD2	3.613
6C6Y	H_ARG_66	NH1	H_ASP_86	OD1	3.184
6C6Y	H_ARG_66	NH1	H_ASP_86	OD2	2.116
6C6Y	H_ARG_66	NH2	H_ASP_86	OD1	3.133

6C6Y	H_ARG_66	NH2	H_ASP_86	OD2	3.619
6C6Y	L_ARG_24	NH1	L_ASP_70	OD1	3.969
6C6Y	L_ARG_24	NH1	L_ASP_70	OD2	3.418
6C6Y	L_ARG_24	NH2	L_ASP_70	OD1	3.004
6C6Y	L_ARG_24	NH2	L_ASP_70	OD2	2.849
6C6Y	L_ARG_61	NH2	L_ASP_82	OD1	2.482
6C6Y	L_ARG_61	NH2	L_ASP_82	OD2	3.036
6C6Y	L_ARG_66	NH1	L_ASP_28	OD1	3.067
6C6Y	L_LYS_103	NZ	L_GLU_165	OE1	2.476
6C6Y	L_ARG_142	NH2	L_GLU_165	OE2	3.885
6C6Y	L_LYS_147	NZ	L_GLU_195	OE1	3.059
6C6Y	L_LYS_147	NZ	L_GLU_195	OE2	3.820
6C6Y	L_LYS_155	NZ	L_GLU_185	OE2	3.070
6C6Y	R_LYS_400	NZ	L_ASP_28	OD2	3.363
6C6Y	R_ARG_401	NH2	R_ASP_444	OD2	3.769
6C6Y	R_LYS_413	NZ	R_GLU_382	OE2	3.002
6C6Y	R_LYS_453	NZ	R_ASP_422	OD2	3.217
6C6Y	R_LYS_502	NZ	R_GLU_513	OE1	3.001
6C6Y	R_LYS_543	NZ	L_GLU_55	OE2	2.973
6C6Y	R_LYS_587	NZ	R_GLU_382	OE1	3.401
6C6Y	R_LYS_587	NZ	R_GLU_382	OE2	2.619
6C6Y	S_LYS_400	NZ	B_ASP_28	OD1	3.764
6C6Y	S_LYS_400	NZ	B_ASP_28	OD2	2.712
6C6Y	S_ARG_401	NH2	S_ASP_444	OD2	2.856
6C6Y	S_LYS_413	NZ	S_GLU_382	OE2	3.998
6C6Y	S_LYS_453	NZ	S_ASP_422	OD2	2.144
6C6Y	S_LYS_502	NZ	S_GLU_513	OE1	3.472
6C6Y	S_LYS_543	NZ	B_GLU_55	OE2	3.134
6C6Y	S_LYS_587	NZ	S_GLU_382	OE1	3.941
6C6Y	S_LYS_587	NZ	S_GLU_382	OE2	2.874
6C6Z	A_ARG_401	NH2	A_ASP_444	OD1	3.459
6C6Z	A_ARG_401	NH2	A_ASP_444	OD2	2.937
6C6Z	A_LYS_453	NZ	A_ASP_422	OD1	3.282
6C6Z	A_LYS_453	NZ	A_ASP_422	OD2	3.866
6C6Z	A_ARG_542	NH1	C_GLU_95	OE1	3.387
6C6Z	A_ARG_542	NH1	C_GLU_95	OE2	2.704
6C6Z	A_ARG_542	NH2	C_GLU_95	OE1	2.635
6C6Z	A_ARG_542	NH2	C_GLU_95	OE2	3.577
6C6Z	B_ARG_401	NH2	B_ASP_444	OD1	3.464
6C6Z	B_ARG_401	NH2	B_ASP_444	OD2	3.103
6C6Z	B_LYS_453	NZ	B_ASP_422	OD2	2.962
6C6Z	B_LYS_502	NZ	B_GLU_513	OE2	2.909
6C6Z	B_ARG_542	NH1	H_GLU_95	OE1	3.238
6C6Z	B_ARG_542	NH1	H_GLU_95	OE2	2.770
6C6Z	B_ARG_542	NH2	H_GLU_95	OE1	2.578
6C6Z	B_ARG_542	NH2	H_GLU_95	OE2	3.689
6C6Z	B_LYS_543	NZ	B_GLU_549	OE2	3.799
6C6Z	C_LYS_12	NZ	C_GLU_10	OE1	3.923
6C6Z	C_ARG_38	NH1	C_ASP_86	OD1	2.775
6C6Z	C_ARG_38	NH2	C_GLU_46	OE1	3.971
6C6Z	C_ARG_38	NH2	C_ASP_86	OD1	3.678
6C6Z	C_LYS_62	NZ	C_GLU_46	OE1	3.517
6C6Z	C_LYS_62	NZ	C_GLU_46	OE2	2.404
6C6Z	C_ARG_66	NH1	C_ASP_86	OD1	3.649
6C6Z	C_ARG_66	NH1	C_ASP_86	OD2	2.887
6C6Z	C_ARG_66	NH2	C_ASP_86	OD1	2.965
6C6Z	C_ARG_66	NH2	C_ASP_86	OD2	3.656
6C6Z	C_LYS_143	NZ	C_ASP_144	OD1	3.698

6C6Z	C_LYS_209	NZ	D_GLU_123	OE1	2.970
6C6Z	C_LYS_209	NZ	D_GLU_123	OE2	3.150
6C6Z	C_LYS_214	NZ	D_ASP_122	OD2	2.844
6C6Z	D_ARG_24	NH2	D_ASP_70	OD1	3.771
6C6Z	D_ARG_24	NH2	D_ASP_70	OD2	3.462
6C6Z	D_HIS_27D	NE2	A_GLU_536	OE1	2.616
6C6Z	D_LYS_39	NZ	D_GLU_81	OE1	3.045
6C6Z	D_ARG_61	NH1	D_ASP_82	OD1	3.547
6C6Z	D_ARG_61	NH1	D_ASP_82	OD2	2.767
6C6Z	D_ARG_61	NH2	D_GLU_79	OE2	3.892
6C6Z	D_ARG_61	NH2	D_ASP_82	OD1	2.888
6C6Z	D_ARG_61	NH2	D_ASP_82	OD2	3.519
6C6Z	D_LYS_103	NZ	D_GLU_105	OE1	3.035
6C6Z	D_LYS_149	NZ	D_GLU_195	OE2	3.680
6C6Z	D_LYS_183	NZ	D_GLU_187	OE1	3.446
6C6Z	D_LYS_183	NZ	D_GLU_187	OE2	2.362
6C6Z	H_LYS_12	NZ	H_GLU_10	OE1	3.627
6C6Z	H_ARG_38	NH1	H_ASP_86	OD1	2.800
6C6Z	H_ARG_38	NH2	H_GLU_46	OE1	3.855
6C6Z	H_ARG_38	NH2	H_ASP_86	OD1	3.819
6C6Z	H_LYS_62	NZ	H_GLU_46	OE1	3.413
6C6Z	H_LYS_62	NZ	H_GLU_46	OE2	2.893
6C6Z	H_ARG_66	NH1	H_ASP_86	OD1	3.573
6C6Z	H_ARG_66	NH1	H_ASP_86	OD2	2.784
6C6Z	H_ARG_66	NH2	H_ASP_86	OD1	2.918
6C6Z	H_ARG_66	NH2	H_ASP_86	OD2	3.610
6C6Z	H_LYS_143	NZ	H_ASP_144	OD1	3.196
6C6Z	H_LYS_143	NZ	H_ASP_144	OD2	3.107
6C6Z	H_LYS_206	NZ	H_ASP_208	OD1	2.733
6C6Z	H_LYS_209	NZ	L_GLU_123	OE1	3.044
6C6Z	H_LYS_209	NZ	L_GLU_123	OE2	3.156
6C6Z	L_HIS_27D	NE2	B_GLU_536	OE1	2.931
6C6Z	L_LYS_39	NZ	L_GLU_81	OE1	3.674
6C6Z	L_ARG_61	NH1	L_ASP_82	OD1	3.616
6C6Z	L_ARG_61	NH1	L_ASP_82	OD2	2.658
6C6Z	L_ARG_61	NH2	L_ASP_82	OD1	2.969
6C6Z	L_ARG_61	NH2	L_ASP_82	OD2	3.526
6C6Z	L_LYS_169	NZ	L_ASP_170	OD2	3.960
6C6Z	L_LYS_183	NZ	L_GLU_187	OE1	2.903
6C6Z	L_LYS_183	NZ	L_GLU_187	OE2	3.197
6C6Z	L_LYS_188	NZ	L_ASP_185	OD1	3.953
6CUJ	A_HIS_325	NE2	A_ASP_359	OD2	3.301
6CUJ	A_ARG_337	NH1	A_GLU_322	OE1	3.884
6CUJ	A_LYS_378	NZ	A_ASP_388	OD2	3.300
6CUJ	B_HIS_327	ND1	B_ASP_359	OD2	3.102
6CUJ	B_HIS_327	NE2	B_GLU_329	OE2	2.543
6CUJ	B_HIS_327	NE2	B_ASP_359	OD2	3.671
6CUJ	B_ARG_337	NH1	B_GLU_322	OE1	3.772
6CUJ	B_HIS_362	ND1	B_ASP_359	OD1	3.012
6CUJ	B_HIS_362	ND1	B_ASP_359	OD2	2.820
6CUJ	B_LYS_404	NZ	A_GLU_292	OE1	3.957
6DC3	H_ARG_38	NH1	H_ASP_86	OD1	2.959
6DC3	H_ARG_38	NH2	H_GLU_46	OE1	3.231
6DC3	H_ARG_38	NH2	H_GLU_46	OE2	3.389
6DC3	H_ARG_66	NH2	H_ASP_86	OD1	3.488
6DC3	H_ARG_66	NH2	H_ASP_86	OD2	2.922
6DC3	H_ARG_94	NH2	H_ASP_101	OD1	3.653
6DC3	H_ARG_94	NH2	H_ASP_101	OD2	2.581

6DC3	H.LYS_143	NZ	L.GLU_125	OE2	3.101
6DC3	H.LYS_209	NZ	L.GLU_124	OE1	3.719
6DC3	H.ARG_210	NH1	H.GLU_212	OE2	3.787
6DC3	H.ARG_210	NH2	H.GLU_212	OE2	3.635
6DC3	L.ARG_61	NH1	L.ASP_82	OD2	2.982
6DC3	L.ARG_61	NH2	L.ASP_82	OD1	2.867
6DC3	L.ARG_61	NH2	L.ASP_82	OD2	2.906
6DC3	F.ARG_49	NH1	F.ASP_368	OD1	2.816
6DC3	F.ARG_49	NH1	F.ASP_368	OD2	3.848
6DC3	F.LYS_166	NZ	F.GLU_163	OE1	2.612
6DC3	F.LYS_168	NZ	H.ASP_53	OD2	2.485
6DC3	F.LYS_176	NZ	F.ASP_263	OD1	3.442
6DC3	F.LYS_176	NZ	F.ASP_263	OD2	3.080
6DC3	F.LYS_191	NZ	F.GLU_60	OE1	2.907
6DC3	F.LYS_191	NZ	F.GLU_60	OE2	3.428
6DC3	F.LYS_196	NZ	F.GLU_295	OE1	2.816
6DC3	F.ARG_229	NH1	F.GLU_256	OE1	3.821
6DC3	F.ARG_229	NH1	F.GLU_256	OE2	2.936
6DC3	F.ARG_229	NH2	F.GLU_256	OE1	2.824
6DC3	F.ARG_229	NH2	F.GLU_256	OE2	3.412
6DC3	F.ARG_235	NH2	F.GLU_232	OE1	3.589
6DC3	F.ARG_235	NH2	F.GLU_232	OE2	3.188
6DC3	F.ARG_336	NH2	F.ASP_338	OD1	3.536
6DC3	F.ARG_336	NH2	F.ASP_338	OD2	3.006
6DC3	F.ARG_364	NH1	F.ASP_310	OD1	3.283
6DC3	F.ARG_364	NH2	F.ASP_310	OD1	2.353
6DC3	F.LYS_394	NZ	F.ASP_489	OD1	2.937
6DC3	F.LYS_433	NZ	F.ASP_440	OD1	3.790
6DC3	F.LYS_433	NZ	F.ASP_440	OD2	2.911
6DC3	F.LYS_461	NZ	F.ASP_448	OD1	3.211
6DC3	F.LYS_498	NZ	F.GLU_487	OE2	3.896
6DC4	H.HIS_35	NE2	H.GLU_52	OE2	2.774
6DC4	H.ARG_38	NH1	H.ASP_86	OD1	2.825
6DC4	H.ARG_38	NH2	H.GLU_46	OE1	3.316
6DC4	H.ARG_38	NH2	H.ASP_86	OD1	3.824
6DC4	H.LYS_62	NZ	H.GLU_46	OE1	3.857
6DC4	H.LYS_62	NZ	H.GLU_46	OE2	2.772
6DC4	H.ARG_66	NH1	H.ASP_86	OD1	3.550
6DC4	H.ARG_66	NH1	H.ASP_86	OD2	2.921
6DC4	H.ARG_66	NH2	H.ASP_86	OD1	2.875
6DC4	H.ARG_66	NH2	H.ASP_86	OD2	3.553
6DC4	H.LYS_143	NZ	H.ASP_144	OD1	2.940
6DC4	H.LYS_143	NZ	H.ASP_144	OD2	2.949
6DC4	H.LYS_209	NZ	L.GLU_123	OE1	3.056
6DC4	H.LYS_210	NZ	H.GLU_212	OE2	2.245
6DC4	L.ARG_24	NH2	L.ASP_70	OD1	2.900
6DC4	L.ARG_24	NH2	L.ASP_70	OD2	3.578
6DC4	L.ARG_61	NH2	L.GLU_81	OE2	3.633
6DC4	L.ARG_61	NH2	L.ASP_82	OD1	2.855
6DC4	L.ARG_61	NH2	L.ASP_82	OD2	3.416
6DC5	A.ARG_49	NH2	A.ASP_368	OD1	3.110
6DC5	A.LYS_85	NZ	A.GLU_82	OE1	3.470
6DC5	A.LYS_87	NZ	A.ASP_84	OD1	3.601
6DC5	A.LYS_156	NZ	D.GLU_463	OE1	3.876
6DC5	A.LYS_166	NZ	A.GLU_163	OE1	3.173
6DC5	A.LYS_166	NZ	A.GLU_163	OE2	3.169
6DC5	A.LYS_168	NZ	A.GLU_294	OE1	3.265
6DC5	A.LYS_176	NZ	A.ASP_263	OD2	2.052

6DC5	A_LYS_191	NZ	A_GLU_60	OE1	3.950
6DC5	A_LYS_196	NZ	A_ASP_200	OD2	2.872
6DC5	A_LYS_196	NZ	A_GLU_295	OE1	2.434
6DC5	A_LYS_196	NZ	A_GLU_295	OE2	3.186
6DC5	A_LYS_226	NZ	A_GLU_222	OE2	3.817
6DC5	A_ARG_229	NH1	A_GLU_256	OE1	3.604
6DC5	A_ARG_229	NH1	A_GLU_256	OE2	2.958
6DC5	A_ARG_229	NH2	A_GLU_256	OE1	2.962
6DC5	A_ARG_229	NH2	A_GLU_256	OE2	3.782
6DC5	A_ARG_235	NH1	A_GLU_232	OE1	2.605
6DC5	A_ARG_235	NH1	A_GLU_232	OE2	2.938
6DC5	A_ARG_336	NH2	A_ASP_338	OD1	3.564
6DC5	A_ARG_336	NH2	A_ASP_338	OD2	2.679
6DC5	A_ARG_364	NH1	A_ASP_310	OD1	2.528
6DC5	A_ARG_364	NH2	A_ASP_310	OD1	3.947
6DC5	A_LYS_394	NZ	A_ASP_489	OD1	2.355
6DC5	A_LYS_394	NZ	A_ASP_489	OD2	3.843
6DC5	A_LYS_399	NZ	G_GLU_497	OE2	2.871
6DC5	A_LYS_427	NZ	A_ASP_448	OD1	3.250
6DC5	A_LYS_427	NZ	A_ASP_448	OD2	2.579
6DC5	A_LYS_461	NZ	A_ASP_448	OD1	2.319
6DC5	A_LYS_498	NZ	A_GLU_487	OE1	3.625
6DC5	A_LYS_498	NZ	A_GLU_487	OE2	2.810
6DC5	D_LYS_42	NZ	D_GLU_31	OE2	3.526
6DC5	D_ARG_49	NH2	D_ASP_368	OD1	2.868
6DC5	D_LYS_75	NZ	G_GLU_218	OE2	2.912
6DC5	D_LYS_85	NZ	D_GLU_82	OE1	3.435
6DC5	D_LYS_166	NZ	D_GLU_163	OE1	3.454
6DC5	D_LYS_166	NZ	D_GLU_163	OE2	3.601
6DC5	D_LYS_168	NZ	D_GLU_294	OE1	3.339
6DC5	D_LYS_168	NZ	D_GLU_294	OE2	3.380
6DC5	D_LYS_176	NZ	D_ASP_263	OD1	3.729
6DC5	D_LYS_176	NZ	D_ASP_263	OD2	2.442
6DC5	D_LYS_196	NZ	D_ASP_200	OD2	2.508
6DC5	D_LYS_196	NZ	D_GLU_295	OE1	2.680
6DC5	D_LYS_196	NZ	D_GLU_295	OE2	3.385
6DC5	D_LYS_209	NZ	E_GLU_53	OE2	3.142
6DC5	D_LYS_209	NZ	E_ASP_100G	OD2	3.755
6DC5	D_LYS_226	NZ	D_GLU_222	OE2	3.264
6DC5	D_ARG_229	NH1	D_GLU_256	OE1	3.363
6DC5	D_ARG_229	NH1	D_GLU_256	OE2	3.131
6DC5	D_ARG_229	NH2	D_GLU_256	OE1	3.395
6DC5	D_ARG_235	NH1	D_GLU_232	OE1	3.378
6DC5	D_ARG_235	NH1	D_GLU_232	OE2	2.564
6DC5	D_ARG_336	NH2	D_ASP_338	OD1	3.496
6DC5	D_ARG_336	NH2	D_ASP_338	OD2	2.373
6DC5	D_ARG_364	NH1	D_ASP_310	OD1	2.428
6DC5	D_ARG_364	NH2	D_ASP_310	OD1	3.463
6DC5	D_LYS_394	NZ	D_ASP_489	OD1	2.520
6DC5	D_LYS_427	NZ	D_ASP_448	OD1	3.113
6DC5	D_LYS_427	NZ	D_ASP_448	OD2	2.130
6DC5	D_LYS_433	NZ	D_ASP_440	OD2	3.766
6DC5	G_ARG_49	NH2	G_ASP_368	OD1	3.771
6DC5	G_LYS_68	NZ	G_GLU_66	OE2	3.905
6DC5	G_LYS_77	NZ	A_GLU_222	OE2	3.675
6DC5	G_LYS_85	NZ	G_GLU_82	OE1	2.899
6DC5	G_LYS_87	NZ	G_ASP_84	OD1	3.393
6DC5	G_LYS_166	NZ	G_GLU_163	OE1	3.829

6DC5	G_LYS_166	NZ	G_GLU_163	OE2	3.728
6DC5	G_LYS_168	NZ	G_GLU_294	OE1	3.141
6DC5	G_LYS_176	NZ	G_ASP_263	OD1	3.769
6DC5	G_LYS_176	NZ	G_ASP_263	OD2	2.528
6DC5	G_LYS_191	NZ	G_GLU_60	OE1	3.637
6DC5	G_LYS_191	NZ	G_GLU_60	OE2	2.059
6DC5	G_LYS_196	NZ	G_GLU_295	OE1	3.725
6DC5	G_LYS_196	NZ	G_GLU_295	OE2	2.152
6DC5	G_LYS_209	NZ	H_GLU_53	OE2	3.533
6DC5	G_LYS_209	NZ	H_ASP_100G	OD2	3.715
6DC5	G_ARG_229	NH1	G_GLU_256	OE1	3.620
6DC5	G_ARG_229	NH1	G_GLU_256	OE2	2.755
6DC5	G_ARG_229	NH2	G_GLU_256	OE1	2.678
6DC5	G_ARG_229	NH2	G_GLU_256	OE2	3.180
6DC5	G_ARG_235	NH1	G_GLU_232	OE1	3.701
6DC5	G_ARG_235	NH1	G_GLU_232	OE2	2.639
6DC5	G_ARG_336	NH2	G_ASP_338	OD1	3.302
6DC5	G_ARG_364	NH1	G_ASP_310	OD1	2.671
6DC5	G_ARG_364	NH2	G_ASP_310	OD1	2.918
6DC5	G_LYS_399	NZ	D_GLU_497	OE1	3.390
6DC5	G_LYS_399	NZ	D_GLU_497	OE2	2.804
6DC5	G_LYS_461	NZ	G_ASP_448	OD1	3.243
6DC5	B_LYS_12	NZ	B_GLU_10	OE1	3.494
6DC5	B_HIS_35	NE2	B_GLU_52	OE2	2.642
6DC5	B_ARG_38	NH1	B_ASP_86	OD1	3.077
6DC5	B_ARG_38	NH2	B_GLU_46	OE1	3.245
6DC5	B_LYS_62	NZ	B_GLU_46	OE2	3.113
6DC5	B_ARG_66	NH1	B_ASP_86	OD1	3.647
6DC5	B_ARG_66	NH1	B_ASP_86	OD2	3.361
6DC5	B_ARG_66	NH2	B_ASP_86	OD1	2.784
6DC5	B_ARG_66	NH2	B_ASP_86	OD2	3.528
6DC5	B_LYS_143	NZ	B_ASP_144	OD1	3.448
6DC5	B_LYS_143	NZ	B_ASP_144	OD2	3.641
6DC5	B_LYS_209	NZ	C_GLU_123	OE1	2.374
6DC5	B_LYS_209	NZ	C_GLU_123	OE2	3.312
6DC5	B_LYS_210	NZ	B_GLU_212	OE2	2.833
6DC5	C_ARG_61	NH2	C_GLU_81	OE2	3.401
6DC5	C_ARG_61	NH2	C_ASP_82	OD1	3.387
6DC5	C_ARG_61	NH2	C_ASP_82	OD2	3.483
6DC5	E_LYS_12	NZ	E_GLU_10	OE1	3.386
6DC5	E_HIS_35	NE2	E_GLU_52	OE2	3.002
6DC5	E_ARG_38	NH1	E_ASP_86	OD1	3.042
6DC5	E_ARG_38	NH2	E_GLU_46	OE1	3.298
6DC5	E_LYS_62	NZ	E_GLU_46	OE1	3.343
6DC5	E_LYS_62	NZ	E_GLU_46	OE2	2.685
6DC5	E_ARG_66	NH1	E_ASP_86	OD1	3.530
6DC5	E_ARG_66	NH1	E_ASP_86	OD2	3.256
6DC5	E_ARG_66	NH2	E_ASP_86	OD1	2.815
6DC5	E_ARG_66	NH2	E_ASP_86	OD2	3.601
6DC5	E_LYS_143	NZ	E_ASP_144	OD1	3.756
6DC5	E_LYS_143	NZ	E_ASP_144	OD2	3.843
6DC5	E_LYS_209	NZ	F_GLU_123	OE1	3.793
6DC5	E_LYS_210	NZ	E_GLU_212	OE2	3.622
6DC5	F_ARG_24	NH1	F_ASP_70	OD1	3.764
6DC5	F_ARG_24	NH2	F_ASP_70	OD1	2.904
6DC5	F_ARG_24	NH2	F_ASP_70	OD2	2.994
6DC5	F_ARG_61	NH2	F_GLU_81	OE2	3.917
6DC5	F_ARG_61	NH2	F_ASP_82	OD1	2.920

6DC5	F_ARG_61	NH2	F_ASP_82	OD2	3.281
6DC5	F_LYS_103	NZ	F_ASP_105	OD1	3.853
6DC5	F_LYS_107	NZ	F_GLU_17	OE1	3.389
6DC5	F_LYS_107	NZ	F_GLU_17	OE2	3.533
6DC5	H_HIS_35	NE2	H_GLU_52	OE2	2.720
6DC5	H_ARG_38	NH1	H_ASP_86	OD1	3.016
6DC5	H_ARG_38	NH2	H_GLU_46	OE1	3.352
6DC5	H_ARG_38	NH2	H_ASP_86	OD1	3.965
6DC5	H_LYS_62	NZ	H_GLU_46	OE1	3.843
6DC5	H_LYS_62	NZ	H_GLU_46	OE2	2.697
6DC5	H_ARG_66	NH1	H_ASP_86	OD1	3.199
6DC5	H_ARG_66	NH1	H_ASP_86	OD2	2.905
6DC5	H_ARG_66	NH2	H_ASP_86	OD1	3.432
6DC5	H_LYS_143	NZ	H_ASP_144	OD1	3.438
6DC5	H_LYS_143	NZ	H_ASP_	OD2	3.755
6DC5	H_LYS_	NZ	I_GLU_	OE1	2.846
6DC5	H_LYS_	NZ	I_ASP_	OD1	3.400
6DC5	H_LYS_	NZ	I_ASP_	OD2	3.825
6DC5	I_ARG_24	NH1	I_ASP_70	OD2	3.681
6DC5	I_ARG_61	NH2	I_ASP_82	OD1	2.828
6DC5	I_ARG_61	NH2	I_ASP_82	OD2	3.083
6DC5	I_LYS_107	NZ	I_GLU_17	OE1	3.661
6DC5	I_LYS_107	NZ	I_GLU_17	OE2	3.133
6DC5	I_LYS_149	NZ	I_GLU_195	OE1	3.809
6DCV	L_ARG_18	NH2	L_ASP_76	OD1	3.175
6DCV	L_ARG_61	NH1	L_ASP_82	OD1	3.860
6DCV	L_ARG_61	NH1	L_ASP_82	OD2	2.769
6DCV	L_ARG_61	NH2	L_ASP_82	OD1	2.985
6DCV	L_ARG_61	NH2	L_ASP_82	OD2	3.307
6DCV	L_LYS_149	NZ	L_GLU_195	OE1	2.823
6DCV	L_LYS_149	NZ	L_GLU_195	OE2	3.954
6DCV	L_LYS_183	NZ	L_GLU_187	OE2	2.410
6DCV	L_LYS_188	NZ	L_ASP_185	OD1	3.076
6DCV	L_HIS_189	ND1	L_ASP_151	OD2	3.050
6DCV	H_ARG_12	NH1	H_GLU_10	OE1	3.321
6DCV	H_ARG_12	NH2	H_GLU_10	OE1	3.424
6DCV	H_LYS_43	NZ	L_ASP_9	OD1	3.193
6DCV	H_ARG_58	NH1	H_ASP_56	OD1	3.128
6DCV	H_ARG_58	NH1	H_ASP_56	OD2	3.930
6DCV	H_HIS_66	ND1	H_ASP_86	OD1	3.802
6DCV	H_HIS_66	NE2	H_ASP_86	OD2	3.695
6DCV	H_ARG_94	NH2	H_ASP_101	OD1	3.792
6DCV	H_ARG_94	NH2	H_ASP_101	OD2	3.895
6DCV	H_ARG_98	NH1	H_ASP_96	OD2	3.931
6DCV	H_ARG_98	NH2	H_ASP_31	OD2	3.613
6DCV	H_LYS_145	NZ	H_ASP_146	OD1	3.176
6DCV	H_LYS_145	NZ	H_ASP_146	OD2	2.821
6DCV	H_LYS_221	NZ	L_GLU_123	OE1	3.166
6DCV	H_ARG_222	NH1	H_GLU_226	OE2	3.915
6DCV	A_ARG_18	NH2	A_ASP_76	OD1	2.925
6DCV	A_ARG_61	NH1	A_ASP_82	OD1	3.927
6DCV	A_ARG_61	NH1	A_ASP_82	OD2	2.798
6DCV	A_ARG_61	NH2	A_ASP_82	OD1	2.940
6DCV	A_ARG_61	NH2	A_ASP_82	OD2	3.262
6DCV	A_LYS_149	NZ	A_GLU_195	OE1	2.726
6DCV	A_HIS_189	ND1	A_ASP_151	OD2	3.062
6DCV	B_ARG_12	NH1	B_GLU_10	OE1	3.306
6DCV	B_ARG_12	NH2	B_GLU_10	OE1	3.831

6DCV	B.LYS_13	NZ	B.GLU_16	OE2	3.930
6DCV	B.LYS_43	NZ	A.ASP_9	OD1	3.127
6DCV	B.ARG_58	NH1	B.ASP_56	OD1	3.719
6DCV	B.ARG_58	NH1	B.ASP_56	OD2	3.964
6DCV	B.ARG_58	NH2	B.ASP_56	OD2	3.300
6DCV	B.HIS_66	NE2	B.ASP_86	OD1	2.995
6DCV	B.HIS_66	NE2	B.ASP_86	OD2	3.037
6DCV	B.ARG_94	NH2	B.ASP_101	OD1	3.995
6DCV	B.ARG_94	NH2	B.ASP_101	OD2	3.590
6DCV	B.ARG_98	NH2	B.ASP_31	OD2	3.052
6DCV	B.LYS_145	NZ	B.ASP_146	OD1	3.023
6DCV	B.LYS_145	NZ	B.ASP_146	OD2	2.799
6DCV	B.LYS_221	NZ	A.GLU_123	OE1	3.096
6DCW	L.ARG_18	NH1	L.ASP_76	OD1	3.895
6DCW	L.ARG_54	NH2	L.ASP_60	OD1	3.555
6DCW	L.ARG_61	NH1	L.ASP_82	OD1	3.666
6DCW	L.ARG_61	NH1	L.ASP_82	OD2	2.742
6DCW	L.ARG_61	NH2	L.ASP_82	OD1	2.952
6DCW	L.ARG_61	NH2	L.ASP_82	OD2	3.481
6DCW	L.LYS_188	NZ	L.ASP_185	OD1	2.731
6DCW	L.HIS_189	ND1	L.ASP_151	OD2	3.503
6DCW	H.ARG_12	NH1	H.GLU_10	OE1	3.120
6DCW	H.ARG_12	NH2	H.GLU_10	OE1	3.789
6DCW	H.LYS_43	NZ	L.ASP_9	OD1	3.018
6DCW	H.ARG_58	NH2	H.ASP_56	OD1	3.918
6DCW	H.ARG_58	NH2	H.ASP_56	OD2	2.896
6DCW	H.HIS_66	NE2	H.ASP_86	OD1	3.111
6DCW	H.HIS_66	NE2	H.ASP_86	OD2	2.753
6DCW	H.ARG_94	NH2	H.ASP_101	OD1	3.488
6DCW	H.ARG_98	NH1	H.ASP_31	OD2	3.894
6DCW	H.ARG_98	NH2	H.ASP_96	OD1	3.809
6DCW	H.ARG_98	NH2	H.ASP_96	OD2	3.209
6DCW	H.LYS_145	NZ	H.ASP_146	OD1	3.440
6DCW	H.LYS_145	NZ	H.ASP_146	OD2	3.529
6DCW	T.LYS_317	NZ	H.ASP_54	OD1	3.849
6DCW	T.LYS_317	NZ	H.ASP_54	OD2	2.833
6DCW	T.LYS_317	NZ	H.ASP_56	OD2	2.597
6DDM	A.ARG_61	NH2	A.GLU_81	OE2	2.977
6DDM	A.ARG_61	NH2	A.ASP_82	OD1	2.747
6DDM	A.ARG_61	NH2	A.ASP_82	OD2	3.496
6DDM	A.LYS_103	NZ	A.GLU_165	OE1	2.802
6DDM	A.LYS_103	NZ	A.GLU_165	OE2	3.912
6DDM	A.LYS_149	NZ	A.GLU_195	OE1	2.933
6DDM	A.ARG_211	NH1	A.GLU_187	OE1	3.736
6DDM	C.ARG_213	NH2	C.GLU_277	OE2	3.529
6DDM	C.ARG_279	NH1	C.GLU_276	OE1	2.719
6DDM	C.ARG_279	NH2	C.ASP_242	OD2	2.805
6DDM	B.LYS_62	NZ	A.GLU_1	OE1	3.434
6DDM	B.LYS_62	NZ	A.GLU_1	OE2	2.992
6DDM	B.LYS_66	NZ	B.ASP_86	OD1	3.688
6DDM	B.LYS_66	NZ	B.ASP_86	OD2	2.870
6DDM	B.LYS_143	NZ	B.ASP_144	OD1	3.301
6DDM	B.LYS_143	NZ	B.ASP_144	OD2	3.964
6DDM	B.LYS_210	NZ	B.GLU_212	OE2	3.002
6DDR	A.ARG_61	NH2	A.GLU_81	OE2	3.323
6DDR	A.ARG_61	NH2	A.ASP_82	OD1	2.814
6DDR	A.ARG_61	NH2	A.ASP_82	OD2	3.435
6DDR	A.LYS_103	NZ	A.GLU_165	OE1	2.937

6DDR	A_LYS_103	NZ	A_GLU_165	OE2	3.642
6DDR	A_LYS_149	NZ	A_GLU_195	OE1	3.062
6DDR	A_LYS_149	NZ	A_GLU_195	OE2	3.956
6DDR	A_HIS_189	ND1	A_ASP_151	OD2	2.733
6DDR	A_HIS_189	NE2	A_ASP_185	OD1	3.597
6DDR	B_LYS_38	NZ	B_ASP_85	OD2	3.921
6DDR	B_ARG_40	NH1	B_ASP_85	OD1	2.696
6DDR	B_ARG_40	NH2	B_GLU_46	OE1	2.989
6DDR	B_ARG_40	NH2	B_ASP_85	OD1	3.981
6DDR	B_LYS_66	NZ	B_ASP_86	OD1	3.678
6DDR	B_LYS_66	NZ	B_ASP_86	OD2	2.732
6DDR	B_LYS_143	NZ	B_ASP_144	OD1	3.277
6DDR	B_LYS_143	NZ	B_ASP_144	OD2	2.811
6DDR	B_LYS_209	NZ	A_GLU_123	OE1	3.270
6DDR	B_LYS_210	NZ	B_GLU_212	OE1	3.192
6DDR	C_ARG_213	NH1	C_GLU_277	OE2	3.507
6DDR	C_ARG_213	NH2	C_GLU_277	OE2	2.893
6DDR	C_HIS_248	NE2	C_ASP_249	OD1	3.810
6DDR	C_ARG_279	NH2	C_ASP_242	OD1	3.644
6DDR	C_ARG_279	NH2	C_ASP_242	OD2	2.939
6DDV	B_LYS_40	NZ	B_GLU_85	OE1	3.350
6DDV	B_LYS_62	NZ	B_GLU_46	OE1	2.630
6DDV	B_LYS_62	NZ	B_GLU_46	OE2	3.425
6DDV	B_ARG_64	NH1	B_ASP_65	OD2	3.653
6DDV	B_LYS_66	NZ	B_ASP_86	OD1	3.869
6DDV	B_LYS_66	NZ	B_ASP_86	OD2	2.750
6DDV	B_LYS_143	NZ	B_ASP_144	OD1	3.440
6DDV	B_LYS_143	NZ	B_ASP_144	OD2	3.403
6DDV	B_LYS_209	NZ	A_GLU_123	OE1	3.050
6DDV	B_LYS_209	NZ	A_GLU_123	OE2	3.197
6DDV	B_LYS_210	NZ	B_GLU_212	OE1	3.943
6DDV	B_LYS_210	NZ	B_GLU_212	OE2	3.102
6DDV	C_ARG_226	NH1	B_ASP_31	OD1	3.652
6DDV	C_ARG_226	NH1	B_ASP_31	OD2	2.831
6DDV	C_ARG_226	NH2	B_ASP_31	OD1	3.123
6DDV	C_ARG_226	NH2	B_ASP_31	OD2	3.778
6DDV	C_ARG_279	NH1	C_GLU_276	OE1	3.430
6DDV	C_ARG_279	NH1	C_GLU_276	OE2	2.920
6DDV	C_ARG_279	NH2	C_ASP_242	OD2	3.431
6DDV	A_LYS_50	NZ	C_ASP_255	OD1	3.063
6DDV	A_LYS_50	NZ	C_ASP_255	OD2	3.312
6DDV	A_ARG_61	NH2	A_ASP_82	OD1	2.731
6DDV	A_ARG_61	NH2	A_ASP_82	OD2	3.820
6DDV	A_LYS_103	NZ	A_GLU_165	OE1	2.682
6DDV	A_LYS_149	NZ	A_GLU_195	OE1	2.706
6DFG	A_LYS_168	NZ	A_ASP_167	OD1	3.182
6DFG	A_LYS_168	NZ	A_ASP_167	OD2	2.721
6DFG	A_LYS_229	NZ	A_GLU_83	OE1	3.608
6DFG	A_LYS_232	NZ	A_GLU_267	OE1	3.152
6DFG	A_LYS_232	NZ	A_GLU_268	OE1	3.241
6DFG	A_LYS_232	NZ	A_GLU_268	OE2	3.886
6DFG	A_LYS_282	NZ	A_GLU_275	OE1	2.361
6DFG	A_ARG_298	NH1	A_GLU_381	OE1	3.634
6DFG	A_ARG_298	NH1	A_GLU_381	OE2	3.774
6DFG	A_ARG_327	NH2	A_ASP_325	OD2	3.456
6DFG	A_ARG_476	NH1	A_ASP_474	OD1	3.432
6DFG	A_ARG_476	NH1	A_ASP_474	OD2	3.733
6DFG	A_ARG_480	NH1	A_ASP_477	OD1	2.382

6DFG	A_LYS_487	NZ	A_GLU_91	OE2	2.524
6DFG	A_LYS_490	NZ	A_GLU_492	OE2	2.373
6DFG	B_HIS_585	ND1	B_GLU_584	OE1	3.794
6DFG	B_HIS_585	NE2	A_GLU_492	OE2	3.210
6DFG	B_ARG_588	NH2	A_GLU_492	OE1	2.981
6DFG	B_ARG_588	NH2	A_GLU_492	OE2	3.149
6DFG	B_ARG_617	NH1	B_GLU_634	OE1	3.067
6DFG	B_ARG_617	NH1	B_GLU_634	OE2	2.965
6DFG	H_HIS_33	NE2	H_ASP_27	OD1	3.974
6DFG	H_ARG_38	NH1	H_ASP_86	OD1	3.005
6DFG	H_ARG_38	NH1	H_ASP_86	OD2	3.826
6DFG	H_ARG_38	NH2	H_GLU_46	OE1	3.689
6DFG	H_ARG_38	NH2	H_GLU_46	OE2	3.014
6DFG	H_ARG_38	NH2	H_ASP_86	OD1	2.880
6DFG	H_ARG_66	NH1	H_ASP_86	OD2	3.544
6DFG	H_ARG_94	NH1	H_ASP_27	OD1	3.807
6DFG	H_ARG_94	NH1	H_ASP_27	OD2	3.737
6DFG	H_ARG_94	NH2	H_ASP_101	OD1	3.688
6DFG	H_ARG_94	NH2	H_ASP_101	OD2	2.491
6DFG	L_ARG_31	NH1	A_ASP_140	OD2	3.569
6DFG	L_ARG_31	NH2	L_ASP_95	OD1	3.542
6DFG	L_ARG_37	NH1	L_ASP_82	OD1	3.979
6DFG	L_ARG_54	NH2	A_ASP_322	OD2	3.922
6DFG	L_ARG_61	NH1	L_ASP_82	OD2	3.243
6DFG	L_ARG_61	NH2	L_ASP_82	OD2	3.425
6DFG	L_LYS_96	NZ	H_ASP_50	OD2	3.294
6DFG	C_LYS_168	NZ	C_ASP_167	OD1	3.183
6DFG	C_LYS_168	NZ	C_ASP_167	OD2	2.721
6DFG	C_LYS_229	NZ	C_GLU_83	OE1	3.608
6DFG	C_LYS_232	NZ	C_GLU_267	OE1	3.151
6DFG	C_LYS_232	NZ	C_GLU_268	OE1	3.240
6DFG	C_LYS_232	NZ	C_GLU_268	OE2	3.886
6DFG	C_LYS_282	NZ	C_GLU_275	OE1	2.361
6DFG	C_ARG_298	NH1	C_GLU_381	OE1	3.635
6DFG	C_ARG_298	NH1	C_GLU_381	OE2	3.774
6DFG	C_ARG_327	NH2	C_ASP_325	OD2	3.457
6DFG	C_ARG_476	NH1	C_ASP_474	OD1	3.431
6DFG	C_ARG_476	NH1	C_ASP_474	OD2	3.733
6DFG	C_ARG_480	NH1	C_ASP_477	OD1	2.383
6DFG	C_LYS_487	NZ	C_GLU_91	OE2	2.525
6DFG	C_LYS_490	NZ	C_GLU_492	OE2	2.372
6DFG	E_HIS_585	ND1	E_GLU_584	OE1	3.793
6DFG	E_HIS_585	NE2	C_GLU_492	OE2	3.225
6DFG	E_ARG_588	NH2	C_GLU_492	OE1	2.984
6DFG	E_ARG_588	NH2	C_GLU_492	OE2	3.072
6DFG	E_ARG_617	NH1	E_GLU_634	OE1	3.067
6DFG	E_ARG_617	NH1	E_GLU_634	OE2	2.965
6DFG	G_HIS_33	NE2	G_ASP_27	OD1	3.974
6DFG	G_ARG_38	NH1	G_ASP_86	OD1	3.004
6DFG	G_ARG_38	NH1	G_ASP_86	OD2	3.826
6DFG	G_ARG_38	NH2	G_GLU_46	OE1	3.689
6DFG	G_ARG_38	NH2	G_GLU_46	OE2	3.013
6DFG	G_ARG_38	NH2	G_ASP_86	OD1	2.880
6DFG	G_ARG_66	NH1	G_ASP_86	OD2	3.543
6DFG	G_ARG_94	NH1	G_ASP_27	OD1	3.807
6DFG	G_ARG_94	NH1	G_ASP_27	OD2	3.738
6DFG	G_ARG_94	NH2	G_ASP_101	OD1	3.688
6DFG	G_ARG_94	NH2	G_ASP_101	OD2	2.492

6DFG	J_ARG_31	NH1	C_ASP_140	OD2	3.924
6DFG	J_ARG_31	NH2	J_ASP_95	OD1	3.542
6DFG	J_ARG_37	NH1	J_ASP_82	OD1	3.978
6DFG	J_ARG_61	NH1	J_ASP_82	OD2	3.243
6DFG	J_ARG_61	NH2	J_ASP_82	OD2	3.425
6DFG	J_LYS_96	NZ	G_ASP_50	OD2	3.096
6DFG	D_LYS_168	NZ	D_ASP_167	OD1	3.183
6DFG	D_LYS_168	NZ	D_ASP_167	OD2	2.721
6DFG	D_LYS_229	NZ	D_GLU_83	OE1	3.608
6DFG	D_LYS_232	NZ	D_GLU_267	OE1	3.152
6DFG	D_LYS_232	NZ	D_GLU_268	OE1	3.241
6DFG	D_LYS_232	NZ	D_GLU_268	OE2	3.886
6DFG	D_LYS_282	NZ	D_GLU_275	OE1	2.361
6DFG	D_ARG_298	NH1	D_GLU_381	OE1	3.634
6DFG	D_ARG_298	NH1	D_GLU_381	OE2	3.773
6DFG	D_ARG_327	NH2	D_ASP_325	OD2	3.457
6DFG	D_ARG_476	NH1	D_ASP_474	OD1	3.432
6DFG	D_ARG_476	NH1	D_ASP_474	OD2	3.733
6DFG	D_ARG_480	NH1	D_ASP_477	OD1	2.383
6DFG	D_LYS_487	NZ	D_GLU_91	OE2	2.524
6DFG	D_LYS_490	NZ	D_GLU_492	OE2	2.374
6DFG	F_HIS_585	ND1	F_GLU_584	OE1	3.793
6DFG	F_HIS_585	NE2	D_GLU_492	OE2	3.337
6DFG	F_ARG_588	NH2	D_GLU_492	OE1	2.974
6DFG	F_ARG_588	NH2	D_GLU_492	OE2	3.036
6DFG	F_ARG_617	NH1	F_GLU_634	OE1	3.067
6DFG	F_ARG_617	NH1	F_GLU_634	OE2	2.965
6DFG	I_HIS_33	NE2	I_ASP_27	OD1	3.975
6DFG	I_ARG_38	NH1	I_ASP_86	OD1	3.005
6DFG	I_ARG_38	NH1	I_ASP_86	OD2	3.826
6DFG	I_ARG_38	NH2	I_GLU_46	OE1	3.689
6DFG	I_ARG_38	NH2	I_GLU_46	OE2	3.014
6DFG	I_ARG_38	NH2	I_ASP_86	OD1	2.879
6DFG	I_ARG_66	NH1	I_ASP_86	OD2	3.544
6DFG	I_ARG_94	NH1	I_ASP_27	OD1	3.807
6DFG	I_ARG_94	NH1	I_ASP_27	OD2	3.738
6DFG	I_ARG_94	NH2	I_ASP_101	OD1	3.687
6DFG	I_ARG_94	NH2	I_ASP_101	OD2	2.491
6DFG	K_ARG_31	NH1	D_ASP_140	OD2	3.732
6DFG	K_ARG_31	NH2	K_ASP_95	OD1	3.542
6DFG	K_ARG_37	NH1	K_ASP_82	OD1	3.979
6DFG	K_ARG_61	NH1	K_ASP_82	OD2	3.243
6DFG	K_ARG_61	NH2	K_ASP_82	OD2	3.426
6DFG	K_LYS_96	NZ	I_ASP_50	OD2	3.268
6DFH	A_LYS_46	NZ	A_GLU_492	OE1	3.414
6DFH	A_HIS_85	NE2	A_GLU_87	OE2	3.841
6DFH	A_LYS_137	NZ	L_ASP_51	OD2	2.491
6DFH	A_ARG_192	NH1	D_GLU_164	OE2	3.939
6DFH	A_HIS_216	NE2	A_ASP_57	OD1	3.108
6DFH	A_HIS_216	NE2	A_ASP_57	OD2	2.891
6DFH	A_LYS_227	NZ	A_GLU_83	OE1	3.845
6DFH	A_LYS_227	NZ	A_GLU_83	OE2	2.457
6DFH	A_LYS_232	NZ	A_GLU_268	OE2	3.725
6DFH	A_HIS_249	NE2	A_GLU_482	OE1	3.926
6DFH	A_LYS_282	NZ	A_GLU_275	OE1	3.019
6DFH	A_LYS_282	NZ	A_GLU_275	OE2	3.829
6DFH	A_LYS_351	NZ	A_GLU_269	OE1	3.844
6DFH	A_LYS_351	NZ	A_GLU_269	OE2	3.223

6DFH	A_ARG_419	NH1	A_GLU_153	OE1	2.923
6DFH	A_ARG_419	NH1	A_GLU_153	OE2	3.091
6DFH	A_ARG_429	NH2	A_ASP_113	OD2	3.911
6DFH	A_ARG_476	NH1	A_GLU_102	OE1	3.544
6DFH	A_ARG_476	NH1	A_GLU_102	OE2	2.438
6DFH	A_ARG_476	NH2	A_ASP_474	OD2	3.340
6DFH	A_ARG_480	NH1	A_ASP_477	OD1	2.443
6DFH	A_LYS_487	NZ	A_ASP_47	OD1	3.477
6DFH	A_LYS_487	NZ	A_ASP_47	OD2	2.691
6DFH	A_LYS_487	NZ	A_GLU_91	OE2	3.894
6DFH	B_ARG_542	NH1	E_GLU_647	OE2	2.777
6DFH	B_LYS_574	NZ	A_ASP_107	OD1	3.419
6DFH	B_LYS_574	NZ	A_ASP_107	OD2	3.383
6DFH	B_ARG_588	NH2	A_GLU_492	OE1	3.118
6DFH	B_ARG_588	NH2	A_GLU_492	OE2	3.874
6DFH	H_ARG_38	NH1	H_ASP_86	OD1	3.690
6DFH	H_ARG_38	NH1	H_ASP_86	OD2	3.393
6DFH	H_ARG_38	NH2	H_GLU_46	OE1	3.255
6DFH	H_ARG_38	NH2	H_ASP_86	OD1	3.023
6DFH	H_ARG_38	NH2	H_ASP_86	OD2	3.384
6DFH	H_ARG_66	NH2	H_ASP_86	OD2	3.900
6DFH	H_ARG_94	NH1	H_ASP_101	OD2	3.387
6DFH	L_LYS_103	NZ	L_ASP_85	OD1	3.975
6DFH	C_LYS_46	NZ	C_GLU_492	OE1	3.413
6DFH	C_HIS_85	NE2	C_GLU_87	OE2	3.840
6DFH	C_LYS_137	NZ	J_ASP_51	OD2	2.536
6DFH	C_ARG_192	NH1	A_GLU_164	OE2	3.905
6DFH	C_HIS_216	NE2	C_ASP_57	OD1	3.108
6DFH	C_HIS_216	NE2	C_ASP_57	OD2	2.892
6DFH	C_LYS_227	NZ	C_GLU_83	OE1	3.845
6DFH	C_LYS_227	NZ	C_GLU_83	OE2	2.456
6DFH	C_LYS_232	NZ	C_GLU_268	OE2	3.726
6DFH	C_HIS_249	NE2	C_GLU_482	OE1	3.927
6DFH	C_LYS_282	NZ	C_GLU_275	OE1	3.018
6DFH	C_LYS_282	NZ	C_GLU_275	OE2	3.829
6DFH	C_LYS_351	NZ	C_GLU_269	OE1	3.844
6DFH	C_LYS_351	NZ	C_GLU_269	OE2	3.223
6DFH	C_ARG_419	NH1	C_GLU_153	OE1	2.923
6DFH	C_ARG_419	NH1	C_GLU_153	OE2	3.092
6DFH	C_ARG_429	NH2	C_ASP_113	OD2	3.910
6DFH	C_ARG_476	NH1	C_GLU_102	OE1	3.543
6DFH	C_ARG_476	NH1	C_GLU_102	OE2	2.438
6DFH	C_ARG_476	NH2	C_ASP_474	OD2	3.339
6DFH	C_ARG_480	NH1	C_ASP_477	OD1	2.443
6DFH	C_LYS_487	NZ	C_ASP_47	OD1	3.476
6DFH	C_LYS_487	NZ	C_ASP_47	OD2	2.691
6DFH	C_LYS_487	NZ	C_GLU_91	OE2	3.893
6DFH	E_ARG_542	NH1	F_GLU_647	OE2	2.777
6DFH	E_LYS_574	NZ	C_ASP_107	OD1	3.423
6DFH	E_LYS_574	NZ	C_ASP_107	OD2	3.381
6DFH	E_ARG_588	NH2	C_GLU_492	OE1	3.158
6DFH	E_ARG_588	NH2	C_GLU_492	OE2	3.904
6DFH	G_ARG_38	NH1	G_ASP_86	OD1	3.690
6DFH	G_ARG_38	NH1	G_ASP_86	OD2	3.393
6DFH	G_ARG_38	NH2	G_GLU_46	OE1	3.255
6DFH	G_ARG_38	NH2	G_ASP_86	OD1	3.022
6DFH	G_ARG_38	NH2	G_ASP_86	OD2	3.383
6DFH	G_ARG_66	NH2	G_ASP_86	OD2	3.900

6DFH	G_ARG_94	NH1	G_ASP_101	OD2	3.387
6DFH	J_LYS_103	NZ	J_ASP_85	OD1	3.976
6DFH	D_LYS_46	NZ	D_GLU_492	OE1	3.413
6DFH	D_HIS_85	NE2	D_GLU_87	OE2	3.840
6DFH	D_LYS_137	NZ	K_ASP_51	OD2	2.448
6DFH	D_ARG_192	NH1	C_GLU_164	OE2	3.902
6DFH	D_HIS_216	NE2	D_ASP_57	OD1	3.108
6DFH	D_HIS_216	NE2	D_ASP_57	OD2	2.891
6DFH	D_LYS_227	NZ	D_GLU_83	OE1	3.845
6DFH	D_LYS_227	NZ	D_GLU_83	OE2	2.456
6DFH	D_LYS_232	NZ	D_GLU_268	OE2	3.726
6DFH	D_HIS_249	NE2	D_GLU_482	OE1	3.926
6DFH	D_LYS_282	NZ	D_GLU_275	OE1	3.019
6DFH	D_LYS_282	NZ	D_GLU_275	OE2	3.830
6DFH	D_LYS_351	NZ	D_GLU_269	OE1	3.845
6DFH	D_LYS_351	NZ	D_GLU_269	OE2	3.223
6DFH	D_ARG_419	NH1	D_GLU_153	OE1	2.923
6DFH	D_ARG_419	NH1	D_GLU_153	OE2	3.092
6DFH	D_ARG_429	NH2	D_ASP_113	OD2	3.910
6DFH	D_ARG_476	NH1	D_GLU_102	OE1	3.543
6DFH	D_ARG_476	NH1	D_GLU_102	OE2	2.438
6DFH	D_ARG_476	NH2	D_ASP_474	OD2	3.339
6DFH	D_ARG_480	NH1	D_ASP_477	OD1	2.443
6DFH	D_LYS_487	NZ	D_ASP_47	OD1	3.476
6DFH	D_LYS_487	NZ	D_ASP_47	OD2	2.691
6DFH	D_LYS_487	NZ	D_GLU_91	OE2	3.894
6DFH	F_ARG_542	NH1	B_GLU_647	OE2	2.778
6DFH	F_LYS_574	NZ	D_ASP_107	OD1	3.408
6DFH	F_LYS_574	NZ	D_ASP_107	OD2	3.378
6DFH	F_ARG_588	NH2	D_GLU_492	OE1	3.059
6DFH	F_ARG_588	NH2	D_GLU_492	OE2	3.839
6DFH	L_ARG_38	NH1	L_ASP_86	OD1	3.691
6DFH	L_ARG_38	NH1	L_ASP_86	OD2	3.393
6DFH	L_ARG_38	NH2	L_GLU_46	OE1	3.255
6DFH	L_ARG_38	NH2	L_ASP_86	OD1	3.023
6DFH	L_ARG_38	NH2	L_ASP_86	OD2	3.383
6DFH	L_ARG_66	NH2	L_ASP_86	OD2	3.901
6DFH	L_ARG_94	NH1	L_ASP_101	OD2	3.386
6DFH	K_LYS_103	NZ	K_ASP_85	OD1	3.976
6DG2	A_HIS_35	NE2	A_GLU_50	OE1	2.810
6DG2	A_ARG_40	NH1	A_GLU_89	OE2	3.382
6DG2	A_ARG_40	NH2	A_GLU_89	OE2	3.578
6DG2	A_ARG_57	NH1	C_GLU_50	OE1	2.686
6DG2	A_ARG_57	NH1	C_GLU_50	OE2	3.712
6DG2	A_ARG_57	NH1	C_ASP_59	OD1	3.923
6DG2	A_ARG_57	NH2	C_GLU_50	OE1	3.412
6DG2	A_ARG_57	NH2	C_GLU_50	OE2	2.876
6DG2	A_LYS_65	NZ	A_GLU_62	OE1	2.446
6DG2	A_LYS_65	NZ	A_GLU_62	OE2	3.885
6DG2	A_LYS_67	NZ	A_ASP_90	OD1	3.375
6DG2	A_LYS_67	NZ	A_ASP_90	OD2	3.355
6DG2	A_ARG_98	NH2	A_ASP_106	OD1	3.809
6DG2	A_ARG_98	NH2	A_ASP_106	OD2	2.951
6DG2	A_LYS_148	NZ	A_ASP_149	OD1	3.488
6DG2	A_LYS_148	NZ	A_ASP_149	OD2	3.887
6DG2	A_LYS_211	NZ	A_ASP_213	OD1	2.323
6DG2	A_LYS_211	NZ	A_ASP_213	OD2	3.618
6DG2	A_LYS_215	NZ	A_GLU_217	OE2	3.590

6DG2	A_LYS_219	NZ	B_ASP_123	OD1	3.620
6DG2	A_LYS_219	NZ	B_ASP_123	OD2	3.832
6DG2	B_ARG_61	NH1	B_ASP_82	OD1	3.334
6DG2	B_ARG_61	NH1	B_ASP_82	OD2	3.815
6DG2	B_ARG_61	NH2	B_GLU_81	OE1	3.510
6DG2	B_ARG_61	NH2	B_ASP_82	OD1	3.338
6DG2	B_ARG_61	NH2	B_ASP_82	OD2	3.953
6DG2	B_LYS_104	NZ	B_GLU_166	OE1	3.797
6DG2	B_LYS_150	NZ	B_GLU_196	OE1	3.711
6DG2	B_LYS_150	NZ	B_GLU_196	OE2	2.891
6DG2	B_LYS_184	NZ	B_GLU_188	OE1	3.697
6DG2	B_LYS_184	NZ	B_GLU_188	OE2	2.997
6DG2	B_LYS_189	NZ	B_ASP_186	OD1	2.377
6DG2	C_HIS_35	NE2	C_GLU_50	OE2	2.691
6DG2	C_LYS_38	NZ	C_ASP_90	OD2	3.933
6DG2	C_ARG_40	NH1	C_GLU_89	OE1	3.263
6DG2	C_ARG_57	NH1	A_GLU_50	OE1	3.739
6DG2	C_ARG_57	NH1	A_GLU_50	OE2	2.758
6DG2	C_ARG_57	NH1	A_ASP_59	OD1	3.719
6DG2	C_ARG_57	NH2	A_GLU_50	OE1	2.935
6DG2	C_ARG_57	NH2	A_GLU_50	OE2	3.488
6DG2	C_LYS_63	NZ	C_GLU_46	OE2	3.257
6DG2	C_LYS_65	NZ	C_GLU_62	OE1	3.990
6DG2	C_LYS_67	NZ	C_ASP_90	OD1	2.743
6DG2	C_LYS_67	NZ	C_ASP_90	OD2	3.331
6DG2	C_ARG_98	NH2	C_ASP_106	OD1	3.590
6DG2	C_ARG_98	NH2	C_ASP_106	OD2	2.787
6DG2	C_LYS_148	NZ	C_ASP_149	OD1	3.517
6DG2	C_LYS_148	NZ	C_ASP_149	OD2	3.956
6DG2	C_LYS_215	NZ	C_GLU_217	OE1	3.786
6DG2	D_LYS_24	NZ	D_ASP_70	OD1	3.383
6DG2	D_LYS_39	NZ	D_GLU_81	OE2	2.693
6DG2	D_ARG_54	NH1	D_ASP_60	OD1	3.820
6DG2	D_ARG_54	NH2	D_ASP_60	OD1	3.271
6DG2	D_ARG_61	NH2	D_GLU_81	OE1	3.822
6DG2	D_ARG_61	NH2	D_ASP_82	OD1	3.113
6DG2	D_LYS_104	NZ	D_GLU_166	OE1	2.780
6DG2	D_LYS_150	NZ	D_GLU_196	OE1	3.724
6DG2	D_LYS_150	NZ	D_GLU_196	OE2	2.441
6E62	P_LYS_307	NZ	P_ASP_386	OD2	3.669
6E62	P_HIS_308	NE2	P_ASP_386	OD2	2.759
6E62	P_HIS_324	NE2	P_GLU_362	OE1	3.607
6E62	P_HIS_324	NE2	P_GLU_362	OE2	3.765
6E62	P_HIS_330	NE2	P_ASP_426	OD1	2.903
6E62	P_HIS_330	NE2	P_ASP_426	OD2	3.266
6E62	P_LYS_394	NZ	P_GLU_385	OE2	3.213
6E62	P_LYS_413	NZ	H_ASP_100	OD1	3.190
6E62	P_LYS_413	NZ	H_ASP_100	OD2	2.736
6E62	P_LYS_416	NZ	L_ASP_51	OD2	2.614
6E62	P_LYS_417	NZ	P_ASP_321	OD1	2.847
6E62	H_ARG_38	NH1	H_GLU_46	OE1	2.901
6E62	H_ARG_38	NH1	H_GLU_46	OE2	3.315
6E62	H_ARG_38	NH2	H_ASP_86	OD2	3.041
6E62	H_LYS_64	NZ	H_ASP_61	OD1	3.685
6E62	H_ARG_66	NH1	H_ASP_86	OD1	3.196
6E62	H_ARG_66	NH2	H_ASP_86	OD1	2.873
6E62	H_ARG_66	NH2	H_ASP_86	OD2	2.687
6E62	H_ARG_94	NH2	H_ASP_101	OD2	2.512

6E62	H_ARG_97	NH1	P_ASP_347	OD2	3.575
6E62	H_ARG_97	NH1	H_ASP_100	OD1	2.302
6E62	H_ARG_97	NH2	H_ASP_100	OD1	3.098
6E62	H_LYS_143	NZ	L_GLU_124	OE2	2.458
6E62	H_LYS_209	NZ	L_GLU_123	OE1	3.996
6E62	H_LYS_209	NZ	L_GLU_123	OE2	3.607
6E62	H_LYS_210	NZ	H_GLU_212	OE1	3.306
6E62	H_LYS_210	NZ	H_GLU_212	OE2	3.355
6E62	L_ARG_61	NH1	L_ASP_82	OD1	2.647
6E62	L_ARG_61	NH1	L_ASP_82	OD2	2.836
6E62	L_ARG_61	NH2	L_ASP_82	OD1	3.964
6E62	L_LYS_110	NZ	L_GLU_198	OE1	3.168
6E62	L_LYS_110	NZ	L_GLU_198	OE2	3.580
6E62	L_HIS_188	NE2	L_ASP_151	OD2	3.831
6E62	A_HIS_308	NE2	A_ASP_386	OD2	3.782
6E62	A_HIS_324	NE2	A_GLU_362	OE2	3.283
6E62	A_HIS_330	NE2	A_ASP_426	OD1	2.479
6E62	A_HIS_330	NE2	A_ASP_426	OD2	3.398
6E62	A_HIS_338	NE2	A_GLU_333	OE2	3.680
6E62	A_LYS_394	NZ	A_GLU_385	OE2	2.787
6E62	A_LYS_413	NZ	B_ASP_100	OD1	3.041
6E62	A_LYS_413	NZ	B_ASP_100	OD2	2.916
6E62	A_LYS_416	NZ	C_ASP_51	OD2	2.944
6E62	A_LYS_417	NZ	A_ASP_321	OD1	2.603
6E62	B_ARG_38	NH1	B_GLU_46	OE1	3.293
6E62	B_ARG_38	NH1	B_GLU_46	OE2	3.910
6E62	B_ARG_38	NH1	B_ASP_86	OD2	3.877
6E62	B_ARG_38	NH2	B_ASP_86	OD2	2.880
6E62	B_ARG_66	NH1	B_ASP_86	OD1	2.876
6E62	B_ARG_66	NH1	B_ASP_86	OD2	3.625
6E62	B_ARG_66	NH2	B_ASP_86	OD1	3.290
6E62	B_ARG_66	NH2	B_ASP_86	OD2	2.657
6E62	B_ARG_83	NH1	H_GLU_1	OE1	3.696
6E62	B_ARG_83	NH1	H_GLU_1	OE2	3.867
6E62	B_ARG_83	NH2	H_GLU_1	OE1	3.783
6E62	B_ARG_83	NH2	H_GLU_1	OE2	3.983
6E62	B_ARG_94	NH2	B_ASP_101	OD2	2.599
6E62	B_ARG_97	NH1	B_ASP_100	OD1	2.912
6E62	B_LYS_143	NZ	C_GLU_124	OE2	2.797
6E62	B_LYS_210	NZ	B_GLU_212	OE1	3.652
6E62	B_LYS_210	NZ	B_GLU_212	OE2	2.960
6E62	C_ARG_54	NH1	C_ASP_60	OD2	3.657
6E62	C_ARG_61	NH1	C_ASP_82	OD2	3.397
6E62	C_ARG_61	NH2	C_ASP_82	OD1	3.278
6E62	C_ARG_61	NH2	C_ASP_82	OD2	2.476
6E62	C_LYS_103	NZ	C_GLU_83	OE2	3.303
6E62	C_LYS_110	NZ	C_GLU_198	OE1	2.849
6E62	C_LYS_110	NZ	C_GLU_198	OE2	3.942
6E62	C_LYS_149	NZ	C_GLU_203	OE1	2.875
6E62	C_LYS_149	NZ	C_GLU_203	OE2	3.215
6E62	C_LYS_156	NZ	L_GLU_81	OE2	3.985
6E62	C_HIS_188	NE2	C_ASP_151	OD2	3.860
6E63	P_LYS_307	NZ	P_ASP_386	OD1	3.127
6E63	P_LYS_307	NZ	P_ASP_386	OD2	2.866
6E63	P_HIS_308	NE2	P_ASP_386	OD2	2.480
6E63	P_HIS_330	NE2	P_ASP_426	OD1	2.711
6E63	P_LYS_394	NZ	P_GLU_385	OE2	3.080
6E63	P_LYS_413	NZ	H_ASP_100	OD1	3.187

6E63	P.LYS_413	NZ	H_ASP_100	OD2	2.904
6E63	P.LYS_416	NZ	L_ASP_51	OD1	3.564
6E63	P.LYS_416	NZ	L_ASP_51	OD2	2.955
6E63	H_ARG_38	NH1	H_GLU_46	OE1	3.318
6E63	H_ARG_38	NH1	H_GLU_46	OE2	3.594
6E63	H_ARG_38	NH2	H_ASP_86	OD1	2.939
6E63	H_LYS_64	NZ	H_ASP_61	OD1	2.864
6E63	H_ARG_66	NH1	H_ASP_86	OD1	3.558
6E63	H_ARG_66	NH1	H_ASP_86	OD2	2.622
6E63	H_ARG_66	NH2	H_ASP_86	OD1	3.266
6E63	H_ARG_66	NH2	H_ASP_86	OD2	3.816
6E63	H_ARG_94	NH2	H_ASP_101	OD2	2.922
6E63	H_ARG_97	NH1	P_ASP_347	OD2	3.407
6E63	H_ARG_97	NH2	H_ASP_100	OD1	2.600
6E63	H_LYS_143	NZ	L_GLU_124	OE2	2.665
6E63	H_LYS_209	NZ	L_GLU_123	OE1	2.498
6E63	L_LYS_17	NZ	B_GLU_85	OE1	3.318
6E63	L_LYS_17	NZ	B_GLU_85	OE2	3.250
6E63	L_ARG_61	NH1	L_ASP_82	OD1	3.684
6E63	L_ARG_61	NH1	L_ASP_82	OD2	2.729
6E63	L_ARG_61	NH2	L_ASP_82	OD1	2.979
6E63	L_ARG_61	NH2	L_ASP_82	OD2	3.405
6E63	A_LYS_307	NZ	A_ASP_386	OD2	3.648
6E63	A_HIS_308	NE2	A_ASP_386	OD2	2.820
6E63	A_HIS_330	NE2	A_ASP_426	OD1	2.686
6E63	A_HIS_330	NE2	A_ASP_426	OD2	3.540
6E63	A_LYS_394	NZ	A_GLU_385	OE2	2.976
6E63	A_LYS_413	NZ	B_ASP_100	OD1	2.369
6E63	A_LYS_413	NZ	B_ASP_100	OD2	3.029
6E63	A_LYS_416	NZ	C_ASP_51	OD2	3.236
6E63	A_LYS_417	NZ	A_ASP_415	OD2	3.741
6E63	B_ARG_38	NH1	B_GLU_46	OE1	3.240
6E63	B_ARG_38	NH1	B_GLU_46	OE2	3.499
6E63	B_ARG_38	NH1	B_ASP_86	OD1	3.761
6E63	B_ARG_38	NH2	B_ASP_86	OD1	2.835
6E63	B_ARG_66	NH1	B_ASP_86	OD1	3.865
6E63	B_ARG_66	NH1	B_ASP_86	OD2	2.829
6E63	B_ARG_66	NH2	B_ASP_86	OD1	3.527
6E63	B_ARG_66	NH2	B_ASP_86	OD2	3.871
6E63	B_LYS_75	NZ	B_ASP_72	OD2	3.854
6E63	B_ARG_83	NH1	L_GLU_13	OE1	3.486
6E63	B_ARG_83	NH1	L_GLU_13	OE2	2.814
6E63	B_ARG_94	NH2	B_ASP_101	OD2	2.586
6E63	B_ARG_97	NH1	A_ASP_347	OD1	3.859
6E63	B_ARG_97	NH2	B_ASP_100	OD2	2.691
6E63	B_LYS_143	NZ	B_ASP_144	OD2	2.985
6E63	C_ARG_61	NH1	C_ASP_82	OD1	3.450
6E63	C_ARG_61	NH1	C_ASP_82	OD2	2.361
6E63	C_ARG_61	NH2	C_ASP_82	OD1	3.192
6E63	C_ARG_61	NH2	C_ASP_82	OD2	3.567
6E63	C_LYS_103	NZ	C_ASP_85	OD1	3.606
6E63	C_LYS_110	NZ	C_GLU_198	OE2	2.744
6E63	C_HIS_188	ND1	C_ASP_151	OD1	2.608
6E64	H_ARG_38	NH1	H_GLU_46	OE1	3.189
6E64	H_ARG_38	NH1	H_GLU_46	OE2	3.661
6E64	H_ARG_38	NH1	H_ASP_86	OD2	3.741
6E64	H_ARG_38	NH2	H_ASP_86	OD2	2.909
6E64	H_ARG_66	NH1	H_ASP_86	OD1	2.379

6E64	H_ARG_66	NH1	H_ASP_86	OD2	3.616
6E64	H_ARG_66	NH2	H_ASP_86	OD1	3.004
6E64	H_ARG_66	NH2	H_ASP_86	OD2	2.769
6E64	H_ARG_83	NH2	H_GLU_85	OE1	3.958
6E64	H_ARG_94	NH2	H_ASP_101	OD2	2.952
6E64	H_ARG_97	NH1	H_ASP_100	OD1	3.380
6E64	H_ARG_97	NH2	H_ASP_100	OD1	3.101
6E64	H_LYS_143	NZ	L_GLU_124	OE2	2.942
6E64	H_LYS_209	NZ	L_GLU_123	OE2	2.774
6E64	H_LYS_210	NZ	H_GLU_212	OE1	3.202
6E64	H_LYS_210	NZ	H_GLU_212	OE2	3.230
6E64	L_ARG_54	NH1	L_ASP_60	OD2	3.879
6E64	L_ARG_61	NH1	L_ASP_82	OD1	3.199
6E64	L_ARG_61	NH1	L_ASP_82	OD2	2.244
6E64	L_ARG_61	NH2	L_GLU_81	OE2	2.926
6E64	L_ARG_61	NH2	L_ASP_82	OD1	3.741
6E64	L_LYS_110	NZ	L_GLU_198	OE1	3.205
6E64	L_LYS_110	NZ	L_GLU_198	OE2	3.935
6E64	L_LYS_149	NZ	L_GLU_203	OE2	3.889
6E64	A_ARG_38	NH1	A_GLU_46	OE1	3.590
6E64	A_ARG_38	NH1	A_GLU_46	OE2	3.959
6E64	A_ARG_38	NH1	A_ASP_86	OD2	3.714
6E64	A_ARG_38	NH2	A_ASP_86	OD2	2.885
6E64	A_ARG_66	NH1	A_ASP_86	OD1	2.673
6E64	A_ARG_66	NH1	A_ASP_86	OD2	3.501
6E64	A_ARG_66	NH2	A_ASP_86	OD2	3.885
6E64	A_ARG_94	NH2	A_ASP_101	OD2	2.800
6E64	A_ARG_97	NH1	A_ASP_100	OD1	2.610
6E64	A_LYS_209	NZ	B_GLU_123	OE1	3.569
6E64	A_LYS_209	NZ	B_GLU_123	OE2	2.777
6E64	A_LYS_210	NZ	A_GLU_212	OE1	2.858
6E64	B_ARG_54	NH1	B_ASP_60	OD2	3.850
6E64	B_ARG_61	NH1	B_ASP_82	OD1	3.141
6E64	B_ARG_61	NH1	B_ASP_82	OD2	2.224
6E64	B_ARG_61	NH2	B_GLU_81	OE2	3.154
6E64	B_LYS_110	NZ	B_GLU_198	OE1	3.325
6E65	L_ARG_61	NH1	L_ASP_82	OD1	3.558
6E65	L_ARG_61	NH1	L_ASP_82	OD2	2.687
6E65	L_ARG_61	NH2	L_ASP_82	OD1	2.921
6E65	L_ARG_61	NH2	L_ASP_82	OD2	3.517
6E65	L_LYS_110	NZ	L_GLU_198	OE1	3.254
6E65	L_LYS_149	NZ	L_GLU_203	OE2	3.192
6E65	H_ARG_38	NH1	H_GLU_46	OE1	3.010
6E65	H_ARG_38	NH1	H_GLU_46	OE2	3.789
6E65	H_ARG_38	NH1	H_ASP_86	OD2	3.921
6E65	H_ARG_38	NH2	H_ASP_86	OD2	2.906
6E65	H_LYS_64	NZ	H_ASP_61	OD1	2.812
6E65	H_ARG_66	NH1	H_ASP_86	OD1	2.716
6E65	H_ARG_66	NH1	H_ASP_86	OD2	3.744
6E65	H_ARG_66	NH2	H_ASP_86	OD1	3.520
6E65	H_ARG_66	NH2	H_ASP_86	OD2	3.030
6E65	H_ARG_94	NH2	H_ASP_101	OD1	3.830
6E65	H_ARG_94	NH2	H_ASP_101	OD2	2.624
6E65	H_ARG_97	NH1	H_ASP_100	OD1	3.182
6E65	H_ARG_97	NH2	H_ASP_100	OD1	2.837
6E65	H_LYS_209	NZ	L_GLU_123	OE1	2.900
6E65	H_LYS_209	NZ	L_GLU_123	OE2	3.402
6E65	H_LYS_210	NZ	H_GLU_212	OE2	3.313

6E8V	A_LYS_58	NZ	A_ASP_183	OD2	3.383
6E8V	A_ARG_64	NH1	A_ASP_115	OD1	3.736
6E8V	A_ARG_64	NH1	A_ASP_115	OD2	3.862
6E8V	A_ARG_64	NH2	A_GLU_72	OE1	2.461
6E8V	A_LYS_69	NZ	H_GLU_114	OE1	3.919
6E8V	A_LYS_69	NZ	H_GLU_114	OE2	3.267
6E8V	A_ARG_92	NH1	A_ASP_115	OD1	3.628
6E8V	A_ARG_92	NH1	A_ASP_115	OD2	2.200
6E8V	A_ARG_92	NH2	A_ASP_115	OD2	3.895
6E8V	A_HIS_129	NE2	A_GLU_179	OE1	3.896
6E8V	A_LYS_290	NZ	B_GLU_128	OE1	3.297
6E8V	A_LYS_290	NZ	B_GLU_128	OE2	3.454
6E8V	B_ARG_62	NH2	B_ASP_83	OD1	3.866
6E8V	B_ARG_62	NH2	B_ASP_83	OD2	3.065
6E8V	B_LYS_154	NZ	E_ASP_98	OD2	3.855
6E8V	B_LYS_212	NZ	B_GLU_215	OE2	3.054
6E8V	E_LYS_58	NZ	E_ASP_183	OD2	3.769
6E8V	E_ARG_64	NH1	E_ASP_115	OD1	3.111
6E8V	E_ARG_64	NH2	E_GLU_72	OE1	2.694
6E8V	E_ARG_64	NH2	E_GLU_72	OE2	3.880
6E8V	E_ARG_64	NH2	E_ASP_115	OD1	3.985
6E8V	E_ARG_92	NH1	E_ASP_115	OD1	2.769
6E8V	E_ARG_92	NH1	E_ASP_115	OD2	3.085
6E8V	E_HIS_129	NE2	E_GLU_179	OE2	3.144
6E8V	E_LYS_290	NZ	F_GLU_128	OE1	2.548
6E8V	E_LYS_290	NZ	F_GLU_128	OE2	3.232
6E8V	F_ARG_63	NH1	F_GLU_83	OE2	3.510
6E8V	F_ARG_63	NH1	F_ASP_84	OD1	3.568
6E8V	F_ARG_63	NH2	F_ASP_84	OD1	3.073
6E8V	F_ARG_63	NH2	F_ASP_84	OD2	2.536
6E8V	F_ARG_68	NH2	F_ASP_53	OD2	3.856
6E8V	H_LYS_58	NZ	H_ASP_183	OD2	3.692
6E8V	H_ARG_64	NH1	H_ASP_115	OD2	3.761
6E8V	H_ARG_64	NH2	H_GLU_72	OE1	3.369
6E8V	H_ARG_64	NH2	H_GLU_72	OE2	2.811
6E8V	H_LYS_69	NZ	H_GLU_72	OE2	3.846
6E8V	H_LYS_69	NZ	H_GLU_114	OE2	2.887
6E8V	H_ARG_92	NH1	H_ASP_115	OD1	3.257
6E8V	H_ARG_92	NH1	H_ASP_115	OD2	2.227
6E8V	H_ARG_92	NH2	H_ASP_115	OD2	3.949
6E8V	H_HIS_125	NE2	H_ASP_183	OD2	3.568
6E8V	H_HIS_129	NE2	H_GLU_179	OE2	2.966
6E8V	H_LYS_290	NZ	L_GLU_127	OE1	2.706
6E8V	H_LYS_290	NZ	L_GLU_127	OE2	2.554
6E8V	J_LYS_58	NZ	J_ASP_183	OD2	3.273
6E8V	J_ARG_64	NH1	J_ASP_115	OD2	3.190
6E8V	J_ARG_64	NH2	J_GLU_72	OE1	3.098
6E8V	J_ARG_92	NH1	J_ASP_115	OD1	2.752
6E8V	J_ARG_92	NH1	J_ASP_115	OD2	2.685
6E8V	J_HIS_129	NE2	J_GLU_179	OE2	3.681
6E8V	J_LYS_290	NZ	K_GLU_128	OE1	3.173
6E8V	J_LYS_290	NZ	K_GLU_128	OE2	2.611
6E8V	K_ARG_63	NH1	K_ASP_84	OD2	3.865
6E8V	K_ARG_63	NH2	K_ASP_84	OD1	2.385
6E8V	K_ARG_63	NH2	K_ASP_84	OD2	3.106
6E8V	K_LYS_212	NZ	H_GLU_101	OE1	3.767
6E8V	K_LYS_212	NZ	H_GLU_101	OE2	3.490
6E8V	K_LYS_212	NZ	K_GLU_215	OE1	3.501

6E8V	L_LYS_211	NZ	L_GLU_214	OE1	3.855
6E8V	L_LYS_211	NZ	L_GLU_214	OE2	3.483
6E8V	O_LYS_58	NZ	O_ASP_183	OD2	2.755
6E8V	O_ARG_64	NH1	O_ASP_115	OD1	2.759
6E8V	O_ARG_64	NH2	O_GLU_72	OE1	3.262
6E8V	O_ARG_64	NH2	O_GLU_72	OE2	2.920
6E8V	O_ARG_64	NH2	O_ASP_115	OD1	3.656
6E8V	O_ARG_92	NH1	O_ASP_115	OD1	3.104
6E8V	O_ARG_92	NH1	O_ASP_115	OD2	2.418
6E8V	O_ARG_92	NH2	O_ASP_115	OD1	3.944
6E8V	O_HIS_129	NE2	L_ASP_61	OD1	3.511
6E8V	O_HIS_129	NE2	O_GLU_179	OE1	3.633
6E8V	O_LYS_290	NZ	P_GLU_128	OE1	3.591
6E8V	P_ARG_56	NH2	P_ASP_62	OD1	3.947
6E8V	P_ARG_63	NH2	P_ASP_84	OD1	2.443
6E8V	P_ARG_63	NH2	P_ASP_84	OD2	3.024
6E8V	P_ARG_68	NH2	P_ASP_53	OD2	3.638
6E8V	P_LYS_171	NZ	P_GLU_85	OE1	3.474
6E8V	P_LYS_212	NZ	P_GLU_215	OE2	3.770
6E8V	U_ARG_64	NH1	U_ASP_115	OD1	2.978
6E8V	U_ARG_64	NH2	U_GLU_72	OE1	3.075
6E8V	U_ARG_64	NH2	U_GLU_72	OE2	3.322
6E8V	U_LYS_69	NZ	U_GLU_72	OE1	2.536
6E8V	U_ARG_92	NH1	U_ASP_115	OD1	3.227
6E8V	U_ARG_92	NH1	U_ASP_115	OD2	2.688
6E8V	U_LYS_290	NZ	V_GLU_128	OE1	2.346
6E8V	U_LYS_290	NZ	V_GLU_128	OE2	3.693
6E8V	V_ARG_63	NH1	V_GLU_83	OE2	3.928
6E8V	V_ARG_63	NH2	V_ASP_84	OD1	2.920
6E8V	V_ARG_63	NH2	V_ASP_84	OD2	2.400
6E8V	V_LYS_154	NZ	V_GLU_199	OE2	3.787
6E8V	V_LYS_212	NZ	V_GLU_215	OE1	3.212
6E8V	Y_ARG_64	NH1	Y_ASP_115	OD1	3.849
6E8V	Y_ARG_64	NH1	Y_ASP_115	OD2	3.924
6E8V	Y_ARG_64	NH2	Y_GLU_72	OE1	3.305
6E8V	Y_ARG_64	NH2	Y_GLU_72	OE2	3.450
6E8V	Y_ARG_64	NH2	Y_ASP_115	OD1	3.987
6E8V	Y_ARG_92	NH1	Y_ASP_115	OD1	3.320
6E8V	Y_ARG_92	NH1	Y_ASP_115	OD2	2.179
6E8V	Y_HIS_129	NE2	Y_GLU_179	OE1	2.918
6E8V	Y_LYS_290	NZ	Z_GLU_128	OE1	3.390
6E8V	Z_ARG_63	NH1	Z_ASP_84	OD1	3.893
6E8V	Z_ARG_63	NH2	Z_ASP_84	OD1	3.228
6E8V	Z_ARG_63	NH2	Z_ASP_84	OD2	2.268
6E8V	Z_LYS_171	NZ	Z_GLU_85	OE1	2.482
6E8V	Z_HIS_202	NE2	Z_GLU_203	OE1	3.581
6E8V	Z_LYS_212	NZ	Z_GLU_215	OE2	3.769
6E8V	c_LYS_58	NZ	c_ASP_183	OD2	3.320
6E8V	c_ARG_64	NH1	c_ASP_115	OD1	3.153
6E8V	c_ARG_64	NH2	c_GLU_72	OE1	2.815
6E8V	c_ARG_64	NH2	c_GLU_72	OE2	3.967
6E8V	c_ARG_92	NH1	c_ASP_115	OD1	2.545
6E8V	c_ARG_92	NH1	c_ASP_115	OD2	2.955
6E8V	c_HIS_125	ND1	K_ASP_62	OD1	3.174
6E8V	c_HIS_125	ND1	K_ASP_62	OD2	3.139
6E8V	c_HIS_125	NE2	c_ASP_183	OD2	2.451
6E8V	c_HIS_129	NE2	c_GLU_179	OE1	3.728
6E8V	c_LYS_290	NZ	d_GLU_128	OE1	2.357

6E8V	c_LYS_290	NZ	d_GLU_128	OE2	3.486
6E8V	d_ARG_63	NH2	d_ASP_84	OD1	3.212
6E8V	d_ARG_63	NH2	d_ASP_84	OD2	2.255
6E8V	d_LYS_154	NZ	d_GLU_199	OE1	2.319
6E8V	d_LYS_154	NZ	d_GLU_199	OE2	3.282
6E9G	A_ARG_38	NH1	A_GLU_46	OE1	3.009
6E9G	A_ARG_38	NH1	A_GLU_46	OE2	3.865
6E9G	A_ARG_38	NH1	A_ASP_89	OD1	3.731
6E9G	A_ARG_38	NH2	A_ASP_89	OD1	2.942
6E9G	A_ARG_124	NH1	A_ASP_126	OD1	3.428
6E9G	A_ARG_124	NH1	A_ASP_126	OD2	3.623
6E9G	A_LYS_259	NZ	A_ASP_261	OD1	3.382
6E9G	A_LYS_262	NZ	B_GLU_127	OE1	3.021
6E9G	A_LYS_262	NZ	B_GLU_127	OE2	3.870
6E9G	B_ARG_55	NH1	B_ASP_61	OD2	3.166
6E9G	B_ARG_55	NH2	B_ASP_61	OD1	3.953
6E9G	B_ARG_55	NH2	B_ASP_61	OD2	3.935
6E9G	B_ARG_62	NH1	B_ASP_83	OD1	3.754
6E9G	B_ARG_62	NH2	B_ASP_83	OD1	2.216
6E9G	B_ARG_62	NH2	B_ASP_83	OD2	3.767
6E9G	B_LYS_114	NZ	B_GLU_202	OE1	3.419
6E9H	A_LYS_58	NZ	A_ASP_57	OD2	3.854
6E9H	A_ARG_64	NH1	A_ASP_115	OD1	2.780
6E9H	A_ARG_64	NH2	A_GLU_72	OE1	3.005
6E9H	A_ARG_64	NH2	A_ASP_115	OD1	3.589
6E9H	A_ARG_92	NH1	A_ASP_115	OD1	3.583
6E9H	A_ARG_92	NH1	A_ASP_115	OD2	2.997
6E9H	A_ARG_92	NH2	A_ASP_115	OD1	3.156
6E9H	A_ARG_92	NH2	A_ASP_115	OD2	3.683
6E9H	A_HIS_125	NE2	A_GLU_181	OE2	3.054
6E9H	A_ARG_147	NH2	A_ASP_160	OD1	3.058
6E9H	A_ARG_147	NH2	A_ASP_160	OD2	3.404
6E9H	A_LYS_292	NZ	B_GLU_128	OE1	2.895
6E9H	A_LYS_292	NZ	B_GLU_128	OE2	3.744
6E9H	B_ARG_56	NH1	B_ASP_62	OD2	3.861
6E9H	B_ARG_56	NH2	B_ASP_62	OD2	3.548
6E9H	B_ARG_63	NH1	B_ASP_84	OD1	2.804
6E9H	B_ARG_63	NH1	B_ASP_84	OD2	3.553
6E9H	B_ARG_63	NH2	B_ASP_84	OD1	3.448
6E9H	B_ARG_63	NH2	B_ASP_84	OD2	2.780
6E9H	B_ARG_68	NH2	B_ASP_53	OD2	3.674
6E9H	B_LYS_154	NZ	B_GLU_199	OE1	3.479
6E9H	B_LYS_154	NZ	B_GLU_199	OE2	3.530
6E9H	B_LYS_171	NZ	B_GLU_85	OE1	2.299
6E9H	B_LYS_171	NZ	B_GLU_85	OE2	3.752
6E9I	A_LYS_58	NZ	A_ASP_182	OD2	3.602
6E9I	A_ARG_64	NH1	A_ASP_115	OD2	2.633
6E9I	A_ARG_64	NH2	A_GLU_72	OE2	3.049
6E9I	A_ARG_64	NH2	A_ASP_115	OD2	3.483
6E9I	A_ARG_92	NH1	A_ASP_115	OD1	3.516
6E9I	A_ARG_92	NH1	A_ASP_115	OD2	2.842
6E9I	A_ARG_92	NH2	A_ASP_115	OD1	3.099
6E9I	A_ARG_92	NH2	A_ASP_115	OD2	3.725
6E9I	A_ARG_109	NH2	D_ASP_95	OD1	3.782
6E9I	A_ARG_109	NH2	D_ASP_95	OD2	3.931
6E9I	A_HIS_125	NE2	A_GLU_178	OE2	3.001
6E9I	A_LYS_289	NZ	B_GLU_128	OE1	3.746
6E9I	A_LYS_289	NZ	B_GLU_128	OE2	2.925

6E9I	B_ARG_63	NH1	B_ASP_84	OD1	2.801
6E9I	B_ARG_63	NH1	B_ASP_84	OD2	2.588
6E9I	B_ARG_68	NH1	B_ASP_53	OD2	3.498
6E9I	B_LYS_171	NZ	B_GLU_85	OE1	2.942
6E9I	C_ARG_64	NH1	C_ASP_115	OD2	2.558
6E9I	C_ARG_64	NH2	C_GLU_72	OE2	2.949
6E9I	C_ARG_64	NH2	C_ASP_115	OD2	3.425
6E9I	C_ARG_92	NH1	C_ASP_115	OD1	3.394
6E9I	C_ARG_92	NH1	C_ASP_115	OD2	2.831
6E9I	C_ARG_92	NH2	C_ASP_115	OD1	3.153
6E9I	C_ARG_92	NH2	C_ASP_115	OD2	3.762
6E9I	C_HIS_125	NE2	C_GLU_178	OE1	3.090
6E9I	C_LYS_289	NZ	D_GLU_128	OE1	2.528
6E9I	C_LYS_289	NZ	D_GLU_128	OE2	3.968
6E9I	D_ARG_63	NH2	D_ASP_84	OD1	2.787
6E9I	D_ARG_63	NH2	D_ASP_84	OD2	2.635
6E9I	D_ARG_68	NH2	D_ASP_53	OD2	3.085
6E9I	D_LYS_115	NZ	D_GLU_203	OE2	3.399
6E9I	D_LYS_171	NZ	D_GLU_85	OE2	3.210
6E9I	H_LYS_58	NZ	H_ASP_57	OD1	3.428
6E9I	H_ARG_64	NH1	H_ASP_115	OD1	2.649
6E9I	H_ARG_64	NH2	H_GLU_72	OE1	2.999
6E9I	H_ARG_64	NH2	H_ASP_115	OD1	3.536
6E9I	H_LYS_69	NZ	H_GLU_114	OE2	3.957
6E9I	H_ARG_92	NH1	H_ASP_115	OD1	2.822
6E9I	H_ARG_92	NH1	H_ASP_115	OD2	3.288
6E9I	H_ARG_92	NH2	H_ASP_115	OD1	3.754
6E9I	H_ARG_92	NH2	H_ASP_115	OD2	3.182
6E9I	H_HIS_125	NE2	H_GLU_178	OE1	3.044
6E9I	H_LYS_289	NZ	L_GLU_128	OE1	3.811
6E9I	H_LYS_289	NZ	L_GLU_128	OE2	2.547
6E9I	L_ARG_56	NH1	L_ASP_62	OD2	3.686
6E9I	L_ARG_56	NH2	L_ASP_62	OD2	3.053
6E9I	L_ARG_63	NH1	L_ASP_84	OD1	3.024
6E9I	L_ARG_63	NH1	L_ASP_84	OD2	2.419
6E9I	L_ARG_63	NH2	L_GLU_83	OE1	3.490
6E9I	L_ARG_63	NH2	L_ASP_84	OD1	3.404
6E9I	L_ARG_68	NH1	L_ASP_53	OD2	3.356
6E9I	L_LYS_171	NZ	L_GLU_85	OE1	2.446
6E9K	A_LYS_32	NZ	A_ASP_31	OD1	2.993
6E9K	A_LYS_32	NZ	A_ASP_31	OD2	3.547
6E9K	A_ARG_38	NH1	A_ASP_89	OD1	2.700
6E9K	A_ARG_38	NH2	A_GLU_46	OE1	3.033
6E9K	A_ARG_38	NH2	A_ASP_89	OD1	3.664
6E9K	A_ARG_66	NH1	A_ASP_89	OD1	3.360
6E9K	A_ARG_66	NH1	A_ASP_89	OD2	2.516
6E9K	A_ARG_66	NH2	A_ASP_89	OD1	3.299
6E9K	A_ARG_66	NH2	A_ASP_89	OD2	3.549
6E9K	A_HIS_99	NE2	A_GLU_146	OE2	3.060
6E9K	A_ARG_103	NH1	A_GLU_146	OE1	3.769
6E9K	A_LYS_104	NZ	A_ASP_143	OD1	2.823
6E9K	A_LYS_104	NZ	A_ASP_143	OD2	3.004
6E9K	A_LYS_257	NZ	B_GLU_128	OE1	3.997
6E9K	A_LYS_257	NZ	B_GLU_128	OE2	3.056
6E9K	B_ARG_63	NH1	B_ASP_84	OD1	3.165
6E9K	B_ARG_63	NH1	B_ASP_84	OD2	2.396
6E9K	B_ARG_63	NH2	B_ASP_84	OD1	2.989
6E9K	B_ARG_63	NH2	B_ASP_84	OD2	3.593

6E9K	B.LYS_115	NZ	B.GLU_203	OE1	3.094
6E9K	B.LYS_154	NZ	B.GLU_199	OE2	3.249
6E9K	B.LYS_171	NZ	B.GLU_85	OE1	2.917
6E9Q	A_ARG_38	NH1	A.ASP_89	OD2	3.963
6E9Q	A_ARG_66	NH1	A.ASP_89	OD1	2.868
6E9Q	A_ARG_66	NH1	A.ASP_89	OD2	2.514
6E9Q	A.HIS_99	NE2	A.GLU_142	OE1	3.452
6E9Q	A.LYS_101	NZ	A.GLU_142	OE2	3.652
6E9Q	A.LYS_253	NZ	B.GLU_128	OE1	3.048
6E9Q	A.LYS_253	NZ	B.GLU_128	OE2	2.978
6E9Q	B_ARG_63	NH2	B.ASP_84	OD1	2.631
6E9Q	B_ARG_63	NH2	B.ASP_84	OD2	2.815
6E9Q	B_ARG_68	NH2	B.ASP_53	OD2	3.543
6E9Q	B.LYS_154	NZ	B.GLU_199	OE1	2.492
6E9Q	B.LYS_171	NZ	B.GLU_85	OE1	2.682
6E9Q	B.LYS_171	NZ	B.GLU_85	OE2	3.666
6E9Q	C_ARG_38	NH1	C.ASP_89	OD1	2.493
6E9Q	C_ARG_38	NH2	C.GLU_46	OE1	2.768
6E9Q	C_ARG_38	NH2	C.GLU_46	OE2	3.894
6E9Q	C_ARG_38	NH2	C.ASP_89	OD1	3.476
6E9Q	C_ARG_66	NH1	C.ASP_89	OD1	3.542
6E9Q	C_ARG_66	NH1	C.ASP_89	OD2	2.437
6E9Q	C_ARG_66	NH2	C.ASP_89	OD1	3.979
6E9Q	C_ARG_66	NH2	C.ASP_89	OD2	3.919
6E9Q	C.HIS_99	NE2	C.GLU_142	OE1	3.707
6E9Q	C.LYS_101	NZ	C.GLU_142	OE1	3.900
6E9Q	D_ARG_56	NH1	D.ASP_62	OD2	3.862
6E9Q	D_ARG_63	NH2	D.ASP_84	OD1	3.419
6E9Q	D_ARG_63	NH2	D.ASP_84	OD2	3.605
6E9Q	D.LYS_154	NZ	D.GLU_199	OE1	3.115
6E9Q	D.LYS_176	NZ	D.ASP_143	OD1	3.925
6E9Q	D.LYS_193	NZ	D.ASP_189	OD1	3.400
6E9Q	E_ARG_38	NH1	E.ASP_89	OD1	3.733
6E9Q	E_ARG_38	NH2	E.GLU_46	OE1	3.706
6E9Q	E_ARG_38	NH2	E.ASP_89	OD1	2.896
6E9Q	E_ARG_66	NH1	E.ASP_89	OD1	3.922
6E9Q	E_ARG_66	NH1	E.ASP_89	OD2	2.529
6E9Q	E_ARG_66	NH2	E.ASP_89	OD2	3.750
6E9Q	E.HIS_99	NE2	E.GLU_142	OE2	3.775
6E9Q	E.LYS_253	NZ	F.GLU_128	OE1	2.966
6E9Q	E.LYS_253	NZ	F.GLU_128	OE2	2.802
6E9Q	F_ARG_63	NH2	F.ASP_84	OD1	2.560
6E9Q	F_ARG_63	NH2	F.ASP_84	OD2	3.515
6E9Q	F_ARG_68	NH2	F.ASP_53	OD2	3.049
6E9Q	F.LYS_171	NZ	F.GLU_85	OE1	3.068
6E9Q	G_ARG_38	NH1	G.ASP_89	OD1	3.204
6E9Q	G_ARG_38	NH2	G.GLU_46	OE1	2.728
6E9Q	G_ARG_38	NH2	G.GLU_46	OE2	3.967
6E9Q	G_ARG_66	NH1	G.ASP_89	OD1	3.146
6E9Q	G_ARG_66	NH1	G.ASP_89	OD2	2.916
6E9Q	G_ARG_66	NH2	G.ASP_89	OD1	3.930
6E9Q	G.HIS_99	NE2	G.GLU_142	OE2	3.698
6E9U	A.LYS_32	NZ	A.ASP_159	OD2	3.058
6E9U	A_ARG_38	NH1	A.ASP_89	OD1	2.696
6E9U	A_ARG_38	NH2	A.GLU_46	OE1	3.019
6E9U	A_ARG_38	NH2	A.ASP_89	OD1	3.469
6E9U	A_ARG_66	NH1	A.ASP_89	OD1	3.553
6E9U	A_ARG_66	NH1	A.ASP_89	OD2	2.571

6E9U	A_ARG_66	NH2	A_ASP_89	OD1	3.370
6E9U	A_ARG_66	NH2	A_ASP_89	OD2	3.619
6E9U	A_HIS_99	NE2	A_GLU_155	OE2	3.178
6E9U	A_LYS_104	NZ	A_ASP_133	OD2	2.359
6E9U	A_ARG_117	NH2	A_ASP_116	OD1	3.439
6E9U	A_ARG_117	NH2	A_ASP_116	OD2	3.943
6E9U	A_LYS_266	NZ	B_GLU_128	OE1	2.942
6E9U	A_LYS_266	NZ	B_GLU_128	OE2	2.747
6E9U	B_ARG_56	NH2	B_ASP_62	OD2	3.549
6E9U	B_ARG_63	NH2	B_ASP_84	OD1	2.519
6E9U	B_ARG_63	NH2	B_ASP_84	OD2	3.472
6E9U	B_ARG_168	NH2	B_ASP_87	OD1	3.330
6E9U	B_ARG_168	NH2	B_ASP_87	OD2	3.181
6EDU	D_LYS_348	NZ	D_GLU_269	OE1	2.947
6EDU	D_LYS_348	NZ	D_GLU_269	OE2	3.576
6EDU	D_LYS_421	NZ	L_GLU_54	OE2	2.920
6EDU	D_LYS_432	NZ	L_GLU_55	OE1	3.655
6EDU	D_LYS_432	NZ	L_GLU_55	OE2	3.439
6EDU	D_ARG_476	NH1	D_GLU_102	OE1	3.942
6EDU	D_ARG_476	NH1	D_GLU_102	OE2	2.435
6EDU	D_ARG_480	NH1	D_ASP_477	OD1	2.572
6EDU	D_LYS_487	NZ	D_GLU_47	OE2	2.857
6EDU	D_LYS_487	NZ	D_GLU_91	OE2	3.215
6EDU	E_LYS_348	NZ	E_GLU_269	OE1	2.948
6EDU	E_LYS_348	NZ	E_GLU_269	OE2	3.576
6EDU	E_LYS_421	NZ	N_GLU_54	OE2	3.004
6EDU	E_LYS_432	NZ	N_GLU_55	OE1	3.579
6EDU	E_LYS_432	NZ	N_GLU_55	OE2	3.398
6EDU	E_ARG_476	NH1	E_GLU_102	OE1	3.943
6EDU	E_ARG_476	NH1	E_GLU_102	OE2	2.436
6EDU	E_ARG_480	NH1	E_ASP_477	OD1	2.573
6EDU	E_LYS_487	NZ	E_GLU_47	OE2	2.857
6EDU	E_LYS_487	NZ	E_GLU_91	OE2	3.215
6EDU	F_LYS_348	NZ	F_GLU_269	OE1	2.947
6EDU	F_LYS_348	NZ	F_GLU_269	OE2	3.576
6EDU	F_LYS_421	NZ	J_GLU_54	OE2	3.064
6EDU	F_LYS_432	NZ	J_GLU_55	OE1	3.805
6EDU	F_LYS_432	NZ	J_GLU_55	OE2	3.577
6EDU	F_ARG_476	NH1	F_GLU_102	OE1	3.943
6EDU	F_ARG_476	NH1	F_GLU_102	OE2	2.437
6EDU	F_ARG_480	NH1	F_ASP_477	OD1	2.573
6EDU	F_LYS_487	NZ	F_GLU_47	OE2	2.856
6EDU	F_LYS_487	NZ	F_GLU_91	OE2	3.215
6EDU	G_LYS_22	NZ	F_GLU_102	OE1	3.040
6EDU	G_ARG_59	NH2	F_ASP_368	OD1	3.059
6EDU	G_LYS_72	NZ	G_ASP_56	OD2	3.829
6EDU	H_LYS_22	NZ	E_GLU_102	OE1	3.174
6EDU	H_ARG_59	NH2	E_ASP_368	OD1	3.166
6EDU	H_LYS_72	NZ	H_ASP_56	OD2	3.828
6EDU	I_LYS_22	NZ	D_GLU_102	OE1	3.053
6EDU	I_ARG_59	NH2	D_ASP_368	OD1	3.238
6EDU	I_LYS_72	NZ	I_ASP_56	OD2	3.828
6EDU	J_ARG_12	NH2	J_GLU_10	OE2	2.569
6EDU	J_LYS_19	NZ	J_GLU_82	OE2	3.419
6EDU	J_ARG_38	NH2	J_GLU_46	OE1	2.774
6EDU	J_ARG_38	NH2	J_GLU_46	OE2	3.579
6EDU	J_LYS_63	NZ	J_GLU_46	OE1	3.894
6EDU	J_LYS_63	NZ	J_GLU_46	OE2	3.217

6EDU	J_ARG.67	NH1	J_ASP_90	OD2	3.399
6EDU	J_ARG.67	NH2	J_ASP_90	OD1	3.817
6EDU	K_ARG.63	NH1	K_ASP_84	OD1	3.667
6EDU	K_ARG.63	NH1	K_ASP_84	OD2	3.012
6EDU	K_ARG.63	NH2	K_ASP_84	OD2	3.643
6EDU	L_ARG.12	NH2	L_GLU_10	OE2	2.570
6EDU	L_LYS.19	NZ	L_GLU_82	OE2	3.420
6EDU	L_ARG.38	NH2	L_GLU_46	OE1	2.773
6EDU	L_ARG.38	NH2	L_GLU_46	OE2	3.579
6EDU	L_LYS.63	NZ	L_GLU_46	OE1	3.894
6EDU	L_LYS.63	NZ	L_GLU_46	OE2	3.217
6EDU	L_ARG.67	NH1	L_ASP_90	OD2	3.399
6EDU	L_ARG.67	NH2	L_ASP_90	OD1	3.816
6EDU	M_ARG.63	NH1	M_ASP_84	OD1	3.667
6EDU	M_ARG.63	NH1	M_ASP_84	OD2	3.013
6EDU	M_ARG.63	NH2	M_ASP_84	OD2	3.645
6EDU	N_ARG.12	NH2	N_GLU_10	OE2	2.569
6EDU	N_LYS.19	NZ	N_GLU_82	OE2	3.419
6EDU	N_ARG.38	NH2	N_GLU_46	OE1	2.773
6EDU	N_ARG.38	NH2	N_GLU_46	OE2	3.579
6EDU	N_LYS.63	NZ	N_GLU_46	OE1	3.894
6EDU	N_LYS.63	NZ	N_GLU_46	OE2	3.217
6EDU	N_ARG.67	NH1	N_ASP_90	OD2	3.398
6EDU	N_ARG.67	NH2	N_ASP_90	OD1	3.817
6EDU	O_ARG.63	NH1	O_ASP_84	OD1	3.667
6EDU	O_ARG.63	NH1	O_ASP_84	OD2	3.013
6EDU	O_ARG.63	NH2	O_ASP_84	OD2	3.644
6EDU	P_ARG.39	NH1	P_ASP_93	OD1	3.407
6EDU	P_ARG.39	NH2	P_GLU_47	OE1	3.894
6EDU	P_ARG.39	NH2	P_GLU_47	OE2	3.043
6EDU	P_ARG.66	NH1	P_ASP_93	OD2	3.616
6EDU	P_ARG.66	NH2	P_ASP_93	OD2	2.801
6EDU	P_LYS.87	NZ	P_GLU_85	OE2	3.427
6EDU	P_LYS.107	NZ	F_GLU_91	OE1	3.324
6EDU	Q_ARG.24	NH1	Q_ASP_71	OD1	3.743
6EDU	Q_ARG.62	NH2	Q_GLU_82	OE2	3.021
6EDU	Q_ARG.62	NH2	Q_ASP_83	OD2	3.975
6EDU	R_ARG.39	NH1	R_ASP_93	OD1	3.408
6EDU	R_ARG.39	NH2	R_GLU_47	OE1	3.894
6EDU	R_ARG.39	NH2	R_GLU_47	OE2	3.044
6EDU	R_ARG.66	NH1	R_ASP_93	OD2	3.616
6EDU	R_ARG.66	NH2	R_ASP_93	OD2	2.800
6EDU	R_LYS.87	NZ	R_GLU_85	OE2	3.427
6EDU	R_LYS.107	NZ	D_GLU_91	OE1	3.704
6EDU	S_ARG.24	NH1	S_ASP_71	OD1	3.743
6EDU	S_ARG.62	NH2	S_GLU_82	OE2	3.020
6EDU	S_ARG.62	NH2	S_ASP_83	OD2	3.975
6EDU	T_ARG.39	NH1	T_ASP_93	OD1	3.408
6EDU	T_ARG.39	NH2	T_GLU_47	OE1	3.894
6EDU	T_ARG.39	NH2	T_GLU_47	OE2	3.043
6EDU	T_ARG.66	NH1	T_ASP_93	OD2	3.616
6EDU	T_ARG.66	NH2	T_ASP_93	OD2	2.801
6EDU	T_LYS.87	NZ	T_GLU_85	OE2	3.426
6EDU	T_LYS.107	NZ	E_GLU_91	OE1	3.475
6EDU	U_ARG.24	NH1	U_ASP_71	OD1	3.744
6EDU	U_ARG.62	NH2	U_GLU_82	OE2	3.020
6EDU	U_ARG.62	NH2	U_ASP_83	OD2	3.976
6EJG	A_LYS.116	NZ	A_ASP_117	OD2	3.986

6EJG	A_LYS_124	NZ	A_ASP_195	OD1	3.544
6EJG	A_LYS_124	NZ	A_ASP_195	OD2	2.697
6EJG	A_LYS_171	NZ	C_ASP_224	OD2	3.396
6EJG	A_LYS_171	NZ	C_ASP_226	OD2	2.901
6EJG	A_HIS_191	NE2	A_ASP_128	OD1	3.062
6EJG	A_HIS_191	NE2	A_ASP_128	OD2	2.636
6EJG	A_LYS_193	NZ	A_ASP_155	OD1	3.682
6EJG	B_LYS_124	NZ	B_ASP_195	OD1	2.725
6EJG	B_LYS_124	NZ	B_ASP_195	OD2	3.034
6EJG	B_LYS_	NZ	B_ASP_	OD2	3.458
6EJG	B_LYS_	NZ	D_ASP_	OD1	3.521
6EJG	B_LYS_	NZ	D_ASP_	OD2	2.547
6EJG	B_LYS_	NZ	D_ASP_	OD2	2.932
6EJG	B_HIS_191	NE2	B_ASP_	OD1	2.701
6EJG	B_HIS_191	NE2	B_ASP_	OD2	3.241
6EJG	C_ARG_62	NH1	C_ASP_112	OD1	3.837
6EJG	C_ARG_62	NH2	C_ASP_112	OD1	3.201
6EJG	C_ARG_62	NH2	C_ASP_112	OD2	3.690
6EJG	C_LYS_65	NZ	C_GLU_135	OE1	3.179
6EJG	C_LYS_91	NZ	C_GLU_97	OE1	3.567
6EJG	C_ARG_103	NH1	C_GLU_123	OE2	3.023
6EJG	C_ARG_103	NH1	C_ASP_124	OD2	3.428
6EJG	C_ARG_103	NH2	C_GLU_121	OE2	3.520
6EJG	C_ARG_209	NH1	C_GLU_258	OE1	3.385
6EJG	C_ARG_209	NH1	C_GLU_258	OE2	3.605
6EJG	C_ARG_219	NH2	C_GLU_268	OE1	2.753
6EJG	C_ARG_219	NH2	C_GLU_268	OE2	3.078
6EJG	C_LYS_236	NZ	C_ASP_259	OD1	3.275
6EJG	C_LYS_236	NZ	C_ASP_259	OD2	2.696
6EJG	C_ARG_277	NH1	C_ASP_273	OD1	3.404
6EJG	C_ARG_277	NH1	C_ASP_273	OD2	3.492
6EJG	C_ARG_277	NH2	C_GLU_97	OE1	3.001
6EJG	D_ARG_	NH1	D_ASP_	OD1	2.944
6EJG	D_ARG_	NH1	D_ASP_	OD2	3.871
6EJG	D_ARG_	NH2	D_ASP_	OD1	3.096
6EJG	D_ARG_	NH2	D_ASP_	OD2	3.874
6EJG	D_LYS_	NZ	D_GLU_	OE1	2.983
6EJG	D_LYS_	NZ	D_GLU_	OE2	3.137
6EJG	D_ARG_	NH1	D_GLU_	OE2	3.108
6EJG	D_ARG_	NH1	D_ASP_	OD2	3.449
6EJG	D_ARG_	NH2	D_ASP_	OD1	2.957
6EJG	D_ARG_	NH2	D_ASP_	OD2	3.232
6EJG	D_LYS_	NZ	D_ASP_	OD1	3.981
6EJG	D_ARG_	NH2	D_GLU_	OE1	2.937
6EJG	D_ARG_	NH2	D_GLU_	OE2	3.024
6EJG	D_LYS_	NZ	D_ASP_	OD1	3.260
6EJG	D_LYS_	NZ	D_ASP_	OD2	2.656
6EJG	D_ARG_	NH1	D_ASP_	OD1	3.140
6EJG	D_ARG_	NH1	D_ASP_	OD2	3.900
6EJG	D_ARG_	NH2	D_GLU_	OE1	3.261
6EJG	D_ARG_	NH2	D_GLU_	OE2	3.642
6EJM	A_LYS_124	NZ	A_ASP_195	OD1	3.195
6EJM	A_LYS_124	NZ	A_ASP_195	OD2	2.580
6EJM	A_HIS_191	NE2	A_ASP_128	OD1	3.203
6EJM	A_HIS_191	NE2	A_ASP_128	OD2	2.407
6EJM	A_HIS_204	ND1	B_GLU_152	OE2	3.786
6EJM	B_LYS_124	NZ	B_ASP_195	OD1	2.563
6EJM	B_LYS_124	NZ	B_ASP_195	OD2	3.251

6EJM	B_HIS_191	NE2	B_ASP_128	OD1	2.629
6EJM	B_HIS_191	NE2	B_ASP_128	OD2	3.201
6EJM	B_LYS_193	NZ	B_GLU_188	OE2	3.576
6EJM	H_ARG_76	NH1	H_GLU_84	OE1	2.904
6EJM	H_ARG_76	NH1	H_ASP_128	OD1	3.983
6EJM	H_ARG_76	NH2	H_ASP_128	OD1	2.619
6EJM	H_ARG_105	NH1	H_ASP_128	OD1	3.929
6EJM	H_ARG_105	NH1	H_ASP_128	OD2	2.801
6EJM	H_ARG_105	NH2	H_ASP_128	OD1	3.282
6EJM	H_ARG_105	NH2	H_ASP_128	OD2	3.596
6EJM	H_LYS_114	NZ	H_ASP_111	OD1	3.878
6EJM	H_LYS_198	NZ	H_ASP_249	OD2	3.812
6EJM	H_ARG_225	NH2	H_ASP_142	OD2	3.513
6EJM	H_ARG_240	NH1	H_GLU_258	OE1	3.177
6EJM	H_ARG_240	NH1	H_GLU_258	OE2	3.066
6EJM	H_ARG_240	NH1	H_GLU_260	OE2	3.276
6EJM	H_ARG_240	NH1	H_ASP_261	OD2	3.562
6EJM	H_ARG_240	NH2	H_ASP_261	OD1	2.537
6EJM	H_ARG_240	NH2	H_ASP_261	OD2	2.801
6EJM	L_ARG_76	NH1	L_GLU_84	OE1	2.878
6EJM	L_ARG_76	NH2	L_ASP_128	OD1	2.699
6EJM	L_ARG_82	NH2	L_GLU_84	OE2	3.006
6EJM	L_ARG_105	NH1	L_ASP_128	OD1	3.783
6EJM	L_ARG_105	NH1	L_ASP_128	OD2	2.828
6EJM	L_ARG_105	NH2	L_ASP_128	OD1	3.082
6EJM	L_ARG_105	NH2	L_ASP_128	OD2	3.617
6EJM	L_ARG_225	NH2	L_ASP_142	OD2	3.785
6EJM	L_ARG_240	NH2	L_ASP_261	OD1	3.449
6EJM	L_ARG_240	NH2	L_ASP_261	OD2	2.659
6EK2	A_LYS_124	NZ	A_ASP_195	OD1	3.535
6EK2	A_LYS_124	NZ	A_ASP_195	OD2	2.854
6EK2	A_LYS_187	NZ	A_ASP_189	OD1	3.611
6EK2	A_HIS_191	NE2	A_ASP_128	OD1	3.936
6EK2	A_HIS_191	NE2	A_ASP_128	OD2	2.649
6EK2	B_LYS_124	NZ	B_ASP_195	OD1	2.644
6EK2	B_LYS_124	NZ	B_ASP_195	OD2	3.630
6EK2	B_LYS_144	NZ	B_ASP_137	OD1	3.085
6EK2	B_HIS_191	NE2	B_ASP_128	OD1	2.602
6EK2	B_HIS_191	NE2	B_ASP_128	OD2	3.758
6EK2	B_LYS_193	NZ	B_ASP_189	OD1	3.150
6EK2	H_LYS_188	NZ	H_ASP_249	OD1	2.862
6EK2	H_HIS_204	NE2	H_ASP_268	OD1	2.734
6EK2	H_ARG_207	NH1	H_GLU_215	OE1	3.268
6EK2	H_ARG_207	NH1	H_GLU_215	OE2	3.622
6EK2	H_ARG_207	NH1	H_GLU_258	OE2	3.557
6EK2	H_ARG_207	NH2	H_ASP_259	OD1	2.945
6EK2	H_ARG_213	NH1	H_GLU_215	OE1	3.256
6EK2	H_ARG_213	NH1	H_GLU_215	OE2	3.614
6EK2	H_ARG_236	NH1	H_ASP_259	OD1	3.179
6EK2	H_ARG_236	NH1	H_ASP_259	OD2	2.190
6EK2	H_ARG_236	NH2	H_GLU_258	OE2	3.829
6EK2	H_ARG_236	NH2	H_ASP_259	OD1	3.282
6EK2	H_ARG_236	NH2	H_ASP_259	OD2	3.781
6EK2	H_LYS_247	NZ	H_ASP_249	OD1	3.816
6EK2	H_LYS_271	NZ	H_ASP_222	OD2	3.418
6EK2	H_LYS_362	NZ	H_ASP_408	OD2	3.909
6EK2	H_ARG_370	NH1	A_GLU_188	OE2	3.014
6EK2	H_ARG_370	NH2	A_GLU_188	OE1	3.920

6EK2	H_ARG_370	NH2	A_GLU_188	OE2	3.261
6EK2	H_ARG_399	NH1	H_ASP_420	OD1	3.412
6EK2	H_ARG_399	NH1	H_ASP_420	OD2	2.682
6EK2	H_LYS_441	NZ	H_GLU_443	OE2	3.288
6EK2	I_LYS_188	NZ	I_ASP_249	OD1	2.854
6EK2	I_HIS_204	NE2	I_ASP_268	OD2	2.800
6EK2	I_ARG_207	NH1	I_GLU_215	OE1	3.248
6EK2	I_ARG_207	NH1	I_GLU_215	OE2	3.625
6EK2	I_ARG_207	NH1	I_GLU_258	OE2	3.570
6EK2	I_ARG_207	NH2	I_ASP_259	OD1	2.867
6EK2	I_ARG_236	NH1	I_ASP_259	OD1	2.843
6EK2	I_ARG_236	NH1	I_ASP_259	OD2	2.628
6EK2	I_LYS_247	NZ	I_ASP_249	OD1	3.833
6EK2	I_LYS_271	NZ	I_ASP_222	OD2	3.427
6EK2	I_LYS_362	NZ	I_ASP_408	OD2	3.921
6EK2	I_ARG_370	NH1	B_GLU_188	OE1	2.817
6EK2	I_ARG_370	NH1	B_GLU_188	OE2	3.286
6EK2	I_ARG_370	NH2	B_GLU_188	OE1	3.837
6EK2	I_ARG_370	NH2	B_GLU_188	OE2	3.095
6EK2	I_ARG_399	NH1	I_ASP_420	OD1	3.393
6EK2	I_ARG_399	NH1	I_ASP_420	OD2	2.676
6EK2	I_LYS_441	NZ	I_GLU_443	OE2	3.785
6EUN	A_LYS_82	NZ	A_GLU_77	OE2	2.937
6EUN	A_LYS_87	NZ	B_GLU_47	OE1	3.058
6EUN	A_LYS_101	NZ	A_ASP_105	OD2	3.752
6EUN	A_LYS_107	NZ	C_ASP_105	OD1	3.488
6EUN	A_LYS_145	NZ	A_GLU_148	OE2	3.702
6EUN	A_LYS_167	NZ	C_ASP_165	OD1	3.883
6EUN	B_LYS_69	NZ	B_ASP_59	OD2	2.842
6EUN	B_LYS_82	NZ	B_GLU_77	OE2	2.936
6EUN	B_LYS_87	NZ	C_GLU_47	OE1	3.021
6EUN	B_LYS_101	NZ	B_ASP_105	OD2	3.762
6EUN	B_LYS_107	NZ	A_ASP_105	OD1	3.579
6EUN	B_LYS_145	NZ	B_GLU_148	OE2	3.617
6EUN	C_LYS_69	NZ	C_ASP_59	OD2	2.843
6EUN	C_LYS_82	NZ	C_GLU_77	OE2	2.928
6EUN	C_LYS_87	NZ	A_GLU_47	OE1	3.007
6EUN	C_LYS_101	NZ	C_ASP_105	OD2	3.754
6EUN	C_LYS_107	NZ	B_ASP_105	OD1	3.525
6EUN	C_LYS_145	NZ	C_GLU_148	OE2	3.782
6EUP	A_LYS_69	NZ	A_ASP_59	OD2	3.593
6EUP	A_LYS_87	NZ	B_GLU_47	OE1	2.842
6EUP	A_LYS_87	NZ	B_ASP_79	OD1	3.786
6EUP	A_LYS_107	NZ	C_ASP_105	OD1	3.538
6EUP	A_LYS_145	NZ	A_GLU_148	OE2	3.961
6EUP	B_LYS_69	NZ	B_ASP_75	OD1	3.179
6EUP	B_LYS_69	NZ	B_ASP_75	OD2	2.780
6EUP	B_LYS_87	NZ	C_GLU_47	OE1	2.811
6EUP	B_LYS_87	NZ	C_ASP_79	OD1	3.799
6EUP	B_LYS_107	NZ	A_ASP_105	OD1	3.723
6EUP	C_LYS_69	NZ	C_ASP_59	OD2	3.592
6EUP	C_LYS_87	NZ	A_GLU_47	OE1	2.814
6EUP	C_LYS_87	NZ	A_ASP_79	OD1	3.752
6EUP	C_LYS_107	NZ	B_ASP_105	OD1	3.560
6EUP	C_LYS_145	NZ	C_GLU_148	OE2	3.928
6EV1	A_ARG_40	NH1	A_GLU_46	OE1	3.790
6EV1	A_ARG_40	NH1	A_GLU_46	OE2	2.696
6EV1	A_ARG_40	NH2	A_GLU_46	OE2	2.910

6EV1	A_LYS_63	NZ	A_GLU_46	OE1	3.383
6EV1	A_LYS_67	NZ	A_ASP_90	OD1	3.842
6EV1	A_LYS_67	NZ	A_ASP_90	OD2	2.754
6EV1	A_LYS_147	NZ	A_ASP_148	OD1	3.932
6EV1	A_LYS_213	NZ	B_GLU_122	OE1	3.565
6EV1	B_HIS_33	NE2	B_ASP_49	OD1	3.832
6EV1	B_ARG_45	NH1	A_ASP_105	OD1	3.400
6EV1	B_LYS_52	NZ	B_ASP_49	OD2	3.765
6EV1	B_ARG_60	NH1	B_GLU_78	OE1	3.819
6EV1	B_ARG_60	NH1	B_GLU_78	OE2	3.655
6EV1	B_ARG_60	NH2	B_GLU_78	OE2	3.561
6EV1	B_ARG_60	NH2	B_GLU_80	OE2	2.733
6EV1	B_ARG_60	NH2	B_ASP_81	OD1	3.048
6EV1	B_ARG_60	NH2	B_ASP_81	OD2	3.747
6EV1	B_LYS_102	NZ	B_GLU_104	OE2	3.444
6EV1	B_LYS_102	NZ	B_GLU_164	OE2	3.563
6EV1	B_ARG_141	NH1	B_GLU_104	OE1	3.542
6EV1	B_ARG_141	NH1	B_GLU_104	OE2	2.887
6EV1	B_ARG_141	NH2	B_GLU_104	OE1	3.560
6EV1	B_ARG_141	NH2	B_GLU_104	OE2	2.857
6EV1	B_LYS_144	NZ	B_GLU_194	OE2	3.954
6EV1	B_LYS_148	NZ	B_GLU_194	OE1	2.745
6EV1	B_LYS_187	NZ	B_ASP_184	OD1	3.196
6EV1	C_LYS_38	NZ	C_GLU_89	OE2	2.747
6EV1	C_LYS_63	NZ	C_GLU_46	OE1	3.586
6EV1	C_LYS_63	NZ	C_GLU_46	OE2	3.868
6EV1	C_LYS_63	NZ	C_GLU_89	OE2	3.610
6EV1	C_LYS_67	NZ	C_ASP_90	OD1	3.419
6EV1	C_LYS_67	NZ	C_ASP_90	OD2	2.576
6EV1	C_LYS_147	NZ	C_ASP_148	OD1	3.591
6EV1	D_LYS_52	NZ	D_ASP_49	OD2	3.936
6EV1	D_ARG_60	NH1	D_GLU_78	OE1	3.982
6EV1	D_ARG_60	NH1	D_ASP_81	OD1	2.686
6EV1	D_ARG_60	NH1	D_ASP_81	OD2	2.341
6EV1	D_ARG_60	NH2	D_GLU_78	OE2	3.908
6EV1	D_ARG_60	NH2	D_GLU_80	OE2	2.672
6EV1	D_ARG_60	NH2	D_ASP_81	OD1	3.533
6EV1	D_LYS_102	NZ	D_GLU_104	OE2	2.957
6EV1	D_LYS_102	NZ	D_GLU_164	OE1	3.066
6EV1	D_ARG_141	NH1	D_GLU_104	OE1	3.100
6EV1	D_ARG_141	NH1	D_GLU_104	OE2	2.729
6EV1	D_ARG_141	NH2	D_GLU_104	OE1	3.502
6EV1	D_LYS_148	NZ	D_GLU_194	OE2	2.419
6EV1	D_LYS_187	NZ	D_ASP_184	OD1	2.568
6EV1	D_LYS_187	NZ	D_ASP_184	OD2	3.848
6EV1	E_ARG_40	NH1	E_GLU_46	OE1	3.238
6EV1	E_LYS_67	NZ	E_ASP_90	OD1	3.136
6EV1	E_LYS_67	NZ	E_ASP_90	OD2	3.150
6EV1	E_LYS_147	NZ	E_ASP_148	OD1	3.641
6EV1	E_LYS_147	NZ	E_ASP_148	OD2	3.538
6EV1	E_LYS_213	NZ	F_GLU_122	OE2	3.696
6EV1	E_LYS_214	NZ	E_GLU_216	OE2	3.745
6EV1	F_ARG_45	NH1	E_ASP_105	OD1	3.598
6EV1	F_LYS_52	NZ	F_ASP_49	OD2	3.409
6EV1	F_ARG_60	NH1	F_GLU_78	OE1	3.963
6EV1	F_ARG_60	NH2	F_GLU_80	OE2	2.462
6EV1	F_ARG_60	NH2	F_ASP_81	OD1	2.838
6EV1	F_ARG_60	NH2	F_ASP_81	OD2	3.378

6EV1	F_LYS_102	NZ	F_GLU_104	OE2	3.200
6EV1	F_LYS_102	NZ	F_GLU_164	OE1	3.253
6EV1	F_LYS_102	NZ	F_GLU_164	OE2	3.819
6EV1	F_ARG_141	NH1	F_GLU_142	OE2	3.956
6EV1	F_ARG_141	NH2	F_GLU_104	OE1	2.879
6EV1	F_ARG_141	NH2	F_GLU_104	OE2	2.315
6EV1	F_LYS_148	NZ	F_GLU_194	OE1	2.676
6EV1	F_LYS_187	NZ	F_ASP_184	OD1	3.320
6EV1	F_LYS_189	NZ	F_GLU_212	OE1	3.396
6EV1	G_ARG_40	NH1	G_GLU_46	OE1	3.181
6EV1	G_LYS_63	NZ	G_GLU_46	OE1	3.941
6EV1	G_LYS_63	NZ	G_GLU_46	OE2	3.486
6EV1	G_LYS_67	NZ	G_ASP_90	OD1	3.844
6EV1	G_LYS_67	NZ	G_ASP_90	OD2	3.076
6EV1	G_LYS_213	NZ	H_GLU_122	OE2	3.127
6EV1	H_HIS_33	NE2	H_ASP_49	OD1	3.831
6EV1	H_ARG_60	NH2	H_GLU_80	OE2	2.685
6EV1	H_ARG_60	NH2	H_ASP_81	OD1	3.172
6EV1	H_ARG_60	NH2	H_ASP_81	OD2	3.902
6EV1	H_LYS_102	NZ	H_GLU_104	OE2	2.463
6EV1	H_LYS_102	NZ	H_GLU_164	OE1	3.887
6EV1	H_LYS_102	NZ	H_GLU_164	OE2	3.148
6EV1	H_ARG_141	NH1	H_GLU_104	OE1	3.993
6EV1	H_ARG_141	NH2	H_GLU_104	OE1	2.709
6EV1	H_ARG_141	NH2	H_GLU_104	OE2	3.012
6EV1	H_HIS_188	ND1	H_ASP_150	OD2	3.547
6EV1	L_ARG_40	NH1	L_GLU_46	OE1	3.727
6EV1	L_ARG_40	NH1	L_GLU_46	OE2	2.502
6EV1	L_ARG_40	NH2	L_GLU_46	OE2	3.081
6EV1	L_LYS_67	NZ	L_ASP_90	OD1	3.185
6EV1	L_LYS_67	NZ	L_ASP_90	OD2	2.453
6EV1	L_LYS_147	NZ	L_ASP_148	OD1	3.802
6EV1	L_LYS_213	NZ	J_GLU_122	OE1	2.884
6EV1	L_LYS_213	NZ	J_GLU_122	OE2	3.812
6EV1	J_ARG_45	NH2	L_ASP_105	OD1	3.213
6EV1	J_ARG_45	NH2	L_ASP_105	OD2	3.457
6EV1	J_ARG_60	NH1	J_GLU_78	OE1	2.996
6EV1	J_ARG_60	NH2	J_GLU_78	OE1	2.740
6EV1	J_ARG_60	NH2	J_GLU_78	OE2	3.438
6EV1	J_ARG_60	NH2	J_GLU_80	OE1	3.708
6EV1	J_ARG_60	NH2	J_ASP_81	OD1	3.548
6EV1	J_LYS_102	NZ	J_GLU_164	OE1	3.206
6EV1	J_LYS_102	NZ	J_GLU_164	OE2	3.357
6EV1	J_ARG_141	NH1	J_GLU_104	OE1	3.574
6EV1	J_ARG_141	NH1	J_GLU_104	OE2	3.837
6EV1	J_ARG_141	NH2	J_GLU_104	OE1	3.635
6EV1	J_ARG_141	NH2	J_GLU_104	OE2	3.025
6EV1	J_LYS_148	NZ	J_GLU_194	OE1	2.568
6EV1	J_LYS_187	NZ	J_ASP_184	OD1	2.786
6EV1	J_HIS_188	ND1	J_ASP_150	OD2	3.581
6EV1	K_LYS_67	NZ	K_ASP_90	OD1	3.821
6EV1	K_LYS_67	NZ	K_ASP_90	OD2	3.131
6EV1	K_LYS_147	NZ	K_ASP_148	OD1	3.891
6EV1	K_LYS_147	NZ	K_ASP_148	OD2	3.991
6EV1	K_HIS_168	NE2	L_ASP_166	OD2	3.740
6EV1	K_LYS_213	NZ	L_GLU_122	OE1	3.450
6EV1	L_ARG_45	NH2	K_ASP_105	OD1	3.857
6EV1	L_LYS_52	NZ	L_ASP_49	OD2	3.305

6EV1	L_ARG_60	NH1	L_GLU_78	OE2	3.656
6EV1	L_ARG_60	NH2	L_GLU_80	OE2	2.289
6EV1	L_ARG_60	NH2	L_ASP_81	OD1	3.740
6EV1	L_LYS_102	NZ	L_GLU_104	OE1	3.803
6EV1	L_LYS_102	NZ	L_GLU_104	OE2	3.397
6EV1	L_LYS_102	NZ	L_GLU_164	OE1	3.211
6EV1	L_ARG_141	NH1	L_GLU_104	OE1	3.719
6EV1	L_LYS_148	NZ	L_GLU_194	OE1	2.763
6EV1	L_LYS_187	NZ	L_ASP_184	OD1	2.439
6EV1	L_LYS_187	NZ	L_ASP_184	OD2	3.983
6EV2	A_LYS_63	NZ	A_GLU_46	OE2	3.111
6EV2	A_LYS_65	NZ	A_ASP_66	OD1	3.842
6EV2	A_LYS_65	NZ	A_ASP_66	OD2	2.879
6EV2	A_LYS_67	NZ	A_ASP_90	OD1	3.783
6EV2	A_LYS_67	NZ	A_ASP_90	OD2	2.679
6EV2	A_LYS_147	NZ	A_ASP_148	OD1	3.638
6EV2	A_LYS_213	NZ	B_GLU_122	OE1	3.442
6EV2	B_ARG_45	NH1	A_ASP_105	OD1	3.088
6EV2	B_LYS_52	NZ	B_ASP_49	OD2	3.559
6EV2	B_ARG_60	NH1	B_GLU_78	OE1	3.644
6EV2	B_ARG_60	NH1	B_GLU_78	OE2	3.977
6EV2	B_ARG_60	NH2	B_GLU_80	OE2	3.107
6EV2	B_ARG_60	NH2	B_ASP_81	OD1	2.872
6EV2	B_ARG_60	NH2	B_ASP_81	OD2	3.612
6EV2	B_LYS_102	NZ	B_GLU_104	OE1	3.573
6EV2	B_LYS_102	NZ	B_GLU_164	OE1	3.299
6EV2	B_LYS_102	NZ	B_GLU_164	OE2	3.878
6EV2	B_ARG_141	NH2	B_GLU_104	OE1	3.798
6EV2	B_ARG_141	NH2	B_GLU_104	OE2	3.715
6EV2	B_LYS_168	NZ	F_GLU_78	OE2	2.948
6EV2	B_LYS_182	NZ	B_GLU_186	OE2	3.804
6EV2	B_HIS_188	ND1	B_ASP_150	OD2	3.294
6EV2	B_HIS_217	NE2	B_GLU_186	OE2	3.191
6EV2	C_LYS_38	NZ	C_GLU_46	OE1	3.925
6EV2	C_ARG_40	NH1	C_GLU_89	OE1	2.530
6EV2	C_ARG_40	NH1	C_GLU_89	OE2	3.940
6EV2	C_ARG_40	NH2	C_GLU_89	OE1	2.841
6EV2	C_LYS_63	NZ	C_GLU_46	OE2	2.910
6EV2	C_LYS_67	NZ	C_ASP_90	OD1	3.799
6EV2	C_LYS_67	NZ	C_ASP_90	OD2	2.689
6EV2	C_LYS_147	NZ	C_ASP_148	OD1	3.909
6EV2	C_LYS_214	NZ	C_GLU_216	OE1	3.019
6EV2	C_LYS_214	NZ	C_GLU_216	OE2	3.275
6EV2	D_LYS_44	NZ	C_ASP_105	OD2	3.822
6EV2	D_ARG_45	NH1	C_ASP_105	OD1	3.142
6EV2	D_LYS_52	NZ	D_ASP_49	OD2	3.541
6EV2	D_ARG_60	NH1	D_GLU_78	OE1	3.997
6EV2	D_ARG_60	NH1	D_GLU_78	OE2	3.666
6EV2	D_ARG_60	NH2	D_GLU_80	OE2	2.969
6EV2	D_ARG_60	NH2	D_ASP_81	OD1	2.871
6EV2	D_ARG_60	NH2	D_ASP_81	OD2	3.679
6EV2	D_LYS_102	NZ	D_GLU_164	OE1	3.482
6EV2	D_ARG_141	NH2	D_GLU_104	OE1	3.236
6EV2	D_ARG_141	NH2	D_GLU_104	OE2	3.266
6EV2	D_LYS_148	NZ	D_GLU_194	OE1	3.886
6EV2	D_LYS_148	NZ	D_GLU_194	OE2	2.872
6EV2	D_LYS_168	NZ	H_GLU_78	OE2	3.198
6EV2	D_HIS_188	ND1	D_ASP_150	OD2	3.510

6EV2	E_ARG_40	NH1	E_GLU_89	OE1	3.472
6EV2	E_ARG_40	NH1	E_GLU_89	OE2	2.763
6EV2	E_ARG_40	NH2	E_GLU_89	OE2	2.889
6EV2	E_LYS_63	NZ	E_GLU_46	OE1	3.154
6EV2	E_LYS_63	NZ	E_GLU_46	OE2	2.770
6EV2	E_LYS_67	NZ	E_ASP_90	OD1	3.680
6EV2	E_LYS_67	NZ	E_ASP_90	OD2	2.852
6EV2	E_LYS_147	NZ	E_ASP_148	OD1	2.804
6EV2	E_LYS_147	NZ	E_ASP_148	OD2	3.429
6EV2	E_LYS_210	NZ	E_ASP_212	OD1	3.724
6EV2	E_LYS_210	NZ	E_ASP_212	OD2	3.578
6EV2	E_LYS_213	NZ	F_GLU_122	OE1	3.493
6EV2	E_LYS_214	NZ	E_GLU_216	OE2	2.823
6EV2	E_LYS_218	NZ	F_ASP_121	OD2	3.835
6EV2	F_ARG_45	NH1	E_ASP_105	OD1	2.818
6EV2	F_LYS_52	NZ	F_ASP_49	OD2	3.921
6EV2	F_ARG_60	NH1	F_GLU_78	OE2	3.617
6EV2	F_ARG_60	NH2	F_GLU_80	OE2	3.106
6EV2	F_ARG_60	NH2	F_ASP_81	OD1	2.910
6EV2	F_ARG_60	NH2	F_ASP_81	OD2	3.493
6EV2	F_LYS_102	NZ	F_GLU_104	OE2	3.866
6EV2	F_LYS_102	NZ	F_GLU_164	OE1	2.823
6EV2	F_LYS_102	NZ	F_GLU_164	OE2	3.600
6EV2	F_LYS_148	NZ	F_GLU_194	OE1	2.349
6EV2	F_LYS_168	NZ	B_GLU_78	OE1	3.747
6EV2	F_LYS_189	NZ	F_GLU_212	OE1	2.964
6EV2	F_LYS_189	NZ	F_GLU_212	OE2	3.194
6EV2	G_LYS_63	NZ	G_GLU_46	OE2	2.652
6EV2	G_LYS_67	NZ	G_ASP_90	OD1	3.758
6EV2	G_LYS_67	NZ	G_ASP_90	OD2	2.774
6EV2	G_LYS_147	NZ	G_ASP_148	OD1	3.806
6EV2	G_LYS_210	NZ	A_ASP_73	OD1	3.883
6EV2	G_LYS_210	NZ	A_ASP_73	OD2	2.404
6EV2	G_LYS_213	NZ	H_GLU_122	OE1	3.330
6EV2	G_LYS_213	NZ	H_GLU_122	OE2	3.779
6EV2	G_LYS_214	NZ	G_GLU_216	OE2	2.730
6EV2	H_ARG_45	NH1	G_ASP_105	OD1	3.108
6EV2	H_ARG_60	NH1	H_GLU_78	OE2	3.921
6EV2	H_ARG_60	NH2	H_GLU_80	OE2	2.991
6EV2	H_ARG_60	NH2	H_ASP_81	OD1	3.423
6EV2	H_ARG_60	NH2	H_ASP_81	OD2	2.856
6EV2	H_LYS_102	NZ	H_GLU_164	OE1	3.383
6EV2	H_ARG_141	NH2	H_GLU_104	OE1	3.404
6EV2	H_ARG_141	NH2	H_GLU_104	OE2	2.455
6EV2	H_LYS_148	NZ	H_GLU_194	OE1	2.710
6EV2	H_LYS_148	NZ	H_GLU_194	OE2	3.785
6EV2	H_LYS_168	NZ	D_GLU_78	OE2	3.686
6EWB	A_ARG_241	NH2	A_ASP_325	OD1	2.936
6EWB	A_ARG_241	NH2	A_ASP_325	OD2	3.696
6EWB	A_LYS_248	NZ	A_GLU_247	OE1	3.886
6EWB	A_ARG_345	NH1	A_GLU_376	OE2	3.889
6EWB	A_HIS_347	NE2	A_ASP_374	OD2	2.911
6EWB	A_HIS_396	ND1	A_ASP_391	OD2	3.943
6EWB	A_ARG_435	NH1	A_ASP_448	OD2	3.551
6EWB	A_ARG_435	NH2	A_ASP_450	OD1	3.333
6EWB	A_ARG_435	NH2	A_ASP_450	OD2	2.720
6EWB	A_ARG_476	NH1	A_ASP_518	OD2	2.712
6EWB	A_ARG_476	NH2	A_GLU_488	OE1	3.271

6EWB	A_LYS_490	NZ	A_GLU_429	OE2	3.221
6EWB	A_ARG_516	NH2	A_ASP_518	OD1	3.815
6EWB	A_ARG_516	NH2	A_ASP_518	OD2	3.445
6EWB	B_ARG_241	NH2	B_ASP_325	OD1	3.075
6EWB	B_ARG_241	NH2	B_ASP_325	OD2	3.936
6EWB	B_LYS_248	NZ	B_GLU_247	OE1	3.679
6EWB	B_ARG_345	NH1	B_GLU_376	OE2	3.796
6EWB	B_ARG_345	NH2	B_GLU_376	OE2	3.815
6EWB	B_HIS_347	ND1	B_ASP_370	OD1	3.328
6EWB	B_HIS_347	NE2	B_ASP_374	OD2	2.654
6EWB	B_ARG_373	NH1	B_ASP_372	OD2	3.813
6EWB	B_ARG_373	NH2	B_ASP_372	OD2	3.329
6EWB	B_ARG_435	NH1	B_ASP_448	OD2	3.850
6EWB	B_ARG_435	NH1	B_ASP_506	OD1	3.944
6EWB	B_ARG_435	NH2	B_ASP_450	OD1	3.359
6EWB	B_ARG_435	NH2	B_ASP_450	OD2	2.788
6EWB	B_ARG_476	NH1	B_ASP_518	OD2	2.823
6EWB	B_ARG_476	NH2	B_GLU_488	OE1	3.165
6EWB	B_LYS_490	NZ	B_GLU_429	OE2	3.030
6EWB	B_ARG_516	NH2	B_ASP_518	OD1	3.365
6EWB	B_ARG_516	NH2	B_ASP_518	OD2	2.936
6EWB	C_ARG_241	NH2	C_ASP_325	OD1	2.915
6EWB	C_ARG_241	NH2	C_ASP_325	OD2	3.721
6EWB	C_LYS_248	NZ	C_GLU_247	OE1	3.894
6EWB	C_ARG_345	NH1	C_GLU_376	OE2	3.422
6EWB	C_ARG_345	NH2	C_GLU_376	OE2	3.471
6EWB	C_HIS_347	ND1	C_ASP_370	OD1	3.346
6EWB	C_HIS_347	NE2	C_ASP_374	OD2	2.797
6EWB	C_HIS_396	ND1	C_ASP_391	OD2	3.992
6EWB	C_ARG_435	NH1	C_ASP_448	OD2	3.511
6EWB	C_ARG_435	NH2	C_ASP_450	OD1	3.163
6EWB	C_ARG_435	NH2	C_ASP_450	OD2	2.800
6EWB	C_ARG_476	NH1	C_GLU_488	OE1	2.525
6EWB	C_ARG_476	NH2	C_ASP_518	OD2	3.985
6EWB	C_LYS_490	NZ	C_GLU_429	OE1	3.972
6EWB	C_LYS_490	NZ	C_GLU_429	OE2	3.084
6EWB	C_ARG_516	NH2	C_ASP_518	OD1	3.755
6EWB	C_ARG_516	NH2	C_ASP_518	OD2	3.482
6EWB	D_ARG_241	NH2	D_ASP_325	OD1	3.023
6EWB	D_ARG_241	NH2	D_ASP_325	OD2	3.955
6EWB	D_LYS_248	NZ	D_GLU_247	OE1	3.969
6EWB	D_ARG_345	NH1	D_GLU_376	OE2	3.830
6EWB	D_HIS_347	ND1	D_ASP_370	OD1	3.312
6EWB	D_HIS_347	NE2	D_ASP_374	OD2	2.724
6EWB	D_HIS_417	NE2	L_GLU_80	OE2	3.932
6EWB	D_ARG_435	NH1	D_ASP_448	OD2	3.638
6EWB	D_ARG_435	NH2	D_ASP_450	OD1	3.210
6EWB	D_ARG_435	NH2	D_ASP_450	OD2	2.891
6EWB	D_ARG_476	NH1	D_ASP_518	OD2	2.514
6EWB	D_ARG_476	NH2	D_GLU_488	OE1	3.217
6EWB	D_LYS_490	NZ	D_GLU_429	OE2	2.925
6EWB	D_ARG_516	NH2	D_ASP_518	OD1	3.559
6EWB	D_ARG_516	NH2	D_ASP_518	OD2	3.083
6EWB	E_LYS_	NZ	E_ASP_	OD1	3.980
6EWB	E_ARG_98	NH1	B_ASP_341	OD1	3.977
6EWB	E_ARG_98	NH2	B_ASP_341	OD1	3.813
6EWB	E_ARG_101	NH1	F_ASP_49	OD1	2.895
6EWB	E_ARG_101	NH1	F_ASP_49	OD2	3.620

6EWB	F_ARG_	NH1	E_ASP_	OD1	3.803
6EWB	F_ARG_	NH1	E_ASP_	OD2	3.536
6EWB	F_LYS_52	NZ	A_ASP_448	OD1	3.722
6EWB	F_LYS_52	NZ	A_ASP_448	OD2	2.304
6EWB	F_LYS_52	NZ	F_ASP_49	OD2	3.153
6EWB	F_ARG_	NH1	F_GLU_	OE2	3.882
6EWB	F_ARG_	NH2	F_GLU_	OE2	2.849
6EWB	F_ARG_	NH2	F_ASP_	OD1	2.744
6EWB	F_ARG_	NH2	F_ASP_	OD2	3.294
6EWB	G_ARG_40	NH1	G_GLU_89	OE1	3.993
6EWB	G_ARG_40	NH2	G_GLU_89	OE2	3.112
6EWB	G_LYS_63	NZ	G_GLU_46	OE1	3.095
6EWB	G_LYS_63	NZ	G_GLU_46	OE2	3.462
6EWB	G_LYS_67	NZ	G_ASP_90	OD2	3.352
6EWB	G_ARG_98	NH1	D_ASP_341	OD1	3.850
6EWB	G_ARG_98	NH2	D_ASP_341	OD1	3.731
6EWB	G_ARG_101	NH1	L_ASP_49	OD1	2.830
6EWB	G_ARG_101	NH1	L_ASP_49	OD2	3.797
6EWB	H_ARG_40	NH1	H_GLU_89	OE1	3.969
6EWB	H_LYS_67	NZ	H_ASP_90	OD2	3.353
6EWB	H_ARG_98	NH1	A_ASP_341	OD2	3.948
6EWB	H_ARG_98	NH2	A_ASP_341	OD2	3.896
6EWB	H_ARG_101	NH1	L_ASP_49	OD1	2.509
6EWB	H_ARG_101	NH1	L_ASP_49	OD2	3.441
6EWB	H_LYS_208	NZ	H_ASP_210	OD1	3.387
6EWB	H_LYS_208	NZ	H_ASP_210	OD2	3.606
6EWB	L_ARG_45	NH1	G_ASP_104	OD1	3.731
6EWB	L_ARG_45	NH1	G_ASP_104	OD2	3.636
6EWB	L_LYS_52	NZ	C_ASP_448	OD1	3.564
6EWB	L_LYS_52	NZ	C_ASP_448	OD2	2.694
6EWB	L_LYS_52	NZ	L_ASP_49	OD2	3.594
6EWB	L_ARG_60	NH1	L_GLU_80	OE2	3.662
6EWB	L_ARG_60	NH2	L_GLU_80	OE2	2.362
6EWB	L_ARG_60	NH2	L_ASP_81	OD1	3.161
6EWB	L_ARG_60	NH2	L_ASP_81	OD2	3.779
6EWB	L_LYS_148	NZ	L_GLU_194	OE1	2.906
6EWB	L_LYS_148	NZ	L_GLU_194	OE2	3.891
6EWB	L_HIS_188	ND1	L_ASP_150	OD2	2.838
6EWB	J_LYS_38	NZ	J_ASP_90	OD1	3.994
6EWB	J_ARG_98	NH1	C_ASP_341	OD2	3.957
6EWB	J_ARG_98	NH2	C_ASP_341	OD2	3.467
6EWB	J_ARG_101	NH1	K_ASP_49	OD1	2.726
6EWB	J_ARG_101	NH1	K_ASP_49	OD2	3.581
6EWB	J_LYS_211	NZ	K_GLU_122	OE2	2.945
6EWB	K_ARG_45	NH1	J_ASP_104	OD2	3.826
6EWB	K_LYS_52	NZ	D_ASP_448	OD1	3.845
6EWB	K_LYS_52	NZ	D_ASP_448	OD2	2.608
6EWB	K_LYS_52	NZ	K_ASP_49	OD2	3.118
6EWB	K_ARG_60	NH2	K_GLU_80	OE1	3.852
6EWB	K_ARG_60	NH2	K_ASP_81	OD1	2.735
6EWB	K_ARG_60	NH2	K_ASP_81	OD2	3.577
6EWB	K_LYS_141	NZ	K_GLU_104	OE1	3.738
6EWB	K_LYS_141	NZ	K_GLU_104	OE2	2.397
6EWB	K_LYS_198	NZ	K_ASP_109	OD2	3.688
6EWB	L_ARG_45	NH1	H_ASP_104	OD1	3.721
6EWB	L_ARG_45	NH1	H_ASP_104	OD2	3.560
6EWB	L_LYS_52	NZ	B_ASP_448	OD1	3.690
6EWB	L_LYS_52	NZ	B_ASP_448	OD2	2.585

6EWB	L_LYS_52	NZ	L_ASP_49	OD2	3.133
6EWB	L_ARG_60	NH1	D_GLU_316	OE1	3.251
6EWB	L_ARG_60	NH1	D_GLU_316	OE2	3.266
6EWB	L_ARG_60	NH2	L_GLU_80	OE1	3.300
6EWB	L_ARG_60	NH2	L_ASP_81	OD1	2.716
6EWB	L_ARG_60	NH2	L_ASP_81	OD2	3.315
6EWB	L_LYS_102	NZ	L_ASP_164	OD2	3.771
6EWB	L_LYS_141	NZ	L_GLU_104	OE2	3.049
6EWB	L_HIS_188	ND1	L_ASP_150	OD1	3.713
6FAB	L_ARG_24	NH1	L_ASP_70	OD1	2.789
6FAB	L_ARG_61	NH1	L_GLU_81	OE2	3.576
6FAB	L_ARG_61	NH2	L_GLU_81	OE1	2.864
6FAB	L_ARG_61	NH2	L_GLU_81	OE2	2.823
6FAB	L_ARG_61	NH2	L_ASP_82	OD1	2.715
6FAB	L_ARG_61	NH2	L_ASP_82	OD2	3.543
6FAB	L_LYS_107	NZ	L_ASP_110	OD1	3.024
6FAB	L_LYS_147	NZ	L_GLU_195	OE2	3.857
6FAB	L_LYS_149	NZ	L_GLU_195	OE1	2.545
6FAB	L_LYS_149	NZ	L_GLU_195	OE2	2.801
6FAB	L_LYS_169	NZ	L_ASP_167	OD1	2.717
6FAB	L_LYS_169	NZ	L_ASP_167	OD2	2.572
6FAB	L_LYS_183	NZ	L_GLU_187	OE1	2.518
6FAB	L_LYS_183	NZ	L_GLU_187	OE2	2.757
6FAB	L_ARG_188	NH1	L_ASP_184	OD1	2.649
6FAB	L_ARG_188	NH1	L_ASP_184	OD2	3.158
6FAB	L_ARG_188	NH2	L_ASP_184	OD1	3.720
6FAB	L_ARG_188	NH2	L_ASP_184	OD2	2.655
6FAB	L_ARG_188	NH2	L_GLU_185	OE1	2.879
6FAB	L_LYS_199	NZ	L_ASP_143	OD1	2.609
6FAB	L_LYS_199	NZ	L_ASP_143	OD2	2.563
6FAB	H_LYS_63	NZ	H_GLU_46	OE1	2.502
6FAB	H_LYS_63	NZ	H_GLU_46	OE2	3.193
6FAB	H_LYS_65	NZ	H_GLU_62	OE1	2.682
6FAB	H_LYS_65	NZ	H_GLU_62	OE2	2.720
6FAB	H_LYS_67	NZ	H_ASP_90	OD1	3.504
6FAB	H_LYS_67	NZ	H_ASP_90	OD2	2.658
6FAB	H_ARG_98	NH2	H_ASP_109	OD1	3.478
6FAB	H_ARG_98	NH2	H_ASP_109	OD2	2.734
6FAB	H_LYS_107	NZ	H_GLU_100	OE2	3.655
6FAB	H_LYS_107	NZ	H_ASP_109	OD2	2.865
6FAB	H_LYS_213	NZ	H_ASP_215	OD1	3.756
6FAB	H_LYS_213	NZ	H_ASP_215	OD2	2.836
6FAB	H_LYS_216	NZ	L_GLU_123	OE1	2.624
6FAB	H_LYS_216	NZ	L_GLU_123	OE2	2.770
6FAB	H_ARG_221	NH2	H_ASP_222	OD1	2.832
6FAB	H_ARG_221	NH2	H_ASP_222	OD2	3.565
6FAX	L_ARG_61	NH2	L_ASP_82	OD1	2.582
6FAX	L_ARG_61	NH2	L_ASP_82	OD2	3.227
6FAX	L_LYS_103	NZ	L_GLU_165	OE1	3.961
6FAX	L_LYS_149	NZ	L_GLU_195	OE1	3.174
6FAX	L_LYS_149	NZ	L_GLU_195	OE2	3.580
6FAX	L_HIS_189	ND1	L_ASP_151	OD2	3.031
6FAX	H_LYS_19	NZ	H_GLU_82	OE1	3.254
6FAX	H_LYS_38	NZ	H_ASP_90	OD1	3.375
6FAX	H_LYS_63	NZ	H_GLU_46	OE1	3.943
6FAX	H_LYS_63	NZ	H_GLU_46	OE2	3.507
6FAX	H_LYS_67	NZ	H_ASP_90	OD2	3.573
6FAX	H_ARG_98	NH2	H_ASP_110	OD1	3.912

6FAX	H_ARG_98	NH2	H_ASP_110	OD2	3.034
6FAX	H_ARG_104	NH1	H_GLU_100	OE2	2.851
6FAX	H_ARG_104	NH2	R_GLU_21	OE1	3.986
6FAX	H_LYS_152	NZ	H_ASP_153	OD1	3.279
6FAX	H_LYS_152	NZ	H_ASP_153	OD2	3.260
6FAX	H_HIS_173	NE2	L_ASP_167	OD1	3.928
6FAX	H_LYS_218	NZ	L_GLU_123	OE1	3.125
6FAX	H_LYS_218	NZ	L_GLU_123	OE2	3.415
6FAX	R_HIS_78	NE2	R_GLU_74	OE1	3.706
6FAX	R_HIS_78	NE2	R_GLU_74	OE2	3.685
6FN1	A_ARG_40	NH1	A_ASP_369	OD1	2.632
6FN1	A_ARG_40	NH1	A_ASP_369	OD2	3.669
6FN1	A_ARG_40	NH2	A_ASP_369	OD1	3.084
6FN1	A_HIS_152	NE2	A_GLU_916	OE2	3.957
6FN1	A_ARG_173	NH2	A_GLU_169	OE1	2.871
6FN1	A_LYS_180	NZ	A_ASP_176	OD1	3.377
6FN1	A_LYS_180	NZ	A_ASP_176	OD2	3.959
6FN1	A_LYS_212	NZ	A_GLU_324	OE1	3.963
6FN1	A_LYS_212	NZ	A_GLU_324	OE2	2.762
6FN1	A_ARG_261	NH2	A_ASP_804	OD1	2.402
6FN1	A_ARG_261	NH2	A_ASP_804	OD2	3.659
6FN1	A_ARG_275	NH1	A_GLU_255	OE2	3.657
6FN1	A_ARG_275	NH1	A_GLU_272	OE1	3.157
6FN1	A_ARG_275	NH2	A_GLU_255	OE2	3.869
6FN1	A_ARG_285	NH2	A_GLU_282	OE2	2.865
6FN1	A_HIS_517	ND1	A_ASP_520	OD1	3.421
6FN1	A_HIS_517	ND1	A_ASP_520	OD2	3.421
6FN1	A_ARG_526	NH1	A_GLU_525	OE1	3.961
6FN1	A_ARG_526	NH1	A_GLU_525	OE2	2.166
6FN1	A_ARG_546	NH2	A_GLU_467	OE2	3.847
6FN1	A_ARG_576	NH2	A_ASP_573	OD1	2.465
6FN1	A_HIS_586	ND1	A_GLU_555	OE1	3.845
6FN1	A_HIS_586	NE2	A_GLU_555	OE2	3.514
6FN1	A_ARG_587	NH1	A_GLU_565	OE1	3.907
6FN1	A_ARG_587	NH2	A_GLU_565	OE1	3.568
6FN1	A_ARG_587	NH2	A_GLU_565	OE2	3.656
6FN1	A_HIS_611	ND1	A_ASP_612	OD1	3.740
6FN1	A_ARG_740	NH1	A_ASP_742	OD1	3.566
6FN1	A_ARG_740	NH1	A_ASP_742	OD2	2.936
6FN1	A_ARG_786	NH2	A_GLU_706	OE2	3.988
6FN1	A_ARG_797	NH1	A_ASP_1018	OD1	3.806
6FN1	A_ARG_797	NH1	A_ASP_1018	OD2	3.974
6FN1	A_LYS_807	NZ	A_ASP_805	OD1	3.714
6FN1	A_ARG_816	NH1	A_ASP_820	OD2	3.588
6FN1	A_LYS_825	NZ	A_GLU_781	OE2	3.696
6FN1	A_ARG_911	NH1	A_GLU_492	OE1	3.944
6FN1	A_LYS_914	NZ	A_GLU_485	OE2	3.976
6FN1	A_LYS_966	NZ	A_GLU_85	OE1	3.505
6FN1	A_LYS_966	NZ	A_GLU_85	OE2	2.563
6FN1	A_ARG_1084	NH2	A_ASP_1087	OD2	3.806
6FN1	A_ARG_1137	NH2	A_GLU_1143	OE1	3.300
6FN1	A_ARG_1137	NH2	A_GLU_1143	OE2	2.684
6FN1	A_ARG_1146	NH1	A_GLU_1142	OE2	3.522
6FN1	A_ARG_1146	NH2	A_GLU_1142	OE2	3.079
6FN1	A_HIS_1154	NE2	A_ASP_1158	OD1	3.475
6FN1	A_HIS_1154	NE2	A_ASP_1158	OD2	3.129
6FN1	A_ARG_1167	NH2	A_ASP_1123	OD1	2.431
6FN1	A_ARG_1167	NH2	A_ASP_1123	OD2	3.170

6FN1	A_ARG_1221	NH1	A_ASP_1218	OD1	3.994
6FN1	A_ARG_1221	NH2	A_ASP_1218	OD1	2.327
6FN1	B_ARG_24	NH1	B_ASP_75	OD1	3.067
6FN1	B_ARG_24	NH2	B_ASP_75	OD1	3.279
6FN1	B_ARG_59	NH1	B_ASP_65	OD1	2.228
6FN1	B_ARG_59	NH2	B_ASP_65	OD1	3.826
6FN1	B_ARG_66	NH1	B_GLU_84	OE1	3.321
6FN1	B_ARG_66	NH1	B_GLU_84	OE2	3.915
6FN1	B_ARG_66	NH1	B_ASP_87	OD2	2.881
6FN1	B_ARG_66	NH2	B_ASP_87	OD2	3.217
6FN1	B_LYS_153	NZ	B_GLU_160	OE1	2.476
6FN1	B_LYS_153	NZ	B_GLU_160	OE2	3.139
6FN1	B_LYS_189	NZ	B_GLU_193	OE1	3.697
6FN1	B_LYS_189	NZ	B_GLU_193	OE2	2.359
6FN1	B_ARG_194	NH1	B_GLU_191	OE1	3.707
6FN1	B_HIS_195	ND1	B_ASP_157	OD2	2.402
6FN1	B_HIS_195	NE2	B_GLU_191	OE2	2.859
6FN1	C_LYS_38	NZ	C_ASP_90	OD1	3.638
6FN1	C_ARG_98	NH1	C_ASP_110	OD1	3.210
6FN1	C_ARG_98	NH1	C_ASP_110	OD2	2.556
6FN1	C_ARG_98	NH2	C_ASP_110	OD2	3.769
6FN1	C_LYS_217	NZ	B_GLU_129	OE1	3.462
6FN1	C_LYS_217	NZ	B_GLU_129	OE2	2.375
6FN4	A_ARG_40	NH1	A_ASP_369	OD1	3.044
6FN4	A_ARG_40	NH1	A_ASP_369	OD2	2.673
6FN4	A_ARG_40	NH2	A_ASP_369	OD1	2.550
6FN4	A_ARG_40	NH2	A_ASP_369	OD2	3.247
6FN4	A_HIS_152	NE2	A_GLU_916	OE2	3.942
6FN4	A_ARG_173	NH1	A_GLU_363	OE1	3.817
6FN4	A_ARG_209	NH1	A_GLU_73	OE2	3.499
6FN4	A_ARG_209	NH2	A_GLU_73	OE2	2.413
6FN4	A_LYS_212	NZ	A_GLU_324	OE2	3.760
6FN4	A_ARG_261	NH2	A_ASP_804	OD1	3.439
6FN4	A_ARG_275	NH1	A_GLU_272	OE2	3.706
6FN4	A_ARG_275	NH2	A_GLU_255	OE2	3.146
6FN4	A_ARG_275	NH2	A_GLU_272	OE1	2.485
6FN4	A_ARG_275	NH2	A_GLU_272	OE2	3.067
6FN4	A_LYS_394	NZ	A_GLU_392	OE2	3.872
6FN4	A_ARG_441	NH2	A_ASP_444	OD1	3.730
6FN4	A_ARG_441	NH2	A_ASP_444	OD2	3.767
6FN4	A_ARG_458	NH1	A_ASP_456	OD2	3.726
6FN4	A_ARG_458	NH2	A_ASP_456	OD2	3.316
6FN4	A_ARG_488	NH1	A_GLU_485	OE2	3.913
6FN4	A_ARG_491	NH2	A_GLU_498	OE1	3.157
6FN4	A_ARG_576	NH2	A_ASP_573	OD1	2.521
6FN4	A_HIS_586	NE2	A_GLU_555	OE2	3.330
6FN4	A_HIS_611	ND1	A_ASP_612	OD1	3.332
6FN4	A_LYS_747	NZ	A_ASP_742	OD1	2.172
6FN4	A_LYS_747	NZ	A_ASP_742	OD2	3.656
6FN4	A_LYS_807	NZ	A_ASP_805	OD1	2.940
6FN4	A_LYS_807	NZ	A_ASP_805	OD2	3.024
6FN4	A_ARG_904	NH2	A_ASP_163	OD2	3.996
6FN4	A_ARG_911	NH1	A_GLU_492	OE2	3.311
6FN4	A_LYS_914	NZ	A_GLU_485	OE1	2.840
6FN4	A_ARG_957	NH2	A_GLU_107	OE2	3.364
6FN4	A_LYS_966	NZ	A_GLU_85	OE2	2.855
6FN4	A_HIS_1006	ND1	A_ASP_820	OD2	3.743
6FN4	A_ARG_1084	NH2	A_ASP_1087	OD2	3.893

6FN4	A_ARG_1137	NH2	A_GLU_1143	OE1	3.629
6FN4	A_ARG_1137	NH2	A_GLU_1143	OE2	3.357
6FN4	A_HIS_1154	ND1	A_ASP_1158	OD2	3.508
6FN4	A_HIS_1154	NE2	A_ASP_1158	OD2	2.806
6FN4	A_LYS_1163	NZ	A_ASP_1158	OD1	3.925
6FN4	A_ARG_1221	NH1	A_ASP_1218	OD1	3.565
6FN4	A_ARG_1221	NH2	A_ASP_1218	OD1	2.235
6FN4	A_ARG_1232	NH1	A_GLU_1210	OE2	2.338
6FN4	B_LYS_55	NZ	A_ASP_743	OD1	2.728
6FN4	B_LYS_55	NZ	A_ASP_743	OD2	3.540
6FN4	B_ARG_59	NH1	B_ASP_65	OD1	2.795
6FN4	B_ARG_59	NH2	B_ASP_65	OD1	2.360
6FN4	B_ARG_66	NH1	B_GLU_84	OE1	3.279
6FN4	B_ARG_66	NH1	B_GLU_84	OE2	3.707
6FN4	B_ARG_66	NH1	B_ASP_87	OD1	3.527
6FN4	B_ARG_66	NH1	B_ASP_87	OD2	2.589
6FN4	B_ARG_66	NH2	B_ASP_87	OD2	2.765
6FN4	B_LYS_155	NZ	B_GLU_201	OE2	2.874
6FN4	B_HIS_195	ND1	B_ASP_157	OD2	2.468
6FN4	B_LYS_205	NZ	B_ASP_149	OD2	3.164
6FN4	C_LYS_38	NZ	C_ASP_90	OD1	3.032
6FN4	C_ARG_98	NH2	C_ASP_110	OD2	2.746
6FN4	C_LYS_217	NZ	B_GLU_129	OE2	3.828
6FRJ	H_ARG_38	NH1	H_ASP_92	OD1	2.898
6FRJ	H_ARG_38	NH2	H_GLU_46	OE1	3.142
6FRJ	H_ARG_38	NH2	H_GLU_46	OE2	3.614
6FRJ	H_ARG_38	NH2	H_ASP_92	OD1	3.948
6FRJ	H_ARG_52	NH1	H_GLU_50	OE2	2.771
6FRJ	H_HIS_61	ND1	H_GLU_50	OE2	2.713
6FRJ	H_ARG_69	NH1	H_ASP_92	OD1	3.677
6FRJ	H_ARG_69	NH1	H_ASP_92	OD2	3.927
6FRJ	H_ARG_69	NH2	H_ASP_92	OD1	3.557
6FRJ	H_ARG_69	NH2	H_ASP_92	OD2	2.452
6FRJ	H_ARG_74	NH2	H_ASP_76	OD1	3.295
6FRJ	H_ARG_89	NH1	H_GLU_91	OE2	3.985
6FRJ	H_HIS_1051	ND1	H_GLU_1047	OE2	3.559
6FRJ	H_ARG_1070	NH2	H_GLU_1090	OE2	3.987
6FRJ	H_ARG_1070	NH2	H_ASP_1091	OD1	2.809
6FRJ	H_ARG_1070	NH2	H_ASP_1091	OD2	3.687
6GK7	L_ARG_67	NH1	L_ASP_88	OD1	3.869
6GK7	L_ARG_67	NH1	L_ASP_88	OD2	2.730
6GK7	L_ARG_67	NH2	L_ASP_88	OD1	3.654
6GK7	L_ARG_67	NH2	L_ASP_88	OD2	3.733
6GK7	L_LYS_155	NZ	L_GLU_201	OE1	2.758
6GK7	L_LYS_194	NZ	L_ASP_191	OD1	3.901
6GK7	L_HIS_195	ND1	L_ASP_157	OD2	3.421
6GK7	H_ARG_12	NH1	H_GLU_10	OE1	3.806
6GK7	H_LYS_43	NZ	L_ASP_9	OD1	3.203
6GK7	H_ARG_59	NH2	H_ASP_57	OD2	3.671
6GK7	H_HIS_67	NE2	H_ASP_90	OD1	2.917
6GK7	H_HIS_67	NE2	H_ASP_90	OD2	3.437
6GK7	H_ARG_98	NH2	H_ASP_110	OD1	3.856
6GK7	H_ARG_98	NH2	H_ASP_110	OD2	2.851
6GK7	H_ARG_102	NH2	H_ASP_100	OD1	3.141
6GK7	H_LYS_152	NZ	H_ASP_153	OD1	3.227
6GK7	H_LYS_152	NZ	H_ASP_153	OD2	3.445
6GK7	H_LYS_218	NZ	L_GLU_129	OE1	3.512
6GK7	H_LYS_218	NZ	L_GLU_129	OE2	3.016

6GK7	H.LYS_223	NZ	L.ASP_128	OD2	3.231
6GK7	A.LYS_317	NZ	H.ASP_55	OD2	2.761
6GK7	A.LYS_317	NZ	H.ASP_57	OD2	2.983
6GK8	H.ARG_38	NH1	H.ASP_90	OD1	3.902
6GK8	H.ARG_38	NH2	H.GLU_46	OE1	3.059
6GK8	H.ARG_38	NH2	H.GLU_46	OE2	3.561
6GK8	H.ARG_59	NH1	H.ASP_57	OD1	3.512
6GK8	H.ARG_59	NH1	H.ASP_57	OD2	2.923
6GK8	H.ARG_59	NH2	H.ASP_57	OD2	3.871
6GK8	H.ARG_59	NH2	L.ASP_65	OD1	3.295
6GK8	H.ARG_101	NH1	L.GLU_62	OE2	2.742
6GK8	H.ARG_101	NH2	L.GLU_62	OE2	3.142
6GK8	H.LYS_104	NZ	L.GLU_62	OE1	2.762
6GK8	H.LYS_104	NZ	L.GLU_62	OE2	3.928
6GK8	H.LYS_151	NZ	H.ASP_152	OD1	3.401
6GK8	H.LYS_151	NZ	H.ASP_152	OD2	3.307
6GK8	H.LYS_222	NZ	L.ASP_128	OD2	2.761
6GK8	L.ARG_32	NH1	L.GLU_57	OE2	3.709
6GK8	L.ARG_67	NH2	L.GLU_87	OE1	3.972
6GK8	L.ARG_67	NH2	L.GLU_87	OE2	2.995
6GK8	L.ARG_67	NH2	L.ASP_88	OD1	3.077
6GK8	L.ARG_67	NH2	L.ASP_88	OD2	3.854
6GK8	L.ARG_109	NH2	L.GLU_111	OE1	3.804
6GK8	L.ARG_148	NH2	L.GLU_171	OE2	3.424
6GK8	L.LYS_155	NZ	L.GLU_201	OE1	3.754
6GK8	L.LYS_194	NZ	L.ASP_191	OD1	3.678
6GK8	L.HIS_195	ND1	L.ASP_157	OD2	2.898
6GK8	I.LYS_67	NZ	H.ASP_55	OD1	3.586
6GK8	I.LYS_67	NZ	H.ASP_55	OD2	3.183
6GK8	I.LYS_67	NZ	H.ASP_57	OD2	3.085
6H2Y	D.HIS_30	ND1	D.ASP_29	OD2	2.968
6H2Y	D.LYS_74	NZ	D.ASP_32	OD1	3.080
6H2Y	D.LYS_74	NZ	D.ASP_32	OD2	3.146
6H2Y	D.LYS_79	NZ	L.ASP_52	OD1	3.126
6H2Y	D.ARG_82	NH1	D.GLU_102	OE1	3.225
6H2Y	D.HIS_110	ND1	D.GLU_144	OE1	3.692
6H2Y	D.LYS_120	NZ	L.ASP_95	OD2	2.910
6H2Y	D.HIS_173	ND1	D.GLU_188	OE2	3.534
6H2Y	D.HIS_173	NE2	D.GLU_188	OE2	3.951
6H2Y	D.ARG_186	NH1	D.GLU_188	OE2	2.556
6H2Y	D.ARG_186	NH2	D.GLU_194	OE1	3.470
6H2Y	D.HIS_189	NE2	D.GLU_188	OE1	3.353
6H2Y	D.LYS_191	NZ	L.ASP_50	OD2	2.715
6H2Y	D.ARG_236	NH1	D.ASP_235	OD2	3.896
6H2Y	D.LYS_260	NZ	D.ASP_78	OD1	3.223
6H2Y	D.LYS_260	NZ	D.ASP_78	OD2	3.636
6H2Y	D.LYS_260	NZ	D.GLU_239	OE2	3.969
6H2Y	H.ARG_38	NH1	H.ASP_90	OD2	2.735
6H2Y	H.ARG_38	NH2	H.GLU_46	OE1	3.600
6H2Y	H.ARG_38	NH2	H.ASP_90	OD2	3.880
6H2Y	H.ARG_56	NH2	D.GLU_58	OE1	3.564
6H2Y	H.ARG_56	NH2	D.GLU_58	OE2	3.905
6H2Y	H.LYS_63	NZ	H.GLU_46	OE1	3.969
6H2Y	H.LYS_63	NZ	H.GLU_46	OE2	2.764
6H2Y	H.ARG_67	NH1	H.ASP_90	OD1	2.793
6H2Y	H.ARG_67	NH1	H.ASP_90	OD2	3.306
6H2Y	H.ARG_67	NH2	H.ASP_90	OD1	3.797
6H2Y	H.ARG_67	NH2	H.ASP_90	OD2	3.132

6H2Y	H.LYS_215	NZ	L_GLU_125	OE1	3.261
6H2Y	H.LYS_215	NZ	L_GLU_125	OE2	2.865
6H2Y	L_ARG_60	NH1	L_ASP_81	OD1	3.946
6H2Y	L_ARG_60	NH1	L_ASP_81	OD2	2.714
6H2Y	L_ARG_60	NH2	L_ASP_81	OD1	2.835
6H2Y	L_ARG_60	NH2	L_ASP_81	OD2	3.155
6H2Y	L_ARG_92	NH1	D_ASP_166	OD2	3.217
6H2Y	L_ARG_92	NH2	D_GLU_119	OE1	3.274
6H2Y	L_ARG_92	NH2	D_GLU_119	OE2	3.244
6H2Y	L_ARG_92	NH2	D_ASP_166	OD1	3.891
6H2Y	L_ARG_92	NH2	D_ASP_166	OD2	2.328
6H2Y	L.LYS_104	NZ	L_ASP_84	OD1	2.864
6H2Y	L.LYS_104	NZ	L_ASP_84	OD2	2.840
6H2Y	L.LYS_168	NZ	L_GLU_82	OE1	2.735
6H2Y	L.LYS_168	NZ	L_GLU_82	OE2	3.700
6H2Y	L.HIS_190	ND1	L_ASP_153	OD2	3.040
6I3Z	A_HIS_73	ND1	A_ASP_74	OD1	3.992
6I3Z	A.LYS_201	NZ	L_ASP_92	OD1	3.556
6I3Z	A.LYS_217	NZ	A_ASP_207	OD1	2.912
6I3Z	A.LYS_222	NZ	A_GLU_204	OE1	2.374
6I3Z	A.LYS_222	NZ	A_GLU_206	OE2	3.231
6I3Z	A.LYS_290	NZ	A_GLU_342	OE1	3.811
6I3Z	A.LYS_290	NZ	H_ASP_33	OD1	3.699
6I3Z	H_ARG_38	NH1	H_GLU_46	OE2	3.015
6I3Z	H_ARG_38	NH2	H_ASP_86	OD1	2.939
6I3Z	H_ARG_66	NH1	H_ASP_86	OD1	3.907
6I3Z	H_ARG_66	NH1	H_ASP_86	OD2	3.045
6I3Z	H_ARG_66	NH2	H_ASP_86	OD1	3.844
6I3Z	L_ARG_53	NH1	A_GLU_204	OE1	2.383
6I3Z	L_ARG_53	NH1	A_GLU_204	OE2	3.516
6I3Z	L_ARG_61	NH1	L_GLU_81	OE2	3.392
6I3Z	L_ARG_61	NH1	L_ASP_82	OD1	3.108
6I3Z	L_ARG_61	NH1	L_ASP_82	OD2	3.395
6I3Z	L_ARG_61	NH2	L_GLU_81	OE2	3.127
6I3Z	L_ARG_61	NH2	L_ASP_82	OD1	3.903
6I3Z	L_ARG_61	NH2	L_ASP_82	OD2	3.066
6I9J	A_ARG_328	NH1	A_ASP_325	OD2	3.806
6I9J	A_ARG_328	NH2	A_ASP_329	OD1	3.559
6I9J	A_ARG_328	NH2	A_ASP_329	OD2	3.170
6IAP	A.LYS_4	NZ	A_GLU_84	OE1	3.796
6IAP	A_ARG_47	NH1	A_GLU_33	OE1	3.554
6IAP	A_ARG_47	NH1	A_GLU_33	OE2	2.707
6IAP	A_ARG_77	NH1	A_GLU_33	OE1	3.589
6IAP	A_ARG_77	NH1	A_GLU_33	OE2	2.806
6IAP	A_ARG_77	NH2	A_GLU_33	OE2	3.449
6IAP	A_ARG_165	NH1	A_GLU_134	OE1	2.832
6IAP	A_ARG_165	NH1	A_GLU_134	OE2	2.932
6IAP	D_ARG_61	NH2	D_ASP_82	OD1	2.957
6IAP	D_ARG_61	NH2	D_ASP_82	OD2	3.990
6IAP	D_ARG_96	NH2	A_GLU_80	OE1	3.466
6IAP	D.LYS_103	NZ	D_GLU_105	OE1	2.801
6IAP	D.LYS_103	NZ	D_GLU_165	OE1	3.070
6IAP	D_ARG_142	NH1	D_GLU_105	OE1	3.560
6IAP	D.LYS_149	NZ	D_GLU_195	OE2	3.829
6IAP	D.LYS_183	NZ	D_GLU_187	OE1	3.913
6IAP	D.HIS_189	ND1	D_ASP_151	OD2	3.610
6IAP	E_HIS_35	NE2	A_GLU_80	OE1	3.445
6IAP	E_ARG_38	NH1	E_GLU_46	OE1	3.245

6IAP	E_ARG_38	NH1	E_ASP_90	OD1	3.826
6IAP	E_ARG_38	NH2	E_ASP_90	OD1	2.938
6IAP	E_LYS_63	NZ	E_GLU_46	OE2	2.856
6IAP	E_ARG_67	NH1	E_ASP_90	OD1	3.217
6IAP	E_ARG_67	NH1	E_ASP_90	OD2	2.832
6IAP	E_ARG_98	NH1	E_ASP_105	OD2	2.742
6IAP	E_LYS_147	NZ	E_ASP_148	OD1	3.224
6IAP	E_LYS_147	NZ	E_ASP_148	OD2	2.946
6IAP	H_ARG_38	NH2	H_GLU_46	OE1	3.468
6IAP	H_LYS_65	NZ	H_GLU_62	OE1	2.882
6IAP	H_LYS_65	NZ	H_GLU_62	OE2	3.834
6IAP	H_ARG_87	NH1	H_GLU_89	OE1	2.796
6IAP	H_ARG_98	NH1	H_ASP_108	OD2	3.622
6IAP	H_ARG_99	NH1	H_GLU_50	OE1	2.819
6IAP	H_ARG_99	NH1	H_GLU_50	OE2	2.819
6IAP	H_ARG_99	NH2	A_ASP_98	OD1	2.689
6IAP	H_LYS_150	NZ	H_ASP_151	OD1	3.562
6IAP	H_LYS_150	NZ	H_ASP_151	OD2	3.534
6IAP	H_ARG_217	NH1	H_GLU_219	OE2	3.357
6IAP	L_ARG_24	NH1	L_ASP_70	OD1	3.449
6IAP	L_ARG_94	NH1	H_GLU_50	OE2	2.973
6IAP	L_ARG_94	NH2	A_ASP_123	OD2	3.888
6IAP	L_LYS_103	NZ	L_GLU_105	OE1	2.667
6IAP	L_LYS_126	NZ	L_GLU_123	OE1	3.630
6IAP	L_ARG_142	NH2	L_GLU_143	OE2	2.909
6IAP	L_LYS_149	NZ	L_GLU_195	OE2	3.247
6IAP	L_LYS_183	NZ	L_GLU_187	OE1	3.970
6IAP	L_HIS_189	ND1	L_ASP_151	OD2	3.405
6JMQ	A_LYS_112	NZ	A_GLU_265	OE2	3.737
6JMQ	A_ARG_419	NH1	A_GLU_426	OE1	3.417
6JMQ	A_ARG_419	NH1	A_GLU_426	OE2	2.358
6JMQ	A_ARG_419	NH2	A_GLU_426	OE1	2.551
6JMQ	A_ARG_419	NH2	A_GLU_426	OE2	3.223
6JMQ	B_ARG_211	NH2	B_ASP_540	OD1	3.901
6JMQ	B_ARG_211	NH2	B_ASP_540	OD2	3.653
6JMQ	B_LYS_298	NZ	B_ASP_343	OD1	3.798
6JMQ	B_LYS_298	NZ	B_ASP_343	OD2	2.773
6JMQ	B_LYS_300	NZ	B_ASP_249	OD1	2.988
6JMQ	B_LYS_300	NZ	B_ASP_249	OD2	3.168
6JMQ	B_ARG_313	NH2	B_ASP_281	OD2	2.986
6JMQ	B_ARG_348	NH1	B_ASP_349	OD2	3.884
6JMQ	B_LYS_354	NZ	B_ASP_355	OD1	3.767
6JMQ	B_LYS_354	NZ	B_ASP_355	OD2	3.182
6JMQ	B_ARG_374	NH1	B_ASP_343	OD1	3.786
6JMQ	B_HIS_414	ND1	B_GLU_413	OE1	3.881
6JMQ	B_HIS_414	NE2	B_GLU_413	OE1	3.761
6JMQ	B_HIS_414	NE2	B_GLU_413	OE2	3.827
6JMQ	B_LYS_510	NZ	B_GLU_493	OE2	3.727
6JMQ	B_ARG_525	NH1	B_GLU_605	OE1	3.564
6JMQ	B_ARG_525	NH1	B_GLU_605	OE2	3.265
6JMQ	B_ARG_525	NH2	B_GLU_605	OE1	2.626
6JMQ	B_ARG_525	NH2	B_GLU_605	OE2	3.608
6JMQ	B_HIS_556	NE2	B_ASP_540	OD2	3.806
6JMQ	B_LYS_592	NZ	B_GLU_610	OE1	3.993
6JMQ	B_ARG_603	NH1	B_GLU_620	OE1	2.595
6JMQ	B_ARG_603	NH1	B_GLU_620	OE2	3.221
6JMQ	B_ARG_613	NH1	B_GLU_610	OE2	3.252
6JMQ	B_HIS_619	ND1	B_ASP_571	OD1	3.990

6JMQ	B_ARG_625	NH2	B_GLU_533	OE2	3.458
6JMQ	B_ARG_625	NH2	B_GLU_561	OE1	3.849
6JMQ	C_ARG_38	NH1	C_ASP_89	OD1	3.785
6JMQ	C_ARG_38	NH2	C_GLU_46	OE1	2.796
6JMQ	C_ARG_38	NH2	C_GLU_46	OE2	3.808
6JMQ	C_ARG_66	NH1	C_ASP_89	OD1	3.398
6JMQ	C_ARG_66	NH1	C_ASP_89	OD2	2.424
6JMQ	C_ARG_66	NH2	C_ASP_89	OD1	3.049
6JMQ	C_ARG_66	NH2	C_ASP_89	OD2	3.597
6JMQ	C_HIS_169	NE2	D_ASP_173	OD2	3.860
6JMQ	C_LYS_213	NZ	D_GLU_129	OE1	3.825
6JMQ	D_ARG_67	NH2	D_ASP_88	OD1	2.846
6JMQ	D_ARG_67	NH2	D_ASP_88	OD2	3.134
6JMQ	D_LYS_109	NZ	D_GLU_111	OE2	3.564
6JMQ	D_LYS_155	NZ	D_GLU_160	OE1	3.318
6JMQ	D_LYS_155	NZ	D_GLU_201	OE1	2.847
6JMQ	D_LYS_155	NZ	D_GLU_201	OE2	3.538
6JMQ	D_ARG_194	NH2	D_GLU_191	OE1	2.521
6JMQ	D_ARG_194	NH2	D_GLU_191	OE2	3.913
6JMQ	D_HIS_195	ND1	D_ASP_157	OD1	3.523
6JMQ	D_HIS_195	ND1	D_ASP_157	OD2	3.075
6JMR	E_ARG_38	NH2	E_GLU_46	OE1	2.993
6JMR	E_ARG_66	NH1	E_ASP_89	OD2	3.421
6JMR	E_ARG_66	NH2	E_ASP_89	OD2	3.938
6JMR	F_LYS_152	NZ	F_GLU_159	OE2	3.268
6JMR	F_LYS_154	NZ	F_GLU_200	OE1	3.337
6JMR	F_LYS_154	NZ	F_GLU_200	OE2	3.361
6JMR	F_ARG_193	NH1	F_ASP_189	OD1	3.350
6JMR	F_ARG_193	NH2	F_GLU_190	OE1	2.696
6JMR	F_HIS_194	ND1	F_ASP_156	OD1	3.981
6JMR	F_HIS_194	ND1	F_ASP_156	OD2	2.412
6JMR	F_HIS_194	NE2	F_GLU_190	OE2	2.764
6JMR	B_ARG_211	NH1	B_ASP_558	OD1	3.360
6JMR	B_ARG_211	NH1	B_ASP_558	OD2	3.537
6JMR	B_ARG_211	NH2	B_ASP_558	OD1	3.693
6JMR	B_ARG_211	NH2	B_ASP_558	OD2	3.265
6JMR	B_LYS_255	NZ	B_ASP_528	OD1	2.933
6JMR	B_LYS_287	NZ	B_ASP_291	OD1	3.700
6JMR	B_LYS_287	NZ	B_ASP_291	OD2	2.415
6JMR	B_LYS_298	NZ	B_ASP_343	OD2	3.993
6JMR	B_LYS_300	NZ	B_ASP_249	OD1	3.273
6JMR	B_LYS_300	NZ	B_ASP_249	OD2	3.592
6JMR	B_ARG_303	NH2	B_ASP_373	OD2	3.818
6JMR	B_ARG_313	NH1	B_ASP_281	OD2	3.856
6JMR	B_ARG_313	NH2	B_ASP_281	OD2	2.988
6JMR	B_ARG_348	NH2	B_ASP_307	OD2	2.462
6JMR	B_LYS_354	NZ	B_ASP_355	OD2	2.401
6JMR	B_ARG_525	NH2	B_GLU_605	OE1	2.922
6JMR	B_ARG_603	NH1	B_GLU_620	OE1	3.059
6JMR	B_ARG_603	NH2	B_GLU_620	OE1	3.650
6JMR	B_HIS_619	ND1	B_ASP_571	OD1	3.672
6JMR	C_ARG_38	NH1	C_ASP_89	OD1	3.534
6JMR	C_ARG_38	NH2	C_ASP_89	OD1	3.797
6JMR	C_HIS_169	NE2	D_ASP_173	OD1	3.922
6JMR	D_ARG_67	NH2	D_ASP_88	OD1	2.789
6JMR	D_ARG_67	NH2	D_ASP_88	OD2	2.868
6JMR	D_LYS_113	NZ	D_GLU_17	OE1	3.374
6JMR	D_LYS_113	NZ	D_GLU_17	OE2	3.100

6JMR	D_LYS_155	NZ	D_GLU_201	OE1	3.651
6JMR	D_LYS_155	NZ	D_GLU_201	OE2	2.757
6JMR	D_LYS_175	NZ	D_GLU_87	OE1	3.592
6JMR	D_ARG_194	NH1	D_GLU_191	OE1	3.814
6JMR	D_ARG_194	NH2	D_GLU_191	OE1	2.418
6JMR	D_ARG_194	NH2	D_GLU_191	OE2	3.613
6JMR	D_HIS_195	ND1	D_ASP_157	OD2	3.249
6JMR	D_HIS_195	NE2	D_GLU_191	OE2	3.086
6K4Z	A_HIS_42	ND1	A_GLU_38	OE2	3.995
6K4Z	A_ARG_61	NH2	A_GLU_81	OE2	3.887
6K4Z	A_ARG_61	NH2	A_ASP_82	OD1	2.751
6K4Z	A_ARG_61	NH2	A_ASP_82	OD2	3.412
6K4Z	A_LYS_1064	NZ	A_GLU_1061	OE2	2.583
6K4Z	A_LYS_1066	NZ	A_ASP_1086	OD1	3.628
6K4Z	A_LYS_1066	NZ	A_ASP_1086	OD2	2.944
6K4Z	A_ARG_1094	NH1	A_ASP_1101	OD1	3.902
6K4Z	A_ARG_1094	NH1	A_ASP_1101	OD2	2.777
6K4Z	B_HIS_42	ND1	B_GLU_38	OE2	3.400
6K4Z	B_ARG_61	NH2	B_GLU_81	OE1	3.807
6K4Z	B_ARG_61	NH2	B_ASP_82	OD1	2.835
6K4Z	B_ARG_61	NH2	B_ASP_82	OD2	3.444
6K4Z	B_LYS_1064	NZ	B_GLU_1061	OE1	3.293
6K4Z	B_LYS_1064	NZ	B_GLU_1061	OE2	3.306
6K4Z	B_LYS_1066	NZ	B_ASP_1086	OD1	2.977
6K4Z	B_LYS_1066	NZ	B_ASP_1086	OD2	3.306
6K4Z	B_ARG_1094	NH2	B_ASP_1101	OD1	3.758
6K4Z	B_ARG_1094	NH2	B_ASP_1101	OD2	2.738
6K7O	A_LYS_5	NZ	A_ASP_88	OD1	2.318
6K7O	A_LYS_5	NZ	A_ASP_88	OD2	3.371
6K7O	A_ARG_36	NH2	A_ASP_38	OD2	3.575
6K7O	A_LYS_55	NZ	A_GLU_53	OE2	3.732
6K7O	A_LYS_55	NZ	H_ASP_106	OD1	3.027
6K7O	A_ARG_72	NH1	A_GLU_40	OE1	3.011
6K7O	A_ARG_72	NH1	A_GLU_40	OE2	2.176
6K7O	A_ARG_74	NH2	A_GLU_40	OE2	2.314
6K7O	A_ARG_78	NH1	L_ASP_94	OD1	3.792
6K7O	A_ARG_78	NH2	L_ASP_94	OD1	2.709
6K7O	B_ARG_39	NH1	B_ASP_92	OD1	2.639
6K7O	B_ARG_39	NH2	B_GLU_47	OE1	3.803
6K7O	B_ARG_39	NH2	B_ASP_92	OD1	3.143
6K7O	B_LYS_67	NZ	B_ASP_64	OD1	3.307
6K7O	B_ARG_69	NH1	B_ASP_92	OD1	3.750
6K7O	B_ARG_69	NH1	B_ASP_92	OD2	2.232
6K7O	B_ARG_69	NH2	B_ASP_92	OD1	2.738
6K7O	B_ARG_69	NH2	B_ASP_92	OD2	2.835
6K7O	B_ARG_100	NH2	B_ASP_110	OD1	3.271
6K7O	B_ARG_100	NH2	B_ASP_110	OD2	3.077
6K7O	B_LYS_152	NZ	B_ASP_153	OD1	2.261
6K7O	B_LYS_152	NZ	B_ASP_153	OD2	3.089
6K7O	B_LYS_218	NZ	C_GLU_127	OE1	3.816
6K7O	B_LYS_218	NZ	C_GLU_127	OE2	2.813
6K7O	B_LYS_219	NZ	B_GLU_221	OE2	3.997
6K7O	B_LYS_223	NZ	C_ASP_126	OD1	2.273
6K7O	B_LYS_223	NZ	C_ASP_126	OD2	2.907
6K7O	C_ARG_62	NH1	C_GLU_82	OE1	3.128
6K7O	C_ARG_62	NH2	C_ASP_83	OD1	2.283
6K7O	C_ARG_62	NH2	C_ASP_83	OD2	3.026
6K7O	C_LYS_107	NZ	C_GLU_169	OE1	3.884

6K7O	C_LYS_153	NZ	C_GLU_199	OE1	2.343
6K7O	C_LYS_153	NZ	C_GLU_199	OE2	3.740
6K7O	C_ARG_215	NH1	C_GLU_191	OE1	3.258
6K7O	D_ARG_39	NH1	D_ASP_92	OD1	3.691
6K7O	D_ARG_39	NH2	D_GLU_47	OE1	3.378
6K7O	D_ARG_69	NH1	D_ASP_92	OD1	3.540
6K7O	D_ARG_69	NH1	D_ASP_92	OD2	3.004
6K7O	D_ARG_100	NH1	D_ASP_28	OD1	3.508
6K7O	D_ARG_100	NH2	D_ASP_110	OD1	3.621
6K7O	D_ARG_100	NH2	D_ASP_110	OD2	2.219
6K7O	D_LYS_152	NZ	D_ASP_153	OD1	2.709
6K7O	D_LYS_152	NZ	D_ASP_153	OD2	2.488
6K7O	D_LYS_215	NZ	G_ASP_189	OD2	2.832
6K7O	D_LYS_218	NZ	E_GLU_127	OE1	2.290
6K7O	D_LYS_218	NZ	E_GLU_127	OE2	3.074
6K7O	D_LYS_219	NZ	D_GLU_221	OE2	3.309
6K7O	D_LYS_223	NZ	E_ASP_126	OD1	3.765
6K7O	D_LYS_223	NZ	E_ASP_126	OD2	3.552
6K7O	E_ARG_62	NH1	E_GLU_82	OE1	3.785
6K7O	E_ARG_62	NH2	E_ASP_83	OD1	2.379
6K7O	E_ARG_62	NH2	E_ASP_83	OD2	2.884
6K7O	E_LYS_107	NZ	E_GLU_169	OE1	3.682
6K7O	E_LYS_107	NZ	E_GLU_169	OE2	3.861
6K7O	E_LYS_153	NZ	E_GLU_199	OE1	3.571
6K7O	E_LYS_187	NZ	E_GLU_191	OE1	3.589
6K7O	E_HIS_193	ND1	E_ASP_155	OD2	2.222
6K7O	E_ARG_215	NH1	E_GLU_191	OE1	3.183
6K7O	E_ARG_215	NH1	E_GLU_191	OE2	3.052
6K7O	F_ARG_39	NH1	F_ASP_92	OD1	3.160
6K7O	F_ARG_39	NH2	F_GLU_47	OE1	3.541
6K7O	F_ARG_39	NH2	F_ASP_92	OD1	3.852
6K7O	F_ARG_69	NH2	F_ASP_92	OD1	3.334
6K7O	F_ARG_69	NH2	F_ASP_92	OD2	2.262
6K7O	F_ARG_100	NH2	F_ASP_110	OD1	3.367
6K7O	F_ARG_100	NH2	F_ASP_110	OD2	2.302
6K7O	F_LYS_152	NZ	F_ASP_153	OD1	2.970
6K7O	F_LYS_152	NZ	F_ASP_153	OD2	3.514
6K7O	F_HIS_173	NE2	G_ASP_171	OD2	3.941
6K7O	G_ARG_51	NH2	F_ASP_106	OD2	3.980
6K7O	G_ARG_62	NH2	G_ASP_83	OD1	2.886
6K7O	G_ARG_62	NH2	G_ASP_83	OD2	2.569
6K7O	G_LYS_107	NZ	G_GLU_169	OE1	3.132
6K7O	G_LYS_107	NZ	G_GLU_169	OE2	2.495
6K7O	G_LYS_153	NZ	G_GLU_199	OE1	3.412
6K7O	G_ARG_215	NH1	G_GLU_191	OE1	2.817
6K7O	H_ARG_39	NH1	H_ASP_92	OD1	3.037
6K7O	H_ARG_39	NH2	H_GLU_47	OE2	3.357
6K7O	H_ARG_39	NH2	H_ASP_92	OD1	3.458
6K7O	H_ARG_69	NH1	H_ASP_92	OD1	3.457
6K7O	H_ARG_69	NH1	H_ASP_92	OD2	2.161
6K7O	H_ARG_69	NH2	H_ASP_92	OD1	3.051
6K7O	H_ARG_69	NH2	H_ASP_92	OD2	3.302
6K7O	H_ARG_100	NH1	H_ASP_28	OD1	3.046
6K7O	H_ARG_100	NH1	H_ASP_28	OD2	3.800
6K7O	H_ARG_100	NH2	H_ASP_110	OD1	3.159
6K7O	H_ARG_100	NH2	H_ASP_110	OD2	2.559
6K7O	H_LYS_152	NZ	H_ASP_153	OD1	3.285
6K7O	H_LYS_152	NZ	H_ASP_153	OD2	3.072

6K7O	H_HIS_173	NE2	L_ASP_171	OD2	3.862
6K7O	H_LYS_218	NZ	L_GLU_127	OE1	3.981
6K7O	H_LYS_219	NZ	H_GLU_221	OE1	3.644
6K7O	H_LYS_223	NZ	L_ASP_126	OD1	3.964
6K7O	L_ARG_62	NH1	L_GLU_82	OE1	3.867
6K7O	L_ARG_62	NH2	L_ASP_83	OD1	2.401
6K7O	L_ARG_62	NH2	L_ASP_83	OD2	2.682
6K7O	L_ARG_215	NH1	L_GLU_191	OE1	2.693
6K7O	P_LYS_5	NZ	P_ASP_88	OD1	3.227
6K7O	P_ARG_36	NH2	P_ASP_38	OD2	3.978
6K7O	P_LYS_55	NZ	B_ASP_106	OD1	3.340
6K7O	P_LYS_55	NZ	P_GLU_53	OE2	3.383
6K7O	P_ARG_72	NH1	P_GLU_40	OE2	3.046
6K7O	P_ARG_74	NH2	P_GLU_40	OE2	2.240
6K7O	P_ARG_78	NH1	C_ASP_94	OD1	2.583
6K7O	P_ARG_78	NH2	C_ASP_94	OD1	2.609
6K7O	R_LYS_5	NZ	R_ASP_88	OD1	2.725
6K7O	R_LYS_5	NZ	R_ASP_88	OD2	3.900
6K7O	R_LYS_55	NZ	F_ASP_106	OD1	2.834
6K7O	R_LYS_55	NZ	R_GLU_53	OE2	3.817
6K7O	R_ARG_72	NH1	R_GLU_40	OE1	3.051
6K7O	R_ARG_72	NH1	R_GLU_40	OE2	2.785
6K7O	R_ARG_74	NH2	R_GLU_40	OE2	2.444
6K7O	Q_LYS_5	NZ	Q_ASP_88	OD1	3.267
6K7O	Q_ARG_36	NH2	Q_ASP_38	OD2	3.639
6K7O	Q_LYS_55	NZ	D_ASP_106	OD1	3.172
6K7O	Q_ARG_59	NH1	H_GLU_221	OE1	3.018
6K7O	Q_ARG_59	NH1	H_GLU_221	OE2	3.413
6K7O	Q_ARG_59	NH2	H_GLU_221	OE1	3.299
6K7O	Q_ARG_59	NH2	H_GLU_221	OE2	2.855
6K7O	Q_ARG_72	NH1	Q_GLU_40	OE1	2.910
6K7O	Q_ARG_72	NH1	Q_GLU_40	OE2	2.362
6K7O	Q_ARG_74	NH2	Q_GLU_40	OE2	3.223
6K7O	Q_ARG_78	NH1	E_ASP_94	OD1	3.546
6K7O	Q_ARG_78	NH2	E_ASP_94	OD1	2.499
6KN9	A_HIS_112	ND1	A_GLU_41	OE1	3.585
6KN9	A_ARG_235	NH2	A_ASP_222	OD1	3.857
6KN9	A_ARG_235	NH2	A_ASP_222	OD2	2.742
6KN9	A_ARG_241	NH2	A_ASP_164	OD1	3.542
6KN9	A_ARG_241	NH2	A_ASP_164	OD2	3.212
6KN9	A_LYS_267	NZ	A_GLU_264	OE1	2.822
6KN9	A_LYS_267	NZ	A_GLU_264	OE2	3.577
6KN9	A_LYS_274	NZ	A_ASP_255	OD2	3.178
6KN9	A_LYS_274	NZ	A_GLU_318	OE2	3.699
6KN9	A_ARG_276	NH2	A_ASP_314	OD1	1.972
6KN9	A_ARG_281	NH1	D_ASP_111	OD1	2.228
6KN9	A_ARG_281	NH1	D_ASP_111	OD2	3.976
6KN9	A_LYS_288	NZ	A_GLU_299	OE1	3.349
6KN9	A_LYS_292	NZ	A_GLU_297	OE1	3.199
6KN9	A_LYS_292	NZ	A_GLU_297	OE2	3.595
6KN9	A_LYS_306	NZ	A_GLU_318	OE1	3.465
6KN9	A_LYS_309	NZ	A_ASP_314	OD2	2.944
6KN9	A_ARG_319	NH2	A_GLU_299	OE2	3.969
6KN9	A_ARG_333	NH1	A_ASP_330	OD1	3.681
6KN9	A_ARG_333	NH2	A_ASP_293	OD2	3.015
6KN9	B_ARG_241	NH2	B_ASP_164	OD2	3.877
6KN9	B_LYS_267	NZ	B_GLU_264	OE1	3.093
6KN9	B_LYS_267	NZ	B_GLU_264	OE2	3.256

6KN9	B_LYS_274	NZ	B_ASP_255	OD2	2.896
6KN9	B_LYS_274	NZ	B_GLU_318	OE1	3.770
6KN9	B_ARG_276	NH2	B_ASP_314	OD1	3.835
6KN9	B_ARG_281	NH2	E_ASP_111	OD1	2.487
6KN9	B_ARG_281	NH2	E_ASP_111	OD2	3.660
6KN9	B_LYS_288	NZ	B_GLU_299	OE1	3.279
6KN9	B_LYS_306	NZ	B_GLU_318	OE2	3.342
6KN9	B_LYS_309	NZ	B_ASP_314	OD2	2.507
6KN9	B_LYS_313	NZ	B_ASP_314	OD2	3.641
6KN9	B_ARG_319	NH1	B_GLU_304	OE1	3.890
6KN9	B_ARG_319	NH2	B_GLU_304	OE1	3.759
6KN9	B_ARG_319	NH2	B_GLU_304	OE2	3.666
6KN9	B_ARG_333	NH2	B_ASP_293	OD2	3.063
6KN9	C_HIS_112	ND1	C_GLU_41	OE1	2.327
6KN9	C_HIS_112	NE2	C_ASP_107	OD2	3.295
6KN9	C_ARG_235	NH2	C_ASP_222	OD1	3.959
6KN9	C_ARG_235	NH2	C_ASP_222	OD2	2.800
6KN9	C_ARG_241	NH2	C_ASP_164	OD1	3.385
6KN9	C_ARG_241	NH2	C_ASP_164	OD2	2.874
6KN9	C_LYS_274	NZ	C_ASP_255	OD2	3.106
6KN9	C_LYS_274	NZ	C_GLU_318	OE1	3.930
6KN9	C_ARG_276	NH2	C_ASP_314	OD1	3.434
6KN9	C_ARG_281	NH2	F_ASP_111	OD2	3.907
6KN9	C_LYS_288	NZ	C_GLU_299	OE1	3.086
6KN9	C_LYS_288	NZ	C_GLU_299	OE2	3.808
6KN9	C_LYS_306	NZ	C_GLU_318	OE2	3.670
6KN9	C_LYS_309	NZ	C_ASP_314	OD2	2.610
6KN9	C_ARG_319	NH1	C_GLU_299	OE2	3.995
6KN9	C_ARG_333	NH1	C_ASP_330	OD1	3.656
6KN9	C_ARG_333	NH2	C_ASP_293	OD2	2.842
6KN9	D_ARG_38	NH1	D_ASP_90	OD1	3.545
6KN9	D_ARG_38	NH2	D_GLU_46	OE1	2.628
6KN9	D_ARG_38	NH2	D_GLU_46	OE2	3.501
6KN9	D_LYS_43	NZ	D_GLU_89	OE1	3.952
6KN9	D_LYS_43	NZ	D_GLU_89	OE2	3.337
6KN9	D_ARG_67	NH1	D_ASP_90	OD1	3.041
6KN9	D_ARG_67	NH1	D_ASP_90	OD2	3.151
6KN9	D_ARG_67	NH2	D_ASP_90	OD1	3.897
6KN9	D_ARG_98	NH1	D_ASP_111	OD2	2.640
6KN9	D_ARG_201	NH2	D_ASP_222	OD1	2.871
6KN9	D_ARG_201	NH2	D_ASP_222	OD2	3.172
6KN9	F_ARG_38	NH1	F_ASP_90	OD1	3.168
6KN9	F_ARG_38	NH2	F_GLU_46	OE1	2.799
6KN9	F_ARG_38	NH2	F_GLU_46	OE2	3.293
6KN9	F_ARG_98	NH1	F_ASP_111	OD1	3.108
6KN9	F_ARG_98	NH1	F_ASP_111	OD2	2.892
6KN9	F_ARG_201	NH2	F_ASP_222	OD1	2.968
6KN9	F_ARG_201	NH2	F_ASP_222	OD2	3.406
6MH2	A_LYS_149	NZ	A_GLU_195	OE1	3.787
6MH2	A_LYS_149	NZ	A_GLU_195	OE2	3.621
6MH2	B_ARG_38	NH1	B_ASP_90	OD1	2.761
6MH2	B_ARG_38	NH2	B_GLU_46	OE1	3.270
6MH2	B_ARG_38	NH2	B_GLU_46	OE2	3.852
6MH2	B_ARG_38	NH2	B_ASP_90	OD1	3.946
6MH2	B_ARG_67	NH1	B_ASP_90	OD1	3.761
6MH2	B_ARG_67	NH1	B_ASP_90	OD2	2.763
6MH2	B_ARG_67	NH2	B_ASP_90	OD1	3.235
6MH2	B_ARG_67	NH2	B_ASP_90	OD2	3.604

6MH2	B.LYS_76	NZ	B.ASP_73	OD2	3.341
6MH2	B.ARG_98	NH2	B.ASP_108	OD1	3.946
6MH2	B.ARG_98	NH2	B.ASP_108	OD2	3.214
6MH2	B.LYS_150	NZ	B.ASP_151	OD1	3.564
6MH2	B.LYS_150	NZ	B.ASP_151	OD2	3.741
6MH2	C.ARG_61	NH2	C.ASP_82	OD1	3.009
6MH2	C.ARG_61	NH2	C.ASP_82	OD2	3.516
6MH2	C.ARG_66	NH1	C.ASP_28	OD1	3.766
6MH2	D.ARG_38	NH1	D.ASP_90	OD1	2.776
6MH2	D.ARG_38	NH2	D.GLU_46	OE1	2.980
6MH2	D.ARG_38	NH2	D.GLU_46	OE2	3.596
6MH2	D.ARG_38	NH2	D.ASP_90	OD1	3.851
6MH2	D.ARG_67	NH1	D.ASP_90	OD1	3.812
6MH2	D.ARG_67	NH1	D.ASP_90	OD2	2.537
6MH2	D.ARG_67	NH2	D.ASP_90	OD1	3.255
6MH2	D.ARG_67	NH2	D.ASP_90	OD2	3.479
6MH2	D.LYS_76	NZ	D.ASP_73	OD2	3.284
6MH2	D.ARG_98	NH2	D.ASP_108	OD2	2.820
6MHR	D.ARG_38	NH1	D.ASP_89	OD1	2.826
6MHR	D.ARG_38	NH2	D.GLU_46	OE1	3.169
6MHR	D.ARG_38	NH2	D.GLU_46	OE2	3.753
6MHR	D.ARG_38	NH2	D.ASP_89	OD1	3.916
6MHR	D.ARG_66	NH1	D.ASP_89	OD1	3.572
6MHR	D.ARG_66	NH1	D.ASP_89	OD2	2.987
6MHR	D.ARG_66	NH2	D.ASP_89	OD1	2.810
6MHR	D.ARG_66	NH2	D.ASP_89	OD2	3.631
6MHR	D.ARG_97	NH2	D.ASP_109	OD1	2.845
6MHR	D.ARG_97	NH2	D.ASP_109	OD2	3.931
6MHR	D.LYS_151	NZ	D.ASP_152	OD1	3.753
6MHR	D.LYS_151	NZ	D.ASP_152	OD2	3.790
6MHR	E.ARG_61	NH2	E.ASP_82	OD1	3.057
6MHR	E.ARG_61	NH2	E.ASP_82	OD2	3.583
6MHR	E.ARG_91	NH1	D.GLU_50	OE1	3.108
6MHR	E.ARG_91	NH1	D.ASP_98	OD2	3.892
6MHR	E.ARG_91	NH2	D.GLU_50	OE1	3.238
6MHR	E.ARG_91	NH2	D.GLU_50	OE2	3.082
6MHR	E.LYS_151	NZ	E.GLU_197	OE1	3.306
6MHR	E.LYS_151	NZ	E.GLU_197	OE2	2.656
6MHR	A.ARG_38	NH1	A.ASP_89	OD1	2.922
6MHR	A.ARG_38	NH2	A.GLU_46	OE1	3.494
6MHR	A.ARG_38	NH2	A.ASP_89	OD1	3.894
6MHR	A.ARG_66	NH1	A.ASP_89	OD1	3.791
6MHR	A.ARG_66	NH2	A.ASP_89	OD1	2.938
6MHR	A.ARG_66	NH2	A.ASP_89	OD2	2.504
6MHR	A.ARG_97	NH2	A.ASP_109	OD1	3.855
6MHR	A.ARG_97	NH2	A.ASP_109	OD2	2.834
6MHR	A.LYS_151	NZ	A.ASP_152	OD2	3.659
6MHR	A.LYS_217	NZ	B.GLU_125	OE2	2.775
6MHR	B.ARG_61	NH1	B.ASP_82	OD1	2.499
6MHR	B.ARG_61	NH1	B.ASP_82	OD2	2.707
6MHR	B.ARG_61	NH2	B.GLU_81	OE2	3.693
6MHR	B.ARG_91	NH1	A.GLU_50	OE1	3.086
6MHR	B.ARG_91	NH1	A.GLU_50	OE2	3.775
6MHR	B.ARG_91	NH1	A.ASP_98	OD2	3.351
6MHR	B.ARG_91	NH2	A.GLU_50	OE1	3.608
6MHR	B.ARG_91	NH2	A.GLU_50	OE2	2.934
6MHR	F.ARG_73	NH2	F.ASP_87	OD2	3.617
6MHR	F.ARG_75	NH1	F.ASP_87	OD1	3.232

6MHR	F_HIS_93	ND1	F_ASP_105	OD1	2.539
6MHR	F_HIS_93	NE2	F_GLU_103	OE1	2.711
6MHR	C_ARG_75	NH2	C_GLU_85	OE2	2.934
6MHR	C_HIS_	ND1	C_ASP_	OD1	2.729
6MHR	C_HIS_93	NE2	C_GLU_103	OE1	2.688
6MHR	C_ARG_	NH1	C_ASP_	OD1	3.364
6MHR	C_ARG_	NH2	C_ASP_	OD1	3.177
6MI2	A_LYS_12	NZ	A_GLU_16	OE2	3.989
6MI2	A_ARG_38	NH2	A_GLU_46	OE1	2.859
6MI2	A_ARG_38	NH2	A_GLU_46	OE2	3.408
6MI2	A_ARG_98	NH2	A_ASP_104	OD2	3.122
6MI2	B_ARG_60	NH2	B_ASP_81	OD1	3.443
6MI2	D_ARG_38	NH2	D_GLU_46	OE1	2.927
6MI2	D_ARG_38	NH2	D_GLU_46	OE2	2.802
6MI2	D_ARG_98	NH2	D_ASP_104	OD1	3.789
6MI2	D_ARG_98	NH2	D_ASP_104	OD2	2.702
6MI2	E_ARG_60	NH2	E_ASP_81	OD1	2.603
6MI2	E_ARG_60	NH2	E_ASP_81	OD2	2.973
6MI2	F_ARG_73	NH2	F_ASP_87	OD2	3.773
6MI2	F_HIS_93	ND1	F_ASP_105	OD1	2.788
6MI2	F_HIS_93	ND1	F_ASP_105	OD2	3.836
6MI2	F_HIS_93	NE2	F_GLU_103	OE2	3.226
6MI2	F_LYS_114	NZ	E_ASP_50	OD1	2.776
6MI2	F_LYS_114	NZ	E_ASP_50	OD2	3.977
6MI2	F_ARG_134	NH2	D_ASP_55	OD2	3.507
6MI2	F_ARG_134	NH2	F_ASP_127	OD1	3.458
6MI2	F_ARG_134	NH2	F_ASP_127	OD2	3.809
6MI2	C_ARG_73	NH2	C_ASP_87	OD1	3.648
6MI2	C_ARG_73	NH2	C_ASP_87	OD2	2.300
6MI2	C_HIS_93	ND1	C_ASP_105	OD1	2.396
6MI2	C_HIS_93	NE2	C_GLU_103	OE2	2.977
6MI2	C_LYS_114	NZ	B_ASP_50	OD1	3.683
6MI2	C_LYS_114	NZ	B_ASP_50	OD2	2.434
6MI2	C_ARG_134	NH1	C_ASP_127	OD2	3.259
6MI2	C_ARG_134	NH2	C_ASP_127	OD1	3.569
6MI2	C_ARG_134	NH2	C_ASP_127	OD2	3.076
6MN7	A_LYS_46	NZ	A_GLU_492	OE1	3.387
6MN7	A_LYS_46	NZ	A_GLU_492	OE2	2.895
6MN7	A_LYS_229	NZ	A_GLU_83	OE1	2.957
6MN7	A_LYS_232	NZ	A_GLU_268	OE1	3.584
6MN7	A_LYS_232	NZ	A_GLU_268	OE2	2.841
6MN7	A_LYS_282	NZ	A_GLU_275	OE1	2.868
6MN7	A_LYS_282	NZ	A_GLU_275	OE2	3.561
6MN7	A_ARG_308	NH2	A_GLU_164	OE1	3.817
6MN7	A_ARG_308	NH2	A_GLU_164	OE2	3.051
6MN7	A_LYS_351	NZ	A_GLU_269	OE1	2.814
6MN7	A_LYS_351	NZ	A_GLU_269	OE2	3.423
6MN7	A_ARG_429	NH1	A_ASP_113	OD1	3.456
6MN7	A_ARG_429	NH1	A_ASP_113	OD2	2.823
6MN7	A_ARG_429	NH2	A_ASP_113	OD2	3.973
6MN7	A_ARG_456	NH2	A_GLU_466	OE1	3.736
6MN7	A_ARG_456	NH2	A_GLU_466	OE2	2.975
6MN7	A_ARG_469	NH1	A_ASP_457	OD1	2.938
6MN7	A_ARG_469	NH2	A_ASP_457	OD1	3.933
6MN7	A_ARG_476	NH1	A_GLU_102	OE1	3.017
6MN7	A_ARG_476	NH1	A_GLU_102	OE2	3.686
6MN7	A_ARG_476	NH2	A_ASP_474	OD2	2.794
6MN7	A_ARG_480	NH1	A_ASP_477	OD1	3.065

6MN7	A_ARG_480	NH2	A_ASP_477	OD1	2.733
6MN7	A_LYS_487	NZ	A_ASP_47	OD1	3.272
6MN7	A_LYS_487	NZ	A_ASP_47	OD2	2.968
6MN7	A_LYS_487	NZ	A_GLU_91	OE2	2.917
6MN7	B_ARG_542	NH1	F_GLU_647	OE2	3.229
6MN7	B_LYS_574	NZ	A_ASP_107	OD1	3.285
6MN7	B_LYS_574	NZ	A_ASP_107	OD2	3.696
6MN7	B_ARG_579	NH2	F_GLU_584	OE1	2.844
6MN7	B_ARG_579	NH2	F_GLU_584	OE2	3.533
6MN7	B_ARG_585	NH1	B_ASP_589	OD1	3.926
6MN7	B_ARG_585	NH1	B_ASP_589	OD2	2.732
6MN7	B_ARG_585	NH2	B_ASP_589	OD2	3.591
6MN7	B_ARG_588	NH2	B_GLU_584	OE2	2.813
6MN7	B_ARG_617	NH1	B_GLU_621	OE2	2.445
6MN7	B_ARG_617	NH2	B_GLU_634	OE1	3.873
6MN7	B_ARG_617	NH2	B_GLU_634	OE2	2.744
6MN7	C_LYS_46	NZ	C_GLU_492	OE1	3.386
6MN7	C_LYS_46	NZ	C_GLU_492	OE2	2.894
6MN7	C_LYS_229	NZ	C_GLU_83	OE1	2.956
6MN7	C_LYS_232	NZ	C_GLU_268	OE1	3.583
6MN7	C_LYS_232	NZ	C_GLU_268	OE2	2.842
6MN7	C_LYS_282	NZ	C_GLU_275	OE1	2.869
6MN7	C_LYS_282	NZ	C_GLU_275	OE2	3.561
6MN7	C_ARG_308	NH2	C_GLU_164	OE1	3.817
6MN7	C_ARG_308	NH2	C_GLU_164	OE2	3.051
6MN7	C_LYS_351	NZ	C_GLU_269	OE1	2.813
6MN7	C_LYS_351	NZ	C_GLU_269	OE2	3.422
6MN7	C_ARG_429	NH1	C_ASP_113	OD1	3.457
6MN7	C_ARG_429	NH1	C_ASP_113	OD2	2.824
6MN7	C_ARG_429	NH2	C_ASP_113	OD2	3.973
6MN7	C_ARG_456	NH2	C_GLU_466	OE1	3.737
6MN7	C_ARG_456	NH2	C_GLU_466	OE2	2.976
6MN7	C_ARG_469	NH1	C_ASP_457	OD1	2.939
6MN7	C_ARG_469	NH2	C_ASP_457	OD1	3.933
6MN7	C_ARG_476	NH1	C_GLU_102	OE1	3.016
6MN7	C_ARG_476	NH1	C_GLU_102	OE2	3.686
6MN7	C_ARG_476	NH2	C_ASP_474	OD2	2.793
6MN7	C_ARG_480	NH1	C_ASP_477	OD1	3.066
6MN7	C_ARG_480	NH2	C_ASP_477	OD1	2.733
6MN7	C_LYS_487	NZ	C_ASP_47	OD1	3.273
6MN7	C_LYS_487	NZ	C_ASP_47	OD2	2.968
6MN7	C_LYS_487	NZ	C_GLU_91	OE2	2.918
6MN7	D_LYS_46	NZ	D_GLU_492	OE1	3.385
6MN7	D_LYS_46	NZ	D_GLU_492	OE2	2.893
6MN7	D_LYS_229	NZ	D_GLU_83	OE1	2.958
6MN7	D_LYS_232	NZ	D_GLU_268	OE1	3.583
6MN7	D_LYS_232	NZ	D_GLU_268	OE2	2.840
6MN7	D_LYS_282	NZ	D_GLU_275	OE1	2.869
6MN7	D_LYS_282	NZ	D_GLU_275	OE2	3.560
6MN7	D_ARG_308	NH2	D_GLU_164	OE1	3.817
6MN7	D_ARG_308	NH2	D_GLU_164	OE2	3.051
6MN7	D_LYS_351	NZ	D_GLU_269	OE1	2.813
6MN7	D_LYS_351	NZ	D_GLU_269	OE2	3.422
6MN7	D_ARG_429	NH1	D_ASP_113	OD1	3.456
6MN7	D_ARG_429	NH1	D_ASP_113	OD2	2.823
6MN7	D_ARG_429	NH2	D_ASP_113	OD2	3.972
6MN7	D_ARG_456	NH2	D_GLU_466	OE1	3.737
6MN7	D_ARG_456	NH2	D_GLU_466	OE2	2.975

6MN7	D_ARG_469	NH1	D_ASP_457	OD1	2.938
6MN7	D_ARG_469	NH2	D_ASP_457	OD1	3.933
6MN7	D_ARG_476	NH1	D_GLU_102	OE1	3.018
6MN7	D_ARG_476	NH1	D_GLU_102	OE2	3.687
6MN7	D_ARG_476	NH2	D_ASP_474	OD2	2.795
6MN7	D_ARG_480	NH1	D_ASP_477	OD1	3.065
6MN7	D_ARG_480	NH2	D_ASP_477	OD1	2.732
6MN7	D_LYS_487	NZ	D_ASP_47	OD1	3.273
6MN7	D_LYS_487	NZ	D_ASP_47	OD2	2.968
6MN7	D_LYS_487	NZ	D_GLU_91	OE2	2.917
6MN7	E_ARG_542	NH1	B_GLU_647	OE2	3.076
6MN7	E_LYS_574	NZ	C_ASP_107	OD1	3.286
6MN7	E_LYS_574	NZ	C_ASP_107	OD2	3.697
6MN7	E_ARG_579	NH2	B_GLU_584	OE1	2.796
6MN7	E_ARG_579	NH2	B_GLU_584	OE2	3.568
6MN7	E_ARG_585	NH1	E_ASP_589	OD1	3.925
6MN7	E_ARG_585	NH1	E_ASP_589	OD2	2.731
6MN7	E_ARG_585	NH2	E_ASP_589	OD2	3.591
6MN7	E_ARG_588	NH2	E_GLU_584	OE2	2.814
6MN7	E_ARG_617	NH1	E_GLU_621	OE2	2.446
6MN7	E_ARG_617	NH2	E_GLU_634	OE1	3.873
6MN7	E_ARG_617	NH2	E_GLU_634	OE2	2.744
6MN7	F_ARG_542	NH1	E_GLU_647	OE2	3.126
6MN7	F_LYS_574	NZ	D_ASP_107	OD1	3.285
6MN7	F_LYS_574	NZ	D_ASP_107	OD2	3.696
6MN7	F_ARG_579	NH2	E_GLU_584	OE1	2.859
6MN7	F_ARG_579	NH2	E_GLU_584	OE2	3.579
6MN7	F_ARG_585	NH1	F_ASP_589	OD1	3.927
6MN7	F_ARG_585	NH1	F_ASP_589	OD2	2.734
6MN7	F_ARG_585	NH2	F_ASP_589	OD2	3.592
6MN7	F_ARG_588	NH2	F_GLU_584	OE2	2.813
6MN7	F_ARG_617	NH1	F_GLU_621	OE2	2.447
6MN7	F_ARG_617	NH2	F_GLU_634	OE1	3.873
6MN7	F_ARG_617	NH2	F_GLU_634	OE2	2.744
6MN7	G_LYS_12	NZ	G_GLU_10	OE1	3.426
6MN7	G_ARG_38	NH1	G_GLU_46	OE1	3.285
6MN7	G_ARG_38	NH1	G_GLU_46	OE2	3.559
6MN7	G_ARG_38	NH1	G_ASP_89	OD1	3.445
6MN7	G_ARG_38	NH1	G_ASP_89	OD2	3.578
6MN7	G_ARG_38	NH2	G_ASP_90	OD1	2.915
6MN7	G_ARG_63	NH1	G_GLU_46	OE2	3.497
6MN7	G_ARG_67	NH1	G_ASP_90	OD1	2.860
6MN7	G_ARG_67	NH1	G_ASP_90	OD2	2.650
6MN7	G_ARG_67	NH2	G_ASP_90	OD1	2.942
6MN7	G_ARG_98	NH1	G_ASP_115	OD2	3.898
6MN7	G_ARG_188	NH1	G_GLU_208	OE2	3.991
6MN7	G_ARG_188	NH1	G_ASP_209	OD1	2.679
6MN7	G_ARG_188	NH1	G_ASP_209	OD2	2.661
6MN7	G_ARG_188	NH2	G_GLU_208	OE2	3.728
6MN7	G_ARG_188	NH2	G_ASP_209	OD1	3.908
6MN7	H_LYS_12	NZ	H_GLU_10	OE1	3.427
6MN7	H_ARG_38	NH1	H_GLU_46	OE1	3.285
6MN7	H_ARG_38	NH1	H_GLU_46	OE2	3.557
6MN7	H_ARG_38	NH1	H_ASP_89	OD1	3.443
6MN7	H_ARG_38	NH1	H_ASP_89	OD2	3.578
6MN7	H_ARG_38	NH2	H_ASP_90	OD1	2.915
6MN7	H_ARG_63	NH1	H_GLU_46	OE2	3.498
6MN7	H_ARG_67	NH1	H_ASP_90	OD1	2.859

6MN7	H_ARG_67	NH1	H_ASP_90	OD2	2.650
6MN7	H_ARG_67	NH2	H_ASP_90	OD1	2.942
6MN7	H_ARG_98	NH1	H_ASP_115	OD2	3.897
6MN7	H_ARG_188	NH1	H_GLU_208	OE2	3.991
6MN7	H_ARG_188	NH1	H_ASP_209	OD1	2.679
6MN7	H_ARG_188	NH1	H_ASP_209	OD2	2.663
6MN7	H_ARG_188	NH2	H_GLU_208	OE2	3.729
6MN7	H_ARG_188	NH2	H_ASP_209	OD1	3.908
6MN7	I_LYS_12	NZ	I_GLU_10	OE1	3.427
6MN7	I_ARG_38	NH1	I_GLU_46	OE1	3.285
6MN7	I_ARG_38	NH1	I_GLU_46	OE2	3.556
6MN7	I_ARG_38	NH1	I_ASP_89	OD1	3.444
6MN7	I_ARG_38	NH1	I_ASP_89	OD2	3.578
6MN7	I_ARG_38	NH2	I_ASP_90	OD1	2.915
6MN7	I_ARG_63	NH1	I_GLU_46	OE2	3.498
6MN7	I_ARG_67	NH1	I_ASP_90	OD1	2.860
6MN7	I_ARG_67	NH1	I_ASP_90	OD2	2.649
6MN7	I_ARG_67	NH2	I_ASP_90	OD1	2.942
6MN7	I_ARG_98	NH1	I_ASP_115	OD2	3.897
6MN7	I_ARG_188	NH1	I_GLU_208	OE2	3.991
6MN7	I_ARG_188	NH1	I_ASP_209	OD1	2.681
6MN7	I_ARG_188	NH1	I_ASP_209	OD2	2.663
6MN7	I_ARG_188	NH2	I_GLU_208	OE2	3.728
6MN7	I_ARG_188	NH2	I_ASP_209	OD1	3.910
6MPG	B_ARG_67	NH1	B_GLU_87	OE2	2.287
6MPG	B_ARG_67	NH1	B_ASP_88	OD1	3.091
6MPG	B_ARG_67	NH1	B_ASP_88	OD2	3.303
6MPG	B_ARG_67	NH2	B_GLU_87	OE2	3.585
6MPG	U_ARG_542	NH2	D_GLU_647	OE1	3.141
6MPG	U_ARG_542	NH2	D_GLU_647	OE2	2.524
6MPG	U_ARG_579	NH2	D_GLU_584	OE1	2.488
6MPG	U_ARG_588	NH2	U_GLU_584	OE2	2.498
6MPG	U_ARG_617	NH1	U_GLU_634	OE1	3.224
6MPG	U_ARG_617	NH1	U_GLU_634	OE2	3.055
6MPG	V_LYS_46	NZ	V_GLU_492	OE2	3.793
6MPG	V_LYS_65	NZ	V_GLU_64	OE2	2.921
6MPG	V_HIS_85	NE2	V_GLU_87	OE1	3.725
6MPG	V_HIS_105	NE2	V_ASP_474	OD1	3.796
6MPG	V_HIS_216	NE2	V_ASP_57	OD1	2.756
6MPG	V_HIS_216	NE2	V_ASP_57	OD2	3.780
6MPG	V_LYS_227	NZ	V_GLU_83	OE1	2.744
6MPG	V_LYS_227	NZ	V_GLU_83	OE2	3.617
6MPG	V_LYS_229	NZ	B_ASP_1	OD1	2.776
6MPG	V_LYS_231	NZ	V_GLU_268	OE1	2.210
6MPG	V_LYS_231	NZ	V_GLU_268	OE2	3.773
6MPG	V_LYS_231	NZ	V_GLU_269	OE1	3.900
6MPG	V_LYS_282	NZ	V_GLU_275	OE1	2.926
6MPG	V_ARG_298	NH1	V_GLU_381	OE1	3.522
6MPG	V_ARG_298	NH1	V_GLU_381	OE2	2.978
6MPG	V_ARG_298	NH2	V_GLU_381	OE1	3.713
6MPG	V_ARG_308	NH1	V_GLU_164	OE1	3.822
6MPG	V_LYS_421	NZ	V_ASP_180	OD1	3.836
6MPG	V_ARG_429	NH1	V_ASP_113	OD2	3.831
6MPG	V_ARG_429	NH2	V_ASP_113	OD1	3.803
6MPG	V_ARG_429	NH2	V_ASP_113	OD2	2.191
6MPG	V_ARG_469	NH2	V_ASP_457	OD2	3.540
6MPG	V_ARG_476	NH1	V_GLU_102	OE1	2.983
6MPG	V_ARG_476	NH1	V_GLU_102	OE2	2.663

6MPG	V_ARG_476	NH2	V_GLU_102	OE1	3.160
6MPG	V_ARG_480	NH1	V_ASP_477	OD1	2.648
6MPG	V_LYS_487	NZ	V_ASP_47	OD1	2.603
6MPG	V_LYS_487	NZ	V_ASP_47	OD2	3.288
6MPG	W_ARG_38	NH1	W_GLU_46	OE2	3.453
6MPG	W_ARG_38	NH1	W_ASP_89	OD1	3.905
6MPG	W_ARG_38	NH2	W_ASP_89	OD1	2.942
6MPG	W_ARG_66	NH2	W_ASP_89	OD2	3.660
6MPG	W_HIS_105	NE2	B_GLU_61	OE2	3.652
6MPG	m_ARG_38	NH1	m_ASP_86	OD1	2.924
6MPG	m_ARG_38	NH2	m_GLU_46	OE1	3.523
6MPG	m_ARG_38	NH2	m_GLU_46	OE2	3.688
6MPG	m_ARG_38	NH2	m_ASP_86	OD1	3.975
6MPG	m_LYS_73	NZ	m_ASP_53	OD1	3.849
6MPG	m_LYS_73	NZ	m_ASP_53	OD2	2.556
6MPG	n_ARG_61	NH1	n_ASP_60	OD1	3.630
6MPG	n_ARG_61	NH1	n_ASP_60	OD2	3.902
6MPG	n_ARG_94	NH1	V_ASP_321A	OD1	3.878
6MPG	n_ARG_95	NH2	n_GLU_25	OE2	3.812
6MPG	q_ARG_38	NH1	q_ASP_86	OD1	3.717
6MPG	q_ARG_38	NH2	q_ASP_86	OD1	3.650
6MPG	q_ARG_66	NH1	q_ASP_86	OD2	3.786
6MPG	q_ARG_66	NH2	q_ASP_86	OD1	3.709
6MPG	q_ARG_66	NH2	q_ASP_86	OD2	2.196
6MPG	r_ARG_60	NH1	r_ASP_81	OD2	3.768
6MPG	r_ARG_60	NH2	r_ASP_81	OD1	3.488
6MPG	r_ARG_60	NH2	r_ASP_81	OD2	2.219
6MPG	2_LYS_46	NZ	2_GLU_492	OE2	3.792
6MPG	2_LYS_65	NZ	2_GLU_64	OE2	2.922
6MPG	2_HIS_85	NE2	2_GLU_87	OE1	3.726
6MPG	2_HIS_105	NE2	2_ASP_474	OD1	3.795
6MPG	2_HIS_216	NE2	2_ASP_57	OD1	2.756
6MPG	2_HIS_216	NE2	2_ASP_57	OD2	3.779
6MPG	2_LYS_227	NZ	2_GLU_83	OE1	2.745
6MPG	2_LYS_227	NZ	2_GLU_83	OE2	3.617
6MPG	2_LYS_229	NZ	4_ASP_1	OD1	2.776
6MPG	2_LYS_231	NZ	2_GLU_268	OE1	2.210
6MPG	2_LYS_231	NZ	2_GLU_268	OE2	3.772
6MPG	2_LYS_231	NZ	2_GLU_269	OE1	3.900
6MPG	2_LYS_282	NZ	2_GLU_275	OE1	2.926
6MPG	2_ARG_298	NH1	2_GLU_381	OE1	3.521
6MPG	2_ARG_298	NH1	2_GLU_381	OE2	2.977
6MPG	2_ARG_298	NH2	2_GLU_381	OE1	3.713
6MPG	2_ARG_308	NH1	2_GLU_164	OE1	3.822
6MPG	2_LYS_421	NZ	2_ASP_180	OD1	3.837
6MPG	2_ARG_429	NH1	2_ASP_113	OD2	3.831
6MPG	2_ARG_429	NH2	2_ASP_113	OD1	3.804
6MPG	2_ARG_429	NH2	2_ASP_113	OD2	2.191
6MPG	2_ARG_469	NH2	2_ASP_457	OD2	3.540
6MPG	2_ARG_476	NH1	2_GLU_102	OE1	2.983
6MPG	2_ARG_476	NH1	2_GLU_102	OE2	2.663
6MPG	2_ARG_476	NH2	2_GLU_102	OE1	3.160
6MPG	2_ARG_480	NH1	2_ASP_477	OD1	2.648
6MPG	2_LYS_487	NZ	2_ASP_47	OD1	2.604
6MPG	2_LYS_487	NZ	2_ASP_47	OD2	3.288
6MPG	3_ARG_38	NH1	3_GLU_46	OE2	3.453
6MPG	3_ARG_38	NH1	3_ASP_89	OD1	3.905
6MPG	3_ARG_38	NH2	3_ASP_89	OD1	2.943

6MPG	3_ARG.66	NH2	3_ASP.89	OD2	3.660
6MPG	3_HIS.105	NE2	4_GLU.61	OE2	3.651
6MPG	4_ARG.67	NH1	4_GLU.87	OE2	2.288
6MPG	4_ARG.67	NH1	4_ASP.88	OD1	3.090
6MPG	4_ARG.67	NH1	4_ASP.88	OD2	3.302
6MPG	4_ARG.67	NH2	4_GLU.87	OE2	3.586
6MPG	5_ARG.38	NH1	5_ASP.86	OD1	2.924
6MPG	5_ARG.38	NH2	5_GLU.46	OE1	3.523
6MPG	5_ARG.38	NH2	5_GLU.46	OE2	3.688
6MPG	5_ARG.38	NH2	5_ASP.86	OD1	3.975
6MPG	5_LYS.73	NZ	5_ASP.53	OD1	3.850
6MPG	5_LYS.73	NZ	5_ASP.53	OD2	2.557
6MPG	6_ARG.61	NH1	6_ASP.60	OD1	3.630
6MPG	6_ARG.61	NH1	6_ASP.60	OD2	3.902
6MPG	6_ARG.94	NH1	2_ASP.321A	OD1	3.878
6MPG	6_ARG.95	NH2	6_GLU.25	OE2	3.812
6MPG	7_ARG.60	NH1	7_ASP.81	OD2	3.768
6MPG	7_ARG.60	NH2	7_ASP.81	OD1	3.488
6MPG	7_ARG.60	NH2	7_ASP.81	OD2	2.218
6MPG	8_ARG.38	NH1	8_ASP.86	OD1	3.717
6MPG	8_ARG.38	NH2	8_ASP.86	OD1	3.651
6MPG	8_ARG.66	NH1	8_ASP.86	OD2	3.787
6MPG	8_ARG.66	NH2	8_ASP.86	OD1	3.708
6MPG	8_ARG.66	NH2	8_ASP.86	OD2	2.195
6MPG	A_ARG.542	NH2	U_GLU.647	OE1	3.132
6MPG	A_ARG.542	NH2	U_GLU.647	OE2	2.525
6MPG	A_ARG.579	NH2	U_GLU.584	OE1	2.474
6MPG	A_ARG.588	NH2	A_GLU.584	OE2	2.498
6MPG	A_ARG.617	NH1	A_GLU.634	OE1	3.224
6MPG	A_ARG.617	NH1	A_GLU.634	OE2	3.054
6MPG	C_LYS.46	NZ	C_GLU.492	OE2	3.793
6MPG	C_LYS.65	NZ	C_GLU.64	OE2	2.921
6MPG	C_HIS.85	NE2	C_GLU.87	OE1	3.726
6MPG	C_HIS.105	NE2	C_ASP.474	OD1	3.796
6MPG	C_HIS.216	NE2	C_ASP.57	OD1	2.756
6MPG	C_HIS.216	NE2	C_ASP.57	OD2	3.780
6MPG	C_LYS.227	NZ	C_GLU.83	OE1	2.745
6MPG	C_LYS.227	NZ	C_GLU.83	OE2	3.617
6MPG	C_LYS.229	NZ	Y_ASP.1	OD1	2.776
6MPG	C_LYS.231	NZ	C_GLU.268	OE1	2.210
6MPG	C_LYS.231	NZ	C_GLU.268	OE2	3.773
6MPG	C_LYS.231	NZ	C_GLU.269	OE1	3.900
6MPG	C_LYS.282	NZ	C_GLU.275	OE1	2.926
6MPG	C_ARG.298	NH1	C_GLU.381	OE1	3.521
6MPG	C_ARG.298	NH1	C_GLU.381	OE2	2.977
6MPG	C_ARG.298	NH2	C_GLU.381	OE1	3.713
6MPG	C_ARG.308	NH1	C_GLU.164	OE1	3.822
6MPG	C_LYS.421	NZ	C_ASP.180	OD1	3.836
6MPG	C_ARG.429	NH1	C_ASP.113	OD2	3.831
6MPG	C_ARG.429	NH2	C_ASP.113	OD1	3.803
6MPG	C_ARG.429	NH2	C_ASP.113	OD2	2.191
6MPG	C_ARG.469	NH2	C_ASP.457	OD2	3.540
6MPG	C_ARG.476	NH1	C_GLU.102	OE1	2.983
6MPG	C_ARG.476	NH1	C_GLU.102	OE2	2.663
6MPG	C_ARG.476	NH2	C_GLU.102	OE1	3.160
6MPG	C_ARG.480	NH1	C_ASP.477	OD1	2.648
6MPG	C_LYS.487	NZ	C_ASP.47	OD1	2.604
6MPG	C_LYS.487	NZ	C_ASP.47	OD2	3.288

6MPG	D_ARG_542	NH2	A_GLU_647	OE1	3.137
6MPG	D_ARG_542	NH2	A_GLU_647	OE2	2.533
6MPG	D_ARG_579	NH2	A_GLU_584	OE1	2.479
6MPG	D_ARG_588	NH2	D_GLU_584	OE2	2.498
6MPG	D_ARG_617	NH1	D_GLU_634	OE1	3.224
6MPG	D_ARG_617	NH1	D_GLU_634	OE2	3.054
6MPG	M_ARG_38	NH1	M_ASP_86	OD1	2.924
6MPG	M_ARG_38	NH2	M_GLU_46	OE1	3.523
6MPG	M_ARG_38	NH2	M_GLU_46	OE2	3.688
6MPG	M_ARG_38	NH2	M_ASP_86	OD1	3.975
6MPG	M_LYS_73	NZ	M_ASP_53	OD1	3.849
6MPG	M_LYS_73	NZ	M_ASP_53	OD2	2.557
6MPG	N_ARG_61	NH1	N_ASP_60	OD1	3.630
6MPG	N_ARG_61	NH1	N_ASP_60	OD2	3.902
6MPG	N_ARG_94	NH1	C_ASP_321A	OD1	3.878
6MPG	N_ARG_95	NH2	N_GLU_25	OE2	3.813
6MPG	Q_ARG_38	NH1	Q_ASP_86	OD1	3.717
6MPG	Q_ARG_38	NH2	Q_ASP_86	OD1	3.651
6MPG	Q_ARG_66	NH1	Q_ASP_86	OD2	3.787
6MPG	Q_ARG_66	NH2	Q_ASP_86	OD1	3.708
6MPG	Q_ARG_66	NH2	Q_ASP_86	OD2	2.196
6MPG	R_ARG_60	NH1	R_ASP_81	OD2	3.768
6MPG	R_ARG_60	NH2	R_ASP_81	OD1	3.488
6MPG	R_ARG_60	NH2	R_ASP_81	OD2	2.219
6MPG	X_ARG_38	NH1	X_GLU_46	OE2	3.453
6MPG	X_ARG_38	NH1	X_ASP_89	OD1	3.905
6MPG	X_ARG_38	NH2	X_ASP_89	OD1	2.942
6MPG	X_ARG_66	NH2	X_ASP_89	OD2	3.661
6MPG	X_HIS_105	NE2	Y_GLU_61	OE2	3.651
6MPG	Y_ARG_67	NH1	Y_GLU_87	OE2	2.288
6MPG	Y_ARG_67	NH1	Y_ASP_88	OD1	3.090
6MPG	Y_ARG_67	NH1	Y_ASP_88	OD2	3.302
6MPG	Y_ARG_67	NH2	Y_GLU_87	OE2	3.586
6MPH	1_LYS_31A	NZ	A_GLU_87	OE1	2.457
6MPH	1_LYS_31A	NZ	A_GLU_87	OE2	3.919
6MPH	1_ARG_38	NH1	1_GLU_46	OE1	3.740
6MPH	1_ARG_38	NH1	1_GLU_46	OE2	2.866
6MPH	2_ARG_61	NH1	2_ASP_82	OD1	3.657
6MPH	2_ARG_96	NH1	1_GLU_95	OE1	3.340
6MPH	2_ARG_96	NH1	1_GLU_95	OE2	2.522
6MPH	3_LYS_31A	NZ	B_GLU_87	OE1	2.448
6MPH	3_LYS_31A	NZ	B_GLU_87	OE2	3.973
6MPH	3_ARG_38	NH1	3_GLU_46	OE1	3.744
6MPH	3_ARG_38	NH1	3_GLU_46	OE2	2.935
6MPH	4_ARG_61	NH1	4_ASP_82	OD1	3.637
6MPH	4_ARG_96	NH1	3_GLU_95	OE1	3.339
6MPH	4_ARG_96	NH1	3_GLU_95	OE2	2.507
6MPH	6_ARG_542	NH1	E_GLU_647	OE2	3.863
6MPH	6_ARG_542	NH2	E_GLU_647	OE1	3.449
6MPH	6_ARG_542	NH2	E_GLU_647	OE2	2.484
6MPH	6_ARG_579	NH2	E_GLU_584	OE1	2.833
6MPH	6_ARG_588	NH2	6_GLU_584	OE2	2.677
6MPH	6_ARG_617	NH1	6_GLU_634	OE2	2.791
6MPH	6_ARG_617	NH2	6_GLU_621	OE2	3.365
6MPH	A_LYS_46	NZ	A_GLU_492	OE2	3.500
6MPH	A_HIS_216	NE2	A_ASP_57	OD1	2.758
6MPH	A_HIS_216	NE2	A_ASP_57	OD2	3.293
6MPH	A_LYS_231	NZ	A_GLU_268	OE1	2.566

6MPH	A_LYS_231	NZ	A_GLU_268	OE2	3.911
6MPH	A_LYS_282	NZ	A_GLU_275	OE1	3.999
6MPH	A_LYS_282	NZ	f_ASP_114	OD1	3.470
6MPH	A_LYS_282	NZ	f_ASP_114	OD2	3.288
6MPH	A_ARG_298	NH1	A_GLU_381	OE1	2.662
6MPH	A_ARG_298	NH1	A_GLU_381	OE2	3.145
6MPH	A_ARG_298	NH2	A_GLU_381	OE1	3.543
6MPH	A_ARG_308	NH1	A_GLU_164	OE2	3.005
6MPH	A_ARG_327	NH2	X_GLU_100I	OE1	3.876
6MPH	A_LYS_351	NZ	A_GLU_269	OE1	3.880
6MPH	A_LYS_421	NZ	A_ASP_180	OD1	3.919
6MPH	A_ARG_429	NH1	A_ASP_113	OD1	3.710
6MPH	A_ARG_429	NH1	A_ASP_113	OD2	3.111
6MPH	A_ARG_429	NH2	A_ASP_113	OD1	3.007
6MPH	A_ARG_429	NH2	A_ASP_113	OD2	2.937
6MPH	A_ARG_469	NH2	A_ASP_457	OD2	3.457
6MPH	A_ARG_476	NH1	A_GLU_102	OE1	3.188
6MPH	A_ARG_476	NH1	A_GLU_102	OE2	2.587
6MPH	A_ARG_476	NH2	A_GLU_102	OE1	3.380
6MPH	A_ARG_480	NH1	A_ASP_477	OD1	2.475
6MPH	A_LYS_487	NZ	A_ASP_47	OD1	2.599
6MPH	A_LYS_487	NZ	A_ASP_47	OD2	3.570
6MPH	A_LYS_487	NZ	A_GLU_91	OE1	3.931
6MPH	B_LYS_46	NZ	B_GLU_492	OE2	3.523
6MPH	B_HIS_216	NE2	B_ASP_57	OD1	2.681
6MPH	B_HIS_216	NE2	B_ASP_57	OD2	3.250
6MPH	B_LYS_231	NZ	B_GLU_268	OE1	2.562
6MPH	B_LYS_231	NZ	B_GLU_268	OE2	3.926
6MPH	B_LYS_282	NZ	B_GLU_275	OE1	3.947
6MPH	B_LYS_282	NZ	g_ASP_114	OD1	3.432
6MPH	B_LYS_282	NZ	g_ASP_114	OD2	3.289
6MPH	B_ARG_298	NH1	B_GLU_381	OE1	2.635
6MPH	B_ARG_298	NH1	B_GLU_381	OE2	3.103
6MPH	B_ARG_298	NH2	B_GLU_381	OE1	3.494
6MPH	B_ARG_308	NH1	B_GLU_164	OE2	3.028
6MPH	B_ARG_327	NH2	Y_GLU_100I	OE1	3.899
6MPH	B_LYS_351	NZ	B_GLU_269	OE1	3.859
6MPH	B_LYS_421	NZ	B_ASP_180	OD1	3.823
6MPH	B_ARG_429	NH1	B_ASP_113	OD1	3.775
6MPH	B_ARG_429	NH1	B_ASP_113	OD2	3.138
6MPH	B_ARG_429	NH2	B_ASP_113	OD1	3.034
6MPH	B_ARG_429	NH2	B_ASP_113	OD2	2.894
6MPH	B_ARG_469	NH2	B_ASP_457	OD2	3.505
6MPH	B_ARG_476	NH1	B_GLU_102	OE1	3.172
6MPH	B_ARG_476	NH1	B_GLU_102	OE2	2.620
6MPH	B_ARG_476	NH2	B_GLU_102	OE1	3.414
6MPH	B_ARG_480	NH1	B_ASP_477	OD1	2.510
6MPH	B_LYS_487	NZ	B_ASP_47	OD1	2.597
6MPH	B_LYS_487	NZ	B_ASP_47	OD2	3.582
6MPH	B_LYS_487	NZ	B_GLU_91	OE1	3.935
6MPH	C_LYS_46	NZ	C_GLU_492	OE2	3.581
6MPH	C_HIS_216	NE2	C_ASP_57	OD1	2.733
6MPH	C_HIS_216	NE2	C_ASP_57	OD2	3.258
6MPH	C_LYS_231	NZ	C_GLU_268	OE1	2.574
6MPH	C_LYS_231	NZ	C_GLU_268	OE2	3.908
6MPH	C_LYS_282	NZ	C_GLU_275	OE1	3.963
6MPH	C_LYS_282	NZ	Q_ASP_114	OD1	3.383
6MPH	C_LYS_282	NZ	Q_ASP_114	OD2	3.272

6MPH	C_ARG.298	NH1	C_GLU.381	OE1	2.658
6MPH	C_ARG.298	NH1	C_GLU.381	OE2	3.166
6MPH	C_ARG.298	NH2	C_GLU.381	OE1	3.611
6MPH	C_ARG.308	NH1	C_GLU.164	OE2	2.979
6MPH	C_ARG.327	NH2	M_GLU.100I	OE1	3.872
6MPH	C_LYS.351	NZ	C_GLU.269	OE1	3.861
6MPH	C_LYS.421	NZ	C_ASP.180	OD1	3.916
6MPH	C_ARG.429	NH1	C_ASP.113	OD1	3.764
6MPH	C_ARG.429	NH1	C_ASP.113	OD2	3.172
6MPH	C_ARG.429	NH2	C_ASP.113	OD1	2.996
6MPH	C_ARG.429	NH2	C_ASP.113	OD2	2.906
6MPH	C_ARG.469	NH2	C_ASP.457	OD2	3.484
6MPH	C_ARG.476	NH1	C_GLU.102	OE1	3.185
6MPH	C_ARG.476	NH1	C_GLU.102	OE2	2.606
6MPH	C_ARG.476	NH2	C_GLU.102	OE1	3.401
6MPH	C_ARG.480	NH1	C_ASP.477	OD1	2.485
6MPH	C_LYS.487	NZ	C_ASP.47	OD1	2.672
6MPH	C_LYS.487	NZ	C_ASP.47	OD2	3.601
6MPH	C_LYS.487	NZ	C_GLU.91	OE1	3.831
6MPH	D_ARG.542	NH1	6_GLU.647	OE2	3.853
6MPH	D_ARG.542	NH2	6_GLU.647	OE1	3.460
6MPH	D_ARG.542	NH2	6_GLU.647	OE2	2.476
6MPH	D_ARG.579	NH2	6_GLU.584	OE1	2.760
6MPH	D_ARG.588	NH2	D_GLU.584	OE2	2.573
6MPH	D_ARG.617	NH1	D_GLU.634	OE2	2.801
6MPH	D_ARG.617	NH2	D_GLU.621	OE2	3.420
6MPH	E_ARG.542	NH1	D_GLU.647	OE2	3.888
6MPH	E_ARG.542	NH2	D_GLU.647	OE1	3.465
6MPH	E_ARG.542	NH2	D_GLU.647	OE2	2.463
6MPH	E_ARG.579	NH2	D_GLU.584	OE1	2.789
6MPH	E_ARG.588	NH2	E_GLU.584	OE2	2.573
6MPH	E_ARG.617	NH1	E_GLU.634	OE2	2.776
6MPH	E_ARG.617	NH2	E_GLU.621	OE2	3.431
6MPH	H_LYS.31A	NZ	C_GLU.87	OE1	2.458
6MPH	H_LYS.31A	NZ	C_GLU.87	OE2	3.969
6MPH	H_ARG.38	NH1	H_GLU.46	OE1	3.668
6MPH	H_ARG.38	NH1	H_GLU.46	OE2	2.976
6MPH	L_ARG.61	NH1	L_ASP.82	OD1	3.612
6MPH	L_ARG.96	NH1	H_GLU.95	OE1	3.309
6MPH	L_ARG.96	NH1	H_GLU.95	OE2	2.530
6MPH	M_ARG.38	NH1	M_ASP.86	OD1	3.017
6MPH	M_ARG.38	NH2	M_GLU.46	OE1	3.135
6MPH	M_ARG.38	NH2	M_GLU.46	OE2	3.398
6MPH	M_ARG.66	NH2	M_ASP.86	OD1	3.623
6MPH	M_LYS.73	NZ	M_ASP.53	OD1	3.608
6MPH	M_LYS.73	NZ	M_ASP.53	OD2	2.901
6MPH	M_LYS.96	NZ	M_ASP.100Q	OD2	3.995
6MPH	N_ARG.61	NH1	N_ASP.60	OD1	3.566
6MPH	N_ARG.94	NH1	C_ASP.321A	OD1	3.859
6MPH	Q_ARG.38	NH1	Q_GLU.46	OE1	3.730
6MPH	Q_ARG.38	NH2	Q_ASP.97	OD1	3.305
6MPH	Q_ARG.67	NH2	Q_ASP.97	OD1	3.545
6MPH	Q_ARG.67	NH2	Q_ASP.97	OD2	3.021
6MPH	Q_ARG.72	NH2	C_ASP.368	OD2	3.534
6MPH	R_ARG.40	NH2	R_GLU.103	OE2	3.768
6MPH	R_ARG.61	NH2	R_ASP.82	OD1	3.293
6MPH	R_ARG.61	NH2	R_ASP.82	OD2	2.978
6MPH	X_ARG.38	NH1	X_ASP.86	OD1	3.079

6MPH	X_ARG_38	NH2	X_GLU_46	OE1	3.140
6MPH	X_ARG_38	NH2	X_GLU_46	OE2	3.408
6MPH	X_ARG_66	NH2	X_ASP_86	OD1	3.580
6MPH	X_LYS_73	NZ	X_ASP_53	OD1	3.586
6MPH	X_LYS_73	NZ	X_ASP_53	OD2	2.898
6MPH	Y_ARG_38	NH1	Y_ASP_86	OD1	3.102
6MPH	Y_ARG_38	NH2	Y_GLU_46	OE1	3.155
6MPH	Y_ARG_38	NH2	Y_GLU_46	OE2	3.384
6MPH	Y_ARG_66	NH2	Y_ASP_86	OD1	3.575
6MPH	Y_LYS_73	NZ	Y_ASP_53	OD1	3.614
6MPH	Y_LYS_73	NZ	Y_ASP_53	OD2	2.911
6MPH	Z_ARG_61	NH1	Z_ASP_60	OD1	3.627
6MPH	Z_ARG_94	NH1	A_ASP_321A	OD1	3.890
6MPH	a_ARG_61	NH1	a_ASP_60	OD1	3.574
6MPH	a_ARG_94	NH1	B_ASP_321A	OD1	3.861
6MPH	f_ARG_38	NH1	f_GLU_46	OE1	3.663
6MPH	f_ARG_38	NH2	f_ASP_97	OD1	3.333
6MPH	f_ARG_67	NH2	f_ASP_97	OD1	3.553
6MPH	f_ARG_67	NH2	f_ASP_97	OD2	3.049
6MPH	f_ARG_72	NH2	A_ASP_368	OD2	3.577
6MPH	g_ARG_38	NH1	g_GLU_46	OE1	3.701
6MPH	g_ARG_38	NH2	g_ASP_97	OD1	3.335
6MPH	g_ARG_67	NH2	g_ASP_97	OD1	3.559
6MPH	g_ARG_67	NH2	g_ASP_97	OD2	3.040
6MPH	g_ARG_72	NH2	B_ASP_368	OD2	3.570
6MPH	h_ARG_40	NH2	h_GLU_103	OE2	3.735
6MPH	h_ARG_61	NH2	h_ASP_82	OD1	3.222
6MPH	h_ARG_61	NH2	h_ASP_82	OD2	2.932
6MPH	i_ARG_40	NH2	i_GLU_103	OE2	3.762
6MPH	i_ARG_61	NH2	i_ASP_82	OD1	3.332
6MPH	i_ARG_61	NH2	i_ASP_82	OD2	3.017
6MQC	A_ARG_	NH1	A_GLU_	OE1	3.064
6MQC	A_ARG_	NH1	A_ASP_	OD1	3.838
6MQC	A_ARG_	NH2	A_ASP_	OD1	3.330
6MQC	A_ARG_	NH2	A_ASP_	OD2	3.244
6MQC	A_ARG_	NH1	A_ASP_	OD1	3.212
6MQC	A_ARG_	NH1	A_ASP_	OD2	2.946
6MQC	A_ARG_	NH1	A_ASP_	OD1	2.770
6MQC	A_ARG_	NH1	B_ASP_	OD1	2.994
6MQC	A_ARG_	NH2	B_ASP_	OD1	2.820
6MQC	A_ARG_	NH2	A_ASP_	OD1	3.694
6MQC	A_ARG_	NH2	A_ASP_	OD2	2.674
6MQC	A_ARG_	NH1	B_ASP_	OD1	3.399
6MQC	A_ARG_	NH1	B_ASP_	OD2	3.078
6MQC	A_ARG_	NH1	B_ASP_	OD1	2.829
6MQC	A_ARG_	NH2	B_ASP_	OD1	2.822
6MQC	A_ARG_	NH2	B_ASP_	OD2	3.673
6MQC	A_ARG_	NH2	A_GLU_	OE2	3.410
6MQC	B_ARG_	NH1	B_ASP_	OD2	3.586
6MQC	B_LYS_	NZ	B_GLU_	OE1	3.361
6MQC	B_ARG_	NH1	B_ASP_	OD1	2.810
6MQC	B_ARG_	NH1	B_ASP_	OD2	3.319
6MQC	B_ARG_	NH2	B_ASP_	OD1	3.618
6MQC	B_ARG_	NH2	B_ASP_	OD2	2.613
6MQC	B_LYS_	NZ	B_GLU_	OE1	3.307
6MQC	B_HIS_	ND1	B_ASP_	OD1	2.832
6MQC	H_ARG_	NH1	H_GLU_	OE1	3.098
6MQC	H_ARG_	NH1	H_ASP_	OD1	3.684

6MQC	H_ARG_	NH2	H_ASP_	OD1	2.690
6MQC	H_ARG_	NH1	H_ASP_	OD1	3.063
6MQC	H_ARG_	NH1	H_ASP_	OD2	3.805
6MQC	H_ARG_	NH2	H_ASP_	OD1	3.624
6MQC	H_ARG_	NH2	H_ASP_	OD2	3.006
6MQC	H_ARG_	NH1	H_ASP_	OD1	2.952
6MQC	H_ARG_	NH1	L_ASP_	OD1	2.906
6MQC	H_ARG_	NH2	L_ASP_	OD1	2.999
6MQC	H_ARG_	NH2	H_ASP_	OD1	3.031
6MQC	H_ARG_	NH2	H_ASP_	OD2	3.958
6MQC	H_ARG_	NH1	L_ASP_	OD1	2.856
6MQC	H_ARG_	NH1	L_ASP_	OD2	3.748
6MQC	H_ARG_	NH2	L_ASP_	OD1	3.439
6MQC	H_ARG_	NH2	L_ASP_	OD2	3.140
6MQC	H_ARG_	NH2	L_ASP_	OD1	2.780
6MQC	H_ARG_	NH2	L_ASP_	OD2	3.923
6MQC	H_LYS_	NZ	H_ASP_	OD1	3.326
6MQC	L_ARG_	NH1	L_ASP_	OD2	3.327
6MQC	L_ARG_	NH1	L_ASP_	OD1	2.916
6MQC	L_ARG_	NH1	L_ASP_	OD2	3.414
6MQC	L_ARG_	NH2	L_ASP_	OD1	3.578
6MQC	L_ARG_	NH2	L_ASP_	OD2	2.554
6MQC	L_LYS_	NZ	L_GLU_	OE2	3.839
6MQC	L_LYS_	NZ	L_GLU_	OE1	3.867
6MQC	L_LYS_	NZ	L_GLU_	OE2	3.648
6MQC	L_HIS_	ND1	L_ASP_	OD1	2.866
6MQC	L_HIS_	NE2	L_GLU_	OE2	3.758
6MQE	B_ARG_61	NH1	B_GLU_81	OE2	2.972
6MQE	B_ARG_61	NH1	B_ASP_82	OD1	3.540
6MQE	B_ARG_61	NH1	B_ASP_82	OD2	3.139
6MQE	B_ARG_61	NH2	B_ASP_82	OD1	2.652
6MQE	B_ARG_61	NH2	B_ASP_82	OD2	3.672
6MQE	B_LYS_103	NZ	B_GLU_165	OE1	3.601
6MQE	B_LYS_126	NZ	B_GLU_122	OE1	2.295
6MQE	B_LYS_147	NZ	B_GLU_195	OE1	2.709
6MQE	B_LYS_149	NZ	B_GLU_195	OE2	3.823
6MQE	B_LYS_155	NZ	B_GLU_185	OE1	3.813
6MQE	B_LYS_155	NZ	B_GLU_185	OE2	2.543
6MQE	B_HIS_189	ND1	B_ASP_151	OD1	3.273
6MQE	B_HIS_189	NE2	B_GLU_185	OE1	2.265
6MQE	B_HIS_189	NE2	B_GLU_185	OE2	2.201
6MQE	A_ARG_38	NH1	A_GLU_46	OE2	3.135
6MQE	A_ARG_38	NH1	A_ASP_86	OD1	3.589
6MQE	A_ARG_38	NH2	A_ASP_86	OD1	2.950
6MQE	A_ARG_66	NH1	A_ASP_86	OD1	3.044
6MQE	A_ARG_66	NH1	A_ASP_86	OD2	2.613
6MQE	A_ARG_66	NH2	A_ASP_86	OD1	3.697
6MQE	A_LYS_75	NZ	A_ASP_72	OD2	2.759
6MQE	A_LYS_75	NZ	A_GLU_77	OE1	3.673
6MQE	A_ARG_95	NH1	A_ASP_101	OD1	3.112
6MQE	A_ARG_95	NH2	B_ASP_91	OD2	3.864
6MQE	A_ARG_100H	NH2	B_ASP_91	OD2	3.610
6MQE	H_ARG_38	NH1	H_GLU_46	OE1	2.700
6MQE	H_ARG_38	NH1	H_GLU_46	OE2	3.912
6MQE	H_ARG_38	NH1	H_ASP_86	OD2	3.737
6MQE	H_ARG_38	NH2	H_ASP_86	OD2	2.834
6MQE	H_ARG_66	NH1	H_ASP_86	OD1	2.676
6MQE	H_ARG_66	NH1	H_ASP_86	OD2	3.146

6MQE	H_ARG.66	NH2	H_ASP.86	OD2	3.716
6MQE	H_LYS.71	NZ	H_GLU.55	OE1	3.815
6MQE	H_LYS.71	NZ	H_GLU.55	OE2	3.654
6MQE	H_ARG.95	NH1	H_ASP.101	OD1	3.185
6MQE	H_ARG.95	NH1	L_ASP.91	OD1	3.360
6MQE	H_ARG.95	NH2	L_ASP.91	OD1	2.956
6MQE	H_ARG.100H	NH1	L_ASP.91	OD1	2.604
6MQE	H_ARG.100H	NH1	L_ASP.91	OD2	3.888
6MQE	H_ARG.210	NH1	H_GLU.212	OE1	2.890
6MQE	H_ARG.210	NH2	H_GLU.212	OE1	3.265
6MQE	L_ARG.61	NH1	L_ASP.82	OD1	2.728
6MQE	L_ARG.61	NH1	L_ASP.82	OD2	3.171
6MQE	L_ARG.61	NH2	L_ASP.82	OD1	3.670
6MQE	L_ARG.61	NH2	L_ASP.82	OD2	2.544
6MQE	L_LYS.103	NZ	L_GLU.165	OE1	2.963
6MQE	L_LYS.103	NZ	L_GLU.165	OE2	3.584
6MQE	L_LYS.126	NZ	L_ASP.123	OD1	3.637
6MQE	L_LYS.155	NZ	A_GLU.56	OE1	2.786
6MQE	L_LYS.155	NZ	L_GLU.185	OE2	3.322
6MQE	L_HIS.189	ND1	L_GLU.185	OE2	3.793
6MQE	L_HIS.189	NE2	A_GLU.56	OE1	3.428
6MQE	L_HIS.189	NE2	A_GLU.56	OE2	2.569
6MQE	L_HIS.189	NE2	L_GLU.185	OE2	3.601
6MQM	A_ARG.38	NH1	A_GLU.46	OE1	3.765
6MQM	A_ARG.38	NH1	A_GLU.46	OE2	2.771
6MQM	A_ARG.38	NH1	A_ASP.86	OD1	3.479
6MQM	A_ARG.38	NH2	A_ASP.86	OD1	2.674
6MQM	A_ARG.66	NH1	A_ASP.86	OD1	3.175
6MQM	A_ARG.66	NH1	A_ASP.86	OD2	3.748
6MQM	A_ARG.66	NH2	A_ASP.86	OD1	3.755
6MQM	A_ARG.66	NH2	A_ASP.86	OD2	2.918
6MQM	A_ARG.94	NH1	A_ASP.101	OD1	3.858
6MQM	A_ARG.94	NH1	A_ASP.101	OD2	3.426
6MQM	A_ARG.94	NH2	A_ASP.101	OD2	3.302
6MQM	A_LYS.206	NZ	A_ASP.208	OD1	3.694
6MQM	A_LYS.206	NZ	A_ASP.208	OD2	3.645
6MQM	A_LYS.210	NZ	A_GLU.212	OE1	3.835
6MQM	A_LYS.210	NZ	A_GLU.212	OE2	2.455
6MQM	B_ARG.61	NH1	B_ASP.82	OD1	3.379
6MQM	B_ARG.61	NH1	B_ASP.82	OD2	3.603
6MQM	B_ARG.96	NH1	A_GLU.95	OE1	3.968
6MQM	B_ARG.96	NH1	A_GLU.95	OE2	2.460
6MQM	B_LYS.103	NZ	B_GLU.165	OE1	3.460
6MQM	B_LYS.103	NZ	B_GLU.165	OE2	2.483
6MQM	B_LYS.126	NZ	B_GLU.122	OE2	3.847
6MQM	B_LYS.149	NZ	B_GLU.195	OE1	3.490
6MQM	D_ARG.38	NH1	D_GLU.46	OE2	3.038
6MQM	D_ARG.38	NH1	D_ASP.86	OD1	3.431
6MQM	D_ARG.38	NH2	D_ASP.86	OD1	2.590
6MQM	D_ARG.66	NH1	D_ASP.86	OD1	2.939
6MQM	D_ARG.66	NH1	D_ASP.86	OD2	2.983
6MQM	D_ARG.66	NH2	D_ASP.86	OD2	3.281
6MQM	D_LYS.206	NZ	D_ASP.208	OD1	3.752
6MQM	D_LYS.210	NZ	D_GLU.212	OE2	3.469
6MQM	E_ARG.61	NH1	E_ASP.82	OD1	3.174
6MQM	E_ARG.61	NH1	E_ASP.82	OD2	3.771
6MQM	E_ARG.96	NH1	D_GLU.95	OE2	2.376
6MQM	E_LYS.103	NZ	E_GLU.165	OE1	3.185

6MQM	E_LYS_103	NZ	E_GLU_165	OE2	2.355
6MQM	E_LYS_149	NZ	E_GLU_195	OE1	2.638
6MQM	E_HIS_189	NE2	E_ASP_185	OD1	3.808
6MQM	G_ARG_38	NH1	G_GLU_46	OE2	3.081
6MQM	G_ARG_38	NH1	G_ASP_86	OD1	3.241
6MQM	G_ARG_38	NH2	G_ASP_86	OD1	2.432
6MQM	G_ARG_66	NH1	G_ASP_86	OD1	3.284
6MQM	G_ARG_66	NH1	G_ASP_86	OD2	3.321
6MQM	G_ARG_66	NH2	G_ASP_86	OD2	2.999
6MQM	G_ARG_94	NH2	G_ASP_101	OD1	3.791
6MQM	G_ARG_94	NH2	G_ASP_101	OD2	2.962
6MQM	G_LYS_206	NZ	G_ASP_208	OD1	3.377
6MQM	G_LYS_206	NZ	G_ASP_208	OD2	3.969
6MQM	G_LYS_210	NZ	G_GLU_212	OE2	3.739
6MQM	H_ARG_61	NH1	H_ASP_82	OD1	3.357
6MQM	H_ARG_61	NH1	H_ASP_82	OD2	3.698
6MQM	H_ARG_61	NH2	H_GLU_79	OE2	3.084
6MQM	H_ARG_96	NH1	G_GLU_95	OE2	2.480
6MQM	H_LYS_103	NZ	H_GLU_165	OE1	2.991
6MQM	H_LYS_103	NZ	H_GLU_165	OE2	2.468
6MQM	H_LYS_126	NZ	H_GLU_122	OE2	3.719
6MQM	H_LYS_149	NZ	H_GLU_195	OE1	2.676
6MQM	H_HIS_189	ND1	H_ASP_151	OD1	3.088
6MQM	H_HIS_189	NE2	H_ASP_185	OD1	3.777
6MQM	J_ARG_38	NH1	J_GLU_46	OE2	3.367
6MQM	J_ARG_38	NH1	J_ASP_86	OD1	3.218
6MQM	J_ARG_38	NH2	J_ASP_86	OD1	2.641
6MQM	J_ARG_66	NH1	J_ASP_86	OD1	2.986
6MQM	J_ARG_66	NH1	J_ASP_86	OD2	3.538
6MQM	J_ARG_66	NH2	J_ASP_86	OD1	3.738
6MQM	J_ARG_66	NH2	J_ASP_86	OD2	2.783
6MQM	J_ARG_94	NH1	J_ASP_101	OD2	3.348
6MQM	J_ARG_94	NH2	J_ASP_101	OD2	2.919
6MQM	J_LYS_206	NZ	J_ASP_208	OD1	3.651
6MQM	J_LYS_206	NZ	J_ASP_208	OD2	3.476
6MQM	J_LYS_	NZ	J_GLU_	OE2	3.487
6MQM	K_ARG_61	NH1	K_ASP_82	OD1	2.973
6MQM	K_ARG_61	NH1	K_ASP_82	OD2	3.285
6MQM	K_ARG_96	NH1	J_GLU_95	OE1	3.782
6MQM	K_ARG_96	NH1	J_GLU_95	OE2	2.262
6MQM	K_LYS_103	NZ	K_GLU_165	OE2	2.763
6MQM	K_LYS_	NZ	K_GLU_	OE1	2.452
6MQM	K_HIS_	ND1	K_ASP_	OD1	3.413
6MQM	K_HIS_	NE2	K_ASP_	OD1	3.837
6MQR	H_ARG_38	NH1	H_GLU_46	OE1	3.085
6MQR	H_ARG_38	NH1	H_ASP_86	OD1	3.945
6MQR	H_ARG_38	NH2	H_ASP_86	OD1	2.835
6MQR	H_ARG_41	NH2	H_GLU_148	OE1	3.805
6MQR	H_ARG_66	NH1	H_ASP_86	OD1	3.097
6MQR	H_ARG_66	NH1	H_ASP_86	OD2	3.599
6MQR	H_ARG_66	NH2	H_ASP_86	OD1	3.722
6MQR	H_ARG_66	NH2	H_ASP_86	OD2	3.135
6MQR	H_ARG_94	NH2	H_ASP_27	OD2	3.095
6MQR	H_ARG_96	NH1	H_ASP_101	OD2	3.599
6MQR	H_ARG_96	NH1	L_GLU_55	OE1	2.553
6MQR	H_LYS_143	NZ	H_ASP_144	OD1	3.883
6MQR	H_LYS_143	NZ	H_ASP_144	OD2	3.358
6MQR	L_LYS_30	NZ	L_ASP_28	OD2	3.556

6MQR	L_ARG_46	NH1	H_ASP_101	OD2	2.970
6MQR	L_ARG_46	NH1	L_GLU_55	OE1	3.253
6MQR	L_ARG_46	NH1	L_GLU_55	OE2	3.148
6MQR	L_ARG_46	NH2	H_GLU_95	OE2	3.587
6MQR	L_ARG_46	NH2	H_ASP_101	OD2	3.723
6MQR	L_HIS_49	ND1	L_GLU_55	OE1	3.996
6MQR	L_HIS_49	ND1	L_GLU_55	OE2	2.804
6MQR	L_ARG_61	NH1	L_GLU_81	OE1	3.715
6MQR	L_ARG_61	NH1	L_ASP_82	OD1	3.745
6MQR	L_ARG_61	NH1	L_ASP_82	OD2	2.987
6MQR	L_LYS_126	NZ	L_GLU_122	OE1	3.993
6MQR	L_ARG_142	NH2	L_GLU_161	OE2	3.937
6MQR	L_LYS_149	NZ	L_GLU_195	OE1	3.817
6MQR	L_LYS_149	NZ	L_GLU_195	OE2	2.808
6MQR	L_LYS_155	NZ	L_GLU_185	OE1	3.064
6MQR	L_LYS_169	NZ	L_ASP_167	OD2	3.796
6MQR	L_HIS_189	ND1	L_ASP_151	OD1	2.846
6MQR	L_HIS_189	NE2	L_GLU_185	OE1	2.682
6MQR	L_HIS_189	NE2	L_GLU_185	OE2	3.307
6MQS	A_ARG_39	NH1	A_ASP_91	OD1	3.081
6MQS	A_ARG_39	NH2	A_GLU_47	OE1	3.112
6MQS	A_ARG_39	NH2	A_ASP_91	OD1	3.076
6MQS	A_LYS_44	NZ	B_ASP_86	OD1	3.511
6MQS	A_ARG_45	NH1	A_GLU_47	OE2	3.645
6MQS	A_ARG_45	NH2	A_GLU_47	OE1	3.366
6MQS	A_ARG_68	NH2	A_ASP_91	OD1	3.145
6MQS	A_ARG_68	NH2	A_ASP_91	OD2	3.136
6MQS	A_ARG_138	NH1	B_GLU_214	OE1	3.046
6MQS	A_ARG_138	NH1	B_GLU_214	OE2	2.728
6MQS	A_LYS_152	NZ	A_ASP_153	OD1	3.592
6MQS	A_LYS_218	NZ	B_GLU_127	OE1	2.743
6MQS	A_LYS_218	NZ	B_GLU_127	OE2	3.002
6MQS	B_LYS_54	NZ	B_GLU_51	OE2	3.430
6MQS	B_ARG_62	NH1	B_ASP_83	OD1	2.524
6MQS	B_ARG_62	NH1	B_ASP_83	OD2	2.782
6MQS	B_LYS_114	NZ	B_GLU_202	OE1	3.365
6MQS	B_LYS_114	NZ	B_GLU_202	OE2	2.522
6MQS	B_LYS_153	NZ	B_GLU_207	OE1	2.539
6MQS	B_LYS_153	NZ	B_GLU_207	OE2	3.433
6MQS	B_LYS_170	NZ	B_GLU_106	OE1	3.760
6MQS	B_LYS_175	NZ	B_ASP_142	OD2	2.550
6MQS	B_HIS_192	ND1	B_ASP_155	OD1	3.151
6MQS	C_ARG_39	NH1	C_ASP_91	OD2	3.128
6MQS	C_ARG_39	NH2	C_GLU_47	OE2	3.179
6MQS	C_ARG_39	NH2	C_ASP_91	OD2	3.775
6MQS	C_LYS_44	NZ	D_ASP_86	OD1	2.946
6MQS	C_ARG_68	NH1	C_ASP_91	OD1	3.157
6MQS	C_ARG_68	NH1	C_ASP_91	OD2	3.255
6MQS	C_ARG_138	NH2	D_GLU_214	OE1	2.736
6MQS	C_ARG_138	NH2	D_GLU_214	OE2	3.220
6MQS	C_LYS_152	NZ	D_GLU_128	OE1	3.230
6MQS	C_LYS_215	NZ	C_ASP_217	OD1	3.836
6MQS	C_LYS_215	NZ	C_ASP_217	OD2	3.808
6MQS	C_LYS_218	NZ	D_GLU_127	OE1	2.641
6MQS	C_LYS_218	NZ	D_GLU_127	OE2	3.160
6MQS	D_LYS_54	NZ	D_GLU_51	OE2	2.149
6MQS	D_ARG_55	NH1	D_ASP_61	OD1	2.947
6MQS	D_ARG_55	NH2	D_ASP_61	OD1	3.758

6MQS	D_ARG.62	NH1	D_ASP.83	OD1	2.603
6MQS	D_ARG.62	NH1	D_ASP.83	OD2	3.278
6MQS	D_ARG.62	NH2	D_ASP.83	OD1	3.570
6MQS	D_ARG.62	NH2	D_ASP.83	OD2	2.546
6MQS	D_LYS.153	NZ	D_GLU.207	OE1	2.843
6MQS	D_LYS.153	NZ	D_GLU.207	OE2	3.321
6MQS	D_LYS.170	NZ	D_GLU.106	OE1	3.583
6MQS	D_HIS.192	ND1	D_ASP.155	OD1	2.450
6N16	A_ARG.38	NH1	A_GLU.46	OE1	3.309
6N16	A_ARG.38	NH1	A_ASP.86	OD1	3.572
6N16	A_ARG.38	NH2	A_ASP.86	OD1	2.610
6N16	A_ARG.66	NH1	A_ASP.86	OD1	3.129
6N16	A_ARG.66	NH1	A_ASP.86	OD2	3.512
6N16	A_ARG.66	NH2	A_ASP.86	OD1	3.997
6N16	A_ARG.66	NH2	A_ASP.86	OD2	3.156
6N16	A_LYS.71	NZ	A_GLU.55	OE2	3.830
6N16	A_ARG.105	NH1	C_GLU.64	OE1	3.566
6N16	A_ARG.105	NH2	C_GLU.64	OE1	3.522
6N16	A_ARG.105	NH2	C_GLU.64	OE2	3.717
6N16	A_HIS.164	NE2	B_ASP.167	OD2	3.486
6N16	A_ARG.210	NH2	A_GLU.212	OE2	3.118
6N16	B_ARG.24	NH1	B_ASP.70	OD1	3.099
6N16	B_ARG.24	NH2	B_ASP.70	OD1	2.017
6N16	B_ARG.24	NH2	B_ASP.70	OD2	3.393
6N16	B_HIS.30E	ND1	B_GLU.50	OE2	3.843
6N16	B_ARG.54	NH1	B_ASP.60	OD1	2.491
6N16	B_ARG.61	NH1	B_GLU.81	OE1	2.899
6N16	B_ARG.61	NH1	B_GLU.81	OE2	3.698
6N16	B_ARG.61	NH1	B_ASP.82	OD2	3.838
6N16	B_ARG.61	NH2	B_GLU.79	OE1	3.749
6N16	B_ARG.61	NH2	B_GLU.79	OE2	2.925
6N16	B_ARG.61	NH2	B_ASP.82	OD1	2.769
6N16	B_ARG.61	NH2	B_ASP.82	OD2	3.263
6N16	B_ARG.77	NH1	B_GLU.79	OE1	3.315
6N16	B_LYS.169	NZ	B_ASP.167	OD2	3.870
6N16	B_HIS.189	ND1	B_ASP.151	OD1	3.412
6N16	H_ARG.38	NH1	H_GLU.46	OE2	3.288
6N16	H_ARG.38	NH1	H_ASP.86	OD1	3.675
6N16	H_ARG.38	NH2	H_ASP.86	OD1	2.691
6N16	H_ARG.66	NH1	H_ASP.86	OD1	3.216
6N16	H_ARG.66	NH1	H_ASP.86	OD2	3.793
6N16	H_ARG.66	NH2	H_ASP.86	OD1	3.587
6N16	H_ARG.66	NH2	H_ASP.86	OD2	3.090
6N16	H_LYS.143	NZ	H_ASP.144	OD1	3.308
6N16	H_LYS.143	NZ	H_ASP.144	OD2	3.890
6N16	H_HIS.164	NE2	L_ASP.167	OD1	3.075
6N16	H_ARG.210	NH1	H_GLU.212	OE1	3.730
6N16	H_ARG.210	NH1	H_GLU.212	OE2	3.198
6N16	H_ARG.210	NH2	H_GLU.212	OE1	3.203
6N16	J_ARG.24	NH1	J_ASP.70	OD1	2.082
6N16	J_ARG.24	NH1	J_ASP.70	OD2	2.995
6N16	J_ARG.24	NH2	J_ASP.70	OD1	2.960
6N16	J_ARG.24	NH2	J_ASP.70	OD2	3.355
6N16	J_ARG.54	NH1	J_ASP.60	OD1	2.428
6N16	J_ARG.54	NH2	J_ASP.60	OD1	2.646
6N16	J_ARG.61	NH1	J_GLU.81	OE2	3.475
6N16	J_ARG.61	NH1	J_ASP.82	OD1	3.146
6N16	J_ARG.61	NH1	J_ASP.82	OD2	3.392

6N16	J_ARG_61	NH2	J_GLU_79	OE1	3.524
6N16	J_ARG_77	NH1	J_GLU_79	OE1	2.977
6N16	J_ARG_77	NH1	J_GLU_79	OE2	2.495
6N16	J_HIS_189	ND1	J_ASP_151	OD1	2.409
6N16	J_LYS_190	NZ	J_ASP_151	OD1	3.722
6N16	J_LYS_190	NZ	J_ASP_151	OD2	3.788
6N16	K_ARG_38	NH1	K_GLU_46	OE1	3.313
6N16	K_ARG_38	NH1	K_ASP_86	OD1	3.587
6N16	K_ARG_38	NH2	K_ASP_86	OD1	2.713
6N16	K_ARG_66	NH1	K_ASP_86	OD1	2.932
6N16	K_ARG_66	NH1	K_ASP_86	OD2	3.658
6N16	K_ARG_66	NH2	K_ASP_86	OD1	3.552
6N16	K_ARG_66	NH2	K_ASP_86	OD2	2.933
6N16	K_LYS_71	NZ	K_GLU_55	OE1	3.671
6N16	K_LYS_71	NZ	K_GLU_55	OE2	3.555
6N16	K_ARG_105	NH2	H_GLU_64	OE1	2.463
6N16	K_ARG_105	NH2	H_GLU_64	OE2	3.174
6N16	K_ARG_210	NH1	K_GLU_212	OE1	2.599
6N16	K_ARG_210	NH1	K_GLU_212	OE2	3.558
6N16	L_ARG_54	NH1	L_ASP_60	OD2	3.141
6N16	L_ARG_61	NH1	L_ASP_82	OD1	2.699
6N16	L_ARG_61	NH1	L_ASP_82	OD2	3.825
6N16	L_ARG_61	NH2	L_GLU_79	OE1	2.631
6N16	L_ARG_61	NH2	L_GLU_79	OE2	3.838
6N16	L_ARG_61	NH2	L_GLU_81	OE2	3.819
6N16	L_ARG_61	NH2	L_ASP_82	OD1	3.883
6N16	L_ARG_61	NH2	L_ASP_82	OD2	3.728
6N16	L_ARG_77	NH1	L_GLU_79	OE2	2.621
6N16	L_ARG_77	NH2	L_GLU_79	OE2	3.210
6N16	L_LYS_103	NZ	L_GLU_165	OE2	3.676
6N16	L_LYS_149	NZ	L_GLU_195	OE2	2.385
6N16	L_LYS_155	NZ	L_GLU_185	OE2	3.497
6N16	L_HIS_189	ND1	L_ASP_151	OD2	2.964
6N16	C_ARG_38	NH1	C_ASP_86	OD1	2.762
6N16	C_ARG_38	NH2	C_GLU_46	OE2	2.909
6N16	C_ARG_38	NH2	C_ASP_86	OD1	3.930
6N16	C_ARG_66	NH1	C_ASP_86	OD1	2.966
6N16	C_ARG_66	NH1	C_ASP_86	OD2	3.602
6N16	C_ARG_66	NH2	C_ASP_86	OD1	3.584
6N16	C_ARG_66	NH2	C_ASP_86	OD2	2.985
6N16	C_LYS_209	NZ	D_ASP_123	OD2	3.251
6N16	C_ARG_210	NH1	C_GLU_212	OE1	2.646
6N16	C_ARG_210	NH2	C_GLU_212	OE1	2.972
6N16	D_ARG_24	NH2	D_ASP_70	OD1	3.142
6N16	D_ARG_24	NH2	D_ASP_70	OD2	3.869
6N16	D_ARG_54	NH1	D_ASP_60	OD1	3.199
6N16	D_ARG_54	NH1	D_ASP_60	OD2	3.672
6N16	D_ARG_54	NH2	D_ASP_60	OD1	3.573
6N16	D_ARG_54	NH2	D_ASP_60	OD2	3.601
6N16	D_ARG_61	NH1	D_GLU_79	OE2	2.680
6N16	D_ARG_61	NH2	D_GLU_79	OE2	3.457
6N16	D_ARG_77	NH2	D_GLU_79	OE1	2.307
6N16	D_ARG_77	NH2	D_GLU_79	OE2	3.456
6N16	D_LYS_103	NZ	D_GLU_165	OE1	3.221
6N16	D_LYS_103	NZ	D_GLU_165	OE2	3.677
6N16	D_LYS_126	NZ	D_GLU_122	OE1	3.518
6N16	D_LYS_149	NZ	D_GLU_195	OE1	3.379
6N1V	3_ARG_39	NH1	3_ASP_91	OD1	3.220

6N1V	3_ARG_39	NH2	3_GLU_47	OE1	2.848
6N1V	3_ARG_39	NH2	3_GLU_47	OE2	2.999
6N1V	3_LYS_44	NZ	4_ASP_86	OD1	3.675
6N1V	3_LYS_44	NZ	4_ASP_86	OD2	2.472
6N1V	3_LYS_44	NZ	4_GLU_106	OE1	3.723
6N1V	3_ARG_45	NH2	3_GLU_47	OE1	3.739
6N1V	3_ARG_138	NH1	4_GLU_214	OE1	2.573
6N1V	3_ARG_138	NH1	4_GLU_214	OE2	3.070
6N1V	3_ARG_138	NH2	4_GLU_214	OE2	3.291
6N1V	3_LYS_152	NZ	3_ASP_153	OD2	3.384
6N1V	3_LYS_218	NZ	4_GLU_127	OE1	3.611
6N1V	3_ARG_219	NH1	3_GLU_221	OE1	3.404
6N1V	4_LYS_54	NZ	4_GLU_51	OE1	3.248
6N1V	4_ARG_62	NH1	4_ASP_83	OD1	3.753
6N1V	4_ARG_62	NH1	4_ASP_83	OD2	3.947
6N1V	4_LYS_114	NZ	4_GLU_202	OE1	3.543
6N1V	4_LYS_114	NZ	4_GLU_202	OE2	2.746
6N1V	4_LYS_153	NZ	4_GLU_207	OE1	3.065
6N1V	4_LYS_153	NZ	4_GLU_207	OE2	3.086
6N1V	4_LYS_170	NZ	4_GLU_84	OE1	2.379
6N1V	4_LYS_175	NZ	4_ASP_142	OD1	3.116
6N1V	4_LYS_175	NZ	4_ASP_142	OD2	2.712
6N1V	4_HIS_192	ND1	4_ASP_155	OD1	3.682
6N1V	4_HIS_192	ND1	4_ASP_155	OD2	2.769
6N1V	B_LYS_46	NZ	B_GLU_492	OE2	2.855
6N1V	B_LYS_231	NZ	B_GLU_268	OE1	3.616
6N1V	B_LYS_231	NZ	B_GLU_268	OE2	2.737
6N1V	B_LYS_282	NZ	g_ASP_114	OD2	3.730
6N1V	B_ARG_298	NH1	B_GLU_381	OE1	3.416
6N1V	B_ARG_298	NH1	B_GLU_381	OE2	3.774
6N1V	B_ARG_298	NH2	B_GLU_381	OE1	3.507
6N1V	B_ARG_308	NH1	B_GLU_164	OE1	3.519
6N1V	B_ARG_308	NH1	B_GLU_164	OE2	2.477
6N1V	B_ARG_429	NH1	B_ASP_113	OD2	3.774
6N1V	B_ARG_429	NH2	B_ASP_113	OD1	3.650
6N1V	B_ARG_429	NH2	B_ASP_113	OD2	2.335
6N1V	B_ARG_469	NH1	B_ASP_457	OD1	3.545
6N1V	B_ARG_469	NH1	B_ASP_457	OD2	2.329
6N1V	B_ARG_476	NH1	B_GLU_102	OE2	3.982
6N1V	B_ARG_476	NH1	B_ASP_474	OD2	3.112
6N1V	B_ARG_476	NH2	B_GLU_102	OE1	3.903
6N1V	B_ARG_476	NH2	B_GLU_102	OE2	3.744
6N1V	B_ARG_480	NH1	B_ASP_477	OD1	2.992
6N1V	B_LYS_487	NZ	B_ASP_47	OD2	2.431
6N1V	B_ARG_504	NH2	D_GLU_657	OE2	3.905
6N1V	F_ARG_542	NH2	D_GLU_647	OE1	3.326
6N1V	F_ARG_542	NH2	D_GLU_647	OE2	2.831
6N1V	F_ARG_579	NH2	D_GLU_584	OE1	3.581
6N1V	F_ARG_588	NH2	F_GLU_584	OE2	2.394
6N1V	F_ARG_617	NH1	F_GLU_634	OE1	2.879
6N1V	F_ARG_617	NH1	F_GLU_634	OE2	2.871
6N1V	F_ARG_617	NH2	F_GLU_621	OE1	3.225
6N1V	Y_ARG_38	NH1	Y_ASP_86	OD1	2.536
6N1V	Y_ARG_38	NH2	Y_GLU_46	OE1	3.284
6N1V	Y_ARG_66	NH1	Y_ASP_86	OD2	3.359
6N1V	Y_ARG_66	NH2	Y_ASP_86	OD1	3.775
6N1V	Y_ARG_66	NH2	Y_ASP_86	OD2	3.105
6N1V	Y_LYS_73	NZ	Y_ASP_53	OD1	3.985

6N1V	Y_LYS_73	NZ	Y_ASP_53	OD2	2.420
6N1V	a_ARG_61	NH1	a_ASP_60	OD1	2.807
6N1V	g_LYS_19	NZ	g_GLU_89	OE1	3.749
6N1V	g_ARG_38	NH1	g_GLU_46	OE1	3.909
6N1V	g_ARG_38	NH1	g_GLU_46	OE2	3.659
6N1V	g_ARG_38	NH2	g_ASP_97	OD1	3.891
6N1V	g_ARG_72	NH1	B_ASP_368	OD2	3.927
6N1V	g_ARG_72	NH2	B_ASP_368	OD2	3.974
6N1V	i_ARG_61	NH2	i_ASP_82	OD1	3.042
6N1V	i_ARG_61	NH2	i_ASP_82	OD2	3.088
6N1V	l_ARG_39	NH1	l_ASP_91	OD1	3.219
6N1V	l_ARG_39	NH2	l_GLU_47	OE1	2.847
6N1V	l_ARG_39	NH2	l_GLU_47	OE2	3.000
6N1V	l_LYS_44	NZ	2_ASP_86	OD1	3.676
6N1V	l_LYS_44	NZ	2_ASP_86	OD2	2.473
6N1V	l_LYS_44	NZ	2_GLU_106	OE1	3.723
6N1V	l_ARG_45	NH2	l_GLU_47	OE1	3.739
6N1V	l_ARG_138	NH1	2_GLU_214	OE1	2.573
6N1V	l_ARG_138	NH1	2_GLU_214	OE2	3.069
6N1V	l_ARG_138	NH2	2_GLU_214	OE2	3.291
6N1V	l_LYS_152	NZ	l_ASP_153	OD2	3.384
6N1V	l_LYS_218	NZ	2_GLU_127	OE1	3.611
6N1V	l_ARG_219	NH1	l_GLU_221	OE1	3.404
6N1V	2_LYS_54	NZ	2_GLU_51	OE1	3.247
6N1V	2_ARG_62	NH1	2_ASP_83	OD1	3.752
6N1V	2_ARG_62	NH1	2_ASP_83	OD2	3.947
6N1V	2_LYS_114	NZ	2_GLU_202	OE1	3.543
6N1V	2_LYS_114	NZ	2_GLU_202	OE2	2.746
6N1V	2_LYS_153	NZ	2_GLU_207	OE1	3.064
6N1V	2_LYS_153	NZ	2_GLU_207	OE2	3.086
6N1V	2_LYS_170	NZ	2_GLU_84	OE1	2.379
6N1V	2_LYS_175	NZ	2_ASP_142	OD1	3.116
6N1V	2_LYS_175	NZ	2_ASP_142	OD2	2.712
6N1V	2_HIS_192	ND1	2_ASP_155	OD1	3.682
6N1V	2_HIS_192	ND1	2_ASP_155	OD2	2.769
6N1V	A_LYS_46	NZ	A_GLU_492	OE2	2.855
6N1V	A_LYS_231	NZ	A_GLU_268	OE1	3.617
6N1V	A_LYS_231	NZ	A_GLU_268	OE2	2.737
6N1V	A_LYS_282	NZ	f_ASP_114	OD2	3.729
6N1V	A_ARG_298	NH1	A_GLU_381	OE1	3.416
6N1V	A_ARG_298	NH1	A_GLU_381	OE2	3.774
6N1V	A_ARG_298	NH2	A_GLU_381	OE1	3.507
6N1V	A_ARG_308	NH1	A_GLU_164	OE1	3.518
6N1V	A_ARG_308	NH1	A_GLU_164	OE2	2.477
6N1V	A_ARG_429	NH1	A_ASP_113	OD2	3.775
6N1V	A_ARG_429	NH2	A_ASP_113	OD1	3.650
6N1V	A_ARG_429	NH2	A_ASP_113	OD2	2.336
6N1V	A_ARG_469	NH1	A_ASP_457	OD1	3.546
6N1V	A_ARG_469	NH1	A_ASP_457	OD2	2.329
6N1V	A_ARG_476	NH1	A_GLU_102	OE2	3.981
6N1V	A_ARG_476	NH1	A_ASP_474	OD2	3.112
6N1V	A_ARG_476	NH2	A_GLU_102	OE1	3.904
6N1V	A_ARG_476	NH2	A_GLU_102	OE2	3.744
6N1V	A_ARG_480	NH1	A_ASP_477	OD1	2.992
6N1V	A_LYS_487	NZ	A_ASP_47	OD2	2.431
6N1V	A_ARG_504	NH2	F_GLU_657	OE2	3.909
6N1V	E_ARG_542	NH2	F_GLU_647	OE1	3.328
6N1V	E_ARG_542	NH2	F_GLU_647	OE2	2.831

6N1V	E_ARG_579	NH2	F_GLU_584	OE1	3.583
6N1V	E_ARG_588	NH2	E_GLU_584	OE2	2.393
6N1V	E_ARG_617	NH1	E_GLU_634	OE1	2.879
6N1V	E_ARG_617	NH1	E_GLU_634	OE2	2.871
6N1V	E_ARG_617	NH2	E_GLU_621	OE1	3.225
6N1V	X_ARG_38	NH1	X_ASP_86	OD1	2.536
6N1V	X_ARG_38	NH2	X_GLU_46	OE1	3.284
6N1V	X_ARG_66	NH1	X_ASP_86	OD2	3.359
6N1V	X_ARG_66	NH2	X_ASP_86	OD1	3.775
6N1V	X_ARG_66	NH2	X_ASP_86	OD2	3.105
6N1V	X_LYS_73	NZ	X_ASP_53	OD1	3.985
6N1V	X_LYS_73	NZ	X_ASP_53	OD2	2.420
6N1V	Z_ARG_61	NH1	Z_ASP_60	OD1	2.807
6N1V	f_LYS_19	NZ	f_GLU_89	OE1	3.748
6N1V	f_ARG_38	NH1	f_GLU_46	OE1	3.909
6N1V	f_ARG_38	NH1	f_GLU_46	OE2	3.659
6N1V	f_ARG_38	NH2	f_ASP_97	OD1	3.891
6N1V	f_ARG_72	NH1	A_ASP_368	OD2	3.927
6N1V	f_ARG_72	NH2	A_ASP_368	OD2	3.974
6N1V	h_ARG_61	NH2	h_ASP_82	OD1	3.042
6N1V	h_ARG_61	NH2	h_ASP_82	OD2	3.088
6N1V	C_LYS_46	NZ	C_GLU_492	OE2	2.855
6N1V	C_LYS_231	NZ	C_GLU_268	OE1	3.617
6N1V	C_LYS_231	NZ	C_GLU_268	OE2	2.737
6N1V	C_LYS_282	NZ	Q_ASP_114	OD2	3.730
6N1V	C_ARG_298	NH1	C_GLU_381	OE1	3.416
6N1V	C_ARG_298	NH1	C_GLU_381	OE2	3.775
6N1V	C_ARG_298	NH2	C_GLU_381	OE1	3.507
6N1V	C_ARG_308	NH1	C_GLU_164	OE1	3.518
6N1V	C_ARG_308	NH1	C_GLU_164	OE2	2.477
6N1V	C_ARG_429	NH1	C_ASP_113	OD2	3.775
6N1V	C_ARG_429	NH2	C_ASP_113	OD1	3.651
6N1V	C_ARG_429	NH2	C_ASP_113	OD2	2.336
6N1V	C_ARG_469	NH1	C_ASP_457	OD1	3.545
6N1V	C_ARG_469	NH1	C_ASP_457	OD2	2.329
6N1V	C_ARG_476	NH1	C_GLU_102	OE2	3.982
6N1V	C_ARG_476	NH1	C_ASP_474	OD2	3.112
6N1V	C_ARG_476	NH2	C_GLU_102	OE1	3.904
6N1V	C_ARG_476	NH2	C_GLU_102	OE2	3.744
6N1V	C_ARG_480	NH1	C_ASP_477	OD1	2.992
6N1V	C_LYS_487	NZ	C_ASP_47	OD2	2.431
6N1V	C_ARG_504	NH2	E_GLU_657	OE2	3.907
6N1V	D_ARG_542	NH2	E_GLU_647	OE1	3.330
6N1V	D_ARG_542	NH2	E_GLU_647	OE2	2.832
6N1V	D_ARG_579	NH2	E_GLU_584	OE1	3.585
6N1V	D_ARG_588	NH2	D_GLU_584	OE2	2.394
6N1V	D_ARG_617	NH1	D_GLU_634	OE1	2.880
6N1V	D_ARG_617	NH1	D_GLU_634	OE2	2.871
6N1V	D_ARG_617	NH2	D_GLU_621	OE1	3.225
6N1V	H_ARG_39	NH1	H_ASP_91	OD1	3.220
6N1V	H_ARG_39	NH2	H_GLU_47	OE1	2.848
6N1V	H_ARG_39	NH2	H_GLU_47	OE2	3.000
6N1V	H_LYS_44	NZ	L_ASP_86	OD1	3.676
6N1V	H_LYS_44	NZ	L_ASP_86	OD2	2.472
6N1V	H_LYS_44	NZ	L_GLU_106	OE1	3.722
6N1V	H_ARG_45	NH2	H_GLU_47	OE1	3.739
6N1V	H_ARG_138	NH1	L_GLU_214	OE1	2.573
6N1V	H_ARG_138	NH1	L_GLU_214	OE2	3.069

6N1V	H_ARG_138	NH2	L_GLU_214	OE2	3.291
6N1V	H_LYS_152	NZ	H_ASP_153	OD2	3.384
6N1V	H_LYS_218	NZ	L_GLU_127	OE1	3.611
6N1V	H_ARG_219	NH1	H_GLU_221	OE1	3.404
6N1V	L_LYS_54	NZ	L_GLU_51	OE1	3.248
6N1V	L_ARG_62	NH1	L_ASP_83	OD1	3.753
6N1V	L_ARG_62	NH1	L_ASP_83	OD2	3.947
6N1V	L_LYS_114	NZ	L_GLU_202	OE1	3.542
6N1V	L_LYS_114	NZ	L_GLU_202	OE2	2.746
6N1V	L_LYS_153	NZ	L_GLU_207	OE1	3.065
6N1V	L_LYS_153	NZ	L_GLU_207	OE2	3.087
6N1V	L_LYS_170	NZ	L_GLU_84	OE1	2.379
6N1V	L_LYS_175	NZ	L_ASP_142	OD1	3.116
6N1V	L_LYS_175	NZ	L_ASP_142	OD2	2.712
6N1V	L_HIS_192	ND1	L_ASP_155	OD1	3.682
6N1V	L_HIS_192	ND1	L_ASP_155	OD2	2.769
6N1V	M_ARG_38	NH1	M_ASP_86	OD1	2.536
6N1V	M_ARG_38	NH2	M_GLU_46	OE1	3.284
6N1V	M_ARG_66	NH1	M_ASP_86	OD2	3.359
6N1V	M_ARG_66	NH2	M_ASP_86	OD1	3.775
6N1V	M_ARG_66	NH2	M_ASP_86	OD2	3.105
6N1V	M_LYS_73	NZ	M_ASP_53	OD1	3.985
6N1V	M_LYS_73	NZ	M_ASP_53	OD2	2.420
6N1V	N_ARG_61	NH1	N_ASP_60	OD1	2.808
6N1V	Q_LYS_19	NZ	Q_GLU_89	OE1	3.749
6N1V	Q_ARG_38	NH1	Q_GLU_46	OE1	3.909
6N1V	Q_ARG_38	NH1	Q_GLU_46	OE2	3.659
6N1V	Q_ARG_38	NH2	Q_ASP_97	OD1	3.891
6N1V	Q_ARG_72	NH1	C_ASP_368	OD2	3.927
6N1V	Q_ARG_72	NH2	C_ASP_368	OD2	3.975
6N1V	R_ARG_61	NH2	R_ASP_82	OD1	3.042
6N1V	R_ARG_61	NH2	R_ASP_82	OD2	3.088
6N1W	2_LYS_46	NZ	2_GLU_492	OE2	3.928
6N1W	2_LYS_227	NZ	2_GLU_83	OE1	2.543
6N1W	2_LYS_231	NZ	2_GLU_268	OE1	2.454
6N1W	2_LYS_231	NZ	2_GLU_268	OE2	3.957
6N1W	2_LYS_231	NZ	2_GLU_269	OE1	3.998
6N1W	2_HIS_249	NE2	2_GLU_83	OE1	3.939
6N1W	2_LYS_282	NZ	2_GLU_275	OE1	3.006
6N1W	2_ARG_298	NH1	2_GLU_381	OE1	3.635
6N1W	2_ARG_298	NH1	2_GLU_381	OE2	2.558
6N1W	2_ARG_298	NH2	2_GLU_381	OE1	3.709
6N1W	2_ARG_298	NH2	2_GLU_381	OE2	3.969
6N1W	2_ARG_308	NH1	2_GLU_164	OE1	3.421
6N1W	2_ARG_308	NH1	2_GLU_164	OE2	3.903
6N1W	2_ARG_327	NH2	m_GLU_100I	OE1	3.996
6N1W	2_LYS_421	NZ	2_ASP_180	OD1	3.450
6N1W	2_ARG_429	NH1	2_ASP_113	OD2	3.966
6N1W	2_ARG_429	NH2	2_ASP_113	OD1	3.893
6N1W	2_ARG_429	NH2	2_ASP_113	OD2	2.506
6N1W	2_ARG_469	NH2	2_ASP_457	OD2	2.809
6N1W	2_ARG_476	NH1	2_GLU_102	OE1	2.957
6N1W	2_ARG_476	NH1	2_GLU_102	OE2	3.101
6N1W	2_ARG_476	NH2	2_GLU_102	OE1	3.474
6N1W	2_ARG_480	NH1	2_ASP_477	OD1	2.941
6N1W	2_LYS_487	NZ	2_ASP_47	OD1	2.806
6N1W	2_LYS_487	NZ	2_ASP_47	OD2	3.509
6N1W	2_ARG_504	NH2	d_GLU_657	OE2	3.118

6N1W	3_ARG_38	NH1	3_GLU_46	OE1	2.665
6N1W	3_ARG_38	NH1	3_GLU_46	OE2	3.250
6N1W	3_ARG_38	NH2	3_ASP_86	OD1	2.625
6N1W	3_ARG_66	NH1	3_ASP_86	OD2	3.781
6N1W	3_LYS_71	NZ	3_GLU_55	OE2	3.265
6N1W	3_ARG_100H	NH1	3_ASP_101	OD2	3.227
6N1W	3_ARG_100H	NH2	4_ASP_91	OD2	3.241
6N1W	4_ARG_61	NH1	4_GLU_81	OE2	3.361
6N1W	4_ARG_61	NH1	4_ASP_82	OD1	3.254
6N1W	4_ARG_61	NH2	4_ASP_82	OD1	3.059
6N1W	4_ARG_61	NH2	4_ASP_82	OD2	2.679
6N1W	5_ARG_38	NH1	5_ASP_86	OD1	2.691
6N1W	5_ARG_38	NH2	5_GLU_46	OE1	3.484
6N1W	5_ARG_38	NH2	5_GLU_46	OE2	3.816
6N1W	5_ARG_38	NH2	5_ASP_86	OD1	3.929
6N1W	5_ARG_66	NH1	5_ASP_86	OD2	3.620
6N1W	5_ARG_66	NH2	5_ASP_86	OD1	3.504
6N1W	5_LYS_73	NZ	5_ASP_53	OD1	3.480
6N1W	5_LYS_73	NZ	5_ASP_53	OD2	2.933
6N1W	7_ARG_60	NH2	7_ASP_81	OD1	2.923
6N1W	7_ARG_60	NH2	7_ASP_81	OD2	2.939
6N1W	8_ARG_38	NH1	8_GLU_46	OE1	3.713
6N1W	8_ARG_38	NH1	8_ASP_86	OD1	3.761
6N1W	8_ARG_38	NH2	8_ASP_86	OD1	3.294
6N1W	8_ARG_66	NH1	8_ASP_86	OD2	3.879
6N1W	8_ARG_66	NH2	8_ASP_86	OD2	2.655
6N1W	A_ARG_542	NH1	d_GLU_647	OE1	3.516
6N1W	A_ARG_542	NH1	d_GLU_647	OE2	3.474
6N1W	A_ARG_542	NH2	d_GLU_647	OE1	2.848
6N1W	A_ARG_579	NH2	d_GLU_584	OE2	3.464
6N1W	A_LYS_601	NZ	d_GLU_654	OE1	3.802
6N1W	A_LYS_601	NZ	d_GLU_654	OE2	3.060
6N1W	A_ARG_617	NH1	A_GLU_634	OE2	3.959
6N1W	A_ARG_617	NH2	A_GLU_621	OE1	3.529
6N1W	C_LYS_46	NZ	C_GLU_492	OE2	3.859
6N1W	C_LYS_97	NZ	C_GLU_275	OE2	3.973
6N1W	C_LYS_227	NZ	C_GLU_83	OE1	2.695
6N1W	C_LYS_231	NZ	C_GLU_268	OE1	2.473
6N1W	C_LYS_231	NZ	C_GLU_268	OE2	3.970
6N1W	C_LYS_231	NZ	C_GLU_269	OE1	3.984
6N1W	C_HIS_249	NE2	C_GLU_83	OE1	3.866
6N1W	C_LYS_282	NZ	C_GLU_275	OE1	3.039
6N1W	C_ARG_298	NH1	C_GLU_381	OE1	3.780
6N1W	C_ARG_298	NH1	C_GLU_381	OE2	2.649
6N1W	C_ARG_298	NH2	C_GLU_381	OE1	3.748
6N1W	C_ARG_298	NH2	C_GLU_381	OE2	3.927
6N1W	C_ARG_308	NH1	C_GLU_164	OE1	3.469
6N1W	C_ARG_308	NH1	C_GLU_164	OE2	3.901
6N1W	C_LYS_421	NZ	C_ASP_180	OD1	3.498
6N1W	C_ARG_429	NH1	C_ASP_113	OD2	3.958
6N1W	C_ARG_429	NH2	C_ASP_113	OD1	3.756
6N1W	C_ARG_429	NH2	C_ASP_113	OD2	2.445
6N1W	C_ARG_469	NH2	C_ASP_457	OD2	2.859
6N1W	C_ARG_476	NH1	C_GLU_102	OE1	3.094
6N1W	C_ARG_476	NH1	C_GLU_102	OE2	3.309
6N1W	C_ARG_476	NH2	C_GLU_102	OE1	3.512
6N1W	C_ARG_480	NH1	C_ASP_477	OD1	2.924
6N1W	C_LYS_487	NZ	C_ASP_47	OD1	2.763

6N1W	C_LYS_487	NZ	C_ASP_47	OD2	3.509
6N1W	C_ARG_504	NH2	A_GLU_657	OE2	3.221
6N1W	D_ARG_542	NH1	A_GLU_647	OE1	3.273
6N1W	D_ARG_542	NH1	A_GLU_647	OE2	3.289
6N1W	D_ARG_542	NH2	A_GLU_647	OE1	2.942
6N1W	D_ARG_579	NH1	A_GLU_584	OE1	3.854
6N1W	D_ARG_579	NH2	A_GLU_584	OE2	3.567
6N1W	D_LYS_601	NZ	A_GLU_654	OE1	3.837
6N1W	D_LYS_601	NZ	A_GLU_654	OE2	3.044
6N1W	D_ARG_617	NH1	D_GLU_634	OE2	3.956
6N1W	D_ARG_617	NH2	D_GLU_621	OE1	3.541
6N1W	H_ARG_38	NH1	H_GLU_46	OE1	2.685
6N1W	H_ARG_38	NH1	H_GLU_46	OE2	3.187
6N1W	H_ARG_38	NH2	H_ASP_86	OD1	2.618
6N1W	H_ARG_66	NH1	H_ASP_86	OD2	3.806
6N1W	H_LYS_71	NZ	H_GLU_55	OE2	3.251
6N1W	H_ARG_100H	NH1	H_ASP_101	OD2	3.211
6N1W	H_ARG_100H	NH2	L_ASP_91	OD2	3.150
6N1W	L_ARG_61	NH1	L_GLU_81	OE2	3.442
6N1W	L_ARG_61	NH1	L_ASP_82	OD1	3.265
6N1W	L_ARG_61	NH2	L_ASP_82	OD1	3.076
6N1W	L_ARG_61	NH2	L_ASP_82	OD2	2.697
6N1W	M_ARG_38	NH1	M_ASP_86	OD1	2.569
6N1W	M_ARG_38	NH2	M_GLU_46	OE1	3.511
6N1W	M_ARG_38	NH2	M_GLU_46	OE2	3.792
6N1W	M_ARG_38	NH2	M_ASP_86	OD1	3.908
6N1W	M_ARG_66	NH1	M_ASP_86	OD2	3.739
6N1W	M_ARG_66	NH2	M_ASP_86	OD1	3.607
6N1W	M_LYS_73	NZ	M_ASP_53	OD1	3.504
6N1W	M_LYS_73	NZ	M_ASP_53	OD2	2.877
6N1W	Q_ARG_38	NH1	Q_GLU_46	OE1	3.699
6N1W	Q_ARG_38	NH1	Q_ASP_86	OD1	3.715
6N1W	Q_ARG_38	NH2	Q_ASP_86	OD1	3.040
6N1W	Q_ARG_66	NH1	Q_ASP_86	OD2	3.762
6N1W	Q_ARG_66	NH2	Q_ASP_86	OD2	2.524
6N1W	R_ARG_60	NH2	R_ASP_81	OD1	2.849
6N1W	R_ARG_60	NH2	R_ASP_81	OD2	2.945
6N1W	c_LYS_46	NZ	c_GLU_492	OE2	3.862
6N1W	c_LYS_227	NZ	c_GLU_83	OE1	2.652
6N1W	c_LYS_231	NZ	c_GLU_268	OE1	2.434
6N1W	c_LYS_231	NZ	c_GLU_268	OE2	3.951
6N1W	c_LYS_231	NZ	c_GLU_269	OE1	3.890
6N1W	c_HIS_249	NE2	c_GLU_83	OE1	3.931
6N1W	c_LYS_282	NZ	c_GLU_275	OE1	3.038
6N1W	c_ARG_298	NH1	c_GLU_381	OE1	3.531
6N1W	c_ARG_298	NH1	c_GLU_381	OE2	2.444
6N1W	c_ARG_298	NH2	c_GLU_381	OE1	3.806
6N1W	c_ARG_308	NH1	c_GLU_164	OE1	3.441
6N1W	c_ARG_308	NH1	c_GLU_164	OE2	3.830
6N1W	c_LYS_421	NZ	c_ASP_180	OD1	3.813
6N1W	c_ARG_429	NH1	c_ASP_113	OD2	3.970
6N1W	c_ARG_429	NH2	c_ASP_113	OD1	3.958
6N1W	c_ARG_429	NH2	c_ASP_113	OD2	2.540
6N1W	c_ARG_469	NH2	c_ASP_457	OD2	2.886
6N1W	c_ARG_476	NH1	c_GLU_102	OE1	2.901
6N1W	c_ARG_476	NH1	c_GLU_102	OE2	3.038
6N1W	c_ARG_476	NH2	c_GLU_102	OE1	3.473
6N1W	c_ARG_480	NH1	c_ASP_477	OD1	2.867

6N1W	c_LYS_487	NZ	c_ASP_47	OD1	2.950
6N1W	c_LYS_487	NZ	c_ASP_47	OD2	3.392
6N1W	c_LYS_487	NZ	c_GLU_91	OE1	3.967
6N1W	c_ARG_504	NH2	D_GLU_657	OE2	3.061
6N1W	d_ARG_542	NH1	D_GLU_647	OE1	3.482
6N1W	d_ARG_542	NH1	D_GLU_647	OE2	3.280
6N1W	d_ARG_542	NH2	D_GLU_647	OE1	2.854
6N1W	d_ARG_579	NH1	D_GLU_584	OE1	3.913
6N1W	d_ARG_579	NH2	D_GLU_584	OE2	3.653
6N1W	d_LYS_601	NZ	D_GLU_654	OE1	3.862
6N1W	d_LYS_601	NZ	D_GLU_654	OE2	3.082
6N1W	d_ARG_617	NH1	d_GLU_634	OE2	3.896
6N1W	d_ARG_617	NH2	d_GLU_621	OE1	3.678
6N1W	h_ARG_38	NH1	h_GLU_46	OE1	2.684
6N1W	h_ARG_38	NH1	h_GLU_46	OE2	3.228
6N1W	h_ARG_38	NH2	h_ASP_86	OD1	2.566
6N1W	h_ARG_66	NH1	h_ASP_86	OD2	3.765
6N1W	h_LYS_71	NZ	h_GLU_55	OE2	3.379
6N1W	h_ARG_100H	NH1	h_ASP_101	OD2	3.191
6N1W	h_ARG_100H	NH2	L_ASP_91	OD2	3.226
6N1W	L_ARG_61	NH1	L_GLU_81	OE2	3.471
6N1W	L_ARG_61	NH1	L_ASP_82	OD1	3.278
6N1W	L_ARG_61	NH2	L_ASP_82	OD1	3.046
6N1W	L_ARG_61	NH2	L_ASP_82	OD2	2.734
6N1W	m_ARG_38	NH1	m_ASP_86	OD1	2.662
6N1W	m_ARG_38	NH2	m_GLU_46	OE1	3.392
6N1W	m_ARG_38	NH2	m_GLU_46	OE2	3.730
6N1W	m_ARG_38	NH2	m_ASP_86	OD1	3.976
6N1W	m_ARG_66	NH1	m_ASP_86	OD2	3.631
6N1W	m_ARG_66	NH2	m_ASP_86	OD1	3.510
6N1W	m_LYS_73	NZ	m_ASP_53	OD1	3.489
6N1W	m_LYS_73	NZ	m_ASP_53	OD2	2.916
6N1W	q_ARG_38	NH1	q_GLU_46	OE1	3.649
6N1W	q_ARG_38	NH1	q_ASP_86	OD1	3.800
6N1W	q_ARG_38	NH2	q_ASP_86	OD1	3.194
6N1W	q_ARG_66	NH1	q_ASP_86	OD2	3.833
6N1W	q_ARG_66	NH2	q_ASP_86	OD2	2.511
6N1W	r_ARG_60	NH2	r_ASP_81	OD1	2.963
6N1W	r_ARG_60	NH2	r_ASP_81	OD2	3.033
6N5B	H_ARG_38	NH1	H_GLU_46	OE1	3.194
6N5B	H_ARG_38	NH1	H_GLU_46	OE2	3.841
6N5B	H_ARG_38	NH2	H_ASP_86	OD1	3.183
6N5B	H_LYS_64	NZ	H_ASP_61	OD1	3.760
6N5B	H_ARG_66	NH1	H_ASP_86	OD1	3.517
6N5B	H_ARG_66	NH1	H_ASP_86	OD2	3.589
6N5B	H_ARG_66	NH2	H_ASP_86	OD2	3.024
6N5B	H_LYS_149	NZ	L_GLU_128	OE2	3.031
6N5B	H_LYS_214	NZ	L_GLU_127	OE2	3.139
6N5B	L_ARG_63	NH2	L_ASP_84	OD1	2.528
6N5B	L_ARG_63	NH2	L_ASP_84	OD2	3.785
6N5B	L_LYS_170	NZ	L_GLU_85	OE2	2.862
6N5B	L_HIS_192	ND1	L_ASP_155	OD2	3.335
6N5B	B_ARG_53	NH1	B_GLU_79	OE1	3.394
6N5B	B_ARG_53	NH2	B_ASP_81	OD1	3.952
6N5B	B_ARG_86	NH2	B_ASP_56	OD1	3.915
6N5B	B_ARG_86	NH2	B_ASP_56	OD2	2.646
6N5B	B_ARG_105	NH2	B_GLU_85	OE1	3.089
6N5B	B_LYS_113	NZ	B_GLU_115	OE1	3.775

6N5B	B_ARG_137	NH1	B_ASP_73	OD1	2.745
6N5B	B_ARG_137	NH1	B_ASP_73	OD2	3.436
6N5B	B_ARG_137	NH2	B_ASP_142	OD2	3.308
6N5B	B_ARG_172	NH1	B_GLU_119	OE2	3.863
6N5B	B_HIS_253	ND1	B_GLU_119	OE1	2.944
6N5B	B_LYS_255	NZ	B_GLU_115	OE2	3.788
6N5D	A_HIS_56	ND1	A_ASP_85	OD2	3.953
6N5D	A_ARG_57	NH2	A_GLU_82	OE1	2.603
6N5D	A_HIS_75	ND1	A_ASP_73	OD1	2.834
6N5D	A_HIS_75	ND1	A_ASP_73	OD2	3.931
6N5D	A_ARG_90	NH2	A_ASP_60	OD1	3.337
6N5D	A_ARG_90	NH2	A_ASP_60	OD2	2.505
6N5D	A_LYS_92	NZ	A_ASP_271	OD2	3.373
6N5D	A_ARG_109	NH1	A_GLU_89	OE1	2.808
6N5D	A_ARG_109	NH1	A_GLU_89	OE2	3.783
6N5D	A_LYS_176	NZ	A_GLU_123	OE2	3.918
6N5D	A_LYS_238	NZ	A_ASP_175	OD1	3.849
6N5D	A_LYS_238	NZ	A_ASP_175	OD2	3.598
6N5D	A_LYS_259	NZ	A_GLU_119	OE2	3.730
6N5D	C_ARG_38	NH2	C_ASP_90	OD1	3.385
6N5D	C_ARG_67	NH1	C_ASP_90	OD1	3.989
6N5D	C_ARG_67	NH1	C_ASP_90	OD2	3.731
6N5D	C_ARG_67	NH2	C_ASP_90	OD1	3.488
6N5D	C_ARG_67	NH2	C_ASP_90	OD2	2.158
6N5D	C_LYS_149	NZ	D_GLU_127	OE2	2.211
6N5D	C_LYS_212	NZ	C_ASP_214	OD1	3.695
6N5D	C_LYS_215	NZ	D_GLU_126	OE1	3.361
6N5D	C_LYS_215	NZ	D_GLU_126	OE2	3.815
6N5D	C_ARG_216	NH1	C_GLU_218	OE1	2.311
6N5D	C_ARG_216	NH1	C_GLU_218	OE2	3.798
6N5D	C_ARG_216	NH2	C_GLU_218	OE1	3.283
6N5D	C_ARG_216	NH2	C_GLU_218	OE2	3.709
6N5D	B_ARG_57	NH2	B_GLU_82	OE1	2.558
6N5D	B_ARG_57	NH2	B_GLU_82	OE2	3.860
6N5D	B_HIS_75	ND1	B_ASP_73	OD1	2.685
6N5D	B_HIS_75	ND1	B_ASP_73	OD2	3.543
6N5D	B_ARG_90	NH2	B_ASP_60	OD1	3.667
6N5D	B_ARG_90	NH2	B_ASP_60	OD2	2.318
6N5D	B_LYS_92	NZ	B_ASP_271	OD2	2.554
6N5D	B_ARG_109	NH1	B_GLU_89	OE1	3.519
6N5D	B_ARG_141	NH1	B_ASP_77	OD2	2.444
6N5D	B_LYS_176	NZ	B_GLU_123	OE1	3.115
6N5D	B_ARG_261	NH2	B_GLU_119	OE1	3.598
6N5D	B_ARG_269	NH2	B_GLU_89	OE1	3.840
6N5D	B_LYS_315	NZ	B_GLU_41	OE1	3.513
6N5D	E_ARG_38	NH1	E_ASP_90	OD1	3.664
6N5D	E_ARG_38	NH2	E_GLU_46	OE1	3.505
6N5D	E_ARG_38	NH2	E_ASP_90	OD1	3.051
6N5D	E_LYS_65	NZ	E_ASP_62	OD1	3.737
6N5D	E_ARG_67	NH1	E_ASP_90	OD2	3.314
6N5D	E_ARG_67	NH2	E_ASP_90	OD1	3.968
6N5D	E_ARG_67	NH2	E_ASP_90	OD2	2.162
6N5D	E_LYS_149	NZ	F_GLU_127	OE2	3.376
6N5D	E_LYS_212	NZ	E_ASP_214	OD1	3.161
6N5D	E_ARG_216	NH2	E_GLU_218	OE2	2.928
6N5D	K_HIS_56	ND1	K_ASP_85	OD2	3.271
6N5D	K_ARG_57	NH2	K_GLU_82	OE1	2.301
6N5D	K_HIS_75	ND1	K_ASP_73	OD1	2.835

6N5D	K_HIS_75	ND1	K_ASP_73	OD2	3.740
6N5D	K_ARG_90	NH2	K_ASP_60	OD1	3.759
6N5D	K_ARG_90	NH2	K_ASP_60	OD2	3.274
6N5D	K_ARG_109	NH1	K_GLU_89	OE1	3.561
6N5D	K_ARG_141	NH1	K_ASP_77	OD2	3.970
6N5D	K_LYS_176	NZ	K_GLU_123	OE2	2.488
6N5D	K_LYS_238	NZ	K_ASP_175	OD1	2.613
6N5D	K_LYS_238	NZ	K_ASP_175	OD2	3.291
6N5D	K_LYS_315	NZ	K_GLU_41	OE1	2.260
6N5D	L_ARG_38	NH1	L_ASP_90	OD1	3.927
6N5D	L_ARG_38	NH2	L_ASP_90	OD1	3.768
6N5D	L_LYS_65	NZ	L_ASP_62	OD2	3.222
6N5D	L_ARG_67	NH1	L_ASP_90	OD1	3.866
6N5D	L_ARG_67	NH1	L_ASP_90	OD2	3.353
6N5D	L_ARG_67	NH2	L_ASP_90	OD1	3.826
6N5D	L_ARG_67	NH2	L_ASP_90	OD2	2.288
6N5D	L_LYS_149	NZ	N_GLU_127	OE2	2.091
6N5D	L_HIS_170	NE2	N_ASP_141	OD2	3.244
6N5D	L_LYS_212	NZ	L_ASP_214	OD1	2.499
6N5D	L_LYS_212	NZ	L_ASP_214	OD2	3.450
6N5D	F_ARG_63	NH2	F_ASP_84	OD1	3.578
6N5D	D_ARG_63	NH2	D_ASP_84	OD1	3.736
6N5D	D_HIS_191	ND1	D_ASP_154	OD1	3.992
6N5D	D_HIS_191	ND1	D_ASP_154	OD2	3.059
6N5E	A_HIS_56	NE2	A_GLU_280	OE2	3.185
6N5E	A_ARG_57	NH2	A_GLU_82	OE1	2.937
6N5E	A_HIS_75	ND1	A_ASP_73	OD1	2.982
6N5E	A_ARG_90	NH2	A_ASP_60	OD2	2.862
6N5E	A_LYS_92	NZ	A_ASP_63	OD1	3.254
6N5E	A_ARG_109	NH2	A_GLU_89	OE1	3.038
6N5E	A_ARG_109	NH2	A_GLU_89	OE2	3.184
6N5E	A_ARG_141	NH1	A_ASP_77	OD2	2.455
6N5E	A_ARG_141	NH2	A_ASP_77	OD2	3.946
6N5E	A_LYS_176	NZ	A_GLU_123	OE1	3.715
6N5E	A_LYS_176	NZ	A_GLU_123	OE2	2.160
6N5E	A_LYS_259	NZ	A_GLU_119	OE2	3.507
6N5E	A_ARG_261	NH2	A_GLU_119	OE1	3.324
6N5E	A_LYS_292	NZ	A_GLU_41	OE1	3.523
6N5E	B_LYS_50	NZ	B_ASP_275	OD2	3.461
6N5E	B_HIS_56	NE2	B_GLU_280	OE1	3.340
6N5E	B_ARG_57	NH2	B_GLU_82	OE1	3.063
6N5E	B_HIS_75	ND1	B_ASP_73	OD1	2.687
6N5E	B_HIS_75	ND1	B_ASP_73	OD2	3.481
6N5E	B_ARG_90	NH2	B_ASP_60	OD1	3.444
6N5E	B_ARG_90	NH2	B_ASP_60	OD2	2.891
6N5E	B_ARG_141	NH1	B_ASP_77	OD2	2.583
6N5E	B_ARG_141	NH2	B_ASP_77	OD2	3.726
6N5E	B_LYS_176	NZ	B_GLU_123	OE1	3.977
6N5E	B_LYS_176	NZ	B_GLU_123	OE2	2.397
6N5E	B_LYS_176	NZ	B_ASP_172	OD1	2.910
6N5E	B_ARG_261	NH2	B_GLU_119	OE1	3.905
6N5E	C_HIS_56	NE2	C_GLU_280	OE1	3.055
6N5E	C_ARG_57	NH2	C_GLU_82	OE1	3.487
6N5E	C_HIS_75	ND1	C_ASP_73	OD1	2.463
6N5E	C_HIS_75	ND1	C_ASP_73	OD2	3.598
6N5E	C_ARG_90	NH2	C_ASP_60	OD1	3.875
6N5E	C_ARG_90	NH2	C_ASP_60	OD2	3.604
6N5E	C_ARG_141	NH1	C_ASP_77	OD1	3.061

6N5E	C_ARG_141	NH1	C_ASP_77	OD2	2.463
6N5E	C_ARG_141	NH2	C_ASP_77	OD1	3.964
6N5E	C_LYS_176	NZ	C_GLU_123	OE2	2.465
6N5E	C_LYS_176	NZ	C_ASP_172	OD2	3.772
6N5E	C_ARG_207	NH1	C_ASP_241	OD1	3.296
6N5E	C_ARG_207	NH2	C_ASP_241	OD1	3.641
6N5E	C_LYS_259	NZ	C_GLU_119	OE1	3.550
6N5E	C_LYS_259	NZ	C_GLU_119	OE2	3.071
6N5E	C_ARG_261	NH2	C_GLU_119	OE1	3.746
6N5E	H_ARG_38	NH2	H_ASP_89	OD1	2.940
6N5E	H_ARG_44	NH2	H_GLU_42	OE1	3.999
6N5E	H_LYS_64	NZ	H_ASP_61	OD1	3.701
6N5E	H_ARG_66	NH1	H_ASP_89	OD2	3.385
6N5E	H_ARG_66	NH2	H_ASP_89	OD2	2.231
6N5E	H_LYS_214	NZ	H_ASP_216	OD1	2.519
6N5E	H_LYS_214	NZ	H_ASP_216	OD2	3.480
6N5E	H_LYS_217	NZ	I_GLU_126	OE2	2.748
6N5E	H_ARG_218	NH1	H_GLU_220	OE2	3.887
6N5E	H_ARG_218	NH2	H_GLU_220	OE2	2.803
6N5E	E_ARG_38	NH1	E_ASP_89	OD1	2.478
6N5E	E_ARG_38	NH2	E_GLU_46	OE1	3.997
6N5E	E_ARG_38	NH2	E_ASP_89	OD1	2.988
6N5E	E_LYS_64	NZ	E_ASP_61	OD1	2.968
6N5E	E_ARG_66	NH1	E_ASP_89	OD1	3.712
6N5E	E_ARG_66	NH1	E_ASP_89	OD2	2.993
6N5E	E_ARG_66	NH2	E_ASP_89	OD2	2.243
6N5E	E_ARG_75	NH1	E_ASP_72	OD2	3.012
6N5E	E_LYS_214	NZ	E_ASP_216	OD1	2.448
6N5E	E_LYS_214	NZ	E_ASP_216	OD2	3.601
6N5E	E_LYS_217	NZ	D_GLU_126	OE1	2.995
6N5E	E_LYS_217	NZ	D_GLU_126	OE2	2.272
6N5E	E_ARG_218	NH1	E_GLU_220	OE1	3.911
6N5E	E_ARG_218	NH1	E_GLU_220	OE2	2.563
6N5E	E_ARG_218	NH2	E_GLU_220	OE2	2.863
6N5E	E_LYS_222	NZ	D_GLU_126	OE1	3.688
6N5E	G_ARG_38	NH1	G_GLU_46	OE2	2.572
6N5E	G_ARG_38	NH2	G_ASP_89	OD1	3.217
6N5E	G_LYS_64	NZ	G_ASP_61	OD1	3.314
6N5E	G_LYS_64	NZ	G_ASP_61	OD2	3.572
6N5E	G_ARG_66	NH2	G_ASP_89	OD1	3.438
6N5E	G_ARG_66	NH2	G_ASP_89	OD2	3.428
6N5E	G_LYS_214	NZ	G_ASP_216	OD1	2.167
6N5E	G_LYS_217	NZ	F_GLU_126	OE2	3.351
6N5E	I_ARG_63	NH2	I_GLU_83	OE1	3.435
6N5E	I_ARG_63	NH2	I_ASP_84	OD1	2.372
6N5E	I_ARG_63	NH2	I_ASP_84	OD2	3.580
6N5E	I_LYS_189	NZ	I_GLU_186	OE1	2.386
6N5E	F_ARG_63	NH2	F_GLU_83	OE2	3.657
6N5E	F_ARG_63	NH2	F_ASP_84	OD1	2.359
6N5E	F_ARG_63	NH2	F_ASP_84	OD2	3.434
6N5E	D_ARG_63	NH2	D_ASP_84	OD1	2.410
6N5E	D_ARG_63	NH2	D_ASP_84	OD2	3.669
6N6B	A_ARG_118	NH1	A_GLU_119	OE2	3.576
6N6B	A_ARG_118	NH2	A_GLU_119	OE2	3.958
6N6B	A_ARG_118	NH2	A_GLU_425	OE1	2.971
6N6B	A_ARG_118	NH2	A_GLU_425	OE2	3.457
6N6B	A_LYS_128	NZ	A_GLU_162	OE1	3.900
6N6B	A_LYS_128	NZ	A_GLU_162	OE2	2.839

6N6B	A_ARG_152	NH2	A_ASP_198	OD1	3.511
6N6B	A_ARG_152	NH2	A_ASP_198	OD2	3.079
6N6B	A_ARG_156	NH1	A_GLU_119	OE1	3.104
6N6B	A_ARG_156	NH1	A_GLU_119	OE2	3.984
6N6B	A_ARG_156	NH2	A_GLU_119	OE1	2.722
6N6B	A_ARG_224	NH2	A_GLU_276	OE2	2.776
6N6B	A_ARG_283	NH2	A_ASP_355	OD2	3.221
6N6B	A_ARG_288	NH1	A_ASP_355	OD1	3.223
6N6B	A_ARG_288	NH1	A_ASP_355	OD2	3.540
6N6B	A_ARG_288	NH2	A_ASP_304	OD1	3.429
6N6B	A_ARG_288	NH2	A_ASP_304	OD2	3.339
6N6B	A_ARG_292	NH1	A_GLU_277	OE1	2.791
6N6B	A_ARG_292	NH1	A_GLU_277	OE2	3.678
6N6B	A_LYS_296	NZ	L_ASP_28	OD1	3.122
6N6B	A_LYS_296	NZ	L_ASP_28	OD2	3.000
6N6B	A_LYS_296	NZ	L_GLU_68	OE2	2.842
6N6B	A_ARG_300	NH1	A_ASP_324	OD1	3.902
6N6B	A_ARG_300	NH2	A_ASP_324	OD1	3.653
6N6B	A_LYS_344	NZ	A_GLU_369	OE1	2.725
6N6B	A_LYS_344	NZ	A_GLU_369	OE2	3.576
6N6B	A_ARG_364	NH1	A_ASP_330	OD1	3.580
6N6B	A_ARG_364	NH2	A_ASP_330	OD1	3.008
6N6B	A_ARG_364	NH2	A_ASP_330	OD2	3.328
6N6B	A_ARG_364	NH2	A_GLU_375	OE2	3.344
6N6B	A_ARG_394	NH2	A_GLU_375	OE1	2.841
6N6B	A_ARG_403	NH1	A_GLU_433	OE1	3.202
6N6B	A_ARG_403	NH2	A_GLU_432	OE1	3.164
6N6B	A_ARG_428	NH1	A_ASP_460	OD2	3.015
6N6B	A_ARG_428	NH2	A_GLU_433	OE1	3.667
6N6B	A_ARG_428	NH2	A_GLU_433	OE2	2.721
6N6B	A_LYS_431	NZ	K_ASP_101	OD1	3.959
6N6B	A_LYS_431	NZ	K_ASP_101	OD2	3.832
6N6B	K_ARG_39	NH1	K_ASP_90	OD1	2.897
6N6B	K_ARG_39	NH2	K_GLU_47	OE2	2.900
6N6B	K_ARG_39	NH2	K_ASP_90	OD1	3.537
6N6B	K_ARG_67	NH1	K_ASP_90	OD1	3.734
6N6B	K_ARG_67	NH1	K_ASP_90	OD2	2.854
6N6B	K_ARG_67	NH2	K_ASP_90	OD1	3.053
6N6B	K_ARG_67	NH2	K_ASP_90	OD2	3.660
6N6B	K_LYS_76	NZ	K_ASP_73	OD2	3.758
6N6B	K_ARG_98	NH2	K_ASP_106	OD1	3.697
6N6B	K_ARG_98	NH2	K_ASP_106	OD2	3.098
6N6B	K_HIS_169	NE2	L_ASP_167	OD1	3.738
6N6B	K_LYS_213	NZ	L_GLU_123	OE1	2.814
6N6B	K_LYS_213	NZ	L_GLU_123	OE2	3.044
6N6B	L_ARG_24	NH2	L_ASP_70	OD1	3.008
6N6B	L_ARG_24	NH2	L_ASP_70	OD2	3.990
6N6B	L_ARG_61	NH1	L_ASP_82	OD1	3.460
6N6B	L_ARG_61	NH1	L_ASP_82	OD2	2.694
6N6B	L_ARG_61	NH2	L_GLU_81	OE1	3.382
6N6B	L_ARG_61	NH2	L_ASP_82	OD1	3.002
6N6B	L_ARG_61	NH2	L_ASP_82	OD2	3.567
6N6B	L_LYS_103	NZ	L_ASP_165	OD2	3.902
6N6B	L_LYS_149	NZ	L_GLU_195	OE2	2.717
6N6B	L_ARG_155	NH1	L_GLU_185	OE2	3.590
6N6B	L_ARG_155	NH2	L_GLU_185	OE1	3.631
6N6B	L_ARG_155	NH2	L_GLU_185	OE2	2.832
6N6B	L_HIS_189	ND1	L_ASP_151	OD2	3.291

6NB6	L_ARG_211	NH1	L_GLU_187	OE1	3.717
6NB5	H_ARG_38	NH1	H_ASP_92	OD2	3.491
6NB5	H_ARG_38	NH2	H_GLU_46	OE1	2.486
6NB5	H_ARG_50	NH2	H_ASP_61	OD2	3.474
6NB5	H_LYS_52	NZ	H_GLU_56	OE2	3.363
6NB5	H_LYS_54	NZ	H_ASP_76	OD2	3.985
6NB5	H_ARG_69	NH1	H_ASP_92	OD1	2.701
6NB5	H_ARG_69	NH1	H_ASP_92	OD2	3.806
6NB5	H_ARG_69	NH2	H_ASP_92	OD1	3.650
6NB5	H_ARG_69	NH2	H_ASP_92	OD2	3.432
6NB5	H_LYS_78	NZ	H_ASP_75	OD2	3.471
6NB5	H_LYS_157	NZ	H_ASP_158	OD1	2.929
6NB5	H_LYS_157	NZ	H_ASP_158	OD2	3.584
6NB5	H_LYS_220	NZ	H_ASP_222	OD1	3.861
6NB5	H_LYS_223	NZ	L_GLU_126	OE1	3.229
6NB5	H_LYS_223	NZ	L_GLU_126	OE2	2.760
6NB5	H_ARG_224	NH2	H_GLU_226	OE2	3.546
6NB5	L_ARG_63	NH2	L_ASP_84	OD1	3.374
6NB5	L_ARG_63	NH2	L_ASP_84	OD2	3.503
6NB5	L_LYS_68	NZ	L_ASP_33	OD2	2.578
6NB5	L_LYS_113	NZ	L_GLU_201	OE1	2.506
6NB5	L_ARG_38	NH1	L_ASP_92	OD1	3.159
6NB5	L_ARG_38	NH2	L_GLU_46	OE1	2.869
6NB5	L_ARG_38	NH2	L_ASP_92	OD1	3.985
6NB5	L_ARG_50	NH1	L_ASP_61	OD2	3.493
6NB5	L_ARG_50	NH2	L_ASP_61	OD1	3.774
6NB5	L_ARG_69	NH1	L_ASP_92	OD1	2.838
6NB5	L_ARG_69	NH1	L_ASP_92	OD2	2.846
6NB5	L_ARG_69	NH2	L_ASP_92	OD1	3.249
6NB5	L_LYS_157	NZ	L_ASP_158	OD1	3.106
6NB5	L_LYS_157	NZ	M_GLU_127	OE2	3.828
6NB5	L_LYS_223	NZ	M_GLU_126	OE2	3.316
6NB5	M_ARG_63	NH1	M_ASP_84	OD1	2.715
6NB5	M_ARG_63	NH1	M_ASP_84	OD2	3.713
6NB5	M_ARG_63	NH2	M_ASP_84	OD1	3.329
6NB5	M_ARG_63	NH2	M_ASP_84	OD2	2.729
6NB5	M_LYS_107	NZ	M_GLU_85	OE1	3.669
6NB5	M_LYS_152	NZ	M_GLU_206	OE1	3.241
6NB5	M_LYS_152	NZ	M_GLU_206	OE2	3.589
6NB5	M_ARG_192	NH1	M_ASP_154	OD2	3.102
6NB8	H_ARG_38	NH1	H_ASP_90	OD1	2.818
6NB8	H_ARG_38	NH2	H_ASP_90	OD1	3.793
6NB8	H_ARG_67	NH1	H_ASP_90	OD1	3.807
6NB8	H_ARG_67	NH1	H_ASP_90	OD2	2.824
6NB8	H_ARG_67	NH2	H_ASP_90	OD1	3.012
6NB8	H_ARG_67	NH2	H_ASP_90	OD2	3.450
6NB8	H_ARG_72	NH2	H_ASP_74	OD1	3.534
6NB8	H_LYS_157	NZ	H_ASP_158	OD1	3.474
6NB8	H_LYS_223	NZ	L_GLU_128	OE1	2.783
6NB8	H_LYS_223	NZ	L_GLU_128	OE2	3.341
6NB8	L_ARG_51	NH1	H_ASP_113	OD1	2.821
6NB8	L_ARG_51	NH2	H_ASP_113	OD1	3.921
6NB8	L_ARG_51	NH2	H_ASP_115	OD1	3.423
6NB8	L_ARG_51	NH2	L_ASP_60	OD1	2.805
6NB8	L_ARG_51	NH2	L_ASP_60	OD2	3.641
6NB8	L_ARG_66	NH2	L_ASP_87	OD1	2.740
6NB8	L_ARG_66	NH2	L_ASP_87	OD2	3.561
6NB8	L_LYS_108	NZ	L_GLU_170	OE1	2.684

6NB8	L_LYS_108	NZ	L_GLU_170	OE2	3.357
6NB8	L_LYS_154	NZ	L_GLU_200	OE1	3.899
6NB8	L_LYS_154	NZ	L_GLU_200	OE2	2.642
6NB8	L_LYS_188	NZ	L_GLU_192	OE1	3.516
6NB8	L_LYS_188	NZ	L_GLU_192	OE2	2.963
6NB8	L_LYS_193	NZ	L_ASP_190	OD1	3.067
6NB8	L_HIS_194	ND1	L_ASP_156	OD2	3.106
6NC2	A_LYS_46	NZ	B_ASP_636	OD1	3.909
6NC2	A_ARG_59	NH1	A_ASP_57	OD1	2.814
6NC2	A_ARG_59	NH1	A_ASP_57	OD2	3.348
6NC2	A_ARG_59	NH2	A_ASP_57	OD1	3.635
6NC2	A_ARG_59	NH2	A_ASP_57	OD2	2.766
6NC2	A_LYS_155	NZ	A_ASP_133	OD1	2.379
6NC2	A_LYS_231	NZ	A_GLU_268	OE2	2.886
6NC2	A_LYS_232	NZ	A_GLU_269	OE1	3.666
6NC2	A_LYS_232	NZ	A_GLU_269	OE2	2.418
6NC2	A_LYS_282	NZ	A_ASP_279	OD2	2.788
6NC2	A_ARG_298	NH1	A_GLU_381	OE1	2.865
6NC2	A_ARG_298	NH1	A_GLU_381	OE2	2.959
6NC2	A_LYS_305	NZ	A_GLU_172	OE1	2.574
6NC2	A_LYS_305	NZ	A_GLU_172	OE2	3.869
6NC2	A_ARG_327	NH2	A_ASP_325	OD2	3.126
6NC2	A_LYS_337	NZ	A_GLU_293	OE1	2.932
6NC2	A_LYS_343	NZ	A_ASP_340	OD1	3.486
6NC2	A_LYS_348	NZ	A_GLU_269	OE1	2.894
6NC2	A_LYS_348	NZ	A_GLU_269	OE2	3.758
6NC2	A_LYS_348	NZ	A_GLU_351	OE2	3.738
6NC2	A_ARG_419	NH2	A_GLU_153	OE2	3.652
6NC2	A_LYS_421	NZ	A_GLU_370	OE2	2.787
6NC2	A_ARG_456	NH2	A_GLU_466	OE1	2.887
6NC2	A_ARG_456	NH2	A_GLU_466	OE2	3.857
6NC2	A_LYS_460	NZ	A_GLU_466	OE1	3.544
6NC2	A_ARG_476	NH1	A_GLU_102	OE1	3.959
6NC2	A_ARG_476	NH1	A_GLU_102	OE2	2.882
6NC2	A_ARG_476	NH2	A_ASP_474	OD1	3.950
6NC2	A_ARG_476	NH2	A_ASP_474	OD2	2.809
6NC2	A_ARG_480	NH2	A_ASP_477	OD1	3.009
6NC2	A_ARG_480	NH2	A_ASP_477	OD2	3.559
6NC2	A_LYS_487	NZ	A_GLU_47	OE1	3.379
6NC2	A_LYS_487	NZ	A_GLU_91	OE1	3.334
6NC2	A_LYS_490	NZ	A_GLU_492	OE1	3.377
6NC2	A_LYS_490	NZ	A_GLU_492	OE2	2.629
6NC2	A_LYS_500	NZ	I_ASP_664	OD1	2.780
6NC2	A_LYS_500	NZ	I_ASP_664	OD2	3.992
6NC2	A_ARG_503	NH1	B_GLU_654	OE1	3.759
6NC2	A_ARG_503	NH1	B_GLU_654	OE2	3.172
6NC2	B_ARG_542	NH1	I_GLU_647	OE1	2.800
6NC2	B_ARG_542	NH1	I_ASP_648	OD1	3.191
6NC2	B_ARG_542	NH2	I_ASP_648	OD1	3.498
6NC2	B_LYS_574	NZ	A_ASP_107	OD1	2.510
6NC2	B_LYS_574	NZ	A_ASP_107	OD2	3.688
6NC2	B_LYS_588	NZ	B_ASP_589	OD1	2.875
6NC2	B_LYS_617	NZ	B_GLU_634	OE2	2.908
6NC2	H_LYS_30	NZ	H_ASP_31	OD1	3.266
6NC2	H_LYS_30	NZ	H_ASP_31	OD2	2.768
6NC2	H_HIS_35	NE2	H_ASP_95	OD1	2.705
6NC2	H_ARG_38	NH1	H_ASP_86	OD1	2.970
6NC2	H_ARG_38	NH2	H_GLU_46	OE1	3.107

6NC2	H_ARG_38	NH2	H_GLU_46	OE2	3.826
6NC2	H_ARG_66	NH2	H_ASP_86	OD1	3.009
6NC2	H_ARG_66	NH2	H_ASP_86	OD2	3.729
6NC2	H_LYS_75	NZ	H_ASP_72	OD2	3.903
6NC2	H_ARG_82B	NH1	H_ASP_82A	OD2	2.740
6NC2	H_ARG_83	NH2	H_GLU_85	OE1	3.718
6NC2	H_ARG_83	NH2	H_GLU_85	OE2	3.237
6NC2	H_LYS_94	NZ	H_ASP_101	OD1	3.921
6NC2	H_ARG_96	NH1	L_ASP_50	OD1	3.082
6NC2	H_ARG_96	NH1	L_ASP_50	OD2	3.706
6NC2	H_ARG_96	NH2	L_ASP_50	OD1	3.892
6NC2	H_ARG_96	NH2	L_ASP_50	OD2	3.158
6NC2	H_ARG_99	NH2	H_ASP_31	OD1	3.800
6NC2	L_LYS_30	NZ	L_ASP_28	OD2	2.906
6NC2	L_ARG_37	NH1	L_ASP_82	OD1	3.215
6NC2	L_ARG_37	NH2	L_GLU_45	OE1	2.891
6NC2	L_ARG_37	NH2	L_GLU_45	OE2	3.981
6NC2	L_LYS_42	NZ	L_GLU_45	OE1	3.768
6NC2	L_LYS_103	NZ	L_GLU_105	OE1	3.671
6NC2	C_LYS_46	NZ	L_ASP_636	OD1	3.909
6NC2	C_ARG_59	NH1	C_ASP_57	OD1	2.814
6NC2	C_ARG_59	NH1	C_ASP_57	OD2	3.348
6NC2	C_ARG_59	NH2	C_ASP_57	OD1	3.635
6NC2	C_ARG_59	NH2	C_ASP_57	OD2	2.765
6NC2	C_LYS_155	NZ	C_ASP_133	OD1	2.379
6NC2	C_LYS_231	NZ	C_GLU_268	OE2	2.886
6NC2	C_LYS_232	NZ	C_GLU_269	OE1	3.666
6NC2	C_LYS_232	NZ	C_GLU_269	OE2	2.418
6NC2	C_LYS_282	NZ	C_ASP_279	OD2	2.788
6NC2	C_ARG_298	NH1	C_GLU_381	OE1	2.865
6NC2	C_ARG_298	NH1	C_GLU_381	OE2	2.960
6NC2	C_LYS_305	NZ	C_GLU_172	OE1	2.574
6NC2	C_LYS_305	NZ	C_GLU_172	OE2	3.869
6NC2	C_ARG_327	NH2	C_ASP_325	OD2	3.126
6NC2	C_LYS_337	NZ	C_GLU_293	OE1	2.932
6NC2	C_LYS_343	NZ	C_ASP_340	OD1	3.486
6NC2	C_LYS_348	NZ	C_GLU_269	OE1	2.894
6NC2	C_LYS_348	NZ	C_GLU_269	OE2	3.757
6NC2	C_LYS_348	NZ	C_GLU_351	OE2	3.738
6NC2	C_ARG_419	NH2	C_GLU_153	OE2	3.652
6NC2	C_LYS_421	NZ	C_GLU_370	OE2	2.787
6NC2	C_ARG_456	NH2	C_GLU_466	OE1	2.887
6NC2	C_ARG_456	NH2	C_GLU_466	OE2	3.857
6NC2	C_LYS_460	NZ	C_GLU_466	OE1	3.544
6NC2	C_ARG_476	NH1	C_GLU_102	OE1	3.959
6NC2	C_ARG_476	NH1	C_GLU_102	OE2	2.882
6NC2	C_ARG_476	NH2	C_ASP_474	OD1	3.950
6NC2	C_ARG_476	NH2	C_ASP_474	OD2	2.809
6NC2	C_ARG_480	NH2	C_ASP_477	OD1	3.009
6NC2	C_ARG_480	NH2	C_ASP_477	OD2	3.559
6NC2	C_LYS_487	NZ	C_GLU_47	OE1	3.379
6NC2	C_LYS_487	NZ	C_GLU_91	OE1	3.334
6NC2	C_LYS_490	NZ	C_GLU_492	OE1	3.377
6NC2	C_LYS_490	NZ	C_GLU_492	OE2	2.629
6NC2	C_LYS_500	NZ	J_ASP_664	OD1	2.780
6NC2	C_LYS_500	NZ	J_ASP_664	OD2	3.991
6NC2	C_ARG_503	NH1	I_GLU_654	OE1	3.760
6NC2	C_ARG_503	NH1	I_GLU_654	OE2	3.173

6NC2	L_ARG_542	NH1	J_GLU_647	OE1	2.801
6NC2	L_ARG_542	NH1	J_ASP_648	OD1	3.190
6NC2	L_ARG_542	NH2	J_ASP_648	OD1	3.498
6NC2	L_LYS_574	NZ	C_ASP_107	OD1	2.510
6NC2	L_LYS_574	NZ	C_ASP_107	OD2	3.688
6NC2	L_LYS_588	NZ	L_ASP_589	OD1	2.875
6NC2	L_LYS_617	NZ	L_GLU_634	OE2	2.908
6NC2	O_LYS_30	NZ	O_ASP_31	OD1	3.267
6NC2	O_LYS_30	NZ	O_ASP_31	OD2	2.768
6NC2	O_HIS_35	NE2	O_ASP_95	OD1	2.705
6NC2	O_ARG_38	NH1	O_ASP_86	OD1	2.971
6NC2	O_ARG_38	NH2	O_GLU_46	OE1	3.107
6NC2	O_ARG_38	NH2	O_GLU_46	OE2	3.826
6NC2	O_ARG_66	NH2	O_ASP_86	OD1	3.008
6NC2	O_ARG_66	NH2	O_ASP_86	OD2	3.729
6NC2	O_LYS_75	NZ	O_ASP_72	OD2	3.903
6NC2	O_ARG_82B	NH1	O_ASP_82A	OD2	2.740
6NC2	O_ARG_83	NH2	O_GLU_85	OE1	3.718
6NC2	O_ARG_83	NH2	O_GLU_85	OE2	3.238
6NC2	O_LYS_94	NZ	O_ASP_101	OD1	3.921
6NC2	O_ARG_96	NH1	T_ASP_50	OD1	3.082
6NC2	O_ARG_96	NH1	T_ASP_50	OD2	3.706
6NC2	O_ARG_96	NH2	T_ASP_50	OD1	3.892
6NC2	O_ARG_96	NH2	T_ASP_50	OD2	3.158
6NC2	O_ARG_99	NH2	O_ASP_31	OD1	3.799
6NC2	T_LYS_30	NZ	T_ASP_28	OD2	2.905
6NC2	T_ARG_37	NH1	T_ASP_82	OD1	3.216
6NC2	T_ARG_37	NH2	T_GLU_45	OE1	2.891
6NC2	T_ARG_37	NH2	T_GLU_45	OE2	3.981
6NC2	T_LYS_42	NZ	T_GLU_45	OE1	3.769
6NC2	T_LYS_103	NZ	T_GLU_105	OE1	3.670
6NC2	D_LYS_46	NZ	J_ASP_636	OD1	3.909
6NC2	D_ARG_59	NH1	D_ASP_57	OD1	2.814
6NC2	D_ARG_59	NH1	D_ASP_57	OD2	3.348
6NC2	D_ARG_59	NH2	D_ASP_57	OD1	3.635
6NC2	D_ARG_59	NH2	D_ASP_57	OD2	2.766
6NC2	D_LYS_155	NZ	D_ASP_133	OD1	2.379
6NC2	D_LYS_231	NZ	D_GLU_268	OE2	2.885
6NC2	D_LYS_232	NZ	D_GLU_269	OE1	3.666
6NC2	D_LYS_232	NZ	D_GLU_269	OE2	2.418
6NC2	D_LYS_282	NZ	D_ASP_279	OD2	2.787
6NC2	D_ARG_298	NH1	D_GLU_381	OE1	2.864
6NC2	D_ARG_298	NH1	D_GLU_381	OE2	2.959
6NC2	D_LYS_305	NZ	D_GLU_172	OE1	2.575
6NC2	D_LYS_305	NZ	D_GLU_172	OE2	3.868
6NC2	D_ARG_327	NH2	D_ASP_325	OD2	3.127
6NC2	D_LYS_337	NZ	D_GLU_293	OE1	2.931
6NC2	D_LYS_343	NZ	D_ASP_340	OD1	3.486
6NC2	D_LYS_348	NZ	D_GLU_269	OE1	2.894
6NC2	D_LYS_348	NZ	D_GLU_269	OE2	3.758
6NC2	D_LYS_348	NZ	D_GLU_351	OE2	3.738
6NC2	D_ARG_419	NH2	D_GLU_153	OE2	3.652
6NC2	D_LYS_421	NZ	D_GLU_370	OE2	2.786
6NC2	D_ARG_456	NH2	D_GLU_466	OE1	2.886
6NC2	D_ARG_456	NH2	D_GLU_466	OE2	3.857
6NC2	D_LYS_460	NZ	D_GLU_466	OE1	3.544
6NC2	D_ARG_476	NH1	D_GLU_102	OE1	3.959
6NC2	D_ARG_476	NH1	D_GLU_102	OE2	2.881

6NC2	D_ARG_476	NH2	D_ASP_474	OD1	3.950
6NC2	D_ARG_476	NH2	D_ASP_474	OD2	2.809
6NC2	D_ARG_480	NH2	D_ASP_477	OD1	3.009
6NC2	D_ARG_480	NH2	D_ASP_477	OD2	3.559
6NC2	D_LYS_487	NZ	D_GLU_47	OE1	3.379
6NC2	D_LYS_487	NZ	D_GLU_91	OE1	3.334
6NC2	D_LYS_490	NZ	D_GLU_492	OE1	3.377
6NC2	D_LYS_490	NZ	D_GLU_492	OE2	2.630
6NC2	D_LYS_500	NZ	B_ASP_664	OD1	2.780
6NC2	D_LYS_500	NZ	B_ASP_664	OD2	3.992
6NC2	D_ARG_503	NH1	J_GLU_654	OE1	3.759
6NC2	D_ARG_503	NH1	J_GLU_654	OE2	3.173
6NC2	J_ARG_542	NH1	B_GLU_647	OE1	2.800
6NC2	J_ARG_542	NH1	B_ASP_648	OD1	3.191
6NC2	J_ARG_542	NH2	B_ASP_648	OD1	3.498
6NC2	J_LYS_574	NZ	D_ASP_107	OD1	2.510
6NC2	J_LYS_574	NZ	D_ASP_107	OD2	3.688
6NC2	J_LYS_588	NZ	J_ASP_589	OD1	2.875
6NC2	J_LYS_617	NZ	J_GLU_634	OE2	2.908
6NC2	P_LYS_30	NZ	P_ASP_31	OD1	3.267
6NC2	P_LYS_30	NZ	P_ASP_31	OD2	2.768
6NC2	P_HIS_35	NE2	P_ASP_95	OD1	2.704
6NC2	P_ARG_38	NH1	P_ASP_86	OD1	2.970
6NC2	P_ARG_38	NH2	P_GLU_46	OE1	3.107
6NC2	P_ARG_38	NH2	P_GLU_46	OE2	3.826
6NC2	P_ARG_66	NH2	P_ASP_86	OD1	3.009
6NC2	P_ARG_66	NH2	P_ASP_86	OD2	3.730
6NC2	P_LYS_75	NZ	P_ASP_72	OD2	3.903
6NC2	P_ARG_82B	NH1	P_ASP_82A	OD2	2.740
6NC2	P_ARG_83	NH2	P_GLU_85	OE1	3.718
6NC2	P_ARG_83	NH2	P_GLU_85	OE2	3.237
6NC2	P_LYS_94	NZ	P_ASP_101	OD1	3.921
6NC2	P_ARG_96	NH1	U_ASP_50	OD1	3.083
6NC2	P_ARG_96	NH1	U_ASP_50	OD2	3.706
6NC2	P_ARG_96	NH2	U_ASP_50	OD1	3.893
6NC2	P_ARG_96	NH2	U_ASP_50	OD2	3.158
6NC2	P_ARG_99	NH2	P_ASP_31	OD1	3.800
6NC2	U_LYS_30	NZ	U_ASP_28	OD2	2.905
6NC2	U_ARG_37	NH1	U_ASP_82	OD1	3.215
6NC2	U_ARG_37	NH2	U_GLU_45	OE1	2.891
6NC2	U_ARG_37	NH2	U_GLU_45	OE2	3.981
6NC2	U_LYS_42	NZ	U_GLU_45	OE1	3.768
6NC2	U_LYS_103	NZ	U_GLU_105	OE1	3.671
6NC2	E_LYS_46	NZ	K_ASP_636	OD1	3.909
6NC2	E_ARG_59	NH1	E_ASP_57	OD1	2.814
6NC2	E_ARG_59	NH1	E_ASP_57	OD2	3.348
6NC2	E_ARG_59	NH2	E_ASP_57	OD1	3.635
6NC2	E_ARG_59	NH2	E_ASP_57	OD2	2.766
6NC2	E_LYS_155	NZ	E_ASP_133	OD1	2.379
6NC2	E_LYS_231	NZ	E_GLU_268	OE2	2.886
6NC2	E_LYS_232	NZ	E_GLU_269	OE1	3.666
6NC2	E_LYS_232	NZ	E_GLU_269	OE2	2.418
6NC2	E_LYS_282	NZ	E_ASP_279	OD2	2.788
6NC2	E_ARG_298	NH1	E_GLU_381	OE1	2.865
6NC2	E_ARG_298	NH1	E_GLU_381	OE2	2.959
6NC2	E_LYS_305	NZ	E_GLU_172	OE1	2.574
6NC2	E_LYS_305	NZ	E_GLU_172	OE2	3.869
6NC2	E_ARG_327	NH2	E_ASP_325	OD2	3.126

6NC2	E_LYS_337	NZ	E_GLU_293	OE1	2.932
6NC2	E_LYS_343	NZ	E_ASP_340	OD1	3.486
6NC2	E_LYS_348	NZ	E_GLU_269	OE1	2.894
6NC2	E_LYS_348	NZ	E_GLU_269	OE2	3.758
6NC2	E_LYS_348	NZ	E_GLU_351	OE2	3.738
6NC2	E_ARG_419	NH2	E_GLU_153	OE2	3.652
6NC2	E_LYS_421	NZ	E_GLU_370	OE2	2.787
6NC2	E_ARG_456	NH2	E_GLU_466	OE1	2.887
6NC2	E_ARG_456	NH2	E_GLU_466	OE2	3.857
6NC2	E_LYS_460	NZ	E_GLU_466	OE1	3.544
6NC2	E_ARG_476	NH1	E_GLU_102	OE1	3.959
6NC2	E_ARG_476	NH1	E_GLU_102	OE2	2.882
6NC2	E_ARG_476	NH2	E_ASP_474	OD1	3.950
6NC2	E_ARG_476	NH2	E_ASP_474	OD2	2.809
6NC2	E_ARG_480	NH2	E_ASP_477	OD1	3.009
6NC2	E_ARG_480	NH2	E_ASP_477	OD2	3.559
6NC2	E_LYS_487	NZ	E_GLU_47	OE1	3.379
6NC2	E_LYS_487	NZ	E_GLU_91	OE1	3.334
6NC2	E_LYS_490	NZ	E_GLU_492	OE1	3.377
6NC2	E_LYS_490	NZ	E_GLU_492	OE2	2.629
6NC2	E_LYS_500	NZ	M_ASP_664	OD1	2.780
6NC2	E_LYS_500	NZ	M_ASP_664	OD2	3.992
6NC2	E_ARG_503	NH1	K_GLU_654	OE1	3.759
6NC2	E_ARG_503	NH1	K_GLU_654	OE2	3.172
6NC2	K_ARG_542	NH1	M_GLU_647	OE1	2.800
6NC2	K_ARG_542	NH1	M_ASP_648	OD1	3.191
6NC2	K_ARG_542	NH2	M_ASP_648	OD1	3.498
6NC2	K_LYS_574	NZ	E_ASP_107	OD1	2.510
6NC2	K_LYS_574	NZ	E_ASP_107	OD2	3.688
6NC2	K_LYS_588	NZ	K_ASP_589	OD1	2.875
6NC2	K_LYS_617	NZ	K_GLU_634	OE2	2.908
6NC2	Q_LYS_30	NZ	Q_ASP_31	OD1	3.266
6NC2	Q_LYS_30	NZ	Q_ASP_31	OD2	2.768
6NC2	Q_HIS_35	NE2	Q_ASP_95	OD1	2.705
6NC2	Q_ARG_38	NH1	Q_ASP_86	OD1	2.970
6NC2	Q_ARG_38	NH2	Q_GLU_46	OE1	3.107
6NC2	Q_ARG_38	NH2	Q_GLU_46	OE2	3.826
6NC2	Q_ARG_66	NH2	Q_ASP_86	OD1	3.009
6NC2	Q_ARG_66	NH2	Q_ASP_86	OD2	3.729
6NC2	Q_LYS_75	NZ	Q_ASP_72	OD2	3.903
6NC2	Q_ARG_82B	NH1	Q_ASP_82A	OD2	2.740
6NC2	Q_ARG_83	NH2	Q_GLU_85	OE1	3.718
6NC2	Q_ARG_83	NH2	Q_GLU_85	OE2	3.237
6NC2	Q_LYS_94	NZ	Q_ASP_101	OD1	3.921
6NC2	Q_ARG_96	NH1	V_ASP_50	OD1	3.082
6NC2	Q_ARG_96	NH1	V_ASP_50	OD2	3.706
6NC2	Q_ARG_96	NH2	V_ASP_50	OD1	3.892
6NC2	Q_ARG_96	NH2	V_ASP_50	OD2	3.158
6NC2	Q_ARG_99	NH2	Q_ASP_31	OD1	3.800
6NC2	V_LYS_30	NZ	V_ASP_28	OD2	2.906
6NC2	V_ARG_37	NH1	V_ASP_82	OD1	3.215
6NC2	V_ARG_37	NH2	V_GLU_45	OE1	2.891
6NC2	V_ARG_37	NH2	V_GLU_45	OE2	3.981
6NC2	V_LYS_42	NZ	V_GLU_45	OE1	3.768
6NC2	V_LYS_103	NZ	V_GLU_105	OE1	3.671
6NC2	F_LYS_46	NZ	M_ASP_636	OD1	3.909
6NC2	F_ARG_59	NH1	F_ASP_57	OD1	2.814
6NC2	F_ARG_59	NH1	F_ASP_57	OD2	3.348

6NC2	F_ARG_59	NH2	F_ASP_57	OD1	3.635
6NC2	F_ARG_59	NH2	F_ASP_57	OD2	2.765
6NC2	F_LYS_155	NZ	F_ASP_133	OD1	2.379
6NC2	F_LYS_231	NZ	F_GLU_268	OE2	2.886
6NC2	F_LYS_232	NZ	F_GLU_269	OE1	3.666
6NC2	F_LYS_232	NZ	F_GLU_269	OE2	2.418
6NC2	F_LYS_282	NZ	F_ASP_279	OD2	2.788
6NC2	F_ARG_298	NH1	F_GLU_381	OE1	2.865
6NC2	F_ARG_298	NH1	F_GLU_381	OE2	2.960
6NC2	F_LYS_305	NZ	F_GLU_172	OE1	2.574
6NC2	F_LYS_305	NZ	F_GLU_172	OE2	3.869
6NC2	F_ARG_327	NH2	F_ASP_325	OD2	3.127
6NC2	F_LYS_337	NZ	F_GLU_293	OE1	2.932
6NC2	F_LYS_343	NZ	F_ASP_340	OD1	3.486
6NC2	F_LYS_348	NZ	F_GLU_269	OE1	2.894
6NC2	F_LYS_348	NZ	F_GLU_269	OE2	3.757
6NC2	F_LYS_348	NZ	F_GLU_351	OE2	3.738
6NC2	F_ARG_419	NH2	F_GLU_153	OE2	3.653
6NC2	F_LYS_421	NZ	F_GLU_370	OE2	2.787
6NC2	F_ARG_456	NH2	F_GLU_466	OE1	2.887
6NC2	F_ARG_456	NH2	F_GLU_466	OE2	3.857
6NC2	F_LYS_460	NZ	F_GLU_466	OE1	3.544
6NC2	F_ARG_476	NH1	F_GLU_102	OE1	3.959
6NC2	F_ARG_476	NH1	F_GLU_102	OE2	2.882
6NC2	F_ARG_476	NH2	F_ASP_474	OD1	3.950
6NC2	F_ARG_476	NH2	F_ASP_474	OD2	2.809
6NC2	F_ARG_480	NH2	F_ASP_477	OD1	3.009
6NC2	F_ARG_480	NH2	F_ASP_477	OD2	3.559
6NC2	F_LYS_487	NZ	F_GLU_47	OE1	3.379
6NC2	F_LYS_487	NZ	F_GLU_91	OE1	3.334
6NC2	F_LYS_490	NZ	F_GLU_492	OE1	3.377
6NC2	F_LYS_490	NZ	F_GLU_492	OE2	2.629
6NC2	F_LYS_500	NZ	N_ASP_664	OD1	2.780
6NC2	F_LYS_500	NZ	N_ASP_664	OD2	3.991
6NC2	F_ARG_503	NH1	M_GLU_654	OE1	3.759
6NC2	F_ARG_503	NH1	M_GLU_654	OE2	3.173
6NC2	M_ARG_542	NH1	N_GLU_647	OE1	2.801
6NC2	M_ARG_542	NH1	N_ASP_648	OD1	3.191
6NC2	M_ARG_542	NH2	N_ASP_648	OD1	3.498
6NC2	M_LYS_574	NZ	F_ASP_107	OD1	2.510
6NC2	M_LYS_574	NZ	F_ASP_107	OD2	3.688
6NC2	M_LYS_588	NZ	M_ASP_589	OD1	2.875
6NC2	M_LYS_617	NZ	M_GLU_634	OE2	2.907
6NC2	R_LYS_30	NZ	R_ASP_31	OD1	3.267
6NC2	R_LYS_30	NZ	R_ASP_31	OD2	2.768
6NC2	R_HIS_35	NE2	R_ASP_95	OD1	2.705
6NC2	R_ARG_38	NH1	R_ASP_86	OD1	2.970
6NC2	R_ARG_38	NH2	R_GLU_46	OE1	3.107
6NC2	R_ARG_38	NH2	R_GLU_46	OE2	3.826
6NC2	R_ARG_66	NH2	R_ASP_86	OD1	3.009
6NC2	R_ARG_66	NH2	R_ASP_86	OD2	3.729
6NC2	R_LYS_75	NZ	R_ASP_72	OD2	3.903
6NC2	R_ARG_82B	NH1	R_ASP_82A	OD2	2.739
6NC2	R_ARG_83	NH2	R_GLU_85	OE1	3.718
6NC2	R_ARG_83	NH2	R_GLU_85	OE2	3.238
6NC2	R_LYS_94	NZ	R_ASP_101	OD1	3.921
6NC2	R_ARG_96	NH1	W_ASP_50	OD1	3.082
6NC2	R_ARG_96	NH1	W_ASP_50	OD2	3.706

6NC2	R_ARG_96	NH2	W_ASP_50	OD1	3.892
6NC2	R_ARG_96	NH2	W_ASP_50	OD2	3.157
6NC2	R_ARG_99	NH2	R_ASP_31	OD1	3.799
6NC2	W_LYS_30	NZ	W_ASP_28	OD2	2.905
6NC2	W_ARG_37	NH1	W_ASP_82	OD1	3.215
6NC2	W_ARG_37	NH2	W_GLU_45	OE1	2.891
6NC2	W_ARG_37	NH2	W_GLU_45	OE2	3.981
6NC2	W_LYS_42	NZ	W_GLU_45	OE1	3.769
6NC2	W_LYS_103	NZ	W_GLU_105	OE1	3.671
6NC2	G_LYS_46	NZ	N_ASP_636	OD1	3.909
6NC2	G_ARG_59	NH1	G_ASP_57	OD1	2.814
6NC2	G_ARG_59	NH1	G_ASP_57	OD2	3.348
6NC2	G_ARG_59	NH2	G_ASP_57	OD1	3.635
6NC2	G_ARG_59	NH2	G_ASP_57	OD2	2.766
6NC2	G_LYS_155	NZ	G_ASP_133	OD1	2.379
6NC2	G_LYS_231	NZ	G_GLU_268	OE2	2.886
6NC2	G_LYS_232	NZ	G_GLU_269	OE1	3.666
6NC2	G_LYS_232	NZ	G_GLU_269	OE2	2.418
6NC2	G_LYS_282	NZ	G_ASP_279	OD2	2.787
6NC2	G_ARG_298	NH1	G_GLU_381	OE1	2.864
6NC2	G_ARG_298	NH1	G_GLU_381	OE2	2.959
6NC2	G_LYS_305	NZ	G_GLU_172	OE1	2.575
6NC2	G_LYS_305	NZ	G_GLU_172	OE2	3.868
6NC2	G_ARG_327	NH2	G_ASP_325	OD2	3.127
6NC2	G_LYS_337	NZ	G_GLU_293	OE1	2.931
6NC2	G_LYS_343	NZ	G_ASP_340	OD1	3.486
6NC2	G_LYS_348	NZ	G_GLU_269	OE1	2.894
6NC2	G_LYS_348	NZ	G_GLU_269	OE2	3.758
6NC2	G_LYS_348	NZ	G_GLU_351	OE2	3.738
6NC2	G_ARG_419	NH2	G_GLU_153	OE2	3.652
6NC2	G_LYS_421	NZ	G_GLU_370	OE2	2.786
6NC2	G_ARG_456	NH2	G_GLU_466	OE1	2.887
6NC2	G_ARG_456	NH2	G_GLU_466	OE2	3.857
6NC2	G_LYS_460	NZ	G_GLU_466	OE1	3.544
6NC2	G_ARG_476	NH1	G_GLU_102	OE1	3.959
6NC2	G_ARG_476	NH1	G_GLU_102	OE2	2.881
6NC2	G_ARG_476	NH2	G_ASP_474	OD1	3.950
6NC2	G_ARG_476	NH2	G_ASP_474	OD2	2.809
6NC2	G_ARG_480	NH2	G_ASP_477	OD1	3.009
6NC2	G_ARG_480	NH2	G_ASP_477	OD2	3.559
6NC2	G_LYS_487	NZ	G_GLU_47	OE1	3.379
6NC2	G_LYS_487	NZ	G_GLU_91	OE1	3.334
6NC2	G_LYS_490	NZ	G_GLU_492	OE1	3.377
6NC2	G_LYS_490	NZ	G_GLU_492	OE2	2.630
6NC2	G_LYS_500	NZ	K_ASP_664	OD1	2.780
6NC2	G_LYS_500	NZ	K_ASP_664	OD2	3.992
6NC2	G_ARG_503	NH1	N_GLU_654	OE1	3.759
6NC2	G_ARG_503	NH1	N_GLU_654	OE2	3.173
6NC2	N_ARG_542	NH1	K_GLU_647	OE1	2.800
6NC2	N_ARG_542	NH1	K_ASP_648	OD1	3.191
6NC2	N_ARG_542	NH2	K_ASP_648	OD1	3.498
6NC2	N_LYS_574	NZ	G_ASP_107	OD1	2.510
6NC2	N_LYS_574	NZ	G_ASP_107	OD2	3.688
6NC2	N_LYS_588	NZ	N_ASP_589	OD1	2.875
6NC2	N_LYS_617	NZ	N_GLU_634	OE2	2.908
6NC2	S_LYS_30	NZ	S_ASP_31	OD1	3.267
6NC2	S_LYS_30	NZ	S_ASP_31	OD2	2.768
6NC2	S_HIS_35	NE2	S_ASP_95	OD1	2.704

6NC2	S_ARG_38	NH1	S_ASP_86	OD1	2.970
6NC2	S_ARG_38	NH2	S_GLU_46	OE1	3.107
6NC2	S_ARG_38	NH2	S_GLU_46	OE2	3.826
6NC2	S_ARG_66	NH2	S_ASP_86	OD1	3.009
6NC2	S_ARG_66	NH2	S_ASP_86	OD2	3.730
6NC2	S_LYS_75	NZ	S_ASP_72	OD2	3.903
6NC2	S_ARG_82B	NH1	S_ASP_82A	OD2	2.740
6NC2	S_ARG_83	NH2	S_GLU_85	OE1	3.718
6NC2	S_ARG_83	NH2	S_GLU_85	OE2	3.237
6NC2	S_LYS_94	NZ	S_ASP_101	OD1	3.921
6NC2	S_ARG_96	NH1	X_ASP_50	OD1	3.082
6NC2	S_ARG_96	NH1	X_ASP_50	OD2	3.706
6NC2	S_ARG_96	NH2	X_ASP_50	OD1	3.892
6NC2	S_ARG_96	NH2	X_ASP_50	OD2	3.158
6NC2	S_ARG_99	NH2	S_ASP_31	OD1	3.800
6NC2	X_LYS_30	NZ	X_ASP_28	OD2	2.906
6NC2	X_ARG_37	NH1	X_ASP_82	OD1	3.215
6NC2	X_ARG_37	NH2	X_GLU_45	OE1	2.891
6NC2	X_ARG_37	NH2	X_GLU_45	OE2	3.981
6NC2	X_LYS_42	NZ	X_GLU_45	OE1	3.768
6NC2	X_LYS_103	NZ	X_GLU_105	OE1	3.671
6NC3	A_LYS_46	NZ	B_ASP_636	OD1	2.912
6NC3	A_LYS_46	NZ	B_ASP_636	OD2	3.719
6NC3	A_HIS_72	ND1	A_GLU_64	OE1	3.735
6NC3	A_LYS_117	NZ	A_ASP_113	OD1	3.847
6NC3	A_LYS_117	NZ	A_ASP_113	OD2	2.492
6NC3	A_LYS_155	NZ	A_ASP_133	OD1	2.486
6NC3	A_LYS_168	NZ	A_ASP_167	OD1	2.679
6NC3	A_LYS_168	NZ	A_ASP_167	OD2	3.249
6NC3	A_ARG_192	NH2	C_ASP_167	OD1	3.709
6NC3	A_ARG_192	NH2	C_ASP_167	OD2	3.548
6NC3	A_LYS_231	NZ	A_GLU_267	OE1	2.789
6NC3	A_LYS_231	NZ	A_GLU_267	OE2	3.511
6NC3	A_LYS_232	NZ	A_GLU_269	OE1	3.765
6NC3	A_LYS_232	NZ	A_GLU_269	OE2	2.544
6NC3	A_HIS_249	NE2	A_GLU_482	OE2	2.721
6NC3	A_LYS_290	NZ	A_GLU_268	OE1	3.516
6NC3	A_ARG_298	NH1	A_GLU_381	OE2	2.878
6NC3	A_LYS_305	NZ	A_GLU_172	OE1	2.502
6NC3	A_LYS_305	NZ	A_GLU_172	OE2	3.928
6NC3	A_LYS_337	NZ	A_GLU_293	OE2	2.661
6NC3	A_LYS_348	NZ	A_GLU_351	OE1	2.941
6NC3	A_LYS_348	NZ	A_GLU_351	OE2	3.643
6NC3	A_LYS_421	NZ	A_GLU_370	OE2	2.811
6NC3	A_LYS_432	NZ	A_ASP_113	OD1	2.553
6NC3	A_LYS_432	NZ	A_ASP_113	OD2	3.774
6NC3	A_LYS_432	NZ	A_GLU_429	OE1	3.926
6NC3	A_ARG_456	NH2	A_GLU_466	OE1	3.636
6NC3	A_ARG_456	NH2	A_GLU_466	OE2	2.864
6NC3	A_ARG_476	NH1	A_GLU_102	OE1	3.922
6NC3	A_ARG_476	NH1	A_GLU_102	OE2	3.112
6NC3	A_ARG_476	NH2	A_ASP_474	OD1	3.856
6NC3	A_ARG_476	NH2	A_ASP_474	OD2	3.033
6NC3	A_ARG_480	NH1	A_ASP_477	OD1	2.738
6NC3	A_ARG_480	NH2	A_ASP_477	OD1	3.897
6NC3	A_LYS_487	NZ	A_GLU_47	OE1	2.894
6NC3	A_LYS_487	NZ	A_GLU_47	OE2	3.821
6NC3	A_LYS_487	NZ	A_GLU_91	OE1	3.879

6NC3	A_ARG_503	NH2	B_GLU_654	OE1	3.773
6NC3	A_ARG_503	NH2	B_GLU_654	OE2	3.161
6NC3	B_ARG_542	NH2	J_GLU_647	OE1	2.826
6NC3	B_ARG_542	NH2	J_ASP_648	OD1	2.949
6NC3	B_ARG_542	NH2	J_ASP_648	OD2	3.670
6NC3	B_LYS_574	NZ	A_ASP_107	OD1	2.582
6NC3	B_LYS_574	NZ	A_ASP_107	OD2	2.711
6NC3	B_ARG_579	NH1	J_GLU_584	OE2	3.194
6NC3	B_ARG_585	NH2	A_GLU_492	OE1	2.939
6NC3	B_ARG_585	NH2	A_GLU_492	OE2	3.498
6NC3	B_LYS_617	NZ	B_GLU_634	OE1	2.815
6NC3	B_LYS_617	NZ	B_GLU_634	OE2	3.445
6NC3	H_LYS_12	NZ	H_GLU_10	OE1	3.786
6NC3	H_HIS_35	NE2	H_ASP_95	OD2	3.813
6NC3	H_ARG_38	NH1	H_ASP_86	OD1	2.638
6NC3	H_ARG_38	NH2	H_GLU_46	OE1	2.857
6NC3	H_ARG_38	NH2	H_GLU_46	OE2	3.919
6NC3	H_ARG_38	NH2	H_ASP_86	OD1	3.489
6NC3	H_LYS_62	NZ	H_GLU_46	OE2	2.819
6NC3	H_ARG_66	NH2	H_ASP_86	OD1	3.294
6NC3	H_ARG_66	NH2	H_ASP_86	OD2	3.014
6NC3	H_ARG_94	NH1	H_GLU_2	OE1	2.960
6NC3	H_ARG_94	NH2	H_GLU_2	OE1	3.018
6NC3	H_LYS_96	NZ	H_ASP_101	OD1	3.648
6NC3	H_LYS_96	NZ	H_ASP_101	OD2	2.449
6NC3	L_ARG_30	NH2	L_GLU_32	OE2	3.023
6NC3	L_ARG_61	NH1	L_GLU_81	OE2	3.991
6NC3	L_ARG_61	NH2	L_GLU_81	OE2	3.260
6NC3	L_ARG_61	NH2	L_ASP_82	OD1	2.918
6NC3	L_ARG_61	NH2	L_ASP_82	OD2	3.280
6NC3	L_LYS_103	NZ	L_GLU_105	OE2	3.920
6NC3	L_LYS_107	NZ	L_ASP_17	OD2	2.904
6NC3	C_LYS_46	NZ	L_ASP_636	OD1	2.913
6NC3	C_LYS_46	NZ	L_ASP_636	OD2	3.719
6NC3	C_HIS_72	ND1	C_GLU_64	OE1	3.735
6NC3	C_LYS_117	NZ	C_ASP_113	OD1	3.848
6NC3	C_LYS_117	NZ	C_ASP_113	OD2	2.492
6NC3	C_LYS_155	NZ	C_ASP_133	OD1	2.487
6NC3	C_LYS_168	NZ	C_ASP_167	OD1	2.679
6NC3	C_LYS_168	NZ	C_ASP_167	OD2	3.249
6NC3	C_ARG_192	NH2	D_ASP_167	OD1	3.709
6NC3	C_ARG_192	NH2	D_ASP_167	OD2	3.548
6NC3	C_LYS_231	NZ	C_GLU_267	OE1	2.789
6NC3	C_LYS_231	NZ	C_GLU_267	OE2	3.511
6NC3	C_LYS_232	NZ	C_GLU_269	OE1	3.765
6NC3	C_LYS_232	NZ	C_GLU_269	OE2	2.544
6NC3	C_HIS_249	NE2	C_GLU_482	OE2	2.721
6NC3	C_LYS_290	NZ	C_GLU_268	OE1	3.516
6NC3	C_ARG_298	NH1	C_GLU_381	OE2	2.878
6NC3	C_LYS_305	NZ	C_GLU_172	OE1	2.502
6NC3	C_LYS_305	NZ	C_GLU_172	OE2	3.929
6NC3	C_LYS_337	NZ	C_GLU_293	OE2	2.662
6NC3	C_LYS_348	NZ	C_GLU_351	OE1	2.941
6NC3	C_LYS_348	NZ	C_GLU_351	OE2	3.643
6NC3	C_LYS_421	NZ	C_GLU_370	OE2	2.811
6NC3	C_LYS_432	NZ	C_ASP_113	OD1	2.553
6NC3	C_LYS_432	NZ	C_ASP_113	OD2	3.774
6NC3	C_LYS_432	NZ	C_GLU_429	OE1	3.927

6NC3	C_ARG_456	NH2	C_GLU_466	OE1	3.636
6NC3	C_ARG_456	NH2	C_GLU_466	OE2	2.864
6NC3	C_ARG_476	NH1	C_GLU_102	OE1	3.922
6NC3	C_ARG_476	NH1	C_GLU_102	OE2	3.112
6NC3	C_ARG_476	NH2	C_ASP_474	OD1	3.856
6NC3	C_ARG_476	NH2	C_ASP_474	OD2	3.032
6NC3	C_ARG_480	NH1	C_ASP_477	OD1	2.738
6NC3	C_ARG_480	NH2	C_ASP_477	OD1	3.897
6NC3	C_LYS_487	NZ	C_GLU_47	OE1	2.894
6NC3	C_LYS_487	NZ	C_GLU_47	OE2	3.821
6NC3	C_LYS_487	NZ	C_GLU_91	OE1	3.878
6NC3	C_ARG_503	NH2	I_GLU_654	OE1	3.773
6NC3	C_ARG_503	NH2	I_GLU_654	OE2	3.161
6NC3	I_ARG_542	NH2	B_GLU_647	OE1	2.826
6NC3	I_ARG_542	NH2	B_ASP_648	OD1	2.949
6NC3	I_ARG_542	NH2	B_ASP_648	OD2	3.670
6NC3	I_LYS_574	NZ	C_ASP_107	OD1	2.581
6NC3	I_LYS_574	NZ	C_ASP_107	OD2	2.711
6NC3	I_ARG_579	NH1	B_GLU_584	OE2	3.194
6NC3	I_ARG_585	NH2	C_GLU_492	OE1	2.939
6NC3	I_ARG_585	NH2	C_GLU_492	OE2	3.498
6NC3	I_LYS_617	NZ	I_GLU_634	OE1	2.815
6NC3	I_LYS_617	NZ	I_GLU_634	OE2	3.445
6NC3	O_LYS_12	NZ	O_GLU_10	OE1	3.786
6NC3	O_HIS_35	NE2	O_ASP_95	OD2	3.813
6NC3	O_ARG_38	NH1	O_ASP_86	OD1	2.638
6NC3	O_ARG_38	NH2	O_GLU_46	OE1	2.857
6NC3	O_ARG_38	NH2	O_GLU_46	OE2	3.919
6NC3	O_ARG_38	NH2	O_ASP_86	OD1	3.489
6NC3	O_LYS_62	NZ	O_GLU_46	OE2	2.819
6NC3	O_ARG_66	NH2	O_ASP_86	OD1	3.294
6NC3	O_ARG_66	NH2	O_ASP_86	OD2	3.013
6NC3	O_ARG_94	NH1	O_GLU_2	OE1	2.959
6NC3	O_ARG_94	NH2	O_GLU_2	OE1	3.018
6NC3	O_LYS_96	NZ	O_ASP_101	OD1	3.647
6NC3	O_LYS_96	NZ	O_ASP_101	OD2	2.449
6NC3	T_ARG_30	NH2	T_GLU_32	OE2	3.022
6NC3	T_ARG_61	NH1	T_GLU_81	OE2	3.990
6NC3	T_ARG_61	NH2	T_GLU_81	OE2	3.260
6NC3	T_ARG_61	NH2	T_ASP_82	OD1	2.918
6NC3	T_ARG_61	NH2	T_ASP_82	OD2	3.280
6NC3	T_LYS_103	NZ	T_GLU_105	OE2	3.920
6NC3	T_LYS_107	NZ	T_ASP_17	OD2	2.904
6NC3	D_LYS_46	NZ	J_ASP_636	OD1	2.913
6NC3	D_LYS_46	NZ	J_ASP_636	OD2	3.719
6NC3	D_HIS_72	ND1	D_GLU_64	OE1	3.734
6NC3	D_LYS_117	NZ	D_ASP_113	OD1	3.848
6NC3	D_LYS_117	NZ	D_ASP_113	OD2	2.492
6NC3	D_LYS_155	NZ	D_ASP_133	OD1	2.487
6NC3	D_LYS_168	NZ	D_ASP_167	OD1	2.679
6NC3	D_LYS_168	NZ	D_ASP_167	OD2	3.249
6NC3	D_ARG_192	NH2	A_ASP_167	OD1	3.708
6NC3	D_ARG_192	NH2	A_ASP_167	OD2	3.548
6NC3	D_LYS_231	NZ	D_GLU_267	OE1	2.789
6NC3	D_LYS_231	NZ	D_GLU_267	OE2	3.510
6NC3	D_LYS_232	NZ	D_GLU_269	OE1	3.765
6NC3	D_LYS_232	NZ	D_GLU_269	OE2	2.544
6NC3	D_HIS_249	NE2	D_GLU_482	OE2	2.721

6NC3	D_LYS_290	NZ	D_GLU_268	OE1	3.516
6NC3	D_ARG_298	NH1	D_GLU_381	OE2	2.878
6NC3	D_LYS_305	NZ	D_GLU_172	OE1	2.502
6NC3	D_LYS_305	NZ	D_GLU_172	OE2	3.929
6NC3	D_LYS_337	NZ	D_GLU_293	OE2	2.661
6NC3	D_LYS_348	NZ	D_GLU_351	OE1	2.941
6NC3	D_LYS_348	NZ	D_GLU_351	OE2	3.643
6NC3	D_LYS_421	NZ	D_GLU_370	OE2	2.811
6NC3	D_LYS_432	NZ	D_ASP_113	OD1	2.553
6NC3	D_LYS_432	NZ	D_ASP_113	OD2	3.775
6NC3	D_LYS_432	NZ	D_GLU_429	OE1	3.926
6NC3	D_ARG_456	NH2	D_GLU_466	OE1	3.636
6NC3	D_ARG_456	NH2	D_GLU_466	OE2	2.864
6NC3	D_ARG_476	NH1	D_GLU_102	OE1	3.922
6NC3	D_ARG_476	NH1	D_GLU_102	OE2	3.112
6NC3	D_ARG_476	NH2	D_ASP_474	OD1	3.856
6NC3	D_ARG_476	NH2	D_ASP_474	OD2	3.032
6NC3	D_ARG_480	NH1	D_ASP_477	OD1	2.738
6NC3	D_ARG_480	NH2	D_ASP_477	OD1	3.897
6NC3	D_LYS_487	NZ	D_GLU_47	OE1	2.894
6NC3	D_LYS_487	NZ	D_GLU_47	OE2	3.821
6NC3	D_LYS_487	NZ	D_GLU_91	OE1	3.878
6NC3	D_ARG_503	NH2	J_GLU_654	OE1	3.773
6NC3	D_ARG_503	NH2	J_GLU_654	OE2	3.160
6NC3	J_ARG_542	NH2	I_GLU_647	OE1	2.825
6NC3	J_ARG_542	NH2	I_ASP_648	OD1	2.949
6NC3	J_ARG_542	NH2	I_ASP_648	OD2	3.670
6NC3	J_LYS_574	NZ	D_ASP_107	OD1	2.581
6NC3	J_LYS_574	NZ	D_ASP_107	OD2	2.710
6NC3	J_ARG_579	NH1	I_GLU_584	OE2	3.194
6NC3	J_ARG_585	NH2	D_GLU_492	OE1	2.939
6NC3	J_ARG_585	NH2	D_GLU_492	OE2	3.498
6NC3	J_LYS_617	NZ	J_GLU_634	OE1	2.815
6NC3	J_LYS_617	NZ	J_GLU_634	OE2	3.445
6NC3	P_LYS_12	NZ	P_GLU_10	OE1	3.785
6NC3	P_HIS_35	NE2	P_ASP_95	OD2	3.813
6NC3	P_ARG_38	NH1	P_ASP_86	OD1	2.638
6NC3	P_ARG_38	NH2	P_GLU_46	OE1	2.856
6NC3	P_ARG_38	NH2	P_GLU_46	OE2	3.919
6NC3	P_ARG_38	NH2	P_ASP_86	OD1	3.489
6NC3	P_LYS_62	NZ	P_GLU_46	OE2	2.819
6NC3	P_ARG_66	NH2	P_ASP_86	OD1	3.294
6NC3	P_ARG_66	NH2	P_ASP_86	OD2	3.014
6NC3	P_ARG_94	NH1	P_GLU_2	OE1	2.959
6NC3	P_ARG_94	NH2	P_GLU_2	OE1	3.018
6NC3	P_LYS_96	NZ	P_ASP_101	OD1	3.648
6NC3	P_LYS_96	NZ	P_ASP_101	OD2	2.449
6NC3	U_ARG_30	NH2	U_GLU_32	OE2	3.022
6NC3	U_ARG_61	NH1	U_GLU_81	OE2	3.991
6NC3	U_ARG_61	NH2	U_GLU_81	OE2	3.260
6NC3	U_ARG_61	NH2	U_ASP_82	OD1	2.918
6NC3	U_ARG_61	NH2	U_ASP_82	OD2	3.280
6NC3	U_LYS_103	NZ	U_GLU_105	OE2	3.920
6NC3	U_LYS_107	NZ	U_ASP_17	OD2	2.904
6NC3	E_LYS_46	NZ	K_ASP_636	OD1	2.912
6NC3	E_LYS_46	NZ	K_ASP_636	OD2	3.719
6NC3	E_HIS_72	ND1	E_GLU_64	OE1	3.735
6NC3	E_LYS_117	NZ	E_ASP_113	OD1	3.847

6NC3	E_LYS_117	NZ	E_ASP_113	OD2	2.492
6NC3	E_LYS_155	NZ	E_ASP_133	OD1	2.486
6NC3	E_LYS_168	NZ	E_ASP_167	OD1	2.679
6NC3	E_LYS_168	NZ	E_ASP_167	OD2	3.249
6NC3	E_ARG_192	NH2	F_ASP_167	OD1	3.709
6NC3	E_ARG_192	NH2	F_ASP_167	OD2	3.548
6NC3	E_LYS_231	NZ	E_GLU_267	OE1	2.789
6NC3	E_LYS_231	NZ	E_GLU_267	OE2	3.511
6NC3	E_LYS_232	NZ	E_GLU_269	OE1	3.765
6NC3	E_LYS_232	NZ	E_GLU_269	OE2	2.544
6NC3	E_HIS_249	NE2	E_GLU_482	OE2	2.721
6NC3	E_LYS_290	NZ	E_GLU_268	OE1	3.516
6NC3	E_ARG_298	NH1	E_GLU_381	OE2	2.878
6NC3	E_LYS_305	NZ	E_GLU_172	OE1	2.502
6NC3	E_LYS_305	NZ	E_GLU_172	OE2	3.928
6NC3	E_LYS_337	NZ	E_GLU_293	OE2	2.661
6NC3	E_LYS_348	NZ	E_GLU_351	OE1	2.941
6NC3	E_LYS_348	NZ	E_GLU_351	OE2	3.643
6NC3	E_LYS_421	NZ	E_GLU_370	OE2	2.811
6NC3	E_LYS_432	NZ	E_ASP_113	OD1	2.553
6NC3	E_LYS_432	NZ	E_ASP_113	OD2	3.774
6NC3	E_LYS_432	NZ	E_GLU_429	OE1	3.926
6NC3	E_ARG_456	NH2	E_GLU_466	OE1	3.636
6NC3	E_ARG_456	NH2	E_GLU_466	OE2	2.864
6NC3	E_ARG_476	NH1	E_GLU_102	OE1	3.922
6NC3	E_ARG_476	NH1	E_GLU_102	OE2	3.112
6NC3	E_ARG_476	NH2	E_ASP_474	OD1	3.856
6NC3	E_ARG_476	NH2	E_ASP_474	OD2	3.033
6NC3	E_ARG_480	NH1	E_ASP_477	OD1	2.738
6NC3	E_ARG_480	NH2	E_ASP_477	OD1	3.897
6NC3	E_LYS_487	NZ	E_GLU_47	OE1	2.894
6NC3	E_LYS_487	NZ	E_GLU_47	OE2	3.821
6NC3	E_LYS_487	NZ	E_GLU_91	OE1	3.879
6NC3	E_ARG_503	NH2	K_GLU_654	OE1	3.773
6NC3	E_ARG_503	NH2	K_GLU_654	OE2	3.161
6NC3	K_ARG_542	NH2	N_GLU_647	OE1	2.826
6NC3	K_ARG_542	NH2	N_ASP_648	OD1	2.949
6NC3	K_ARG_542	NH2	N_ASP_648	OD2	3.670
6NC3	K_LYS_574	NZ	E_ASP_107	OD1	2.582
6NC3	K_LYS_574	NZ	E_ASP_107	OD2	2.711
6NC3	K_ARG_579	NH1	N_GLU_584	OE2	3.194
6NC3	K_ARG_585	NH2	E_GLU_492	OE1	2.939
6NC3	K_ARG_585	NH2	E_GLU_492	OE2	3.498
6NC3	K_LYS_617	NZ	K_GLU_634	OE1	2.815
6NC3	K_LYS_617	NZ	K_GLU_634	OE2	3.445
6NC3	Q_LYS_12	NZ	Q_GLU_10	OE1	3.786
6NC3	Q_HIS_35	NE2	Q_ASP_95	OD2	3.813
6NC3	Q_ARG_38	NH1	Q_ASP_86	OD1	2.638
6NC3	Q_ARG_38	NH2	Q_GLU_46	OE1	2.857
6NC3	Q_ARG_38	NH2	Q_GLU_46	OE2	3.919
6NC3	Q_ARG_38	NH2	Q_ASP_86	OD1	3.489
6NC3	Q_LYS_62	NZ	Q_GLU_46	OE2	2.819
6NC3	Q_ARG_66	NH2	Q_ASP_86	OD1	3.294
6NC3	Q_ARG_66	NH2	Q_ASP_86	OD2	3.014
6NC3	Q_ARG_94	NH1	Q_GLU_2	OE1	2.960
6NC3	Q_ARG_94	NH2	Q_GLU_2	OE1	3.018
6NC3	Q_LYS_96	NZ	Q_ASP_101	OD1	3.648
6NC3	Q_LYS_96	NZ	Q_ASP_101	OD2	2.449

6NC3	V_ARG_30	NH2	V_GLU_32	OE2	3.023
6NC3	V_ARG_61	NH1	V_GLU_81	OE2	3.991
6NC3	V_ARG_61	NH2	V_GLU_81	OE2	3.260
6NC3	V_ARG_61	NH2	V_ASP_82	OD1	2.918
6NC3	V_ARG_61	NH2	V_ASP_82	OD2	3.280
6NC3	V_LYS_103	NZ	V_GLU_105	OE2	3.920
6NC3	V_LYS_107	NZ	V_ASP_17	OD2	2.904
6NC3	F_LYS_46	NZ	M_ASP_636	OD1	2.913
6NC3	F_LYS_46	NZ	M_ASP_636	OD2	3.719
6NC3	F_HIS_72	ND1	F_GLU_64	OE1	3.734
6NC3	F_LYS_117	NZ	F_ASP_113	OD1	3.848
6NC3	F_LYS_117	NZ	F_ASP_113	OD2	2.492
6NC3	F_LYS_155	NZ	F_ASP_133	OD1	2.487
6NC3	F_LYS_168	NZ	F_ASP_167	OD1	2.679
6NC3	F_LYS_168	NZ	F_ASP_167	OD2	3.249
6NC3	F_ARG_192	NH2	G_ASP_167	OD1	3.709
6NC3	F_ARG_192	NH2	G_ASP_167	OD2	3.548
6NC3	F_LYS_231	NZ	F_GLU_267	OE1	2.789
6NC3	F_LYS_231	NZ	F_GLU_267	OE2	3.511
6NC3	F_LYS_232	NZ	F_GLU_269	OE1	3.765
6NC3	F_LYS_232	NZ	F_GLU_269	OE2	2.544
6NC3	F_HIS_249	NE2	F_GLU_482	OE2	2.721
6NC3	F_LYS_290	NZ	F_GLU_268	OE1	3.516
6NC3	F_ARG_298	NH1	F_GLU_381	OE2	2.878
6NC3	F_LYS_305	NZ	F_GLU_172	OE1	2.502
6NC3	F_LYS_305	NZ	F_GLU_172	OE2	3.929
6NC3	F_LYS_337	NZ	F_GLU_293	OE2	2.662
6NC3	F_LYS_348	NZ	F_GLU_351	OE1	2.941
6NC3	F_LYS_348	NZ	F_GLU_351	OE2	3.643
6NC3	F_LYS_421	NZ	F_GLU_370	OE2	2.811
6NC3	F_LYS_432	NZ	F_ASP_113	OD1	2.553
6NC3	F_LYS_432	NZ	F_ASP_113	OD2	3.774
6NC3	F_LYS_432	NZ	F_GLU_429	OE1	3.927
6NC3	F_ARG_456	NH2	F_GLU_466	OE1	3.636
6NC3	F_ARG_456	NH2	F_GLU_466	OE2	2.864
6NC3	F_ARG_476	NH1	F_GLU_102	OE1	3.922
6NC3	F_ARG_476	NH1	F_GLU_102	OE2	3.112
6NC3	F_ARG_476	NH2	F_ASP_474	OD1	3.856
6NC3	F_ARG_476	NH2	F_ASP_474	OD2	3.032
6NC3	F_ARG_480	NH1	F_ASP_477	OD1	2.738
6NC3	F_ARG_480	NH2	F_ASP_477	OD1	3.897
6NC3	F_LYS_487	NZ	F_GLU_47	OE1	2.894
6NC3	F_LYS_487	NZ	F_GLU_47	OE2	3.821
6NC3	F_LYS_487	NZ	F_GLU_91	OE1	3.878
6NC3	F_ARG_503	NH2	M_GLU_654	OE1	3.773
6NC3	F_ARG_503	NH2	M_GLU_654	OE2	3.161
6NC3	M_ARG_542	NH2	K_GLU_647	OE1	2.826
6NC3	M_ARG_542	NH2	K_ASP_648	OD1	2.949
6NC3	M_ARG_542	NH2	K_ASP_648	OD2	3.670
6NC3	M_LYS_574	NZ	F_ASP_107	OD1	2.581
6NC3	M_LYS_574	NZ	F_ASP_107	OD2	2.711
6NC3	M_ARG_579	NH1	K_GLU_584	OE2	3.194
6NC3	M_ARG_585	NH2	F_GLU_492	OE1	2.939
6NC3	M_ARG_585	NH2	F_GLU_492	OE2	3.498
6NC3	M_LYS_617	NZ	M_GLU_634	OE1	2.815
6NC3	M_LYS_617	NZ	M_GLU_634	OE2	3.445
6NC3	R_LYS_12	NZ	R_GLU_10	OE1	3.786
6NC3	R_HIS_35	NE2	R_ASP_95	OD2	3.813

6NC3	R_ARG_38	NH1	R_ASP_86	OD1	2.638
6NC3	R_ARG_38	NH2	R_GLU_46	OE1	2.857
6NC3	R_ARG_38	NH2	R_GLU_46	OE2	3.919
6NC3	R_ARG_38	NH2	R_ASP_86	OD1	3.489
6NC3	R_LYS_62	NZ	R_GLU_46	OE2	2.819
6NC3	R_ARG_66	NH2	R_ASP_86	OD1	3.294
6NC3	R_ARG_66	NH2	R_ASP_86	OD2	3.013
6NC3	R_ARG_94	NH1	R_GLU_2	OE1	2.959
6NC3	R_ARG_94	NH2	R_GLU_2	OE1	3.018
6NC3	R_LYS_96	NZ	R_ASP_101	OD1	3.647
6NC3	R_LYS_96	NZ	R_ASP_101	OD2	2.449
6NC3	W_ARG_30	NH2	W_GLU_32	OE2	3.022
6NC3	W_ARG_61	NH1	W_GLU_81	OE2	3.990
6NC3	W_ARG_61	NH2	W_GLU_81	OE2	3.260
6NC3	W_ARG_61	NH2	W_ASP_82	OD1	2.918
6NC3	W_ARG_61	NH2	W_ASP_82	OD2	3.280
6NC3	W_LYS_103	NZ	W_GLU_105	OE2	3.920
6NC3	W_LYS_107	NZ	W_ASP_17	OD2	2.904
6NC3	G_LYS_46	NZ	N_ASP_636	OD1	2.913
6NC3	G_LYS_46	NZ	N_ASP_636	OD2	3.719
6NC3	G_HIS_72	ND1	G_GLU_64	OE1	3.735
6NC3	G_LYS_117	NZ	G_ASP_113	OD1	3.847
6NC3	G_LYS_117	NZ	G_ASP_113	OD2	2.492
6NC3	G_LYS_155	NZ	G_ASP_133	OD1	2.487
6NC3	G_LYS_168	NZ	G_ASP_167	OD1	2.679
6NC3	G_LYS_168	NZ	G_ASP_167	OD2	3.249
6NC3	G_ARG_192	NH2	E_ASP_167	OD1	3.708
6NC3	G_ARG_192	NH2	E_ASP_167	OD2	3.548
6NC3	G_LYS_231	NZ	G_GLU_267	OE1	2.789
6NC3	G_LYS_231	NZ	G_GLU_267	OE2	3.510
6NC3	G_LYS_232	NZ	G_GLU_269	OE1	3.765
6NC3	G_LYS_232	NZ	G_GLU_269	OE2	2.544
6NC3	G_HIS_249	NE2	G_GLU_482	OE2	2.721
6NC3	G_LYS_290	NZ	G_GLU_268	OE1	3.516
6NC3	G_ARG_298	NH1	G_GLU_381	OE2	2.878
6NC3	G_LYS_305	NZ	G_GLU_172	OE1	2.502
6NC3	G_LYS_305	NZ	G_GLU_172	OE2	3.929
6NC3	G_LYS_337	NZ	G_GLU_293	OE2	2.661
6NC3	G_LYS_348	NZ	G_GLU_351	OE1	2.941
6NC3	G_LYS_348	NZ	G_GLU_351	OE2	3.643
6NC3	G_LYS_421	NZ	G_GLU_370	OE2	2.811
6NC3	G_LYS_432	NZ	G_ASP_113	OD1	2.553
6NC3	G_LYS_432	NZ	G_ASP_113	OD2	3.775
6NC3	G_LYS_432	NZ	G_GLU_429	OE1	3.926
6NC3	G_ARG_456	NH2	G_GLU_466	OE1	3.636
6NC3	G_ARG_456	NH2	G_GLU_466	OE2	2.864
6NC3	G_ARG_476	NH1	G_GLU_102	OE1	3.922
6NC3	G_ARG_476	NH1	G_GLU_102	OE2	3.112
6NC3	G_ARG_476	NH2	G_ASP_474	OD1	3.856
6NC3	G_ARG_476	NH2	G_ASP_474	OD2	3.032
6NC3	G_ARG_480	NH1	G_ASP_477	OD1	2.738
6NC3	G_ARG_480	NH2	G_ASP_477	OD1	3.897
6NC3	G_LYS_487	NZ	G_GLU_47	OE1	2.894
6NC3	G_LYS_487	NZ	G_GLU_47	OE2	3.821
6NC3	G_LYS_487	NZ	G_GLU_91	OE1	3.878
6NC3	G_ARG_503	NH2	N_GLU_654	OE1	3.773
6NC3	G_ARG_503	NH2	N_GLU_654	OE2	3.160
6NC3	N_ARG_542	NH2	M_GLU_647	OE1	2.825

6NC3	N_ARG_542	NH2	M_ASP_648	OD1	2.949
6NC3	N_ARG_542	NH2	M_ASP_648	OD2	3.670
6NC3	N_LYS_574	NZ	G_ASP_107	OD1	2.581
6NC3	N_LYS_574	NZ	G_ASP_107	OD2	2.710
6NC3	N_ARG_579	NH1	M_GLU_584	OE2	3.194
6NC3	N_ARG_585	NH2	G_GLU_492	OE1	2.939
6NC3	N_ARG_585	NH2	G_GLU_492	OE2	3.498
6NC3	N_LYS_617	NZ	N_GLU_634	OE1	2.815
6NC3	N_LYS_617	NZ	N_GLU_634	OE2	3.445
6NC3	S_LYS_12	NZ	S_GLU_10	OE1	3.785
6NC3	S_HIS_35	NE2	S_ASP_95	OD2	3.813
6NC3	S_ARG_38	NH1	S_ASP_86	OD1	2.638
6NC3	S_ARG_38	NH2	S_GLU_46	OE1	2.856
6NC3	S_ARG_38	NH2	S_GLU_46	OE2	3.919
6NC3	S_ARG_38	NH2	S_ASP_86	OD1	3.489
6NC3	S_LYS_62	NZ	S_GLU_46	OE2	2.819
6NC3	S_ARG_66	NH2	S_ASP_86	OD1	3.294
6NC3	S_ARG_66	NH2	S_ASP_86	OD2	3.014
6NC3	S_ARG_94	NH1	S_GLU_2	OE1	2.959
6NC3	S_ARG_94	NH2	S_GLU_2	OE1	3.018
6NC3	S_LYS_96	NZ	S_ASP_101	OD1	3.648
6NC3	S_LYS_96	NZ	S_ASP_101	OD2	2.449
6NC3	X_ARG_30	NH2	X_GLU_32	OE2	3.022
6NC3	X_ARG_61	NH1	X_GLU_81	OE2	3.991
6NC3	X_ARG_61	NH2	X_GLU_81	OE2	3.260
6NC3	X_ARG_61	NH2	X_ASP_82	OD1	2.918
6NC3	X_ARG_61	NH2	X_ASP_82	OD2	3.280
6NC3	X_LYS_103	NZ	X_GLU_105	OE2	3.920
6NC3	X_LYS_107	NZ	X_ASP_17	OD2	2.904
6NEX	L_ARG_	NH2	L_GLU_	OE2	2.737
6NEX	L_ARG_	NH2	L_ASP_	OD1	2.840
6NEX	L_ARG_	NH2	L_ASP_	OD2	3.473
6NEX	L_LYS_	NZ	L_GLU_	OE2	3.642
6NEX	H_ARG_	NH1	H_ASP_	OD1	2.811
6NEX	H_ARG_	NH2	H_GLU_	OE1	2.941
6NEX	H_ARG_	NH2	H_GLU_	OE2	3.733
6NEX	H_ARG_	NH1	H_ASP_	OD1	3.160
6NEX	H_ARG_	NH1	H_ASP_	OD2	3.548
6NEX	H_ARG_	NH2	H_ASP_	OD1	3.762
6NEX	H_ARG_	NH2	H_ASP_	OD2	2.737
6NEX	H_LYS_	NZ	H_ASP_	OD1	3.770
6NEX	H_ARG_210	NH1	H_GLU_212	OE2	3.708
6NEX	H_ARG_210	NH2	H_GLU_212	OE1	3.957
6NEX	H_ARG_210	NH2	H_GLU_212	OE2	2.338
6NEX	A_ARG_	NH2	A_GLU_	OE2	2.672
6NEX	A_ARG_	NH2	A_ASP_	OD1	2.826
6NEX	A_ARG_	NH2	A_ASP_	OD2	3.589
6NEX	A_LYS_	NZ	A_GLU_	OE1	3.636
6NEX	A_LYS_	NZ	A_GLU_	OE2	3.384
6NEX	B_ARG_	NH1	B_ASP_	OD1	2.934
6NEX	B_ARG_	NH2	B_GLU_	OE2	2.957
6NEX	B_ARG_	NH2	B_ASP_	OD1	3.823
6NEX	B_LYS_	NZ	B_ASP_	OD1	3.270
6NEX	B_ARG_	NH1	B_ASP_	OD1	3.264
6NEX	B_ARG_	NH1	B_ASP_	OD2	3.612
6NEX	B_ARG_	NH2	B_ASP_	OD2	3.065
6NEX	B_ARG_	NH1	B_GLU_	OE2	2.598
6NEX	B_LYS_	NZ	B_ASP_	OD1	3.942

6NEX	B.LYS_209	NZ	A_GLU_126	OE2	3.298
6NF2	A.LYS_46	NZ	A_GLU_492	OE2	2.493
6NF2	A.LYS_46	NZ	I_ASP_632	OD2	2.876
6NF2	A_HIS_216	NE2	A_ASP_57	OD1	2.861
6NF2	A_HIS_216	NE2	A_ASP_57	OD2	2.990
6NF2	A.LYS_227	NZ	A_GLU_83	OE1	2.516
6NF2	A.LYS_227	NZ	A_GLU_83	OE2	3.523
6NF2	A.LYS_282	NZ	A_GLU_275	OE1	3.484
6NF2	A.LYS_282	NZ	A_GLU_275	OE2	3.921
6NF2	A_ARG_419	NH1	A_GLU_153	OE1	3.359
6NF2	A_ARG_419	NH2	A_GLU_153	OE1	3.820
6NF2	A.LYS_421	NZ	A_GLU_370	OE2	3.954
6NF2	A_ARG_429	NH1	A_ASP_113	OD1	2.605
6NF2	A_ARG_429	NH1	A_ASP_113	OD2	3.059
6NF2	A_ARG_429	NH2	A_ASP_113	OD1	3.615
6NF2	A_ARG_456	NH1	A_GLU_466	OE1	3.082
6NF2	A_ARG_456	NH1	A_GLU_466	OE2	3.859
6NF2	A_ARG_476	NH2	A_ASP_474	OD1	3.180
6NF2	A.LYS_487	NZ	A_ASP_47	OD1	2.705
6NF2	A.LYS_487	NZ	A_ASP_47	OD2	3.456
6NF2	A.LYS_487	NZ	A_GLU_91	OE1	3.205
6NF2	A.LYS_490	NZ	A_GLU_492	OE1	3.081
6NF2	A_ARG_504	NH2	R_GLU_657	OE2	3.927
6NF2	B_ARG_579	NH1	I_GLU_584	OE2	3.681
6NF2	B.LYS_601	NZ	I_GLU_654	OE1	2.983
6NF2	B.LYS_601	NZ	I_GLU_654	OE2	3.256
6NF2	B_ARG_617	NH1	B_GLU_634	OE1	3.898
6NF2	B_ARG_617	NH1	B_GLU_634	OE2	3.558
6NF2	B_ARG_617	NH2	B_GLU_634	OE1	2.451
6NF2	B_ARG_617	NH2	B_GLU_634	OE2	3.092
6NF2	C.LYS_19	NZ	C_GLU_81	OE2	3.460
6NF2	C_ARG_38	NH1	C_GLU_46	OE1	2.376
6NF2	C_ARG_38	NH2	C_ASP_86	OD1	2.835
6NF2	C_ARG_38	NH2	C_ASP_86	OD2	3.913
6NF2	C_ARG_61	NH1	G_GLU_466	OE1	3.610
6NF2	C_ARG_61	NH2	G_GLU_466	OE2	3.748
6NF2	C_ARG_66	NH2	C_ASP_86	OD2	2.541
6NF2	C_ARG_71	NH2	G_ASP_368	OD1	3.504
6NF2	D_ARG_38	NH1	D_ASP_81	OD2	3.918
6NF2	D_ARG_52	NH1	D_ASP_49	OD2	2.507
6NF2	D_ARG_60	NH1	D_ASP_78	OD1	3.451
6NF2	D_ARG_60	NH1	D_ASP_78	OD2	2.551
6NF2	D_ARG_60	NH1	D_ASP_81	OD1	3.827
6NF2	D_ARG_60	NH2	D_ASP_78	OD2	3.741
6NF2	D_ARG_60	NH2	D_ASP_81	OD1	2.673
6NF2	E_ARG_30	NH1	E_ASP_53	OD1	3.557
6NF2	E_ARG_30	NH1	E_ASP_53	OD2	3.208
6NF2	E_ARG_30	NH2	E_ASP_53	OD2	3.963
6NF2	E_ARG_38	NH2	E_GLU_46	OE1	2.920
6NF2	F_ARG_31	NH2	F_ASP_92	OD2	3.578
6NF2	F_ARG_61	NH2	F_GLU_79	OE1	2.683
6NF2	F_ARG_61	NH2	F_GLU_79	OE2	3.530
6NF2	F_ARG_61	NH2	F_ASP_82	OD1	3.710
6NF2	F_ARG_95	NH1	F_GLU_25	OE1	2.962
6NF2	F_ARG_95	NH1	F_ASP_92	OD2	3.472
6NF2	G.LYS_46	NZ	B_ASP_632	OD2	2.943
6NF2	G.LYS_46	NZ	G_GLU_492	OE2	2.493
6NF2	G_HIS_216	NE2	G_ASP_57	OD1	2.861

6NF2	G_HIS_216	NE2	G_ASP_57	OD2	2.990
6NF2	G_LYS_227	NZ	G_GLU_83	OE1	2.516
6NF2	G_LYS_227	NZ	G_GLU_83	OE2	3.523
6NF2	G_LYS_282	NZ	G_GLU_275	OE1	3.483
6NF2	G_LYS_282	NZ	G_GLU_275	OE2	3.920
6NF2	G_ARG_419	NH1	G_GLU_153	OE1	3.359
6NF2	G_ARG_419	NH2	G_GLU_153	OE1	3.821
6NF2	G_LYS_421	NZ	G_GLU_370	OE2	3.954
6NF2	G_ARG_429	NH1	G_ASP_113	OD1	2.606
6NF2	G_ARG_429	NH1	G_ASP_113	OD2	3.059
6NF2	G_ARG_429	NH2	G_ASP_113	OD1	3.615
6NF2	G_ARG_456	NH1	G_GLU_466	OE1	3.082
6NF2	G_ARG_456	NH1	G_GLU_466	OE2	3.857
6NF2	G_ARG_476	NH2	G_ASP_474	OD1	3.180
6NF2	G_LYS_487	NZ	G_ASP_47	OD1	2.706
6NF2	G_LYS_487	NZ	G_ASP_47	OD2	3.456
6NF2	G_LYS_487	NZ	G_GLU_91	OE1	3.206
6NF2	G_LYS_490	NZ	G_GLU_492	OE1	3.082
6NF2	G_ARG_504	NH2	L_GLU_657	OE2	3.805
6NF2	H_LYS_13	NZ	H_GLU_16	OE1	3.322
6NF2	H_ARG_66	NH1	H_ASP_86	OD1	2.849
6NF2	H_ARG_66	NH1	H_ASP_86	OD2	2.841
6NF2	H_ARG_100F	NH1	L_ASP_50	OD2	2.403
6NF2	H_ARG_100F	NH2	L_ASP_50	OD2	3.926
6NF2	L_ARG_579	NH1	R_GLU_584	OE2	3.624
6NF2	L_LYS_601	NZ	R_GLU_654	OE1	3.068
6NF2	L_LYS_601	NZ	R_GLU_654	OE2	3.333
6NF2	L_ARG_617	NH1	L_GLU_634	OE1	3.897
6NF2	L_ARG_617	NH1	L_GLU_634	OE2	3.558
6NF2	L_ARG_617	NH2	L_GLU_634	OE1	2.451
6NF2	L_ARG_617	NH2	L_GLU_634	OE2	3.093
6NF2	J_ARG_30	NH1	J_ASP_53	OD1	3.558
6NF2	J_ARG_30	NH1	J_ASP_53	OD2	3.207
6NF2	J_ARG_30	NH2	J_ASP_53	OD2	3.963
6NF2	J_ARG_38	NH2	J_GLU_46	OE1	2.921
6NF2	K_ARG_31	NH2	K_ASP_92	OD2	3.577
6NF2	K_ARG_61	NH2	K_GLU_79	OE1	2.684
6NF2	K_ARG_61	NH2	K_GLU_79	OE2	3.531
6NF2	K_ARG_61	NH2	K_ASP_82	OD1	3.710
6NF2	K_ARG_95	NH1	K_GLU_25	OE1	2.961
6NF2	K_ARG_95	NH1	K_ASP_92	OD2	3.471
6NF2	L_ARG_24	NH1	L_ASP_70	OD2	2.515
6NF2	L_ARG_54	NH1	L_ASP_60	OD1	3.948
6NF2	L_ARG_54	NH2	L_ASP_60	OD1	2.933
6NF2	L_ARG_61	NH1	L_GLU_79	OE1	3.691
6NF2	L_ARG_61	NH1	L_GLU_79	OE2	3.057
6NF2	L_ARG_61	NH2	L_GLU_79	OE1	3.745
6NF2	M_ARG_38	NH1	M_ASP_81	OD2	3.919
6NF2	M_ARG_52	NH1	M_ASP_49	OD2	2.507
6NF2	M_ARG_60	NH1	M_ASP_78	OD1	3.451
6NF2	M_ARG_60	NH1	M_ASP_78	OD2	2.551
6NF2	M_ARG_60	NH1	M_ASP_81	OD1	3.826
6NF2	M_ARG_60	NH2	M_ASP_78	OD2	3.741
6NF2	M_ARG_60	NH2	M_ASP_81	OD1	2.674
6NF2	N_LYS_19	NZ	N_GLU_81	OE2	3.461
6NF2	N_ARG_38	NH1	N_GLU_46	OE1	2.376
6NF2	N_ARG_38	NH2	N_ASP_86	OD1	2.835
6NF2	N_ARG_38	NH2	N_ASP_86	OD2	3.913

6NF2	N_ARG.61	NH1	A_GLU_466	OE1	3.592
6NF2	N_ARG.61	NH2	A_GLU_466	OE2	3.737
6NF2	N_ARG.66	NH2	N_ASP_86	OD2	2.541
6NF2	N_ARG.71	NH2	A_ASP_368	OD1	3.532
6NF2	O_LYS.13	NZ	O_GLU_16	OE1	3.322
6NF2	O_ARG.66	NH1	O_ASP_86	OD1	2.849
6NF2	O_ARG.66	NH1	O_ASP_86	OD2	2.841
6NF2	O_ARG.100F	NH1	P_ASP_50	OD2	2.825
6NF2	P_ARG.24	NH1	P_ASP_70	OD2	2.514
6NF2	P_ARG.54	NH1	P_ASP_60	OD1	3.948
6NF2	P_ARG.54	NH2	P_ASP_60	OD1	2.932
6NF2	P_ARG.61	NH1	P_GLU_79	OE1	3.692
6NF2	P_ARG.61	NH1	P_GLU_79	OE2	3.058
6NF2	P_ARG.61	NH2	P_GLU_79	OE1	3.745
6NF2	Q_LYS.46	NZ	Q_GLU_492	OE2	2.491
6NF2	Q_LYS.46	NZ	R_ASP_632	OD2	2.912
6NF2	Q_HIS.216	NE2	Q_ASP_57	OD1	2.861
6NF2	Q_HIS.216	NE2	Q_ASP_57	OD2	2.990
6NF2	Q_LYS.227	NZ	Q_GLU_83	OE1	2.514
6NF2	Q_LYS.227	NZ	Q_GLU_83	OE2	3.524
6NF2	Q_LYS.282	NZ	Q_GLU_275	OE1	3.483
6NF2	Q_LYS.282	NZ	Q_GLU_275	OE2	3.921
6NF2	Q_ARG.419	NH1	Q_GLU_153	OE1	3.360
6NF2	Q_ARG.419	NH2	Q_GLU_153	OE1	3.820
6NF2	Q_LYS.421	NZ	Q_GLU_370	OE2	3.955
6NF2	Q_ARG.429	NH1	Q_ASP_113	OD1	2.604
6NF2	Q_ARG.429	NH1	Q_ASP_113	OD2	3.059
6NF2	Q_ARG.429	NH2	Q_ASP_113	OD1	3.616
6NF2	Q_ARG.456	NH1	Q_GLU_466	OE1	3.084
6NF2	Q_ARG.456	NH1	Q_GLU_466	OE2	3.860
6NF2	Q_ARG.476	NH2	Q_ASP_474	OD1	3.179
6NF2	Q_LYS.487	NZ	Q_ASP_47	OD1	2.706
6NF2	Q_LYS.487	NZ	Q_ASP_47	OD2	3.457
6NF2	Q_LYS.487	NZ	Q_GLU_91	OE1	3.205
6NF2	Q_LYS.490	NZ	Q_GLU_492	OE1	3.080
6NF2	Q_ARG.504	NH2	B_GLU_657	OE2	3.920
6NF2	R_ARG.579	NH1	B_GLU_584	OE2	3.657
6NF2	R_LYS.601	NZ	B_GLU_654	OE1	3.130
6NF2	R_LYS.601	NZ	B_GLU_654	OE2	3.363
6NF2	R_ARG.617	NH1	R_GLU_634	OE1	3.896
6NF2	R_ARG.617	NH1	R_GLU_634	OE2	3.558
6NF2	R_ARG.617	NH2	R_GLU_634	OE1	2.450
6NF2	R_ARG.617	NH2	R_GLU_634	OE2	3.092
6NF2	S_ARG.30	NH1	S_ASP_53	OD1	3.557
6NF2	S_ARG.30	NH1	S_ASP_53	OD2	3.207
6NF2	S_ARG.30	NH2	S_ASP_53	OD2	3.964
6NF2	S_ARG.38	NH2	S_GLU_46	OE1	2.919
6NF2	T_ARG.31	NH2	T_ASP_92	OD2	3.577
6NF2	T_ARG.61	NH2	T_GLU_79	OE1	2.683
6NF2	T_ARG.61	NH2	T_GLU_79	OE2	3.530
6NF2	T_ARG.61	NH2	T_ASP_82	OD1	3.710
6NF2	T_ARG.95	NH1	T_GLU_25	OE1	2.962
6NF2	T_ARG.95	NH1	T_ASP_92	OD2	3.472
6NF2	U_ARG.38	NH1	U_ASP_81	OD2	3.919
6NF2	U_ARG.52	NH1	U_ASP_49	OD2	2.509
6NF2	U_ARG.60	NH1	U_ASP_78	OD1	3.451
6NF2	U_ARG.60	NH1	U_ASP_78	OD2	2.550
6NF2	U_ARG.60	NH1	U_ASP_81	OD1	3.827

6NF2	U_ARG_60	NH2	U_ASP_78	OD2	3.741
6NF2	U_ARG_60	NH2	U_ASP_81	OD1	2.673
6NF2	V_LYS_19	NZ	V_GLU_81	OE2	3.461
6NF2	V_ARG_38	NH1	V_GLU_46	OE1	2.376
6NF2	V_ARG_38	NH2	V_ASP_86	OD1	2.836
6NF2	V_ARG_38	NH2	V_ASP_86	OD2	3.912
6NF2	V_ARG_61	NH1	Q_GLU_466	OE1	3.626
6NF2	V_ARG_61	NH2	Q_GLU_466	OE2	3.762
6NF2	V_ARG_66	NH2	V_ASP_86	OD2	2.542
6NF2	V_ARG_71	NH2	Q_ASP_368	OD1	3.511
6NF2	W_LYS_13	NZ	W_GLU_16	OE1	3.322
6NF2	W_ARG_66	NH1	W_ASP_86	OD1	2.849
6NF2	W_ARG_66	NH1	W_ASP_86	OD2	2.842
6NF2	W_ARG_100F	NH1	X_ASP_50	OD2	2.242
6NF2	W_ARG_100F	NH2	X_ASP_50	OD2	3.856
6NF2	X_ARG_24	NH1	X_ASP_70	OD2	2.514
6NF2	X_ARG_54	NH1	X_ASP_60	OD1	3.949
6NF2	X_ARG_54	NH2	X_ASP_60	OD1	2.932
6NF2	X_ARG_61	NH1	X_GLU_79	OE1	3.693
6NF2	X_ARG_61	NH1	X_GLU_79	OE2	3.059
6NF2	X_ARG_61	NH2	X_GLU_79	OE1	3.746
6NF5	A_LYS_46	NZ	B_ASP_632	OD2	2.410
6NF5	A_LYS_97	NZ	A_GLU_275	OE2	3.695
6NF5	A_LYS_137	NZ	L_ASP_51	OD2	2.736
6NF5	A_LYS_168	NZ	A_ASP_167	OD2	2.451
6NF5	A_ARG_178	NH2	A_GLU_153	OE1	3.939
6NF5	A_ARG_192	NH1	J_GLU_164	OE2	3.009
6NF5	A_ARG_192	NH2	J_GLU_164	OE2	3.825
6NF5	A_LYS_229	NZ	A_GLU_83	OE2	2.843
6NF5	A_LYS_232	NZ	A_GLU_268	OE1	2.483
6NF5	A_HIS_249	NE2	A_GLU_482	OE1	3.152
6NF5	A_LYS_282	NZ	A_GLU_275	OE1	3.676
6NF5	A_LYS_421	NZ	A_GLU_370	OE2	2.968
6NF5	A_ARG_456	NH1	A_GLU_466	OE1	2.887
6NF5	A_ARG_469	NH1	A_ASP_457	OD1	2.731
6NF5	A_ARG_469	NH1	A_ASP_457	OD2	2.912
6NF5	A_ARG_476	NH1	A_GLU_102	OE1	3.769
6NF5	A_ARG_476	NH1	A_GLU_102	OE2	2.949
6NF5	A_ARG_476	NH2	A_ASP_474	OD1	3.812
6NF5	A_ARG_476	NH2	A_ASP_474	OD2	2.863
6NF5	A_ARG_480	NH1	A_ASP_477	OD1	2.619
6NF5	A_LYS_485	NZ	A_GLU_267	OE2	3.474
6NF5	A_LYS_487	NZ	A_ASP_47	OD1	2.966
6NF5	A_LYS_487	NZ	A_ASP_47	OD2	2.855
6NF5	A_LYS_487	NZ	A_GLU_91	OE1	3.852
6NF5	A_LYS_490	NZ	A_GLU_492	OE2	3.881
6NF5	B_ARG_542	NH1	D_GLU_647	OE1	3.182
6NF5	B_ARG_542	NH1	D_GLU_647	OE2	3.535
6NF5	B_ARG_542	NH2	D_GLU_647	OE1	3.979
6NF5	B_LYS_574	NZ	A_ASP_107	OD1	2.887
6NF5	B_HIS_585	NE2	A_GLU_492	OE1	3.726
6NF5	B_HIS_585	NE2	B_ASP_589	OD1	3.861
6NF5	B_HIS_585	NE2	B_ASP_589	OD2	3.640
6NF5	B_LYS_601	NZ	D_GLU_657	OE1	3.026
6NF5	B_ARG_617	NH1	B_GLU_634	OE1	2.939
6NF5	B_ARG_617	NH1	B_GLU_634	OE2	3.518
6NF5	B_ARG_617	NH2	B_GLU_621	OE2	3.903
6NF5	H_ARG_38	NH1	H_ASP_86	OD1	2.711

6NF5	H_ARG_38	NH2	H_GLU_46	OE1	2.805
6NF5	H_ARG_38	NH2	H_GLU_46	OE2	3.660
6NF5	H_ARG_38	NH2	H_ASP_86	OD1	3.921
6NF5	H_ARG_50	NH1	H_GLU_95	OE1	3.017
6NF5	H_ARG_66	NH1	H_ASP_86	OD1	3.025
6NF5	H_ARG_66	NH1	H_ASP_86	OD2	3.679
6NF5	H_ARG_66	NH2	H_ASP_86	OD1	3.529
6NF5	H_ARG_66	NH2	H_ASP_86	OD2	2.747
6NF5	L_ARG_61	NH2	L_ASP_82	OD1	3.053
6NF5	L_ARG_61	NH2	L_ASP_82	OD2	3.487
6NF5	L_LYS_103	NZ	L_ASP_85	OD1	2.813
6NF5	L_LYS_103	NZ	L_ASP_85	OD2	3.823
6NF5	K_ARG_38	NH1	K_ASP_86	OD1	3.164
6NF5	K_ARG_38	NH2	K_ASP_86	OD1	2.934
6NF5	K_ARG_53	NH1	B_ASP_659	OD1	3.261
6NF5	K_ARG_53	NH1	B_ASP_659	OD2	3.240
6NF5	K_ARG_53	NH2	B_ASP_659	OD1	3.591
6NF5	K_ARG_53	NH2	B_ASP_659	OD2	2.651
6NF5	K_ARG_66	NH1	K_ASP_86	OD1	3.713
6NF5	K_ARG_66	NH1	K_ASP_86	OD2	2.791
6NF5	K_ARG_66	NH2	K_ASP_86	OD1	3.225
6NF5	K_ARG_66	NH2	K_ASP_86	OD2	3.737
6NF5	K_LYS_75	NZ	K_ASP_72	OD2	3.956
6NF5	K_LYS_100E	NZ	K_ASP_101	OD1	3.994
6NF5	K_LYS_100E	NZ	K_ASP_101	OD2	2.688
6NF5	N_ARG_54	NH2	N_ASP_60	OD1	2.562
6NF5	N_ARG_61	NH2	N_ASP_82	OD1	3.061
6NF5	N_ARG_61	NH2	N_ASP_82	OD2	3.668
6NF5	N_ARG_103	NH1	N_ASP_85	OD1	3.116
6NF5	C_LYS_46	NZ	D_ASP_632	OD2	2.410
6NF5	C_LYS_97	NZ	C_GLU_275	OE2	3.696
6NF5	C_LYS_137	NZ	F_ASP_51	OD2	2.736
6NF5	C_LYS_168	NZ	C_ASP_167	OD2	2.451
6NF5	C_ARG_178	NH2	C_GLU_153	OE1	3.938
6NF5	C_ARG_192	NH1	A_GLU_164	OE2	3.009
6NF5	C_ARG_192	NH2	A_GLU_164	OE2	3.825
6NF5	C_LYS_229	NZ	C_GLU_83	OE2	2.843
6NF5	C_LYS_232	NZ	C_GLU_268	OE1	2.483
6NF5	C_HIS_249	NE2	C_GLU_482	OE1	3.152
6NF5	C_LYS_282	NZ	C_GLU_275	OE1	3.676
6NF5	C_LYS_421	NZ	C_GLU_370	OE2	2.968
6NF5	C_ARG_456	NH1	C_GLU_466	OE1	2.887
6NF5	C_ARG_469	NH1	C_ASP_457	OD1	2.731
6NF5	C_ARG_469	NH1	C_ASP_457	OD2	2.913
6NF5	C_ARG_476	NH1	C_GLU_102	OE1	3.769
6NF5	C_ARG_476	NH1	C_GLU_102	OE2	2.949
6NF5	C_ARG_476	NH2	C_ASP_474	OD1	3.813
6NF5	C_ARG_476	NH2	C_ASP_474	OD2	2.863
6NF5	C_ARG_480	NH1	C_ASP_477	OD1	2.619
6NF5	C_LYS_485	NZ	C_GLU_267	OE2	3.473
6NF5	C_LYS_487	NZ	C_ASP_47	OD1	2.966
6NF5	C_LYS_487	NZ	C_ASP_47	OD2	2.856
6NF5	C_LYS_487	NZ	C_GLU_91	OE1	3.852
6NF5	C_LYS_490	NZ	C_GLU_492	OE2	3.881
6NF5	D_ARG_542	NH1	M_GLU_647	OE1	3.182
6NF5	D_ARG_542	NH1	M_GLU_647	OE2	3.535
6NF5	D_ARG_542	NH2	M_GLU_647	OE1	3.978
6NF5	D_LYS_574	NZ	C_ASP_107	OD1	2.887

6NF5	D_HIS_585	NE2	C_GLU_492	OE1	3.725
6NF5	D_HIS_585	NE2	D_ASP_589	OD1	3.861
6NF5	D_HIS_585	NE2	D_ASP_589	OD2	3.640
6NF5	D_LYS_601	NZ	M_GLU_657	OE1	3.026
6NF5	D_ARG_617	NH1	D_GLU_634	OE1	2.940
6NF5	D_ARG_617	NH1	D_GLU_634	OE2	3.518
6NF5	D_ARG_617	NH2	D_GLU_621	OE2	3.903
6NF5	E_ARG_38	NH1	E_ASP_86	OD1	2.712
6NF5	E_ARG_38	NH2	E_GLU_46	OE1	2.805
6NF5	E_ARG_38	NH2	E_GLU_46	OE2	3.659
6NF5	E_ARG_38	NH2	E_ASP_86	OD1	3.922
6NF5	E_ARG_50	NH1	E_GLU_95	OE1	3.018
6NF5	E_ARG_66	NH1	E_ASP_86	OD1	3.025
6NF5	E_ARG_66	NH1	E_ASP_86	OD2	3.680
6NF5	E_ARG_66	NH2	E_ASP_86	OD1	3.528
6NF5	E_ARG_66	NH2	E_ASP_86	OD2	2.747
6NF5	F_ARG_61	NH2	F_ASP_82	OD1	3.053
6NF5	F_ARG_61	NH2	F_ASP_82	OD2	3.487
6NF5	F_LYS_103	NZ	F_ASP_85	OD1	2.813
6NF5	F_LYS_103	NZ	F_ASP_85	OD2	3.823
6NF5	G_ARG_38	NH1	G_ASP_86	OD1	3.165
6NF5	G_ARG_38	NH2	G_ASP_86	OD1	2.935
6NF5	G_ARG_53	NH1	D_ASP_659	OD1	3.261
6NF5	G_ARG_53	NH1	D_ASP_659	OD2	3.240
6NF5	G_ARG_53	NH2	D_ASP_659	OD1	3.591
6NF5	G_ARG_53	NH2	D_ASP_659	OD2	2.651
6NF5	G_ARG_66	NH1	G_ASP_86	OD1	3.712
6NF5	G_ARG_66	NH1	G_ASP_86	OD2	2.791
6NF5	G_ARG_66	NH2	G_ASP_86	OD1	3.225
6NF5	G_ARG_66	NH2	G_ASP_86	OD2	3.738
6NF5	G_LYS_75	NZ	G_ASP_72	OD2	3.956
6NF5	G_LYS_100E	NZ	G_ASP_101	OD1	3.994
6NF5	G_LYS_100E	NZ	G_ASP_101	OD2	2.688
6NF5	I_ARG_54	NH2	I_ASP_60	OD1	2.564
6NF5	I_ARG_61	NH2	I_ASP_82	OD1	3.061
6NF5	I_ARG_61	NH2	I_ASP_82	OD2	3.668
6NF5	I_ARG_103	NH1	I_ASP_85	OD1	3.116
6NF5	J_LYS_46	NZ	M_ASP_632	OD2	2.410
6NF5	J_LYS_97	NZ	J_GLU_275	OE2	3.696
6NF5	J_LYS_137	NZ	P_ASP_51	OD2	2.735
6NF5	J_LYS_168	NZ	J_ASP_167	OD2	2.451
6NF5	J_ARG_178	NH2	J_GLU_153	OE1	3.938
6NF5	J_ARG_192	NH1	C_GLU_164	OE2	3.010
6NF5	J_ARG_192	NH2	C_GLU_164	OE2	3.825
6NF5	J_LYS_229	NZ	J_GLU_83	OE2	2.843
6NF5	J_LYS_232	NZ	J_GLU_268	OE1	2.482
6NF5	J_HIS_249	NE2	J_GLU_482	OE1	3.151
6NF5	J_LYS_282	NZ	J_GLU_275	OE1	3.676
6NF5	J_LYS_421	NZ	J_GLU_370	OE2	2.968
6NF5	J_ARG_456	NH1	J_GLU_466	OE1	2.887
6NF5	J_ARG_469	NH1	J_ASP_457	OD1	2.730
6NF5	J_ARG_469	NH1	J_ASP_457	OD2	2.913
6NF5	J_ARG_476	NH1	J_GLU_102	OE1	3.770
6NF5	J_ARG_476	NH1	J_GLU_102	OE2	2.949
6NF5	J_ARG_476	NH2	J_ASP_474	OD1	3.812
6NF5	J_ARG_476	NH2	J_ASP_474	OD2	2.862
6NF5	J_ARG_480	NH1	J_ASP_477	OD1	2.619
6NF5	J_LYS_485	NZ	J_GLU_267	OE2	3.474

6NF5	J_LYS_487	NZ	J_ASP_47	OD1	2.966
6NF5	J_LYS_487	NZ	J_ASP_47	OD2	2.856
6NF5	J_LYS_487	NZ	J_GLU_91	OE1	3.851
6NF5	J_LYS_490	NZ	J_GLU_492	OE2	3.881
6NF5	M_ARG_542	NH1	B_GLU_647	OE1	3.182
6NF5	M_ARG_542	NH1	B_GLU_647	OE2	3.534
6NF5	M_ARG_542	NH2	B_GLU_647	OE1	3.979
6NF5	M_LYS_574	NZ	J_ASP_107	OD1	2.887
6NF5	M_HIS_585	NE2	J_GLU_492	OE1	3.726
6NF5	M_HIS_585	NE2	M_ASP_589	OD1	3.860
6NF5	M_HIS_585	NE2	M_ASP_589	OD2	3.640
6NF5	M_LYS_601	NZ	B_GLU_657	OE1	3.027
6NF5	M_ARG_617	NH1	M_GLU_634	OE1	2.940
6NF5	M_ARG_617	NH1	M_GLU_634	OE2	3.518
6NF5	M_ARG_617	NH2	M_GLU_621	OE2	3.902
6NF5	O_ARG_38	NH1	O_ASP_86	OD1	2.712
6NF5	O_ARG_38	NH2	O_GLU_46	OE1	2.805
6NF5	O_ARG_38	NH2	O_GLU_46	OE2	3.659
6NF5	O_ARG_38	NH2	O_ASP_86	OD1	3.922
6NF5	O_ARG_50	NH1	O_GLU_95	OE1	3.017
6NF5	O_ARG_66	NH1	O_ASP_86	OD1	3.025
6NF5	O_ARG_66	NH1	O_ASP_86	OD2	3.680
6NF5	O_ARG_66	NH2	O_ASP_86	OD1	3.529
6NF5	O_ARG_66	NH2	O_ASP_86	OD2	2.748
6NF5	P_ARG_61	NH2	P_ASP_82	OD1	3.053
6NF5	P_ARG_61	NH2	P_ASP_82	OD2	3.487
6NF5	P_LYS_103	NZ	P_ASP_85	OD1	2.813
6NF5	P_LYS_103	NZ	P_ASP_85	OD2	3.823
6NF5	Q_ARG_38	NH1	Q_ASP_86	OD1	3.164
6NF5	Q_ARG_38	NH2	Q_ASP_86	OD1	2.933
6NF5	Q_ARG_53	NH1	M_ASP_659	OD1	3.262
6NF5	Q_ARG_53	NH1	M_ASP_659	OD2	3.240
6NF5	Q_ARG_53	NH2	M_ASP_659	OD1	3.591
6NF5	Q_ARG_53	NH2	M_ASP_659	OD2	2.650
6NF5	Q_ARG_66	NH1	Q_ASP_86	OD1	3.713
6NF5	Q_ARG_66	NH1	Q_ASP_86	OD2	2.791
6NF5	Q_ARG_66	NH2	Q_ASP_86	OD1	3.225
6NF5	Q_ARG_66	NH2	Q_ASP_86	OD2	3.737
6NF5	Q_LYS_75	NZ	Q_ASP_72	OD2	3.956
6NF5	Q_LYS_100E	NZ	Q_ASP_101	OD1	3.994
6NF5	Q_LYS_100E	NZ	Q_ASP_101	OD2	2.688
6NF5	R_ARG_54	NH2	R_ASP_60	OD1	2.562
6NF5	R_ARG_61	NH2	R_ASP_82	OD1	3.061
6NF5	R_ARG_61	NH2	R_ASP_82	OD2	3.667
6NF5	R_ARG_103	NH1	R_ASP_85	OD1	3.116
6NFC	C_ARG_38	NH1	C_ASP_86	OD1	3.197
6NFC	C_ARG_38	NH2	C_ASP_86	OD1	2.953
6NFC	C_LYS_43	NZ	C_GLU_46	OE1	2.792
6NFC	C_LYS_43	NZ	C_GLU_46	OE2	3.534
6NFC	C_ARG_53	NH1	I_ASP_659	OD1	3.890
6NFC	C_ARG_53	NH1	I_ASP_659	OD2	2.842
6NFC	C_ARG_53	NH2	I_ASP_659	OD2	2.675
6NFC	C_LYS_64	NZ	C_ASP_61	OD1	2.498
6NFC	C_ARG_66	NH1	C_ASP_86	OD1	3.737
6NFC	C_ARG_66	NH1	C_ASP_86	OD2	2.795
6NFC	C_ARG_66	NH2	C_ASP_86	OD1	3.194
6NFC	C_ARG_66	NH2	C_ASP_86	OD2	3.686
6NFC	C_LYS_100E	NZ	C_ASP_101	OD2	2.741

6NFC	D_ARG_54	NH1	D_ASP_60	OD1	3.484
6NFC	D_ARG_61	NH1	D_ASP_82	OD1	3.021
6NFC	D_ARG_61	NH1	D_ASP_82	OD2	3.736
6NFC	D_ARG_103	NH2	D_ASP_85	OD1	3.716
6NFC	D_ARG_103	NH2	D_ASP_85	OD2	3.091
6NFC	A_LYS_46	NZ	B_ASP_632	OD1	3.913
6NFC	A_LYS_46	NZ	B_ASP_632	OD2	2.455
6NFC	A_LYS_97	NZ	A_GLU_275	OE2	3.627
6NFC	A_LYS_137	NZ	L_ASP_51	OD2	2.690
6NFC	A_ARG_178	NH2	A_GLU_153	OE1	3.848
6NFC	A_ARG_178	NH2	A_GLU_153	OE2	3.063
6NFC	A_LYS_227	NZ	A_GLU_83	OE1	2.893
6NFC	A_LYS_229	NZ	A_GLU_83	OE2	2.829
6NFC	A_LYS_231	NZ	A_GLU_268	OE2	3.327
6NFC	A_LYS_232	NZ	A_GLU_268	OE1	3.542
6NFC	A_LYS_232	NZ	A_GLU_269	OE2	3.983
6NFC	A_LYS_282	NZ	A_GLU_275	OE1	3.354
6NFC	A_ARG_298	NH2	A_GLU_381	OE1	3.053
6NFC	A_ARG_308	NH1	A_GLU_164	OE2	2.885
6NFC	A_LYS_335	NZ	A_ASP_412	OD2	2.571
6NFC	A_LYS_351	NZ	A_GLU_269	OE1	3.918
6NFC	A_LYS_351	NZ	A_GLU_269	OE2	3.924
6NFC	A_ARG_429	NH2	A_ASP_113	OD2	3.338
6NFC	A_ARG_456	NH2	A_GLU_466	OE1	2.989
6NFC	A_ARG_456	NH2	A_GLU_466	OE2	3.574
6NFC	A_ARG_469	NH2	A_ASP_457	OD1	3.689
6NFC	A_ARG_469	NH2	A_ASP_457	OD2	3.083
6NFC	A_ARG_476	NH1	A_ASP_474	OD1	3.258
6NFC	A_ARG_476	NH1	A_ASP_474	OD2	3.799
6NFC	A_ARG_476	NH2	A_GLU_102	OE1	3.757
6NFC	A_ARG_476	NH2	A_GLU_102	OE2	3.100
6NFC	A_ARG_480	NH1	A_ASP_477	OD1	2.962
6NFC	A_LYS_487	NZ	A_ASP_47	OD1	2.724
6NFC	A_LYS_487	NZ	A_ASP_47	OD2	3.863
6NFC	A_LYS_487	NZ	A_GLU_91	OE1	3.844
6NFC	B_ARG_542	NH1	G_GLU_647	OE1	3.297
6NFC	B_ARG_542	NH1	G_GLU_647	OE2	3.640
6NFC	B_LYS_574	NZ	A_GLU_106	OE1	3.608
6NFC	B_LYS_574	NZ	A_GLU_106	OE2	2.473
6NFC	B_ARG_579	NH2	G_GLU_584	OE1	3.071
6NFC	B_ARG_579	NH2	G_GLU_584	OE2	3.850
6NFC	B_HIS_585	NE2	B_ASP_589	OD2	3.555
6NFC	B_ARG_617	NH1	B_GLU_634	OE1	2.878
6NFC	B_ARG_617	NH1	B_GLU_634	OE2	3.440
6NFC	B_ARG_617	NH2	B_GLU_621	OE2	2.967
6NFC	H_LYS_19	NZ	H_GLU_81	OE1	3.943
6NFC	H_HIS_35	NE2	H_ASP_95	OD2	2.826
6NFC	H_ARG_38	NH1	H_ASP_86	OD1	2.925
6NFC	H_ARG_38	NH2	H_GLU_46	OE1	2.914
6NFC	H_ARG_38	NH2	H_GLU_46	OE2	3.729
6NFC	H_LYS_62	NZ	H_GLU_46	OE2	3.377
6NFC	H_ARG_66	NH2	H_ASP_86	OD1	2.882
6NFC	H_ARG_66	NH2	H_ASP_86	OD2	3.067
6NFC	H_ARG_98	NH2	H_ASP_95	OD1	3.740
6NFC	L_LYS_50	NZ	H_GLU_99	OE1	3.024
6NFC	L_ARG_61	NH1	L_GLU_81	OE2	3.132
6NFC	L_ARG_61	NH1	L_ASP_82	OD1	3.859
6NFC	L_ARG_61	NH1	L_ASP_82	OD2	2.905

6NFC	L_LYS_103	NZ	L_ASP_85	OD1	2.838
6NFC	L_LYS_103	NZ	L_ASP_85	OD2	3.467
6NFC	J_ARG_38	NH1	J_ASP_86	OD1	3.229
6NFC	J_ARG_38	NH2	J_ASP_86	OD1	2.989
6NFC	J_LYS_43	NZ	J_GLU_46	OE1	2.802
6NFC	J_LYS_43	NZ	J_GLU_46	OE2	3.573
6NFC	J_ARG_53	NH1	J_ASP_52A	OD1	3.966
6NFC	J_ARG_53	NH1	G_ASP_659	OD1	3.783
6NFC	J_ARG_53	NH1	G_ASP_659	OD2	2.774
6NFC	J_ARG_53	NH2	G_ASP_659	OD2	2.735
6NFC	J_LYS_64	NZ	J_ASP_61	OD1	2.518
6NFC	J_ARG_66	NH1	J_ASP_86	OD1	3.718
6NFC	J_ARG_66	NH1	J_ASP_86	OD2	2.782
6NFC	J_ARG_66	NH2	J_ASP_86	OD1	3.192
6NFC	J_ARG_66	NH2	J_ASP_86	OD2	3.698
6NFC	J_LYS_75	NZ	J_ASP_72	OD2	2.500
6NFC	J_LYS_100E	NZ	J_ASP_101	OD2	2.686
6NFC	M_ARG_103	NH2	M_ASP_85	OD1	3.649
6NFC	M_ARG_103	NH2	M_ASP_85	OD2	3.061
6NFC	E_LYS_46	NZ	E_GLU_492	OE1	2.958
6NFC	E_LYS_46	NZ	G_ASP_632	OD1	3.927
6NFC	E_LYS_46	NZ	G_ASP_632	OD2	2.442
6NFC	E_HIS_85	NE2	E_GLU_87	OE1	3.993
6NFC	E_ARG_178	NH2	E_GLU_153	OE1	3.884
6NFC	E_ARG_178	NH2	E_GLU_153	OE2	3.098
6NFC	E_LYS_227	NZ	E_GLU_83	OE1	2.898
6NFC	E_LYS_229	NZ	E_GLU_83	OE2	2.894
6NFC	E_LYS_232	NZ	E_GLU_269	OE2	3.820
6NFC	E_HIS_249	NE2	E_GLU_482	OE1	3.961
6NFC	E_LYS_282	NZ	E_GLU_275	OE1	2.898
6NFC	E_LYS_282	NZ	E_GLU_275	OE2	3.574
6NFC	E_ARG_298	NH1	E_GLU_381	OE2	3.008
6NFC	E_ARG_308	NH1	E_GLU_164	OE2	2.931
6NFC	E_LYS_335	NZ	E_ASP_412	OD1	3.769
6NFC	E_LYS_335	NZ	E_ASP_412	OD2	2.805
6NFC	E_LYS_351	NZ	E_GLU_269	OE2	3.378
6NFC	E_ARG_429	NH2	E_ASP_113	OD2	3.262
6NFC	E_ARG_456	NH2	E_GLU_466	OE1	2.769
6NFC	E_ARG_456	NH2	E_GLU_466	OE2	3.322
6NFC	E_ARG_469	NH2	E_ASP_457	OD1	3.712
6NFC	E_ARG_469	NH2	E_ASP_457	OD2	3.034
6NFC	E_ARG_476	NH1	E_ASP_474	OD1	3.318
6NFC	E_ARG_476	NH1	E_ASP_474	OD2	3.890
6NFC	E_ARG_476	NH2	E_GLU_102	OE1	3.764
6NFC	E_ARG_476	NH2	E_GLU_102	OE2	3.083
6NFC	E_ARG_480	NH1	E_ASP_477	OD1	2.952
6NFC	E_LYS_487	NZ	E_ASP_47	OD1	2.725
6NFC	E_LYS_487	NZ	E_ASP_47	OD2	3.874
6NFC	E_LYS_487	NZ	E_GLU_91	OE1	3.818
6NFC	E_ARG_500	NH2	I_ASP_664	OD1	2.950
6NFC	E_ARG_500	NH2	I_ASP_664	OD2	3.747
6NFC	G_ARG_542	NH1	I_GLU_647	OE1	3.321
6NFC	G_ARG_542	NH1	I_GLU_647	OE2	3.884
6NFC	G_LYS_574	NZ	E_GLU_106	OE1	3.312
6NFC	G_LYS_574	NZ	E_GLU_106	OE2	2.741
6NFC	G_ARG_579	NH2	I_GLU_584	OE1	3.032
6NFC	G_ARG_579	NH2	I_GLU_584	OE2	3.885
6NFC	G_HIS_585	NE2	G_ASP_589	OD2	3.475

6NFC	G_LYS_601	NZ	I_GLU_657	OE1	2.933
6NFC	G_LYS_601	NZ	I_GLU_657	OE2	3.730
6NFC	G_ARG_617	NH1	G_GLU_634	OE1	3.252
6NFC	G_ARG_617	NH1	G_GLU_634	OE2	3.637
6NFC	G_ARG_617	NH2	G_GLU_621	OE2	3.149
6NFC	F_LYS_46	NZ	F_GLU_492	OE1	3.791
6NFC	F_LYS_46	NZ	I_ASP_632	OD1	3.960
6NFC	F_LYS_46	NZ	I_ASP_632	OD2	2.474
6NFC	F_LYS_117	NZ	F_ASP_113	OD1	3.918
6NFC	F_LYS_117	NZ	F_ASP_113	OD2	2.461
6NFC	F_ARG_178	NH2	F_GLU_153	OE1	3.758
6NFC	F_LYS_227	NZ	F_GLU_83	OE1	2.903
6NFC	F_LYS_229	NZ	F_GLU_83	OE2	2.947
6NFC	F_LYS_232	NZ	F_GLU_268	OE1	3.618
6NFC	F_LYS_232	NZ	F_GLU_269	OE2	3.891
6NFC	F_HIS_249	NE2	F_GLU_482	OE1	3.968
6NFC	F_LYS_282	NZ	F_GLU_275	OE1	2.886
6NFC	F_LYS_282	NZ	F_GLU_275	OE2	3.568
6NFC	F_ARG_298	NH2	F_GLU_381	OE1	3.051
6NFC	F_ARG_308	NH1	F_GLU_164	OE2	2.946
6NFC	F_LYS_335	NZ	F_ASP_412	OD2	2.846
6NFC	F_LYS_351	NZ	F_GLU_269	OE1	3.913
6NFC	F_LYS_351	NZ	F_GLU_269	OE2	3.773
6NFC	F_ARG_429	NH1	F_ASP_113	OD1	3.014
6NFC	F_ARG_429	NH2	F_ASP_113	OD1	2.930
6NFC	F_ARG_456	NH2	F_GLU_466	OE1	2.974
6NFC	F_ARG_456	NH2	F_GLU_466	OE2	3.635
6NFC	F_ARG_469	NH2	F_ASP_457	OD1	3.660
6NFC	F_ARG_469	NH2	F_ASP_457	OD2	3.070
6NFC	F_ARG_476	NH1	F_ASP_474	OD1	3.311
6NFC	F_ARG_476	NH1	F_ASP_474	OD2	3.824
6NFC	F_ARG_476	NH2	F_GLU_102	OE1	3.903
6NFC	F_ARG_480	NH1	F_ASP_477	OD1	2.871
6NFC	F_LYS_487	NZ	F_ASP_47	OD1	2.719
6NFC	F_LYS_487	NZ	F_ASP_47	OD2	3.910
6NFC	F_LYS_502	NZ	B_ASP_664	OD1	3.023
6NFC	I_ARG_542	NH1	B_GLU_647	OE1	3.339
6NFC	I_ARG_542	NH1	B_GLU_647	OE2	3.856
6NFC	I_LYS_574	NZ	F_ASP_107	OD1	2.742
6NFC	I_ARG_579	NH2	B_GLU_584	OE1	3.222
6NFC	I_ARG_579	NH2	B_GLU_584	OE2	3.762
6NFC	I_HIS_585	NE2	I_ASP_589	OD2	3.720
6NFC	I_LYS_601	NZ	B_GLU_657	OE1	3.945
6NFC	I_ARG_617	NH1	I_GLU_634	OE1	3.726
6NFC	K_ARG_38	NH1	K_ASP_86	OD1	3.022
6NFC	K_ARG_38	NH2	K_GLU_46	OE1	2.916
6NFC	K_ARG_38	NH2	K_GLU_46	OE2	3.525
6NFC	K_ARG_53	NH1	B_ASP_659	OD1	3.915
6NFC	K_ARG_53	NH1	B_ASP_659	OD2	2.784
6NFC	K_ARG_53	NH2	B_ASP_659	OD2	2.738
6NFC	K_LYS_64	NZ	K_ASP_61	OD1	3.796
6NFC	K_ARG_66	NH1	K_ASP_86	OD1	3.739
6NFC	K_ARG_66	NH1	K_ASP_86	OD2	2.801
6NFC	K_ARG_66	NH2	K_ASP_86	OD1	3.263
6NFC	K_ARG_66	NH2	K_ASP_86	OD2	3.749
6NFC	K_LYS_75	NZ	K_ASP_72	OD2	3.979
6NFC	K_LYS_100E	NZ	K_ASP_101	OD2	2.756
6NFC	N_ARG_54	NH1	N_ASP_60	OD1	3.576

6NFC	N_ARG.61	NH1	N_ASP.82	OD1	2.937
6NFC	N_ARG.61	NH1	N_ASP.82	OD2	3.695
6NFC	N_ARG.103	NH2	N_ASP.85	OD1	3.716
6NFC	N_ARG.103	NH2	N_ASP.85	OD2	3.096
6NMR	L_ARG.24	NH1	L_GLU.70	OE2	3.158
6NMR	L_ARG.39	NH2	L_GLU.81	OE1	3.616
6NMR	L_ARG.61	NH1	L_GLU.81	OE2	3.707
6NMR	L_ARG.61	NH1	L_ASP.82	OD1	2.354
6NMR	L_ARG.61	NH1	L_ASP.82	OD2	2.889
6NMR	L_ARG.61	NH2	L_GLU.81	OE2	2.699
6NMR	L_ARG.61	NH2	L_ASP.82	OD1	3.976
6NMR	L_LYS.150	NZ	L_GLU.196	OE1	3.160
6NMR	L_HIS.190	ND1	L_ASP.152	OD2	3.477
6NMR	L_ARG.212	NH1	L_GLU.188	OE1	3.201
6NMR	H_ARG.38	NH1	H_GLU.46	OE2	3.009
6NMR	H_ARG.38	NH1	H_ASP.88	OD1	3.678
6NMR	H_ARG.38	NH2	H_ASP.88	OD1	2.935
6NMR	H_ARG.65	NH1	H_ASP.88	OD1	3.496
6NMR	H_ARG.65	NH1	H_ASP.88	OD2	2.506
6NMR	H_ARG.65	NH2	H_ASP.88	OD1	3.005
6NMR	H_ARG.65	NH2	H_ASP.88	OD2	3.455
6NMR	H_LYS.96	NZ	H_ASP.108	OD1	3.882
6NMR	H_LYS.96	NZ	H_ASP.108	OD2	2.332
6NMR	H_LYS.150	NZ	H_ASP.151	OD1	3.197
6NMR	H_LYS.150	NZ	H_ASP.151	OD2	3.273
6NMR	H_LYS.216	NZ	L_GLU.124	OE1	3.273
6NMR	H_LYS.216	NZ	L_GLU.124	OE2	3.010
6NMR	H_LYS.217	NZ	H_GLU.219	OE1	3.365
6NMR	H_LYS.217	NZ	H_GLU.219	OE2	3.978
6NMR	S_ARG.24	NH1	S_ASP.10	OD2	3.980
6NMR	S_ARG.24	NH2	S_ASP.10	OD1	3.502
6NMR	S_ARG.40	NH2	S_GLU.47	OE2	2.570
6NMR	S_ARG.46	NH1	S_GLU.103	OE1	3.842
6NMR	S_ARG.46	NH1	S_GLU.103	OE2	3.579
6NMR	S_ARG.46	NH2	S_GLU.103	OE2	2.903
6NMR	S_ARG.59	NH1	S_ASP.85	OD1	3.806
6NMR	S_ARG.59	NH1	S_ASP.85	OD2	3.028
6NMR	S_ARG.59	NH2	S_ASP.85	OD2	2.222
6NMR	S_ARG.69	NH1	L_GLU.55	OE1	3.247
6NMR	S_ARG.69	NH1	L_GLU.55	OE2	3.038
6NMR	S_ARG.69	NH2	L_GLU.55	OE2	3.173
6NMR	B_ARG.39	NH2	B_GLU.81	OE2	3.427
6NMR	B_ARG.61	NH1	B_ASP.82	OD1	2.926
6NMR	B_ARG.61	NH1	B_ASP.82	OD2	2.375
6NMR	B_ARG.61	NH2	B_GLU.81	OE2	3.579
6NMR	B_ARG.61	NH2	B_ASP.82	OD1	3.952
6NMR	B_LYS.189	NZ	B_ASP.186	OD1	3.729
6NMR	B_ARG.212	NH1	B_GLU.188	OE1	3.038
6NMR	A_ARG.38	NH1	A_GLU.46	OE1	2.680
6NMR	A_ARG.38	NH1	A_GLU.87	OE2	3.236
6NMR	A_ARG.38	NH2	A_GLU.87	OE2	3.845
6NMR	A_ARG.65	NH1	A_ASP.88	OD1	3.503
6NMR	A_ARG.65	NH1	A_ASP.88	OD2	2.589
6NMR	A_ARG.65	NH2	A_ASP.88	OD1	2.928
6NMR	A_ARG.65	NH2	A_ASP.88	OD2	3.469
6NMR	A_LYS.74	NZ	A_ASP.71	OD2	3.116
6NMR	A_LYS.150	NZ	A_ASP.151	OD1	3.635
6NMR	A_LYS.150	NZ	A_ASP.151	OD2	3.589

6NMR	E_ARG_40	NH1	E_GLU_47	OE1	3.843
6NMR	E_ARG_40	NH1	E_GLU_47	OE2	3.651
6NMR	E_ARG_59	NH1	E_ASP_85	OD2	3.106
6NMR	E_ARG_69	NH1	B_GLU_55	OE1	2.733
6NMR	E_ARG_69	NH1	B_GLU_55	OE2	2.469
6NMR	E_ARG_69	NH2	B_GLU_55	OE1	2.510
6NMR	E_ARG_69	NH2	B_GLU_55	OE2	3.637
6NMR	G_ARG_24	NH1	G_GLU_70	OE2	3.551
6NMR	G_ARG_61	NH1	G_GLU_81	OE1	3.642
6NMR	G_ARG_61	NH2	G_GLU_81	OE1	3.695
6NMR	G_ARG_61	NH2	G_ASP_82	OD1	3.089
6NMR	G_ARG_61	NH2	G_ASP_82	OD2	3.380
6NMR	G_LYS_150	NZ	G_GLU_196	OE1	2.752
6NMR	G_HIS_190	ND1	G_ASP_152	OD2	3.424
6NMR	G_HIS_190	NE2	G_ASP_186	OD1	3.299
6NMR	G_ARG_212	NH1	G_GLU_188	OE1	3.625
6NMR	F_ARG_38	NH1	F_GLU_46	OE1	2.763
6NMR	F_ARG_38	NH2	F_ASP_88	OD1	3.207
6NMR	F_LYS_63	NZ	F_ASP_60	OD1	3.920
6NMR	F_ARG_65	NH1	F_ASP_88	OD2	3.068
6NMR	F_ARG_65	NH2	F_ASP_88	OD1	3.379
6NMR	F_ARG_65	NH2	F_ASP_88	OD2	3.500
6NMR	F_LYS_96	NZ	F_ASP_108	OD1	3.703
6NMR	F_LYS_96	NZ	F_ASP_108	OD2	2.983
6NMR	F_LYS_150	NZ	F_ASP_151	OD2	3.277
6NMR	F_LYS_217	NZ	F_GLU_219	OE1	3.922
6NMR	L_ARG_46	NH1	L_GLU_103	OE2	3.225
6NMR	L_ARG_46	NH2	L_GLU_103	OE2	3.674
6NMR	L_ARG_69	NH1	G_GLU_55	OE1	3.183
6NMR	L_ARG_69	NH1	G_GLU_55	OE2	2.119
6NMR	L_ARG_69	NH1	F_ASP_108	OD2	3.629
6NMR	L_ARG_69	NH2	G_GLU_55	OE1	2.639
6NMR	L_ARG_69	NH2	G_GLU_55	OE2	3.327
6NMR	K_ARG_54	NH2	K_GLU_60	OE2	3.656
6NMR	K_ARG_61	NH1	K_GLU_81	OE1	3.042
6NMR	K_ARG_61	NH2	K_GLU_81	OE1	3.659
6NMR	K_ARG_61	NH2	K_ASP_82	OD1	2.679
6NMR	K_ARG_61	NH2	K_ASP_82	OD2	3.306
6NMR	K_LYS_104	NZ	K_GLU_106	OE2	3.287
6NMR	K_LYS_150	NZ	K_GLU_196	OE1	3.084
6NMR	K_HIS_190	ND1	K_ASP_186	OD1	3.859
6NMR	K_ARG_212	NH1	K_GLU_188	OE2	3.131
6NMR	J_ARG_38	NH1	J_GLU_46	OE1	3.889
6NMR	J_ARG_38	NH1	J_GLU_46	OE2	3.293
6NMR	J_ARG_38	NH1	J_ASP_88	OD1	3.807
6NMR	J_ARG_38	NH2	J_ASP_88	OD1	2.826
6NMR	J_ARG_65	NH1	J_ASP_88	OD1	3.631
6NMR	J_ARG_65	NH1	J_ASP_88	OD2	2.729
6NMR	J_ARG_65	NH2	J_ASP_88	OD1	3.014
6NMR	J_ARG_65	NH2	J_ASP_88	OD2	3.359
6NMR	M_ARG_24	NH1	M_ASP_10	OD1	3.002
6NMR	M_ARG_24	NH1	M_ASP_10	OD2	3.370
6NMR	M_ARG_59	NH1	M_ASP_85	OD1	3.222
6NMR	M_ARG_59	NH1	M_ASP_85	OD2	2.493
6NMR	M_ARG_59	NH2	M_ASP_85	OD1	2.536
6NMR	M_ARG_59	NH2	M_ASP_85	OD2	3.074
6NMR	M_ARG_69	NH1	J_ASP_108	OD1	3.945
6NMR	M_ARG_69	NH1	J_ASP_108	OD2	3.140

6NMR	M_ARG_69	NH2	K_GLU_55	OE1	3.608
6NMR	M_ARG_69	NH2	J_ASP_108	OD1	1.901
6NMR	M_ARG_69	NH2	J_ASP_108	OD2	2.331
6NMS	L_ARG_24	NH2	L_GLU_70	OE2	3.738
6NMS	L_ARG_54	NH1	L_ASP_60	OD1	3.255
6NMS	L_ARG_61	NH2	L_ASP_82	OD1	2.892
6NMS	L_ARG_61	NH2	L_ASP_82	OD2	3.481
6NMS	L_ARG_94	NH2	S_GLU_111	OE1	3.728
6NMS	L_LYS_104	NZ	L_GLU_166	OE1	2.765
6NMS	L_LYS_104	NZ	L_GLU_166	OE2	3.798
6NMS	L_LYS_184	NZ	L_GLU_188	OE2	3.523
6NMS	L_LYS_189	NZ	L_ASP_186	OD1	3.714
6NMS	L_HIS_190	ND1	L_ASP_152	OD2	3.478
6NMS	L_ARG_212	NH1	L_GLU_188	OE1	3.865
6NMS	H_ARG_38	NH1	H_ASP_90	OD1	2.876
6NMS	H_ARG_38	NH2	H_GLU_46	OE1	3.437
6NMS	H_ARG_38	NH2	H_GLU_46	OE2	3.436
6NMS	H_ARG_67	NH1	H_ASP_90	OD2	2.785
6NMS	H_ARG_67	NH2	H_ASP_90	OD1	3.162
6NMS	H_ARG_67	NH2	H_ASP_90	OD2	3.281
6NMS	H_LYS_98	NZ	H_ASP_107	OD2	3.621
6NMS	H_ARG_104	NH1	H_ASP_33	OD2	3.391
6NMS	H_ARG_104	NH1	H_GLU_99	OE1	2.855
6NMS	H_ARG_104	NH1	H_GLU_99	OE2	3.265
6NMS	H_ARG_104	NH2	S_GLU_111	OE1	3.455
6NMS	H_ARG_104	NH2	S_GLU_111	OE2	2.500
6NMS	H_LYS_149	NZ	H_ASP_150	OD1	3.443
6NMS	H_LYS_149	NZ	H_ASP_150	OD2	3.773
6NMS	H_LYS_215	NZ	L_GLU_124	OE1	3.565
6NMS	H_LYS_215	NZ	L_GLU_124	OE2	3.270
6NMS	H_LYS_220	NZ	L_GLU_214	OE1	3.397
6NMS	S_LYS_11	NZ	H_ASP_33	OD1	3.001
6NMS	S_LYS_11	NZ	H_GLU_99	OE1	2.549
6NMS	S_ARG_40	NH2	S_GLU_47	OE1	2.801
6NMS	S_ARG_46	NH1	S_GLU_103	OE2	2.751
6NMS	S_ARG_46	NH2	S_GLU_103	OE2	3.693
6NMS	S_LYS_53	NZ	S_ASP_101	OD2	3.950
6NMS	S_HIS_56	ND1	A_ASP_60	OD2	2.658
6NMS	S_ARG_59	NH1	S_ASP_85	OD1	2.788
6NMS	S_ARG_59	NH1	S_ASP_85	OD2	3.425
6NMS	S_ARG_59	NH2	S_ASP_85	OD1	3.472
6NMS	S_ARG_59	NH2	S_ASP_85	OD2	2.622
6NMS	A_ARG_54	NH1	A_ASP_60	OD1	3.517
6NMS	A_ARG_61	NH2	A_GLU_81	OE2	3.125
6NMS	A_ARG_61	NH2	A_ASP_82	OD1	2.833
6NMS	A_ARG_61	NH2	A_ASP_82	OD2	3.517
6NMS	A_ARG_94	NH2	C_GLU_111	OE2	3.453
6NMS	A_LYS_104	NZ	A_GLU_166	OE1	3.888
6NMS	A_LYS_104	NZ	A_GLU_166	OE2	3.097
6NMS	A_LYS_189	NZ	A_ASP_186	OD1	3.508
6NMS	A_HIS_190	ND1	A_ASP_152	OD2	3.250
6NMS	A_ARG_212	NH1	A_GLU_188	OE2	2.785
6NMS	B_ARG_38	NH1	B_ASP_90	OD1	2.896
6NMS	B_ARG_38	NH2	B_GLU_46	OE1	3.127
6NMS	B_ARG_38	NH2	B_GLU_46	OE2	3.624
6NMS	B_ARG_67	NH1	B_ASP_90	OD2	3.000
6NMS	B_ARG_67	NH2	B_ASP_90	OD1	3.281
6NMS	B_ARG_67	NH2	B_ASP_90	OD2	3.615

6NMS	B_LYS_98	NZ	B_ASP_108	OD2	3.767
6NMS	B_ARG_104	NH1	B_ASP_33	OD2	2.846
6NMS	B_ARG_104	NH1	B_GLU_99	OE1	2.968
6NMS	B_ARG_104	NH1	B_GLU_99	OE2	3.409
6NMS	B_ARG_104	NH2	C_GLU_111	OE1	2.703
6NMS	B_ARG_104	NH2	C_GLU_111	OE2	3.000
6NMS	B_LYS_149	NZ	B_ASP_150	OD1	3.211
6NMS	B_LYS_149	NZ	B_ASP_150	OD2	3.461
6NMS	C_LYS_11	NZ	B_ASP_33	OD2	3.490
6NMS	C_LYS_11	NZ	B_GLU_99	OE1	2.892
6NMS	C_ARG_24	NH1	C_ASP_10	OD1	2.731
6NMS	C_ARG_24	NH1	C_ASP_10	OD2	2.859
6NMS	C_ARG_40	NH2	C_GLU_47	OE1	2.382
6NMS	C_ARG_46	NH1	C_GLU_103	OE2	2.805
6NMS	C_ARG_46	NH2	C_GLU_103	OE2	3.029
6NMS	C_ARG_59	NH1	C_ASP_85	OD1	3.855
6NMS	C_ARG_59	NH1	C_ASP_85	OD2	3.301
6NMS	C_ARG_59	NH2	C_ASP_85	OD1	2.480
6NMS	C_ARG_59	NH2	C_ASP_85	OD2	3.376
6NMS	C_ARG_115	NH1	B_GLU_56	OE2	3.579
6NMS	C_ARG_115	NH2	B_GLU_56	OE2	2.699
6NMT	A_ARG_26	NH1	A_ASP_46	OD2	3.596
6NMT	A_ARG_26	NH2	C_ASP_10	OD1	3.433
6NMT	A_ARG_26	NH2	C_ASP_10	OD2	3.182
6NMT	A_ARG_56	NH2	A_ASP_76	OD1	3.261
6NMT	A_ARG_56	NH2	A_ASP_77	OD1	2.770
6NMT	A_ARG_56	NH2	A_ASP_77	OD2	3.625
6NMT	A_LYS_144	NZ	A_GLU_190	OE1	2.725
6NMT	A_HIS_184	ND1	A_ASP_146	OD2	2.798
6NMT	A_LYS_185	NZ	A_GLU_208	OE2	2.842
6NMT	A_ARG_206	NH1	A_GLU_182	OE1	3.022
6NMT	B_ARG_38	NH1	B_ASP_89	OD1	2.805
6NMT	B_ARG_38	NH2	B_GLU_46	OE1	2.846
6NMT	B_ARG_38	NH2	B_ASP_89	OD1	3.887
6NMT	B_ARG_56	NH2	C_GLU_111	OE2	3.542
6NMT	B_ARG_66	NH1	B_ASP_89	OD1	3.742
6NMT	B_ARG_66	NH1	B_ASP_89	OD2	2.824
6NMT	B_ARG_66	NH2	B_ASP_89	OD1	2.986
6NMT	B_ARG_66	NH2	B_ASP_89	OD2	3.478
6NMT	B_ARG_97	NH2	B_ASP_107	OD1	3.422
6NMT	B_ARG_97	NH2	B_ASP_107	OD2	2.766
6NMT	B_LYS_149	NZ	B_ASP_150	OD1	3.170
6NMT	B_LYS_149	NZ	B_ASP_150	OD2	2.917
6NMT	B_LYS_215	NZ	A_GLU_118	OE2	3.496
6NMT	C_LYS_11	NZ	A_ASP_91	OD1	2.678
6NMT	C_LYS_11	NZ	A_ASP_91	OD2	3.319
6NMT	C_ARG_40	NH2	C_GLU_47	OE2	2.784
6NMT	C_ARG_46	NH1	C_GLU_103	OE1	3.083
6NMT	C_ARG_46	NH2	C_GLU_103	OE1	3.045
6NMT	C_ARG_59	NH1	C_ASP_85	OD1	3.125
6NMT	C_ARG_59	NH1	C_ASP_85	OD2	3.925
6NMT	C_ARG_59	NH2	C_ASP_85	OD1	3.454
6NMT	C_ARG_59	NH2	C_ASP_85	OD2	2.809
6NMT	C_LYS_105	NZ	C_GLU_3	OE1	2.957
6NMU	L_ARG_24	NH1	L_ASP_70	OD1	3.847
6NMU	L_ARG_24	NH1	L_ASP_70	OD2	3.464
6NMU	L_LYS_32	NZ	S_ASP_85	OD1	3.326
6NMU	L_ARG_61	NH1	L_ASP_82	OD2	2.822

6NMU	L_ARG_61	NH2	L_ASP_82	OD1	2.930
6NMU	L_ARG_61	NH2	L_ASP_82	OD2	3.243
6NMU	L_LYS_150	NZ	L_GLU_196	OE1	3.282
6NMU	L_HIS_190	ND1	L_ASP_152	OD2	3.169
6NMU	H_ARG_13	NH1	H_GLU_16	OE2	3.522
6NMU	H_ARG_13	NH2	H_GLU_16	OE2	3.940
6NMU	H_ARG_38	NH1	H_ASP_90	OD2	3.008
6NMU	H_ARG_38	NH2	H_GLU_46	OE1	3.672
6NMU	H_ARG_38	NH2	H_GLU_46	OE2	3.384
6NMU	H_ARG_50	NH1	S_GLU_47	OE1	3.597
6NMU	H_ARG_50	NH1	S_GLU_47	OE2	3.084
6NMU	H_ARG_50	NH2	S_GLU_47	OE1	2.989
6NMU	H_ARG_50	NH2	S_GLU_47	OE2	3.577
6NMU	H_ARG_67	NH1	H_ASP_90	OD1	2.716
6NMU	H_ARG_67	NH1	H_ASP_90	OD2	3.953
6NMU	H_ARG_67	NH2	H_ASP_90	OD1	3.430
6NMU	H_ARG_67	NH2	H_ASP_90	OD2	3.165
6NMU	H_LYS_98	NZ	H_ASP_107	OD2	2.857
6NMU	H_LYS_149	NZ	H_ASP_150	OD1	3.438
6NMU	S_ARG_24	NH2	S_ASP_10	OD1	3.643
6NMU	S_ARG_24	NH2	S_ASP_10	OD2	2.829
6NMU	S_ARG_46	NH1	S_GLU_103	OE1	3.107
6NMU	S_ARG_46	NH2	S_GLU_103	OE1	3.375
6NMU	S_LYS_53	NZ	S_ASP_101	OD1	3.593
6NMU	S_LYS_53	NZ	S_ASP_101	OD2	3.819
6NMU	S_ARG_59	NH1	S_ASP_85	OD1	2.826
6NMU	S_ARG_59	NH1	S_ASP_85	OD2	3.250
6NMU	S_ARG_59	NH2	H_ASP_101	OD2	3.444
6NMU	S_ARG_59	NH2	S_ASP_85	OD1	3.666
6NMU	S_ARG_59	NH2	S_ASP_85	OD2	2.554
6NMU	A_LYS_32	NZ	C_ASP_85	OD1	3.635
6NMU	A_ARG_61	NH1	A_ASP_82	OD2	2.912
6NMU	A_ARG_61	NH2	A_ASP_82	OD1	3.034
6NMU	A_ARG_61	NH2	A_ASP_82	OD2	3.051
6NMU	A_ARG_98	NH2	A_GLU_1	OE2	3.553
6NMU	B_ARG_38	NH1	B_ASP_90	OD1	3.513
6NMU	B_ARG_38	NH2	B_GLU_46	OE1	3.545
6NMU	B_ARG_38	NH2	B_GLU_46	OE2	3.227
6NMU	B_ARG_50	NH1	C_GLU_47	OE1	3.989
6NMU	B_ARG_50	NH1	C_GLU_47	OE2	3.035
6NMU	B_ARG_50	NH2	C_GLU_47	OE1	2.804
6NMU	B_ARG_50	NH2	C_GLU_47	OE2	3.091
6NMU	B_ARG_67	NH1	B_ASP_90	OD1	3.761
6NMU	B_ARG_67	NH1	B_ASP_90	OD2	2.940
6NMU	B_ARG_67	NH2	B_ASP_90	OD1	2.900
6NMU	B_ARG_67	NH2	B_ASP_90	OD2	3.596
6NMU	B_LYS_98	NZ	B_ASP_107	OD1	2.896
6NMU	B_LYS_149	NZ	B_ASP_150	OD1	3.427
6NMU	B_LYS_149	NZ	B_ASP_150	OD2	3.506
6NMU	B_LYS_215	NZ	A_GLU_124	OE1	3.494
6NMU	B_LYS_215	NZ	A_GLU_124	OE2	3.379
6NMU	B_LYS_216	NZ	B_GLU_218	OE1	3.942
6NMU	C_ARG_24	NH1	C_ASP_10	OD1	3.661
6NMU	C_ARG_24	NH1	C_ASP_10	OD2	3.733
6NMU	C_ARG_24	NH2	C_ASP_10	OD1	3.751
6NMU	C_ARG_46	NH1	C_GLU_103	OE1	2.724
6NMU	C_ARG_46	NH2	C_GLU_103	OE1	3.025
6NMU	C_ARG_59	NH1	B_ASP_101	OD1	3.720

6NMU	C_ARG_59	NH1	B_ASP_101	OD2	2.808
6NMU	C_ARG_59	NH1	C_ASP_85	OD2	3.825
6NMU	C_ARG_59	NH2	C_ASP_85	OD1	2.746
6NMU	C_ARG_59	NH2	C_ASP_85	OD2	3.128
6NMV	S_ARG_40	NH2	S_GLU_47	OE2	2.928
6NMV	S_ARG_46	NH1	S_GLU_103	OE1	2.838
6NMV	S_ARG_46	NH1	S_GLU_103	OE2	3.875
6NMV	S_ARG_46	NH2	S_GLU_103	OE1	3.070
6NMV	S_ARG_59	NH1	S_ASP_85	OD1	2.912
6NMV	S_ARG_59	NH1	S_ASP_85	OD2	3.273
6NMV	S_ARG_59	NH2	S_ASP_85	OD1	3.839
6NMV	S_ARG_59	NH2	S_ASP_85	OD2	2.616
6NMV	S_LYS_96	NZ	S_ASP_101	OD1	2.456
6NMV	S_LYS_96	NZ	S_ASP_101	OD2	3.521
6NMV	H_ARG_38	NH1	H_ASP_90	OD2	2.817
6NMV	H_ARG_38	NH2	H_ASP_90	OD2	3.510
6NMV	H_ARG_67	NH1	H_ASP_90	OD1	2.934
6NMV	H_ARG_67	NH1	H_ASP_90	OD2	3.250
6NMV	H_ARG_67	NH2	H_ASP_90	OD1	3.025
6NMV	H_ARG_67	NH2	H_ASP_90	OD2	2.954
6NMV	H_LYS_76	NZ	H_ASP_73	OD1	2.991
6NMV	H_LYS_76	NZ	H_ASP_73	OD2	2.854
6NMV	H_HIS_103	ND1	H_ASP_102	OD1	3.753
6NMV	H_HIS_103	ND1	H_ASP_102	OD2	3.398
6NMV	H_LYS_211	NZ	H_GLU_213	OE2	3.838
6NMV	L_ARG_56	NH2	L_GLU_76	OE1	3.634
6NMV	L_ARG_56	NH2	L_GLU_76	OE2	3.096
6NMV	L_ARG_56	NH2	L_ASP_77	OD1	2.690
6NMV	L_ARG_56	NH2	L_ASP_77	OD2	3.240
6NMV	L_LYS_162	NZ	L_GLU_78	OE2	3.175
6NMV	L_ARG_185	NH1	L_ASP_147	OD2	3.022
6O9B	A_HIS_3	ND1	A_ASP_29	OD1	3.484
6O9B	A_HIS_3	ND1	A_ASP_29	OD2	2.647
6O9B	A_ARG_6	NH2	A_ASP_102	OD1	3.670
6O9B	A_ARG_14	NH1	A_ASP_39	OD1	2.811
6O9B	A_ARG_14	NH1	A_ASP_39	OD2	3.600
6O9B	A_ARG_14	NH2	A_ASP_39	OD1	3.638
6O9B	A_ARG_14	NH2	A_ASP_39	OD2	2.902
6O9B	A_ARG_21	NH2	A_ASP_37	OD1	3.576
6O9B	A_ARG_21	NH2	A_ASP_37	OD2	2.758
6O9B	A_ARG_35	NH1	B_ASP_73	OD1	2.773
6O9B	A_ARG_35	NH1	B_ASP_73	OD2	3.974
6O9B	A_ARG_35	NH2	A_GLU_46	OE1	3.894
6O9B	A_ARG_35	NH2	A_GLU_46	OE2	3.171
6O9B	A_ARG_44	NH1	A_ASP_61	OD1	3.041
6O9B	A_ARG_44	NH2	A_ASP_61	OD1	3.227
6O9B	A_ARG_48	NH2	B_ASP_73	OD2	3.479
6O9B	A_ARG_75	NH1	A_GLU_19	OE2	3.730
6O9B	A_HIS_93	ND1	A_ASP_119	OD1	3.532
6O9B	A_HIS_93	ND1	A_ASP_119	OD2	2.838
6O9B	A_ARG_111	NH1	A_GLU_128	OE1	3.371
6O9B	A_ARG_111	NH2	A_ASP_102	OD2	3.967
6O9B	A_ARG_114	NH1	A_ASP_116	OD1	3.450
6O9B	A_ARG_114	NH1	A_ASP_116	OD2	2.611
6O9B	A_HIS_151	ND1	A_GLU_154	OE1	3.521
6O9B	A_HIS_151	ND1	A_GLU_154	OE2	3.425
6O9B	A_ARG_169	NH1	A_GLU_166	OE2	3.051
6O9B	A_ARG_170	NH1	A_GLU_166	OE1	3.610

6O9B	A_LYS_176	NZ	A_GLU_173	OE2	2.914
6O9B	A_ARG_181	NH1	A_ASP_183	OD2	2.854
6O9B	A_HIS_191	NE2	A_GLU_254	OE2	2.884
6O9B	A_HIS_192	ND1	B_ASP_118	OD2	3.864
6O9B	A_ARG_256	NH1	A_GLU_253	OE2	3.337
6O9B	A_ARG_256	NH2	A_ASP_220	OD1	3.231
6O9B	A_ARG_256	NH2	A_ASP_220	OD2	3.184
6O9B	B_ARG_65	NH2	B_ASP_58	OD1	3.970
6O9B	B_LYS_95	NZ	B_GLU_94	OE2	3.964
6O9B	B_ARG_101	NH1	B_ASP_58	OD2	3.244
6O9B	C_LYS_9	NZ	A_ASP_116	OD2	2.706
6O9C	A_HIS_3	ND1	A_ASP_29	OD1	3.533
6O9C	A_HIS_3	ND1	A_ASP_29	OD2	2.591
6O9C	A_ARG_14	NH2	A_ASP_39	OD1	3.395
6O9C	A_ARG_14	NH2	A_ASP_39	OD2	3.458
6O9C	A_ARG_21	NH1	A_ASP_39	OD2	3.725
6O9C	A_ARG_21	NH2	A_ASP_37	OD1	3.787
6O9C	A_ARG_21	NH2	A_ASP_37	OD2	3.069
6O9C	A_ARG_35	NH1	A_ASP_37	OD2	3.939
6O9C	A_ARG_35	NH1	B_ASP_73	OD1	3.395
6O9C	A_ARG_35	NH2	A_GLU_46	OE1	3.628
6O9C	A_ARG_35	NH2	A_GLU_46	OE2	2.787
6O9C	A_ARG_44	NH1	A_ASP_61	OD1	3.116
6O9C	A_ARG_44	NH2	A_ASP_61	OD1	2.964
6O9C	A_ARG_48	NH1	A_GLU_46	OE1	3.653
6O9C	A_ARG_48	NH2	A_GLU_46	OE1	3.457
6O9C	A_HIS_93	ND1	A_ASP_119	OD1	3.563
6O9C	A_HIS_93	ND1	A_ASP_119	OD2	2.884
6O9C	A_ARG_108	NH2	A_ASP_106	OD1	3.075
6O9C	A_ARG_111	NH1	A_ASP_102	OD2	3.448
6O9C	A_ARG_114	NH1	A_ASP_116	OD1	3.523
6O9C	A_ARG_114	NH1	A_ASP_116	OD2	2.739
6O9C	A_ARG_169	NH2	A_GLU_166	OE2	3.041
6O9C	A_ARG_170	NH1	A_GLU_166	OE1	3.871
6O9C	A_LYS_176	NZ	A_GLU_173	OE2	3.474
6O9C	A_HIS_191	NE2	A_GLU_254	OE2	2.693
6O9C	A_HIS_192	NE2	B_ASP_118	OD2	3.199
6O9C	A_ARG_202	NH1	B_ASP_118	OD2	3.014
6O9C	A_ARG_256	NH1	A_ASP_220	OD2	3.945
6O9C	A_ARG_256	NH1	A_GLU_253	OE2	3.454
6O9C	A_ARG_256	NH2	A_ASP_220	OD1	3.827
6O9C	A_ARG_256	NH2	A_ASP_220	OD2	2.698
6O9C	B_ARG_23	NH1	B_ASP_79	OD2	3.597
6O9C	B_LYS_26	NZ	A_GLU_232	OE2	3.913
6O9C	B_LYS_39	NZ	B_GLU_36	OE1	3.574
6O9C	B_ARG_65	NH1	B_ASP_58	OD1	3.907
6O9C	B_ARG_65	NH1	B_GLU_67	OE2	3.387
6O9C	B_ARG_101	NH2	B_ASP_58	OD2	3.040
6O9C	C_LYS_9	NZ	A_ASP_77	OD2	3.855
6O9C	C_LYS_9	NZ	A_ASP_116	OD2	2.984
6OGX	C_LYS_12	NZ	C_GLU_10	OE2	3.904
6OGX	C_ARG_38	NH1	C_ASP_90	OD1	2.937
6OGX	C_ARG_38	NH2	C_GLU_46	OE2	3.462
6OGX	C_ARG_67	NH1	C_ASP_90	OD1	3.674
6OGX	C_ARG_67	NH1	C_ASP_90	OD2	2.808
6OGX	C_ARG_67	NH2	C_ASP_90	OD1	2.780
6OGX	C_ARG_67	NH2	C_ASP_90	OD2	3.408
6OGX	C_ARG_101	NH2	C_ASP_50	OD1	2.908

6OGX	C_ARG_101	NH2	C_ASP_50	OD2	3.364
6OGX	C_LYS_147	NZ	C_ASP_148	OD1	3.403
6OGX	C_LYS_147	NZ	C_ASP_148	OD2	3.834
6OGX	C_LYS_213	NZ	D_GLU_123	OE1	2.791
6OGX	C_LYS_213	NZ	D_GLU_123	OE2	3.773
6OGX	C_LYS_218	NZ	D_ASP_122	OD2	3.785
6OGX	D_ARG_24	NH1	D_ASP_70	OD1	2.881
6OGX	D_ARG_24	NH2	D_ASP_70	OD1	3.409
6OGX	D_ARG_24	NH2	D_ASP_70	OD2	3.280
6OGX	D_ARG_55	NH2	G_ASP_117	OD1	2.990
6OGX	D_ARG_61	NH2	D_GLU_81	OE1	3.619
6OGX	D_ARG_61	NH2	D_ASP_82	OD1	2.844
6OGX	D_ARG_61	NH2	D_ASP_82	OD2	3.707
6OGX	D_HIS_189	ND1	D_ASP_151	OD2	3.260
6OGX	D_LYS_190	NZ	D_GLU_213	OE1	3.539
6OGX	G_ARG_95	NH1	H_ASP_99	OD1	3.462
6OGX	G_ARG_95	NH1	H_ASP_99	OD2	2.833
6OGX	G_ARG_95	NH2	H_ASP_99	OD1	2.923
6OGX	G_ARG_95	NH2	H_ASP_99	OD2	3.646
6OGX	G_LYS_96	NZ	G_GLU_94	OE2	3.997
6OGX	G_ARG_110	NH2	G_GLU_94	OE1	3.529
6OGX	G_LYS_120	NZ	G_ASP_117	OD1	3.499
6OGX	G_LYS_120	NZ	G_ASP_117	OD2	3.674
6OGX	H_LYS_12	NZ	H_GLU_10	OE1	3.316
6OGX	H_ARG_38	NH1	H_ASP_90	OD2	2.947
6OGX	H_ARG_38	NH2	H_GLU_46	OE1	3.229
6OGX	H_ARG_38	NH2	H_ASP_90	OD2	3.994
6OGX	H_LYS_63	NZ	H_GLU_46	OE1	3.798
6OGX	H_LYS_63	NZ	H_GLU_46	OE2	2.760
6OGX	H_ARG_67	NH1	H_ASP_90	OD1	3.110
6OGX	H_ARG_67	NH1	H_ASP_90	OD2	3.101
6OGX	H_ARG_67	NH2	H_ASP_90	OD1	3.614
6OGX	H_ARG_67	NH2	H_ASP_90	OD2	2.757
6OGX	H_ARG_87	NH2	H_GLU_89	OE2	3.153
6OGX	H_ARG_98	NH1	H_ASP_102	OD1	3.528
6OGX	H_ARG_98	NH1	H_ASP_102	OD2	2.722
6OGX	H_ARG_100	NH1	L_GLU_55	OE1	3.516
6OGX	H_ARG_100	NH1	L_GLU_55	OE2	2.787
6OGX	H_LYS_144	NZ	H_ASP_145	OD1	3.450
6OGX	H_LYS_144	NZ	H_ASP_145	OD2	2.902
6OGX	H_LYS_211	NZ	H_GLU_213	OE1	2.815
6OGX	L_ARG_61	NH2	L_ASP_82	OD1	2.857
6OGX	L_ARG_61	NH2	L_ASP_82	OD2	3.713
6OGX	L_LYS_103	NZ	L_GLU_165	OE1	2.789
6OGX	L_LYS_103	NZ	L_GLU_165	OE2	3.599
6OKM	H_LYS_12	NZ	H_GLU_10	OE1	3.648
6OKM	H_LYS_19	NZ	H_GLU_82	OE2	3.437
6OKM	H_ARG_38	NH1	H_ASP_90	OD1	2.918
6OKM	H_ARG_38	NH2	H_GLU_46	OE1	3.013
6OKM	H_ARG_38	NH2	H_ASP_90	OD1	3.782
6OKM	H_LYS_63	NZ	H_GLU_46	OE1	3.808
6OKM	H_LYS_63	NZ	H_GLU_46	OE2	2.757
6OKM	H_LYS_65	NZ	H_GLU_62	OE2	2.941
6OKM	H_ARG_67	NH1	H_ASP_90	OD1	3.731
6OKM	H_ARG_67	NH1	H_ASP_90	OD2	2.994
6OKM	H_ARG_67	NH2	H_ASP_90	OD1	2.792
6OKM	H_ARG_67	NH2	H_ASP_90	OD2	3.476
6OKM	H_ARG_98	NH1	H_ASP_102	OD1	3.580

6OKM	H_ARG_98	NH1	H_ASP_102	OD2	3.014
6OKM	H_ARG_100	NH1	L_GLU_55	OE1	2.851
6OKM	H_LYS_144	NZ	H_ASP_145	OD1	3.343
6OKM	H_LYS_144	NZ	H_ASP_145	OD2	2.800
6OKM	H_HIS_165	NE2	L_ASP_167	OD1	3.460
6OKM	H_LYS_210	NZ	L_GLU_123	OE2	3.540
6OKM	H_LYS_211	NZ	H_GLU_213	OE1	3.622
6OKM	H_LYS_215	NZ	L_ASP_122	OD1	3.237
6OKM	H_LYS_215	NZ	L_ASP_122	OD2	3.538
6OKM	L_HIS_24	ND1	L_ASP_70	OD1	2.785
6OKM	L_HIS_24	ND1	L_ASP_70	OD2	3.925
6OKM	L_ARG_61	NH2	L_GLU_81	OE2	3.773
6OKM	L_ARG_61	NH2	L_ASP_82	OD1	2.807
6OKM	L_ARG_61	NH2	L_ASP_82	OD2	3.536
6OKM	L_ARG_142	NH1	L_GLU_105	OE2	2.944
6OKM	L_ARG_142	NH1	L_GLU_165	OE1	3.753
6OKM	L_ARG_142	NH2	L_GLU_165	OE1	3.529
6OKM	L_ARG_142	NH2	L_GLU_165	OE2	2.617
6OKM	L_LYS_145	NZ	L_GLU_195	OE2	2.987
6OKM	L_LYS_183	NZ	L_GLU_187	OE1	3.533
6OKM	R_HIS_44	NE2	R_ASP_34	OD1	3.867
6OKM	R_ARG_47	NH1	R_ASP_34	OD1	3.651
6OKM	R_LYS_82	NZ	R_ASP_74	OD1	3.045
6OKM	R_ARG_95	NH1	H_ASP_99	OD1	3.347
6OKM	R_ARG_95	NH1	H_ASP_99	OD2	3.783
6OKM	R_ARG_95	NH2	H_ASP_99	OD1	3.371
6OKM	R_ARG_95	NH2	H_ASP_99	OD2	2.555
6OKN	A_LYS_12	NZ	A_GLU_10	OE2	3.091
6OKN	A_ARG_38	NH1	A_ASP_90	OD1	2.825
6OKN	A_ARG_38	NH2	A_GLU_46	OE2	3.132
6OKN	A_LYS_63	NZ	A_GLU_46	OE1	3.198
6OKN	A_ARG_67	NH1	A_ASP_90	OD1	3.100
6OKN	A_ARG_67	NH1	A_ASP_90	OD2	3.478
6OKN	A_ARG_67	NH2	A_ASP_90	OD1	3.897
6OKN	A_ARG_67	NH2	A_ASP_90	OD2	2.783
6OKN	A_ARG_87	NH1	A_GLU_89	OE2	3.350
6OKN	A_ARG_101	NH2	A_ASP_50	OD1	2.814
6OKN	A_ARG_101	NH2	A_ASP_50	OD2	3.671
6OKN	A_LYS_210	NZ	A_ASP_212	OD1	3.571
6OKN	A_LYS_210	NZ	A_ASP_212	OD2	2.910
6OKN	A_LYS_213	NZ	B_GLU_123	OE1	3.312
6OKN	A_LYS_213	NZ	B_GLU_123	OE2	2.829
6OKN	A_LYS_214	NZ	A_GLU_216	OE1	2.957
6OKN	B_ARG_24	NH2	B_ASP_70	OD2	2.962
6OKN	B_ARG_61	NH2	B_ASP_82	OD1	2.800
6OKN	B_ARG_61	NH2	B_ASP_82	OD2	3.520
6OKN	B_LYS_103	NZ	B_GLU_165	OE1	3.396
6OKN	B_ARG_142	NH2	B_GLU_165	OE2	3.573
6OKN	B_LYS_149	NZ	B_GLU_195	OE1	3.927
6OKN	B_LYS_149	NZ	B_GLU_195	OE2	3.761
6OKN	B_LYS_183	NZ	B_GLU_187	OE2	3.169
6OKN	B_LYS_188	NZ	B_ASP_185	OD2	3.891
6OKN	B_HIS_189	ND1	B_ASP_151	OD2	2.830
6OKN	C_LYS_12	NZ	C_GLU_10	OE2	3.089
6OKN	C_LYS_19	NZ	C_GLU_82	OE1	3.422
6OKN	C_ARG_38	NH1	C_ASP_90	OD1	2.800
6OKN	C_ARG_38	NH2	C_GLU_46	OE2	3.128
6OKN	C_ARG_67	NH2	C_ASP_90	OD1	3.311

6OKN	C_ARG_67	NH2	C_ASP_90	OD2	2.765
6OKN	C_ARG_87	NH1	C_GLU_89	OE2	3.419
6OKN	C_LYS_147	NZ	C_ASP_148	OD1	3.408
6OKN	C_LYS_147	NZ	C_ASP_148	OD2	3.266
6OKN	C_LYS_210	NZ	C_ASP_212	OD1	3.569
6OKN	C_LYS_210	NZ	C_ASP_212	OD2	2.918
6OKN	C_LYS_213	NZ	D_GLU_123	OE1	3.356
6OKN	C_LYS_213	NZ	D_GLU_123	OE2	2.896
6OKN	C_LYS_214	NZ	C_GLU_216	OE1	2.949
6OKN	C_LYS_218	NZ	D_ASP_122	OD2	3.923
6OKN	D_ARG_24	NH2	D_ASP_70	OD2	2.953
6OKN	D_ARG_61	NH2	D_ASP_82	OD1	2.797
6OKN	D_ARG_61	NH2	D_ASP_82	OD2	3.516
6OKN	D_LYS_103	NZ	D_GLU_165	OE1	3.551
6OKN	D_ARG_142	NH1	D_GLU_143	OE2	3.897
6OKN	D_LYS_149	NZ	D_GLU_195	OE1	2.973
6OKN	D_LYS_149	NZ	D_GLU_195	OE2	3.725
6OKN	D_LYS_183	NZ	D_GLU_187	OE2	3.166
6OKN	D_LYS_188	NZ	D_ASP_185	OD1	3.552
6OKN	D_LYS_188	NZ	D_ASP_185	OD2	2.987
6OKN	D_HIS_189	ND1	D_ASP_151	OD2	2.861
6OKN	E_ARG_108	NH1	E_ASP_137	OD1	3.561
6OKN	E_ARG_110	NH1	E_GLU_94	OE2	3.361
6OKN	E_ARG_110	NH2	E_GLU_94	OE2	3.771
6OKN	R_ARG_108	NH2	R_ASP_137	OD1	3.846
6OKN	R_ARG_110	NH2	R_GLU_94	OE2	3.184
6OOR	A_ARG_25	NH1	A_ASP_43	OD1	3.325
6OOR	A_ARG_25	NH1	A_ASP_43	OD2	3.379
6OOR	A_ARG_25	NH2	A_ASP_43	OD2	3.436
6OOR	A_LYS_51	NZ	A_GLU_243	OE1	2.738
6OOR	A_LYS_51	NZ	A_GLU_243	OE2	3.127
6OOR	A_LYS_148	NZ	H_ASP_55	OD2	3.250
6OOR	A_HIS_203	ND1	A_ASP_252	OD1	2.639
6OOR	A_HIS_203	ND1	A_ASP_252	OD2	3.969
6OOR	A_ARG_264	NH2	A_ASP_274	OD2	3.670
6OOR	A_LYS_266	NZ	A_ASP_274	OD2	2.771
6OOR	B_ARG_12	NH2	A_ASP_242	OD1	3.946
6OOR	B_ARG_12	NH2	A_ASP_242	OD2	2.705
6OOR	B_HIS_34	NE2	A_GLU_97	OE1	2.803
6OOR	B_HIS_34	NE2	A_GLU_97	OE2	3.580
6OOR	B_LYS_48	NZ	B_GLU_50	OE2	3.789
6OOR	B_LYS_48	NZ	B_GLU_69	OE2	3.855
6OOR	L_ARG_66	NH2	L_GLU_86	OE2	3.235
6OOR	L_ARG_66	NH2	L_ASP_87	OD1	2.858
6OOR	L_ARG_66	NH2	L_ASP_87	OD2	3.400
6OOR	L_LYS_152	NZ	L_GLU_159	OE2	3.764
6OOR	L_LYS_154	NZ	L_GLU_200	OE1	2.808
6OOR	L_LYS_154	NZ	L_GLU_200	OE2	3.333
6OOR	L_ARG_160	NH2	L_ASP_190	OD1	3.044
6OOR	L_ARG_160	NH2	L_ASP_190	OD2	3.065
6OOR	L_ARG_161	NH2	L_GLU_159	OE1	3.906
6OOR	L_ARG_161	NH2	L_GLU_159	OE2	3.222
6OOR	L_HIS_194	ND1	L_ASP_190	OD1	3.947
6OOR	L_LYS_204	NZ	L_ASP_115	OD1	3.329
6OOR	L_LYS_204	NZ	L_ASP_115	OD2	2.404
6OOR	H_ARG_38	NH1	H_ASP_90	OD1	3.007
6OOR	H_ARG_38	NH2	H_GLU_46	OE2	2.874
6OOR	H_ARG_52	NH1	H_ASP_33	OD2	2.683

6OOR	H_ARG_61	NH1	H_GLU_46	OE1	3.910
6OOR	H_ARG_61	NH2	H_GLU_46	OE1	3.595
6OOR	H_ARG_67	NH1	H_ASP_90	OD1	3.879
6OOR	H_ARG_67	NH2	H_ASP_90	OD1	3.229
6OOR	H_ARG_67	NH2	H_ASP_90	OD2	2.355
6OOR	H_ARG_98	NH2	H_ASP_115	OD2	3.198
6OOR	H_ARG_109	NH2	A_ASP_80	OD1	2.917
6OOR	H_ARG_109	NH2	A_ASP_80	OD2	3.352
6OOR	H_LYS_220	NZ	L_GLU_128	OE1	2.677
6OOR	H_LYS_220	NZ	L_GLU_128	OE2	2.872
6OSY	2_HIS_216	NE2	2_ASP_57	OD1	3.190
6OSY	2_LYS_229	NZ	2_GLU_83	OE1	3.622
6OSY	2_LYS_229	NZ	2_GLU_83	OE2	2.450
6OSY	2_LYS_231	NZ	2_GLU_269	OE1	3.698
6OSY	2_LYS_231	NZ	2_GLU_269	OE2	3.406
6OSY	2_LYS_282	NZ	8_ASP_100C	OD2	3.941
6OSY	2_ARG_298	NH1	2_GLU_381	OE1	3.961
6OSY	2_ARG_469	NH1	2_ASP_457	OD1	3.797
6OSY	2_ARG_469	NH1	2_ASP_457	OD2	2.471
6OSY	2_ARG_469	NH2	2_ASP_457	OD2	3.905
6OSY	2_ARG_480	NH1	2_ASP_477	OD1	2.969
6OSY	2_LYS_487	NZ	2_ASP_47	OD1	2.484
6OSY	2_LYS_487	NZ	2_GLU_91	OE1	3.279
6OSY	5_ARG_38	NH1	5_ASP_86	OD1	2.426
6OSY	5_ARG_38	NH2	5_ASP_86	OD1	3.798
6OSY	5_HIS_52	ND1	5_ASP_53	OD1	3.541
6OSY	5_HIS_52	NE2	5_ASP_53	OD1	2.927
6OSY	5_ARG_66	NH2	5_ASP_86	OD1	2.765
6OSY	5_ARG_66	NH2	5_ASP_86	OD2	3.200
6OSY	6_ARG_54	NH1	6_ASP_60	OD2	3.135
6OSY	6_ARG_54	NH2	6_ASP_60	OD1	3.545
6OSY	6_ARG_54	NH2	6_ASP_60	OD2	3.739
6OSY	6_ARG_61	NH2	6_GLU_79	OE1	3.562
6OSY	6_ARG_61	NH2	6_GLU_79	OE2	2.945
6OSY	7_ARG_60	NH2	7_ASP_78	OD1	3.680
6OSY	7_LYS_76	NZ	7_ASP_78	OD1	3.618
6OSY	8_ARG_38	NH2	8_ASP_86	OD1	2.575
6OSY	8_ARG_61	NH1	2_GLU_466	OE2	3.827
6OSY	8_ARG_71	NH1	2_ASP_368	OD2	3.948
6OSY	8_ARG_71	NH2	2_ASP_368	OD2	3.279
6OSY	A_ARG_542	NH1	Q_GLU_647	OE2	3.907
6OSY	A_ARG_542	NH2	Q_GLU_647	OE1	3.187
6OSY	A_ARG_542	NH2	Q_GLU_647	OE2	2.660
6OSY	A_ARG_579	NH2	Q_GLU_584	OE1	3.706
6OSY	A_ARG_588	NH2	A_GLU_584	OE2	3.896
6OSY	A_ARG_617	NH1	A_GLU_634	OE1	3.782
6OSY	A_ARG_617	NH1	A_GLU_634	OE2	2.878
6OSY	B_HIS_85	NE2	B_GLU_87	OE2	3.796
6OSY	B_HIS_216	NE2	B_ASP_57	OD1	3.161
6OSY	B_LYS_229	NZ	B_GLU_83	OE1	3.600
6OSY	B_LYS_229	NZ	B_GLU_83	OE2	2.450
6OSY	B_LYS_231	NZ	B_GLU_269	OE1	3.715
6OSY	B_LYS_231	NZ	B_GLU_269	OE2	3.368
6OSY	B_LYS_282	NZ	F_ASP_100C	OD1	3.567
6OSY	B_LYS_282	NZ	F_ASP_100C	OD2	3.346
6OSY	B_LYS_421	NZ	B_ASP_180	OD1	3.951
6OSY	B_ARG_469	NH1	B_ASP_457	OD1	3.948
6OSY	B_ARG_469	NH1	B_ASP_457	OD2	2.695

6OSY	B_ARG_469	NH2	B_ASP_457	OD2	3.861
6OSY	B_ARG_480	NH1	B_ASP_477	OD1	3.023
6OSY	B_LYS_487	NZ	B_ASP_47	OD1	2.451
6OSY	B_LYS_487	NZ	B_GLU_91	OE1	3.497
6OSY	C_ARG_38	NH1	C_ASP_86	OD1	2.431
6OSY	C_ARG_38	NH2	C_ASP_86	OD1	3.856
6OSY	C_HIS_52	ND1	C_ASP_53	OD1	3.516
6OSY	C_HIS_52	NE2	C_ASP_53	OD1	2.951
6OSY	C_ARG_66	NH2	C_ASP_86	OD1	2.899
6OSY	C_ARG_66	NH2	C_ASP_86	OD2	3.310
6OSY	D_ARG_54	NH1	D_ASP_60	OD1	3.203
6OSY	D_ARG_54	NH2	D_ASP_60	OD1	3.673
6OSY	D_ARG_54	NH2	D_ASP_60	OD2	3.335
6OSY	D_ARG_61	NH2	D_GLU_79	OE1	3.529
6OSY	D_ARG_61	NH2	D_GLU_79	OE2	2.917
6OSY	E_ARG_60	NH2	E_ASP_78	OD1	3.663
6OSY	E_LYS_76	NZ	E_ASP_78	OD1	3.632
6OSY	F_ARG_38	NH1	F_ASP_86	OD1	3.966
6OSY	F_ARG_38	NH2	F_ASP_86	OD1	2.680
6OSY	F_ARG_66	NH1	F_ASP_86	OD2	3.886
6OSY	F_ARG_71	NH2	B_ASP_368	OD2	3.635
6OSY	G_ARG_542	NH1	A_GLU_647	OE2	3.983
6OSY	G_ARG_542	NH2	A_GLU_647	OE1	3.165
6OSY	G_ARG_542	NH2	A_GLU_647	OE2	2.705
6OSY	G_ARG_579	NH2	A_GLU_584	OE1	3.899
6OSY	G_ARG_588	NH2	G_GLU_584	OE2	3.357
6OSY	G_ARG_617	NH1	G_GLU_634	OE1	3.355
6OSY	G_ARG_617	NH1	G_GLU_634	OE2	2.448
6OSY	H_ARG_38	NH1	H_GLU_46	OE1	2.885
6OSY	H_ARG_38	NH1	H_GLU_46	OE2	3.190
6OSY	H_ARG_38	NH1	H_ASP_86	OD2	3.298
6OSY	H_ARG_38	NH2	H_ASP_86	OD2	2.451
6OSY	H_ARG_66	NH1	H_ASP_86	OD1	3.016
6OSY	H_ARG_66	NH1	H_ASP_86	OD2	2.795
6OSY	H_ARG_66	NH2	H_ASP_86	OD1	2.574
6OSY	H_ARG_66	NH2	H_ASP_86	OD2	3.909
6OSY	H_ARG_96	NH1	L_GLU_55	OE1	3.662
6OSY	H_HIS_100	ND1	2_GLU_87	OE2	3.031
6OSY	H_HIS_100	NE2	2_GLU_87	OE2	3.785
6OSY	I_ARG_38	NH1	I_GLU_46	OE1	2.963
6OSY	I_ARG_38	NH1	I_GLU_46	OE2	3.677
6OSY	I_ARG_38	NH1	I_ASP_86	OD1	3.365
6OSY	I_ARG_38	NH2	I_ASP_86	OD1	2.431
6OSY	I_ARG_66	NH1	I_ASP_86	OD1	2.805
6OSY	I_ARG_66	NH1	I_ASP_86	OD2	3.496
6OSY	I_ARG_66	NH2	I_ASP_86	OD1	3.389
6OSY	I_ARG_66	NH2	I_ASP_86	OD2	2.439
6OSY	I_ARG_96	NH1	J_GLU_55	OE2	3.419
6OSY	I_HIS_100	ND1	B_GLU_87	OE2	3.029
6OSY	I_HIS_100	NE2	B_GLU_87	OE2	3.781
6OSY	J_ARG_24	NH1	J_GLU_70	OE2	3.291
6OSY	J_LYS_30	NZ	J_ASP_28	OD2	3.933
6OSY	J_ARG_46	NH1	I_ASP_101	OD1	3.411
6OSY	J_ARG_46	NH1	I_ASP_101	OD2	2.599
6OSY	J_ARG_46	NH1	J_GLU_55	OE2	3.676
6OSY	J_ARG_61	NH1	J_GLU_81	OE1	2.792
6OSY	J_ARG_61	NH1	J_ASP_82	OD1	2.601
6OSY	J_ARG_61	NH1	J_ASP_82	OD2	3.417

6OSY	J_ARG_61	NH2	J_GLU_81	OE1	2.918
6OSY	K_HIS_85	NE2	K_GLU_87	OE2	3.406
6OSY	K_HIS_216	NE2	K_ASP_57	OD1	3.206
6OSY	K_LYS_229	NZ	K_GLU_83	OE1	3.712
6OSY	K_LYS_229	NZ	K_GLU_83	OE2	2.837
6OSY	K_LYS_231	NZ	K_GLU_269	OE1	3.711
6OSY	K_LYS_231	NZ	K_GLU_269	OE2	3.385
6OSY	K_LYS_282	NZ	P_ASP_100C	OD2	3.859
6OSY	K_LYS_421	NZ	K_ASP_180	OD1	3.938
6OSY	K_ARG_469	NH1	K_ASP_457	OD1	3.854
6OSY	K_ARG_469	NH1	K_ASP_457	OD2	2.579
6OSY	K_ARG_469	NH2	K_ASP_457	OD2	3.974
6OSY	K_ARG_480	NH1	K_ASP_477	OD1	3.037
6OSY	K_LYS_487	NZ	K_ASP_47	OD1	2.530
6OSY	K_LYS_487	NZ	K_ASP_47	OD2	3.781
6OSY	K_LYS_487	NZ	K_GLU_91	OE1	2.961
6OSY	L_ARG_24	NH1	L_GLU_70	OE2	3.285
6OSY	L_LYS_30	NZ	L_ASP_28	OD2	3.882
6OSY	L_ARG_46	NH1	H_ASP_101	OD1	3.509
6OSY	L_ARG_46	NH1	H_ASP_101	OD2	2.485
6OSY	L_ARG_46	NH1	L_GLU_55	OE1	3.489
6OSY	L_ARG_61	NH1	L_GLU_81	OE1	2.728
6OSY	L_ARG_61	NH1	L_ASP_82	OD1	2.575
6OSY	L_ARG_61	NH1	L_ASP_82	OD2	3.365
6OSY	L_ARG_61	NH2	L_GLU_81	OE1	2.971
6OSY	M_ARG_38	NH1	M_ASP_86	OD1	2.434
6OSY	M_ARG_38	NH2	M_ASP_86	OD1	3.790
6OSY	M_HIS_52	ND1	M_ASP_53	OD1	3.529
6OSY	M_HIS_52	NE2	M_ASP_53	OD1	2.931
6OSY	M_ARG_66	NH2	M_ASP_86	OD1	2.638
6OSY	M_ARG_66	NH2	M_ASP_86	OD2	3.176
6OSY	N_ARG_54	NH1	N_ASP_60	OD2	3.198
6OSY	N_ARG_54	NH2	N_ASP_60	OD1	3.491
6OSY	N_ARG_54	NH2	N_ASP_60	OD2	3.714
6OSY	N_ARG_61	NH2	N_GLU_79	OE1	3.680
6OSY	N_ARG_61	NH2	N_GLU_79	OE2	2.924
6OSY	O_ARG_60	NH2	O_ASP_78	OD1	3.714
6OSY	O_LYS_76	NZ	O_ASP_78	OD1	3.603
6OSY	P_ARG_38	NH1	P_ASP_86	OD1	3.657
6OSY	P_ARG_38	NH2	P_ASP_86	OD1	2.467
6OSY	P_ARG_66	NH1	P_ASP_86	OD2	3.897
6OSY	P_ARG_71	NH1	K_ASP_368	OD2	3.949
6OSY	P_ARG_71	NH2	K_ASP_368	OD2	3.325
6OSY	Q_ARG_542	NH1	G_GLU_647	OE2	3.913
6OSY	Q_ARG_542	NH2	G_GLU_647	OE1	3.228
6OSY	Q_ARG_542	NH2	G_GLU_647	OE2	2.706
6OSY	Q_ARG_617	NH1	Q_GLU_634	OE1	3.307
6OSY	Q_ARG_617	NH1	Q_GLU_634	OE2	2.450
6OSY	R_ARG_38	NH1	R_GLU_46	OE1	2.894
6OSY	R_ARG_38	NH1	R_ASP_86	OD1	3.489
6OSY	R_ARG_38	NH2	R_ASP_86	OD1	2.425
6OSY	R_ARG_66	NH1	R_ASP_86	OD1	3.291
6OSY	R_ARG_66	NH1	R_ASP_86	OD2	2.545
6OSY	R_ARG_66	NH2	R_ASP_86	OD1	3.724
6OSY	R_ARG_96	NH1	S_GLU_55	OE2	3.423
6OSY	R_HIS_100	ND1	K_GLU_87	OE1	3.719
6OSY	R_HIS_100	ND1	K_GLU_87	OE2	2.905
6OSY	R_HIS_100	NE2	K_GLU_87	OE1	3.960

6OSY	S_ARG_24	NH1	S_GLU_70	OE2	3.276
6OSY	S_LYS_30	NZ	S_ASP_28	OD1	3.818
6OSY	S_ARG_46	NH1	R_ASP_101	OD1	3.488
6OSY	S_ARG_46	NH1	R_ASP_101	OD2	2.503
6OSY	S_ARG_46	NH1	S_GLU_55	OE2	3.494
6OSY	S_ARG_61	NH1	S_GLU_81	OE1	2.746
6OSY	S_ARG_61	NH1	S_ASP_82	OD1	3.377
6OSY	S_ARG_61	NH1	S_ASP_82	OD2	2.556
6OSY	S_ARG_61	NH2	S_GLU_81	OE1	2.966
6OT1	B_ARG_542	NH2	D_GLU_647	OE1	2.021
6OT1	B_ARG_542	NH2	D_GLU_647	OE2	3.827
6OT1	B_ARG_588	NH2	B_GLU_584	OE2	2.977
6OT1	B_LYS_601	NZ	D_GLU_657	OE1	3.960
6OT1	B_LYS_601	NZ	D_GLU_657	OE2	3.832
6OT1	B_ARG_617	NH1	B_GLU_634	OE1	3.167
6OT1	B_ARG_617	NH1	B_GLU_634	OE2	2.669
6OT1	B_ARG_617	NH2	B_GLU_621	OE1	3.234
6OT1	B_ARG_617	NH2	B_GLU_621	OE2	3.259
6OT1	G_HIS_85	NE2	G_GLU_87	OE2	3.938
6OT1	G_HIS_216	NE2	G_ASP_57	OD1	2.810
6OT1	G_HIS_216	NE2	G_ASP_57	OD2	3.156
6OT1	G_LYS_229	NZ	G_GLU_83	OE2	3.683
6OT1	G_LYS_231	NZ	G_GLU_268	OE1	3.079
6OT1	G_LYS_231	NZ	G_GLU_268	OE2	3.577
6OT1	G_HIS_249	NE2	G_GLU_482	OE1	3.787
6OT1	G_LYS_282	NZ	G_GLU_275	OE2	3.607
6OT1	G_LYS_282	NZ	q_ASP_100C	OD2	3.404
6OT1	G_ARG_298	NH1	G_GLU_381	OE1	2.421
6OT1	G_ARG_298	NH1	G_GLU_381	OE2	3.196
6OT1	G_ARG_327	NH2	m_GLU_100I	OE1	3.817
6OT1	G_LYS_351	NZ	G_GLU_269	OE1	3.548
6OT1	G_ARG_429	NH1	G_ASP_113	OD1	3.405
6OT1	G_ARG_429	NH1	G_ASP_113	OD2	2.495
6OT1	G_ARG_469	NH1	G_ASP_457	OD1	2.847
6OT1	G_ARG_476	NH1	G_GLU_102	OE1	3.389
6OT1	G_ARG_476	NH1	G_ASP_474	OD2	3.647
6OT1	G_ARG_476	NH2	G_GLU_102	OE1	3.349
6OT1	G_ARG_476	NH2	G_GLU_102	OE2	3.433
6OT1	G_ARG_480	NH1	G_ASP_477	OD1	3.354
6OT1	G_LYS_487	NZ	G_ASP_47	OD1	2.584
6OT1	G_LYS_487	NZ	G_ASP_47	OD2	3.393
6OT1	G_LYS_487	NZ	G_GLU_91	OE2	2.597
6OT1	H_ARG_38	NH2	H_ASP_86	OD1	3.494
6OT1	H_LYS_71	NZ	H_GLU_55	OE2	3.697
6OT1	L_ARG_54	NH2	L_ASP_60	OD2	3.975
6OT1	L_ARG_61	NH1	L_GLU_81	OE2	3.772
6OT1	L_ARG_61	NH2	L_GLU_81	OE2	2.479
6OT1	m_ARG_38	NH1	m_ASP_86	OD1	3.011
6OT1	m_ARG_38	NH2	m_GLU_46	OE1	2.859
6OT1	m_ARG_38	NH2	m_GLU_46	OE2	3.063
6OT1	m_ARG_38	NH2	m_ASP_86	OD1	3.767
6OT1	m_HIS_52	ND1	m_ASP_53	OD1	3.328
6OT1	m_HIS_52	NE2	m_ASP_53	OD1	3.028
6OT1	m_ARG_66	NH1	m_ASP_86	OD2	2.461
6OT1	m_ARG_66	NH2	m_ASP_86	OD1	3.460
6OT1	m_ARG_66	NH2	m_ASP_86	OD2	3.125
6OT1	m_LYS_73	NZ	m_ASP_53	OD2	3.345
6OT1	m_LYS_96	NZ	m_ASP_100Q	OD1	3.813

6OT1	m_LYS_96	NZ	m_ASP_100Q	OD2	2.475
6OT1	n_ARG_31	NH1	n_ASP_92	OD2	2.719
6OT1	n_ARG_54	NH2	n_ASP_60	OD1	3.737
6OT1	n_ARG_54	NH2	n_ASP_60	OD2	2.630
6OT1	n_ARG_61	NH1	n_ASP_82	OD2	3.959
6OT1	n_ARG_61	NH2	n_GLU_79	OE2	3.140
6OT1	n_ARG_61	NH2	n_ASP_82	OD1	3.334
6OT1	n_ARG_61	NH2	n_ASP_82	OD2	3.994
6OT1	n_ARG_95	NH2	n_GLU_25	OE1	3.478
6OT1	q_ARG_38	NH1	q_ASP_86	OD1	2.452
6OT1	q_ARG_38	NH1	q_ASP_86	OD2	3.996
6OT1	q_ARG_38	NH2	q_GLU_46	OE1	2.492
6OT1	q_ARG_38	NH2	q_GLU_46	OE2	3.367
6OT1	q_ARG_66	NH2	q_ASP_86	OD2	2.599
6OT1	q_ARG_71	NH2	G_ASP_368	OD2	3.596
6OT1	r_LYS_24	NZ	r_ASP_69	OD1	3.076
6OT1	r_ARG_52	NH2	r_ASP_49	OD2	3.108
6OT1	r_ARG_53	NH1	r_ASP_59	OD1	3.647
6OT1	r_ARG_60	NH2	r_ASP_81	OD1	3.037
6OT1	r_ARG_60	NH2	r_ASP_81	OD2	2.674
6OT1	O_ARG_542	NH2	B_GLU_647	OE1	2.048
6OT1	O_ARG_542	NH2	B_GLU_647	OE2	3.874
6OT1	O_ARG_588	NH2	O_GLU_584	OE2	2.978
6OT1	O_LYS_601	NZ	B_GLU_657	OE1	3.934
6OT1	O_LYS_601	NZ	B_GLU_657	OE2	3.759
6OT1	O_ARG_617	NH1	O_GLU_634	OE1	3.167
6OT1	O_ARG_617	NH1	O_GLU_634	OE2	2.669
6OT1	O_ARG_617	NH2	O_GLU_621	OE1	3.234
6OT1	O_ARG_617	NH2	O_GLU_621	OE2	3.261
6OT1	E_HIS_85	NE2	E_GLU_87	OE2	3.938
6OT1	E_HIS_216	NE2	E_ASP_57	OD1	2.811
6OT1	E_HIS_216	NE2	E_ASP_57	OD2	3.156
6OT1	E_LYS_229	NZ	E_GLU_83	OE2	3.683
6OT1	E_LYS_231	NZ	E_GLU_268	OE1	3.077
6OT1	E_LYS_231	NZ	E_GLU_268	OE2	3.575
6OT1	E_HIS_249	NE2	E_GLU_482	OE1	3.787
6OT1	E_LYS_282	NZ	E_GLU_275	OE2	3.608
6OT1	E_LYS_282	NZ	J_ASP_100C	OD2	3.404
6OT1	E_ARG_298	NH1	E_GLU_381	OE1	2.420
6OT1	E_ARG_298	NH1	E_GLU_381	OE2	3.196
6OT1	E_ARG_327	NH2	F_GLU_100I	OE1	3.817
6OT1	E_LYS_351	NZ	E_GLU_269	OE1	3.548
6OT1	E_ARG_429	NH1	E_ASP_113	OD1	3.405
6OT1	E_ARG_429	NH1	E_ASP_113	OD2	2.495
6OT1	E_ARG_469	NH1	E_ASP_457	OD1	2.847
6OT1	E_ARG_476	NH1	E_GLU_102	OE1	3.389
6OT1	E_ARG_476	NH1	E_ASP_474	OD2	3.648
6OT1	E_ARG_476	NH2	E_GLU_102	OE1	3.349
6OT1	E_ARG_476	NH2	E_GLU_102	OE2	3.433
6OT1	E_ARG_480	NH1	E_ASP_477	OD1	3.353
6OT1	E_LYS_487	NZ	E_ASP_47	OD1	2.586
6OT1	E_LYS_487	NZ	E_ASP_47	OD2	3.398
6OT1	E_LYS_487	NZ	E_GLU_91	OE2	2.596
6OT1	A_ARG_38	NH2	A_ASP_86	OD1	3.495
6OT1	A_LYS_71	NZ	A_GLU_55	OE2	3.697
6OT1	C_ARG_54	NH2	C_ASP_60	OD2	3.977
6OT1	C_ARG_61	NH1	C_GLU_81	OE2	3.768
6OT1	C_ARG_61	NH2	C_GLU_81	OE2	2.478

6OT1	F_ARG_38	NH1	F_ASP_86	OD1	3.011
6OT1	F_ARG_38	NH2	F_GLU_46	OE1	2.859
6OT1	F_ARG_38	NH2	F_GLU_46	OE2	3.063
6OT1	F_ARG_38	NH2	F_ASP_86	OD1	3.766
6OT1	F_HIS_52	ND1	F_ASP_53	OD1	3.327
6OT1	F_HIS_52	NE2	F_ASP_53	OD1	3.026
6OT1	F_ARG_66	NH1	F_ASP_86	OD2	2.462
6OT1	F_ARG_66	NH2	F_ASP_86	OD1	3.460
6OT1	F_ARG_66	NH2	F_ASP_86	OD2	3.125
6OT1	F_LYS_73	NZ	F_ASP_53	OD2	3.344
6OT1	F_LYS_96	NZ	F_ASP_100Q	OD1	3.814
6OT1	F_LYS_96	NZ	F_ASP_100Q	OD2	2.475
6OT1	L_ARG_31	NH1	L_ASP_92	OD2	2.719
6OT1	L_ARG_54	NH2	L_ASP_60	OD1	3.738
6OT1	L_ARG_54	NH2	L_ASP_60	OD2	2.630
6OT1	L_ARG_61	NH1	L_ASP_82	OD2	3.959
6OT1	L_ARG_61	NH2	L_GLU_79	OE2	3.139
6OT1	L_ARG_61	NH2	L_ASP_82	OD1	3.334
6OT1	L_ARG_61	NH2	L_ASP_82	OD2	3.993
6OT1	L_ARG_95	NH2	L_GLU_25	OE1	3.478
6OT1	J_ARG_38	NH1	J_ASP_86	OD1	2.453
6OT1	J_ARG_38	NH1	J_ASP_86	OD2	3.995
6OT1	J_ARG_38	NH2	J_GLU_46	OE1	2.492
6OT1	J_ARG_38	NH2	J_GLU_46	OE2	3.368
6OT1	J_ARG_66	NH2	J_ASP_86	OD2	2.596
6OT1	J_ARG_71	NH2	E_ASP_368	OD2	3.599
6OT1	K_LYS_24	NZ	K_ASP_69	OD1	3.078
6OT1	K_ARG_52	NH2	K_ASP_49	OD2	3.106
6OT1	K_ARG_53	NH1	K_ASP_59	OD1	3.648
6OT1	K_ARG_60	NH2	K_ASP_81	OD1	3.037
6OT1	K_ARG_60	NH2	K_ASP_81	OD2	2.675
6OT1	D_ARG_542	NH2	O_GLU_647	OE1	2.015
6OT1	D_ARG_542	NH2	O_GLU_647	OE2	3.816
6OT1	D_ARG_588	NH2	D_GLU_584	OE2	2.978
6OT1	D_LYS_601	NZ	O_GLU_657	OE2	3.900
6OT1	D_ARG_617	NH1	D_GLU_634	OE1	3.168
6OT1	D_ARG_617	NH1	D_GLU_634	OE2	2.668
6OT1	D_ARG_617	NH2	D_GLU_621	OE1	3.233
6OT1	D_ARG_617	NH2	D_GLU_621	OE2	3.260
6OT1	P_HIS_85	NE2	P_GLU_87	OE2	3.938
6OT1	P_HIS_216	NE2	P_ASP_57	OD1	2.811
6OT1	P_HIS_216	NE2	P_ASP_57	OD2	3.156
6OT1	P_LYS_229	NZ	P_GLU_83	OE2	3.683
6OT1	P_LYS_231	NZ	P_GLU_268	OE1	3.078
6OT1	P_LYS_231	NZ	P_GLU_268	OE2	3.576
6OT1	P_HIS_249	NE2	P_GLU_482	OE1	3.788
6OT1	P_LYS_282	NZ	P_GLU_275	OE2	3.608
6OT1	P_LYS_282	NZ	S_ASP_100C	OD2	3.405
6OT1	P_ARG_298	NH1	P_GLU_381	OE1	2.420
6OT1	P_ARG_298	NH1	P_GLU_381	OE2	3.195
6OT1	P_ARG_327	NH2	Q_GLU_100I	OE1	3.817
6OT1	P_LYS_351	NZ	P_GLU_269	OE1	3.548
6OT1	P_ARG_429	NH1	P_ASP_113	OD1	3.405
6OT1	P_ARG_429	NH1	P_ASP_113	OD2	2.495
6OT1	P_ARG_469	NH1	P_ASP_457	OD1	2.848
6OT1	P_ARG_476	NH1	P_GLU_102	OE1	3.390
6OT1	P_ARG_476	NH1	P_ASP_474	OD2	3.647
6OT1	P_ARG_476	NH2	P_GLU_102	OE1	3.349

6OT1	P_ARG_476	NH2	P_GLU_102	OE2	3.433
6OT1	P_ARG_480	NH1	P_ASP_477	OD1	3.353
6OT1	P_LYS_487	NZ	P_ASP_47	OD1	2.584
6OT1	P_LYS_487	NZ	P_ASP_47	OD2	3.393
6OT1	P_LYS_487	NZ	P_GLU_91	OE2	2.596
6OT1	M_ARG_38	NH2	M_ASP_86	OD1	3.493
6OT1	M_LYS_71	NZ	M_GLU_55	OE2	3.697
6OT1	N_ARG_54	NH2	N_ASP_60	OD2	3.974
6OT1	N_ARG_61	NH1	N_GLU_81	OE2	3.770
6OT1	N_ARG_61	NH2	N_GLU_81	OE2	2.479
6OT1	Q_ARG_38	NH1	Q_ASP_86	OD1	3.012
6OT1	Q_ARG_38	NH2	Q_GLU_46	OE1	2.859
6OT1	Q_ARG_38	NH2	Q_GLU_46	OE2	3.063
6OT1	Q_ARG_38	NH2	Q_ASP_86	OD1	3.766
6OT1	Q_HIS_52	ND1	Q_ASP_53	OD1	3.327
6OT1	Q_HIS_52	NE2	Q_ASP_53	OD1	3.026
6OT1	Q_ARG_66	NH1	Q_ASP_86	OD2	2.462
6OT1	Q_ARG_66	NH2	Q_ASP_86	OD1	3.460
6OT1	Q_ARG_66	NH2	Q_ASP_86	OD2	3.125
6OT1	Q_LYS_73	NZ	Q_ASP_53	OD2	3.344
6OT1	Q_LYS_96	NZ	Q_ASP_100Q	OD1	3.814
6OT1	Q_LYS_96	NZ	Q_ASP_100Q	OD2	2.476
6OT1	R_ARG_31	NH1	R_ASP_92	OD2	2.718
6OT1	R_ARG_54	NH2	R_ASP_60	OD1	3.737
6OT1	R_ARG_54	NH2	R_ASP_60	OD2	2.630
6OT1	R_ARG_61	NH1	R_ASP_82	OD2	3.960
6OT1	R_ARG_61	NH2	R_GLU_79	OE2	3.139
6OT1	R_ARG_61	NH2	R_ASP_82	OD1	3.334
6OT1	R_ARG_61	NH2	R_ASP_82	OD2	3.995
6OT1	R_ARG_95	NH2	R_GLU_25	OE1	3.477
6OT1	S_ARG_38	NH1	S_ASP_86	OD1	2.452
6OT1	S_ARG_38	NH1	S_ASP_86	OD2	3.995
6OT1	S_ARG_38	NH2	S_GLU_46	OE1	2.492
6OT1	S_ARG_38	NH2	S_GLU_46	OE2	3.367
6OT1	S_ARG_66	NH2	S_ASP_86	OD2	2.599
6OT1	S_ARG_71	NH2	P_ASP_368	OD2	3.597
6OT1	T_LYS_24	NZ	T_ASP_69	OD1	3.076
6OT1	T_ARG_52	NH2	T_ASP_49	OD2	3.107
6OT1	T_ARG_53	NH1	T_ASP_59	OD1	3.647
6OT1	T_ARG_60	NH2	T_ASP_81	OD1	3.038
6OT1	T_ARG_60	NH2	T_ASP_81	OD2	2.673
6P62	A_LYS_46	NZ	A_ASP_632	OD2	2.721
6P62	A_LYS_97	NZ	A_GLU_275	OE2	3.366
6P62	A_ARG_151	NH2	A_ASP_140	OD1	3.754
6P62	A_LYS_168	NZ	B_GLU_190	OE2	3.547
6P62	A_LYS_229	NZ	A_GLU_83	OE1	3.953
6P62	A_LYS_229	NZ	A_GLU_83	OE2	2.773
6P62	A_LYS_231	NZ	A_GLU_267	OE1	3.655
6P62	A_LYS_232	NZ	A_GLU_268	OE2	3.138
6P62	A_LYS_232	NZ	A_GLU_269	OE2	2.749
6P62	A_HIS_249	NE2	A_GLU_482	OE1	3.132
6P62	A_LYS_282	NZ	A_GLU_275	OE1	3.423
6P62	A_ARG_298	NH1	A_GLU_381	OE2	2.910
6P62	A_ARG_298	NH2	A_GLU_381	OE2	3.307
6P62	A_LYS_335	NZ	A_ASP_412	OD2	2.410
6P62	A_LYS_351	NZ	A_GLU_269	OE1	3.133
6P62	A_LYS_421	NZ	A_GLU_370	OE2	2.730
6P62	A_ARG_429	NH1	A_ASP_113	OD1	3.526

6P62	A_ARG_429	NH1	A_ASP_113	OD2	2.935
6P62	A_ARG_429	NH2	A_ASP_113	OD1	2.818
6P62	A_ARG_429	NH2	A_ASP_113	OD2	3.695
6P62	A_ARG_476	NH1	A_ASP_474	OD1	3.290
6P62	A_ARG_476	NH1	A_ASP_474	OD2	3.909
6P62	A_ARG_476	NH2	A_GLU_102	OE1	3.634
6P62	A_ARG_476	NH2	A_GLU_102	OE2	3.089
6P62	A_LYS_487	NZ	A_ASP_47	OD1	3.073
6P62	A_LYS_487	NZ	A_ASP_47	OD2	2.842
6P62	A_LYS_490	NZ	A_GLU_492	OE2	3.504
6P62	A_ARG_520	NH2	A_GLU_87	OE1	3.537
6P62	A_ARG_542	NH1	B_GLU_647	OE1	2.629
6P62	A_ARG_542	NH1	B_GLU_647	OE2	3.985
6P62	A_ARG_542	NH2	B_GLU_648	OE2	3.131
6P62	A_LYS_574	NZ	A_ASP_107	OD1	2.481
6P62	A_LYS_574	NZ	A_ASP_107	OD2	3.953
6P62	A_ARG_579	NH1	B_GLU_584	OE1	3.453
6P62	A_ARG_579	NH1	B_GLU_584	OE2	2.953
6P62	A_ARG_585	NH2	A_GLU_492	OE1	3.953
6P62	A_ARG_585	NH2	A_GLU_492	OE2	2.999
6P62	A_ARG_588	NH1	A_GLU_584	OE1	3.660
6P62	A_ARG_588	NH2	A_GLU_584	OE1	3.069
6P62	A_ARG_617	NH1	A_GLU_634	OE1	3.708
6P62	A_ARG_617	NH1	A_GLU_634	OE2	3.595
6P62	H_ARG_38	NH1	H_ASP_86	OD1	3.041
6P62	H_ARG_38	NH2	H_GLU_46	OE1	2.920
6P62	H_ARG_94	NH2	H_ASP_101	OD1	3.646
6P62	H_ARG_94	NH2	H_ASP_101	OD2	2.930
6P62	L_LYS_22	NZ	L_GLU_70	OE2	3.542
6P62	L_ARG_61	NH1	L_GLU_79	OE2	3.423
6P62	L_ARG_61	NH1	L_ASP_82	OD2	3.764
6P62	L_ARG_61	NH2	L_ASP_77	OD2	2.844
6P62	L_ARG_61	NH2	L_GLU_79	OE2	2.955
6P62	B_LYS_46	NZ	B_ASP_632	OD2	2.722
6P62	B_LYS_97	NZ	B_GLU_275	OE2	3.366
6P62	B_ARG_151	NH2	B_ASP_140	OD1	3.754
6P62	B_LYS_168	NZ	E_GLU_190	OE2	3.547
6P62	B_LYS_229	NZ	B_GLU_83	OE1	3.953
6P62	B_LYS_229	NZ	B_GLU_83	OE2	2.774
6P62	B_LYS_231	NZ	B_GLU_267	OE1	3.655
6P62	B_LYS_232	NZ	B_GLU_268	OE2	3.139
6P62	B_LYS_232	NZ	B_GLU_269	OE2	2.750
6P62	B_HIS_249	NE2	B_GLU_482	OE1	3.131
6P62	B_LYS_282	NZ	B_GLU_275	OE1	3.424
6P62	B_ARG_298	NH1	B_GLU_381	OE2	2.910
6P62	B_ARG_298	NH2	B_GLU_381	OE2	3.308
6P62	B_LYS_335	NZ	B_ASP_412	OD2	2.410
6P62	B_LYS_351	NZ	B_GLU_269	OE1	3.133
6P62	B_LYS_421	NZ	B_GLU_370	OE2	2.731
6P62	B_ARG_429	NH1	B_ASP_113	OD1	3.526
6P62	B_ARG_429	NH1	B_ASP_113	OD2	2.934
6P62	B_ARG_429	NH2	B_ASP_113	OD1	2.819
6P62	B_ARG_429	NH2	B_ASP_113	OD2	3.695
6P62	B_ARG_476	NH1	B_ASP_474	OD1	3.291
6P62	B_ARG_476	NH1	B_ASP_474	OD2	3.909
6P62	B_ARG_476	NH2	B_GLU_102	OE1	3.634
6P62	B_ARG_476	NH2	B_GLU_102	OE2	3.089
6P62	B_LYS_487	NZ	B_ASP_47	OD1	3.072

6P62	B_LYS_487	NZ	B_ASP_47	OD2	2.841
6P62	B_LYS_490	NZ	B_GLU_492	OE2	3.504
6P62	B_ARG_520	NH2	B_GLU_87	OE1	3.537
6P62	B_ARG_542	NH1	E_GLU_647	OE1	2.630
6P62	B_ARG_542	NH1	E_GLU_647	OE2	3.986
6P62	B_ARG_542	NH2	E_GLU_648	OE2	3.130
6P62	B_LYS_574	NZ	B_ASP_107	OD1	2.481
6P62	B_LYS_574	NZ	B_ASP_107	OD2	3.954
6P62	B_ARG_579	NH1	E_GLU_584	OE1	3.454
6P62	B_ARG_579	NH1	E_GLU_584	OE2	2.952
6P62	B_ARG_585	NH2	B_GLU_492	OE1	3.952
6P62	B_ARG_585	NH2	B_GLU_492	OE2	2.998
6P62	B_ARG_588	NH1	B_GLU_584	OE1	3.660
6P62	B_ARG_588	NH2	B_GLU_584	OE1	3.069
6P62	B_ARG_617	NH1	B_GLU_634	OE1	3.708
6P62	B_ARG_617	NH1	B_GLU_634	OE2	3.595
6P62	C_ARG_38	NH1	C_ASP_86	OD1	3.041
6P62	C_ARG_38	NH2	C_GLU_46	OE1	2.920
6P62	C_ARG_94	NH2	C_ASP_101	OD1	3.646
6P62	C_ARG_94	NH2	C_ASP_101	OD2	2.930
6P62	D_LYS_22	NZ	D_GLU_70	OE2	3.542
6P62	D_ARG_61	NH1	D_GLU_79	OE2	3.423
6P62	D_ARG_61	NH1	D_ASP_82	OD2	3.764
6P62	D_ARG_61	NH2	D_ASP_77	OD2	2.845
6P62	D_ARG_61	NH2	D_GLU_79	OE2	2.955
6P62	E_LYS_46	NZ	E_ASP_632	OD2	2.721
6P62	E_LYS_97	NZ	E_GLU_275	OE2	3.366
6P62	E_ARG_151	NH2	E_ASP_140	OD1	3.754
6P62	E_LYS_168	NZ	A_GLU_190	OE2	3.547
6P62	E_LYS_229	NZ	E_GLU_83	OE1	3.953
6P62	E_LYS_229	NZ	E_GLU_83	OE2	2.773
6P62	E_LYS_231	NZ	E_GLU_267	OE1	3.656
6P62	E_LYS_232	NZ	E_GLU_268	OE2	3.139
6P62	E_LYS_232	NZ	E_GLU_269	OE2	2.749
6P62	E_HIS_249	NE2	E_GLU_482	OE1	3.131
6P62	E_LYS_282	NZ	E_GLU_275	OE1	3.424
6P62	E_ARG_298	NH1	E_GLU_381	OE2	2.909
6P62	E_ARG_298	NH2	E_GLU_381	OE2	3.307
6P62	E_LYS_335	NZ	E_ASP_412	OD2	2.409
6P62	E_LYS_351	NZ	E_GLU_269	OE1	3.133
6P62	E_LYS_421	NZ	E_GLU_370	OE2	2.731
6P62	E_ARG_429	NH1	E_ASP_113	OD1	3.526
6P62	E_ARG_429	NH1	E_ASP_113	OD2	2.935
6P62	E_ARG_429	NH2	E_ASP_113	OD1	2.819
6P62	E_ARG_429	NH2	E_ASP_113	OD2	3.695
6P62	E_ARG_476	NH1	E_ASP_474	OD1	3.291
6P62	E_ARG_476	NH1	E_ASP_474	OD2	3.910
6P62	E_ARG_476	NH2	E_GLU_102	OE1	3.634
6P62	E_ARG_476	NH2	E_GLU_102	OE2	3.089
6P62	E_LYS_487	NZ	E_ASP_47	OD1	3.071
6P62	E_LYS_487	NZ	E_ASP_47	OD2	2.841
6P62	E_LYS_490	NZ	E_GLU_492	OE2	3.504
6P62	E_ARG_520	NH2	E_GLU_87	OE1	3.537
6P62	E_ARG_542	NH1	A_GLU_647	OE1	2.629
6P62	E_ARG_542	NH1	A_GLU_647	OE2	3.985
6P62	E_ARG_542	NH2	A_GLU_648	OE2	3.130
6P62	E_LYS_574	NZ	E_ASP_107	OD1	2.480
6P62	E_LYS_574	NZ	E_ASP_107	OD2	3.952

6P62	E_ARG_579	NH1	A_GLU_584	OE1	3.453
6P62	E_ARG_579	NH1	A_GLU_584	OE2	2.952
6P62	E_ARG_585	NH2	E_GLU_492	OE1	3.953
6P62	E_ARG_585	NH2	E_GLU_492	OE2	2.998
6P62	E_ARG_588	NH1	E_GLU_584	OE1	3.660
6P62	E_ARG_588	NH2	E_GLU_584	OE1	3.069
6P62	E_ARG_617	NH1	E_GLU_634	OE1	3.708
6P62	E_ARG_617	NH1	E_GLU_634	OE2	3.595
6P62	F_ARG_38	NH1	F_ASP_86	OD1	3.041
6P62	F_ARG_38	NH2	F_GLU_46	OE1	2.921
6P62	F_ARG_94	NH2	F_ASP_101	OD1	3.646
6P62	F_ARG_94	NH2	F_ASP_101	OD2	2.930
6P62	G_LYS_22	NZ	G_GLU_70	OE2	3.542
6P62	G_ARG_61	NH1	G_GLU_79	OE2	3.423
6P62	G_ARG_61	NH1	G_ASP_82	OD2	3.763
6P62	G_ARG_61	NH2	G_ASP_77	OD2	2.844
6P62	G_ARG_61	NH2	G_GLU_79	OE2	2.955
6P65	A_LYS_46	NZ	A_ASP_632	OD2	2.391
6P65	A_LYS_185D	NZ	A_GLU_185A	OE1	3.592
6P65	A_LYS_185D	NZ	A_GLU_185A	OE2	3.302
6P65	A_LYS_227	NZ	A_GLU_83	OE1	2.949
6P65	A_LYS_227	NZ	A_GLU_83	OE2	3.484
6P65	A_HIS_249	NE2	A_GLU_482	OE1	3.021
6P65	A_LYS_282	NZ	A_GLU_275	OE1	2.833
6P65	A_LYS_282	NZ	A_GLU_275	OE2	3.523
6P65	A_ARG_298	NH2	A_GLU_381	OE1	3.069
6P65	A_LYS_305	NZ	A_ASP_322	OD1	2.972
6P65	A_LYS_305	NZ	A_ASP_322	OD2	2.511
6P65	A_ARG_340	NH2	A_ASP_337	OD1	2.733
6P65	A_ARG_340	NH2	A_ASP_337	OD2	3.882
6P65	A_ARG_344	NH1	A_GLU_290	OE1	3.426
6P65	A_ARG_344	NH1	A_GLU_290	OE2	3.021
6P65	A_LYS_348	NZ	A_GLU_351	OE1	2.894
6P65	A_LYS_348	NZ	A_GLU_351	OE2	3.938
6P65	A_ARG_419	NH2	A_GLU_153	OE1	2.875
6P65	A_LYS_421	NZ	A_GLU_370	OE2	2.921
6P65	A_ARG_429	NH1	A_ASP_113	OD1	3.603
6P65	A_ARG_429	NH1	A_ASP_113	OD2	2.908
6P65	A_ARG_429	NH2	A_ASP_113	OD1	2.815
6P65	A_ARG_429	NH2	A_ASP_113	OD2	3.611
6P65	A_LYS_446	NZ	A_GLU_293	OE2	3.260
6P65	A_ARG_456	NH1	A_GLU_466	OE1	3.094
6P65	A_ARG_456	NH1	A_GLU_466	OE2	3.849
6P65	A_ARG_469	NH1	A_ASP_457	OD2	2.839
6P65	A_ARG_469	NH2	A_ASP_457	OD2	3.804
6P65	A_ARG_476	NH1	A_ASP_474	OD1	3.178
6P65	A_ARG_476	NH1	A_ASP_474	OD2	3.851
6P65	A_ARG_476	NH2	A_GLU_102	OE1	3.708
6P65	A_ARG_476	NH2	A_GLU_102	OE2	3.051
6P65	A_LYS_485	NZ	A_GLU_267	OE2	2.827
6P65	A_LYS_487	NZ	A_ASP_47	OD1	2.922
6P65	A_LYS_487	NZ	A_ASP_47	OD2	2.883
6P65	A_LYS_492	NZ	A_GLU_490	OE1	3.434
6P65	A_LYS_492	NZ	A_GLU_490	OE2	2.781
6P65	A_ARG_500	NH1	L_GLU_30	OE1	3.144
6P65	A_ARG_500	NH1	L_GLU_30	OE2	3.804
6P65	A_ARG_500	NH2	L_GLU_30	OE1	3.741
6P65	A_ARG_500	NH2	L_GLU_30	OE2	2.979

6P65	A_ARG_542	NH2	B_ASP_648	OD1	3.154
6P65	A_LYS_574	NZ	A_ASP_107	OD1	2.461
6P65	A_LYS_574	NZ	A_ASP_107	OD2	3.497
6P65	A_LYS_588	NZ	A_GLU_584	OE2	2.713
6P65	A_LYS_617	NZ	A_GLU_634	OE1	3.411
6P65	A_LYS_658	NZ	A_GLU_654	OE1	2.575
6P65	H_ARG_38	NH2	H_GLU_46	OE1	3.002
6P65	H_LYS_71	NZ	A_GLU_87	OE1	2.936
6P65	H_LYS_71	NZ	A_GLU_87	OE2	2.864
6P65	H_ARG_94	NH2	H_ASP_33	OD1	3.585
6P65	H_ARG_94	NH2	H_ASP_33	OD2	3.145
6P65	H_LYS_100H	NZ	L_ASP_50	OD1	2.708
6P65	H_LYS_100H	NZ	L_ASP_50	OD2	2.597
6P65	L_ARG_95B	NH2	L_ASP_95D	OD2	3.668
6P65	B_LYS_46	NZ	B_ASP_632	OD2	2.391
6P65	B_LYS_185D	NZ	B_GLU_185A	OE1	3.593
6P65	B_LYS_185D	NZ	B_GLU_185A	OE2	3.302
6P65	B_LYS_227	NZ	B_GLU_83	OE1	2.949
6P65	B_LYS_227	NZ	B_GLU_83	OE2	3.484
6P65	B_HIS_249	NE2	B_GLU_482	OE1	3.021
6P65	B_LYS_282	NZ	B_GLU_275	OE1	2.833
6P65	B_LYS_282	NZ	B_GLU_275	OE2	3.523
6P65	B_ARG_298	NH2	B_GLU_381	OE1	3.068
6P65	B_LYS_305	NZ	B_ASP_322	OD1	2.972
6P65	B_LYS_305	NZ	B_ASP_322	OD2	2.511
6P65	B_ARG_340	NH2	B_ASP_337	OD1	2.733
6P65	B_ARG_340	NH2	B_ASP_337	OD2	3.883
6P65	B_ARG_344	NH1	B_GLU_290	OE1	3.427
6P65	B_ARG_344	NH1	B_GLU_290	OE2	3.022
6P65	B_LYS_348	NZ	B_GLU_351	OE1	2.895
6P65	B_LYS_348	NZ	B_GLU_351	OE2	3.939
6P65	B_ARG_419	NH2	B_GLU_153	OE1	2.875
6P65	B_LYS_421	NZ	B_GLU_370	OE2	2.921
6P65	B_ARG_429	NH1	B_ASP_113	OD1	3.603
6P65	B_ARG_429	NH1	B_ASP_113	OD2	2.908
6P65	B_ARG_429	NH2	B_ASP_113	OD1	2.816
6P65	B_ARG_429	NH2	B_ASP_113	OD2	3.612
6P65	B_LYS_446	NZ	B_GLU_293	OE2	3.260
6P65	B_ARG_456	NH1	B_GLU_466	OE1	3.095
6P65	B_ARG_456	NH1	B_GLU_466	OE2	3.849
6P65	B_ARG_469	NH1	B_ASP_457	OD2	2.839
6P65	B_ARG_469	NH2	B_ASP_457	OD2	3.803
6P65	B_ARG_476	NH1	B_ASP_474	OD1	3.178
6P65	B_ARG_476	NH1	B_ASP_474	OD2	3.851
6P65	B_ARG_476	NH2	B_GLU_102	OE1	3.708
6P65	B_ARG_476	NH2	B_GLU_102	OE2	3.050
6P65	B_LYS_485	NZ	B_GLU_267	OE2	2.826
6P65	B_LYS_487	NZ	B_ASP_47	OD1	2.922
6P65	B_LYS_487	NZ	B_ASP_47	OD2	2.883
6P65	B_LYS_492	NZ	B_GLU_490	OE1	3.434
6P65	B_LYS_492	NZ	B_GLU_490	OE2	2.782
6P65	B_ARG_500	NH1	D_GLU_30	OE1	3.143
6P65	B_ARG_500	NH1	D_GLU_30	OE2	3.804
6P65	B_ARG_500	NH2	D_GLU_30	OE1	3.741
6P65	B_ARG_500	NH2	D_GLU_30	OE2	2.979
6P65	B_ARG_542	NH2	E_ASP_648	OD1	3.155
6P65	B_LYS_574	NZ	B_ASP_107	OD1	2.460
6P65	B_LYS_574	NZ	B_ASP_107	OD2	3.496

6P65	B_LYS_588	NZ	B_GLU_584	OE2	2.714
6P65	B_LYS_617	NZ	B_GLU_634	OE1	3.411
6P65	B_LYS_658	NZ	B_GLU_654	OE1	2.576
6P65	C_ARG_38	NH2	C_GLU_46	OE1	3.002
6P65	C_LYS_71	NZ	B_GLU_87	OE1	2.936
6P65	C_LYS_71	NZ	B_GLU_87	OE2	2.864
6P65	C_ARG_94	NH2	C_ASP_33	OD1	3.585
6P65	C_ARG_94	NH2	C_ASP_33	OD2	3.145
6P65	C_LYS_100H	NZ	D_ASP_50	OD1	2.708
6P65	C_LYS_100H	NZ	D_ASP_50	OD2	2.597
6P65	D_ARG_95B	NH2	D_ASP_95D	OD2	3.668
6P65	E_LYS_46	NZ	E_ASP_632	OD2	2.391
6P65	E_LYS_185D	NZ	E_GLU_185A	OE1	3.592
6P65	E_LYS_185D	NZ	E_GLU_185A	OE2	3.302
6P65	E_LYS_227	NZ	E_GLU_83	OE1	2.949
6P65	E_LYS_227	NZ	E_GLU_83	OE2	3.484
6P65	E_HIS_249	NE2	E_GLU_482	OE1	3.021
6P65	E_LYS_282	NZ	E_GLU_275	OE1	2.834
6P65	E_LYS_282	NZ	E_GLU_275	OE2	3.523
6P65	E_ARG_298	NH2	E_GLU_381	OE1	3.068
6P65	E_LYS_305	NZ	E_ASP_322	OD1	2.973
6P65	E_LYS_305	NZ	E_ASP_322	OD2	2.510
6P65	E_ARG_340	NH2	E_ASP_337	OD1	2.733
6P65	E_ARG_340	NH2	E_ASP_337	OD2	3.883
6P65	E_ARG_344	NH1	E_GLU_290	OE1	3.426
6P65	E_ARG_344	NH1	E_GLU_290	OE2	3.021
6P65	E_LYS_348	NZ	E_GLU_351	OE1	2.895
6P65	E_LYS_348	NZ	E_GLU_351	OE2	3.939
6P65	E_ARG_419	NH2	E_GLU_153	OE1	2.874
6P65	E_LYS_421	NZ	E_GLU_370	OE2	2.921
6P65	E_ARG_429	NH1	E_ASP_113	OD1	3.603
6P65	E_ARG_429	NH1	E_ASP_113	OD2	2.907
6P65	E_ARG_429	NH2	E_ASP_113	OD1	2.816
6P65	E_ARG_429	NH2	E_ASP_113	OD2	3.611
6P65	E_LYS_446	NZ	E_GLU_293	OE2	3.260
6P65	E_ARG_456	NH1	E_GLU_466	OE1	3.094
6P65	E_ARG_456	NH1	E_GLU_466	OE2	3.849
6P65	E_ARG_469	NH1	E_ASP_457	OD2	2.839
6P65	E_ARG_469	NH2	E_ASP_457	OD2	3.804
6P65	E_ARG_476	NH1	E_ASP_474	OD1	3.178
6P65	E_ARG_476	NH1	E_ASP_474	OD2	3.850
6P65	E_ARG_476	NH2	E_GLU_102	OE1	3.708
6P65	E_ARG_476	NH2	E_GLU_102	OE2	3.050
6P65	E_LYS_485	NZ	E_GLU_267	OE2	2.828
6P65	E_LYS_487	NZ	E_ASP_47	OD1	2.921
6P65	E_LYS_487	NZ	E_ASP_47	OD2	2.883
6P65	E_LYS_492	NZ	E_GLU_490	OE1	3.434
6P65	E_LYS_492	NZ	E_GLU_490	OE2	2.782
6P65	E_ARG_500	NH1	G_GLU_30	OE1	3.143
6P65	E_ARG_500	NH1	G_GLU_30	OE2	3.804
6P65	E_ARG_500	NH2	G_GLU_30	OE1	3.741
6P65	E_ARG_500	NH2	G_GLU_30	OE2	2.979
6P65	E_ARG_542	NH2	A_ASP_648	OD1	3.154
6P65	E_LYS_574	NZ	E_ASP_107	OD1	2.460
6P65	E_LYS_574	NZ	E_ASP_107	OD2	3.496
6P65	E_LYS_588	NZ	E_GLU_584	OE2	2.714
6P65	E_LYS_617	NZ	E_GLU_634	OE1	3.411
6P65	E_LYS_658	NZ	E_GLU_654	OE1	2.576

6P65	F_ARG_38	NH2	F_GLU_46	OE1	3.002
6P65	F_LYS_71	NZ	E_GLU_87	OE1	2.935
6P65	F_LYS_71	NZ	E_GLU_87	OE2	2.865
6P65	F_ARG_94	NH2	F_ASP_33	OD1	3.585
6P65	F_ARG_94	NH2	F_ASP_33	OD2	3.145
6P65	F_LYS_100H	NZ	G_ASP_50	OD1	2.708
6P65	F_LYS_100H	NZ	G_ASP_50	OD2	2.596
6P65	G_ARG_95B	NH2	G_ASP_95D	OD2	3.668
6PE8	A_ARG_38	NH1	A_ASP_90	OD1	3.071
6PE8	A_ARG_38	NH2	A_GLU_46	OE1	3.098
6PE8	A_ARG_38	NH2	A_ASP_90	OD1	3.704
6PE8	A_LYS_65	NZ	A_ASP_62	OD1	3.575
6PE8	A_ARG_67	NH1	A_ASP_90	OD1	3.779
6PE8	A_ARG_67	NH1	A_ASP_90	OD2	2.688
6PE8	A_ARG_67	NH2	A_ASP_90	OD1	3.147
6PE8	A_ARG_67	NH2	A_ASP_90	OD2	3.558
6PE8	A_ARG_98	NH2	A_ASP_104	OD2	2.902
6PE8	A_LYS_212	NZ	B_GLU_129	OE1	3.617
6PE8	A_LYS_212	NZ	B_GLU_129	OE2	2.921
6PE8	A_LYS_213	NZ	A_GLU_215	OE2	2.893
6PE8	A_LYS_217	NZ	B_ASP_128	OD2	3.408
6PE8	B_LYS_24	NZ	B_ASP_76	OD1	3.379
6PE8	B_LYS_36	NZ	U_GLU_98	OE2	3.943
6PE8	B_ARG_67	NH2	B_ASP_88	OD1	2.504
6PE8	B_ARG_67	NH2	B_ASP_88	OD2	3.136
6PE8	B_LYS_109	NZ	B_GLU_111	OE2	3.226
6PE8	B_LYS_155	NZ	B_GLU_201	OE2	3.818
6PE8	B_HIS_195	ND1	B_ASP_157	OD2	3.341
6PE8	H_ARG_38	NH1	H_ASP_90	OD1	3.238
6PE8	H_ARG_38	NH2	H_GLU_46	OE2	3.230
6PE8	H_ARG_38	NH2	H_ASP_90	OD1	3.857
6PE8	H_LYS_65	NZ	H_ASP_62	OD1	3.030
6PE8	H_ARG_67	NH1	H_ASP_90	OD1	3.620
6PE8	H_ARG_67	NH1	H_ASP_90	OD2	2.656
6PE8	H_ARG_67	NH2	H_ASP_90	OD1	3.125
6PE8	H_ARG_67	NH2	H_ASP_90	OD2	3.678
6PE8	H_ARG_98	NH2	H_ASP_104	OD1	3.497
6PE8	H_ARG_98	NH2	H_ASP_104	OD2	2.823
6PE8	H_LYS_146	NZ	H_ASP_147	OD1	3.006
6PE8	H_LYS_146	NZ	H_ASP_147	OD2	3.312
6PE8	H_LYS_212	NZ	L_GLU_129	OE1	2.763
6PE8	H_LYS_212	NZ	L_GLU_129	OE2	3.237
6PE8	L_LYS_36	NZ	T_GLU_98	OE1	3.975
6PE8	L_LYS_36	NZ	T_GLU_98	OE2	3.494
6PE8	L_ARG_67	NH1	L_ASP_88	OD1	2.489
6PE8	L_ARG_67	NH1	L_ASP_88	OD2	2.664
6PE8	L_ARG_67	NH2	L_GLU_87	OE2	3.818
6PE8	L_LYS_109	NZ	L_GLU_171	OE1	2.957
6PE8	L_LYS_109	NZ	L_GLU_171	OE2	3.577
6PE8	L_HIS_195	ND1	L_ASP_191	OD1	3.228
6PE8	L_ARG_217	NH1	L_GLU_193	OE2	3.407
6PE8	T_LYS_46	NZ	T_GLU_66	OE1	3.537
6PE8	T_HIS_78	NE2	T_GLU_74	OE2	3.145
6PE8	T_LYS_81	NZ	T_GLU_117	OE2	3.858
6PE8	T_ARG_90	NH1	T_GLU_106	OE2	3.299
6PE8	T_ARG_90	NH2	H_ASP_62	OD1	3.932
6PE8	T_LYS_94	NZ	L_ASP_97	OD1	2.502
6PE8	T_LYS_94	NZ	L_ASP_97	OD2	3.872

6PE8	T_ARG_123	NH1	T_ASP_140	OD2	3.487
6PE8	T_ARG_123	NH2	T_ASP_140	OD2	3.475
6PE8	U_HIS_78	NE2	U_GLU_74	OE2	3.728
6PE8	U_HIS_162	NE2	U_GLU_159	OE1	3.858
6PE8	U_HIS_162	NE2	U_GLU_159	OE2	3.289
6PE9	A_ARG_38	NH1	A_ASP_90	OD1	2.798
6PE9	A_ARG_38	NH2	A_GLU_46	OE1	3.159
6PE9	A_ARG_38	NH2	A_GLU_46	OE2	3.251
6PE9	A_ARG_38	NH2	A_ASP_90	OD1	3.887
6PE9	A_ARG_67	NH1	A_ASP_90	OD1	3.800
6PE9	A_ARG_67	NH1	A_ASP_90	OD2	2.750
6PE9	A_ARG_67	NH2	A_ASP_90	OD1	2.777
6PE9	A_ARG_67	NH2	A_ASP_90	OD2	3.300
6PE9	A_ARG_87	NH1	A_ASP_90	OD1	3.204
6PE9	A_ARG_98	NH2	A_ASP_104	OD1	3.991
6PE9	A_ARG_98	NH2	A_ASP_104	OD2	3.023
6PE9	A_LYS_146	NZ	A_ASP_147	OD1	3.217
6PE9	A_LYS_146	NZ	A_ASP_147	OD2	3.463
6PE9	A_LYS_212	NZ	B_GLU_129	OE1	3.227
6PE9	A_LYS_212	NZ	B_GLU_129	OE2	3.311
6PE9	A_LYS_213	NZ	A_GLU_215	OE2	2.756
6PE9	A_LYS_217	NZ	B_ASP_128	OD1	3.061
6PE9	A_LYS_217	NZ	B_ASP_128	OD2	3.113
6PE9	B_ARG_60	NH2	B_ASP_66	OD2	3.733
6PE9	B_ARG_67	NH2	B_GLU_87	OE2	3.721
6PE9	B_ARG_67	NH2	B_ASP_88	OD1	2.626
6PE9	B_ARG_67	NH2	B_ASP_88	OD2	3.531
6PE9	B_LYS_109	NZ	B_GLU_171	OE1	3.224
6PE9	B_LYS_109	NZ	B_GLU_171	OE2	3.604
6PE9	B_LYS_155	NZ	B_GLU_201	OE1	2.857
6PE9	B_LYS_155	NZ	B_GLU_201	OE2	3.583
6PE9	B_LYS_189	NZ	B_GLU_193	OE1	2.706
6PE9	B_HIS_195	ND1	B_ASP_157	OD2	3.250
6PE9	B_HIS_195	NE2	B_ASP_191	OD1	3.630
6PE9	C_LYS_13	NZ	U_GLU_107	OE2	3.461
6PE9	C_ARG_38	NH1	C_ASP_90	OD1	2.834
6PE9	C_ARG_38	NH2	C_GLU_46	OE1	3.774
6PE9	C_ARG_38	NH2	C_ASP_90	OD1	3.862
6PE9	C_ARG_67	NH1	C_ASP_90	OD1	3.690
6PE9	C_ARG_67	NH1	C_ASP_90	OD2	2.701
6PE9	C_ARG_67	NH2	C_ASP_90	OD1	3.027
6PE9	C_ARG_67	NH2	C_ASP_90	OD2	3.482
6PE9	C_ARG_87	NH1	C_GLU_89	OE1	2.999
6PE9	C_ARG_87	NH2	C_GLU_89	OE1	3.050
6PE9	C_ARG_98	NH2	C_ASP_104	OD1	3.544
6PE9	C_ARG_98	NH2	C_ASP_104	OD2	2.696
6PE9	C_LYS_212	NZ	D_GLU_129	OE1	2.716
6PE9	D_LYS_24	NZ	D_ASP_76	OD2	3.066
6PE9	D_LYS_36	NZ	G_GLU_98	OE2	3.800
6PE9	D_ARG_67	NH2	D_GLU_87	OE2	3.276
6PE9	D_ARG_67	NH2	D_ASP_88	OD1	2.629
6PE9	D_ARG_67	NH2	D_ASP_88	OD2	2.960
6PE9	D_LYS_109	NZ	D_GLU_111	OE2	3.968
6PE9	D_ARG_148	NH1	D_GLU_111	OE1	3.574
6PE9	D_ARG_148	NH1	D_GLU_111	OE2	3.676
6PE9	D_LYS_155	NZ	D_GLU_201	OE1	3.155
6PE9	D_LYS_189	NZ	D_GLU_193	OE2	3.713
6PE9	D_HIS_195	ND1	D_ASP_157	OD2	3.268

6PE9	D_HIS_195	NE2	D_ASP_191	OD1	3.868
6PE9	D_LYS_196	NZ	D_GLU_219	OE1	3.644
6PE9	D_LYS_196	NZ	D_GLU_219	OE2	3.664
6PE9	E_LYS_13	NZ	G_GLU_107	OE2	3.510
6PE9	E_ARG_38	NH1	E_ASP_90	OD1	3.156
6PE9	E_ARG_38	NH2	E_GLU_46	OE1	3.279
6PE9	E_ARG_38	NH2	E_ASP_90	OD1	3.604
6PE9	E_LYS_65	NZ	E_ASP_62	OD1	3.311
6PE9	E_ARG_67	NH1	E_ASP_90	OD1	3.553
6PE9	E_ARG_67	NH1	E_ASP_90	OD2	2.749
6PE9	E_ARG_67	NH2	E_ASP_90	OD1	2.879
6PE9	E_ARG_67	NH2	E_ASP_90	OD2	3.602
6PE9	E_ARG_87	NH1	E_GLU_89	OE1	2.875
6PE9	E_ARG_98	NH2	E_ASP_104	OD1	3.656
6PE9	E_ARG_98	NH2	E_ASP_104	OD2	2.618
6PE9	E_LYS_212	NZ	F_GLU_129	OE1	3.511
6PE9	E_LYS_212	NZ	F_GLU_129	OE2	3.915
6PE9	F_LYS_36	NZ	U_GLU_98	OE2	3.769
6PE9	F_ARG_67	NH2	F_GLU_87	OE2	3.406
6PE9	F_ARG_67	NH2	F_ASP_88	OD1	3.433
6PE9	F_ARG_67	NH2	F_ASP_88	OD2	3.747
6PE9	F_ARG_148	NH1	F_GLU_149	OE1	2.587
6PE9	F_LYS_155	NZ	F_GLU_201	OE1	2.986
6PE9	F_LYS_189	NZ	F_GLU_193	OE1	3.673
6PE9	F_HIS_195	ND1	F_ASP_157	OD2	2.583
6PE9	F_ARG_217	NH1	F_GLU_193	OE2	2.594
6PE9	F_ARG_217	NH2	F_GLU_193	OE2	3.577
6PE9	G_ARG_73	NH1	J_GLU_74	OE1	3.140
6PE9	G_ARG_73	NH2	J_GLU_74	OE1	2.423
6PE9	G_ARG_73	NH2	J_GLU_74	OE2	3.851
6PE9	G_LYS_94	NZ	D_ASP_97	OD1	2.957
6PE9	G_HIS_110	ND1	G_ASP_140	OD1	3.723
6PE9	G_HIS_110	ND1	G_ASP_140	OD2	3.419
6PE9	G_HIS_110	NE2	G_ASP_140	OD2	3.595
6PE9	H_ARG_38	NH1	H_ASP_90	OD1	2.812
6PE9	H_ARG_38	NH2	H_GLU_46	OE1	3.356
6PE9	H_ARG_38	NH2	H_ASP_90	OD1	3.422
6PE9	H_ARG_67	NH1	H_ASP_90	OD1	3.929
6PE9	H_ARG_67	NH1	H_ASP_90	OD2	2.687
6PE9	H_ARG_67	NH2	H_ASP_90	OD1	3.445
6PE9	H_ARG_67	NH2	H_ASP_90	OD2	3.625
6PE9	H_ARG_98	NH2	H_ASP_104	OD1	3.718
6PE9	H_ARG_98	NH2	H_ASP_104	OD2	3.048
6PE9	I_LYS_29	NZ	U_ASP_69	OD2	3.034
6PE9	I_ARG_73	NH1	U_GLU_74	OE1	3.681
6PE9	I_ARG_73	NH1	U_GLU_74	OE2	2.345
6PE9	I_ARG_73	NH2	U_GLU_74	OE2	3.507
6PE9	I_LYS_	NZ	I_GLU_	OE2	3.108
6PE9	J_ARG_73	NH1	G_GLU_74	OE1	3.931
6PE9	J_ARG_73	NH1	G_GLU_74	OE2	3.429
6PE9	K_ARG_38	NH1	K_ASP_90	OD1	3.525
6PE9	K_ARG_38	NH2	K_GLU_46	OE1	3.767
6PE9	K_ARG_38	NH2	K_GLU_46	OE2	3.741
6PE9	K_LYS_65	NZ	K_ASP_62	OD1	3.669
6PE9	K_ARG_67	NH1	K_ASP_90	OD2	2.819
6PE9	K_ARG_67	NH2	K_ASP_90	OD1	3.281
6PE9	K_ARG_67	NH2	K_ASP_90	OD2	2.919
6PE9	K_ARG_98	NH2	K_ASP_104	OD2	3.783

6PE9	L_LYS_24	NZ	L_ASP_76	OD1	3.672
6PE9	L_LYS_24	NZ	L_ASP_76	OD2	3.497
6PE9	L_ARG_67	NH2	L_ASP_88	OD1	2.613
6PE9	L_ARG_67	NH2	L_ASP_88	OD2	3.007
6PE9	L_LYS_109	NZ	L_GLU_111	OE2	2.907
6PE9	L_LYS_155	NZ	L_GLU_201	OE1	3.099
6PE9	L_LYS_155	NZ	L_GLU_201	OE2	3.866
6PE9	L_LYS_194	NZ	L_ASP_191	OD1	2.988
6PE9	L_LYS_196	NZ	L_GLU_219	OE1	3.947
6PE9	L_LYS_196	NZ	L_GLU_219	OE2	3.563
6PE9	M_LYS_24	NZ	M_ASP_76	OD2	2.801
6PE9	M_LYS_36	NZ	J_GLU_98	OE1	2.716
6PE9	M_ARG_67	NH2	M_GLU_87	OE2	3.490
6PE9	M_ARG_67	NH2	M_ASP_88	OD1	2.820
6PE9	M_ARG_67	NH2	M_ASP_88	OD2	3.597
6PE9	U_LYS_	NZ	I_ASP_	OD2	3.835
6PE9	U_LYS_	NZ	U_GLU_	OE1	3.844
6PE9	U_ARG_	NH2	I_GLU_	OE1	3.379
6PE9	U_ARG_	NH2	I_GLU_	OE2	2.907
6PE9	U_ARG_90	NH2	U_GLU_107	OE1	3.607
6PE9	U_LYS_94	NZ	F_ASP_97	OD1	2.940
6PE9	U_HIS_110	ND1	U_ASP_140	OD1	3.870
6PE9	U_HIS_110	NE2	U_ASP_140	OD2	3.135
6PE9	V_LYS_46	NZ	V_GLU_66	OE1	3.793
6PE9	V_LYS_81	NZ	V_ASP_100	OD2	3.343
6PE9	V_ARG_90	NH1	L_ASP_1	OD1	3.701
6PE9	V_ARG_90	NH1	V_GLU_106	OE1	3.470
6PE9	V_ARG_90	NH1	V_GLU_106	OE2	3.555
6PE9	V_ARG_90	NH2	L_ASP_1	OD1	3.047
6PE9	V_LYS_94	NZ	L_ASP_97	OD1	3.203
6PHB	I_HIS_20	NE2	I_GLU_22	OE2	2.552
6PHB	I_LYS_43	NZ	D_ASP_27	OD2	2.797
6PHB	I_LYS_47	NZ	C_GLU_55	OE1	3.460
6PHB	I_LYS_47	NZ	C_GLU_55	OE2	3.396
6PHB	I_LYS_47	NZ	D_ASP_105	OD2	2.626
6PHB	I_LYS_98	NZ	I_GLU_22	OE1	3.315
6PHB	I_LYS_98	NZ	I_GLU_22	OE2	2.997
6PHB	I_LYS_118	NZ	I_ASP_131	OD1	2.829
6PHB	C_ARG_61	NH2	C_GLU_81	OE2	3.398
6PHB	C_ARG_61	NH2	C_ASP_82	OD1	2.798
6PHB	C_ARG_61	NH2	C_ASP_82	OD2	3.548
6PHB	C_ARG_95	NH1	I_ASP_28	OD2	3.551
6PHB	C_ARG_95	NH1	I_GLU_39	OE2	3.728
6PHB	C_LYS_104	NZ	C_GLU_166	OE2	2.738
6PHB	C_LYS_150	NZ	C_GLU_196	OE1	2.587
6PHB	C_LYS_150	NZ	C_GLU_196	OE2	3.892
6PHB	C_LYS_189	NZ	C_ASP_186	OD1	3.064
6PHB	C_ARG_212	NH1	C_GLU_188	OE1	3.096
6PHB	D_ARG_38	NH1	D_ASP_89	OD1	2.792
6PHB	D_ARG_38	NH2	D_GLU_46	OE1	3.039
6PHB	D_ARG_38	NH2	D_GLU_46	OE2	3.983
6PHB	D_ARG_38	NH2	D_ASP_89	OD1	3.789
6PHB	D_ARG_50	NH1	I_GLU_39	OE2	3.791
6PHB	D_ARG_50	NH2	I_GLU_39	OE2	2.945
6PHB	D_ARG_66	NH1	D_ASP_89	OD1	3.229
6PHB	D_ARG_66	NH1	D_ASP_89	OD2	3.729
6PHB	D_ARG_66	NH2	D_ASP_89	OD1	3.250
6PHB	D_ARG_66	NH2	D_ASP_89	OD2	2.491

6PHB	D_LYS_147	NZ	D_ASP_148	OD1	3.275
6PHB	D_LYS_147	NZ	D_ASP_148	OD2	3.674
6PHB	D_LYS_213	NZ	C_GLU_124	OE1	2.534
6PHB	D_LYS_213	NZ	C_GLU_124	OE2	3.508
6PHB	E_HIS_20	NE2	E_GLU_22	OE1	2.558
6PHB	E_LYS_43	NZ	B_ASP_27	OD2	3.033
6PHB	E_LYS_47	NZ	A_GLU_55	OE1	3.560
6PHB	E_LYS_47	NZ	A_GLU_55	OE2	3.516
6PHB	E_LYS_47	NZ	B_ASP_105	OD1	2.522
6PHB	E_LYS_98	NZ	E_GLU_22	OE1	3.054
6PHB	E_LYS_98	NZ	E_GLU_22	OE2	3.330
6PHB	E_LYS_118	NZ	E_ASP_131	OD1	2.740
6PHB	E_LYS_142	NZ	E_GLU_145	OE2	3.699
6PHB	A_ARG_61	NH2	A_GLU_81	OE2	3.390
6PHB	A_ARG_61	NH2	A_ASP_82	OD1	2.898
6PHB	A_ARG_61	NH2	A_ASP_82	OD2	3.663
6PHB	A_ARG_95	NH1	E_ASP_28	OD1	3.463
6PHB	A_ARG_95	NH1	E_GLU_39	OE2	3.694
6PHB	A_LYS_104	NZ	A_GLU_166	OE1	2.724
6PHB	A_LYS_150	NZ	A_GLU_196	OE1	2.544
6PHB	A_LYS_150	NZ	A_GLU_196	OE2	3.867
6PHB	A_LYS_189	NZ	A_ASP_186	OD1	3.061
6PHB	A_ARG_212	NH2	A_GLU_188	OE2	2.964
6PHB	B_ARG_38	NH1	B_ASP_89	OD1	2.781
6PHB	B_ARG_38	NH2	B_GLU_46	OE1	3.033
6PHB	B_ARG_38	NH2	B_GLU_46	OE2	3.957
6PHB	B_ARG_38	NH2	B_ASP_89	OD1	3.799
6PHB	B_ARG_50	NH1	E_GLU_39	OE2	3.771
6PHB	B_ARG_50	NH2	E_GLU_39	OE2	2.963
6PHB	B_ARG_66	NH1	B_ASP_89	OD1	3.245
6PHB	B_ARG_66	NH1	B_ASP_89	OD2	3.725
6PHB	B_ARG_66	NH2	B_ASP_89	OD1	3.258
6PHB	B_ARG_66	NH2	B_ASP_89	OD2	2.482
6PHB	B_LYS_147	NZ	B_ASP_148	OD1	3.294
6PHB	B_LYS_147	NZ	B_ASP_148	OD2	3.635
6PHB	B_LYS_213	NZ	A_GLU_124	OE1	3.629
6PHB	B_LYS_213	NZ	A_GLU_124	OE2	2.552
6PHC	I_LYS_2	NZ	A_GLU_96	OE1	3.433
6PHC	I_HIS_20	NE2	I_GLU_22	OE2	2.559
6PHC	I_LYS_40	NZ	I_ASP_28	OD1	2.981
6PHC	I_LYS_40	NZ	I_ASP_28	OD2	3.595
6PHC	I_LYS_98	NZ	I_GLU_22	OE2	3.581
6PHC	I_LYS_139	NZ	I_ASP_6	OD1	2.833
6PHC	A_ARG_38	NH1	A_ASP_86	OD1	2.881
6PHC	A_ARG_38	NH2	A_GLU_46	OE1	3.768
6PHC	A_ARG_38	NH2	A_GLU_46	OE2	2.978
6PHC	A_ARG_38	NH2	A_ASP_86	OD1	3.793
6PHC	A_LYS_64	NZ	A_ASP_61	OD2	2.874
6PHC	A_ARG_66	NH1	A_ASP_86	OD1	3.869
6PHC	A_ARG_66	NH2	A_ASP_86	OD1	3.269
6PHC	A_ARG_66	NH2	A_ASP_86	OD2	2.372
6PHC	A_ARG_94	NH2	A_ASP_101	OD1	3.528
6PHC	A_ARG_94	NH2	A_ASP_101	OD2	2.665
6PHC	A_LYS_143	NZ	A_ASP_144	OD1	3.692
6PHC	A_LYS_206	NZ	A_ASP_208	OD1	2.966
6PHC	A_LYS_206	NZ	A_ASP_208	OD2	3.137
6PHC	A_LYS_209	NZ	B_GLU_122	OE2	3.367
6PHC	A_LYS_210	NZ	A_GLU_212	OE2	2.900

6PHC	B_ARG_24	NH1	B_ASP_70	OD1	3.336
6PHC	B_ARG_61	NH1	B_ASP_82	OD1	3.307
6PHC	B_ARG_61	NH1	B_ASP_82	OD2	2.292
6PHC	B_ARG_61	NH2	B_GLU_81	OE2	3.528
6PHC	B_ARG_61	NH2	B_ASP_82	OD1	3.098
6PHC	B_ARG_61	NH2	B_ASP_82	OD2	3.416
6PHC	B_ARG_102	NH1	B_GLU_164	OE1	2.853
6PHC	B_LYS_106	NZ	B_GLU_17	OE2	3.611
6PHC	B_ARG_141	NH1	B_GLU_104	OE1	3.956
6PHC	B_ARG_141	NH2	B_GLU_104	OE1	2.662
6PHC	B_ARG_141	NH2	B_GLU_104	OE2	2.894
6PHC	B_LYS_148	NZ	B_GLU_194	OE1	2.588
6PHC	B_LYS_187	NZ	B_ASP_184	OD1	3.568
6PHC	E_LYS_2	NZ	C_GLU_96	OE2	3.166
6PHC	E_HIS_20	NE2	E_GLU_22	OE2	2.761
6PHC	E_LYS_118	NZ	E_ASP_131	OD1	3.884
6PHC	E_LYS_118	NZ	E_ASP_131	OD2	3.881
6PHC	E_LYS_139	NZ	E_ASP_6	OD1	2.752
6PHC	E_LYS_139	NZ	E_ASP_6	OD2	3.907
6PHC	E_LYS_155	NZ	E_ASP_157	OD2	3.939
6PHC	C_ARG_38	NH1	C_ASP_86	OD1	2.792
6PHC	C_ARG_38	NH2	C_GLU_46	OE1	3.747
6PHC	C_ARG_38	NH2	C_GLU_46	OE2	2.839
6PHC	C_ARG_38	NH2	C_ASP_86	OD1	3.865
6PHC	C_LYS_64	NZ	C_ASP_61	OD1	3.164
6PHC	C_ARG_66	NH2	C_ASP_86	OD1	3.190
6PHC	C_ARG_66	NH2	C_ASP_86	OD2	2.357
6PHC	C_LYS_75	NZ	A_GLU_1	OE1	3.102
6PHC	C_ARG_94	NH2	C_ASP_101	OD1	3.594
6PHC	C_ARG_94	NH2	C_ASP_101	OD2	2.564
6PHC	C_LYS_143	NZ	C_ASP_144	OD1	3.602
6PHC	C_LYS_143	NZ	C_ASP_144	OD2	3.997
6PHC	C_LYS_209	NZ	D_GLU_122	OE2	3.075
6PHC	D_ARG_24	NH1	D_ASP_70	OD1	2.338
6PHC	D_ARG_24	NH1	D_ASP_70	OD2	2.957
6PHC	D_ARG_24	NH2	D_ASP_70	OD1	3.768
6PHC	D_ARG_61	NH2	D_GLU_81	OE2	3.370
6PHC	D_ARG_61	NH2	D_ASP_82	OD1	3.166
6PHC	D_ARG_61	NH2	D_ASP_82	OD2	3.703
6PHC	D_LYS_106	NZ	D_GLU_17	OE2	3.862
6PHC	D_ARG_141	NH1	D_GLU_104	OE1	3.512
6PHC	D_ARG_141	NH1	D_GLU_104	OE2	3.995
6PHC	D_ARG_141	NH2	D_GLU_104	OE1	3.237
6PHC	D_ARG_141	NH2	D_GLU_104	OE2	2.397
6PHC	D_LYS_187	NZ	D_ASP_184	OD1	3.752
6PHD	H_HIS_3	NE2	H_GLU_1	OE1	3.723
6PHD	H_HIS_3	NE2	H_GLU_1	OE2	3.479
6PHD	H_ARG_38	NH1	H_ASP_92	OD1	3.022
6PHD	H_ARG_38	NH2	H_GLU_46	OE1	3.293
6PHD	H_ARG_38	NH2	H_GLU_46	OE2	3.635
6PHD	H_ARG_38	NH2	H_ASP_92	OD1	3.809
6PHD	H_ARG_50	NH1	H_ASP_35	OD1	3.977
6PHD	H_ARG_50	NH1	H_ASP_35	OD2	3.398
6PHD	H_ARG_52	NH1	H_ASP_61	OD2	3.597
6PHD	H_ARG_52	NH2	H_ASP_61	OD2	3.257
6PHD	H_ARG_52	NH2	C_ASP_131	OD2	3.559
6PHD	H_ARG_69	NH1	H_ASP_92	OD1	3.736
6PHD	H_ARG_69	NH1	H_ASP_92	OD2	2.629

6PHD	H_ARG_69	NH2	H_ASP_92	OD1	3.118
6PHD	H_ARG_69	NH2	H_ASP_92	OD2	3.528
6PHD	H_ARG_74	NH2	H_ASP_76	OD1	3.389
6PHD	H_ARG_100	NH2	H_ASP_116	OD1	3.601
6PHD	H_ARG_100	NH2	H_ASP_116	OD2	2.413
6PHD	H_ARG_107	NH1	H_GLU_106	OE2	3.946
6PHD	H_LYS_158	NZ	L_GLU_128	OE2	2.649
6PHD	H_LYS_224	NZ	L_GLU_127	OE1	2.532
6PHD	H_LYS_224	NZ	L_GLU_127	OE2	2.992
6PHD	H_LYS_225	NZ	H_GLU_227	OE2	3.183
6PHD	L_ARG_61	NH2	L_GLU_81	OE1	3.579
6PHD	L_ARG_61	NH2	L_ASP_82	OD1	3.221
6PHD	L_ARG_61	NH2	L_ASP_82	OD2	3.791
6PHD	L_LYS_106	NZ	L_ASP_85	OD1	3.546
6PHD	L_LYS_114	NZ	L_GLU_202	OE1	3.497
6PHD	L_HIS_192	ND1	L_ASP_155	OD2	4.000
6PHD	C_ARG_11	NH1	C_GLU_39	OE2	3.811
6PHD	C_ARG_11	NH2	C_GLU_39	OE1	3.053
6PHD	C_ARG_11	NH2	C_GLU_39	OE2	3.487
6PHD	C_HIS_20	NE2	C_GLU_22	OE1	3.024
6PHD	C_LYS_90	NZ	C_ASP_78	OD2	3.307
6PHD	C_LYS_98	NZ	C_GLU_22	OE1	2.852
6PHD	C_LYS_98	NZ	C_GLU_22	OE2	3.209
6PHD	C_LYS_118	NZ	H_ASP_109	OD1	3.874
6PHD	C_LYS_118	NZ	C_ASP_131	OD1	3.023
6PHD	C_LYS_127	NZ	C_ASP_124	OD1	3.895
6PHD	C_LYS_135	NZ	L_ASP_51	OD2	3.166
6PHD	C_LYS_139	NZ	C_ASP_6	OD1	3.503
6PHD	C_LYS_148	NZ	C_ASP_157	OD2	3.726
6PHD	C_LYS_148	NZ	C_ASP_160	OD1	3.495
6PHF	A_ARG_12	NH2	A_GLU_10	OE1	2.765
6PHF	A_ARG_38	NH1	A_ASP_90	OD1	3.178
6PHF	A_ARG_38	NH2	A_GLU_46	OE1	3.769
6PHF	A_ARG_38	NH2	A_GLU_89	OE1	3.880
6PHF	A_ARG_38	NH2	A_GLU_89	OE2	3.467
6PHF	A_LYS_63	NZ	A_GLU_46	OE2	2.996
6PHF	A_LYS_63	NZ	C_GLU_89	OE2	2.941
6PHF	A_ARG_67	NH1	A_ASP_90	OD1	3.640
6PHF	A_ARG_67	NH2	A_ASP_90	OD1	3.213
6PHF	A_ARG_67	NH2	A_ASP_90	OD2	2.825
6PHF	A_ARG_87	NH2	A_GLU_89	OE1	3.635
6PHF	A_ARG_98	NH1	A_ASP_108	OD1	3.223
6PHF	A_ARG_98	NH1	A_ASP_108	OD2	2.645
6PHF	A_ARG_98	NH2	A_ASP_108	OD2	3.048
6PHF	A_LYS_150	NZ	B_GLU_123	OE1	3.782
6PHF	A_LYS_216	NZ	B_GLU_122	OE1	2.642
6PHF	A_LYS_216	NZ	B_GLU_122	OE2	2.832
6PHF	G_HIS_20	NE2	G_GLU_22	OE2	2.627
6PHF	G_LYS_72	NZ	G_ASP_78	OD1	3.015
6PHF	G_LYS_98	NZ	G_GLU_22	OE1	3.385
6PHF	G_LYS_98	NZ	G_GLU_22	OE2	2.989
6PHF	G_LYS_118	NZ	G_ASP_131	OD1	2.874
6PHF	G_LYS_130	NZ	A_GLU_59	OE2	2.793
6PHF	G_LYS_135	NZ	B_ASP_48	OD1	3.917
6PHF	G_LYS_135	NZ	B_ASP_48	OD2	2.691
6PHF	G_LYS_148	NZ	G_ASP_160	OD1	2.301
6PHF	G_LYS_148	NZ	G_ASP_160	OD2	3.905
6PHF	B_LYS_28	NZ	B_ASP_89	OD2	3.634

6PHF	B.LYS_50	NZ	G_ASP_160	OD1	3.948
6PHF	B.LYS_50	NZ	G_ASP_160	OD2	3.455
6PHF	B_ARG_58	NH1	B_ASP_79	OD2	3.097
6PHF	B_ARG_58	NH2	B_ASP_79	OD1	3.588
6PHF	B_ARG_58	NH2	B_ASP_79	OD2	3.661
6PHF	B.LYS_165	NZ	B_GLU_80	OE1	2.830
6PHF	C_ARG_12	NH2	C_GLU_10	OE1	2.671
6PHF	C_ARG_38	NH1	C_ASP_90	OD1	3.218
6PHF	C.LYS_63	NZ	A_GLU_89	OE2	3.050
6PHF	C.LYS_63	NZ	C_GLU_46	OE2	3.084
6PHF	C_ARG_67	NH2	C_ASP_90	OD1	3.179
6PHF	C_ARG_87	NH1	C_GLU_89	OE1	3.091
6PHF	C_ARG_87	NH2	C_GLU_89	OE1	2.353
6PHF	C_ARG_87	NH2	C_ASP_90	OD1	3.900
6PHF	C_ARG_98	NH2	C_ASP_108	OD2	3.438
6PHF	C.LYS_150	NZ	D_GLU_123	OE2	2.663
6PHF	C.LYS_216	NZ	D_GLU_122	OE1	2.759
6PHF	C.LYS_216	NZ	D_GLU_122	OE2	3.120
6PHF	E.HIS_20	NE2	E_GLU_22	OE1	3.442
6PHF	E.LYS_72	NZ	E_ASP_78	OD1	3.439
6PHF	E.LYS_98	NZ	E_GLU_22	OE1	2.929
6PHF	E.LYS_98	NZ	E_GLU_22	OE2	3.612
6PHF	E.LYS_118	NZ	E_ASP_131	OD1	2.864
6PHF	E.LYS_130	NZ	C_GLU_59	OE2	2.474
6PHF	E.LYS_135	NZ	D_ASP_48	OD1	3.909
6PHF	E.LYS_135	NZ	D_ASP_48	OD2	2.579
6PHF	E.LYS_139	NZ	E_ASP_6	OD1	2.802
6PHF	D.LYS_24	NZ	D_ASP_23	OD1	3.810
6PHF	D.LYS_28	NZ	D_ASP_89	OD1	3.365
6PHF	D_ARG_58	NH2	D_ASP_79	OD1	2.632
6PHF	D_ARG_58	NH2	D_ASP_79	OD2	2.899
6PHG	A_ARG_38	NH1	A_ASP_90	OD1	2.955
6PHG	A_ARG_38	NH2	A_GLU_46	OE1	3.239
6PHG	A_ARG_38	NH2	A_ASP_90	OD1	3.782
6PHG	A.LYS_65	NZ	A_ASP_62	OD1	3.774
6PHG	A_ARG_67	NH1	A_ASP_90	OD1	3.754
6PHG	A_ARG_67	NH1	A_ASP_90	OD2	2.801
6PHG	A_ARG_67	NH2	A_ASP_90	OD1	2.872
6PHG	A_ARG_67	NH2	A_ASP_90	OD2	3.428
6PHG	A.LYS_76	NZ	A_ASP_73	OD2	3.739
6PHG	A_ARG_98	NH2	A_ASP_113	OD1	3.705
6PHG	A_ARG_98	NH2	A_ASP_113	OD2	2.616
6PHG	A.LYS_155	NZ	A_ASP_156	OD1	3.341
6PHG	A.LYS_155	NZ	A_ASP_156	OD2	2.879
6PHG	A.LYS_221	NZ	B_GLU_126	OE2	3.079
6PHG	A.LYS_222	NZ	A_GLU_224	OE1	3.525
6PHG	B_ARG_65	NH1	B_GLU_83	OE1	3.253
6PHG	B_ARG_65	NH1	B_GLU_83	OE2	3.558
6PHG	B_ARG_65	NH2	B_GLU_83	OE1	3.939
6PHG	B_ARG_65	NH2	B_ASP_86	OD1	2.611
6PHG	B_ARG_65	NH2	B_ASP_86	OD2	2.992
6PHG	B_ARG_81	NH2	B_GLU_83	OE2	2.886
6PHG	B_ARG_106	NH1	B_GLU_168	OE2	3.259
6PHG	B.LYS_152	NZ	B_GLU_198	OE1	3.024
6PHG	B.LYS_191	NZ	B_ASP_188	OD1	3.125
6PHG	B_ARG_214	NH1	B_GLU_190	OE1	3.537
6PHH	C_ARG_38	NH1	C_ASP_90	OD1	2.886
6PHH	C_ARG_38	NH2	C_GLU_46	OE1	3.069

6PHH	C_ARG_38	NH2	C_GLU_46	OE2	3.921
6PHH	C_ARG_38	NH2	C_ASP_90	OD1	3.682
6PHH	C_ARG_67	NH1	C_ASP_90	OD1	3.146
6PHH	C_ARG_67	NH1	C_ASP_90	OD2	3.531
6PHH	C_ARG_67	NH2	C_ASP_90	OD1	3.933
6PHH	C_ARG_67	NH2	C_ASP_90	OD2	2.855
6PHH	C_LYS_76	NZ	A_GLU_1	OE1	3.897
6PHH	C_ARG_98	NH2	C_ASP_113	OD1	3.626
6PHH	C_ARG_98	NH2	C_ASP_113	OD2	2.534
6PHH	C_LYS_155	NZ	C_ASP_156	OD1	3.705
6PHH	D_ARG_58	NH2	D_ASP_64	OD1	3.542
6PHH	D_ARG_65	NH2	D_ASP_86	OD1	2.596
6PHH	D_ARG_65	NH2	D_ASP_86	OD2	2.751
6PHH	D_ARG_106	NH1	D_GLU_168	OE1	3.672
6PHH	D_ARG_106	NH1	D_GLU_168	OE2	2.329
6PHH	A_ARG_38	NH1	A_ASP_90	OD1	2.820
6PHH	A_ARG_38	NH2	A_GLU_46	OE1	2.997
6PHH	A_ARG_38	NH2	A_GLU_46	OE2	3.785
6PHH	A_ARG_38	NH2	A_ASP_90	OD1	3.734
6PHH	A_LYS_65	NZ	A_ASP_62	OD1	2.552
6PHH	A_ARG_67	NH1	A_ASP_90	OD1	3.908
6PHH	A_ARG_67	NH1	A_ASP_90	OD2	2.904
6PHH	A_ARG_67	NH2	A_ASP_90	OD1	3.309
6PHH	A_ARG_67	NH2	A_ASP_90	OD2	3.733
6PHH	A_LYS_76	NZ	C_GLU_1	OE1	3.451
6PHH	A_ARG_98	NH2	A_GLU_100	OE1	3.744
6PHH	A_ARG_98	NH2	A_ASP_113	OD1	3.536
6PHH	A_ARG_98	NH2	A_ASP_113	OD2	2.500
6PHH	A_LYS_218	NZ	A_ASP_220	OD1	2.774
6PHH	A_LYS_218	NZ	A_ASP_220	OD2	3.847
6PHH	A_LYS_221	NZ	B_GLU_126	OE2	3.327
6PHH	B_ARG_24	NH1	B_ASP_74	OD1	3.370
6PHH	B_ARG_24	NH1	B_ASP_74	OD2	3.208
6PHH	B_ARG_24	NH2	B_ASP_74	OD1	3.944
6PHH	B_ARG_58	NH2	B_ASP_64	OD1	3.009
6PHH	B_ARG_65	NH2	B_ASP_86	OD1	2.841
6PHH	B_ARG_65	NH2	B_ASP_86	OD2	2.510
6PHH	B_ARG_106	NH1	B_GLU_168	OE2	2.682
6PHH	B_ARG_214	NH1	B_GLU_190	OE1	3.673
6PI7	A_HIS_317	NE2	A_GLU_316	OE1	3.899
6PI7	A_HIS_320	ND1	A_GLU_316	OE2	2.374
6PI7	A_HIS_320	NE2	A_GLU_418	OE2	2.831
6PI7	A_HIS_355	ND1	A_ASP_358	OD1	3.681
6PI7	A_HIS_355	ND1	A_ASP_358	OD2	2.824
6PI7	A_ARG_372	NH2	A_ASP_390	OD1	2.751
6PI7	A_ARG_372	NH2	A_ASP_390	OD2	3.246
6PI7	A_ARG_406	NH2	A_ASP_408	OD1	3.871
6PI7	A_ARG_406	NH2	A_ASP_408	OD2	2.514
6PI7	A_ARG_423	NH1	A_GLU_494	OE1	3.880
6PI7	A_HIS_444	NE2	A_ASP_473	OD2	2.887
6PI7	A_LYS_449	NZ	A_ASP_447	OD2	3.499
6PI7	A_LYS_489	NZ	A_GLU_485	OE1	2.489
6PI7	B_ARG_62	NH2	B_ASP_83	OD1	2.896
6PI7	B_ARG_62	NH2	B_ASP_83	OD2	3.659
6PI7	B_ARG_67	NH2	A_GLU_345	OE2	3.601
6PI7	C_ARG_41	NH1	C_GLU_49	OE1	3.463
6PI7	C_ARG_41	NH1	C_GLU_49	OE2	3.574
6PI7	C_ARG_41	NH1	C_ASP_93	OD1	3.486

6PI7	C_ARG_41	NH2	C_ASP_93	OD1	3.043
6PI7	C_ARG_70	NH1	C_ASP_93	OD1	3.039
6PI7	C_ARG_70	NH1	C_ASP_93	OD2	3.416
6PI7	C_ARG_70	NH2	C_ASP_93	OD1	3.898
6PI7	C_ARG_70	NH2	C_ASP_93	OD2	3.164
6PI7	C_ARG_101	NH2	C_ASP_115	OD1	3.986
6PI7	C_ARG_101	NH2	C_ASP_115	OD2	2.837
6PI7	C_HIS_103	NE2	C_ASP_115	OD2	3.124
6PI7	C_ARG_105	NH1	A_ASP_334	OD1	2.888
6PI7	D_HIS_317	NE2	D_GLU_316	OE1	3.914
6PI7	D_HIS_320	ND1	D_GLU_316	OE2	2.372
6PI7	D_HIS_320	NE2	D_GLU_418	OE2	2.836
6PI7	D_HIS_355	ND1	D_ASP_358	OD2	3.434
6PI7	D_ARG_372	NH2	D_ASP_390	OD1	2.758
6PI7	D_ARG_372	NH2	D_ASP_390	OD2	3.271
6PI7	D_ARG_406	NH2	D_ASP_408	OD1	3.860
6PI7	D_ARG_406	NH2	D_ASP_408	OD2	2.528
6PI7	D_ARG_423	NH1	D_GLU_494	OE1	3.849
6PI7	D_HIS_444	NE2	D_ASP_473	OD2	2.883
6PI7	D_LYS_449	NZ	D_ASP_447	OD2	3.509
6PI7	E_ARG_62	NH2	E_ASP_83	OD1	2.890
6PI7	E_ARG_62	NH2	E_ASP_83	OD2	3.662
6PI7	E_LYS_104	NZ	E_GLU_106	OE2	3.467
6PI7	E_LYS_150	NZ	E_GLU_196	OE1	3.393
6PI7	E_LYS_150	NZ	E_GLU_196	OE2	3.111
6PI7	F_ARG_41	NH1	F_GLU_49	OE1	3.460
6PI7	F_ARG_41	NH1	F_GLU_49	OE2	3.581
6PI7	F_ARG_41	NH1	F_ASP_93	OD1	3.467
6PI7	F_ARG_41	NH2	F_ASP_93	OD1	3.047
6PI7	F_ARG_70	NH1	F_ASP_93	OD1	3.056
6PI7	F_ARG_70	NH1	F_ASP_93	OD2	3.386
6PI7	F_ARG_70	NH2	F_ASP_93	OD1	3.902
6PI7	F_ARG_70	NH2	F_ASP_93	OD2	3.180
6PI7	F_ARG_101	NH2	F_ASP_115	OD1	3.992
6PI7	F_ARG_101	NH2	F_ASP_115	OD2	2.859
6PI7	F_HIS_103	NE2	F_ASP_115	OD2	3.117
6PI7	F_ARG_105	NH1	D_ASP_334	OD1	3.009
6PI7	G_ARG_4	NH1	A_ASP_385	OD1	3.497
6PI7	G_ARG_4	NH1	A_ASP_385	OD2	3.823
6PI7	G_ARG_4	NH2	A_ASP_385	OD1	3.602
6PI7	G_ARG_4	NH2	A_ASP_385	OD2	3.033
6PI7	G_ARG_6	NH1	A_GLU_433	OE2	2.847
6PI7	G_ARG_6	NH1	A_ASP_437	OD1	3.619
6PI7	G_ARG_6	NH2	A_ASP_437	OD1	2.997
6PI7	G_ARG_6	NH2	A_ASP_440	OD2	2.762
6PYC	H_ARG_67	NH2	H_GLU_87	OE2	3.339
6PYC	H_ARG_67	NH2	H_ASP_88	OD1	3.284
6PYC	H_ARG_67	NH2	H_ASP_88	OD2	3.903
6PYC	H_LYS_109	NZ	H_GLU_147	OE1	3.975
6PYC	H_LYS_142	NZ	H_ASP_143	OD1	3.360
6PYC	H_LYS_208	NZ	L_GLU_124	OE1	2.557
6PYC	H_LYS_208	NZ	L_GLU_124	OE2	3.571
6PYC	L_ARG_62	NH2	L_GLU_82	OE1	3.870
6PYC	L_ARG_62	NH2	L_ASP_83	OD1	2.885
6PYC	L_ARG_62	NH2	L_ASP_83	OD2	3.362
6PYC	L_LYS_108	NZ	B_ASP_32	OD1	2.949
6PYC	L_LYS_150	NZ	L_GLU_196	OE1	3.695
6PYC	L_LYS_184	NZ	L_GLU_188	OE1	2.615

6PYC	L_LYS_189	NZ	L_ASP_186	OD1	3.942
6PYC	A_ARG_38	NH1	A_ASP_90	OD1	2.858
6PYC	A_ARG_38	NH2	A_GLU_46	OE1	3.193
6PYC	A_ARG_38	NH2	A_GLU_46	OE2	3.336
6PYC	A_LYS_67	NZ	A_ASP_90	OD1	3.714
6PYC	A_LYS_67	NZ	A_ASP_90	OD2	3.477
6PYC	A_ARG_99	NH1	B_ASP_91	OD1	3.714
6PYC	B_LYS_53	NZ	L_GLU_17	OE1	3.141
6PYC	B_LYS_53	NZ	L_GLU_17	OE2	3.254
6PYC	B_ARG_61	NH1	B_GLU_81	OE2	3.676
6PYC	B_ARG_61	NH1	B_ASP_82	OD1	2.683
6PYC	B_ARG_61	NH1	B_ASP_82	OD2	3.599
6PYC	B_LYS_149	NZ	B_GLU_195	OE1	3.962
6PYC	B_LYS_149	NZ	B_GLU_195	OE2	3.345
6PYC	B_ARG_155	NH1	B_GLU_185	OE1	3.962
6PYC	B_ARG_155	NH1	B_GLU_185	OE2	3.253
6PYC	B_ARG_155	NH2	B_GLU_185	OE1	2.747
6PYC	B_ARG_155	NH2	B_GLU_185	OE2	3.418
6PYC	B_ARG_188	NH2	B_GLU_185	OE2	3.932
6PYC	B_LYS_199	NZ	B_ASP_110	OD2	3.197
6PYD	H_ARG_38	NH1	H_ASP_89	OD1	2.746
6PYD	H_ARG_38	NH2	H_GLU_46	OE1	2.703
6PYD	H_ARG_38	NH2	H_ASP_89	OD1	3.577
6PYD	H_ARG_66	NH1	H_ASP_89	OD1	3.629
6PYD	H_ARG_66	NH2	H_ASP_89	OD1	3.377
6PYD	H_ARG_66	NH2	H_ASP_89	OD2	2.647
6PYD	H_ARG_97	NH1	H_ASP_27	OD2	2.986
6PYD	H_ARG_97	NH2	H_ASP_105	OD1	3.627
6PYD	H_ARG_97	NH2	H_ASP_105	OD2	2.550
6PYD	H_LYS_147	NZ	H_ASP_148	OD1	3.103
6PYD	H_LYS_147	NZ	H_ASP_148	OD2	3.216
6PYD	H_LYS_213	NZ	L_GLU_127	OE1	3.352
6PYD	L_ARG_24	NH2	L_ASP_74	OD2	3.949
6PYD	L_ARG_65	NH1	L_GLU_83	OE2	3.750
6PYD	L_ARG_65	NH2	L_GLU_83	OE1	3.672
6PYD	L_ARG_65	NH2	L_GLU_85	OE1	3.120
6PYD	L_ARG_65	NH2	L_ASP_86	OD1	2.800
6PYD	L_ARG_65	NH2	L_ASP_86	OD2	3.601
6PYD	L_LYS_107	NZ	L_GLU_169	OE1	2.362
6PYD	L_HIS_193	ND1	L_ASP_155	OD2	3.270
6PYD	A_ARG_38	NH1	A_ASP_89	OD1	2.732
6PYD	A_ARG_38	NH2	A_GLU_46	OE1	2.704
6PYD	A_ARG_38	NH2	A_ASP_89	OD1	3.554
6PYD	A_ARG_66	NH1	A_ASP_89	OD1	3.626
6PYD	A_ARG_66	NH2	A_ASP_89	OD1	3.375
6PYD	A_ARG_66	NH2	A_ASP_89	OD2	2.645
6PYD	A_ARG_97	NH1	A_ASP_27	OD2	2.978
6PYD	A_ARG_97	NH2	A_ASP_105	OD1	3.618
6PYD	A_ARG_97	NH2	A_ASP_105	OD2	2.545
6PYD	A_LYS_147	NZ	A_ASP_148	OD1	3.105
6PYD	A_LYS_147	NZ	A_ASP_148	OD2	3.217
6PYD	A_LYS_213	NZ	B_GLU_127	OE1	3.596
6PYD	B_ARG_24	NH2	B_ASP_74	OD2	3.946
6PYD	B_ARG_65	NH1	B_GLU_83	OE2	3.749
6PYD	B_ARG_65	NH2	B_GLU_83	OE1	3.670
6PYD	B_ARG_65	NH2	B_GLU_85	OE1	3.121
6PYD	B_ARG_65	NH2	B_ASP_86	OD1	2.790
6PYD	B_ARG_65	NH2	B_ASP_86	OD2	3.597

6PYD	B_LYS_107	NZ	B_GLU_169	OE1	2.353
6PYD	B_LYS_192	NZ	B_ASP_189	OD1	3.073
6PZW	A_HIS_98	NE2	B_GLU_214	OE2	3.848
6PZW	A_ARG_118	NH2	A_GLU_425	OE1	3.722
6PZW	A_ARG_118	NH2	A_GLU_425	OE2	3.231
6PZW	A_ARG_130	NH1	A_GLU_128	OE2	2.902
6PZW	A_ARG_141	NH1	A_GLU_110	OE2	3.585
6PZW	A_ARG_156	NH2	A_GLU_119	OE2	2.799
6PZW	A_ARG_172	NH2	A_GLU_174	OE1	3.990
6PZW	A_ARG_172	NH2	A_GLU_174	OE2	3.068
6PZW	A_ARG_189	NH2	A_ASP_125	OD1	2.667
6PZW	A_ARG_224	NH2	A_GLU_276	OE2	3.019
6PZW	A_ARG_253	NH1	K_ASP_53	OD2	2.854
6PZW	A_ARG_253	NH2	A_ASP_251	OD1	3.916
6PZW	A_ARG_253	NH2	A_ASP_251	OD2	3.037
6PZW	A_ARG_253	NH2	K_ASP_53	OD2	2.999
6PZW	A_LYS_264	NZ	A_GLU_266	OE2	3.655
6PZW	A_LYS_273	NZ	A_ASP_339	OD1	2.481
6PZW	A_HIS_274	NE2	A_GLU_276	OE2	2.952
6PZW	A_ARG_292	NH2	A_GLU_276	OE1	2.826
6PZW	A_ARG_292	NH2	A_GLU_277	OE1	3.803
6PZW	A_ARG_292	NH2	A_GLU_277	OE2	3.606
6PZW	A_ARG_300	NH2	A_ASP_324	OD1	3.849
6PZW	A_HIS_312	ND1	A_GLU_266	OE1	2.834
6PZW	A_ARG_364	NH1	A_ASP_330	OD1	3.531
6PZW	A_ARG_364	NH1	A_ASP_330	OD2	3.075
6PZW	A_ARG_364	NH2	A_ASP_330	OD2	3.882
6PZW	A_ARG_364	NH2	A_GLU_375	OE2	3.232
6PZW	A_ARG_387	NH1	A_ASP_386	OD1	3.540
6PZW	A_ARG_387	NH1	A_ASP_386	OD2	2.586
6PZW	A_ARG_419	NH1	B_GLU_214	OE2	3.897
6PZW	A_ARG_428	NH1	A_ASP_460	OD2	2.906
6PZW	A_ARG_428	NH2	A_GLU_433	OE1	3.580
6PZW	A_ARG_428	NH2	A_GLU_433	OE2	3.020
6PZW	A_LYS_435	NZ	A_GLU_465	OE2	3.897
6PZW	L_ARG_61	NH1	L_ASP_82	OD1	3.701
6PZW	L_ARG_61	NH1	L_ASP_82	OD2	2.929
6PZW	L_ARG_61	NH2	L_ASP_82	OD1	2.966
6PZW	L_ARG_61	NH2	L_ASP_82	OD2	3.633
6PZW	L_LYS_103	NZ	L_ASP_85	OD1	2.829
6PZW	L_LYS_103	NZ	L_ASP_85	OD2	3.336
6PZW	K_HIS_35	NE2	K_ASP_95	OD2	2.981
6PZW	K_ARG_38	NH1	K_ASP_86	OD1	2.818
6PZW	K_ARG_38	NH2	K_GLU_46	OE1	3.500
6PZW	K_ARG_38	NH2	K_GLU_46	OE2	3.095
6PZW	K_ARG_38	NH2	K_ASP_86	OD1	3.867
6PZW	K_ARG_66	NH1	K_ASP_86	OD1	3.642
6PZW	K_ARG_66	NH1	K_ASP_86	OD2	2.868
6PZW	K_ARG_66	NH2	K_ASP_86	OD1	3.050
6PZW	K_ARG_66	NH2	K_ASP_86	OD2	3.680
6PZW	K_LYS_75	NZ	K_ASP_72	OD2	2.805
6PZW	K_LYS_94	NZ	K_ASP_101	OD2	2.905
6PZW	K_LYS_96	NZ	K_ASP_101	OD1	2.573
6PZW	K_LYS_96	NZ	K_ASP_101	OD2	3.869
6PZW	K_ARG_97	NH2	L_ASP_50	OD1	2.825
6PZW	K_ARG_97	NH2	L_ASP_50	OD2	3.390
6PZW	D_HIS_98	NE2	A_GLU_214	OE2	3.848
6PZW	D_ARG_118	NH2	D_GLU_425	OE1	3.722

6PZW	D_ARG.118	NH2	D_GLU_425	OE2	3.231
6PZW	D_ARG.130	NH1	D_GLU_128	OE2	2.902
6PZW	D_ARG.141	NH1	D_GLU_110	OE2	3.585
6PZW	D_ARG.156	NH2	D_GLU_119	OE2	2.799
6PZW	D_ARG.172	NH2	D_GLU_174	OE1	3.990
6PZW	D_ARG.172	NH2	D_GLU_174	OE2	3.068
6PZW	D_ARG.189	NH2	D_ASP_125	OD1	2.667
6PZW	D_ARG.224	NH2	D_GLU_276	OE2	3.019
6PZW	D_ARG.253	NH1	F_ASP_53	OD2	2.854
6PZW	D_ARG.253	NH2	D_ASP_251	OD1	3.916
6PZW	D_ARG.253	NH2	D_ASP_251	OD2	3.037
6PZW	D_ARG.253	NH2	F_ASP_53	OD2	2.999
6PZW	D_LYS_264	NZ	D_GLU_266	OE2	3.655
6PZW	D_LYS_273	NZ	D_ASP_339	OD1	2.481
6PZW	D_HIS_274	NE2	D_GLU_276	OE2	2.952
6PZW	D_ARG.292	NH2	D_GLU_276	OE1	2.826
6PZW	D_ARG.292	NH2	D_GLU_277	OE1	3.803
6PZW	D_ARG.292	NH2	D_GLU_277	OE2	3.606
6PZW	D_ARG.300	NH2	D_ASP_324	OD1	3.849
6PZW	D_HIS_312	ND1	D_GLU_266	OE1	2.834
6PZW	D_ARG.364	NH1	D_ASP_330	OD1	3.531
6PZW	D_ARG.364	NH1	D_ASP_330	OD2	3.075
6PZW	D_ARG.364	NH2	D_ASP_330	OD2	3.882
6PZW	D_ARG.364	NH2	D_GLU_375	OE2	3.232
6PZW	D_ARG.387	NH1	D_ASP_386	OD1	3.540
6PZW	D_ARG.387	NH1	D_ASP_386	OD2	2.586
6PZW	D_ARG.419	NH1	A_GLU_214	OE2	3.897
6PZW	D_ARG.428	NH1	D_ASP_460	OD2	2.906
6PZW	D_ARG.428	NH2	D_GLU_433	OE1	3.580
6PZW	D_ARG.428	NH2	D_GLU_433	OE2	3.020
6PZW	D_LYS_435	NZ	D_GLU_465	OE2	3.897
6PZW	E_ARG.61	NH1	E_ASP_82	OD1	3.701
6PZW	E_ARG.61	NH1	E_ASP_82	OD2	2.929
6PZW	E_ARG.61	NH2	E_ASP_82	OD1	2.966
6PZW	E_ARG.61	NH2	E_ASP_82	OD2	3.633
6PZW	E_LYS_103	NZ	E_ASP_85	OD1	2.829
6PZW	E_LYS_103	NZ	E_ASP_85	OD2	3.336
6PZW	F_HIS_35	NE2	F_ASP_95	OD2	2.981
6PZW	F_ARG.38	NH1	F_ASP_86	OD1	2.818
6PZW	F_ARG.38	NH2	F_GLU_46	OE1	3.500
6PZW	F_ARG.38	NH2	F_GLU_46	OE2	3.095
6PZW	F_ARG.38	NH2	F_ASP_86	OD1	3.867
6PZW	F_ARG.66	NH1	F_ASP_86	OD1	3.642
6PZW	F_ARG.66	NH1	F_ASP_86	OD2	2.868
6PZW	F_ARG.66	NH2	F_ASP_86	OD1	3.050
6PZW	F_ARG.66	NH2	F_ASP_86	OD2	3.680
6PZW	F_LYS_75	NZ	F_ASP_72	OD2	2.805
6PZW	F_LYS_94	NZ	F_ASP_101	OD2	2.905
6PZW	F_LYS_96	NZ	F_ASP_101	OD1	2.573
6PZW	F_LYS_96	NZ	F_ASP_101	OD2	3.869
6PZW	F_ARG.97	NH2	E_ASP_50	OD1	2.825
6PZW	F_ARG.97	NH2	E_ASP_50	OD2	3.390
6PZW	G_ARG.61	NH1	G_ASP_82	OD1	3.701
6PZW	G_ARG.61	NH1	G_ASP_82	OD2	2.929
6PZW	G_ARG.61	NH2	G_ASP_82	OD1	2.966
6PZW	G_ARG.61	NH2	G_ASP_82	OD2	3.633
6PZW	G_LYS_103	NZ	G_ASP_85	OD1	2.829
6PZW	G_LYS_103	NZ	G_ASP_85	OD2	3.336

6PZW	J_HIS_35	NE2	J_ASP_95	OD2	2.981
6PZW	J_ARG_38	NH1	J_ASP_86	OD1	2.818
6PZW	J_ARG_38	NH2	J_GLU_46	OE1	3.500
6PZW	J_ARG_38	NH2	J_GLU_46	OE2	3.095
6PZW	J_ARG_38	NH2	J_ASP_86	OD1	3.867
6PZW	J_ARG_66	NH1	J_ASP_86	OD1	3.642
6PZW	J_ARG_66	NH1	J_ASP_86	OD2	2.868
6PZW	J_ARG_66	NH2	J_ASP_86	OD1	3.050
6PZW	J_ARG_66	NH2	J_ASP_86	OD2	3.680
6PZW	J_LYS_75	NZ	J_ASP_72	OD2	2.805
6PZW	J_LYS_94	NZ	J_ASP_101	OD2	2.905
6PZW	J_LYS_96	NZ	J_ASP_101	OD1	2.573
6PZW	J_LYS_96	NZ	J_ASP_101	OD2	3.869
6PZW	J_ARG_97	NH2	G_ASP_50	OD1	2.825
6PZW	J_ARG_97	NH2	G_ASP_50	OD2	3.390
6PZW	C_HIS_98	NE2	D_GLU_214	OE2	3.848
6PZW	C_ARG_118	NH2	C_GLU_425	OE1	3.722
6PZW	C_ARG_118	NH2	C_GLU_425	OE2	3.231
6PZW	C_ARG_130	NH1	C_GLU_128	OE2	2.902
6PZW	C_ARG_141	NH1	C_GLU_110	OE2	3.585
6PZW	C_ARG_156	NH2	C_GLU_119	OE2	2.799
6PZW	C_ARG_172	NH2	C_GLU_174	OE1	3.990
6PZW	C_ARG_172	NH2	C_GLU_174	OE2	3.068
6PZW	C_ARG_189	NH2	C_ASP_125	OD1	2.667
6PZW	C_ARG_224	NH2	C_GLU_276	OE2	3.019
6PZW	C_ARG_253	NH1	J_ASP_53	OD2	2.854
6PZW	C_ARG_253	NH2	J_ASP_53	OD2	2.999
6PZW	C_ARG_253	NH2	C_ASP_251	OD1	3.916
6PZW	C_ARG_253	NH2	C_ASP_251	OD2	3.037
6PZW	C_LYS_264	NZ	C_GLU_266	OE2	3.655
6PZW	C_LYS_273	NZ	C_ASP_339	OD1	2.481
6PZW	C_HIS_274	NE2	C_GLU_276	OE2	2.952
6PZW	C_ARG_292	NH2	C_GLU_276	OE1	2.826
6PZW	C_ARG_292	NH2	C_GLU_277	OE1	3.803
6PZW	C_ARG_292	NH2	C_GLU_277	OE2	3.606
6PZW	C_ARG_300	NH2	C_ASP_324	OD1	3.849
6PZW	C_HIS_312	ND1	C_GLU_266	OE1	2.834
6PZW	C_ARG_364	NH1	C_ASP_330	OD1	3.531
6PZW	C_ARG_364	NH1	C_ASP_330	OD2	3.075
6PZW	C_ARG_364	NH2	C_ASP_330	OD2	3.882
6PZW	C_ARG_364	NH2	C_GLU_375	OE2	3.232
6PZW	C_ARG_387	NH1	C_ASP_386	OD1	3.540
6PZW	C_ARG_387	NH1	C_ASP_386	OD2	2.586
6PZW	C_ARG_419	NH1	D_GLU_214	OE2	3.897
6PZW	C_ARG_428	NH1	C_ASP_460	OD2	2.906
6PZW	C_ARG_428	NH2	C_GLU_433	OE1	3.580
6PZW	C_ARG_428	NH2	C_GLU_433	OE2	3.020
6PZW	C_LYS_435	NZ	C_GLU_465	OE2	3.897
6PZW	B_HIS_98	NE2	C_GLU_214	OE2	3.848
6PZW	B_ARG_118	NH2	B_GLU_425	OE1	3.722
6PZW	B_ARG_118	NH2	B_GLU_425	OE2	3.231
6PZW	B_ARG_130	NH1	B_GLU_128	OE2	2.902
6PZW	B_ARG_141	NH1	B_GLU_110	OE2	3.585
6PZW	B_ARG_156	NH2	B_GLU_119	OE2	2.799
6PZW	B_ARG_172	NH2	B_GLU_174	OE1	3.990
6PZW	B_ARG_172	NH2	B_GLU_174	OE2	3.068
6PZW	B_ARG_189	NH2	B_ASP_125	OD1	2.667
6PZW	B_ARG_224	NH2	B_GLU_276	OE2	3.019

6PZW	B_ARG_253	NH1	H_ASP_53	OD2	2.854
6PZW	B_ARG_253	NH2	B_ASP_251	OD1	3.916
6PZW	B_ARG_253	NH2	B_ASP_251	OD2	3.037
6PZW	B_ARG_253	NH2	H_ASP_53	OD2	2.999
6PZW	B_LYS_264	NZ	B_GLU_266	OE2	3.655
6PZW	B_LYS_273	NZ	B_ASP_339	OD1	2.481
6PZW	B_HIS_274	NE2	B_GLU_276	OE2	2.952
6PZW	B_ARG_292	NH2	B_GLU_276	OE1	2.826
6PZW	B_ARG_292	NH2	B_GLU_277	OE1	3.803
6PZW	B_ARG_292	NH2	B_GLU_277	OE2	3.606
6PZW	B_ARG_300	NH2	B_ASP_324	OD1	3.849
6PZW	B_HIS_312	ND1	B_GLU_266	OE1	2.834
6PZW	B_ARG_364	NH1	B_ASP_330	OD1	3.531
6PZW	B_ARG_364	NH1	B_ASP_330	OD2	3.075
6PZW	B_ARG_364	NH2	B_ASP_330	OD2	3.882
6PZW	B_ARG_364	NH2	B_GLU_375	OE2	3.232
6PZW	B_ARG_387	NH1	B_ASP_386	OD1	3.540
6PZW	B_ARG_387	NH1	B_ASP_386	OD2	2.586
6PZW	B_ARG_419	NH1	C_GLU_214	OE2	3.897
6PZW	B_ARG_428	NH1	B_ASP_460	OD2	2.906
6PZW	B_ARG_428	NH2	B_GLU_433	OE1	3.580
6PZW	B_ARG_428	NH2	B_GLU_433	OE2	3.020
6PZW	B_LYS_435	NZ	B_GLU_465	OE2	3.897
6PZW	L_ARG_61	NH1	L_ASP_82	OD1	3.701
6PZW	L_ARG_61	NH1	L_ASP_82	OD2	2.929
6PZW	L_ARG_61	NH2	L_ASP_82	OD1	2.966
6PZW	L_ARG_61	NH2	L_ASP_82	OD2	3.633
6PZW	L_LYS_103	NZ	L_ASP_85	OD1	2.829
6PZW	L_LYS_103	NZ	L_ASP_85	OD2	3.336
6PZW	H_HIS_35	NE2	H_ASP_95	OD2	2.981
6PZW	H_ARG_38	NH1	H_ASP_86	OD1	2.818
6PZW	H_ARG_38	NH2	H_GLU_46	OE1	3.500
6PZW	H_ARG_38	NH2	H_GLU_46	OE2	3.095
6PZW	H_ARG_38	NH2	H_ASP_86	OD1	3.867
6PZW	H_ARG_66	NH1	H_ASP_86	OD1	3.642
6PZW	H_ARG_66	NH1	H_ASP_86	OD2	2.868
6PZW	H_ARG_66	NH2	H_ASP_86	OD1	3.050
6PZW	H_ARG_66	NH2	H_ASP_86	OD2	3.680
6PZW	H_LYS_75	NZ	H_ASP_72	OD2	2.805
6PZW	H_LYS_94	NZ	H_ASP_101	OD2	2.905
6PZW	H_LYS_96	NZ	H_ASP_101	OD1	2.573
6PZW	H_LYS_96	NZ	H_ASP_101	OD2	3.869
6PZW	H_ARG_97	NH2	L_ASP_50	OD1	2.825
6PZW	H_ARG_97	NH2	L_ASP_50	OD2	3.390
6RPS	A_HIS_34	ND1	A_ASP_32	OD2	2.928
6RPS	A_HIS_34	NE2	A_ASP_36	OD1	3.392
6RPS	A_HIS_34	NE2	B_ASP_102	OD2	3.097
6RPS	A_HIS_64	NE2	H_ASP_54	OD2	2.837
6RPS	A_HIS_96	ND1	A_GLU_106	OE1	3.812
6RPS	A_HIS_96	ND1	A_GLU_106	OE2	3.696
6RPS	A_HIS_96	NE2	A_GLU_106	OE1	3.203
6RPS	A_HIS_103	ND1	A_ASP_102	OD1	3.719
6RPS	A_HIS_107	ND1	A_GLU_117	OE1	3.830
6RPS	A_HIS_107	ND1	A_GLU_117	OE2	2.892
6RPS	A_HIS_119	ND1	A_GLU_106	OE1	3.943
6RPS	A_HIS_119	NE2	A_GLU_117	OE2	2.681
6RPS	A_LYS_170	NZ	H_ASP_54	OD1	3.636
6RPS	A_LYS_170	NZ	H_ASP_54	OD2	2.590

6RPS	A_LYS_170	NZ	H_ASP_56	OD2	2.821
6RPS	A_ARG_213	NH1	A_GLU_190	OE1	3.317
6RPS	A_ARG_213	NH1	A_GLU_190	OE2	3.527
6RPS	A_HIS_234	ND1	H_ASP_56	OD2	3.904
6RPS	A_LYS_250	NZ	B_GLU_13	OE2	2.734
6RPS	B_HIS_34	ND1	B_ASP_32	OD2	2.934
6RPS	B_HIS_34	NE2	B_ASP_36	OD1	3.758
6RPS	B_HIS_34	NE2	B_ASP_36	OD2	3.233
6RPS	B_HIS_64	NE2	N_ASP_54	OD2	2.859
6RPS	B_HIS_96	ND1	B_GLU_106	OE1	3.814
6RPS	B_HIS_96	ND1	B_GLU_106	OE2	3.680
6RPS	B_HIS_96	NE2	B_GLU_106	OE1	3.214
6RPS	B_HIS_103	ND1	A_ASP_36	OD1	3.129
6RPS	B_HIS_103	ND1	A_ASP_36	OD2	3.954
6RPS	B_HIS_103	ND1	B_ASP_102	OD1	3.019
6RPS	B_HIS_107	ND1	B_GLU_117	OE1	3.839
6RPS	B_HIS_107	ND1	B_GLU_117	OE2	2.888
6RPS	B_HIS_119	ND1	B_GLU_106	OE1	3.928
6RPS	B_HIS_119	NE2	B_GLU_117	OE2	2.683
6RPS	B_LYS_170	NZ	N_ASP_54	OD1	3.719
6RPS	B_LYS_170	NZ	N_ASP_54	OD2	2.644
6RPS	B_LYS_170	NZ	N_ASP_56	OD2	2.839
6RPS	B_ARG_213	NH1	B_GLU_190	OE1	3.106
6RPS	B_ARG_213	NH1	B_GLU_190	OE2	3.685
6RPS	B_HIS_234	ND1	N_ASP_56	OD2	3.922
6RPS	B_LYS_250	NZ	A_GLU_13	OE2	2.991
6RPS	M_ARG_24	NH1	M_ASP_70	OD2	3.891
6RPS	M_ARG_61	NH1	M_GLU_79	OE1	3.422
6RPS	M_ARG_61	NH1	M_GLU_79	OE2	3.489
6RPS	M_ARG_61	NH2	M_GLU_79	OE1	3.623
6RPS	M_ARG_61	NH2	M_GLU_81	OE1	3.600
6RPS	M_ARG_61	NH2	M_ASP_82	OD1	2.623
6RPS	M_ARG_61	NH2	M_ASP_82	OD2	3.076
6RPS	M_LYS_149	NZ	M_GLU_195	OE1	3.183
6RPS	M_LYS_149	NZ	M_GLU_195	OE2	3.364
6RPS	N_ARG_38	NH1	N_GLU_86	OE2	2.950
6RPS	N_ARG_38	NH2	N_GLU_46	OE1	3.142
6RPS	N_ARG_38	NH2	N_GLU_46	OE2	3.953
6RPS	N_ARG_38	NH2	N_GLU_86	OE2	3.241
6RPS	N_ARG_50	NH2	N_ASP_95	OD2	3.876
6RPS	N_ARG_66	NH1	N_GLU_86	OE2	3.240
6RPS	N_ARG_66	NH2	N_GLU_86	OE1	2.816
6RPS	N_ARG_66	NH2	N_GLU_86	OE2	2.704
6RPS	N_ARG_94	NH2	N_ASP_101	OD2	3.208
6RPS	N_LYS_143	NZ	N_ASP_144	OD1	3.314
6RPS	N_LYS_143	NZ	N_ASP_144	OD2	3.375
6RPS	N_LYS_210	NZ	N_GLU_212	OE1	3.241
6RPS	N_LYS_214	NZ	M_ASP_122	OD1	3.095
6RPS	N_LYS_214	NZ	M_ASP_122	OD2	3.107
6RPS	L_ARG_24	NH1	L_ASP_70	OD2	3.896
6RPS	L_LYS_39	NZ	L_GLU_81	OE2	3.206
6RPS	L_ARG_45	NH2	L_GLU_81	OE2	3.948
6RPS	L_ARG_61	NH1	L_GLU_79	OE1	3.428
6RPS	L_ARG_61	NH1	L_GLU_79	OE2	3.496
6RPS	L_ARG_61	NH2	L_GLU_79	OE1	3.620
6RPS	L_ARG_61	NH2	L_ASP_82	OD1	2.624
6RPS	L_ARG_61	NH2	L_ASP_82	OD2	3.082
6RPS	L_LYS_149	NZ	L_GLU_195	OE1	3.146

6RPS	L_LYS_149	NZ	L_GLU_195	OE2	3.433
6RPS	H_ARG_38	NH1	H_GLU_86	OE2	2.972
6RPS	H_ARG_38	NH2	H_GLU_46	OE1	3.141
6RPS	H_ARG_38	NH2	H_GLU_46	OE2	3.931
6RPS	H_ARG_38	NH2	H_GLU_86	OE2	3.242
6RPS	H_ARG_50	NH2	H_ASP_95	OD2	3.877
6RPS	H_ARG_66	NH1	H_GLU_86	OE2	3.250
6RPS	H_ARG_66	NH2	H_GLU_86	OE1	2.806
6RPS	H_ARG_66	NH2	H_GLU_86	OE2	2.709
6RPS	H_ARG_94	NH2	H_ASP_101	OD2	3.183
6RPS	H_LYS_143	NZ	H_ASP_144	OD1	3.311
6RPS	H_LYS_143	NZ	H_ASP_144	OD2	3.365
6RPS	H_LYS_209	NZ	L_GLU_123	OE1	2.780
6RPS	H_LYS_209	NZ	L_GLU_123	OE2	3.710
6RPS	H_LYS_210	NZ	H_GLU_212	OE1	3.232
6S3T	A_HIS_48	ND1	A_ASP_79	OD1	3.030
6S3T	A_LYS_49	NZ	C_GLU_158	OE1	3.663
6S3T	A_ARG_66	NH1	A_ASP_140	OD2	3.290
6S3T	A_ARG_66	NH2	A_ASP_140	OD1	3.561
6S3T	A_ARG_66	NH2	A_ASP_343	OD1	2.921
6S3T	A_ARG_66	NH2	A_ASP_343	OD2	3.772
6S3T	A_LYS_90	NZ	A_ASP_63	OD1	3.963
6S3T	A_LYS_90	NZ	A_ASP_63	OD2	2.710
6S3T	A_LYS_110	NZ	A_GLU_82	OE1	3.367
6S3T	A_LYS_110	NZ	A_GLU_82	OE2	3.373
6S3T	A_ARG_141	NH1	A_ASP_210	OD1	3.859
6S3T	A_ARG_141	NH1	A_ASP_210	OD2	3.679
6S3T	A_ARG_141	NH2	A_ASP_61	OD1	2.655
6S3T	A_ARG_141	NH2	A_ASP_61	OD2	3.839
6S3T	A_LYS_148	NZ	A_ASP_131	OD1	3.035
6S3T	A_LYS_222	NZ	A_GLU_158	OE2	3.425
6S3T	A_LYS_222	NZ	A_GLU_162	OE2	3.965
6S3T	A_LYS_268	NZ	A_GLU_308	OE1	3.868
6S3T	A_LYS_306	NZ	A_ASP_334	OD1	3.070
6S3T	A_LYS_306	NZ	A_ASP_334	OD2	3.336
6S3T	A_LYS_327	NZ	A_ASP_324	OD1	3.861
6S3T	A_LYS_341	NZ	A_ASP_140	OD1	3.192
6S3T	A_ARG_355	NH1	A_GLU_82	OE1	3.960
6S3T	A_ARG_355	NH1	A_GLU_82	OE2	3.091
6S3T	A_ARG_366	NH1	A_ASP_150	OD2	3.723
6S3T	A_ARG_366	NH2	A_ASP_150	OD2	3.506
6S3T	A_LYS_383	NZ	A_ASP_156	OD2	3.389
6S3T	B_HIS_48	ND1	B_ASP_79	OD1	3.029
6S3T	B_LYS_49	NZ	L_GLU_158	OE1	3.761
6S3T	B_ARG_66	NH1	B_ASP_140	OD2	3.289
6S3T	B_ARG_66	NH2	B_ASP_140	OD1	3.563
6S3T	B_ARG_66	NH2	B_ASP_343	OD1	2.924
6S3T	B_ARG_66	NH2	B_ASP_343	OD2	3.774
6S3T	B_LYS_90	NZ	B_ASP_63	OD1	3.964
6S3T	B_LYS_90	NZ	B_ASP_63	OD2	2.710
6S3T	B_LYS_110	NZ	B_GLU_82	OE1	3.367
6S3T	B_LYS_110	NZ	B_GLU_82	OE2	3.374
6S3T	B_ARG_141	NH1	B_ASP_210	OD1	3.858
6S3T	B_ARG_141	NH1	B_ASP_210	OD2	3.682
6S3T	B_ARG_141	NH2	B_ASP_61	OD1	2.654
6S3T	B_ARG_141	NH2	B_ASP_61	OD2	3.837
6S3T	B_LYS_148	NZ	B_ASP_131	OD1	3.032
6S3T	B_LYS_175	NZ	B_ASP_177	OD2	3.891

6S3T	B.LYS_222	NZ	B.GLU_158	OE2	3.419
6S3T	B.LYS_222	NZ	B.GLU_162	OE2	3.964
6S3T	B.LYS_282	NZ	B.GLU_241	OE2	3.757
6S3T	B.LYS_306	NZ	B.ASP_334	OD1	3.070
6S3T	B.LYS_306	NZ	B.ASP_334	OD2	3.338
6S3T	B.LYS_327	NZ	B.ASP_324	OD1	3.858
6S3T	B.LYS_341	NZ	B.ASP_140	OD1	3.192
6S3T	B.ARG_355	NH1	B.GLU_352	OE1	2.881
6S3T	B.ARG_366	NH2	B.ASP_150	OD2	3.496
6S3T	B.LYS_383	NZ	B.ASP_156	OD2	3.383
6S3T	C.ARG_24	NH2	C.ASP_74	OD1	3.093
6S3T	C.ARG_24	NH2	C.ASP_74	OD2	3.742
6S3T	C.ARG_65	NH1	C.ASP_86	OD1	3.788
6S3T	C.ARG_65	NH1	C.ASP_86	OD2	2.683
6S3T	C.ARG_65	NH2	C.GLU_83	OE1	3.619
6S3T	C.ARG_65	NH2	C.ASP_86	OD1	3.107
6S3T	C.ARG_65	NH2	C.ASP_86	OD2	3.458
6S3T	C.LYS_151	NZ	C.GLU_158	OE2	3.956
6S3T	C.LYS_153	NZ	C.GLU_199	OE2	2.738
6S3T	D.ARG_35	NH1	S.ASP_332	OD1	3.467
6S3T	D.ARG_35	NH1	S.ASP_332	OD2	2.946
6S3T	D.ARG_35	NH2	S.ASP_332	OD2	3.071
6S3T	D.ARG_35	NH2	S.ASP_334	OD1	3.408
6S3T	D.ARG_40	NH1	D.GLU_48	OE1	3.019
6S3T	D.ARG_40	NH2	D.ASP_91	OD2	3.639
6S3T	D.ARG_68	NH1	D.ASP_91	OD1	3.381
6S3T	D.ARG_68	NH1	D.ASP_91	OD2	3.003
6S3T	D.ARG_68	NH2	D.ASP_91	OD1	3.560
6S3T	D.ARG_73	NH2	D.ASP_57	OD2	3.930
6S3T	D.HIS_171	NE2	C.ASP_171	OD2	3.832
6S3T	D.LYS_215	NZ	C.GLU_127	OE1	2.814
6S3T	D.LYS_215	NZ	C.GLU_127	OE2	3.990
6S3T	D.LYS_216	NZ	D.GLU_218	OE2	3.949
6S3T	I.ARG_24	NH2	I.ASP_74	OD1	3.090
6S3T	I.ARG_24	NH2	I.ASP_74	OD2	3.744
6S3T	I.ARG_65	NH1	I.GLU_83	OE1	3.576
6S3T	I.ARG_65	NH1	I.ASP_86	OD1	3.791
6S3T	I.ARG_65	NH1	I.ASP_86	OD2	2.684
6S3T	I.ARG_65	NH2	I.ASP_86	OD1	3.110
6S3T	I.ARG_65	NH2	I.ASP_86	OD2	3.459
6S3T	I.LYS_107	NZ	I.GLU_109	OE2	3.962
6S3T	I.LYS_151	NZ	I.GLU_158	OE1	3.422
6S3T	I.LYS_153	NZ	I.GLU_199	OE2	2.741
6S3T	E.ARG_35	NH1	T.ASP_332	OD1	3.561
6S3T	E.ARG_35	NH1	T.ASP_332	OD2	3.035
6S3T	E.ARG_35	NH2	T.ASP_332	OD2	3.163
6S3T	E.ARG_35	NH2	T.ASP_334	OD1	3.432
6S3T	E.ARG_40	NH1	E.ASP_91	OD1	3.668
6S3T	E.ARG_40	NH1	E.ASP_91	OD2	3.638
6S3T	E.ARG_40	NH2	E.GLU_48	OE1	2.851
6S3T	E.ARG_68	NH1	E.ASP_91	OD1	3.381
6S3T	E.ARG_68	NH1	E.ASP_91	OD2	3.005
6S3T	E.ARG_68	NH2	E.ASP_91	OD1	3.559
6S3T	E.ARG_73	NH2	E.ASP_57	OD2	3.938
6S3T	E.HIS_171	NE2	I.ASP_171	OD2	3.931
6S3T	E.LYS_215	NZ	I.GLU_127	OE1	3.013
6S3T	E.LYS_216	NZ	E.GLU_218	OE2	3.946
6S3T	M.ARG_24	NH2	M.ASP_74	OD1	3.084

6S3T	M_ARG_24	NH2	M_ASP_74	OD2	3.751
6S3T	M_ARG_65	NH1	M_GLU_83	OE1	3.576
6S3T	M_ARG_65	NH1	M_ASP_86	OD1	3.781
6S3T	M_ARG_65	NH1	M_ASP_86	OD2	2.680
6S3T	M_ARG_65	NH2	M_ASP_86	OD1	3.107
6S3T	M_ARG_65	NH2	M_ASP_86	OD2	3.455
6S3T	M_LYS_151	NZ	M_GLU_158	OE2	3.920
6S3T	M_LYS_153	NZ	M_GLU_199	OE1	3.748
6S3T	M_LYS_153	NZ	M_GLU_199	OE2	2.775
6S3T	N_ARG_35	NH1	A_ASP_332	OD1	3.796
6S3T	N_ARG_35	NH1	A_ASP_332	OD2	3.195
6S3T	N_ARG_35	NH2	A_ASP_332	OD1	3.883
6S3T	N_ARG_35	NH2	A_ASP_332	OD2	2.517
6S3T	N_ARG_35	NH2	A_ASP_334	OD2	3.989
6S3T	N_ARG_40	NH1	N_GLU_48	OE1	3.017
6S3T	N_ARG_40	NH2	N_ASP_91	OD2	3.633
6S3T	N_ARG_68	NH1	N_ASP_91	OD1	3.379
6S3T	N_ARG_68	NH1	N_ASP_91	OD2	3.002
6S3T	N_ARG_68	NH2	N_ASP_91	OD1	3.568
6S3T	N_ARG_73	NH2	S_GLU_44	OE2	2.482
6S3T	N_HIS_171	NE2	M_ASP_171	OD2	3.181
6S3T	N_LYS_215	NZ	M_GLU_127	OE1	2.964
6S3T	N_LYS_215	NZ	M_GLU_127	OE2	3.944
6S3T	N_LYS_216	NZ	N_GLU_218	OE2	3.948
6S3T	Q_ARG_24	NH2	Q_ASP_74	OD1	3.083
6S3T	Q_ARG_24	NH2	Q_ASP_74	OD2	3.750
6S3T	Q_ARG_65	NH1	Q_GLU_83	OE1	3.574
6S3T	Q_ARG_65	NH1	Q_ASP_86	OD1	3.785
6S3T	Q_ARG_65	NH1	Q_ASP_86	OD2	2.681
6S3T	Q_ARG_65	NH2	Q_ASP_86	OD1	3.108
6S3T	Q_ARG_65	NH2	Q_ASP_86	OD2	3.458
6S3T	Q_LYS_151	NZ	Q_GLU_199	OE1	2.666
6S3T	Q_LYS_151	NZ	Q_GLU_199	OE2	3.849
6S3T	Q_LYS_153	NZ	Q_GLU_199	OE2	2.742
6S3T	R_ARG_35	NH1	B_ASP_332	OD1	3.511
6S3T	R_ARG_35	NH1	B_ASP_332	OD2	2.943
6S3T	R_ARG_35	NH2	B_ASP_332	OD2	2.873
6S3T	R_ARG_35	NH2	B_ASP_334	OD1	3.424
6S3T	R_ARG_40	NH1	R_GLU_48	OE1	3.017
6S3T	R_ARG_40	NH2	R_ASP_91	OD2	3.634
6S3T	R_ARG_68	NH1	R_ASP_91	OD1	3.379
6S3T	R_ARG_68	NH1	R_ASP_91	OD2	3.002
6S3T	R_ARG_68	NH2	R_ASP_91	OD1	3.566
6S3T	R_ARG_73	NH2	T_GLU_44	OE2	2.709
6S3T	R_HIS_171	NE2	Q_ASP_171	OD2	3.265
6S3T	R_LYS_215	NZ	Q_GLU_127	OE1	2.948
6S3T	R_LYS_215	NZ	Q_GLU_127	OE2	3.831
6S3T	R_LYS_216	NZ	R_GLU_218	OE2	3.945
6S3T	S_HIS_48	ND1	S_ASP_79	OD1	3.027
6S3T	S_ARG_66	NH1	S_ASP_140	OD2	3.289
6S3T	S_ARG_66	NH2	S_ASP_140	OD1	3.557
6S3T	S_ARG_66	NH2	S_ASP_343	OD1	2.918
6S3T	S_ARG_66	NH2	S_ASP_343	OD2	3.764
6S3T	S_LYS_90	NZ	S_ASP_63	OD1	3.967
6S3T	S_LYS_90	NZ	S_ASP_63	OD2	2.710
6S3T	S_LYS_110	NZ	S_GLU_82	OE2	3.372
6S3T	S_ARG_141	NH1	S_ASP_210	OD1	3.860
6S3T	S_ARG_141	NH1	S_ASP_210	OD2	3.676

6S3T	S_ARG_141	NH2	S_ASP_61	OD1	2.655
6S3T	S_ARG_141	NH2	S_ASP_61	OD2	3.848
6S3T	S_LYS_148	NZ	S_ASP_131	OD1	3.009
6S3T	S_LYS_175	NZ	S_ASP_177	OD2	3.891
6S3T	S_LYS_306	NZ	S_ASP_334	OD1	3.069
6S3T	S_LYS_306	NZ	S_ASP_334	OD2	3.337
6S3T	S_LYS_327	NZ	S_ASP_324	OD1	3.856
6S3T	S_LYS_341	NZ	S_ASP_140	OD1	3.205
6S3T	S_LYS_383	NZ	S_ASP_156	OD2	3.396
6S3T	T_HIS_48	ND1	T_ASP_79	OD1	3.029
6S3T	T_ARG_66	NH1	T_ASP_140	OD2	3.288
6S3T	T_ARG_66	NH2	T_ASP_140	OD1	3.559
6S3T	T_ARG_66	NH2	T_ASP_343	OD1	2.920
6S3T	T_ARG_66	NH2	T_ASP_343	OD2	3.765
6S3T	T_LYS_90	NZ	T_ASP_63	OD1	3.971
6S3T	T_LYS_90	NZ	T_ASP_63	OD2	2.711
6S3T	T_LYS_110	NZ	T_GLU_82	OE1	3.369
6S3T	T_LYS_110	NZ	T_GLU_82	OE2	3.374
6S3T	T_ARG_141	NH1	T_ASP_210	OD1	3.860
6S3T	T_ARG_141	NH1	T_ASP_210	OD2	3.680
6S3T	T_ARG_141	NH2	T_ASP_61	OD1	2.654
6S3T	T_ARG_141	NH2	T_ASP_61	OD2	3.845
6S3T	T_LYS_148	NZ	T_ASP_131	OD1	3.022
6S3T	T_LYS_175	NZ	T_ASP_177	OD1	2.862
6S3T	T_LYS_306	NZ	T_ASP_334	OD1	3.070
6S3T	T_LYS_306	NZ	T_ASP_334	OD2	3.338
6S3T	T_LYS_327	NZ	T_ASP_324	OD1	3.858
6S3T	T_LYS_341	NZ	T_ASP_140	OD1	3.202
6S3T	T_ARG_355	NH1	T_GLU_82	OE1	3.957
6S3T	T_ARG_355	NH1	T_GLU_82	OE2	3.099
6S3T	T_ARG_366	NH1	T_GLU_370	OE2	3.935
6S3T	T_LYS_383	NZ	T_ASP_156	OD2	3.383
6U02	A_HIS_98	NE2	B_GLU_214	OE2	3.838
6U02	A_ARG_118	NH2	A_GLU_425	OE1	3.303
6U02	A_ARG_118	NH2	A_GLU_425	OE2	3.788
6U02	A_ARG_130	NH1	A_GLU_128	OE1	3.104
6U02	A_ARG_156	NH2	A_GLU_119	OE1	3.056
6U02	A_ARG_172	NH2	A_GLU_174	OE2	3.004
6U02	A_ARG_189	NH2	A_ASP_125	OD1	2.704
6U02	A_ARG_209	NH1	J_GLU_128	OE2	3.226
6U02	A_ARG_210	NH2	J_ASP_412	OD1	3.355
6U02	A_ARG_210	NH2	J_ASP_412	OD2	3.535
6U02	A_ARG_224	NH2	A_GLU_276	OE2	2.857
6U02	A_ARG_253	NH2	A_ASP_251	OD1	3.915
6U02	A_ARG_253	NH2	A_ASP_251	OD2	3.078
6U02	A_LYS_264	NZ	A_GLU_266	OE2	3.592
6U02	A_ARG_292	NH1	A_GLU_276	OE1	3.981
6U02	A_ARG_292	NH2	A_GLU_276	OE1	3.522
6U02	A_ARG_292	NH2	A_GLU_277	OE1	3.270
6U02	A_ARG_292	NH2	A_GLU_277	OE2	3.103
6U02	A_ARG_300	NH2	A_ASP_324	OD1	3.840
6U02	A_HIS_312	ND1	A_GLU_266	OE1	2.873
6U02	A_ARG_364	NH1	A_ASP_330	OD1	3.366
6U02	A_ARG_364	NH1	A_ASP_330	OD2	3.020
6U02	A_ARG_364	NH2	A_ASP_330	OD2	3.213
6U02	A_ARG_364	NH2	A_GLU_375	OE2	3.763
6U02	A_ARG_419	NH1	B_GLU_214	OE2	3.906
6U02	A_ARG_428	NH1	A_ASP_460	OD2	2.812

6U02	A_ARG_428	NH2	A_GLU_433	OE1	3.662
6U02	A_ARG_428	NH2	A_GLU_433	OE2	3.046
6U02	L_ARG_24	NH2	L_ASP_70	OD1	2.974
6U02	L_ARG_61	NH2	L_GLU_81	OE1	3.909
6U02	L_ARG_61	NH2	L_ASP_82	OD1	2.859
6U02	L_ARG_61	NH2	L_ASP_82	OD2	3.591
6U02	L_LYS_103	NZ	L_GLU_105	OE2	3.418
6U02	H_ARG_38	NH1	H_ASP_86	OD1	2.942
6U02	H_ARG_38	NH2	H_ASP_86	OD1	3.941
6U02	H_LYS_52	NZ	H_GLU_56	OE2	2.823
6U02	H_LYS_64	NZ	H_ASP_61	OD1	2.817
6U02	H_ARG_66	NH1	H_ASP_86	OD1	3.307
6U02	H_ARG_66	NH1	H_ASP_86	OD2	3.771
6U02	H_ARG_66	NH2	H_ASP_86	OD1	3.561
6U02	H_ARG_66	NH2	H_ASP_86	OD2	2.624
6U02	B_HIS_98	NE2	E_GLU_214	OE2	3.839
6U02	B_ARG_118	NH2	B_GLU_425	OE1	3.304
6U02	B_ARG_118	NH2	B_GLU_425	OE2	3.788
6U02	B_ARG_130	NH1	B_GLU_128	OE1	3.105
6U02	B_ARG_156	NH2	B_GLU_119	OE1	3.056
6U02	B_ARG_172	NH2	B_GLU_174	OE2	3.004
6U02	B_ARG_189	NH2	B_ASP_125	OD1	2.703
6U02	B_ARG_209	NH1	A_GLU_128	OE2	3.226
6U02	B_ARG_210	NH2	A_ASP_412	OD1	3.355
6U02	B_ARG_210	NH2	A_ASP_412	OD2	3.535
6U02	B_ARG_224	NH2	B_GLU_276	OE2	2.857
6U02	B_ARG_253	NH2	B_ASP_251	OD1	3.915
6U02	B_ARG_253	NH2	B_ASP_251	OD2	3.077
6U02	B_LYS_264	NZ	B_GLU_266	OE2	3.593
6U02	B_ARG_292	NH1	B_GLU_276	OE1	3.982
6U02	B_ARG_292	NH2	B_GLU_276	OE1	3.522
6U02	B_ARG_292	NH2	B_GLU_277	OE1	3.270
6U02	B_ARG_292	NH2	B_GLU_277	OE2	3.103
6U02	B_ARG_300	NH2	B_ASP_324	OD1	3.839
6U02	B_HIS_312	ND1	B_GLU_266	OE1	2.872
6U02	B_ARG_364	NH1	B_ASP_330	OD1	3.367
6U02	B_ARG_364	NH1	B_ASP_330	OD2	3.022
6U02	B_ARG_364	NH2	B_ASP_330	OD2	3.214
6U02	B_ARG_364	NH2	B_GLU_375	OE2	3.764
6U02	B_ARG_419	NH1	E_GLU_214	OE2	3.906
6U02	B_ARG_428	NH1	B_ASP_460	OD2	2.812
6U02	B_ARG_428	NH2	B_GLU_433	OE1	3.662
6U02	B_ARG_428	NH2	B_GLU_433	OE2	3.045
6U02	C_ARG_24	NH2	C_ASP_70	OD1	2.974
6U02	C_ARG_61	NH2	C_GLU_81	OE1	3.909
6U02	C_ARG_61	NH2	C_ASP_82	OD1	2.859
6U02	C_ARG_61	NH2	C_ASP_82	OD2	3.591
6U02	C_LYS_103	NZ	C_GLU_105	OE2	3.418
6U02	D_ARG_38	NH1	D_ASP_86	OD1	2.941
6U02	D_ARG_38	NH2	D_ASP_86	OD1	3.942
6U02	D_LYS_52	NZ	D_GLU_56	OE2	2.822
6U02	D_LYS_64	NZ	D_ASP_61	OD1	2.818
6U02	D_ARG_66	NH1	D_ASP_86	OD1	3.308
6U02	D_ARG_66	NH1	D_ASP_86	OD2	3.771
6U02	D_ARG_66	NH2	D_ASP_86	OD1	3.562
6U02	D_ARG_66	NH2	D_ASP_86	OD2	2.624
6U02	E_HIS_98	NE2	J_GLU_214	OE2	3.838
6U02	E_ARG_118	NH2	E_GLU_425	OE1	3.304

6U02	E_ARG_118	NH2	E_GLU_425	OE2	3.789
6U02	E_ARG_130	NH1	E_GLU_128	OE1	3.104
6U02	E_ARG_156	NH2	E_GLU_119	OE1	3.056
6U02	E_ARG_172	NH2	E_GLU_174	OE2	3.004
6U02	E_ARG_189	NH2	E_ASP_125	OD1	2.704
6U02	E_ARG_209	NH1	B_GLU_128	OE2	3.226
6U02	E_ARG_210	NH2	B_ASP_412	OD1	3.355
6U02	E_ARG_210	NH2	B_ASP_412	OD2	3.536
6U02	E_ARG_224	NH2	E_GLU_276	OE2	2.858
6U02	E_ARG_253	NH2	E_ASP_251	OD1	3.916
6U02	E_ARG_253	NH2	E_ASP_251	OD2	3.078
6U02	E_LYS_264	NZ	E_GLU_266	OE2	3.592
6U02	E_ARG_292	NH1	E_GLU_276	OE1	3.982
6U02	E_ARG_292	NH2	E_GLU_276	OE1	3.522
6U02	E_ARG_292	NH2	E_GLU_277	OE1	3.270
6U02	E_ARG_292	NH2	E_GLU_277	OE2	3.103
6U02	E_ARG_300	NH2	E_ASP_324	OD1	3.839
6U02	E_HIS_312	ND1	E_GLU_266	OE1	2.873
6U02	E_ARG_364	NH1	E_ASP_330	OD1	3.366
6U02	E_ARG_364	NH1	E_ASP_330	OD2	3.021
6U02	E_ARG_364	NH2	E_ASP_330	OD2	3.214
6U02	E_ARG_364	NH2	E_GLU_375	OE2	3.764
6U02	E_ARG_419	NH1	J_GLU_214	OE2	3.906
6U02	E_ARG_428	NH1	E_ASP_460	OD2	2.812
6U02	E_ARG_428	NH2	E_GLU_433	OE1	3.663
6U02	E_ARG_428	NH2	E_GLU_433	OE2	3.046
6U02	F_ARG_24	NH2	F_ASP_70	OD1	2.973
6U02	F_ARG_61	NH2	F_GLU_81	OE1	3.909
6U02	F_ARG_61	NH2	F_ASP_82	OD1	2.860
6U02	F_ARG_61	NH2	F_ASP_82	OD2	3.591
6U02	F_LYS_103	NZ	F_GLU_105	OE2	3.417
6U02	G_ARG_38	NH1	G_ASP_86	OD1	2.942
6U02	G_ARG_38	NH2	G_ASP_86	OD1	3.942
6U02	G_LYS_52	NZ	G_GLU_56	OE2	2.823
6U02	G_LYS_64	NZ	G_ASP_61	OD1	2.819
6U02	G_ARG_66	NH1	G_ASP_86	OD1	3.308
6U02	G_ARG_66	NH1	G_ASP_86	OD2	3.771
6U02	G_ARG_66	NH2	G_ASP_86	OD1	3.561
6U02	G_ARG_66	NH2	G_ASP_86	OD2	2.624
6U02	J_HIS_98	NE2	A_GLU_214	OE2	3.838
6U02	J_ARG_118	NH2	J_GLU_425	OE1	3.304
6U02	J_ARG_118	NH2	J_GLU_425	OE2	3.788
6U02	J_ARG_130	NH1	J_GLU_128	OE1	3.104
6U02	J_ARG_156	NH2	J_GLU_119	OE1	3.055
6U02	J_ARG_172	NH2	J_GLU_174	OE2	3.005
6U02	J_ARG_189	NH2	J_ASP_125	OD1	2.704
6U02	J_ARG_209	NH1	E_GLU_128	OE2	3.226
6U02	J_ARG_210	NH2	E_ASP_412	OD1	3.356
6U02	J_ARG_210	NH2	E_ASP_412	OD2	3.535
6U02	J_ARG_224	NH2	J_GLU_276	OE2	2.857
6U02	J_ARG_253	NH2	J_ASP_251	OD1	3.916
6U02	J_ARG_253	NH2	J_ASP_251	OD2	3.078
6U02	J_LYS_264	NZ	J_GLU_266	OE2	3.593
6U02	J_ARG_292	NH1	J_GLU_276	OE1	3.982
6U02	J_ARG_292	NH2	J_GLU_276	OE1	3.522
6U02	J_ARG_292	NH2	J_GLU_277	OE1	3.270
6U02	J_ARG_292	NH2	J_GLU_277	OE2	3.103
6U02	J_ARG_300	NH2	J_ASP_324	OD1	3.839

6U02	J_HIS_312	ND1	J_GLU_266	OE1	2.872
6U02	J_ARG_364	NH1	J_ASP_330	OD1	3.366
6U02	J_ARG_364	NH1	J_ASP_330	OD2	3.021
6U02	J_ARG_364	NH2	J_ASP_330	OD2	3.215
6U02	J_ARG_364	NH2	J_GLU_375	OE2	3.763
6U02	J_ARG_419	NH1	A_GLU_214	OE2	3.906
6U02	J_ARG_428	NH1	J_ASP_460	OD2	2.812
6U02	J_ARG_428	NH2	J_GLU_433	OE1	3.663
6U02	J_ARG_428	NH2	J_GLU_433	OE2	3.047
6U02	L_ARG_24	NH2	L_ASP_70	OD1	2.974
6U02	L_ARG_61	NH2	L_GLU_81	OE1	3.910
6U02	L_ARG_61	NH2	L_ASP_82	OD1	2.860
6U02	L_ARG_61	NH2	L_ASP_82	OD2	3.591
6U02	L_LYS_103	NZ	L_GLU_105	OE2	3.418
6U02	K_ARG_38	NH1	K_ASP_86	OD1	2.942
6U02	K_ARG_38	NH2	K_ASP_86	OD1	3.942
6U02	K_LYS_52	NZ	K_GLU_56	OE2	2.823
6U02	K_LYS_64	NZ	K_ASP_61	OD1	2.819
6U02	K_ARG_66	NH1	K_ASP_86	OD1	3.307
6U02	K_ARG_66	NH1	K_ASP_86	OD2	3.771
6U02	K_ARG_66	NH2	K_ASP_86	OD1	3.561
6U02	K_ARG_66	NH2	K_ASP_86	OD2	2.624
6U1T	H_ARG_38	NH1	H_ASP_90	OD1	2.918
6U1T	H_ARG_38	NH2	H_GLU_46	OE1	3.164
6U1T	H_ARG_38	NH2	H_ASP_90	OD1	3.940
6U1T	H_ARG_67	NH1	H_ASP_90	OD1	3.821
6U1T	H_ARG_67	NH1	H_ASP_90	OD2	2.731
6U1T	H_ARG_67	NH2	H_ASP_90	OD1	3.017
6U1T	H_ARG_67	NH2	H_ASP_90	OD2	3.451
6U1T	L_ARG_61	NH2	L_ASP_82	OD1	2.857
6U1T	L_ARG_61	NH2	L_ASP_82	OD2	3.548
6U1T	L_LYS_142	NZ	L_GLU_105	OE1	3.135
6U1T	L_LYS_149	NZ	L_GLU_195	OE1	3.622
6U1T	L_LYS_149	NZ	L_GLU_195	OE2	2.931
6U1T	L_ARG_155	NH1	L_GLU_185	OE1	3.214
6U1T	L_ARG_155	NH1	L_GLU_185	OE2	3.203
6U1T	L_ARG_155	NH2	L_GLU_185	OE1	3.040
6U1T	L_HIS_189	ND1	L_ASP_151	OD2	3.058
6U1T	L_LYS_199	NZ	L_ASP_110	OD2	3.885
6U59	A_LYS_34	NZ	B_ASP_612	OD1	2.489
6U59	A_LYS_46	NZ	A_GLU_492	OE1	2.715
6U59	A_LYS_170	NZ	A_GLU_172	OE2	3.768
6U59	A_LYS_227	NZ	A_GLU_83	OE1	3.011
6U59	A_LYS_227	NZ	A_GLU_83	OE2	3.430
6U59	A_LYS_231	NZ	A_GLU_268	OE2	2.869
6U59	A_HIS_249	NE2	A_GLU_482	OE2	2.821
6U59	A_LYS_282	NZ	A_ASP_279	OD2	2.817
6U59	A_ARG_298	NH1	A_GLU_381	OE2	3.452
6U59	A_ARG_298	NH2	A_GLU_381	OE1	3.785
6U59	A_ARG_298	NH2	A_GLU_381	OE2	3.680
6U59	A_ARG_327	NH1	A_ASP_148A	OD1	3.884
6U59	A_ARG_327	NH1	A_ASP_148A	OD2	3.044
6U59	A_LYS_335	NZ	A_GLU_408	OE1	3.651
6U59	A_ARG_337	NH1	A_GLU_290	OE1	2.993
6U59	A_ARG_337	NH2	A_GLU_290	OE1	2.941
6U59	A_LYS_356	NZ	A_GLU_466	OE2	2.969
6U59	A_ARG_399	NH1	A_ASP_401	OD2	3.230
6U59	A_ARG_419	NH2	A_GLU_153	OE2	3.607

6U59	A_LYS_421	NZ	A_GLU_370	OE2	3.544
6U59	A_LYS_432	NZ	A_ASP_113	OD1	2.692
6U59	A_LYS_432	NZ	A_ASP_113	OD2	2.690
6U59	A_ARG_456	NH2	A_GLU_466	OE1	2.731
6U59	A_ARG_456	NH2	A_GLU_466	OE2	3.143
6U59	A_ARG_469	NH2	A_ASP_457	OD2	2.912
6U59	A_ARG_476	NH2	A_GLU_102	OE1	3.714
6U59	A_ARG_476	NH2	A_GLU_102	OE2	3.058
6U59	A_ARG_480	NH1	A_ASP_477	OD1	2.833
6U59	A_LYS_487	NZ	A_GLU_47	OE1	3.413
6U59	A_LYS_487	NZ	A_GLU_91	OE2	2.867
6U59	A_LYS_490	NZ	A_GLU_492	OE2	3.991
6U59	A_ARG_504	NH1	I_GLU_662	OE1	3.209
6U59	A_ARG_504	NH1	I_GLU_662	OE2	2.833
6U59	A_ARG_504	NH2	I_GLU_662	OE2	3.911
6U59	B_LYS_574	NZ	A_ASP_107	OD1	2.403
6U59	B_ARG_579	NH2	I_GLU_584	OE1	3.024
6U59	B_ARG_588	NH2	B_GLU_584	OE2	3.079
6U59	B_LYS_617	NZ	B_GLU_634	OE1	2.908
6U59	B_LYS_617	NZ	B_GLU_634	OE2	3.808
6U59	L_ARG_28	NH2	L_ASP_95D	OD2	3.021
6U59	L_ARG_50	NH1	A_GLU_269	OE2	3.175
6U59	L_ARG_50	NH2	A_GLU_268	OE1	2.965
6U59	L_ARG_50	NH2	A_GLU_269	OE2	3.221
6U59	L_ARG_61	NH1	L_GLU_79	OE1	3.076
6U59	L_ARG_61	NH1	L_ASP_82	OD2	2.866
6U59	L_ARG_61	NH2	L_ASP_77	OD2	3.575
6U59	L_ARG_61	NH2	L_GLU_79	OE1	3.931
6U59	L_ARG_95A	NH1	A_GLU_350	OE2	3.796
6U59	L_ARG_95A	NH2	A_GLU_350	OE1	3.217
6U59	L_ARG_95A	NH2	A_GLU_350	OE2	3.041
6U59	L_ARG_95A	NH2	A_GLU_351	OE1	3.921
6U59	H_ARG_38	NH1	H_ASP_86	OD1	2.876
6U59	H_ARG_38	NH2	H_GLU_46	OE1	2.785
6U59	H_ARG_38	NH2	H_GLU_46	OE2	3.942
6U59	H_ARG_66	NH1	H_ASP_86	OD1	2.903
6U59	H_ARG_66	NH1	H_ASP_86	OD2	3.436
6U59	C_LYS_34	NZ	D_ASP_612	OD1	2.489
6U59	C_LYS_46	NZ	C_GLU_492	OE1	2.715
6U59	C_LYS_170	NZ	C_GLU_172	OE2	3.768
6U59	C_LYS_227	NZ	C_GLU_83	OE1	3.011
6U59	C_LYS_227	NZ	C_GLU_83	OE2	3.430
6U59	C_LYS_231	NZ	C_GLU_268	OE2	2.869
6U59	C_HIS_249	NE2	C_GLU_482	OE2	2.820
6U59	C_LYS_282	NZ	C_ASP_279	OD2	2.817
6U59	C_ARG_298	NH1	C_GLU_381	OE2	3.453
6U59	C_ARG_298	NH2	C_GLU_381	OE1	3.785
6U59	C_ARG_298	NH2	C_GLU_381	OE2	3.680
6U59	C_ARG_327	NH1	C_ASP_148A	OD1	3.883
6U59	C_ARG_327	NH1	C_ASP_148A	OD2	3.044
6U59	C_LYS_335	NZ	C_GLU_408	OE1	3.651
6U59	C_ARG_337	NH1	C_GLU_290	OE1	2.993
6U59	C_ARG_337	NH2	C_GLU_290	OE1	2.942
6U59	C_LYS_356	NZ	C_GLU_466	OE2	2.969
6U59	C_ARG_399	NH1	C_ASP_401	OD2	3.229
6U59	C_ARG_419	NH2	C_GLU_153	OE2	3.607
6U59	C_LYS_421	NZ	C_GLU_370	OE2	3.543
6U59	C_LYS_432	NZ	C_ASP_113	OD1	2.692

6U59	C_LYS_432	NZ	C_ASP_113	OD2	2.691
6U59	C_ARG_456	NH2	C_GLU_466	OE1	2.732
6U59	C_ARG_456	NH2	C_GLU_466	OE2	3.144
6U59	C_ARG_469	NH2	C_ASP_457	OD2	2.911
6U59	C_ARG_476	NH2	C_GLU_102	OE1	3.714
6U59	C_ARG_476	NH2	C_GLU_102	OE2	3.058
6U59	C_ARG_480	NH1	C_ASP_477	OD1	2.832
6U59	C_LYS_487	NZ	C_GLU_47	OE1	3.414
6U59	C_LYS_487	NZ	C_GLU_91	OE2	2.866
6U59	C_LYS_490	NZ	C_GLU_492	OE2	3.991
6U59	C_ARG_504	NH1	B_GLU_662	OE1	3.208
6U59	C_ARG_504	NH1	B_GLU_662	OE2	2.832
6U59	C_ARG_504	NH2	B_GLU_662	OE2	3.910
6U59	D_LYS_574	NZ	C_ASP_107	OD1	2.403
6U59	D_ARG_579	NH2	B_GLU_584	OE1	3.024
6U59	D_ARG_588	NH2	D_GLU_584	OE2	3.079
6U59	D_LYS_617	NZ	D_GLU_634	OE1	2.908
6U59	D_LYS_617	NZ	D_GLU_634	OE2	3.808
6U59	E_ARG_28	NH2	E_ASP_95D	OD2	3.022
6U59	E_ARG_50	NH1	C_GLU_269	OE2	3.175
6U59	E_ARG_50	NH2	C_GLU_268	OE1	2.965
6U59	E_ARG_50	NH2	C_GLU_269	OE2	3.221
6U59	E_ARG_61	NH1	E_GLU_79	OE1	3.076
6U59	E_ARG_61	NH1	E_ASP_82	OD2	2.865
6U59	E_ARG_61	NH2	E_ASP_77	OD2	3.574
6U59	E_ARG_61	NH2	E_GLU_79	OE1	3.931
6U59	E_ARG_95A	NH1	C_GLU_350	OE2	3.795
6U59	E_ARG_95A	NH2	C_GLU_350	OE1	3.216
6U59	E_ARG_95A	NH2	C_GLU_350	OE2	3.040
6U59	E_ARG_95A	NH2	C_GLU_351	OE1	3.921
6U59	F_ARG_38	NH1	F_ASP_86	OD1	2.877
6U59	F_ARG_38	NH2	F_GLU_46	OE1	2.786
6U59	F_ARG_38	NH2	F_GLU_46	OE2	3.943
6U59	F_ARG_66	NH1	F_ASP_86	OD1	2.903
6U59	F_ARG_66	NH1	F_ASP_86	OD2	3.437
6U59	G_LYS_34	NZ	I_ASP_612	OD1	2.489
6U59	G_LYS_46	NZ	G_GLU_492	OE1	2.715
6U59	G_LYS_170	NZ	G_GLU_172	OE2	3.768
6U59	G_LYS_227	NZ	G_GLU_83	OE1	3.011
6U59	G_LYS_227	NZ	G_GLU_83	OE2	3.430
6U59	G_LYS_231	NZ	G_GLU_268	OE2	2.869
6U59	G_HIS_249	NE2	G_GLU_482	OE2	2.821
6U59	G_LYS_282	NZ	G_ASP_279	OD2	2.816
6U59	G_ARG_298	NH1	G_GLU_381	OE2	3.452
6U59	G_ARG_298	NH2	G_GLU_381	OE1	3.785
6U59	G_ARG_298	NH2	G_GLU_381	OE2	3.679
6U59	G_ARG_327	NH1	G_ASP_148A	OD1	3.883
6U59	G_ARG_327	NH1	G_ASP_148A	OD2	3.044
6U59	G_LYS_335	NZ	G_GLU_408	OE1	3.651
6U59	G_ARG_337	NH1	G_GLU_290	OE1	2.994
6U59	G_ARG_337	NH2	G_GLU_290	OE1	2.942
6U59	G_LYS_356	NZ	G_GLU_466	OE2	2.969
6U59	G_ARG_399	NH1	G_ASP_401	OD2	3.230
6U59	G_ARG_419	NH2	G_GLU_153	OE2	3.607
6U59	G_LYS_421	NZ	G_GLU_370	OE2	3.543
6U59	G_LYS_432	NZ	G_ASP_113	OD1	2.692
6U59	G_LYS_432	NZ	G_ASP_113	OD2	2.691
6U59	G_ARG_456	NH2	G_GLU_466	OE1	2.731

6U59	G_ARG_456	NH2	G_GLU_466	OE2	3.144
6U59	G_ARG_469	NH2	G_ASP_457	OD2	2.912
6U59	G_ARG_476	NH2	G_GLU_102	OE1	3.714
6U59	G_ARG_476	NH2	G_GLU_102	OE2	3.058
6U59	G_ARG_480	NH1	G_ASP_477	OD1	2.833
6U59	G_LYS_487	NZ	G_GLU_47	OE1	3.414
6U59	G_LYS_487	NZ	G_GLU_91	OE2	2.866
6U59	G_LYS_490	NZ	G_GLU_492	OE2	3.990
6U59	G_ARG_504	NH1	D_GLU_662	OE1	3.209
6U59	G_ARG_504	NH1	D_GLU_662	OE2	2.833
6U59	G_ARG_504	NH2	D_GLU_662	OE2	3.910
6U59	I_LYS_574	NZ	G_ASP_107	OD1	2.403
6U59	I_ARG_579	NH2	D_GLU_584	OE1	3.025
6U59	I_ARG_588	NH2	I_GLU_584	OE2	3.079
6U59	I_LYS_617	NZ	I_GLU_634	OE1	2.907
6U59	I_LYS_617	NZ	I_GLU_634	OE2	3.808
6U59	J_ARG_28	NH2	J_ASP_95D	OD2	3.022
6U59	J_ARG_50	NH1	G_GLU_269	OE2	3.175
6U59	J_ARG_50	NH2	G_GLU_268	OE1	2.965
6U59	J_ARG_50	NH2	G_GLU_269	OE2	3.220
6U59	J_ARG_61	NH1	J_GLU_79	OE1	3.077
6U59	J_ARG_61	NH1	J_ASP_82	OD2	2.866
6U59	J_ARG_61	NH2	J_ASP_77	OD2	3.574
6U59	J_ARG_61	NH2	J_GLU_79	OE1	3.931
6U59	J_ARG_95A	NH1	G_GLU_350	OE2	3.796
6U59	J_ARG_95A	NH2	G_GLU_350	OE1	3.217
6U59	J_ARG_95A	NH2	G_GLU_350	OE2	3.041
6U59	J_ARG_95A	NH2	G_GLU_351	OE1	3.921
6U59	K_ARG_38	NH1	K_ASP_86	OD1	2.876
6U59	K_ARG_38	NH2	K_GLU_46	OE1	2.786
6U59	K_ARG_38	NH2	K_GLU_46	OE2	3.943
6U59	K_ARG_66	NH1	K_ASP_86	OD1	2.904
6U59	K_ARG_66	NH1	K_ASP_86	OD2	3.437
6UG7	L_ARG_60	NH1	L_GLU_78	OE1	3.385
6UG7	L_ARG_60	NH1	L_GLU_78	OE2	3.452
6UG7	L_ARG_60	NH2	L_GLU_78	OE1	3.649
6UG7	L_ARG_60	NH2	L_GLU_80	OE2	2.876
6UG7	L_ARG_60	NH2	L_ASP_81	OD1	2.780
6UG7	L_ARG_60	NH2	L_ASP_81	OD2	3.537
6UG7	L_LYS_148	NZ	L_GLU_194	OE2	2.618
6UG7	L_LYS_168	NZ	L_ASP_166	OD1	3.206
6UG7	L_LYS_168	NZ	L_ASP_166	OD2	3.551
6UG7	L_HIS_188	ND1	L_ASP_150	OD2	3.280
6UG7	H_ARG_38	NH1	H_ASP_89	OD1	2.846
6UG7	H_ARG_38	NH2	H_ASP_89	OD1	3.706
6UG7	H_HIS_60	NE2	L_GLU_1	OE1	2.854
6UG7	H_HIS_60	NE2	L_GLU_1	OE2	3.808
6UG7	H_ARG_66	NH1	H_ASP_89	OD1	3.754
6UG7	H_ARG_66	NH1	H_ASP_89	OD2	2.880
6UG7	H_ARG_66	NH2	H_ASP_89	OD1	3.067
6UG7	H_ARG_66	NH2	H_ASP_89	OD2	3.547
6UG7	H_LYS_147	NZ	H_ASP_148	OD1	3.523
6UG7	H_LYS_213	NZ	L_GLU_122	OE1	2.927
6UG7	H_LYS_213	NZ	L_GLU_122	OE2	3.960
6UG7	H_LYS_214	NZ	H_GLU_216	OE1	3.060
6UG8	L_ARG_60	NH1	L_GLU_78	OE1	3.498
6UG8	L_ARG_60	NH2	L_GLU_78	OE1	3.557
6UG8	L_ARG_60	NH2	L_GLU_80	OE2	2.819

6UG8	L_ARG_60	NH2	L_ASP_81	OD1	2.739
6UG8	L_ARG_60	NH2	L_ASP_81	OD2	3.504
6UG8	L_LYS_148	NZ	L_GLU_194	OE1	2.956
6UG8	L_LYS_148	NZ	L_GLU_194	OE2	3.899
6UG8	L_HIS_188	ND1	L_ASP_184	OD1	3.549
6UG8	H_ARG_38	NH1	H_ASP_89	OD1	2.810
6UG8	H_ARG_38	NH2	H_GLU_46	OE1	3.785
6UG8	H_ARG_38	NH2	H_GLU_46	OE2	2.904
6UG8	H_ARG_38	NH2	H_ASP_89	OD1	3.679
6UG8	H_HIS_60	NE2	L_GLU_1	OE1	3.688
6UG8	H_ARG_66	NH1	H_ASP_89	OD1	3.627
6UG8	H_ARG_66	NH1	H_ASP_89	OD2	2.995
6UG8	H_ARG_66	NH2	H_ASP_89	OD1	2.888
6UG8	H_ARG_66	NH2	H_ASP_89	OD2	3.572
6UG8	H_LYS_75	NZ	H_ASP_72	OD2	3.818
6UG8	H_LYS_147	NZ	H_ASP_148	OD1	3.749
6UG8	H_LYS_147	NZ	H_ASP_148	OD2	3.867
6UG8	H_LYS_213	NZ	L_GLU_122	OE1	2.779
6UG8	H_LYS_213	NZ	L_GLU_122	OE2	3.811
6UG8	H_LYS_214	NZ	H_GLU_216	OE1	3.891
6UG9	L_ARG_60	NH1	L_GLU_78	OE1	3.657
6UG9	L_ARG_60	NH2	L_GLU_80	OE2	2.753
6UG9	L_ARG_60	NH2	L_ASP_81	OD1	2.737
6UG9	L_ARG_60	NH2	L_ASP_81	OD2	3.762
6UG9	L_LYS_102	NZ	L_GLU_164	OE1	3.252
6UG9	L_LYS_102	NZ	L_GLU_164	OE2	2.915
6UG9	L_LYS_106	NZ	L_GLU_17	OE2	3.780
6UG9	L_ARG_141	NH1	L_GLU_164	OE2	3.279
6UG9	L_ARG_141	NH2	L_GLU_104	OE1	3.321
6UG9	L_ARG_141	NH2	L_GLU_104	OE2	3.680
6UG9	L_ARG_210	NH1	L_GLU_186	OE2	3.814
6UG9	H_ARG_38	NH1	H_ASP_89	OD1	2.732
6UG9	H_ARG_38	NH2	H_GLU_46	OE2	3.364
6UG9	H_ARG_38	NH2	H_ASP_89	OD1	3.514
6UG9	H_HIS_60	NE2	L_GLU_1	OE2	3.673
6UG9	H_HIS_60	NE2	H_GLU_46	OE1	3.948
6UG9	H_ARG_66	NH1	H_ASP_89	OD1	3.412
6UG9	H_ARG_66	NH1	H_ASP_89	OD2	3.392
6UG9	H_ARG_66	NH2	H_ASP_89	OD1	3.881
6UG9	H_ARG_66	NH2	H_ASP_89	OD2	2.589
6UG9	H_LYS_147	NZ	H_ASP_148	OD1	3.376
6UG9	H_LYS_147	NZ	H_ASP_148	OD2	3.331
6UG9	H_LYS_213	NZ	L_GLU_122	OE1	3.853
6UG9	H_LYS_214	NZ	H_GLU_216	OE2	3.824
6UG9	B_LYS_52	NZ	B_ASP_49	OD2	3.304
6UG9	B_ARG_60	NH2	B_GLU_80	OE2	3.597
6UG9	B_ARG_60	NH2	B_ASP_81	OD1	2.874
6UG9	B_ARG_60	NH2	B_ASP_81	OD2	3.455
6UG9	B_LYS_102	NZ	B_GLU_164	OE1	3.160
6UG9	B_LYS_102	NZ	B_GLU_164	OE2	3.546
6UG9	B_ARG_141	NH1	B_GLU_104	OE1	3.634
6UG9	B_ARG_141	NH1	B_GLU_104	OE2	3.870
6UG9	B_LYS_148	NZ	B_GLU_194	OE1	3.810
6UG9	B_LYS_148	NZ	B_GLU_194	OE2	3.615
6UG9	B_HIS_188	ND1	B_ASP_150	OD2	3.288
6UG9	B_ARG_210	NH1	B_GLU_186	OE1	3.776
6UG9	A_ARG_38	NH1	A_ASP_89	OD1	2.722
6UG9	A_ARG_38	NH2	A_GLU_46	OE2	3.287

6UG9	A_ARG_38	NH2	A_ASP_89	OD1	3.758
6UG9	A_HIS_60	NE2	B_GLU_1	OE1	3.507
6UG9	A_ARG_66	NH1	A_ASP_89	OD1	3.675
6UG9	A_ARG_66	NH1	A_ASP_89	OD2	2.753
6UG9	A_ARG_66	NH2	A_ASP_89	OD1	3.070
6UG9	A_ARG_66	NH2	A_ASP_89	OD2	3.506
6UG9	A_LYS_147	NZ	A_ASP_148	OD1	3.442
6UG9	A_LYS_147	NZ	A_ASP_148	OD2	3.550
6UG9	A_LYS_213	NZ	B_GLU_122	OE1	2.877
6UG9	A_LYS_214	NZ	A_GLU_216	OE1	2.984
6UG9	K_ARG_60	NH1	K_GLU_78	OE1	3.075
6UG9	K_ARG_60	NH1	K_GLU_78	OE2	3.972
6UG9	K_ARG_60	NH1	K_GLU_80	OE2	3.745
6UG9	K_ARG_60	NH1	K_ASP_81	OD1	2.816
6UG9	K_ARG_60	NH1	K_ASP_81	OD2	2.993
6UG9	K_ARG_60	NH2	K_GLU_78	OE1	3.769
6UG9	K_ARG_60	NH2	K_GLU_80	OE2	2.923
6UG9	K_LYS_102	NZ	K_GLU_104	OE1	3.987
6UG9	K_LYS_102	NZ	K_GLU_164	OE1	3.455
6UG9	K_LYS_102	NZ	K_GLU_164	OE2	3.139
6UG9	K_ARG_141	NH1	K_GLU_104	OE1	3.193
6UG9	K_ARG_141	NH1	K_GLU_104	OE2	2.932
6UG9	K_ARG_141	NH2	K_GLU_104	OE1	2.602
6UG9	K_ARG_141	NH2	K_GLU_104	OE2	3.840
6UG9	K_LYS_148	NZ	K_GLU_194	OE1	3.594
6UG9	K_LYS_148	NZ	K_GLU_194	OE2	2.938
6UG9	K_HIS_188	ND1	K_ASP_150	OD2	3.205
6UG9	K_HIS_188	NE2	K_ASP_184	OD1	3.818
6UG9	K_ARG_210	NH1	K_GLU_186	OE2	3.933
6UG9	J_ARG_38	NH1	J_ASP_89	OD1	2.782
6UG9	J_ARG_38	NH2	J_GLU_46	OE2	3.597
6UG9	J_ARG_38	NH2	J_ASP_89	OD1	3.861
6UG9	J_HIS_60	NE2	K_GLU_1	OE1	3.585
6UG9	J_ARG_66	NH2	J_ASP_89	OD1	2.909
6UG9	J_ARG_66	NH2	J_ASP_89	OD2	2.772
6UG9	J_LYS_75	NZ	J_ASP_72	OD2	3.024
6UG9	J_LYS_147	NZ	J_ASP_148	OD1	3.646
6UG9	J_LYS_213	NZ	K_GLU_122	OE1	2.648
6UG9	J_LYS_213	NZ	K_GLU_122	OE2	3.296
6UG9	J_LYS_214	NZ	J_GLU_216	OE1	3.149
6UGA	L_HIS_33	ND1	L_ASP_49	OD1	3.961
6UGA	L_LYS_52	NZ	L_ASP_49	OD2	3.704
6UGA	L_ARG_60	NH2	L_GLU_80	OE2	3.278
6UGA	L_ARG_60	NH2	L_ASP_81	OD1	2.749
6UGA	L_ARG_60	NH2	L_ASP_81	OD2	3.568
6UGA	L_LYS_102	NZ	L_GLU_104	OE2	3.070
6UGA	L_LYS_148	NZ	L_GLU_194	OE2	2.966
6UGA	L_LYS_182	NZ	L_GLU_186	OE2	3.117
6UGA	L_HIS_188	ND1	L_ASP_150	OD2	2.852
6UGA	H_ARG_38	NH1	H_ASP_89	OD1	2.990
6UGA	H_ARG_38	NH2	H_GLU_46	OE1	3.017
6UGA	H_ARG_38	NH2	H_ASP_89	OD1	3.417
6UGA	H_HIS_60	NE2	L_GLU_1	OE1	3.306
6UGA	H_ARG_66	NH1	H_ASP_89	OD1	3.849
6UGA	H_ARG_66	NH1	H_ASP_89	OD2	2.855
6UGA	H_ARG_66	NH2	H_ASP_89	OD1	2.858
6UGA	H_ARG_66	NH2	H_ASP_89	OD2	3.277
6UGA	H_LYS_147	NZ	H_ASP_148	OD1	3.129

6UGA	A_LYS_52	NZ	A_ASP_49	OD2	3.881
6UGA	A_ARG_60	NH1	A_GLU_80	OE1	3.935
6UGA	A_ARG_60	NH2	A_GLU_80	OE1	2.878
6UGA	A_ARG_60	NH2	A_ASP_81	OD1	2.757
6UGA	A_ARG_60	NH2	A_ASP_81	OD2	3.485
6UGA	A_LYS_144	NZ	A_GLU_194	OE1	3.405
6UGA	A_LYS_144	NZ	A_GLU_194	OE2	2.645
6UGA	A_LYS_182	NZ	A_GLU_186	OE2	3.697
6UGA	A_LYS_187	NZ	A_ASP_184	OD1	3.052
6UGA	A_ARG_210	NH2	A_GLU_186	OE1	3.370
6UGA	B_ARG_38	NH1	B_ASP_89	OD1	2.951
6UGA	B_ARG_38	NH2	B_ASP_89	OD1	3.625
6UGA	B_HIS_60	NE2	A_GLU_1	OE2	3.932
6UGA	B_ARG_66	NH1	B_ASP_89	OD1	3.747
6UGA	B_ARG_66	NH1	B_ASP_89	OD2	3.050
6UGA	B_ARG_66	NH2	B_ASP_89	OD1	3.323
6UGA	B_ARG_66	NH2	B_ASP_89	OD2	3.833
6UGA	B_LYS_147	NZ	B_ASP_148	OD1	3.437
6UGA	B_LYS_147	NZ	B_ASP_148	OD2	3.600
6UGA	B_HIS_168	NE2	A_ASP_166	OD1	3.218
6UGA	B_LYS_213	NZ	A_GLU_122	OE1	3.352

Table 1: Salt bridging networks within the PDB entries of all experimentally determined antigen-antibody-related structures. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1A14	N.LYS_432	NZ	H.ASP_56	OD1	3.071
1A2Y	A.ARG_96	NH1	B.GLU_98	OE1	2.846
1A2Y	A.ARG_96	NH1	B.GLU_98	OE2	3.664
1A2Y	A.ARG_96	NH2	B.GLU_98	OE1	3.545
1A2Y	A.ARG_96	NH2	B.GLU_98	OE2	2.882
1A7L	A.LYS_219	NZ	B.GLU_131	OE1	3.835
1A7N	L.ARG_96	NH1	H.GLU_298	OE1	2.957
1A7N	L.ARG_96	NH1	H.GLU_298	OE2	3.249
1A7N	L.ARG_96	NH2	H.GLU_298	OE2	3.297
1A7P	L.ARG_96	NH2	H.GLU_298	OE1	3.845
1A7P	L.ARG_96	NH2	H.GLU_298	OE2	2.867
1A7Q	L.ARG_96	NH1	H.GLU_298	OE1	2.615
1A7Q	L.ARG_96	NH1	H.GLU_298	OE2	3.239
1A7Q	L.ARG_96	NH2	H.GLU_298	OE1	3.431
1A7Q	L.ARG_96	NH2	H.GLU_298	OE2	2.621
1A7R	L.ARG_96	NH1	H.GLU_298	OE1	2.658
1A7R	L.ARG_96	NH1	H.GLU_298	OE2	3.535
1A7R	L.ARG_96	NH2	H.GLU_298	OE1	3.614
1A7R	L.ARG_96	NH2	H.GLU_298	OE2	2.905
1ADQ	A.ARG_255	NH2	H.ASP_31	OD2	2.929
1ADQ	A.HIS_433	NE2	L.ASP_50	OD1	3.394
1ADQ	A.HIS_433	NE2	L.ASP_50	OD2	3.883
1ADQ	L.HIS_95B	NE2	H.ASP_61	OD2	3.425
1BJ1	H.LYS_219	NZ	L.GLU_123	OE1	2.948
1BJ1	H.LYS_224	NZ	L.ASP_122	OD2	2.691
1BJ1	V.ARG_23	NH1	W.GLU_30	OE1	3.305
1BJ1	W.ARG_23	NH1	V.GLU_30	OE1	3.351
1BLN	B.LYS_221	NZ	A.GLU_123	OE2	2.688
1BLN	D.LYS_221	NZ	C.GLU_123	OE2	2.694
1BQL	L.LYS_44	NZ	H.ASP_104	OD1	3.995
1BQL	L.ARG_45	NH2	H.ASP_104	OD2	3.212
1BQL	H.LYS_211	NZ	L.GLU_121	OE1	2.714
1BQL	H.LYS_211	NZ	L.GLU_121	OE2	2.963
1BQL	Y.ARG_45	NH1	H.GLU_50	OE1	3.800
1BQL	Y.ARG_45	NH1	H.GLU_50	OE2	2.920
1BQL	Y.LYS_68	NZ	H.GLU_50	OE1	3.561
1BVK	A.ARG_96	NH2	B.GLU_98	OE1	2.978
1BVK	A.ARG_96	NH2	B.GLU_98	OE2	2.932
1BVK	D.ARG_96	NH2	E.GLU_98	OE1	2.525
1BVK	D.ARG_96	NH2	E.GLU_98	OE2	2.753
1C08	C.LYS_97	NZ	B.ASP_32	OD1	2.620
1C08	C.LYS_97	NZ	B.ASP_32	OD2	3.999
1C08	C.LYS_97	NZ	B.ASP_99	OD2	2.365
1C12	B.LYS_508	NZ	A.GLU_123	OE2	3.314
1CE1	L.ARG_94	NH2	H.GLU_61	OE2	3.979
1CE1	L.ARG_96	NH1	H.GLU_101	OE1	2.707
1CE1	L.ARG_96	NH1	H.GLU_101	OE2	3.562
1CE1	L.ARG_96	NH2	H.GLU_101	OE1	3.509
1CE1	L.ARG_96	NH2	H.GLU_101	OE2	2.787
1CE1	H.ARG_52	NH2	P.ASP_7	OD1	3.481
1CE1	H.LYS_56	NZ	P.ASP_7	OD2	2.951
1CFS	B.LYS_207	NZ	A.GLU_123	OE1	3.526
1CFT	B.LYS_207	NZ	A.GLU_123	OE1	2.550
1CFT	C.LYS_2	NZ	A.ASP_92	OD1	2.682
1CG9	A.ARG_17	NH1	B.ASP_35	OD2	3.201
1CG9	A.ARG_17	NH2	B.ASP_35	OD1	3.038
1CG9	A.ARG_17	NH2	B.ASP_35	OD2	3.401

1CG9	A_ARG_48	NH2	B_ASP_54	OD1	3.456
1CG9	A_ARG_48	NH2	B_ASP_54	OD2	3.762
1CG9	A_HIS_192	ND1	B_ASP_99	OD2	3.812
1CG9	B_LYS_7	NZ	A_GLU_232	OE1	3.887
1CLZ	L_LYS_207	NZ	H_ASP_130	OD1	3.119
1CLZ	L_LYS_207	NZ	H_ASP_130	OD2	3.445
1CLZ	H_ARG_172	NH1	L_ASP_170	OD2	3.885
1CLZ	H_ARG_172	NH2	L_ASP_170	OD2	3.384
1CLZ	H_LYS_221	NZ	L_GLU_123	OE1	3.750
1CLZ	H_LYS_221	NZ	L_GLU_123	OE2	2.509
1CZ8	V_ARG_23	NH1	W_GLU_30	OE1	3.162
1CZ8	V_ARG_23	NH1	W_GLU_30	OE2	3.558
1CZ8	W_ARG_23	NH1	V_GLU_30	OE1	3.011
1CZ8	W_ARG_23	NH1	V_GLU_30	OE2	3.663
1CZ8	H_LYS_219	NZ	L_GLU_123	OE1	3.027
1CZ8	H_LYS_224	NZ	L_ASP_122	OD1	2.846
1CZ8	H_LYS_224	NZ	L_ASP_122	OD2	3.185
1CZ8	Y_LYS_219	NZ	X_GLU_123	OE2	3.832
1DBJ	H_LYS_221	NZ	L_GLU_123	OE1	3.386
1DBJ	H_LYS_221	NZ	L_GLU_123	OE2	2.770
1DBK	H_HIS_172	ND1	L_ASP_167	OD2	3.619
1DBK	H_LYS_221	NZ	L_GLU_123	OE2	3.030
1DBM	H_LYS_221	NZ	L_GLU_123	OE2	3.277
1DEE	A_ARG_24	NH1	D_GLU_1555	OE1	3.510
1DEE	B_ARG_674	NH1	A_ASP_167	OD2	3.579
1DEE	B_LYS_719	NZ	A_GLU_123	OE1	2.730
1DEE	B_LYS_719	NZ	A_GLU_123	OE2	3.113
1DEE	D_ARG_1519	NH1	G_ASP_1834	OD1	3.122
1DEE	D_ARG_1519	NH1	G_ASP_1834	OD2	3.064
1DEE	D_ARG_1519	NH2	G_ASP_1834	OD1	3.684
1DEE	D_ARG_1519	NH2	G_ASP_1834	OD2	2.875
1DEE	D_ARG_1674	NH1	C_ASP_1167	OD2	3.619
1DEE	D_LYS_1719	NZ	C_GLU_1123	OE1	3.687
1DEE	D_LYS_1719	NZ	C_GLU_1123	OE2	2.890
1DEE	F_ARG_2519	NH1	H_ASP_2834	OD1	3.463
1DEE	F_ARG_2519	NH1	H_ASP_2834	OD2	2.731
1DEE	F_ARG_2519	NH2	H_ASP_2834	OD1	3.523
1DEE	F_ARG_2519	NH2	H_ASP_2834	OD2	3.444
1DEE	F_ARG_2674	NH1	E_ASP_2167	OD2	3.989
1DEE	F_LYS_2719	NZ	E_GLU_2123	OE1	2.882
1DEE	F_LYS_2719	NZ	E_GLU_2123	OE2	3.779
1DQD	H_LYS_217	NZ	L_GLU_122	OE2	3.953
1DQJ	B_LYS_219	NZ	A_GLU_123	OE2	2.598
1DQJ	C_LYS_97	NZ	B_ASP_32	OD2	2.665
1DQM	L_LYS_207	NZ	H_ASP_130	OD1	3.491
1DQM	L_LYS_207	NZ	H_ASP_130	OD2	3.782
1DQQ	A_LYS_49	NZ	B_ASP_101	OD1	2.957
1DQQ	B_LYS_216	NZ	D_ASP_218	OD1	2.965
1DQQ	B_LYS_219	NZ	A_GLU_123	OE2	2.763
1DQQ	C_LYS_49	NZ	D_ASP_101	OD1	3.456
1DQQ	C_LYS_49	NZ	D_ASP_101	OD2	3.943
1DQQ	D_LYS_219	NZ	C_GLU_123	OE1	3.088
1DVF	A_ARG_96	NH1	B_GLU_98	OE1	2.616
1DVF	A_ARG_96	NH1	B_GLU_98	OE2	3.746
1DVF	A_ARG_96	NH2	B_GLU_98	OE1	3.400
1DVF	A_ARG_96	NH2	B_GLU_98	OE2	2.958
1DVF	D_HIS_33	NE2	B_ASP_100	OD1	3.569
1DVF	D_HIS_33	NE2	B_ASP_100	OD2	3.052

1DZB	A_LYS_63	NZ	B_GLU_89	OE1	3.983
1DZB	A_LYS_67	NZ	B_ASP_90	OD2	3.792
1DZB	X_ARG_61	NH2	A_ASP_256	OD2	3.887
1DZB	X_LYS_73	NZ	A_ASP_256	OD1	3.412
1DZB	X_LYS_73	NZ	A_ASP_256	OD2	3.290
1DZB	X_ARG_112	NH2	A_ASP_31	OD2	3.878
1DZB	Y_LYS_73	NZ	B_ASP_256	OD1	3.559
1E4W	H_LYS_205	NZ	L_GLU_123	OE1	3.384
1E4W	H_LYS_205	NZ	L_GLU_123	OE2	3.066
1E4X	L_LYS_205	NZ	M_GLU_123	OE1	2.874
1E4X	L_LYS_205	NZ	M_GLU_123	OE2	3.751
1E4X	Q_HIS_4	NE2	L_ASP_98	OD2	3.960
1E6J	H_LYS_215	NZ	L_GLU_121	OE1	3.273
1E6J	H_LYS_215	NZ	L_GLU_121	OE2	3.199
1E6O	H_LYS_215	NZ	L_GLU_121	OE1	2.731
1E6O	H_LYS_215	NZ	L_GLU_121	OE2	3.094
1EJO	L_HIS_2038	NE2	H_ASP_2603	OD1	3.217
1EJO	H_ARG_2598	NH2	P_ASP_3143	OD1	3.795
1EJO	H_ARG_2598	NH2	P_ASP_3143	OD2	2.982
1EJO	H_LYS_2714	NZ	L_GLU_2127	OE1	2.933
1EJO	H_LYS_2714	NZ	L_GLU_2127	OE2	3.046
1EJO	P_ARG_3141	NH1	L_GLU_2027	OE2	3.696
1EJO	P_ARG_3141	NH1	L_GLU_2097	OE1	2.675
1EJO	P_ARG_3141	NH2	L_GLU_2027	OE2	3.441
1EMT	H_LYS_63	NZ	L_ASP_1	OD1	3.310
1EMT	H_LYS_211	NZ	L_GLU_123	OE1	2.945
1EMT	H_LYS_211	NZ	L_GLU_123	OE2	2.554
1ETZ	L_ARG_186	NH1	B_GLU_48	OE1	2.771
1ETZ	L_ARG_186	NH1	B_GLU_48	OE2	3.248
1ETZ	L_ARG_190	NH2	B_GLU_48	OE2	3.331
1ETZ	H_LYS_156	NZ	L_GLU_127	OE2	3.377
1ETZ	H_LYS_221	NZ	L_GLU_126	OE1	3.184
1ETZ	A_ARG_186	NH1	H_GLU_45	OE2	3.236
1ETZ	A_ARG_186	NH2	H_GLU_48	OE1	3.518
1ETZ	B_LYS_156	NZ	A_GLU_127	OE2	2.979
1ETZ	B_LYS_221	NZ	A_GLU_126	OE1	3.572
1F11	B_LYS_221	NZ	A_GLU_123	OE2	3.880
1F11	D_LYS_221	NZ	C_GLU_123	OE2	3.786
1F4W	H_LYS_147	NZ	L_GLU_127	OE2	2.611
1F4W	H_LYS_212	NZ	L_GLU_126	OE1	2.614
1F4W	H_LYS_212	NZ	L_GLU_126	OE2	2.379
1F4X	H_LYS_147	NZ	L_GLU_127	OE2	2.699
1F4X	H_LYS_212	NZ	L_GLU_126	OE1	2.421
1F4X	H_LYS_212	NZ	L_GLU_126	OE2	2.990
1F4Y	H_LYS_212	NZ	L_GLU_126	OE2	3.609
1F8T	L_ARG_96	NH1	H_ASP_97	OD1	3.105
1F8T	L_ARG_96	NH1	H_ASP_97	OD2	3.586
1F8T	L_ARG_96	NH2	H_ASP_97	OD1	3.395
1F8T	L_ARG_96	NH2	H_ASP_97	OD2	2.424
1F8T	H_LYS_221	NZ	L_GLU_123	OE1	3.087
1F90	L_LYS_30	NZ	E_GLU_4	OE1	2.620
1F90	L_LYS_30	NZ	E_GLU_4	OE2	2.679
1F90	L_ARG_96	NH2	H_ASP_97	OD1	2.720
1F90	L_ARG_96	NH2	H_ASP_97	OD2	2.722
1F90	H_LYS_221	NZ	L_GLU_123	OE2	3.675
1FBI	H_LYS_63	NZ	L_ASP_1	OD1	2.933
1FBI	H_LYS_63	NZ	L_ASP_1	OD2	2.804
1FBI	H_LYS_217	NZ	L_GLU_123	OE1	3.667

1FBI	X_HIS_15	ND1	H_ASP_55	OD1	3.190
1FBI	X_HIS_15	ND1	H_ASP_55	OD2	3.649
1FBI	X_LYS_96	NZ	H_ASP_52	OD2	2.922
1FBI	X_LYS_97	NZ	H_GLU_50	OE1	3.586
1FBI	X_LYS_97	NZ	H_GLU_50	OE2	2.898
1FBI	Q_LYS_63	NZ	P_ASP_1	OD1	3.020
1FBI	Q_LYS_63	NZ	P_ASP_1	OD2	3.850
1FBI	Y_HIS_15	ND1	Q_ASP_55	OD1	3.335
1FBI	Y_HIS_15	ND1	Q_ASP_55	OD2	3.838
1FBI	Y_LYS_96	NZ	Q_ASP_52	OD2	2.727
1FBI	Y_LYS_97	NZ	Q_GLU_50	OE1	2.828
1FBI	Y_LYS_97	NZ	Q_GLU_50	OE2	3.159
1FCC	A_LYS_370	NZ	B_GLU_357	OE2	2.948
1FCC	A_LYS_409	NZ	B_ASP_399	OD2	2.859
1FCC	A_LYS_439	NZ	B_GLU_356	OE1	3.550
1FCC	A_LYS_439	NZ	B_GLU_356	OE2	3.522
1FCC	C_LYS_28	NZ	A_GLU_380	OE1	2.730
1FCC	C_LYS_28	NZ	A_GLU_380	OE2	3.982
1FCC	C_LYS_28	NZ	A_GLU_382	OE1	3.879
1FCC	C_LYS_28	NZ	A_GLU_382	OE2	2.866
1FCC	B_LYS_370	NZ	A_GLU_357	OE2	2.633
1FCC	B_LYS_409	NZ	A_ASP_399	OD2	3.360
1FCC	B_LYS_439	NZ	A_GLU_356	OE1	3.166
1FCC	B_LYS_439	NZ	A_GLU_356	OE2	3.295
1FCC	D_LYS_28	NZ	B_GLU_380	OE1	2.730
1FCC	D_LYS_28	NZ	B_GLU_380	OE2	3.982
1FCC	D_LYS_28	NZ	B_GLU_382	OE1	3.879
1FCC	D_LYS_28	NZ	B_GLU_382	OE2	2.865
1FDL	L_ARG_96	NH1	H_GLU_98	OE1	3.307
1FDL	L_ARG_96	NH1	H_GLU_98	OE2	2.802
1FDL	L_ARG_96	NH2	H_GLU_98	OE1	2.754
1FDL	L_ARG_96	NH2	H_GLU_98	OE2	3.656
1FDL	H_LYS_211	NZ	L_GLU_123	OE1	2.896
1FDL	H_LYS_211	NZ	L_GLU_123	OE2	3.291
1FJ1	A_ARG_188	NH2	E_GLU_196	OE2	3.475
1FJ1	A_HIS_189	ND1	E_GLU_196	OE1	3.723
1FJ1	A_HIS_189	NE2	E_GLU_196	OE1	3.502
1FJ1	B_ARG_47	NH1	A_ASP_1	OD1	3.251
1FJ1	B_ARG_47	NH2	A_ASP_1	OD1	2.492
1FJ1	C_HIS_189	NE2	F_GLU_196	OE1	3.808
1FJ1	D_ARG_47	NH1	C_ASP_1	OD1	3.296
1FJ1	D_ARG_47	NH2	C_ASP_1	OD1	2.800
1FRG	L_LYS_213	NZ	H_ASP_354	OD1	3.324
1FRG	H_ARG_316	NH1	L_ASP_97	OD1	2.879
1FRG	H_ARG_316	NH2	L_ASP_97	OD1	3.078
1FRG	H_ARG_316	NH2	P_ASP_5	OD2	2.959
1FRG	H_LYS_322	NZ	L_GLU_61	OE1	2.861
1FRG	H_LYS_322	NZ	L_GLU_61	OE2	3.997
1FRG	H_LYS_432	NZ	L_GLU_129	OE1	3.086
1FRG	H_LYS_432	NZ	L_GLU_129	OE2	3.769
1FUJ	A_LYS_187	NZ	B_GLU_97	OE1	3.506
1FUJ	B_ARG_143	NH1	A_ASP_61	OD2	3.455
1FUJ	B_LYS_187	NZ	A_GLU_97	OE1	3.870
1FUJ	C_ARG_143	NH2	D_ASP_61	OD1	3.394
1FUJ	C_ARG_143	NH2	D_ASP_61	OD2	3.428
1FUJ	C_LYS_187	NZ	D_GLU_97	OE2	2.917
1FUJ	D_HIS_147	ND1	C_GLU_97	OE1	3.734
1FUJ	D_LYS_187	NZ	C_GLU_97	OE1	3.930

1FVD	A_ARG_18	NH1	C_ASP_70	OD2	3.361
1FVD	B_LYS_216	NZ	A_GLU_123	OE2	3.426
1FVD	C_ARG_18	NH1	A_ASP_70	OD2	3.065
1FVD	D_LYS_216	NZ	C_GLU_123	OE1	2.737
1FVE	A_ARG_18	NH1	C_ASP_70	OD1	3.613
1FVE	A_ARG_18	NH1	C_ASP_70	OD2	3.316
1FVE	B_LYS_216	NZ	A_GLU_123	OE2	3.328
1G6V	K_ARG_907	NH1	A_GLU_187	OE2	2.962
1G6V	K_ARG_909	NH1	A_GLU_187	OE1	3.909
1G6V	K_ARG_909	NH2	A_GLU_187	OE1	3.477
1G7H	A_ARG_96	NH1	B_GLU_98	OE1	2.788
1G7H	A_ARG_96	NH1	B_GLU_98	OE2	3.317
1G7H	A_ARG_96	NH2	B_GLU_98	OE1	3.736
1G7H	A_ARG_96	NH2	B_GLU_98	OE2	2.819
1G7I	A_ARG_96	NH1	B_GLU_98	OE1	2.881
1G7I	A_ARG_96	NH1	B_GLU_98	OE2	3.589
1G7I	A_ARG_96	NH2	B_GLU_98	OE1	3.599
1G7I	A_ARG_96	NH2	B_GLU_98	OE2	2.841
1G7J	A_ARG_96	NH1	B_GLU_98	OE1	2.834
1G7J	A_ARG_96	NH1	B_GLU_98	OE2	3.535
1G7J	A_ARG_96	NH2	B_GLU_98	OE1	3.524
1G7J	A_ARG_96	NH2	B_GLU_98	OE2	2.694
1G7L	A_ARG_96	NH1	B_GLU_98	OE1	2.744
1G7L	A_ARG_96	NH1	B_GLU_98	OE2	3.483
1G7L	A_ARG_96	NH2	B_GLU_98	OE1	3.535
1G7L	A_ARG_96	NH2	B_GLU_98	OE2	2.761
1G7M	A_ARG_96	NH1	B_GLU_98	OE1	2.792
1G7M	A_ARG_96	NH1	B_GLU_98	OE2	3.493
1G7M	A_ARG_96	NH2	B_GLU_98	OE1	3.544
1G7M	A_ARG_96	NH2	B_GLU_98	OE2	2.732
1G9M	G_ARG_419	NH1	H_GLU_103	OE2	3.773
1G9M	G_ARG_419	NH2	H_GLU_103	OE2	2.762
1G9M	G_ARG_419	NH2	H_GLU_108	OE2	3.794
1G9M	C_LYS_29	NZ	G_ASP_279	OD2	3.077
1G9M	C_ARG_59	NH1	G_ASP_368	OD1	3.576
1G9M	C_ARG_59	NH1	G_ASP_368	OD2	3.197
1G9M	C_ARG_59	NH2	G_ASP_368	OD1	2.550
1G9M	C_ARG_59	NH2	G_ASP_368	OD2	3.360
1G9N	G_ARG_419	NH1	H_GLU_106	OE1	2.930
1G9N	G_ARG_419	NH1	H_GLU_106	OE2	3.665
1G9N	G_ARG_419	NH2	H_GLU_103	OE1	2.300
1G9N	G_ARG_419	NH2	H_GLU_106	OE2	3.990
1G9N	C_LYS_35	NZ	G_ASP_457	OD2	3.608
1G9N	C_ARG_59	NH1	G_ASP_368	OD1	3.032
1G9N	C_ARG_59	NH1	G_ASP_368	OD2	3.045
1G9N	C_ARG_59	NH2	G_ASP_368	OD1	2.609
1G9N	C_ARG_59	NH2	G_ASP_368	OD2	3.355
1G9N	H_LYS_224	NZ	L_GLU_125	OE1	3.507
1G9N	H_LYS_224	NZ	L_GLU_125	OE2	3.538
1G9N	H_LYS_229	NZ	L_ASP_124	OD2	3.557
1GC1	G_ARG_419	NH1	H_GLU_106	OE1	2.761
1GC1	G_ARG_419	NH2	H_GLU_106	OE1	2.942
1GC1	G_ARG_419	NH2	H_GLU_108	OE1	3.887
1GC1	G_ARG_419	NH2	H_GLU_108	OE2	3.401
1GC1	C_LYS_29	NZ	G_ASP_279	OD1	2.748
1GC1	C_ARG_59	NH1	G_ASP_368	OD1	2.780
1GC1	C_ARG_59	NH1	G_ASP_368	OD2	3.645
1GC1	C_ARG_59	NH2	G_ASP_368	OD1	3.062

1GC1	C_ARG_59	NH2	G_ASP_368	OD2	2.481
1GC1	H_LYS_224	NZ	L_GLU_125	OE1	2.581
1GC1	H_LYS_224	NZ	L_GLU_125	OE2	3.963
1GGB	H_ARG_58	NH1	L_ASP_94	OD1	3.623
1GGB	H_ARG_58	NH2	L_ASP_94	OD1	2.873
1GGB	H_LYS_221	NZ	L_GLU_123	OE1	2.690
1GGB	H_LYS_221	NZ	L_GLU_123	OE2	3.205
1GGC	H_ARG_58	NH2	L_ASP_94	OD1	3.221
1GGC	H_LYS_221	NZ	L_GLU_123	OE1	2.942
1GGI	H_ARG_58	NH2	L_ASP_94	OD2	3.749
1GGI	H_LYS_221	NZ	L_GLU_123	OE2	3.900
1GGI	P_LYS_312	NZ	H_ASP_54	OD1	2.914
1GGI	P_LYS_312	NZ	H_ASP_54	OD2	3.188
1GGI	P_LYS_312	NZ	H_ASP_56	OD1	2.830
1GGI	P_LYS_312	NZ	H_ASP_56	OD2	3.728
1GGI	J_ARG_58	NH2	M_ASP_94	OD2	3.966
1GGI	J_HIS_172	NE2	M_ASP_167	OD2	3.287
1GGI	J_LYS_221	NZ	M_GLU_123	OE1	3.528
1GGI	J_LYS_221	NZ	M_GLU_123	OE2	3.781
1GGI	Q_LYS_312	NZ	J_ASP_54	OD1	3.299
1GGI	Q_LYS_312	NZ	J_ASP_54	OD2	2.967
1GGI	Q_LYS_312	NZ	J_ASP_56	OD1	3.964
1GGI	Q_LYS_312	NZ	J_ASP_56	OD2	3.120
1GPO	L_LYS_54	NZ	H_ASP_101	OD1	2.768
1GPO	L_LYS_54	NZ	H_ASP_101	OD2	3.525
1GPO	H_LYS_208	NZ	L_GLU_128	OE2	3.848
1GPO	M_LYS_54	NZ	I_ASP_101	OD1	3.704
1GPO	I_LYS_208	NZ	M_GLU_128	OE2	3.367
1HEZ	A_ARG_24	NH1	C_ASP_70	OD1	3.567
1HEZ	A_ARG_24	NH1	C_ASP_70	OD2	3.209
1HEZ	B_LYS_219	NZ	A_GLU_123	OE1	2.923
1HEZ	B_LYS_219	NZ	A_GLU_123	OE2	2.722
1HEZ	C_ARG_24	NH1	E_ASP_855	OD1	2.717
1HEZ	C_LYS_107	NZ	E_ASP_867	OD1	2.620
1HGD	A_LYS_27	NZ	B_GLU_97	OE1	2.787
1HGD	A_LYS_27	NZ	B_GLU_97	OE2	2.801
1HGD	A_ARG_109	NH2	B_GLU_67	OE1	3.474
1HGD	A_ARG_109	NH2	B_GLU_67	OE2	2.826
1HGD	A_LYS_238	NZ	F_GLU_72	OE1	2.925
1HGD	A_LYS_238	NZ	F_GLU_72	OE2	2.815
1HGD	A_ARG_269	NH1	B_GLU_67	OE1	2.758
1HGD	A_ARG_269	NH2	B_GLU_67	OE1	3.754
1HGD	A_LYS_299	NZ	B_GLU_69	OE2	2.769
1HGD	A_LYS_310	NZ	B_ASP_86	OD1	2.861
1HGD	A_LYS_310	NZ	B_ASP_90	OD1	2.569
1HGD	A_LYS_326	NZ	B_GLU_15	OE1	3.037
1HGD	A_LYS_326	NZ	B_GLU_15	OE2	2.743
1HGD	B_ARG_25	NH1	A_GLU_325	OE2	3.743
1HGD	B_ARG_25	NH2	A_GLU_325	OE2	3.016
1HGD	B_ARG_54	NH1	F_GLU_97	OE2	3.275
1HGD	B_ARG_54	NH2	F_GLU_97	OE2	2.774
1HGD	B_LYS_62	NZ	F_ASP_86	OD1	2.852
1HGD	B_LYS_62	NZ	F_ASP_86	OD2	2.612
1HGD	B_LYS_62	NZ	F_ASP_90	OD1	3.620
1HGD	B_LYS_62	NZ	F_ASP_90	OD2	2.727
1HGD	B_ARG_76	NH1	D_GLU_74	OE1	3.558
1HGD	B_ARG_76	NH1	D_GLU_74	OE2	2.838
1HGD	B_ARG_76	NH2	D_GLU_74	OE1	2.751

1HGD	B_ARG_76	NH2	D_GLU_74	OE2	3.529
1HGD	B_ARG_76	NH2	D_GLU_81	OE1	2.707
1HGD	B_ARG_76	NH2	D_GLU_81	OE2	3.498
1HGD	B_ARG_123	NH2	F_GLU_132	OE1	3.169
1HGD	B_ARG_124	NH2	F_GLU_132	OE1	3.011
1HGD	B_ARG_124	NH2	F_GLU_132	OE2	3.294
1HGD	B_ARG_127	NH1	F_GLU_131	OE1	2.471
1HGD	B_ARG_163	NH2	F_GLU_131	OE1	2.583
1HGD	B_ARG_163	NH2	F_GLU_131	OE2	2.596
1HGD	B_ARG_170	NH1	D_GLU_128	OE1	3.354
1HGD	B_ARG_170	NH1	D_GLU_128	OE2	3.628
1HGD	B_LYS_174	NZ	D_ASP_164	OD1	2.787
1HGD	B_LYS_174	NZ	D_ASP_164	OD2	2.517
1HGD	C_LYS_27	NZ	D_GLU_97	OE1	2.760
1HGD	C_LYS_27	NZ	D_GLU_97	OE2	2.799
1HGD	C_ARG_109	NH2	D_GLU_67	OE1	3.480
1HGD	C_ARG_109	NH2	D_GLU_67	OE2	2.867
1HGD	C_LYS_238	NZ	B_GLU_72	OE1	2.801
1HGD	C_LYS_238	NZ	B_GLU_72	OE2	2.746
1HGD	C_ARG_269	NH1	D_GLU_67	OE1	2.720
1HGD	C_ARG_269	NH2	D_GLU_67	OE1	3.733
1HGD	C_LYS_299	NZ	D_GLU_69	OE2	2.796
1HGD	C_LYS_310	NZ	D_ASP_86	OD1	2.878
1HGD	C_LYS_310	NZ	D_ASP_90	OD1	2.526
1HGD	C_LYS_326	NZ	D_GLU_15	OE1	2.784
1HGD	C_LYS_326	NZ	D_GLU_15	OE2	3.881
1HGD	D_ARG_54	NH1	B_GLU_97	OE2	3.293
1HGD	D_ARG_54	NH2	B_GLU_97	OE2	2.793
1HGD	D_LYS_62	NZ	B_ASP_86	OD1	2.884
1HGD	D_LYS_62	NZ	B_ASP_86	OD2	2.567
1HGD	D_LYS_62	NZ	B_ASP_90	OD1	3.576
1HGD	D_LYS_62	NZ	B_ASP_90	OD2	2.617
1HGD	D_ARG_76	NH1	F_GLU_74	OE1	3.379
1HGD	D_ARG_76	NH1	F_GLU_74	OE2	2.785
1HGD	D_ARG_76	NH2	F_GLU_74	OE1	2.687
1HGD	D_ARG_76	NH2	F_GLU_74	OE2	3.593
1HGD	D_ARG_76	NH2	F_GLU_81	OE1	2.649
1HGD	D_ARG_76	NH2	F_GLU_81	OE2	3.537
1HGD	D_ARG_123	NH2	B_GLU_132	OE1	3.120
1HGD	D_ARG_124	NH2	B_GLU_132	OE1	2.998
1HGD	D_ARG_124	NH2	B_GLU_132	OE2	3.261
1HGD	D_ARG_127	NH1	B_GLU_131	OE1	2.513
1HGD	D_ARG_163	NH2	B_GLU_131	OE1	2.583
1HGD	D_ARG_163	NH2	B_GLU_131	OE2	2.616
1HGD	D_ARG_170	NH1	F_GLU_128	OE1	3.487
1HGD	D_ARG_170	NH1	F_GLU_128	OE2	3.741
1HGD	D_LYS_174	NZ	F_ASP_164	OD1	2.806
1HGD	D_LYS_174	NZ	F_ASP_164	OD2	2.686
1HGD	E_LYS_27	NZ	F_GLU_97	OE1	2.794
1HGD	E_LYS_27	NZ	F_GLU_97	OE2	2.792
1HGD	E_ARG_109	NH2	F_GLU_67	OE1	3.474
1HGD	E_ARG_109	NH2	F_GLU_67	OE2	2.818
1HGD	E_LYS_238	NZ	D_GLU_72	OE1	2.872
1HGD	E_LYS_238	NZ	D_GLU_72	OE2	2.843
1HGD	E_ARG_269	NH1	F_GLU_67	OE1	2.732
1HGD	E_ARG_269	NH2	F_GLU_67	OE1	3.760
1HGD	E_LYS_299	NZ	F_GLU_69	OE2	2.767
1HGD	E_LYS_310	NZ	F_ASP_86	OD1	2.884

1HGD	E_LYS_310	NZ	F_ASP_90	OD1	2.533
1HGD	E_LYS_326	NZ	F_GLU_15	OE1	2.967
1HGD	E_LYS_326	NZ	F_GLU_15	OE2	3.203
1HGD	F_ARG_54	NH1	D_GLU_97	OE2	3.306
1HGD	F_ARG_54	NH2	D_GLU_97	OE2	2.719
1HGD	F_LYS_62	NZ	D_ASP_86	OD1	2.854
1HGD	F_LYS_62	NZ	D_ASP_86	OD2	2.590
1HGD	F_LYS_62	NZ	D_ASP_90	OD1	3.656
1HGD	F_LYS_62	NZ	D_ASP_90	OD2	2.713
1HGD	F_HIS_64	NE2	D_ASP_79	OD2	3.996
1HGD	F_ARG_76	NH1	B_GLU_74	OE1	3.419
1HGD	F_ARG_76	NH1	B_GLU_74	OE2	2.766
1HGD	F_ARG_76	NH2	B_GLU_74	OE1	2.711
1HGD	F_ARG_76	NH2	B_GLU_74	OE2	3.568
1HGD	F_ARG_76	NH2	B_GLU_81	OE1	2.637
1HGD	F_ARG_76	NH2	B_GLU_81	OE2	3.557
1HGD	F_ARG_123	NH2	D_GLU_132	OE1	3.156
1HGD	F_ARG_124	NH2	D_GLU_132	OE1	3.098
1HGD	F_ARG_124	NH2	D_GLU_132	OE2	3.292
1HGD	F_ARG_127	NH1	D_GLU_131	OE1	2.558
1HGD	F_ARG_163	NH2	D_GLU_131	OE1	2.583
1HGD	F_ARG_163	NH2	D_GLU_131	OE2	2.699
1HGD	F_ARG_170	NH1	B_GLU_128	OE1	3.398
1HGD	F_ARG_170	NH1	B_GLU_128	OE2	3.736
1HGD	F_LYS_174	NZ	B_ASP_164	OD1	2.545
1HGD	F_LYS_174	NZ	B_ASP_164	OD2	2.838
1HGE	A_LYS_27	NZ	B_GLU_97	OE1	2.881
1HGE	A_LYS_27	NZ	B_GLU_97	OE2	2.803
1HGE	A_ARG_109	NH2	B_GLU_67	OE1	3.666
1HGE	A_ARG_109	NH2	B_GLU_67	OE2	2.737
1HGE	A_LYS_238	NZ	F_GLU_72	OE1	2.915
1HGE	A_LYS_238	NZ	F_GLU_72	OE2	2.732
1HGE	A_ARG_269	NH1	B_GLU_67	OE1	2.727
1HGE	A_ARG_269	NH2	B_GLU_67	OE1	3.813
1HGE	A_LYS_299	NZ	B_GLU_69	OE2	2.765
1HGE	A_LYS_310	NZ	B_ASP_86	OD1	2.860
1HGE	A_LYS_310	NZ	B_ASP_90	OD1	2.586
1HGE	A_LYS_310	NZ	B_ASP_90	OD2	3.982
1HGE	A_LYS_326	NZ	B_GLU_15	OE1	3.112
1HGE	A_LYS_326	NZ	B_GLU_15	OE2	2.788
1HGE	B_ARG_25	NH1	A_GLU_325	OE2	3.901
1HGE	B_ARG_25	NH2	A_GLU_325	OE2	3.058
1HGE	B_ARG_54	NH1	F_GLU_97	OE2	3.352
1HGE	B_ARG_54	NH2	F_GLU_97	OE2	2.840
1HGE	B_LYS_62	NZ	F_ASP_86	OD1	2.965
1HGE	B_LYS_62	NZ	F_ASP_86	OD2	2.602
1HGE	B_LYS_62	NZ	F_ASP_90	OD1	3.562
1HGE	B_LYS_62	NZ	F_ASP_90	OD2	2.691
1HGE	B_ARG_76	NH1	D_GLU_74	OE1	3.487
1HGE	B_ARG_76	NH1	D_GLU_74	OE2	2.838
1HGE	B_ARG_76	NH2	D_GLU_74	OE1	2.788
1HGE	B_ARG_76	NH2	D_GLU_74	OE2	3.585
1HGE	B_ARG_76	NH2	D_GLU_81	OE1	2.698
1HGE	B_ARG_76	NH2	D_GLU_81	OE2	3.486
1HGE	B_ARG_123	NH2	F_GLU_132	OE1	3.159
1HGE	B_ARG_124	NH2	F_GLU_132	OE1	3.028
1HGE	B_ARG_124	NH2	F_GLU_132	OE2	3.444
1HGE	B_ARG_127	NH1	F_GLU_131	OE1	2.492

1HGE	B_ARG_163	NH2	F_GLU_131	OE1	2.609
1HGE	B_ARG_163	NH2	F_GLU_131	OE2	2.622
1HGE	B_ARG_170	NH1	D_GLU_128	OE1	3.351
1HGE	B_ARG_170	NH1	D_GLU_128	OE2	3.595
1HGE	B_LYS_174	NZ	D_ASP_164	OD1	2.542
1HGE	B_LYS_174	NZ	D_ASP_164	OD2	2.784
1HGE	C_LYS_27	NZ	D_GLU_97	OE1	2.850
1HGE	C_LYS_27	NZ	D_GLU_97	OE2	2.792
1HGE	C_ARG_109	NH2	D_GLU_67	OE1	3.673
1HGE	C_ARG_109	NH2	D_GLU_67	OE2	2.784
1HGE	C_LYS_238	NZ	B_GLU_72	OE1	2.779
1HGE	C_LYS_238	NZ	B_GLU_72	OE2	2.668
1HGE	C_ARG_269	NH1	D_GLU_67	OE1	2.720
1HGE	C_ARG_269	NH2	D_GLU_67	OE1	3.811
1HGE	C_LYS_299	NZ	D_GLU_69	OE2	2.808
1HGE	C_LYS_310	NZ	D_ASP_86	OD1	2.890
1HGE	C_LYS_310	NZ	D_ASP_90	OD1	2.566
1HGE	C_LYS_310	NZ	D_ASP_90	OD2	3.955
1HGE	C_LYS_326	NZ	D_GLU_15	OE1	2.739
1HGE	C_LYS_326	NZ	D_GLU_15	OE2	3.731
1HGE	D_ARG_54	NH1	B_GLU_97	OE2	3.383
1HGE	D_ARG_54	NH2	B_GLU_97	OE2	2.866
1HGE	D_LYS_62	NZ	B_ASP_86	OD1	3.023
1HGE	D_LYS_62	NZ	B_ASP_86	OD2	2.550
1HGE	D_LYS_62	NZ	B_ASP_90	OD1	3.565
1HGE	D_LYS_62	NZ	B_ASP_90	OD2	2.627
1HGE	D_ARG_76	NH1	F_GLU_74	OE1	3.355
1HGE	D_ARG_76	NH1	F_GLU_74	OE2	2.783
1HGE	D_ARG_76	NH2	F_GLU_74	OE1	2.745
1HGE	D_ARG_76	NH2	F_GLU_74	OE2	3.636
1HGE	D_ARG_76	NH2	F_GLU_81	OE1	2.634
1HGE	D_ARG_76	NH2	F_GLU_81	OE2	3.497
1HGE	D_ARG_123	NH2	B_GLU_132	OE1	3.118
1HGE	D_ARG_124	NH2	B_GLU_132	OE1	3.002
1HGE	D_ARG_124	NH2	B_GLU_132	OE2	3.417
1HGE	D_ARG_127	NH1	B_GLU_131	OE1	2.524
1HGE	D_ARG_163	NH2	B_GLU_131	OE1	2.587
1HGE	D_ARG_163	NH2	B_GLU_131	OE2	2.600
1HGE	D_ARG_170	NH1	F_GLU_128	OE1	3.477
1HGE	D_ARG_170	NH1	F_GLU_128	OE2	3.701
1HGE	D_LYS_174	NZ	F_ASP_164	OD1	2.678
1HGE	D_LYS_174	NZ	F_ASP_164	OD2	2.785
1HGE	E_LYS_27	NZ	F_GLU_97	OE1	2.844
1HGE	E_LYS_27	NZ	F_GLU_97	OE2	2.791
1HGE	E_ARG_109	NH2	F_GLU_67	OE1	3.658
1HGE	E_ARG_109	NH2	F_GLU_67	OE2	2.776
1HGE	E_LYS_238	NZ	D_GLU_72	OE1	2.851
1HGE	E_LYS_238	NZ	D_GLU_72	OE2	2.740
1HGE	E_ARG_269	NH1	F_GLU_67	OE1	2.696
1HGE	E_ARG_269	NH2	F_GLU_67	OE1	3.784
1HGE	E_LYS_299	NZ	F_GLU_69	OE2	2.768
1HGE	E_LYS_310	NZ	F_ASP_86	OD1	2.863
1HGE	E_LYS_310	NZ	F_ASP_90	OD1	2.577
1HGE	E_LYS_310	NZ	F_ASP_90	OD2	3.952
1HGE	E_LYS_326	NZ	F_GLU_15	OE1	2.987
1HGE	E_LYS_326	NZ	F_GLU_15	OE2	3.095
1HGE	F_ARG_54	NH1	D_GLU_97	OE2	3.384
1HGE	F_ARG_54	NH2	D_GLU_97	OE2	2.800

1HGE	F_LYS_62	NZ	D_ASP_86	OD1	2.945
1HGE	F_LYS_62	NZ	D_ASP_86	OD2	2.535
1HGE	F_LYS_62	NZ	D_ASP_90	OD1	3.592
1HGE	F_LYS_62	NZ	D_ASP_90	OD2	2.671
1HGE	F_ARG_76	NH1	B_GLU_74	OE1	3.326
1HGE	F_ARG_76	NH1	B_GLU_74	OE2	2.732
1HGE	F_ARG_76	NH2	B_GLU_74	OE1	2.705
1HGE	F_ARG_76	NH2	B_GLU_74	OE2	3.590
1HGE	F_ARG_76	NH2	B_GLU_81	OE1	2.650
1HGE	F_ARG_76	NH2	B_GLU_81	OE2	3.592
1HGE	F_ARG_123	NH2	D_GLU_132	OE1	3.161
1HGE	F_ARG_124	NH2	D_GLU_132	OE1	3.085
1HGE	F_ARG_124	NH2	D_GLU_132	OE2	3.468
1HGE	F_ARG_127	NH1	D_GLU_131	OE1	2.578
1HGE	F_ARG_163	NH2	D_GLU_131	OE1	2.628
1HGE	F_ARG_163	NH2	D_GLU_131	OE2	2.698
1HGE	F_ARG_170	NH1	B_GLU_128	OE1	3.389
1HGE	F_ARG_170	NH1	B_GLU_128	OE2	3.679
1HGE	F_LYS_174	NZ	B_ASP_164	OD1	2.537
1HGE	F_LYS_174	NZ	B_ASP_164	OD2	2.796
1HGF	A_LYS_27	NZ	B_GLU_97	OE1	2.809
1HGF	A_LYS_27	NZ	B_GLU_97	OE2	2.791
1HGF	A_ARG_109	NH2	B_GLU_67	OE1	3.699
1HGF	A_ARG_109	NH2	B_GLU_67	OE2	2.917
1HGF	A_LYS_238	NZ	F_GLU_72	OE1	2.852
1HGF	A_LYS_238	NZ	F_GLU_72	OE2	2.778
1HGF	A_ARG_269	NH1	B_GLU_67	OE1	2.939
1HGF	A_LYS_299	NZ	B_GLU_69	OE2	3.681
1HGF	A_LYS_310	NZ	B_ASP_86	OD1	2.820
1HGF	A_LYS_310	NZ	B_ASP_90	OD1	2.555
1HGF	A_LYS_310	NZ	B_ASP_90	OD2	3.978
1HGF	A_LYS_326	NZ	B_GLU_15	OE1	3.851
1HGF	A_LYS_326	NZ	B_GLU_15	OE2	3.863
1HGF	B_ARG_25	NH1	A_GLU_325	OE2	3.563
1HGF	B_ARG_25	NH2	A_GLU_325	OE2	2.989
1HGF	B_ARG_54	NH1	F_GLU_97	OE2	3.282
1HGF	B_ARG_54	NH2	F_GLU_97	OE2	2.831
1HGF	B_LYS_62	NZ	F_ASP_86	OD1	3.116
1HGF	B_LYS_62	NZ	F_ASP_86	OD2	2.708
1HGF	B_LYS_62	NZ	F_ASP_90	OD1	3.733
1HGF	B_LYS_62	NZ	F_ASP_90	OD2	2.767
1HGF	B_ARG_76	NH1	D_GLU_74	OE1	2.859
1HGF	B_ARG_76	NH1	D_GLU_74	OE2	3.561
1HGF	B_ARG_76	NH2	D_GLU_74	OE1	3.524
1HGF	B_ARG_76	NH2	D_GLU_74	OE2	2.746
1HGF	B_ARG_76	NH2	D_GLU_81	OE1	2.726
1HGF	B_ARG_76	NH2	D_GLU_81	OE2	3.662
1HGF	B_ARG_123	NH2	F_GLU_132	OE1	3.495
1HGF	B_ARG_124	NH2	F_GLU_132	OE1	3.111
1HGF	B_ARG_124	NH2	F_GLU_132	OE2	3.495
1HGF	B_ARG_127	NH1	F_GLU_131	OE1	2.468
1HGF	B_ARG_163	NH2	F_GLU_131	OE1	2.740
1HGF	B_ARG_163	NH2	F_GLU_131	OE2	2.533
1HGF	B_ARG_170	NH1	D_GLU_128	OE1	3.455
1HGF	B_ARG_170	NH1	D_GLU_128	OE2	3.294
1HGF	B_LYS_174	NZ	D_ASP_164	OD2	3.813
1HGF	C_LYS_27	NZ	D_GLU_97	OE1	2.824
1HGF	C_LYS_27	NZ	D_GLU_97	OE2	2.808

1HGF	C_ARG_109	NH2	D_GLU_67	OE1	3.698
1HGF	C_ARG_109	NH2	D_GLU_67	OE2	2.914
1HGF	C_LYS_238	NZ	B_GLU_72	OE1	2.746
1HGF	C_LYS_238	NZ	B_GLU_72	OE2	2.727
1HGF	C_ARG_269	NH1	D_GLU_67	OE1	2.900
1HGF	C_LYS_299	NZ	D_GLU_69	OE2	3.732
1HGF	C_LYS_310	NZ	D_ASP_86	OD1	2.839
1HGF	C_LYS_310	NZ	D_ASP_90	OD1	2.507
1HGF	C_LYS_310	NZ	D_ASP_90	OD2	3.941
1HGF	C_LYS_326	NZ	D_GLU_15	OE1	3.713
1HGF	D_ARG_54	NH1	B_GLU_97	OE2	3.314
1HGF	D_ARG_54	NH2	B_GLU_97	OE2	2.840
1HGF	D_LYS_62	NZ	B_ASP_86	OD1	3.122
1HGF	D_LYS_62	NZ	B_ASP_86	OD2	2.686
1HGF	D_LYS_62	NZ	B_ASP_90	OD1	3.703
1HGF	D_LYS_62	NZ	B_ASP_90	OD2	2.682
1HGF	D_ARG_76	NH1	F_GLU_74	OE1	2.790
1HGF	D_ARG_76	NH1	F_GLU_74	OE2	3.379
1HGF	D_ARG_76	NH2	F_GLU_74	OE1	3.594
1HGF	D_ARG_76	NH2	F_GLU_74	OE2	2.697
1HGF	D_ARG_76	NH2	F_GLU_81	OE1	2.644
1HGF	D_ARG_76	NH2	F_GLU_81	OE2	3.691
1HGF	D_ARG_123	NH2	B_GLU_132	OE1	3.407
1HGF	D_ARG_124	NH2	B_GLU_132	OE1	3.100
1HGF	D_ARG_124	NH2	B_GLU_132	OE2	3.442
1HGF	D_ARG_127	NH1	B_GLU_131	OE1	2.516
1HGF	D_ARG_163	NH2	B_GLU_131	OE1	2.704
1HGF	D_ARG_163	NH2	B_GLU_131	OE2	2.556
1HGF	D_ARG_170	NH1	F_GLU_128	OE1	3.604
1HGF	D_ARG_170	NH1	F_GLU_128	OE2	3.428
1HGF	E_LYS_27	NZ	F_GLU_97	OE1	2.793
1HGF	E_LYS_27	NZ	F_GLU_97	OE2	2.754
1HGF	E_ARG_109	NH2	F_GLU_67	OE1	3.694
1HGF	E_ARG_109	NH2	F_GLU_67	OE2	2.878
1HGF	E_LYS_238	NZ	D_GLU_72	OE1	2.831
1HGF	E_LYS_238	NZ	D_GLU_72	OE2	2.834
1HGF	E_ARG_269	NH1	F_GLU_67	OE1	2.906
1HGF	E_LYS_299	NZ	F_GLU_69	OE2	3.655
1HGF	E_LYS_310	NZ	F_ASP_86	OD1	2.832
1HGF	E_LYS_310	NZ	F_ASP_90	OD1	2.514
1HGF	E_LYS_310	NZ	F_ASP_90	OD2	3.973
1HGF	E_LYS_326	NZ	F_GLU_15	OE1	3.652
1HGF	E_LYS_326	NZ	F_GLU_15	OE2	3.771
1HGF	F_ARG_54	NH1	D_GLU_97	OE2	3.368
1HGF	F_ARG_54	NH2	D_GLU_97	OE2	2.791
1HGF	F_LYS_62	NZ	D_ASP_86	OD1	3.076
1HGF	F_LYS_62	NZ	D_ASP_86	OD2	2.672
1HGF	F_LYS_62	NZ	D_ASP_90	OD1	3.773
1HGF	F_LYS_62	NZ	D_ASP_90	OD2	2.752
1HGF	F_ARG_76	NH1	B_GLU_74	OE1	2.779
1HGF	F_ARG_76	NH1	B_GLU_74	OE2	3.420
1HGF	F_ARG_76	NH2	B_GLU_74	OE1	3.542
1HGF	F_ARG_76	NH2	B_GLU_74	OE2	2.707
1HGF	F_ARG_76	NH2	B_GLU_81	OE1	2.689
1HGF	F_ARG_76	NH2	B_GLU_81	OE2	3.716
1HGF	F_ARG_123	NH2	D_GLU_132	OE1	3.469
1HGF	F_ARG_124	NH2	D_GLU_132	OE1	3.198
1HGF	F_ARG_124	NH2	D_GLU_132	OE2	3.522

1HGF	F_ARG_127	NH1	D_GLU_131	OE1	2.568
1HGF	F_ARG_163	NH2	D_GLU_131	OE1	2.689
1HGF	F_ARG_163	NH2	D_GLU_131	OE2	2.644
1HGF	F_ARG_170	NH1	B_GLU_128	OE1	3.432
1HGF	F_ARG_170	NH1	B_GLU_128	OE2	3.366
1HGF	F_LYS_174	NZ	B_ASP_164	OD2	3.837
1HGG	A_LYS_27	NZ	B_GLU_97	OE1	2.679
1HGG	A_LYS_27	NZ	B_GLU_97	OE2	2.904
1HGG	A_ARG_109	NH2	B_GLU_67	OE1	3.854
1HGG	A_ARG_109	NH2	B_GLU_67	OE2	2.838
1HGG	A_LYS_238	NZ	F_GLU_72	OE1	2.931
1HGG	A_LYS_238	NZ	F_GLU_72	OE2	2.744
1HGG	A_ARG_269	NH1	B_GLU_67	OE1	2.694
1HGG	A_ARG_269	NH2	B_GLU_67	OE1	3.814
1HGG	A_LYS_299	NZ	B_GLU_69	OE2	2.915
1HGG	A_LYS_310	NZ	B_ASP_86	OD1	2.852
1HGG	A_LYS_310	NZ	B_ASP_90	OD1	2.700
1HGG	A_LYS_310	NZ	B_ASP_90	OD2	3.923
1HGG	A_LYS_326	NZ	B_GLU_15	OE1	3.039
1HGG	A_LYS_326	NZ	B_GLU_15	OE2	2.830
1HGG	B_ARG_25	NH1	A_GLU_325	OE2	3.770
1HGG	B_ARG_25	NH2	A_GLU_325	OE2	2.944
1HGG	B_ARG_54	NH1	F_GLU_97	OE2	3.410
1HGG	B_ARG_54	NH2	F_GLU_97	OE2	2.750
1HGG	B_LYS_62	NZ	F_ASP_86	OD1	2.889
1HGG	B_LYS_62	NZ	F_ASP_86	OD2	2.639
1HGG	B_LYS_62	NZ	F_ASP_90	OD1	3.716
1HGG	B_LYS_62	NZ	F_ASP_90	OD2	2.650
1HGG	B_ARG_76	NH1	D_GLU_74	OE1	2.882
1HGG	B_ARG_76	NH1	D_GLU_74	OE2	3.580
1HGG	B_ARG_76	NH2	D_GLU_74	OE1	3.459
1HGG	B_ARG_76	NH2	D_GLU_74	OE2	2.820
1HGG	B_ARG_76	NH2	D_GLU_81	OE1	2.731
1HGG	B_ARG_76	NH2	D_GLU_81	OE2	3.473
1HGG	B_ARG_123	NH2	F_GLU_132	OE1	2.827
1HGG	B_ARG_124	NH2	F_GLU_132	OE1	3.221
1HGG	B_ARG_124	NH2	F_GLU_132	OE2	3.297
1HGG	B_ARG_127	NH1	F_GLU_131	OE1	2.465
1HGG	B_ARG_163	NH2	F_GLU_131	OE1	2.594
1HGG	B_ARG_163	NH2	F_GLU_131	OE2	2.562
1HGG	B_ARG_170	NH1	D_GLU_128	OE1	3.236
1HGG	B_ARG_170	NH1	D_GLU_128	OE2	3.289
1HGG	B_LYS_174	NZ	D_ASP_164	OD1	2.736
1HGG	B_LYS_174	NZ	D_ASP_164	OD2	2.575
1HGG	C_LYS_27	NZ	D_GLU_97	OE1	2.683
1HGG	C_LYS_27	NZ	D_GLU_97	OE2	2.941
1HGG	C_ARG_109	NH2	D_GLU_67	OE1	3.869
1HGG	C_ARG_109	NH2	D_GLU_67	OE2	2.853
1HGG	C_LYS_238	NZ	B_GLU_72	OE1	2.830
1HGG	C_LYS_238	NZ	B_GLU_72	OE2	2.699
1HGG	C_ARG_269	NH1	D_GLU_67	OE1	2.688
1HGG	C_ARG_269	NH2	D_GLU_67	OE1	3.820
1HGG	C_LYS_299	NZ	D_GLU_69	OE2	2.932
1HGG	C_LYS_310	NZ	D_ASP_86	OD1	2.859
1HGG	C_LYS_310	NZ	D_ASP_90	OD1	2.651
1HGG	C_LYS_310	NZ	D_ASP_90	OD2	3.858
1HGG	C_LYS_326	NZ	D_GLU_15	OE1	2.591
1HGG	C_LYS_326	NZ	D_GLU_15	OE2	3.450

1HGG	D_ARG.54	NH1	B_GLU_97	OE2	3.442
1HGG	D_ARG.54	NH2	B_GLU_97	OE2	2.764
1HGG	D_LYS.62	NZ	B_ASP_86	OD1	2.924
1HGG	D_LYS.62	NZ	B_ASP_86	OD2	2.567
1HGG	D_LYS.62	NZ	B_ASP_90	OD1	3.695
1HGG	D_LYS.62	NZ	B_ASP_90	OD2	2.575
1HGG	D_ARG.76	NH1	F_GLU_74	OE1	2.783
1HGG	D_ARG.76	NH1	F_GLU_74	OE2	3.379
1HGG	D_ARG.76	NH2	F_GLU_74	OE1	3.480
1HGG	D_ARG.76	NH2	F_GLU_74	OE2	2.737
1HGG	D_ARG.76	NH2	F_GLU_81	OE1	2.674
1HGG	D_ARG.76	NH2	F_GLU_81	OE2	3.521
1HGG	D_ARG.123	NH2	B_GLU_132	OE1	2.793
1HGG	D_ARG.124	NH2	B_GLU_132	OE1	3.241
1HGG	D_ARG.124	NH2	B_GLU_132	OE2	3.297
1HGG	D_ARG.127	NH1	B_GLU_131	OE1	2.475
1HGG	D_ARG.163	NH2	B_GLU_131	OE1	2.580
1HGG	D_ARG.163	NH2	B_GLU_131	OE2	2.598
1HGG	D_ARG.170	NH1	F_GLU_128	OE1	3.365
1HGG	D_ARG.170	NH1	F_GLU_128	OE2	3.390
1HGG	D_LYS.174	NZ	F_ASP_164	OD1	2.763
1HGG	D_LYS.174	NZ	F_ASP_164	OD2	2.711
1HGG	E_LYS.27	NZ	F_GLU_97	OE1	2.689
1HGG	E_LYS.27	NZ	F_GLU_97	OE2	2.909
1HGG	E_ARG.109	NH2	F_GLU_67	OE1	3.891
1HGG	E_ARG.109	NH2	F_GLU_67	OE2	2.876
1HGG	E_LYS.238	NZ	D_GLU_72	OE1	2.893
1HGG	E_LYS.238	NZ	D_GLU_72	OE2	2.782
1HGG	E_ARG.269	NH1	F_GLU_67	OE1	2.691
1HGG	E_ARG.269	NH2	F_GLU_67	OE1	3.830
1HGG	E_LYS.299	NZ	F_GLU_69	OE2	2.920
1HGG	E_LYS.310	NZ	F_ASP_86	OD1	2.871
1HGG	E_LYS.310	NZ	F_ASP_90	OD1	2.639
1HGG	E_LYS.310	NZ	F_ASP_90	OD2	3.900
1HGG	E_LYS.326	NZ	F_GLU_15	OE1	2.975
1HGG	E_LYS.326	NZ	F_GLU_15	OE2	3.000
1HGG	F_ARG.54	NH1	D_GLU_97	OE2	3.483
1HGG	F_ARG.54	NH2	D_GLU_97	OE2	2.727
1HGG	F_LYS.62	NZ	D_ASP_86	OD1	2.904
1HGG	F_LYS.62	NZ	D_ASP_86	OD2	2.582
1HGG	F_LYS.62	NZ	D_ASP_90	OD1	3.752
1HGG	F_LYS.62	NZ	D_ASP_90	OD2	2.595
1HGG	F_ARG.76	NH1	B_GLU_74	OE1	2.750
1HGG	F_ARG.76	NH1	B_GLU_74	OE2	3.432
1HGG	F_ARG.76	NH2	B_GLU_74	OE1	3.456
1HGG	F_ARG.76	NH2	B_GLU_74	OE2	2.786
1HGG	F_ARG.76	NH2	B_GLU_81	OE1	2.674
1HGG	F_ARG.76	NH2	B_GLU_81	OE2	3.545
1HGG	F_ARG.123	NH2	D_GLU_132	OE1	2.843
1HGG	F_ARG.124	NH2	D_GLU_132	OE1	3.317
1HGG	F_ARG.124	NH2	D_GLU_132	OE2	3.342
1HGG	F_ARG.127	NH1	D_GLU_131	OE1	2.523
1HGG	F_ARG.163	NH2	D_GLU_131	OE1	2.589
1HGG	F_ARG.163	NH2	D_GLU_131	OE2	2.640
1HGG	F_ARG.170	NH1	B_GLU_128	OE1	3.237
1HGG	F_ARG.170	NH1	B_GLU_128	OE2	3.354
1HGG	F_LYS.174	NZ	B_ASP_164	OD1	2.757
1HGG	F_LYS.174	NZ	B_ASP_164	OD2	2.547

1HGH	A_LYS_27	NZ	B_GLU_97	OE1	2.856
1HGH	A_LYS_27	NZ	B_GLU_97	OE2	2.781
1HGH	A_ARG_109	NH2	B_GLU_67	OE1	3.697
1HGH	A_ARG_109	NH2	B_GLU_67	OE2	2.864
1HGH	A_LYS_238	NZ	F_GLU_72	OE1	2.921
1HGH	A_LYS_238	NZ	F_GLU_72	OE2	2.736
1HGH	A_ARG_269	NH1	B_GLU_67	OE1	2.720
1HGH	A_ARG_269	NH2	B_GLU_67	OE1	3.718
1HGH	A_LYS_299	NZ	B_GLU_69	OE2	2.918
1HGH	A_LYS_310	NZ	B_ASP_86	OD1	2.712
1HGH	A_LYS_310	NZ	B_ASP_90	OD1	2.578
1HGH	A_LYS_310	NZ	B_ASP_90	OD2	3.975
1HGH	A_LYS_326	NZ	B_GLU_15	OE1	3.092
1HGH	A_LYS_326	NZ	B_GLU_15	OE2	2.707
1HGH	B_ARG_25	NH1	A_GLU_325	OE2	3.971
1HGH	B_ARG_25	NH2	A_GLU_325	OE2	3.017
1HGH	B_ARG_54	NH1	F_GLU_97	OE2	3.285
1HGH	B_ARG_54	NH2	F_GLU_97	OE2	2.823
1HGH	B_LYS_62	NZ	F_ASP_86	OD1	3.064
1HGH	B_LYS_62	NZ	F_ASP_86	OD2	2.661
1HGH	B_LYS_62	NZ	F_ASP_90	OD1	3.547
1HGH	B_LYS_62	NZ	F_ASP_90	OD2	2.683
1HGH	B_ARG_76	NH1	D_GLU_74	OE1	3.707
1HGH	B_ARG_76	NH1	D_GLU_74	OE2	2.912
1HGH	B_ARG_76	NH2	D_GLU_74	OE1	2.889
1HGH	B_ARG_76	NH2	D_GLU_74	OE2	3.526
1HGH	B_ARG_76	NH2	D_GLU_81	OE1	2.765
1HGH	B_ARG_76	NH2	D_GLU_81	OE2	3.411
1HGH	B_ARG_123	NH2	F_GLU_132	OE1	3.134
1HGH	B_ARG_124	NH2	F_GLU_132	OE1	3.005
1HGH	B_ARG_124	NH2	F_GLU_132	OE2	3.302
1HGH	B_ARG_127	NH1	F_GLU_131	OE1	2.524
1HGH	B_ARG_163	NH2	F_GLU_131	OE1	2.607
1HGH	B_ARG_163	NH2	F_GLU_131	OE2	2.538
1HGH	B_ARG_170	NH1	D_GLU_128	OE1	3.253
1HGH	B_ARG_170	NH1	D_GLU_128	OE2	3.577
1HGH	B_LYS_174	NZ	D_ASP_164	OD1	2.767
1HGH	B_LYS_174	NZ	D_ASP_164	OD2	2.573
1HGH	C_LYS_27	NZ	D_GLU_97	OE1	2.897
1HGH	C_LYS_27	NZ	D_GLU_97	OE2	2.815
1HGH	C_ARG_109	NH2	D_GLU_67	OE1	3.686
1HGH	C_ARG_109	NH2	D_GLU_67	OE2	2.856
1HGH	C_LYS_238	NZ	B_GLU_72	OE1	2.713
1HGH	C_LYS_238	NZ	B_GLU_72	OE2	2.597
1HGH	C_ARG_269	NH1	D_GLU_67	OE1	2.732
1HGH	C_ARG_269	NH2	D_GLU_67	OE1	3.725
1HGH	C_LYS_299	NZ	D_GLU_69	OE2	2.939
1HGH	C_LYS_310	NZ	D_ASP_86	OD1	2.734
1HGH	C_LYS_310	NZ	D_ASP_90	OD1	2.551
1HGH	C_LYS_310	NZ	D_ASP_90	OD2	3.913
1HGH	C_LYS_326	NZ	D_GLU_15	OE1	2.774
1HGH	C_LYS_326	NZ	D_GLU_15	OE2	3.676
1HGH	D_ARG_54	NH1	B_GLU_97	OE2	3.277
1HGH	D_ARG_54	NH2	B_GLU_97	OE2	2.797
1HGH	D_LYS_62	NZ	B_ASP_86	OD1	3.011
1HGH	D_LYS_62	NZ	B_ASP_86	OD2	2.510
1HGH	D_LYS_62	NZ	B_ASP_90	OD1	3.543
1HGH	D_LYS_62	NZ	B_ASP_90	OD2	2.589

1HGH	D_ARG_76	NH1	F_GLU_74	OE1	3.430
1HGH	D_ARG_76	NH1	F_GLU_74	OE2	2.765
1HGH	D_ARG_76	NH2	F_GLU_74	OE1	2.747
1HGH	D_ARG_76	NH2	F_GLU_74	OE2	3.553
1HGH	D_ARG_76	NH2	F_GLU_81	OE1	2.698
1HGH	D_ARG_76	NH2	F_GLU_81	OE2	3.487
1HGH	D_ARG_123	NH2	B_GLU_132	OE1	3.141
1HGH	D_ARG_124	NH2	B_GLU_132	OE1	3.050
1HGH	D_ARG_124	NH2	B_GLU_132	OE2	3.354
1HGH	D_ARG_127	NH1	B_GLU_131	OE1	2.536
1HGH	D_ARG_163	NH2	B_GLU_131	OE1	2.609
1HGH	D_ARG_163	NH2	B_GLU_131	OE2	2.570
1HGH	D_ARG_170	NH1	F_GLU_128	OE1	3.352
1HGH	D_ARG_170	NH1	F_GLU_128	OE2	3.641
1HGH	D_LYS_174	NZ	F_ASP_164	OD1	2.863
1HGH	D_LYS_174	NZ	F_ASP_164	OD2	2.724
1HGH	E_LYS_27	NZ	F_GLU_97	OE1	2.917
1HGH	E_LYS_27	NZ	F_GLU_97	OE2	2.767
1HGH	E_ARG_109	NH2	F_GLU_67	OE1	3.698
1HGH	E_ARG_109	NH2	F_GLU_67	OE2	2.878
1HGH	E_LYS_238	NZ	D_GLU_72	OE1	2.870
1HGH	E_LYS_238	NZ	D_GLU_72	OE2	2.766
1HGH	E_ARG_269	NH1	F_GLU_67	OE1	2.705
1HGH	E_ARG_269	NH2	F_GLU_67	OE1	3.715
1HGH	E_LYS_299	NZ	F_GLU_69	OE2	2.896
1HGH	E_LYS_310	NZ	F_ASP_86	OD1	2.740
1HGH	E_LYS_310	NZ	F_ASP_90	OD1	2.571
1HGH	E_LYS_310	NZ	F_ASP_90	OD2	3.948
1HGH	E_LYS_326	NZ	F_GLU_15	OE1	2.900
1HGH	E_LYS_326	NZ	F_GLU_15	OE2	3.072
1HGH	F_ARG_54	NH1	D_GLU_97	OE2	3.293
1HGH	F_ARG_54	NH2	D_GLU_97	OE2	2.723
1HGH	F_LYS_62	NZ	D_ASP_86	OD1	3.012
1HGH	F_LYS_62	NZ	D_ASP_86	OD2	2.546
1HGH	F_LYS_62	NZ	D_ASP_90	OD1	3.612
1HGH	F_LYS_62	NZ	D_ASP_90	OD2	2.682
1HGH	F_ARG_76	NH1	B_GLU_74	OE1	3.509
1HGH	F_ARG_76	NH1	B_GLU_74	OE2	2.732
1HGH	F_ARG_76	NH2	B_GLU_74	OE1	2.780
1HGH	F_ARG_76	NH2	B_GLU_74	OE2	3.488
1HGH	F_ARG_76	NH2	B_GLU_81	OE1	2.709
1HGH	F_ARG_76	NH2	B_GLU_81	OE2	3.513
1HGH	F_ARG_123	NH2	D_GLU_132	OE1	3.148
1HGH	F_ARG_124	NH2	D_GLU_132	OE1	3.099
1HGH	F_ARG_124	NH2	D_GLU_132	OE2	3.356
1HGH	F_ARG_127	NH1	D_GLU_131	OE1	2.577
1HGH	F_ARG_163	NH2	D_GLU_131	OE1	2.600
1HGH	F_ARG_163	NH2	D_GLU_131	OE2	2.611
1HGH	F_ARG_170	NH1	B_GLU_128	OE1	3.225
1HGH	F_ARG_170	NH1	B_GLU_128	OE2	3.576
1HGH	F_LYS_174	NZ	B_ASP_164	OD1	2.776
1HGH	F_LYS_174	NZ	B_ASP_164	OD2	2.495
1HGI	A_LYS_27	NZ	B_GLU_97	OE1	2.940
1HGI	A_LYS_27	NZ	B_GLU_97	OE2	2.900
1HGI	A_ARG_109	NH2	B_GLU_67	OE1	3.638
1HGI	A_ARG_109	NH2	B_GLU_67	OE2	2.797
1HGI	A_LYS_238	NZ	F_GLU_72	OE1	2.849
1HGI	A_LYS_238	NZ	F_GLU_72	OE2	2.839

1HGI	A_ARG_269	NH1	B_GLU_67	OE1	2.748
1HGI	A_ARG_269	NH2	B_GLU_67	OE1	3.823
1HGI	A_LYS_299	NZ	B_GLU_69	OE2	2.728
1HGI	A_LYS_310	NZ	B_ASP_86	OD1	2.759
1HGI	A_LYS_310	NZ	B_ASP_90	OD1	2.527
1HGI	A_LYS_326	NZ	B_GLU_15	OE1	3.374
1HGI	A_LYS_326	NZ	B_GLU_15	OE2	2.794
1HGI	B_ARG_25	NH1	A_GLU_325	OE2	3.734
1HGI	B_ARG_25	NH2	A_GLU_325	OE2	2.929
1HGI	B_ARG_54	NH1	F_GLU_97	OE2	3.222
1HGI	B_ARG_54	NH2	F_GLU_97	OE2	2.806
1HGI	B_LYS_62	NZ	F_ASP_86	OD1	2.942
1HGI	B_LYS_62	NZ	F_ASP_86	OD2	2.668
1HGI	B_LYS_62	NZ	F_ASP_90	OD1	3.332
1HGI	B_LYS_62	NZ	F_ASP_90	OD2	2.667
1HGI	B_ARG_76	NH1	D_GLU_74	OE1	3.625
1HGI	B_ARG_76	NH1	D_GLU_74	OE2	2.918
1HGI	B_ARG_76	NH2	D_GLU_74	OE1	2.861
1HGI	B_ARG_76	NH2	D_GLU_74	OE2	3.621
1HGI	B_ARG_76	NH2	D_GLU_81	OE1	2.708
1HGI	B_ARG_76	NH2	D_GLU_81	OE2	3.474
1HGI	B_ARG_123	NH2	F_GLU_132	OE1	3.105
1HGI	B_ARG_124	NH2	F_GLU_132	OE1	3.081
1HGI	B_ARG_124	NH2	F_GLU_132	OE2	3.356
1HGI	B_ARG_127	NH1	F_GLU_131	OE1	2.493
1HGI	B_ARG_163	NH2	F_GLU_131	OE1	2.586
1HGI	B_ARG_163	NH2	F_GLU_131	OE2	2.598
1HGI	B_ARG_170	NH1	D_GLU_128	OE1	3.640
1HGI	B_ARG_170	NH1	D_GLU_128	OE2	3.301
1HGI	B_LYS_174	NZ	D_ASP_164	OD1	2.745
1HGI	B_LYS_174	NZ	D_ASP_164	OD2	2.560
1HGI	C_LYS_27	NZ	D_GLU_97	OE1	2.951
1HGI	C_LYS_27	NZ	D_GLU_97	OE2	2.876
1HGI	C_ARG_109	NH2	D_GLU_67	OE1	3.637
1HGI	C_ARG_109	NH2	D_GLU_67	OE2	2.819
1HGI	C_LYS_238	NZ	B_GLU_72	OE1	2.671
1HGI	C_LYS_238	NZ	B_GLU_72	OE2	2.721
1HGI	C_ARG_269	NH1	D_GLU_67	OE1	2.753
1HGI	C_ARG_269	NH2	D_GLU_67	OE1	3.850
1HGI	C_LYS_299	NZ	D_GLU_69	OE2	2.739
1HGI	C_LYS_310	NZ	D_ASP_86	OD1	2.772
1HGI	C_LYS_310	NZ	D_ASP_90	OD1	2.525
1HGI	C_LYS_326	NZ	D_GLU_15	OE1	2.825
1HGI	C_LYS_326	NZ	D_GLU_15	OE2	3.570
1HGI	D_ARG_54	NH1	B_GLU_97	OE2	3.254
1HGI	D_ARG_54	NH2	B_GLU_97	OE2	2.808
1HGI	D_LYS_62	NZ	B_ASP_86	OD1	2.962
1HGI	D_LYS_62	NZ	B_ASP_86	OD2	2.570
1HGI	D_LYS_62	NZ	B_ASP_90	OD1	3.335
1HGI	D_LYS_62	NZ	B_ASP_90	OD2	2.541
1HGI	D_ARG_76	NH1	F_GLU_74	OE1	3.375
1HGI	D_ARG_76	NH1	F_GLU_74	OE2	2.776
1HGI	D_ARG_76	NH2	F_GLU_74	OE1	2.760
1HGI	D_ARG_76	NH2	F_GLU_74	OE2	3.657
1HGI	D_ARG_76	NH2	F_GLU_81	OE1	2.608
1HGI	D_ARG_76	NH2	F_GLU_81	OE2	3.506
1HGI	D_ARG_123	NH2	B_GLU_132	OE1	3.093
1HGI	D_ARG_124	NH2	B_GLU_132	OE1	3.096

1HGI	D_ARG_124	NH2	B_GLU_132	OE2	3.377
1HGI	D_ARG_127	NH1	B_GLU_131	OE1	2.513
1HGI	D_ARG_163	NH2	B_GLU_131	OE1	2.590
1HGI	D_ARG_163	NH2	B_GLU_131	OE2	2.616
1HGI	D_ARG_170	NH1	F_GLU_128	OE1	3.797
1HGI	D_ARG_170	NH1	F_GLU_128	OE2	3.417
1HGI	D_LYS_174	NZ	F_ASP_164	OD1	2.814
1HGI	D_LYS_174	NZ	F_ASP_164	OD2	2.727
1HGI	E_LYS_27	NZ	F_GLU_97	OE1	2.961
1HGI	E_LYS_27	NZ	F_GLU_97	OE2	2.862
1HGI	E_ARG_109	NH2	F_GLU_67	OE1	3.649
1HGI	E_ARG_109	NH2	F_GLU_67	OE2	2.781
1HGI	E_LYS_238	NZ	D_GLU_72	OE1	2.803
1HGI	E_LYS_238	NZ	D_GLU_72	OE2	2.859
1HGI	E_ARG_269	NH1	F_GLU_67	OE1	2.720
1HGI	E_ARG_269	NH2	F_GLU_67	OE1	3.815
1HGI	E_LYS_299	NZ	F_GLU_69	OE2	2.715
1HGI	E_LYS_310	NZ	F_ASP_86	OD1	2.757
1HGI	E_LYS_310	NZ	F_ASP_90	OD1	2.523
1HGI	E_LYS_326	NZ	F_GLU_15	OE1	2.882
1HGI	E_LYS_326	NZ	F_GLU_15	OE2	3.090
1HGI	F_ARG_54	NH1	D_GLU_97	OE2	3.254
1HGI	F_ARG_54	NH2	D_GLU_97	OE2	2.750
1HGI	F_LYS_62	NZ	D_ASP_86	OD1	2.884
1HGI	F_LYS_62	NZ	D_ASP_86	OD2	2.563
1HGI	F_LYS_62	NZ	D_ASP_90	OD1	3.358
1HGI	F_LYS_62	NZ	D_ASP_90	OD2	2.609
1HGI	F_ARG_76	NH1	B_GLU_74	OE1	3.420
1HGI	F_ARG_76	NH1	B_GLU_74	OE2	2.771
1HGI	F_ARG_76	NH2	B_GLU_74	OE1	2.763
1HGI	F_ARG_76	NH2	B_GLU_74	OE2	3.604
1HGI	F_ARG_76	NH2	B_GLU_81	OE1	2.645
1HGI	F_ARG_76	NH2	B_GLU_81	OE2	3.592
1HGI	F_ARG_123	NH2	D_GLU_132	OE1	3.144
1HGI	F_ARG_124	NH2	D_GLU_132	OE1	3.185
1HGI	F_ARG_124	NH2	D_GLU_132	OE2	3.386
1HGI	F_ARG_127	NH1	D_GLU_131	OE1	2.561
1HGI	F_ARG_163	NH2	D_GLU_131	OE1	2.567
1HGI	F_ARG_163	NH2	D_GLU_131	OE2	2.692
1HGI	F_ARG_170	NH1	B_GLU_128	OE1	3.621
1HGI	F_ARG_170	NH1	B_GLU_128	OE2	3.345
1HGI	F_LYS_174	NZ	B_ASP_164	OD1	2.789
1HGI	F_LYS_174	NZ	B_ASP_164	OD2	2.521
1HGJ	A_LYS_27	NZ	B_GLU_97	OE1	2.775
1HGJ	A_LYS_27	NZ	B_GLU_97	OE2	2.807
1HGJ	A_ARG_109	NH2	B_GLU_67	OE1	3.648
1HGJ	A_ARG_109	NH2	B_GLU_67	OE2	2.748
1HGJ	A_LYS_238	NZ	F_GLU_72	OE1	2.903
1HGJ	A_LYS_238	NZ	F_GLU_72	OE2	2.788
1HGJ	A_ARG_269	NH1	B_GLU_67	OE1	2.736
1HGJ	A_ARG_269	NH2	B_GLU_67	OE1	3.791
1HGJ	A_LYS_299	NZ	B_GLU_69	OE2	2.821
1HGJ	A_LYS_310	NZ	B_ASP_86	OD1	2.922
1HGJ	A_LYS_310	NZ	B_ASP_90	OD1	2.569
1HGJ	A_LYS_326	NZ	B_GLU_15	OE1	3.187
1HGJ	A_LYS_326	NZ	B_GLU_15	OE2	2.826
1HGJ	B_ARG_25	NH1	A_GLU_325	OE2	3.775
1HGJ	B_ARG_25	NH2	A_GLU_325	OE2	2.974

1HGJ	B_ARG_54	NH1	F_GLU_97	OE2	3.272
1HGJ	B_ARG_54	NH2	F_GLU_97	OE2	2.774
1HGJ	B_LYS_62	NZ	F_ASP_86	OD1	2.863
1HGJ	B_LYS_62	NZ	F_ASP_86	OD2	2.651
1HGJ	B_LYS_62	NZ	F_ASP_90	OD1	3.453
1HGJ	B_LYS_62	NZ	F_ASP_90	OD2	2.738
1HGJ	B_ARG_76	NH1	D_GLU_74	OE1	3.648
1HGJ	B_ARG_76	NH1	D_GLU_74	OE2	2.885
1HGJ	B_ARG_76	NH2	D_GLU_74	OE1	2.846
1HGJ	B_ARG_76	NH2	D_GLU_74	OE2	3.547
1HGJ	B_ARG_76	NH2	D_GLU_81	OE1	2.721
1HGJ	B_ARG_76	NH2	D_GLU_81	OE2	3.500
1HGJ	B_ARG_123	NH2	F_GLU_132	OE1	3.120
1HGJ	B_ARG_124	NH2	F_GLU_132	OE1	3.095
1HGJ	B_ARG_124	NH2	F_GLU_132	OE2	3.375
1HGJ	B_ARG_127	NH1	F_GLU_131	OE1	2.484
1HGJ	B_ARG_163	NH2	F_GLU_131	OE1	2.591
1HGJ	B_ARG_163	NH2	F_GLU_131	OE2	2.571
1HGJ	B_ARG_170	NH1	D_GLU_128	OE1	3.291
1HGJ	B_ARG_170	NH1	D_GLU_128	OE2	3.706
1HGJ	B_LYS_174	NZ	D_ASP_164	OD1	2.810
1HGJ	B_LYS_174	NZ	D_ASP_164	OD2	2.550
1HGJ	C_LYS_27	NZ	D_GLU_97	OE1	2.755
1HGJ	C_LYS_27	NZ	D_GLU_97	OE2	2.824
1HGJ	C_ARG_109	NH2	D_GLU_67	OE1	3.638
1HGJ	C_ARG_109	NH2	D_GLU_67	OE2	2.758
1HGJ	C_LYS_238	NZ	B_GLU_72	OE1	2.749
1HGJ	C_LYS_238	NZ	B_GLU_72	OE2	2.713
1HGJ	C_ARG_269	NH1	D_GLU_67	OE1	2.708
1HGJ	C_ARG_269	NH2	D_GLU_67	OE1	3.781
1HGJ	C_LYS_299	NZ	D_GLU_69	OE2	2.827
1HGJ	C_LYS_310	NZ	D_ASP_86	OD1	2.943
1HGJ	C_LYS_310	NZ	D_ASP_90	OD1	2.532
1HGJ	C_LYS_326	NZ	D_GLU_15	OE1	2.911
1HGJ	C_LYS_326	NZ	D_GLU_15	OE2	3.904
1HGJ	D_ARG_54	NH1	B_GLU_97	OE2	3.338
1HGJ	D_ARG_54	NH2	B_GLU_97	OE2	2.835
1HGJ	D_LYS_62	NZ	B_ASP_86	OD1	2.910
1HGJ	D_LYS_62	NZ	B_ASP_86	OD2	2.574
1HGJ	D_LYS_62	NZ	B_ASP_90	OD1	3.419
1HGJ	D_LYS_62	NZ	B_ASP_90	OD2	2.622
1HGJ	D_ARG_76	NH1	F_GLU_74	OE1	3.424
1HGJ	D_ARG_76	NH1	F_GLU_74	OE2	2.763
1HGJ	D_ARG_76	NH2	F_GLU_74	OE1	2.714
1HGJ	D_ARG_76	NH2	F_GLU_74	OE2	3.550
1HGJ	D_ARG_76	NH2	F_GLU_81	OE1	2.684
1HGJ	D_ARG_76	NH2	F_GLU_81	OE2	3.574
1HGJ	D_ARG_123	NH2	B_GLU_132	OE1	3.075
1HGJ	D_ARG_124	NH2	B_GLU_132	OE1	3.055
1HGJ	D_ARG_124	NH2	B_GLU_132	OE2	3.342
1HGJ	D_ARG_127	NH1	B_GLU_131	OE1	2.514
1HGJ	D_ARG_163	NH2	B_GLU_131	OE1	2.599
1HGJ	D_ARG_163	NH2	B_GLU_131	OE2	2.594
1HGJ	D_ARG_170	NH1	F_GLU_128	OE1	3.405
1HGJ	D_ARG_170	NH1	F_GLU_128	OE2	3.769
1HGJ	D_LYS_174	NZ	F_ASP_164	OD1	2.824
1HGJ	D_LYS_174	NZ	F_ASP_164	OD2	2.673
1HGJ	E_LYS_27	NZ	F_GLU_97	OE1	2.779

1HGJ	E_LYS_27	NZ	F_GLU_97	OE2	2.813
1HGJ	E_ARG_109	NH2	F_GLU_67	OE1	3.635
1HGJ	E_ARG_109	NH2	F_GLU_67	OE2	2.759
1HGJ	E_LYS_238	NZ	D_GLU_72	OE1	2.865
1HGJ	E_LYS_238	NZ	D_GLU_72	OE2	2.804
1HGJ	E_ARG_269	NH1	F_GLU_67	OE1	2.691
1HGJ	E_ARG_269	NH2	F_GLU_67	OE1	3.759
1HGJ	E_LYS_299	NZ	F_GLU_69	OE2	2.806
1HGJ	E_LYS_310	NZ	F_ASP_86	OD1	2.930
1HGJ	E_LYS_310	NZ	F_ASP_90	OD1	2.553
1HGJ	E_LYS_326	NZ	F_GLU_15	OE1	2.874
1HGJ	E_LYS_326	NZ	F_GLU_15	OE2	3.254
1HGJ	F_ARG_54	NH1	D_GLU_97	OE2	3.349
1HGJ	F_ARG_54	NH2	D_GLU_97	OE2	2.771
1HGJ	F_LYS_62	NZ	D_ASP_86	OD1	2.846
1HGJ	F_LYS_62	NZ	D_ASP_86	OD2	2.568
1HGJ	F_LYS_62	NZ	D_ASP_90	OD1	3.467
1HGJ	F_LYS_62	NZ	D_ASP_90	OD2	2.658
1HGJ	F_ARG_76	NH1	B_GLU_74	OE1	3.383
1HGJ	F_ARG_76	NH1	B_GLU_74	OE2	2.704
1HGJ	F_ARG_76	NH2	B_GLU_74	OE1	2.715
1HGJ	F_ARG_76	NH2	B_GLU_74	OE2	3.551
1HGJ	F_ARG_76	NH2	B_GLU_81	OE1	2.654
1HGJ	F_ARG_76	NH2	B_GLU_81	OE2	3.611
1HGJ	F_ARG_123	NH2	D_GLU_132	OE1	3.110
1HGJ	F_ARG_124	NH2	D_GLU_132	OE1	3.125
1HGJ	F_ARG_124	NH2	D_GLU_132	OE2	3.360
1HGJ	F_ARG_127	NH1	D_GLU_131	OE1	2.554
1HGJ	F_ARG_163	NH2	D_GLU_131	OE1	2.636
1HGJ	F_ARG_163	NH2	D_GLU_131	OE2	2.696
1HGJ	F_ARG_170	NH1	B_GLU_128	OE1	3.311
1HGJ	F_ARG_170	NH1	B_GLU_128	OE2	3.766
1HGJ	F_LYS_174	NZ	B_ASP_164	OD1	2.859
1HGJ	F_LYS_174	NZ	B_ASP_164	OD2	2.554
1HIL	A_LYS_28	NZ	B_ASP_99	OD1	3.388
1HIL	A_LYS_28	NZ	B_ASP_99	OD2	3.371
1HIL	A_LYS_30	NZ	B_ASP_99	OD2	3.991
1HIL	B_ARG_95	NH1	A_ASP_91	OD1	2.828
1HIL	B_ARG_95	NH1	A_ASP_91	OD2	3.804
1HIL	B_ARG_95	NH2	A_ASP_91	OD1	3.160
1HIL	B_ARG_95	NH2	A_ASP_91	OD2	3.904
1HIL	B_HIS_172	NE2	A_ASP_167	OD2	3.701
1HIL	B_LYS_221	NZ	A_GLU_123	OE1	2.980
1HIL	C_LYS_28	NZ	D_ASP_99	OD1	3.565
1HIL	C_LYS_28	NZ	D_ASP_99	OD2	3.509
1HIL	D_ARG_95	NH1	C_ASP_91	OD1	2.906
1HIL	D_ARG_95	NH1	C_ASP_91	OD2	3.993
1HIL	D_ARG_95	NH2	C_ASP_91	OD1	3.045
1HIL	D_ARG_95	NH2	C_ASP_91	OD2	3.822
1HIL	D_LYS_221	NZ	C_GLU_123	OE1	2.896
1HIL	D_LYS_221	NZ	C_GLU_123	OE2	3.091
1HIM	L_ARG_95	NH1	H_ASP_91	OD1	3.100
1HIM	L_ARG_95	NH2	H_ASP_91	OD1	3.427
1HIM	L_ARG_95	NH2	P_ASP_104	OD1	3.909
1HIM	L_ARG_95	NH2	P_ASP_104	OD2	3.079
1HIM	L_LYS_221	NZ	H_GLU_123	OE1	3.486
1HIM	L_LYS_221	NZ	H_GLU_123	OE2	2.924
1HIM	J_LYS_28	NZ	M_GLU_100	OE1	3.991

1HIM	J_LYS_28	NZ	M_GLU_100	OE2	3.433
1HIM	M_ARG_95	NH1	J_ASP_91	OD1	2.854
1HIM	M_ARG_95	NH2	J_ASP_91	OD1	3.712
1HIM	M_ARG_95	NH2	R_ASP_104	OD1	2.834
1HIM	M_ARG_95	NH2	R_ASP_104	OD2	3.540
1HIN	L_LYS_28	NZ	H_GLU_100	OE2	2.975
1HIN	H_ARG_95	NH1	L_ASP_91	OD1	3.169
1HIN	H_ARG_95	NH1	P_ASP_104	OD1	3.889
1HIN	H_ARG_95	NH2	L_ASP_91	OD1	2.746
1I8I	B_LYS_343	NZ	A_ASP_85	OD1	3.777
1I8I	C_LYS_502	NZ	A_GLU_50	OE1	3.673
1I8I	C_LYS_502	NZ	A_GLU_50	OE2	3.232
1I8K	B_LYS_343	NZ	A_ASP_85	OD1	3.688
1I8K	B_LYS_343	NZ	A_ASP_85	OD2	2.833
1I8K	C_LYS_502	NZ	A_GLU_50	OE1	3.381
1I8K	C_LYS_502	NZ	A_GLU_50	OE2	3.653
1I8M	H_LYS_208	NZ	L_GLU_123	OE1	2.918
1I8M	B_LYS_208	NZ	A_GLU_123	OE2	2.887
1IC4	Y_LYS_97	NZ	H_ASP_99	OD1	2.657
1IC4	Y_LYS_97	NZ	H_ASP_99	OD2	3.938
1IC5	Y_LYS_97	NZ	H_ASP_32	OD1	2.694
1IFH	H_ARG_95	NH1	L_ASP_91	OD1	2.782
1IFH	H_ARG_95	NH2	P_ASP_104	OD1	2.974
1IFH	H_ARG_95	NH2	P_ASP_104	OD2	2.813
1IFH	H_LYS_221	NZ	L_GLU_123	OE1	3.267
1IFH	H_LYS_221	NZ	L_GLU_123	OE2	2.926
1IGF	L_LYS_50	NZ	H_ASP_98	OD2	3.036
1IGF	H_LYS_221	NZ	L_GLU_123	OE1	3.549
1IGF	J_LYS_221	NZ	M_GLU_123	OE1	3.800
1IGF	J_LYS_221	NZ	M_GLU_123	OE2	3.750
1IND	H_LYS_143	NZ	L_GLU_127	OE2	2.765
1IND	H_HIS_164	NE2	L_ASP_141	OD1	3.891
1INE	H_LYS_143	NZ	L_GLU_127	OE2	2.920
1INE	H_HIS_164	NE2	L_ASP_141	OD2	3.817
1IQW	L_ARG_100	NH2	H_GLU_50	OE1	2.572
1IQW	L_ARG_100	NH2	H_GLU_50	OE2	2.799
1IQW	H_HIS_172	NE2	L_ASP_171	OD1	3.594
1IT9	L_ARG_100	NH2	H_GLU_50	OE2	3.105
1IT9	H_LYS_217	NZ	L_GLU_127	OE1	3.545
1IT9	H_LYS_217	NZ	L_GLU_127	OE2	3.302
1J05	H_LYS_58	NZ	L_ASP_94	OD2	2.663
1J05	B_LYS_58	NZ	A_ASP_94	OD2	2.870
1J1O	Y_LYS_97	NZ	H_ASP_32	OD1	2.636
1J1O	Y_LYS_97	NZ	H_ASP_32	OD2	3.985
1J1O	Y_LYS_97	NZ	H_ASP_99	OD1	3.590
1J1O	Y_LYS_97	NZ	H_ASP_99	OD2	2.896
1J1P	Y_LYS_97	NZ	H_ASP_32	OD1	2.700
1J1P	Y_LYS_97	NZ	H_ASP_99	OD1	3.721
1J1P	Y_LYS_97	NZ	H_ASP_99	OD2	2.595
1J1X	Y_LYS_97	NZ	H_ASP_32	OD1	2.655
1J1X	Y_LYS_97	NZ	H_ASP_32	OD2	3.935
1J1X	Y_LYS_97	NZ	H_ASP_99	OD1	3.479
1J1X	Y_LYS_97	NZ	H_ASP_99	OD2	2.956
1JFQ	H_LYS_516	NZ	L_GLU_123	OE1	3.003
1JFQ	H_LYS_516	NZ	L_GLU_123	OE2	3.095
1JHL	A_ARG_112	NH1	H_ASP_55	OD1	3.828
1JHL	A_ARG_112	NH1	H_ASP_55	OD2	3.112
1JHL	A_LYS_116	NZ	H_ASP_99	OD1	3.763

1JHL	A_LYS_116	NZ	H_ASP_99	OD2	3.232
1JPS	T_LYS_201	NZ	H_ASP_52	OD1	2.781
1JPT	H_LYS_213	NZ	L_GLU_123	OE1	3.226
1JPT	H_LYS_213	NZ	L_GLU_123	OE2	3.740
1JRH	I_LYS_52	NZ	H_ASP_54	OD1	3.471
1JRH	I_LYS_52	NZ	H_ASP_54	OD2	2.819
1JRH	I_LYS_52	NZ	H_ASP_56	OD2	2.824
1JRH	I_ARG_84	NH2	L_GLU_27	OE1	3.652
1JRH	I_ARG_84	NH2	L_GLU_27	OE2	3.984
1K6Q	H_HIS_168	NE2	L_ASP_167	OD1	3.896
1KB5	A_ARG_93	NH1	B_GLU_105	OE1	2.975
1KB5	A_ARG_93	NH1	B_GLU_105	OE2	3.412
1KB5	A_ARG_101	NH2	H_ASP_98	OD1	2.690
1KB5	L_LYS_27	NZ	B_ASP_54	OD1	3.460
1KB5	H_ARG_96	NH1	A_ASP_26	OD1	2.599
1KB5	H_ARG_96	NH1	A_ASP_26	OD2	2.834
1KB5	H_ARG_96	NH2	L_GLU_56	OE2	2.981
1KC5	H_LYS_211	NZ	L_GLU_123	OE2	2.759
1KCS	H_LYS_211	NZ	L_GLU_123	OE1	3.340
1KCS	H_LYS_211	NZ	L_GLU_123	OE2	2.904
1KIP	A_ARG_96	NH1	B_GLU_98	OE1	2.773
1KIP	A_ARG_96	NH1	B_GLU_98	OE2	3.817
1KIP	A_ARG_96	NH2	B_GLU_98	OE1	3.280
1KIP	A_ARG_96	NH2	B_GLU_98	OE2	2.802
1KIQ	A_ARG_96	NH1	B_GLU_98	OE1	2.812
1KIQ	A_ARG_96	NH1	B_GLU_98	OE2	3.589
1KIQ	A_ARG_96	NH2	B_GLU_98	OE1	3.677
1KIQ	A_ARG_96	NH2	B_GLU_98	OE2	2.919
1KIR	A_ARG_96	NH1	B_GLU_98	OE1	2.757
1KIR	A_ARG_96	NH1	B_GLU_98	OE2	3.582
1KIR	A_ARG_96	NH2	B_GLU_98	OE1	3.625
1KIR	A_ARG_96	NH2	B_GLU_98	OE2	2.980
1KTR	P_HIS_4	NE2	L_ASP_183	OD1	3.445
1KTR	P_HIS_4	NE2	L_ASP_183	OD2	2.673
1KTR	P_HIS_6	ND1	L_GLU_39	OE1	3.223
1KTR	P_HIS_6	ND1	L_GLU_39	OE2	2.811
1KTR	P_HIS_6	NE2	L_GLU_230	OE1	3.040
1KTR	P_HIS_6	NE2	L_GLU_230	OE2	3.199
1L7I	H_LYS_209	NZ	L_GLU_123	OE1	2.718
1LK3	A_LYS_130	NZ	L_ASP_1	OD1	2.906
1LK3	L_ARG_31	NH1	A_GLU_133	OE1	2.703
1LK3	H_LYS_23	NZ	L_GLU_121	OE2	2.800
1LK3	H_LYS_214	NZ	L_GLU_122	OE1	2.517
1LK3	B_LYS_130	NZ	M_ASP_1	OD1	2.851
1LK3	M_ARG_31	NH1	B_GLU_133	OE1	2.693
1LK3	I_LYS_63	NZ	M_ASP_1	OD2	3.881
1LK3	I_LYS_214	NZ	M_GLU_122	OE2	2.753
1M7I	B_ARG_164	NH1	A_ASP_167	OD2	3.246
1M7I	B_ARG_164	NH1	A_ASP_170	OD1	3.912
1M7I	B_ARG_164	NH2	A_ASP_167	OD2	2.886
1M7I	B_LYS_208	NZ	A_GLU_123	OE1	2.546
1M7I	B_LYS_208	NZ	A_GLU_123	OE2	3.594
1M7D	B_ARG_164	NH1	A_ASP_167	OD2	3.313
1M7D	B_ARG_164	NH1	A_ASP_170	OD1	3.795
1M7D	B_ARG_164	NH2	A_ASP_167	OD2	3.482
1M7D	B_LYS_208	NZ	A_GLU_123	OE1	2.586
1M7D	B_LYS_208	NZ	A_GLU_123	OE2	3.420
1M7I	B_ARG_164	NH1	A_ASP_167	OD2	3.340

1M7I	B_ARG_164	NH1	A_ASP_170	OD1	3.884
1M7I	B_ARG_164	NH2	A_ASP_167	OD2	3.473
1M7I	B_LYS_208	NZ	A_GLU_123	OE1	3.031
1M7I	B_LYS_208	NZ	A_GLU_123	OE2	3.016
1MFB	H_LYS_398	NZ	L_GLU_127	OE2	2.924
1MFB	H_LYS_463	NZ	L_GLU_126	OE1	3.780
1MFC	H_LYS_398	NZ	L_GLU_127	OE2	2.815
1MFC	H_LYS_463	NZ	L_GLU_126	OE1	3.807
1MHH	B_LYS_208	NZ	A_GLU_123	OE2	3.019
1MHH	C_ARG_188	NH1	E_ASP_831	OD2	3.196
1MHH	C_ARG_188	NH2	E_ASP_831	OD2	3.360
1MHH	E_LYS_833	NZ	C_GLU_185	OE2	2.489
1MHH	F_LYS_1833	NZ	C_GLU_17	OE1	3.798
1MLB	B_LYS_211	NZ	A_GLU_123	OE1	3.556
1MLC	E_ARG_45	NH2	B_GLU_50	OE2	3.032
1MLC	E_ARG_68	NH1	B_GLU_50	OE2	3.781
1MLC	E_ARG_68	NH2	B_GLU_35	OE2	2.927
1MLC	E_ARG_68	NH2	B_GLU_50	OE1	2.510
1MLC	E_ARG_68	NH2	B_GLU_50	OE2	3.189
1MLC	F_ARG_45	NH2	D_GLU_50	OE2	2.431
1MLC	F_ARG_68	NH2	D_GLU_35	OE2	3.266
1MLC	F_ARG_68	NH2	D_GLU_50	OE1	2.710
1MLC	F_ARG_68	NH2	D_GLU_50	OE2	3.606
1N64	H_LYS_208	NZ	L_GLU_123	OE1	3.752
1NBY	B_LYS_508	NZ	A_GLU_123	OE1	2.458
1NBY	B_LYS_508	NZ	A_GLU_123	OE2	3.274
1NBY	C_LYS_697	NZ	B_ASP_332	OD1	3.949
1NBY	C_LYS_697	NZ	B_ASP_332	OD2	2.515
1NDG	B_HIS_360	NE2	A_ASP_1	OD2	3.716
1NDG	B_LYS_519	NZ	A_GLU_123	OE2	2.645
1NDG	C_LYS_697	NZ	B_ASP_332	OD1	3.996
1NDG	C_LYS_697	NZ	B_ASP_332	OD2	2.706
1NDG	C_LYS_697	NZ	B_ASP_399	OD1	2.922
1NDG	C_LYS_697	NZ	B_ASP_399	OD2	3.579
1NDM	B_LYS_519	NZ	A_GLU_123	OE1	3.184
1NDM	C_LYS_697	NZ	B_ASP_332	OD1	3.954
1NDM	C_LYS_697	NZ	B_ASP_332	OD2	2.468
1NDM	C_LYS_697	NZ	B_GLU_399	OE1	2.743
1NGW	H_HIS_165	NE2	L_ASP_167	OD1	3.771
1NGW	H_LYS_210	NZ	L_GLU_123	OE1	3.544
1NGW	H_LYS_210	NZ	L_GLU_123	OE2	3.092
1NGW	B_HIS_165	NE2	A_ASP_167	OD1	3.804
1NGW	B_LYS_210	NZ	A_GLU_123	OE1	3.662
1NGW	B_LYS_210	NZ	A_GLU_123	OE2	3.240
1NGX	B_LYS_210	NZ	A_GLU_123	OE1	3.994
1NGX	L_LYS_45	NZ	H_ASP_102	OD2	3.800
1NGX	H_LYS_210	NZ	L_GLU_123	OE1	3.804
1NGY	B_LYS_215	NZ	A_ASP_122	OD1	3.713
1NGY	B_LYS_215	NZ	A_ASP_122	OD2	3.325
1NGZ	B_LYS_	NZ	A_GLU_	OE2	3.517
1NLB	H_LYS_208	NZ	L_GLU_123	OE1	3.572
1NMC	N_LYS_432	NZ	H_ASP_56	OD1	2.750
1NMC	A_LYS_432	NZ	B_ASP_56	OD1	2.750
1OB1	A_ARG_61	NH2	F_ASP_59	OD1	3.421
1OB1	A_ARG_61	NH2	F_ASP_59	OD2	2.223
1OB1	B_HIS_164	NE2	A_ASP_166	OD2	3.671
1OB1	C_LYS_10	NZ	B_ASP_100	OD1	2.437
1OB1	C_LYS_80	NZ	D_GLU_79	OE1	3.373

1OB1	C_LYS_80	NZ	D_GLU_81	OE1	3.553
1OB1	C_LYS_80	NZ	D_GLU_81	OE2	2.714
1OB1	D_ARG_61	NH2	C_ASP_59	OD1	3.599
1OB1	D_ARG_61	NH2	C_ASP_59	OD2	2.460
1OB1	E_ARG_98	NH1	F_ASP_39	OD1	2.706
1OB1	E_HIS_164	NE2	D_ASP_166	OD2	3.790
1OB1	F_LYS_10	NZ	E_ASP_100	OD1	2.524
1OB1	F_LYS_80	NZ	A_GLU_79	OE1	3.743
1OB1	F_LYS_80	NZ	A_GLU_81	OE1	3.454
1OB1	F_LYS_80	NZ	A_GLU_81	OE2	2.796
1OB1	F_HIS_96	NE2	A_GLU_79	OE1	3.773
1OP9	B_LYS_97	NZ	A_GLU_97	OE1	2.570
1OP9	B_ARG_101	NH1	A_ASP_109	OD1	3.213
1OP9	B_ARG_101	NH1	A_ASP_109	OD2	2.829
1OP9	B_ARG_101	NH2	A_ASP_109	OD1	2.793
1OP9	B_ARG_101	NH2	A_ASP_109	OD2	3.765
1OSP	H_ARG_99	NH1	L_GLU_55	OE1	3.970
1OSP	H_ARG_99	NH1	L_GLU_55	OE2	2.686
1OSP	H_ARG_99	NH2	O_ASP_92	OD1	3.355
1OSP	H_ARG_99	NH2	O_ASP_92	OD2	2.514
1OSP	H_LYS_215	NZ	L_GLU_123	OE1	2.783
1OSP	H_LYS_215	NZ	L_GLU_123	OE2	3.079
1OSP	O_LYS_46	NZ	L_ASP_66	OD2	3.087
1P2C	A_ARG_188	NH2	F_ASP_1518	OD1	2.778
1P2C	B_LYS_511	NZ	A_GLU_123	OE1	3.498
1P2C	C_ARG_645	NH2	B_GLU_350	OE1	2.980
1P2C	C_ARG_668	NH1	B_GLU_350	OE1	3.355
1P2C	C_ARG_668	NH1	B_GLU_350	OE2	3.681
1P2C	C_ARG_668	NH2	B_GLU_335	OE2	3.090
1P2C	C_ARG_668	NH2	B_GLU_350	OE1	3.316
1P2C	C_ARG_668	NH2	B_GLU_350	OE2	2.404
1P2C	E_LYS_1411	NZ	D_GLU_1023	OE1	3.897
1P2C	F_ARG_1545	NH2	E_GLU_1250	OE1	2.861
1P2C	F_ARG_1568	NH1	E_GLU_1250	OE1	3.580
1P2C	F_ARG_1568	NH1	E_GLU_1250	OE2	3.708
1P2C	F_ARG_1568	NH2	E_GLU_1235	OE2	2.833
1P2C	F_ARG_1568	NH2	E_GLU_1250	OE1	3.551
1P2C	F_ARG_1568	NH2	E_GLU_1250	OE2	2.418
1P4B	P_HIS_2	NE2	H_ASP_65	OD1	3.248
1P4B	P_HIS_2	NE2	H_ASP_65	OD2	3.747
1P4B	P_ARG_9	NH1	H_ASP_137	OD1	2.804
1P4B	P_ARG_9	NH1	H_ASP_137	OD2	3.838
1P4B	P_ARG_9	NH2	H_ASP_137	OD1	3.399
1P4B	P_ARG_9	NH2	H_ASP_137	OD2	3.080
1P7K	H_LYS_62	NZ	L_GLU_1	OE2	3.723
1P7K	H_LYS_208	NZ	L_GLU_123	OE1	3.517
1P7K	H_LYS_208	NZ	L_GLU_123	OE2	2.802
1P7K	B_LYS_62	NZ	A_GLU_1	OE2	2.848
1PG7	H_LYS_209	NZ	L_GLU_123	OE1	2.828
1PG7	H_LYS_209	NZ	L_GLU_123	OE2	3.697
1PG7	L_LYS_209	NZ	M_GLU_123	OE1	2.829
1PG7	L_LYS_209	NZ	M_GLU_123	OE2	3.963
1PG7	L_LYS_30	NZ	X_GLU_95	OE1	3.476
1PG7	L_LYS_30	NZ	X_GLU_95	OE2	2.795
1PG7	M_LYS_30	NZ	Z_GLU_95	OE2	3.166
1PG7	X_ARG_94	NH1	H_GLU_53	OE1	3.386
1PG7	X_ARG_94	NH1	H_GLU_53	OE2	3.321
1PG7	X_ARG_94	NH2	H_GLU_53	OE1	3.937

1PG7	X_ARG_94	NH2	H_GLU_53	OE2	2.866
1PG7	X_ARG_98	NH2	H_ASP_95	OD1	2.990
1PG7	X_ARG_98	NH2	H_ASP_95	OD2	3.561
1PG7	X_LYS_143	NZ	W_GLU_125	OE2	2.675
1PG7	X_HIS_164	NE2	W_GLU_139	OE2	3.801
1PG7	X_LYS_208	NZ	W_GLU_124	OE2	2.927
1PG7	Z_ARG_94	NH1	I_GLU_53	OE1	3.259
1PG7	Z_ARG_94	NH1	I_GLU_53	OE2	3.931
1PG7	Z_ARG_94	NH2	I_GLU_53	OE1	2.918
1PG7	Z_ARG_94	NH2	I_GLU_53	OE2	2.525
1PG7	Z_ARG_98	NH2	I_ASP_95	OD1	3.168
1PG7	Z_ARG_98	NH2	I_ASP_95	OD2	3.781
1PG7	Z_LYS_143	NZ	Y_GLU_125	OE2	2.901
1PG7	Z_LYS_208	NZ	Y_GLU_124	OE2	3.302
1PZ5	A_HIS_27D	NE2	C_ASP_2	OD1	2.720
1PZ5	B_ARG_164	NH1	A_ASP_167	OD2	3.218
1PZ5	B_ARG_164	NH2	A_ASP_167	OD2	3.712
1PZ5	B_LYS_208	NZ	A_GLU_123	OE1	2.648
1PZ5	B_LYS_208	NZ	A_GLU_123	OE2	3.713
1Q9K	A_ARG_95	NH2	B_ASP_95	OD1	3.932
1Q9K	A_ARG_95	NH2	B_ASP_95	OD2	3.226
1Q9K	B_HIS_162	NE2	A_ASP_166	OD1	3.847
1Q9L	B_LYS_206	NZ	A_GLU_122	OE2	3.242
1Q9L	D_ARG_100B	NH1	B_GLU_85	OE1	3.618
1Q9L	D_ARG_100B	NH1	B_GLU_85	OE2	3.115
1Q9L	D_HIS_162	NE2	C_ASP_166	OD1	3.172
1Q9L	A_ARG_95	NH2	B_ASP_95	OD2	3.284
1Q9L	C_ARG_95	NH2	D_ASP_95	OD2	3.309
1Q9O	B_ARG_100	NH1	A_GLU_55	OE1	3.447
1Q9O	B_ARG_100	NH1	A_GLU_55	OE2	3.466
1Q9O	B_ARG_100	NH2	A_GLU_55	OE1	3.378
1Q9O	B_ARG_100	NH2	A_GLU_55	OE2	2.999
1Q9O	B_LYS_206	NZ	A_GLU_122	OE2	3.964
1Q9O	D_ARG_100	NH1	C_GLU_55	OE1	3.493
1Q9O	D_ARG_100	NH1	C_GLU_55	OE2	3.040
1Q9O	D_ARG_100	NH2	C_GLU_55	OE1	3.391
1Q9O	D_ARG_100	NH2	C_GLU_55	OE2	3.047
1Q9O	A_ARG_95	NH2	B_ASP_95	OD1	2.958
1Q9O	A_ARG_95	NH2	B_ASP_95	OD2	3.717
1Q9O	C_ARG_95	NH2	D_ASP_95	OD1	3.672
1Q9O	C_ARG_95	NH2	D_ASP_95	OD2	2.974
1Q9W	A_ARG_95	NH2	B_ASP_95	OD1	2.949
1Q9W	A_ARG_95	NH2	B_ASP_95	OD2	3.845
1Q9W	B_ARG_100	NH1	A_GLU_55	OE1	2.615
1Q9W	B_ARG_100	NH1	A_GLU_55	OE2	3.657
1Q9W	B_ARG_100	NH2	A_GLU_55	OE1	2.891
1Q9W	B_ARG_100	NH2	A_GLU_55	OE2	3.820
1Q9W	C_ARG_95	NH2	D_ASP_95	OD1	2.929
1Q9W	C_ARG_95	NH2	D_ASP_95	OD2	3.831
1Q9W	D_ARG_100	NH1	C_GLU_55	OE1	3.356
1Q9W	D_ARG_100	NH1	C_GLU_55	OE2	3.002
1Q9W	D_ARG_100	NH2	C_GLU_55	OE1	3.373
1Q9W	D_ARG_100	NH2	C_GLU_55	OE2	3.045
1QBL	H_LYS_212	NZ	L_GLU_123	OE1	3.581
1QBM	H_LYS_212	NZ	L_GLU_123	OE1	2.762
1QBM	H_LYS_212	NZ	L_GLU_123	OE2	3.773
1QGC	1_ARG_124	NH1	2_ASP_41	OD1	3.642
1QGC	1_ARG_124	NH1	2_ASP_41	OD2	2.877

1QGC	1_ARG_124	NH2	2_ASP_41	OD1	3.740
1QGC	2_ARG_167	NH2	3_ASP_166	OD1	2.757
1QGC	2_ARG_167	NH2	3_ASP_166	OD2	2.777
1QGC	A_ARG_99	NH2	5_ASP_143	OD1	3.483
1QGC	A_LYS_215	NZ	4_GLU_127	OE2	3.716
1QKZ	H_LYS_208	NZ	L_GLU_123	OE2	2.582
1RZJ	G_ARG_419	NH2	H_GLU_99	OE2	2.591
1RZJ	C_LYS_29	NZ	G_ASP_279	OD2	3.209
1RZJ	C_LYS_35	NZ	G_ASP_457	OD2	3.838
1RZJ	C_ARG_59	NH1	G_ASP_368	OD1	3.788
1RZJ	C_ARG_59	NH1	G_ASP_368	OD2	3.342
1RZJ	C_ARG_59	NH2	G_ASP_368	OD1	2.531
1RZJ	C_ARG_59	NH2	G_ASP_368	OD2	3.174
1RZJ	H_LYS_209	NZ	L_GLU_123	OE1	3.812
1RZK	G_ARG_419	NH1	H_GLU_100B	OE1	2.999
1RZK	G_ARG_419	NH1	H_GLU_100B	OE2	3.674
1RZK	G_ARG_419	NH2	H_GLU_99	OE1	2.292
1RZK	G_ARG_419	NH2	H_GLU_100B	OE2	3.969
1RZK	C_LYS_35	NZ	G_ASP_457	OD2	3.741
1RZK	C_ARG_59	NH1	G_ASP_368	OD1	3.343
1RZK	C_ARG_59	NH1	G_ASP_368	OD2	3.154
1RZK	C_ARG_59	NH2	G_ASP_368	OD1	2.433
1RZK	C_ARG_59	NH2	G_ASP_368	OD2	2.977
1RZK	H_HIS_164	NE2	L_ASP_167	OD1	3.880
1RZK	H_HIS_164	NE2	L_ASP_167	OD2	2.505
1RZK	H_LYS_209	NZ	L_GLU_123	OE1	3.513
1RZK	H_LYS_209	NZ	L_GLU_123	OE2	3.584
1S5I	L_ARG_96	NH1	H_ASP_97	OD1	3.601
1S5I	L_ARG_96	NH2	H_ASP_97	OD1	2.496
1S5I	L_ARG_96	NH2	H_ASP_97	OD2	2.511
1S5I	H_HIS_172	NE2	L_ASP_167	OD2	3.741
1S5I	H_LYS_221	NZ	L_GLU_123	OE2	3.213
1S78	D_HIS_164	NE2	C_ASP_167	OD1	3.839
1S78	D_LYS_209	NZ	C_GLU_123	OE1	3.290
1S78	D_LYS_214	NZ	C_ASP_122	OD1	3.484
1SM3	H_LYS_143	NZ	L_GLU_124	OE2	2.757
1SQ2	L_ARG_73	NH2	N_ASP_93	OD1	3.549
1SQ2	L_ARG_73	NH2	N_ASP_93	OD2	3.002
1SQ2	N_ARG_100	NH1	L_ASP_52	OD1	3.032
1SQ2	N_ARG_100	NH1	L_ASP_52	OD2	3.454
1SQ2	N_ARG_100	NH2	L_ASP_52	OD1	3.561
1SQ2	N_ARG_100	NH2	L_ASP_52	OD2	3.218
1T6V	L_ARG_73	NH1	N_ASP_93	OD2	3.564
1T6V	L_ARG_73	NH2	N_ASP_93	OD1	3.874
1T6V	L_ARG_73	NH2	N_ASP_93	OD2	2.603
1T6V	N_ARG_100	NH1	L_ASP_52	OD1	2.973
1T6V	N_ARG_100	NH1	L_ASP_52	OD2	3.510
1T6V	N_ARG_100	NH2	L_ASP_52	OD1	3.501
1T6V	N_ARG_100	NH2	L_ASP_52	OD2	3.094
1T6V	M_ARG_73	NH2	O_ASP_93	OD1	3.734
1T6V	M_ARG_73	NH2	O_ASP_93	OD2	2.904
1T6V	M_LYS_97	NZ	N_ASP_106	OD1	3.749
1T6V	M_LYS_97	NZ	N_ASP_106	OD2	2.853
1T6V	O_ARG_100	NH1	M_ASP_52	OD1	3.232
1T6V	O_ARG_100	NH1	M_ASP_52	OD2	2.872
1T6V	O_ARG_100	NH2	M_ASP_52	OD1	3.920
1T6V	O_ARG_100	NH2	M_ASP_52	OD2	2.990
1TYE	A_HIS_30	ND1	E_ASP_429	OD2	3.896

1TYE	A_ARG_32	NH1	E_ASP_429	OD1	3.657
1TYE	A_ARG_32	NH1	E_ASP_429	OD2	2.825
1TYE	A_ARG_73	NH1	C_ASP_71	OD1	3.528
1TYE	A_ARG_73	NH1	C_ASP_71	OD2	3.396
1TYE	A_ARG_73	NH2	C_ASP_71	OD2	2.714
1TYE	A_ARG_73	NH2	C_GLU_75	OE1	3.907
1TYE	B_ARG_216	NH1	A_GLU_123	OE1	2.702
1TYE	B_LYS_253	NZ	A_ASP_232	OD2	3.290
1TYE	C_ARG_73	NH1	A_ASP_71	OD1	3.491
1TYE	C_ARG_73	NH2	A_ASP_71	OD1	3.688
1TYE	C_ARG_73	NH2	A_ASP_71	OD2	3.197
1TYE	D_ARG_216	NH1	C_GLU_123	OE1	2.914
1TYE	D_ARG_216	NH1	C_GLU_123	OE2	3.969
1TYE	D_LYS_253	NZ	C_ASP_232	OD2	3.400
1TYE	E_ARG_368	NH2	A_ASP_429	OD2	3.921
1TYE	F_ARG_216	NH1	E_GLU_123	OE1	2.938
1TYE	F_ARG_216	NH1	E_GLU_123	OE2	3.244
1TYE	F_LYS_253	NZ	E_ASP_232	OD2	3.394
1TZH	V_ARG_23	NH1	W_GLU_30	OE2	3.100
1TZH	V_HIS_90	NE2	H_ASP_33	OD1	2.826
1TZH	V_HIS_90	NE2	H_ASP_33	OD2	2.524
1TZH	W_ARG_23	NH1	V_GLU_30	OE1	3.346
1TZH	W_HIS_90	NE2	B_ASP_33	OD1	3.121
1TZH	W_HIS_90	NE2	B_ASP_33	OD2	2.585
1TZH	B_LYS_209	NZ	A_GLU_123	OE2	3.903
1TZH	H_HIS_164	NE2	L_ASP_167	OD1	3.495
1TZH	H_LYS_209	NZ	L_GLU_123	OE1	2.754
1TZH	H_LYS_209	NZ	L_GLU_123	OE2	3.404
1TZI	B_LYS_209	NZ	A_GLU_123	OE2	3.786
1UA6	H_HIS_164	NE2	L_ASP_167	OD1	3.994
1UA6	Y_LYS_97	NZ	H_ASP_32	OD1	2.722
1UA6	Y_LYS_97	NZ	H_ASP_99	OD2	2.674
1UAC	Y_LYS_97	NZ	H_ASP_32	OD1	2.750
1UAC	Y_LYS_97	NZ	H_ASP_32	OD2	3.845
1UAC	Y_LYS_97	NZ	H_ASP_99	OD2	2.749
1UCB	L_LYS_50	NZ	H_ASP_98	OD1	3.160
1UCB	H_LYS_221	NZ	L_GLU_123	OE1	3.128
1UJ3	A_HIS_91	NE2	B_ASP_399	OD1	3.708
1UJ3	A_HIS_91	NE2	B_ASP_399	OD2	2.884
1UJ3	B_LYS_513	NZ	A_GLU_123	OE1	3.554
1UJ3	B_LYS_513	NZ	A_GLU_123	OE2	3.075
1UJ3	C_LYS_766	NZ	A_ASP_1	OD1	3.997
1UJ3	C_LYS_769	NZ	B_ASP_399	OD1	2.791
1UJ3	C_LYS_769	NZ	B_ASP_399	OD2	3.372
1UJ3	C_LYS_801	NZ	B_ASP_352	OD1	2.774
1UJ3	C_LYS_801	NZ	B_ASP_352	OD2	3.632
1UWX	H_HIS_164	NE2	L_ASP_168	OD2	3.899
1UWX	H_LYS_208	NZ	L_GLU_124	OE2	2.744
1UWX	M_LYS_208	NZ	K_GLU_124	OE2	2.705
1UZ6	F_ARG_164	NH1	E_ASP_166	OD1	3.662
1UZ6	F_ARG_164	NH2	E_ASP_166	OD1	3.708
1UZ6	F_ARG_164	NH2	E_ASP_169	OD2	3.554
1UZ6	F_LYS_208	NZ	E_GLU_122	OE1	3.883
1UZ6	F_ARG_209	NH1	E_GLU_122	OE2	3.531
1UZ6	H_ARG_164	NH1	L_ASP_166	OD1	3.603
1UZ6	H_ARG_164	NH2	L_ASP_166	OD1	3.557
1UZ6	H_ARG_164	NH2	L_ASP_169	OD2	3.746
1UZ6	H_LYS_208	NZ	L_GLU_122	OE1	3.795

1UZ6	H_ARG_209	NH1	L_GLU_122	OE2	3.180
1UZ6	P_ARG_164	NH1	M_ASP_166	OD1	3.636
1UZ6	P_ARG_164	NH2	M_ASP_166	OD1	3.666
1UZ6	P_ARG_164	NH2	M_ASP_166	OD2	3.901
1UZ6	P_ARG_164	NH2	M_ASP_169	OD2	3.942
1UZ6	P_LYS_208	NZ	M_GLU_122	OE1	3.361
1UZ6	W_ARG_164	NH2	V_ASP_166	OD1	3.892
1UZ6	W_LYS_208	NZ	V_GLU_122	OE1	3.069
1UZ8	B_ARG_164	NH1	A_ASP_166	OD1	3.299
1UZ8	B_ARG_164	NH2	A_ASP_166	OD1	3.745
1UZ8	B_ARG_164	NH2	A_ASP_169	OD2	3.660
1UZ8	H_ARG_164	NH1	L_ASP_166	OD1	3.385
1UZ8	H_ARG_164	NH2	L_ASP_166	OD1	3.573
1UZ8	H_ARG_164	NH2	L_ASP_169	OD2	3.234
1V7M	L_ARG_95	NH1	H_GLU_50	OE1	3.532
1V7M	V_ARG_98	NH2	H_ASP_31	OD1	3.697
1V7M	M_ARG_95	NH1	L_GLU_50	OE1	3.801
1V7M	X_ARG_98	NH2	L_ASP_31	OD1	3.214
1V7N	L_ARG_95	NH1	H_GLU_50	OE1	3.194
1V7N	L_ARG_107	NH1	O_GLU_78	OE2	3.587
1V7N	L_ARG_107	NH2	O_GLU_78	OE1	3.844
1V7N	L_ARG_107	NH2	O_GLU_78	OE2	2.214
1V7N	H_ARG_216	NH2	Z_ASP_123	OD2	3.997
1V7N	M_ARG_95	NH1	L_GLU_50	OE1	2.984
1V7N	M_ARG_107	NH1	N_GLU_78	OE2	3.960
1V7N	M_ARG_107	NH2	N_GLU_78	OE1	3.607
1V7N	M_ARG_107	NH2	N_GLU_78	OE2	2.132
1V7N	N_ARG_95	NH1	J_GLU_50	OE1	3.631
1V7N	N_ARG_107	NH2	M_GLU_78	OE1	2.980
1V7N	N_ARG_107	NH2	M_GLU_78	OE2	2.369
1V7N	J_ARG_216	NH2	X_ASP_123	OD2	3.982
1V7N	O_ARG_95	NH1	K_GLU_50	OE1	2.735
1V7N	O_ARG_107	NH1	L_GLU_78	OE1	3.650
1V7N	O_ARG_107	NH1	L_GLU_78	OE2	3.114
1V7N	O_ARG_107	NH2	L_GLU_78	OE2	2.402
1V7N	V_ARG_98	NH2	H_ASP_31	OD1	3.580
1V7N	X_ARG_98	NH2	L_ASP_31	OD1	3.389
1V7N	X_HIS_121	ND1	J_ASP_217	OD1	2.619
1V7N	X_HIS_121	NE2	J_ASP_217	OD1	3.422
1V7N	Y_HIS_20	ND1	H_ASP_217	OD1	3.368
1V7N	Y_HIS_20	ND1	H_ASP_217	OD2	3.116
1V7N	Y_HIS_20	NE2	H_ASP_217	OD1	3.862
1V7N	Y_HIS_121	ND1	L_ASP_217	OD1	3.108
1V7N	Z_ARG_98	NH2	K_ASP_31	OD1	3.622
1V7N	Z_ARG_140	NH2	M_GLU_212	OE1	3.768
1VES	A_ARG_25	NH1	B_ASP_4	OD1	3.636
1VES	A_ARG_25	NH1	B_ASP_4	OD2	2.836
1VES	A_ARG_25	NH2	B_ASP_4	OD1	2.879
1VES	A_ARG_25	NH2	B_ASP_4	OD2	3.552
1VES	B_ARG_25	NH1	A_ASP_4	OD1	3.762
1VES	B_ARG_25	NH1	A_ASP_4	OD2	2.782
1VES	B_ARG_25	NH2	A_ASP_4	OD1	3.070
1VES	B_ARG_25	NH2	A_ASP_4	OD2	3.548
1VFA	A_ARG_96	NH1	B_GLU_98	OE1	2.794
1VFA	A_ARG_96	NH1	B_GLU_98	OE2	3.600
1VFA	A_ARG_96	NH2	B_GLU_98	OE1	3.537
1VFA	A_ARG_96	NH2	B_GLU_98	OE2	2.928
1VFB	A_ARG_96	NH1	B_GLU_98	OE1	2.821

1VFB	A_ARG_96	NH1	B_GLU_98	OE2	3.695
1VFB	A_ARG_96	NH2	B_GLU_98	OE1	3.393
1VFB	A_ARG_96	NH2	B_GLU_98	OE2	2.813
1W72	A_ARG_35	NH1	B_ASP_53	OD1	2.945
1W72	A_ARG_48	NH1	B_ASP_53	OD2	3.978
1W72	A_ARG_48	NH2	B_ASP_53	OD1	3.455
1W72	A_ARG_48	NH2	B_ASP_53	OD2	2.916
1W72	A_ARG_65	NH1	H_ASP_30	OD1	3.409
1W72	A_ARG_65	NH1	H_ASP_31	OD1	2.977
1W72	A_ARG_114	NH1	C_ASP_3	OD2	3.999
1W72	A_LYS_146	NZ	L_ASP_95A	OD1	3.112
1W72	A_LYS_146	NZ	L_ASP_95A	OD2	3.996
1W72	A_ARG_156	NH1	C_ASP_3	OD1	3.704
1W72	A_ARG_156	NH1	C_ASP_3	OD2	2.953
1W72	A_ARG_163	NH1	C_GLU_1	OE1	3.400
1W72	A_ARG_163	NH2	C_GLU_1	OE1	3.293
1W72	A_ARG_163	NH2	C_GLU_1	OE2	3.482
1W72	A_ARG_170	NH1	C_GLU_1	OE2	3.205
1W72	A_ARG_170	NH2	C_GLU_1	OE2	2.677
1W72	A_HIS_192	NE2	B_ASP_98	OD1	3.224
1W72	A_HIS_192	NE2	B_ASP_98	OD2	2.823
1W72	B_LYS_6	NZ	A_GLU_232	OE1	3.881
1W72	D_ARG_35	NH2	E_ASP_53	OD1	3.761
1W72	D_ARG_65	NH1	I_ASP_30	OD1	2.970
1W72	D_ARG_65	NH1	I_ASP_31	OD1	3.035
1W72	D_LYS_146	NZ	M_ASP_95A	OD2	3.397
1W72	D_ARG_156	NH1	F_ASP_3	OD1	3.644
1W72	D_ARG_156	NH1	F_ASP_3	OD2	3.082
1W72	D_ARG_163	NH1	F_GLU_1	OE1	3.609
1W72	D_ARG_163	NH1	F_GLU_1	OE2	3.022
1W72	D_HIS_192	NE2	E_ASP_98	OD2	3.123
1W72	E_LYS_6	NZ	D_GLU_232	OE2	2.863
1W72	H_LYS_145	NZ	L_GLU_124	OE2	2.720
1W72	H_LYS_221	NZ	L_GLU_123	OE1	2.737
1W72	H_LYS_221	NZ	L_GLU_123	OE2	3.946
1W72	I_LYS_145	NZ	M_GLU_124	OE2	2.470
1W72	I_LYS_228	NZ	M_GLU_123	OE2	3.514
1W72	M_HIS_95B	NE2	I_ASP_61	OD2	3.924
1WEJ	L_HIS_30	ND1	F_GLU_104	OE1	2.984
1WEJ	L_HIS_30	ND1	F_GLU_104	OE2	2.758
1WEJ	H_ARG_50	NH1	F_GLU_62	OE2	3.319
1WEJ	H_ARG_50	NH2	F_GLU_62	OE2	2.823
1WEJ	H_LYS_212	NZ	L_GLU_123	OE2	3.963
1WEJ	F_LYS_60	NZ	H_ASP_100	OD2	3.322
1XF2	H_LYS_208	NZ	L_GLU_123	OE1	3.369
1XF2	H_LYS_208	NZ	L_GLU_123	OE2	2.577
1XF2	B_LYS_208	NZ	A_GLU_123	OE2	2.913
1XGY	L_ARG_50	NH2	P_GLU_6	OE1	2.621
1XGY	H_LYS_208	NZ	L_GLU_123	OE2	3.768
1XGY	M_ARG_50	NH2	Q_GLU_6	OE1	3.022
1XGY	I_LYS_208	NZ	M_GLU_123	OE2	3.551
1XIW	A_ARG_80	NH1	D_ASP_106	OD2	2.879
1XIW	A_ARG_94	NH2	B_GLU_7	OE1	3.648
1XIW	A_ARG_94	NH2	B_GLU_7	OE2	2.974
1XIW	B_LYS_2	NZ	A_ASP_42	OD1	3.017
1XIW	B_LYS_2	NZ	A_ASP_42	OD2	2.678
1XIW	C_ARG_31	NH1	A_ASP_86	OD1	2.919
1XIW	C_ARG_31	NH1	A_ASP_86	OD2	3.491

1XIW	C_ARG_31	NH2	A_ASP_86	OD1	3.709
1XIW	C_ARG_31	NH2	A_ASP_86	OD2	2.755
1XIW	C_ARG_54	NH1	F_GLU_6	OE1	2.951
1XIW	C_ARG_54	NH2	F_GLU_6	OE1	3.193
1XIW	C_ARG_54	NH2	F_GLU_6	OE2	3.073
1XIW	C_HIS_56	ND1	F_GLU_9	OE1	3.139
1XIW	C_HIS_56	ND1	F_GLU_9	OE2	2.963
1XIW	D_LYS_55	NZ	A_ASP_57	OD1	3.690
1XIW	E_ARG_80	NH1	H_ASP_106	OD2	2.741
1XIW	E_ARG_94	NH2	F_GLU_7	OE2	3.577
1XIW	F_LYS_2	NZ	E_ASP_42	OD1	3.079
1XIW	F_LYS_2	NZ	E_ASP_42	OD2	3.491
1XIW	G_ARG_31	NH1	E_ASP_86	OD1	3.076
1XIW	G_ARG_31	NH1	E_ASP_86	OD2	3.219
1XIW	G_ARG_31	NH2	E_ASP_86	OD2	2.817
1XIW	G_ARG_54	NH1	B_GLU_6	OE1	2.839
1XIW	G_ARG_54	NH2	B_GLU_6	OE1	3.146
1XIW	G_ARG_54	NH2	B_GLU_6	OE2	3.222
1XIW	G_HIS_56	ND1	B_GLU_9	OE1	2.509
1XIW	G_HIS_56	ND1	B_GLU_9	OE2	3.961
1YEI	L_LYS_30	NZ	H_GLU_100B	OE1	2.979
1YEI	L_LYS_45	NZ	H_ASP_101	OD1	2.746
1YEI	L_LYS_45	NZ	H_ASP_101	OD2	3.891
1YEI	L_ARG_46	NH2	H_ASP_101	OD1	3.707
1YEI	L_HIS_49	NE2	H_ASP_100C	OD1	3.542
1YEJ	L_LYS_45	NZ	H_ASP_101	OD1	2.790
1YEJ	L_LYS_45	NZ	H_ASP_101	OD2	3.988
1YEJ	L_ARG_46	NH2	H_ASP_101	OD1	3.745
1YEJ	L_HIS_49	NE2	H_ASP_100C	OD1	3.536
1YEJ	L_LYS_53	NZ	H_ASP_100C	OD1	3.377
1YEJ	L_LYS_53	NZ	H_ASP_100C	OD2	3.298
1YEK	L_LYS_30	NZ	H_GLU_100B	OE1	2.464
1YEK	L_LYS_45	NZ	H_ASP_101	OD1	2.830
1YEK	L_ARG_46	NH2	H_ASP_101	OD1	3.853
1YEK	L_HIS_49	NE2	H_ASP_100C	OD1	3.610
1YNT	A_ARG_24	NH1	C_ASP_1070	OD2	3.114
1YNT	A_ARG_24	NH2	C_ASP_1070	OD2	3.728
1YNT	B_LYS_563	NZ	A_ASP_1	OD1	2.935
1YNT	B_LYS_563	NZ	A_ASP_1	OD2	3.384
1YNT	B_LYS_713	NZ	A_GLU_123	OE1	3.645
1YNT	C_ARG_1024	NH1	A_ASP_70	OD2	3.173
1YNT	C_ARG_1024	NH2	A_ASP_70	OD2	3.802
1YNT	C_LYS_1107	NZ	E_GLU_869	OE1	3.719
1YNT	D_LYS_1563	NZ	C_ASP_1001	OD1	2.913
1YNT	D_LYS_1563	NZ	C_ASP_1001	OD2	3.385
1YNT	D_LYS_1713	NZ	C_GLU_1123	OE1	3.557
1YNT	E_LYS_824	NZ	A_ASP_143	OD1	3.012
1YNT	E_LYS_824	NZ	A_ASP_143	OD2	3.238
1YNT	E_LYS_833	NZ	A_ASP_17	OD2	3.941
1YQV	L_ARG_46	NH2	H_ASP_101	OD2	3.072
1YQV	H_LYS_221	NZ	L_GLU_123	OE1	3.123
1YQV	H_LYS_221	NZ	L_GLU_123	OE2	2.724
1YQV	Y_ARG_45	NH1	H_GLU_50	OE1	3.514
1YQV	Y_ARG_45	NH1	H_GLU_50	OE2	2.957
1YQV	Y_ARG_68	NH1	H_GLU_50	OE1	2.746
1YQV	Y_ARG_68	NH1	H_GLU_50	OE2	3.759
1YQV	Y_ARG_68	NH2	H_GLU_50	OE1	3.492
1YQV	Y_ARG_68	NH2	H_GLU_50	OE2	2.963

1YYL	G_ARG_419	NH1	H_GLU_100D	OE2	3.749
1YYL	G_ARG_419	NH2	H_GLU_99	OE2	2.852
1YYL	G_ARG_419	NH2	H_GLU_100D	OE1	3.510
1YYL	G_ARG_419	NH2	H_GLU_100D	OE2	2.773
1YYL	H_LYS_209	NZ	L_GLU_123	OE1	2.745
1YYL	H_LYS_209	NZ	L_GLU_123	OE2	3.202
1YYL	P_ARG_1419	NH1	R_GLU_1100B	OE1	3.247
1YYL	P_ARG_1419	NH2	R_GLU_1099	OE1	2.456
1YYL	P_ARG_1419	NH2	R_GLU_1100D	OE1	3.853
1YYL	R_LYS_1201	NZ	H_GLU_10	OE1	3.633
1YYL	R_LYS_1209	NZ	Q_GLU_1123	OE2	3.934
1YYL	S_ARG_1009	NH1	P_ASP_1368	OD2	3.204
1YYL	S_ARG_1009	NH2	P_ASP_1368	OD2	2.930
1YYM	G_ARG_419	NH2	H_GLU_99	OE2	2.868
1YYM	G_ARG_419	NH2	H_GLU_100D	OE1	3.511
1YYM	H_LYS_209	NZ	L_GLU_123	OE1	2.715
1YYM	H_LYS_209	NZ	L_GLU_123	OE2	2.976
1YYM	P_ARG_1419	NH1	R_GLU_1100B	OE1	2.635
1YYM	P_ARG_1419	NH2	R_GLU_1099	OE1	3.192
1YYM	S_ARG_1009	NH1	P_ASP_1368	OD2	3.572
1YYM	S_ARG_1009	NH2	P_ASP_1368	OD2	2.725
1ZEA	H_ARG_95	NH1	L_GLU_34	OE1	2.842
1ZEA	H_ARG_95	NH1	L_GLU_34	OE2	3.642
1ZEA	H_ARG_95	NH2	L_GLU_34	OE1	3.613
1ZEA	H_ARG_95	NH2	L_GLU_34	OE2	2.859
1ZEA	H_LYS_208	NZ	L_GLU_123	OE2	2.817
2AAB	H_LYS_208	NZ	L_GLU_123	OE1	3.545
2B2X	A_HIS_261	NE2	H_ASP_101	OD2	3.121
2B2X	H_HIS_169	NE2	L_ASP_171	OD2	3.832
2B2X	H_LYS_213	NZ	L_GLU_127	OE1	2.709
2B2X	H_LYS_213	NZ	L_GLU_127	OE2	3.416
2B2X	L_HIS_31	NE2	A_GLU_259	OE2	3.821
2B2X	B_HIS_261	NE2	L_ASP_101	OD2	3.107
2B2X	L_HIS_169	NE2	M_ASP_171	OD2	3.874
2B2X	L_LYS_213	NZ	M_GLU_127	OE2	3.245
2B2X	M_HIS_31	NE2	B_GLU_259	OE2	3.848
2B4C	G_ARG_	NH1	H_ASP_	OD2	3.237
2B4C	G_ARG_	NH2	H_ASP_	OD2	2.859
2B4C	G_LYS_	NZ	H_ASP_	OD2	2.598
2B4C	C_ARG_	NH1	H_GLU_	OE2	3.957
2B4C	C_ARG_	NH2	H_GLU_	OE2	3.405
2B4C	C_ARG_	NH1	G_ASP_	OD1	2.937
2B4C	C_ARG_	NH1	G_ASP_	OD2	3.245
2B4C	H_LYS_	NZ	L_GLU_	OE1	3.365
2B4C	H_LYS_209	NZ	L_GLU_123	OE2	3.837
2BDN	A_LYS_56	NZ	H_ASP_52	OD1	2.539
2BDN	A_LYS_56	NZ	H_ASP_52	OD2	3.792
2BDN	L_ARG_32	NH1	A_ASP_65	OD1	3.196
2BDN	L_ARG_32	NH1	A_ASP_68	OD1	2.578
2BDN	L_ARG_32	NH2	A_ASP_65	OD1	2.774
2BDN	H_ARG_98	NH1	A_GLU_39	OE2	3.155
2BDN	H_LYS_212	NZ	L_GLU_123	OE2	3.177
2BRR	H_ARG_213	NH1	L_GLU_123	OE1	2.600
2BRR	H_ARG_213	NH1	L_GLU_123	OE2	3.932
2BRR	H_ARG_213	NH2	L_GLU_123	OE1	3.110
2BRR	H_ARG_213	NH2	L_GLU_123	OE2	3.029
2BRR	P_LYS_7	NZ	H_ASP_95	OD1	3.067
2BRR	P_LYS_7	NZ	H_ASP_95	OD2	2.549

2BRR	P_HIS_11	ND1	Y_ASP_95	OD2	2.841
2BRR	Y_LYS_208	NZ	X_GLU_123	OE2	3.359
2BRR	Y_ARG_213	NH1	X_GLU_123	OE1	2.523
2BRR	Y_ARG_213	NH1	X_GLU_123	OE2	3.327
2BRR	Y_ARG_213	NH2	X_GLU_123	OE1	3.468
2BRR	Y_ARG_213	NH2	X_GLU_123	OE2	2.546
2DBL	H_LYS_221	NZ	L_GLU_123	OE2	3.660
2DQC	Y_LYS_97	NZ	H_ASP_32	OD1	2.612
2DQC	Y_LYS_97	NZ	H_ASP_32	OD2	3.998
2DQC	Y_LYS_97	NZ	H_ASP_99	OD1	3.500
2DQC	Y_LYS_97	NZ	H_ASP_99	OD2	2.637
2DQD	Y_LYS_97	NZ	H_ASP_32	OD1	2.767
2DQD	Y_LYS_97	NZ	H_ASP_32	OD2	3.965
2DQD	Y_LYS_97	NZ	H_ASP_99	OD1	3.334
2DQD	Y_LYS_97	NZ	H_ASP_99	OD2	3.048
2DQE	Y_LYS_97	NZ	H_ASP_32	OD1	2.650
2DQE	Y_LYS_97	NZ	H_ASP_99	OD1	3.314
2DQE	Y_LYS_97	NZ	H_ASP_99	OD2	2.899
2DQF	A_ARG_45	NH1	E_ASP_1	OD2	3.511
2DQF	A_LYS_49	NZ	B_ASP_99	OD1	3.470
2DQF	A_ARG_61	NH1	E_ASP_27	OD1	3.814
2DQF	C_LYS_97	NZ	B_ASP_99	OD1	3.543
2DQF	C_LYS_97	NZ	B_ASP_99	OD2	2.851
2DQF	D_LYS_39	NZ	B_ASP_1	OD1	3.005
2DQF	D_ARG_61	NH1	B_ASP_27	OD1	3.581
2DQF	F_LYS_97	NZ	E_ASP_99	OD2	3.165
2DQG	Y_LYS_97	NZ	H_ASP_32	OD1	3.992
2DQG	Y_LYS_97	NZ	H_ASP_32	OD2	2.695
2DQG	Y_LYS_97	NZ	H_ASP_99	OD1	3.156
2DQG	Y_LYS_97	NZ	H_ASP_99	OD2	3.019
2DQH	Y_LYS_97	NZ	H_ASP_32	OD1	2.777
2DQH	Y_LYS_97	NZ	H_ASP_99	OD1	3.694
2DQH	Y_LYS_97	NZ	H_ASP_99	OD2	2.635
2DQI	L_LYS_49	NZ	H_ASP_99	OD1	2.843
2DQI	L_LYS_49	NZ	H_ASP_101	OD1	3.541
2DQI	L_LYS_49	NZ	H_ASP_101	OD2	3.285
2DQI	Y_LYS_97	NZ	H_ASP_32	OD1	2.729
2DQJ	Y_LYS_97	NZ	H_ASP_32	OD1	2.638
2DQJ	Y_LYS_97	NZ	H_ASP_32	OD2	3.939
2DQJ	Y_LYS_97	NZ	H_ASP_99	OD1	3.482
2DQJ	Y_LYS_97	NZ	H_ASP_99	OD2	2.865
2DQT	L_LYS_50	NZ	H_ASP_100C	OD1	3.056
2DQT	H_ARG_100B	NH2	L_ASP_30	OD1	3.486
2DQT	H_ARG_100B	NH2	L_ASP_30	OD2	3.745
2DQU	L_LYS_50	NZ	H_ASP_100C	OD1	2.628
2DQU	L_LYS_50	NZ	H_ASP_100C	OD2	3.616
2DQU	H_ARG_100B	NH2	L_ASP_30	OD2	2.721
2DQU	H_LYS_208	NZ	L_GLU_123	OE2	2.915
2DQU	H_ARG_213	NH1	L_GLU_123	OE1	3.471
2FB4	H_LYS_148	NZ	L_GLU_126	OE2	2.805
2FB4	H_LYS_214	NZ	L_GLU_125	OE1	3.053
2FB4	H_LYS_214	NZ	L_GLU_125	OE2	2.759
2FD6	A_HIS_87	ND1	U_ASP_11	OD2	3.705
2FD6	H_HIS_98	ND1	L_GLU_50	OE1	3.050
2FD6	H_HIS_98	ND1	L_GLU_50	OE2	3.997
2FD6	H_LYS_203	NZ	L_GLU_122	OE2	2.585
2FD6	U_ARG_192	NH1	H_GLU_58	OE2	2.359
2FD6	U_ARG_192	NH2	H_GLU_58	OE2	3.898

2FR4	H.LYS_208	NZ	L_GLU_123	OE2	3.199
2FR4	B.LYS_208	NZ	A_GLU_123	OE1	2.539
2H32	H.ARG_59	NH1	A_GLU_106	OE1	3.937
2H32	H.ARG_59	NH1	A_GLU_106	OE2	3.372
2H32	H.ARG_59	NH2	A_GLU_106	OE2	3.412
2H9G	B.HIS_53	ND1	R_GLU_36	OE2	3.471
2H9G	B.LYS_209	NZ	A_GLU_123	OE1	2.713
2H9G	H.LYS_209	NZ	L_GLU_123	OE1	2.570
2HFG	H.ARG_95	NH2	R_ASP_26	OD1	2.783
2HFG	H.ARG_95	NH2	R_ASP_26	OD2	3.667
2HFG	H.LYS_209	NZ	L_GLU_122	OE1	3.336
2HFG	H.LYS_209	NZ	L_GLU_122	OE2	2.886
2HKF	L.LYS_55	NZ	P_ASP_6	OD1	2.651
2HKF	H.ARG_50	NH2	P_GLU_5	OE1	3.869
2HKF	H.ARG_50	NH2	P_GLU_5	OE2	2.886
2HKF	H.ARG_52	NH2	P_GLU_5	OE1	3.116
2HKF	H.LYS_214	NZ	L_GLU_128	OE2	2.891
2HMG	A.LYS_27	NZ	B_GLU_97	OE1	2.762
2HMG	A.LYS_27	NZ	B_GLU_97	OE2	3.001
2HMG	A.ARG_109	NH1	B_GLU_67	OE1	3.634
2HMG	A.ARG_109	NH1	B_GLU_67	OE2	2.959
2HMG	A.ARG_269	NH2	B_GLU_67	OE1	2.999
2HMG	A.LYS_299	NZ	B_GLU_69	OE1	3.169
2HMG	B.ARG_54	NH1	F_GLU_97	OE1	2.721
2HMG	B.ARG_54	NH2	F_GLU_97	OE1	3.280
2HMG	B.LYS_62	NZ	F_ASP_86	OD1	3.023
2HMG	B.LYS_62	NZ	F_ASP_86	OD2	2.718
2HMG	B.LYS_62	NZ	F_ASP_90	OD1	3.256
2HMG	B.LYS_62	NZ	F_ASP_90	OD2	2.780
2HMG	B.HIS_64	NE2	F_ASP_79	OD2	3.863
2HMG	B.ARG_76	NH1	D_GLU_74	OE1	3.508
2HMG	B.ARG_76	NH1	D_GLU_74	OE2	2.816
2HMG	B.ARG_76	NH1	D_GLU_81	OE1	2.774
2HMG	B.ARG_76	NH1	D_GLU_81	OE2	3.655
2HMG	B.ARG_76	NH2	D_GLU_74	OE1	2.915
2HMG	B.ARG_76	NH2	D_GLU_74	OE2	3.598
2HMG	B.ARG_123	NH1	F_GLU_132	OE2	3.122
2HMG	B.ARG_124	NH1	F_GLU_132	OE1	3.544
2HMG	B.ARG_124	NH1	F_GLU_132	OE2	3.040
2HMG	B.ARG_127	NH2	F_GLU_131	OE1	2.502
2HMG	B.ARG_163	NH1	F_GLU_131	OE1	2.668
2HMG	B.ARG_163	NH1	F_GLU_131	OE2	2.605
2HMG	B.ARG_170	NH1	D_GLU_128	OE1	3.860
2HMG	B.ARG_170	NH2	D_GLU_128	OE1	2.750
2HMG	B.ARG_170	NH2	D_GLU_128	OE2	3.837
2HMG	C.LYS_27	NZ	D_GLU_97	OE1	2.819
2HMG	C.LYS_27	NZ	D_GLU_97	OE2	3.060
2HMG	C.ARG_109	NH1	D_GLU_67	OE1	3.653
2HMG	C.ARG_109	NH1	D_GLU_67	OE2	2.947
2HMG	C.ARG_269	NH2	D_GLU_67	OE1	2.972
2HMG	C.LYS_299	NZ	D_GLU_69	OE1	3.147
2HMG	D.ARG_54	NH1	B_GLU_97	OE1	2.735
2HMG	D.ARG_54	NH2	B_GLU_97	OE1	3.312
2HMG	D.LYS_62	NZ	B_ASP_86	OD1	3.037
2HMG	D.LYS_62	NZ	B_ASP_86	OD2	2.683
2HMG	D.LYS_62	NZ	B_ASP_90	OD1	3.222
2HMG	D.LYS_62	NZ	B_ASP_90	OD2	2.673
2HMG	D.HIS_64	NE2	B_ASP_79	OD2	3.737

2HMG	D_ARG_76	NH1	F_GLU_74	OE1	3.549
2HMG	D_ARG_76	NH1	F_GLU_74	OE2	2.731
2HMG	D_ARG_76	NH1	F_GLU_81	OE1	2.698
2HMG	D_ARG_76	NH1	F_GLU_81	OE2	3.690
2HMG	D_ARG_76	NH2	F_GLU_74	OE1	2.828
2HMG	D_ARG_76	NH2	F_GLU_74	OE2	3.390
2HMG	D_ARG_123	NH1	B_GLU_132	OE2	3.058
2HMG	D_ARG_124	NH1	B_GLU_132	OE1	3.508
2HMG	D_ARG_124	NH1	B_GLU_132	OE2	3.040
2HMG	D_ARG_127	NH2	B_GLU_131	OE1	2.517
2HMG	D_ARG_163	NH1	B_GLU_131	OE1	2.667
2HMG	D_ARG_163	NH1	B_GLU_131	OE2	2.648
2HMG	D_ARG_170	NH1	F_GLU_128	OE1	3.974
2HMG	D_ARG_170	NH2	F_GLU_128	OE1	2.843
2HMG	E_LYS_27	NZ	F_GLU_97	OE1	2.743
2HMG	E_LYS_27	NZ	F_GLU_97	OE2	3.029
2HMG	E_ARG_109	NH1	F_GLU_67	OE1	3.629
2HMG	E_ARG_109	NH1	F_GLU_67	OE2	2.891
2HMG	E_ARG_269	NH2	F_GLU_67	OE1	2.967
2HMG	E_LYS_299	NZ	F_GLU_69	OE1	3.127
2HMG	F_ARG_54	NH1	D_GLU_97	OE1	2.701
2HMG	F_ARG_54	NH2	D_GLU_97	OE1	3.310
2HMG	F_LYS_62	NZ	D_ASP_86	OD1	2.945
2HMG	F_LYS_62	NZ	D_ASP_86	OD2	2.624
2HMG	F_LYS_62	NZ	D_ASP_90	OD1	3.290
2HMG	F_LYS_62	NZ	D_ASP_90	OD2	2.741
2HMG	F_HIS_64	NE2	D_ASP_79	OD2	3.679
2HMG	F_ARG_76	NH1	B_GLU_74	OE1	3.499
2HMG	F_ARG_76	NH1	B_GLU_74	OE2	2.732
2HMG	F_ARG_76	NH1	B_GLU_81	OE1	2.710
2HMG	F_ARG_76	NH1	B_GLU_81	OE2	3.754
2HMG	F_ARG_76	NH2	B_GLU_74	OE1	2.743
2HMG	F_ARG_76	NH2	B_GLU_74	OE2	3.373
2HMG	F_ARG_123	NH1	D_GLU_132	OE2	3.112
2HMG	F_ARG_124	NH1	D_GLU_132	OE1	3.531
2HMG	F_ARG_124	NH1	D_GLU_132	OE2	3.090
2HMG	F_ARG_127	NH2	D_GLU_131	OE1	2.569
2HMG	F_ARG_163	NH1	D_GLU_131	OE1	2.672
2HMG	F_ARG_163	NH1	D_GLU_131	OE2	2.717
2HMG	F_ARG_170	NH1	B_GLU_128	OE1	3.849
2HMG	F_ARG_170	NH2	B_GLU_128	OE1	2.798
2HMG	F_ARG_170	NH2	B_GLU_128	OE2	3.855
2HRP	L_LYS_30	NZ	H_ASP_100B	OD2	3.323
2HRP	L_ARG_61	NH1	M_GLU_79	OE1	2.692
2HRP	L_ARG_61	NH1	M_GLU_79	OE2	2.607
2HRP	L_ARG_108	NH1	N_ASP_1	OD1	3.613
2HRP	L_ARG_108	NH1	N_ASP_1	OD2	2.869
2HRP	L_ARG_108	NH2	N_ASP_1	OD1	3.306
2HRP	L_ARG_108	NH2	N_ASP_1	OD2	3.988
2HRP	H_LYS_205	NZ	N_ASP_207	OD2	3.339
2HRP	H_LYS_208	NZ	L_GLU_123	OE1	2.834
2HRP	M_LYS_30	NZ	N_ASP_100B	OD2	3.922
2HRP	M_ARG_61	NH1	L_GLU_79	OE1	2.827
2HRP	M_ARG_61	NH1	L_GLU_79	OE2	2.489
2HRP	M_ARG_61	NH2	L_GLU_79	OE1	3.658
2HRP	M_ARG_108	NH1	H_ASP_1	OD2	3.449
2HRP	N_LYS_208	NZ	M_GLU_123	OE1	2.875
2HRP	N_LYS_208	NZ	M_GLU_123	OE2	3.117

2I25	N_ARG_25	NH1	O_ASP_101	OD1	3.459
2I25	N_ARG_25	NH1	O_ASP_101	OD2	3.204
2I25	N_ARG_25	NH2	O_ASP_101	OD1	2.762
2I25	N_ARG_25	NH2	O_ASP_101	OD2	3.967
2I25	N_ARG_88	NH2	L_ASP_101	OD1	2.875
2I25	N_ARG_88	NH2	L_ASP_101	OD2	3.303
2I25	L_ARG_61	NH2	N_ASP_101	OD2	3.227
2I25	L_ARG_73	NH1	N_GLU_86	OE1	3.764
2I25	L_ARG_73	NH1	N_GLU_86	OE2	2.771
2I25	L_ARG_112	NH2	N_ASP_93	OD1	2.693
2I25	O_ARG_44	NH2	N_GLU_57	OE1	3.011
2I25	O_ARG_88	NH2	M_ASP_101	OD1	2.850
2I25	O_ARG_88	NH2	M_ASP_101	OD2	3.440
2I25	M_ARG_61	NH2	O_ASP_101	OD2	2.975
2I25	M_ARG_73	NH1	O_GLU_86	OE1	3.850
2I25	M_ARG_73	NH1	O_GLU_86	OE2	2.851
2I25	M_ARG_112	NH1	O_ASP_93	OD1	3.660
2I25	M_ARG_112	NH2	O_ASP_93	OD1	3.176
2I26	N_ARG_88	NH2	L_ASP_101	OD1	3.268
2I26	N_ARG_88	NH2	L_ASP_101	OD2	3.652
2I26	L_ARG_73	NH1	N_GLU_86	OE2	3.511
2I26	L_ARG_73	NH2	N_GLU_86	OE1	3.590
2I26	L_ARG_73	NH2	N_GLU_86	OE2	3.542
2I26	L_ARG_112	NH1	N_ASP_93	OD2	3.838
2I26	L_ARG_112	NH2	N_ASP_93	OD2	3.391
2I26	O_ARG_88	NH1	M_ASP_101	OD1	2.648
2I26	O_ARG_88	NH1	M_ASP_101	OD2	2.840
2I26	M_ARG_73	NH1	O_GLU_86	OE1	2.832
2I26	M_ARG_73	NH1	O_GLU_86	OE2	3.677
2I26	M_ARG_112	NH1	O_ASP_93	OD2	3.127
2I26	M_ARG_112	NH2	O_ASP_93	OD2	3.198
2I26	P_ARG_88	NH1	Q_ASP_101	OD1	3.139
2I26	P_ARG_88	NH1	Q_ASP_101	OD2	3.016
2I26	Q_ARG_61	NH2	P_ASP_101	OD2	3.115
2I26	Q_ARG_73	NH1	P_GLU_86	OE2	2.623
2I26	Q_ARG_112	NH1	P_ASP_93	OD2	3.805
2I26	Q_ARG_112	NH2	P_ASP_93	OD2	3.685
2I27	N_ARG_25	NH2	O_GLU_46	OE2	3.350
2I5Y	G_ARG_419	NH1	H_GLU_100B	OE1	3.248
2I5Y	G_ARG_419	NH2	H_GLU_99	OE2	3.146
2I5Y	G_ARG_419	NH2	H_GLU_100D	OE2	2.601
2I5Y	H_LYS_201	NZ	R_GLU_10	OE2	3.615
2I5Y	H_LYS_209	NZ	L_GLU_123	OE1	2.531
2I5Y	H_LYS_209	NZ	L_GLU_123	OE2	3.403
2I5Y	P_ARG_419	NH1	R_GLU_99	OE2	3.800
2I5Y	P_ARG_419	NH1	R_GLU_100D	OE1	2.563
2I5Y	P_ARG_419	NH1	R_GLU_100D	OE2	3.898
2I5Y	R_LYS_209	NZ	Q_GLU_123	OE2	3.373
2I5Y	S_ARG_9	NH1	P_ASP_368	OD2	2.853
2I5Y	S_ARG_9	NH2	P_ASP_368	OD2	3.453
2I60	G_ARG_419	NH2	H_GLU_99	OE1	3.736
2I60	G_ARG_419	NH2	H_GLU_99	OE2	2.767
2I60	G_ARG_419	NH2	H_GLU_100D	OE2	3.611
2I60	H_LYS_209	NZ	L_GLU_123	OE1	3.997
2I60	P_ARG_419	NH1	R_GLU_100B	OE1	3.610
2I60	P_ARG_419	NH2	R_GLU_99	OE1	3.892
2I60	R_LYS_209	NZ	Q_GLU_123	OE2	3.485
2I60	S_ARG_9	NH1	P_ASP_368	OD2	3.268

2I60	S_ARG_9	NH2	P_ASP_368	OD1	3.938
2I60	S_ARG_9	NH2	P_ASP_368	OD2	2.664
2IFF	L_LYS_44	NZ	H_ASP_104	OD1	2.935
2IFF	L_ARG_45	NH2	H_ASP_104	OD2	3.348
2IFF	H_LYS_211	NZ	L_GLU_121	OE1	3.040
2IFF	H_LYS_211	NZ	L_GLU_121	OE2	2.921
2IFF	Y_ARG_45	NH1	H_GLU_50	OE1	3.425
2IFF	Y_ARG_45	NH1	H_GLU_50	OE2	2.959
2IG2	H_LYS_148	NZ	L_GLU_126	OE2	2.854
2IG2	H_LYS_214	NZ	L_GLU_125	OE1	3.816
2IG2	H_LYS_214	NZ	L_GLU_125	OE2	2.866
2IGF	H_LYS_221	NZ	L_GLU_123	OE1	3.203
2IGF	P_LYS_75	NZ	L_ASP_28	OD1	3.253
2IGF	P_LYS_75	NZ	L_ASP_28	OD2	2.849
2IGF	P_LYS_75	NZ	L_ASP_30	OD2	3.458
2J4W	D_LYS_427	NZ	H_ASP_52A	OD1	3.478
2J4W	D_LYS_427	NZ	H_ASP_52A	OD2	2.864
2J4W	H_LYS_221	NZ	L_GLU_123	OE1	3.280
2J4W	H_LYS_221	NZ	L_GLU_123	OE2	3.313
2J5L	A_LYS_485	NZ	C_ASP_52A	OD1	3.476
2J5L	A_LYS_485	NZ	C_ASP_52A	OD2	3.193
2JB6	B_LYS_216	NZ	A_GLU_128	OE2	3.078
2JEL	L_LYS_50	NZ	H_GLU_98	OE1	2.874
2JEL	L_LYS_50	NZ	P_GLU_66	OE1	3.050
2JEL	L_LYS_50	NZ	P_GLU_66	OE2	3.051
2NXY	A_ARG_419	NH1	D_GLU_3103	OE2	3.305
2NXY	A_ARG_419	NH2	D_GLU_3103	OE2	2.288
2NXY	B_LYS_1029	NZ	A_ASP_279	OD2	2.892
2NXY	B_ARG_1059	NH1	A_ASP_368	OD1	3.350
2NXY	B_ARG_1059	NH1	A_ASP_368	OD2	2.835
2NXY	B_ARG_1059	NH2	A_ASP_368	OD1	2.856
2NXY	B_ARG_1059	NH2	A_ASP_368	OD2	3.647
2NXY	D_LYS_3224	NZ	C_GLU_2125	OE2	3.113
2NXZ	A_ARG_419	NH1	D_GLU_3103	OE2	3.647
2NXZ	A_ARG_419	NH2	D_GLU_3103	OE2	2.536
2NXZ	B_LYS_1029	NZ	A_ASP_279	OD2	3.046
2NXZ	B_ARG_1059	NH1	A_ASP_368	OD1	3.623
2NXZ	B_ARG_1059	NH1	A_ASP_368	OD2	3.029
2NXZ	B_ARG_1059	NH2	A_ASP_368	OD1	2.916
2NXZ	B_ARG_1059	NH2	A_ASP_368	OD2	3.612
2NXZ	D_HIS_3179	NE2	C_ASP_2169	OD2	3.986
2NXZ	D_LYS_3224	NZ	C_GLU_2125	OE1	3.503
2NXZ	D_LYS_3224	NZ	C_GLU_2125	OE2	2.801
2NY0	A_ARG_419	NH1	D_GLU_3103	OE2	3.320
2NY0	A_ARG_419	NH2	D_GLU_3103	OE2	2.328
2NY0	B_LYS_1029	NZ	A_ASP_279	OD2	2.858
2NY0	B_ARG_1059	NH1	A_ASP_368	OD1	3.389
2NY0	B_ARG_1059	NH1	A_ASP_368	OD2	2.874
2NY0	B_ARG_1059	NH2	A_ASP_368	OD1	2.859
2NY0	B_ARG_1059	NH2	A_ASP_368	OD2	3.661
2NY0	D_LYS_3224	NZ	C_GLU_2125	OE2	3.518
2NY1	A_ARG_419	NH1	D_GLU_3103	OE2	3.396
2NY1	A_ARG_419	NH2	D_GLU_3103	OE1	3.789
2NY1	A_ARG_419	NH2	D_GLU_3103	OE2	2.363
2NY1	B_LYS_1029	NZ	A_ASP_279	OD2	3.031
2NY1	B_ARG_1059	NH1	A_ASP_368	OD1	3.481
2NY1	B_ARG_1059	NH1	A_ASP_368	OD2	3.131
2NY1	B_ARG_1059	NH2	A_ASP_368	OD1	2.526

2NY1	B_ARG_1059	NH2	A_ASP_368	OD2	3.458
2NY1	D_LYS_3224	NZ	C_GLU_2125	OE1	3.100
2NY1	D_LYS_3224	NZ	C_GLU_2125	OE2	3.945
2NY2	A_ARG_419	NH1	D_GLU_3103	OE2	2.325
2NY2	A_ARG_419	NH2	D_GLU_3103	OE2	3.124
2NY2	B_LYS_1029	NZ	A_ASP_279	OD2	2.981
2NY2	B_ARG_1059	NH1	A_ASP_368	OD1	3.464
2NY2	B_ARG_1059	NH1	A_ASP_368	OD2	2.895
2NY2	B_ARG_1059	NH2	A_ASP_368	OD1	2.934
2NY2	B_ARG_1059	NH2	A_ASP_368	OD2	3.638
2NY2	D_LYS_3224	NZ	C_GLU_2125	OE2	2.721
2NY3	A_ARG_419	NH1	D_GLU_3103	OE2	3.671
2NY3	A_ARG_419	NH2	D_GLU_3103	OE1	3.681
2NY3	A_ARG_419	NH2	D_GLU_3103	OE2	2.058
2NY3	B_LYS_1029	NZ	A_ASP_279	OD2	3.124
2NY3	B_ARG_1059	NH1	A_ASP_368	OD1	2.775
2NY3	B_ARG_1059	NH1	A_ASP_368	OD2	3.550
2NY3	B_ARG_1059	NH2	A_ASP_368	OD1	3.449
2NY3	B_ARG_1059	NH2	A_ASP_368	OD2	2.862
2NY3	D_LYS_3224	NZ	C_GLU_2125	OE1	3.624
2NY3	D_LYS_3224	NZ	C_GLU_2125	OE2	2.832
2NY4	A_ARG_419	NH1	D_GLU_3103	OE2	3.167
2NY4	A_ARG_419	NH2	D_GLU_3103	OE2	2.562
2NY4	B_LYS_1029	NZ	A_ASP_279	OD2	3.126
2NY4	B_ARG_1059	NH1	A_ASP_368	OD1	3.376
2NY4	B_ARG_1059	NH1	A_ASP_368	OD2	2.816
2NY4	B_ARG_1059	NH2	A_ASP_368	OD1	2.784
2NY4	B_ARG_1059	NH2	A_ASP_368	OD2	3.537
2NY4	D_LYS_3224	NZ	C_GLU_2125	OE1	3.625
2NY4	D_LYS_3224	NZ	C_GLU_2125	OE2	3.179
2NY5	G_ARG_419	NH2	H_GLU_3103	OE2	3.818
2NY5	C_LYS_1029	NZ	G_ASP_279	OD2	3.358
2NY5	C_ARG_1059	NH1	G_ASP_368	OD1	3.253
2NY5	C_ARG_1059	NH1	G_ASP_368	OD2	2.656
2NY5	C_ARG_1059	NH2	G_ASP_368	OD1	2.825
2NY5	C_ARG_1059	NH2	G_ASP_368	OD2	3.554
2NY5	H_LYS_3224	NZ	L_GLU_2125	OE1	3.285
2NY5	H_LYS_3224	NZ	L_GLU_2125	OE2	3.364
2NY6	A_ARG_419	NH2	D_GLU_3103	OE1	3.563
2NY6	A_ARG_419	NH2	D_GLU_3103	OE2	2.589
2NY6	B_LYS_1029	NZ	A_ASP_279	OD2	3.061
2NY6	B_ARG_1059	NH1	A_ASP_368	OD1	2.945
2NY6	B_ARG_1059	NH1	A_ASP_368	OD2	2.767
2NY6	B_ARG_1059	NH2	A_ASP_368	OD1	3.097
2NY6	D_LYS_3224	NZ	C_GLU_2125	OE1	3.158
2NY6	D_LYS_3224	NZ	C_GLU_2125	OE2	2.701
2NY7	H_LYS_221	NZ	L_GLU_123	OE1	3.153
2NY7	L_ARG_32	NH1	H_ASP_100F	OD2	2.962
2OR9	H_ARG_53	NH2	P_GLU_8	OE2	3.967
2OR9	L_LYS_208	NZ	M_GLU_123	OE2	3.803
2OSL	L_HIS_33	NE2	H_ASP_105	OD1	3.260
2OSL	L_HIS_33	NE2	H_ASP_105	OD2	2.885
2OSL	L_ARG_107	NH2	B_GLU_194	OE2	3.976
2OSL	B_HIS_33	ND1	A_ASP_105	OD2	3.615
2OSL	B_HIS_33	NE2	A_ASP_105	OD2	3.957
2OSL	A_LYS_217	NZ	B_GLU_122	OE1	2.793
2OTU	B_LYS_87	NZ	F_ASP_31	OD1	3.793
2OTU	B_LYS_87	NZ	F_ASP_31	OD2	2.711

2OTU	F_ARG_100	NH1	E_ASP_60	OD1	3.255
2OTU	F_ARG_100	NH1	E_ASP_60	OD2	3.915
2OTU	H_ARG_44	NH1	C_ASP_60	OD1	3.017
2OTU	H_ARG_44	NH1	C_ASP_60	OD2	3.518
2OTU	H_ARG_44	NH2	C_ASP_60	OD1	3.945
2OTU	H_ARG_44	NH2	C_ASP_60	OD2	3.013
2OTU	H_LYS_87	NZ	D_ASP_31	OD1	3.910
2OTU	H_LYS_87	NZ	D_ASP_31	OD2	2.759
2OTW	B_LYS_87	NZ	D_ASP_31	OD1	3.659
2OTW	B_LYS_87	NZ	D_ASP_31	OD2	2.671
2OTW	B_ARG_100	NH1	A_ASP_60	OD1	3.223
2OTW	B_ARG_100	NH1	A_ASP_60	OD2	3.943
2OTW	D_ARG_100	NH1	C_ASP_60	OD1	3.882
2OTW	D_ARG_100	NH1	C_ASP_60	OD2	3.653
2P8L	A_HIS_96	NE2	C_ASP_5	OD1	2.766
2P8L	B_ARG_58	NH1	C_GLU_3	OE1	1.911
2P8L	B_ARG_58	NH1	C_GLU_3	OE2	3.223
2P8L	B_ARG_58	NH2	C_GLU_3	OE1	3.943
2P8L	B_ARG_95	NH1	C_ASP_5	OD1	2.951
2P8L	B_ARG_95	NH1	C_ASP_5	OD2	3.619
2P8L	B_ARG_95	NH2	C_ASP_5	OD1	3.420
2P8L	B_ARG_95	NH2	C_ASP_5	OD2	2.971
2P8L	B_ARG_96	NH1	A_GLU_55	OE1	3.236
2P8L	B_ARG_96	NH1	A_GLU_55	OE2	3.320
2P8L	B_ARG_96	NH2	A_GLU_55	OE1	3.018
2P8L	B_LYS_209	NZ	A_GLU_123	OE1	3.743
2P8L	C_LYS_6	NZ	B_ASP_54	OD1	3.641
2P8L	C_LYS_6	NZ	B_ASP_54	OD2	3.025
2P8L	C_LYS_6	NZ	B_ASP_56	OD1	2.878
2P8M	A_HIS_96	NE2	C_ASP_3	OD2	2.613
2P8M	B_ARG_1	NH2	A_GLU_55	OE2	3.915
2P8M	B_ARG_58	NH2	C_GLU_1	OE1	2.510
2P8M	B_ARG_95	NH1	C_ASP_3	OD1	2.973
2P8M	B_ARG_95	NH1	C_ASP_3	OD2	3.042
2P8M	B_ARG_95	NH2	C_ASP_3	OD1	3.169
2P8M	B_ARG_96	NH1	A_GLU_55	OE1	3.351
2P8M	B_ARG_96	NH1	A_GLU_55	OE2	3.448
2P8M	B_ARG_96	NH2	A_GLU_55	OE1	3.393
2P8M	B_LYS_209	NZ	A_GLU_123	OE1	3.649
2P8M	C_LYS_4	NZ	B_ASP_54	OD1	2.903
2P8M	C_LYS_4	NZ	B_ASP_54	OD2	2.371
2P8M	C_LYS_4	NZ	B_ASP_56	OD2	3.183
2P8P	A_HIS_96	NE2	C_ASP_3	OD1	3.214
2P8P	B_ARG_58	NH2	C_GLU_1	OE2	3.147
2P8P	B_ARG_95	NH1	C_ASP_3	OD1	2.805
2P8P	B_ARG_95	NH1	C_ASP_3	OD2	3.510
2P8P	B_ARG_95	NH2	C_ASP_3	OD1	3.459
2P8P	B_ARG_95	NH2	C_ASP_3	OD2	2.629
2P8P	B_ARG_96	NH1	A_GLU_55	OE1	3.239
2P8P	B_ARG_96	NH1	A_GLU_55	OE2	3.518
2P8P	B_ARG_96	NH2	A_GLU_55	OE1	3.128
2P8P	B_LYS_210	NZ	A_GLU_123	OE1	3.349
2P8P	B_LYS_210	NZ	A_GLU_123	OE2	3.192
2P8P	C_LYS_4	NZ	B_ASP_54	OD1	3.623
2P8P	C_LYS_4	NZ	B_ASP_54	OD2	3.010
2P8P	C_LYS_4	NZ	B_ASP_56	OD2	2.836
2PR4	H_ARG_101	NH1	L_GLU_55	OE1	3.296
2PR4	H_ARG_101	NH1	L_GLU_55	OE2	3.376

2PR4	H_ARG_101	NH2	L_GLU_55	OE1	3.286
2PR4	H_LYS_228	NZ	L_GLU_123	OE1	3.151
2Q8A	A_LYS_203	NZ	L_ASP_32	OD1	3.044
2Q8A	A_LYS_203	NZ	L_ASP_32	OD2	2.513
2Q8A	L_ARG_96	NH1	A_ASP_204	OD1	2.971
2Q8A	L_ARG_96	NH1	A_ASP_204	OD2	2.580
2Q8A	L_ARG_96	NH2	A_ASP_204	OD1	2.882
2Q8A	L_ARG_96	NH2	A_ASP_204	OD2	3.927
2Q8A	L_ARG_96	NH2	H_GLU_59	OE2	3.755
2Q8A	H_HIS_35	NE2	A_ASP_204	OD2	3.930
2Q8B	A_LYS_203	NZ	L_ASP_32	OD1	3.779
2Q8B	A_LYS_203	NZ	L_ASP_32	OD2	2.847
2Q8B	L_ARG_96	NH1	A_ASP_204	OD1	3.458
2Q8B	L_ARG_96	NH1	A_ASP_204	OD2	2.952
2Q8B	L_ARG_96	NH2	A_ASP_204	OD1	2.667
2Q8B	L_ARG_96	NH2	A_ASP_204	OD2	3.462
2QAD	B_ARG_59	NH1	A_ASP_368	OD1	3.394
2QAD	B_ARG_59	NH1	A_ASP_368	OD2	2.749
2QAD	B_ARG_59	NH2	A_ASP_368	OD1	3.764
2QAD	C_LYS_50	NZ	D_GLU_100F	OE2	2.989
2QAD	C_LYS_55	NZ	D_ASP_101	OD1	3.312
2QAD	C_LYS_55	NZ	D_ASP_101	OD2	3.736
2QAD	F_ARG_59	NH1	E_ASP_368	OD1	2.855
2QAD	F_ARG_59	NH1	E_ASP_368	OD2	2.624
2QAD	F_ARG_59	NH2	E_ASP_368	OD1	3.681
2QAD	G_LYS_50	NZ	H_GLU_100F	OE2	3.151
2QAD	G_LYS_55	NZ	H_ASP_101	OD1	3.191
2QAD	G_LYS_55	NZ	H_ASP_101	OD2	3.496
2QQN	H_LYS_209	NZ	L_GLU_123	OE1	2.782
2QQN	H_LYS_209	NZ	L_GLU_123	OE2	3.506
2QQN	H_LYS_214	NZ	L_ASP_122	OD1	3.854
2R29	A_LYS_307	NZ	H_ASP_99	OD1	2.956
2R29	A_LYS_307	NZ	L_GLU_59	OE1	3.335
2R29	A_LYS_310	NZ	H_ASP_52	OD1	3.449
2R29	A_LYS_310	NZ	H_ASP_52	OD2	2.764
2R29	H_LYS_59	NZ	L_ASP_98	OD2	3.485
2R29	L_ARG_54	NH2	H_GLU_101	OE1	3.814
2R29	L_ARG_54	NH2	H_GLU_101	OE2	3.270
2R29	L_LYS_107	NZ	H_GLU_42	OE1	3.937
2R69	A_LYS_307	NZ	H_ASP_99	OD2	3.631
2R69	H_LYS_59	NZ	L_ASP_98	OD2	3.723
2R69	H_LYS_211	NZ	L_GLU_127	OE1	3.695
2R69	H_LYS_211	NZ	L_GLU_127	OE2	3.159
2R69	L_ARG_31	NH2	A_GLU_311	OE2	3.151
2R69	L_ARG_54	NH2	H_GLU_101	OE1	2.992
2R69	L_ARG_54	NH2	H_GLU_101	OE2	2.911
2UYL	A_ARG_101	NH1	B_GLU_99	OE1	3.183
2UYL	A_ARG_101	NH1	B_GLU_99	OE2	3.530
2UYL	A_ARG_101	NH2	B_GLU_99	OE2	3.803
2UYL	M_ARG_101	NH1	N_GLU_99	OE1	3.058
2UYL	M_ARG_101	NH1	N_GLU_99	OE2	3.775
2UYL	M_ARG_101	NH2	N_GLU_99	OE2	3.923
2UYL	N_HIS_170	NE2	M_ASP_172	OD1	3.811
2UYL	V_ARG_101	NH1	W_GLU_99	OE1	2.958
2UYL	V_ARG_101	NH1	W_GLU_99	OE2	3.417
2UYL	V_ARG_101	NH2	W_GLU_99	OE2	3.369
2UYL	X_ARG_101	NH1	Y_GLU_99	OE1	2.789
2UYL	X_ARG_101	NH1	Y_GLU_99	OE2	3.483

2UYL	X_ARG_101	NH2	Y_GLU_99	OE2	3.405
2VC2	A_ARG_77	NH1	H_ASP_102	OD1	3.536
2VC2	A_ARG_77	NH1	H_ASP_102	OD2	3.007
2VC2	A_ARG_77	NH2	H_ASP_102	OD1	2.794
2VC2	A_ARG_77	NH2	H_ASP_102	OD2	3.630
2VC2	B_ARG_216	NH2	A_GLU_123	OE2	3.081
2VC2	B_LYS_253	NZ	A_ASP_232	OD2	2.805
2VC2	H_LYS_214	NZ	L_GLU_123	OE2	3.240
2VDK	A_ARG_77	NH1	H_ASP_102	OD1	3.535
2VDK	A_ARG_77	NH1	H_ASP_102	OD2	3.168
2VDK	A_ARG_77	NH2	H_ASP_102	OD1	2.738
2VDK	A_ARG_77	NH2	H_ASP_102	OD2	3.673
2VDK	B_ARG_216	NH2	A_GLU_123	OE2	3.072
2VDK	B_LYS_253	NZ	A_ASP_232	OD2	2.921
2VDK	H_LYS_214	NZ	L_GLU_123	OE2	3.461
2VDL	A_ARG_77	NH1	H_ASP_102	OD1	3.566
2VDL	A_ARG_77	NH1	H_ASP_102	OD2	3.106
2VDL	A_ARG_77	NH2	H_ASP_102	OD1	2.722
2VDL	A_ARG_77	NH2	H_ASP_102	OD2	3.538
2VDL	B_ARG_216	NH2	A_GLU_123	OE2	3.160
2VDL	B_LYS_253	NZ	A_ASP_232	OD2	2.886
2VDL	H_LYS_59	NZ	A_GLU_117	OE2	3.964
2VDL	H_LYS_214	NZ	L_GLU_123	OE2	3.400
2VDM	A_ARG_77	NH1	H_ASP_102	OD1	3.512
2VDM	A_ARG_77	NH1	H_ASP_102	OD2	3.196
2VDM	A_ARG_77	NH2	H_ASP_102	OD1	2.762
2VDM	A_ARG_77	NH2	H_ASP_102	OD2	3.757
2VDM	B_ARG_216	NH2	A_GLU_123	OE2	2.982
2VDM	B_LYS_253	NZ	A_ASP_232	OD2	3.306
2VDM	H_LYS_214	NZ	L_GLU_123	OE2	3.334
2VDN	A_ARG_77	NH1	H_ASP_102	OD1	3.491
2VDN	A_ARG_77	NH1	H_ASP_102	OD2	3.169
2VDN	A_ARG_77	NH2	H_ASP_102	OD1	2.808
2VDN	A_ARG_77	NH2	H_ASP_102	OD2	3.762
2VDN	B_ARG_216	NH2	A_GLU_123	OE2	2.995
2VDN	H_LYS_214	NZ	L_GLU_123	OE2	3.685
2VDO	A_ARG_77	NH1	H_ASP_102	OD1	3.703
2VDO	A_ARG_77	NH1	H_ASP_102	OD2	3.042
2VDO	A_ARG_77	NH2	H_ASP_102	OD1	2.789
2VDO	A_ARG_77	NH2	H_ASP_102	OD2	3.375
2VDO	B_ARG_216	NH2	A_GLU_123	OE2	3.092
2VDO	B_LYS_253	NZ	A_ASP_232	OD2	2.836
2VDO	C_LYS_406	NZ	A_ASP_224	OD1	2.673
2VDO	C_LYS_406	NZ	A_ASP_224	OD2	3.263
2VDP	A_ARG_77	NH1	H_ASP_102	OD1	3.519
2VDP	A_ARG_77	NH1	H_ASP_102	OD2	3.089
2VDP	A_ARG_77	NH2	H_ASP_102	OD1	2.733
2VDP	A_ARG_77	NH2	H_ASP_102	OD2	3.585
2VDP	B_ARG_216	NH2	A_GLU_123	OE2	3.038
2VDP	B_LYS_253	NZ	A_ASP_232	OD2	2.914
2VDP	C_LYS_406	NZ	A_ASP_224	OD1	2.604
2VDP	C_LYS_406	NZ	A_ASP_224	OD2	3.297
2VDP	H_LYS_214	NZ	L_GLU_123	OE2	3.425
2VDQ	A_ARG_77	NH1	H_ASP_102	OD1	3.603
2VDQ	A_ARG_77	NH1	H_ASP_102	OD2	3.057
2VDQ	A_ARG_77	NH2	H_ASP_102	OD1	2.765
2VDQ	A_ARG_77	NH2	H_ASP_102	OD2	3.398
2VDQ	B_ARG_216	NH2	A_GLU_123	OE2	2.900

2VDQ	B.LYS_253	NZ	A.ASP_232	OD2	3.522
2VDQ	C.ARG_408	NH1	A.ASP_224	OD1	3.059
2VDQ	C.ARG_408	NH1	A.ASP_224	OD2	3.490
2VDQ	C.ARG_408	NH2	A.ASP_224	OD1	3.054
2VDQ	C.ARG_408	NH2	A.ASP_224	OD2	3.761
2VDQ	H.LYS_59	NZ	A.GLU_117	OE2	3.921
2VDQ	H.LYS_214	NZ	L.GLU_123	OE2	3.223
2VDR	A.ARG_77	NH1	H.ASP_102	OD1	3.703
2VDR	A.ARG_77	NH1	H.ASP_102	OD2	3.091
2VDR	A.ARG_77	NH2	H.ASP_102	OD1	2.791
2VDR	A.ARG_77	NH2	H.ASP_102	OD2	3.414
2VDR	B.ARG_216	NH2	A.GLU_123	OE2	2.956
2VDR	B.LYS_253	NZ	A.ASP_232	OD2	3.191
2VDR	C.ARG_408	NH1	A.ASP_224	OD1	3.062
2VDR	C.ARG_408	NH1	A.ASP_224	OD2	3.850
2VDR	C.ARG_408	NH2	A.ASP_224	OD1	3.028
2VDR	C.ARG_408	NH2	A.ASP_224	OD2	3.839
2VDR	H.LYS_214	NZ	L.GLU_123	OE2	3.860
2VIR	B.LYS_	NZ	A.GLU_127	OE2	3.017
2VIR	B.HIS_173	NE2	A.ASP_141	OD1	3.726
2VIR	B.HIS_173	NE2	A.ASP_141	OD2	3.076
2VIR	B.LYS_217	NZ	A.GLU_126	OE2	3.903
2VIS	B.LYS_	NZ	A.GLU_127	OE2	2.999
2VIS	B.HIS_173	NE2	A.ASP_141	OD1	3.763
2VIS	B.HIS_173	NE2	A.ASP_141	OD2	3.158
2VIS	B.LYS_217	NZ	A.GLU_126	OE2	3.709
2VIT	B.LYS_	NZ	A.GLU_127	OE2	2.939
2VIT	B.HIS_173	NE2	A.ASP_141	OD1	3.614
2VIT	B.HIS_173	NE2	A.ASP_141	OD2	3.333
2VIT	B.LYS_217	NZ	A.GLU_126	OE2	3.872
2VIU	A.LYS_27	NZ	B.GLU_97	OE1	3.686
2VIU	A.LYS_27	NZ	B.GLU_97	OE2	2.721
2VIU	A.ARG_109	NH1	B.GLU_67	OE1	3.978
2VIU	A.ARG_109	NH1	B.GLU_67	OE2	3.053
2VIU	A.ARG_269	NH1	B.GLU_67	OE1	2.986
2VIU	A.LYS_310	NZ	B.ASP_90	OD1	2.868
2VXS	H.LYS_143	NZ	L.GLU_125	OE2	2.772
2VXS	I.LYS_214	NZ	M.GLU_124	OE1	3.186
2VXS	J.LYS_	NZ	N.GLU_	OE1	2.922
2VXS	K.LYS_214	NZ	O.GLU_124	OE1	3.391
2VXS	N.LYS_	NZ	J.ASP_	OD2	3.949
2VXT	H.ARG_94	NH2	I.GLU_179	OE1	2.816
2VXT	H.ARG_94	NH2	I.GLU_179	OE2	3.466
2VXT	H.ARG_101	NH1	I.GLU_179	OE1	2.914
2VXT	H.LYS_208	NZ	L.GLU_123	OE2	2.940
2VXT	I.HIS_145	NE2	H.ASP_50	OD1	2.753
2VXT	I.LYS_148	NZ	H.ASP_56	OD2	2.664
2VXU	H.LYS_43	NZ	L.ASP_85	OD1	3.097
2VXU	I.LYS_208	NZ	M.GLU_123	OE1	2.734
2VXU	I.LYS_208	NZ	M.GLU_123	OE2	2.893
2VXV	H.LYS_214	NZ	L.ASP_122	OD1	3.721
2VXV	H.LYS_214	NZ	L.ASP_122	OD2	2.868
2XZQ	H.LYS_150	NZ	L.GLU_127	OE2	3.822
2XZQ	H.LYS_215	NZ	L.GLU_126	OE2	2.689
2Y06	H.LYS_215	NZ	L.GLU_126	OE2	2.373
2Y07	H.LYS_215	NZ	L.GLU_126	OE2	2.390
2Y36	H.LYS_150	NZ	L.GLU_127	OE2	3.849
2Y36	H.LYS_215	NZ	L.GLU_126	OE2	2.707

2Y7S	A_ARG_127	NH1	B_GLU_118	OE1	3.457
2Y7S	A_LYS_218	NZ	B_ASP_85	OD1	3.014
2Y7S	B_ARG_41	NH2	A_GLU_238	OE2	2.757
2YPV	A_ARG_130	NH2	L_ASP_92	OD1	2.916
2YPV	A_LYS_219	NZ	H_ASP_52	OD2	3.469
2YPV	A_LYS_241	NZ	H_ASP_99	OD2	2.741
2YPV	H_LYS_214	NZ	L_GLU_123	OE1	2.788
2YPV	H_LYS_214	NZ	L_GLU_123	OE2	2.975
2YPV	L_ARG_50	NH2	A_GLU_239	OE1	3.110
2YPV	L_ARG_50	NH2	A_GLU_239	OE2	3.975
2YWY	A_LYS_48	NZ	B_GLU_32	OE1	3.306
2YWY	A_LYS_48	NZ	B_GLU_32	OE2	2.998
2YWY	A_LYS_61	NZ	B_GLU_57	OE1	2.550
2YWY	A_LYS_61	NZ	B_GLU_57	OE2	3.211
2YWY	A_LYS_82	NZ	C_ASP_89	OD1	3.260
2YWY	B_ARG_33	NH2	A_GLU_32	OE1	3.506
2YWY	B_LYS_48	NZ	A_GLU_32	OE1	3.520
2YWY	B_LYS_48	NZ	A_GLU_32	OE2	2.757
2YWY	B_LYS_61	NZ	A_GLU_57	OE1	3.086
2YWY	C_LYS_48	NZ	D_GLU_32	OE1	2.723
2YWY	C_LYS_48	NZ	D_GLU_32	OE2	3.404
2YWY	C_LYS_61	NZ	D_GLU_57	OE1	2.801
2YWY	C_LYS_61	NZ	D_GLU_57	OE2	3.948
2YWY	D_LYS_48	NZ	C_GLU_32	OE1	3.239
2YWY	D_LYS_48	NZ	C_GLU_32	OE2	2.447
2YWY	D_LYS_61	NZ	C_GLU_57	OE1	2.837
2YWY	D_LYS_61	NZ	C_GLU_57	OE2	3.637
2ZCH	P_LYS_178	NZ	H_ASP_96	OD1	3.502
2ZCH	P_LYS_178	NZ	H_ASP_96	OD2	3.400
2ZCH	P_ARG_235	NH1	L_ASP_28	OD2	2.443
2ZCH	P_ARG_235	NH2	L_ASP_28	OD2	3.166
2ZCH	P_LYS_236	NZ	H_GLU_100C	OE2	3.089
2ZCH	H_ARG_50	NH2	L_ASP_94	OD1	2.658
2ZCH	H_ARG_50	NH2	L_ASP_94	OD2	2.887
2ZCH	H_LYS_208	NZ	L_GLU_123	OE1	3.921
2ZCH	H_LYS_208	NZ	L_GLU_123	OE2	3.396
2ZCK	P_LYS_178	NZ	H_ASP_96	OD1	3.892
2ZCK	P_LYS_178	NZ	H_ASP_96	OD2	3.060
2ZCK	P_ARG_236	NH2	L_ASP_28	OD1	3.496
2ZCK	H_ARG_50	NH2	L_ASP_94	OD1	3.095
2ZCK	H_ARG_50	NH2	L_ASP_94	OD2	2.679
2ZCK	H_LYS_208	NZ	L_GLU_123	OE2	2.731
2ZCL	P_LYS_178	NZ	H_ASP_96	OD1	3.272
2ZCL	P_LYS_178	NZ	H_ASP_96	OD2	2.771
2ZCL	P_ARG_235	NH2	L_ASP_28	OD1	3.392
2ZCL	H_ARG_50	NH2	L_ASP_94	OD1	3.155
2ZCL	H_ARG_50	NH2	L_ASP_94	OD2	2.864
2ZNW	Y_LYS_97	NZ	A_ASP_154	OD1	2.612
2ZNW	Y_LYS_97	NZ	A_ASP_154	OD2	3.786
2ZNW	Y_LYS_97	NZ	A_ASP_221	OD1	3.143
2ZNW	Y_LYS_97	NZ	A_ASP_221	OD2	3.719
2ZNW	Y_LYS_116	NZ	B_ASP_203	OD1	2.664
2ZNW	Z_LYS_97	NZ	B_ASP_154	OD1	3.042
2ZNW	Z_LYS_97	NZ	B_ASP_221	OD1	2.782
2ZNW	Z_LYS_97	NZ	B_ASP_221	OD2	3.319
2ZNW	Z_LYS_116	NZ	A_ASP_203	OD1	2.989
2ZNX	Y_LYS_97	NZ	A_ASP_154	OD1	2.701
2ZNX	Y_LYS_97	NZ	A_ASP_221	OD1	2.716

2ZNX	Y_LYS_97	NZ	A_ASP_221	OD2	3.355
2ZNX	Y_LYS_116	NZ	B_ASP_203	OD1	3.871
2ZNX	Y_LYS_116	NZ	B_ASP_203	OD2	2.956
2ZNX	B_LYS_135	NZ	Y_ASP_119	OD2	3.744
2ZNX	Z_LYS_97	NZ	B_ASP_154	OD1	2.804
2ZNX	Z_LYS_97	NZ	B_ASP_221	OD1	3.005
2ZNX	Z_LYS_97	NZ	B_ASP_221	OD2	3.520
2ZNX	Z_LYS_116	NZ	A_ASP_203	OD1	3.699
2ZNX	Z_LYS_116	NZ	A_ASP_203	OD2	3.427
2ZPK	L_HIS_95	NE2	H_ASP_62	OD1	3.977
2ZPK	H_LYS_143	NZ	L_GLU_125	OE2	2.882
2ZPK	H_LYS_208	NZ	L_GLU_124	OE2	3.548
2ZPK	I_LYS_143	NZ	M_GLU_125	OE2	2.672
2ZPK	I_LYS_208	NZ	M_GLU_124	OE2	3.137
32C2	B_LYS_214	NZ	A_GLU_126	OE1	3.056
32C2	B_LYS_214	NZ	A_GLU_126	OE2	3.702
3A67	Y_LYS_96	NZ	L_ASP_31	OD1	2.774
3A67	Y_LYS_96	NZ	L_ASP_31	OD2	3.727
3A67	Y_LYS_97	NZ	H_ASP_32	OD1	2.657
3A67	Y_LYS_97	NZ	H_ASP_99	OD1	3.291
3A67	Y_LYS_97	NZ	H_ASP_99	OD2	2.885
3A6B	Y_LYS_96	NZ	L_ASP_32	OD1	2.734
3A6B	Y_LYS_97	NZ	H_ASP_32	OD1	2.700
3A6B	Y_LYS_97	NZ	H_ASP_32	OD2	3.941
3A6B	Y_LYS_97	NZ	H_ASP_99	OD1	2.956
3A6B	Y_LYS_97	NZ	H_ASP_99	OD2	3.259
3A6C	Y_LYS_97	NZ	H_ASP_32	OD1	2.672
3A6C	Y_LYS_97	NZ	H_ASP_32	OD2	3.916
3A6C	Y_LYS_97	NZ	H_ASP_99	OD1	2.965
3A6C	Y_LYS_97	NZ	H_ASP_99	OD2	3.291
3B9K	H_LYS_221	NZ	L_GLU_123	OE1	2.886
3B9K	A_LYS_13	NZ	B_ASP_42	OD2	3.894
3B9K	B_LYS_27	NZ	H_ASP_32	OD1	2.409
3B9K	B_ARG_77	NH2	L_ASP_92	OD1	3.184
3B9K	B_ARG_78	NH2	L_ASP_92	OD1	2.834
3B9K	B_LYS_103	NZ	A_ASP_66	OD1	3.058
3B9K	D_LYS_221	NZ	C_GLU_123	OE1	3.178
3B9K	F_LYS_27	NZ	D_ASP_32	OD1	2.318
3B9K	F_ARG_77	NH2	C_ASP_92	OD1	2.984
3B9K	F_ARG_78	NH2	C_ASP_92	OD1	3.141
3B9K	F_ARG_78	NH2	C_ASP_92	OD2	3.951
3B9K	F_LYS_103	NZ	E_ASP_	OD1	3.044
3BDY	H_LYS_211	NZ	L_GLU_123	OE2	2.706
3BE1	H_ARG_50	NH1	A_ASP_560	OD2	3.215
3BE1	H_ARG_50	NH2	A_GLU_558	OE1	3.092
3BE1	H_ARG_50	NH2	A_GLU_558	OE2	3.263
3BE1	H_ARG_50	NH2	A_ASP_560	OD1	3.492
3BE1	H_ARG_50	NH2	A_ASP_560	OD2	3.175
3BGF	S_ARG_426	NH1	H_ASP_56	OD1	3.504
3BGF	S_ARG_426	NH1	H_ASP_56	OD2	2.403
3BGF	S_LYS_439	NZ	A_ASP_480	OD2	3.161
3BGF	A_LYS_439	NZ	S_ASP_480	OD2	2.520
3BGF	H_LYS_210	NZ	L_GLU_123	OE1	3.997
3BIK	A_ARG_113	NH2	B_GLU_136	OE2	3.149
3BIK	A_ARG_125	NH2	B_GLU_136	OE1	3.033
3BIK	A_ARG_125	NH2	B_GLU_136	OE2	3.001
3BKY	H_LYS_138	NZ	L_GLU_212	OE2	2.743
3BO8	A_ARG_35	NH1	B_ASP_53	OD1	3.541

3BO8	A_ARG_48	NH1	B_ASP_53	OD1	3.101
3BO8	A_ARG_48	NH1	B_ASP_53	OD2	3.041
3BO8	A_ARG_48	NH2	B_ASP_53	OD1	3.771
3BO8	A_ARG_48	NH2	B_ASP_53	OD2	3.368
3BO8	A_ARG_156	NH1	C_ASP_3	OD1	3.842
3BO8	A_ARG_156	NH1	C_ASP_3	OD2	2.711
3BO8	A_ARG_163	NH2	C_GLU_1	OE1	3.484
3BO8	A_ARG_163	NH2	C_GLU_1	OE2	2.848
3BO8	A_ARG_170	NH1	C_GLU_1	OE2	2.801
3BO8	A_ARG_170	NH2	C_GLU_1	OE2	3.023
3BO8	A_HIS_192	NE2	B_ASP_98	OD1	3.566
3BO8	A_HIS_192	NE2	B_ASP_98	OD2	3.950
3BT2	A_HIS_87	ND1	U_ASP_11	OD2	3.629
3BT2	H_HIS_98	ND1	L_GLU_50	OE1	2.845
3BT2	H_HIS_98	ND1	L_GLU_50	OE2	2.191
3BT2	H_HIS_98	NE2	L_GLU_50	OE1	3.301
3BT2	H_HIS_98	NE2	L_GLU_50	OE2	3.904
3BT2	H_LYS_203	NZ	L_GLU_122	OE2	3.715
3BT2	U_ARG_91	NH1	B_ASP_22	OD1	3.502
3BT2	U_ARG_91	NH1	B_ASP_22	OD2	3.574
3BT2	U_ARG_91	NH2	B_ASP_22	OD1	3.066
3BT2	U_ARG_192	NH1	H_GLU_58	OE2	2.836
3BZ4	A_LYS_27	NZ	E_ASP_1	OD1	3.348
3BZ4	A_LYS_27	NZ	E_ASP_1	OD2	3.551
3BZ4	A_ARG_96	NH2	B_GLU_50	OE1	3.591
3BZ4	A_ARG_96	NH2	B_GLU_50	OE2	2.914
3BZ4	B_LYS_210	NZ	A_GLU_123	OE2	2.839
3BZ4	C_ARG_96	NH2	D_GLU_50	OE1	3.615
3BZ4	C_ARG_96	NH2	D_GLU_50	OE2	2.938
3BZ4	D_LYS_210	NZ	C_GLU_123	OE2	2.929
3BZ4	E_ARG_96	NH2	F_GLU_50	OE1	3.659
3BZ4	E_ARG_96	NH2	F_GLU_50	OE2	3.062
3BZ4	F_LYS_210	NZ	E_GLU_123	OE2	2.855
3BZ4	G_ARG_96	NH2	H_GLU_50	OE1	3.659
3BZ4	G_ARG_96	NH2	H_GLU_50	OE2	3.021
3BZ4	G_LYS_147	NZ	C_GLU_154	OE1	3.559
3C09	L_HIS_93	NE2	D_ASP_434	OD1	2.739
3C09	L_HIS_93	NE2	D_ASP_434	OD2	3.466
3C09	H_ARG_57	NH2	D_GLU_431	OE1	3.682
3C09	A_LYS_454	NZ	C_ASP_100	OD1	2.467
3C09	A_LYS_463	NZ	B_ASP_49	OD2	2.856
3C09	B_HIS_93	NE2	A_ASP_434	OD1	2.346
3C09	D_LYS_454	NZ	H_ASP_100	OD2	3.482
3C09	D_LYS_463	NZ	L_ASP_49	OD2	3.418
3C5S	A_ARG_96	NH2	B_GLU_50	OE1	3.517
3C5S	A_ARG_96	NH2	B_GLU_50	OE2	2.932
3C5S	B_LYS_210	NZ	A_GLU_123	OE2	3.553
3C5S	C_ARG_96	NH2	D_GLU_50	OE1	3.571
3C5S	C_ARG_96	NH2	D_GLU_50	OE2	2.973
3C6S	A_LYS_27	NZ	F_GLU_61	OE1	2.945
3C6S	A_ARG_96	NH2	B_GLU_50	OE1	3.551
3C6S	A_ARG_96	NH2	B_GLU_50	OE2	2.936
3C6S	B_LYS_210	NZ	A_GLU_123	OE2	2.871
3C6S	C_ARG_96	NH2	D_GLU_50	OE1	3.699
3C6S	C_ARG_96	NH2	D_GLU_50	OE2	2.915
3C6S	D_LYS_115	NZ	H_GLU_85	OE1	3.000
3C6S	D_LYS_115	NZ	H_GLU_85	OE2	3.884
3C6S	D_LYS_210	NZ	C_GLU_123	OE2	2.801

3C6S	E_LYS_27	NZ	A_ASP_1	OD1	3.387
3C6S	E_LYS_27	NZ	A_ASP_1	OD2	3.431
3C6S	E_ARG_96	NH2	F_GLU_50	OE1	3.703
3C6S	E_ARG_96	NH2	F_GLU_50	OE2	3.164
3C6S	F_LYS_210	NZ	E_GLU_123	OE2	3.016
3C6S	G_ARG_96	NH2	H_GLU_50	OE1	3.733
3C6S	G_ARG_96	NH2	H_GLU_50	OE2	2.958
3C6S	H_LYS_210	NZ	G_GLU_123	OE2	2.402
3CVH	A_ARG_48	NH1	B_ASP_53	OD2	3.820
3CVH	A_ARG_48	NH2	B_ASP_53	OD2	2.637
3CVH	A_ARG_62	NH1	L_GLU_26	OE1	3.514
3CVH	A_ARG_62	NH1	L_GLU_26	OE2	3.458
3CVH	A_ARG_62	NH2	L_GLU_26	OE1	3.664
3CVH	A_ARG_108	NH2	M_GLU_223	OE2	3.938
3CVH	A_HIS_192	ND1	B_ASP_98	OD2	3.410
3CVH	C_LYS_7	NZ	H_ASP_49	OD1	3.577
3CVH	C_LYS_7	NZ	H_ASP_49	OD2	3.552
3CVH	H_LYS_215	NZ	L_GLU_122	OE2	2.643
3CVH	M_ARG_48	NH1	N_ASP_53	OD2	3.601
3CVH	M_ARG_48	NH2	N_ASP_53	OD2	2.621
3CVH	M_ARG_62	NH1	R_GLU_26	OE1	3.418
3CVH	M_ARG_62	NH2	R_GLU_26	OE1	3.162
3CVH	M_ARG_62	NH2	R_GLU_26	OE2	2.706
3CVH	M_ARG_108	NH2	A_GLU_223	OE1	3.207
3CVH	M_ARG_108	NH2	A_GLU_223	OE2	3.250
3CVH	M_ARG_169	NH1	A_GLU_268	OE2	3.364
3CVH	O_LYS_7	NZ	Q_ASP_49	OD1	3.648
3CVH	O_LYS_7	NZ	Q_ASP_49	OD2	3.052
3CVH	Q_LYS_215	NZ	R_GLU_122	OE1	3.557
3CXD	H_ARG_52	NH1	P_ASP_47	OD1	3.830
3CXD	H_ARG_52	NH1	P_ASP_47	OD2	3.528
3D0L	A_HIS_96	NE2	C_ASP_5	OD1	3.014
3D0L	B_ARG_58	NH2	C_GLU_3	OE1	3.473
3D0L	B_ARG_58	NH2	C_GLU_3	OE2	3.109
3D0L	B_ARG_95	NH1	C_ASP_5	OD1	2.695
3D0L	B_ARG_95	NH1	C_ASP_5	OD2	3.449
3D0L	B_ARG_95	NH2	C_ASP_5	OD1	3.596
3D0L	B_ARG_95	NH2	C_ASP_5	OD2	3.078
3D0L	B_ARG_96	NH1	A_GLU_55	OE1	3.284
3D0L	B_ARG_96	NH1	A_GLU_55	OE2	3.522
3D0L	B_ARG_96	NH2	A_GLU_55	OE1	3.455
3D0L	C_LYS_6	NZ	B_ASP_54	OD1	2.251
3D0L	C_LYS_6	NZ	B_ASP_54	OD2	2.930
3D0L	C_LYS_6	NZ	B_ASP_56	OD2	3.751
3D0V	A_HIS_96	NE2	C_ASP_5	OD1	2.775
3D0V	B_ARG_58	NH2	C_GLU_3	OE1	2.733
3D0V	B_ARG_95	NH1	C_ASP_5	OD1	2.808
3D0V	B_ARG_95	NH1	C_ASP_5	OD2	3.484
3D0V	B_ARG_95	NH2	C_ASP_5	OD1	3.359
3D0V	B_ARG_95	NH2	C_ASP_5	OD2	2.831
3D0V	B_ARG_96	NH1	A_GLU_55	OE1	3.250
3D0V	B_ARG_96	NH1	A_GLU_55	OE2	3.216
3D0V	B_ARG_96	NH2	A_GLU_55	OE1	3.184
3D0V	B_LYS_209	NZ	A_GLU_123	OE1	3.487
3D0V	C_LYS_6	NZ	B_ASP_54	OD1	3.609
3D0V	C_LYS_6	NZ	B_ASP_54	OD2	2.826
3D0V	C_LYS_6	NZ	B_ASP_56	OD1	3.006
3D9A	C_LYS_697	NZ	H_ASP_332	OD2	2.741

3D9A	C.LYS_697	NZ	H.ASP_399	OD1	2.864
3D9A	C.LYS_697	NZ	H.ASP_399	OD2	3.300
3D9A	H.LYS_508	NZ	L.GLU_123	OE1	3.029
3D9A	H.LYS_508	NZ	L.GLU_123	OE2	3.809
3DRO	B.ARG_95	NH1	P.ASP_5	OD1	3.590
3DRO	B.ARG_95	NH1	P.ASP_5	OD2	3.370
3DRO	B.ARG_95	NH2	P.ASP_5	OD2	3.007
3DRO	B.ARG_96	NH2	A.GLU_55	OE1	2.727
3DRO	B.ARG_96	NH2	A.GLU_55	OE2	3.426
3DRO	B.LYS_209	NZ	A.GLU_123	OE1	3.782
3DRO	P.LYS_6	NZ	B.ASP_54	OD1	2.913
3DRO	P.LYS_6	NZ	B.ASP_54	OD2	3.775
3DRO	P.LYS_6	NZ	B.ASP_56	OD1	3.330
3DRO	P.LYS_6	NZ	B.ASP_56	OD2	3.868
3DRQ	A.HIS_96	NE2	C.ASP_5	OD1	2.866
3DRQ	B.ARG_58	NH2	C.GLU_3	OE1	3.516
3DRQ	B.ARG_95	NH1	C.ASP_5	OD1	2.806
3DRQ	B.ARG_95	NH1	C.ASP_5	OD2	3.209
3DRQ	B.ARG_95	NH2	C.ASP_5	OD1	3.572
3DRQ	B.ARG_95	NH2	C.ASP_5	OD2	2.688
3DRQ	B.ARG_96	NH1	A.GLU_55	OE1	2.721
3DRQ	B.ARG_96	NH1	A.GLU_55	OE2	2.397
3DRQ	B.ARG_96	NH2	A.GLU_55	OE1	3.293
3DRQ	B.LYS_209	NZ	A.GLU_123	OE1	3.837
3DRQ	C.LYS_6	NZ	B.ASP_54	OD1	2.921
3DRQ	C.LYS_6	NZ	B.ASP_54	OD2	2.342
3DRQ	C.LYS_6	NZ	B.ASP_56	OD1	3.006
3DSF	H.ARG_52	NH1	P.ASP_47	OD2	3.172
3EBA	B.LYS_97	NZ	A.GLU_97	OE2	3.240
3EBA	B.ARG_101	NH1	A.ASP_109	OD1	3.083
3EBA	B.ARG_101	NH1	A.ASP_109	OD2	2.691
3EBA	B.ARG_101	NH2	A.ASP_109	OD1	3.308
3EBA	B.ARG_101	NH2	A.ASP_109	OD2	3.134
3EOA	H.LYS_217	NZ	L.GLU_123	OE2	3.037
3EOA	I.LYS_197	NZ	H.ASP_55	OD1	3.170
3EOA	I.LYS_197	NZ	H.GLU_57	OE1	2.719
3EOA	I.HIS_198	NE2	H.GLU_57	OE1	3.638
3EOA	I.HIS_198	NE2	H.GLU_57	OE2	3.098
3EOA	B.LYS_	NZ	A.GLU_	OE2	3.673
3EOA	J.LYS_197	NZ	B.ASP_55	OD1	2.626
3EOA	J.LYS_197	NZ	B.ASP_55	OD2	2.997
3EOA	J.LYS_197	NZ	B.GLU_57	OE1	2.784
3EOA	J.HIS_198	NE2	B.GLU_57	OE1	3.322
3EOA	J.HIS_198	NE2	B.GLU_57	OE2	2.793
3EOB	H.LYS_217	NZ	L.GLU_123	OE2	3.176
3EOB	I.LYS_197	NZ	H.GLU_57	OE1	2.792
3EOB	I.LYS_197	NZ	H.GLU_57	OE2	3.051
3EOB	I.HIS_198	ND1	H.GLU_57	OE2	3.691
3EOB	I.HIS_198	NE2	H.GLU_57	OE1	2.182
3EOB	I.HIS_198	NE2	H.GLU_57	OE2	2.522
3EOB	I.HIS_264	NE2	J.GLU_241	OE1	2.369
3EOB	I.HIS_264	NE2	J.GLU_241	OE2	2.595
3EOB	B.LYS_	NZ	A.GLU_	OE1	3.788
3EOB	B.LYS_	NZ	A.GLU_	OE2	3.219
3EOB	J.LYS_197	NZ	B.ASP_55	OD1	3.833
3EOB	J.LYS_197	NZ	B.GLU_57	OE1	2.107
3EOB	J.LYS_197	NZ	B.GLU_57	OE2	3.802
3EOB	J.HIS_198	ND1	B.GLU_57	OE2	3.839

3EOB	J_HIS_198	NE2	B_GLU_57	OE1	2.356
3EOB	J_HIS_198	NE2	B_GLU_57	OE2	2.609
3EOB	J_HIS_264	NE2	L_GLU_241	OE1	2.434
3EOB	J_HIS_264	NE2	L_GLU_241	OE2	2.722
3ESV	F_LYS_0	NZ	G_ASP_1054	OD1	3.499
3ESV	F_LYS_0	NZ	G_ASP_1054	OD2	2.774
3ESV	F_LYS_0	NZ	G_ASP_1056	OD2	3.090
3ESV	G_ARG_53	NH1	F_ASP_1056	OD1	2.802
3ESV	G_ARG_53	NH2	F_ASP_1056	OD1	3.489
3ETB	F_ARG_24	NH1	G_ASP_70	OD1	3.579
3ETB	F_ARG_24	NH1	G_ASP_70	OD2	3.034
3ETB	F_ARG_24	NH2	G_ASP_70	OD1	3.608
3ETB	F_ARG_24	NH2	G_ASP_70	OD2	3.774
3ETB	F_ARG_30	NH1	J_ASP_658	OD2	3.129
3ETB	F_ARG_53	NH1	J_GLU_654	OE1	3.838
3ETB	F_ARG_53	NH2	J_GLU_654	OE1	3.771
3ETB	F_ARG_1050	NH2	J_ASP_683	OD2	3.114
3ETB	G_ARG_24	NH1	F_ASP_70	OD1	3.633
3ETB	G_ARG_24	NH1	F_ASP_70	OD2	3.127
3ETB	G_ARG_24	NH2	F_ASP_70	OD1	3.702
3ETB	G_ARG_24	NH2	F_ASP_70	OD2	3.878
3ETB	G_ARG_30	NH1	K_ASP_658	OD2	3.266
3ETB	G_ARG_53	NH2	K_ASP_648	OD2	3.972
3ETB	G_ARG_53	NH2	K_GLU_654	OE1	3.990
3ETB	G_ARG_1050	NH2	K_ASP_683	OD1	3.853
3ETB	G_ARG_1050	NH2	K_ASP_683	OD2	2.796
3ETB	H_ARG_24	NH1	L_ASP_70	OD1	3.544
3ETB	H_ARG_24	NH1	L_ASP_70	OD2	3.118
3ETB	H_ARG_24	NH2	L_ASP_70	OD1	3.662
3ETB	H_ARG_24	NH2	L_ASP_70	OD2	3.905
3ETB	H_ARG_30	NH1	L_ASP_658	OD1	3.824
3ETB	H_ARG_30	NH1	L_ASP_658	OD2	2.913
3ETB	H_ARG_53	NH1	L_GLU_654	OE1	3.771
3ETB	H_ARG_53	NH2	L_GLU_654	OE1	3.669
3ETB	H_ARG_1050	NH2	L_ASP_683	OD2	3.159
3ETB	L_ARG_24	NH1	H_ASP_70	OD1	3.448
3ETB	L_ARG_24	NH1	H_ASP_70	OD2	2.998
3ETB	L_ARG_24	NH2	H_ASP_70	OD1	3.537
3ETB	L_ARG_24	NH2	H_ASP_70	OD2	3.789
3ETB	L_ARG_30	NH1	M_ASP_658	OD2	3.315
3ETB	L_ARG_53	NH1	M_GLU_654	OE1	3.885
3ETB	L_ARG_53	NH2	M_GLU_654	OE1	3.890
3ETB	L_ARG_1050	NH2	M_ASP_683	OD2	3.093
3ETB	J_LYS_653	NZ	G_ASP_17	OD1	2.972
3ETB	J_LYS_684	NZ	F_ASP_1054	OD1	3.728
3ETB	J_LYS_684	NZ	F_ASP_1054	OD2	3.401
3ETB	J_LYS_684	NZ	F_ASP_1056	OD1	3.220
3ETB	J_LYS_684	NZ	F_ASP_1056	OD2	3.481
3ETB	K_LYS_653	NZ	F_ASP_17	OD1	3.083
3ETB	K_LYS_684	NZ	G_ASP_1054	OD1	3.379
3ETB	K_LYS_684	NZ	G_ASP_1054	OD2	3.075
3ETB	K_LYS_684	NZ	G_ASP_1056	OD1	3.162
3ETB	K_LYS_684	NZ	G_ASP_1056	OD2	3.578
3ETB	L_LYS_653	NZ	L_ASP_17	OD1	2.978
3ETB	L_LYS_684	NZ	H_ASP_1056	OD1	3.616
3ETB	L_LYS_684	NZ	H_ASP_1056	OD2	3.187
3ETB	M_LYS_653	NZ	H_ASP_17	OD1	3.060
3ETB	M_LYS_684	NZ	L_ASP_1054	OD1	3.625

3ETB	M.LYS_684	NZ	L.ASP_1054	OD2	3.167
3ETB	M.LYS_684	NZ	L.ASP_1056	OD1	3.241
3ETB	M.LYS_684	NZ	L.ASP_1056	OD2	3.478
3EYV	L.LYS_55	NZ	H.ASP_102	OD2	3.565
3EYV	H.LYS_215	NZ	L.GLU_128	OE2	3.627
3EYV	A.LYS_55	NZ	B.ASP_102	OD2	3.151
3EYV	B.LYS_220	NZ	A.ASP_127	OD2	3.402
3FMG	L.LYS_50	NZ	H.ASP_106	OD1	3.132
3FMG	H.LYS_64	NZ	L.ASP_1	OD2	3.241
3G3A	B.ARG_61	NH2	A.ASP_59	OD2	3.447
3G3A	B.ARG_73	NH1	A.ASP_61	OD1	2.630
3G3A	B.ARG_73	NH1	A.ASP_61	OD2	3.494
3G3A	B.ARG_73	NH2	A.ASP_59	OD2	3.260
3G3A	B.ARG_73	NH2	A.ASP_61	OD1	3.287
3G3A	B.ARG_73	NH2	A.ASP_61	OD2	2.479
3G3A	B.ARG_112	NH1	A.ASP_141	OD1	3.611
3G3A	B.ARG_112	NH1	A.ASP_141	OD2	2.906
3G3A	B.ARG_112	NH2	A.ASP_141	OD1	2.901
3G3A	B.ARG_112	NH2	A.ASP_141	OD2	3.689
3G3A	B.ARG_112	NH2	A.ASP_143	OD2	3.389
3G3A	D.ARG_61	NH1	C.ASP_59	OD2	3.676
3G3A	D.ARG_61	NH2	C.ASP_59	OD1	3.900
3G3A	D.ARG_61	NH2	C.ASP_59	OD2	3.137
3G3A	D.ARG_73	NH1	C.ASP_61	OD1	3.720
3G3A	D.ARG_73	NH1	C.ASP_61	OD2	2.705
3G3A	D.ARG_73	NH2	C.ASP_59	OD2	2.913
3G3A	D.ARG_73	NH2	C.ASP_61	OD1	2.638
3G3A	D.ARG_73	NH2	C.ASP_61	OD2	3.209
3G3A	D.ARG_112	NH1	C.ASP_141	OD1	3.483
3G3A	D.ARG_112	NH1	C.ASP_141	OD2	2.837
3G3A	D.ARG_112	NH2	C.ASP_141	OD1	2.752
3G3A	D.ARG_112	NH2	C.ASP_141	OD2	3.622
3G3A	D.ARG_112	NH2	C.ASP_143	OD2	3.602
3G3A	F.ARG_61	NH1	E.ASP_59	OD2	3.922
3G3A	F.ARG_61	NH2	E.ASP_59	OD1	3.681
3G3A	F.ARG_61	NH2	E.ASP_59	OD2	2.804
3G3A	F.ARG_73	NH1	E.ASP_61	OD1	3.367
3G3A	F.ARG_73	NH1	E.ASP_61	OD2	2.915
3G3A	F.ARG_73	NH2	E.ASP_59	OD2	2.686
3G3A	F.ARG_73	NH2	E.ASP_61	OD1	2.874
3G3A	F.ARG_73	NH2	E.ASP_61	OD2	3.960
3G3A	F.ARG_112	NH1	E.ASP_141	OD1	3.733
3G3A	F.ARG_112	NH1	E.ASP_141	OD2	3.195
3G3A	F.ARG_112	NH2	E.ASP_141	OD1	3.001
3G3A	F.ARG_112	NH2	E.ASP_141	OD2	3.839
3G3A	F.ARG_112	NH2	E.ASP_143	OD2	3.491
3G3A	H.ARG_61	NH2	G.ASP_59	OD2	3.367
3G3A	H.ARG_73	NH1	G.ASP_59	OD2	3.259
3G3A	H.ARG_73	NH2	G.ASP_59	OD2	3.473
3G3A	H.ARG_73	NH2	G.ASP_61	OD1	2.486
3G3A	H.ARG_73	NH2	G.ASP_61	OD2	2.698
3G3A	H.ARG_112	NH1	G.ASP_141	OD1	3.280
3G3A	H.ARG_112	NH1	G.ASP_143	OD2	3.578
3G3A	H.ARG_112	NH2	G.ASP_141	OD1	3.102
3G3A	H.ARG_112	NH2	G.ASP_141	OD2	2.609
3G3B	B.ARG_61	NH2	A.ASP_59	OD1	3.551
3G3B	B.ARG_61	NH2	A.ASP_59	OD2	3.590
3G3B	B.ARG_73	NH1	A.ASP_61	OD1	2.527

3G3B	B_ARG_73	NH1	A_ASP_61	OD2	3.439
3G3B	B_ARG_73	NH2	A_ASP_59	OD2	2.967
3G3B	B_ARG_73	NH2	A_ASP_61	OD1	3.469
3G3B	B_ARG_73	NH2	A_ASP_61	OD2	2.765
3G3B	B_ARG_112	NH1	A_ASP_141	OD1	3.569
3G3B	B_ARG_112	NH1	A_ASP_141	OD2	2.625
3G3B	B_ARG_112	NH2	A_ASP_141	OD1	2.926
3G3B	B_ARG_112	NH2	A_ASP_141	OD2	3.538
3G3B	B_ARG_112	NH2	A_ASP_143	OD2	3.804
3G3B	D_ARG_61	NH2	C_ASP_59	OD1	3.954
3G3B	D_ARG_73	NH1	C_ASP_61	OD1	2.753
3G3B	D_ARG_73	NH1	C_ASP_61	OD2	3.824
3G3B	D_ARG_73	NH2	C_ASP_59	OD2	3.136
3G3B	D_ARG_73	NH2	C_ASP_61	OD1	3.224
3G3B	D_ARG_73	NH2	C_ASP_61	OD2	2.702
3G3B	D_ARG_112	NH1	C_ASP_141	OD1	3.812
3G3B	D_ARG_112	NH1	C_ASP_141	OD2	2.690
3G3B	D_ARG_112	NH2	C_ASP_141	OD1	2.826
3G3B	D_ARG_112	NH2	C_ASP_141	OD2	3.301
3G3B	D_ARG_112	NH2	C_ASP_143	OD2	3.656
3G3B	F_ARG_61	NH2	E_ASP_59	OD2	3.820
3G3B	F_ARG_73	NH1	E_ASP_61	OD1	2.535
3G3B	F_ARG_73	NH1	E_ASP_61	OD2	3.949
3G3B	F_ARG_73	NH2	E_ASP_59	OD2	2.812
3G3B	F_ARG_73	NH2	E_ASP_61	OD1	3.056
3G3B	F_ARG_73	NH2	E_ASP_61	OD2	2.934
3G3B	F_ARG_112	NH1	E_ASP_141	OD2	2.714
3G3B	F_ARG_112	NH2	E_ASP_141	OD1	3.020
3G3B	F_ARG_112	NH2	E_ASP_141	OD2	3.176
3G3B	F_ARG_112	NH2	E_ASP_143	OD2	3.737
3G3B	H_ARG_73	NH1	G_ASP_61	OD1	2.839
3G3B	H_ARG_73	NH1	G_ASP_61	OD2	3.791
3G3B	H_ARG_73	NH2	G_ASP_59	OD2	2.431
3G3B	H_ARG_73	NH2	G_ASP_61	OD1	3.464
3G3B	H_ARG_73	NH2	G_ASP_61	OD2	2.896
3G3B	H_ARG_112	NH1	G_ASP_141	OD1	3.676
3G3B	H_ARG_112	NH1	G_ASP_141	OD2	2.564
3G3B	H_ARG_112	NH2	G_ASP_141	OD1	2.813
3G3B	H_ARG_112	NH2	G_ASP_141	OD2	3.280
3G3B	H_ARG_112	NH2	G_ASP_143	OD2	3.506
3GGW	A_ARG_96	NH2	B_GLU_50	OE1	3.590
3GGW	A_ARG_96	NH2	B_GLU_50	OE2	2.762
3GGW	B_ARG_52	NH1	E_ASP_4	OD2	3.092
3GGW	B_LYS_210	NZ	A_GLU_123	OE2	3.208
3GGW	C_ARG_96	NH2	D_GLU_50	OE1	3.555
3GGW	C_ARG_96	NH2	D_GLU_50	OE2	2.962
3GGW	D_ARG_52	NH1	F_ASP_4	OD2	3.127
3GGW	D_LYS_210	NZ	C_GLU_123	OE2	2.871
3GGW	D_ARG_215	NH2	C_GLU_213	OE1	3.834
3GGW	D_ARG_215	NH2	C_GLU_213	OE2	2.618
3GHB	H_LYS_143	NZ	L_GLU_124	OE2	2.614
3GHB	H_LYS_209	NZ	L_GLU_123	OE1	2.751
3GHB	H_LYS_209	NZ	L_GLU_123	OE2	3.411
3GHB	P_LYS_305	NZ	H_GLU_100E	OE1	3.508
3GHB	P_LYS_305	NZ	H_ASP_100F	OD2	3.835
3GHB	LLYS_143	NZ	M_GLU_124	OE2	2.607
3GHB	LLYS_209	NZ	M_GLU_123	OE1	2.988
3GHB	LLYS_209	NZ	M_GLU_123	OE2	3.773

3GHB	Q_LYS_305	NZ	L_ASP_100F	OD1	3.174
3GHE	H_LYS_143	NZ	L_GLU_124	OE2	2.684
3GHE	H_LYS_209	NZ	L_GLU_123	OE1	2.541
3GHE	H_LYS_209	NZ	L_GLU_123	OE2	3.149
3GHE	P_ARG_304	NH1	H_ASP_100A	OD1	3.397
3GHE	P_ARG_304	NH2	H_ASP_100A	OD1	3.243
3GHE	P_ARG_304	NH2	H_ASP_100A	OD2	3.833
3GHE	P_HIS_308	ND1	H_ASP_100H	OD2	3.415
3GHE	P_ARG_315	NH1	H_GLU_95	OE1	3.518
3GHE	P_ARG_315	NH1	H_GLU_95	OE2	2.720
3GHE	P_ARG_315	NH2	H_GLU_95	OE2	3.104
3GJF	A_ARG_48	NH2	B_ASP_53	OD2	3.786
3GJF	A_ARG_65	NH1	L_ASP_52	OD1	3.134
3GJF	A_ARG_65	NH1	L_ASP_52	OD2	3.382
3GJF	A_ARG_65	NH2	L_ASP_52	OD1	2.989
3GJF	A_ARG_65	NH2	L_ASP_52	OD2	3.338
3GJF	D_ARG_35	NH2	E_ASP_53	OD1	3.050
3GJF	D_ARG_35	NH2	E_ASP_53	OD2	3.940
3GJF	D_ARG_48	NH2	E_ASP_53	OD1	3.764
3GJF	D_ARG_48	NH2	E_ASP_53	OD2	3.452
3GJF	D_ARG_65	NH1	K_ASP_52	OD1	3.173
3GJF	D_ARG_65	NH1	K_ASP_52	OD2	3.530
3GJF	D_ARG_65	NH2	K_ASP_52	OD1	3.166
3GJF	D_ARG_65	NH2	K_ASP_52	OD2	2.445
3GJF	E_LYS_6	NZ	D_GLU_232	OE1	3.774
3GJF	E_LYS_6	NZ	D_GLU_232	OE2	2.502
3GJF	M_LYS_215	NZ	K_GLU_126	OE1	3.244
3GJF	M_LYS_215	NZ	K_GLU_126	OE2	2.553
3GNM	H_ARG_169	NH1	L_ASP_172	OD1	3.348
3GNM	H_ARG_169	NH2	L_ASP_172	OD1	3.542
3GNM	H_ARG_169	NH2	L_ASP_175	OD1	3.297
3GNM	H_LYS_213	NZ	L_GLU_128	OE1	2.721
3GNM	H_LYS_213	NZ	L_GLU_128	OE2	3.840
3GO1	H_LYS_209	NZ	L_GLU_123	OE1	2.728
3GO1	H_LYS_209	NZ	L_GLU_123	OE2	3.471
3GO1	P_LYS_305	NZ	L_ASP_51	OD1	2.931
3GO1	P_ARG_315	NH1	H_GLU_95	OE2	3.127
3GO1	P_ARG_315	NH2	H_GLU_95	OE2	2.921
3GO1	P_ARG_315	NH2	H_ASP_100A	OD2	3.393
3HAE	A_ARG_35	NH1	B_ASP_53	OD1	3.527
3HAE	A_ARG_35	NH1	B_ASP_53	OD2	2.844
3HAE	A_ARG_48	NH2	B_ASP_53	OD2	3.583
3HAE	A_ARG_65	NH1	L_ASP_52	OD1	3.495
3HAE	A_ARG_65	NH1	L_ASP_52	OD2	2.908
3HAE	A_ARG_65	NH2	L_ASP_52	OD1	3.452
3HAE	A_ARG_65	NH2	L_ASP_52	OD2	3.099
3HAE	B_LYS_6	NZ	A_GLU_232	OE2	2.622
3HAE	D_ARG_35	NH1	E_ASP_53	OD1	3.949
3HAE	D_ARG_35	NH1	E_ASP_53	OD2	3.963
3HAE	D_ARG_35	NH2	E_ASP_53	OD1	3.106
3HAE	D_ARG_48	NH2	E_ASP_53	OD2	3.593
3HAE	D_ARG_65	NH1	G_ASP_52	OD1	3.201
3HAE	D_ARG_65	NH2	G_ASP_52	OD1	2.885
3HAE	D_ARG_65	NH2	G_ASP_52	OD2	3.031
3HAE	J_ARG_35	NH2	K_ASP_53	OD1	3.520
3HAE	J_ARG_48	NH2	K_ASP_53	OD1	3.945
3HAE	J_ARG_48	NH2	K_ASP_53	OD2	3.051
3HAE	J_ARG_65	NH1	N_ASP_52	OD1	3.749

3HAE	J_ARG.65	NH2	N_ASP_52	OD1	2.440
3HAE	J_ARG.65	NH2	N_ASP_52	OD2	2.989
3HAE	P_ARG.35	NH1	Q_ASP_53	OD2	3.921
3HAE	P_ARG.48	NH2	Q_ASP_53	OD1	3.566
3HAE	P_ARG.48	NH2	Q_ASP_53	OD2	2.872
3HAE	P_ARG.65	NH1	S_ASP_52	OD1	3.579
3HAE	P_ARG.65	NH1	S_ASP_52	OD2	3.466
3HAE	P_ARG.65	NH2	S_ASP_52	OD1	3.120
3HAE	P_ARG.65	NH2	S_ASP_52	OD2	2.826
3HAE	Q_LYS.6	NZ	P_GLU_232	OE2	3.965
3HAE	N_LYS_132	NZ	O_ASP_150	OD2	3.615
3HAE	H_LYS_215	NZ	L_GLU_126	OE1	3.537
3HAE	H_LYS_215	NZ	L_GLU_126	OE2	3.674
3HAE	I_LYS_215	NZ	G_GLU_126	OE1	3.678
3HAE	O_LYS_215	NZ	N_GLU_126	OE2	3.736
3HAE	T_LYS_215	NZ	S_GLU_126	OE1	2.660
3HAE	T_LYS_215	NZ	S_GLU_126	OE2	3.779
3HFM	L_HIS_34	ND1	H_ASP_99	OD1	3.756
3HFM	L_HIS_34	ND1	H_ASP_99	OD2	3.698
3HFM	L_LYS_49	NZ	H_ASP_99	OD1	3.423
3HFM	H_LYS_209	NZ	L_GLU_123	OE1	2.622
3HFM	H_ARG_213	NH2	L_GLU_123	OE1	3.991
3HFM	Y_LYS_97	NZ	H_ASP_32	OD1	3.609
3HI6	H_LYS_216	NZ	L_GLU_122	OE1	2.896
3HI6	H_LYS_216	NZ	L_GLU_122	OE2	3.887
3HI6	X_LYS_216	NZ	Y_GLU_122	OE1	3.212
3HMG	A_ARG_109	NH1	B_GLU_67	OE1	3.372
3HMG	A_ARG_109	NH1	B_GLU_67	OE2	2.849
3HMG	A_LYS_238	NZ	F_GLU_72	OE2	2.747
3HMG	A_ARG_269	NH2	B_GLU_67	OE1	2.883
3HMG	A_LYS_299	NZ	B_GLU_69	OE1	3.233
3HMG	A_LYS_310	NZ	B_ASP_90	OD1	2.577
3HMG	B_ARG_25	NH1	A_GLU_325	OE1	3.777
3HMG	B_ARG_54	NH1	F_GLU_97	OE1	2.798
3HMG	B_ARG_54	NH2	F_GLU_97	OE1	3.127
3HMG	B_LYS_62	NZ	F_ASP_86	OD1	2.986
3HMG	B_LYS_62	NZ	F_ASP_86	OD2	2.761
3HMG	B_LYS_62	NZ	F_ASP_90	OD1	3.490
3HMG	B_LYS_62	NZ	F_ASP_90	OD2	2.774
3HMG	B_HIS_64	NE2	F_ASP_79	OD1	3.991
3HMG	B_HIS_64	NE2	F_ASP_79	OD2	3.618
3HMG	B_ARG_76	NH1	D_GLU_74	OE1	3.445
3HMG	B_ARG_76	NH1	D_GLU_74	OE2	2.823
3HMG	B_ARG_76	NH1	D_GLU_81	OE1	2.738
3HMG	B_ARG_76	NH1	D_GLU_81	OE2	3.615
3HMG	B_ARG_76	NH2	D_GLU_74	OE1	2.830
3HMG	B_ARG_76	NH2	D_GLU_74	OE2	3.630
3HMG	B_ARG_123	NH1	F_GLU_132	OE2	3.281
3HMG	B_ARG_124	NH1	F_GLU_132	OE1	3.422
3HMG	B_ARG_124	NH1	F_GLU_132	OE2	3.128
3HMG	B_ARG_127	NH2	F_GLU_131	OE1	2.404
3HMG	B_ARG_163	NH1	F_GLU_131	OE1	2.713
3HMG	B_ARG_163	NH1	F_GLU_131	OE2	2.661
3HMG	B_ARG_170	NH2	D_GLU_128	OE1	3.667
3HMG	B_ARG_170	NH2	D_GLU_128	OE2	3.704
3HMG	C_ARG_109	NH1	D_GLU_67	OE1	3.376
3HMG	C_ARG_109	NH1	D_GLU_67	OE2	2.842
3HMG	C_LYS_238	NZ	B_GLU_72	OE2	2.625

3HMG	C_ARG_269	NH2	D_GLU_67	OE1	2.813
3HMG	C_LYS_299	NZ	D_GLU_69	OE1	3.251
3HMG	C_LYS_310	NZ	D_ASP_90	OD1	2.544
3HMG	D_ARG_54	NH1	B_GLU_97	OE1	2.804
3HMG	D_ARG_54	NH2	B_GLU_97	OE1	3.138
3HMG	D_LYS_62	NZ	B_ASP_86	OD1	2.985
3HMG	D_LYS_62	NZ	B_ASP_86	OD2	2.721
3HMG	D_LYS_62	NZ	B_ASP_90	OD1	3.453
3HMG	D_LYS_62	NZ	B_ASP_90	OD2	2.701
3HMG	D_HIS_64	NE2	B_ASP_79	OD1	3.960
3HMG	D_HIS_64	NE2	B_ASP_79	OD2	3.444
3HMG	D_ARG_76	NH1	F_GLU_74	OE1	3.513
3HMG	D_ARG_76	NH1	F_GLU_74	OE2	2.767
3HMG	D_ARG_76	NH1	F_GLU_81	OE1	2.643
3HMG	D_ARG_76	NH1	F_GLU_81	OE2	3.636
3HMG	D_ARG_76	NH2	F_GLU_74	OE1	2.766
3HMG	D_ARG_76	NH2	F_GLU_74	OE2	3.449
3HMG	D_ARG_123	NH1	B_GLU_132	OE2	3.299
3HMG	D_ARG_124	NH1	B_GLU_132	OE1	3.459
3HMG	D_ARG_124	NH1	B_GLU_132	OE2	3.169
3HMG	D_ARG_127	NH2	B_GLU_131	OE1	2.449
3HMG	D_ARG_163	NH1	B_GLU_131	OE1	2.694
3HMG	D_ARG_163	NH1	B_GLU_131	OE2	2.707
3HMG	D_ARG_170	NH2	F_GLU_128	OE1	3.716
3HMG	D_ARG_170	NH2	F_GLU_128	OE2	3.859
3HMG	E_ARG_109	NH1	F_GLU_67	OE1	3.402
3HMG	E_ARG_109	NH1	F_GLU_67	OE2	2.841
3HMG	E_LYS_238	NZ	D_GLU_72	OE2	2.745
3HMG	E_ARG_269	NH2	F_GLU_67	OE1	2.840
3HMG	E_LYS_299	NZ	F_GLU_69	OE1	3.192
3HMG	E_LYS_310	NZ	F_ASP_90	OD1	2.563
3HMG	F_ARG_25	NH1	E_GLU_325	OE2	3.879
3HMG	F_ARG_25	NH2	E_GLU_325	OE2	3.668
3HMG	F_ARG_54	NH1	D_GLU_97	OE1	2.700
3HMG	F_ARG_54	NH2	D_GLU_97	OE1	3.155
3HMG	F_LYS_62	NZ	D_ASP_86	OD1	2.928
3HMG	F_LYS_62	NZ	D_ASP_86	OD2	2.697
3HMG	F_LYS_62	NZ	D_ASP_90	OD1	3.563
3HMG	F_LYS_62	NZ	D_ASP_90	OD2	2.800
3HMG	F_HIS_64	NE2	D_ASP_79	OD1	3.875
3HMG	F_HIS_64	NE2	D_ASP_79	OD2	3.441
3HMG	F_ARG_76	NH1	B_GLU_74	OE1	3.414
3HMG	F_ARG_76	NH1	B_GLU_74	OE2	2.793
3HMG	F_ARG_76	NH1	B_GLU_81	OE1	2.687
3HMG	F_ARG_76	NH1	B_GLU_81	OE2	3.711
3HMG	F_ARG_76	NH2	B_GLU_74	OE1	2.734
3HMG	F_ARG_76	NH2	B_GLU_74	OE2	3.548
3HMG	F_ARG_123	NH1	D_GLU_132	OE2	3.319
3HMG	F_ARG_124	NH1	D_GLU_132	OE1	3.517
3HMG	F_ARG_124	NH1	D_GLU_132	OE2	3.294
3HMG	F_ARG_127	NH2	D_GLU_131	OE1	2.559
3HMG	F_ARG_163	NH1	D_GLU_131	OE1	2.673
3HMG	F_ARG_163	NH1	D_GLU_131	OE2	2.666
3HMG	F_ARG_170	NH2	B_GLU_128	OE1	3.705
3HMG	F_ARG_170	NH2	B_GLU_128	OE2	3.753
3HZK	A_ARG_95	NH2	B_ASP_95	OD1	3.611
3HZK	A_ARG_95	NH2	B_ASP_95	OD2	2.795
3HZK	B_LYS_207	NZ	A_GLU_122	OE2	3.993

3HZM	A_ARG_95	NH2	B_ASP_95	OD1	3.493
3HZM	A_ARG_95	NH2	B_ASP_95	OD2	2.771
3HZM	A_ARG_95	NH2	B_ASP_100E	OD1	3.831
3HZM	B_LYS_207	NZ	A_GLU_122	OE2	3.353
3HZV	A_ARG_95	NH2	B_ASP_95	OD1	3.498
3HZV	A_ARG_95	NH2	B_ASP_95	OD2	2.821
3HZV	A_ARG_95	NH2	B_ASP_100E	OD1	3.905
3HZV	B_LYS_207	NZ	A_GLU_122	OE2	3.521
3HZY	A_ARG_95	NH2	B_ASP_95	OD1	3.688
3HZY	A_ARG_95	NH2	B_ASP_95	OD2	3.045
3HZY	A_ARG_95	NH2	B_ASP_100E	OD1	3.820
3HZY	B_LYS_207	NZ	A_GLU_122	OE2	3.902
3I02	A_ARG_95	NH2	B_ASP_95	OD2	3.028
3I02	C_ARG_95	NH2	D_ASP_95	OD1	3.601
3I02	C_ARG_95	NH2	D_ASP_95	OD2	2.826
3I02	D_LYS_208	NZ	C_GLU_122	OE2	3.585
3IET	A_LYS_50	NZ	X_GLU_8	OE1	3.701
3IET	A_LYS_50	NZ	X_GLU_8	OE2	3.403
3IET	B_LYS_208	NZ	A_GLU_123	OE1	3.818
3IET	D_HIS_55	ND1	A_ASP_143	OD1	3.412
3IET	D_HIS_55	ND1	A_ASP_143	OD2	3.385
3IET	D_LYS_208	NZ	C_GLU_123	OE2	3.321
3IF1	D_LYS_52B	NZ	A_ASP_143	OD2	3.658
3IF1	D_HIS_55	ND1	A_ASP_143	OD1	3.559
3IF1	D_HIS_55	ND1	A_ASP_143	OD2	3.251
3IJH	A_ARG_95	NH2	B_ASP_95	OD1	3.392
3IJH	A_ARG_95	NH2	B_ASP_95	OD2	2.832
3IJH	A_ARG_95	NH2	B_GLU_100E	OE1	3.920
3IJH	B_ARG_164	NH1	A_ASP_166	OD1	3.428
3IJH	B_ARG_164	NH2	A_ASP_166	OD1	3.938
3IJH	B_LYS_208	NZ	A_GLU_122	OE1	2.744
3IJH	C_ARG_95	NH2	D_ASP_95	OD1	3.394
3IJH	C_ARG_95	NH2	D_ASP_95	OD2	2.734
3IJH	D_ARG_164	NH1	C_ASP_166	OD1	3.593
3IJH	D_ARG_164	NH2	C_ASP_166	OD1	3.440
3IJS	A_ARG_95	NH2	B_ASP_95	OD1	3.603
3IJS	A_ARG_95	NH2	B_ASP_95	OD2	3.018
3IJS	A_ARG_95	NH2	B_GLU_100E	OE1	3.734
3IJS	B_ARG_164	NH1	A_ASP_166	OD1	3.855
3IJS	B_LYS_208	NZ	A_GLU_122	OE1	2.963
3IJS	C_ARG_95	NH2	D_ASP_95	OD1	3.466
3IJS	C_ARG_95	NH2	D_ASP_95	OD2	2.795
3IJS	C_ARG_95	NH2	D_GLU_100E	OE1	3.752
3IJS	D_ARG_164	NH1	C_ASP_166	OD1	3.815
3IJS	D_ARG_164	NH2	C_ASP_166	OD1	3.576
3IJS	D_LYS_208	NZ	C_GLU_122	OE1	3.219
3IJS	D_LYS_208	NZ	C_GLU_122	OE2	2.679
3IJY	A_ARG_95	NH2	B_ASP_95	OD1	3.420
3IJY	A_ARG_95	NH2	B_ASP_95	OD2	2.800
3IJY	A_ARG_95	NH2	B_GLU_100E	OE1	3.751
3IJY	B_ARG_164	NH2	A_ASP_166	OD1	3.730
3IJY	B_ARG_164	NH2	A_ASP_166	OD2	3.693
3IJY	B_LYS_208	NZ	A_GLU_122	OE1	2.748
3IJY	C_ARG_95	NH2	D_ASP_95	OD1	2.992
3IJY	C_ARG_95	NH2	D_ASP_95	OD2	2.767
3IJY	C_ARG_95	NH2	D_GLU_100E	OE1	3.905
3IJY	D_ARG_164	NH2	C_ASP_166	OD1	3.199
3IKC	A_ARG_95	NH2	B_ASP_95	OD1	3.326

3IKC	A_ARG_95	NH2	B_ASP_95	OD2	2.867
3IKC	A_ARG_95	NH2	B_GLU_100E	OE1	3.865
3IKC	B_LYS_208	NZ	A_GLU_122	OE1	3.042
3IKC	C_ARG_95	NH2	D_ASP_95	OD1	3.250
3IKC	C_ARG_95	NH2	D_ASP_95	OD2	2.670
3IKC	D_ARG_164	NH1	C_ASP_166	OD1	3.903
3IKC	D_ARG_164	NH2	C_ASP_166	OD1	3.107
3IU3	A_ARG_29	NH2	K_ASP_6	OD1	2.779
3IU3	A_LYS_211	NZ	B_GLU_120	OE1	2.457
3IU3	B_ARG_90	NH1	K_ASP_56	OD2	3.059
3IU3	C_ARG_29	NH1	J_ASP_6	OD1	3.038
3IU3	C_ARG_29	NH1	J_ASP_6	OD2	3.788
3IU3	C_ARG_29	NH2	J_ASP_6	OD1	3.464
3IU3	C_LYS_211	NZ	D_GLU_120	OE2	3.231
3IU3	D_ARG_90	NH2	J_ASP_56	OD2	3.101
3IU3	H_ARG_29	NH1	I_ASP_6	OD1	3.964
3IU3	H_ARG_29	NH1	I_ASP_6	OD2	3.865
3IU3	H_ARG_29	NH2	I_ASP_6	OD1	2.749
3IU3	H_ARG_29	NH2	I_ASP_6	OD2	3.378
3IU3	H_HIS_166	NE2	L_ASP_164	OD1	3.898
3IU3	H_LYS_211	NZ	L_GLU_120	OE2	3.694
3IU3	L_ARG_29	NH2	I_ASP_56	OD2	3.164
3IU3	L_ARG_90	NH2	I_ASP_56	OD1	2.806
3IU3	L_ARG_36	NH1	H_ASP_55	OD1	3.819
3IU3	L_ARG_36	NH2	H_ASP_55	OD1	3.008
3IU3	L_ARG_36	NH2	H_ASP_55	OD2	2.747
3J5M	A_ARG_429	NH2	D_ASP_74	OD1	3.207
3J5M	A_ARG_429	NH2	D_ASP_74	OD2	3.203
3J5M	D_LYS_52	NZ	A_ASP_474	OD2	2.827
3J5M	D_ARG_64	NH2	A_ASP_457	OD2	3.079
3J5M	D_LYS_209	NZ	C_GLU_123	OE1	3.480
3J5M	D_LYS_209	NZ	C_GLU_123	OE2	2.844
3J5M	D_LYS_214	NZ	C_ASP_122	OD2	2.841
3J5M	E_ARG_429	NH2	H_ASP_74	OD1	3.207
3J5M	E_ARG_429	NH2	H_ASP_74	OD2	3.202
3J5M	H_LYS_52	NZ	E_ASP_474	OD2	2.827
3J5M	H_ARG_64	NH2	E_ASP_457	OD2	3.078
3J5M	H_LYS_209	NZ	G_GLU_123	OE1	3.479
3J5M	H_LYS_209	NZ	G_GLU_123	OE2	2.843
3J5M	H_LYS_214	NZ	G_ASP_122	OD2	2.842
3J5M	L_ARG_429	NH2	L_ASP_74	OD1	3.207
3J5M	L_ARG_429	NH2	L_ASP_74	OD2	3.202
3J5M	L_LYS_52	NZ	I_ASP_474	OD2	2.827
3J5M	L_ARG_64	NH2	I_ASP_457	OD2	3.078
3J5M	L_LYS_209	NZ	K_GLU_123	OE1	3.480
3J5M	L_LYS_209	NZ	K_GLU_123	OE2	2.844
3J5M	L_LYS_214	NZ	K_ASP_122	OD2	2.841
3J70	A_ARG_64	NH2	B_ASP_1	OD1	2.676
3J70	A_LYS_209	NZ	B_GLU_123	OE1	3.744
3J70	A_LYS_209	NZ	B_GLU_123	OE2	2.604
3J70	C_LYS_29	NZ	D_ASP_279	OD2	2.704
3J70	C_ARG_59	NH1	D_ASP_368	OD1	3.842
3J70	C_ARG_59	NH1	D_ASP_368	OD2	2.986
3J70	C_ARG_59	NH2	D_ASP_368	OD1	2.621
3J70	C_ARG_59	NH2	D_ASP_368	OD2	3.173
3J70	D_ARG_146	NH1	C_GLU_169	OE1	2.841
3J70	D_ARG_146	NH1	C_GLU_169	OE2	2.796
3J70	D_ARG_146	NH2	C_GLU_169	OE1	3.599

3J70	D_LYS_171	NZ	C_GLU_13	OE1	3.949
3J70	D_LYS_322	NZ	A_ASP_95	OD2	2.908
3J70	D_ARG_327	NH2	A_ASP_52	OD2	3.286
3J70	D_ARG_419	NH1	A_ASP_54	OD1	3.985
3J70	M_ARG_64	NH2	N_ASP_1	OD1	2.677
3J70	M_LYS_209	NZ	N_GLU_123	OE1	3.744
3J70	M_LYS_209	NZ	N_GLU_123	OE2	2.604
3J70	O_LYS_29	NZ	P_ASP_279	OD2	2.704
3J70	O_ARG_59	NH1	P_ASP_368	OD1	3.842
3J70	O_ARG_59	NH1	P_ASP_368	OD2	2.986
3J70	O_ARG_59	NH2	P_ASP_368	OD1	2.620
3J70	O_ARG_59	NH2	P_ASP_368	OD2	3.173
3J70	P_ARG_146	NH1	O_GLU_169	OE1	2.841
3J70	P_ARG_146	NH1	O_GLU_169	OE2	2.796
3J70	P_ARG_146	NH2	O_GLU_169	OE1	3.599
3J70	P_LYS_171	NZ	O_GLU_13	OE1	3.948
3J70	P_LYS_322	NZ	M_ASP_95	OD2	2.909
3J70	P_ARG_327	NH2	M_ASP_52	OD2	3.286
3J70	P_ARG_419	NH1	M_ASP_54	OD1	3.985
3J70	R_ARG_64	NH2	S_ASP_1	OD1	2.677
3J70	R_LYS_209	NZ	S_GLU_123	OE1	3.743
3J70	R_LYS_209	NZ	S_GLU_123	OE2	2.603
3J70	T_LYS_29	NZ	U_ASP_279	OD2	2.704
3J70	T_ARG_59	NH1	U_ASP_368	OD1	3.842
3J70	T_ARG_59	NH1	U_ASP_368	OD2	2.986
3J70	T_ARG_59	NH2	U_ASP_368	OD1	2.621
3J70	T_ARG_59	NH2	U_ASP_368	OD2	3.174
3J70	U_ARG_146	NH1	T_GLU_169	OE1	2.840
3J70	U_ARG_146	NH1	T_GLU_169	OE2	2.796
3J70	U_ARG_146	NH2	T_GLU_169	OE1	3.599
3J70	U_LYS_171	NZ	T_GLU_13	OE1	3.949
3J70	U_LYS_322	NZ	R_ASP_95	OD2	2.909
3J70	U_ARG_327	NH2	R_ASP_52	OD2	3.287
3J70	U_ARG_419	NH1	R_ASP_54	OD1	3.985
3JCC	A_ARG_429	NH2	D_ASP_63	OD2	3.854
3JCC	C_LYS_207	NZ	B_GLU_124	OE1	3.629
3JCC	D_ARG_59	NH2	A_ASP_368	OD1	2.961
3JCC	D_ARG_59	NH2	A_ASP_368	OD2	3.986
3KS0	H_LYS_39	NZ	L_GLU_40	OE1	3.686
3KS0	H_LYS_39	NZ	L_GLU_40	OE2	2.843
3KS0	H_LYS_147	NZ	L_GLU_127	OE2	3.112
3KS0	H_LYS_212	NZ	L_GLU_126	OE1	3.920
3KS0	H_LYS_212	NZ	L_GLU_126	OE2	3.042
3KS0	K_LYS_39	NZ	J_GLU_40	OE1	3.754
3KS0	K_LYS_39	NZ	J_GLU_40	OE2	2.934
3KS0	K_LYS_147	NZ	J_GLU_127	OE2	3.169
3KS0	K_LYS_212	NZ	J_GLU_126	OE1	3.344
3KS0	K_LYS_212	NZ	J_GLU_126	OE2	2.562
3L7E	H_LYS_217	NZ	L_GLU_123	OE1	3.175
3L7E	B_LYS_217	NZ	A_GLU_123	OE1	2.697
3L7E	B_LYS_217	NZ	A_GLU_123	OE2	3.970
3LZF	A_ARG_109	NH2	B_GLU_69	OE1	3.970
3LZF	A_ARG_109	NH2	B_GLU_69	OE2	2.555
3LZF	A_LYS_157	NZ	H_ASP_52	OD1	3.712
3LZF	A_LYS_157	NZ	H_ASP_52	OD2	3.952
3LZF	A_LYS_157	NZ	H_ASP_54	OD2	2.960
3LZF	A_LYS_166	NZ	L_ASP_93	OD1	2.890
3LZF	A_LYS_166	NZ	L_ASP_93	OD2	2.667

3LZF	A_ARG_310	NH1	B_ASP_90	OD1	2.412
3LZF	A_ARG_310	NH2	B_ASP_90	OD1	3.228
3LZF	B_LYS_68	NZ	A_GLU_110	OE1	3.290
3LZF	B_LYS_68	NZ	A_GLU_110	OE2	2.778
3LZF	H_LYS_221	NZ	L_GLU_123	OE2	3.483
3MLR	H_LYS_129	NZ	L_ASP_142	OD2	3.806
3MLR	H_LYS_209	NZ	L_GLU_127	OE2	3.182
3MLR	P_LYS_304	NZ	H_ASP_31	OD1	3.470
3MLR	P_LYS_305	NZ	H_ASP_54	OD1	2.683
3MLR	P_LYS_305	NZ	H_ASP_54	OD2	3.624
3MLR	P_LYS_305	NZ	H_ASP_56	OD2	3.011
3MLS	H_LYS_73	NZ	I_ASP_31	OD1	3.962
3MLS	H_LYS_73	NZ	I_ASP_31	OD2	2.716
3MLS	H_LYS_73	NZ	I_ASP_53	OD1	3.242
3MLS	H_LYS_73	NZ	I_ASP_53	OD2	3.339
3MLS	H_LYS_117	NZ	J_GLU_10	OE1	3.515
3MLS	H_LYS_143	NZ	L_GLU_128	OE2	2.664
3MLS	H_LYS_209	NZ	L_GLU_127	OE1	2.677
3MLS	P_ARG_11	NH1	H_GLU_99	OE1	3.690
3MLS	P_ARG_11	NH1	H_GLU_99	OE2	3.548
3MLS	P_ARG_11	NH2	H_GLU_99	OE1	3.097
3MLS	P_ARG_11	NH2	H_GLU_99	OE2	3.355
3MLS	P_LYS_12	NZ	H_ASP_54	OD1	3.420
3MLS	P_LYS_12	NZ	H_ASP_54	OD2	2.807
3MLS	P_LYS_12	NZ	H_ASP_56	OD1	3.833
3MLS	P_LYS_12	NZ	H_ASP_56	OD2	3.175
3MLS	I_LYS_143	NZ	M_GLU_128	OE2	2.744
3MLS	Q_LYS_12	NZ	I_ASP_54	OD1	2.683
3MLS	Q_LYS_12	NZ	I_ASP_54	OD2	3.484
3MLS	Q_LYS_12	NZ	I_ASP_56	OD1	3.650
3MLS	N_LYS_97	NZ	J_GLU_64	OE2	3.402
3MLS	J_LYS_117	NZ	H_GLU_10	OE1	3.984
3MLS	J_LYS_209	NZ	N_GLU_127	OE2	3.428
3MLS	R_LYS_12	NZ	J_ASP_54	OD1	2.569
3MLS	R_LYS_12	NZ	J_ASP_54	OD2	3.629
3MLS	R_LYS_12	NZ	J_ASP_56	OD2	2.975
3MLS	K_LYS_117	NZ	I_GLU_10	OE1	3.985
3MLS	S_LYS_12	NZ	K_ASP_54	OD1	2.573
3MLS	S_LYS_12	NZ	K_ASP_54	OD2	3.736
3MLS	S_LYS_12	NZ	K_ASP_56	OD2	3.122
3MLT	P_ARG_304	NH1	H_ASP_31	OD1	2.766
3MLT	P_LYS_305	NZ	H_ASP_54	OD1	2.503
3MLT	P_LYS_305	NZ	H_ASP_54	OD2	3.276
3MLT	P_LYS_305	NZ	H_ASP_56	OD2	2.482
3MLT	B_LYS_209	NZ	A_GLU_127	OE2	3.807
3MLT	C_LYS_305	NZ	B_ASP_54	OD1	3.099
3MLT	C_LYS_305	NZ	B_ASP_54	OD2	3.737
3MLT	C_LYS_305	NZ	B_ASP_56	OD2	3.095
3MLT	E_LYS_209	NZ	D_GLU_127	OE2	3.591
3MLT	I_LYS_209	NZ	G_GLU_127	OE2	3.669
3MLU	L_LYS_133	NZ	H_ASP_144	OD2	3.641
3MLU	P_LYS_305	NZ	H_ASP_54	OD1	2.586
3MLU	P_LYS_305	NZ	H_ASP_54	OD2	3.496
3MLU	P_LYS_305	NZ	H_ASP_56	OD2	3.684
3MLV	P_ARG_304	NH1	H_ASP_31	OD1	3.750
3MLV	P_LYS_305	NZ	H_ASP_54	OD1	2.508
3MLV	P_LYS_305	NZ	H_ASP_54	OD2	3.477
3MLV	P_LYS_305	NZ	H_ASP_56	OD2	2.918

3MLV	M_LYS_97	NZ	N_GLU_64	OE1	2.901
3MLV	Q_ARG_304	NH1	N_GLU_99	OE2	3.900
3MLV	Q_ARG_304	NH2	N_GLU_99	OE2	3.849
3MLV	Q_LYS_305	NZ	N_ASP_54	OD1	3.154
3MLV	Q_LYS_305	NZ	N_ASP_54	OD2	3.686
3MLV	Q_LYS_305	NZ	N_ASP_56	OD2	2.702
3MLW	L_ARG_50	NH1	H_ASP_100G	OD1	2.178
3MLW	L_ARG_50	NH1	H_ASP_100G	OD2	3.432
3MLW	L_LYS_129	NZ	H_ASP_144	OD2	3.472
3MLW	H_ARG_58	NH1	L_ASP_95D	OD1	3.535
3MLW	H_ARG_58	NH1	L_ASP_95D	OD2	2.585
3MLW	P_LYS_303	NZ	H_ASP_31	OD2	3.075
3MLW	P_ARG_304	NH1	H_ASP_31	OD1	3.646
3MLW	P_LYS_305	NZ	H_ASP_54	OD1	3.646
3MLW	P_LYS_305	NZ	H_ASP_54	OD2	2.863
3MLW	P_LYS_305	NZ	H_ASP_56	OD1	3.537
3MLW	P_ARG_315	NH1	L_ASP_93	OD1	2.718
3MLW	P_ARG_315	NH1	L_ASP_93	OD2	3.239
3MLW	M_ARG_50	NH2	L_ASP_100G	OD1	2.708
3MLW	M_ARG_50	NH2	L_ASP_100G	OD2	3.923
3MLW	L_ARG_58	NH1	M_ASP_95D	OD1	2.653
3MLW	L_ARG_58	NH1	M_ASP_95D	OD2	3.643
3MLW	L_LYS_209	NZ	M_GLU_123	OE1	2.581
3MLW	L_LYS_209	NZ	M_GLU_123	OE2	3.213
3MLW	Q_LYS_305	NZ	L_ASP_54	OD2	3.005
3MLW	Q_LYS_305	NZ	L_ASP_56	OD1	2.747
3MLW	Q_ARG_315	NH1	M_ASP_93	OD1	3.021
3MLX	H_LYS_143	NZ	L_GLU_124	OE2	3.021
3MLX	P_HIS_308	ND1	H_GLU_98	OE2	3.800
3MLX	P_HIS_308	NE2	H_GLU_98	OE2	3.892
3MLX	L_LYS_143	NZ	M_GLU_124	OE2	2.608
3MLX	L_LYS_214	NZ	M_GLU_123	OE1	3.588
3MLX	Q_HIS_308	ND1	L_GLU_98	OE1	3.280
3MLY	H_LYS_143	NZ	L_GLU_124	OE2	3.991
3MLY	H_LYS_214	NZ	L_GLU_123	OE1	3.745
3MLY	P_LYS_308	NZ	L_GLU_50	OE1	3.397
3MLY	P_LYS_308	NZ	L_GLU_50	OE2	3.390
3MLY	L_LYS_143	NZ	M_GLU_124	OE2	2.661
3MLY	L_LYS_214	NZ	M_GLU_123	OE1	3.594
3MLZ	H_LYS_	NZ	L_GLU_	OE1	3.724
3MLZ	H_LYS_	NZ	L_GLU_	OE2	3.184
3MLZ	H_LYS_	NZ	L_GLU_	OE2	2.805
3MLZ	H_LYS_	NZ	L_GLU_	OE1	3.039
3MLZ	H_LYS_	NZ	L_GLU_	OE2	3.262
3NFP	A_ARG_33	NH1	K_ASP_4	OD1	3.227
3NFP	A_ARG_33	NH2	K_ASP_6	OD1	3.995
3NFP	A_ARG_33	NH2	K_ASP_6	OD2	2.804
3NFP	A_HIS_35	NE2	K_ASP_4	OD1	3.568
3NFP	A_HIS_35	NE2	K_ASP_4	OD2	3.384
3NFP	H_ARG_33	NH1	L_ASP_4	OD2	2.868
3NFP	H_ARG_33	NH2	L_ASP_6	OD2	3.531
3NFP	H_HIS_35	NE2	L_ASP_4	OD1	3.314
3NFP	H_HIS_35	NE2	L_ASP_4	OD2	3.660
3NFP	H_LYS_212	NZ	L_GLU_122	OE1	3.767
3NFP	L_HIS_120	NE2	H_GLU_59	OE1	3.799
3NFP	L_HIS_120	NE2	H_GLU_59	OE2	3.285
3NFP	K_HIS_120	NE2	A_GLU_59	OE2	3.393
3NGB	G_LYS_97	NZ	H_ASP_99	OD2	3.903

3NGB	H_ARG_71	NH1	G_ASP_368	OD1	3.623
3NGB	H_ARG_71	NH1	G_ASP_368	OD2	3.004
3NGB	H_ARG_71	NH2	G_ASP_368	OD1	2.815
3NGB	H_ARG_71	NH2	G_ASP_368	OD2	3.723
3NGB	H_LYS_209	NZ	L_GLU_125	OE1	3.421
3NGB	H_LYS_209	NZ	L_GLU_125	OE2	3.841
3NGB	A_LYS_97	NZ	B_ASP_99	OD2	3.768
3NGB	B_ARG_71	NH1	A_ASP_368	OD1	3.647
3NGB	B_ARG_71	NH1	A_ASP_368	OD2	2.944
3NGB	B_ARG_71	NH2	A_ASP_368	OD1	2.895
3NGB	B_ARG_71	NH2	A_ASP_368	OD2	3.718
3NGB	B_LYS_209	NZ	C_GLU_125	OE1	2.774
3NGB	B_LYS_209	NZ	C_GLU_125	OE2	2.799
3NGB	D_LYS_97	NZ	E_ASP_99	OD1	3.709
3NGB	E_ARG_71	NH1	D_ASP_368	OD1	3.715
3NGB	E_ARG_71	NH1	D_ASP_368	OD2	3.074
3NGB	E_ARG_71	NH2	D_ASP_368	OD1	3.026
3NGB	E_ARG_71	NH2	D_ASP_368	OD2	3.848
3NGB	E_HIS_164	ND1	F_ASP_169	OD1	3.984
3NGB	E_LYS_	NZ	F_GLU_	OE1	3.345
3NGB	E_LYS_	NZ	F_GLU_	OE2	2.927
3NGB	I_LYS_97	NZ	J_ASP_99	OD1	3.443
3NGB	J_ARG_71	NH1	I_ASP_368	OD1	3.645
3NGB	J_ARG_71	NH1	I_ASP_368	OD2	3.125
3NGB	J_ARG_71	NH2	I_ASP_368	OD1	3.120
3NGB	J_LYS_209	NZ	K_GLU_125	OE1	2.929
3NGB	J_LYS_209	NZ	K_GLU_125	OE2	3.060
3NGB	J_LYS_214	NZ	K_ASP_124	OD1	3.305
3NH7	H_ARG_98	NH1	A_ASP_67	OD2	3.819
3NH7	H_ARG_98	NH2	A_ASP_67	OD1	2.850
3NH7	H_ARG_98	NH2	A_ASP_67	OD2	2.389
3NH7	H_ARG_100	NH2	A_GLU_64	OE2	3.004
3NH7	H_HIS_102	ND1	A_GLU_64	OE1	2.378
3NH7	H_ARG_104	NH2	A_GLU_81	OE1	3.515
3NH7	H_ARG_104	NH2	A_GLU_81	OE2	2.462
3NH7	H_LYS_216	NZ	L_GLU_125	OE2	3.557
3NH7	A_LYS_79	NZ	L_ASP_50	OD1	3.333
3NH7	A_LYS_79	NZ	L_ASP_50	OD2	3.058
3NH7	A_LYS_92	NZ	H_GLU_99	OE1	3.975
3NH7	A_LYS_92	NZ	H_GLU_99	OE2	3.561
3NH7	I_ARG_98	NH1	B_ASP_67	OD2	3.924
3NH7	I_ARG_98	NH2	B_ASP_67	OD1	3.388
3NH7	I_ARG_98	NH2	B_ASP_67	OD2	2.296
3NH7	I_ARG_100	NH2	B_GLU_64	OE2	2.996
3NH7	I_HIS_102	ND1	B_GLU_64	OE1	2.707
3NH7	I_ARG_104	NH2	B_GLU_81	OE1	3.637
3NH7	I_ARG_104	NH2	B_GLU_81	OE2	2.502
3NH7	I_LYS_216	NZ	M_GLU_125	OE1	3.301
3NH7	I_LYS_216	NZ	M_GLU_125	OE2	3.320
3NH7	B_LYS_79	NZ	M_ASP_50	OD1	3.625
3NH7	B_LYS_79	NZ	M_ASP_50	OD2	2.953
3NH7	B_LYS_92	NZ	I_GLU_99	OE1	3.831
3NH7	B_LYS_92	NZ	I_GLU_99	OE2	3.683
3NH7	J_ARG_98	NH1	C_ASP_67	OD2	3.893
3NH7	J_ARG_98	NH2	C_ASP_67	OD1	3.313
3NH7	J_ARG_98	NH2	C_ASP_67	OD2	2.401
3NH7	J_ARG_100	NH2	C_GLU_64	OE2	3.173
3NH7	J_HIS_102	ND1	C_GLU_64	OE1	2.668

3NH7	J_ARG_104	NH2	C_GLU_81	OE1	3.595
3NH7	J_ARG_104	NH2	C_GLU_81	OE2	2.634
3NH7	J_LYS_216	NZ	N_GLU_125	OE1	2.816
3NH7	J_LYS_216	NZ	N_GLU_125	OE2	3.044
3NH7	C_LYS_79	NZ	N_ASP_50	OD1	3.064
3NH7	C_LYS_79	NZ	N_ASP_50	OD2	3.315
3NH7	C_LYS_92	NZ	J_GLU_99	OE1	3.721
3NH7	C_LYS_92	NZ	J_GLU_99	OE2	3.806
3NH7	K_ARG_98	NH1	D_ASP_67	OD2	3.348
3NH7	K_ARG_98	NH2	D_ASP_67	OD1	3.350
3NH7	K_ARG_98	NH2	D_ASP_67	OD2	2.647
3NH7	K_ARG_100	NH2	D_GLU_64	OE2	3.101
3NH7	K_HIS_102	ND1	D_GLU_64	OE1	2.313
3NH7	K_ARG_104	NH2	D_GLU_81	OE1	3.830
3NH7	K_ARG_104	NH2	D_GLU_81	OE2	2.800
3NH7	K_LYS_216	NZ	O_GLU_125	OE1	3.159
3NH7	K_LYS_216	NZ	O_GLU_125	OE2	3.376
3NH7	D_LYS_79	NZ	O_ASP_50	OD1	3.661
3NH7	D_LYS_79	NZ	O_ASP_50	OD2	3.355
3NH7	D_LYS_92	NZ	K_GLU_99	OE1	3.766
3NH7	D_LYS_92	NZ	K_GLU_99	OE2	3.832
3NZ8	A_HIS_164	NE2	B_ASP_167	OD1	3.115
3NZ8	A_LYS_208	NZ	B_GLU_123	OE2	3.283
3NZ8	H_LYS_208	NZ	L_GLU_123	OE2	3.808
3O2D	L_ARG_95	NH1	H_GLU_95	OE2	2.847
3O2D	L_ARG_95	NH2	H_GLU_95	OE2	3.717
3O2D	H_LYS_209	NZ	L_GLU_122	OE1	2.503
3O2D	H_LYS_209	NZ	L_GLU_122	OE2	3.547
3O41	H_ARG_94	NH1	A_GLU_191	OE1	2.970
3O41	H_ARG_94	NH1	A_GLU_191	OE2	3.394
3O41	H_ARG_94	NH2	A_GLU_191	OE1	3.744
3O41	H_ARG_94	NH2	A_GLU_191	OE2	2.660
3O41	H_LYS_208	NZ	L_GLU_123	OE2	3.054
3O41	A_LYS_208	NZ	B_GLU_123	OE2	2.651
3O41	P_LYS_433	NZ	H_ASP_54	OD1	3.659
3O41	P_LYS_433	NZ	H_ASP_54	OD2	2.887
3O41	P_LYS_433	NZ	H_ASP_56	OD2	2.760
3O41	C_LYS_433	NZ	A_ASP_54	OD1	3.503
3O41	C_LYS_433	NZ	A_ASP_54	OD2	2.671
3O41	C_LYS_433	NZ	A_ASP_56	OD2	2.936
3O45	H_ARG_94	NH1	A_GLU_191	OE1	3.085
3O45	H_ARG_94	NH1	A_GLU_191	OE2	3.621
3O45	H_ARG_94	NH2	A_GLU_191	OE1	3.709
3O45	H_ARG_94	NH2	A_GLU_191	OE2	2.802
3O45	H_LYS_208	NZ	L_GLU_123	OE2	3.033
3O45	A_LYS_208	NZ	B_GLU_123	OE2	2.878
3O45	P_LYS_433	NZ	H_ASP_54	OD1	3.518
3O45	P_LYS_433	NZ	H_ASP_54	OD2	2.818
3O45	P_LYS_433	NZ	H_ASP_56	OD2	2.927
3O45	C_LYS_433	NZ	A_ASP_54	OD1	3.297
3O45	C_LYS_433	NZ	A_ASP_54	OD2	2.723
3O45	C_LYS_433	NZ	A_ASP_56	OD2	2.899
3OJD	B_LYS_208	NZ	A_GLU_123	OE2	3.588
3OJD	B_ARG_213	NH1	A_GLU_213	OE2	3.118
3OJD	B_ARG_213	NH2	A_GLU_213	OE2	3.609
3P0Y	A_LYS_463	NZ	H_GLU_95	OE2	2.859
3P0Y	A_LYS_465	NZ	H_GLU_50	OE1	2.656
3P0Y	A_LYS_465	NZ	H_GLU_50	OE2	3.845

3P0Y	A_LYS_465	NZ	H_GLU_95	OE1	2.777
3P0Y	A_LYS_465	NZ	H_GLU_95	OE2	3.671
3P0Y	H_ARG_97	NH1	A_ASP_436	OD1	2.876
3P0Y	H_ARG_97	NH1	A_ASP_436	OD2	3.533
3P0Y	H_ARG_97	NH2	A_ASP_436	OD1	3.647
3P0Y	H_ARG_97	NH2	A_ASP_436	OD2	2.823
3P0Y	H_LYS_209	NZ	L_GLU_123	OE1	2.674
3P0Y	H_LYS_209	NZ	L_GLU_123	OE2	3.317
3P11	A_ARG_441	NH1	H_ASP_58	OD2	3.356
3P11	A_ARG_441	NH1	L_GLU_94	OE1	2.859
3P11	A_ARG_441	NH1	L_GLU_94	OE2	3.310
3P11	A_ARG_441	NH2	L_GLU_94	OE2	3.075
3P11	A_LYS_466	NZ	H_GLU_95	OE1	2.568
3P11	A_LYS_466	NZ	H_GLU_95	OE2	3.227
3P11	A_HIS_467	ND1	H_GLU_50	OE2	3.466
3P11	A_HIS_467	ND1	L_GLU_94	OE2	3.926
3P11	A_HIS_467	NE2	H_GLU_50	OE1	3.754
3P11	A_HIS_467	NE2	H_GLU_50	OE2	3.679
3P11	A_HIS_467	NE2	H_GLU_95	OE2	3.533
3PGF	L_ARG_66	NH1	A_GLU_309	OE2	3.045
3PGF	L_ARG_66	NH2	A_GLU_309	OE2	2.501
3PNW	B_ARG_104	NH1	C_GLU_599	OE1	3.048
3PNW	D_ARG_25	NH1	J_GLU_82	OE1	2.858
3PNW	D_ARG_25	NH1	J_GLU_82	OE2	3.430
3PNW	D_ARG_25	NH2	J_GLU_82	OE1	3.626
3PNW	D_ARG_25	NH2	J_GLU_82	OE2	3.034
3PNW	E_ARG_104	NH1	F_GLU_599	OE2	2.653
3PNW	H_ARG_104	NH1	I_GLU_599	OE1	3.020
3PNW	K_ARG_104	NH1	L_GLU_599	OE1	2.888
3PNW	K_ARG_104	NH1	L_GLU_599	OE2	2.772
3PNW	K_ARG_104	NH2	L_GLU_599	OE2	3.083
3PNW	Q_ARG_104	NH1	R_GLU_599	OE1	3.284
3PNW	T_ARG_104	NH1	U_GLU_599	OE2	2.955
3PNW	W_ARG_104	NH2	X_GLU_599	OE2	3.113
3PP4	H_LYS_215	NZ	L_GLU_128	OE1	3.038
3PP4	H_LYS_215	NZ	L_GLU_128	OE2	2.948
3PP4	P_LYS_175	NZ	H_ASP_57	OD2	3.518
3Q3G	C_LYS_109	NZ	D_GLU_44	OE1	3.620
3Q3G	D_LYS_21	NZ	H_GLU_202	OE2	2.633
3Q3G	D_ARG_52	NH1	G_GLU_179	OE2	3.405
3Q3G	D_ARG_52	NH2	G_GLU_178	OE1	2.845
3Q3G	D_ARG_52	NH2	G_GLU_179	OE2	2.628
3Q3G	D_LYS_219	NZ	C_GLU_129	OE2	3.237
3Q3G	G_ARG_208	NH1	D_GLU_101	OE1	3.693
3Q3G	G_ARG_208	NH1	D_GLU_101	OE2	2.792
3Q3G	G_ARG_208	NH2	D_GLU_101	OE1	2.994
3Q3G	G_ARG_208	NH2	D_GLU_101	OE2	3.045
3Q3G	B_LYS_21	NZ	K_GLU_202	OE2	2.668
3Q3G	B_ARG_52	NH1	E_GLU_179	OE2	3.409
3Q3G	B_ARG_52	NH2	E_GLU_178	OE1	2.858
3Q3G	B_ARG_52	NH2	E_GLU_179	OE2	2.617
3Q3G	B_LYS_219	NZ	A_GLU_129	OE2	3.294
3Q3G	E_ARG_208	NH1	B_GLU_101	OE1	3.701
3Q3G	E_ARG_208	NH1	B_GLU_101	OE2	2.888
3Q3G	E_ARG_208	NH2	B_GLU_101	OE1	3.046
3Q3G	E_ARG_208	NH2	B_GLU_101	OE2	3.227
3Q3G	H_ARG_52	NH1	I_GLU_179	OE2	3.532
3Q3G	H_ARG_52	NH2	I_GLU_178	OE1	2.972

3Q3G	H_ARG_52	NH2	I_GLU_179	OE2	2.629
3Q3G	H_LYS_61	NZ	I_GLU_179	OE2	3.923
3Q3G	H_LYS_219	NZ	F_GLU_129	OE2	3.319
3Q3G	I_ARG_208	NH1	H_GLU_101	OE1	3.704
3Q3G	I_ARG_208	NH1	H_GLU_101	OE2	2.809
3Q3G	I_ARG_208	NH2	H_GLU_101	OE1	3.098
3Q3G	I_ARG_208	NH2	H_GLU_101	OE2	3.125
3Q3G	J_LYS_109	NZ	K_GLU_44	OE1	3.972
3Q3G	K_ARG_52	NH1	L_GLU_179	OE2	3.394
3Q3G	K_ARG_52	NH2	L_GLU_178	OE1	2.871
3Q3G	K_ARG_52	NH2	L_GLU_179	OE2	2.626
3Q3G	K_LYS_219	NZ	J_GLU_129	OE2	3.216
3Q3G	L_ARG_208	NH1	K_GLU_101	OE1	3.706
3Q3G	L_ARG_208	NH1	K_GLU_101	OE2	2.777
3Q3G	L_ARG_208	NH2	K_GLU_101	OE1	3.099
3Q3G	L_ARG_208	NH2	K_GLU_101	OE2	3.162
3QA3	C_LYS_109	NZ	D_GLU_44	OE1	3.919
3QA3	D_LYS_21	NZ	B_GLU_202	OE2	2.710
3QA3	D_ARG_52	NH1	G_GLU_179	OE2	3.492
3QA3	D_ARG_52	NH2	G_GLU_178	OE1	3.012
3QA3	D_ARG_52	NH2	G_GLU_179	OE2	2.776
3QA3	D_LYS_61	NZ	G_GLU_179	OE1	3.896
3QA3	D_LYS_61	NZ	G_GLU_179	OE2	3.867
3QA3	D_LYS_219	NZ	C_GLU_129	OE2	3.586
3QA3	G_ARG_208	NH1	D_GLU_101	OE1	3.094
3QA3	G_ARG_208	NH1	D_GLU_101	OE2	3.755
3QA3	G_ARG_208	NH2	D_GLU_101	OE1	2.802
3QA3	G_LYS_306	NZ	F_GLU_61	OE1	2.676
3QA3	G_LYS_306	NZ	F_GLU_61	OE2	3.962
3QA3	B_ARG_52	NH1	E_GLU_179	OE2	3.674
3QA3	B_ARG_52	NH2	E_GLU_178	OE1	3.139
3QA3	B_ARG_52	NH2	E_GLU_179	OE2	2.772
3QA3	B_LYS_61	NZ	E_GLU_179	OE1	3.626
3QA3	B_LYS_61	NZ	E_GLU_179	OE2	3.531
3QA3	B_LYS_219	NZ	A_GLU_129	OE2	3.689
3QA3	E_ARG_208	NH1	B_GLU_101	OE1	3.112
3QA3	E_ARG_208	NH1	B_GLU_101	OE2	3.639
3QA3	E_ARG_208	NH2	B_GLU_101	OE1	2.913
3QA3	E_ARG_208	NH2	B_GLU_101	OE2	3.978
3QA3	H_LYS_21	NZ	K_GLU_202	OE1	2.630
3QA3	H_ARG_52	NH1	I_GLU_179	OE2	3.536
3QA3	H_ARG_52	NH2	I_GLU_178	OE1	3.079
3QA3	H_ARG_52	NH2	I_GLU_179	OE2	2.753
3QA3	H_LYS_61	NZ	I_GLU_179	OE1	3.833
3QA3	H_LYS_61	NZ	I_GLU_179	OE2	3.714
3QA3	H_LYS_219	NZ	F_GLU_129	OE2	3.683
3QA3	I_ARG_208	NH1	H_GLU_101	OE1	2.952
3QA3	I_ARG_208	NH1	H_GLU_101	OE2	3.280
3QA3	I_ARG_208	NH2	H_GLU_101	OE1	2.858
3QA3	I_ARG_208	NH2	H_GLU_101	OE2	3.749
3QA3	I_LYS_306	NZ	C_GLU_61	OE1	3.836
3QA3	J_LYS_109	NZ	K_GLU_44	OE1	3.982
3QA3	K_ARG_52	NH1	L_GLU_179	OE2	3.477
3QA3	K_ARG_52	NH2	L_GLU_178	OE1	3.052
3QA3	K_ARG_52	NH2	L_GLU_179	OE2	2.734
3QA3	K_LYS_61	NZ	L_GLU_179	OE1	3.839
3QA3	K_LYS_61	NZ	L_GLU_179	OE2	3.819
3QA3	K_LYS_219	NZ	J_GLU_129	OE2	3.538

3QA3	L_ARG_208	NH1	K_GLU_101	OE1	3.296
3QA3	L_ARG_208	NH1	K_GLU_101	OE2	3.152
3QA3	L_ARG_208	NH2	K_GLU_101	OE1	3.120
3QA3	L_ARG_208	NH2	K_GLU_101	OE2	3.548
3QG6	A_ARG_188	NH1	H_ASP_86	OD2	3.997
3QG6	A_ARG_188	NH2	H_ASP_86	OD1	3.422
3QG6	A_HIS_189	NE2	H_GLU_85	OE1	3.361
3QG6	A_HIS_189	NE2	H_GLU_85	OE2	3.215
3QG6	B_LYS_44	NZ	L_ASP_151	OD2	2.912
3QG6	B_LYS_64	NZ	L_GLU_187	OE1	3.778
3QG6	B_LYS_221	NZ	A_GLU_123	OE1	2.433
3QG6	H_LYS_44	NZ	A_ASP_151	OD2	2.924
3QG6	H_LYS_64	NZ	A_GLU_187	OE1	3.924
3QG6	H_LYS_221	NZ	L_GLU_123	OE1	2.733
3QG6	L_HIS_189	NE2	B_GLU_85	OE1	3.320
3QG6	L_HIS_189	NE2	B_GLU_85	OE2	3.623
3QG7	H_LYS_221	NZ	L_GLU_123	OE2	2.769
3QO1	B_ARG_101	NH1	A_GLU_39	OE1	3.830
3QO1	B_ARG_101	NH1	A_GLU_39	OE2	2.711
3QO1	B_ARG_101	NH2	A_GLU_39	OE1	2.782
3QO1	B_ARG_101	NH2	A_GLU_39	OE2	3.238
3QO1	B_LYS_215	NZ	A_GLU_128	OE1	3.939
3QUM	P_ARG_36	NH1	A_ASP_94	OD2	3.603
3QUM	P_ARG_36	NH1	B_GLU_58	OE1	3.234
3QUM	P_ARG_36	NH1	B_GLU_58	OE2	3.373
3QUM	P_ARG_36	NH2	B_GLU_58	OE1	3.423
3QUM	P_LYS_62	NZ	B_GLU_58	OE2	3.762
3QUM	P_LYS_119	NZ	H_ASP_54	OD1	2.788
3QUM	P_LYS_119	NZ	H_ASP_54	OD2	3.700
3QUM	P_LYS_119	NZ	H_ASP_56	OD2	3.000
3QUM	L_ARG_50	NH2	P_GLU_23	OE1	2.715
3QUM	H_ARG_98	NH2	P_ASP_159	OD1	3.868
3QUM	H_ARG_98	NH2	P_ASP_159	OD2	3.474
3QUM	H_HIS_164	NE2	L_ASP_167	OD1	3.746
3QUM	H_LYS_208	NZ	L_GLU_123	OE1	3.317
3QUM	A_LYS_207	NZ	M_ASP_70	OD2	3.646
3QUM	B_LYS_62	NZ	A_ASP_1	OD1	3.967
3QUM	B_LYS_62	NZ	A_ASP_1	OD2	3.654
3QUM	B_LYS_209	NZ	A_GLU_123	OE1	3.994
3QUM	B_LYS_209	NZ	A_GLU_123	OE2	2.553
3QUM	Q_LYS_119	NZ	K_ASP_54	OD1	3.579
3QUM	Q_LYS_119	NZ	K_ASP_54	OD2	2.557
3QUM	Q_LYS_119	NZ	K_ASP_56	OD2	3.138
3QUM	M_ARG_24	NH2	B_ASP_131	OD1	2.867
3QUM	M_ARG_24	NH2	B_ASP_131	OD2	3.402
3QUM	M_ARG_50	NH1	Q_GLU_21	OE2	3.456
3QUM	M_ARG_50	NH2	Q_GLU_21	OE2	3.792
3QUM	K_LYS_58	NZ	Q_ASP_116	OD2	3.811
3QUM	K_LYS_62	NZ	M_ASP_1	OD1	2.803
3QUM	K_ARG_98	NH2	Q_ASP_159	OD2	3.098
3QUM	K_LYS_208	NZ	M_GLU_123	OE1	3.358
3QUM	D_ARG_97	NH1	C_GLU_55	OE1	3.578
3QUM	D_ARG_97	NH1	C_GLU_55	OE2	3.784
3QUM	D_ARG_97	NH2	Q_GLU_110	OE2	3.547
3R08	L_LYS_207	NZ	H_ASP_129	OD1	3.653
3R08	L_LYS_207	NZ	H_ASP_129	OD2	2.868
3R08	H_LYS_58	NZ	E_GLU_4	OE2	3.175
3R08	H_LYS_99	NZ	L_ASP_56	OD2	3.746

3SE8	G_LYS_282	NZ	H_ASP_100C	OD2	3.668
3SE8	H_ARG_71	NH1	G_ASP_368	OD1	3.115
3SE8	H_ARG_71	NH1	G_ASP_368	OD2	3.763
3SE8	H_ARG_71	NH2	G_ASP_368	OD1	3.733
3SE8	H_ARG_71	NH2	G_ASP_368	OD2	2.907
3SE8	H_LYS_209	NZ	L_GLU_123	OE1	3.768
3SE9	H_ARG_64	NH1	G_ASP_457	OD2	3.853
3SE9	H_ARG_64	NH2	G_ASP_457	OD1	3.358
3SE9	H_ARG_64	NH2	G_ASP_457	OD2	3.280
3SE9	H_ARG_71	NH1	G_ASP_368	OD1	3.515
3SE9	H_ARG_71	NH1	G_ASP_368	OD2	2.768
3SE9	H_ARG_71	NH2	G_ASP_368	OD1	3.012
3SE9	H_ARG_71	NH2	G_ASP_368	OD2	3.769
3SE9	H_LYS_209	NZ	L_GLU_123	OE1	3.388
3SE9	H_LYS_214	NZ	L_ASP_122	OD1	3.332
3SGD	L_LYS_204	NZ	J_ASP_75	OD1	3.665
3SGD	L_LYS_204	NZ	J_ASP_75	OD2	3.246
3SGD	H_LYS_43	NZ	J_ASP_68	OD1	3.910
3SGD	H_LYS_210	NZ	L_GLU_128	OE1	3.898
3SGD	J_LYS_19	NZ	L_ASP_148	OD1	3.248
3SGD	J_LYS_19	NZ	L_ASP_148	OD2	2.952
3SKJ	L_ARG_96	NH1	H_GLU_100I	OE1	2.505
3SKJ	L_ARG_96	NH1	H_GLU_100I	OE2	2.799
3SKJ	H_HIS_31	NE2	E_GLU_133	OE2	3.297
3SKJ	H_HIS_161	NE2	L_ASP_167	OD2	3.763
3SKJ	H_LYS_206	NZ	L_GLU_123	OE1	2.501
3SKJ	H_LYS_206	NZ	L_GLU_123	OE2	3.323
3SKJ	M_ARG_96	NH2	L_GLU_100I	OE1	3.081
3SKJ	M_ARG_96	NH2	L_GLU_100I	OE2	3.831
3SKJ	L_LYS_43	NZ	L_ASP_1	OD1	3.862
3SKJ	L_LYS_211	NZ	M_ASP_122	OD2	3.816
3SKJ	L_LYS_211	NZ	M_GLU_123	OE1	3.612
3SY0	A_ARG_95	NH2	B_ASP_95	OD1	3.609
3SY0	A_ARG_95	NH2	B_ASP_95	OD2	2.821
3SY0	B_ARG_100B	NH1	A_GLU_55	OE1	2.843
3SY0	B_ARG_100B	NH1	A_GLU_55	OE2	3.786
3SY0	B_LYS_206	NZ	A_GLU_122	OE1	3.980
3T4Y	A_ARG_95	NH2	B_ASP_95	OD1	3.796
3T4Y	A_ARG_95	NH2	B_ASP_95	OD2	2.951
3T4Y	B_ARG_100B	NH1	A_GLU_55	OE1	3.824
3T4Y	B_ARG_100B	NH1	A_GLU_55	OE2	2.840
3T4Y	B_LYS_206	NZ	A_GLU_122	OE2	2.652
3T65	B_ARG_100B	NH1	A_GLU_55	OE1	3.841
3T65	B_ARG_100B	NH1	A_GLU_55	OE2	2.883
3T65	A_ARG_95	NH2	B_ASP_95	OD1	3.666
3T65	A_ARG_95	NH2	B_ASP_95	OD2	2.866
3T77	A_ARG_95	NH2	B_ASP_95	OD1	3.723
3T77	A_ARG_95	NH2	B_ASP_95	OD2	2.997
3T77	B_ARG_100B	NH1	A_GLU_55	OE1	3.125
3T77	B_ARG_100B	NH1	A_GLU_55	OE2	2.687
3T77	B_LYS_206	NZ	A_GLU_122	OE2	3.917
3THM	F_LYS_45	NZ	L_GLU_97	OE2	3.172
3THM	F_LYS_78	NZ	L_ASP_52	OD1	3.702
3U1S	L_HIS_27D	NE2	H_ASP_100B	OD2	2.859
3U1S	H_LYS_214	NZ	L_GLU_123	OE1	3.475
3U2S	L_ARG_54	NH2	C_ASP_167	OD1	3.525
3U2S	L_ARG_54	NH2	C_ASP_167	OD2	3.282
3U2S	L_ARG_95A	NH1	H_ASP_61	OD1	2.794

3U2S	L_ARG_95A	NH1	H_ASP_61	OD2	3.373
3U2S	L_ARG_95A	NH2	H_ASP_61	OD1	2.338
3U2S	L_ARG_96	NH2	H_GLU_95	OE1	3.743
3U2S	L_ARG_96	NH2	H_GLU_95	OE2	2.869
3U2S	L_LYS_129	NZ	H_ASP_144	OD1	3.881
3U2S	G_ARG_168	NH2	H_ASP_100L	OD1	3.358
3U2S	G_ARG_168	NH2	H_ASP_100L	OD2	3.104
3U2S	G_LYS_171	NZ	H_ASP_100I	OD1	3.178
3U2S	A_LYS_143	NZ	B_GLU_124	OE2	3.550
3U2S	B_ARG_95A	NH1	A_ASP_61	OD1	2.632
3U2S	B_ARG_95A	NH1	A_ASP_61	OD2	3.483
3U2S	B_ARG_95A	NH2	A_ASP_61	OD1	3.270
3U2S	B_ARG_96	NH2	A_GLU_95	OE1	3.738
3U2S	B_ARG_96	NH2	A_GLU_95	OE2	2.983
3U2S	C_ARG_168	NH2	A_ASP_100L	OD1	2.424
3U2S	C_ARG_168	NH2	A_ASP_100L	OD2	3.228
3U2S	C_LYS_171	NZ	A_ASP_100I	OD1	3.279
3U36	L_LYS_89	NZ	H_GLU_95	OE1	3.857
3U36	L_ARG_95A	NH1	H_ASP_61	OD1	3.290
3U36	L_ARG_95A	NH1	H_ASP_61	OD2	1.959
3U36	L_ARG_95A	NH2	H_ASP_61	OD1	3.530
3U36	L_ARG_95A	NH2	H_ASP_61	OD2	3.624
3U36	L_ARG_96	NH2	H_GLU_95	OE2	3.606
3U36	B_LYS_89	NZ	A_GLU_95	OE1	3.772
3U36	B_ARG_95A	NH1	A_ASP_61	OD1	3.519
3U36	B_ARG_95A	NH1	A_ASP_61	OD2	2.198
3U36	B_ARG_95A	NH2	A_ASP_61	OD1	3.831
3U36	B_ARG_95A	NH2	A_ASP_61	OD2	3.817
3U36	B_ARG_96	NH2	A_GLU_95	OE2	3.395
3U36	B_LYS_129	NZ	A_ASP_144	OD1	3.769
3U36	D_LYS_89	NZ	C_GLU_95	OE1	3.877
3U36	D_ARG_95A	NH1	C_ASP_61	OD1	3.266
3U36	D_ARG_95A	NH1	C_ASP_61	OD2	2.045
3U36	D_ARG_95A	NH2	C_ASP_61	OD1	3.629
3U36	D_ARG_95A	NH2	C_ASP_61	OD2	3.782
3U36	D_ARG_96	NH2	C_GLU_95	OE2	3.569
3U36	F_ARG_95A	NH1	E_ASP_61	OD1	3.076
3U36	F_ARG_95A	NH1	E_ASP_61	OD2	1.876
3U36	F_ARG_95A	NH2	E_ASP_61	OD1	3.424
3U36	F_ARG_95A	NH2	E_ASP_61	OD2	3.670
3U36	F_ARG_96	NH2	E_GLU_95	OE2	3.739
3UBX	A_ARG_39	NH2	B_ASP_53	OD2	3.336
3UBX	A_HIS_282	NE2	B_ASP_98	OD1	3.815
3UBX	A_HIS_282	NE2	B_ASP_98	OD2	3.128
3UBX	B_ARG_12	NH2	A_ASP_242	OD1	3.715
3UBX	B_ARG_12	NH2	A_ASP_242	OD2	3.324
3UBX	D_ARG_	NH2	E_ASP_	OD2	3.464
3UBX	D_HIS_	NE2	E_ASP_	OD1	3.963
3UBX	D_HIS_	NE2	E_ASP_	OD2	3.193
3UBX	E_ARG_	NH2	D_ASP_	OD1	3.594
3UBX	E_ARG_	NH2	D_ASP_	OD2	3.257
3UBX	E_HIS_	ND1	D_GLU_97	OE1	3.846
3UBX	L_ARG_32	NH2	A_ASP_80	OD1	3.479
3UBX	L_ARG_32	NH2	A_ASP_80	OD2	3.348
3UBX	L_ARG_32	NH2	A_ASP_153	OD2	3.795
3UBX	L_LYS_169	NZ	I_GLU_81	OE1	3.852
3UBX	L_LYS_169	NZ	I_GLU_81	OE2	3.096
3UBX	H_ARG_103	NH2	A_ASP_80	OD1	2.578

3UBX	H.LYS_215	NZ	L_GLU_123	OE1	3.082
3UBX	H.LYS_215	NZ	L_GLU_123	OE2	3.481
3UBX	L_ARG_32	NH2	D_ASP_80	OD1	3.383
3UBX	L_ARG_32	NH2	D_ASP_80	OD2	3.294
3UBX	L_ARG_32	NH2	D_ASP_153	OD2	3.950
3UBX	L.LYS_169	NZ	L_GLU_81	OE1	3.837
3UBX	L.LYS_169	NZ	L_GLU_81	OE2	3.130
3UBX	G_ARG_103	NH2	D_ASP_80	OD1	2.614
3UBX	G.LYS_215	NZ	L_GLU_123	OE1	3.204
3UBX	G.LYS_215	NZ	L_GLU_123	OE2	3.514
3UJI	H.LYS_143	NZ	L_GLU_124	OE2	2.632
3UJI	H.LYS_209	NZ	L_GLU_123	OE1	3.097
3UJI	H.LYS_209	NZ	L_GLU_123	OE2	2.701
3UJI	P.LYS_305	NZ	H_ASP_54	OD1	2.722
3UJI	P.LYS_305	NZ	H_ASP_54	OD2	3.687
3UJI	P.LYS_305	NZ	H_ASP_56	OD2	2.744
3UJI	P.HIS_308	ND1	H_GLU_98	OE1	2.731
3UJI	P.HIS_308	ND1	H_GLU_98	OE2	3.371
3UJJ	H.LYS_209	NZ	L_GLU_123	OE1	2.859
3UJJ	H.LYS_209	NZ	L_GLU_123	OE2	2.771
3UJJ	P.LYS_305	NZ	H_ASP_54	OD1	3.600
3UJJ	P.LYS_305	NZ	H_ASP_54	OD2	2.628
3UJJ	P.LYS_305	NZ	H_ASP_56	OD2	2.857
3UJJ	P_ARG_308	NH2	L_GLU_50	OE2	2.898
3UJT	H.LYS_143	NZ	M_ASP_60	OD2	3.914
3UJT	H.LYS_208	NZ	L_GLU_123	OE2	2.966
3UJT	L.HIS_164	NE2	M_ASP_167	OD1	3.917
3UJT	L.LYS_208	NZ	M_GLU_123	OE2	3.024
3UO1	H.LYS_212	NZ	L_GLU_127	OE2	2.634
3UYR	H.LYS_212	NZ	L_GLU_127	OE2	2.869
3V4P	B_ARG_194	NH1	H_ASP_102	OD1	2.860
3V4P	B_ARG_194	NH1	H_ASP_102	OD2	2.764
3V4P	B_ARG_200	NH2	H_ASP_102	OD1	3.172
3V4P	D_ARG_194	NH1	M_ASP_102	OD1	2.738
3V4P	D_ARG_194	NH1	M_ASP_102	OD2	2.760
3V4P	D_ARG_200	NH2	M_ASP_102	OD1	3.233
3V4P	H.HIS_172	ND1	L_ASP_172	OD2	3.780
3V4P	H.LYS_216	NZ	L_GLU_128	OE2	3.270
3V4P	M.HIS_172	ND1	N_ASP_172	OD2	3.600
3V4P	M.LYS_216	NZ	N_GLU_128	OE2	3.408
3V4U	H.LYS_212	NZ	L_GLU_127	OE2	2.667
3V4V	B_ARG_194	NH1	H_ASP_102	OD1	2.874
3V4V	B_ARG_194	NH1	H_ASP_102	OD2	3.211
3V4V	B_ARG_200	NH2	H_ASP_102	OD1	3.237
3V4V	H.HIS_172	ND1	L_ASP_172	OD1	3.644
3V4V	H.LYS_216	NZ	L_GLU_128	OE2	3.607
3V4V	D_ARG_194	NH1	M_ASP_102	OD1	2.657
3V4V	D_ARG_194	NH1	M_ASP_102	OD2	2.923
3V4V	D_ARG_200	NH2	M_ASP_102	OD1	3.070
3V4V	M.HIS_172	ND1	N_ASP_172	OD1	3.594
3V4V	M.LYS_216	NZ	N_GLU_128	OE2	3.217
3V52	H.LYS_212	NZ	L_GLU_127	OE2	2.929
3V6F	A.LYS_213	NZ	B_GLU_130	OE1	3.799
3V6F	C.LYS_213	NZ	D_GLU_130	OE1	3.956
3V6F	E.LYS_213	NZ	F_GLU_130	OE1	3.763
3V6F	H.HIS_169	NE2	L_ASP_174	OD1	3.656
3WIH	H.LYS_214	NZ	L_GLU_123	OE2	3.755
3WIH	L.LYS_214	NZ	M_GLU_123	OE1	2.678

3WIH	I.LYS_214	NZ	M.GLU_123	OE2	3.619
3WN5	A.LYS_370	NZ	B.GLU_357	OE2	3.815
3WN5	A.LYS_409	NZ	B.ASP_399	OD2	3.327
3WN5	B.LYS_370	NZ	A.GLU_357	OE1	3.801
3WN5	B.LYS_409	NZ	A.ASP_399	OD1	3.830
3WN5	B.LYS_409	NZ	A.ASP_399	OD2	3.511
3WN5	C.LYS_117	NZ	B.ASP_265	OD2	2.853
3WN5	C.HIS_131	NE2	B.ASP_270	OD1	3.342
3WN5	C.HIS_131	NE2	B.ASP_270	OD2	2.619
3WN5	D.LYS_370	NZ	E.GLU_357	OE2	3.279
3WN5	D.LYS_409	NZ	E.ASP_399	OD2	3.246
3WN5	E.LYS_370	NZ	D.GLU_357	OE1	3.843
3WN5	E.LYS_409	NZ	D.ASP_399	OD2	2.789
3WN5	F.LYS_117	NZ	E.ASP_265	OD2	3.157
3WN5	F.HIS_131	NE2	E.ASP_270	OD2	2.923
4A6Y	A.ARG_186	NH2	H.ASP_180	OD2	3.656
4A6Y	A.ARG_190	NH1	H.GLU_89	OE2	3.969
4A6Y	B.LYS_150	NZ	A.GLU_127	OE2	3.258
4A6Y	H.LYS_150	NZ	L.GLU_127	OE2	3.131
4A6Y	H.HIS_171	NE2	L.ASP_141	OD1	3.968
4A6Y	L.ARG_190	NH2	B.GLU_89	OE2	3.440
4AG4	H.LYS_208	NZ	L.GLU_123	OE2	2.708
4C83	C.LYS_208	NZ	D.GLU_123	OE1	2.304
4C83	C.LYS_208	NZ	D.GLU_123	OE2	2.598
4DAG	H.ARG_101	NH2	A.GLU_33	OE1	3.620
4DAG	H.ARG_101	NH2	A.GLU_33	OE2	2.107
4DAG	L.LYS_46	NZ	A.ASP_414	OD1	3.558
4DAG	L.LYS_46	NZ	A.ASP_414	OD2	3.550
4DGV	H.LYS_209	NZ	L.GLU_123	OE1	2.915
4DGV	H.LYS_209	NZ	L.GLU_123	OE2	3.422
4DGY	H.LYS_214	NZ	L.ASP_122	OD1	3.699
4DGY	H.LYS_214	NZ	L.ASP_122	OD2	2.517
4EBQ	H.LYS_215	NZ	L.GLU_123	OE2	2.960
4EDW	H.LYS_209	NZ	L.GLU_123	OE2	2.707
4EDX	W.LYS_32	NZ	H.ASP_58	OD1	2.886
4EDX	W.LYS_32	NZ	H.ASP_58	OD2	2.677
4EDX	A.ARG_53	NH1	W.GLU_11	OE1	2.795
4EDX	B.LYS_221	NZ	A.GLU_123	OE2	3.878
4EDX	V.LYS_32	NZ	B.ASP_58	OD1	3.117
4EDX	V.LYS_32	NZ	B.ASP_58	OD2	2.681
4EDX	V.LYS_88	NZ	B.ASP_54	OD2	3.805
4EDX	L.ARG_53	NH1	V.GLU_11	OE1	3.269
4EDX	H.LYS_221	NZ	L.GLU_123	OE2	3.893
4ETQ	H.ARG_60	NH1	C.ASP_179	OD1	3.609
4ETQ	H.ARG_60	NH2	C.ASP_179	OD1	3.375
4ETQ	H.ARG_103	NH1	C.GLU_217	OE1	3.862
4ETQ	H.ARG_103	NH1	C.GLU_217	OE2	2.754
4ETQ	H.ARG_103	NH2	C.GLU_217	OE2	2.933
4ETQ	H.LYS_215	NZ	L.GLU_123	OE2	3.075
4ETQ	A.ARG_103	NH1	X.GLU_217	OE1	2.753
4ETQ	A.ARG_103	NH1	X.GLU_217	OE2	3.565
4ETQ	A.ARG_103	NH2	X.GLU_217	OE1	2.983
4ETQ	A.ARG_103	NH2	X.GLU_217	OE2	3.995
4ETQ	A.LYS_215	NZ	B.GLU_123	OE2	3.774
4ETQ	X.ARG_44	NH1	A.GLU_56	OE1	3.611
4ETQ	X.ARG_44	NH1	A.GLU_56	OE2	3.023
4ETQ	X.LYS_108	NZ	A.GLU_58	OE2	3.014
4ETQ	X.ARG_220	NH1	A.ASP_105	OD1	3.937

4ETQ	X_ARG.220	NH2	A_ASP.105	OD1	2.929
4ETQ	C_ARG.44	NH1	H_GLU.56	OE1	2.601
4ETQ	C_ARG.220	NH1	H_ASP.105	OD1	3.872
4ETQ	C_ARG.220	NH2	H_ASP.105	OD1	3.103
4F33	B_LYS.215	NZ	A_GLU.123	OE1	2.676
4F33	B_LYS.215	NZ	A_GLU.123	OE2	3.528
4F33	D_LYS.215	NZ	C_GLU.123	OE1	2.787
4F33	D_LYS.215	NZ	C_GLU.123	OE2	3.695
4F33	F_LYS.212	NZ	D_ASP.214	OD2	3.519
4F33	F_LYS.215	NZ	E_GLU.123	OE1	2.609
4F33	F_LYS.215	NZ	E_GLU.123	OE2	3.626
4F33	H_LYS.215	NZ	G_GLU.123	OE1	2.968
4F33	H_LYS.215	NZ	G_GLU.123	OE2	3.966
4F3F	A_HIS.94	NE2	C_GLU.18	OE1	3.664
4F3F	A_HIS.94	NE2	C_GLU.18	OE2	3.880
4F3F	C_LYS.24	NZ	A_ASP.50	OD1	2.832
4F3F	C_LYS.24	NZ	A_ASP.50	OD2	3.865
4FFV	A_ARG.659	NH2	B_GLU.242	OE2	2.683
4FFV	A_HIS.755	ND1	B_ASP.730	OD1	2.996
4FFV	B_ARG.659	NH2	A_GLU.242	OE2	2.592
4FFV	B_HIS.755	ND1	A_ASP.730	OD1	2.989
4FFV	B_HIS.755	ND1	A_ASP.730	OD2	3.942
4FFV	D_LYS.54	NZ	B_GLU.89	OE1	3.460
4FFV	D_LYS.54	NZ	B_GLU.89	OE2	3.556
4FFV	H_LYS.54	NZ	A_GLU.89	OE1	3.584
4FFV	H_LYS.54	NZ	A_GLU.89	OE2	3.871
4FFV	H_HIS.168	NE2	L_ASP.166	OD1	3.178
4FFV	H_HIS.168	NE2	L_ASP.166	OD2	3.870
4FFW	A_ARG.659	NH2	B_GLU.242	OE2	3.187
4FFW	A_HIS.755	ND1	B_ASP.730	OD1	3.111
4FFW	B_ARG.659	NH2	A_GLU.242	OE2	3.068
4FFW	D_LYS.54	NZ	B_GLU.89	OE1	3.085
4FFW	D_LYS.54	NZ	B_GLU.89	OE2	3.381
4FFW	H_LYS.54	NZ	A_GLU.89	OE1	3.517
4FFW	H_LYS.54	NZ	A_GLU.89	OE2	3.666
4FFW	H_HIS.168	NE2	L_ASP.166	OD1	3.737
4FQH	H_LYS.143	NZ	L_GLU.124	OE2	2.906
4FQH	H_LYS.214	NZ	L_GLU.123	OE1	3.752
4FQH	H_LYS.214	NZ	L_GLU.123	OE2	2.217
4FQH	A_LYS.143	NZ	B_GLU.124	OE2	3.049
4FQH	A_LYS.214	NZ	B_GLU.123	OE1	3.132
4FQI	A_LYS.109	NZ	B_GLU.69	OE1	2.615
4FQI	A_LYS.109	NZ	B_GLU.69	OE2	3.205
4FQI	A_LYS.307	NZ	B_GLU.64	OE2	3.371
4FQI	A_LYS.310	NZ	B_ASP.90	OD1	2.687
4FQI	A_LYS.310	NZ	B_ASP.90	OD2	3.739
4FQI	H_LYS.143	NZ	L_GLU.124	OE2	2.947
4G6A	C_ARG.64	NH1	D_ASP.94	OD1	3.792
4G6A	C_ARG.64	NH1	D_ASP.94	OD2	3.701
4G6A	C_LYS.209	NZ	D_GLU.123	OE1	2.784
4G6A	C_LYS.209	NZ	D_GLU.123	OE2	3.529
4G6A	D_ARG.18	NH2	L_GLU.27	OE2	3.721
4G6A	H_ARG.64	NH2	L_ASP.94	OD1	3.443
4G6A	H_ARG.64	NH2	L_ASP.94	OD2	3.275
4G6A	H_LYS.209	NZ	L_GLU.123	OE1	2.940
4G6A	H_LYS.209	NZ	L_GLU.123	OE2	3.622
4G6F	H_LYS.143	NZ	L_GLU.125	OE2	3.341
4G6F	H_LYS.209	NZ	L_GLU.124	OE1	3.080

4G6F	H.LYS_209	NZ	L_GLU_124	OE2	2.558
4G6F	B.LYS_143	NZ	D_GLU_125	OE2	2.735
4G6F	B.LYS_209	NZ	D_GLU_124	OE1	3.470
4G6F	B.LYS_209	NZ	D_GLU_124	OE2	2.107
4G6F	L.HIS_31	ND1	H_GLU_100I	OE2	2.912
4G6F	L.ARG_91	NH1	H_GLU_100J	OE2	2.715
4G6F	L.ARG_91	NH2	H_GLU_100J	OE2	2.951
4G6F	D.HIS_31	ND1	B_GLU_100I	OE2	2.954
4G6F	D.ARG_91	NH1	B_GLU_100J	OE2	2.854
4G6F	D.ARG_91	NH2	B_GLU_100J	OE2	2.880
4G6F	D.ARG_95B	NH2	B.ASP_58	OD1	3.343
4GMT	H.HIS_164	NE2	L.ASP_167	OD2	3.650
4GXU	A.LYS_	NZ	F_GLU_	OE1	3.529
4GXU	A.LYS_	NZ	F_GLU_	OE2	3.469
4GXU	A.ARG_109	NH2	B_GLU_69	OE1	3.987
4GXU	A.ARG_109	NH2	B_GLU_69	OE2	3.286
4GXU	A.ARG_	NH1	B.ASP_	OD1	2.648
4GXU	A.ARG_	NH2	B.ASP_	OD1	2.545
4GXU	B.LYS_58	NZ	D_GLU_97	OE1	3.748
4GXU	B.LYS_68	NZ	A_GLU_110	OE2	3.492
4GXU	B.ARG_76	NH1	F_GLU_74	OE1	3.015
4GXU	B.ARG_76	NH1	F_GLU_74	OE2	2.935
4GXU	B.ARG_76	NH2	E_GLU_107	OE2	3.559
4GXU	B.ARG_76	NH2	F_GLU_74	OE2	2.547
4GXU	B.LYS_83	NZ	F.ASP_85	OD1	3.431
4GXU	B.LYS_83	NZ	F.ASP_85	OD2	3.614
4GXU	B.ARG_	NH2	D.ASP_	OD2	3.432
4GXU	B.ARG_	NH1	F_GLU_	OE1	3.168
4GXU	B.ARG_	NH2	F_GLU_	OE1	3.085
4GXU	B.ARG_	NH2	F_GLU_	OE2	3.110
4GXU	C.LYS_32	NZ	B_GLU_57	OE1	3.823
4GXU	C.LYS_32	NZ	B_GLU_57	OE2	3.681
4GXU	C.ARG_109	NH2	D_GLU_69	OE1	3.507
4GXU	C.ARG_109	NH2	D_GLU_69	OE2	3.205
4GXU	C.ARG_310	NH1	D.ASP_90	OD1	3.385
4GXU	C.ARG_310	NH2	D.ASP_90	OD1	3.336
4GXU	D.LYS_68	NZ	C_GLU_110	OE2	3.981
4GXU	D.ARG_76	NH1	B_GLU_74	OE1	2.948
4GXU	D.ARG_76	NH1	B_GLU_74	OE2	3.453
4GXU	D.ARG_76	NH2	A_GLU_107	OE2	3.465
4GXU	D.ARG_76	NH2	B_GLU_74	OE1	3.835
4GXU	D.ARG_76	NH2	B_GLU_74	OE2	2.916
4GXU	D.LYS_83	NZ	B.ASP_85	OD1	3.057
4GXU	D.LYS_83	NZ	B.ASP_85	OD2	3.527
4GXU	D.ARG_	NH2	F.ASP_	OD2	3.392
4GXU	D.ARG_	NH1	B_GLU_	OE1	2.743
4GXU	D.ARG_	NH1	B_GLU_	OE2	3.931
4GXU	D.ARG_	NH2	B_GLU_	OE1	2.897
4GXU	D.ARG_	NH2	B_GLU_	OE2	2.579
4GXU	E.LYS_	NZ	D_GLU_	OE1	3.848
4GXU	E.LYS_	NZ	D_GLU_	OE2	3.549
4GXU	E.ARG_109	NH2	F_GLU_69	OE1	3.819
4GXU	E.ARG_109	NH2	F_GLU_69	OE2	3.459
4GXU	E.ARG_310	NH1	F.ASP_90	OD1	2.704
4GXU	E.ARG_310	NH2	F.ASP_90	OD1	2.770
4GXU	F.LYS_	NZ	B_GLU_	OE1	3.893
4GXU	F.LYS_68	NZ	E_GLU_110	OE2	3.968
4GXU	F.ARG_76	NH1	D_GLU_74	OE1	2.787

4GXU	F_ARG_76	NH1	D_GLU_74	OE2	3.366
4GXU	F_ARG_76	NH2	C_GLU_107	OE2	3.548
4GXU	F_ARG_76	NH2	D_GLU_74	OE1	3.616
4GXU	F_ARG_76	NH2	D_GLU_74	OE2	2.732
4GXU	F_LYS_83	NZ	D_ASP_85	OD1	3.339
4GXU	F_LYS_83	NZ	D_ASP_85	OD2	3.717
4GXU	F_ARG_	NH2	B_ASP_	OD2	3.670
4GXU	F_ARG_	NH1	D_GLU_	OE1	3.077
4GXU	F_ARG_	NH2	D_GLU_	OE1	2.952
4GXU	F_ARG_	NH2	D_GLU_	OE2	3.074
4GXU	G_LYS_	NZ	J_GLU_	OE1	3.601
4GXU	G_LYS_	NZ	J_GLU_	OE2	3.403
4GXU	G_ARG_	NH2	H_GLU_	OE2	3.183
4GXU	G_ARG_	NH1	H_ASP_	OD1	2.337
4GXU	G_ARG_	NH2	H_ASP_	OD1	2.900
4GXU	H_LYS_	NZ	L_GLU_	OE1	3.639
4GXU	H_LYS_	NZ	G_GLU_	OE2	3.438
4GXU	H_ARG_	NH1	J_GLU_	OE1	2.612
4GXU	H_ARG_	NH1	J_GLU_	OE2	3.374
4GXU	H_ARG_	NH2	I_GLU_	OE2	3.506
4GXU	H_ARG_	NH2	J_GLU_	OE1	3.326
4GXU	H_ARG_	NH2	J_GLU_	OE2	2.517
4GXU	H_LYS_	NZ	J_ASP_	OD1	2.938
4GXU	H_LYS_	NZ	J_ASP_	OD2	3.368
4GXU	H_ARG_	NH2	L_ASP_	OD2	3.212
4GXU	H_ARG_	NH1	J_GLU_	OE1	3.044
4GXU	H_ARG_	NH2	J_GLU_	OE1	2.714
4GXU	H_ARG_	NH2	J_GLU_	OE2	3.067
4GXU	L_LYS_	NZ	L_GLU_	OE1	3.747
4GXU	L_LYS_	NZ	L_GLU_	OE2	3.353
4GXU	L_ARG_	NH2	J_GLU_	OE1	3.762
4GXU	L_ARG_	NH2	J_GLU_	OE2	2.924
4GXU	L_ARG_	NH1	J_ASP_	OD1	2.388
4GXU	L_ARG_	NH2	J_ASP_	OD1	2.649
4GXU	J_LYS_	NZ	H_GLU_	OE1	3.949
4GXU	J_LYS_	NZ	I_GLU_	OE2	3.674
4GXU	J_ARG_	NH1	L_GLU_	OE1	2.912
4GXU	J_ARG_	NH1	L_GLU_	OE2	3.322
4GXU	J_ARG_	NH2	K_GLU_	OE2	3.542
4GXU	J_ARG_	NH2	L_GLU_	OE1	3.621
4GXU	J_ARG_	NH2	L_GLU_	OE2	2.520
4GXU	J_LYS_	NZ	L_ASP_	OD1	3.139
4GXU	J_LYS_	NZ	L_ASP_	OD2	3.566
4GXU	J_ARG_	NH2	H_ASP_	OD2	3.270
4GXU	J_ARG_	NH1	L_GLU_	OE1	3.377
4GXU	J_ARG_	NH2	L_GLU_	OE1	2.504
4GXU	J_ARG_	NH2	L_GLU_	OE2	3.208
4GXU	K_LYS_	NZ	H_GLU_	OE2	3.068
4GXU	K_ARG_	NH2	L_GLU_	OE1	3.835
4GXU	K_ARG_	NH2	L_GLU_	OE2	3.159
4GXU	K_ARG_	NH1	L_ASP_	OD1	2.447
4GXU	K_ARG_	NH2	L_ASP_	OD1	2.754
4GXU	L_LYS_	NZ	J_GLU_	OE1	3.674
4GXU	L_LYS_	NZ	K_GLU_	OE2	3.305
4GXU	L_ARG_	NH1	H_GLU_	OE1	2.958
4GXU	L_ARG_	NH1	H_GLU_	OE2	3.138
4GXU	L_ARG_	NH2	G_GLU_	OE2	3.886
4GXU	L_ARG_	NH2	H_GLU_	OE1	3.887

4GXU	L_ARG_	NH2	H_GLU_	OE2	2.595
4GXU	L_LYS_	NZ	H_ASP_	OD1	2.732
4GXU	L_LYS_	NZ	H_ASP_	OD2	3.190
4GXU	L_ARG_	NH2	J_ASP_	OD2	3.583
4GXU	L_ARG_	NH1	H_GLU_	OE1	3.044
4GXU	L_ARG_	NH2	H_GLU_	OE1	2.477
4GXU	L_ARG_	NH2	H_GLU_	OE2	3.036
4GXU	M_ARG_	NH2	H_GLU_	OE2	3.356
4GXU	M_LYS_	NZ	N_GLU_	OE2	2.851
4GXU	M_LYS_	NZ	N_GLU_	OE1	3.371
4GXU	Q_LYS_143	NZ	R_GLU_124	OE2	3.025
4GXU	Q_LYS_209	NZ	R_GLU_123	OE1	3.619
4GXU	Q_LYS_209	NZ	R_GLU_123	OE2	3.564
4GXV	H_LYS_143	NZ	L_GLU_124	OE2	2.866
4GXV	H_LYS_209	NZ	L_GLU_123	OE1	3.472
4GXV	H_LYS_209	NZ	L_GLU_123	OE2	2.731
4GXV	I_LYS_143	NZ	M_GLU_124	OE2	2.455
4GXV	I_LYS_209	NZ	M_GLU_123	OE1	2.930
4GXV	I_LYS_209	NZ	M_GLU_123	OE2	3.487
4GXX	A_LYS_32	NZ	D_GLU_57	OE1	3.386
4GXX	A_ARG_109	NH2	B_GLU_69	OE2	3.594
4GXX	A_ARG_310	NH1	B_ASP_90	OD1	2.488
4GXX	A_ARG_310	NH2	B_ASP_90	OD1	2.951
4GXX	B_LYS_58	NZ	F_GLU_97	OE1	3.721
4GXX	B_LYS_68	NZ	A_GLU_110	OE2	2.734
4GXX	B_ARG_76	NH1	D_GLU_74	OE1	2.782
4GXX	B_ARG_76	NH1	D_GLU_74	OE2	3.511
4GXX	B_ARG_76	NH2	C_GLU_107	OE2	3.651
4GXX	B_ARG_76	NH2	D_GLU_74	OE1	3.625
4GXX	B_ARG_76	NH2	D_GLU_74	OE2	2.818
4GXX	B_LYS_83	NZ	D_ASP_85	OD1	2.661
4GXX	B_LYS_83	NZ	D_ASP_85	OD2	3.421
4GXX	B_ARG_106	NH2	F_ASP_109	OD2	3.780
4GXX	B_ARG_116	NH2	D_GLU_120	OE1	2.669
4GXX	C_LYS_32	NZ	F_GLU_57	OE2	3.165
4GXX	C_ARG_109	NH2	D_GLU_69	OE1	3.802
4GXX	C_ARG_109	NH2	D_GLU_69	OE2	3.427
4GXX	C_ARG_310	NH1	D_ASP_90	OD1	2.336
4GXX	C_ARG_310	NH2	D_ASP_86	OD1	3.727
4GXX	C_ARG_310	NH2	D_ASP_90	OD1	3.012
4GXX	D_LYS_58	NZ	B_GLU_97	OE1	3.529
4GXX	D_LYS_68	NZ	C_GLU_110	OE2	2.872
4GXX	D_ARG_76	NH1	F_GLU_74	OE1	2.910
4GXX	D_ARG_76	NH1	F_GLU_74	OE2	3.571
4GXX	D_ARG_76	NH2	E_GLU_107	OE2	3.622
4GXX	D_ARG_76	NH2	F_GLU_74	OE1	3.615
4GXX	D_ARG_76	NH2	F_GLU_74	OE2	2.803
4GXX	D_LYS_83	NZ	F_ASP_85	OD1	2.774
4GXX	D_LYS_83	NZ	F_ASP_85	OD2	3.514
4GXX	D_ARG_106	NH2	B_ASP_109	OD2	3.920
4GXX	D_ARG_116	NH1	F_GLU_120	OE1	3.357
4GXX	D_ARG_116	NH2	F_GLU_120	OE1	3.225
4GXX	D_ARG_116	NH2	F_GLU_120	OE2	3.007
4GXX	E_LYS_32	NZ	B_GLU_57	OE2	3.237
4GXX	E_ARG_109	NH2	F_GLU_69	OE1	3.858
4GXX	E_ARG_109	NH2	F_GLU_69	OE2	2.773
4GXX	E_ARG_310	NH1	F_ASP_90	OD1	2.470
4GXX	E_ARG_310	NH2	F_ASP_90	OD1	2.925

4GXX	F_LYS_58	NZ	D_GLU_97	OE1	3.142
4GXX	F_LYS_68	NZ	E_GLU_110	OE2	2.982
4GXX	F_ARG_76	NH1	B_GLU_74	OE1	2.798
4GXX	F_ARG_76	NH1	B_GLU_74	OE2	3.572
4GXX	F_ARG_76	NH2	A_GLU_107	OE2	3.644
4GXX	F_ARG_76	NH2	B_GLU_74	OE1	3.566
4GXX	F_ARG_76	NH2	B_GLU_74	OE2	2.823
4GXX	F_LYS_83	NZ	B_ASP_85	OD1	2.859
4GXX	F_LYS_83	NZ	B_ASP_85	OD2	3.462
4GXX	F_ARG_106	NH2	D_ASP_109	OD2	3.576
4GXX	F_ARG_116	NH1	B_GLU_120	OE1	2.775
4GXX	F_ARG_116	NH1	B_GLU_120	OE2	3.643
4GXX	F_ARG_116	NH2	B_GLU_120	OE1	3.285
4GXX	F_ARG_116	NH2	B_GLU_120	OE2	2.552
4H8W	H_ARG_55	NH1	G_ASP_107	OD1	3.623
4H8W	H_ARG_55	NH1	G_ASP_107	OD2	3.025
4H8W	H_LYS_209	NZ	L_GLU_124	OE1	2.673
4H8W	H_LYS_209	NZ	L_GLU_124	OE2	2.808
4H8W	C_ARG_59	NH1	G_ASP_368	OD1	2.952
4H8W	C_ARG_59	NH1	G_ASP_368	OD2	3.318
4H8W	C_ARG_59	NH2	G_ASP_368	OD1	3.741
4H8W	C_ARG_59	NH2	G_ASP_368	OD2	2.611
4HF5	A_LYS_109	NZ	B_GLU_69	OE1	3.017
4HF5	A_ARG_137	NH1	H_ASP_97	OD2	2.969
4HF5	A_ARG_137	NH2	H_ASP_97	OD1	3.008
4HF5	A_ARG_137	NH2	H_ASP_97	OD2	2.797
4HF5	A_LYS_269	NZ	B_GLU_69	OE1	2.931
4HF5	A_LYS_269	NZ	B_GLU_69	OE2	3.200
4HF5	A_LYS_307	NZ	B_GLU_64	OE2	3.558
4HF5	A_LYS_310	NZ	B_ASP_90	OD1	2.877
4HF5	B_LYS_143	NZ	A_ASP_11	OD2	3.934
4HGK	C_LYS_65	NZ	B_GLU_230	OE1	3.917
4HGK	C_ARG_103	NH1	B_GLU_230	OE1	3.099
4HGK	C_ARG_103	NH2	B_GLU_230	OE1	3.263
4HGK	C_ARG_103	NH2	B_GLU_230	OE2	3.968
4HGK	D_LYS_65	NZ	A_GLU_230	OE1	3.741
4HGK	D_ARG_103	NH1	A_GLU_230	OE1	3.115
4HGK	D_ARG_103	NH2	A_GLU_230	OE1	3.112
4HGK	D_ARG_103	NH2	A_GLU_230	OE2	3.907
4HH9	A_ARG_54	NH1	C_ASP_50	OD2	3.238
4HH9	A_ARG_54	NH2	C_ASP_50	OD2	3.183
4HH9	B_LYS_209	NZ	A_GLU_123	OE1	3.274
4HH9	B_LYS_209	NZ	A_GLU_123	OE2	3.488
4HH9	B_LYS_214	NZ	A_ASP_122	OD1	3.788
4HH9	C_ARG_54	NH1	A_ASP_50	OD2	2.782
4HH9	C_ARG_54	NH2	A_ASP_50	OD2	3.752
4HH9	D_LYS_129	NZ	C_GLU_213	OE1	3.401
4HH9	D_LYS_129	NZ	C_GLU_213	OE2	3.163
4HH9	D_LYS_209	NZ	C_GLU_123	OE2	3.057
4HH9	D_LYS_214	NZ	C_ASP_122	OD2	3.367
4HHA	B_HIS_32	ND1	P_GLU_1	OE1	4.000
4HHA	B_HIS_32	NE2	P_GLU_1	OE1	3.076
4HHA	B_HIS_32	NE2	P_GLU_1	OE2	2.639
4HHA	B_ARG_94	NH1	P_GLU_1	OE2	3.723
4HHA	B_ARG_94	NH2	P_GLU_1	OE2	3.026
4HHA	B_HIS_164	NE2	A_ASP_167	OD1	3.917
4HHA	B_LYS_209	NZ	A_GLU_123	OE2	2.754
4HIE	A_ARG_91	NH2	B_GLU_95	OE1	3.457

4HIE	A_ARG_91	NH2	B_GLU_95	OE2	3.317
4HIH	A_ARG_91	NH2	B_GLU_95	OE1	3.470
4HIH	A_ARG_91	NH2	B_GLU_95	OE2	3.314
4HIH	B_LYS_209	NZ	A_GLU_123	OE1	2.853
4HIH	B_LYS_209	NZ	A_GLU_123	OE2	3.685
4HIH	C_ARG_91	NH2	D_GLU_95	OE1	3.527
4HIH	C_ARG_91	NH2	D_GLU_95	OE2	3.339
4HIH	D_LYS_209	NZ	C_GLU_123	OE1	2.616
4HIH	D_LYS_209	NZ	C_GLU_123	OE2	2.820
4HII	A_ARG_91	NH2	B_GLU_95	OE1	3.439
4HII	A_ARG_91	NH2	B_GLU_95	OE2	3.542
4HII	B_LYS_209	NZ	A_GLU_123	OE1	2.845
4HII	B_LYS_209	NZ	A_GLU_123	OE2	2.723
4HII	C_ARG_91	NH1	D_GLU_95	OE2	3.915
4HII	C_ARG_91	NH2	D_GLU_95	OE1	3.687
4HII	C_ARG_91	NH2	D_GLU_95	OE2	3.380
4HIJ	A_ARG_91	NH1	B_GLU_95	OE2	3.962
4HIJ	A_ARG_91	NH2	B_GLU_95	OE1	3.390
4HIJ	A_ARG_91	NH2	B_GLU_95	OE2	3.274
4HIJ	C_ARG_91	NH2	D_GLU_95	OE1	3.772
4HIJ	C_ARG_91	NH2	D_GLU_95	OE2	3.260
4HIJ	D_LYS_209	NZ	C_GLU_123	OE2	3.644
4HK0	A_LYS_222	NZ	B_GLU_125	OE2	2.735
4HK0	C_ARG_104	NH2	D_ASP_95	OD2	3.573
4HK0	D_LYS_104	NZ	B_ASP_50	OD1	3.601
4HK0	D_LYS_104	NZ	B_ASP_50	OD2	2.755
4HK3	J_LYS_222	NZ	N_GLU_125	OE2	3.801
4HKB	J_LYS_23	NZ	C_ASP_73	OD1	3.505
4HKB	J_ARG_72	NH2	A_GLU_10	OE1	3.065
4HKB	J_ARG_72	NH2	A_GLU_10	OE2	2.664
4HKB	J_LYS_222	NZ	N_GLU_125	OE1	3.188
4HKB	J_LYS_222	NZ	N_GLU_125	OE2	3.564
4HKB	A_ARG_72	NH2	C_GLU_10	OE1	3.154
4HKB	A_ARG_72	NH2	C_GLU_10	OE2	2.755
4HKB	A_LYS_156	NZ	B_GLU_126	OE2	3.919
4HKB	A_LYS_222	NZ	B_GLU_125	OE1	3.019
4HKB	A_LYS_222	NZ	B_GLU_125	OE2	3.903
4HKB	C_LYS_63	NZ	E_ASP_89	OD1	3.939
4HKB	C_LYS_63	NZ	E_ASP_89	OD2	3.374
4HKB	C_ARG_87	NH2	E_ASP_90	OD1	3.045
4HKB	C_ARG_87	NH2	E_ASP_90	OD2	2.962
4HKB	C_LYS_222	NZ	D_GLU_125	OE1	3.332
4HKB	C_LYS_222	NZ	D_GLU_125	OE2	3.836
4HKB	E_LYS_23	NZ	G_ASP_73	OD1	2.630
4HKB	E_LYS_63	NZ	C_ASP_89	OD1	3.625
4HKB	E_LYS_63	NZ	C_ASP_89	OD2	3.095
4HKB	E_ARG_72	NH1	I_GLU_10	OE1	2.874
4HKB	E_ARG_72	NH1	I_GLU_10	OE2	2.849
4HKB	E_ARG_87	NH1	C_ASP_90	OD1	3.489
4HKB	E_ARG_87	NH1	C_ASP_90	OD2	3.954
4HKB	E_ARG_87	NH2	C_ASP_90	OD1	3.930
4HKB	E_ARG_87	NH2	C_ASP_90	OD2	3.219
4HKB	E_LYS_222	NZ	F_GLU_125	OE2	3.327
4HKB	G_ARG_87	NH1	J_ASP_90	OD1	3.108
4HKB	G_ARG_87	NH1	J_ASP_90	OD2	3.912
4HKB	G_ARG_87	NH2	J_ASP_90	OD2	3.607
4HKB	I_ARG_72	NH2	G_GLU_10	OE1	3.560
4HKB	I_ARG_72	NH2	G_GLU_10	OE2	2.553

4HKB	I_LYS_222	NZ	K_GLU_125	OE2	3.211
4HKB	N_ARG_29	NH1	J_ASP_107	OD1	3.664
4HKB	N_ARG_29	NH1	J_ASP_107	OD2	2.469
4HKB	N_LYS_131	NZ	J_ASP_157	OD2	3.951
4HKB	B_ARG_29	NH1	A_ASP_107	OD2	3.659
4HKB	D_ARG_29	NH1	C_ASP_107	OD2	3.254
4HKB	H_ARG_29	NH1	G_ASP_107	OD2	3.325
4HKB	H_ARG_29	NH2	G_ASP_107	OD2	3.189
4HKB	K_ARG_31	NH1	I_ASP_107	OD2	3.242
4HKX	E_ARG_192	NH1	B_ASP_95	OD2	3.293
4HKX	E_LYS_219	NZ	B_ASP_93	OD1	2.877
4HKX	E_LYS_219	NZ	B_ASP_93	OD2	3.792
4HKX	A_LYS_222	NZ	B_GLU_125	OE1	3.981
4HKX	B_ARG_29	NH2	A_ASP_107	OD2	3.853
4HKX	B_LYS_131	NZ	A_ASP_157	OD2	3.310
4HLZ	A_LYS_109	NZ	B_GLU_69	OE1	3.478
4HLZ	A_LYS_109	NZ	B_GLU_69	OE2	2.999
4HLZ	A_LYS_310	NZ	B_ASP_90	OD1	2.429
4HLZ	A_LYS_310	NZ	B_ASP_90	OD2	3.948
4HLZ	B_LYS_58	NZ	F_GLU_97	OE1	3.865
4HLZ	B_LYS_58	NZ	F_GLU_97	OE2	3.885
4HLZ	B_ARG_76	NH1	D_GLU_74	OE1	2.838
4HLZ	B_ARG_76	NH1	D_GLU_74	OE2	3.993
4HLZ	B_ARG_76	NH2	D_GLU_74	OE1	3.145
4HLZ	B_ARG_76	NH2	D_GLU_74	OE2	2.917
4HLZ	B_LYS_83	NZ	D_GLU_85	OE2	2.459
4HLZ	B_ARG_106	NH2	F_ASP_109	OD2	3.278
4HLZ	B_LYS_143	NZ	A_ASP_11	OD1	3.527
4HLZ	B_LYS_143	NZ	A_ASP_11	OD2	3.714
4HLZ	C_ARG_32	NH1	F_GLU_57	OE1	3.413
4HLZ	C_LYS_109	NZ	D_GLU_69	OE1	2.904
4HLZ	C_LYS_109	NZ	D_GLU_69	OE2	3.394
4HLZ	C_LYS_310	NZ	D_ASP_86	OD2	2.827
4HLZ	C_LYS_310	NZ	D_ASP_90	OD1	2.357
4HLZ	C_LYS_310	NZ	D_ASP_90	OD2	3.459
4HLZ	D_LYS_58	NZ	B_GLU_97	OE1	2.796
4HLZ	D_ARG_76	NH1	F_GLU_74	OE1	3.279
4HLZ	D_ARG_76	NH1	F_GLU_74	OE2	2.976
4HLZ	D_ARG_76	NH2	E_GLU_107	OE2	3.277
4HLZ	D_ARG_76	NH2	F_GLU_74	OE2	2.480
4HLZ	D_LYS_83	NZ	F_GLU_85	OE2	2.714
4HLZ	D_ARG_106	NH2	B_ASP_109	OD2	3.865
4HLZ	D_LYS_131	NZ	F_ASP_128	OD1	3.317
4HLZ	E_LYS_109	NZ	F_GLU_69	OE1	2.572
4HLZ	E_LYS_109	NZ	F_GLU_69	OE2	3.930
4HLZ	E_LYS_310	NZ	F_ASP_86	OD1	3.890
4HLZ	E_LYS_310	NZ	F_ASP_90	OD1	3.800
4HLZ	F_LYS_58	NZ	D_GLU_97	OE1	3.641
4HLZ	F_ARG_76	NH1	B_GLU_74	OE1	3.514
4HLZ	F_ARG_76	NH1	B_GLU_74	OE2	3.227
4HLZ	F_ARG_76	NH2	B_GLU_74	OE1	3.962
4HLZ	F_ARG_76	NH2	B_GLU_74	OE2	2.467
4HLZ	I_LYS_96	NZ	D_ASP_46	OD1	2.912
4HLZ	I_LYS_96	NZ	D_ASP_46	OD2	3.655
4HLZ	I_LYS_208	NZ	J_GLU_125	OE2	3.495
4HLZ	I_ARG_213	NH2	J_GLU_125	OE1	3.227
4HLZ	I_ARG_213	NH2	J_GLU_125	OE2	3.829
4HMG	A_LYS_27	NZ	B_GLU_97	OE1	2.795

4HMG	A_LYS_27	NZ	B_GLU_97	OE2	3.247
4HMG	A_ARG_109	NH1	B_GLU_67	OE1	3.584
4HMG	A_ARG_109	NH1	B_GLU_67	OE2	2.773
4HMG	A_LYS_238	NZ	F_GLU_72	OE2	2.782
4HMG	A_ARG_269	NH2	B_GLU_67	OE1	2.783
4HMG	A_LYS_310	NZ	B_ASP_90	OD1	3.350
4HMG	A_LYS_310	NZ	B_ASP_90	OD2	2.711
4HMG	B_ARG_54	NH1	F_GLU_97	OE1	3.078
4HMG	B_ARG_54	NH2	E_ASP_32	OD2	3.863
4HMG	B_ARG_54	NH2	F_GLU_97	OE1	3.088
4HMG	B_LYS_62	NZ	F_ASP_86	OD1	2.890
4HMG	B_LYS_62	NZ	F_ASP_86	OD2	2.630
4HMG	B_LYS_62	NZ	F_ASP_90	OD1	3.620
4HMG	B_LYS_62	NZ	F_ASP_90	OD2	3.931
4HMG	B_HIS_64	NE2	F_ASP_79	OD2	3.785
4HMG	B_ARG_76	NH1	D_GLU_74	OE1	2.796
4HMG	B_ARG_76	NH1	D_GLU_74	OE2	3.711
4HMG	B_ARG_76	NH1	D_GLU_81	OE1	2.672
4HMG	B_ARG_76	NH1	D_GLU_81	OE2	3.308
4HMG	B_ARG_76	NH2	D_GLU_74	OE1	3.404
4HMG	B_ARG_76	NH2	D_GLU_74	OE2	2.827
4HMG	B_ARG_123	NH1	F_GLU_132	OE2	3.178
4HMG	B_ARG_124	NH1	F_GLU_132	OE1	3.359
4HMG	B_ARG_124	NH1	F_GLU_132	OE2	3.102
4HMG	B_ARG_127	NH2	F_GLU_131	OE1	2.525
4HMG	B_ARG_163	NH1	F_GLU_131	OE1	3.338
4HMG	B_ARG_163	NH1	F_GLU_131	OE2	2.796
4HMG	B_ARG_163	NH2	F_GLU_131	OE1	2.694
4HMG	B_ARG_163	NH2	F_GLU_131	OE2	3.492
4HMG	B_ARG_170	NH2	D_GLU_128	OE1	3.784
4HMG	B_ARG_170	NH2	D_GLU_128	OE2	3.698
4HMG	C_LYS_27	NZ	D_GLU_97	OE1	2.789
4HMG	C_LYS_27	NZ	D_GLU_97	OE2	3.246
4HMG	C_ARG_109	NH1	D_GLU_67	OE1	3.616
4HMG	C_ARG_109	NH1	D_GLU_67	OE2	2.791
4HMG	C_LYS_238	NZ	B_GLU_72	OE2	2.606
4HMG	C_ARG_269	NH2	D_GLU_67	OE1	2.764
4HMG	C_LYS_310	NZ	D_ASP_90	OD1	3.321
4HMG	C_LYS_310	NZ	D_ASP_90	OD2	2.697
4HMG	C_LYS_326	NZ	D_GLU_15	OE1	3.836
4HMG	C_LYS_326	NZ	D_GLU_15	OE2	2.684
4HMG	D_ARG_54	NH1	B_GLU_97	OE1	3.076
4HMG	D_ARG_54	NH2	A_ASP_32	OD2	3.995
4HMG	D_ARG_54	NH2	B_GLU_97	OE1	3.112
4HMG	D_LYS_62	NZ	B_ASP_86	OD1	2.940
4HMG	D_LYS_62	NZ	B_ASP_86	OD2	2.591
4HMG	D_LYS_62	NZ	B_ASP_90	OD1	3.586
4HMG	D_LYS_62	NZ	B_ASP_90	OD2	3.891
4HMG	D_HIS_64	NE2	B_ASP_79	OD2	3.731
4HMG	D_ARG_76	NH1	F_GLU_74	OE1	2.745
4HMG	D_ARG_76	NH1	F_GLU_74	OE2	3.756
4HMG	D_ARG_76	NH1	F_GLU_81	OE1	2.644
4HMG	D_ARG_76	NH1	F_GLU_81	OE2	3.314
4HMG	D_ARG_76	NH2	F_GLU_74	OE1	3.255
4HMG	D_ARG_76	NH2	F_GLU_74	OE2	2.777
4HMG	D_ARG_123	NH1	B_GLU_132	OE2	3.157
4HMG	D_ARG_124	NH1	B_GLU_132	OE1	3.347
4HMG	D_ARG_124	NH1	B_GLU_132	OE2	3.074

4HMG	D_ARG_127	NH2	B_GLU_131	OE1	2.541
4HMG	D_ARG_163	NH1	B_GLU_131	OE1	3.321
4HMG	D_ARG_163	NH1	B_GLU_131	OE2	2.801
4HMG	D_ARG_163	NH2	B_GLU_131	OE1	2.729
4HMG	D_ARG_163	NH2	B_GLU_131	OE2	3.526
4HMG	D_ARG_170	NH2	F_GLU_128	OE1	3.859
4HMG	D_ARG_170	NH2	F_GLU_128	OE2	3.829
4HMG	E_LYS_27	NZ	F_GLU_97	OE1	2.764
4HMG	E_LYS_27	NZ	F_GLU_97	OE2	3.247
4HMG	E_ARG_109	NH1	F_GLU_67	OE1	3.614
4HMG	E_ARG_109	NH1	F_GLU_67	OE2	2.773
4HMG	E_LYS_238	NZ	D_GLU_72	OE2	2.707
4HMG	E_ARG_269	NH2	F_GLU_67	OE1	2.739
4HMG	E_LYS_310	NZ	F_ASP_90	OD1	3.300
4HMG	E_LYS_310	NZ	F_ASP_90	OD2	2.685
4HMG	F_ARG_25	NH1	E_GLU_325	OE1	3.853
4HMG	F_ARG_54	NH1	D_GLU_97	OE1	3.052
4HMG	F_ARG_54	NH2	C_ASP_32	OD2	3.923
4HMG	F_ARG_54	NH2	D_GLU_97	OE1	3.130
4HMG	F_LYS_62	NZ	D_ASP_86	OD1	2.900
4HMG	F_LYS_62	NZ	D_ASP_86	OD2	2.597
4HMG	F_LYS_62	NZ	D_ASP_90	OD1	3.664
4HMG	F_LYS_62	NZ	D_ASP_90	OD2	3.951
4HMG	F_HIS_64	NE2	D_ASP_79	OD2	3.646
4HMG	F_ARG_76	NH1	B_GLU_74	OE1	2.714
4HMG	F_ARG_76	NH1	B_GLU_74	OE2	3.687
4HMG	F_ARG_76	NH1	B_GLU_81	OE1	2.651
4HMG	F_ARG_76	NH1	B_GLU_81	OE2	3.434
4HMG	F_ARG_76	NH2	B_GLU_74	OE1	3.281
4HMG	F_ARG_76	NH2	B_GLU_74	OE2	2.711
4HMG	F_ARG_123	NH1	D_GLU_132	OE2	3.178
4HMG	F_ARG_124	NH1	D_GLU_132	OE1	3.402
4HMG	F_ARG_124	NH1	D_GLU_132	OE2	3.132
4HMG	F_ARG_127	NH2	D_GLU_131	OE1	2.579
4HMG	F_ARG_163	NH1	D_GLU_131	OE1	3.299
4HMG	F_ARG_163	NH1	D_GLU_131	OE2	2.816
4HMG	F_ARG_163	NH2	D_GLU_131	OE1	2.752
4HMG	F_ARG_163	NH2	D_GLU_131	OE2	3.575
4HMG	F_ARG_170	NH2	B_GLU_128	OE1	3.815
4HMG	F_ARG_170	NH2	B_GLU_128	OE2	3.719
4HXB	A_ARG_230	NH2	H_ASP_56	OD2	3.246
4HXB	H_LYS_215	NZ	L_GLU_120	OE2	3.469
4HXA	H_ARG_98	NH1	L_ASP_50	OD1	2.959
4HXA	H_ARG_98	NH1	L_ASP_50	OD2	3.607
4HXA	H_HIS_164	NE2	L_ASP_167	OD1	3.601
4HXB	H_ARG_96	NH1	L_ASP_94	OD1	3.212
4HXB	H_ARG_96	NH1	L_ASP_94	OD2	2.665
4HXB	H_ARG_96	NH2	L_ASP_94	OD1	2.669
4HXB	H_ARG_96	NH2	L_ASP_94	OD2	3.708
4I2X	B_LYS_59	NZ	E_GLU_10	OE2	3.418
4I2X	B_LYS_65	NZ	E_ASP_208	OD1	3.256
4I2X	B_LYS_214	NZ	A_GLU_123	OE2	3.742
4I2X	D_LYS_63	NZ	C_ASP_1	OD2	3.656
4I2X	D_LYS_65	NZ	F_ASP_208	OD1	3.848
4I2X	D_HIS_170	ND1	C_ASP_167	OD2	3.958
4I2X	D_LYS_214	NZ	C_GLU_123	OE2	3.815
4I2X	F_ARG_180	NH1	E_GLU_47	OE1	3.834
4I3R	G_LYS_282	NZ	H_GLU_33	OE1	3.996

4I3R	G_LYS_282	NZ	H_GLU_33	OE2	2.684
4I3R	H_ARG_64	NH2	G_ASP_457	OD1	3.551
4I3R	H_ARG_64	NH2	G_ASP_457	OD2	3.482
4I3R	H_ARG_71	NH1	G_ASP_368	OD1	3.996
4I3R	H_ARG_71	NH1	G_ASP_368	OD2	2.319
4I3R	H_ARG_71	NH2	G_ASP_368	OD1	3.997
4I3R	H_ARG_71	NH2	G_ASP_368	OD2	3.530
4I3R	H_LYS_209	NZ	L_GLU_123	OE2	2.484
4I3S	G_LYS_282	NZ	H_GLU_33	OE1	3.669
4I3S	G_LYS_282	NZ	H_GLU_33	OE2	3.690
4I3S	H_ARG_64	NH2	G_ASP_457	OD1	3.430
4I3S	H_ARG_64	NH2	G_ASP_457	OD2	3.082
4I3S	H_ARG_71	NH1	G_ASP_368	OD1	3.370
4I3S	H_ARG_71	NH1	G_ASP_368	OD2	3.053
4I3S	H_ARG_71	NH2	G_ASP_368	OD1	3.484
4I3S	H_LYS_209	NZ	L_GLU_123	OE1	2.882
4JAM	H_LYS_209	NZ	L_GLU_123	OE2	3.865
4JAM	A_LYS_209	NZ	B_GLU_123	OE2	3.814
4JAN	H_ARG_97	NH2	G_ASP_368	OD2	2.609
4JAN	H_ARG_97	NH2	G_GLU_370	OE1	2.554
4JAN	H_LYS_143	NZ	L_GLU_124	OE2	3.811
4JAN	H_LYS_209	NZ	L_GLU_123	OE1	2.888
4JAN	L_LYS_129	NZ	H_ASP_144	OD2	3.458
4JAN	A_ARG_97	NH2	L_ASP_368	OD1	2.825
4JAN	A_ARG_97	NH2	L_ASP_368	OD2	3.792
4JAN	A_ARG_97	NH2	L_GLU_370	OE1	3.106
4JAN	A_LYS_209	NZ	B_GLU_123	OE1	3.788
4JAN	A_LYS_209	NZ	B_GLU_123	OE2	3.189
4JHW	F_LYS_209	NZ	H_ASP_101	OD2	3.535
4JHW	F_LYS_209	NZ	L_GLU_55	OE1	2.845
4JHW	F_LYS_209	NZ	L_GLU_55	OE2	3.356
4JO1	P_ARG_304	NH1	H_ASP_34	OD1	3.045
4JO1	P_ARG_304	NH1	H_ASP_34	OD2	3.346
4JO1	P_ARG_304	NH2	H_ASP_34	OD2	2.892
4JO1	Q_ARG_304	NH1	L_ASP_34	OD1	2.949
4JO1	Q_ARG_304	NH1	L_ASP_34	OD2	3.344
4JO1	Q_ARG_304	NH2	L_ASP_34	OD1	3.946
4JO1	Q_ARG_304	NH2	L_ASP_34	OD2	2.878
4JO2	P_ARG_304	NH1	H_ASP_34	OD1	2.726
4JO2	P_ARG_304	NH1	H_ASP_34	OD2	3.333
4JO2	P_ARG_304	NH2	H_ASP_34	OD1	3.721
4JO2	P_ARG_304	NH2	H_ASP_34	OD2	2.854
4JO2	Q_ARG_304	NH1	L_ASP_34	OD1	2.965
4JO2	Q_ARG_304	NH1	L_ASP_34	OD2	3.252
4JO2	Q_ARG_304	NH2	L_ASP_34	OD2	3.328
4JO3	H_ARG_54	NH1	P_GLU_321	OE1	3.970
4JO3	P_ARG_327	NH1	L_ASP_1	OD1	2.994
4JO3	P_ARG_327	NH2	L_ASP_1	OD1	2.732
4JO3	P_ARG_327	NH2	L_GLU_27	OE1	3.272
4JO3	P_ARG_327	NH2	L_GLU_27	OE2	3.099
4JO3	Q_ARG_327	NH1	M_ASP_1	OD1	3.248
4JO3	Q_ARG_327	NH2	M_ASP_1	OD1	2.447
4JO3	Q_ARG_327	NH2	M_ASP_1	OD2	3.524
4JO3	Q_ARG_327	NH2	M_GLU_27	OE1	3.837
4JO3	Q_ARG_327	NH2	M_GLU_27	OE2	3.723
4K24	A_LYS_46	NZ	U_GLU_33	OE2	3.632
4K24	A_LYS_46	NZ	U_GLU_36	OE2	2.856
4K24	A_HIS_87	ND1	U_ASP_11	OD1	3.994

4K24	H.LYS_62	NZ	L.ASP_1	OD1	3.610
4K24	H.LYS_208	NZ	L.GLU_123	OE1	2.286
4K24	H.LYS_208	NZ	L.GLU_123	OE2	3.345
4K24	U.ARG_91	NH1	B.ASP_22	OD2	3.233
4K24	U.ARG_91	NH2	B.ASP_22	OD1	3.988
4K24	U.ARG_91	NH2	B.ASP_22	OD2	3.635
4K2U	H.LYS_	NZ	L.ASP_	OD2	2.646
4K2U	H.LYS_	NZ	L.GLU_	OE2	3.160
4K2U	L.LYS_	NZ	M.ASP_	OD2	2.895
4K2U	L.ARG_	NH1	A.GLU_	OE1	2.808
4K2U	L.ARG_	NH1	A.GLU_	OE2	3.439
4K2U	L.ARG_	NH2	A.GLU_	OE1	3.591
4K2U	L.ARG_	NH2	A.GLU_	OE2	2.619
4K2U	M.ARG_	NH1	B.GLU_	OE1	2.744
4K2U	M.ARG_	NH1	B.GLU_	OE2	3.321
4K2U	M.ARG_	NH2	B.GLU_	OE1	3.489
4K2U	M.ARG_	NH2	B.GLU_	OE2	2.673
4K2U	M.HIS_	ND1	L.GLU_	OE2	3.997
4KI5	C.LYS_211	NZ	D.GLU_122	OE2	2.907
4KI5	E.LYS_217	NZ	F.GLU_123	OE2	3.401
4KI5	E.ARG_222	NH1	F.GLU_123	OE1	3.106
4KI5	E.ARG_222	NH1	F.GLU_123	OE2	3.925
4KI5	E.ARG_222	NH2	F.GLU_123	OE1	3.823
4KI5	E.ARG_222	NH2	F.GLU_123	OE2	3.234
4KI5	M.ARG_2215	NH1	C.ASP_100	OD1	2.868
4KI5	M.ARG_2215	NH1	C.ASP_100	OD2	3.241
4KI5	M.ARG_2215	NH2	C.ASP_100	OD1	3.324
4KI5	M.ARG_2215	NH2	C.ASP_100	OD2	2.939
4KI5	M.ARG_2215	NH2	C.ASP_101	OD2	3.819
4KI5	M.LYS_2227	NZ	E.GLU_50	OE1	3.493
4KJY	A.LYS_39	NZ	B.ASP_100	OD1	2.809
4KJY	B.ARG_53	NH1	A.GLU_97	OE2	3.571
4KJY	B.ARG_53	NH1	A.GLU_106	OE1	3.135
4KJY	B.ARG_69	NH1	A.GLU_35	OE1	2.737
4KJY	B.ARG_69	NH1	A.GLU_35	OE2	3.607
4KJY	B.ARG_69	NH1	A.GLU_100	OE2	2.961
4KJY	B.ARG_69	NH2	A.GLU_35	OE1	3.476
4KJY	B.ARG_69	NH2	A.GLU_35	OE2	2.813
4KJY	B.LYS_96	NZ	A.GLU_97	OE1	2.567
4KJY	D.ARG_40	NH1	A.GLU_29	OE1	3.310
4KJY	D.ARG_40	NH2	A.GLU_29	OE1	3.253
4KJY	D.ARG_40	NH2	A.GLU_29	OE2	2.999
4KJY	D.ARG_40	NH2	B.GLU_70	OE1	3.440
4KJY	D.ARG_53	NH1	C.GLU_97	OE2	3.949
4KJY	D.ARG_53	NH2	C.GLU_104	OE1	3.112
4KJY	D.ARG_53	NH2	C.GLU_104	OE2	3.607
4KJY	D.ARG_69	NH1	C.GLU_35	OE1	2.786
4KJY	D.ARG_69	NH1	C.GLU_35	OE2	3.903
4KJY	D.ARG_69	NH1	C.GLU_100	OE2	3.005
4KJY	D.ARG_69	NH2	C.GLU_35	OE1	3.286
4KJY	D.ARG_69	NH2	C.GLU_35	OE2	2.868
4KJY	D.LYS_96	NZ	C.GLU_97	OE1	2.747
4KPH	L.ARG_61	NH2	L.GLU_85	OE2	3.345
4KPH	H.LYS_208	NZ	L.GLU_123	OE2	2.903
4KPH	L.LYS_208	NZ	M.GLU_123	OE2	2.312
4KRL	B.ARG_30	NH1	A.ASP_355	OD1	3.258
4KRL	B.ARG_30	NH1	A.ASP_355	OD2	2.275
4KRL	B.ARG_30	NH2	A.ASP_355	OD1	3.549

4KRL	B_ARG_30	NH2	A_ASP_355	OD2	3.938
4KRL	A_ARG_353	NH1	B_GLU_110	OE1	2.654
4KRL	A_ARG_353	NH2	B_ASP_112	OD1	3.873
4KRL	A_ARG_353	NH2	B_ASP_112	OD2	2.978
4KRM	A_ARG_353	NH1	B_GLU_110	OE1	2.811
4KRM	A_ARG_353	NH2	B_ASP_112	OD1	3.965
4KRM	A_ARG_353	NH2	B_ASP_112	OD2	2.932
4KRM	A_LYS_407	NZ	H_GLU_5	OE1	3.498
4KRM	A_LYS_407	NZ	H_GLU_5	OE2	3.022
4KRM	B_ARG_30	NH1	A_ASP_355	OD1	3.162
4KRM	B_ARG_30	NH1	A_ASP_355	OD2	2.423
4KRM	B_ARG_30	NH2	A_ASP_355	OD1	3.525
4KRM	C_ARG_353	NH1	D_GLU_110	OE1	2.866
4KRM	C_ARG_353	NH2	D_ASP_112	OD2	3.218
4KRM	D_ARG_30	NH1	C_ASP_355	OD1	3.295
4KRM	D_ARG_30	NH1	C_ASP_355	OD2	2.452
4KRM	D_ARG_30	NH2	C_ASP_355	OD1	3.096
4KRM	D_ARG_30	NH2	C_ASP_355	OD2	3.699
4KRM	E_ARG_353	NH1	F_GLU_110	OE1	2.855
4KRM	E_ARG_353	NH2	F_ASP_112	OD2	2.965
4KRM	E_LYS_407	NZ	L_GLU_5	OE1	3.054
4KRM	E_LYS_407	NZ	L_GLU_5	OE2	2.995
4KRM	F_ARG_30	NH1	E_ASP_355	OD1	3.119
4KRM	F_ARG_30	NH1	E_ASP_355	OD2	2.396
4KRM	F_ARG_30	NH2	E_ASP_355	OD1	3.504
4KRM	G_ARG_353	NH1	H_GLU_110	OE1	3.021
4KRM	G_ARG_353	NH2	H_ASP_112	OD2	3.118
4KRM	G_LYS_407	NZ	B_GLU_5	OE1	3.493
4KRM	G_LYS_407	NZ	B_GLU_5	OE2	2.984
4KRM	H_ARG_27	NH1	G_ASP_323	OD1	2.688
4KRM	H_ARG_27	NH2	G_ASP_323	OD1	3.952
4KRM	H_ARG_30	NH1	G_ASP_355	OD1	3.358
4KRM	H_ARG_30	NH1	G_ASP_355	OD2	2.448
4KRM	H_ARG_30	NH2	G_ASP_355	OD1	3.423
4KRM	H_ARG_30	NH2	G_ASP_355	OD2	3.935
4KRM	I_ARG_353	NH1	J_GLU_110	OE1	2.862
4KRM	I_ARG_353	NH2	J_ASP_112	OD2	2.998
4KRM	J_ARG_30	NH1	I_ASP_355	OD1	3.164
4KRM	J_ARG_30	NH1	I_ASP_355	OD2	2.382
4KRM	J_ARG_30	NH2	I_ASP_355	OD1	3.707
4KRM	K_ARG_353	NH1	L_GLU_110	OE1	2.887
4KRM	K_ARG_353	NH1	L_ASP_112	OD2	3.973
4KRM	K_ARG_353	NH2	L_ASP_112	OD2	2.890
4KRM	L_ARG_30	NH1	K_ASP_355	OD1	3.487
4KRM	L_ARG_30	NH1	K_ASP_355	OD2	2.441
4KRM	L_ARG_30	NH2	K_ASP_355	OD1	3.452
4KRM	L_ARG_30	NH2	K_ASP_355	OD2	3.835
4KRO	A_ARG_403	NH2	B_ASP_118	OD2	3.168
4KRO	A_ARG_405	NH2	B_ASP_118	OD1	3.123
4KRO	A_ARG_405	NH2	B_ASP_118	OD2	3.849
4KRO	A_LYS_443	NZ	D_ASP_58	OD1	2.597
4KRO	A_LYS_443	NZ	D_ASP_58	OD2	3.457
4KRO	A_LYS_465	NZ	D_ASP_103	OD2	2.400
4KRO	B_ARG_27	NH1	A_GLU_431	OE1	3.073
4KRO	B_ARG_27	NH2	A_GLU_431	OE1	3.933
4KRO	C_LYS_49	NZ	D_GLU_105	OE2	3.247
4KRP	A_ARG_403	NH2	B_ASP_115	OD2	3.818
4KRP	A_ARG_405	NH1	B_GLU_113	OE1	2.923

4KRP	A_ARG_405	NH2	B_GLU_113	OE1	3.376
4KRP	A_ARG_405	NH2	B_ASP_115	OD1	2.626
4KRP	A_LYS_443	NZ	D_ASP_58	OD1	2.649
4KRP	A_LYS_443	NZ	D_ASP_58	OD2	3.951
4KRP	A_LYS_465	NZ	D_ASP_103	OD2	2.931
4KRP	B_ARG_27	NH1	A_GLU_431	OE1	3.144
4KV5	C_LYS_60	NZ	G_ASP_56	OD2	3.911
4KV5	C_LYS_60	NZ	G_GLU_74	OE2	3.252
4KV5	C_ARG_94	NH1	E_ASP_231	OD2	3.776
4KV5	D_LYS_60	NZ	E_GLU_74	OE2	3.237
4KV5	A_ARG_94	NH1	H_ASP_231	OD2	3.628
4KV5	B_LYS_60	NZ	H_ASP_56	OD2	3.938
4KV5	B_LYS_60	NZ	H_GLU_74	OE2	3.524
4KXZ	A_ARG_60	NH2	J_GLU_74	OE1	3.804
4KXZ	B_ARG_60	NH2	H_ASP_56	OD1	3.585
4KXZ	B_ARG_60	NH2	H_GLU_74	OE1	3.374
4KXZ	B_ARG_60	NH2	H_GLU_74	OE2	3.199
4KXZ	D_ARG_60	NH1	N_GLU_74	OE2	3.775
4KXZ	D_ARG_60	NH2	N_GLU_74	OE2	2.746
4KXZ	E_ARG_60	NH1	Q_GLU_74	OE1	3.619
4KXZ	H_HIS_219	NE2	Q_ASP_56	OD2	3.789
4KXZ	H_HIS_223	ND1	Q_GLU_82	OE1	3.688
4KXZ	H_HIS_223	ND1	Q_GLU_82	OE2	3.984
4KXZ	H_HIS_223	ND1	L_ASP_123	OD1	3.085
4KXZ	H_HIS_223	NE2	Q_GLU_82	OE2	3.368
4KXZ	H_HIS_223	NE2	L_ASP_123	OD1	3.457
4KXZ	J_LYS_216	NZ	I_GLU_124	OE1	2.736
4KXZ	J_LYS_216	NZ	I_GLU_124	OE2	3.105
4KXZ	N_HIS_219	NE2	J_ASP_56	OD2	3.889
4KXZ	N_HIS_223	ND1	J_GLU_82	OE1	3.240
4KXZ	N_HIS_223	ND1	M_ASP_123	OD1	3.197
4KXZ	N_HIS_223	NE2	J_GLU_82	OE1	3.650
4KXZ	N_HIS_223	NE2	J_GLU_82	OE2	3.394
4KXZ	N_HIS_223	NE2	M_ASP_123	OD1	3.310
4LQF	H_LYS_212	NZ	L_GLU_129	OE1	2.714
4LQF	H_LYS_212	NZ	L_GLU_129	OE2	3.879
4LQF	L_LYS_55	NZ	A_ASP_170	OD2	2.731
4LSS	G_LYS_97	NZ	H_ASP_99	OD2	3.791
4LSS	G_ARG_476	NH2	H_ASP_31	OD1	3.839
4LSS	H_ARG_61	NH2	G_GLU_466	OE1	3.951
4LSS	H_ARG_71	NH1	G_ASP_368	OD1	3.719
4LSS	H_ARG_71	NH1	G_ASP_368	OD2	3.126
4LSS	H_ARG_71	NH2	G_ASP_368	OD1	3.278
4LSS	H_LYS_209	NZ	L_GLU_125	OE1	3.429
4LSS	H_LYS_209	NZ	L_GLU_125	OE2	3.562
4LST	G_LYS_357	NZ	L_GLU_1	OE1	2.783
4LST	H_ARG_61	NH1	G_GLU_466	OE1	3.812
4LST	H_ARG_61	NH2	G_ASP_461	OD1	2.947
4LST	H_ARG_71	NH1	G_ASP_368	OD1	3.527
4LST	H_ARG_71	NH1	G_ASP_368	OD2	2.632
4LST	H_ARG_71	NH2	G_ASP_368	OD1	2.939
4LST	H_ARG_71	NH2	G_ASP_368	OD2	3.624
4LST	H_LYS_209	NZ	L_GLU_125	OE2	3.921
4LST	H_LYS_214	NZ	L_ASP_124	OD1	3.010
4LST	H_LYS_214	NZ	L_ASP_124	OD2	3.020
4LU5	H_ARG_98	NH2	B_ASP_168	OD2	3.392
4LU5	H_LYS_208	NZ	L_GLU_128	OE1	3.058
4LU5	H_LYS_208	NZ	L_GLU_128	OE2	3.445

4LU5	L_ARG_51	NH1	H_ASP_101	OD1	3.227
4LU5	L_ARG_51	NH2	H_ASP_101	OD1	2.925
4LU5	L_ARG_98	NH2	A_ASP_168	OD2	3.317
4LU5	M_ARG_51	NH1	L_ASP_101	OD2	3.086
4LU5	M_ARG_51	NH2	L_ASP_101	OD1	3.927
4LU5	M_ARG_51	NH2	L_ASP_101	OD2	2.770
4M1D	L_LYS_129	NZ	H_ASP_144	OD2	3.436
4M1D	H_LYS_143	NZ	L_GLU_124	OE2	2.547
4M1D	H_LYS_209	NZ	L_GLU_123	OE1	2.798
4M1D	H_LYS_209	NZ	L_GLU_123	OE2	2.782
4M1D	P_ARG_315	NH2	H_ASP_95	OD2	3.175
4M1D	L_LYS_209	NZ	M_GLU_123	OE1	3.060
4M1D	L_LYS_209	NZ	M_GLU_123	OE2	2.485
4M1D	Q_ARG_315	NH2	L_ASP_95	OD2	3.051
4M1G	H_LYS_213	NZ	L_GLU_124	OE2	2.837
4M1G	H_ARG_218	NH2	L_GLU_124	OE1	2.657
4M1G	H_ARG_218	NH2	L_GLU_124	OE2	3.648
4M1G	A_LYS_161	NZ	H_ASP_31	OD1	3.895
4M5Y	H_LYS_143	NZ	L_GLU_124	OE2	2.602
4M5Y	L_LYS_143	NZ	M_GLU_124	OE2	2.668
4M7J	H_LYS_208	NZ	L_GLU_123	OE1	3.727
4M7J	H_LYS_208	NZ	L_GLU_123	OE2	3.593
4M7Z	B_LYS_208	NZ	C_GLU_123	OE1	3.318
4M7Z	B_LYS_208	NZ	C_GLU_123	OE2	3.881
4M7Z	H_LYS_208	NZ	L_GLU_123	OE1	3.192
4M93	H_LYS_208	NZ	L_GLU_123	OE1	3.795
4M93	B_LYS_208	NZ	C_GLU_123	OE1	3.203
4MA1	B_LYS_5	NZ	F_GLU_187	OE1	3.315
4MA1	B_LYS_208	NZ	C_GLU_123	OE1	3.857
4MA1	H_LYS_208	NZ	L_GLU_123	OE1	3.752
4N0Y	H_LYS_209	NZ	L_GLU_123	OE1	2.939
4N1H	A_LYS_111	NZ	C_GLU_202	OE1	3.097
4N1H	A_LYS_111	NZ	C_GLU_202	OE2	2.712
4N1H	A_HIS_112	ND1	C_GLU_205	OE2	3.407
4N1H	A_HIS_112	NE2	C_GLU_202	OE1	2.950
4N1H	A_HIS_112	NE2	C_GLU_205	OE2	3.971
4N1H	A_ARG_128	NH1	C_GLU_89	OE1	3.101
4N1H	A_LYS_150	NZ	B_ASP_115	OD2	2.748
4N1H	A_ARG_153	NH2	B_ASP_106	OD1	3.262
4N1H	A_ARG_153	NH2	B_ASP_106	OD2	3.262
4N1H	C_LYS_149	NZ	D_ASP_106	OD1	3.587
4N1H	C_LYS_149	NZ	D_ASP_106	OD2	3.735
4N1H	C_LYS_150	NZ	D_ASP_115	OD1	3.157
4N1H	C_ARG_153	NH2	D_ASP_106	OD1	2.772
4N1H	C_ARG_204	NH2	A_GLU_121	OE2	3.425
4NC1	A_ARG_133	NH1	D_ASP_115	OD2	3.145
4NC1	C_ARG_114	NH1	D_ASP_115	OD1	3.051
4NC1	C_ARG_114	NH1	D_ASP_115	OD2	3.046
4NC1	C_ARG_114	NH2	D_ASP_115	OD1	2.896
4NC1	B_ARG_133	NH2	C_ASP_115	OD2	3.404
4NC1	D_ARG_63	NH1	B_ASP_112	OD2	3.125
4NC1	D_ARG_114	NH1	C_ASP_115	OD1	2.908
4NC1	D_ARG_114	NH2	C_ASP_115	OD1	2.942
4NGH	H_LYS_228	NZ	L_ASP_122	OD1	3.887
4NIK	A_LYS_153	NZ	B_ASP_104	OD1	3.730
4NIK	A_LYS_153	NZ	B_ASP_104	OD2	2.794
4NIK	A_LYS_153	NZ	B_GLU_186	OE2	2.639
4NZR	H_LYS_60	NZ	L_GLU_1	OE1	3.647

4NZR	H_HIS_97	NE2	L_GLU_50	OE2	3.635
4NZR	H_HIS_98	NE2	L_GLU_50	OE1	2.875
4NZR	H_HIS_172	NE2	L_ASP_167	OD2	3.398
4NZR	H_LYS_221	NZ	L_GLU_123	OE2	2.989
4NZR	M_LYS_114	NZ	L_GLU_17	OE1	3.119
4NZR	M_ARG_384	NH2	L_GLU_81	OE1	3.444
4NZR	M_ARG_384	NH2	L_GLU_81	OE2	3.239
4NZR	M_ARG_457	NH1	H_ASP_31E	OD1	2.958
4NZR	M_ARG_457	NH1	H_ASP_31E	OD2	3.096
4NZR	M_ARG_457	NH2	H_ASP_31E	OD1	3.746
4NZR	M_ARG_457	NH2	H_ASP_31E	OD2	2.554
4NZT	M_ARG_99	NH2	L_ASP_60	OD1	3.096
4NZT	M_ARG_384	NH2	L_GLU_81	OE1	3.193
4NZT	M_ARG_384	NH2	L_GLU_81	OE2	3.684
4NZT	H_LYS_145	NZ	L_GLU_124	OE2	2.541
4NZU	H_LYS_100E	NZ	L_ASP_50	OD1	3.991
4NZU	H_LYS_100E	NZ	L_ASP_50	OD2	2.752
4NZU	H_LYS_221	NZ	L_GLU_123	OE2	2.899
4O5L	H_LYS_100I	NZ	L_ASP_93	OD1	2.723
4O5L	H_LYS_100I	NZ	L_ASP_93	OD2	3.455
4OLU	G_LYS_97	NZ	H_ASP_100B	OD1	3.513
4OLU	G_LYS_97	NZ	H_ASP_100B	OD2	2.385
4OLU	H_ARG_61	NH1	G_GLU_466	OE1	2.734
4OLU	H_ARG_71	NH1	G_ASP_368	OD1	3.753
4OLU	H_ARG_71	NH1	G_ASP_368	OD2	2.863
4OLU	H_ARG_71	NH2	G_ASP_368	OD1	3.092
4OLU	H_ARG_71	NH2	G_ASP_368	OD2	3.692
4OLU	H_LYS_209	NZ	L_GLU_125	OE1	3.927
4OLU	H_LYS_209	NZ	L_GLU_125	OE2	3.166
4OLV	G_LYS_97	NZ	H_ASP_100B	OD1	3.067
4OLV	G_LYS_97	NZ	H_ASP_100B	OD2	2.942
4OLV	H_ARG_61	NH1	G_GLU_466	OE1	2.769
4OLV	H_ARG_71	NH1	G_ASP_368	OD1	3.700
4OLV	H_ARG_71	NH1	G_ASP_368	OD2	2.815
4OLV	H_ARG_71	NH2	G_ASP_368	OD1	3.136
4OLV	H_ARG_71	NH2	G_ASP_368	OD2	3.717
4OLV	H_LYS_209	NZ	L_GLU_125	OE1	3.978
4OLV	H_LYS_209	NZ	L_GLU_125	OE2	3.214
4OLW	G_LYS_97	NZ	H_ASP_100B	OD1	3.637
4OLW	G_LYS_97	NZ	H_ASP_100B	OD2	3.575
4OLW	H_ARG_61	NH1	G_GLU_466	OE1	2.598
4OLW	H_ARG_61	NH2	G_GLU_466	OE1	3.969
4OLW	H_ARG_71	NH1	G_ASP_368	OD1	3.570
4OLW	H_ARG_71	NH1	G_ASP_368	OD2	2.966
4OLW	H_ARG_71	NH2	G_ASP_368	OD1	3.028
4OLW	H_ARG_71	NH2	G_ASP_368	OD2	3.898
4OLW	H_ARG_100A	NH2	G_GLU_106	OE1	3.908
4OLW	H_LYS_209	NZ	L_GLU_125	OE1	2.861
4OLW	H_LYS_209	NZ	L_GLU_125	OE2	2.764
4OLW	H_LYS_214	NZ	L_ASP_124	OD1	3.031
4OLW	H_LYS_214	NZ	L_ASP_124	OD2	3.691
4OLX	G_LYS_97	NZ	H_ASP_100B	OD1	3.339
4OLX	G_LYS_97	NZ	H_ASP_100B	OD2	2.904
4OLX	H_ARG_61	NH1	G_GLU_466	OE1	2.655
4OLX	H_ARG_71	NH1	G_ASP_368	OD1	3.883
4OLX	H_ARG_71	NH1	G_ASP_368	OD2	2.896
4OLX	H_ARG_71	NH2	G_ASP_368	OD1	3.066
4OLX	H_ARG_71	NH2	G_ASP_368	OD2	3.572

4OLX	H_ARG_100A	NH2	G_GLU_106	OE1	3.646
4OLX	H_LYS_209	NZ	L_GLU_125	OE2	3.132
4OLY	G_LYS_97	NZ	H_ASP_100B	OD1	3.240
4OLY	G_LYS_97	NZ	H_ASP_100B	OD2	2.829
4OLY	H_ARG_61	NH1	G_GLU_466	OE1	2.641
4OLY	H_ARG_71	NH1	G_ASP_368	OD1	3.538
4OLY	H_ARG_71	NH1	G_ASP_368	OD2	2.816
4OLY	H_ARG_71	NH2	G_ASP_368	OD1	3.002
4OLY	H_ARG_71	NH2	G_ASP_368	OD2	3.765
4OLY	H_LYS_209	NZ	L_GLU_125	OE1	3.888
4OLY	H_LYS_209	NZ	L_GLU_125	OE2	3.336
4OLZ	G_LYS_97	NZ	H_ASP_100B	OD1	3.552
4OLZ	G_LYS_97	NZ	H_ASP_100B	OD2	3.545
4OLZ	H_ARG_61	NH1	G_GLU_466	OE1	2.620
4OLZ	H_ARG_71	NH1	G_ASP_368	OD1	3.472
4OLZ	H_ARG_71	NH1	G_ASP_368	OD2	2.715
4OLZ	H_ARG_71	NH2	G_ASP_368	OD1	2.877
4OLZ	H_ARG_71	NH2	G_ASP_368	OD2	3.685
4OLZ	H_LYS_209	NZ	L_GLU_125	OE1	3.703
4OLZ	H_LYS_209	NZ	L_GLU_125	OE2	3.063
4OLZ	H_LYS_214	NZ	L_ASP_124	OD1	3.528
4OLZ	H_LYS_214	NZ	L_ASP_124	OD2	3.896
4OM0	G_LYS_97	NZ	H_ASP_100B	OD1	3.843
4OM0	G_LYS_97	NZ	H_ASP_100B	OD2	3.296
4OM0	H_ARG_61	NH1	G_GLU_466	OE1	2.871
4OM0	H_ARG_71	NH1	G_ASP_368	OD1	3.724
4OM0	H_ARG_71	NH1	G_ASP_368	OD2	2.771
4OM0	H_ARG_71	NH2	G_ASP_368	OD1	3.189
4OM0	H_ARG_71	NH2	G_ASP_368	OD2	3.713
4OM0	H_LYS_209	NZ	L_GLU_125	OE2	3.121
4OM1	G_LYS_97	NZ	H_ASP_100B	OD1	3.927
4OM1	G_LYS_97	NZ	H_ASP_100B	OD2	3.635
4OM1	G_LYS_357	NZ	L_GLU_1	OE2	3.763
4OM1	H_ARG_71	NH1	G_ASP_368	OD1	3.565
4OM1	H_ARG_71	NH1	G_ASP_368	OD2	2.752
4OM1	H_ARG_71	NH2	G_ASP_368	OD1	3.031
4OM1	H_ARG_71	NH2	G_ASP_368	OD2	3.734
4OM1	H_LYS_209	NZ	L_GLU_125	OE1	3.639
4OM1	H_LYS_209	NZ	L_GLU_125	OE2	3.008
4OT1	H_LYS_161	NZ	L_GLU_127	OE2	2.572
4OT1	H_LYS_227	NZ	L_GLU_126	OE1	2.521
4OT1	H_LYS_227	NZ	L_GLU_126	OE2	3.241
4OT1	L_LYS_67	NZ	A_GLU_361	OE2	3.026
4P9H	C_ARG_59	NH1	G_ASP_368	OD1	2.832
4P9H	C_ARG_59	NH1	G_ASP_368	OD2	3.395
4P9H	C_ARG_59	NH2	G_ASP_368	OD1	3.561
4P9H	C_ARG_59	NH2	G_ASP_368	OD2	2.514
4P9H	H_HIS_61	NE2	L_ASP_1	OD2	3.817
4PTT	A_ARG_91	NH2	B_GLU_95	OE1	3.477
4PTT	A_ARG_91	NH2	B_GLU_95	OE2	3.208
4PTT	B_LYS_209	NZ	A_GLU_123	OE2	3.476
4PTU	A_ARG_91	NH2	B_GLU_95	OE1	3.438
4PTU	A_ARG_91	NH2	B_GLU_95	OE2	3.334
4PTU	B_LYS_209	NZ	A_GLU_123	OE1	3.628
4Q6I	A_LYS_49	NZ	B_ASP_100A	OD1	2.964
4Q6I	B_LYS_208	NZ	A_GLU_123	OE2	2.822
4Q6I	C_LYS_50	NZ	L_GLU_93	OE2	2.549
4Q6I	C_LYS_181	NZ	G_GLU_56	OE1	2.499

4Q6I	D.LYS_49	NZ	E.ASP_100A	OD1	3.008
4Q6I	E.LYS_208	NZ	D.GLU_123	OE2	3.047
4Q6I	F.LYS_49	NZ	G.ASP_100A	OD1	3.146
4Q6I	G.LYS_208	NZ	F.GLU_123	OE2	3.409
4Q6I	H.LYS_208	NZ	L.GLU_123	OE2	3.045
4Q6I	I.LYS_50	NZ	F.GLU_93	OE2	2.473
4Q6I	I.LYS_181	NZ	H.GLU_56	OE1	3.345
4Q6I	J.LYS_50	NZ	D.GLU_93	OE2	2.666
4Q6I	K.LYS_50	NZ	A.GLU_93	OE2	2.835
4Q6I	L.LYS_49	NZ	H.ASP_100A	OD1	3.063
4Q9B	A.ARG_309	NH1	B.GLU_255	OE1	3.484
4Q9B	A.ARG_309	NH1	B.GLU_255	OE2	2.912
4Q9B	A.ARG_309	NH2	B.GLU_255	OE2	3.212
4Q9B	B.ARG_309	NH1	A.GLU_255	OE1	3.145
4Q9B	B.ARG_309	NH1	A.GLU_255	OE2	2.858
4QEX	A.LYS_341	NZ	H.ASP_53	OD1	3.875
4QEX	A.ARG_422	NH2	H.ASP_97	OD2	3.116
4QHU	B.LYS_145	NZ	A.GLU_126	OE2	2.821
4QHU	C.HIS_29	ND1	D.GLU_113	OE1	3.672
4QHU	C.ARG_31	NH1	D.GLU_113	OE2	3.297
4QHU	C.ARG_31	NH2	D.GLU_113	OE1	3.241
4QHU	C.ARG_31	NH2	D.GLU_113	OE2	3.844
4QHU	C.ARG_39	NH1	L.ASP_52	OD1	3.835
4QHU	C.ARG_39	NH1	L.ASP_52	OD2	2.646
4QHU	C.ARG_55	NH1	L.ASP_49	OD1	2.860
4QHU	C.ARG_55	NH1	L.ASP_49	OD2	3.543
4QTI	H.LYS_217	NZ	L.GLU_123	OE2	2.684
4QTI	U.ARG_58	NH2	H.ASP_103	OD2	2.819
4QTI	U.ARG_89	NH1	H.ASP_99	OD2	3.048
4QTI	U.ARG_91	NH1	H.ASP_99	OD1	2.759
4QTI	U.ARG_91	NH1	H.ASP_99	OD2	2.751
4QTI	U.ARG_91	NH2	H.ASP_99	OD2	3.786
4QTI	U.ARG_116	NH1	H.ASP_103	OD2	3.777
4QTI	U.ARG_116	NH2	H.ASP_103	OD1	3.889
4QXG	H.LYS_213	NZ	L.GLU_124	OE2	3.477
4R2G	F.LYS_29	NZ	E.ASP_279	OD2	2.979
4R2G	F.ARG_59	NH1	E.ASP_368	OD1	2.950
4R2G	F.ARG_59	NH1	E.ASP_368	OD2	2.577
4R2G	F.ARG_59	NH2	E.ASP_368	OD2	3.352
4R2G	Q.ARG_100	NH2	P.ASP_66A	OD2	2.815
4R2G	Q.LYS_227	NZ	P.GLU_124	OE2	3.083
4R2G	B.LYS_29	NZ	O.ASP_279	OD2	3.448
4R2G	B.ARG_59	NH1	O.ASP_368	OD1	2.838
4R2G	B.ARG_59	NH1	O.ASP_368	OD2	3.428
4R2G	B.ARG_59	NH2	O.ASP_368	OD1	3.471
4R2G	B.ARG_59	NH2	O.ASP_368	OD2	2.776
4R2G	D.ARG_100	NH2	C.ASP_66A	OD2	3.131
4R2G	D.LYS_227	NZ	C.GLU_124	OE1	3.473
4R2G	D.LYS_227	NZ	C.GLU_124	OE2	3.405
4R2G	H.LYS_29	NZ	K.ASP_279	OD1	2.934
4R2G	H.ARG_59	NH1	K.ASP_368	OD1	2.502
4R2G	H.ARG_59	NH1	K.ASP_368	OD2	3.259
4R2G	J.ARG_100	NH2	L.ASP_66A	OD2	3.189
4R2G	J.LYS_161	NZ	I.GLU_125	OE2	3.537
4R2G	L.LYS_29	NZ	A.ASP_279	OD1	3.450
4R2G	L.ARG_59	NH1	A.ASP_368	OD1	2.642
4R2G	L.ARG_59	NH1	A.ASP_368	OD2	2.825
4R2G	L.ARG_59	NH2	A.ASP_368	OD1	3.793

4R2G	L_ARG_59	NH2	A_ASP_368	OD2	2.422
4R2G	N_ARG_100	NH2	M_ASP_66A	OD2	3.592
4R2G	N_LYS_161	NZ	M_GLU_125	OE2	2.706
4R2G	O_ARG_327	NH1	D_GLU_100I	OE2	3.858
4R2G	A_ARG_327	NH1	N_GLU_100I	OE1	3.235
4R4H	B_LYS_29	NZ	A_ASP_279	OD1	2.795
4R4H	B_ARG_59	NH1	A_ASP_367	OD1	3.294
4R4H	B_ARG_59	NH1	A_ASP_367	OD2	3.409
4R4H	B_ARG_59	NH2	A_ASP_367	OD2	3.834
4R4H	H_LYS_52	NZ	A_ASP_78	OD1	3.615
4R4H	H_LYS_	NZ	L_ASP_	OD2	3.470
4R7D	A_LYS_214	NZ	B_GLU_123	OE1	3.736
4R7D	B_LYS_107	NZ	D_ASP_9	OD2	3.947
4R7D	D_LYS_18	NZ	B_ASP_70	OD2	3.792
4R7D	D_LYS_107	NZ	B_ASP_9	OD2	3.503
4R7D	E_LYS_214	NZ	F_GLU_123	OE1	3.862
4R7D	E_LYS_214	NZ	F_GLU_123	OE2	3.571
4R7D	I_HIS_169	NE2	J_ASP_167	OD1	3.970
4R7D	J_LYS_18	NZ	N_ASP_70	OD1	3.913
4R7D	J_ARG_24	NH2	N_GLU_17	OE1	3.275
4R7D	J_ARG_24	NH2	N_GLU_17	OE2	2.135
4R7D	K_HIS_169	NE2	L_ASP_167	OD2	3.666
4R7D	K_LYS_214	NZ	L_GLU_123	OE1	3.074
4R7D	L_LYS_49	NZ	K_ASP_100	OD2	3.591
4R7D	M_LYS_214	NZ	N_GLU_123	OE1	3.058
4R7D	M_LYS_214	NZ	N_GLU_123	OE2	2.866
4R7D	N_LYS_107	NZ	J_ASP_9	OD2	3.244
4R7D	O_LYS_214	NZ	P_GLU_123	OE1	2.454
4R7D	O_LYS_214	NZ	P_GLU_123	OE2	3.167
4R7N	A_LYS_214	NZ	B_GLU_123	OE1	3.674
4R7N	A_LYS_214	NZ	B_GLU_123	OE2	3.683
4R7N	B_ARG_24	NH2	J_GLU_17	OE1	3.625
4R7N	B_ARG_24	NH2	J_GLU_17	OE2	2.355
4R7N	B_LYS_107	NZ	J_ASP_9	OD2	3.605
4R7N	C_LYS_214	NZ	D_GLU_123	OE1	2.537
4R7N	C_LYS_214	NZ	D_GLU_123	OE2	3.321
4R7N	D_ARG_24	NH2	F_GLU_17	OE1	3.787
4R7N	D_ARG_24	NH2	F_GLU_17	OE2	2.414
4R7N	D_LYS_107	NZ	F_ASP_9	OD2	3.633
4R7N	E_HIS_169	NE2	F_ASP_167	OD1	3.616
4R7N	E_HIS_169	NE2	F_ASP_167	OD2	3.474
4R7N	E_LYS_214	NZ	F_GLU_123	OE2	3.072
4R7N	F_ARG_24	NH2	D_GLU_17	OE1	3.696
4R7N	F_ARG_24	NH2	D_GLU_17	OE2	2.325
4R7N	F_LYS_107	NZ	D_ASP_9	OD2	3.641
4R7N	G_LYS_214	NZ	H_GLU_123	OE1	2.389
4R7N	G_LYS_214	NZ	H_GLU_123	OE2	3.440
4R7N	H_ARG_24	NH2	L_GLU_17	OE1	3.413
4R7N	H_ARG_24	NH2	L_GLU_17	OE2	2.312
4R7N	I_LYS_214	NZ	J_GLU_123	OE1	3.635
4R7N	I_LYS_214	NZ	J_GLU_123	OE2	2.942
4R7N	J_ARG_24	NH2	B_GLU_17	OE1	3.555
4R7N	J_ARG_24	NH2	B_GLU_17	OE2	2.304
4R7N	K_LYS_214	NZ	L_GLU_123	OE2	3.794
4R7N	L_ARG_24	NH2	H_GLU_17	OE1	3.531
4R7N	L_ARG_24	NH2	H_GLU_17	OE2	2.313
4R7N	N_ARG_24	NH2	P_GLU_17	OE1	3.814
4R7N	N_ARG_24	NH2	P_GLU_17	OE2	2.289

4R7N	N.LYS_107	NZ	P.ASP_9	OD2	3.591
4R7N	O.HIS_169	NE2	P.ASP_167	OD2	3.725
4R7N	P.ARG_24	NH2	N.GLU_17	OE1	3.525
4R7N	P.ARG_24	NH2	N.GLU_17	OE2	2.277
4R7N	Q.LYS_211	NZ	G.ASP_213	OD2	3.009
4R7N	Q.LYS_214	NZ	R.GLU_123	OE1	3.438
4R7N	Q.LYS_214	NZ	R.GLU_123	OE2	3.002
4R7N	R.LYS_145	NZ	F.ASP_93	OD2	3.627
4R7N	S.LYS_214	NZ	T.GLU_123	OE1	3.934
4R7N	S.LYS_214	NZ	T.GLU_123	OE2	3.931
4R9Y	H.LYS_214	NZ	L.GLU_148	OE2	2.745
4R9Y	N.LYS_	NZ	M.GLU_	OE2	3.272
4RAU	A.LYS_95	NZ	C.ASP_7	OD1	3.997
4RAU	A.LYS_95	NZ	C.ASP_7	OD2	3.077
4RAU	D.LYS_95	NZ	F.ASP_7	OD1	3.860
4RAU	G.LYS_95	NZ	I.ASP_7	OD1	3.805
4RAU	G.LYS_95	NZ	I.ASP_7	OD2	2.755
4RAU	K.LYS_216	NZ	J.GLU_125	OE2	3.935
4RAU	O.ARG_49	NH2	X.ASP_7	OD1	2.993
4RAU	O.ARG_49	NH2	X.ASP_7	OD2	3.647
4RAU	P.LYS_	NZ	R.ASP_	OD1	3.104
4RAU	V.LYS_95	NZ	X.ASP_7	OD1	3.972
4RAU	V.LYS_95	NZ	X.ASP_7	OD2	3.050
4RAU	X.ARG_49	NH2	O.ASP_7	OD1	2.791
4RAU	X.ARG_49	NH2	O.ASP_7	OD2	3.699
4RRP	G.LYS_214	NZ	A.ASP_122	OD1	3.271
4RRP	G.LYS_214	NZ	A.ASP_122	OD2	3.253
4RRP	B.ARG_61	NH1	Q.GLU_32	OE1	3.055
4RRP	B.ARG_61	NH1	Q.GLU_32	OE2	3.683
4RRP	B.ARG_61	NH2	Q.GLU_32	OE2	3.637
4RRP	J.LYS_214	NZ	D.ASP_122	OD1	3.176
4RRP	J.LYS_214	NZ	D.ASP_122	OD2	2.924
4RRP	L.HIS_164	NE2	F.ASP_167	OD1	3.853
4RRP	L.LYS_214	NZ	F.ASP_122	OD2	3.247
4RRP	M.LYS_10	NZ	N.GLU_29	OE1	3.876
4RRP	M.LYS_10	NZ	N.GLU_29	OE2	3.237
4RRP	N.LYS_10	NZ	M.GLU_29	OE1	3.319
4RRP	N.LYS_10	NZ	M.GLU_29	OE2	2.389
4RRP	O.ARG_123	NH1	Q.ASP_54	OD1	3.356
4RRP	O.ARG_123	NH1	Q.ASP_54	OD2	3.533
4RRP	O.ARG_123	NH2	Q.ASP_54	OD2	3.134
4RRP	O.HIS_134	NE2	N.GLU_121	OE1	3.780
4RRP	O.HIS_134	NE2	N.GLU_121	OE2	3.192
4RRP	O.ARG_145	NH2	Q.GLU_116	OE1	3.921
4RRP	O.ARG_145	NH2	Q.GLU_116	OE2	3.324
4RRP	Q.ARG_145	NH1	O.GLU_116	OE2	3.050
4RRP	Q.ARG_145	NH2	O.GLU_116	OE2	3.244
4TRP	H.LYS_208	NZ	L.GLU_129	OE2	3.281
4TUK	H.LYS_208	NZ	L.GLU_129	OE2	3.061
4TUL	H.LYS_208	NZ	L.GLU_129	OE1	3.059
4TUL	H.LYS_208	NZ	L.GLU_129	OE2	2.741
4TUO	A.LYS_208	NZ	B.GLU_129	OE1	3.043
4TUO	B.LYS_153	NZ	C.GLU_10	OE2	3.051
4TUO	C.LYS_208	NZ	D.GLU_129	OE1	2.720
4TUO	C.LYS_208	NZ	D.GLU_129	OE2	3.136
4U0Q	A.HIS_495	NE2	D.GLU_31	OE1	3.802
4U0Q	A.HIS_495	NE2	D.GLU_31	OE2	2.620
4U0Q	A.HIS_496	ND1	D.GLU_31	OE1	3.680

4U0Q	B_HIS_170	ND1	D_GLU_172	OE1	2.788
4U0Q	C_HIS_495	ND1	B_ASP_32	OD2	3.411
4U0Q	D_HIS_170	ND1	B_GLU_172	OE1	2.879
4U0Q	D_HIS_170	ND1	B_GLU_172	OE2	2.959
4U0Q	D_LYS_191	NZ	C_GLU_362	OE2	3.108
4U3X	A_HIS_106	NE2	B_GLU_35	OE1	2.597
4U3X	A_HIS_106	NE2	B_GLU_35	OE2	3.650
4U3X	B_ARG_61	NH1	A_ASP_33	OD2	2.723
4U3X	B_ARG_61	NH2	A_ASP_33	OD2	2.983
4U3X	B_ARG_112	NH2	A_ASP_109	OD1	3.763
4U3X	B_ARG_112	NH2	A_ASP_109	OD2	3.035
4U3X	C_HIS_106	NE2	D_GLU_35	OE1	2.720
4U3X	C_HIS_106	NE2	D_GLU_35	OE2	3.669
4U3X	D_ARG_61	NH1	C_ASP_33	OD2	3.116
4U3X	D_ARG_61	NH2	C_ASP_33	OD2	3.400
4U3X	D_ARG_112	NH2	C_ASP_109	OD2	3.567
4U6G	H_LYS_143	NZ	L_GLU_125	OE2	3.603
4U6G	H_LYS_209	NZ	L_GLU_124	OE1	2.829
4U6G	H_LYS_209	NZ	L_GLU_124	OE2	2.866
4U6G	L_HIS_31	ND1	H_GLU_100I	OE2	3.196
4U6G	L_ARG_61	NH1	B_GLU_81	OE1	3.298
4U6G	L_ARG_91	NH1	H_GLU_100J	OE1	3.679
4U6G	L_ARG_91	NH1	H_GLU_100J	OE2	3.478
4U6G	L_ARG_91	NH2	H_GLU_100J	OE2	3.428
4U6G	A_LYS_143	NZ	B_GLU_125	OE2	3.217
4U6G	A_LYS_201	NZ	H_ASP_30	OD1	3.983
4U6G	A_LYS_209	NZ	B_GLU_124	OE1	2.769
4U6G	A_LYS_209	NZ	B_GLU_124	OE2	3.063
4U6G	B_HIS_31	ND1	A_GLU_100I	OE2	3.102
4U6G	B_ARG_91	NH1	A_GLU_100J	OE1	3.587
4U6G	B_ARG_91	NH1	A_GLU_100J	OE2	3.310
4U6G	B_ARG_91	NH2	A_GLU_100J	OE2	3.407
4U6V	H_ARG_99	NH2	L_GLU_55	OE1	2.660
4U6V	H_ARG_99	NH2	L_GLU_55	OE2	2.823
4U6V	H_HIS_105	NE2	A_ASP_183	OD1	3.150
4U6V	H_HIS_105	NE2	A_ASP_183	OD2	3.236
4U6V	H_LYS_218	NZ	L_GLU_122	OE1	2.258
4U6V	H_LYS_218	NZ	L_GLU_122	OE2	3.923
4U6V	A_ARG_200	NH1	H_ASP_56	OD1	3.722
4U6V	A_ARG_200	NH1	H_ASP_56	OD2	3.481
4U6V	A_LYS_266	NZ	L_ASP_93	OD1	2.981
4U6V	K_ARG_99	NH2	M_GLU_55	OE1	2.606
4U6V	K_ARG_99	NH2	M_GLU_55	OE2	2.857
4U6V	K_HIS_105	NE2	B_ASP_183	OD1	2.992
4U6V	K_HIS_105	NE2	B_ASP_183	OD2	3.142
4U6V	K_LYS_218	NZ	M_GLU_122	OE1	2.653
4U6V	B_ARG_200	NH1	K_ASP_56	OD1	3.809
4U6V	B_ARG_200	NH1	K_ASP_56	OD2	3.557
4U6V	B_LYS_266	NZ	M_ASP_93	OD1	3.145
4UAO	A_ARG_317	NH1	C_GLU_100B	OE2	3.537
4UAO	A_ARG_317	NH2	C_GLU_100B	OE1	3.794
4UAO	A_ARG_317	NH2	C_GLU_100B	OE2	2.800
4UAO	C_ARG_56	NH1	A_GLU_81	OE2	2.819
4UAO	C_ARG_56	NH2	A_ASP_174	OD1	3.129
4UAO	C_ARG_56	NH2	A_ASP_174	OD2	2.857
4UAO	C_ARG_95	NH2	A_GLU_173	OE2	3.027
4UV6	B_ARG_180	NH2	A_GLU_396	OE2	2.784
4UV6	B_ARG_313	NH2	A_GLU_60	OE1	2.768

4WEU	D.LYS_887	NZ	A_GLU_145	OE1	3.143
4WEU	A_ARG_96	NH1	B_GLU_94	OE1	3.636
4WEU	A_ARG_96	NH1	B_GLU_94	OE2	3.058
4WEU	A_ARG_96	NH2	B_GLU_94	OE1	2.949
4WEU	A_ARG_96	NH2	B_GLU_94	OE2	3.852
4WEU	A_ARG_136	NH1	D_GLU_889	OE1	2.898
4WEU	B_ARG_96	NH1	A_GLU_94	OE1	3.754
4WEU	B_ARG_96	NH1	A_GLU_94	OE2	2.795
4WEU	B_ARG_96	NH2	A_GLU_94	OE1	2.707
4WEU	B_ARG_96	NH2	A_GLU_94	OE2	3.344
4WHT	A_LYS_207	NZ	B_GLU_127	OE1	2.607
4WHT	A_LYS_207	NZ	B_GLU_127	OE2	3.670
4WHT	C_LYS_207	NZ	D_GLU_127	OE1	3.293
4WHT	E_LYS_207	NZ	F_GLU_127	OE1	3.118
4WHT	G_LYS_204	NZ	U_ASP_206	OD2	3.854
4WHT	I_LYS_65	NZ	R_GLU_84	OE2	3.044
4WHT	I_LYS_207	NZ	J_GLU_127	OE1	2.774
4WHT	I_LYS_207	NZ	J_GLU_127	OE2	3.846
4WHT	K_LYS_207	NZ	L_GLU_127	OE1	2.813
4WHT	M_LYS_204	NZ	K_ASP_206	OD2	2.701
4WHT	M_LYS_207	NZ	N_GLU_127	OE1	3.186
4WHT	O_LYS_207	NZ	P_GLU_127	OE1	3.812
4WHT	O_LYS_207	NZ	P_GLU_127	OE2	2.822
4WHT	Q_LYS_207	NZ	R_GLU_127	OE1	2.572
4WHT	Q_LYS_207	NZ	R_GLU_127	OE2	3.627
4WHT	S_LYS_207	NZ	T_GLU_127	OE1	3.197
4WHT	U_LYS_204	NZ	G_ASP_206	OD2	3.954
4WHT	U_LYS_207	NZ	V_GLU_127	OE1	3.622
4WHT	X_LYS_207	NZ	Y_GLU_127	OE2	2.718
4WHT	B_LYS_111	NZ	J_GLU_73	OE2	3.842
4WHT	D_LYS_151	NZ	L_GLU_191	OE2	3.259
4WHT	D_LYS_187	NZ	I_GLU_114	OE1	3.576
4WHT	D_LYS_187	NZ	I_GLU_114	OE2	3.498
4WHT	H_ARG_66	NH1	Q_ASP_62	OD2	3.949
4WHT	N_LYS_187	NZ	K_GLU_114	OE1	3.270
4WHT	N_LYS_187	NZ	K_GLU_114	OE2	3.221
4WHT	V_LYS_187	NZ	G_GLU_114	OE1	3.353
4WHT	V_LYS_187	NZ	G_GLU_114	OE2	3.189
4WHY	K_LYS_204	NZ	G_ASP_206	OD2	3.182
4WHY	K_LYS_207	NZ	L_GLU_127	OE1	3.798
4WHY	L_LYS_187	NZ	G_GLU_114	OE1	3.275
4WHY	L_LYS_187	NZ	G_GLU_114	OE2	3.634
4WHY	M_LYS_207	NZ	N_GLU_127	OE1	3.795
4WHY	N_LYS_187	NZ	I_GLU_114	OE1	2.397
4WHY	N_LYS_187	NZ	I_GLU_114	OE2	3.551
4WUU	A_ARG_35	NH1	B_ASP_53	OD1	3.025
4WUU	A_ARG_35	NH1	B_ASP_53	OD2	3.278
4WUU	A_ARG_48	NH2	B_ASP_53	OD1	3.607
4WUU	A_ARG_48	NH2	B_ASP_53	OD2	3.368
4WUU	E_ARG_50	NH1	A_GLU_166	OE2	3.181
4WUU	E_ARG_50	NH2	A_GLU_166	OE1	3.839
4WUU	E_ARG_50	NH2	A_GLU_166	OE2	2.671
4XVJ	A_ARG_1	NH2	L_ASP_51	OD1	3.482
4YHP	P_LYS_4	NZ	H_ASP_62	OD1	3.318
4YHP	A_LYS_222	NZ	B_ASP_123	OD2	3.677
4YHP	Q_LYS_4	NZ	C_ASP_62	OD1	3.313
4YHP	C_LYS_222	NZ	D_ASP_123	OD1	3.776
4YHP	C_LYS_222	NZ	D_ASP_123	OD2	3.442

4YHP	D.HIS_190	NE2	L_GLU_59	OE2	2.478
4YHP	E.LYS_222	NZ	F_ASP_123	OD1	3.304
4YHP	E.LYS_222	NZ	F_ASP_123	OD2	2.842
4YHZ	H.ARG_102	NH1	L_ASP_52	OD2	3.952
4YNY	A.LYS_166	NZ	B_GLU_146	OE2	2.702
4YNY	C.LYS_166	NZ	D_GLU_146	OE2	2.776
4YO0	A.LYS_76	NZ	E_ASP_11	OD1	3.807
4YO0	A.LYS_76	NZ	E_ASP_11	OD2	3.094
4YO0	A.LYS_166	NZ	B_GLU_146	OE2	2.816
4YO0	C.LYS_76	NZ	F_GLU_10	OE2	3.111
4YO0	C.LYS_76	NZ	F_ASP_11	OD1	3.515
4YO0	C.LYS_76	NZ	F_ASP_11	OD2	2.782
4YO0	C.LYS_166	NZ	D_GLU_146	OE2	2.660
4YO0	C.LYS_231	NZ	D_GLU_145	OE1	3.828
4YO0	C.LYS_231	NZ	D_GLU_145	OE2	3.815
4Z0X	C.LYS_446	NZ	A_ASP_50	OD1	3.873
4Z0X	C.LYS_446	NZ	A_ASP_50	OD2	2.440
4ZD3	H.HIS_108	NE2	L_GLU_68	OE1	2.549
4ZD3	H.HIS_108	NE2	L_GLU_68	OE2	3.986
4ZD3	H.LYS_224	NZ	L_GLU_143	OE2	2.997
4ZFF	A.LYS_209	NZ	B_GLU_123	OE1	3.193
4ZFF	C.ARG_23	NH1	D_GLU_30	OE1	3.414
4ZFF	H.LYS_209	NZ	L_GLU_123	OE1	3.731
4ZFG	H.LYS_209	NZ	L_GLU_123	OE1	2.808
4ZFO	F.HIS_19	NE2	A_GLU_50	OE1	2.994
4ZFO	F.HIS_19	NE2	A_GLU_50	OE2	3.320
4ZFO	H.ARG_39	NH1	L_GLU_85	OE2	3.425
4ZFO	H.ARG_39	NH2	L_GLU_85	OE1	3.703
4ZFO	H.ARG_39	NH2	L_GLU_85	OE2	2.644
4ZFO	H.LYS_216	NZ	L_GLU_123	OE2	3.666
4ZFO	A.ARG_39	NH1	B_GLU_85	OE1	3.845
4ZFO	A.ARG_39	NH2	B_GLU_85	OE1	2.855
4ZFO	A.ARG_39	NH2	B_GLU_85	OE2	3.746
4ZFO	K.HIS_19	NE2	H_GLU_50	OE1	2.755
4ZFO	K.HIS_19	NE2	H_GLU_50	OE2	3.392
5A7X	A.ARG_419	NH1	D_GLU_100B	OE1	3.000
5A7X	A.ARG_419	NH1	D_GLU_100B	OE2	3.675
5A7X	A.ARG_419	NH2	D_GLU_99	OE1	2.292
5A7X	A.ARG_419	NH2	D_GLU_100B	OE2	3.969
5A7X	B.LYS_35	NZ	A_ASP_457	OD1	3.741
5A7X	B.ARG_59	NH1	A_ASP_368	OD1	3.154
5A7X	B.ARG_59	NH1	A_ASP_368	OD2	3.344
5A7X	B.ARG_59	NH2	A_ASP_368	OD1	2.976
5A7X	B.ARG_59	NH2	A_ASP_368	OD2	2.433
5A7X	D.HIS_164	NE2	C_ASP_167	OD1	3.880
5A7X	D.HIS_164	NE2	C_ASP_167	OD2	2.506
5A7X	D.LYS_209	NZ	C_GLU_123	OE1	3.513
5A7X	D.LYS_209	NZ	C_GLU_123	OE2	3.583
5A7X	E.ARG_419	NH1	H_GLU_100B	OE1	2.998
5A7X	E.ARG_419	NH1	H_GLU_100B	OE2	3.674
5A7X	E.ARG_419	NH2	H_GLU_99	OE1	2.293
5A7X	E.ARG_419	NH2	H_GLU_100B	OE2	3.968
5A7X	F.LYS_35	NZ	E_ASP_457	OD1	3.741
5A7X	F.ARG_59	NH1	E_ASP_368	OD1	3.154
5A7X	F.ARG_59	NH1	E_ASP_368	OD2	3.343
5A7X	F.ARG_59	NH2	E_ASP_368	OD1	2.977
5A7X	F.ARG_59	NH2	E_ASP_368	OD2	2.434
5A7X	H.HIS_164	NE2	G_ASP_167	OD1	3.880

5A7X	H_HIS_164	NE2	G_ASP_167	OD2	2.505
5A7X	H_LYS_209	NZ	G_GLU_123	OE1	3.512
5A7X	H_LYS_209	NZ	G_GLU_123	OE2	3.584
5A7X	I_ARG_419	NH1	L_GLU_100B	OE1	2.999
5A7X	I_ARG_419	NH1	L_GLU_100B	OE2	3.675
5A7X	I_ARG_419	NH2	L_GLU_99	OE1	2.293
5A7X	I_ARG_419	NH2	L_GLU_100B	OE2	3.968
5A7X	J_LYS_35	NZ	I_ASP_457	OD1	3.740
5A7X	J_ARG_59	NH1	I_ASP_368	OD1	3.154
5A7X	J_ARG_59	NH1	I_ASP_368	OD2	3.344
5A7X	J_ARG_59	NH2	I_ASP_368	OD1	2.976
5A7X	J_ARG_59	NH2	I_ASP_368	OD2	2.433
5A7X	L_HIS_164	NE2	K_ASP_167	OD1	3.880
5A7X	L_HIS_164	NE2	K_ASP_167	OD2	2.504
5A7X	L_LYS_209	NZ	K_GLU_123	OE1	3.514
5A7X	L_LYS_209	NZ	K_GLU_123	OE2	3.585
5A8H	A_ARG_419	NH1	D_GLU_100B	OE1	2.999
5A8H	A_ARG_419	NH1	D_GLU_100B	OE2	3.674
5A8H	A_ARG_419	NH2	D_GLU_99	OE1	2.292
5A8H	A_ARG_419	NH2	D_GLU_100B	OE2	3.968
5A8H	B_LYS_35	NZ	A_ASP_457	OD1	3.740
5A8H	B_ARG_59	NH1	A_ASP_368	OD1	3.154
5A8H	B_ARG_59	NH1	A_ASP_368	OD2	3.342
5A8H	B_ARG_59	NH2	A_ASP_368	OD1	2.977
5A8H	B_ARG_59	NH2	A_ASP_368	OD2	2.433
5A8H	D_HIS_164	NE2	C_ASP_167	OD1	3.880
5A8H	D_HIS_164	NE2	C_ASP_167	OD2	2.505
5A8H	D_LYS_209	NZ	C_GLU_123	OE1	3.514
5A8H	D_LYS_209	NZ	C_GLU_123	OE2	3.584
5A8H	F_LYS_100	NZ	A_GLU_91	OE1	3.015
5A8H	F_LYS_100	NZ	A_GLU_91	OE2	3.536
5A8H	G_ARG_419	NH1	J_GLU_100B	OE1	2.998
5A8H	G_ARG_419	NH1	J_GLU_100B	OE2	3.675
5A8H	G_ARG_419	NH2	J_GLU_99	OE1	2.292
5A8H	G_ARG_419	NH2	J_GLU_100B	OE2	3.969
5A8H	H_LYS_35	NZ	G_ASP_457	OD1	3.741
5A8H	H_ARG_59	NH1	G_ASP_368	OD1	3.154
5A8H	H_ARG_59	NH1	G_ASP_368	OD2	3.343
5A8H	H_ARG_59	NH2	G_ASP_368	OD1	2.977
5A8H	H_ARG_59	NH2	G_ASP_368	OD2	2.433
5A8H	J_HIS_164	NE2	I_ASP_167	OD1	3.881
5A8H	J_HIS_164	NE2	I_ASP_167	OD2	2.505
5A8H	J_LYS_209	NZ	I_GLU_123	OE1	3.513
5A8H	J_LYS_209	NZ	I_GLU_123	OE2	3.584
5A8H	L_LYS_100	NZ	G_GLU_87	OE1	2.922
5A8H	L_LYS_100	NZ	G_GLU_87	OE2	3.552
5A8H	L_HIS_100E	NE2	G_GLU_91	OE2	3.049
5A8H	M_ARG_419	NH1	P_GLU_100B	OE1	2.999
5A8H	M_ARG_419	NH1	P_GLU_100B	OE2	3.675
5A8H	M_ARG_419	NH2	P_GLU_99	OE1	2.292
5A8H	M_ARG_419	NH2	P_GLU_100B	OE2	3.969
5A8H	N_LYS_35	NZ	M_ASP_457	OD1	3.741
5A8H	N_ARG_59	NH1	M_ASP_368	OD1	3.154
5A8H	N_ARG_59	NH1	M_ASP_368	OD2	3.343
5A8H	N_ARG_59	NH2	M_ASP_368	OD1	2.977
5A8H	N_ARG_59	NH2	M_ASP_368	OD2	2.433
5A8H	O_LYS_145	NZ	C_GLU_17	OE1	3.474
5A8H	O_LYS_145	NZ	C_GLU_17	OE2	2.123

5A8H	P_HIS_164	NE2	O_ASP_167	OD1	3.881
5A8H	P_HIS_164	NE2	O_ASP_167	OD2	2.505
5A8H	P_LYS_209	NZ	O_GLU_123	OE1	3.514
5A8H	P_LYS_209	NZ	O_GLU_123	OE2	3.584
5A8H	R_HIS_100E	ND1	M_GLU_87	OE2	2.709
5A8H	R_HIS_100E	NE2	M_GLU_87	OE2	3.097
5AZE	L_HIS_36	NE2	H_GLU_105	OE2	2.756
5AZE	H_LYS_137	NZ	L_ASP_143	OD2	2.939
5AZE	H_LYS_217	NZ	L_GLU_128	OE2	2.701
5BW7	A_LYS_370	NZ	B_GLU_357	OE2	3.993
5BW7	A_LYS_409	NZ	B_ASP_399	OD1	3.864
5BW7	A_LYS_409	NZ	B_ASP_399	OD2	2.990
5BW7	B_LYS_370	NZ	A_GLU_357	OE2	3.748
5BW7	B_LYS_409	NZ	A_ASP_399	OD1	3.328
5BW7	B_LYS_409	NZ	A_ASP_399	OD2	2.988
5BW7	C_LYS_120	NZ	A_ASP_265	OD2	2.730
5BW7	C_LYS_131	NZ	A_GLU_269	OE1	3.414
5BW7	C_LYS_131	NZ	A_GLU_269	OE2	2.642
5CMA	B_LYS_214	NZ	A_GLU_123	OE1	2.706
5CMA	B_LYS_214	NZ	A_GLU_123	OE2	3.531
5CP3	H_LYS_207	NZ	A_GLU_128	OE2	2.762
5CP7	B_LYS_207	NZ	C_GLU_128	OE2	3.335
5CP7	C_LYS_58	NZ	H_ASP_1	OD1	3.663
5CP7	C_LYS_58	NZ	H_ASP_1	OD2	3.316
5CP7	D_LYS_207	NZ	E_GLU_128	OE2	2.825
5CP7	F_HIS_163	ND1	G_ASP_172	OD2	3.652
5CP7	F_LYS_207	NZ	G_GLU_128	OE2	3.951
5CP7	H_LYS_207	NZ	A_GLU_128	OE2	3.290
5DFV	A_LYS_171	NZ	C_ASP_288	OD1	3.582
5DFV	A_LYS_171	NZ	C_ASP_288	OD2	2.737
5DFV	A_LYS_171	NZ	C_ASP_290	OD2	2.874
5DFV	B_LYS_171	NZ	E_ASP_288	OD1	3.695
5DFV	B_LYS_171	NZ	E_ASP_288	OD2	3.653
5DFV	B_LYS_171	NZ	E_ASP_290	OD2	2.646
5DFV	C_ARG_398	NH2	D_GLU_698	OE1	3.277
5DFV	E_ARG_398	NH1	F_GLU_698	OE2	3.319
5DFV	E_LYS_1094	NZ	F_GLU_2015	OE1	3.713
5DFV	E_ARG_1099	NH1	F_GLU_2105	OE2	3.679
5DFW	A_LYS_171	NZ	H_ASP_156	OD2	2.691
5DFW	A_LYS_171	NZ	H_ASP_253	OD1	2.751
5DFW	A_LYS_171	NZ	H_ASP_253	OD2	3.799
5DFW	H_ARG_251	NH2	A_ASP_138	OD1	3.392
5DFW	H_ARG_251	NH2	A_ASP_138	OD2	2.698
5DFW	H_LYS_292	NZ	A_ASP_138	OD1	3.884
5DFW	H_LYS_292	NZ	A_ASP_138	OD2	2.950
5DFW	H_LYS_292	NZ	A_ASP_139	OD1	3.019
5DMI	A_LYS_46	NZ	L_ASP_31	OD1	2.761
5DMI	A_LYS_46	NZ	L_ASP_31	OD2	3.234
5DMI	A_HIS_76	ND1	H_ASP_100A	OD2	3.977
5DMI	H_LYS_221	NZ	L_GLU_123	OE2	3.105
5DMJ	B_ARG_83	NH2	G_ASP_72	OD1	3.449
5DMJ	G_LYS_75	NZ	B_GLU_85	OE1	3.187
5DWU	H_ARG_52	NH1	A_ASP_107	OD1	3.435
5DWU	H_ARG_52	NH1	A_ASP_107	OD2	2.568
5DWU	H_ARG_52	NH2	A_ASP_107	OD1	2.685
5DWU	H_ARG_52	NH2	A_ASP_107	OD2	3.250
5ERW	A_ARG_103	NH1	B_ASP_49	OD2	2.990
5ERW	A_LYS_214	NZ	B_GLU_122	OE1	2.490

5ERW	C.LYS_446	NZ	B.ASP_50	OD1	3.926
5ERW	C.LYS_446	NZ	B.ASP_50	OD2	2.398
5EZI	L.ARG_120	NH1	H.GLU_64	OE1	3.561
5EZI	L.ARG_120	NH1	H.GLU_64	OE2	2.826
5EZJ	A.LYS_228	NZ	B.GLU_147	OE1	3.274
5EZJ	B.ARG_120	NH1	A.GLU_64	OE1	3.637
5EZJ	B.ARG_120	NH1	A.GLU_64	OE2	2.843
5EZL	A.LYS_228	NZ	B.GLU_147	OE1	3.314
5EZL	B.ARG_120	NH1	A.GLU_64	OE1	3.901
5EZL	B.ARG_120	NH1	A.GLU_64	OE2	2.804
5EZL	H.LYS_228	NZ	L.GLU_147	OE2	3.445
5EZL	L.ARG_120	NH1	H.GLU_64	OE1	3.668
5EZL	L.ARG_120	NH1	H.GLU_64	OE2	2.626
5EZN	A.ARG_58	NH1	E.ASP_336	OD2	3.940
5EZN	A.ARG_58	NH2	E.ASP_336	OD2	2.479
5EZN	E.LYS_204	NZ	A.GLU_113	OE1	2.243
5EZN	E.LYS_204	NZ	A.GLU_113	OE2	3.142
5EZN	E.LYS_251	NZ	B.GLU_72	OE2	3.130
5EZN	B.ARG_135	NH1	G.GLU_206	OE2	3.927
5EZN	B.ARG_135	NH2	G.GLU_206	OE2	3.596
5EZN	G.LYS_204	NZ	B.GLU_112	OE1	2.749
5EZN	G.LYS_204	NZ	B.GLU_112	OE2	3.972
5EZN	G.LYS_204	NZ	B.GLU_113	OE2	3.260
5EZO	H.LYS_232	NZ	L.GLU_143	OE1	3.314
5EZO	H.LYS_232	NZ	L.GLU_143	OE2	2.456
5EZO	L.ARG_50	NH1	A.ASP_66	OD1	3.943
5EZO	L.ARG_50	NH1	A.ASP_66	OD2	3.721
5EZO	L.ARG_116	NH1	H.GLU_68	OE1	3.718
5EZO	L.ARG_116	NH1	H.GLU_68	OE2	2.774
5GGV	H.ARG_101	NH1	Y.GLU_97	OE2	3.572
5GGV	H.LYS_221	NZ	L.GLU_123	OE1	2.304
5GGV	H.LYS_221	NZ	L.GLU_123	OE2	3.975
5GKR	A.LYS_143	NZ	B.GLU_125	OE2	2.806
5GKR	A.LYS_209	NZ	B.GLU_124	OE1	2.825
5GKR	A.LYS_209	NZ	B.GLU_124	OE2	3.325
5GKR	B.LYS_130	NZ	A.ASP_144	OD2	3.639
5GKR	C.LYS_143	NZ	D.GLU_125	OE2	2.591
5GKR	C.LYS_209	NZ	D.GLU_124	OE1	2.486
5GKR	C.LYS_209	NZ	D.GLU_124	OE2	2.893
5GKR	D.LYS_130	NZ	C.ASP_144	OD2	3.574
5GKS	A.LYS_	NZ	B.GLU_124	OE1	3.518
5GKS	A.LYS_	NZ	B.GLU_124	OE2	2.790
5GKS	B.LYS_130	NZ	A.ASP_144	OD2	3.783
5GKS	C.LYS_	NZ	D.GLU_	OE1	3.455
5GKS	C.LYS_	NZ	D.GLU_	OE2	2.665
5HDQ	A.HIS_234	ND1	H.ASP_97	OD2	3.865
5HDQ	H.LYS_95	NZ	A.ASP_256	OD2	3.739
5HDQ	H.LYS_208	NZ	L.GLU_123	OE1	2.947
5HMG	A.LYS_27	NZ	B.GLU_97	OE1	2.931
5HMG	A.LYS_27	NZ	B.GLU_97	OE2	3.005
5HMG	A.ARG_109	NH1	B.GLU_67	OE1	2.841
5HMG	A.ARG_109	NH1	B.GLU_67	OE2	3.185
5HMG	A.ARG_269	NH1	B.GLU_67	OE1	3.577
5HMG	A.ARG_269	NH2	B.GLU_67	OE1	3.220
5HMG	A.LYS_299	NZ	B.GLU_69	OE1	3.343
5HMG	A.LYS_310	NZ	B.ASP_86	OD1	3.434
5HMG	A.LYS_310	NZ	B.ASP_90	OD1	2.661
5HMG	B.ARG_54	NH1	F.GLU_97	OE1	2.843

5HMG	B_ARG_54	NH2	F_GLU_97	OE1	2.937
5HMG	B_LYS_58	NZ	F_GLU_97	OE1	3.606
5HMG	B_LYS_58	NZ	F_GLU_97	OE2	3.524
5HMG	B_LYS_62	NZ	F_ASP_86	OD1	3.085
5HMG	B_LYS_62	NZ	F_ASP_86	OD2	2.792
5HMG	B_LYS_62	NZ	F_ASP_90	OD1	3.679
5HMG	B_LYS_62	NZ	F_ASP_90	OD2	2.748
5HMG	B_HIS_64	NE2	F_ASP_79	OD2	3.617
5HMG	B_ARG_76	NH1	D_GLU_74	OE1	3.275
5HMG	B_ARG_76	NH1	D_GLU_74	OE2	2.882
5HMG	B_ARG_76	NH1	D_GLU_81	OE1	2.781
5HMG	B_ARG_76	NH1	D_GLU_81	OE2	3.484
5HMG	B_ARG_76	NH2	D_GLU_74	OE1	2.814
5HMG	B_ARG_76	NH2	D_GLU_74	OE2	3.691
5HMG	B_ARG_123	NH1	F_GLU_132	OE2	3.002
5HMG	B_ARG_124	NH1	F_GLU_132	OE1	3.424
5HMG	B_ARG_124	NH1	F_GLU_132	OE2	3.265
5HMG	B_ARG_127	NH2	F_GLU_131	OE1	2.537
5HMG	B_ARG_163	NH1	F_GLU_131	OE1	2.770
5HMG	B_ARG_163	NH1	F_GLU_131	OE2	2.532
5HMG	B_ARG_170	NH1	D_GLU_128	OE1	3.169
5HMG	B_ARG_170	NH1	D_GLU_128	OE2	3.597
5HMG	C_LYS_27	NZ	D_GLU_97	OE1	2.934
5HMG	C_LYS_27	NZ	D_GLU_97	OE2	2.988
5HMG	C_ARG_109	NH1	D_GLU_67	OE1	2.853
5HMG	C_ARG_109	NH1	D_GLU_67	OE2	3.184
5HMG	C_ARG_269	NH1	D_GLU_67	OE1	3.552
5HMG	C_ARG_269	NH2	D_GLU_67	OE1	3.173
5HMG	C_LYS_299	NZ	D_GLU_69	OE1	3.348
5HMG	C_LYS_310	NZ	D_ASP_86	OD1	3.449
5HMG	C_LYS_310	NZ	D_ASP_90	OD1	2.638
5HMG	D_ARG_54	NH1	B_GLU_97	OE1	2.819
5HMG	D_ARG_54	NH2	B_GLU_97	OE1	2.943
5HMG	D_LYS_58	NZ	B_GLU_97	OE1	3.646
5HMG	D_LYS_58	NZ	B_GLU_97	OE2	3.528
5HMG	D_LYS_62	NZ	B_ASP_86	OD1	3.110
5HMG	D_LYS_62	NZ	B_ASP_86	OD2	2.718
5HMG	D_LYS_62	NZ	B_ASP_90	OD1	3.686
5HMG	D_LYS_62	NZ	B_ASP_90	OD2	2.685
5HMG	D_HIS_64	NE2	B_ASP_79	OD2	3.446
5HMG	D_ARG_76	NH1	F_GLU_74	OE1	3.349
5HMG	D_ARG_76	NH1	F_GLU_74	OE2	2.805
5HMG	D_ARG_76	NH1	F_GLU_81	OE1	2.685
5HMG	D_ARG_76	NH1	F_GLU_81	OE2	3.513
5HMG	D_ARG_76	NH2	F_GLU_74	OE1	2.710
5HMG	D_ARG_76	NH2	F_GLU_74	OE2	3.478
5HMG	D_ARG_123	NH1	B_GLU_132	OE2	2.981
5HMG	D_ARG_124	NH1	B_GLU_132	OE1	3.466
5HMG	D_ARG_124	NH1	B_GLU_132	OE2	3.303
5HMG	D_ARG_127	NH2	B_GLU_131	OE1	2.578
5HMG	D_ARG_163	NH1	B_GLU_131	OE1	2.694
5HMG	D_ARG_163	NH1	B_GLU_131	OE2	2.571
5HMG	D_ARG_170	NH1	F_GLU_128	OE1	3.252
5HMG	D_ARG_170	NH1	F_GLU_128	OE2	3.705
5HMG	E_LYS_27	NZ	F_GLU_97	OE1	2.935
5HMG	E_LYS_27	NZ	F_GLU_97	OE2	3.012
5HMG	E_ARG_109	NH1	F_GLU_67	OE1	2.825
5HMG	E_ARG_109	NH1	F_GLU_67	OE2	3.180

5HMG	E_ARG_269	NH1	F_GLU_67	OE1	3.584
5HMG	E_ARG_269	NH2	F_GLU_67	OE1	3.233
5HMG	E_LYS_299	NZ	F_GLU_69	OE1	3.318
5HMG	E_LYS_310	NZ	F_ASP_86	OD1	3.440
5HMG	E_LYS_310	NZ	F_ASP_90	OD1	2.621
5HMG	F_ARG_54	NH1	D_GLU_97	OE1	2.726
5HMG	F_ARG_54	NH2	D_GLU_97	OE1	2.912
5HMG	F_LYS_58	NZ	D_GLU_97	OE1	3.765
5HMG	F_LYS_58	NZ	D_GLU_97	OE2	3.593
5HMG	F_LYS_62	NZ	D_ASP_86	OD1	3.013
5HMG	F_LYS_62	NZ	D_ASP_86	OD2	2.694
5HMG	F_LYS_62	NZ	D_ASP_90	OD1	3.718
5HMG	F_LYS_62	NZ	D_ASP_90	OD2	2.750
5HMG	F_HIS_64	NE2	D_ASP_79	OD1	3.885
5HMG	F_HIS_64	NE2	D_ASP_79	OD2	3.364
5HMG	F_ARG_76	NH1	B_GLU_74	OE1	3.251
5HMG	F_ARG_76	NH1	B_GLU_74	OE2	2.826
5HMG	F_ARG_76	NH1	B_GLU_81	OE1	2.735
5HMG	F_ARG_76	NH1	B_GLU_81	OE2	3.601
5HMG	F_ARG_76	NH2	B_GLU_74	OE1	2.649
5HMG	F_ARG_76	NH2	B_GLU_74	OE2	3.569
5HMG	F_ARG_123	NH1	D_GLU_132	OE2	2.992
5HMG	F_ARG_124	NH1	D_GLU_132	OE1	3.514
5HMG	F_ARG_124	NH1	D_GLU_132	OE2	3.395
5HMG	F_ARG_127	NH2	D_GLU_131	OE1	2.609
5HMG	F_ARG_163	NH1	D_GLU_131	OE1	2.712
5HMG	F_ARG_163	NH1	D_GLU_131	OE2	2.596
5HMG	F_ARG_170	NH1	B_GLU_128	OE1	3.210
5HMG	F_ARG_170	NH1	B_GLU_128	OE2	3.530
5I76	A_LYS_49	NZ	B_GLU_105	OE1	3.995
5I76	B_LYS_215	NZ	A_GLU_123	OE1	2.731
5I76	B_LYS_215	NZ	A_GLU_123	OE2	2.888
5I76	B_LYS_220	NZ	A_ASP_122	OD2	3.474
5I76	C_ARG_24	NH1	A_ASP_70	OD1	3.725
5I76	C_ARG_24	NH1	A_ASP_70	OD2	2.949
5I76	C_ARG_24	NH2	A_ASP_70	OD1	3.138
5I76	C_ARG_24	NH2	A_ASP_70	OD2	3.394
5I76	D_LYS_215	NZ	C_GLU_123	OE1	2.596
5I76	D_LYS_215	NZ	C_GLU_123	OE2	3.738
5ITB	H_ARG_111	NH1	L_GLU_68	OE1	3.426
5ITB	H_ARG_111	NH2	L_GLU_68	OE1	2.856
5ITB	H_LYS_224	NZ	L_GLU_143	OE1	3.323
5ITB	H_LYS_224	NZ	L_GLU_143	OE2	2.099
5J3D	A_ARG_111	NH2	B_GLU_68	OE1	3.664
5J3D	A_LYS_224	NZ	B_GLU_143	OE1	3.390
5J3D	A_LYS_229	NZ	B_ASP_142	OD1	3.902
5J3D	A_LYS_229	NZ	B_ASP_142	OD2	3.196
5J3D	C_ARG_111	NH2	D_GLU_68	OE1	3.489
5J3D	C_LYS_	NZ	D_GLU_	OE1	3.377
5J3D	C_LYS_	NZ	D_ASP_	OD1	2.847
5J3D	C_LYS_	NZ	D_ASP_	OD2	2.791
5J3D	E_ARG_49	NH2	F_ASP_368	OD1	2.801
5J3D	E_ARG_49	NH2	F_ASP_368	OD2	3.628
5J3D	F_LYS_	NZ	I_GLU_	OE2	3.850
5J3D	F_LYS_196	NZ	I_ASP_489	OD1	2.634
5J3D	F_LYS_196	NZ	I_ASP_489	OD2	3.067
5J3D	F_ARG_235	NH1	I_GLU_232	OE1	3.071
5J3D	F_ARG_235	NH1	I_GLU_232	OE2	2.514

5J3D	F_LYS_272	NZ	B_ASP_56	OD2	3.606
5J3D	F_LYS_399	NZ	K_ASP_392	OD1	3.567
5J3D	F_LYS_470	NZ	J_GLU_60	OE1	3.190
5J3D	F_LYS_470	NZ	J_GLU_60	OE2	3.891
5J3D	G_ARG_49	NH2	I_ASP_368	OD1	3.151
5J3D	H_ARG_111	NH2	L_GLU_68	OE1	3.466
5J3D	H_LYS_224	NZ	L_GLU_143	OE1	3.364
5J3D	H_LYS_	NZ	L_ASP_	OD1	3.352
5J3D	H_LYS_	NZ	L_ASP_	OD2	3.692
5J3D	I_LYS_	NZ	K_GLU_	OE1	3.226
5J3D	I_LYS_	NZ	K_GLU_	OE2	3.914
5J3D	I_LYS_196	NZ	K_ASP_489	OD1	2.833
5J3D	I_LYS_196	NZ	K_ASP_489	OD2	3.027
5J3D	I_ARG_235	NH1	K_GLU_232	OE1	3.110
5J3D	I_ARG_235	NH1	K_GLU_232	OE2	2.664
5J3D	I_LYS_272	NZ	D_ASP_56	OD2	3.795
5J3D	I_LYS_399	NZ	F_ASP_392	OD1	3.746
5J3D	I_LYS_470	NZ	E_GLU_60	OE1	3.634
5J3D	I_LYS_470	NZ	E_GLU_60	OE2	3.872
5J3D	J_ARG_49	NH2	K_ASP_368	OD1	3.049
5J3D	J_ARG_49	NH2	K_ASP_368	OD2	3.898
5J3D	J_LYS_87	NZ	K_GLU_294	OE1	3.791
5J3D	K_LYS_	NZ	F_GLU_	OE1	2.905
5J3D	K_LYS_196	NZ	F_ASP_489	OD1	2.822
5J3D	K_LYS_196	NZ	F_ASP_489	OD2	3.022
5J3D	K_ARG_235	NH1	F_GLU_232	OE1	2.445
5J3D	K_ARG_235	NH1	F_GLU_232	OE2	2.683
5J3D	K_ARG_235	NH2	F_GLU_232	OE2	3.814
5J3D	K_LYS_399	NZ	I_ASP_392	OD1	3.598
5J3D	K_LYS_470	NZ	G_GLU_60	OE1	3.953
5JO5	H_LYS_143	NZ	L_GLU_124	OE2	2.459
5JO5	H_LYS_209	NZ	L_GLU_	OE2	2.531
5JO5	L_ARG_91	NH1	H_GLU_100J	OE2	3.301
5JO5	L_ARG_91	NH2	H_GLU_100J	OE2	2.691
5JO5	L_ARG_95B	NH2	H_ASP_58	OD1	3.439
5JO5	A_LYS_143	NZ	B_GLU_124	OE2	2.618
5JO5	A_LYS_209	NZ	B_GLU_123	OE2	2.545
5JO5	B_ARG_91	NH1	A_GLU_100J	OE2	3.353
5JO5	B_ARG_91	NH2	A_GLU_100J	OE2	3.038
5JO5	C_LYS_143	NZ	D_GLU_124	OE2	2.788
5JO5	C_LYS_209	NZ	D_GLU_123	OE2	2.583
5JO5	D_ARG_91	NH1	C_GLU_100J	OE2	3.302
5JO5	D_ARG_91	NH2	C_GLU_100J	OE2	3.077
5JO5	D_ARG_95B	NH2	C_ASP_58	OD1	3.978
5JO5	E_LYS_143	NZ	F_GLU_124	OE2	2.545
5JO5	E_LYS_209	NZ	F_GLU_123	OE2	2.567
5JO5	F_ARG_91	NH1	E_GLU_100J	OE2	3.369
5JO5	F_ARG_91	NH2	E_GLU_100J	OE2	2.722
5JO5	F_ARG_95B	NH2	E_ASP_58	OD1	3.518
5JOF	H_LYS_212	NZ	L_GLU_123	OE2	3.883
5JOF	H_LYS_217	NZ	L_ASP_122	OD2	3.165
5JOF	A_LYS_209	NZ	B_GLU_123	OE1	3.449
5JOF	A_LYS_209	NZ	B_GLU_123	OE2	3.809
5JOF	B_ARG_24	NH1	C_ASP_99	OD1	2.692
5JOF	B_ARG_24	NH1	C_ASP_99	OD2	3.960
5JOF	C_ARG_94	NH1	B_GLU_1	OE2	2.653
5JOF	C_ARG_94	NH2	B_GLU_1	OE2	3.195
5JOF	C_LYS_214	NZ	D_ASP_122	OD2	3.772

5JOF	C_LYS_214	NZ	D_GLU_123	OE1	2.987
5JOF	C_LYS_214	NZ	D_GLU_123	OE2	3.631
5JOF	E_LYS_209	NZ	F_GLU_123	OE1	2.331
5JOF	E_LYS_209	NZ	F_GLU_123	OE2	3.588
5JOF	E_LYS_214	NZ	F_ASP_122	OD2	3.802
5JR1	H_HIS_164	NE2	L_ASP_139	OD1	3.232
5JR1	H_HIS_164	NE2	L_ASP_139	OD2	3.168
5JR1	L_HIS_31	ND1	H_ASP_100	OD2	3.496
5JR1	L_HIS_31	ND1	H_GLU_100I	OE2	3.149
5JR1	L_ARG_95B	NH1	H_ASP_58	OD1	3.367
5JR1	L_ARG_95B	NH1	H_ASP_58	OD2	3.787
5JR1	L_ARG_95B	NH2	H_ASP_58	OD1	3.502
5JR1	L_ARG_95B	NH2	H_ASP_58	OD2	2.474
5JUE	H_LYS_208	NZ	L_GLU_123	OE1	2.809
5JUE	H_LYS_208	NZ	L_GLU_123	OE2	2.812
5JXA	H_LYS_209	NZ	L_GLU_123	OE1	3.277
5JXA	H_LYS_214	NZ	L_ASP_122	OD1	2.755
5JXA	H_LYS_214	NZ	L_ASP_122	OD2	3.275
5KZP	H_LYS_224	NZ	L_ASP_122	OD2	3.852
5KZP	E_ARG_65	NH2	K_GLU_1	OE2	3.580
5KZP	E_LYS_219	NZ	L_GLU_123	OE1	2.944
5KZP	E_LYS_219	NZ	L_GLU_123	OE2	2.510
5KZP	F_LYS_139	NZ	J_GLU_213	OE2	2.615
5KZP	G_LYS_219	NZ	K_GLU_123	OE2	3.381
5LDN	H_LYS_	NZ	L_GLU_	OE1	3.019
5MO9	H_LYS_212	NZ	L_GLU_128	OE2	3.509
5MO9	L_LYS_55	NZ	X_GLU_371	OE2	2.811
5MO9	X_LYS_364	NZ	H_GLU_33	OE2	2.799
5MO9	X_LYS_364	NZ	H_ASP_52	OD1	3.966
5N4J	L_ARG_38	NH1	H_ASP_100	OD1	2.794
5N4J	L_ARG_38	NH1	H_ASP_100	OD2	3.589
5N4J	H_LYS_210	NZ	L_GLU_131	OE1	2.936
5N4J	H_LYS_210	NZ	L_GLU_131	OE2	3.282
5N7W	A_LYS_149	NZ	B_GLU_126	OE2	2.961
5N7W	A_LYS_215	NZ	B_GLU_125	OE1	2.755
5N7W	A_LYS_215	NZ	B_GLU_125	OE2	3.335
5N7W	H_LYS_149	NZ	L_GLU_126	OE2	2.605
5NPH	H_LYS_215	NZ	L_GLU_123	OE2	2.787
5NPH	L_LYS_93	NZ	A_GLU_533	OE1	3.679
5NPI	A_HIS_181	NE2	B_GLU_10	OE1	3.570
5NPI	A_HIS_181	NE2	B_GLU_10	OE2	3.750
5NPI	B_HIS_181	NE2	A_GLU_10	OE1	3.757
5NPI	B_HIS_181	NE2	A_GLU_10	OE2	3.882
5NPI	B_LYS_233	NZ	E_GLU_533	OE1	3.924
5NPJ	A_HIS_181	NE2	B_GLU_10	OE1	3.540
5NPJ	A_HIS_181	NE2	B_GLU_10	OE2	3.793
5NPJ	B_HIS_181	NE2	A_GLU_10	OE1	3.734
5NPJ	B_HIS_181	NE2	A_GLU_10	OE2	3.967
5NST	A_ARG_39	NH1	C_GLU_81	OE1	3.260
5NST	A_ARG_39	NH1	C_GLU_81	OE2	3.263
5NST	A_ARG_39	NH2	C_GLU_81	OE1	3.038
5NST	B_LYS_345	NZ	A_GLU_123	OE1	3.069
5NST	C_ARG_39	NH1	A_GLU_81	OE1	3.247
5NST	C_ARG_39	NH1	A_GLU_81	OE2	3.139
5NST	C_ARG_39	NH2	A_GLU_81	OE1	3.004
5NST	D_LYS_345	NZ	C_GLU_123	OE2	3.272
5NUZ	A_ARG_95	NH1	C_ASP_114	OD1	3.502
5NUZ	A_ARG_95	NH1	C_ASP_114	OD2	2.701

5NUZ	A_ARG_95	NH2	C_ASP_114	OD1	2.822
5NUZ	A_ARG_95	NH2	C_ASP_114	OD2	3.585
5NUZ	A_LYS_208	NZ	B_GLU_123	OE1	3.889
5NUZ	A_LYS_208	NZ	B_GLU_123	OE2	2.684
5NUZ	H_ARG_95	NH1	D_ASP_114	OD1	3.679
5NUZ	H_ARG_95	NH1	D_ASP_114	OD2	2.753
5NUZ	H_ARG_95	NH2	D_ASP_114	OD1	2.850
5NUZ	H_ARG_95	NH2	D_ASP_114	OD2	3.470
5NUZ	H_LYS_208	NZ	L_GLU_123	OE2	2.982
5NUZ	B_ARG_61	NH2	L_GLU_79	OE1	3.072
5NUZ	B_ARG_61	NH2	L_GLU_79	OE2	3.676
5NUZ	C_LYS_211	NZ	A_ASP_54	OD1	3.758
5NUZ	C_LYS_211	NZ	A_ASP_54	OD2	3.058
5NUZ	C_LYS_211	NZ	A_ASP_56	OD2	2.861
5NUZ	L_ARG_61	NH2	B_GLU_79	OE1	3.765
5NUZ	L_ARG_61	NH2	B_GLU_79	OE2	2.966
5NUZ	D_LYS_211	NZ	H_ASP_54	OD1	3.910
5NUZ	D_LYS_211	NZ	H_ASP_54	OD2	3.105
5NUZ	D_LYS_211	NZ	H_ASP_56	OD2	2.803
5O14	A_LYS_185	NZ	H_ASP_55	OD1	3.249
5O14	A_LYS_185	NZ	H_ASP_55	OD2	2.764
5O14	A_LYS_185	NZ	H_ASP_57	OD2	2.802
5O14	A_ARG_204	NH1	B_GLU_218	OE1	3.625
5O14	B_LYS_185	NZ	C_ASP_55	OD1	3.234
5O14	B_LYS_185	NZ	C_ASP_55	OD2	2.720
5O14	B_LYS_185	NZ	C_ASP_57	OD2	2.736
5O14	C_ARG_54	NH2	B_ASP_161	OD1	2.870
5O14	C_ARG_54	NH2	B_ASP_161	OD2	3.505
5O14	C_LYS_218	NZ	D_GLU_124	OE1	3.107
5O14	D_ARG_18	NH1	A_GLU_218	OE1	3.301
5O14	H_ARG_54	NH1	A_ASP_161	OD1	2.861
5O14	H_ARG_54	NH1	A_ASP_161	OD2	3.283
5O14	H_ARG_59	NH1	L_ASP_94	OD1	3.733
5O14	H_ARG_59	NH1	L_ASP_94	OD2	3.698
5O1R	A_ARG_339	NH1	H_ASP_100	OD1	3.968
5O1R	A_ARG_339	NH1	H_ASP_100	OD2	3.203
5O1R	B_ARG_339	NH1	I_ASP_100	OD1	3.595
5O1R	B_ARG_339	NH1	I_ASP_100	OD2	2.991
5OLM	A_HIS_0	NE2	B_GLU_97	OE1	2.769
5OLM	A_HIS_0	NE2	B_GLU_97	OE2	2.598
5OLM	A_ARG_6	NH2	B_GLU_82	OE1	3.071
5OLM	B_HIS_0	NE2	A_GLU_97	OE1	2.741
5OLM	B_HIS_0	NE2	A_GLU_97	OE2	3.001
5OLM	B_ARG_6	NH2	A_GLU_82	OE2	2.559
5OPY	H_LYS_212	NZ	L_GLU_123	OE2	3.578
5T6P	A_LYS_58	NZ	F_ASP_3	OD2	1.997
5T6P	A_LYS_174	NZ	C_GLU_128	OE2	3.605
5T6P	C_ARG_55	NH1	E_ASP_3	OD2	3.191
5T6P	C_LYS_58	NZ	E_ASP_3	OD2	2.925
5T6P	E_ARG_5	NH2	C_GLU_39	OE1	3.351
5T6P	E_ARG_5	NH2	C_GLU_39	OE2	2.626
5T6P	F_ARG_5	NH2	A_GLU_39	OE1	3.661
5T6P	F_ARG_5	NH2	A_GLU_39	OE2	2.718
5T78	A_LYS_58	NZ	F_ASP_3	OD1	2.579
5T78	A_LYS_58	NZ	F_ASP_3	OD2	3.334
5T78	F_ARG_5	NH1	A_GLU_39	OE1	2.678
5T78	F_ARG_5	NH1	A_GLU_39	OE2	2.480
5T78	C_ARG_55	NH2	E_ASP_3	OD1	3.685

5T78	C.LYS_58	NZ	E.ASP_3	OD1	2.753
5T78	C.LYS_58	NZ	E.ASP_3	OD2	2.872
5T78	D.LYS_211	NZ	C.GLU_128	OE1	3.376
5T78	E.ARG_5	NH1	C.GLU_39	OE1	2.693
5T78	E.ARG_5	NH1	C.GLU_39	OE2	2.664
5TIH	A.LYS_66	NZ	L.ASP_92	OD1	3.482
5TIH	H.HIS_35	NE2	A.ASP_69	OD1	2.973
5TIH	H.HIS_35	NE2	A.ASP_69	OD2	3.535
5TIH	H.ARG_100	NH2	A.ASP_69	OD1	3.080
5TIH	H.ARG_101	NH2	A.GLU_119	OE1	3.357
5TIH	H.ARG_101	NH2	A.GLU_119	OE2	3.359
5TIK	A.HIS_3	ND1	D.GLU_9	OE2	3.832
5TIK	A.HIS_3	NE2	B.GLU_9	OE2	3.597
5TIK	B.HIS_3	NE2	A.GLU_9	OE1	3.627
5TIK	B.HIS_3	NE2	A.GLU_9	OE2	3.175
5TIK	B.HIS_3	NE2	C.GLU_9	OE1	3.296
5TIK	B.HIS_3	NE2	C.GLU_9	OE2	3.823
5TIK	B.LYS_290	NZ	A.GLU_281	OE1	3.703
5TIK	C.HIS_3	NE2	B.GLU_9	OE1	2.908
5TIK	C.ARG_29	NH2	B.ASP_259	OD2	3.311
5TIK	D.HIS_3	NE2	A.GLU_9	OE1	2.950
5TIK	D.HIS_3	NE2	A.GLU_9	OE2	2.918
5TL5	H.ARG_50	NH1	L.ASP_98	OD1	2.887
5TL5	H.ARG_50	NH1	L.ASP_98	OD2	3.532
5TL5	H.ARG_50	NH2	L.ASP_98	OD1	3.785
5TL5	H.ARG_50	NH2	L.ASP_98	OD2	2.933
5TL5	H.LYS_216	NZ	L.GLU_127	OE1	3.027
5TL5	H.LYS_216	NZ	L.GLU_127	OE2	3.571
5TL5	A.LYS_17	NZ	H.ASP_55	OD1	3.610
5TL5	A.LYS_17	NZ	H.ASP_55	OD2	2.637
5TL5	A.LYS_17	NZ	H.ASP_57	OD1	2.990
5TL5	A.HIS_36	NE2	H.ASP_104	OD1	3.017
5TL5	A.HIS_36	NE2	H.ASP_104	OD2	2.947
5TL5	A.ARG_37	NH2	H.ASP_104	OD2	2.895
5TLJ	B.ARG_50	NH1	A.ASP_98	OD1	2.672
5TLJ	B.ARG_50	NH1	A.ASP_98	OD2	3.926
5TLJ	D.ARG_100	NH1	X.ASP_43	OD2	3.396
5TLJ	D.ARG_100	NH2	C.GLU_59	OE1	2.703
5TLJ	D.ARG_100	NH2	C.GLU_59	OE2	3.403
5TLJ	D.ARG_100	NH2	X.ASP_43	OD2	3.844
5TLJ	F.ARG_50	NH1	E.ASP_98	OD1	3.689
5TLJ	F.ARG_50	NH1	E.ASP_98	OD2	2.897
5TLJ	F.ARG_50	NH2	E.ASP_98	OD1	3.671
5TLJ	F.ARG_50	NH2	E.ASP_98	OD2	3.575
5TLJ	F.HIS_171	ND1	E.ASP_171	OD1	3.892
5TLJ	F.HIS_171	NE2	E.ASP_171	OD2	3.411
5TLJ	H.ARG_100	NH2	G.GLU_59	OE1	2.761
5TLJ	X.LYS_17	NZ	B.ASP_57	OD2	3.053
5TLJ	X.HIS_36	NE2	B.ASP_104	OD1	3.121
5TLJ	X.HIS_36	NE2	B.ASP_104	OD2	2.886
5TLK	B.ARG_50	NH1	A.ASP_98	OD1	3.277
5TLK	B.ARG_50	NH1	A.ASP_98	OD2	2.898
5TLK	B.ARG_50	NH2	A.ASP_98	OD1	2.923
5TLK	B.LYS_216	NZ	A.GLU_127	OE1	3.067
5TLK	B.LYS_216	NZ	A.GLU_127	OE2	3.588
5TLK	C.ARG_57	NH2	X.ASP_43	OD1	3.384
5TLK	D.ARG_100	NH1	X.ASP_43	OD2	2.904
5TLK	D.ARG_100	NH2	C.GLU_59	OE1	2.708

5TLK	D_ARG_100	NH2	C_GLU_59	OE2	3.299
5TLK	D_ARG_100	NH2	X_ASP_43	OD2	3.882
5TLK	F_ARG_50	NH1	E_ASP_98	OD1	3.086
5TLK	F_ARG_50	NH1	E_ASP_98	OD2	3.224
5TLK	F_ARG_50	NH2	E_ASP_98	OD1	2.767
5TLK	F_ARG_50	NH2	E_ASP_98	OD2	3.943
5TLK	G_ARG_33	NH1	Y_GLU_24	OE2	3.993
5TLK	G_ARG_33	NH2	Y_GLU_24	OE2	3.475
5TLK	H_ARG_100	NH1	G_GLU_59	OE1	3.531
5TLK	H_ARG_100	NH1	Y_ASP_43	OD2	3.423
5TLK	H_ARG_100	NH2	G_GLU_59	OE1	2.787
5TLK	H_ARG_100	NH2	G_GLU_59	OE2	3.306
5TLK	H_LYS_213	NZ	G_GLU_127	OE1	3.569
5TLK	X_LYS_17	NZ	B_ASP_55	OD1	3.914
5TLK	X_LYS_17	NZ	B_ASP_55	OD2	3.018
5TLK	X_LYS_17	NZ	B_ASP_57	OD2	3.114
5TLK	X_HIS_36	NE2	B_ASP_104	OD1	3.010
5TLK	X_HIS_36	NE2	B_ASP_104	OD2	2.891
5TLK	X_ARG_37	NH2	B_ASP_104	OD1	2.703
5TLK	Y_LYS_17	NZ	F_ASP_55	OD1	3.581
5TLK	Y_LYS_17	NZ	F_ASP_55	OD2	3.170
5TLK	Y_LYS_17	NZ	F_ASP_57	OD2	3.380
5TLK	Y_HIS_36	NE2	F_ASP_104	OD1	3.198
5TLK	Y_HIS_36	NE2	F_ASP_104	OD2	2.793
5TLK	Y_ARG_37	NH2	F_ASP_104	OD1	3.616
5TRU	h_HIS_169	NE2	L_ASP_168	OD2	3.995
5TZ2	H_ARG_101	NH1	C_ASP_46	OD2	3.182
5TZ2	H_HIS_105	NE2	C_ASP_51	OD1	2.798
5TZ2	H_HIS_105	NE2	C_ASP_51	OD2	2.654
5TZ2	C_LYS_56	NZ	H_ASP_55	OD1	3.222
5TZ2	C_LYS_56	NZ	H_ASP_55	OD2	2.489
5TZ2	C_LYS_56	NZ	H_ASP_57	OD2	3.354
5TZT	B_ARG_82	NH2	H_ASP_31	OD1	2.783
5TZT	B_ARG_82	NH2	H_ASP_31	OD2	3.806
5TZT	A_HIS_102	ND1	D_GLU_104	OE2	3.803
5TZT	L_LYS_55	NZ	C_GLU_104	OE1	3.704
5TZT	L_LYS_55	NZ	C_GLU_104	OE2	2.899
5TZT	H_HIS_102	ND1	C_GLU_104	OE1	2.856
5TZU	L_LYS_49	NZ	C_ASP_51	OD1	3.523
5TZU	L_LYS_49	NZ	C_ASP_51	OD2	2.772
5TZU	L_ARG_96	NH1	C_GLU_104	OE1	3.230
5TZU	L_ARG_96	NH1	C_GLU_104	OE2	3.808
5TZU	L_ARG_96	NH2	C_GLU_104	OE1	2.901
5TZU	H_LYS_214	NZ	L_GLU_123	OE1	2.584
5TZU	H_LYS_214	NZ	L_GLU_123	OE2	3.416
5TZU	C_LYS_39	NZ	L_ASP_31	OD1	3.076
5TZU	C_LYS_39	NZ	L_ASP_31	OD2	2.978
5U3J	H_ARG_52A	NH1	A_ASP_674	OD1	3.805
5U3J	H_ARG_52A	NH1	A_ASP_674	OD2	3.646
5U3J	H_ARG_52A	NH2	A_ASP_674	OD2	3.216
5U3J	H_LYS_52C	NZ	A_ASP_674	OD1	3.151
5U3J	H_LYS_52C	NZ	A_ASP_674	OD2	3.836
5U3J	H_LYS_209	NZ	L_GLU_123	OE1	3.171
5U3J	H_LYS_209	NZ	L_GLU_123	OE2	2.412
5U3N	H_ARG_52A	NH1	A_ASP_674	OD2	2.997
5U3N	H_ARG_52A	NH2	A_ASP_674	OD1	3.173
5U3N	H_ARG_52A	NH2	A_ASP_674	OD2	3.047
5U3N	H_ARG_100B	NH1	L_ASP_31	OD1	3.593

5U3N	H_ARG_100B	NH1	L_ASP_31	OD2	2.967
5U3N	H_ARG_100B	NH2	L_ASP_31	OD1	2.974
5U3N	H_ARG_100B	NH2	L_ASP_31	OD2	3.816
5U3N	H_LYS_209	NZ	L_GLU_123	OE1	3.254
5U3N	L_LYS_30	NZ	H_GLU_100E	OE1	3.899
5U3N	L_ARG_55	NH2	H_ASP_101	OD1	3.682
5U3N	L_ARG_55	NH2	H_ASP_101	OD2	2.901
5UCB	L_ARG_66	NH2	B_ASP_51	OD1	2.894
5UCB	B_ARG_144	NH2	L_ASP_91	OD1	2.844
5UCB	B_ARG_144	NH2	L_ASP_91	OD2	3.495
5UEA	X_LYS_10	NZ	D_GLU_29	OE1	3.740
5UEA	X_LYS_10	NZ	D_GLU_29	OE2	2.855
5UEA	X_LYS_71	NZ	D_GLU_29	OE2	3.320
5UEA	D_LYS_10	NZ	X_GLU_29	OE1	3.485
5UEA	D_LYS_10	NZ	X_GLU_29	OE2	2.490
5UEA	D_LYS_70	NZ	X_GLU_29	OE2	3.861
5UEK	A_ARG_145	NH2	L_ASP_91	OD1	2.787
5UEK	A_ARG_145	NH2	L_ASP_91	OD2	3.426
5UEK	L_ARG_66	NH2	A_ASP_52	OD1	2.873
5UG0	A_ARG_106	NH1	B_GLU_69	OE1	3.096
5UG0	A_ARG_106	NH1	B_GLU_69	OE2	3.964
5UG0	A_ARG_106	NH2	B_GLU_69	OE1	3.415
5UG0	A_ARG_106	NH2	B_GLU_69	OE2	3.059
5UG0	A_LYS_222	NZ	D_ASP_107	OD2	3.472
5UG0	A_ARG_311	NH1	B_ASP_90	OD1	2.840
5UG0	A_ARG_311	NH2	B_ASP_86	OD1	2.770
5UG0	A_ARG_311	NH2	B_ASP_90	OD1	3.313
5UG0	B_LYS_68	NZ	A_GLU_107	OE2	3.009
5UG0	D_ARG_100	NH1	A_ASP_190	OD1	3.522
5UG0	D_ARG_100	NH1	A_ASP_190	OD2	3.877
5UG0	D_HIS_178	NE2	C_ASP_169	OD2	3.490
5UG0	D_LYS_223	NZ	C_GLU_125	OE2	3.392
5UJZ	A_ARG_106	NH1	B_GLU_569	OE2	3.797
5UJZ	A_ARG_106	NH2	B_GLU_569	OE1	3.958
5UJZ	A_ARG_106	NH2	B_GLU_569	OE2	3.070
5UJZ	A_ARG_311	NH1	B_ASP_586	OD1	3.689
5UJZ	A_ARG_311	NH1	B_ASP_590	OD1	3.217
5UJZ	A_ARG_311	NH1	B_ASP_590	OD2	3.955
5UJZ	A_ARG_311	NH2	B_ASP_586	OD1	2.782
5UJZ	B_LYS_558	NZ	F_GLU_597	OE1	3.688
5UJZ	B_LYS_558	NZ	F_GLU_597	OE2	3.874
5UJZ	B_ARG_576	NH1	D_GLU_574	OE1	3.986
5UJZ	B_ARG_576	NH1	D_GLU_574	OE2	3.042
5UJZ	B_ARG_576	NH2	C_GLU_104	OE2	3.168
5UJZ	B_LYS_583	NZ	D_ASP_585	OD1	3.717
5UJZ	B_ARG_606	NH2	F_ASP_609	OD2	2.744
5UJZ	B_LYS_643	NZ	A_GLU_4	OE1	2.954
5UJZ	B_LYS_643	NZ	A_ASP_5	OD1	2.763
5UJZ	B_LYS_643	NZ	A_ASP_5	OD2	3.863
5UJZ	C_ARG_106	NH1	D_GLU_569	OE2	3.872
5UJZ	C_ARG_106	NH2	D_GLU_569	OE2	3.260
5UJZ	C_ARG_311	NH1	D_ASP_586	OD1	3.865
5UJZ	C_ARG_311	NH1	D_ASP_590	OD1	3.148
5UJZ	C_ARG_311	NH1	D_ASP_590	OD2	3.998
5UJZ	C_ARG_311	NH2	D_ASP_586	OD1	2.921
5UJZ	D_LYS_558	NZ	B_GLU_597	OE1	3.772
5UJZ	D_LYS_572	NZ	E_GLU_238	OE1	3.910
5UJZ	D_ARG_576	NH1	F_GLU_574	OE1	3.863

5UJZ	D_ARG_576	NH1	F_GLU_574	OE2	2.716
5UJZ	D_ARG_576	NH2	E_GLU_104	OE2	3.170
5UJZ	D_LYS_583	NZ	F_ASP_585	OD1	3.807
5UJZ	D_ARG_606	NH2	B_ASP_609	OD2	2.766
5UJZ	D_LYS_643	NZ	C_GLU_4	OE1	3.185
5UJZ	D_LYS_643	NZ	C_ASP_5	OD1	2.519
5UJZ	D_LYS_643	NZ	C_ASP_5	OD2	3.642
5UJZ	E_ARG_106	NH2	F_GLU_569	OE2	3.361
5UJZ	E_ARG_311	NH1	F_ASP_586	OD1	3.477
5UJZ	E_ARG_311	NH1	F_ASP_590	OD1	3.629
5UJZ	E_ARG_311	NH2	F_ASP_586	OD1	2.793
5UJZ	F_ARG_576	NH1	B_GLU_574	OE1	3.655
5UJZ	F_ARG_576	NH1	B_GLU_574	OE2	2.847
5UJZ	F_ARG_576	NH2	A_GLU_104	OE2	3.211
5UJZ	F_LYS_583	NZ	B_ASP_585	OD1	3.548
5UJZ	F_ARG_606	NH2	D_ASP_609	OD2	2.609
5UJZ	F_LYS_643	NZ	E_GLU_4	OE1	3.009
5UJZ	F_LYS_643	NZ	E_ASP_5	OD1	2.882
5UJZ	F_LYS_643	NZ	E_ASP_5	OD2	3.935
5UJZ	G_ARG_225	NH1	A_ASP_190	OD1	3.090
5UJZ	G_ARG_225	NH1	A_ASP_190	OD2	3.996
5UJZ	G_ARG_225	NH2	A_ASP_190	OD1	3.715
5UJZ	G_ARG_225	NH2	A_ASP_190	OD2	3.410
5UJZ	H_ARG_225	NH1	C_ASP_190	OD1	3.041
5UJZ	H_ARG_225	NH2	C_ASP_190	OD1	3.552
5UJZ	H_ARG_225	NH2	C_ASP_190	OD2	3.366
5UJZ	I_ARG_225	NH1	E_ASP_190	OD1	3.119
5UJZ	I_ARG_225	NH1	E_ASP_190	OD2	3.970
5UJZ	I_ARG_225	NH2	E_ASP_190	OD1	3.713
5UJZ	I_ARG_225	NH2	E_ASP_190	OD2	3.347
5UK0	A_ARG_106	NH1	B_GLU_569	OE2	3.967
5UK0	A_ARG_106	NH2	B_GLU_569	OE2	3.244
5UK0	A_ARG_220	NH2	C_ASP_241	OD1	3.711
5UK0	A_ARG_220	NH2	C_ASP_241	OD2	3.819
5UK0	A_ARG_311	NH1	B_ASP_590	OD1	3.139
5UK0	A_ARG_311	NH1	B_ASP_590	OD2	3.961
5UK0	A_ARG_311	NH2	B_ASP_586	OD1	3.197
5UK0	B_LYS_558	NZ	F_GLU_597	OE1	3.717
5UK0	B_LYS_568	NZ	A_GLU_107	OE2	3.962
5UK0	B_ARG_576	NH1	D_GLU_574	OE1	2.500
5UK0	B_ARG_576	NH1	D_GLU_574	OE2	3.431
5UK0	B_ARG_576	NH2	C_GLU_104	OE2	3.446
5UK0	B_ARG_576	NH2	D_GLU_574	OE1	3.430
5UK0	B_ARG_576	NH2	D_GLU_574	OE2	3.016
5UK0	B_ARG_606	NH2	F_ASP_609	OD2	2.765
5UK0	B_LYS_643	NZ	A_GLU_4	OE1	2.724
5UK0	B_LYS_643	NZ	A_ASP_5	OD1	2.705
5UK0	B_LYS_643	NZ	A_ASP_5	OD2	3.831
5UK0	C_ARG_106	NH1	D_GLU_569	OE2	3.998
5UK0	C_ARG_106	NH2	D_GLU_569	OE2	3.213
5UK0	C_ARG_220	NH2	E_ASP_241	OD1	3.755
5UK0	C_ARG_220	NH2	E_ASP_241	OD2	3.891
5UK0	C_ARG_311	NH1	D_ASP_586	OD1	3.901
5UK0	C_ARG_311	NH1	D_ASP_590	OD1	3.110
5UK0	C_ARG_311	NH1	D_ASP_590	OD2	3.851
5UK0	C_ARG_311	NH2	D_ASP_586	OD1	2.981
5UK0	D_LYS_558	NZ	B_GLU_597	OE1	3.800
5UK0	D_LYS_572	NZ	E_GLU_238	OE1	3.723

5UK0	D_ARG_576	NH1	F_GLU_574	OE1	2.823
5UK0	D_ARG_576	NH1	F_GLU_574	OE2	3.743
5UK0	D_ARG_576	NH2	E_GLU_104	OE2	3.003
5UK0	D_ARG_576	NH2	F_GLU_574	OE1	3.596
5UK0	D_ARG_576	NH2	F_GLU_574	OE2	3.278
5UK0	D_ARG_606	NH2	B_ASP_609	OD2	2.683
5UK0	D_LYS_643	NZ	C_GLU_4	OE1	2.844
5UK0	D_LYS_643	NZ	C_ASP_5	OD1	2.693
5UK0	D_LYS_643	NZ	C_ASP_5	OD2	3.673
5UK0	E_ARG_106	NH1	F_GLU_569	OE2	3.924
5UK0	E_ARG_106	NH2	F_GLU_569	OE2	3.130
5UK0	E_ARG_220	NH2	A_ASP_241	OD1	3.703
5UK0	E_ARG_220	NH2	A_ASP_241	OD2	3.860
5UK0	E_ARG_311	NH1	F_ASP_586	OD1	3.927
5UK0	E_ARG_311	NH1	F_ASP_590	OD1	3.174
5UK0	E_ARG_311	NH1	F_ASP_590	OD2	3.882
5UK0	E_ARG_311	NH2	F_ASP_586	OD1	3.095
5UK0	F_LYS_558	NZ	D_GLU_597	OE1	3.758
5UK0	F_LYS_568	NZ	E_GLU_107	OE2	3.989
5UK0	F_LYS_572	NZ	A_GLU_238	OE1	3.995
5UK0	F_ARG_576	NH1	B_GLU_574	OE1	2.515
5UK0	F_ARG_576	NH1	B_GLU_574	OE2	3.607
5UK0	F_ARG_576	NH2	A_GLU_104	OE2	3.281
5UK0	F_ARG_576	NH2	B_GLU_574	OE1	3.248
5UK0	F_ARG_576	NH2	B_GLU_574	OE2	3.003
5UK0	F_ARG_606	NH2	D_ASP_609	OD2	2.740
5UK0	F_LYS_643	NZ	E_GLU_4	OE1	2.987
5UK0	F_LYS_643	NZ	E_ASP_5	OD1	2.694
5UK0	F_LYS_643	NZ	E_ASP_5	OD2	3.721
5UK0	G_ARG_225	NH1	A_ASP_190	OD1	3.056
5UK0	G_ARG_225	NH1	A_ASP_190	OD2	3.844
5UK0	G_ARG_225	NH2	A_ASP_190	OD1	3.909
5UK0	G_ARG_225	NH2	A_ASP_190	OD2	3.442
5UK0	H_ARG_225	NH1	C_ASP_190	OD1	3.008
5UK0	H_ARG_225	NH1	C_ASP_190	OD2	3.873
5UK0	H_ARG_225	NH2	C_ASP_190	OD1	3.782
5UK0	H_ARG_225	NH2	C_ASP_190	OD2	3.377
5UK0	I_ARG_225	NH1	E_ASP_190	OD1	3.078
5UK0	I_ARG_225	NH1	E_ASP_190	OD2	3.875
5UK0	I_ARG_225	NH2	E_ASP_190	OD1	3.886
5UK0	I_ARG_225	NH2	E_ASP_190	OD2	3.433
5UK1	A_ARG_106	NH1	B_GLU_569	OE2	3.892
5UK1	A_ARG_106	NH2	B_GLU_569	OE2	2.755
5UK1	A_ARG_311	NH1	B_ASP_590	OD1	2.545
5UK1	A_ARG_311	NH1	B_ASP_590	OD2	3.367
5UK1	A_ARG_311	NH2	B_ASP_586	OD1	3.117
5UK1	B_LYS_558	NZ	F_GLU_597	OE1	3.470
5UK1	B_ARG_576	NH1	D_GLU_574	OE1	3.845
5UK1	B_ARG_576	NH1	D_GLU_574	OE2	3.273
5UK1	B_ARG_576	NH2	C_GLU_104	OE2	2.839
5UK1	B_ARG_606	NH2	F_ASP_609	OD2	3.320
5UK1	B_LYS_643	NZ	A_GLU_4	OE1	2.898
5UK1	B_LYS_643	NZ	A_ASP_5	OD1	2.632
5UK1	B_LYS_643	NZ	A_ASP_5	OD2	3.703
5UK1	C_ARG_106	NH2	D_GLU_569	OE2	3.108
5UK1	C_ARG_311	NH1	D_ASP_590	OD1	2.901
5UK1	C_ARG_311	NH1	D_ASP_590	OD2	3.798
5UK1	C_ARG_311	NH2	D_ASP_586	OD1	3.261

5UK1	D_LYS_558	NZ	B_GLU_597	OE1	3.543
5UK1	D_ARG_576	NH1	F_GLU_574	OE1	3.490
5UK1	D_ARG_576	NH1	F_GLU_574	OE2	3.058
5UK1	D_ARG_576	NH2	E_GLU_104	OE2	3.186
5UK1	D_ARG_606	NH2	B_ASP_609	OD2	3.177
5UK1	D_LYS_643	NZ	C_GLU_4	OE1	3.015
5UK1	D_LYS_643	NZ	C_ASP_5	OD1	2.615
5UK1	D_LYS_643	NZ	C_ASP_5	OD2	3.806
5UK1	E_ARG_106	NH2	F_GLU_569	OE2	2.991
5UK1	E_ARG_311	NH1	F_ASP_590	OD1	2.696
5UK1	E_ARG_311	NH1	F_ASP_590	OD2	3.637
5UK1	E_ARG_311	NH2	F_ASP_586	OD1	3.291
5UK1	F_LYS_558	NZ	D_GLU_597	OE1	3.566
5UK1	F_ARG_576	NH1	B_GLU_574	OE1	3.570
5UK1	F_ARG_576	NH1	B_GLU_574	OE2	3.065
5UK1	F_ARG_576	NH2	A_GLU_104	OE2	3.295
5UK1	F_ARG_606	NH2	D_ASP_609	OD2	3.182
5UK1	F_LYS_643	NZ	E_GLU_4	OE1	3.024
5UK1	F_LYS_643	NZ	E_ASP_5	OD1	2.503
5UK1	F_LYS_643	NZ	E_ASP_5	OD2	3.650
5UK1	G_ARG_225	NH1	A_ASP_190	OD1	2.887
5UK1	G_ARG_225	NH1	A_ASP_190	OD2	3.709
5UK1	G_ARG_225	NH2	A_ASP_190	OD1	3.956
5UK1	G_ARG_225	NH2	A_ASP_190	OD2	3.555
5UK1	H_ARG_225	NH1	C_ASP_190	OD1	2.683
5UK1	H_ARG_225	NH1	C_ASP_190	OD2	3.511
5UK1	H_ARG_225	NH2	C_ASP_190	OD1	3.809
5UK1	H_ARG_225	NH2	C_ASP_190	OD2	3.346
5UK1	I_ARG_225	NH1	E_ASP_190	OD1	2.885
5UK1	I_ARG_225	NH1	E_ASP_190	OD2	3.789
5UK1	I_ARG_225	NH2	E_ASP_190	OD1	3.888
5UK1	I_ARG_225	NH2	E_ASP_190	OD2	3.567
5UK2	A_ARG_106	NH1	B_GLU_569	OE2	3.935
5UK2	A_ARG_106	NH2	B_GLU_569	OE2	2.216
5UK2	A_ARG_311	NH1	B_ASP_586	OD1	3.877
5UK2	A_ARG_311	NH1	B_ASP_590	OD1	2.946
5UK2	A_ARG_311	NH1	B_ASP_590	OD2	3.729
5UK2	A_ARG_311	NH2	B_ASP_586	OD1	3.044
5UK2	B_LYS_558	NZ	F_GLU_597	OE1	3.672
5UK2	B_LYS_568	NZ	A_GLU_107	OE1	3.896
5UK2	B_ARG_576	NH1	D_GLU_574	OE1	3.949
5UK2	B_ARG_576	NH1	D_GLU_574	OE2	2.806
5UK2	B_ARG_576	NH2	C_GLU_104	OE2	3.501
5UK2	B_LYS_583	NZ	D_ASP_585	OD1	3.241
5UK2	B_LYS_583	NZ	D_ASP_585	OD2	3.954
5UK2	B_ARG_606	NH2	F_ASP_609	OD2	2.779
5UK2	B_LYS_643	NZ	A_GLU_4	OE1	3.076
5UK2	B_LYS_643	NZ	A_ASP_5	OD1	2.565
5UK2	B_LYS_643	NZ	A_ASP_5	OD2	3.717
5UK2	C_ARG_106	NH1	D_GLU_569	OE2	3.977
5UK2	C_ARG_106	NH2	D_GLU_569	OE2	2.287
5UK2	C_ARG_311	NH1	D_ASP_586	OD1	3.894
5UK2	C_ARG_311	NH1	D_ASP_590	OD1	2.932
5UK2	C_ARG_311	NH1	D_ASP_590	OD2	3.727
5UK2	C_ARG_311	NH2	D_ASP_586	OD1	3.043
5UK2	D_LYS_558	NZ	B_GLU_597	OE1	3.518
5UK2	D_LYS_558	NZ	B_GLU_597	OE2	3.929
5UK2	D_LYS_568	NZ	C_GLU_107	OE1	3.830

5UK2	D_ARG_576	NH1	F_GLU_574	OE1	3.823
5UK2	D_ARG_576	NH1	F_GLU_574	OE2	2.724
5UK2	D_ARG_576	NH2	E_GLU_104	OE2	3.539
5UK2	D_LYS_583	NZ	F_ASP_585	OD1	3.067
5UK2	D_LYS_583	NZ	F_ASP_585	OD2	3.783
5UK2	D_ARG_606	NH2	B_ASP_609	OD2	2.604
5UK2	D_LYS_643	NZ	C_GLU_4	OE1	3.112
5UK2	D_LYS_643	NZ	C_ASP_5	OD1	2.525
5UK2	D_LYS_643	NZ	C_ASP_5	OD2	3.631
5UK2	E_ARG_106	NH1	F_GLU_569	OE2	3.948
5UK2	E_ARG_106	NH2	F_GLU_569	OE2	2.300
5UK2	E_ARG_311	NH1	F_ASP_586	OD1	3.963
5UK2	E_ARG_311	NH1	F_ASP_590	OD1	2.962
5UK2	E_ARG_311	NH1	F_ASP_590	OD2	3.800
5UK2	E_ARG_311	NH2	F_ASP_586	OD1	3.154
5UK2	F_LYS_558	NZ	D_GLU_597	OE1	3.583
5UK2	F_LYS_558	NZ	D_GLU_597	OE2	3.900
5UK2	F_LYS_568	NZ	E_GLU_107	OE1	3.789
5UK2	F_ARG_576	NH1	B_GLU_574	OE1	3.881
5UK2	F_ARG_576	NH1	B_GLU_574	OE2	2.699
5UK2	F_ARG_576	NH2	A_GLU_104	OE2	3.688
5UK2	F_LYS_583	NZ	B_ASP_585	OD1	3.058
5UK2	F_LYS_583	NZ	B_ASP_585	OD2	3.745
5UK2	F_ARG_606	NH2	D_ASP_609	OD2	2.605
5UK2	F_LYS_643	NZ	E_GLU_4	OE1	3.293
5UK2	F_LYS_643	NZ	E_ASP_5	OD1	2.450
5UK2	F_LYS_643	NZ	E_ASP_5	OD2	3.677
5UK2	G_ARG_225	NH1	A_ASP_190	OD1	2.979
5UK2	G_ARG_225	NH1	A_ASP_190	OD2	3.894
5UK2	G_ARG_225	NH2	A_ASP_190	OD1	3.206
5UK2	G_ARG_225	NH2	A_ASP_190	OD2	2.785
5UK2	H_ARG_225	NH1	C_ASP_190	OD1	3.085
5UK2	H_ARG_225	NH2	C_ASP_190	OD1	3.195
5UK2	H_ARG_225	NH2	C_ASP_190	OD2	2.865
5UK2	I_ARG_225	NH1	E_ASP_190	OD1	2.888
5UK2	I_ARG_225	NH1	E_ASP_190	OD2	3.869
5UK2	I_ARG_225	NH2	E_ASP_190	OD1	3.014
5UK2	I_ARG_225	NH2	E_ASP_190	OD2	2.625
5UR8	A_ARG_59	NH1	B_ASP_95	OD1	3.084
5UR8	A_ARG_59	NH1	B_ASP_95	OD2	3.357
5UR8	A_LYS_138	NZ	B_GLU_215	OE2	2.961
5VL3	Q_HIS_213	NE2	H_GLU_58	OE2	3.352
5VL3	R_ARG_120	NH2	T_GLU_54	OE2	3.782
5VL3	R_LYS_127	NZ	T_GLU_54	OE1	2.927
5VL3	R_LYS_127	NZ	T_GLU_122	OE1	2.999
5VL3	R_HIS_213	NE2	A_GLU_58	OE2	3.157
5VL3	S_HIS_213	NE2	C_GLU_58	OE2	3.140
5VL3	T_LYS_127	NZ	R_GLU_54	OE1	3.658
5VL3	T_LYS_127	NZ	R_GLU_122	OE1	3.863
5VL3	T_HIS_213	NE2	E_GLU_58	OE2	3.636
5VL3	A_ARG_53	NH2	R_ASP_232	OD1	3.883
5VL3	A_ARG_53	NH2	R_ASP_232	OD2	3.340
5VL3	A_ARG_95	NH1	R_GLU_179	OE1	3.121
5VL3	A_ARG_95	NH1	R_GLU_179	OE2	3.607
5VL3	A_ARG_95	NH2	R_GLU_179	OE2	3.046
5VL3	A_LYS_210	NZ	B_GLU_124	OE2	3.976
5VL3	C_ARG_53	NH2	S_ASP_232	OD2	3.370
5VL3	C_ARG_95	NH1	S_GLU_179	OE1	3.505

5VL3	C_ARG_95	NH1	S_GLU_179	OE2	3.184
5VL3	C_ARG_95	NH2	S_GLU_179	OE2	3.815
5VL3	E_ARG_53	NH2	T_ASP_232	OD1	3.852
5VL3	E_ARG_53	NH2	T_ASP_232	OD2	3.470
5VL3	E_ARG_95	NH1	T_GLU_179	OE1	2.688
5VL3	E_ARG_95	NH1	T_GLU_179	OE2	2.993
5VL3	E_ARG_95	NH2	T_GLU_179	OE2	3.079
5VL3	E_LYS_210	NZ	F_GLU_	OE2	3.778
5VL3	E_LYS_	NZ	F_ASP_	OD2	3.984
5VL3	H_ARG_53	NH2	Q_ASP_232	OD1	3.950
5VL3	H_ARG_53	NH2	Q_ASP_232	OD2	3.411
5VL3	H_ARG_95	NH1	Q_GLU_179	OE1	3.431
5VL3	H_ARG_95	NH1	Q_GLU_179	OE2	3.819
5VL3	H_ARG_95	NH2	Q_GLU_179	OE2	3.149
5VL3	L_ARG_18	NH2	R_GLU_36	OE2	3.892
5VN8	G_LYS_34	NZ	A_ASP_612	OD1	3.263
5VN8	G_LYS_46	NZ	A_GLU_632	OE1	3.416
5VN8	G_LYS_46	NZ	A_GLU_632	OE2	2.866
5VN8	A_ARG_542	NH2	C_GLU_647	OE2	2.749
5VN8	A_ARG_579	NH1	C_GLU_584	OE1	3.931
5VN8	H_ARG_28	NH1	G_ASP_457	OD1	2.893
5VN8	L_HIS_49	ND1	H_ASP_101	OD1	3.097
5VN8	D_LYS_34	NZ	B_ASP_612	OD1	3.397
5VN8	D_LYS_46	NZ	B_GLU_632	OE1	3.407
5VN8	D_LYS_46	NZ	B_GLU_632	OE2	2.853
5VN8	B_ARG_542	NH2	A_GLU_647	OE1	3.985
5VN8	B_ARG_542	NH2	A_GLU_647	OE2	2.712
5VN8	B_ARG_579	NH1	A_GLU_584	OE1	3.986
5VN8	F_ARG_28	NH1	D_ASP_457	OD1	2.808
5VN8	J_HIS_49	ND1	F_ASP_101	OD1	3.213
5VN8	E_LYS_34	NZ	C_ASP_612	OD1	3.266
5VN8	E_LYS_46	NZ	C_GLU_632	OE1	3.380
5VN8	E_LYS_46	NZ	C_GLU_632	OE2	2.776
5VN8	C_ARG_542	NH2	B_GLU_647	OE2	2.738
5VN8	C_ARG_579	NH1	B_GLU_584	OE1	3.772
5VN8	I_ARG_28	NH1	E_ASP_457	OD1	3.234
5VN8	K_HIS_49	ND1	I_ASP_101	OD1	3.072
5VN8	K_HIS_49	NE2	I_ASP_101	OD1	3.981
5VXJ	B_ARG_19	NH2	A_ASP_97	OD1	2.652
5VXJ	B_ARG_50	NH1	I_GLU_200	OE1	2.921
5VXJ	B_ARG_50	NH2	I_GLU_200	OE1	3.757
5VXJ	B_LYS_76	NZ	A_GLU_122	OE1	2.874
5VXJ	B_HIS_80	NE2	A_ASP_144	OD1	3.165
5VXJ	B_HIS_80	NE2	A_ASP_144	OD2	3.364
5VXJ	D_ARG_19	NH1	C_ASP_97	OD1	3.252
5VXJ	D_ARG_50	NH1	E_GLU_200	OE1	3.721
5VXJ	D_ARG_50	NH2	E_GLU_200	OE1	3.781
5VXJ	D_LYS_76	NZ	C_GLU_122	OE1	3.854
5VXJ	D_HIS_80	NE2	C_ASP_144	OD1	3.067
5VXJ	D_HIS_80	NE2	C_ASP_144	OD2	3.196
5VXJ	E_LYS_137	NZ	F_ASP_73	OD1	3.543
5VXJ	E_LYS_137	NZ	F_ASP_73	OD2	2.771
5VXJ	F_ARG_19	NH2	E_ASP_97	OD1	2.921
5VXJ	F_ARG_50	NH1	G_GLU_200	OE1	3.576
5VXJ	F_ARG_50	NH2	G_GLU_200	OE1	2.702
5VXJ	F_LYS_76	NZ	E_GLU_122	OE1	3.693
5VXJ	F_HIS_80	NE2	E_ASP_144	OD1	3.009
5VXJ	F_HIS_80	NE2	E_ASP_144	OD2	3.134

5VXJ	G_LYS_137	NZ	H_ASP_73	OD1	3.131
5VXJ	G_LYS_137	NZ	H_ASP_73	OD2	2.336
5VXJ	H_ARG_19	NH2	G_ASP_97	OD1	2.467
5VXJ	H_LYS_76	NZ	G_ASP_124	OD2	3.951
5VXJ	H_HIS_80	NE2	G_ASP_144	OD1	3.186
5VXJ	H_HIS_80	NE2	G_ASP_144	OD2	3.321
5VXJ	I_LYS_137	NZ	J_ASP_73	OD1	3.804
5VXJ	I_LYS_137	NZ	J_ASP_73	OD2	2.902
5VXJ	J_ARG_19	NH2	I_ASP_97	OD1	2.772
5VXJ	J_LYS_76	NZ	I_GLU_122	OE2	2.338
5VXJ	J_HIS_80	NE2	I_ASP_144	OD1	3.036
5VXJ	J_HIS_80	NE2	I_ASP_144	OD2	3.151
5VXL	A_LYS_205	NZ	B_ASP_52	OD2	2.998
5VXL	B_ARG_102	NH1	A_GLU_201	OE1	3.097
5VXL	B_ARG_102	NH2	A_GLU_201	OE1	3.202
5VXL	B_ARG_102	NH2	A_GLU_201	OE2	2.871
5VXM	A_LYS_205	NZ	B_ASP_53	OD1	3.221
5VXM	A_LYS_205	NZ	B_ASP_53	OD2	3.090
5VXM	B_ARG_59	NH2	A_GLU_201	OE1	3.364
5VXR	H_LYS_214	NZ	L_GLU_123	OE2	2.932
5VZR	H_LYS_219	NZ	L_GLU_123	OE2	3.208
5VZR	L_ARG_96	NH2	H_ASP_100C	OD2	3.042
5VZR	A_LYS_219	NZ	B_GLU_123	OE1	3.381
5VZR	B_ARG_96	NH2	A_ASP_100C	OD2	2.983
5W9H	A_ARG_758	NH1	p_ASP_740	OD1	3.106
5W9H	A_ARG_1113	NH2	D_GLU_1105	OE1	3.583
5W9H	A_ARG_1179	NH2	B_ASP_31	OD1	2.752
5W9H	C_ARG_96	NH1	B_ASP_100C	OD2	2.859
5W9H	C_ARG_96	NH2	A_GLU_1183	OE1	3.871
5W9H	C_ARG_96	NH2	A_GLU_1183	OE2	2.827
5W9H	C_ARG_96	NH2	B_ASP_100C	OD2	2.885
5W9H	D_ARG_1113	NH1	G_GLU_1105	OE1	3.247
5W9H	F_ARG_96	NH1	E_ASP_100C	OD2	2.830
5W9H	F_ARG_96	NH2	E_ASP_100C	OD2	2.948
5W9H	G_ARG_758	NH1	r_ASP_740	OD1	2.922
5W9H	G_ARG_1113	NH2	A_GLU_1105	OE1	3.110
5W9H	G_ARG_1179	NH2	H_ASP_31	OD1	2.809
5W9H	I_ARG_96	NH1	H_ASP_100C	OD2	2.791
5W9H	I_ARG_96	NH2	G_GLU_1183	OE2	2.911
5W9H	I_ARG_96	NH2	H_ASP_100C	OD2	2.950
5W9H	p_HIS_681	NE2	D_ASP_910	OD1	2.819
5W9H	p_HIS_681	NE2	D_ASP_910	OD2	3.760
5W9H	r_HIS_681	NE2	A_ASP_910	OD1	2.850
5W9H	r_HIS_681	NE2	A_ASP_910	OD2	3.840
5W9I	A_ARG_758	NH1	B_ASP_740	OD1	2.830
5W9I	A_ARG_847	NH1	F_ASP_726	OD1	3.733
5W9I	A_ARG_847	NH1	F_ASP_726	OD2	2.884
5W9I	A_ARG_1113	NH2	I_GLU_1105	OE2	2.773
5W9I	A_ARG_1179	NH2	C_ASP_31	OD1	2.834
5W9I	B_HIS_681	NE2	I_ASP_910	OD1	2.801
5W9I	B_HIS_681	NE2	I_ASP_910	OD2	3.893
5W9I	D_ARG_96	NH1	C_ASP_100C	OD2	2.837
5W9I	D_ARG_96	NH2	A_GLU_1183	OE2	2.862
5W9I	D_ARG_96	NH2	C_ASP_100C	OD2	2.920
5W9I	E_ARG_758	NH1	F_ASP_740	OD1	2.820
5W9I	E_ARG_847	NH1	J_ASP_726	OD1	3.709
5W9I	E_ARG_847	NH1	J_ASP_726	OD2	2.881
5W9I	E_ARG_1179	NH2	G_ASP_31	OD1	2.831

5W9I	F_HIS_681	NE2	A_ASP_910	OD1	2.878
5W9I	F_HIS_681	NE2	A_ASP_910	OD2	3.982
5W9I	H_ARG_96	NH1	G_ASP_100C	OD2	2.856
5W9I	H_ARG_96	NH2	E_GLU_1183	OE2	2.871
5W9I	H_ARG_96	NH2	G_ASP_100C	OD2	2.925
5W9I	I_ARG_758	NH1	J_ASP_740	OD1	2.804
5W9I	I_ARG_847	NH1	B_ASP_726	OD1	3.716
5W9I	I_ARG_847	NH1	B_ASP_726	OD2	2.881
5W9I	I_ARG_1113	NH2	E_GLU_1105	OE2	2.821
5W9I	I_ARG_1179	NH2	K_ASP_31	OD1	2.785
5W9I	J_HIS_681	NE2	E_ASP_910	OD1	2.832
5W9I	L_ARG_96	NH1	K_ASP_100C	OD2	2.856
5W9I	L_ARG_96	NH2	I_GLU_1183	OE2	2.872
5W9I	L_ARG_96	NH2	K_ASP_100C	OD2	2.922
5W9J	D_ARG_1113	NH2	G_GLU_1105	OE1	3.627
5W9J	D_ARG_1113	NH2	G_GLU_1105	OE2	2.779
5W9J	F_ARG_96	NH1	E_ASP_100C	OD1	3.873
5W9J	F_ARG_96	NH1	E_ASP_100C	OD2	3.469
5W9J	A_ARG_1113	NH2	D_GLU_1105	OE1	3.626
5W9J	A_ARG_1113	NH2	D_GLU_1105	OE2	2.778
5W9J	C_ARG_96	NH1	B_ASP_100C	OD1	3.873
5W9J	C_ARG_96	NH1	B_ASP_100C	OD2	3.470
5W9J	G_ARG_1113	NH2	A_GLU_1105	OE1	3.626
5W9J	G_ARG_1113	NH2	A_GLU_1105	OE2	2.777
5W9J	I_ARG_96	NH1	H_ASP_100C	OD1	3.873
5W9J	I_ARG_96	NH1	H_ASP_100C	OD2	3.470
5W9K	A_ARG_758	NH1	J_ASP_740	OD1	3.054
5W9K	A_ARG_1113	NH2	D_GLU_1105	OE1	3.698
5W9K	C_ARG_96	NH1	B_ASP_100C	OD2	2.822
5W9K	C_ARG_96	NH2	A_GLU_1183	OE1	3.683
5W9K	C_ARG_96	NH2	B_ASP_100C	OD2	3.420
5W9K	D_ARG_847	NH2	A_GLU_1017	OE2	3.108
5W9K	D_ARG_1113	NH1	G_GLU_1105	OE2	3.336
5W9K	F_ARG_96	NH1	E_ASP_100C	OD2	2.856
5W9K	F_ARG_96	NH2	D_GLU_1183	OE2	3.059
5W9K	F_ARG_96	NH2	E_ASP_100C	OD2	3.317
5W9K	G_ARG_758	NH1	L_ASP_740	OD1	3.028
5W9K	G_ARG_758	NH2	L_ASP_740	OD1	3.483
5W9K	G_ARG_847	NH1	K_ASP_726	OD2	3.336
5W9K	G_ARG_1113	NH2	A_GLU_1105	OE2	3.565
5W9K	I_ARG_96	NH1	H_ASP_100C	OD2	2.828
5W9K	I_ARG_96	NH2	G_GLU_1183	OE2	3.651
5W9K	I_ARG_96	NH2	H_ASP_100C	OD2	3.553
5W9K	J_HIS_681	NE2	D_ASP_910	OD1	2.963
5W9K	J_ARG_700	NH2	A_GLU_756	OE2	2.841
5W9K	L_HIS_681	NE2	A_ASP_910	OD1	3.027
5W9K	L_HIS_681	NE2	A_ASP_910	OD2	3.875
5W9K	L_ARG_700	NH2	G_GLU_756	OE2	2.893
5W9L	A_ARG_758	NH1	B_ASP_740	OD1	2.964
5W9L	A_ARG_758	NH2	B_ASP_740	OD1	3.858
5W9L	A_ARG_1113	NH2	D_GLU_1105	OE1	3.448
5W9L	A_ARG_1113	NH2	D_GLU_1105	OE2	2.879
5W9L	F_ARG_96	NH1	E_ASP_100C	OD2	3.246
5W9L	F_ARG_96	NH2	D_GLU_1183	OE2	2.643
5W9L	F_ARG_96	NH2	E_ASP_100C	OD2	3.370
5W9L	G_ARG_758	NH1	J_ASP_740	OD1	2.859
5W9L	G_ARG_758	NH2	J_ASP_740	OD1	3.792
5W9L	G_ARG_1179	NH2	H_ASP_31	OD1	2.753

5W9L	L_ARG.96	NH1	H_ASP.100C	OD2	2.945
5W9L	L_ARG.96	NH2	H_ASP.100C	OD2	2.982
5W9L	B_HIS.681	NE2	D_ASP.910	OD1	2.803
5W9L	B_HIS.681	NE2	D_ASP.910	OD2	3.795
5W9L	B_ARG.700	NH1	A_GLU.756	OE2	2.893
5W9L	J_HIS.681	NE2	A_ASP.910	OD1	2.810
5W9L	J_HIS.681	NE2	A_ASP.910	OD2	3.815
5W9M	A_ARG.758	NH1	E_ASP.740	OD1	2.862
5W9M	A_ARG.758	NH2	E_ASP.740	OD1	2.970
5W9M	A_ARG.847	NH1	J_ASP.726	OD2	3.850
5W9M	C_ARG.96	NH1	B_ASP.100C	OD2	2.894
5W9M	C_ARG.96	NH2	A_GLU.1183	OE2	2.938
5W9M	C_ARG.96	NH2	B_ASP.100C	OD2	2.940
5W9M	D_ARG.847	NH1	A_GLU.1017	OE2	3.300
5W9M	D_ARG.847	NH2	A_GLU.1017	OE2	3.532
5W9M	G_ARG.758	NH1	J_ASP.740	OD1	2.816
5W9M	G_ARG.758	NH2	J_ASP.740	OD1	3.407
5W9M	G_ARG.1113	NH2	A_GLU.1105	OE1	3.823
5W9M	G_ARG.1113	NH2	A_GLU.1105	OE2	2.800
5W9M	G_ARG.1179	NH1	H_ASP.31	OD1	3.713
5W9M	L_ARG.96	NH1	H_ASP.100C	OD2	2.840
5W9M	L_ARG.96	NH2	G_GLU.1183	OE2	2.957
5W9M	L_ARG.96	NH2	H_ASP.100C	OD2	3.363
5W9M	E_HIS.681	NE2	D_ASP.910	OD1	2.869
5W9M	E_HIS.681	NE2	D_ASP.910	OD2	3.974
5W9M	E_ARG.700	NH2	A_GLU.756	OE1	3.024
5W9M	E_ARG.700	NH2	A_GLU.756	OE2	3.469
5W9M	F_HIS.681	NE2	G_ASP.910	OD1	2.934
5W9M	F_HIS.681	NE2	G_ASP.910	OD2	3.892
5W9M	J_HIS.681	NE2	A_ASP.910	OD1	3.021
5W9N	A_ARG.758	NH1	H_ASP.740	OD1	3.061
5W9N	A_ARG.758	NH2	H_ASP.740	OD1	3.534
5W9N	C_ARG.96	NH1	B_ASP.100C	OD2	2.860
5W9N	C_ARG.96	NH2	A_GLU.1183	OE2	2.942
5W9N	C_ARG.96	NH2	B_ASP.100C	OD2	3.629
5W9N	F_ARG.96	NH1	E_ASP.100C	OD2	2.898
5W9N	F_ARG.96	NH2	D_GLU.1183	OE2	3.465
5W9N	F_ARG.96	NH2	E_ASP.100C	OD2	3.359
5W9N	G_ARG.758	NH1	J_ASP.740	OD1	2.883
5W9N	G_ARG.758	NH2	J_ASP.740	OD1	3.992
5W9N	G_ARG.1113	NH2	A_GLU.1105	OE1	3.089
5W9N	H_HIS.681	NE2	D_ASP.910	OD1	2.909
5W9N	H_HIS.681	NE2	D_ASP.910	OD2	3.885
5W9N	J_HIS.681	NE2	A_ASP.910	OD1	2.923
5W9N	J_HIS.681	NE2	A_ASP.910	OD2	3.770
5W9O	A_ARG.758	NH1	J_ASP.740	OD1	2.989
5W9O	A_ARG.1113	NH2	D_GLU.1105	OE1	3.178
5W9O	A_ARG.1179	NH2	B_ASP.31	OD1	2.796
5W9O	C_ARG.96	NH1	B_ASP.100C	OD2	3.180
5W9O	C_ARG.96	NH2	B_ASP.100C	OD2	2.879
5W9O	D_ARG.847	NH1	J_ASP.726	OD2	2.979
5W9O	D_ARG.1113	NH1	G_GLU.1105	OE1	3.664
5W9O	F_ARG.96	NH1	E_ASP.100C	OD2	2.799
5W9O	F_ARG.96	NH2	D_GLU.1183	OE2	3.799
5W9O	F_ARG.96	NH2	E_ASP.100C	OD2	3.255
5W9O	G_ARG.758	NH1	L_ASP.740	OD1	2.934
5W9O	G_ARG.847	NH1	K_ASP.726	OD2	3.097
5W9O	G_ARG.1179	NH2	H_ASP.31	OD1	2.843

5W9O	L_ARG_96	NH1	H_ASP_100C	OD2	3.979
5W9O	L_ARG_96	NH2	G_GLU_1183	OE2	2.715
5W9O	L_ARG_96	NH2	H_ASP_100C	OD2	3.993
5W9O	J_HIS_681	NE2	D_ASP_910	OD1	2.932
5W9O	J_ARG_700	NH2	A_GLU_756	OE1	3.931
5W9O	J_ARG_700	NH2	A_GLU_756	OE2	2.914
5W9O	L_HIS_681	NE2	A_ASP_910	OD1	3.028
5W9O	L_HIS_681	NE2	A_ASP_910	OD2	3.886
5W9P	J_ARG_758	NH2	A_ASP_740	OD1	2.970
5W9P	J_ARG_847	NH1	C_ASP_726	OD1	3.573
5W9P	J_ARG_847	NH1	C_ASP_726	OD2	2.973
5W9P	J_ARG_1113	NH2	H_GLU_1105	OE1	3.990
5W9P	J_ARG_1113	NH2	H_GLU_1105	OE2	2.796
5W9P	J_ARG_1179	NH2	F_ASP_31	OD1	2.888
5W9P	A_HIS_681	NE2	H_ASP_910	OD1	3.149
5W9P	A_HIS_681	NE2	H_ASP_910	OD2	3.352
5W9P	A_ARG_691	NH2	H_GLU_818	OE2	2.969
5W9P	A_ARG_700	NH2	J_GLU_756	OE2	2.978
5W9P	G_ARG_1212	NH1	J_GLU_1183	OE2	3.421
5W9P	G_ARG_1212	NH2	J_GLU_1183	OE2	2.921
5W9P	G_ARG_1212	NH2	F_ASP_100C	OD2	2.848
5W9P	B_ARG_758	NH2	C_ASP_740	OD1	2.971
5W9P	B_ARG_847	NH1	I_ASP_726	OD1	3.572
5W9P	B_ARG_847	NH1	I_ASP_726	OD2	2.973
5W9P	B_ARG_1113	NH2	J_GLU_1105	OE1	3.989
5W9P	B_ARG_1113	NH2	J_GLU_1105	OE2	2.795
5W9P	B_ARG_1179	NH2	D_ASP_31	OD1	2.887
5W9P	C_HIS_681	NE2	J_ASP_910	OD1	3.149
5W9P	C_HIS_681	NE2	J_ASP_910	OD2	3.352
5W9P	C_ARG_691	NH2	J_GLU_818	OE2	2.970
5W9P	C_ARG_700	NH2	B_GLU_756	OE2	2.978
5W9P	E_ARG_1212	NH1	B_GLU_1183	OE2	3.420
5W9P	E_ARG_1212	NH2	B_GLU_1183	OE2	2.920
5W9P	E_ARG_1212	NH2	D_ASP_100C	OD2	2.848
5W9P	H_ARG_758	NH2	I_ASP_740	OD1	2.969
5W9P	H_ARG_847	NH1	A_ASP_726	OD1	3.572
5W9P	H_ARG_847	NH1	A_ASP_726	OD2	2.973
5W9P	H_ARG_1113	NH2	B_GLU_1105	OE1	3.989
5W9P	H_ARG_1113	NH2	B_GLU_1105	OE2	2.795
5W9P	H_ARG_1179	NH2	K_ASP_31	OD1	2.888
5W9P	I_HIS_681	NE2	B_ASP_910	OD1	3.149
5W9P	I_HIS_681	NE2	B_ASP_910	OD2	3.352
5W9P	I_ARG_691	NH2	B_GLU_818	OE2	2.970
5W9P	I_ARG_700	NH2	H_GLU_756	OE2	2.977
5W9P	L_ARG_1212	NH1	H_GLU_1183	OE2	3.420
5W9P	L_ARG_1212	NH2	H_GLU_1183	OE2	2.921
5W9P	L_ARG_1212	NH2	K_ASP_100C	OD2	2.848
5WK4	D_ARG_29	NH2	E_ASP_36	OD1	3.168
5WK4	D_ARG_29	NH2	E_ASP_36	OD2	3.056
5WK4	D_ARG_101	NH2	E_ASP_50	OD2	3.021
5WK4	A_HIS_174	NE2	D_GLU_65	OE2	2.738
5WK4	B_ARG_29	NH2	C_ASP_36	OD1	3.257
5WK4	B_ARG_29	NH2	C_ASP_36	OD2	2.944
5WK4	B_ARG_101	NH1	C_ASP_50	OD2	3.997
5WK4	B_ARG_101	NH2	C_ASP_50	OD2	2.811
5WK4	C_ARG_29	NH2	B_ASP_36	OD1	3.196
5WK4	C_ARG_29	NH2	B_ASP_36	OD2	3.146
5WK4	C_ARG_101	NH1	B_ASP_50	OD2	3.840

5WK4	C_ARG_101	NH2	B_ASP_50	OD2	2.874
5WK4	E_ARG_29	NH2	D_ASP_36	OD1	3.889
5WK4	E_ARG_101	NH2	D_ASP_50	OD2	2.922
5WKQ	A_ARG_135	NH1	B_ASP_212	OD1	3.924
5WKQ	A_ARG_135	NH2	B_ASP_212	OD1	3.057
5WKQ	B_HIS_207	ND1	A_GLU_131	OE1	3.383
5WKQ	B_HIS_207	ND1	A_GLU_131	OE2	2.652
5WNA	H_LYS_220	NZ	L_GLU_122	OE2	3.667
5WNA	H_LYS_225	NZ	L_ASP_121	OD1	3.706
5WNA	L_LYS_39	NZ	D_GLU_81	OE1	2.898
5WNA	L_LYS_39	NZ	D_GLU_81	OE2	2.887
5WNA	C_LYS_220	NZ	D_GLU_122	OE2	3.567
5WNA	D_LYS_39	NZ	L_GLU_81	OE1	3.744
5WNB	H_LYS_140	NZ	L_GLU_212	OE1	3.467
5WNB	H_LYS_140	NZ	L_GLU_212	OE2	3.708
5WNB	L_ARG_61	NH1	M_GLU_79	OE2	3.612
5XBM	A_LYS_205	NZ	B_ASP_139	OD1	3.654
5XBM	B_LYS_217	NZ	A_GLU_121	OE1	2.614
5XBM	B_LYS_217	NZ	A_GLU_121	OE2	3.625
5XBM	E_LYS_217	NZ	D_GLU_121	OE2	3.463
5XBM	F_ARG_77	NH1	D_ASP_31	OD1	3.188
5XBM	F_ARG_77	NH2	D_ASP_31	OD1	3.156
5XBM	F_ARG_77	NH2	D_ASP_31	OD2	3.938
5XBM	F_LYS_161	NZ	C_GLU_154	OE2	3.149
5XCQ	A_LYS_13	NZ	B_ASP_154	OD1	3.910
5XCQ	B_LYS_144	NZ	A_GLU_142	OE1	3.005
5XCQ	B_LYS_144	NZ	A_GLU_142	OE2	2.931
5XCR	A_LYS_13	NZ	B_ASP_154	OD1	3.316
5XCR	A_LYS_13	NZ	B_ASP_154	OD2	2.938
5XCR	A_ARG_147	NH2	B_GLU_135	OE2	3.104
5XCR	A_LYS_149	NZ	B_ASP_41	OD1	2.692
5XCR	A_LYS_149	NZ	B_ASP_41	OD2	3.682
5XCR	A_LYS_153	NZ	B_ASP_41	OD1	3.567
5XCR	A_LYS_153	NZ	B_ASP_41	OD2	3.385
5XCR	B_LYS_144	NZ	A_GLU_142	OE1	2.665
5XCR	B_LYS_144	NZ	A_GLU_142	OE2	3.686
5XCR	D_LYS_149	NZ	E_ASP_41	OD1	2.596
5XCR	D_LYS_149	NZ	E_ASP_41	OD2	3.537
5XCR	D_LYS_149	NZ	E_GLU_137	OE1	2.552
5XCR	D_LYS_149	NZ	E_GLU_137	OE2	3.483
5XCR	D_ARG_154	NH2	E_ASP_131	OD1	2.972
5XCR	E_LYS_144	NZ	D_GLU_142	OE1	2.644
5XCR	E_LYS_144	NZ	D_GLU_142	OE2	3.385
5XCS	A_LYS_43	NZ	B_GLU_140	OE2	2.517
5XCS	A_ARG_95	NH1	B_ASP_91	OD1	2.738
5XCS	A_ARG_95	NH1	B_ASP_91	OD2	3.741
5XCS	A_ARG_95	NH2	B_ASP_91	OD1	3.421
5XCS	A_ARG_95	NH2	C_ASP_7	OD1	3.700
5XCS	A_ARG_95	NH2	C_ASP_7	OD2	2.872
5XCS	A_LYS_100A	NZ	B_GLU_55	OE1	2.609
5XCS	A_LYS_100A	NZ	B_GLU_55	OE2	3.239
5XCS	A_LYS_149	NZ	B_GLU_137	OE1	3.069
5XCS	A_LYS_149	NZ	B_GLU_137	OE2	3.874
5XCS	B_HIS_94	NE2	C_ASP_7	OD2	3.772
5XCS	B_LYS_144	NZ	A_GLU_142	OE1	3.111
5XCS	B_LYS_144	NZ	A_GLU_142	OE2	3.511
5XCS	B_ARG_149	NH1	A_ASP_136	OD1	2.816
5XCT	B_LYS_144	NZ	A_GLU_142	OE1	2.822

5XCT	B.LYS_144	NZ	A_GLU_142	OE2	3.117
5XCU	A.LYS_13	NZ	B_ASP_154	OD2	3.098
5XCU	A_ARG_95	NH1	B_ASP_91	OD1	2.822
5XCU	A_ARG_95	NH1	B_ASP_91	OD2	3.880
5XCU	A_ARG_95	NH2	B_ASP_91	OD1	3.668
5XCU	A_ARG_95	NH2	C_ASP_7	OD1	3.592
5XCU	A_ARG_95	NH2	C_ASP_7	OD2	2.664
5XCU	A_LYS_100A	NZ	B_GLU_55	OE1	3.292
5XCU	A_LYS_100A	NZ	B_GLU_55	OE2	3.457
5XCU	A_LYS_149	NZ	B_GLU_137	OE1	3.142
5XCU	A_LYS_149	NZ	B_GLU_137	OE2	3.674
5XCU	B_HIS_94	NE2	C_ASP_7	OD2	3.530
5XCU	B_ARG_142	NH2	D_GLU_100	OE1	3.626
5XCU	B_ARG_142	NH2	D_GLU_100	OE2	3.496
5XCU	B.LYS_144	NZ	A_GLU_142	OE1	2.843
5XCU	B.LYS_144	NZ	A_GLU_142	OE2	2.719
5XCU	B_ARG_149	NH2	A_ASP_136	OD1	3.520
5XCU	D.LYS_13	NZ	E_ASP_154	OD2	2.965
5XCU	D_ARG_52A	NH1	A_GLU_144	OE1	3.014
5XCU	D_ARG_52A	NH1	A_GLU_144	OE2	3.323
5XCU	D_ARG_52A	NH2	A_GLU_144	OE2	3.086
5XCU	D_ARG_95	NH1	E_ASP_91	OD1	2.736
5XCU	D_ARG_95	NH1	E_ASP_91	OD2	3.660
5XCU	D_ARG_95	NH2	E_ASP_91	OD1	3.272
5XCU	D_ARG_95	NH2	F_ASP_7	OD1	3.878
5XCU	D_ARG_95	NH2	F_ASP_7	OD2	3.169
5XCU	D_LYS_100A	NZ	E_GLU_55	OE1	3.852
5XCU	D_LYS_100A	NZ	E_GLU_55	OE2	2.994
5XCU	D_LYS_149	NZ	E_GLU_137	OE1	2.785
5XCU	D_LYS_149	NZ	E_GLU_137	OE2	3.293
5XCU	E.LYS_30F	NZ	B_GLU_139	OE1	2.662
5XCU	E.LYS_30F	NZ	B_GLU_139	OE2	3.287
5XCU	E_HIS_94	NE2	F_ASP_7	OD2	3.551
5XCU	E_ARG_142	NH2	D_GLU_140	OE2	3.967
5XCU	E.LYS_144	NZ	D_GLU_142	OE1	3.438
5XCU	E.LYS_144	NZ	D_GLU_142	OE2	2.648
5XCV	A.LYS_56	NZ	C_GLU_10	OE2	3.165
5XCV	A.LYS_56	NZ	C_ASP_11	OD1	3.842
5XCV	A.LYS_56	NZ	C_ASP_11	OD2	2.877
5XCV	A_ARG_131	NH1	D_GLU_142	OE2	2.857
5XCV	A_ARG_131	NH2	D_GLU_142	OE2	3.651
5XCV	A.LYS_149	NZ	B_GLU_137	OE1	3.135
5XCV	A.LYS_149	NZ	B_GLU_137	OE2	2.706
5XCV	A_ARG_154	NH2	B_ASP_131	OD1	2.532
5XCV	B.LYS_144	NZ	A_GLU_142	OE1	2.798
5XCV	B.LYS_144	NZ	A_GLU_142	OE2	3.295
5XCV	B_ARG_149	NH2	A_ASP_136	OD1	3.863
5XCV	B_ARG_149	NH2	A_ASP_136	OD2	3.941
5XCV	D_ARG_131	NH1	A_GLU_142	OE2	2.791
5XCV	D_ARG_131	NH2	A_GLU_142	OE2	3.693
5XCV	D.LYS_149	NZ	E_GLU_137	OE1	2.622
5XCV	D.LYS_149	NZ	E_GLU_137	OE2	3.565
5XCV	D.LYS_153	NZ	E_GLU_40	OE2	3.944
5XCV	E.LYS_144	NZ	D_GLU_142	OE1	2.798
5XCV	E.LYS_144	NZ	D_GLU_142	OE2	3.738
5XRT	A.LYS_27	NZ	B_GLU_97	OE2	3.178
5XRT	A_ARG_109	NH1	B_GLU_67	OE2	3.059
5XRT	A_ARG_109	NH2	B_GLU_67	OE2	3.511

5XRT	A_LYS_238	NZ	F_GLU_72	OE1	3.452
5XRT	A_LYS_238	NZ	F_GLU_72	OE2	2.683
5XRT	A_ARG_269	NH1	B_GLU_67	OE1	3.465
5XRT	A_ARG_307	NH1	F_ASP_90	OD2	3.867
5XRT	A_ARG_307	NH2	F_ASP_90	OD2	3.590
5XRT	A_LYS_310	NZ	B_ASP_90	OD1	2.844
5XRT	A_LYS_326	NZ	B_GLU_11	OE1	2.808
5XRT	A_LYS_326	NZ	B_GLU_11	OE2	2.925
5XRT	B_ARG_54	NH1	F_GLU_97	OE2	3.836
5XRT	B_ARG_54	NH2	F_GLU_97	OE2	2.767
5XRT	B_LYS_62	NZ	F_ASP_86	OD1	3.336
5XRT	B_LYS_62	NZ	F_ASP_86	OD2	2.617
5XRT	B_LYS_62	NZ	F_ASP_90	OD1	3.654
5XRT	B_LYS_62	NZ	F_ASP_90	OD2	2.589
5XRT	B_HIS_64	NE2	F_ASP_79	OD2	3.582
5XRT	B_ARG_76	NH1	D_GLU_74	OE1	3.704
5XRT	B_ARG_76	NH1	D_GLU_74	OE2	3.032
5XRT	B_ARG_76	NH2	D_GLU_74	OE1	2.984
5XRT	B_ARG_76	NH2	D_GLU_74	OE2	3.801
5XRT	B_ARG_76	NH2	D_GLU_81	OE1	2.864
5XRT	B_ARG_76	NH2	D_GLU_81	OE2	3.722
5XRT	B_ARG_123	NH2	F_ASP_132	OD2	3.663
5XRT	B_ARG_124	NH1	F_ASP_132	OD2	2.812
5XRT	B_ARG_127	NH2	F_GLU_131	OE1	3.103
5XRT	B_ARG_163	NH1	F_GLU_131	OE1	3.194
5XRT	B_ARG_163	NH1	F_GLU_131	OE2	3.563
5XRT	B_ARG_163	NH2	F_GLU_131	OE1	3.596
5XRT	B_ARG_163	NH2	F_GLU_131	OE2	2.598
5XRT	B_ARG_170	NH2	D_GLU_128	OE1	3.449
5XRT	B_ARG_170	NH2	D_GLU_128	OE2	3.578
5XRT	C_LYS_27	NZ	D_GLU_97	OE1	3.926
5XRT	C_LYS_27	NZ	D_GLU_97	OE2	3.340
5XRT	C_ARG_109	NH1	D_GLU_67	OE2	2.932
5XRT	C_LYS_238	NZ	B_GLU_72	OE2	3.031
5XRT	C_ARG_269	NH1	D_GLU_67	OE1	3.251
5XRT	C_ARG_307	NH2	B_ASP_90	OD2	3.134
5XRT	C_LYS_310	NZ	D_ASP_90	OD1	3.206
5XRT	C_LYS_310	NZ	D_ASP_90	OD2	3.892
5XRT	D_ARG_54	NH2	B_GLU_97	OE2	3.066
5XRT	D_LYS_62	NZ	B_ASP_86	OD1	3.579
5XRT	D_LYS_62	NZ	B_ASP_86	OD2	3.058
5XRT	D_LYS_62	NZ	B_ASP_90	OD1	3.574
5XRT	D_LYS_62	NZ	B_ASP_90	OD2	2.797
5XRT	D_HIS_64	NE2	B_ASP_79	OD2	3.856
5XRT	D_ARG_76	NH1	F_GLU_74	OE1	3.338
5XRT	D_ARG_76	NH1	F_GLU_74	OE2	2.885
5XRT	D_ARG_76	NH2	F_GLU_74	OE1	2.652
5XRT	D_ARG_76	NH2	F_GLU_74	OE2	3.749
5XRT	D_ARG_76	NH2	F_GLU_81	OE1	2.506
5XRT	D_ARG_76	NH2	F_GLU_81	OE2	3.677
5XRT	D_ARG_123	NH2	B_ASP_132	OD2	3.975
5XRT	D_ARG_124	NH1	B_ASP_132	OD1	3.986
5XRT	D_ARG_124	NH1	B_ASP_132	OD2	2.717
5XRT	D_ARG_127	NH2	B_GLU_131	OE1	2.649
5XRT	D_ARG_163	NH1	B_GLU_131	OE1	3.152
5XRT	D_ARG_163	NH1	B_GLU_131	OE2	3.070
5XRT	D_ARG_163	NH2	B_GLU_131	OE1	3.267
5XRT	D_ARG_163	NH2	B_GLU_131	OE2	2.951

5XRT	D_ARG_170	NH2	F_GLU_128	OE1	2.950
5XRT	D_ARG_170	NH2	F_GLU_128	OE2	3.791
5XRT	E_LYS_27	NZ	F_GLU_97	OE1	3.896
5XRT	E_LYS_27	NZ	F_GLU_97	OE2	3.675
5XRT	E_ARG_109	NH1	F_GLU_67	OE2	2.719
5XRT	E_ARG_109	NH2	F_GLU_67	OE2	3.732
5XRT	E_LYS_238	NZ	D_GLU_72	OE2	3.742
5XRT	E_ARG_269	NH1	F_GLU_67	OE1	2.954
5XRT	E_ARG_269	NH1	F_GLU_67	OE2	3.996
5XRT	E_ARG_307	NH1	D_ASP_90	OD2	3.580
5XRT	E_ARG_307	NH2	D_ASP_90	OD2	3.837
5XRT	E_LYS_310	NZ	F_ASP_90	OD1	3.115
5XRT	E_LYS_326	NZ	F_GLU_11	OE1	3.300
5XRT	F_ARG_54	NH2	D_GLU_97	OE2	3.005
5XRT	F_LYS_62	NZ	D_ASP_86	OD1	3.549
5XRT	F_LYS_62	NZ	D_ASP_86	OD2	2.499
5XRT	F_LYS_62	NZ	D_ASP_90	OD1	3.666
5XRT	F_LYS_62	NZ	D_ASP_90	OD2	2.972
5XRT	F_HIS_64	NE2	D_ASP_79	OD2	3.194
5XRT	F_ARG_76	NH1	B_GLU_74	OE1	3.311
5XRT	F_ARG_76	NH1	B_GLU_74	OE2	3.105
5XRT	F_ARG_76	NH2	B_GLU_74	OE1	2.768
5XRT	F_ARG_76	NH2	B_GLU_74	OE2	3.989
5XRT	F_ARG_76	NH2	B_GLU_81	OE1	2.869
5XRT	F_ARG_76	NH2	B_GLU_81	OE2	3.812
5XRT	F_ARG_124	NH1	D_ASP_132	OD2	3.024
5XRT	F_ARG_127	NH2	D_GLU_131	OE1	2.415
5XRT	F_ARG_163	NH1	D_GLU_131	OE1	3.516
5XRT	F_ARG_163	NH2	D_GLU_131	OE1	3.296
5XRT	F_ARG_163	NH2	D_GLU_131	OE2	2.611
5XRT	F_ARG_170	NH2	B_GLU_128	OE1	3.475
5XRT	F_ARG_170	NH2	B_GLU_128	OE2	3.657
5XRT	F_LYS_174	NZ	B_ASP_160	OD1	3.902
5XRT	G_LYS_27	NZ	H_GLU_97	OE2	3.228
5XRT	G_LYS_82	NZ	E_GLU_119	OE1	3.805
5XRT	G_ARG_109	NH1	H_GLU_67	OE1	3.826
5XRT	G_ARG_109	NH1	H_GLU_67	OE2	2.804
5XRT	G_ARG_269	NH1	H_GLU_67	OE1	3.306
5XRT	G_LYS_299	NZ	H_GLU_69	OE2	3.918
5XRT	G_LYS_310	NZ	H_ASP_90	OD1	2.955
5XWD	A_ARG_353	NH2	D_ASP_96	OD2	3.335
5XWD	A_HIS_409	NE2	H_ASP_108	OD2	2.707
5XWD	A_LYS_443	NZ	D_ASP_51	OD2	2.907
5XWD	A_LYS_465	NZ	D_ASP_53	OD2	3.314
5YC5	A_LYS_409	NZ	B_ASP_399	OD1	3.635
5YC5	A_LYS_409	NZ	B_ASP_399	OD2	2.875
5YC5	A_LYS_439	NZ	B_ASP_356	OD1	3.309
5YC5	B_LYS_409	NZ	A_ASP_399	OD1	3.731
5YC5	B_LYS_409	NZ	A_ASP_399	OD2	2.920
5YC5	C_LYS_120	NZ	A_ASP_265	OD2	2.563
5YC5	C_LYS_131	NZ	A_GLU_269	OE1	3.549
5YC5	C_LYS_131	NZ	A_GLU_269	OE2	2.940
5ZV3	A_LYS_67	NZ	H_ASP_54	OD1	3.656
5ZV3	A_LYS_67	NZ	H_ASP_54	OD2	2.636
5ZV3	A_LYS_67	NZ	H_ASP_56	OD2	3.213
5ZV3	H_ARG_58	NH2	A_ASP_65	OD1	3.187
5ZV3	H_ARG_97	NH1	A_GLU_62	OE2	3.412
5ZV3	H_ARG_97	NH2	A_GLU_62	OE1	3.676

5ZV3	H_ARG_97	NH2	A_GLU_62	OE2	3.134
5ZV3	H_LYS_100	NZ	A_GLU_62	OE1	2.715
5ZV3	H_LYS_209	NZ	L_GLU_123	OE1	3.860
6A3V	E_ARG_193	NH1	C_ASP_184	OD1	3.333
6A3V	I_ARG_193	NH1	K_ASP_184	OD1	3.791
6A3V	U_ARG_193	NH1	W_ASP_184	OD1	2.218
6A3V	U_ARG_193	NH1	W_ASP_184	OD2	3.282
6A3V	U_ARG_193	NH2	W_ASP_184	OD1	3.966
6A3V	U_ARG_193	NH2	W_ASP_184	OD2	3.892
6A3W	C_LYS_107	NZ	E_ASP_30	OD2	3.465
6A3W	C_LYS_114	NZ	B_ASP_51	OD2	2.835
6A3W	C_ARG_134	NH2	A_ASP_55	OD2	3.122
6A3W	D_LYS_43	NZ	K_ASP_26	OD1	2.407
6A3W	D_LYS_43	NZ	K_ASP_26	OD2	3.696
6A3W	F_LYS_114	NZ	E_ASP_51	OD2	2.834
6A3W	F_ARG_134	NH2	D_ASP_55	OD1	3.962
6A3W	F_ARG_134	NH2	D_ASP_55	OD2	2.895
6A3W	I_LYS_114	NZ	H_ASP_51	OD2	2.757
6A3W	I_LYS_115	NZ	L_ASP_119	OD1	3.708
6A3W	I_LYS_115	NZ	L_ASP_119	OD2	3.946
6A3W	I_ARG_134	NH2	G_ASP_55	OD1	3.740
6A3W	I_ARG_134	NH2	G_ASP_55	OD2	2.630
6A3W	I_ARG_154	NH1	E_ASP_26	OD1	2.965
6A3W	I_ARG_154	NH2	E_ASP_26	OD1	3.042
6A3W	L_LYS_107	NZ	H_ASP_30	OD1	3.282
6A3W	L_LYS_107	NZ	H_ASP_30	OD2	2.525
6A3W	L_LYS_114	NZ	K_ASP_51	OD2	2.893
6A3W	L_ARG_134	NH2	J_ASP_55	OD1	3.749
6A3W	L_ARG_134	NH2	J_ASP_55	OD2	2.496
6A76	H_LYS_213	NZ	L_GLU_123	OE1	3.460
6A77	A_ARG_67	NH1	H_GLU_97	OE1	2.680
6A77	A_ARG_67	NH2	H_GLU_97	OE1	3.115
6A77	A_ARG_67	NH2	H_GLU_97	OE2	3.032
6A78	A_LYS_57	NZ	H_GLU_97	OE1	3.795
6A78	I_LYS_63	NZ	B_ASP_23	OD1	3.699
6A79	B_ARG_67	NH1	I_GLU_97	OE2	3.582
6AL5	A_LYS_155	NZ	H_GLU_74	OE1	3.542
6AL5	A_LYS_220	NZ	H_ASP_55	OD1	3.389
6AL5	A_LYS_220	NZ	H_ASP_55	OD2	2.832
6AL5	A_LYS_220	NZ	H_ASP_57	OD2	3.301
6AL5	H_ARG_106	NH2	L_ASP_54	OD1	3.142
6AL5	H_ARG_106	NH2	L_ASP_54	OD2	3.298
6AL5	H_LYS_220	NZ	L_GLU_127	OE1	3.220
6AND	H_LYS_209	NZ	L_GLU_123	OE1	2.684
6AND	H_LYS_209	NZ	L_GLU_123	OE2	3.876
6AND	L_LYS_50	NZ	H_ASP_100	OD1	3.188
6ANI	H_LYS_209	NZ	L_GLU_123	OE1	2.397
6ANI	I_LYS_209	NZ	M_GLU_123	OE2	3.950
6AQ7	H_HIS_34	NE2	A_GLU_199	OE1	3.934
6AQ7	H_HIS_34	NE2	A_GLU_199	OE2	2.717
6AQ7	H_ARG_49	NH1	A_GLU_199	OE2	2.744
6AQ7	H_LYS_209	NZ	L_GLU_127	OE2	2.651
6ATT	H_LYS_217	NZ	L_GLU_129	OE1	3.069
6ATT	H_LYS_222	NZ	L_ASP_128	OD1	2.688
6ATT	L_ARG_32	NH1	A_GLU_216	OE1	2.742
6AZZ	F_LYS_209	NZ	E_GLU_124	OE2	3.461
6AZZ	E_ARG_77	NH1	B_GLU_79	OE2	3.685
6AZZ	E_ARG_77	NH2	B_GLU_79	OE1	3.407

6AZZ	E_ARG_77	NH2	B_GLU_79	OE2	3.489
6AZZ	E_LYS_130	NZ	F_ASP_144	OD2	3.330
6AZZ	C_LYS_209	NZ	B_GLU_124	OE1	3.784
6AZZ	C_LYS_209	NZ	B_GLU_124	OE2	2.655
6AZZ	B_LYS_130	NZ	C_ASP_144	OD2	3.121
6AZZ	A_LYS_90	NZ	B_ASP_51	OD1	3.552
6AZZ	A_LYS_90	NZ	B_ASP_51	OD2	2.501
6AZZ	A_LYS_108	NZ	B_ASP_53	OD2	3.868
6AZZ	D_LYS_90	NZ	E_ASP_51	OD1	3.639
6AZZ	D_LYS_90	NZ	E_ASP_51	OD2	2.901
6B08	C_LYS_143	NZ	B_GLU_125	OE2	2.599
6B08	A_LYS_90	NZ	B_ASP_51	OD1	2.529
6B08	A_LYS_90	NZ	B_ASP_51	OD2	3.708
6B0E	B_HIS_164	ND1	A_ASP_167	OD2	3.677
6B0E	E_LYS_155	NZ	B_ASP_98	OD2	3.864
6B0G	D_ARG_100B	NH1	C_ASP_91	OD2	3.003
6B0G	D_ARG_100B	NH2	C_ASP_91	OD2	3.130
6B0G	D_LYS_214	NZ	C_GLU_123	OE2	3.176
6B0G	E_LYS_155	NZ	D_ASP_98	OD2	2.837
6BE2	H_LYS_154	NZ	L_GLU_129	OE2	2.747
6BE2	L_LYS_49	NZ	H_GLU_108	OE2	2.828
6BE2	L_ARG_100	NH2	H_ASP_98	OD1	2.914
6BE3	H_LYS_154	NZ	L_GLU_129	OE2	2.742
6BE3	H_LYS_220	NZ	L_GLU_128	OE1	3.265
6BE3	H_LYS_220	NZ	L_GLU_128	OE2	2.896
6BE3	L_LYS_49	NZ	H_GLU_108	OE2	2.860
6BE3	L_ARG_100	NH2	H_ASP_98	OD1	3.147
6BE3	L_ARG_100	NH2	H_ASP_109	OD1	3.865
6BE4	H_LYS_154	NZ	L_GLU_129	OE1	2.824
6BE4	L_ARG_100	NH2	H_ASP_98	OD1	3.253
6BE4	L_ARG_100	NH2	H_ASP_109	OD1	3.926
6BIT	I_HIS_35	NE2	H_GLU_54	OE1	3.340
6BIT	I_ARG_50	NH2	H_ASP_100	OD1	3.331
6BIT	I_ARG_50	NH2	H_ASP_101	OD1	3.135
6BIT	I_ARG_50	NH2	H_ASP_101	OD2	3.871
6BIT	I_LYS_59	NZ	H_ASP_100	OD1	3.680
6BIT	I_LYS_208	NZ	K_GLU_123	OE2	3.567
6BIT	I_ARG_213	NH1	L_ASP_143	OD1	3.423
6BIT	K_ARG_96	NH1	H_GLU_54	OE1	3.223
6BIT	K_ARG_96	NH2	H_GLU_54	OE1	2.904
6BIT	K_ARG_96	NH2	H_GLU_54	OE2	3.687
6BIT	H_LYS_53	NZ	I_ASP_52	OD1	3.518
6BIT	H_LYS_53	NZ	I_GLU_54	OE1	2.817
6BIT	H_LYS_96	NZ	I_ASP_52	OD2	2.786
6BIT	H_LYS_96	NZ	I_ASP_55	OD1	3.426
6BIT	H_LYS_96	NZ	I_ASP_55	OD2	2.655
6BIT	H_LYS_96	NZ	I_GLU_57	OE1	2.771
6BIT	J_HIS_35	NE2	G_GLU_54	OE1	3.221
6BIT	J_ARG_50	NH2	G_ASP_100	OD1	3.724
6BIT	J_ARG_50	NH2	G_ASP_101	OD1	3.330
6BIT	J_LYS_208	NZ	L_GLU_123	OE2	3.539
6BIT	L_ARG_96	NH1	G_GLU_54	OE1	3.007
6BIT	L_ARG_96	NH2	G_GLU_54	OE1	2.768
6BIT	L_ARG_96	NH2	G_GLU_54	OE2	3.419
6BIT	G_LYS_53	NZ	J_ASP_52	OD1	2.843
6BIT	G_LYS_53	NZ	J_ASP_52	OD2	3.656
6BIT	G_LYS_53	NZ	J_GLU_54	OE1	2.681
6BIT	G_LYS_96	NZ	J_ASP_52	OD2	2.719

6BIT	G.LYS_96	NZ	J_ASP_55	OD1	3.165
6BIT	G.LYS_96	NZ	J_ASP_55	OD2	2.701
6BIT	G.LYS_96	NZ	J_GLU_57	OE2	2.943
6BXA	A_ARG_37	NH1	C_GLU_101	OE1	3.957
6BXA	A_ARG_37	NH1	C_GLU_101	OE2	3.920
6BXA	A_ARG_37	NH2	C_GLU_101	OE1	3.689
6BXA	A_ARG_37	NH2	C_GLU_101	OE2	2.525
6BXA	A_LYS_77	NZ	C_ASP_34	OD2	2.860
6BXA	A_LYS_102	NZ	C_ASP_34	OD1	2.955
6BXA	A_LYS_184	NZ	B_ASP_133	OD2	2.709
6BXA	B_ARG_37	NH2	D_GLU_101	OE1	3.840
6BXA	B_ARG_37	NH2	D_GLU_101	OE2	2.839
6BXA	B_LYS_77	NZ	D_ASP_34	OD1	2.907
6BXA	B_LYS_102	NZ	D_ASP_34	OD2	3.845
6BXA	B_LYS_184	NZ	A_ASP_133	OD2	2.771
6BXC	A_LYS_184	NZ	C_ASP_34	OD2	3.851
6BXC	A_HIS_198	NE2	D_GLU_65	OE2	3.317
6BXC	B_LYS_159	NZ	D_ASP_34	OD2	3.891
6BXC	B_LYS_182	NZ	D_GLU_81	OE2	3.361
6BXC	B_LYS_184	NZ	D_ASP_34	OD2	3.547
6BXE	A_HIS_125	NE2	B_GLU_81	OE2	2.552
6BXE	B_HIS_125	NE2	A_GLU_81	OE2	3.833
6BZU	A_ARG_64	NH2	B_ASP_94	OD1	3.703
6BZU	A_LYS_209	NZ	B_GLU_123	OE2	3.980
6BZU	B_ARG_18	NH2	F_ASP_70	OD2	2.642
6BZU	B_ARG_24	NH1	F_ASP_76	OD1	3.597
6BZU	B_ARG_24	NH1	F_ASP_76	OD2	2.861
6BZU	C_ARG_64	NH2	D_ASP_94	OD1	3.618
6BZU	E_ARG_64	NH2	F_ASP_94	OD1	3.701
6BZU	F_ARG_24	NH1	B_ASP_76	OD1	3.333
6BZU	F_ARG_24	NH1	B_ASP_76	OD2	3.080
6BZU	G_ARG_64	NH2	H_ASP_94	OD1	3.197
6BZU	G_ARG_64	NH2	H_ASP_94	OD2	3.837
6BZU	G_LYS_209	NZ	H_GLU_123	OE1	2.734
6BZU	G_LYS_209	NZ	H_GLU_123	OE2	3.547
6BZV	E_ARG_66	NH1	C_GLU_85	OE2	3.540
6BZV	E_ARG_66	NH2	C_GLU_85	OE2	3.482
6BZV	E_LYS_206	NZ	G_ASP_208	OD2	3.271
6BZV	E_LYS_209	NZ	F_GLU_123	OE1	3.953
6BZV	E_LYS_209	NZ	F_GLU_123	OE2	2.713
6BZV	A_LYS_209	NZ	B_GLU_123	OE1	2.709
6BZV	A_LYS_209	NZ	B_GLU_123	OE2	3.439
6BZV	C_LYS_209	NZ	D_GLU_123	OE1	2.619
6BZV	C_LYS_209	NZ	D_GLU_123	OE2	2.945
6BZV	G_HIS_164	NE2	H_ASP_167	OD1	3.817
6BZV	G_LYS_209	NZ	H_GLU_123	OE1	3.054
6BZV	G_LYS_209	NZ	H_GLU_123	OE2	3.192
6BZW	C_LYS_209	NZ	D_GLU_123	OE1	2.857
6BZW	C_LYS_209	NZ	D_GLU_123	OE2	3.990
6BZW	D_ARG_18	NH2	H_GLU_93	OE1	3.070
6BZW	A_LYS_209	NZ	B_GLU_123	OE1	2.988
6BZW	E_LYS_209	NZ	F_GLU_123	OE1	2.583
6BZW	E_LYS_209	NZ	F_GLU_123	OE2	3.254
6BZW	G_LYS_209	NZ	H_GLU_123	OE1	2.709
6BZW	G_LYS_209	NZ	H_GLU_123	OE2	2.569
6C5H	H_LYS_208	NZ	L_GLU_123	OE1	3.569
6C5I	H_HIS_164	NE2	L_ASP_167	OD2	3.802
6C5I	H_LYS_208	NZ	L_GLU_123	OE1	3.192

6C5J	H_HIS_164	ND1	L_ASP_167	OD1	3.598
6C6X	B_LYS_207	NZ	A_GLU_133	OE1	3.861
6C6Y	R_LYS_400	NZ	L_ASP_28	OD2	3.363
6C6Y	R_LYS_543	NZ	L_GLU_55	OE2	2.973
6C6Y	S_LYS_400	NZ	B_ASP_28	OD1	3.764
6C6Y	S_LYS_400	NZ	B_ASP_28	OD2	2.712
6C6Y	S_LYS_543	NZ	B_GLU_55	OE2	3.134
6C6Z	A_ARG_542	NH1	C_GLU_95	OE1	3.387
6C6Z	A_ARG_542	NH1	C_GLU_95	OE2	2.704
6C6Z	A_ARG_542	NH2	C_GLU_95	OE1	2.635
6C6Z	A_ARG_542	NH2	C_GLU_95	OE2	3.577
6C6Z	B_ARG_542	NH1	H_GLU_95	OE1	3.238
6C6Z	B_ARG_542	NH1	H_GLU_95	OE2	2.770
6C6Z	B_ARG_542	NH2	H_GLU_95	OE1	2.578
6C6Z	B_ARG_542	NH2	H_GLU_95	OE2	3.689
6C6Z	C_LYS_209	NZ	D_GLU_123	OE1	2.970
6C6Z	C_LYS_209	NZ	D_GLU_123	OE2	3.150
6C6Z	C_LYS_214	NZ	D_ASP_122	OD2	2.844
6C6Z	D_HIS_27D	NE2	A_GLU_536	OE1	2.616
6C6Z	H_LYS_209	NZ	L_GLU_123	OE1	3.044
6C6Z	H_LYS_209	NZ	L_GLU_123	OE2	3.156
6C6Z	L_HIS_27D	NE2	B_GLU_536	OE1	2.931
6CUJ	B_LYS_404	NZ	A_GLU_292	OE1	3.957
6DC3	H_LYS_143	NZ	L_GLU_125	OE2	3.101
6DC3	H_LYS_209	NZ	L_GLU_124	OE1	3.719
6DC3	F_LYS_168	NZ	H_ASP_53	OD2	2.485
6DC4	H_LYS_209	NZ	L_GLU_123	OE1	3.056
6DC5	A_LYS_156	NZ	D_GLU_463	OE1	3.876
6DC5	A_LYS_399	NZ	G_GLU_497	OE2	2.871
6DC5	D_LYS_75	NZ	G_GLU_218	OE2	2.912
6DC5	D_LYS_209	NZ	E_GLU_53	OE2	3.142
6DC5	D_LYS_209	NZ	E_ASP_100G	OD2	3.755
6DC5	G_LYS_77	NZ	A_GLU_222	OE2	3.675
6DC5	G_LYS_209	NZ	H_GLU_53	OE2	3.533
6DC5	G_LYS_209	NZ	H_ASP_100G	OD2	3.715
6DC5	G_LYS_399	NZ	D_GLU_497	OE1	3.390
6DC5	G_LYS_399	NZ	D_GLU_497	OE2	2.804
6DC5	B_LYS_209	NZ	C_GLU_123	OE1	2.374
6DC5	B_LYS_209	NZ	C_GLU_123	OE2	3.312
6DC5	E_LYS_209	NZ	F_GLU_123	OE1	3.793
6DC5	H_LYS_	NZ	I_GLU_	OE1	2.846
6DC5	H_LYS_	NZ	I_ASP_	OD1	3.400
6DC5	H_LYS_	NZ	I_ASP_	OD2	3.825
6DCV	H_LYS_43	NZ	L_ASP_9	OD1	3.193
6DCV	H_LYS_221	NZ	L_GLU_123	OE1	3.166
6DCV	B_LYS_43	NZ	A_ASP_9	OD1	3.127
6DCV	B_LYS_221	NZ	A_GLU_123	OE1	3.096
6DCW	H_LYS_43	NZ	L_ASP_9	OD1	3.018
6DCW	T_LYS_317	NZ	H_ASP_54	OD1	3.849
6DCW	T_LYS_317	NZ	H_ASP_54	OD2	2.833
6DCW	T_LYS_317	NZ	H_ASP_56	OD2	2.597
6DDM	B_LYS_62	NZ	A_GLU_1	OE1	3.434
6DDM	B_LYS_62	NZ	A_GLU_1	OE2	2.992
6DDR	B_LYS_209	NZ	A_GLU_123	OE1	3.270
6DDV	B_LYS_209	NZ	A_GLU_123	OE1	3.050
6DDV	B_LYS_209	NZ	A_GLU_123	OE2	3.197
6DDV	C_ARG_226	NH1	B_ASP_31	OD1	3.652
6DDV	C_ARG_226	NH1	B_ASP_31	OD2	2.831

6DDV	C_ARG_226	NH2	B_ASP_31	OD1	3.123
6DDV	C_ARG_226	NH2	B_ASP_31	OD2	3.778
6DDV	A_LYS_50	NZ	C_ASP_255	OD1	3.063
6DDV	A_LYS_50	NZ	C_ASP_255	OD2	3.312
6DFG	B_HIS_585	NE2	A_GLU_492	OE2	3.210
6DFG	B_ARG_588	NH2	A_GLU_492	OE1	2.981
6DFG	B_ARG_588	NH2	A_GLU_492	OE2	3.149
6DFG	L_ARG_31	NH1	A_ASP_140	OD2	3.569
6DFG	L_ARG_54	NH2	A_ASP_322	OD2	3.922
6DFG	L_LYS_96	NZ	H_ASP_50	OD2	3.294
6DFG	E_HIS_585	NE2	C_GLU_492	OE2	3.225
6DFG	E_ARG_588	NH2	C_GLU_492	OE1	2.984
6DFG	E_ARG_588	NH2	C_GLU_492	OE2	3.072
6DFG	J_ARG_31	NH1	C_ASP_140	OD2	3.924
6DFG	J_LYS_96	NZ	G_ASP_50	OD2	3.096
6DFG	F_HIS_585	NE2	D_GLU_492	OE2	3.337
6DFG	F_ARG_588	NH2	D_GLU_492	OE1	2.974
6DFG	F_ARG_588	NH2	D_GLU_492	OE2	3.036
6DFG	K_ARG_31	NH1	D_ASP_140	OD2	3.732
6DFG	K_LYS_96	NZ	I_ASP_50	OD2	3.268
6DFH	A_LYS_137	NZ	L_ASP_51	OD2	2.491
6DFH	A_ARG_192	NH1	D_GLU_164	OE2	3.939
6DFH	B_ARG_542	NH1	E_GLU_647	OE2	2.777
6DFH	B_LYS_574	NZ	A_ASP_107	OD1	3.419
6DFH	B_LYS_574	NZ	A_ASP_107	OD2	3.383
6DFH	B_ARG_588	NH2	A_GLU_492	OE1	3.118
6DFH	B_ARG_588	NH2	A_GLU_492	OE2	3.874
6DFH	C_LYS_137	NZ	J_ASP_51	OD2	2.536
6DFH	C_ARG_192	NH1	A_GLU_164	OE2	3.905
6DFH	E_ARG_542	NH1	F_GLU_647	OE2	2.777
6DFH	E_LYS_574	NZ	C_ASP_107	OD1	3.423
6DFH	E_LYS_574	NZ	C_ASP_107	OD2	3.381
6DFH	E_ARG_588	NH2	C_GLU_492	OE1	3.158
6DFH	E_ARG_588	NH2	C_GLU_492	OE2	3.904
6DFH	D_LYS_137	NZ	K_ASP_51	OD2	2.448
6DFH	D_ARG_192	NH1	C_GLU_164	OE2	3.902
6DFH	F_ARG_542	NH1	B_GLU_647	OE2	2.778
6DFH	F_LYS_574	NZ	D_ASP_107	OD1	3.408
6DFH	F_LYS_574	NZ	D_ASP_107	OD2	3.378
6DFH	F_ARG_588	NH2	D_GLU_492	OE1	3.059
6DFH	F_ARG_588	NH2	D_GLU_492	OE2	3.839
6DG2	A_ARG_57	NH1	C_GLU_50	OE1	2.686
6DG2	A_ARG_57	NH1	C_GLU_50	OE2	3.712
6DG2	A_ARG_57	NH1	C_ASP_59	OD1	3.923
6DG2	A_ARG_57	NH2	C_GLU_50	OE1	3.412
6DG2	A_ARG_57	NH2	C_GLU_50	OE2	2.876
6DG2	A_LYS_219	NZ	B_ASP_123	OD1	3.620
6DG2	A_LYS_219	NZ	B_ASP_123	OD2	3.832
6DG2	C_ARG_57	NH1	A_GLU_50	OE1	3.739
6DG2	C_ARG_57	NH1	A_GLU_50	OE2	2.758
6DG2	C_ARG_57	NH1	A_ASP_59	OD1	3.719
6DG2	C_ARG_57	NH2	A_GLU_50	OE1	2.935
6DG2	C_ARG_57	NH2	A_GLU_50	OE2	3.488
6E62	P_LYS_413	NZ	H_ASP_100	OD1	3.190
6E62	P_LYS_413	NZ	H_ASP_100	OD2	2.736
6E62	P_LYS_416	NZ	L_ASP_51	OD2	2.614
6E62	H_ARG_97	NH1	P_ASP_347	OD2	3.575
6E62	H_LYS_143	NZ	L_GLU_124	OE2	2.458

6E62	H.LYS_209	NZ	L_GLU_123	OE1	3.996
6E62	H.LYS_209	NZ	L_GLU_123	OE2	3.607
6E62	A.LYS_413	NZ	B_ASP_100	OD1	3.041
6E62	A.LYS_413	NZ	B_ASP_100	OD2	2.916
6E62	A.LYS_416	NZ	C_ASP_51	OD2	2.944
6E62	B_ARG_83	NH1	H_GLU_1	OE1	3.696
6E62	B_ARG_83	NH1	H_GLU_1	OE2	3.867
6E62	B_ARG_83	NH2	H_GLU_1	OE1	3.783
6E62	B_ARG_83	NH2	H_GLU_1	OE2	3.983
6E62	B.LYS_143	NZ	C_GLU_124	OE2	2.797
6E62	C.LYS_156	NZ	L_GLU_81	OE2	3.985
6E63	P.LYS_413	NZ	H_ASP_100	OD1	3.187
6E63	P.LYS_413	NZ	H_ASP_100	OD2	2.904
6E63	P.LYS_416	NZ	L_ASP_51	OD1	3.564
6E63	P.LYS_416	NZ	L_ASP_51	OD2	2.955
6E63	H_ARG_97	NH1	P_ASP_347	OD2	3.407
6E63	H.LYS_143	NZ	L_GLU_124	OE2	2.665
6E63	H.LYS_209	NZ	L_GLU_123	OE1	2.498
6E63	L.LYS_17	NZ	B_GLU_85	OE1	3.318
6E63	L.LYS_17	NZ	B_GLU_85	OE2	3.250
6E63	A.LYS_413	NZ	B_ASP_100	OD1	2.369
6E63	A.LYS_413	NZ	B_ASP_100	OD2	3.029
6E63	A.LYS_416	NZ	C_ASP_51	OD2	3.236
6E63	B_ARG_83	NH1	L_GLU_13	OE1	3.486
6E63	B_ARG_83	NH1	L_GLU_13	OE2	2.814
6E63	B_ARG_97	NH1	A_ASP_347	OD1	3.859
6E64	H.LYS_143	NZ	L_GLU_124	OE2	2.942
6E64	H.LYS_209	NZ	L_GLU_123	OE2	2.774
6E64	A.LYS_209	NZ	B_GLU_123	OE1	3.569
6E64	A.LYS_209	NZ	B_GLU_123	OE2	2.777
6E65	H.LYS_209	NZ	L_GLU_123	OE1	2.900
6E65	H.LYS_209	NZ	L_GLU_123	OE2	3.402
6E8V	A.LYS_69	NZ	H_GLU_114	OE1	3.919
6E8V	A.LYS_69	NZ	H_GLU_114	OE2	3.267
6E8V	A.LYS_290	NZ	B_GLU_128	OE1	3.297
6E8V	A.LYS_290	NZ	B_GLU_128	OE2	3.454
6E8V	B.LYS_154	NZ	E_ASP_98	OD2	3.855
6E8V	E.LYS_290	NZ	F_GLU_128	OE1	2.548
6E8V	E.LYS_290	NZ	F_GLU_128	OE2	3.232
6E8V	H.LYS_290	NZ	L_GLU_127	OE1	2.706
6E8V	H.LYS_290	NZ	L_GLU_127	OE2	2.554
6E8V	J.LYS_290	NZ	K_GLU_128	OE1	3.173
6E8V	J.LYS_290	NZ	K_GLU_128	OE2	2.611
6E8V	K.LYS_212	NZ	H_GLU_101	OE1	3.767
6E8V	K.LYS_212	NZ	H_GLU_101	OE2	3.490
6E8V	O.HIS_129	NE2	L_ASP_61	OD1	3.511
6E8V	O.LYS_290	NZ	P_GLU_128	OE1	3.591
6E8V	U.LYS_290	NZ	V_GLU_128	OE1	2.346
6E8V	U.LYS_290	NZ	V_GLU_128	OE2	3.693
6E8V	Y.LYS_290	NZ	Z_GLU_128	OE1	3.390
6E8V	c.HIS_125	ND1	K_ASP_62	OD1	3.174
6E8V	c.HIS_125	ND1	K_ASP_62	OD2	3.139
6E8V	c.LYS_290	NZ	d_GLU_128	OE1	2.357
6E8V	c.LYS_290	NZ	d_GLU_128	OE2	3.486
6E9G	A.LYS_262	NZ	B_GLU_127	OE1	3.021
6E9G	A.LYS_262	NZ	B_GLU_127	OE2	3.870
6E9H	A.LYS_292	NZ	B_GLU_128	OE1	2.895
6E9H	A.LYS_292	NZ	B_GLU_128	OE2	3.744

6E9I	A_ARG_109	NH2	D_ASP_95	OD1	3.782
6E9I	A_ARG_109	NH2	D_ASP_95	OD2	3.931
6E9I	A_LYS_289	NZ	B_GLU_128	OE1	3.746
6E9I	A_LYS_289	NZ	B_GLU_128	OE2	2.925
6E9I	C_LYS_289	NZ	D_GLU_128	OE1	2.528
6E9I	C_LYS_289	NZ	D_GLU_128	OE2	3.968
6E9I	H_LYS_289	NZ	L_GLU_128	OE1	3.811
6E9I	H_LYS_289	NZ	L_GLU_128	OE2	2.547
6E9K	A_LYS_257	NZ	B_GLU_128	OE1	3.997
6E9K	A_LYS_257	NZ	B_GLU_128	OE2	3.056
6E9Q	A_LYS_253	NZ	B_GLU_128	OE1	3.048
6E9Q	A_LYS_253	NZ	B_GLU_128	OE2	2.978
6E9Q	E_LYS_253	NZ	F_GLU_128	OE1	2.966
6E9Q	E_LYS_253	NZ	F_GLU_128	OE2	2.802
6E9U	A_LYS_266	NZ	B_GLU_128	OE1	2.942
6E9U	A_LYS_266	NZ	B_GLU_128	OE2	2.747
6EDU	D_LYS_421	NZ	L_GLU_54	OE2	2.920
6EDU	D_LYS_432	NZ	L_GLU_55	OE1	3.655
6EDU	D_LYS_432	NZ	L_GLU_55	OE2	3.439
6EDU	E_LYS_421	NZ	N_GLU_54	OE2	3.004
6EDU	E_LYS_432	NZ	N_GLU_55	OE1	3.579
6EDU	E_LYS_432	NZ	N_GLU_55	OE2	3.398
6EDU	F_LYS_421	NZ	J_GLU_54	OE2	3.064
6EDU	F_LYS_432	NZ	J_GLU_55	OE1	3.805
6EDU	F_LYS_432	NZ	J_GLU_55	OE2	3.577
6EDU	G_LYS_22	NZ	F_GLU_102	OE1	3.040
6EDU	G_ARG_59	NH2	F_ASP_368	OD1	3.059
6EDU	H_LYS_22	NZ	E_GLU_102	OE1	3.174
6EDU	H_ARG_59	NH2	E_ASP_368	OD1	3.166
6EDU	I_LYS_22	NZ	D_GLU_102	OE1	3.053
6EDU	I_ARG_59	NH2	D_ASP_368	OD1	3.238
6EDU	P_LYS_107	NZ	F_GLU_91	OE1	3.324
6EDU	R_LYS_107	NZ	D_GLU_91	OE1	3.704
6EDU	T_LYS_107	NZ	E_GLU_91	OE1	3.475
6EJG	A_LYS_171	NZ	C_ASP_224	OD2	3.396
6EJG	A_LYS_171	NZ	C_ASP_226	OD2	2.901
6EJG	B_LYS_	NZ	D_ASP_	OD1	3.521
6EJG	B_LYS_	NZ	D_ASP_	OD2	2.547
6EJG	B_LYS_	NZ	D_ASP_	OD2	2.932
6EJM	A_HIS_204	ND1	B_GLU_152	OE2	3.786
6EK2	H_ARG_370	NH1	A_GLU_188	OE2	3.014
6EK2	H_ARG_370	NH2	A_GLU_188	OE1	3.920
6EK2	H_ARG_370	NH2	A_GLU_188	OE2	3.261
6EK2	I_ARG_370	NH1	B_GLU_188	OE1	2.817
6EK2	I_ARG_370	NH1	B_GLU_188	OE2	3.286
6EK2	I_ARG_370	NH2	B_GLU_188	OE1	3.837
6EK2	I_ARG_370	NH2	B_GLU_188	OE2	3.095
6EUN	A_LYS_87	NZ	B_GLU_47	OE1	3.058
6EUN	A_LYS_107	NZ	C_ASP_105	OD1	3.488
6EUN	A_LYS_167	NZ	C_ASP_165	OD1	3.883
6EUN	B_LYS_87	NZ	C_GLU_47	OE1	3.021
6EUN	B_LYS_107	NZ	A_ASP_105	OD1	3.579
6EUN	C_LYS_87	NZ	A_GLU_47	OE1	3.007
6EUN	C_LYS_107	NZ	B_ASP_105	OD1	3.525
6EUP	A_LYS_87	NZ	B_GLU_47	OE1	2.842
6EUP	A_LYS_87	NZ	B_ASP_79	OD1	3.786
6EUP	A_LYS_107	NZ	C_ASP_105	OD1	3.538
6EUP	B_LYS_87	NZ	C_GLU_47	OE1	2.811

6EUP	B.LYS_87	NZ	C_ASP_79	OD1	3.799
6EUP	B.LYS_107	NZ	A_ASP_105	OD1	3.723
6EUP	C.LYS_87	NZ	A_GLU_47	OE1	2.814
6EUP	C.LYS_87	NZ	A_ASP_79	OD1	3.752
6EUP	C.LYS_107	NZ	B_ASP_105	OD1	3.560
6EV1	A.LYS_213	NZ	B_GLU_122	OE1	3.565
6EV1	B_ARG_45	NH1	A_ASP_105	OD1	3.400
6EV1	E.LYS_213	NZ	F_GLU_122	OE2	3.696
6EV1	F_ARG_45	NH1	E_ASP_105	OD1	3.598
6EV1	G.LYS_213	NZ	H_GLU_122	OE2	3.127
6EV1	I.LYS_213	NZ	J_GLU_122	OE1	2.884
6EV1	I.LYS_213	NZ	J_GLU_122	OE2	3.812
6EV1	J_ARG_45	NH2	I_ASP_105	OD1	3.213
6EV1	J_ARG_45	NH2	I_ASP_105	OD2	3.457
6EV1	K_HIS_168	NE2	L_ASP_166	OD2	3.740
6EV1	K.LYS_213	NZ	L_GLU_122	OE1	3.450
6EV1	L_ARG_45	NH2	K_ASP_105	OD1	3.857
6EV2	A.LYS_213	NZ	B_GLU_122	OE1	3.442
6EV2	B_ARG_45	NH1	A_ASP_105	OD1	3.088
6EV2	B.LYS_168	NZ	F_GLU_78	OE2	2.948
6EV2	D.LYS_44	NZ	C_ASP_105	OD2	3.822
6EV2	D_ARG_45	NH1	C_ASP_105	OD1	3.142
6EV2	D.LYS_168	NZ	H_GLU_78	OE2	3.198
6EV2	E.LYS_213	NZ	F_GLU_122	OE1	3.493
6EV2	E.LYS_218	NZ	F_ASP_121	OD2	3.835
6EV2	F_ARG_45	NH1	E_ASP_105	OD1	2.818
6EV2	F.LYS_168	NZ	B_GLU_78	OE1	3.747
6EV2	G.LYS_210	NZ	A_ASP_73	OD1	3.883
6EV2	G.LYS_210	NZ	A_ASP_73	OD2	2.404
6EV2	G.LYS_213	NZ	H_GLU_122	OE1	3.330
6EV2	G.LYS_213	NZ	H_GLU_122	OE2	3.779
6EV2	H_ARG_45	NH1	G_ASP_105	OD1	3.108
6EV2	H.LYS_168	NZ	D_GLU_78	OE2	3.686
6EWB	D.HIS_417	NE2	L_GLU_80	OE2	3.932
6EWB	E_ARG_98	NH1	B_ASP_341	OD1	3.977
6EWB	E_ARG_98	NH2	B_ASP_341	OD1	3.813
6EWB	E_ARG_101	NH1	F_ASP_49	OD1	2.895
6EWB	E_ARG_101	NH1	F_ASP_49	OD2	3.620
6EWB	F_ARG_	NH1	E_ASP_	OD1	3.803
6EWB	F_ARG_	NH1	E_ASP_	OD2	3.536
6EWB	F.LYS_52	NZ	A_ASP_448	OD1	3.722
6EWB	F.LYS_52	NZ	A_ASP_448	OD2	2.304
6EWB	G_ARG_98	NH1	D_ASP_341	OD1	3.850
6EWB	G_ARG_98	NH2	D_ASP_341	OD1	3.731
6EWB	G_ARG_101	NH1	I_ASP_49	OD1	2.830
6EWB	G_ARG_101	NH1	I_ASP_49	OD2	3.797
6EWB	H_ARG_98	NH1	A_ASP_341	OD2	3.948
6EWB	H_ARG_98	NH2	A_ASP_341	OD2	3.896
6EWB	H_ARG_101	NH1	L_ASP_49	OD1	2.509
6EWB	H_ARG_101	NH1	L_ASP_49	OD2	3.441
6EWB	I_ARG_45	NH1	G_ASP_104	OD1	3.731
6EWB	I_ARG_45	NH1	G_ASP_104	OD2	3.636
6EWB	I.LYS_52	NZ	C_ASP_448	OD1	3.564
6EWB	I.LYS_52	NZ	C_ASP_448	OD2	2.694
6EWB	J_ARG_98	NH1	C_ASP_341	OD2	3.957
6EWB	J_ARG_98	NH2	C_ASP_341	OD2	3.467
6EWB	J_ARG_101	NH1	K_ASP_49	OD1	2.726
6EWB	J_ARG_101	NH1	K_ASP_49	OD2	3.581

6EWB	J_LYS_211	NZ	K_GLU_122	OE2	2.945
6EWB	K_ARG_45	NH1	J_ASP_104	OD2	3.826
6EWB	K_LYS_52	NZ	D_ASP_448	OD1	3.845
6EWB	K_LYS_52	NZ	D_ASP_448	OD2	2.608
6EWB	L_ARG_45	NH1	H_ASP_104	OD1	3.721
6EWB	L_ARG_45	NH1	H_ASP_104	OD2	3.560
6EWB	L_LYS_52	NZ	B_ASP_448	OD1	3.690
6EWB	L_LYS_52	NZ	B_ASP_448	OD2	2.585
6EWB	L_ARG_60	NH1	D_GLU_316	OE1	3.251
6EWB	L_ARG_60	NH1	D_GLU_316	OE2	3.266
6FAB	H_LYS_216	NZ	L_GLU_123	OE1	2.624
6FAB	H_LYS_216	NZ	L_GLU_123	OE2	2.770
6FAX	H_ARG_104	NH2	R_GLU_21	OE1	3.986
6FAX	H_HIS_173	NE2	L_ASP_167	OD1	3.928
6FAX	H_LYS_218	NZ	L_GLU_123	OE1	3.125
6FAX	H_LYS_218	NZ	L_GLU_123	OE2	3.415
6FN1	C_LYS_217	NZ	B_GLU_129	OE1	3.462
6FN1	C_LYS_217	NZ	B_GLU_129	OE2	2.375
6FN4	B_LYS_55	NZ	A_ASP_743	OD1	2.728
6FN4	B_LYS_55	NZ	A_ASP_743	OD2	3.540
6FN4	C_LYS_217	NZ	B_GLU_129	OE2	3.828
6GK7	H_LYS_43	NZ	L_ASP_9	OD1	3.203
6GK7	H_LYS_218	NZ	L_GLU_129	OE1	3.512
6GK7	H_LYS_218	NZ	L_GLU_129	OE2	3.016
6GK7	H_LYS_223	NZ	L_ASP_128	OD2	3.231
6GK7	A_LYS_317	NZ	H_ASP_55	OD2	2.761
6GK7	A_LYS_317	NZ	H_ASP_57	OD2	2.983
6GK8	H_ARG_59	NH2	L_ASP_65	OD1	3.295
6GK8	H_ARG_101	NH1	L_GLU_62	OE2	2.742
6GK8	H_ARG_101	NH2	L_GLU_62	OE2	3.142
6GK8	H_LYS_104	NZ	L_GLU_62	OE1	2.762
6GK8	H_LYS_104	NZ	L_GLU_62	OE2	3.928
6GK8	H_LYS_222	NZ	L_ASP_128	OD2	2.761
6GK8	L_ARG_32	NH1	L_GLU_57	OE2	3.709
6GK8	L_LYS_67	NZ	H_ASP_55	OD1	3.586
6GK8	L_LYS_67	NZ	H_ASP_55	OD2	3.183
6GK8	L_LYS_67	NZ	H_ASP_57	OD2	3.085
6H2Y	D_LYS_79	NZ	L_ASP_52	OD1	3.126
6H2Y	D_LYS_120	NZ	L_ASP_95	OD2	2.910
6H2Y	D_LYS_191	NZ	L_ASP_50	OD2	2.715
6H2Y	H_ARG_56	NH2	D_GLU_58	OE1	3.564
6H2Y	H_ARG_56	NH2	D_GLU_58	OE2	3.905
6H2Y	H_LYS_215	NZ	L_GLU_125	OE1	3.261
6H2Y	H_LYS_215	NZ	L_GLU_125	OE2	2.865
6H2Y	L_ARG_92	NH1	D_ASP_166	OD2	3.217
6H2Y	L_ARG_92	NH2	D_GLU_119	OE1	3.274
6H2Y	L_ARG_92	NH2	D_GLU_119	OE2	3.244
6H2Y	L_ARG_92	NH2	D_ASP_166	OD1	3.891
6H2Y	L_ARG_92	NH2	D_ASP_166	OD2	2.328
6I3Z	A_LYS_201	NZ	L_ASP_92	OD1	3.556
6I3Z	A_LYS_290	NZ	H_ASP_33	OD1	3.699
6I3Z	L_ARG_53	NH1	A_GLU_204	OE1	2.383
6I3Z	L_ARG_53	NH1	A_GLU_204	OE2	3.516
6IAP	D_ARG_96	NH2	A_GLU_80	OE1	3.466
6IAP	E_HIS_35	NE2	A_GLU_80	OE1	3.445
6IAP	H_ARG_99	NH2	A_ASP_98	OD1	2.689
6IAP	L_ARG_94	NH1	H_GLU_50	OE2	2.973
6IAP	L_ARG_94	NH2	A_ASP_123	OD2	3.888

6JMQ	C.HIS_169	NE2	D.ASP_173	OD2	3.860
6JMQ	C.LYS_213	NZ	D.GLU_129	OE1	3.825
6JMR	C.HIS_169	NE2	D.ASP_173	OD1	3.922
6K7O	A.LYS_55	NZ	H.ASP_106	OD1	3.027
6K7O	A.ARG_78	NH1	L.ASP_94	OD1	3.792
6K7O	A.ARG_78	NH2	L.ASP_94	OD1	2.709
6K7O	B.LYS_218	NZ	C.GLU_127	OE1	3.816
6K7O	B.LYS_218	NZ	C.GLU_127	OE2	2.813
6K7O	B.LYS_223	NZ	C.ASP_126	OD1	2.273
6K7O	B.LYS_223	NZ	C.ASP_126	OD2	2.907
6K7O	D.LYS_215	NZ	G.ASP_189	OD2	2.832
6K7O	D.LYS_218	NZ	E.GLU_127	OE1	2.290
6K7O	D.LYS_218	NZ	E.GLU_127	OE2	3.074
6K7O	D.LYS_223	NZ	E.ASP_126	OD1	3.765
6K7O	D.LYS_223	NZ	E.ASP_126	OD2	3.552
6K7O	F.HIS_173	NE2	G.ASP_171	OD2	3.941
6K7O	G.ARG_51	NH2	F.ASP_106	OD2	3.980
6K7O	H.HIS_173	NE2	L.ASP_171	OD2	3.862
6K7O	H.LYS_218	NZ	L.GLU_127	OE1	3.981
6K7O	H.LYS_223	NZ	L.ASP_126	OD1	3.964
6K7O	P.LYS_55	NZ	B.ASP_106	OD1	3.340
6K7O	P.ARG_78	NH1	C.ASP_94	OD1	2.583
6K7O	P.ARG_78	NH2	C.ASP_94	OD1	2.609
6K7O	R.LYS_55	NZ	F.ASP_106	OD1	2.834
6K7O	Q.LYS_55	NZ	D.ASP_106	OD1	3.172
6K7O	Q.ARG_59	NH1	H.GLU_221	OE1	3.018
6K7O	Q.ARG_59	NH1	H.GLU_221	OE2	3.413
6K7O	Q.ARG_59	NH2	H.GLU_221	OE1	3.299
6K7O	Q.ARG_59	NH2	H.GLU_221	OE2	2.855
6K7O	Q.ARG_78	NH1	E.ASP_94	OD1	3.546
6K7O	Q.ARG_78	NH2	E.ASP_94	OD1	2.499
6KN9	A.ARG_281	NH1	D.ASP_111	OD1	2.228
6KN9	A.ARG_281	NH1	D.ASP_111	OD2	3.976
6KN9	B.ARG_281	NH2	E.ASP_111	OD1	2.487
6KN9	B.ARG_281	NH2	E.ASP_111	OD2	3.660
6KN9	C.ARG_281	NH2	F.ASP_111	OD2	3.907
6MHR	E.ARG_91	NH1	D.GLU_50	OE1	3.108
6MHR	E.ARG_91	NH1	D.ASP_98	OD2	3.892
6MHR	E.ARG_91	NH2	D.GLU_50	OE1	3.238
6MHR	E.ARG_91	NH2	D.GLU_50	OE2	3.082
6MHR	A.LYS_217	NZ	B.GLU_125	OE2	2.775
6MHR	B.ARG_91	NH1	A.GLU_50	OE1	3.086
6MHR	B.ARG_91	NH1	A.GLU_50	OE2	3.775
6MHR	B.ARG_91	NH1	A.ASP_98	OD2	3.351
6MHR	B.ARG_91	NH2	A.GLU_50	OE1	3.608
6MHR	B.ARG_91	NH2	A.GLU_50	OE2	2.934
6MI2	F.LYS_114	NZ	E.ASP_50	OD1	2.776
6MI2	F.LYS_114	NZ	E.ASP_50	OD2	3.977
6MI2	F.ARG_134	NH2	D.ASP_55	OD2	3.507
6MI2	C.LYS_114	NZ	B.ASP_50	OD1	3.683
6MI2	C.LYS_114	NZ	B.ASP_50	OD2	2.434
6MN7	B.ARG_542	NH1	F.GLU_647	OE2	3.229
6MN7	B.LYS_574	NZ	A.ASP_107	OD1	3.285
6MN7	B.LYS_574	NZ	A.ASP_107	OD2	3.696
6MN7	B.ARG_579	NH2	F.GLU_584	OE1	2.844
6MN7	B.ARG_579	NH2	F.GLU_584	OE2	3.533
6MN7	E.ARG_542	NH1	B.GLU_647	OE2	3.076
6MN7	E.LYS_574	NZ	C.ASP_107	OD1	3.286

6MN7	E_LYS_574	NZ	C_ASP_107	OD2	3.697
6MN7	E_ARG_579	NH2	B_GLU_584	OE1	2.796
6MN7	E_ARG_579	NH2	B_GLU_584	OE2	3.568
6MN7	F_ARG_542	NH1	E_GLU_647	OE2	3.126
6MN7	F_LYS_574	NZ	D_ASP_107	OD1	3.285
6MN7	F_LYS_574	NZ	D_ASP_107	OD2	3.696
6MN7	F_ARG_579	NH2	E_GLU_584	OE1	2.859
6MN7	F_ARG_579	NH2	E_GLU_584	OE2	3.579
6MPG	U_ARG_542	NH2	D_GLU_647	OE1	3.141
6MPG	U_ARG_542	NH2	D_GLU_647	OE2	2.524
6MPG	U_ARG_579	NH2	D_GLU_584	OE1	2.488
6MPG	V_LYS_229	NZ	B_ASP_1	OD1	2.776
6MPG	W_HIS_105	NE2	B_GLU_61	OE2	3.652
6MPG	n_ARG_94	NH1	V_ASP_321A	OD1	3.878
6MPG	2_LYS_229	NZ	4_ASP_1	OD1	2.776
6MPG	3_HIS_105	NE2	4_GLU_61	OE2	3.651
6MPG	6_ARG_94	NH1	2_ASP_321A	OD1	3.878
6MPG	A_ARG_542	NH2	U_GLU_647	OE1	3.132
6MPG	A_ARG_542	NH2	U_GLU_647	OE2	2.525
6MPG	A_ARG_579	NH2	U_GLU_584	OE1	2.474
6MPG	C_LYS_229	NZ	Y_ASP_1	OD1	2.776
6MPG	D_ARG_542	NH2	A_GLU_647	OE1	3.137
6MPG	D_ARG_542	NH2	A_GLU_647	OE2	2.533
6MPG	D_ARG_579	NH2	A_GLU_584	OE1	2.479
6MPG	N_ARG_94	NH1	C_ASP_321A	OD1	3.878
6MPG	X_HIS_105	NE2	Y_GLU_61	OE2	3.651
6MPH	1_LYS_31A	NZ	A_GLU_87	OE1	2.457
6MPH	1_LYS_31A	NZ	A_GLU_87	OE2	3.919
6MPH	2_ARG_96	NH1	1_GLU_95	OE1	3.340
6MPH	2_ARG_96	NH1	1_GLU_95	OE2	2.522
6MPH	3_LYS_31A	NZ	B_GLU_87	OE1	2.448
6MPH	3_LYS_31A	NZ	B_GLU_87	OE2	3.973
6MPH	4_ARG_96	NH1	3_GLU_95	OE1	3.339
6MPH	4_ARG_96	NH1	3_GLU_95	OE2	2.507
6MPH	6_ARG_542	NH1	E_GLU_647	OE2	3.863
6MPH	6_ARG_542	NH2	E_GLU_647	OE1	3.449
6MPH	6_ARG_542	NH2	E_GLU_647	OE2	2.484
6MPH	6_ARG_579	NH2	E_GLU_584	OE1	2.833
6MPH	A_LYS_282	NZ	f_ASP_114	OD1	3.470
6MPH	A_LYS_282	NZ	f_ASP_114	OD2	3.288
6MPH	A_ARG_327	NH2	X_GLU_100I	OE1	3.876
6MPH	B_LYS_282	NZ	g_ASP_114	OD1	3.432
6MPH	B_LYS_282	NZ	g_ASP_114	OD2	3.289
6MPH	B_ARG_327	NH2	Y_GLU_100I	OE1	3.899
6MPH	C_LYS_282	NZ	Q_ASP_114	OD1	3.383
6MPH	C_LYS_282	NZ	Q_ASP_114	OD2	3.272
6MPH	C_ARG_327	NH2	M_GLU_100I	OE1	3.872
6MPH	D_ARG_542	NH1	6_GLU_647	OE2	3.853
6MPH	D_ARG_542	NH2	6_GLU_647	OE1	3.460
6MPH	D_ARG_542	NH2	6_GLU_647	OE2	2.476
6MPH	D_ARG_579	NH2	6_GLU_584	OE1	2.760
6MPH	E_ARG_542	NH1	D_GLU_647	OE2	3.888
6MPH	E_ARG_542	NH2	D_GLU_647	OE1	3.465
6MPH	E_ARG_542	NH2	D_GLU_647	OE2	2.463
6MPH	E_ARG_579	NH2	D_GLU_584	OE1	2.789
6MPH	H_LYS_31A	NZ	C_GLU_87	OE1	2.458
6MPH	H_LYS_31A	NZ	C_GLU_87	OE2	3.969
6MPH	L_ARG_96	NH1	H_GLU_95	OE1	3.309

6MPH	L_ARG_96	NH1	H_GLU_95	OE2	2.530
6MPH	N_ARG_94	NH1	C_ASP_321A	OD1	3.859
6MPH	Q_ARG_72	NH2	C_ASP_368	OD2	3.534
6MPH	Z_ARG_94	NH1	A_ASP_321A	OD1	3.890
6MPH	a_ARG_94	NH1	B_ASP_321A	OD1	3.861
6MPH	f_ARG_72	NH2	A_ASP_368	OD2	3.577
6MPH	g_ARG_72	NH2	B_ASP_368	OD2	3.570
6MQC	A_ARG_	NH1	B_ASP_	OD1	2.994
6MQC	A_ARG_	NH2	B_ASP_	OD1	2.820
6MQC	A_ARG_	NH1	B_ASP_	OD1	3.399
6MQC	A_ARG_	NH1	B_ASP_	OD2	3.078
6MQC	A_ARG_	NH1	B_ASP_	OD1	2.829
6MQC	A_ARG_	NH2	B_ASP_	OD1	2.822
6MQC	A_ARG_	NH2	B_ASP_	OD2	3.673
6MQC	H_ARG_	NH1	L_ASP_	OD1	2.906
6MQC	H_ARG_	NH2	L_ASP_	OD1	2.999
6MQC	H_ARG_	NH1	L_ASP_	OD1	2.856
6MQC	H_ARG_	NH1	L_ASP_	OD2	3.748
6MQC	H_ARG_	NH2	L_ASP_	OD1	3.439
6MQC	H_ARG_	NH2	L_ASP_	OD2	3.140
6MQC	H_ARG_	NH2	L_ASP_	OD1	2.780
6MQC	H_ARG_	NH2	L_ASP_	OD2	3.923
6MQE	A_ARG_95	NH2	B_ASP_91	OD2	3.864
6MQE	A_ARG_100H	NH2	B_ASP_91	OD2	3.610
6MQE	H_ARG_95	NH1	L_ASP_91	OD1	3.360
6MQE	H_ARG_95	NH2	L_ASP_91	OD1	2.956
6MQE	H_ARG_100H	NH1	L_ASP_91	OD1	2.604
6MQE	H_ARG_100H	NH1	L_ASP_91	OD2	3.888
6MQE	L_LYS_155	NZ	A_GLU_56	OE1	2.786
6MQE	L_HIS_189	NE2	A_GLU_56	OE1	3.428
6MQE	L_HIS_189	NE2	A_GLU_56	OE2	2.569
6MQM	B_ARG_96	NH1	A_GLU_95	OE1	3.968
6MQM	B_ARG_96	NH1	A_GLU_95	OE2	2.460
6MQM	E_ARG_96	NH1	D_GLU_95	OE2	2.376
6MQM	H_ARG_96	NH1	G_GLU_95	OE2	2.480
6MQM	K_ARG_96	NH1	J_GLU_95	OE1	3.782
6MQM	K_ARG_96	NH1	J_GLU_95	OE2	2.262
6MQR	H_ARG_96	NH1	L_GLU_55	OE1	2.553
6MQR	L_ARG_46	NH1	H_ASP_101	OD2	2.970
6MQR	L_ARG_46	NH2	H_GLU_95	OE2	3.587
6MQR	L_ARG_46	NH2	H_ASP_101	OD2	3.723
6MQS	A_LYS_44	NZ	B_ASP_86	OD1	3.511
6MQS	A_ARG_138	NH1	B_GLU_214	OE1	3.046
6MQS	A_ARG_138	NH1	B_GLU_214	OE2	2.728
6MQS	A_LYS_218	NZ	B_GLU_127	OE1	2.743
6MQS	A_LYS_218	NZ	B_GLU_127	OE2	3.002
6MQS	C_LYS_44	NZ	D_ASP_86	OD1	2.946
6MQS	C_ARG_138	NH2	D_GLU_214	OE1	2.736
6MQS	C_ARG_138	NH2	D_GLU_214	OE2	3.220
6MQS	C_LYS_152	NZ	D_GLU_128	OE1	3.230
6MQS	C_LYS_218	NZ	D_GLU_127	OE1	2.641
6MQS	C_LYS_218	NZ	D_GLU_127	OE2	3.160
6N16	A_ARG_105	NH1	C_GLU_64	OE1	3.566
6N16	A_ARG_105	NH2	C_GLU_64	OE1	3.522
6N16	A_ARG_105	NH2	C_GLU_64	OE2	3.717
6N16	A_HIS_164	NE2	B_ASP_167	OD2	3.486
6N16	H_HIS_164	NE2	L_ASP_167	OD1	3.075
6N16	K_ARG_105	NH2	H_GLU_64	OE1	2.463

6N16	K_ARG_105	NH2	H_GLU_64	OE2	3.174
6N16	C_LYS_209	NZ	D_ASP_123	OD2	3.251
6N1V	3_LYS_44	NZ	4_ASP_86	OD1	3.675
6N1V	3_LYS_44	NZ	4_ASP_86	OD2	2.472
6N1V	3_LYS_44	NZ	4_GLU_106	OE1	3.723
6N1V	3_ARG_138	NH1	4_GLU_214	OE1	2.573
6N1V	3_ARG_138	NH1	4_GLU_214	OE2	3.070
6N1V	3_ARG_138	NH2	4_GLU_214	OE2	3.291
6N1V	3_LYS_218	NZ	4_GLU_127	OE1	3.611
6N1V	B_LYS_282	NZ	g_ASP_114	OD2	3.730
6N1V	B_ARG_504	NH2	D_GLU_657	OE2	3.905
6N1V	F_ARG_542	NH2	D_GLU_647	OE1	3.326
6N1V	F_ARG_542	NH2	D_GLU_647	OE2	2.831
6N1V	F_ARG_579	NH2	D_GLU_584	OE1	3.581
6N1V	g_ARG_72	NH1	B_ASP_368	OD2	3.927
6N1V	g_ARG_72	NH2	B_ASP_368	OD2	3.974
6N1V	1_LYS_44	NZ	2_ASP_86	OD1	3.676
6N1V	1_LYS_44	NZ	2_ASP_86	OD2	2.473
6N1V	1_LYS_44	NZ	2_GLU_106	OE1	3.723
6N1V	1_ARG_138	NH1	2_GLU_214	OE1	2.573
6N1V	1_ARG_138	NH1	2_GLU_214	OE2	3.069
6N1V	1_ARG_138	NH2	2_GLU_214	OE2	3.291
6N1V	1_LYS_218	NZ	2_GLU_127	OE1	3.611
6N1V	A_LYS_282	NZ	f_ASP_114	OD2	3.729
6N1V	A_ARG_504	NH2	F_GLU_657	OE2	3.909
6N1V	E_ARG_542	NH2	F_GLU_647	OE1	3.328
6N1V	E_ARG_542	NH2	F_GLU_647	OE2	2.831
6N1V	E_ARG_579	NH2	F_GLU_584	OE1	3.583
6N1V	f_ARG_72	NH1	A_ASP_368	OD2	3.927
6N1V	f_ARG_72	NH2	A_ASP_368	OD2	3.974
6N1V	C_LYS_282	NZ	Q_ASP_114	OD2	3.730
6N1V	C_ARG_504	NH2	E_GLU_657	OE2	3.907
6N1V	D_ARG_542	NH2	E_GLU_647	OE1	3.330
6N1V	D_ARG_542	NH2	E_GLU_647	OE2	2.832
6N1V	D_ARG_579	NH2	E_GLU_584	OE1	3.585
6N1V	H_LYS_44	NZ	L_ASP_86	OD1	3.676
6N1V	H_LYS_44	NZ	L_ASP_86	OD2	2.472
6N1V	H_LYS_44	NZ	L_GLU_106	OE1	3.722
6N1V	H_ARG_138	NH1	L_GLU_214	OE1	2.573
6N1V	H_ARG_138	NH1	L_GLU_214	OE2	3.069
6N1V	H_ARG_138	NH2	L_GLU_214	OE2	3.291
6N1V	H_LYS_218	NZ	L_GLU_127	OE1	3.611
6N1V	Q_ARG_72	NH1	C_ASP_368	OD2	3.927
6N1V	Q_ARG_72	NH2	C_ASP_368	OD2	3.975
6N1W	2_ARG_327	NH2	m_GLU_100I	OE1	3.996
6N1W	2_ARG_504	NH2	d_GLU_657	OE2	3.118
6N1W	3_ARG_100H	NH2	4_ASP_91	OD2	3.241
6N1W	A_ARG_542	NH1	d_GLU_647	OE1	3.516
6N1W	A_ARG_542	NH1	d_GLU_647	OE2	3.474
6N1W	A_ARG_542	NH2	d_GLU_647	OE1	2.848
6N1W	A_ARG_579	NH2	d_GLU_584	OE2	3.464
6N1W	A_LYS_601	NZ	d_GLU_654	OE1	3.802
6N1W	A_LYS_601	NZ	d_GLU_654	OE2	3.060
6N1W	C_ARG_504	NH2	A_GLU_657	OE2	3.221
6N1W	D_ARG_542	NH1	A_GLU_647	OE1	3.273
6N1W	D_ARG_542	NH1	A_GLU_647	OE2	3.289
6N1W	D_ARG_542	NH2	A_GLU_647	OE1	2.942
6N1W	D_ARG_579	NH1	A_GLU_584	OE1	3.854

6N1W	D_ARG_579	NH2	A_GLU_584	OE2	3.567
6N1W	D_LYS_601	NZ	A_GLU_654	OE1	3.837
6N1W	D_LYS_601	NZ	A_GLU_654	OE2	3.044
6N1W	H_ARG_100H	NH2	L_ASP_91	OD2	3.150
6N1W	c_ARG_504	NH2	D_GLU_657	OE2	3.061
6N1W	d_ARG_542	NH1	D_GLU_647	OE1	3.482
6N1W	d_ARG_542	NH1	D_GLU_647	OE2	3.280
6N1W	d_ARG_542	NH2	D_GLU_647	OE1	2.854
6N1W	d_ARG_579	NH1	D_GLU_584	OE1	3.913
6N1W	d_ARG_579	NH2	D_GLU_584	OE2	3.653
6N1W	d_LYS_601	NZ	D_GLU_654	OE1	3.862
6N1W	d_LYS_601	NZ	D_GLU_654	OE2	3.082
6N1W	h_ARG_100H	NH2	L_ASP_91	OD2	3.226
6N5B	H_LYS_149	NZ	L_GLU_128	OE2	3.031
6N5B	H_LYS_214	NZ	L_GLU_127	OE2	3.139
6N5D	C_LYS_149	NZ	D_GLU_127	OE2	2.211
6N5D	C_LYS_215	NZ	D_GLU_126	OE1	3.361
6N5D	C_LYS_215	NZ	D_GLU_126	OE2	3.815
6N5D	E_LYS_149	NZ	F_GLU_127	OE2	3.376
6N5D	L_LYS_149	NZ	N_GLU_127	OE2	2.091
6N5D	L_HIS_170	NE2	N_ASP_141	OD2	3.244
6N5E	H_LYS_217	NZ	L_GLU_126	OE2	2.748
6N5E	E_LYS_217	NZ	D_GLU_126	OE1	2.995
6N5E	E_LYS_217	NZ	D_GLU_126	OE2	2.272
6N5E	E_LYS_222	NZ	D_GLU_126	OE1	3.688
6N5E	G_LYS_217	NZ	F_GLU_126	OE2	3.351
6N6B	A_LYS_296	NZ	L_ASP_28	OD1	3.122
6N6B	A_LYS_296	NZ	L_ASP_28	OD2	3.000
6N6B	A_LYS_296	NZ	L_GLU_68	OE2	2.842
6N6B	A_LYS_431	NZ	K_ASP_101	OD1	3.959
6N6B	A_LYS_431	NZ	K_ASP_101	OD2	3.832
6N6B	K_HIS_169	NE2	L_ASP_167	OD1	3.738
6N6B	K_LYS_213	NZ	L_GLU_123	OE1	2.814
6N6B	K_LYS_213	NZ	L_GLU_123	OE2	3.044
6NB5	H_LYS_223	NZ	L_GLU_126	OE1	3.229
6NB5	H_LYS_223	NZ	L_GLU_126	OE2	2.760
6NB5	I_LYS_157	NZ	M_GLU_127	OE2	3.828
6NB5	I_LYS_223	NZ	M_GLU_126	OE2	3.316
6NB8	H_LYS_223	NZ	L_GLU_128	OE1	2.783
6NB8	H_LYS_223	NZ	L_GLU_128	OE2	3.341
6NB8	L_ARG_51	NH1	H_ASP_113	OD1	2.821
6NB8	L_ARG_51	NH2	H_ASP_113	OD1	3.921
6NB8	L_ARG_51	NH2	H_ASP_115	OD1	3.423
6NC2	A_LYS_46	NZ	B_ASP_636	OD1	3.909
6NC2	A_LYS_500	NZ	L_ASP_664	OD1	2.780
6NC2	A_LYS_500	NZ	L_ASP_664	OD2	3.992
6NC2	A_ARG_503	NH1	B_GLU_654	OE1	3.759
6NC2	A_ARG_503	NH1	B_GLU_654	OE2	3.172
6NC2	B_ARG_542	NH1	L_GLU_647	OE1	2.800
6NC2	B_ARG_542	NH1	L_ASP_648	OD1	3.191
6NC2	B_ARG_542	NH2	L_ASP_648	OD1	3.498
6NC2	B_LYS_574	NZ	A_ASP_107	OD1	2.510
6NC2	B_LYS_574	NZ	A_ASP_107	OD2	3.688
6NC2	H_ARG_96	NH1	L_ASP_50	OD1	3.082
6NC2	H_ARG_96	NH1	L_ASP_50	OD2	3.706
6NC2	H_ARG_96	NH2	L_ASP_50	OD1	3.892
6NC2	H_ARG_96	NH2	L_ASP_50	OD2	3.158
6NC2	C_LYS_46	NZ	L_ASP_636	OD1	3.909

6NC2	C_LYS_500	NZ	J_ASP_664	OD1	2.780
6NC2	C_LYS_500	NZ	J_ASP_664	OD2	3.991
6NC2	C_ARG_503	NH1	I_GLU_654	OE1	3.760
6NC2	C_ARG_503	NH1	I_GLU_654	OE2	3.173
6NC2	I_ARG_542	NH1	J_GLU_647	OE1	2.801
6NC2	I_ARG_542	NH1	J_ASP_648	OD1	3.190
6NC2	I_ARG_542	NH2	J_ASP_648	OD1	3.498
6NC2	I_LYS_574	NZ	C_ASP_107	OD1	2.510
6NC2	I_LYS_574	NZ	C_ASP_107	OD2	3.688
6NC2	O_ARG_96	NH1	T_ASP_50	OD1	3.082
6NC2	O_ARG_96	NH1	T_ASP_50	OD2	3.706
6NC2	O_ARG_96	NH2	T_ASP_50	OD1	3.892
6NC2	O_ARG_96	NH2	T_ASP_50	OD2	3.158
6NC2	D_LYS_46	NZ	J_ASP_636	OD1	3.909
6NC2	D_LYS_500	NZ	B_ASP_664	OD1	2.780
6NC2	D_LYS_500	NZ	B_ASP_664	OD2	3.992
6NC2	D_ARG_503	NH1	J_GLU_654	OE1	3.759
6NC2	D_ARG_503	NH1	J_GLU_654	OE2	3.173
6NC2	J_ARG_542	NH1	B_GLU_647	OE1	2.800
6NC2	J_ARG_542	NH1	B_ASP_648	OD1	3.191
6NC2	J_ARG_542	NH2	B_ASP_648	OD1	3.498
6NC2	J_LYS_574	NZ	D_ASP_107	OD1	2.510
6NC2	J_LYS_574	NZ	D_ASP_107	OD2	3.688
6NC2	P_ARG_96	NH1	U_ASP_50	OD1	3.083
6NC2	P_ARG_96	NH1	U_ASP_50	OD2	3.706
6NC2	P_ARG_96	NH2	U_ASP_50	OD1	3.893
6NC2	P_ARG_96	NH2	U_ASP_50	OD2	3.158
6NC2	E_LYS_46	NZ	K_ASP_636	OD1	3.909
6NC2	E_LYS_500	NZ	M_ASP_664	OD1	2.780
6NC2	E_LYS_500	NZ	M_ASP_664	OD2	3.992
6NC2	E_ARG_503	NH1	K_GLU_654	OE1	3.759
6NC2	E_ARG_503	NH1	K_GLU_654	OE2	3.172
6NC2	K_ARG_542	NH1	M_GLU_647	OE1	2.800
6NC2	K_ARG_542	NH1	M_ASP_648	OD1	3.191
6NC2	K_ARG_542	NH2	M_ASP_648	OD1	3.498
6NC2	K_LYS_574	NZ	E_ASP_107	OD1	2.510
6NC2	K_LYS_574	NZ	E_ASP_107	OD2	3.688
6NC2	Q_ARG_96	NH1	V_ASP_50	OD1	3.082
6NC2	Q_ARG_96	NH1	V_ASP_50	OD2	3.706
6NC2	Q_ARG_96	NH2	V_ASP_50	OD1	3.892
6NC2	Q_ARG_96	NH2	V_ASP_50	OD2	3.158
6NC2	F_LYS_46	NZ	M_ASP_636	OD1	3.909
6NC2	F_LYS_500	NZ	N_ASP_664	OD1	2.780
6NC2	F_LYS_500	NZ	N_ASP_664	OD2	3.991
6NC2	F_ARG_503	NH1	M_GLU_654	OE1	3.759
6NC2	F_ARG_503	NH1	M_GLU_654	OE2	3.173
6NC2	M_ARG_542	NH1	N_GLU_647	OE1	2.801
6NC2	M_ARG_542	NH1	N_ASP_648	OD1	3.191
6NC2	M_ARG_542	NH2	N_ASP_648	OD1	3.498
6NC2	M_LYS_574	NZ	F_ASP_107	OD1	2.510
6NC2	M_LYS_574	NZ	F_ASP_107	OD2	3.688
6NC2	R_ARG_96	NH1	W_ASP_50	OD1	3.082
6NC2	R_ARG_96	NH1	W_ASP_50	OD2	3.706
6NC2	R_ARG_96	NH2	W_ASP_50	OD1	3.892
6NC2	R_ARG_96	NH2	W_ASP_50	OD2	3.157
6NC2	G_LYS_46	NZ	N_ASP_636	OD1	3.909
6NC2	G_LYS_500	NZ	K_ASP_664	OD1	2.780
6NC2	G_LYS_500	NZ	K_ASP_664	OD2	3.992

6NC2	G_ARG_503	NH1	N_GLU_654	OE1	3.759
6NC2	G_ARG_503	NH1	N_GLU_654	OE2	3.173
6NC2	N_ARG_542	NH1	K_GLU_647	OE1	2.800
6NC2	N_ARG_542	NH1	K_ASP_648	OD1	3.191
6NC2	N_ARG_542	NH2	K_ASP_648	OD1	3.498
6NC2	N_LYS_574	NZ	G_ASP_107	OD1	2.510
6NC2	N_LYS_574	NZ	G_ASP_107	OD2	3.688
6NC2	S_ARG_96	NH1	X_ASP_50	OD1	3.082
6NC2	S_ARG_96	NH1	X_ASP_50	OD2	3.706
6NC2	S_ARG_96	NH2	X_ASP_50	OD1	3.892
6NC2	S_ARG_96	NH2	X_ASP_50	OD2	3.158
6NC3	A_LYS_46	NZ	B_ASP_636	OD1	2.912
6NC3	A_LYS_46	NZ	B_ASP_636	OD2	3.719
6NC3	A_ARG_192	NH2	C_ASP_167	OD1	3.709
6NC3	A_ARG_192	NH2	C_ASP_167	OD2	3.548
6NC3	A_ARG_503	NH2	B_GLU_654	OE1	3.773
6NC3	A_ARG_503	NH2	B_GLU_654	OE2	3.161
6NC3	B_ARG_542	NH2	J_GLU_647	OE1	2.826
6NC3	B_ARG_542	NH2	J_ASP_648	OD1	2.949
6NC3	B_ARG_542	NH2	J_ASP_648	OD2	3.670
6NC3	B_LYS_574	NZ	A_ASP_107	OD1	2.582
6NC3	B_LYS_574	NZ	A_ASP_107	OD2	2.711
6NC3	B_ARG_579	NH1	J_GLU_584	OE2	3.194
6NC3	B_ARG_585	NH2	A_GLU_492	OE1	2.939
6NC3	B_ARG_585	NH2	A_GLU_492	OE2	3.498
6NC3	C_LYS_46	NZ	I_ASP_636	OD1	2.913
6NC3	C_LYS_46	NZ	I_ASP_636	OD2	3.719
6NC3	C_ARG_192	NH2	D_ASP_167	OD1	3.709
6NC3	C_ARG_192	NH2	D_ASP_167	OD2	3.548
6NC3	C_ARG_503	NH2	I_GLU_654	OE1	3.773
6NC3	C_ARG_503	NH2	I_GLU_654	OE2	3.161
6NC3	I_ARG_542	NH2	B_GLU_647	OE1	2.826
6NC3	I_ARG_542	NH2	B_ASP_648	OD1	2.949
6NC3	I_ARG_542	NH2	B_ASP_648	OD2	3.670
6NC3	I_LYS_574	NZ	C_ASP_107	OD1	2.581
6NC3	I_LYS_574	NZ	C_ASP_107	OD2	2.711
6NC3	I_ARG_579	NH1	B_GLU_584	OE2	3.194
6NC3	I_ARG_585	NH2	C_GLU_492	OE1	2.939
6NC3	I_ARG_585	NH2	C_GLU_492	OE2	3.498
6NC3	D_LYS_46	NZ	J_ASP_636	OD1	2.913
6NC3	D_LYS_46	NZ	J_ASP_636	OD2	3.719
6NC3	D_ARG_192	NH2	A_ASP_167	OD1	3.708
6NC3	D_ARG_192	NH2	A_ASP_167	OD2	3.548
6NC3	D_ARG_503	NH2	J_GLU_654	OE1	3.773
6NC3	D_ARG_503	NH2	J_GLU_654	OE2	3.160
6NC3	J_ARG_542	NH2	I_GLU_647	OE1	2.825
6NC3	J_ARG_542	NH2	I_ASP_648	OD1	2.949
6NC3	J_ARG_542	NH2	I_ASP_648	OD2	3.670
6NC3	J_LYS_574	NZ	D_ASP_107	OD1	2.581
6NC3	J_LYS_574	NZ	D_ASP_107	OD2	2.710
6NC3	J_ARG_579	NH1	I_GLU_584	OE2	3.194
6NC3	J_ARG_585	NH2	D_GLU_492	OE1	2.939
6NC3	J_ARG_585	NH2	D_GLU_492	OE2	3.498
6NC3	E_LYS_46	NZ	K_ASP_636	OD1	2.912
6NC3	E_LYS_46	NZ	K_ASP_636	OD2	3.719
6NC3	E_ARG_192	NH2	F_ASP_167	OD1	3.709
6NC3	E_ARG_192	NH2	F_ASP_167	OD2	3.548
6NC3	E_ARG_503	NH2	K_GLU_654	OE1	3.773

6NC3	E_ARG_503	NH2	K_GLU_654	OE2	3.161
6NC3	K_ARG_542	NH2	N_GLU_647	OE1	2.826
6NC3	K_ARG_542	NH2	N_ASP_648	OD1	2.949
6NC3	K_ARG_542	NH2	N_ASP_648	OD2	3.670
6NC3	K_LYS_574	NZ	E_ASP_107	OD1	2.582
6NC3	K_LYS_574	NZ	E_ASP_107	OD2	2.711
6NC3	K_ARG_579	NH1	N_GLU_584	OE2	3.194
6NC3	K_ARG_585	NH2	E_GLU_492	OE1	2.939
6NC3	K_ARG_585	NH2	E_GLU_492	OE2	3.498
6NC3	F_LYS_46	NZ	M_ASP_636	OD1	2.913
6NC3	F_LYS_46	NZ	M_ASP_636	OD2	3.719
6NC3	F_ARG_192	NH2	G_ASP_167	OD1	3.709
6NC3	F_ARG_192	NH2	G_ASP_167	OD2	3.548
6NC3	F_ARG_503	NH2	M_GLU_654	OE1	3.773
6NC3	F_ARG_503	NH2	M_GLU_654	OE2	3.161
6NC3	M_ARG_542	NH2	K_GLU_647	OE1	2.826
6NC3	M_ARG_542	NH2	K_ASP_648	OD1	2.949
6NC3	M_ARG_542	NH2	K_ASP_648	OD2	3.670
6NC3	M_LYS_574	NZ	F_ASP_107	OD1	2.581
6NC3	M_LYS_574	NZ	F_ASP_107	OD2	2.711
6NC3	M_ARG_579	NH1	K_GLU_584	OE2	3.194
6NC3	M_ARG_585	NH2	F_GLU_492	OE1	2.939
6NC3	M_ARG_585	NH2	F_GLU_492	OE2	3.498
6NC3	G_LYS_46	NZ	N_ASP_636	OD1	2.913
6NC3	G_LYS_46	NZ	N_ASP_636	OD2	3.719
6NC3	G_ARG_192	NH2	E_ASP_167	OD1	3.708
6NC3	G_ARG_192	NH2	E_ASP_167	OD2	3.548
6NC3	G_ARG_503	NH2	N_GLU_654	OE1	3.773
6NC3	G_ARG_503	NH2	N_GLU_654	OE2	3.160
6NC3	N_ARG_542	NH2	M_GLU_647	OE1	2.825
6NC3	N_ARG_542	NH2	M_ASP_648	OD1	2.949
6NC3	N_ARG_542	NH2	M_ASP_648	OD2	3.670
6NC3	N_LYS_574	NZ	G_ASP_107	OD1	2.581
6NC3	N_LYS_574	NZ	G_ASP_107	OD2	2.710
6NC3	N_ARG_579	NH1	M_GLU_584	OE2	3.194
6NC3	N_ARG_585	NH2	G_GLU_492	OE1	2.939
6NC3	N_ARG_585	NH2	G_GLU_492	OE2	3.498
6NEX	B_LYS_209	NZ	A_GLU_126	OE2	3.298
6NF2	A_LYS_46	NZ	L_ASP_632	OD2	2.876
6NF2	A_ARG_504	NH2	R_GLU_657	OE2	3.927
6NF2	B_ARG_579	NH1	L_GLU_584	OE2	3.681
6NF2	B_LYS_601	NZ	L_GLU_654	OE1	2.983
6NF2	B_LYS_601	NZ	L_GLU_654	OE2	3.256
6NF2	C_ARG_61	NH1	G_GLU_466	OE1	3.610
6NF2	C_ARG_61	NH2	G_GLU_466	OE2	3.748
6NF2	C_ARG_71	NH2	G_ASP_368	OD1	3.504
6NF2	G_LYS_46	NZ	B_ASP_632	OD2	2.943
6NF2	G_ARG_504	NH2	L_GLU_657	OE2	3.805
6NF2	H_ARG_100F	NH1	L_ASP_50	OD2	2.403
6NF2	H_ARG_100F	NH2	L_ASP_50	OD2	3.926
6NF2	I_ARG_579	NH1	R_GLU_584	OE2	3.624
6NF2	I_LYS_601	NZ	R_GLU_654	OE1	3.068
6NF2	I_LYS_601	NZ	R_GLU_654	OE2	3.333
6NF2	N_ARG_61	NH1	A_GLU_466	OE1	3.592
6NF2	N_ARG_61	NH2	A_GLU_466	OE2	3.737
6NF2	N_ARG_71	NH2	A_ASP_368	OD1	3.532
6NF2	O_ARG_100F	NH1	P_ASP_50	OD2	2.825
6NF2	Q_LYS_46	NZ	R_ASP_632	OD2	2.912

6NF2	Q_ARG_504	NH2	B_GLU_657	OE2	3.920
6NF2	R_ARG_579	NH1	B_GLU_584	OE2	3.657
6NF2	R_LYS_601	NZ	B_GLU_654	OE1	3.130
6NF2	R_LYS_601	NZ	B_GLU_654	OE2	3.363
6NF2	V_ARG_61	NH1	Q_GLU_466	OE1	3.626
6NF2	V_ARG_61	NH2	Q_GLU_466	OE2	3.762
6NF2	V_ARG_71	NH2	Q_ASP_368	OD1	3.511
6NF2	W_ARG_100F	NH1	X_ASP_50	OD2	2.242
6NF2	W_ARG_100F	NH2	X_ASP_50	OD2	3.856
6NF5	A_LYS_46	NZ	B_ASP_632	OD2	2.410
6NF5	A_LYS_137	NZ	L_ASP_51	OD2	2.736
6NF5	A_ARG_192	NH1	J_GLU_164	OE2	3.009
6NF5	A_ARG_192	NH2	J_GLU_164	OE2	3.825
6NF5	B_ARG_542	NH1	D_GLU_647	OE1	3.182
6NF5	B_ARG_542	NH1	D_GLU_647	OE2	3.535
6NF5	B_ARG_542	NH2	D_GLU_647	OE1	3.979
6NF5	B_LYS_574	NZ	A_ASP_107	OD1	2.887
6NF5	B_HIS_585	NE2	A_GLU_492	OE1	3.726
6NF5	B_LYS_601	NZ	D_GLU_657	OE1	3.026
6NF5	K_ARG_53	NH1	B_ASP_659	OD1	3.261
6NF5	K_ARG_53	NH1	B_ASP_659	OD2	3.240
6NF5	K_ARG_53	NH2	B_ASP_659	OD1	3.591
6NF5	K_ARG_53	NH2	B_ASP_659	OD2	2.651
6NF5	C_LYS_46	NZ	D_ASP_632	OD2	2.410
6NF5	C_LYS_137	NZ	F_ASP_51	OD2	2.736
6NF5	C_ARG_192	NH1	A_GLU_164	OE2	3.009
6NF5	C_ARG_192	NH2	A_GLU_164	OE2	3.825
6NF5	D_ARG_542	NH1	M_GLU_647	OE1	3.182
6NF5	D_ARG_542	NH1	M_GLU_647	OE2	3.535
6NF5	D_ARG_542	NH2	M_GLU_647	OE1	3.978
6NF5	D_LYS_574	NZ	C_ASP_107	OD1	2.887
6NF5	D_HIS_585	NE2	C_GLU_492	OE1	3.725
6NF5	D_LYS_601	NZ	M_GLU_657	OE1	3.026
6NF5	G_ARG_53	NH1	D_ASP_659	OD1	3.261
6NF5	G_ARG_53	NH1	D_ASP_659	OD2	3.240
6NF5	G_ARG_53	NH2	D_ASP_659	OD1	3.591
6NF5	G_ARG_53	NH2	D_ASP_659	OD2	2.651
6NF5	J_LYS_46	NZ	M_ASP_632	OD2	2.410
6NF5	J_LYS_137	NZ	P_ASP_51	OD2	2.735
6NF5	J_ARG_192	NH1	C_GLU_164	OE2	3.010
6NF5	J_ARG_192	NH2	C_GLU_164	OE2	3.825
6NF5	M_ARG_542	NH1	B_GLU_647	OE1	3.182
6NF5	M_ARG_542	NH1	B_GLU_647	OE2	3.534
6NF5	M_ARG_542	NH2	B_GLU_647	OE1	3.979
6NF5	M_LYS_574	NZ	J_ASP_107	OD1	2.887
6NF5	M_HIS_585	NE2	J_GLU_492	OE1	3.726
6NF5	M_LYS_601	NZ	B_GLU_657	OE1	3.027
6NF5	Q_ARG_53	NH1	M_ASP_659	OD1	3.262
6NF5	Q_ARG_53	NH1	M_ASP_659	OD2	3.240
6NF5	Q_ARG_53	NH2	M_ASP_659	OD1	3.591
6NF5	Q_ARG_53	NH2	M_ASP_659	OD2	2.650
6NFC	C_ARG_53	NH1	I_ASP_659	OD1	3.890
6NFC	C_ARG_53	NH1	I_ASP_659	OD2	2.842
6NFC	C_ARG_53	NH2	I_ASP_659	OD2	2.675
6NFC	A_LYS_46	NZ	B_ASP_632	OD1	3.913
6NFC	A_LYS_46	NZ	B_ASP_632	OD2	2.455
6NFC	A_LYS_137	NZ	L_ASP_51	OD2	2.690
6NFC	B_ARG_542	NH1	G_GLU_647	OE1	3.297

6NFC	B_ARG_542	NH1	G_GLU_647	OE2	3.640
6NFC	B_LYS_574	NZ	A_GLU_106	OE1	3.608
6NFC	B_LYS_574	NZ	A_GLU_106	OE2	2.473
6NFC	B_ARG_579	NH2	G_GLU_584	OE1	3.071
6NFC	B_ARG_579	NH2	G_GLU_584	OE2	3.850
6NFC	L_LYS_50	NZ	H_GLU_99	OE1	3.024
6NFC	J_ARG_53	NH1	G_ASP_659	OD1	3.783
6NFC	J_ARG_53	NH1	G_ASP_659	OD2	2.774
6NFC	J_ARG_53	NH2	G_ASP_659	OD2	2.735
6NFC	E_LYS_46	NZ	G_ASP_632	OD1	3.927
6NFC	E_LYS_46	NZ	G_ASP_632	OD2	2.442
6NFC	E_ARG_500	NH2	I_ASP_664	OD1	2.950
6NFC	E_ARG_500	NH2	I_ASP_664	OD2	3.747
6NFC	G_ARG_542	NH1	I_GLU_647	OE1	3.321
6NFC	G_ARG_542	NH1	I_GLU_647	OE2	3.884
6NFC	G_LYS_574	NZ	E_GLU_106	OE1	3.312
6NFC	G_LYS_574	NZ	E_GLU_106	OE2	2.741
6NFC	G_ARG_579	NH2	I_GLU_584	OE1	3.032
6NFC	G_ARG_579	NH2	I_GLU_584	OE2	3.885
6NFC	G_LYS_601	NZ	I_GLU_657	OE1	2.933
6NFC	G_LYS_601	NZ	I_GLU_657	OE2	3.730
6NFC	F_LYS_46	NZ	I_ASP_632	OD1	3.960
6NFC	F_LYS_46	NZ	I_ASP_632	OD2	2.474
6NFC	F_LYS_502	NZ	B_ASP_664	OD1	3.023
6NFC	I_ARG_542	NH1	B_GLU_647	OE1	3.339
6NFC	I_ARG_542	NH1	B_GLU_647	OE2	3.856
6NFC	I_LYS_574	NZ	F_ASP_107	OD1	2.742
6NFC	I_ARG_579	NH2	B_GLU_584	OE1	3.222
6NFC	I_ARG_579	NH2	B_GLU_584	OE2	3.762
6NFC	I_LYS_601	NZ	B_GLU_657	OE1	3.945
6NFC	K_ARG_53	NH1	B_ASP_659	OD1	3.915
6NFC	K_ARG_53	NH1	B_ASP_659	OD2	2.784
6NFC	K_ARG_53	NH2	B_ASP_659	OD2	2.738
6NMR	H_LYS_216	NZ	L_GLU_124	OE1	3.273
6NMR	H_LYS_216	NZ	L_GLU_124	OE2	3.010
6NMR	S_ARG_69	NH1	L_GLU_55	OE1	3.247
6NMR	S_ARG_69	NH1	L_GLU_55	OE2	3.038
6NMR	S_ARG_69	NH2	L_GLU_55	OE2	3.173
6NMR	E_ARG_69	NH1	B_GLU_55	OE1	2.733
6NMR	E_ARG_69	NH1	B_GLU_55	OE2	2.469
6NMR	E_ARG_69	NH2	B_GLU_55	OE1	2.510
6NMR	E_ARG_69	NH2	B_GLU_55	OE2	3.637
6NMR	I_ARG_69	NH1	G_GLU_55	OE1	3.183
6NMR	I_ARG_69	NH1	G_GLU_55	OE2	2.119
6NMR	I_ARG_69	NH1	F_ASP_108	OD2	3.629
6NMR	I_ARG_69	NH2	G_GLU_55	OE1	2.639
6NMR	I_ARG_69	NH2	G_GLU_55	OE2	3.327
6NMR	M_ARG_69	NH1	J_ASP_108	OD1	3.945
6NMR	M_ARG_69	NH1	J_ASP_108	OD2	3.140
6NMR	M_ARG_69	NH2	K_GLU_55	OE1	3.608
6NMR	M_ARG_69	NH2	J_ASP_108	OD1	1.901
6NMR	M_ARG_69	NH2	J_ASP_108	OD2	2.331
6NMS	L_ARG_94	NH2	S_GLU_111	OE1	3.728
6NMS	H_ARG_104	NH2	S_GLU_111	OE1	3.455
6NMS	H_ARG_104	NH2	S_GLU_111	OE2	2.500
6NMS	H_LYS_215	NZ	L_GLU_124	OE1	3.565
6NMS	H_LYS_215	NZ	L_GLU_124	OE2	3.270
6NMS	H_LYS_220	NZ	L_GLU_214	OE1	3.397

6NMS	S_LYS_11	NZ	H_ASP_33	OD1	3.001
6NMS	S_LYS_11	NZ	H_GLU_99	OE1	2.549
6NMS	S_HIS_56	ND1	A_ASP_60	OD2	2.658
6NMS	A_ARG_94	NH2	C_GLU_111	OE2	3.453
6NMS	B_ARG_104	NH2	C_GLU_111	OE1	2.703
6NMS	B_ARG_104	NH2	C_GLU_111	OE2	3.000
6NMS	C_LYS_11	NZ	B_ASP_33	OD2	3.490
6NMS	C_LYS_11	NZ	B_GLU_99	OE1	2.892
6NMS	C_ARG_115	NH1	B_GLU_56	OE2	3.579
6NMS	C_ARG_115	NH2	B_GLU_56	OE2	2.699
6NMT	A_ARG_26	NH2	C_ASP_10	OD1	3.433
6NMT	A_ARG_26	NH2	C_ASP_10	OD2	3.182
6NMT	B_ARG_56	NH2	C_GLU_111	OE2	3.542
6NMT	B_LYS_215	NZ	A_GLU_118	OE2	3.496
6NMT	C_LYS_11	NZ	A_ASP_91	OD1	2.678
6NMT	C_LYS_11	NZ	A_ASP_91	OD2	3.319
6NMU	L_LYS_32	NZ	S_ASP_85	OD1	3.326
6NMU	H_ARG_50	NH1	S_GLU_47	OE1	3.597
6NMU	H_ARG_50	NH1	S_GLU_47	OE2	3.084
6NMU	H_ARG_50	NH2	S_GLU_47	OE1	2.989
6NMU	H_ARG_50	NH2	S_GLU_47	OE2	3.577
6NMU	S_ARG_59	NH2	H_ASP_101	OD2	3.444
6NMU	A_LYS_32	NZ	C_ASP_85	OD1	3.635
6NMU	B_ARG_50	NH1	C_GLU_47	OE1	3.989
6NMU	B_ARG_50	NH1	C_GLU_47	OE2	3.035
6NMU	B_ARG_50	NH2	C_GLU_47	OE1	2.804
6NMU	B_ARG_50	NH2	C_GLU_47	OE2	3.091
6NMU	B_LYS_215	NZ	A_GLU_124	OE1	3.494
6NMU	B_LYS_215	NZ	A_GLU_124	OE2	3.379
6NMU	C_ARG_59	NH1	B_ASP_101	OD1	3.720
6NMU	C_ARG_59	NH1	B_ASP_101	OD2	2.808
6O9B	A_ARG_35	NH1	B_ASP_73	OD1	2.773
6O9B	A_ARG_35	NH1	B_ASP_73	OD2	3.974
6O9B	A_ARG_48	NH2	B_ASP_73	OD2	3.479
6O9B	A_HIS_192	ND1	B_ASP_118	OD2	3.864
6O9B	C_LYS_9	NZ	A_ASP_116	OD2	2.706
6O9C	A_ARG_35	NH1	B_ASP_73	OD1	3.395
6O9C	A_HIS_192	NE2	B_ASP_118	OD2	3.199
6O9C	A_ARG_202	NH1	B_ASP_118	OD2	3.014
6O9C	B_LYS_26	NZ	A_GLU_232	OE2	3.913
6O9C	C_LYS_9	NZ	A_ASP_77	OD2	3.855
6O9C	C_LYS_9	NZ	A_ASP_116	OD2	2.984
6OGX	C_LYS_213	NZ	D_GLU_123	OE1	2.791
6OGX	C_LYS_213	NZ	D_GLU_123	OE2	3.773
6OGX	C_LYS_218	NZ	D_ASP_122	OD2	3.785
6OGX	D_ARG_55	NH2	G_ASP_117	OD1	2.990
6OGX	G_ARG_95	NH1	H_ASP_99	OD1	3.462
6OGX	G_ARG_95	NH1	H_ASP_99	OD2	2.833
6OGX	G_ARG_95	NH2	H_ASP_99	OD1	2.923
6OGX	G_ARG_95	NH2	H_ASP_99	OD2	3.646
6OGX	H_ARG_100	NH1	L_GLU_55	OE1	3.516
6OGX	H_ARG_100	NH1	L_GLU_55	OE2	2.787
6OKM	H_ARG_100	NH1	L_GLU_55	OE1	2.851
6OKM	H_HIS_165	NE2	L_ASP_167	OD1	3.460
6OKM	H_LYS_210	NZ	L_GLU_123	OE2	3.540
6OKM	H_LYS_215	NZ	L_ASP_122	OD1	3.237
6OKM	H_LYS_215	NZ	L_ASP_122	OD2	3.538
6OKM	R_ARG_95	NH1	H_ASP_99	OD1	3.347

6OKM	R_ARG_95	NH1	H_ASP_99	OD2	3.783
6OKM	R_ARG_95	NH2	H_ASP_99	OD1	3.371
6OKM	R_ARG_95	NH2	H_ASP_99	OD2	2.555
6OKN	A_LYS_213	NZ	B_GLU_123	OE1	3.312
6OKN	A_LYS_213	NZ	B_GLU_123	OE2	2.829
6OKN	C_LYS_213	NZ	D_GLU_123	OE1	3.356
6OKN	C_LYS_213	NZ	D_GLU_123	OE2	2.896
6OKN	C_LYS_218	NZ	D_ASP_122	OD2	3.923
6OOR	A_LYS_148	NZ	H_ASP_55	OD2	3.250
6OOR	B_ARG_12	NH2	A_ASP_242	OD1	3.946
6OOR	B_ARG_12	NH2	A_ASP_242	OD2	2.705
6OOR	B_HIS_34	NE2	A_GLU_97	OE1	2.803
6OOR	B_HIS_34	NE2	A_GLU_97	OE2	3.580
6OOR	H_ARG_109	NH2	A_ASP_80	OD1	2.917
6OOR	H_ARG_109	NH2	A_ASP_80	OD2	3.352
6OOR	H_LYS_220	NZ	L_GLU_128	OE1	2.677
6OOR	H_LYS_220	NZ	L_GLU_128	OE2	2.872
6OSY	2_LYS_282	NZ	8_ASP_100C	OD2	3.941
6OSY	8_ARG_61	NH1	2_GLU_466	OE2	3.827
6OSY	8_ARG_71	NH1	2_ASP_368	OD2	3.948
6OSY	8_ARG_71	NH2	2_ASP_368	OD2	3.279
6OSY	A_ARG_542	NH1	Q_GLU_647	OE2	3.907
6OSY	A_ARG_542	NH2	Q_GLU_647	OE1	3.187
6OSY	A_ARG_542	NH2	Q_GLU_647	OE2	2.660
6OSY	A_ARG_579	NH2	Q_GLU_584	OE1	3.706
6OSY	B_LYS_282	NZ	F_ASP_100C	OD1	3.567
6OSY	B_LYS_282	NZ	F_ASP_100C	OD2	3.346
6OSY	F_ARG_71	NH2	B_ASP_368	OD2	3.635
6OSY	G_ARG_542	NH1	A_GLU_647	OE2	3.983
6OSY	G_ARG_542	NH2	A_GLU_647	OE1	3.165
6OSY	G_ARG_542	NH2	A_GLU_647	OE2	2.705
6OSY	G_ARG_579	NH2	A_GLU_584	OE1	3.899
6OSY	H_ARG_96	NH1	L_GLU_55	OE1	3.662
6OSY	H_HIS_100	ND1	2_GLU_87	OE2	3.031
6OSY	H_HIS_100	NE2	2_GLU_87	OE2	3.785
6OSY	I_ARG_96	NH1	J_GLU_55	OE2	3.419
6OSY	I_HIS_100	ND1	B_GLU_87	OE2	3.029
6OSY	I_HIS_100	NE2	B_GLU_87	OE2	3.781
6OSY	J_ARG_46	NH1	I_ASP_101	OD1	3.411
6OSY	J_ARG_46	NH1	I_ASP_101	OD2	2.599
6OSY	K_LYS_282	NZ	P_ASP_100C	OD2	3.859
6OSY	L_ARG_46	NH1	H_ASP_101	OD1	3.509
6OSY	L_ARG_46	NH1	H_ASP_101	OD2	2.485
6OSY	P_ARG_71	NH1	K_ASP_368	OD2	3.949
6OSY	P_ARG_71	NH2	K_ASP_368	OD2	3.325
6OSY	Q_ARG_542	NH1	G_GLU_647	OE2	3.913
6OSY	Q_ARG_542	NH2	G_GLU_647	OE1	3.228
6OSY	Q_ARG_542	NH2	G_GLU_647	OE2	2.706
6OSY	R_ARG_96	NH1	S_GLU_55	OE2	3.423
6OSY	R_HIS_100	ND1	K_GLU_87	OE1	3.719
6OSY	R_HIS_100	ND1	K_GLU_87	OE2	2.905
6OSY	R_HIS_100	NE2	K_GLU_87	OE1	3.960
6OSY	S_ARG_46	NH1	R_ASP_101	OD1	3.488
6OSY	S_ARG_46	NH1	R_ASP_101	OD2	2.503
6OT1	B_ARG_542	NH2	D_GLU_647	OE1	2.021
6OT1	B_ARG_542	NH2	D_GLU_647	OE2	3.827
6OT1	B_LYS_601	NZ	D_GLU_657	OE1	3.960
6OT1	B_LYS_601	NZ	D_GLU_657	OE2	3.832

6OT1	G_LYS_282	NZ	q-ASP_100C	OD2	3.404
6OT1	G_ARG_327	NH2	m_GLU_100I	OE1	3.817
6OT1	q_ARG_71	NH2	G_ASP_368	OD2	3.596
6OT1	O_ARG_542	NH2	B_GLU_647	OE1	2.048
6OT1	O_ARG_542	NH2	B_GLU_647	OE2	3.874
6OT1	O_LYS_601	NZ	B_GLU_657	OE1	3.934
6OT1	O_LYS_601	NZ	B_GLU_657	OE2	3.759
6OT1	E_LYS_282	NZ	J_ASP_100C	OD2	3.404
6OT1	E_ARG_327	NH2	F_GLU_100I	OE1	3.817
6OT1	J_ARG_71	NH2	E_ASP_368	OD2	3.599
6OT1	D_ARG_542	NH2	O_GLU_647	OE1	2.015
6OT1	D_ARG_542	NH2	O_GLU_647	OE2	3.816
6OT1	D_LYS_601	NZ	O_GLU_657	OE2	3.900
6OT1	P_LYS_282	NZ	S_ASP_100C	OD2	3.405
6OT1	P_ARG_327	NH2	Q_GLU_100I	OE1	3.817
6OT1	S_ARG_71	NH2	P_ASP_368	OD2	3.597
6P62	A_LYS_168	NZ	B_GLU_190	OE2	3.547
6P62	A_ARG_542	NH1	B_GLU_647	OE1	2.629
6P62	A_ARG_542	NH1	B_GLU_647	OE2	3.985
6P62	A_ARG_542	NH2	B_GLU_648	OE2	3.131
6P62	A_ARG_579	NH1	B_GLU_584	OE1	3.453
6P62	A_ARG_579	NH1	B_GLU_584	OE2	2.953
6P62	B_LYS_168	NZ	E_GLU_190	OE2	3.547
6P62	B_ARG_542	NH1	E_GLU_647	OE1	2.630
6P62	B_ARG_542	NH1	E_GLU_647	OE2	3.986
6P62	B_ARG_542	NH2	E_GLU_648	OE2	3.130
6P62	B_ARG_579	NH1	E_GLU_584	OE1	3.454
6P62	B_ARG_579	NH1	E_GLU_584	OE2	2.952
6P62	E_LYS_168	NZ	A_GLU_190	OE2	3.547
6P62	E_ARG_542	NH1	A_GLU_647	OE1	2.629
6P62	E_ARG_542	NH1	A_GLU_647	OE2	3.985
6P62	E_ARG_542	NH2	A_GLU_648	OE2	3.130
6P62	E_ARG_579	NH1	A_GLU_584	OE1	3.453
6P62	E_ARG_579	NH1	A_GLU_584	OE2	2.952
6P65	A_ARG_500	NH1	L_GLU_30	OE1	3.144
6P65	A_ARG_500	NH1	L_GLU_30	OE2	3.804
6P65	A_ARG_500	NH2	L_GLU_30	OE1	3.741
6P65	A_ARG_500	NH2	L_GLU_30	OE2	2.979
6P65	A_ARG_542	NH2	B_ASP_648	OD1	3.154
6P65	H_LYS_71	NZ	A_GLU_87	OE1	2.936
6P65	H_LYS_71	NZ	A_GLU_87	OE2	2.864
6P65	H_LYS_100H	NZ	L_ASP_50	OD1	2.708
6P65	H_LYS_100H	NZ	L_ASP_50	OD2	2.597
6P65	B_ARG_500	NH1	D_GLU_30	OE1	3.143
6P65	B_ARG_500	NH1	D_GLU_30	OE2	3.804
6P65	B_ARG_500	NH2	D_GLU_30	OE1	3.741
6P65	B_ARG_500	NH2	D_GLU_30	OE2	2.979
6P65	B_ARG_542	NH2	E_ASP_648	OD1	3.155
6P65	C_LYS_71	NZ	B_GLU_87	OE1	2.936
6P65	C_LYS_71	NZ	B_GLU_87	OE2	2.864
6P65	C_LYS_100H	NZ	D_ASP_50	OD1	2.708
6P65	C_LYS_100H	NZ	D_ASP_50	OD2	2.597
6P65	E_ARG_500	NH1	G_GLU_30	OE1	3.143
6P65	E_ARG_500	NH1	G_GLU_30	OE2	3.804
6P65	E_ARG_500	NH2	G_GLU_30	OE1	3.741
6P65	E_ARG_500	NH2	G_GLU_30	OE2	2.979
6P65	E_ARG_542	NH2	A_ASP_648	OD1	3.154
6P65	F_LYS_71	NZ	E_GLU_87	OE1	2.935

6P65	F_LYS_71	NZ	E_GLU_87	OE2	2.865
6P65	F_LYS_100H	NZ	G_ASP_50	OD1	2.708
6P65	F_LYS_100H	NZ	G_ASP_50	OD2	2.596
6PE8	A_LYS_212	NZ	B_GLU_129	OE1	3.617
6PE8	A_LYS_212	NZ	B_GLU_129	OE2	2.921
6PE8	A_LYS_217	NZ	B_ASP_128	OD2	3.408
6PE8	B_LYS_36	NZ	U_GLU_98	OE2	3.943
6PE8	H_LYS_212	NZ	L_GLU_129	OE1	2.763
6PE8	H_LYS_212	NZ	L_GLU_129	OE2	3.237
6PE8	L_LYS_36	NZ	T_GLU_98	OE1	3.975
6PE8	L_LYS_36	NZ	T_GLU_98	OE2	3.494
6PE8	T_ARG_90	NH2	H_ASP_62	OD1	3.932
6PE8	T_LYS_94	NZ	L_ASP_97	OD1	2.502
6PE8	T_LYS_94	NZ	L_ASP_97	OD2	3.872
6PE9	A_LYS_212	NZ	B_GLU_129	OE1	3.227
6PE9	A_LYS_212	NZ	B_GLU_129	OE2	3.311
6PE9	A_LYS_217	NZ	B_ASP_128	OD1	3.061
6PE9	A_LYS_217	NZ	B_ASP_128	OD2	3.113
6PE9	C_LYS_13	NZ	U_GLU_107	OE2	3.461
6PE9	C_LYS_212	NZ	D_GLU_129	OE1	2.716
6PE9	D_LYS_36	NZ	G_GLU_98	OE2	3.800
6PE9	E_LYS_13	NZ	G_GLU_107	OE2	3.510
6PE9	E_LYS_212	NZ	F_GLU_129	OE1	3.511
6PE9	E_LYS_212	NZ	F_GLU_129	OE2	3.915
6PE9	F_LYS_36	NZ	U_GLU_98	OE2	3.769
6PE9	G_ARG_73	NH1	J_GLU_74	OE1	3.140
6PE9	G_ARG_73	NH2	J_GLU_74	OE1	2.423
6PE9	G_ARG_73	NH2	J_GLU_74	OE2	3.851
6PE9	G_LYS_94	NZ	D_ASP_97	OD1	2.957
6PE9	I_LYS_29	NZ	U_ASP_69	OD2	3.034
6PE9	I_ARG_73	NH1	U_GLU_74	OE1	3.681
6PE9	I_ARG_73	NH1	U_GLU_74	OE2	2.345
6PE9	I_ARG_73	NH2	U_GLU_74	OE2	3.507
6PE9	J_ARG_73	NH1	G_GLU_74	OE1	3.931
6PE9	J_ARG_73	NH1	G_GLU_74	OE2	3.429
6PE9	M_LYS_36	NZ	J_GLU_98	OE1	2.716
6PE9	U_LYS_	NZ	L_ASP_	OD2	3.835
6PE9	U_ARG_	NH2	I_GLU_	OE1	3.379
6PE9	U_ARG_	NH2	I_GLU_	OE2	2.907
6PE9	U_LYS_94	NZ	F_ASP_97	OD1	2.940
6PE9	V_ARG_90	NH1	L_ASP_1	OD1	3.701
6PE9	V_ARG_90	NH2	L_ASP_1	OD1	3.047
6PE9	V_LYS_94	NZ	L_ASP_97	OD1	3.203
6PHB	I_LYS_43	NZ	D_ASP_27	OD2	2.797
6PHB	I_LYS_47	NZ	C_GLU_55	OE1	3.460
6PHB	I_LYS_47	NZ	C_GLU_55	OE2	3.396
6PHB	I_LYS_47	NZ	D_ASP_105	OD2	2.626
6PHB	C_ARG_95	NH1	L_ASP_28	OD2	3.551
6PHB	C_ARG_95	NH1	I_GLU_39	OE2	3.728
6PHB	D_ARG_50	NH1	I_GLU_39	OE2	3.791
6PHB	D_ARG_50	NH2	I_GLU_39	OE2	2.945
6PHB	D_LYS_213	NZ	C_GLU_124	OE1	2.534
6PHB	D_LYS_213	NZ	C_GLU_124	OE2	3.508
6PHB	E_LYS_43	NZ	B_ASP_27	OD2	3.033
6PHB	E_LYS_47	NZ	A_GLU_55	OE1	3.560
6PHB	E_LYS_47	NZ	A_GLU_55	OE2	3.516
6PHB	E_LYS_47	NZ	B_ASP_105	OD1	2.522
6PHB	A_ARG_95	NH1	E_ASP_28	OD1	3.463

6PHB	A_ARG_95	NH1	E_GLU_39	OE2	3.694
6PHB	B_ARG_50	NH1	E_GLU_39	OE2	3.771
6PHB	B_ARG_50	NH2	E_GLU_39	OE2	2.963
6PHB	B_LYS_213	NZ	A_GLU_124	OE1	3.629
6PHB	B_LYS_213	NZ	A_GLU_124	OE2	2.552
6PHC	I_LYS_2	NZ	A_GLU_96	OE1	3.433
6PHC	A_LYS_209	NZ	B_GLU_122	OE2	3.367
6PHC	E_LYS_2	NZ	C_GLU_96	OE2	3.166
6PHC	C_LYS_75	NZ	A_GLU_1	OE1	3.102
6PHC	C_LYS_209	NZ	D_GLU_122	OE2	3.075
6PHD	H_ARG_52	NH2	C_ASP_131	OD2	3.559
6PHD	H_LYS_158	NZ	L_GLU_128	OE2	2.649
6PHD	H_LYS_224	NZ	L_GLU_127	OE1	2.532
6PHD	H_LYS_224	NZ	L_GLU_127	OE2	2.992
6PHD	C_LYS_118	NZ	H_ASP_109	OD1	3.874
6PHD	C_LYS_135	NZ	L_ASP_51	OD2	3.166
6PHF	A_LYS_63	NZ	C_GLU_89	OE2	2.941
6PHF	A_LYS_150	NZ	B_GLU_123	OE1	3.782
6PHF	A_LYS_216	NZ	B_GLU_122	OE1	2.642
6PHF	A_LYS_216	NZ	B_GLU_122	OE2	2.832
6PHF	G_LYS_130	NZ	A_GLU_59	OE2	2.793
6PHF	G_LYS_135	NZ	B_ASP_48	OD1	3.917
6PHF	G_LYS_135	NZ	B_ASP_48	OD2	2.691
6PHF	B_LYS_50	NZ	G_ASP_160	OD1	3.948
6PHF	B_LYS_50	NZ	G_ASP_160	OD2	3.455
6PHF	C_LYS_63	NZ	A_GLU_89	OE2	3.050
6PHF	C_LYS_150	NZ	D_GLU_123	OE2	2.663
6PHF	C_LYS_216	NZ	D_GLU_122	OE1	2.759
6PHF	C_LYS_216	NZ	D_GLU_122	OE2	3.120
6PHF	E_LYS_130	NZ	C_GLU_59	OE2	2.474
6PHF	E_LYS_135	NZ	D_ASP_48	OD1	3.909
6PHF	E_LYS_135	NZ	D_ASP_48	OD2	2.579
6PHG	A_LYS_221	NZ	B_GLU_126	OE2	3.079
6PHH	C_LYS_76	NZ	A_GLU_1	OE1	3.897
6PHH	A_LYS_76	NZ	C_GLU_1	OE1	3.451
6PHH	A_LYS_221	NZ	B_GLU_126	OE2	3.327
6PI7	B_ARG_67	NH2	A_GLU_345	OE2	3.601
6PI7	C_ARG_105	NH1	A_ASP_334	OD1	2.888
6PI7	F_ARG_105	NH1	D_ASP_334	OD1	3.009
6PI7	G_ARG_4	NH1	A_ASP_385	OD1	3.497
6PI7	G_ARG_4	NH1	A_ASP_385	OD2	3.823
6PI7	G_ARG_4	NH2	A_ASP_385	OD1	3.602
6PI7	G_ARG_4	NH2	A_ASP_385	OD2	3.033
6PI7	G_ARG_6	NH1	A_GLU_433	OE2	2.847
6PI7	G_ARG_6	NH1	A_ASP_437	OD1	3.619
6PI7	G_ARG_6	NH2	A_ASP_437	OD1	2.997
6PI7	G_ARG_6	NH2	A_ASP_440	OD2	2.762
6PYC	H_LYS_208	NZ	L_GLU_124	OE1	2.557
6PYC	H_LYS_208	NZ	L_GLU_124	OE2	3.571
6PYC	L_LYS_108	NZ	B_ASP_32	OD1	2.949
6PYC	A_ARG_99	NH1	B_ASP_91	OD1	3.714
6PYC	B_LYS_53	NZ	L_GLU_17	OE1	3.141
6PYC	B_LYS_53	NZ	L_GLU_17	OE2	3.254
6PYD	H_LYS_213	NZ	L_GLU_127	OE1	3.352
6PYD	A_LYS_213	NZ	B_GLU_127	OE1	3.596
6PZW	A_HIS_98	NE2	B_GLU_214	OE2	3.848
6PZW	A_ARG_253	NH1	K_ASP_53	OD2	2.854
6PZW	A_ARG_253	NH2	K_ASP_53	OD2	2.999

6PZW	A_ARG_419	NH1	B_GLU_214	OE2	3.897
6PZW	K_ARG_97	NH2	L ASP_50	OD1	2.825
6PZW	K_ARG_97	NH2	L ASP_50	OD2	3.390
6PZW	D_HIS_98	NE2	A_GLU_214	OE2	3.848
6PZW	D_ARG_253	NH1	F ASP_53	OD2	2.854
6PZW	D_ARG_253	NH2	F ASP_53	OD2	2.999
6PZW	D_ARG_419	NH1	A_GLU_214	OE2	3.897
6PZW	F_ARG_97	NH2	E ASP_50	OD1	2.825
6PZW	F_ARG_97	NH2	E ASP_50	OD2	3.390
6PZW	J_ARG_97	NH2	G ASP_50	OD1	2.825
6PZW	J_ARG_97	NH2	G ASP_50	OD2	3.390
6PZW	C_HIS_98	NE2	D_GLU_214	OE2	3.848
6PZW	C_ARG_253	NH1	J ASP_53	OD2	2.854
6PZW	C_ARG_253	NH2	J ASP_53	OD2	2.999
6PZW	C_ARG_419	NH1	D_GLU_214	OE2	3.897
6PZW	B_HIS_98	NE2	C_GLU_214	OE2	3.848
6PZW	B_ARG_253	NH1	H ASP_53	OD2	2.854
6PZW	B_ARG_253	NH2	H ASP_53	OD2	2.999
6PZW	B_ARG_419	NH1	C_GLU_214	OE2	3.897
6PZW	H_ARG_97	NH2	L ASP_50	OD1	2.825
6PZW	H_ARG_97	NH2	L ASP_50	OD2	3.390
6RPS	A_HIS_34	NE2	B ASP_102	OD2	3.097
6RPS	A_HIS_64	NE2	H ASP_54	OD2	2.837
6RPS	A_LYS_170	NZ	H ASP_54	OD1	3.636
6RPS	A_LYS_170	NZ	H ASP_54	OD2	2.590
6RPS	A_LYS_170	NZ	H ASP_56	OD2	2.821
6RPS	A_HIS_234	ND1	H ASP_56	OD2	3.904
6RPS	A_LYS_250	NZ	B_GLU_13	OE2	2.734
6RPS	B_HIS_64	NE2	N ASP_54	OD2	2.859
6RPS	B_HIS_103	ND1	A ASP_36	OD1	3.129
6RPS	B_HIS_103	ND1	A ASP_36	OD2	3.954
6RPS	B_LYS_170	NZ	N ASP_54	OD1	3.719
6RPS	B_LYS_170	NZ	N ASP_54	OD2	2.644
6RPS	B_LYS_170	NZ	N ASP_56	OD2	2.839
6RPS	B_HIS_234	ND1	N ASP_56	OD2	3.922
6RPS	B_LYS_250	NZ	A_GLU_13	OE2	2.991
6RPS	N_LYS_214	NZ	M ASP_122	OD1	3.095
6RPS	N_LYS_214	NZ	M ASP_122	OD2	3.107
6RPS	H_LYS_209	NZ	L_GLU_123	OE1	2.780
6RPS	H_LYS_209	NZ	L_GLU_123	OE2	3.710
6S3T	A_LYS_49	NZ	C_GLU_158	OE1	3.663
6S3T	B_LYS_49	NZ	L_GLU_158	OE1	3.761
6S3T	D_ARG_35	NH1	S ASP_332	OD1	3.467
6S3T	D_ARG_35	NH1	S ASP_332	OD2	2.946
6S3T	D_ARG_35	NH2	S ASP_332	OD2	3.071
6S3T	D_ARG_35	NH2	S ASP_334	OD1	3.408
6S3T	D_HIS_171	NE2	C ASP_171	OD2	3.832
6S3T	D_LYS_215	NZ	C_GLU_127	OE1	2.814
6S3T	D_LYS_215	NZ	C_GLU_127	OE2	3.990
6S3T	E_ARG_35	NH1	T ASP_332	OD1	3.561
6S3T	E_ARG_35	NH1	T ASP_332	OD2	3.035
6S3T	E_ARG_35	NH2	T ASP_332	OD2	3.163
6S3T	E_ARG_35	NH2	T ASP_334	OD1	3.432
6S3T	E_HIS_171	NE2	I ASP_171	OD2	3.931
6S3T	E_LYS_215	NZ	L_GLU_127	OE1	3.013
6S3T	N_ARG_35	NH1	A ASP_332	OD1	3.796
6S3T	N_ARG_35	NH1	A ASP_332	OD2	3.195
6S3T	N_ARG_35	NH2	A ASP_332	OD1	3.883

6S3T	N_ARG_35	NH2	A_ASP_332	OD2	2.517
6S3T	N_ARG_35	NH2	A_ASP_334	OD2	3.989
6S3T	N_ARG_73	NH2	S_GLU_44	OE2	2.482
6S3T	N_HIS_171	NE2	M_ASP_171	OD2	3.181
6S3T	N_LYS_215	NZ	M_GLU_127	OE1	2.964
6S3T	N_LYS_215	NZ	M_GLU_127	OE2	3.944
6S3T	R_ARG_35	NH1	B_ASP_332	OD1	3.511
6S3T	R_ARG_35	NH1	B_ASP_332	OD2	2.943
6S3T	R_ARG_35	NH2	B_ASP_332	OD2	2.873
6S3T	R_ARG_35	NH2	B_ASP_334	OD1	3.424
6S3T	R_ARG_73	NH2	T_GLU_44	OE2	2.709
6S3T	R_HIS_171	NE2	Q_ASP_171	OD2	3.265
6S3T	R_LYS_215	NZ	Q_GLU_127	OE1	2.948
6S3T	R_LYS_215	NZ	Q_GLU_127	OE2	3.831
6U02	A_HIS_98	NE2	B_GLU_214	OE2	3.838
6U02	A_ARG_209	NH1	J_GLU_128	OE2	3.226
6U02	A_ARG_210	NH2	J_ASP_412	OD1	3.355
6U02	A_ARG_210	NH2	J_ASP_412	OD2	3.535
6U02	A_ARG_419	NH1	B_GLU_214	OE2	3.906
6U02	B_HIS_98	NE2	E_GLU_214	OE2	3.839
6U02	B_ARG_209	NH1	A_GLU_128	OE2	3.226
6U02	B_ARG_210	NH2	A_ASP_412	OD1	3.355
6U02	B_ARG_210	NH2	A_ASP_412	OD2	3.535
6U02	B_ARG_419	NH1	E_GLU_214	OE2	3.906
6U02	E_HIS_98	NE2	J_GLU_214	OE2	3.838
6U02	E_ARG_209	NH1	B_GLU_128	OE2	3.226
6U02	E_ARG_210	NH2	B_ASP_412	OD1	3.355
6U02	E_ARG_210	NH2	B_ASP_412	OD2	3.536
6U02	E_ARG_419	NH1	J_GLU_214	OE2	3.906
6U02	J_HIS_98	NE2	A_GLU_214	OE2	3.838
6U02	J_ARG_209	NH1	E_GLU_128	OE2	3.226
6U02	J_ARG_210	NH2	E_ASP_412	OD1	3.356
6U02	J_ARG_210	NH2	E_ASP_412	OD2	3.535
6U02	J_ARG_419	NH1	A_GLU_214	OE2	3.906
6U59	A_LYS_34	NZ	B_ASP_612	OD1	2.489
6U59	A_ARG_504	NH1	I_GLU_662	OE1	3.209
6U59	A_ARG_504	NH1	I_GLU_662	OE2	2.833
6U59	A_ARG_504	NH2	I_GLU_662	OE2	3.911
6U59	B_LYS_574	NZ	A_ASP_107	OD1	2.403
6U59	B_ARG_579	NH2	I_GLU_584	OE1	3.024
6U59	L_ARG_50	NH1	A_GLU_269	OE2	3.175
6U59	L_ARG_50	NH2	A_GLU_268	OE1	2.965
6U59	L_ARG_50	NH2	A_GLU_269	OE2	3.221
6U59	L_ARG_95A	NH1	A_GLU_350	OE2	3.796
6U59	L_ARG_95A	NH2	A_GLU_350	OE1	3.217
6U59	L_ARG_95A	NH2	A_GLU_350	OE2	3.041
6U59	L_ARG_95A	NH2	A_GLU_351	OE1	3.921
6U59	C_LYS_34	NZ	D_ASP_612	OD1	2.489
6U59	C_ARG_504	NH1	B_GLU_662	OE1	3.208
6U59	C_ARG_504	NH1	B_GLU_662	OE2	2.832
6U59	C_ARG_504	NH2	B_GLU_662	OE2	3.910
6U59	D_LYS_574	NZ	C_ASP_107	OD1	2.403
6U59	D_ARG_579	NH2	B_GLU_584	OE1	3.024
6U59	E_ARG_50	NH1	C_GLU_269	OE2	3.175
6U59	E_ARG_50	NH2	C_GLU_268	OE1	2.965
6U59	E_ARG_50	NH2	C_GLU_269	OE2	3.221
6U59	E_ARG_95A	NH1	C_GLU_350	OE2	3.795
6U59	E_ARG_95A	NH2	C_GLU_350	OE1	3.216

6U59	E_ARG_95A	NH2	C_GLU_350	OE2	3.040
6U59	E_ARG_95A	NH2	C_GLU_351	OE1	3.921
6U59	G_LYS_34	NZ	I_ASP_612	OD1	2.489
6U59	G_ARG_504	NH1	D_GLU_662	OE1	3.209
6U59	G_ARG_504	NH1	D_GLU_662	OE2	2.833
6U59	G_ARG_504	NH2	D_GLU_662	OE2	3.910
6U59	I_LYS_574	NZ	G_ASP_107	OD1	2.403
6U59	I_ARG_579	NH2	D_GLU_584	OE1	3.025
6U59	J_ARG_50	NH1	G_GLU_269	OE2	3.175
6U59	J_ARG_50	NH2	G_GLU_268	OE1	2.965
6U59	J_ARG_50	NH2	G_GLU_269	OE2	3.220
6U59	J_ARG_95A	NH1	G_GLU_350	OE2	3.796
6U59	J_ARG_95A	NH2	G_GLU_350	OE1	3.217
6U59	J_ARG_95A	NH2	G_GLU_350	OE2	3.041
6U59	J_ARG_95A	NH2	G_GLU_351	OE1	3.921
6UG7	H_HIS_60	NE2	L_GLU_1	OE1	2.854
6UG7	H_HIS_60	NE2	L_GLU_1	OE2	3.808
6UG7	H_LYS_213	NZ	L_GLU_122	OE1	2.927
6UG7	H_LYS_213	NZ	L_GLU_122	OE2	3.960
6UG8	H_HIS_60	NE2	L_GLU_1	OE1	3.688
6UG8	H_LYS_213	NZ	L_GLU_122	OE1	2.779
6UG8	H_LYS_213	NZ	L_GLU_122	OE2	3.811
6UG9	H_HIS_60	NE2	L_GLU_1	OE2	3.673
6UG9	H_LYS_213	NZ	L_GLU_122	OE1	3.853
6UG9	A_HIS_60	NE2	B_GLU_1	OE1	3.507
6UG9	A_LYS_213	NZ	B_GLU_122	OE1	2.877
6UG9	J_HIS_60	NE2	K_GLU_1	OE1	3.585
6UG9	J_LYS_213	NZ	K_GLU_122	OE1	2.648
6UG9	J_LYS_213	NZ	K_GLU_122	OE2	3.296
6UGA	H_HIS_60	NE2	L_GLU_1	OE1	3.306
6UGA	B_HIS_60	NE2	A_GLU_1	OE2	3.932
6UGA	B_HIS_168	NE2	A_ASP_166	OD1	3.218
6UGA	B_LYS_213	NZ	A_GLU_122	OE1	3.352

Table 2: Interfacial salt bridging networks within the PDB entries of all experimentally determined antigen-antibody-related structures. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

Count	Residue A	Residue B
1945	ARG61	ASP82
1576	ARG66	ASP86
1226	ARG38	GLU46
902	ARG67	ASP90
811	ARG38	ASP86
539	LYS149	GLU195
512	ARG61	GLU79
486	ARG61	GLU81
429	ARG94	ASP101
380	ARG24	ASP70
373	ARG155	GLU185
367	ARG66	ASP89
347	ARG38	ASP90
304	HIS189	ASP151
267	ARG	ASP
262	LYS183	GLU187
245	LYS143	ASP144
222	ARG60	ASP81
217	LYS199	ASP110
200	ARG	GLU
200	LYS67	ASP90
191	ARG38	ASP89
185	LYS	GLU
178	ARG76	GLU74
177	ARG125	ASP119
173	LYS209	GLU123
171	ARG66	ASP87
160	ARG63	ASP84
157	ARG456	GLU466
156	LYS103	GLU165
153	ARG476	GLU102
149	LYS63	GLU46
141	ARG469	ASP457
138	LYS62	GLU46
138	LYS66	ASP86
131	ARG476	ASP474
128	LYS103	GLU105
122	ARG480	ASP477
117	ARG261	GLU119
116	ARG170	GLU128
114	ARG69	ASP92
113	LYS1	GLU7
111	LYS148	GLU194
111	ARG54	ASP60
109	LYS210	GLU212
107	LYS	ASP
106	LYS487	ASP47
105	ARG109	GLU89
105	LYS282	GLU275
103	LYS147	GLU154
101	ARG65	ASP86
101	ARG54	ASP78
100	LYS487	GLU91
98	ARG298	GLU381
98	ARG62	ASP83
97	ARG429	ASP113
94	ARG141	ASP77

92	LYS75	ASP72
88	ARG542	GLU647
88	ARG59	ASP368
87	ARG90	ASP60
87	ARG123	GLU120
86	HIS75	ASP73
86	LYS207	GLU381
86	ARG83	GLU85
83	ARG163	GLU131
83	HIS189	GLU185
83	ARG211	GLU187
82	LYS348	GLU351
81	HIS249	GLU482
80	ARG71	ASP368
80	LYS208	GLU123
76	LYS68	GLU85
76	ARG57	GLU82
75	ARG54	ASP77
75	ARG66	GLU84
75	ARG109	GLU67
74	LYS64	ASP61
74	LYS348	GLU269
73	LYS142	GLU105
73	ARG60	GLU78
73	ARG24	ASP75
72	LYS62	ASP90
72	ARG76	GLU81
72	LYS117	GLU114
72	LYS62	ASP86
72	ARG1113	GLU1105
71	ARG96	GLU98
71	ARG617	GLU634
70	ARG54	GLU97
70	LYS24	ASP70
70	LYS27	GLU97
69	LYS65	ASP62
69	LYS188	ASP185
69	ARG67	ASP88
68	ARG98	ASP100
67	LYS39	ASP81
66	LYS153	GLU199
66	ARG124	GLU132
65	LYS264	ASP85
65	LYS39	GLU81
65	ARG61	ASP48
63	LYS292	ASP291
62	LYS103	ASP85
62	ARG188	GLU185
61	ARG60	GLU80
60	ARG39	ASP90
60	ARG54	GLU57
60	ARG269	GLU67
59	LYS124	ASP195
59	LYS103	ASP165
59	HIS188	ASP150
59	LYS310	ASP90
59	LYS176	GLU123
59	ARG39	GLU47

58	HIS191	ASP128
58	ARG40	GLU89
57	LYS12	GLU10
56	ARG154	GLU184
55	LYS574	ASP107
54	ARG159	ASP189
54	LYS221	GLU123
53	ARG98	ASP108
53	ARG59	ASP85
53	LYS206	ASP208
52	LYS238	GLU72
52	LYS214	GLU123
51	LYS231	GLU268
51	LYS147	ASP148
51	ARG210	GLU212
51	ARG629	ASP644
50	LYS46	GLU492
50	ARG14	ASP39
50	ARG106	GLU85
49	ARG70	ASP93
49	ARG579	GLU584
49	ARG188	ASP184
49	LYS801	ASP843
48	ARG68	ASP91
47	ARG98	ASP105
47	LYS51	GLU103
47	ARG95	ASP95
46	ARG401	ASP444
46	LYS76	ASP73
46	ARG225	ASP190
46	ARG66	GLU86
45	ARG64	ASP86
44	ARG96	ASP100C
44	LYS155	GLU201
43	LYS326	GLU15
43	LYS50	ASP275
43	HIS159	ASP160
43	ARG58	ASP56
43	LYS150	GLU196
42	LYS227	GLU83
42	ARG141	GLU104
42	LYS107	GLU17
41	LYS807	GLU818
41	ARG98	ASP109
41	LYS182	GLU186
41	LYS150	ASP151
41	LYS154	GLU200
40	HIS	ASP
40	LYS1102	GLU793
40	LYS64	GLU61
39	ARG40	GLU46
39	ARG92	ASP115
39	ARG65	ASP88
39	ARG71	ASP73
39	ARG416	GLU388
39	ARG235	GLU188
39	LYS198	ASP109
39	HIS1020	ASP1024

38	LYS29	GLU85
38	ARG170	GLU131
38	LYS174	ASP164
38	ARG87	GLU89
37	LYS97	ASP99
37	ARG142	GLU105
37	LYS490	GLU492
36	ARG127	GLU131
36	ARG67	GLU87
36	ARG77	ASP102
36	LYS73	ASP53
36	ARG1054	ASP1078
36	ARG887	ASP892
36	ARG160	GLU190
35	ARG62	GLU82
35	ARG1059	ASP368
35	ARG3067	ASP3090
35	ARG841	GLU1090
35	LYS151	GLU197
35	ARG59	ASP57
34	HIS75	ASP63
34	HIS681	ASP910
34	ARG40	GLU48
34	LYS169	ASP167
34	LYS315	GLU41
34	LYS149	ASP150
34	HIS194	ASP156
34	ARG364	ASP330
34	HIS183	GLU190
34	ARG52	GLU50
34	LYS94	ASP101
33	ARG38	ASP92
33	ARG123	GLU132
33	HIS216	ASP57
33	ARG153	GLU150
33	LYS205	ASP116
33	ARG77	GLU79
32	LYS357	GLU466
32	ARG97	ASP104
32	LYS816	ASP1064
32	ARG46	ASP55
32	ARG119	ASP54
32	LYS232	GLU269
31	LYS299	GLU69
31	ARG124	GLU120
31	LYS487	GLU47
31	ARG82A	GLU81
31	HIS35	GLU50
31	LYS147	GLU195
31	ARG847	ASP844
31	ARG229	GLU256
31	LYS229	GLU83
31	LYS151	ASP152
31	ARG208	GLU101
30	HIS93	ASP119
30	LYS502	GLU513
30	ARG21	ASP37
30	HIS61	GLU52

30	HIS35	ASP95
30	ARG576	GLU574
30	LYS66	ASP51
30	ARG112	ASP141
30	ARG73	ASP61
30	HIS164	ASP167
30	HIS35	GLU95
30	ARG262	GLU175
29	HIS66	GLU64
29	LYS102	GLU104
29	LYS110	GLU198
29	LYS187	GLU191
29	LYS148	ASP149
29	LYS152	ASP153
29	LYS97	ASP32
29	LYS95	ASP100C
28	LYS351	GLU269
28	LYS143	GLU124
28	LYS52	ASP49
28	ARG46	GLU103
27	ARG422	ASP24
27	ARG6	ASP102
27	HIS	GLU
27	LYS142	GLU252
27	ARG31	ASP100A
27	LYS102	GLU164
27	ARG335	ASP326
27	ARG542	ASP648
27	LYS617	GLU634
27	LYS421	GLU370
27	ARG308	GLU164
27	ARG95	ASP91
26	ARG41	GLU49
26	LYS310	ASP86
26	LYS8	GLU119
26	LYS476	GLU102
26	ARG1058	GLU1013
26	ARG588	GLU584
26	LYS43	GLU46
26	ARG104	ASP102
26	LYS97	GLU275
26	ARG41	ASP93
26	LYS99	GLU32
26	ARG170	GLU55
25	ARG106A	ASP85
25	ARG214	ASP179
25	ARG56	GLU38
25	ARG321	GLU31
25	LYS728	ASP726
25	ARG24	GLU70
25	LYS65	GLU62
25	ARG30	ASP355
25	LYS104	ASP84
25	HIS189	ASP185
25	ARG758	ASP740
25	ARG40	GLU85
25	ARG190	ASP24
24	HIS27D	ASP28

24	LYS214	ASP122
24	ARG419	GLU153
24	ARG118	GLU425
24	ARG98	ASP104
24	ARG98	ASP107
24	LYS643	ASP5
24	LYS218	ASP220
24	ARG503	GLU654
24	LYS136	ASP153
24	HIS54	GLU52
24	LYS337	GLU293
24	LYS204	ASP206
24	LYS121	GLU429
24	LYS305	GLU172
24	LYS209	GLU211
24	ARG96	GLU55
24	ARG96	GLU50
24	HIS274	ASP270
24	ARG163	GLU171
24	ARG96	ASP50
24	LYS143	ASP145
24	ARG164	ASP166
24	ARG428	GLU433
24	ARG12	GLU10
24	ARG52	GLU58
24	ARG292	GLU277
24	HIS255	ASP217
23	ARG149	ASP77
23	LYS159	ASP224
23	ARG419	GLU100B
23	ARG201	ASP224
23	ARG98	ASP106
23	LYS231	GLU267
23	ARG311	ASP590
23	ARG18	ASP76
23	ARG165	ASP163
23	ARG617	GLU621
23	HIS194	GLU32
23	LYS302	ASP233
23	HIS195	ASP157
23	LYS146	GLU153
23	ARG65	GLU83
23	LYS96	ASP101
23	LYS53	ASP50
23	LYS38	ASP90
23	LYS779	GLU1148
23	LYS209	GLU125
23	LYS232	GLU268
23	ARG153	GLU120
23	ARG24	ASP74
23	LYS27	GLU93
22	LYS104	GLU166
22	ARG50	ASP58
22	LYS98	GLU22
22	ARG48	ASP53
22	ARG63	GLU83
22	LYS215	GLU123
22	ARG95A	ASP61

22	ARG65	ASP52
22	ARG134	ASP153
22	ARG694	ASP343
22	ARG40	ASP91
22	ARG94	GLU96
22	HIS3	ASP29
22	ARG165	GLU123
22	LYS187	ASP155
22	ARG106	GLU569
22	ARG52	GLU56
22	LYS144	ASP145
21	ARG94	ASP27
21	ARG161	GLU191
21	ARG96	ASP101
21	LYS168	ASP167
21	ARG53	ASP659
21	ARG334	ASP330
21	LYS188	GLU192
21	ARG100	ASP109
21	LYS13	ASP18
21	ARG64	ASP115
21	HIS190	ASP152
21	LYS205	ASP207
21	ARG327	GLU283
21	ARG223	ASP104
21	LYS338	GLU430
21	ARG25	ASP4
21	LYS185	GLU189
21	LYS204	ASP115
20	ARG91	GLU95
20	ARG266	ASP289
20	ARG96	GLU95
20	ARG82	GLU42
20	LYS238	ASP175
20	ARG98	ASP110
20	ARG311	ASP586
20	ARG38	GLU89
20	LYS203	ASP114
20	HIS1138	GLU793
20	LYS187	ASP184
20	HIS107	ASP105
20	ARG2061	ASP2082
20	ARG55	ASP73
20	ARG50	GLU100J
20	LYS210	GLU123
20	HIS64	ASP79
20	ARG1057	ASP1053
19	ARG188	ASP211
19	HIS24	ASP70
19	LYS12	GLU16
19	ARG100	GLU55
19	ARG62	GLU46
19	LYS110	ASP83
19	ARG61	GLU46
19	LYS145	ASP146
19	ARG74	ASP97
19	ARG73	ASP87
19	ARG57	ASP59

19	LYS305	ASP54
19	ARG23	ASP71
19	LYS142	ASP143
19	HIS193	ASP189
19	LYS113	GLU17
19	ARG82	GLU46
19	ARG95	ASP5
19	ARG103	ASP85
19	ARG64	GLU72
19	ARG35	GLU46
19	ARG403	GLU376
19	ARG366	ASP389
19	ARG74	ASP76
19	ARG108	GLU105
19	ARG419	GLU3103
19	LYS183	ASP184
19	ARG81	GLU57
19	ARG266	ASP260
19	LYS213	GLU122
19	LYS212	ASP214
18	LYS407	ASP434
18	ARG24	GLU17
18	ARG66	ASP28
18	ARG585	GLU492
18	LYS3158	ASP3159
18	ARG91	GLU100J
18	LYS144	GLU142
18	LYS57	ASP55
18	LYS110	ASP108
18	LYS27	ASP92
18	LYS432	ASP113
18	ARG1061	ASP1082
18	ARG25	GLU325
18	ARG3038	ASP3090
18	ARG50	ASP98
18	ARG58	GLU13
18	LYS58	GLU61
18	LYS149	GLU203
18	LYS209	GLU124
18	LYS46	ASP632
18	LYS153	GLU207
18	ARG55	ASP61
18	ARG2	ASP4
18	ARG44	ASP61
18	LYS46	ASP636
18	ARG235	ASP24
18	ARG24	ASP71
18	HIS188	GLU184
18	ARG3031	ASP3105
17	ARG37	ASP82
17	LYS168	ASP166
17	LYS113	GLU201
17	ARG404	GLU364
17	ARG98	ASP114
17	HIS57	ASP102
17	LYS207	GLU127
17	ARG99	ASP108
17	ARG61	GLU466

17	ARG235	GLU232
17	ARG215	GLU217
17	LYS1066	ASP1086
17	ARG427	ASP498
17	LYS149	GLU156
17	HIS193	ASP155
17	ARG102	ASP100
17	ARG156	GLU119
17	LYS1174	GLU1183
17	LYS72	ASP109
17	ARG364	ASP310
16	ARG100	ASP52
16	ARG63	GLU46
16	LYS248	GLU380
16	ARG37	GLU45
16	ARG614	GLU605
16	ARG52	GLU179
16	ARG67	GLU89
16	HIS188	ASP151
16	ARG87	ASP90
16	LYS97	ASP100B
16	HIS191	ASP153
16	ARG847	ASP726
16	LYS71	GLU55
16	ARG172	GLU174
16	ARG96	GLU1183
16	HIS78	GLU74
16	ARG224	GLU276
16	ARG561	ASP557
16	ARG411	ASP106
16	ARG68	ASP66
16	LYS51	GLU57
16	ARG220	GLU258
16	LYS38	ASP86
16	ARG61	ASP59
16	ARG253	ASP251
16	LYS92	GLU93
16	ARG190	ASP714
16	ARG86	ASP109
16	ARG192	GLU198
16	ARG300	ASP324
15	LYS222	GLU226
15	LYS779	ASP771
15	LYS3224	GLU2125
15	LYS117	ASP113
15	ARG50	GLU97
15	ARG155	ASP143
15	LYS282	ASP279
15	ARG40	GLU47
15	LYS171	GLU169
15	HIS93	GLU103
15	ARG163	ASP214
15	ARG3038	GLU3046
15	ARG336	ASP338
15	ARG24	ASP10
15	ARG83	ASP85
15	ARG51	ASP60
15	LYS354	GLU356

15	ARG45	ASP62
15	LYS118	ASP131
15	ARG419	GLU99
15	ARG96	ASP16
15	ARG187	GLU184
15	LYS159	ASP160
15	LYS153	GLU160
15	ARG256	ASP220
15	ARG159	GLU189
15	LYS409	ASP399
15	LYS68	ASP91
15	LYS153	ASP154
15	HIS20	GLU22
15	HIS192	ASP155
15	LYS162	ASP142
15	ARG196	GLU155
15	LYS190	GLU213
14	ARG304	ASP34
14	ARG50	GLU78
14	ARG194	ASP217
14	LYS106	GLU168
14	HIS191	GLU254
14	LYS19	GLU82
14	ARG130	GLU92
14	LYS109	GLU17
14	ARG108	ASP170
14	LYS215	GLU126
14	ARG38	GLU85
14	LYS3	GLU5
14	ARG65	GLU85
14	LYS320	GLU333
14	ARG75	ASP98
14	HIS94	ASP101
14	ARG216	GLU123
14	HIS66	ASP86
14	LYS58	GLU97
14	ARG211	GLU132
14	ARG35	ASP53
14	ARG75	GLU19
14	LYS1029	GLU1085
14	HIS189	ASP152
14	LYS158	ASP159
14	LYS30	ASP31
14	LYS665	GLU357
14	LYS558	GLU597
13	LYS66	GLU63
13	LYS69	ASP92
13	ARG25	ASP71
13	LYS152	GLU198
13	ARG96	GLU298
13	ARG31	ASP33
13	ARG210	GLU186
13	ARG199	ASP187
13	ARG35	ASP332
13	LYS114	GLU202
13	LYS587	GLU382
13	ARG89	GLU91
13	ARG83	ASP86

13	ARG239	ASP113
13	HIS191	ASP154
13	LYS171	GLU85
13	LYS143	GLU125
13	ARG153	GLU157
13	LYS203	ASP254
13	LYS139	ASP6
13	ARG130	GLU128
13	LYS31	ASP30
13	ARG142	GLU165
13	LYS83	GLU85
13	LYS86	GLU90
13	LYS38	GLU46
13	HIS208	GLU238
13	ARG116	GLU120
13	ARG208	ASP241
13	LYS216	GLU218
13	LYS214	GLU216
13	LYS16	GLU79
13	ARG138	GLU214
13	ARG75	GLU78
13	LYS219	GLU123
13	LYS189	ASP186
13	ARG134	ASP127
13	ARG39	ASP45
13	ARG109	GLU69
12	ARG500	GLU30
12	ARG614	GLU367
12	LYS144	GLU148
12	ARG310	ASP90
12	LYS231	GLU269
12	ARG1177	ASP1198
12	LYS88	GLU75
12	ARG100	ASP58
12	ARG201	ASP222
12	ARG95	GLU179
12	LYS50	GLU77
12	ARG215	GLU191
12	ARG73	ASP96
12	ARG72	ASP93
12	LYS643	GLU4
12	HIS255	ASP158
12	LYS149	GLU137
12	LYS601	GLU654
12	HIS312	GLU266
12	ARG94	ASP100
12	ARG94	ASP102
12	ARG232	ASP242
12	ARG101	GLU99
12	ARG94	GLU2
12	LYS174	GLU116
12	LYS661	GLU647
12	LYS217	GLU221
12	ARG11	GLU39
12	LYS218	GLU127
12	ARG337	GLU290
12	ARG98	ASP67
12	ARG36	ASP88

12	ARG360	GLU358
12	ARG1179	ASP31
12	ARG75	ASP87
12	HIS52	ASP53
12	ARG46	ASP101
12	LYS582	ASP586
12	ARG364	GLU375
12	ARG60	ASP78
12	HIS35	ASP100C
12	ARG367	ASP390
12	ARG172	GLU180
12	ARG96	ASP108
12	ARG428	ASP460
12	LYS496	GLU536
12	ARG606	ASP609
12	HIS394	GLU397
12	LYS83	ASP85
12	ARG61	ASP60
12	ARG192	ASP167
12	HIS85	GLU87
12	LYS500	ASP664
12	HIS81	ASP80
12	ARG292	GLU276
12	ARG670	GLU671
12	HIS255	ASP259
12	LYS623	GLU632
12	ARG659	ASP661
12	ARG399	GLU390
12	ARG841	ASP844
12	ARG54	ASP56
12	LYS1021	GLU793
12	ARG588	GLU492
12	ARG134	GLU150
12	ARG59	ASP65
12	LYS114	GLU116
12	LYS155	ASP133
12	LYS290	GLU128
12	ARG305	ASP329
12	ARG629	GLU376
12	LYS167	GLU83
12	ARG69	GLU55
12	ARG576	GLU104
12	LYS151	GLU147
12	LYS643	GLU529
12	LYS107	GLU169
11	LYS13	GLU16
11	ARG75	GLU85
11	ARG19	GLU81
11	LYS148	GLU111
11	LYS222	GLU125
11	LYS90	ASP63
11	LYS253	ASP232
11	LYS169	ASP170
11	ARG55	ASP309
11	ARG379	ASP211
11	LYS184	GLU188
11	LYS151	GLU158
11	ARG98	GLU50

11	HIS244	ASP113
11	LYS208	GLU122
11	LYS10	GLU25
11	LYS390	ASP393
11	ARG60	ASP66
11	LYS152	GLU159
11	LYS169	GLU85
11	ARG127	ASP160
11	HIS217	ASP104
11	ARG189	ASP125
11	LYS29	ASP279
11	ARG187	ASP183
11	LYS343	GLU347
11	ARG104	ASP107
11	LYS201	ASP112
11	ARG105	ASP71
11	ARG49	ASP368
11	LYS53	GLU50
11	LYS421	ASP180
11	ARG73	ASP71
11	LYS601	GLU657
11	ARG412	GLU299
11	ARG142	GLU103
11	ARG19	ASP81
11	LYS1062	GLU1046
11	LYS543	GLU549
11	ARG98	ASP111
11	LYS197	GLU201
11	HIS55	ASP73
11	HIS93	ASP105
11	HIS27	GLU85
11	LYS62	ASP46
11	LYS209	GLU206
11	LYS215	GLU217
11	ARG84	ASP108
11	ARG279	GLU268
11	LYS213	GLU123
11	LYS212	GLU129
11	ARG280	ASP230
11	HIS102	GLU101
11	ARG269	GLU252
11	LYS298	GLU297
11	HIS30	GLU136
11	LYS413	GLU382
11	ARG107	GLU78
10	ARG1024	ASP1069
10	ARG39	GLU81
10	ARG97	ASP100
10	ARG81	ASP104
10	LYS30	ASP28
10	ARG146	GLU169
10	LYS485	GLU267
10	ARG96	GLU94
10	ARG199	ASP220
10	ARG213	GLU123
10	ARG34	ASP39
10	LYS187	GLU114
10	ARG98	ASP102

10	ARG44	GLU42
10	ARG700	GLU756
10	ARG181	ASP174
10	LYS24	ASP76
10	LYS97	ASP101
10	ARG238	GLU246
10	ARG98	ASP115
10	HIS3063	GLU3046
10	LYS79	ASP76
10	ARG5	GLU7
10	ARG105	GLU103
10	LYS305	ASP56
10	LYS208	GLU238
10	ARG55	GLU57
10	HIS80	ASP144
10	LYS196	ASP261
10	LYS66	GLU31
10	LYS174	GLU119
10	ARG100	ASP110
10	ARG108	ASP106
10	ARG255	ASP249
10	LYS169	GLU81
10	LYS45	ASP41
10	ARG40	ASP92
10	ARG338	ASP389
10	HIS190	ASP153
10	HIS198	GLU57
10	ARG327	ASP325
10	ARG477	GLU485
10	ARG111	GLU128
10	ARG1094	ASP1101
10	ARG73	GLU86
10	LYS350	ASP395
10	LYS107	ASP17
10	LYS24	ASP75
10	ARG297	ASP304
10	LYS211	GLU123
10	ARG208	GLU178
10	ARG205	ASP226
10	ARG353	ASP112
10	LYS6	ASP54
10	ARG84	GLU82
10	ARG211	GLU213
10	LYS412	GLU365
10	LYS65	ASP6
10	LYS67	ASP28
10	ARG100	ASP100B
10	ARG64	ASP457
10	ARG95	ASP99
10	LYS155	GLU185
10	LYS264	GLU266
10	LYS665	GLU666
10	ARG212	GLU188
10	ARG101	ASP50
10	ARG66	GLU85
10	LYS211	ASP213
10	ARG3050	GLU3101
10	ARG91	ASP113

10	ARG127	GLU112
10	ARG91	GLU60
10	LYS216	ASP218
10	LYS46	ASP62
10	ARG238	ASP289
10	HIS86	ASP84
10	LYS151	GLU199
10	ARG88	ASP101
10	ARG249	GLU187
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10	ARG53	ASP254
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9	ARG61	ASP81
9	HIS585	ASP589
9	ARG96	ASP97
9	LYS52	GLU30
9	ARG45	ASP105
9	ARG95	GLU25
9	ARG101	ASP97
9	HIS35	ASP99
9	LYS65	ASP59
9	ARG30	ASP53
9	ARG585	ASP589
9	ARG53	ASP31
9	ARG209	GLU174
9	LYS583	ASP585
9	LYS217	GLU219
9	ARG192	GLU164
9	LYS35	ASP457
9	ARG327	GLU100I
9	LYS19	GLU81
9	ARG230	ASP134
9	HIS134	ASP118
9	LYS109	GLU69
9	ARG135	ASP96
9	LYS58	GLU57
9	ARG3084	GLU3082
9	ARG181	ASP183
9	ARG2061	GLU2081
9	HIS3	GLU9
9	LYS282	ASP114
9	LYS218	GLU220
9	HIS56	GLU280
9	HIS3117	GLU3001
9	LYS90	GLU85
9	ARG82	GLU89
9	HIS345	GLU137
9	LYS1008	GLU1119
9	ARG156	GLU186
9	ARG23	GLU30
9	ARG38	ASP77
9	LYS551	GLU603
9	LYS144	ASP138
9	HIS33	ASP49
9	ARG207	ASP241
9	HIS58	GLU50
9	LYS144	GLU107
9	ARG73	GLU201

9	ARG338	GLU346
9	LYS155	ASP156
9	LYS205	ASP166
9	LYS168	GLU82
9	LYS214	ASP216
9	HIS280	ASP278
9	ARG209	GLU211
9	ARG41	ASP38
9	ARG42	ASP40
9	ARG68	GLU50
9	ARG104	GLU599
9	ARG19	ASP80
9	LYS1171	GLU1169
9	ARG103	GLU100
9	ARG193	ASP189
9	ARG112	ASP93
9	ARG72	ASP368
9	ARG100D	ASP100B
9	LYS85	GLU87
9	LYS85	GLU82
9	LYS212	GLU126
9	ARG73	ASP59
9	HIS96	GLU106
9	ARG504	GLU662
9	LYS94	ASP97
9	LYS109	GLU89
9	ARG504	GLU657
9	LYS305	GLU308
9	LYS108	GLU170
9	LYS1029	ASP279
9	ARG130	ASP105
9	ARG95A	GLU350
9	ARG64	ASP94
9	LYS100E	ASP101
9	HIS160	ASP158
9	ARG188	ASP209
9	LYS61	GLU179
9	ARG56	ASP62
8	ARG334	GLU337
8	ARG598	ASP596
8	LYS44	ASP86
8	ARG98	ASP35
8	HIS192	ASP154
8	LYS166	GLU163
8	ARG316	GLU669
8	HIS36	ASP104
8	ARG96	GLU65
8	LYS601	GLU607
8	LYS637	GLU641
8	ARG134	ASP55
8	HIS238	GLU243
8	HIS224	GLU156
8	ARG419	ASP325
8	ARG354	ASP114
8	ARG253	ASP53
8	ARG21	ASP39
8	ARG141	GLU164
8	ARG100	GLU59

8	ARG189	ASP151
8	ARG419	GLU100D
8	ARG68	ASP53
8	ARG98	ASP31
8	HIS377	ASP453
8	HIS293	ASP289
8	LYS117	ASP124
8	LYS2190	ASP2187
8	ARG98	ASP101
8	ARG81	ASP38
8	ARG195	GLU192
8	ARG98	ASP113
8	ARG72	ASP74
8	LYS79	ASP50
8	LYS180	ASP244
8	LYS152	ASP119
8	ARG317	GLU315
8	LYS24	ASP74
8	HIS36	ASP102
8	ARG94	ASP106
8	ARG52	GLU178
8	ARG80	GLU44
8	ARG178	GLU153
8	LYS684	ASP1056
8	ARG39	ASP84
8	ARG43	GLU51
8	LYS413	ASP100
8	ARG230	ASP132
8	ARG120	GLU64
8	ARG94	ASP117
8	LYS208	GLU124
8	ARG97	ASP105
8	ARG527	GLU436
8	ARG400	GLU64
8	ARG101	ASP117
8	ARG241	ASP325
8	ARG378	ASP422
8	ARG435	ASP450
8	ARG63	GLU81
8	LYS306	ASP334
8	ARG52	ASP104
8	LYS330	ASP361
8	HIS741	ASP709
8	ARG480	ASP474
8	ARG66	ASP343
8	ARG157	GLU161
8	LYS215	GLU127
8	ARG419	GLU214
8	ARG69	GLU35
8	LYS217	GLU123
8	ARG181	ASP184
8	ARG66	ASP140
8	LYS68	GLU110
8	LYS104	GLU106
8	ARG370	ASP666
8	LYS73	ASP55
8	HIS96	GLU100A
8	ARG31	ASP92

8	ARG121	ASP189
8	LYS455	GLU489
8	ARG101	ASP109
8	ARG141	ASP61
8	HIS181	GLU10
8	ARG288	GLU316
8	LYS10	GLU29
8	HIS32	GLU50
8	ARG94	GLU191
8	HIS60	GLU1
8	HIS66	ASP61
8	ARG94	ASP100D
8	LYS372	GLU397
8	HIS553	GLU425
8	ARG94	GLU53
8	ARG65	ASP62
8	ARG45	GLU50
8	LYS216	GLU125
8	ARG57	GLU50
8	LYS147	GLU193
8	ARG2024	GLU2070
8	ARG26	ASP27
8	LYS163	GLU246
8	ARG400	GLU397
8	ARG73	GLU74
8	ARG50	GLU47
8	ARG170	ASP128
8	ARG152	ASP149
8	ARG94	ASP96
8	LYS166	GLU83
8	ARG141	ASP210
8	LYS219	GLU129
8	ARG45	GLU47
8	ARG95B	ASP1
8	ARG96	ASP204
8	ARG98	ASP341
8	ARG255	GLU145
8	ARG72	GLU10
8	ARG344	GLU153
8	ARG669	ASP671
8	LYS282	ASP100C
8	HIS274	GLU276
8	HIS99	GLU73
8	ARG227	GLU232
8	ARG384	GLU386
8	ARG98	GLU6
8	LYS235	GLU262
8	ARG117	GLU113
8	ARG410	GLU383
8	LYS154	ASP155
8	LYS52	ASP448
8	ARG194	ASP102
8	LYS181	GLU185
8	HIS2191	ASP2153
8	ARG105	ASP128
8	LYS152	GLU206
8	ARG82	GLU84
8	LYS105	ASP167

8	ARG332	GLU357
8	ARG387	ASP386
8	ARG867	ASP890
8	ARG154	ASP184
8	ARG101	ASP49
8	ARG64	ASP87
8	LYS176	ASP263
8	LYS136	GLU150
8	ARG542	GLU95
8	ARG516	ASP518
8	ARG69	ASP16
8	LYS154	GLU199
8	HIS109	ASP108
8	ARG46	GLU44
8	ARG344	ASP401
8	LYS88	ASP71
8	LYS81	ASP104
8	LYS186	GLU190
8	LYS92	GLU99
8	ARG127	ASP159
8	ARG160	ASP211
8	ARG112	ASP143
8	ARG29	ASP6
8	ARG97	ASP50
8	LYS54	GLU89
8	LYS48	GLU32
8	ARG36	GLU44
8	ARG85	ASP106
8	ARG164	ASP167
8	HIS98	GLU214
8	LYS12	ASP54
8	ARG216	GLU218
8	ARG210	ASP412
8	ARG196	GLU162
8	ARG51	ASP50
8	ARG27	GLU157
8	LYS433	ASP54
8	ARG95B	ASP58
8	LYS126	GLU88
8	ARG5	GLU39
8	ARG408	ASP224
8	LYS189	GLU193
8	ARG100B	GLU55
8	LYS146	ASP147
8	ARG95	ASP114
8	ARG55	ASP53
8	ARG104	GLU81
8	LYS370	GLU357
8	LYS72	ASP56
8	HIS56	ASP85
8	ARG218	GLU220
8	ARG94	ASP32
8	ARG725	ASP719
8	LYS97	ASP221
7	LYS220	GLU222
7	HIS110	ASP140
7	ARG205	GLU223
7	HIS141	GLU70

7	ARG200	ASP182
7	LYS110	GLU82
7	LYS214	ASP124
7	ARG95	ASP104
7	ARG58	ASP54
7	HIS98	GLU50
7	ARG217	GLU193
7	ARG304	GLU436
7	ARG48	GLU46
7	LYS216	GLU122
7	ARG88	ASP90
7	ARG73	ASP93
7	LYS2151	GLU2197
7	LYS173	GLU219
7	LYS157	ASP166
7	LYS232	GLU351
7	LYS196	GLU295
7	LYS149	GLU138
7	HIS129	GLU179
7	ARG141	GLU110
7	HIS58	ASP76
7	ARG90	ASP49
7	LYS219	GLU227
7	ARG53	GLU654
7	ARG44	GLU46
7	LYS19	ASP82
7	LYS207	ASP209
7	ARG370	ASP369
7	LYS159	ASP193
7	ARG204	GLU125
7	ARG44	ASP42
7	LYS102	GLU46
7	ARG390	ASP369
7	LYS317	ASP312
7	LYS210	ASP212
7	ARG221	GLU223
7	LYS59	ASP63
7	ARG179	GLU209
7	ARG39	ASP92
7	ARG204	ASP233
7	LYS668	ASP355
7	LYS175	ASP142
7	LYS175	GLU84
7	LYS82	ASP86
7	ARG57	ASP109
7	ARG865	ASP888
7	LYS326	GLU325
7	ARG39	ASP91
7	LYS109	ASP171
7	ARG87	ASP89
7	LYS107	ASP9
7	LYS94	ASP27
7	ARG108	ASP59
7	HIS172	ASP167
7	LYS44	GLU86
7	LYS1183	GLU1187
7	ARG31	ASP86
7	ARG76	GLU107

7	LYS30	ASP91
7	LYS123	GLU132
7	ARG176	GLU174
7	LYS150	GLU204
7	LYS217	GLU126
7	ARG157	ASP179
7	ARG53	ASP232
7	HIS79	ASP81
7	ARG29	ASP36
7	ARG194	GLU191
7	HIS3	GLU1
7	LYS463	ASP436
7	LYS106	GLU17
7	LYS209	GLU127
7	ARG31	ASP93
7	ARG199	GLU217
7	ARG161	ASP208
7	ARG118	GLU119
7	LYS149	ASP145
7	ARG427	GLU397
7	ARG45	GLU53
7	LYS46	ASP56
7	HIS100	GLU87
7	LYS99	ASP34
7	LYS205	GLU308
7	ARG95	ASP3
7	LYS606	GLU505
7	ARG45	GLU42
7	ARG66	GLU28
7	LYS63	ASP1
7	ARG25	GLU42
7	LYS121	GLU118
7	LYS137	ASP51
7	HIS330	ASP426
7	HIS394	ASP369
7	ARG29	ASP107
7	LYS96	ASP100Q
7	ARG370	GLU188
7	ARG112	ASP121
7	ARG1066	ASP1086
7	HIS228	ASP226
7	ARG1061	GLU1081
7	LYS111	GLU199
7	ARG838	GLU846
7	ARG72	GLU40
7	ARG505	GLU549
7	HIS377	GLU424
7	LYS104	ASP80
7	ARG100	ASP98
7	ARG103	GLU217
7	ARG98	GLU100
7	ARG103	GLU105
7	ARG62	ASP60
7	LYS356	GLU466
7	ARG123	ASP140
7	HIS19	ASP16
7	ARG45	ASP104
7	ARG40	ASP369

7	LYS208	GLU129
7	LYS59	GLU56
7	LYS61	GLU57
7	ARG255	ASP133
7	LYS95	ASP7
7	LYS335	ASP412
7	LYS42	GLU45
7	LYS213	GLU215
7	LYS63	GLU89
7	LYS140	ASP136
7	ARG163	GLU1
7	ARG582	ASP606
7	LYS212	GLU123
7	ARG67	GLU65
7	LYS697	ASP332
7	ARG91	GLU50
7	ARG480	GLU102
7	HIS162	GLU159
7	LYS275	ASP272
7	HIS151	GLU154
7	ARG172	ASP224
7	ARG107	GLU84
7	ARG154	ASP177
7	ARG58	GLU3
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7	ARG353	GLU110
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6	LYS222	GLU224
6	ARG228	GLU234
6	ARG156	ASP3
6	ARG144	GLU146
6	LYS178	ASP96
6	ARG50	ASP95
6	LYS116	GLU113
6	LYS492	GLU490
6	ARG250	ASP378
6	ARG96	ASP103
6	LYS341	ASP173
6	LYS180	GLU182
6	HIS171	ASP171
6	ARG345	GLU376
6	ARG72	GLU92
6	ARG191	ASP153
6	LYS40	ASP92
6	LYS185D	GLU185A
6	ARG284	ASP224
6	ARG114	ASP116
6	ARG45	ASP97
6	LYS209	GLU122
6	LYS277	GLU281
6	HIS75	ASP72
6	HIS56	GLU408
6	HIS33	ASP97
6	ARG463	GLU457
6	LYS215	ASP217
6	HIS160	GLU175
6	ARG27	GLU93

6	HIS223	GLU82
6	LYS432	GLU429
6	HIS268	GLU294
6	ARG194	ASP190
6	LYS58	ASP183
6	LYS290	GLU268
6	ARG348	ASP356
6	LYS137	ASP73
6	LYS653	GLU650
6	LYS189	GLU160
6	ARG163	GLU128
6	HIS72	GLU64
6	LYS317	ASP340
6	HIS49	ASP55
6	ARG100	ASP60
6	LYS631	GLU639
6	ARG256	GLU253
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6	ARG188	GLU208
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6	ARG31	ASP102
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6	ARG39	GLU85
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6	ARG220	ASP241
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6	ARG485	GLU383
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6	ARG123	GLU203
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6	LYS110	ASP55
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6	HIS42	GLU38
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6	ARG106	GLU177
6	LYS148	GLU152
6	ARG316	ASP236

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6	LYS107	GLU64
6	LYS305	ASP322
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6	LYS112	GLU200
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6	ARG199	GLU219
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6	ARG166	ASP143
6	LYS59	ASP57
6	LYS313	GLU296
6	LYS407	GLU5
6	ARG691	ASP343
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6	ARG100H	ASP91
6	LYS17	ASP55
6	ARG64	ASP61
6	ARG107	ASP114
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6	ARG57	GLU65
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6	ARG95	GLU100E
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6	ARG80	GLU92
6	LYS5	ASP88
6	LYS71	GLU87
6	ARG185	ASP159
6	ARG327	ASP148A
6	LYS243	GLU153
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6	ARG103	GLU230
6	ARG52A	ASP674

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6	HIS162	ASP226
6	ARG429	ASP74
6	ARG62	GLU26
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6	ARG143	GLU106
6	LYS58	ASP3
6	ARG193	ASP184
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6	LYS588	ASP589
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6	LYS213	GLU127
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6	ARG249	GLU381
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6	HIS585	GLU492
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6	LYS155	ASP193
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6	ARG112	ASP198
6	ARG293	ASP294
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6	ARG239	GLU243
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5	ARG19	ASP97
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5	LYS13	ASP154
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5	ARG117	ASP183
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5	ARG114	ASP115
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5	ARG25	ASP22
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5	ARG106	ASP109
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5	LYS31	ASP92
5	HIS168	ASP166
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4	LYS215	ASP122
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4	LYS28	GLU382
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4	ARG457	ASP31E

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4	HIS32	ASP31
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4	ARG279	ASP242
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4	ARG419	GLU426
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4	ARG348	GLU450

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4	HIS15	ASP55
4	ARG560	ASP488
4	ARG552	GLU550
4	LYS406	ASP106
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4	ARG98	ASP103
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4	ARG303	ASP301
4	LYS423	ASP358
4	LYS339	GLU336
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4	LYS329	GLU333
4	ARG414	GLU367
4	HIS20	GLU157
4	ARG96	GLU100I
4	LYS62	GLU1
4	LYS218	GLU261
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4	LYS557	ASP560
4	LYS31	GLU20
4	LYS212	GLU127
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4	LYS49	ASP100A
4	LYS247	ASP251
4	ARG100	ASP104
4	LYS208	GLU128
4	LYS192	ASP160
4	ARG337	GLU333
4	LYS435	GLU465
4	ARG236	ASP44
4	LYS461	ASP448
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4	ARG6	GLU100
4	LYS224	GLU125
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4	ARG99	ASP114
4	LYS307	ASP386
4	HIS274	ASP179
4	LYS230	ASP274
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4	LYS215	GLU121
4	HIS90	ASP33
4	ARG106	GLU168
4	ARG101	GLU60
4	ARG43	GLU46
4	LYS150	GLU127

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4	ARG2598	ASP2603
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4	ARG41	GLU165
4	ARG38	GLU87
4	ARG38	GLU86
4	ARG536	GLU457
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4	ARG941	ASP362
4	ARG52	ASP107
4	ARG155	GLU152
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4	ARG12	ASP242
4	ARG668	GLU350
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4	ARG209	GLU128
4	ARG499	ASP489
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4	LYS124	ASP122
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4	ARG1009	ASP1368
4	HIS308	ASP386
4	HIS196	GLU192
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4	LYS208	ASP206
4	ARG99	ASP109
4	LYS17	ASP57
4	ARG99	ASP104
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4	ARG190	GLU188
4	ARG216	ASP217
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4	LYS217	GLU129
4	LYS653	ASP17
4	ARG476	ASP518
4	ARG536	ASP534
4	LYS69	ASP29
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4	ARG95	ASP95D
4	ARG852	GLU849
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4	HIS111	ASP23
4	ARG2519	ASP2834
4	HIS689	GLU672
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4	LYS168	GLU78
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4	ARG220	ASP105

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4	ARG111	ASP102
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4	ARG110	GLU450
4	ARG334	GLU302
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4	HIS33	ASP105
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4	ARG284	ASP307
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4	LYS323	GLU358
4	ARG213	GLU218
4	ARG363	ASP106
4	ARG168	ASP100L
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4	LYS103	ASP83
4	ARG380	GLU383
4	ARG58	ASP95D
4	HIS452	GLU450
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4	ARG153	GLU183

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4	LYS312	ASP56
4	LYS312	ASP54
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4	HIS189	GLU85
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4	ARG162	GLU192
4	LYS251	ASP164
4	ARG624	ASP621
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4	LYS80	ASP72
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4	ARG439	GLU377
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4	HIS55	ASP143
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4	LYS439	GLU356

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4	LYS394	GLU385
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4	ARG429	ASP408
4	ARG13	GLU16
4	HIS32	ASP97
4	LYS171	ASP137
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4	ARG567	ASP590
4	HIS377	GLU425
4	ARG94	GLU68
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4	LYS284	ASP312
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4	ARG170	GLU1
4	ARG366	ASP386

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4	ARG339	GLU322
4	LYS168	ASP169
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4	LYS76	GLU122
4	LYS289	GLU313
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4	HIS100G	GLU95
4	ARG54	ASP50
4	ARG124	ASP132
4	ARG136	GLU134
4	ARG97	ASP27
4	ARG384	GLU360
4	LYS114	ASP50
4	LYS114	ASP51
4	HIS35	ASP4
4	HIS553	ASP387
4	LYS32	ASP58
4	LYS176	GLU173
4	ARG379	ASP330
4	LYS253	GLU128
4	ARG495	ASP429
4	HIS49	ASP101
4	ARG251	GLU351
4	ARG184	ASP63
4	ARG35	GLU32
4	LYS181	GLU173
4	LYS47	GLU55
4	HIS29	ASP12
4	ARG135	GLU206
4	LYS491	GLU495
4	ARG110	GLU94
4	ARG213	GLU189
4	HIS28	ASP138
4	ARG235	ASP222
4	ARG100	ASP66A
4	ARG275	GLU272
4	ARG171	ASP173
4	ARG484	ASP408
4	ARG98	ASP72
4	LYS1207	GLU1381
4	ARG302	GLU305
4	LYS633	ASP634
4	LYS402	GLU404
4	LYS55	ASP101
4	LYS55	ASP106
4	ARG511	ASP509
4	HIS274	ASP278
4	LYS248	GLU247
4	HIS100	ASP96
4	HIS19	GLU50

4	HIS102	GLU64
4	LYS28	ASP99
4	ARG276	ASP273
4	ARG63	GLU138
4	LYS406	ASP224
4	ARG66	GLU83
4	ARG128	ASP103
4	ARG336	GLU333
4	ARG44	ASP60
4	LYS96	ASP108
4	ARG25	GLU82
4	LYS300	ASP249
4	LYS187	GLU97
4	ARG149	ASP136
4	ARG211	ASP558
4	HIS35	ASP33
4	ARG131	GLU142
4	ARG354	GLU404
4	ARG128	ASP124
4	ARG152	GLU150
4	HIS68	ASP21
4	LYS203	ASP32
4	ARG99	ASP53
4	ARG59	GLU221
4	ARG86	ASP107
4	ARG3087	ASP3089
4	LYS161	ASP146
4	LYS47	GLU54
4	LYS23	ASP69
4	ARG80	GLU35
4	ARG25	ASP101
4	LYS513	ASP557
4	LYS446	ASP50
4	ARG316	ASP295
4	LYS207	ASP130
4	ARG313	GLU310
4	ARG550	GLU527
4	ARG25	ASP27
4	LYS145	GLU143
4	HIS35	GLU52
4	HIS35	ASP98
4	LYS39	GLU40
4	LYS532	GLU535
4	ARG97	ASP109
4	LYS157	GLU160
4	LYS665	ASP355
4	LYS433	ASP56
4	LYS267	GLU264
4	HIS142	ASP143
4	LYS179	GLU181
4	ARG50	GLU57
4	ARG75	GLU71
4	LYS224	ASP122
4	HIS96	ASP5
4	LYS62	ASP83
4	ARG147	GLU142
4	LYS62	ASP1
4	LYS233	ASP237

4	LYS69	ASP59
4	ARG145	GLU116
4	ARG484	ASP405
4	LYS197	ASP55
4	ARG162	ASP90
4	HIS56	GLU9
4	ARG398	ASP394
4	LYS138	ASP169
4	ARG118	GLU12
4	ARG102	ASP92
4	ARG476	GLU488
4	LYS443	ASP58
4	ARG327	GLU27
4	HIS573	ASP567
4	ARG107	ASP169
4	ARG24	GLU3
4	ARG250	GLU437
4	ARG66	GLU88
4	ARG355	GLU82
4	ARG257	GLU153
4	LYS109	GLU171
4	LYS221	GLU126
4	ARG4	ASP385
4	ARG52	GLU49
4	LYS66	ASP89
4	ARG514	GLU531
4	LYS347	GLU299
4	LYS109	GLU111
4	HIS242	GLU243
4	ARG372	ASP390
4	LYS7	ASP49
4	LYS55	GLU59
4	ARG47	ASP1
4	HIS213	GLU58
3	LYS213	GLU130
3	ARG319	GLU304
3	ARG40	ASP68
3	ARG88	GLU61
3	ARG304	ASP31
3	LYS76	GLU85
3	ARG315	ASP93
3	ARG50	ASP61
3	LYS175	GLU174
3	ARG220	GLU221
3	ARG143	ASP61
3	ARG170	GLU166
3	LYS67	ASP64
3	ARG97	ASP32
3	LYS72	ASP69
3	LYS287	GLU273
3	ARG221	GLU218
3	LYS245	ASP242
3	LYS155	ASP157
3	LYS260	ASP232
3	HIS123	ASP106
3	HIS105	GLU61
3	LYS127	ASP123
3	LYS161	GLU149

3	LYS200	ASP111
3	HIS35	GLU33
3	ARG97	ASP368
3	LYS50	ASP100C
3	ARG219	GLU197
3	LYS84	GLU86
3	HIS20	ASP217
3	LYS74	ASP56
3	LYS326	GLU11
3	ARG50	GLU95
3	LYS309	ASP314
3	ARG100	ASP28
3	ARG	ASP70
3	ARG1024	ASP1070
3	LYS96	ASP50
3	HIS414	GLU391
3	ARG186	GLU48
3	ARG255	GLU162
3	LYS192	ASP137
3	LYS87	ASP90
3	ARG97	GLU62
3	LYS103	GLU83
3	ARG100	GLU50
3	ARG90	ASP56
3	ARG61	ASP101
3	ARG101	GLU55
3	ARG192	GLU58
3	HIS189	GLU196
3	LYS201	ASP200
3	HIS61	GLU50
3	HIS260	ASP262
3	LYS164	ASP85
3	LYS126	ASP122
3	LYS98	ASP107
3	LYS204	GLU112
3	LYS104	GLU3
3	ARG119	GLU83
3	LYS73	ASP256
3	LYS572	GLU238
3	ARG92	ASP166
3	HIS134	ASP133
3	ARG102	GLU201
3	ARG65	ASP59
3	ARG59	ASP102
3	ARG171	ASP138
3	ARG909	ASP912
3	ARG275	GLU255
3	LYS354	ASP355
3	ARG74	ASP58
3	LYS306	GLU318
3	HIS347	ASP370
3	HIS19	GLU15
3	ARG38	ASP81
3	HIS119	GLU117
3	LYS232	ASP253
3	LYS125	GLU122
3	LYS30	GLU95
3	ARG1055	GLU1085

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3	LYS143	ASP11
3	HIS106	GLU102
3	ARG107	ASP17
3	LYS154	GLU129
3	HIS34	ASP36
3	ARG847	GLU1017
3	LYS45	ASP97
3	ARG37	GLU46
3	LYS101	ASP105
3	LYS107	GLU91
3	LYS298	ASP343
3	LYS421	GLU145
3	ARG209	GLU354
3	ARG193	GLU190
3	HIS152	GLU125
3	ARG42	GLU91
3	LYS347	GLU312
3	LYS142	GLU249
3	LYS142	GLU247
3	ARG419	GLU103
3	LYS74	ASP71
3	LYS212	GLU230
3	LYS121	ASP113
3	LYS154	GLU208
3	HIS586	GLU555
3	HIS104	ASP105
3	HIS108	ASP106
3	LYS175	ASP177
3	ARG151	ASP140
3	ARG50	ASP275
3	LYS227	GLU188
3	ARG182	ASP180
3	HIS113	GLU129
3	LYS48	ASP35
3	HIS195	ASP191
3	ARG203	ASP177
3	LYS76	ASP78
3	HIS467	GLU50
3	LYS149	GLU127
3	LYS148	ASP160
3	ARG94	GLU7
3	ARG97	ASP110
3	ARG163	ASP162
3	HIS324	GLU362
3	ARG75	ASP65
3	LYS274	GLU318
3	ARG419	ASP54
3	ARG111	GLU102
3	ARG41	GLU90
3	HIS27	GLU1
3	LYS223	ASP134
3	ARG50	GLU100I
3	LYS120	ASP740
3	LYS99	GLU96
3	HIS125	GLU178
3	ARG62	GLU80
3	ARG31	GLU113

3	HIS87	ASP11
3	LYS22	GLU102
3	HIS96	ASP97
3	LYS217	ASP128
3	LYS87	GLU89
3	ARG176	ASP150
3	LYS306	GLU61
3	LYS279	GLU244
3	LYS30	GLU54
3	LYS88	GLU85
3	ARG1070	GLU1090
3	ARG172	GLU123
3	ARG50	ASP560
3	LYS384	GLU306
3	ARG277	GLU275
3	LYS326	GLU322
3	LYS287	GLU290
3	ARG1567	ASP1590
3	ARG50	GLU166
3	HIS164	ASP162
3	ARG2	ASP74
3	HIS134	GLU148
3	ARG40	GLU29
3	LYS103	ASP105
3	ARG54	ASP32
3	ARG27	GLU431
3	LYS146	GLU202
3	LYS218	GLU122
3	ARG108	GLU223
3	LYS121	ASP137
3	ARG2024	ASP2070
3	LYS127	GLU122
3	LYS83	GLU36
3	ARG104	GLU166
3	ARG213	ASP214
3	ARG76	ASP54
3	LYS69	GLU72
3	LYS399	GLU497
3	ARG213	GLU277
3	ARG97	GLU27
3	HIS19	ASP24
3	LYS415	ASP378
3	LYS22	GLU70
3	ARG59	ASP367
3	HIS32	GLU1
3	ARG198	GLU152
3	ARG198	GLU150
3	ARG327	ASP52
3	ARG155	ASP185
3	LYS80	ASP84
3	LYS144	GLU194
3	LYS229	ASP1
3	ARG37	ASP104
3	HIS33	ASP27
3	HIS164	GLU166
3	LYS150	GLU202
3	LYS212	GLU324
3	LYS232	GLU267

3	ARG28	ASP26
3	ARG62	ASP112
3	ARG67	GLU25
3	HIS205	ASP220
3	LYS36	GLU32
3	LYS807	ASP805
3	LYS201	ASP196
3	LYS221	GLU189
3	ARG419	GLU108
3	LYS49	GLU240
3	LYS107	ASP30
3	ARG103	GLU165
3	LYS350	GLU347
3	LYS228	GLU147
3	HIS76	ASP92
3	LYS1064	GLU1061
3	LYS443	GLU422
3	ARG95A	GLU351
3	LYS77	ASP53
3	ARG294	GLU285
3	ARG75	ASP97
3	ARG31	ASP95
3	HIS155	GLU152
3	LYS399	ASP392
3	LYS697	GLU694
3	LYS12	GLU57
3	ARG2566	ASP2589
3	LYS71	GLU25
3	ARG77	GLU33
3	LYS87	ASP79
3	LYS585	ASP563
3	LYS446	GLU293
3	LYS46	ASP44
3	HIS120	GLU59
3	LYS203	GLU255
3	LYS217	GLU121
3	LYS52	GLU55
3	LYS63	ASP61
3	ARG95	GLU413
3	LYS610	GLU703
3	ARG29	ASP26
3	ARG91	ASP99
3	ARG71	ASP72
3	ARG110	GLU108
3	HIS618	GLU716
3	ARG430	ASP408
3	LYS49	GLU53
3	ARG313	ASP281
3	ARG142	GLU135
3	LYS81	GLU59
3	HIS34	ASP52
3	ARG123	ASP132
3	LYS130	GLU132
3	HIS355	ASP358
3	ARG1099	GLU1097
3	LYS65	GLU64
3	ARG44	GLU56
3	ARG97	ASP347

3	LYS98	GLU32
3	ARG113	ASP116
3	ARG14	ASP17
3	LYS53	ASP101
3	HIS31	ASP28
3	ARG61	GLU32
3	ARG59	ASP101
3	ARG304	ASP100A
3	LYS65	ASP88
3	ARG838	GLU887
3	HIS110	GLU106
3	ARG36	ASP38
3	HIS585	GLU584
3	ARG30	ASP93
3	ARG124	ASP41
3	LYS128	ASP190
3	ARG124	ASP216
3	ARG78	ASP92
3	ARG354	GLU379
3	ARG267	ASP41
3	ARG276	ASP314
3	ARG8	ASP106
3	ARG520	GLU87
3	ARG587	GLU565
3	ARG74	GLU76
3	ARG52	ASP47
3	LYS556	GLU755
3	ARG169	GLU166
3	LYS54	ASP101
3	LYS274	ASP255
3	LYS21	ASP23
3	ARG60	ASP55
3	ARG103	GLU29
3	ARG1094	ASP1024
3	HIS49	ASP100C
3	ARG85	GLU105
3	LYS225	ASP296
3	ARG1031	GLU1099
3	LYS292	GLU133
3	ARG36	ASP55
3	ARG102	ASP67
3	LYS400	ASP28
3	LYS19	GLU89
3	LYS211	GLU120
3	LYS343	ASP85
3	HIS257	GLU264
3	ARG64	ASP1
3	LYS182	ASP165
3	LYS130	GLU150
3	ARG91	ASP50
3	HIS121	ASP217
3	ARG61	ASP79
3	HIS52A	GLU52B
3	ARG30	GLU37
3	HIS120	ASP106
3	HIS1051	GLU1047
3	HIS105	ASP474
3	LYS60	GLU74

3	ARG209	ASP324
3	ARG95	ASP100E
3	HIS27	ASP25
3	LYS50	ASP30
3	ARG172	GLU149
3	HIS192	ASP125
3	HIS108	GLU50
3	LYS43	GLU64
3	HIS43	GLU46
3	ARG469	GLU477
3	ARG31	ASP94
3	LYS49	ASP99
3	LYS306	GLU322
3	ARG229	GLU231
3	HIS211	ASP253
3	ARG366	ASP150
3	ARG105	GLU71
3	ARG17	ASP35
3	LYS171	GLU87
3	LYS169	GLU215
3	ARG31	ASP140
3	LYS50	ASP254
3	HIS42	ASP41
3	ARG932	ASP89
3	LYS280	GLU304
3	ARG211	GLU189
3	ARG100H	ASP101
3	ARG50	GLU268
3	HIS249	GLU83
3	LYS87	GLU85
3	ARG69	GLU77
3	HIS560	GLU537
3	ARG98	ASP96
3	ARG542	GLU648
3	LYS322	GLU333
3	ARG153	ASP106
3	LYS189	ASP358
3	LYS126	GLU123
3	LYS28	GLU100
3	ARG90	GLU106
3	LYS293	GLU295
3	ARG95B	ASP95D
3	LYS214	GLU122
3	LYS360	GLU362
3	LYS170	GLU84
3	ARG50	GLU101
3	LYS190	ASP158
3	LYS73	GLU166
3	ARG2567	ASP2590
3	ARG28	ASP457
3	LYS335	GLU408
3	LYS1035	GLU1039
3	LYS100	ASP124
3	ARG217	GLU219
3	LYS1219	GLU1221
3	LYS149	GLU154
3	LYS145	GLU124
3	LYS	GLU127

3	LYS223	GLU126
3	ARG95	ASP92
3	ARG1038	ASP1086
3	LYS175	GLU94
3	ARG68	GLU65
3	LYS176	GLU177
3	ARG317	GLU100B
3	ARG334	GLU184
3	HIS70	GLU21
3	LYS144	ASP137
3	ARG50	ASP101
3	HIS203	ASP252
3	ARG337	GLU340
3	ARG112	ASP109
3	HIS170	GLU172
3	ARG49	ASP52
3	ARG36	GLU58
3	LYS55	ASP35
3	LYS24	ASP69
3	HIS220	GLU218
3	LYS174	ASP171
3	ARG77	ASP31
3	ARG123	ASP54
3	LYS227	GLU124
3	LYS363	GLU346
3	LYS123	GLU185
3	ARG1155	GLU1185
3	ARG691	GLU818
3	LYS72	ASP71
3	ARG194	ASP156
3	ARG100	GLU113
3	LYS58	ASP57
3	ARG100B	ASP30
3	LYS391	ASP134
3	HIS1042	ASP1041
3	LYS3012	GLU3010
3	LYS247	GLU249
3	LYS344	GLU340
3	ARG52	GLU61
3	ARG204	ASP149
3	ARG59	GLU106
3	ARG120	GLU123
3	ARG82A	ASP65
3	LYS588	GLU584
3	ARG399	ASP401
3	ARG102	ASP108
3	ARG705	GLU725
3	ARG66	ASP51
3	LYS89	GLU95
3	ARG705	GLU727
3	HIS394	ASP392
3	LYS168	GLU190
3	ARG1212	ASP100C
3	LYS52	ASP474
3	ARG52A	GLU144
3	HIS1189	ASP1151
3	LYS432	ASP56
3	ARG87	GLU65

3	LYS44	GLU106
3	HIS84	ASP105
3	LYS146	ASP95A
3	ARG304	GLU286
3	ARG441	GLU94
3	ARG56	GLU76
3	ARG261	ASP804
3	ARG204	GLU196
3	ARG279	GLU276
3	ARG333	ASP293
3	ARG28	ASP95D
3	ARG117	ASP45
3	LYS105	GLU3
3	ARG106	GLU100
3	LYS171	GLU13
3	ARG144	GLU167
3	ARG35	ASP73
3	ARG32	ASP28
3	LYS159	GLU168
3	LYS658	GLU654
3	HIS327	ASP359
3	ARG1476	ASP1474
3	ARG96	GLU104
3	HIS94	ASP7
3	LYS1021	GLU1017
3	HIS240	ASP282
3	LYS194	ASP191
3	HIS53	ASP54
3	ARG90	GLU92
3	HIS165	ASP167
3	ARG137	ASP97
3	ARG33	ASP6
3	ARG235	ASP28
3	LYS117	GLU10
3	LYS40	GLU85
3	ARG98	ASP159
3	LYS94	ASP102
3	ARG225	ASP233
3	HIS325	ASP359
3	ARG141	ASP146
3	ARG40	GLU103
3	LYS322	ASP95
3	ARG39	ASP93
3	ARG1038	GLU1046
3	ARG164	ASP170
3	HIS414	GLU413
3	ARG164	ASP179
3	HIS44	GLU40
3	LYS143	ASP29
3	ARG33	ASP27
3	LYS103	ASP233
3	HIS131	ASP270
3	LYS137	ASP124
3	HIS86	ASP88
3	LYS421	GLU54
3	ARG1456	GLU1466
3	LYS417	GLU358
3	ARG74	ASP72

3	LYS966	GLU85
3	HIS93	ASP434
3	ARG50	GLU49
3	ARG310	GLU376
3	LYS82	GLU77
3	ARG145	ASP234
3	LYS156	ASP191
3	LYS107	GLU84
3	LYS55	GLU53
3	ARG76	ASP128
2	ARG85	ASP110
2	HIS282	ASP98
2	LYS102	ASP169
2	LYS290	GLU127
2	ARG54	GLU77
2	ARG441	ASP454
2	HIS191	ASP
2	ARG315	ASP95
2	ARG100A	GLU106
2	LYS1142	GLU1105
2	LYS345	GLU123
2	LYS174	ASP172
2	LYS40	GLU90
2	LYS153	ASP104
2	LYS449	ASP447
2	LYS216	ASP113
2	LYS914	GLU485
2	LYS191	ASP188
2	LYS35	ASP50
2	LYS44	ASP89
2	HIS30	GLU104
2	LYS391	ASP393
2	LYS13	GLU17
2	LYS30	GLU4
2	LYS49	GLU105
2	LYS101	GLU103
2	LYS232	ASP230
2	HIS50	ASP264
2	LYS49	GLU108
2	ARG31	GLU133
2	ARG2537	ASP2589
2	LYS2663	ASP2669
2	ARG97	ASP107
2	ARG207	GLU258
2	ARG277	ASP273
2	ARG106	ASP116
2	HIS84	GLU82
2	LYS287	GLU301
2	LYS239	ASP240
2	LYS64	GLU187
2	ARG73	GLU288
2	LYS110	GLU100
2	LYS46	GLU44
2	ARG311	ASP90
2	ARG526	GLU525
2	ARG144	GLU142
2	ARG144	GLU141
2	LYS1357	GLU1466

2	ARG145	ASP91
2	ARG216	GLU231
2	LYS78	ASP90
2	HIS50	GLU95
2	LYS205	ASP219
2	ARG338	ASP390
2	ARG106	GLU129
2	LYS206	ASP212
2	ARG437	GLU438
2	ARG120	ASP216
2	LYS107	ASP89
2	HIS53	GLU52
2	ARG271	GLU257
2	LYS81	ASP100
2	ARG194	GLU216
2	LYS212	ASP203
2	ARG160	ASP190
2	ARG506	ASP482
2	HIS288	ASP257
2	LYS490	GLU49
2	LYS107	ASP109
2	ARG40	ASP336
2	LYS120	ASP117
2	LYS40	ASP38
2	HIS489	GLU168
2	ARG65	ASP66
2	LYS3	ASP1
2	LYS287	ASP291
2	ARG53	GLU104
2	ARG135E	ASP133E
2	LYS117	ASP118
2	LYS312	GLU282
2	LYS156	ASP188
2	LYS431	ASP101
2	ARG101	GLU33
2	LYS25	ASP4
2	ARG423	ASP162
2	ARG124	ASP126
2	ARG441	ASP444
2	LYS11	ASP91
2	LYS96	GLU57
2	HIS35	ASP69
2	LYS44	GLU46
2	LYS266	GLU128
2	ARG95	ASP28
2	ARG98	ASP100A
2	ARG1167	ASP1123
2	LYS198	ASP163
2	LYS219	ASP123
2	ARG84	GLU60
2	LYS76	GLU1
2	LYS769	ASP399
2	ARG58	GLU69
2	ARG162	ASP166
2	ARG103	ASP101
2	ARG167	ASP166
2	ARG93	GLU105
2	LYS13	GLU63

2	LYS93	ASP116
2	ARG98	ASP27
2	LYS269	GLU69
2	LYS204	ASP75
2	ARG53	GLU11
2	LYS69	ASP75
2	LYS65	ASP66
2	LYS262	GLU266
2	HIS24	GLU10
2	ARG92	ASP87
2	LYS102	ASP84
2	LYS242	GLU214
2	HIS133	ASP117
2	LYS2	GLU96
2	ARG213	GLU125
2	ARG1538	GLU1546
2	LYS316	GLU302
2	HIS204	GLU203
2	LYS14	GLU11
2	LYS14	ASP25
2	ARG51	ASP113
2	LYS6	GLU38
2	ARG63	ASP83
2	HIS21	GLU27
2	LYS147	GLU111
2	LYS231	GLU145
2	LYS218	GLU123
2	LYS191	GLU214
2	HIS361	GLU359
2	ARG1587	GLU1589
2	ARG38	ASP
2	LYS140	GLU212
2	ARG18	GLU85
2	ARG513	GLU541
2	LYS131	ASP157
2	LYS261	GLU83A
2	LYS623	ASP621
2	HIS874	GLU869
2	LYS205	ASP53
2	ARG106	ASP54
2	ARG95	ASP26
2	ARG398	ASP405
2	ARG1024	ASP70
2	ARG2097	ASP2001
2	ARG398	ASP400
2	ARG398	ASP409
2	LYS70	ASP72
2	HIS73	ASP72
2	ARG112	GLU98
2	LYS308	GLU50
2	LYS99	GLU33
2	LYS	GLU195
2	LYS327	ASP331
2	HIS213	ASP175
2	ARG107	GLU17
2	LYS357	ASP464
2	LYS44	ASP104
2	HIS566	ASP553

2	ARG50	GLU62
2	LYS95	ASP92
2	ARG	ASP82
2	HIS194	ASP190
2	ARG65	ASP58
2	LYS100	GLU91
2	ARG140	GLU117
2	ARG97	GLU95
2	ARG167	GLU164
2	ARG168	ASP214
2	LYS177	GLU180
2	ARG255	GLU119
2	ARG171	GLU73
2	LYS177	GLU219
2	LYS255	ASP259
2	LYS115	GLU85
2	LYS156	GLU127
2	LYS310	ASP52
2	ARG106	ASP17
2	ARG49	GLU88
2	ARG144	ASP91
2	ARG98	ASP50
2	LYS52C	ASP674
2	LYS40	GLU76
2	LYS39	GLU42
2	ARG287	GLU235
2	ARG54	ASP167
2	HIS81	GLU77
2	LYS311	ASP285
2	HIS87	GLU166
2	ARG161	GLU159
2	ARG50	GLU5
2	ARG197	ASP218
2	LYS105	GLU17
2	LYS250	GLU13
2	LYS441	GLU443
2	LYS232	GLU143
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2	ARG264	ASP274
2	ARG155	ASP201
2	ARG90	ASP1
2	LYS80	GLU79
2	LYS189	ASP190
2	ARG1298	ASP1300
2	LYS41	ASP46
2	ARG188	ASP831
2	LYS514	GLU541
2	ARG553	ASP107
2	LYS14	ASP18
2	LYS212	GLU101
2	ARG1469	ASP1457
2	ARG405	ASP118
2	HIS152	GLU916
2	LYS129	GLU213
2	ARG101	GLU119
2	ARG277	GLU250
2	ARG50	ASP35
2	LYS105	GLU85

2	ARG27	ASP323
2	ARG582	GLU605
2	LYS219	ASP93
2	ARG136	GLU145
2	LYS161	GLU125
2	LYS98	ASP111
2	ARG28	ASP93
2	LYS368	ASP227
2	HIS94	GLU18
2	LYS745	ASP907
2	ARG10	ASP255
2	LYS344	GLU369
2	LYS73	GLU45
2	HIS34	ASP32
2	LYS37	GLU45
2	LYS369	ASP352
2	ARG101	ASP113
2	LYS50	GLU66
2	ARG373	ASP372
2	LYS185	ASP57
2	LYS41	GLU39
2	ARG407	ASP435
2	ARG32	ASP65
2	ARG294	ASP368
2	ARG59	ASP80
2	ARG1099	ASP1101
2	LYS240	GLU217
2	LYS120	ASP265
2	LYS100	GLU87
2	LYS184	ASP211
2	ARG269	ASP217
2	LYS357	GLU464
2	ARG38	ASP100
2	LYS387	ASP386
2	HIS47	GLU45
2	ARG73	GLU44
2	LYS466	GLU95
2	ARG538	ASP590
2	ARG151	GLU154
2	LYS152	ASP127
2	ARG98	ASP119
2	LYS50	ASP98
2	LYS224	GLU127
2	LYS40	GLU47
2	LYS150	GLU123
2	HIS32	ASP102
2	ARG193	GLU274
2	LYS93	GLU3
2	ARG45	GLU111
2	ARG838	ASP890
2	ARG84	GLU45
2	LYS7	ASP80
2	ARG385	ASP324
2	HIS273	ASP275
2	ARG213	GLU213
2	HIS198	GLU199
2	LYS122	ASP216
2	LYS141	GLU172

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2	ARG337	GLU322
2	ARG466	ASP458
2	HIS4	ASP183
2	ARG42	GLU7
2	LYS26	ASP108
2	ARG94	GLU179
2	ARG48	ASP54
2	HIS125	ASP62
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2	ARG261	GLU279
2	LYS149	GLU126
2	LYS75	GLU74
2	LYS419	GLU451
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2	ARG184	ASP147
2	LYS266	ASP93
2	LYS225	ASP227
2	ARG228	GLU118
2	ARG104	ASP33
2	ARG216	ASP123
2	ARG135	ASP212
2	HIS100E	GLU87
2	ARG316	ASP97
2	ARG93	GLU95
2	LYS162	ASP168
2	ARG116	GLU68
2	ARG39	ASP81
2	LYS145	GLU161
2	HIS320	GLU418
2	LYS2149	GLU2195
2	ARG179	ASP37
2	LYS82	GLU102
2	ARG107	GLU104
2	HIS102	GLU104
2	HIS619	ASP571
2	ARG740	ASP742
2	LYS30	ASP100B
2	LYS222	GLU158
2	LYS333	GLU331
2	HIS121	ASP119
2	LYS18	ASP70
2	LYS340	GLU318
2	ARG24	ASP131
2	ARG109	ASP80
2	LYS613	ASP618
2	LYS265	GLU243
2	LYS139	GLU137
2	LYS73	ASP72
2	ARG1476	GLU1102
2	ARG59	ASP94
2	LYS44	ASP151
2	LYS157	ASP160
2	ARG911	GLU492
2	ARG1	ASP101
2	ARG219	ASP220
2	LYS50	ASP160

2	LYS85	ASP108
2	LYS62	GLU80
2	HIS81	GLU64
2	LYS66	GLU26
2	LYS317	ASP54
2	HIS171	GLU185
2	ARG341	GLU322
2	HIS317	GLU316
2	ARG485	GLU450
2	LYS65	GLU230
2	HIS611	ASP612
2	ARG147	GLU144
2	LYS31	GLU27
2	LYS100E	ASP50
2	ARG48	GLU32
2	LYS60	GLU29
2	ARG154	ASP131
2	ARG838	ASP888
2	HIS119	GLU106
2	ARG2065	ASP2086
2	ARG2065	ASP2085
2	LYS170	ASP180
2	ARG53	GLU204
2	ARG97	GLU55
2	LYS210	ASP207
2	LYS2598	ASP2609
2	LYS441	GLU465
2	HIS108	ASP116
2	ARG112	ASP174
2	ARG109	ASP95
2	LYS302	ASP305
2	ARG99	ASP110
2	LYS434	GLU465
2	LYS11	GLU99
2	LYS66	ASP63
2	ARG410	GLU438
2	ARG65	ASP31
2	LYS106	GLU108
2	LYS186	GLU102
2	ARG125	GLU136
2	HIS115	GLU1
2	LYS41	GLU106
2	HIS288	ASP177
2	ARG101	GLU62
2	ARG329	GLU330
2	LYS304	GLU307
2	ARG45	ASP42
2	ARG218	GLU215
2	HIS125	GLU81
2	LYS1719	GLU1123
2	LYS117	ASP265
2	LYS649	GLU700
2	LYS189	GLU186
2	ARG2538	GLU2546
2	ARG209	GLU73
2	ARG97	ASP102
2	LYS47	ASP105
2	ARG95	GLU8

2	ARG661	ASP648
2	LYS267	GLU178
2	LYS292	ASP138
2	ARG186	GLU158
2	LYS378	ASP362
2	ARG65	GLU96
2	LYS336	ASP333
2	ARG3141	GLU2027
2	LYS189	GLU268
2	LYS121	GLU17
2	LYS24	ASP50
2	LYS114	GLU17
2	ARG99	ASP100R
2	ARG476	ASP473
2	HIS34	ASP99
2	HIS87	GLU85
2	ARG219	ASP232
2	ARG2543	GLU2545
2	ARG110	GLU125
2	LYS209	ASP211
2	LYS271	ASP185
2	LYS163	ASP169
2	ARG339	ASP356
2	ARG47	GLU33
2	LYS497	GLU582
2	LYS127	GLU129
2	ARG134	GLU127
2	LYS67	ASP55
2	LYS32	ASP31
2	LYS143	GLU128
2	ARG155	GLU153
2	ARG50	GLU6
2	LYS180	ASP176
2	ARG455	GLU466
2	ARG82	GLU581
2	LYS2183	GLU2187
2	LYS172	GLU170
2	ARG456	GLU429
2	HIS9	GLU6
2	ARG84	GLU27
2	HIS287	ASP289
2	ARG100	ASP116
2	LYS266	ASP274
2	LYS222	GLU162
2	LYS1095	GLU1097
2	ARG95	ASP101
2	ARG190	GLU89
2	LYS107	GLU109
2	HIS192	ASP118
2	HIS558	ASP101
2	LYS104	ASP50
2	ARG167	GLU159
2	ARG2598	ASP3143
2	LYS39	GLU90
2	LYS13	GLU121
2	LYS96	GLU97
2	LYS10	ASP100
2	HIS2	GLU5

2	ARG80	ASP106
2	LYS215	GLU122
2	ARG3	GLU93
2	LYS292	GLU297
2	LYS719	GLU741
2	LYS54	ASP31
2	HIS6	GLU39
2	ARG125	GLU127
2	ARG1598	ASP1606
2	LYS217	GLU127
2	LYS212	GLU214
2	LYS728	GLU666
2	ARG246	GLU227
2	HIS63	GLU84
2	ARG209	GLU122
2	ARG77	ASP92
2	ARG1084	ASP1087
2	LYS143	GLU127
2	LYS217	GLU122
2	HIS105	GLU86
2	ARG100B	GLU85
2	LYS46	ASP414
2	LYS398	GLU127
2	ARG115	GLU56
2	ARG94	ASP95
2	HIS53	GLU51
2	HIS314	GLU290
2	LYS65	ASP113
2	LYS514	ASP516
2	ARG209	GLU258
2	ARG296	GLU288
2	HIS169	ASP171
2	ARG191	ASP263
2	LYS1348	GLU1351
2	ARG119	ASP121
2	ARG114	GLU78
2	LYS209	GLU55
2	LYS225	ASP165
2	LYS221	ASP172
2	ARG194	GLU190
2	LYS246	ASP242
2	HIS54	GLU55
2	HIS108	GLU68
2	LYS39	ASP31
2	ARG96	GLU97
2	LYS463	ASP49
2	LYS188	ASP249
2	LYS121	ASP122
2	LYS10	GLU35
2	ARG39	ASP52
2	ARG94	ASP231
2	ARG61	ASP27
2	HIS517	ASP520
2	HIS32	GLU27
2	LYS96	GLU101
2	ARG227	ASP101
2	ARG52	ASP4
2	ARG242	ASP240

2	ARG281	GLU229
2	ARG426	ASP56
2	HIS261	ASP101
2	HIS115	ASP99
2	HIS320	GLU316
2	LYS170	GLU106
2	ARG497	GLU495
2	LYS53	GLU63
2	HIS327	GLU329
2	HIS27D	GLU536
2	ARG149	ASP171
2	HIS99	ASP120
2	LYS77	ASP34
2	LYS222	ASP128
2	LYS2719	GLU2123
2	HIS120	ASP4
2	LYS49	ASP51
2	HIS234	ASP56
2	LYS313	ASP27
2	LYS223	GLU128
2	ARG134	GLU167
2	HIS104	ASP135
2	LYS198	ASP68
2	HIS444	ASP473
2	LYS260	ASP78
2	LYS193	ASP189
2	ARG184	ASP272
2	LYS35	ASP31
2	HIS2705	ASP2720
2	LYS262	GLU127
2	LYS2154	GLU2252
2	LYS30	GLU35
2	HIS33	ASP100
2	LYS247	ASP249
2	HIS393	ASP349
2	LYS60	ASP56
2	LYS519	GLU123
2	HIS427	ASP162
2	LYS169	ASP223
2	ARG28	GLU31
2	LYS97	GLU97
2	LYS240	ASP256
2	LYS375	GLU308
2	HIS196	GLU236
2	ARG319	GLU322
2	LYS663	ASP669
2	ARG438	GLU426
2	HIS164	ASP139
2	ARG288	ASP355
2	LYS463	GLU126
2	LYS148	GLU126
2	HIS67	ASP90
2	ARG86	ASP88
2	ARG339	ASP336
2	ARG458	ASP456
2	LYS63	ASP65
2	LYS67	GLU69
2	ARG169	GLU167

2	LYS36	GLU280
2	ARG304	GLU99
2	LYS28	ASP89
2	ARG1419	GLU1100B
2	ARG91	ASP98
2	LYS62	GLU45
2	LYS184	ASP34
2	LYS41	GLU78
2	HIS35	GLU54
2	HIS159	GLU158
2	ARG1419	GLU1099
2	LYS102	ASP34
2	ARG35	ASP92
2	LYS320	ASP311
2	LYS222	GLU104
2	LYS51	ASP44
2	HIS173	GLU188
2	LYS59	ASP98
2	HIS1249	GLU1482
2	ARG152	ASP151
2	ARG76	GLU84
2	ARG10	GLU6
2	ARG83	GLU13
2	LYS202	ASP187
2	LYS4	ASP56
2	HIS134	GLU121
2	LYS1103	GLU1165
2	LYS107	GLU67
2	LYS119	ASP56
2	LYS119	GLU255
2	ARG56	ASP174
2	LYS75	ASP28
2	LYS153	ASP41
2	ARG66	ASP83
2	ARG213	GLU215
2	ARG	GLU46
2	ARG668	ASP666
2	LYS437	GLU381
2	LYS317	ASP280
2	ARG69	GLU100
2	LYS305	ASP321
2	ARG53	GLU97
2	LYS100I	ASP93
2	ARG207	ASP197
2	LYS563	ASP1
2	LYS193	ASP190
2	ARG354	GLU358
2	ARG315	GLU317
2	LYS364	GLU361
2	LYS53	GLU17
2	HIS125	ASP183
2	LYS123	GLU120
2	LYS138	ASP45
2	LYS52	ASP100I
2	LYS97	GLU64
2	LYS85	GLU250
2	LYS105	GLU167
2	LYS65	ASP208

2	LYS862	ASP529
2	ARG2304	ASP2233
2	LYS206	GLU123
2	ARG363	ASP923
2	LYS1	GLU5
2	LYS1282	GLU1275
2	LYS145	GLU17
2	ARG116	ASP182
2	LYS109	GLU106
2	ARG77	ASP78
2	ARG278	ASP275
2	ARG107	ASP108
2	LYS100A	ASP99
2	ARG92	GLU119
2	LYS52	GLU49
2	LYS98	ASP113
2	LYS305	ASP100F
2	HIS396	ASP391
2	ARG51	ASP57
2	LYS197	ASP194
2	ARG251	ASP276
2	ARG416	ASP412
2	LYS272	ASP56
2	ARG463	ASP444
2	LYS83	ASP80
2	LYS199	ASP201
2	LYS119	GLU120
2	ARG53	ASP1056
2	ARG37	ASP39
2	LYS140	ASP141
2	LYS	GLU119
2	LYS362	ASP408
2	LYS163	ASP162
2	LYS193	ASP205
2	ARG95	GLU95
2	LYS181	ASP37
2	HIS291	ASP228
2	ARG99	GLU50
2	ARG99	GLU58
2	ARG68	GLU35
2	ARG18	ASP80
2	LYS166	ASP93
2	ARG601	ASP587
2	ARG94	ASP92
2	LYS4	ASP62
2	LYS143	GLU106
2	LYS146	GLU109
2	ARG204	GLU258
2	ARG81	GLU101
2	ARG97	GLU370
2	LYS73	ASP57
2	ARG105	ASP334
2	LYS80	GLU73
2	LYS302	ASP265
2	LYS11	GLU27
2	LYS252	ASP249
2	ARG55	ASP3
2	LYS115	ASP119

2	LYS236	ASP240
2	ARG94	GLU111
2	LYS824	ASP143
2	LYS130	ASP1
2	LYS56	ASP55
2	ARG60	ASP58
2	HIS34	GLU97
2	ARG93	GLU64
2	LYS454	ASP100
2	LYS30F	GLU139
2	LYS164	GLU236
2	ARG53	GLU59
2	ARG109	GLU125
2	ARG148	GLU111
2	ARG99	ASP92
2	LYS149	GLU72
2	LYS17	GLU85
2	ARG99	GLU52B
2	ARG237	ASP255
2	ARG101	ASP116
2	LYS205	GLU156
2	ARG545	ASP391
2	LYS346	GLU382
2	ARG80	ASP101
2	LYS207	GLU380
2	LYS123	ASP185
2	ARG221	ASP242
2	ARG63	ASP115
2	LYS211	GLU127
2	ARG746	GLU743
2	ARG145	GLU141
2	ARG675	GLU920
2	LYS79	ASP35
2	ARG82	ASP31
2	LYS245	GLU213
2	LYS49	GLU158
2	ARG444	ASP454
2	HIS204	ASP268
2	ARG576	ASP573
2	LYS149	GLU206
2	LYS13	GLU107
2	LYS19	ASP148
2	ARG215	GLU213
2	LYS271	ASP222
2	LYS139	GLU142
2	LYS116	ASP120
2	LYS24	GLU22
2	LYS516	GLU123
2	LYS256	ASP367
2	LYS32	ASP85
2	LYS2665	GLU2704
2	LYS357	GLU1
2	ARG319	GLU299
2	ARG67	ASP27
2	LYS155	GLU160
2	LYS465	ASP103
2	ARG454	ASP412
2	LYS273	ASP255

2	LYS171	ASP290
2	ARG160	GLU158
2	LYS307	ASP99
2	ARG1031	ASP1100A
2	LYS251	ASP157
2	LYS58	ASP1
2	ARG372	GLU358
2	LYS171	ASP100I
2	ARG211	GLU199
2	ARG86	ASP56
2	LYS292	GLU128
2	LYS53	GLU54
2	LYS7	ASP95
2	ARG59	ASP95
2	LYS747	ASP742
2	LYS465	GLU95
2	ARG221	ASP222
2	ARG56	GLU58
2	ARG397	ASP401
2	LYS513	GLU123
2	LYS1714	GLU1716
2	ARG3	ASP6
2	LYS360	ASP63
2	LYS218	ASP122
2	ARG262	GLU
2	HIS898	ASP725
2	LYS167	ASP165
2	LYS117	GLU211
2	LYS181	GLU56
2	LYS9	ASP116
2	LYS378	ASP375
2	ARG190	ASP186
2	LYS138	ASP62
2	ARG98	GLU95
2	LYS48	ASP94
2	LYS196	ASP200
2	HIS173	ASP171
2	LYS722	ASP778
2	ARG1050	GLU1097
2	ARG1082A	GLU1081
2	ARG221	ASP306
2	ARG240	GLU258
2	ARG393	ASP390
2	ARG36	GLU38
2	LYS58	ASP94
2	ARG101	ASP111
2	HIS103	ASP115
2	ARG797	ASP1018
2	LYS46	ASP31
2	ARG221	GLU241
2	HIS31	GLU259
2	ARG423	GLU494
2	LYS37	ASP89
2	LYS129	ASP105
2	ARG58	ASP336
2	ARG444	GLU452
2	ARG427	GLU495
2	HIS164	ASP166

2	HIS169	ASP173
2	ARG116	ASP103
2	LYS343	GLU171
2	ARG485	ASP488
2	HIS38	ASP56
2	ARG219	GLU268
2	LYS127	GLU54
2	LYS9	GLU26
2	ARG168	ASP87
2	LYS257	GLU128
2	LYS104	ASP143
2	LYS199	GLU276
2	LYS50	ASP255
2	HIS218	GLU120
2	HIS105	ASP51
2	ARG1146	GLU1142
2	ARG302	ASP300
2	LYS	GLU139
2	ARG281	ASP246
2	LYS247	GLU266
2	LYS30	GLU100B
2	HIS112	GLU205
2	ARG193	ASP155
2	LYS343	GLU395
2	LYS209	ASP100G
2	LYS98	ASP49
2	LYS56	ASP11
2	ARG198	GLU67
2	ARG117	ASP116
2	LYS598	ASP609
2	HIS219	ASP56
2	HIS495	GLU31
2	HIS107	ASP138
2	LYS211	GLU122
2	LYS67	ASP54
2	ARG60	GLU316
2	LYS173	ASP171
2	ARG52	ASP61
2	LYS130	GLU59
2	HIS174	ASP169
2	LYS101	GLU142
2	ARG158	ASP211
2	LYS86	GLU93
2	ARG65	ASP30
2	LYS304	GLU301
2	ARG62	GLU78
2	LYS229	ASP142
2	ARG160	ASP165
2	ARG6	ASP437
2	LYS224	ASP295
2	HIS378	GLU381
2	ARG53	ASP105
2	LYS150	ASP115
2	LYS157	ASP52
2	HIS95B	ASP61
2	ARG142	GLU100
2	ARG98	ASP168
2	HIS91	ASP399

2	ARG89	ASP75
2	ARG301	GLU302
2	ARG190	GLU189
2	ARG33	GLU24
2	LYS188	ASP159
2	ARG398	GLU698
2	LYS209	GLU212
2	LYS214	GLU124
2	LYS214	GLU126
2	ARG101	ASP58
2	LYS531	GLU535
2	LYS235	ASP231
2	ARG79	GLU81
2	HIS34	GLU199
2	ARG2159	GLU2189
2	LYS52	ASP54
2	LYS190	GLU425
2	LYS172	ASP139
2	ARG82	GLU79
2	LYS207	GLU123
2	ARG102	ASP41
2	ARG95	GLU93
2	ARG117	GLU106
2	LYS149	ASP106
2	LYS485	ASP52A
2	HIS30	ASP28
2	LYS190	ASP152
2	LYS176	ASP143
2	LYS225	ASP135
2	LYS40	ASP28
2	ARG103	ASP80
2	LYS289	GLU311
2	ARG961	ASP982
2	ARG37	ASP64
2	LYS58	ASP62
2	ARG251	ASP138
2	ARG144	GLU107
2	ARG280	GLU227
2	LYS	GLU124
2	LYS120	GLU89
2	HIS103	ASP36
2	LYS61	GLU146
2	LYS220	GLU122
2	ARG100B	ASP91
2	ARG437	ASP442
2	ARG310	ASP307
2	HIS1051	ASP1050
2	ARG1038	ASP1088
2	ARG169	ASP172
2	HIS489	GLU239
2	ARG61	ASP58
2	ARG1538	ASP1590
2	ARG308	ASP304
2	LYS162	GLU131
2	ARG133	ASP115
2	HIS236	GLU126
2	ARG152	ASP198
2	ARG94	ASP63

2	HIS433	GLU436
2	ARG160	GLU285
2	ARG225	ASP142
2	LYS29	GLU28
2	ARG285	GLU237
2	ARG64	GLU26
2	LYS300	GLU229
2	LYS82	GLU46
2	LYS210	GLU131
2	LYS56	ASP52
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2	ARG55	ASP101
2	ARG61	ASP
2	ARG55	ASP107
2	ARG245	ASP148
2	LYS284	ASP309
2	LYS164	GLU158
2	ARG137	ASP73
2	ARG6	GLU82
2	LYS59	GLU117
2	LYS310	ASP230
2	ARG207	ASP259
2	ARG235	ASP224
2	ARG308	GLU310
2	ARG97	GLU1
2	LYS427	ASP52A
2	ARG96	ASP26
2	ARG270	ASP178
2	ARG445	GLU442
2	LYS59	GLU57
2	HIS198	ASP143
2	HIS67	GLU76
2	LYS68	ASP92
2	LYS305	GLU318
2	ARG32	GLU57
2	LYS321	ASP318
2	HIS341	GLU85
2	HIS49	GLU55
2	LYS343	ASP350
2	HIS207	GLU131
2	LYS203	ASP324
2	LYS43	ASP27
2	LYS43	ASP26
2	ARG154	ASP26
2	ARG69	GLU27
2	ARG932	GLU630
2	LYS432	GLU129
2	ARG234	ASP272
2	LYS23	ASP73
2	LYS111	GLU202
2	ARG311	GLU136
2	HIS6	GLU230
2	ARG165	GLU134
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2	ARG107	ASP113
2	LYS227	GLU126
2	LYS55	ASP743

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2	HIS164	ASP141
2	LYS74	ASP32
2	LYS207	ASP129
2	LYS210	ASP73
2	LYS417	ASP321
2	LYS130	ASP165
2	ARG405	GLU113
2	LYS4	ASP77
2	LYS1348	GLU1269
2	LYS203	GLU206
2	ARG95	GLU39
2	LYS58	ASP56
2	ARG73	ASP57
2	LYS97	ASP33
2	LYS50	GLU8
2	ARG500	ASP664
2	ARG186	ASP182
2	LYS1199	ASP1110
2	LYS51	GLU289
2	ARG266	GLU259
2	HIS174	GLU128
2	HIS123	ASP264
2	LYS147	GLU175
2	LYS97	GLU52B
2	LYS13	ASP83
2	LYS228	GLU123
2	LYS1	GLU92
2	LYS175	ASP182
2	ARG97	GLU113
2	LYS215	ASP194
2	ARG100	ASP107
2	ARG147	ASP160
2	ARG99	ASP107
2	HIS84	GLU163
2	HIS157	ASP106
2	HIS62	GLU46
2	ARG68	ASP27C
2	LYS96	ASP46
2	ARG82	ASP127
2	ARG50	GLU21
2	LYS1848	GLU1845
2	ARG188	ASP86
2	LYS543	GLU55
2	ARG140	GLU152
2	ARG288	ASP304
2	ARG2	GLU16
2	ARG381	GLU162
2	HIS162	ASP166
2	LYS505	ASP501
2	LYS2714	GLU2127
2	ARG167	ASP339
2	LYS66	GLU85
2	LYS242	GLU261
2	ARG66	GLU309
2	LYS262	GLU83
2	LYS0	ASP1054
2	LYS1663	ASP1669

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2	LYS1563	ASP1001
2	LYS68	ASP66
2	HIS170	GLU168
2	ARG58	ASP64
2	ARG40	ASP85
2	HIS15	ASP87
2	LYS55	ASP102
2	LYS296	ASP28
2	ARG163	ASP166
2	LYS50	GLU100F
2	HIS133	ASP45
2	ARG909	GLU187
2	ARG93	ASP101
2	ARG55	ASP49
2	LYS5	GLU3
2	LYS1038	ASP1086
2	ARG598	ASP606
2	ARG8	GLU27
2	ARG328	ASP329
2	ARG	GLU81
2	HIS84	GLU100
2	LYS222	ASP225
2	HIS193	GLU189
2	ARG175	ASP171
2	ARG172	ASP170
2	ARG237	GLU285
2	ARG250	GLU268
2	LYS67	GLU89
2	LYS251	GLU253
2	LYS593	ASP570
2	ARG24	ASP69
2	LYS155	ASP98
2	ARG116	ASP125
2	LYS363	ASP361
2	ARG26	ASP10
2	LYS186	GLU236
2	LYS19	GLU10
2	LYS9	GLU24
2	LYS128	GLU162
2	LYS41	GLU97
2	LYS190	GLU187
2	LYS122	ASP178
2	LYS114	GLU95
2	ARG218	GLU124
2	LYS714	GLU716
2	LYS427	ASP362
2	LYS719	GLU123
2	LYS226	GLU222
2	HIS189	GLU56
2	LYS202	ASP113
2	LYS148	GLU155
2	LYS143	GLU29
2	LYS801	ASP352
2	LYS157	GLU168
2	HIS96	ASP3
2	HIS209	ASP205
2	HIS64	ASP54

2	LYS50	GLU28
2	ARG56	ASP108
2	ARG50	GLU239
2	ARG47	ASP45
2	LYS50	GLU275
2	LYS153	GLU150
2	ARG33	GLU135
2	ARG50	GLU59
2	ARG112	ASP55
2	LYS225	GLU227
2	ARG66	ASP64
2	HIS738	ASP682
2	LYS1598	ASP1609
2	ARG169	GLU118
2	HIS433	ASP50
2	LYS465	GLU50
2	HIS171	GLU175
2	LYS307	GLU64
2	LYS51	GLU16
2	LYS171	ASP253
2	LYS259	GLU116C
2	ARG333	ASP330
2	LYS1210	GLU1212
2	ARG211	ASP540
2	ARG33	ASP4
2	HIS149	ASP146
2	LYS213	GLU129
2	LYS220	ASP55
2	ARG184	ASP152
2	ARG100	ASP190
2	ARG24	ASP1070
2	LYS211	ASP56
2	HIS225	ASP222
2	ARG292	GLU272
2	ARG103	ASP165
2	ARG24	ASP99
2	ARG99	ASP27
2	LYS63	GLU65
2	HIS567	GLU544
2	ARG1625	ASP1619
2	ARG212	GLU214
2	ARG58	GLU1
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2	LYS203	GLU122
2	LYS53	ASP100C
2	ARG32	ASP429
2	LYS20	ASP18
2	HIS112	GLU41
2	LYS184	ASP133
2	ARG106	ASP102
2	ARG221	GLU288
2	ARG87	GLU148
2	ARG117	GLU72
2	ARG50	GLU558
2	LYS73	ASP31
2	ARG45	ASP100
2	LYS447	ASP448
2	LYS218	GLU129

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2	ARG50	ASP66
2	LYS665	GLU704
2	LYS41	GLU83
2	LYS11	ASP33
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2	LYS27	GLU98
2	ARG398	ASP866
2	LYS116	ASP99
2	LYS148	GLU145
2	ARG114	GLU11
2	ARG60	ASP179
2	ARG1109	ASP1112
2	LYS151	GLU205
2	HIS123	GLU189
2	HIS30	ASP92
2	HIS2	ASP65
2	LYS209	GLU53
2	LYS72	ASP78
2	LYS322	GLU61
2	HIS928	ASP639
2	HIS197	ASP142
2	LYS356	GLU412
2	LYS218	GLU216
2	ARG222	ASP233
2	LYS170	ASP56
2	LYS145	GLU193
2	LYS145	GLU195
2	LYS878	ASP867
2	ARG95	ASP100A
2	ARG105	GLU113
2	LYS211	GLU215
2	LYS211	GLU214
2	ARG65	ASP
2	HIS126	ASP128
2	LYS370	GLU420
2	LYS236	ASP259
2	LYS89	GLU72
2	LYS573	GLU394
2	ARG108	ASP137
2	LYS55	GLU52
2	ARG74	GLU110
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1	ARG155	ASP157
1	LYS205	GLU465
1	HIS34	ASP102
1	LYS9	ASP77
1	ARG351	GLU379
1	ARG57	GLU431
1	HIS35	ASP50
1	LYS510	GLU493
1	LYS249	GLU247
1	ARG242	GLU236
1	ARG123	GLU116
1	LYS44	ASP61
1	LYS222	GLU227
1	LYS219	ASP130
1	LYS	ASP23

1	ARG345	ASP341
1	LYS175	GLU178
1	LYS2227	GLU50
1	LYS	ASP76
1	HIS594	ASP588
1	ARG98	ASP39
1	ARG538	GLU546
1	LYS58	ASP182
1	LYS1090	GLU1085
1	ARG400	ASP422
1	ARG31	GLU311
1	LYS295	GLU291
1	LYS212	GLU128
1	LYS185	GLU208
1	LYS379	GLU359
1	ARG433	GLU516
1	LYS176	GLU66
1	ARG25	GLU68
1	LYS187	ASP316
1	LYS50	ASP111
1	ARG41	GLU148
1	LYS30	ASP29
1	HIS51	GLU50
1	LYS290	ASP33
1	ARG49	GLU199
1	ARG668	GLU335
1	LYS79	ASP52
1	HIS486	GLU565
1	LYS82	GLU119
1	ARG52	GLU5
1	LYS75	GLU218
1	LYS162	ASP163
1	LYS410	ASP434
1	LYS463	GLU95
1	ARG50	ASP59
1	ARG73	GLU75
1	ARG18	GLU93
1	LYS42	GLU31
1	ARG186	ASP180
1	LYS122	ASP116
1	HIS26	ASP25
1	ARG37	ASP88
1	HIS3245	GLU3243
1	ARG57	ASP43
1	LYS27	GLU61
1	ARG180	GLU47
1	LYS45	GLU83
1	LYS45	GLU81
1	ARG184	GLU145
1	LYS45	GLU87
1	HIS189	GLU188
1	LYS241	ASP99
1	LYS218	GLU187
1	HIS198	GLU65
1	LYS109	GLU107
1	ARG1099	GLU2105
1	LYS15	ASP14
1	HIS98	ASP31

1	ARG18	ASP17
1	ARG58	ASP103
1	LYS26	ASP30
1	HIS99	GLU146
1	HIS61	ASP1
1	LYS152	GLU128
1	HIS50	GLU189
1	ARG53	GLU106
1	ARG44	ASP87
1	LYS106	ASP17
1	ARG144	ASP119
1	LYS193	GLU208
1	LYS288	ASP32
1	LYS118	ASP109
1	ARG130	ASP92
1	LYS153	GLU186
1	LYS62	GLU58
1	HIS43	GLU89
1	ARG186	GLU45
1	ARG54	ASP322
1	HIS221	ASP232
1	ARG120	GLU54
1	ARG140	GLU212
1	ARG213	ASP124
1	LYS341	ASP53
1	LYS648	GLU662
1	LYS84	GLU99
1	LYS112	ASP54
1	LYS44	GLU42
1	LYS59	GLU10
1	LYS180	GLU184
1	LYS76	GLU53
1	ARG100A	GLU100N
1	ARG152	GLU303
1	HIS335	ASP399
1	ARG180	ASP169
1	HIS59	ASP57
1	LYS193	ASP116
1	HIS133	GLU118
1	LYS175	GLU146
1	LYS44	ASP90
1	LYS207	GLU49
1	ARG157	GLU187
1	ARG31	GLU30
1	ARG587	GLU589
1	LYS100	GLU62
1	ARG236	GLU258
1	HIS57	ASP59
1	HIS417	GLU80
1	ARG141	GLU160
1	LYS103	GLU85
1	LYS262	GLU265
1	ARG27	GLU1
1	ARG24	ASP855
1	ARG19	GLU82
1	ARG19	GLU83
1	LYS222	GLU126
1	LYS155	GLU56

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1	HIS236	ASP125
1	HIS99	GLU155
1	ARG101	ASP98
1	ARG17	ASP39
1	HIS248	ASP249
1	LYS255	ASP528
1	LYS174	ASP175
1	LYS125	ASP193
1	ARG99	ASP143
1	ARG236	ASP235
1	ARG56	GLU111
1	ARG374	ASP343
1	LYS96	GLU94
1	LYS672	GLU674
1	ARG146	ASP133
1	ARG105	GLU85
1	LYS140	GLU100
1	ARG2674	ASP2167
1	ARG126	GLU81
1	LYS98	ASP108
1	LYS98	ASP100
1	HIS112	ASP107
1	ARG40	GLU70
1	LYS119	ASP116
1	ARG2825	GLU2822
1	LYS372	ASP369
1	ARG35	ASP29
1	LYS348	ASP269
1	LYS282	ASP275
1	ARG101	GLU179
1	LYS	GLU75
1	ARG209	GLU185
1	LYS439	ASP356
1	LYS157	ASP54
1	ARG514	GLU516
1	HIS73	ASP74
1	ARG25	ASP76
1	LYS1576	ASP1573
1	LYS113	GLU115
1	ARG491	GLU498
1	LYS159	ASP180
1	ARG169	ASP170
1	LYS257	ASP41
1	LYS69	ASP67
1	ARG169	ASP175
1	LYS130	ASP87
1	LYS313	ASP309
1	HIS95	ASP62
1	LYS394	GLU392
1	LYS50	GLU98
1	LYS3231	GLU3229
1	LYS181	GLU77
1	LYS220	ASP122
1	ARG348	ASP349
1	LYS120	ASP95
1	ARG66	ASP52

1	HIS108	GLU35
1	ARG148	GLU149
1	LYS32	ASP159
1	LYS307	GLU59
1	ARG44	GLU61
1	HIS184	ASP146
1	LYS108	GLU17
1	LYS129	GLU131
1	LYS156	GLU126
1	ARG77	GLU73
1	ARG128	GLU343
1	ARG207	GLU209
1	LYS39	GLU46
1	LYS262	ASP175
1	LYS222	GLU206
1	ARG103	GLU123
1	LYS68	GLU66
1	HIS317	GLU368
1	ARG53	ASP52A
1	ARG82	ASP65
1	ARG51	ASP115
1	LYS132	GLU27
1	ARG90	ASP62
1	ARG194	ASP191
1	LYS42	ASP37
1	ARG225	GLU227
1	LYS1107	ASP1017
1	ARG21	ASP23
1	LYS125	GLU121
1	LYS168	ASP53
1	ARG373	GLU575
1	LYS65	GLU84
1	ARG313	GLU60
1	LYS214	GLU148
1	ARG72	ASP77
1	LYS149	GLU195B
1	ARG277	ASP32
1	LYS155	GLU74
1	HIS496	GLU31
1	LYS42	GLU97
1	ARG76	GLU59
1	LYS13	GLU113
1	LYS43	ASP68
1	HIS51	GLU74
1	LYS133	ASP144
1	LYS3	ASP59
1	LYS17	GLU72
1	ARG106	GLU103
1	LYS215	GLU118
1	HIS27D	ASP100B
1	LYS103	ASP66
1	LYS198	ASP142
1	HIS95	ASP92
1	ARG103	ASP124
1	LYS389	GLU393
1	HIS110	GLU144
1	LYS105	GLU83
1	HIS30	ASP429

1	ARG282	GLU286
1	LYS86	ASP83
1	ARG	GLU187
1	ARG441	ASP58
1	LYS161	GLU127
1	LYS290	ASP278
1	LYS204	GLU115
1	LYS467	GLU80
1	LYS874	ASP871
1	ARG35	ASP39
1	LYS106	ASP85
1	ARG55	ASP80
1	ARG32	GLU216
1	ARG310	ASP86
1	LYS43	ASP86
1	LYS157	GLU127
1	LYS105	ASP103
1	LYS82	ASP144
1	LYS313	ASP317
1	LYS59	GLU101
1	ARG1674	ASP1167
1	LYS50	GLU68
1	ARG224	GLU226
1	ARG32	ASP68
1	LYS887	GLU145
1	ARG316	ASP5
1	ARG353	ASP96
1	HIS275	GLU272
1	LYS489	GLU485
1	LYS7	ASP11
1	LYS646	GLU662
1	LYS175	ASP176
1	LYS15	GLU24
1	LYS127	ASP189
1	ARG204	GLU121
1	ARG48	GLU73
1	LYS70	GLU29
1	LYS833	ASP17
1	LYS428	ASP390
1	LYS1232	GLU1351
1	ARG45	ASP1
1	LYS114	ASP111
1	LYS90	GLU92
1	ARG213	ASP143
1	HIS338	GLU333
1	ARG196	ASP148
1	LYS191	ASP50
1	ARG246	GLU240
1	HIS119	ASP116
1	HIS80	ASP73
1	LYS59	GLU37
1	LYS76	GLU72
1	HIS32	ASP100
1	LYS68	ASP33
1	LYS168	GLU238
1	LYS174	GLU89
1	ARG142	GLU161
1	ARG179	GLU77

1	LYS93	GLU27
1	ARG82	ASP71
1	LYS111	GLU73
1	ARG674	ASP167
1	LYS220	GLU214
1	LYS317	ASP314
1	LYS113	ASP171
1	ARG247	GLU188
1	LYS175	ASP98
1	HIS192	ASP188
1	LYS114	ASP173
1	ARG304	ASP306
1	LYS189	ASP184
1	LYS20	ASP58
1	LYS75	GLU77
1	ARG255	ASP307
1	LYS487	ASP92
1	ARG64	ASP65
1	LYS282	GLU241
1	ARG101	GLU97
1	ARG126	ASP125
1	HIS30E	GLU50
1	LYS80	GLU581
1	LYS71	GLU29
1	LYS143	ASP60
1	LYS135	ASP51
1	LYS196	GLU60
1	ARG625	GLU533
1	LYS105	GLU187
1	LYS105	GLU188
1	LYS76	ASP71
1	ARG226	GLU212
1	ARG44	GLU57
1	LYS231	GLU129
1	LYS255	GLU115
1	HIS556	ASP540
1	LYS187	ASP189
1	LYS330	ASP307
1	ARG75	ASP123
1	HIS161	ASP167
1	LYS33	GLU76
1	LYS19	ASP78
1	ARG2209	ASP2187
1	LYS109	ASP107
1	LYS343	GLU405
1	LYS1411	GLU1023
1	ARG223	GLU225
1	ARG11	GLU26
1	LYS49	ASP100
1	LYS148	ASP170
1	LYS64	ASP
1	LYS199	GLU110
1	HIS1705	ASP1720
1	LYS259	ASP261
1	LYS76	ASP124
1	LYS90	GLU273
1	ARG39	ASP53
1	ARG31	ASP107

1	ARG8	GLU6
1	LYS75	GLU1
1	ARG95	ASP100C
1	HIS125	GLU181
1	LYS107	GLU42
1	HIS4	ASP19
1	ARG121	ASP119
1	HIS217	GLU186
1	LYS364	GLU33
1	ARG332	ASP328
1	LYS56	ASP57
1	ARG403	GLU431
1	LYS127	ASP154
1	LYS62	GLU85
1	ARG308	GLU50
1	LYS317	ASP55
1	ARG50	GLU100C
1	LYS372	ASP370
1	ARG65	GLU1
1	HIS172	ASP171
1	HIS76	GLU74
1	LYS82	ASP89
1	LYS130	GLU85
1	LYS713	GLU123
1	ARG94	ASP119
1	LYS102	GLU79
1	LYS102	GLU78
1	LYS59	ASP100
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1	LYS1713	GLU1123
1	ARG61	GLU85
1	ARG62	GLU85
1	LYS353	GLU273
1	LYS40	GLU55
1	LYS305	ASP51
1	LYS243	GLU260
1	LYS303	GLU296
1	ARG114	ASP92
1	HIS705	ASP720
1	LYS77	ASP74
1	ARG41	GLU238
1	LYS1263	GLU1246
1	ARG204	GLU218
1	ARG111	ASP126
1	LYS236	GLU100C
1	ARG172	GLU119
1	ARG83	GLU81
1	LYS135	ASP119
1	LYS30	ASP99
1	ARG100B	ASP101
1	LYS208	GLU125
1	ARG137	ASP142
1	ARG350	ASP397
1	LYS237	ASP232
1	ARG186	ASP187
1	LYS217	ASP122
1	LYS175	ASP81

1	LYS222	ASP107
1	HIS202	GLU203
1	HIS346	ASP344
1	LYS254	GLU251
1	LYS128	ASP124
1	HIS58	ASP56
1	ARG670	GLU204
1	LYS250	GLU276
1	LYS66	ASP92
1	ARG102	GLU164
1	ARG61	ASP461
1	ARG202	ASP118
1	LYS170	GLU139
1	LYS94	GLU77
1	ARG255	GLU263
1	LYS427	GLU435
1	ARG89	ASP99
1	LYS322	ASP323
1	LYS88	GLU92
1	LYS233	GLU235
1	ARG74	ASP80
1	LYS42	GLU39
1	ARG101	ASP120
1	ARG503	ASP513
1	LYS88	GLU86
1	ARG109	GLU111
1	LYS132	GLU144
1	LYS57	GLU97
1	LYS250	GLU381
1	HIS100E	GLU91
1	LYS138	GLU215
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1	LYS305	GLU100E
1	LYS69	GLU4
1	LYS79	GLU75
1	ARG6	ASP30
1	LYS46	ASP66
1	LYS46	ASP63
1	HIS74	ASP77
1	LYS109	GLU147
1	ARG219	GLU222
1	HIS25	GLU77
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1	HIS35	ASP204
1	ARG924	ASP970
1	LYS95	GLU94
1	ARG131	ASP116
1	LYS143	GLU88
1	LYS221	GLU225
1	LYS189	GLU188
1	HIS28	ASP27
1	ARG29	ASP307
1	LYS400	ASP397
1	LYS244	GLU242
1	LYS99	GLU61
1	ARG22	ASP70
1	HIS3179	ASP2169

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1	LYS573	ASP577
1	LYS39	GLU36
1	ARG188	ASP1518
1	ARG63	GLU82
1	LYS3019	GLU3082
1	LYS144	GLU190
1	ARG2537	GLU2545
1	ARG112	ASP31
1	LYS351	GLU343
1	ARG266	GLU264
1	HIS145	ASP50
1	LYS139	GLU213
1	ARG2543	GLU2541
1	LYS218	GLU124
1	ARG255	GLU124
1	HIS172	ASP169
1	LYS483	ASP910
1	LYS56	GLU10
1	LYS268	GLU308
1	ARG230	ASP56
1	LYS411	ASP408
1	LYS1100	ASP1101
1	LYS292	GLU41
1	LYS759	ASP780
1	LYS155	GLU151
1	LYS2565	ASP2562
1	ARG115	GLU146
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1	LYS586	ASP74
1	HIS192	ASP99
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1	ARG33	ASP56
1	ARG97	GLU110
1	LYS99	ASP102
1	LYS18	GLU165
1	LYS174	GLU86
1	ARG65	ASP85
1	LYS186	GLU232
1	LYS82	ASP79
1	LYS107	GLU100
1	ARG355	GLU352
1	LYS82	ASP74
1	ARG60	ASP61
1	HIS107	ASP85
1	ARG48	ASP73
1	ARG315	ASP100A
1	LYS205	ASP52
1	ARG142	GLU140
1	HIS104	ASP121
1	LYS175	GLU87
1	LYS5	GLU187
1	LYS95	ASP256
1	LYS4	GLU57
1	LYS39	GLU97
1	ARG136	GLU889
1	HIS113	ASP102

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1	ARG185	GLU313
1	LYS209	ASP101
1	ARG61	ASP256
1	LYS215	GLU120
1	ARG23	ASP79
1	HIS204	GLU152
1	ARG957	GLU107
1	ARG240	GLU260
1	ARG65	GLU67
1	LYS362	ASP363
1	LYS116	GLU120
1	HIS96	GLU79
1	LYS440	ASP447
1	LYS217	GLU125
1	LYS217	GLU128
1	HIS166	ASP164
1	LYS194	GLU217
1	LYS296	ASP294
1	HIS27D	ASP2
1	ARG104	GLU21
1	ARG50	ASP72
1	ARG94	ASP97
1	LYS3074	ASP3056
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1	LYS228	GLU238
1	HIS169	ASP174
1	ARG52	ASP131
1	LYS228	GLU230
1	ARG128	GLU89
1	LYS16	GLU116
1	LYS99	ASP56
1	ARG114	GLU77
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1	ARG852	GLU845
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1	LYS39	ASP33
1	ARG35	ASP87
1	LYS171	ASP226
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1	ARG97	ASP53
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1	LYS127	ASP139
1	ARG57	ASP96
1	LYS100	GLU102
1	ARG45	GLU81
1	LYS205	ASP139
1	ARG469	ASP473
1	LYS137	ASP143
1	ARG422	ASP97
1	LYS478	ASP377
1	LYS50	ASP60
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1	LYS129	ASP142
1	ARG904	ASP163
1	ARG1568	GLU1235
1	LYS181	ASP205
1	HIS36	GLU105
1	HIS70	GLU77
1	ARG372	ASP369
1	ARG38	ASP46
1	ARG59	GLU201
1	ARG113	GLU136
1	ARG100	ASP30
1	LYS833	GLU185
1	LYS2187	ASP2188
1	ARG81	GLU83
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1	LYS46	GLU36
1	LYS87	GLU294
1	HIS97	GLU50
1	ARG301	GLU293
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1	LYS108	ASP170
1	ARG189	ASP185
1	HIS230	GLU181
1	ARG438	ASP396
1	ARG157	GLU155
1	ARG157	GLU154
1	ARG338	ASP386
1	ARG79	ASP85
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1	LYS35	ASP32
1	HIS113	ASP115
1	LYS52	ASP55
1	HIS60	GLU46
1	ARG147	GLU135
1	HIS44	ASP34
1	LYS38	GLU85
1	LYS227	ASP225
1	LYS201	ASP30
1	LYS156	GLU463
1	LYS170	GLU83
1	HIS129	ASP61
1	ARG265	ASP231
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1	ARG94	ASP123
1	LYS174	GLU220
1	ARG522	GLU401
1	LYS504	ASP368
1	LYS212	GLU208
1	ARG538	ASP394
1	HIS56	ASP54
1	LYS219	ASP52
1	LYS165	GLU246
1	ARG329	ASP386
1	LYS412	GLU409
1	ARG480	ASP99
1	LYS46	ASP47

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1	ARG77	ASP61
1	HIS31	ASP100
1	LYS52B	ASP143
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1	LYS220	ASP57
1	ARG53	GLU79
1	HIS52	GLU87
1	ARG128	ASP190
1	ARG86	ASP89
1	ARG114	ASP3
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1	LYS104	GLU101
1	ARG	GLU357
1	LYS172	GLU116
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1	LYS58	GLU4
1	ARG454	ASP411
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1	ARG1419	GLU1100D
1	ARG454	ASP408
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1	LYS280	GLU278
1	LYS344	GLU338
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1	ARG95G	GLU218
1	ARG107	GLU83
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1	LYS107	ASP169
1	LYS159	ASP156
1	ARG403	ASP118
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1	LYS684	ASP652
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1	LYS220	ASP245
1	LYS164	ASP160
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1	HIS34	ASP50
1	ARG277	GLU97
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1	LYS502	ASP664
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1	ARG73	ASP38
1	HIS147	GLU97
1	HIS170	ASP141
1	ARG476	ASP31
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1	LYS207	ASP70
1	LYS14	GLU27
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1	LYS27	ASP54
1	LYS103	ASP

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1	ARG2142	GLU2165
1	ARG82	ASP39
1	ARG6	GLU433
1	LYS171	ASP224
1	LYS175	ASP57
1	LYS159	ASP34
1	LYS81	GLU69
1	HIS40	ASP58
1	HIS2189	ASP2151
1	LYS303	ASP31
1	ARG101	ASP46
1	ARG24	GLU1555
1	LYS840	GLU838
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1	LYS126	ASP123
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1	ARG107	GLU194
1	LYS45	ASP102
1	ARG56	GLU153
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1	LYS138	GLU212
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1	ARG304	GLU302
1	ARG405	ASP115
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1	ARG2103	GLU2079
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1	LYS862	ASP526
1	LYS148	ASP55
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1	ARG63	GLU71
1	ARG98	GLU1
1	LYS76	GLU10
1	ARG50	GLU58
1	LYS26	GLU232
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1	LYS99	GLU93
1	ARG7	GLU9
1	LYS1099	ASP1010
1	HIS247	ASP249
1	ARG546	GLU467

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1	ARG438	GLU427
1	ARG85	GLU61
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1	ARG1480	ASP1477
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1	LYS251	GLU72
1	LYS108	ASP32
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1	ARG158	GLU188
1	LYS125	GLU130
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1	ARG64	ASP116
1	LYS221	ASP222
1	LYS317	ASP56
1	ARG52	ASP7
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1	LYS151	GLU154
1	LYS191	GLU362
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1	LYS146	GLU104
1	HIS29	GLU113
1	LYS43	GLU91
1	LYS80	ASP71
1	ARG114	GLU116
1	LYS378	ASP388
1	HIS35	GLU99
1	LYS75	ASP30
1	ARG102	GLU40
1	ARG99	ASP98
1	HIS196	ASP141
1	LYS186	ASP195
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1	ARG907	GLU187
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1	LYS153	GLU40
1	LYS149	GLU128
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1	ARG35	GLU43
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1	LYS290	GLU342
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1	LYS131	GLU128
1	ARG60	ASP56
1	ARG40	ASP89
1	ARG634	GLU630
1	LYS294	ASP290
1	LYS141	ASP142
1	LYS98	ASP52

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1	LYS169	GLU171
1	ARG166	ASP167
1	ARG74	GLU78
1	LYS56	ASP7
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1	ARG377	ASP379
1	ARG99	ASP91
1	ARG122	GLU119
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1	ARG403	ASP115
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1	ARG303	ASP373
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1	ARG78	ASP61
1	LYS149	GLU193
1	LYS69	ASP70
1	LYS139	GLU143
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1	LYS107	ASP110
1	HIS197	GLU198
1	LYS104	ASP133
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1	ARG103	GLU121
1	ARG169	ASP257
1	LYS208	GLU
1	LYS145	GLU126
1	ARG294	GLU361
1	LYS16	ASP13
1	LYS359	GLU356
1	LYS215	GLU213
1	LYS766	ASP1
1	ARG29	ASP56
1	HIS54	GLU68
1	ARG188	GLU196
1	LYS190	ASP187
1	ARG330	ASP328
1	LYS206	GLU204
1	LYS215	GLU265
1	LYS2036	ASP2089

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1	ARG30	GLU39
1	ARG42	GLU48
1	ARG59	GLU79
1	HIS11	ASP95
1	LYS173	ASP140
1	LYS155	ASP185
1	ARG299	ASP304
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1	LYS87	GLU90
1	LYS154	ASP152
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1	LYS122	GLU84
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1	LYS62	GLU33
1	HIS200	GLU201
1	ARG459	GLU445
1	LYS46	GLU62
1	LYS414	GLU329
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1	LYS574	ASP346
1	ARG2215	ASP101
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1	LYS218	ASP85
1	ARG311	ASP86
1	LYS155	ASP152
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1	LYS166	GLU320
1	ARG173	GLU363
1	LYS233	GLU533
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1	LYS58	ASP116
1	LYS301	GLU296
1	LYS156	GLU81
1	ARG74	ASP77
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1	ARG79	GLU77
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1	ARG148	GLU171
1	LYS67	GLU361
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1	LYS55	ASP57
1	ARG180	GLU210
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1	ARG82	GLU354
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1	ARG164	GLU174
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1	LYS209	GLU126
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1	ARG120	GLU146
1	HIS164	ASP168
1	LYS364	ASP52
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1	HIS173	ASP174
1	ARG158	GLU166
1	LYS238	ASP291
1	ARG2141	GLU2100
1	ARG171	GLU4
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1	ARG98	GLU39
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1	ARG146	GLU109
1	LYS217	ASP207
1	HIS106	GLU6
1	LYS310	GLU308
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1	ARG104	ASP122
1	LYS	GLU131
1	HIS53	GLU88
1	LYS174	ASP141
1	ARG3141	GLU2097
1	LYS53	GLU59
1	HIS129	ASP62
1	LYS143	ASP
1	LYS30	GLU100E
1	HIS112	GLU202
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1	ARG1	ASP51
1	LYS36	ASP88
1	ARG104	ASP95
1	ARG141	GLU142
1	LYS64	ASP1
1	ARG52	ASP33
1	ARG394	GLU375
1	ARG212	GLU217
1	ARG104	GLU100
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1	LYS312	GLU345
1	LYS465	ASP53
1	ARG18	GLU218
1	LYS228	ASP230
1	LYS33	GLU63
1	LYS173	ASP170
1	LYS192	ASP217

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1	ARG59	ASP16
1	HIS66	ASP96
1	LYS117	ASP144
1	ARG198	ASP142
1	ARG131	GLU422
1	ARG27	ASP23
1	ARG56	GLU81
1	HIS1006	ASP820
1	ARG94	GLU61
1	ARG53	GLU56
1	LYS167	ASP83
1	ARG786	GLU706
1	HIS31	GLU133
1	HIS2245	GLU2243
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1	LYS304	GLU306
1	LYS92	ASP63
1	LYS82	ASP84
1	ARG235	GLU236
1	LYS122	GLU220
1	LYS161	ASP31
1	ARG236	ASP28
1	LYS69	GLU74
1	LYS240	ASP241
1	HIS214	GLU210
1	HIS248	GLU239
1	HIS928	ASP636
1	HIS332	ASP280
1	ARG429	ASP63
1	ARG192	ASP95
1	ARG62	GLU38
1	LYS148	ASP157
1	LYS55	GLU371
1	LYS214	GLU128
1	ARG159	ASP161
1	LYS153	GLU10
1	ARG51	ASP106
1	LYS48	GLU50
1	ARG100	ASP93
1	ARG90	GLU107
1	LYS52	ASP53
1	LYS52	ASP56
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1	ARG18	GLU36
1	LYS207	GLU124
1	LYS511	GLU123
1	ARG355	GLU324
1	ARG67	GLU345
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1	LYS1267	ASP1290
1	ARG126	ASP152
1	HIS204	ASP200
1	ARG513	GLU483
1	LYS63	ASP23
1	LYS166	GLU129
1	ARG203	ASP235

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1	ARG120	ASP148
1	LYS72	GLU76
1	ARG397	ASP332
1	LYS158	GLU128
1	ARG357	ASP122
1	LYS213	ASP354
1	HIS52	ASP31G
1	LYS23	ASP50
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1	LYS201	GLU10
1	LYS210	GLU128
1	ARG103	GLU146
1	LYS133A	GLU131
1	ARG366	GLU370
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1	LYS391	ASP388
1	LYS205	ASP149
1	LYS185	ASP182
1	LYS108	GLU88
1	HIS209	ASP221
1	ARG255	ASP31
1	LYS50	ASP100
1	LYS683	GLU911
1	ARG645	GLU350
1	ARG447	GLU442
1	LYS1665	GLU1704
1	HIS170	ASP172
1	ARG159	GLU158
1	ARG2051	ASP2078
1	ARG96	GLU59
1	ARG96	GLU56
1	LYS39	ASP100
1	ARG625	GLU561
1	HIS2038	ASP2603
1	ARG100	ASP69
1	LYS357	ASP461
1	HIS495	ASP32
1	ARG153	ASP115
1	ARG269	GLU89
1	LYS165	GLU162
1	HIS184	GLU216
1	ARG337	GLU341
1	ARG63	ASP112
1	LYS182	GLU81
1	LYS50	GLU99
1	ARG198	GLU118
1	ARG33	GLU32
1	HIS403	GLU401
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1	ARG1545	GLU1250
1	LYS44	ASP105
1	LYS2115	ASP2014
1	HIS45	ASP43
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1	ARG46	GLU48

1	ARG871	GLU920
1	ARG435	ASP506
1	LYS223	GLU125
1	ARG20	ASP15
1	ARG192	ASP154
1	LYS75	GLU85
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1	LYS1103	GLU1083
1	LYS67	ASP57
1	ARG350	GLU370
1	LYS209	ASP123
1	LYS207	GLU133
1	LYS220	ASP127
1	LYS172	ASP129
1	HIS15	GLU14
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1	LYS165	GLU216
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1	LYS21	ASP69
1	LYS42	GLU44
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1	LYS238	GLU293
1	LYS54	ASP51
1	LYS115	ASP173
1	LYS145	GLU152
1	ARG169	GLU268
1	ARG77	GLU99
1	ARG29	GLU50
1	LYS592	GLU610
1	LYS697	GLU399
1	HIS	GLU97
1	HIS409	ASP108
1	LYS419	GLU420
1	LYS212	GLU122
1	HIS4	ASP98
1	HIS3246	ASP3147
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1	LYS210	GLU124
1	LYS107	ASP867
1	ARG283	ASP355
1	LYS806	GLU808
1	LYS1565	ASP1562
1	ARG356	ASP300
1	HIS102	ASP111
1	HIS381	ASP375
1	HIS52A	ASP33
1	ARG308	ASP285
1	ARG926	ASP639
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1	LYS260	GLU233
1	LYS344	GLU290
1	HIS115	GLU112
1	LYS171	ASP156
1	LYS63	ASP60
1	HIS170	ASP167

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1	HIS164	GLU139
1	ARG50	GLU23
1	LYS1833	GLU17
1	LYS219	GLU131
1	ARG56	GLU99
1	ARG145	ASP136
1	ARG27D	ASP70
1	ARG41	ASP70
1	ARG87	GLU63
1	ARG168	GLU154
1	LYS43	GLU36
1	LYS0	ASP1056
1	LYS154	ASP98
1	ARG97	ASP100A
1	LYS67	ASP56
1	LYS72	GLU70
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1	ARG58	ASP65
1	ARG188	ASP185
1	ARG26	ASP46
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1	ARG58	GLU56
1	HIS215	GLU216
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1	ARG349	GLU269
1	ARG180	GLU396
1	ARG103	GLU61
1	ARG587	ASP590
1	LYS189	ASP151
1	LYS167	GLU164
1	HIS171	ASP141
1	LYS1538	ASP1590
1	ARG23	ASP19
1	ARG43	GLU15
1	LYS174	ASP160
1	ARG103	ASP49
1	LYS23	GLU121
1	LYS485	ASP493
1	HIS134	ASP98
1	LYS81	GLU117
1	HIS90	ASP93
1	LYS88	GLU81
1	ARG363	ASP359
1	LYS67	GLU80
1	ARG33	ASP53
1	HIS193	ASP156
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1	HIS223	GLU212
1	ARG216	GLU214
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1	ARG39	ASP37
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1	ARG186	GLU194
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1	LYS222	GLU204
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1	ARG328	ASP325
1	LYS333	GLU367
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1	HIS143	GLU106
1	LYS228	ASP122
1	ARG53	ASP648
1	LYS417	ASP415
1	LYS165	GLU80
1	LYS171	ASP169
1	LYS1121	GLU1429
1	HIS1089	ASP1051
1	LYS144	ASP142
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1	ARG50	ASP52
1	LYS225	GLU229
1	HIS100C	ASP100B
1	ARG	ASP53
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1	ARG127	GLU118
1	ARG469	ASP456
1	LYS32	GLU30
1	HIS234	ASP97
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1	LYS183	ASP228
1	LYS574	ASP348
1	LYS62	ASP60
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1	ARG3	ASP59
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1	LYS3115	ASP3014
1	HIS169	ASP168
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1	ARG242	GLU228
1	ARG613	GLU610
1	HIS174	GLU65
1	LYS2039	GLU2087
1	ARG107	GLU106
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1	ARG192	ASP194
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1	ARG212	ASP210
1	LYS68	GLU50
1	LYS16	ASP132
1	ARG9	GLU6
1	LYS35	GLU156
1	LYS404	GLU292
1	LYS108	GLU58
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1	HIS653	GLU649
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1	ARG163	ASP177
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1	LYS615	GLU698
1	ARG202	GLU229
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1	ARG94	GLU50
1	HIS53	GLU36
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1	ARG403	GLU432
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1	LYS41	GLU175
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1	LYS2169	ASP2214
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1	LYS45	GLU97
1	ARG488	GLU485
1	HIS35	GLU80
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1	ARG497	GLU510
1	ARG56	ASP76
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1	LYS443	ASP51
1	ARG402	GLU373
1	LYS293	GLU288
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1	HIS33	ASP52
1	ARG134	GLU165
1	LYS63	GLU64
1	ARG428	GLU425
1	HIS111	GLU108
1	LYS250	ASP179
1	ARG29	ASP259
1	LYS27	ASP26
1	LYS27	ASP25
1	ARG6	ASP440
1	LYS1163	ASP1158
1	HIS190	GLU59

Table 3: Counting of side chain salt bridging networks within the PDB entries of all experimentally determined antigen-antibody-related structures. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

Count	Residue A	Residue B
178	ARG76	GLU74
173	LYS209	GLU123
88	ARG542	GLU647
88	ARG59	ASP368
83	ARG163	GLU131
80	LYS208	GLU123
80	ARG71	ASP368
75	ARG109	GLU67
74	ARG170	GLU128
72	LYS62	ASP90
72	ARG76	GLU81
72	LYS62	ASP86
70	ARG54	GLU97
68	LYS27	GLU97
66	ARG124	GLU132
60	ARG269	GLU67
59	LYS310	ASP90
56	ARG96	GLU98
54	LYS221	GLU123
52	ARG	GLU
52	LYS238	GLU72
52	LYS214	GLU123
49	ARG579	GLU584

47	ARG95	ASP95
46	ARG225	ASP190
44	ARG96	ASP100C
43	LYS326	GLU15
43	LYS574	ASP107
42	LYS	GLU
38	ARG	ASP
38	LYS174	ASP164
37	LYS97	ASP99
36	ARG77	ASP102
36	ARG127	GLU131
35	ARG1059	ASP368
34	HIS681	ASP910
33	ARG123	GLU132
31	LYS299	GLU69
31	ARG208	GLU101
30	ARG576	GLU574
30	ARG112	ASP141
30	ARG73	ASP61
30	HIS164	ASP167
29	LYS97	ASP32
28	LYS143	GLU124
27	ARG1113	GLU1105
27	ARG95	ASP91
27	ARG542	ASP648
26	LYS310	ASP86
25	ARG30	ASP355
25	ARG758	ASP740
24	LYS214	ASP122
24	ARG503	GLU654
24	ARG96	GLU55
24	ARG96	GLU50
24	LYS643	ASP5
24	ARG96	ASP50
24	ARG164	ASP166
23	ARG419	GLU100B
23	LYS209	GLU125
23	LYS	ASP
23	ARG311	ASP590
22	ARG48	ASP53
22	ARG95A	ASP61
22	LYS215	GLU123
22	ARG106	GLU569
22	ARG65	ASP52
22	ARG24	ASP70
21	ARG53	ASP659
20	ARG91	GLU95
20	ARG96	GLU95
20	ARG311	ASP586
20	LYS210	GLU123
20	HIS64	ASP79
19	ARG100	GLU55
19	LYS305	ASP54
19	ARG95	ASP5
19	ARG419	GLU3103
19	LYS213	GLU122
18	LYS144	GLU142
18	ARG24	GLU17

18	ARG91	GLU100J
18	ARG25	GLU325
18	LYS209	GLU124
18	LYS46	ASP636
17	ARG61	GLU466
17	LYS207	GLU127
17	ARG50	ASP98
16	ARG52	GLU179
16	ARG847	ASP726
16	ARG96	GLU1183
16	ARG61	ASP59
16	LYS97	ASP100B
15	LYS3224	GLU2125
15	ARG419	GLU99
15	LYS409	ASP399
14	ARG304	ASP34
14	LYS215	GLU126
14	LYS558	GLU597
14	ARG216	GLU123
14	LYS58	GLU97
14	ARG35	ASP53
13	ARG96	GLU298
13	LYS143	GLU125
13	ARG35	ASP332
13	LYS219	GLU123
13	ARG138	GLU214
13	ARG109	GLU69
12	LYS290	GLU128
12	ARG100	ASP52
12	ARG585	GLU492
12	ARG310	ASP90
12	LYS500	ASP664
12	LYS643	GLU4
12	LYS149	GLU137
12	LYS601	GLU654
12	ARG101	GLU99
12	LYS218	GLU127
12	ARG98	ASP67
12	ARG46	ASP101
12	ARG95	GLU179
12	LYS83	ASP85
12	ARG192	ASP167
12	ARG606	ASP609
12	ARG576	GLU104
12	ARG588	GLU492
12	ARG1179	ASP31
12	ARG500	GLU30
12	ARG69	GLU55
12	LYS46	ASP632
11	LYS253	ASP232
11	LYS208	GLU122
11	LYS222	GLU125
11	LYS601	GLU657
11	LYS29	ASP279
11	LYS213	GLU123
11	LYS212	GLU129
11	ARG107	GLU78
10	ARG213	GLU123

10	LYS187	GLU114
10	ARG61	GLU79
10	ARG700	GLU756
10	LYS305	ASP56
10	HIS80	ASP144
10	HIS198	GLU57
10	ARG73	GLU86
10	ARG353	ASP112
10	LYS6	ASP54
10	LYS211	GLU123
10	ARG64	ASP457
10	ARG88	ASP101
9	ARG96	ASP97
9	ARG192	GLU164
9	ARG146	GLU169
9	LYS583	ASP585
9	LYS35	ASP457
9	ARG87	ASP90
9	ARG104	GLU599
9	LYS109	GLU69
9	HIS3	GLU9
9	ARG95A	GLU350
9	LYS282	ASP114
9	ARG23	GLU30
9	ARG327	GLU100I
9	LYS1029	ASP279
9	ARG68	GLU50
9	ARG112	ASP93
9	ARG72	ASP368
9	ARG64	ASP94
9	LYS212	GLU126
9	ARG73	ASP59
9	ARG504	GLU662
9	ARG504	GLU657
9	ARG45	ASP105
9	LYS61	GLU179
8	LYS44	ASP86
8	HIS36	ASP104
8	ARG73	GLU74
8	ARG134	ASP55
8	ARG96	GLU94
8	ARG253	ASP53
8	ARG100	GLU59
8	ARG419	GLU100D
8	LYS52	ASP448
8	LYS79	ASP50
8	ARG52	GLU178
8	LYS684	ASP1056
8	LYS282	ASP100C
8	ARG94	GLU53
8	ARG120	GLU64
8	LYS208	GLU124
8	LYS48	GLU32
8	ARG94	GLU191
8	LYS215	GLU127
8	LYS217	GLU123
8	LYS68	GLU110
8	ARG101	ASP109

8	HIS181	GLU10
8	ARG210	ASP412
8	ARG100B	GLU55
8	HIS60	GLU1
8	ARG116	GLU120
8	ARG419	GLU214
8	ARG45	GLU50
8	LYS216	GLU125
8	ARG112	ASP143
8	ARG97	ASP50
8	ARG29	ASP6
8	ARG96	ASP204
8	ARG98	ASP341
8	ARG72	GLU10
8	ARG95	ASP99
8	ARG194	ASP102
8	ARG69	GLU35
8	ARG101	ASP49
8	ARG57	GLU50
8	ARG542	GLU95
8	HIS98	GLU214
8	LYS92	GLU99
8	ARG25	ASP4
8	LYS413	ASP100
8	LYS54	GLU89
8	ARG164	ASP167
8	LYS433	ASP54
8	ARG95B	ASP58
8	ARG5	GLU39
8	ARG408	ASP224
8	LYS219	GLU129
8	LYS10	GLU29
8	ARG104	GLU81
8	LYS370	GLU357
8	LYS12	ASP54
8	ARG95	ASP114
8	ARG50	GLU47
8	LYS97	ASP221
7	LYS214	ASP124
7	ARG95	ASP104
7	HIS98	GLU50
7	ARG73	ASP93
7	ARG53	GLU654
7	LYS208	GLU129
7	LYS137	ASP51
7	ARG370	GLU188
7	LYS63	ASP1
7	ARG31	ASP86
7	LYS217	GLU126
7	ARG29	ASP36
7	LYS209	GLU127
7	LYS216	GLU122
7	ARG95	ASP3
7	ARG53	ASP232
7	ARG353	GLU110
7	ARG235	GLU232
7	ARG76	GLU107
7	ARG103	GLU217

7	HIS100	GLU87
7	LYS61	GLU57
7	LYS95	ASP7
7	ARG163	GLU1
7	LYS212	GLU123
7	LYS697	ASP332
7	ARG91	GLU50
7	ARG29	ASP107
7	ARG58	GLU3
7	ARG45	ASP104
7	LYS107	ASP9
6	ARG39	GLU81
6	ARG39	GLU85
6	ARG156	ASP3
6	LYS100A	GLU55
6	LYS178	ASP96
6	LYS107	ASP105
6	HIS171	ASP171
6	ARG50	GLU269
6	HIS223	GLU82
6	ARG73	ASP71
6	LYS137	ASP73
6	ARG100	ASP60
6	ARG50	GLU200
6	LYS684	ASP1054
6	ARG220	ASP241
6	LYS90	ASP51
6	LYS46	GLU632
6	HIS192	ASP98
6	LYS17	ASP55
6	LYS197	GLU57
6	LYS209	GLU122
6	LYS407	GLU5
6	LYS87	ASP31
6	LYS196	ASP489
6	HIS169	ASP167
6	LYS216	GLU123
6	LYS71	GLU87
6	ARG78	ASP94
6	LYS87	GLU47
6	ARG95	ASP7
6	ARG95	GLU100E
6	ARG99	GLU55
6	ARG103	GLU230
6	ARG52A	ASP674
6	ARG94	ASP321A
6	HIS173	ASP141
6	ARG429	ASP74
6	ARG62	GLU26
6	ARG100H	ASP91
6	ARG54	GLU6
6	LYS6	ASP56
6	ARG91	ASP22
6	ARG95	GLU50
6	LYS36	GLU98
6	ARG1212	GLU1183
6	ARG50	ASP94
6	LYS58	ASP3

6	ARG193	ASP184
6	ARG96	GLU54
6	LYS432	GLU55
6	LYS100H	ASP50
6	ARG101	ASP50
6	HIS585	GLU492
6	LYS116	ASP203
6	LYS34	ASP612
6	LYS6	GLU232
6	ARG37	GLU101
6	LYS213	GLU127
6	ARG60	GLU74
6	LYS213	GLU124
6	LYS289	GLU128
6	LYS31A	GLU87
5	ARG98	ASP31
5	ARG108	ASP1
5	ARG315	GLU95
5	ARG309	GLU255
5	ARG100	ASP43
5	ARG307	ASP90
5	ARG1050	ASP683
5	ARG18	ASP70
5	LYS206	GLU122
5	LYS13	ASP154
5	ARG9	ASP368
5	HIS172	ASP167
5	LYS224	GLU143
5	ARG100F	ASP50
5	LYS129	ASP144
5	ARG281	ASP111
5	ARG419	GLU106
5	ARG69	ASP108
5	LYS222	ASP123
5	LYS32	GLU57
5	LYS216	GLU128
5	HIS308	GLU98
5	LYS45	ASP101
5	LYS223	ASP126
5	LYS568	GLU107
5	ARG105	GLU64
5	ARG111	GLU68
5	ARG327	ASP1
5	ARG49	ASP368
5	LYS470	GLU60
5	ARG51	ASP101
5	LYS207	GLU128
5	ARG58	ASP94
5	LYS416	ASP51
5	LYS49	ASP101
5	ARG19	ASP97
5	LYS97	ASP154
5	LYS94	ASP97
5	ARG164	ASP169
5	ARG114	ASP115
5	HIS31	GLU100I
5	ARG30	ASP658
5	ARG106	ASP109

5	LYS130	ASP144
5	LYS508	GLU123
5	LYS12	ASP56
5	HIS168	ASP166
4	LYS149	ASP41
4	ARG1568	GLU1250
4	LYS215	ASP122
4	LYS28	GLU380
4	LYS28	GLU382
4	ARG100	GLU64
4	ARG96	ASP94
4	LYS147	GLU127
4	HIS105	ASP183
4	ARG4	ASP385
4	LYS96	ASP52
4	LYS96	ASP55
4	LYS43	ASP9
4	ARG384	GLU81
4	LYS76	ASP11
4	ARG200	ASP56
4	ARG104	GLU111
4	ARG168	ASP100L
4	LYS50	GLU93
4	HIS102	GLU64
4	ARG95	GLU34
4	ARG124	ASP132
4	LYS39	GLU40
4	ARG54	ASP161
4	HIS755	ASP730
4	ARG659	GLU242
4	LYS166	GLU146
4	LYS63	ASP89
4	ARG83	GLU1
4	ARG339	ASP100
4	ARG97	ASP436
4	ARG67	GLU97
4	LYS76	GLU122
4	HIS19	GLU50
4	LYS205	GLU123
4	LYS224	GLU125
4	HIS264	GLU241
4	ARG50	ASP100G
4	HIS15	ASP55
4	ARG145	GLU116
4	ARG9	ASP137
4	ARG1009	ASP1368
4	ARG94	GLU1
4	ARG96	GLU100I
4	LYS62	GLU1
4	HIS172	ASP172
4	LYS49	ASP100A
4	LYS253	GLU128
4	LYS208	GLU128
4	ARG25	GLU82
4	LYS203	ASP32
4	ARG2215	ASP100
4	LYS215	GLU121
4	HIS90	ASP33

4	LYS150	GLU127
4	ARG226	ASP31
4	ARG61	ASP33
4	ARG52	ASP107
4	ARG12	ASP242
4	ARG668	GLU350
4	LYS215	GLU128
4	LYS215	GLU125
4	LYS215	GLU124
4	ARG209	GLU128
4	HIS0	GLU97
4	LYS217	GLU129
4	LYS653	ASP17
4	LYS17	ASP57
4	LYS169	GLU81
4	ARG2519	ASP2834
4	ARG49	ASP7
4	ARG220	ASP105
4	HIS106	GLU35
4	HIS96	ASP5
4	ARG32	ASP80
4	ARG327	GLU27
4	LYS4	ASP54
4	ARG1519	ASP1834
4	LYS119	ASP54
4	ARG457	ASP31E
4	LYS502	GLU50
4	ARG96	GLU101
4	LYS204	ASP206
4	LYS216	GLU127
4	LYS216	GLU124
4	LYS80	GLU81
4	LYS109	GLU44
4	LYS185	ASP55
4	ARG58	ASP95D
4	LYS697	ASP399
4	ARG35	ASP334
4	LYS312	ASP56
4	LYS312	ASP54
4	HIS189	GLU85
4	LYS168	GLU78
4	HIS33	ASP105
4	ARG222	GLU123
4	LYS170	ASP54
4	HIS55	ASP143
4	ARG59	GLU221
4	ARG170	GLU1
4	LYS2	ASP42
4	LYS131	GLU269
4	LYS439	GLU356
4	ARG106	GLU69
4	LYS21	GLU202
4	ARG101	GLU39
4	HIS223	ASP123
4	LYS171	ASP288
4	LYS211	GLU121
4	LYS282	GLU33
4	LYS27	ASP1

4	ARG131	GLU142
4	ARG98	ASP95
4	ARG54	GLU101
4	LYS214	GLU125
4	LYS207	GLU122
4	ARG11	GLU99
4	LYS97	GLU50
4	ARG54	ASP50
4	LYS220	GLU128
4	LYS114	ASP50
4	LYS114	ASP51
4	HIS35	ASP4
4	LYS32	ASP58
4	ARG50	GLU39
4	HIS49	ASP101
4	ARG100	ASP66A
4	LYS55	ASP101
4	LYS55	ASP106
4	LYS28	ASP99
4	LYS406	ASP224
4	ARG100B	ASP31
4	LYS212	GLU127
4	ARG44	ASP60
4	LYS187	GLU97
4	ARG149	ASP136
4	LYS47	GLU55
4	ARG25	ASP101
4	LYS446	ASP50
4	LYS207	ASP130
4	LYS433	ASP56
4	ARG200	ASP102
4	LYS224	ASP122
4	LYS135	ASP48
4	LYS574	GLU106
4	LYS62	ASP1
4	LYS211	ASP54
4	HIS56	GLU9
4	ARG24	ASP76
4	LYS221	GLU126
4	LYS197	ASP55
4	LYS443	ASP58
4	LYS7	ASP49
4	ARG47	ASP1
4	HIS213	GLU58
3	ARG304	ASP31
3	ARG315	ASP93
3	ARG143	ASP61
3	ARG97	ASP368
3	LYS50	ASP100C
3	HIS20	ASP217
3	LYS326	GLU11
3	LYS107	GLU91
3	LYS96	ASP50
3	ARG186	GLU48
3	ARG97	GLU62
3	ARG100	GLU50
3	ARG90	ASP56
3	ARG61	ASP101

3	HIS189	GLU196
3	LYS73	ASP256
3	LYS572	GLU238
3	ARG108	GLU223
3	LYS168	GLU190
3	ARG50	ASP101
3	LYS143	ASP11
3	ARG50	GLU166
3	LYS154	GLU129
3	ARG847	GLU1017
3	LYS204	GLU113
3	LYS229	ASP1
3	ARG95A	GLU351
3	ARG44	GLU56
3	LYS149	GLU127
3	ARG94	GLU7
3	ARG419	ASP54
3	ARG95	ASP100E
3	HIS87	ASP11
3	LYS217	ASP128
3	LYS52	ASP474
3	LYS39	GLU81
3	LYS306	GLU61
3	ARG317	GLU100B
3	ARG50	ASP560
3	ARG40	GLU29
3	ARG54	ASP32
3	ARG192	GLU58
3	LYS218	GLU122
3	LYS399	GLU497
3	LYS53	ASP52
3	HIS32	GLU1
3	ARG123	ASP54
3	ARG327	ASP52
3	ARG37	ASP104
3	ARG419	GLU103
3	ARG419	GLU108
3	LYS107	ASP30
3	LYS228	GLU147
3	LYS22	GLU102
3	ARG52A	GLU144
3	LYS223	GLU126
3	ARG542	GLU648
3	LYS399	ASP392
3	ARG28	ASP457
3	LYS87	ASP79
3	HIS120	GLU59
3	LYS217	GLU121
3	ARG91	ASP99
3	ARG31	ASP140
3	HIS467	GLU50
3	LYS213	GLU130
3	ARG61	GLU32
3	ARG59	ASP101
3	ARG304	ASP100A
3	ARG92	ASP166
3	ARG124	ASP41
3	ARG78	ASP92

3	ARG52	ASP47
3	LYS54	ASP101
3	ARG96	GLU104
3	HIS49	ASP100C
3	ARG101	GLU55
3	HIS165	ASP167
3	ARG36	ASP55
3	LYS400	ASP28
3	LYS30	GLU95
3	LYS211	GLU120
3	HIS121	ASP217
3	ARG235	ASP28
3	LYS60	GLU74
3	ARG137	ASP97
3	LYS49	ASP99
3	ARG17	ASP35
3	ARG50	GLU268
3	ARG77	GLU79
3	ARG27	GLU431
3	ARG153	ASP106
3	ARG64	ASP1
3	LYS28	GLU100
3	LYS214	GLU122
3	ARG100	ASP98
3	LYS145	GLU124
3	LYS	GLU127
3	ARG112	ASP109
3	HIS170	GLU172
3	ARG36	GLU58
3	ARG77	ASP31
3	LYS227	GLU124
3	ARG691	GLU818
3	ARG100B	ASP30
3	ARG59	GLU106
3	LYS89	GLU95
3	ARG1212	ASP100C
3	LYS432	ASP56
3	LYS44	GLU106
3	LYS146	ASP95A
3	ARG31	GLU113
3	ARG97	ASP347
3	LYS171	GLU13
3	ARG35	ASP73
3	HIS94	ASP7
3	LYS343	ASP85
3	ARG33	ASP6
3	ARG59	ASP367
3	LYS117	GLU10
3	ARG98	ASP159
3	LYS322	ASP95
3	ARG102	GLU201
3	ARG164	ASP170
3	HIS131	ASP270
3	LYS63	GLU89
3	HIS105	GLU61
3	ARG441	GLU94
3	LYS421	GLU54
3	HIS93	ASP434

2	HIS282	ASP98
2	LYS290	GLU127
2	HIS	ASP
2	ARG315	ASP95
2	ARG50	ASP100
2	LYS345	GLU123
2	HIS30	GLU104
2	LYS69	GLU114
2	LYS30	GLU4
2	LYS49	GLU105
2	LYS49	GLU108
2	ARG31	GLU133
2	ARG144	ASP91
2	HIS94	GLU18
2	LYS64	GLU187
2	HIS108	GLU68
2	LYS153	ASP104
2	ARG39	ASP52
2	ARG53	GLU104
2	LYS127	GLU54
2	LYS11	GLU99
2	LYS56	ASP11
2	ARG94	ASP231
2	LYS11	ASP91
2	HIS35	ASP69
2	ARG304	GLU99
2	ARG95	ASP28
2	LYS219	ASP123
2	LYS769	ASP399
2	ARG167	ASP166
2	ARG93	GLU105
2	ARG53	GLU11
2	ARG60	GLU316
2	LYS2	GLU96
2	ARG213	GLU125
2	LYS17	GLU85
2	LYS129	GLU213
2	LYS50	ASP160
2	LYS231	GLU145
2	LYS140	GLU212
2	LYS131	ASP157
2	LYS257	GLU128
2	ARG56	GLU58
2	ARG106	ASP54
2	ARG95	ASP26
2	ARG1024	ASP70
2	ARG169	ASP172
2	LYS44	ASP104
2	ARG50	GLU62
2	LYS100	GLU91
2	ARG95	GLU39
2	LYS96	ASP46
2	LYS115	GLU85
2	LYS156	GLU127
2	LYS310	ASP52
2	LYS52C	ASP674
2	LYS205	ASP53
2	ARG54	ASP167

2	LYS80	GLU79
2	ARG188	ASP831
2	HIS103	ASP36
2	ARG27	ASP323
2	LYS219	ASP93
2	LYS204	GLU112
2	LYS161	GLU125
2	HIS207	GLU131
2	LYS50	GLU66
2	ARG32	ASP65
2	ARG32	ASP153
2	LYS120	ASP265
2	LYS100	GLU87
2	ARG24	ASP131
2	LYS97	ASP106
2	LYS224	GLU127
2	ARG213	GLU213
2	LYS104	GLU62
2	HIS4	ASP183
2	LYS266	ASP93
2	ARG32	GLU57
2	ARG216	ASP123
2	ARG135	ASP212
2	ARG100B	ASP91
2	HIS100E	GLU87
2	ARG316	ASP97
2	ARG116	GLU68
2	LYS149	GLU126
2	HIS105	ASP51
2	LYS115	ASP119
2	ARG109	ASP80
2	LYS431	ASP101
2	ARG59	ASP95
2	ARG59	ASP94
2	ARG57	ASP59
2	LYS210	ASP73
2	ARG6	GLU82
2	ARG142	GLU100
2	ARG398	GLU698
2	LYS65	GLU230
2	LYS466	GLU95
2	LYS100E	ASP50
2	LYS49	ASP51
2	ARG100	ASP109
2	ARG53	GLU204
2	ARG97	GLU55
2	ARG92	GLU119
2	LYS155	ASP98
2	LYS50	ASP98
2	HIS125	ASP62
2	ARG50	GLU239
2	ARG125	GLU136
2	HIS125	GLU81
2	LYS1719	GLU1123
2	LYS117	ASP265
2	LYS150	GLU123
2	ARG109	ASP95
2	LYS47	ASP105

2	LYS292	ASP138
2	LYS44	ASP151
2	ARG3141	GLU2027
2	LYS203	GLU122
2	LYS24	ASP50
2	HIS34	ASP99
2	LYS218	GLU129
2	LYS218	GLU123
2	LYS127	GLU122
2	ARG50	GLU5
2	ARG50	GLU6
2	LYS232	GLU143
2	ARG84	GLU27
2	ARG94	GLU179
2	ARG190	GLU89
2	LYS30	ASP100B
2	LYS104	ASP50
2	ARG2598	ASP3143
2	ARG154	ASP131
2	LYS10	ASP100
2	ARG80	ASP106
2	LYS215	GLU122
2	HIS6	GLU39
2	ARG209	GLU122
2	ARG77	ASP92
2	LYS143	GLU127
2	LYS217	GLU122
2	LYS217	GLU127
2	ARG100B	GLU85
2	LYS398	GLU127
2	LYS143	GLU128
2	ARG115	GLU56
2	HIS169	ASP173
2	HIS169	ASP171
2	ARG48	ASP54
2	LYS209	GLU55
2	LYS209	GLU53
2	LYS39	ASP31
2	LYS463	ASP49
2	ARG61	ASP27
2	LYS166	ASP93
2	LYS73	ASP53
2	ARG426	ASP56
2	HIS27D	GLU536
2	ARG98	ASP50
2	LYS222	ASP128
2	LYS2719	GLU2123
2	HIS234	ASP56
2	LYS130	GLU59
2	LYS223	GLU128
2	LYS262	GLU127
2	LYS60	ASP56
2	LYS519	GLU123
2	LYS719	GLU123
2	LYS97	GLU97
2	LYS43	ASP27
2	LYS43	ASP26
2	HIS164	ASP139

2	LYS463	GLU126
2	LYS148	GLU126
2	LYS96	GLU57
2	ARG1419	GLU1100B
2	ARG91	ASP98
2	ARG26	ASP10
2	HIS35	GLU54
2	HIS96	ASP3
2	ARG1419	GLU1099
2	LYS102	ASP34
2	LYS171	ASP253
2	ARG69	GLU100
2	LYS11	ASP33
2	ARG83	GLU13
2	LYS4	ASP56
2	LYS119	ASP56
2	LYS75	ASP28
2	LYS153	ASP41
2	ARG82	ASP31
2	LYS130	ASP1
2	LYS204	ASP75
2	ARG53	GLU97
2	LYS100I	ASP93
2	LYS563	ASP1
2	LYS292	GLU128
2	ARG405	ASP118
2	LYS97	GLU64
2	LYS65	ASP208
2	LYS185	ASP57
2	LYS53	GLU17
2	LYS206	GLU123
2	LYS145	GLU17
2	LYS305	ASP100F
2	LYS272	ASP56
2	ARG53	ASP1056
2	ARG95	GLU95
2	LYS439	ASP480
2	ARG68	GLU35
2	ARG52	ASP4
2	LYS4	ASP62
2	HIS173	ASP171
2	LYS77	ASP34
2	ARG97	GLU370
2	HIS33	ASP100
2	ARG105	ASP334
2	ARG55	ASP3
2	LYS184	ASP133
2	HIS134	GLU121
2	LYS824	ASP143
2	HIS34	GLU97
2	LYS454	ASP100
2	LYS30F	GLU139
2	ARG311	ASP90
2	ARG99	ASP92
2	LYS170	ASP56
2	LYS19	ASP148
2	ARG215	GLU213
2	LYS211	GLU127

2	LYS211	GLU122
2	LYS516	GLU123
2	ARG145	ASP91
2	ARG123	ASP132
2	LYS357	GLU1
2	LYS465	ASP103
2	LYS171	ASP290
2	LYS46	ASP414
2	LYS307	ASP99
2	LYS171	ASP100I
2	LYS53	GLU54
2	ARG38	ASP100
2	LYS7	ASP95
2	LYS181	GLU56
2	LYS465	GLU95
2	LYS513	GLU123
2	LYS218	ASP122
2	ARG24	ASP1070
2	ARG51	ASP113
2	LYS58	ASP94
2	ARG100A	GLU106
2	LYS46	ASP31
2	HIS31	GLU259
2	ARG101	GLU33
2	ARG58	ASP336
2	ARG154	ASP26
2	HIS164	ASP166
2	ARG116	ASP103
2	LYS50	ASP255
2	LYS250	GLU13
2	LYS269	GLU69
2	LYS212	GLU101
2	ARG101	GLU119
2	LYS30	GLU100B
2	HIS112	GLU205
2	LYS209	ASP100G
2	ARG90	ASP1
2	HIS219	ASP56
2	HIS495	GLU31
2	LYS83	GLU85
2	LYS18	ASP70
2	ARG65	ASP30
2	ARG65	ASP31
2	LYS229	ASP142
2	ARG6	ASP437
2	LYS150	ASP115
2	LYS157	ASP52
2	HIS95B	ASP61
2	HIS192	ASP118
2	ARG98	ASP168
2	HIS91	ASP399
2	ARG33	GLU24
2	LYS214	GLU124
2	LYS214	GLU126
2	HIS261	ASP101
2	LYS52	ASP54
2	LYS207	GLU123
2	LYS59	ASP98

2	LYS149	ASP106
2	LYS485	ASP52A
2	LYS96	GLU97
2	ARG103	ASP80
2	ARG251	ASP138
2	LYS	GLU124
2	LYS220	GLU122
2	LYS58	ASP1
2	ARG133	ASP115
2	LYS76	GLU1
2	LYS13	GLU107
2	LYS56	ASP55
2	LYS56	ASP52
2	ARG55	ASP101
2	ARG55	ASP107
2	ARG135	GLU206
2	LYS59	GLU117
2	LYS55	GLU104
2	LYS427	ASP52A
2	ARG96	ASP26
2	LYS55	ASP102
2	LYS432	GLU129
2	LYS23	ASP73
2	LYS111	GLU202
2	HIS6	GLU230
2	LYS227	GLU126
2	LYS55	ASP743
2	LYS213	GLU128
2	HIS164	ASP141
2	LYS207	ASP129
2	ARG405	GLU113
2	ARG66	GLU85
2	ARG73	GLU44
2	LYS210	GLU131
2	LYS50	GLU8
2	ARG500	ASP664
2	LYS228	GLU123
2	LYS266	GLU128
2	LYS308	GLU50
2	ARG50	GLU21
2	LYS49	GLU158
2	ARG188	ASP86
2	LYS184	ASP34
2	HIS162	ASP166
2	LYS2714	GLU2127
2	ARG66	GLU309
2	LYS0	ASP1054
2	LYS1563	ASP1001
2	LYS67	ASP54
2	LYS67	ASP55
2	HIS102	GLU104
2	LYS50	GLU100F
2	ARG909	GLU187
2	LYS317	ASP54
2	ARG55	ASP49
2	ARG101	GLU62
2	HIS34	GLU199
2	ARG172	ASP170

2	LYS9	ASP116
2	ARG218	GLU124
2	HIS189	GLU56
2	HIS64	ASP54
2	LYS801	ASP352
2	ARG56	ASP174
2	ARG112	ASP55
2	LYS27	ASP32
2	LYS296	ASP28
2	HIS433	ASP50
2	LYS465	GLU50
2	LYS307	GLU64
2	LYS96	ASP31
2	ARG33	ASP4
2	LYS220	ASP55
2	ARG100	ASP190
2	LYS211	ASP56
2	ARG24	ASP99
2	ARG58	GLU1
2	ARG94	GLU111
2	LYS53	ASP100C
2	ARG32	ASP429
2	ARG50	GLU558
2	LYS73	ASP31
2	ARG50	ASP66
2	LYS116	ASP99
2	ARG60	ASP179
2	HIS2	ASP65
2	LYS322	GLU61
2	LYS543	GLU55
2	LYS32	ASP85
1	LYS9	ASP77
1	ARG57	GLU431
1	HIS	GLU97
1	LYS153	GLU186
1	LYS155	GLU56
1	ARG98	ASP39
1	HIS178	ASP169
1	LYS120	ASP95
1	ARG31	GLU311
1	LYS212	GLU128
1	ARG90	ASP62
1	LYS43	ASP85
1	LYS290	ASP33
1	ARG49	GLU199
1	LYS201	ASP92
1	ARG46	GLU95
1	ARG52	GLU5
1	LYS75	GLU218
1	LYS463	GLU95
1	ARG73	GLU75
1	ARG18	GLU93
1	ARG39	ASP53
1	LYS108	ASP32
1	LYS27	GLU61
1	ARG32	GLU216
1	LYS66	ASP92
1	LYS364	ASP52

1	ARG58	ASP103
1	ARG53	GLU106
1	ARG130	ASP92
1	LYS62	GLU58
1	ARG186	GLU45
1	ARG120	GLU54
1	ARG140	GLU212
1	LYS341	ASP53
1	ARG94	ASP123
1	LYS59	GLU10
1	LYS209	ASP123
1	LYS191	GLU362
1	LYS43	ASP1
1	LYS222	GLU126
1	ARG101	ASP98
1	LYS2227	GLU50
1	ARG97	GLU110
1	ARG99	ASP143
1	HIS	GLU
1	ARG67	GLU345
1	ARG2674	ASP2167
1	ARG40	GLU70
1	LYS161	GLU127
1	ARG101	GLU179
1	LYS95	ASP256
1	LYS77	GLU222
1	LYS157	ASP54
1	HIS29	GLU113
1	ARG169	ASP175
1	HIS95	ASP62
1	ARG313	GLU60
1	LYS50	GLU98
1	LYS50	GLU99
1	LYS220	ASP127
1	LYS220	ASP122
1	ARG6	ASP440
1	LYS156	GLU126
1	LYS56	GLU10
1	LYS205	ASP52
1	ARG96	GLU80
1	HIS495	ASP32
1	HIS234	ASP97
1	ARG180	GLU47
1	LYS214	GLU148
1	LYS155	GLU74
1	HIS496	GLU31
1	LYS79	ASP52
1	LYS82	GLU119
1	LYS43	ASP68
1	LYS133	ASP144
1	LYS215	GLU118
1	ARG41	GLU238
1	ARG441	ASP58
1	LYS157	GLU127
1	ARG1674	ASP1167
1	ARG353	ASP96
1	ARG32	ASP68
1	ARG316	ASP5

1	LYS70	GLU29
1	ARG57	ASP43
1	LYS833	ASP17
1	ARG31	ASP107
1	ARG45	ASP1
1	ARG213	ASP143
1	LYS0	ASP1056
1	LYS156	GLU463
1	ARG56	GLU111
1	LYS43	GLU140
1	LYS111	GLU73
1	ARG674	ASP167
1	ARG100	ASP69
1	LYS209	ASP101
1	ARG101	GLU97
1	LYS143	ASP60
1	LYS502	ASP664
1	ARG44	GLU57
1	HIS161	ASP167
1	LYS1411	GLU1023
1	LYS149	GLU128
1	ARG29	ASP56
1	LYS75	GLU1
1	LYS107	GLU42
1	ARG308	GLU50
1	LYS317	ASP55
1	ARG18	GLU218
1	HIS172	ASP171
1	LYS82	ASP89
1	LYS713	GLU123
1	LYS59	ASP100
1	LYS1713	GLU1123
1	LYS305	ASP51
1	ARG204	GLU218
1	LYS236	GLU100C
1	LYS135	ASP119
1	LYS208	GLU125
1	LYS217	ASP122
1	LYS222	ASP107
1	ARG61	ASP461
1	ARG202	ASP118
1	ARG89	ASP99
1	ARG2215	ASP101
1	HIS100E	GLU91
1	ARG36	ASP94
1	LYS305	GLU100E
1	LYS46	ASP66
1	ARG104	ASP95
1	LYS152	GLU128
1	HIS3179	ASP2169
1	LYS292	ASP139
1	ARG188	ASP1518
1	ARG112	ASP31
1	LYS114	GLU17
1	LYS100	GLU62
1	HIS145	ASP50
1	LYS139	GLU213
1	LYS218	GLU124

1	LYS2	ASP92
1	ARG230	ASP56
1	LYS76	GLU10
1	HIS360	ASP1
1	HIS192	ASP99
1	ARG204	GLU121
1	ARG48	ASP73
1	ARG315	ASP100A
1	ARG142	GLU140
1	LYS5	GLU187
1	LYS364	GLU33
1	LYS30	ASP99
1	ARG61	ASP256
1	LYS215	GLU120
1	LYS147	GLU154
1	HIS204	GLU152
1	HIS96	GLU79
1	LYS217	GLU125
1	LYS217	GLU128
1	HIS166	ASP164
1	HIS27D	ASP2
1	ARG104	GLU21
1	LYS129	ASP142
1	LYS118	ASP109
1	HIS169	ASP174
1	ARG128	GLU89
1	LYS99	ASP56
1	LYS171	ASP224
1	LYS171	ASP226
1	HIS308	ASP100H
1	LYS205	ASP139
1	ARG52	ASP7
1	LYS137	ASP143
1	ARG422	ASP97
1	HIS163	ASP172
1	ARG1568	GLU1235
1	ARG113	GLU136
1	LYS46	GLU36
1	LYS46	GLU33
1	LYS87	GLU294
1	LYS223	GLU125
1	ARG147	GLU135
1	LYS201	ASP30
1	HIS129	ASP61
1	HIS417	GLU80
1	LYS219	ASP52
1	LYS71	GLU29
1	LYS131	ASP128
1	HIS31	ASP100
1	ARG1	GLU55
1	LYS220	ASP57
1	ARG114	ASP3
1	ARG1419	GLU1100D
1	LYS76	ASP124
1	LYS210	GLU
1	LYS68	GLU107
1	LYS60	GLU1
1	ARG403	ASP115

1	HIS169	ASP168
1	ARG136	GLU889
1	LYS93	GLU533
1	HIS173	ASP167
1	HIS147	GLU97
1	ARG476	ASP31
1	LYS207	ASP70
1	LYS27	ASP54
1	ARG668	GLU335
1	LYS241	ASP99
1	ARG94	GLU50
1	LYS175	ASP57
1	LYS159	ASP34
1	LYS303	ASP31
1	ARG24	GLU1555
1	ARG190	GLU48
1	LYS135	ASP51
1	ARG95	GLU173
1	LYS1209	GLU1123
1	LYS65	GLU84
1	LYS168	ASP53
1	LYS138	GLU212
1	LYS138	GLU215
1	ARG405	ASP115
1	LYS78	ASP52
1	HIS467	GLU95
1	HIS467	GLU94
1	HIS27D	ASP100B
1	LYS57	GLU97
1	LYS145	GLU126
1	LYS13	ASP42
1	ARG368	ASP429
1	HIS198	GLU65
1	ARG52	ASP131
1	LYS1201	GLU10
1	LYS174	GLU128
1	LYS75	ASP30
1	LYS205	ASP207
1	ARG907	GLU187
1	LYS153	GLU40
1	LYS229	ASP124
1	LYS210	GLU124
1	ARG60	ASP56
1	LYS45	ASP102
1	ARG25	GLU46
1	ARG32	ASP100F
1	LYS223	ASP128
1	LYS56	ASP7
1	ARG99	ASP98
1	ARG99	ASP91
1	LYS55	ASP170
1	LYS108	ASP53
1	LYS296	GLU68
1	LYS465	ASP53
1	LYS211	GLU128
1	LYS766	ASP1
1	ARG188	GLU196
1	LYS887	GLU145

1	HIS11	ASP95
1	LYS833	GLU185
1	LYS218	ASP121
1	LYS88	ASP54
1	LYS251	GLU72
1	LYS218	ASP85
1	LYS167	ASP165
1	LYS148	ASP56
1	ARG311	ASP86
1	LYS132	ASP150
1	LYS233	GLU533
1	LYS58	ASP116
1	LYS156	GLU81
1	ARG99	ASP60
1	HIS34	ASP102
1	LYS67	GLU361
1	LYS55	ASP57
1	ARG1099	GLU2105
1	ARG51	ASP115
1	ARG102	ASP52
1	LYS209	GLU126
1	LYS60	ASP100
1	LYS103	ASP66
1	ARG24	ASP855
1	HIS164	ASP168
1	HIS164	ASP169
1	LYS225	ASP121
1	ARG98	GLU39
1	HIS35	GLU80
1	LYS7	GLU232
1	LYS55	ASP6
1	ARG3141	GLU2097
1	LYS30	GLU100E
1	HIS112	GLU202
1	ARG1	ASP51
1	LYS26	GLU232
1	LYS191	ASP50
1	LYS64	ASP1
1	LYS215	ASP189
1	ARG94	GLU61
1	HIS31	GLU133
1	HIS56	ASP60
1	ARG55	ASP117
1	LYS161	ASP31
1	ARG236	ASP28
1	ARG429	ASP63
1	ARG192	ASP95
1	LYS55	GLU371
1	LYS214	GLU128
1	LYS29	ASP69
1	LYS214	GLU127
1	HIS36	GLU105
1	ARG51	ASP106
1	LYS67	ASP90
1	LYS52	ASP56
1	ARG18	GLU36
1	LYS207	GLU124
1	LYS511	GLU123

1	LYS52B	ASP143
1	LYS103	ASP
1	ARG101	ASP46
1	ARG107	GLU194
1	LYS63	ASP23
1	ARG59	GLU201
1	LYS158	GLU128
1	LYS213	ASP354
1	LYS201	GLU10
1	LYS210	GLU128
1	LYS220	GLU127
1	ARG255	ASP31
1	LYS50	ASP100
1	ARG645	GLU350
1	HIS170	ASP172
1	ARG59	ASP65
1	LYS56	ASP57
1	ARG96	GLU59
1	ARG96	GLU56
1	LYS39	ASP100
1	HIS2038	ASP2603
1	LYS290	GLU281
1	ARG63	ASP112
1	LYS182	GLU81
1	ARG33	GLU32
1	ARG1545	GLU1250
1	LYS44	ASP105
1	ARG169	GLU268
1	LYS75	GLU85
1	LYS67	ASP56
1	LYS67	ASP57
1	LYS49	ASP100
1	LYS207	GLU133
1	ARG54	GLU321
1	LYS697	GLU399
1	HIS409	ASP108
1	LYS212	GLU122
1	LYS211	ASP213
1	HIS4	ASP98
1	LYS1107	GLU869
1	ARG186	ASP180
1	LYS107	ASP867
1	HIS61	ASP1
1	HIS30	ASP429
1	LYS171	ASP156
1	HIS170	ASP167
1	HIS164	GLU139
1	LYS307	GLU59
1	ARG50	GLU23
1	ARG66	ASP51
1	ARG66	ASP52
1	LYS1833	GLU17
1	LYS219	GLU131
1	LYS108	GLU58
1	LYS154	ASP98
1	ARG54	ASP322
1	ARG58	ASP65
1	LYS201	ASP52

1	ARG61	GLU81
1	ARG61	GLU85
1	ARG18	GLU27
1	LYS317	ASP57
1	LYS317	ASP56
1	ARG180	GLU396
1	LYS52	ASP78
1	HIS171	ASP141
1	LYS174	ASP160
1	ARG103	ASP49
1	LYS23	GLU121
1	ARG29	ASP259
1	LYS212	ASP214
1	LYS304	ASP31
1	LYS153	GLU10
1	LYS1094	GLU2015
1	LYS209	GLU
1	LYS58	GLU4
1	ARG6	GLU433
1	LYS228	ASP122
1	ARG53	ASP648
1	HIS97	GLU50
1	ARG66	ASP62
1	ARG53	GLU8
1	ARG127	GLU118
1	ARG56	GLU81
1	LYS96	ASP32
1	ARG403	ASP118
1	LYS220	GLU214
1	LYS213	GLU129
1	HIS174	GLU65
1	LYS145	ASP93
1	LYS39	ASP1
1	ARG65	GLU1
1	ARG83	ASP72
1	LYS216	ASP218
1	LYS68	GLU50
1	HIS76	ASP100A
1	LYS211	ASP122
1	LYS50	ASP106
1	LYS148	ASP55
1	HIS53	GLU36
1	LYS206	ASP208
1	LYS161	GLU154
1	LYS151	GLU191
1	LYS45	GLU97
1	HIS35	ASP204
1	LYS439	ASP356
1	ARG310	ASP86
1	HIS168	ASP167
1	LYS404	GLU292
1	LYS443	ASP51
1	HIS170	ASP141
1	HIS190	GLU59

Table 4: Counting of interfacial side chain salt bridging networks within the PDB entries of all experimentally determined antigen-antibody-related structures. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1A14.PDB	O, H_SER_25	N, H_GLN_3	H, H_GLN_3	2.77	1.89	21.99
1A14.PDB	OG, H_SER_25	NE2, H_GLN_5	HE21, H_GLN_5	2.94	2.02	15.87
1A14.PDB	O, H_TYR_90	NE2, H_GLN_6	HE21, H_GLN_6	2.72	1.83	18.57
1A14.PDB	O, H_THR_108	N, H_GLU_10	H, H_GLU_10	2.84	1.94	19.84
1A14.PDB	O, H_THR_110	N, H_VAL_12	H, H_VAL_12	2.96	2.06	20.79
1A14.PDB	O, H_LEU_82C	N, H_GLY_15	H, H_GLY_15	2.91	2.08	27.09
1A14.PDB	O, H_GLN_5	N, H_LYS_23	H, H_LYS_23	2.75	1.80	7.95
1A14.PDB	O, H_ASN_76	N, H_ALA_24	H, H_ALA_24	2.78	1.85	14.53
1A14.PDB	O, H_THR_28	N, H_ASN_31	H, H_ASN_31	2.81	1.88	13.65
1A14.PDB	O, H_PHE_51	N, H_MET_34	H, H_MET_34	2.88	1.94	13.17
1A14.PDB	O, H_ALA_93	N, H_TYR_35	H, H_TYR_35	2.86	1.93	13.77
1A14.PDB	O, H_TYR_91	N, H_VAL_37	H, H_VAL_37	2.95	2.02	16.35
1A14.PDB	O, H_GLU_46	N, H_LYS_38	H, H_LYS_38	2.72	1.78	11.05
1A14.PDB	OE1, L_GLN_38	NE2, H_GLN_39	HE21, H_GLN_39	2.62	1.69	9.24
1A14.PDB	O, H_SER_40	N, H_GLN_43	H, H_GLN_43	2.91	2.06	24.59
1A14.PDB	O, H_TRP_36	N, H_ILE_48	H, H_ILE_48	2.85	1.93	16.00
1A14.PDB	O, H_SER_58	N, H_ILE_50	H, H_ILE_50	2.72	1.81	16.55
1A14.PDB	O, H_MET_34	N, H_PHE_51	H, H_PHE_51	2.91	2.00	17.30
1A14.PDB	O, H_ASP_56	N, H_TYR_52	H, H_TYR_52	2.91	1.96	11.43
1A14.PDB	OD1, H_ASN_54	N, H_ASP_56	H, H_ASP_56	2.82	2.01	27.91
1A14.PDB	O, H_ILE_48	N, H_ASN_60	H, H_ASN_60	2.52	1.70	23.11
1A14.PDB	O, H_TRP_47	ND2, H_ASN_60	HD22, H_ASN_60	2.76	1.87	19.57
1A14.PDB	O, H_PHE_63	N, H_ALA_67	H, H_ALA_67	2.95	1.99	5.88
1A14.PDB	OH, H_TYR_59	N, H_LEU_69	H, H_LEU_69	2.81	1.86	9.44
1A14.PDB	O, H_THR_77	N, H_ASP_72	H, H_ASP_72	2.72	1.79	11.50
1A14.PDB	OD2, H_ASP_72	N, H_SER_75	H, H_SER_75	2.80	1.92	19.95
1A14.PDB	OG1, H_THR_77	OG, H_SER_75	HG, H_SER_75	2.86	2.04	27.11
1A14.PDB	O, H_ASP_72	N, H_THR_77	H, H_THR_77	2.99	2.04	11.91
1A14.PDB	O, H_CYS_22	N, H_ALA_78	H, H_ALA_78	2.74	1.87	21.95
1A14.PDB	O, H_MET_20	N, H_MET_80	H, H_MET_80	2.96	2.07	20.70
1A14.PDB	OE2, H_GLU_85	OG, H_SER_84	HG, H_SER_84	2.91	1.99	12.42
1A14.PDB	O, H_THR_83	N, H_ASP_86	H, H_ASP_86	2.92	1.98	13.36
1A14.PDB	O, H_TYR_102	N, H_ARG_94	H, H_ARG_94	2.71	1.83	20.03
1A14.PDB	OD2, H_ASP_101	NH2, H_ARG_94	HH21, H_ARG_94	2.75	1.83	16.91
1A14.PDB	O, H_GLY_97	N, H_ARG_100	H, H_ARG_100	2.82	1.90	14.18
1A14.PDB	OH, L_TYR_36	N, H_PHE_100E	H, H_PHE_100E	2.73	1.81	13.85
1A14.PDB	OE1, H_GLN_6	N, H_GLY_106	H, H_GLY_106	2.85	1.98	22.46
1A14.PDB	O, H_ALA_88	N, H_VAL_109	H, H_VAL_109	2.80	1.86	11.06
1A14.PDB	O, H_GLU_10	N, H_THR_110	H, H_THR_110	2.78	1.95	26.41
1A14.PDB	O, H_GLU_10	OG1, H_THR_110	HG1, H_THR_110	2.94	1.99	6.65
1A14.PDB	OG, H_SER_87	N, H_VAL_111	H, H_VAL_111	2.68	1.82	20.55
1E6J.PDB	O, H_TYR_94	NE2, H_GLN_6	HE22, H_GLN_6	2.85	1.90	10.79
1E6J.PDB	O, H_GLN_6	NE2, H_GLN_112	HE22, H_GLN_112	2.88	2.04	26.17
1E6J.PDB	O, L_TYR_85	NE2, L_GLN_6	HE22, L_GLN_6	2.85	1.96	20.67
1E6J.PDB	OH, L_TYR_85	NE2, L_GLN_36	HE21, L_GLN_36	2.83	1.87	8.49
1E6J.PDB	OE1, H_GLN_39	NE2, L_GLN_37	HE22, L_GLN_37	2.69	1.84	23.98
1E6J.PDB	OG, L_SER_129	NE2, L_GLN_122	HE22, L_GLN_122	2.94	2.00	13.76
1E6J.PDB	O, L_ILE_104	NE2, L_GLN_164	HE22, L_GLN_164	2.87	1.92	11.35
1E6J.PDB	O, P_GLU_159	NE2, P_GLN_155	HE21, P_GLN_155	2.82	1.93	20.03
1F3R.PDB	O, A_ASN_68	N, A_TYR_72	H, A_TYR_72	2.96	1.94	7.79
1F3R.PDB	O, B_ASN_230	OH, A_TYR_72	HH, A_TYR_72	2.67	1.70	2.56
1F3R.PDB	O, B_THR_21	N, B_SER_7	H, B_SER_7	2.87	1.87	9.61
1F3R.PDB	O, B_LEU_85	N, B_SER_15	H, B_SER_15	2.82	1.79	2.70
1F3R.PDB	OD1, B_ASN_83	OG1, B_THR_17	HG1, B_THR_17	2.73	1.80	13.32
1F3R.PDB	O, B_LEU_80	N, B_LEU_20	H, B_LEU_20	2.98	2.06	21.36
1F3R.PDB	O, B_VAL_78	N, B_CYS_22	H, B_CYS_22	2.90	1.88	6.63
1F3R.PDB	O, B_ASN_76	N, B_VAL_24	H, B_VAL_24	2.91	1.89	6.46

1F3R.PDB	O, B_SER_28	OG, B_SER_31	HG, B_SER_31	2.64	1.68	8.32
1F3R.PDB	O, B_THR_96	N, B_SER_35	H, B_SER_35	2.97	1.94	2.64
1F3R.PDB	O, B_GLY_49	N, B_TRP_36	H, B_TRP_36	2.92	1.90	3.05
1F3R.PDB	O, B_THR_90	N, B_SER_41	H, B_SER_41	2.88	1.87	9.24
1F3R.PDB	O, B_ARG_38	N, B_GLU_46	H, B_GLU_46	2.92	1.91	7.52
1F3R.PDB	O, B_TRP_36	N, B_MET_48	H, B_MET_48	2.89	1.95	18.67
1F3R.PDB	O, B_ALA_58	N, B_ARG_50	H, B_ARG_50	2.87	1.86	10.08
1F3R.PDB	O, A_GLY_70	NH2, B_ARG_50	HH21, B_ARG_50	2.81	1.79	6.29
1F3R.PDB	O, B_TYR_100	OH, B_TYR_53	HH, B_TYR_53	2.66	1.70	6.56
1F3R.PDB	O, B_LEU_67	OH, B_TYR_59	HH, B_TYR_59	2.69	1.77	15.53
1F3R.PDB	O, B_TRP_47	ND2, B_ASN_60	HD21, B_ASN_60	2.98	1.99	12.26
1F3R.PDB	NE1, A_TRP_67	OG, B_SER_61	HG, B_SER_61	2.86	1.89	6.31
1F3R.PDB	O, B_GLN_77	N, B_ASP_72	H, B_ASP_72	2.95	1.93	8.00
1F3R.PDB	O, B_SER_70	N, B_PHE_79	H, B_PHE_79	2.87	1.91	16.42
1F3R.PDB	O, B_LEU_20	N, B_LEU_80	H, B_LEU_80	2.97	1.97	11.86
1F3R.PDB	O, B_SER_68	N, B_LYS_81	H, B_LYS_81	3.00	2.04	17.31
1F3R.PDB	O, B_LEU_18	N, B_MET_82	H, B_MET_82	2.89	1.88	9.85
1F3R.PDB	O, B_ARG_66	N, B_ASN_83	H, B_ASN_83	2.93	1.91	7.12
1F3R.PDB	O, B_ASP_89	OH, B_TYR_93	HH, B_TYR_93	2.65	1.76	18.66
1F3R.PDB	O, B_VAL_37	N, B_TYR_94	H, B_TYR_94	2.86	1.87	13.22
1F3R.PDB	O, B_SER_35	N, B_THR_96	H, B_THR_96	2.85	1.83	6.85
1F3R.PDB	O, B_PHE_112	N, B_ARG_97	H, B_ARG_97	2.97	1.94	0.13
1F3R.PDB	O, B_TYR_109	N, B_LEU_99	H, B_LEU_99	2.82	1.80	6.09
1F3R.PDB	O, B_LEU_105	OH, B_TYR_100	HH, B_TYR_100	2.81	1.87	9.55
1F3R.PDB	O, B_ARG_97	N, B_ASP_111	H, B_ASP_111	3.00	1.99	8.87
1F3R.PDB	OD2, B_ASP_111	N, B_PHE_112	H, B_PHE_112	2.95	1.99	17.02
1F3R.PDB	O, B_CYS_95	N, B_GLY_114	H, B_GLY_114	2.93	1.91	8.69
1F3R.PDB	O, B_GLY_91	N, B_VAL_119	H, B_VAL_119	2.99	2.03	17.54
1F3R.PDB	O, B_GLY_10	N, B_THR_120	H, B_THR_120	2.83	1.81	7.39
1F3R.PDB	O, B_ASN_257	N, B_LEU_142	H, B_LEU_142	2.85	1.82	6.57
1F3R.PDB	O, B_LYS_162	OG1, B_THR_143	HG1, B_THR_143	2.81	1.98	25.43
1F3R.PDB	O, B_TYR_224	NE2, B_GLN_144	HE22, B_GLN_144	2.91	1.91	11.14
1F3R.PDB	O, B_SER_160	N, B_SER_145	H, B_SER_145	2.97	1.94	2.29
1F3R.PDB	O, B_GLY_238	OG, B_SER_147	HG, B_SER_147	2.70	1.74	5.62
1F3R.PDB	O, B_LEU_216	N, B_GLY_154	H, B_GLY_154	2.96	1.97	13.26
1F3R.PDB	OG1, B_THR_212	OG1, B_THR_158	HG1, B_THR_158	2.80	1.87	11.10
1F3R.PDB	O, B_LEU_211	N, B_LEU_159	H, B_LEU_159	2.93	1.90	5.82
1F3R.PDB	O, B_SER_145	N, B_SER_160	H, B_SER_160	2.85	1.84	8.61
1F3R.PDB	O, B_TYR_209	N, B_CYS_161	H, B_CYS_161	2.83	1.82	9.85
1F3R.PDB	O, B_THR_143	N, B_LYS_162	H, B_LYS_162	2.92	1.94	14.43
1F3R.PDB	O, A_ILE_75	OH, B_TYR_170	HH, B_TYR_170	2.72	1.77	10.88
1F3R.PDB	O, B_ILE_186	N, B_TRP_173	H, B_TRP_173	2.96	1.95	8.06
1F3R.PDB	O, B_PHE_225	N, B_TYR_174	H, B_TYR_174	2.93	1.90	0.94
1F3R.PDB	O, B_LYS_183	N, B_GLN_175	H, B_GLN_175	2.88	1.90	13.28
1F3R.PDB	O, B_THR_223	N, B_GLN_176	H, B_GLN_176	2.93	1.91	6.88
1F3R.PDB	O, B_TRP_173	N, B_LEU_185	H, B_LEU_185	2.95	2.01	19.35
1F3R.PDB	O, B_SER_191	N, B_TYR_187	H, B_TYR_187	2.91	1.92	11.97
1F3R.PDB	O, B_LEU_171	N, B_THR_189	H, B_THR_189	2.92	1.94	15.09
1F3R.PDB	O, B_ASN_169	OG1, B_THR_189	HG1, B_THR_189	2.78	1.86	13.97
1F3R.PDB	O, B_ASN_188	N, B_ASN_190	H, B_ASN_190	2.99	2.10	24.68
1F3R.PDB	O, B_ASN_190	OG, B_SER_191	HG, B_SER_191	2.83	1.89	11.19
1F3R.PDB	O, B_PRO_197	N, B_ARG_199	H, B_ARG_199	2.94	2.05	24.65
1F3R.PDB	OD1, B_ASP_220	NH1, B_ARG_199	HH12, B_ARG_199	2.89	1.98	22.15
1F3R.PDB	O, B_THR_210	N, B_SER_203	H, B_SER_203	2.88	1.86	4.33
1F3R.PDB	O, B_ASN_168	N, B_GLY_206	H, B_GLY_206	2.87	1.85	8.80
1F3R.PDB	O, B_CYS_161	N, B_TYR_209	H, B_TYR_209	2.98	1.97	8.84
1F3R.PDB	O, B_GLY_206	OH, B_TYR_209	HH, B_TYR_209	2.72	1.77	8.74
1F3R.PDB	O, B_SER_203	N, B_THR_210	H, B_THR_210	2.89	1.91	14.26

1F3R.PDB	O, B_SER.203	OG1, B_THR.210	HG1, B_THR.210	2.67	1.72	9.35
1F3R.PDB	O, B_LEU.159	N, B_LEU.211	H, B_LEU.211	2.96	1.94	7.42
1F3R.PDB	O, B_VAL.157	N, B_ILE.213	H, B_ILE.213	2.95	1.95	11.15
1F3R.PDB	O, B_ARG.199	OG, B_SER.214	HG, B_SER.214	2.60	1.65	8.60
1F3R.PDB	OG, B_SER.214	N, B_SER.215	H, B_SER.215	2.99	2.14	28.78
1F3R.PDB	OE1, B_GLN.217	OG, B_SER.215	HG, B_SER.215	2.66	1.72	13.57
1F3R.PDB	O, B_GLN.217	N, B_ASP.220	H, B_ASP.220	2.93	1.97	17.91
1F3R.PDB	O, B_GLN.176	N, B_THR.223	H, B_THR.223	2.88	1.86	6.84
1F3R.PDB	O, B_THR.239	OG1, B_THR.223	HG1, B_THR.223	2.65	1.69	5.79
1F3R.PDB	O, B_ASP.220	OH, B_TYR.224	HH, B_TYR.224	2.64	1.71	12.61
1F3R.PDB	O, B_TYR.174	N, B_PHE.225	H, B_PHE.225	2.92	1.99	20.78
1F3R.PDB	O, B_ALA.172	N, B_TYR.227	H, B_TYR.227	3.00	2.00	11.62
1F3R.PDB	NE1, B_TRP.47	OH, B_TYR.227	HH, B_TYR.227	2.99	2.20	29.73
1F3R.PDB	O, B_TYR.170	N, B_TYR.229	H, B_TYR.229	2.94	1.91	4.24
1F3R.PDB	OD1, B_ASN.188	OH, B_TYR.229	HH, B_TYR.229	2.66	1.70	7.44
1F3R.PDB	OD1, B_ASN.231	N, B_GLY.232	H, B_GLY.232	2.89	1.87	6.19
1F3R.PDB	O, A_ASP.71	OH, B_TYR.233	HH, B_TYR.233	2.71	1.89	25.38
1F3R.PDB	OE1, B_GLN.144	N, B_GLY.238	H, B_GLY.238	2.97	1.99	15.42
1F3R.PDB	O, B_SER.147	N, B_LYS.240	H, B_LYS.240	2.89	1.86	4.01
1F3R.PDB	O, B_LEU.149	OE2, B_GLU.242	HE2, B_GLU.242	2.59	1.65	10.05
1F3R.PDB	O, B_LEU.243	NE2, B_GLN.248	HE21, B_GLN.248	2.97	2.01	16.74
1F3R.PDB	O, B_GLY.136	N, B_ILE.251	H, B_ILE.251	2.88	1.88	10.81
1F3R.PDB	O, B_SER.41	OE2, B_GLU.253	HE2, B_GLU.253	2.63	1.68	6.51
1F3R.PDB	O, B_ASP.139	N, B_ASP.255	H, B_ASP.255	2.95	1.95	13.03
1HCV.PDB	O, A_THR.110	N, A_VAL.12	H, A_VAL.12	2.93	2.02	18.33
1HCV.PDB	O, A_SER.112	N, A_ALA.14	H, A_ALA.14	2.93	2.13	29.46
1HCV.PDB	O, A_LEU.82C	N, A_GLY.15	H, A_GLY.15	2.71	1.79	13.54
1HCV.PDB	O, A_GLN.13	N, A_GLY.16	H, A_GLY.16	2.86	1.94	16.16
1HCV.PDB	O, A_MET.82	N, A_LEU.18	H, A_LEU.18	2.92	1.99	16.49
1HCV.PDB	O, A_LEU.80	N, A_LEU.20	H, A_LEU.20	2.95	1.97	7.19
1HCV.PDB	O, A_SER.7	N, A_SER.21	H, A_SER.21	2.87	1.92	9.29
1HCV.PDB	O, A_VAL.78	N, A_CYS.22	H, A_CYS.22	2.90	2.03	23.01
1HCV.PDB	O, A_GLN.5	N, A_ALA.23	H, A_ALA.23	2.91	1.94	8.72
1HCV.PDB	O, A_LYS.76	N, A_ALA.24	H, A_ALA.24	2.84	1.87	5.65
1HCV.PDB	O, A_GLY.95	N, A_ASP.33	H, A_ASP.33	2.78	1.82	4.32
1HCV.PDB	O, A_ILE.51	N, A_MET.34	H, A_MET.34	2.93	1.96	6.74
1HCV.PDB	O, A_GLY.93	N, A_GLY.35	H, A_GLY.35	2.81	1.88	14.94
1HCV.PDB	O, A_ALA.49	N, A_TRP.36	H, A_TRP.36	2.79	1.84	9.16
1HCV.PDB	O, A_THR.91	N, A_PHE.37	H, A_PHE.37	2.79	1.88	17.50
1HCV.PDB	O, A_GLU.46	N, A_ARG.38	H, A_ARG.38	2.85	1.92	14.14
1HCV.PDB	OE2, A_GLU.46	NE, A_ARG.38	HE, A_ARG.38	2.98	2.01	4.47
1HCV.PDB	OH, A_TYR.90	NH1, A_ARG.38	HH11, A_ARG.38	2.93	1.98	14.34
1HCV.PDB	OD1, A_ASP.86	NH1, A_ARG.38	HH12, A_ARG.38	2.86	1.90	11.61
1HCV.PDB	O, A_VAL.89	N, A_GLN.39	H, A_GLN.39	2.97	2.07	19.93
1HCV.PDB	O, A_LYS.43	NE2, A_GLN.39	HE22, A_GLN.39	2.89	1.95	12.02
1HCV.PDB	O, A_ALA.40	N, A_LYS.43	H, A_LYS.43	2.92	2.01	18.86
1HCV.PDB	O, A_ARG.38	N, A_GLU.46	H, A_GLU.46	2.84	1.93	16.72
1HCV.PDB	O, A_TRP.36	N, A_VAL.48	H, A_VAL.48	2.86	1.95	18.09
1HCV.PDB	O, A_MET.34	N, A_ILE.51	H, A_ILE.51	2.83	1.91	16.34
1HCV.PDB	O, A_ARG.56	N, A_ASN.52	H, A_ASN.52	2.98	2.06	16.59
1HCV.PDB	O, A_ASN.52	N, A_ALA.55	H, A_ALA.55	2.92	2.11	28.15
1HCV.PDB	O, A_TYR.59	NE, A_ARG.64	HE, A_ARG.64	2.96	2.11	24.27
1HCV.PDB	O, A_TYR.59	NH2, A_ARG.64	HH21, A_ARG.64	2.85	1.95	21.66
1HCV.PDB	O, A_VAL.63	N, A_ARG.66	H, A_ARG.66	2.97	2.05	16.00
1HCV.PDB	O, A_GLN.81	N, A_THR.68	H, A_THR.68	2.89	1.97	16.73
1HCV.PDB	OH, A_TYR.59	N, A_ILE.69	H, A_ILE.69	2.86	1.90	7.83
1HCV.PDB	O, A_TRP.52A	NE, A_ARG.71	HE, A_ARG.71	2.79	1.83	3.79
1HCV.PDB	O, A_THR.77	N, A_ASP.72	H, A_ASP.72	2.82	1.84	2.73

1HCV.PDB	OD1, A_ASP_72	N, A_LYS_75	H, A_LYS_75	2.94	2.05	18.63
1HCV.PDB	O, A_CYS_22	N, A_VAL_78	H, A_VAL_78	2.93	1.97	8.95
1HCV.PDB	O, A_SER_70	N, A_TYR_79	H, A_TYR_79	2.83	1.88	10.07
1HCV.PDB	O, A_LEU_20	N, A_LEU_80	H, A_LEU_80	2.95	2.00	12.10
1HCV.PDB	O, A_THR_68	N, A_GLN_81	H, A_GLN_81	2.77	1.81	7.49
1HCV.PDB	O, A_LEU_18	N, A_MET_82	H, A_MET_82	2.84	1.89	10.75
1HCV.PDB	OD2, A_ASP_86	N, A_LYS_83	H, A_LYS_83	2.81	1.93	18.86
1HCV.PDB	O, A_LYS_83	N, A_ASP_86	H, A_ASP_86	2.78	1.84	11.83
1HCV.PDB	O, A_THR_107	N, A_TYR_90	H, A_TYR_90	2.77	1.82	10.83
1HCV.PDB	O, A_ASP_86	OH, A_TYR_90	HH, A_TYR_90	2.78	1.82	4.95
1HCV.PDB	O, A_PHE_37	N, A_THR_91	H, A_THR_91	2.79	1.83	10.98
1HCV.PDB	OE2, A_GLU_6	N, A_CYS_92	H, A_CYS_92	2.92	1.93	9.32
1HCV.PDB	O, A_GLY_35	N, A_GLY_93	H, A_GLY_93	2.87	1.92	15.71
1HCV.PDB	O, A_ALA_94	N, A_ASP_101	H, A_ASP_101	2.95	2.03	16.44
1HCV.PDB	O, A_CYS_92	N, A_GLY_104	H, A_GLY_104	2.85	1.98	21.84
1HCV.PDB	OE2, A_GLU_6	N, A_GLY_106	H, A_GLY_106	2.97	2.18	29.00
1HCV.PDB	O, A_TYR_90	N, A_THR_107	H, A_THR_107	2.83	1.98	25.29
1HCV.PDB	O, A_GLY_10	N, A_THR_110	H, A_THR_110	2.96	1.98	5.57
1HGD.PDB	O, B_ILE_140	N, A_ALA_11	H, A_ALA_11	2.90	2.03	23.17
1HGD.PDB	O, B_PHE_138	N, A_LEU_13	H, A_LEU_13	2.95	2.00	13.08
1HGD.PDB	O, B_ARG_25	N, A_CYS_14	H, A_CYS_14	2.89	1.92	6.63
1HGD.PDB	O, B_GLY_136	N, A_LEU_15	H, A_LEU_15	2.87	1.90	8.68
1HGD.PDB	O, B_GLY_23	N, A_GLY_16	H, A_GLY_16	2.93	2.02	18.64
1HGD.PDB	O, A_HIS_18	ND1, A_HIS_17	HD1, A_HIS_17	2.93	2.05	21.54
1HGD.PDB	O, B_TRP_21	N, A_HIS_18	H, A_HIS_18	2.86	2.01	24.44
1HGD.PDB	OD1, A_ASN_322	N, A_VAL_20	H, A_VAL_20	2.77	1.82	9.61
1HGD.PDB	O, A_VAL_36	N, A_THR_24	H, A_THR_24	2.85	1.96	19.97
1HGD.PDB	O, A_ILE_34	N, A_VAL_26	H, A_VAL_26	2.82	1.91	17.04
1HGD.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.80	1.78	9.95
1HGD.PDB	O, A_VAL_26	N, A_ILE_34	H, A_ILE_34	2.88	1.94	11.85
1HGD.PDB	O, A_THR_24	N, A_VAL_36	H, A_VAL_36	2.80	1.84	8.97
1HGD.PDB	O, A_MET_320	N, A_THR_37	H, A_THR_37	2.84	1.87	4.46
1HGD.PDB	O, A_LEU_316	N, A_THR_40	H, A_THR_40	2.81	1.96	24.53
1HGD.PDB	O, A_LEU_314	N, A_LEU_42	H, A_LEU_42	2.82	1.97	25.11
1HGD.PDB	O, A_PHE_294	N, A_GLN_44	H, A_GLN_44	2.82	1.85	6.79
1HGD.PDB	O, A_SER_46	NE2, A_GLN_44	HE22, A_GLN_44	2.87	1.99	21.11
1HGD.PDB	OD2, A_ASP_275	NZ, A_LYS_50	HZ1, A_LYS_50	2.70	1.79	23.99
1HGD.PDB	O, A_PRO_273	N, A_ILE_51	H, A_ILE_51	2.81	1.86	10.46
1HGD.PDB	O, A_ASP_275	N, A_ASN_53	H, A_ASN_53	2.82	1.93	20.82
1HGD.PDB	OD2, A_ASP_85	N, A_ARG_57	H, A_ARG_57	2.86	1.92	12.52
1HGD.PDB	O, A_THR_83	NE, A_ARG_57	HE, A_ARG_57	2.79	1.82	8.87
1HGD.PDB	O, A_LEU_86	N, A_LEU_59	H, A_LEU_59	2.85	1.91	13.74
1HGD.PDB	O, A_VAL_88	N, A_GLY_61	H, A_GLY_61	2.95	2.09	23.46
1HGD.PDB	OD1, A_ASP_60	N, A_ILE_62	H, A_ILE_62	2.87	1.95	16.02
1HGD.PDB	O, A_GLY_61	N, A_CYS_64	H, A_CYS_64	2.88	1.96	16.57
1HGD.PDB	OE2, A_GLU_89	N, A_LEU_66	H, A_LEU_66	2.99	2.02	7.24
1HGD.PDB	O, A_LEU_66	N, A_LEU_70	H, A_LEU_70	2.89	2.00	21.06
1HGD.PDB	O, A_ILE_67	N, A_LEU_71	H, A_LEU_71	2.83	1.86	7.61
1HGD.PDB	O, A_ASP_68	N, A_GLY_72	H, A_GLY_72	2.86	1.93	13.78
1HGD.PDB	OD1, A_ASP_73	N, A_HIS_75	H, A_HIS_75	2.94	2.08	23.98
1HGD.PDB	OD1, A_ASP_73	ND1, A_HIS_75	HD1, A_HIS_75	2.82	1.92	19.21
1HGD.PDB	O, A_ASP_63	NE2, A_HIS_75	HE2, A_HIS_75	2.89	1.98	18.26
1HGD.PDB	O, A_ASP_73	N, A_CYS_76	H, A_CYS_76	2.82	1.87	12.30
1HGD.PDB	O, A_PRO_74	N, A_ASP_77	H, A_ASP_77	2.96	2.01	12.30
1HGD.PDB	OE1, A_GLU_82	N, A_THR_83	H, A_THR_83	2.91	2.00	18.21
1HGD.PDB	O, A_ARG_57	N, A_ASP_85	H, A_ASP_85	2.78	1.87	17.48
1HGD.PDB	O, A_LEU_59	N, A_VAL_88	H, A_VAL_88	2.92	1.95	5.25
1HGD.PDB	O, A_MET_268	N, A_GLU_89	H, A_GLU_89	2.76	1.82	11.67

1HGD.PDB	OD1, A_ASP_60	NE, A_ARG_90	HE, A_ARG_90	2.88	1.91	7.55
1HGD.PDB	O, A_SER_270	NH1, A_ARG_90	HH11, A_ARG_90	2.66	1.79	24.65
1HGD.PDB	O, A_ALA_272	NH1, A_ARG_90	HH12, A_ARG_90	2.63	1.70	17.53
1HGD.PDB	OD2, A_ASP_60	NH2, A_ARG_90	HH21, A_ARG_90	2.80	1.82	10.07
1HGD.PDB	OD1, A_ASP_271	N, A_SER_91	H, A_SER_91	2.89	1.92	6.25
1HGD.PDB	OD1, A_ASP_271	OG, A_SER_91	HG, A_SER_91	2.93	2.12	28.00
1HGD.PDB	OD2, A_ASP_271	OG, A_SER_91	HG, A_SER_91	2.81	1.91	17.78
1HGD.PDB	OD2, A_ASP_68	OG, A_SER_95	HG, A_SER_95	2.92	1.99	16.11
1HGD.PDB	OD2, A_ASP_73	N, A_ASN_96	H, A_ASN_96	2.94	1.97	9.87
1HGD.PDB	OD1, A_ASP_68	OH, A_TYR_100	HH, A_TYR_100	2.88	1.90	0.98
1HGD.PDB	OD2, A_ASP_104	OG, A_SER_107	HG, A_SER_107	2.86	1.96	19.52
1HGD.PDB	O, A_TYR_105	N, A_ARG_109	H, A_ARG_109	2.82	1.85	4.81
1HGD.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.83	1.84	13.41
1HGD.PDB	OD2, F_ASP_79	OG, A_SER_110	HG, A_SER_110	2.92	1.96	11.03
1HGD.PDB	O, A_SER_107	N, A_LEU_111	H, A_LEU_111	2.89	1.94	11.30
1HGD.PDB	O, A_LEU_108	N, A_VAL_112	H, A_VAL_112	2.97	2.01	7.23
1HGD.PDB	O, A_ARG_109	N, A_ALA_113	H, A_ALA_113	2.92	2.01	17.77
1HGD.PDB	O, A_SER_110	N, A_SER_114	H, A_SER_114	2.96	2.05	17.15
1HGD.PDB	OE2, A_GLU_119	OG1, A_THR_117	HG1, A_THR_117	2.87	1.92	9.92
1HGD.PDB	O, A_GLU_82	N, A_LEU_118	H, A_LEU_118	2.91	1.98	15.32
1HGD.PDB	O, A_TYR_257	N, A_ILE_121	H, A_ILE_121	2.85	1.89	7.79
1HGD.PDB	O, A_ARG_255	N, A_GLU_123	H, A_GLU_123	2.91	1.96	11.30
1HGD.PDB	O, A_THR_155	N, A_THR_131	H, A_THR_131	2.76	1.86	18.36
1HGD.PDB	OD1, A_ASN_152	N, A_ASN_133	H, A_ASN_133	2.80	1.88	15.39
1HGD.PDB	O, A_GLY_146	N, A_SER_136	H, A_SER_136	2.72	1.80	14.38
1HGD.PDB	O, A_GLY_144	NZ, A_LYS_140	HZ1, A_LYS_140	2.72	1.75	16.12
1HGD.PDB	OD1, A_ASN_137	NZ, A_LYS_140	HZ2, A_LYS_140	2.76	1.82	19.96
1HGD.PDB	OD2, A_ASP_77	NE, A_ARG_141	HE, A_ARG_141	2.80	1.97	26.87
1HGD.PDB	O, A_PHE_147	NH1, A_ARG_141	HH12, A_ARG_141	2.57	1.62	14.73
1HGD.PDB	OD1, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.86	1.95	21.98
1HGD.PDB	OD2, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.74	1.86	23.87
1HGD.PDB	O, A_GLY_72	NH2, A_ARG_141	HH22, A_ARG_141	2.95	1.97	11.26
1HGD.PDB	O, A_SER_136	N, A_GLY_146	H, A_GLY_146	2.96	2.04	13.96
1HGD.PDB	O, A_GLY_72	N, A_SER_149	H, A_SER_149	2.84	1.94	17.77
1HGD.PDB	O, A_ALA_253	N, A_ASN_152	H, A_ASN_152	2.80	1.94	23.17
1HGD.PDB	OH, A_TYR_195	NE1, A_TRP_153	HE1, A_TRP_153	2.81	1.92	20.45
1HGD.PDB	O, A_LEU_194	N, A_LYS_156	H, A_LYS_156	2.95	2.06	19.92
1HGD.PDB	O, A_SER_193	NZ, A_LYS_156	HZ2, A_LYS_156	2.80	1.80	13.32
1HGD.PDB	O, A_SER_247	N, A_LEU_164	H, A_LEU_164	2.66	1.83	25.34
1HGD.PDB	O, A_ILE_245	N, A_VAL_166	H, A_VAL_166	2.93	1.97	10.28
1HGD.PDB	O, A_LEU_243	OG1, A_THR_167	HG1, A_THR_167	2.93	2.00	13.12
1HGD.PDB	O, A_LEU_243	N, A_MET_168	H, A_MET_168	2.89	1.96	14.94
1HGD.PDB	O, A_ASP_241	N, A_ASN_170	H, A_ASN_170	2.96	1.98	6.23
1HGD.PDB	O, A_PHE_174	ND2, A_ASN_170	HD21, A_ASN_170	2.82	1.87	11.30
1HGD.PDB	O, A_VAL_237	ND2, A_ASN_170	HD22, A_ASN_170	2.83	2.02	27.43
1HGD.PDB	O, A_VAL_237	N, A_LYS_176	H, A_LYS_176	2.97	2.05	17.24
1HGD.PDB	OE2, A_GLU_123	NZ, A_LYS_176	HZ2, A_LYS_176	2.69	1.80	25.20
1HGD.PDB	O, A_THR_235	N, A_TYR_178	H, A_TYR_178	2.79	1.82	5.26
1HGD.PDB	OE1, A_GLU_123	OH, A_TYR_178	HH, A_TYR_178	2.75	1.82	12.48
1HGD.PDB	OG1, A_THR_235	NE1, A_TRP_180	HE1, A_TRP_180	2.94	1.95	4.39
1HGD.PDB	O, A_ASN_250	N, A_HIS_183	H, A_HIS_183	2.86	1.94	16.37
1HGD.PDB	O, A_ARG_229	N, A_HIS_184	H, A_HIS_184	2.80	1.84	6.46
1HGD.PDB	OG, A_SER_231	NE2, A_HIS_184	HE2, A_HIS_184	2.78	1.93	25.06
1HGD.PDB	OE1, A_GLU_190	N, A_SER_186	H, A_SER_186	2.93	1.98	11.85
1HGD.PDB	OG1, A_THR_187	N, A_GLU_190	H, A_GLU_190	2.88	1.93	10.33
1HGD.PDB	O, A_GLN_197	NE2, A_GLN_191	HE22, A_GLN_191	2.88	1.95	15.50
1HGD.PDB	O, A_ASN_188	OG1, A_THR_192	HG1, A_THR_192	2.99	2.04	7.10
1HGD.PDB	O, A_GLN_189	N, A_SER_193	H, A_SER_193	2.80	1.83	3.68

1HGD.PDB	O, A_GLU_190	N, A_LEU_194	H, A_LEU_194	2.97	2.01	9.56
1HGD.PDB	O, A_GLN_191	N, A_TYR_195	H, A_TYR_195	2.77	1.82	9.83
1HGD.PDB	O, A_TYR_161	NE2, A_GLN_197	HE21, A_GLN_197	2.91	1.96	11.57
1HGD.PDB	O, A_ASN_248	NE2, A_GLN_197	HE22, A_GLN_197	2.95	2.02	15.49
1HGD.PDB	OD1, A_ASN_246	NH2, A_ARG_201	HH21, A_ARG_201	2.59	1.75	26.83
1HGD.PDB	O, A_ILE_213	N, A_VAL_202	H, A_VAL_202	3.00	2.02	5.97
1HGD.PDB	O, A_ASN_246	N, A_THR_203	H, A_THR_203	2.83	1.91	16.65
1HGD.PDB	O, A_GLN_211	N, A_VAL_204	H, A_VAL_204	2.85	1.94	18.50
1HGD.PDB	O, A_SER_209	N, A_THR_206	H, A_THR_206	2.89	1.92	7.99
1HGD.PDB	OD1, A_ASP_241	N, A_ARG_207	H, A_ARG_207	2.92	1.95	8.05
1HGD.PDB	OG1, A_THR_206	OG, A_SER_209	HG, A_SER_209	2.90	1.96	11.12
1HGD.PDB	OD1, E_ASP_101	NE2, A_GLN_210	HE22, A_GLN_210	3.00	2.15	26.33
1HGD.PDB	O, A_VAL_204	N, A_GLN_211	H, A_GLN_211	2.82	1.90	17.10
1HGD.PDB	OG1, A_THR_203	OG1, A_THR_212	HG1, A_THR_212	2.90	1.94	6.68
1HGD.PDB	O, A_VAL_202	N, A_ILE_213	H, A_ILE_213	2.87	1.94	15.45
1HGD.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.78	1.86	19.99
1HGD.PDB	O, A_ASN_216	NH2, A_ARG_220	HH22, A_ARG_220	2.74	1.85	22.34
1HGD.PDB	O, A_LEU_226	N, A_VAL_223	H, A_VAL_223	2.88	1.93	9.40
1HGD.PDB	O, A_CYS_97	NE, A_ARG_224	HE, A_ARG_224	2.82	1.98	25.92
1HGD.PDB	O, A_CYS_97	NH2, A_ARG_224	HH21, A_ARG_224	2.84	1.96	24.52
1HGD.PDB	O, A_VAL_223	N, A_LEU_226	H, A_LEU_226	2.93	1.98	11.82
1HGD.PDB	OE2, A_GLU_190	OG, A_SER_228	HG, A_SER_228	2.98	2.00	5.61
1HGD.PDB	O, A_SER_228	NH1, A_ARG_229	HH11, A_ARG_229	2.71	1.76	17.21
1HGD.PDB	O, A_PRO_221	NH2, A_ARG_229	HH22, A_ARG_229	2.60	1.67	16.74
1HGD.PDB	OD1, A_ASP_101	OG, A_SER_231	HG, A_SER_231	2.84	1.88	8.92
1HGD.PDB	O, A_ASP_101	N, A_ILE_232	H, A_ILE_232	2.89	1.95	14.22
1HGD.PDB	O, A_TRP_180	N, A_TYR_233	H, A_TYR_233	2.92	1.95	10.20
1HGD.PDB	O, A_TYR_178	N, A_THR_235	H, A_THR_235	2.88	1.99	20.72
1HGD.PDB	O, A_LYS_176	N, A_VAL_237	H, A_VAL_237	2.78	1.85	14.71
1HGD.PDB	O, F_SER_71	NZ, A_LYS_238	HZ2, A_LYS_238	2.63	1.73	23.20
1HGD.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.93	1.92	13.44
1HGD.PDB	O, A_ASN_170	N, A_GLY_240	H, A_GLY_240	2.86	1.99	22.42
1HGD.PDB	O, A_LYS_238	N, A_ASP_241	H, A_ASP_241	2.97	2.03	13.82
1HGD.PDB	OD1, A_ASP_241	N, A_VAL_242	H, A_VAL_242	2.76	1.95	27.32
1HGD.PDB	O, A_MET_168	N, A_LEU_243	H, A_LEU_243	2.90	1.93	5.35
1HGD.PDB	O, A_SER_205	N, A_VAL_244	H, A_VAL_244	2.96	2.02	12.84
1HGD.PDB	O, A_VAL_166	N, A_ILE_245	H, A_ILE_245	2.91	1.97	12.42
1HGD.PDB	O, A_THR_203	N, A_ASN_246	H, A_ASN_246	2.92	1.96	6.49
1HGD.PDB	OD1, A_ASN_165	ND2, A_ASN_246	HD22, A_ASN_246	2.92	1.97	12.69
1HGD.PDB	O, A_LEU_164	N, A_SER_247	H, A_SER_247	2.92	2.01	18.72
1HGD.PDB	O, A_SER_199	ND2, A_ASN_248	HD21, A_ASN_248	3.00	2.19	29.63
1HGD.PDB	OE1, A_GLN_191	ND2, A_ASN_250	HD21, A_ASN_250	2.94	1.98	9.96
1HGD.PDB	O, A_HIS_183	ND2, A_ASN_250	HD22, A_ASN_250	2.85	1.91	14.80
1HGD.PDB	O, A_ASN_152	N, A_ALA_253	H, A_ALA_253	2.86	1.95	18.07
1HGD.PDB	OD1, A_ASN_133	NH2, A_ARG_255	HH22, A_ARG_255	2.53	1.69	26.82
1HGD.PDB	O, A_ILE_121	N, A_TYR_257	H, A_TYR_257	2.95	2.09	24.12
1HGD.PDB	O, A_LEU_177	N, A_PHE_258	H, A_PHE_258	2.93	1.97	8.57
1HGD.PDB	OE2, A_GLU_119	NH1, A_ARG_261	HH12, A_ARG_261	2.65	1.81	27.93
1HGD.PDB	OE1, A_GLU_119	NH2, A_ARG_261	HH22, A_ARG_261	2.88	1.97	22.77
1HGD.PDB	OD2, A_ASP_85	NZ, A_LYS_264	HZ3, A_LYS_264	2.85	1.86	16.67
1HGD.PDB	O, A_PHE_87	N, A_MET_268	H, A_MET_268	2.83	1.94	19.49
1HGD.PDB	O, A_PRO_284	OG, A_SER_270	HG, A_SER_270	2.85	1.89	8.52
1HGD.PDB	OG, A_SER_270	N, A_ALA_272	H, A_ALA_272	2.92	1.98	12.23
1HGD.PDB	O, A_ILE_51	N, A_ASP_275	H, A_ASP_275	2.87	1.97	19.56
1HGD.PDB	OD1, A_ASP_275	N, A_THR_276	H, A_THR_276	2.83	1.98	24.15
1HGD.PDB	O, A_ASN_54	N, A_SER_279	H, A_SER_279	2.79	1.86	14.12
1HGD.PDB	O, A_TYR_302	N, A_ILE_282	H, A_ILE_282	2.86	1.91	10.03
1HGD.PDB	O, A_THR_283	N, A_GLY_286	H, A_GLY_286	2.82	1.91	15.39

1HGD.PDB	O, A_LYS_50	N, A_SER_287	H, A_SER_287	2.87	1.90	3.72
1HGD.PDB	O, A_ALA_304	ND2, A_ASN_290	HD22, A_ASN_290	2.80	1.90	19.37
1HGD.PDB	OE1, A_GLN_44	NZ, A_LYS_292	HZ1, A_LYS_292	2.71	1.70	11.58
1HGD.PDB	OD2, A_ASP_291	NZ, A_LYS_292	HZ3, A_LYS_292	2.78	1.85	22.68
1HGD.PDB	O, A_LYS_307	N, A_GLN_295	H, A_GLN_295	2.79	1.92	22.70
1HGD.PDB	O, A_ASN_298	NE2, A_GLN_295	HE21, A_GLN_295	2.79	1.82	3.80
1HGD.PDB	O, A_GLN_44	N, A_ASN_296	H, A_ASN_296	2.83	1.90	14.13
1HGD.PDB	OE1, A_GLN_295	N, A_VAL_297	H, A_VAL_297	2.66	1.88	29.86
1HGD.PDB	OD1, A_ASN_285	ND2, A_ASN_298	HD22, A_ASN_298	2.98	2.04	13.52
1HGD.PDB	O, B_LYS_68	NZ, A_LYS_299	HZ2, A_LYS_299	2.96	1.95	12.60
1HGD.PDB	OD1, A_ASN_298	N, A_ILE_300	H, A_ILE_300	2.94	2.01	15.36
1HGD.PDB	O, A_ILE_282	N, A_TYR_302	H, A_TYR_302	2.90	2.05	25.49
1HGD.PDB	O, B_LYS_62	N, A_GLY_303	H, A_GLY_303	2.91	1.96	9.72
1HGD.PDB	O, A_GLN_295	N, A_VAL_309	H, A_VAL_309	2.97	2.17	29.89
1HGD.PDB	OG, B_SER_93	N, A_LYS_310	H, A_LYS_310	2.92	1.97	11.29
1HGD.PDB	OE2, A_GLU_41	N, A_LEU_314	H, A_LEU_314	2.80	1.88	15.00
1HGD.PDB	OE1, A_GLU_41	NZ, A_LYS_315	HZ3, A_LYS_315	2.76	1.81	20.40
1HGD.PDB	O, A_THR_40	N, A_LEU_316	H, A_LEU_316	2.77	1.84	12.70
1HGD.PDB	OD1, B_ASN_104	N, A_ALA_317	H, A_ALA_317	2.78	1.85	14.55
1HGD.PDB	O, A_ASN_38	N, A_THR_318	H, A_THR_318	2.93	2.00	15.92
1HGD.PDB	O, A_VAL_20	ND2, A_ASN_322	HD21, A_ASN_322	2.87	1.96	17.38
1HGD.PDB	OE2, A_GLU_35	ND2, A_ASN_322	HD22, A_ASN_322	2.84	1.97	23.40
1HGD.PDB	O, A_PRO_21	NE2, A_GLN_327	HE22, A_GLN_327	2.81	1.92	20.13
1HGD.PDB	OD2, B_ASP_112	N, B_GLY_1	H2, B_GLY_1	2.82	1.82	14.61
1HGD.PDB	OD1, B_ASP_109	N, B_LEU_2	H, B_LEU_2	2.82	1.95	22.22
1HGD.PDB	OD2, B_ASP_112	N, B_PHE_3	H, B_PHE_3	2.80	1.98	27.04
1HGD.PDB	OD2, B_ASP_112	N, B_GLY_4	H, B_GLY_4	2.93	2.05	20.30
1HGD.PDB	OD1, B_ASP_112	N, B_ALA_5	H, B_ALA_5	2.88	1.99	20.94
1HGD.PDB	O, B_GLY_4	N, B_PHE_9	H, B_PHE_9	2.78	1.84	12.99
1HGD.PDB	O, B_GLY_13	ND2, B_ASN_12	HD22, B_ASN_12	2.80	1.93	22.87
1HGD.PDB	O, A_VAL_323	N, B_GLY_13	H, B_GLY_13	2.71	1.77	11.58
1HGD.PDB	O, A_HIS_17	N, B_TRP_14	H, B_TRP_14	2.85	1.93	15.85
1HGD.PDB	OG1, B_THR_41	N, B_TRP_21	H, B_TRP_21	2.86	1.96	18.16
1HGD.PDB	O, A_GLY_16	N, B_GLY_23	H, B_GLY_23	2.92	1.99	15.76
1HGD.PDB	O, B_ALA_35	N, B_PHE_24	H, B_PHE_24	2.78	1.82	5.68
1HGD.PDB	O, A_CYS_14	N, B_ARG_25	H, B_ARG_25	2.96	2.02	13.01
1HGD.PDB	OE1, B_GLN_34	NE, B_ARG_25	HE, B_ARG_25	2.65	1.77	20.51
1HGD.PDB	O, B_GLY_33	N, B_HIS_26	H, B_HIS_26	2.63	1.81	26.83
1HGD.PDB	O, B_GLY_31	N, B_ASN_28	H, B_ASN_28	2.74	1.82	15.78
1HGD.PDB	O, B_HIS_26	N, B_GLY_33	H, B_GLY_33	2.76	1.88	21.28
1HGD.PDB	O, B_TYR_22	N, B_ASP_37	H, B_ASP_37	2.70	1.77	14.05
1HGD.PDB	OD2, B_ASP_37	N, B_SER_40	H, B_SER_40	2.90	1.95	12.27
1HGD.PDB	O, B_ASP_37	OG1, B_THR_41	HG1, B_THR_41	2.77	1.84	15.28
1HGD.PDB	O, B_LEU_38	N, B_GLN_42	H, B_GLN_42	2.99	2.05	13.49
1HGD.PDB	OD1, B_ASP_46	NE2, B_GLN_42	HE22, B_GLN_42	2.84	1.95	20.63
1HGD.PDB	O, B_LYS_39	N, B_ALA_43	H, B_ALA_43	2.96	2.04	16.02
1HGD.PDB	O, B_SER_40	N, B_ALA_44	H, B_ALA_44	2.96	1.99	5.57
1HGD.PDB	O, B_THR_41	N, B_ILE_45	H, B_ILE_45	2.90	1.93	6.90
1HGD.PDB	O, B_GLN_42	N, B_ASP_46	H, B_ASP_46	2.81	1.84	1.31
1HGD.PDB	O, B_ALA_43	NE2, B_GLN_47	HE22, B_GLN_47	2.89	1.99	19.00
1HGD.PDB	O, B_ILE_45	N, B_ASN_49	H, B_ASN_49	2.87	1.93	13.87
1HGD.PDB	O, B_ASP_46	N, B_GLY_50	H, B_GLY_50	2.87	1.98	20.63
1HGD.PDB	OG1, B_THR_107	NZ, B_LYS_51	HZ1, B_LYS_51	2.96	1.97	16.32
1HGD.PDB	OE1, B_GLU_103	NZ, B_LYS_51	HZ2, B_LYS_51	2.73	1.71	9.93
1HGD.PDB	ND1, B_HIS_106	NZ, B_LYS_51	HZ3, B_LYS_51	2.75	1.79	17.84
1HGD.PDB	O, B_ILE_48	N, B_LEU_52	H, B_LEU_52	2.92	2.00	15.14
1HGD.PDB	O, B_ASN_49	N, B_ASN_53	H, B_ASN_53	2.88	1.92	9.70
1HGD.PDB	OE1, B_GLU_57	NH1, B_ARG_54	HH11, B_ARG_54	2.86	1.87	11.55

1HGD.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.77	1.80	12.79
1HGD.PDB	OE2, B_GLU_61	NZ, B_LYS_58	HZ2, B_LYS_58	2.91	1.88	11.49
1HGD.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ1, B_LYS_62	2.61	1.78	29.53
1HGD.PDB	OD2, F_ASP_90	NZ, B_LYS_62	HZ3, B_LYS_62	2.73	1.84	25.56
1HGD.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.96	2.01	12.34
1HGD.PDB	O, A_LYS_299	NZ, B_LYS_68	HZ1, B_LYS_68	2.92	1.90	10.17
1HGD.PDB	OE2, B_GLU_85	NZ, B_LYS_68	HZ2, B_LYS_68	2.76	1.74	9.73
1HGD.PDB	OG, C_SER_107	N, B_ARG_76	H, B_ARG_76	2.80	1.86	12.47
1HGD.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.88	1.91	8.67
1HGD.PDB	OE2, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.84	1.82	2.51
1HGD.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.71	1.71	6.80
1HGD.PDB	OE1, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.75	1.75	3.21
1HGD.PDB	OE1, B_GLU_74	NE2, B_GLN_78	HE22, B_GLN_78	2.92	1.97	11.55
1HGD.PDB	O, B_GLY_75	N, B_ASP_79	H, B_ASP_79	2.93	1.97	10.45
1HGD.PDB	O, B_GLN_78	N, B_LYS_82	H, B_LYS_82	2.98	2.01	8.27
1HGD.PDB	O, B_ASP_79	N, B_TYR_83	H, B_TYR_83	2.92	1.98	12.82
1HGD.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.65	1.81	23.27
1HGD.PDB	O, B_LEU_80	N, B_VAL_84	H, B_VAL_84	2.91	1.93	4.90
1HGD.PDB	O, B_LYS_82	N, B_ASP_86	H, B_ASP_86	2.94	1.97	5.83
1HGD.PDB	O, B_TYR_83	N, B_THR_87	H, B_THR_87	2.89	1.93	10.17
1HGD.PDB	O, B_VAL_84	N, B_LYS_88	H, B_LYS_88	2.91	1.99	16.72
1HGD.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.76	1.72	5.59
1HGD.PDB	O, B_GLU_85	N, B_ILE_89	H, B_ILE_89	2.85	1.88	3.45
1HGD.PDB	O, B_LYS_88	N, B_TRP_92	H, B_TRP_92	2.96	1.98	5.21
1HGD.PDB	O, B_ILE_89	N, B_SER_93	H, B_SER_93	2.89	1.98	17.56
1HGD.PDB	O, B_ILE_89	OG, B_SER_93	HG, B_SER_93	2.80	1.87	12.12
1HGD.PDB	O, B_ASP_90	N, B_TYR_94	H, B_TYR_94	2.87	1.95	15.58
1HGD.PDB	O, B_TRP_92	N, B_ALA_96	H, B_ALA_96	2.88	1.94	15.13
1HGD.PDB	O, B_SER_93	N, B_GLU_97	H, B_GLU_97	2.98	2.02	8.64
1HGD.PDB	O, B_TYR_94	N, B_LEU_98	H, B_LEU_98	2.95	1.97	4.16
1HGD.PDB	O, B_ASN_95	N, B_LEU_99	H, B_LEU_99	2.94	2.03	17.77
1HGD.PDB	O, B_LEU_98	N, B_LEU_102	H, B_LEU_102	3.00	2.02	4.33
1HGD.PDB	O, B_LEU_99	N, B_GLU_103	H, B_GLU_103	2.95	1.99	9.69
1HGD.PDB	O, B_VAL_100	N, B_ASN_104	H, B_ASN_104	2.89	1.92	9.01
1HGD.PDB	O, A_LYS_27	ND2, B_ASN_104	HD22, B_ASN_104	2.94	1.98	9.01
1HGD.PDB	O, B_LEU_102	N, B_HIS_106	H, B_HIS_106	2.93	1.96	7.40
1HGD.PDB	O, B_GLU_103	N, B_THR_107	H, B_THR_107	2.77	1.89	20.47
1HGD.PDB	O, B_ASN_104	N, B_ILE_108	H, B_ILE_108	2.98	2.01	9.27
1HGD.PDB	O, B_HIS_106	N, B_LEU_110	H, B_LEU_110	2.82	1.87	10.47
1HGD.PDB	O, B_THR_107	OG1, B_THR_111	HG1, B_THR_111	2.97	2.00	4.65
1HGD.PDB	O, B_ASP_109	N, B_SER_113	H, B_SER_113	2.81	1.86	10.44
1HGD.PDB	O, F_LEU_2	OG, B_SER_113	HG, B_SER_113	2.69	1.91	29.59
1HGD.PDB	O, B_SER_113	N, B_LYS_117	H, B_LYS_117	2.72	1.85	22.52
1HGD.PDB	O, B_MET_115	N, B_PHE_119	H, B_PHE_119	3.00	2.05	11.89
1HGD.PDB	O, B_ASN_116	N, B_GLU_120	H, B_GLU_120	2.91	1.94	4.94
1HGD.PDB	O, B_LYS_117	N, B_LYS_121	H, B_LYS_121	2.92	2.03	20.84
1HGD.PDB	O, B_PHE_119	N, B_ARG_123	H, B_ARG_123	2.95	1.99	8.27
1HGD.PDB	OE2, B_GLU_120	NH1, B_ARG_123	HH11, B_ARG_123	2.79	1.91	24.17
1HGD.PDB	O, B_GLU_120	N, B_ARG_124	H, B_ARG_124	2.97	2.00	6.65
1HGD.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.83	2.02	28.17
1HGD.PDB	OE2, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.88	2.01	22.00
1HGD.PDB	O, B_HIS_159	ND2, B_ASN_129	HD21, B_ASN_129	2.97	2.01	9.55
1HGD.PDB	OH, B_TYR_157	ND2, B_ASN_129	HD22, B_ASN_129	2.78	1.83	11.22
1HGD.PDB	O, B_LYS_139	N, B_GLU_131	H, B_GLU_131	2.96	2.05	17.87
1HGD.PDB	O, B_CYS_137	N, B_MET_133	H, B_MET_133	2.86	1.91	11.95
1HGD.PDB	O, A_LEU_13	N, B_PHE_138	H, B_PHE_138	2.71	1.82	20.20
1HGD.PDB	O, B_GLU_131	N, B_LYS_139	H, B_LYS_139	2.85	1.91	12.79
1HGD.PDB	O, A_ALA_11	N, B_ILE_140	H, B_ILE_140	2.81	1.89	16.38

1HGD.PDB	O, B_ASN_129	N, B_TYR_141	H, B_TYR_141	2.94	2.01	16.23
1HGD.PDB	O, B_LYS_143	ND1, B_HIS_142	HD1, B_HIS_142	2.98	2.08	18.98
1HGD.PDB	OE2, B_GLU_165	N, B_LYS_143	H, B_LYS_143	2.93	1.99	13.81
1HGD.PDB	O, B_ASP_145	N, B_ILE_149	H, B_ILE_149	2.84	1.89	10.47
1HGD.PDB	O, B_ASN_146	N, B_GLU_150	H, B_GLU_150	2.92	1.97	11.35
1HGD.PDB	O, B_ALA_147	N, B_SER_151	H, B_SER_151	2.92	2.06	22.74
1HGD.PDB	O, B_CYS_148	OG, B_SER_151	HG, B_SER_151	2.66	1.81	21.47
1HGD.PDB	O, B_GLU_150	N, B_ASN_154	H, B_ASN_154	2.80	1.83	3.48
1HGD.PDB	OE2, B_GLU_150	ND2, B_ASN_154	HD21, B_ASN_154	2.98	2.09	22.34
1HGD.PDB	O, B_SER_151	N, B_THR_156	H, B_THR_156	2.74	1.92	27.01
1HGD.PDB	OD1, B_ASN_154	OG1, B_THR_156	HG1, B_THR_156	2.75	1.84	16.14
1HGD.PDB	OD1, B_ASP_158	N, B_ASP_160	H, B_ASP_160	2.88	2.02	24.02
1HGD.PDB	O, B_HIS_159	N, B_TYR_162	H, B_TYR_162	2.92	2.06	23.47
1HGD.PDB	O, F_ARG_170	NH1, B_ARG_163	HH12, B_ARG_163	2.75	1.79	14.15
1HGD.PDB	O, B_TYR_162	N, B_ALA_166	H, B_ALA_166	2.93	1.95	5.06
1HGD.PDB	O, B_ARG_163	N, B_LEU_167	H, B_LEU_167	2.77	1.81	7.70
1HGD.PDB	O, B_ASP_164	N, B_ASN_168	H, B_ASN_168	2.97	2.02	11.42
1HGD.PDB	O, B_GLU_165	ND2, B_ASN_169	HD22, B_ASN_169	2.96	2.00	8.67
1HGD.PDB	O, B_ALA_166	N, B_ARG_170	H, B_ARG_170	2.80	1.92	20.27
1HGD.PDB	O, B_GLU_128	NE, B_ARG_170	HE, B_ARG_170	2.73	1.86	22.68
1HGD.PDB	OE2, B_GLU_131	NH1, B_ARG_170	HH11, B_ARG_170	2.78	1.79	7.42
1HGD.PDB	O, B_LEU_167	N, B_PHE_171	H, B_PHE_171	2.95	2.04	17.43
1HGD.PDB	O, D_ILE_140	N, C_ALA_11	H, C_ALA_11	2.91	2.01	19.96
1HGD.PDB	O, D_GLN_27	N, C_THR_12	H, C_THR_12	2.92	1.96	10.52
1HGD.PDB	O, D_PHE_138	N, C_LEU_13	H, C_LEU_13	2.98	2.02	9.60
1HGD.PDB	O, D_ARG_25	N, C_CYS_14	H, C_CYS_14	2.74	1.84	19.68
1HGD.PDB	O, D_GLY_136	N, C_LEU_15	H, C_LEU_15	2.88	1.91	5.44
1HGD.PDB	O, D_GLY_23	N, C_GLY_16	H, C_GLY_16	2.97	2.07	19.04
1HGD.PDB	O, C_HIS_18	ND1, C_HIS_17	HD1, C_HIS_17	2.93	2.06	23.26
1HGD.PDB	O, D_TRP_21	N, C_HIS_18	H, C_HIS_18	2.85	1.99	23.00
1HGD.PDB	OD1, C_ASN_322	N, C_VAL_20	H, C_VAL_20	2.80	1.83	3.81
1HGD.PDB	O, C_VAL_36	N, C_THR_24	H, C_THR_24	2.84	1.91	15.31
1HGD.PDB	O, C_ILE_34	N, C_VAL_26	H, C_VAL_26	2.82	1.89	14.49
1HGD.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.80	1.77	7.54
1HGD.PDB	O, C_VAL_26	N, C_ILE_34	H, C_ILE_34	2.89	1.94	12.21
1HGD.PDB	O, C_THR_24	N, C_VAL_36	H, C_VAL_36	2.79	1.83	9.80
1HGD.PDB	O, C_MET_320	N, C_THR_37	H, C_THR_37	2.88	1.90	4.85
1HGD.PDB	O, C_LEU_316	N, C_THR_40	H, C_THR_40	2.84	1.97	22.14
1HGD.PDB	O, C_LEU_314	N, C_LEU_42	H, C_LEU_42	2.78	1.93	24.47
1HGD.PDB	O, C_PHE_294	N, C_GLN_44	H, C_GLN_44	2.79	1.83	6.90
1HGD.PDB	O, C_SER_46	NE2, C_GLN_44	HE22, C_GLN_44	2.85	1.96	21.38
1HGD.PDB	O, C_ASN_285	OG, C_SER_47	HG, C_SER_47	2.81	1.90	15.43
1HGD.PDB	OD2, C_ASP_275	NZ, C_LYS_50	HZ1, C_LYS_50	2.66	1.78	25.77
1HGD.PDB	O, C_PRO_273	N, C_ILE_51	H, C_ILE_51	2.78	1.83	8.71
1HGD.PDB	O, C_ASP_275	N, C_ASN_53	H, C_ASN_53	2.80	1.94	23.81
1HGD.PDB	OD2, C_ASP_85	N, C_ARG_57	H, C_ARG_57	2.85	1.91	10.75
1HGD.PDB	O, C_THR_83	NE, C_ARG_57	HE, C_ARG_57	2.80	1.83	7.46
1HGD.PDB	O, C_LEU_86	N, C_LEU_59	H, C_LEU_59	2.86	1.91	11.22
1HGD.PDB	O, C_VAL_88	N, C_GLY_61	H, C_GLY_61	2.98	2.11	22.39
1HGD.PDB	OD1, C_ASP_60	N, C_ILE_62	H, C_ILE_62	2.86	1.95	16.63
1HGD.PDB	O, C_GLY_61	N, C_CYS_64	H, C_CYS_64	2.87	1.95	15.76
1HGD.PDB	OE2, C_GLU_89	N, C_LEU_66	H, C_LEU_66	2.99	2.02	7.77
1HGD.PDB	O, C_LEU_66	N, C_LEU_70	H, C_LEU_70	2.88	2.00	21.00
1HGD.PDB	O, C_ILE_67	N, C_LEU_71	H, C_LEU_71	2.81	1.86	10.52
1HGD.PDB	O, C_ASP_68	N, C_GLY_72	H, C_GLY_72	2.84	1.91	15.63
1HGD.PDB	OD1, C_ASP_73	N, C_HIS_75	H, C_HIS_75	2.89	2.01	22.22
1HGD.PDB	OD1, C_ASP_73	ND1, C_HIS_75	HD1, C_HIS_75	2.77	1.87	19.67
1HGD.PDB	O, C_ASP_63	NE2, C_HIS_75	HE2, C_HIS_75	2.86	1.94	17.12

1HGD.PDB	O, C_ASP_73	N, C_CYS_76	H, C_CYS_76	2.80	1.86	11.97
1HGD.PDB	O, C_PRO_74	N, C_ASP_77	H, C_ASP_77	2.94	1.99	12.51
1HGD.PDB	O, C_ARG_57	N, C_ASP_85	H, C_ASP_85	2.79	1.90	19.56
1HGD.PDB	O, C_LEU_59	N, C_VAL_88	H, C_VAL_88	2.93	1.95	4.90
1HGD.PDB	O, C_MET_268	N, C_GLU_89	H, C_GLU_89	2.78	1.84	12.72
1HGD.PDB	OD1, C_ASP_60	NE, C_ARG_90	HE, C_ARG_90	2.86	1.89	9.66
1HGD.PDB	O, C_SER_270	NH1, C_ARG_90	HH11, C_ARG_90	2.68	1.81	24.44
1HGD.PDB	O, C_ALA_272	NH1, C_ARG_90	HH12, C_ARG_90	2.62	1.70	17.91
1HGD.PDB	OD2, C_ASP_60	NH2, C_ARG_90	HH21, C_ARG_90	2.78	1.79	10.49
1HGD.PDB	OD1, C_ASP_271	N, C_SER_91	H, C_SER_91	2.89	1.92	5.66
1HGD.PDB	OD1, C_ASP_271	OG, C_SER_91	HG, C_SER_91	2.93	2.11	26.93
1HGD.PDB	OD2, C_ASP_271	OG, C_SER_91	HG, C_SER_91	2.86	1.96	18.80
1HGD.PDB	OD2, C_ASP_68	OG, C_SER_95	HG, C_SER_95	2.88	1.96	15.18
1HGD.PDB	OD2, C_ASP_73	N, C_ASN_96	H, C_ASN_96	2.93	1.97	11.12
1HGD.PDB	OD1, C_ASP_68	OH, C_TYR_100	HH, C_TYR_100	2.89	1.96	14.39
1HGD.PDB	OD2, C_ASP_104	OG, C_SER_107	HG, C_SER_107	2.91	2.00	17.92
1HGD.PDB	O, C_TYR_105	N, C_ARG_109	H, C_ARG_109	2.82	1.85	5.75
1HGD.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.87	1.88	13.44
1HGD.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.73	1.84	19.59
1HGD.PDB	O, C_SER_107	N, C_LEU_111	H, C_LEU_111	2.87	1.93	12.86
1HGD.PDB	O, C_ARG_109	N, C_ALA_113	H, C_ALA_113	2.95	2.03	17.38
1HGD.PDB	OE2, C_GLU_119	OG1, C_THR_117	HG1, C_THR_117	2.86	1.93	10.42
1HGD.PDB	O, C_GLU_82	N, C_LEU_118	H, C_LEU_118	2.89	1.96	15.85
1HGD.PDB	O, C_TYR_257	N, C_ILE_121	H, C_ILE_121	2.88	1.91	7.92
1HGD.PDB	O, C_ARG_255	N, C_GLU_123	H, C_GLU_123	2.91	1.95	11.07
1HGD.PDB	O, C_THR_155	N, C_THR_131	H, C_THR_131	2.77	1.87	18.56
1HGD.PDB	OD1, C_ASN_152	N, C_ASN_133	H, C_ASN_133	2.82	1.89	13.60
1HGD.PDB	O, C_GLY_146	N, C_SER_136	H, C_SER_136	2.73	1.81	14.22
1HGD.PDB	O, C_GLY_144	NZ, C_LYS_140	HZ1, C_LYS_140	2.66	1.71	18.26
1HGD.PDB	OD1, C_ASN_137	NZ, C_LYS_140	HZ2, C_LYS_140	2.78	1.84	20.52
1HGD.PDB	OD2, C_ASP_77	NE, C_ARG_141	HE, C_ARG_141	2.80	1.97	27.06
1HGD.PDB	O, C_PHE_147	NH1, C_ARG_141	HH12, C_ARG_141	2.57	1.62	14.51
1HGD.PDB	OD1, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.87	1.96	21.76
1HGD.PDB	OD2, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.75	1.86	23.93
1HGD.PDB	O, C_GLY_72	NH2, C_ARG_141	HH22, C_ARG_141	2.96	1.99	11.64
1HGD.PDB	OD1, C_ASN_137	OG, C_SER_145	HG, C_SER_145	2.98	2.13	22.87
1HGD.PDB	O, C_SER_136	N, C_GLY_146	H, C_GLY_146	2.97	2.04	13.75
1HGD.PDB	O, C_GLY_72	N, C_SER_149	H, C_SER_149	2.83	1.92	17.38
1HGD.PDB	O, C_ALA_253	N, C_ASN_152	H, C_ASN_152	2.78	1.92	22.70
1HGD.PDB	OH, C_TYR_195	NE1, C_TRP_153	HE1, C_TRP_153	2.80	1.95	24.25
1HGD.PDB	O, C_LEU_194	N, C_LYS_156	H, C_LYS_156	2.95	2.05	20.33
1HGD.PDB	O, C_SER_247	N, C_LEU_164	H, C_LEU_164	2.68	1.84	25.44
1HGD.PDB	O, C_ILE_245	N, C_VAL_166	H, C_VAL_166	2.92	1.97	10.65
1HGD.PDB	O, C_LEU_243	OG1, C_THR_167	HG1, C_THR_167	2.91	2.00	16.96
1HGD.PDB	O, C_LEU_243	N, C_MET_168	H, C_MET_168	2.93	2.00	16.08
1HGD.PDB	O, C_ASP_241	N, C_ASN_170	H, C_ASN_170	2.92	1.95	7.54
1HGD.PDB	O, C_PHE_174	ND2, C_ASN_170	HD21, C_ASN_170	2.81	1.86	10.36
1HGD.PDB	O, C_VAL_237	ND2, C_ASN_170	HD22, C_ASN_170	2.83	2.02	27.86
1HGD.PDB	O, C_VAL_237	N, C_LYS_176	H, C_LYS_176	2.96	2.03	15.89
1HGD.PDB	OE2, C_GLU_123	NZ, C_LYS_176	HZ2, C_LYS_176	2.69	1.80	25.35
1HGD.PDB	O, C_THR_235	N, C_TYR_178	H, C_TYR_178	2.78	1.82	3.58
1HGD.PDB	OE1, C_GLU_123	OH, C_TYR_178	HH, C_TYR_178	2.73	1.80	13.21
1HGD.PDB	OG1, C_THR_235	NE1, C_TRP_180	HE1, C_TRP_180	2.91	1.93	2.97
1HGD.PDB	O, C_ASN_250	N, C_HIS_183	H, C_HIS_183	2.86	1.94	17.04
1HGD.PDB	O, C_ARG_229	N, C_HIS_184	H, C_HIS_184	2.84	1.87	6.25
1HGD.PDB	OG, C_SER_231	NE2, C_HIS_184	HE2, C_HIS_184	2.75	1.91	25.20
1HGD.PDB	OE1, C_GLU_190	N, C_SER_186	H, C_SER_186	2.94	1.99	11.52
1HGD.PDB	OG1, C_THR_187	N, C_GLU_190	H, C_GLU_190	2.91	1.96	11.66

1HGD.PDB	OD1, C_ASN_250	NE2, C_GLN_191	HE21, C_GLN_191	2.98	2.02	9.43
1HGD.PDB	O, C_GLN_197	NE2, C_GLN_191	HE22, C_GLN_191	2.89	1.96	15.69
1HGD.PDB	O, C_GLN_189	OG1, C_THR_192	HG1, C_THR_192	2.81	1.97	23.75
1HGD.PDB	O, C_GLN_189	N, C_SER_193	H, C_SER_193	2.79	1.85	12.90
1HGD.PDB	O, C_GLN_191	N, C_TYR_195	H, C_TYR_195	2.80	1.85	11.05
1HGD.PDB	O, C_TYR_161	NE2, C_GLN_197	HE21, C_GLN_197	2.91	1.96	11.66
1HGD.PDB	O, C_ASN_248	NE2, C_GLN_197	HE22, C_GLN_197	2.97	2.05	15.65
1HGD.PDB	OD1, C_ASN_246	NH2, C_ARG_201	HH21, C_ARG_201	2.60	1.77	27.30
1HGD.PDB	O, C_ILE_213	N, C_VAL_202	H, C_VAL_202	3.00	2.04	9.35
1HGD.PDB	O, C_ASN_246	N, C_THR_203	H, C_THR_203	2.89	1.94	12.58
1HGD.PDB	OG1, C_THR_212	OG1, C_THR_203	HG1, C_THR_203	2.89	1.96	13.30
1HGD.PDB	O, C_GLN_211	N, C_VAL_204	H, C_VAL_204	2.87	1.96	17.77
1HGD.PDB	O, C_SER_209	N, C_THR_206	H, C_THR_206	2.90	1.94	8.48
1HGD.PDB	OD1, C_ASP_241	N, C_ARG_207	H, C_ARG_207	2.91	1.95	9.04
1HGD.PDB	OD2, C_ASP_241	NE, C_ARG_208	HE, C_ARG_208	2.97	2.08	21.42
1HGD.PDB	OG1, C_THR_206	OG, C_SER_209	HG, C_SER_209	2.92	1.98	10.99
1HGD.PDB	OD1, A_ASP_101	NE2, C_GLN_210	HE22, C_GLN_210	2.97	2.13	27.21
1HGD.PDB	O, C_VAL_204	N, C_GLN_211	H, C_GLN_211	2.82	1.89	16.07
1HGD.PDB	O, C_VAL_202	N, C_ILE_213	H, C_ILE_213	2.87	1.94	15.07
1HGD.PDB	O, C_ASN_216	NH1, C_ARG_220	HH12, C_ARG_220	2.88	2.06	29.71
1HGD.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.69	1.80	23.00
1HGD.PDB	O, C_ASN_216	NH2, C_ARG_220	HH22, C_ARG_220	2.74	1.85	22.78
1HGD.PDB	O, C_LEU_226	N, C_VAL_223	H, C_VAL_223	2.86	1.90	8.93
1HGD.PDB	O, C_CYS_97	NE, C_ARG_224	HE, C_ARG_224	2.81	1.97	26.63
1HGD.PDB	O, C_CYS_97	NH2, C_ARG_224	HH21, C_ARG_224	2.83	1.96	24.41
1HGD.PDB	O, C_VAL_223	N, C_LEU_226	H, C_LEU_226	2.96	2.01	12.56
1HGD.PDB	OE2, C_GLU_190	OG, C_SER_228	HG, C_SER_228	3.00	2.02	4.69
1HGD.PDB	O, C_SER_228	NH1, C_ARG_229	HH11, C_ARG_229	2.69	1.75	17.13
1HGD.PDB	O, C_PRO_221	NH2, C_ARG_229	HH22, C_ARG_229	2.59	1.67	18.22
1HGD.PDB	OD1, C_ASP_101	OG, C_SER_231	HG, C_SER_231	2.87	1.90	8.39
1HGD.PDB	O, C_ASP_101	N, C_ILE_232	H, C_ILE_232	2.91	1.97	13.69
1HGD.PDB	O, C_TRP_180	N, C_TYR_233	H, C_TYR_233	2.92	1.96	10.09
1HGD.PDB	O, C_TYR_178	N, C_THR_235	H, C_THR_235	2.86	1.97	20.86
1HGD.PDB	O, C_LYS_176	N, C_VAL_237	H, C_VAL_237	2.76	1.84	16.40
1HGD.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.80	1.83	17.68
1HGD.PDB	O, B_SER_71	NZ, C_LYS_238	HZ3, C_LYS_238	2.57	1.67	23.33
1HGD.PDB	O, C_ASN_170	N, C_GLY_240	H, C_GLY_240	2.86	1.98	22.33
1HGD.PDB	O, C_LYS_238	N, C_ASP_241	H, C_ASP_241	2.97	2.04	14.16
1HGD.PDB	OD1, C_ASP_241	N, C_VAL_242	H, C_VAL_242	2.79	1.97	27.05
1HGD.PDB	O, C_MET_168	N, C_LEU_243	H, C_LEU_243	2.90	1.93	5.78
1HGD.PDB	O, C_SER_205	N, C_VAL_244	H, C_VAL_244	2.99	2.03	11.79
1HGD.PDB	O, C_VAL_166	N, C_ILE_245	H, C_ILE_245	2.96	2.02	13.67
1HGD.PDB	O, C_THR_203	N, C_ASN_246	H, C_ASN_246	2.93	1.96	5.65
1HGD.PDB	OD1, C_ASN_165	ND2, C_ASN_246	HD22, C_ASN_246	2.91	1.96	13.56
1HGD.PDB	O, C_LEU_164	N, C_SER_247	H, C_SER_247	2.95	2.05	18.82
1HGD.PDB	OE1, C_GLN_191	ND2, C_ASN_250	HD21, C_ASN_250	2.90	1.95	10.99
1HGD.PDB	O, C_HIS_183	ND2, C_ASN_250	HD22, C_ASN_250	2.89	1.96	14.74
1HGD.PDB	O, C_ASN_152	N, C_ALA_253	H, C_ALA_253	2.86	1.97	19.68
1HGD.PDB	OD1, C_ASN_133	NH2, C_ARG_255	HH22, C_ARG_255	2.52	1.69	27.35
1HGD.PDB	O, C_ILE_121	N, C_TYR_257	H, C_TYR_257	2.92	2.07	24.63
1HGD.PDB	O, C_LEU_177	N, C_PHE_258	H, C_PHE_258	2.93	1.97	8.49
1HGD.PDB	OE2, C_GLU_119	NH1, C_ARG_261	HH12, C_ARG_261	2.66	1.83	27.96
1HGD.PDB	OE1, C_GLU_119	NH2, C_ARG_261	HH22, C_ARG_261	2.90	2.00	23.32
1HGD.PDB	OD2, C_ASP_85	NZ, C_LYS_264	HZ3, C_LYS_264	2.82	1.84	16.88
1HGD.PDB	O, C_PHE_87	N, C_MET_268	H, C_MET_268	2.82	1.92	19.58
1HGD.PDB	O, C_PRO_284	OG, C_SER_270	HG, C_SER_270	2.86	1.93	14.34
1HGD.PDB	OG, C_SER_270	N, C_ALA_272	H, C_ALA_272	2.88	1.93	11.04
1HGD.PDB	O, C_ILE_51	N, C_ASP_275	H, C_ASP_275	2.89	2.02	21.61

1HGD.PDB	OD1, C_ASP_275	N, C_THR_276	H, C_THR_276	2.82	1.97	24.34
1HGD.PDB	O, C_ASN_54	N, C_SER_279	H, C_SER_279	2.80	1.87	14.30
1HGD.PDB	O, C_TYR_302	N, C_ILE_282	H, C_ILE_282	2.89	1.91	5.26
1HGD.PDB	O, C_THR_283	N, C_GLY_286	H, C_GLY_286	2.83	1.91	15.19
1HGD.PDB	O, C_LYS_50	N, C_SER_287	H, C_SER_287	2.85	1.88	6.04
1HGD.PDB	O, C_ALA_304	ND2, C_ASN_290	HD22, C_ASN_290	2.83	1.94	20.74
1HGD.PDB	OE1, C_GLN_44	NZ, C_LYS_292	HZ1, C_LYS_292	2.73	1.73	12.00
1HGD.PDB	OD2, C_ASP_291	NZ, C_LYS_292	HZ3, C_LYS_292	2.79	1.88	23.81
1HGD.PDB	O, C_LYS_307	N, C_GLN_295	H, C_GLN_295	2.80	1.93	22.24
1HGD.PDB	O, C_ASN_298	NE2, C_GLN_295	HE21, C_GLN_295	2.78	1.81	6.87
1HGD.PDB	O, C_GLN_44	N, C_ASN_296	H, C_ASN_296	2.84	1.92	15.89
1HGD.PDB	OE1, C_GLN_295	N, C_VAL_297	H, C_VAL_297	2.67	1.87	28.66
1HGD.PDB	OD1, C_ASN_285	ND2, C_ASN_298	HD22, C_ASN_298	2.96	2.02	13.09
1HGD.PDB	O, D_LYS_68	NZ, C_LYS_299	HZ2, C_LYS_299	2.97	1.97	13.11
1HGD.PDB	OD1, C_ASN_298	N, C_ILE_300	H, C_ILE_300	2.91	2.01	18.95
1HGD.PDB	O, C_ILE_282	N, C_TYR_302	H, C_TYR_302	2.86	2.02	25.59
1HGD.PDB	O, D_LYS_62	N, C_GLY_303	H, C_GLY_303	2.92	1.97	11.11
1HGD.PDB	O, C_GLN_295	N, C_VAL_309	H, C_VAL_309	2.96	2.15	29.17
1HGD.PDB	OG, D_SER_93	N, C_LYS_310	H, C_LYS_310	2.96	2.01	12.70
1HGD.PDB	OE2, C_GLU_41	N, C_LEU_314	H, C_LEU_314	2.81	1.88	14.84
1HGD.PDB	OE1, C_GLU_41	NZ, C_LYS_315	HZ3, C_LYS_315	2.78	1.84	20.99
1HGD.PDB	O, C_THR_40	N, C_LEU_316	H, C_LEU_316	2.76	1.82	12.19
1HGD.PDB	OD1, D_ASN_104	N, C_ALA_317	H, C_ALA_317	2.76	1.81	11.23
1HGD.PDB	O, C_ASN_38	N, C_THR_318	H, C_THR_318	2.95	2.04	17.98
1HGD.PDB	O, C_VAL_20	ND2, C_ASN_322	HD21, C_ASN_322	2.90	1.99	17.62
1HGD.PDB	OE2, C_GLU_35	ND2, C_ASN_322	HD22, C_ASN_322	2.83	1.94	21.17
1HGD.PDB	OE1, D_GLU_15	NZ, C_LYS_326	HZ1, C_LYS_326	2.78	1.77	11.96
1HGD.PDB	OXT, C_THR_328	NE2, C_GLN_327	HE22, C_GLN_327	2.97	2.03	15.01
1HGD.PDB	OD2, D_ASP_112	N, D_GLY_1	H2, D_GLY_1	2.80	1.80	13.51
1HGD.PDB	OD1, D_ASP_109	N, D_LEU_2	H, D_LEU_2	2.86	1.98	21.55
1HGD.PDB	OD2, D_ASP_112	N, D_PHE_3	H, D_PHE_3	2.84	2.05	29.38
1HGD.PDB	OD2, D_ASP_112	N, D_GLY_4	H, D_GLY_4	2.94	2.04	18.50
1HGD.PDB	OD1, D_ASP_112	N, D_ALA_5	H, D_ALA_5	2.90	2.02	22.02
1HGD.PDB	O, D_GLY_4	N, D_PHE_9	H, D_PHE_9	2.79	1.85	14.03
1HGD.PDB	O, D_GLY_13	ND2, D_ASN_12	HD22, D_ASN_12	2.84	1.96	21.33
1HGD.PDB	O, C_VAL_323	N, D_GLY_13	H, D_GLY_13	2.70	1.78	14.49
1HGD.PDB	O, C_HIS_17	N, D_TRP_14	H, D_TRP_14	2.85	1.91	13.36
1HGD.PDB	OG1, D_THR_41	N, D_TRP_21	H, D_TRP_21	2.90	2.00	19.11
1HGD.PDB	O, C_GLY_16	N, D_GLY_23	H, D_GLY_23	2.93	2.01	16.45
1HGD.PDB	O, D_ALA_35	N, D_PHE_24	H, D_PHE_24	2.81	1.84	5.01
1HGD.PDB	O, C_CYS_14	N, D_ARG_25	H, D_ARG_25	2.91	1.95	9.92
1HGD.PDB	OE1, D_GLN_34	NE, D_ARG_25	HE, D_ARG_25	2.61	1.77	24.43
1HGD.PDB	O, D_GLY_33	N, D_HIS_26	H, D_HIS_26	2.84	1.92	15.70
1HGD.PDB	O, C_THR_12	N, D_GLN_27	H, D_GLN_27	2.91	1.98	16.00
1HGD.PDB	O, D_GLY_31	N, D_ASN_28	H, D_ASN_28	2.90	1.95	12.05
1HGD.PDB	OD1, D_ASN_146	ND2, D_ASN_28	HD21, D_ASN_28	3.00	2.03	9.16
1HGD.PDB	O, D_PHE_24	N, D_ALA_35	H, D_ALA_35	2.79	1.99	28.44
1HGD.PDB	O, D_TYR_22	N, D_ASP_37	H, D_ASP_37	2.70	1.79	16.23
1HGD.PDB	OD2, D_ASP_37	N, D_SER_40	H, D_SER_40	2.91	1.96	11.03
1HGD.PDB	OD2, D_ASP_37	OG, D_SER_40	HG, D_SER_40	2.86	1.96	18.80
1HGD.PDB	O, D_ASP_37	OG1, D_THR_41	HG1, D_THR_41	2.74	1.83	16.22
1HGD.PDB	O, D_LEU_38	N, D_GLN_42	H, D_GLN_42	2.97	2.03	13.89
1HGD.PDB	OD1, D_ASP_46	NE2, D_GLN_42	HE22, D_GLN_42	2.84	1.95	20.82
1HGD.PDB	O, D_LYS_39	N, D_ALA_43	H, D_ALA_43	2.97	2.02	11.21
1HGD.PDB	O, D_SER_40	N, D_ALA_44	H, D_ALA_44	2.97	2.00	5.30
1HGD.PDB	O, D_THR_41	N, D_ILE_45	H, D_ILE_45	2.92	1.97	10.66
1HGD.PDB	O, D_GLN_42	N, D_ASP_46	H, D_ASP_46	2.81	1.84	5.79
1HGD.PDB	O, D_ALA_43	NE2, D_GLN_47	HE22, D_GLN_47	2.86	1.96	18.91

1HGD.PDB	O, D_ILE_45	N, D_ASN_49	H, D_ASN_49	2.87	1.93	14.90
1HGD.PDB	O, D_ASP_46	N, D_GLY_50	H, D_GLY_50	2.89	1.97	17.25
1HGD.PDB	OG1, D_THR_107	NZ, D_LYS_51	HZ1, D_LYS_51	2.96	1.98	16.97
1HGD.PDB	OE1, D_GLU_103	NZ, D_LYS_51	HZ2, D_LYS_51	2.74	1.72	8.47
1HGD.PDB	ND1, D_HIS_106	NZ, D_LYS_51	HZ3, D_LYS_51	2.74	1.78	16.91
1HGD.PDB	O, D_ILE_48	N, D_LEU_52	H, D_LEU_52	2.95	2.04	18.99
1HGD.PDB	O, D_ASN_49	N, D_ASN_53	H, D_ASN_53	2.85	1.90	9.27
1HGD.PDB	O, A_THR_28	NE, D_ARG_54	HE, D_ARG_54	3.00	2.06	13.94
1HGD.PDB	OE1, D_GLU_57	NH1, D_ARG_54	HH11, D_ARG_54	2.85	1.86	12.06
1HGD.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.79	1.82	13.03
1HGD.PDB	OE2, D_GLU_61	NZ, D_LYS_58	HZ2, D_LYS_58	2.90	1.87	10.86
1HGD.PDB	OD2, B_ASP_90	NZ, D_LYS_62	HZ3, D_LYS_62	2.62	1.79	29.99
1HGD.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.96	1.98	5.65
1HGD.PDB	O, C_LYS_299	NZ, D_LYS_68	HZ1, D_LYS_68	2.93	1.92	12.36
1HGD.PDB	OE2, D_GLU_85	NZ, D_LYS_68	HZ2, D_LYS_68	2.78	1.76	10.92
1HGD.PDB	OG, E_SER_107	N, D_ARG_76	H, D_ARG_76	2.86	1.90	9.40
1HGD.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.83	1.87	10.56
1HGD.PDB	OE2, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.78	1.77	3.14
1HGD.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.65	1.67	9.42
1HGD.PDB	OE1, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.69	1.70	6.24
1HGD.PDB	OE1, D_GLU_74	NE2, D_GLN_78	HE22, D_GLN_78	2.94	1.97	10.43
1HGD.PDB	O, D_GLY_75	N, D_ASP_79	H, D_ASP_79	2.94	1.98	9.81
1HGD.PDB	O, D_GLN_78	N, D_LYS_82	H, D_LYS_82	2.95	1.98	5.44
1HGD.PDB	O, D_ASP_79	N, D_TYR_83	H, D_TYR_83	2.91	1.98	15.53
1HGD.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.57	1.79	29.87
1HGD.PDB	O, D_LEU_80	N, D_VAL_84	H, D_VAL_84	2.86	1.89	6.82
1HGD.PDB	O, D_LYS_82	N, D_ASP_86	H, D_ASP_86	2.94	1.97	2.92
1HGD.PDB	O, D_TYR_83	N, D_THR_87	H, D_THR_87	2.90	1.95	11.15
1HGD.PDB	O, D_VAL_84	N, D_LYS_88	H, D_LYS_88	2.90	2.00	19.38
1HGD.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.76	1.72	5.75
1HGD.PDB	O, D_GLU_85	N, D_ILE_89	H, D_ILE_89	2.85	1.88	3.25
1HGD.PDB	O, D_LYS_88	N, D_TRP_92	H, D_TRP_92	2.93	1.96	4.18
1HGD.PDB	O, D_ILE_89	N, D_SER_93	H, D_SER_93	2.87	1.96	17.31
1HGD.PDB	O, D_ILE_89	OG, D_SER_93	HG, D_SER_93	2.77	1.86	16.92
1HGD.PDB	O, D_ASP_90	N, D_TYR_94	H, D_TYR_94	2.87	1.97	18.94
1HGD.PDB	O, D_TRP_92	N, D_ALA_96	H, D_ALA_96	2.89	1.94	12.43
1HGD.PDB	O, D_TYR_94	N, D_LEU_98	H, D_LEU_98	2.91	1.95	7.12
1HGD.PDB	O, D_ASN_95	N, D_LEU_99	H, D_LEU_99	2.95	2.03	17.99
1HGD.PDB	O, D_LEU_98	N, D_LEU_102	H, D_LEU_102	2.99	2.01	6.26
1HGD.PDB	O, D_LEU_99	N, D_GLU_103	H, D_GLU_103	2.96	2.00	10.90
1HGD.PDB	O, D_VAL_100	N, D_ASN_104	H, D_ASN_104	2.84	1.88	8.49
1HGD.PDB	O, C_LYS_27	ND2, D_ASN_104	HD22, D_ASN_104	2.96	2.00	10.74
1HGD.PDB	O, D_LEU_102	N, D_HIS_106	H, D_HIS_106	2.92	1.96	8.43
1HGD.PDB	O, D_GLU_103	N, D_THR_107	H, D_THR_107	2.81	1.91	18.55
1HGD.PDB	O, D_ASN_104	N, D_ILE_108	H, D_ILE_108	2.99	2.03	8.56
1HGD.PDB	O, D_HIS_106	N, D_LEU_110	H, D_LEU_110	2.82	1.88	11.88
1HGD.PDB	O, D_ASP_109	N, D_SER_113	H, D_SER_113	2.84	1.89	12.44
1HGD.PDB	O, D_SER_113	N, D_LYS_117	H, D_LYS_117	2.74	1.87	21.85
1HGD.PDB	O, D_MET_115	N, D_PHE_119	H, D_PHE_119	2.99	2.05	13.34
1HGD.PDB	O, D_ASN_116	N, D_GLU_120	H, D_GLU_120	2.89	1.91	1.87
1HGD.PDB	O, D_LYS_117	N, D_LYS_121	H, D_LYS_121	2.92	2.02	19.68
1HGD.PDB	O, D_PHE_119	N, D_ARG_123	H, D_ARG_123	2.95	1.99	11.55
1HGD.PDB	OE2, D_GLU_120	NH1, D_ARG_123	HH11, D_ARG_123	2.80	1.92	24.08
1HGD.PDB	O, D_GLU_120	N, D_ARG_124	H, D_ARG_124	2.98	2.01	7.42
1HGD.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.80	2.01	29.31
1HGD.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.82	1.95	21.73
1HGD.PDB	O, D_HIS_159	ND2, D_ASN_129	HD21, D_ASN_129	2.95	1.98	9.02
1HGD.PDB	OH, D_TYR_157	ND2, D_ASN_129	HD22, D_ASN_129	2.79	1.82	6.93

1HGD.PDB	O, D_CYS_137	N, D_MET_133	H, D_MET_133	2.89	1.94	11.36
1HGD.PDB	O, C_LEU_13	N, D_PHE_138	H, D_PHE_138	2.74	1.85	19.25
1HGD.PDB	O, D_GLU_131	N, D_LYS_139	H, D_LYS_139	2.83	1.88	9.21
1HGD.PDB	O, C_ALA_11	N, D_ILE_140	H, D_ILE_140	2.85	1.94	17.95
1HGD.PDB	O, D_ASN_129	N, D_TYR_141	H, D_TYR_141	2.95	2.00	12.47
1HGD.PDB	O, D_LYS_143	ND1, D_HIS_142	HD1, D_HIS_142	2.95	2.07	22.42
1HGD.PDB	OE2, D_GLU_165	N, D_LYS_143	H, D_LYS_143	2.98	2.08	20.43
1HGD.PDB	OE2, D_GLU_30	N, D_ASN_146	H, D_ASN_146	2.83	1.93	17.92
1HGD.PDB	O, D_ASP_145	N, D_ILE_149	H, D_ILE_149	2.88	1.92	11.10
1HGD.PDB	O, D_ASN_146	N, D_GLU_150	H, D_GLU_150	2.93	2.00	14.93
1HGD.PDB	O, D_ALA_147	N, D_SER_151	H, D_SER_151	2.95	2.03	16.03
1HGD.PDB	O, D_CYS_148	OG, D_SER_151	HG, D_SER_151	2.69	1.83	21.65
1HGD.PDB	O, D_GLU_150	N, D_ASN_154	H, D_ASN_154	2.80	1.83	6.06
1HGD.PDB	OE2, D_GLU_150	ND2, D_ASN_154	HD21, D_ASN_154	2.88	2.05	27.54
1HGD.PDB	OD1, D_ASN_154	OG1, D_THR_156	HG1, D_THR_156	2.79	1.83	8.53
1HGD.PDB	NE2, D_HIS_142	OH, D_TYR_157	HH, D_TYR_157	2.78	1.89	18.65
1HGD.PDB	OD1, D_ASP_158	N, D_ASP_160	H, D_ASP_160	2.88	2.02	23.43
1HGD.PDB	O, D_HIS_159	N, D_TYR_162	H, D_TYR_162	2.96	2.10	23.77
1HGD.PDB	O, B_ARG_170	NH1, D_ARG_163	HH12, D_ARG_163	2.77	1.79	12.64
1HGD.PDB	O, D_TYR_162	N, D_ALA_166	H, D_ALA_166	2.92	1.95	4.89
1HGD.PDB	O, D_ARG_163	N, D_LEU_167	H, D_LEU_167	2.76	1.80	8.07
1HGD.PDB	O, D_ASP_164	N, D_ASN_168	H, D_ASN_168	2.96	2.00	8.71
1HGD.PDB	O, D_GLU_165	ND2, D_ASN_169	HD22, D_ASN_169	2.94	1.98	8.39
1HGD.PDB	O, D_ALA_166	N, D_ARG_170	H, D_ARG_170	2.81	1.93	20.44
1HGD.PDB	O, D_GLU_128	NE, D_ARG_170	HE, D_ARG_170	2.73	1.86	22.22
1HGD.PDB	OE2, D_GLU_131	NH1, D_ARG_170	HH11, D_ARG_170	2.77	1.78	7.65
1HGD.PDB	O, D_LEU_167	N, D_PHE_171	H, D_PHE_171	2.96	2.02	14.05
1HGD.PDB	O, F_ILE_140	N, E_ALA_11	H, E_ALA_11	2.92	2.03	20.36
1HGD.PDB	O, F_GLN_27	N, E_THR_12	H, E_THR_12	2.97	2.03	14.03
1HGD.PDB	O, F_PHE_138	N, E_LEU_13	H, E_LEU_13	2.98	2.02	11.10
1HGD.PDB	O, F_ARG_25	N, E_CYS_14	H, E_CYS_14	2.65	1.79	21.42
1HGD.PDB	O, F_GLY_136	N, E_LEU_15	H, E_LEU_15	2.85	1.88	5.88
1HGD.PDB	O, F_GLY_23	N, E_GLY_16	H, E_GLY_16	2.93	2.04	20.98
1HGD.PDB	O, E_HIS_18	ND1, E_HIS_17	HD1, E_HIS_17	2.90	2.05	24.96
1HGD.PDB	O, F_TRP_21	N, E_HIS_18	H, E_HIS_18	2.83	1.98	25.03
1HGD.PDB	OD1, E_ASN_322	N, E_VAL_20	H, E_VAL_20	2.79	1.83	7.78
1HGD.PDB	O, E_VAL_36	N, E_THR_24	H, E_THR_24	2.83	1.94	19.94
1HGD.PDB	O, E_ILE_34	N, E_VAL_26	H, E_VAL_26	2.83	1.90	15.73
1HGD.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.79	1.77	8.77
1HGD.PDB	O, E_VAL_26	N, E_ILE_34	H, E_ILE_34	2.86	1.91	10.68
1HGD.PDB	O, E_THR_24	N, E_VAL_36	H, E_VAL_36	2.80	1.85	11.38
1HGD.PDB	O, E_MET_320	N, E_THR_37	H, E_THR_37	2.88	1.91	4.25
1HGD.PDB	O, E_LEU_316	N, E_THR_40	H, E_THR_40	2.82	1.95	22.86
1HGD.PDB	O, E_LEU_314	N, E_LEU_42	H, E_LEU_42	2.82	1.94	21.92
1HGD.PDB	O, E_PHE_294	N, E_GLN_44	H, E_GLN_44	2.85	1.88	5.47
1HGD.PDB	O, E_SER_46	NE2, E_GLN_44	HE22, E_GLN_44	2.85	1.97	21.62
1HGD.PDB	O, E_ASN_285	OG, E_SER_47	HG, E_SER_47	2.85	1.99	21.23
1HGD.PDB	OD2, E_ASP_275	NZ, E_LYS_50	HZ1, E_LYS_50	2.69	1.80	25.14
1HGD.PDB	O, E_PRO_273	N, E_ILE_51	H, E_ILE_51	2.79	1.84	10.59
1HGD.PDB	O, E_ASP_275	N, E_ASN_53	H, E_ASN_53	2.81	1.95	23.64
1HGD.PDB	OD2, E_ASP_85	N, E_ARG_57	H, E_ARG_57	2.85	1.91	12.33
1HGD.PDB	O, E_THR_83	NE, E_ARG_57	HE, E_ARG_57	2.81	1.84	7.04
1HGD.PDB	O, E_LEU_86	N, E_LEU_59	H, E_LEU_59	2.86	1.91	10.61
1HGD.PDB	O, E_VAL_88	N, E_GLY_61	H, E_GLY_61	2.96	2.07	21.18
1HGD.PDB	OD1, E_ASP_60	N, E_ILE_62	H, E_ILE_62	2.88	1.95	15.04
1HGD.PDB	O, E_GLY_61	N, E_CYS_64	H, E_CYS_64	2.89	1.98	17.49
1HGD.PDB	OE2, E_GLU_89	N, E_LEU_66	H, E_LEU_66	2.97	1.99	5.61
1HGD.PDB	O, E_LEU_66	N, E_LEU_70	H, E_LEU_70	2.90	2.02	20.74

1HGD.PDB	O, E_ILE_67	N, E_LEU_71	H, E_LEU_71	2.80	1.84	6.52
1HGD.PDB	O, E_ASP_68	N, E_GLY_72	H, E_GLY_72	2.91	1.98	15.31
1HGD.PDB	OD1, E_ASP_73	N, E_HIS_75	H, E_HIS_75	2.96	2.07	21.14
1HGD.PDB	OD1, E_ASP_73	ND1, E_HIS_75	HD1, E_HIS_75	2.79	1.88	18.25
1HGD.PDB	O, E_ASP_63	NE2, E_HIS_75	HE2, E_HIS_75	2.89	1.97	16.27
1HGD.PDB	O, E_ASP_73	N, E_CYS_76	H, E_CYS_76	2.81	1.87	13.32
1HGD.PDB	O, E_PRO_74	N, E_ASP_77	H, E_ASP_77	2.91	1.96	10.31
1HGD.PDB	O, E_ARG_57	N, E_ASP_85	H, E_ASP_85	2.78	1.89	18.76
1HGD.PDB	O, E_LEU_59	N, E_VAL_88	H, E_VAL_88	2.91	1.94	5.45
1HGD.PDB	O, E_MET_268	N, E_GLU_89	H, E_GLU_89	2.76	1.82	11.82
1HGD.PDB	OD1, E_ASP_60	NE, E_ARG_90	HE, E_ARG_90	2.88	1.91	7.90
1HGD.PDB	O, E_SER_270	NH1, E_ARG_90	HH11, E_ARG_90	2.66	1.80	24.67
1HGD.PDB	O, E_ALA_272	NH1, E_ARG_90	HH12, E_ARG_90	2.60	1.68	18.53
1HGD.PDB	OD2, E_ASP_60	NH2, E_ARG_90	HH21, E_ARG_90	2.82	1.83	10.15
1HGD.PDB	OD1, E_ASP_271	N, E_SER_91	H, E_SER_91	2.88	1.92	9.41
1HGD.PDB	OD1, E_ASP_271	OG, E_SER_91	HG, E_SER_91	2.94	2.13	28.39
1HGD.PDB	OD2, E_ASP_271	OG, E_SER_91	HG, E_SER_91	2.84	1.93	17.47
1HGD.PDB	OD2, E_ASP_68	OG, E_SER_95	HG, E_SER_95	2.91	1.98	14.66
1HGD.PDB	OD2, E_ASP_73	N, E_ASN_96	H, E_ASN_96	2.95	1.99	11.30
1HGD.PDB	OD1, E_ASP_68	OH, E_TYR_100	HH, E_TYR_100	2.86	1.93	14.06
1HGD.PDB	OD2, E_ASP_104	OG, E_SER_107	HG, E_SER_107	2.90	1.98	16.44
1HGD.PDB	O, E_TYR_105	N, E_ARG_109	H, E_ARG_109	2.86	1.88	0.77
1HGD.PDB	OE2, E_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.82	1.85	14.73
1HGD.PDB	OD2, E_ASP_79	OG, E_SER_110	HG, E_SER_110	2.81	1.89	15.50
1HGD.PDB	O, E_SER_107	N, E_LEU_111	H, E_LEU_111	2.92	1.96	10.24
1HGD.PDB	O, E_LEU_108	N, E_VAL_112	H, E_VAL_112	2.98	2.02	7.44
1HGD.PDB	O, E_ARG_109	N, E_ALA_113	H, E_ALA_113	2.92	2.02	18.83
1HGD.PDB	O, E_SER_110	N, E_SER_114	H, E_SER_114	2.98	2.03	12.50
1HGD.PDB	OE2, E_GLU_119	OG1, E_THR_117	HG1, E_THR_117	2.90	1.95	9.79
1HGD.PDB	O, E_GLU_82	N, E_LEU_118	H, E_LEU_118	2.92	1.99	15.84
1HGD.PDB	O, E_TYR_257	N, E_ILE_121	H, E_ILE_121	2.87	1.90	6.59
1HGD.PDB	O, E_ARG_255	N, E_GLU_123	H, E_GLU_123	2.92	1.97	11.75
1HGD.PDB	O, E_THR_155	N, E_THR_131	H, E_THR_131	2.76	1.86	18.28
1HGD.PDB	OD1, E_ASN_152	N, E_ASN_133	H, E_ASN_133	2.85	1.91	14.28
1HGD.PDB	O, E_GLY_146	N, E_SER_136	H, E_SER_136	2.73	1.79	12.16
1HGD.PDB	O, E_GLY_144	NZ, E_LYS_140	HZ1, E_LYS_140	2.69	1.72	15.78
1HGD.PDB	OD1, E_ASN_137	NZ, E_LYS_140	HZ2, E_LYS_140	2.79	1.84	19.51
1HGD.PDB	OD2, E_ASP_77	NE, E_ARG_141	HE, E_ARG_141	2.82	1.98	26.95
1HGD.PDB	O, E_PHE_147	NH1, E_ARG_141	HH12, E_ARG_141	2.57	1.63	15.28
1HGD.PDB	OD1, E_ASP_77	NH2, E_ARG_141	HH21, E_ARG_141	2.88	1.95	21.13
1HGD.PDB	OD2, E_ASP_77	NH2, E_ARG_141	HH21, E_ARG_141	2.75	1.86	24.62
1HGD.PDB	O, E_GLY_72	NH2, E_ARG_141	HH22, E_ARG_141	2.94	1.97	11.68
1HGD.PDB	O, E_SER_136	N, E_GLY_146	H, E_GLY_146	2.97	2.03	13.31
1HGD.PDB	O, E_GLY_72	N, E_SER_149	H, E_SER_149	2.84	1.94	18.94
1HGD.PDB	O, E_ALA_253	N, E_ASN_152	H, E_ASN_152	2.83	1.97	23.36
1HGD.PDB	OH, E_TYR_195	NE1, E_TRP_153	HE1, E_TRP_153	2.82	1.91	19.17
1HGD.PDB	O, E_LEU_194	N, E_LYS_156	H, E_LYS_156	2.96	2.06	18.57
1HGD.PDB	O, E_SER_193	NZ, E_LYS_156	HZ2, E_LYS_156	2.80	1.84	19.27
1HGD.PDB	O, E_SER_247	N, E_LEU_164	H, E_LEU_164	2.67	1.83	24.46
1HGD.PDB	O, E_ILE_245	N, E_VAL_166	H, E_VAL_166	2.95	1.99	10.02
1HGD.PDB	O, E_LEU_243	OG1, E_THR_167	HG1, E_THR_167	2.95	2.08	21.06
1HGD.PDB	O, E_LEU_243	N, E_MET_168	H, E_MET_168	2.92	1.99	16.02
1HGD.PDB	O, E_ASP_241	N, E_ASN_170	H, E_ASN_170	2.93	1.96	7.59
1HGD.PDB	O, E_PHE_174	ND2, E_ASN_170	HD21, E_ASN_170	2.84	1.88	9.66
1HGD.PDB	O, E_VAL_237	ND2, E_ASN_170	HD22, E_ASN_170	2.82	2.02	28.84
1HGD.PDB	O, E_VAL_237	N, E_LYS_176	H, E_LYS_176	2.95	2.02	16.27
1HGD.PDB	OE2, E_GLU_123	NZ, E_LYS_176	HZ2, E_LYS_176	2.69	1.80	25.12
1HGD.PDB	O, E_THR_235	N, E_TYR_178	H, E_TYR_178	2.82	1.85	5.66

1HGD.PDB	OE1, E_GLU_123	OH, E_TYR_178	HH, E_TYR_178	2.75	1.83	13.46
1HGD.PDB	OG1, E_THR_235	NE1, E_TRP_180	HE1, E_TRP_180	2.93	1.94	3.75
1HGD.PDB	O, E_ASN_250	N, E_HIS_183	H, E_HIS_183	2.87	1.97	19.16
1HGD.PDB	O, E_ARG_229	N, E_HIS_184	H, E_HIS_184	2.83	1.87	8.20
1HGD.PDB	OG, E_SER_231	NE2, E_HIS_184	HE2, E_HIS_184	2.80	1.95	25.42
1HGD.PDB	OE1, E_GLU_190	N, E_SER_186	H, E_SER_186	2.91	1.96	11.07
1HGD.PDB	OG1, E_THR_187	N, E_GLU_190	H, E_GLU_190	2.91	1.97	13.39
1HGD.PDB	O, E_GLN_197	NE2, E_GLN_191	HE22, E_GLN_191	2.89	1.97	15.90
1HGD.PDB	O, E_ASN_188	OG1, E_THR_192	HG1, E_THR_192	2.98	2.03	7.22
1HGD.PDB	O, E_GLN_189	N, E_SER_193	H, E_SER_193	2.81	1.84	3.50
1HGD.PDB	O, E_GLU_190	N, E_LEU_194	H, E_LEU_194	2.98	2.02	10.79
1HGD.PDB	O, E_GLN_191	N, E_TYR_195	H, E_TYR_195	2.77	1.82	10.72
1HGD.PDB	O, E_TYR_161	NE2, E_GLN_197	HE21, E_GLN_197	2.91	1.96	10.54
1HGD.PDB	O, E_ASN_248	NE2, E_GLN_197	HE22, E_GLN_197	2.95	2.02	14.25
1HGD.PDB	OD1, E_ASN_246	NH2, E_ARG_201	HH21, E_ARG_201	2.60	1.77	27.54
1HGD.PDB	O, E_ASN_246	N, E_THR_203	H, E_THR_203	2.88	1.92	8.43
1HGD.PDB	OG1, E_THR_212	OG1, E_THR_203	HG1, E_THR_203	2.93	1.99	12.22
1HGD.PDB	O, E_GLN_211	N, E_VAL_204	H, E_VAL_204	2.87	1.96	17.47
1HGD.PDB	O, E_SER_209	N, E_THR_206	H, E_THR_206	2.95	1.99	8.08
1HGD.PDB	OD1, E_ASP_241	N, E_ARG_207	H, E_ARG_207	2.90	1.93	8.79
1HGD.PDB	OG1, E_THR_206	OG, E_SER_209	HG, E_SER_209	2.91	1.97	11.26
1HGD.PDB	OD1, C_ASP_101	NE2, E_GLN_210	HE22, E_GLN_210	2.98	2.14	27.07
1HGD.PDB	O, E_VAL_204	N, E_GLN_211	H, E_GLN_211	2.82	1.90	15.66
1HGD.PDB	O, E_VAL_202	N, E_ILE_213	H, E_ILE_213	2.89	1.96	14.67
1HGD.PDB	O, E_ASN_216	NH1, E_ARG_220	HH12, E_ARG_220	2.89	2.08	29.65
1HGD.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.77	1.90	25.11
1HGD.PDB	O, E_ASN_216	NH2, E_ARG_220	HH22, E_ARG_220	2.74	1.86	23.30
1HGD.PDB	O, E_LEU_226	N, E_VAL_223	H, E_VAL_223	2.87	1.91	7.72
1HGD.PDB	O, E_CYS_97	NE, E_ARG_224	HE, E_ARG_224	2.84	2.00	26.20
1HGD.PDB	O, E_CYS_97	NH2, E_ARG_224	HH21, E_ARG_224	2.84	1.97	24.48
1HGD.PDB	O, E_VAL_223	N, E_LEU_226	H, E_LEU_226	2.93	1.99	12.03
1HGD.PDB	OE2, E_GLU_190	OG, E_SER_228	HG, E_SER_228	2.96	1.98	4.78
1HGD.PDB	O, E_SER_228	NH1, E_ARG_229	HH11, E_ARG_229	2.70	1.76	17.46
1HGD.PDB	O, E_PRO_221	NH2, E_ARG_229	HH22, E_ARG_229	2.58	1.65	17.47
1HGD.PDB	OD1, E_ASP_101	OG, E_SER_231	HG, E_SER_231	2.85	1.91	13.25
1HGD.PDB	O, E_ASP_101	N, E_ILE_232	H, E_ILE_232	2.91	1.98	14.92
1HGD.PDB	O, E_TRP_180	N, E_TYR_233	H, E_TYR_233	2.93	1.97	9.20
1HGD.PDB	O, E_TYR_178	N, E_THR_235	H, E_THR_235	2.86	1.97	20.35
1HGD.PDB	O, E_LYS_176	N, E_VAL_237	H, E_VAL_237	2.77	1.86	16.39
1HGD.PDB	O, D_SER_71	NZ, E_LYS_238	HZ2, E_LYS_238	2.73	1.80	21.39
1HGD.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ3, E_LYS_238	2.87	1.86	13.40
1HGD.PDB	O, E_ASN_170	N, E_GLY_240	H, E_GLY_240	2.89	2.02	22.44
1HGD.PDB	O, E_LYS_238	N, E_ASP_241	H, E_ASP_241	2.96	2.03	13.52
1HGD.PDB	OD1, E_ASP_241	N, E_VAL_242	H, E_VAL_242	2.79	1.95	26.27
1HGD.PDB	O, E_MET_168	N, E_LEU_243	H, E_LEU_243	2.89	1.92	5.48
1HGD.PDB	O, E_VAL_166	N, E_ILE_245	H, E_ILE_245	2.95	2.01	13.26
1HGD.PDB	O, E_THR_203	N, E_ASN_246	H, E_ASN_246	2.94	1.96	4.93
1HGD.PDB	OD1, E_ASN_165	ND2, E_ASN_246	HD22, E_ASN_246	2.91	1.96	12.66
1HGD.PDB	O, E_LEU_164	N, E_SER_247	H, E_SER_247	2.95	2.04	18.22
1HGD.PDB	OE1, E_GLN_191	ND2, E_ASN_250	HD21, E_ASN_250	2.95	1.99	9.92
1HGD.PDB	O, E_HIS_183	ND2, E_ASN_250	HD22, E_ASN_250	2.86	1.93	15.05
1HGD.PDB	O, E_ASN_152	N, E_ALA_253	H, E_ALA_253	2.88	1.99	19.87
1HGD.PDB	OD1, E_ASN_133	NH2, E_ARG_255	HH22, E_ARG_255	2.52	1.69	27.28
1HGD.PDB	O, E_ILE_121	N, E_TYR_257	H, E_TYR_257	2.94	2.11	26.29
1HGD.PDB	O, E_LEU_177	N, E_PHE_258	H, E_PHE_258	2.92	1.95	7.16
1HGD.PDB	OE2, E_GLU_119	NH1, E_ARG_261	HH12, E_ARG_261	2.64	1.81	27.92
1HGD.PDB	OE1, E_GLU_119	NH2, E_ARG_261	HH22, E_ARG_261	2.88	1.97	22.94
1HGD.PDB	OD2, E_ASP_85	NZ, E_LYS_264	HZ3, E_LYS_264	2.87	1.88	16.50

1HGD.PDB	O, E_PHE.87	N, E_MET.268	H, E_MET.268	2.81	1.92	20.02
1HGD.PDB	O, E_PRO.284	OG, E_SER.270	HG, E_SER.270	2.87	1.93	12.39
1HGD.PDB	OG, E_SER.270	N, E_ALA.272	H, E_ALA.272	2.92	1.98	12.12
1HGD.PDB	O, E_ILE.51	N, E_ASP.275	H, E_ASP.275	2.91	2.01	19.96
1HGD.PDB	OD1, E_ASP.275	N, E_THR.276	H, E_THR.276	2.81	1.96	24.15
1HGD.PDB	O, E_ASN.54	N, E_SER.279	H, E_SER.279	2.80	1.87	14.43
1HGD.PDB	O, E_TYR.302	N, E_ILE.282	H, E_ILE.282	2.87	1.90	8.73
1HGD.PDB	O, E_THR.283	N, E_GLY.286	H, E_GLY.286	2.82	1.89	12.51
1HGD.PDB	O, E_LYS.50	N, E_SER.287	H, E_SER.287	2.87	1.90	5.78
1HGD.PDB	O, E_ALA.304	ND2, E_ASN.290	HD22, E_ASN.290	2.83	1.94	19.46
1HGD.PDB	OE1, E_GLN.44	NZ, E_LYS.292	HZ1, E_LYS.292	2.70	1.70	12.87
1HGD.PDB	OD2, E_ASP.291	NZ, E_LYS.292	HZ3, E_LYS.292	2.83	1.91	23.60
1HGD.PDB	O, E_LYS.307	N, E_GLN.295	H, E_GLN.295	2.78	1.92	23.12
1HGD.PDB	O, E_ASN.298	NE2, E_GLN.295	HE21, E_GLN.295	2.76	1.79	7.00
1HGD.PDB	O, E_GLN.44	N, E_ASN.296	H, E_ASN.296	2.84	1.90	13.14
1HGD.PDB	OE1, E_GLN.295	N, E_VAL.297	H, E_VAL.297	2.67	1.86	28.12
1HGD.PDB	OD1, E_ASN.285	ND2, E_ASN.298	HD22, E_ASN.298	2.95	2.01	14.15
1HGD.PDB	O, F_LYS.68	NZ, E_LYS.299	HZ1, E_LYS.299	2.98	1.98	14.54
1HGD.PDB	OD1, E_ASN.298	N, E_ILE.300	H, E_ILE.300	2.90	1.99	17.71
1HGD.PDB	O, E_ILE.282	N, E_TYR.302	H, E_TYR.302	2.88	2.05	26.69
1HGD.PDB	O, E_LYS.264	OH, E_TYR.302	HH, E_TYR.302	2.65	1.86	28.82
1HGD.PDB	O, F_LYS.62	N, E_GLY.303	H, E_GLY.303	2.94	1.98	8.87
1HGD.PDB	O, E_GLN.295	N, E_VAL.309	H, E_VAL.309	2.96	2.15	28.43
1HGD.PDB	OG, F_SER.93	N, E_LYS.310	H, E_LYS.310	2.95	2.00	12.05
1HGD.PDB	OE2, E_GLU.41	N, E_LEU.314	H, E_LEU.314	2.81	1.89	15.95
1HGD.PDB	OE1, E_GLU.41	NZ, E_LYS.315	HZ3, E_LYS.315	2.76	1.83	22.10
1HGD.PDB	O, E_THR.40	N, E_LEU.316	H, E_LEU.316	2.76	1.83	14.34
1HGD.PDB	OD1, F_ASN.104	N, E_ALA.317	H, E_ALA.317	2.79	1.84	10.01
1HGD.PDB	O, E_ASN.38	N, E_THR.318	H, E_THR.318	2.97	2.03	14.24
1HGD.PDB	O, E_VAL.20	ND2, E_ASN.322	HD21, E_ASN.322	2.90	2.00	18.79
1HGD.PDB	OE2, E_GLU.35	ND2, E_ASN.322	HD22, E_ASN.322	2.82	1.95	23.13
1HGD.PDB	OE2, F_GLU.15	N, E_GLU.325	H, E_GLU.325	2.91	2.10	28.29
1HGD.PDB	O, E_GLN.327	NZ, E_LYS.326	HZ1, E_LYS.326	2.81	1.89	22.57
1HGD.PDB	OE1, F_GLU.15	NZ, E_LYS.326	HZ3, E_LYS.326	2.97	1.97	16.19
1HGD.PDB	O, E_LYS.326	NE2, E_GLN.327	HE22, E_GLN.327	2.85	1.95	19.55
1HGD.PDB	OD2, F_ASP.112	N, F_GLY.1	H2, F_GLY.1	2.81	1.81	13.59
1HGD.PDB	OD1, F_ASP.109	N, F_LEU.2	H, F_LEU.2	2.86	1.96	19.63
1HGD.PDB	OD2, F_ASP.112	N, F_PHE.3	H, F_PHE.3	2.81	2.02	29.56
1HGD.PDB	OD2, F_ASP.112	N, F_GLY.4	H, F_GLY.4	2.92	2.06	23.22
1HGD.PDB	OD1, F_ASP.112	N, F_ALA.5	H, F_ALA.5	2.89	2.02	22.37
1HGD.PDB	O, F_GLY.4	N, F_PHE.9	H, F_PHE.9	2.78	1.84	12.30
1HGD.PDB	O, F_GLY.13	ND2, F_ASN.12	HD22, F_ASN.12	2.80	1.95	24.70
1HGD.PDB	O, E_VAL.323	N, F_GLY.13	H, F_GLY.13	2.71	1.79	15.38
1HGD.PDB	O, E_HIS.17	N, F_TRP.14	H, F_TRP.14	2.87	1.92	12.04
1HGD.PDB	OG1, F_THR.41	N, F_TRP.21	H, F_TRP.21	2.87	1.95	16.02
1HGD.PDB	O, E_GLY.16	N, F_GLY.23	H, F_GLY.23	2.91	2.00	17.89
1HGD.PDB	O, F_ALA.35	N, F_PHE.24	H, F_PHE.24	2.81	1.84	4.26
1HGD.PDB	O, E_CYS.14	N, F_ARG.25	H, F_ARG.25	2.88	1.94	13.26
1HGD.PDB	OE1, F_GLN.34	NE, F_ARG.25	HE, F_ARG.25	2.93	2.07	24.69
1HGD.PDB	OE1, F_GLN.34	NH2, F_ARG.25	HH21, F_ARG.25	2.80	1.89	20.31
1HGD.PDB	O, F_GLY.33	N, F_HIS.26	H, F_HIS.26	2.91	2.03	21.54
1HGD.PDB	O, E_THR.12	N, F_GLN.27	H, F_GLN.27	2.97	2.04	16.25
1HGD.PDB	O, F_GLY.31	N, F_ASN.28	H, F_ASN.28	2.78	1.85	13.40
1HGD.PDB	OD1, F_ASN.146	ND2, F_ASN.28	HD21, F_ASN.28	2.81	1.89	15.27
1HGD.PDB	O, F_CYS.144	ND2, F_ASN.28	HD22, F_ASN.28	2.83	1.93	18.14
1HGD.PDB	O, F_HIS.26	N, F_GLY.33	H, F_GLY.33	2.97	2.11	23.75
1HGD.PDB	O, F_PHE.24	N, F_ALA.35	H, F_ALA.35	2.78	1.98	28.59
1HGD.PDB	O, F_TYR.22	N, F_ASP.37	H, F_ASP.37	2.69	1.77	12.88

1HGD.PDB	OD2, F_ASP_37	N, F_SER_40	H, F_SER_40	2.92	1.96	9.75
1HGD.PDB	OD2, F_ASP_37	OG, F_SER_40	HG, F_SER_40	2.84	1.98	23.42
1HGD.PDB	O, F_ASP_37	OG1, F_THR_41	HG1, F_THR_41	2.75	1.88	21.07
1HGD.PDB	O, F_LEU_38	N, F_GLN_42	H, F_GLN_42	2.93	2.03	18.28
1HGD.PDB	OD1, F_ASP_46	NE2, F_GLN_42	HE22, F_GLN_42	2.83	1.94	21.51
1HGD.PDB	O, F_LYS_39	N, F_ALA_43	H, F_ALA_43	2.93	1.98	11.56
1HGD.PDB	O, F_SER_40	N, F_ALA_44	H, F_ALA_44	2.97	1.99	2.55
1HGD.PDB	O, F_THR_41	N, F_ILE_45	H, F_ILE_45	2.91	1.96	10.99
1HGD.PDB	O, F_GLN_42	N, F_ASP_46	H, F_ASP_46	2.80	1.82	0.60
1HGD.PDB	O, F_ALA_43	NE2, F_GLN_47	HE22, F_GLN_47	2.90	2.01	20.21
1HGD.PDB	O, F_ILE_45	N, F_ASN_49	H, F_ASN_49	2.84	1.94	18.12
1HGD.PDB	O, F_ASP_46	N, F_GLY_50	H, F_GLY_50	2.84	1.95	20.14
1HGD.PDB	OE1, F_GLU_103	NZ, F_LYS_51	HZ2, F_LYS_51	2.72	1.70	8.28
1HGD.PDB	ND1, F_HIS_106	NZ, F_LYS_51	HZ3, F_LYS_51	2.73	1.76	16.89
1HGD.PDB	O, F_ILE_48	N, F_LEU_52	H, F_LEU_52	2.94	2.02	16.22
1HGD.PDB	O, F_ASN_49	N, F_ASN_53	H, F_ASN_53	2.85	1.92	14.75
1HGD.PDB	OE1, F_GLU_57	NH1, F_ARG_54	HH11, F_ARG_54	2.86	1.85	10.37
1HGD.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.72	1.75	12.85
1HGD.PDB	OE2, F_GLU_61	NZ, F_LYS_58	HZ2, F_LYS_58	2.92	1.89	10.22
1HGD.PDB	OD2, D_ASP_90	NZ, F_LYS_62	HZ3, F_LYS_62	2.71	1.86	28.09
1HGD.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.95	1.98	9.92
1HGD.PDB	O, E_LYS_299	NZ, F_LYS_68	HZ1, F_LYS_68	2.97	1.94	5.85
1HGD.PDB	OE2, F_GLU_85	NZ, F_LYS_68	HZ2, F_LYS_68	2.72	1.77	19.94
1HGD.PDB	OG, A_SER_107	N, F_ARG_76	H, F_ARG_76	2.82	1.86	9.34
1HGD.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.86	1.90	10.66
1HGD.PDB	OE2, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.77	1.75	1.42
1HGD.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.64	1.65	5.37
1HGD.PDB	OE1, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.71	1.72	7.42
1HGD.PDB	OE1, F_GLU_74	NE2, F_GLN_78	HE22, F_GLN_78	2.96	1.99	9.91
1HGD.PDB	O, F_GLY_75	N, F_ASP_79	H, F_ASP_79	2.93	1.98	10.55
1HGD.PDB	O, F_GLN_78	N, F_LYS_82	H, F_LYS_82	2.98	2.01	9.35
1HGD.PDB	O, F_ASP_79	N, F_TYR_83	H, F_TYR_83	2.93	1.99	14.99
1HGD.PDB	OE1, B_GLU_85	OH, F_TYR_83	HH, F_TYR_83	2.53	1.75	27.84
1HGD.PDB	O, F_LEU_80	N, F_VAL_84	H, F_VAL_84	2.89	1.92	3.19
1HGD.PDB	O, F_LYS_82	N, F_ASP_86	H, F_ASP_86	2.94	1.97	9.39
1HGD.PDB	O, F_TYR_83	N, F_THR_87	H, F_THR_87	2.90	1.96	11.94
1HGD.PDB	O, F_VAL_84	N, F_LYS_88	H, F_LYS_88	2.92	1.96	11.08
1HGD.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.67	1.66	8.83
1HGD.PDB	O, F_GLU_85	N, F_ILE_89	H, F_ILE_89	2.88	1.90	4.38
1HGD.PDB	O, F_LYS_88	N, F_TRP_92	H, F_TRP_92	2.95	1.98	4.36
1HGD.PDB	O, F_ILE_89	N, F_SER_93	H, F_SER_93	2.85	1.95	19.01
1HGD.PDB	O, F_ILE_89	OG, F_SER_93	HG, F_SER_93	2.82	1.88	12.37
1HGD.PDB	O, F_ASP_90	N, F_TYR_94	H, F_TYR_94	2.87	1.95	17.83
1HGD.PDB	O, F_TRP_92	N, F_ALA_96	H, F_ALA_96	2.93	1.99	13.63
1HGD.PDB	O, F_SER_93	N, F_GLU_97	H, F_GLU_97	2.98	2.03	11.78
1HGD.PDB	O, F_TYR_94	N, F_LEU_98	H, F_LEU_98	2.95	1.97	4.49
1HGD.PDB	O, F_ASN_95	N, F_LEU_99	H, F_LEU_99	2.94	2.01	15.31
1HGD.PDB	O, F_LEU_99	N, F_GLU_103	H, F_GLU_103	2.96	2.00	11.56
1HGD.PDB	O, F_VAL_100	N, F_ASN_104	H, F_ASN_104	2.88	1.92	8.65
1HGD.PDB	O, E_LYS_27	ND2, F_ASN_104	HD22, F_ASN_104	2.95	1.99	8.95
1HGD.PDB	O, F_LEU_102	N, F_HIS_106	H, F_HIS_106	2.94	1.97	6.97
1HGD.PDB	O, F_GLU_103	N, F_THR_107	H, F_THR_107	2.81	1.90	17.76
1HGD.PDB	O, F_ASN_104	N, F_ILE_108	H, F_ILE_108	2.98	2.03	11.71
1HGD.PDB	O, F_HIS_106	N, F_LEU_110	H, F_LEU_110	2.80	1.85	9.01
1HGD.PDB	O, F_ASP_109	N, F_SER_113	H, F_SER_113	2.83	1.87	7.95
1HGD.PDB	O, D_LEU_2	OG, F_SER_113	HG, F_SER_113	2.74	1.91	25.98
1HGD.PDB	O, F_SER_113	N, F_LYS_117	H, F_LYS_117	2.74	1.84	18.35
1HGD.PDB	O, F_MET_115	N, F_PHE_119	H, F_PHE_119	3.00	2.07	16.22

1HGD.PDB	O, F_ASN.116	N, F_GLU.120	H, F_GLU.120	2.89	1.91	4.65
1HGD.PDB	O, F_LYS.117	N, F_LYS.121	H, F_LYS.121	2.95	2.02	15.04
1HGD.PDB	O, F_PHE.119	N, F_ARG.123	H, F_ARG.123	2.94	2.00	14.04
1HGD.PDB	OE2, F_GLU.120	NH1, F_ARG.123	HH11, F_ARG.123	2.77	1.88	23.82
1HGD.PDB	O, F_GLU.120	N, F_ARG.124	H, F_ARG.124	2.95	1.97	3.23
1HGD.PDB	OE1, D_GLU.132	NE, F_ARG.124	HE, F_ARG.124	2.96	2.14	28.71
1HGD.PDB	OE2, D_GLU.132	NE, F_ARG.124	HE, F_ARG.124	2.94	2.05	20.84
1HGD.PDB	O, F_HIS.159	ND2, F_ASN.129	HD21, F_ASN.129	2.96	2.01	10.95
1HGD.PDB	OH, F_TYR.157	ND2, F_ASN.129	HD22, F_ASN.129	2.80	1.85	12.13
1HGD.PDB	O, F_LYS.139	N, F_GLU.131	H, F_GLU.131	2.97	2.05	16.87
1HGD.PDB	O, F_CYS.137	N, F_MET.133	H, F_MET.133	2.88	1.93	10.80
1HGD.PDB	O, E_LEU.13	N, F_PHE.138	H, F_PHE.138	2.72	1.85	21.62
1HGD.PDB	O, F_GLU.131	N, F_LYS.139	H, F_LYS.139	2.85	1.89	9.90
1HGD.PDB	O, E_ALA.11	N, F_ILE.140	H, F_ILE.140	2.82	1.92	18.45
1HGD.PDB	O, F_ASN.129	N, F_TYR.141	H, F_TYR.141	2.97	2.05	16.46
1HGD.PDB	OE2, F_GLU.165	N, F_LYS.143	H, F_LYS.143	2.96	2.04	17.35
1HGD.PDB	O, F_ASP.145	N, F_ILE.149	H, F_ILE.149	2.86	1.91	11.09
1HGD.PDB	O, F_ASN.146	N, F_GLU.150	H, F_GLU.150	2.91	1.98	15.29
1HGD.PDB	O, F_ALA.147	N, F_SER.151	H, F_SER.151	2.97	2.10	22.90
1HGD.PDB	O, F_CYS.148	OG, F_SER.151	HG, F_SER.151	2.68	1.83	22.68
1HGD.PDB	O, F_GLU.150	N, F_ASN.154	H, F_ASN.154	2.77	1.80	3.19
1HGD.PDB	OD1, F_ASP.158	N, F_ASP.160	H, F_ASP.160	2.93	2.09	25.30
1HGD.PDB	O, F_HIS.159	N, F_TYR.162	H, F_TYR.162	2.96	2.06	19.25
1HGD.PDB	O, D_ARG.170	NH1, F_ARG.163	HH12, F_ARG.163	2.94	1.98	14.11
1HGD.PDB	O, F_TYR.162	N, F_ALA.166	H, F_ALA.166	2.95	1.98	6.51
1HGD.PDB	O, F_ARG.163	N, F_LEU.167	H, F_LEU.167	2.76	1.80	7.00
1HGD.PDB	O, F_ASP.164	N, F_ASN.168	H, F_ASN.168	2.95	1.99	8.58
1HGD.PDB	O, F_GLU.165	ND2, F_ASN.169	HD22, F_ASN.169	3.00	2.04	9.28
1HGD.PDB	O, F_ALA.166	N, F_ARG.170	H, F_ARG.170	2.83	1.97	23.51
1HGD.PDB	O, F_GLU.128	NE, F_ARG.170	HE, F_ARG.170	2.72	1.86	23.45
1HGD.PDB	OE2, F_GLU.131	NH1, F_ARG.170	HH11, F_ARG.170	2.76	1.77	6.97
1HGD.PDB	O, F_LEU.167	N, F_PHE.171	H, F_PHE.171	2.98	2.05	14.52
1HGE.PDB	O, B_ILE.140	N, A_ALA.11	H, A_ALA.11	2.81	1.93	21.75
1HGE.PDB	O, B_PHE.138	N, A_LEU.13	H, A_LEU.13	2.99	2.04	13.41
1HGE.PDB	O, B_ARG.25	N, A_CYS.14	H, A_CYS.14	2.88	1.92	6.83
1HGE.PDB	O, B_GLY.136	N, A_LEU.15	H, A_LEU.15	2.86	1.90	7.71
1HGE.PDB	O, B_GLY.23	N, A_GLY.16	H, A_GLY.16	2.95	2.03	17.76
1HGE.PDB	O, A_HIS.18	ND1, A_HIS.17	HD1, A_HIS.17	2.99	2.09	20.69
1HGE.PDB	O, B_TRP.21	N, A_HIS.18	H, A_HIS.18	2.85	1.97	21.20
1HGE.PDB	OD1, A_ASN.322	N, A_VAL.20	H, A_VAL.20	2.78	1.83	11.31
1HGE.PDB	O, A_VAL.36	N, A_THR.24	H, A_THR.24	2.84	1.95	19.98
1HGE.PDB	O, A_ILE.34	N, A_VAL.26	H, A_VAL.26	2.81	1.88	13.67
1HGE.PDB	OE2, B_GLU.97	NZ, A_LYS.27	HZ1, A_LYS.27	2.80	1.78	10.14
1HGE.PDB	O, A_VAL.26	N, A_ILE.34	H, A_ILE.34	2.90	1.96	12.32
1HGE.PDB	O, A_THR.24	N, A_VAL.36	H, A_VAL.36	2.80	1.84	9.48
1HGE.PDB	O, A_MET.320	N, A_THR.37	H, A_THR.37	2.86	1.89	5.71
1HGE.PDB	O, A_LEU.316	N, A_THR.40	H, A_THR.40	2.78	1.95	26.07
1HGE.PDB	O, A_LEU.314	N, A_LEU.42	H, A_LEU.42	2.81	1.99	27.51
1HGE.PDB	O, A_PHE.294	N, A_GLN.44	H, A_GLN.44	2.80	1.84	7.08
1HGE.PDB	O, A_SER.46	NE2, A_GLN.44	HE22, A_GLN.44	2.87	1.99	22.46
1HGE.PDB	OD2, A_ASP.275	NZ, A_LYS.50	HZ1, A_LYS.50	2.75	1.80	21.09
1HGE.PDB	O, A_PRO.273	N, A_ILE.51	H, A_ILE.51	2.81	1.86	12.28
1HGE.PDB	O, A_ASP.275	N, A_ASN.53	H, A_ASN.53	2.79	1.91	21.52
1HGE.PDB	OD2, A_ASP.85	N, A_ARG.57	H, A_ARG.57	2.92	1.99	13.17
1HGE.PDB	O, A_THR.83	NE, A_ARG.57	HE, A_ARG.57	2.79	1.83	9.22
1HGE.PDB	O, A_LEU.86	N, A_LEU.59	H, A_LEU.59	2.90	1.96	12.31
1HGE.PDB	O, A_VAL.88	N, A_GLY.61	H, A_GLY.61	2.97	2.14	26.58
1HGE.PDB	OD1, A_ASP.60	N, A_ILE.62	H, A_ILE.62	2.87	1.94	14.68

1HGE.PDB	O, A_GLY_61	N, A_CYS_64	H, A_CYS_64	2.85	1.93	16.81
1HGE.PDB	O, A_LEU_66	N, A_LEU_70	H, A_LEU_70	2.85	1.96	19.99
1HGE.PDB	O, A_ILE_67	N, A_LEU_71	H, A_LEU_71	2.84	1.88	8.15
1HGE.PDB	O, A_ASP_68	N, A_GLY_72	H, A_GLY_72	2.86	1.94	15.74
1HGE.PDB	OD1, A_ASP_73	ND1, A_HIS_75	HD1, A_HIS_75	2.80	1.89	17.62
1HGE.PDB	O, A_ASP_63	NE2, A_HIS_75	HE2, A_HIS_75	2.86	1.95	18.71
1HGE.PDB	O, A_ASP_73	N, A_CYS_76	H, A_CYS_76	2.78	1.83	10.81
1HGE.PDB	O, A_PRO_74	N, A_ASP_77	H, A_ASP_77	2.92	1.97	11.94
1HGE.PDB	O, A_CYS_76	N, A_PHE_79	H, A_PHE_79	3.00	2.02	2.98
1HGE.PDB	OE1, A_GLU_82	N, A_THR_83	H, A_THR_83	2.93	2.04	19.92
1HGE.PDB	O, A_ARG_57	N, A_ASP_85	H, A_ASP_85	2.80	1.89	17.89
1HGE.PDB	O, A_LEU_59	N, A_VAL_88	H, A_VAL_88	2.95	1.98	5.20
1HGE.PDB	O, A_MET_268	N, A_GLU_89	H, A_GLU_89	2.78	1.83	9.22
1HGE.PDB	OD1, A_ASP_60	NE, A_ARG_90	HE, A_ARG_90	2.85	1.89	7.94
1HGE.PDB	O, A_SER_270	NH1, A_ARG_90	HH11, A_ARG_90	2.62	1.75	23.79
1HGE.PDB	O, A_ALA_272	NH1, A_ARG_90	HH12, A_ARG_90	2.62	1.69	16.06
1HGE.PDB	OD2, A_ASP_60	NH2, A_ARG_90	HH21, A_ARG_90	2.79	1.80	8.90
1HGE.PDB	OD1, A_ASP_271	N, A_SER_91	H, A_SER_91	2.91	1.94	6.37
1HGE.PDB	OD2, A_ASP_271	OG, A_SER_91	HG, A_SER_91	2.81	1.90	18.10
1HGE.PDB	OD2, A_ASP_68	OG, A_SER_95	HG, A_SER_95	2.90	1.97	15.50
1HGE.PDB	OD2, A_ASP_73	N, A_ASN_96	H, A_ASN_96	2.90	1.93	6.89
1HGE.PDB	OD1, A_ASP_68	OH, A_TYR_100	HH, A_TYR_100	2.91	1.93	2.88
1HGE.PDB	O, A_ILE_230	N, A_ASP_101	H, A_ASP_101	3.00	2.11	21.52
1HGE.PDB	OD2, A_ASP_104	OG, A_SER_107	HG, A_SER_107	2.86	1.94	16.59
1HGE.PDB	O, A_TYR_105	N, A_ARG_109	H, A_ARG_109	2.83	1.86	3.58
1HGE.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.74	1.75	12.19
1HGE.PDB	OD2, F_ASP_79	OG, A_SER_110	HG, A_SER_110	2.90	1.95	11.19
1HGE.PDB	O, A_SER_107	N, A_LEU_111	H, A_LEU_111	2.85	1.87	2.87
1HGE.PDB	O, A_LEU_108	N, A_VAL_112	H, A_VAL_112	2.99	2.03	8.13
1HGE.PDB	O, A_ARG_109	N, A_ALA_113	H, A_ALA_113	2.94	2.03	18.27
1HGE.PDB	O, A_SER_110	N, A_SER_114	H, A_SER_114	2.87	1.96	18.01
1HGE.PDB	OE2, A_GLU_119	OG1, A_THR_117	HG1, A_THR_117	2.90	1.95	8.88
1HGE.PDB	O, A_GLU_82	N, A_LEU_118	H, A_LEU_118	2.96	2.03	16.11
1HGE.PDB	O, A_TYR_257	N, A_ILE_121	H, A_ILE_121	2.88	1.91	6.47
1HGE.PDB	O, A_ARG_255	N, A_GLU_123	H, A_GLU_123	2.93	1.98	10.93
1HGE.PDB	O, A_THR_155	N, A_THR_131	H, A_THR_131	2.74	1.84	18.66
1HGE.PDB	OD1, A_ASN_152	N, A_ASN_133	H, A_ASN_133	2.88	1.96	16.29
1HGE.PDB	O, A_TRP_153	N, A_GLY_134	H, A_GLY_134	2.96	2.06	19.55
1HGE.PDB	O, A_GLY_146	N, A_SER_136	H, A_SER_136	2.83	1.88	10.81
1HGE.PDB	OG, A_SER_136	N, A_ALA_138	H, A_ALA_138	2.95	2.01	13.95
1HGE.PDB	O, A_GLY_144	NZ, A_LYS_140	HZ1, A_LYS_140	2.75	1.77	16.24
1HGE.PDB	OD1, A_ASN_137	NZ, A_LYS_140	HZ2, A_LYS_140	2.81	1.83	16.67
1HGE.PDB	OD2, A_ASP_77	NE, A_ARG_141	HE, A_ARG_141	2.81	1.97	26.71
1HGE.PDB	O, A_PHE_147	NH1, A_ARG_141	HH12, A_ARG_141	2.55	1.62	16.38
1HGE.PDB	OD1, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.89	1.98	21.76
1HGE.PDB	OD2, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.75	1.86	23.90
1HGE.PDB	O, A_GLY_72	NH2, A_ARG_141	HH22, A_ARG_141	2.93	1.96	12.25
1HGE.PDB	O, A_GLY_72	N, A_SER_149	H, A_SER_149	2.83	1.92	17.48
1HGE.PDB	O, A_ALA_253	N, A_ASN_152	H, A_ASN_152	2.79	1.91	21.99
1HGE.PDB	OH, A_TYR_195	NE1, A_TRP_153	HE1, A_TRP_153	2.88	1.99	20.14
1HGE.PDB	O, A_LEU_194	N, A_LYS_156	H, A_LYS_156	2.98	2.08	19.15
1HGE.PDB	O, A_SER_193	NZ, A_LYS_156	HZ2, A_LYS_156	2.68	1.68	12.99
1HGE.PDB	O, A_THR_160	N, A_SER_157	H, A_SER_157	2.99	2.09	20.22
1HGE.PDB	O, A_SER_247	N, A_LEU_164	H, A_LEU_164	2.68	1.85	26.14
1HGE.PDB	O, A_ILE_245	N, A_VAL_166	H, A_VAL_166	2.88	1.93	12.18
1HGE.PDB	O, A_LEU_243	OG1, A_THR_167	HG1, A_THR_167	2.88	1.97	16.07
1HGE.PDB	O, A_LEU_243	N, A_MET_168	H, A_MET_168	2.92	1.99	15.75
1HGE.PDB	O, A_ASP_241	N, A_ASN_170	H, A_ASN_170	2.93	1.96	5.62

1HGE.PDB	O, A_PHE.174	ND2, A_ASN.170	HD21, A_ASN.170	2.84	1.88	9.34
1HGE.PDB	O, A_VAL.237	ND2, A_ASN.170	HD22, A_ASN.170	2.86	2.05	28.37
1HGE.PDB	O, A_VAL.237	N, A_LYS.176	H, A_LYS.176	2.98	2.05	15.51
1HGE.PDB	OE2, A_GLU.123	NZ, A_LYS.176	HZ1, A_LYS.176	2.71	1.79	22.78
1HGE.PDB	O, A_THR.235	N, A_TYR.178	H, A_TYR.178	2.82	1.86	5.77
1HGE.PDB	OE1, A_GLU.123	OH, A_TYR.178	HH, A_TYR.178	2.75	1.82	10.80
1HGE.PDB	O, A_TYR.233	N, A_TRP.180	H, A_TRP.180	2.99	2.02	8.32
1HGE.PDB	OG1, A_THR.235	NE1, A_TRP.180	HE1, A_TRP.180	2.92	1.93	3.33
1HGE.PDB	O, A_ASN.250	N, A_HIS.183	H, A_HIS.183	2.92	2.01	18.32
1HGE.PDB	O, A_ARG.229	N, A_HIS.184	H, A_HIS.184	2.86	1.90	8.10
1HGE.PDB	OG, A_SER.231	NE2, A_HIS.184	HE2, A_HIS.184	2.72	1.88	25.40
1HGE.PDB	OG1, A_THR.187	N, A_GLU.190	H, A_GLU.190	2.97	2.02	10.04
1HGE.PDB	O, A_GLN.197	NE2, A_GLN.191	HE22, A_GLN.191	2.96	2.04	16.90
1HGE.PDB	O, A_ASN.188	OG1, A_THR.192	HG1, A_THR.192	3.00	2.04	5.15
1HGE.PDB	O, A_GLN.189	N, A_SER.193	H, A_SER.193	2.84	1.87	3.05
1HGE.PDB	O, A_GLU.190	N, A_LEU.194	H, A_LEU.194	2.96	1.99	8.69
1HGE.PDB	O, A_GLN.191	N, A_TYR.195	H, A_TYR.195	2.77	1.82	9.81
1HGE.PDB	O, A_TYR.161	NE2, A_GLN.197	HE21, A_GLN.197	2.88	1.93	11.11
1HGE.PDB	O, A_ASN.248	NE2, A_GLN.197	HE22, A_GLN.197	2.92	1.99	15.44
1HGE.PDB	OD1, A_ASN.246	NH2, A_ARG.201	HH21, A_ARG.201	2.60	1.73	24.24
1HGE.PDB	O, A_ILE.213	N, A_VAL.202	H, A_VAL.202	2.96	1.99	9.62
1HGE.PDB	O, A_ASN.246	N, A_THR.203	H, A_THR.203	2.84	1.92	16.80
1HGE.PDB	O, A_GLN.211	N, A_VAL.204	H, A_VAL.204	2.83	1.93	18.95
1HGE.PDB	O, A_SER.209	N, A_THR.206	H, A_THR.206	2.97	2.00	7.75
1HGE.PDB	OD1, A_ASP.241	N, A_ARG.207	H, A_ARG.207	2.90	1.93	8.60
1HGE.PDB	OG1, A_THR.206	OG, A_SER.209	HG, A_SER.209	2.97	2.03	10.25
1HGE.PDB	OD1, E_ASP.101	NE2, A_GLN.210	HE22, A_GLN.210	2.91	2.05	24.48
1HGE.PDB	O, A_VAL.204	N, A_GLN.211	H, A_GLN.211	2.84	1.93	17.53
1HGE.PDB	OG1, A_THR.203	OG1, A_THR.212	HG1, A_THR.212	2.85	1.89	3.04
1HGE.PDB	O, A_VAL.202	N, A_ILE.213	H, A_ILE.213	2.83	1.91	16.11
1HGE.PDB	OE1, C_GLN.210	NH2, A_ARG.220	HH21, A_ARG.220	2.71	1.78	19.14
1HGE.PDB	O, A_ASN.216	NH2, A_ARG.220	HH22, A_ARG.220	2.65	1.77	22.20
1HGE.PDB	O, A_LEU.226	N, A_VAL.223	H, A_VAL.223	2.87	1.92	10.90
1HGE.PDB	O, A_CYS.97	NE, A_ARG.224	HE, A_ARG.224	2.88	2.06	27.84
1HGE.PDB	O, A_CYS.97	NH2, A_ARG.224	HH21, A_ARG.224	2.81	1.91	22.36
1HGE.PDB	O, A_VAL.223	N, A_LEU.226	H, A_LEU.226	2.91	1.96	11.44
1HGE.PDB	O, A_SER.228	NH1, A_ARG.229	HH11, A_ARG.229	2.68	1.74	17.50
1HGE.PDB	O, A_PRO.221	NH2, A_ARG.229	HH22, A_ARG.229	2.64	1.68	14.09
1HGE.PDB	OD1, A_ASP.101	OG, A_SER.231	HG, A_SER.231	2.85	1.89	7.16
1HGE.PDB	O, A_ASP.101	N, A_ILE.232	H, A_ILE.232	2.93	2.00	16.40
1HGE.PDB	O, A_TRP.180	N, A_TYR.233	H, A_TYR.233	2.87	1.90	8.23
1HGE.PDB	O, A_TYR.178	N, A_THR.235	H, A_THR.235	2.87	1.97	18.03
1HGE.PDB	O, A_LYS.176	N, A_VAL.237	H, A_VAL.237	2.80	1.88	15.84
1HGE.PDB	O, F_SER.71	NZ, A_LYS.238	HZ2, A_LYS.238	2.67	1.73	19.84
1HGE.PDB	OE1, F_GLU.72	NZ, A_LYS.238	HZ3, A_LYS.238	2.91	1.89	11.73
1HGE.PDB	O, A_ASN.170	N, A_GLY.240	H, A_GLY.240	2.86	1.99	22.30
1HGE.PDB	O, A_LYS.238	N, A_ASP.241	H, A_ASP.241	2.94	2.01	14.08
1HGE.PDB	OD1, A_ASP.241	N, A_VAL.242	H, A_VAL.242	2.76	1.94	27.44
1HGE.PDB	O, A_MET.168	N, A_LEU.243	H, A_LEU.243	2.90	1.93	4.25
1HGE.PDB	O, A_SER.205	N, A_VAL.244	H, A_VAL.244	2.95	2.01	13.31
1HGE.PDB	O, A_VAL.166	N, A_ILE.245	H, A_ILE.245	2.85	1.92	14.45
1HGE.PDB	O, A_THR.203	N, A_ASN.246	H, A_ASN.246	2.90	1.93	7.70
1HGE.PDB	OD1, A_ASN.165	ND2, A_ASN.246	HD22, A_ASN.246	2.88	1.94	13.15
1HGE.PDB	O, A_LEU.164	N, A_SER.247	H, A_SER.247	2.96	2.05	18.81
1HGE.PDB	OE1, A_GLN.191	ND2, A_ASN.250	HD21, A_ASN.250	2.94	1.97	8.25
1HGE.PDB	O, A_HIS.183	ND2, A_ASN.250	HD22, A_ASN.250	2.88	1.92	10.41
1HGE.PDB	O, A_ASN.152	N, A_ALA.253	H, A_ALA.253	2.86	1.98	21.30
1HGE.PDB	OD1, A_ASN.133	NH2, A_ARG.255	HH22, A_ARG.255	2.48	1.67	28.93

1HGE.PDB	O, A_LEU_177	N, A_PHE_258	H, A_PHE_258	2.96	1.99	5.50
1HGE.PDB	OE2, A_GLU_119	NH1, A_ARG_261	HH12, A_ARG_261	2.64	1.81	27.97
1HGE.PDB	OE1, A_GLU_119	NH2, A_ARG_261	HH22, A_ARG_261	2.84	1.95	24.23
1HGE.PDB	OD2, A_ASP_85	NZ, A_LYS_264	HZ3, A_LYS_264	2.77	1.79	16.96
1HGE.PDB	O, A_PHE_87	N, A_MET_268	H, A_MET_268	2.82	1.93	21.12
1HGE.PDB	O, A_PRO_284	OG, A_SER_270	HG, A_SER_270	2.79	1.85	11.32
1HGE.PDB	OG, A_SER_270	N, A_ALA_272	H, A_ALA_272	2.96	2.01	11.61
1HGE.PDB	O, A_ILE_51	N, A_ASP_275	H, A_ASP_275	2.94	2.05	20.45
1HGE.PDB	OD1, A_ASP_275	N, A_THR_276	H, A_THR_276	2.79	1.94	23.69
1HGE.PDB	O, A_ASN_54	N, A_SER_279	H, A_SER_279	2.78	1.85	13.75
1HGE.PDB	O, A_TYR_302	N, A_ILE_282	H, A_ILE_282	2.91	1.94	8.25
1HGE.PDB	O, A_THR_283	N, A_GLY_286	H, A_GLY_286	2.83	1.90	13.31
1HGE.PDB	O, A_LYS_50	N, A_SER_287	H, A_SER_287	2.88	1.91	2.15
1HGE.PDB	O, A_ALA_304	ND2, A_ASN_290	HD22, A_ASN_290	2.81	1.91	18.81
1HGE.PDB	OE1, A_GLN_44	NZ, A_LYS_292	HZ1, A_LYS_292	2.69	1.69	12.67
1HGE.PDB	OD2, A_ASP_291	NZ, A_LYS_292	HZ3, A_LYS_292	2.82	1.86	19.03
1HGE.PDB	O, A_LYS_307	N, A_GLN_295	H, A_GLN_295	2.84	1.95	20.46
1HGE.PDB	O, A_ASN_298	NE2, A_GLN_295	HE21, A_GLN_295	2.75	1.79	6.17
1HGE.PDB	O, A_GLN_44	N, A_ASN_296	H, A_ASN_296	2.80	1.87	13.84
1HGE.PDB	OE1, A_GLN_295	N, A_VAL_297	H, A_VAL_297	2.67	1.87	28.35
1HGE.PDB	O, B_LYS_68	NZ, A_LYS_299	HZ2, A_LYS_299	2.95	1.93	10.27
1HGE.PDB	OD1, A_ASN_298	N, A_ILE_300	H, A_ILE_300	2.94	2.01	15.45
1HGE.PDB	O, A_ILE_282	N, A_TYR_302	H, A_TYR_302	2.95	2.08	23.09
1HGE.PDB	O, B_LYS_62	N, A_GLY_303	H, A_GLY_303	2.95	1.98	8.88
1HGE.PDB	OG, B_SER_93	N, A_LYS_310	H, A_LYS_310	2.91	1.95	10.06
1HGE.PDB	OE2, A_GLU_41	N, A_LEU_314	H, A_LEU_314	2.82	1.89	14.30
1HGE.PDB	OE1, A_GLU_41	NZ, A_LYS_315	HZ3, A_LYS_315	2.82	1.87	21.00
1HGE.PDB	O, A_THR_40	N, A_LEU_316	H, A_LEU_316	2.80	1.85	10.41
1HGE.PDB	OD1, B_ASN_104	N, A_ALA_317	H, A_ALA_317	2.72	1.81	16.15
1HGE.PDB	O, A_ASN_38	N, A_THR_318	H, A_THR_318	2.85	1.93	17.18
1HGE.PDB	O, A_VAL_20	ND2, A_ASN_322	HD21, A_ASN_322	2.93	2.01	15.29
1HGE.PDB	OE2, A_GLU_35	ND2, A_ASN_322	HD22, A_ASN_322	2.88	1.99	21.26
1HGE.PDB	OE1, A_GLU_325	NZ, A_LYS_326	HZ3, A_LYS_326	2.85	1.86	15.04
1HGE.PDB	O, A_PRO_21	NE2, A_GLN_327	HE22, A_GLN_327	2.79	1.93	23.89
1HGE.PDB	OD2, B_ASP_112	N, B_GLY_1	H2, B_GLY_1	2.79	1.81	15.88
1HGE.PDB	OD1, B_ASP_109	N, B_LEU_2	H, B_LEU_2	2.80	1.92	21.49
1HGE.PDB	OD2, B_ASP_112	N, B_PHE_3	H, B_PHE_3	2.74	1.95	29.38
1HGE.PDB	OD2, B_ASP_112	N, B_GLY_4	H, B_GLY_4	2.91	2.02	19.87
1HGE.PDB	OD1, B_ASP_112	N, B_ALA_5	H, B_ALA_5	2.93	2.03	18.95
1HGE.PDB	O, B_GLY_4	N, B_PHE_9	H, B_PHE_9	2.82	1.87	12.40
1HGE.PDB	O, B_GLY_13	ND2, B_ASN_12	HD22, B_ASN_12	2.77	1.94	25.78
1HGE.PDB	O, A_VAL_323	N, B_GLY_13	H, B_GLY_13	2.72	1.79	12.30
1HGE.PDB	O, A_HIS_17	N, B_TRP_14	H, B_TRP_14	2.85	1.92	15.18
1HGE.PDB	OG1, B_THR_41	N, B_TRP_21	H, B_TRP_21	2.88	1.97	18.39
1HGE.PDB	O, A_GLY_16	N, B_GLY_23	H, B_GLY_23	2.92	2.01	18.67
1HGE.PDB	O, B_ALA_35	N, B_PHE_24	H, B_PHE_24	2.78	1.82	3.34
1HGE.PDB	O, A_CYS_14	N, B_ARG_25	H, B_ARG_25	3.00	2.06	13.87
1HGE.PDB	OE1, B_GLN_34	NE, B_ARG_25	HE, B_ARG_25	2.59	1.77	25.60
1HGE.PDB	O, B_GLY_33	N, B_HIS_26	H, B_HIS_26	2.68	1.83	22.72
1HGE.PDB	OG1, B_THR_32	NE2, B_GLN_27	HE22, B_GLN_27	2.99	2.08	18.28
1HGE.PDB	O, B_GLY_31	N, B_ASN_28	H, B_ASN_28	2.82	1.91	16.99
1HGE.PDB	O, B_ASN_28	N, B_GLY_31	H, B_GLY_31	3.00	2.09	18.25
1HGE.PDB	O, B_HIS_26	N, B_GLY_33	H, B_GLY_33	2.86	1.95	17.40
1HGE.PDB	O, B_TYR_22	N, B_ASP_37	H, B_ASP_37	2.72	1.79	12.23
1HGE.PDB	OD2, B_ASP_37	N, B_SER_40	H, B_SER_40	2.87	1.91	9.83
1HGE.PDB	O, B_ASP_37	OG1, B_THR_41	HG1, B_THR_41	2.70	1.82	19.30
1HGE.PDB	O, B_LEU_38	N, B_GLN_42	H, B_GLN_42	2.86	1.93	14.86
1HGE.PDB	OD1, B_ASP_46	NE2, B_GLN_42	HE22, B_GLN_42	2.87	1.96	19.05

1HGE.PDB	O, B_LYS_39	N, B_ALA_43	H, B_ALA_43	2.94	2.00	12.81
1HGE.PDB	O, B_SER_40	N, B_ALA_44	H, B_ALA_44	2.93	1.95	3.59
1HGE.PDB	O, B_GLN_42	N, B_ASP_46	H, B_ASP_46	2.81	1.84	1.45
1HGE.PDB	O, B_ALA_43	NE2, B_GLN_47	HE22, B_GLN_47	2.88	1.96	16.21
1HGE.PDB	O, B_ILE_45	N, B_ASN_49	H, B_ASN_49	2.85	1.89	11.27
1HGE.PDB	O, B_ASP_46	N, B_GLY_50	H, B_GLY_50	2.84	1.93	18.21
1HGE.PDB	OG1, B_THR_107	NZ, B_LYS_51	HZ1, B_LYS_51	2.97	1.99	17.16
1HGE.PDB	OE1, B_GLU_103	NZ, B_LYS_51	HZ2, B_LYS_51	2.76	1.73	6.92
1HGE.PDB	ND1, B_HIS_106	NZ, B_LYS_51	HZ3, B_LYS_51	2.73	1.78	18.14
1HGE.PDB	O, B_ILE_48	N, B_LEU_52	H, B_LEU_52	2.84	1.93	16.73
1HGE.PDB	O, B_ASN_49	N, B_ASN_53	H, B_ASN_53	2.78	1.86	14.52
1HGE.PDB	OE1, B_GLU_57	NH1, B_ARG_54	HH11, B_ARG_54	2.83	1.84	12.19
1HGE.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.84	1.86	12.76
1HGE.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ1, B_LYS_62	2.60	1.76	28.82
1HGE.PDB	OD2, F_ASP_90	NZ, B_LYS_62	HZ3, B_LYS_62	2.69	1.82	26.81
1HGE.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.97	2.02	12.36
1HGE.PDB	O, B_PHE_63	NE2, B_GLN_65	HE22, B_GLN_65	2.99	2.02	6.59
1HGE.PDB	O, A_LYS_299	NZ, B_LYS_68	HZ1, B_LYS_68	2.93	1.92	11.15
1HGE.PDB	OE2, B_GLU_85	NZ, B_LYS_68	HZ2, B_LYS_68	2.78	1.76	9.50
1HGE.PDB	OG, C_SER_107	N, B_ARG_76	H, B_ARG_76	2.82	1.86	9.28
1HGE.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.87	1.91	11.56
1HGE.PDB	OE2, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.84	1.83	5.81
1HGE.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.70	1.70	6.45
1HGE.PDB	OE1, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.79	1.79	3.91
1HGE.PDB	OE1, B_GLU_74	NE2, B_GLN_78	HE22, B_GLN_78	2.97	2.00	7.88
1HGE.PDB	O, B_GLY_75	N, B_ASP_79	H, B_ASP_79	2.91	1.96	12.34
1HGE.PDB	O, B_ILE_77	N, B_GLU_81	H, B_GLU_81	2.94	1.98	9.95
1HGE.PDB	O, B_ASP_79	N, B_TYR_83	H, B_TYR_83	2.93	2.00	15.72
1HGE.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.65	1.81	24.86
1HGE.PDB	O, B_LEU_80	N, B_VAL_84	H, B_VAL_84	2.83	1.87	9.05
1HGE.PDB	O, B_LYS_82	N, B_ASP_86	H, B_ASP_86	2.93	1.97	10.28
1HGE.PDB	O, B_TYR_83	N, B_THR_87	H, B_THR_87	2.93	1.97	8.81
1HGE.PDB	O, B_VAL_84	N, B_LYS_88	H, B_LYS_88	2.94	2.02	16.73
1HGE.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.75	1.71	5.62
1HGE.PDB	O, B_GLU_85	N, B_ILE_89	H, B_ILE_89	2.88	1.90	4.71
1HGE.PDB	O, B_LYS_88	N, B_TRP_92	H, B_TRP_92	2.97	1.99	5.16
1HGE.PDB	O, B_ILE_89	N, B_SER_93	H, B_SER_93	2.85	1.95	18.50
1HGE.PDB	O, B_ILE_89	OG, B_SER_93	HG, B_SER_93	2.88	1.95	13.07
1HGE.PDB	O, B_ASP_90	N, B_TYR_94	H, B_TYR_94	2.86	1.94	16.10
1HGE.PDB	O, B_TRP_92	N, B_ALA_96	H, B_ALA_96	2.95	2.01	14.83
1HGE.PDB	O, B_TYR_94	N, B_LEU_98	H, B_LEU_98	2.99	2.01	4.40
1HGE.PDB	O, B_ASN_95	N, B_LEU_99	H, B_LEU_99	2.90	1.98	15.69
1HGE.PDB	O, B_LEU_98	N, B_LEU_102	H, B_LEU_102	2.96	1.99	5.20
1HGE.PDB	O, B_LEU_99	N, B_GLU_103	H, B_GLU_103	2.88	1.92	7.57
1HGE.PDB	O, B_VAL_100	N, B_ASN_104	H, B_ASN_104	2.90	1.95	12.33
1HGE.PDB	O, A_LYS_27	ND2, B_ASN_104	HD22, B_ASN_104	2.93	1.97	10.25
1HGE.PDB	O, B_LEU_102	N, B_HIS_106	H, B_HIS_106	2.92	1.96	11.10
1HGE.PDB	O, B_GLU_103	N, B_THR_107	H, B_THR_107	2.81	1.94	21.77
1HGE.PDB	O, B_ASN_104	N, B_ILE_108	H, B_ILE_108	2.89	1.93	10.01
1HGE.PDB	O, B_HIS_106	N, B_LEU_110	H, B_LEU_110	2.83	1.87	9.77
1HGE.PDB	O, B_THR_107	OG1, B_THR_111	HG1, B_THR_111	2.88	1.91	3.54
1HGE.PDB	O, B_ASP_109	N, B_SER_113	H, B_SER_113	2.82	1.87	9.66
1HGE.PDB	O, B_LEU_110	N, B_GLU_114	H, B_GLU_114	2.93	1.98	10.47
1HGE.PDB	O, B_ASP_112	N, B_ASN_116	H, B_ASN_116	2.97	2.00	6.50
1HGE.PDB	O, B_SER_113	N, B_LYS_117	H, B_LYS_117	2.76	1.88	21.74
1HGE.PDB	O, B_GLU_114	N, B_LEU_118	H, B_LEU_118	2.98	2.03	12.99
1HGE.PDB	O, B_MET_115	N, B_PHE_119	H, B_PHE_119	3.00	2.05	11.74
1HGE.PDB	O, B_ASN_116	N, B_GLU_120	H, B_GLU_120	2.94	1.96	5.48

1HGE.PDB	O, B_LYS_117	N, B_LYS_121	H, B_LYS_121	2.93	2.04	20.65
1HGE.PDB	O, B_PHE_119	N, B_ARG_123	H, B_ARG_123	2.92	1.95	6.37
1HGE.PDB	OE2, B_GLU_120	NH1, B_ARG_123	HH11, B_ARG_123	2.84	1.95	23.29
1HGE.PDB	O, B_GLU_120	N, B_ARG_124	H, B_ARG_124	2.99	2.03	10.10
1HGE.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.80	1.98	27.36
1HGE.PDB	OE2, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.94	2.06	21.65
1HGE.PDB	O, B_LEU_126	N, B_ASN_129	H, B_ASN_129	2.92	1.98	14.64
1HGE.PDB	O, B_HIS_159	ND2, B_ASN_129	HD21, B_ASN_129	2.96	2.01	10.21
1HGE.PDB	OH, B_TYR_157	ND2, B_ASN_129	HD22, B_ASN_129	2.79	1.85	12.68
1HGE.PDB	O, B_LYS_139	N, B_GLU_131	H, B_GLU_131	2.95	2.03	17.07
1HGE.PDB	O, B_CYS_137	N, B_MET_133	H, B_MET_133	2.86	1.91	11.42
1HGE.PDB	O, A_LEU_13	N, B_PHE_138	H, B_PHE_138	2.71	1.84	21.33
1HGE.PDB	O, B_GLU_131	N, B_LYS_139	H, B_LYS_139	2.81	1.88	12.91
1HGE.PDB	O, A_ALA_11	N, B_ILE_140	H, B_ILE_140	2.75	1.86	18.72
1HGE.PDB	O, B_ASN_129	N, B_TYR_141	H, B_TYR_141	2.86	1.94	15.94
1HGE.PDB	OD2, B_ASP_145	NZ, B_LYS_143	HZ1, B_LYS_143	2.79	1.94	29.42
1HGE.PDB	OE1, B_GLU_30	N, B_ASN_146	H, B_ASN_146	2.97	2.02	12.34
1HGE.PDB	O, B_ASP_145	N, B_ILE_149	H, B_ILE_149	2.91	1.95	10.07
1HGE.PDB	O, B_ASN_146	N, B_GLU_150	H, B_GLU_150	2.95	2.00	12.08
1HGE.PDB	O, B_ALA_147	N, B_SER_151	H, B_SER_151	2.90	2.05	24.74
1HGE.PDB	O, B_CYS_148	OG, B_SER_151	HG, B_SER_151	2.68	1.83	21.90
1HGE.PDB	O, B_GLU_150	N, B_ASN_154	H, B_ASN_154	2.81	1.84	3.57
1HGE.PDB	OE2, B_GLU_150	ND2, B_ASN_154	HD21, B_ASN_154	2.93	2.05	22.48
1HGE.PDB	O, B_SER_151	N, B_THR_156	H, B_THR_156	2.73	1.90	26.23
1HGE.PDB	OD1, B_ASN_154	OG1, B_THR_156	HG1, B_THR_156	2.71	1.82	17.99
1HGE.PDB	OD1, B_ASP_158	N, B_ASP_160	H, B_ASP_160	2.83	1.98	24.58
1HGE.PDB	O, B_HIS_159	N, B_TYR_162	H, B_TYR_162	2.90	2.00	20.06
1HGE.PDB	O, F_ARG_170	NH1, B_ARG_163	HH12, B_ARG_163	2.78	1.81	13.88
1HGE.PDB	O, B_TYR_162	N, B_ALA_166	H, B_ALA_166	2.88	1.91	5.46
1HGE.PDB	O, B_ARG_163	N, B_LEU_167	H, B_LEU_167	2.76	1.81	10.04
1HGE.PDB	O, B_ALA_166	N, B_ARG_170	H, B_ARG_170	2.82	1.95	21.77
1HGE.PDB	O, B_GLU_128	NE, B_ARG_170	HE, B_ARG_170	2.74	1.87	22.54
1HGE.PDB	OE2, B_GLU_131	NH1, B_ARG_170	HH11, B_ARG_170	2.80	1.80	6.47
1HGE.PDB	O, B_LEU_167	N, B_PHE_171	H, B_PHE_171	2.90	1.98	16.40
1HGE.PDB	O, D_ILE_140	N, C_ALA_11	H, C_ALA_11	2.80	1.91	19.98
1HGE.PDB	O, D_PHE_138	N, C_LEU_13	H, C_LEU_13	2.99	2.04	12.20
1HGE.PDB	O, D_ARG_25	N, C_CYS_14	H, C_CYS_14	2.73	1.82	16.85
1HGE.PDB	O, D_GLY_136	N, C_LEU_15	H, C_LEU_15	2.89	1.92	5.03
1HGE.PDB	O, D_GLY_23	N, C_GLY_16	H, C_GLY_16	2.98	2.07	18.60
1HGE.PDB	O, C_HIS_18	ND1, C_HIS_17	HD1, C_HIS_17	3.00	2.12	21.91
1HGE.PDB	O, D_TRP_21	N, C_HIS_18	H, C_HIS_18	2.85	1.96	19.89
1HGE.PDB	OD1, C_ASN_322	N, C_VAL_20	H, C_VAL_20	2.80	1.84	8.99
1HGE.PDB	O, C_VAL_36	N, C_THR_24	H, C_THR_24	2.83	1.91	16.33
1HGE.PDB	O, C_ILE_34	N, C_VAL_26	H, C_VAL_26	2.82	1.87	10.60
1HGE.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.79	1.77	8.74
1HGE.PDB	O, C_VAL_26	N, C_ILE_34	H, C_ILE_34	2.90	1.95	12.39
1HGE.PDB	O, C_THR_24	N, C_VAL_36	H, C_VAL_36	2.79	1.83	9.59
1HGE.PDB	O, C_MET_320	N, C_THR_37	H, C_THR_37	2.87	1.90	5.65
1HGE.PDB	O, C_LEU_316	N, C_THR_40	H, C_THR_40	2.80	1.96	24.94
1HGE.PDB	O, C_LEU_314	N, C_LEU_42	H, C_LEU_42	2.79	1.97	26.99
1HGE.PDB	O, C_PHE_294	N, C_GLN_44	H, C_GLN_44	2.81	1.85	7.78
1HGE.PDB	O, C_SER_46	NE2, C_GLN_44	HE22, C_GLN_44	2.87	1.98	21.20
1HGE.PDB	O, C_ASN_285	OG, C_SER_47	HG, C_SER_47	2.85	1.92	13.60
1HGE.PDB	OG1, C_THR_48	N, C_LYS_50	H, C_LYS_50	2.99	2.04	10.77
1HGE.PDB	OD2, C_ASP_275	NZ, C_LYS_50	HZ1, C_LYS_50	2.70	1.77	22.15
1HGE.PDB	O, C_PRO_273	N, C_ILE_51	H, C_ILE_51	2.80	1.85	11.79
1HGE.PDB	O, C_ASP_275	N, C_ASN_53	H, C_ASN_53	2.75	1.91	24.79
1HGE.PDB	OD2, C_ASP_85	N, C_ARG_57	H, C_ARG_57	2.90	1.96	11.88

1HGE.PDB	O, C_THR_83	NE, C_ARG_57	HE, C_ARG_57	2.79	1.83	9.16
1HGE.PDB	O, C_LEU_86	N, C_LEU_59	H, C_LEU_59	2.93	1.97	10.15
1HGE.PDB	O, C_VAL_88	N, C_GLY_61	H, C_GLY_61	2.98	2.14	25.88
1HGE.PDB	OD1, C_ASP_60	N, C_ILE_62	H, C_ILE_62	2.86	1.94	15.66
1HGE.PDB	O, C_GLY_61	N, C_CYS_64	H, C_CYS_64	2.85	1.93	16.26
1HGE.PDB	O, C_LEU_66	N, C_LEU_70	H, C_LEU_70	2.86	1.97	20.20
1HGE.PDB	O, C_ILE_67	N, C_LEU_71	H, C_LEU_71	2.82	1.86	10.15
1HGE.PDB	O, C_ASP_68	N, C_GLY_72	H, C_GLY_72	2.84	1.92	16.44
1HGE.PDB	OD1, C_ASP_73	ND1, C_HIS_75	HD1, C_HIS_75	2.76	1.85	18.20
1HGE.PDB	O, C_ASP_63	NE2, C_HIS_75	HE2, C_HIS_75	2.82	1.90	17.58
1HGE.PDB	O, C_ASP_73	N, C_CYS_76	H, C_CYS_76	2.77	1.82	10.67
1HGE.PDB	O, C_PRO_74	N, C_ASP_77	H, C_ASP_77	2.88	1.93	11.27
1HGE.PDB	O, C_CYS_76	N, C_PHE_79	H, C_PHE_79	2.99	2.01	4.04
1HGE.PDB	O, C_ARG_57	N, C_ASP_85	H, C_ASP_85	2.79	1.90	19.22
1HGE.PDB	O, C_LEU_59	N, C_VAL_88	H, C_VAL_88	2.96	1.98	5.43
1HGE.PDB	O, C_MET_268	N, C_GLU_89	H, C_GLU_89	2.78	1.83	10.28
1HGE.PDB	OD1, C_ASP_60	NE, C_ARG_90	HE, C_ARG_90	2.84	1.88	10.34
1HGE.PDB	O, C_SER_270	NH1, C_ARG_90	HH11, C_ARG_90	2.64	1.77	24.86
1HGE.PDB	O, C_ALA_272	NH1, C_ARG_90	HH12, C_ARG_90	2.61	1.68	16.52
1HGE.PDB	OD2, C_ASP_60	NH2, C_ARG_90	HH21, C_ARG_90	2.77	1.78	9.61
1HGE.PDB	OD1, C_ASP_271	N, C_SER_91	H, C_SER_91	2.89	1.92	5.94
1HGE.PDB	OD2, C_ASP_271	OG, C_SER_91	HG, C_SER_91	2.80	1.91	19.19
1HGE.PDB	OD2, C_ASP_68	OG, C_SER_95	HG, C_SER_95	2.88	1.95	14.90
1HGE.PDB	OD2, C_ASP_73	N, C_ASN_96	H, C_ASN_96	2.89	1.91	7.72
1HGE.PDB	OD1, C_ASP_68	OH, C_TYR_100	HH, C_TYR_100	2.89	1.97	15.01
1HGE.PDB	O, C_ILE_230	N, C_ASP_101	H, C_ASP_101	2.99	2.10	21.29
1HGE.PDB	OD2, C_ASP_104	OG, C_SER_107	HG, C_SER_107	2.88	1.96	15.70
1HGE.PDB	O, C_TYR_105	N, C_ARG_109	H, C_ARG_109	2.82	1.85	4.05
1HGE.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.78	1.79	11.19
1HGE.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.78	1.86	15.09
1HGE.PDB	O, C_SER_107	N, C_LEU_111	H, C_LEU_111	2.85	1.88	4.99
1HGE.PDB	O, C_ARG_109	N, C_ALA_113	H, C_ALA_113	2.95	2.04	18.55
1HGE.PDB	O, C_SER_110	N, C_SER_114	H, C_SER_114	2.89	1.95	14.50
1HGE.PDB	OE2, C_GLU_119	OG1, C_THR_117	HG1, C_THR_117	2.89	1.94	9.29
1HGE.PDB	O, C_GLU_82	N, C_LEU_118	H, C_LEU_118	2.97	2.03	15.52
1HGE.PDB	O, C_TYR_257	N, C_ILE_121	H, C_ILE_121	2.88	1.91	6.31
1HGE.PDB	O, C_ARG_255	N, C_GLU_123	H, C_GLU_123	2.94	1.98	10.94
1HGE.PDB	O, C_THR_155	N, C_THR_131	H, C_THR_131	2.77	1.87	18.82
1HGE.PDB	OD1, C_ASN_152	N, C_ASN_133	H, C_ASN_133	2.88	1.96	16.12
1HGE.PDB	O, C_TRP_153	N, C_GLY_134	H, C_GLY_134	2.94	2.05	19.45
1HGE.PDB	O, C_GLY_146	N, C_SER_136	H, C_SER_136	2.85	1.90	10.46
1HGE.PDB	OG, C_SER_136	N, C_ALA_138	H, C_ALA_138	2.96	2.02	13.07
1HGE.PDB	O, C_GLY_144	NZ, C_LYS_140	HZ1, C_LYS_140	2.72	1.75	17.13
1HGE.PDB	OD1, C_ASN_137	NZ, C_LYS_140	HZ2, C_LYS_140	2.83	1.86	16.66
1HGE.PDB	OD2, C_ASP_77	NE, C_ARG_141	HE, C_ARG_141	2.80	1.97	26.96
1HGE.PDB	O, C_PHE_147	NH1, C_ARG_141	HH12, C_ARG_141	2.55	1.62	15.87
1HGE.PDB	OD1, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.88	1.96	21.42
1HGE.PDB	OD2, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.74	1.86	24.30
1HGE.PDB	O, C_GLY_72	NH2, C_ARG_141	HH22, C_ARG_141	2.91	1.94	12.79
1HGE.PDB	O, C_GLY_72	N, C_SER_149	H, C_SER_149	2.84	1.92	17.14
1HGE.PDB	O, C_ALA_253	N, C_ASN_152	H, C_ASN_152	2.77	1.90	22.09
1HGE.PDB	OH, C_TYR_195	NE1, C_TRP_153	HE1, C_TRP_153	2.85	1.98	22.78
1HGE.PDB	O, C_LEU_194	N, C_LYS_156	H, C_LYS_156	2.97	2.07	19.03
1HGE.PDB	O, C_THR_160	N, C_SER_157	H, C_SER_157	2.96	2.05	18.03
1HGE.PDB	O, C_SER_247	N, C_LEU_164	H, C_LEU_164	2.70	1.87	25.69
1HGE.PDB	O, C_ILE_245	N, C_VAL_166	H, C_VAL_166	2.88	1.93	12.26
1HGE.PDB	O, C_LEU_243	OG1, C_THR_167	HG1, C_THR_167	2.89	2.00	19.24
1HGE.PDB	O, C_LEU_243	N, C_MET_168	H, C_MET_168	2.95	2.03	16.73

1HGE.PDB	O, C_ASP_241	N, C_ASN_170	H, C_ASN_170	2.90	1.92	6.43
1HGE.PDB	O, C_PHE_174	ND2, C_ASN_170	HD21, C_ASN_170	2.84	1.87	8.31
1HGE.PDB	O, C_VAL_237	ND2, C_ASN_170	HD22, C_ASN_170	2.85	2.06	29.16
1HGE.PDB	O, C_VAL_237	N, C_LYS_176	H, C_LYS_176	2.96	2.03	15.33
1HGE.PDB	OE2, C_GLU_123	NZ, C_LYS_176	HZ1, C_LYS_176	2.71	1.80	23.44
1HGE.PDB	O, C_PHE_258	N, C_LEU_177	H, C_LEU_177	2.95	1.98	5.56
1HGE.PDB	O, C_THR_235	N, C_TYR_178	H, C_TYR_178	2.82	1.85	5.01
1HGE.PDB	OE1, C_GLU_123	OH, C_TYR_178	HH, C_TYR_178	2.73	1.80	12.29
1HGE.PDB	OG1, C_THR_235	NE1, C_TRP_180	HE1, C_TRP_180	2.92	1.93	1.68
1HGE.PDB	O, C_ASN_250	N, C_HIS_183	H, C_HIS_183	2.90	2.00	18.95
1HGE.PDB	O, C_ARG_229	N, C_HIS_184	H, C_HIS_184	2.88	1.92	7.36
1HGE.PDB	OG, C_SER_231	NE2, C_HIS_184	HE2, C_HIS_184	2.71	1.87	25.48
1HGE.PDB	OG1, C_THR_187	N, C_GLU_190	H, C_GLU_190	2.99	2.05	11.81
1HGE.PDB	OD1, C_ASN_250	NE2, C_GLN_191	HE21, C_GLN_191	3.00	2.03	7.73
1HGE.PDB	O, C_GLN_197	NE2, C_GLN_191	HE22, C_GLN_191	2.95	2.03	16.39
1HGE.PDB	O, C_GLN_189	OG1, C_THR_192	HG1, C_THR_192	2.80	1.94	21.49
1HGE.PDB	O, C_GLN_189	N, C_SER_193	H, C_SER_193	2.84	1.90	12.38
1HGE.PDB	O, C_GLU_190	N, C_LEU_194	H, C_LEU_194	3.00	2.03	8.39
1HGE.PDB	O, C_GLN_191	N, C_TYR_195	H, C_TYR_195	2.79	1.84	10.35
1HGE.PDB	O, C_TYR_161	NE2, C_GLN_197	HE21, C_GLN_197	2.87	1.92	10.94
1HGE.PDB	O, C_ASN_248	NE2, C_GLN_197	HE22, C_GLN_197	2.96	2.03	16.11
1HGE.PDB	OD1, C_ASN_246	NH2, C_ARG_201	HH21, C_ARG_201	2.62	1.75	24.53
1HGE.PDB	O, C_ILE_213	N, C_VAL_202	H, C_VAL_202	2.99	2.05	14.11
1HGE.PDB	O, C_ASN_246	N, C_THR_203	H, C_THR_203	2.91	1.96	12.23
1HGE.PDB	OG1, C_THR_212	OG1, C_THR_203	HG1, C_THR_203	2.89	1.94	9.07
1HGE.PDB	O, C_GLN_211	N, C_VAL_204	H, C_VAL_204	2.84	1.94	18.37
1HGE.PDB	O, C_SER_209	N, C_THR_206	H, C_THR_206	2.97	2.00	8.35
1HGE.PDB	OD1, C_ASP_241	N, C_ARG_207	H, C_ARG_207	2.89	1.93	9.60
1HGE.PDB	OG1, C_THR_206	OG1, C_SER_209	HG, C_SER_209	2.98	2.03	9.68
1HGE.PDB	OD1, A_ASP_101	NE2, C_GLN_210	HE22, C_GLN_210	2.93	2.07	24.92
1HGE.PDB	O, C_VAL_204	N, C_GLN_211	H, C_GLN_211	2.83	1.91	16.68
1HGE.PDB	O, C_VAL_202	N, C_ILE_213	H, C_ILE_213	2.84	1.91	15.11
1HGE.PDB	ND1, C_HIS_184	N, C_ASN_216	H, C_ASN_216	2.76	1.97	29.84
1HGE.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.64	1.76	23.09
1HGE.PDB	O, C_ASN_216	NH2, C_ARG_220	HH22, C_ARG_220	2.68	1.79	22.17
1HGE.PDB	O, C_LEU_226	N, C_VAL_223	H, C_VAL_223	2.85	1.89	10.14
1HGE.PDB	O, C_CYS_97	NE, C_ARG_224	HE, C_ARG_224	2.86	2.04	28.35
1HGE.PDB	O, C_CYS_97	NH2, C_ARG_224	HH21, C_ARG_224	2.80	1.90	22.90
1HGE.PDB	O, C_VAL_223	N, C_LEU_226	H, C_LEU_226	2.92	1.98	11.69
1HGE.PDB	O, C_SER_228	NH1, C_ARG_229	HH11, C_ARG_229	2.66	1.73	17.65
1HGE.PDB	O, C_PRO_221	NH2, C_ARG_229	HH22, C_ARG_229	2.66	1.70	14.45
1HGE.PDB	OD1, C_ASP_101	OG, C_SER_231	HG, C_SER_231	2.89	1.93	7.03
1HGE.PDB	O, C_ASP_101	N, C_ILE_232	H, C_ILE_232	2.94	2.01	16.06
1HGE.PDB	O, C_TRP_180	N, C_TYR_233	H, C_TYR_233	2.87	1.91	8.74
1HGE.PDB	O, C_TYR_178	N, C_THR_235	H, C_THR_235	2.86	1.95	17.72
1HGE.PDB	O, C_LYS_176	N, C_VAL_237	H, C_VAL_237	2.76	1.86	18.21
1HGE.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.78	1.80	16.75
1HGE.PDB	O, B_SER_71	NZ, C_LYS_238	HZ3, C_LYS_238	2.65	1.71	19.56
1HGE.PDB	O, C_ASN_170	N, C_GLY_240	H, C_GLY_240	2.86	1.99	22.04
1HGE.PDB	O, C_LYS_238	N, C_ASP_241	H, C_ASP_241	2.92	1.99	14.19
1HGE.PDB	OD1, C_ASP_241	N, C_VAL_242	H, C_VAL_242	2.80	1.97	26.99
1HGE.PDB	O, C_MET_168	N, C_LEU_243	H, C_LEU_243	2.92	1.94	4.20
1HGE.PDB	O, C_SER_205	N, C_VAL_244	H, C_VAL_244	2.96	2.01	12.41
1HGE.PDB	O, C_VAL_166	N, C_ILE_245	H, C_ILE_245	2.89	1.96	15.45
1HGE.PDB	O, C_THR_203	N, C_ASN_246	H, C_ASN_246	2.90	1.93	6.52
1HGE.PDB	OD1, C_ASN_165	ND2, C_ASN_246	HD22, C_ASN_246	2.89	1.94	13.09
1HGE.PDB	O, C_LEU_164	N, C_SER_247	H, C_SER_247	2.96	2.05	18.85
1HGE.PDB	O, C_ARG_201	OG, C_SER_247	HG, C_SER_247	2.74	1.95	29.12

1HGE.PDB	OE1, C_GLN_191	ND2, C_ASN_250	HD21, C_ASN_250	2.89	1.93	9.19
1HGE.PDB	O, C_HIS_183	ND2, C_ASN_250	HD22, C_ASN_250	2.90	1.94	11.40
1HGE.PDB	O, C_ASN_152	N, C_ALA_253	H, C_ALA_253	2.88	2.01	23.02
1HGE.PDB	OD1, C_ASN_133	NH2, C_ARG_255	HH22, C_ARG_255	2.48	1.68	29.46
1HGE.PDB	O, C_ILE_121	N, C_TYR_257	H, C_TYR_257	2.98	2.14	25.04
1HGE.PDB	O, C_LEU_177	N, C_PHE_258	H, C_PHE_258	2.95	1.97	4.47
1HGE.PDB	OE2, C_GLU_119	NH1, C_ARG_261	HH12, C_ARG_261	2.65	1.82	27.69
1HGE.PDB	OE1, C_GLU_119	NH2, C_ARG_261	HH22, C_ARG_261	2.84	1.95	24.41
1HGE.PDB	OD2, C_ASP_85	NZ, C_LYS_264	HZ3, C_LYS_264	2.77	1.79	16.79
1HGE.PDB	O, C_PHE_87	N, C_MET_268	H, C_MET_268	2.81	1.93	20.65
1HGE.PDB	O, C_PRO_284	OG, C_SER_270	HG, C_SER_270	2.77	1.85	14.90
1HGE.PDB	OG, C_SER_270	N, C_ALA_272	H, C_ALA_272	2.95	2.00	10.98
1HGE.PDB	O, C_ILE_51	N, C_ASP_275	H, C_ASP_275	2.98	2.09	21.88
1HGE.PDB	OD1, C_ASP_275	N, C_THR_276	H, C_THR_276	2.79	1.93	23.11
1HGE.PDB	O, C_ASN_54	N, C_SER_279	H, C_SER_279	2.78	1.85	13.73
1HGE.PDB	O, C_TYR_302	N, C_ILE_282	H, C_ILE_282	2.90	1.93	4.89
1HGE.PDB	O, C_THR_283	N, C_GLY_286	H, C_GLY_286	2.85	1.91	13.86
1HGE.PDB	O, C_LYS_50	N, C_SER_287	H, C_SER_287	2.85	1.88	3.50
1HGE.PDB	O, C_ALA_304	ND2, C_ASN_290	HD22, C_ASN_290	2.82	1.93	19.75
1HGE.PDB	OE1, C_GLN_44	NZ, C_LYS_292	HZ1, C_LYS_292	2.72	1.72	12.77
1HGE.PDB	OD2, C_ASP_291	NZ, C_LYS_292	HZ3, C_LYS_292	2.84	1.88	19.72
1HGE.PDB	O, C_LYS_307	N, C_GLN_295	H, C_GLN_295	2.83	1.94	20.43
1HGE.PDB	O, C_ASN_298	NE2, C_GLN_295	HE21, C_GLN_295	2.74	1.79	8.05
1HGE.PDB	O, C_GLN_44	N, C_ASN_296	H, C_ASN_296	2.82	1.89	15.19
1HGE.PDB	OE1, C_GLN_295	N, C_VAL_297	H, C_VAL_297	2.70	1.88	26.95
1HGE.PDB	OD1, C_ASN_285	ND2, C_ASN_298	HD22, C_ASN_298	2.99	2.05	12.60
1HGE.PDB	O, D_LYS_68	NZ, C_LYS_299	HZ2, C_LYS_299	2.96	1.94	10.83
1HGE.PDB	OD1, C_ASN_298	N, C_ILE_300	H, C_ILE_300	2.91	2.01	19.01
1HGE.PDB	O, C_ILE_282	N, C_TYR_302	H, C_TYR_302	2.93	2.07	24.01
1HGE.PDB	O, C_LYS_264	OH, C_TYR_302	HH, C_TYR_302	2.65	1.87	29.65
1HGE.PDB	O, D_LYS_62	N, C_GLY_303	H, C_GLY_303	2.94	1.98	10.89
1HGE.PDB	OG, D_SER_93	N, C_LYS_310	H, C_LYS_310	2.92	1.96	11.23
1HGE.PDB	OE2, C_GLU_41	N, C_LEU_314	H, C_LEU_314	2.83	1.89	13.54
1HGE.PDB	OE1, C_GLU_41	NZ, C_LYS_315	HZ3, C_LYS_315	2.82	1.88	21.70
1HGE.PDB	O, C_THR_40	N, C_LEU_316	H, C_LEU_316	2.80	1.84	9.83
1HGE.PDB	OD1, D_ASN_104	N, C_ALA_317	H, C_ALA_317	2.73	1.80	14.37
1HGE.PDB	O, C_ASN_38	N, C_THR_318	H, C_THR_318	2.85	1.95	18.88
1HGE.PDB	O, C_VAL_20	ND2, C_ASN_322	HD21, C_ASN_322	2.96	2.03	15.20
1HGE.PDB	OE2, C_GLU_35	ND2, C_ASN_322	HD22, C_ASN_322	2.89	2.00	20.86
1HGE.PDB	OE1, D_GLU_15	NZ, C_LYS_326	HZ1, C_LYS_326	2.74	1.73	12.73
1HGE.PDB	OXT, C_THR_328	NE2, C_GLN_327	HE22, C_GLN_327	2.97	2.01	12.27
1HGE.PDB	OD2, D_ASP_112	N, D_GLY_1	H2, D_GLY_1	2.75	1.76	15.00
1HGE.PDB	OD1, D_ASP_109	N, D_LEU_2	H, D_LEU_2	2.82	1.93	20.06
1HGE.PDB	OD2, D_ASP_112	N, D_PHE_3	H, D_PHE_3	2.80	2.00	29.38
1HGE.PDB	OD2, D_ASP_112	N, D_GLY_4	H, D_GLY_4	2.92	2.03	19.66
1HGE.PDB	OD1, D_ASP_112	N, D_ALA_5	H, D_ALA_5	2.94	2.04	19.74
1HGE.PDB	O, D_GLY_4	N, D_PHE_9	H, D_PHE_9	2.82	1.88	13.73
1HGE.PDB	O, D_GLY_13	ND2, D_ASN_12	HD22, D_ASN_12	2.81	1.95	23.47
1HGE.PDB	O, C_VAL_323	N, D_GLY_13	H, D_GLY_13	2.71	1.79	14.79
1HGE.PDB	O, C_HIS_17	N, D_TRP_14	H, D_TRP_14	2.88	1.94	13.07
1HGE.PDB	OG1, D_THR_41	N, D_TRP_21	H, D_TRP_21	2.86	1.96	18.92
1HGE.PDB	O, C_GLY_16	N, D_GLY_23	H, D_GLY_23	2.94	2.04	19.95
1HGE.PDB	O, D_ALA_35	N, D_PHE_24	H, D_PHE_24	2.84	1.86	3.41
1HGE.PDB	O, C_CYS_14	N, D_ARG_25	H, D_ARG_25	2.94	1.98	9.40
1HGE.PDB	OE1, D_GLN_34	NE, D_ARG_25	HE, D_ARG_25	2.56	1.76	28.50
1HGE.PDB	O, D_GLY_33	N, D_HIS_26	H, D_HIS_26	2.85	1.95	19.13
1HGE.PDB	O, C_THR_12	N, D_GLN_27	H, D_GLN_27	2.86	1.95	18.04
1HGE.PDB	O, D_GLY_31	N, D_ASN_28	H, D_ASN_28	2.82	1.88	13.03

1HGE.PDB	OD1, D_ASN_28	N, D_GLU_30	H, D_GLU_30	2.96	2.16	29.70
1HGE.PDB	O, D_ASN_28	N, D_GLY_31	H, D_GLY_31	2.97	2.06	18.30
1HGE.PDB	O, D_PHE_24	N, D_ALA_35	H, D_ALA_35	2.79	1.99	28.92
1HGE.PDB	O, D_TYR_22	N, D_ASP_37	H, D_ASP_37	2.72	1.80	13.99
1HGE.PDB	OD2, D_ASP_37	N, D_SER_40	H, D_SER_40	2.88	1.92	10.60
1HGE.PDB	OD2, D_ASP_37	OG, D_SER_40	HG, D_SER_40	2.78	1.93	24.10
1HGE.PDB	O, D_ASP_37	OG1, D_THR_41	HG1, D_THR_41	2.71	1.83	19.19
1HGE.PDB	O, D_LEU_38	N, D_GLN_42	H, D_GLN_42	2.87	1.94	14.92
1HGE.PDB	OD1, D_ASP_46	NE2, D_GLN_42	HE22, D_GLN_42	2.87	1.96	19.33
1HGE.PDB	O, D_LYS_39	N, D_ALA_43	H, D_ALA_43	2.95	2.00	11.25
1HGE.PDB	O, D_SER_40	N, D_ALA_44	H, D_ALA_44	2.93	1.96	3.43
1HGE.PDB	O, D_GLN_42	N, D_ASP_46	H, D_ASP_46	2.80	1.83	3.78
1HGE.PDB	OE2, D_GLU_114	NE2, D_GLN_47	HE21, D_GLN_47	2.99	2.06	16.53
1HGE.PDB	O, D_ALA_43	NE2, D_GLN_47	HE22, D_GLN_47	2.87	1.96	16.48
1HGE.PDB	O, D_ILE_45	N, D_ASN_49	H, D_ASN_49	2.89	1.94	10.31
1HGE.PDB	O, D_ASP_46	N, D_GLY_50	H, D_GLY_50	2.85	1.93	16.23
1HGE.PDB	OG1, D_THR_107	NZ, D_LYS_51	HZ1, D_LYS_51	2.96	1.98	16.83
1HGE.PDB	OE1, D_GLU_103	NZ, D_LYS_51	HZ2, D_LYS_51	2.76	1.73	6.47
1HGE.PDB	ND1, D_HIS_106	NZ, D_LYS_51	HZ3, D_LYS_51	2.77	1.82	18.39
1HGE.PDB	O, D_ILE_48	N, D_LEU_52	H, D_LEU_52	2.84	1.95	19.97
1HGE.PDB	O, D_ASN_49	N, D_ASN_53	H, D_ASN_53	2.80	1.87	13.93
1HGE.PDB	OE1, D_GLU_57	NH1, D_ARG_54	HH11, D_ARG_54	2.82	1.84	12.42
1HGE.PDB	OE2, D_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.87	1.89	12.82
1HGE.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.96	1.98	6.23
1HGE.PDB	O, C_LYS_299	NZ, D_LYS_68	HZ1, D_LYS_68	2.92	1.91	12.00
1HGE.PDB	OE2, D_GLU_85	NZ, D_LYS_68	HZ2, D_LYS_68	2.80	1.78	10.75
1HGE.PDB	OG, E_SER_107	N, D_ARG_76	H, D_ARG_76	2.87	1.90	6.58
1HGE.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.79	1.85	14.06
1HGE.PDB	OE2, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.78	1.78	7.91
1HGE.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.63	1.67	11.36
1HGE.PDB	OE1, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.74	1.75	7.04
1HGE.PDB	OE1, D_GLU_74	NE2, D_GLN_78	HE22, D_GLN_78	2.96	1.99	8.03
1HGE.PDB	O, D_GLY_75	N, D_ASP_79	H, D_ASP_79	2.95	2.00	12.34
1HGE.PDB	O, D_ILE_77	N, D_GLU_81	H, D_GLU_81	2.96	2.00	10.54
1HGE.PDB	O, D_ASP_79	N, D_TYR_83	H, D_TYR_83	2.91	1.99	16.75
1HGE.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.58	1.80	29.40
1HGE.PDB	O, D_LEU_80	N, D_VAL_84	H, D_VAL_84	2.82	1.87	12.05
1HGE.PDB	O, D_LYS_82	N, D_ASP_86	H, D_ASP_86	2.94	1.98	8.49
1HGE.PDB	O, D_TYR_83	N, D_THR_87	H, D_THR_87	2.92	1.95	7.61
1HGE.PDB	O, D_VAL_84	N, D_LYS_88	H, D_LYS_88	2.93	2.04	19.95
1HGE.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.71	1.68	6.52
1HGE.PDB	O, D_GLU_85	N, D_ILE_89	H, D_ILE_89	2.88	1.90	2.66
1HGE.PDB	O, D_LYS_88	N, D_TRP_92	H, D_TRP_92	2.96	1.98	4.29
1HGE.PDB	O, D_ILE_89	N, D_SER_93	H, D_SER_93	2.83	1.92	17.54
1HGE.PDB	O, D_ILE_89	OG, D_SER_93	HG, D_SER_93	2.86	1.94	14.79
1HGE.PDB	O, D_ASP_90	N, D_TYR_94	H, D_TYR_94	2.87	1.96	18.12
1HGE.PDB	O, D_TRP_92	N, D_ALA_96	H, D_ALA_96	2.95	2.01	13.60
1HGE.PDB	O, D_TYR_94	N, D_LEU_98	H, D_LEU_98	2.96	1.98	4.20
1HGE.PDB	O, D_ASN_95	N, D_LEU_99	H, D_LEU_99	2.91	1.98	15.66
1HGE.PDB	O, D_LEU_98	N, D_LEU_102	H, D_LEU_102	2.98	2.00	6.37
1HGE.PDB	O, D_LEU_99	N, D_GLU_103	H, D_GLU_103	2.91	1.94	7.56
1HGE.PDB	O, D_VAL_100	N, D_ASN_104	H, D_ASN_104	2.91	1.96	12.51
1HGE.PDB	O, C_LYS_27	ND2, D_ASN_104	HD22, D_ASN_104	2.96	2.00	10.88
1HGE.PDB	O, D_LEU_102	N, D_HIS_106	H, D_HIS_106	2.92	1.97	11.35
1HGE.PDB	O, D_GLU_103	N, D_THR_107	H, D_THR_107	2.85	1.96	20.31
1HGE.PDB	O, D_ASN_104	N, D_ILE_108	H, D_ILE_108	2.91	1.95	9.12
1HGE.PDB	O, D_HIS_106	N, D_LEU_110	H, D_LEU_110	2.80	1.85	9.79
1HGE.PDB	O, D_THR_107	OG1, D_THR_111	HG1, D_THR_111	2.87	1.91	5.65

1HGE.PDB	O, D_ASP_109	N, D_SER_113	H, D_SER_113	2.84	1.89	10.30
1HGE.PDB	O, D_LEU_110	N, D_GLU_114	H, D_GLU_114	2.93	1.97	9.88
1HGE.PDB	O, D_ASP_112	N, D_ASN_116	H, D_ASN_116	2.98	2.01	8.80
1HGE.PDB	O, D_SER_113	N, D_LYS_117	H, D_LYS_117	2.78	1.90	20.87
1HGE.PDB	O, D_MET_115	N, D_PHE_119	H, D_PHE_119	3.00	2.05	13.31
1HGE.PDB	O, D_ASN_116	N, D_GLU_120	H, D_GLU_120	2.94	1.96	2.22
1HGE.PDB	O, D_LYS_117	N, D_LYS_121	H, D_LYS_121	2.93	2.03	20.11
1HGE.PDB	O, D_PHE_119	N, D_ARG_123	H, D_ARG_123	2.91	1.95	8.55
1HGE.PDB	OE2, D_GLU_120	NH1, D_ARG_123	HH11, D_ARG_123	2.83	1.93	23.01
1HGE.PDB	O, D_GLU_120	N, D_ARG_124	H, D_ARG_124	3.00	2.04	10.14
1HGE.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.78	1.98	28.90
1HGE.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.90	2.01	20.41
1HGE.PDB	O, D_LEU_126	N, D_ASN_129	H, D_ASN_129	2.94	1.99	12.91
1HGE.PDB	O, D_HIS_159	ND2, D_ASN_129	HD21, D_ASN_129	2.92	1.97	10.53
1HGE.PDB	OH, D_TYR_157	ND2, D_ASN_129	HD22, D_ASN_129	2.81	1.85	9.24
1HGE.PDB	O, D_LYS_139	N, D_GLU_131	H, D_GLU_131	2.97	2.05	17.56
1HGE.PDB	O, D_CYS_137	N, D_MET_133	H, D_MET_133	2.89	1.93	10.58
1HGE.PDB	O, C_LEU_13	N, D_PHE_138	H, D_PHE_138	2.74	1.87	21.30
1HGE.PDB	O, D_GLU_131	N, D_LYS_139	H, D_LYS_139	2.81	1.87	11.30
1HGE.PDB	O, C_ALA_11	N, D_ILE_140	H, D_ILE_140	2.78	1.88	18.97
1HGE.PDB	O, D_ASN_129	N, D_TYR_141	H, D_TYR_141	2.89	1.95	13.56
1HGE.PDB	OE2, D_GLU_30	N, D_ASN_146	H, D_ASN_146	2.83	1.92	17.98
1HGE.PDB	O, D_ASP_145	N, D_ILE_149	H, D_ILE_149	2.93	1.97	9.93
1HGE.PDB	O, D_ASN_146	N, D_GLU_150	H, D_GLU_150	2.95	2.02	14.34
1HGE.PDB	O, D_ALA_147	N, D_SER_151	H, D_SER_151	2.92	2.03	19.70
1HGE.PDB	O, D_CYS_148	OG, D_SER_151	HG, D_SER_151	2.69	1.84	22.52
1HGE.PDB	O, D_GLU_150	N, D_ASN_154	H, D_ASN_154	2.82	1.85	7.63
1HGE.PDB	O, D_SER_151	N, D_THR_156	H, D_THR_156	2.75	1.94	27.92
1HGE.PDB	OD1, D_ASN_154	OG1, D_THR_156	HG1, D_THR_156	2.74	1.81	12.51
1HGE.PDB	NE2, D_HIS_142	OH, D_TYR_157	HH, D_TYR_157	2.73	1.86	21.01
1HGE.PDB	OD1, D_ASP_158	N, D_ASP_160	H, D_ASP_160	2.84	1.98	23.52
1HGE.PDB	O, D_HIS_159	N, D_TYR_162	H, D_TYR_162	2.91	2.02	20.55
1HGE.PDB	O, D_ASP_160	N, D_ARG_163	H, D_ARG_163	2.99	2.03	9.92
1HGE.PDB	O, B_ARG_170	NH1, D_ARG_163	HH12, D_ARG_163	2.79	1.82	14.16
1HGE.PDB	O, D_TYR_162	N, D_ALA_166	H, D_ALA_166	2.87	1.90	5.91
1HGE.PDB	O, D_ARG_163	N, D_LEU_167	H, D_LEU_167	2.73	1.80	11.73
1HGE.PDB	O, D_ALA_166	N, D_ARG_170	H, D_ARG_170	2.84	1.97	22.00
1HGE.PDB	O, D_GLU_128	NE, D_ARG_170	HE, D_ARG_170	2.74	1.87	22.62
1HGE.PDB	OE2, D_GLU_131	NH1, D_ARG_170	HH11, D_ARG_170	2.79	1.79	6.83
1HGE.PDB	O, D_LEU_167	N, D_PHE_171	H, D_PHE_171	2.89	1.96	14.77
1HGE.PDB	O, F_ILE_140	N, E_ALA_11	H, E_ALA_11	2.82	1.93	19.79
1HGE.PDB	O, F_GLN_27	N, E_THR_12	H, E_THR_12	2.91	1.97	12.43
1HGE.PDB	O, F_PHE_138	N, E_LEU_13	H, E_LEU_13	2.98	2.03	12.93
1HGE.PDB	O, F_ARG_25	N, E_CYS_14	H, E_CYS_14	2.61	1.80	26.88
1HGE.PDB	O, F_GLY_136	N, E_LEU_15	H, E_LEU_15	2.88	1.90	5.56
1HGE.PDB	O, F_GLY_23	N, E_GLY_16	H, E_GLY_16	2.95	2.06	19.95
1HGE.PDB	O, E_HIS_18	ND1, E_HIS_17	HD1, E_HIS_17	2.98	2.10	22.18
1HGE.PDB	O, F_TRP_21	N, E_HIS_18	H, E_HIS_18	2.85	1.97	21.43
1HGE.PDB	OD1, E_ASN_322	N, E_VAL_20	H, E_VAL_20	2.81	1.86	11.30
1HGE.PDB	O, E_VAL_36	N, E_THR_24	H, E_THR_24	2.83	1.94	19.47
1HGE.PDB	O, E_ILE_34	N, E_VAL_26	H, E_VAL_26	2.83	1.88	11.74
1HGE.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.79	1.77	9.75
1HGE.PDB	O, E_LYS_27	OG1, E_THR_28	HG1, E_THR_28	2.99	2.20	29.66
1HGE.PDB	O, E_VAL_26	N, E_ILE_34	H, E_ILE_34	2.89	1.94	12.30
1HGE.PDB	O, E_THR_24	N, E_VAL_36	H, E_VAL_36	2.81	1.85	9.59
1HGE.PDB	O, E_MET_320	N, E_THR_37	H, E_THR_37	2.89	1.91	5.80
1HGE.PDB	O, E_LEU_316	N, E_THR_40	H, E_THR_40	2.78	1.93	24.64
1HGE.PDB	O, E_LEU_314	N, E_LEU_42	H, E_LEU_42	2.80	1.97	26.27

1HGE.PDB	O, E_PHE.294	N, E_GLN.44	H, E_GLN.44	2.81	1.85	6.62
1HGE.PDB	O, E_SER.46	NE2, E_GLN.44	HE22, E_GLN.44	2.85	1.98	22.39
1HGE.PDB	O, E_ASN.285	OG, E_SER.47	HG, E_SER.47	2.87	1.96	16.37
1HGE.PDB	OD2, E_ASP.275	NZ, E_LYS.50	HZ1, E_LYS.50	2.73	1.80	21.86
1HGE.PDB	O, E_PRO.273	N, E_ILE.51	H, E_ILE.51	2.78	1.85	13.53
1HGE.PDB	O, E_ASP.275	N, E_ASN.53	H, E_ASN.53	2.78	1.91	23.30
1HGE.PDB	OD2, E_ASP.85	N, E_ARG.57	H, E_ARG.57	2.91	1.97	12.45
1HGE.PDB	O, E_THR.83	NE, E_ARG.57	HE, E_ARG.57	2.83	1.86	9.17
1HGE.PDB	O, E_LEU.86	N, E_LEU.59	H, E_LEU.59	2.93	1.97	10.59
1HGE.PDB	O, E_VAL.88	N, E_GLY.61	H, E_GLY.61	2.95	2.10	25.32
1HGE.PDB	OD1, E_ASP.60	N, E_ILE.62	H, E_ILE.62	2.86	1.93	15.29
1HGE.PDB	O, E_GLY.61	N, E_CYS.64	H, E_CYS.64	2.87	1.96	17.48
1HGE.PDB	O, E_LEU.66	N, E_LEU.70	H, E_LEU.70	2.86	1.97	20.45
1HGE.PDB	O, E_ILE.67	N, E_LEU.71	H, E_LEU.71	2.83	1.87	6.72
1HGE.PDB	O, E_ASP.68	N, E_GLY.72	H, E_GLY.72	2.87	1.96	17.08
1HGE.PDB	OD1, E_ASP.73	ND1, E_HIS.75	HD1, E_HIS.75	2.77	1.85	16.90
1HGE.PDB	O, E_ASP.63	NE2, E_HIS.75	HE2, E_HIS.75	2.86	1.94	17.47
1HGE.PDB	O, E_ASP.73	N, E_CYS.76	H, E_CYS.76	2.76	1.81	11.37
1HGE.PDB	O, E_PRO.74	N, E_ASP.77	H, E_ASP.77	2.86	1.91	10.86
1HGE.PDB	O, E_CYS.76	N, E_PHE.79	H, E_PHE.79	2.97	1.99	3.02
1HGE.PDB	OE1, E_GLU.82	N, E_THR.83	H, E_THR.83	2.88	1.98	19.27
1HGE.PDB	O, E_ARG.57	N, E_ASP.85	H, E_ASP.85	2.78	1.89	19.36
1HGE.PDB	O, E_LEU.59	N, E_VAL.88	H, E_VAL.88	2.96	1.98	5.16
1HGE.PDB	O, E_MET.268	N, E_GLU.89	H, E_GLU.89	2.77	1.81	8.69
1HGE.PDB	OD1, E_ASP.60	NE, E_ARG.90	HE, E_ARG.90	2.88	1.91	8.59
1HGE.PDB	O, E_SER.270	NH1, E_ARG.90	HH11, E_ARG.90	2.63	1.77	25.17
1HGE.PDB	O, E_ALA.272	NH1, E_ARG.90	HH12, E_ARG.90	2.61	1.68	16.51
1HGE.PDB	OD2, E_ASP.60	NH2, E_ARG.90	HH21, E_ARG.90	2.80	1.80	8.94
1HGE.PDB	OD1, E_ASP.271	N, E_SER.91	H, E_SER.91	2.89	1.92	7.24
1HGE.PDB	OD2, E_ASP.271	OG, E_SER.91	HG, E_SER.91	2.83	1.92	17.26
1HGE.PDB	OD2, E_ASP.68	OG, E_SER.95	HG, E_SER.95	2.91	1.97	13.28
1HGE.PDB	OD2, E_ASP.73	N, E_ASN.96	H, E_ASN.96	2.90	1.94	8.49
1HGE.PDB	OD1, E_ASP.68	OH, E_TYR.100	HH, E_TYR.100	2.88	1.95	14.25
1HGE.PDB	OD2, E_ASP.104	OG, E_SER.107	HG, E_SER.107	2.86	1.93	15.15
1HGE.PDB	O, E_TYR.105	N, E_ARG.109	H, E_ARG.109	2.86	1.88	1.80
1HGE.PDB	OE2, F_GLU.67	NH2, E_ARG.109	HH21, E_ARG.109	2.78	1.79	11.63
1HGE.PDB	OD2, D_ASP.79	OG, E_SER.110	HG, E_SER.110	2.82	1.89	14.19
1HGE.PDB	O, E_SER.107	N, E_LEU.111	H, E_LEU.111	2.87	1.89	3.10
1HGE.PDB	O, E_ARG.109	N, E_ALA.113	H, E_ALA.113	2.93	2.03	20.07
1HGE.PDB	O, E_SER.110	N, E_SER.114	H, E_SER.114	2.88	1.93	13.24
1HGE.PDB	OE2, E_GLU.119	OG1, E_THR.117	HG1, E_THR.117	2.93	1.97	8.29
1HGE.PDB	O, E_GLU.82	N, E_LEU.118	H, E_LEU.118	2.98	2.05	15.39
1HGE.PDB	O, E_TYR.257	N, E_ILE.121	H, E_ILE.121	2.89	1.92	6.39
1HGE.PDB	O, E_ARG.255	N, E_GLU.123	H, E_GLU.123	2.92	1.96	10.72
1HGE.PDB	O, E_THR.155	N, E_THR.131	H, E_THR.131	2.77	1.88	19.94
1HGE.PDB	OD1, E_ASN.152	N, E_ASN.133	H, E_ASN.133	2.90	1.97	15.58
1HGE.PDB	O, E_TRP.153	N, E_GLY.134	H, E_GLY.134	2.95	2.06	19.92
1HGE.PDB	O, E_GLY.146	N, E_SER.136	H, E_SER.136	2.84	1.87	9.56
1HGE.PDB	OG, E_SER.136	N, E_ALA.138	H, E_ALA.138	2.99	2.05	13.25
1HGE.PDB	O, E_GLY.144	NZ, E_LYS.140	HZ1, E_LYS.140	2.71	1.74	16.73
1HGE.PDB	OD1, E_ASN.137	NZ, E_LYS.140	HZ2, E_LYS.140	2.84	1.86	16.83
1HGE.PDB	OD2, E_ASP.77	NE, E_ARG.141	HE, E_ARG.141	2.80	1.96	26.48
1HGE.PDB	O, E_PHE.147	NH1, E_ARG.141	HH12, E_ARG.141	2.55	1.62	17.30
1HGE.PDB	OD1, E_ASP.77	NH2, E_ARG.141	HH21, E_ARG.141	2.91	2.00	21.55
1HGE.PDB	OD2, E_ASP.77	NH2, E_ARG.141	HH21, E_ARG.141	2.75	1.87	24.36
1HGE.PDB	O, E_GLY.72	NH2, E_ARG.141	HH22, E_ARG.141	2.92	1.95	12.66
1HGE.PDB	O, E_GLY.72	N, E_SER.149	H, E_SER.149	2.84	1.93	17.58
1HGE.PDB	OD1, E_ASP.77	OG, E_SER.149	HG, E_SER.149	2.99	2.14	24.93

1HGE.PDB	O, E_ALA_253	N, E_ASN_152	H, E_ASN_152	2.82	1.95	22.18
1HGE.PDB	OH, E_TYR_195	NE1, E_TRP_153	HE1, E_TRP_153	2.90	1.99	18.82
1HGE.PDB	O, E_LEU_194	N, E_LYS_156	H, E_LYS_156	2.96	2.06	18.56
1HGE.PDB	O, E_SER_193	NZ, E_LYS_156	HZ2, E_LYS_156	2.79	1.81	17.51
1HGE.PDB	O, E_THR_160	N, E_SER_157	H, E_SER_157	2.99	2.08	19.06
1HGE.PDB	O, E_SER_247	N, E_LEU_164	H, E_LEU_164	2.69	1.86	25.19
1HGE.PDB	O, E_ILE_245	N, E_VAL_166	H, E_VAL_166	2.91	1.96	12.45
1HGE.PDB	O, E_LEU_243	OG1, E_THR_167	HG1, E_THR_167	2.92	2.05	21.37
1HGE.PDB	O, E_LEU_243	N, E_MET_168	H, E_MET_168	2.94	2.02	16.59
1HGE.PDB	O, E_ASP_241	N, E_ASN_170	H, E_ASN_170	2.92	1.94	6.42
1HGE.PDB	O, E_PHE_174	ND2, E_ASN_170	HD21, E_ASN_170	2.85	1.88	8.67
1HGE.PDB	O, E_VAL_237	ND2, E_ASN_170	HD22, E_ASN_170	2.84	2.05	29.41
1HGE.PDB	O, E_VAL_237	N, E_LYS_176	H, E_LYS_176	2.97	2.04	15.22
1HGE.PDB	OE2, E_GLU_123	NZ, E_LYS_176	HZ1, E_LYS_176	2.73	1.81	23.24
1HGE.PDB	O, E_PHE_258	N, E_LEU_177	H, E_LEU_177	2.99	2.02	5.44
1HGE.PDB	O, E_THR_235	N, E_TYR_178	H, E_TYR_178	2.85	1.89	6.94
1HGE.PDB	OE1, E_GLU_123	OH, E_TYR_178	HH, E_TYR_178	2.75	1.82	12.06
1HGE.PDB	O, E_TYR_233	N, E_TRP_180	H, E_TRP_180	2.98	2.01	9.33
1HGE.PDB	OG1, E_THR_235	NE1, E_TRP_180	HE1, E_TRP_180	2.93	1.94	2.48
1HGE.PDB	O, E_ASN_250	N, E_HIS_183	H, E_HIS_183	2.93	2.02	18.57
1HGE.PDB	O, E_ARG_229	N, E_HIS_184	H, E_HIS_184	2.91	1.95	9.81
1HGE.PDB	OG, E_SER_231	NE2, E_HIS_184	HE2, E_HIS_184	2.75	1.91	25.72
1HGE.PDB	OG1, E_THR_187	N, E_GLU_190	H, E_GLU_190	3.00	2.05	12.79
1HGE.PDB	O, E_GLN_197	NE2, E_GLN_191	HE22, E_GLN_191	2.96	2.04	16.74
1HGE.PDB	O, E_GLN_189	N, E_SER_193	H, E_SER_193	2.85	1.87	3.50
1HGE.PDB	O, E_GLU_190	N, E_LEU_194	H, E_LEU_194	2.96	2.00	9.57
1HGE.PDB	O, E_GLN_191	N, E_TYR_195	H, E_TYR_195	2.77	1.82	10.43
1HGE.PDB	O, E_TYR_161	NE2, E_GLN_197	HE21, E_GLN_197	2.88	1.92	10.46
1HGE.PDB	O, E_ASN_248	NE2, E_GLN_197	HE22, E_GLN_197	2.96	2.02	14.87
1HGE.PDB	OD1, E_ASN_246	NH2, E_ARG_201	HH21, E_ARG_201	2.61	1.75	25.36
1HGE.PDB	O, E_ILE_213	N, E_VAL_202	H, E_VAL_202	2.98	2.03	12.89
1HGE.PDB	O, E_ASN_246	N, E_THR_203	H, E_THR_203	2.89	1.93	9.46
1HGE.PDB	OG1, E_THR_212	OG1, E_THR_203	HG1, E_THR_203	2.89	1.95	10.14
1HGE.PDB	O, E_GLN_211	N, E_VAL_204	H, E_VAL_204	2.86	1.96	18.79
1HGE.PDB	OD1, E_ASP_241	N, E_ARG_207	H, E_ARG_207	2.88	1.92	9.18
1HGE.PDB	OG1, E_THR_206	OG, E_SER_209	HG, E_SER_209	2.98	2.04	10.06
1HGE.PDB	OD1, C_ASP_101	NE2, E_GLN_210	HE22, E_GLN_210	2.89	2.04	25.02
1HGE.PDB	O, E_VAL_204	N, E_GLN_211	H, E_GLN_211	2.84	1.92	15.49
1HGE.PDB	O, E_VAL_202	N, E_ILE_213	H, E_ILE_213	2.85	1.92	15.02
1HGE.PDB	ND1, E_HIS_184	N, E_ASN_216	H, E_ASN_216	2.79	1.98	28.16
1HGE.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.74	1.87	25.04
1HGE.PDB	O, E_ASN_216	NH2, E_ARG_220	HH22, E_ARG_220	2.66	1.79	23.30
1HGE.PDB	O, E_LEU_226	N, E_VAL_223	H, E_VAL_223	2.87	1.91	9.50
1HGE.PDB	O, E_CYS_97	NE, E_ARG_224	HE, E_ARG_224	2.88	2.06	27.97
1HGE.PDB	O, E_CYS_97	NH2, E_ARG_224	HH21, E_ARG_224	2.81	1.92	22.85
1HGE.PDB	O, E_VAL_223	N, E_LEU_226	H, E_LEU_226	2.92	1.97	11.57
1HGE.PDB	O, E_SER_228	NH1, E_ARG_229	HH11, E_ARG_229	2.68	1.75	17.61
1HGE.PDB	O, E_PRO_221	NH2, E_ARG_229	HH22, E_ARG_229	2.62	1.67	14.07
1HGE.PDB	OD1, E_ASP_101	OG, E_SER_231	HG, E_SER_231	2.87	1.92	12.10
1HGE.PDB	O, E_ASP_101	N, E_ILE_232	H, E_ILE_232	2.95	2.02	16.05
1HGE.PDB	O, E_TRP_180	N, E_TYR_233	H, E_TYR_233	2.88	1.91	8.62
1HGE.PDB	O, E_TYR_178	N, E_THR_235	H, E_THR_235	2.87	1.96	17.45
1HGE.PDB	O, E_LYS_176	N, E_VAL_237	H, E_VAL_237	2.79	1.88	17.98
1HGE.PDB	O, D_SER_71	NZ, E_LYS_238	HZ2, E_LYS_238	2.75	1.79	18.19
1HGE.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ3, E_LYS_238	2.85	1.84	12.25
1HGE.PDB	O, E_ASN_170	N, E_GLY_240	H, E_GLY_240	2.89	2.02	22.60
1HGE.PDB	O, E_LYS_238	N, E_ASP_241	H, E_ASP_241	2.92	1.99	13.81
1HGE.PDB	OD1, E_ASP_241	N, E_VAL_242	H, E_VAL_242	2.79	1.97	26.69

1HGE.PDB	O, E_MET_168	N, E_LEU_243	H, E_LEU_243	2.88	1.91	4.05
1HGE.PDB	O, E_SER_205	N, E_VAL_244	H, E_VAL_244	2.98	2.03	12.64
1HGE.PDB	O, E_VAL_166	N, E_ILE_245	H, E_ILE_245	2.88	1.95	14.55
1HGE.PDB	O, E_THR_203	N, E_ASN_246	H, E_ASN_246	2.93	1.96	6.89
1HGE.PDB	OD1, E_ASN_165	ND2, E_ASN_246	HD22, E_ASN_246	2.88	1.93	12.25
1HGE.PDB	O, E_LEU_164	N, E_SER_247	H, E_SER_247	2.96	2.05	17.92
1HGE.PDB	O, E_ARG_201	OG, E_SER_247	HG, E_SER_247	2.74	1.94	28.66
1HGE.PDB	OE1, E_GLN_191	ND2, E_ASN_250	HD21, E_ASN_250	2.94	1.97	8.28
1HGE.PDB	O, E_HIS_183	ND2, E_ASN_250	HD22, E_ASN_250	2.89	1.94	10.81
1HGE.PDB	O, E_ASN_152	N, E_ALA_253	H, E_ALA_253	2.87	2.00	21.77
1HGE.PDB	OD1, E_ASN_133	NH2, E_ARG_255	HH22, E_ARG_255	2.49	1.68	28.65
1HGE.PDB	O, E_ILE_121	N, E_TYR_257	H, E_TYR_257	3.00	2.15	25.48
1HGE.PDB	O, E_LEU_177	N, E_PHE_258	H, E_PHE_258	2.95	1.98	4.40
1HGE.PDB	OE2, E_GLU_119	NH1, E_ARG_261	HH12, E_ARG_261	2.65	1.81	27.82
1HGE.PDB	OE1, E_GLU_119	NH2, E_ARG_261	HH22, E_ARG_261	2.83	1.95	24.52
1HGE.PDB	OD2, E_ASP_85	NZ, E_LYS_264	HZ3, E_LYS_264	2.81	1.83	16.30
1HGE.PDB	O, E_PHE_87	N, E_MET_268	H, E_MET_268	2.79	1.90	20.72
1HGE.PDB	O, E_PRO_284	OG, E_SER_270	HG, E_SER_270	2.79	1.86	13.35
1HGE.PDB	OG, E_SER_270	N, E_ALA_272	H, E_ALA_272	2.97	2.02	11.52
1HGE.PDB	O, E_ILE_51	N, E_ASP_275	H, E_ASP_275	2.97	2.07	20.34
1HGE.PDB	OD1, E_ASP_275	N, E_THR_276	H, E_THR_276	2.78	1.93	23.65
1HGE.PDB	O, E_ASN_54	N, E_SER_279	H, E_SER_279	2.80	1.87	14.21
1HGE.PDB	O, E_TYR_302	N, E_ILE_282	H, E_ILE_282	2.89	1.92	7.96
1HGE.PDB	O, E_THR_283	N, E_GLY_286	H, E_GLY_286	2.82	1.88	11.76
1HGE.PDB	O, E_LYS_50	N, E_SER_287	H, E_SER_287	2.88	1.91	4.05
1HGE.PDB	O, E_ALA_304	ND2, E_ASN_290	HD22, E_ASN_290	2.85	1.96	19.63
1HGE.PDB	OE1, E_GLN_44	NZ, E_LYS_292	HZ1, E_LYS_292	2.72	1.72	11.93
1HGE.PDB	OD2, E_ASP_291	NZ, E_LYS_292	HZ3, E_LYS_292	2.84	1.89	19.87
1HGE.PDB	O, E_LYS_307	N, E_GLN_295	H, E_GLN_295	2.82	1.93	20.26
1HGE.PDB	O, E_ASN_298	NE2, E_GLN_295	HE21, E_GLN_295	2.75	1.80	8.98
1HGE.PDB	O, E_GLN_44	N, E_ASN_296	H, E_ASN_296	2.82	1.88	13.69
1HGE.PDB	OE1, E_GLN_295	N, E_VAL_297	H, E_VAL_297	2.67	1.86	27.79
1HGE.PDB	OD1, E_ASN_285	ND2, E_ASN_298	HD22, E_ASN_298	2.98	2.04	13.10
1HGE.PDB	O, F_LYS_68	NZ, E_LYS_299	HZ2, E_LYS_299	2.95	1.93	11.73
1HGE.PDB	OD1, E_ASN_298	N, E_ILE_300	H, E_ILE_300	2.89	1.97	16.82
1HGE.PDB	O, E_ILE_282	N, E_TYR_302	H, E_TYR_302	2.94	2.07	23.45
1HGE.PDB	O, F_LYS_62	N, E_GLY_303	H, E_GLY_303	2.95	1.98	8.29
1HGE.PDB	OG, F_SER_93	N, E_LYS_310	H, E_LYS_310	2.93	1.97	10.15
1HGE.PDB	OD1, F_ASP_86	NZ, E_LYS_310	HZ3, E_LYS_310	2.86	2.02	29.64
1HGE.PDB	OE2, E_GLU_41	N, E_LEU_314	H, E_LEU_314	2.81	1.89	15.15
1HGE.PDB	OE1, E_GLU_41	NZ, E_LYS_315	HZ3, E_LYS_315	2.80	1.87	22.54
1HGE.PDB	O, E_THR_40	N, E_LEU_316	H, E_LEU_316	2.80	1.85	9.95
1HGE.PDB	OD1, F_ASN_104	N, E_ALA_317	H, E_ALA_317	2.73	1.80	13.22
1HGE.PDB	O, E_ASN_38	N, E_THR_318	H, E_THR_318	2.85	1.93	15.97
1HGE.PDB	O, E_VAL_20	ND2, E_ASN_322	HD21, E_ASN_322	2.99	2.07	17.11
1HGE.PDB	OE2, E_GLU_35	ND2, E_ASN_322	HD22, E_ASN_322	2.87	1.98	21.90
1HGE.PDB	O, E_GLN_327	NZ, E_LYS_326	HZ1, E_LYS_326	2.74	1.86	25.33
1HGE.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.99	2.00	17.08
1HGE.PDB	O, E_LYS_326	NE2, E_GLN_327	HE22, E_GLN_327	2.76	1.89	22.95
1HGE.PDB	OD2, F_ASP_112	N, F_GLY_1	H2, F_GLY_1	2.78	1.80	14.95
1HGE.PDB	OD1, F_ASP_109	N, F_LEU_2	H, F_LEU_2	2.80	1.91	20.53
1HGE.PDB	OD2, F_ASP_112	N, F_GLY_4	H, F_GLY_4	2.92	2.04	21.78
1HGE.PDB	OD1, F_ASP_112	N, F_ALA_5	H, F_ALA_5	2.92	2.02	19.47
1HGE.PDB	O, F_GLY_4	N, F_PHE_9	H, F_PHE_9	2.81	1.87	11.92
1HGE.PDB	O, F_GLY_13	ND2, F_ASN_12	HD22, F_ASN_12	2.79	1.96	26.47
1HGE.PDB	O, E_VAL_323	N, F_GLY_13	H, F_GLY_13	2.72	1.79	12.93
1HGE.PDB	O, E_HIS_17	N, F_TRP_14	H, F_TRP_14	2.85	1.91	12.63
1HGE.PDB	OG1, F_THR_41	N, F_TRP_21	H, F_TRP_21	2.88	1.97	17.81

1HGE.PDB	O, E_GLY_16	N, F_GLY_23	H, F_GLY_23	2.91	2.01	19.90
1HGE.PDB	O, F_ALA_35	N, F_PHE_24	H, F_PHE_24	2.82	1.85	3.58
1HGE.PDB	O, E_CYS_14	N, F_ARG_25	H, F_ARG_25	2.88	1.93	12.79
1HGE.PDB	OE1, F_GLN_34	NE, F_ARG_25	HE, F_ARG_25	2.92	2.07	24.83
1HGE.PDB	OE1, F_GLN_34	NH2, F_ARG_25	HH21, F_ARG_25	2.81	1.90	20.25
1HGE.PDB	O, F_GLY_33	N, F_HIS_26	H, F_HIS_26	2.96	2.07	20.60
1HGE.PDB	O, E_THR_12	N, F_GLN_27	H, F_GLN_27	2.82	1.90	16.16
1HGE.PDB	O, F_GLY_31	N, F_ASN_28	H, F_ASN_28	2.84	1.88	9.14
1HGE.PDB	OD1, F_ASN_146	ND2, F_ASN_28	HD21, F_ASN_28	2.81	1.89	15.75
1HGE.PDB	O, F_CYS_144	ND2, F_ASN_28	HD22, F_ASN_28	2.90	1.97	14.42
1HGE.PDB	O, F_ASN_28	N, F_GLY_31	H, F_GLY_31	2.92	2.08	25.93
1HGE.PDB	O, F_PHE_24	N, F_ALA_35	H, F_ALA_35	2.77	1.97	29.32
1HGE.PDB	O, F_TYR_22	N, F_ASP_37	H, F_ASP_37	2.73	1.79	11.31
1HGE.PDB	OD2, F_ASP_37	N, F_SER_40	H, F_SER_40	2.89	1.93	8.53
1HGE.PDB	OD2, F_ASP_37	OG, F_SER_40	HG, F_SER_40	2.76	1.94	26.96
1HGE.PDB	O, F_ASP_37	OG1, F_THR_41	HG1, F_THR_41	2.69	1.84	22.88
1HGE.PDB	O, F_LEU_38	N, F_GLN_42	H, F_GLN_42	2.83	1.92	17.33
1HGE.PDB	OD1, F_ASP_46	NE2, F_GLN_42	HE22, F_GLN_42	2.86	1.96	19.38
1HGE.PDB	O, F_LYS_39	N, F_ALA_43	H, F_ALA_43	2.93	1.98	9.94
1HGE.PDB	O, F_SER_40	N, F_ALA_44	H, F_ALA_44	2.92	1.94	4.84
1HGE.PDB	O, F_GLN_42	N, F_ASP_46	H, F_ASP_46	2.81	1.84	1.16
1HGE.PDB	OE2, F_GLU_114	NE2, F_GLN_47	HE21, F_GLN_47	3.00	2.09	17.78
1HGE.PDB	O, F_ALA_43	NE2, F_GLN_47	HE22, F_GLN_47	2.91	2.00	18.24
1HGE.PDB	O, F_ILE_45	N, F_ASN_49	H, F_ASN_49	2.83	1.89	13.28
1HGE.PDB	O, F_ASP_46	N, F_GLY_50	H, F_GLY_50	2.83	1.91	17.15
1HGE.PDB	OG1, F_THR_107	NZ, F_LYS_51	HZ1, F_LYS_51	2.97	2.00	18.12
1HGE.PDB	OE1, F_GLU_103	NZ, F_LYS_51	HZ2, F_LYS_51	2.77	1.74	6.40
1HGE.PDB	ND1, F_HIS_106	NZ, F_LYS_51	HZ3, F_LYS_51	2.74	1.79	17.89
1HGE.PDB	O, F_ILE_48	N, F_LEU_52	H, F_LEU_52	2.89	1.97	17.49
1HGE.PDB	O, F_ASN_49	N, F_ASN_53	H, F_ASN_53	2.78	1.88	17.70
1HGE.PDB	OE1, F_GLU_57	NH1, F_ARG_54	HH11, F_ARG_54	2.82	1.83	11.59
1HGE.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.80	1.82	12.52
1HGE.PDB	OD2, D_ASP_90	NZ, F_LYS_62	HZ2, F_LYS_62	2.67	1.83	29.15
1HGE.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.94	1.97	9.11
1HGE.PDB	O, E_LYS_299	NZ, F_LYS_68	HZ1, F_LYS_68	2.97	1.93	4.62
1HGE.PDB	OE2, F_GLU_85	NZ, F_LYS_68	HZ2, F_LYS_68	2.75	1.78	18.51
1HGE.PDB	OG, A_SER_107	N, F_ARG_76	H, F_ARG_76	2.81	1.83	4.38
1HGE.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.85	1.89	11.64
1HGE.PDB	OE2, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.73	1.73	6.19
1HGE.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.65	1.66	5.51
1HGE.PDB	OE1, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.70	1.73	9.07
1HGE.PDB	OE1, F_GLU_74	NE2, F_GLN_78	HE22, F_GLN_78	2.96	1.99	8.87
1HGE.PDB	O, F_GLY_75	N, F_ASP_79	H, F_ASP_79	2.92	1.98	13.37
1HGE.PDB	O, F_ILE_77	N, F_GLU_81	H, F_GLU_81	2.95	1.99	8.53
1HGE.PDB	O, F_ASP_79	N, F_TYR_83	H, F_TYR_83	2.94	2.02	17.09
1HGE.PDB	OE1, B_GLU_85	OH, F_TYR_83	HH, F_TYR_83	2.51	1.76	30.00
1HGE.PDB	O, F_LEU_80	N, F_VAL_84	H, F_VAL_84	2.83	1.87	8.33
1HGE.PDB	O, F_LYS_82	N, F_ASP_86	H, F_ASP_86	2.92	1.97	11.17
1HGE.PDB	O, F_TYR_83	N, F_THR_87	H, F_THR_87	2.93	1.97	9.90
1HGE.PDB	O, F_VAL_84	N, F_LYS_88	H, F_LYS_88	2.95	2.01	12.83
1HGE.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.67	1.65	8.34
1HGE.PDB	O, F_GLU_85	N, F_ILE_89	H, F_ILE_89	2.92	1.94	4.91
1HGE.PDB	O, F_LYS_88	N, F_TRP_92	H, F_TRP_92	2.97	2.00	5.01
1HGE.PDB	O, F_ILE_89	N, F_SER_93	H, F_SER_93	2.84	1.93	17.22
1HGE.PDB	O, F_ILE_89	OG, F_SER_93	HG, F_SER_93	2.85	1.93	13.60
1HGE.PDB	O, F_ASP_90	N, F_TYR_94	H, F_TYR_94	2.85	1.93	16.45
1HGE.PDB	O, F_TYR_94	N, F_LEU_98	H, F_LEU_98	2.97	1.99	3.80
1HGE.PDB	O, F_ASN_95	N, F_LEU_99	H, F_LEU_99	2.92	1.99	14.65

1HGE.PDB	O, F_LEU_98	N, F_LEU_102	H, F_LEU_102	2.96	1.98	4.54
1HGE.PDB	O, F_LEU_99	N, F_GLU_103	H, F_GLU_103	2.90	1.93	9.01
1HGE.PDB	O, F_VAL_100	N, F_ASN_104	H, F_ASN_104	2.88	1.94	12.72
1HGE.PDB	O, E_LYS_27	ND2, F_ASN_104	HD22, F_ASN_104	2.94	1.99	10.01
1HGE.PDB	O, F_LEU_102	N, F_HIS_106	H, F_HIS_106	2.93	1.98	10.60
1HGE.PDB	O, F_GLU_103	N, F_THR_107	H, F_THR_107	2.85	1.95	19.04
1HGE.PDB	O, F_ASN_104	N, F_ILE_108	H, F_ILE_108	2.91	1.95	10.63
1HGE.PDB	O, F_HIS_106	N, F_LEU_110	H, F_LEU_110	2.81	1.84	7.77
1HGE.PDB	O, F_THR_107	OG1, F_THR_111	HG1, F_THR_111	2.90	1.93	1.70
1HGE.PDB	O, F_ASP_109	N, F_SER_113	H, F_SER_113	2.83	1.87	8.23
1HGE.PDB	O, F_LEU_110	N, F_GLU_114	H, F_GLU_114	2.90	1.94	9.48
1HGE.PDB	O, F_SER_113	N, F_LYS_117	H, F_LYS_117	2.79	1.89	18.58
1HGE.PDB	O, F_GLU_114	N, F_LEU_118	H, F_LEU_118	2.97	2.01	10.63
1HGE.PDB	O, F_ASN_116	N, F_GLU_120	H, F_GLU_120	2.93	1.96	5.04
1HGE.PDB	O, F_LYS_117	N, F_LYS_121	H, F_LYS_121	2.93	2.01	16.80
1HGE.PDB	O, F_PHE_119	N, F_ARG_123	H, F_ARG_123	2.92	1.96	9.49
1HGE.PDB	OE2, F_GLU_120	NH1, F_ARG_123	HH11, F_ARG_123	2.81	1.92	23.28
1HGE.PDB	O, F_GLU_120	N, F_ARG_124	H, F_ARG_124	2.97	2.00	7.42
1HGE.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.92	2.09	27.36
1HGE.PDB	O, F_LEU_126	N, F_ASN_129	H, F_ASN_129	2.94	2.00	13.52
1HGE.PDB	O, F_HIS_159	ND2, F_ASN_129	HD21, F_ASN_129	2.95	2.00	10.63
1HGE.PDB	OH, F_TYR_157	ND2, F_ASN_129	HD22, F_ASN_129	2.80	1.87	15.30
1HGE.PDB	O, F_LYS_139	N, F_GLU_131	H, F_GLU_131	2.96	2.04	15.90
1HGE.PDB	O, F_CYS_137	N, F_MET_133	H, F_MET_133	2.88	1.92	10.66
1HGE.PDB	O, E_LEU_13	N, F_PHE_138	H, F_PHE_138	2.73	1.86	22.03
1HGE.PDB	O, F_GLU_131	N, F_LYS_139	H, F_LYS_139	2.82	1.86	10.37
1HGE.PDB	O, E_ALA_11	N, F_ILE_140	H, F_ILE_140	2.75	1.87	19.65
1HGE.PDB	O, F_ASN_129	N, F_TYR_141	H, F_TYR_141	2.90	1.98	16.42
1HGE.PDB	O, F_ASP_145	N, F_ILE_149	H, F_ILE_149	2.91	1.95	10.01
1HGE.PDB	O, F_ASN_146	N, F_GLU_150	H, F_GLU_150	2.93	1.99	14.06
1HGE.PDB	O, F_ALA_147	N, F_SER_151	H, F_SER_151	2.92	2.06	23.67
1HGE.PDB	O, F_CYS_148	OG, F_SER_151	HG, F_SER_151	2.68	1.84	23.64
1HGE.PDB	O, F_GLU_150	N, F_ASN_154	H, F_ASN_154	2.79	1.81	1.42
1HGE.PDB	OD1, F_ASP_158	N, F_ASP_160	H, F_ASP_160	2.88	2.02	24.16
1HGE.PDB	O, F_HIS_159	N, F_TYR_162	H, F_TYR_162	2.92	2.01	17.85
1HGE.PDB	O, D_ARG_170	NH1, F_ARG_163	HH12, F_ARG_163	2.95	1.99	14.32
1HGE.PDB	O, F_TYR_162	N, F_ALA_166	H, F_ALA_166	2.88	1.91	5.83
1HGE.PDB	O, F_ARG_163	N, F_LEU_167	H, F_LEU_167	2.74	1.79	10.43
1HGE.PDB	O, F_ALA_166	N, F_ARG_170	H, F_ARG_170	2.84	1.99	23.33
1HGE.PDB	O, F_GLU_128	NE, F_ARG_170	HE, F_ARG_170	2.74	1.87	22.99
1HGE.PDB	OE2, F_GLU_131	NH1, F_ARG_170	HH11, F_ARG_170	2.78	1.79	6.04
1HGE.PDB	O, F_LEU_167	N, F_PHE_171	H, F_PHE_171	2.91	1.98	14.72
1HGF.PDB	O, B_ILE_140	N, A_ALA_11	H, A_ALA_11	2.90	2.03	22.48
1HGF.PDB	O, B_PHE_138	N, A_LEU_13	H, A_LEU_13	2.96	1.99	8.07
1HGF.PDB	O, B_ARG_25	N, A_CYS_14	H, A_CYS_14	2.98	2.02	8.89
1HGF.PDB	O, B_GLY_136	N, A_LEU_15	H, A_LEU_15	2.92	1.95	7.83
1HGF.PDB	O, B_GLY_23	N, A_GLY_16	H, A_GLY_16	2.92	2.03	19.80
1HGF.PDB	O, B_TRP_21	N, A_HIS_18	H, A_HIS_18	2.92	2.01	18.08
1HGF.PDB	OD1, A_ASN_322	N, A_VAL_20	H, A_VAL_20	2.80	1.83	7.05
1HGF.PDB	O, A_VAL_36	N, A_THR_24	H, A_THR_24	2.86	1.98	20.85
1HGF.PDB	O, A_ILE_34	N, A_VAL_26	H, A_VAL_26	2.85	1.90	12.10
1HGF.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.79	1.86	21.55
1HGF.PDB	O, A_ASP_31	N, A_THR_28	H, A_THR_28	2.70	1.89	28.68
1HGF.PDB	O, A_VAL_26	N, A_ILE_34	H, A_ILE_34	2.96	2.01	12.92
1HGF.PDB	O, A_THR_24	N, A_VAL_36	H, A_VAL_36	2.81	1.84	5.89
1HGF.PDB	O, A_MET_320	N, A_THR_37	H, A_THR_37	2.89	1.91	4.82
1HGF.PDB	O, A_LEU_316	N, A_THR_40	H, A_THR_40	2.76	1.85	17.44
1HGF.PDB	O, A_LEU_314	N, A_LEU_42	H, A_LEU_42	2.79	1.94	25.04

1HGF.PDB	O, A_PHE_294	N, A_GLN_44	H, A_GLN_44	2.99	2.01	3.16
1HGF.PDB	O, A_SER_46	NE2, A_GLN_44	HE21, A_GLN_44	2.84	1.96	21.79
1HGF.PDB	OD2, A_ASP_275	NZ, A_LYS_50	HZ2, A_LYS_50	2.91	1.91	15.13
1HGF.PDB	O, A_PRO_273	N, A_ILE_51	H, A_ILE_51	2.77	1.81	8.80
1HGF.PDB	O, A_ASP_275	N, A_ASN_53	H, A_ASN_53	2.88	1.94	13.18
1HGF.PDB	OD2, A_ASP_85	N, A_ARG_57	H, A_ARG_57	2.93	1.98	11.29
1HGF.PDB	O, A_THR_83	NE, A_ARG_57	HE, A_ARG_57	2.79	1.82	4.94
1HGF.PDB	O, A_LEU_86	N, A_LEU_59	H, A_LEU_59	2.87	1.93	13.63
1HGF.PDB	OD1, A_ASP_60	N, A_ILE_62	H, A_ILE_62	2.92	1.97	12.05
1HGF.PDB	O, A_GLY_61	N, A_CYS_64	H, A_CYS_64	2.90	1.96	15.17
1HGF.PDB	O, A_LEU_66	N, A_LEU_70	H, A_LEU_70	2.80	1.89	17.51
1HGF.PDB	O, A_ILE_67	N, A_LEU_71	H, A_LEU_71	2.92	1.94	5.50
1HGF.PDB	O, A_ASP_68	N, A_GLY_72	H, A_GLY_72	2.85	1.95	18.27
1HGF.PDB	OD1, A_ASP_73	N, A_HIS_75	H, A_HIS_75	2.98	2.09	20.20
1HGF.PDB	OD1, A_ASP_73	ND1, A_HIS_75	HD1, A_HIS_75	2.84	1.91	15.59
1HGF.PDB	O, A_ASP_63	NE2, A_HIS_75	HE2, A_HIS_75	2.88	1.95	16.02
1HGF.PDB	O, A_ASP_73	N, A_CYS_76	H, A_CYS_76	2.81	1.89	15.96
1HGF.PDB	O, A_PRO_74	N, A_ASP_77	H, A_ASP_77	2.94	1.99	11.05
1HGF.PDB	O, A_CYS_76	N, A_PHE_79	H, A_PHE_79	2.97	2.00	8.63
1HGF.PDB	OE1, A_GLU_82	N, A_THR_83	H, A_THR_83	2.98	2.09	20.75
1HGF.PDB	O, A_ARG_57	N, A_ASP_85	H, A_ASP_85	2.83	1.91	16.22
1HGF.PDB	O, A_MET_268	N, A_GLU_89	H, A_GLU_89	2.80	1.87	13.08
1HGF.PDB	OD1, A_ASP_60	NE, A_ARG_90	HE, A_ARG_90	2.77	1.85	16.11
1HGF.PDB	O, A_SER_270	NH1, A_ARG_90	HH11, A_ARG_90	2.64	1.79	25.97
1HGF.PDB	O, A_ALA_272	NH1, A_ARG_90	HH12, A_ARG_90	2.67	1.74	16.70
1HGF.PDB	OD2, A_ASP_60	NH2, A_ARG_90	HH21, A_ARG_90	2.84	1.84	8.73
1HGF.PDB	OD1, A_ASP_271	N, A_SER_91	H, A_SER_91	2.96	1.99	10.09
1HGF.PDB	OD2, A_ASP_271	OG, A_SER_91	HG, A_SER_91	2.85	1.91	12.59
1HGF.PDB	OD2, A_ASP_73	N, A_ASN_96	H, A_ASN_96	2.89	1.95	14.63
1HGF.PDB	O, A_ILE_230	N, A_ASP_101	H, A_ASP_101	2.99	2.15	25.68
1HGF.PDB	OD2, A_ASP_104	OG, A_SER_107	HG, A_SER_107	2.89	1.97	16.55
1HGF.PDB	O, A_TYR_105	N, A_ARG_109	H, A_ARG_109	2.87	1.89	3.75
1HGF.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.92	1.92	10.51
1HGF.PDB	OD2, F_ASP_79	OG, A_SER_110	HG, A_SER_110	2.82	1.90	15.87
1HGF.PDB	O, A_SER_107	N, A_LEU_111	H, A_LEU_111	2.96	2.00	9.75
1HGF.PDB	O, A_LEU_108	N, A_VAL_112	H, A_VAL_112	2.99	2.02	7.62
1HGF.PDB	O, A_ARG_109	N, A_ALA_113	H, A_ALA_113	2.92	2.00	16.71
1HGF.PDB	O, A_SER_110	N, A_SER_114	H, A_SER_114	2.94	2.06	21.84
1HGF.PDB	OE2, A_GLU_119	OG1, A_THR_117	HG1, A_THR_117	2.95	1.98	3.95
1HGF.PDB	O, A_GLU_82	N, A_LEU_118	H, A_LEU_118	2.98	2.00	4.41
1HGF.PDB	O, A_TYR_257	N, A_ILE_121	H, A_ILE_121	2.82	1.84	1.82
1HGF.PDB	O, A_ARG_255	N, A_GLU_123	H, A_GLU_123	2.84	1.88	9.80
1HGF.PDB	O, A_THR_155	N, A_THR_131	H, A_THR_131	2.73	1.79	9.00
1HGF.PDB	O, A_LYS_156	OG1, A_THR_131	HG1, A_THR_131	2.73	1.79	7.60
1HGF.PDB	ND2, A_ASN_152	NE2, A_GLN_132	HE21, A_GLN_132	2.94	2.00	10.26
1HGF.PDB	OD1, A_ASN_152	N, A_ASN_133	H, A_ASN_133	2.91	1.97	13.50
1HGF.PDB	O, A_TRP_153	N, A_GLY_134	H, A_GLY_134	3.00	2.07	15.59
1HGF.PDB	O, A_GLY_146	N, A_SER_136	H, A_SER_136	2.70	1.84	23.70
1HGF.PDB	O, A_GLY_144	NZ, A_LYS_140	HZ2, A_LYS_140	2.83	1.99	29.88
1HGF.PDB	O, A_GLY_144	N, A_ARG_141	H, A_ARG_141	2.92	2.09	26.49
1HGF.PDB	OD2, A_ASP_77	NE, A_ARG_141	HE, A_ARG_141	2.91	2.06	25.46
1HGF.PDB	O, A_PHE_147	NH1, A_ARG_141	HH12, A_ARG_141	2.58	1.65	16.41
1HGF.PDB	OD1, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.84	1.97	26.05
1HGF.PDB	OD2, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.78	1.86	20.91
1HGF.PDB	O, A_SER_136	N, A_GLY_146	H, A_GLY_146	2.98	2.14	25.61
1HGF.PDB	O, A_GLY_72	N, A_SER_149	H, A_SER_149	2.87	1.95	15.87
1HGF.PDB	O, A_ALA_253	N, A_ASN_152	H, A_ASN_152	2.85	1.95	19.48
1HGF.PDB	OH, A_TYR_195	NE1, A_TRP_153	HE1, A_TRP_153	2.84	1.90	13.02

1HGF.PDB	O, A_THR_131	N, A_THR_155	H, A_THR_155	2.99	2.03	10.01
1HGF.PDB	O, A_LEU_194	N, A_LYS_156	H, A_LYS_156	2.84	1.97	22.10
1HGF.PDB	O, A_THR_160	N, A_SER_157	H, A_SER_157	3.00	2.11	20.90
1HGF.PDB	O, A_SER_247	N, A_LEU_164	H, A_LEU_164	2.70	1.86	25.60
1HGF.PDB	O, A_ILE_245	N, A_VAL_166	H, A_VAL_166	2.89	1.93	10.88
1HGF.PDB	O, A_LEU_243	N, A_MET_168	H, A_MET_168	3.00	2.06	14.85
1HGF.PDB	O, A_ASP_241	N, A_ASN_170	H, A_ASN_170	2.88	1.90	0.71
1HGF.PDB	O, A_PHE_174	ND2, A_ASN_170	HD22, A_ASN_170	2.75	1.81	11.59
1HGF.PDB	O, A_VAL_237	N, A_LYS_176	H, A_LYS_176	2.94	2.04	19.01
1HGF.PDB	OE2, A_GLU_123	NZ, A_LYS_176	HZ1, A_LYS_176	2.72	1.80	23.85
1HGF.PDB	O, A_THR_235	N, A_TYR_178	H, A_TYR_178	2.82	1.85	7.11
1HGF.PDB	OG1, A_THR_235	NE1, A_TRP_180	HE1, A_TRP_180	2.87	1.89	5.46
1HGF.PDB	O, A_ASN_250	N, A_HIS_183	H, A_HIS_183	2.77	1.92	24.91
1HGF.PDB	OH, A_TYR_98	NE2, A_HIS_183	HE2, A_HIS_183	2.90	1.98	15.32
1HGF.PDB	O, A_ARG_229	N, A_HIS_184	H, A_HIS_184	2.84	1.88	9.30
1HGF.PDB	OG, A_SER_231	NE2, A_HIS_184	HE2, A_HIS_184	2.68	1.88	29.05
1HGF.PDB	OD1, A_ASN_250	NE2, A_GLN_191	HE22, A_GLN_191	2.90	1.94	8.27
1HGF.PDB	O, A_ASN_188	N, A_THR_192	H, A_THR_192	2.96	2.06	18.82
1HGF.PDB	O, A_GLN_189	N, A_SER_193	H, A_SER_193	2.83	1.90	13.84
1HGF.PDB	O, A_GLU_190	N, A_LEU_194	H, A_LEU_194	2.93	1.96	8.30
1HGF.PDB	O, A_GLN_191	N, A_TYR_195	H, A_TYR_195	2.75	1.81	10.35
1HGF.PDB	O, A_TYR_195	N, A_GLN_197	H, A_GLN_197	2.73	1.94	29.33
1HGF.PDB	O, A_ASN_248	NE2, A_GLN_197	HE21, A_GLN_197	2.87	2.00	23.13
1HGF.PDB	O, A_TYR_161	NE2, A_GLN_197	HE22, A_GLN_197	2.98	2.03	11.50
1HGF.PDB	O, A_ILE_213	N, A_VAL_202	H, A_VAL_202	2.99	2.02	6.97
1HGF.PDB	O, A_ASN_246	N, A_THR_203	H, A_THR_203	2.96	2.06	19.01
1HGF.PDB	O, A_GLN_211	N, A_VAL_204	H, A_VAL_204	2.92	1.99	15.84
1HGF.PDB	O, A_SER_209	N, A_THR_206	H, A_THR_206	2.95	2.03	15.35
1HGF.PDB	OD1, A_ASP_241	N, A_ARG_207	H, A_ARG_207	2.92	1.95	7.62
1HGF.PDB	O, A_VAL_204	N, A_GLN_211	H, A_GLN_211	2.87	1.98	21.25
1HGF.PDB	OG1, A_THR_203	OG1, A_THR_212	HG1, A_THR_212	2.83	1.91	15.11
1HGF.PDB	O, A_VAL_202	N, A_ILE_213	H, A_ILE_213	2.85	1.94	17.93
1HGF.PDB	ND1, A_HIS_184	N, A_ASN_216	H, A_ASN_216	2.73	1.89	25.27
1HGF.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.64	1.76	23.62
1HGF.PDB	O, A_ASN_216	NH2, A_ARG_220	HH22, A_ARG_220	2.77	1.87	21.15
1HGF.PDB	O, A_LEU_226	N, A_VAL_223	H, A_VAL_223	2.86	1.91	11.57
1HGF.PDB	O, A_CYS_97	NE, A_ARG_224	HE, A_ARG_224	2.81	1.94	23.65
1HGF.PDB	O, A_CYS_97	NH2, A_ARG_224	HH21, A_ARG_224	2.95	2.11	27.74
1HGF.PDB	O, A_VAL_223	N, A_LEU_226	H, A_LEU_226	2.93	1.98	11.09
1HGF.PDB	O, A_SER_228	NH1, A_ARG_229	HH11, A_ARG_229	2.75	1.83	19.84
1HGF.PDB	O, A_PRO_221	NH2, A_ARG_229	HH22, A_ARG_229	2.63	1.68	15.15
1HGF.PDB	O, A_PRO_99	N, A_ILE_230	H, A_ILE_230	2.95	2.09	24.07
1HGF.PDB	OD1, A_ASP_101	OG, A_SER_231	HG, A_SER_231	2.83	1.87	7.29
1HGF.PDB	O, A_ASP_101	N, A_ILE_232	H, A_ILE_232	2.89	1.95	14.12
1HGF.PDB	O, A_TRP_180	N, A_TYR_233	H, A_TYR_233	2.93	1.97	10.39
1HGF.PDB	O, A_TYR_178	N, A_THR_235	H, A_THR_235	2.85	1.97	21.16
1HGF.PDB	O, A_LYS_176	N, A_VAL_237	H, A_VAL_237	2.78	1.84	14.11
1HGF.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ2, A_LYS_238	2.85	1.85	14.58
1HGF.PDB	O, F_SER_71	NZ, A_LYS_238	HZ3, A_LYS_238	2.63	1.67	16.71
1HGF.PDB	O, A_ASN_170	N, A_GLY_240	H, A_GLY_240	2.91	2.09	27.97
1HGF.PDB	O, A_MET_168	N, A_LEU_243	H, A_LEU_243	2.94	1.98	7.98
1HGF.PDB	O, A_SER_205	N, A_VAL_244	H, A_VAL_244	2.89	1.97	15.63
1HGF.PDB	O, A_VAL_166	N, A_ILE_245	H, A_ILE_245	2.94	2.01	15.58
1HGF.PDB	O, A_THR_203	N, A_ASN_246	H, A_ASN_246	2.92	1.96	10.40
1HGF.PDB	OD1, A_ASN_165	ND2, A_ASN_246	HD21, A_ASN_246	2.93	2.03	19.92
1HGF.PDB	O, A_LEU_164	N, A_SER_247	H, A_SER_247	2.90	2.00	19.06
1HGF.PDB	OG, A_SER_247	N, A_GLY_249	H, A_GLY_249	2.99	2.00	4.05
1HGF.PDB	O, A_HIS_183	ND2, A_ASN_250	HD21, A_ASN_250	2.77	1.81	6.63

1HGF.PDB	OE1, A_GLN_191	ND2, A_ASN_250	HD22, A_ASN_250	2.86	1.90	9.57
1HGF.PDB	O, A_ASN_152	N, A_ALA_253	H, A_ALA_253	2.98	2.05	15.63
1HGF.PDB	OD1, A_ASN_133	NH2, A_ARG_255	HH22, A_ARG_255	2.49	1.67	28.52
1HGF.PDB	O, A_LEU_177	N, A_PHE_258	H, A_PHE_258	2.98	2.01	4.56
1HGF.PDB	OE1, A_GLU_119	NH2, A_ARG_261	HH22, A_ARG_261	2.74	1.90	27.76
1HGF.PDB	O, A_PHE_87	N, A_MET_268	H, A_MET_268	2.93	2.03	19.50
1HGF.PDB	O, A_PRO_284	OG, A_SER_270	HG, A_SER_270	2.80	1.83	2.11
1HGF.PDB	OG, A_SER_270	N, A_ALA_272	H, A_ALA_272	2.94	2.02	16.24
1HGF.PDB	O, A_ILE_51	N, A_ASP_275	H, A_ASP_275	2.90	2.00	18.80
1HGF.PDB	OD1, A_ASP_275	N, A_THR_276	H, A_THR_276	2.77	1.92	24.49
1HGF.PDB	O, A_ASN_54	N, A_SER_279	H, A_SER_279	2.78	1.84	13.06
1HGF.PDB	O, A_TYR_302	N, A_ILE_282	H, A_ILE_282	2.94	1.97	5.53
1HGF.PDB	O, A_THR_283	N, A_GLY_286	H, A_GLY_286	2.80	1.86	12.05
1HGF.PDB	O, A_LYS_50	N, A_SER_287	H, A_SER_287	2.81	1.89	15.58
1HGF.PDB	O, A_ALA_304	ND2, A_ASN_290	HD21, A_ASN_290	2.79	1.88	15.92
1HGF.PDB	OE1, A_GLN_44	NZ, A_LYS_292	HZ1, A_LYS_292	2.87	1.83	0.68
1HGF.PDB	OD1, A_ASP_291	NZ, A_LYS_292	HZ2, A_LYS_292	2.86	1.83	8.47
1HGF.PDB	O, A_LYS_307	N, A_GLN_295	H, A_GLN_295	2.82	1.98	25.98
1HGF.PDB	O, A_ASN_298	NE2, A_GLN_295	HE22, A_GLN_295	2.74	1.81	14.12
1HGF.PDB	O, A_GLN_44	N, A_ASN_296	H, A_ASN_296	2.86	1.90	9.96
1HGF.PDB	OD1, A_ASN_298	N, A_ILE_300	H, A_ILE_300	2.89	2.00	19.34
1HGF.PDB	O, A_ILE_282	N, A_TYR_302	H, A_TYR_302	2.80	1.95	24.99
1HGF.PDB	O, B_LYS_62	N, A_GLY_303	H, A_GLY_303	2.90	1.93	4.88
1HGF.PDB	O, A_GLN_295	N, A_VAL_309	H, A_VAL_309	2.94	2.08	24.38
1HGF.PDB	OG, B_SER_93	N, A_LYS_310	H, A_LYS_310	2.89	1.97	16.03
1HGF.PDB	OE1, A_GLU_41	OG1, A_THR_313	HG1, A_THR_313	2.68	1.87	27.57
1HGF.PDB	OE2, A_GLU_41	N, A_LEU_314	H, A_LEU_314	2.78	1.85	12.25
1HGF.PDB	OG1, A_THR_313	NZ, A_LYS_315	HZ2, A_LYS_315	2.95	2.00	20.61
1HGF.PDB	O, A_THR_40	N, A_LEU_316	H, A_LEU_316	2.77	1.84	13.98
1HGF.PDB	OD1, B_ASN_104	N, A_ALA_317	H, A_ALA_317	2.74	1.82	15.07
1HGF.PDB	O, A_ASN_38	N, A_THR_318	H, A_THR_318	2.85	1.92	14.74
1HGF.PDB	OE2, A_GLU_35	ND2, A_ASN_322	HD21, A_ASN_322	2.76	1.93	26.44
1HGF.PDB	O, A_VAL_20	ND2, A_ASN_322	HD22, A_ASN_322	2.95	2.02	15.09
1HGF.PDB	O, A_PRO_21	NE2, A_GLN_327	HE21, A_GLN_327	2.80	2.01	29.67
1HGF.PDB	OD2, B_ASP_112	N, B_GLY_1	H1, B_GLY_1	2.90	1.93	18.51
1HGF.PDB	OD1, B_ASP_109	N, B_LEU_2	H, B_LEU_2	2.91	2.01	19.54
1HGF.PDB	OD2, B_ASP_112	N, B_PHE_3	H, B_PHE_3	2.80	1.99	27.59
1HGF.PDB	OD2, B_ASP_112	N, B_GLY_4	H, B_GLY_4	2.97	2.05	16.11
1HGF.PDB	OD1, B_ASP_112	N, B_ALA_5	H, B_ALA_5	2.98	2.10	21.76
1HGF.PDB	O, B_GLY_4	N, B_PHE_9	H, B_PHE_9	2.80	1.88	14.94
1HGF.PDB	O, B_GLY_13	ND2, B_ASN_12	HD21, B_ASN_12	2.79	1.93	22.97
1HGF.PDB	O, A_VAL_323	N, B_GLY_13	H, B_GLY_13	2.74	1.86	21.47
1HGF.PDB	O, A_HIS_17	N, B_TRP_14	H, B_TRP_14	2.87	1.97	19.18
1HGF.PDB	OG1, B_THR_41	N, B_TRP_21	H, B_TRP_21	2.88	1.96	17.54
1HGF.PDB	O, B_ALA_35	N, B_PHE_24	H, B_PHE_24	2.83	1.86	5.03
1HGF.PDB	O, A_CYS_14	N, B_ARG_25	H, B_ARG_25	2.97	2.03	13.73
1HGF.PDB	OE1, B_GLN_34	NE, B_ARG_25	HE, B_ARG_25	2.64	1.77	20.89
1HGF.PDB	OE1, B_GLN_34	NH2, B_ARG_25	HH21, B_ARG_25	2.81	1.99	28.67
1HGF.PDB	OE2, A_GLU_325	NH2, B_ARG_25	HH22, B_ARG_25	2.99	2.04	16.52
1HGF.PDB	O, B_GLY_31	N, B_ASN_28	H, B_ASN_28	2.76	1.82	13.38
1HGF.PDB	O, B_TYR_22	N, B_ASP_37	H, B_ASP_37	2.72	1.76	1.26
1HGF.PDB	OD2, B_ASP_37	N, B_SER_40	H, B_SER_40	2.89	1.91	1.46
1HGF.PDB	O, B_ASP_37	OG1, B_THR_41	HG1, B_THR_41	2.68	1.88	27.80
1HGF.PDB	O, B_LEU_38	N, B_GLN_42	H, B_GLN_42	2.87	1.93	12.73
1HGF.PDB	OD1, B_ASP_46	NE2, B_GLN_42	HE21, B_GLN_42	2.87	1.99	22.40
1HGF.PDB	O, B_LYS_39	N, B_ALA_43	H, B_ALA_43	2.92	1.97	11.63
1HGF.PDB	O, B_SER_40	N, B_ALA_44	H, B_ALA_44	2.94	1.96	4.26
1HGF.PDB	O, B_GLN_42	N, B_ASP_46	H, B_ASP_46	2.81	1.84	4.31

1HGF.PDB	O, B_ALA_43	NE2, B_GLN_47	HE21, B_GLN_47	2.89	1.94	12.17
1HGF.PDB	O, B_ILE_45	N, B_ASN_49	H, B_ASN_49	2.90	1.97	14.22
1HGF.PDB	O, B_ASP_46	N, B_GLY_50	H, B_GLY_50	2.85	1.93	16.88
1HGF.PDB	O, B_GLN_47	N, B_LYS_51	H, B_LYS_51	2.96	2.00	10.44
1HGF.PDB	OE1, B_GLU_103	NZ, B_LYS_51	HZ1, B_LYS_51	2.74	1.70	5.26
1HGF.PDB	ND1, B_HIS_106	NZ, B_LYS_51	HZ3, B_LYS_51	2.67	1.72	18.38
1HGF.PDB	O, B_ILE_48	N, B_LEU_52	H, B_LEU_52	2.92	2.01	17.60
1HGF.PDB	O, B_ASN_49	N, B_ASN_53	H, B_ASN_53	2.84	1.91	14.80
1HGF.PDB	O, E_THR_28	NE, B_ARG_54	HE, B_ARG_54	2.92	1.94	6.13
1HGF.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.83	1.86	13.50
1HGF.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ2, B_LYS_62	2.71	1.70	11.44
1HGF.PDB	OD2, F_ASP_90	NZ, B_LYS_62	HZ3, B_LYS_62	2.77	1.82	20.37
1HGF.PDB	OG, A_SER_266	ND1, B_HIS_64	HD1, B_HIS_64	2.66	1.79	20.68
1HGF.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.89	1.92	10.70
1HGF.PDB	O, B_PHE_63	NE2, B_GLN_65	HE21, B_GLN_65	2.92	1.95	7.46
1HGF.PDB	OE2, B_GLU_85	NZ, B_LYS_68	HZ1, B_LYS_68	2.67	1.75	22.44
1HGF.PDB	O, A_LYS_299	NZ, B_LYS_68	HZ2, B_LYS_68	2.93	1.89	4.53
1HGF.PDB	OG, C_SER_107	N, B_ARG_76	H, B_ARG_76	2.84	1.90	13.38
1HGF.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.92	1.92	2.47
1HGF.PDB	OE1, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.86	1.84	3.80
1HGF.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.73	1.74	10.29
1HGF.PDB	OE2, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.75	1.74	3.91
1HGF.PDB	O, B_GLY_75	N, B_ASP_79	H, B_ASP_79	2.96	2.00	9.52
1HGF.PDB	O, B_ILE_77	N, B_GLU_81	H, B_GLU_81	2.94	1.98	10.87
1HGF.PDB	O, B_GLN_78	N, B_LYS_82	H, B_LYS_82	3.00	2.09	18.29
1HGF.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.57	1.80	29.66
1HGF.PDB	O, B_LEU_80	N, B_VAL_84	H, B_VAL_84	2.91	1.98	14.24
1HGF.PDB	O, B_LYS_82	N, B_ASP_86	H, B_ASP_86	2.93	1.99	11.73
1HGF.PDB	O, B_TYR_83	N, B_THR_87	H, B_THR_87	2.99	2.04	12.38
1HGF.PDB	O, B_VAL_84	N, B_LYS_88	H, B_LYS_88	2.93	2.07	23.33
1HGF.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.72	1.70	9.91
1HGF.PDB	O, B_GLU_85	N, B_ILE_89	H, B_ILE_89	2.93	1.96	7.36
1HGF.PDB	O, B_LYS_88	N, B_TRP_92	H, B_TRP_92	2.91	1.95	10.80
1HGF.PDB	O, B_ILE_89	N, B_SER_93	H, B_SER_93	2.91	2.02	20.72
1HGF.PDB	O, B_ILE_89	OG, B_SER_93	HG, B_SER_93	2.78	1.94	24.66
1HGF.PDB	O, B_ASP_90	N, B_TYR_94	H, B_TYR_94	3.00	2.07	16.60
1HGF.PDB	O, B_TRP_92	N, B_ALA_96	H, B_ALA_96	2.98	2.04	14.15
1HGF.PDB	O, B_TYR_94	N, B_LEU_98	H, B_LEU_98	2.94	1.99	11.23
1HGF.PDB	O, B_ASN_95	N, B_LEU_99	H, B_LEU_99	3.00	2.03	11.07
1HGF.PDB	O, B_LEU_98	N, B_LEU_102	H, B_LEU_102	2.98	2.01	7.33
1HGF.PDB	O, B_LEU_99	N, B_GLU_103	H, B_GLU_103	2.91	1.94	8.79
1HGF.PDB	O, B_VAL_100	N, B_ASN_104	H, B_ASN_104	2.86	1.91	12.70
1HGF.PDB	O, A_LYS_27	ND2, B_ASN_104	HD21, B_ASN_104	2.88	1.94	13.97
1HGF.PDB	O, B_LEU_102	N, B_HIS_106	H, B_HIS_106	2.90	1.94	9.48
1HGF.PDB	O, B_GLU_103	N, B_THR_107	H, B_THR_107	2.84	1.94	18.07
1HGF.PDB	O, B_ASN_104	N, B_ILE_108	H, B_ILE_108	2.93	1.99	13.61
1HGF.PDB	O, B_HIS_106	N, B_LEU_110	H, B_LEU_110	2.78	1.84	12.67
1HGF.PDB	O, B_ASP_109	N, B_SER_113	H, B_SER_113	2.79	1.85	13.76
1HGF.PDB	O, F_LEU_2	OG, B_SER_113	HG, B_SER_113	2.68	1.90	29.80
1HGF.PDB	O, B_SER_113	N, B_LYS_117	H, B_LYS_117	2.74	1.85	20.16
1HGF.PDB	O, B_GLU_114	N, B_LEU_118	H, B_LEU_118	2.99	2.05	15.07
1HGF.PDB	O, B_MET_115	N, B_PHE_119	H, B_PHE_119	2.97	2.01	9.96
1HGF.PDB	O, B_ASN_116	N, B_GLU_120	H, B_GLU_120	2.92	1.94	1.95
1HGF.PDB	OE2, B_GLU_120	NH1, B_ARG_123	HH11, B_ARG_123	2.78	1.93	26.74
1HGF.PDB	O, B_GLU_120	N, B_ARG_124	H, B_ARG_124	2.96	2.04	16.03
1HGF.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.80	1.86	13.00
1HGF.PDB	OH, B_TYR_157	ND2, B_ASN_129	HD21, B_ASN_129	2.81	1.86	11.58
1HGF.PDB	O, B_HIS_159	ND2, B_ASN_129	HD22, B_ASN_129	2.97	2.06	17.16

1HGF.PDB	O, B_LYS_139	N, B_GLU_131	H, B_GLU_131	2.94	2.04	19.21
1HGF.PDB	O, B_CYS_137	N, B_MET_133	H, B_MET_133	2.88	1.93	11.45
1HGF.PDB	O, A_LEU_13	N, B_PHE_138	H, B_PHE_138	2.73	1.88	23.58
1HGF.PDB	O, B_GLU_131	N, B_LYS_139	H, B_LYS_139	2.85	1.91	11.21
1HGF.PDB	O, A_ALA_11	N, B_ILE_140	H, B_ILE_140	2.80	1.87	14.66
1HGF.PDB	O, B_ASN_129	N, B_TYR_141	H, B_TYR_141	2.87	1.93	12.99
1HGF.PDB	OD2, B_ASP_145	N, B_ALA_147	H, B_ALA_147	2.86	1.98	21.48
1HGF.PDB	O, B_ASP_145	N, B_ILE_149	H, B_ILE_149	2.90	1.94	9.97
1HGF.PDB	O, B_ASN_146	N, B_GLU_150	H, B_GLU_150	2.94	1.99	11.66
1HGF.PDB	O, B_ALA_147	N, B_SER_151	H, B_SER_151	2.85	2.06	29.61
1HGF.PDB	O, B_CYS_148	OG, B_SER_151	HG, B_SER_151	2.68	1.81	19.96
1HGF.PDB	O, B_GLU_150	N, B_ASN_154	H, B_ASN_154	2.87	1.89	5.04
1HGF.PDB	O, B_SER_151	N, B_THR_156	H, B_THR_156	2.77	1.91	23.09
1HGF.PDB	OD1, B_ASN_154	OG1, B_THR_156	HG1, B_THR_156	2.68	1.80	19.09
1HGF.PDB	OD1, B_ASP_158	N, B_ASP_160	H, B_ASP_160	2.97	2.10	23.68
1HGF.PDB	O, B_HIS_159	N, B_TYR_162	H, B_TYR_162	2.85	2.05	29.20
1HGF.PDB	O, F_ARG_170	NH1, B_ARG_163	HH12, B_ARG_163	2.79	1.78	1.27
1HGF.PDB	OE1, F_GLU_131	NH2, B_ARG_163	HH21, B_ARG_163	2.74	1.86	24.20
1HGF.PDB	O, B_TYR_162	N, B_ALA_166	H, B_ALA_166	2.86	1.89	4.35
1HGF.PDB	O, B_ARG_163	N, B_LEU_167	H, B_LEU_167	2.79	1.83	5.57
1HGF.PDB	O, B_GLU_165	ND2, B_ASN_169	HD21, B_ASN_169	3.00	2.06	13.38
1HGF.PDB	O, B_ALA_166	N, B_ARG_170	H, B_ARG_170	2.82	1.94	21.74
1HGF.PDB	O, B_GLU_128	NE, B_ARG_170	HE, B_ARG_170	2.78	1.88	20.28
1HGF.PDB	OE2, B_GLU_131	NH1, B_ARG_170	HH11, B_ARG_170	2.84	1.84	5.96
1HGF.PDB	O, B_LEU_167	N, B_PHE_171	H, B_PHE_171	2.90	1.97	15.47
1HGF.PDB	O, D_ILE_140	N, C_ALA_11	H, C_ALA_11	2.89	2.00	20.42
1HGF.PDB	O, D_GLN_27	N, C_THR_12	H, C_THR_12	2.90	1.96	12.68
1HGF.PDB	O, D_PHE_138	N, C_LEU_13	H, C_LEU_13	2.97	1.99	7.01
1HGF.PDB	O, D_ARG_25	N, C_CYS_14	H, C_CYS_14	2.79	1.86	15.57
1HGF.PDB	O, D_GLY_136	N, C_LEU_15	H, C_LEU_15	2.95	1.97	3.72
1HGF.PDB	O, D_GLY_23	N, C_GLY_16	H, C_GLY_16	2.95	2.05	18.06
1HGF.PDB	O, D_TRP_21	N, C_HIS_18	H, C_HIS_18	2.91	2.01	18.40
1HGF.PDB	OD1, C_ASN_322	N, C_VAL_20	H, C_VAL_20	2.80	1.83	2.80
1HGF.PDB	O, C_VAL_36	N, C_THR_24	H, C_THR_24	2.88	1.97	16.83
1HGF.PDB	O, C_ILE_34	N, C_VAL_26	H, C_VAL_26	2.85	1.90	10.38
1HGF.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.81	1.85	19.93
1HGF.PDB	O, C_ASP_31	N, C_THR_28	H, C_THR_28	2.69	1.91	29.80
1HGF.PDB	O, C_VAL_26	N, C_ILE_34	H, C_ILE_34	2.94	1.99	12.34
1HGF.PDB	O, C_THR_24	N, C_VAL_36	H, C_VAL_36	2.81	1.85	7.51
1HGF.PDB	O, C_MET_320	N, C_THR_37	H, C_THR_37	2.93	1.95	5.43
1HGF.PDB	O, C_LEU_316	N, C_THR_40	H, C_THR_40	2.80	1.89	17.62
1HGF.PDB	O, C_LEU_314	N, C_LEU_42	H, C_LEU_42	2.77	1.92	23.28
1HGF.PDB	O, C_PHE_294	N, C_GLN_44	H, C_GLN_44	2.95	1.98	8.35
1HGF.PDB	O, C_SER_46	NE2, C_GLN_44	HE21, C_GLN_44	2.83	1.96	22.13
1HGF.PDB	O, C_ASN_285	OG, C_SER_47	HG, C_SER_47	2.88	1.94	10.85
1HGF.PDB	OD2, C_ASP_275	NZ, C_LYS_50	HZ2, C_LYS_50	2.88	1.87	13.71
1HGF.PDB	O, C_PRO_273	N, C_ILE_51	H, C_ILE_51	2.76	1.80	7.14
1HGF.PDB	O, C_ASP_275	N, C_ASN_53	H, C_ASN_53	2.87	1.97	19.35
1HGF.PDB	OD2, C_ASP_85	N, C_ARG_57	H, C_ARG_57	2.92	1.96	10.20
1HGF.PDB	O, C_THR_83	NE, C_ARG_57	HE, C_ARG_57	2.76	1.82	12.66
1HGF.PDB	O, C_LEU_86	N, C_LEU_59	H, C_LEU_59	2.88	1.92	8.76
1HGF.PDB	O, C_VAL_88	N, C_GLY_61	H, C_GLY_61	2.99	2.18	28.94
1HGF.PDB	OD1, C_ASP_60	N, C_ILE_62	H, C_ILE_62	2.90	1.96	13.08
1HGF.PDB	O, C_GLY_61	N, C_CYS_64	H, C_CYS_64	2.89	1.95	14.15
1HGF.PDB	O, C_THR_65	N, C_ALA_69	H, C_ALA_69	2.99	2.03	9.48
1HGF.PDB	O, C_LEU_66	N, C_LEU_70	H, C_LEU_70	2.84	1.91	15.42
1HGF.PDB	O, C_ILE_67	N, C_LEU_71	H, C_LEU_71	2.90	1.93	5.47
1HGF.PDB	O, C_ASP_68	N, C_GLY_72	H, C_GLY_72	2.81	1.92	21.42

1HGF.PDB	OD1, C_ASP_73	N, C_HIS_75	H, C_HIS_75	2.97	2.06	19.07
1HGF.PDB	OD1, C_ASP_73	ND1, C_HIS_75	HD1, C_HIS_75	2.84	1.90	12.73
1HGF.PDB	O, C_ASP_63	NE2, C_HIS_75	HE2, C_HIS_75	2.86	1.91	13.30
1HGF.PDB	O, C_ASP_73	N, C_CYS_76	H, C_CYS_76	2.82	1.90	14.90
1HGF.PDB	O, C_PRO_74	N, C_ASP_77	H, C_ASP_77	2.92	1.97	11.55
1HGF.PDB	O, C_CYS_76	N, C_PHE_79	H, C_PHE_79	2.95	1.98	6.66
1HGF.PDB	OE1, C_GLU_82	N, C_THR_83	H, C_THR_83	2.95	2.02	15.89
1HGF.PDB	O, C_ARG_57	N, C_ASP_85	H, C_ASP_85	2.80	1.92	20.17
1HGF.PDB	O, C_MET_268	N, C_GLU_89	H, C_GLU_89	2.83	1.88	10.14
1HGF.PDB	OD1, C_ASP_60	NE, C_ARG_90	HE, C_ARG_90	2.76	1.85	16.46
1HGF.PDB	O, C_SER_270	NH1, C_ARG_90	HH11, C_ARG_90	2.67	1.81	25.78
1HGF.PDB	O, C_ALA_272	NH1, C_ARG_90	HH12, C_ARG_90	2.65	1.72	16.33
1HGF.PDB	OD2, C_ASP_60	NH2, C_ARG_90	HH21, C_ARG_90	2.84	1.85	9.99
1HGF.PDB	OD1, C_ASP_271	N, C_SER_91	H, C_SER_91	2.94	1.98	10.16
1HGF.PDB	OD1, C_ASP_271	OG, C_SER_91	HG, C_SER_91	2.91	2.11	29.01
1HGF.PDB	OD2, C_ASP_271	OG, C_SER_91	HG, C_SER_91	2.86	1.95	16.65
1HGF.PDB	OD2, C_ASP_73	N, C_ASN_96	H, C_ASN_96	2.88	1.95	14.97
1HGF.PDB	SG, C_CYS_97	N, C_TYR_98	H, C_TYR_98	2.99	2.15	25.59
1HGF.PDB	OD1, C_ASP_68	OH, C_TYR_100	HH, C_TYR_100	2.97	2.03	12.15
1HGF.PDB	O, C_ILE_230	N, C_ASP_101	H, C_ASP_101	2.99	2.16	26.80
1HGF.PDB	OD2, C_ASP_104	OG, C_SER_107	HG, C_SER_107	2.91	1.98	14.76
1HGF.PDB	O, C_TYR_105	N, C_ARG_109	H, C_ARG_109	2.87	1.90	5.89
1HGF.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.91	1.92	11.49
1HGF.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.69	1.85	25.37
1HGF.PDB	O, C_SER_107	N, C_LEU_111	H, C_LEU_111	2.95	2.00	12.48
1HGF.PDB	O, C_ARG_109	N, C_ALA_113	H, C_ALA_113	2.94	2.02	17.14
1HGF.PDB	O, C_SER_110	N, C_SER_114	H, C_SER_114	2.95	2.04	18.89
1HGF.PDB	O, C_VAL_112	N, C_GLY_116	H, C_GLY_116	3.00	2.03	6.34
1HGF.PDB	OE2, C_GLU_119	OG1, C_THR_117	HG1, C_THR_117	2.97	2.00	2.16
1HGF.PDB	O, C_GLU_82	N, C_LEU_118	H, C_LEU_118	2.97	2.00	8.06
1HGF.PDB	OD1, C_ASN_81	N, C_PHE_120	H, C_PHE_120	3.00	2.07	15.52
1HGF.PDB	O, C_TYR_257	N, C_ILE_121	H, C_ILE_121	2.83	1.85	1.84
1HGF.PDB	O, C_ARG_255	N, C_GLU_123	H, C_GLU_123	2.86	1.90	9.31
1HGF.PDB	O, C_THR_155	N, C_THR_131	H, C_THR_131	2.75	1.81	11.67
1HGF.PDB	ND2, C_ASN_152	NE2, C_GLN_132	HE21, C_GLN_132	2.94	2.00	12.42
1HGF.PDB	OD1, C_ASN_152	N, C_ASN_133	H, C_ASN_133	2.91	1.95	9.50
1HGF.PDB	O, C_TRP_153	N, C_GLY_134	H, C_GLY_134	2.99	2.07	16.29
1HGF.PDB	O, C_GLY_146	N, C_SER_136	H, C_SER_136	2.71	1.85	23.34
1HGF.PDB	O, C_GLY_144	N, C_ARG_141	H, C_ARG_141	2.89	2.08	28.20
1HGF.PDB	OD2, C_ASP_77	NE, C_ARG_141	HE, C_ARG_141	2.91	2.05	25.56
1HGF.PDB	O, C_PHE_147	NH1, C_ARG_141	HH12, C_ARG_141	2.59	1.66	16.99
1HGF.PDB	OD1, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.84	1.98	26.48
1HGF.PDB	OD2, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.79	1.86	20.63
1HGF.PDB	O, C_SER_136	N, C_GLY_146	H, C_GLY_146	2.99	2.14	25.31
1HGF.PDB	O, C_GLY_72	N, C_SER_149	H, C_SER_149	2.87	1.95	17.40
1HGF.PDB	O, C_ALA_253	N, C_ASN_152	H, C_ASN_152	2.81	1.90	18.05
1HGF.PDB	OH, C_TYR_195	NE1, C_TRP_153	HE1, C_TRP_153	2.82	1.92	18.47
1HGF.PDB	O, C_LEU_194	N, C_LYS_156	H, C_LYS_156	2.86	2.00	23.97
1HGF.PDB	O, C_THR_160	N, C_SER_157	H, C_SER_157	2.96	2.07	20.42
1HGF.PDB	O, C_SER_247	N, C_LEU_164	H, C_LEU_164	2.70	1.88	26.53
1HGF.PDB	O, C_ILE_245	N, C_VAL_166	H, C_VAL_166	2.89	1.93	11.49
1HGF.PDB	O, C_LEU_243	OG1, C_THR_167	HG1, C_THR_167	2.95	2.01	11.60
1HGF.PDB	O, C_ASP_241	N, C_ASN_170	H, C_ASN_170	2.84	1.87	6.38
1HGF.PDB	O, C_PHE_174	ND2, C_ASN_170	HD22, C_ASN_170	2.74	1.80	12.05
1HGF.PDB	O, C_VAL_237	N, C_LYS_176	H, C_LYS_176	2.93	1.99	14.60
1HGF.PDB	OE2, C_GLU_123	NZ, C_LYS_176	HZ1, C_LYS_176	2.72	1.80	22.47
1HGF.PDB	O, C_THR_235	N, C_TYR_178	H, C_TYR_178	2.78	1.81	4.50
1HGF.PDB	OG1, C_THR_235	NE1, C_TRP_180	HE1, C_TRP_180	2.86	1.88	3.91

1HGF.PDB	O, C_ASN_250	N, C_HIS_183	H, C_HIS_183	2.79	1.92	22.35
1HGF.PDB	OH, C_TYR_98	NE2, C_HIS_183	HE2, C_HIS_183	2.89	1.99	18.89
1HGF.PDB	O, C_ARG_229	N, C_HIS_184	H, C_HIS_184	2.87	1.90	8.03
1HGF.PDB	OG, C_SER_231	NE2, C_HIS_184	HE2, C_HIS_184	2.67	1.86	27.83
1HGF.PDB	OD1, C_ASN_250	NE2, C_GLN_191	HE22, C_GLN_191	2.91	1.94	7.66
1HGF.PDB	O, C_ASN_188	N, C_THR_192	H, C_THR_192	2.94	2.00	14.19
1HGF.PDB	O, C_GLN_189	OG1, C_THR_192	HG1, C_THR_192	2.86	2.05	27.70
1HGF.PDB	O, C_GLN_189	N, C_SER_193	H, C_SER_193	2.81	1.91	19.71
1HGF.PDB	O, C_GLU_190	N, C_LEU_194	H, C_LEU_194	2.96	2.00	9.41
1HGF.PDB	O, C_GLN_191	N, C_TYR_195	H, C_TYR_195	2.79	1.84	10.04
1HGF.PDB	O, C_ASN_248	NE2, C_GLN_197	HE21, C_GLN_197	2.92	2.05	22.87
1HGF.PDB	O, C_TYR_161	NE2, C_GLN_197	HE22, C_GLN_197	2.98	2.03	10.03
1HGF.PDB	OG1, C_THR_212	OG1, C_THR_203	HG1, C_THR_203	2.82	1.90	14.76
1HGF.PDB	O, C_GLN_211	N, C_VAL_204	H, C_VAL_204	2.93	2.00	14.76
1HGF.PDB	O, C_SER_209	N, C_THR_206	H, C_THR_206	2.97	2.04	14.71
1HGF.PDB	OD1, C_ASP_241	N, C_ARG_207	H, C_ARG_207	2.91	1.95	9.01
1HGF.PDB	O, C_VAL_204	N, C_GLN_211	H, C_GLN_211	2.84	1.94	18.99
1HGF.PDB	O, C_VAL_202	N, C_ILE_213	H, C_ILE_213	2.85	1.95	18.52
1HGF.PDB	ND1, C_HIS_184	N, C_ASN_216	H, C_ASN_216	2.71	1.89	26.19
1HGF.PDB	O, C_ASN_216	NH1, C_ARG_220	HH12, C_ARG_220	2.97	2.15	29.93
1HGF.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.56	1.72	26.72
1HGF.PDB	O, C_ASN_216	NH2, C_ARG_220	HH22, C_ARG_220	2.74	1.84	20.57
1HGF.PDB	O, C_LEU_226	N, C_VAL_223	H, C_VAL_223	2.83	1.89	12.06
1HGF.PDB	O, C_CYS_97	NE, C_ARG_224	HE, C_ARG_224	2.75	1.89	23.47
1HGF.PDB	O, C_CYS_97	NH2, C_ARG_224	HH21, C_ARG_224	2.93	2.09	27.24
1HGF.PDB	O, C_VAL_223	N, C_LEU_226	H, C_LEU_226	2.93	1.99	12.10
1HGF.PDB	O, C_SER_228	NH1, C_ARG_229	HH11, C_ARG_229	2.74	1.82	20.52
1HGF.PDB	O, C_PRO_221	NH2, C_ARG_229	HH22, C_ARG_229	2.64	1.70	16.37
1HGF.PDB	O, C_PRO_99	N, C_ILE_230	H, C_ILE_230	2.97	2.09	21.38
1HGF.PDB	OD1, C_ASP_101	OG, C_SER_231	HG, C_SER_231	2.86	1.89	4.34
1HGF.PDB	O, C_ASP_101	N, C_ILE_232	H, C_ILE_232	2.92	1.98	14.28
1HGF.PDB	O, C_TRP_180	N, C_TYR_233	H, C_TYR_233	2.92	1.97	12.47
1HGF.PDB	O, C_TYR_178	N, C_THR_235	H, C_THR_235	2.83	1.96	22.49
1HGF.PDB	O, C_LYS_176	N, C_VAL_237	H, C_VAL_237	2.78	1.86	15.74
1HGF.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ2, C_LYS_238	2.75	1.78	18.48
1HGF.PDB	O, B_SER_71	NZ, C_LYS_238	HZ3, C_LYS_238	2.61	1.62	12.67
1HGF.PDB	O, C_ASN_170	N, C_GLY_240	H, C_GLY_240	2.91	2.11	29.28
1HGF.PDB	O, C_LYS_238	N, C_ASP_241	H, C_ASP_241	2.98	2.06	15.29
1HGF.PDB	O, C_MET_168	N, C_LEU_243	H, C_LEU_243	2.96	1.99	7.32
1HGF.PDB	O, C_SER_205	N, C_VAL_244	H, C_VAL_244	2.94	1.99	13.35
1HGF.PDB	O, C_VAL_166	N, C_ILE_245	H, C_ILE_245	2.97	2.05	16.82
1HGF.PDB	O, C_THR_203	N, C_ASN_246	H, C_ASN_246	2.92	1.97	10.97
1HGF.PDB	OD1, C_ASN_165	ND2, C_ASN_246	HD21, C_ASN_246	2.93	2.04	21.38
1HGF.PDB	O, C_LEU_164	N, C_SER_247	H, C_SER_247	2.93	2.02	18.68
1HGF.PDB	OG, C_SER_247	N, C_GLY_249	H, C_GLY_249	2.99	2.02	6.95
1HGF.PDB	O, C_HIS_183	ND2, C_ASN_250	HD21, C_ASN_250	2.81	1.85	7.16
1HGF.PDB	OE1, C_GLN_191	ND2, C_ASN_250	HD22, C_ASN_250	2.84	1.89	10.62
1HGF.PDB	O, C_ASN_152	N, C_ALA_253	H, C_ALA_253	2.97	2.05	17.09
1HGF.PDB	OD1, C_ASN_133	NH2, C_ARG_255	HH22, C_ARG_255	2.47	1.67	28.90
1HGF.PDB	O, C_ILE_121	N, C_TYR_257	H, C_TYR_257	2.98	2.13	24.91
1HGF.PDB	O, C_LEU_177	N, C_PHE_258	H, C_PHE_258	3.00	2.02	5.00
1HGF.PDB	OE1, C_GLU_119	NH2, C_ARG_261	HH22, C_ARG_261	2.72	1.88	28.14
1HGF.PDB	O, C_PHE_87	N, C_MET_268	H, C_MET_268	2.91	1.98	16.01
1HGF.PDB	OG, C_SER_270	N, C_ALA_272	H, C_ALA_272	2.93	2.02	16.95
1HGF.PDB	O, C_ILE_51	N, C_ASP_275	H, C_ASP_275	2.92	2.05	22.55
1HGF.PDB	OD1, C_ASP_275	N, C_THR_276	H, C_THR_276	2.75	1.92	25.58
1HGF.PDB	O, C_ASN_54	N, C_SER_279	H, C_SER_279	2.77	1.83	12.02
1HGF.PDB	O, C_TYR_302	N, C_ILE_282	H, C_ILE_282	2.94	1.96	4.09

1HGF.PDB	O, C_THR_283	N, C_GLY_286	H, C_GLY_286	2.80	1.85	9.72
1HGF.PDB	O, C_LYS_50	N, C_SER_287	H, C_SER_287	2.77	1.82	8.64
1HGF.PDB	O, C_ALA_304	ND2, C_ASN_290	HD21, C_ASN_290	2.81	1.90	17.53
1HGF.PDB	OE1, C_GLN_44	NZ, C_LYS_292	HZ1, C_LYS_292	2.89	1.84	2.00
1HGF.PDB	OD1, C_ASP_291	NZ, C_LYS_292	HZ2, C_LYS_292	2.88	1.85	8.89
1HGF.PDB	O, C_LYS_307	N, C_GLN_295	H, C_GLN_295	2.79	1.95	25.63
1HGF.PDB	O, C_ASN_298	NE2, C_GLN_295	HE22, C_GLN_295	2.74	1.82	15.41
1HGF.PDB	O, C_GLN_44	N, C_ASN_296	H, C_ASN_296	2.86	1.91	11.96
1HGF.PDB	OD1, C_ASN_298	N, C_ILE_300	H, C_ILE_300	2.86	2.02	25.28
1HGF.PDB	O, C_ILE_282	N, C_TYR_302	H, C_TYR_302	2.79	1.95	25.47
1HGF.PDB	O, D_LYS_62	N, C_GLY_303	H, C_GLY_303	2.91	1.95	8.09
1HGF.PDB	O, C_GLN_295	N, C_VAL_309	H, C_VAL_309	2.90	2.02	21.20
1HGF.PDB	OG, D_SER_93	N, C_LYS_310	H, C_LYS_310	2.89	1.98	17.69
1HGF.PDB	OE1, C_GLU_41	OG1, C_THR_313	HG1, C_THR_313	2.66	1.87	29.10
1HGF.PDB	OE2, C_GLU_41	N, C_LEU_314	H, C_LEU_314	2.78	1.84	12.61
1HGF.PDB	OG1, C_THR_313	NZ, C_LYS_315	HZ2, C_LYS_315	2.92	1.98	21.54
1HGF.PDB	O, C_THR_40	N, C_LEU_316	H, C_LEU_316	2.78	1.85	14.66
1HGF.PDB	OD1, D_ASN_104	N, C_ALA_317	H, C_ALA_317	2.78	1.83	11.25
1HGF.PDB	O, C_ASN_38	N, C_THR_318	H, C_THR_318	2.88	1.93	11.29
1HGF.PDB	OE2, C_GLU_35	ND2, C_ASN_322	HD21, C_ASN_322	2.77	1.93	25.57
1HGF.PDB	O, C_VAL_20	ND2, C_ASN_322	HD22, C_ASN_322	2.97	2.05	15.45
1HGF.PDB	OXT, C_THR_328	NE2, C_GLN_327	HE21, C_GLN_327	2.93	2.09	26.28
1HGF.PDB	OD2, D_ASP_112	N, D_GLY_1	H1, D_GLY_1	2.88	1.90	17.37
1HGF.PDB	OD1, D_ASP_109	N, D_LEU_2	H, D_LEU_2	2.92	2.02	20.08
1HGF.PDB	O, D_GLY_4	N, D_PHE_9	H, D_PHE_9	2.80	1.88	16.46
1HGF.PDB	O, D_GLY_13	ND2, D_ASN_12	HD21, D_ASN_12	2.79	1.92	22.00
1HGF.PDB	O, C_VAL_323	N, D_GLY_13	H, D_GLY_13	2.72	1.85	21.39
1HGF.PDB	O, C_HIS_17	N, D_TRP_14	H, D_TRP_14	2.87	1.96	16.75
1HGF.PDB	OG1, D_THR_41	N, D_TRP_21	H, D_TRP_21	2.91	2.00	17.91
1HGF.PDB	O, D_ALA_35	N, D_PHE_24	H, D_PHE_24	2.85	1.87	3.45
1HGF.PDB	O, C_CYS_14	N, D_ARG_25	H, D_ARG_25	2.90	1.93	7.59
1HGF.PDB	OE1, D_GLN_34	NE, D_ARG_25	HE, D_ARG_25	2.69	1.78	17.17
1HGF.PDB	O, D_GLY_33	N, D_HIS_26	H, D_HIS_26	2.88	2.02	23.62
1HGF.PDB	O, C_THR_12	N, D_GLN_27	H, D_GLN_27	2.86	1.94	17.23
1HGF.PDB	O, D_GLY_31	N, D_ASN_28	H, D_ASN_28	2.96	1.98	6.01
1HGF.PDB	OD1, D_ASN_146	ND2, D_ASN_28	HD22, D_ASN_28	2.89	1.97	17.31
1HGF.PDB	O, D_ASN_28	N, D_GLY_31	H, D_GLY_31	2.88	1.99	19.79
1HGF.PDB	O, D_HIS_26	N, D_GLY_33	H, D_GLY_33	2.97	2.16	28.69
1HGF.PDB	O, D_PHE_24	N, D_ALA_35	H, D_ALA_35	2.78	1.98	29.25
1HGF.PDB	O, D_TYR_22	N, D_ASP_37	H, D_ASP_37	2.72	1.76	4.61
1HGF.PDB	OD2, D_ASP_37	N, D_SER_40	H, D_SER_40	2.90	1.92	1.16
1HGF.PDB	OD2, D_ASP_37	OG, D_SER_40	HG, D_SER_40	2.85	1.95	18.29
1HGF.PDB	O, D_ASP_37	OG1, D_THR_41	HG1, D_THR_41	2.68	1.81	21.66
1HGF.PDB	O, D_LEU_38	N, D_GLN_42	H, D_GLN_42	2.88	1.96	16.52
1HGF.PDB	OD1, D_ASP_46	NE2, D_GLN_42	HE21, D_GLN_42	2.85	1.97	22.40
1HGF.PDB	O, D_LYS_39	N, D_ALA_43	H, D_ALA_43	2.92	1.96	7.79
1HGF.PDB	O, D_SER_40	N, D_ALA_44	H, D_ALA_44	2.95	1.98	3.84
1HGF.PDB	O, D_GLN_42	N, D_ASP_46	H, D_ASP_46	2.80	1.83	2.08
1HGF.PDB	O, D_ALA_43	NE2, D_GLN_47	HE21, D_GLN_47	2.88	1.93	11.54
1HGF.PDB	O, D_ILE_45	N, D_ASN_49	H, D_ASN_49	2.91	1.99	16.85
1HGF.PDB	O, D_ASP_46	N, D_GLY_50	H, D_GLY_50	2.87	1.93	13.85
1HGF.PDB	O, D_GLN_47	N, D_LYS_51	H, D_LYS_51	2.95	1.98	9.03
1HGF.PDB	OE1, D_GLU_103	NZ, D_LYS_51	HZ1, D_LYS_51	2.74	1.71	5.53
1HGF.PDB	ND1, D_HIS_106	NZ, D_LYS_51	HZ3, D_LYS_51	2.69	1.73	17.89
1HGF.PDB	O, D_ILE_48	N, D_LEU_52	H, D_LEU_52	2.91	2.04	22.13
1HGF.PDB	O, D_ASN_49	N, D_ASN_53	H, D_ASN_53	2.86	1.92	13.32
1HGF.PDB	O, A_THR_28	NE, D_ARG_54	HE, D_ARG_54	2.88	1.90	8.46
1HGF.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.84	1.86	12.74

1HGF.PDB	OD2, B_ASP_86	NZ, D_LYS_62	HZ2, D_LYS_62	2.69	1.69	13.49
1HGF.PDB	OD2, B_ASP_90	NZ, D_LYS_62	HZ3, D_LYS_62	2.68	1.77	22.81
1HGF.PDB	OG, C_SER_266	ND1, D_HIS_64	HD1, D_HIS_64	2.64	1.83	27.58
1HGF.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.90	1.92	7.33
1HGF.PDB	O, D_PHE_63	NE2, D_GLN_65	HE21, D_GLN_65	2.97	2.00	7.06
1HGF.PDB	OE2, D_GLU_85	NZ, D_LYS_68	HZ1, D_LYS_68	2.73	1.78	19.48
1HGF.PDB	O, C_LYS_299	NZ, D_LYS_68	HZ2, D_LYS_68	2.93	1.89	4.98
1HGF.PDB	OG, E_SER_107	N, D_ARG_76	H, D_ARG_76	2.91	1.94	7.76
1HGF.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.82	1.85	5.34
1HGF.PDB	OE1, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.79	1.78	3.81
1HGF.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.64	1.68	12.43
1HGF.PDB	OE2, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.70	1.71	7.38
1HGF.PDB	O, D_GLY_75	N, D_ASP_79	H, D_ASP_79	2.98	2.03	12.51
1HGF.PDB	O, D_ILE_77	N, D_GLU_81	H, D_GLU_81	2.96	2.00	8.84
1HGF.PDB	O, D_GLN_78	N, D_LYS_82	H, D_LYS_82	2.96	2.03	15.61
1HGF.PDB	O, D_ASP_79	N, D_TYR_83	H, D_TYR_83	2.99	2.06	16.44
1HGF.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.58	1.80	29.87
1HGF.PDB	O, D_LEU_80	N, D_VAL_84	H, D_VAL_84	2.89	1.96	15.53
1HGF.PDB	O, D_LYS_82	N, D_ASP_86	H, D_ASP_86	2.88	1.93	10.60
1HGF.PDB	O, D_TYR_83	N, D_THR_87	H, D_THR_87	2.98	2.05	15.57
1HGF.PDB	O, D_VAL_84	N, D_LYS_88	H, D_LYS_88	2.92	2.03	20.52
1HGF.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.68	1.69	13.85
1HGF.PDB	O, D_GLU_85	N, D_ILE_89	H, D_ILE_89	2.92	1.94	5.05
1HGF.PDB	O, D_LYS_88	N, D_TRP_92	H, D_TRP_92	2.90	1.93	7.06
1HGF.PDB	O, D_ILE_89	N, D_SER_93	H, D_SER_93	2.93	2.03	18.97
1HGF.PDB	O, D_ILE_89	OG, D_SER_93	HG, D_SER_93	2.79	1.87	14.25
1HGF.PDB	O, D_ASP_90	N, D_TYR_94	H, D_TYR_94	2.98	2.09	20.66
1HGF.PDB	O, D_TRP_92	N, D_ALA_96	H, D_ALA_96	2.99	2.03	9.70
1HGF.PDB	O, D_TYR_94	N, D_LEU_98	H, D_LEU_98	2.90	1.96	13.51
1HGF.PDB	O, D_ASN_95	N, D_LEU_99	H, D_LEU_99	2.97	2.01	11.18
1HGF.PDB	O, D_LEU_98	N, D_LEU_102	H, D_LEU_102	2.98	2.02	11.36
1HGF.PDB	O, D_LEU_99	N, D_GLU_103	H, D_GLU_103	2.92	1.96	10.07
1HGF.PDB	O, D_VAL_100	N, D_ASN_104	H, D_ASN_104	2.84	1.89	11.66
1HGF.PDB	O, C_LYS_27	ND2, D_ASN_104	HD21, D_ASN_104	2.89	1.96	15.72
1HGF.PDB	O, D_LEU_102	N, D_HIS_106	H, D_HIS_106	2.92	1.97	11.28
1HGF.PDB	O, D_GLU_103	N, D_THR_107	H, D_THR_107	2.85	1.92	13.38
1HGF.PDB	O, D_ASN_104	N, D_ILE_108	H, D_ILE_108	2.97	2.03	13.33
1HGF.PDB	O, D_HIS_106	N, D_LEU_110	H, D_LEU_110	2.77	1.83	11.73
1HGF.PDB	O, D_ASP_109	N, D_SER_113	H, D_SER_113	2.82	1.90	15.73
1HGF.PDB	O, D_SER_113	N, D_LYS_117	H, D_LYS_117	2.74	1.83	18.58
1HGF.PDB	O, D_MET_115	N, D_PHE_119	H, D_PHE_119	2.96	2.01	11.81
1HGF.PDB	O, D_ASN_116	N, D_GLU_120	H, D_GLU_120	2.90	1.92	4.93
1HGF.PDB	O, D_PHE_119	N, D_ARG_123	H, D_ARG_123	3.00	2.03	9.49
1HGF.PDB	OE2, D_GLU_120	NH1, D_ARG_123	HH11, D_ARG_123	2.79	1.92	25.71
1HGF.PDB	O, D_GLU_120	N, D_ARG_124	H, D_ARG_124	2.96	2.04	16.78
1HGF.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.79	1.88	16.40
1HGF.PDB	OH, D_TYR_157	ND2, D_ASN_129	HD21, D_ASN_129	2.81	1.84	5.39
1HGF.PDB	O, D_HIS_159	ND2, D_ASN_129	HD22, D_ASN_129	2.94	2.01	14.46
1HGF.PDB	O, D_LYS_139	N, D_GLU_131	H, D_GLU_131	2.98	2.08	19.93
1HGF.PDB	O, D_CYS_137	N, D_MET_133	H, D_MET_133	2.92	1.96	10.87
1HGF.PDB	OD1, D_ASN_135	N, D_CYS_137	H, D_CYS_137	2.83	1.95	20.45
1HGF.PDB	O, C_LEU_13	N, D_PHE_138	H, D_PHE_138	2.75	1.91	24.76
1HGF.PDB	O, D_GLU_131	N, D_LYS_139	H, D_LYS_139	2.83	1.88	9.91
1HGF.PDB	O, C_ALA_11	N, D_ILE_140	H, D_ILE_140	2.82	1.90	15.68
1HGF.PDB	O, D_ASN_129	N, D_TYR_141	H, D_TYR_141	2.87	1.92	10.75
1HGF.PDB	OG, D_SER_29	NZ, D_LYS_143	HZ1, D_LYS_143	2.83	1.89	20.16
1HGF.PDB	OE2, D_GLU_30	N, D_ASN_146	H, D_ASN_146	2.80	1.88	14.92
1HGF.PDB	OD2, D_ASP_145	N, D_ALA_147	H, D_ALA_147	2.87	2.00	23.24

1HGF.PDB	O, D_ASP_145	N, D_ILE_149	H, D_ILE_149	2.93	1.97	10.46
1HGF.PDB	O, D_ASN_146	N, D_GLU_150	H, D_GLU_150	2.94	2.01	15.42
1HGF.PDB	O, D_ALA_147	N, D_SER_151	H, D_SER_151	2.89	2.02	22.93
1HGF.PDB	O, D_CYS_148	OG, D_SER_151	HG, D_SER_151	2.73	1.81	12.37
1HGF.PDB	O, D_GLU_150	N, D_ASN_154	H, D_ASN_154	2.87	1.89	5.22
1HGF.PDB	O, D_SER_151	N, D_THR_156	H, D_THR_156	2.79	1.97	26.84
1HGF.PDB	OD1, D_ASN_154	OG1, D_THR_156	HG1, D_THR_156	2.72	1.80	12.72
1HGF.PDB	NE2, D_HIS_142	OH, D_TYR_157	HH, D_TYR_157	2.72	1.85	19.75
1HGF.PDB	OD1, D_ASP_158	N, D_ASP_160	H, D_ASP_160	3.00	2.13	23.50
1HGF.PDB	O, D_HIS_159	N, D_TYR_162	H, D_TYR_162	2.89	2.08	29.06
1HGF.PDB	O, D_ASP_160	N, D_ARG_163	H, D_ARG_163	3.00	2.09	17.80
1HGF.PDB	O, B_ARG_170	NH1, D_ARG_163	HH12, D_ARG_163	2.84	1.83	3.71
1HGF.PDB	OE1, B_GLU_131	NH2, D_ARG_163	HH21, D_ARG_163	2.70	1.83	24.43
1HGF.PDB	O, D_TYR_162	N, D_ALA_166	H, D_ALA_166	2.86	1.89	3.57
1HGF.PDB	O, D_ARG_163	N, D_LEU_167	H, D_LEU_167	2.79	1.83	4.62
1HGF.PDB	O, D_GLU_165	ND2, D_ASN_169	HD21, D_ASN_169	2.97	2.03	11.99
1HGF.PDB	O, D_ALA_166	N, D_ARG_170	H, D_ARG_170	2.84	1.97	21.75
1HGF.PDB	O, D_GLU_128	NE, D_ARG_170	HE, D_ARG_170	2.76	1.87	20.27
1HGF.PDB	OE2, D_GLU_131	NH1, D_ARG_170	HH11, D_ARG_170	2.84	1.84	5.29
1HGF.PDB	O, D_LEU_167	N, D_PHE_171	H, D_PHE_171	2.90	1.96	12.84
1HGF.PDB	O, F_ILE_140	N, E_ALA_11	H, E_ALA_11	2.95	2.06	20.63
1HGF.PDB	O, F_GLN_27	N, E_THR_12	H, E_THR_12	2.87	1.93	12.24
1HGF.PDB	O, F_PHE_138	N, E_LEU_13	H, E_LEU_13	2.96	1.99	8.43
1HGF.PDB	O, F_ARG_25	N, E_CYS_14	H, E_CYS_14	2.65	1.83	26.13
1HGF.PDB	O, F_GLY_136	N, E_LEU_15	H, E_LEU_15	2.91	1.93	3.45
1HGF.PDB	O, F_GLY_23	N, E_GLY_16	H, E_GLY_16	2.94	2.06	22.45
1HGF.PDB	O, E_HIS_18	ND1, E_HIS_17	HD1, E_HIS_17	2.99	2.14	25.53
1HGF.PDB	O, F_TRP_21	N, E_HIS_18	H, E_HIS_18	2.91	2.00	17.81
1HGF.PDB	OD1, E_ASN_322	N, E_VAL_20	H, E_VAL_20	2.80	1.82	2.55
1HGF.PDB	O, E_VAL_36	N, E_THR_24	H, E_THR_24	2.87	1.98	19.96
1HGF.PDB	O, E_ILE_34	N, E_VAL_26	H, E_VAL_26	2.89	1.93	10.60
1HGF.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.75	1.83	22.30
1HGF.PDB	O, E_VAL_26	N, E_ILE_34	H, E_ILE_34	2.94	1.98	10.18
1HGF.PDB	O, E_THR_24	N, E_VAL_36	H, E_VAL_36	2.81	1.85	7.38
1HGF.PDB	O, E_MET_320	N, E_THR_37	H, E_THR_37	2.91	1.94	5.79
1HGF.PDB	O, E_LEU_316	N, E_THR_40	H, E_THR_40	2.78	1.86	16.07
1HGF.PDB	O, E_LEU_314	N, E_LEU_42	H, E_LEU_42	2.78	1.90	19.77
1HGF.PDB	O, E_PHE_294	N, E_GLN_44	H, E_GLN_44	2.96	1.98	3.65
1HGF.PDB	O, E_SER_46	NE2, E_GLN_44	HE21, E_GLN_44	2.83	1.95	21.77
1HGF.PDB	O, E_ASN_285	OG, E_SER_47	HG, E_SER_47	2.86	1.95	16.70
1HGF.PDB	OD2, E_ASP_275	NZ, E_LYS_50	HZ2, E_LYS_50	2.90	1.90	14.56
1HGF.PDB	O, E_PRO_273	N, E_ILE_51	H, E_ILE_51	2.76	1.81	9.83
1HGF.PDB	O, E_ASP_275	N, E_ASN_53	H, E_ASN_53	2.89	1.97	17.56
1HGF.PDB	OD2, E_ASP_85	N, E_ARG_57	H, E_ARG_57	2.93	1.98	11.47
1HGF.PDB	O, E_THR_83	NE, E_ARG_57	HE, E_ARG_57	2.82	1.86	10.06
1HGF.PDB	O, E_LEU_86	N, E_LEU_59	H, E_LEU_59	2.87	1.91	9.41
1HGF.PDB	OD1, E_ASP_60	N, E_ILE_62	H, E_ILE_62	2.91	1.96	11.31
1HGF.PDB	O, E_GLY_61	N, E_CYS_64	H, E_CYS_64	2.88	1.96	16.75
1HGF.PDB	O, E_THR_65	N, E_ALA_69	H, E_ALA_69	3.00	2.07	14.88
1HGF.PDB	O, E_LEU_66	N, E_LEU_70	H, E_LEU_70	2.82	1.89	15.13
1HGF.PDB	O, E_ILE_67	N, E_LEU_71	H, E_LEU_71	2.91	1.95	6.47
1HGF.PDB	O, E_ASP_68	N, E_GLY_72	H, E_GLY_72	2.87	1.99	21.64
1HGF.PDB	OD1, E_ASP_73	ND1, E_HIS_75	HD1, E_HIS_75	2.85	1.91	12.17
1HGF.PDB	O, E_ASP_63	NE2, E_HIS_75	HE2, E_HIS_75	2.89	1.94	12.08
1HGF.PDB	O, E_ASP_73	N, E_CYS_76	H, E_CYS_76	2.81	1.88	15.29
1HGF.PDB	O, E_PRO_74	N, E_ASP_77	H, E_ASP_77	2.90	1.94	7.27
1HGF.PDB	O, E_CYS_76	N, E_PHE_79	H, E_PHE_79	2.95	1.97	5.01
1HGF.PDB	O, E_ARG_57	N, E_ASP_85	H, E_ASP_85	2.81	1.92	19.34

1HGF.PDB	O, E_MET_268	N, E_GLU_89	H, E_GLU_89	2.79	1.84	8.93
1HGF.PDB	OD1, E_ASP_60	NE, E_ARG_90	HE, E_ARG_90	2.80	1.85	10.51
1HGF.PDB	O, E_SER_270	NH1, E_ARG_90	HH11, E_ARG_90	2.63	1.77	25.28
1HGF.PDB	O, E_ALA_272	NH1, E_ARG_90	HH12, E_ARG_90	2.66	1.73	17.47
1HGF.PDB	OD2, E_ASP_60	NH2, E_ARG_90	HH21, E_ARG_90	2.88	1.89	10.22
1HGF.PDB	OD1, E_ASP_271	N, E_SER_91	H, E_SER_91	2.94	1.98	11.41
1HGF.PDB	OD2, E_ASP_73	N, E_ASN_96	H, E_ASN_96	2.93	1.99	16.05
1HGF.PDB	OD2, E_ASP_104	OG, E_SER_107	HG, E_SER_107	2.88	1.94	12.45
1HGF.PDB	O, E_TYR_105	N, E_ARG_109	H, E_ARG_109	2.91	1.93	1.03
1HGF.PDB	OE2, E_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.88	1.88	11.28
1HGF.PDB	OD2, E_ASP_79	OG, E_SER_110	HG, E_SER_110	2.78	1.90	21.69
1HGF.PDB	O, E_SER_107	N, E_LEU_111	H, E_LEU_111	2.99	2.02	8.11
1HGF.PDB	O, E_ARG_109	N, E_ALA_113	H, E_ALA_113	2.91	2.02	19.90
1HGF.PDB	O, E_SER_110	N, E_SER_114	H, E_SER_114	2.94	2.02	16.55
1HGF.PDB	OE2, E_GLU_119	OG1, E_THR_117	HG1, E_THR_117	2.96	1.99	6.08
1HGF.PDB	O, E_TYR_257	N, E_ILE_121	H, E_ILE_121	2.83	1.86	2.31
1HGF.PDB	O, E_ARG_255	N, E_GLU_123	H, E_GLU_123	2.87	1.92	11.49
1HGF.PDB	O, E_GLU_123	N, E_PHE_125	H, E_PHE_125	2.96	2.16	29.94
1HGF.PDB	O, E_THR_155	N, E_THR_131	H, E_THR_131	2.77	1.83	12.18
1HGF.PDB	ND2, E_ASN_152	NE2, E_GLN_132	HE21, E_GLN_132	2.95	2.01	11.55
1HGF.PDB	OD1, E_ASN_152	N, E_ASN_133	H, E_ASN_133	2.94	1.99	11.33
1HGF.PDB	O, E_TRP_153	N, E_GLY_134	H, E_GLY_134	2.99	2.07	16.55
1HGF.PDB	O, E_GLY_146	N, E_SER_136	H, E_SER_136	2.71	1.82	20.23
1HGF.PDB	OD2, E_ASP_77	NE, E_ARG_141	HE, E_ARG_141	2.92	2.06	25.46
1HGF.PDB	O, E_PHE_147	NH1, E_ARG_141	HH12, E_ARG_141	2.60	1.67	17.74
1HGF.PDB	OD1, E_ASP_77	NH2, E_ARG_141	HH21, E_ARG_141	2.83	1.96	25.41
1HGF.PDB	OD2, E_ASP_77	NH2, E_ARG_141	HH21, E_ARG_141	2.77	1.86	21.24
1HGF.PDB	O, E_SER_136	N, E_GLY_146	H, E_GLY_146	2.98	2.12	24.01
1HGF.PDB	O, E_GLY_72	N, E_SER_149	H, E_SER_149	2.88	1.98	19.21
1HGF.PDB	O, E_ALA_253	N, E_ASN_152	H, E_ASN_152	2.87	1.95	17.97
1HGF.PDB	OH, E_TYR_195	NE1, E_TRP_153	HE1, E_TRP_153	2.83	1.89	12.15
1HGF.PDB	O, E_LEU_194	N, E_LYS_156	H, E_LYS_156	2.87	1.98	19.42
1HGF.PDB	O, E_THR_160	N, E_SER_157	H, E_SER_157	2.99	2.11	21.85
1HGF.PDB	O, E_SER_247	N, E_LEU_164	H, E_LEU_164	2.72	1.84	21.47
1HGF.PDB	O, E_ILE_245	N, E_VAL_166	H, E_VAL_166	2.90	1.96	13.03
1HGF.PDB	O, E_ASP_241	N, E_ASN_170	H, E_ASN_170	2.87	1.90	4.85
1HGF.PDB	O, E_PHE_174	ND2, E_ASN_170	HD22, E_ASN_170	2.77	1.82	9.34
1HGF.PDB	O, E_VAL_237	N, E_LYS_176	H, E_LYS_176	2.92	1.99	15.75
1HGF.PDB	OE2, E_GLU_123	NZ, E_LYS_176	HZ1, E_LYS_176	2.76	1.80	18.44
1HGF.PDB	O, E_THR_235	N, E_TYR_178	H, E_TYR_178	2.83	1.85	2.97
1HGF.PDB	OE1, E_GLU_123	OH, E_TYR_178	HH, E_TYR_178	2.88	1.93	11.71
1HGF.PDB	OG1, E_THR_235	NE1, E_TRP_180	HE1, E_TRP_180	2.85	1.87	2.94
1HGF.PDB	O, E_ASN_250	N, E_HIS_183	H, E_HIS_183	2.80	1.96	25.59
1HGF.PDB	OH, E_TYR_98	NE2, E_HIS_183	HE2, E_HIS_183	2.91	1.99	15.99
1HGF.PDB	O, E_ARG_229	N, E_HIS_184	H, E_HIS_184	2.88	1.94	13.07
1HGF.PDB	OG, E_SER_231	NE2, E_HIS_184	HE2, E_HIS_184	2.70	1.89	28.56
1HGF.PDB	OD1, E_ASN_250	NE2, E_GLN_191	HE22, E_GLN_191	2.96	1.99	7.90
1HGF.PDB	O, E_ASN_188	N, E_THR_192	H, E_THR_192	2.94	2.01	14.37
1HGF.PDB	O, E_GLN_189	N, E_SER_193	H, E_SER_193	2.83	1.90	13.82
1HGF.PDB	O, E_GLU_190	N, E_LEU_194	H, E_LEU_194	2.94	1.99	12.89
1HGF.PDB	O, E_GLN_191	N, E_TYR_195	H, E_TYR_195	2.77	1.83	10.66
1HGF.PDB	O, E_ASN_248	NE2, E_GLN_197	HE21, E_GLN_197	2.89	2.01	21.02
1HGF.PDB	O, E_TYR_161	NE2, E_GLN_197	HE22, E_GLN_197	2.98	2.02	7.72
1HGF.PDB	O, E_ASN_246	N, E_THR_203	H, E_THR_203	2.97	2.01	9.92
1HGF.PDB	OG1, E_THR_212	OG1, E_THR_203	HG1, E_THR_203	2.89	1.95	9.70
1HGF.PDB	O, E_GLN_211	N, E_VAL_204	H, E_VAL_204	2.94	2.02	15.91
1HGF.PDB	OD1, E_ASP_241	N, E_ARG_207	H, E_ARG_207	2.90	1.94	9.22
1HGF.PDB	O, E_VAL_204	N, E_GLN_211	H, E_GLN_211	2.86	1.97	20.41

1HGF.PDB	O, E_VAL_202	N, E_ILE_213	H, E_ILE_213	2.88	1.97	17.74
1HGF.PDB	ND1, E_HIS_184	N, E_ASN_216	H, E_ASN_216	2.74	1.89	23.44
1HGF.PDB	O, E_ASN_216	NH1, E_ARG_220	HH12, E_ARG_220	2.97	2.15	29.37
1HGF.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.65	1.79	25.97
1HGF.PDB	O, E_ASN_216	NH2, E_ARG_220	HH22, E_ARG_220	2.76	1.86	21.47
1HGF.PDB	O, E_LEU_226	N, E_VAL_223	H, E_VAL_223	2.85	1.89	8.19
1HGF.PDB	O, E_CYS_97	NE, E_ARG_224	HE, E_ARG_224	2.78	1.93	24.07
1HGF.PDB	O, E_CYS_97	NH2, E_ARG_224	HH21, E_ARG_224	2.92	2.07	26.92
1HGF.PDB	O, E_VAL_223	N, E_LEU_226	H, E_LEU_226	2.92	1.97	10.75
1HGF.PDB	O, E_SER_228	NH1, E_ARG_229	HH11, E_ARG_229	2.73	1.81	20.22
1HGF.PDB	O, E_PRO_221	NH2, E_ARG_229	HH22, E_ARG_229	2.63	1.68	15.58
1HGF.PDB	O, E_PRO_99	N, E_ILE_230	H, E_ILE_230	2.96	2.12	25.49
1HGF.PDB	OD1, E_ASP_101	OG, E_SER_231	HG, E_SER_231	2.82	1.90	15.36
1HGF.PDB	O, E_ASP_101	N, E_ILE_232	H, E_ILE_232	2.91	1.98	14.67
1HGF.PDB	O, E_TRP_180	N, E_TYR_233	H, E_TYR_233	2.95	1.99	9.60
1HGF.PDB	O, E_TYR_178	N, E_THR_235	H, E_THR_235	2.86	1.98	21.39
1HGF.PDB	O, E_LYS_176	N, E_VAL_237	H, E_VAL_237	2.79	1.87	16.02
1HGF.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ2, E_LYS_238	2.83	1.84	16.42
1HGF.PDB	O, D_SER_71	NZ, E_LYS_238	HZ3, E_LYS_238	2.74	1.75	13.85
1HGF.PDB	O, E_ASN_170	N, E_GLY_240	H, E_GLY_240	2.92	2.12	29.34
1HGF.PDB	O, E_LYS_238	N, E_ASP_241	H, E_ASP_241	2.98	2.04	13.06
1HGF.PDB	OD1, E_ASP_241	N, E_VAL_242	H, E_VAL_242	2.72	1.93	29.38
1HGF.PDB	O, E_MET_168	N, E_LEU_243	H, E_LEU_243	2.94	1.97	6.95
1HGF.PDB	O, E_SER_205	N, E_VAL_244	H, E_VAL_244	2.94	1.98	11.07
1HGF.PDB	O, E_VAL_166	N, E_ILE_245	H, E_ILE_245	2.96	2.03	15.13
1HGF.PDB	O, E_THR_203	N, E_ASN_246	H, E_ASN_246	2.93	1.96	7.07
1HGF.PDB	OD1, E_ASN_165	ND2, E_ASN_246	HD21, E_ASN_246	2.93	2.02	19.67
1HGF.PDB	O, E_LEU_164	N, E_SER_247	H, E_SER_247	2.91	2.00	17.82
1HGF.PDB	O, E_ARG_201	OG, E_SER_247	HG, E_SER_247	2.77	1.98	29.79
1HGF.PDB	OG, E_SER_247	N, E_GLY_249	H, E_GLY_249	3.00	2.01	1.54
1HGF.PDB	O, E_HIS_183	ND2, E_ASN_250	HD21, E_ASN_250	2.78	1.81	7.40
1HGF.PDB	OE1, E_GLN_191	ND2, E_ASN_250	HD22, E_ASN_250	2.87	1.91	8.14
1HGF.PDB	O, E_ASN_152	N, E_ALA_253	H, E_ALA_253	2.95	2.04	17.49
1HGF.PDB	OD1, E_ASN_133	NH2, E_ARG_255	HH22, E_ARG_255	2.47	1.67	29.09
1HGF.PDB	O, E_ILE_121	N, E_TYR_257	H, E_TYR_257	2.99	2.17	27.08
1HGF.PDB	O, E_LEU_177	N, E_PHE_258	H, E_PHE_258	2.97	1.99	6.56
1HGF.PDB	OE1, E_GLU_119	NH2, E_ARG_261	HH22, E_ARG_261	2.73	1.89	28.16
1HGF.PDB	O, E_PHE_87	N, E_MET_268	H, E_MET_268	2.88	1.97	18.30
1HGF.PDB	O, E_PRO_284	OG, E_SER_270	HG, E_SER_270	2.78	1.84	9.58
1HGF.PDB	OG, E_SER_270	N, E_ALA_272	H, E_ALA_272	2.96	2.02	14.55
1HGF.PDB	O, E_ILE_51	N, E_ASP_275	H, E_ASP_275	2.91	2.03	21.67
1HGF.PDB	OD1, E_ASP_275	N, E_THR_276	H, E_THR_276	2.76	1.89	22.50
1HGF.PDB	O, E_ASN_54	N, E_SER_279	H, E_SER_279	2.78	1.83	11.19
1HGF.PDB	O, E_TYR_302	N, E_ILE_282	H, E_ILE_282	2.94	1.96	6.32
1HGF.PDB	O, E_THR_283	N, E_GLY_286	H, E_GLY_286	2.80	1.84	8.27
1HGF.PDB	O, E_LYS_50	N, E_SER_287	H, E_SER_287	2.79	1.82	5.70
1HGF.PDB	O, E_ALA_304	ND2, E_ASN_290	HD21, E_ASN_290	2.83	1.91	16.09
1HGF.PDB	OE1, E_GLN_44	NZ, E_LYS_292	HZ1, E_LYS_292	2.90	1.86	1.40
1HGF.PDB	OD1, E_ASP_291	NZ, E_LYS_292	HZ2, E_LYS_292	2.87	1.84	9.03
1HGF.PDB	O, E_LYS_307	N, E_GLN_295	H, E_GLN_295	2.82	1.98	25.22
1HGF.PDB	O, E_ASN_298	NE2, E_GLN_295	HE22, E_GLN_295	2.75	1.83	15.52
1HGF.PDB	O, E_GLN_44	N, E_ASN_296	H, E_ASN_296	2.89	1.94	10.75
1HGF.PDB	OD1, E_ASN_298	N, E_ILE_300	H, E_ILE_300	2.86	1.98	21.35
1HGF.PDB	O, E_ILE_282	N, E_TYR_302	H, E_TYR_302	2.78	1.95	26.52
1HGF.PDB	O, F_LYS_62	N, E_GLY_303	H, E_GLY_303	2.90	1.93	6.18
1HGF.PDB	O, E_GLN_295	N, E_VAL_309	H, E_VAL_309	2.93	2.06	22.44
1HGF.PDB	OG, F_SER_93	N, E_LYS_310	H, E_LYS_310	2.86	1.93	14.59
1HGF.PDB	OE1, E_GLU_41	OG1, E_THR_313	HG1, E_THR_313	2.68	1.89	29.15

1HGF.PDB	OE2, E_GLU_41	N, E_LEU_314	H, E_LEU_314	2.77	1.85	15.04
1HGF.PDB	OG1, E_THR_313	NZ, E_LYS_315	HZ2, E_LYS_315	2.94	2.00	21.30
1HGF.PDB	O, E_THR_40	N, E_LEU_316	H, E_LEU_316	2.76	1.85	16.85
1HGF.PDB	OD1, F_ASN_104	N, E_ALA_317	H, E_ALA_317	2.72	1.78	10.77
1HGF.PDB	O, E_ASN_38	N, E_THR_318	H, E_THR_318	2.90	1.95	12.98
1HGF.PDB	OE2, E_GLU_35	ND2, E_ASN_322	HD21, E_ASN_322	2.77	1.93	26.11
1HGF.PDB	O, E_VAL_20	ND2, E_ASN_322	HD22, E_ASN_322	2.96	2.04	16.53
1HGF.PDB	O, E_GLN_327	NZ, E_LYS_326	HZ2, E_LYS_326	2.70	1.74	17.93
1HGF.PDB	O, E_LYS_326	NE2, E_GLN_327	HE21, E_GLN_327	2.79	1.87	16.74
1HGF.PDB	OD2, F_ASP_112	N, F_GLY_1	H1, F_GLY_1	2.89	1.91	17.14
1HGF.PDB	OD1, F_ASP_109	N, F_LEU_2	H, F_LEU_2	2.91	2.00	18.77
1HGF.PDB	OD2, F_ASP_112	N, F_GLY_4	H, F_GLY_4	2.97	2.08	20.30
1HGF.PDB	OD1, F_ASP_112	N, F_ALA_5	H, F_ALA_5	2.98	2.11	23.47
1HGF.PDB	O, F_GLY_4	N, F_PHE_9	H, F_PHE_9	2.81	1.86	10.76
1HGF.PDB	O, F_GLY_13	ND2, F_ASN_12	HD21, F_ASN_12	2.77	1.93	24.90
1HGF.PDB	O, E_VAL_323	N, F_GLY_13	H, F_GLY_13	2.75	1.85	19.07
1HGF.PDB	O, E_HIS_17	N, F_TRP_14	H, F_TRP_14	2.87	1.96	16.52
1HGF.PDB	OG1, F_THR_41	N, F_TRP_21	H, F_TRP_21	2.91	1.99	16.39
1HGF.PDB	O, F_ALA_35	N, F_PHE_24	H, F_PHE_24	2.84	1.87	3.09
1HGF.PDB	O, E_CYS_14	N, F_ARG_25	H, F_ARG_25	2.91	1.94	8.25
1HGF.PDB	OE1, F_GLN_34	NE, F_ARG_25	HE, F_ARG_25	2.89	2.02	23.18
1HGF.PDB	OE1, F_GLN_34	NH2, F_ARG_25	HH21, F_ARG_25	2.91	2.03	24.46
1HGF.PDB	O, E_THR_12	N, F_GLN_27	H, F_GLN_27	3.00	2.08	17.91
1HGF.PDB	O, F_GLY_31	N, F_ASN_28	H, F_ASN_28	2.88	1.94	13.45
1HGF.PDB	O, F_CYS_144	ND2, F_ASN_28	HD21, F_ASN_28	2.81	1.91	20.19
1HGF.PDB	OD1, F_ASN_146	ND2, F_ASN_28	HD22, F_ASN_28	2.88	2.02	23.75
1HGF.PDB	O, F_ASN_28	N, F_GLY_31	H, F_GLY_31	2.91	2.04	22.35
1HGF.PDB	O, F_PHE_24	N, F_ALA_35	H, F_ALA_35	2.75	1.95	28.87
1HGF.PDB	O, F_TYR_22	N, F_ASP_37	H, F_ASP_37	2.72	1.77	3.63
1HGF.PDB	OD2, F_ASP_37	N, F_SER_40	H, F_SER_40	2.90	1.92	3.34
1HGF.PDB	O, F_ASP_37	OG1, F_THR_41	HG1, F_THR_41	2.65	1.82	24.28
1HGF.PDB	O, F_LEU_38	N, F_GLN_42	H, F_GLN_42	2.83	1.96	21.43
1HGF.PDB	OD1, F_ASP_46	NE2, F_GLN_42	HE21, F_GLN_42	2.86	1.99	23.71
1HGF.PDB	O, F_LYS_39	N, F_ALA_43	H, F_ALA_43	2.91	1.95	8.37
1HGF.PDB	O, F_SER_40	N, F_ALA_44	H, F_ALA_44	2.92	1.95	0.99
1HGF.PDB	O, F_GLN_42	N, F_ASP_46	H, F_ASP_46	2.79	1.83	7.98
1HGF.PDB	O, F_ALA_43	NE2, F_GLN_47	HE21, F_GLN_47	2.92	1.97	13.01
1HGF.PDB	O, F_ILE_45	N, F_ASN_49	H, F_ASN_49	2.88	1.99	20.58
1HGF.PDB	O, F_ASP_46	N, F_GLY_50	H, F_GLY_50	2.83	1.92	17.00
1HGF.PDB	O, F_GLN_47	N, F_LYS_51	H, F_LYS_51	2.95	1.98	4.87
1HGF.PDB	OE1, F_GLU_103	NZ, F_LYS_51	HZ1, F_LYS_51	2.72	1.69	6.79
1HGF.PDB	ND1, F_HIS_106	NZ, F_LYS_51	HZ3, F_LYS_51	2.66	1.70	17.89
1HGF.PDB	O, F_ILE_48	N, F_LEU_52	H, F_LEU_52	2.92	2.02	18.86
1HGF.PDB	O, F_ASN_49	N, F_ASN_53	H, F_ASN_53	2.83	1.96	22.00
1HGF.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.79	1.81	11.74
1HGF.PDB	OD2, D_ASP_86	NZ, F_LYS_62	HZ2, F_LYS_62	2.67	1.68	13.64
1HGF.PDB	OD2, D_ASP_90	NZ, F_LYS_62	HZ3, F_LYS_62	2.75	1.81	20.23
1HGF.PDB	OG, E_SER_266	ND1, F_HIS_64	HD1, F_HIS_64	2.65	1.77	20.25
1HGF.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.89	1.92	9.46
1HGF.PDB	O, F_PHE_63	NE2, F_GLN_65	HE21, F_GLN_65	2.97	2.00	6.66
1HGF.PDB	OE2, F_GLU_85	NZ, F_LYS_68	HZ1, F_LYS_68	2.64	1.77	26.62
1HGF.PDB	O, E_LYS_299	NZ, F_LYS_68	HZ2, F_LYS_68	2.97	1.95	8.70
1HGF.PDB	OG, A_SER_107	N, F_ARG_76	H, F_ARG_76	2.83	1.87	9.12
1HGF.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.86	1.88	5.84
1HGF.PDB	OE1, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.78	1.77	1.59
1HGF.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.69	1.70	7.61
1HGF.PDB	OE2, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.71	1.73	8.88
1HGF.PDB	O, F_GLY_75	N, F_ASP_79	H, F_ASP_79	2.99	2.05	14.09

1HGF.PDB	O, F_ILE_77	N, F_GLU_81	H, F_GLU_81	2.97	2.01	7.31
1HGF.PDB	O, F_GLN_78	N, F_LYS_82	H, F_LYS_82	2.99	2.12	23.13
1HGF.PDB	O, F_ASP_79	N, F_TYR_83	H, F_TYR_83	2.99	2.06	15.58
1HGF.PDB	O, F_LEU_80	N, F_VAL_84	H, F_VAL_84	2.90	1.94	9.23
1HGF.PDB	O, F_LYS_82	N, F_ASP_86	H, F_ASP_86	2.91	2.00	17.05
1HGF.PDB	O, F_TYR_83	N, F_THR_87	H, F_THR_87	2.99	2.06	14.57
1HGF.PDB	O, F_VAL_84	N, F_LYS_88	H, F_LYS_88	2.93	1.98	10.82
1HGF.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.55	1.63	21.75
1HGF.PDB	O, F_GLU_85	N, F_ILE_89	H, F_ILE_89	2.95	2.00	10.35
1HGF.PDB	O, F_LYS_88	N, F_TRP_92	H, F_TRP_92	2.92	1.96	8.47
1HGF.PDB	O, F_ILE_89	N, F_SER_93	H, F_SER_93	2.89	2.01	22.68
1HGF.PDB	O, F_ASP_90	N, F_TYR_94	H, F_TYR_94	2.99	2.08	18.84
1HGF.PDB	O, F_TRP_92	N, F_ALA_96	H, F_ALA_96	3.00	2.04	10.19
1HGF.PDB	O, F_TYR_94	N, F_LEU_98	H, F_LEU_98	2.95	2.00	11.08
1HGF.PDB	O, F_ASN_95	N, F_LEU_99	H, F_LEU_99	2.97	2.00	8.54
1HGF.PDB	O, F_LEU_98	N, F_LEU_102	H, F_LEU_102	2.99	2.02	4.18
1HGF.PDB	O, F_LEU_99	N, F_GLU_103	H, F_GLU_103	2.91	1.96	12.29
1HGF.PDB	O, F_VAL_100	N, F_ASN_104	H, F_ASN_104	2.82	1.88	14.39
1HGF.PDB	O, E_LYS_27	ND2, F_ASN_104	HD21, F_ASN_104	2.91	1.99	15.12
1HGF.PDB	O, F_LEU_102	N, F_HIS_106	H, F_HIS_106	2.96	1.99	6.92
1HGF.PDB	O, F_GLU_103	N, F_THR_107	H, F_THR_107	2.86	1.92	13.75
1HGF.PDB	O, F_ASN_104	N, F_ILE_108	H, F_ILE_108	2.95	2.03	17.77
1HGF.PDB	O, F_HIS_106	N, F_LEU_110	H, F_LEU_110	2.80	1.84	8.75
1HGF.PDB	O, F_ASP_109	N, F_SER_113	H, F_SER_113	2.83	1.88	9.86
1HGF.PDB	O, D_LEU_2	OG, F_SER_113	HG, F_SER_113	2.73	1.92	27.40
1HGF.PDB	O, F_SER_113	N, F_LYS_117	H, F_LYS_117	2.77	1.85	14.47
1HGF.PDB	O, F_GLU_114	N, F_LEU_118	H, F_LEU_118	2.99	2.05	13.43
1HGF.PDB	O, F_MET_115	N, F_PHE_119	H, F_PHE_119	2.96	2.03	15.65
1HGF.PDB	O, F_ASN_116	N, F_GLU_120	H, F_GLU_120	2.89	1.91	2.90
1HGF.PDB	O, F_PHE_119	N, F_ARG_123	H, F_ARG_123	2.99	2.04	11.96
1HGF.PDB	OE2, F_GLU_120	NH1, F_ARG_123	HH11, F_ARG_123	2.79	1.92	25.30
1HGF.PDB	O, F_GLU_120	N, F_ARG_124	H, F_ARG_124	2.94	1.99	12.33
1HGF.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.90	1.96	15.73
1HGF.PDB	OH, F_TYR_157	ND2, F_ASN_129	HD21, F_ASN_129	2.83	1.89	13.44
1HGF.PDB	O, F_HIS_159	ND2, F_ASN_129	HD22, F_ASN_129	2.96	2.06	18.90
1HGF.PDB	O, F_LYS_139	N, F_GLU_131	H, F_GLU_131	2.97	2.06	18.31
1HGF.PDB	O, F_CYS_137	N, F_MET_133	H, F_MET_133	2.91	1.96	10.70
1HGF.PDB	O, E_LEU_13	N, F_PHE_138	H, F_PHE_138	2.75	1.92	26.04
1HGF.PDB	O, F_GLU_131	N, F_LYS_139	H, F_LYS_139	2.85	1.90	10.44
1HGF.PDB	O, E_ALA_11	N, F_ILE_140	H, F_ILE_140	2.82	1.90	16.36
1HGF.PDB	O, F_ASN_129	N, F_TYR_141	H, F_TYR_141	2.91	1.97	14.31
1HGF.PDB	OD2, F_ASP_145	N, F_ALA_147	H, F_ALA_147	2.85	1.95	18.91
1HGF.PDB	O, F_ASP_145	N, F_ILE_149	H, F_ILE_149	2.92	1.96	9.99
1HGF.PDB	O, F_ASN_146	N, F_GLU_150	H, F_GLU_150	2.92	2.01	16.83
1HGF.PDB	O, F_GLU_150	N, F_ASN_154	H, F_ASN_154	2.85	1.95	19.47
1HGF.PDB	O, F_SER_151	N, F_THR_156	H, F_THR_156	2.79	1.97	27.62
1HGF.PDB	O, F_HIS_159	N, F_TYR_162	H, F_TYR_162	2.90	2.05	24.52
1HGF.PDB	OE1, D_GLU_131	NH2, F_ARG_163	HH21, F_ARG_163	2.69	1.84	27.00
1HGF.PDB	O, F_TYR_162	N, F_ALA_166	H, F_ALA_166	2.88	1.92	7.02
1HGF.PDB	O, F_ARG_163	N, F_LEU_167	H, F_LEU_167	2.80	1.84	8.02
1HGF.PDB	O, F_GLU_165	ND2, F_ASN_169	HD21, F_ASN_169	3.00	2.05	10.68
1HGF.PDB	O, F_ALA_166	N, F_ARG_170	H, F_ARG_170	2.86	2.02	25.68
1HGF.PDB	O, F_GLU_128	NE, F_ARG_170	HE, F_ARG_170	2.79	1.90	20.12
1HGF.PDB	OE2, F_GLU_131	NH1, F_ARG_170	HH11, F_ARG_170	2.85	1.84	3.96
1HGF.PDB	O, F_LEU_167	N, F_PHE_171	H, F_PHE_171	2.90	1.96	11.83
1HGG.PDB	O, B_ILE_140	N, A_ALA_11	H, A_ALA_11	2.90	1.98	16.87
1HGG.PDB	O, B_PHE_138	N, A_LEU_13	H, A_LEU_13	2.97	2.01	10.10
1HGG.PDB	O, B_ARG_25	N, A_CYS_14	H, A_CYS_14	2.92	1.97	11.02

1HGG.PDB	O, B_GLY_136	N, A_LEU_15	H, A_LEU_15	2.86	1.89	7.78
1HGG.PDB	O, B_GLY_23	N, A_GLY_16	H, A_GLY_16	2.90	2.00	20.11
1HGG.PDB	O, B_TRP_21	N, A_HIS_18	H, A_HIS_18	2.90	1.99	17.50
1HGG.PDB	OD1, A_ASN_322	N, A_VAL_20	H, A_VAL_20	2.82	1.84	4.55
1HGG.PDB	O, A_VAL_36	N, A_THR_24	H, A_THR_24	2.85	1.98	22.87
1HGG.PDB	O, A_ILE_34	N, A_VAL_26	H, A_VAL_26	2.77	1.83	12.78
1HGG.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.90	1.87	9.15
1HGG.PDB	O, A_VAL_26	N, A_ILE_34	H, A_ILE_34	2.94	2.01	14.94
1HGG.PDB	O, A_THR_24	N, A_VAL_36	H, A_VAL_36	2.80	1.84	7.79
1HGG.PDB	O, A_MET_320	N, A_THR_37	H, A_THR_37	2.90	1.93	7.41
1HGG.PDB	O, A_LEU_316	N, A_THR_40	H, A_THR_40	2.81	1.95	23.35
1HGG.PDB	O, A_LEU_314	N, A_LEU_42	H, A_LEU_42	2.87	2.00	23.31
1HGG.PDB	O, A_PHE_294	N, A_GLN_44	H, A_GLN_44	2.82	1.86	8.73
1HGG.PDB	OD2, A_ASP_275	NZ, A_LYS_50	HZ1, A_LYS_50	2.71	1.78	22.40
1HGG.PDB	O, A_PRO_273	N, A_ILE_51	H, A_ILE_51	2.76	1.80	7.18
1HGG.PDB	O, A_ASP_275	N, A_ASN_53	H, A_ASN_53	2.78	1.93	24.69
1HGG.PDB	OD2, A_ASP_85	N, A_ARG_57	H, A_ARG_57	2.88	1.93	11.04
1HGG.PDB	O, A_THR_83	NE, A_ARG_57	HE, A_ARG_57	2.76	1.79	4.99
1HGG.PDB	O, A_LEU_86	N, A_LEU_59	H, A_LEU_59	2.94	1.98	9.64
1HGG.PDB	O, A_VAL_88	N, A_GLY_61	H, A_GLY_61	2.99	2.14	24.72
1HGG.PDB	OD1, A_ASP_60	N, A_ILE_62	H, A_ILE_62	2.86	1.94	14.24
1HGG.PDB	O, A_GLY_61	N, A_CYS_64	H, A_CYS_64	2.94	2.01	15.60
1HGG.PDB	O, A_LEU_66	N, A_LEU_70	H, A_LEU_70	2.85	1.95	18.25
1HGG.PDB	O, A_ILE_67	N, A_LEU_71	H, A_LEU_71	2.83	1.86	6.13
1HGG.PDB	O, A_ASP_68	N, A_GLY_72	H, A_GLY_72	2.84	1.93	17.70
1HGG.PDB	OD1, A_ASP_73	N, A_HIS_75	H, A_HIS_75	2.97	2.06	18.51
1HGG.PDB	OD1, A_ASP_73	ND1, A_HIS_75	HD1, A_HIS_75	2.77	1.87	17.99
1HGG.PDB	O, A_ASP_63	NE2, A_HIS_75	HE2, A_HIS_75	2.83	1.88	12.09
1HGG.PDB	O, A_ASP_73	N, A_CYS_76	H, A_CYS_76	2.73	1.81	15.45
1HGG.PDB	O, A_PRO_74	N, A_ASP_77	H, A_ASP_77	2.92	1.97	11.68
1HGG.PDB	O, A_CYS_76	N, A_PHE_79	H, A_PHE_79	2.99	2.02	6.69
1HGG.PDB	O, A_PHE_79	N, A_GLU_82	H, A_GLU_82	3.00	2.09	17.80
1HGG.PDB	O, A_ARG_57	N, A_ASP_85	H, A_ASP_85	2.86	1.95	17.16
1HGG.PDB	O, A_SER_266	N, A_PHE_87	H, A_PHE_87	2.98	2.05	14.85
1HGG.PDB	O, A_LEU_59	N, A_VAL_88	H, A_VAL_88	2.95	1.98	7.50
1HGG.PDB	O, A_MET_268	N, A_GLU_89	H, A_GLU_89	2.80	1.85	11.55
1HGG.PDB	OD1, A_ASP_60	NE, A_ARG_90	HE, A_ARG_90	2.94	1.96	6.92
1HGG.PDB	O, A_SER_270	NH1, A_ARG_90	HH11, A_ARG_90	2.63	1.77	25.03
1HGG.PDB	O, A_ALA_272	NH1, A_ARG_90	HH12, A_ARG_90	2.66	1.75	18.96
1HGG.PDB	OD2, A_ASP_60	NH2, A_ARG_90	HH21, A_ARG_90	2.79	1.81	10.63
1HGG.PDB	OD1, A_ASP_271	N, A_SER_91	H, A_SER_91	2.92	1.99	16.08
1HGG.PDB	OD1, A_ASP_271	OG, A_SER_91	HG, A_SER_91	2.86	2.03	25.78
1HGG.PDB	OD2, A_ASP_271	OG, A_SER_91	HG, A_SER_91	2.85	1.97	21.46
1HGG.PDB	O, A_ASP_63	N, A_PHE_94	H, A_PHE_94	3.00	2.04	11.56
1HGG.PDB	OD2, A_ASP_68	OG, A_SER_95	HG, A_SER_95	2.94	1.99	11.26
1HGG.PDB	OD2, A_ASP_73	N, A_ASN_96	H, A_ASN_96	2.86	1.92	13.44
1HGG.PDB	SG, A_CYS_97	N, A_TYR_98	H, A_TYR_98	2.99	2.16	26.19
1HGG.PDB	OD1, A_ASP_68	OH, A_TYR_100	HH, A_TYR_100	2.94	1.99	11.28
1HGG.PDB	O, A_ILE_230	N, A_ASP_101	H, A_ASP_101	2.99	2.10	21.45
1HGG.PDB	OD1, A_ASP_104	N, A_SER_107	H, A_SER_107	2.91	2.03	21.37
1HGG.PDB	OD2, A_ASP_104	OG, A_SER_107	HG, A_SER_107	2.84	1.92	16.45
1HGG.PDB	O, A_TYR_105	N, A_ARG_109	H, A_ARG_109	2.79	1.82	3.79
1HGG.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.84	1.86	14.43
1HGG.PDB	OD2, F_ASP_79	OG, A_SER_110	HG, A_SER_110	2.88	1.95	14.29
1HGG.PDB	O, A_SER_107	N, A_LEU_111	H, A_LEU_111	2.81	1.85	7.66
1HGG.PDB	O, A_ARG_109	N, A_ALA_113	H, A_ALA_113	2.89	1.98	17.55
1HGG.PDB	O, A_SER_110	N, A_SER_114	H, A_SER_114	2.94	2.01	15.84
1HGG.PDB	OE2, A_GLU_119	OG1, A_THR_117	HG1, A_THR_117	2.88	1.93	9.58

1HGG.PDB	O, A_TYR_257	N, A_ILE_121	H, A_ILE_121	2.89	1.92	8.73
1HGG.PDB	O, A_ARG_255	N, A_GLU_123	H, A_GLU_123	2.94	2.00	13.79
1HGG.PDB	O, A_THR_155	N, A_THR_131	H, A_THR_131	2.73	1.83	17.36
1HGG.PDB	OD1, A_ASN_152	N, A_ASN_133	H, A_ASN_133	2.89	1.97	16.60
1HGG.PDB	O, A_GLY_146	N, A_SER_136	H, A_SER_136	2.76	1.85	17.88
1HGG.PDB	OG, A_SER_136	N, A_ALA_138	H, A_ALA_138	2.88	1.92	8.65
1HGG.PDB	O, A_GLY_144	NZ, A_LYS_140	HZ1, A_LYS_140	2.89	1.90	15.38
1HGG.PDB	OD1, A_ASN_137	NZ, A_LYS_140	HZ2, A_LYS_140	2.76	1.76	13.87
1HGG.PDB	OD2, A_ASP_77	NE, A_ARG_141	HE, A_ARG_141	2.89	2.07	28.91
1HGG.PDB	O, A_PHE_147	NH1, A_ARG_141	HH12, A_ARG_141	2.49	1.65	25.86
1HGG.PDB	OD1, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.76	1.85	22.03
1HGG.PDB	OD2, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.76	1.87	24.00
1HGG.PDB	O, A_GLY_72	NH2, A_ARG_141	HH22, A_ARG_141	2.92	1.93	7.80
1HGG.PDB	O, A_SER_136	N, A_GLY_146	H, A_GLY_146	2.98	2.09	20.80
1HGG.PDB	O, A_GLY_72	N, A_SER_149	H, A_SER_149	2.90	1.98	16.68
1HGG.PDB	O, A_ALA_253	N, A_ASN_152	H, A_ASN_152	2.72	1.87	24.29
1HGG.PDB	OH, A_TYR_195	NE1, A_TRP_153	HE1, A_TRP_153	2.91	1.96	13.96
1HGG.PDB	O, A_THR_131	N, A_THR_155	H, A_THR_155	2.93	1.99	12.97
1HGG.PDB	O, A_LEU_194	N, A_LYS_156	H, A_LYS_156	2.97	2.08	20.53
1HGG.PDB	O, A_SER_193	NZ, A_LYS_156	HZ2, A_LYS_156	2.65	1.69	18.25
1HGG.PDB	O, A_THR_160	N, A_SER_157	H, A_SER_157	2.97	2.06	18.87
1HGG.PDB	O, A_ILE_245	N, A_VAL_166	H, A_VAL_166	2.87	1.91	9.82
1HGG.PDB	O, A_LEU_243	OG1, A_THR_167	HG1, A_THR_167	2.86	1.98	20.98
1HGG.PDB	O, A_LEU_243	N, A_MET_168	H, A_MET_168	2.89	1.96	15.80
1HGG.PDB	O, A_ASP_241	N, A_ASN_170	H, A_ASN_170	2.91	1.93	5.10
1HGG.PDB	O, A_PHE_174	ND2, A_ASN_170	HD21, A_ASN_170	2.81	1.87	12.89
1HGG.PDB	O, A_VAL_237	ND2, A_ASN_170	HD22, A_ASN_170	2.85	1.98	22.66
1HGG.PDB	O, A_VAL_237	N, A_LYS_176	H, A_LYS_176	2.93	1.99	14.07
1HGG.PDB	OE2, A_GLU_123	NZ, A_LYS_176	HZ1, A_LYS_176	2.65	1.77	25.92
1HGG.PDB	O, A_THR_235	N, A_TYR_178	H, A_TYR_178	2.78	1.81	6.55
1HGG.PDB	OE1, A_GLU_123	OH, A_TYR_178	HH, A_TYR_178	2.78	1.83	8.16
1HGG.PDB	OG1, A_THR_235	NE1, A_TRP_180	HE1, A_TRP_180	2.92	1.93	2.35
1HGG.PDB	O, A_ASN_250	N, A_HIS_183	H, A_HIS_183	2.79	1.91	21.79
1HGG.PDB	O, A_ARG_229	N, A_HIS_184	H, A_HIS_184	2.85	1.88	5.64
1HGG.PDB	OG, A_SER_231	NE2, A_HIS_184	HE2, A_HIS_184	2.80	1.92	21.87
1HGG.PDB	OG1, A_THR_187	N, A_GLU_190	H, A_GLU_190	2.84	1.88	9.16
1HGG.PDB	O, A_THR_187	N, A_GLN_191	H, A_GLN_191	3.00	2.05	11.25
1HGG.PDB	O, A_GLN_197	NE2, A_GLN_191	HE22, A_GLN_191	2.89	1.99	19.48
1HGG.PDB	O, A_ASN_188	OG1, A_THR_192	HG1, A_THR_192	2.94	2.01	12.14
1HGG.PDB	O, A_GLN_189	N, A_SER_193	H, A_SER_193	2.84	1.87	5.56
1HGG.PDB	O, A_GLN_189	OG, A_SER_193	HG, A_SER_193	2.70	1.82	19.80
1HGG.PDB	O, A_GLU_190	N, A_LEU_194	H, A_LEU_194	2.99	2.04	11.68
1HGG.PDB	O, A_GLN_191	N, A_TYR_195	H, A_TYR_195	2.81	1.87	11.54
1HGG.PDB	O, A_THR_192	N, A_VAL_196	H, A_VAL_196	2.94	2.12	27.19
1HGG.PDB	O, A_TYR_161	NE2, A_GLN_197	HE21, A_GLN_197	2.91	1.94	6.31
1HGG.PDB	O, A_ASN_248	NE2, A_GLN_197	HE22, A_GLN_197	2.93	2.04	20.44
1HGG.PDB	OD1, A_ASN_246	NH2, A_ARG_201	HH21, A_ARG_201	2.65	1.72	18.81
1HGG.PDB	O, A_ILE_213	N, A_VAL_202	H, A_VAL_202	2.91	1.94	9.19
1HGG.PDB	O, A_ASN_246	N, A_THR_203	H, A_THR_203	2.82	1.89	14.13
1HGG.PDB	O, A_GLN_211	N, A_VAL_204	H, A_VAL_204	2.88	1.97	18.00
1HGG.PDB	O, A_SER_209	N, A_THR_206	H, A_THR_206	2.97	2.00	7.26
1HGG.PDB	OD1, A_ASP_241	N, A_ARG_207	H, A_ARG_207	2.89	1.94	12.62
1HGG.PDB	OD2, A_ASP_241	NE, A_ARG_208	HE, A_ARG_208	2.96	2.06	20.34
1HGG.PDB	OG1, A_THR_206	OG, A_SER_209	HG, A_SER_209	2.95	2.03	14.98
1HGG.PDB	OD1, E_ASP_101	NE2, A_GLN_210	HE22, A_GLN_210	2.99	2.07	17.95
1HGG.PDB	O, A_VAL_204	N, A_GLN_211	H, A_GLN_211	2.83	1.92	18.11
1HGG.PDB	OG1, A_THR_203	OG1, A_THR_212	HG1, A_THR_212	2.88	1.92	6.20
1HGG.PDB	O, A_VAL_202	N, A_ILE_213	H, A_ILE_213	2.82	1.90	15.67

1HGG.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.73	1.78	15.93
1HGG.PDB	O, A_ASN_216	NH2, A_ARG_220	HH22, A_ARG_220	2.70	1.79	20.31
1HGG.PDB	O, A_LEU_226	N, A_VAL_223	H, A_VAL_223	2.90	1.94	11.61
1HGG.PDB	O, A_CYS_97	NE, A_ARG_224	HE, A_ARG_224	2.79	1.96	26.10
1HGG.PDB	O, A_CYS_97	NH2, A_ARG_224	HH21, A_ARG_224	2.82	1.96	25.99
1HGG.PDB	O, A_VAL_223	N, A_LEU_226	H, A_LEU_226	2.95	2.01	13.46
1HGG.PDB	O, A_SER_228	NH1, A_ARG_229	HH11, A_ARG_229	2.74	1.81	18.53
1HGG.PDB	O, A_PRO_221	NH2, A_ARG_229	HH22, A_ARG_229	2.60	1.67	16.87
1HGG.PDB	OD1, A_ASP_101	OG, A_SER_231	HG, A_SER_231	2.88	1.92	8.82
1HGG.PDB	O, A_ASP_101	N, A_ILE_232	H, A_ILE_232	2.92	2.00	16.64
1HGG.PDB	O, A_TRP_180	N, A_TYR_233	H, A_TYR_233	2.89	1.93	10.84
1HGG.PDB	O, A_TYR_178	N, A_THR_235	H, A_THR_235	2.90	2.00	18.55
1HGG.PDB	O, A_LYS_176	N, A_VAL_237	H, A_VAL_237	2.81	1.85	9.01
1HGG.PDB	O, F_SER_71	NZ, A_LYS_238	HZ2, A_LYS_238	2.70	1.77	20.55
1HGG.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.93	1.93	14.31
1HGG.PDB	OE2, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.74	1.91	29.92
1HGG.PDB	O, A_ASN_170	N, A_GLY_240	H, A_GLY_240	2.85	1.99	23.50
1HGG.PDB	O, A_LYS_238	N, A_ASP_241	H, A_ASP_241	2.97	2.05	16.90
1HGG.PDB	OD1, A_ASP_241	N, A_VAL_242	H, A_VAL_242	2.79	1.98	28.57
1HGG.PDB	O, A_MET_168	N, A_LEU_243	H, A_LEU_243	2.88	1.91	4.58
1HGG.PDB	O, A_SER_205	N, A_VAL_244	H, A_VAL_244	2.92	1.98	13.47
1HGG.PDB	O, A_VAL_166	N, A_ILE_245	H, A_ILE_245	2.93	2.00	14.39
1HGG.PDB	O, A_THR_203	N, A_ASN_246	H, A_ASN_246	2.89	1.94	11.24
1HGG.PDB	OD1, A_ASN_165	ND2, A_ASN_246	HD22, A_ASN_246	2.90	1.98	17.02
1HGG.PDB	O, A_LEU_164	N, A_SER_247	H, A_SER_247	2.90	1.99	18.81
1HGG.PDB	OE1, A_GLN_191	ND2, A_ASN_250	HD21, A_ASN_250	2.92	1.96	11.11
1HGG.PDB	O, A_HIS_183	ND2, A_ASN_250	HD22, A_ASN_250	2.85	1.89	9.48
1HGG.PDB	O, A_ASN_152	N, A_ALA_253	H, A_ALA_253	2.86	1.94	16.70
1HGG.PDB	OD1, A_ASN_133	NH2, A_ARG_255	HH22, A_ARG_255	2.52	1.66	24.50
1HGG.PDB	O, A_ILE_121	N, A_TYR_257	H, A_TYR_257	2.96	2.12	25.89
1HGG.PDB	O, A_LEU_177	N, A_PHE_258	H, A_PHE_258	2.95	2.01	12.69
1HGG.PDB	OG, A_SER_115	N, A_ARG_261	H, A_ARG_261	2.99	2.03	11.53
1HGG.PDB	OE2, A_GLU_119	NH1, A_ARG_261	HH12, A_ARG_261	2.68	1.87	29.79
1HGG.PDB	OE1, A_GLU_119	NH2, A_ARG_261	HH22, A_ARG_261	2.74	1.88	26.75
1HGG.PDB	OH, A_TYR_302	NZ, A_LYS_264	HZ1, A_LYS_264	2.93	1.98	19.58
1HGG.PDB	ND1, A_HIS_56	NZ, A_LYS_264	HZ2, A_LYS_264	2.66	1.73	19.87
1HGG.PDB	OD2, A_ASP_85	NZ, A_LYS_264	HZ3, A_LYS_264	2.83	1.83	12.74
1HGG.PDB	O, A_PHE_87	N, A_MET_268	H, A_MET_268	2.85	1.96	20.36
1HGG.PDB	OE1, B_GLU_67	NH1, A_ARG_269	HH12, A_ARG_269	2.69	1.86	28.34
1HGG.PDB	O, A_PRO_284	OG, A_SER_270	HG, A_SER_270	2.78	1.86	15.49
1HGG.PDB	OG, A_SER_270	N, A_ALA_272	H, A_ALA_272	2.95	2.00	11.38
1HGG.PDB	O, A_ILE_51	N, A_ASP_275	H, A_ASP_275	2.83	1.95	21.40
1HGG.PDB	OD1, A_ASP_275	N, A_THR_276	H, A_THR_276	2.80	1.95	24.62
1HGG.PDB	O, A_ASN_54	N, A_SER_279	H, A_SER_279	2.79	1.85	12.05
1HGG.PDB	O, A_TYR_302	N, A_ILE_282	H, A_ILE_282	2.87	1.93	13.76
1HGG.PDB	O, A_THR_283	N, A_GLY_286	H, A_GLY_286	2.80	1.86	11.09
1HGG.PDB	O, A_LYS_50	N, A_SER_287	H, A_SER_287	2.87	1.90	6.27
1HGG.PDB	O, A_ALA_304	ND2, A_ASN_290	HD22, A_ASN_290	2.86	1.98	20.93
1HGG.PDB	OE1, A_GLN_44	NZ, A_LYS_292	HZ1, A_LYS_292	2.74	1.73	11.51
1HGG.PDB	OD2, A_ASP_291	NZ, A_LYS_292	HZ3, A_LYS_292	2.77	1.90	27.56
1HGG.PDB	O, A_LYS_307	N, A_GLN_295	H, A_GLN_295	2.78	1.90	20.19
1HGG.PDB	O, A_ASN_298	NE2, A_GLN_295	HE21, A_GLN_295	2.82	1.86	7.25
1HGG.PDB	O, A_GLN_44	N, A_ASN_296	H, A_ASN_296	2.89	1.94	10.48
1HGG.PDB	OD1, A_ASN_285	ND2, A_ASN_298	HD22, A_ASN_298	2.97	2.01	11.28
1HGG.PDB	O, B_LYS_68	NZ, A_LYS_299	HZ1, A_LYS_299	2.91	1.88	9.16
1HGG.PDB	OD1, A_ASN_298	N, A_ILE_300	H, A_ILE_300	2.88	1.94	13.01
1HGG.PDB	O, A_ILE_282	N, A_TYR_302	H, A_TYR_302	2.82	1.93	21.11
1HGG.PDB	O, A_LYS_264	OH, A_TYR_302	HH, A_TYR_302	2.68	1.87	27.38

1HGG.PDB	O, B_LYS_62	N, A_GLY_303	H, A_GLY_303	2.91	1.94	6.06
1HGG.PDB	O, A_GLN_295	N, A_VAL_309	H, A_VAL_309	2.91	2.09	27.06
1HGG.PDB	OG, B_SER_93	N, A_LYS_310	H, A_LYS_310	2.89	1.96	14.59
1HGG.PDB	OD1, B_ASP_90	NZ, A_LYS_310	HZ2, A_LYS_310	2.70	1.74	18.08
1HGG.PDB	OE2, A_GLU_41	N, A_LEU_314	H, A_LEU_314	2.82	1.91	16.70
1HGG.PDB	OE1, A_GLU_41	NZ, A_LYS_315	HZ3, A_LYS_315	2.73	1.81	23.14
1HGG.PDB	O, A_THR_40	N, A_LEU_316	H, A_LEU_316	2.77	1.85	15.18
1HGG.PDB	OD1, B_ASN_104	N, A_ALA_317	H, A_ALA_317	2.79	1.88	16.20
1HGG.PDB	O, A_ASN_38	N, A_THR_318	H, A_THR_318	2.90	1.97	14.69
1HGG.PDB	O, A_VAL_20	ND2, A_ASN_322	HD21, A_ASN_322	2.85	1.93	15.64
1HGG.PDB	OE2, A_GLU_35	ND2, A_ASN_322	HD22, A_ASN_322	2.81	1.95	25.01
1HGG.PDB	OE2, B_GLU_15	NZ, A_LYS_326	HZ1, A_LYS_326	2.83	1.89	21.04
1HGG.PDB	OE1, A_GLU_325	NZ, A_LYS_326	HZ3, A_LYS_326	2.82	1.86	18.51
1HGG.PDB	OD2, B_ASP_112	N, B_GLY_1	H2, B_GLY_1	2.70	1.71	13.07
1HGG.PDB	OD1, B_ASP_109	N, B_LEU_2	H, B_LEU_2	2.95	2.05	19.45
1HGG.PDB	OD2, B_ASP_112	N, B_PHE_3	H, B_PHE_3	2.84	2.02	27.93
1HGG.PDB	OD2, B_ASP_112	N, B_GLY_4	H, B_GLY_4	2.94	2.03	17.01
1HGG.PDB	OD1, B_ASP_112	N, B_ALA_5	H, B_ALA_5	2.91	2.04	23.33
1HGG.PDB	O, B_GLY_4	N, B_PHE_9	H, B_PHE_9	2.76	1.84	15.80
1HGG.PDB	O, A_VAL_323	N, B_GLY_13	H, B_GLY_13	2.71	1.78	13.00
1HGG.PDB	O, A_HIS_17	N, B_TRP_14	H, B_TRP_14	2.79	1.88	17.76
1HGG.PDB	OG1, B_THR_41	N, B_TRP_21	H, B_TRP_21	2.85	1.90	11.01
1HGG.PDB	O, A_GLY_16	N, B_GLY_23	H, B_GLY_23	2.99	2.09	20.32
1HGG.PDB	O, B_ALA_35	N, B_PHE_24	H, B_PHE_24	2.82	1.86	7.34
1HGG.PDB	OE1, B_GLN_34	NE, B_ARG_25	HE, B_ARG_25	2.80	1.89	18.36
1HGG.PDB	OE1, B_GLN_34	NH2, B_ARG_25	HH21, B_ARG_25	2.91	2.04	24.97
1HGG.PDB	OE2, A_GLU_325	NH2, B_ARG_25	HH22, B_ARG_25	2.94	1.96	12.23
1HGG.PDB	O, B_GLY_33	N, B_HIS_26	H, B_HIS_26	2.74	1.85	19.00
1HGG.PDB	O, B_GLY_31	N, B_ASN_28	H, B_ASN_28	2.71	1.77	11.36
1HGG.PDB	O, B_ASN_28	N, B_GLY_31	H, B_GLY_31	2.90	1.97	14.90
1HGG.PDB	O, B_PHE_24	N, B_ALA_35	H, B_ALA_35	2.88	2.07	28.80
1HGG.PDB	O, B_TYR_22	N, B_ASP_37	H, B_ASP_37	2.72	1.76	2.83
1HGG.PDB	OD2, B_ASP_37	N, B_SER_40	H, B_SER_40	2.85	1.90	11.78
1HGG.PDB	OD2, B_ASP_37	OG, B_SER_40	HG, B_SER_40	2.80	1.93	21.69
1HGG.PDB	O, B_ASP_37	OG1, B_THR_41	HG1, B_THR_41	2.72	1.82	17.56
1HGG.PDB	O, B_LEU_38	N, B_GLN_42	H, B_GLN_42	2.94	1.99	12.08
1HGG.PDB	OD1, B_ASP_46	NE2, B_GLN_42	HE22, B_GLN_42	2.83	1.95	21.37
1HGG.PDB	O, B_LYS_39	N, B_ALA_43	H, B_ALA_43	2.99	2.02	7.45
1HGG.PDB	O, B_SER_40	N, B_ALA_44	H, B_ALA_44	2.94	1.96	2.17
1HGG.PDB	O, B_THR_41	N, B_ILE_45	H, B_ILE_45	2.95	2.02	15.56
1HGG.PDB	O, B_GLN_42	N, B_ASP_46	H, B_ASP_46	2.79	1.82	3.46
1HGG.PDB	OE2, B_GLU_114	NE2, B_GLN_47	HE21, B_GLN_47	2.96	2.05	17.92
1HGG.PDB	O, B_ALA_43	NE2, B_GLN_47	HE22, B_GLN_47	2.97	2.06	17.51
1HGG.PDB	O, B_ILE_45	N, B_ASN_49	H, B_ASN_49	2.86	1.94	16.30
1HGG.PDB	O, B_ASP_46	N, B_GLY_50	H, B_GLY_50	2.92	2.06	23.80
1HGG.PDB	O, B_GLN_47	N, B_LYS_51	H, B_LYS_51	2.94	1.96	0.16
1HGG.PDB	OG1, B_THR_107	NZ, B_LYS_51	HZ1, B_LYS_51	2.97	2.00	18.19
1HGG.PDB	OE1, B_GLU_103	NZ, B_LYS_51	HZ2, B_LYS_51	2.76	1.73	5.86
1HGG.PDB	ND1, B_HIS_106	NZ, B_LYS_51	HZ3, B_LYS_51	2.77	1.79	14.96
1HGG.PDB	O, B_ILE_48	N, B_LEU_52	H, B_LEU_52	2.89	1.99	19.12
1HGG.PDB	O, B_ASN_49	N, B_ASN_53	H, B_ASN_53	2.89	1.99	19.14
1HGG.PDB	O, E_THR_28	NE, B_ARG_54	HE, B_ARG_54	2.94	1.97	7.82
1HGG.PDB	OE1, B_GLU_57	NH1, B_ARG_54	HH11, B_ARG_54	2.86	1.86	11.23
1HGG.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.75	1.76	9.96
1HGG.PDB	OE2, B_GLU_61	NZ, B_LYS_58	HZ3, B_LYS_58	2.94	1.92	12.53
1HGG.PDB	OD2, F_ASP_90	NZ, B_LYS_62	HZ2, B_LYS_62	2.65	1.82	29.87
1HGG.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ3, B_LYS_62	2.64	1.73	23.35
1HGG.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.90	1.96	14.63

1HGG.PDB	O, B.PHE.63	NE2, B.GLN.65	HE22, B.GLN.65	2.94	1.96	4.34
1HGG.PDB	O, A.LYS.299	NZ, B.LYS.68	HZ1, B.LYS.68	2.86	1.83	9.73
1HGG.PDB	OE2, B.GLU.85	NZ, B.LYS.68	HZ2, B.LYS.68	2.75	1.72	7.06
1HGG.PDB	OE2, B.GLU.72	OG, B.SER.71	HG, B.SER.71	2.84	2.03	27.31
1HGG.PDB	OG, C.SER.107	N, B.ARG.76	H, B.ARG.76	2.77	1.82	10.45
1HGG.PDB	OE2, D.GLU.81	NE, B.ARG.76	HE, B.ARG.76	2.94	1.96	10.47
1HGG.PDB	OE1, D.GLU.74	NH1, B.ARG.76	HH12, B.ARG.76	2.88	1.89	10.69
1HGG.PDB	OE1, D.GLU.81	NH2, B.ARG.76	HH21, B.ARG.76	2.73	1.73	5.91
1HGG.PDB	OE2, D.GLU.74	NH2, B.ARG.76	HH22, B.ARG.76	2.82	1.82	7.26
1HGG.PDB	O, B.GLY.75	N, B.ASP.79	H, B.ASP.79	2.85	1.93	16.05
1HGG.PDB	OE1, D.GLU.85	OH, B.TYR.83	HH, B.TYR.83	2.68	1.80	19.99
1HGG.PDB	O, B.LEU.80	N, B.VAL.84	H, B.VAL.84	2.87	1.91	8.71
1HGG.PDB	O, B.LYS.82	N, B.ASP.86	H, B.ASP.86	2.95	2.00	10.58
1HGG.PDB	O, B.TYR.83	N, B.THR.87	H, B.THR.87	2.90	1.95	10.43
1HGG.PDB	O, B.VAL.84	N, B.LYS.88	H, B.LYS.88	2.87	2.00	23.09
1HGG.PDB	OH, F.TYR.83	NZ, B.LYS.88	HZ1, B.LYS.88	2.77	1.73	5.14
1HGG.PDB	O, B.GLU.85	N, B.ILE.89	H, B.ILE.89	2.84	1.88	8.66
1HGG.PDB	O, B.LYS.88	N, B.TRP.92	H, B.TRP.92	2.93	1.96	6.86
1HGG.PDB	O, B.ILE.89	N, B.SER.93	H, B.SER.93	2.84	1.95	20.72
1HGG.PDB	O, B.ILE.89	OG, B.SER.93	HG, B.SER.93	2.79	1.89	17.30
1HGG.PDB	O, B.ASP.90	N, B.TYR.94	H, B.TYR.94	2.97	2.04	15.33
1HGG.PDB	O, B.TRP.92	N, B.ALA.96	H, B.ALA.96	2.98	2.05	15.46
1HGG.PDB	O, B.TYR.94	N, B.LEU.98	H, B.LEU.98	2.95	2.00	9.66
1HGG.PDB	O, B.ASN.95	N, B.LEU.99	H, B.LEU.99	2.89	1.99	18.59
1HGG.PDB	O, B.ALA.96	N, B.VAL.100	H, B.VAL.100	2.98	2.01	8.53
1HGG.PDB	O, B.LEU.98	N, B.LEU.102	H, B.LEU.102	2.92	1.98	12.12
1HGG.PDB	O, B.VAL.100	N, B.ASN.104	H, B.ASN.104	2.85	1.94	17.67
1HGG.PDB	O, A.LYS.27	ND2, B.ASN.104	HD22, B.ASN.104	2.88	1.95	14.60
1HGG.PDB	O, B.LEU.102	N, B.HIS.106	H, B.HIS.106	2.96	2.00	9.47
1HGG.PDB	O, B.GLU.103	N, B.THR.107	H, B.THR.107	2.81	1.95	23.40
1HGG.PDB	O, B.HIS.106	N, B.LEU.110	H, B.LEU.110	2.81	1.86	11.06
1HGG.PDB	O, B.THR.107	N, B.THR.111	H, B.THR.111	2.99	2.04	11.06
1HGG.PDB	O, B.THR.107	OG1, B.THR.111	HG1, B.THR.111	2.84	1.91	11.39
1HGG.PDB	O, B.ASP.109	N, B.SER.113	H, B.SER.113	2.78	1.86	16.47
1HGG.PDB	O, B.SER.113	N, B.LYS.117	H, B.LYS.117	2.73	1.85	21.24
1HGG.PDB	O, B.GLU.114	N, B.LEU.118	H, B.LEU.118	2.99	2.06	15.73
1HGG.PDB	O, B.MET.115	N, B.PHE.119	H, B.PHE.119	3.00	2.05	12.47
1HGG.PDB	O, B.ASN.116	N, B.GLU.120	H, B.GLU.120	2.95	1.97	4.00
1HGG.PDB	O, B.LYS.117	N, B.LYS.121	H, B.LYS.121	2.90	2.02	20.57
1HGG.PDB	O, B.LEU.118	N, B.THR.122	H, B.THR.122	2.96	1.98	6.92
1HGG.PDB	O, B.PHE.119	N, B.ARG.123	H, B.ARG.123	2.91	1.95	9.73
1HGG.PDB	OE2, B.GLU.120	NH1, B.ARG.123	HH11, B.ARG.123	2.73	1.87	25.50
1HGG.PDB	O, B.GLU.120	N, B.ARG.124	H, B.ARG.124	2.98	2.01	8.72
1HGG.PDB	OE1, F.GLU.132	NE, B.ARG.124	HE, B.ARG.124	2.84	1.98	22.96
1HGG.PDB	OE2, F.GLU.132	NE, B.ARG.124	HE, B.ARG.124	2.81	1.98	25.54
1HGG.PDB	O, B.HIS.159	ND2, B.ASN.129	HD21, B.ASN.129	2.98	2.03	11.68
1HGG.PDB	OH, B.TYR.157	ND2, B.ASN.129	HD22, B.ASN.129	2.80	1.86	13.18
1HGG.PDB	O, B.LYS.139	N, B.GLU.131	H, B.GLU.131	2.96	2.02	13.20
1HGG.PDB	O, B.CYS.137	N, B.MET.133	H, B.MET.133	2.89	1.98	18.42
1HGG.PDB	O, A.LEU.13	N, B.PHE.138	H, B.PHE.138	2.70	1.86	24.49
1HGG.PDB	O, B.GLU.131	N, B.LYS.139	H, B.LYS.139	2.86	1.90	8.51
1HGG.PDB	O, A.ALA.11	N, B.ILE.140	H, B.ILE.140	2.77	1.86	18.05
1HGG.PDB	O, B.ASN.129	N, B.TYR.141	H, B.TYR.141	2.90	1.92	3.10
1HGG.PDB	OE2, B.GLU.165	N, B.LYS.143	H, B.LYS.143	2.97	2.08	21.83
1HGG.PDB	OD1, B.ASP.145	N, B.ALA.147	H, B.ALA.147	2.99	2.19	29.06
1HGG.PDB	O, B.ASP.145	N, B.ILE.149	H, B.ILE.149	2.94	1.98	9.40
1HGG.PDB	O, B.ASN.146	N, B.GLU.150	H, B.GLU.150	2.89	1.95	12.57
1HGG.PDB	O, B.ALA.147	N, B.SER.151	H, B.SER.151	2.85	1.98	22.55

1HGG.PDB	O, B_CYS_148	OG, B_SER_151	HG, B_SER_151	2.71	1.85	21.43
1HGG.PDB	O, B_GLU_150	N, B_ASN_154	H, B_ASN_154	2.84	1.87	3.20
1HGG.PDB	O, B_SER_151	N, B_THR_156	H, B_THR_156	2.76	1.93	25.42
1HGG.PDB	OD1, B_ASN_154	OG1, B_THR_156	HG1, B_THR_156	2.71	1.81	17.64
1HGG.PDB	OD1, B_ASP_158	N, B_ASP_160	H, B_ASP_160	2.97	2.06	18.02
1HGG.PDB	O, B_HIS_159	N, B_TYR_162	H, B_TYR_162	2.94	2.02	17.18
1HGG.PDB	O, B_ASP_160	N, B_ARG_163	H, B_ARG_163	2.91	1.94	6.47
1HGG.PDB	O, F_ARG_170	NH1, B_ARG_163	HH12, B_ARG_163	2.76	1.82	18.13
1HGG.PDB	O, B_TYR_162	N, B_ALA_166	H, B_ALA_166	2.87	1.91	8.33
1HGG.PDB	O, B_ARG_163	N, B_LEU_167	H, B_LEU_167	2.76	1.83	12.88
1HGG.PDB	O, B_ALA_166	N, B_ARG_170	H, B_ARG_170	2.86	1.99	22.15
1HGG.PDB	O, B_GLU_128	NE, B_ARG_170	HE, B_ARG_170	2.71	1.86	24.52
1HGG.PDB	OE2, B_GLU_131	NH1, B_ARG_170	HH11, B_ARG_170	2.85	1.85	6.28
1HGG.PDB	O, B_LEU_167	N, B_PHE_171	H, B_PHE_171	2.94	1.99	10.53
1HGG.PDB	O, D_ILE_140	N, C_ALA_11	H, C_ALA_11	2.88	1.96	16.67
1HGG.PDB	O, D_PHE_138	N, C_LEU_13	H, C_LEU_13	3.00	2.04	10.72
1HGG.PDB	O, D_ARG_25	N, C_CYS_14	H, C_CYS_14	2.73	1.80	13.70
1HGG.PDB	O, D_GLY_136	N, C_LEU_15	H, C_LEU_15	2.90	1.94	8.49
1HGG.PDB	O, D_GLY_23	N, C_GLY_16	H, C_GLY_16	2.91	2.01	20.14
1HGG.PDB	O, D_TRP_21	N, C_HIS_18	H, C_HIS_18	2.90	2.00	17.75
1HGG.PDB	OD1, C_ASN_322	N, C_VAL_20	H, C_VAL_20	2.83	1.86	5.96
1HGG.PDB	O, C_VAL_36	N, C_THR_24	H, C_THR_24	2.85	1.97	21.07
1HGG.PDB	O, C_ILE_34	N, C_VAL_26	H, C_VAL_26	2.78	1.85	13.27
1HGG.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.94	1.91	8.28
1HGG.PDB	O, C_VAL_26	N, C_ILE_34	H, C_ILE_34	2.94	2.00	14.30
1HGG.PDB	O, C_THR_24	N, C_VAL_36	H, C_VAL_36	2.78	1.83	9.33
1HGG.PDB	O, C_MET_320	N, C_THR_37	H, C_THR_37	2.95	1.98	6.39
1HGG.PDB	O, C_LEU_316	N, C_THR_40	H, C_THR_40	2.80	1.94	23.65
1HGG.PDB	O, C_LEU_314	N, C_LEU_42	H, C_LEU_42	2.84	1.98	23.25
1HGG.PDB	O, C_PHE_294	N, C_GLN_44	H, C_GLN_44	2.77	1.82	9.57
1HGG.PDB	O, C_ASN_285	OG, C_SER_47	HG, C_SER_47	2.86	1.92	11.28
1HGG.PDB	OD2, C_ASP_275	NZ, C_LYS_50	HZ1, C_LYS_50	2.68	1.77	23.74
1HGG.PDB	O, C_PRO_273	N, C_ILE_51	H, C_ILE_51	2.76	1.81	7.91
1HGG.PDB	O, C_ASP_275	N, C_ASN_53	H, C_ASN_53	2.74	1.92	26.97
1HGG.PDB	OD2, C_ASP_85	N, C_ARG_57	H, C_ARG_57	2.86	1.92	11.42
1HGG.PDB	O, C_THR_83	NE, C_ARG_57	HE, C_ARG_57	2.73	1.76	4.62
1HGG.PDB	OE1, C_GLU_82	NH2, C_ARG_57	HH21, C_ARG_57	2.59	1.77	28.22
1HGG.PDB	O, C_LEU_86	N, C_LEU_59	H, C_LEU_59	2.91	1.94	7.95
1HGG.PDB	O, C_VAL_88	N, C_GLY_61	H, C_GLY_61	2.96	2.11	24.97
1HGG.PDB	OD1, C_ASP_60	N, C_ILE_62	H, C_ILE_62	2.85	1.92	14.37
1HGG.PDB	O, C_GLY_61	N, C_CYS_64	H, C_CYS_64	2.95	2.02	15.64
1HGG.PDB	O, C_LEU_66	N, C_LEU_70	H, C_LEU_70	2.88	1.98	18.83
1HGG.PDB	O, C_ILE_67	N, C_LEU_71	H, C_LEU_71	2.81	1.85	6.57
1HGG.PDB	O, C_ASP_68	N, C_GLY_72	H, C_GLY_72	2.83	1.91	16.32
1HGG.PDB	OD1, C_ASP_73	N, C_HIS_75	H, C_HIS_75	2.95	2.04	19.03
1HGG.PDB	OD1, C_ASP_73	ND1, C_HIS_75	HD1, C_HIS_75	2.72	1.84	20.87
1HGG.PDB	O, C_ASP_63	NE2, C_HIS_75	HE2, C_HIS_75	2.81	1.85	11.39
1HGG.PDB	O, C_ASP_73	N, C_CYS_76	H, C_CYS_76	2.75	1.83	14.81
1HGG.PDB	O, C_PRO_74	N, C_ASP_77	H, C_ASP_77	2.88	1.94	12.22
1HGG.PDB	O, C_PHE_79	N, C_GLU_82	H, C_GLU_82	2.98	2.06	16.43
1HGG.PDB	O, C_ARG_57	N, C_ASP_85	H, C_ASP_85	2.82	1.92	18.11
1HGG.PDB	O, C_LEU_59	N, C_VAL_88	H, C_VAL_88	2.94	1.97	7.31
1HGG.PDB	O, C_MET_268	N, C_GLU_89	H, C_GLU_89	2.84	1.90	11.81
1HGG.PDB	OD1, C_ASP_60	NE, C_ARG_90	HE, C_ARG_90	2.93	1.95	8.71
1HGG.PDB	O, C_SER_270	NH1, C_ARG_90	HH11, C_ARG_90	2.63	1.77	25.40
1HGG.PDB	O, C_ALA_272	NH1, C_ARG_90	HH12, C_ARG_90	2.64	1.73	19.40
1HGG.PDB	OD2, C_ASP_60	NH2, C_ARG_90	HH21, C_ARG_90	2.79	1.80	9.72
1HGG.PDB	OD1, C_ASP_271	N, C_SER_91	H, C_SER_91	2.91	1.98	14.77

1HGG.PDB	OD1, C_ASP_271	OG, C_SER_91	HG, C_SER_91	2.89	2.06	25.85
1HGG.PDB	OD2, C_ASP_271	OG, C_SER_91	HG, C_SER_91	2.90	2.02	21.44
1HGG.PDB	O, C_ASP_63	N, C_PHE_94	H, C_PHE_94	2.99	2.03	11.00
1HGG.PDB	OD2, C_ASP_68	OG, C_SER_95	HG, C_SER_95	2.90	1.95	11.80
1HGG.PDB	OD2, C_ASP_73	N, C_ASN_96	H, C_ASN_96	2.84	1.91	15.44
1HGG.PDB	SG, C_CYS_97	N, C_TYR_98	H, C_TYR_98	2.98	2.13	24.49
1HGG.PDB	OD1, C_ASP_68	OH, C_TYR_100	HH, C_TYR_100	2.93	1.98	11.50
1HGG.PDB	O, C_ILE_230	N, C_ASP_101	H, C_ASP_101	2.95	2.06	21.39
1HGG.PDB	OD1, C_ASP_104	N, C_SER_107	H, C_SER_107	2.96	2.07	20.96
1HGG.PDB	OD2, C_ASP_104	OG, C_SER_107	HG, C_SER_107	2.88	1.95	15.82
1HGG.PDB	O, C_TYR_105	N, C_ARG_109	H, C_ARG_109	2.77	1.80	4.85
1HGG.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.85	1.88	14.56
1HGG.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.76	1.86	17.83
1HGG.PDB	O, C_SER_107	N, C_LEU_111	H, C_LEU_111	2.84	1.88	8.80
1HGG.PDB	O, C_ARG_109	N, C_ALA_113	H, C_ALA_113	2.92	2.01	17.55
1HGG.PDB	O, C_SER_110	N, C_SER_114	H, C_SER_114	2.96	2.00	11.10
1HGG.PDB	OE2, C_GLU_119	OG1, C_THR_117	HG1, C_THR_117	2.92	1.97	8.69
1HGG.PDB	O, C_GLU_82	N, C_LEU_118	H, C_LEU_118	2.98	2.02	11.62
1HGG.PDB	O, C_TYR_257	N, C_ILE_121	H, C_ILE_121	2.89	1.93	9.59
1HGG.PDB	O, C_ARG_255	N, C_GLU_123	H, C_GLU_123	2.97	2.02	13.93
1HGG.PDB	O, C_THR_155	N, C_THR_131	H, C_THR_131	2.76	1.85	16.88
1HGG.PDB	OD1, C_ASN_152	N, C_ASN_133	H, C_ASN_133	2.89	1.97	17.25
1HGG.PDB	O, C_GLY_146	N, C_SER_136	H, C_SER_136	2.76	1.84	16.68
1HGG.PDB	OG, C_SER_136	N, C_ALA_138	H, C_ALA_138	2.90	1.94	8.35
1HGG.PDB	O, C_GLY_144	NZ, C_LYS_140	HZ1, C_LYS_140	2.87	1.89	15.96
1HGG.PDB	OD1, C_ASN_137	NZ, C_LYS_140	HZ2, C_LYS_140	2.78	1.78	13.21
1HGG.PDB	OD2, C_ASP_77	NE, C_ARG_141	HE, C_ARG_141	2.87	2.06	29.23
1HGG.PDB	O, C_PHE_147	NH1, C_ARG_141	HH12, C_ARG_141	2.49	1.65	25.79
1HGG.PDB	OD1, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.76	1.85	22.10
1HGG.PDB	OD2, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.74	1.86	24.28
1HGG.PDB	O, C_GLY_72	NH2, C_ARG_141	HH22, C_ARG_141	2.93	1.94	7.19
1HGG.PDB	OD1, C_ASN_137	OG, C_SER_145	HG, C_SER_145	2.90	2.03	20.82
1HGG.PDB	O, C_SER_136	N, C_GLY_146	H, C_GLY_146	2.99	2.11	21.11
1HGG.PDB	O, C_GLY_72	N, C_SER_149	H, C_SER_149	2.87	1.95	15.72
1HGG.PDB	O, C_ALA_253	N, C_ASN_152	H, C_ASN_152	2.70	1.87	25.79
1HGG.PDB	OH, C_TYR_195	NE1, C_TRP_153	HE1, C_TRP_153	2.90	1.98	17.08
1HGG.PDB	O, C_THR_131	N, C_THR_155	H, C_THR_155	2.97	2.01	10.26
1HGG.PDB	O, C_LEU_194	N, C_LYS_156	H, C_LYS_156	2.96	2.09	22.28
1HGG.PDB	O, C_THR_160	N, C_SER_157	H, C_SER_157	2.94	2.03	17.38
1HGG.PDB	O, C_ILE_245	N, C_VAL_166	H, C_VAL_166	2.88	1.92	11.02
1HGG.PDB	O, C_LEU_243	OG1, C_THR_167	HG1, C_THR_167	2.88	1.99	19.69
1HGG.PDB	O, C_LEU_243	N, C_MET_168	H, C_MET_168	2.95	2.02	15.96
1HGG.PDB	O, C_ASP_241	N, C_ASN_170	H, C_ASN_170	2.87	1.89	5.24
1HGG.PDB	O, C_PHE_174	ND2, C_ASN_170	HD21, C_ASN_170	2.80	1.86	12.52
1HGG.PDB	O, C_VAL_237	ND2, C_ASN_170	HD22, C_ASN_170	2.86	2.00	22.88
1HGG.PDB	O, C_VAL_237	N, C_LYS_176	H, C_LYS_176	2.90	1.97	14.96
1HGG.PDB	OE2, C_GLU_123	NZ, C_LYS_176	HZ1, C_LYS_176	2.63	1.76	26.89
1HGG.PDB	O, C_PHE_258	N, C_LEU_177	H, C_LEU_177	2.95	1.99	9.21
1HGG.PDB	O, C_THR_235	N, C_TYR_178	H, C_TYR_178	2.76	1.80	6.43
1HGG.PDB	OE1, C_GLU_123	OH, C_TYR_178	HH, C_TYR_178	2.78	1.82	5.18
1HGG.PDB	OG1, C_THR_235	NE1, C_TRP_180	HE1, C_TRP_180	2.92	1.93	1.99
1HGG.PDB	O, C_ASN_250	N, C_HIS_183	H, C_HIS_183	2.79	1.93	23.13
1HGG.PDB	O, C_ARG_229	N, C_HIS_184	H, C_HIS_184	2.88	1.91	4.45
1HGG.PDB	OG, C_SER_231	NE2, C_HIS_184	HE2, C_HIS_184	2.79	1.91	21.48
1HGG.PDB	OG1, C_THR_187	N, C_GLU_190	H, C_GLU_190	2.85	1.91	12.50
1HGG.PDB	OD1, C_ASN_250	NE2, C_GLN_191	HE21, C_GLN_191	2.95	1.99	11.16
1HGG.PDB	O, C_GLN_197	NE2, C_GLN_191	HE22, C_GLN_191	2.91	2.02	19.58
1HGG.PDB	O, C_GLN_189	OG1, C_THR_192	HG1, C_THR_192	2.78	1.95	25.67

1HGG.PDB	O, C_GLN_189	N, C_SER_193	H, C_SER_193	2.82	1.90	15.79
1HGG.PDB	O, C_GLN_191	N, C_TYR_195	H, C_TYR_195	2.84	1.90	11.98
1HGG.PDB	O, C_THR_192	N, C_VAL_196	H, C_VAL_196	2.94	2.12	27.31
1HGG.PDB	O, C_TYR_161	NE2, C_GLN_197	HE21, C_GLN_197	2.93	1.96	5.46
1HGG.PDB	O, C_ASN_248	NE2, C_GLN_197	HE22, C_GLN_197	2.96	2.07	20.53
1HGG.PDB	OD1, C_ASN_246	NH2, C_ARG_201	HH21, C_ARG_201	2.66	1.74	19.39
1HGG.PDB	O, C_ILE_213	N, C_VAL_202	H, C_VAL_202	2.95	2.00	11.94
1HGG.PDB	O, C_ASN_246	N, C_THR_203	H, C_THR_203	2.86	1.90	8.48
1HGG.PDB	OG1, C_THR_212	OG1, C_THR_203	HG1, C_THR_203	2.83	1.91	13.70
1HGG.PDB	O, C_GLN_211	N, C_VAL_204	H, C_VAL_204	2.89	1.98	18.00
1HGG.PDB	O, C_SER_209	N, C_THR_206	H, C_THR_206	2.98	2.01	7.02
1HGG.PDB	OD1, C_ASP_241	N, C_ARG_207	H, C_ARG_207	2.89	1.95	13.44
1HGG.PDB	OD2, C_ASP_241	NE, C_ARG_208	HE, C_ARG_208	2.93	2.03	20.59
1HGG.PDB	OG1, C_THR_206	OG, C_SER_209	HG, C_SER_209	2.99	2.06	14.06
1HGG.PDB	O, C_VAL_204	N, C_GLN_211	H, C_GLN_211	2.82	1.90	16.88
1HGG.PDB	O, C_VAL_202	N, C_ILE_213	H, C_ILE_213	2.82	1.89	15.37
1HGG.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.61	1.71	21.26
1HGG.PDB	O, C_ASN_216	NH2, C_ARG_220	HH22, C_ARG_220	2.71	1.81	20.71
1HGG.PDB	O, C_LEU_226	N, C_VAL_223	H, C_VAL_223	2.85	1.90	10.41
1HGG.PDB	O, C_CYS_97	NE, C_ARG_224	HE, C_ARG_224	2.77	1.94	26.89
1HGG.PDB	O, C_CYS_97	NH2, C_ARG_224	HH21, C_ARG_224	2.80	1.94	26.26
1HGG.PDB	O, C_VAL_223	N, C_LEU_226	H, C_LEU_226	2.98	2.05	14.11
1HGG.PDB	O, C_ARG_220	OG, C_SER_227	HG, C_SER_227	2.93	1.98	9.94
1HGG.PDB	O, C_SER_228	NH1, C_ARG_229	HH11, C_ARG_229	2.73	1.79	17.88
1HGG.PDB	O, C_PRO_221	NH2, C_ARG_229	HH22, C_ARG_229	2.58	1.66	18.11
1HGG.PDB	OD1, C_ASP_101	OG, C_SER_231	HG, C_SER_231	2.91	1.95	9.20
1HGG.PDB	O, C_ASP_101	N, C_ILE_232	H, C_ILE_232	2.94	2.02	16.10
1HGG.PDB	O, C_TRP_180	N, C_TYR_233	H, C_TYR_233	2.88	1.93	12.54
1HGG.PDB	O, C_TYR_178	N, C_THR_235	H, C_THR_235	2.88	1.98	19.07
1HGG.PDB	O, C_LYS_176	N, C_VAL_237	H, C_VAL_237	2.77	1.82	10.57
1HGG.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.83	1.86	17.18
1HGG.PDB	OE2, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.70	1.87	29.85
1HGG.PDB	O, B_SER_71	NZ, C_LYS_238	HZ3, C_LYS_238	2.64	1.71	20.39
1HGG.PDB	O, C_ASN_170	N, C_GLY_240	H, C_GLY_240	2.87	2.00	22.99
1HGG.PDB	O, C_LYS_238	N, C_ASP_241	H, C_ASP_241	2.94	2.02	16.73
1HGG.PDB	OD1, C_ASP_241	N, C_VAL_242	H, C_VAL_242	2.79	1.98	28.74
1HGG.PDB	O, C_MET_168	N, C_LEU_243	H, C_LEU_243	2.90	1.93	4.41
1HGG.PDB	O, C_SER_205	N, C_VAL_244	H, C_VAL_244	2.94	1.99	13.16
1HGG.PDB	O, C_VAL_166	N, C_ILE_245	H, C_ILE_245	2.96	2.03	15.63
1HGG.PDB	O, C_THR_203	N, C_ASN_246	H, C_ASN_246	2.89	1.94	11.37
1HGG.PDB	OD1, C_ASN_165	ND2, C_ASN_246	HD22, C_ASN_246	2.88	1.97	17.94
1HGG.PDB	O, C_LEU_164	N, C_SER_247	H, C_SER_247	2.93	2.03	18.95
1HGG.PDB	OE1, C_GLN_191	ND2, C_ASN_250	HD21, C_ASN_250	2.88	1.93	11.32
1HGG.PDB	O, C_HIS_183	ND2, C_ASN_250	HD22, C_ASN_250	2.88	1.92	9.88
1HGG.PDB	O, C_ASN_152	N, C_ALA_253	H, C_ALA_253	2.89	1.98	18.52
1HGG.PDB	OD1, C_ASN_133	NH2, C_ARG_255	HH22, C_ARG_255	2.54	1.68	24.43
1HGG.PDB	O, C_ILE_121	N, C_TYR_257	H, C_TYR_257	2.94	2.10	25.61
1HGG.PDB	O, C_LEU_177	N, C_PHE_258	H, C_PHE_258	2.95	2.00	12.32
1HGG.PDB	OG, C_SER_115	N, C_ARG_261	H, C_ARG_261	2.98	2.02	10.79
1HGG.PDB	OE2, C_GLU_119	NH1, C_ARG_261	HH12, C_ARG_261	2.67	1.86	29.79
1HGG.PDB	OE1, C_GLU_119	NH2, C_ARG_261	HH22, C_ARG_261	2.73	1.87	26.76
1HGG.PDB	OH, C_TYR_302	NZ, C_LYS_264	HZ1, C_LYS_264	2.88	1.92	18.77
1HGG.PDB	ND1, C_HIS_56	NZ, C_LYS_264	HZ2, C_LYS_264	2.66	1.73	19.57
1HGG.PDB	OD2, C_ASP_85	NZ, C_LYS_264	HZ3, C_LYS_264	2.85	1.83	11.83
1HGG.PDB	O, C_PHE_87	N, C_MET_268	H, C_MET_268	2.84	1.93	18.75
1HGG.PDB	OE1, D_GLU_67	NH1, C_ARG_269	HH12, C_ARG_269	2.69	1.85	27.75
1HGG.PDB	O, C_PRO_284	OG, C_SER_270	HG, C_SER_270	2.81	1.87	12.03
1HGG.PDB	OG, C_SER_270	N, C_ALA_272	H, C_ALA_272	2.94	2.00	11.74

1HGG.PDB	O, C_ILE_51	N, C_ASP_275	H, C_ASP_275	2.84	1.97	21.56
1HGG.PDB	OD1, C_ASP_275	N, C_THR_276	H, C_THR_276	2.78	1.93	24.05
1HGG.PDB	O, C_ASN_54	N, C_SER_279	H, C_SER_279	2.77	1.82	11.28
1HGG.PDB	O, C_TYR_302	N, C_ILE_282	H, C_ILE_282	2.90	1.95	12.03
1HGG.PDB	O, C_THR_283	N, C_GLY_286	H, C_GLY_286	2.78	1.84	12.37
1HGG.PDB	O, C_LYS_50	N, C_SER_287	H, C_SER_287	2.83	1.87	6.69
1HGG.PDB	O, C_ALA_304	ND2, C_ASN_290	HD22, C_ASN_290	2.88	2.00	21.32
1HGG.PDB	OE1, C_GLN_44	NZ, C_LYS_292	HZ1, C_LYS_292	2.77	1.76	11.69
1HGG.PDB	OD2, C_ASP_291	NZ, C_LYS_292	HZ3, C_LYS_292	2.78	1.91	27.51
1HGG.PDB	O, C_LYS_307	N, C_GLN_295	H, C_GLN_295	2.80	1.92	20.69
1HGG.PDB	O, C_ASN_298	NE2, C_GLN_295	HE21, C_GLN_295	2.82	1.85	7.30
1HGG.PDB	O, C_GLN_44	N, C_ASN_296	H, C_ASN_296	2.86	1.91	11.10
1HGG.PDB	OD1, C_ASN_285	ND2, C_ASN_298	HD22, C_ASN_298	2.95	2.00	10.88
1HGG.PDB	O, D_LYS_68	NZ, C_LYS_299	HZ1, C_LYS_299	2.94	1.91	9.55
1HGG.PDB	OD1, C_ASN_298	N, C_ILE_300	H, C_ILE_300	2.84	1.92	15.94
1HGG.PDB	O, C_ILE_282	N, C_TYR_302	H, C_TYR_302	2.82	1.94	22.26
1HGG.PDB	O, C_LYS_264	OH, C_TYR_302	HH, C_TYR_302	2.69	1.86	25.98
1HGG.PDB	O, D_LYS_62	N, C_GLY_303	H, C_GLY_303	2.91	1.94	5.10
1HGG.PDB	O, C_GLN_295	N, C_VAL_309	H, C_VAL_309	2.92	2.09	26.95
1HGG.PDB	OG, D_SER_93	N, C_LYS_310	H, C_LYS_310	2.89	1.96	14.95
1HGG.PDB	OD1, D_ASP_90	NZ, C_LYS_310	HZ2, C_LYS_310	2.65	1.73	21.74
1HGG.PDB	OE2, C_GLU_41	N, C_LEU_314	H, C_LEU_314	2.79	1.88	17.71
1HGG.PDB	OE1, C_GLU_41	NZ, C_LYS_315	HZ3, C_LYS_315	2.73	1.82	23.48
1HGG.PDB	O, C_THR_40	N, C_LEU_316	H, C_LEU_316	2.76	1.85	16.07
1HGG.PDB	OD1, D_ASN_104	N, C_ALA_317	H, C_ALA_317	2.78	1.87	17.02
1HGG.PDB	O, C_ASN_38	N, C_THR_318	H, C_THR_318	2.91	1.99	16.68
1HGG.PDB	O, C_VAL_20	ND2, C_ASN_322	HD21, C_ASN_322	2.89	1.97	16.73
1HGG.PDB	OE2, C_GLU_35	ND2, C_ASN_322	HD22, C_ASN_322	2.82	1.96	24.18
1HGG.PDB	OXT, C_THR_328	NE2, C_GLN_327	HE22, C_GLN_327	2.99	2.05	16.22
1HGG.PDB	OD2, D_ASP_112	N, D_GLY_1	H2, D_GLY_1	2.72	1.72	12.91
1HGG.PDB	OD1, D_ASP_109	N, D_LEU_2	H, D_LEU_2	2.98	2.06	18.06
1HGG.PDB	OD2, D_ASP_112	N, D_PHE_3	H, D_PHE_3	2.89	2.07	26.93
1HGG.PDB	OD2, D_ASP_112	N, D_GLY_4	H, D_GLY_4	2.95	2.04	17.54
1HGG.PDB	OD1, D_ASP_112	N, D_ALA_5	H, D_ALA_5	2.93	2.07	23.70
1HGG.PDB	O, D_GLY_4	N, D_PHE_9	H, D_PHE_9	2.79	1.86	14.01
1HGG.PDB	O, C_VAL_323	N, D_GLY_13	H, D_GLY_13	2.71	1.79	13.39
1HGG.PDB	O, C_HIS_17	N, D_TRP_14	H, D_TRP_14	2.80	1.89	17.21
1HGG.PDB	OG1, D_THR_41	N, D_TRP_21	H, D_TRP_21	2.88	1.93	11.49
1HGG.PDB	O, C_GLY_16	N, D_GLY_23	H, D_GLY_23	2.99	2.09	20.18
1HGG.PDB	O, D_ALA_35	N, D_PHE_24	H, D_PHE_24	2.85	1.88	4.85
1HGG.PDB	O, C_CYS_14	N, D_ARG_25	H, D_ARG_25	2.94	1.98	8.24
1HGG.PDB	OE1, D_GLN_34	NE, D_ARG_25	HE, D_ARG_25	2.69	1.81	20.51
1HGG.PDB	OE1, D_GLN_34	NH2, D_ARG_25	HH21, D_ARG_25	2.92	2.08	27.66
1HGG.PDB	O, D_GLY_33	N, D_HIS_26	H, D_HIS_26	2.93	2.01	17.07
1HGG.PDB	O, D_GLY_31	N, D_ASN_28	H, D_ASN_28	2.87	1.91	10.16
1HGG.PDB	OD1, D_ASN_146	ND2, D_ASN_28	HD21, D_ASN_28	2.95	1.98	8.75
1HGG.PDB	O, D_HIS_26	N, D_GLY_33	H, D_GLY_33	2.99	2.09	19.19
1HGG.PDB	O, D_PHE_24	N, D_ALA_35	H, D_ALA_35	2.88	2.07	28.42
1HGG.PDB	O, D_TYR_22	N, D_ASP_37	H, D_ASP_37	2.74	1.77	2.87
1HGG.PDB	OD2, D_ASP_37	N, D_SER_40	H, D_SER_40	2.86	1.92	11.90
1HGG.PDB	OD2, D_ASP_37	OG, D_SER_40	HG, D_SER_40	2.77	1.93	24.58
1HGG.PDB	O, D_ASP_37	OG1, D_THR_41	HG1, D_THR_41	2.70	1.81	19.22
1HGG.PDB	O, D_LEU_38	N, D_GLN_42	H, D_GLN_42	2.95	2.02	14.26
1HGG.PDB	OD1, D_ASP_46	NE2, D_GLN_42	HE22, D_GLN_42	2.85	1.96	21.08
1HGG.PDB	O, D_LYS_39	N, D_ALA_43	H, D_ALA_43	2.99	2.03	8.86
1HGG.PDB	O, D_SER_40	N, D_ALA_44	H, D_ALA_44	2.95	1.97	1.83
1HGG.PDB	O, D_THR_41	N, D_ILE_45	H, D_ILE_45	2.97	2.03	14.64
1HGG.PDB	O, D_GLN_42	N, D_ASP_46	H, D_ASP_46	2.77	1.81	4.12

1HGG.PDB	OE2, D_GLU_114	NE2, D_GLN_47	HE21, D_GLN_47	2.97	2.05	17.17
1HGG.PDB	O, D_ALA_43	NE2, D_GLN_47	HE22, D_GLN_47	2.95	2.03	16.72
1HGG.PDB	O, D_ILE_45	N, D_ASN_49	H, D_ASN_49	2.86	1.93	14.78
1HGG.PDB	O, D_ASP_46	N, D_GLY_50	H, D_GLY_50	2.93	2.07	23.90
1HGG.PDB	O, D_GLN_47	N, D_LYS_51	H, D_LYS_51	2.93	1.95	0.82
1HGG.PDB	OG1, D_THR_107	NZ, D_LYS_51	HZ1, D_LYS_51	2.98	2.00	17.66
1HGG.PDB	OE1, D_GLU_103	NZ, D_LYS_51	HZ2, D_LYS_51	2.77	1.73	6.39
1HGG.PDB	ND1, D_HIS_106	NZ, D_LYS_51	HZ3, D_LYS_51	2.76	1.78	15.09
1HGG.PDB	O, D_ILE_48	N, D_LEU_52	H, D_LEU_52	2.86	1.96	19.21
1HGG.PDB	O, D_ASN_49	N, D_ASN_53	H, D_ASN_53	2.89	1.99	19.47
1HGG.PDB	O, A_THR_28	NE, D_ARG_54	HE, D_ARG_54	2.88	1.91	8.15
1HGG.PDB	OE1, D_GLU_57	NH1, D_ARG_54	HH11, D_ARG_54	2.86	1.86	11.12
1HGG.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.76	1.78	10.56
1HGG.PDB	O, D_ASN_53	N, D_ILE_56	H, D_ILE_56	2.92	2.12	28.93
1HGG.PDB	OE2, D_GLU_61	NZ, D_LYS_58	HZ3, D_LYS_58	2.91	1.89	12.30
1HGG.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.86	1.90	9.42
1HGG.PDB	O, D_PHE_63	NE2, D_GLN_65	HE22, D_GLN_65	2.97	2.00	6.28
1HGG.PDB	O, C_LYS_299	NZ, D_LYS_68	HZ1, D_LYS_68	2.84	1.83	12.46
1HGG.PDB	OE2, D_GLU_85	NZ, D_LYS_68	HZ2, D_LYS_68	2.77	1.74	6.59
1HGG.PDB	OE2, D_GLU_72	OG, D_SER_71	HG, D_SER_71	2.82	2.00	26.77
1HGG.PDB	OG, E_SER_107	N, D_ARG_76	H, D_ARG_76	2.84	1.88	7.98
1HGG.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.86	1.89	9.57
1HGG.PDB	OE1, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.78	1.80	12.10
1HGG.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.67	1.68	6.66
1HGG.PDB	OE2, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.74	1.75	9.29
1HGG.PDB	O, D_GLY_75	N, D_ASP_79	H, D_ASP_79	2.89	1.95	14.50
1HGG.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.59	1.78	26.83
1HGG.PDB	O, D_LEU_80	N, D_VAL_84	H, D_VAL_84	2.86	1.90	9.21
1HGG.PDB	O, D_LYS_82	N, D_ASP_86	H, D_ASP_86	2.98	2.01	8.40
1HGG.PDB	O, D_TYR_83	N, D_THR_87	H, D_THR_87	2.88	1.92	7.85
1HGG.PDB	O, D_VAL_84	N, D_LYS_88	H, D_LYS_88	2.88	2.03	24.81
1HGG.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.73	1.70	8.35
1HGG.PDB	O, D_GLU_85	N, D_ILE_89	H, D_ILE_89	2.83	1.87	9.71
1HGG.PDB	O, D_LYS_88	N, D_TRP_92	H, D_TRP_92	2.89	1.92	6.21
1HGG.PDB	O, D_ILE_89	N, D_SER_93	H, D_SER_93	2.82	1.94	21.49
1HGG.PDB	O, D_ILE_89	OG, D_SER_93	HG, D_SER_93	2.77	1.87	18.00
1HGG.PDB	O, D_ASP_90	N, D_TYR_94	H, D_TYR_94	2.96	2.03	15.50
1HGG.PDB	O, D_TRP_92	N, D_ALA_96	H, D_ALA_96	3.00	2.06	15.10
1HGG.PDB	O, D_TYR_94	N, D_LEU_98	H, D_LEU_98	2.95	1.99	9.12
1HGG.PDB	O, D_ASN_95	N, D_LEU_99	H, D_LEU_99	2.88	1.98	19.51
1HGG.PDB	O, D_ALA_96	N, D_VAL_100	H, D_VAL_100	2.99	2.02	8.75
1HGG.PDB	O, D_LEU_98	N, D_LEU_102	H, D_LEU_102	2.93	1.97	11.16
1HGG.PDB	O, D_VAL_100	N, D_ASN_104	H, D_ASN_104	2.84	1.93	18.38
1HGG.PDB	O, C_LYS_27	ND2, D_ASN_104	HD22, D_ASN_104	2.86	1.93	13.53
1HGG.PDB	O, D_LEU_102	N, D_HIS_106	H, D_HIS_106	2.95	2.00	11.00
1HGG.PDB	O, D_GLU_103	N, D_THR_107	H, D_THR_107	2.82	1.97	24.04
1HGG.PDB	O, D_HIS_106	N, D_LEU_110	H, D_LEU_110	2.77	1.83	11.18
1HGG.PDB	O, D_THR_107	N, D_THR_111	H, D_THR_111	2.98	2.03	10.32
1HGG.PDB	O, D_THR_107	OG1, D_THR_111	HG1, D_THR_111	2.86	1.91	10.45
1HGG.PDB	O, D_ASP_109	N, D_SER_113	H, D_SER_113	2.78	1.86	15.73
1HGG.PDB	O, D_ASP_112	N, D_ASN_116	H, D_ASN_116	3.00	2.01	4.28
1HGG.PDB	O, D_SER_113	N, D_LYS_117	H, D_LYS_117	2.76	1.87	19.86
1HGG.PDB	O, D_ASN_116	N, D_GLU_120	H, D_GLU_120	2.94	1.96	4.15
1HGG.PDB	O, D_LYS_117	N, D_LYS_121	H, D_LYS_121	2.89	1.99	19.16
1HGG.PDB	O, D_LEU_118	N, D_THR_122	H, D_THR_122	2.95	1.98	8.05
1HGG.PDB	O, D_PHE_119	N, D_ARG_123	H, D_ARG_123	2.95	1.99	9.23
1HGG.PDB	OE2, D_GLU_120	NH1, D_ARG_123	HH11, D_ARG_123	2.73	1.87	25.59
1HGG.PDB	O, D_GLU_120	N, D_ARG_124	H, D_ARG_124	2.99	2.02	7.97

1HGG.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.86	2.00	22.57
1HGG.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.78	1.96	26.12
1HGG.PDB	O, D_HIS_159	ND2, D_ASN_129	HD21, D_ASN_129	2.94	1.99	11.72
1HGG.PDB	OH, D_TYR_157	ND2, D_ASN_129	HD22, D_ASN_129	2.80	1.84	10.50
1HGG.PDB	O, D_LYS_139	N, D_GLU_131	H, D_GLU_131	2.99	2.04	13.39
1HGG.PDB	O, D_CYS_137	N, D_MET_133	H, D_MET_133	2.90	1.98	17.30
1HGG.PDB	OD1, D_ASN_135	N, D_CYS_137	H, D_CYS_137	3.00	2.10	19.46
1HGG.PDB	O, C_LEU_13	N, D_PHE_138	H, D_PHE_138	2.73	1.88	23.87
1HGG.PDB	O, D_GLU_131	N, D_LYS_139	H, D_LYS_139	2.86	1.90	10.04
1HGG.PDB	O, C_ALA_11	N, D_ILE_140	H, D_ILE_140	2.80	1.89	17.21
1HGG.PDB	O, D_ASN_129	N, D_TYR_141	H, D_TYR_141	2.89	1.92	4.81
1HGG.PDB	OE2, D_GLU_30	N, D_ASN_146	H, D_ASN_146	2.84	1.92	15.86
1HGG.PDB	O, D_ASP_145	N, D_ILE_149	H, D_ILE_149	2.98	2.02	9.24
1HGG.PDB	O, D_ASN_146	N, D_GLU_150	H, D_GLU_150	2.89	1.95	13.07
1HGG.PDB	O, D_ALA_147	N, D_SER_151	H, D_SER_151	2.89	2.01	20.94
1HGG.PDB	O, D_CYS_148	OG, D_SER_151	HG, D_SER_151	2.72	1.85	20.20
1HGG.PDB	O, D_GLU_150	N, D_ASN_154	H, D_ASN_154	2.84	1.87	4.45
1HGG.PDB	O, D_SER_151	N, D_THR_156	H, D_THR_156	2.78	1.93	25.02
1HGG.PDB	OD1, D_ASN_154	OG1, D_THR_156	HG1, D_THR_156	2.73	1.82	15.46
1HGG.PDB	NE2, D_HIS_142	OH, D_TYR_157	HH, D_TYR_157	2.72	1.85	20.87
1HGG.PDB	OD1, D_ASP_158	N, D_ASP_160	H, D_ASP_160	2.97	2.05	17.87
1HGG.PDB	O, D_HIS_159	N, D_TYR_162	H, D_TYR_162	2.93	2.01	16.79
1HGG.PDB	O, D_ASP_160	N, D_ARG_163	H, D_ARG_163	2.89	1.92	6.62
1HGG.PDB	O, B_ARG_170	NH1, D_ARG_163	HH12, D_ARG_163	2.79	1.85	17.60
1HGG.PDB	O, D_TYR_162	N, D_ALA_166	H, D_ALA_166	2.86	1.90	8.06
1HGG.PDB	O, D_ARG_163	N, D_LEU_167	H, D_LEU_167	2.77	1.84	14.60
1HGG.PDB	O, D_ALA_166	N, D_ARG_170	H, D_ARG_170	2.87	2.00	22.89
1HGG.PDB	O, D_GLU_128	NE, D_ARG_170	HE, D_ARG_170	2.70	1.85	24.63
1HGG.PDB	OE2, D_GLU_131	NH1, D_ARG_170	HH11, D_ARG_170	2.85	1.86	6.70
1HGG.PDB	O, D_LEU_167	N, D_PHE_171	H, D_PHE_171	2.94	1.98	10.64
1HGG.PDB	O, F_ILE_140	N, E_ALA_11	H, E_ALA_11	2.91	1.98	15.76
1HGG.PDB	O, F_GLN_27	N, E_THR_12	H, E_THR_12	2.92	1.99	15.18
1HGG.PDB	O, F_PHE_138	N, E_LEU_13	H, E_LEU_13	2.97	2.01	11.10
1HGG.PDB	O, F_ARG_25	N, E_CYS_14	H, E_CYS_14	2.71	1.83	19.57
1HGG.PDB	O, F_GLY_136	N, E_LEU_15	H, E_LEU_15	2.87	1.90	6.84
1HGG.PDB	O, F_GLY_23	N, E_GLY_16	H, E_GLY_16	2.91	2.01	19.19
1HGG.PDB	O, F_TRP_21	N, E_HIS_18	H, E_HIS_18	2.89	1.99	18.05
1HGG.PDB	OD1, E_ASN_322	N, E_VAL_20	H, E_VAL_20	2.81	1.84	7.14
1HGG.PDB	O, E_VAL_36	N, E_THR_24	H, E_THR_24	2.86	1.99	23.32
1HGG.PDB	O, E_ILE_34	N, E_VAL_26	H, E_VAL_26	2.80	1.86	12.97
1HGG.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.91	1.88	8.89
1HGG.PDB	O, E_VAL_26	N, E_ILE_34	H, E_ILE_34	2.91	1.98	15.06
1HGG.PDB	O, E_THR_24	N, E_VAL_36	H, E_VAL_36	2.79	1.84	9.17
1HGG.PDB	O, E_MET_320	N, E_THR_37	H, E_THR_37	2.93	1.96	8.79
1HGG.PDB	O, E_LEU_316	N, E_THR_40	H, E_THR_40	2.83	1.96	23.13
1HGG.PDB	O, E_LEU_314	N, E_LEU_42	H, E_LEU_42	2.84	1.97	22.62
1HGG.PDB	O, E_PHE_294	N, E_GLN_44	H, E_GLN_44	2.82	1.86	8.10
1HGG.PDB	O, E_ASN_285	OG, E_SER_47	HG, E_SER_47	2.85	1.92	11.49
1HGG.PDB	OD2, E_ASP_275	NZ, E_LYS_50	HZ1, E_LYS_50	2.68	1.77	24.10
1HGG.PDB	O, E_PRO_273	N, E_ILE_51	H, E_ILE_51	2.76	1.80	7.93
1HGG.PDB	O, E_ASP_275	N, E_ASN_53	H, E_ASN_53	2.76	1.93	26.21
1HGG.PDB	OD2, E_ASP_85	N, E_ARG_57	H, E_ARG_57	2.88	1.93	10.58
1HGG.PDB	O, E_THR_83	NE, E_ARG_57	HE, E_ARG_57	2.76	1.79	2.44
1HGG.PDB	O, E_LEU_86	N, E_LEU_59	H, E_LEU_59	2.92	1.95	8.87
1HGG.PDB	O, E_VAL_88	N, E_GLY_61	H, E_GLY_61	2.97	2.12	24.82
1HGG.PDB	OD1, E_ASP_60	N, E_ILE_62	H, E_ILE_62	2.87	1.94	14.20
1HGG.PDB	O, E_GLY_61	N, E_CYS_64	H, E_CYS_64	2.97	2.05	16.18
1HGG.PDB	O, E_LEU_66	N, E_LEU_70	H, E_LEU_70	2.87	1.97	18.30

1HGG.PDB	O, E_ILE.67	N, E_LEU.71	H, E_LEU.71	2.81	1.85	7.87
1HGG.PDB	O, E_ASP.68	N, E_GLY.72	H, E_GLY.72	2.86	1.95	17.48
1HGG.PDB	OD1, E_ASP.73	ND1, E_HIS.75	HD1, E_HIS.75	2.75	1.85	17.34
1HGG.PDB	O, E_ASP.63	NE2, E_HIS.75	HE2, E_HIS.75	2.82	1.87	11.87
1HGG.PDB	O, E_ASP.73	N, E_CYS.76	H, E_CYS.76	2.74	1.82	15.22
1HGG.PDB	O, E_PRO.74	N, E_ASP.77	H, E_ASP.77	2.89	1.94	11.95
1HGG.PDB	O, E_PHE.79	N, E_GLU.82	H, E_GLU.82	3.00	2.09	17.70
1HGG.PDB	OE1, E_GLU.82	N, E_THR.83	H, E_THR.83	2.96	2.07	21.15
1HGG.PDB	O, E_ARG.57	N, E_ASP.85	H, E_ASP.85	2.82	1.91	18.08
1HGG.PDB	O, E_LEU.59	N, E_VAL.88	H, E_VAL.88	2.92	1.95	6.94
1HGG.PDB	O, E_MET.268	N, E_GLU.89	H, E_GLU.89	2.82	1.88	11.27
1HGG.PDB	OD1, E_ASP.60	NE, E_ARG.90	HE, E_ARG.90	2.91	1.94	9.27
1HGG.PDB	O, E_SER.270	NH1, E_ARG.90	HH11, E_ARG.90	2.66	1.80	25.54
1HGG.PDB	O, E_ALA.272	NH1, E_ARG.90	HH12, E_ARG.90	2.63	1.72	18.75
1HGG.PDB	OD2, E_ASP.60	NH2, E_ARG.90	HH21, E_ARG.90	2.83	1.84	9.64
1HGG.PDB	OD1, E_ASP.271	N, E_SER.91	H, E_SER.91	2.89	1.97	16.48
1HGG.PDB	OD1, E_ASP.271	OG, E_SER.91	HG, E_SER.91	2.92	2.07	24.79
1HGG.PDB	OD2, E_ASP.271	OG, E_SER.91	HG, E_SER.91	2.93	2.06	22.08
1HGG.PDB	O, E_ASP.63	N, E_PHE.94	H, E_PHE.94	3.00	2.05	12.31
1HGG.PDB	OD2, E_ASP.68	OG, E_SER.95	HG, E_SER.95	2.93	1.98	13.19
1HGG.PDB	OD2, E_ASP.73	N, E_ASN.96	H, E_ASN.96	2.88	1.94	14.23
1HGG.PDB	SG, E_CYS.97	N, E_TYR.98	H, E_TYR.98	2.97	2.12	24.47
1HGG.PDB	OD1, E_ASP.68	OH, E_TYR.100	HH, E_TYR.100	2.92	1.96	10.90
1HGG.PDB	O, E_ILE.230	N, E_ASP.101	H, E_ASP.101	2.99	2.10	20.87
1HGG.PDB	OD1, E_ASP.104	N, E_SER.107	H, E_SER.107	2.92	2.04	21.12
1HGG.PDB	OD2, E_ASP.104	OG, E_SER.107	HG, E_SER.107	2.85	1.93	15.56
1HGG.PDB	O, E_ASP.104	N, E_LEU.108	H, E_LEU.108	2.97	2.01	9.00
1HGG.PDB	O, E_TYR.105	N, E_ARG.109	H, E_ARG.109	2.81	1.84	2.88
1HGG.PDB	OE2, E_GLU.67	NH2, E_ARG.109	HH21, E_ARG.109	2.88	1.90	14.20
1HGG.PDB	OD2, E_ASP.79	OG, E_SER.110	HG, E_SER.110	2.79	1.88	16.48
1HGG.PDB	O, E_SER.107	N, E_LEU.111	H, E_LEU.111	2.86	1.89	6.99
1HGG.PDB	O, E_ARG.109	N, E_ALA.113	H, E_ALA.113	2.89	1.98	18.53
1HGG.PDB	O, E_SER.110	N, E_SER.114	H, E_SER.114	2.92	1.95	9.29
1HGG.PDB	OE2, E_GLU.119	OG1, E_THR.117	HG1, E_THR.117	2.95	1.99	7.33
1HGG.PDB	O, E_TYR.257	N, E_ILE.121	H, E_ILE.121	2.88	1.93	10.40
1HGG.PDB	O, E_ARG.255	N, E_GLU.123	H, E_GLU.123	2.93	1.99	13.52
1HGG.PDB	O, E_THR.155	N, E_THR.131	H, E_THR.131	2.74	1.86	19.96
1HGG.PDB	OD1, E_ASN.152	N, E_ASN.133	H, E_ASN.133	2.93	2.01	17.35
1HGG.PDB	O, E_GLY.146	N, E_SER.136	H, E_SER.136	2.75	1.83	16.47
1HGG.PDB	OG, E_SER.136	N, E_ALA.138	H, E_ALA.138	2.92	1.95	8.13
1HGG.PDB	O, E_GLY.144	NZ, E_LYS.140	HZ1, E_LYS.140	2.88	1.90	15.75
1HGG.PDB	OD1, E_ASN.137	NZ, E_LYS.140	HZ2, E_LYS.140	2.76	1.76	13.40
1HGG.PDB	OD2, E_ASP.77	NE, E_ARG.141	HE, E_ARG.141	2.90	2.09	29.10
1HGG.PDB	O, E_PHE.147	NH1, E_ARG.141	HH12, E_ARG.141	2.48	1.65	26.20
1HGG.PDB	OD1, E_ASP.77	NH2, E_ARG.141	HH21, E_ARG.141	2.80	1.90	22.17
1HGG.PDB	OD2, E_ASP.77	NH2, E_ARG.141	HH21, E_ARG.141	2.74	1.86	23.74
1HGG.PDB	O, E_GLY.72	NH2, E_ARG.141	HH22, E_ARG.141	2.91	1.92	8.01
1HGG.PDB	OD1, E_ASN.137	OG, E_SER.145	HG, E_SER.145	2.95	2.08	20.42
1HGG.PDB	O, E_SER.136	N, E_GLY.146	H, E_GLY.146	2.98	2.09	20.70
1HGG.PDB	O, E_GLY.72	N, E_SER.149	H, E_SER.149	2.94	2.02	16.43
1HGG.PDB	O, E_ALA.253	N, E_ASN.152	H, E_ASN.152	2.76	1.91	24.30
1HGG.PDB	OH, E_TYR.195	NE1, E_TRP.153	HE1, E_TRP.153	2.91	1.97	14.69
1HGG.PDB	O, E_LEU.194	N, E_LYS.156	H, E_LYS.156	2.96	2.09	22.38
1HGG.PDB	O, E_SER.193	NZ, E_LYS.156	HZ2, E_LYS.156	2.92	2.00	22.42
1HGG.PDB	O, E_THR.160	N, E_SER.157	H, E_SER.157	2.97	2.06	18.55
1HGG.PDB	O, E_ILE.245	N, E_VAL.166	H, E_VAL.166	2.88	1.92	9.84
1HGG.PDB	O, E_LEU.243	OG1, E_THR.167	HG1, E_THR.167	2.89	2.02	20.67
1HGG.PDB	O, E_LEU.243	N, E_MET.168	H, E_MET.168	2.91	1.99	16.43

1HGG.PDB	O, E_ASP_241	N, E_ASN_170	H, E_ASN_170	2.89	1.91	4.36
1HGG.PDB	O, E_PHE_174	ND2, E_ASN_170	HD21, E_ASN_170	2.83	1.89	11.99
1HGG.PDB	O, E_VAL_237	ND2, E_ASN_170	HD22, E_ASN_170	2.85	1.99	23.32
1HGG.PDB	O, E_VAL_237	N, E_LYS_176	H, E_LYS_176	2.89	1.95	13.18
1HGG.PDB	OE2, E_GLU_123	NZ, E_LYS_176	HZ1, E_LYS_176	2.65	1.78	26.50
1HGG.PDB	O, E_THR_235	N, E_TYR_178	H, E_TYR_178	2.81	1.85	6.71
1HGG.PDB	OE1, E_GLU_123	OH, E_TYR_178	HH, E_TYR_178	2.80	1.84	8.47
1HGG.PDB	OG1, E_THR_235	NE1, E_TRP_180	HE1, E_TRP_180	2.93	1.94	2.01
1HGG.PDB	O, E_ASN_250	N, E_HIS_183	H, E_HIS_183	2.79	1.92	22.01
1HGG.PDB	O, E_ARG_229	N, E_HIS_184	H, E_HIS_184	2.88	1.92	7.25
1HGG.PDB	OG, E_SER_231	NE2, E_HIS_184	HE2, E_HIS_184	2.81	1.94	22.49
1HGG.PDB	OG1, E_THR_187	N, E_GLU_190	H, E_GLU_190	2.87	1.93	12.79
1HGG.PDB	O, E_GLN_197	NE2, E_GLN_191	HE22, E_GLN_191	2.91	2.01	19.48
1HGG.PDB	O, E_ASN_188	OG1, E_THR_192	HG1, E_THR_192	2.94	1.99	8.04
1HGG.PDB	O, E_GLN_189	N, E_SER_193	H, E_SER_193	2.85	1.88	6.48
1HGG.PDB	O, E_GLN_191	N, E_TYR_195	H, E_TYR_195	2.82	1.87	11.82
1HGG.PDB	O, E_THR_192	N, E_VAL_196	H, E_VAL_196	2.95	2.13	27.67
1HGG.PDB	O, E_TYR_161	NE2, E_GLN_197	HE21, E_GLN_197	2.93	1.96	5.53
1HGG.PDB	O, E_ASN_248	NE2, E_GLN_197	HE22, E_GLN_197	2.94	2.04	19.72
1HGG.PDB	OD1, E_ASN_246	NH2, E_ARG_201	HH21, E_ARG_201	2.66	1.74	20.08
1HGG.PDB	O, E_ILE_213	N, E_VAL_202	H, E_VAL_202	2.94	1.98	10.96
1HGG.PDB	O, E_ASN_246	N, E_THR_203	H, E_THR_203	2.86	1.89	5.92
1HGG.PDB	OG1, E_THR_212	OG1, E_THR_203	HG1, E_THR_203	2.88	1.95	13.34
1HGG.PDB	O, E_GLN_211	N, E_VAL_204	H, E_VAL_204	2.86	1.96	18.23
1HGG.PDB	OD1, E_ASP_241	N, E_ARG_207	H, E_ARG_207	2.89	1.94	12.68
1HGG.PDB	OD2, E_ASP_241	NE, E_ARG_208	HE, E_ARG_208	2.96	2.05	19.90
1HGG.PDB	OG1, E_THR_206	OG, E_SER_209	HG, E_SER_209	2.99	2.07	14.54
1HGG.PDB	OD1, E_ASP_101	NE2, E_GLN_210	HE22, E_GLN_210	2.96	2.04	17.70
1HGG.PDB	O, E_VAL_204	N, E_GLN_211	H, E_GLN_211	2.83	1.91	15.52
1HGG.PDB	O, E_VAL_202	N, E_ILE_213	H, E_ILE_213	2.83	1.91	15.44
1HGG.PDB	OE1, E_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.72	1.80	20.26
1HGG.PDB	O, E_ASN_216	NH2, E_ARG_220	HH22, E_ARG_220	2.70	1.80	21.11
1HGG.PDB	O, E_LEU_226	N, E_VAL_223	H, E_VAL_223	2.87	1.91	9.88
1HGG.PDB	O, E_CYS_97	NE, E_ARG_224	HE, E_ARG_224	2.79	1.95	26.52
1HGG.PDB	O, E_CYS_97	NH2, E_ARG_224	HH21, E_ARG_224	2.81	1.95	25.91
1HGG.PDB	O, E_VAL_223	N, E_LEU_226	H, E_LEU_226	2.99	2.06	14.12
1HGG.PDB	O, E_ARG_220	OG, E_SER_227	HG, E_SER_227	2.91	1.97	11.08
1HGG.PDB	O, E_SER_228	NH1, E_ARG_229	HH11, E_ARG_229	2.74	1.81	18.43
1HGG.PDB	O, E_PRO_221	NH2, E_ARG_229	HH22, E_ARG_229	2.61	1.67	16.25
1HGG.PDB	O, E_ILE_182	N, E_SER_231	H, E_SER_231	3.00	2.12	21.85
1HGG.PDB	OD1, E_ASP_101	OG, E_SER_231	HG, E_SER_231	2.91	1.96	10.31
1HGG.PDB	O, E_ASP_101	N, E_ILE_232	H, E_ILE_232	2.93	2.00	14.76
1HGG.PDB	O, E_TRP_180	N, E_TYR_233	H, E_TYR_233	2.93	1.97	11.34
1HGG.PDB	O, E_TYR_178	N, E_THR_235	H, E_THR_235	2.90	2.00	18.66
1HGG.PDB	O, E_LYS_176	N, E_VAL_237	H, E_VAL_237	2.79	1.84	9.36
1HGG.PDB	OE1, E_GLU_72	NZ, E_LYS_238	HZ1, E_LYS_238	2.89	1.89	13.93
1HGG.PDB	O, E_SER_71	NZ, E_LYS_238	HZ3, E_LYS_238	2.80	1.86	20.00
1HGG.PDB	O, E_ASN_170	N, E_GLY_240	H, E_GLY_240	2.86	1.99	23.07
1HGG.PDB	O, E_LYS_238	N, E_ASP_241	H, E_ASP_241	2.93	2.02	17.28
1HGG.PDB	OD1, E_ASP_241	N, E_VAL_242	H, E_VAL_242	2.79	1.99	28.45
1HGG.PDB	O, E_MET_168	N, E_LEU_243	H, E_LEU_243	2.88	1.91	4.89
1HGG.PDB	O, E_SER_205	N, E_VAL_244	H, E_VAL_244	2.93	1.99	13.01
1HGG.PDB	O, E_VAL_166	N, E_ILE_245	H, E_ILE_245	2.98	2.06	15.80
1HGG.PDB	O, E_THR_203	N, E_ASN_246	H, E_ASN_246	2.92	1.97	11.38
1HGG.PDB	OD1, E_ASN_165	ND2, E_ASN_246	HD22, E_ASN_246	2.88	1.96	17.66
1HGG.PDB	O, E_LEU_164	N, E_SER_247	H, E_SER_247	2.92	2.01	18.12
1HGG.PDB	OE1, E_GLN_191	ND2, E_ASN_250	HD21, E_ASN_250	2.89	1.94	10.20
1HGG.PDB	O, E_HIS_183	ND2, E_ASN_250	HD22, E_ASN_250	2.88	1.93	10.21

1HGG.PDB	O, E_ASN_152	N, E_ALA_253	H, E_ALA_253	2.90	1.98	17.67
1HGG.PDB	OD1, E_ASN_133	NH2, E_ARG_255	HH22, E_ARG_255	2.55	1.68	24.24
1HGG.PDB	O, E_ILE_121	N, E_TYR_257	H, E_TYR_257	2.94	2.10	26.15
1HGG.PDB	O, E_LEU_177	N, E_PHE_258	H, E_PHE_258	2.94	2.00	12.72
1HGG.PDB	OG, E_SER_115	N, E_ARG_261	H, E_ARG_261	2.99	2.04	12.07
1HGG.PDB	OE2, E_GLU_119	NH1, E_ARG_261	HH12, E_ARG_261	2.69	1.87	29.29
1HGG.PDB	OE1, E_GLU_119	NH2, E_ARG_261	HH22, E_ARG_261	2.74	1.88	26.67
1HGG.PDB	OH, E_TYR_302	NZ, E_LYS_264	HZ1, E_LYS_264	2.90	1.93	18.14
1HGG.PDB	ND1, E_HIS_56	NZ, E_LYS_264	HZ2, E_LYS_264	2.66	1.73	20.09
1HGG.PDB	OD2, E_ASP_85	NZ, E_LYS_264	HZ3, E_LYS_264	2.85	1.83	11.84
1HGG.PDB	O, E_PHE_87	N, E_MET_268	H, E_MET_268	2.81	1.91	19.55
1HGG.PDB	OE1, F_GLU_67	NH1, E_ARG_269	HH12, E_ARG_269	2.69	1.85	27.32
1HGG.PDB	O, E_PRO_284	OG, E_SER_270	HG, E_SER_270	2.76	1.85	15.69
1HGG.PDB	OG, E_SER_270	N, E_ALA_272	H, E_ALA_272	2.95	2.00	11.61
1HGG.PDB	O, E_ILE_51	N, E_ASP_275	H, E_ASP_275	2.87	1.99	21.60
1HGG.PDB	OD1, E_ASP_275	N, E_THR_276	H, E_THR_276	2.79	1.94	24.39
1HGG.PDB	O, E_ASN_54	N, E_SER_279	H, E_SER_279	2.79	1.84	11.36
1HGG.PDB	O, E_TYR_302	N, E_ILE_282	H, E_ILE_282	2.87	1.92	10.52
1HGG.PDB	O, E_THR_283	N, E_GLY_286	H, E_GLY_286	2.79	1.84	9.62
1HGG.PDB	O, E_LYS_50	N, E_SER_287	H, E_SER_287	2.89	1.92	6.20
1HGG.PDB	O, E_ALA_304	ND2, E_ASN_290	HD22, E_ASN_290	2.87	2.00	21.60
1HGG.PDB	OE1, E_GLN_44	NZ, E_LYS_292	HZ1, E_LYS_292	2.77	1.75	10.61
1HGG.PDB	OD2, E_ASP_291	NZ, E_LYS_292	HZ3, E_LYS_292	2.76	1.90	27.94
1HGG.PDB	O, E_LYS_307	N, E_GLN_295	H, E_GLN_295	2.79	1.91	20.65
1HGG.PDB	O, E_ASN_298	NE2, E_GLN_295	HE21, E_GLN_295	2.79	1.83	8.95
1HGG.PDB	O, E_GLN_44	N, E_ASN_296	H, E_ASN_296	2.89	1.93	10.60
1HGG.PDB	OD1, E_ASN_285	ND2, E_ASN_298	HD22, E_ASN_298	2.95	2.00	11.31
1HGG.PDB	O, F_LYS_68	NZ, E_LYS_299	HZ1, E_LYS_299	2.93	1.91	9.86
1HGG.PDB	OD1, E_ASN_298	N, E_ILE_300	H, E_ILE_300	2.82	1.91	16.92
1HGG.PDB	O, E_ILE_282	N, E_TYR_302	H, E_TYR_302	2.82	1.94	21.27
1HGG.PDB	O, E_LYS_264	OH, E_TYR_302	HH, E_TYR_302	2.63	1.84	28.99
1HGG.PDB	O, F_LYS_62	N, E_GLY_303	H, E_GLY_303	2.92	1.95	6.71
1HGG.PDB	O, E_GLN_295	N, E_VAL_309	H, E_VAL_309	2.89	2.05	25.47
1HGG.PDB	OG, F_SER_93	N, E_LYS_310	H, E_LYS_310	2.89	1.95	15.34
1HGG.PDB	OD1, F_ASP_90	NZ, E_LYS_310	HZ2, E_LYS_310	2.64	1.72	22.12
1HGG.PDB	OE2, E_GLU_41	N, E_LEU_314	H, E_LEU_314	2.79	1.89	17.95
1HGG.PDB	OE1, E_GLU_41	NZ, E_LYS_315	HZ3, E_LYS_315	2.68	1.80	26.22
1HGG.PDB	O, E_THR_40	N, E_LEU_316	H, E_LEU_316	2.77	1.85	15.13
1HGG.PDB	OD1, F_ASN_104	N, E_ALA_317	H, E_ALA_317	2.80	1.89	16.99
1HGG.PDB	O, E_ASN_38	N, E_THR_318	H, E_THR_318	2.92	1.99	14.27
1HGG.PDB	O, E_VAL_20	ND2, E_ASN_322	HD21, E_ASN_322	2.88	1.96	16.01
1HGG.PDB	OE2, E_GLU_35	ND2, E_ASN_322	HD22, E_ASN_322	2.79	1.94	25.02
1HGG.PDB	OE2, F_GLU_15	N, E_GLU_325	H, E_GLU_325	2.88	2.08	28.79
1HGG.PDB	O, E_GLN_327	NZ, E_LYS_326	HZ1, E_LYS_326	2.71	1.82	24.99
1HGG.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.98	1.97	15.13
1HGG.PDB	O, E_LYS_326	NE2, E_GLN_327	HE22, E_GLN_327	2.77	1.84	14.97
1HGG.PDB	OD2, F_ASP_112	N, F_GLY_1	H2, F_GLY_1	2.68	1.70	14.41
1HGG.PDB	OD1, F_ASP_109	N, F_LEU_2	H, F_LEU_2	2.94	2.03	18.76
1HGG.PDB	OD2, F_ASP_112	N, F_PHE_3	H, F_PHE_3	2.87	2.05	27.28
1HGG.PDB	OD2, F_ASP_112	N, F_GLY_4	H, F_GLY_4	2.93	2.02	17.67
1HGG.PDB	OD1, F_ASP_112	N, F_ALA_5	H, F_ALA_5	2.93	2.06	23.45
1HGG.PDB	O, F_GLY_4	N, F_PHE_9	H, F_PHE_9	2.76	1.83	14.86
1HGG.PDB	O, E_VAL_323	N, F_GLY_13	H, F_GLY_13	2.73	1.78	9.21
1HGG.PDB	O, E_HIS_17	N, F_TRP_14	H, F_TRP_14	2.81	1.90	18.17
1HGG.PDB	OG1, F_THR_41	N, F_TRP_21	H, F_TRP_21	2.87	1.92	11.28
1HGG.PDB	O, E_GLY_16	N, F_GLY_23	H, F_GLY_23	2.97	2.08	20.37
1HGG.PDB	O, F_ALA_35	N, F_PHE_24	H, F_PHE_24	2.85	1.88	5.77
1HGG.PDB	O, E_CYS_14	N, F_ARG_25	H, F_ARG_25	2.99	2.04	12.72

1HGG.PDB	O, F_GLY_33	N, F_HIS_26	H, F_HIS_26	2.87	1.99	21.57
1HGG.PDB	O, E_THR_12	N, F_GLN_27	H, F_GLN_27	2.98	2.05	15.41
1HGG.PDB	O, F_GLY_31	N, F_ASN_28	H, F_ASN_28	2.80	1.85	12.20
1HGG.PDB	O, F_CYS_144	ND2, F_ASN_28	HD22, F_ASN_28	2.83	1.93	18.95
1HGG.PDB	O, F_PHE_24	N, F_ALA_35	H, F_ALA_35	2.83	2.02	27.51
1HGG.PDB	O, F_TYR_22	N, F_ASP_37	H, F_ASP_37	2.73	1.77	4.79
1HGG.PDB	OD2, F_ASP_37	N, F_SER_40	H, F_SER_40	2.88	1.93	12.27
1HGG.PDB	OD2, F_ASP_37	OG, F_SER_40	HG, F_SER_40	2.74	1.92	26.19
1HGG.PDB	O, F_ASP_37	OG1, F_THR_41	HG1, F_THR_41	2.71	1.82	18.81
1HGG.PDB	O, F_LEU_38	N, F_GLN_42	H, F_GLN_42	2.91	1.98	13.94
1HGG.PDB	OD1, F_ASP_46	NE2, F_GLN_42	HE22, F_GLN_42	2.82	1.94	21.99
1HGG.PDB	O, F_LYS_39	N, F_ALA_43	H, F_ALA_43	2.96	1.99	8.07
1HGG.PDB	O, F_SER_40	N, F_ALA_44	H, F_ALA_44	2.94	1.96	1.69
1HGG.PDB	O, F_THR_41	N, F_ILE_45	H, F_ILE_45	2.95	2.01	14.67
1HGG.PDB	O, F_GLN_42	N, F_ASP_46	H, F_ASP_46	2.77	1.80	0.61
1HGG.PDB	OE2, F_GLU_114	NE2, F_GLN_47	HE21, F_GLN_47	2.97	2.06	18.05
1HGG.PDB	O, F_ALA_43	NE2, F_GLN_47	HE22, F_GLN_47	2.99	2.07	16.84
1HGG.PDB	O, F_ILE_45	N, F_ASN_49	H, F_ASN_49	2.83	1.91	16.15
1HGG.PDB	O, F_ASP_46	N, F_GLY_50	H, F_GLY_50	2.91	2.04	23.57
1HGG.PDB	O, F_GLN_47	N, F_LYS_51	H, F_LYS_51	2.91	1.93	0.37
1HGG.PDB	OG1, F_THR_107	NZ, F_LYS_51	HZ1, F_LYS_51	2.98	2.02	18.55
1HGG.PDB	OE1, F_GLU_103	NZ, F_LYS_51	HZ2, F_LYS_51	2.79	1.76	6.25
1HGG.PDB	ND1, F_HIS_106	NZ, F_LYS_51	HZ3, F_LYS_51	2.72	1.74	15.22
1HGG.PDB	O, F_ILE_48	N, F_LEU_52	H, F_LEU_52	2.90	2.00	18.64
1HGG.PDB	O, F_ASN_49	N, F_ASN_53	H, F_ASN_53	2.88	1.99	19.93
1HGG.PDB	OE1, F_GLU_57	NH1, F_ARG_54	HH11, F_ARG_54	2.85	1.85	10.83
1HGG.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.73	1.74	10.16
1HGG.PDB	O, F_ASN_53	N, F_ILE_56	H, F_ILE_56	2.96	2.16	29.26
1HGG.PDB	OE2, F_GLU_61	NZ, F_LYS_58	HZ3, F_LYS_58	2.94	1.92	12.48
1HGG.PDB	OD2, D_ASP_86	NZ, F_LYS_62	HZ3, F_LYS_62	2.58	1.75	29.01
1HGG.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.87	1.91	10.03
1HGG.PDB	O, F_PHE_63	NE2, F_GLN_65	HE22, F_GLN_65	2.98	2.01	5.05
1HGG.PDB	O, E_LYS_299	NZ, F_LYS_68	HZ1, F_LYS_68	2.85	1.83	8.63
1HGG.PDB	OE2, F_GLU_85	NZ, F_LYS_68	HZ2, F_LYS_68	2.75	1.74	10.05
1HGG.PDB	OE2, F_GLU_72	OG, F_SER_71	HG, F_SER_71	2.86	2.03	26.49
1HGG.PDB	OG, A_SER_107	N, F_ARG_76	H, F_ARG_76	2.79	1.82	4.90
1HGG.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.88	1.92	11.44
1HGG.PDB	OE1, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.75	1.76	9.13
1HGG.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.67	1.68	1.99
1HGG.PDB	OE2, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.79	1.81	10.64
1HGG.PDB	O, F_GLY_75	N, F_ASP_79	H, F_ASP_79	2.85	1.92	13.80
1HGG.PDB	O, F_LEU_80	N, F_VAL_84	H, F_VAL_84	2.86	1.90	9.26
1HGG.PDB	O, F_LYS_82	N, F_ASP_86	H, F_ASP_86	2.94	1.98	10.58
1HGG.PDB	O, F_TYR_83	N, F_THR_87	H, F_THR_87	2.89	1.95	12.08
1HGG.PDB	O, F_VAL_84	N, F_LYS_88	H, F_LYS_88	2.90	2.00	19.38
1HGG.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.68	1.67	10.46
1HGG.PDB	O, F_GLU_85	N, F_ILE_89	H, F_ILE_89	2.87	1.91	8.62
1HGG.PDB	O, F_LYS_88	N, F_TRP_92	H, F_TRP_92	2.93	1.97	10.23
1HGG.PDB	O, F_ILE_89	N, F_SER_93	H, F_SER_93	2.82	1.93	20.13
1HGG.PDB	O, F_ILE_89	OG, F_SER_93	HG, F_SER_93	2.82	1.91	16.61
1HGG.PDB	O, F_ASP_90	N, F_TYR_94	H, F_TYR_94	2.98	2.04	13.91
1HGG.PDB	O, F_TYR_94	N, F_LEU_98	H, F_LEU_98	2.96	1.99	8.41
1HGG.PDB	O, F_ASN_95	N, F_LEU_99	H, F_LEU_99	2.87	1.98	19.54
1HGG.PDB	O, F_LEU_98	N, F_LEU_102	H, F_LEU_102	2.91	1.95	11.26
1HGG.PDB	O, F_VAL_100	N, F_ASN_104	H, F_ASN_104	2.83	1.90	15.88
1HGG.PDB	O, E_LYS_27	ND2, F_ASN_104	HD22, F_ASN_104	2.91	1.98	14.98
1HGG.PDB	O, F_LEU_102	N, F_HIS_106	H, F_HIS_106	2.95	2.00	11.41
1HGG.PDB	O, F_GLU_103	N, F_THR_107	H, F_THR_107	2.84	1.97	22.50

1HGG.PDB	O, F_HIS_106	N, F_LEU_110	H, F_LEU_110	2.81	1.85	10.10
1HGG.PDB	O, F_THR_107	N, F_THR_111	H, F_THR_111	2.97	2.01	8.66
1HGG.PDB	O, F_THR_107	OG1, F_THR_111	HG1, F_THR_111	2.90	1.95	9.89
1HGG.PDB	O, F_ASP_109	N, F_SER_113	H, F_SER_113	2.78	1.87	15.88
1HGG.PDB	O, F_ASP_112	N, F_ASN_116	H, F_ASN_116	2.99	2.01	3.50
1HGG.PDB	O, F_SER_113	N, F_LYS_117	H, F_LYS_117	2.76	1.88	19.98
1HGG.PDB	O, F_ASN_116	N, F_GLU_120	H, F_GLU_120	2.92	1.95	3.79
1HGG.PDB	O, F_LYS_117	N, F_LYS_121	H, F_LYS_121	2.87	1.96	17.48
1HGG.PDB	O, F_LEU_118	N, F_THR_122	H, F_THR_122	2.98	2.04	13.60
1HGG.PDB	O, F_PHE_119	N, F_ARG_123	H, F_ARG_123	2.90	1.95	11.29
1HGG.PDB	OE2, F_GLU_120	NH1, F_ARG_123	HH11, F_ARG_123	2.72	1.86	25.68
1HGG.PDB	O, F_GLU_120	N, F_ARG_124	H, F_ARG_124	2.96	1.99	8.37
1HGG.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.96	2.09	22.59
1HGG.PDB	OE2, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.87	2.01	24.00
1HGG.PDB	O, F_HIS_159	ND2, F_ASN_129	HD21, F_ASN_129	2.99	2.04	11.15
1HGG.PDB	OH, F_TYR_157	ND2, F_ASN_129	HD22, F_ASN_129	2.79	1.86	14.20
1HGG.PDB	O, F_LYS_139	N, F_GLU_131	H, F_GLU_131	2.96	2.01	12.55
1HGG.PDB	O, F_CYS_137	N, F_MET_133	H, F_MET_133	2.88	1.96	16.91
1HGG.PDB	O, E_LEU_13	N, F_PHE_138	H, F_PHE_138	2.72	1.87	23.38
1HGG.PDB	O, F_GLU_131	N, F_LYS_139	H, F_LYS_139	2.84	1.88	8.34
1HGG.PDB	O, E_ALA_11	N, F_ILE_140	H, F_ILE_140	2.79	1.89	17.86
1HGG.PDB	O, F_ASN_129	N, F_TYR_141	H, F_TYR_141	2.91	1.94	4.20
1HGG.PDB	OE2, F_GLU_165	N, F_LYS_143	H, F_LYS_143	2.98	2.11	23.38
1HGG.PDB	OE2, F_GLU_30	N, F_ASN_146	H, F_ASN_146	2.87	1.90	7.26
1HGG.PDB	OD1, F_ASP_145	N, F_ALA_147	H, F_ALA_147	2.98	2.17	28.99
1HGG.PDB	O, F_ASP_145	N, F_ILE_149	H, F_ILE_149	2.98	2.02	9.29
1HGG.PDB	O, F_ASN_146	N, F_GLU_150	H, F_GLU_150	2.88	1.93	11.94
1HGG.PDB	O, F_ALA_147	N, F_SER_151	H, F_SER_151	2.86	1.99	21.94
1HGG.PDB	O, F_CYS_148	OG, F_SER_151	HG, F_SER_151	2.70	1.85	23.21
1HGG.PDB	O, F_GLU_150	N, F_ASN_154	H, F_ASN_154	2.81	1.84	3.77
1HGG.PDB	O, F_HIS_159	N, F_TYR_162	H, F_TYR_162	2.96	2.05	18.31
1HGG.PDB	O, F_ASP_160	N, F_ARG_163	H, F_ARG_163	2.93	1.96	6.26
1HGG.PDB	O, D_ARG_170	NH1, F_ARG_163	HH12, F_ARG_163	2.94	2.00	17.69
1HGG.PDB	O, F_TYR_162	N, F_ALA_166	H, F_ALA_166	2.88	1.92	7.73
1HGG.PDB	O, F_ARG_163	N, F_LEU_167	H, F_LEU_167	2.76	1.84	14.20
1HGG.PDB	O, F_ALA_166	N, F_ARG_170	H, F_ARG_170	2.89	2.02	22.61
1HGG.PDB	O, F_GLU_128	NE, F_ARG_170	HE, F_ARG_170	2.70	1.85	24.72
1HGG.PDB	OE2, F_GLU_131	NH1, F_ARG_170	HH11, F_ARG_170	2.84	1.84	6.38
1HGG.PDB	O, F_LEU_167	N, F_PHE_171	H, F_PHE_171	2.94	1.99	11.68
1HGH.PDB	O, B_ILE_140	N, A_ALA_11	H, A_ALA_11	2.91	2.03	21.75
1HGH.PDB	O, B_PHE_138	N, A_LEU_13	H, A_LEU_13	2.96	1.99	9.24
1HGH.PDB	O, B_ARG_25	N, A_CYS_14	H, A_CYS_14	2.90	1.93	6.13
1HGH.PDB	O, B_GLY_136	N, A_LEU_15	H, A_LEU_15	2.89	1.92	5.59
1HGH.PDB	O, B_GLY_23	N, A_GLY_16	H, A_GLY_16	2.92	2.07	24.71
1HGH.PDB	O, B_TRP_21	N, A_HIS_18	H, A_HIS_18	2.92	2.03	20.10
1HGH.PDB	OD1, A_ASN_322	N, A_VAL_20	H, A_VAL_20	2.77	1.82	11.72
1HGH.PDB	O, A_VAL_36	N, A_THR_24	H, A_THR_24	2.85	1.96	20.21
1HGH.PDB	O, A_ILE_34	N, A_VAL_26	H, A_VAL_26	2.81	1.89	15.81
1HGH.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.78	1.76	9.03
1HGH.PDB	O, A_ASP_31	N, A_THR_28	H, A_THR_28	2.74	1.91	26.60
1HGH.PDB	O, A_VAL_26	N, A_ILE_34	H, A_ILE_34	2.88	1.93	10.35
1HGH.PDB	O, A_THR_24	N, A_VAL_36	H, A_VAL_36	2.78	1.83	9.24
1HGH.PDB	O, A_MET_320	N, A_THR_37	H, A_THR_37	2.90	1.93	5.37
1HGH.PDB	O, A_LEU_316	N, A_THR_40	H, A_THR_40	2.78	1.95	25.57
1HGH.PDB	O, A_LEU_314	N, A_LEU_42	H, A_LEU_42	2.85	1.99	23.14
1HGH.PDB	O, A_PHE_294	N, A_GLN_44	H, A_GLN_44	2.90	1.92	4.45
1HGH.PDB	O, A_SER_46	NE2, A_GLN_44	HE22, A_GLN_44	2.81	1.96	24.37
1HGH.PDB	OD2, A_ASP_275	NZ, A_LYS_50	HZ1, A_LYS_50	2.79	1.83	19.36

1HGH.PDB	O, A_PRO_273	N, A_ILE_51	H, A_ILE_51	2.82	1.89	14.41
1HGH.PDB	O, A_ASP_275	N, A_ASN_53	H, A_ASN_53	2.86	1.97	20.86
1HGH.PDB	O, A_GLU_280	NE2, A_HIS_56	HE2, A_HIS_56	2.98	2.02	10.58
1HGH.PDB	OD2, A_ASP_85	N, A_ARG_57	H, A_ARG_57	2.81	1.91	18.42
1HGH.PDB	O, A_THR_83	NE, A_ARG_57	HE, A_ARG_57	2.77	1.81	8.25
1HGH.PDB	O, A_LEU_86	N, A_LEU_59	H, A_LEU_59	2.96	2.03	13.96
1HGH.PDB	O, A_VAL_88	N, A_GLY_61	H, A_GLY_61	2.98	2.14	25.31
1HGH.PDB	OD1, A_ASP_60	N, A_ILE_62	H, A_ILE_62	2.86	1.93	13.55
1HGH.PDB	O, A_GLY_61	N, A_CYS_64	H, A_CYS_64	2.88	1.98	19.17
1HGH.PDB	OE2, A_GLU_89	N, A_LEU_66	H, A_LEU_66	2.90	1.95	10.87
1HGH.PDB	O, A_LEU_66	N, A_LEU_70	H, A_LEU_70	2.83	1.95	21.65
1HGH.PDB	O, A_ILE_67	N, A_LEU_71	H, A_LEU_71	2.79	1.83	6.52
1HGH.PDB	O, A_ASP_68	N, A_GLY_72	H, A_GLY_72	2.91	1.99	15.72
1HGH.PDB	OD1, A_ASP_73	ND1, A_HIS_75	HD1, A_HIS_75	2.74	1.85	19.20
1HGH.PDB	O, A_ASP_63	NE2, A_HIS_75	HE2, A_HIS_75	2.75	1.84	17.13
1HGH.PDB	O, A_ASP_73	N, A_CYS_76	H, A_CYS_76	2.78	1.88	17.74
1HGH.PDB	O, A_PRO_74	N, A_ASP_77	H, A_ASP_77	2.92	1.95	6.24
1HGH.PDB	O, A_PHE_79	N, A_GLU_82	H, A_GLU_82	2.94	2.02	16.23
1HGH.PDB	OE1, A_GLU_82	N, A_THR_83	H, A_THR_83	2.95	2.06	20.13
1HGH.PDB	O, A_ARG_57	N, A_ASP_85	H, A_ASP_85	2.82	1.89	15.27
1HGH.PDB	O, A_MET_268	N, A_GLU_89	H, A_GLU_89	2.83	1.89	11.77
1HGH.PDB	OD1, A_ASP_60	NE, A_ARG_90	HE, A_ARG_90	2.85	1.88	8.50
1HGH.PDB	O, A_SER_270	NH1, A_ARG_90	HH11, A_ARG_90	2.64	1.77	24.75
1HGH.PDB	O, A_ALA_272	NH1, A_ARG_90	HH12, A_ARG_90	2.63	1.72	19.06
1HGH.PDB	OD2, A_ASP_60	NH2, A_ARG_90	HH21, A_ARG_90	2.79	1.80	9.33
1HGH.PDB	OD1, A_ASP_271	N, A_SER_91	H, A_SER_91	2.85	1.90	11.89
1HGH.PDB	OD2, A_ASP_271	OG, A_SER_91	HG, A_SER_91	2.76	1.89	21.30
1HGH.PDB	OD2, A_ASP_68	OG, A_SER_95	HG, A_SER_95	2.83	1.95	21.96
1HGH.PDB	OD2, A_ASP_73	N, A_ASN_96	H, A_ASN_96	2.91	1.94	7.26
1HGH.PDB	OD1, A_ASP_68	OH, A_TYR_100	HH, A_TYR_100	2.95	2.07	21.37
1HGH.PDB	O, A_ILE_230	N, A_ASP_101	H, A_ASP_101	2.93	2.05	22.44
1HGH.PDB	OD2, A_ASP_104	OG, A_SER_107	HG, A_SER_107	2.88	1.94	14.34
1HGH.PDB	O, A_TYR_105	N, A_ARG_109	H, A_ARG_109	2.84	1.87	3.70
1HGH.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.86	1.88	13.48
1HGH.PDB	OD2, F_ASP_79	OG, A_SER_110	HG, A_SER_110	2.97	2.01	11.65
1HGH.PDB	O, A_SER_107	N, A_LEU_111	H, A_LEU_111	2.86	1.91	11.39
1HGH.PDB	O, A_LEU_108	N, A_VAL_112	H, A_VAL_112	2.97	2.00	6.33
1HGH.PDB	O, A_ARG_109	N, A_ALA_113	H, A_ALA_113	2.87	1.97	18.74
1HGH.PDB	O, A_SER_110	N, A_SER_114	H, A_SER_114	2.97	2.06	18.17
1HGH.PDB	OE2, A_GLU_119	OG1, A_THR_117	HG1, A_THR_117	2.86	1.91	8.00
1HGH.PDB	O, A_GLU_82	N, A_LEU_118	H, A_LEU_118	2.97	2.03	14.27
1HGH.PDB	O, A_TYR_257	N, A_ILE_121	H, A_ILE_121	2.88	1.93	10.50
1HGH.PDB	O, A_ARG_255	N, A_GLU_123	H, A_GLU_123	2.86	1.91	11.35
1HGH.PDB	O, A_THR_155	N, A_THR_131	H, A_THR_131	2.70	1.82	20.96
1HGH.PDB	O, A_LYS_156	OG1, A_THR_131	HG1, A_THR_131	2.65	1.86	28.53
1HGH.PDB	OD1, A_ASN_152	N, A_ASN_133	H, A_ASN_133	2.91	2.01	19.83
1HGH.PDB	O, A_TRP_153	N, A_GLY_134	H, A_GLY_134	2.97	2.05	15.71
1HGH.PDB	O, A_GLY_146	N, A_SER_136	H, A_SER_136	2.71	1.82	19.78
1HGH.PDB	OG, A_SER_136	N, A_ALA_138	H, A_ALA_138	2.92	1.99	15.62
1HGH.PDB	O, A_GLY_144	NZ, A_LYS_140	HZ1, A_LYS_140	2.88	1.90	16.19
1HGH.PDB	OD1, A_ASN_137	NZ, A_LYS_140	HZ2, A_LYS_140	2.74	1.73	12.09
1HGH.PDB	OD2, A_ASP_77	NE, A_ARG_141	HE, A_ARG_141	2.85	2.03	27.72
1HGH.PDB	O, A_PHE_147	NH1, A_ARG_141	HH12, A_ARG_141	2.57	1.64	17.56
1HGH.PDB	OD1, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.86	1.95	21.78
1HGH.PDB	OD2, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.74	1.85	23.60
1HGH.PDB	O, A_GLY_72	NH2, A_ARG_141	HH22, A_ARG_141	2.97	1.99	11.22
1HGH.PDB	O, A_SER_136	N, A_GLY_146	H, A_GLY_146	2.94	1.99	12.07
1HGH.PDB	O, A_GLY_72	N, A_SER_149	H, A_SER_149	2.87	1.96	17.76

1HGH.PDB	O, A_ALA_253	N, A_ASN_152	H, A_ASN_152	2.72	1.90	27.60
1HGH.PDB	OH, A_TYR_195	NE1, A_TRP_153	HE1, A_TRP_153	2.96	2.05	18.96
1HGH.PDB	O, A_THR_131	N, A_THR_155	H, A_THR_155	2.98	2.04	12.93
1HGH.PDB	O, A_LEU_194	N, A_LYS_156	H, A_LYS_156	2.93	1.99	14.05
1HGH.PDB	O, A_SER_193	NZ, A_LYS_156	HZ2, A_LYS_156	2.80	1.78	10.99
1HGH.PDB	O, A_THR_160	N, A_SER_157	H, A_SER_157	2.94	2.03	18.60
1HGH.PDB	O, A_SER_247	N, A_LEU_164	H, A_LEU_164	2.69	1.86	25.54
1HGH.PDB	O, A_ILE_245	N, A_VAL_166	H, A_VAL_166	2.85	1.89	11.06
1HGH.PDB	O, A_LEU_243	OG1, A_THR_167	HG1, A_THR_167	2.91	1.96	8.56
1HGH.PDB	O, A_LEU_243	N, A_MET_168	H, A_MET_168	2.82	1.89	14.71
1HGH.PDB	O, A_ASP_241	N, A_ASN_170	H, A_ASN_170	2.96	1.99	7.35
1HGH.PDB	O, A_PHE_174	ND2, A_ASN_170	HD21, A_ASN_170	2.81	1.86	12.55
1HGH.PDB	O, A_VAL_237	ND2, A_ASN_170	HD22, A_ASN_170	2.88	2.03	25.05
1HGH.PDB	O, A_VAL_237	N, A_LYS_176	H, A_LYS_176	3.00	2.06	14.88
1HGH.PDB	OE2, A_GLU_123	NZ, A_LYS_176	HZ1, A_LYS_176	2.68	1.79	24.70
1HGH.PDB	O, A_PHE_258	N, A_LEU_177	H, A_LEU_177	2.99	2.01	5.13
1HGH.PDB	O, A_THR_235	N, A_TYR_178	H, A_TYR_178	2.85	1.88	6.04
1HGH.PDB	OE1, A_GLU_123	OH, A_TYR_178	HH, A_TYR_178	2.75	1.81	10.37
1HGH.PDB	OG1, A_THR_235	NE1, A_TRP_180	HE1, A_TRP_180	2.89	1.90	1.65
1HGH.PDB	O, A_ASN_250	N, A_HIS_183	H, A_HIS_183	2.85	1.97	21.49
1HGH.PDB	O, A_ARG_229	N, A_HIS_184	H, A_HIS_184	2.86	1.93	14.05
1HGH.PDB	OG, A_SER_231	NE2, A_HIS_184	HE2, A_HIS_184	2.74	1.90	25.48
1HGH.PDB	OG1, A_THR_187	N, A_GLU_190	H, A_GLU_190	2.92	1.98	12.65
1HGH.PDB	O, A_THR_187	N, A_GLN_191	H, A_GLN_191	2.99	2.03	10.21
1HGH.PDB	OD1, A_ASN_250	NE2, A_GLN_191	HE21, A_GLN_191	2.96	2.00	8.72
1HGH.PDB	O, A_GLN_197	NE2, A_GLN_191	HE22, A_GLN_191	2.95	2.00	12.41
1HGH.PDB	O, A_GLN_189	N, A_SER_193	H, A_SER_193	2.92	1.94	4.94
1HGH.PDB	O, A_GLN_189	OG, A_SER_193	HG, A_SER_193	2.79	2.00	29.43
1HGH.PDB	O, A_GLU_190	N, A_LEU_194	H, A_LEU_194	2.95	1.99	10.19
1HGH.PDB	O, A_GLN_191	N, A_TYR_195	H, A_TYR_195	2.79	1.83	8.10
1HGH.PDB	O, A_TYR_161	NE2, A_GLN_197	HE21, A_GLN_197	2.92	1.97	11.79
1HGH.PDB	O, A_ASN_248	NE2, A_GLN_197	HE22, A_GLN_197	2.87	1.96	16.95
1HGH.PDB	OD1, A_ASN_246	NH2, A_ARG_201	HH21, A_ARG_201	2.63	1.71	19.32
1HGH.PDB	O, A_ILE_213	N, A_VAL_202	H, A_VAL_202	2.95	2.00	12.25
1HGH.PDB	O, A_ASN_246	N, A_THR_203	H, A_THR_203	2.81	1.89	15.97
1HGH.PDB	O, A_GLN_211	N, A_VAL_204	H, A_VAL_204	2.84	1.93	17.60
1HGH.PDB	O, A_SER_209	N, A_THR_206	H, A_THR_206	2.88	1.91	6.84
1HGH.PDB	OD1, A_ASP_241	N, A_ARG_207	H, A_ARG_207	2.88	1.92	8.24
1HGH.PDB	OG1, A_THR_206	OG, A_SER_209	HG, A_SER_209	2.93	1.98	8.14
1HGH.PDB	OD1, E_ASP_101	NE2, A_GLN_210	HE22, A_GLN_210	2.97	2.14	27.61
1HGH.PDB	O, A_VAL_204	N, A_GLN_211	H, A_GLN_211	2.88	1.95	14.72
1HGH.PDB	OG1, A_THR_203	OG1, A_THR_212	HG1, A_THR_212	2.93	1.98	7.92
1HGH.PDB	O, A_VAL_202	N, A_ILE_213	H, A_ILE_213	2.89	1.95	14.76
1HGH.PDB	ND1, A_HIS_184	N, A_ASN_216	H, A_ASN_216	2.75	1.96	29.57
1HGH.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.66	1.73	18.15
1HGH.PDB	O, A_ASN_216	NH2, A_ARG_220	HH22, A_ARG_220	2.69	1.79	20.62
1HGH.PDB	O, A_LEU_226	N, A_VAL_223	H, A_VAL_223	2.87	1.91	10.54
1HGH.PDB	O, A_CYS_97	NE, A_ARG_224	HE, A_ARG_224	2.80	1.97	26.34
1HGH.PDB	O, A_CYS_97	NH2, A_ARG_224	HH21, A_ARG_224	2.81	1.94	24.94
1HGH.PDB	O, A_VAL_223	N, A_LEU_226	H, A_LEU_226	2.81	1.89	14.05
1HGH.PDB	O, A_SER_228	NH1, A_ARG_229	HH11, A_ARG_229	2.68	1.73	15.83
1HGH.PDB	O, A_PRO_221	NH2, A_ARG_229	HH22, A_ARG_229	2.59	1.64	14.22
1HGH.PDB	OD1, A_ASP_101	OG, A_SER_231	HG, A_SER_231	2.86	1.91	11.01
1HGH.PDB	O, A_ASP_101	N, A_ILE_232	H, A_ILE_232	2.88	1.97	18.41
1HGH.PDB	O, A_TRP_180	N, A_TYR_233	H, A_TYR_233	2.88	1.92	10.18
1HGH.PDB	O, A_TYR_178	N, A_THR_235	H, A_THR_235	2.91	2.01	18.50
1HGH.PDB	O, A_LYS_176	N, A_VAL_237	H, A_VAL_237	2.76	1.84	16.06
1HGH.PDB	O, F_SER_71	NZ, A_LYS_238	HZ2, A_LYS_238	2.69	1.74	19.56

1HGH.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.92	1.93	15.64
1HGH.PDB	O, A_ASN_170	N, A_GLY_240	H, A_GLY_240	2.92	2.05	22.76
1HGH.PDB	O, A_LYS_238	N, A_ASP_241	H, A_ASP_241	2.96	2.03	14.77
1HGH.PDB	OD1, A_ASP_241	N, A_VAL_242	H, A_VAL_242	2.75	1.93	27.28
1HGH.PDB	O, A_MET_168	N, A_LEU_243	H, A_LEU_243	2.84	1.87	3.34
1HGH.PDB	O, A_SER_205	N, A_VAL_244	H, A_VAL_244	2.95	2.00	12.06
1HGH.PDB	O, A_VAL_166	N, A_ILE_245	H, A_ILE_245	2.85	1.91	12.74
1HGH.PDB	O, A_THR_203	N, A_ASN_246	H, A_ASN_246	2.92	1.96	9.76
1HGH.PDB	OD1, A_ASN_165	ND2, A_ASN_246	HD22, A_ASN_246	2.95	1.98	10.57
1HGH.PDB	O, A_LEU_164	N, A_SER_247	H, A_SER_247	2.89	1.97	17.06
1HGH.PDB	OE1, A_GLN_191	ND2, A_ASN_250	HD21, A_ASN_250	2.87	1.90	5.96
1HGH.PDB	O, A_HIS_183	ND2, A_ASN_250	HD22, A_ASN_250	2.85	1.88	6.67
1HGH.PDB	O, A_GLY_181	N, A_ILE_252	H, A_ILE_252	2.94	1.99	11.06
1HGH.PDB	O, A_ASN_152	N, A_ALA_253	H, A_ALA_253	2.83	1.93	19.98
1HGH.PDB	O, A_ILE_121	N, A_TYR_257	H, A_TYR_257	3.00	2.13	23.55
1HGH.PDB	O, A_LEU_177	N, A_PHE_258	H, A_PHE_258	2.88	1.93	9.88
1HGH.PDB	OG, A_SER_115	N, A_ARG_261	H, A_ARG_261	2.95	1.99	11.60
1HGH.PDB	OE2, A_GLU_119	NH1, A_ARG_261	HH12, A_ARG_261	2.62	1.81	29.53
1HGH.PDB	OE1, A_GLU_119	NH2, A_ARG_261	HH22, A_ARG_261	2.87	1.97	23.64
1HGH.PDB	OD2, A_ASP_85	NZ, A_LYS_264	HZ3, A_LYS_264	2.81	1.82	15.33
1HGH.PDB	O, A_PHE_87	N, A_MET_268	H, A_MET_268	2.83	1.97	23.14
1HGH.PDB	O, A_GLU_89	N, A_SER_270	H, A_SER_270	3.00	2.03	9.88
1HGH.PDB	O, A_PRO_284	OG, A_SER_270	HG, A_SER_270	2.79	1.85	11.64
1HGH.PDB	OG, A_SER_270	N, A_ALA_272	H, A_ALA_272	2.97	2.03	13.38
1HGH.PDB	O, A_ILE_51	N, A_ASP_275	H, A_ASP_275	2.90	1.99	17.90
1HGH.PDB	OD1, A_ASP_275	N, A_THR_276	H, A_THR_276	2.83	1.96	22.54
1HGH.PDB	O, A_ASN_54	N, A_SER_279	H, A_SER_279	2.78	1.84	12.84
1HGH.PDB	O, A_TYR_302	N, A_ILE_282	H, A_ILE_282	2.85	1.90	11.45
1HGH.PDB	O, A_THR_283	N, A_GLY_286	H, A_GLY_286	2.81	1.91	17.80
1HGH.PDB	O, A_LYS_50	N, A_SER_287	H, A_SER_287	2.92	1.95	4.60
1HGH.PDB	O, A_ALA_304	ND2, A_ASN_290	HD22, A_ASN_290	2.87	1.97	19.64
1HGH.PDB	OE1, A_GLN_44	NZ, A_LYS_292	HZ1, A_LYS_292	2.68	1.67	11.56
1HGH.PDB	OD2, A_ASP_291	NZ, A_LYS_292	HZ3, A_LYS_292	2.82	1.85	18.01
1HGH.PDB	O, A_LYS_307	N, A_GLN_295	H, A_GLN_295	2.87	1.98	21.43
1HGH.PDB	O, A_ASN_298	NE2, A_GLN_295	HE21, A_GLN_295	2.73	1.78	8.62
1HGH.PDB	O, A_GLN_44	N, A_ASN_296	H, A_ASN_296	2.92	1.96	9.49
1HGH.PDB	O, B_LYS_68	NZ, A_LYS_299	HZ1, A_LYS_299	2.98	1.97	13.59
1HGH.PDB	OD1, A_ASN_298	N, A_ILE_300	H, A_ILE_300	2.92	1.97	10.82
1HGH.PDB	O, A_ILE_282	N, A_TYR_302	H, A_TYR_302	2.84	2.02	27.55
1HGH.PDB	O, A_LYS_264	OH, A_TYR_302	HH, A_TYR_302	2.68	1.89	29.18
1HGH.PDB	O, B_LYS_62	N, A_GLY_303	H, A_GLY_303	3.00	2.03	6.35
1HGH.PDB	O, A_GLN_295	N, A_VAL_309	H, A_VAL_309	2.94	2.11	27.12
1HGH.PDB	OG, B_SER_93	N, A_LYS_310	H, A_LYS_310	2.90	1.94	8.41
1HGH.PDB	OD1, B_ASP_86	NZ, A_LYS_310	HZ2, A_LYS_310	2.71	1.84	27.09
1HGH.PDB	OE2, A_GLU_41	N, A_LEU_314	H, A_LEU_314	2.82	1.88	12.85
1HGH.PDB	OE1, A_GLU_41	NZ, A_LYS_315	HZ3, A_LYS_315	2.87	1.90	18.83
1HGH.PDB	O, A_THR_40	N, A_LEU_316	H, A_LEU_316	2.77	1.84	14.60
1HGH.PDB	OD1, B_ASN_104	N, A_ALA_317	H, A_ALA_317	2.74	1.80	10.38
1HGH.PDB	O, A_ASN_38	N, A_THR_318	H, A_THR_318	2.93	1.99	13.50
1HGH.PDB	N, A_GLU_35	N, A_ASN_322	H, A_ASN_322	2.96	1.98	2.64
1HGH.PDB	O, A_VAL_20	ND2, A_ASN_322	HD21, A_ASN_322	2.83	1.91	15.77
1HGH.PDB	OE2, A_GLU_35	ND2, A_ASN_322	HD22, A_ASN_322	2.83	1.93	20.02
1HGH.PDB	OE1, A_GLU_325	NZ, A_LYS_326	HZ3, A_LYS_326	2.84	1.87	17.61
1HGH.PDB	O, A_PRO_21	NE2, A_GLN_327	HE22, A_GLN_327	2.76	1.93	26.05
1HGH.PDB	OD2, B_ASP_112	N, B_GLY_1	H2, B_GLY_1	2.83	1.83	12.80
1HGH.PDB	OD1, B_ASP_109	N, B_LEU_2	H, B_LEU_2	2.87	1.94	15.91
1HGH.PDB	OD2, B_ASP_112	N, B_PHE_3	H, B_PHE_3	2.80	1.99	28.74
1HGH.PDB	OD2, B_ASP_112	N, B_GLY_4	H, B_GLY_4	2.97	2.08	20.13

1HGH.PDB	OD1, B_ASP_112	N, B_ALA_5	H, B_ALA_5	2.90	2.00	18.43
1HGH.PDB	O, B_GLY_4	N, B_PHE_9	H, B_PHE_9	2.83	1.90	13.47
1HGH.PDB	O, B_GLY_13	ND2, B_ASN_12	HD22, B_ASN_12	2.81	1.93	21.84
1HGH.PDB	O, A_VAL_323	N, B_GLY_13	H, B_GLY_13	2.69	1.78	16.40
1HGH.PDB	O, A_HIS_17	N, B_TRP_14	H, B_TRP_14	2.80	1.87	14.18
1HGH.PDB	OG1, B_THR_41	N, B_TRP_21	H, B_TRP_21	2.88	1.96	16.52
1HGH.PDB	O, A_GLY_16	N, B_GLY_23	H, B_GLY_23	2.92	2.01	18.42
1HGH.PDB	O, B_ALA_35	N, B_PHE_24	H, B_PHE_24	2.84	1.87	5.30
1HGH.PDB	O, A_CYS_14	N, B_ARG_25	H, B_ARG_25	2.97	2.02	12.29
1HGH.PDB	OE1, B_GLN_34	NE, B_ARG_25	HE, B_ARG_25	2.67	1.79	21.37
1HGH.PDB	OE1, B_GLN_34	NH2, B_ARG_25	HH21, B_ARG_25	2.91	2.10	29.24
1HGH.PDB	O, B_GLY_33	N, B_HIS_26	H, B_HIS_26	2.69	1.85	24.63
1HGH.PDB	O, B_GLY_31	N, B_ASN_28	H, B_ASN_28	2.77	1.84	14.31
1HGH.PDB	O, B_ASN_28	N, B_GLY_31	H, B_GLY_31	2.97	2.09	21.15
1HGH.PDB	O, B_HIS_26	N, B_GLY_33	H, B_GLY_33	2.87	1.95	17.09
1HGH.PDB	O, B_PHE_24	N, B_ALA_35	H, B_ALA_35	2.82	2.00	27.92
1HGH.PDB	O, B_TYR_22	N, B_ASP_37	H, B_ASP_37	2.71	1.77	10.18
1HGH.PDB	OD2, B_ASP_37	N, B_SER_40	H, B_SER_40	2.86	1.90	7.81
1HGH.PDB	O, B_ASP_37	OG1, B_THR_41	HG1, B_THR_41	2.73	1.82	16.31
1HGH.PDB	O, B_LEU_38	N, B_GLN_42	H, B_GLN_42	2.96	2.02	13.86
1HGH.PDB	OD1, B_ASP_46	NE2, B_GLN_42	HE22, B_GLN_42	2.86	1.97	20.47
1HGH.PDB	O, B_LYS_39	N, B_ALA_43	H, B_ALA_43	2.95	2.01	14.38
1HGH.PDB	O, B_SER_40	N, B_ALA_44	H, B_ALA_44	2.94	1.96	4.02
1HGH.PDB	O, B_THR_41	N, B_ILE_45	H, B_ILE_45	2.92	1.98	12.98
1HGH.PDB	O, B_GLN_42	N, B_ASP_46	H, B_ASP_46	2.79	1.82	1.49
1HGH.PDB	O, B_ALA_43	NE2, B_GLN_47	HE22, B_GLN_47	2.86	1.96	17.99
1HGH.PDB	O, B_ILE_45	N, B_ASN_49	H, B_ASN_49	2.86	1.93	14.26
1HGH.PDB	O, B_ASP_46	N, B_GLY_50	H, B_GLY_50	2.92	2.02	19.62
1HGH.PDB	O, B_GLN_47	N, B_LYS_51	H, B_LYS_51	2.97	2.01	11.02
1HGH.PDB	OE1, B_GLU_103	NZ, B_LYS_51	HZ1, B_LYS_51	2.79	1.76	7.63
1HGH.PDB	ND1, B_HIS_106	NZ, B_LYS_51	HZ2, B_LYS_51	2.80	1.85	18.51
1HGH.PDB	OG1, B_THR_107	NZ, B_LYS_51	HZ3, B_LYS_51	2.89	1.91	15.99
1HGH.PDB	O, B_ILE_48	N, B_LEU_52	H, B_LEU_52	2.93	2.02	17.94
1HGH.PDB	O, B_ASN_49	N, B_ASN_53	H, B_ASN_53	2.82	1.92	18.53
1HGH.PDB	OE1, B_GLU_57	NH1, B_ARG_54	HH11, B_ARG_54	2.86	1.87	11.36
1HGH.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.82	1.86	15.60
1HGH.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ1, B_LYS_62	2.66	1.80	27.71
1HGH.PDB	OD2, F_ASP_90	NZ, B_LYS_62	HZ3, B_LYS_62	2.68	1.82	27.13
1HGH.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.87	1.91	11.96
1HGH.PDB	O, B_PHE_63	NE2, B_GLN_65	HE22, B_GLN_65	2.98	2.01	7.37
1HGH.PDB	O, A_LYS_299	NZ, B_LYS_68	HZ1, B_LYS_68	2.89	1.86	6.42
1HGH.PDB	OE2, B_GLU_85	NZ, B_LYS_68	HZ2, B_LYS_68	2.73	1.71	6.94
1HGH.PDB	OG, C_SER_107	N, B_ARG_76	H, B_ARG_76	2.88	1.92	9.13
1HGH.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.87	1.90	9.70
1HGH.PDB	OE2, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.91	1.90	8.45
1HGH.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.77	1.76	5.47
1HGH.PDB	OE1, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.89	1.87	2.83
1HGH.PDB	O, B_GLU_72	NE2, B_GLN_78	HE21, B_GLN_78	2.94	1.96	7.72
1HGH.PDB	OE1, B_GLU_74	NE2, B_GLN_78	HE22, B_GLN_78	2.91	1.95	10.12
1HGH.PDB	O, B_GLY_75	N, B_ASP_79	H, B_ASP_79	2.86	1.93	16.21
1HGH.PDB	O, B_ASP_79	N, B_TYR_83	H, B_TYR_83	2.90	2.00	19.79
1HGH.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.69	1.84	23.96
1HGH.PDB	O, B_LEU_80	N, B_VAL_84	H, B_VAL_84	2.72	1.80	14.22
1HGH.PDB	O, B_LYS_82	N, B_ASP_86	H, B_ASP_86	2.94	2.00	12.60
1HGH.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.74	1.71	7.44
1HGH.PDB	O, B_GLU_85	N, B_ILE_89	H, B_ILE_89	2.85	1.87	2.68
1HGH.PDB	O, B_LYS_88	N, B_TRP_92	H, B_TRP_92	2.92	1.94	4.60
1HGH.PDB	O, B_ILE_89	N, B_SER_93	H, B_SER_93	2.91	2.02	21.18

1HGH.PDB	O, B_ILE_89	OG, B_SER_93	HG, B_SER_93	2.79	1.87	15.47
1HGH.PDB	O, B_ASP_90	N, B_TYR_94	H, B_TYR_94	2.88	1.97	17.78
1HGH.PDB	O, B_LEU_91	N, B_ASN_95	H, B_ASN_95	3.00	2.02	1.45
1HGH.PDB	O, B_TRP_92	N, B_ALA_96	H, B_ALA_96	2.97	2.04	15.59
1HGH.PDB	O, B_TYR_94	N, B_LEU_98	H, B_LEU_98	2.93	1.96	5.82
1HGH.PDB	O, B_ASN_95	N, B_LEU_99	H, B_LEU_99	2.94	2.02	15.77
1HGH.PDB	O, B_VAL_100	N, B_ASN_104	H, B_ASN_104	2.89	1.94	12.26
1HGH.PDB	O, A_LYS_27	ND2, B_ASN_104	HD22, B_ASN_104	2.88	1.93	11.07
1HGH.PDB	O, B_LEU_102	N, B_HIS_106	H, B_HIS_106	2.96	1.99	8.01
1HGH.PDB	O, B_GLU_103	N, B_THR_107	H, B_THR_107	2.84	1.93	17.70
1HGH.PDB	O, B_HIS_106	N, B_LEU_110	H, B_LEU_110	2.80	1.84	8.73
1HGH.PDB	O, B_THR_107	OG1, B_THR_111	HG1, B_THR_111	2.85	1.90	7.42
1HGH.PDB	O, B_ASP_109	N, B_SER_113	H, B_SER_113	2.77	1.82	9.55
1HGH.PDB	O, B_ASP_112	N, B_ASN_116	H, B_ASN_116	3.00	2.02	6.31
1HGH.PDB	O, B_SER_113	N, B_LYS_117	H, B_LYS_117	2.71	1.89	26.84
1HGH.PDB	O, B_GLU_114	N, B_LEU_118	H, B_LEU_118	2.99	2.02	7.88
1HGH.PDB	O, B_ASN_116	N, B_GLU_120	H, B_GLU_120	2.94	1.96	2.10
1HGH.PDB	O, B_LYS_117	N, B_LYS_121	H, B_LYS_121	2.86	1.96	18.76
1HGH.PDB	O, B_LEU_118	N, B_THR_122	H, B_THR_122	2.99	2.01	4.84
1HGH.PDB	O, B_PHE_119	N, B_ARG_123	H, B_ARG_123	2.90	1.94	9.49
1HGH.PDB	OE2, B_GLU_120	NH1, B_ARG_123	HH11, B_ARG_123	2.74	1.85	22.74
1HGH.PDB	O, B_GLU_120	N, B_ARG_124	H, B_ARG_124	2.98	2.02	10.15
1HGH.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.76	1.94	26.47
1HGH.PDB	OE2, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.83	1.98	23.62
1HGH.PDB	O, B_LEU_126	N, B_ASN_129	H, B_ASN_129	2.97	2.04	14.58
1HGH.PDB	OH, B_TYR_157	ND2, B_ASN_129	HD22, B_ASN_129	2.83	1.87	11.09
1HGH.PDB	O, B_LYS_139	N, B_GLU_131	H, B_GLU_131	2.93	2.01	16.63
1HGH.PDB	O, B_CYS_137	N, B_MET_133	H, B_MET_133	2.84	1.90	13.58
1HGH.PDB	O, A_LEU_13	N, B_PHE_138	H, B_PHE_138	2.71	1.82	19.17
1HGH.PDB	O, B_GLU_131	N, B_LYS_139	H, B_LYS_139	2.85	1.89	6.05
1HGH.PDB	O, A_ALA_11	N, B_ILE_140	H, B_ILE_140	2.77	1.85	16.34
1HGH.PDB	O, B_ASN_129	N, B_TYR_141	H, B_TYR_141	2.84	1.90	13.40
1HGH.PDB	O, B_ILE_140	N, B_HIS_142	H, B_HIS_142	3.00	2.21	29.95
1HGH.PDB	OE2, B_GLU_165	N, B_LYS_143	H, B_LYS_143	2.98	2.03	13.49
1HGH.PDB	OE1, B_GLU_30	N, B_ASN_146	H, B_ASN_146	2.90	1.99	19.37
1HGH.PDB	O, B_ASP_145	N, B_ILE_149	H, B_ILE_149	2.89	1.93	10.45
1HGH.PDB	O, B_ASN_146	N, B_GLU_150	H, B_GLU_150	2.91	1.99	15.45
1HGH.PDB	O, B_ALA_147	N, B_SER_151	H, B_SER_151	2.92	2.08	25.20
1HGH.PDB	O, B_CYS_148	OG, B_SER_151	HG, B_SER_151	2.72	1.85	19.70
1HGH.PDB	O, B_GLU_150	N, B_ASN_154	H, B_ASN_154	2.82	1.84	0.36
1HGH.PDB	OE2, B_GLU_150	ND2, B_ASN_154	HD21, B_ASN_154	2.97	2.10	23.74
1HGH.PDB	O, B_SER_151	N, B_THR_156	H, B_THR_156	2.77	1.95	26.55
1HGH.PDB	OD1, B_ASN_154	OG1, B_THR_156	HG1, B_THR_156	2.66	1.78	19.28
1HGH.PDB	OD1, B_ASP_158	N, B_ASP_160	H, B_ASP_160	2.94	2.06	21.76
1HGH.PDB	O, B_HIS_159	N, B_TYR_162	H, B_TYR_162	2.90	2.01	20.57
1HGH.PDB	O, F_ARG_170	NH1, B_ARG_163	HH12, B_ARG_163	2.69	1.71	10.72
1HGH.PDB	O, B_TYR_162	N, B_ALA_166	H, B_ALA_166	2.89	1.91	4.63
1HGH.PDB	O, B_ARG_163	N, B_LEU_167	H, B_LEU_167	2.82	1.86	7.93
1HGH.PDB	O, B_GLU_165	ND2, B_ASN_169	HD22, B_ASN_169	2.96	1.99	6.61
1HGH.PDB	O, B_ALA_166	N, B_ARG_170	H, B_ARG_170	2.78	1.91	21.64
1HGH.PDB	O, B_GLU_128	NE, B_ARG_170	HE, B_ARG_170	2.74	1.88	23.26
1HGH.PDB	OE2, B_GLU_131	NH1, B_ARG_170	HH11, B_ARG_170	2.83	1.83	5.81
1HGH.PDB	O, B_LEU_167	N, B_PHE_171	H, B_PHE_171	2.96	2.03	15.44
1HGH.PDB	O, D_ILE_140	N, C_ALA_11	H, C_ALA_11	2.90	2.02	21.17
1HGH.PDB	O, D_GLN_27	N, C_THR_12	H, C_THR_12	2.94	1.99	10.37
1HGH.PDB	O, D_PHE_138	N, C_LEU_13	H, C_LEU_13	2.98	2.01	8.63
1HGH.PDB	O, D_ARG_25	N, C_CYS_14	H, C_CYS_14	2.74	1.80	11.01
1HGH.PDB	O, D_GLY_136	N, C_LEU_15	H, C_LEU_15	2.92	1.95	6.34

1HGH.PDB	O, D_GLY_23	N, C_GLY_16	H, C_GLY_16	2.95	2.08	23.40
1HGH.PDB	O, D_TRP_21	N, C_HIS_18	H, C_HIS_18	2.93	2.04	20.66
1HGH.PDB	OD1, C_ASN_322	N, C_VAL_20	H, C_VAL_20	2.77	1.84	13.32
1HGH.PDB	O, C_VAL_36	N, C_THR_24	H, C_THR_24	2.84	1.94	18.88
1HGH.PDB	O, C_ILE_34	N, C_VAL_26	H, C_VAL_26	2.81	1.89	15.19
1HGH.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.82	1.78	7.61
1HGH.PDB	O, C_ASP_31	N, C_THR_28	H, C_THR_28	2.72	1.89	26.38
1HGH.PDB	O, C_VAL_26	N, C_ILE_34	H, C_ILE_34	2.87	1.91	10.12
1HGH.PDB	O, C_THR_24	N, C_VAL_36	H, C_VAL_36	2.79	1.83	8.93
1HGH.PDB	O, C_MET_320	N, C_THR_37	H, C_THR_37	2.94	1.96	4.71
1HGH.PDB	O, C_LEU_316	N, C_THR_40	H, C_THR_40	2.84	2.01	25.77
1HGH.PDB	O, C_LEU_314	N, C_LEU_42	H, C_LEU_42	2.83	1.98	24.51
1HGH.PDB	O, C_PHE_294	N, C_GLN_44	H, C_GLN_44	2.92	1.94	4.18
1HGH.PDB	O, C_SER_46	NE2, C_GLN_44	HE22, C_GLN_44	2.81	1.95	23.93
1HGH.PDB	O, C_ASN_285	OG, C_SER_47	HG, C_SER_47	2.78	1.85	12.35
1HGH.PDB	OD2, C_ASP_275	NZ, C_LYS_50	HZ1, C_LYS_50	2.77	1.81	19.74
1HGH.PDB	O, C_PRO_273	N, C_ILE_51	H, C_ILE_51	2.79	1.88	17.33
1HGH.PDB	O, C_ASP_275	N, C_ASN_53	H, C_ASN_53	2.82	1.92	18.86
1HGH.PDB	O, C_GLU_280	NE2, C_HIS_56	HE2, C_HIS_56	2.96	2.00	11.12
1HGH.PDB	OD2, C_ASP_85	N, C_ARG_57	H, C_ARG_57	2.82	1.94	21.49
1HGH.PDB	O, C_THR_83	NE, C_ARG_57	HE, C_ARG_57	2.74	1.79	9.49
1HGH.PDB	O, C_LEU_86	N, C_LEU_59	H, C_LEU_59	2.97	2.04	15.48
1HGH.PDB	O, C_VAL_88	N, C_GLY_61	H, C_GLY_61	2.96	2.15	28.24
1HGH.PDB	OD1, C_ASP_60	N, C_ILE_62	H, C_ILE_62	2.88	1.94	12.53
1HGH.PDB	O, C_GLY_61	N, C_CYS_64	H, C_CYS_64	2.87	1.98	20.97
1HGH.PDB	OE2, C_GLU_89	N, C_LEU_66	H, C_LEU_66	2.91	1.94	8.58
1HGH.PDB	O, C_LEU_66	N, C_LEU_70	H, C_LEU_70	2.86	2.00	23.48
1HGH.PDB	O, C_ILE_67	N, C_LEU_71	H, C_LEU_71	2.80	1.84	8.28
1HGH.PDB	O, C_ASP_68	N, C_GLY_72	H, C_GLY_72	2.90	1.96	13.34
1HGH.PDB	OD1, C_ASP_73	ND1, C_HIS_75	HD1, C_HIS_75	2.71	1.84	22.23
1HGH.PDB	O, C_ASP_63	NE2, C_HIS_75	HE2, C_HIS_75	2.74	1.84	19.08
1HGH.PDB	O, C_ASP_73	N, C_CYS_76	H, C_CYS_76	2.76	1.88	21.08
1HGH.PDB	O, C_PRO_74	N, C_ASP_77	H, C_ASP_77	2.92	1.94	6.05
1HGH.PDB	O, C_CYS_76	N, C_PHE_79	H, C_PHE_79	2.99	2.01	3.05
1HGH.PDB	O, C_PHE_79	N, C_GLU_82	H, C_GLU_82	2.96	2.04	15.86
1HGH.PDB	OE1, C_GLU_82	N, C_THR_83	H, C_THR_83	2.89	2.00	20.79
1HGH.PDB	O, C_ARG_57	N, C_ASP_85	H, C_ASP_85	2.82	1.87	10.67
1HGH.PDB	O, C_MET_268	N, C_GLU_89	H, C_GLU_89	2.85	1.91	11.22
1HGH.PDB	OD1, C_ASP_60	NE, C_ARG_90	HE, C_ARG_90	2.80	1.87	15.44
1HGH.PDB	O, C_SER_270	NH1, C_ARG_90	HH11, C_ARG_90	2.64	1.80	26.46
1HGH.PDB	O, C_ALA_272	NH1, C_ARG_90	HH12, C_ARG_90	2.63	1.73	20.12
1HGH.PDB	OD2, C_ASP_60	NH2, C_ARG_90	HH21, C_ARG_90	2.76	1.77	8.79
1HGH.PDB	OD1, C_ASP_271	N, C_SER_91	H, C_SER_91	2.85	1.89	10.15
1HGH.PDB	OD2, C_ASP_271	OG, C_SER_91	HG, C_SER_91	2.80	1.87	12.62
1HGH.PDB	OD2, C_ASP_68	OG, C_SER_95	HG, C_SER_95	2.83	1.92	18.04
1HGH.PDB	OD2, C_ASP_73	N, C_ASN_96	H, C_ASN_96	2.88	1.92	9.38
1HGH.PDB	OD1, C_ASP_68	OH, C_TYR_100	HH, C_TYR_100	2.94	2.01	15.20
1HGH.PDB	O, C_ILE_230	N, C_ASP_101	H, C_ASP_101	2.88	2.00	21.91
1HGH.PDB	OD2, C_ASP_104	OG, C_SER_107	HG, C_SER_107	2.88	1.96	17.02
1HGH.PDB	O, C_TYR_105	N, C_ARG_109	H, C_ARG_109	2.83	1.86	3.16
1HGH.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.86	1.88	13.66
1HGH.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.78	1.85	13.87
1HGH.PDB	O, C_SER_107	N, C_LEU_111	H, C_LEU_111	2.85	1.90	10.01
1HGH.PDB	O, C_ARG_109	N, C_ALA_113	H, C_ALA_113	2.90	1.99	17.86
1HGH.PDB	O, C_SER_110	N, C_SER_114	H, C_SER_114	2.98	2.02	11.21
1HGH.PDB	OE2, C_GLU_119	OG1, C_THR_117	HG1, C_THR_117	2.87	1.92	8.14
1HGH.PDB	O, C_GLU_82	N, C_LEU_118	H, C_LEU_118	2.94	1.98	9.54
1HGH.PDB	O, C_TYR_257	N, C_ILE_121	H, C_ILE_121	2.91	1.96	13.11

1HGH.PDB	O, C_ARG_255	N, C_GLU_123	H, C_GLU_123	2.84	1.89	11.27
1HGH.PDB	O, C_THR_155	N, C_THR_131	H, C_THR_131	2.73	1.84	19.41
1HGH.PDB	OD1, C_ASN_152	N, C_ASN_133	H, C_ASN_133	2.88	2.02	23.07
1HGH.PDB	O, C_TRP_153	N, C_GLY_134	H, C_GLY_134	3.00	2.07	15.16
1HGH.PDB	O, C_GLY_146	N, C_SER_136	H, C_SER_136	2.72	1.83	18.30
1HGH.PDB	OG, C_SER_136	N, C_ALA_138	H, C_ALA_138	2.92	2.02	18.99
1HGH.PDB	O, C_GLY_144	NZ, C_LYS_140	HZ1, C_LYS_140	2.84	1.87	16.40
1HGH.PDB	OD1, C_ASN_137	NZ, C_LYS_140	HZ2, C_LYS_140	2.76	1.74	10.11
1HGH.PDB	OD2, C_ASP_77	NE, C_ARG_141	HE, C_ARG_141	2.85	2.02	26.86
1HGH.PDB	O, C_PHE_147	NH1, C_ARG_141	HH12, C_ARG_141	2.56	1.64	18.32
1HGH.PDB	OD1, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.88	1.98	22.59
1HGH.PDB	OD2, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.75	1.86	23.43
1HGH.PDB	O, C_GLY_72	NH2, C_ARG_141	HH22, C_ARG_141	2.92	1.95	11.58
1HGH.PDB	OD1, C_ASN_137	OG, C_SER_145	HG, C_SER_145	2.89	2.04	23.42
1HGH.PDB	O, C_SER_136	N, C_GLY_146	H, C_GLY_146	2.94	2.00	12.32
1HGH.PDB	O, C_GLY_72	N, C_SER_149	H, C_SER_149	2.86	1.93	14.59
1HGH.PDB	OH, C_TYR_195	NE1, C_TRP_153	HE1, C_TRP_153	2.92	2.00	17.94
1HGH.PDB	O, C_LEU_194	N, C_LYS_156	H, C_LYS_156	2.95	2.02	15.17
1HGH.PDB	O, C_THR_160	N, C_SER_157	H, C_SER_157	2.91	1.98	14.73
1HGH.PDB	O, C_SER_247	N, C_LEU_164	H, C_LEU_164	2.74	1.91	26.14
1HGH.PDB	O, C_ILE_245	N, C_VAL_166	H, C_VAL_166	2.84	1.89	12.07
1HGH.PDB	O, C_LEU_243	OG1, C_THR_167	HG1, C_THR_167	2.87	1.97	18.05
1HGH.PDB	O, C_LEU_243	N, C_MET_168	H, C_MET_168	2.84	1.91	14.36
1HGH.PDB	O, C_ASP_241	N, C_ASN_170	H, C_ASN_170	2.92	1.95	6.13
1HGH.PDB	O, C_PHE_174	ND2, C_ASN_170	HD21, C_ASN_170	2.82	1.87	11.99
1HGH.PDB	O, C_VAL_237	ND2, C_ASN_170	HD22, C_ASN_170	2.87	2.05	26.77
1HGH.PDB	O, C_VAL_237	N, C_LYS_176	H, C_LYS_176	2.98	2.08	18.97
1HGH.PDB	OE2, C_GLU_123	NZ, C_LYS_176	HZ1, C_LYS_176	2.65	1.80	28.51
1HGH.PDB	O, C_PHE_258	N, C_LEU_177	H, C_LEU_177	2.96	1.98	4.25
1HGH.PDB	O, C_THR_235	N, C_TYR_178	H, C_TYR_178	2.84	1.89	11.44
1HGH.PDB	OE1, C_GLU_123	OH, C_TYR_178	HH, C_TYR_178	2.74	1.81	11.36
1HGH.PDB	OG1, C_THR_235	NE1, C_TRP_180	HE1, C_TRP_180	2.88	1.89	0.71
1HGH.PDB	O, C_ASN_250	N, C_HIS_183	H, C_HIS_183	2.86	2.01	24.69
1HGH.PDB	O, C_ARG_229	N, C_HIS_184	H, C_HIS_184	2.88	1.93	10.57
1HGH.PDB	OG, C_SER_231	NE2, C_HIS_184	HE2, C_HIS_184	2.77	1.92	24.69
1HGH.PDB	OG1, C_THR_187	N, C_GLU_190	H, C_GLU_190	2.94	2.00	12.64
1HGH.PDB	OD1, C_ASN_250	NE2, C_GLN_191	HE21, C_GLN_191	2.95	1.99	9.46
1HGH.PDB	O, C_GLN_197	NE2, C_GLN_191	HE22, C_GLN_191	2.94	1.99	11.67
1HGH.PDB	O, C_GLN_189	OG1, C_THR_192	HG1, C_THR_192	2.82	1.90	13.51
1HGH.PDB	O, C_GLN_189	N, C_SER_193	H, C_SER_193	2.90	1.95	11.34
1HGH.PDB	O, C_GLU_190	N, C_LEU_194	H, C_LEU_194	2.97	1.99	6.33
1HGH.PDB	O, C_GLN_191	N, C_TYR_195	H, C_TYR_195	2.80	1.84	8.79
1HGH.PDB	O, C_TYR_195	N, C_GLN_197	H, C_GLN_197	2.68	1.90	29.95
1HGH.PDB	O, C_TYR_161	NE2, C_GLN_197	HE21, C_GLN_197	2.92	1.98	11.92
1HGH.PDB	O, C_ASN_248	NE2, C_GLN_197	HE22, C_GLN_197	2.88	1.96	16.62
1HGH.PDB	OD1, C_ASN_246	NH2, C_ARG_201	HH21, C_ARG_201	2.65	1.73	20.02
1HGH.PDB	O, C_ILE_213	N, C_VAL_202	H, C_VAL_202	2.96	2.02	14.06
1HGH.PDB	O, C_ASN_246	N, C_THR_203	H, C_THR_203	2.85	1.89	9.27
1HGH.PDB	OG1, C_THR_212	OG1, C_THR_203	HG1, C_THR_203	2.92	1.98	11.43
1HGH.PDB	O, C_GLN_211	N, C_VAL_204	H, C_VAL_204	2.86	1.95	18.48
1HGH.PDB	O, C_SER_209	N, C_THR_206	H, C_THR_206	2.88	1.91	6.25
1HGH.PDB	OD1, C_ASP_241	N, C_ARG_207	H, C_ARG_207	2.87	1.91	10.07
1HGH.PDB	OD2, C_ASP_241	NE, C_ARG_208	HE, C_ARG_208	2.97	2.08	22.63
1HGH.PDB	OG1, C_THR_206	OG, C_SER_209	HG, C_SER_209	2.95	2.00	8.11
1HGH.PDB	OD1, A_ASP_101	NE2, C_GLN_210	HE22, C_GLN_210	2.93	2.07	24.87
1HGH.PDB	O, C_VAL_204	N, C_GLN_211	H, C_GLN_211	2.87	1.94	15.75
1HGH.PDB	O, C_VAL_202	N, C_ILE_213	H, C_ILE_213	2.87	1.94	14.37
1HGH.PDB	ND1, C_HIS_184	N, C_ASN_216	H, C_ASN_216	2.74	1.94	28.49

1HGH.PDB	O, C_ASN_216	NH1, C_ARG_220	HH12, C_ARG_220	2.90	2.08	29.68
1HGH.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.57	1.72	26.03
1HGH.PDB	O, C_ASN_216	NH2, C_ARG_220	HH22, C_ARG_220	2.69	1.80	21.79
1HGH.PDB	O, C_LEU_226	N, C_VAL_223	H, C_VAL_223	2.85	1.88	8.82
1HGH.PDB	O, C_CYS_97	NE, C_ARG_224	HE, C_ARG_224	2.79	1.97	28.26
1HGH.PDB	O, C_CYS_97	NH2, C_ARG_224	HH21, C_ARG_224	2.81	1.96	27.50
1HGH.PDB	O, C_VAL_223	N, C_LEU_226	H, C_LEU_226	2.85	1.93	15.63
1HGH.PDB	O, C_ARG_220	OG, C_SER_227	HG, C_SER_227	2.97	2.04	13.65
1HGH.PDB	O, C_SER_228	NH1, C_ARG_229	HH11, C_ARG_229	2.65	1.70	16.09
1HGH.PDB	O, C_PRO_221	NH2, C_ARG_229	HH22, C_ARG_229	2.62	1.66	13.46
1HGH.PDB	OD1, C_ASP_101	OG, C_SER_231	HG, C_SER_231	2.86	1.92	12.68
1HGH.PDB	O, C_ASP_101	N, C_ILE_232	H, C_ILE_232	2.90	1.98	16.86
1HGH.PDB	O, C_TRP_180	N, C_TYR_233	H, C_TYR_233	2.89	1.92	6.98
1HGH.PDB	O, C_TYR_178	N, C_THR_235	H, C_THR_235	2.90	1.98	17.23
1HGH.PDB	O, C_LYS_176	N, C_VAL_237	H, C_VAL_237	2.74	1.82	16.60
1HGH.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.71	1.80	22.72
1HGH.PDB	O, B_SER_71	NZ, C_LYS_238	HZ3, C_LYS_238	2.68	1.75	20.57
1HGH.PDB	O, C_ASN_170	N, C_GLY_240	H, C_GLY_240	2.92	2.04	20.96
1HGH.PDB	O, C_LYS_238	N, C_ASP_241	H, C_ASP_241	2.93	1.99	14.39
1HGH.PDB	OD1, C_ASP_241	N, C_VAL_242	H, C_VAL_242	2.78	1.96	27.73
1HGH.PDB	O, C_MET_168	N, C_LEU_243	H, C_LEU_243	2.86	1.89	2.64
1HGH.PDB	O, C_SER_205	N, C_VAL_244	H, C_VAL_244	2.96	2.02	14.40
1HGH.PDB	O, C_VAL_166	N, C_ILE_245	H, C_ILE_245	2.87	1.93	13.03
1HGH.PDB	O, C_THR_203	N, C_ASN_246	H, C_ASN_246	2.89	1.95	12.42
1HGH.PDB	OD1, C_ASN_165	ND2, C_ASN_246	HD22, C_ASN_246	2.97	2.00	10.03
1HGH.PDB	O, C_LEU_164	N, C_SER_247	H, C_SER_247	2.91	2.00	17.54
1HGH.PDB	O, C_ARG_201	OG, C_SER_247	HG, C_SER_247	2.73	1.94	29.65
1HGH.PDB	OE1, C_GLN_191	ND2, C_ASN_250	HD21, C_ASN_250	2.86	1.89	6.98
1HGH.PDB	O, C_HIS_183	ND2, C_ASN_250	HD22, C_ASN_250	2.87	1.90	8.13
1HGH.PDB	O, C_GLY_181	N, C_ILE_252	H, C_ILE_252	2.97	2.02	11.25
1HGH.PDB	O, C_ASN_152	N, C_ALA_253	H, C_ALA_253	2.87	2.00	22.06
1HGH.PDB	O, C_ILE_121	N, C_TYR_257	H, C_TYR_257	2.97	2.09	21.43
1HGH.PDB	O, C_LEU_177	N, C_PHE_258	H, C_PHE_258	2.89	1.95	13.32
1HGH.PDB	O, C_GLU_119	N, C_LYS_259	H, C_LYS_259	2.98	2.10	21.28
1HGH.PDB	OG, C_SER_115	N, C_ARG_261	H, C_ARG_261	2.95	2.00	12.02
1HGH.PDB	OE2, C_GLU_119	NH1, C_ARG_261	HH12, C_ARG_261	2.64	1.82	29.37
1HGH.PDB	OE1, C_GLU_119	NH2, C_ARG_261	HH22, C_ARG_261	2.85	1.97	24.44
1HGH.PDB	OD2, C_ASP_85	NZ, C_LYS_264	HZ3, C_LYS_264	2.79	1.81	15.90
1HGH.PDB	O, C_PHE_87	N, C_MET_268	H, C_MET_268	2.82	1.96	23.69
1HGH.PDB	O, C_GLU_89	N, C_SER_270	H, C_SER_270	2.99	2.02	9.99
1HGH.PDB	O, C_PRO_284	OG, C_SER_270	HG, C_SER_270	2.79	1.83	6.01
1HGH.PDB	OG, C_SER_270	N, C_ALA_272	H, C_ALA_272	2.92	1.99	14.61
1HGH.PDB	O, C_ILE_51	N, C_ASP_275	H, C_ASP_275	2.92	1.99	15.40
1HGH.PDB	OD1, C_ASP_275	N, C_THR_276	H, C_THR_276	2.82	1.95	22.45
1HGH.PDB	O, C_ASN_54	N, C_SER_279	H, C_SER_279	2.78	1.84	13.60
1HGH.PDB	O, C_TYR_302	N, C_ILE_282	H, C_ILE_282	2.88	1.95	15.61
1HGH.PDB	O, C_THR_283	N, C_GLY_286	H, C_GLY_286	2.83	1.94	19.20
1HGH.PDB	O, C_LYS_50	N, C_SER_287	H, C_SER_287	2.85	1.88	2.68
1HGH.PDB	O, C_ALA_304	ND2, C_ASN_290	HD22, C_ASN_290	2.89	2.00	20.66
1HGH.PDB	OE1, C_GLN_44	NZ, C_LYS_292	HZ1, C_LYS_292	2.68	1.68	11.00
1HGH.PDB	OD2, C_ASP_291	NZ, C_LYS_292	HZ3, C_LYS_292	2.82	1.84	17.38
1HGH.PDB	O, C_LYS_307	N, C_GLN_295	H, C_GLN_295	2.85	2.00	24.78
1HGH.PDB	O, C_ASN_298	NE2, C_GLN_295	HE21, C_GLN_295	2.73	1.77	6.42
1HGH.PDB	O, C_GLN_44	N, C_ASN_296	H, C_ASN_296	2.89	1.94	9.83
1HGH.PDB	OD1, C_ASN_285	ND2, C_ASN_298	HD22, C_ASN_298	2.99	2.06	14.92
1HGH.PDB	OD1, C_ASN_298	N, C_ILE_300	H, C_ILE_300	2.90	1.96	12.51
1HGH.PDB	O, C_ILE_282	N, C_TYR_302	H, C_TYR_302	2.82	1.98	25.76
1HGH.PDB	O, C_GLN_295	N, C_VAL_309	H, C_VAL_309	2.93	2.12	28.37

1HGH.PDB	OG, D_SER_93	N, C_LYS_310	H, C_LYS_310	2.93	1.96	8.29
1HGH.PDB	OD1, D_ASP_86	NZ, C_LYS_310	HZ2, C_LYS_310	2.73	1.85	26.20
1HGH.PDB	OE2, C_GLU_41	N, C_LEU_314	H, C_LEU_314	2.81	1.86	11.11
1HGH.PDB	OE1, C_GLU_41	NZ, C_LYS_315	HZ3, C_LYS_315	2.87	1.91	19.47
1HGH.PDB	O, C_THR_40	N, C_LEU_316	H, C_LEU_316	2.77	1.83	12.11
1HGH.PDB	OD1, D_ASN_104	N, C_ALA_317	H, C_ALA_317	2.74	1.81	14.42
1HGH.PDB	O, C_ASN_38	N, C_THR_318	H, C_THR_318	2.94	1.99	12.96
1HGH.PDB	O, C_GLU_35	N, C_ASN_322	H, C_ASN_322	2.96	1.98	1.89
1HGH.PDB	O, C_VAL_20	ND2, C_ASN_322	HD21, C_ASN_322	2.84	1.92	16.39
1HGH.PDB	OE2, C_GLU_35	ND2, C_ASN_322	HD22, C_ASN_322	2.82	1.91	18.57
1HGH.PDB	OE1, D_GLU_15	NZ, C_LYS_326	HZ1, C_LYS_326	2.77	1.75	11.00
1HGH.PDB	OXT, C_THR_328	NE2, C_GLN_327	HE22, C_GLN_327	2.93	1.99	14.57
1HGH.PDB	OD2, D_ASP_112	N, D_GLY_1	H2, D_GLY_1	2.82	1.82	12.93
1HGH.PDB	OD1, D_ASP_109	N, D_LEU_2	H, D_LEU_2	2.90	1.96	14.04
1HGH.PDB	OD2, D_ASP_112	N, D_PHE_3	H, D_PHE_3	2.83	2.03	28.69
1HGH.PDB	OD2, D_ASP_112	N, D_GLY_4	H, D_GLY_4	2.96	2.09	21.45
1HGH.PDB	OD1, D_ASP_112	N, D_ALA_5	H, D_ALA_5	2.95	2.04	18.20
1HGH.PDB	O, D_GLY_4	N, D_PHE_9	H, D_PHE_9	2.82	1.88	12.35
1HGH.PDB	O, D_GLY_13	ND2, D_ASN_12	HD22, D_ASN_12	2.83	1.93	18.16
1HGH.PDB	O, C_VAL_323	N, D_GLY_13	H, D_GLY_13	2.68	1.77	15.36
1HGH.PDB	O, C_HIS_17	N, D_TRP_14	H, D_TRP_14	2.80	1.87	13.64
1HGH.PDB	OG1, D_THR_41	N, D_TRP_21	H, D_TRP_21	2.88	1.96	16.44
1HGH.PDB	O, C_GLY_16	N, D_GLY_23	H, D_GLY_23	2.92	2.01	18.18
1HGH.PDB	O, D_ALA_35	N, D_PHE_24	H, D_PHE_24	2.87	1.90	5.65
1HGH.PDB	O, C_CYS_14	N, D_ARG_25	H, D_ARG_25	2.90	1.94	10.42
1HGH.PDB	OE1, D_GLN_34	NE, D_ARG_25	HE, D_ARG_25	2.91	1.96	12.36
1HGH.PDB	O, D_GLY_33	N, D_HIS_26	H, D_HIS_26	2.85	1.94	18.22
1HGH.PDB	O, C_THR_12	N, D_GLN_27	H, D_GLN_27	2.91	1.98	14.85
1HGH.PDB	O, D_GLY_31	N, D_ASN_28	H, D_ASN_28	2.93	1.97	10.70
1HGH.PDB	OD1, D_ASN_28	N, D_GLU_30	H, D_GLU_30	2.88	2.06	26.85
1HGH.PDB	O, D_HIS_26	N, D_GLY_33	H, D_GLY_33	2.86	2.05	27.85
1HGH.PDB	O, D_PHE_24	N, D_ALA_35	H, D_ALA_35	2.81	1.99	27.43
1HGH.PDB	O, D_TYR_22	N, D_ASP_37	H, D_ASP_37	2.72	1.78	9.80
1HGH.PDB	OD2, D_ASP_37	N, D_SER_40	H, D_SER_40	2.86	1.91	10.58
1HGH.PDB	OD2, D_ASP_37	OG, D_SER_40	HG, D_SER_40	2.74	1.93	27.28
1HGH.PDB	O, D_ASP_37	OG1, D_THR_41	HG1, D_THR_41	2.73	1.83	18.40
1HGH.PDB	O, D_LEU_38	N, D_GLN_42	H, D_GLN_42	2.92	1.99	14.71
1HGH.PDB	OD1, D_ASP_46	NE2, D_GLN_42	HE22, D_GLN_42	2.87	1.96	19.71
1HGH.PDB	O, D_LYS_39	N, D_ALA_43	H, D_ALA_43	2.95	2.04	17.64
1HGH.PDB	O, D_SER_40	N, D_ALA_44	H, D_ALA_44	2.94	1.96	3.83
1HGH.PDB	O, D_THR_41	N, D_ILE_45	H, D_ILE_45	2.94	1.99	10.18
1HGH.PDB	O, D_GLN_42	N, D_ASP_46	H, D_ASP_46	2.79	1.82	1.60
1HGH.PDB	O, D_ALA_43	NE2, D_GLN_47	HE22, D_GLN_47	2.84	1.94	17.94
1HGH.PDB	O, D_ILE_45	N, D_ASN_49	H, D_ASN_49	2.88	1.92	10.54
1HGH.PDB	O, D_ASP_46	N, D_GLY_50	H, D_GLY_50	2.97	2.07	20.28
1HGH.PDB	O, D_GLN_47	N, D_LYS_51	H, D_LYS_51	2.96	2.00	10.33
1HGH.PDB	OE1, D_GLU_103	NZ, D_LYS_51	HZ1, D_LYS_51	2.74	1.72	7.43
1HGH.PDB	ND1, D_HIS_106	NZ, D_LYS_51	HZ2, D_LYS_51	2.80	1.84	18.41
1HGH.PDB	OG1, D_THR_107	NZ, D_LYS_51	HZ3, D_LYS_51	2.90	1.93	16.98
1HGH.PDB	O, D_ILE_48	N, D_LEU_52	H, D_LEU_52	2.94	2.02	16.46
1HGH.PDB	O, D_ASN_49	N, D_ASN_53	H, D_ASN_53	2.80	1.89	17.97
1HGH.PDB	O, A_THR_28	NE, D_ARG_54	HE, D_ARG_54	2.96	1.98	3.97
1HGH.PDB	OE1, D_GLU_57	NH1, D_ARG_54	HH11, D_ARG_54	2.86	1.86	11.45
1HGH.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.80	1.85	16.64
1HGH.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.84	1.88	10.18
1HGH.PDB	O, C_LYS_299	NZ, D_LYS_68	HZ1, D_LYS_68	2.88	1.85	6.67
1HGH.PDB	OE2, D_GLU_85	NZ, D_LYS_68	HZ2, D_LYS_68	2.75	1.73	9.37
1HGH.PDB	OG, E_SER_107	N, D_ARG_76	H, D_ARG_76	2.91	1.94	8.23

1HGH.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.79	1.84	10.45
1HGH.PDB	OE2, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.77	1.77	10.38
1HGH.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.70	1.70	6.41
1HGH.PDB	OE1, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.75	1.75	5.88
1HGH.PDB	O, D_GLU_72	NE2, D_GLN_78	HE21, D_GLN_78	2.93	1.96	8.18
1HGH.PDB	OE1, D_GLU_74	NE2, D_GLN_78	HE22, D_GLN_78	2.92	1.96	9.79
1HGH.PDB	O, D_GLY_75	N, D_ASP_79	H, D_ASP_79	2.84	1.88	10.94
1HGH.PDB	O, D_ASP_79	N, D_TYR_83	H, D_TYR_83	2.86	1.93	15.47
1HGH.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.59	1.81	29.86
1HGH.PDB	O, D_LEU_80	N, D_VAL_84	H, D_VAL_84	2.71	1.80	16.30
1HGH.PDB	O, D_LYS_82	N, D_ASP_86	H, D_ASP_86	2.95	1.99	9.46
1HGH.PDB	O, D_VAL_84	N, D_LYS_88	H, D_LYS_88	2.98	2.09	19.67
1HGH.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.66	1.64	7.83
1HGH.PDB	O, D_GLU_85	N, D_ILE_89	H, D_ILE_89	2.85	1.88	5.79
1HGH.PDB	O, D_LYS_88	N, D_TRP_92	H, D_TRP_92	2.90	1.92	5.72
1HGH.PDB	O, D_ILE_89	N, D_SER_93	H, D_SER_93	2.89	1.99	19.16
1HGH.PDB	O, D_ILE_89	OG, D_SER_93	HG, D_SER_93	2.76	1.84	13.71
1HGH.PDB	O, D_ASP_90	N, D_TYR_94	H, D_TYR_94	2.86	1.93	14.89
1HGH.PDB	O, D_LEU_91	N, D_ASN_95	H, D_ASN_95	3.00	2.01	2.40
1HGH.PDB	O, D_TRP_92	N, D_ALA_96	H, D_ALA_96	2.97	2.07	19.88
1HGH.PDB	O, D_TYR_94	N, D_LEU_98	H, D_LEU_98	2.95	1.98	4.96
1HGH.PDB	O, D_ASN_95	N, D_LEU_99	H, D_LEU_99	2.96	2.05	17.05
1HGH.PDB	O, D_VAL_100	N, D_ASN_104	H, D_ASN_104	2.87	1.94	14.58
1HGH.PDB	O, C_LYS_27	ND2, D_ASN_104	HD22, D_ASN_104	2.89	1.94	11.70
1HGH.PDB	O, D_LEU_102	N, D_HIS_106	H, D_HIS_106	2.95	1.98	8.89
1HGH.PDB	O, D_GLU_103	N, D_THR_107	H, D_THR_107	2.84	1.94	18.36
1HGH.PDB	O, D_HIS_106	N, D_LEU_110	H, D_LEU_110	2.82	1.86	9.68
1HGH.PDB	O, D_THR_107	OG1, D_THR_111	HG1, D_THR_111	2.89	1.92	2.49
1HGH.PDB	O, D_ASP_109	N, D_SER_113	H, D_SER_113	2.77	1.82	8.06
1HGH.PDB	O, D_ASP_112	N, D_ASN_116	H, D_ASN_116	2.96	1.98	6.25
1HGH.PDB	O, D_SER_113	N, D_LYS_117	H, D_LYS_117	2.75	1.92	25.56
1HGH.PDB	O, D_GLU_114	N, D_LEU_118	H, D_LEU_118	3.00	2.03	9.32
1HGH.PDB	O, D_ASN_116	N, D_GLU_120	H, D_GLU_120	2.93	1.95	1.97
1HGH.PDB	O, D_LYS_117	N, D_LYS_121	H, D_LYS_121	2.85	1.95	19.21
1HGH.PDB	O, D_LEU_118	N, D_THR_122	H, D_THR_122	2.98	2.00	5.78
1HGH.PDB	O, D_PHE_119	N, D_ARG_123	H, D_ARG_123	2.89	1.93	8.77
1HGH.PDB	OE2, D_GLU_120	NH1, D_ARG_123	HH11, D_ARG_123	2.77	1.87	22.36
1HGH.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.80	1.98	26.35
1HGH.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.84	1.99	23.38
1HGH.PDB	O, D_LEU_126	N, D_ASN_129	H, D_ASN_129	2.98	2.04	13.91
1HGH.PDB	O, D_HIS_159	ND2, D_ASN_129	HD21, D_ASN_129	2.99	2.06	14.65
1HGH.PDB	OH, D_TYR_157	ND2, D_ASN_129	HD22, D_ASN_129	2.83	1.87	7.67
1HGH.PDB	O, D_LYS_139	N, D_GLU_131	H, D_GLU_131	2.96	2.04	16.55
1HGH.PDB	O, D_CYS_137	N, D_MET_133	H, D_MET_133	2.85	1.91	13.04
1HGH.PDB	OD1, D_ASN_135	N, D_CYS_137	H, D_CYS_137	2.95	2.05	19.26
1HGH.PDB	O, C_LEU_13	N, D_PHE_138	H, D_PHE_138	2.75	1.85	18.05
1HGH.PDB	O, D_GLU_131	N, D_LYS_139	H, D_LYS_139	2.80	1.84	6.99
1HGH.PDB	O, C_ALA_11	N, D_ILE_140	H, D_ILE_140	2.83	1.90	15.57
1HGH.PDB	O, D_ASN_129	N, D_TYR_141	H, D_TYR_141	2.84	1.91	14.49
1HGH.PDB	OE2, D_GLU_30	N, D_ASN_146	H, D_ASN_146	2.90	1.97	15.32
1HGH.PDB	O, D_ASP_145	N, D_ILE_149	H, D_ILE_149	2.92	1.97	10.33
1HGH.PDB	O, D_ASN_146	N, D_GLU_150	H, D_GLU_150	2.92	1.99	14.54
1HGH.PDB	O, D_ALA_147	N, D_SER_151	H, D_SER_151	2.94	2.07	23.02
1HGH.PDB	O, D_CYS_148	OG, D_SER_151	HG, D_SER_151	2.73	1.84	17.19
1HGH.PDB	O, D_GLU_150	N, D_ASN_154	H, D_ASN_154	2.82	1.84	3.73
1HGH.PDB	O, D_SER_151	N, D_THR_156	H, D_THR_156	2.80	1.97	26.19
1HGH.PDB	OD1, D_ASN_154	OG1, D_THR_156	HG1, D_THR_156	2.69	1.80	16.96
1HGH.PDB	NE2, D_HIS_142	OH, D_TYR_157	HH, D_TYR_157	2.68	1.87	26.02

1HGH.PDB	OD1, D_ASP_158	N, D_ASP_160	H, D_ASP_160	2.94	2.07	22.26
1HGH.PDB	O, D_HIS_159	N, D_TYR_162	H, D_TYR_162	2.94	2.06	20.90
1HGH.PDB	O, B_ARG_170	NH1, D_ARG_163	HH12, D_ARG_163	2.75	1.77	10.76
1HGH.PDB	O, D_TYR_162	N, D_ALA_166	H, D_ALA_166	2.89	1.92	5.05
1HGH.PDB	O, D_ARG_163	N, D_LEU_167	H, D_LEU_167	2.82	1.86	8.99
1HGH.PDB	O, D_ASP_164	N, D_ASN_168	H, D_ASN_168	2.99	2.02	7.50
1HGH.PDB	O, D_GLU_165	ND2, D_ASN_169	HD22, D_ASN_169	2.97	2.00	7.05
1HGH.PDB	O, D_ALA_166	N, D_ARG_170	H, D_ARG_170	2.80	1.93	21.90
1HGH.PDB	O, D_GLU_128	NE, D_ARG_170	HE, D_ARG_170	2.74	1.87	23.06
1HGH.PDB	OE2, D_GLU_131	NH1, D_ARG_170	HH11, D_ARG_170	2.83	1.83	5.85
1HGH.PDB	O, D_LEU_167	N, D_PHE_171	H, D_PHE_171	2.95	2.02	15.80
1HGH.PDB	O, F_ILE_140	N, E_ALA_11	H, E_ALA_11	2.92	2.02	19.53
1HGH.PDB	O, F_PHE_138	N, E_LEU_13	H, E_LEU_13	2.96	1.99	9.34
1HGH.PDB	O, F_ARG_25	N, E_CYS_14	H, E_CYS_14	2.64	1.78	21.59
1HGH.PDB	O, F_GLY_136	N, E_LEU_15	H, E_LEU_15	2.90	1.93	5.74
1HGH.PDB	O, F_GLY_23	N, E_GLY_16	H, E_GLY_16	2.92	2.05	22.72
1HGH.PDB	O, E_HIS_18	ND1, E_HIS_17	HD1, E_HIS_17	2.99	2.08	18.51
1HGH.PDB	O, F_TRP_21	N, E_HIS_18	H, E_HIS_18	2.92	2.03	19.54
1HGH.PDB	OD1, E_ASN_322	N, E_VAL_20	H, E_VAL_20	2.74	1.82	16.04
1HGH.PDB	O, E_VAL_36	N, E_THR_24	H, E_THR_24	2.82	1.93	20.03
1HGH.PDB	O, E_ILE_34	N, E_VAL_26	H, E_VAL_26	2.82	1.88	13.02
1HGH.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.77	1.74	8.08
1HGH.PDB	O, E_ASP_31	N, E_THR_28	H, E_THR_28	2.77	1.94	26.92
1HGH.PDB	O, E_VAL_26	N, E_ILE_34	H, E_ILE_34	2.87	1.92	12.72
1HGH.PDB	O, E_THR_24	N, E_VAL_36	H, E_VAL_36	2.79	1.83	5.74
1HGH.PDB	O, E_MET_320	N, E_THR_37	H, E_THR_37	2.91	1.94	5.98
1HGH.PDB	O, E_LEU_316	N, E_THR_40	H, E_THR_40	2.81	1.97	25.58
1HGH.PDB	O, E_LEU_314	N, E_LEU_42	H, E_LEU_42	2.86	1.99	23.51
1HGH.PDB	O, E_PHE_294	N, E_GLN_44	H, E_GLN_44	2.90	1.92	3.60
1HGH.PDB	O, E_SER_46	NE2, E_GLN_44	HE22, E_GLN_44	2.79	1.94	24.07
1HGH.PDB	O, E_ASN_285	OG, E_SER_47	HG, E_SER_47	2.82	1.86	5.68
1HGH.PDB	OD2, E_ASP_275	NZ, E_LYS_50	HZ1, E_LYS_50	2.78	1.83	20.38
1HGH.PDB	O, E_PRO_273	N, E_ILE_51	H, E_ILE_51	2.79	1.86	14.05
1HGH.PDB	O, E_ASP_275	N, E_ASN_53	H, E_ASN_53	2.84	1.95	20.03
1HGH.PDB	O, E_GLU_280	NE2, E_HIS_56	HE2, E_HIS_56	3.00	2.04	11.75
1HGH.PDB	OD2, E_ASP_85	N, E_ARG_57	H, E_ARG_57	2.80	1.92	20.20
1HGH.PDB	O, E_THR_83	NE, E_ARG_57	HE, E_ARG_57	2.76	1.81	9.61
1HGH.PDB	O, E_LEU_86	N, E_LEU_59	H, E_LEU_59	2.94	2.02	16.24
1HGH.PDB	O, E_VAL_88	N, E_GLY_61	H, E_GLY_61	2.97	2.17	29.53
1HGH.PDB	OD1, E_ASP_60	N, E_ILE_62	H, E_ILE_62	2.88	1.95	12.63
1HGH.PDB	O, E_GLY_61	N, E_CYS_64	H, E_CYS_64	2.91	2.01	19.21
1HGH.PDB	OE2, E_GLU_89	N, E_LEU_66	H, E_LEU_66	2.90	1.94	8.52
1HGH.PDB	O, E_LEU_66	N, E_LEU_70	H, E_LEU_70	2.83	1.96	22.59
1HGH.PDB	O, E_ILE_67	N, E_LEU_71	H, E_LEU_71	2.80	1.85	10.15
1HGH.PDB	O, E_ASP_68	N, E_GLY_72	H, E_GLY_72	2.92	1.98	13.98
1HGH.PDB	OD1, E_ASP_73	ND1, E_HIS_75	HD1, E_HIS_75	2.70	1.83	21.52
1HGH.PDB	O, E_ASP_63	NE2, E_HIS_75	HE2, E_HIS_75	2.76	1.85	18.40
1HGH.PDB	O, E_ASP_73	N, E_CYS_76	H, E_CYS_76	2.77	1.88	19.19
1HGH.PDB	O, E_PRO_74	N, E_ASP_77	H, E_ASP_77	2.89	1.93	8.73
1HGH.PDB	O, E_CYS_76	N, E_PHE_79	H, E_PHE_79	2.99	2.02	3.39
1HGH.PDB	O, E_PHE_79	N, E_GLU_82	H, E_GLU_82	2.96	2.03	14.49
1HGH.PDB	OE1, E_GLU_82	N, E_THR_83	H, E_THR_83	2.87	2.01	22.92
1HGH.PDB	O, E_ARG_57	N, E_ASP_85	H, E_ASP_85	2.80	1.87	13.06
1HGH.PDB	O, E_MET_268	N, E_GLU_89	H, E_GLU_89	2.80	1.86	11.55
1HGH.PDB	OD1, E_ASP_60	NE, E_ARG_90	HE, E_ARG_90	2.82	1.87	13.57
1HGH.PDB	O, E_SER_270	NH1, E_ARG_90	HH11, E_ARG_90	2.65	1.80	26.29
1HGH.PDB	O, E_ALA_272	NH1, E_ARG_90	HH12, E_ARG_90	2.63	1.72	19.05
1HGH.PDB	OD2, E_ASP_60	NH2, E_ARG_90	HH21, E_ARG_90	2.82	1.82	8.69

1HGH.PDB	OD1, E_ASP_271	N, E_SER_91	H, E_SER_91	2.82	1.87	11.20
1HGH.PDB	OD2, E_ASP_271	OG, E_SER_91	HG, E_SER_91	2.81	1.88	14.87
1HGH.PDB	OD2, E_ASP_68	OG, E_SER_95	HG, E_SER_95	2.88	1.94	13.28
1HGH.PDB	OD2, E_ASP_73	N, E_ASN_96	H, E_ASN_96	2.91	1.94	6.86
1HGH.PDB	OD1, E_ASP_68	OH, E_TYR_100	HH, E_TYR_100	2.91	1.97	12.96
1HGH.PDB	O, E_ILE_230	N, E_ASP_101	H, E_ASP_101	2.92	2.05	22.42
1HGH.PDB	OD2, E_ASP_104	OG, E_SER_107	HG, E_SER_107	2.88	1.97	18.12
1HGH.PDB	O, E_TYR_105	N, E_ARG_109	H, E_ARG_109	2.86	1.89	4.60
1HGH.PDB	OE2, F_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.88	1.90	13.56
1HGH.PDB	OD2, D_ASP_79	OG, E_SER_110	HG, E_SER_110	2.90	1.94	9.49
1HGH.PDB	O, E_SER_107	N, E_LEU_111	H, E_LEU_111	2.88	1.93	12.85
1HGH.PDB	O, E_ARG_109	N, E_ALA_113	H, E_ALA_113	2.87	1.96	17.46
1HGH.PDB	O, E_SER_110	N, E_SER_114	H, E_SER_114	2.96	2.00	10.70
1HGH.PDB	OE2, E_GLU_119	OG1, E_THR_117	HG1, E_THR_117	2.88	1.94	11.16
1HGH.PDB	O, E_GLU_82	N, E_LEU_118	H, E_LEU_118	2.97	2.01	10.67
1HGH.PDB	O, E_TYR_257	N, E_ILE_121	H, E_ILE_121	2.91	1.96	12.67
1HGH.PDB	O, E_ARG_255	N, E_GLU_123	H, E_GLU_123	2.88	1.92	10.98
1HGH.PDB	O, E_THR_155	N, E_THR_131	H, E_THR_131	2.72	1.85	21.27
1HGH.PDB	OD1, E_ASN_152	N, E_ASN_133	H, E_ASN_133	2.90	2.03	22.25
1HGH.PDB	O, E_TRP_153	N, E_GLY_134	H, E_GLY_134	2.97	2.04	15.57
1HGH.PDB	O, E_GLY_146	N, E_SER_136	H, E_SER_136	2.72	1.83	19.86
1HGH.PDB	OG, E_SER_136	N, E_ALA_138	H, E_ALA_138	2.95	2.04	18.21
1HGH.PDB	O, E_GLY_144	NZ, E_LYS_140	HZ1, E_LYS_140	2.90	1.92	16.43
1HGH.PDB	OD1, E_ASN_137	NZ, E_LYS_140	HZ2, E_LYS_140	2.75	1.75	11.91
1HGH.PDB	OD2, E_ASP_77	NE, E_ARG_141	HE, E_ARG_141	2.85	2.01	27.16
1HGH.PDB	O, E_PHE_147	NH1, E_ARG_141	HH12, E_ARG_141	2.56	1.64	18.71
1HGH.PDB	OD1, E_ASP_77	NH2, E_ARG_141	HH21, E_ARG_141	2.89	1.99	22.46
1HGH.PDB	OD2, E_ASP_77	NH2, E_ARG_141	HH21, E_ARG_141	2.74	1.84	23.25
1HGH.PDB	O, E_GLY_72	NH2, E_ARG_141	HH22, E_ARG_141	2.94	1.96	11.25
1HGH.PDB	OD1, E_ASN_137	OG, E_SER_145	HG, E_SER_145	2.98	2.07	15.03
1HGH.PDB	O, E_SER_136	N, E_GLY_146	H, E_GLY_146	2.94	1.99	13.35
1HGH.PDB	O, E_GLY_72	N, E_SER_149	H, E_SER_149	2.91	1.97	14.68
1HGH.PDB	O, E_ALA_253	N, E_ASN_152	H, E_ASN_152	2.75	1.96	29.93
1HGH.PDB	OH, E_TYR_195	NE1, E_TRP_153	HE1, E_TRP_153	2.94	2.03	18.49
1HGH.PDB	O, E_LEU_194	N, E_LYS_156	H, E_LYS_156	2.95	2.04	17.92
1HGH.PDB	O, E_SER_193	NZ, E_LYS_156	HZ2, E_LYS_156	2.74	1.77	17.07
1HGH.PDB	O, E_THR_160	N, E_SER_157	H, E_SER_157	2.95	2.02	16.56
1HGH.PDB	O, E_SER_247	N, E_LEU_164	H, E_LEU_164	2.73	1.90	26.43
1HGH.PDB	O, E_ILE_245	N, E_VAL_166	H, E_VAL_166	2.87	1.94	14.01
1HGH.PDB	O, E_LEU_243	OG1, E_THR_167	HG1, E_THR_167	2.95	2.02	14.19
1HGH.PDB	O, E_LEU_243	N, E_MET_168	H, E_MET_168	2.85	1.92	14.04
1HGH.PDB	O, E_ASP_241	N, E_ASN_170	H, E_ASN_170	2.95	1.97	5.59
1HGH.PDB	O, E_PHE_174	ND2, E_ASN_170	HD21, E_ASN_170	2.82	1.88	12.75
1HGH.PDB	O, E_VAL_237	ND2, E_ASN_170	HD22, E_ASN_170	2.89	2.06	25.88
1HGH.PDB	O, E_VAL_237	N, E_LYS_176	H, E_LYS_176	2.98	2.06	17.00
1HGH.PDB	OE2, E_GLU_123	NZ, E_LYS_176	HZ1, E_LYS_176	2.69	1.82	26.87
1HGH.PDB	O, E_PHE_258	N, E_LEU_177	H, E_LEU_177	2.97	2.00	4.18
1HGH.PDB	O, E_THR_235	N, E_TYR_178	H, E_TYR_178	2.86	1.90	10.67
1HGH.PDB	OE1, E_GLU_123	OH, E_TYR_178	HH, E_TYR_178	2.77	1.82	8.79
1HGH.PDB	OG1, E_THR_235	NE1, E_TRP_180	HE1, E_TRP_180	2.88	1.89	0.99
1HGH.PDB	O, E_ASN_250	N, E_HIS_183	H, E_HIS_183	2.86	1.99	21.99
1HGH.PDB	O, E_ARG_229	N, E_HIS_184	H, E_HIS_184	2.88	1.94	12.21
1HGH.PDB	OG, E_SER_231	NE2, E_HIS_184	HE2, E_HIS_184	2.78	1.93	25.10
1HGH.PDB	OG1, E_THR_187	N, E_GLU_190	H, E_GLU_190	2.95	2.00	11.05
1HGH.PDB	OD1, E_ASN_250	NE2, E_GLN_191	HE21, E_GLN_191	2.99	2.02	8.22
1HGH.PDB	O, E_GLN_197	NE2, E_GLN_191	HE22, E_GLN_191	2.93	1.98	11.58
1HGH.PDB	O, E_GLN_189	N, E_SER_193	H, E_SER_193	2.93	1.94	3.87
1HGH.PDB	O, E_GLU_190	N, E_LEU_194	H, E_LEU_194	2.96	1.97	5.03

1HGH.PDB	O, E_GLN_191	N, E_TYR_195	H, E_TYR_195	2.79	1.83	8.93
1HGH.PDB	O, E_TYR_195	N, E_GLN_197	H, E_GLN_197	2.65	1.86	29.33
1HGH.PDB	O, E_TYR_161	NE2, E_GLN_197	HE21, E_GLN_197	2.94	1.99	11.18
1HGH.PDB	O, E_ASN_248	NE2, E_GLN_197	HE22, E_GLN_197	2.86	1.94	17.19
1HGH.PDB	OD1, E_ASN_246	NH2, E_ARG_201	HH21, E_ARG_201	2.64	1.73	21.41
1HGH.PDB	O, E_ILE_213	N, E_VAL_202	H, E_VAL_202	2.96	2.00	10.60
1HGH.PDB	O, E_ASN_246	N, E_THR_203	H, E_THR_203	2.87	1.91	9.98
1HGH.PDB	OG1, E_THR_212	OG1, E_THR_203	HG1, E_THR_203	2.98	2.08	17.30
1HGH.PDB	O, E_GLN_211	N, E_VAL_204	H, E_VAL_204	2.87	1.97	20.15
1HGH.PDB	O, E_SER_209	N, E_THR_206	H, E_THR_206	2.92	1.96	6.97
1HGH.PDB	OD1, E_ASP_241	N, E_ARG_207	H, E_ARG_207	2.86	1.90	9.49
1HGH.PDB	OG1, E_THR_206	OG, E_SER_209	HG, E_SER_209	2.95	2.00	8.64
1HGH.PDB	OD1, C_ASP_101	NE2, E_GLN_210	HE22, E_GLN_210	2.95	2.09	25.33
1HGH.PDB	O, E_VAL_204	N, E_GLN_211	H, E_GLN_211	2.89	1.95	12.74
1HGH.PDB	O, E_VAL_202	N, E_ILE_213	H, E_ILE_213	2.90	1.97	14.56
1HGH.PDB	ND1, E_HIS_184	N, E_ASN_216	H, E_ASN_216	2.77	1.96	27.61
1HGH.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.68	1.79	22.30
1HGH.PDB	O, E_ASN_216	NH2, E_ARG_220	HH22, E_ARG_220	2.67	1.78	21.90
1HGH.PDB	O, E_LEU_226	N, E_VAL_223	H, E_VAL_223	2.86	1.90	9.88
1HGH.PDB	O, E_CYS_97	NE, E_ARG_224	HE, E_ARG_224	2.82	1.98	26.83
1HGH.PDB	O, E_CYS_97	NH2, E_ARG_224	HH21, E_ARG_224	2.83	1.97	26.23
1HGH.PDB	O, E_VAL_223	N, E_LEU_226	H, E_LEU_226	2.83	1.91	14.82
1HGH.PDB	O, E_ARG_220	OG, E_SER_227	HG, E_SER_227	2.98	2.06	16.39
1HGH.PDB	O, E_SER_228	NH1, E_ARG_229	HH11, E_ARG_229	2.68	1.73	16.77
1HGH.PDB	O, E_PRO_221	NH2, E_ARG_229	HH22, E_ARG_229	2.59	1.64	14.71
1HGH.PDB	OD1, E_ASP_101	OG, E_SER_231	HG, E_SER_231	2.86	1.91	11.78
1HGH.PDB	O, E_ASP_101	N, E_ILE_232	H, E_ILE_232	2.89	1.97	15.99
1HGH.PDB	O, E_TRP_180	N, E_TYR_233	H, E_TYR_233	2.91	1.95	8.91
1HGH.PDB	O, E_TYR_178	N, E_THR_235	H, E_THR_235	2.90	1.99	17.41
1HGH.PDB	O, E_LYS_176	N, E_VAL_237	H, E_VAL_237	2.74	1.82	15.90
1HGH.PDB	O, D_SER_71	NZ, E_LYS_238	HZ2, E_LYS_238	2.84	1.88	19.22
1HGH.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ3, E_LYS_238	2.87	1.88	15.42
1HGH.PDB	O, E_ASN_170	N, E_GLY_240	H, E_GLY_240	2.93	2.05	21.68
1HGH.PDB	O, E_LYS_238	N, E_ASP_241	H, E_ASP_241	2.93	2.01	15.54
1HGH.PDB	OD1, E_ASP_241	N, E_VAL_242	H, E_VAL_242	2.78	1.96	27.21
1HGH.PDB	O, E_MET_168	N, E_LEU_243	H, E_LEU_243	2.84	1.87	3.13
1HGH.PDB	O, E_SER_205	N, E_VAL_244	H, E_VAL_244	2.97	2.03	14.34
1HGH.PDB	O, E_VAL_166	N, E_ILE_245	H, E_ILE_245	2.86	1.92	13.73
1HGH.PDB	O, E_THR_203	N, E_ASN_246	H, E_ASN_246	2.93	2.00	14.46
1HGH.PDB	OD1, E_ASN_165	ND2, E_ASN_246	HD22, E_ASN_246	2.98	2.01	10.13
1HGH.PDB	O, E_LEU_164	N, E_SER_247	H, E_SER_247	2.90	1.99	17.74
1HGH.PDB	OE1, E_GLN_191	ND2, E_ASN_250	HD21, E_ASN_250	2.89	1.92	6.88
1HGH.PDB	O, E_HIS_183	ND2, E_ASN_250	HD22, E_ASN_250	2.85	1.88	7.17
1HGH.PDB	O, E_GLY_181	N, E_ILE_252	H, E_ILE_252	2.96	2.00	10.43
1HGH.PDB	O, E_ASN_152	N, E_ALA_253	H, E_ALA_253	2.86	1.96	18.53
1HGH.PDB	O, E_ILE_121	N, E_TYR_257	H, E_TYR_257	2.97	2.09	21.21
1HGH.PDB	O, E_LEU_177	N, E_PHE_258	H, E_PHE_258	2.87	1.92	12.22
1HGH.PDB	OG, E_SER_115	N, E_ARG_261	H, E_ARG_261	2.96	2.00	11.47
1HGH.PDB	OE2, E_GLU_119	NH1, E_ARG_261	HH12, E_ARG_261	2.63	1.81	29.30
1HGH.PDB	OE1, E_GLU_119	NH2, E_ARG_261	HH22, E_ARG_261	2.85	1.96	24.42
1HGH.PDB	OD2, E_ASP_85	NZ, E_LYS_264	HZ3, E_LYS_264	2.81	1.82	14.94
1HGH.PDB	O, E_PHE_87	N, E_MET_268	H, E_MET_268	2.82	1.95	22.70
1HGH.PDB	OE1, F_GLU_67	NH1, E_ARG_269	HH12, E_ARG_269	2.71	1.88	29.19
1HGH.PDB	O, E_GLU_89	N, E_SER_270	H, E_SER_270	2.97	2.01	10.37
1HGH.PDB	O, E_PRO_284	OG, E_SER_270	HG, E_SER_270	2.79	1.83	6.34
1HGH.PDB	OG, E_SER_270	N, E_ALA_272	H, E_ALA_272	2.93	2.00	13.96
1HGH.PDB	O, E_ILE_51	N, E_ASP_275	H, E_ASP_275	2.89	1.98	17.07
1HGH.PDB	OD1, E_ASP_275	N, E_THR_276	H, E_THR_276	2.81	1.94	22.67

1HGH.PDB	O, E_ASN_54	N, E_SER_279	H, E_SER_279	2.79	1.85	12.96
1HGH.PDB	O, E_TYR_302	N, E_ILE_282	H, E_ILE_282	2.90	1.96	14.02
1HGH.PDB	O, E_THR_283	N, E_GLY_286	H, E_GLY_286	2.82	1.92	18.13
1HGH.PDB	O, E_LYS_50	N, E_SER_287	H, E_SER_287	2.89	1.92	2.42
1HGH.PDB	O, E_ALA_304	ND2, E_ASN_290	HD22, E_ASN_290	2.86	1.98	20.69
1HGH.PDB	OE1, E_GLN_44	NZ, E_LYS_292	HZ1, E_LYS_292	2.67	1.66	10.24
1HGH.PDB	OD2, E_ASP_291	NZ, E_LYS_292	HZ3, E_LYS_292	2.84	1.86	17.36
1HGH.PDB	O, E_LYS_307	N, E_GLN_295	H, E_GLN_295	2.84	1.97	22.67
1HGH.PDB	O, E_ASN_298	NE2, E_GLN_295	HE21, E_GLN_295	2.75	1.79	8.52
1HGH.PDB	O, E_GLN_44	N, E_ASN_296	H, E_ASN_296	2.90	1.94	9.06
1HGH.PDB	OD1, E_ASN_298	N, E_ILE_300	H, E_ILE_300	2.92	1.98	13.95
1HGH.PDB	O, E_ILE_282	N, E_TYR_302	H, E_TYR_302	2.84	2.00	26.34
1HGH.PDB	O, F_LYS_62	N, E_GLY_303	H, E_GLY_303	2.98	2.01	7.92
1HGH.PDB	O, E_PRO_293	N, E_LYS_307	H, E_LYS_307	3.00	2.03	9.04
1HGH.PDB	O, E_GLN_295	N, E_VAL_309	H, E_VAL_309	2.91	2.07	25.95
1HGH.PDB	OG, F_SER_93	N, E_LYS_310	H, E_LYS_310	2.93	1.97	10.42
1HGH.PDB	OD1, F_ASP_86	NZ, E_LYS_310	HZ2, E_LYS_310	2.74	1.87	26.77
1HGH.PDB	O, F_SER_93	NE2, E_GLN_311	HE21, E_GLN_311	2.99	2.02	4.65
1HGH.PDB	OE2, E_GLU_41	N, E_LEU_314	H, E_LEU_314	2.81	1.87	11.19
1HGH.PDB	OE1, E_GLU_41	NZ, E_LYS_315	HZ3, E_LYS_315	2.85	1.89	19.70
1HGH.PDB	O, E_THR_40	N, E_LEU_316	H, E_LEU_316	2.77	1.82	9.99
1HGH.PDB	OD1, F_ASN_104	N, E_ALA_317	H, E_ALA_317	2.75	1.81	11.69
1HGH.PDB	O, E_ASN_38	N, E_THR_318	H, E_THR_318	2.95	2.00	12.19
1HGH.PDB	O, E_GLU_35	N, E_ASN_322	H, E_ASN_322	2.96	1.98	2.25
1HGH.PDB	O, E_VAL_20	ND2, E_ASN_322	HD21, E_ASN_322	2.82	1.91	16.60
1HGH.PDB	OE2, E_GLU_35	ND2, E_ASN_322	HD22, E_ASN_322	2.80	1.90	19.14
1HGH.PDB	OE2, F_GLU_15	N, E_GLU_325	H, E_GLU_325	2.97	2.16	28.37
1HGH.PDB	O, E_GLN_327	NZ, E_LYS_326	HZ1, E_LYS_326	2.85	1.92	22.31
1HGH.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.90	1.89	12.96
1HGH.PDB	O, E_LYS_326	NE2, E_GLN_327	HE22, E_GLN_327	2.81	1.89	16.48
1HGH.PDB	OD2, F_ASP_112	N, F_GLY_1	H2, F_GLY_1	2.82	1.82	13.22
1HGH.PDB	OD1, F_ASP_109	N, F_LEU_2	H, F_LEU_2	2.91	1.98	15.54
1HGH.PDB	OD2, F_ASP_112	N, F_PHE_3	H, F_PHE_3	2.80	2.01	28.96
1HGH.PDB	OD2, F_ASP_112	N, F_GLY_4	H, F_GLY_4	2.95	2.06	19.48
1HGH.PDB	OD1, F_ASP_112	N, F_ALA_5	H, F_ALA_5	2.92	2.00	17.34
1HGH.PDB	O, F_GLY_4	N, F_PHE_9	H, F_PHE_9	2.86	1.91	12.98
1HGH.PDB	O, F_GLY_13	ND2, F_ASN_12	HD22, F_ASN_12	2.80	1.92	21.14
1HGH.PDB	O, E_VAL_323	N, F_GLY_13	H, F_GLY_13	2.70	1.77	11.97
1HGH.PDB	O, E_HIS_17	N, F_TRP_14	H, F_TRP_14	2.81	1.87	12.50
1HGH.PDB	OG1, F_THR_41	N, F_TRP_21	H, F_TRP_21	2.88	1.96	16.20
1HGH.PDB	O, E_GLY_16	N, F_GLY_23	H, F_GLY_23	2.91	2.00	17.53
1HGH.PDB	O, F_ALA_35	N, F_PHE_24	H, F_PHE_24	2.86	1.89	4.90
1HGH.PDB	O, E_CYS_14	N, F_ARG_25	H, F_ARG_25	2.90	1.98	16.77
1HGH.PDB	OE1, F_GLN_34	NH2, F_ARG_25	HH21, F_ARG_25	2.92	2.03	23.48
1HGH.PDB	O, F_GLY_33	N, F_HIS_26	H, F_HIS_26	2.90	2.03	21.65
1HGH.PDB	O, E_THR_12	N, F_GLN_27	H, F_GLN_27	2.91	2.03	20.46
1HGH.PDB	O, F_GLY_31	N, F_ASN_28	H, F_ASN_28	2.72	1.81	16.52
1HGH.PDB	OD1, F_ASN_146	ND2, F_ASN_28	HD21, F_ASN_28	2.91	1.96	12.69
1HGH.PDB	O, F_CYS_144	ND2, F_ASN_28	HD22, F_ASN_28	2.96	2.10	23.78
1HGH.PDB	O, F_PHE_24	N, F_ALA_35	H, F_ALA_35	2.81	2.00	28.47
1HGH.PDB	O, F_TYR_22	N, F_ASP_37	H, F_ASP_37	2.69	1.76	12.03
1HGH.PDB	OD2, F_ASP_37	N, F_SER_40	H, F_SER_40	2.86	1.90	9.36
1HGH.PDB	OD2, F_ASP_37	OG, F_SER_40	HG, F_SER_40	2.73	1.92	26.94
1HGH.PDB	O, F_ASP_37	OG1, F_THR_41	HG1, F_THR_41	2.73	1.82	16.92
1HGH.PDB	O, F_LEU_38	N, F_GLN_42	H, F_GLN_42	2.93	1.99	14.39
1HGH.PDB	OD1, F_ASP_46	NE2, F_GLN_42	HE22, F_GLN_42	2.85	1.95	20.25
1HGH.PDB	O, F_LYS_39	N, F_ALA_43	H, F_ALA_43	2.92	1.99	14.06
1HGH.PDB	O, F_SER_40	N, F_ALA_44	H, F_ALA_44	2.94	1.96	3.72

1HGH.PDB	O, F_THR_41	N, F_ILE_45	H, F_ILE_45	2.94	2.00	13.08
1HGH.PDB	O, F_GLN_42	N, F_ASP_46	H, F_ASP_46	2.77	1.80	1.50
1HGH.PDB	OE2, F_GLU_114	NE2, F_GLN_47	HE21, F_GLN_47	2.99	2.08	19.28
1HGH.PDB	O, F_ALA_43	NE2, F_GLN_47	HE22, F_GLN_47	2.86	1.96	18.47
1HGH.PDB	O, F_ILE_45	N, F_ASN_49	H, F_ASN_49	2.86	1.91	11.74
1HGH.PDB	O, F_ASP_46	N, F_GLY_50	H, F_GLY_50	2.93	2.01	18.13
1HGH.PDB	O, F_GLN_47	N, F_LYS_51	H, F_LYS_51	2.95	2.01	12.39
1HGH.PDB	OE1, F_GLU_103	NZ, F_LYS_51	HZ1, F_LYS_51	2.75	1.72	7.02
1HGH.PDB	ND1, F_HIS_106	NZ, F_LYS_51	HZ2, F_LYS_51	2.77	1.82	19.11
1HGH.PDB	OG1, F_THR_107	NZ, F_LYS_51	HZ3, F_LYS_51	2.93	1.96	17.40
1HGH.PDB	O, F_ILE_48	N, F_LEU_52	H, F_LEU_52	2.94	2.03	18.13
1HGH.PDB	O, F_ASN_49	N, F_ASN_53	H, F_ASN_53	2.82	1.91	17.65
1HGH.PDB	OE1, F_GLU_57	NH1, F_ARG_54	HH11, F_ARG_54	2.88	1.88	10.86
1HGH.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.72	1.77	15.67
1HGH.PDB	OD2, D_ASP_90	NZ, F_LYS_62	HZ2, F_LYS_62	2.68	1.83	28.02
1HGH.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.87	1.91	9.23
1HGH.PDB	O, E_LYS_299	NZ, F_LYS_68	HZ1, F_LYS_68	2.91	1.87	1.37
1HGH.PDB	OE2, F_GLU_85	NZ, F_LYS_68	HZ2, F_LYS_68	2.73	1.74	15.07
1HGH.PDB	OG, A_SER_107	N, F_ARG_76	H, F_ARG_76	2.80	1.83	4.45
1HGH.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.84	1.87	10.72
1HGH.PDB	OE2, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.73	1.73	5.34
1HGH.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.71	1.70	1.21
1HGH.PDB	OE1, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.78	1.78	7.19
1HGH.PDB	O, F_GLU_72	NE2, F_GLN_78	HE21, F_GLN_78	2.90	1.94	9.41
1HGH.PDB	OE1, F_GLU_74	NE2, F_GLN_78	HE22, F_GLN_78	2.92	1.95	8.97
1HGH.PDB	O, F_GLY_75	N, F_ASP_79	H, F_ASP_79	2.84	1.89	11.67
1HGH.PDB	O, F_ASP_79	N, F_TYR_83	H, F_TYR_83	2.85	1.92	14.40
1HGH.PDB	OE1, B_GLU_85	OH, F_TYR_83	HH, F_TYR_83	2.53	1.74	27.23
1HGH.PDB	O, F_LEU_80	N, F_VAL_84	H, F_VAL_84	2.73	1.81	14.79
1HGH.PDB	O, F_LYS_82	N, F_ASP_86	H, F_ASP_86	2.93	1.98	9.76
1HGH.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.65	1.63	9.88
1HGH.PDB	O, F_GLU_85	N, F_ILE_89	H, F_ILE_89	2.87	1.89	5.28
1HGH.PDB	O, F_LYS_88	N, F_TRP_92	H, F_TRP_92	2.94	1.97	7.63
1HGH.PDB	O, F_ILE_89	N, F_SER_93	H, F_SER_93	2.86	1.97	18.83
1HGH.PDB	O, F_ILE_89	OG, F_SER_93	HG, F_SER_93	2.78	1.88	16.61
1HGH.PDB	O, F_ASP_90	N, F_TYR_94	H, F_TYR_94	2.84	1.92	15.99
1HGH.PDB	O, F_LEU_91	N, F_ASN_95	H, F_ASN_95	3.00	2.02	3.46
1HGH.PDB	O, F_TRP_92	N, F_ALA_96	H, F_ALA_96	2.98	2.07	17.48
1HGH.PDB	O, F_TYR_94	N, F_LEU_98	H, F_LEU_98	2.95	1.97	6.50
1HGH.PDB	O, F_ASN_95	N, F_LEU_99	H, F_LEU_99	2.94	2.05	19.69
1HGH.PDB	O, F_LEU_98	N, F_LEU_102	H, F_LEU_102	3.00	2.02	4.44
1HGH.PDB	O, F_VAL_100	N, F_ASN_104	H, F_ASN_104	2.88	1.93	12.02
1HGH.PDB	O, E_LYS_27	ND2, F_ASN_104	HD22, F_ASN_104	2.90	1.95	12.28
1HGH.PDB	O, F_LEU_102	N, F_HIS_106	H, F_HIS_106	2.96	2.00	11.13
1HGH.PDB	O, F_GLU_103	N, F_THR_107	H, F_THR_107	2.86	1.95	17.81
1HGH.PDB	O, F_HIS_106	N, F_LEU_110	H, F_LEU_110	2.81	1.86	10.81
1HGH.PDB	O, F_THR_107	OG1, F_THR_111	HG1, F_THR_111	2.90	1.94	2.05
1HGH.PDB	O, F_ASP_109	N, F_SER_113	H, F_SER_113	2.77	1.83	10.08
1HGH.PDB	O, F_ASP_112	N, F_ASN_116	H, F_ASN_116	2.97	1.99	5.76
1HGH.PDB	O, F_SER_113	N, F_LYS_117	H, F_LYS_117	2.73	1.90	25.90
1HGH.PDB	O, F_GLU_114	N, F_LEU_118	H, F_LEU_118	2.99	2.02	8.75
1HGH.PDB	O, F_ASN_116	N, F_GLU_120	H, F_GLU_120	2.90	1.92	2.56
1HGH.PDB	O, F_LYS_117	N, F_LYS_121	H, F_LYS_121	2.86	1.95	17.55
1HGH.PDB	O, F_LEU_118	N, F_THR_122	H, F_THR_122	3.00	2.04	9.77
1HGH.PDB	O, F_PHE_119	N, F_ARG_123	H, F_ARG_123	2.88	1.91	8.40
1HGH.PDB	OE2, F_GLU_120	NH1, F_ARG_123	HH11, F_ARG_123	2.74	1.84	22.63
1HGH.PDB	O, F_GLU_120	N, F_ARG_124	H, F_ARG_124	2.97	2.00	8.45
1HGH.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.89	2.06	26.55

1HGH.PDB	OE2, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.92	2.03	21.52
1HGH.PDB	O, F_LEU_126	N, F_ASN_129	H, F_ASN_129	2.97	2.04	14.05
1HGH.PDB	OH, F_TYR_157	ND2, F_ASN_129	HD22, F_ASN_129	2.82	1.88	14.11
1HGH.PDB	O, F_LYS_139	N, F_GLU_131	H, F_GLU_131	2.96	2.04	16.53
1HGH.PDB	O, F_CYS_137	N, F_MET_133	H, F_MET_133	2.86	1.92	14.22
1HGH.PDB	O, E_LEU_13	N, F_PHE_138	H, F_PHE_138	2.71	1.82	18.02
1HGH.PDB	O, F_GLU_131	N, F_LYS_139	H, F_LYS_139	2.82	1.86	5.73
1HGH.PDB	O, E_ALA_11	N, F_ILE_140	H, F_ILE_140	2.79	1.87	15.45
1HGH.PDB	O, F_ASN_129	N, F_TYR_141	H, F_TYR_141	2.86	1.92	14.36
1HGH.PDB	OE2, F_GLU_165	N, F_LYS_143	H, F_LYS_143	2.98	2.04	16.16
1HGH.PDB	O, F_ASP_145	N, F_ILE_149	H, F_ILE_149	2.90	1.94	10.21
1HGH.PDB	O, F_ASN_146	N, F_GLU_150	H, F_GLU_150	2.92	1.99	14.40
1HGH.PDB	O, F_ALA_147	N, F_SER_151	H, F_SER_151	2.95	2.08	22.59
1HGH.PDB	O, F_CYS_148	OG, F_SER_151	HG, F_SER_151	2.76	1.89	20.46
1HGH.PDB	O, F_GLU_150	N, F_ASN_154	H, F_ASN_154	2.79	1.82	2.73
1HGH.PDB	OD1, F_ASP_158	N, F_ASP_160	H, F_ASP_160	2.98	2.10	21.90
1HGH.PDB	O, F_HIS_159	N, F_TYR_162	H, F_TYR_162	2.95	2.07	22.27
1HGH.PDB	O, D_ARG_170	NH1, F_ARG_163	HH12, F_ARG_163	2.89	1.90	10.67
1HGH.PDB	O, F_TYR_162	N, F_ALA_166	H, F_ALA_166	2.94	1.96	4.91
1HGH.PDB	O, F_ARG_163	N, F_LEU_167	H, F_LEU_167	2.82	1.86	8.96
1HGH.PDB	O, F_GLU_165	ND2, F_ASN_169	HD22, F_ASN_169	2.99	2.03	7.50
1HGH.PDB	O, F_ALA_166	N, F_ARG_170	H, F_ARG_170	2.83	1.95	20.78
1HGH.PDB	O, F_GLU_128	NE, F_ARG_170	HE, F_ARG_170	2.76	1.89	22.46
1HGH.PDB	OE2, F_GLU_131	NH1, F_ARG_170	HH11, F_ARG_170	2.84	1.84	5.40
1HGH.PDB	O, F_LEU_167	N, F_PHE_171	H, F_PHE_171	2.96	2.05	17.03
1HGI.PDB	O, B_ILE_140	N, A_ALA_11	H, A_ALA_11	2.84	1.92	15.59
1HGI.PDB	O, B_PHE_138	N, A_LEU_13	H, A_LEU_13	3.00	2.03	9.98
1HGI.PDB	O, B_ARG_25	N, A_CYS_14	H, A_CYS_14	2.96	2.03	15.50
1HGI.PDB	O, B_GLY_136	N, A_LEU_15	H, A_LEU_15	2.93	1.96	7.25
1HGI.PDB	O, B_GLY_23	N, A_GLY_16	H, A_GLY_16	2.98	2.12	23.40
1HGI.PDB	O, A_HIS_18	ND1, A_HIS_17	HD1, A_HIS_17	2.95	2.05	20.26
1HGI.PDB	O, B_TRP_21	N, A_HIS_18	H, A_HIS_18	2.89	1.98	18.40
1HGI.PDB	OD1, A_ASN_322	N, A_VAL_20	H, A_VAL_20	2.77	1.82	10.44
1HGI.PDB	O, A_VAL_36	N, A_THR_24	H, A_THR_24	2.83	1.89	12.49
1HGI.PDB	O, A_ILE_34	N, A_VAL_26	H, A_VAL_26	2.77	1.82	9.67
1HGI.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.90	1.86	7.66
1HGI.PDB	O, A_ASP_31	N, A_THR_28	H, A_THR_28	2.78	1.96	27.36
1HGI.PDB	O, A_VAL_26	N, A_ILE_34	H, A_ILE_34	2.91	2.01	18.80
1HGI.PDB	O, A_THR_24	N, A_VAL_36	H, A_VAL_36	2.78	1.82	5.76
1HGI.PDB	O, A_MET_320	N, A_THR_37	H, A_THR_37	2.84	1.88	8.46
1HGI.PDB	O, A_LEU_316	N, A_THR_40	H, A_THR_40	2.88	2.01	22.14
1HGI.PDB	O, A_LEU_314	N, A_LEU_42	H, A_LEU_42	2.85	1.98	22.93
1HGI.PDB	OE2, A_GLU_41	N, A_VAL_43	H, A_VAL_43	2.99	2.05	14.68
1HGI.PDB	O, A_PHE_294	N, A_GLN_44	H, A_GLN_44	2.83	1.87	6.80
1HGI.PDB	O, A_SER_46	NE2, A_GLN_44	HE22, A_GLN_44	2.80	1.99	27.53
1HGI.PDB	OD2, A_ASP_275	NZ, A_LYS_50	HZ1, A_LYS_50	2.71	1.78	22.79
1HGI.PDB	O, A_PRO_273	N, A_ILE_51	H, A_ILE_51	2.80	1.85	10.62
1HGI.PDB	O, A_ASP_275	N, A_ASN_53	H, A_ASN_53	2.87	2.01	23.36
1HGI.PDB	O, A_GLU_280	NE2, A_HIS_56	HE2, A_HIS_56	2.99	2.05	14.61
1HGI.PDB	OD2, A_ASP_85	N, A_ARG_57	H, A_ARG_57	2.87	1.92	11.71
1HGI.PDB	O, A_THR_83	NE, A_ARG_57	HE, A_ARG_57	2.85	1.87	3.06
1HGI.PDB	O, A_LEU_86	N, A_LEU_59	H, A_LEU_59	2.86	1.91	10.36
1HGI.PDB	O, A_VAL_88	N, A_GLY_61	H, A_GLY_61	2.97	2.12	24.22
1HGI.PDB	OD1, A_ASP_60	N, A_ILE_62	H, A_ILE_62	2.84	1.91	13.27
1HGI.PDB	O, A_GLY_61	N, A_CYS_64	H, A_CYS_64	2.89	1.98	18.14
1HGI.PDB	OE2, A_GLU_89	N, A_LEU_66	H, A_LEU_66	3.00	2.06	15.37
1HGI.PDB	O, A_LEU_66	N, A_LEU_70	H, A_LEU_70	2.81	1.92	20.22
1HGI.PDB	O, A_ILE_67	N, A_LEU_71	H, A_LEU_71	2.84	1.88	6.23

1HGI.PDB	O, A_ASP_68	N, A_GLY_72	H, A_GLY_72	2.79	1.85	12.70
1HGI.PDB	OD1, A_ASP_73	ND1, A_HIS_75	HD1, A_HIS_75	2.90	1.96	15.34
1HGI.PDB	O, A_ASP_63	NE2, A_HIS_75	HE2, A_HIS_75	2.84	1.90	14.11
1HGI.PDB	O, A_ASP_73	N, A_CYS_76	H, A_CYS_76	2.75	1.84	16.03
1HGI.PDB	O, A_PRO_74	N, A_ASP_77	H, A_ASP_77	2.94	1.98	10.08
1HGI.PDB	O, A_CYS_76	N, A_PHE_79	H, A_PHE_79	2.96	1.99	3.40
1HGI.PDB	OE1, A_GLU_82	N, A_THR_83	H, A_THR_83	2.96	2.07	20.90
1HGI.PDB	O, A_ARG_57	N, A_ASP_85	H, A_ASP_85	2.81	1.90	17.53
1HGI.PDB	O, A_MET_268	N, A_GLU_89	H, A_GLU_89	2.81	1.85	7.54
1HGI.PDB	OD1, A_ASP_60	NE, A_ARG_90	HE, A_ARG_90	2.89	1.91	4.93
1HGI.PDB	O, A_SER_270	NH1, A_ARG_90	HH11, A_ARG_90	2.65	1.78	23.88
1HGI.PDB	O, A_ALA_272	NH1, A_ARG_90	HH12, A_ARG_90	2.62	1.72	20.22
1HGI.PDB	OD2, A_ASP_60	NH2, A_ARG_90	HH21, A_ARG_90	2.83	1.85	11.60
1HGI.PDB	OD1, A_ASP_271	N, A_SER_91	H, A_SER_91	2.91	1.95	10.73
1HGI.PDB	OD1, A_ASP_271	OG, A_SER_91	HG, A_SER_91	2.93	2.10	25.86
1HGI.PDB	OD2, A_ASP_271	OG, A_SER_91	HG, A_SER_91	2.80	1.92	20.51
1HGI.PDB	OD2, A_ASP_68	OG, A_SER_95	HG, A_SER_95	2.89	1.96	14.00
1HGI.PDB	OD2, A_ASP_73	N, A_ASN_96	H, A_ASN_96	2.87	1.92	13.04
1HGI.PDB	OD1, A_ASP_68	OH, A_TYR_100	HH, A_TYR_100	2.99	2.05	13.08
1HGI.PDB	OD2, A_ASP_104	OG, A_SER_107	HG, A_SER_107	2.89	1.96	15.23
1HGI.PDB	O, A_TYR_105	N, A_ARG_109	H, A_ARG_109	2.86	1.88	3.08
1HGI.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.80	1.81	13.24
1HGI.PDB	O, A_SER_107	N, A_LEU_111	H, A_LEU_111	2.85	1.89	7.63
1HGI.PDB	O, A_LEU_108	N, A_VAL_112	H, A_VAL_112	2.97	1.99	2.18
1HGI.PDB	O, A_ARG_109	N, A_ALA_113	H, A_ALA_113	2.95	2.04	17.40
1HGI.PDB	O, A_SER_110	N, A_SER_114	H, A_SER_114	2.94	2.06	20.96
1HGI.PDB	OE2, A_GLU_119	OG1, A_THR_117	HG1, A_THR_117	2.93	2.01	15.43
1HGI.PDB	O, A_GLU_82	N, A_LEU_118	H, A_LEU_118	2.94	2.01	15.84
1HGI.PDB	O, A_TYR_257	N, A_ILE_121	H, A_ILE_121	2.92	1.95	6.91
1HGI.PDB	O, A_ARG_255	N, A_GLU_123	H, A_GLU_123	2.88	1.93	11.84
1HGI.PDB	O, A_THR_155	N, A_THR_131	H, A_THR_131	2.73	1.85	20.63
1HGI.PDB	OD1, A_ASN_152	N, A_ASN_133	H, A_ASN_133	2.84	1.92	17.02
1HGI.PDB	O, A_GLY_146	N, A_SER_136	H, A_SER_136	2.75	1.87	20.99
1HGI.PDB	OG, A_SER_136	N, A_ALA_138	H, A_ALA_138	2.84	1.93	17.99
1HGI.PDB	O, A_GLY_144	NZ, A_LYS_140	HZ1, A_LYS_140	2.89	1.92	16.20
1HGI.PDB	OD1, A_ASN_137	NZ, A_LYS_140	HZ2, A_LYS_140	2.79	1.79	13.01
1HGI.PDB	OD2, A_ASP_77	NE, A_ARG_141	HE, A_ARG_141	2.82	2.01	29.43
1HGI.PDB	O, A_PHE_147	NH1, A_ARG_141	HH12, A_ARG_141	2.56	1.66	20.36
1HGI.PDB	OD1, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.93	2.01	20.43
1HGI.PDB	OD2, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.69	1.82	24.99
1HGI.PDB	O, A_GLY_72	NH2, A_ARG_141	HH22, A_ARG_141	3.00	2.01	9.22
1HGI.PDB	O, A_SER_136	N, A_GLY_146	H, A_GLY_146	2.98	2.04	14.64
1HGI.PDB	O, A_GLY_72	N, A_SER_149	H, A_SER_149	2.91	1.98	15.28
1HGI.PDB	O, A_ALA_253	N, A_ASN_152	H, A_ASN_152	2.76	1.90	23.60
1HGI.PDB	OH, A_TYR_195	NE1, A_TRP_153	HE1, A_TRP_153	2.87	1.98	21.02
1HGI.PDB	O, A_THR_131	N, A_THR_155	H, A_THR_155	2.95	1.99	10.46
1HGI.PDB	O, A_LEU_194	N, A_LYS_156	H, A_LYS_156	2.87	1.97	18.02
1HGI.PDB	O, A_SER_193	NZ, A_LYS_156	HZ2, A_LYS_156	2.75	1.76	15.14
1HGI.PDB	O, A_THR_160	N, A_SER_157	H, A_SER_157	2.90	2.01	20.69
1HGI.PDB	OG1, A_THR_131	OG, A_SER_157	HG, A_SER_157	2.97	2.02	9.12
1HGI.PDB	O, A_SER_247	N, A_LEU_164	H, A_LEU_164	2.71	1.88	25.60
1HGI.PDB	O, A_ILE_245	N, A_VAL_166	H, A_VAL_166	2.88	1.93	12.13
1HGI.PDB	O, A_LEU_243	OG1, A_THR_167	HG1, A_THR_167	2.87	2.00	20.84
1HGI.PDB	O, A_LEU_243	N, A_MET_168	H, A_MET_168	2.94	2.01	15.31
1HGI.PDB	O, A_ASP_241	N, A_ASN_170	H, A_ASN_170	2.98	2.00	3.78
1HGI.PDB	O, A_PHE_174	ND2, A_ASN_170	HD21, A_ASN_170	2.83	1.88	13.11
1HGI.PDB	O, A_VAL_237	ND2, A_ASN_170	HD22, A_ASN_170	2.97	2.11	23.66
1HGI.PDB	O, A_VAL_237	N, A_LYS_176	H, A_LYS_176	2.96	2.02	13.33

1HGI.PDB	OE2, A_GLU_123	NZ, A_LYS_176	HZ1, A_LYS_176	2.68	1.79	25.50
1HGI.PDB	O, A_THR_235	N, A_TYR_178	H, A_TYR_178	2.83	1.86	3.17
1HGI.PDB	OE1, A_GLU_123	OH, A_TYR_178	HH, A_TYR_178	2.78	1.82	7.33
1HGI.PDB	OG1, A_THR_235	NE1, A_TRP_180	HE1, A_TRP_180	2.85	1.87	3.02
1HGI.PDB	O, A_ILE_252	N, A_GLY_181	H, A_GLY_181	2.99	2.17	27.41
1HGI.PDB	O, A_ASN_250	N, A_HIS_183	H, A_HIS_183	2.91	2.02	20.40
1HGI.PDB	O, A_ARG_229	N, A_HIS_184	H, A_HIS_184	2.87	1.91	8.12
1HGI.PDB	OG, A_SER_231	NE2, A_HIS_184	HE2, A_HIS_184	2.81	1.93	22.19
1HGI.PDB	OE1, A_GLU_190	N, A_SER_186	H, A_SER_186	2.97	2.07	20.08
1HGI.PDB	OD1, A_ASN_250	NE2, A_GLN_191	HE21, A_GLN_191	2.93	1.97	11.19
1HGI.PDB	O, A_GLN_197	NE2, A_GLN_191	HE22, A_GLN_191	2.94	1.98	10.63
1HGI.PDB	O, A_ASN_188	N, A_THR_192	H, A_THR_192	2.97	2.03	12.91
1HGI.PDB	O, A_ASN_188	OG1, A_THR_192	HG1, A_THR_192	2.95	1.99	5.36
1HGI.PDB	O, A_GLN_189	N, A_SER_193	H, A_SER_193	2.83	1.86	5.01
1HGI.PDB	O, A_GLN_191	N, A_TYR_195	H, A_TYR_195	2.74	1.78	5.84
1HGI.PDB	O, A_TYR_161	NE2, A_GLN_197	HE21, A_GLN_197	2.98	2.02	10.94
1HGI.PDB	O, A_ASN_248	NE2, A_GLN_197	HE22, A_GLN_197	2.92	2.01	18.40
1HGI.PDB	OD1, A_ASN_246	NH2, A_ARG_201	HH21, A_ARG_201	2.54	1.71	26.99
1HGI.PDB	O, A_ILE_213	N, A_VAL_202	H, A_VAL_202	2.93	1.95	5.55
1HGI.PDB	O, A_ASN_246	N, A_THR_203	H, A_THR_203	2.85	1.91	12.85
1HGI.PDB	O, A_GLN_211	N, A_VAL_204	H, A_VAL_204	2.83	1.91	15.32
1HGI.PDB	O, A_VAL_244	N, A_SER_205	H, A_SER_205	2.95	2.02	15.55
1HGI.PDB	O, A_SER_209	N, A_THR_206	H, A_THR_206	2.90	1.93	7.39
1HGI.PDB	OD1, A_ASP_241	N, A_ARG_207	H, A_ARG_207	2.92	1.95	9.91
1HGI.PDB	OD2, A_ASP_241	NE, A_ARG_208	HE, A_ARG_208	2.96	2.05	19.55
1HGI.PDB	O, A_VAL_204	N, A_GLN_211	H, A_GLN_211	2.90	1.98	16.08
1HGI.PDB	OG1, A_THR_203	OG1, A_THR_212	HG1, A_THR_212	2.96	2.00	2.15
1HGI.PDB	O, A_VAL_202	N, A_ILE_213	H, A_ILE_213	2.83	1.91	15.65
1HGI.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.65	1.73	18.55
1HGI.PDB	O, A_ASN_216	NH2, A_ARG_220	HH22, A_ARG_220	2.69	1.79	20.57
1HGI.PDB	O, A_LEU_226	N, A_VAL_223	H, A_VAL_223	2.88	1.91	8.35
1HGI.PDB	O, A_CYS_97	NE, A_ARG_224	HE, A_ARG_224	2.78	1.93	25.49
1HGI.PDB	O, A_CYS_97	NH2, A_ARG_224	HH21, A_ARG_224	2.83	1.97	25.33
1HGI.PDB	O, A_VAL_223	N, A_LEU_226	H, A_LEU_226	2.93	2.00	15.45
1HGI.PDB	O, A_SER_228	NH1, A_ARG_229	HH11, A_ARG_229	2.68	1.75	18.52
1HGI.PDB	O, A_PRO_221	NH2, A_ARG_229	HH22, A_ARG_229	2.62	1.67	14.70
1HGI.PDB	O, A_PRO_99	N, A_ILE_230	H, A_ILE_230	2.99	2.15	25.83
1HGI.PDB	O, A_ILE_182	N, A_SER_231	H, A_SER_231	2.99	2.14	24.63
1HGI.PDB	OD1, A_ASP_101	OG, A_SER_231	HG, A_SER_231	2.96	2.01	11.74
1HGI.PDB	O, A_ASP_101	N, A_ILE_232	H, A_ILE_232	2.92	1.99	15.11
1HGI.PDB	O, A_TRP_180	N, A_TYR_233	H, A_TYR_233	2.89	1.92	9.03
1HGI.PDB	O, A_TYR_178	N, A_THR_235	H, A_THR_235	2.82	1.93	19.14
1HGI.PDB	O, A_LYS_176	N, A_VAL_237	H, A_VAL_237	2.80	1.86	12.56
1HGI.PDB	O, F_SER_71	NZ, A_LYS_238	HZ2, A_LYS_238	2.65	1.80	28.67
1HGI.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.85	1.85	15.00
1HGI.PDB	O, A_ASN_170	N, A_GLY_240	H, A_GLY_240	2.91	2.07	25.35
1HGI.PDB	OD1, A_ASP_241	N, A_VAL_242	H, A_VAL_242	2.74	1.94	29.06
1HGI.PDB	O, A_MET_168	N, A_LEU_243	H, A_LEU_243	2.93	1.96	6.54
1HGI.PDB	O, A_SER_205	N, A_VAL_244	H, A_VAL_244	2.95	2.00	12.56
1HGI.PDB	O, A_VAL_166	N, A_ILE_245	H, A_ILE_245	2.98	2.04	14.27
1HGI.PDB	O, A_THR_203	N, A_ASN_246	H, A_ASN_246	2.86	1.93	15.27
1HGI.PDB	O, A_LEU_164	N, A_SER_247	H, A_SER_247	2.86	1.96	18.93
1HGI.PDB	O, A_ARG_201	OG, A_SER_247	HG, A_SER_247	2.80	2.00	29.04
1HGI.PDB	OE1, A_GLN_191	ND2, A_ASN_250	HD21, A_ASN_250	2.89	1.93	10.00
1HGI.PDB	O, A_HIS_183	ND2, A_ASN_250	HD22, A_ASN_250	2.85	1.88	5.42
1HGI.PDB	O, A_GLY_181	N, A_ILE_252	H, A_ILE_252	2.93	1.97	10.35
1HGI.PDB	O, A_ASN_152	N, A_ALA_253	H, A_ALA_253	2.80	1.92	21.29
1HGI.PDB	O, A_LEU_177	N, A_PHE_258	H, A_PHE_258	2.93	1.97	9.46

1HGI.PDB	OE2, A_GLU_119	NH1, A_ARG_261	HH12, A_ARG_261	2.66	1.83	28.46
1HGI.PDB	OE1, A_GLU_119	NH2, A_ARG_261	HH22, A_ARG_261	2.85	1.99	27.12
1HGI.PDB	OD2, A_ASP_85	NZ, A_LYS_264	HZ3, A_LYS_264	2.82	1.85	17.23
1HGI.PDB	O, A_PHE_87	N, A_MET_268	H, A_MET_268	2.89	2.01	22.03
1HGI.PDB	O, A_PRO_284	OG, A_SER_270	HG, A_SER_270	2.81	1.87	11.59
1HGI.PDB	OG, A_SER_270	N, A_ALA_272	H, A_ALA_272	2.98	2.03	12.37
1HGI.PDB	O, A_ILE_51	N, A_ASP_275	H, A_ASP_275	2.92	2.02	19.41
1HGI.PDB	OD1, A_ASP_275	N, A_THR_276	H, A_THR_276	2.85	2.00	24.58
1HGI.PDB	O, A_ASN_54	N, A_SER_279	H, A_SER_279	2.79	1.86	13.88
1HGI.PDB	O, A_TYR_302	N, A_ILE_282	H, A_ILE_282	2.88	1.92	8.64
1HGI.PDB	O, A_THR_283	N, A_GLY_286	H, A_GLY_286	2.81	1.89	14.79
1HGI.PDB	O, A_LYS_50	N, A_SER_287	H, A_SER_287	2.89	1.91	3.39
1HGI.PDB	O, A_ALA_304	ND2, A_ASN_290	HD22, A_ASN_290	2.73	1.85	20.49
1HGI.PDB	OE1, A_GLN_44	NZ, A_LYS_292	HZ1, A_LYS_292	2.74	1.74	11.73
1HGI.PDB	OD2, A_ASP_291	NZ, A_LYS_292	HZ3, A_LYS_292	2.81	1.89	23.33
1HGI.PDB	O, A_LYS_307	N, A_GLN_295	H, A_GLN_295	2.85	1.96	20.30
1HGI.PDB	O, A_ASN_298	NE2, A_GLN_295	HE21, A_GLN_295	2.82	1.86	9.08
1HGI.PDB	O, A_GLN_44	N, A_ASN_296	H, A_ASN_296	2.91	1.97	13.42
1HGI.PDB	OE1, A_GLN_295	N, A_VAL_297	H, A_VAL_297	2.73	1.93	28.60
1HGI.PDB	OD1, A_ASN_298	N, A_ILE_300	H, A_ILE_300	2.93	1.98	12.80
1HGI.PDB	O, A_ILE_282	N, A_TYR_302	H, A_TYR_302	2.98	2.09	21.95
1HGI.PDB	O, A_LYS_264	OH, A_TYR_302	HH, A_TYR_302	2.75	1.94	27.71
1HGI.PDB	O, B_LYS_62	N, A_GLY_303	H, A_GLY_303	2.96	1.99	7.07
1HGI.PDB	O, A_GLN_295	N, A_VAL_309	H, A_VAL_309	2.99	2.14	25.08
1HGI.PDB	OG, B_SER_93	N, A_LYS_310	H, A_LYS_310	2.98	2.05	15.58
1HGI.PDB	OD1, B_ASP_86	NZ, A_LYS_310	HZ3, A_LYS_310	2.76	1.92	29.34
1HGI.PDB	OE2, A_GLU_41	N, A_LEU_314	H, A_LEU_314	2.86	1.90	8.56
1HGI.PDB	OE1, A_GLU_41	NZ, A_LYS_315	HZ3, A_LYS_315	2.77	1.82	19.86
1HGI.PDB	O, A_THR_40	N, A_LEU_316	H, A_LEU_316	2.86	1.94	16.90
1HGI.PDB	OD1, B_ASN_104	N, A_ALA_317	H, A_ALA_317	2.74	1.83	15.76
1HGI.PDB	O, A_ASN_38	N, A_THR_318	H, A_THR_318	2.82	1.93	19.87
1HGI.PDB	O, A_VAL_20	ND2, A_ASN_322	HD21, A_ASN_322	2.87	1.93	13.77
1HGI.PDB	OE2, A_GLU_35	ND2, A_ASN_322	HD22, A_ASN_322	2.93	1.97	12.34
1HGI.PDB	OE2, B_GLU_15	NZ, A_LYS_326	HZ1, A_LYS_326	2.79	1.93	27.33
1HGI.PDB	OE1, A_GLU_325	NZ, A_LYS_326	HZ3, A_LYS_326	2.91	1.94	17.77
1HGI.PDB	OE1, B_GLU_15	N, A_THR_328	H, A_THR_328	2.87	1.93	12.65
1HGI.PDB	OD2, B_ASP_112	N, B_GLY_1	H2, B_GLY_1	2.79	1.78	11.80
1HGI.PDB	OD1, B_ASP_109	N, B_LEU_2	H, B_LEU_2	2.89	1.95	13.58
1HGI.PDB	OD2, B_ASP_112	N, B_PHE_3	H, B_PHE_3	2.82	2.00	27.10
1HGI.PDB	OD2, B_ASP_112	N, B_GLY_4	H, B_GLY_4	2.93	2.02	17.65
1HGI.PDB	OD1, B_ASP_112	N, B_ALA_5	H, B_ALA_5	2.82	1.90	16.18
1HGI.PDB	O, B_GLY_4	N, B_PHE_9	H, B_PHE_9	2.84	1.90	12.47
1HGI.PDB	O, B_GLY_13	ND2, B_ASN_12	HD22, B_ASN_12	2.81	1.91	19.43
1HGI.PDB	O, A_VAL_323	N, B_GLY_13	H, B_GLY_13	2.68	1.79	18.45
1HGI.PDB	O, A_HIS_17	N, B_TRP_14	H, B_TRP_14	2.78	1.88	17.65
1HGI.PDB	OG1, B_THR_41	N, B_TRP_21	H, B_TRP_21	2.98	2.13	25.10
1HGI.PDB	O, A_GLY_16	N, B_GLY_23	H, B_GLY_23	2.97	2.06	17.58
1HGI.PDB	O, B_ALA_35	N, B_PHE_24	H, B_PHE_24	2.80	1.84	7.18
1HGI.PDB	OE1, B_GLN_34	NE, B_ARG_25	HE, B_ARG_25	2.60	1.78	26.17
1HGI.PDB	OE1, B_GLN_34	NH2, B_ARG_25	HH21, B_ARG_25	2.75	1.92	27.98
1HGI.PDB	OE2, A_GLU_325	NH2, B_ARG_25	HH22, B_ARG_25	2.93	1.95	13.46
1HGI.PDB	O, B_GLY_33	N, B_HIS_26	H, B_HIS_26	2.73	1.82	16.37
1HGI.PDB	O, B_GLY_31	N, B_ASN_28	H, B_ASN_28	2.73	1.84	19.89
1HGI.PDB	O, B_ASN_28	N, B_GLY_31	H, B_GLY_31	2.85	2.01	25.49
1HGI.PDB	O, B_PHE_24	N, B_ALA_35	H, B_ALA_35	2.80	2.01	29.31
1HGI.PDB	O, B_TYR_22	N, B_ASP_37	H, B_ASP_37	2.70	1.78	14.64
1HGI.PDB	OD2, B_ASP_37	N, B_SER_40	H, B_SER_40	2.90	1.93	5.57
1HGI.PDB	O, B_ASP_37	OG1, B_THR_41	HG1, B_THR_41	2.74	1.83	15.44

1HGI.PDB	OD1, B_ASP_46	NE2, B_GLN_42	HE22, B_GLN_42	2.89	2.02	23.36
1HGI.PDB	O, B_SER_40	N, B_ALA_44	H, B_ALA_44	2.95	1.97	3.32
1HGI.PDB	O, B_THR_41	N, B_ILE_45	H, B_ILE_45	2.96	2.03	14.49
1HGI.PDB	O, B_GLN_42	N, B_ASP_46	H, B_ASP_46	2.71	1.76	6.05
1HGI.PDB	O, B_ALA_43	NE2, B_GLN_47	HE22, B_GLN_47	2.94	2.02	16.15
1HGI.PDB	O, B_ILE_45	N, B_ASN_49	H, B_ASN_49	2.87	1.98	20.49
1HGI.PDB	O, B_ASP_46	N, B_GLY_50	H, B_GLY_50	2.94	2.01	16.14
1HGI.PDB	O, B_GLN_47	N, B_LYS_51	H, B_LYS_51	3.00	2.02	5.35
1HGI.PDB	OG1, B_THR_107	NZ, B_LYS_51	HZ1, B_LYS_51	2.96	1.97	15.88
1HGI.PDB	OE1, B_GLU_103	NZ, B_LYS_51	HZ2, B_LYS_51	2.82	1.78	6.88
1HGI.PDB	ND1, B_HIS_106	NZ, B_LYS_51	HZ3, B_LYS_51	2.81	1.87	19.52
1HGI.PDB	O, B_ILE_48	N, B_LEU_52	H, B_LEU_52	2.94	2.01	15.10
1HGI.PDB	O, B_ASN_49	N, B_ASN_53	H, B_ASN_53	2.79	1.92	22.20
1HGI.PDB	O, E_THR_28	NE, B_ARG_54	HE, B_ARG_54	2.88	1.92	10.21
1HGI.PDB	OE1, B_GLU_57	NH1, B_ARG_54	HH11, B_ARG_54	2.86	1.87	11.02
1HGI.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.81	1.84	14.63
1HGI.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ1, B_LYS_62	2.67	1.78	25.75
1HGI.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.87	1.89	8.13
1HGI.PDB	O, B_PHE_63	NE2, B_GLN_65	HE22, B_GLN_65	2.93	1.95	3.70
1HGI.PDB	O, A_LYS_299	NZ, B_LYS_68	HZ1, B_LYS_68	2.81	1.78	9.15
1HGI.PDB	OE2, B_GLU_85	NZ, B_LYS_68	HZ2, B_LYS_68	2.79	1.75	2.13
1HGI.PDB	OG, C_SER_107	N, B_ARG_76	H, B_ARG_76	2.85	1.90	10.66
1HGI.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.86	1.89	7.04
1HGI.PDB	OE2, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.92	1.89	1.72
1HGI.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.71	1.72	8.42
1HGI.PDB	OE1, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.86	1.86	6.93
1HGI.PDB	O, B_GLU_72	NE2, B_GLN_78	HE21, B_GLN_78	2.96	1.98	5.26
1HGI.PDB	OE1, B_GLU_74	NE2, B_GLN_78	HE22, B_GLN_78	2.94	1.97	8.23
1HGI.PDB	O, B_ASP_79	N, B_TYR_83	H, B_TYR_83	2.91	2.00	18.32
1HGI.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.78	1.84	13.46
1HGI.PDB	O, B_LEU_80	N, B_VAL_84	H, B_VAL_84	2.75	1.83	14.22
1HGI.PDB	O, B_LYS_82	N, B_ASP_86	H, B_ASP_86	2.90	1.94	10.51
1HGI.PDB	O, B_TYR_83	N, B_THR_87	H, B_THR_87	2.96	2.01	11.07
1HGI.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.65	1.64	9.94
1HGI.PDB	O, B_GLU_85	N, B_ILE_89	H, B_ILE_89	2.86	1.89	9.56
1HGI.PDB	O, B_LYS_88	N, B_TRP_92	H, B_TRP_92	2.97	1.99	6.73
1HGI.PDB	O, B_ILE_89	N, B_SER_93	H, B_SER_93	2.87	1.94	14.62
1HGI.PDB	O, B_ILE_89	OG, B_SER_93	HG, B_SER_93	2.83	1.94	18.39
1HGI.PDB	O, B_ASP_90	N, B_TYR_94	H, B_TYR_94	2.94	2.02	16.85
1HGI.PDB	O, B_TRP_92	N, B_ALA_96	H, B_ALA_96	2.90	1.95	10.47
1HGI.PDB	O, B_TYR_94	N, B_LEU_98	H, B_LEU_98	2.90	1.94	9.73
1HGI.PDB	O, B_ASN_95	N, B_LEU_99	H, B_LEU_99	2.85	1.96	19.61
1HGI.PDB	O, B_ALA_96	N, B_VAL_100	H, B_VAL_100	2.99	2.03	8.76
1HGI.PDB	O, B_LEU_98	N, B_LEU_102	H, B_LEU_102	2.99	2.01	3.39
1HGI.PDB	O, B_LEU_99	N, B_GLU_103	H, B_GLU_103	2.93	1.96	7.47
1HGI.PDB	O, B_VAL_100	N, B_ASN_104	H, B_ASN_104	2.87	1.90	6.79
1HGI.PDB	O, A_LYS_27	ND2, B_ASN_104	HD22, B_ASN_104	2.86	1.90	10.00
1HGI.PDB	O, B_LEU_102	N, B_HIS_106	H, B_HIS_106	2.92	1.98	15.03
1HGI.PDB	O, B_GLU_103	N, B_THR_107	H, B_THR_107	2.76	1.89	21.30
1HGI.PDB	O, B_ASN_104	N, B_ILE_108	H, B_ILE_108	2.93	1.97	9.63
1HGI.PDB	O, B_HIS_106	N, B_LEU_110	H, B_LEU_110	2.81	1.86	12.25
1HGI.PDB	O, B_THR_107	OG1, B_THR_111	HG1, B_THR_111	2.94	1.97	3.25
1HGI.PDB	O, B_ASP_109	N, B_SER_113	H, B_SER_113	2.80	1.86	12.43
1HGI.PDB	O, F_LEU_2	OG, B_SER_113	HG, B_SER_113	2.77	1.90	22.05
1HGI.PDB	O, B_LEU_110	N, B_GLU_114	H, B_GLU_114	2.95	1.99	9.30
1HGI.PDB	O, B_ASP_112	N, B_ASN_116	H, B_ASN_116	2.96	2.02	13.43
1HGI.PDB	O, B_SER_113	N, B_LYS_117	H, B_LYS_117	2.68	1.82	23.27
1HGI.PDB	O, B_ASN_116	N, B_GLU_120	H, B_GLU_120	2.93	1.95	4.31

1HGI.PDB	O, B_LYS_117	N, B_LYS_121	H, B_LYS_121	2.92	2.00	16.22
1HGI.PDB	OE2, B_GLU_120	NH1, B_ARG_123	HH11, B_ARG_123	2.84	1.97	25.22
1HGI.PDB	O, B_GLU_120	N, B_ARG_124	H, B_ARG_124	2.91	1.93	5.01
1HGI.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.81	1.96	23.50
1HGI.PDB	OE2, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.86	2.02	24.92
1HGI.PDB	O, B_LEU_126	N, B_ASN_129	H, B_ASN_129	2.99	2.06	15.00
1HGI.PDB	O, B_HIS_159	ND2, B_ASN_129	HD21, B_ASN_129	3.00	2.06	13.30
1HGI.PDB	OH, B_TYR_157	ND2, B_ASN_129	HD22, B_ASN_129	2.81	1.86	9.72
1HGI.PDB	O, B_LYS_139	N, B_GLU_131	H, B_GLU_131	2.91	1.98	14.55
1HGI.PDB	O, B_CYS_137	N, B_MET_133	H, B_MET_133	2.81	1.88	13.30
1HGI.PDB	O, A_LEU_13	N, B_PHE_138	H, B_PHE_138	2.74	1.89	23.78
1HGI.PDB	O, B_GLU_131	N, B_LYS_139	H, B_LYS_139	2.82	1.86	8.55
1HGI.PDB	O, A_ALA_11	N, B_ILE_140	H, B_ILE_140	2.77	1.87	18.46
1HGI.PDB	O, B_ASN_129	N, B_TYR_141	H, B_TYR_141	2.82	1.85	4.69
1HGI.PDB	OE2, B_GLU_165	N, B_LYS_143	H, B_LYS_143	2.87	1.93	14.38
1HGI.PDB	OE1, B_GLU_30	N, B_ASN_146	H, B_ASN_146	2.95	2.07	23.02
1HGI.PDB	O, B_ASP_145	N, B_ILE_149	H, B_ILE_149	2.90	1.94	7.96
1HGI.PDB	O, B_ASN_146	N, B_GLU_150	H, B_GLU_150	2.83	1.92	17.44
1HGI.PDB	O, B_ALA_147	N, B_SER_151	H, B_SER_151	2.90	2.01	20.08
1HGI.PDB	O, B_CYS_148	OG, B_SER_151	HG, B_SER_151	2.68	1.84	23.42
1HGI.PDB	O, B_GLU_150	N, B_ASN_154	H, B_ASN_154	2.81	1.83	1.94
1HGI.PDB	OE2, B_GLU_150	ND2, B_ASN_154	HD21, B_ASN_154	2.84	2.01	27.47
1HGI.PDB	O, B_SER_151	N, B_THR_156	H, B_THR_156	2.77	1.94	25.73
1HGI.PDB	OD1, B_ASN_154	OG1, B_THR_156	HG1, B_THR_156	2.64	1.78	21.15
1HGI.PDB	O, B_HIS_159	N, B_TYR_162	H, B_TYR_162	2.88	2.01	22.48
1HGI.PDB	O, F_ARG_170	NH1, B_ARG_163	HH12, B_ARG_163	2.73	1.76	13.86
1HGI.PDB	O, B_TYR_162	N, B_ALA_166	H, B_ALA_166	2.86	1.88	1.82
1HGI.PDB	O, B_ARG_163	N, B_LEU_167	H, B_LEU_167	2.77	1.81	5.67
1HGI.PDB	O, B_ALA_166	N, B_ARG_170	H, B_ARG_170	2.78	1.90	21.33
1HGI.PDB	O, B_GLU_128	NE, B_ARG_170	HE, B_ARG_170	2.72	1.88	25.72
1HGI.PDB	OE2, B_GLU_131	NH1, B_ARG_170	HH11, B_ARG_170	2.77	1.77	6.54
1HGI.PDB	O, B_LEU_167	N, B_PHE_171	H, B_PHE_171	2.90	1.96	12.85
1HGI.PDB	O, D_ILE_140	N, C_ALA_11	H, C_ALA_11	2.86	1.93	15.33
1HGI.PDB	O, D_GLN_27	N, C_THR_12	H, C_THR_12	2.98	2.01	4.69
1HGI.PDB	O, D_PHE_138	N, C_LEU_13	H, C_LEU_13	2.99	2.03	9.93
1HGI.PDB	O, D_ARG_25	N, C_CYS_14	H, C_CYS_14	2.67	1.83	24.75
1HGI.PDB	O, D_GLY_136	N, C_LEU_15	H, C_LEU_15	2.95	1.98	7.51
1HGI.PDB	O, D_GLY_23	N, C_GLY_16	H, C_GLY_16	2.99	2.12	22.96
1HGI.PDB	O, C_HIS_18	ND1, C_HIS_17	HD1, C_HIS_17	2.96	2.07	20.32
1HGI.PDB	O, D_TRP_21	N, C_HIS_18	H, C_HIS_18	2.88	1.97	18.12
1HGI.PDB	OD1, C_ASN_322	N, C_VAL_20	H, C_VAL_20	2.78	1.82	9.40
1HGI.PDB	O, C_VAL_36	N, C_THR_24	H, C_THR_24	2.85	1.90	11.53
1HGI.PDB	O, C_ILE_34	N, C_VAL_26	H, C_VAL_26	2.78	1.84	11.07
1HGI.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.88	1.83	6.58
1HGI.PDB	O, C_ASP_31	N, C_THR_28	H, C_THR_28	2.76	1.94	27.36
1HGI.PDB	O, C_VAL_26	N, C_ILE_34	H, C_ILE_34	2.92	2.01	18.98
1HGI.PDB	O, C_THR_24	N, C_VAL_36	H, C_VAL_36	2.78	1.82	7.09
1HGI.PDB	O, C_MET_320	N, C_THR_37	H, C_THR_37	2.89	1.92	7.75
1HGI.PDB	O, C_LEU_316	N, C_THR_40	H, C_THR_40	2.92	2.04	21.59
1HGI.PDB	O, C_LEU_314	N, C_LEU_42	H, C_LEU_42	2.81	1.95	23.61
1HGI.PDB	OE2, C_GLU_41	N, C_VAL_43	H, C_VAL_43	2.99	2.05	14.73
1HGI.PDB	O, C_PHE_294	N, C_GLN_44	H, C_GLN_44	2.82	1.86	6.96
1HGI.PDB	O, C_SER_46	NE2, C_GLN_44	HE22, C_GLN_44	2.83	2.00	26.47
1HGI.PDB	O, C_ASN_285	OG, C_SER_47	HG, C_SER_47	2.79	1.92	20.46
1HGI.PDB	OD2, C_ASP_275	NZ, C_LYS_50	HZ1, C_LYS_50	2.68	1.77	23.91
1HGI.PDB	O, C_PRO_273	N, C_ILE_51	H, C_ILE_51	2.79	1.84	11.72
1HGI.PDB	O, C_ASP_275	N, C_ASN_53	H, C_ASN_53	2.84	1.98	23.59
1HGI.PDB	O, C_GLU_280	NE2, C_HIS_56	HE2, C_HIS_56	3.00	2.06	15.07

1HGI.PDB	OD2, C_ASP_85	N, C_ARG_57	H, C_ARG_57	2.85	1.91	11.94
1HGI.PDB	O, C_THR_83	NE, C_ARG_57	HE, C_ARG_57	2.81	1.84	5.65
1HGI.PDB	O, C_LEU_86	N, C_LEU_59	H, C_LEU_59	2.86	1.90	10.05
1HGI.PDB	O, C_VAL_88	N, C_GLY_61	H, C_GLY_61	2.94	2.11	25.94
1HGI.PDB	OD1, C_ASP_60	N, C_ILE_62	H, C_ILE_62	2.85	1.91	12.59
1HGI.PDB	O, C_GLY_61	N, C_CYS_64	H, C_CYS_64	2.89	1.99	19.13
1HGI.PDB	O, C_LEU_66	N, C_LEU_70	H, C_LEU_70	2.83	1.94	20.67
1HGI.PDB	O, C_ILE_67	N, C_LEU_71	H, C_LEU_71	2.84	1.87	6.00
1HGI.PDB	O, C_ASP_68	N, C_GLY_72	H, C_GLY_72	2.79	1.85	12.61
1HGI.PDB	OD1, C_ASP_73	ND1, C_HIS_75	HD1, C_HIS_75	2.88	1.94	15.46
1HGI.PDB	O, C_ASP_63	NE2, C_HIS_75	HE2, C_HIS_75	2.82	1.88	14.02
1HGI.PDB	O, C_ASP_73	N, C_CYS_76	H, C_CYS_76	2.75	1.84	16.01
1HGI.PDB	O, C_PRO_74	N, C_ASP_77	H, C_ASP_77	2.91	1.96	10.58
1HGI.PDB	O, C_CYS_76	N, C_PHE_79	H, C_PHE_79	2.94	1.96	2.92
1HGI.PDB	OE1, C_GLU_82	N, C_THR_83	H, C_THR_83	2.93	2.02	17.21
1HGI.PDB	O, C_ARG_57	N, C_ASP_85	H, C_ASP_85	2.81	1.91	18.21
1HGI.PDB	O, C_MET_268	N, C_GLU_89	H, C_GLU_89	2.80	1.84	7.26
1HGI.PDB	OD1, C_ASP_60	NE, C_ARG_90	HE, C_ARG_90	2.83	1.88	11.13
1HGI.PDB	O, C_SER_270	NH1, C_ARG_90	HH11, C_ARG_90	2.67	1.81	25.47
1HGI.PDB	O, C_ALA_272	NH1, C_ARG_90	HH12, C_ARG_90	2.60	1.70	21.36
1HGI.PDB	OD2, C_ASP_60	NH2, C_ARG_90	HH21, C_ARG_90	2.77	1.79	11.02
1HGI.PDB	OD1, C_ASP_271	N, C_SER_91	H, C_SER_91	2.90	1.94	8.90
1HGI.PDB	OD1, C_ASP_271	OG, C_SER_91	HG, C_SER_91	2.95	2.13	27.22
1HGI.PDB	OD2, C_ASP_271	OG, C_SER_91	HG, C_SER_91	2.83	1.94	19.64
1HGI.PDB	OD2, C_ASP_68	OG, C_SER_95	HG, C_SER_95	2.89	1.96	14.85
1HGI.PDB	OD2, C_ASP_73	N, C_ASN_96	H, C_ASN_96	2.88	1.93	14.25
1HGI.PDB	OD1, C_ASP_68	OH, C_TYR_100	HH, C_TYR_100	2.94	1.99	10.92
1HGI.PDB	OD2, C_ASP_104	OG, C_SER_107	HG, C_SER_107	2.90	1.96	13.90
1HGI.PDB	O, C_TYR_105	N, C_ARG_109	H, C_ARG_109	2.86	1.89	3.57
1HGI.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.82	1.84	15.02
1HGI.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.85	1.90	11.29
1HGI.PDB	O, C_SER_107	N, C_LEU_111	H, C_LEU_111	2.85	1.89	7.56
1HGI.PDB	O, C_LEU_108	N, C_VAL_112	H, C_VAL_112	3.00	2.02	3.49
1HGI.PDB	O, C_ARG_109	N, C_ALA_113	H, C_ALA_113	2.96	2.06	18.71
1HGI.PDB	O, C_SER_110	N, C_SER_114	H, C_SER_114	2.95	2.00	13.25
1HGI.PDB	OE2, C_GLU_119	OG1, C_THR_117	HG1, C_THR_117	2.95	2.03	14.67
1HGI.PDB	O, C_GLU_82	N, C_LEU_118	H, C_LEU_118	2.88	1.95	16.18
1HGI.PDB	O, C_TYR_257	N, C_ILE_121	H, C_ILE_121	2.94	1.97	6.04
1HGI.PDB	O, C_ARG_255	N, C_GLU_123	H, C_GLU_123	2.89	1.94	11.68
1HGI.PDB	O, C_THR_155	N, C_THR_131	H, C_THR_131	2.76	1.87	19.24
1HGI.PDB	OD1, C_ASN_152	N, C_ASN_133	H, C_ASN_133	2.83	1.91	16.95
1HGI.PDB	O, C_GLY_146	N, C_SER_136	H, C_SER_136	2.76	1.88	20.67
1HGI.PDB	OG, C_SER_136	N, C_ALA_138	H, C_ALA_138	2.86	1.95	18.03
1HGI.PDB	O, C_GLY_144	NZ, C_LYS_140	HZ1, C_LYS_140	2.86	1.89	16.83
1HGI.PDB	OD1, C_ASN_137	NZ, C_LYS_140	HZ2, C_LYS_140	2.83	1.83	12.62
1HGI.PDB	OD2, C_ASP_77	NE, C_ARG_141	HE, C_ARG_141	2.83	2.02	29.40
1HGI.PDB	O, C_PHE_147	NH1, C_ARG_141	HH12, C_ARG_141	2.56	1.65	20.19
1HGI.PDB	OD1, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.93	2.01	20.50
1HGI.PDB	OD2, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.70	1.83	25.10
1HGI.PDB	O, C_GLY_72	NH2, C_ARG_141	HH22, C_ARG_141	2.97	1.99	9.60
1HGI.PDB	O, C_SER_136	N, C_GLY_146	H, C_GLY_146	2.99	2.05	14.57
1HGI.PDB	O, C_GLY_72	N, C_SER_149	H, C_SER_149	2.90	1.97	15.40
1HGI.PDB	O, C_ALA_253	N, C_ASN_152	H, C_ASN_152	2.73	1.88	24.43
1HGI.PDB	OH, C_TYR_195	NE1, C_TRP_153	HE1, C_TRP_153	2.82	1.96	22.98
1HGI.PDB	O, C_LEU_194	N, C_LYS_156	H, C_LYS_156	2.88	1.99	20.12
1HGI.PDB	O, C_THR_160	N, C_SER_157	H, C_SER_157	2.87	1.98	19.55
1HGI.PDB	O, C_SER_247	N, C_LEU_164	H, C_LEU_164	2.73	1.90	26.15
1HGI.PDB	O, C_ILE_245	N, C_VAL_166	H, C_VAL_166	2.88	1.93	12.15

1HGI.PDB	O, C_LEU_243	OG1, C_THR_167	HG1, C_THR_167	2.85	1.95	18.23
1HGI.PDB	O, C_LEU_243	N, C_MET_168	H, C_MET_168	2.97	2.05	16.15
1HGI.PDB	O, C_ASP_241	N, C_ASN_170	H, C_ASN_170	2.92	1.94	4.90
1HGI.PDB	O, C_PHE_174	ND2, C_ASN_170	HD21, C_ASN_170	2.83	1.88	12.32
1HGI.PDB	O, C_VAL_237	ND2, C_ASN_170	HD22, C_ASN_170	2.96	2.10	24.31
1HGI.PDB	O, C_VAL_237	N, C_LYS_176	H, C_LYS_176	2.94	2.00	13.35
1HGI.PDB	OE2, C_GLU_123	NZ, C_LYS_176	HZ1, C_LYS_176	2.68	1.80	26.11
1HGI.PDB	O, C_PHE_258	N, C_LEU_177	H, C_LEU_177	2.96	1.99	8.81
1HGI.PDB	O, C_THR_235	N, C_TYR_178	H, C_TYR_178	2.82	1.85	3.86
1HGI.PDB	OE1, C_GLU_123	OH, C_TYR_178	HH, C_TYR_178	2.75	1.80	7.25
1HGI.PDB	OG1, C_THR_235	NE1, C_TRP_180	HE1, C_TRP_180	2.84	1.86	3.22
1HGI.PDB	O, C_ILE_252	N, C_GLY_181	H, C_GLY_181	2.98	2.16	27.47
1HGI.PDB	O, C_ASN_250	N, C_HIS_183	H, C_HIS_183	2.91	2.02	20.05
1HGI.PDB	O, C_ARG_229	N, C_HIS_184	H, C_HIS_184	2.89	1.92	8.40
1HGI.PDB	OG, C_SER_231	NE2, C_HIS_184	HE2, C_HIS_184	2.81	1.93	22.34
1HGI.PDB	OE1, C_GLU_190	N, C_SER_186	H, C_SER_186	3.00	2.10	20.23
1HGI.PDB	OD1, C_ASN_250	NE2, C_GLN_191	HE21, C_GLN_191	2.86	1.91	10.94
1HGI.PDB	O, C_GLN_197	NE2, C_GLN_191	HE22, C_GLN_191	2.97	2.02	11.67
1HGI.PDB	O, C_ASN_188	N, C_THR_192	H, C_THR_192	2.98	2.00	5.60
1HGI.PDB	O, C_GLN_189	OG1, C_THR_192	HG1, C_THR_192	2.81	1.90	15.34
1HGI.PDB	O, C_GLN_189	N, C_SER_193	H, C_SER_193	2.84	1.90	13.29
1HGI.PDB	O, C_GLN_191	N, C_TYR_195	H, C_TYR_195	2.76	1.80	7.13
1HGI.PDB	O, C_TYR_161	NE2, C_GLN_197	HE21, C_GLN_197	2.96	2.01	11.19
1HGI.PDB	O, C_ASN_248	NE2, C_GLN_197	HE22, C_GLN_197	2.92	2.02	18.87
1HGI.PDB	OD1, C_ASN_246	NH2, C_ARG_201	HH21, C_ARG_201	2.55	1.72	27.61
1HGI.PDB	O, C_ILE_213	N, C_VAL_202	H, C_VAL_202	2.94	1.98	9.08
1HGI.PDB	O, C_ASN_246	N, C_THR_203	H, C_THR_203	2.86	1.89	7.88
1HGI.PDB	OG1, C_THR_212	OG1, C_THR_203	HG1, C_THR_203	2.94	2.00	11.06
1HGI.PDB	O, C_GLN_211	N, C_VAL_204	H, C_VAL_204	2.84	1.92	15.35
1HGI.PDB	O, C_VAL_244	N, C_SER_205	H, C_SER_205	2.96	2.05	17.13
1HGI.PDB	O, C_SER_209	N, C_THR_206	H, C_THR_206	2.90	1.93	7.31
1HGI.PDB	OD1, C_ASP_241	N, C_ARG_207	H, C_ARG_207	2.90	1.95	10.96
1HGI.PDB	OD2, C_ASP_241	NE, C_ARG_208	HE, C_ARG_208	2.92	2.01	19.66
1HGI.PDB	O, C_VAL_204	N, C_GLN_211	H, C_GLN_211	2.87	1.93	14.30
1HGI.PDB	O, C_VAL_202	N, C_ILE_213	H, C_ILE_213	2.82	1.89	14.72
1HGI.PDB	O, C_ASN_216	NH1, C_ARG_220	HH12, C_ARG_220	2.89	2.08	29.98
1HGI.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.62	1.75	23.70
1HGI.PDB	O, C_ASN_216	NH2, C_ARG_220	HH22, C_ARG_220	2.69	1.79	20.70
1HGI.PDB	O, C_LEU_226	N, C_VAL_223	H, C_VAL_223	2.85	1.88	6.86
1HGI.PDB	O, C_CYS_97	NE, C_ARG_224	HE, C_ARG_224	2.75	1.92	26.67
1HGI.PDB	O, C_CYS_97	NH2, C_ARG_224	HH21, C_ARG_224	2.83	1.98	26.45
1HGI.PDB	O, C_VAL_223	N, C_LEU_226	H, C_LEU_226	2.94	2.02	16.27
1HGI.PDB	O, C_SER_228	NH1, C_ARG_229	HH11, C_ARG_229	2.65	1.73	19.05
1HGI.PDB	O, C_PRO_221	NH2, C_ARG_229	HH22, C_ARG_229	2.65	1.69	14.06
1HGI.PDB	OD1, C_ASP_101	OG, C_SER_231	HG, C_SER_231	2.97	2.02	12.14
1HGI.PDB	O, C_ASP_101	N, C_ILE_232	H, C_ILE_232	2.92	1.98	14.17
1HGI.PDB	O, C_TRP_180	N, C_TYR_233	H, C_TYR_233	2.88	1.92	9.12
1HGI.PDB	O, C_TYR_178	N, C_THR_235	H, C_THR_235	2.81	1.91	19.71
1HGI.PDB	O, C_LYS_176	N, C_VAL_237	H, C_VAL_237	2.80	1.87	14.88
1HGI.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.67	1.77	23.68
1HGI.PDB	O, B_SER_71	NZ, C_LYS_238	HZ3, C_LYS_238	2.57	1.73	28.43
1HGI.PDB	O, C_ASN_170	N, C_GLY_240	H, C_GLY_240	2.88	2.03	25.25
1HGI.PDB	OD1, C_ASP_241	N, C_VAL_242	H, C_VAL_242	2.77	1.97	28.83
1HGI.PDB	O, C_MET_168	N, C_LEU_243	H, C_LEU_243	2.92	1.95	6.19
1HGI.PDB	O, C_SER_205	N, C_VAL_244	H, C_VAL_244	2.97	2.02	12.13
1HGI.PDB	O, C_VAL_166	N, C_ILE_245	H, C_ILE_245	2.97	2.04	14.87
1HGI.PDB	O, C_THR_203	N, C_ASN_246	H, C_ASN_246	2.85	1.92	14.46
1HGI.PDB	O, C_LEU_164	N, C_SER_247	H, C_SER_247	2.86	1.95	18.44

1HGI.PDB	O, C_ARG_201	OG, C_SER_247	HG, C_SER_247	2.81	2.01	28.50
1HGI.PDB	OE1, C_GLN_191	ND2, C_ASN_250	HD21, C_ASN_250	2.87	1.92	11.00
1HGI.PDB	O, C_HIS_183	ND2, C_ASN_250	HD22, C_ASN_250	2.85	1.88	5.75
1HGI.PDB	O, C_ASN_152	N, C_ALA_253	H, C_ALA_253	2.82	1.96	22.89
1HGI.PDB	O, C_ILE_121	N, C_TYR_257	H, C_TYR_257	2.97	2.10	23.39
1HGI.PDB	O, C_LEU_177	N, C_PHE_258	H, C_PHE_258	2.92	1.96	9.71
1HGI.PDB	OE2, C_GLU_119	NH1, C_ARG_261	HH12, C_ARG_261	2.66	1.84	29.01
1HGI.PDB	OE1, C_GLU_119	NH2, C_ARG_261	HH22, C_ARG_261	2.84	1.99	27.78
1HGI.PDB	OD2, C_ASP_85	NZ, C_LYS_264	HZ3, C_LYS_264	2.83	1.86	17.28
1HGI.PDB	O, C_PHE_87	N, C_MET_268	H, C_MET_268	2.86	1.97	20.48
1HGI.PDB	O, C_PRO_284	OG, C_SER_270	HG, C_SER_270	2.81	1.86	9.17
1HGI.PDB	OG, C_SER_270	N, C_ALA_272	H, C_ALA_272	2.97	2.03	11.96
1HGI.PDB	O, C_ILE_51	N, C_ASP_275	H, C_ASP_275	2.97	2.06	19.21
1HGI.PDB	OD1, C_ASP_275	N, C_THR_276	H, C_THR_276	2.80	1.96	24.61
1HGI.PDB	O, C_ASN_54	N, C_SER_279	H, C_SER_279	2.76	1.83	13.77
1HGI.PDB	O, C_TYR_302	N, C_ILE_282	H, C_ILE_282	2.89	1.93	9.00
1HGI.PDB	O, C_THR_283	N, C_GLY_286	H, C_GLY_286	2.81	1.89	16.23
1HGI.PDB	O, C_LYS_50	N, C_SER_287	H, C_SER_287	2.84	1.87	3.21
1HGI.PDB	O, C_ALA_304	ND2, C_ASN_290	HD22, C_ASN_290	2.76	1.88	20.58
1HGI.PDB	OE1, C_GLN_44	NZ, C_LYS_292	HZ1, C_LYS_292	2.75	1.75	12.02
1HGI.PDB	OD2, C_ASP_291	NZ, C_LYS_292	HZ3, C_LYS_292	2.82	1.90	23.36
1HGI.PDB	O, C_LYS_307	N, C_GLN_295	H, C_GLN_295	2.80	1.92	20.79
1HGI.PDB	O, C_ASN_298	NE2, C_GLN_295	HE21, C_GLN_295	2.79	1.83	9.85
1HGI.PDB	O, C_GLN_44	N, C_ASN_296	H, C_ASN_296	2.86	1.93	14.90
1HGI.PDB	OE1, C_GLN_295	N, C_VAL_297	H, C_VAL_297	2.80	1.98	27.59
1HGI.PDB	OD1, C_ASN_285	ND2, C_ASN_298	HD22, C_ASN_298	3.00	2.03	7.73
1HGI.PDB	OD1, C_ASN_298	N, C_ILE_300	H, C_ILE_300	2.91	2.01	18.61
1HGI.PDB	O, C_ILE_282	N, C_TYR_302	H, C_TYR_302	2.94	2.06	21.76
1HGI.PDB	O, C_LYS_264	OH, C_TYR_302	HH, C_TYR_302	2.75	1.95	27.81
1HGI.PDB	O, D_LYS_62	N, C_GLY_303	H, C_GLY_303	2.97	2.00	7.92
1HGI.PDB	O, C_PRO_293	N, C_LYS_307	H, C_LYS_307	2.99	2.03	8.70
1HGI.PDB	O, C_GLN_295	N, C_VAL_309	H, C_VAL_309	2.93	2.08	24.45
1HGI.PDB	OD1, D_ASP_86	NZ, C_LYS_310	HZ3, C_LYS_310	2.77	1.93	29.51
1HGI.PDB	OE2, C_GLU_41	N, C_LEU_314	H, C_LEU_314	2.83	1.87	8.52
1HGI.PDB	OE1, C_GLU_41	NZ, C_LYS_315	HZ3, C_LYS_315	2.75	1.80	20.43
1HGI.PDB	O, C_THR_40	N, C_LEU_316	H, C_LEU_316	2.83	1.90	15.29
1HGI.PDB	OD1, D_ASN_104	N, C_ALA_317	H, C_ALA_317	2.74	1.83	16.29
1HGI.PDB	O, C_ASN_38	N, C_THR_318	H, C_THR_318	2.87	1.98	20.30
1HGI.PDB	O, C_VAL_20	ND2, C_ASN_322	HD21, C_ASN_322	2.87	1.94	14.86
1HGI.PDB	OE2, C_GLU_35	ND2, C_ASN_322	HD22, C_ASN_322	2.90	1.95	11.70
1HGI.PDB	OE1, D_GLU_15	NZ, C_LYS_326	HZ1, C_LYS_326	2.83	1.84	16.25
1HGI.PDB	OD2, D_ASP_112	N, D_GLY_1	H1, D_GLY_1	2.77	1.76	11.64
1HGI.PDB	OD1, D_ASP_109	N, D_LEU_2	H, D_LEU_2	2.92	1.97	13.20
1HGI.PDB	OD2, D_ASP_112	N, D_PHE_3	H, D_PHE_3	2.88	2.06	26.84
1HGI.PDB	OD2, D_ASP_112	N, D_GLY_4	H, D_GLY_4	2.95	2.06	19.72
1HGI.PDB	OD1, D_ASP_112	N, D_ALA_5	H, D_ALA_5	2.82	1.91	16.74
1HGI.PDB	O, D_GLY_4	N, D_PHE_9	H, D_PHE_9	2.83	1.89	12.42
1HGI.PDB	O, D_GLY_13	ND2, D_ASN_12	HD22, D_ASN_12	2.80	1.89	16.05
1HGI.PDB	O, C_VAL_323	N, D_GLY_13	H, D_GLY_13	2.65	1.77	19.23
1HGI.PDB	O, C_HIS_17	N, D_TRP_14	H, D_TRP_14	2.83	1.92	16.86
1HGI.PDB	OG1, D_THR_41	N, D_TRP_21	H, D_TRP_21	2.98	2.14	26.03
1HGI.PDB	O, C_GLY_16	N, D_GLY_23	H, D_GLY_23	2.94	2.02	16.89
1HGI.PDB	O, D_ALA_35	N, D_PHE_24	H, D_PHE_24	2.82	1.86	6.63
1HGI.PDB	O, C_CYS_14	N, D_ARG_25	H, D_ARG_25	2.88	1.94	13.44
1HGI.PDB	OE1, D_GLN_34	NE, D_ARG_25	HE, D_ARG_25	2.62	1.78	23.70
1HGI.PDB	O, D_GLY_33	N, D_HIS_26	H, D_HIS_26	2.88	1.93	11.28
1HGI.PDB	O, C_THR_12	N, D_GLN_27	H, D_GLN_27	2.95	2.00	13.47
1HGI.PDB	O, D_GLY_31	N, D_ASN_28	H, D_ASN_28	2.97	2.06	18.59

1HGI.PDB	OD1, D_ASN_146	ND2, D_ASN_28	HD21, D_ASN_28	2.93	1.98	12.39
1HGI.PDB	OD1, D_ASN_28	N, D_GLU_30	H, D_GLU_30	2.83	1.95	21.69
1HGI.PDB	O, D_HIS_26	N, D_GLY_33	H, D_GLY_33	2.99	2.10	20.01
1HGI.PDB	O, D_PHE_24	N, D_ALA_35	H, D_ALA_35	2.80	1.98	27.73
1HGI.PDB	O, D_TYR_22	N, D_ASP_37	H, D_ASP_37	2.72	1.78	11.42
1HGI.PDB	OD2, D_ASP_37	N, D_SER_40	H, D_SER_40	2.89	1.92	6.59
1HGI.PDB	OD2, D_ASP_37	OG, D_SER_40	HG, D_SER_40	2.78	1.93	23.19
1HGI.PDB	O, D_ASP_37	OG1, D_THR_41	HG1, D_THR_41	2.73	1.82	16.18
1HGI.PDB	OD1, D_ASP_46	NE2, D_GLN_42	HE22, D_GLN_42	2.88	2.01	23.38
1HGI.PDB	O, D_SER_40	N, D_ALA_44	H, D_ALA_44	2.93	1.95	3.19
1HGI.PDB	O, D_THR_41	N, D_ILE_45	H, D_ILE_45	2.97	2.03	13.52
1HGI.PDB	O, D_GLN_42	N, D_ASP_46	H, D_ASP_46	2.71	1.76	6.20
1HGI.PDB	O, D_ALA_43	NE2, D_GLN_47	HE22, D_GLN_47	2.88	1.96	16.19
1HGI.PDB	O, D_ILE_45	N, D_ASN_49	H, D_ASN_49	2.89	1.98	17.77
1HGI.PDB	O, D_ASP_46	N, D_GLY_50	H, D_GLY_50	2.98	2.04	15.66
1HGI.PDB	O, D_GLN_47	N, D_LYS_51	H, D_LYS_51	2.98	2.01	5.63
1HGI.PDB	OE1, D_GLU_103	NZ, D_LYS_51	HZ2, D_LYS_51	2.81	1.77	5.89
1HGI.PDB	ND1, D_HIS_106	NZ, D_LYS_51	HZ3, D_LYS_51	2.78	1.83	18.78
1HGI.PDB	O, D_ILE_48	N, D_LEU_52	H, D_LEU_52	2.93	2.01	16.44
1HGI.PDB	O, D_ASN_49	N, D_ASN_53	H, D_ASN_53	2.77	1.91	22.51
1HGI.PDB	O, A_THR_28	NE, D_ARG_54	HE, D_ARG_54	2.83	1.87	10.21
1HGI.PDB	OE1, D_GLU_57	NH1, D_ARG_54	HH11, D_ARG_54	2.85	1.86	11.80
1HGI.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.81	1.85	15.40
1HGI.PDB	OE2, D_GLU_61	NZ, D_LYS_58	HZ2, D_LYS_58	3.00	2.01	17.14
1HGI.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.83	1.85	2.78
1HGI.PDB	O, D_PHE_63	NE2, D_GLN_65	HE22, D_GLN_65	2.98	2.00	3.57
1HGI.PDB	O, C_LYS_299	NZ, D_LYS_68	HZ1, D_LYS_68	2.79	1.78	10.55
1HGI.PDB	OE2, D_GLU_85	NZ, D_LYS_68	HZ2, D_LYS_68	2.81	1.76	2.16
1HGI.PDB	OG, E_SER_107	N, D_ARG_76	H, D_ARG_76	2.89	1.92	9.17
1HGI.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.80	1.82	5.40
1HGI.PDB	OE2, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.78	1.76	4.18
1HGI.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.61	1.67	15.38
1HGI.PDB	OE1, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.76	1.77	8.75
1HGI.PDB	O, D_GLU_72	NE2, D_GLN_78	HE21, D_GLN_78	2.97	2.00	4.85
1HGI.PDB	OE1, D_GLU_74	NE2, D_GLN_78	HE22, D_GLN_78	2.92	1.95	8.47
1HGI.PDB	O, D_ASP_79	N, D_TYR_83	H, D_TYR_83	2.89	2.00	19.78
1HGI.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.69	1.81	20.41
1HGI.PDB	O, D_LEU_80	N, D_VAL_84	H, D_VAL_84	2.72	1.83	17.89
1HGI.PDB	O, D_LYS_82	N, D_ASP_86	H, D_ASP_86	2.90	1.94	8.30
1HGI.PDB	O, D_TYR_83	N, D_THR_87	H, D_THR_87	2.92	1.96	7.87
1HGI.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.66	1.64	7.30
1HGI.PDB	O, D_GLU_85	N, D_ILE_89	H, D_ILE_89	2.88	1.92	10.07
1HGI.PDB	O, D_ASP_86	N, D_ASP_90	H, D_ASP_90	2.97	2.00	6.24
1HGI.PDB	O, D_LYS_88	N, D_TRP_92	H, D_TRP_92	2.97	2.00	6.54
1HGI.PDB	O, D_ILE_89	N, D_SER_93	H, D_SER_93	2.87	1.94	14.13
1HGI.PDB	O, D_ILE_89	OG, D_SER_93	HG, D_SER_93	2.80	1.92	19.66
1HGI.PDB	O, D_ASP_90	N, D_TYR_94	H, D_TYR_94	2.93	2.00	16.49
1HGI.PDB	O, D_TRP_92	N, D_ALA_96	H, D_ALA_96	2.93	1.97	9.70
1HGI.PDB	O, D_TYR_94	N, D_LEU_98	H, D_LEU_98	2.90	1.94	9.34
1HGI.PDB	O, D_ASN_95	N, D_LEU_99	H, D_LEU_99	2.84	1.96	21.05
1HGI.PDB	O, D_LEU_98	N, D_LEU_102	H, D_LEU_102	2.99	2.02	4.46
1HGI.PDB	O, D_LEU_99	N, D_GLU_103	H, D_GLU_103	2.97	2.00	7.39
1HGI.PDB	O, D_VAL_100	N, D_ASN_104	H, D_ASN_104	2.87	1.91	10.16
1HGI.PDB	O, C_LYS_27	ND2, D_ASN_104	HD22, D_ASN_104	2.83	1.88	11.60
1HGI.PDB	O, D_LEU_102	N, D_HIS_106	H, D_HIS_106	2.93	2.00	15.62
1HGI.PDB	O, D_GLU_103	N, D_THR_107	H, D_THR_107	2.78	1.91	22.01
1HGI.PDB	O, D_ASN_104	N, D_ILE_108	H, D_ILE_108	2.95	2.00	10.44
1HGI.PDB	O, D_HIS_106	N, D_LEU_110	H, D_LEU_110	2.81	1.86	10.24

1HGI.PDB	O, D_THR_107	OG1, D_THR_111	HG1, D_THR_111	2.94	1.97	4.08
1HGI.PDB	O, D_ASP_109	N, D_SER_113	H, D_SER_113	2.82	1.87	9.43
1HGI.PDB	O, B_LEU_2	OG, D_SER_113	HG, D_SER_113	2.77	1.91	22.96
1HGI.PDB	O, D_LEU_110	N, D_GLU_114	H, D_GLU_114	2.96	2.00	9.06
1HGI.PDB	O, D_ASP_112	N, D_ASN_116	H, D_ASN_116	2.95	2.00	13.00
1HGI.PDB	O, D_SER_113	N, D_LYS_117	H, D_LYS_117	2.70	1.83	21.74
1HGI.PDB	O, D_ASN_116	N, D_GLU_120	H, D_GLU_120	2.92	1.95	4.03
1HGI.PDB	O, D_LYS_117	N, D_LYS_121	H, D_LYS_121	2.93	2.00	15.48
1HGI.PDB	OE2, D_GLU_120	NH1, D_ARG_123	HH11, D_ARG_123	2.83	1.97	25.69
1HGI.PDB	O, D_GLU_120	N, D_ARG_124	H, D_ARG_124	2.93	1.95	3.12
1HGI.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.84	1.98	23.95
1HGI.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.88	2.03	24.96
1HGI.PDB	O, D_LEU_126	N, D_ASN_129	H, D_ASN_129	3.00	2.06	14.34
1HGI.PDB	O, D_HIS_159	ND2, D_ASN_129	HD21, D_ASN_129	2.99	2.04	12.91
1HGI.PDB	OH, D_TYR_157	ND2, D_ASN_129	HD22, D_ASN_129	2.81	1.84	5.40
1HGI.PDB	O, D_LYS_139	N, D_GLU_131	H, D_GLU_131	2.93	2.00	14.77
1HGI.PDB	O, D_CYS_137	N, D_MET_133	H, D_MET_133	2.81	1.87	12.15
1HGI.PDB	OD1, D_ASN_135	N, D_CYS_137	H, D_CYS_137	2.87	1.99	20.31
1HGI.PDB	O, C_LEU_13	N, D_PHE_138	H, D_PHE_138	2.79	1.92	22.46
1HGI.PDB	O, D_GLU_131	N, D_LYS_139	H, D_LYS_139	2.79	1.84	9.37
1HGI.PDB	O, C_ALA_11	N, D_ILE_140	H, D_ILE_140	2.81	1.91	18.30
1HGI.PDB	O, D_ASN_129	N, D_TYR_141	H, D_TYR_141	2.85	1.88	4.18
1HGI.PDB	OE2, D_GLU_165	N, D_LYS_143	H, D_LYS_143	2.89	1.96	16.92
1HGI.PDB	OE2, D_GLU_30	N, D_ASN_146	H, D_ASN_146	2.90	1.95	12.47
1HGI.PDB	O, D_ASP_145	N, D_ILE_149	H, D_ILE_149	2.94	1.98	8.42
1HGI.PDB	O, D_ASN_146	N, D_GLU_150	H, D_GLU_150	2.83	1.93	18.07
1HGI.PDB	O, D_ALA_147	N, D_SER_151	H, D_SER_151	2.92	2.00	16.50
1HGI.PDB	O, D_CYS_148	OG, D_SER_151	HG, D_SER_151	2.71	1.85	21.05
1HGI.PDB	O, D_GLU_150	N, D_ASN_154	H, D_ASN_154	2.81	1.83	1.56
1HGI.PDB	O, D_SER_151	N, D_THR_156	H, D_THR_156	2.80	1.97	25.47
1HGI.PDB	OD1, D_ASN_154	OG1, D_THR_156	HG1, D_THR_156	2.68	1.79	17.62
1HGI.PDB	NE2, D_HIS_142	OH, D_TYR_157	HH, D_TYR_157	2.72	1.85	20.80
1HGI.PDB	O, D_HIS_159	N, D_TYR_162	H, D_TYR_162	2.90	2.02	21.56
1HGI.PDB	O, B_ARG_170	NH1, D_ARG_163	HH12, D_ARG_163	2.80	1.83	13.94
1HGI.PDB	O, D_TYR_162	N, D_ALA_166	H, D_ALA_166	2.86	1.89	1.04
1HGI.PDB	O, D_ARG_163	N, D_LEU_167	H, D_LEU_167	2.77	1.81	6.36
1HGI.PDB	O, D_ALA_166	N, D_ARG_170	H, D_ARG_170	2.80	1.93	22.25
1HGI.PDB	O, D_GLU_128	NE, D_ARG_170	HE, D_ARG_170	2.72	1.87	25.38
1HGI.PDB	OE2, D_GLU_131	NH1, D_ARG_170	HH11, D_ARG_170	2.77	1.78	6.80
1HGI.PDB	O, D_LEU_167	N, D_PHE_171	H, D_PHE_171	2.90	1.96	13.08
1HGI.PDB	O, F_ILE_140	N, E_ALA_11	H, E_ALA_11	2.89	1.95	14.83
1HGI.PDB	O, F_GLN_27	N, E_THR_12	H, E_THR_12	2.94	2.00	13.31
1HGI.PDB	O, F_PHE_138	N, E_LEU_13	H, E_LEU_13	2.97	2.02	11.46
1HGI.PDB	O, F_ARG_25	N, E_CYS_14	H, E_CYS_14	2.66	1.84	26.53
1HGI.PDB	O, F_GLY_136	N, E_LEU_15	H, E_LEU_15	2.92	1.95	6.28
1HGI.PDB	O, F_GLY_23	N, E_GLY_16	H, E_GLY_16	2.99	2.12	22.78
1HGI.PDB	O, E_HIS_18	ND1, E_HIS_17	HD1, E_HIS_17	2.91	2.01	19.98
1HGI.PDB	O, F_TRP_21	N, E_HIS_18	H, E_HIS_18	2.89	1.99	19.14
1HGI.PDB	OD1, E_ASN_322	N, E_VAL_20	H, E_VAL_20	2.75	1.81	12.01
1HGI.PDB	O, E_VAL_36	N, E_THR_24	H, E_THR_24	2.83	1.90	13.27
1HGI.PDB	O, E_ILE_34	N, E_VAL_26	H, E_VAL_26	2.80	1.85	10.53
1HGI.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.86	1.82	7.44
1HGI.PDB	O, E_ASP_31	N, E_THR_28	H, E_THR_28	2.81	2.00	28.11
1HGI.PDB	O, E_VAL_26	N, E_ILE_34	H, E_ILE_34	2.91	2.01	19.08
1HGI.PDB	O, E_THR_24	N, E_VAL_36	H, E_VAL_36	2.78	1.82	6.19
1HGI.PDB	O, E_MET_320	N, E_THR_37	H, E_THR_37	2.83	1.86	7.80
1HGI.PDB	O, E_LEU_316	N, E_THR_40	H, E_THR_40	2.86	1.98	21.93
1HGI.PDB	O, E_LEU_314	N, E_LEU_42	H, E_LEU_42	2.82	1.95	22.62

1HGI.PDB	O, E_PHE_294	N, E_GLN_44	H, E_GLN_44	2.83	1.86	6.11
1HGI.PDB	O, E_SER_46	NE2, E_GLN_44	HE22, E_GLN_44	2.78	1.97	27.44
1HGI.PDB	O, E_ASN_285	OG, E_SER_47	HG, E_SER_47	2.82	1.91	15.52
1HGI.PDB	OD2, E_ASP_275	NZ, E_LYS_50	HZ1, E_LYS_50	2.70	1.78	22.89
1HGI.PDB	O, E_PRO_273	N, E_ILE_51	H, E_ILE_51	2.78	1.83	10.95
1HGI.PDB	O, E_ASP_275	N, E_ASN_53	H, E_ASN_53	2.86	2.00	23.91
1HGI.PDB	O, E_GLU_280	NE2, E_HIS_56	HE2, E_HIS_56	3.00	2.06	15.06
1HGI.PDB	OD2, E_ASP_85	N, E_ARG_57	H, E_ARG_57	2.84	1.90	11.96
1HGI.PDB	O, E_THR_83	NE, E_ARG_57	HE, E_ARG_57	2.81	1.83	5.10
1HGI.PDB	O, E_LEU_86	N, E_LEU_59	H, E_LEU_59	2.85	1.89	9.90
1HGI.PDB	O, E_VAL_88	N, E_GLY_61	H, E_GLY_61	2.94	2.11	26.55
1HGI.PDB	OD1, E_ASP_60	N, E_ILE_62	H, E_ILE_62	2.85	1.91	12.99
1HGI.PDB	O, E_GLY_61	N, E_CYS_64	H, E_CYS_64	2.89	1.99	18.65
1HGI.PDB	OE2, E_GLU_89	N, E_LEU_66	H, E_LEU_66	2.99	2.04	13.34
1HGI.PDB	O, E_LEU_66	N, E_LEU_70	H, E_LEU_70	2.83	1.95	21.53
1HGI.PDB	O, E_ILE_67	N, E_LEU_71	H, E_LEU_71	2.87	1.90	5.23
1HGI.PDB	O, E_ASP_68	N, E_GLY_72	H, E_GLY_72	2.81	1.87	13.53
1HGI.PDB	OD1, E_ASP_73	ND1, E_HIS_75	HD1, E_HIS_75	2.87	1.94	15.26
1HGI.PDB	O, E_ASP_63	NE2, E_HIS_75	HE2, E_HIS_75	2.82	1.88	13.89
1HGI.PDB	O, E_ASP_73	N, E_CYS_76	H, E_CYS_76	2.75	1.83	16.25
1HGI.PDB	O, E_PRO_74	N, E_ASP_77	H, E_ASP_77	2.91	1.96	9.76
1HGI.PDB	O, E_CYS_76	N, E_PHE_79	H, E_PHE_79	2.93	1.96	3.56
1HGI.PDB	OE1, E_GLU_82	N, E_THR_83	H, E_THR_83	2.89	2.00	21.36
1HGI.PDB	O, E_ARG_57	N, E_ASP_85	H, E_ASP_85	2.76	1.87	19.11
1HGI.PDB	O, E_MET_268	N, E_GLU_89	H, E_GLU_89	2.77	1.81	7.27
1HGI.PDB	OD1, E_ASP_60	NE, E_ARG_90	HE, E_ARG_90	2.89	1.92	8.33
1HGI.PDB	O, E_SER_270	NH1, E_ARG_90	HH11, E_ARG_90	2.67	1.80	24.87
1HGI.PDB	O, E_ALA_272	NH1, E_ARG_90	HH12, E_ARG_90	2.58	1.69	21.42
1HGI.PDB	OD2, E_ASP_60	NH2, E_ARG_90	HH21, E_ARG_90	2.84	1.85	10.04
1HGI.PDB	OD1, E_ASP_271	N, E_SER_91	H, E_SER_91	2.90	1.95	11.41
1HGI.PDB	OD1, E_ASP_271	OG, E_SER_91	HG, E_SER_91	2.94	2.11	26.21
1HGI.PDB	OD2, E_ASP_271	OG, E_SER_91	HG, E_SER_91	2.82	1.93	20.43
1HGI.PDB	OD2, E_ASP_68	OG, E_SER_95	HG, E_SER_95	2.90	1.96	13.54
1HGI.PDB	OD2, E_ASP_73	N, E_ASN_96	H, E_ASN_96	2.90	1.96	13.19
1HGI.PDB	OD1, E_ASP_68	OH, E_TYR_100	HH, E_TYR_100	2.94	1.98	8.32
1HGI.PDB	OD2, E_ASP_104	OG, E_SER_107	HG, E_SER_107	2.91	1.98	14.52
1HGI.PDB	O, E_TYR_105	N, E_ARG_109	H, E_ARG_109	2.90	1.93	4.30
1HGI.PDB	OE2, E_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.78	1.80	14.37
1HGI.PDB	OD2, E_ASP_79	OG, E_SER_110	HG, E_SER_110	2.90	1.94	10.08
1HGI.PDB	O, E_SER_107	N, E_LEU_111	H, E_LEU_111	2.87	1.91	6.91
1HGI.PDB	O, E_LEU_108	N, E_VAL_112	H, E_VAL_112	2.97	1.99	3.20
1HGI.PDB	O, E_ARG_109	N, E_ALA_113	H, E_ALA_113	2.98	2.07	18.10
1HGI.PDB	O, E_SER_110	N, E_SER_114	H, E_SER_114	2.94	2.00	13.83
1HGI.PDB	OE2, E_GLU_119	OG1, E_THR_117	HG1, E_THR_117	2.98	2.05	12.54
1HGI.PDB	O, E_GLU_82	N, E_LEU_118	H, E_LEU_118	2.91	1.97	15.20
1HGI.PDB	O, E_TYR_257	N, E_ILE_121	H, E_ILE_121	2.92	1.95	7.25
1HGI.PDB	O, E_ARG_255	N, E_GLU_123	H, E_GLU_123	2.89	1.94	11.77
1HGI.PDB	O, E_THR_155	N, E_THR_131	H, E_THR_131	2.77	1.89	21.32
1HGI.PDB	OD1, E_ASN_152	N, E_ASN_133	H, E_ASN_133	2.84	1.93	17.00
1HGI.PDB	O, E_GLY_146	N, E_SER_136	H, E_SER_136	2.77	1.88	19.62
1HGI.PDB	OG, E_SER_136	N, E_ALA_138	H, E_ALA_138	2.87	1.96	18.10
1HGI.PDB	O, E_GLY_144	NZ, E_LYS_140	HZ1, E_LYS_140	2.89	1.92	16.40
1HGI.PDB	OD1, E_ASN_137	NZ, E_LYS_140	HZ2, E_LYS_140	2.83	1.82	12.93
1HGI.PDB	OD2, E_ASP_77	NE, E_ARG_141	HE, E_ARG_141	2.83	2.01	29.05
1HGI.PDB	O, E_PHE_147	NH1, E_ARG_141	HH12, E_ARG_141	2.55	1.65	20.15
1HGI.PDB	OD1, E_ASP_77	NH2, E_ARG_141	HH21, E_ARG_141	2.94	2.01	20.45
1HGI.PDB	OD2, E_ASP_77	NH2, E_ARG_141	HH21, E_ARG_141	2.70	1.83	24.80
1HGI.PDB	O, E_GLY_72	NH2, E_ARG_141	HH22, E_ARG_141	2.98	2.00	9.93

1HGI.PDB	OD1, E_ASN_137	OG, E_SER_145	HG, E_SER_145	2.92	2.15	29.94
1HGI.PDB	O, E_SER_136	N, E_GLY_146	H, E_GLY_146	2.98	2.04	14.06
1HGI.PDB	O, E_GLY_72	N, E_SER_149	H, E_SER_149	2.92	1.99	15.35
1HGI.PDB	O, E_ALA_253	N, E_ASN_152	H, E_ASN_152	2.77	1.92	24.49
1HGI.PDB	OH, E_TYR_195	NE1, E_TRP_153	HE1, E_TRP_153	2.87	1.98	20.67
1HGI.PDB	O, E_LEU_194	N, E_LYS_156	H, E_LYS_156	2.89	2.00	19.98
1HGI.PDB	O, E_SER_193	NZ, E_LYS_156	HZ2, E_LYS_156	2.74	1.75	15.56
1HGI.PDB	O, E_THR_160	N, E_SER_157	H, E_SER_157	2.90	2.00	19.80
1HGI.PDB	O, E_SER_247	N, E_LEU_164	H, E_LEU_164	2.73	1.89	25.21
1HGI.PDB	O, E_ILE_245	N, E_VAL_166	H, E_VAL_166	2.92	1.98	12.27
1HGI.PDB	O, E_LEU_243	OG1, E_THR_167	HG1, E_THR_167	2.89	2.00	19.18
1HGI.PDB	O, E_LEU_243	N, E_MET_168	H, E_MET_168	2.98	2.05	15.68
1HGI.PDB	O, E_ASP_241	N, E_ASN_170	H, E_ASN_170	2.96	1.98	4.05
1HGI.PDB	O, E_PHE_174	ND2, E_ASN_170	HD21, E_ASN_170	2.85	1.90	12.31
1HGI.PDB	O, E_VAL_237	ND2, E_ASN_170	HD22, E_ASN_170	2.95	2.11	25.03
1HGI.PDB	O, E_VAL_237	N, E_LYS_176	H, E_LYS_176	2.94	2.00	12.53
1HGI.PDB	OE2, E_GLU_123	NZ, E_LYS_176	HZ1, E_LYS_176	2.69	1.80	25.89
1HGI.PDB	O, E_PHE_258	N, E_LEU_177	H, E_LEU_177	2.98	2.01	8.00
1HGI.PDB	O, E_THR_235	N, E_TYR_178	H, E_TYR_178	2.83	1.86	3.40
1HGI.PDB	OE1, E_GLU_123	OH, E_TYR_178	HH, E_TYR_178	2.77	1.82	8.27
1HGI.PDB	OG1, E_THR_235	NE1, E_TRP_180	HE1, E_TRP_180	2.85	1.87	2.03
1HGI.PDB	O, E_ASN_250	N, E_HIS_183	H, E_HIS_183	2.94	2.04	20.19
1HGI.PDB	O, E_ARG_229	N, E_HIS_184	H, E_HIS_184	2.89	1.93	8.27
1HGI.PDB	OG, E_SER_231	NE2, E_HIS_184	HE2, E_HIS_184	2.81	1.95	23.57
1HGI.PDB	OD1, E_ASN_250	NE2, E_GLN_191	HE21, E_GLN_191	2.93	1.97	10.64
1HGI.PDB	O, E_GLN_197	NE2, E_GLN_191	HE22, E_GLN_191	2.95	1.99	10.71
1HGI.PDB	O, E_ASN_188	N, E_THR_192	H, E_THR_192	2.98	2.03	12.25
1HGI.PDB	O, E_ASN_188	OG1, E_THR_192	HG1, E_THR_192	2.95	1.99	2.99
1HGI.PDB	O, E_GLN_189	N, E_SER_193	H, E_SER_193	2.85	1.88	3.98
1HGI.PDB	O, E_GLN_191	N, E_TYR_195	H, E_TYR_195	2.76	1.80	5.82
1HGI.PDB	O, E_TYR_161	NE2, E_GLN_197	HE21, E_GLN_197	3.00	2.04	10.17
1HGI.PDB	O, E_ASN_248	NE2, E_GLN_197	HE22, E_GLN_197	2.91	2.00	18.24
1HGI.PDB	OD1, E_ASN_246	NH2, E_ARG_201	HH21, E_ARG_201	2.57	1.74	27.51
1HGI.PDB	O, E_ILE_213	N, E_VAL_202	H, E_VAL_202	2.95	1.98	8.47
1HGI.PDB	O, E_ASN_246	N, E_THR_203	H, E_THR_203	2.89	1.92	4.39
1HGI.PDB	O, E_GLN_211	N, E_VAL_204	H, E_VAL_204	2.85	1.92	15.24
1HGI.PDB	O, E_VAL_244	N, E_SER_205	H, E_SER_205	2.97	2.05	16.25
1HGI.PDB	O, E_SER_209	N, E_THR_206	H, E_THR_206	2.94	1.97	8.14
1HGI.PDB	OD1, E_ASP_241	N, E_ARG_207	H, E_ARG_207	2.91	1.95	10.57
1HGI.PDB	OD2, E_ASP_241	NE, E_ARG_208	HE, E_ARG_208	2.98	2.07	19.52
1HGI.PDB	O, E_VAL_204	N, E_GLN_211	H, E_GLN_211	2.91	1.97	13.40
1HGI.PDB	O, E_VAL_202	N, E_ILE_213	H, E_ILE_213	2.85	1.92	15.12
1HGI.PDB	ND1, E_HIS_184	N, E_ASN_216	H, E_ASN_216	2.74	1.94	28.99
1HGI.PDB	O, E_ASN_216	NH1, E_ARG_220	HH12, E_ARG_220	2.87	2.06	29.75
1HGI.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.69	1.80	23.03
1HGI.PDB	O, E_ASN_216	NH2, E_ARG_220	HH22, E_ARG_220	2.70	1.80	21.47
1HGI.PDB	O, E_LEU_226	N, E_VAL_223	H, E_VAL_223	2.88	1.90	5.13
1HGI.PDB	O, E_CYS_97	NE, E_ARG_224	HE, E_ARG_224	2.81	1.97	26.09
1HGI.PDB	O, E_CYS_97	NH2, E_ARG_224	HH21, E_ARG_224	2.85	1.99	25.73
1HGI.PDB	O, E_VAL_223	N, E_LEU_226	H, E_LEU_226	2.93	2.00	15.87
1HGI.PDB	O, E_SER_228	NH1, E_ARG_229	HH11, E_ARG_229	2.68	1.75	18.51
1HGI.PDB	O, E_PRO_221	NH2, E_ARG_229	HH22, E_ARG_229	2.66	1.70	13.51
1HGI.PDB	OD1, E_ASP_101	OG, E_SER_231	HG, E_SER_231	2.99	2.05	12.53
1HGI.PDB	O, E_ASP_101	N, E_ILE_232	H, E_ILE_232	2.94	2.00	13.40
1HGI.PDB	O, E_TRP_180	N, E_TYR_233	H, E_TYR_233	2.90	1.93	7.29
1HGI.PDB	O, E_TYR_178	N, E_THR_235	H, E_THR_235	2.82	1.92	19.31
1HGI.PDB	O, E_LYS_176	N, E_VAL_237	H, E_VAL_237	2.80	1.86	13.21
1HGI.PDB	O, D_SER_71	NZ, E_LYS_238	HZ2, E_LYS_238	2.75	1.87	26.62

1HGI.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ3, E_LYS_238	2.80	1.81	15.90
1HGI.PDB	O, E_ASN_170	N, E_GLY_240	H, E_GLY_240	2.90	2.05	25.02
1HGI.PDB	OD1, E_ASP_241	N, E_VAL_242	H, E_VAL_242	2.76	1.96	28.65
1HGI.PDB	O, E_MET_168	N, E_LEU_243	H, E_LEU_243	2.92	1.95	5.56
1HGI.PDB	O, E_SER_205	N, E_VAL_244	H, E_VAL_244	2.99	2.04	11.95
1HGI.PDB	O, E_THR_203	N, E_ASN_246	H, E_ASN_246	2.86	1.93	15.06
1HGI.PDB	O, E_LEU_164	N, E_SER_247	H, E_SER_247	2.89	1.98	17.96
1HGI.PDB	O, E_ARG_201	OG, E_SER_247	HG, E_SER_247	2.86	2.05	28.14
1HGI.PDB	OE1, E_GLN_191	ND2, E_ASN_250	HD21, E_ASN_250	2.90	1.94	10.02
1HGI.PDB	O, E_HIS_183	ND2, E_ASN_250	HD22, E_ASN_250	2.84	1.87	6.39
1HGI.PDB	O, E_ASN_152	N, E_ALA_253	H, E_ALA_253	2.82	1.94	21.84
1HGI.PDB	O, E_ILE_121	N, E_TYR_257	H, E_TYR_257	2.96	2.09	22.80
1HGI.PDB	O, E_LEU_177	N, E_PHE_258	H, E_PHE_258	2.90	1.94	8.58
1HGI.PDB	OE2, E_GLU_119	NH1, E_ARG_261	HH12, E_ARG_261	2.65	1.83	28.50
1HGI.PDB	OE1, E_GLU_119	NH2, E_ARG_261	HH22, E_ARG_261	2.84	1.99	27.52
1HGI.PDB	OD2, E_ASP_85	NZ, E_LYS_264	HZ3, E_LYS_264	2.86	1.87	16.39
1HGI.PDB	O, E_ASP_85	N, E_SER_266	H, E_SER_266	2.99	2.14	25.54
1HGI.PDB	O, E_PHE_87	N, E_MET_268	H, E_MET_268	2.85	1.97	21.63
1HGI.PDB	O, E_PRO_284	OG, E_SER_270	HG, E_SER_270	2.79	1.85	10.23
1HGI.PDB	OG, E_SER_270	N, E_ALA_272	H, E_ALA_272	2.98	2.03	12.01
1HGI.PDB	O, E_ILE_51	N, E_ASP_275	H, E_ASP_275	2.93	2.03	19.68
1HGI.PDB	OD1, E_ASP_275	N, E_THR_276	H, E_THR_276	2.83	1.98	25.02
1HGI.PDB	O, E_ASN_54	N, E_SER_279	H, E_SER_279	2.79	1.86	14.40
1HGI.PDB	O, E_TYR_302	N, E_ILE_282	H, E_ILE_282	2.87	1.91	9.87
1HGI.PDB	O, E_THR_283	N, E_GLY_286	H, E_GLY_286	2.80	1.87	13.74
1HGI.PDB	O, E_LYS_50	N, E_SER_287	H, E_SER_287	2.85	1.88	3.05
1HGI.PDB	O, E_ALA_304	ND2, E_ASN_290	HD22, E_ASN_290	2.75	1.86	20.40
1HGI.PDB	OE1, E_GLN_44	NZ, E_LYS_292	HZ1, E_LYS_292	2.73	1.72	12.13
1HGI.PDB	OD2, E_ASP_291	NZ, E_LYS_292	HZ3, E_LYS_292	2.87	1.94	23.09
1HGI.PDB	O, E_LYS_307	N, E_GLN_295	H, E_GLN_295	2.79	1.91	21.81
1HGI.PDB	O, E_ASN_298	NE2, E_GLN_295	HE21, E_GLN_295	2.78	1.83	10.67
1HGI.PDB	O, E_GLN_44	N, E_ASN_296	H, E_ASN_296	2.87	1.95	15.01
1HGI.PDB	OE1, E_GLN_295	N, E_VAL_297	H, E_VAL_297	2.74	1.92	27.74
1HGI.PDB	OD1, E_ASN_285	ND2, E_ASN_298	HD22, E_ASN_298	2.97	2.00	7.97
1HGI.PDB	OD1, E_ASN_298	N, E_ILE_300	H, E_ILE_300	2.91	1.99	17.07
1HGI.PDB	O, E_ILE_282	N, E_TYR_302	H, E_TYR_302	2.94	2.05	21.12
1HGI.PDB	O, E_LYS_264	OH, E_TYR_302	HH, E_TYR_302	2.73	1.93	27.81
1HGI.PDB	O, F_LYS_62	N, E_GLY_303	H, E_GLY_303	2.93	1.96	6.65
1HGI.PDB	O, E_PRO_293	N, E_LYS_307	H, E_LYS_307	2.98	2.02	9.39
1HGI.PDB	O, E_GLN_295	N, E_VAL_309	H, E_VAL_309	2.93	2.07	24.14
1HGI.PDB	OG, F_SER_93	N, E_LYS_310	H, E_LYS_310	2.99	2.05	13.79
1HGI.PDB	OD1, F_ASP_86	NZ, E_LYS_310	HZ3, E_LYS_310	2.76	1.91	29.16
1HGI.PDB	OE2, E_GLU_41	N, E_LEU_314	H, E_LEU_314	2.84	1.88	8.62
1HGI.PDB	OE1, E_GLU_41	NZ, E_LYS_315	HZ3, E_LYS_315	2.74	1.81	21.50
1HGI.PDB	O, E_THR_40	N, E_LEU_316	H, E_LEU_316	2.81	1.89	15.98
1HGI.PDB	OD1, F_ASN_104	N, E_ALA_317	H, E_ALA_317	2.72	1.81	15.78
1HGI.PDB	O, E_ASN_38	N, E_THR_318	H, E_THR_318	2.88	1.97	18.20
1HGI.PDB	O, E_VAL_20	ND2, E_ASN_322	HD21, E_ASN_322	2.90	1.97	15.71
1HGI.PDB	OE2, E_GLU_35	ND2, E_ASN_322	HD22, E_ASN_322	2.92	1.96	12.59
1HGI.PDB	O, E_GLN_327	NZ, E_LYS_326	HZ1, E_LYS_326	2.69	1.77	22.48
1HGI.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.88	1.86	11.05
1HGI.PDB	O, E_LYS_326	NE2, E_GLN_327	HE22, E_GLN_327	2.82	1.87	11.22
1HGI.PDB	OD2, F_ASP_112	N, F_GLY_1	H1, F_GLY_1	2.78	1.77	11.25
1HGI.PDB	OD1, F_ASP_109	N, F_LEU_2	H, F_LEU_2	2.91	1.97	13.16
1HGI.PDB	OD2, F_ASP_112	N, F_PHE_3	H, F_PHE_3	2.84	2.03	27.46
1HGI.PDB	OD2, F_ASP_112	N, F_GLY_4	H, F_GLY_4	2.93	2.03	18.14
1HGI.PDB	OD1, F_ASP_112	N, F_ALA_5	H, F_ALA_5	2.81	1.90	16.38
1HGI.PDB	O, F_GLY_4	N, F_PHE_9	H, F_PHE_9	2.85	1.90	11.24

1HGI.PDB	O, F_GLY_13	ND2, F_ASN_12	HD22, F_ASN_12	2.79	1.91	21.41
1HGI.PDB	O, E_VAL_323	N, F_GLY_13	H, F_GLY_13	2.66	1.77	18.62
1HGI.PDB	O, E_HIS_17	N, F_TRP_14	H, F_TRP_14	2.84	1.93	16.42
1HGI.PDB	OG1, F_THR_41	N, F_TRP_21	H, F_TRP_21	2.99	2.14	24.96
1HGI.PDB	O, E_GLY_16	N, F_GLY_23	H, F_GLY_23	2.97	2.05	16.89
1HGI.PDB	O, F_ALA_35	N, F_PHE_24	H, F_PHE_24	2.82	1.85	6.25
1HGI.PDB	O, E_CYS_14	N, F_ARG_25	H, F_ARG_25	2.91	2.04	22.96
1HGI.PDB	OE1, F_GLN_34	NH2, F_ARG_25	HH21, F_ARG_25	2.91	1.98	18.85
1HGI.PDB	O, F_GLY_33	N, F_HIS_26	H, F_HIS_26	2.85	1.94	17.98
1HGI.PDB	O, E_THR_12	N, F_GLN_27	H, F_GLN_27	2.93	1.99	14.92
1HGI.PDB	O, F_GLY_31	N, F_ASN_28	H, F_ASN_28	2.87	1.90	8.27
1HGI.PDB	OD1, F_ASN_146	ND2, F_ASN_28	HD21, F_ASN_28	2.93	2.01	16.48
1HGI.PDB	O, F_CYS_144	ND2, F_ASN_28	HD22, F_ASN_28	3.00	2.14	23.86
1HGI.PDB	O, F_PHE_24	N, F_ALA_35	H, F_ALA_35	2.77	1.97	29.03
1HGI.PDB	O, F_TYR_22	N, F_ASP_37	H, F_ASP_37	2.70	1.78	13.02
1HGI.PDB	OD2, F_ASP_37	N, F_SER_40	H, F_SER_40	2.93	1.96	6.56
1HGI.PDB	OD2, F_ASP_37	OG, F_SER_40	HG, F_SER_40	2.76	1.92	24.70
1HGI.PDB	O, F_ASP_37	OG1, F_THR_41	HG1, F_THR_41	2.70	1.81	18.66
1HGI.PDB	O, F_LEU_38	N, F_GLN_42	H, F_GLN_42	3.00	2.08	17.54
1HGI.PDB	OD1, F_ASP_46	NE2, F_GLN_42	HE22, F_GLN_42	2.86	1.99	23.93
1HGI.PDB	O, F_LYS_39	N, F_ALA_43	H, F_ALA_43	2.96	2.00	7.28
1HGI.PDB	O, F_SER_40	N, F_ALA_44	H, F_ALA_44	2.94	1.96	3.55
1HGI.PDB	O, F_THR_41	N, F_ILE_45	H, F_ILE_45	2.94	2.00	13.26
1HGI.PDB	O, F_GLN_42	N, F_ASP_46	H, F_ASP_46	2.71	1.76	8.22
1HGI.PDB	O, F_ALA_43	NE2, F_GLN_47	HE22, F_GLN_47	2.92	1.99	15.42
1HGI.PDB	O, F_ILE_45	N, F_ASN_49	H, F_ASN_49	2.88	1.98	19.70
1HGI.PDB	O, F_ASP_46	N, F_GLY_50	H, F_GLY_50	2.94	2.01	15.37
1HGI.PDB	OE1, F_GLU_103	NZ, F_LYS_51	HZ2, F_LYS_51	2.80	1.76	5.82
1HGI.PDB	ND1, F_HIS_106	NZ, F_LYS_51	HZ3, F_LYS_51	2.75	1.80	19.60
1HGI.PDB	O, F_ILE_48	N, F_LEU_52	H, F_LEU_52	2.96	2.03	15.82
1HGI.PDB	O, F_ASN_49	N, F_ASN_53	H, F_ASN_53	2.80	1.95	24.38
1HGI.PDB	O, C_THR_28	NE, F_ARG_54	HE, F_ARG_54	2.95	1.99	9.70
1HGI.PDB	OE1, F_GLU_57	NH1, F_ARG_54	HH11, F_ARG_54	2.83	1.84	11.68
1HGI.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.75	1.79	14.82
1HGI.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.84	1.87	3.62
1HGI.PDB	O, E_LYS_299	NZ, F_LYS_68	HZ1, F_LYS_68	2.80	1.76	2.37
1HGI.PDB	OE2, F_GLU_85	NZ, F_LYS_68	HZ2, F_LYS_68	2.74	1.72	8.70
1HGI.PDB	OG, A_SER_107	N, F_ARG_76	H, F_ARG_76	2.79	1.83	7.22
1HGI.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.85	1.88	7.37
1HGI.PDB	OE2, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.77	1.76	3.93
1HGI.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.64	1.66	4.79
1HGI.PDB	OE1, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.76	1.78	10.40
1HGI.PDB	O, F_GLU_72	NE2, F_GLN_78	HE21, F_GLN_78	2.93	1.96	6.67
1HGI.PDB	OE1, F_GLU_74	NE2, F_GLN_78	HE22, F_GLN_78	2.95	1.98	8.40
1HGI.PDB	O, F_ASP_79	N, F_TYR_83	H, F_TYR_83	2.90	1.99	17.92
1HGI.PDB	OE1, B_GLU_85	OH, F_TYR_83	HH, F_TYR_83	2.58	1.75	24.06
1HGI.PDB	O, F_LEU_80	N, F_VAL_84	H, F_VAL_84	2.77	1.86	16.15
1HGI.PDB	O, F_LYS_82	N, F_ASP_86	H, F_ASP_86	2.91	1.96	11.16
1HGI.PDB	O, F_TYR_83	N, F_THR_87	H, F_THR_87	2.92	1.97	10.81
1HGI.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.61	1.62	12.49
1HGI.PDB	O, F_GLU_85	N, F_ILE_89	H, F_ILE_89	2.88	1.92	9.04
1HGI.PDB	O, F_LYS_88	N, F_TRP_92	H, F_TRP_92	2.96	1.99	7.36
1HGI.PDB	O, F_ILE_89	N, F_SER_93	H, F_SER_93	2.88	1.94	13.75
1HGI.PDB	O, F_ILE_89	OG, F_SER_93	HG, F_SER_93	2.83	1.94	18.22
1HGI.PDB	O, F_ASP_90	N, F_TYR_94	H, F_TYR_94	2.93	2.00	16.36
1HGI.PDB	O, F_TRP_92	N, F_ALA_96	H, F_ALA_96	2.93	1.97	9.62
1HGI.PDB	O, F_TYR_94	N, F_LEU_98	H, F_LEU_98	2.91	1.95	9.75
1HGI.PDB	O, F_ASN_95	N, F_LEU_99	H, F_LEU_99	2.85	1.97	20.80

1HGI.PDB	O, F_LEU_99	N, F_GLU_103	H, F_GLU_103	2.93	1.96	7.51
1HGI.PDB	O, F_VAL_100	N, F_ASN_104	H, F_ASN_104	2.86	1.89	6.57
1HGI.PDB	O, E_LYS_27	ND2, F_ASN_104	HD22, F_ASN_104	2.88	1.93	10.77
1HGI.PDB	O, F_LEU_102	N, F_HIS_106	H, F_HIS_106	2.94	2.01	16.17
1HGI.PDB	O, F_GLU_103	N, F_THR_107	H, F_THR_107	2.77	1.88	20.29
1HGI.PDB	O, F_ASN_104	N, F_ILE_108	H, F_ILE_108	2.98	2.02	10.32
1HGI.PDB	O, F_HIS_106	N, F_LEU_110	H, F_LEU_110	2.83	1.87	10.55
1HGI.PDB	O, F_THR_107	OG1, F_THR_111	HG1, F_THR_111	2.97	2.00	2.90
1HGI.PDB	O, F_ASP_109	N, F_SER_113	H, F_SER_113	2.84	1.88	8.44
1HGI.PDB	O, D_LEU_2	OG, F_SER_113	HG, F_SER_113	2.78	1.94	24.17
1HGI.PDB	O, F_LEU_110	N, F_GLU_114	H, F_GLU_114	2.93	1.97	9.47
1HGI.PDB	O, F_THR_111	N, F_MET_115	H, F_MET_115	3.00	2.05	12.25
1HGI.PDB	O, F_ASP_112	N, F_ASN_116	H, F_ASN_116	2.97	2.03	13.76
1HGI.PDB	O, F_SER_113	N, F_LYS_117	H, F_LYS_117	2.72	1.85	21.38
1HGI.PDB	O, F_GLU_114	N, F_LEU_118	H, F_LEU_118	2.97	2.00	4.23
1HGI.PDB	O, F_ASN_116	N, F_GLU_120	H, F_GLU_120	2.90	1.92	4.14
1HGI.PDB	O, F_LYS_117	N, F_LYS_121	H, F_LYS_121	2.95	2.01	14.18
1HGI.PDB	O, F_LEU_118	OG1, F_THR_122	HG1, F_THR_122	2.94	1.99	9.77
1HGI.PDB	OE2, F_GLU_120	NH1, F_ARG_123	HH11, F_ARG_123	2.81	1.95	25.91
1HGI.PDB	O, F_GLU_120	N, F_ARG_124	H, F_ARG_124	2.91	1.93	3.14
1HGI.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.96	2.09	23.50
1HGI.PDB	OE2, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.96	2.09	23.34
1HGI.PDB	O, F_LEU_126	N, F_ASN_129	H, F_ASN_129	2.99	2.06	14.77
1HGI.PDB	OH, F_TYR_157	ND2, F_ASN_129	HD22, F_ASN_129	2.81	1.86	11.53
1HGI.PDB	O, F_LYS_139	N, F_GLU_131	H, F_GLU_131	2.91	1.97	13.98
1HGI.PDB	O, F_CYS_137	N, F_MET_133	H, F_MET_133	2.82	1.88	11.89
1HGI.PDB	O, E_LEU_13	N, F_PHE_138	H, F_PHE_138	2.75	1.89	22.82
1HGI.PDB	O, F_GLU_131	N, F_LYS_139	H, F_LYS_139	2.80	1.85	8.12
1HGI.PDB	O, E_ALA_11	N, F_ILE_140	H, F_ILE_140	2.78	1.89	18.92
1HGI.PDB	O, F_ASN_129	N, F_TYR_141	H, F_TYR_141	2.85	1.88	5.59
1HGI.PDB	OE2, F_GLU_165	N, F_LYS_143	H, F_LYS_143	2.88	1.95	16.12
1HGI.PDB	OE1, F_GLU_30	N, F_ASN_146	H, F_ASN_146	2.87	1.93	13.21
1HGI.PDB	O, F_ASP_145	N, F_ILE_149	H, F_ILE_149	2.92	1.96	7.67
1HGI.PDB	O, F_ASN_146	N, F_GLU_150	H, F_GLU_150	2.82	1.91	17.13
1HGI.PDB	O, F_ALA_147	N, F_SER_151	H, F_SER_151	2.94	2.03	17.96
1HGI.PDB	O, F_CYS_148	OG, F_SER_151	HG, F_SER_151	2.72	1.86	20.78
1HGI.PDB	O, F_GLU_150	N, F_ASN_154	H, F_ASN_154	2.78	1.81	2.53
1HGI.PDB	O, F_HIS_159	N, F_TYR_162	H, F_TYR_162	2.91	2.05	22.85
1HGI.PDB	O, D_ARG_170	NH1, F_ARG_163	HH12, F_ARG_163	2.92	1.95	13.55
1HGI.PDB	OE2, D_GLU_131	NH2, F_ARG_163	HH22, F_ARG_163	2.69	1.85	26.81
1HGI.PDB	O, F_TYR_162	N, F_ALA_166	H, F_ALA_166	2.89	1.91	1.45
1HGI.PDB	O, F_ARG_163	N, F_LEU_167	H, F_LEU_167	2.78	1.81	5.41
1HGI.PDB	O, F_ALA_166	N, F_ARG_170	H, F_ARG_170	2.82	1.95	21.63
1HGI.PDB	O, F_GLU_128	NE, F_ARG_170	HE, F_ARG_170	2.73	1.88	25.04
1HGI.PDB	OE2, F_GLU_131	NH1, F_ARG_170	HH11, F_ARG_170	2.75	1.76	6.67
1HGI.PDB	O, F_LEU_167	N, F_PHE_171	H, F_PHE_171	2.92	1.98	13.87
1HGJ.PDB	O, B_ILE_140	N, A_ALA_11	H, A_ALA_11	2.85	1.95	18.97
1HGJ.PDB	O, B_PHE_138	N, A_LEU_13	H, A_LEU_13	2.97	2.00	8.62
1HGJ.PDB	O, B_ARG_25	N, A_CYS_14	H, A_CYS_14	2.88	1.94	12.89
1HGJ.PDB	O, B_GLY_136	N, A_LEU_15	H, A_LEU_15	2.93	1.95	2.37
1HGJ.PDB	O, B_GLY_23	N, A_GLY_16	H, A_GLY_16	2.86	1.96	18.97
1HGJ.PDB	O, A_HIS_18	ND1, A_HIS_17	HD1, A_HIS_17	2.94	2.07	22.50
1HGJ.PDB	O, B_TRP_21	N, A_HIS_18	H, A_HIS_18	2.85	1.98	21.54
1HGJ.PDB	OD1, A_ASN_322	N, A_VAL_20	H, A_VAL_20	2.76	1.81	10.35
1HGJ.PDB	O, A_VAL_36	N, A_THR_24	H, A_THR_24	2.86	1.95	16.84
1HGJ.PDB	O, A_ILE_34	N, A_VAL_26	H, A_VAL_26	2.80	1.86	12.04
1HGJ.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.81	1.78	9.30
1HGJ.PDB	O, A_ASP_31	N, A_THR_28	H, A_THR_28	2.73	1.88	24.26

1HGJ.PDB	O, A_VAL_26	N, A_ILE_34	H, A_ILE_34	2.90	1.95	11.45
1HGJ.PDB	O, A_THR_24	N, A_VAL_36	H, A_VAL_36	2.81	1.84	5.48
1HGJ.PDB	O, A_MET_320	N, A_THR_37	H, A_THR_37	2.87	1.90	7.32
1HGJ.PDB	O, A_LEU_316	N, A_THR_40	H, A_THR_40	2.84	2.00	24.78
1HGJ.PDB	O, A_LEU_314	N, A_LEU_42	H, A_LEU_42	2.83	1.95	21.41
1HGJ.PDB	O, A_PHE_294	N, A_GLN_44	H, A_GLN_44	2.83	1.86	6.97
1HGJ.PDB	O, A_SER_46	NE2, A_GLN_44	HE22, A_GLN_44	2.92	2.02	20.25
1HGJ.PDB	OD2, A_ASP_275	NZ, A_LYS_50	HZ1, A_LYS_50	2.74	1.82	22.91
1HGJ.PDB	O, A_PRO_273	N, A_ILE_51	H, A_ILE_51	2.86	1.90	9.76
1HGJ.PDB	O, A_ASP_275	N, A_ASN_53	H, A_ASN_53	2.80	1.95	24.33
1HGJ.PDB	O, A_GLU_280	NE2, A_HIS_56	HE2, A_HIS_56	2.97	2.05	17.77
1HGJ.PDB	OD2, A_ASP_85	N, A_ARG_57	H, A_ARG_57	2.86	1.92	12.38
1HGJ.PDB	O, A_THR_83	NE, A_ARG_57	HE, A_ARG_57	2.77	1.80	8.03
1HGJ.PDB	O, A_LEU_86	N, A_LEU_59	H, A_LEU_59	2.86	1.91	11.37
1HGJ.PDB	O, A_VAL_88	N, A_GLY_61	H, A_GLY_61	2.97	2.09	22.25
1HGJ.PDB	OD1, A_ASP_60	N, A_ILE_62	H, A_ILE_62	2.87	1.94	15.09
1HGJ.PDB	O, A_GLY_61	N, A_CYS_64	H, A_CYS_64	2.89	1.97	17.07
1HGJ.PDB	O, A_LEU_66	N, A_LEU_70	H, A_LEU_70	2.88	1.99	19.66
1HGJ.PDB	O, A_ILE_67	N, A_LEU_71	H, A_LEU_71	2.83	1.87	6.71
1HGJ.PDB	O, A_ASP_68	N, A_GLY_72	H, A_GLY_72	2.88	1.97	18.26
1HGJ.PDB	OD1, A_ASP_73	N, A_HIS_75	H, A_HIS_75	2.98	2.07	18.75
1HGJ.PDB	OD1, A_ASP_73	ND1, A_HIS_75	HD1, A_HIS_75	2.83	1.91	17.40
1HGJ.PDB	O, A_ASP_63	NE2, A_HIS_75	HE2, A_HIS_75	2.85	1.95	19.40
1HGJ.PDB	O, A_ASP_73	N, A_CYS_76	H, A_CYS_76	2.78	1.84	13.08
1HGJ.PDB	O, A_PRO_74	N, A_ASP_77	H, A_ASP_77	2.97	2.01	11.14
1HGJ.PDB	O, A_ARG_57	N, A_ASP_85	H, A_ASP_85	2.81	1.89	16.54
1HGJ.PDB	O, A_LEU_59	N, A_VAL_88	H, A_VAL_88	2.98	2.01	7.07
1HGJ.PDB	O, A_MET_268	N, A_GLU_89	H, A_GLU_89	2.79	1.84	8.85
1HGJ.PDB	OD1, A_ASP_60	NE, A_ARG_90	HE, A_ARG_90	2.88	1.91	7.56
1HGJ.PDB	O, A_SER_270	NH1, A_ARG_90	HH11, A_ARG_90	2.70	1.81	23.07
1HGJ.PDB	O, A_ALA_272	NH1, A_ARG_90	HH12, A_ARG_90	2.62	1.70	17.78
1HGJ.PDB	OD2, A_ASP_60	NH2, A_ARG_90	HH21, A_ARG_90	2.81	1.82	10.05
1HGJ.PDB	OD1, A_ASP_271	N, A_SER_91	H, A_SER_91	2.92	1.95	7.81
1HGJ.PDB	OD1, A_ASP_271	OG, A_SER_91	HG, A_SER_91	2.98	2.13	24.27
1HGJ.PDB	OD2, A_ASP_271	OG, A_SER_91	HG, A_SER_91	2.78	1.90	20.01
1HGJ.PDB	OD2, A_ASP_68	OG, A_SER_95	HG, A_SER_95	2.95	2.05	19.19
1HGJ.PDB	OD2, A_ASP_73	N, A_ASN_96	H, A_ASN_96	2.89	1.93	9.91
1HGJ.PDB	O, A_ILE_230	N, A_ASP_101	H, A_ASP_101	2.95	2.08	23.05
1HGJ.PDB	OD2, A_ASP_104	OG, A_SER_107	HG, A_SER_107	2.84	1.95	18.85
1HGJ.PDB	O, A_TYR_105	N, A_ARG_109	H, A_ARG_109	2.84	1.86	2.92
1HGJ.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.75	1.77	12.07
1HGJ.PDB	OD2, F_ASP_79	OG, A_SER_110	HG, A_SER_110	2.94	1.98	10.39
1HGJ.PDB	O, A_SER_107	N, A_LEU_111	H, A_LEU_111	2.86	1.89	5.37
1HGJ.PDB	O, A_ARG_109	N, A_ALA_113	H, A_ALA_113	2.93	2.03	18.98
1HGJ.PDB	O, A_SER_110	N, A_SER_114	H, A_SER_114	2.89	1.97	15.80
1HGJ.PDB	OE2, A_GLU_119	OG1, A_THR_117	HG1, A_THR_117	2.87	1.94	12.44
1HGJ.PDB	O, A_GLU_82	N, A_LEU_118	H, A_LEU_118	2.93	2.00	16.05
1HGJ.PDB	O, A_TYR_257	N, A_ILE_121	H, A_ILE_121	2.85	1.88	7.23
1HGJ.PDB	O, A_ARG_255	N, A_GLU_123	H, A_GLU_123	2.94	1.98	10.39
1HGJ.PDB	O, A_THR_155	N, A_THR_131	H, A_THR_131	2.71	1.83	19.42
1HGJ.PDB	OD1, A_ASN_152	N, A_ASN_133	H, A_ASN_133	2.86	1.94	16.50
1HGJ.PDB	O, A_GLY_146	N, A_SER_136	H, A_SER_136	2.74	1.85	19.18
1HGJ.PDB	OG, A_SER_136	N, A_ALA_138	H, A_ALA_138	2.90	1.96	14.29
1HGJ.PDB	O, A_GLY_144	NZ, A_LYS_140	HZ1, A_LYS_140	2.76	1.78	16.23
1HGJ.PDB	OD1, A_ASN_137	NZ, A_LYS_140	HZ2, A_LYS_140	2.70	1.70	13.62
1HGJ.PDB	OD2, A_ASP_77	NE, A_ARG_141	HE, A_ARG_141	2.82	1.99	27.09
1HGJ.PDB	O, A_PHE_147	NH1, A_ARG_141	HH12, A_ARG_141	2.55	1.62	16.97
1HGJ.PDB	OD1, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.82	1.90	21.48

1HGJ.PDB	OD2, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.75	1.86	24.28
1HGJ.PDB	O, A_GLY_72	NH2, A_ARG_141	HH22, A_ARG_141	2.89	1.91	10.49
1HGJ.PDB	O, A_SER_136	N, A_GLY_146	H, A_GLY_146	2.92	1.99	15.16
1HGJ.PDB	O, A_GLY_72	N, A_SER_149	H, A_SER_149	2.81	1.92	19.89
1HGJ.PDB	O, A_ALA_253	N, A_ASN_152	H, A_ASN_152	2.77	1.94	25.94
1HGJ.PDB	OH, A_TYR_195	NE1, A_TRP_153	HE1, A_TRP_153	2.85	1.94	18.91
1HGJ.PDB	O, A_THR_131	N, A_THR_155	H, A_THR_155	2.98	2.03	13.10
1HGJ.PDB	O, A_LEU_194	N, A_LYS_156	H, A_LYS_156	2.96	2.04	16.82
1HGJ.PDB	O, A_SER_193	NZ, A_LYS_156	HZ2, A_LYS_156	2.76	1.77	15.28
1HGJ.PDB	O, A_SER_247	N, A_LEU_164	H, A_LEU_164	2.71	1.86	23.94
1HGJ.PDB	O, A_ILE_245	N, A_VAL_166	H, A_VAL_166	2.96	2.01	11.11
1HGJ.PDB	O, A_LEU_243	OG1, A_THR_167	HG1, A_THR_167	2.95	2.00	7.14
1HGJ.PDB	O, A_LEU_243	N, A_MET_168	H, A_MET_168	2.88	1.96	15.85
1HGJ.PDB	O, A_ASP_241	N, A_ASN_170	H, A_ASN_170	2.94	1.97	10.04
1HGJ.PDB	O, A_PHE_174	ND2, A_ASN_170	HD21, A_ASN_170	2.85	1.90	10.43
1HGJ.PDB	O, A_VAL_237	ND2, A_ASN_170	HD22, A_ASN_170	2.88	2.05	26.57
1HGJ.PDB	O, A_VAL_237	N, A_LYS_176	H, A_LYS_176	2.93	1.99	13.19
1HGJ.PDB	OE2, A_GLU_123	NZ, A_LYS_176	HZ1, A_LYS_176	2.68	1.78	24.65
1HGJ.PDB	O, A_THR_235	N, A_TYR_178	H, A_TYR_178	2.81	1.83	1.66
1HGJ.PDB	OE1, A_GLU_123	OH, A_TYR_178	HH, A_TYR_178	2.79	1.84	8.91
1HGJ.PDB	OG1, A_THR_235	NE1, A_TRP_180	HE1, A_TRP_180	2.92	1.93	4.44
1HGJ.PDB	O, A_ASN_250	N, A_HIS_183	H, A_HIS_183	2.90	1.98	16.84
1HGJ.PDB	O, A_ARG_229	N, A_HIS_184	H, A_HIS_184	2.83	1.87	9.59
1HGJ.PDB	OG, A_SER_231	NE2, A_HIS_184	HE2, A_HIS_184	2.75	1.92	26.36
1HGJ.PDB	OG1, A_THR_187	N, A_GLU_190	H, A_GLU_190	2.88	1.93	10.33
1HGJ.PDB	O, A_GLN_197	NE2, A_GLN_191	HE22, A_GLN_191	2.90	1.98	16.92
1HGJ.PDB	O, A_ASN_188	OG1, A_THR_192	HG1, A_THR_192	2.97	2.01	7.08
1HGJ.PDB	O, A_GLN_189	N, A_SER_193	H, A_SER_193	2.85	1.87	2.99
1HGJ.PDB	O, A_GLU_190	N, A_LEU_194	H, A_LEU_194	2.97	2.00	9.61
1HGJ.PDB	O, A_GLN_191	N, A_TYR_195	H, A_TYR_195	2.80	1.85	9.60
1HGJ.PDB	O, A_TYR_161	NE2, A_GLN_197	HE21, A_GLN_197	2.87	1.93	12.14
1HGJ.PDB	O, A_ASN_248	NE2, A_GLN_197	HE22, A_GLN_197	2.87	1.94	14.83
1HGJ.PDB	OD1, A_ASN_246	NH2, A_ARG_201	HH21, A_ARG_201	2.58	1.73	25.49
1HGJ.PDB	O, A_ILE_213	N, A_VAL_202	H, A_VAL_202	2.97	2.02	12.20
1HGJ.PDB	O, A_ASN_246	N, A_THR_203	H, A_THR_203	2.90	1.99	17.82
1HGJ.PDB	O, A_GLN_211	N, A_VAL_204	H, A_VAL_204	2.83	1.93	18.94
1HGJ.PDB	O, A_SER_209	N, A_THR_206	H, A_THR_206	2.89	1.93	8.74
1HGJ.PDB	OD1, A_ASP_241	N, A_ARG_207	H, A_ARG_207	2.88	1.92	9.03
1HGJ.PDB	OG1, A_THR_206	OG, A_SER_209	HG, A_SER_209	3.00	2.04	8.15
1HGJ.PDB	O, A_VAL_204	N, A_GLN_211	H, A_GLN_211	2.91	2.00	17.89
1HGJ.PDB	OG1, A_THR_203	OG1, A_THR_212	HG1, A_THR_212	2.89	1.93	3.12
1HGJ.PDB	O, A_VAL_202	N, A_ILE_213	H, A_ILE_213	2.84	1.92	16.69
1HGJ.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.67	1.78	22.50
1HGJ.PDB	O, A_ASN_216	NH2, A_ARG_220	HH22, A_ARG_220	2.78	1.89	22.30
1HGJ.PDB	O, A_LEU_226	N, A_VAL_223	H, A_VAL_223	2.84	1.88	10.14
1HGJ.PDB	O, A_CYS_97	NE, A_ARG_224	HE, A_ARG_224	2.80	1.95	24.47
1HGJ.PDB	O, A_CYS_97	NH2, A_ARG_224	HH21, A_ARG_224	2.93	2.07	26.25
1HGJ.PDB	O, A_VAL_223	N, A_LEU_226	H, A_LEU_226	2.91	1.97	13.14
1HGJ.PDB	O, A_SER_228	NH1, A_ARG_229	HH11, A_ARG_229	2.72	1.77	16.65
1HGJ.PDB	O, A_PRO_221	NH2, A_ARG_229	HH22, A_ARG_229	2.62	1.66	13.73
1HGJ.PDB	OD1, A_ASP_101	OG, A_SER_231	HG, A_SER_231	2.87	1.91	9.73
1HGJ.PDB	O, A_ASP_101	N, A_ILE_232	H, A_ILE_232	2.86	1.94	17.01
1HGJ.PDB	O, A_TRP_180	N, A_TYR_233	H, A_TYR_233	2.94	1.96	7.60
1HGJ.PDB	O, A_TYR_178	N, A_THR_235	H, A_THR_235	2.91	2.02	19.93
1HGJ.PDB	O, A_LYS_176	N, A_VAL_237	H, A_VAL_237	2.80	1.86	14.26
1HGJ.PDB	O, F_SER_71	NZ, A_LYS_238	HZ2, A_LYS_238	2.62	1.72	23.44
1HGJ.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.90	1.90	13.91
1HGJ.PDB	O, A_ASN_170	N, A_GLY_240	H, A_GLY_240	2.83	1.97	23.20

1HGJ.PDB	OD1, A_ASP_241	N, A_VAL_242	H, A_VAL_242	2.77	1.93	25.51
1HGJ.PDB	O, A_MET_168	N, A_LEU_243	H, A_LEU_243	2.93	1.96	5.60
1HGJ.PDB	O, A_SER_205	N, A_VAL_244	H, A_VAL_244	2.98	2.03	12.76
1HGJ.PDB	O, A_VAL_166	N, A_ILE_245	H, A_ILE_245	2.88	1.93	13.19
1HGJ.PDB	O, A_THR_203	N, A_ASN_246	H, A_ASN_246	2.93	1.96	5.50
1HGJ.PDB	OD1, A_ASN_165	ND2, A_ASN_246	HD22, A_ASN_246	2.91	1.95	11.26
1HGJ.PDB	O, A_LEU_164	N, A_SER_247	H, A_SER_247	2.91	2.00	18.09
1HGJ.PDB	O, A_HIS_183	ND2, A_ASN_250	HD22, A_ASN_250	2.81	1.86	11.47
1HGJ.PDB	O, A_GLY_181	N, A_ILE_252	H, A_ILE_252	2.95	1.99	11.10
1HGJ.PDB	O, A_ASN_152	N, A_ALA_253	H, A_ALA_253	2.89	2.00	20.87
1HGJ.PDB	OD1, A_ASN_133	NH2, A_ARG_255	HH22, A_ARG_255	2.53	1.70	27.52
1HGJ.PDB	O, A_ILE_121	N, A_TYR_257	H, A_TYR_257	2.95	2.11	25.99
1HGJ.PDB	O, A_LEU_177	N, A_PHE_258	H, A_PHE_258	2.93	1.97	8.17
1HGJ.PDB	OG, A_SER_115	N, A_ARG_261	H, A_ARG_261	2.93	1.99	14.40
1HGJ.PDB	OE2, A_GLU_119	NH1, A_ARG_261	HH12, A_ARG_261	2.65	1.82	28.35
1HGJ.PDB	OE1, A_GLU_119	NH2, A_ARG_261	HH22, A_ARG_261	2.90	1.99	23.18
1HGJ.PDB	OD2, A_ASP_85	NZ, A_LYS_264	HZ3, A_LYS_264	2.84	1.85	15.53
1HGJ.PDB	O, A_PHE_87	N, A_MET_268	H, A_MET_268	2.87	1.96	18.47
1HGJ.PDB	O, A_PRO_284	OG, A_SER_270	HG, A_SER_270	2.82	1.88	11.71
1HGJ.PDB	OG, A_SER_270	N, A_ALA_272	H, A_ALA_272	2.99	2.05	13.78
1HGJ.PDB	O, A_ILE_51	N, A_ASP_275	H, A_ASP_275	2.92	2.02	19.32
1HGJ.PDB	OD1, A_ASP_275	N, A_THR_276	H, A_THR_276	2.81	1.96	23.63
1HGJ.PDB	O, A_ASN_54	N, A_SER_279	H, A_SER_279	2.81	1.88	14.91
1HGJ.PDB	O, A_TYR_302	N, A_ILE_282	H, A_ILE_282	2.92	1.95	7.78
1HGJ.PDB	O, A_THR_283	N, A_GLY_286	H, A_GLY_286	2.78	1.86	14.62
1HGJ.PDB	O, A_LYS_50	N, A_SER_287	H, A_SER_287	2.84	1.87	6.72
1HGJ.PDB	O, A_ALA_304	ND2, A_ASN_290	HD22, A_ASN_290	2.82	1.91	18.14
1HGJ.PDB	OE1, A_GLN_44	NZ, A_LYS_292	HZ1, A_LYS_292	2.71	1.70	11.30
1HGJ.PDB	OD2, A_ASP_291	NZ, A_LYS_292	HZ3, A_LYS_292	2.80	1.82	17.27
1HGJ.PDB	O, A_LYS_307	N, A_GLN_295	H, A_GLN_295	2.89	1.99	19.47
1HGJ.PDB	O, A_ASN_298	NE2, A_GLN_295	HE21, A_GLN_295	2.78	1.82	8.78
1HGJ.PDB	O, A_GLN_44	N, A_ASN_296	H, A_ASN_296	2.84	1.91	14.48
1HGJ.PDB	OE1, A_GLN_295	N, A_VAL_297	H, A_VAL_297	2.74	1.95	29.44
1HGJ.PDB	O, B_LYS_68	NZ, A_LYS_299	HZ2, A_LYS_299	2.95	1.96	14.91
1HGJ.PDB	OD1, A_ASN_298	N, A_ILE_300	H, A_ILE_300	2.86	1.95	16.95
1HGJ.PDB	O, A_ILE_282	N, A_TYR_302	H, A_TYR_302	2.88	2.05	26.62
1HGJ.PDB	O, A_LYS_264	OH, A_TYR_302	HH, A_TYR_302	2.66	1.88	29.88
1HGJ.PDB	O, B_LYS_62	N, A_GLY_303	H, A_GLY_303	2.93	1.97	8.41
1HGJ.PDB	O, A_GLN_295	N, A_VAL_309	H, A_VAL_309	2.92	2.10	27.87
1HGJ.PDB	OE2, A_GLU_41	N, A_LEU_314	H, A_LEU_314	2.79	1.86	13.81
1HGJ.PDB	OE1, A_GLU_41	NZ, A_LYS_315	HZ3, A_LYS_315	2.85	1.90	20.12
1HGJ.PDB	O, A_THR_40	N, A_LEU_316	H, A_LEU_316	2.80	1.86	11.89
1HGJ.PDB	OD1, B_ASN_104	N, A_ALA_317	H, A_ALA_317	2.74	1.81	13.01
1HGJ.PDB	O, A_ASN_38	N, A_THR_318	H, A_THR_318	2.86	1.94	16.91
1HGJ.PDB	O, A_VAL_20	ND2, A_ASN_322	HD21, A_ASN_322	2.87	1.93	14.22
1HGJ.PDB	OE2, A_GLU_35	ND2, A_ASN_322	HD22, A_ASN_322	2.88	1.99	20.96
1HGJ.PDB	OE1, A_GLU_325	NZ, A_LYS_326	HZ3, A_LYS_326	2.92	1.93	15.95
1HGJ.PDB	O, A_PRO_21	NE2, A_GLN_327	HE22, A_GLN_327	2.76	1.91	24.52
1HGJ.PDB	OE1, B_GLU_15	N, A_THR_328	H, A_THR_328	2.99	2.03	9.44
1HGJ.PDB	OD2, B_ASP_112	N, B_GLY_1	H2, B_GLY_1	2.78	1.79	13.86
1HGJ.PDB	OD1, B_ASP_109	N, B_LEU_2	H, B_LEU_2	2.86	1.98	21.89
1HGJ.PDB	OD2, B_ASP_112	N, B_PHE_3	H, B_PHE_3	2.78	1.97	28.02
1HGJ.PDB	OD2, B_ASP_112	N, B_GLY_4	H, B_GLY_4	2.88	1.96	16.60
1HGJ.PDB	OD1, B_ASP_112	N, B_ALA_5	H, B_ALA_5	2.84	1.99	24.18
1HGJ.PDB	OD1, B_ASP_112	N, B_ILE_6	H, B_ILE_6	3.00	2.08	16.65
1HGJ.PDB	O, B_GLY_4	N, B_PHE_9	H, B_PHE_9	2.78	1.85	13.96
1HGJ.PDB	O, B_GLY_13	ND2, B_ASN_12	HD22, B_ASN_12	2.87	1.99	21.80
1HGJ.PDB	O, A_VAL_323	N, B_GLY_13	H, B_GLY_13	2.69	1.76	11.68

1HGJ.PDB	O, A_HIS_17	N, B_TRP_14	H, B_TRP_14	2.84	1.89	12.22
1HGJ.PDB	OG1, B_THR_41	N, B_TRP_21	H, B_TRP_21	2.94	2.02	16.97
1HGJ.PDB	O, A_GLY_16	N, B_GLY_23	H, B_GLY_23	2.94	2.02	17.07
1HGJ.PDB	O, B_ALA_35	N, B_PHE_24	H, B_PHE_24	2.82	1.86	8.22
1HGJ.PDB	O, A_CYS_14	N, B_ARG_25	H, B_ARG_25	2.98	2.05	15.51
1HGJ.PDB	OE1, B_GLN_34	NE, B_ARG_25	HE, B_ARG_25	2.57	1.79	29.34
1HGJ.PDB	OE2, A_GLU_325	NH2, B_ARG_25	HH22, B_ARG_25	2.97	2.01	15.94
1HGJ.PDB	O, B_GLY_33	N, B_HIS_26	H, B_HIS_26	2.69	1.82	21.72
1HGJ.PDB	O, B_GLY_31	N, B_ASN_28	H, B_ASN_28	2.73	1.80	14.27
1HGJ.PDB	O, B_ASN_28	N, B_GLY_31	H, B_GLY_31	2.95	2.06	20.54
1HGJ.PDB	O, B_HIS_26	N, B_GLY_33	H, B_GLY_33	2.91	1.99	16.91
1HGJ.PDB	O, B_PHE_24	N, B_ALA_35	H, B_ALA_35	2.77	1.91	23.35
1HGJ.PDB	O, B_TYR_22	N, B_ASP_37	H, B_ASP_37	2.68	1.76	13.66
1HGJ.PDB	OD2, B_ASP_37	N, B_SER_40	H, B_SER_40	2.93	1.96	8.36
1HGJ.PDB	O, B_ASP_37	OG1, B_THR_41	HG1, B_THR_41	2.75	1.82	13.86
1HGJ.PDB	O, B_LEU_38	N, B_GLN_42	H, B_GLN_42	2.95	2.02	15.28
1HGJ.PDB	OD1, B_ASP_46	NE2, B_GLN_42	HE22, B_GLN_42	2.81	1.92	21.14
1HGJ.PDB	O, B_LYS_39	N, B_ALA_43	H, B_ALA_43	2.97	2.02	10.62
1HGJ.PDB	O, B_SER_40	N, B_ALA_44	H, B_ALA_44	2.96	1.98	1.15
1HGJ.PDB	O, B_THR_41	N, B_ILE_45	H, B_ILE_45	2.88	1.92	10.00
1HGJ.PDB	O, B_GLN_42	N, B_ASP_46	H, B_ASP_46	2.77	1.81	2.39
1HGJ.PDB	OE2, B_GLU_114	NE2, B_GLN_47	HE21, B_GLN_47	2.96	2.05	17.93
1HGJ.PDB	O, B_ALA_43	NE2, B_GLN_47	HE22, B_GLN_47	2.92	2.04	21.05
1HGJ.PDB	O, B_ILE_45	N, B_ASN_49	H, B_ASN_49	2.87	1.94	16.22
1HGJ.PDB	O, B_ASP_46	N, B_GLY_50	H, B_GLY_50	2.84	1.96	21.96
1HGJ.PDB	OG1, B_THR_107	NZ, B_LYS_51	HZ1, B_LYS_51	2.96	1.99	17.76
1HGJ.PDB	OE1, B_GLU_103	NZ, B_LYS_51	HZ2, B_LYS_51	2.78	1.74	6.16
1HGJ.PDB	ND1, B_HIS_106	NZ, B_LYS_51	HZ3, B_LYS_51	2.79	1.82	16.46
1HGJ.PDB	O, B_ILE_48	N, B_LEU_52	H, B_LEU_52	2.87	1.97	17.59
1HGJ.PDB	O, B_ASN_49	N, B_ASN_53	H, B_ASN_53	2.88	1.95	13.58
1HGJ.PDB	O, E_THR_28	NE, B_ARG_54	HE, B_ARG_54	3.00	2.04	10.82
1HGJ.PDB	OE1, B_GLU_57	NH1, B_ARG_54	HH11, B_ARG_54	2.87	1.87	9.43
1HGJ.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.77	1.81	15.09
1HGJ.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ1, B_LYS_62	2.65	1.75	23.55
1HGJ.PDB	OD2, F_ASP_90	NZ, B_LYS_62	HZ3, B_LYS_62	2.74	1.89	28.52
1HGJ.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.89	1.93	11.21
1HGJ.PDB	O, A_LYS_299	NZ, B_LYS_68	HZ1, B_LYS_68	2.90	1.89	11.39
1HGJ.PDB	OE2, B_GLU_85	NZ, B_LYS_68	HZ2, B_LYS_68	2.78	1.76	8.72
1HGJ.PDB	OG, C_SER_107	N, B_ARG_76	H, B_ARG_76	2.84	1.89	10.24
1HGJ.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.90	1.93	10.80
1HGJ.PDB	OE2, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.88	1.87	5.28
1HGJ.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.72	1.72	3.64
1HGJ.PDB	OE1, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.85	1.84	3.19
1HGJ.PDB	OE1, B_GLU_74	NE2, B_GLN_78	HE22, B_GLN_78	2.90	1.95	12.93
1HGJ.PDB	O, B_GLY_75	N, B_ASP_79	H, B_ASP_79	2.93	2.00	14.44
1HGJ.PDB	O, B_ILE_77	N, B_GLU_81	H, B_GLU_81	2.99	2.02	6.22
1HGJ.PDB	O, B_GLN_78	N, B_LYS_82	H, B_LYS_82	2.95	1.99	7.96
1HGJ.PDB	O, B_ASP_79	N, B_TYR_83	H, B_TYR_83	2.84	1.90	13.83
1HGJ.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.67	1.83	24.12
1HGJ.PDB	O, B_LEU_80	N, B_VAL_84	H, B_VAL_84	2.83	1.86	5.05
1HGJ.PDB	O, B_LYS_82	N, B_ASP_86	H, B_ASP_86	2.93	1.98	11.14
1HGJ.PDB	O, B_TYR_83	N, B_THR_87	H, B_THR_87	2.88	1.94	13.57
1HGJ.PDB	O, B_VAL_84	N, B_LYS_88	H, B_LYS_88	2.97	2.03	12.68
1HGJ.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.78	1.75	7.42
1HGJ.PDB	O, B_GLU_85	N, B_ILE_89	H, B_ILE_89	2.86	1.88	2.57
1HGJ.PDB	O, B_LYS_88	N, B_TRP_92	H, B_TRP_92	2.95	1.97	4.34
1HGJ.PDB	O, B_ILE_89	N, B_SER_93	H, B_SER_93	2.84	1.96	21.34
1HGJ.PDB	O, B_ILE_89	OG, B_SER_93	HG, B_SER_93	2.85	1.94	16.10

1HGJ.PDB	O, B_ASP_90	N, B_TYR_94	H, B_TYR_94	2.84	1.94	19.37
1HGJ.PDB	O, B_TRP_92	N, B_ALA_96	H, B_ALA_96	2.98	2.03	11.55
1HGJ.PDB	O, B_TYR_94	N, B_LEU_98	H, B_LEU_98	2.96	1.99	5.51
1HGJ.PDB	O, B_ASN_95	N, B_LEU_99	H, B_LEU_99	2.87	1.95	16.33
1HGJ.PDB	O, B_LEU_98	N, B_LEU_102	H, B_LEU_102	2.95	1.98	7.34
1HGJ.PDB	O, B_LEU_99	N, B_GLU_103	H, B_GLU_103	2.95	1.99	9.27
1HGJ.PDB	O, B_VAL_100	N, B_ASN_104	H, B_ASN_104	2.84	1.88	10.60
1HGJ.PDB	O, A_LYS_27	ND2, B_ASN_104	HD22, B_ASN_104	2.89	1.94	10.52
1HGJ.PDB	O, B_LEU_102	N, B_HIS_106	H, B_HIS_106	2.93	1.97	8.51
1HGJ.PDB	O, B_GLU_103	N, B_THR_107	H, B_THR_107	2.83	1.93	19.44
1HGJ.PDB	O, B_HIS_106	N, B_LEU_110	H, B_LEU_110	2.81	1.85	8.24
1HGJ.PDB	O, B_THR_107	OG1, B_THR_111	HG1, B_THR_111	2.81	1.92	19.54
1HGJ.PDB	O, B_ASP_109	N, B_SER_113	H, B_SER_113	2.79	1.83	7.83
1HGJ.PDB	O, F_LEU_2	OG, B_SER_113	HG, B_SER_113	2.74	1.91	25.16
1HGJ.PDB	O, B_LEU_110	N, B_GLU_114	H, B_GLU_114	2.95	1.99	10.32
1HGJ.PDB	O, B_ASP_112	N, B_ASN_116	H, B_ASN_116	2.97	2.01	9.78
1HGJ.PDB	O, B_SER_113	N, B_LYS_117	H, B_LYS_117	2.71	1.84	21.48
1HGJ.PDB	O, B_GLU_114	N, B_LEU_118	H, B_LEU_118	2.97	2.01	9.85
1HGJ.PDB	O, B_ASN_116	N, B_GLU_120	H, B_GLU_120	2.95	1.98	2.37
1HGJ.PDB	O, B_LYS_117	N, B_LYS_121	H, B_LYS_121	2.92	2.02	19.46
1HGJ.PDB	O, B_PHE_119	N, B_ARG_123	H, B_ARG_123	2.95	1.98	8.48
1HGJ.PDB	OE2, B_GLU_120	NH1, B_ARG_123	HH11, B_ARG_123	2.74	1.86	23.95
1HGJ.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.82	2.00	27.29
1HGJ.PDB	OE2, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.91	2.02	20.91
1HGJ.PDB	O, B_HIS_159	ND2, B_ASN_129	HD21, B_ASN_129	2.96	2.00	9.85
1HGJ.PDB	OH, B_TYR_157	ND2, B_ASN_129	HD22, B_ASN_129	2.77	1.84	15.18
1HGJ.PDB	O, B_LYS_139	N, B_GLU_131	H, B_GLU_131	2.92	1.98	12.78
1HGJ.PDB	O, B_CYS_137	N, B_MET_133	H, B_MET_133	2.85	1.92	15.10
1HGJ.PDB	O, A_LEU_13	N, B_PHE_138	H, B_PHE_138	2.71	1.86	23.78
1HGJ.PDB	O, B_GLU_131	N, B_LYS_139	H, B_LYS_139	2.83	1.87	8.18
1HGJ.PDB	O, A_ALA_11	N, B_ILE_140	H, B_ILE_140	2.77	1.86	16.77
1HGJ.PDB	O, B_ASN_129	N, B_TYR_141	H, B_TYR_141	2.93	1.98	12.18
1HGJ.PDB	OE2, B_GLU_165	N, B_LYS_143	H, B_LYS_143	2.97	2.02	13.21
1HGJ.PDB	OE1, B_GLU_30	N, B_ASN_146	H, B_ASN_146	2.90	1.96	14.42
1HGJ.PDB	O, B_ASP_145	N, B_ILE_149	H, B_ILE_149	2.89	1.94	10.22
1HGJ.PDB	O, B_ASN_146	N, B_GLU_150	H, B_GLU_150	2.88	1.95	15.40
1HGJ.PDB	O, B_ALA_147	N, B_SER_151	H, B_SER_151	2.86	1.97	19.97
1HGJ.PDB	O, B_CYS_148	OG, B_SER_151	HG, B_SER_151	2.69	1.85	23.77
1HGJ.PDB	O, B_GLU_150	N, B_ASN_154	H, B_ASN_154	2.80	1.82	1.74
1HGJ.PDB	OE2, B_GLU_150	ND2, B_ASN_154	HD21, B_ASN_154	2.81	2.00	28.55
1HGJ.PDB	O, B_SER_151	N, B_THR_156	H, B_THR_156	2.71	1.89	26.64
1HGJ.PDB	OD1, B_ASN_154	OG1, B_THR_156	HG1, B_THR_156	2.67	1.80	19.98
1HGJ.PDB	OD1, B_ASP_158	N, B_ASP_160	H, B_ASP_160	2.91	2.05	23.96
1HGJ.PDB	O, B_HIS_159	N, B_TYR_162	H, B_TYR_162	2.94	2.06	21.10
1HGJ.PDB	O, F_ARG_170	NH1, B_ARG_163	HH12, B_ARG_163	2.72	1.75	12.61
1HGJ.PDB	O, B_TYR_162	N, B_ALA_166	H, B_ALA_166	2.86	1.89	2.61
1HGJ.PDB	O, B_ARG_163	N, B_LEU_167	H, B_LEU_167	2.77	1.81	8.42
1HGJ.PDB	O, B_ALA_166	N, B_ARG_170	H, B_ARG_170	2.83	1.95	21.36
1HGJ.PDB	O, B_GLU_128	NE, B_ARG_170	HE, B_ARG_170	2.79	1.92	22.95
1HGJ.PDB	OE2, B_GLU_131	NH1, B_ARG_170	HH11, B_ARG_170	2.80	1.80	6.39
1HGJ.PDB	O, B_LEU_167	N, B_PHE_171	H, B_PHE_171	2.93	2.01	16.69
1HGJ.PDB	O, D_ILE_140	N, C_ALA_11	H, C_ALA_11	2.85	1.95	19.06
1HGJ.PDB	O, D_GLN_27	N, C_THR_12	H, C_THR_12	2.99	2.03	8.05
1HGJ.PDB	O, D_PHE_138	N, C_LEU_13	H, C_LEU_13	2.99	2.02	7.89
1HGJ.PDB	O, D_ARG_25	N, C_CYS_14	H, C_CYS_14	2.76	1.85	16.80
1HGJ.PDB	O, D_GLY_136	N, C_LEU_15	H, C_LEU_15	2.95	1.97	3.95
1HGJ.PDB	O, D_GLY_23	N, C_GLY_16	H, C_GLY_16	2.89	1.98	18.54
1HGJ.PDB	O, C_HIS_18	ND1, C_HIS_17	HD1, C_HIS_17	2.94	2.08	23.78

1HGJ.PDB	O, D_TRP_21	N, C_HIS_18	H, C_HIS_18	2.86	1.97	20.63
1HGJ.PDB	OD1, C_ASN_322	N, C_VAL_20	H, C_VAL_20	2.78	1.82	9.76
1HGJ.PDB	O, C_VAL_36	N, C_THR_24	H, C_THR_24	2.86	1.93	13.58
1HGJ.PDB	O, C_ILE_34	N, C_VAL_26	H, C_VAL_26	2.80	1.85	11.08
1HGJ.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.82	1.80	8.63
1HGJ.PDB	O, C_ASP_31	N, C_THR_28	H, C_THR_28	2.73	1.88	23.51
1HGJ.PDB	O, C_VAL_26	N, C_ILE_34	H, C_ILE_34	2.90	1.95	12.50
1HGJ.PDB	O, C_THR_24	N, C_VAL_36	H, C_VAL_36	2.82	1.85	5.74
1HGJ.PDB	O, C_MET_320	N, C_THR_37	H, C_THR_37	2.89	1.92	6.83
1HGJ.PDB	O, C_LEU_316	N, C_THR_40	H, C_THR_40	2.90	2.05	25.12
1HGJ.PDB	O, C_LEU_314	N, C_LEU_42	H, C_LEU_42	2.80	1.93	22.39
1HGJ.PDB	O, C_PHE_294	N, C_GLN_44	H, C_GLN_44	2.82	1.85	7.42
1HGJ.PDB	O, C_SER_46	NE2, C_GLN_44	HE22, C_GLN_44	2.90	2.00	19.73
1HGJ.PDB	O, C_ASN_285	OG, C_SER_47	HG, C_SER_47	2.83	1.92	15.29
1HGJ.PDB	OD2, C_ASP_275	NZ, C_LYS_50	HZ1, C_LYS_50	2.74	1.82	22.76
1HGJ.PDB	O, C_PRO_273	N, C_ILE_51	H, C_ILE_51	2.85	1.89	9.03
1HGJ.PDB	O, C_ASP_275	N, C_ASN_53	H, C_ASN_53	2.78	1.94	25.31
1HGJ.PDB	O, C_GLU_280	NE2, C_HIS_56	HE2, C_HIS_56	2.97	2.05	17.85
1HGJ.PDB	OD2, C_ASP_85	N, C_ARG_57	H, C_ARG_57	2.84	1.90	12.58
1HGJ.PDB	O, C_THR_83	NE, C_ARG_57	HE, C_ARG_57	2.76	1.80	8.04
1HGJ.PDB	O, C_LEU_86	N, C_LEU_59	H, C_LEU_59	2.87	1.92	10.21
1HGJ.PDB	O, C_VAL_88	N, C_GLY_61	H, C_GLY_61	2.97	2.10	22.49
1HGJ.PDB	OD1, C_ASP_60	N, C_ILE_62	H, C_ILE_62	2.85	1.93	15.07
1HGJ.PDB	O, C_GLY_61	N, C_CYS_64	H, C_CYS_64	2.87	1.96	17.46
1HGJ.PDB	O, C_LEU_66	N, C_LEU_70	H, C_LEU_70	2.89	2.00	19.99
1HGJ.PDB	O, C_ILE_67	N, C_LEU_71	H, C_LEU_71	2.82	1.86	8.52
1HGJ.PDB	O, C_ASP_68	N, C_GLY_72	H, C_GLY_72	2.86	1.96	18.14
1HGJ.PDB	OD1, C_ASP_73	N, C_HIS_75	H, C_HIS_75	2.96	2.05	18.04
1HGJ.PDB	OD1, C_ASP_73	ND1, C_HIS_75	HD1, C_HIS_75	2.80	1.89	17.49
1HGJ.PDB	O, C_ASP_63	NE2, C_HIS_75	HE2, C_HIS_75	2.82	1.92	19.39
1HGJ.PDB	O, C_ASP_73	N, C_CYS_76	H, C_CYS_76	2.78	1.84	12.95
1HGJ.PDB	O, C_PRO_74	N, C_ASP_77	H, C_ASP_77	2.96	2.00	11.06
1HGJ.PDB	O, C_ARG_57	N, C_ASP_85	H, C_ASP_85	2.81	1.90	16.89
1HGJ.PDB	O, C_LEU_59	N, C_VAL_88	H, C_VAL_88	2.97	2.00	6.49
1HGJ.PDB	O, C_MET_268	N, C_GLU_89	H, C_GLU_89	2.80	1.85	10.39
1HGJ.PDB	OD1, C_ASP_60	NE, C_ARG_90	HE, C_ARG_90	2.88	1.91	9.03
1HGJ.PDB	O, C_SER_270	NH1, C_ARG_90	HH11, C_ARG_90	2.68	1.80	24.07
1HGJ.PDB	O, C_ALA_272	NH1, C_ARG_90	HH12, C_ARG_90	2.62	1.70	18.50
1HGJ.PDB	OD2, C_ASP_60	NH2, C_ARG_90	HH21, C_ARG_90	2.78	1.79	9.66
1HGJ.PDB	OD1, C_ASP_271	N, C_SER_91	H, C_SER_91	2.92	1.95	7.70
1HGJ.PDB	OD1, C_ASP_271	OG, C_SER_91	HG, C_SER_91	2.99	2.16	26.38
1HGJ.PDB	OD2, C_ASP_271	OG, C_SER_91	HG, C_SER_91	2.81	1.92	18.67
1HGJ.PDB	OD2, C_ASP_68	OG, C_SER_95	HG, C_SER_95	2.93	1.99	14.68
1HGJ.PDB	OD2, C_ASP_73	N, C_ASN_96	H, C_ASN_96	2.87	1.92	11.70
1HGJ.PDB	OD1, C_ASP_68	OH, C_TYR_100	HH, C_TYR_100	2.88	1.95	14.58
1HGJ.PDB	O, C_ILE_230	N, C_ASP_101	H, C_ASP_101	2.91	2.04	23.02
1HGJ.PDB	OD2, C_ASP_104	OG, C_SER_107	HG, C_SER_107	2.90	1.99	17.96
1HGJ.PDB	O, C_TYR_105	N, C_ARG_109	H, C_ARG_109	2.82	1.85	3.87
1HGJ.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.76	1.78	13.33
1HGJ.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.79	1.87	14.95
1HGJ.PDB	O, C_SER_107	N, C_LEU_111	H, C_LEU_111	2.85	1.89	7.06
1HGJ.PDB	O, C_ARG_109	N, C_ALA_113	H, C_ALA_113	2.95	2.06	19.71
1HGJ.PDB	O, C_SER_110	N, C_SER_114	H, C_SER_114	2.92	1.97	12.30
1HGJ.PDB	OE2, C_GLU_119	OG1, C_THR_117	HG1, C_THR_117	2.88	1.94	11.85
1HGJ.PDB	O, C_GLU_82	N, C_LEU_118	H, C_LEU_118	2.91	1.97	15.15
1HGJ.PDB	O, C_TYR_257	N, C_ILE_121	H, C_ILE_121	2.86	1.89	7.41
1HGJ.PDB	O, C_ARG_255	N, C_GLU_123	H, C_GLU_123	2.93	1.97	10.38
1HGJ.PDB	O, C_THR_155	N, C_THR_131	H, C_THR_131	2.74	1.84	18.58

1HGJ.PDB	OD1, C_ASN_152	N, C_ASN_133	H, C_ASN_133	2.86	1.94	15.99
1HGJ.PDB	O, C_GLY_146	N, C_SER_136	H, C_SER_136	2.75	1.85	18.24
1HGJ.PDB	OG, C_SER_136	N, C_ALA_138	H, C_ALA_138	2.91	1.97	13.65
1HGJ.PDB	O, C_GLY_144	NZ, C_LYS_140	HZ1, C_LYS_140	2.72	1.76	17.33
1HGJ.PDB	OD1, C_ASN_137	NZ, C_LYS_140	HZ2, C_LYS_140	2.71	1.72	13.24
1HGJ.PDB	OD2, C_ASP_77	NE, C_ARG_141	HE, C_ARG_141	2.82	1.99	27.42
1HGJ.PDB	O, C_PHE_147	NH1, C_ARG_141	HH12, C_ARG_141	2.55	1.62	17.29
1HGJ.PDB	OD1, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.81	1.89	21.37
1HGJ.PDB	OD2, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.74	1.86	24.47
1HGJ.PDB	O, C_GLY_72	NH2, C_ARG_141	HH22, C_ARG_141	2.89	1.91	10.48
1HGJ.PDB	OD1, C_ASN_137	OG, C_SER_145	HG, C_SER_145	2.92	2.08	24.33
1HGJ.PDB	O, C_SER_136	N, C_GLY_146	H, C_GLY_146	2.93	2.00	15.25
1HGJ.PDB	O, C_GLY_72	N, C_SER_149	H, C_SER_149	2.81	1.91	18.87
1HGJ.PDB	O, C_ALA_253	N, C_ASN_152	H, C_ASN_152	2.77	1.94	26.39
1HGJ.PDB	OH, C_TYR_195	NE1, C_TRP_153	HE1, C_TRP_153	2.84	1.96	21.72
1HGJ.PDB	O, C_THR_131	N, C_THR_155	H, C_THR_155	2.99	2.03	9.79
1HGJ.PDB	O, C_LEU_194	N, C_LYS_156	H, C_LYS_156	2.97	2.05	16.86
1HGJ.PDB	O, C_SER_247	N, C_LEU_164	H, C_LEU_164	2.72	1.87	24.03
1HGJ.PDB	O, C_ILE_245	N, C_VAL_166	H, C_VAL_166	2.96	2.01	10.78
1HGJ.PDB	O, C_LEU_243	OG1, C_THR_167	HG1, C_THR_167	2.93	2.04	19.65
1HGJ.PDB	O, C_LEU_243	N, C_MET_168	H, C_MET_168	2.91	1.99	17.19
1HGJ.PDB	O, C_ASP_241	N, C_ASN_170	H, C_ASN_170	2.89	1.92	9.78
1HGJ.PDB	O, C_PHE_174	ND2, C_ASN_170	HD21, C_ASN_170	2.84	1.88	9.63
1HGJ.PDB	O, C_VAL_237	ND2, C_ASN_170	HD22, C_ASN_170	2.87	2.05	26.94
1HGJ.PDB	O, C_VAL_237	N, C_LYS_176	H, C_LYS_176	2.90	1.97	14.44
1HGJ.PDB	OE2, C_GLU_123	NZ, C_LYS_176	HZ1, C_LYS_176	2.69	1.80	24.96
1HGJ.PDB	O, C_PHE_258	N, C_LEU_177	H, C_LEU_177	2.97	2.00	6.71
1HGJ.PDB	O, C_THR_235	N, C_TYR_178	H, C_TYR_178	2.79	1.83	4.13
1HGJ.PDB	OE1, C_GLU_123	OH, C_TYR_178	HH, C_TYR_178	2.77	1.82	8.51
1HGJ.PDB	OG1, C_THR_235	NE1, C_TRP_180	HE1, C_TRP_180	2.91	1.92	4.72
1HGJ.PDB	O, C_ASN_250	N, C_HIS_183	H, C_HIS_183	2.91	2.00	17.12
1HGJ.PDB	O, C_ARG_229	N, C_HIS_184	H, C_HIS_184	2.88	1.92	8.64
1HGJ.PDB	OG, C_SER_231	NE2, C_HIS_184	HE2, C_HIS_184	2.74	1.91	26.34
1HGJ.PDB	OG1, C_THR_187	N, C_GLU_190	H, C_GLU_190	2.91	1.96	12.15
1HGJ.PDB	OD1, C_ASN_250	NE2, C_GLN_191	HE21, C_GLN_191	2.99	2.02	8.22
1HGJ.PDB	O, C_GLN_197	NE2, C_GLN_191	HE22, C_GLN_191	2.89	1.97	17.35
1HGJ.PDB	O, C_GLN_189	OG1, C_THR_192	HG1, C_THR_192	2.84	1.97	20.14
1HGJ.PDB	O, C_GLN_189	N, C_SER_193	H, C_SER_193	2.85	1.90	9.95
1HGJ.PDB	O, C_GLN_191	N, C_TYR_195	H, C_TYR_195	2.82	1.86	10.13
1HGJ.PDB	O, C_TYR_161	NE2, C_GLN_197	HE21, C_GLN_197	2.90	1.95	11.26
1HGJ.PDB	O, C_ASN_248	NE2, C_GLN_197	HE22, C_GLN_197	2.87	1.94	15.42
1HGJ.PDB	OD1, C_ASN_246	NH2, C_ARG_201	HH21, C_ARG_201	2.59	1.74	25.86
1HGJ.PDB	O, C_ILE_213	N, C_VAL_202	H, C_VAL_202	2.99	2.07	16.15
1HGJ.PDB	O, C_ASN_246	N, C_THR_203	H, C_THR_203	2.94	2.00	13.61
1HGJ.PDB	OG1, C_THR_212	OG1, C_THR_203	HG1, C_THR_203	2.89	1.94	9.95
1HGJ.PDB	O, C_GLN_211	N, C_VAL_204	H, C_VAL_204	2.83	1.93	19.04
1HGJ.PDB	O, C_SER_209	N, C_THR_206	H, C_THR_206	2.91	1.95	8.75
1HGJ.PDB	OD1, C_ASP_241	N, C_ARG_207	H, C_ARG_207	2.88	1.92	10.11
1HGJ.PDB	O, C_VAL_204	N, C_GLN_211	H, C_GLN_211	2.90	1.98	16.77
1HGJ.PDB	O, C_VAL_202	N, C_ILE_213	H, C_ILE_213	2.84	1.92	15.65
1HGJ.PDB	O, C_ASN_216	NH1, C_ARG_220	HH12, C_ARG_220	2.91	2.10	29.44
1HGJ.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.66	1.82	26.85
1HGJ.PDB	O, C_ASN_216	NH2, C_ARG_220	HH22, C_ARG_220	2.76	1.88	22.85
1HGJ.PDB	O, C_LEU_226	N, C_VAL_223	H, C_VAL_223	2.82	1.86	9.59
1HGJ.PDB	O, C_CYS_97	NE, C_ARG_224	HE, C_ARG_224	2.77	1.91	24.59
1HGJ.PDB	O, C_CYS_97	NH2, C_ARG_224	HH21, C_ARG_224	2.94	2.09	27.65
1HGJ.PDB	O, C_VAL_223	N, C_LEU_226	H, C_LEU_226	2.93	1.99	13.69
1HGJ.PDB	O, C_SER_228	NH1, C_ARG_229	HH11, C_ARG_229	2.68	1.74	16.79

1HGJ.PDB	O, C_PRO_221	NH2, C_ARG_229	HH22, C_ARG_229	2.63	1.67	13.79
1HGJ.PDB	OD1, C_ASP_101	OG, C_SER_231	HG, C_SER_231	2.91	1.95	9.37
1HGJ.PDB	O, C_ASP_101	N, C_ILE_232	H, C_ILE_232	2.88	1.96	16.46
1HGJ.PDB	O, C_TRP_180	N, C_TYR_233	H, C_TYR_233	2.93	1.96	7.62
1HGJ.PDB	O, C_TYR_178	N, C_THR_235	H, C_THR_235	2.88	1.98	19.28
1HGJ.PDB	O, C_LYS_176	N, C_VAL_237	H, C_VAL_237	2.78	1.87	16.51
1HGJ.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.75	1.79	18.67
1HGJ.PDB	O, B_SER_71	NZ, C_LYS_238	HZ3, C_LYS_238	2.55	1.67	24.42
1HGJ.PDB	O, C_ASN_170	N, C_GLY_240	H, C_GLY_240	2.83	1.96	22.49
1HGJ.PDB	O, C_LYS_238	N, C_ASP_241	H, C_ASP_241	3.00	2.07	14.48
1HGJ.PDB	OD1, C_ASP_241	N, C_VAL_242	H, C_VAL_242	2.79	1.95	25.43
1HGJ.PDB	O, C_MET_168	N, C_LEU_243	H, C_LEU_243	2.93	1.95	4.94
1HGJ.PDB	O, C_SER_205	N, C_VAL_244	H, C_VAL_244	2.99	2.04	12.22
1HGJ.PDB	O, C_VAL_166	N, C_ILE_245	H, C_ILE_245	2.91	1.98	14.47
1HGJ.PDB	O, C_THR_203	N, C_ASN_246	H, C_ASN_246	2.94	1.97	6.29
1HGJ.PDB	OD1, C_ASN_165	ND2, C_ASN_246	HD22, C_ASN_246	2.89	1.93	12.15
1HGJ.PDB	O, C_LEU_164	N, C_SER_247	H, C_SER_247	2.92	2.00	17.46
1HGJ.PDB	O, C_HIS_183	ND2, C_ASN_250	HD22, C_ASN_250	2.86	1.91	11.73
1HGJ.PDB	O, C_GLY_181	N, C_ILE_252	H, C_ILE_252	3.00	2.04	10.63
1HGJ.PDB	O, C_ASN_152	N, C_ALA_253	H, C_ALA_253	2.89	2.00	20.86
1HGJ.PDB	OD1, C_ASN_133	NH2, C_ARG_255	HH22, C_ARG_255	2.54	1.71	27.08
1HGJ.PDB	O, C_ILE_121	N, C_TYR_257	H, C_TYR_257	2.90	2.06	24.92
1HGJ.PDB	O, C_LEU_177	N, C_PHE_258	H, C_PHE_258	2.92	1.95	7.10
1HGJ.PDB	OG, C_SER_115	N, C_ARG_261	H, C_ARG_261	2.96	2.02	14.08
1HGJ.PDB	OE2, C_GLU_119	NH1, C_ARG_261	HH12, C_ARG_261	2.65	1.83	28.56
1HGJ.PDB	OE1, C_GLU_119	NH2, C_ARG_261	HH22, C_ARG_261	2.92	2.03	23.97
1HGJ.PDB	OD2, C_ASP_85	NZ, C_LYS_264	HZ3, C_LYS_264	2.82	1.83	14.94
1HGJ.PDB	O, C_PHE_87	N, C_MET_268	H, C_MET_268	2.85	1.94	18.47
1HGJ.PDB	O, C_PRO_284	OG, C_SER_270	HG, C_SER_270	2.82	1.88	11.05
1HGJ.PDB	O, C_ILE_51	N, C_ASP_275	H, C_ASP_275	2.97	2.06	19.32
1HGJ.PDB	OD1, C_ASP_275	N, C_THR_276	H, C_THR_276	2.79	1.94	23.72
1HGJ.PDB	O, C_ASN_54	N, C_SER_279	H, C_SER_279	2.79	1.87	15.26
1HGJ.PDB	O, C_TYR_302	N, C_ILE_282	H, C_ILE_282	2.92	1.95	6.05
1HGJ.PDB	O, C_THR_283	N, C_GLY_286	H, C_GLY_286	2.79	1.87	14.96
1HGJ.PDB	O, C_LYS_50	N, C_SER_287	H, C_SER_287	2.81	1.85	7.28
1HGJ.PDB	O, C_ALA_304	ND2, C_ASN_290	HD22, C_ASN_290	2.84	1.93	18.26
1HGJ.PDB	OE1, C_GLN_44	NZ, C_LYS_292	HZ1, C_LYS_292	2.73	1.72	10.59
1HGJ.PDB	OD2, C_ASP_291	NZ, C_LYS_292	HZ3, C_LYS_292	2.82	1.84	16.66
1HGJ.PDB	O, C_LYS_307	N, C_GLN_295	H, C_GLN_295	2.91	2.01	20.39
1HGJ.PDB	O, C_ASN_298	NE2, C_GLN_295	HE21, C_GLN_295	2.78	1.83	8.19
1HGJ.PDB	O, C_GLN_44	N, C_ASN_296	H, C_ASN_296	2.84	1.91	13.62
1HGJ.PDB	OE1, C_GLN_295	N, C_VAL_297	H, C_VAL_297	2.75	1.95	28.92
1HGJ.PDB	O, D_LYS_68	NZ, C_LYS_299	HZ2, C_LYS_299	2.96	1.96	14.80
1HGJ.PDB	OD1, C_ASN_298	N, C_ILE_300	H, C_ILE_300	2.82	1.93	19.65
1HGJ.PDB	O, C_ILE_282	N, C_TYR_302	H, C_TYR_302	2.87	2.05	27.80
1HGJ.PDB	O, C_LYS_264	OH, C_TYR_302	HH, C_TYR_302	2.65	1.87	29.71
1HGJ.PDB	O, D_LYS_62	N, C_GLY_303	H, C_GLY_303	2.93	1.98	10.54
1HGJ.PDB	O, C_GLN_295	N, C_VAL_309	H, C_VAL_309	2.88	2.06	26.91
1HGJ.PDB	OG, D_SER_93	N, C_LYS_310	H, C_LYS_310	3.00	2.04	11.61
1HGJ.PDB	OD1, D_ASP_86	NZ, C_LYS_310	HZ3, C_LYS_310	2.94	2.10	29.37
1HGJ.PDB	OE2, C_GLU_41	N, C_LEU_314	H, C_LEU_314	2.78	1.85	13.27
1HGJ.PDB	OE1, C_GLU_41	NZ, C_LYS_315	HZ3, C_LYS_315	2.86	1.91	20.22
1HGJ.PDB	O, C_THR_40	N, C_LEU_316	H, C_LEU_316	2.82	1.87	11.05
1HGJ.PDB	OD1, D_ASN_104	N, C_ALA_317	H, C_ALA_317	2.74	1.82	13.77
1HGJ.PDB	O, C_ASN_38	N, C_THR_318	H, C_THR_318	2.92	2.00	16.68
1HGJ.PDB	O, C_VAL_20	ND2, C_ASN_322	HD21, C_ASN_322	2.87	1.94	14.85
1HGJ.PDB	OE2, C_GLU_35	ND2, C_ASN_322	HD22, C_ASN_322	2.88	1.97	19.99
1HGJ.PDB	OE1, D_GLU_15	NZ, C_LYS_326	HZ1, C_LYS_326	2.91	1.86	5.48

1HGJ.PDB	OD2, D_ASP_112	N, D_GLY_1	H2, D_GLY_1	2.78	1.78	13.54
1HGJ.PDB	OD1, D_ASP_109	N, D_LEU_2	H, D_LEU_2	2.88	1.99	20.57
1HGJ.PDB	OD2, D_ASP_112	N, D_PHE_3	H, D_PHE_3	2.81	2.00	27.45
1HGJ.PDB	OD2, D_ASP_112	N, D_GLY_4	H, D_GLY_4	2.87	1.96	16.53
1HGJ.PDB	OD1, D_ASP_112	N, D_ALA_5	H, D_ALA_5	2.85	1.99	23.99
1HGJ.PDB	O, D_GLY_4	N, D_PHE_9	H, D_PHE_9	2.80	1.87	14.24
1HGJ.PDB	O, D_GLY_13	ND2, D_ASN_12	HD22, D_ASN_12	2.90	2.01	19.14
1HGJ.PDB	O, C_VAL_323	N, D_GLY_13	H, D_GLY_13	2.70	1.77	13.01
1HGJ.PDB	O, C_HIS_17	N, D_TRP_14	H, D_TRP_14	2.84	1.88	10.47
1HGJ.PDB	OG1, D_THR_41	N, D_TRP_21	H, D_TRP_21	2.94	2.03	16.88
1HGJ.PDB	O, C_GLY_16	N, D_GLY_23	H, D_GLY_23	2.95	2.03	16.60
1HGJ.PDB	O, D_ALA_35	N, D_PHE_24	H, D_PHE_24	2.84	1.87	6.75
1HGJ.PDB	O, C_CYS_14	N, D_ARG_25	H, D_ARG_25	2.96	2.03	15.69
1HGJ.PDB	OE1, D_GLN_34	NE, D_ARG_25	HE, D_ARG_25	2.65	1.80	23.08
1HGJ.PDB	O, D_GLY_33	N, D_HIS_26	H, D_HIS_26	2.87	1.95	17.26
1HGJ.PDB	O, C_THR_12	N, D_GLN_27	H, D_GLN_27	2.96	2.04	16.68
1HGJ.PDB	O, D_GLY_31	N, D_ASN_28	H, D_ASN_28	2.92	1.97	10.77
1HGJ.PDB	OD1, D_ASN_146	ND2, D_ASN_28	HD21, D_ASN_28	2.98	2.03	11.81
1HGJ.PDB	OD1, D_ASN_28	N, D_GLU_30	H, D_GLU_30	2.82	1.99	26.55
1HGJ.PDB	O, D_HIS_26	N, D_GLY_33	H, D_GLY_33	2.97	2.10	23.23
1HGJ.PDB	O, D_PHE_24	N, D_ALA_35	H, D_ALA_35	2.80	1.92	21.75
1HGJ.PDB	O, D_TYR_22	N, D_ASP_37	H, D_ASP_37	2.70	1.76	11.08
1HGJ.PDB	OD2, D_ASP_37	N, D_SER_40	H, D_SER_40	2.95	1.99	9.26
1HGJ.PDB	OD2, D_ASP_37	OG, D_SER_40	HG, D_SER_40	2.82	1.96	22.49
1HGJ.PDB	O, D_ASP_37	OG1, D_THR_41	HG1, D_THR_41	2.76	1.85	16.95
1HGJ.PDB	O, D_LEU_38	N, D_GLN_42	H, D_GLN_42	2.96	2.03	15.57
1HGJ.PDB	OD1, D_ASP_46	NE2, D_GLN_42	HE22, D_GLN_42	2.81	1.92	21.12
1HGJ.PDB	O, D_LYS_39	N, D_ALA_43	H, D_ALA_43	2.97	2.01	10.81
1HGJ.PDB	O, D_SER_40	N, D_ALA_44	H, D_ALA_44	2.97	1.99	1.97
1HGJ.PDB	O, D_THR_41	N, D_ILE_45	H, D_ILE_45	2.89	1.93	10.07
1HGJ.PDB	O, D_GLN_42	N, D_ASP_46	H, D_ASP_46	2.76	1.79	4.41
1HGJ.PDB	OE2, D_GLU_114	NE2, D_GLN_47	HE21, D_GLN_47	2.94	2.03	18.44
1HGJ.PDB	O, D_ALA_43	NE2, D_GLN_47	HE22, D_GLN_47	2.90	2.02	20.80
1HGJ.PDB	O, D_ILE_45	N, D_ASN_49	H, D_ASN_49	2.90	1.96	15.06
1HGJ.PDB	O, D_ASP_46	N, D_GLY_50	H, D_GLY_50	2.88	2.00	21.98
1HGJ.PDB	OG1, D_THR_107	NZ, D_LYS_51	HZ1, D_LYS_51	2.97	1.99	16.18
1HGJ.PDB	OE1, D_GLU_103	NZ, D_LYS_51	HZ2, D_LYS_51	2.80	1.76	6.89
1HGJ.PDB	ND1, D_HIS_106	NZ, D_LYS_51	HZ3, D_LYS_51	2.79	1.82	16.80
1HGJ.PDB	O, D_ILE_48	N, D_LEU_52	H, D_LEU_52	2.89	1.98	17.52
1HGJ.PDB	O, D_ASN_49	N, D_ASN_53	H, D_ASN_53	2.86	1.92	13.12
1HGJ.PDB	O, A_THR_28	NE, D_ARG_54	HE, D_ARG_54	2.94	1.98	10.71
1HGJ.PDB	OE1, D_GLU_57	NH1, D_ARG_54	HH11, D_ARG_54	2.87	1.86	9.17
1HGJ.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.84	1.88	15.58
1HGJ.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.89	1.91	5.59
1HGJ.PDB	O, C_LYS_299	NZ, D_LYS_68	HZ1, D_LYS_68	2.93	1.91	11.63
1HGJ.PDB	OE2, D_GLU_85	NZ, D_LYS_68	HZ2, D_LYS_68	2.82	1.80	11.23
1HGJ.PDB	OG, E_SER_107	N, D_ARG_76	H, D_ARG_76	2.86	1.90	9.67
1HGJ.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.85	1.89	10.87
1HGJ.PDB	OE2, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.76	1.76	7.89
1HGJ.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.68	1.69	5.65
1HGJ.PDB	OE1, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.71	1.72	5.59
1HGJ.PDB	OE1, D_GLU_74	NE2, D_GLN_78	HE22, D_GLN_78	2.88	1.94	14.79
1HGJ.PDB	O, D_GLY_75	N, D_ASP_79	H, D_ASP_79	2.96	2.02	12.85
1HGJ.PDB	O, D_GLN_78	N, D_LYS_82	H, D_LYS_82	2.93	1.96	6.74
1HGJ.PDB	O, D_ASP_79	N, D_TYR_83	H, D_TYR_83	2.85	1.90	12.33
1HGJ.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.63	1.81	25.72
1HGJ.PDB	O, D_LEU_80	N, D_VAL_84	H, D_VAL_84	2.81	1.84	7.09
1HGJ.PDB	O, D_LYS_82	N, D_ASP_86	H, D_ASP_86	2.93	1.96	7.56

1HGJ.PDB	O, D_TYR_83	N, D_THR_87	H, D_THR_87	2.89	1.94	10.26
1HGJ.PDB	O, D_VAL_84	N, D_LYS_88	H, D_LYS_88	2.98	2.07	17.30
1HGJ.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.75	1.72	7.31
1HGJ.PDB	O, D_GLU_85	N, D_ILE_89	H, D_ILE_89	2.85	1.88	2.88
1HGJ.PDB	O, D_LYS_88	N, D_TRP_92	H, D_TRP_92	2.93	1.96	4.62
1HGJ.PDB	O, D_ILE_89	N, D_SER_93	H, D_SER_93	2.81	1.94	21.33
1HGJ.PDB	O, D_ILE_89	OG, D_SER_93	HG, D_SER_93	2.87	1.95	15.74
1HGJ.PDB	O, D_ASP_90	N, D_TYR_94	H, D_TYR_94	2.84	1.94	18.59
1HGJ.PDB	O, D_LEU_91	N, D_ASN_95	H, D_ASN_95	2.98	2.00	5.61
1HGJ.PDB	O, D_TYR_94	N, D_LEU_98	H, D_LEU_98	2.94	1.97	5.79
1HGJ.PDB	O, D_ASN_95	N, D_LEU_99	H, D_LEU_99	2.89	1.98	17.69
1HGJ.PDB	O, D_LEU_98	N, D_LEU_102	H, D_LEU_102	2.94	1.98	8.88
1HGJ.PDB	O, D_LEU_99	N, D_GLU_103	H, D_GLU_103	2.96	1.99	8.34
1HGJ.PDB	O, D_VAL_100	N, D_ASN_104	H, D_ASN_104	2.80	1.86	13.01
1HGJ.PDB	O, C_LYS_27	ND2, D_ASN_104	HD22, D_ASN_104	2.90	1.94	10.67
1HGJ.PDB	O, D_LEU_102	N, D_HIS_106	H, D_HIS_106	2.93	1.97	8.46
1HGJ.PDB	O, D_GLU_103	N, D_THR_107	H, D_THR_107	2.85	1.96	20.31
1HGJ.PDB	N, D_HIS_106	N, D_LEU_110	H, D_LEU_110	2.79	1.83	9.65
1HGJ.PDB	O, D_THR_107	OG1, D_THR_111	HG1, D_THR_111	2.84	1.88	5.73
1HGJ.PDB	O, D_ASP_109	N, D_SER_113	H, D_SER_113	2.82	1.86	7.21
1HGJ.PDB	O, B_LEU_2	OG, D_SER_113	HG, D_SER_113	2.68	1.87	27.58
1HGJ.PDB	O, D_LEU_110	N, D_GLU_114	H, D_GLU_114	2.94	1.99	11.05
1HGJ.PDB	O, D_ASP_112	N, D_ASN_116	H, D_ASN_116	2.97	2.01	9.82
1HGJ.PDB	O, D_SER_113	N, D_LYS_117	H, D_LYS_117	2.74	1.86	21.58
1HGJ.PDB	O, D_GLU_114	N, D_LEU_118	H, D_LEU_118	2.99	2.04	11.08
1HGJ.PDB	O, D_ASN_116	N, D_GLU_120	H, D_GLU_120	2.94	1.96	1.58
1HGJ.PDB	O, D_LYS_117	N, D_LYS_121	H, D_LYS_121	2.92	2.02	18.90
1HGJ.PDB	O, D_PHE_119	N, D_ARG_123	H, D_ARG_123	2.94	1.98	8.81
1HGJ.PDB	OE2, D_GLU_120	NH1, D_ARG_123	HH11, D_ARG_123	2.74	1.85	23.39
1HGJ.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.80	1.98	27.33
1HGJ.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.87	2.00	21.99
1HGJ.PDB	OH, B_TYR_141	NH1, D_ARG_127	HH12, D_ARG_127	2.99	2.02	12.89
1HGJ.PDB	O, D_HIS_159	ND2, D_ASN_129	HD21, D_ASN_129	2.95	1.99	10.63
1HGJ.PDB	OH, D_TYR_157	ND2, D_ASN_129	HD22, D_ASN_129	2.79	1.84	10.20
1HGJ.PDB	O, D_LYS_139	N, D_GLU_131	H, D_GLU_131	2.95	2.01	13.86
1HGJ.PDB	O, D_CYS_137	N, D_MET_133	H, D_MET_133	2.85	1.92	14.74
1HGJ.PDB	OD1, D_ASN_135	N, D_CYS_137	H, D_CYS_137	2.89	1.99	19.26
1HGJ.PDB	O, C_LEU_13	N, D_PHE_138	H, D_PHE_138	2.74	1.87	22.25
1HGJ.PDB	O, D_GLU_131	N, D_LYS_139	H, D_LYS_139	2.81	1.86	10.15
1HGJ.PDB	O, C_ALA_11	N, D_ILE_140	H, D_ILE_140	2.80	1.87	15.19
1HGJ.PDB	O, D_ASN_129	N, D_TYR_141	H, D_TYR_141	2.96	2.02	12.67
1HGJ.PDB	OE2, D_GLU_30	N, D_ASN_146	H, D_ASN_146	2.86	1.92	14.29
1HGJ.PDB	O, D_ASP_145	N, D_ILE_149	H, D_ILE_149	2.91	1.96	10.44
1HGJ.PDB	O, D_ASN_146	N, D_GLU_150	H, D_GLU_150	2.91	1.98	15.92
1HGJ.PDB	O, D_ALA_147	N, D_SER_151	H, D_SER_151	2.90	1.98	17.07
1HGJ.PDB	O, D_CYS_148	OG, D_SER_151	HG, D_SER_151	2.70	1.86	22.84
1HGJ.PDB	O, D_GLU_150	N, D_ASN_154	H, D_ASN_154	2.80	1.83	5.11
1HGJ.PDB	O, D_SER_151	N, D_THR_156	H, D_THR_156	2.73	1.90	25.93
1HGJ.PDB	OD1, D_ASN_154	OG1, D_THR_156	HG1, D_THR_156	2.71	1.81	16.75
1HGJ.PDB	NE2, D_HIS_142	OH, D_TYR_157	HH, D_TYR_157	2.78	1.88	18.06
1HGJ.PDB	OD1, D_ASP_158	N, D_ASP_160	H, D_ASP_160	2.92	2.05	23.79
1HGJ.PDB	O, D_HIS_159	N, D_TYR_162	H, D_TYR_162	2.94	2.05	20.16
1HGJ.PDB	O, B_ARG_170	NH1, D_ARG_163	HH12, D_ARG_163	2.74	1.76	11.80
1HGJ.PDB	O, D_TYR_162	N, D_ALA_166	H, D_ALA_166	2.85	1.88	3.22
1HGJ.PDB	O, D_ARG_163	N, D_LEU_167	H, D_LEU_167	2.76	1.82	10.09
1HGJ.PDB	O, D_ASP_164	N, D_ASN_168	H, D_ASN_168	3.00	2.04	9.26
1HGJ.PDB	O, D_ALA_166	N, D_ARG_170	H, D_ARG_170	2.83	1.97	22.68
1HGJ.PDB	O, D_GLU_128	NE, D_ARG_170	HE, D_ARG_170	2.77	1.90	22.62

1HGJ.PDB	OE2, D_GLU_131	NH1, D_ARG_170	HH11, D_ARG_170	2.79	1.80	6.55
1HGJ.PDB	O, D_LEU_167	N, D_PHE_171	H, D_PHE_171	2.92	2.00	16.37
1HGJ.PDB	O, F_ILE_140	N, E_ALA_11	H, E_ALA_11	2.86	1.96	18.18
1HGJ.PDB	O, F_GLN_27	N, E_THR_12	H, E_THR_12	2.93	2.00	15.55
1HGJ.PDB	O, F_PHE_138	N, E_LEU_13	H, E_LEU_13	2.96	1.99	8.56
1HGJ.PDB	O, F_ARG_25	N, E_CYS_14	H, E_CYS_14	2.66	1.82	24.90
1HGJ.PDB	O, F_GLY_136	N, E_LEU_15	H, E_LEU_15	2.91	1.94	3.68
1HGJ.PDB	O, F_GLY_23	N, E_GLY_16	H, E_GLY_16	2.87	1.96	18.32
1HGJ.PDB	O, E_HIS_18	ND1, E_HIS_17	HD1, E_HIS_17	2.90	2.02	21.78
1HGJ.PDB	O, F_TRP_21	N, E_HIS_18	H, E_HIS_18	2.83	1.96	22.19
1HGJ.PDB	OD1, E_ASN_322	N, E_VAL_20	H, E_VAL_20	2.78	1.83	10.50
1HGJ.PDB	O, E_VAL_36	N, E_THR_24	H, E_THR_24	2.85	1.93	16.11
1HGJ.PDB	O, E_ILE_34	N, E_VAL_26	H, E_VAL_26	2.82	1.87	11.16
1HGJ.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.81	1.79	8.50
1HGJ.PDB	O, E_ASP_31	N, E_THR_28	H, E_THR_28	2.74	1.89	24.59
1HGJ.PDB	O, E_VAL_26	N, E_ILE_34	H, E_ILE_34	2.87	1.93	12.94
1HGJ.PDB	O, E_THR_24	N, E_VAL_36	H, E_VAL_36	2.82	1.85	5.68
1HGJ.PDB	O, E_MET_320	N, E_THR_37	H, E_THR_37	2.86	1.90	7.27
1HGJ.PDB	O, E_LEU_316	N, E_THR_40	H, E_THR_40	2.85	2.00	25.13
1HGJ.PDB	O, E_LEU_314	N, E_LEU_42	H, E_LEU_42	2.82	1.95	22.41
1HGJ.PDB	O, E_PHE_294	N, E_GLN_44	H, E_GLN_44	2.85	1.88	6.55
1HGJ.PDB	O, E_SER_46	NE2, E_GLN_44	HE22, E_GLN_44	2.90	2.00	19.51
1HGJ.PDB	O, E_ASN_285	OG, E_SER_47	HG, E_SER_47	2.83	1.92	15.25
1HGJ.PDB	OD2, E_ASP_275	NZ, E_LYS_50	HZ1, E_LYS_50	2.74	1.82	22.90
1HGJ.PDB	O, E_PRO_273	N, E_ILE_51	H, E_ILE_51	2.84	1.88	9.36
1HGJ.PDB	O, E_ASP_275	N, E_ASN_53	H, E_ASN_53	2.80	1.95	24.30
1HGJ.PDB	O, E_GLU_280	NE2, E_HIS_56	HE2, E_HIS_56	2.98	2.06	17.67
1HGJ.PDB	OD2, E_ASP_85	N, E_ARG_57	H, E_ARG_57	2.82	1.89	13.47
1HGJ.PDB	O, E_THR_83	NE, E_ARG_57	HE, E_ARG_57	2.78	1.81	7.69
1HGJ.PDB	O, E_LEU_86	N, E_LEU_59	H, E_LEU_59	2.87	1.91	10.09
1HGJ.PDB	O, E_VAL_88	N, E_GLY_61	H, E_GLY_61	2.97	2.10	22.60
1HGJ.PDB	OD1, E_ASP_60	N, E_ILE_62	H, E_ILE_62	2.86	1.94	15.40
1HGJ.PDB	O, E_GLY_61	N, E_CYS_64	H, E_CYS_64	2.90	1.99	17.47
1HGJ.PDB	O, E_LEU_66	N, E_LEU_70	H, E_LEU_70	2.91	2.02	20.49
1HGJ.PDB	O, E_ILE_67	N, E_LEU_71	H, E_LEU_71	2.82	1.86	7.76
1HGJ.PDB	O, E_ASP_68	N, E_GLY_72	H, E_GLY_72	2.90	1.99	18.41
1HGJ.PDB	OD1, E_ASP_73	ND1, E_HIS_75	HD1, E_HIS_75	2.80	1.88	17.19
1HGJ.PDB	O, E_ASP_63	NE2, E_HIS_75	HE2, E_HIS_75	2.86	1.95	19.12
1HGJ.PDB	O, E_ASP_73	N, E_CYS_76	H, E_CYS_76	2.76	1.82	13.01
1HGJ.PDB	O, E_PRO_74	N, E_ASP_77	H, E_ASP_77	2.93	1.97	10.57
1HGJ.PDB	O, E_CYS_76	N, E_PHE_79	H, E_PHE_79	2.99	2.02	4.96
1HGJ.PDB	O, E_ARG_57	N, E_ASP_85	H, E_ASP_85	2.80	1.90	17.59
1HGJ.PDB	O, E_LEU_59	N, E_VAL_88	H, E_VAL_88	2.98	2.01	5.78
1HGJ.PDB	O, E_MET_268	N, E_GLU_89	H, E_GLU_89	2.79	1.83	9.12
1HGJ.PDB	OD1, E_ASP_60	NE, E_ARG_90	HE, E_ARG_90	2.91	1.94	8.87
1HGJ.PDB	O, E_SER_270	NH1, E_ARG_90	HH11, E_ARG_90	2.71	1.84	24.06
1HGJ.PDB	O, E_ALA_272	NH1, E_ARG_90	HH12, E_ARG_90	2.60	1.68	18.01
1HGJ.PDB	OD2, E_ASP_60	NH2, E_ARG_90	HH21, E_ARG_90	2.83	1.83	8.62
1HGJ.PDB	OD1, E_ASP_271	N, E_SER_91	H, E_SER_91	2.91	1.94	8.21
1HGJ.PDB	OD1, E_ASP_271	OG, E_SER_91	HG, E_SER_91	2.99	2.15	25.95
1HGJ.PDB	OD2, E_ASP_271	OG, E_SER_91	HG, E_SER_91	2.82	1.92	18.47
1HGJ.PDB	OD2, E_ASP_68	OG, E_SER_95	HG, E_SER_95	2.94	2.00	13.81
1HGJ.PDB	OD2, E_ASP_73	N, E_ASN_96	H, E_ASN_96	2.91	1.95	10.69
1HGJ.PDB	OD1, E_ASP_68	OH, E_TYR_100	HH, E_TYR_100	2.88	1.94	12.28
1HGJ.PDB	O, E_ILE_230	N, E_ASP_101	H, E_ASP_101	2.96	2.10	23.29
1HGJ.PDB	OD2, E_ASP_104	OG, E_SER_107	HG, E_SER_107	2.85	1.94	18.67
1HGJ.PDB	O, E_TYR_105	N, E_ARG_109	H, E_ARG_109	2.87	1.90	3.75
1HGJ.PDB	OE2, F_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.76	1.77	12.82

1HGJ.PDB	OD2, D_ASP_79	OG, E_SER_110	HG, E_SER_110	2.79	1.87	15.96
1HGJ.PDB	O, E_SER_107	N, E_LEU_111	H, E_LEU_111	2.87	1.90	6.50
1HGJ.PDB	O, E_ARG_109	N, E_ALA_113	H, E_ALA_113	2.94	2.05	20.26
1HGJ.PDB	O, E_SER_110	N, E_SER_114	H, E_SER_114	2.90	1.95	11.85
1HGJ.PDB	OE2, E_GLU_119	OG1, E_THR_117	HG1, E_THR_117	2.91	1.96	10.96
1HGJ.PDB	O, E_GLU_82	N, E_LEU_118	H, E_LEU_118	2.93	2.00	15.98
1HGJ.PDB	O, E_TYR_257	N, E_ILE_121	H, E_ILE_121	2.86	1.90	7.59
1HGJ.PDB	O, E_ARG_255	N, E_GLU_123	H, E_GLU_123	2.95	1.98	9.79
1HGJ.PDB	O, E_THR_155	N, E_THR_131	H, E_THR_131	2.73	1.86	21.20
1HGJ.PDB	OD1, E_ASN_152	N, E_ASN_133	H, E_ASN_133	2.87	1.94	15.99
1HGJ.PDB	O, E_GLY_146	N, E_SER_136	H, E_SER_136	2.74	1.83	17.73
1HGJ.PDB	OG, E_SER_136	N, E_ALA_138	H, E_ALA_138	2.94	2.00	14.03
1HGJ.PDB	O, E_GLY_144	NZ, E_LYS_140	HZ1, E_LYS_140	2.75	1.78	16.45
1HGJ.PDB	OD1, E_ASN_137	NZ, E_LYS_140	HZ2, E_LYS_140	2.71	1.72	13.56
1HGJ.PDB	OD2, E_ASP_77	NE, E_ARG_141	HE, E_ARG_141	2.84	2.00	27.31
1HGJ.PDB	O, E_PHE_147	NH1, E_ARG_141	HH12, E_ARG_141	2.54	1.62	17.41
1HGJ.PDB	OD1, E_ASP_77	NH2, E_ARG_141	HH21, E_ARG_141	2.84	1.92	21.35
1HGJ.PDB	OD2, E_ASP_77	NH2, E_ARG_141	HH21, E_ARG_141	2.75	1.86	24.32
1HGJ.PDB	O, E_GLY_72	NH2, E_ARG_141	HH22, E_ARG_141	2.88	1.90	10.71
1HGJ.PDB	OD1, E_ASN_137	OG, E_SER_145	HG, E_SER_145	2.96	2.12	24.46
1HGJ.PDB	O, E_SER_136	N, E_GLY_146	H, E_GLY_146	2.92	1.99	15.20
1HGJ.PDB	O, E_GLY_72	N, E_SER_149	H, E_SER_149	2.83	1.94	19.83
1HGJ.PDB	O, E_ALA_253	N, E_ASN_152	H, E_ASN_152	2.81	1.98	26.27
1HGJ.PDB	OH, E_TYR_195	NE1, E_TRP_153	HE1, E_TRP_153	2.83	1.93	19.26
1HGJ.PDB	O, E_LEU_194	N, E_LYS_156	H, E_LYS_156	2.96	2.04	16.52
1HGJ.PDB	O, E_SER_193	NZ, E_LYS_156	HZ2, E_LYS_156	2.72	1.80	21.90
1HGJ.PDB	O, E_SER_247	N, E_LEU_164	H, E_LEU_164	2.72	1.87	23.95
1HGJ.PDB	O, E_ILE_245	N, E_VAL_166	H, E_VAL_166	2.99	2.04	11.20
1HGJ.PDB	O, E_LEU_243	OG1, E_THR_167	HG1, E_THR_167	2.97	2.09	21.09
1HGJ.PDB	O, E_LEU_243	N, E_MET_168	H, E_MET_168	2.90	1.98	16.52
1HGJ.PDB	O, E_ASP_241	N, E_ASN_170	H, E_ASN_170	2.90	1.94	11.02
1HGJ.PDB	O, E_PHE_174	ND2, E_ASN_170	HD21, E_ASN_170	2.85	1.90	10.04
1HGJ.PDB	O, E_VAL_237	ND2, E_ASN_170	HD22, E_ASN_170	2.87	2.05	27.43
1HGJ.PDB	O, E_VAL_237	N, E_LYS_176	H, E_LYS_176	2.91	1.97	13.40
1HGJ.PDB	OE2, E_GLU_123	NZ, E_LYS_176	HZ1, E_LYS_176	2.69	1.80	25.95
1HGJ.PDB	O, E_PHE_258	N, E_LEU_177	H, E_LEU_177	2.99	2.02	6.31
1HGJ.PDB	O, E_THR_235	N, E_TYR_178	H, E_TYR_178	2.83	1.86	3.63
1HGJ.PDB	OE1, E_GLU_123	OH, E_TYR_178	HH, E_TYR_178	2.77	1.83	11.08
1HGJ.PDB	OG1, E_THR_235	NE1, E_TRP_180	HE1, E_TRP_180	2.94	1.96	4.45
1HGJ.PDB	O, E_ASN_250	N, E_HIS_183	H, E_HIS_183	2.92	2.00	17.04
1HGJ.PDB	O, E_ARG_229	N, E_HIS_184	H, E_HIS_184	2.87	1.92	10.49
1HGJ.PDB	OG, E_SER_231	NE2, E_HIS_184	HE2, E_HIS_184	2.75	1.92	26.56
1HGJ.PDB	OG1, E_THR_187	N, E_GLU_190	H, E_GLU_190	2.90	1.96	12.58
1HGJ.PDB	O, E_GLN_197	NE2, E_GLN_191	HE22, E_GLN_191	2.91	1.99	17.51
1HGJ.PDB	O, E_ASN_188	OG1, E_THR_192	HG1, E_THR_192	2.94	1.98	6.07
1HGJ.PDB	O, E_GLN_189	N, E_SER_193	H, E_SER_193	2.85	1.87	2.13
1HGJ.PDB	O, E_GLU_190	N, E_LEU_194	H, E_LEU_194	2.97	2.00	9.20
1HGJ.PDB	O, E_GLN_191	N, E_TYR_195	H, E_TYR_195	2.80	1.85	9.91
1HGJ.PDB	O, E_TYR_195	N, E_GLN_197	H, E_GLN_197	2.71	1.92	29.63
1HGJ.PDB	O, E_TYR_161	NE2, E_GLN_197	HE21, E_GLN_197	2.91	1.96	10.54
1HGJ.PDB	O, E_ASN_248	NE2, E_GLN_197	HE22, E_GLN_197	2.87	1.94	14.62
1HGJ.PDB	OD1, E_ASN_246	NH2, E_ARG_201	HH21, E_ARG_201	2.59	1.74	26.30
1HGJ.PDB	O, E_ILE_213	N, E_VAL_202	H, E_VAL_202	3.00	2.07	14.91
1HGJ.PDB	O, E_ASN_246	N, E_THR_203	H, E_THR_203	2.93	1.98	11.44
1HGJ.PDB	OG1, E_THR_212	OG1, E_THR_203	HG1, E_THR_203	2.93	1.99	12.00
1HGJ.PDB	O, E_GLN_211	N, E_VAL_204	H, E_VAL_204	2.84	1.94	19.22
1HGJ.PDB	O, E_SER_209	N, E_THR_206	H, E_THR_206	2.94	1.97	8.33
1HGJ.PDB	OD1, E_ASP_241	N, E_ARG_207	H, E_ARG_207	2.88	1.92	9.33

1HGJ.PDB	OD1, C_ASP_101	NE2, E_GLN_210	HE22, E_GLN_210	2.94	2.10	26.45
1HGJ.PDB	O, E_VAL_204	N, E_GLN_211	H, E_GLN_211	2.90	1.97	16.00
1HGJ.PDB	O, E_VAL_202	N, E_ILE_213	H, E_ILE_213	2.86	1.94	15.90
1HGJ.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.69	1.86	28.41
1HGJ.PDB	O, E_ASN_216	NH2, E_ARG_220	HH22, E_ARG_220	2.77	1.90	23.93
1HGJ.PDB	O, E_LEU_226	N, E_VAL_223	H, E_VAL_223	2.82	1.86	9.44
1HGJ.PDB	O, E_CYS_97	NE, E_ARG_224	HE, E_ARG_224	2.81	1.96	24.68
1HGJ.PDB	O, E_CYS_97	NH2, E_ARG_224	HH21, E_ARG_224	2.94	2.09	27.02
1HGJ.PDB	O, E_VAL_223	N, E_LEU_226	H, E_LEU_226	2.92	1.98	13.32
1HGJ.PDB	O, E_SER_228	NH1, E_ARG_229	HH11, E_ARG_229	2.73	1.78	16.61
1HGJ.PDB	O, E_PRO_221	NH2, E_ARG_229	HH22, E_ARG_229	2.62	1.66	13.20
1HGJ.PDB	OD1, E_ASP_101	OG, E_SER_231	HG, E_SER_231	2.90	1.95	11.36
1HGJ.PDB	O, E_ASP_101	N, E_ILE_232	H, E_ILE_232	2.88	1.96	15.95
1HGJ.PDB	O, E_TRP_180	N, E_TYR_233	H, E_TYR_233	2.94	1.97	6.84
1HGJ.PDB	O, E_TYR_178	N, E_THR_235	H, E_THR_235	2.90	2.00	19.30
1HGJ.PDB	O, E_LYS_176	N, E_VAL_237	H, E_VAL_237	2.80	1.88	15.33
1HGJ.PDB	O, D_SER_71	NZ, E_LYS_238	HZ2, E_LYS_238	2.65	1.73	22.71
1HGJ.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ3, E_LYS_238	2.87	1.86	13.82
1HGJ.PDB	O, E_ASN_170	N, E_GLY_240	H, E_GLY_240	2.85	1.98	22.38
1HGJ.PDB	OD1, E_ASP_241	N, E_VAL_242	H, E_VAL_242	2.79	1.95	25.35
1HGJ.PDB	O, E_MET_168	N, E_LEU_243	H, E_LEU_243	2.92	1.95	5.02
1HGJ.PDB	O, E_VAL_166	N, E_ILE_245	H, E_ILE_245	2.90	1.96	13.71
1HGJ.PDB	O, E_THR_203	N, E_ASN_246	H, E_ASN_246	2.96	1.99	5.52
1HGJ.PDB	OD1, E_ASN_165	ND2, E_ASN_246	HD22, E_ASN_246	2.89	1.94	11.88
1HGJ.PDB	O, E_LEU_164	N, E_SER_247	H, E_SER_247	2.94	2.02	17.47
1HGJ.PDB	O, E_HIS_183	ND2, E_ASN_250	HD22, E_ASN_250	2.83	1.88	12.22
1HGJ.PDB	O, E_ASN_152	N, E_ALA_253	H, E_ALA_253	2.89	2.00	20.06
1HGJ.PDB	OD1, E_ASN_133	NH2, E_ARG_255	HH22, E_ARG_255	2.55	1.71	26.62
1HGJ.PDB	O, E_ILE_121	N, E_TYR_257	H, E_TYR_257	2.92	2.08	25.41
1HGJ.PDB	O, E_LEU_177	N, E_PHE_258	H, E_PHE_258	2.92	1.95	7.34
1HGJ.PDB	OG, E_SER_115	N, E_ARG_261	H, E_ARG_261	2.94	2.00	14.60
1HGJ.PDB	OE2, E_GLU_119	NH1, E_ARG_261	HH12, E_ARG_261	2.65	1.82	28.15
1HGJ.PDB	OE1, E_GLU_119	NH2, E_ARG_261	HH22, E_ARG_261	2.91	2.01	23.66
1HGJ.PDB	OD2, E_ASP_85	NZ, E_LYS_264	HZ3, E_LYS_264	2.86	1.86	15.01
1HGJ.PDB	O, E_PHE_87	N, E_MET_268	H, E_MET_268	2.83	1.92	18.18
1HGJ.PDB	O, E_PRO_284	OG, E_SER_270	HG, E_SER_270	2.82	1.88	11.49
1HGJ.PDB	OG, E_SER_270	N, E_ALA_272	H, E_ALA_272	2.99	2.05	12.84
1HGJ.PDB	O, E_ILE_51	N, E_ASP_275	H, E_ASP_275	2.93	2.03	19.50
1HGJ.PDB	OD1, E_ASP_275	N, E_THR_276	H, E_THR_276	2.79	1.94	24.04
1HGJ.PDB	O, E_ASN_54	N, E_SER_279	H, E_SER_279	2.81	1.88	14.80
1HGJ.PDB	O, E_TYR_302	N, E_ILE_282	H, E_ILE_282	2.91	1.94	6.79
1HGJ.PDB	O, E_THR_283	N, E_GLY_286	H, E_GLY_286	2.81	1.88	13.99
1HGJ.PDB	O, E_LYS_50	N, E_SER_287	H, E_SER_287	2.83	1.86	7.05
1HGJ.PDB	O, E_ALA_304	ND2, E_ASN_290	HD22, E_ASN_290	2.82	1.92	17.80
1HGJ.PDB	OE1, E_GLN_44	NZ, E_LYS_292	HZ1, E_LYS_292	2.72	1.70	10.33
1HGJ.PDB	OD2, E_ASP_291	NZ, E_LYS_292	HZ3, E_LYS_292	2.83	1.86	17.49
1HGJ.PDB	O, E_LYS_307	N, E_GLN_295	H, E_GLN_295	2.87	1.98	20.11
1HGJ.PDB	O, E_ASN_298	NE2, E_GLN_295	HE21, E_GLN_295	2.74	1.78	8.06
1HGJ.PDB	O, E_GLN_44	N, E_ASN_296	H, E_ASN_296	2.84	1.90	13.41
1HGJ.PDB	OE1, E_GLN_295	N, E_VAL_297	H, E_VAL_297	2.70	1.91	29.61
1HGJ.PDB	O, F_LYS_68	NZ, E_LYS_299	HZ1, E_LYS_299	2.94	1.95	15.31
1HGJ.PDB	OD1, E_ASN_298	N, E_ILE_300	H, E_ILE_300	2.84	1.96	20.15
1HGJ.PDB	O, E_ILE_282	N, E_TYR_302	H, E_TYR_302	2.88	2.04	26.30
1HGJ.PDB	O, E_LYS_264	OH, E_TYR_302	HH, E_TYR_302	2.66	1.88	29.67
1HGJ.PDB	O, F_LYS_62	N, E_GLY_303	H, E_GLY_303	2.92	1.96	9.12
1HGJ.PDB	O, E_GLN_295	N, E_VAL_309	H, E_VAL_309	2.91	2.08	26.42
1HGJ.PDB	OG, F_SER_93	N, E_LYS_310	H, E_LYS_310	2.99	2.03	10.38
1HGJ.PDB	OD1, F_ASP_86	NZ, E_LYS_310	HZ3, E_LYS_310	2.93	2.08	29.22

1HGJ.PDB	OE2, E_GLU_41	N, E_LEU_314	H, E_LEU_314	2.79	1.86	13.14
1HGJ.PDB	OE1, E_GLU_41	NZ, E_LYS_315	HZ3, E_LYS_315	2.86	1.91	20.65
1HGJ.PDB	O, E_THR_40	N, E_LEU_316	H, E_LEU_316	2.79	1.84	10.66
1HGJ.PDB	OD1, F_ASN_104	N, E_ALA_317	H, E_ALA_317	2.73	1.80	11.35
1HGJ.PDB	O, E_ASN_38	N, E_THR_318	H, E_THR_318	2.91	1.98	16.58
1HGJ.PDB	O, E_VAL_20	ND2, E_ASN_322	HD21, E_ASN_322	2.87	1.94	14.58
1HGJ.PDB	OE2, E_GLU_35	ND2, E_ASN_322	HD22, E_ASN_322	2.86	1.96	20.74
1HGJ.PDB	OE2, F_GLU_15	N, E_GLU_325	H, E_GLU_325	2.88	2.08	29.65
1HGJ.PDB	O, E_GLN_327	NZ, E_LYS_326	HZ1, E_LYS_326	2.81	1.90	23.82
1HGJ.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.87	1.86	12.83
1HGJ.PDB	O, E_LYS_326	NE2, E_GLN_327	HE22, E_GLN_327	2.82	1.90	17.58
1HGJ.PDB	OD2, F_ASP_112	N, F_GLY_1	H2, F_GLY_1	2.75	1.76	14.31
1HGJ.PDB	OD1, F_ASP_109	N, F_LEU_2	H, F_LEU_2	2.87	1.99	21.90
1HGJ.PDB	OD2, F_ASP_112	N, F_PHE_3	H, F_PHE_3	2.83	2.02	27.46
1HGJ.PDB	OD2, F_ASP_112	N, F_GLY_4	H, F_GLY_4	2.87	1.95	16.24
1HGJ.PDB	OD1, F_ASP_112	N, F_ALA_5	H, F_ALA_5	2.84	1.98	23.38
1HGJ.PDB	OD1, F_ASP_112	N, F_ILE_6	H, F_ILE_6	3.00	2.08	18.28
1HGJ.PDB	O, F_GLY_4	N, F_PHE_9	H, F_PHE_9	2.79	1.86	13.96
1HGJ.PDB	O, F_GLY_13	ND2, F_ASN_12	HD22, F_ASN_12	2.89	2.02	22.28
1HGJ.PDB	O, E_VAL_323	N, F_GLY_13	H, F_GLY_13	2.69	1.76	10.96
1HGJ.PDB	O, E_HIS_17	N, F_TRP_14	H, F_TRP_14	2.84	1.89	11.67
1HGJ.PDB	OG1, F_THR_41	N, F_TRP_21	H, F_TRP_21	2.96	2.04	16.61
1HGJ.PDB	O, E_GLY_16	N, F_GLY_23	H, F_GLY_23	2.93	2.01	16.90
1HGJ.PDB	O, F_ALA_35	N, F_PHE_24	H, F_PHE_24	2.82	1.85	6.05
1HGJ.PDB	O, E_CYS_14	N, F_ARG_25	H, F_ARG_25	2.87	1.99	20.85
1HGJ.PDB	OE1, F_GLN_34	NE, F_ARG_25	HE, F_ARG_25	2.86	2.05	28.42
1HGJ.PDB	OE1, F_GLN_34	NH2, F_ARG_25	HH21, F_ARG_25	2.64	1.73	20.69
1HGJ.PDB	O, F_GLY_33	N, F_HIS_26	H, F_HIS_26	2.93	2.04	19.59
1HGJ.PDB	O, E_THR_12	N, F_GLN_27	H, F_GLN_27	2.89	1.97	15.73
1HGJ.PDB	O, F_GLY_31	N, F_ASN_28	H, F_ASN_28	2.76	1.81	11.08
1HGJ.PDB	OD1, F_ASN_146	ND2, F_ASN_28	HD21, F_ASN_28	2.81	1.89	16.64
1HGJ.PDB	O, F_CYS_144	ND2, F_ASN_28	HD22, F_ASN_28	2.86	1.94	16.87
1HGJ.PDB	O, F_PHE_24	N, F_ALA_35	H, F_ALA_35	2.77	1.91	22.75
1HGJ.PDB	O, F_TYR_22	N, F_ASP_37	H, F_ASP_37	2.70	1.77	12.58
1HGJ.PDB	OD2, F_ASP_37	N, F_SER_40	H, F_SER_40	2.96	1.99	8.62
1HGJ.PDB	OD2, F_ASP_37	OG, F_SER_40	HG, F_SER_40	2.80	1.95	24.06
1HGJ.PDB	O, F_ASP_37	OG1, F_THR_41	HG1, F_THR_41	2.72	1.84	19.21
1HGJ.PDB	O, F_LEU_38	N, F_GLN_42	H, F_GLN_42	2.93	2.00	15.35
1HGJ.PDB	OD1, F_ASP_46	NE2, F_GLN_42	HE22, F_GLN_42	2.80	1.92	21.18
1HGJ.PDB	O, F_LYS_39	N, F_ALA_43	H, F_ALA_43	2.93	1.97	8.45
1HGJ.PDB	O, F_SER_40	N, F_ALA_44	H, F_ALA_44	2.96	1.98	2.14
1HGJ.PDB	O, F_THR_41	N, F_ILE_45	H, F_ILE_45	2.88	1.94	11.66
1HGJ.PDB	O, F_GLN_42	N, F_ASP_46	H, F_ASP_46	2.77	1.80	2.95
1HGJ.PDB	OE2, F_GLU_114	NE2, F_GLN_47	HE21, F_GLN_47	2.95	2.04	18.06
1HGJ.PDB	O, F_ALA_43	NE2, F_GLN_47	HE22, F_GLN_47	2.95	2.07	21.45
1HGJ.PDB	O, F_ILE_45	N, F_ASN_49	H, F_ASN_49	2.87	1.94	15.82
1HGJ.PDB	O, F_ASP_46	N, F_GLY_50	H, F_GLY_50	2.83	1.94	20.73
1HGJ.PDB	OE1, F_GLU_103	NZ, F_LYS_51	HZ2, F_LYS_51	2.79	1.75	5.77
1HGJ.PDB	ND1, F_HIS_106	NZ, F_LYS_51	HZ3, F_LYS_51	2.75	1.79	17.21
1HGJ.PDB	O, F_ILE_48	N, F_LEU_52	H, F_LEU_52	2.90	1.98	16.71
1HGJ.PDB	O, F_ASN_49	N, F_ASN_53	H, F_ASN_53	2.87	1.94	13.91
1HGJ.PDB	OE1, F_GLU_57	NH1, F_ARG_54	HH11, F_ARG_54	2.86	1.86	9.70
1HGJ.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.77	1.81	14.54
1HGJ.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.90	1.93	7.02
1HGJ.PDB	O, E_LYS_299	NZ, F_LYS_68	HZ1, F_LYS_68	2.93	1.90	4.77
1HGJ.PDB	OE2, F_GLU_85	NZ, F_LYS_68	HZ2, F_LYS_68	2.74	1.77	18.09
1HGJ.PDB	OG, A_SER_107	N, F_ARG_76	H, F_ARG_76	2.85	1.88	6.29
1HGJ.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.85	1.89	12.57

1HGJ.PDB	OE2, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.70	1.70	4.55
1HGJ.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.65	1.66	2.84
1HGJ.PDB	OE1, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.72	1.73	7.95
1HGJ.PDB	OE1, F_GLU_74	NE2, F_GLN_78	HE22, F_GLN_78	2.92	1.97	13.10
1HGJ.PDB	O, F_GLY_75	N, F_ASP_79	H, F_ASP_79	2.96	2.02	12.63
1HGJ.PDB	O, F_GLN_78	N, F_LYS_82	H, F_LYS_82	2.96	1.99	6.52
1HGJ.PDB	O, F_ASP_79	N, F_TYR_83	H, F_TYR_83	2.83	1.89	13.63
1HGJ.PDB	OE1, B_GLU_85	OH, F_TYR_83	HH, F_TYR_83	2.53	1.75	28.54
1HGJ.PDB	O, F_LEU_80	N, F_VAL_84	H, F_VAL_84	2.82	1.86	7.45
1HGJ.PDB	O, F_LYS_82	N, F_ASP_86	H, F_ASP_86	2.93	1.97	9.90
1HGJ.PDB	O, F_TYR_83	N, F_THR_87	H, F_THR_87	2.88	1.95	13.71
1HGJ.PDB	O, F_VAL_84	N, F_LYS_88	H, F_LYS_88	2.98	2.03	12.44
1HGJ.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.70	1.68	8.19
1HGJ.PDB	O, F_GLU_85	N, F_ILE_89	H, F_ILE_89	2.86	1.88	2.87
1HGJ.PDB	O, F_LYS_88	N, F_TRP_92	H, F_TRP_92	2.93	1.96	5.23
1HGJ.PDB	O, F_ILE_89	N, F_SER_93	H, F_SER_93	2.83	1.94	19.77
1HGJ.PDB	O, F_ILE_89	OG, F_SER_93	HG, F_SER_93	2.86	1.95	15.80
1HGJ.PDB	O, F_ASP_90	N, F_TYR_94	H, F_TYR_94	2.83	1.93	19.07
1HGJ.PDB	O, F_TYR_94	N, F_LEU_98	H, F_LEU_98	2.95	1.98	6.19
1HGJ.PDB	O, F_ASN_95	N, F_LEU_99	H, F_LEU_99	2.87	1.97	18.16
1HGJ.PDB	O, F_LEU_98	N, F_LEU_102	H, F_LEU_102	2.95	1.98	8.07
1HGJ.PDB	O, F_LEU_99	N, F_GLU_103	H, F_GLU_103	2.95	1.99	9.09
1HGJ.PDB	O, F_VAL_100	N, F_ASN_104	H, F_ASN_104	2.81	1.86	11.07
1HGJ.PDB	O, E_LYS_27	ND2, F_ASN_104	HD22, F_ASN_104	2.91	1.96	11.78
1HGJ.PDB	O, F_LEU_102	N, F_HIS_106	H, F_HIS_106	2.94	1.98	8.79
1HGJ.PDB	O, F_GLU_103	N, F_THR_107	H, F_THR_107	2.86	1.95	17.68
1HGJ.PDB	O, F_HIS_106	N, F_LEU_110	H, F_LEU_110	2.80	1.84	7.98
1HGJ.PDB	O, F_THR_107	OG1, F_THR_111	HG1, F_THR_111	2.89	1.92	1.87
1HGJ.PDB	O, F_ASP_109	N, F_SER_113	H, F_SER_113	2.81	1.84	6.27
1HGJ.PDB	O, D_LEU_2	OG, F_SER_113	HG, F_SER_113	2.74	1.92	26.51
1HGJ.PDB	O, F_LEU_110	N, F_GLU_114	H, F_GLU_114	2.93	1.97	10.83
1HGJ.PDB	O, F_ASP_112	N, F_ASN_116	H, F_ASN_116	2.99	2.03	9.83
1HGJ.PDB	O, F_SER_113	N, F_LYS_117	H, F_LYS_117	2.74	1.86	21.34
1HGJ.PDB	O, F_GLU_114	N, F_LEU_118	H, F_LEU_118	2.96	2.00	9.84
1HGJ.PDB	O, F_ASN_116	N, F_GLU_120	H, F_GLU_120	2.93	1.95	2.43
1HGJ.PDB	O, F_LYS_117	N, F_LYS_121	H, F_LYS_121	2.95	2.03	16.46
1HGJ.PDB	O, F_PHE_119	N, F_ARG_123	H, F_ARG_123	2.92	1.97	10.33
1HGJ.PDB	OE2, F_GLU_120	NH1, F_ARG_123	HH11, F_ARG_123	2.73	1.86	24.44
1HGJ.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.92	2.09	27.65
1HGJ.PDB	OE2, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.96	2.06	20.98
1HGJ.PDB	O, F_HIS_159	ND2, F_ASN_129	HD21, F_ASN_129	2.97	2.01	8.92
1HGJ.PDB	OH, F_TYR_157	ND2, F_ASN_129	HD22, F_ASN_129	2.75	1.85	17.65
1HGJ.PDB	O, F_LYS_139	N, F_GLU_131	H, F_GLU_131	2.94	1.99	12.85
1HGJ.PDB	O, F_CYS_137	N, F_MET_133	H, F_MET_133	2.84	1.91	14.51
1HGJ.PDB	OD1, F_ASN_135	N, F_CYS_137	H, F_CYS_137	2.98	2.16	26.53
1HGJ.PDB	O, E_LEU_13	N, F_PHE_138	H, F_PHE_138	2.73	1.87	22.18
1HGJ.PDB	O, F_GLU_131	N, F_LYS_139	H, F_LYS_139	2.81	1.86	9.38
1HGJ.PDB	O, E_ALA_11	N, F_ILE_140	H, F_ILE_140	2.78	1.87	17.89
1HGJ.PDB	O, F_ASN_129	N, F_TYR_141	H, F_TYR_141	2.96	2.03	14.20
1HGJ.PDB	OE2, F_GLU_165	N, F_LYS_143	H, F_LYS_143	2.99	2.05	14.57
1HGJ.PDB	O, F_ASP_145	N, F_ILE_149	H, F_ILE_149	2.90	1.95	10.28
1HGJ.PDB	O, F_ASN_146	N, F_GLU_150	H, F_GLU_150	2.89	1.95	14.81
1HGJ.PDB	O, F_ALA_147	N, F_SER_151	H, F_SER_151	2.90	2.00	18.77
1HGJ.PDB	O, F_CYS_148	OG, F_SER_151	HG, F_SER_151	2.72	1.92	27.65
1HGJ.PDB	O, F_GLU_150	N, F_ASN_154	H, F_ASN_154	2.78	1.81	1.94
1HGJ.PDB	OD1, F_ASP_158	N, F_ASP_160	H, F_ASP_160	2.95	2.08	23.42
1HGJ.PDB	O, F_HIS_159	N, F_TYR_162	H, F_TYR_162	2.96	2.07	20.30
1HGJ.PDB	O, D_ARG_170	NH1, F_ARG_163	HH12, F_ARG_163	2.89	1.91	11.37

1HGJ.PDB	O, F_TYR_162	N, F_ALA_166	H, F_ALA_166	2.89	1.92	3.44
1HGJ.PDB	O, F_ARG_163	N, F_LEU_167	H, F_LEU_167	2.76	1.81	9.28
1HGJ.PDB	O, F_ASP_164	N, F_ASN_168	H, F_ASN_168	2.99	2.03	9.70
1HGJ.PDB	O, F_ALA_166	N, F_ARG_170	H, F_ARG_170	2.86	1.98	21.69
1HGJ.PDB	O, F_GLU_128	NE, F_ARG_170	HE, F_ARG_170	2.77	1.90	22.39
1HGJ.PDB	OE2, F_GLU_131	NH1, F_ARG_170	HH11, F_ARG_170	2.79	1.80	6.77
1HGJ.PDB	O, F_LEU_167	N, F_PHE_171	H, F_PHE_171	2.94	2.02	16.73
1OSP.PDB	OG, L_SER_26	N, L_GLN_3	H, L_GLN_3	2.70	1.79	13.92
1OSP.PDB	O, L_LYS_24	N, L_SER_5	H, L_SER_5	2.66	1.74	13.88
1OSP.PDB	O, L_TYR_86	NE2, L_GLN_6	HE21, L_GLN_6	2.96	2.00	8.59
1OSP.PDB	O, L_LYS_103	N, L_PHE_11	H, L_PHE_11	2.89	1.98	18.16
1OSP.PDB	O, L_GLU_105	N, L_VAL_13	H, L_VAL_13	2.80	1.85	11.83
1OSP.PDB	O, L_LEU_78	N, L_GLY_16	H, L_GLY_16	2.67	1.75	12.23
1OSP.PDB	OD1, L_ASP_17	N, L_ARG_18	H, L_ARG_18	2.90	2.10	29.03
1OSP.PDB	O, L_ILE_75	N, L_VAL_19	H, L_VAL_19	2.73	1.79	10.56
1OSP.PDB	O, L_LEU_73	N, L_ILE_21	H, L_ILE_21	2.79	1.84	10.88
1OSP.PDB	O, L_TYR_71	N, L_CYS_23	H, L_CYS_23	2.71	1.82	18.30
1OSP.PDB	O, L_SER_5	N, L_LYS_24	H, L_LYS_24	2.95	2.04	17.66
1OSP.PDB	OH, L_TYR_71	N, L_SER_31	H, L_SER_31	2.95	2.08	22.39
1OSP.PDB	O, L_TYR_30	NH1, L_ARG_32	HH11, L_ARG_32	2.63	1.69	15.15
1OSP.PDB	O, O_LYS_44	NH1, L_ARG_32	HH12, L_ARG_32	2.98	2.09	22.73
1OSP.PDB	O, O_SER_43	NH2, L_ARG_32	HH22, L_ARG_32	2.91	1.93	9.19
1OSP.PDB	O, L_SER_31	N, L_LEU_33	H, L_LEU_33	2.98	2.14	25.04
1OSP.PDB	O, L_GLN_89	N, L_ALA_34	H, L_ALA_34	2.77	1.82	10.76
1OSP.PDB	O, L_ILE_48	N, L_TRP_35	H, L_TRP_35	2.95	2.03	16.19
1OSP.PDB	O, L_PHE_87	N, L_TYR_36	H, L_TYR_36	2.75	1.89	22.90
1OSP.PDB	OE1, L_GLN_89	OH, L_TYR_36	HH, L_TYR_36	2.81	1.86	10.05
1OSP.PDB	O, L_ARG_45	N, L_GLN_37	H, L_GLN_37	2.92	1.98	13.78
1OSP.PDB	O, L_THR_85	N, L_GLN_38	H, L_GLN_38	2.68	1.77	15.79
1OSP.PDB	O, L_ASN_42	NE2, L_GLN_38	HE22, L_GLN_38	2.84	1.91	14.33
1OSP.PDB	O, L_GLN_37	N, L_ARG_45	H, L_ARG_45	2.71	1.86	23.84
1OSP.PDB	O, L_TRP_35	N, L_LEU_47	H, L_LEU_47	2.77	1.81	8.27
1OSP.PDB	O, L_SER_53	N, L_SER_49	H, L_SER_49	2.83	1.86	5.93
1OSP.PDB	OH, L_TYR_91	N, L_GLY_50	H, L_GLY_50	2.94	2.04	18.66
1OSP.PDB	O, L_LEU_33	N, L_ALA_51	H, L_ALA_51	2.85	1.96	19.10
1OSP.PDB	O, L_GLY_50	N, L_THR_52	H, L_THR_52	2.84	2.01	25.88
1OSP.PDB	O, L_SER_49	N, L_SER_53	H, L_SER_53	2.91	2.11	29.67
1OSP.PDB	O, L_LEU_47	N, L_GLU_55	H, L_GLU_55	2.98	2.09	21.52
1OSP.PDB	O, L_LEU_46	NE1, L_TRP_57	HE1, L_TRP_57	2.86	1.90	10.61
1OSP.PDB	O, L_SER_74	N, L_SER_63	H, L_SER_63	2.92	2.11	28.83
1OSP.PDB	O, L_THR_72	N, L_SER_65	H, L_SER_65	2.98	2.07	17.30
1OSP.PDB	O, L_CYS_23	N, L_TYR_71	H, L_TYR_71	2.86	1.98	20.08
1OSP.PDB	O, L_ILE_21	N, L_LEU_73	H, L_LEU_73	2.87	1.98	20.14
1OSP.PDB	O, L_SER_63	N, L_SER_74	H, L_SER_74	2.74	1.79	7.99
1OSP.PDB	O, L_VAL_19	N, L_ILE_75	H, L_ILE_75	2.84	1.89	12.51
1OSP.PDB	O, L_ASP_17	N, L_LEU_78	H, L_LEU_78	2.81	1.87	13.11
1OSP.PDB	O, L_GLN_79	N, L_ASP_82	H, L_ASP_82	2.86	1.91	11.93
1OSP.PDB	O, L_GLN_38	N, L_THR_85	H, L_THR_85	2.92	1.95	4.18
1OSP.PDB	O, L_THR_102	N, L_TYR_86	H, L_TYR_86	2.89	1.93	8.08
1OSP.PDB	O, L_ASP_82	OH, L_TYR_86	HH, L_TYR_86	2.85	1.91	12.11
1OSP.PDB	O, L_TYR_36	N, L_PHE_87	H, L_PHE_87	2.96	2.01	13.11
1OSP.PDB	O, L_ALA_34	N, L_GLN_89	H, L_GLN_89	2.85	2.04	28.87
1OSP.PDB	O, L_GLN_90	NE2, L_GLN_89	HE22, L_GLN_89	2.86	2.00	23.53
1OSP.PDB	O, L_THR_97	N, L_GLN_90	H, L_GLN_90	2.93	2.01	16.17
1OSP.PDB	O, L_SER_93	NE2, L_GLN_90	HE21, L_GLN_90	2.98	2.01	7.86
1OSP.PDB	OG1, L_THR_97	NE2, L_GLN_90	HE22, L_GLN_90	3.00	2.06	15.72
1OSP.PDB	O, L_ARG_32	N, L_TYR_91	H, L_TYR_91	2.95	1.99	9.54
1OSP.PDB	OE1, L_GLN_90	N, L_TRP_92	H, L_TRP_92	2.79	1.98	27.96

1OSP.PDB	O, L_CYS_88	N, L_GLY_99	H, L_GLY_99	2.75	1.80	9.69
1OSP.PDB	OE1, L_GLN_6	N, L_GLY_101	H, L_GLY_101	2.85	1.99	22.93
1OSP.PDB	O, L_TYR_86	N, L_THR_102	H, L_THR_102	2.94	2.02	17.58
1OSP.PDB	O, L_SER_8	OG1, L_THR_102	HG1, L_THR_102	2.69	1.79	17.03
1OSP.PDB	O, L_SER_9	N, L_LYS_103	H, L_LYS_103	2.69	1.74	5.66
1OSP.PDB	O, L_ALA_84	N, L_LEU_104	H, L_LEU_104	2.92	2.02	18.72
1OSP.PDB	O, L_PHE_11	N, L_GLU_105	H, L_GLU_105	2.91	2.04	22.49
1OSP.PDB	OE1, L_GLN_166	N, L_ILE_106	H, L_ILE_106	2.92	1.96	10.71
1OSP.PDB	O, L_VAL_13	N, L_LYS_107	H, L_LYS_107	2.80	1.92	21.29
1OSP.PDB	O, L_ALA_109	NE, L_ARG_108	HE, L_ARG_108	2.74	1.82	13.78
1OSP.PDB	O, L ASP_170	NH1, L_ARG_108	HH11, L_ARG_108	2.91	1.95	11.72
1OSP.PDB	O, L_TYR_140	N, L_ALA_111	H, L_ALA_111	2.99	2.03	8.54
1OSP.PDB	O, L ASN_137	N, L_THR_114	H, L_THR_114	2.83	1.86	3.43
1OSP.PDB	O, L_PHE_135	N, L_SER_116	H, L_SER_116	2.91	2.00	18.69
1OSP.PDB	O, L_VAL_133	N, L_PHE_118	H, L_PHE_118	2.70	1.85	23.89
1OSP.PDB	O, L_SER_122	N, L_THR_126	H, L_THR_126	2.83	1.95	20.51
1OSP.PDB	O, L_SER_122	OG1, L_THR_126	HG1, L_THR_126	2.68	1.79	17.62
1OSP.PDB	O, L_LEU_125	N, L_GLY_128	H, L_GLY_128	2.89	1.98	18.00
1OSP.PDB	OE1, L_GLN_124	N, L_SER_131	H, L_SER_131	2.84	2.03	28.15
1OSP.PDB	O, L_LEU_179	N, L_VAL_132	H, L_VAL_132	2.99	2.03	9.27
1OSP.PDB	O, L_PHE_118	N, L_VAL_133	H, L_VAL_133	2.94	1.99	10.25
1OSP.PDB	O, L_SER_177	N, L_CYS_134	H, L_CYS_134	2.87	1.96	17.37
1OSP.PDB	O, L_SER_116	N, L_PHE_135	H, L_PHE_135	2.92	2.02	19.40
1OSP.PDB	O, L_MET_175	N, L_LEU_136	H, L_LEU_136	2.84	1.89	10.42
1OSP.PDB	O, L_THR_114	N, L ASN_137	H, L ASN_137	2.82	1.87	10.96
1OSP.PDB	O, L_TYR_173	N, L_PHE_139	H, L_PHE_139	2.82	1.85	4.99
1OSP.PDB	OE1, L_GLU_105	OH, L_TYR_140	HH, L_TYR_140	2.90	2.03	21.23
1OSP.PDB	O, L_THR_197	N, L ASN_145	H, L ASN_145	2.93	2.05	21.16
1OSP.PDB	O, L_GLU_195	N, L_LYS_147	H, L_LYS_147	2.84	1.90	13.83
1OSP.PDB	OG, L_SER_177	NE1, L_TRP_148	HE1, L_TRP_148	2.94	1.97	6.03
1OSP.PDB	O, L_THR_193	N, L_LYS_149	H, L_LYS_149	2.86	1.89	5.27
1OSP.PDB	O, L_SER_153	N, L_ILE_150	H, L_ILE_150	2.73	1.84	20.13
1OSP.PDB	O, L_SER_191	N, L ASP_151	H, L ASP_151	2.90	1.94	7.97
1OSP.PDB	O, L_TRP_148	N, L_ARG_155	H, L_ARG_155	2.67	1.85	27.49
1OSP.PDB	O, L_SER_176	N, L_SER_162	H, L_SER_162	2.90	1.97	13.57
1OSP.PDB	O, L_ILE_106	NE2, L_GLN_166	HE21, L_GLN_166	2.72	1.85	21.90
1OSP.PDB	OD1, L ASP_167	N, L_LYS_169	H, L_LYS_169	2.91	2.06	23.22
1OSP.PDB	OD1, L ASP_167	N, L ASP_170	H, L ASP_170	2.97	2.06	17.28
1OSP.PDB	OD1, L ASP_170	N, L_THR_172	H, L_THR_172	2.93	1.99	11.17
1OSP.PDB	O, L_PHE_139	N, L_TYR_173	H, L_TYR_173	2.78	1.85	13.38
1OSP.PDB	O, L_LEU_136	N, L_MET_175	H, L_MET_175	2.90	2.00	19.13
1OSP.PDB	O, L_SER_162	N, L_SER_176	H, L_SER_176	2.94	1.99	10.89
1OSP.PDB	O, L_CYS_134	N, L_SER_177	H, L_SER_177	2.92	1.98	13.57
1OSP.PDB	O, L_LEU_160	N, L_THR_178	H, L_THR_178	2.95	1.99	8.96
1OSP.PDB	O, L_VAL_132	N, L_LEU_179	H, L_LEU_179	2.86	1.89	6.54
1OSP.PDB	O, L_GLY_158	N, L_THR_180	H, L_THR_180	2.81	1.87	11.29
1OSP.PDB	OG, L_SER_131	OG1, L_THR_180	HG1, L_THR_180	2.85	1.92	11.66
1OSP.PDB	O, L_ALA_130	N, L_LEU_181	H, L_LEU_181	2.78	1.82	7.56
1OSP.PDB	O, L_GLY_128	N, L_LYS_183	H, L_LYS_183	2.85	1.89	9.20
1OSP.PDB	O, L_THR_182	N, L_TYR_186	H, L_TYR_186	2.97	2.01	7.10
1OSP.PDB	O, L_LYS_183	N, L_GLU_187	H, L_GLU_187	2.92	1.97	10.78
1OSP.PDB	O, L_GLU_185	N, L_ARG_188	H, L_ARG_188	2.88	2.00	21.14
1OSP.PDB	O, L_PHE_209	N, L_TYR_192	H, L_TYR_192	2.89	1.92	5.15
1OSP.PDB	O, L_LYS_207	N, L_CYS_194	H, L_CYS_194	3.00	2.06	13.98
1OSP.PDB	O, L_LYS_147	N, L_GLU_195	H, L_GLU_195	2.86	1.93	14.83
1OSP.PDB	O, L_ILE_205	N, L_ALA_196	H, L_ALA_196	2.74	1.78	0.99
1OSP.PDB	O, L ASN_145	N, L_THR_197	H, L_THR_197	2.74	1.79	7.28
1OSP.PDB	OD2, L ASP_110	NZ, L_LYS_199	HZ3, L_LYS_199	2.64	1.82	29.88

1OSP.PDB	O, L_ALA_196	N, L_ILE_205	H, L_ILE_205	2.88	2.01	22.87
1OSP.PDB	O, L_TYR_192	N, L_PHE_209	H, L_PHE_209	2.99	2.09	20.05
1OSP.PDB	O, L_ASN_190	N, L_ARG_211	H, L_ARG_211	2.57	1.73	22.30
1OSP.PDB	OD1, L_ASN_190	N, L_ASN_212	H, L_ASN_212	2.63	1.70	14.44
1OSP.PDB	O, H_THR_25	N, H_GLN_3	H, H_GLN_3	2.84	1.98	24.33
1OSP.PDB	O, H_THR_21	N, H_SER_7	H, H_SER_7	2.81	1.95	22.81
1OSP.PDB	O, H_THR_117	N, H_VAL_12	H, H_VAL_12	2.94	2.00	13.37
1OSP.PDB	O, H_VAL_85	N, H_SER_15	H, H_SER_15	2.92	1.95	6.64
1OSP.PDB	O, H_LYS_13	N, H_GLN_16	H, H_GLN_16	3.00	2.09	18.64
1OSP.PDB	OD1, H_ASN_83	OG1, H_THR_17	HG1, H_THR_17	2.79	1.95	24.49
1OSP.PDB	O, H_LEU_82	N, H_LEU_18	H, H_LEU_18	2.68	1.78	16.36
1OSP.PDB	O, H_LEU_80	N, H_LEU_20	H, H_LEU_20	2.94	1.99	11.52
1OSP.PDB	O, H_SER_7	N, H_THR_21	H, H_THR_21	2.82	1.88	11.48
1OSP.PDB	O, H_TYR_78	N, H_CYS_22	H, H_CYS_22	2.86	1.91	11.66
1OSP.PDB	O, H_GLN_5	N, H_SER_23	H, H_SER_23	2.89	1.92	6.27
1OSP.PDB	O, H_GLN_3	N, H_THR_25	H, H_THR_25	2.88	1.93	10.50
1OSP.PDB	OD1, H_ASN_76	N, H_ILE_29	H, H_ILE_29	2.92	1.99	15.63
1OSP.PDB	O, H_ILE_51	N, H_TRP_34	H, H_TRP_34	2.95	1.99	10.12
1OSP.PDB	O, H_SER_31	NE1, H_TRP_34	HE1, H_TRP_34	2.85	1.98	23.03
1OSP.PDB	O, H_ALA_96	N, H_ASP_35	H, H_ASP_35	2.77	1.81	7.66
1OSP.PDB	O, H_GLY_49	N, H_TRP_36	H, H_TRP_36	2.89	2.03	23.14
1OSP.PDB	O, H_TYR_94	N, H_ILE_37	H, H_ILE_37	2.84	1.87	8.13
1OSP.PDB	O, H_GLU_46	N, H_ARG_38	H, H_ARG_38	2.95	1.99	11.63
1OSP.PDB	OE1, H_GLU_46	NH1, H_ARG_38	HH11, H_ARG_38	2.77	1.80	9.20
1OSP.PDB	OH, H_TYR_93	NH2, H_ARG_38	HH21, H_ARG_38	2.83	1.87	12.82
1OSP.PDB	OD1, H_ASP_89	NH2, H_ARG_38	HH22, H_ARG_38	2.83	1.91	19.07
1OSP.PDB	O, H_THR_92	N, H_LYS_39	H, H_LYS_39	2.72	1.83	19.36
1OSP.PDB	O, H_LYS_44	N, H_PHE_40	H, H_PHE_40	2.72	1.83	18.74
1OSP.PDB	O, H_PHE_40	N, H_ASN_43	H, H_ASN_43	2.74	1.91	24.90
1OSP.PDB	O, H_ARG_38	N, H_GLU_46	H, H_GLU_46	2.94	2.08	24.27
1OSP.PDB	O, H_TRP_36	N, H_MET_48	H, H_MET_48	2.82	1.92	18.56
1OSP.PDB	O, H_TRP_34	N, H_ILE_51	H, H_ILE_51	2.94	2.01	16.05
1OSP.PDB	O, H_GLY_56	N, H_ARG_52	H, H_ARG_52	2.70	1.82	20.54
1OSP.PDB	O, H_ARG_52	N, H_GLY_55	H, H_GLY_55	2.98	2.16	28.05
1OSP.PDB	O, H_MET_48	N, H_ASN_60	H, H_ASN_60	2.81	1.84	4.94
1OSP.PDB	O, H_PHE_47	ND2, H_ASN_60	HD22, H_ASN_60	2.80	1.84	6.91
1OSP.PDB	OD1, H_ASN_60	N, H_SER_62	H, H_SER_62	2.92	1.99	15.17
1OSP.PDB	OD2, L_ASP_1	OG, H_SER_62	HG, H_SER_62	2.98	2.17	26.53
1OSP.PDB	O, H_GLN_81	N, H_SER_68	H, H_SER_68	2.92	2.02	18.77
1OSP.PDB	OH, H_TYR_59	N, H_ILE_69	H, H_ILE_69	2.83	1.90	13.21
1OSP.PDB	O, H_HIS_77	N, H_ASP_72	H, H_ASP_72	2.76	1.83	13.63
1OSP.PDB	OD1, H_ASP_72	N, H_LYS_75	H, H_LYS_75	2.98	2.11	21.21
1OSP.PDB	O, H_GLU_27	ND2, H_ASN_76	HD21, H_ASN_76	2.87	1.93	13.17
1OSP.PDB	O, H_VAL_24	ND2, H_ASN_76	HD22, H_ASN_76	2.88	1.97	18.51
1OSP.PDB	O, H_ASN_76	ND1, H_HIS_77	HD1, H_HIS_77	2.92	1.96	10.26
1OSP.PDB	O, H_THR_70	N, H_TYR_79	H, H_TYR_79	2.78	1.83	9.64
1OSP.PDB	O, H_SER_68	N, H_GLN_81	H, H_GLN_81	2.98	2.10	21.73
1OSP.PDB	O, H_LEU_18	N, H_LEU_82	H, H_LEU_82	2.92	1.99	15.92
1OSP.PDB	O, H_GLN_16	N, H_VAL_85	H, H_VAL_85	2.82	1.85	6.22
1OSP.PDB	OD2, H_ASP_89	N, H_VAL_86	H, H_VAL_86	2.80	1.88	11.59
1OSP.PDB	O, H_VAL_86	N, H_ASP_89	H, H_ASP_89	2.89	1.96	13.81
1OSP.PDB	O, H_THR_114	N, H_TYR_93	H, H_TYR_93	2.83	1.88	11.95
1OSP.PDB	O, H_ASP_89	OH, H_TYR_93	HH, H_TYR_93	2.70	1.77	11.96
1OSP.PDB	O, H_ILE_37	N, H_TYR_94	H, H_TYR_94	2.68	1.76	13.41
1OSP.PDB	OE2, H_GLU_6	N, H_CYS_95	H, H_CYS_95	2.95	2.01	11.90
1OSP.PDB	O, H_PHE_109	N, H_ARG_97	H, H_ARG_97	2.87	1.96	17.07
1OSP.PDB	O, H_PHE_33	N, H_SER_98	H, H_SER_98	2.89	1.95	12.66
1OSP.PDB	O, H_GLY_106	N, H_ARG_99	H, H_ARG_99	2.65	1.77	20.05

1OSP.PDB	OG, H_SER_105	N, H_ASP_100	H, H_ASP_100	2.96	2.05	15.15
1OSP.PDB	O, O_ASP_93	N, H_TYR_101	H, H_TYR_101	2.96	2.00	9.88
1OSP.PDB	OH, L_TYR_36	N, H_PHE_107	H, H_PHE_107	2.90	1.92	4.68
1OSP.PDB	O, H_PHE_107	NE1, H_TRP_110	HE1, H_TRP_110	2.73	1.93	28.89
1OSP.PDB	OE1, H_GLU_6	N, H_GLY_113	H, H_GLY_113	2.71	1.88	24.91
1OSP.PDB	O, H_ALA_91	N, H_VAL_116	H, H_VAL_116	2.85	1.88	5.20
1OSP.PDB	O, H_SER_10	N, H_THR_117	H, H_THR_117	2.78	1.82	8.67
1OSP.PDB	O, H_LYS_150	N, H_SER_127	H, H_SER_127	2.92	1.96	10.41
1OSP.PDB	O, H_LEU_148	N, H_TYR_129	H, H_TYR_129	2.81	1.85	8.10
1OSP.PDB	O, H_GLY_146	N, H_LEU_131	H, H_LEU_131	2.76	1.84	15.39
1OSP.PDB	O, H_VAL_190	N, H_VAL_143	H, H_VAL_143	2.73	1.81	13.86
1OSP.PDB	O, H_VAL_188	N, H_LEU_145	H, H_LEU_145	2.82	1.87	9.83
1OSP.PDB	O, H_LEU_131	N, H_GLY_146	H, H_GLY_146	2.94	2.07	22.39
1OSP.PDB	O, H_SER_186	N, H_CYS_147	H, H_CYS_147	3.00	2.12	21.82
1OSP.PDB	O, H_TYR_129	N, H_LEU_148	H, H_LEU_148	2.83	1.89	14.70
1OSP.PDB	O, H_MET_184	N, H_VAL_149	H, H_VAL_149	2.83	1.86	7.67
1OSP.PDB	O, H_SER_127	N, H_LYS_150	H, H_LYS_150	2.86	1.89	5.15
1OSP.PDB	O, H_THR_124	N, H_PHE_153	H, H_PHE_153	2.99	2.11	20.08
1OSP.PDB	OE1, H_GLU_155	N, H_SER_156	H, H_SER_156	2.82	1.96	21.80
1OSP.PDB	O, H_SER_203	N, H_THR_160	H, H_THR_160	2.81	1.86	11.32
1OSP.PDB	OG, H_SER_186	NE1, H_TRP_161	HE1, H_TRP_161	2.94	1.96	6.92
1OSP.PDB	O, H_SER_187	N, H_HIS_171	H, H_HIS_171	2.90	1.95	12.27
1OSP.PDB	O, H_SER_185	N, H_PHE_173	H, H_PHE_173	2.83	1.89	14.13
1OSP.PDB	O, H_LEU_181	N, H_GLN_178	H, H_GLN_178	2.99	2.02	8.47
1OSP.PDB	O, H_TYR_152	N, H_TYR_182	H, H_TYR_182	2.70	1.78	13.65
1OSP.PDB	O, H_VAL_149	N, H_MET_184	H, H_MET_184	2.88	1.94	12.78
1OSP.PDB	OG, L_SER_176	OG, H_SER_185	HG, H_SER_185	2.74	1.91	24.72
1OSP.PDB	O, H_HIS_171	N, H_SER_187	H, H_SER_187	2.79	1.91	19.94
1OSP.PDB	O, H_LEU_145	N, H_VAL_188	H, H_VAL_188	2.91	1.95	10.57
1OSP.PDB	O, H_SER_169	N, H_THR_189	H, H_THR_189	2.97	2.10	22.89
1OSP.PDB	O, H_VAL_143	N, H_VAL_190	H, H_VAL_190	2.87	1.94	15.00
1OSP.PDB	O, H_SER_141	N, H_SER_192	H, H_SER_192	2.75	1.80	9.03
1OSP.PDB	O, H_PRO_191	N, H_THR_194	H, H_THR_194	2.85	1.95	18.47
1OSP.PDB	O, H_PRO_191	OG1, H_THR_194	HG1, H_THR_194	2.70	1.91	28.34
1OSP.PDB	O, H_ASN_162	N, H_THR_201	H, H_THR_201	2.71	1.81	16.91
1OSP.PDB	O, H_LYS_215	N, H_CYS_202	H, H_CYS_202	2.91	1.95	9.86
1OSP.PDB	O, H_THR_160	N, H_SER_203	H, H_SER_203	2.69	1.78	14.42
1OSP.PDB	O, H_VAL_213	N, H_VAL_204	H, H_VAL_204	2.76	1.80	5.73
1OSP.PDB	O, H_THR_158	N, H_ALA_205	H, H_ALA_205	2.97	2.01	9.69
1OSP.PDB	O, H_THR_211	N, H_HIS_206	H, H_HIS_206	2.87	1.90	7.50
1OSP.PDB	OG, H_SER_209	ND1, H_HIS_206	HD1, H_HIS_206	2.73	1.88	25.05
1OSP.PDB	O, H_PRO_154	NE2, H_HIS_206	HE2, H_HIS_206	2.71	1.78	13.27
1OSP.PDB	O, H_PRO_207	N, H_SER_210	H, H_SER_210	2.91	1.98	12.92
1OSP.PDB	O, H_VAL_204	N, H_VAL_213	H, H_VAL_213	2.78	1.87	17.04
1OSP.PDB	O, H_CYS_202	N, H_LYS_215	H, H_LYS_215	2.75	1.83	14.50
1OSP.PDB	OE1, L_GLU_123	NZ, H_LYS_215	HZ2, H_LYS_215	2.78	1.85	20.53
1OSP.PDB	O, H_VAL_200	N, H_LEU_217	H, H_LEU_217	2.88	1.93	11.66
1OSP.PDB	O, O_ASP_25	OG, O_SER_29	HG, O_SER_29	2.96	2.06	17.60
1OSP.PDB	O, O_VAL_42	N, O_VAL_30	H, O_VAL_30	2.74	1.80	11.57
1OSP.PDB	O, O_VAL_40	N, O_VAL_32	H, O_VAL_32	2.79	1.86	14.04
1OSP.PDB	O, O_MET_38	N, O_LEU_34	H, O_LEU_34	2.77	1.93	25.21
1OSP.PDB	OD1, O_ASP_33	NZ, O_LYS_39	HZ2, O_LYS_39	2.81	1.85	17.76
1OSP.PDB	O, O_VAL_32	N, O_VAL_40	H, O_VAL_40	2.85	1.95	18.60
1OSP.PDB	O, O_ILE_55	N, O_LEU_41	H, O_LEU_41	2.73	1.77	2.80
1OSP.PDB	O, O_VAL_30	N, O_VAL_42	H, O_VAL_42	2.79	1.83	5.03
1OSP.PDB	O, O_LYS_51	N, O_ASN_47	H, O_ASN_47	2.68	1.74	7.05
1OSP.PDB	OD1, O_ASN_47	N, O_ASP_49	H, O_ASP_49	2.77	1.90	22.03
1OSP.PDB	O, O_ASN_47	N, O_GLY_50	H, O_GLY_50	2.81	1.86	10.63

1OSP.PDB	OD1, O_ASN_47	N, O_LYS_51	H, O_LYS_51	2.98	2.06	16.48
1OSP.PDB	O, O_SER_67	N, O_TYR_52	H, O_TYR_52	2.69	1.80	18.76
1OSP.PDB	OG, O_SER_43	N, O_ASP_53	H, O_ASP_53	2.84	1.87	5.15
1OSP.PDB	O, O_GLY_65	N, O_LEU_54	H, O_LEU_54	2.75	1.89	23.21
1OSP.PDB	O, O_LEU_61	N, O_VAL_58	H, O_VAL_58	2.83	1.87	9.77
1OSP.PDB	O, O_ALA_56	N, O_LEU_63	H, O_LEU_63	2.76	1.81	6.30
1OSP.PDB	O, O_GLU_77	N, O_LYS_64	H, O_LYS_64	2.80	1.86	12.67
1OSP.PDB	O, O_TYR_52	N, O_SER_67	H, O_SER_67	2.91	2.05	23.91
1OSP.PDB	O, O_LEU_88	N, O_LEU_76	H, O_LEU_76	2.81	1.86	9.34
1OSP.PDB	O, O_LYS_64	N, O_GLU_77	H, O_GLU_77	2.89	2.01	22.35
1OSP.PDB	O, O_VAL_86	N, O_GLY_78	H, O_GLY_78	2.92	2.04	22.03
1OSP.PDB	O, O_CYS_84	N, O_LYS_80	H, O_LYS_80	2.88	1.91	7.18
1OSP.PDB	O, O_LYS_80	N, O_LYS_83	H, O_LYS_83	2.97	2.11	23.34
1OSP.PDB	OD1, O_ASP_82	N, O_CYS_84	H, O_CYS_84	2.94	2.02	12.85
1OSP.PDB	O, O_GLY_78	N, O_VAL_86	H, O_VAL_86	2.78	1.82	7.53
1OSP.PDB	O, O_GLU_100	N, O_LYS_87	H, O_LYS_87	2.83	1.86	6.51
1OSP.PDB	O, O_LEU_76	N, O_LEU_88	H, O_LEU_88	2.85	1.88	3.67
1OSP.PDB	O, O_THR_98	N, O_THR_89	H, O_THR_89	2.87	1.91	8.56
1OSP.PDB	O, O_GLY_74	N, O_ILE_90	H, O_ILE_90	2.80	1.83	2.30
1OSP.PDB	O, O_GLN_96	N, O_SER_91	H, O_SER_91	2.90	1.92	4.64
1OSP.PDB	O, O_SER_91	N, O_LEU_94	H, O_LEU_94	2.77	1.86	16.57
1OSP.PDB	O, O_THR_115	N, O_THR_97	H, O_THR_97	2.95	2.01	13.77
1OSP.PDB	O, O_THR_89	N, O_THR_98	H, O_THR_98	2.94	2.04	19.56
1OSP.PDB	O, O_LYS_113	N, O_LEU_99	H, O_LEU_99	2.95	1.99	7.52
1OSP.PDB	O, O_LYS_87	N, O_GLU_100	H, O_GLU_100	2.86	1.89	3.85
1OSP.PDB	O, O_LYS_85	N, O_PHE_102	H, O_PHE_102	2.73	1.77	4.67
1OSP.PDB	O, O_THR_108	N, O_LYS_103	H, O_LYS_103	2.81	1.88	14.70
1OSP.PDB	O, O_LYS_103	N, O_GLY_106	H, O_GLY_106	2.79	1.88	17.21
1OSP.PDB	O, O_VAL_101	N, O_VAL_110	H, O_VAL_110	2.84	1.89	11.58
1OSP.PDB	O, O_GLU_124	N, O_LYS_112	H, O_LYS_112	2.97	2.14	27.43
1OSP.PDB	O, O_LEU_99	N, O_LYS_113	H, O_LYS_113	2.94	1.98	9.26
1OSP.PDB	O, O_THR_122	N, O_VAL_114	H, O_VAL_114	2.91	1.95	10.05
1OSP.PDB	O, O_THR_97	N, O_THR_115	H, O_THR_115	2.93	1.98	12.74
1OSP.PDB	O, O_SER_120	N, O_SER_116	H, O_SER_116	2.84	1.87	6.23
1OSP.PDB	O, O_GLY_95	N, O_LYS_117	H, O_LYS_117	2.85	2.02	26.58
1OSP.PDB	O, O_SER_116	N, O_LYS_119	H, O_LYS_119	3.00	2.13	23.54
1OSP.PDB	OD1, O_ASP_118	N, O_SER_120	H, O_SER_120	2.97	2.05	14.24
1OSP.PDB	O, O_THR_138	N, O_SER_121	H, O_SER_121	2.84	1.93	17.68
1OSP.PDB	O, O_VAL_114	N, O_THR_122	H, O_THR_122	2.89	1.97	16.41
1OSP.PDB	O, O_ILE_136	N, O_GLU_123	H, O_GLU_123	2.84	1.88	8.73
1OSP.PDB	O, O_LYS_112	N, O_GLU_124	H, O_GLU_124	2.76	1.80	4.84
1OSP.PDB	O, O_GLU_134	N, O_LYS_125	H, O_LYS_125	2.97	2.02	11.11
1OSP.PDB	O, O_GLU_131	N, O_ASN_127	H, O_ASN_127	2.72	1.91	28.14
1OSP.PDB	OD1, O_ASN_127	N, O_LYS_129	H, O_LYS_129	2.89	2.06	25.72
1OSP.PDB	O, O_ASN_127	N, O_GLY_130	H, O_GLY_130	2.88	1.93	10.26
1OSP.PDB	OD1, O_ASN_127	N, O_GLU_131	H, O_GLU_131	2.98	2.04	13.29
1OSP.PDB	O, O_LYS_125	N, O_SER_133	H, O_SER_133	2.75	1.83	15.11
1OSP.PDB	O, O_TYR_147	N, O_LYS_135	H, O_LYS_135	2.89	1.94	12.24
1OSP.PDB	O, O_GLU_123	N, O_ILE_136	H, O_ILE_136	2.91	1.99	16.85
1OSP.PDB	O, O_LEU_145	N, O_ILE_137	H, O_ILE_137	2.93	1.95	4.82
1OSP.PDB	O, O_SER_121	N, O_THR_138	H, O_THR_138	2.76	1.86	18.89
1OSP.PDB	O, O_THR_143	N, O_ARG_139	H, O_ARG_139	2.90	1.93	8.66
1OSP.PDB	OG1, O_THR_143	NH1, O_ARG_139	HH11, O_ARG_139	2.73	1.78	14.74
1OSP.PDB	OE2, O_GLU_160	NH2, O_ARG_139	HH22, O_ARG_139	2.96	2.05	19.95
1OSP.PDB	O, O_ARG_139	N, O_GLY_142	H, O_GLY_142	2.82	1.89	14.20
1OSP.PDB	O, O_VAL_161	N, O_ARG_144	H, O_ARG_144	2.86	1.92	11.75
1OSP.PDB	O, O_LYS_159	N, O_GLU_146	H, O_GLU_146	2.74	1.79	9.08
1OSP.PDB	O, O_LYS_135	N, O_TYR_147	H, O_TYR_147	2.76	1.82	11.54

1OSP.PDB	O, O_SER_155	N, O_LYS_151	H, O_LYS_151	2.82	1.90	16.12
1OSP.PDB	O, O_LYS_151	N, O_GLY_154	H, O_GLY_154	3.00	2.15	24.39
1OSP.PDB	O, O_THR_148	N, O_LYS_157	H, O_LYS_157	2.96	2.06	18.52
1OSP.PDB	O, O_GLU_146	N, O_LYS_159	H, O_LYS_159	2.90	2.10	29.35
1OSP.PDB	O, O_LEU_167	N, O_GLU_160	H, O_GLU_160	2.80	1.84	8.36
1OSP.PDB	O, O_ARG_144	N, O_VAL_161	H, O_VAL_161	2.67	1.80	21.27
1OSP.PDB	O, O_TYR_165	N, O_LEU_162	H, O_LEU_162	2.97	2.08	19.74
1OSP.PDB	O, O_GLU_160	N, O_LEU_167	H, O_LEU_167	2.98	2.02	8.76
1OSP.PDB	O, O_THR_177	N, O_THR_170	H, O_THR_170	2.94	2.08	23.59
1OSP.PDB	O, O_GLY_156	N, O_LEU_171	H, O_LEU_171	2.97	2.15	28.04
1OSP.PDB	O, O_ILE_191	N, O_THR_176	H, O_THR_176	2.77	1.81	7.44
1OSP.PDB	O, O_THR_170	N, O_THR_177	H, O_THR_177	2.90	1.94	8.28
1OSP.PDB	O, O_LYS_189	N, O_LEU_178	H, O_LEU_178	2.85	1.91	12.14
1OSP.PDB	O, O_GLU_168	N, O_VAL_179	H, O_VAL_179	2.80	1.83	5.32
1OSP.PDB	O, O_LEU_187	N, O_VAL_180	H, O_VAL_180	2.82	1.89	14.25
1OSP.PDB	O, O_GLU_182	N, O_VAL_185	H, O_VAL_185	2.98	2.06	16.93
1OSP.PDB	O, O_ASN_202	N, O_THR_186	H, O_THR_186	2.75	1.80	6.91
1OSP.PDB	O, O_VAL_180	N, O_LEU_187	H, O_LEU_187	2.73	1.77	7.01
1OSP.PDB	O, O_GLU_200	N, O_SER_188	H, O_SER_188	2.94	1.96	4.07
1OSP.PDB	O, O_LEU_178	N, O_LYS_189	H, O_LYS_189	2.81	1.84	6.92
1OSP.PDB	OE1, O_GLU_160	NZ, O_LYS_189	HZ1, O_LYS_189	2.95	1.93	9.44
1OSP.PDB	O, O_SER_198	N, O_ASN_190	H, O_ASN_190	2.85	1.88	7.09
1OSP.PDB	OG, O_SER_198	ND2, O_ASN_190	HD22, O_ASN_190	2.97	2.02	11.75
1OSP.PDB	O, O_THR_176	N, O_ILE_191	H, O_ILE_191	2.86	1.92	14.23
1OSP.PDB	O, O_GLU_196	N, O_SER_192	H, O_SER_192	2.84	1.90	12.51
1OSP.PDB	O, O_SER_192	N, O_GLY_195	H, O_GLY_195	2.80	1.87	14.11
1OSP.PDB	O, O_THR_186	N, O_ASN_202	H, O_ASN_202	2.98	2.04	13.31
1OSP.PDB	O, O_THR_184	N, O_THR_204	H, O_THR_204	2.90	1.95	13.33
1OSP.PDB	OD1, O_ASP_203	N, O_ASP_205	H, O_ASP_205	2.93	2.02	16.29
1OSP.PDB	O, O_SER_207	N, O_THR_210	H, O_THR_210	2.99	2.05	13.36
1OSP.PDB	OD2, O_ASP_203	N, O_LYS_212	H, O_LYS_212	2.91	1.95	1.32
1OSP.PDB	O, O_THR_210	NZ, O_LYS_212	HZ1, O_LYS_212	2.94	1.97	16.29
1OSP.PDB	O, O_THR_224	N, O_ALA_215	H, O_ALA_215	2.95	2.06	20.55
1OSP.PDB	O, O_THR_222	N, O_ASN_217	H, O_ASN_217	2.94	2.00	14.86
1OSP.PDB	O, O_SER_218	N, O_SER_221	H, O_SER_221	2.93	2.08	24.26
1OSP.PDB	O, O_LEU_235	N, O_LEU_223	H, O_LEU_223	2.82	1.86	8.38
1OSP.PDB	O, O_ALA_215	N, O_THR_224	H, O_THR_224	2.90	1.97	14.17
1OSP.PDB	OD1, O_ASP_234	OG1, O_THR_224	HG1, O_THR_224	2.71	1.92	27.50
1OSP.PDB	O, O_LYS_233	N, O_ILE_225	H, O_ILE_225	2.88	1.93	10.58
1OSP.PDB	O, O_THR_213	N, O_THR_226	H, O_THR_226	2.78	1.85	13.98
1OSP.PDB	O, O_LYS_230	N, O_VAL_227	H, O_VAL_227	2.89	1.96	15.17
1OSP.PDB	O, O_VAL_227	N, O_LYS_230	H, O_LYS_230	2.93	2.00	15.15
1OSP.PDB	O, O_SER_250	NZ, O_LYS_230	HZ1, O_LYS_230	2.95	1.95	11.76
1OSP.PDB	O, O_ILE_225	N, O_THR_232	H, O_THR_232	2.81	1.85	8.22
1OSP.PDB	O, O_GLN_246	N, O_ASP_234	H, O_ASP_234	2.97	2.05	16.64
1OSP.PDB	O, O_LEU_223	N, O_LEU_235	H, O_LEU_235	2.73	1.78	7.98
1OSP.PDB	O, O_THR_244	N, O_VAL_236	H, O_VAL_236	2.90	1.94	9.91
1OSP.PDB	O, O_SER_221	N, O_PHE_237	H, O_PHE_237	2.91	1.92	1.81
1OSP.PDB	O, O_VAL_236	N, O_THR_244	H, O_THR_244	2.91	2.01	19.80
1OSP.PDB	O, O_VAL_260	N, O_VAL_245	H, O_VAL_245	2.75	1.81	11.28
1OSP.PDB	O, O_GLU_256	NE2, O_GLN_246	HE22, O_GLN_246	2.92	1.95	7.48
1OSP.PDB	O, O_THR_232	N, O_TYR_248	H, O_TYR_248	2.90	2.01	20.77
1OSP.PDB	OD1, O_ASP_234	OH, O_TYR_248	HH, O_TYR_248	2.73	1.90	24.06
1OSP.PDB	O, O_LYS_254	N, O_ASP_249	H, O_ASP_249	2.87	1.94	14.75
1OSP.PDB	O, O_ASP_249	N, O_GLY_252	H, O_GLY_252	2.85	1.98	21.02
1OSP.PDB	OD2, O_ASP_249	N, O_LYS_254	H, O_LYS_254	2.80	1.86	5.31
1OSP.PDB	O, O_GLN_247	N, O_GLU_256	H, O_GLU_256	2.93	1.98	13.89
1OSP.PDB	O, O_VAL_245	N, O_VAL_260	H, O_VAL_260	2.77	1.81	5.97

1OSP.PDB	O, O_ILE_243	N, O_ILE_262	H, O_ILE_262	2.80	1.83	3.81
1OSP.PDB	OE1, O_GLU_267	N, O_THR_263	H, O_THR_263	2.83	1.90	11.29
1OSP.PDB	O, O_ASP_266	N, O_ASN_270	H, O_ASN_270	2.79	1.90	19.11
1PSK.PDB	O, L_TYR_85	NE2, L_GLN_6	HE21, L_GLN_6	2.81	1.89	16.29
1PSK.PDB	O, L_LYS_102	N, L_MET_11	H, L_MET_11	2.72	1.89	26.00
1PSK.PDB	O, L_GLU_104	N, L_ALA_13	H, L_ALA_13	2.83	1.92	17.43
1PSK.PDB	O, L_MET_77	N, L_GLY_16	H, L_GLY_16	2.73	1.77	6.44
1PSK.PDB	O, L_ILE_74	N, L_VAL_19	H, L_VAL_19	2.88	2.00	21.06
1PSK.PDB	O, L_LEU_72	N, L_ILE_21	H, L_ILE_21	2.81	1.98	26.09
1PSK.PDB	O, L_SER_7	N, L_THR_22	H, L_THR_22	2.98	2.05	14.20
1PSK.PDB	O, L_TYR_70	N, L_CYS_23	H, L_CYS_23	2.74	1.94	28.83
1PSK.PDB	O, L_THR_68	N, L_ALA_25	H, L_ALA_25	2.80	1.83	4.30
1PSK.PDB	O, L_VAL_3	N, L_SER_26	H, L_SER_26	2.84	1.92	15.77
1PSK.PDB	O, L_GLN_88	N, L_HIS_33	H, L_HIS_33	2.77	1.93	24.90
1PSK.PDB	O, L_ILE_47	N, L_TRP_34	H, L_TRP_34	2.73	1.83	16.95
1PSK.PDB	O, L_TYR_86	N, L_PHE_35	H, L_PHE_35	2.70	1.82	20.29
1PSK.PDB	O, L_LYS_44	N, L_GLN_36	H, L_GLN_36	2.74	1.81	13.25
1PSK.PDB	O, L_THR_41	NE2, L_GLN_37	HE22, L_GLN_37	2.64	1.76	19.44
1PSK.PDB	O, L_GLU_80	NZ, L_LYS_38	HZ2, L_LYS_38	2.69	1.82	26.34
1PSK.PDB	O, L_LYS_38	N, L_THR_41	H, L_THR_41	2.90	1.99	18.24
1PSK.PDB	O, L_TRP_34	N, L_TRP_46	H, L_TRP_46	2.75	1.83	15.53
1PSK.PDB	O, L_THR_52	N, L_TYR_48	H, L_TYR_48	2.90	2.05	25.41
1PSK.PDB	O, L_ILE_32	N, L_THR_50	H, L_THR_50	2.83	2.01	27.59
1PSK.PDB	O, L_SER_49	N, L_SER_51	H, L_SER_51	2.81	1.95	22.62
1PSK.PDB	O, L_SER_71	N, L_SER_64	H, L_SER_64	2.93	2.00	15.47
1PSK.PDB	O, L_SER_69	N, L_SER_66	H, L_SER_66	2.87	2.04	26.16
1PSK.PDB	O, L_CYS_23	N, L_TYR_70	H, L_TYR_70	2.88	1.92	9.26
1PSK.PDB	O, L_SER_64	N, L_SER_71	H, L_SER_71	2.83	1.87	10.56
1PSK.PDB	O, L_ILE_21	N, L_LEU_72	H, L_LEU_72	2.84	1.87	7.12
1PSK.PDB	O, L_VAL_19	N, L_ILE_74	H, L_ILE_74	2.66	1.77	18.08
1PSK.PDB	O, L_ARG_60	N, L_SER_75	H, L_SER_75	2.95	2.02	15.07
1PSK.PDB	O, L_GLU_17	N, L_MET_77	H, L_MET_77	2.56	1.73	24.40
1PSK.PDB	O, L_THR_101	N, L_TYR_85	H, L_TYR_85	2.97	2.05	16.35
1PSK.PDB	O, L_PHE_35	N, L_TYR_86	H, L_TYR_86	2.89	2.04	24.71
1PSK.PDB	OE1, L_GLN_6	N, L_CYS_87	H, L_CYS_87	2.90	2.04	23.69
1PSK.PDB	O, L_HIS_33	N, L_GLN_88	H, L_GLN_88	2.64	1.77	19.96
1PSK.PDB	O, L_ALA_9	N, L_LYS_102	H, L_LYS_102	2.79	1.82	7.68
1PSK.PDB	O, L_ALA_83	N, L_LEU_103	H, L_LEU_103	2.67	1.77	17.39
1PSK.PDB	O, L_MET_11	N, L_GLU_104	H, L_GLU_104	2.63	1.81	26.11
1PSK.PDB	O, L_ALA_13	N, L_LYS_106	H, L_LYS_106	2.86	1.91	10.19
1PSK.PDB	O, L_ALA_108	NE, L_ARG_107	HE, L_ARG_107	2.69	1.87	26.11
1PSK.PDB	O, L_ASP_169	NH1, L_ARG_107	HH11, L_ARG_107	2.89	1.94	13.94
1PSK.PDB	O, L_ALA_108	NH2, L_ARG_107	HH21, L_ARG_107	2.77	1.96	29.27
1PSK.PDB	O, L_TYR_139	N, L_ALA_110	H, L_ALA_110	2.80	1.90	19.51
1PSK.PDB	O, L_ASN_136	N, L_THR_113	H, L_THR_113	2.79	1.85	11.43
1PSK.PDB	O, L_SER_120	N, L_LEU_124	H, L_LEU_124	2.82	1.86	7.62
1PSK.PDB	O, L_SER_121	N, L_THR_125	H, L_THR_125	2.73	1.80	12.63
1PSK.PDB	O, L_SER_121	OG1, L_THR_125	HG1, L_THR_125	2.84	1.90	10.36
1PSK.PDB	O, L_GLU_122	OG, L_SER_126	HG, L_SER_126	2.94	2.08	22.24
1PSK.PDB	O, L_LEU_180	N, L_ALA_129	H, L_ALA_129	2.84	1.94	18.85
1PSK.PDB	O, L_LEU_178	N, L_VAL_131	H, L_VAL_131	2.87	2.03	25.59
1PSK.PDB	OG, L_SER_173	N, L_ASN_137	H, L_ASN_137	2.92	1.98	12.28
1PSK.PDB	O, L_TYR_172	N, L_PHE_138	H, L_PHE_138	2.85	1.88	6.49
1PSK.PDB	O, L_GLU_194	N, L_LYS_146	H, L_LYS_146	2.97	2.01	10.09
1PSK.PDB	OG, L_SER_176	NE1, L_TRP_147	HE1, L_TRP_147	2.73	1.78	10.14
1PSK.PDB	O, L_THR_192	N, L_LYS_148	H, L_LYS_148	2.68	1.78	17.05
1PSK.PDB	O, L_SER_152	N, L_ILE_149	H, L_ILE_149	2.76	1.81	9.00
1PSK.PDB	O, L_SER_190	N, L_ASP_150	H, L_ASP_150	2.82	1.85	2.71

1PSK.PDB	O, L_ILE_149	N, L_SER_152	H, L_SER_152	2.78	1.90	20.78
1PSK.PDB	OE1, L_GLN_155	N, L_ASN_156	H, L_ASN_156	2.98	2.05	13.77
1PSK.PDB	O, L_THR_177	N, L_LEU_159	H, L_LEU_159	2.87	2.02	24.21
1PSK.PDB	O, H_PRO_168	OG, L_SER_161	HG, L_SER_161	2.76	1.90	22.64
1PSK.PDB	O, L_ILE_105	NE2, L_GLN_165	HE21, L_GLN_165	2.92	2.00	17.26
1PSK.PDB	O, L_THR_171	N, L_ASP_166	H, L_ASP_166	2.81	1.87	10.96
1PSK.PDB	OD2, L_ASP_166	N, L_ASP_169	H, L_ASP_169	2.99	2.04	7.95
1PSK.PDB	O, L_PHE_138	N, L_TYR_172	H, L_TYR_172	2.85	1.92	14.74
1PSK.PDB	O, L_LEU_135	N, L_MET_174	H, L_MET_174	2.76	1.79	2.98
1PSK.PDB	O, L_CYS_133	N, L_SER_176	H, L_SER_176	2.88	1.92	9.72
1PSK.PDB	OD1, L_ASN_160	OG, L_SER_176	HG, L_SER_176	2.79	1.87	14.99
1PSK.PDB	O, L_GLY_157	N, L_THR_179	H, L_THR_179	2.95	2.12	26.59
1PSK.PDB	O, L_ALA_129	N, L_LEU_180	H, L_LEU_180	2.80	1.83	2.82
1PSK.PDB	O, L_THR_181	N, L_TYR_185	H, L_TYR_185	2.95	2.01	13.19
1PSK.PDB	O, L_LYS_182	N, L_GLU_186	H, L_GLU_186	2.95	1.99	9.74
1PSK.PDB	O, L_PHE_208	N, L_TYR_191	H, L_TYR_191	2.94	1.97	6.75
1PSK.PDB	O, L_LYS_148	N, L_THR_192	H, L_THR_192	2.84	1.87	6.81
1PSK.PDB	O, L_LYS_146	N, L_GLU_194	H, L_GLU_194	2.94	2.02	16.13
1PSK.PDB	O, L_ILE_204	N, L_ALA_195	H, L_ALA_195	2.94	2.01	15.37
1PSK.PDB	O, L_ASN_144	N, L_THR_196	H, L_THR_196	2.65	1.83	27.50
1PSK.PDB	O, L_TYR_191	N, L_PHE_208	H, L_PHE_208	2.94	2.02	17.53
1PSK.PDB	O, L_ASN_189	N, L_ARG_210	H, L_ARG_210	2.72	1.78	9.08
1PSK.PDB	O, L_HIS_188	NH1, L_ARG_210	HH11, L_ARG_210	2.85	1.95	20.39
1PSK.PDB	O, H_TYR_94	NE2, H_GLN_6	HE21, H_GLN_6	2.75	1.83	14.83
1PSK.PDB	O, H_THR_109	N, H_GLU_10	H, H_GLU_10	2.94	2.04	19.11
1PSK.PDB	O, H_THR_111	N, H_VAL_12	H, H_VAL_12	2.75	1.86	19.89
1PSK.PDB	O, H_LYS_13	N, H_ALA_16	H, H_ALA_16	2.98	2.05	15.84
1PSK.PDB	O, H_LEU_83	N, H_VAL_18	H, H_VAL_18	2.94	2.01	16.46
1PSK.PDB	OG, H_SER_7	N, H_SER_21	H, H_SER_21	2.91	1.95	7.05
1PSK.PDB	O, H_THR_77	N, H_THR_24	H, H_THR_24	2.84	1.91	14.03
1PSK.PDB	O, H_THR_97	N, H_HIS_35	H, H_HIS_35	2.81	1.88	13.42
1PSK.PDB	NE1, H_TRP_47	ND1, H_HIS_35	HD1, H_HIS_35	2.92	2.03	20.19
1PSK.PDB	O, H_TYR_95	N, H_VAL_37	H, H_VAL_37	2.78	1.85	13.12
1PSK.PDB	O, H_GLU_46	N, H_LYS_38	H, H_LYS_38	2.74	1.81	11.82
1PSK.PDB	O, H_VAL_93	N, H_GLN_39	H, H_GLN_39	2.70	1.83	20.61
1PSK.PDB	O, H_SER_40	NE2, H_GLN_39	HE22, H_GLN_39	2.98	2.06	16.51
1PSK.PDB	O, H_SER_44	N, H_SER_40	H, H_SER_40	2.86	1.90	10.36
1PSK.PDB	O, H_LYS_38	N, H_GLU_46	H, H_GLU_46	2.72	1.82	17.92
1PSK.PDB	O, H_TRP_36	N, H_ILE_48	H, H_ILE_48	2.97	2.07	18.37
1PSK.PDB	O, H_ASN_59	N, H_ASP_50	H, H_ASP_50	2.89	1.96	16.23
1PSK.PDB	O, H_GLY_57	N, H_ASN_52	H, H_ASN_52	2.75	1.93	27.30
1PSK.PDB	O, H_PRO_53	N, H_ASN_55	H, H_ASN_55	2.75	1.87	20.51
1PSK.PDB	O, H_PRO_53	ND2, H_ASN_55	HD22, H_ASN_55	2.76	1.94	26.77
1PSK.PDB	O, H_ILE_48	N, H_ASN_61	H, H_ASN_61	2.93	2.02	18.42
1PSK.PDB	O, H_TRP_47	ND2, H_ASN_61	HD22, H_ASN_61	2.88	1.97	18.24
1PSK.PDB	OD1, H_ASN_61	N, H_LYS_63	H, H_LYS_63	2.93	2.01	16.11
1PSK.PDB	O, H_PHE_64	N, H_ALA_68	H, H_ALA_68	2.83	1.93	18.74
1PSK.PDB	OH, H_TYR_60	N, H_LEU_70	H, H_LEU_70	2.73	1.84	18.80
1PSK.PDB	O, H_THR_78	N, H_HIS_73	H, H_HIS_73	2.82	2.01	28.97
1PSK.PDB	OG1, H_THR_78	OG, H_SER_76	HG, H_SER_76	2.94	2.03	16.27
1PSK.PDB	O, H_THR_71	N, H_TYR_80	H, H_TYR_80	2.94	2.09	24.76
1PSK.PDB	O, H_VAL_18	N, H_LEU_83	H, H_LEU_83	2.81	1.85	9.28
1PSK.PDB	OD2, H_ASP_90	N, H_THR_87	H, H_THR_87	2.99	2.12	22.62
1PSK.PDB	O, H_THR_87	N, H_ASP_90	H, H_ASP_90	2.83	1.90	13.61
1PSK.PDB	O, H_SER_88	OG, H_SER_91	HG, H_SER_91	2.90	1.97	12.52
1PSK.PDB	O, H_GLN_39	N, H_VAL_93	H, H_VAL_93	2.97	1.99	0.74
1PSK.PDB	O, H_THR_108	N, H_TYR_94	H, H_TYR_94	2.81	1.89	15.61
1PSK.PDB	O, H_ASP_90	OH, H_TYR_94	HH, H_TYR_94	2.77	1.87	17.15

1PSK.PDB	O, H_VAL_37	N, H_TYR_95	H, H_TYR_95	2.95	1.97	7.17
1PSK.PDB	O, H_HIS_35	N, H_THR_97	H, H_THR_97	2.81	1.92	20.68
1PSK.PDB	O, H_TYR_103	N, H_SER_98	H, H_SER_98	2.80	1.88	15.11
1PSK.PDB	OH, H_TYR_27	OG, H_SER_98	HG, H_SER_98	2.95	2.06	19.06
1PSK.PDB	O, H_TYR_94	N, H_THR_108	H, H_THR_108	2.86	2.00	23.11
1PSK.PDB	O, H_SER_7	OG1, H_THR_108	HG1, H_THR_108	2.62	1.79	24.94
1PSK.PDB	O, H_ALA_92	N, H_LEU_110	H, H_LEU_110	2.97	2.02	12.06
1PSK.PDB	O, H_GLU_10	N, H_THR_111	H, H_THR_111	2.77	1.82	9.08
1PSK.PDB	O, H_LYS_144	N, H_SER_121	H, H_SER_121	2.81	1.84	4.61
1PSK.PDB	O, H_LEU_142	N, H_TYR_123	H, H_TYR_123	2.75	1.89	23.66
1PSK.PDB	O, H_GLY_140	N, H_LEU_125	H, H_LEU_125	2.83	1.96	22.70
1PSK.PDB	O, H_VAL_182	N, H_LEU_139	H, H_LEU_139	2.94	1.97	6.89
1PSK.PDB	O, H_SER_180	N, H_CYS_141	H, H_CYS_141	2.84	1.96	21.90
1PSK.PDB	O, H_TYR_123	N, H_LEU_142	H, H_LEU_142	2.94	1.96	5.65
1PSK.PDB	O, H_LEU_178	N, H_VAL_143	H, H_VAL_143	2.80	1.85	10.99
1PSK.PDB	O, H_SER_121	N, H_LYS_144	H, H_LYS_144	2.73	1.77	7.35
1PSK.PDB	O, H_LEU_175	N, H_GLN_172	H, H_GLN_172	2.99	2.02	7.12
1PSK.PDB	O, H_TYR_146	N, H_TYR_176	H, H_TYR_176	2.73	1.77	6.58
1PSK.PDB	O, H_VAL_170	N, H_THR_177	H, H_THR_177	3.00	2.15	24.71
1PSK.PDB	O, H_HIS_165	N, H_SER_181	H, H_SER_181	2.93	1.97	9.97
1PSK.PDB	O, H_GLY_163	N, H_THR_183	H, H_THR_183	2.96	2.11	24.27
1PSK.PDB	O, H_VAL_137	N, H_VAL_184	H, H_VAL_184	2.80	1.88	17.57
1PSK.PDB	O, H_THR_188	N, H_GLN_192	H, H_GLN_192	2.60	1.80	26.98
1PSK.PDB	OD1, H_ASN_156	N, H_THR_195	H, H_THR_195	2.91	1.95	9.28
1PSK.PDB	O, H_THR_154	N, H_ASN_197	H, H_ASN_197	2.76	1.83	13.92
1PSK.PDB	O, H_LYS_206	N, H_VAL_198	H, H_VAL_198	2.73	1.84	18.50
1PSK.PDB	O, H_HIS_200	N, H_SER_204	H, H_SER_204	2.75	1.84	15.81
1PSK.PDB	O, H_VAL_198	N, H_LYS_206	H, H_LYS_206	2.77	1.84	13.06
1PSK.PDB	O, H_PRO_120	NZ, H_LYS_206	HZ1, H_LYS_206	2.63	1.80	29.01
1R21-1.PDB	O, A_ARG_96	N, A_VAL_8	H, A_VAL_8	2.92	2.11	28.07
1R21-1.PDB	O, A_ILE_51	N, A_CYS_27	H, A_CYS_27	2.73	1.80	13.77
1R21-1.PDB	O, A_CYS_49	N, A_PHE_29	H, A_PHE_29	2.63	1.76	21.39
1R21-1.PDB	O, A_GLY_32	N, A_CYS_35	H, A_CYS_35	2.97	2.04	15.31
1R21-1.PDB	O, A_LEU_28	N, A_ILE_37	H, A_ILE_37	2.58	1.63	11.44
1R21-1.PDB	O, A_CYS_27	N, A_ILE_51	H, A_ILE_51	2.59	1.74	23.78
1R21-1.PDB	O, A_ILE_59	N, A_GLU_52	H, A_GLU_52	2.42	1.47	10.01
1R21-1.PDB	O, A_SER_25	N, A_ILE_53	H, A_ILE_53	2.91	2.02	20.16
1R21-1.PDB	O, A_GLU_57	N, A_HIS_54	H, A_HIS_54	2.41	1.54	20.64
1R21-1.PDB	O, A_GLU_52	N, A_ILE_59	H, A_ILE_59	2.67	1.74	15.06
1R21-1.PDB	OG1, A_THR_69	ND2, A_ASN_62	HD21, A_ASN_62	2.86	1.99	21.79
1R21-1.PDB	ND2, A_ASN_62	N, A_THR_69	H, A_THR_69	2.75	1.81	12.35
1R21-1.PDB	O, A_THR_89	N, A_GLN_70	H, A_GLN_70	2.50	1.71	28.49
1R21-1.PDB	O, A_SER_74	N, A_VAL_71	H, A_VAL_71	2.82	1.84	3.74
1R21-1.PDB	O, A_VAL_87	N, A_ASN_72	H, A_ASN_72	2.95	2.00	10.39
1R21-1.PDB	O, A_VAL_71	N, A_SER_74	H, A_SER_74	2.47	1.61	23.41
1R21-1.PDB	OD2, A_ASP_86	N, A_LYS_83	H, A_LYS_83	2.35	1.40	9.85
1R21-1.PDB	O, A_TYR_97	N, A_GLY_85	H, A_GLY_85	2.98	2.05	14.93
1R21-1.PDB	O, A_PHE_95	N, A_ILE_88	H, A_ILE_88	2.64	1.67	7.14
1R21-1.PDB	O, A_GLN_70	N, A_THR_89	H, A_THR_89	2.52	1.55	4.70
1R21-1.PDB	O, A_ARG_93	N, A_ILE_90	H, A_ILE_90	2.76	1.81	12.04
1R21-1.PDB	O, A_ILE_88	N, A_PHE_95	H, A_PHE_95	2.52	1.55	6.84
1R21-1.PDB	O, A_VAL_8	N, A_ARG_96	H, A_ARG_96	2.54	1.67	21.94
1R21-1.PDB	O, A_ARG_6	N, A_GLU_98	H, A_GLU_98	2.97	1.99	7.38
1R21-1.PDB	ND1, A_HIS_84	N, A_ASN_99	H, A_ASN_99	2.78	1.83	11.23
1R21-10.PDB	O, A_PHE_20	N, A_LEU_7	H, A_LEU_7	2.54	1.63	17.03
1R21-10.PDB	O, A_ARG_96	N, A_VAL_8	H, A_VAL_8	2.88	1.97	16.93
1R21-10.PDB	O, A_PRO_18	N, A_THR_9	H, A_THR_9	2.64	1.77	22.03
1R21-10.PDB	O, A_ARG_5	N, A_LEU_22	H, A_LEU_22	2.90	2.07	26.17

1R21-10.PDB	O, A_ILE.51	N, A_CYS.27	H, A_CYS.27	2.90	1.97	15.62
1R21-10.PDB	O, A_CYS.49	N, A_PHE.29	H, A_PHE.29	2.63	1.76	20.96
1R21-10.PDB	O, A_LEU.28	N, A_ILE.37	H, A_ILE.37	2.61	1.66	11.11
1R21-10.PDB	O, A_GLY.30	N, A_ILE.39	H, A_ILE.39	2.86	1.97	19.93
1R21-10.PDB	O, A_LEU.41	N, A_VAL.44	H, A_VAL.44	2.90	2.09	27.66
1R21-10.PDB	O, A_CYS.27	N, A_ILE.51	H, A_ILE.51	2.67	1.79	22.06
1R21-10.PDB	O, A_ILE.59	N, A_GLU.52	H, A_GLU.52	2.49	1.61	19.99
1R21-10.PDB	O, A_GLU.57	N, A_HIS.54	H, A_HIS.54	2.63	1.74	19.91
1R21-10.PDB	O, A_GLU.52	N, A_ILE.59	H, A_ILE.59	2.58	1.65	14.41
1R21-10.PDB	O, A_VAL.80	N, A_LEU.60	H, A_LEU.60	2.98	2.07	18.84
1R21-10.PDB	OG1, A_THR.69	ND2, A_ASN.62	HD21, A_ASN.62	2.90	2.06	25.22
1R21-10.PDB	ND2, A_ASN.62	N, A_THR.69	H, A_THR.69	2.86	1.92	14.24
1R21-10.PDB	O, A_SER.74	N, A_VAL.71	H, A_VAL.71	2.72	1.74	5.16
1R21-10.PDB	O, A_VAL.87	N, A_ASN.72	H, A_ASN.72	2.98	2.03	12.85
1R21-10.PDB	O, A_VAL.71	N, A_SER.74	H, A_SER.74	2.40	1.47	14.75
1R21-10.PDB	O, A_THR.69	N, A_ILE.76	H, A_ILE.76	2.93	2.09	24.54
1R21-10.PDB	O, A_ALA.58	N, A_LEU.82	H, A_LEU.82	2.93	2.12	28.18
1R21-10.PDB	OD2, A_ASP.86	N, A_LYS.83	H, A_LYS.83	2.34	1.37	8.83
1R21-10.PDB	O, A_TYR.97	N, A_GLY.85	H, A_GLY.85	2.85	2.03	27.50
1R21-10.PDB	O, A_LYS.83	N, A_ASP.86	H, A_ASP.86	2.93	2.10	26.57
1R21-10.PDB	O, A_PHE.95	N, A_ILE.88	H, A_ILE.88	2.55	1.60	10.99
1R21-10.PDB	O, A_GLN.70	N, A_THR.89	H, A_THR.89	2.70	1.75	9.37
1R21-10.PDB	O, A_ARG.93	N, A_ILE.90	H, A_ILE.90	2.66	1.70	9.59
1R21-10.PDB	O, A_ILE.88	N, A_PHE.95	H, A_PHE.95	2.60	1.73	21.06
1R21-10.PDB	O, A_VAL.8	N, A_ARG.96	H, A_ARG.96	2.52	1.64	21.43
1R21-10.PDB	ND1, A_HIS.84	N, A_ASN.99	H, A_ASN.99	2.77	1.80	7.83
1R21-11.PDB	O, A_LEU.7	N, A_PHE.20	H, A_PHE.20	2.62	1.83	29.77
1R21-11.PDB	O, A_ILE.51	N, A_CYS.27	H, A_CYS.27	2.93	1.97	9.94
1R21-11.PDB	O, A_CYS.49	N, A_PHE.29	H, A_PHE.29	2.82	1.94	21.59
1R21-11.PDB	O, A_LEU.28	N, A_ILE.37	H, A_ILE.37	2.67	1.76	16.89
1R21-11.PDB	O, A_GLY.30	N, A_ILE.39	H, A_ILE.39	2.89	1.99	18.61
1R21-11.PDB	O, A_LEU.41	N, A_VAL.44	H, A_VAL.44	2.87	2.01	24.14
1R21-11.PDB	O, A_CYS.27	N, A_ILE.51	H, A_ILE.51	2.91	2.09	27.62
1R21-11.PDB	O, A_ILE.59	N, A_GLU.52	H, A_GLU.52	2.50	1.54	7.92
1R21-11.PDB	O, A_GLU.57	N, A_HIS.54	H, A_HIS.54	2.47	1.52	11.34
1R21-11.PDB	O, A_GLU.52	N, A_ILE.59	H, A_ILE.59	2.50	1.53	7.38
1R21-11.PDB	O, A_LYS.50	N, A_HIS.61	H, A_HIS.61	2.34	1.55	28.69
1R21-11.PDB	OG, A_SER.64	ND2, A_ASN.62	HD22, A_ASN.62	2.35	1.48	21.77
1R21-11.PDB	ND2, A_ASN.62	N, A_THR.69	H, A_THR.69	2.87	1.91	9.38
1R21-11.PDB	O, A_THR.89	N, A_GLN.70	H, A_GLN.70	2.52	1.62	18.25
1R21-11.PDB	O, A_VAL.71	N, A_SER.74	H, A_SER.74	2.43	1.53	18.84
1R21-11.PDB	O, A_VAL.71	OG, A_SER.74	HG, A_SER.74	2.65	1.87	28.98
1R21-11.PDB	N, A_GLY.85	ND1, A_HIS.84	HD1, A_HIS.84	2.62	1.77	24.61
1R21-11.PDB	O, A_LYS.83	N, A_ASP.86	H, A_ASP.86	2.93	2.08	25.03
1R21-11.PDB	O, A_PHE.95	N, A_ILE.88	H, A_ILE.88	2.49	1.58	17.48
1R21-11.PDB	O, A_GLN.70	N, A_THR.89	H, A_THR.89	2.50	1.53	3.27
1R21-11.PDB	O, A_ARG.93	N, A_ILE.90	H, A_ILE.90	2.78	1.90	20.94
1R21-11.PDB	O, A_ILE.88	N, A_PHE.95	H, A_PHE.95	2.50	1.61	19.58
1R21-11.PDB	O, A_VAL.8	N, A_ARG.96	H, A_ARG.96	2.62	1.79	25.65
1R21-11.PDB	O, A_ASP.86	N, A_TYR.97	H, A_TYR.97	2.89	1.91	5.12
1R21-12.PDB	O, A_HIS.54	NH1, A_ARG.5	HH12, A_ARG.5	2.35	1.46	20.98
1R21-12.PDB	O, A_ASP.16	N, A_LYS.11	H, A_LYS.11	2.75	1.92	26.57
1R21-12.PDB	O, A_LEU.7	N, A_PHE.20	H, A_PHE.20	2.75	1.93	26.79
1R21-12.PDB	O, A_ILE.51	N, A_CYS.27	H, A_CYS.27	2.63	1.69	14.10
1R21-12.PDB	O, A_CYS.49	N, A_PHE.29	H, A_PHE.29	2.60	1.71	19.44
1R21-12.PDB	O, A_LEU.28	N, A_ILE.37	H, A_ILE.37	2.57	1.63	12.93
1R21-12.PDB	O, A_LEU.41	N, A_VAL.44	H, A_VAL.44	2.87	2.03	25.37
1R21-12.PDB	O, A_CYS.27	N, A_ILE.51	H, A_ILE.51	2.54	1.72	26.76

1R21-12.PDB	O, A_ILE_59	N, A_GLU_52	H, A_GLU_52	2.50	1.60	18.41
1R21-12.PDB	O, A_SER_25	N, A_ILE_53	H, A_ILE_53	2.75	1.90	23.58
1R21-12.PDB	O, A_GLU_57	N, A_HIS_54	H, A_HIS_54	2.53	1.59	12.83
1R21-12.PDB	O, A_GLU_52	N, A_ILE_59	H, A_ILE_59	2.53	1.55	3.06
1R21-12.PDB	OD1, A_ASN_67	OG1, A_THR_66	HG1, A_THR_66	2.34	1.38	3.67
1R21-12.PDB	ND2, A_ASN_62	N, A_THR_69	H, A_THR_69	2.95	1.98	4.80
1R21-12.PDB	O, A_SER_74	N, A_VAL_71	H, A_VAL_71	2.74	1.76	4.25
1R21-12.PDB	O, A_VAL_87	N, A_ASN_72	H, A_ASN_72	2.97	2.02	11.55
1R21-12.PDB	O, A_VAL_71	N, A_SER_74	H, A_SER_74	2.46	1.58	19.54
1R21-12.PDB	O, A_TYR_97	N, A_GLY_85	H, A_GLY_85	2.87	2.02	24.88
1R21-12.PDB	O, A_PHE_95	N, A_ILE_88	H, A_ILE_88	2.84	1.89	12.15
1R21-12.PDB	O, A_GLN_70	N, A_THR_89	H, A_THR_89	2.50	1.53	5.45
1R21-12.PDB	O, A_ARG_93	N, A_ILE_90	H, A_ILE_90	2.66	1.75	17.37
1R21-12.PDB	O, A_ILE_88	N, A_PHE_95	H, A_PHE_95	2.61	1.63	4.84
1R21-12.PDB	O, A_VAL_8	N, A_ARG_96	H, A_ARG_96	2.92	2.06	24.15
1R21-12.PDB	ND1, A_HIS_84	N, A_ASN_99	H, A_ASN_99	2.78	1.81	6.29
1R21-13.PDB	O, A_PHE_20	N, A_LEU_7	H, A_LEU_7	2.91	1.96	10.96
1R21-13.PDB	O, A_LEU_7	N, A_PHE_20	H, A_PHE_20	2.60	1.77	25.97
1R21-13.PDB	O, A_ILE_51	N, A_CYS_27	H, A_CYS_27	2.75	1.81	13.78
1R21-13.PDB	O, A_CYS_49	N, A_PHE_29	H, A_PHE_29	2.85	1.88	7.67
1R21-13.PDB	O, A_GLY_32	N, A_CYS_35	H, A_CYS_35	2.95	2.05	19.20
1R21-13.PDB	O, A_LEU_28	N, A_ILE_37	H, A_ILE_37	2.62	1.65	8.44
1R21-13.PDB	OG, A_SER_45	N, A_GLN_47	H, A_GLN_47	2.99	2.17	27.24
1R21-13.PDB	O, A_CYS_27	N, A_ILE_51	H, A_ILE_51	2.43	1.49	12.20
1R21-13.PDB	O, A_ILE_59	N, A_GLU_52	H, A_GLU_52	2.43	1.54	19.61
1R21-13.PDB	O, A_GLU_57	N, A_HIS_54	H, A_HIS_54	2.39	1.45	12.69
1R21-13.PDB	O, A_GLU_52	N, A_ILE_59	H, A_ILE_59	2.60	1.64	9.03
1R21-13.PDB	O, A_LYS_50	N, A_HIS_61	H, A_HIS_61	2.72	1.77	12.00
1R21-13.PDB	OG1, A_THR_69	ND2, A_ASN_62	HD22, A_ASN_62	2.50	1.62	19.65
1R21-13.PDB	O, A_HIS_48	N, A_PHE_63	H, A_PHE_63	2.98	2.08	19.86
1R21-13.PDB	O, A_HIS_48	N, A_SER_64	H, A_SER_64	3.00	2.09	18.58
1R21-13.PDB	O, A_THR_89	N, A_GLN_70	H, A_GLN_70	2.61	1.74	22.03
1R21-13.PDB	O, A_SER_74	N, A_VAL_71	H, A_VAL_71	2.72	1.81	16.96
1R21-13.PDB	O, A_VAL_71	N, A_SER_74	H, A_SER_74	2.42	1.47	9.86
1R21-13.PDB	O, A_PHE_95	N, A_ILE_88	H, A_ILE_88	2.49	1.53	9.17
1R21-13.PDB	O, A_GLN_70	N, A_THR_89	H, A_THR_89	2.84	1.88	8.15
1R21-13.PDB	O, A_ARG_93	N, A_ILE_90	H, A_ILE_90	2.77	1.79	2.62
1R21-13.PDB	O, A_ILE_88	N, A_PHE_95	H, A_PHE_95	2.53	1.57	8.67
1R21-13.PDB	O, A_VAL_8	N, A_ARG_96	H, A_ARG_96	2.67	1.79	21.65
1R21-13.PDB	ND1, A_HIS_84	N, A_ASN_99	H, A_ASN_99	2.75	1.78	6.35
1R21-13.PDB	OH, A_TYR_97	ND2, A_ASN_99	HD21, A_ASN_99	2.51	1.54	7.69
1R21-14.PDB	O, A_LYS_11	N, A_GLY_14	H, A_GLY_14	2.87	1.98	19.78
1R21-14.PDB	O, A_LEU_7	N, A_PHE_20	H, A_PHE_20	2.54	1.58	9.83
1R21-14.PDB	O, A_ILE_51	N, A_CYS_27	H, A_CYS_27	2.51	1.56	10.89
1R21-14.PDB	O, A_CYS_49	N, A_PHE_29	H, A_PHE_29	2.67	1.74	15.50
1R21-14.PDB	O, A_LEU_28	N, A_ILE_37	H, A_ILE_37	2.59	1.64	10.66
1R21-14.PDB	O, A_GLY_30	N, A_ILE_39	H, A_ILE_39	2.98	2.01	7.49
1R21-14.PDB	O, A_CYS_27	N, A_ILE_51	H, A_ILE_51	2.41	1.51	18.34
1R21-14.PDB	O, A_ILE_59	N, A_GLU_52	H, A_GLU_52	2.40	1.49	17.73
1R21-14.PDB	O, A_GLU_57	N, A_HIS_54	H, A_HIS_54	2.54	1.66	20.37
1R21-14.PDB	O, A_GLU_52	N, A_ILE_59	H, A_ILE_59	2.44	1.48	8.49
1R21-14.PDB	OG1, A_THR_69	ND2, A_ASN_62	HD21, A_ASN_62	2.52	1.57	12.09
1R21-14.PDB	ND2, A_ASN_62	N, A_THR_69	H, A_THR_69	2.79	1.90	20.15
1R21-14.PDB	O, A_SER_74	N, A_VAL_71	H, A_VAL_71	2.76	1.80	9.73
1R21-14.PDB	O, A_VAL_71	N, A_SER_74	H, A_SER_74	2.68	1.86	26.85
1R21-14.PDB	O, A_THR_69	N, A_ILE_76	H, A_ILE_76	2.74	1.79	12.00
1R21-14.PDB	OE1, A_GLU_57	NE, A_ARG_81	HE, A_ARG_81	2.82	2.02	29.06
1R21-14.PDB	OE2, A_GLU_57	NH2, A_ARG_81	HH21, A_ARG_81	2.46	1.50	12.90

1R21-14.PDB	O, A_LYS_83	N, A_ASP_86	H, A_ASP_86	2.90	2.01	20.84
1R21-14.PDB	O, A_PHE_95	N, A_ILE_88	H, A_ILE_88	2.88	1.96	15.69
1R21-14.PDB	O, A_GLN_70	N, A_THR_89	H, A_THR_89	2.35	1.46	19.02
1R21-14.PDB	O, A_ARG_93	N, A_ILE_90	H, A_ILE_90	2.73	1.76	5.94
1R21-14.PDB	O, A_ILE_88	N, A_PHE_95	H, A_PHE_95	2.68	1.71	6.73
1R21-14.PDB	O, A_VAL_8	N, A_ARG_96	H, A_ARG_96	2.64	1.79	24.33
1R21-14.PDB	ND1, A_HIS_84	N, A_ASN_99	H, A_ASN_99	2.72	1.75	7.22
1R21-14.PDB	OH, A_TYR_97	ND2, A_ASN_99	HD22, A_ASN_99	2.66	1.70	8.32
1R21-14.PDB	O, A_THR_4	N, A_GLU_100	H, A_GLU_100	2.70	1.78	16.06
1R21-15.PDB	O, A_ARG_96	N, A_VAL_8	H, A_VAL_8	2.88	1.93	10.65
1R21-15.PDB	O, A_SER_13	N, A_VAL_15	H, A_VAL_15	2.35	1.44	16.35
1R21-15.PDB	O, A_LEU_7	N, A_PHE_20	H, A_PHE_20	2.72	1.80	16.28
1R21-15.PDB	O, A_ILE_51	N, A_CYS_27	H, A_CYS_27	2.61	1.66	12.03
1R21-15.PDB	O, A_CYS_49	N, A_PHE_29	H, A_PHE_29	2.69	1.83	22.46
1R21-15.PDB	O, A_LEU_28	N, A_ILE_37	H, A_ILE_37	2.63	1.74	19.85
1R21-15.PDB	O, A_GLY_30	N, A_ILE_39	H, A_ILE_39	2.35	1.52	25.02
1R21-15.PDB	O, A_LEU_41	N, A_VAL_44	H, A_VAL_44	2.84	1.98	24.12
1R21-15.PDB	O, A_CYS_27	N, A_ILE_51	H, A_ILE_51	2.47	1.55	15.28
1R21-15.PDB	O, A_ILE_59	N, A_GLU_52	H, A_GLU_52	2.51	1.64	21.23
1R21-15.PDB	O, A_SER_25	N, A_ILE_53	H, A_ILE_53	2.58	1.68	18.87
1R21-15.PDB	O, A_GLU_57	N, A_HIS_54	H, A_HIS_54	2.77	1.90	21.35
1R21-15.PDB	O, A_GLU_52	N, A_ILE_59	H, A_ILE_59	2.58	1.61	8.20
1R21-15.PDB	ND2, A_ASN_62	N, A_THR_69	H, A_THR_69	2.81	1.84	7.15
1R21-15.PDB	O, A_THR_89	N, A_GLN_70	H, A_GLN_70	2.43	1.52	17.31
1R21-15.PDB	O, A_SER_74	N, A_VAL_71	H, A_VAL_71	2.74	1.76	5.74
1R21-15.PDB	O, A_VAL_87	N, A_ASN_72	H, A_ASN_72	2.86	1.91	10.94
1R21-15.PDB	O, A_VAL_71	N, A_SER_74	H, A_SER_74	2.38	1.51	21.59
1R21-15.PDB	O, A_LYS_83	N, A_ASP_86	H, A_ASP_86	2.97	2.11	23.04
1R21-15.PDB	O, A_PHE_95	N, A_ILE_88	H, A_ILE_88	2.57	1.60	8.14
1R21-15.PDB	O, A_GLN_70	N, A_THR_89	H, A_THR_89	2.38	1.41	5.21
1R21-15.PDB	O, A_ARG_93	N, A_ILE_90	H, A_ILE_90	2.86	1.91	12.34
1R21-15.PDB	O, A_ILE_88	N, A_PHE_95	H, A_PHE_95	2.57	1.60	6.79
1R21-15.PDB	O, A_VAL_8	N, A_ARG_96	H, A_ARG_96	2.52	1.57	12.45
1R21-15.PDB	O, A_ASP_86	N, A_TYR_97	H, A_TYR_97	2.93	1.95	3.90
1R21-15.PDB	ND1, A_HIS_84	N, A_ASN_99	H, A_ASN_99	2.69	1.85	25.22
1R21-16.PDB	O, A_GLN_56	NH2, A_ARG_5	HH22, A_ARG_5	2.34	1.43	18.03
1R21-16.PDB	O, A_PRO_18	N, A_THR_9	H, A_THR_9	2.87	1.96	17.95
1R21-16.PDB	O, A_LEU_7	N, A_PHE_20	H, A_PHE_20	2.79	1.90	20.16
1R21-16.PDB	O, A_ILE_51	N, A_CYS_27	H, A_CYS_27	2.97	2.01	9.41
1R21-16.PDB	O, A_CYS_49	N, A_PHE_29	H, A_PHE_29	2.70	1.82	20.83
1R21-16.PDB	O, A_LEU_28	N, A_ILE_37	H, A_ILE_37	2.64	1.66	6.75
1R21-16.PDB	O, A_GLY_30	N, A_ILE_39	H, A_ILE_39	2.92	2.04	21.29
1R21-16.PDB	O, A_LEU_41	N, A_VAL_44	H, A_VAL_44	2.78	1.86	16.48
1R21-16.PDB	N, A_LYS_50	SG, A_CYS_49	HG, A_CYS_49	2.71	1.94	29.78
1R21-16.PDB	O, A_CYS_27	N, A_ILE_51	H, A_ILE_51	2.66	1.76	18.43
1R21-16.PDB	O, A_ILE_59	N, A_GLU_52	H, A_GLU_52	2.35	1.42	13.61
1R21-16.PDB	O, A_GLU_57	N, A_HIS_54	H, A_HIS_54	2.48	1.61	21.21
1R21-16.PDB	O, A_GLU_52	N, A_ILE_59	H, A_ILE_59	2.45	1.49	8.62
1R21-16.PDB	O, A_LYS_50	N, A_HIS_61	H, A_HIS_61	2.79	1.86	14.54
1R21-16.PDB	O, A_ASN_67	OG, A_SER_64	HG, A_SER_64	2.30	1.47	23.15
1R21-16.PDB	ND2, A_ASN_62	N, A_THR_69	H, A_THR_69	2.78	1.82	9.93
1R21-16.PDB	O, A_THR_89	N, A_GLN_70	H, A_GLN_70	2.50	1.67	25.41
1R21-16.PDB	O, A_SER_74	N, A_VAL_71	H, A_VAL_71	2.80	1.83	8.69
1R21-16.PDB	O, A_VAL_87	N, A_ASN_72	H, A_ASN_72	2.98	2.02	10.53
1R21-16.PDB	O, A_VAL_71	N, A_SER_74	H, A_SER_74	2.44	1.53	16.98
1R21-16.PDB	OE1, A_GLU_57	NE, A_ARG_81	HE, A_ARG_81	2.43	1.60	25.79
1R21-16.PDB	OD2, A_ASP_86	N, A_LYS_83	H, A_LYS_83	2.35	1.45	17.98
1R21-16.PDB	O, A_PHE_95	N, A_ILE_88	H, A_ILE_88	2.63	1.69	13.56

1R21-16.PDB	O, A_GLN_70	N, A_THR_89	H, A_THR_89	2.63	1.67	7.81
1R21-16.PDB	O, A_ARG_93	N, A_ILE_90	H, A_ILE_90	2.81	1.86	12.00
1R21-16.PDB	O, A_ILE_88	N, A_PHE_95	H, A_PHE_95	2.55	1.60	9.47
1R21-16.PDB	O, A_VAL_8	N, A_ARG_96	H, A_ARG_96	2.56	1.67	20.20
1R21-16.PDB	ND1, A_HIS_84	N, A_ASN_99	H, A_ASN_99	2.73	1.80	13.70
1R21-17.PDB	ND2, A_ASN_99	NE, A_ARG_5	HE, A_ARG_5	2.79	1.84	10.87
1R21-17.PDB	O, A_MET_1	NH2, A_ARG_6	HH21, A_ARG_6	2.74	1.87	24.11
1R21-17.PDB	O, A_LYS_11	N, A_GLY_14	H, A_GLY_14	2.90	2.08	27.87
1R21-17.PDB	O, A_ILE_51	N, A_CYS_27	H, A_CYS_27	2.92	1.99	13.70
1R21-17.PDB	O, A_CYS_49	N, A_PHE_29	H, A_PHE_29	2.53	1.61	15.83
1R21-17.PDB	O, A_LEU_28	N, A_ILE_37	H, A_ILE_37	2.62	1.67	11.05
1R21-17.PDB	O, A_LEU_41	N, A_VAL_44	H, A_VAL_44	2.81	1.91	19.33
1R21-17.PDB	N, A_LYS_50	SG, A_CYS_49	HG, A_CYS_49	2.88	2.09	29.10
1R21-17.PDB	O, A_CYS_27	N, A_ILE_51	H, A_ILE_51	2.65	1.79	22.63
1R21-17.PDB	O, A_ILE_59	N, A_GLU_52	H, A_GLU_52	2.52	1.59	14.29
1R21-17.PDB	O, A_GLU_57	N, A_HIS_54	H, A_HIS_54	2.65	1.75	18.68
1R21-17.PDB	OH, A_TYR_97	N, A_ALA_58	H, A_ALA_58	2.72	1.89	26.01
1R21-17.PDB	O, A_GLU_52	N, A_ILE_59	H, A_ILE_59	2.54	1.61	14.09
1R21-17.PDB	ND2, A_ASN_62	N, A_THR_69	H, A_THR_69	2.79	1.83	10.71
1R21-17.PDB	O, A_THR_89	N, A_GLN_70	H, A_GLN_70	2.59	1.75	25.37
1R21-17.PDB	O, A_SER_74	N, A_VAL_71	H, A_VAL_71	2.94	1.96	5.72
1R21-17.PDB	O, A_VAL_71	N, A_SER_74	H, A_SER_74	2.46	1.58	20.03
1R21-17.PDB	OD2, A_ASP_86	N, A_LYS_83	H, A_LYS_83	2.55	1.59	9.81
1R21-17.PDB	O, A_LYS_83	N, A_ASP_86	H, A_ASP_86	2.89	2.09	28.87
1R21-17.PDB	O, A_GLN_70	N, A_THR_89	H, A_THR_89	2.44	1.48	5.59
1R21-17.PDB	OG1, A_SER_94	OG1, A_THR_89	HG1, A_THR_89	2.85	1.94	16.35
1R21-17.PDB	O, A_ARG_93	N, A_ILE_90	H, A_ILE_90	2.85	1.87	5.40
1R21-17.PDB	O, A_ILE_88	N, A_PHE_95	H, A_PHE_95	2.73	1.78	13.00
1R21-17.PDB	O, A_VAL_8	N, A_ARG_96	H, A_ARG_96	2.69	1.78	16.86
1R21-17.PDB	ND1, A_HIS_84	N, A_ASN_99	H, A_ASN_99	2.76	1.87	19.62
1R21-18.PDB	O, A_ARG_96	N, A_VAL_8	H, A_VAL_8	2.73	1.79	13.70
1R21-18.PDB	O, A_LEU_7	N, A_PHE_20	H, A_PHE_20	2.72	1.86	23.59
1R21-18.PDB	O, A_ILE_51	N, A_CYS_27	H, A_CYS_27	2.72	1.82	18.54
1R21-18.PDB	O, A_CYS_49	N, A_PHE_29	H, A_PHE_29	2.70	1.85	23.94
1R21-18.PDB	O, A_LEU_28	N, A_ILE_37	H, A_ILE_37	2.69	1.74	12.20
1R21-18.PDB	O, A_LEU_41	N, A_VAL_44	H, A_VAL_44	2.84	2.03	28.77
1R21-18.PDB	O, A_CYS_27	N, A_ILE_51	H, A_ILE_51	2.61	1.76	24.32
1R21-18.PDB	O, A_ILE_59	N, A_GLU_52	H, A_GLU_52	2.43	1.48	11.54
1R21-18.PDB	O, A_GLU_57	N, A_HIS_54	H, A_HIS_54	2.49	1.54	10.72
1R21-18.PDB	O, A_GLU_52	N, A_ILE_59	H, A_ILE_59	2.56	1.66	18.64
1R21-18.PDB	OD1, A_ASN_67	OG1, A_THR_66	HG1, A_THR_66	2.60	1.66	10.07
1R21-18.PDB	ND2, A_ASN_62	N, A_THR_69	H, A_THR_69	2.83	1.90	12.87
1R21-18.PDB	O, A_THR_89	N, A_GLN_70	H, A_GLN_70	2.37	1.53	24.51
1R21-18.PDB	O, A_SER_74	N, A_VAL_71	H, A_VAL_71	2.79	1.82	9.69
1R21-18.PDB	O, A_VAL_71	N, A_SER_74	H, A_SER_74	2.46	1.62	24.85
1R21-18.PDB	OE2, A_GLU_100	NE2, A_HIS_84	HE2, A_HIS_84	2.44	1.60	25.14
1R21-18.PDB	O, A_PHE_95	N, A_ILE_88	H, A_ILE_88	2.60	1.64	8.44
1R21-18.PDB	O, A_GLN_70	N, A_THR_89	H, A_THR_89	2.43	1.45	2.51
1R21-18.PDB	O, A_ARG_93	N, A_ILE_90	H, A_ILE_90	2.78	1.81	6.62
1R21-18.PDB	O, A_ILE_88	N, A_PHE_95	H, A_PHE_95	2.57	1.60	5.68
1R21-18.PDB	O, A_VAL_8	N, A_ARG_96	H, A_ARG_96	2.51	1.63	20.84
1R21-18.PDB	ND1, A_HIS_84	N, A_ASN_99	H, A_ASN_99	2.90	1.93	9.14
1R21-19.PDB	O, A_ARG_96	N, A_VAL_8	H, A_VAL_8	2.99	2.07	17.19
1R21-19.PDB	O, A_LEU_7	N, A_PHE_20	H, A_PHE_20	2.60	1.69	17.39
1R21-19.PDB	O, A_ILE_51	N, A_CYS_27	H, A_CYS_27	2.92	1.99	15.89
1R21-19.PDB	O, A_CYS_49	N, A_PHE_29	H, A_PHE_29	2.60	1.72	21.65
1R21-19.PDB	O, A_LEU_28	N, A_ILE_37	H, A_ILE_37	2.59	1.64	12.32
1R21-19.PDB	OE2, A_GLU_34	NE2, A_GLN_47	HE21, A_GLN_47	2.80	1.93	22.82

1R21-19.PDB	O, A_CYS_27	N, A_ILE_51	H, A_ILE_51	2.77	1.98	29.09
1R21-19.PDB	O, A_ILE_59	N, A_GLU_52	H, A_GLU_52	2.43	1.48	11.27
1R21-19.PDB	O, A_GLU_57	N, A_HIS_54	H, A_HIS_54	2.56	1.64	15.53
1R21-19.PDB	OH, A_TYR_97	N, A_ALA_58	H, A_ALA_58	2.88	2.06	27.15
1R21-19.PDB	O, A_GLU_52	N, A_ILE_59	H, A_ILE_59	2.44	1.53	17.22
1R21-19.PDB	OG1, A_THR_69	ND2, A_ASN_62	HD21, A_ASN_62	2.83	2.03	29.57
1R21-19.PDB	ND2, A_ASN_62	N, A_THR_69	H, A_THR_69	2.67	1.78	19.68
1R21-19.PDB	O, A_THR_89	N, A_GLN_70	H, A_GLN_70	2.64	1.78	22.36
1R21-19.PDB	O, A_SER_74	N, A_VAL_71	H, A_VAL_71	2.64	1.69	11.33
1R21-19.PDB	O, A_VAL_71	N, A_SER_74	H, A_SER_74	2.48	1.59	19.12
1R21-19.PDB	O, A_THR_69	N, A_ILE_76	H, A_ILE_76	2.76	1.93	26.34
1R21-19.PDB	O, A_LYS_83	N, A_ASP_86	H, A_ASP_86	2.90	2.02	21.05
1R21-19.PDB	O, A_PHE_95	N, A_ILE_88	H, A_ILE_88	2.84	1.95	19.79
1R21-19.PDB	O, A_GLN_70	N, A_THR_89	H, A_THR_89	2.66	1.69	6.71
1R21-19.PDB	O, A_ARG_93	N, A_ILE_90	H, A_ILE_90	2.72	1.76	8.86
1R21-19.PDB	O, A_ILE_88	N, A_PHE_95	H, A_PHE_95	2.54	1.63	17.83
1R21-19.PDB	O, A_VAL_8	N, A_ARG_96	H, A_ARG_96	2.59	1.69	17.99
1R21-19.PDB	ND1, A_HIS_84	N, A_ASN_99	H, A_ASN_99	2.84	1.89	10.70
1R21-2.PDB	N, A_ARG_5	OG1, A_THR_4	HG1, A_THR_4	2.74	1.85	17.56
1R21-2.PDB	O, A_PHE_20	N, A_LEU_7	H, A_LEU_7	2.95	1.98	8.03
1R21-2.PDB	O, A_LEU_7	N, A_PHE_20	H, A_PHE_20	2.59	1.74	24.59
1R21-2.PDB	O, A_CYS_49	N, A_PHE_29	H, A_PHE_29	2.72	1.83	19.71
1R21-2.PDB	O, A_LEU_28	N, A_ILE_37	H, A_ILE_37	2.57	1.60	6.95
1R21-2.PDB	OE2, A_GLU_34	NE2, A_GLN_47	HE21, A_GLN_47	2.62	1.65	7.42
1R21-2.PDB	O, A_CYS_27	N, A_ILE_51	H, A_ILE_51	2.67	1.82	25.05
1R21-2.PDB	O, A_ILE_59	N, A_GLU_52	H, A_GLU_52	2.42	1.55	22.16
1R21-2.PDB	O, A_GLU_57	N, A_HIS_54	H, A_HIS_54	2.50	1.69	27.80
1R21-2.PDB	O, A_GLU_52	N, A_ILE_59	H, A_ILE_59	2.46	1.49	3.05
1R21-2.PDB	OG1, A_THR_69	ND2, A_ASN_62	HD21, A_ASN_62	2.81	1.92	20.56
1R21-2.PDB	OG, A_SER_64	ND2, A_ASN_62	HD22, A_ASN_62	2.42	1.53	18.22
1R21-2.PDB	ND2, A_ASN_62	N, A_THR_69	H, A_THR_69	2.76	1.81	12.74
1R21-2.PDB	O, A_THR_89	N, A_GLN_70	H, A_GLN_70	2.51	1.65	23.32
1R21-2.PDB	O, A_VAL_87	N, A_ASN_72	H, A_ASN_72	2.97	2.02	10.02
1R21-2.PDB	O, A_VAL_71	N, A_SER_74	H, A_SER_74	2.58	1.65	14.58
1R21-2.PDB	OD2, A_ASP_86	N, A_LYS_83	H, A_LYS_83	2.34	1.53	27.15
1R21-2.PDB	O, A_TYR_97	N, A_GLY_85	H, A_GLY_85	2.88	2.06	27.73
1R21-2.PDB	O, A_PHE_95	N, A_ILE_88	H, A_ILE_88	2.71	1.73	6.39
1R21-2.PDB	O, A_GLN_70	N, A_THR_89	H, A_THR_89	2.55	1.58	6.68
1R21-2.PDB	OG, A_SER_94	OG1, A_THR_89	HG1, A_THR_89	2.98	2.02	6.58
1R21-2.PDB	N, A_ARG_93	N, A_ILE_90	H, A_ILE_90	2.82	1.89	14.80
1R21-2.PDB	O, A_ILE_88	N, A_PHE_95	H, A_PHE_95	2.61	1.65	9.22
1R21-2.PDB	O, A_VAL_8	N, A_ARG_96	H, A_ARG_96	2.61	1.75	22.96
1R21-2.PDB	OD2, A_ASP_16	NH1, A_ARG_96	HH12, A_ARG_96	2.71	1.87	26.03
1R21-2.PDB	ND1, A_HIS_84	N, A_ASN_99	H, A_ASN_99	2.71	1.73	1.63
1R21-20.PDB	O, A_PHE_20	N, A_LEU_7	H, A_LEU_7	2.89	1.97	16.40
1R21-20.PDB	O, A_LEU_7	N, A_PHE_20	H, A_PHE_20	2.54	1.59	11.23
1R21-20.PDB	O, A_ILE_51	N, A_CYS_27	H, A_CYS_27	2.71	1.75	9.33
1R21-20.PDB	O, A_CYS_49	N, A_PHE_29	H, A_PHE_29	2.67	1.77	18.32
1R21-20.PDB	O, A_LEU_28	N, A_ILE_37	H, A_ILE_37	2.61	1.64	6.85
1R21-20.PDB	N, A_LYS_46	OG, A_SER_45	HG, A_SER_45	2.70	1.79	15.25
1R21-20.PDB	O, A_CYS_27	N, A_ILE_51	H, A_ILE_51	2.42	1.58	23.81
1R21-20.PDB	O, A_ILE_59	N, A_GLU_52	H, A_GLU_52	2.32	1.45	21.34
1R21-20.PDB	O, A_GLU_57	N, A_HIS_54	H, A_HIS_54	2.45	1.51	12.30
1R21-20.PDB	O, A_GLU_52	N, A_ILE_59	H, A_ILE_59	2.48	1.51	4.91
1R21-20.PDB	O, A_VAL_80	N, A_LEU_60	H, A_LEU_60	2.94	1.97	6.46
1R21-20.PDB	O, A_LYS_50	N, A_HIS_61	H, A_HIS_61	2.71	1.83	20.97
1R21-20.PDB	ND2, A_ASN_62	N, A_THR_69	H, A_THR_69	2.81	1.85	8.55
1R21-20.PDB	O, A_THR_89	N, A_GLN_70	H, A_GLN_70	2.55	1.71	24.95

1R21-20.PDB	O, A_VAL_87	N, A_ASN_72	H, A_ASN_72	2.84	1.89	10.53
1R21-20.PDB	O, A_VAL_71	N, A_SER_74	H, A_SER_74	2.53	1.62	17.33
1R21-20.PDB	O, A_VAL_71	OG, A_SER_74	HG, A_SER_74	2.49	1.70	27.88
1R21-20.PDB	O, A_PHE_95	N, A_ILE_88	H, A_ILE_88	2.46	1.49	5.80
1R21-20.PDB	O, A_GLN_70	N, A_THR_89	H, A_THR_89	2.46	1.50	7.24
1R21-20.PDB	O, A_ARG_93	N, A_ILE_90	H, A_ILE_90	2.66	1.69	6.47
1R21-20.PDB	O, A_ILE_88	N, A_PHE_95	H, A_PHE_95	2.54	1.58	8.65
1R21-20.PDB	O, A_VAL_8	N, A_ARG_96	H, A_ARG_96	2.64	1.79	24.11
1R21-20.PDB	ND1, A_HIS_84	N, A_ASN_99	H, A_ASN_99	2.96	2.01	12.19
1R21-21.PDB	O, A_PHE_20	N, A_LEU_7	H, A_LEU_7	2.96	2.07	20.84
1R21-21.PDB	O, A_ARG_96	N, A_VAL_8	H, A_VAL_8	2.59	1.62	4.25
1R21-21.PDB	O, A_LEU_7	N, A_PHE_20	H, A_PHE_20	2.61	1.64	5.69
1R21-21.PDB	O, A_ILE_51	N, A_CYS_27	H, A_CYS_27	2.91	1.95	10.90
1R21-21.PDB	O, A_CYS_49	N, A_PHE_29	H, A_PHE_29	2.68	1.81	22.17
1R21-21.PDB	O, A_LEU_28	N, A_ILE_37	H, A_ILE_37	2.56	1.62	13.05
1R21-21.PDB	O, A_LEU_41	N, A_VAL_44	H, A_VAL_44	2.91	2.06	24.25
1R21-21.PDB	O, A_CYS_27	N, A_ILE_51	H, A_ILE_51	2.73	1.89	24.96
1R21-21.PDB	O, A_ILE_59	N, A_GLU_52	H, A_GLU_52	2.35	1.50	22.81
1R21-21.PDB	O, A_GLU_57	N, A_HIS_54	H, A_HIS_54	2.92	1.97	10.24
1R21-21.PDB	O, A_GLU_52	N, A_ILE_59	H, A_ILE_59	2.54	1.70	24.70
1R21-21.PDB	ND2, A_ASN_62	N, A_THR_69	H, A_THR_69	2.75	1.85	18.29
1R21-21.PDB	O, A_THR_89	N, A_GLN_70	H, A_GLN_70	2.65	1.74	16.82
1R21-21.PDB	O, A_SER_74	N, A_VAL_71	H, A_VAL_71	2.64	1.68	10.54
1R21-21.PDB	O, A_VAL_87	N, A_ASN_72	H, A_ASN_72	2.70	1.73	7.44
1R21-21.PDB	O, A_VAL_71	N, A_SER_74	H, A_SER_74	2.70	1.91	29.55
1R21-21.PDB	OD2, A_ASP_86	N, A_LYS_83	H, A_LYS_83	2.35	1.45	17.97
1R21-21.PDB	OD1, A_ASN_72	N, A_VAL_87	H, A_VAL_87	2.99	2.03	10.40
1R21-21.PDB	O, A_PHE_95	N, A_ILE_88	H, A_ILE_88	2.42	1.51	16.26
1R21-21.PDB	O, A_GLN_70	N, A_THR_89	H, A_THR_89	2.52	1.56	6.68
1R21-21.PDB	O, A_ARG_93	N, A_ILE_90	H, A_ILE_90	2.78	1.92	23.35
1R21-21.PDB	O, A_ILE_88	N, A_PHE_95	H, A_PHE_95	2.32	1.44	19.20
1R21-21.PDB	O, A_VAL_8	N, A_ARG_96	H, A_ARG_96	2.40	1.50	17.53
1R21-21.PDB	ND1, A_HIS_84	N, A_ASN_99	H, A_ASN_99	2.69	1.78	18.43
1R21-22.PDB	O, A_LYS_11	N, A_GLY_14	H, A_GLY_14	2.92	1.99	15.41
1R21-22.PDB	OD1, A_ASP_16	N, A_GLY_17	H, A_GLY_17	2.32	1.45	19.59
1R21-22.PDB	O, A_LEU_7	N, A_PHE_20	H, A_PHE_20	2.61	1.65	9.53
1R21-22.PDB	O, A_ILE_51	N, A_CYS_27	H, A_CYS_27	2.87	1.96	17.01
1R21-22.PDB	O, A_CYS_49	N, A_PHE_29	H, A_PHE_29	2.60	1.70	18.19
1R21-22.PDB	O, A_VAL_44	NH1, A_ARG_31	HH11, A_ARG_31	2.32	1.43	20.44
1R21-22.PDB	O, A_LEU_28	N, A_ILE_37	H, A_ILE_37	2.50	1.57	14.67
1R21-22.PDB	O, A_GLY_30	N, A_ILE_39	H, A_ILE_39	2.87	1.93	13.15
1R21-22.PDB	O, A_CYS_27	N, A_ILE_51	H, A_ILE_51	2.68	1.88	28.33
1R21-22.PDB	O, A_ILE_59	N, A_GLU_52	H, A_GLU_52	2.35	1.46	18.95
1R21-22.PDB	O, A_SER_25	N, A_ILE_53	H, A_ILE_53	2.75	1.92	25.97
1R21-22.PDB	O, A_GLU_57	N, A_HIS_54	H, A_HIS_54	2.43	1.49	13.42
1R21-22.PDB	O, A_GLU_52	N, A_ILE_59	H, A_ILE_59	2.51	1.56	11.28
1R21-22.PDB	OG, A_SER_64	ND2, A_ASN_62	HD22, A_ASN_62	2.37	1.45	16.21
1R21-22.PDB	ND2, A_ASN_62	N, A_THR_69	H, A_THR_69	2.75	1.81	13.92
1R21-22.PDB	O, A_THR_89	N, A_GLN_70	H, A_GLN_70	2.39	1.49	18.52
1R21-22.PDB	O, A_SER_74	N, A_VAL_71	H, A_VAL_71	2.73	1.76	7.13
1R21-22.PDB	O, A_VAL_71	N, A_SER_74	H, A_SER_74	2.40	1.54	22.50
1R21-22.PDB	OD2, A_ASP_86	N, A_LYS_83	H, A_LYS_83	2.34	1.47	21.74
1R21-22.PDB	O, A_TYR_97	N, A_GLY_85	H, A_GLY_85	2.95	2.10	24.40
1R21-22.PDB	O, A_PHE_95	N, A_ILE_88	H, A_ILE_88	2.63	1.67	6.98
1R21-22.PDB	O, A_GLN_70	N, A_THR_89	H, A_THR_89	2.41	1.52	18.90
1R21-22.PDB	O, A_ARG_93	N, A_ILE_90	H, A_ILE_90	2.74	1.77	6.10
1R21-22.PDB	O, A_ILE_88	N, A_PHE_95	H, A_PHE_95	2.64	1.72	15.76
1R21-22.PDB	O, A_VAL_8	N, A_ARG_96	H, A_ARG_96	2.37	1.47	18.14

1R21-22.PDB	O, A_ASP_86	N, A_TYR_97	H, A_TYR_97	2.99	2.03	9.81
1R21-22.PDB	ND1, A_HIS_84	N, A_ASN_99	H, A_ASN_99	2.84	1.90	14.56
1R21-23.PDB	O, A_ARG_96	N, A_VAL_8	H, A_VAL_8	2.86	1.92	13.31
1R21-23.PDB	O, A_CYS_49	N, A_PHE_29	H, A_PHE_29	2.64	1.75	19.18
1R21-23.PDB	O, A_LEU_28	N, A_ILE_37	H, A_ILE_37	2.58	1.62	9.88
1R21-23.PDB	O, A_CYS_27	N, A_ILE_51	H, A_ILE_51	2.71	1.91	29.18
1R21-23.PDB	O, A_SER_25	N, A_ILE_53	H, A_ILE_53	2.69	1.85	24.46
1R21-23.PDB	O, A_GLU_57	N, A_HIS_54	H, A_HIS_54	2.99	2.01	4.94
1R21-23.PDB	ND1, A_HIS_54	N, A_GLU_57	H, A_GLU_57	2.90	2.03	23.13
1R21-23.PDB	O, A_GLU_52	N, A_ILE_59	H, A_ILE_59	2.62	1.77	23.57
1R21-23.PDB	ND2, A_ASN_62	N, A_THR_69	H, A_THR_69	2.86	1.89	7.90
1R21-23.PDB	O, A_VAL_71	N, A_SER_74	H, A_SER_74	2.40	1.48	15.27
1R21-23.PDB	OE1, A_GLU_57	NE, A_ARG_81	HE, A_ARG_81	2.65	1.70	11.54
1R21-23.PDB	OD2, A_ASP_86	N, A_LYS_83	H, A_LYS_83	2.56	1.66	17.59
1R21-23.PDB	O, A_PHE_95	N, A_ILE_88	H, A_ILE_88	2.67	1.71	9.77
1R21-23.PDB	O, A_GLN_70	N, A_THR_89	H, A_THR_89	2.44	1.47	4.21
1R21-23.PDB	O, A_ARG_93	N, A_ILE_90	H, A_ILE_90	2.77	1.83	11.81
1R21-23.PDB	O, A_ILE_88	N, A_PHE_95	H, A_PHE_95	2.62	1.66	9.26
1R21-23.PDB	O, A_VAL_8	N, A_ARG_96	H, A_ARG_96	2.53	1.67	22.54
1R21-23.PDB	ND1, A_HIS_84	N, A_ASN_99	H, A_ASN_99	2.78	1.83	12.42
1R21-3.PDB	O, A_PRO_18	N, A_THR_9	H, A_THR_9	2.75	1.82	15.55
1R21-3.PDB	OD1, A_ASP_16	NE2, A_HIS_19	HE2, A_HIS_19	2.71	1.85	23.51
1R21-3.PDB	O, A_LEU_7	N, A_PHE_20	H, A_PHE_20	2.81	2.01	29.61
1R21-3.PDB	O, A_ILE_51	N, A_CYS_27	H, A_CYS_27	2.79	1.88	18.32
1R21-3.PDB	O, A_CYS_49	N, A_PHE_29	H, A_PHE_29	2.76	1.82	13.22
1R21-3.PDB	O, A_LEU_28	N, A_ILE_37	H, A_ILE_37	2.65	1.72	14.66
1R21-3.PDB	O, A_GLY_30	N, A_ILE_39	H, A_ILE_39	2.90	1.94	10.95
1R21-3.PDB	OE2, A_GLU_34	NE2, A_GLN_47	HE22, A_GLN_47	2.72	1.92	29.24
1R21-3.PDB	O, A_ILE_59	N, A_GLU_52	H, A_GLU_52	2.41	1.46	10.14
1R21-3.PDB	O, A_SER_25	N, A_ILE_53	H, A_ILE_53	2.44	1.55	19.50
1R21-3.PDB	O, A_GLU_57	N, A_HIS_54	H, A_HIS_54	2.46	1.55	16.84
1R21-3.PDB	O, A_GLU_52	N, A_ILE_59	H, A_ILE_59	2.65	1.70	10.74
1R21-3.PDB	O, A_LYS_50	N, A_HIS_61	H, A_HIS_61	2.72	1.91	28.48
1R21-3.PDB	OG1, A_THR_69	ND2, A_ASN_62	HD21, A_ASN_62	2.87	2.01	23.40
1R21-3.PDB	O, A_HIS_48	N, A_PHE_63	H, A_PHE_63	2.66	1.74	15.84
1R21-3.PDB	ND2, A_ASN_62	N, A_THR_69	H, A_THR_69	2.80	1.85	9.14
1R21-3.PDB	O, A_SER_74	N, A_VAL_71	H, A_VAL_71	2.76	1.79	6.23
1R21-3.PDB	O, A_VAL_87	N, A_ASN_72	H, A_ASN_72	2.81	1.87	12.50
1R21-3.PDB	O, A_VAL_71	N, A_SER_74	H, A_SER_74	2.52	1.65	22.26
1R21-3.PDB	O, A_PHE_95	N, A_ILE_88	H, A_ILE_88	2.38	1.42	9.04
1R21-3.PDB	O, A_GLN_70	N, A_THR_89	H, A_THR_89	2.58	1.62	7.30
1R21-3.PDB	O, A_ARG_93	N, A_ILE_90	H, A_ILE_90	2.88	1.98	18.52
1R21-3.PDB	O, A_ILE_88	N, A_PHE_95	H, A_PHE_95	2.49	1.52	2.60
1R21-3.PDB	O, A_VAL_8	N, A_ARG_96	H, A_ARG_96	2.86	1.93	15.31
1R21-3.PDB	ND1, A_HIS_84	N, A_ASN_99	H, A_ASN_99	2.73	1.81	16.46
1R21-4.PDB	O, A_GLN_56	NH2, A_ARG_5	HH21, A_ARG_5	2.90	2.09	29.83
1R21-4.PDB	O, A_LEU_7	N, A_PHE_20	H, A_PHE_20	2.67	1.82	24.01
1R21-4.PDB	O, A_ILE_51	N, A_CYS_27	H, A_CYS_27	2.66	1.75	17.27
1R21-4.PDB	O, A_CYS_49	N, A_PHE_29	H, A_PHE_29	2.65	1.73	16.15
1R21-4.PDB	O, A_LEU_28	N, A_ILE_37	H, A_ILE_37	2.58	1.63	11.12
1R21-4.PDB	O, A_GLY_30	N, A_ILE_39	H, A_ILE_39	2.96	2.02	14.09
1R21-4.PDB	O, A_LEU_41	N, A_VAL_44	H, A_VAL_44	2.78	1.93	24.60
1R21-4.PDB	O, A_CYS_27	N, A_ILE_51	H, A_ILE_51	2.64	1.83	27.83
1R21-4.PDB	O, A_ILE_59	N, A_GLU_52	H, A_GLU_52	2.49	1.57	16.14
1R21-4.PDB	O, A_SER_25	N, A_ILE_53	H, A_ILE_53	2.85	2.00	24.05
1R21-4.PDB	N, A_GLU_55	ND1, A_HIS_54	HD1, A_HIS_54	2.58	1.78	28.52
1R21-4.PDB	O, A_GLU_52	N, A_ILE_59	H, A_ILE_59	2.59	1.66	14.45
1R21-4.PDB	OD1, A_ASN_67	OG1, A_THR_66	HG1, A_THR_66	2.40	1.45	5.76

1R21-4.PDB	ND2, A_ASN_62	N, A_THR_69	H, A_THR_69	2.80	1.85	11.39
1R21-4.PDB	O, A_THR_89	N, A_GLN_70	H, A_GLN_70	2.55	1.67	20.25
1R21-4.PDB	O, A_SER_74	N, A_VAL_71	H, A_VAL_71	2.68	1.77	17.57
1R21-4.PDB	O, A_VAL_71	N, A_SER_74	H, A_SER_74	2.43	1.52	16.62
1R21-4.PDB	OE1, A_GLU_57	NE, A_ARG_81	HE, A_ARG_81	2.76	1.87	19.46
1R21-4.PDB	OE1, A_GLU_57	NH2, A_ARG_81	HH21, A_ARG_81	2.93	2.10	27.48
1R21-4.PDB	OD2, A_ASP_86	N, A_LYS_83	H, A_LYS_83	2.52	1.72	28.30
1R21-4.PDB	O, A_PHE_95	N, A_ILE_88	H, A_ILE_88	2.41	1.51	17.89
1R21-4.PDB	O, A_GLN_70	N, A_THR_89	H, A_THR_89	2.59	1.62	4.11
1R21-4.PDB	O, A_ARG_93	N, A_ILE_90	H, A_ILE_90	2.76	1.91	24.78
1R21-4.PDB	O, A_ILE_88	N, A_PHE_95	H, A_PHE_95	2.36	1.44	14.85
1R21-4.PDB	ND1, A_HIS_84	N, A_ASN_99	H, A_ASN_99	2.80	1.85	12.02
1R21-5.PDB	O, A_VAL_15	N, A_LYS_11	H, A_LYS_11	2.78	1.94	24.72
1R21-5.PDB	O, A_LYS_11	N, A_GLY_14	H, A_GLY_14	2.58	1.71	22.29
1R21-5.PDB	O, A_LEU_7	N, A_PHE_20	H, A_PHE_20	2.74	1.95	29.42
1R21-5.PDB	O, A_ILE_51	N, A_CYS_27	H, A_CYS_27	2.96	2.03	16.24
1R21-5.PDB	O, A_CYS_49	N, A_PHE_29	H, A_PHE_29	2.56	1.68	20.60
1R21-5.PDB	O, A_GLY_32	N, A_CYS_35	H, A_CYS_35	3.00	2.10	20.00
1R21-5.PDB	O, A_LEU_28	N, A_ILE_37	H, A_ILE_37	2.63	1.66	7.71
1R21-5.PDB	O, A_CYS_27	N, A_ILE_51	H, A_ILE_51	2.67	1.84	25.60
1R21-5.PDB	O, A_ILE_59	N, A_GLU_52	H, A_GLU_52	2.45	1.51	13.28
1R21-5.PDB	O, A_SER_25	N, A_ILE_53	H, A_ILE_53	2.88	2.00	20.92
1R21-5.PDB	O, A_GLU_57	N, A_HIS_54	H, A_HIS_54	2.45	1.55	17.67
1R21-5.PDB	O, A_GLU_52	N, A_ILE_59	H, A_ILE_59	2.73	1.80	15.41
1R21-5.PDB	OG1, A_THR_69	ND2, A_ASN_62	HD22, A_ASN_62	2.62	1.75	21.48
1R21-5.PDB	O, A_THR_89	N, A_GLN_70	H, A_GLN_70	2.61	1.83	29.99
1R21-5.PDB	O, A_VAL_87	N, A_ASN_72	H, A_ASN_72	2.99	2.02	8.39
1R21-5.PDB	O, A_VAL_71	N, A_SER_74	H, A_SER_74	2.41	1.47	13.31
1R21-5.PDB	OD2, A_ASP_86	N, A_LYS_83	H, A_LYS_83	2.31	1.52	27.57
1R21-5.PDB	O, A_PHE_95	N, A_ILE_88	H, A_ILE_88	2.66	1.72	14.09
1R21-5.PDB	O, A_GLN_70	N, A_THR_89	H, A_THR_89	2.73	1.76	5.33
1R21-5.PDB	O, A_ARG_93	N, A_ILE_90	H, A_ILE_90	2.64	1.71	14.23
1R21-5.PDB	O, A_ILE_88	N, A_PHE_95	H, A_PHE_95	2.55	1.58	4.54
1R21-5.PDB	O, A_VAL_8	N, A_ARG_96	H, A_ARG_96	2.68	1.85	26.28
1R21-5.PDB	ND1, A_HIS_84	N, A_ASN_99	H, A_ASN_99	2.79	1.81	1.91
1R21-6.PDB	O, A_LEU_7	N, A_PHE_20	H, A_PHE_20	2.66	1.77	20.35
1R21-6.PDB	O, A_CYS_49	N, A_PHE_29	H, A_PHE_29	2.75	1.83	16.30
1R21-6.PDB	O, A_LEU_28	N, A_ILE_37	H, A_ILE_37	2.59	1.63	9.82
1R21-6.PDB	O, A_GLY_30	N, A_ILE_39	H, A_ILE_39	2.91	2.07	25.97
1R21-6.PDB	O, A_LEU_41	N, A_VAL_44	H, A_VAL_44	2.95	2.04	17.93
1R21-6.PDB	N, A_LYS_50	SG, A_CYS_49	HG, A_CYS_49	2.71	1.89	25.56
1R21-6.PDB	O, A_CYS_27	N, A_ILE_51	H, A_ILE_51	2.75	1.91	25.39
1R21-6.PDB	O, A_ILE_59	N, A_GLU_52	H, A_GLU_52	2.40	1.53	21.67
1R21-6.PDB	O, A_GLU_57	N, A_HIS_54	H, A_HIS_54	2.79	1.89	19.06
1R21-6.PDB	O, A_GLU_52	N, A_ILE_59	H, A_ILE_59	2.58	1.61	5.50
1R21-6.PDB	OG1, A_THR_69	ND2, A_ASN_62	HD21, A_ASN_62	2.81	1.95	22.23
1R21-6.PDB	OD1, A_ASN_67	OG1, A_THR_66	HG1, A_THR_66	2.30	1.42	18.29
1R21-6.PDB	ND2, A_ASN_62	N, A_THR_69	H, A_THR_69	2.77	1.82	9.89
1R21-6.PDB	O, A_THR_89	N, A_GLN_70	H, A_GLN_70	2.74	1.83	16.28
1R21-6.PDB	O, A_SER_74	N, A_VAL_71	H, A_VAL_71	2.71	1.73	5.25
1R21-6.PDB	O, A_VAL_87	N, A_ASN_72	H, A_ASN_72	2.81	1.83	4.97
1R21-6.PDB	O, A_VAL_71	N, A_SER_74	H, A_SER_74	2.47	1.57	18.72
1R21-6.PDB	O, A_TYR_97	N, A_GLY_85	H, A_GLY_85	2.85	1.98	22.19
1R21-6.PDB	O, A_PHE_95	N, A_ILE_88	H, A_ILE_88	2.58	1.60	5.92
1R21-6.PDB	O, A_GLN_70	N, A_THR_89	H, A_THR_89	2.72	1.76	7.04
1R21-6.PDB	O, A_ARG_93	N, A_ILE_90	H, A_ILE_90	2.73	1.78	11.89
1R21-6.PDB	O, A_ILE_88	N, A_PHE_95	H, A_PHE_95	2.50	1.55	9.80
1R21-6.PDB	O, A_VAL_8	N, A_ARG_96	H, A_ARG_96	2.94	2.02	15.77

1R21-6.PDB	ND1, A_HIS_84	N, A_ASN_99	H, A_ASN_99	2.78	1.82	10.56
1R21-6.PDB	O, A_THR_4	N, A_GLU_100	H, A_GLU_100	2.69	1.89	28.90
1R21-7.PDB	O, A_ARG_96	N, A_VAL_8	H, A_VAL_8	2.93	2.00	14.50
1R21-7.PDB	O, A_SER_94	N, A_ILE_10	H, A_ILE_10	2.75	1.83	17.27
1R21-7.PDB	O, A_LEU_7	N, A_PHE_20	H, A_PHE_20	2.62	1.73	19.92
1R21-7.PDB	O, A_ILE_51	N, A_CYS_27	H, A_CYS_27	2.70	1.75	13.12
1R21-7.PDB	O, A_CYS_49	N, A_PHE_29	H, A_PHE_29	2.69	1.79	18.19
1R21-7.PDB	O, A_LEU_28	N, A_ILE_37	H, A_ILE_37	2.66	1.71	12.73
1R21-7.PDB	O, A_GLY_30	N, A_ILE_39	H, A_ILE_39	2.93	2.03	19.31
1R21-7.PDB	O, A_CYS_27	N, A_ILE_51	H, A_ILE_51	2.59	1.76	25.78
1R21-7.PDB	O, A_ILE_59	N, A_GLU_52	H, A_GLU_52	2.42	1.57	22.98
1R21-7.PDB	O, A_SER_25	N, A_ILE_53	H, A_ILE_53	2.58	1.70	20.39
1R21-7.PDB	O, A_GLU_57	N, A_HIS_54	H, A_HIS_54	2.55	1.59	6.66
1R21-7.PDB	O, A_GLU_52	N, A_ILE_59	H, A_ILE_59	2.51	1.62	19.11
1R21-7.PDB	OD1, A_ASN_67	OG1, A_THR_66	HG1, A_THR_66	2.91	2.05	21.54
1R21-7.PDB	ND2, A_ASN_62	N, A_THR_69	H, A_THR_69	2.80	1.87	14.50
1R21-7.PDB	O, A_THR_89	N, A_GLN_70	H, A_GLN_70	2.81	2.02	29.36
1R21-7.PDB	O, A_SER_74	N, A_VAL_71	H, A_VAL_71	2.67	1.70	5.32
1R21-7.PDB	O, A_VAL_71	N, A_SER_74	H, A_SER_74	2.40	1.46	12.46
1R21-7.PDB	O, A_PHE_95	N, A_ILE_88	H, A_ILE_88	2.42	1.50	16.16
1R21-7.PDB	O, A_GLN_70	N, A_THR_89	H, A_THR_89	2.72	1.75	6.96
1R21-7.PDB	O, A_ARG_93	N, A_ILE_90	H, A_ILE_90	2.79	1.96	26.27
1R21-7.PDB	O, A_ILE_88	N, A_PHE_95	H, A_PHE_95	2.39	1.47	15.58
1R21-7.PDB	O, A_VAL_8	N, A_ARG_96	H, A_ARG_96	2.62	1.75	22.19
1R21-7.PDB	O, A_ASP_86	N, A_TYR_97	H, A_TYR_97	2.95	1.97	3.22
1R21-7.PDB	ND1, A_HIS_84	N, A_ASN_99	H, A_ASN_99	2.74	1.77	3.18
1R21-7.PDB	O, A_THR_4	N, A_GLU_100	H, A_GLU_100	2.96	1.98	1.07
1R21-8.PDB	O, A_LEU_7	N, A_PHE_20	H, A_PHE_20	2.64	1.67	5.83
1R21-8.PDB	O, A_ILE_51	N, A_CYS_27	H, A_CYS_27	2.97	2.06	18.29
1R21-8.PDB	O, A_CYS_49	N, A_PHE_29	H, A_PHE_29	2.74	1.82	17.14
1R21-8.PDB	O, A_GLY_32	N, A_CYS_35	H, A_CYS_35	2.97	2.06	17.41
1R21-8.PDB	O, A_LEU_28	N, A_ILE_37	H, A_ILE_37	2.56	1.64	16.71
1R21-8.PDB	O, A_CYS_27	N, A_ILE_51	H, A_ILE_51	2.90	2.08	27.50
1R21-8.PDB	O, A_ILE_59	N, A_GLU_52	H, A_GLU_52	2.39	1.51	20.05
1R21-8.PDB	O, A_SER_25	N, A_ILE_53	H, A_ILE_53	2.86	1.97	19.70
1R21-8.PDB	O, A_GLU_57	N, A_HIS_54	H, A_HIS_54	2.63	1.73	17.57
1R21-8.PDB	O, A_GLU_52	N, A_ILE_59	H, A_ILE_59	2.67	1.74	13.79
1R21-8.PDB	O, A_HIS_48	N, A_PHE_63	H, A_PHE_63	2.95	1.99	8.40
1R21-8.PDB	ND2, A_ASN_62	N, A_THR_69	H, A_THR_69	2.77	1.82	11.69
1R21-8.PDB	O, A_THR_89	N, A_GLN_70	H, A_GLN_70	2.54	1.69	23.06
1R21-8.PDB	O, A_SER_74	N, A_VAL_71	H, A_VAL_71	2.87	1.96	17.78
1R21-8.PDB	O, A_VAL_87	N, A_ASN_72	H, A_ASN_72	2.79	1.84	10.06
1R21-8.PDB	O, A_VAL_71	N, A_SER_74	H, A_SER_74	2.39	1.49	18.17
1R21-8.PDB	OD2, A_ASP_86	N, A_LYS_83	H, A_LYS_83	2.70	1.83	21.74
1R21-8.PDB	O, A_LYS_83	N, A_ASP_86	H, A_ASP_86	2.99	2.13	23.27
1R21-8.PDB	O, A_PHE_95	N, A_ILE_88	H, A_ILE_88	2.50	1.64	22.70
1R21-8.PDB	O, A_GLN_70	N, A_THR_89	H, A_THR_89	2.52	1.55	4.58
1R21-8.PDB	O, A_ARG_93	N, A_ILE_90	H, A_ILE_90	2.80	1.96	25.17
1R21-8.PDB	O, A_ILE_88	N, A_PHE_95	H, A_PHE_95	2.40	1.51	18.62
1R21-8.PDB	O, A_VAL_8	N, A_ARG_96	H, A_ARG_96	2.59	1.64	10.89
1R21-8.PDB	ND1, A_HIS_84	N, A_ASN_99	H, A_ASN_99	2.79	1.82	9.29
1R21-9.PDB	O, A_ARG_96	N, A_VAL_8	H, A_VAL_8	2.95	2.02	15.16
1R21-9.PDB	O, A_VAL_15	N, A_LYS_11	H, A_LYS_11	2.46	1.54	16.41
1R21-9.PDB	O, A_LYS_11	N, A_GLY_14	H, A_GLY_14	2.77	1.83	13.31
1R21-9.PDB	O, A_THR_9	N, A_GLY_17	H, A_GLY_17	2.92	2.09	26.43
1R21-9.PDB	O, A_LEU_7	N, A_PHE_20	H, A_PHE_20	2.73	1.90	26.46
1R21-9.PDB	O, A_ILE_51	N, A_CYS_27	H, A_CYS_27	2.80	1.95	24.06
1R21-9.PDB	O, A_CYS_49	N, A_PHE_29	H, A_PHE_29	2.58	1.68	18.54

1R21-9.PDB	O, A_LEU_28	N, A_ILE_37	H, A_ILE_37	2.61	1.66	11.75
1R21-9.PDB	O, A_GLY_30	N, A_ILE_39	H, A_ILE_39	2.95	2.00	11.86
1R21-9.PDB	O, A_CYS_27	N, A_ILE_51	H, A_ILE_51	2.58	1.76	26.53
1R21-9.PDB	O, A_ILE_59	N, A_GLU_52	H, A_GLU_52	2.41	1.49	15.40
1R21-9.PDB	O, A_GLU_57	N, A_HIS_54	H, A_HIS_54	2.39	1.49	17.88
1R21-9.PDB	O, A_GLU_52	N, A_ILE_59	H, A_ILE_59	2.53	1.64	19.17
1R21-9.PDB	OG1, A_THR_69	ND2, A_ASN_62	HD21, A_ASN_62	2.59	1.65	13.02
1R21-9.PDB	ND2, A_ASN_62	N, A_THR_69	H, A_THR_69	2.80	1.88	16.74
1R21-9.PDB	O, A_THR_89	N, A_GLN_70	H, A_GLN_70	2.54	1.65	19.35
1R21-9.PDB	O, A_SER_74	N, A_VAL_71	H, A_VAL_71	2.88	1.97	18.35
1R21-9.PDB	O, A_VAL_71	N, A_SER_74	H, A_SER_74	2.82	1.99	26.19
1R21-9.PDB	O, A_LYS_83	N, A_ASP_86	H, A_ASP_86	2.95	2.09	23.46
1R21-9.PDB	O, A_PHE_95	N, A_ILE_88	H, A_ILE_88	2.79	1.83	9.96
1R21-9.PDB	O, A_GLN_70	N, A_THR_89	H, A_THR_89	2.38	1.46	15.43
1R21-9.PDB	O, A_ARG_93	N, A_ILE_90	H, A_ILE_90	2.76	1.79	6.89
1R21-9.PDB	O, A_ILE_88	N, A_PHE_95	H, A_PHE_95	2.67	1.69	5.04
1R21-9.PDB	O, A_VAL_8	N, A_ARG_96	H, A_ARG_96	2.57	1.73	25.04
1R21-9.PDB	ND1, A_HIS_84	N, A_ASN_99	H, A_ASN_99	2.74	1.83	17.89
1S4H-8.PDB	OE1, A_GLU_2	N, A_GLU_1	H3, A_GLU_1	3.00	2.12	26.52
1S4J-1.PDB	O, A_MET_7	N, A_SER_3	H, A_SER_3	2.68	1.88	28.39
1S4J-10.PDB	O, A_MET_7	N, A_SER_3	H, A_SER_3	2.70	1.89	28.31
1S4J-10.PDB	OD2, A_ASP_5	N, A_LEU_11	H, A_LEU_11	2.97	2.11	23.51
1S4J-11.PDB	O, A_MET_7	N, A_SER_3	H, A_SER_3	2.71	1.88	26.65
1S4J-12.PDB	O, A_MET_7	N, A_SER_3	H, A_SER_3	2.58	1.69	19.82
1S4J-14.PDB	O, A_MET_7	N, A_SER_3	H, A_SER_3	2.62	1.79	26.02
1S4J-14.PDB	OD2, A_ASP_5	N, A_LEU_11	H, A_LEU_11	2.83	2.00	26.13
1S4J-15.PDB	O, A_MET_7	N, A_SER_3	H, A_SER_3	2.73	1.91	26.73
1S4J-16.PDB	O, A_MET_7	N, A_SER_3	H, A_SER_3	2.76	1.95	28.49
1S4J-17.PDB	O, A_MET_7	N, A_SER_3	H, A_SER_3	2.73	1.90	26.91
1S4J-18.PDB	O, A_MET_7	N, A_SER_3	H, A_SER_3	2.72	1.86	23.67
1S4J-19.PDB	O, A_MET_7	N, A_SER_3	H, A_SER_3	2.72	1.87	24.36
1S4J-2.PDB	O, A_MET_7	N, A_SER_3	H, A_SER_3	2.72	1.90	26.68
1S4J-20.PDB	O, A_MET_7	N, A_SER_3	H, A_SER_3	2.77	1.95	27.92
1S4J-20.PDB	O, A_GLY_10	N, A_PHE_12	H, A_PHE_12	2.84	1.99	23.23
1S4J-3.PDB	O, A_MET_7	N, A_SER_3	H, A_SER_3	2.75	1.93	27.51
1S4J-5.PDB	O, A_MET_7	N, A_SER_3	H, A_SER_3	2.72	1.90	26.53
1S4J-6.PDB	O, A_MET_7	N, A_SER_3	H, A_SER_3	2.73	1.90	26.66
1S4J-7.PDB	O, A_MET_7	N, A_SER_3	H, A_SER_3	2.73	1.90	26.44
1S4J-8.PDB	O, A_MET_7	N, A_SER_3	H, A_SER_3	2.73	1.90	26.61
1S4J-9.PDB	O, A_MET_7	N, A_SER_3	H, A_SER_3	2.64	1.83	27.37
1S4J-9.PDB	OD2, A_ASP_5	N, A_LEU_11	H, A_LEU_11	2.83	2.00	25.25
1TOR-5.PDB	O, A_ASN_2	N, A_ASP_5	H, A_ASP_5	2.95	2.03	21.29
1TOS-2.PDB	O, A_ASN_2	N, A_ASP_5	H, A_ASP_5	2.88	1.98	23.42
1VFB.PDB	OG, A_SER_26	N, A_VAL_3	H, A_VAL_3	2.94	1.97	6.30
1VFB.PDB	O, A_ARG_24	N, A_THR_5	H, A_THR_5	2.90	1.93	5.77
1VFB.PDB	O, A_THR_22	N, A_SER_7	H, A_SER_7	2.99	2.11	22.15
1VFB.PDB	O, A_LYS_103	N, A_LEU_11	H, A_LEU_11	2.94	2.05	20.26
1VFB.PDB	O, A_GLU_105	N, A_ALA_13	H, A_ALA_13	2.80	1.93	21.73
1VFB.PDB	O, A_LEU_78	N, A_GLY_16	H, A_GLY_16	2.82	1.99	26.99
1VFB.PDB	O, A_LEU_73	N, A_ILE_21	H, A_ILE_21	2.85	1.95	18.65
1VFB.PDB	O, A_SER_7	N, A_THR_22	H, A_THR_22	2.95	1.97	3.77
1VFB.PDB	O, A_TYR_71	N, A_CYS_23	H, A_CYS_23	2.89	1.95	12.19
1VFB.PDB	O, A_THR_5	N, A_ARG_24	H, A_ARG_24	2.86	1.97	19.64
1VFB.PDB	O, A_THR_69	N, A_ALA_25	H, A_ALA_25	2.80	1.83	9.00
1VFB.PDB	OD1, A_ASN_28	N, A_HIS_30	H, A_HIS_30	2.87	2.03	25.94
1VFB.PDB	O, A_GLN_89	N, A_ALA_34	H, A_ALA_34	2.86	1.95	17.31
1VFB.PDB	O, A_VAL_48	N, A_TRP_35	H, A_TRP_35	2.90	1.96	12.47
1VFB.PDB	O, A_TYR_87	N, A_TYR_36	H, A_TYR_36	2.90	1.97	14.82

1VFB.PDB	OE1, A_GLN_89	OH, A_TYR_36	HH, A_TYR_36	2.84	2.00	25.31
1VFB.PDB	O, A_GLN_45	N, A_GLN_37	H, A_GLN_37	2.94	2.00	11.43
1VFB.PDB	O, A_SER_85	N, A_GLN_38	H, A_GLN_38	2.78	1.86	16.10
1VFB.PDB	O, A_LYS_42	NE2, A_GLN_38	HE22, A_GLN_38	2.95	2.03	15.93
1VFB.PDB	O, A_LYS_39	N, A_LYS_42	H, A_LYS_42	2.94	2.06	21.86
1VFB.PDB	O, A_GLN_37	N, A_GLN_45	H, A_GLN_45	2.83	1.94	20.43
1VFB.PDB	O, A_TRP_35	N, A_LEU_47	H, A_LEU_47	2.87	1.94	14.84
1VFB.PDB	O, A_THR_53	N, A_TYR_49	H, A_TYR_49	2.88	1.94	13.56
1VFB.PDB	O, A_TYR_49	N, A_THR_53	H, A_THR_53	2.96	2.04	16.01
1VFB.PDB	O, A_LEU_47	N, A_ALA_55	H, A_ALA_55	2.84	1.93	17.83
1VFB.PDB	OD2, A ASP_82	NE, A_ARG_61	HE, A_ARG_61	2.88	1.96	15.15
1VFB.PDB	OD1, A ASP_82	NH2, A_ARG_61	HH21, A_ARG_61	2.85	1.87	9.42
1VFB.PDB	O, A_LYS_74	N, A_SER_63	H, A_SER_63	2.88	1.93	11.55
1VFB.PDB	O, A_SER_72	N, A_SER_65	H, A_SER_65	2.96	2.03	16.59
1VFB.PDB	O, A_CYS_23	N, A_TYR_71	H, A_TYR_71	2.90	2.02	21.95
1VFB.PDB	O, A_GLY_68	OH, A_TYR_71	HH, A_TYR_71	2.83	1.87	7.60
1VFB.PDB	O, A_SER_65	N, A_SER_72	H, A_SER_72	2.93	1.97	9.57
1VFB.PDB	O, A_ILE_21	N, A_LEU_73	H, A_LEU_73	2.93	1.98	10.05
1VFB.PDB	O, A_SER_63	N, A_LYS_74	H, A_LYS_74	2.78	1.85	14.93
1VFB.PDB	O, A_VAL_19	N, A_ILE_75	H, A_ILE_75	3.00	2.05	11.89
1VFB.PDB	O, A_ARG_61	N, A_ASN_76	H, A_ASN_76	2.94	1.97	4.92
1VFB.PDB	O, A_GLU_17	N, A_LEU_78	H, A_LEU_78	2.98	2.01	6.59
1VFB.PDB	OD2, A ASP_82	N, A_GLN_79	H, A_GLN_79	2.99	2.09	19.33
1VFB.PDB	O, A_GLN_79	N, A ASP_82	H, A ASP_82	2.90	1.94	8.94
1VFB.PDB	O, A_GLN_38	N, A_SER_85	H, A_SER_85	2.92	1.96	9.01
1VFB.PDB	O, A_THR_102	N, A_TYR_86	H, A_TYR_86	2.97	2.09	22.04
1VFB.PDB	O, A ASP_82	OH, A_TYR_86	HH, A_TYR_86	2.70	1.75	6.61
1VFB.PDB	O, A_ALA_34	N, A_GLN_89	H, A_GLN_89	2.89	2.00	22.07
1VFB.PDB	O, A_TYR_32	N, A_PHE_91	H, A_PHE_91	2.82	1.88	13.65
1VFB.PDB	OE1, C_GLN_121	N, A_SER_93	H, A_SER_93	2.89	1.92	8.17
1VFB.PDB	OE1, B_GLU_98	NH1, A_ARG_96	HH12, A_ARG_96	2.82	1.84	8.38
1VFB.PDB	OE2, B_GLU_98	NH2, A_ARG_96	HH22, A_ARG_96	2.81	1.85	10.74
1VFB.PDB	O, A_CYS_88	N, A_GLY_99	H, A_GLY_99	2.78	1.86	15.50
1VFB.PDB	O, A_TYR_86	N, A_THR_102	H, A_THR_102	2.95	2.08	22.50
1VFB.PDB	O, A_PRO_8	OG1, A_THR_102	HG1, A_THR_102	2.77	1.85	14.39
1VFB.PDB	O, A_ALA_9	N, A_LYS_103	H, A_LYS_103	2.90	1.93	7.79
1VFB.PDB	O, A_GLY_84	N, A_LEU_104	H, A_LEU_104	2.88	1.91	5.85
1VFB.PDB	O, A_LEU_11	N, A_GLU_105	H, A_GLU_105	2.89	1.94	12.21
1VFB.PDB	O, B_SER_25	N, B_GLN_3	H, B_GLN_3	2.88	1.92	9.87
1VFB.PDB	O, B_THR_23	N, B_GLN_5	H, B_GLN_5	2.98	2.10	21.16
1VFB.PDB	O, B_THR_21	N, B_SER_7	H, B_SER_7	2.85	2.00	24.61
1VFB.PDB	O, B_PRO_9	N, B_LEU_11	H, B_LEU_11	2.92	2.13	29.55
1VFB.PDB	OE1, B_GLN_16	N, B_ALA_13	H, B_ALA_13	2.78	1.85	14.74
1VFB.PDB	O, B_ALA_13	N, B_GLN_16	H, B_GLN_16	2.90	1.97	15.84
1VFB.PDB	O, B_MET_82	N, B_LEU_18	H, B_LEU_18	2.72	1.87	23.78
1VFB.PDB	O, B_LEU_80	N, B_ILE_20	H, B_ILE_20	2.91	2.00	17.66
1VFB.PDB	O, B_SER_7	N, B_THR_21	H, B_THR_21	2.89	1.93	9.84
1VFB.PDB	O, B_VAL_78	N, B_CYS_22	H, B_CYS_22	2.86	1.89	3.27
1VFB.PDB	O, B_GLN_5	N, B_THR_23	H, B_THR_23	2.86	1.92	12.65
1VFB.PDB	O, B_SER_76	N, B_VAL_24	H, B_VAL_24	2.97	2.00	3.39
1VFB.PDB	O, B_GLN_3	N, B_SER_25	H, B_SER_25	2.93	2.07	23.55
1VFB.PDB	OG, B_SER_28	OG1, B_THR_30	HG1, B_THR_30	2.97	2.08	19.82
1VFB.PDB	O, B_ILE_51	N, B_VAL_34	H, B_VAL_34	2.91	2.01	18.80
1VFB.PDB	O, B_ALA_96	N, B_ASN_35	H, B_ASN_35	2.89	1.92	5.93
1VFB.PDB	OE1, B_GLU_98	ND2, B_ASN_35	HD21, B_ASN_35	2.85	2.00	23.37
1VFB.PDB	O, B_GLY_49	N, B_TRP_36	H, B_TRP_36	2.96	2.02	15.17
1VFB.PDB	O, B_TYR_94	N, B_VAL_37	H, B_VAL_37	2.92	1.95	9.63
1VFB.PDB	O, B_GLU_46	N, B_ARG_38	H, B_ARG_38	2.89	1.95	14.15

1VFB.PDB	OD1, B.ASP_89	NH1, B.ARG_38	HH12, B.ARG_38	3.00	2.07	17.31
1VFB.PDB	O, B.ARG_92	N, B.GLN_39	H, B.GLN_39	2.82	1.90	16.49
1VFB.PDB	OE1, A.GLN_38	NE2, B.GLN_39	HE21, B.GLN_39	2.95	1.98	8.04
1VFB.PDB	O, B.LYS_43	NE2, B.GLN_39	HE22, B.GLN_39	2.95	2.05	19.96
1VFB.PDB	O, B.PRO_40	N, B.LYS_43	H, B.LYS_43	2.85	1.98	21.72
1VFB.PDB	O, B.ARG_38	N, B.GLU_46	H, B.GLU_46	2.84	1.96	21.55
1VFB.PDB	OD1, B.ASN_35	NE1, B.TRP_47	HE1, B.TRP_47	2.80	1.83	5.78
1VFB.PDB	O, B.TRP_36	N, B.LEU_48	H, B.LEU_48	2.92	1.98	13.84
1VFB.PDB	O, B.ASP_58	N, B.MET_50	H, B.MET_50	2.89	1.97	17.18
1VFB.PDB	O, B.ASN_56	N, B.TRP_52	H, B.TRP_52	2.90	1.95	9.28
1VFB.PDB	O, B.TRP_52	N, B.GLY_55	H, B.GLY_55	2.85	1.92	14.57
1VFB.PDB	O, B.LEU_48	N, B.ASN_60	H, B.ASN_60	2.94	1.98	8.25
1VFB.PDB	O, B.TRP_47	ND2, B.ASN_60	HD22, B.ASN_60	2.87	1.90	6.16
1VFB.PDB	OD1, B.ASN_60	N, B.ALA_62	H, B.ALA_62	2.90	2.08	27.74
1VFB.PDB	O, B.LEU_63	N, B.ARG_66	H, B.ARG_66	2.99	2.04	12.74
1VFB.PDB	OD2, B.ASP_89	NH1, B.ARG_66	HH12, B.ARG_66	2.89	1.97	19.13
1VFB.PDB	OD1, B.ASP_89	NH2, B.ARG_66	HH22, B.ARG_66	2.93	1.93	3.85
1VFB.PDB	O, B.LYS_81	N, B.SER_68	H, B.SER_68	2.97	2.10	22.66
1VFB.PDB	OH, B.TYR_59	N, B.ILE_69	H, B.ILE_69	2.97	2.01	7.63
1VFB.PDB	OD1, B.ASN_73	NZ, B.LYS_71	HZ1, B.LYS_71	2.93	2.08	28.65
1VFB.PDB	O, B.GLY_53	NZ, B.LYS_71	HZ3, B.LYS_71	2.92	2.04	25.68
1VFB.PDB	O, B.GLN_77	N, B.ASP_72	H, B.ASP_72	2.85	1.88	5.90
1VFB.PDB	O, B.CYS_22	N, B.VAL_78	H, B.VAL_78	2.96	2.07	20.13
1VFB.PDB	O, B.SER_70	N, B.PHE_79	H, B.PHE_79	2.82	1.89	14.11
1VFB.PDB	O, B.SER_68	N, B.LYS_81	H, B.LYS_81	2.78	1.89	20.09
1VFB.PDB	OG, B.SER_70	NZ, B.LYS_81	HZ2, B.LYS_81	2.92	2.05	26.58
1VFB.PDB	O, B.LEU_18	N, B.MET_82	H, B.MET_82	2.84	1.92	15.27
1VFB.PDB	OD1, B.ASN_83	OG, B.SER_84	HG, B.SER_84	2.99	2.04	8.51
1VFB.PDB	OD2, B.ASP_89	N, B.HIS_86	H, B.HIS_86	3.00	2.17	27.32
1VFB.PDB	O, B.THR_87	OG1, B.THR_90	HG1, B.THR_90	2.90	1.94	9.38
1VFB.PDB	O, B.GLN_39	N, B.ARG_92	H, B.ARG_92	2.99	2.02	2.81
1VFB.PDB	O, B.THR_110	N, B.TYR_93	H, B.TYR_93	2.83	1.90	15.51
1VFB.PDB	OE2, B.GLU_6	N, B.CYS_95	H, B.CYS_95	2.85	2.00	23.74
1VFB.PDB	O, B.ASN_35	N, B.ALA_96	H, B.ALA_96	2.98	2.12	24.00
1VFB.PDB	O, B.TYR_105	N, B.ARG_97	H, B.ARG_97	2.78	1.93	24.54
1VFB.PDB	OD1, B.ASP_104	NE, B.ARG_97	HE, B.ARG_97	2.99	2.02	4.50
1VFB.PDB	OD2, B.ASP_104	NH2, B.ARG_97	HH21, B.ARG_97	2.86	1.87	3.52
1VFB.PDB	O, B.GLY_33	N, B.GLU_98	H, B.GLU_98	2.83	1.86	4.19
1VFB.PDB	O, B.ARG_102	N, B.ARG_99	H, B.ARG_99	2.95	2.00	10.93
1VFB.PDB	O, B.ASP_100	NH1, B.ARG_102	HH11, B.ARG_102	3.00	2.15	26.78
1VFB.PDB	O, C.GLY_22	NH1, B.ARG_102	HH12, B.ARG_102	2.82	1.90	18.81
1VFB.PDB	O, B.CYS_95	N, B.GLY_107	H, B.GLY_107	2.97	2.01	8.78
1VFB.PDB	OE1, B.GLU_6	N, B.GLY_109	H, B.GLY_109	2.89	1.99	17.04
1VFB.PDB	O, B.TYR_93	N, B.THR_110	H, B.THR_110	2.94	2.04	19.36
1VFB.PDB	O, B.ALA_91	N, B.LEU_112	H, B.LEU_112	2.81	1.84	5.13
1VFB.PDB	O, B.GLY_10	N, B.THR_113	H, B.THR_113	2.88	1.92	9.03
1VFB.PDB	OG1, B.THR_90	N, B.VAL_114	H, B.VAL_114	2.95	1.97	3.76
1VFB.PDB	O, B.VAL_12	N, B.SER_115	H, B.SER_115	2.89	1.92	7.04
1VFB.PDB	OG1, C.THR_40	N, C.LYS_1	H1, C.LYS_1	2.88	1.92	18.01
1VFB.PDB	O, C.PHE_38	N, C.PHE_3	H, C.PHE_3	2.97	2.01	11.57
1VFB.PDB	O, C.ARG_5	N, C.ALA_9	H, C.ALA_9	2.93	1.95	4.49
1VFB.PDB	O, C.CYS_6	N, C.ALA_10	H, C.ALA_10	2.92	1.95	7.61
1VFB.PDB	O, C.LEU_8	N, C.MET_12	H, C.MET_12	2.84	1.91	15.62
1VFB.PDB	O, C.ALA_9	N, C.LYS_13	H, C.LYS_13	2.90	1.96	13.16
1VFB.PDB	O, C.ALA_11	ND1, C.HIS_15	HD1, C.HIS_15	2.83	1.90	15.15
1VFB.PDB	OG1, C.THR_89	NE2, C.HIS_15	HE2, C.HIS_15	2.84	1.94	19.37
1VFB.PDB	O, C.ASN_19	N, C.GLY_22	H, C.GLY_22	2.99	2.09	19.97
1VFB.PDB	O, C.TYR_20	N, C.TYR_23	H, C.TYR_23	2.95	1.99	10.86

1VFB.PDB	OD2, B_ASP_100	N, C_SER_24	H, C_SER_24	2.91	2.09	27.47
1VFB.PDB	O, C_GLY_26	N, C_CYS_30	H, C_CYS_30	2.84	1.96	21.71
1VFB.PDB	O, C_ASN_27	N, C_ALA_31	H, C_ALA_31	2.91	1.97	11.60
1VFB.PDB	O, C_ALA_31	N, C_GLU_35	H, C_GLU_35	2.82	1.95	22.11
1VFB.PDB	O, C_ALA_32	N, C_SER_36	H, C_SER_36	2.95	2.06	19.79
1VFB.PDB	O, C_ILE_55	OG, C_SER_36	HG, C_SER_36	2.79	1.88	15.77
1VFB.PDB	O, C_LYS_1	N, C_THR_40	H, C_THR_40	2.90	1.95	9.98
1VFB.PDB	OE1, C_GLN_41	OG1, C_THR_40	HG1, C_THR_40	2.88	1.98	18.75
1VFB.PDB	OD1, C_ASN_39	N, C_GLN_41	H, C_GLN_41	2.92	2.01	18.23
1VFB.PDB	O, C_LEU_84	NE2, C_GLN_41	HE21, C_GLN_41	2.78	1.99	29.59
1VFB.PDB	O, C_ASP_52	N, C_ASN_44	H, C_ASN_44	2.91	2.02	19.92
1VFB.PDB	O, C_SER_50	ND2, C_ASN_46	HD22, C_ASN_46	2.86	1.97	19.52
1VFB.PDB	O, C_ASN_46	N, C_ASP_48	H, C_ASP_48	2.84	1.95	20.51
1VFB.PDB	OG, C_SER_60	N, C_THR_51	H, C_THR_51	2.85	1.89	9.75
1VFB.PDB	O, C_ASN_44	N, C_ASP_52	H, C_ASP_52	2.77	1.89	21.40
1VFB.PDB	O, C_ILE_58	N, C_TYR_53	H, C_TYR_53	2.84	1.91	14.87
1VFB.PDB	O, C_ALA_42	N, C_GLY_54	H, C_GLY_54	2.75	1.87	21.13
1VFB.PDB	O, C_GLY_54	NE2, C_GLN_57	HE22, C_GLN_57	2.80	1.83	6.26
1VFB.PDB	OG1, C_THR_69	OG, C_SER_60	HG, C_SER_60	2.78	1.84	10.98
1VFB.PDB	O, C_PRO_70	NE, C_ARG_61	HE, C_ARG_61	2.72	1.91	27.72
1VFB.PDB	O, C_ILE_78	N, C_ASN_65	H, C_ASN_65	2.88	1.94	12.38
1VFB.PDB	O, C_SER_60	OG, C_SER_72	HG, C_SER_72	2.95	1.99	6.61
1VFB.PDB	O, C_ARG_61	N, C_ARG_73	H, C_ARG_73	2.84	1.87	6.21
1VFB.PDB	O, C_TRP_62	N, C_LEU_75	H, C_LEU_75	2.82	1.88	12.22
1VFB.PDB	O, C_TRP_63	N, C_CYS_76	H, C_CYS_76	2.88	1.99	20.44
1VFB.PDB	O, C_ASN_74	N, C_ASN_77	H, C_ASN_77	2.92	2.10	27.67
1VFB.PDB	O, C_ASN_65	N, C_CYS_80	H, C_CYS_80	2.95	1.99	9.67
1VFB.PDB	O, C_PRO_79	N, C_ALA_82	H, C_ALA_82	2.89	1.99	18.39
1VFB.PDB	O, C_ILE_88	N, C_VAL_92	H, C_VAL_92	2.91	2.06	24.26
1VFB.PDB	O, C_THR_89	N, C_ASN_93	H, C_ASN_93	2.88	1.92	8.98
1VFB.PDB	O, C_VAL_92	N, C_LYS_96	H, C_LYS_96	2.88	1.94	14.28
1VFB.PDB	O, C_ALA_95	N, C_VAL_99	H, C_VAL_99	2.93	2.05	20.53
1VFB.PDB	O, C_ASP_101	N, C_GLY_104	H, C_GLY_104	2.99	2.10	19.98
1VFB.PDB	O, C_LEU_56	NE1, C_TRP_108	HE1, C_TRP_108	2.75	1.86	21.02
1VFB.PDB	OD1, C_ASN_27	NE1, C_TRP_111	HE1, C_TRP_111	2.95	2.01	14.04
1VFB.PDB	O, C_VAL_109	N, C_ASN_113	H, C_ASN_113	2.97	2.00	6.92
1VFB.PDB	O, C_ALA_110	N, C_ARG_114	H, C_ARG_114	2.73	1.86	21.81
1VFB.PDB	O, C_TRP_111	N, C_CYS_115	H, C_CYS_115	2.84	1.99	24.09
1VFB.PDB	O, C_TRP_111	N, C_LYS_116	H, C_LYS_116	2.81	1.93	20.73
1VFB.PDB	O, C_CYS_115	N, C_THR_118	H, C_THR_118	2.99	2.13	23.03
1VFB.PDB	O, C_CYS_115	OG1, C_THR_118	HG1, C_THR_118	2.73	1.80	11.89
1VFB.PDB	O, C_THR_118	N, C_VAL_120	H, C_VAL_120	2.89	2.08	27.51
1VFB.PDB	O, A_PHE_91	NE2, C_GLN_121	HE21, C_GLN_121	2.82	1.88	14.37
1VFB.PDB	O, C_GLN_121	N, C_ILE_124	H, C_ILE_124	2.94	2.00	13.68
1VFB.PDB	OE1, C_GLN_121	NH1, C_ARG_125	HH11, C_ARG_125	2.96	2.02	16.36
2MKL-1.PDB	O, C_VAL_32	N, C_SER_8	H, C_SER_8	2.87	1.94	15.13
2MKL-1.PDB	O, C_GLU_30	N, C_SER_10	H, C_SER_10	2.78	1.81	7.07
2MKL-1.PDB	O, C_VAL_28	N, C_LEU_12	H, C_LEU_12	2.85	1.96	21.36
2MKL-1.PDB	OXT, C_ALA_105	NZ, C_LYS_13	HZ3, C_LYS_13	2.65	1.63	10.83
2MKL-1.PDB	OD1, C_ASP_80	OG1, C_THR_21	HG1, C_THR_21	2.65	1.79	22.35
2MKL-1.PDB	OD2, C_ASP_80	NE2, C_GLN_22	HE21, C_GLN_22	2.86	1.96	18.61
2MKL-1.PDB	O, C_VAL_74	OG1, C_THR_24	HG1, C_THR_24	2.53	1.57	5.32
2MKL-1.PDB	O, C_LEU_72	N, C_ILE_27	H, C_ILE_27	2.90	1.93	8.25
2MKL-1.PDB	O, C_SER_70	N, C_CYS_29	H, C_CYS_29	2.74	1.79	13.45
2MKL-1.PDB	O, C_SER_10	N, C_GLU_30	H, C_GLU_30	2.74	1.77	7.68
2MKL-1.PDB	O, C_ILE_68	N, C_ILE_31	H, C_ILE_31	2.71	1.73	3.33
2MKL-1.PDB	O, C_SER_8	N, C_VAL_32	H, C_VAL_32	2.86	1.94	16.02
2MKL-1.PDB	O, C_SER_66	N, C_TYR_33	H, C_TYR_33	2.96	2.02	12.76

2MKL-1.PDB	O, C_GLU_90	N, C_LYS_40	H, C_LYS_40	2.75	1.77	6.32
2MKL-1.PDB	O, C_LEU_88	N, C_PHE_42	H, C_PHE_42	2.83	1.96	23.06
2MKL-1.PDB	O, C_VAL_86	N, C_GLN_44	H, C_GLN_44	2.98	2.06	17.99
2MKL-1.PDB	O, C_VAL_48	N, C_VAL_45	H, C_VAL_45	2.89	1.93	11.14
2MKL-1.PDB	O, C_VAL_45	N, C_VAL_48	H, C_VAL_48	2.85	1.96	20.78
2MKL-1.PDB	O, C_TRP_43	NH1, C_ARG_50	HH11, C_ARG_50	2.73	1.80	17.42
2MKL-1.PDB	O, C_LYS_71	N, C_GLU_55	H, C_GLU_55	2.87	2.01	24.71
2MKL-1.PDB	O, C_VAL_69	N, C_GLN_57	H, C_GLN_57	2.76	1.79	7.63
2MKL-1.PDB	O, C_THR_67	N, C_GLU_60	H, C_GLU_60	2.78	1.84	14.09
2MKL-1.PDB	O, C_LYS_65	N, C_SER_62	H, C_SER_62	2.90	1.94	10.66
2MKL-1.PDB	O, C_SER_62	N, C_LYS_65	H, C_LYS_65	2.95	2.06	20.90
2MKL-1.PDB	OG, C_SER_34	NZ, C_LYS_65	HZ2, C_LYS_65	2.81	1.84	16.47
2MKL-1.PDB	O, C_TYR_33	N, C_SER_66	H, C_SER_66	2.85	2.01	24.96
2MKL-1.PDB	O, C_GLU_60	N, C_THR_67	H, C_THR_67	2.81	1.89	17.79
2MKL-1.PDB	O, C_ILE_31	N, C_ILE_68	H, C_ILE_68	2.81	1.84	9.32
2MKL-1.PDB	O, C_CYS_29	N, C_SER_70	H, C_SER_70	2.78	1.84	15.75
2MKL-1.PDB	O, C_GLU_55	N, C_LYS_71	H, C_LYS_71	2.94	2.02	16.84
2MKL-1.PDB	O, C_ILE_27	N, C_LEU_72	H, C_LEU_72	2.65	1.82	25.39
2MKL-1.PDB	O, C_GLY_53	N, C_LYS_73	H, C_LYS_73	2.72	1.81	18.13
2MKL-1.PDB	O, C_ALA_25	NZ, C_LYS_73	HZ3, C_LYS_73	2.77	1.77	11.66
2MKL-1.PDB	O, C_ALA_76	N, C_ASP_80	H, C_ASP_80	2.69	1.74	10.81
2MKL-1.PDB	O, C_GLU_78	N, C_SER_81	H, C_SER_81	2.94	2.13	29.26
2MKL-1.PDB	O, C_TRP_79	N, C_GLY_82	H, C_GLY_82	2.98	2.06	17.42
2MKL-1.PDB	OE1, C_GLU_78	OG1, C_THR_83	HG1, C_THR_83	2.66	1.70	8.48
2MKL-1.PDB	O, C_ALA_100	N, C_CYS_87	H, C_CYS_87	2.70	1.74	9.85
2MKL-1.PDB	O, C_PHE_42	N, C_LEU_88	H, C_LEU_88	2.74	1.76	6.64
2MKL-1.PDB	O, C_VAL_98	N, C_VAL_89	H, C_VAL_89	2.86	1.96	19.19
2MKL-1.PDB	O, C_LYS_40	N, C_GLU_90	H, C_GLU_90	2.85	1.91	13.13
2MKL-1.PDB	OD2, C_ASP_91	N, C_GLU_93	H, C_GLU_93	2.91	2.06	25.41
2MKL-1.PDB	O, C_ASP_91	N, C_LEU_94	H, C_LEU_94	2.97	2.04	16.30
2MKL-1.PDB	O, C_CYS_87	N, C_ALA_100	H, C_ALA_100	2.87	2.07	29.58
2MKL-1.PDB	O, C_TYR_85	N, C_ILE_102	H, C_ILE_102	2.75	1.93	27.29
2MKL-1.PDB	OD1, C_ASP_80	NZ, C_LYS_104	HZ1, C_LYS_104	2.72	1.78	20.43
2MKL-1.PDB	O, C_ASP_80	NZ, C_LYS_104	HZ3, C_LYS_104	2.71	1.81	23.71
2MKL-10.PDB	O, C_VAL_32	N, C_SER_8	H, C_SER_8	2.91	1.92	0.91
2MKL-10.PDB	O, C_GLU_30	N, C_SER_10	H, C_SER_10	2.77	1.80	6.96
2MKL-10.PDB	O, C_VAL_28	N, C_LEU_12	H, C_LEU_12	2.68	1.71	4.93
2MKL-10.PDB	O, C_PRO_15	NE2, C_GLN_22	HE21, C_GLN_22	2.70	1.72	5.44
2MKL-10.PDB	O, C_LEU_72	OG1, C_THR_26	HG1, C_THR_26	2.68	1.73	10.60
2MKL-10.PDB	O, C_LEU_72	N, C_ILE_27	H, C_ILE_27	2.84	2.02	27.43
2MKL-10.PDB	O, C_LEU_12	N, C_VAL_28	H, C_VAL_28	2.99	2.05	14.29
2MKL-10.PDB	O, C_SER_70	N, C_CYS_29	H, C_CYS_29	2.68	1.70	4.32
2MKL-10.PDB	O, C_SER_10	N, C_GLU_30	H, C_GLU_30	2.73	1.81	16.56
2MKL-10.PDB	O, C_SER_8	N, C_VAL_32	H, C_VAL_32	2.77	1.79	4.04
2MKL-10.PDB	O, C_SER_66	N, C_TYR_33	H, C_TYR_33	2.97	2.01	10.13
2MKL-10.PDB	OD1, C_ASP_91	N, C_GLU_37	H, C_GLU_37	2.80	1.93	22.75
2MKL-10.PDB	O, C_GLU_90	N, C_LYS_40	H, C_LYS_40	2.92	1.97	11.19
2MKL-10.PDB	OE2, C_GLU_90	NZ, C_LYS_40	HZ2, C_LYS_40	2.58	1.67	23.06
2MKL-10.PDB	O, C_LEU_88	N, C_PHE_42	H, C_PHE_42	2.92	1.94	6.40
2MKL-10.PDB	O, C_VAL_48	N, C_VAL_45	H, C_VAL_45	2.84	1.89	12.91
2MKL-10.PDB	O, C_VAL_45	N, C_VAL_48	H, C_VAL_48	2.85	2.01	25.64
2MKL-10.PDB	O, C_LYS_71	N, C_GLU_55	H, C_GLU_55	2.68	1.75	14.91
2MKL-10.PDB	O, C_VAL_69	N, C_GLN_57	H, C_GLN_57	2.86	1.90	10.97
2MKL-10.PDB	O, C_THR_67	N, C_GLU_60	H, C_GLU_60	2.97	2.01	8.51
2MKL-10.PDB	O, C_SER_62	N, C_LYS_65	H, C_LYS_65	2.88	1.95	14.30
2MKL-10.PDB	O, C_TYR_33	N, C_SER_66	H, C_SER_66	2.72	1.86	23.25
2MKL-10.PDB	OG, C_SER_62	OG1, C_THR_67	HG1, C_THR_67	2.83	1.88	6.13
2MKL-10.PDB	O, C_CYS_29	N, C_SER_70	H, C_SER_70	2.83	1.85	7.06

2MKL-10.PDB	O, C_GLU_55	N, C_LYS_71	H, C_LYS_71	2.73	1.76	7.85
2MKL-10.PDB	O, C_ILE_27	N, C_LEU_72	H, C_LEU_72	2.69	1.71	7.54
2MKL-10.PDB	O, C_GLY_53	N, C_LYS_73	H, C_LYS_73	2.74	1.76	5.67
2MKL-10.PDB	O, C_ALA_76	N, C_ASP_80	H, C_ASP_80	2.74	1.79	12.95
2MKL-10.PDB	O, C_GLU_78	N, C_SER_81	H, C_SER_81	2.92	2.10	27.95
2MKL-10.PDB	O, C_TRP_79	N, C_GLY_82	H, C_GLY_82	2.95	2.02	15.81
2MKL-10.PDB	O, C_ALA_100	N, C_CYS_87	H, C_CYS_87	2.74	1.76	5.71
2MKL-10.PDB	O, C_PHE_42	N, C_LEU_88	H, C_LEU_88	2.71	1.75	9.91
2MKL-10.PDB	O, C_VAL_98	N, C_VAL_89	H, C_VAL_89	2.70	1.81	20.27
2MKL-10.PDB	O, C_LYS_40	N, C_GLU_90	H, C_GLU_90	2.78	1.93	24.87
2MKL-10.PDB	OD2, C_ASP_91	N, C_GLU_93	H, C_GLU_93	2.71	1.82	20.62
2MKL-10.PDB	O, C_VAL_89	N, C_VAL_98	H, C_VAL_98	2.95	1.97	2.47
2MKL-10.PDB	O, C_CYS_87	N, C_ALA_100	H, C_ALA_100	2.90	2.06	26.13
2MKL-10.PDB	O, C_TYR_85	N, C_ILE_102	H, C_ILE_102	2.78	1.86	16.84
2MKL-10.PDB	OXT, C_ALA_105	NZ, C_LYS_104	HZ3, C_LYS_104	2.68	1.72	17.77
2MKL-2.PDB	OD1, C_ASP_6	N, C_GLY_2	H, C_GLY_2	2.76	1.77	3.72
2MKL-2.PDB	O, C_ARG_3	N, C_THR_5	H, C_THR_5	2.70	1.90	29.18
2MKL-2.PDB	O, C_VAL_32	N, C_SER_8	H, C_SER_8	2.91	1.93	2.96
2MKL-2.PDB	O, C_GLU_30	N, C_SER_10	H, C_SER_10	2.85	1.91	14.14
2MKL-2.PDB	O, C_VAL_28	N, C_LEU_12	H, C_LEU_12	2.67	1.73	13.23
2MKL-2.PDB	OXT, C_ALA_105	NZ, C_LYS_13	HZ3, C_LYS_13	2.61	1.67	20.57
2MKL-2.PDB	O, C_PRO_14	N, C_PHE_16	H, C_PHE_16	2.68	1.84	24.86
2MKL-2.PDB	O, C_THR_24	N, C_THR_26	H, C_THR_26	2.87	2.01	23.54
2MKL-2.PDB	O, C_LEU_72	OG1, C_THR_26	HG1, C_THR_26	2.63	1.69	10.64
2MKL-2.PDB	O, C_LEU_72	N, C_ILE_27	H, C_ILE_27	2.90	2.08	27.91
2MKL-2.PDB	O, C_SER_70	N, C_CYS_29	H, C_CYS_29	2.73	1.79	13.27
2MKL-2.PDB	O, C_SER_10	N, C_GLU_30	H, C_GLU_30	2.88	1.96	17.58
2MKL-2.PDB	O, C_ILE_68	N, C_ILE_31	H, C_ILE_31	2.87	1.90	7.16
2MKL-2.PDB	O, C_SER_8	N, C_VAL_32	H, C_VAL_32	2.78	1.81	9.22
2MKL-2.PDB	O, C_SER_66	N, C_TYR_33	H, C_TYR_33	2.94	2.00	12.67
2MKL-2.PDB	OD1, C_ASP_35	OG, C_SER_34	HG, C_SER_34	2.77	1.81	5.76
2MKL-2.PDB	O, C_GLU_90	N, C_LYS_40	H, C_LYS_40	2.89	1.95	12.75
2MKL-2.PDB	O, C_LEU_88	N, C_PHE_42	H, C_PHE_42	2.81	1.85	8.44
2MKL-2.PDB	O, C_VAL_48	N, C_VAL_45	H, C_VAL_45	2.78	1.87	17.34
2MKL-2.PDB	O, C_VAL_45	N, C_VAL_48	H, C_VAL_48	2.84	2.02	27.01
2MKL-2.PDB	OH, C_TYR_85	NH1, C_ARG_50	HH11, C_ARG_50	2.66	1.70	14.67
2MKL-2.PDB	OE2, C_GLU_78	NH1, C_ARG_50	HH12, C_ARG_50	2.73	1.79	17.34
2MKL-2.PDB	O, C_LYS_71	N, C_GLU_55	H, C_GLU_55	2.70	1.82	21.14
2MKL-2.PDB	O, C_THR_67	N, C_GLU_60	H, C_GLU_60	2.77	1.81	9.91
2MKL-2.PDB	O, C_SER_62	N, C_LYS_65	H, C_LYS_65	2.89	2.03	23.66
2MKL-2.PDB	O, C_TYR_33	N, C_SER_66	H, C_SER_66	2.85	2.01	26.03
2MKL-2.PDB	O, C_GLU_60	N, C_THR_67	H, C_THR_67	2.83	1.98	24.85
2MKL-2.PDB	O, C_ILE_31	N, C_ILE_68	H, C_ILE_68	2.88	1.91	9.29
2MKL-2.PDB	O, C_CYS_29	N, C_SER_70	H, C_SER_70	2.83	1.87	10.79
2MKL-2.PDB	O, C_GLU_55	N, C_LYS_71	H, C_LYS_71	2.73	1.79	13.88
2MKL-2.PDB	OE1, C_GLU_55	NZ, C_LYS_71	HZ1, C_LYS_71	2.72	1.71	11.97
2MKL-2.PDB	O, C_ILE_27	N, C_LEU_72	H, C_LEU_72	2.68	1.70	2.15
2MKL-2.PDB	O, C_GLY_53	N, C_LYS_73	H, C_LYS_73	2.69	1.73	8.58
2MKL-2.PDB	O, C_ALA_76	N, C_ASP_80	H, C_ASP_80	2.99	2.07	17.02
2MKL-2.PDB	O, C_SER_77	OG, C_SER_81	HG, C_SER_81	2.59	1.64	9.12
2MKL-2.PDB	O, C_TRP_79	N, C_GLY_82	H, C_GLY_82	2.99	2.06	16.33
2MKL-2.PDB	OD1, C_ASN_46	OG1, C_THR_83	HG1, C_THR_83	2.72	1.91	26.52
2MKL-2.PDB	O, C_GLN_44	N, C_VAL_86	H, C_VAL_86	2.87	1.99	21.54
2MKL-2.PDB	O, C_ALA_100	N, C_CYS_87	H, C_CYS_87	2.71	1.74	6.36
2MKL-2.PDB	O, C_PHE_42	N, C_LEU_88	H, C_LEU_88	2.70	1.72	2.99
2MKL-2.PDB	O, C_VAL_98	N, C_VAL_89	H, C_VAL_89	2.79	1.88	17.49
2MKL-2.PDB	OD2, C_ASP_91	N, C_GLU_93	H, C_GLU_93	2.95	2.05	18.82
2MKL-2.PDB	O, C_ASP_91	N, C_LEU_94	H, C_LEU_94	2.91	2.01	20.37

2MKL-2.PDB	O, C_VAL_89	N, C_VAL_98	H, C_VAL_98	2.92	1.98	13.93
2MKL-2.PDB	O, C_CYS_87	N, C_ALA_100	H, C_ALA_100	2.93	2.10	27.00
2MKL-2.PDB	O, C_TYR_85	OG, C_SER_101	HG, C_SER_101	2.98	2.03	8.67
2MKL-2.PDB	O, C_TYR_85	N, C_ILE_102	H, C_ILE_102	2.79	1.86	15.51
2MKL-3.PDB	OE1, C_GLU_93	NH1, C_ARG_3	HH12, C_ARG_3	2.68	1.70	11.24
2MKL-3.PDB	O, C_VAL_32	N, C_SER_8	H, C_SER_8	2.88	1.97	17.61
2MKL-3.PDB	O, C_GLU_30	N, C_SER_10	H, C_SER_10	2.89	1.92	6.89
2MKL-3.PDB	O, C_VAL_28	N, C_LEU_12	H, C_LEU_12	2.65	1.67	5.19
2MKL-3.PDB	OXT, C_ALA_105	NZ, C_LYS_13	HZ1, C_LYS_13	2.67	1.72	19.52
2MKL-3.PDB	O, C_TRP_20	OG1, C_THR_21	HG1, C_THR_21	2.91	1.97	13.27
2MKL-3.PDB	O, C_THR_24	N, C_THR_26	H, C_THR_26	2.76	1.91	24.64
2MKL-3.PDB	O, C_LEU_72	OG1, C_THR_26	HG1, C_THR_26	2.58	1.64	12.96
2MKL-3.PDB	O, C_SER_70	N, C_CYS_29	H, C_CYS_29	2.68	1.74	12.62
2MKL-3.PDB	O, C_SER_10	N, C_GLU_30	H, C_GLU_30	2.90	1.95	12.95
2MKL-3.PDB	O, C_ILE_68	N, C_ILE_31	H, C_ILE_31	2.92	1.94	7.65
2MKL-3.PDB	O, C_SER_8	N, C_VAL_32	H, C_VAL_32	2.84	1.90	14.60
2MKL-3.PDB	O, C_SER_66	N, C_TYR_33	H, C_TYR_33	2.81	1.86	12.33
2MKL-3.PDB	OD1, C_ASP_91	N, C_GLU_37	H, C_GLU_37	2.74	1.89	24.66
2MKL-3.PDB	O, C_GLU_90	N, C_LYS_40	H, C_LYS_40	2.97	1.99	6.05
2MKL-3.PDB	O, C_LEU_88	N, C_PHE_42	H, C_PHE_42	2.73	1.79	14.89
2MKL-3.PDB	OE2, C_GLU_84	N, C_GLY_47	H, C_GLY_47	2.89	2.08	28.18
2MKL-3.PDB	O, C_VAL_45	N, C_VAL_48	H, C_VAL_48	2.92	2.02	19.65
2MKL-3.PDB	O, C_LYS_71	N, C_GLU_55	H, C_GLU_55	2.68	1.79	20.49
2MKL-3.PDB	O, C_VAL_69	N, C_GLN_57	H, C_GLN_57	2.76	1.79	7.77
2MKL-3.PDB	O, C_GLY_63	NE1, C_TRP_61	HE1, C_TRP_61	2.71	1.80	19.18
2MKL-3.PDB	O, C_LYS_65	N, C_SER_62	H, C_SER_62	2.68	1.70	4.43
2MKL-3.PDB	O, C_SER_62	N, C_LYS_65	H, C_LYS_65	2.91	1.97	14.37
2MKL-3.PDB	OG, C_SER_34	NZ, C_LYS_65	HZ3, C_LYS_65	2.80	1.76	6.92
2MKL-3.PDB	O, C_TYR_33	N, C_SER_66	H, C_SER_66	2.69	1.79	19.81
2MKL-3.PDB	O, C_GLU_60	N, C_THR_67	H, C_THR_67	2.89	1.96	15.80
2MKL-3.PDB	O, C_ILE_31	N, C_ILE_68	H, C_ILE_68	2.71	1.77	14.66
2MKL-3.PDB	O, C_CYS_29	N, C_SER_70	H, C_SER_70	2.78	1.85	15.96
2MKL-3.PDB	O, C_GLU_55	N, C_LYS_71	H, C_LYS_71	2.82	1.90	15.66
2MKL-3.PDB	OE2, C_GLU_55	NZ, C_LYS_71	HZ1, C_LYS_71	2.64	1.59	1.73
2MKL-3.PDB	OG1, C_THR_26	NZ, C_LYS_71	HZ3, C_LYS_71	2.86	1.95	23.23
2MKL-3.PDB	O, C_ILE_27	N, C_LEU_72	H, C_LEU_72	2.71	1.73	2.63
2MKL-3.PDB	O, C_GLY_53	N, C_LYS_73	H, C_LYS_73	2.74	1.75	3.68
2MKL-3.PDB	O, C_ALA_76	N, C_ASP_80	H, C_ASP_80	2.72	1.79	14.15
2MKL-3.PDB	O, C_GLU_78	N, C_SER_81	H, C_SER_81	2.92	2.06	23.97
2MKL-3.PDB	O, C_TRP_79	N, C_GLY_82	H, C_GLY_82	2.95	2.01	14.70
2MKL-3.PDB	OD1, C_ASN_46	OG1, C_THR_83	HG1, C_THR_83	2.91	1.97	11.57
2MKL-3.PDB	O, C_ALA_100	N, C_CYS_87	H, C_CYS_87	2.69	1.73	11.27
2MKL-3.PDB	O, C_PHE_42	N, C_LEU_88	H, C_LEU_88	2.93	2.02	18.64
2MKL-3.PDB	O, C_VAL_98	N, C_VAL_89	H, C_VAL_89	2.70	1.79	17.71
2MKL-3.PDB	O, C_LYS_40	N, C_GLU_90	H, C_GLU_90	2.89	1.98	17.88
2MKL-3.PDB	OD2, C_ASP_91	N, C_GLU_93	H, C_GLU_93	2.68	1.74	15.47
2MKL-3.PDB	O, C_ASP_91	N, C_LEU_94	H, C_LEU_94	2.96	2.02	14.82
2MKL-3.PDB	O, C_VAL_89	N, C_VAL_98	H, C_VAL_98	2.70	1.73	7.23
2MKL-3.PDB	O, C_TYR_85	N, C_ILE_102	H, C_ILE_102	2.70	1.82	21.56
2MKL-3.PDB	OD1, C_ASP_80	NZ, C_LYS_104	HZ2, C_LYS_104	2.61	1.56	1.39
2MKL-4.PDB	OD1, C_ASP_6	N, C_GLY_2	H, C_GLY_2	2.67	1.68	4.84
2MKL-4.PDB	O, C_VAL_32	N, C_SER_8	H, C_SER_8	2.78	1.82	11.31
2MKL-4.PDB	O, C_GLU_30	N, C_SER_10	H, C_SER_10	2.90	2.00	20.41
2MKL-4.PDB	O, C_VAL_28	N, C_LEU_12	H, C_LEU_12	2.69	1.71	3.92
2MKL-4.PDB	O, C_ALA_105	NZ, C_LYS_13	HZ1, C_LYS_13	2.63	1.64	14.05
2MKL-4.PDB	OE1, C_GLU_17	NE1, C_TRP_20	HE1, C_TRP_20	2.69	1.70	6.61
2MKL-4.PDB	O, C_THR_24	N, C_THR_26	H, C_THR_26	2.90	2.07	26.74
2MKL-4.PDB	O, C_LEU_72	OG1, C_THR_26	HG1, C_THR_26	2.72	1.81	15.12

2MKL-4.PDB	O, C_SER.70	N, C_CYS.29	H, C_CYS.29	2.72	1.78	13.99
2MKL-4.PDB	O, C_SER.10	N, C_GLU.30	H, C_GLU.30	2.82	1.87	12.27
2MKL-4.PDB	O, C_ILE.68	N, C_ILE.31	H, C_ILE.31	2.81	1.83	5.53
2MKL-4.PDB	O, C_SER.8	N, C_VAL.32	H, C_VAL.32	2.75	1.77	3.26
2MKL-4.PDB	O, C_SER.66	N, C_TYR.33	H, C_TYR.33	2.94	1.97	7.56
2MKL-4.PDB	O, C_SER.64	OG, C_SER.34	HG, C_SER.34	2.77	1.80	1.75
2MKL-4.PDB	OE1, C_GLU.37	ND2, C_ASN.38	HD21, C_ASN.38	2.75	1.84	18.89
2MKL-4.PDB	O, C_LEU.88	N, C_PHE.42	H, C_PHE.42	2.69	1.73	9.14
2MKL-4.PDB	O, C_VAL.48	N, C_VAL.45	H, C_VAL.45	2.71	1.78	15.12
2MKL-4.PDB	OE1, C_GLU.84	ND2, C_ASN.46	HD21, C_ASN.46	2.79	1.87	17.49
2MKL-4.PDB	O, C_VAL.45	N, C_VAL.48	H, C_VAL.48	2.77	1.89	22.69
2MKL-4.PDB	OH, C_TYR.85	NE, C_ARG.50	HE, C_ARG.50	2.95	2.07	22.98
2MKL-4.PDB	OE1, C_GLU.78	NH2, C_ARG.50	HH21, C_ARG.50	2.70	1.74	15.78
2MKL-4.PDB	O, C_LYS.71	N, C_GLU.55	H, C_GLU.55	2.71	1.81	18.61
2MKL-4.PDB	O, C_VAL.69	N, C_GLN.57	H, C_GLN.57	2.73	1.78	11.53
2MKL-4.PDB	O, C_SER.62	N, C_LYS.65	H, C_LYS.65	2.84	1.85	4.44
2MKL-4.PDB	O, C_TYR.33	N, C_SER.66	H, C_SER.66	2.69	1.77	16.96
2MKL-4.PDB	O, C_ILE.31	N, C_ILE.68	H, C_ILE.68	2.81	1.88	14.11
2MKL-4.PDB	O, C_CYS.29	N, C_SER.70	H, C_SER.70	2.73	1.81	16.08
2MKL-4.PDB	O, C_GLU.55	N, C_LYS.71	H, C_LYS.71	2.71	1.78	13.91
2MKL-4.PDB	OE2, C_GLU.55	NZ, C_LYS.71	HZ1, C_LYS.71	2.65	1.66	15.29
2MKL-4.PDB	O, C_ILE.27	N, C_LEU.72	H, C_LEU.72	2.71	1.73	8.37
2MKL-4.PDB	O, C_GLY.53	N, C_LYS.73	H, C_LYS.73	2.76	1.78	6.24
2MKL-4.PDB	OE1, C_GLU.78	N, C_MET.75	H, C_MET.75	2.82	1.87	13.55
2MKL-4.PDB	O, C_ALA.76	N, C_ASP.80	H, C_ASP.80	2.90	2.02	21.07
2MKL-4.PDB	O, C_TRP.79	N, C_GLY.82	H, C_GLY.82	2.93	2.03	19.45
2MKL-4.PDB	O, C_ALA.100	N, C_CYS.87	H, C_CYS.87	2.67	1.71	9.36
2MKL-4.PDB	O, C_PHE.42	N, C_LEU.88	H, C_LEU.88	2.83	2.00	27.21
2MKL-4.PDB	O, C_VAL.98	N, C_VAL.89	H, C_VAL.89	2.69	1.75	13.90
2MKL-4.PDB	O, C_LYS.40	N, C_GLU.90	H, C_GLU.90	2.95	1.97	6.05
2MKL-4.PDB	OD2, C_ASP.91	N, C_GLU.93	H, C_GLU.93	2.83	1.95	21.47
2MKL-4.PDB	O, C_VAL.89	N, C_VAL.98	H, C_VAL.98	2.84	1.87	7.29
2MKL-4.PDB	O, C_TYR.85	N, C_ILE.102	H, C_ILE.102	2.72	1.78	13.87
2MKL-5.PDB	OG1, C_THR.5	NE2, C_GLN.4	HE21, C_GLN.4	2.80	1.92	21.71
2MKL-5.PDB	O, C_VAL.32	N, C_SER.8	H, C_SER.8	2.85	1.89	10.14
2MKL-5.PDB	O, C_GLU.30	N, C_SER.10	H, C_SER.10	2.70	1.73	5.85
2MKL-5.PDB	O, C_VAL.28	N, C_LEU.12	H, C_LEU.12	2.69	1.72	7.27
2MKL-5.PDB	O, C_ALA.105	NZ, C_LYS.13	HZ2, C_LYS.13	2.70	1.67	8.50
2MKL-5.PDB	O, C_LEU.72	N, C_ILE.27	H, C_ILE.27	2.84	2.03	28.89
2MKL-5.PDB	O, C_SER.70	N, C_CYS.29	H, C_CYS.29	2.69	1.72	7.41
2MKL-5.PDB	O, C_SER.10	N, C_GLU.30	H, C_GLU.30	2.79	1.82	7.58
2MKL-5.PDB	O, C_ILE.68	N, C_ILE.31	H, C_ILE.31	2.79	1.81	2.50
2MKL-5.PDB	O, C_SER.8	N, C_VAL.32	H, C_VAL.32	2.80	1.83	9.41
2MKL-5.PDB	O, C_SER.66	N, C_TYR.33	H, C_TYR.33	2.93	1.97	10.84
2MKL-5.PDB	OD1, C_ASP.35	OG, C_SER.34	HG, C_SER.34	2.85	1.91	12.30
2MKL-5.PDB	O, C_GLU.90	N, C_LYS.40	H, C_LYS.40	2.94	1.96	3.61
2MKL-5.PDB	O, C_LEU.88	N, C_PHE.42	H, C_PHE.42	2.90	1.95	11.88
2MKL-5.PDB	O, C_VAL.48	N, C_VAL.45	H, C_VAL.45	2.81	1.90	17.99
2MKL-5.PDB	O, C_VAL.45	N, C_VAL.48	H, C_VAL.48	2.85	1.99	24.39
2MKL-5.PDB	OE1, C_GLU.78	NH2, C_ARG.50	HH22, C_ARG.50	2.76	1.81	16.18
2MKL-5.PDB	O, C_LYS.71	N, C_GLU.55	H, C_GLU.55	2.78	1.82	12.33
2MKL-5.PDB	O, C_VAL.69	N, C_GLN.57	H, C_GLN.57	2.78	1.80	6.57
2MKL-5.PDB	O, C_THR.67	N, C_GLU.60	H, C_GLU.60	2.84	1.94	20.40
2MKL-5.PDB	O, C_SER.62	N, C_SER.64	H, C_SER.64	2.53	1.70	25.66
2MKL-5.PDB	OD2, C_ASP.6	NZ, C_LYS.65	HZ2, C_LYS.65	2.68	1.69	14.66
2MKL-5.PDB	O, C_TYR.33	N, C_SER.66	H, C_SER.66	2.80	1.91	20.20
2MKL-5.PDB	O, C_ILE.31	N, C_ILE.68	H, C_ILE.68	2.76	1.80	8.71
2MKL-5.PDB	O, C_CYS.29	N, C_SER.70	H, C_SER.70	2.77	1.81	10.20

2MKL-5.PDB	O, C_GLU_55	N, C_LYS_71	H, C_LYS_71	2.74	1.78	6.80
2MKL-5.PDB	O, C_ILE_27	N, C_LEU_72	H, C_LEU_72	2.68	1.70	3.69
2MKL-5.PDB	O, C_GLY_53	N, C_LYS_73	H, C_LYS_73	2.68	1.72	8.29
2MKL-5.PDB	O, C_ALA_76	N, C_ASP_80	H, C_ASP_80	2.74	1.77	7.96
2MKL-5.PDB	O, C_TRP_79	N, C_GLY_82	H, C_GLY_82	2.89	1.97	17.29
2MKL-5.PDB	OE2, C_GLU_78	OG1, C_THR_83	HG1, C_THR_83	2.81	1.87	12.01
2MKL-5.PDB	O, C_ALA_100	N, C_CYS_87	H, C_CYS_87	2.72	1.76	9.78
2MKL-5.PDB	O, C_PHE_42	N, C_LEU_88	H, C_LEU_88	2.71	1.74	7.08
2MKL-5.PDB	O, C_VAL_98	N, C_VAL_89	H, C_VAL_89	2.71	1.78	15.68
2MKL-5.PDB	OD2, C_ASP_91	N, C_GLU_93	H, C_GLU_93	2.93	2.06	22.91
2MKL-5.PDB	O, C_VAL_89	N, C_VAL_98	H, C_VAL_98	2.95	1.98	7.21
2MKL-5.PDB	O, C_CYS_87	N, C_ALA_100	H, C_ALA_100	2.91	2.10	28.19
2MKL-5.PDB	O, C_TYR_85	N, C_ILE_102	H, C_ILE_102	2.65	1.75	17.77
2MKL-5.PDB	OXT, C_ALA_105	NZ, C_LYS_104	HZ2, C_LYS_104	2.74	1.74	13.81
2MKL-6.PDB	O, C_VAL_32	N, C_SER_8	H, C_SER_8	2.70	1.80	19.33
2MKL-6.PDB	O, C_VAL_28	N, C_LEU_12	H, C_LEU_12	2.64	1.67	9.36
2MKL-6.PDB	OXT, C_ALA_105	NZ, C_LYS_13	HZ2, C_LYS_13	2.64	1.69	18.78
2MKL-6.PDB	OE2, C_GLU_17	NZ, C_LYS_13	HZ3, C_LYS_13	2.63	1.59	5.83
2MKL-6.PDB	O, C_VAL_74	OG1, C_THR_24	HG1, C_THR_24	2.63	1.68	6.20
2MKL-6.PDB	O, C_LEU_72	N, C_ILE_27	H, C_ILE_27	2.81	1.83	4.74
2MKL-6.PDB	O, C_SER_70	N, C_CYS_29	H, C_CYS_29	2.68	1.72	9.63
2MKL-6.PDB	O, C_SER_10	N, C_GLU_30	H, C_GLU_30	2.74	1.79	11.80
2MKL-6.PDB	O, C_SER_8	N, C_VAL_32	H, C_VAL_32	2.94	1.99	13.64
2MKL-6.PDB	O, C_SER_66	N, C_TYR_33	H, C_TYR_33	2.94	1.99	12.36
2MKL-6.PDB	OD2, C_ASP_91	N, C_GLU_37	H, C_GLU_37	2.93	1.96	8.54
2MKL-6.PDB	O, C_GLU_90	N, C_LYS_40	H, C_LYS_40	2.93	1.96	4.64
2MKL-6.PDB	O, C_LEU_88	N, C_PHE_42	H, C_PHE_42	2.84	1.91	15.28
2MKL-6.PDB	O, C_GLY_47	NE2, C_GLN_44	HE21, C_GLN_44	2.88	2.02	23.44
2MKL-6.PDB	O, C_VAL_48	N, C_VAL_45	H, C_VAL_45	2.83	1.89	14.07
2MKL-6.PDB	OE1, C_GLU_84	ND2, C_ASN_46	HD21, C_ASN_46	2.90	1.97	15.36
2MKL-6.PDB	O, C_VAL_45	N, C_VAL_48	H, C_VAL_48	2.91	2.02	21.18
2MKL-6.PDB	OE2, C_GLU_78	NH2, C_ARG_50	HH22, C_ARG_50	2.72	1.70	3.73
2MKL-6.PDB	O, C_LYS_71	N, C_GLU_55	H, C_GLU_55	2.82	1.99	26.45
2MKL-6.PDB	O, C_VAL_69	N, C_GLN_57	H, C_GLN_57	2.71	1.75	9.51
2MKL-6.PDB	O, C_THR_67	N, C_GLU_60	H, C_GLU_60	2.83	1.87	9.90
2MKL-6.PDB	O, C_LYS_65	N, C_SER_62	H, C_SER_62	2.99	2.02	8.78
2MKL-6.PDB	O, C_SER_62	N, C_LYS_65	H, C_LYS_65	2.93	2.00	16.12
2MKL-6.PDB	OD2, C_ASP_6	NZ, C_LYS_65	HZ3, C_LYS_65	2.59	1.63	17.95
2MKL-6.PDB	O, C_TYR_33	N, C_SER_66	H, C_SER_66	2.80	1.88	16.03
2MKL-6.PDB	O, C_GLU_60	N, C_THR_67	H, C_THR_67	2.90	2.10	28.48
2MKL-6.PDB	O, C_ILE_31	N, C_ILE_68	H, C_ILE_68	2.89	1.92	9.05
2MKL-6.PDB	O, C_CYS_29	N, C_SER_70	H, C_SER_70	2.88	1.94	13.67
2MKL-6.PDB	O, C_GLU_55	N, C_LYS_71	H, C_LYS_71	2.76	1.80	10.17
2MKL-6.PDB	OE2, C_GLU_55	NZ, C_LYS_71	HZ1, C_LYS_71	2.70	1.72	16.34
2MKL-6.PDB	O, C_ILE_27	N, C_LEU_72	H, C_LEU_72	2.65	1.75	19.43
2MKL-6.PDB	O, C_GLY_53	N, C_LYS_73	H, C_LYS_73	2.75	1.77	6.62
2MKL-6.PDB	O, C_ALA_76	N, C_ASP_80	H, C_ASP_80	2.70	1.73	7.99
2MKL-6.PDB	O, C_TRP_79	N, C_GLY_82	H, C_GLY_82	2.93	2.02	19.18
2MKL-6.PDB	OD1, C_ASN_46	OG1, C_THR_83	HG1, C_THR_83	2.65	1.71	11.83
2MKL-6.PDB	O, C_ALA_100	N, C_CYS_87	H, C_CYS_87	2.74	1.76	5.40
2MKL-6.PDB	O, C_PHE_42	N, C_LEU_88	H, C_LEU_88	2.76	1.79	7.22
2MKL-6.PDB	O, C_VAL_98	N, C_VAL_89	H, C_VAL_89	2.69	1.77	16.78
2MKL-6.PDB	O, C_VAL_89	N, C_VAL_98	H, C_VAL_98	2.99	2.01	1.37
2MKL-6.PDB	O, C_CYS_87	N, C_ALA_100	H, C_ALA_100	2.94	2.11	26.98
2MKL-6.PDB	O, C_TYR_85	N, C_ILE_102	H, C_ILE_102	2.75	1.80	12.64
2MKL-6.PDB	OD1, C_ASP_80	NZ, C_LYS_104	HZ1, C_LYS_104	2.64	1.71	20.84
2MKL-7.PDB	OD1, C_ASP_6	NE, C_ARG_3	HE, C_ARG_3	2.80	1.90	20.83
2MKL-7.PDB	OD2, C_ASP_6	NE, C_ARG_3	HE, C_ARG_3	2.95	2.13	27.86

2MKL-7.PDB	OD2, C_ASP_6	NH2, C_ARG_3	HH21, C_ARG_3	2.72	1.79	18.49
2MKL-7.PDB	O, C_GLY_2	N, C_GLN_4	H, C_GLN_4	2.91	2.07	25.29
2MKL-7.PDB	O, C_VAL_32	N, C_SER_8	H, C_SER_8	2.86	1.92	13.37
2MKL-7.PDB	O, C_GLU_30	N, C_SER_10	H, C_SER_10	2.76	1.78	0.59
2MKL-7.PDB	O, C_VAL_28	N, C_LEU_12	H, C_LEU_12	2.69	1.70	3.11
2MKL-7.PDB	O, C_PRO_14	N, C_PHE_16	H, C_PHE_16	2.65	1.73	16.96
2MKL-7.PDB	O, C_PHE_16	N, C_GLU_18	H, C_GLU_18	2.58	1.74	25.12
2MKL-7.PDB	O, C_PHE_16	N, C_TRP_20	H, C_TRP_20	2.98	2.12	23.41
2MKL-7.PDB	O, C_GLN_22	N, C_THR_24	H, C_THR_24	2.67	1.86	27.69
2MKL-7.PDB	O, C_LEU_72	OG1, C_THR_26	HG1, C_THR_26	2.61	1.71	16.80
2MKL-7.PDB	O, C_LEU_72	N, C_ILE_27	H, C_ILE_27	2.83	2.01	27.24
2MKL-7.PDB	O, C_SER_70	N, C_CYS_29	H, C_CYS_29	2.71	1.75	8.90
2MKL-7.PDB	O, C_SER_10	N, C_GLU_30	H, C_GLU_30	2.79	1.83	10.18
2MKL-7.PDB	O, C_ILE_68	N, C_ILE_31	H, C_ILE_31	2.98	2.00	2.29
2MKL-7.PDB	O, C_SER_8	N, C_VAL_32	H, C_VAL_32	2.74	1.76	3.52
2MKL-7.PDB	O, C_SER_66	N, C_TYR_33	H, C_TYR_33	2.95	2.00	12.03
2MKL-7.PDB	O, C_SER_64	OG, C_SER_34	HG, C_SER_34	2.66	1.69	4.53
2MKL-7.PDB	O, C_LEU_88	N, C_PHE_42	H, C_PHE_42	2.87	1.89	4.70
2MKL-7.PDB	O, C_VAL_45	N, C_VAL_48	H, C_VAL_48	2.96	2.07	20.95
2MKL-7.PDB	O, C_VAL_54	NZ, C_LYS_52	HZ1, C_LYS_52	2.71	1.68	7.22
2MKL-7.PDB	O, C_LYS_71	N, C_GLU_55	H, C_GLU_55	2.76	1.91	24.53
2MKL-7.PDB	O, C_VAL_69	N, C_GLN_57	H, C_GLN_57	2.73	1.77	10.49
2MKL-7.PDB	O, C_THR_67	N, C_GLU_60	H, C_GLU_60	2.81	1.87	13.84
2MKL-7.PDB	OE1, C_GLU_60	N, C_TRP_61	H, C_TRP_61	2.86	1.94	17.90
2MKL-7.PDB	O, C_LYS_65	N, C_SER_62	H, C_SER_62	2.88	1.90	4.45
2MKL-7.PDB	O, C_SER_62	N, C_LYS_65	H, C_LYS_65	2.88	1.96	16.75
2MKL-7.PDB	OD1, C_ASP_6	NZ, C_LYS_65	HZ2, C_LYS_65	2.61	1.57	4.07
2MKL-7.PDB	O, C_TYR_33	N, C_SER_66	H, C_SER_66	2.78	1.94	25.87
2MKL-7.PDB	O, C_GLU_60	N, C_THR_67	H, C_THR_67	2.69	1.81	21.94
2MKL-7.PDB	O, C_ILE_31	N, C_ILE_68	H, C_ILE_68	2.96	1.98	7.22
2MKL-7.PDB	O, C_CYS_29	N, C_SER_70	H, C_SER_70	2.75	1.80	11.18
2MKL-7.PDB	O, C_GLU_55	N, C_LYS_71	H, C_LYS_71	2.75	1.91	24.82
2MKL-7.PDB	O, C_ILE_27	N, C_LEU_72	H, C_LEU_72	2.67	1.73	13.09
2MKL-7.PDB	O, C_GLY_53	N, C_LYS_73	H, C_LYS_73	2.80	1.82	6.40
2MKL-7.PDB	OG1, C_THR_24	NZ, C_LYS_73	HZ1, C_LYS_73	2.79	1.84	19.74
2MKL-7.PDB	O, C_ALA_76	N, C_ASP_80	H, C_ASP_80	2.73	1.79	13.61
2MKL-7.PDB	O, C_GLU_78	N, C_SER_81	H, C_SER_81	2.92	2.09	26.88
2MKL-7.PDB	O, C_TRP_79	N, C_GLY_82	H, C_GLY_82	2.96	2.03	15.54
2MKL-7.PDB	OE2, C_GLU_78	OG1, C_THR_83	HG1, C_THR_83	2.59	1.64	9.74
2MKL-7.PDB	O, C_ALA_100	N, C_CYS_87	H, C_CYS_87	2.73	1.75	2.91
2MKL-7.PDB	O, C_PHE_42	N, C_LEU_88	H, C_LEU_88	2.67	1.75	17.26
2MKL-7.PDB	O, C_VAL_98	N, C_VAL_89	H, C_VAL_89	2.85	1.96	20.95
2MKL-7.PDB	OD2, C_ASP_91	N, C_GLU_93	H, C_GLU_93	2.83	1.89	14.21
2MKL-7.PDB	O, C_VAL_89	N, C_VAL_98	H, C_VAL_98	2.92	1.95	4.26
2MKL-7.PDB	O, C_CYS_87	N, C_ALA_100	H, C_ALA_100	2.86	2.03	26.56
2MKL-7.PDB	O, C_TYR_85	N, C_ILE_102	H, C_ILE_102	2.82	1.93	20.79
2MKL-7.PDB	O, C_ALA_105	NZ, C_LYS_104	HZ3, C_LYS_104	2.60	1.63	17.04
2MKL-8.PDB	O, C_VAL_32	N, C_SER_8	H, C_SER_8	2.76	1.79	7.90
2MKL-8.PDB	O, C_GLU_30	N, C_SER_10	H, C_SER_10	2.88	1.92	12.44
2MKL-8.PDB	O, C_VAL_28	N, C_LEU_12	H, C_LEU_12	2.63	1.65	4.98
2MKL-8.PDB	O, C_ALA_105	NZ, C_LYS_13	HZ2, C_LYS_13	2.61	1.57	5.41
2MKL-8.PDB	OE2, C_GLU_17	N, C_GLU_18	H, C_GLU_18	2.97	2.09	21.14
2MKL-8.PDB	O, C_LEU_72	OG1, C_THR_26	HG1, C_THR_26	2.97	2.06	16.54
2MKL-8.PDB	O, C_LEU_72	N, C_ILE_27	H, C_ILE_27	2.76	1.84	17.21
2MKL-8.PDB	O, C_SER_70	N, C_CYS_29	H, C_CYS_29	2.80	1.87	15.66
2MKL-8.PDB	O, C_SER_10	N, C_GLU_30	H, C_GLU_30	2.74	1.81	16.35
2MKL-8.PDB	O, C_ILE_68	N, C_ILE_31	H, C_ILE_31	2.87	1.90	7.35
2MKL-8.PDB	O, C_SER_8	N, C_VAL_32	H, C_VAL_32	2.73	1.75	6.64

2MKL-8.PDB	O, C_SER_64	OG, C_SER_34	HG, C_SER_34	2.72	1.87	22.15
2MKL-8.PDB	OD2, C_ASP_91	N, C_ASN_38	H, C_ASN_38	2.62	1.64	4.38
2MKL-8.PDB	O, C_GLU_37	ND2, C_ASN_38	HD21, C_ASN_38	2.58	1.65	16.81
2MKL-8.PDB	O, C_LEU_88	N, C_PHE_42	H, C_PHE_42	2.73	1.76	7.97
2MKL-8.PDB	OG, C_SER_70	NE1, C_TRP_43	HE1, C_TRP_43	2.82	1.83	2.10
2MKL-8.PDB	O, C_VAL_86	N, C_GLN_44	H, C_GLN_44	3.00	2.07	16.25
2MKL-8.PDB	O, C_VAL_48	N, C_VAL_45	H, C_VAL_45	2.73	1.82	17.50
2MKL-8.PDB	O, C_VAL_45	N, C_VAL_48	H, C_VAL_48	2.98	2.08	19.95
2MKL-8.PDB	OE2, C_GLU_78	NH1, C_ARG_50	HH12, C_ARG_50	2.63	1.62	3.58
2MKL-8.PDB	O, C_LYS_73	NH2, C_ARG_50	HH21, C_ARG_50	2.93	1.96	12.60
2MKL-8.PDB	O, C_GLU_49	NZ, C_LYS_51	HZ2, C_LYS_51	2.93	1.94	14.57
2MKL-8.PDB	O, C_LYS_71	N, C_GLU_55	H, C_GLU_55	2.75	1.82	14.98
2MKL-8.PDB	O, C_VAL_69	N, C_GLN_57	H, C_GLN_57	2.96	2.01	12.37
2MKL-8.PDB	O, C_THR_67	N, C_GLU_60	H, C_GLU_60	2.98	2.10	22.35
2MKL-8.PDB	O, C_SER_62	N, C_LYS_65	H, C_LYS_65	2.98	2.01	8.55
2MKL-8.PDB	OD2, C_ASP_6	NZ, C_LYS_65	HZ3, C_LYS_65	2.64	1.68	18.41
2MKL-8.PDB	O, C_TYR_33	N, C_SER_66	H, C_SER_66	2.73	1.81	16.99
2MKL-8.PDB	O, C_ILE_31	N, C_ILE_68	H, C_ILE_68	2.80	1.84	10.07
2MKL-8.PDB	O, C_CYS_29	N, C_SER_70	H, C_SER_70	2.86	1.88	5.47
2MKL-8.PDB	O, C_GLU_55	N, C_LYS_71	H, C_LYS_71	2.77	1.80	6.52
2MKL-8.PDB	O, C_ILE_27	N, C_LEU_72	H, C_LEU_72	2.69	1.74	12.28
2MKL-8.PDB	O, C_GLY_53	N, C_LYS_73	H, C_LYS_73	2.71	1.74	7.49
2MKL-8.PDB	O, C_ALA_25	N, C_VAL_74	H, C_VAL_74	2.97	2.03	14.41
2MKL-8.PDB	OE1, C_GLU_78	N, C_MET_75	H, C_MET_75	2.72	1.76	9.33
2MKL-8.PDB	O, C_ALA_76	N, C_ASP_80	H, C_ASP_80	2.65	1.71	13.15
2MKL-8.PDB	O, C_GLU_78	N, C_SER_81	H, C_SER_81	2.97	2.14	27.36
2MKL-8.PDB	O, C_SER_77	OG, C_SER_81	HG, C_SER_81	2.56	1.60	6.14
2MKL-8.PDB	O, C_TRP_79	N, C_GLY_82	H, C_GLY_82	2.98	2.06	16.79
2MKL-8.PDB	O, C_ALA_100	N, C_CYS_87	H, C_CYS_87	2.71	1.76	12.28
2MKL-8.PDB	O, C_PHE_42	N, C_LEU_88	H, C_LEU_88	2.77	1.80	5.62
2MKL-8.PDB	O, C_LYS_40	N, C_GLU_90	H, C_GLU_90	2.83	1.87	9.17
2MKL-8.PDB	OD1, C_ASP_91	N, C_GLU_93	H, C_GLU_93	2.62	1.67	12.30
2MKL-8.PDB	O, C_CYS_87	N, C_ALA_100	H, C_ALA_100	2.89	2.08	28.20
2MKL-8.PDB	O, C_TYR_85	N, C_ILE_102	H, C_ILE_102	2.83	1.93	19.99
2MKL-8.PDB	O, C_GLY_82	NH1, C_ARG_103	HH11, C_ARG_103	2.70	1.75	16.11
2MKL-8.PDB	OD1, C_ASP_80	NZ, C_LYS_104	HZ1, C_LYS_104	2.61	1.59	9.01
2MKL-9.PDB	OG1, C_THR_96	N, C_MET_1	H2, C_MET_1	2.76	1.75	11.34
2MKL-9.PDB	O, C_VAL_9	OG, C_SER_10	HG, C_SER_10	2.88	1.94	11.21
2MKL-9.PDB	O, C_VAL_28	N, C_LEU_12	H, C_LEU_12	2.61	1.63	7.07
2MKL-9.PDB	O, C_THR_24	N, C_THR_26	H, C_THR_26	2.89	2.03	23.40
2MKL-9.PDB	O, C_LEU_72	OG1, C_THR_26	HG1, C_THR_26	2.65	1.69	6.28
2MKL-9.PDB	O, C_LEU_72	N, C_ILE_27	H, C_ILE_27	2.89	2.04	24.93
2MKL-9.PDB	O, C_SER_70	N, C_CYS_29	H, C_CYS_29	2.74	1.78	9.84
2MKL-9.PDB	O, C_SER_10	N, C_GLU_30	H, C_GLU_30	2.88	1.91	6.77
2MKL-9.PDB	O, C_ILE_68	N, C_ILE_31	H, C_ILE_31	2.89	1.92	7.18
2MKL-9.PDB	O, C_SER_8	N, C_VAL_32	H, C_VAL_32	2.76	1.81	11.14
2MKL-9.PDB	O, C_SER_66	N, C_TYR_33	H, C_TYR_33	2.98	2.04	15.18
2MKL-9.PDB	O, C_LEU_88	N, C_PHE_42	H, C_PHE_42	2.92	1.99	16.26
2MKL-9.PDB	O, C_GLY_47	NE2, C_GLN_44	HE21, C_GLN_44	2.91	2.11	28.91
2MKL-9.PDB	O, C_VAL_48	N, C_VAL_45	H, C_VAL_45	2.81	1.87	13.63
2MKL-9.PDB	O, C_VAL_45	N, C_VAL_48	H, C_VAL_48	2.87	2.01	23.76
2MKL-9.PDB	OE2, C_GLU_78	NH2, C_ARG_50	HH22, C_ARG_50	2.68	1.69	8.63
2MKL-9.PDB	O, C_LYS_71	N, C_GLU_55	H, C_GLU_55	2.70	1.82	21.75
2MKL-9.PDB	O, C_THR_67	N, C_GLU_60	H, C_GLU_60	2.71	1.77	13.93
2MKL-9.PDB	O, C_LYS_65	N, C_SER_62	H, C_SER_62	2.85	1.92	15.49
2MKL-9.PDB	O, C_SER_62	N, C_LYS_65	H, C_LYS_65	2.77	1.83	13.89
2MKL-9.PDB	OD2, C_ASP_6	NZ, C_LYS_65	HZ2, C_LYS_65	2.75	1.71	7.05
2MKL-9.PDB	O, C_ILE_31	N, C_ILE_68	H, C_ILE_68	2.77	1.81	8.93

2MKL-9.PDB	O, C_CYS_29	N, C_SER_70	H, C_SER_70	2.85	1.87	7.34
2MKL-9.PDB	O, C_GLU_55	N, C_LYS_71	H, C_LYS_71	2.73	1.77	9.92
2MKL-9.PDB	O, C_ILE_27	N, C_LEU_72	H, C_LEU_72	2.68	1.70	5.96
2MKL-9.PDB	O, C_GLY_53	N, C_LYS_73	H, C_LYS_73	2.69	1.71	1.06
2MKL-9.PDB	O, C_ALA_76	N, C_ASP_80	H, C_ASP_80	2.94	2.03	18.41
2MKL-9.PDB	O, C_GLU_78	N, C_SER_81	H, C_SER_81	2.94	2.11	27.71
2MKL-9.PDB	O, C_TRP_79	N, C_GLY_82	H, C_GLY_82	2.94	2.01	15.71
2MKL-9.PDB	O, C_ALA_100	N, C_CYS_87	H, C_CYS_87	2.71	1.74	7.57
2MKL-9.PDB	O, C_PHE_42	N, C_LEU_88	H, C_LEU_88	2.76	1.77	3.30
2MKL-9.PDB	O, C_VAL_98	N, C_VAL_89	H, C_VAL_89	2.84	1.93	17.52
2MKL-9.PDB	OE2, C_GLU_37	OG, C_SER_92	HG, C_SER_92	3.00	2.20	28.49
2MKL-9.PDB	O, C_ASP_91	N, C_LEU_94	H, C_LEU_94	2.98	2.06	17.03
2MKL-9.PDB	O, C_CYS_87	N, C_ALA_100	H, C_ALA_100	2.97	2.14	27.19
2MKL-9.PDB	O, C_TYR_85	OG, C_SER_101	HG, C_SER_101	2.85	1.92	13.62
2MKL-9.PDB	O, C_TYR_85	N, C_ILE_102	H, C_ILE_102	2.74	1.79	13.03
2RLL.PDB	O, A_PRO_8	N, A_ASP_11	H, A_ASP_11	2.97	2.17	28.89
3SE8.PDB	OE2, G_GLU_91	NE1, G_TRP_45	HE1, G_TRP_45	2.78	2.03	24.08
3SE8.PDB	OE1, G_GLN_103	N, G_LEU_52	H, G_LEU_52	2.91	2.05	3.20
3SE8.PDB	O, G_HIS_216	N, G_ALA_55	H, G_ALA_55	2.90	2.11	20.01
3SE8.PDB	O, G_VAL_75	N, G_SER_56	H, G_SER_56	2.97	2.22	24.79
3SE8.PDB	OD1, G_ASN_67	N, G_LYS_59	H, G_LYS_59	2.79	1.96	12.33
3SE8.PDB	O, G_SER_209	N, G_VAL_65	H, G_VAL_65	2.99	2.15	12.16
3SE8.PDB	OE2, G_GLU_64	N, G_HIS_66	H, G_HIS_66	2.94	2.09	3.80
3SE8.PDB	OE2, G_GLU_64	ND1, G_HIS_66	HD1, G_HIS_66	2.82	1.98	11.41
3SE8.PDB	OE1, G_GLU_64	N, G_ASN_67	H, G_ASN_67	2.93	2.14	18.64
3SE8.PDB	OE1, G_GLU_64	ND2, G_ASN_67	HD22, G_ASN_67	2.82	2.00	14.84
3SE8.PDB	O, G_HIS_66	N, G_ALA_70	H, G_ALA_70	2.99	2.14	6.51
3SE8.PDB	O, G_ASN_67	N, G_THR_71	H, G_THR_71	2.92	2.13	19.42
3SE8.PDB	O, G_ALA_70	N, G_CYS_74	H, G_CYS_74	2.70	1.91	18.43
3SE8.PDB	O, G_CYS_54	N, G_VAL_75	H, G_VAL_75	2.88	2.07	16.86
3SE8.PDB	OD1, G_ASP_78	N, G_ASN_80	H, G_ASN_80	2.97	2.17	18.12
3SE8.PDB	O, G_SER_244	N, G_ILE_84	H, G_ILE_84	2.94	2.12	14.64
3SE8.PDB	O, G_VAL_242	N, G_LEU_86	H, G_LEU_86	2.80	1.94	0.64
3SE8.PDB	O, G_CYS_239	N, G_GLU_91	H, G_GLU_91	2.91	2.11	18.25
3SE8.PDB	O, G_GLY_237	N, G_PHE_93	H, G_PHE_93	2.87	2.06	15.53
3SE8.PDB	O, G_GLY_235	N, G_MET_95	H, G_MET_95	2.80	1.96	10.44
3SE8.PDB	O, G_ASN_94	N, G_LYS_97	H, G_LYS_97	2.95	2.11	10.82
3SE8.PDB	O, G_ASN_98	N, G_VAL_101	H, G_VAL_101	2.85	2.03	14.99
3SE8.PDB	O, G_THR_50	NE2, G_GLN_103	HE21, G_GLN_103	2.73	1.97	22.93
3SE8.PDB	OD1, G_ASN_99	NE2, G_GLN_103	HE22, G_GLN_103	2.99	2.17	14.68
3SE8.PDB	O, G_VAL_101	N, G_GLN_105	H, G_GLN_105	2.96	2.12	10.76
3SE8.PDB	O, G_MET_104	N, G_VAL_108	H, G_VAL_108	2.93	2.11	15.74
3SE8.PDB	O, G_GLN_105	N, G_ILE_109	H, G_ILE_109	2.97	2.12	7.19
3SE8.PDB	O, G_GLU_106	N, G_SER_110	H, G_SER_110	2.87	2.05	13.15
3SE8.PDB	O, G_ASP_107	N, G_LEU_111	H, G_LEU_111	2.87	2.07	18.28
3SE8.PDB	O, G_VAL_108	N, G_TRP_112	H, G_TRP_112	2.94	2.10	9.73
3SE8.PDB	O, G_ILE_109	N, G_ASP_113	H, G_ASP_113	2.91	2.13	20.04
3SE8.PDB	O, G_TRP_112	N, G_LEU_116	H, G_LEU_116	2.87	2.03	11.15
3SE8.PDB	O, G_ILE_201	N, G_LYS_121	H, G_LYS_121	2.84	2.08	23.60
3SE8.PDB	O, G_GLN_432	N, G_LEU_122	H, G_LEU_122	2.84	1.98	3.70
3SE8.PDB	OE2, G_GLU_381	NZ, G_LYS_207	HZ2, G_LYS_207	2.74	1.86	4.82
3SE8.PDB	OE2, G_GLU_64	N, G_ASP_211	H, G_ASP_211	2.86	2.06	17.85
3SE8.PDB	O, G_ILE_251	N, G_ILE_215	H, G_ILE_215	2.86	2.03	14.34
3SE8.PDB	O, G_ALA_55	N, G_HIS_216	H, G_HIS_216	2.88	2.03	9.08
3SE8.PDB	O, G_THR_248	ND1, G_HIS_216	HD1, G_HIS_216	2.90	2.07	13.28
3SE8.PDB	O, G_PHE_53	N, G_CYS_218	H, G_CYS_218	2.89	2.13	22.85
3SE8.PDB	O, G_VAL_489	N, G_VAL_224	H, G_VAL_224	2.98	2.17	16.77
3SE8.PDB	O, G_LYS_487	N, G_LEU_226	H, G_LEU_226	2.72	1.91	15.99

3SE8.PDB	O, G_SER_243	N, G_LYS_227	H, G_LYS_227	2.80	1.97	12.53
3SE8.PDB	O, G_LYS_485	N, G_CYS_228	H, G_CYS_228	2.74	1.93	16.67
3SE8.PDB	O, G_ASN_241	N, G_ASN_229	H, G_ASN_229	2.73	1.90	11.23
3SE8.PDB	O, G_GLU_91	N, G_CYS_239	H, G_CYS_239	2.59	1.79	18.72
3SE8.PDB	OD2, G_ASP_230	N, G_LYS_240	H, G_LYS_240	2.98	2.13	6.94
3SE8.PDB	OD1, G_ASP_230	N, G_ASN_241	H, G_ASN_241	2.67	1.87	17.74
3SE8.PDB	O, G_LYS_227	N, G_SER_243	H, G_SER_243	2.97	2.15	15.16
3SE8.PDB	OE2, G_GLU_83	OG, G_SER_243	HG, G_SER_243	2.64	1.83	7.57
3SE8.PDB	O, G_ILE_84	N, G_SER_244	H, G_SER_244	2.68	1.89	18.10
3SE8.PDB	O, G_ILE_225	N, G_VAL_245	H, G_VAL_245	2.90	2.07	10.51
3SE8.PDB	O, G_TYR_217	N, G_THR_248	H, G_THR_248	2.72	1.92	16.92
3SE8.PDB	OH, G_TYR_486	ND1, G_HIS_249	HD1, G_HIS_249	2.64	1.81	12.83
3SE8.PDB	OE1, G_GLU_482	NE2, G_HIS_249	HE2, G_HIS_249	3.00	2.16	9.93
3SE8.PDB	O, G_ILE_215	N, G_ILE_251	H, G_ILE_251	2.96	2.12	9.55
3SE8.PDB	O, G_HIS_375	N, G_THR_257	H, G_THR_257	2.97	2.23	26.05
3SE8.PDB	O, G_THR_257	N, G_LEU_259	H, G_LEU_259	2.81	2.06	25.63
3SE8.PDB	O, G_GLY_451	N, G_LEU_260	H, G_LEU_260	2.87	2.03	11.95
3SE8.PDB	O, G_ASN_448	N, G_ASN_262	H, G_ASN_262	2.71	1.88	12.07
3SE8.PDB	OE2, G_GLU_482	N, G_SER_264	H, G_SER_264	2.73	1.91	13.91
3SE8.PDB	O, G_LEU_288	N, G_ALA_266	H, G_ALA_266	2.78	2.00	20.85
3SE8.PDB	O, G_ILE_285	N, G_ARG_273	H, G_ARG_273	2.79	1.98	16.42
3SE8.PDB	O, G_PHE_233	NH2, G_ARG_273	HH22, G_ARG_273	2.82	2.02	18.59
3SE8.PDB	O, G_ASN_276	N, G_ASN_279	H, G_ASN_279	2.78	1.96	14.69
3SE8.PDB	OD1, G_ASN_279	N, G_ALA_281	H, G_ALA_281	2.86	2.06	17.39
3SE8.PDB	O, G_LEU_454	N, G_ILE_284	H, G_ILE_284	2.84	1.98	2.93
3SE8.PDB	O, G_ARG_273	N, G_ILE_285	H, G_ILE_285	2.70	1.87	12.33
3SE8.PDB	O, G_ILE_452	N, G_VAL_286	H, G_VAL_286	2.88	2.04	10.30
3SE8.PDB	O, G_ILE_271	N, G_HIS_287	H, G_HIS_287	2.82	1.96	3.43
3SE8.PDB	O, G_SER_264	NE2, G_HIS_287	HE2, G_HIS_287	2.67	1.83	10.99
3SE8.PDB	O, G_SER_447	N, G_ILE_294	H, G_ILE_294	2.75	1.94	17.22
3SE8.PDB	O, G_GLU_332	N, G_ASN_295	H, G_ASN_295	2.93	2.13	18.46
3SE8.PDB	O, G_TYR_330	N, G_THR_297	H, G_THR_297	2.85	2.02	13.88
3SE8.PDB	O, G_ILE_443	N, G_ARG_298	H, G_ARG_298	2.74	1.91	12.06
3SE8.PDB	O, G_ILE_326	NH1, G_ARG_298	HH11, G_ARG_298	2.83	2.00	11.83
3SE8.PDB	O, G_GLY_441	NH2, G_ARG_298	HH21, G_ARG_298	2.55	1.70	4.64
3SE8.PDB	O, G_ILE_439	NH2, G_ARG_298	HH22, G_ARG_298	2.90	2.10	18.34
3SE8.PDB	O, G_CYS_418	N, G_ALA_329	H, G_ALA_329	2.90	2.06	11.88
3SE8.PDB	O, G_LEU_416	N, G_CYS_331	H, G_CYS_331	2.98	2.19	20.31
3SE8.PDB	O, G_ASN_295	N, G_GLU_332	H, G_GLU_332	2.74	1.92	15.11
3SE8.PDB	O, G_ILE_414	N, G_ILE_333	H, G_ILE_333	2.90	2.08	15.80
3SE8.PDB	O, G_GLY_412	N, G_GLY_335	H, G_GLY_335	2.61	1.86	25.24
3SE8.PDB	OD1, G_ASN_334	N, G_LYS_337	H, G_LYS_337	2.85	2.02	13.75
3SE8.PDB	O, G_ASN_334	N, G_TRP_338	H, G_TRP_338	2.85	2.04	16.18
3SE8.PDB	O, G_LEU_390	NE1, G_TRP_338	HE1, G_TRP_338	2.58	1.76	15.13
3SE8.PDB	O, G_GLY_335	N, G_ASN_339	H, G_ASN_339	2.74	1.88	4.81
3SE8.PDB	O, G_TRP_338	N, G_LEU_342	H, G_LEU_342	2.77	1.94	11.71
3SE8.PDB	O, G_VAL_341	N, G_VAL_345	H, G_VAL_345	2.89	2.13	23.16
3SE8.PDB	O, G_LEU_342	N, G_THR_346	H, G_THR_346	2.94	2.12	14.67
3SE8.PDB	O, G_LYS_343	OG1, G_THR_346	HG1, G_THR_346	2.65	1.92	23.05
3SE8.PDB	O, G_LYS_343	N, G_GLU_347	H, G_GLU_347	3.00	2.22	21.50
3SE8.PDB	O, G_GLN_344	N, G_LYS_348	H, G_LYS_348	2.99	2.19	18.12
3SE8.PDB	OE2, G_GLU_269	NZ, G_LYS_348	HZ1, G_LYS_348	2.90	2.14	25.94
3SE8.PDB	OE1, G_GLU_351	NZ, G_LYS_348	HZ3, G_LYS_348	2.96	2.10	14.00
3SE8.PDB	O, G_VAL_345	N, G_LEU_349	H, G_LEU_349	2.94	2.12	15.13
3SE8.PDB	O, G_LYS_350	N, G_ASN_355	H, G_ASN_355	2.97	2.13	9.29
3SE8.PDB	O, G_PHE_353	N, G_LYS_357	H, G_LYS_357	2.81	1.95	2.88
3SE8.PDB	OD1, G_ASN_393	N, G_PHE_361	H, G_PHE_361	2.89	2.04	5.90
3SE8.PDB	O, G_PHE_468	N, G_GLN_362	H, G_GLN_362	2.83	2.01	15.06

3SE8.PDB	O, H_TRP_54	N, G_ASP_368	H, G_ASP_368	2.75	1.91	10.72
3SE8.PDB	O, G_LEU_369	N, G_MET_373	H, G_MET_373	3.00	2.23	22.44
3SE8.PDB	O, G_CYS_385	N, G_HIS_374	H, G_HIS_374	2.81	2.03	21.55
3SE8.PDB	O, G_THR_257	ND1, G_HIS_374	HD1, G_HIS_374	2.91	2.06	7.53
3SE8.PDB	O, G_PHE_383	ND1, G_HIS_375	HD1, G_HIS_375	2.96	2.19	22.53
3SE8.PDB	O, G_GLU_381	N, G_CYS_378	H, G_CYS_378	2.90	2.12	21.09
3SE8.PDB	O, G_CYS_378	N, G_GLU_381	H, G_GLU_381	2.88	2.03	7.72
3SE8.PDB	O, G_PHE_376	N, G_PHE_383	H, G_PHE_383	2.77	1.95	13.43
3SE8.PDB	O, G_HIS_374	N, G_CYS_385	H, G_CYS_385	2.80	1.98	13.95
3SE8.PDB	OD1, G_ASN_386	N, G_THR_388	H, G_THR_388	2.94	2.09	9.87
3SE8.PDB	O, G_THR_387	N, G_LEU_390	H, G_LEU_390	2.83	2.03	19.01
3SE8.PDB	O, G_PHE_361	ND2, G_ASN_393	HD22, G_ASN_393	2.82	1.99	12.21
3SE8.PDB	OD1, G_ASN_392	N, G_THR_394	H, G_THR_394	2.97	2.24	26.64
3SE8.PDB	O, G_ILE_333	N, G_ILE_414	H, G_ILE_414	2.79	2.00	18.93
3SE8.PDB	O, G_CYS_331	N, G_LEU_416	H, G_LEU_416	2.80	2.05	24.46
3SE8.PDB	O, G_ALA_329	N, G_CYS_418	H, G_CYS_418	2.89	2.04	8.98
3SE8.PDB	O, G_TYR_384	N, G_LYS_419	H, G_LYS_419	2.92	2.14	22.08
3SE8.PDB	O, G_ARG_327	N, G_ILE_420	H, G_ILE_420	2.82	2.00	14.23
3SE8.PDB	O, G_ALA_433	N, G_ILE_424	H, G_ILE_424	2.88	2.06	14.47
3SE8.PDB	OE2, G_GLU_370	N, G_ASN_425	H, G_ASN_425	2.74	1.89	6.23
3SE8.PDB	O, G_GLY_431	N, G_MET_426	H, G_MET_426	2.76	1.90	1.16
3SE8.PDB	O, G_MET_426	N, G_GLY_429	H, G_GLY_429	2.90	2.07	12.32
3SE8.PDB	O, G_ILE_424	N, G_ALA_433	H, G_ALA_433	2.84	2.01	13.80
3SE8.PDB	O, G_VAL_120	N, G_MET_434	H, G_MET_434	2.89	2.08	16.32
3SE8.PDB	O, G_GLN_422	N, G_TYR_435	H, G_TYR_435	2.70	1.89	15.98
3SE8.PDB	OD1, G_ASN_295	ND2, G_ASN_444	HD21, G_ASN_444	2.87	2.12	25.11
3SE8.PDB	OG1, G_THR_297	ND2, G_ASN_444	HD22, G_ASN_444	2.77	1.99	20.73
3SE8.PDB	O, G_ILE_294	N, G_SER_447	H, G_SER_447	2.93	2.10	11.64
3SE8.PDB	O, G_LEU_260	N, G_THR_450	H, G_THR_450	2.91	2.08	13.27
3SE8.PDB	O, G_VAL_286	N, G_ILE_452	H, G_ILE_452	3.00	2.20	19.52
3SE8.PDB	O, G_GLN_258	N, G_LEU_453	H, G_LEU_453	2.85	2.00	5.65
3SE8.PDB	O, G_ILE_284	N, G_LEU_454	H, G_LEU_454	2.99	2.16	13.70
3SE8.PDB	O, G_ARG_469	N, G_THR_455	H, G_THR_455	2.90	2.07	11.48
3SE8.PDB	O, G_THR_467	N, G_ASP_457	H, G_ASP_457	2.94	2.11	12.90
3SE8.PDB	OE2, L_GLU_96	N, G_GLY_459	H, G_GLY_459	2.81	1.99	15.35
3SE8.PDB	O, G_THR_358	N, G_GLU_466	H, G_GLU_466	2.85	2.09	22.90
3SE8.PDB	O, G_ILE_360	N, G_PHE_468	H, G_PHE_468	2.81	2.00	17.29
3SE8.PDB	O, G_THR_455	N, G_ARG_469	H, G_ARG_469	2.91	2.11	19.07
3SE8.PDB	OD2, G_ASP_457	NE, G_ARG_469	HE, G_ARG_469	2.90	2.06	8.93
3SE8.PDB	O, G_PRO_363	NH1, G_ARG_469	HH11, G_ARG_469	2.85	2.03	15.65
3SE8.PDB	OD1, G_ASP_457	NH2, G_ARG_469	HH21, G_ARG_469	2.93	2.11	16.29
3SE8.PDB	O, G_ASN_474	N, G_ASP_477	H, G_ASP_477	2.86	2.03	13.09
3SE8.PDB	OE1, G_GLN_105	NE1, G_TRP_479	HE1, G_TRP_479	2.68	1.92	22.70
3SE8.PDB	O, G_LYS_476	N, G_ARG_480	H, G_ARG_480	2.90	2.07	12.50
3SE8.PDB	O, G_ASP_477	N, G_SER_481	H, G_SER_481	2.99	2.24	26.03
3SE8.PDB	O, G_TRP_479	N, G_LEU_483	H, G_LEU_483	2.88	2.12	23.01
3SE8.PDB	O, G_LEU_226	N, G_LYS_487	H, G_LYS_487	2.94	2.15	19.58
3SE8.PDB	OE1, G_GLU_91	NZ, G_LYS_487	HZ1, G_LYS_487	2.58	1.77	20.55
3SE8.PDB	OD1, G_ASP_47	NZ, G_LYS_487	HZ2, G_LYS_487	2.90	2.08	19.02
3SE8.PDB	O, G_ASN_92	NZ, G_LYS_487	HZ3, G_LYS_487	2.95	2.08	10.80
3SE8.PDB	O, G_VAL_224	N, G_VAL_489	H, G_VAL_489	2.91	2.06	7.65
3SE8.PDB	O, G_LYS_46	N, G_GLN_490	H, G_GLN_490	2.88	2.05	12.76
3SE8.PDB	O, H_SER_25	N, H_GLN_3	H, H_GLN_3	2.90	2.11	20.10
3SE8.PDB	O, H_ARG_23	N, H_VAL_5	H, H_VAL_5	2.88	2.06	15.74
3SE8.PDB	OE1, H_GLN_105	N, H_GLN_6	H, H_GLN_6	2.87	2.02	5.14
3SE8.PDB	O, H_TYR_90	NE2, H_GLN_6	HE22, H_GLN_6	2.89	2.04	7.71
3SE8.PDB	O, H_VAL_110	N, H_LYS_12	H, H_LYS_12	2.75	1.91	10.56
3SE8.PDB	O, H_LEU_82C	N, H_GLY_15	H, H_GLY_15	2.89	2.09	17.72

3SE8.PDB	O, H_THR_13	N, H_SER_16	H, H_SER_16	2.97	2.16	15.50
3SE8.PDB	O, H_PHE_82	N, H_VAL_18	H, H_VAL_18	2.79	1.98	16.37
3SE8.PDB	O, H_MET_80	N, H_ILE_20	H, H_ILE_20	2.76	1.91	7.97
3SE8.PDB	O, H_ALA_78	N, H_CYS_22	H, H_CYS_22	2.72	2.02	29.24
3SE8.PDB	O, H_VAL_5	N, H_ARG_23	H, H_ARG_23	2.79	1.98	14.71
3SE8.PDB	O, H_GLY_76G	N, H_ALA_24	H, H_ALA_24	2.79	1.93	5.97
3SE8.PDB	O, H_GLN_3	N, H_SER_25	H, H_SER_25	2.94	2.16	21.94
3SE8.PDB	O, H_ASP_76E	N, H_PHE_29	H, H_PHE_29	2.78	1.95	13.33
3SE8.PDB	O, H_ILE_51	N, H_ILE_34	H, H_ILE_34	3.00	2.20	18.68
3SE8.PDB	O, H_VAL_93	N, H_HIS_35	H, H_HIS_35	2.89	2.07	13.75
3SE8.PDB	O, H_GLY_49	N, H_TRP_36	H, H_TRP_36	2.94	2.13	16.16
3SE8.PDB	O, H_PHE_91	N, H_VAL_37	H, H_VAL_37	2.86	2.04	15.75
3SE8.PDB	O, H_GLU_46	N, H_ARG_38	H, H_ARG_38	2.88	2.04	10.56
3SE8.PDB	OE1, H_GLU_46	NH1, H_ARG_38	HH11, H_ARG_38	2.64	1.78	1.94
3SE8.PDB	OH, H_TYR_90	NH2, H_ARG_38	HH21, H_ARG_38	2.79	1.95	9.66
3SE8.PDB	OD1, H_ASP_86	NH2, H_ARG_38	HH22, H_ARG_38	2.67	1.83	8.41
3SE8.PDB	O, H_GLU_89	N, H_LEU_39	H, H_LEU_39	2.83	1.99	10.37
3SE8.PDB	O, H_GLY_44	N, H_ILE_40	H, H_ILE_40	2.78	1.93	4.45
3SE8.PDB	O, H_ILE_40	N, H_LYS_43	H, H_LYS_43	2.97	2.13	10.43
3SE8.PDB	O, H_ILE_40	N, H_GLY_44	H, H_GLY_44	2.89	2.10	18.47
3SE8.PDB	O, H_ARG_38	N, H_GLU_46	H, H_GLU_46	2.75	1.95	18.36
3SE8.PDB	O, H_TRP_36	N, H_ILE_48	H, H_ILE_48	2.84	1.99	6.89
3SE8.PDB	O, H_SER_58	N, H_TRP_50	H, H_TRP_50	2.96	2.22	26.23
3SE8.PDB	OD1, G_ASN_280	NE1, H_TRP_50	HE1, H_TRP_50	3.00	2.21	20.49
3SE8.PDB	O, H_ILE_34	N, H_ILE_51	H, H_ILE_51	2.93	2.15	20.77
3SE8.PDB	O, H_ALA_56	N, H_LYS_52	H, H_LYS_52	2.80	1.97	14.43
3SE8.PDB	O, G_GLY_473	NE1, H_TRP_54	HE1, H_TRP_54	2.82	1.98	10.03
3SE8.PDB	O, H_ILE_48	N, H_ALA_60	H, H_ALA_60	2.88	2.02	4.64
3SE8.PDB	O, G_GLY_458	N, H_ARG_61	H, H_ARG_61	2.91	2.08	12.24
3SE8.PDB	OE2, H_GLU_46	NE2, H_GLN_62	HE21, H_GLN_62	2.91	2.06	7.60
3SE8.PDB	O, H_ALA_60	N, H_LEU_63	H, H_LEU_63	2.83	1.99	9.80
3SE8.PDB	OD1, G_ASP_457	NE2, H_GLN_64	HE22, H_GLN_64	2.94	2.12	14.23
3SE8.PDB	O, H_LEU_63	N, H_ARG_66	H, H_ARG_66	2.92	2.10	15.21
3SE8.PDB	OD2, H_ASP_86	NH2, H_ARG_66	HH22, H_ARG_66	2.60	1.84	23.72
3SE8.PDB	O, H_GLU_81	N, H_SER_68	H, H_SER_68	2.93	2.16	21.80
3SE8.PDB	OH, H_TYR_59	N, H_MET_69	H, H_MET_69	2.92	2.08	11.45
3SE8.PDB	O, H_PRO_52A	NE, H_ARG_71	HE, H_ARG_71	2.71	2.00	28.51
3SE8.PDB	OD2, G_ASP_368	NH2, H_ARG_71	HH22, H_ARG_71	2.91	2.05	6.24
3SE8.PDB	O, H_VAL_77	N, H_GLN_72	H, H_GLN_72	2.77	1.96	16.92
3SE8.PDB	O, H_ASP_76C	OG, H_SER_74	HG, H_SER_74	2.69	1.89	9.03
3SE8.PDB	O, H_GLN_72	N, H_VAL_77	H, H_VAL_77	2.77	1.94	13.20
3SE8.PDB	O, H_CYS_22	N, H_ALA_78	H, H_ALA_78	2.93	2.10	11.74
3SE8.PDB	O, H_THR_70	N, H_TYR_79	H, H_TYR_79	2.81	1.96	9.20
3SE8.PDB	O, H_ILE_20	N, H_MET_80	H, H_MET_80	2.83	2.02	15.19
3SE8.PDB	O, H_SER_68	N, H_GLU_81	H, H_GLU_81	2.84	2.00	11.16
3SE8.PDB	O, H_VAL_18	N, H_PHE_82	H, H_PHE_82	2.77	1.96	15.74
3SE8.PDB	O, H_ARG_66	N, H_SER_82A	H, H_SER_82A	2.80	2.01	18.90
3SE8.PDB	OD2, H_ASP_86	N, H_THR_83	H, H_THR_83	2.93	2.13	19.14
3SE8.PDB	O, H_THR_83	N, H_ASP_86	H, H_ASP_86	2.81	1.97	9.27
3SE8.PDB	O, H_PRO_84	N, H_THR_87	H, H_THR_87	2.98	2.14	8.29
3SE8.PDB	O, H_THR_107	N, H_TYR_90	H, H_TYR_90	2.78	1.92	6.22
3SE8.PDB	O, H_VAL_37	N, H_PHE_91	H, H_PHE_91	2.68	1.83	4.53
3SE8.PDB	O, H_HIS_35	N, H_VAL_93	H, H_VAL_93	2.86	2.07	20.12
3SE8.PDB	O, H_TYR_102	N, H_ARG_94	H, H_ARG_94	2.96	2.18	21.24
3SE8.PDB	O, H_ARG_95	NE, H_ARG_94	HE, H_ARG_94	2.79	1.97	14.73
3SE8.PDB	OH, L_TYR_36	N, H_TRP_100F	H, H_TRP_100F	2.89	2.04	6.32
3SE8.PDB	O, H_CYS_92	N, H_CYS_104	H, H_CYS_104	2.93	2.08	5.94
3SE8.PDB	O, H_TYR_90	N, H_THR_107	H, H_THR_107	2.73	1.94	19.33

3SE8.PDB	O, H_ALA_88	N, H_VAL_109	H, H_VAL_109	2.95	2.10	5.90
3SE8.PDB	O, H_LYS_12	N, H_SER_112	H, H_SER_112	2.88	2.11	21.39
3SE8.PDB	OG, H_SER_112	N, H_ALA_114	H, H_ALA_114	2.93	2.08	8.21
3SE8.PDB	O, H_PHE_146	N, H_LYS_117	H, H_LYS_117	2.70	1.88	13.27
3SE8.PDB	O, H_ASP_144	NZ, H_LYS_117	HZ2, H_LYS_117	2.77	2.03	28.12
3SE8.PDB	O, H_LYS_143	N, H_SER_120	H, H_SER_120	2.76	1.96	18.99
3SE8.PDB	O, H_LEU_141	N, H_PHE_122	H, H_PHE_122	2.84	2.01	11.61
3SE8.PDB	O, H_GLY_139	N, H_LEU_124	H, H_LEU_124	2.75	1.90	4.08
3SE8.PDB	O, H_VAL_184	N, H_ALA_136	H, H_ALA_136	2.84	2.00	9.22
3SE8.PDB	O, H_LEU_124	N, H_GLY_139	H, H_GLY_139	2.85	2.13	28.46
3SE8.PDB	O, H_SER_180	N, H_CYS_140	H, H_CYS_140	2.74	1.94	18.37
3SE8.PDB	O, H_PHE_122	N, H_LEU_141	H, H_LEU_141	2.66	1.82	9.87
3SE8.PDB	O, H_LEU_178	N, H_VAL_142	H, H_VAL_142	2.68	1.85	13.60
3SE8.PDB	O, H_SER_120	N, H_LYS_143	H, H_LYS_143	2.76	1.90	5.34
3SE8.PDB	O, H_LYS_117	N, H_PHE_146	H, H_PHE_146	2.83	2.03	17.73
3SE8.PDB	O, H_ASN_199	N, H_THR_151	H, H_THR_151	2.89	2.07	15.54
3SE8.PDB	O, H_ASN_197	N, H_SER_153	H, H_SER_153	2.93	2.14	19.75
3SE8.PDB	OG, H_SER_180	NE1, H_TRP_154	HE1, H_TRP_154	2.94	2.09	7.62
3SE8.PDB	O, H_ILE_195	N, H_ASN_155	H, H_ASN_155	2.71	1.87	10.52
3SE8.PDB	OD1, H_ASN_197	N, H_SER_156	H, H_SER_156	2.66	1.83	13.48
3SE8.PDB	O, H_TRP_154	N, H_GLY_157	H, H_GLY_157	2.82	2.03	19.36
3SE8.PDB	O, H_VAL_181	N, H_HIS_164	H, H_HIS_164	2.78	1.96	13.60
3SE8.PDB	O, H_SER_179	N, H_PHE_166	H, H_PHE_166	2.99	2.15	9.97
3SE8.PDB	O, H_SER_177	N, H_VAL_169	H, H_VAL_169	2.82	1.98	12.77
3SE8.PDB	O, H_LEU_175	N, H_GLN_171	H, H_GLN_171	2.92	2.07	8.88
3SE8.PDB	OD1, H_ASP_144	NE2, H_GLN_171	HE22, H_GLN_171	2.79	1.98	16.20
3SE8.PDB	O, H_GLN_171	N, H_GLY_174	H, H_GLY_174	2.99	2.14	9.14
3SE8.PDB	O, H_TYR_145	N, H_TYR_176	H, H_TYR_176	2.78	1.96	14.03
3SE8.PDB	O, H_VAL_169	N, H_SER_177	H, H_SER_177	2.95	2.22	27.00
3SE8.PDB	O, H_VAL_142	N, H_LEU_178	H, H_LEU_178	2.89	2.07	14.62
3SE8.PDB	O, H_CYS_140	N, H_SER_180	H, H_SER_180	2.90	2.08	15.09
3SE8.PDB	O, H_HIS_164	N, H_VAL_181	H, H_VAL_181	2.92	2.09	11.34
3SE8.PDB	O, H_LEU_138	N, H_VAL_182	H, H_VAL_182	2.88	2.09	19.86
3SE8.PDB	O, H_ALA_136	N, H_VAL_184	H, H_VAL_184	2.91	2.10	16.13
3SE8.PDB	O, H_SER_188	N, H_GLN_192	H, H_GLN_192	2.74	1.90	10.09
3SE8.PDB	OD1, H_ASN_155	N, H_ILE_195	H, H_ILE_195	2.81	2.01	16.89
3SE8.PDB	O, H_LYS_209	N, H_CYS_196	H, H_CYS_196	2.96	2.16	17.85
3SE8.PDB	O, H_SER_153	N, H_ASN_197	H, H_ASN_197	2.75	1.91	9.58
3SE8.PDB	O, H_VAL_207	N, H_VAL_198	H, H_VAL_198	2.77	1.92	5.89
3SE8.PDB	O, H_THR_151	N, H_ASN_199	H, H_ASN_199	2.84	2.01	12.61
3SE8.PDB	O, H_THR_205	N, H_HIS_200	H, H_HIS_200	2.70	1.84	5.53
3SE8.PDB	OG, H_SER_203	ND1, H_HIS_200	HD1, H_HIS_200	2.45	1.61	10.75
3SE8.PDB	O, H_PRO_147	NE2, H_HIS_200	HE2, H_HIS_200	2.78	1.97	17.41
3SE8.PDB	O, H_LYS_201	N, H_ASN_204	H, H_ASN_204	2.85	2.06	18.91
3SE8.PDB	O, H_HIS_200	N, H_THR_205	H, H_THR_205	2.88	2.03	7.09
3SE8.PDB	O, H_VAL_198	N, H_VAL_207	H, H_VAL_207	2.80	1.98	15.00
3SE8.PDB	O, H_CYS_196	N, H_LYS_209	H, H_LYS_209	2.95	2.10	10.01
3SE8.PDB	O, H_TYR_194	N, H_VAL_211	H, H_VAL_211	2.83	1.97	6.68
3SE8.PDB	OG, L_SER_26	N, L_VAL_3	H, L_VAL_3	2.82	1.96	2.57
3SE8.PDB	O, L_LYS_24	N, L_THR_5	H, L_THR_5	2.89	2.05	11.05
3SE8.PDB	O, L_TYR_86	NE2, L_GLN_6	HE22, L_GLN_6	2.87	2.04	13.32
3SE8.PDB	O, L_GLU_103	N, L_LEU_11	H, L_LEU_11	2.80	1.97	11.47
3SE8.PDB	OE1, L_GLU_17	N, L_SER_14	H, L_SER_14	2.71	1.87	8.08
3SE8.PDB	O, L_LEU_78	N, L_GLY_16	H, L_GLY_16	2.93	2.19	25.85
3SE8.PDB	O, L_ILE_75	N, L_ALA_19	H, L_ALA_19	2.95	2.15	18.92
3SE8.PDB	O, L_LEU_73	N, L_LEU_21	H, L_LEU_21	2.86	2.04	13.81
3SE8.PDB	O, L_SER_7	N, L_PHE_22	H, L_PHE_22	2.87	2.02	8.84
3SE8.PDB	O, L_PHE_71	N, L_CYS_23	H, L_CYS_23	2.82	2.00	14.57

3SE8.PDB	O, L_THR_5	N, L_LYS_24	H, L_LYS_24	2.96	2.11	8.02
3SE8.PDB	OD1, L_ASP_70	NZ, L_LYS_24	HZ3, L_LYS_24	2.62	1.80	18.41
3SE8.PDB	O, L_THR_69	N, L_ALA_25	H, L_ALA_25	2.86	2.08	21.04
3SE8.PDB	OG1, L_THR_51	N, L_MET_33	H, L_MET_33	2.91	2.13	21.08
3SE8.PDB	O, L_ILE_48	N, L_TRP_35	H, L_TRP_35	2.90	2.11	18.66
3SE8.PDB	O, L_TYR_87	N, L_TYR_36	H, L_TYR_36	2.80	1.98	13.67
3SE8.PDB	O, L_ARG_45	N, L_GLN_37	H, L_GLN_37	2.76	1.94	13.35
3SE8.PDB	OH, L_TYR_86	NE2, L_GLN_37	HE21, L_GLN_37	2.98	2.15	12.85
3SE8.PDB	O, L_VAL_85	N, L_LYS_38	H, L_LYS_38	2.76	1.91	8.80
3SE8.PDB	O, L_ARG_39	N, L_GLN_42	H, L_GLN_42	2.97	2.15	14.92
3SE8.PDB	O, L_GLN_37	N, L_ARG_45	H, L_ARG_45	2.81	2.02	18.98
3SE8.PDB	O, L_TRP_35	N, L_LEU_47	H, L_LEU_47	2.85	1.99	4.76
3SE8.PDB	O, L_ARG_53	N, L_TYR_49	H, L_TYR_49	2.85	2.04	17.02
3SE8.PDB	O, L_MET_33	N, L_THR_51	H, L_THR_51	2.77	1.98	19.97
3SE8.PDB	O, L_ASP_50	N, L_SER_52	H, L_SER_52	2.85	2.14	29.05
3SE8.PDB	O, L_TYR_49	N, L_ARG_53	H, L_ARG_53	2.91	2.09	16.37
3SE8.PDB	OD2, L_ASP_50	NE, L_ARG_53	HE, L_ARG_53	2.87	2.02	8.47
3SE8.PDB	O, L_VAL_58	NH1, L_ARG_54	HH11, L_ARG_54	2.73	1.98	24.33
3SE8.PDB	O, L_LEU_47	N, L_ALA_55	H, L_ALA_55	2.80	1.97	13.40
3SE8.PDB	OE1, H_GLN_101	N, L_SER_56	H, L_SER_56	2.97	2.12	7.63
3SE8.PDB	OD2, L_ASP_82	NE, L_ARG_61	HE, L_ARG_61	2.91	2.18	26.35
3SE8.PDB	OD1, L_ASP_82	NH2, L_ARG_61	HH21, L_ARG_61	2.77	1.91	2.48
3SE8.PDB	O, L_THR_74	N, L_VAL_63	H, L_VAL_63	2.77	1.99	20.80
3SE8.PDB	O, L_ASP_70	N, L_SER_67	H, L_SER_67	2.93	2.14	19.36
3SE8.PDB	O, L_CYS_23	N, L_PHE_71	H, L_PHE_71	2.87	2.10	23.31
3SE8.PDB	O, L_SER_65	N, L_PHE_72	H, L_PHE_72	2.87	2.05	15.57
3SE8.PDB	O, L_LEU_21	N, L_LEU_73	H, L_LEU_73	2.88	2.10	20.44
3SE8.PDB	O, L_VAL_63	N, L_THR_74	H, L_THR_74	2.77	1.92	5.55
3SE8.PDB	O, L_ALA_19	N, L_ILE_75	H, L_ILE_75	2.87	2.05	14.86
3SE8.PDB	O, L_ARG_61	N, L_ASN_76	H, L_ASN_76	2.80	1.97	11.69
3SE8.PDB	O, L_GLU_17	N, L_LEU_78	H, L_LEU_78	2.85	2.02	13.66
3SE8.PDB	OD2, L_ASP_82	N, L_ASP_79	H, L_ASP_79	2.69	1.83	4.70
3SE8.PDB	OD2, L_ASP_79	N, L_GLU_81	H, L_GLU_81	2.90	2.04	2.10
3SE8.PDB	O, L_ASP_79	N, L_ASP_82	H, L_ASP_82	2.84	2.00	9.57
3SE8.PDB	O, L_SER_102	N, L_TYR_86	H, L_TYR_86	2.84	2.02	14.87
3SE8.PDB	O, L_TYR_36	N, L_TYR_87	H, L_TYR_87	2.95	2.14	16.13
3SE8.PDB	O, L_THR_34	N, L_GLN_89	H, L_GLN_89	2.91	2.20	29.11
3SE8.PDB	O, L_PHE_97	N, L_GLN_90	H, L_GLN_90	2.96	2.20	22.66
3SE8.PDB	O, L_GLN_90	N, L_PHE_97	H, L_PHE_97	2.91	2.07	11.26
3SE8.PDB	O, L_CYS_88	N, L_GLY_99	H, L_GLY_99	2.90	2.07	12.93
3SE8.PDB	OE1, L_GLN_6	N, L_GLY_101	H, L_GLY_101	2.82	2.11	29.29
3SE8.PDB	O, L_TYR_86	N, L_SER_102	H, L_SER_102	2.87	2.06	17.39
3SE8.PDB	O, L_GLY_9	N, L_GLU_103	H, L_GLU_103	2.90	2.06	7.87
3SE8.PDB	O, L_ALA_84	N, L_LEU_104	H, L_LEU_104	2.85	2.00	5.96
3SE8.PDB	O, L_LEU_11	N, L_GLU_105	H, L_GLU_105	2.77	1.92	5.93
3SE8.PDB	O, L_LEU_13	N, L_HIS_107	H, L_HIS_107	2.81	1.97	8.56
3SE8.PDB	O, L_THR_109	NE, L_ARG_108	HE, L_ARG_108	2.88	2.04	10.14
3SE8.PDB	O, L_ASP_170	NH1, L_ARG_108	HH11, L_ARG_108	2.96	2.12	9.70
3SE8.PDB	O, L_TYR_140	N, L_ALA_111	H, L_ALA_111	2.78	1.95	13.81
3SE8.PDB	O, L_LEU_135	N, L_PHE_116	H, L_PHE_116	2.96	2.16	19.15
3SE8.PDB	O, L_VAL_133	N, L_PHE_118	H, L_PHE_118	2.81	2.01	18.69
3SE8.PDB	OG, L_SER_131	NE2, L_GLN_124	HE22, L_GLN_124	2.53	1.70	11.07
3SE8.PDB	O, L_ASP_122	N, L_LYS_126	H, L_LYS_126	2.78	1.93	8.17
3SE8.PDB	O, L_GLN_124	N, L_SER_127	H, L_SER_127	2.84	2.04	18.54
3SE8.PDB	O, L_LEU_125	N, L_GLY_128	H, L_GLY_128	2.82	1.97	6.06
3SE8.PDB	O, L_LEU_181	N, L_ALA_130	H, L_ALA_130	2.63	1.79	9.50
3SE8.PDB	OE1, L_GLN_124	N, L_SER_131	H, L_SER_131	2.86	2.08	21.14
3SE8.PDB	O, L_LEU_179	N, L_VAL_132	H, L_VAL_132	2.81	1.96	9.07

3SE8.PDB	O, L.SER.177	N, L.CYS.134	H, L.CYS.134	2.82	1.99	11.76
3SE8.PDB	O, L.PHE.116	N, L.LEU.135	H, L.LEU.135	2.83	2.00	13.84
3SE8.PDB	O, L.LEU.175	N, L.LEU.136	H, L.LEU.136	2.76	1.91	3.24
3SE8.PDB	O, L.SER.114	N, L.ASN.137	H, L.ASN.137	2.82	1.98	11.18
3SE8.PDB	O, L.TYR.173	N, L.PHE.139	H, L.PHE.139	2.79	1.99	16.94
3SE8.PDB	O, L.ALA.111	N, L.TYR.140	H, L.TYR.140	2.99	2.17	14.53
3SE8.PDB	OE2, L.GLU.103	NH2, L.ARG.142	HH22, L.ARG.142	2.84	2.00	11.39
3SE8.PDB	O, L.THR.197	N, L.LYS.145	H, L.LYS.145	2.99	2.15	9.49
3SE8.PDB	O, L.GLU.195	N, L.GLN.147	H, L.GLN.147	2.92	2.09	11.46
3SE8.PDB	OE1, L.GLU.195	NE2, L.GLN.147	HE21, L.GLN.147	2.66	1.93	26.32
3SE8.PDB	OG, L.SER.177	NE1, L.TRP.148	HE1, L.TRP.148	2.88	2.08	18.18
3SE8.PDB	O, L.ALA.193	N, L.LYS.149	H, L.LYS.149	2.82	1.98	10.28
3SE8.PDB	O, L.ALA.153	N, L.VAL.150	H, L.VAL.150	2.96	2.16	18.37
3SE8.PDB	O, L.VAL.191	N, L.ASP.151	H, L.ASP.151	2.77	1.95	13.90
3SE8.PDB	O, L.TRP.148	N, L.GLN.155	H, L.GLN.155	2.82	1.99	12.31
3SE8.PDB	O, L.ALA.153	NE2, L.GLN.155	HE21, L.GLN.155	2.94	2.12	14.25
3SE8.PDB	O, L.SER.176	N, L.SER.162	H, L.SER.162	2.99	2.21	20.46
3SE8.PDB	O, H.PRO.167	OG, L.SER.162	HG, L.SER.162	2.71	1.98	23.05
3SE8.PDB	O, L.SER.174	N, L.THR.164	H, L.THR.164	2.92	2.10	13.88
3SE8.PDB	O, L.SER.171	NE2, L.GLN.166	HE21, L.GLN.166	2.94	2.11	13.32
3SE8.PDB	O, L.VAL.106	NE2, L.GLN.166	HE22, L.GLN.166	2.84	2.02	15.85
3SE8.PDB	O, L.THR.172	N, L.ASP.167	H, L.ASP.167	2.84	1.99	3.58
3SE8.PDB	OD2, L.ASP.167	N, L.LYS.169	H, L.LYS.169	2.88	2.07	16.82
3SE8.PDB	OD2, L.ASP.167	N, L.ASP.170	H, L.ASP.170	2.87	2.05	15.65
3SE8.PDB	OD1, L.ASP.170	N, L.THR.172	H, L.THR.172	2.93	2.11	15.74
3SE8.PDB	OD1, L.ASP.170	OG1, L.THR.172	HG1, L.THR.172	2.49	1.68	7.38
3SE8.PDB	O, L.PHE.139	N, L.TYR.173	H, L.TYR.173	2.84	2.00	11.94
3SE8.PDB	OG1, L.THR.164	N, L.SER.174	H, L.SER.174	2.99	2.17	15.57
3SE8.PDB	O, L.LEU.136	N, L.LEU.175	H, L.LEU.175	2.83	2.02	17.07
3SE8.PDB	O, L.SER.162	N, L.SER.176	H, L.SER.176	2.98	2.17	16.25
3SE8.PDB	O, L.CYS.134	N, L.SER.177	H, L.SER.177	2.87	2.05	14.69
3SE8.PDB	O, L.GLN.160	N, L.THR.178	H, L.THR.178	2.92	2.11	17.07
3SE8.PDB	O, L.VAL.132	N, L.LEU.179	H, L.LEU.179	2.77	2.01	22.55
3SE8.PDB	O, L.ASN.158	N, L.THR.180	H, L.THR.180	2.97	2.13	11.98
3SE8.PDB	O, L.ALA.130	N, L.LEU.181	H, L.LEU.181	2.83	1.98	9.00
3SE8.PDB	O, L.GLY.128	N, L.LYS.183	H, L.LYS.183	2.93	2.10	13.14
3SE8.PDB	O, L.SER.182	N, L.TYR.186	H, L.TYR.186	2.84	2.00	10.56
3SE8.PDB	O, L.LYS.183	N, L.GLU.187	H, L.GLU.187	2.94	2.13	17.20
3SE8.PDB	OD1, L.ASP.151	N, L.VAL.191	H, L.VAL.191	2.92	2.06	1.84
3SE8.PDB	O, L.PHE.209	N, L.TYR.192	H, L.TYR.192	2.97	2.12	6.17
3SE8.PDB	O, L.LYS.149	N, L.ALA.193	H, L.ALA.193	2.91	2.16	23.94
3SE8.PDB	O, L.LYS.207	N, L.CYS.194	H, L.CYS.194	2.97	2.16	16.78
3SE8.PDB	O, L.GLN.147	N, L.GLU.195	H, L.GLU.195	2.83	1.99	10.05
3SE8.PDB	O, L.VAL.205	N, L.VAL.196	H, L.VAL.196	2.74	1.90	10.53
3SE8.PDB	O, L.LYS.145	N, L.THR.197	H, L.THR.197	2.83	2.01	13.35
3SE8.PDB	O, L.PRO.141	NE2, L.HIS.198	HE2, L.HIS.198	2.98	2.16	13.12
3SE8.PDB	ND1, L.HIS.198	N, L.GLY.200	H, L.GLY.200	2.98	2.13	8.19
3SE8.PDB	O, L.HIS.198	N, L.LEU.201	H, L.LEU.201	2.88	2.03	8.01
3SE8.PDB	O, L.VAL.196	N, L.VAL.205	H, L.VAL.205	2.94	2.17	21.99
3SE8.PDB	O, L.TYR.192	N, L.PHE.209	H, L.PHE.209	2.99	2.20	20.60
3SE8.PDB	O, L.LYS.190	N, L.ARG.211	H, L.ARG.211	2.70	1.88	14.42
3SE8.PDB	O, L.HIS.189	NE, L.ARG.211	HE, L.ARG.211	2.74	1.90	11.40
3SE9.PDB	OE1, G.GLN.103	N, G.LEU.52	H, G.LEU.52	2.89	2.03	2.17
3SE9.PDB	O, G.CYS.218	N, G.PHE.53	H, G.PHE.53	2.97	2.17	17.99
3SE9.PDB	O, G.HIS.216	N, G.ALA.55	H, G.ALA.55	2.87	2.11	23.70
3SE9.PDB	O, G.VAL.75	N, G.SER.56	H, G.SER.56	2.93	2.15	21.60
3SE9.PDB	OG, G.SER.56	N, G.ALA.58	H, G.ALA.58	2.98	2.14	10.37
3SE9.PDB	OD1, G.ASN.67	N, G.LYS.59	H, G.LYS.59	2.90	2.07	12.58

3SE9.PDB	OE2, G_GLU_62	N, G_GLU_64	H, G_GLU_64	2.88	2.04	11.06
3SE9.PDB	O, G_SER_209	N, G_VAL_65	H, G_VAL_65	2.97	2.18	19.43
3SE9.PDB	OE2, G_GLU_64	ND1, G_HIS_66	HD1, G_HIS_66	2.73	1.88	8.47
3SE9.PDB	OE1, G_GLU_64	N, G_ASN_67	H, G_ASN_67	2.81	1.99	14.35
3SE9.PDB	OE1, G_GLU_64	ND2, G_ASN_67	HD21, G_ASN_67	2.83	2.01	14.03
3SE9.PDB	O, G_VAL_65	N, G_TRP_69	H, G_TRP_69	2.98	2.13	9.76
3SE9.PDB	O, G_HIS_66	N, G_ALA_70	H, G_ALA_70	2.90	2.08	14.89
3SE9.PDB	O, G_ASN_67	N, G_THR_71	H, G_THR_71	2.96	2.22	26.00
3SE9.PDB	O, G_TRP_69	N, G_ALA_73	H, G_ALA_73	2.87	2.02	9.06
3SE9.PDB	O, G_ALA_70	N, G_CYS_74	H, G_CYS_74	2.89	2.10	19.93
3SE9.PDB	O, G_CYS_54	N, G_VAL_75	H, G_VAL_75	2.97	2.15	14.48
3SE9.PDB	OD2, G_ASP_78	N, G_ASN_80	H, G_ASN_80	2.89	2.12	23.01
3SE9.PDB	O, G_SER_244	N, G_ILE_84	H, G_ILE_84	2.90	2.12	20.23
3SE9.PDB	O, G_VAL_242	N, G_LEU_86	H, G_LEU_86	2.84	1.98	4.71
3SE9.PDB	O, G_GLY_237	N, G_PHE_93	H, G_PHE_93	2.80	1.98	13.97
3SE9.PDB	O, G_GLY_235	N, G_MET_95	H, G_MET_95	2.84	2.07	22.25
3SE9.PDB	O, G_ASN_98	N, G_VAL_101	H, G_VAL_101	2.89	2.09	18.37
3SE9.PDB	OD1, G_ASN_99	NE2, G_GLN_103	HE21, G_GLN_103	2.75	1.96	19.57
3SE9.PDB	O, G_THR_50	NE2, G_GLN_103	HE22, G_GLN_103	2.73	1.94	19.46
3SE9.PDB	O, G_VAL_101	N, G_GLN_105	H, G_GLN_105	2.94	2.12	13.43
3SE9.PDB	O, G_MET_104	N, G_VAL_108	H, G_VAL_108	2.99	2.15	12.10
3SE9.PDB	O, G_GLN_105	N, G_ILE_109	H, G_ILE_109	2.94	2.09	6.88
3SE9.PDB	O, G_GLU_106	N, G_SER_110	H, G_SER_110	2.94	2.14	17.70
3SE9.PDB	O, G_ASP_107	N, G_LEU_111	H, G_LEU_111	2.78	1.94	10.68
3SE9.PDB	O, G_VAL_108	N, G_TRP_112	H, G_TRP_112	2.98	2.14	9.89
3SE9.PDB	O, G_ILE_109	N, G_ASP_113	H, G_ASP_113	2.94	2.20	25.93
3SE9.PDB	O, G_TRP_112	N, G_LEU_116	H, G_LEU_116	2.84	2.03	15.60
3SE9.PDB	O, G_ILE_201	N, G_LYS_121	H, G_LYS_121	2.90	2.06	12.24
3SE9.PDB	OE1, G_GLN_117	NZ, G_LYS_121	HZ3, G_LYS_121	2.58	1.83	27.32
3SE9.PDB	O, G_GLN_432	N, G_LEU_122	H, G_LEU_122	2.88	2.03	6.48
3SE9.PDB	O, G_LYS_121	N, G_ILE_201	H, G_ILE_201	2.95	2.11	10.92
3SE9.PDB	O, G_PRO_437	NZ, G_LYS_207	HZ2, G_LYS_207	2.83	2.09	27.83
3SE9.PDB	OE2, G_GLU_64	N, G_ASP_211	H, G_ASP_211	2.75	1.90	8.78
3SE9.PDB	O, G_ILE_251	N, G_ILE_215	H, G_ILE_215	2.82	1.98	12.02
3SE9.PDB	O, G_ALA_55	N, G_HIS_216	H, G_HIS_216	2.77	1.91	2.26
3SE9.PDB	OG1, G_THR_248	N, G_TYR_217	H, G_TYR_217	2.95	2.09	2.54
3SE9.PDB	O, G_PHE_53	N, G_CYS_218	H, G_CYS_218	2.85	2.07	20.62
3SE9.PDB	O, G_VAL_489	N, G_VAL_224	H, G_VAL_224	2.98	2.16	15.19
3SE9.PDB	O, G_LYS_487	N, G_LEU_226	H, G_LEU_226	2.88	2.08	18.00
3SE9.PDB	O, G_SER_243	N, G_LYS_227	H, G_LYS_227	2.60	1.80	16.43
3SE9.PDB	O, G_LYS_485	N, G_CYS_228	H, G_CYS_228	2.85	2.03	14.69
3SE9.PDB	O, G_ASN_241	N, G_ASN_229	H, G_ASN_229	2.78	1.96	14.08
3SE9.PDB	O, G_PHE_93	N, G_GLY_237	H, G_GLY_237	2.96	2.25	29.34
3SE9.PDB	O, G_GLU_91	N, G_CYS_239	H, G_CYS_239	2.74	2.00	26.00
3SE9.PDB	OD2, G_ASP_230	N, G_LYS_240	H, G_LYS_240	2.84	2.00	11.61
3SE9.PDB	OD1, G_ASP_230	N, G_ASN_241	H, G_ASN_241	2.75	2.01	25.57
3SE9.PDB	O, G_LYS_227	N, G_SER_243	H, G_SER_243	2.98	2.15	13.38
3SE9.PDB	OE2, G_GLU_83	OG, G_SER_243	HG, G_SER_243	2.65	1.89	17.63
3SE9.PDB	O, G_ILE_84	N, G_SER_244	H, G_SER_244	2.82	2.02	19.32
3SE9.PDB	O, G_ILE_225	N, G_VAL_245	H, G_VAL_245	2.83	2.01	13.24
3SE9.PDB	O, G_TYR_217	N, G_THR_248	H, G_THR_248	2.73	1.92	16.59
3SE9.PDB	OH, G_TYR_486	ND1, G_HIS_249	HD1, G_HIS_249	2.73	1.91	13.84
3SE9.PDB	O, G_ILE_215	N, G_ILE_251	H, G_ILE_251	2.80	1.94	2.64
3SE9.PDB	O, G_LYS_252	N, G_VAL_254	H, G_VAL_254	2.91	2.20	29.72
3SE9.PDB	O, G_HIS_375	N, G_THR_257	H, G_THR_257	3.00	2.26	26.89
3SE9.PDB	O, G_GLU_370	OG1, G_THR_257	HG1, G_THR_257	2.66	1.88	15.46
3SE9.PDB	O, G_ILE_371	NE2, G_GLN_258	HE22, G_GLN_258	2.86	2.01	8.57
3SE9.PDB	O, G_THR_257	N, G_LEU_259	H, G_LEU_259	2.60	1.87	26.09

3SE9.PDB	O, G_GLY_451	N, G_LEU_260	H, G_LEU_260	2.95	2.15	18.25
3SE9.PDB	O, G_ASN_448	N, G_ASN_262	H, G_ASN_262	2.69	1.86	13.26
3SE9.PDB	OE2, G_GLU_482	N, G_SER_264	H, G_SER_264	2.65	1.82	11.12
3SE9.PDB	O, G_LEU_288	N, G_ALA_266	H, G_ALA_266	2.85	2.12	26.29
3SE9.PDB	O, G_ILE_285	N, G_ARG_273	H, G_ARG_273	2.81	2.03	21.22
3SE9.PDB	O, G_ASN_276	N, G_ASN_279	H, G_ASN_279	2.76	1.96	18.81
3SE9.PDB	OD1, G_ASN_279	N, G_ALA_281	H, G_ALA_281	2.99	2.19	18.54
3SE9.PDB	O, G_ASN_279	N, G_LYS_282	H, G_LYS_282	2.89	2.04	7.99
3SE9.PDB	O, G_LEU_454	N, G_ILE_284	H, G_ILE_284	2.90	2.04	2.40
3SE9.PDB	O, G_ARG_273	N, G_ILE_285	H, G_ILE_285	2.83	1.99	11.82
3SE9.PDB	O, G_ILE_452	N, G_VAL_286	H, G_VAL_286	2.83	1.98	5.93
3SE9.PDB	O, G_ILE_271	N, G_HIS_287	H, G_HIS_287	2.81	1.96	6.79
3SE9.PDB	O, G_SER_264	NE2, G_HIS_287	HE2, G_HIS_287	2.74	1.92	14.77
3SE9.PDB	O, G_THR_450	N, G_LEU_288	H, G_LEU_288	3.00	2.19	16.95
3SE9.PDB	O, G_SER_447	N, G_ILE_294	H, G_ILE_294	2.94	2.13	15.34
3SE9.PDB	O, G_GLU_332	N, G_ASN_295	H, G_ASN_295	2.88	2.07	17.19
3SE9.PDB	O, G_TYR_330	N, G_THR_297	H, G_THR_297	2.76	1.95	15.38
3SE9.PDB	O, G_ILE_443	N, G_ARG_298	H, G_ARG_298	2.81	1.99	16.03
3SE9.PDB	O, G_ILE_326	NH1, G_ARG_298	HH11, G_ARG_298	2.73	1.91	14.56
3SE9.PDB	O, G_GLY_441	NH2, G_ARG_298	HH21, G_ARG_298	2.64	1.78	1.00
3SE9.PDB	O, G_ILE_439	NH2, G_ARG_298	HH22, G_ARG_298	2.74	1.95	20.11
3SE9.PDB	OD1, G_ASP_325	N, G_ARG_327	H, G_ARG_327	2.97	2.13	12.25
3SE9.PDB	OE1, G_GLN_422	NH1, G_ARG_327	HH11, G_ARG_327	2.62	1.84	19.91
3SE9.PDB	O, G_THR_297	N, G_TYR_330	H, G_TYR_330	2.97	2.18	20.21
3SE9.PDB	O, G_LEU_416	N, G_CYS_331	H, G_CYS_331	2.98	2.20	20.74
3SE9.PDB	O, G_ASN_295	N, G_GLU_332	H, G_GLU_332	2.81	1.99	12.99
3SE9.PDB	O, G_ILE_414	N, G_ILE_333	H, G_ILE_333	2.98	2.19	19.45
3SE9.PDB	O, G_ASN_334	N, G_TRP_338	H, G_TRP_338	2.98	2.12	4.45
3SE9.PDB	O, G_LEU_390	NE1, G_TRP_338	HE1, G_TRP_338	2.40	1.59	15.54
3SE9.PDB	O, G_GLY_335	N, G_ASN_339	H, G_ASN_339	2.97	2.13	11.25
3SE9.PDB	O, G_TRP_338	N, G_LEU_342	H, G_LEU_342	2.95	2.13	14.49
3SE9.PDB	O, G_ASN_339	N, G_LYS_343	H, G_LYS_343	2.90	2.16	25.67
3SE9.PDB	O, G_VAL_341	N, G_VAL_345	H, G_VAL_345	2.84	2.07	22.06
3SE9.PDB	O, G_GLN_344	N, G_LYS_348	H, G_LYS_348	2.93	2.17	23.65
3SE9.PDB	O, G_VAL_345	N, G_LEU_349	H, G_LEU_349	2.90	2.08	13.64
3SE9.PDB	O, G_THR_346	N, G_LYS_350	H, G_LYS_350	2.84	2.03	16.44
3SE9.PDB	O, G_LEU_349	N, G_HIS_352	H, G_HIS_352	2.89	2.18	29.71
3SE9.PDB	O, G_LYS_350	N, G_ASN_355	H, G_ASN_355	2.78	1.99	18.73
3SE9.PDB	O, G_PHE_353	N, G_LYS_357	H, G_LYS_357	2.82	1.98	9.00
3SE9.PDB	O, G_GLU_466	N, G_ILE_360	H, G_ILE_360	2.86	2.07	19.89
3SE9.PDB	OD1, G_ASN_393	N, G_PHE_361	H, G_PHE_361	2.87	2.02	7.09
3SE9.PDB	O, G_PHE_468	N, G_GLN_362	H, G_GLN_362	2.86	2.06	18.17
3SE9.PDB	O, G_PHE_361	NE2, G_GLN_362	HE22, G_GLN_362	2.61	1.80	15.95
3SE9.PDB	O, H_THR_53	N, G_ASP_368	H, G_ASP_368	2.97	2.15	15.24
3SE9.PDB	O, G_ASP_368	N, G_ILE_371	H, G_ILE_371	2.96	2.14	15.47
3SE9.PDB	O, G_ASP_368	N, G_THR_372	H, G_THR_372	2.96	2.15	17.04
3SE9.PDB	O, G_CYS_385	N, G_HIS_374	H, G_HIS_374	2.80	2.04	23.10
3SE9.PDB	O, G_THR_257	ND1, G_HIS_374	HD1, G_HIS_374	2.94	2.14	18.49
3SE9.PDB	O, G_GLU_381	N, G_CYS_378	H, G_CYS_378	2.81	2.03	21.46
3SE9.PDB	O, G_CYS_378	N, G_GLU_381	H, G_GLU_381	2.91	2.07	11.74
3SE9.PDB	O, G_PHE_376	N, G_PHE_383	H, G_PHE_383	2.77	1.93	9.82
3SE9.PDB	O, G_LYS_419	N, G_TYR_384	H, G_TYR_384	2.88	2.12	23.39
3SE9.PDB	O, G_HIS_374	N, G_CYS_385	H, G_CYS_385	2.82	2.01	16.28
3SE9.PDB	OD1, G_ASN_386	N, G_THR_388	H, G_THR_388	2.98	2.13	7.03
3SE9.PDB	O, G_THR_415	NE2, G_GLN_389	HE21, G_GLN_389	2.67	1.89	20.77
3SE9.PDB	O, G_THR_387	N, G_LEU_390	H, G_LEU_390	2.79	2.00	19.51
3SE9.PDB	O, G_PHE_361	ND2, G_ASN_393	HD21, G_ASN_393	2.74	1.88	3.74
3SE9.PDB	O, G_ILE_333	N, G_ILE_414	H, G_ILE_414	2.79	1.93	6.04

3SE9.PDB	O, G_CYS_331	N, G_LEU_416	H, G_LEU_416	2.86	2.03	11.55
3SE9.PDB	O, G_ALA_329	N, G_CYS_418	H, G_CYS_418	2.84	2.00	9.75
3SE9.PDB	O, G_TYR_384	N, G_LYS_419	H, G_LYS_419	2.88	2.10	21.78
3SE9.PDB	O, G_ARG_327	N, G_ILE_420	H, G_ILE_420	2.87	2.06	16.89
3SE9.PDB	O, G_ALA_433	N, G_ILE_424	H, G_ILE_424	2.96	2.14	15.31
3SE9.PDB	OE2, G_GLU_370	N, G_ASN_425	H, G_ASN_425	2.82	1.97	7.07
3SE9.PDB	OE1, G_GLU_370	ND2, G_ASN_425	HD21, G_ASN_425	2.86	2.02	9.78
3SE9.PDB	O, G_GLY_431	N, G_MET_426	H, G_MET_426	2.79	1.93	2.68
3SE9.PDB	O, G_MET_426	N, G_GLY_429	H, G_GLY_429	2.72	1.88	8.66
3SE9.PDB	O, G_ILE_424	N, G_ALA_433	H, G_ALA_433	2.93	2.10	11.85
3SE9.PDB	O, G_VAL_120	N, G_MET_434	H, G_MET_434	2.93	2.19	26.00
3SE9.PDB	O, G_GLN_422	N, G_TYR_435	H, G_TYR_435	2.67	1.86	16.15
3SE9.PDB	O, G_ARG_298	N, G_ILE_443	H, G_ILE_443	2.97	2.13	10.43
3SE9.PDB	OD1, G_ASN_295	ND2, G_ASN_444	HD21, G_ASN_444	2.93	2.17	24.18
3SE9.PDB	OG1, G_THR_297	ND2, G_ASN_444	HD22, G_ASN_444	2.97	2.23	26.41
3SE9.PDB	O, G_ILE_294	N, G_SER_447	H, G_SER_447	2.99	2.16	12.03
3SE9.PDB	O, G_VAL_292	N, G_ILE_449	H, G_ILE_449	2.90	2.05	8.11
3SE9.PDB	O, G_VAL_286	N, G_ILE_452	H, G_ILE_452	2.96	2.20	22.66
3SE9.PDB	O, G_GLN_258	N, G_LEU_453	H, G_LEU_453	2.91	2.06	4.64
3SE9.PDB	O, G_ILE_284	N, G_LEU_454	H, G_LEU_454	2.88	2.08	17.98
3SE9.PDB	O, G_ARG_469	N, G_THR_455	H, G_THR_455	2.88	2.05	12.96
3SE9.PDB	OE2, G_GLU_466	NH1, G_ARG_456	HH11, G_ARG_456	2.71	1.88	12.87
3SE9.PDB	O, G_THR_467	N, G_ASP_457	H, G_ASP_457	2.81	1.96	8.69
3SE9.PDB	O, G_THR_358	N, G_GLU_466	H, G_GLU_466	2.63	1.83	17.35
3SE9.PDB	O, G_ILE_360	N, G_PHE_468	H, G_PHE_468	2.76	1.94	14.82
3SE9.PDB	O, G_THR_455	N, G_ARG_469	H, G_ARG_469	2.95	2.15	17.67
3SE9.PDB	O, G_LEU_453	N, G_GLY_471	H, G_GLY_471	2.80	2.02	20.51
3SE9.PDB	OE1, G_GLN_105	NE1, G_TRP_479	HE1, G_TRP_479	2.69	1.89	17.56
3SE9.PDB	O, G_LYS_476	N, G_ARG_480	H, G_ARG_480	2.94	2.14	18.76
3SE9.PDB	O, G_ASP_477	N, G_SER_481	H, G_SER_481	2.99	2.25	26.30
3SE9.PDB	O, G_TRP_479	N, G_LEU_483	H, G_LEU_483	2.82	2.04	21.47
3SE9.PDB	O, G_LEU_483	N, G_TYR_486	H, G_TYR_486	2.94	2.11	13.26
3SE9.PDB	O, G_ASN_92	NZ, G_LYS_487	HZ2, G_LYS_487	2.93	2.06	7.72
3SE9.PDB	OE1, G_GLU_91	NZ, G_LYS_487	HZ3, G_LYS_487	2.63	1.86	24.78
3SE9.PDB	O, G_VAL_224	N, G_VAL_489	H, G_VAL_489	2.96	2.10	4.39
3SE9.PDB	O, G_LYS_46	N, G_GLN_490	H, G_GLN_490	2.80	1.98	15.13
3SE9.PDB	O, G_GLY_222	N, G_ILE_491	H, G_ILE_491	2.99	2.20	21.02
3SE9.PDB	O, G_VAL_44	N, G_GLU_492	H, G_GLU_492	2.87	2.09	21.24
3SE9.PDB	O, H_TRP_23	N, H_VAL_5	H, H_VAL_5	2.93	2.09	11.74
3SE9.PDB	O, H_TYR_90	NE2, H_GLN_6	HE21, H_GLN_6	2.96	2.10	4.89
3SE9.PDB	O, H_LEU_108	N, H_GLY_10	H, H_GLY_10	2.94	2.16	21.74
3SE9.PDB	O, H_VAL_110	N, H_LYS_12	H, H_LYS_12	2.90	2.09	15.31
3SE9.PDB	O, H_LEU_82C	N, H_GLY_15	H, H_GLY_15	2.64	1.84	17.68
3SE9.PDB	O, H_ILE_82	N, H_VAL_18	H, H_VAL_18	2.83	2.05	20.43
3SE9.PDB	OD1, H_ASP_81	NE, H_ARG_19	HE, H_ARG_19	2.75	1.91	10.76
3SE9.PDB	O, H_MET_80	N, H_VAL_20	H, H_VAL_20	2.85	2.01	10.21
3SE9.PDB	OG, H_SER_7	N, H_SER_21	H, H_SER_21	2.77	1.92	7.84
3SE9.PDB	O, H_VAL_5	N, H_TRP_23	H, H_TRP_23	2.93	2.15	21.94
3SE9.PDB	O, H_SER_25	N, H_PHE_29	H, H_PHE_29	2.88	2.03	6.53
3SE9.PDB	O, H_GLU_26	N, H_GLU_30	H, H_GLU_30	2.87	2.05	15.53
3SE9.PDB	O, H_GLN_95	N, H_GLU_33	H, H_GLU_33	2.91	2.13	21.88
3SE9.PDB	O, H_VAL_51	N, H_ILE_35	H, H_ILE_35	2.94	2.15	19.12
3SE9.PDB	O, H_ALA_93	N, H_HIS_35A	H, H_HIS_35A	2.77	1.93	10.56
3SE9.PDB	O, H_GLY_49	N, H_TRP_36	H, H_TRP_36	2.93	2.09	11.34
3SE9.PDB	O, H_PHE_91	N, H_VAL_37	H, H_VAL_37	2.94	2.12	14.35
3SE9.PDB	O, H_GLU_46	N, H_ARG_38	H, H_ARG_38	2.93	2.12	16.03
3SE9.PDB	OH, H_TYR_90	NH1, H_ARG_38	HH11, H_ARG_38	2.99	2.21	21.73
3SE9.PDB	OD1, H_ASP_86	NH1, H_ARG_38	HH12, H_ARG_38	2.86	2.03	12.66

3SE9.PDB	O, H_THR_89	N, H_GLN_39	H, H_GLN_39	2.91	2.10	16.25
3SE9.PDB	O, H_GLN_43	NE2, H_GLN_39	HE21, H_GLN_39	2.88	2.07	16.30
3SE9.PDB	O, H_ALA_40	N, H_GLN_43	H, H_GLN_43	2.88	2.07	16.77
3SE9.PDB	O, H_ARG_38	N, H_GLU_46	H, H_GLU_46	2.90	2.11	20.67
3SE9.PDB	O, H_TRP_36	N, H_ILE_48	H, H_ILE_48	2.76	1.91	8.76
3SE9.PDB	O, H_ASN_57	N, H_TRP_50	H, H_TRP_50	2.97	2.24	26.24
3SE9.PDB	OD1, G_ASN_280	NE1, H_TRP_50	HE1, H_TRP_50	2.86	2.03	11.46
3SE9.PDB	O, H_ALA_55	N, H_LYS_52	H, H_LYS_52	2.82	2.02	18.64
3SE9.PDB	O, H_GLU_33	N, H_THR_52A	H, H_THR_52A	2.97	2.15	15.80
3SE9.PDB	O, H_LYS_52	N, H_GLY_54	H, H_GLY_54	2.87	2.11	23.24
3SE9.PDB	O, G_ARG_456	ND2, H_ASN_57	HD22, H_ASN_57	2.82	1.98	10.42
3SE9.PDB	O, H_ILE_48	N, H_GLY_59	H, H_GLY_59	2.88	2.11	22.31
3SE9.PDB	O, H_SER_60	N, H_ARG_64	H, H_ARG_64	2.81	1.98	12.96
3SE9.PDB	OG, G_SER_365	NH1, H_ARG_64	HH11, H_ARG_64	2.81	2.04	21.79
3SE9.PDB	O, H_PRO_61	N, H_GLN_65	H, H_GLN_65	2.78	2.04	25.46
3SE9.PDB	O, H_ASP_62	N, H_ARG_66	H, H_ARG_66	2.94	2.23	28.48
3SE9.PDB	OD2, H_ASP_86	NH2, H_ARG_66	HH22, H_ARG_66	2.37	1.62	23.34
3SE9.PDB	O, H_PHE_63	N, H_VAL_67	H, H_VAL_67	2.84	2.04	18.39
3SE9.PDB	O, H_ASP_81	N, H_SER_68	H, H_SER_68	2.86	2.04	15.98
3SE9.PDB	O, H_THR_52A	NE, H_ARG_71	HE, H_ARG_71	2.71	1.89	14.64
3SE9.PDB	OD2, G_ASP_368	NH1, H_ARG_71	HH12, H_ARG_71	2.77	1.92	7.25
3SE9.PDB	O, H_THR_77	N, H_ASP_72	H, H_ASP_72	2.80	1.97	12.39
3SE9.PDB	O, G_GLY_429	NH1, H_ARG_73	HH12, H_ARG_73	2.99	2.23	23.32
3SE9.PDB	O, H_LEU_75	OG1, H_THR_77	HG1, H_THR_77	2.67	1.90	16.77
3SE9.PDB	O, H_CYS_22	N, H_ALA_78	H, H_ALA_78	2.72	1.89	13.13
3SE9.PDB	O, H_THR_70	N, H_HIS_79	H, H_HIS_79	2.97	2.14	11.35
3SE9.PDB	OG, H_SER_21	ND1, H_HIS_79	HD1, H_HIS_79	2.69	1.93	23.16
3SE9.PDB	O, H_VAL_20	N, H_MET_80	H, H_MET_80	2.71	1.86	8.21
3SE9.PDB	O, H_SER_68	N, H_ASP_81	H, H_ASP_81	2.93	2.09	10.84
3SE9.PDB	O, H_VAL_18	N, H_ILE_82	H, H_ILE_82	2.83	2.01	14.83
3SE9.PDB	OG, H_SER_68	NH1, H_ARG_82A	HH12, H_ARG_82A	2.84	2.02	15.25
3SE9.PDB	OD2, H_ASP_86	N, H_THR_83	H, H_THR_83	2.88	2.05	13.61
3SE9.PDB	O, H_THR_83	N, H_ASP_86	H, H_ASP_86	2.95	2.11	10.53
3SE9.PDB	O, H_GLN_39	N, H_THR_89	H, H_THR_89	2.98	2.19	19.31
3SE9.PDB	O, H_THR_107	N, H_TYR_90	H, H_TYR_90	2.82	1.97	6.56
3SE9.PDB	O, H_VAL_37	N, H_PHE_91	H, H_PHE_91	2.71	1.86	7.71
3SE9.PDB	OE1, H_GLN_6	N, H_CYS_92	H, H_CYS_92	2.90	2.06	12.06
3SE9.PDB	O, H_HIS_35A	N, H_ALA_93	H, H_ALA_93	2.82	2.09	27.40
3SE9.PDB	O, H_LEU_102	N, H_ARG_94	H, H_ARG_94	2.99	2.16	14.50
3SE9.PDB	OD1, H_ASP_101	NH2, H_ARG_94	HH21, H_ARG_94	2.74	1.90	10.49
3SE9.PDB	O, H_LEU_34	N, H_GLN_95	H, H_GLN_95	2.93	2.08	7.14
3SE9.PDB	OH, H_TYR_100E	NE2, H_GLN_100B	HE22, H_GLN_100B	2.88	2.05	12.80
3SE9.PDB	OD1, G_ASN_279	NE1, H_TRP_100D	HE1, H_TRP_100D	2.86	2.13	26.83
3SE9.PDB	OH, L_TYR_36	N, H_PHE_100F	H, H_PHE_100F	2.88	2.05	11.59
3SE9.PDB	O, H_CYS_92	N, H_GLY_104	H, H_GLY_104	2.87	2.02	7.22
3SE9.PDB	O, H_GLN_6	NH2, H_ARG_105	HH21, H_ARG_105	2.67	1.92	23.91
3SE9.PDB	O, H_TYR_90	N, H_THR_107	H, H_THR_107	2.73	1.92	16.56
3SE9.PDB	OG, H_SER_9	N, H_LEU_108	H, H_LEU_108	2.69	1.93	23.13
3SE9.PDB	O, H_ALA_88	N, H_ILE_109	H, H_ILE_109	2.93	2.07	6.87
3SE9.PDB	OG1, H_THR_87	N, H_VAL_111	H, H_VAL_111	2.93	2.08	7.05
3SE9.PDB	OG, H_SER_112	N, H_ALA_114	H, H_ALA_114	2.96	2.13	12.08
3SE9.PDB	O, H_PHE_146	N, H_LYS_117	H, H_LYS_117	2.71	1.88	12.05
3SE9.PDB	O, H_ASP_144	NZ, H_LYS_117	HZ2, H_LYS_117	2.71	1.95	26.51
3SE9.PDB	O, H_LYS_143	N, H_SER_120	H, H_SER_120	2.94	2.18	23.30
3SE9.PDB	O, H_LEU_141	N, H_PHE_122	H, H_PHE_122	2.83	1.99	10.34
3SE9.PDB	O, H_GLY_139	N, H_LEU_124	H, H_LEU_124	2.72	1.86	7.35
3SE9.PDB	O, H_VAL_184	N, H_ALA_136	H, H_ALA_136	2.58	1.73	7.05
3SE9.PDB	O, H_VAL_182	N, H_LEU_138	H, H_LEU_138	2.98	2.14	9.89

3SE9.PDB	O, H_SER_180	N, H_CYS_140	H, H_CYS_140	2.81	2.02	19.42
3SE9.PDB	O, H_PHE_122	N, H_LEU_141	H, H_LEU_141	2.71	1.87	9.85
3SE9.PDB	O, H_LEU_178	N, H_VAL_142	H, H_VAL_142	2.67	1.83	9.14
3SE9.PDB	O, H_SER_120	N, H_LYS_143	H, H_LYS_143	2.81	1.96	4.58
3SE9.PDB	O, H_LYS_117	N, H_PHE_146	H, H_PHE_146	2.83	2.04	19.01
3SE9.PDB	O, H_ASN_199	N, H_THR_151	H, H_THR_151	2.82	2.01	15.51
3SE9.PDB	OG, H_SER_180	NE1, H_TRP_154	HE1, H_TRP_154	2.83	2.00	12.34
3SE9.PDB	O, H_ILE_195	N, H_ASN_155	H, H_ASN_155	2.72	1.88	10.78
3SE9.PDB	OD1, H_ASN_197	N, H_SER_156	H, H_SER_156	2.63	1.82	16.31
3SE9.PDB	O, H_TRP_154	N, H_GLY_157	H, H_GLY_157	2.94	2.17	22.03
3SE9.PDB	O, H_VAL_181	N, H_HIS_164	H, H_HIS_164	2.79	1.95	10.78
3SE9.PDB	OD1, L_ASN_138	NE2, H_HIS_164	HE2, H_HIS_164	2.87	2.10	22.18
3SE9.PDB	O, H_SER_179	N, H_PHE_166	H, H_PHE_166	2.83	1.98	8.83
3SE9.PDB	O, H_SER_177	N, H_VAL_169	H, H_VAL_169	2.79	1.97	15.38
3SE9.PDB	O, H_LEU_175	N, H_GLN_171	H, H_GLN_171	2.88	2.03	9.89
3SE9.PDB	OD1, H_ASP_144	NE2, H_GLN_171	HE22, H_GLN_171	2.70	1.89	15.22
3SE9.PDB	O, H_GLN_171	N, H_GLY_174	H, H_GLY_174	2.82	1.98	10.33
3SE9.PDB	O, H_TYR_145	N, H_TYR_176	H, H_TYR_176	2.80	1.95	9.52
3SE9.PDB	O, H_VAL_169	N, H_SER_177	H, H_SER_177	2.92	2.11	17.68
3SE9.PDB	O, H_VAL_142	N, H_LEU_178	H, H_LEU_178	2.84	2.05	18.79
3SE9.PDB	O, H_HIS_164	N, H_VAL_181	H, H_VAL_181	2.77	1.93	11.77
3SE9.PDB	O, H_LEU_138	N, H_VAL_182	H, H_VAL_182	2.73	1.91	15.41
3SE9.PDB	O, H_ALA_136	N, H_VAL_184	H, H_VAL_184	2.65	1.82	11.73
3SE9.PDB	O, H_GLY_134	N, H_SER_186	H, H_SER_186	2.77	1.92	8.30
3SE9.PDB	O, H_PRO_185	N, H_SER_188	H, H_SER_188	2.84	2.03	16.03
3SE9.PDB	OD1, H_ASN_155	N, H_ILE_195	H, H_ILE_195	2.88	2.07	17.09
3SE9.PDB	O, H_SER_153	N, H_ASN_197	H, H_ASN_197	2.68	1.83	7.88
3SE9.PDB	OD1, H_ASP_208	ND2, H_ASN_197	HD21, H_ASN_197	2.90	2.07	13.74
3SE9.PDB	O, H_VAL_207	N, H_VAL_198	H, H_VAL_198	2.67	1.81	3.24
3SE9.PDB	O, H_THR_151	N, H_ASN_199	H, H_ASN_199	2.88	2.05	12.73
3SE9.PDB	O, H_THR_205	N, H_HIS_200	H, H_HIS_200	2.70	1.85	4.09
3SE9.PDB	OG, H_SER_203	ND1, H_HIS_200	HD1, H_HIS_200	2.68	1.84	9.59
3SE9.PDB	O, H_PRO_147	NE2, H_HIS_200	HE2, H_HIS_200	2.74	1.92	15.55
3SE9.PDB	O, H_LYS_201	N, H_ASN_204	H, H_ASN_204	2.85	2.04	15.88
3SE9.PDB	O, H_VAL_198	N, H_VAL_207	H, H_VAL_207	2.76	1.95	16.29
3SE9.PDB	O, H_CYS_196	N, H_LYS_209	H, H_LYS_209	2.96	2.13	12.56
3SE9.PDB	O, H_TYR_194	N, H_VAL_211	H, H_VAL_211	2.84	1.98	5.32
3SE9.PDB	OE1, L_GLN_100	N, L_GLN_6	H, L_GLN_6	2.87	2.05	13.27
3SE9.PDB	O, L_TYR_86	NE2, L_GLN_6	HE21, L_GLN_6	2.65	1.87	19.42
3SE9.PDB	O, L_SER_22	N, L_SER_7	H, L_SER_7	2.91	2.10	15.22
3SE9.PDB	O, L_ARG_103	N, L_LEU_11	H, L_LEU_11	2.81	2.03	20.07
3SE9.PDB	OE2, L_GLU_17	N, L_SER_14	H, L_SER_14	2.75	1.90	8.71
3SE9.PDB	O, L_MET_78	N, L_GLY_16	H, L_GLY_16	2.86	2.12	26.24
3SE9.PDB	O, L_SER_14	N, L_GLU_17	H, L_GLU_17	3.00	2.15	9.67
3SE9.PDB	O, L_ILE_75	N, L_ALA_19	H, L_ALA_19	2.75	1.95	18.77
3SE9.PDB	O, L_LEU_73	N, L_LEU_21	H, L_LEU_21	2.92	2.06	4.08
3SE9.PDB	O, L_SER_7	N, L_SER_22	H, L_SER_22	2.90	2.04	6.45
3SE9.PDB	O, L_TYR_71	N, L_CYS_23	H, L_CYS_23	2.61	1.79	13.38
3SE9.PDB	O, L_THR_5	N, L_THR_24	H, L_THR_24	2.87	2.04	10.61
3SE9.PDB	O, L_VAL_3	N, L_ALA_26	H, L_ALA_26	2.84	2.01	13.56
3SE9.PDB	OH, L_TYR_71	N, L_GLY_31	H, L_GLY_31	2.83	1.99	8.85
3SE9.PDB	O, L_GLN_89	N, L_THR_34	H, L_THR_34	2.89	2.12	22.07
3SE9.PDB	O, L_ILE_48	N, L_TRP_35	H, L_TRP_35	2.92	2.14	20.82
3SE9.PDB	O, L_TYR_87	N, L_TYR_36	H, L_TYR_36	2.80	1.96	11.38
3SE9.PDB	O, L_LYS_45	N, L_GLN_37	H, L_GLN_37	2.89	2.10	19.91
3SE9.PDB	O, L_ARG_85	N, L_LYS_38	H, L_LYS_38	2.86	2.11	24.20
3SE9.PDB	O, L_GLN_42	NZ, L_LYS_38	HZ2, L_LYS_38	2.69	1.95	28.64
3SE9.PDB	O, L_GLU_81	NZ, L_LYS_39	HZ3, L_LYS_39	2.86	2.10	26.41

3SE9.PDB	O, L_GLN_37	N, L_LYS_45	H, L_LYS_45	2.78	1.95	13.05
3SE9.PDB	O, L_TRP_35	N, L_LEU_47	H, L_LEU_47	2.87	2.05	13.50
3SE9.PDB	O, L_LYS_53	N, L_PHE_49	H, L_PHE_49	2.83	2.01	14.47
3SE9.PDB	O, L_MET_33	N, L_THR_51	H, L_THR_51	2.85	2.05	18.27
3SE9.PDB	O, L_ALA_50	N, L_SER_52	H, L_SER_52	2.77	2.03	26.37
3SE9.PDB	O, L_PHE_49	N, L_LYS_53	H, L_LYS_53	2.88	2.12	23.41
3SE9.PDB	O, L_THR_74	N, L_SER_63	H, L_SER_63	2.83	2.02	16.49
3SE9.PDB	O, L_GLY_68	NE2, L_GLN_66	HE21, L_GLN_66	2.85	2.01	10.87
3SE9.PDB	O, L_GLN_70	N, L_PHE_67	H, L_PHE_67	2.77	1.98	19.75
3SE9.PDB	O, L_PHE_67	N, L_GLN_70	H, L_GLN_70	2.81	1.99	14.85
3SE9.PDB	O, L_CYS_23	N, L_TYR_71	H, L_TYR_71	2.90	2.05	8.86
3SE9.PDB	O, L_SER_65	N, L_THR_72	H, L_THR_72	2.92	2.08	10.66
3SE9.PDB	O, L_LEU_21	N, L_LEU_73	H, L_LEU_73	2.70	1.90	17.14
3SE9.PDB	O, L_SER_63	N, L_THR_74	H, L_THR_74	2.72	1.87	5.98
3SE9.PDB	O, L_GLU_17	N, L_MET_78	H, L_MET_78	2.89	2.06	12.71
3SE9.PDB	OD2, L_ASP_82	N, L_GLU_79	H, L_GLU_79	2.83	1.97	2.91
3SE9.PDB	O, L_GLU_79	N, L_ASP_82	H, L_ASP_82	2.98	2.15	13.63
3SE9.PDB	O, L_THR_102	N, L_TYR_86	H, L_TYR_86	2.81	2.08	27.06
3SE9.PDB	O, L_THR_34	N, L_GLN_89	H, L_GLN_89	2.81	2.01	18.78
3SE9.PDB	O, L_LEU_91	NE2, L_GLN_89	HE22, L_GLN_89	2.88	2.12	24.17
3SE9.PDB	O, L_PHE_97	N, L_GLN_90	H, L_GLN_90	2.90	2.18	28.93
3SE9.PDB	O, L_SER_27	NE2, L_GLN_90	HE21, L_GLN_90	2.99	2.17	16.35
3SE9.PDB	O, L_CYS_88	N, L_GLY_99	H, L_GLY_99	2.80	1.97	11.46
3SE9.PDB	O, L_TYR_86	N, L_THR_102	H, L_THR_102	2.76	1.99	22.12
3SE9.PDB	O, L_ALA_84	N, L_LEU_104	H, L_LEU_104	2.90	2.05	7.67
3SE9.PDB	O, L_LEU_11	N, L_GLU_105	H, L_GLU_105	2.83	2.02	16.12
3SE9.PDB	OE1, L_GLN_166	N, L_ILE_106	H, L_ILE_106	2.83	2.02	16.05
3SE9.PDB	O, L_LEU_13	N, L_ARG_107	H, L_ARG_107	2.82	1.98	9.67
3SE9.PDB	O, L_TYR_140	N, L_ALA_111	H, L_ALA_111	2.91	2.10	17.28
3SE9.PDB	O, L_VAL_133	N, L_PHE_118	H, L_PHE_118	2.77	1.97	18.18
3SE9.PDB	OG, L_SER_131	NE2, L_GLN_124	HE21, L_GLN_124	2.87	2.02	8.09
3SE9.PDB	O, L_GLN_124	N, L_SER_127	H, L_SER_127	2.85	2.11	25.81
3SE9.PDB	O, L_LEU_125	N, L_GLY_128	H, L_GLY_128	2.77	1.93	7.72
3SE9.PDB	O, L_LEU_181	N, L_ALA_130	H, L_ALA_130	2.85	2.00	6.88
3SE9.PDB	O, L_LEU_179	N, L_VAL_132	H, L_VAL_132	2.65	1.81	8.60
3SE9.PDB	O, L_SER_177	N, L_CYS_134	H, L_CYS_134	2.87	2.03	11.55
3SE9.PDB	O, L_PHE_116	N, L_LEU_135	H, L_LEU_135	2.83	2.01	13.22
3SE9.PDB	O, L_LEU_175	N, L_LEU_136	H, L_LEU_136	2.80	1.94	5.67
3SE9.PDB	O, L_SER_114	N, L_ASN_137	H, L_ASN_137	2.87	2.06	16.53
3SE9.PDB	OG, L_SER_174	N, L_ASN_138	H, L_ASN_138	2.87	2.02	6.61
3SE9.PDB	O, L_TYR_173	N, L_PHE_139	H, L_PHE_139	2.71	1.88	11.74
3SE9.PDB	O, L_ALA_111	N, L_TYR_140	H, L_TYR_140	2.97	2.14	13.63
3SE9.PDB	O, L_GLU_195	N, L_GLN_147	H, L_GLN_147	2.88	2.05	13.30
3SE9.PDB	OG, L_SER_177	NE1, L_TRP_148	HE1, L_TRP_148	2.88	2.05	13.01
3SE9.PDB	O, L_ALA_193	N, L_LYS_149	H, L_LYS_149	2.85	2.03	13.91
3SE9.PDB	O, L_ALA_153	N, L_VAL_150	H, L_VAL_150	2.92	2.10	13.17
3SE9.PDB	O, L_VAL_191	N, L_ASP_151	H, L_ASP_151	2.74	1.91	13.52
3SE9.PDB	O, L_VAL_150	N, L_ALA_153	H, L_ALA_153	2.87	2.02	9.15
3SE9.PDB	O, L_TRP_148	N, L_GLN_155	H, L_GLN_155	3.00	2.16	10.91
3SE9.PDB	O, L_THR_178	N, L_GLN_160	H, L_GLN_160	2.99	2.20	19.65
3SE9.PDB	O, L_SER_176	N, L_SER_162	H, L_SER_162	2.81	2.05	22.68
3SE9.PDB	O, H_PRO_167	OG, L_SER_162	HG, L_SER_162	2.60	1.89	25.20
3SE9.PDB	O, L_SER_174	N, L_THR_164	H, L_THR_164	2.97	2.14	12.76
3SE9.PDB	O, L_ILE_106	NE2, L_GLN_166	HE21, L_GLN_166	2.82	2.03	19.63
3SE9.PDB	O, L_SER_171	NE2, L_GLN_166	HE22, L_GLN_166	2.91	2.08	11.92
3SE9.PDB	O, L_THR_172	N, L_ASP_167	H, L_ASP_167	2.88	2.05	12.43
3SE9.PDB	OD2, L_ASP_167	N, L_LYS_169	H, L_LYS_169	2.73	1.98	24.54
3SE9.PDB	OD2, L_ASP_167	N, L_ASP_170	H, L_ASP_170	2.87	2.10	21.70

3SE9.PDB	OD1, L_ASP_170	OG1, L_THR_172	HG1, L_THR_172	2.48	1.71	16.29
3SE9.PDB	O, L_PHE_139	N, L_TYR_173	H, L_TYR_173	2.70	1.86	11.73
3SE9.PDB	O, L_LEU_136	N, L_LEU_175	H, L_LEU_175	2.79	1.97	15.48
3SE9.PDB	O, L_SER_162	N, L_SER_176	H, L_SER_176	2.85	2.02	11.18
3SE9.PDB	O, L_CYS_134	N, L_SER_177	H, L_SER_177	2.95	2.11	11.27
3SE9.PDB	O, L_GLN_160	N, L_THR_178	H, L_THR_178	2.80	1.96	9.46
3SE9.PDB	O, L_VAL_132	N, L_LEU_179	H, L_LEU_179	2.70	1.87	12.38
3SE9.PDB	O, L_ASN_158	N, L_THR_180	H, L_THR_180	3.00	2.16	11.07
3SE9.PDB	O, L_ALA_130	N, L_LEU_181	H, L_LEU_181	2.86	2.02	11.27
3SE9.PDB	O, L_GLY_128	N, L_LYS_183	H, L_LYS_183	2.82	2.01	15.80
3SE9.PDB	OE1, L_GLU_187	NZ, L_LYS_183	HZ3, L_LYS_183	2.82	2.09	29.82
3SE9.PDB	O, L_LYS_183	N, L_GLU_187	H, L_GLU_187	2.93	2.13	19.51
3SE9.PDB	OD2, L_ASP_151	ND1, L_HIS_189	HD1, L_HIS_189	2.89	2.18	29.99
3SE9.PDB	OD1, L_ASP_151	N, L_VAL_191	H, L_VAL_191	2.92	2.06	1.45
3SE9.PDB	O, L_PHE_209	N, L_TYR_192	H, L_TYR_192	2.96	2.10	3.54
3SE9.PDB	O, L_LYS_149	N, L_ALA_193	H, L_ALA_193	2.83	2.03	17.72
3SE9.PDB	O, L_LYS_207	N, L_CYS_194	H, L_CYS_194	2.79	1.94	6.54
3SE9.PDB	O, L_GLN_147	N, L_GLU_195	H, L_GLU_195	2.78	1.93	8.55
3SE9.PDB	O, L_VAL_205	N, L_VAL_196	H, L_VAL_196	2.74	1.90	9.26
3SE9.PDB	O, L_LYS_145	N, L_THR_197	H, L_THR_197	2.89	2.05	9.75
3SE9.PDB	ND1, L_HIS_198	N, L_GLY_200	H, L_GLY_200	3.00	2.16	11.89
3SE9.PDB	O, L_HIS_198	N, L_LEU_201	H, L_LEU_201	2.74	1.90	9.36
3SE9.PDB	O, L_VAL_196	N, L_VAL_205	H, L_VAL_205	2.96	2.24	27.95
3SE9.PDB	O, L_CYS_194	N, L_LYS_207	H, L_LYS_207	2.92	2.12	17.78
3SE9.PDB	O, L_TYR_192	N, L_PHE_209	H, L_PHE_209	2.89	2.14	24.10
3SE9.PDB	O, L_LYS_190	N, L_ARG_211	H, L_ARG_211	2.77	1.94	11.39
3THM.PDB	N, L_VAL_3	OG, L_SER_2	HG, L_SER_2	2.83	2.12	25.75
3THM.PDB	OG, L_SER_2	N, L_LEU_4	H, L_LEU_4	2.87	2.06	16.74
3THM.PDB	O, L_SER_23	N, L_THR_5	H, L_THR_5	2.87	2.03	10.68
3THM.PDB	O, L_TYR_87	NE2, L_GLN_6	HE21, L_GLN_6	2.88	2.03	6.32
3THM.PDB	OE1, L_GLU_12	N, L_ALA_13	H, L_ALA_13	2.70	1.91	19.84
3THM.PDB	O, L_LEU_79	N, L_ARG_15	H, L_ARG_15	2.74	1.88	4.28
3THM.PDB	O, L_LEU_74	N, L_ILE_20	H, L_ILE_20	2.80	1.96	9.35
3THM.PDB	O, L_THR_5	N, L_SER_23	H, L_SER_23	2.90	2.09	16.08
3THM.PDB	O, L_THR_70	N, L_GLY_24	H, L_GLY_24	2.84	2.07	23.10
3THM.PDB	OD1, L_ASN_28	N, L_ASN_25	H, L_ASN_25	2.96	2.18	18.32
3THM.PDB	OD1, L_ASP_93	ND2, L_ASN_28	HD21, L_ASN_28	2.85	2.01	9.28
3THM.PDB	OD1, L_ASN_28	N, L_ILE_29	H, L_ILE_29	2.67	1.87	18.36
3THM.PDB	O, L_ASN_25	N, L_GLY_30	H, L_GLY_30	2.96	2.12	9.14
3THM.PDB	O, L_ASN_28	N, L_TYR_32	H, L_TYR_32	2.89	2.11	20.74
3THM.PDB	OD2, L_ASP_52	N, L_VAL_34	H, L_VAL_34	2.76	2.01	24.28
3THM.PDB	O, L_SER_90	N, L_ASN_35	H, L_ASN_35	2.89	2.07	14.41
3THM.PDB	O, H_ALA_117	ND2, L_ASN_35	HD21, L_ASN_35	2.77	1.97	17.79
3THM.PDB	O, L_ILE_49	N, L_TRP_36	H, L_TRP_36	2.81	1.98	12.62
3THM.PDB	O, L_TYR_88	N, L_TYR_37	H, L_TYR_37	2.84	2.02	14.79
3THM.PDB	O, L_LYS_46	N, L_GLN_38	H, L_GLN_38	2.87	2.08	19.68
3THM.PDB	OH, L_TYR_87	NE2, L_GLN_38	HE21, L_GLN_38	2.86	2.05	16.36
3THM.PDB	O, L_ASP_86	N, L_GLN_39	H, L_GLN_39	2.67	1.81	4.75
3THM.PDB	O, L_LEU_40	N, L_LYS_43	H, L_LYS_43	2.88	2.04	10.22
3THM.PDB	O, L_GLN_38	N, L_LYS_46	H, L_LYS_46	2.84	2.05	18.96
3THM.PDB	O, L_TRP_36	N, L_LEU_48	H, L_LEU_48	2.82	1.98	12.51
3THM.PDB	O, L_LEU_54	N, L_TYR_50	H, L_TYR_50	2.87	2.06	17.25
3THM.PDB	OD1, L_ASN_35	N, L_SER_51	H, L_SER_51	2.98	2.18	17.87
3THM.PDB	O, L_VAL_34	N, L_ASP_52	H, L_ASP_52	2.82	1.98	11.63
3THM.PDB	O, L_ASP_61	NH2, L_ARG_55	HH21, L_ARG_55	2.95	2.23	28.54
3THM.PDB	OD1, L_ASP_83	NE, L_ARG_62	HE, L_ARG_62	2.86	2.03	12.52
3THM.PDB	OD2, L_ASP_83	NH2, L_ARG_62	HH21, L_ARG_62	2.63	1.79	10.74
3THM.PDB	O, L_ALA_75	N, L_SER_64	H, L_SER_64	2.96	2.14	13.06

3THM.PDB	O, L.SER.73	N, L.SER.66	H, L.SER.66	2.95	2.17	20.65
3THM.PDB	O, L.THR.71	N, L.SER.68	H, L.SER.68	2.93	2.09	7.96
3THM.PDB	O, L.SER.68	N, L.THR.71	H, L.THR.71	2.94	2.09	5.15
3THM.PDB	O, L.CYS.22	N, L.ALA.72	H, L.ALA.72	2.80	1.98	14.59
3THM.PDB	O, L.SER.66	N, L.SER.73	H, L.SER.73	2.76	1.91	7.29
3THM.PDB	O, L.ILE.20	N, L.LEU.74	H, L.LEU.74	2.97	2.15	14.37
3THM.PDB	O, L.SER.64	N, L.ALA.75	H, L.ALA.75	2.82	2.00	15.44
3THM.PDB	O, L.VAL.18	N, L.ILE.76	H, L.ILE.76	2.90	2.07	11.54
3THM.PDB	OD2, L.ASP.78	NH1, L.ARG.77	HH11, L.ARG.77	2.79	2.00	19.01
3THM.PDB	O, L.GLN.16	N, L.LEU.79	H, L.LEU.79	2.98	2.13	4.45
3THM.PDB	OD1, L.ASP.83	N, L.LEU.80	H, L.LEU.80	2.94	2.09	0.76
3THM.PDB	O, L.LEU.80	N, L.ASP.83	H, L.ASP.83	2.90	2.06	10.43
3THM.PDB	O, L.GLN.39	N, L.ASP.86	H, L.ASP.86	2.98	2.17	16.25
3THM.PDB	O, L.THR.105	N, L.TYR.87	H, L.TYR.87	2.83	2.01	15.92
3THM.PDB	O, L.TYR.37	N, L.TYR.88	H, L.TYR.88	2.90	2.08	14.37
3THM.PDB	O, L.SER.27	N, L.ASP.94	H, L.ASP.94	2.91	2.10	16.82
3THM.PDB	OD2, L.ASP.93	N, L.THR.95	H, L.THR.95	2.93	2.14	20.81
3THM.PDB	OD2, L.ASP.93	N, L.LEU.96	H, L.LEU.96	2.88	2.03	8.57
3THM.PDB	O, L.THR.91	N, L.VAL.100	H, L.VAL.100	2.85	2.00	6.96
3THM.PDB	O, L.CYS.89	N, L.GLY.102	H, L.GLY.102	2.91	2.09	13.69
3THM.PDB	O, L.TYR.87	N, L.THR.105	H, L.THR.105	2.90	2.14	23.36
3THM.PDB	O, L.PRO.8	N, L.LYS.106	H, L.LYS.106	2.93	2.09	11.49
3THM.PDB	O, L.ALA.85	N, L.VAL.107	H, L.VAL.107	2.85	2.01	9.33
3THM.PDB	OE1, L.GLU.84	N, L.VAL.109	H, L.VAL.109	2.88	2.08	17.71
3THM.PDB	O, L.GLU.12	N, L.LEU.110	H, L.LEU.110	2.93	2.10	11.26
3THM.PDB	OH, L.TYR.144	N, L.GLY.111	H, L.GLY.111	2.94	2.13	15.64
3THM.PDB	O, L.TYR.144	N, L.ALA.115	H, L.ALA.115	2.97	2.15	12.90
3THM.PDB	O, L.SER.141	N, L.SER.118	H, L.SER.118	2.88	2.05	12.08
3THM.PDB	O, L.LEU.139	N, L.THR.120	H, L.THR.120	2.88	2.06	14.03
3THM.PDB	O, L.VAL.137	N, L.PHE.122	H, L.PHE.122	2.87	2.03	12.38
3THM.PDB	O, L.LEU.129	N, L.ASN.132	H, L.ASN.132	2.78	1.99	19.66
3THM.PDB	OE1, L.GLU.128	N, L.THR.135	H, L.THR.135	2.71	1.92	18.59
3THM.PDB	O, L.LEU.182	N, L.LEU.136	H, L.LEU.136	2.87	2.02	9.82
3THM.PDB	O, L.SER.180	N, L.CYS.138	H, L.CYS.138	2.84	1.98	5.42
3THM.PDB	O, L.THR.120	N, L.LEU.139	H, L.LEU.139	2.76	1.90	6.56
3THM.PDB	O, L.ALA.178	N, L.ILE.140	H, L.ILE.140	2.89	2.15	25.14
3THM.PDB	O, L.SER.118	N, L.SER.141	H, L.SER.141	2.99	2.18	16.95
3THM.PDB	O, L.THR.200	N, L.THR.149	H, L.THR.149	2.96	2.13	13.40
3THM.PDB	O, L.GLN.198	N, L.ALA.151	H, L.ALA.151	2.90	2.07	13.36
3THM.PDB	OG, L.SER.180	NE1, L.TRP.152	HE1, L.TRP.152	2.84	1.99	7.64
3THM.PDB	O, L.SER.196	N, L.LYS.153	H, L.LYS.153	2.89	2.09	18.48
3THM.PDB	O, L.SER.157	N, L.ALA.154	H, L.ALA.154	2.77	1.99	21.42
3THM.PDB	O, L.SER.194	N, L.ASP.155	H, L.ASP.155	2.71	1.86	0.53
3THM.PDB	O, L.ALA.154	N, L.SER.157	H, L.SER.157	2.85	2.02	12.03
3THM.PDB	O, L.TYR.181	N, L.GLU.164	H, L.GLU.164	2.88	2.07	15.71
3THM.PDB	O, L.SER.179	N, L.THR.166	H, L.THR.166	2.84	2.02	13.98
3THM.PDB	O, L.ALA.177	N, L.SER.169	H, L.SER.169	2.84	2.02	15.98
3THM.PDB	O, L.LYS.175	N, L.GLN.171	H, L.GLN.171	2.63	1.80	12.05
3THM.PDB	OD1, L.ASP.142	NE2, L.GLN.171	HE22, L.GLN.171	2.87	2.03	8.80
3THM.PDB	O, L.GLN.171	N, L.ASN.174	H, L.ASN.174	2.95	2.14	16.29
3THM.PDB	OD1, L.ASN.173	N, L.LYS.175	H, L.LYS.175	2.86	2.05	16.58
3THM.PDB	O, L.SER.169	N, L.ALA.177	H, L.ALA.177	2.84	2.05	18.78
3THM.PDB	O, L.ILE.140	N, L.ALA.178	H, L.ALA.178	2.72	1.90	14.30
3THM.PDB	OG1, L.THR.166	N, L.SER.179	H, L.SER.179	2.86	2.02	12.53
3THM.PDB	O, L.CYS.138	N, L.SER.180	H, L.SER.180	2.89	2.07	15.30
3THM.PDB	O, L.GLU.164	N, L.TYR.181	H, L.TYR.181	2.72	1.88	12.14
3THM.PDB	O, L.GLY.162	N, L.SER.183	H, L.SER.183	2.89	2.05	9.19
3THM.PDB	O, L.ALA.134	N, L.LEU.184	H, L.LEU.184	2.75	1.90	5.72

3THM.PDB	OD1, L_ASP_155	ND1, L_HIS_192	HD1, L_HIS_192	2.84	1.98	0.83
3THM.PDB	O, L_LYS_153	N, L_SER_196	H, L_SER_196	2.82	2.02	17.68
3THM.PDB	O, L_LYS_208	N, L_CYS_197	H, L_CYS_197	2.89	2.14	23.69
3THM.PDB	O, L_ALA_151	N, L_GLN_198	H, L_GLN_198	2.69	1.85	10.52
3THM.PDB	O, L_VAL_206	N, L_VAL_199	H, L_VAL_199	2.87	2.03	11.90
3THM.PDB	O, L_THR_149	N, L_THR_200	H, L_THR_200	2.80	1.94	5.73
3THM.PDB	OG1, L_THR_205	OG1, L_THR_200	HG1, L_THR_200	2.83	2.04	14.40
3THM.PDB	O, L_SER_204	N, L_HIS_201	H, L_HIS_201	2.89	2.07	13.82
3THM.PDB	O, L_PRO_145	NE2, L_HIS_201	HE2, L_HIS_201	2.93	2.13	17.58
3THM.PDB	O, L_CYS_197	N, L_LYS_208	H, L_LYS_208	3.00	2.18	15.53
3THM.PDB	O, L_TYR_195	N, L_VAL_210	H, L_VAL_210	2.99	2.18	15.60
3THM.PDB	O, H_THR_21	N, H_SER_7	H, H_SER_7	2.99	2.26	26.55
3THM.PDB	O, H_PRO_9	N, H_LEU_11	H, H_LEU_11	2.71	1.97	25.47
3THM.PDB	O, H_THR_129	N, H_VAL_12	H, H_VAL_12	2.92	2.10	14.43
3THM.PDB	O, H_VAL_92	N, H_SER_15	H, H_SER_15	2.84	2.00	9.85
3THM.PDB	O, H_LEU_89	N, H_LEU_18	H, H_LEU_18	2.73	1.90	12.52
3THM.PDB	O, H_LEU_87	N, H_LEU_20	H, H_LEU_20	2.81	1.97	10.10
3THM.PDB	O, H_VAL_85	N, H_CYS_22	H, H_CYS_22	2.69	1.90	18.57
3THM.PDB	O, H_GLN_5	N, H_THR_23	H, H_THR_23	2.91	2.06	9.33
3THM.PDB	O, H_ASN_83	N, H_VAL_24	H, H_VAL_24	2.95	2.09	5.07
3THM.PDB	O, H_GLN_3	N, H_SER_25	H, H_SER_25	2.97	2.14	12.04
3THM.PDB	OD1, H_ASN_83	N, H_ILE_29	H, H_ILE_29	2.98	2.13	8.25
3THM.PDB	O, H_TYR_55	N, H_TYR_34	H, H_TYR_34	2.87	2.06	17.59
3THM.PDB	O, H_ILE_53	N, H_GLY_36	H, H_GLY_36	2.90	2.14	23.00
3THM.PDB	O, H_ALA_103	N, H_VAL_37	H, H_VAL_37	2.92	2.10	13.94
3THM.PDB	O, H_TYR_101	N, H_VAL_39	H, H_VAL_39	2.92	2.10	14.86
3THM.PDB	O, H_GLU_48	N, H_ARG_40	H, H_ARG_40	2.87	2.07	18.62
3THM.PDB	OE1, H_GLU_48	NE, H_ARG_40	HE, H_ARG_40	2.92	2.11	16.36
3THM.PDB	OD1, H_ASP_96	NH1, H_ARG_40	HH12, H_ARG_40	2.76	1.92	9.45
3THM.PDB	O, H_LEU_99	N, H_GLN_41	H, H_GLN_41	2.75	1.96	19.23
3THM.PDB	OE1, L_GLN_39	NE2, H_GLN_41	HE22, H_GLN_41	2.98	2.14	9.35
3THM.PDB	O, H_SER_42	N, H_LYS_45	H, H_LYS_45	2.83	2.00	12.10
3THM.PDB	O, H_ARG_40	N, H_GLU_48	H, H_GLU_48	2.98	2.23	24.84
3THM.PDB	OG, H_SER_52	NE1, H_TRP_49	HE1, H_TRP_49	2.98	2.27	29.23
3THM.PDB	O, H_TRP_38	N, H_VAL_50	H, H_VAL_50	2.78	1.93	5.54
3THM.PDB	O, H_GLY_36	N, H_ILE_53	H, H_ILE_53	2.92	2.11	15.71
3THM.PDB	O, H_SER_63	N, H_ALA_54	H, H_ALA_54	2.85	2.03	14.59
3THM.PDB	O, H_TYR_34	N, H_TYR_55	H, H_TYR_55	2.70	1.86	8.19
3THM.PDB	O, H_SER_61	N, H_ARG_56	H, H_ARG_56	2.79	1.94	3.04
3THM.PDB	O, H_TRP_49	ND2, H_ASN_67	HD21, H_ASN_67	2.99	2.17	14.54
3THM.PDB	OD1, H_ASN_67	N, H_SER_69	H, H_SER_69	2.88	2.04	9.73
3THM.PDB	O, H_PRO_68	N, H_LYS_71	H, H_LYS_71	2.99	2.15	9.73
3THM.PDB	O, H_LEU_70	N, H_ARG_73	H, H_ARG_73	2.98	2.17	16.28
3THM.PDB	O, H_THR_90	NH1, H_ARG_73	HH11, H_ARG_73	2.99	2.22	21.63
3THM.PDB	OD1, H_ASP_96	NH2, H_ARG_73	HH22, H_ARG_73	2.91	2.05	3.20
3THM.PDB	O, H_ARG_88	N, H_THR_75	H, H_THR_75	2.81	1.99	15.03
3THM.PDB	OH, H_TYR_66	N, H_VAL_76	H, H_VAL_76	2.75	1.94	15.65
3THM.PDB	O, H_GLN_84	N, H_ASP_79	H, H_ASP_79	2.81	1.97	8.52
3THM.PDB	O, H_ALA_27	ND2, H_ASN_83	HD21, H_ASN_83	2.72	1.92	17.02
3THM.PDB	O, H_VAL_24	ND2, H_ASN_83	HD22, H_ASN_83	2.73	1.93	16.56
3THM.PDB	O, H_CYS_22	N, H_VAL_85	H, H_VAL_85	2.95	2.13	13.75
3THM.PDB	O, H_SER_77	N, H_SER_86	H, H_SER_86	2.75	1.94	17.86
3THM.PDB	O, H_LEU_20	N, H_LEU_87	H, H_LEU_87	2.98	2.17	15.66
3THM.PDB	O, H_THR_75	N, H_ARG_88	H, H_ARG_88	2.85	2.03	14.81
3THM.PDB	O, H_LEU_18	N, H_LEU_89	H, H_LEU_89	2.80	2.02	20.86
3THM.PDB	O, H_ARG_73	N, H_THR_90	H, H_THR_90	2.97	2.15	16.37
3THM.PDB	OD2, H_ASP_96	N, H_THR_93	H, H_THR_93	2.92	2.12	16.99
3THM.PDB	O, H_THR_93	N, H_ASP_96	H, H_ASP_96	2.87	2.02	6.72

3THM.PDB	O, H_VAL_128	N, H_ALA_98	H, H_ALA_98	2.97	2.18	20.37
3THM.PDB	O, H_GLN_41	N, H_LEU_99	H, H_LEU_99	2.82	2.04	20.70
3THM.PDB	O, H_THR_126	N, H_TYR_100	H, H_TYR_100	2.79	1.94	6.57
3THM.PDB	O, H_VAL_39	N, H_TYR_101	H, H_TYR_101	2.82	1.97	6.69
3THM.PDB	OE2, H_GLU_6	N, H_CYS_102	H, H_CYS_102	2.91	2.11	17.93
3THM.PDB	O, H_VAL_37	N, H_ALA_103	H, H_ALA_103	2.92	2.15	22.20
3THM.PDB	O, H_VAL_121	N, H_ARG_104	H, H_ARG_104	2.93	2.16	22.36
3THM.PDB	OD1, H_ASP_120	NE, H_ARG_104	HE, H_ARG_104	2.94	2.10	9.96
3THM.PDB	OD2, H_ASP_120	NH2, H_ARG_104	HH21, H_ARG_104	2.75	2.00	25.31
3THM.PDB	O, H_TYR_35	N, H_ARG_105	H, H_ARG_105	2.94	2.12	13.20
3THM.PDB	O, F_CYS_43	NH1, H_ARG_105	HH12, H_ARG_105	2.85	2.05	18.46
3THM.PDB	O, H_ALA_118	N, H_GLN_106	H, H_GLN_106	2.92	2.09	11.12
3THM.PDB	O, H_TRP_116	N, H_LEU_108	H, H_LEU_108	2.87	2.01	4.97
3THM.PDB	O, H_TYR_114	N, H_ASP_110	H, H_ASP_110	2.97	2.20	22.11
3THM.PDB	OD2, H_ASP_110	N, H_THR_112	H, H_THR_112	2.71	1.90	15.44
3THM.PDB	OD2, H_ASP_110	OG1, H_THR_112	HG1, H_THR_112	2.76	1.95	7.38
3THM.PDB	OD1, H_ASP_109	NE2, H_GLN_115	HE21, H_GLN_115	2.80	1.96	11.40
3THM.PDB	O, H_CYS_102	N, H_GLY_123	H, H_GLY_123	2.94	2.12	14.27
3THM.PDB	OE1, H_GLU_6	N, H_GLY_125	H, H_GLY_125	2.63	1.81	15.46
3THM.PDB	O, H_TYR_100	N, H_THR_126	H, H_THR_126	2.88	2.07	16.47
3THM.PDB	O, H_ALA_98	N, H_VAL_128	H, H_VAL_128	2.86	2.04	14.39
3THM.PDB	O, H_GLY_10	N, H_THR_129	H, H_THR_129	2.91	2.10	17.08
3THM.PDB	OG1, H_THR_97	N, H_VAL_130	H, H_VAL_130	2.80	1.94	1.61
3THM.PDB	O, H_VAL_12	N, H_SER_131	H, H_SER_131	2.82	2.03	20.60
3THM.PDB	OG, H_SER_131	N, H_ALA_133	H, H_ALA_133	2.89	2.06	13.32
3THM.PDB	O, H_PHE_165	N, H_LYS_136	H, H_LYS_136	2.85	2.08	21.01
3THM.PDB	O, H_LYS_162	N, H_SER_139	H, H_SER_139	2.99	2.21	21.41
3THM.PDB	O, H_LEU_160	N, H_PHE_141	H, H_PHE_141	2.90	2.07	13.94
3THM.PDB	O, H_GLY_158	N, H_LEU_143	H, H_LEU_143	2.66	1.82	10.00
3THM.PDB	O, H_LEU_143	N, H_GLY_158	H, H_GLY_158	2.93	2.12	16.47
3THM.PDB	O, H_SER_199	N, H_ACYS_159	H, H_ACYS_159	2.87	2.09	19.75
3THM.PDB	O, H_SER_199	N, H_BCYS_159	H, H_BCYS_159	2.93	2.18	25.13
3THM.PDB	O, H_PHE_141	N, H_LEU_160	H, H_LEU_160	2.78	1.98	17.74
3THM.PDB	O, H_LEU_197	N, H_VAL_161	H, H_VAL_161	2.77	1.93	8.59
3THM.PDB	O, H_SER_139	N, H_LYS_162	H, H_LYS_162	2.85	2.00	5.79
3THM.PDB	OG, L_SER_183	NZ, H_LYS_162	HZ1, H_LYS_162	2.77	1.97	21.34
3THM.PDB	OG1, L_THR_135	NZ, H_LYS_162	HZ2, H_LYS_162	2.85	2.02	17.75
3THM.PDB	OG, H_SER_196	N, H_ASP_163	H, H_ASP_163	2.90	2.06	10.60
3THM.PDB	O, H_TYR_195	N, H_TYR_164	H, H_TYR_164	2.87	2.08	20.27
3THM.PDB	OG, H_SER_199	NE1, H_TRP_173	HE1, H_TRP_173	3.00	2.15	7.78
3THM.PDB	O, H_ILE_214	N, H_ASN_174	H, H_ASN_174	2.65	1.83	15.08
3THM.PDB	OD1, H_ASN_216	N, H_SER_175	H, H_SER_175	2.77	2.04	26.97
3THM.PDB	O, H_TRP_173	N, H_GLY_176	H, H_GLY_176	2.79	2.00	19.31
3THM.PDB	O, H_ASN_174	N, H_ALA_177	H, H_ALA_177	2.93	2.12	16.59
3THM.PDB	O, H_VAL_200	N, H_HIS_183	H, H_HIS_183	2.68	1.84	8.83
3THM.PDB	O, H_SER_198	N, H_PHE_185	H, H_PHE_185	2.88	2.05	11.29
3THM.PDB	O, H_SER_196	N, H_VAL_188	H, H_VAL_188	2.78	2.06	27.88
3THM.PDB	O, H_LEU_194	N, H_GLN_190	H, H_GLN_190	2.87	2.07	17.50
3THM.PDB	O, H_GLN_190	N, H_GLY_193	H, H_GLY_193	2.85	2.01	11.86
3THM.PDB	O, H_TYR_164	N, H_TYR_195	H, H_TYR_195	2.86	2.01	9.29
3THM.PDB	O, H_VAL_188	N, H_SER_196	H, H_SER_196	2.94	2.15	19.84
3THM.PDB	O, H_VAL_161	N, H_LEU_197	H, H_LEU_197	2.93	2.14	18.92
3THM.PDB	O, H_HIS_183	N, H_VAL_200	H, H_VAL_200	2.86	2.01	9.19
3THM.PDB	O, H_LEU_157	N, H_VAL_201	H, H_VAL_201	2.69	1.85	11.90
3THM.PDB	O, H_GLY_181	N, H_THR_202	H, H_THR_202	3.00	2.19	16.64
3THM.PDB	O, H_PRO_204	N, H_SER_207	H, H_SER_207	2.96	2.23	27.46
3THM.PDB	O, H_SER_207	N, H_GLN_211	H, H_GLN_211	2.68	1.84	9.21
3THM.PDB	OD1, H_ASN_174	N, H_ILE_214	H, H_ILE_214	2.87	2.13	26.27

3THM.PDB	O, H_LYS_228	N, H_CYS_215	H, H_CYS_215	2.84	2.07	22.53
3THM.PDB	O, H_SER_172	N, H_ASN_216	H, H_ASN_216	2.73	1.89	10.25
3THM.PDB	OD1, H_ASP_227	ND2, H_ASN_216	HD22, H_ASN_216	2.86	2.03	14.19
3THM.PDB	O, H_VAL_226	N, H_VAL_217	H, H_VAL_217	2.70	1.86	9.29
3THM.PDB	O, H_THR_170	N, H_ASN_218	H, H_ASN_218	2.97	2.15	14.77
3THM.PDB	O, H_THR_224	N, H_HIS_219	H, H_HIS_219	2.94	2.09	7.91
3THM.PDB	OG, H_SER_222	ND1, H_HIS_219	HD1, H_HIS_219	2.82	2.08	24.90
3THM.PDB	O, H_PRO_166	NE2, H_HIS_219	HE2, H_HIS_219	2.71	1.87	10.58
3THM.PDB	O, H_LYS_220	N, H_ASN_223	H, H_ASN_223	2.76	2.01	25.66
3THM.PDB	O, H_VAL_217	N, H_VAL_226	H, H_VAL_226	2.74	1.90	11.00
3THM.PDB	O, H_CYS_215	N, H_LYS_228	H, H_LYS_228	2.89	2.06	14.00
3THM.PDB	O, H_TYR_213	N, H_VAL_230	H, H_VAL_230	2.80	1.96	9.90
3THM.PDB	OD2, F_ASP_56	ND1, F_HIS_38	HD1, F_HIS_38	2.77	1.98	19.59
3THM.PDB	O, F_GLY_40	N, F_CYS_43	H, F_CYS_43	2.96	2.13	13.45
3THM.PDB	OE2, F_GLU_63	N, F_HIS_44	H, F_HIS_44	2.86	2.00	4.98
3THM.PDB	OH, H_TYR_35	ND1, F_HIS_44	HD1, F_HIS_44	2.69	1.83	5.98
3THM.PDB	OG, H_SER_63	NE2, F_HIS_44	HE2, F_HIS_44	2.83	2.07	23.36
3THM.PDB	OE1, F_GLU_63	N, F_LYS_45	H, F_LYS_45	2.81	1.99	14.79
3THM.PDB	O, F_HIS_80	N, F_CYS_47	H, F_CYS_47	2.76	1.92	10.08
3THM.PDB	OG1, F_THR_76	N, F_GLY_50	H, F_GLY_50	2.93	2.22	29.13
3THM.PDB	O, F_VAL_67	N, F_ARG_52	H, F_ARG_52	2.76	2.01	24.49
3THM.PDB	O, F_ASP_65	N, F_ALA_54	H, F_ALA_54	2.91	2.11	18.55
3THM.PDB	OG1, F_THR_58	N, F_GLY_61	H, F_GLY_61	2.96	2.22	26.61
3THM.PDB	O, F_ARG_52	N, F_VAL_67	H, F_VAL_67	2.78	1.94	11.01
3THM.PDB	O, F_GLY_50	N, F_CYS_69	H, F_CYS_69	2.95	2.13	14.13
3THM.PDB	O, F_GLN_70	N, F_LYS_73	H, F_LYS_73	2.88	2.05	12.43
3THM.PDB	O, F_GLN_70	N, F_GLU_74	H, F_GLU_74	2.89	2.05	11.11
3THM.PDB	O, F_ARG_86	N, F_TYR_75	H, F_TYR_75	2.78	2.03	24.45
3THM.PDB	O, F_ARG_105	N, F_THR_76	H, F_THR_76	2.94	2.15	19.85
3THM.PDB	O, L_SER_51	NZ, F_LYS_78	HZ2, F_LYS_78	3.00	2.15	15.09
3THM.PDB	O, F_GLU_51	NE2, F_HIS_80	HE2, F_HIS_80	2.76	1.91	6.66
3THM.PDB	O, F_TYR_75	N, F_ARG_86	H, F_ARG_86	2.77	1.94	13.51
3THM.PDB	O, F_LYS_73	N, F_CYS_88	H, F_CYS_88	2.79	1.94	5.08
3THM.PDB	OD1, F_ASN_108	N, F_ARG_89	H, F_ARG_89	2.64	1.87	22.68
3THM.PDB	O, F_GLN_107	N, F_THR_104	H, F_THR_104	2.82	1.99	12.71
3TJE.PDB	OG, L_SER_2	N, L_LEU_4	H, L_LEU_4	2.98	2.19	19.51
3TJE.PDB	O, L_SER_23	N, L_THR_5	H, L_THR_5	2.89	2.05	11.59
3TJE.PDB	O, L_TYR_87	NE2, L_GLN_6	HE21, L_GLN_6	2.84	2.01	11.61
3TJE.PDB	O, L_LYS_106	N, L_VAL_10	H, L_VAL_10	2.95	2.15	17.08
3TJE.PDB	OE1, L_GLU_12	N, L_ALA_13	H, L_ALA_13	2.73	1.95	20.14
3TJE.PDB	O, L_LEU_79	N, L_ARG_15	H, L_ARG_15	2.84	2.01	13.10
3TJE.PDB	O, L_LEU_74	N, L_ILE_20	H, L_ILE_20	2.71	1.88	13.42
3TJE.PDB	O, L_THR_5	N, L_SER_23	H, L_SER_23	2.97	2.17	18.20
3TJE.PDB	O, L_THR_70	N, L_GLY_24	H, L_GLY_24	2.81	1.98	12.07
3TJE.PDB	OD1, L_ASN_28	N, L_ASN_25	H, L_ASN_25	2.88	2.06	15.65
3TJE.PDB	OD1, L_ASN_25	N, L_PHE_27	H, L_PHE_27	2.67	1.88	19.71
3TJE.PDB	OD1, L_ASP_93	ND2, L_ASN_28	HD21, L_ASN_28	2.73	1.89	10.95
3TJE.PDB	OD1, L_ASN_28	N, L_ILE_29	H, L_ILE_29	2.67	1.87	18.78
3TJE.PDB	O, L_ASN_25	N, L_GLY_30	H, L_GLY_30	2.98	2.19	18.64
3TJE.PDB	O, L_ASN_28	N, L_ARG_31	H, L_ARG_31	2.87	2.03	11.14
3TJE.PDB	OD1, L_ASP_94	NH1, L_ARG_31	HH11, L_ARG_31	2.81	2.04	22.49
3TJE.PDB	O, L_ASN_28	N, L_TYR_32	H, L_TYR_32	2.86	2.10	23.81
3TJE.PDB	OD1, L_ASN_52	N, L_VAL_34	H, L_VAL_34	2.85	2.02	12.87
3TJE.PDB	O, L_SER_90	N, L_ASN_35	H, L_ASN_35	2.92	2.09	12.93
3TJE.PDB	O, H_ALA_117	ND2, L_ASN_35	HD21, L_ASN_35	2.81	2.01	17.88
3TJE.PDB	O, L_ILE_49	N, L_TRP_36	H, L_TRP_36	2.75	1.91	11.08
3TJE.PDB	O, L_TYR_88	N, L_TYR_37	H, L_TYR_37	2.81	1.99	14.58
3TJE.PDB	O, L_LYS_46	N, L_GLN_38	H, L_GLN_38	2.87	2.07	18.73

3TJE.PDB	OH, L_TYR_87	NE2, L_GLN_38	HE21, L_GLN_38	2.91	2.10	17.00
3TJE.PDB	O, L_ASP_86	N, L_GLN_39	H, L_GLN_39	2.75	1.92	11.44
3TJE.PDB	O, L_LYS_43	NE2, L_GLN_39	HE21, L_GLN_39	2.96	2.17	20.11
3TJE.PDB	O, L_LEU_40	N, L_LYS_43	H, L_LYS_43	2.81	1.96	7.60
3TJE.PDB	O, L_GLN_38	N, L_LYS_46	H, L_LYS_46	2.89	2.11	21.83
3TJE.PDB	O, L_TRP_36	N, L_LEU_48	H, L_LEU_48	2.96	2.15	16.44
3TJE.PDB	O, L_LEU_54	N, L_TYR_50	H, L_TYR_50	2.88	2.07	15.46
3TJE.PDB	O, L_VAL_34	N, L_ASN_52	H, L_ASN_52	2.84	2.00	11.32
3TJE.PDB	O, L_TYR_51	N, L_ASN_53	H, L_ASN_53	2.85	2.14	29.08
3TJE.PDB	O, L_TYR_50	N, L_LEU_54	H, L_LEU_54	2.99	2.17	16.15
3TJE.PDB	O, L_PHE_63	NH1, L_ARG_55	HH11, L_ARG_55	2.88	2.12	23.88
3TJE.PDB	OD2, L_ASP_83	NH1, L_ARG_62	HH12, L_ARG_62	2.77	1.98	19.25
3TJE.PDB	OD1, L_ASP_83	NH2, L_ARG_62	HH22, L_ARG_62	2.87	2.01	3.19
3TJE.PDB	O, L_SER_73	N, L_SER_66	H, L_SER_66	2.91	2.14	21.13
3TJE.PDB	O, L_BSER_73	N, L_SER_66	H, L_SER_66	2.91	2.13	20.97
3TJE.PDB	O, L_TYR_32	NZ, L_LYS_67	HZ2, L_LYS_67	2.82	2.02	22.26
3TJE.PDB	O, L_SER_71	N, L_SER_68	H, L_SER_68	2.88	2.03	8.39
3TJE.PDB	O, L_SER_68	N, L_SER_71	H, L_SER_71	2.99	2.15	8.41
3TJE.PDB	O, L_CYS_22	N, L_ALA_72	H, L_ALA_72	2.87	2.04	13.56
3TJE.PDB	O, L_SER_66	N, L_ASER_73	H, L_ASER_73	2.83	2.04	18.54
3TJE.PDB	O, L_SER_66	N, L_BSER_73	H, L_BSER_73	2.85	2.06	19.36
3TJE.PDB	O, L_ILE_20	N, L_LEU_74	H, L_LEU_74	2.94	2.12	13.68
3TJE.PDB	O, L_SER_64	N, L_ALA_75	H, L_ALA_75	2.88	2.03	9.17
3TJE.PDB	O, L_VAL_18	N, L_ILE_76	H, L_ILE_76	2.93	2.11	14.42
3TJE.PDB	OD2, L_ASP_78	NH1, L_ARG_77	HH11, L_ARG_77	2.74	1.93	16.91
3TJE.PDB	O, L_GLN_16	N, L_LEU_79	H, L_LEU_79	2.98	2.14	10.89
3TJE.PDB	OD2, L_ASP_83	N, L_LEU_80	H, L_LEU_80	2.81	1.96	7.20
3TJE.PDB	O, L_LEU_80	N, L_ASP_83	H, L_ASP_83	2.88	2.03	9.91
3TJE.PDB	O, L_THR_105	N, L_TYR_87	H, L_TYR_87	2.92	2.12	18.00
3TJE.PDB	O, L_TYR_37	N, L_TYR_88	H, L_TYR_88	2.91	2.09	14.23
3TJE.PDB	O, L_PRO_33	OG1, L_THR_91	HG1, L_THR_91	2.76	2.04	23.18
3TJE.PDB	O, L_GLY_98	N, L_ASP_93	H, L_ASP_93	2.88	2.03	9.26
3TJE.PDB	O, L_PHE_27	N, L_ASP_94	H, L_ASP_94	2.94	2.09	6.58
3TJE.PDB	OD2, L_ASP_93	N, L_LEU_96	H, L_LEU_96	2.80	2.01	19.19
3TJE.PDB	O, L_THR_91	N, L_VAL_100	H, L_VAL_100	2.77	1.92	9.60
3TJE.PDB	O, L_CYS_89	N, L_GLY_102	H, L_GLY_102	2.86	2.05	17.43
3TJE.PDB	O, L_TYR_87	N, L_THR_105	H, L_THR_105	2.85	2.08	21.91
3TJE.PDB	O, L_PRO_7	OG1, L_THR_105	HG1, L_THR_105	2.71	1.92	11.71
3TJE.PDB	O, L_PRO_8	N, L_LYS_106	H, L_LYS_106	2.83	1.98	10.06
3TJE.PDB	O, L_ALA_85	N, L_VAL_107	H, L_VAL_107	2.95	2.10	8.53
3TJE.PDB	OE2, L_GLU_84	N, L_VAL_109	H, L_VAL_109	2.88	2.05	12.54
3TJE.PDB	O, L_GLU_12	N, L_LEU_110	H, L_LEU_110	2.90	2.08	14.25
3TJE.PDB	OH, L_TYR_144	N, L_GLY_111	H, L_GLY_111	2.92	2.12	17.61
3TJE.PDB	O, L_TYR_144	N, L_ALA_115	H, L_ALA_115	2.80	2.00	16.96
3TJE.PDB	O, L_SER_141	N, L_SER_118	H, L_SER_118	2.91	2.14	22.45
3TJE.PDB	O, L_LEU_139	N, L_THR_120	H, L_THR_120	2.96	2.12	10.98
3TJE.PDB	O, L_VAL_137	N, L_PHE_122	H, L_PHE_122	2.77	1.92	8.56
3TJE.PDB	O, L_LEU_129	N, L_ASN_132	H, L_ASN_132	2.97	2.15	16.34
3TJE.PDB	OE2, L_GLU_128	OG1, L_THR_135	HG1, L_THR_135	2.52	1.76	18.95
3TJE.PDB	O, L_LEU_182	N, L_LEU_136	H, L_LEU_136	2.82	1.99	11.01
3TJE.PDB	O, L_SER_180	N, L_CYS_138	H, L_CYS_138	2.78	1.93	6.24
3TJE.PDB	O, L_THR_120	N, L_LEU_139	H, L_LEU_139	2.87	2.03	10.47
3TJE.PDB	O, L_ALA_178	N, L_ILE_140	H, L_ILE_140	2.83	2.07	23.88
3TJE.PDB	OE1, L_GLN_171	N, L_ASP_142	H, L_ASP_142	2.90	2.05	8.27
3TJE.PDB	O, L_ALA_115	N, L_TYR_144	H, L_TYR_144	2.95	2.16	19.36
3TJE.PDB	O, L_THR_200	N, L_THR_149	H, L_THR_149	2.90	2.10	17.11
3TJE.PDB	O, L_GLN_198	N, L_ALA_151	H, L_ALA_151	2.89	2.08	16.72
3TJE.PDB	OG, L_SER_180	NE1, L_TRP_152	HE1, L_TRP_152	2.95	2.10	8.91

3TJE.PDB	O, L.SER.157	N, L.ALA.154	H, L.ALA.154	2.87	2.03	11.03
3TJE.PDB	O, L.SER.194	N, L.ASP.155	H, L.ASP.155	2.88	2.03	6.45
3TJE.PDB	O, L.ALA.154	N, L.SER.157	H, L.SER.157	2.84	2.00	9.67
3TJE.PDB	O, L.SER.179	N, L.THR.166	H, L.THR.166	2.85	2.03	14.19
3TJE.PDB	O, L.ALA.177	N, L.SER.169	H, L.SER.169	2.80	1.99	16.63
3TJE.PDB	O, L.LYS.175	N, L.GLN.171	H, L.GLN.171	2.71	1.85	3.49
3TJE.PDB	OD1, L.ASP.142	NE2, L.GLN.171	HE21, L.GLN.171	2.80	1.98	15.09
3TJE.PDB	O, L.GLN.171	N, L.ASN.174	H, L.ASN.174	2.96	2.12	11.80
3TJE.PDB	OD1, L.ASN.173	N, L.LYS.175	H, L.LYS.175	2.90	2.05	7.85
3TJE.PDB	O, L.PHE.143	N, L.TYR.176	H, L.TYR.176	2.84	2.01	10.88
3TJE.PDB	O, L.SER.169	N, L.ALA.177	H, L.ALA.177	2.94	2.12	14.89
3TJE.PDB	O, L.ILE.140	N, L.ALA.178	H, L.ALA.178	2.67	1.87	18.00
3TJE.PDB	OG1, L.THR.166	N, L.SER.179	H, L.SER.179	2.90	2.10	18.20
3TJE.PDB	O, L.CYS.138	N, L.SER.180	H, L.SER.180	2.89	2.09	17.42
3TJE.PDB	O, L.GLU.164	N, L.TYR.181	H, L.TYR.181	2.81	1.99	15.18
3TJE.PDB	O, L.LEU.136	N, L.LEU.182	H, L.LEU.182	2.96	2.15	16.77
3TJE.PDB	O, L.GLY.162	N, L.SER.183	H, L.SER.183	2.95	2.11	9.60
3TJE.PDB	O, L.ALA.134	N, L.LEU.184	H, L.LEU.184	2.91	2.06	5.00
3TJE.PDB	OG1, L.THR.185	N, L.GLN.188	H, L.GLN.188	2.93	2.09	10.43
3TJE.PDB	O, L.THR.185	N, L.TRP.189	H, L.TRP.189	2.96	2.12	11.25
3TJE.PDB	O, L.VAL.210	N, L.TYR.195	H, L.TYR.195	2.89	2.08	15.12
3TJE.PDB	O, L.LYS.153	N, L.SER.196	H, L.SER.196	2.96	2.16	17.59
3TJE.PDB	O, L.LYS.208	N, L.CYS.197	H, L.CYS.197	2.95	2.14	16.29
3TJE.PDB	O, L.ALA.151	N, L.GLN.198	H, L.GLN.198	2.79	1.94	4.13
3TJE.PDB	O, L.VAL.206	N, L.VAL.199	H, L.VAL.199	2.84	2.01	12.78
3TJE.PDB	O, L.THR.149	N, L.THR.200	H, L.THR.200	2.81	1.96	9.64
3TJE.PDB	OG1, L.THR.205	OG1, L.THR.200	HG1, L.THR.200	2.75	1.97	15.90
3TJE.PDB	O, L.SER.204	N, L.HIS.201	H, L.HIS.201	2.96	2.13	12.24
3TJE.PDB	O, L.PRO.145	NE2, L.HIS.201	HE2, L.HIS.201	2.93	2.12	17.78
3TJE.PDB	O, L.TYR.195	N, L.VAL.210	H, L.VAL.210	2.98	2.16	15.92
3TJE.PDB	O, H.SER.25	N, H.GLN.3	H, H.GLN.3	2.88	2.06	14.24
3TJE.PDB	O, H.THR.21	N, H.SER.7	H, H.SER.7	2.87	2.11	23.93
3TJE.PDB	O, H.THR.129	N, H.VAL.12	H, H.VAL.12	2.84	2.01	13.76
3TJE.PDB	O, H.VAL.92	N, H.SER.15	H, H.SER.15	2.99	2.17	15.06
3TJE.PDB	O, H.LEU.89	N, H.LEU.18	H, H.LEU.18	2.80	1.97	12.54
3TJE.PDB	O, H.LEU.87	N, H.LEU.20	H, H.LEU.20	2.91	2.09	15.75
3TJE.PDB	O, H.SER.7	N, H.THR.21	H, H.THR.21	2.91	2.07	9.29
3TJE.PDB	O, H.VAL.85	N, H.CYS.22	H, H.CYS.22	2.64	1.80	12.14
3TJE.PDB	O, H.GLN.5	N, H.THR.23	H, H.THR.23	2.80	1.95	6.62
3TJE.PDB	O, H.ASN.83	N, H.VAL.24	H, H.VAL.24	2.83	1.97	5.09
3TJE.PDB	O, H.GLN.3	N, H.SER.25	H, H.SER.25	2.89	2.05	10.07
3TJE.PDB	OD1, H.ASN.83	N, H.ILE.29	H, H.ILE.29	2.95	2.10	5.57
3TJE.PDB	O, H.TYR.55	N, H.TYR.34	H, H.TYR.34	2.89	2.10	20.67
3TJE.PDB	O, H.ILE.53	N, H.GLY.36	H, H.GLY.36	2.94	2.15	19.40
3TJE.PDB	O, H.ALA.103	N, H.VAL.37	H, H.VAL.37	2.90	2.07	11.42
3TJE.PDB	O, H.TYR.101	N, H.VAL.39	H, H.VAL.39	2.86	2.03	12.06
3TJE.PDB	O, H.GLU.48	N, H.ARG.40	H, H.ARG.40	2.80	1.98	14.17
3TJE.PDB	OE1, H.GLU.48	NE, H.ARG.40	HE, H.ARG.40	2.72	1.90	14.58
3TJE.PDB	OD1, H.ASP.96	NH1, H.ARG.40	HH12, H.ARG.40	2.84	2.01	12.94
3TJE.PDB	O, H.LEU.99	N, H.GLN.41	H, H.GLN.41	2.86	2.14	27.68
3TJE.PDB	OE1, L.GLN.39	NE2, H.GLN.41	HE21, H.GLN.41	2.98	2.15	10.85
3TJE.PDB	O, H.LYS.45	NE2, H.GLN.41	HE22, H.GLN.41	2.99	2.23	24.37
3TJE.PDB	O, H.SER.42	N, H.LYS.45	H, H.LYS.45	2.68	1.88	17.77
3TJE.PDB	O, H.ARG.40	N, H.GLU.48	H, H.GLU.48	2.85	2.11	26.04
3TJE.PDB	O, H.TRP.38	N, H.VAL.50	H, H.VAL.50	2.78	1.93	6.45
3TJE.PDB	O, H.GLY.36	N, H.ILE.53	H, H.ILE.53	2.93	2.12	17.64
3TJE.PDB	O, H.SER.63	N, H.ALA.54	H, H.ALA.54	2.78	1.96	13.18
3TJE.PDB	O, H.TYR.34	N, H.TYR.55	H, H.TYR.55	2.89	2.08	16.16

3TJE.PDB	O, H_SER_61	N, H_ARG_56	H, H_ARG_56	2.85	1.99	1.86
3TJE.PDB	O, H_ALA_54	N, H_SER_63	H, H_SER_63	2.78	2.05	26.84
3TJE.PDB	O, H_VAL_50	N, H_ASN_67	H, H_ASN_67	2.97	2.11	4.12
3TJE.PDB	O, H_TRP_49	ND2, H_ASN_67	HD21, H_ASN_67	2.89	2.04	7.41
3TJE.PDB	OD1, H_ASN_67	N, H_SER_69	H, H_SER_69	2.97	2.12	5.43
3TJE.PDB	O, H_LEU_70	N, H_ARG_73	H, H_ARG_73	2.89	2.05	11.17
3TJE.PDB	OD2, H_ASP_96	NH1, H_ARG_73	HH12, H_ARG_73	2.84	2.09	24.31
3TJE.PDB	OD1, H_ASP_96	NH2, H_ARG_73	HH22, H_ARG_73	2.94	2.09	3.77
3TJE.PDB	O, H_ARG_88	N, H_THR_75	H, H_THR_75	2.86	2.06	17.69
3TJE.PDB	OH, H_TYR_66	N, H_VAL_76	H, H_VAL_76	2.78	1.97	16.41
3TJE.PDB	O, H_GLN_84	N, H_ASP_79	H, H_ASP_79	2.90	2.07	12.81
3TJE.PDB	OD2, H_ASP_79	OG, H_SER_81	HG, H_SER_81	2.85	2.15	27.35
3TJE.PDB	O, H_ALA_27	ND2, H_ASN_83	HD21, H_ASN_83	2.68	1.91	21.50
3TJE.PDB	O, H_VAL_24	ND2, H_ASN_83	HD22, H_ASN_83	2.83	2.02	14.94
3TJE.PDB	O, H_CYS_22	N, H_VAL_85	H, H_VAL_85	2.88	2.08	16.90
3TJE.PDB	O, H_SER_77	N, H_SER_86	H, H_SER_86	2.83	2.01	15.98
3TJE.PDB	O, H_LEU_20	N, H_LEU_87	H, H_LEU_87	2.94	2.13	16.25
3TJE.PDB	O, H_THR_75	N, H_ARG_88	H, H_ARG_88	2.86	2.03	13.96
3TJE.PDB	O, H_LEU_18	N, H_LEU_89	H, H_LEU_89	2.84	2.02	14.49
3TJE.PDB	O, H_ARG_73	N, H_THR_90	H, H_THR_90	2.85	2.04	16.07
3TJE.PDB	O, H_THR_93	N, H_ASP_96	H, H_ASP_96	2.94	2.10	9.54
3TJE.PDB	O, H_GLN_41	N, H_LEU_99	H, H_LEU_99	2.74	1.92	14.43
3TJE.PDB	O, H_THR_126	N, H_TYR_100	H, H_TYR_100	2.79	1.93	2.67
3TJE.PDB	O, H_VAL_39	N, H_TYR_101	H, H_TYR_101	2.77	1.93	10.43
3TJE.PDB	OE2, H_GLU_6	N, H_CYS_102	H, H_CYS_102	2.72	1.91	15.94
3TJE.PDB	O, H_VAL_121	N, H_ARG_104	H, H_ARG_104	2.91	2.13	21.28
3TJE.PDB	OD1, H_ASP_120	NE, H_ARG_104	HE, H_ARG_104	2.87	2.06	15.55
3TJE.PDB	OD2, H_ASP_120	NH2, H_ARG_104	HH21, H_ARG_104	2.68	1.96	27.63
3TJE.PDB	O, H_TYR_35	N, H_ARG_105	H, H_ARG_105	2.94	2.12	13.39
3TJE.PDB	O, F_CYS_43	NH1, H_ARG_105	HH12, H_ARG_105	2.85	2.08	23.11
3TJE.PDB	O, H_ALA_118	N, H_GLN_106	H, H_GLN_106	2.87	2.03	10.40
3TJE.PDB	O, H_TRP_116	N, H_LEU_108	H, H_LEU_108	2.87	2.02	4.86
3TJE.PDB	O, H_TYR_114	N, H_ASP_110	H, H_ASP_110	2.92	2.19	27.17
3TJE.PDB	OD2, H_ASP_110	N, H_THR_112	H, H_THR_112	3.00	2.17	12.16
3TJE.PDB	O, H_LEU_108	N, H_TRP_116	H, H_TRP_116	3.00	2.21	20.70
3TJE.PDB	OH, L_TYR_37	N, H_PHE_119	H, H_PHE_119	2.96	2.10	4.74
3TJE.PDB	O, H_CYS_102	N, H_GLY_123	H, H_GLY_123	2.82	2.01	17.20
3TJE.PDB	OE1, H_GLU_6	N, H_GLY_125	H, H_GLY_125	2.75	1.92	11.39
3TJE.PDB	O, H_TYR_100	N, H_THR_126	H, H_THR_126	2.90	2.10	17.97
3TJE.PDB	O, H_ALA_98	N, H_VAL_128	H, H_VAL_128	2.90	2.08	14.31
3TJE.PDB	O, H_GLY_10	N, H_THR_129	H, H_THR_129	2.80	1.96	9.76
3TJE.PDB	O, H_VAL_12	N, H_SER_131	H, H_SER_131	3.00	2.24	24.52
3TJE.PDB	O, H_PHE_165	N, H_LYS_136	H, H_LYS_136	2.83	2.02	16.58
3TJE.PDB	O, H_ASP_163	NZ, H_LYS_136	HZ2, H_LYS_136	2.77	1.97	20.93
3TJE.PDB	O, H_LEU_160	N, H_PHE_141	H, H_PHE_141	2.88	2.04	12.24
3TJE.PDB	O, H_GLY_158	N, H_LEU_143	H, H_LEU_143	2.57	1.72	7.54
3TJE.PDB	O, H_VAL_203	N, H_ALA_155	H, H_ALA_155	2.69	1.91	20.72
3TJE.PDB	O, H_LEU_143	N, H_GLY_158	H, H_GLY_158	2.85	2.05	18.58
3TJE.PDB	O, H_SER_199	N, H_CYS_159	H, H_CYS_159	2.99	2.22	22.42
3TJE.PDB	O, H_PHE_141	N, H_LEU_160	H, H_LEU_160	2.79	1.97	14.71
3TJE.PDB	O, H_LEU_197	N, H_VAL_161	H, H_VAL_161	2.81	1.97	8.46
3TJE.PDB	O, H_SER_139	N, H_ALYS_162	H, H_ALYS_162	2.77	1.93	9.67
3TJE.PDB	O, H_SER_139	N, H_BLYS_162	H, H_BLYS_162	2.78	1.95	10.83
3TJE.PDB	N, H_ALYS_162	N, H_BLYS_162	H, H_BLYS_162	0.01	0.85	29.33
3TJE.PDB	O, H_TYR_195	N, H_TYR_164	H, H_TYR_164	2.92	2.13	20.02
3TJE.PDB	OG, H_SER_199	NE1, H_TRP_173	HE1, H_TRP_173	2.95	2.10	8.21
3TJE.PDB	O, H_ILE_214	N, H_ASN_174	H, H_ASN_174	2.64	1.81	12.80
3TJE.PDB	O, H_THR_212	ND2, H_ASN_174	HD21, H_ASN_174	2.99	2.18	18.13

3TJE.PDB	OD1, H.ASN.216	N, H.SER.175	H, H.SER.175	2.79	2.01	20.02
3TJE.PDB	O, H.TRP.173	N, H.GLY.176	H, H.GLY.176	2.73	1.90	13.59
3TJE.PDB	O, H.VAL.200	N, H.HIS.183	H, H.HIS.183	2.76	1.93	13.04
3TJE.PDB	O, H.SER.198	N, H.PHE.185	H, H.PHE.185	2.93	2.09	11.93
3TJE.PDB	O, H.SER.196	N, H.VAL.188	H, H.VAL.188	2.92	2.13	19.94
3TJE.PDB	O, H.LEU.194	N, H.GLN.190	H, H.GLN.190	2.89	2.03	2.73
3TJE.PDB	OD1, H.ASP.163	NE2, H.GLN.190	HE21, H.GLN.190	2.74	1.93	16.43
3TJE.PDB	O, H.LEU.194	NE2, H.GLN.190	HE22, H.GLN.190	2.91	2.07	10.67
3TJE.PDB	O, H.GLN.190	N, H.GLY.193	H, H.GLY.193	2.82	1.99	10.97
3TJE.PDB	O, H.TYR.164	N, H.TYR.195	H, H.TYR.195	2.85	2.00	9.32
3TJE.PDB	O, H.HIS.183	N, H.VAL.200	H, H.VAL.200	2.82	2.00	16.33
3TJE.PDB	O, H.LEU.157	N, H.VAL.201	H, H.VAL.201	2.89	2.05	10.36
3TJE.PDB	O, H.ALA.155	N, H.VAL.203	H, H.VAL.203	2.94	2.10	10.75
3TJE.PDB	O, H.GLY.153	N, H.SER.205	H, H.SER.205	2.57	1.73	10.17
3TJE.PDB	OD1, H.ASN.174	N, H.ILE.214	H, H.ILE.214	2.72	1.92	17.15
3TJE.PDB	O, H.SER.172	N, H.ASN.216	H, H.ASN.216	2.85	2.03	15.86
3TJE.PDB	OD1, H.ASP.227	ND2, H.ASN.216	HD22, H.ASN.216	2.79	1.98	17.28
3TJE.PDB	O, H.VAL.226	N, H.VAL.217	H, H.VAL.217	2.75	1.89	4.56
3TJE.PDB	O, H.THR.170	N, H.AASN.218	H, H.AASN.218	2.99	2.16	12.40
3TJE.PDB	O, H.THR.170	N, H.BASN.218	H, H.BASN.218	2.97	2.14	13.28
3TJE.PDB	O, H.PRO.166	NE2, H.HIS.219	HE2, H.HIS.219	2.74	1.90	8.90
3TJE.PDB	O, H.LYS.220	N, H.ASN.223	H, H.ASN.223	2.92	2.10	14.79
3TJE.PDB	OG1, H.SER.222	OG1, H.THR.224	HG1, H.THR.224	2.65	1.92	22.20
3TJE.PDB	O, H.VAL.217	N, H.VAL.226	H, H.VAL.226	2.85	2.02	13.83
3TJE.PDB	O, H.CYS.215	N, H.LYS.228	H, H.LYS.228	2.90	2.09	15.61
3TJE.PDB	O, H.TYR.213	N, H.VAL.230	H, H.VAL.230	2.88	2.03	8.45
3TJE.PDB	O, F.GLY.40	N, F.CYS.43	H, F.CYS.43	2.88	2.06	15.38
3TJE.PDB	OE2, F.GLU.63	N, F.HIS.44	H, F.HIS.44	2.91	2.05	1.72
3TJE.PDB	OH, H.TYR.35	ND1, F.HIS.44	HD1, F.HIS.44	2.56	1.70	3.69
3TJE.PDB	OE1, F.GLU.63	N, F.LYS.45	H, F.LYS.45	2.91	2.10	15.27
3TJE.PDB	O, F.HIS.80	N, F.CYS.47	H, F.CYS.47	2.82	1.98	10.44
3TJE.PDB	OG1, F.THR.76	N, F.GLY.50	H, F.GLY.50	2.74	2.01	27.76
3TJE.PDB	O, F.VAL.67	N, F.ARG.52	H, F.ARG.52	2.89	2.17	27.83
3TJE.PDB	O, F.SER.82	N, F.LYS.53	H, F.LYS.53	2.94	2.10	9.60
3TJE.PDB	O, F.ASP.65	N, F.ALA.54	H, F.ALA.54	2.88	2.07	15.43
3TJE.PDB	O, F.ARG.52	N, F.VAL.67	H, F.VAL.67	2.77	1.94	11.91
3TJE.PDB	O, F.GLY.50	N, F.CYS.69	H, F.CYS.69	2.96	2.12	10.65
3TJE.PDB	O, F.GLN.70	N, F.LYS.73	H, F.LYS.73	2.97	2.14	11.31
3TJE.PDB	O, F.GLN.70	N, F.GLU.74	H, F.GLU.74	2.91	2.06	7.91
3TJE.PDB	O, F.ARG.86	N, F.TYR.75	H, F.TYR.75	2.68	1.90	20.37
3TJE.PDB	O, F.ARG.105	N, F.THR.76	H, F.THR.76	2.92	2.12	18.47
3TJE.PDB	O, F.GLU.51	NE2, F.HIS.80	HE2, F.HIS.80	2.72	1.86	5.72
3TJE.PDB	O, F.TYR.75	N, F.ARG.86	H, F.ARG.86	2.68	1.83	6.97
3TJE.PDB	O, F.LYS.73	N, F.CYS.88	H, F.CYS.88	2.78	1.92	5.80
3TJE.PDB	OD1, F.ASN.108	N, F.AARG.89	H, F.AARG.89	2.87	2.04	11.64
3TJE.PDB	OD1, F.ASN.108	N, F.BARG.89	H, F.BARG.89	2.83	1.98	7.34
3TJE.PDB	OD1, F.ASP.92	N, F.GLY.94	H, F.GLY.94	2.84	2.05	19.77
3TJE.PDB	O, F.ASP.92	N, F.HIS.95	H, F.HIS.95	2.97	2.16	18.09
3TJE.PDB	O, F.GLU.93	N, F.GLY.96	H, F.GLY.96	2.71	1.88	12.35
3TJE.PDB	O, F.ARG.112	N, F.GLU.98	H, F.GLU.98	2.94	2.15	19.49
3TJE.PDB	O, F.LYS.110	N, F.GLU.100	H, F.GLU.100	2.61	1.76	9.32
3TJE.PDB	O, F.GLN.107	N, F.THR.104	H, F.THR.104	2.82	1.98	10.85
3TJE.PDB	O, F.ILE.101	N, F.LYS.110	H, F.LYS.110	2.83	1.99	9.81
3TJE.PDB	OE2, F.GLU.98	NE, F.ARG.112	HE, F.ARG.112	2.97	2.20	22.98
3TJE.PDB	O, F.GLY.96	N, F.LYS.114	H, F.LYS.114	2.92	2.14	21.07
3TJE.PDB	O, F.LYS.114	N, F.PHE.117	H, F.PHE.117	2.97	2.13	10.64
3TJE.PDB	O, F.ASP.128	N, F.PHE.118	H, F.PHE.118	2.93	2.18	24.79
3TJE.PDB	O, F.HIS.95	N, F.CYS.127	H, F.CYS.127	2.92	2.09	13.51

3U2S.PDB	O, H_SER_25	N, H_ARG_3	H, H_ARG_3	2.89	2.07	15.49
3U2S.PDB	O, H_SER_21	N, H_SER_7	H, H_SER_7	2.84	2.05	19.48
3U2S.PDB	O, H_THR_110	N, H_VAL_12	H, H_VAL_12	2.86	2.03	11.16
3U2S.PDB	O, H_LEU_82C	N, H_GLY_15	H, H_GLY_15	2.74	1.93	16.73
3U2S.PDB	O, H_MET_82	N, H_LEU_18	H, H_LEU_18	2.81	2.03	20.52
3U2S.PDB	O, H_LEU_80	N, H_LEU_20	H, H_LEU_20	2.85	2.03	14.92
3U2S.PDB	O, H_SER_7	N, H_SER_21	H, H_SER_21	2.93	2.09	10.95
3U2S.PDB	O, H_VAL_5	N, H_ALA_23	H, H_ALA_23	2.92	2.11	16.83
3U2S.PDB	O, H_ASP_76	N, H_ALA_24	H, H_ALA_24	2.96	2.10	4.40
3U2S.PDB	O, H_ASP_100L	NE, H_ARG_31	HE, H_ARG_31	2.89	2.12	21.23
3U2S.PDB	O, H_ASP_100L	NH2, H_ARG_31	HH21, H_ARG_31	2.93	2.18	24.99
3U2S.PDB	O, H_VAL_93	N, H_HIS_35	H, H_HIS_35	2.77	1.93	11.33
3U2S.PDB	OE1, H_GLU_95	NE2, H_HIS_35	HE2, H_HIS_35	2.64	1.80	11.05
3U2S.PDB	O, H_ALA_49	N, H_TRP_36	H, H_TRP_36	2.96	2.24	28.24
3U2S.PDB	O, H_TYR_79	NE1, H_TRP_36	HE1, H_TRP_36	2.98	2.22	24.67
3U2S.PDB	O, H_PHE_91	N, H_VAL_37	H, H_VAL_37	2.97	2.15	14.01
3U2S.PDB	O, H_GLU_46	N, H_ARG_38	H, H_ARG_38	2.90	2.05	8.68
3U2S.PDB	OE2, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.80	2.01	18.34
3U2S.PDB	OD1, H_ASP_86	NH1, H_ARG_38	HH12, H_ARG_38	2.84	2.00	11.28
3U2S.PDB	OE2, H_GLU_46	NH2, H_ARG_38	HH21, H_ARG_38	2.92	2.18	25.81
3U2S.PDB	O, H_THR_89	N, H_GLN_39	H, H_GLN_39	2.85	2.11	25.60
3U2S.PDB	OE1, H_GLN_38	NE2, H_GLN_39	HE22, H_GLN_39	2.89	2.04	8.55
3U2S.PDB	O, H_ALA_40	N, H_GLN_43	H, H_GLN_43	2.91	2.10	16.74
3U2S.PDB	O, H_ARG_38	N, H_GLU_46	H, H_GLU_46	2.82	2.01	17.41
3U2S.PDB	O, H_TRP_36	N, H_VAL_48	H, H_VAL_48	2.95	2.12	14.22
3U2S.PDB	O, H_TYR_58	N, H_PHE_50	H, H_PHE_50	2.96	2.16	17.41
3U2S.PDB	O, H_MET_34	N, H_ILE_51	H, H_ILE_51	2.86	2.05	16.44
3U2S.PDB	O, H_GLU_56	N, H_LYS_52	H, H_LYS_52	2.94	2.08	3.51
3U2S.PDB	O, H_PHE_100J	OH, H_TYR_52A	HH, H_TYR_52A	2.62	1.87	20.61
3U2S.PDB	O, H_LYS_52	N, H_GLY_54	H, H_GLY_54	2.83	2.01	14.33
3U2S.PDB	O, H_PHE_50	N, H_TYR_58	H, H_TYR_58	2.91	2.10	17.46
3U2S.PDB	O, H_VAL_48	N, H_ALA_60	H, H_ALA_60	2.97	2.15	15.16
3U2S.PDB	OE1, H_GLU_46	OG, H_SER_62	HG, H_SER_62	2.75	1.94	7.42
3U2S.PDB	O, H_VAL_63	N, H_ARG_66	H, H_ARG_66	2.80	2.00	17.44
3U2S.PDB	OD2, H_ASP_86	NH1, H_ARG_66	HH12, H_ARG_66	2.53	1.74	19.65
3U2S.PDB	OD1, H_ASP_86	NH2, H_ARG_66	HH22, H_ARG_66	2.93	2.08	7.53
3U2S.PDB	O, H_VAL_63	N, H_LEU_67	H, H_LEU_67	2.93	2.08	6.74
3U2S.PDB	O, H_GLN_81	N, H_SER_68	H, H_SER_68	2.87	2.07	17.94
3U2S.PDB	OD1, H_ASN_73	NE, H_ARG_71	HE, H_ARG_71	2.77	1.98	19.66
3U2S.PDB	O, H_GLN_32	NH1, H_ARG_71	HH12, H_ARG_71	2.91	2.17	26.10
3U2S.PDB	O, H_THR_77	N, H_ASP_72	H, H_ASP_72	2.85	2.01	9.05
3U2S.PDB	O, H_TYR_52A	ND2, H_ASN_73	HD22, H_ASN_73	2.99	2.13	6.14
3U2S.PDB	O, H_LYS_75	OG1, H_THR_77	HG1, H_THR_77	2.81	2.01	11.82
3U2S.PDB	O, H_CYS_22	N, H_LEU_78	H, H_LEU_78	2.95	2.13	14.49
3U2S.PDB	O, H_SER_70	N, H_TYR_79	H, H_TYR_79	2.84	1.99	5.70
3U2S.PDB	O, H_LEU_20	N, H_LEU_80	H, H_LEU_80	2.94	2.14	17.83
3U2S.PDB	O, H_SER_68	N, H_GLN_81	H, H_GLN_81	2.80	1.98	14.94
3U2S.PDB	O, H_LEU_18	N, H_MET_82	H, H_MET_82	2.77	1.95	13.17
3U2S.PDB	O, H_ARG_66	N, H_ASN_82A	H, H_ASN_82A	2.84	2.00	7.73
3U2S.PDB	OD2, H_ASP_86	N, H_ARG_83	H, H_ARG_83	2.90	2.08	14.43
3U2S.PDB	O, H_ARG_83	N, H_ASP_86	H, H_ASP_86	2.86	2.02	10.14
3U2S.PDB	O, H_VAL_84	N, H_THR_87	H, H_THR_87	2.92	2.08	10.30
3U2S.PDB	O, H_VAL_109	N, H_ALA_88	H, H_ALA_88	2.93	2.20	26.51
3U2S.PDB	O, H_GLN_39	N, H_THR_89	H, H_THR_89	2.92	2.16	23.30
3U2S.PDB	O, H_THR_107	N, H_TYR_90	H, H_TYR_90	2.86	2.02	9.16
3U2S.PDB	O, H_VAL_37	N, H_PHE_91	H, H_PHE_91	2.69	1.83	4.03
3U2S.PDB	OE2, H_GLU_6	N, H_CYS_92	H, H_CYS_92	2.82	1.99	11.94
3U2S.PDB	O, H_HIS_35	N, H_VAL_93	H, H_VAL_93	2.98	2.21	22.76

3U2S.PDB	O, H_VAL_102	N, H_ARG_94	H, H_ARG_94	2.86	2.04	14.82
3U2S.PDB	OD1, H_ASP_101	NE, H_ARG_94	HE, H_ARG_94	2.95	2.09	2.87
3U2S.PDB	OD2, H_ASP_101	NH2, H_ARG_94	HH21, H_ARG_94	2.85	2.03	14.60
3U2S.PDB	O, H_TYR_100S	N, H_ALA_96	H, H_ALA_96	2.80	1.96	10.51
3U2S.PDB	O, H_TYR_100E	N, H_ARG_100B	H, H_ARG_100B	2.95	2.16	20.33
3U2S.PDB	O, H_ARG_100B	N, H_TYR_100E	H, H_TYR_100E	2.87	2.03	10.02
3U2S.PDB	O, H_GLY_100M	N, H_ASP_100I	H, H_ASP_100I	2.85	2.06	18.58
3U2S.PDB	OD1, H_ASP_100I	N, H_PHE_100J	H, H_PHE_100J	2.74	2.00	25.64
3U2S.PDB	O, H_ARG_31	N, H_TYR_100N	H, H_TYR_100N	2.93	2.08	7.40
3U2S.PDB	O, H_GLY_98	N, H_TYR_100O	H, H_TYR_100O	2.86	2.13	27.57
3U2S.PDB	O, H_ALA_96	N, H_TYR_100Q	H, H_TYR_100Q	2.80	1.95	7.01
3U2S.PDB	OH, L_TYR_36	N, H_MET_100T	H, H_MET_100T	2.95	2.15	18.41
3U2S.PDB	OE1, H_GLU_6	N, H_GLY_106	H, H_GLY_106	2.86	2.05	16.47
3U2S.PDB	O, H_TYR_90	N, H_THR_107	H, H_THR_107	2.97	2.17	19.03
3U2S.PDB	O, H_ALA_88	N, H_VAL_109	H, H_VAL_109	2.87	2.02	6.55
3U2S.PDB	O, H_GLY_10	N, H_THR_110	H, H_THR_110	2.97	2.13	11.00
3U2S.PDB	OG1, H_THR_87	N, H_VAL_111	H, H_VAL_111	2.85	1.99	5.74
3U2S.PDB	O, H_VAL_12	N, H_SER_112	H, H_SER_112	2.94	2.12	13.79
3U2S.PDB	OG, H_SER_112	N, H_ALA_114	H, H_ALA_114	2.87	2.03	9.67
3U2S.PDB	O, H_PHE_146	N, H_LYS_117	H, H_LYS_117	2.83	1.99	11.04
3U2S.PDB	O, H_ASP_144	NZ, H_LYS_117	HZ2, H_LYS_117	2.56	1.71	13.65
3U2S.PDB	O, H_LYS_143	N, H_SER_120	H, H_SER_120	2.85	2.04	16.72
3U2S.PDB	O, H_LEU_141	N, H_PHE_122	H, H_PHE_122	2.95	2.11	11.99
3U2S.PDB	O, H_GLY_139	N, H_LEU_124	H, H_LEU_124	2.81	1.97	10.93
3U2S.PDB	O, H_VAL_184	N, H_ALA_136	H, H_ALA_136	2.85	2.04	17.15
3U2S.PDB	O, H_SER_180	N, H_CYS_140	H, H_CYS_140	2.86	2.06	19.17
3U2S.PDB	O, H_PHE_122	N, H_LEU_141	H, H_LEU_141	2.84	2.00	10.39
3U2S.PDB	O, H_LEU_178	N, H_VAL_142	H, H_VAL_142	2.75	1.92	11.05
3U2S.PDB	O, H_SER_120	N, H_LYS_143	H, H_LYS_143	2.79	1.93	5.65
3U2S.PDB	O, H_LYS_117	N, H_PHE_146	H, H_PHE_146	2.94	2.13	15.74
3U2S.PDB	O, H_ASN_199	N, H_THR_151	H, H_THR_151	2.99	2.18	16.40
3U2S.PDB	O, H_ASN_197	N, H_SER_153	H, H_SER_153	2.95	2.14	16.70
3U2S.PDB	OG, H_SER_180	NE1, H_TRP_154	HE1, H_TRP_154	2.93	2.08	7.46
3U2S.PDB	O, H_ILE_195	N, H_ASN_155	H, H_ASN_155	2.79	1.95	11.05
3U2S.PDB	OD1, H_ASN_197	N, H_SER_156	H, H_SER_156	2.71	1.93	20.75
3U2S.PDB	O, H_TRP_154	N, H_GLY_157	H, H_GLY_157	2.86	2.13	26.48
3U2S.PDB	O, H_ASN_155	N, H_ALA_158	H, H_ALA_158	2.95	2.09	5.38
3U2S.PDB	O, H_VAL_181	N, H_HIS_164	H, H_HIS_164	2.77	1.95	14.28
3U2S.PDB	OG, L_SER_165	NE2, H_HIS_164	HE2, H_HIS_164	2.93	2.12	16.97
3U2S.PDB	O, H_SER_179	N, H_PHE_166	H, H_PHE_166	2.88	2.02	1.67
3U2S.PDB	O, H_SER_177	N, H_VAL_169	H, H_VAL_169	2.82	2.01	16.07
3U2S.PDB	O, H_LEU_175	NE2, H_GLN_171	HE21, H_GLN_171	2.97	2.11	6.21
3U2S.PDB	OD2, H_ASP_144	NE2, H_GLN_171	HE22, H_GLN_171	2.87	2.09	20.57
3U2S.PDB	O, H_GLN_171	N, H_GLY_174	H, H_GLY_174	2.90	2.05	6.90
3U2S.PDB	O, H_TYR_145	N, H_TYR_176	H, H_TYR_176	2.78	1.93	7.16
3U2S.PDB	O, H_VAL_169	N, H_SER_177	H, H_SER_177	2.99	2.22	22.23
3U2S.PDB	O, H_VAL_142	N, H_LEU_178	H, H_LEU_178	2.92	2.13	19.87
3U2S.PDB	O, H_CYS_140	N, H_SER_180	H, H_SER_180	2.96	2.15	15.32
3U2S.PDB	O, H_HIS_164	N, H_VAL_181	H, H_VAL_181	2.88	2.05	12.91
3U2S.PDB	O, H_LEU_138	N, H_VAL_182	H, H_VAL_182	2.85	2.03	14.42
3U2S.PDB	O, H_ALA_136	N, H_VAL_184	H, H_VAL_184	2.90	2.07	11.08
3U2S.PDB	O, H_PRO_185	N, H_SER_188	H, H_SER_188	2.91	2.12	19.48
3U2S.PDB	O, H_SER_188	N, H_GLN_192	H, H_GLN_192	2.76	1.90	4.37
3U2S.PDB	OD1, H_ASN_155	N, H_ILE_195	H, H_ILE_195	2.89	2.08	16.84
3U2S.PDB	O, H_LYS_209	N, H_CYS_196	H, H_CYS_196	2.96	2.19	21.56
3U2S.PDB	O, H_SER_153	N, H_ASN_197	H, H_ASN_197	2.74	1.90	9.86
3U2S.PDB	OD2, H_ASP_208	ND2, H_ASN_197	HD21, H_ASN_197	2.76	1.92	10.02
3U2S.PDB	O, H_VAL_207	N, H_VAL_198	H, H_VAL_198	2.74	1.88	1.51

3U2S.PDB	O, H_THR_151	N, H_ASN_199	H, H_ASN_199	2.98	2.15	13.83
3U2S.PDB	O, H_THR_205	N, H_HIS_200	H, H_HIS_200	2.86	2.01	7.91
3U2S.PDB	OG, H_SER_203	ND1, H_HIS_200	HD1, H_HIS_200	2.77	1.92	6.39
3U2S.PDB	O, H_PRO_147	NE2, H_HIS_200	HE2, H_HIS_200	2.63	1.80	12.76
3U2S.PDB	O, H_LYS_201	N, H_ASN_204	H, H_ASN_204	2.93	2.10	12.81
3U2S.PDB	O, H_VAL_198	N, H_VAL_207	H, H_VAL_207	2.81	1.98	12.69
3U2S.PDB	O, H_CYS_196	N, H_LYS_209	H, H_LYS_209	2.98	2.15	13.52
3U2S.PDB	O, H_TYR_194	N, H_VAL_211	H, H_VAL_211	2.76	1.91	7.74
3U2S.PDB	O, L_GLN_24	N, L_THR_5	H, L_THR_5	2.92	2.09	11.98
3U2S.PDB	O, L_TYR_86	NE2, L_GLN_6	HE22, L_GLN_6	2.90	2.07	12.85
3U2S.PDB	O, L_LYS_103	N, L_VAL_11	H, L_VAL_11	2.95	2.14	17.04
3U2S.PDB	O, L_LEU_78	N, L_GLY_16	H, L_GLY_16	2.87	2.09	21.13
3U2S.PDB	O, L_ILE_75	N, L_ILE_19	H, L_ILE_19	3.00	2.19	17.55
3U2S.PDB	OG1, L_THR_74	OG1, L_THR_20	HG1, L_THR_20	2.83	2.11	23.78
3U2S.PDB	O, L_LEU_73	N, L_ILE_21	H, L_ILE_21	2.80	1.99	15.96
3U2S.PDB	O, L_THR_5	N, L_GLN_24	H, L_GLN_24	2.89	2.07	13.09
3U2S.PDB	O, L_ASN_69	N, L_GLY_25	H, L_GLY_25	2.76	1.90	2.23
3U2S.PDB	OD1, L_ASP_27B	N, L_THR_26	H, L_THR_26	2.75	1.92	10.72
3U2S.PDB	OD2, L_ASP_27B	OG1, L_THR_26	HG1, L_THR_26	2.86	2.11	19.40
3U2S.PDB	OD1, L_ASP_27B	N, L_VAL_27C	H, L_VAL_27C	2.60	1.80	17.74
3U2S.PDB	O, L_THR_26	N, L_GLY_28	H, L_GLY_28	2.91	2.07	11.04
3U2S.PDB	O, L_ASP_27B	N, L_GLY_29	H, L_GLY_29	2.99	2.17	15.01
3U2S.PDB	O, L_LYS_89	N, L_SER_34	H, L_SER_34	2.88	2.09	20.40
3U2S.PDB	O, L_ILE_48	N, L_TRP_35	H, L_TRP_35	2.79	1.99	17.98
3U2S.PDB	O, L_TYR_87	N, L_TYR_36	H, L_TYR_36	2.86	2.11	24.00
3U2S.PDB	O, L_LYS_45	N, L_GLN_37	H, L_GLN_37	2.86	2.04	13.48
3U2S.PDB	OH, L_TYR_86	NE2, L_GLN_37	HE21, L_GLN_37	2.82	1.97	2.95
3U2S.PDB	O, L_ASP_85	N, L_GLN_38	H, L_GLN_38	2.74	1.95	19.17
3U2S.PDB	O, L_LYS_42	NE2, L_GLN_38	HE21, L_GLN_38	2.89	2.06	12.72
3U2S.PDB	OE1, H_GLN_39	NE2, L_GLN_38	HE22, L_GLN_38	2.91	2.09	13.75
3U2S.PDB	O, L_GLN_37	N, L_LYS_45	H, L_LYS_45	2.88	2.16	27.52
3U2S.PDB	O, L_TRP_35	N, L_VAL_47	H, L_VAL_47	2.82	1.99	13.03
3U2S.PDB	O, L_LYS_53	N, L_TYR_49	H, L_TYR_49	2.89	2.08	17.33
3U2S.PDB	O, L_VAL_33	N, L_VAL_51	H, L_VAL_51	2.83	1.98	6.67
3U2S.PDB	O, L_ASP_50	N, L_SER_52	H, L_SER_52	2.90	2.20	29.99
3U2S.PDB	O, L_TYR_49	N, L_LYS_53	H, L_LYS_53	2.86	2.03	13.95
3U2S.PDB	OD2, L_ASP_50	NZ, L_LYS_53	HZ2, L_LYS_53	2.84	1.96	4.63
3U2S.PDB	O, L_PHE_62	NH1, L_ARG_54	HH11, L_ARG_54	2.99	2.19	18.54
3U2S.PDB	OD2, C_ASP_167	ND2, L_ASN_60	HD22, L_ASN_60	2.90	2.14	22.76
3U2S.PDB	OD2, L_ASP_82	NH1, L_ARG_61	HH12, L_ARG_61	2.86	2.09	21.77
3U2S.PDB	OD1, L_ASP_82	NH2, L_ARG_61	HH22, L_ARG_61	2.97	2.11	4.14
3U2S.PDB	O, L_THR_74	N, L_SER_63	H, L_SER_63	2.98	2.16	15.11
3U2S.PDB	O, L_SER_72	N, L_SER_65	H, L_SER_65	2.99	2.19	18.65
3U2S.PDB	OE2, L_GLU_31	NZ, L_LYS_66	HZ1, L_LYS_66	2.99	2.15	15.69
3U2S.PDB	O, L_VAL_27C	NZ, L_LYS_66	HZ3, L_LYS_66	2.87	2.07	20.96
3U2S.PDB	O, L_THR_70	N, L_SER_67	H, L_SER_67	2.98	2.14	11.28
3U2S.PDB	O, L_CYS_23	N, L_ALA_71	H, L_ALA_71	2.87	2.04	13.61
3U2S.PDB	O, L_SER_65	N, L_SER_72	H, L_SER_72	2.80	1.98	13.45
3U2S.PDB	O, L_ILE_21	N, L_LEU_73	H, L_LEU_73	2.88	2.06	14.21
3U2S.PDB	O, L_SER_63	N, L_THR_74	H, L_THR_74	2.87	2.03	10.26
3U2S.PDB	O, L_ILE_19	N, L_ILE_75	H, L_ILE_75	2.92	2.10	15.07
3U2S.PDB	O, L_GLN_17	N, L_LEU_78	H, L_LEU_78	2.99	2.15	10.36
3U2S.PDB	OD2, L_ASP_82	N, L_GLN_79	H, L_GLN_79	2.81	1.96	8.38
3U2S.PDB	O, L_GLN_79	N, L_ASP_82	H, L_ASP_82	2.92	2.07	8.13
3U2S.PDB	O, L_GLN_38	N, L_ASP_85	H, L_ASP_85	2.89	2.05	8.81
3U2S.PDB	O, L_THR_102	N, L_TYR_86	H, L_TYR_86	2.77	1.96	15.94
3U2S.PDB	OE1, L_GLN_6	N, L_CYS_88	H, L_CYS_88	2.99	2.16	12.72
3U2S.PDB	O, L_ARG_95A	N, L_THR_92	H, L_THR_92	2.99	2.23	24.29

3U2S.PDB	O, L_THR_92	N, L_ARG_95	H, L_ARG_95	2.97	2.16	16.66
3U2S.PDB	OD1, H_ASP_61	NH2, L_ARG_95A	HH22, L_ARG_95A	2.34	1.58	22.53
3U2S.PDB	OE2, H_GLU_95	NH2, L_ARG_96	HH21, L_ARG_96	2.87	2.05	15.72
3U2S.PDB	O, L_CYS_88	N, L_GLY_99	H, L_GLY_99	2.79	1.97	14.65
3U2S.PDB	O, L_TYR_86	N, L_THR_102	H, L_THR_102	2.76	2.00	23.00
3U2S.PDB	O, L_PRO_7	OG1, L_THR_102	HG1, L_THR_102	2.63	1.82	4.45
3U2S.PDB	O, L_ALA_8	N, L_LYS_103	H, L_LYS_103	2.97	2.12	6.71
3U2S.PDB	O, L_GLY_84	N, L_LEU_104	H, L_LEU_104	2.88	2.02	5.05
3U2S.PDB	O, L_VAL_11	N, L_THR_105	H, L_THR_105	2.95	2.13	14.49
3U2S.PDB	OE1, L_GLU_83	N, L_VAL_106	H, L_VAL_106	2.89	2.07	15.38
3U2S.PDB	O, L_GLY_13	N, L_LEU_106A	H, L_LEU_106A	2.94	2.12	14.62
3U2S.PDB	O, L_TYR_140	N, L_ALA_111	H, L_ALA_111	2.82	1.98	11.85
3U2S.PDB	O, L_SER_137	N, L_SER_114	H, L_SER_114	2.77	1.94	12.77
3U2S.PDB	O, L_LEU_135	N, L_THR_116	H, L_THR_116	2.87	2.04	11.07
3U2S.PDB	O, L_VAL_133	N, L_PHE_118	H, L_PHE_118	2.76	1.92	9.67
3U2S.PDB	O, L_SER_122	N, L_GLN_126	H, L_GLN_126	2.90	2.12	21.06
3U2S.PDB	O, L_GLU_124	N, L_ALA_127	H, L_ALA_127	2.91	2.17	26.56
3U2S.PDB	O, L_LEU_125	N, L_ASN_128	H, L_ASN_128	2.96	2.14	16.25
3U2S.PDB	OE2, L_GLU_124	OG1, L_THR_131	HG1, L_THR_131	2.54	1.83	25.31
3U2S.PDB	O, L_LEU_178	N, L_LEU_132	H, L_LEU_132	2.88	2.05	12.78
3U2S.PDB	O, L_SER_176	N, L_CYS_134	H, L_CYS_134	2.76	1.90	1.60
3U2S.PDB	O, L_THR_116	N, L_LEU_135	H, L_LEU_135	2.74	1.89	1.47
3U2S.PDB	O, L_ALA_174	N, L_ILE_136	H, L_ILE_136	2.84	2.02	15.96
3U2S.PDB	O, L_SER_114	N, L_SER_137	H, L_SER_137	2.84	2.03	17.34
3U2S.PDB	OE1, L_GLN_167	N, L_ASP_138	H, L_ASP_138	2.90	2.06	11.00
3U2S.PDB	O, L_ALA_111	N, L_TYR_140	H, L_TYR_140	2.92	2.12	18.95
3U2S.PDB	O, L_PRO_141	N, L_ALA_143	H, L_ALA_143	2.92	2.21	29.24
3U2S.PDB	O, L_THR_196	N, L_THR_145	H, L_THR_145	2.91	2.08	11.19
3U2S.PDB	O, L_GLN_194	N, L_ALA_147	H, L_ALA_147	2.84	2.02	14.58
3U2S.PDB	OG, L_SER_176	NE1, L_TRP_148	HE1, L_TRP_148	2.93	2.09	11.15
3U2S.PDB	O, L_SER_192	N, L_LYS_149	H, L_LYS_149	2.92	2.14	21.71
3U2S.PDB	O, L_SER_153	N, L_ALA_150	H, L_ALA_150	2.77	2.00	21.57
3U2S.PDB	O, L_SER_190	N, L_ASP_151	H, L_ASP_151	2.62	1.78	11.93
3U2S.PDB	O, L_TRP_148	N, L_VAL_155	H, L_VAL_155	2.98	2.16	15.40
3U2S.PDB	O, L_SER_175	N, L_THR_162	H, L_THR_162	2.82	2.00	14.91
3U2S.PDB	O, L_ALA_173	N, L_SER_165	H, L_SER_165	2.74	1.91	13.98
3U2S.PDB	O, L_LYS_171	N, L_GLN_167	H, L_GLN_167	2.73	1.88	8.55
3U2S.PDB	OD1, L_ASP_138	NE2, L_GLN_167	HE22, L_GLN_167	2.82	2.00	15.99
3U2S.PDB	OD1, L_ASP_138	ND2, L_ASN_169	HD22, L_ASN_169	2.92	2.10	15.30
3U2S.PDB	O, L_GLN_167	N, L_ASN_170	H, L_ASN_170	2.88	2.04	11.78
3U2S.PDB	OD1, L_ASN_169	N, L_LYS_171	H, L_LYS_171	2.91	2.07	8.70
3U2S.PDB	O, L_PHE_139	N, L_TYR_172	H, L_TYR_172	2.84	2.05	19.75
3U2S.PDB	O, L_SER_165	N, L_ALA_173	H, L_ALA_173	2.93	2.10	13.60
3U2S.PDB	O, L_ILE_136	N, L_ALA_174	H, L_ALA_174	2.74	1.97	22.21
3U2S.PDB	OG1, L_THR_162	N, L_SER_175	H, L_SER_175	2.92	2.13	19.21
3U2S.PDB	O, L_CYS_134	N, L_SER_176	H, L_SER_176	2.86	2.05	17.04
3U2S.PDB	O, L_GLU_160	N, L_TYR_177	H, L_TYR_177	2.73	1.94	18.58
3U2S.PDB	O, L_GLY_158	N, L_SER_179	H, L_SER_179	2.88	2.05	11.87
3U2S.PDB	O, L_ALA_130	N, L_LEU_180	H, L_LEU_180	2.86	2.01	7.38
3U2S.PDB	OE1, L_GLN_184	N, L_THR_181	H, L_THR_181	2.99	2.19	18.35
3U2S.PDB	O, L_VAL_206	N, L_TYR_191	H, L_TYR_191	2.95	2.11	11.29
3U2S.PDB	O, L_LYS_149	N, L_SER_192	H, L_SER_192	2.91	2.11	17.67
3U2S.PDB	O, L_ALA_147	N, L_GLN_194	H, L_GLN_194	2.75	1.91	11.28
3U2S.PDB	O, L_VAL_202	N, L_VAL_195	H, L_VAL_195	2.80	1.94	3.08
3U2S.PDB	O, L_THR_145	N, L_THR_196	H, L_THR_196	2.78	1.97	15.99
3U2S.PDB	OG1, L_THR_201	OG1, L_THR_196	HG1, L_THR_196	2.99	2.20	12.41
3U2S.PDB	O, L_SER_200	N, L_HIS_197	H, L_HIS_197	2.83	1.99	8.72
3U2S.PDB	O, L_PRO_141	NE2, L_HIS_197	HE2, L_HIS_197	2.95	2.17	20.02

3U2S.PDB	O, L_HIS_197	N, L_SER_200	H, L_SER_200	2.95	2.10	9.03
3U2S.PDB	O, L_VAL_195	N, L_VAL_202	H, L_VAL_202	2.82	1.99	11.70
3U2S.PDB	O, L_VAL_115	NZ, L_LYS_204	HZ2, L_LYS_204	2.85	2.09	26.22
3U2S.PDB	O, L_TYR_191	N, L_VAL_206	H, L_VAL_206	2.98	2.18	18.28
3U2S.PDB	O, G_THR_201	N, G_PHE_121	H, G_PHE_121	2.70	1.87	12.95
3U2S.PDB	O, G_PHE_235	N, G_ALA_124	H, G_ALA_124	2.87	2.04	12.10
3U2S.PDB	O, G_GLN_197	N, G_ALA_125	H, G_ALA_125	2.88	2.10	21.74
3U2S.PDB	O, G_VAL_237	N, G_CYS_126	H, G_CYS_126	2.73	1.95	20.04
3U2S.PDB	O, G_SER_195	N, G_VAL_127	H, G_VAL_127	2.86	2.06	17.61
3U2S.PDB	O, G_LEU_193	N, G_LEU_129	H, G_LEU_129	2.74	1.88	2.50
3U2S.PDB	O, G_TYR_191	N, G_CYS_131	H, G_CYS_131	2.75	1.91	8.80
3U2S.PDB	O, G_HIS_156	N, G_THR_132	H, G_THR_132	2.82	2.00	14.90
3U2S.PDB	O, G_PHE_176	N, G_LYS_155	H, G_LYS_155	2.81	1.97	9.94
3U2S.PDB	O, G_ALA_174	N, G_CYS_157	H, G_CYS_157	2.84	2.08	23.82
3U2S.PDB	O, G_GLN_170	N, G_ILE_161	H, G_ILE_161	2.99	2.16	11.12
3U2S.PDB	O, H_ASN_100F	N, G_LYS_169	H, G_LYS_169	2.84	1.99	7.68
3U2S.PDB	O, G_ILE_161	N, G_GLN_170	H, G_GLN_170	2.91	2.11	17.48
3U2S.PDB	O, G_PHE_159	N, G_VAL_172	H, G_VAL_172	2.63	1.79	10.86
3U2S.PDB	OH, H_TYR_100K	ND2, G_ASN_173	HD21, G_ASN_173	2.97	2.13	8.87
3U2S.PDB	O, G_LYS_155	N, G_PHE_176	H, G_PHE_176	2.95	2.13	15.03
3U2S.PDB	O, G_CYS_131	N, G_TYR_191	H, G_TYR_191	2.70	1.86	8.47
3U2S.PDB	O, G_LEU_129	N, G_LEU_193	H, G_LEU_193	2.86	2.06	17.04
3U2S.PDB	O, G_VAL_127	N, G_SER_195	H, G_SER_195	2.90	2.06	10.61
3U2S.PDB	O, G_ALA_125	N, G_GLN_197	H, G_GLN_197	2.97	2.17	17.81
3U2S.PDB	O, G_ALA_209	N, G_PHE_213	H, G_PHE_213	2.92	2.06	4.30
3U2S.PDB	O, G_ALA_210	N, G_LYS_214	H, G_LYS_214	2.72	1.91	16.83
3U2S.PDB	O, G_VAL_212	N, G_TYR_216	H, G_TYR_216	2.98	2.15	13.12
3U2S.PDB	O, G_LYS_214	N, G_ASN_218	H, G_ASN_218	2.94	2.11	12.77
3U2S.PDB	O, G_GLN_215	N, G_ASP_219	H, G_ASP_219	2.86	2.06	18.20
3U2S.PDB	O, G_THR_232	OG1, G_THR_234	HG1, G_THR_234	2.83	2.05	16.75
3U2S.PDB	O, G_LYS_122	N, G_PHE_235	H, G_PHE_235	2.85	2.08	22.39
3U2S.PDB	O, G_THR_227	N, G_THR_236	H, G_THR_236	2.90	2.11	19.48
3U2S.PDB	O, G_ALA_124	N, G_VAL_237	H, G_VAL_237	2.94	2.12	15.29
3U2S.PDB	O, G_CYS_126	N, G_GLU_239	H, G_GLU_239	2.92	2.11	16.99
3U2S.PDB	O, A_SER_25	N, A_ARG_3	H, A_ARG_3	2.90	2.11	19.62
3U2S.PDB	O, A_ALA_23	N, A_VAL_5	H, A_VAL_5	2.99	2.20	19.87
3U2S.PDB	O, A_SER_21	N, A_SER_7	H, A_SER_7	2.83	2.05	20.30
3U2S.PDB	O, A_THR_110	N, A_VAL_12	H, A_VAL_12	2.89	2.06	13.20
3U2S.PDB	O, A_LEU_82C	N, A_GLY_15	H, A_GLY_15	2.82	2.05	22.09
3U2S.PDB	O, A_MET_82	N, A_LEU_18	H, A_LEU_18	2.86	2.07	19.99
3U2S.PDB	OE1, A_GLN_81	NH1, A_ARG_19	HH11, A_ARG_19	2.87	2.10	22.03
3U2S.PDB	O, A_LEU_80	N, A_LEU_20	H, A_LEU_20	2.84	2.01	14.35
3U2S.PDB	O, A_SER_7	N, A_SER_21	H, A_SER_21	2.96	2.12	10.61
3U2S.PDB	O, A_VAL_5	N, A_ALA_23	H, A_ALA_23	2.92	2.09	13.34
3U2S.PDB	O, A_ASP_76	N, A_ALA_24	H, A_ALA_24	2.97	2.11	3.15
3U2S.PDB	O, A_ARG_3	N, A_SER_25	H, A_SER_25	2.95	2.14	17.02
3U2S.PDB	O, A_ASP_100L	NE, A_ARG_31	HE, A_ARG_31	2.88	2.08	17.86
3U2S.PDB	O, A_VAL_93	N, A_HIS_35	H, A_HIS_35	2.73	1.90	11.49
3U2S.PDB	OE1, A_GLU_95	NE2, A_HIS_35	HE2, A_HIS_35	2.70	1.86	8.94
3U2S.PDB	O, A_ALA_49	N, A_TRP_36	H, A_TRP_36	3.00	2.25	25.82
3U2S.PDB	O, A_TYR_79	NE1, A_TRP_36	HE1, A_TRP_36	2.96	2.23	27.73
3U2S.PDB	O, A_PHE_91	N, A_VAL_37	H, A_VAL_37	2.92	2.09	14.10
3U2S.PDB	O, A_GLU_46	N, A_ARG_38	H, A_ARG_38	2.87	2.03	8.46
3U2S.PDB	OE2, A_GLU_46	NE, A_ARG_38	HE, A_ARG_38	2.74	1.98	23.65
3U2S.PDB	OH, A_TYR_90	NH1, A_ARG_38	HH11, A_ARG_38	2.88	2.07	17.44
3U2S.PDB	OD1, A_ASP_86	NH1, A_ARG_38	HH12, A_ARG_38	2.89	2.04	8.28
3U2S.PDB	OE2, A_GLU_46	NH2, A_ARG_38	HH21, A_ARG_38	2.90	2.18	27.83
3U2S.PDB	O, A_THR_89	N, A_GLN_39	H, A_GLN_39	2.91	2.16	24.75

3U2S.PDB	OE1, B_GLN_38	NE2, A_GLN_39	HE22, A_GLN_39	2.92	2.07	7.34
3U2S.PDB	O, A_ALA_40	N, A_GLN_43	H, A_GLN_43	2.87	2.06	15.56
3U2S.PDB	O, A_ARG_38	N, A_GLU_46	H, A_GLU_46	2.76	1.99	21.51
3U2S.PDB	O, A_TYR_58	N, A_PHE_50	H, A_PHE_50	2.89	2.09	18.19
3U2S.PDB	O, A_MET_34	N, A_ILE_51	H, A_ILE_51	2.92	2.12	18.53
3U2S.PDB	O, A_GLU_56	N, A_LYS_52	H, A_LYS_52	2.97	2.12	7.01
3U2S.PDB	O, A_PHE_100J	OH, A_TYR_52A	HH, A_TYR_52A	2.59	1.88	24.42
3U2S.PDB	O, A_LYS_52	N, A_GLY_54	H, A_GLY_54	2.87	2.03	9.21
3U2S.PDB	OD2, A_ASP_53	N, A_SER_55	H, A_SER_55	2.98	2.16	14.39
3U2S.PDB	O, A_PHE_50	N, A_TYR_58	H, A_TYR_58	2.79	1.96	13.05
3U2S.PDB	O, A_VAL_48	N, A_ALA_60	H, A_ALA_60	2.95	2.13	13.20
3U2S.PDB	O, A_VAL_63	N, A_ARG_66	H, A_ARG_66	2.73	1.88	9.69
3U2S.PDB	OD2, A_ASP_86	NH1, A_ARG_66	HH12, A_ARG_66	2.48	1.66	13.42
3U2S.PDB	O, A_VAL_63	N, A_LEU_67	H, A_LEU_67	2.90	2.05	9.26
3U2S.PDB	O, A_GLN_81	N, A_SER_68	H, A_SER_68	2.85	2.08	21.35
3U2S.PDB	OD1, A_ASN_73	NE, A_ARG_71	HE, A_ARG_71	2.81	2.03	20.92
3U2S.PDB	O, A_GLN_32	NH1, A_ARG_71	HH12, A_ARG_71	2.95	2.21	26.35
3U2S.PDB	O, A_THR_77	N, A_ASP_72	H, A_ASP_72	2.91	2.06	7.19
3U2S.PDB	O, A_TYR_52A	ND2, A_ASN_73	HD22, A_ASN_73	2.92	2.06	5.19
3U2S.PDB	O, A_LYS_75	OG1, A_THR_77	HG1, A_THR_77	2.85	2.08	17.09
3U2S.PDB	O, A_CYS_22	N, A_LEU_78	H, A_LEU_78	2.91	2.12	18.34
3U2S.PDB	O, A_SER_70	N, A_TYR_79	H, A_TYR_79	2.82	1.97	5.95
3U2S.PDB	O, A_LEU_20	N, A_LEU_80	H, A_LEU_80	2.92	2.11	16.81
3U2S.PDB	O, A_SER_68	N, A_GLN_81	H, A_GLN_81	2.79	1.96	12.01
3U2S.PDB	O, A_LEU_18	N, A_MET_82	H, A_MET_82	2.72	1.90	13.43
3U2S.PDB	O, A_ARG_66	N, A_ASN_82A	H, A_ASN_82A	2.72	1.94	20.65
3U2S.PDB	OD2, A_ASP_86	N, A_ARG_83	H, A_ARG_83	2.76	1.95	16.59
3U2S.PDB	OE1, A_GLU_85	NH1, A_ARG_83	HH11, A_ARG_83	2.91	2.14	21.39
3U2S.PDB	O, A_ARG_83	N, A_ASP_86	H, A_ASP_86	2.84	2.01	13.57
3U2S.PDB	O, A_VAL_84	N, A_THR_87	H, A_THR_87	2.99	2.15	12.03
3U2S.PDB	O, A_VAL_84	OG1, A_THR_87	HG1, A_THR_87	2.79	2.12	29.92
3U2S.PDB	O, A_GLN_39	N, A_THR_89	H, A_THR_89	2.88	2.07	17.15
3U2S.PDB	O, A_THR_107	N, A_TYR_90	H, A_TYR_90	2.83	1.98	6.95
3U2S.PDB	O, A_VAL_37	N, A_PHE_91	H, A_PHE_91	2.67	1.82	6.67
3U2S.PDB	OE2, A_GLU_6	N, A_CYS_92	H, A_CYS_92	2.72	1.89	13.80
3U2S.PDB	O, A_HIS_35	N, A_VAL_93	H, A_VAL_93	2.96	2.18	20.19
3U2S.PDB	O, A_VAL_102	N, A_ARG_94	H, A_ARG_94	2.84	2.03	15.63
3U2S.PDB	OD1, A_ASP_101	NE, A_ARG_94	HE, A_ARG_94	2.84	1.98	4.74
3U2S.PDB	OD2, A_ASP_101	NH2, A_ARG_94	HH21, A_ARG_94	2.90	2.12	20.79
3U2S.PDB	O, A_TYR_100S	N, A_ALA_96	H, A_ALA_96	2.80	1.96	10.95
3U2S.PDB	O, A_TYR_100E	N, A_ARG_100B	H, A_ARG_100B	2.98	2.15	11.35
3U2S.PDB	O, A_ARG_100B	N, A_TYR_100E	H, A_TYR_100E	2.79	1.94	7.07
3U2S.PDB	O, C_ASP_167	N, A_ASN_100F	H, A_ASN_100F	2.97	2.14	14.21
3U2S.PDB	O, A_GLY_100M	N, A_ASP_100I	H, A_ASP_100I	2.82	1.97	9.87
3U2S.PDB	OD1, A_ASP_100I	N, A_PHE_100J	H, A_PHE_100J	2.78	2.05	27.11
3U2S.PDB	O, A_ARG_31	N, A_TYR_100N	H, A_TYR_100N	2.94	2.09	8.42
3U2S.PDB	O, A_GLY_98	N, A_TYR_100O	H, A_TYR_100O	2.92	2.19	26.39
3U2S.PDB	O, A_ALA_96	N, A_TYR_100Q	H, A_TYR_100Q	2.75	1.90	9.19
3U2S.PDB	OE1, A_GLU_6	N, A_GLY_106	H, A_GLY_106	2.86	2.06	17.09
3U2S.PDB	O, A_TYR_90	N, A_THR_107	H, A_THR_107	2.98	2.19	19.53
3U2S.PDB	O, A_ALA_88	N, A_VAL_109	H, A_VAL_109	2.92	2.07	4.29
3U2S.PDB	O, A_GLY_10	N, A_THR_110	H, A_THR_110	2.86	2.01	7.11
3U2S.PDB	OG1, A_THR_87	N, A_VAL_111	H, A_VAL_111	2.87	2.02	8.59
3U2S.PDB	O, A_VAL_12	N, A_SER_112	H, A_SER_112	2.92	2.11	15.36
3U2S.PDB	O, A_PHE_146	N, A_LYS_117	H, A_LYS_117	2.83	2.02	16.74
3U2S.PDB	O, A_ASP_144	NZ, A_LYS_117	HZ2, A_LYS_117	2.78	2.05	29.01
3U2S.PDB	O, A_LYS_143	N, A_SER_120	H, A_SER_120	2.88	2.06	14.03
3U2S.PDB	O, A_GLY_139	N, A_LEU_124	H, A_LEU_124	2.65	1.84	16.74

3U2S.PDB	O, A_LEU_124	N, A_GLY_139	H, A_GLY_139	2.96	2.16	18.70
3U2S.PDB	O, A_SER_180	N, A_CYS_140	H, A_CYS_140	2.75	1.94	16.77
3U2S.PDB	O, A_PHE_122	N, A_LEU_141	H, A_LEU_141	2.88	2.03	7.64
3U2S.PDB	O, A_LEU_178	N, A_VAL_142	H, A_VAL_142	2.79	1.98	17.03
3U2S.PDB	O, A_SER_120	N, A_LYS_143	H, A_LYS_143	2.78	1.92	1.74
3U2S.PDB	OG1, B_THR_131	NZ, A_LYS_143	HZ2, A_LYS_143	2.41	1.67	27.35
3U2S.PDB	O, A_TYR_176	N, A_TYR_145	H, A_TYR_145	2.98	2.17	17.16
3U2S.PDB	O, A_LYS_117	N, A_PHE_146	H, A_PHE_146	2.95	2.17	21.41
3U2S.PDB	O, A_ASN_199	N, A_THR_151	H, A_THR_151	2.98	2.16	15.19
3U2S.PDB	O, A_ILE_195	N, A_ASN_155	H, A_ASN_155	2.78	1.93	7.52
3U2S.PDB	O, A_VAL_181	N, A_HIS_164	H, A_HIS_164	2.87	2.03	10.09
3U2S.PDB	O, A_SER_179	N, A_PHE_166	H, A_PHE_166	2.98	2.12	5.94
3U2S.PDB	O, A_SER_177	N, A_VAL_169	H, A_VAL_169	2.72	1.90	14.55
3U2S.PDB	OD2, A_ASP_144	NE2, A_GLN_171	HE22, A_GLN_171	2.82	1.98	10.06
3U2S.PDB	O, A_GLN_171	N, A_GLY_174	H, A_GLY_174	2.97	2.11	5.23
3U2S.PDB	O, A_TYR_145	N, A_TYR_176	H, A_TYR_176	2.71	1.86	5.46
3U2S.PDB	O, A_VAL_169	N, A_SER_177	H, A_SER_177	2.96	2.16	18.03
3U2S.PDB	O, A_VAL_142	N, A_LEU_178	H, A_LEU_178	2.98	2.19	18.64
3U2S.PDB	O, A_CYS_140	N, A_SER_180	H, A_SER_180	2.98	2.18	18.33
3U2S.PDB	O, A_LEU_138	N, A_VAL_182	H, A_VAL_182	2.84	2.04	17.50
3U2S.PDB	O, A_GLY_162	N, A_THR_183	H, A_THR_183	2.90	2.11	19.30
3U2S.PDB	O, A_SER_153	N, A_ASN_197	H, A_ASN_197	2.76	1.95	14.90
3U2S.PDB	O, A_VAL_207	N, A_VAL_198	H, A_VAL_198	2.76	1.93	12.35
3U2S.PDB	O, A_THR_151	N, A_ASN_199	H, A_ASN_199	2.98	2.16	15.76
3U2S.PDB	O, A_THR_205	N, A_HIS_200	H, A_HIS_200	2.74	1.90	9.41
3U2S.PDB	OG, A_SER_203	ND1, A_HIS_200	HD1, A_HIS_200	2.63	1.78	5.16
3U2S.PDB	O, A_PRO_147	NE2, A_HIS_200	HE2, A_HIS_200	2.75	1.94	15.51
3U2S.PDB	O, A_VAL_198	N, A_VAL_207	H, A_VAL_207	2.82	1.98	12.41
3U2S.PDB	O, A_TYR_194	N, A_VAL_211	H, A_VAL_211	2.94	2.09	7.62
3U2S.PDB	O, B_GLN_24	N, B_THR_5	H, B_THR_5	2.92	2.09	11.05
3U2S.PDB	O, B_TYR_86	NE2, B_GLN_6	HE22, B_GLN_6	2.85	2.02	13.19
3U2S.PDB	O, B_LYS_103	N, B_VAL_11	H, B_VAL_11	2.85	2.04	16.11
3U2S.PDB	OE1, B_GLN_17	N, B_SER_14	H, B_SER_14	2.92	2.13	20.55
3U2S.PDB	O, B_LEU_78	N, B_GLY_16	H, B_GLY_16	2.87	2.07	17.65
3U2S.PDB	O, B_ILE_75	N, B_ILE_19	H, B_ILE_19	2.93	2.15	21.26
3U2S.PDB	OG1, B_THR_74	OG1, B_THR_20	HG1, B_THR_20	2.88	2.16	24.36
3U2S.PDB	O, B_LEU_73	N, B_ILE_21	H, B_ILE_21	2.82	2.00	14.83
3U2S.PDB	O, B_THR_5	N, B_GLN_24	H, B_GLN_24	2.91	2.09	15.35
3U2S.PDB	O, B_ASN_69	N, B_GLY_25	H, B_GLY_25	2.73	1.88	3.63
3U2S.PDB	OD1, B_ASP_27B	N, B_THR_26	H, B_THR_26	2.84	2.02	14.26
3U2S.PDB	OD2, B_ASP_27B	OG1, B_THR_26	HG1, B_THR_26	2.89	2.14	20.81
3U2S.PDB	OD1, B_ASP_27B	N, B_VAL_27C	H, B_VAL_27C	2.70	1.91	19.64
3U2S.PDB	O, B_THR_26	N, B_GLY_28	H, B_GLY_28	2.91	2.08	12.42
3U2S.PDB	O, B_ASP_27B	N, B_GLY_29	H, B_GLY_29	2.89	2.05	10.78
3U2S.PDB	O, B_LYS_89	N, B_SER_34	H, B_SER_34	2.84	2.04	18.48
3U2S.PDB	O, B_ILE_48	N, B_TRP_35	H, B_TRP_35	2.89	2.10	19.01
3U2S.PDB	O, B_TYR_87	N, B_TYR_36	H, B_TYR_36	2.89	2.14	24.66
3U2S.PDB	O, B_LYS_45	N, B_GLN_37	H, B_GLN_37	2.82	2.00	13.80
3U2S.PDB	OH, B_TYR_86	NE2, B_GLN_37	HE21, B_GLN_37	2.88	2.02	1.18
3U2S.PDB	O, B_ASP_85	N, B_GLN_38	H, B_GLN_38	2.78	1.98	17.35
3U2S.PDB	O, B_LYS_42	NE2, B_GLN_38	HE21, B_GLN_38	2.90	2.07	13.31
3U2S.PDB	OE1, A_GLN_39	NE2, B_GLN_38	HE22, B_GLN_38	2.92	2.08	10.61
3U2S.PDB	O, B_GLN_37	N, B_LYS_45	H, B_LYS_45	2.81	2.08	26.63
3U2S.PDB	O, B_TRP_35	N, B_VAL_47	H, B_VAL_47	2.86	2.02	10.13
3U2S.PDB	O, B_LYS_53	N, B_TYR_49	H, B_TYR_49	2.92	2.11	17.26
3U2S.PDB	O, B_VAL_33	N, B_VAL_51	H, B_VAL_51	2.86	2.01	7.74
3U2S.PDB	O, B_ASP_50	N, B_SER_52	H, B_SER_52	2.89	2.18	28.89
3U2S.PDB	O, B_TYR_49	N, B_LYS_53	H, B_LYS_53	2.90	2.09	16.83

3U2S.PDB	OD2, B.ASP_50	NZ, B.LYS_53	HZ2, B.LYS_53	2.75	1.88	8.80
3U2S.PDB	O, B.VAL_58	NH1, B.ARG_54	HH11, B.ARG_54	2.92	2.11	16.82
3U2S.PDB	O, B.SER_76	NH1, B.ARG_61	HH11, B.ARG_61	2.99	2.17	14.44
3U2S.PDB	OD2, B.ASP_82	NH1, B.ARG_61	HH12, B.ARG_61	2.78	1.98	19.10
3U2S.PDB	OD1, B.ASP_82	NH2, B.ARG_61	HH22, B.ARG_61	2.93	2.07	0.82
3U2S.PDB	O, B.VAL_27C	NZ, B.LYS_66	HZ3, B.LYS_66	2.85	2.03	18.40
3U2S.PDB	O, B.THR_70	N, B.SER_67	H, B.SER_67	2.96	2.13	11.57
3U2S.PDB	O, B.CYS_23	N, B.ALA_71	H, B.ALA_71	2.85	2.05	17.45
3U2S.PDB	O, B.SER_65	N, B.SER_72	H, B.SER_72	2.89	2.07	15.07
3U2S.PDB	O, B.ILE_21	N, B.LEU_73	H, B.LEU_73	2.90	2.08	14.34
3U2S.PDB	O, B.SER_63	N, B.THR_74	H, B.THR_74	2.87	2.04	12.52
3U2S.PDB	O, B.ILE_19	N, B.ILE_75	H, B.ILE_75	2.92	2.11	16.75
3U2S.PDB	O, B.ARG_61	N, B.SER_76	H, B.SER_76	2.95	2.11	12.03
3U2S.PDB	O, B.GLN_17	N, B.LEU_78	H, B.LEU_78	2.82	1.97	8.22
3U2S.PDB	OD2, B.ASP_82	N, B.GLN_79	H, B.GLN_79	2.84	2.01	11.59
3U2S.PDB	OG1, H.THR_160	N, B.ALA_80	H, B.ALA_80	2.90	2.08	14.44
3U2S.PDB	O, B.GLN_79	N, B.ASP_82	H, B.ASP_82	2.90	2.05	8.49
3U2S.PDB	O, B.ALA_80	N, B.GLU_83	H, B.GLU_83	2.99	2.13	4.82
3U2S.PDB	O, B.THR_102	N, B.TYR_86	H, B.TYR_86	2.83	2.04	18.67
3U2S.PDB	O, B.ARG_95A	N, B.THR_92	H, B.THR_92	2.98	2.24	26.76
3U2S.PDB	O, B.THR_92	N, B.ARG_95	H, B.ARG_95	2.98	2.15	13.06
3U2S.PDB	OD1, A.ASP_61	NH1, B.ARG_95A	HH12, B.ARG_95A	2.63	1.91	26.97
3U2S.PDB	OE2, A.GLU_95	NH2, B.ARG_96	HH21, B.ARG_96	2.98	2.16	13.77
3U2S.PDB	O, B.CYS_88	N, B.GLY_99	H, B.GLY_99	2.84	2.02	13.65
3U2S.PDB	O, B.TYR_86	N, B.THR_102	H, B.THR_102	2.88	2.13	24.78
3U2S.PDB	O, B.PRO_7	OG1, B.THR_102	HG1, B.THR_102	2.64	1.82	5.54
3U2S.PDB	O, B.GLY_84	N, B.LEU_104	H, B.LEU_104	2.79	1.94	4.02
3U2S.PDB	O, B.VAL_11	N, B.THR_105	H, B.THR_105	2.99	2.17	14.21
3U2S.PDB	OH, B.TYR_140	N, B.GLY_107	H, B.GLY_107	2.85	2.06	20.14
3U2S.PDB	O, B.TYR_140	N, B.ALA_111	H, B.ALA_111	2.98	2.14	10.58
3U2S.PDB	O, B.SER_137	N, B.SER_114	H, B.SER_114	2.93	2.10	13.38
3U2S.PDB	O, B.LEU_135	N, B.THR_116	H, B.THR_116	2.97	2.16	15.84
3U2S.PDB	O, B.VAL_133	N, B.PHE_118	H, B.PHE_118	2.87	2.04	12.26
3U2S.PDB	O, B.LEU_125	N, B.ASN_128	H, B.ASN_128	2.97	2.18	18.83
3U2S.PDB	O, B.SER_176	N, B.CYS_134	H, B.CYS_134	2.86	2.01	7.06
3U2S.PDB	O, B.THR_116	N, B.LEU_135	H, B.LEU_135	2.78	1.93	5.65
3U2S.PDB	O, B.ALA_174	N, B.ILE_136	H, B.ILE_136	2.93	2.14	18.97
3U2S.PDB	O, B.SER_114	N, B.SER_137	H, B.SER_137	2.99	2.19	18.33
3U2S.PDB	OE1, B.GLN_167	N, B.ASP_138	H, B.ASP_138	2.95	2.17	20.82
3U2S.PDB	O, B.ALA_111	N, B.TYR_140	H, B.TYR_140	2.94	2.14	17.27
3U2S.PDB	O, B.PRO_141	N, B.ALA_143	H, B.ALA_143	3.00	2.29	29.69
3U2S.PDB	O, B.GLN_194	N, B.ALA_147	H, B.ALA_147	2.93	2.10	11.92
3U2S.PDB	OG, B.SER_176	NE1, B.TRP_148	HE1, B.TRP_148	2.87	2.03	9.65
3U2S.PDB	O, B.SER_190	N, B.ASP_151	H, B.ASP_151	2.76	1.91	5.32
3U2S.PDB	O, B.TRP_148	N, B.VAL_155	H, B.VAL_155	2.92	2.16	22.91
3U2S.PDB	O, B.TYR_177	N, B.GLU_160	H, B.GLU_160	2.79	1.97	13.97
3U2S.PDB	O, B.SER_175	N, B.THR_162	H, B.THR_162	2.92	2.09	12.18
3U2S.PDB	O, B.ALA_173	N, B.SER_165	H, B.SER_165	2.94	2.13	16.38
3U2S.PDB	O, B.LYS_171	N, B.GLN_167	H, B.GLN_167	2.56	1.71	7.13
3U2S.PDB	OD1, B.ASN_169	NE2, B.GLN_167	HE21, B.GLN_167	2.93	2.16	22.14
3U2S.PDB	OD1, B.ASP_138	NE2, B.GLN_167	HE22, B.GLN_167	2.75	1.90	7.18
3U2S.PDB	OD1, B.ASN_169	N, B.LYS_171	H, B.LYS_171	2.90	2.06	11.66
3U2S.PDB	O, B.PHE_139	N, B.TYR_172	H, B.TYR_172	2.94	2.14	18.70
3U2S.PDB	O, B.SER_165	N, B.ALA_173	H, B.ALA_173	2.91	2.10	18.16
3U2S.PDB	O, B.ILE_136	N, B.ALA_174	H, B.ALA_174	2.80	1.97	12.77
3U2S.PDB	O, B.CYS_134	N, B.SER_176	H, B.SER_176	2.86	2.06	18.58
3U2S.PDB	O, B.GLU_160	N, B.TYR_177	H, B.TYR_177	2.64	1.81	12.56
3U2S.PDB	O, B.GLY_158	N, B.SER_179	H, B.SER_179	2.87	2.03	11.48

3U2S.PDB	O, B_ALA_130	N, B_LEU_180	H, B_LEU_180	2.96	2.11	5.53
3U2S.PDB	O, B_PRO_182	N, B_LYS_186	H, B_LYS_186	2.96	2.16	17.55
3U2S.PDB	OD1, B_ASP_151	N, B_SER_190	H, B_SER_190	2.97	2.20	22.59
3U2S.PDB	O, B_VAL_206	N, B_TYR_191	H, B_TYR_191	2.92	2.10	13.48
3U2S.PDB	O, B_LYS_149	N, B_SER_192	H, B_SER_192	2.99	2.21	20.57
3U2S.PDB	O, B_LYS_204	N, B_CYS_193	H, B_CYS_193	2.92	2.14	21.01
3U2S.PDB	O, B_ALA_147	N, B_GLN_194	H, B_GLN_194	2.80	1.97	13.29
3U2S.PDB	O, B_VAL_202	N, B_VAL_195	H, B_VAL_195	2.78	1.93	3.68
3U2S.PDB	O, B_THR_145	N, B_THR_196	H, B_THR_196	2.86	2.00	5.33
3U2S.PDB	OG1, B_THR_201	OG1, B_THR_196	HG1, B_THR_196	2.79	1.99	11.66
3U2S.PDB	O, B_SER_200	N, B_HIS_197	H, B_HIS_197	2.90	2.05	7.61
3U2S.PDB	O, B_PRO_141	NE2, B_HIS_197	HE2, B_HIS_197	2.83	2.07	23.66
3U2S.PDB	O, B_HIS_197	N, B_SER_200	H, B_SER_200	2.92	2.07	5.55
3U2S.PDB	O, B_VAL_195	N, B_VAL_202	H, B_VAL_202	2.72	1.88	10.92
3U2S.PDB	O, B_TYR_191	N, B_VAL_206	H, B_VAL_206	2.88	2.06	14.38
3U2S.PDB	O, C_THR_201	N, C_PHE_121	H, C_PHE_121	2.92	2.06	2.96
3U2S.PDB	O, C_LYS_233	N, C_LYS_122	H, C_LYS_122	2.76	1.94	13.22
3U2S.PDB	O, C_THR_199	N, C_LEU_123	H, C_LEU_123	2.83	2.01	15.42
3U2S.PDB	O, C_PHE_235	N, C_ALA_124	H, C_ALA_124	2.96	2.15	16.72
3U2S.PDB	O, C_GLN_197	N, C_ALA_125	H, C_ALA_125	2.97	2.18	19.36
3U2S.PDB	O, C_VAL_237	N, C_CYS_126	H, C_CYS_126	2.89	2.18	29.45
3U2S.PDB	O, C_SER_195	N, C_VAL_127	H, C_VAL_127	2.78	2.00	19.73
3U2S.PDB	O, C_LEU_193	N, C_LEU_129	H, C_LEU_129	2.58	1.72	4.21
3U2S.PDB	O, C_SER_158	N, C_ALA_130	H, C_ALA_130	2.91	2.07	10.47
3U2S.PDB	O, C_TYR_191	N, C_CYS_131	H, C_CYS_131	2.97	2.14	13.58
3U2S.PDB	O, C_HIS_156	N, C_THR_132	H, C_THR_132	2.87	2.10	22.75
3U2S.PDB	O, C_PHE_176	N, C_LYS_155	H, C_LYS_155	2.92	2.08	9.76
3U2S.PDB	O, C_ALA_174	N, C_CYS_157	H, C_CYS_157	2.85	2.01	11.36
3U2S.PDB	O, C_GLN_170	N, C_ILE_161	H, C_ILE_161	2.98	2.15	12.25
3U2S.PDB	OG1, C_THR_163	N, C_VAL_165	H, C_VAL_165	2.97	2.12	10.44
3U2S.PDB	O, A_ASN_100F	N, C_LYS_169	H, C_LYS_169	2.91	2.08	13.24
3U2S.PDB	O, C_ILE_161	N, C_GLN_170	H, C_GLN_170	2.89	2.09	17.25
3U2S.PDB	O, C_PHE_159	N, C_VAL_172	H, C_VAL_172	2.73	1.89	10.39
3U2S.PDB	O, C_LYS_155	N, C_PHE_176	H, C_PHE_176	2.99	2.16	12.58
3U2S.PDB	O, C_CYS_131	N, C_TYR_191	H, C_TYR_191	2.87	2.05	15.43
3U2S.PDB	O, C_LEU_129	N, C_LEU_193	H, C_LEU_193	2.96	2.21	25.28
3U2S.PDB	O, C_VAL_127	N, C_SER_195	H, C_SER_195	2.88	2.02	5.76
3U2S.PDB	O, C_ALA_125	N, C_GLN_197	H, C_GLN_197	2.93	2.12	15.95
3U2S.PDB	O, C_LEU_123	N, C_THR_199	H, C_THR_199	2.87	2.07	18.73
3U2S.PDB	O, C_ALA_206	N, C_ALA_210	H, C_ALA_210	2.93	2.14	20.34
3U2S.PDB	O, C_THR_232	OG1, C_THR_234	HG1, C_THR_234	2.76	1.97	14.48
3U2S.PDB	O, C_LYS_122	N, C_PHE_235	H, C_PHE_235	2.66	1.87	18.30
3U2S.PDB	O, C_THR_227	N, C_THR_236	H, C_THR_236	2.92	2.14	20.62
3U2S.PDB	O, C_ALA_124	N, C_VAL_237	H, C_VAL_237	2.99	2.14	7.85
3UYR.PDB	O, H_THR_23	N, H_VAL_5	H, H_VAL_5	2.87	2.05	15.70
3UYR.PDB	O, H_SER_21	N, H_SER_7	H, H_SER_7	2.82	2.03	20.07
3UYR.PDB	O, H_THR_112	N, H_GLY_10	H, H_GLY_10	2.77	1.94	13.13
3UYR.PDB	O, H_THR_114	N, H_VAL_12	H, H_VAL_12	2.88	2.07	16.54
3UYR.PDB	O, H_LEU_86	N, H_GLY_15	H, H_GLY_15	2.68	1.86	14.42
3UYR.PDB	O, H_MET_83	N, H_MET_18	H, H_MET_18	2.83	2.00	14.86
3UYR.PDB	O, H_LEU_81	N, H_LEU_20	H, H_LEU_20	2.86	2.03	15.99
3UYR.PDB	OG, H_SER_7	N, H_SER_21	H, H_SER_21	2.96	2.12	9.95
3UYR.PDB	O, H_VAL_5	N, H_THR_23	H, H_THR_23	2.80	1.98	14.92
3UYR.PDB	O, H_THR_28	N, H_ASP_31	H, H_ASP_31	2.78	1.97	17.10
3UYR.PDB	O, H_ILE_51	N, H_MET_34	H, H_MET_34	2.92	2.09	17.05
3UYR.PDB	O, H_ALA_97	N, H_ALA_35	H, H_ALA_35	2.83	2.02	16.97
3UYR.PDB	O, H_ALA_49	N, H_TRP_36	H, H_TRP_36	2.81	2.00	15.63
3UYR.PDB	O, H_TYR_95	N, H_VAL_37	H, H_VAL_37	2.95	2.10	10.85

3UYR.PDB	O, H_GLU_46	N, H_ARG_38	H, H_ARG_38	2.89	2.05	12.16
3UYR.PDB	OE1, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.84	2.03	16.92
3UYR.PDB	O, H_THR_93	N, H_GLN_39	H, H_GLN_39	2.74	1.95	18.61
3UYR.PDB	O, H_ARG_38	N, H_GLU_46	H, H_GLU_46	2.90	2.11	20.15
3UYR.PDB	OD1, H_ASN_50	NE1, H_TRP_47	HE1, H_TRP_47	2.95	2.18	22.72
3UYR.PDB	O, H_TRP_36	N, H_VAL_48	H, H_VAL_48	2.89	2.08	15.29
3UYR.PDB	O, H_TYR_59	N, H_ASN_50	H, H_ASN_50	2.85	2.06	20.39
3UYR.PDB	O, H_MET_34	N, H_ILE_51	H, H_ILE_51	2.84	2.04	20.05
3UYR.PDB	OD1, H_ASP_54	N, H_SER_56	H, H_SER_56	3.00	2.18	14.88
3UYR.PDB	O, H_ASN_50	N, H_TYR_59	H, H_TYR_59	2.85	2.02	13.64
3UYR.PDB	O, H_VAL_48	N, H_LEU_61	H, H_LEU_61	2.98	2.13	7.86
3UYR.PDB	O, H_ASP_62	N, H_LYS_65	H, H_LYS_65	2.99	2.13	4.39
3UYR.PDB	O, H_LEU_64	N, H_ARG_67	H, H_ARG_67	2.98	2.13	8.99
3UYR.PDB	O, H_SER_84	NH1, H_ARG_67	HH11, H_ARG_67	2.94	2.14	18.03
3UYR.PDB	O, H_GLN_82	N, H_ILE_69	H, H_ILE_69	2.76	1.97	19.91
3UYR.PDB	OH, H_TYR_60	N, H_ILE_70	H, H_ILE_70	2.89	2.08	16.21
3UYR.PDB	O, H_TYR_32	NH1, H_ARG_72	HH12, H_ARG_72	2.89	2.11	20.18
3UYR.PDB	O, H_ILE_78	N, H_ASP_73	H, H_ASP_73	2.70	1.96	26.09
3UYR.PDB	OD1, H_ASP_73	N, H_ALA_75	H, H_ALA_75	3.00	2.29	29.64
3UYR.PDB	O, H_ASP_73	N, H_ILE_78	H, H_ILE_78	2.94	2.08	11.87
3UYR.PDB	O, H_CYS_22	N, H_LEU_79	H, H_LEU_79	2.83	1.98	6.29
3UYR.PDB	O, H_SER_71	N, H_TYR_80	H, H_TYR_80	2.75	1.91	7.16
3UYR.PDB	O, H_LEU_20	N, H_LEU_81	H, H_LEU_81	2.86	2.02	12.02
3UYR.PDB	O, H_ILE_69	N, H_GLN_82	H, H_GLN_82	2.78	1.98	18.27
3UYR.PDB	O, H_MET_18	N, H_MET_83	H, H_MET_83	2.76	1.93	11.89
3UYR.PDB	O, H_SER_16	N, H_LEU_86	H, H_LEU_86	2.97	2.14	12.64
3UYR.PDB	O, H_SER_85	NH1, H_ARG_87	HH11, H_ARG_87	2.82	2.10	28.67
3UYR.PDB	O, H_ARG_87	N, H_ASP_90	H, H_ASP_90	2.99	2.14	6.54
3UYR.PDB	O, H_VAL_113	N, H_ALA_92	H, H_ALA_92	2.99	2.22	22.62
3UYR.PDB	O, H_GLN_39	N, H_THR_93	H, H_THR_93	2.87	2.02	7.65
3UYR.PDB	O, H_THR_111	N, H_TYR_94	H, H_TYR_94	2.77	1.93	7.70
3UYR.PDB	O, H_VAL_37	N, H_TYR_95	H, H_TYR_95	2.76	1.92	4.33
3UYR.PDB	OE2, H_GLU_6	N, H_CYS_96	H, H_CYS_96	2.87	2.06	15.59
3UYR.PDB	O, H_ALA_35	N, H_ALA_97	H, H_ALA_97	2.87	2.05	15.28
3UYR.PDB	O, H_VAL_106	N, H_ARG_98	H, H_ARG_98	2.80	2.00	18.41
3UYR.PDB	OD1, H_ASP_105	NE, H_ARG_98	HE, H_ARG_98	2.98	2.16	14.38
3UYR.PDB	OD2, H_ASP_105	NH2, H_ARG_98	HH21, H_ARG_98	2.92	2.07	8.84
3UYR.PDB	O, H_TYR_103	N, H_THR_100	H, H_THR_100	2.82	1.97	9.07
3UYR.PDB	OE1, P_GLN_48	N, H_ASN_101	H, H_ASN_101	2.90	2.08	14.57
3UYR.PDB	O, H_THR_100	N, H_TYR_103	H, H_TYR_103	2.94	2.08	4.35
3UYR.PDB	OH, L_TYR_41	N, H_LEU_104	H, H_LEU_104	2.91	2.05	4.02
3UYR.PDB	O, H_CYS_96	N, H_GLY_108	H, H_GLY_108	2.80	1.99	17.37
3UYR.PDB	O, H_TYR_94	N, H_THR_111	H, H_THR_111	2.80	2.01	19.20
3UYR.PDB	O, H_ALA_92	N, H_VAL_113	H, H_VAL_113	2.86	2.03	11.74
3UYR.PDB	O, H_GLY_10	N, H_THR_114	H, H_THR_114	2.91	2.06	9.85
3UYR.PDB	OG1, H_THR_91	N, H_VAL_115	H, H_VAL_115	2.95	2.09	4.97
3UYR.PDB	O, H_VAL_12	N, H_SER_116	H, H_SER_116	2.87	2.10	23.24
3UYR.PDB	O, H_PHE_150	N, H_THR_121	H, H_THR_121	2.88	2.05	13.74
3UYR.PDB	O, H_LYS_147	N, H_SER_124	H, H_SER_124	2.80	1.96	9.50
3UYR.PDB	O, H_LEU_145	N, H_TYR_126	H, H_TYR_126	2.81	1.98	12.02
3UYR.PDB	O, H_GLY_143	N, H_LEU_128	H, H_LEU_128	2.77	1.99	20.76
3UYR.PDB	O, H_VAL_187	N, H_VAL_140	H, H_VAL_140	2.79	1.98	16.70
3UYR.PDB	O, H_VAL_185	N, H_LEU_142	H, H_LEU_142	2.82	1.97	8.16
3UYR.PDB	O, H_LEU_128	N, H_GLY_143	H, H_GLY_143	2.84	2.04	17.93
3UYR.PDB	O, H_SER_183	N, H_CYS_144	H, H_CYS_144	2.83	2.03	18.84
3UYR.PDB	O, H_TYR_126	N, H_LEU_145	H, H_LEU_145	2.83	1.98	9.31
3UYR.PDB	O, H_MET_181	N, H_VAL_146	H, H_VAL_146	2.78	1.94	7.21
3UYR.PDB	O, H_SER_124	N, H_LYS_147	H, H_LYS_147	2.85	2.00	9.15

3UYR.PDB	O, H_THR_121	N, H_PHE_150	H, H_PHE_150	2.94	2.13	17.37
3UYR.PDB	O, H_ALA_202	N, H_THR_155	H, H_THR_155	2.91	2.09	17.68
3UYR.PDB	O, H_SER_200	N, H_THR_157	H, H_THR_157	2.85	2.03	15.50
3UYR.PDB	OG, H_SER_183	NE1, H_TRP_158	HE1, H_TRP_158	2.93	2.08	7.42
3UYR.PDB	O, H_THR_198	N, H_ASN_159	H, H_ASN_159	2.85	2.00	6.81
3UYR.PDB	O, H_THR_196	ND2, H_ASN_159	HD21, H_ASN_159	2.99	2.16	12.25
3UYR.PDB	O, H_SER_184	N, H_HIS_168	H, H_HIS_168	2.82	2.01	16.83
3UYR.PDB	O, H_SER_182	N, H_PHE_170	H, H_PHE_170	2.87	2.01	1.94
3UYR.PDB	O, H_THR_180	N, H_LEU_173	H, H_LEU_173	2.80	1.98	14.35
3UYR.PDB	O, H_LEU_178	N, H_GLU_175	H, H_GLU_175	2.86	2.02	11.60
3UYR.PDB	O, H_TYR_149	N, H_TYR_179	H, H_TYR_179	2.88	2.02	4.66
3UYR.PDB	O, H_LEU_173	N, H_THR_180	H, H_THR_180	2.85	2.02	14.69
3UYR.PDB	O, H_VAL_146	N, H_MET_181	H, H_MET_181	2.84	2.01	13.98
3UYR.PDB	O, H_CYS_144	N, H_SER_183	H, H_SER_183	2.93	2.11	17.38
3UYR.PDB	O, H_HIS_168	N, H_SER_184	H, H_SER_184	2.81	2.00	15.83
3UYR.PDB	O, H_LEU_142	N, H_VAL_185	H, H_VAL_185	2.88	2.04	12.88
3UYR.PDB	O, H_VAL_140	N, H_VAL_187	H, H_VAL_187	2.92	2.09	16.07
3UYR.PDB	O, H_SER_138	N, H_SER_189	H, H_SER_189	2.93	2.08	7.47
3UYR.PDB	O, H_THR_191	N, H_GLN_195	H, H_GLN_195	2.89	2.08	16.64
3UYR.PDB	OD1, H_ASN_159	N, H_THR_198	H, H_THR_198	2.89	2.14	25.42
3UYR.PDB	O, H_LYS_212	N, H_CYS_199	H, H_CYS_199	2.82	2.04	21.76
3UYR.PDB	O, H_THR_157	N, H_SER_200	H, H_SER_200	2.77	1.94	8.80
3UYR.PDB	O, H_VAL_210	N, H_VAL_201	H, H_VAL_201	2.74	1.93	14.32
3UYR.PDB	O, H_THR_155	N, H_ALA_202	H, H_ALA_202	2.84	2.00	11.25
3UYR.PDB	O, H_THR_208	N, H_HIS_203	H, H_HIS_203	2.84	2.01	11.63
3UYR.PDB	OG, H_SER_206	ND1, H_HIS_203	HD1, H_HIS_203	2.81	2.06	24.47
3UYR.PDB	O, H_PRO_151	NE2, H_HIS_203	HE2, H_HIS_203	2.78	1.95	12.82
3UYR.PDB	O, H_PRO_204	N, H_SER_207	H, H_SER_207	2.93	2.11	16.45
3UYR.PDB	O, H_SER_206	OG1, H_THR_208	HG1, H_THR_208	2.92	2.11	9.83
3UYR.PDB	O, H_VAL_201	N, H_VAL_210	H, H_VAL_210	2.82	2.01	15.56
3UYR.PDB	O, H_CYS_199	N, H_LYS_212	H, H_LYS_212	2.72	1.97	24.25
3UYR.PDB	OE2, L_GLU_127	NZ, H_LYS_212	HZ3, H_LYS_212	2.87	2.08	23.12
3UYR.PDB	O, H_VAL_197	N, H_LEU_214	H, H_LEU_214	2.84	1.98	4.90
3UYR.PDB	OG, L_SER_26	N, L_VAL_3	H, L_VAL_3	2.88	2.07	15.64
3UYR.PDB	O, L_ARG_24	N, L_THR_5	H, L_THR_5	2.82	1.98	11.17
3UYR.PDB	O, L_TYR_91	NE2, L_GLN_6	HE21, L_GLN_6	2.91	2.06	4.88
3UYR.PDB	O, L_SER_22	N, L_THR_7	H, L_THR_7	2.88	2.05	13.60
3UYR.PDB	O, L_LYS_107	N, L_LEU_11	H, L_LEU_11	2.78	1.95	12.54
3UYR.PDB	O, L_GLU_109	N, L_VAL_13	H, L_VAL_13	2.83	2.02	17.58
3UYR.PDB	O, L_VAL_83	N, L_GLY_16	H, L_GLY_16	2.85	2.01	12.40
3UYR.PDB	O, L_ILE_80	N, L_ALA_19	H, L_ALA_19	2.80	1.98	15.31
3UYR.PDB	O, L_LEU_78	N, L_ILE_21	H, L_ILE_21	2.80	1.97	13.25
3UYR.PDB	O, L_THR_7	N, L_SER_22	H, L_SER_22	2.80	1.95	7.59
3UYR.PDB	O, L_PHE_76	N, L_CYS_23	H, L_CYS_23	2.89	2.03	7.24
3UYR.PDB	O, L_THR_5	N, L_ARG_24	H, L_ARG_24	2.90	2.05	9.82
3UYR.PDB	O, L_THR_74	N, L_SER_25	H, L_SER_25	2.93	2.14	19.27
3UYR.PDB	O, L_GLY_73	N, L_LEU_29	H, L_LEU_29	2.94	2.10	10.63
3UYR.PDB	O, L_ASN_35	N, L_HIS_31	H, L_HIS_31	2.79	1.96	11.60
3UYR.PDB	O, P_PRO_50	NE2, L_HIS_31	HE2, L_HIS_31	2.91	2.13	21.00
3UYR.PDB	O, L_HIS_31	N, L_GLY_34	H, L_GLY_34	2.88	2.04	11.36
3UYR.PDB	OD1, L_ASN_33	N, L_ASN_35	H, L_ASN_35	2.92	2.06	4.57
3UYR.PDB	O, L_SER_94	N, L_HIS_39	H, L_HIS_39	2.84	2.01	14.97
3UYR.PDB	O, L_ILE_53	N, L_TRP_40	H, L_TRP_40	2.74	1.91	12.06
3UYR.PDB	O, L_PHE_92	N, L_TYR_41	H, L_TYR_41	2.85	1.99	7.67
3UYR.PDB	O, L_ASN_50	N, L_LEU_42	H, L_LEU_42	2.87	2.07	16.83
3UYR.PDB	O, L_VAL_90	N, L_GLN_43	H, L_GLN_43	2.80	1.95	5.26
3UYR.PDB	O, L_LEU_42	N, L_ASN_50	H, L_ASN_50	2.86	2.10	23.14
3UYR.PDB	O, L_TRP_40	N, L_LEU_52	H, L_LEU_52	2.84	2.01	12.79

3UYR.PDB	O, L_ASN_58	N, L_TYR_54	H, L_TYR_54	2.84	2.05	19.87
3UYR.PDB	O, L_LEU_38	N, L_VAL_56	H, L_VAL_56	2.77	1.91	6.14
3UYR.PDB	O, L_LYS_55	N, L_SER_57	H, L_SER_57	2.83	2.11	28.35
3UYR.PDB	O, L_TYR_54	N, L_ASN_58	H, L_ASN_58	3.00	2.19	16.78
3UYR.PDB	O, L_LEU_52	N, L_PHE_60	H, L_PHE_60	2.97	2.11	3.95
3UYR.PDB	O, L_PHE_60	N, L_VAL_63	H, L_VAL_63	2.97	2.12	9.01
3UYR.PDB	OD2, L_ASP_87	NH1, L_ARG_66	HH12, L_ARG_66	2.92	2.12	17.99
3UYR.PDB	O, L_LYS_79	N, L_SER_68	H, L_SER_68	2.85	2.02	11.95
3UYR.PDB	O, L_THR_77	N, L_SER_70	H, L_SER_70	2.85	2.05	19.01
3UYR.PDB	O, L_ASP_75	N, L_SER_72	H, L_SER_72	2.90	2.11	22.40
3UYR.PDB	O, L_SER_72	N, L_ASP_75	H, L_ASP_75	2.99	2.11	2.04
3UYR.PDB	O, L_CYS_23	N, L_PHE_76	H, L_PHE_76	2.88	2.06	17.75
3UYR.PDB	O, L_SER_70	N, L_THR_77	H, L_THR_77	2.91	2.06	11.18
3UYR.PDB	O, L_ILE_21	N, L_LEU_78	H, L_LEU_78	2.85	2.02	13.64
3UYR.PDB	O, L_SER_68	N, L_LYS_79	H, L_LYS_79	2.81	1.95	3.66
3UYR.PDB	O, L_ALA_19	N, L_ILE_80	H, L_ILE_80	2.83	2.00	12.62
3UYR.PDB	O, L_ARG_66	N, L_SER_81	H, L_SER_81	2.98	2.14	10.19
3UYR.PDB	O, L_ASP_17	N, L_VAL_83	H, L_VAL_83	2.95	2.10	8.86
3UYR.PDB	OD2, L_ASP_87	N, L_GLU_84	H, L_GLU_84	2.89	2.03	6.75
3UYR.PDB	O, L_GLU_84	N, L_ASP_87	H, L_ASP_87	2.87	2.03	9.35
3UYR.PDB	O, L_GLN_43	N, L_VAL_90	H, L_VAL_90	2.88	2.03	9.40
3UYR.PDB	O, L_THR_106	N, L_TYR_91	H, L_TYR_91	2.84	1.99	8.33
3UYR.PDB	O, L_TYR_41	N, L_PHE_92	H, L_PHE_92	2.86	2.03	13.68
3UYR.PDB	OE1, L_GLN_6	N, L_CYS_93	H, L_CYS_93	3.00	2.19	17.32
3UYR.PDB	O, L_HIS_39	N, L_SER_94	H, L_SER_94	2.83	2.06	23.28
3UYR.PDB	O, L_THR_101	N, L_GLN_95	H, L_GLN_95	2.94	2.12	15.68
3UYR.PDB	O, L_TYR_37	N, L_SER_96	H, L_SER_96	2.94	2.15	18.38
3UYR.PDB	OE1, L_GLN_95	N, L_HIS_98	H, L_HIS_98	2.95	2.09	2.48
3UYR.PDB	O, L_SER_28	NE2, L_HIS_98	HE2, L_HIS_98	2.88	2.05	12.63
3UYR.PDB	O, L_CYS_93	N, L_GLY_103	H, L_GLY_103	2.78	1.93	6.25
3UYR.PDB	O, L_TYR_91	N, L_THR_106	H, L_THR_106	2.84	2.03	18.62
3UYR.PDB	O, L_GLY_89	N, L_LEU_108	H, L_LEU_108	2.94	2.13	16.80
3UYR.PDB	O, L_LEU_11	N, L_GLU_109	H, L_GLU_109	2.82	1.97	7.29
3UYR.PDB	OE1, L_GLN_170	N, L_ILE_110	H, L_ILE_110	2.98	2.14	10.85
3UYR.PDB	O, L_VAL_13	N, L_LYS_111	H, L_LYS_111	2.91	2.06	8.31
3UYR.PDB	O, L_ALA_113	NE, L_ARG_112	HE, L_ARG_112	2.77	1.91	2.87
3UYR.PDB	O, L_ASP_174	NH1, L_ARG_112	HH11, L_ARG_112	2.84	2.02	14.52
3UYR.PDB	O, L_TYR_144	N, L_ALA_115	H, L_ALA_115	2.82	2.03	20.71
3UYR.PDB	O, L_ASN_141	N, L_THR_118	H, L_THR_118	2.86	2.01	9.08
3UYR.PDB	O, L_PHE_139	N, L_SER_120	H, L_SER_120	2.86	2.03	15.20
3UYR.PDB	O, L_VAL_137	N, L_PHE_122	H, L_PHE_122	2.78	2.00	21.33
3UYR.PDB	OG, L_SER_135	NE2, L_GLN_128	HE22, L_GLN_128	2.97	2.12	5.23
3UYR.PDB	O, L_SER_126	N, L_THR_130	H, L_THR_130	2.82	2.00	15.78
3UYR.PDB	O, L_GLN_128	N, L_SER_131	H, L_SER_131	2.96	2.14	14.42
3UYR.PDB	O, L_LEU_185	N, L_ALA_134	H, L_ALA_134	2.87	2.07	19.29
3UYR.PDB	OE1, L_GLN_128	N, L_SER_135	H, L_SER_135	2.90	2.07	13.80
3UYR.PDB	O, L_LEU_183	N, L_VAL_136	H, L_VAL_136	2.80	1.97	12.38
3UYR.PDB	O, L_PHE_122	N, L_VAL_137	H, L_VAL_137	2.95	2.10	12.15
3UYR.PDB	O, L_SER_181	N, L_CYS_138	H, L_CYS_138	2.83	1.98	8.48
3UYR.PDB	O, L_SER_120	N, L_PHE_139	H, L_PHE_139	2.80	2.03	23.03
3UYR.PDB	O, L_MET_179	N, L_LEU_140	H, L_LEU_140	2.85	1.99	0.89
3UYR.PDB	O, L_THR_118	N, L_ASN_141	H, L_ASN_141	2.83	1.99	11.90
3UYR.PDB	OG, L_SER_178	N, L_ASN_142	H, L_ASN_142	2.99	2.15	11.11
3UYR.PDB	O, L_TYR_177	N, L_PHE_143	H, L_PHE_143	2.85	2.04	16.59
3UYR.PDB	O, L_ALA_115	N, L_TYR_144	H, L_TYR_144	2.91	2.10	16.84
3UYR.PDB	O, L_THR_201	N, L_ASN_149	H, L_ASN_149	2.86	2.00	8.27
3UYR.PDB	O, L_GLU_199	N, L_LYS_151	H, L_LYS_151	2.82	2.00	15.42
3UYR.PDB	O, L_THR_197	N, L_LYS_153	H, L_LYS_153	2.84	2.01	13.66

3UYR.PDB	O, L.SER.157	N, L.ILE.154	H, L.ILE.154	2.87	2.03	11.53
3UYR.PDB	O, L.SER.195	N, L.ASP.155	H, L.ASP.155	2.87	2.05	15.34
3UYR.PDB	O, L.ILE.154	N, L.SER.157	H, L.SER.157	2.89	2.05	8.75
3UYR.PDB	O, L.THR.182	N, L.LEU.164	H, L.LEU.164	2.83	2.00	12.39
3UYR.PDB	O, L.SER.180	N, L.SER.166	H, L.SER.166	2.84	2.01	13.00
3UYR.PDB	O, H.PRO.171	OG, L.SER.166	HG, L.SER.166	2.72	1.97	20.46
3UYR.PDB	O, L.SER.178	N, L.THR.168	H, L.THR.168	2.87	2.04	12.69
3UYR.PDB	O, L.ILE.110	NE2, L.GLN.170	HE21, L.GLN.170	2.74	1.92	14.96
3UYR.PDB	O, L.SER.175	NE2, L.GLN.170	HE22, L.GLN.170	2.95	2.10	7.23
3UYR.PDB	O, L.THR.176	N, L.ASP.171	H, L.ASP.171	2.94	2.09	6.43
3UYR.PDB	OD1, L.ASP.174	OG1, L.THR.176	HG1, L.THR.176	2.78	1.97	7.90
3UYR.PDB	O, L.PHE.143	N, L.TYR.177	H, L.TYR.177	2.87	2.01	4.97
3UYR.PDB	O, L.LEU.140	N, L.MET.179	H, L.MET.179	2.90	2.09	17.57
3UYR.PDB	O, L.SER.166	N, L.SER.180	H, L.SER.180	2.83	2.01	15.72
3UYR.PDB	O, L.CYS.138	N, L.SER.181	H, L.SER.181	2.84	1.99	8.90
3UYR.PDB	O, L.LEU.164	N, L.THR.182	H, L.THR.182	2.82	1.99	13.16
3UYR.PDB	O, L.VAL.136	N, L.LEU.183	H, L.LEU.183	2.83	1.99	11.27
3UYR.PDB	O, L.ALA.134	N, L.LEU.185	H, L.LEU.185	2.79	1.94	5.06
3UYR.PDB	O, L.THR.186	N, L.TYR.190	H, L.TYR.190	2.96	2.12	12.41
3UYR.PDB	O, L.LYS.187	N, L.GLU.191	H, L.GLU.191	2.81	2.00	16.98
3UYR.PDB	OD2, L.ASP.155	ND1, L.HIS.193	HD1, L.HIS.193	2.93	2.16	21.52
3UYR.PDB	ND2, L.ASN.216	ND2, L.ASN.194	HD22, L.ASN.194	2.90	2.18	28.48
3UYR.PDB	O, L.PHE.213	N, L.TYR.196	H, L.TYR.196	2.86	2.00	4.60
3UYR.PDB	O, L.LYS.153	N, L.THR.197	H, L.THR.197	2.91	2.08	15.26
3UYR.PDB	O, L.LYS.211	N, L.CYS.198	H, L.CYS.198	2.83	2.02	16.54
3UYR.PDB	O, L.LYS.151	N, L.GLU.199	H, L.GLU.199	2.79	1.98	16.73
3UYR.PDB	O, L.ILE.209	N, L.ALA.200	H, L.ALA.200	2.74	1.92	13.71
3UYR.PDB	O, L.ASN.149	N, L.THR.201	H, L.THR.201	2.78	1.96	14.01
3UYR.PDB	OG1, L.THR.204	ND1, L.HIS.202	HD1, L.HIS.202	2.78	1.93	6.06
3UYR.PDB	O, L.ALA.200	N, L.ILE.209	H, L.ILE.209	2.92	2.18	25.89
3UYR.PDB	O, L.CYS.198	N, L.LYS.211	H, L.LYS.211	2.90	2.05	8.10
3UYR.PDB	O, L.TYR.196	N, L.PHE.213	H, L.PHE.213	2.87	2.05	16.74
3UYR.PDB	O, L.ASN.194	N, L.ARG.215	H, L.ARG.215	2.75	1.97	21.32
3UYR.PDB	O, L.HIS.193	NE, L.ARG.215	HE, L.ARG.215	2.87	2.04	12.99
3UYR.PDB	OD1, H.ASN.101	NE2, P.GLN.48	HE22, P.GLN.48	2.57	1.87	29.89
3X0E.PDB	O, A.PHE.198	NZ, A.LYS.116	HZ3, A.LYS.116	2.72	1.88	16.62
3X0E.PDB	OD1, A.ASP.122	NE2, A.GLN.118	HE21, A.GLN.118	2.93	2.22	29.07
3X0E.PDB	O, A.ASN.115	N, A.ILE.119	H, A.ILE.119	2.94	2.11	11.48
3X0E.PDB	O, A.GLN.118	N, A.ASP.122	H, A.ASP.122	2.95	2.12	13.26
3X0E.PDB	O, A.ILE.119	N, A.VAL.123	H, A.VAL.123	2.88	2.05	13.75
3X0E.PDB	OD2, A.ASP.195	NZ, A.LYS.124	HZ1, A.LYS.124	3.00	2.19	21.32
3X0E.PDB	O, A.ASP.122	N, A.PHE.126	H, A.PHE.126	2.90	2.08	15.30
3X0E.PDB	O, A.VAL.123	N, A.TYR.127	H, A.TYR.127	2.95	2.12	11.57
3X0E.PDB	O, A.LYS.124	N, A.ASP.128	H, A.ASP.128	2.92	2.07	7.55
3X0E.PDB	O, A.GLN.125	N, A.GLN.129	H, A.GLN.129	2.88	2.03	7.18
3X0E.PDB	O, A.TYR.127	N, A.LEU.131	H, A.LEU.131	2.82	2.00	14.74
3X0E.PDB	O, A.ASP.128	N, A.GLN.132	H, A.GLN.132	2.95	2.12	11.27
3X0E.PDB	O, A.ALA.130	N, A.ALA.134	H, A.ALA.134	2.77	1.95	14.29
3X0E.PDB	O, A.GLN.133	N, A.ASP.137	H, A.ASP.137	2.92	2.17	25.03
3X0E.PDB	O, A.ASN.141	N, A.ALA.145	H, A.ALA.145	2.97	2.17	18.25
3X0E.PDB	O, A.ASN.142	N, A.VAL.146	H, A.VAL.146	2.81	1.98	12.77
3X0E.PDB	O, A.LYS.144	N, A.LYS.148	H, A.LYS.148	2.95	2.10	7.95
3X0E.PDB	O, A.ALA.145	N, A.THR.149	H, A.THR.149	2.85	2.06	19.27
3X0E.PDB	O, A.VAL.146	N, A.PHE.150	H, A.PHE.150	2.92	2.09	13.09
3X0E.PDB	O, A.VAL.147	N, A.HIS.151	H, A.HIS.151	2.86	2.05	17.72
3X0E.PDB	O, A.LEU.174	ND1, A.HIS.151	HD1, A.HIS.151	2.63	1.79	9.32
3X0E.PDB	O, A.THR.149	N, A.THR.153	H, A.THR.153	2.90	2.06	11.00
3X0E.PDB	O, A.PHE.150	N, A.LEU.154	H, A.LEU.154	2.90	2.06	10.44

3X0E.PDB	OD2, A_ASP_189	N, A_SER_160	H, A_SER_160	2.87	2.16	28.56
3X0E.PDB	OD2, A_ASP_128	OG1, A_THR_161	HG1, A_THR_161	2.92	2.13	12.66
3X0E.PDB	O, A_LEU_162	N, A_LEU_165	H, A_LEU_165	2.87	2.07	18.34
3X0E.PDB	O, A_SER_168	N, A_ASN_172	H, A_ASN_172	2.80	2.05	24.69
3X0E.PDB	O, A_SER_168	ND2, A_ASN_172	HD22, A_ASN_172	2.72	1.93	18.83
3X0E.PDB	O, A_LEU_170	N, A_ASN_173	H, A_ASN_173	2.82	1.98	11.48
3X0E.PDB	O, A_PRO_176	N, A_SER_179	H, A_SER_179	2.96	2.12	10.85
3X0E.PDB	O, A_CYS_157	ND2, A_ASN_184	HD21, A_ASN_184	2.90	2.04	5.52
3X0E.PDB	OD1, A_ASP_155	NZ, A_LYS_187	HZ1, A_LYS_187	2.84	2.07	26.10
3X0E.PDB	OD2, A_ASP_189	N, A_HIS_191	H, A_HIS_191	2.94	2.18	22.64
3X0E.PDB	O, A_CYS_190	N, A_ILE_194	H, A_ILE_194	2.84	2.02	14.86
3X0E.PDB	O, A_HIS_191	N, A_ASP_195	H, A_ASP_195	2.95	2.12	12.91
3X0E.PDB	O, A_GLN_192	N, A_ASP_196	H, A_ASP_196	2.86	2.06	18.82
3X0E.PDB	O, A_ASP_196	N, A_LYS_201	H, A_LYS_201	2.89	2.07	14.52
3X0E.PDB	OD1, B_ASN_115	N, B_GLN_118	H, B_GLN_118	2.83	2.07	23.69
3X0E.PDB	O, B_LYS_116	N, B_ALA_120	H, B_ALA_120	2.96	2.13	11.70
3X0E.PDB	O, B_GLN_118	N, B_ASP_122	H, B_ASP_122	2.91	2.08	11.40
3X0E.PDB	O, B_ILE_119	N, B_VAL_123	H, B_VAL_123	2.88	2.07	15.19
3X0E.PDB	O, B_ALA_120	N, B_LYS_124	H, B_LYS_124	2.98	2.18	17.57
3X0E.PDB	OD1, B_ASP_195	NZ, B_LYS_124	HZ1, B_LYS_124	2.75	2.02	29.74
3X0E.PDB	O, B_VAL_123	N, B_TYR_127	H, B_TYR_127	2.87	2.05	14.21
3X0E.PDB	O, B_LYS_124	N, B_ASP_128	H, B_ASP_128	2.82	1.97	7.12
3X0E.PDB	O, B_GLN_125	N, B_GLN_129	H, B_GLN_129	2.95	2.09	4.29
3X0E.PDB	O, B_TYR_127	N, B_LEU_131	H, B_LEU_131	2.80	2.02	19.97
3X0E.PDB	O, B_GLN_129	N, B_GLN_133	H, B_GLN_133	2.90	2.04	5.41
3X0E.PDB	O, B_ALA_130	N, B_ALA_134	H, B_ALA_134	2.78	2.05	26.00
3X0E.PDB	O, B_GLN_132	N, B_VAL_136	H, B_VAL_136	2.97	2.12	6.76
3X0E.PDB	O, B_LYS_144	N, B_LYS_148	H, B_LYS_148	2.88	2.03	4.95
3X0E.PDB	O, B_ALA_145	N, B_THR_149	H, B_THR_149	2.96	2.14	15.45
3X0E.PDB	O, B_ALA_145	OG1, B_THR_149	HG1, B_THR_149	2.91	2.17	22.45
3X0E.PDB	O, B_VAL_146	N, B_PHE_150	H, B_PHE_150	2.95	2.10	9.14
3X0E.PDB	O, B_VAL_147	N, B_HIS_151	H, B_HIS_151	2.89	2.04	9.03
3X0E.PDB	O, B_LEU_174	ND1, B_HIS_151	HD1, B_HIS_151	2.75	1.90	7.86
3X0E.PDB	O, B_LYS_148	N, B_GLU_152	H, B_GLU_152	2.88	2.06	15.18
3X0E.PDB	O, B_THR_149	N, B_THR_153	H, B_THR_153	2.82	1.98	10.07
3X0E.PDB	O, B_PHE_150	N, B_LEU_154	H, B_LEU_154	2.87	2.04	11.99
3X0E.PDB	OG1, B_THR_166	N, B_SER_159	H, B_SER_159	2.96	2.14	15.38
3X0E.PDB	OD2, B_ASP_189	N, B_SER_160	H, B_SER_160	2.78	1.93	3.69
3X0E.PDB	OG, B_SER_159	OG1, B_THR_161	HG1, B_THR_161	2.79	1.98	7.89
3X0E.PDB	O, B_SER_159	N, B_LEU_162	H, B_LEU_162	2.92	2.08	12.42
3X0E.PDB	O, B_LEU_162	N, B_THR_166	H, B_THR_166	2.94	2.18	23.20
3X0E.PDB	O, B_LEU_162	OG1, B_THR_166	HG1, B_THR_166	2.88	2.11	16.63
3X0E.PDB	O, B_THR_163	N, B_THR_167	H, B_THR_167	2.85	2.03	14.83
3X0E.PDB	O, B_LEU_165	N, B_VAL_169	H, B_VAL_169	2.94	2.17	21.85
3X0E.PDB	O, B_THR_166	N, B_LEU_170	H, B_LEU_170	2.95	2.19	24.26
3X0E.PDB	O, B_THR_167	N, B_LYS_171	H, B_LYS_171	2.99	2.15	11.05
3X0E.PDB	O, B_ASN_184	N, B_GLU_188	H, B_GLU_188	2.89	2.05	8.79
3X0E.PDB	OD1, B_ASP_128	NE2, B_HIS_191	HE2, B_HIS_191	2.68	1.83	6.07
3X0E.PDB	OD1, B_ASP_189	N, B_GLN_192	H, B_GLN_192	2.88	2.05	11.35
3X0E.PDB	O, B_ASP_189	N, B_LYS_193	H, B_LYS_193	2.99	2.20	19.70
3X0E.PDB	O, B_CYS_190	N, B_ILE_194	H, B_ILE_194	2.95	2.13	14.03
3X0E.PDB	O, B_GLN_192	N, B_ASP_196	H, B_ASP_196	2.94	2.14	18.40
3X0E.PDB	O, B_LYS_193	N, B_LEU_197	H, B_LEU_197	2.89	2.17	28.98
3X0E.PDB	O, B_ASP_196	N, B_LYS_201	H, B_LYS_201	2.91	2.09	15.23
3X0F.PDB	OD1, A_ASN_115	N, A_ASP_117	H, A_ASP_117	2.76	2.05	29.22
3X0F.PDB	O, A_LYS_116	N, A_ALA_120	H, A_ALA_120	2.96	2.10	6.18
3X0F.PDB	O, A_GLN_118	N, A_ASP_122	H, A_ASP_122	2.90	2.09	15.79
3X0F.PDB	O, A_ILE_119	N, A_VAL_123	H, A_VAL_123	2.92	2.11	16.68

3X0F.PDB	O, A_ALA_120	N, A_LYS_124	H, A_LYS_124	2.96	2.13	12.80
3X0F.PDB	OD1, A_ASP_195	NZ, A_LYS_124	HZ3, A_LYS_124	2.91	2.03	6.30
3X0F.PDB	O, A_ASP_122	N, A_PHE_126	H, A_PHE_126	2.92	2.10	14.97
3X0F.PDB	O, A_VAL_123	N, A_TYR_127	H, A_TYR_127	2.88	2.05	12.59
3X0F.PDB	O, A_LYS_124	N, A_ASP_128	H, A_ASP_128	2.89	2.08	15.92
3X0F.PDB	O, A_TYR_127	N, A_LEU_131	H, A_LEU_131	2.80	1.98	14.29
3X0F.PDB	O, A_ALA_130	N, A_ALA_134	H, A_ALA_134	2.84	2.00	11.20
3X0F.PDB	O, A_GLN_133	N, A_ASP_137	H, A_ASP_137	2.91	2.07	8.58
3X0F.PDB	OD1, A_ASP_137	N, A_ASP_139	H, A_ASP_139	2.85	1.99	3.86
3X0F.PDB	O, A_ALA_140	N, A_LYS_144	H, A_LYS_144	2.97	2.14	11.74
3X0F.PDB	O, A_ALA_134	NZ, A_LYS_144	HZ3, A_LYS_144	2.61	1.87	27.66
3X0F.PDB	O, A_ASN_142	N, A_VAL_146	H, A_VAL_146	2.93	2.09	11.09
3X0F.PDB	O, A_ALA_143	N, A_VAL_147	H, A_VAL_147	2.89	2.04	7.77
3X0F.PDB	O, A_LYS_144	N, A_LYS_148	H, A_LYS_148	2.90	2.05	7.59
3X0F.PDB	O, A_SER_173	NZ, A_LYS_148	HZ3, A_LYS_148	2.88	2.00	7.58
3X0F.PDB	O, A_ALA_145	OG1, A_THR_149	HG1, A_THR_149	2.91	2.14	15.86
3X0F.PDB	O, A_VAL_147	N, A_HIS_151	H, A_HIS_151	2.90	2.06	9.89
3X0F.PDB	O, A_LEU_174	ND1, A_HIS_151	HD1, A_HIS_151	2.77	1.98	20.06
3X0F.PDB	O, A_LYS_148	N, A_GLU_152	H, A_GLU_152	2.93	2.09	11.11
3X0F.PDB	O, A_THR_149	N, A_THR_153	H, A_THR_153	2.90	2.09	16.44
3X0F.PDB	O, A_PHE_150	N, A_LEU_154	H, A_LEU_154	2.81	2.01	18.57
3X0F.PDB	OG1, A_THR_163	N, A_ASN_160	H, A_ASN_160	2.95	2.21	26.42
3X0F.PDB	OG, A_SER_159	OG1, A_THR_163	HG1, A_THR_163	2.77	1.96	7.35
3X0F.PDB	O, A_ASN_160	N, A_THR_164	H, A_THR_164	2.88	2.07	16.97
3X0F.PDB	O, A_ASN_160	OG1, A_THR_164	HG1, A_THR_164	2.73	2.01	24.68
3X0F.PDB	O, A_LEU_162	N, A_THR_166	H, A_THR_166	2.92	2.10	13.93
3X0F.PDB	O, A_THR_163	OG1, A_THR_167	HG1, A_THR_167	2.89	2.12	16.26
3X0F.PDB	O, A_THR_166	N, A_LEU_170	H, A_LEU_170	2.90	2.06	12.50
3X0F.PDB	O, A_THR_167	N, A_ARG_171	H, A_ARG_171	2.82	2.01	17.53
3X0F.PDB	O, A_ARG_171	N, A_LEU_174	H, A_LEU_174	2.93	2.08	5.89
3X0F.PDB	O, A_ASN_172	N, A_CYS_175	H, A_CYS_175	3.00	2.20	18.23
3X0F.PDB	OG1, A_THR_183	N, A_ASN_180	H, A_ASN_180	2.96	2.18	19.92
3X0F.PDB	OD1, A_ASN_180	N, A_LEU_182	H, A_LEU_182	2.45	1.71	25.25
3X0F.PDB	O, A_THR_183	N, A_LEU_186	H, A_LEU_186	2.99	2.15	11.85
3X0F.PDB	O, A_PRO_184	N, A_GLN_187	H, A_GLN_187	2.97	2.13	7.84
3X0F.PDB	OE1, A_GLN_192	N, A_ASP_189	H, A_ASP_189	2.95	2.17	21.65
3X0F.PDB	O, A_GLY_158	N, A_CYS_190	H, A_CYS_190	2.80	1.94	6.85
3X0F.PDB	OD1, A_ASP_128	NE2, A_HIS_191	HE2, A_HIS_191	2.65	1.83	14.50
3X0F.PDB	OD1, A_ASP_189	N, A_GLN_192	H, A_GLN_192	2.76	1.93	12.98
3X0F.PDB	O, A_CYS_190	N, A_ILE_194	H, A_ILE_194	2.92	2.08	11.33
3X0F.PDB	O, A_HIS_191	N, A_ASP_195	H, A_ASP_195	2.89	2.05	8.32
3X0F.PDB	OD1, B_ASN_115	N, B_ASP_117	H, B_ASP_117	2.83	2.09	25.59
3X0F.PDB	O, B_ILE_119	N, B_VAL_123	H, B_VAL_123	2.90	2.08	14.90
3X0F.PDB	O, B_ALA_120	N, B_LYS_124	H, B_LYS_124	2.96	2.13	14.11
3X0F.PDB	O, B_ASP_122	N, B_PHE_126	H, B_PHE_126	2.92	2.10	15.77
3X0F.PDB	O, B_VAL_123	N, B_TYR_127	H, B_TYR_127	2.83	1.99	10.66
3X0F.PDB	O, B_LYS_124	N, B_ASP_128	H, B_ASP_128	2.91	2.10	15.77
3X0F.PDB	O, B_TYR_127	N, B_LEU_131	H, B_LEU_131	2.83	2.00	14.03
3X0F.PDB	O, B_ASP_128	N, B_GLN_132	H, B_GLN_132	2.94	2.11	13.87
3X0F.PDB	O, B_ALA_130	N, B_ALA_134	H, B_ALA_134	2.84	1.99	5.94
3X0F.PDB	O, B_GLN_133	N, B_ASP_137	H, B_ASP_137	2.83	1.99	9.88
3X0F.PDB	OD1, B_ASP_137	N, B_ASP_139	H, B_ASP_139	2.78	1.95	12.28
3X0F.PDB	O, B_ASN_141	N, B_ALA_145	H, B_ALA_145	2.98	2.19	18.75
3X0F.PDB	O, B_ASN_142	N, B_VAL_146	H, B_VAL_146	2.93	2.10	14.03
3X0F.PDB	O, B_ALA_143	N, B_VAL_147	H, B_VAL_147	2.90	2.05	8.67
3X0F.PDB	O, B_LYS_144	N, B_LYS_148	H, B_LYS_148	2.93	2.08	6.49
3X0F.PDB	O, B_ALA_145	OG1, B_THR_149	HG1, B_THR_149	2.77	1.99	16.05
3X0F.PDB	O, B_VAL_147	N, B_HIS_151	H, B_HIS_151	2.84	2.00	10.99

3X0F.PDB	O, B_LEU.174	ND1, B_HIS.151	HD1, B_HIS.151	2.65	1.84	15.99
3X0F.PDB	OH, B_TYR.127	NE2, B_HIS.151	HE2, B_HIS.151	2.81	2.02	19.67
3X0F.PDB	O, B_LYS.148	N, B_GLU.152	H, B_GLU.152	2.77	1.92	6.84
3X0F.PDB	O, B_THR.149	N, B_THR.153	H, B_THR.153	2.95	2.13	14.83
3X0F.PDB	O, B_PHE.150	N, B_LEU.154	H, B_LEU.154	2.85	2.04	17.17
3X0F.PDB	OG1, B_THR.163	OG, B_SER.159	HG, B_SER.159	2.96	2.16	10.94
3X0F.PDB	O, B_ASN.160	OG1, B_THR.164	HG1, B_THR.164	2.57	1.80	16.52
3X0F.PDB	O, B_LEU.162	N, B_THR.166	H, B_THR.166	2.76	1.93	11.31
3X0F.PDB	O, B_THR.163	N, B_THR.167	H, B_THR.167	2.99	2.18	15.60
3X0F.PDB	O, B_THR.166	N, B_LEU.170	H, B_LEU.170	2.87	2.06	18.01
3X0F.PDB	O, B_GLY.158	N, B_CYS.190	H, B_CYS.190	2.83	2.05	20.10
3X0F.PDB	OD1, B_ASP.128	NE2, B_HIS.191	HE2, B_HIS.191	2.69	1.83	1.74
3X0F.PDB	O, B_CYS.190	N, B_ILE.194	H, B_ILE.194	2.81	1.97	10.56
3X0F.PDB	O, B_GLN.192	N, B_GLU.196	H, B_GLU.196	2.96	2.13	13.52
3X0F.PDB	O, B_LYS.193	N, B_LEU.197	H, B_LEU.197	2.98	2.18	18.16
3X0F.PDB	O, B_ILE.194	N, B_PHE.198	H, B_PHE.198	2.87	2.06	16.88
3X0F.PDB	O, B_ASP.195	N, B_SER.199	H, B_SER.199	2.79	2.06	26.20
4F33.PDB	OG, A_SER.27	N, A_GLU.4	H, A_GLU.4	2.93	2.12	15.90
4F33.PDB	O, A_SER.25	N, A_THR.6	H, A_THR.6	2.82	1.97	4.01
4F33.PDB	O, A_TYR.86	NE2, A_GLN.7	HE22, A_GLN.7	2.87	2.09	21.54
4F33.PDB	O, A_THR.23	N, A_SER.8	H, A_SER.8	2.88	2.08	17.40
4F33.PDB	O, A_LYS.103	N, A_MET.12	H, A_MET.12	2.89	2.08	17.33
4F33.PDB	OE2, A_GLU.18	N, A_SER.15	H, A_SER.15	2.97	2.12	6.98
4F33.PDB	O, A_VAL.78	N, A_GLY.17	H, A_GLY.17	2.85	2.06	20.41
4F33.PDB	O, A_ILE.75	N, A_VAL.20	H, A_VAL.20	2.97	2.17	19.12
4F33.PDB	O, A_LEU.73	N, A_MET.22	H, A_MET.22	2.86	2.02	10.29
4F33.PDB	O, A_SER.8	N, A_THR.23	H, A_THR.23	2.78	1.93	7.24
4F33.PDB	O, A_TYR.71	N, A_CYS.24	H, A_CYS.24	2.78	1.93	6.93
4F33.PDB	O, A_THR.6	N, A_SER.25	H, A_SER.25	2.80	1.94	5.80
4F33.PDB	O, A_ASN.69	N, A_ALA.26	H, A_ALA.26	2.83	1.99	8.87
4F33.PDB	O, A_ILE.48	N, A_TRP.35	H, A_TRP.35	2.69	1.86	13.25
4F33.PDB	O, A_TYR.87	N, A_TYR.36	H, A_TYR.36	2.79	1.98	16.56
4F33.PDB	O, A_LYS.45	N, A_GLN.37	H, A_GLN.37	2.93	2.17	24.56
4F33.PDB	O, A_THR.85	N, A_GLN.38	H, A_GLN.38	2.78	1.94	8.77
4F33.PDB	O, A_THR.42	NE2, A_GLN.38	HE21, A_GLN.38	2.85	2.01	10.50
4F33.PDB	OE1, B_GLN.39	NE2, A_GLN.38	HE22, A_GLN.38	2.96	2.13	12.75
4F33.PDB	O, A_GLU.81	NZ, A_LYS.39	HZ1, A_LYS.39	2.81	1.96	14.34
4F33.PDB	O, A_ASP.83	NZ, A_LYS.39	HZ3, A_LYS.39	2.88	2.10	24.06
4F33.PDB	O, A_LYS.39	OG1, A_THR.42	HG1, A_THR.42	2.81	1.99	3.65
4F33.PDB	O, B_GLY.110	OG, A_SER.43	HG, A_SER.43	2.65	1.95	25.99
4F33.PDB	O, A_GLN.37	N, A_LYS.45	H, A_LYS.45	2.79	1.96	13.89
4F33.PDB	O, B_ARG.104	NH1, A_ARG.46	HH11, A_ARG.46	2.62	1.83	18.99
4F33.PDB	O, A_TRP.35	N, A_TRP.47	H, A_TRP.47	2.84	2.05	19.82
4F33.PDB	O, A_LYS.53	N, A_TYR.49	H, A_TYR.49	2.79	1.99	16.95
4F33.PDB	O, A_MET.33	N, A_THR.51	H, A_THR.51	2.74	1.92	15.06
4F33.PDB	O, A_ASP.50	N, A_SER.52	H, A_SER.52	2.84	2.12	28.76
4F33.PDB	O, A_TYR.49	N, A_LYS.53	H, A_LYS.53	2.87	2.05	15.09
4F33.PDB	OD2, A_ASP.82	NE, A_ARG.61	HE, A_ARG.61	2.81	2.09	28.09
4F33.PDB	OD1, A_ASP.82	NH2, A_ARG.61	HH21, A_ARG.61	2.71	1.85	4.82
4F33.PDB	O, A_THR.74	N, A_SER.63	H, A_SER.63	2.91	2.14	22.09
4F33.PDB	O, A_ALA.26	ND2, A_ASN.69	HD21, A_ASN.69	2.95	2.09	2.58
4F33.PDB	O, A_SER.67	N, A_SER.70	H, A_SER.70	2.98	2.12	3.48
4F33.PDB	O, A_CYS.24	N, A_TYR.71	H, A_TYR.71	2.94	2.09	7.81
4F33.PDB	O, A_VAL.30	OH, A_TYR.71	HH, A_TYR.71	2.83	2.13	26.33
4F33.PDB	O, A_SER.65	N, A_SER.72	H, A_SER.72	2.82	1.99	12.37
4F33.PDB	O, A_MET.22	N, A_LEU.73	H, A_LEU.73	2.90	2.08	15.13
4F33.PDB	O, A_SER.63	N, A_THR.74	H, A_THR.74	2.86	2.01	8.97
4F33.PDB	OG1, A_THR.21	OG1, A_THR.74	HG1, A_THR.74	2.73	1.99	21.82

4F33.PDB	O, A_VAL_20	N, A_ILE_75	H, A_ILE_75	2.86	2.05	16.70
4F33.PDB	O, A_ARG_61	N, A_SER_76	H, A_SER_76	2.74	1.93	15.27
4F33.PDB	O, A_GLU_18	N, A_VAL_78	H, A_VAL_78	2.98	2.22	23.09
4F33.PDB	OD2, A_ASP_82	N, A_GLU_79	H, A_GLU_79	2.83	1.97	5.35
4F33.PDB	O, A_GLU_79	N, A_ASP_82	H, A_ASP_82	2.82	1.98	10.48
4F33.PDB	O, A_GLN_38	N, A_THR_85	H, A_THR_85	2.93	2.09	10.56
4F33.PDB	O, A_THR_102	N, A_TYR_86	H, A_TYR_86	2.88	2.05	12.33
4F33.PDB	O, A_TYR_36	N, A_TYR_87	H, A_TYR_87	2.86	2.04	15.05
4F33.PDB	OG1, A_THR_97	NE2, A_GLN_90	HE21, A_GLN_90	2.97	2.15	14.62
4F33.PDB	O, A_TYR_32	NE1, A_TRP_91	HE1, A_TRP_91	2.74	1.96	21.98
4F33.PDB	O, A_ILE_3	OG1, A_THR_97	HG1, A_THR_97	2.86	2.07	13.11
4F33.PDB	O, A_CYS_88	N, A_GLY_99	H, A_GLY_99	2.86	2.04	15.33
4F33.PDB	OE1, A_GLN_7	N, A_GLY_101	H, A_GLY_101	2.83	2.06	22.47
4F33.PDB	O, A_TYR_86	N, A_THR_102	H, A_THR_102	2.93	2.11	14.73
4F33.PDB	O, A_PRO_9	OG1, A_THR_102	HG1, A_THR_102	2.73	1.96	15.99
4F33.PDB	O, A_ALA_10	N, A_LYS_103	H, A_LYS_103	2.90	2.06	9.01
4F33.PDB	O, A_ALA_84	N, A_VAL_104	H, A_VAL_104	2.88	2.03	4.65
4F33.PDB	O, A_MET_12	N, A_GLU_105	H, A_GLU_105	2.79	1.94	7.59
4F33.PDB	OE1, A_GLN_166	N, A_ILE_106	H, A_ILE_106	2.90	2.05	6.64
4F33.PDB	O, A_ALA_14	N, A_LYS_107	H, A_LYS_107	2.83	2.00	10.77
4F33.PDB	OG, A_SER_13	NZ, A_LYS_107	HZ3, A_LYS_107	2.94	2.07	9.78
4F33.PDB	O, A_THR_109	NE, A_ARG_108	HE, A_ARG_108	2.77	1.91	3.92
4F33.PDB	O, A_ASP_170	NH1, A_ARG_108	HH11, A_ARG_108	2.95	2.12	11.15
4F33.PDB	O, A_TYR_140	N, A_ALA_111	H, A_ALA_111	2.85	2.01	10.73
4F33.PDB	O, A_LEU_135	N, A_PHE_116	H, A_PHE_116	2.94	2.15	19.06
4F33.PDB	O, A_VAL_133	N, A_PHE_118	H, A_PHE_118	2.80	2.01	19.24
4F33.PDB	OG, A_SER_131	NE2, A_GLN_124	HE22, A_GLN_124	2.81	1.96	5.54
4F33.PDB	O, A_LEU_125	N, A_GLY_128	H, A_GLY_128	2.79	1.95	9.52
4F33.PDB	O, A_LEU_181	N, A_ALA_130	H, A_ALA_130	2.76	1.92	9.83
4F33.PDB	OE1, A_GLN_124	N, A_SER_131	H, A_SER_131	2.96	2.15	16.54
4F33.PDB	O, A_LEU_179	N, A_VAL_132	H, A_VAL_132	2.82	1.98	11.91
4F33.PDB	O, A_SER_177	N, A_CYS_134	H, A_CYS_134	2.86	2.01	7.49
4F33.PDB	O, A_PHE_116	N, A_LEU_135	H, A_LEU_135	2.76	1.92	8.98
4F33.PDB	O, A_LEU_175	N, A_LEU_136	H, A_LEU_136	2.76	1.90	4.04
4F33.PDB	O, A_SER_114	N, A_ASN_137	H, A_ASN_137	2.84	2.02	13.99
4F33.PDB	O, A_TYR_173	N, A_PHE_139	H, A_PHE_139	2.85	2.04	16.43
4F33.PDB	O, A_ALA_111	N, A_TYR_140	H, A_TYR_140	2.90	2.09	16.65
4F33.PDB	O, A_THR_197	N, A_LYS_145	H, A_LYS_145	2.98	2.16	14.92
4F33.PDB	O, A_GLU_195	N, A_GLN_147	H, A_GLN_147	2.86	2.02	11.34
4F33.PDB	OG, A_SER_177	NE1, A_TRP_148	HE1, A_TRP_148	2.91	2.09	14.52
4F33.PDB	O, A_ALA_193	N, A_LYS_149	H, A_LYS_149	2.87	2.03	10.60
4F33.PDB	OE1, A_GLU_195	NZ, A_LYS_149	HZ2, A_LYS_149	2.59	1.85	28.21
4F33.PDB	O, A_VAL_191	N, A_ASP_151	H, A_ASP_151	2.75	1.92	13.23
4F33.PDB	O, A_VAL_150	N, A_ALA_153	H, A_ALA_153	2.85	2.00	6.45
4F33.PDB	O, A_TRP_148	N, A_GLN_155	H, A_GLN_155	2.92	2.11	17.54
4F33.PDB	OE1, A_GLN_155	ND2, A_ASN_158	HD22, A_ASN_158	2.89	2.06	12.00
4F33.PDB	O, A_THR_178	N, A_GLN_160	H, A_GLN_160	2.98	2.22	22.84
4F33.PDB	O, A_SER_176	N, A_SER_162	H, A_SER_162	2.94	2.15	19.03
4F33.PDB	O, B_PRO_173	OG, A_SER_162	HG, A_SER_162	2.76	2.03	23.18
4F33.PDB	O, A_SER_174	N, A_THR_164	H, A_THR_164	2.92	2.09	12.25
4F33.PDB	O, A_SER_171	NE2, A_GLN_166	HE21, A_GLN_166	2.92	2.09	13.24
4F33.PDB	O, A_ILE_106	NE2, A_GLN_166	HE22, A_GLN_166	2.72	1.92	18.36
4F33.PDB	OD1, A_ASP_167	N, A_LYS_169	H, A_LYS_169	2.65	1.81	10.48
4F33.PDB	O, A_ASP_167	N, A_SER_171	H, A_SER_171	2.90	2.19	29.27
4F33.PDB	OD1, A_ASP_170	N, A_THR_172	H, A_THR_172	2.86	2.04	14.41
4F33.PDB	OD1, A_ASP_170	OG1, A_THR_172	HG1, A_THR_172	2.68	1.86	4.02
4F33.PDB	O, A_PHE_139	N, A_TYR_173	H, A_TYR_173	2.78	1.94	7.95
4F33.PDB	OG1, A_THR_164	N, A_SER_174	H, A_SER_174	2.96	2.13	11.32

4F33.PDB	O, A_LEU_136	N, A_LEU_175	H, A_LEU_175	2.82	2.01	16.11
4F33.PDB	O, A_SER_162	N, A_SER_176	H, A_SER_176	2.89	2.07	14.35
4F33.PDB	O, A_CYS_134	N, A_SER_177	H, A_SER_177	2.92	2.09	13.76
4F33.PDB	O, A_GLN_160	N, A_THR_178	H, A_THR_178	2.88	2.04	10.18
4F33.PDB	O, A_VAL_132	N, A_LEU_179	H, A_LEU_179	2.84	2.02	14.45
4F33.PDB	O, A_ASN_158	N, A_THR_180	H, A_THR_180	2.95	2.12	11.92
4F33.PDB	O, A_ALA_130	N, A_LEU_181	H, A_LEU_181	2.88	2.05	13.17
4F33.PDB	O, A_GLY_128	N, A_LYS_183	H, A_LYS_183	2.98	2.19	19.73
4F33.PDB	OG, A_SER_182	N, A_ASP_185	H, A_ASP_185	2.87	2.04	12.72
4F33.PDB	O, A_SER_182	N, A_TYR_186	H, A_TYR_186	2.80	1.98	14.27
4F33.PDB	O, A_LYS_183	N, A_GLU_187	H, A_GLU_187	2.86	2.04	14.84
4F33.PDB	OD2, A_ASP_151	N, A_LYS_190	H, A_LYS_190	2.95	2.15	18.90
4F33.PDB	OD1, A_ASP_151	N, A_VAL_191	H, A_VAL_191	2.83	1.98	4.63
4F33.PDB	O, A_PHE_209	N, A_TYR_192	H, A_TYR_192	2.96	2.11	7.57
4F33.PDB	O, A_LYS_149	N, A_ALA_193	H, A_ALA_193	2.92	2.11	16.79
4F33.PDB	O, A_LYS_207	N, A_CYS_194	H, A_CYS_194	2.99	2.20	20.51
4F33.PDB	O, A_GLN_147	N, A_GLU_195	H, A_GLU_195	2.80	1.96	10.16
4F33.PDB	O, A_VAL_205	N, A_VAL_196	H, A_VAL_196	2.72	1.89	12.89
4F33.PDB	O, A_LYS_145	N, A_THR_197	H, A_THR_197	2.87	2.04	14.20
4F33.PDB	O, A_HIS_198	N, A_LEU_201	H, A_LEU_201	2.83	1.98	4.49
4F33.PDB	O, A_VAL_196	N, A_VAL_205	H, A_VAL_205	2.93	2.11	14.32
4F33.PDB	O, A_TYR_192	N, A_PHE_209	H, A_PHE_209	2.97	2.19	21.09
4F33.PDB	O, A_LYS_190	N, A_ARG_211	H, A_ARG_211	2.77	1.94	10.87
4F33.PDB	O, A_HIS_189	NE, A_ARG_211	HE, A_ARG_211	2.95	2.11	10.88
4F33.PDB	O, B_LYS_23	N, B_GLN_5	H, B_GLN_5	2.89	2.04	6.23
4F33.PDB	O, B_TYR_94	NE2, B_GLN_6	HE22, B_GLN_6	2.91	2.10	17.22
4F33.PDB	O, B_SER_21	N, B_SER_7	H, B_SER_7	2.99	2.26	27.49
4F33.PDB	O, B_PRO_114	N, B_GLU_10	H, B_GLU_10	2.94	2.16	20.47
4F33.PDB	O, B_LEU_86	N, B_GLY_15	H, B_GLY_15	2.71	1.91	16.40
4F33.PDB	O, B_LEU_83	N, B_VAL_18	H, B_VAL_18	2.93	2.17	23.19
4F33.PDB	O, B_MET_81	N, B_ILE_20	H, B_ILE_20	2.82	1.99	11.32
4F33.PDB	OG, B_SER_7	N, B_SER_21	H, B_SER_21	2.96	2.11	7.69
4F33.PDB	O, B_ALA_79	N, B_CYS_22	H, B_CYS_22	2.82	2.06	23.47
4F33.PDB	O, B_GLN_5	N, B_LYS_23	H, B_LYS_23	2.73	1.90	11.88
4F33.PDB	O, B_SER_77	N, B_ALA_24	H, B_ALA_24	2.97	2.12	8.25
4F33.PDB	O, B_GLN_3	N, B_SER_25	H, B_SER_25	2.93	2.12	17.16
4F33.PDB	O, B_SER_28	N, B_GLY_31	H, B_GLY_31	2.98	2.12	6.95
4F33.PDB	O, B_GLY_99	N, B_THR_33	H, B_THR_33	2.98	2.22	23.44
4F33.PDB	O, B_ALA_97	N, B_ASN_35	H, B_ASN_35	2.80	1.95	8.88
4F33.PDB	O, B_PHE_95	N, B_VAL_37	H, B_VAL_37	2.85	2.06	19.95
4F33.PDB	O, B_GLU_46	N, B_LYS_38	H, B_LYS_38	2.82	2.01	16.68
4F33.PDB	O, B_GLU_89	NZ, B_LYS_38	HZ1, B_LYS_38	2.86	1.98	5.39
4F33.PDB	O, B_VAL_93	N, B_GLN_39	H, B_GLN_39	2.87	2.01	5.84
4F33.PDB	OE1, A_GLN_38	NE2, B_GLN_39	HE22, B_GLN_39	2.82	1.97	5.31
4F33.PDB	O, B_SER_40	N, B_LYS_43	H, B_LYS_43	2.88	2.06	15.26
4F33.PDB	O, B_LYS_38	N, B_GLU_46	H, B_GLU_46	2.87	2.06	16.90
4F33.PDB	O, B_TRP_36	N, B_ILE_48	H, B_ILE_48	2.80	1.95	7.15
4F33.PDB	O, B_SER_59	N, B_LEU_50	H, B_LEU_50	2.87	2.08	19.32
4F33.PDB	O, B_MET_34	N, B_ILE_51	H, B_ILE_51	2.89	2.09	18.35
4F33.PDB	O, B_ALA_57	N, B_THR_52	H, B_THR_52	2.92	2.09	13.37
4F33.PDB	O, B_THR_52	N, B_GLY_56	H, B_GLY_56	2.89	2.15	26.20
4F33.PDB	OD1, B_ASN_55	N, B_ALA_57	H, B_ALA_57	2.85	2.00	7.05
4F33.PDB	O, B_LEU_50	N, B_SER_59	H, B_SER_59	2.88	2.09	19.09
4F33.PDB	O, B_ILE_48	N, B_ASN_61	H, B_ASN_61	2.90	2.09	17.36
4F33.PDB	O, B_TRP_47	ND2, B_ASN_61	HD21, B_ASN_61	2.94	2.11	14.44
4F33.PDB	OE2, B_GLU_46	NZ, B_LYS_63	HZ3, B_LYS_63	2.70	1.89	19.35
4F33.PDB	O, B_ASN_61	N, B_PHE_64	H, B_PHE_64	2.77	1.93	12.05
4F33.PDB	OD2, B_ASP_90	NZ, B_LYS_67	HZ2, B_LYS_67	2.73	1.86	7.48

4F33.PDB	O, B_LEU_84	NZ, B_LYS_67	HZ3, B_LYS_67	2.85	2.01	15.38
4F33.PDB	O, B_PHE_64	N, B_ALA_68	H, B_ALA_68	2.93	2.14	19.80
4F33.PDB	O, B_ASP_82	N, B_THR_69	H, B_THR_69	2.92	2.16	23.54
4F33.PDB	OH, B_TYR_60	N, B_LEU_70	H, B_LEU_70	2.92	2.07	9.07
4F33.PDB	O, B_THR_78	N, B_ASP_73	H, B_ASP_73	2.75	1.91	10.75
4F33.PDB	O, B_CYS_22	N, B_ALA_79	H, B_ALA_79	2.91	2.08	13.58
4F33.PDB	O, B_THR_71	N, B_TYR_80	H, B_TYR_80	2.83	1.97	4.70
4F33.PDB	O, B_ILE_20	N, B_MET_81	H, B_MET_81	2.96	2.15	15.91
4F33.PDB	O, B_THR_69	N, B_ASP_82	H, B_ASP_82	2.88	2.06	13.69
4F33.PDB	O, B_VAL_18	N, B_LEU_83	H, B_LEU_83	2.80	1.96	11.41
4F33.PDB	O, B_LYS_67	N, B_LEU_84	H, B_LEU_84	2.92	2.11	17.58
4F33.PDB	O, B_ALA_16	N, B_LEU_86	H, B_LEU_86	2.87	2.02	6.19
4F33.PDB	OD2, B_ASP_90	N, B_THR_87	H, B_THR_87	2.83	2.02	16.35
4F33.PDB	O, B_THR_87	N, B_ASP_90	H, B_ASP_90	2.88	2.04	10.12
4F33.PDB	O, B_SER_88	N, B_SER_91	H, B_SER_91	2.97	2.12	6.19
4F33.PDB	O, B_VAL_115	N, B_ALA_92	H, B_ALA_92	2.98	2.25	27.22
4F33.PDB	O, B_GLN_39	N, B_VAL_93	H, B_VAL_93	2.95	2.11	9.70
4F33.PDB	O, B_THR_113	N, B_TYR_94	H, B_TYR_94	2.86	2.02	9.76
4F33.PDB	O, B_VAL_37	N, B_PHE_95	H, B_PHE_95	2.79	1.94	9.71
4F33.PDB	O, B_ASN_35	N, B_ALA_97	H, B_ALA_97	2.79	2.04	25.47
4F33.PDB	O, B_TYR_108	N, B_ARG_98	H, B_ARG_98	2.80	2.01	18.50
4F33.PDB	OD2, B_ASP_107	NH2, B_ARG_98	HH21, B_ARG_98	2.74	1.88	6.50
4F33.PDB	O, B_THR_33	N, B_GLY_99	H, B_GLY_99	2.94	2.10	10.07
4F33.PDB	OD1, B_ASP_102	NE, B_ARG_104	HE, B_ARG_104	2.87	2.03	8.81
4F33.PDB	OD2, B_ASP_107	NH1, B_ARG_104	HH11, B_ARG_104	2.78	1.96	13.74
4F33.PDB	OD2, B_ASP_102	NH2, B_ARG_104	HH21, B_ARG_104	2.87	2.08	19.19
4F33.PDB	OH, A_TYR_36	N, B_PHE_106	H, B_PHE_106	2.97	2.12	7.79
4F33.PDB	O, B_CYS_96	N, B_GLY_110	H, B_GLY_110	2.83	1.98	5.16
4F33.PDB	OE1, B_GLN_6	N, B_GLY_112	H, B_GLY_112	2.90	2.10	18.34
4F33.PDB	O, B_TYR_94	N, B_THR_113	H, B_THR_113	2.81	1.99	14.66
4F33.PDB	O, B_SER_7	OG1, B_THR_113	HG1, B_THR_113	2.83	2.05	14.68
4F33.PDB	O, B_ALA_92	N, B_VAL_115	H, B_VAL_115	2.84	1.99	7.09
4F33.PDB	OG, B_SER_91	N, B_VAL_117	H, B_VAL_117	2.86	2.01	9.50
4F33.PDB	O, B_GLU_12	N, B_SER_118	H, B_SER_118	2.87	2.07	16.95
4F33.PDB	O, B_PHE_152	N, B_LYS_123	H, B_LYS_123	2.81	1.98	13.03
4F33.PDB	O, B_ASP_150	NZ, B_LYS_123	HZ2, B_LYS_123	2.83	2.00	16.92
4F33.PDB	O, B_GLY_124	NZ, B_LYS_123	HZ3, B_LYS_123	2.99	2.25	28.99
4F33.PDB	OE2, G_GLU_123	N, B_GLY_124	H, B_GLY_124	2.73	1.87	2.75
4F33.PDB	O, B_LYS_149	N, B_SER_126	H, B_SER_126	2.95	2.16	19.58
4F33.PDB	O, B_LEU_147	N, B_PHE_128	H, B_PHE_128	2.87	2.05	14.02
4F33.PDB	O, B_GLY_145	N, B_LEU_130	H, B_LEU_130	2.71	1.85	5.41
4F33.PDB	OG, B_SER_136	N, B_SER_133	H, B_SER_133	2.90	2.08	15.18
4F33.PDB	OG, B_SER_133	N, B_LYS_135	H, B_LYS_135	2.89	2.11	19.85
4F33.PDB	O, B_SER_133	OG1, B_THR_137	HG1, B_THR_137	2.92	2.21	25.24
4F33.PDB	O, B_SER_138	N, B_THR_141	H, B_THR_141	2.82	1.98	11.03
4F33.PDB	O, B_VAL_190	N, B_ALA_142	H, B_ALA_142	2.81	1.95	3.27
4F33.PDB	O, B_SER_136	N, B_ALA_143	H, B_ALA_143	2.75	1.93	14.52
4F33.PDB	O, B_LEU_130	N, B_GLY_145	H, B_GLY_145	2.97	2.22	25.31
4F33.PDB	O, B_PHE_128	N, B_LEU_147	H, B_LEU_147	2.81	1.97	10.25
4F33.PDB	O, B_LEU_184	N, B_VAL_148	H, B_VAL_148	2.76	1.91	7.90
4F33.PDB	O, B_SER_126	N, B_LYS_149	H, B_LYS_149	2.79	1.93	4.11
4F33.PDB	O, B_LYS_123	N, B_PHE_152	H, B_PHE_152	2.89	2.09	18.27
4F33.PDB	O, B_ASN_203	N, B_SER_159	H, B_SER_159	2.96	2.15	17.06
4F33.PDB	OG, B_SER_186	NE1, B_TRP_160	HE1, B_TRP_160	2.97	2.13	10.43
4F33.PDB	O, B_ILE_201	N, B_ASN_161	H, B_ASN_161	2.81	1.97	10.56
4F33.PDB	OD1, B_ASN_203	N, B_SER_162	H, B_SER_162	2.81	2.00	15.00
4F33.PDB	O, B_TRP_160	N, B_GLY_163	H, B_GLY_163	2.93	2.14	20.08
4F33.PDB	O, B_VAL_187	N, B_HIS_170	H, B_HIS_170	2.81	1.98	12.68

4F33.PDB	O, B_SER_185	N, B_PHE_172	H, B_PHE_172	3.00	2.14	5.14
4F33.PDB	O, B_SER_183	N, B_VAL_175	H, B_VAL_175	2.90	2.08	14.90
4F33.PDB	O, B_LEU_181	N, B_GLN_177	H, B_GLN_177	2.81	1.96	6.18
4F33.PDB	OD1, B_ASP_150	NE2, B_GLN_177	HE22, B_GLN_177	2.84	2.07	21.15
4F33.PDB	O, B_TYR_151	N, B_TYR_182	H, B_TYR_182	2.85	2.02	11.23
4F33.PDB	O, B_VAL_148	N, B_LEU_184	H, B_LEU_184	2.91	2.10	17.00
4F33.PDB	O, B_CYS_146	N, B_SER_186	H, B_SER_186	2.97	2.15	14.23
4F33.PDB	O, B_HIS_170	N, B_VAL_187	H, B_VAL_187	2.83	1.99	10.23
4F33.PDB	O, B_LEU_144	N, B_VAL_188	H, B_VAL_188	2.83	2.04	19.81
4F33.PDB	O, B_ALA_142	N, B_VAL_190	H, B_VAL_190	2.79	1.97	14.47
4F33.PDB	O, B_GLY_140	N, B_SER_192	H, B_SER_192	2.87	2.03	10.06
4F33.PDB	O, B_PRO_191	N, B_SER_194	H, B_SER_194	2.87	2.02	9.35
4F33.PDB	O, B_SER_194	N, B_GLN_198	H, B_GLN_198	2.75	1.90	4.61
4F33.PDB	O, B_THR_199	NE2, B_GLN_198	HE21, B_GLN_198	2.96	2.10	2.10
4F33.PDB	OD1, B_ASN_161	N, B_ILE_201	H, B_ILE_201	2.82	2.00	13.45
4F33.PDB	O, B_LYS_215	N, B_CYS_202	H, B_CYS_202	2.94	2.15	19.46
4F33.PDB	O, B_SER_159	N, B_ASN_203	H, B_ASN_203	2.77	1.92	6.83
4F33.PDB	OD1, B_ASP_214	ND2, B_ASN_203	HD21, B_ASN_203	2.97	2.12	8.15
4F33.PDB	O, B_VAL_213	N, B_VAL_204	H, B_VAL_204	2.74	1.90	9.17
4F33.PDB	O, B_THR_157	N, B_ASN_205	H, B_ASN_205	2.86	2.01	7.37
4F33.PDB	O, B_THR_211	N, B_HIS_206	H, B_HIS_206	2.85	2.00	6.46
4F33.PDB	OG, B_SER_209	ND1, B_HIS_206	HD1, B_HIS_206	2.61	1.78	12.57
4F33.PDB	O, B_PRO_153	NE2, B_HIS_206	HE2, B_HIS_206	2.85	2.02	12.89
4F33.PDB	O, B_LYS_207	N, B_ASN_210	H, B_ASN_210	2.94	2.11	13.00
4F33.PDB	O, H_ASP_214	N, B_LYS_212	H, B_LYS_212	2.81	2.00	15.02
4F33.PDB	O, B_VAL_204	N, B_VAL_213	H, B_VAL_213	2.80	1.98	15.11
4F33.PDB	O, H_LYS_212	N, B_ASP_214	H, B_ASP_214	2.84	2.02	15.98
4F33.PDB	O, B_CYS_202	N, B_LYS_215	H, B_LYS_215	2.91	2.09	16.20
4F33.PDB	OE1, A_GLU_123	NZ, B_LYS_215	HZ1, B_LYS_215	2.68	1.82	12.44
4F33.PDB	OG1, H_THR_211	NZ, B_LYS_215	HZ2, B_LYS_215	2.83	1.95	7.37
4F33.PDB	O, B_TYR_200	N, B_VAL_217	H, B_VAL_217	2.89	2.04	8.29
4F33.PDB	OG, C_SER_27	N, C_GLU_4	H, C_GLU_4	2.91	2.10	15.68
4F33.PDB	O, C_SER_25	N, C_THR_6	H, C_THR_6	2.79	1.94	4.69
4F33.PDB	O, C_TYR_86	NE2, C_GLN_7	HE22, C_GLN_7	2.91	2.14	22.16
4F33.PDB	O, C_THR_23	N, C_SER_8	H, C_SER_8	2.94	2.13	16.69
4F33.PDB	O, C_LYS_103	N, C_MET_12	H, C_MET_12	2.88	2.06	16.35
4F33.PDB	OE2, C_GLU_18	N, C_SER_15	H, C_SER_15	2.79	1.94	9.08
4F33.PDB	O, C_VAL_78	N, C_GLY_17	H, C_GLY_17	2.81	2.02	19.83
4F33.PDB	O, C_LEU_73	N, C_MET_22	H, C_MET_22	2.85	2.01	10.93
4F33.PDB	O, C_SER_8	N, C_THR_23	H, C_THR_23	2.77	1.93	10.15
4F33.PDB	O, C_TYR_71	N, C_CYS_24	H, C_CYS_24	2.75	1.90	8.61
4F33.PDB	O, C_THR_6	N, C_SER_25	H, C_SER_25	2.79	1.94	6.02
4F33.PDB	O, C_ASN_69	N, C_ALA_26	H, C_ALA_26	2.82	1.97	9.46
4F33.PDB	O, C_GLN_89	N, C_HIS_34	H, C_HIS_34	2.95	2.09	1.08
4F33.PDB	O, C_ILE_48	N, C_TRP_35	H, C_TRP_35	2.66	1.84	15.50
4F33.PDB	O, C_TYR_87	N, C_TYR_36	H, C_TYR_36	2.75	1.94	16.72
4F33.PDB	O, C_LYS_45	N, C_GLN_37	H, C_GLN_37	2.94	2.17	21.42
4F33.PDB	O, C_THR_85	N, C_GLN_38	H, C_GLN_38	2.81	1.97	10.54
4F33.PDB	O, C_THR_42	NE2, C_GLN_38	HE21, C_GLN_38	2.84	2.00	10.36
4F33.PDB	O, C_GLU_81	NZ, C_LYS_39	HZ1, C_LYS_39	2.82	1.94	9.21
4F33.PDB	O, C_ASP_83	NZ, C_LYS_39	HZ3, C_LYS_39	2.78	1.95	17.23
4F33.PDB	O, C_LYS_39	OG1, C_THR_42	HG1, C_THR_42	2.80	1.99	2.97
4F33.PDB	O, D_GLY_110	OG, C_SER_43	HG, C_SER_43	2.70	1.98	23.76
4F33.PDB	O, C_GLN_37	N, C_LYS_45	H, C_LYS_45	2.82	2.00	13.68
4F33.PDB	O, D_ARG_104	NH1, C_ARG_46	HH11, C_ARG_46	2.70	1.92	20.25
4F33.PDB	O, C_TRP_35	N, C_TRP_47	H, C_TRP_47	2.85	2.05	17.44
4F33.PDB	O, C_LYS_53	N, C_TYR_49	H, C_TYR_49	2.78	1.99	18.60
4F33.PDB	O, C_MET_33	N, C_THR_51	H, C_THR_51	2.75	1.94	16.16

4F33.PDB	O, C_ASP_50	N, C_SER_52	H, C_SER_52	2.86	2.16	29.76
4F33.PDB	O, C_TYR_49	N, C_LYS_53	H, C_LYS_53	2.90	2.09	16.92
4F33.PDB	OD2, C_ASP_82	NE, C_ARG_61	HE, C_ARG_61	2.88	2.06	14.32
4F33.PDB	OD1, C_ASP_82	NH2, C_ARG_61	HH21, C_ARG_61	2.91	2.08	14.25
4F33.PDB	O, C_THR_74	N, C_SER_63	H, C_SER_63	2.94	2.17	23.62
4F33.PDB	O, C_ALA_26	ND2, C_ASN_69	HD21, C_ASN_69	2.94	2.09	4.35
4F33.PDB	O, C_CYS_24	N, C_TYR_71	H, C_TYR_71	2.98	2.13	6.28
4F33.PDB	O, C_VAL_30	OH, C_TYR_71	HH, C_TYR_71	2.83	2.11	24.09
4F33.PDB	O, C_SER_65	N, C_SER_72	H, C_SER_72	2.76	1.92	10.63
4F33.PDB	O, C_MET_22	N, C_LEU_73	H, C_LEU_73	2.91	2.10	15.81
4F33.PDB	O, C_SER_63	N, C_THR_74	H, C_THR_74	2.85	2.00	8.73
4F33.PDB	OG1, C_THR_21	OG1, C_THR_74	HG1, C_THR_74	2.68	1.93	19.90
4F33.PDB	O, C_VAL_20	N, C_ILE_75	H, C_ILE_75	2.88	2.07	17.51
4F33.PDB	O, C_ARG_61	N, C_SER_76	H, C_SER_76	2.77	1.94	14.06
4F33.PDB	O, C_GLU_18	N, C_VAL_78	H, C_VAL_78	2.97	2.17	18.03
4F33.PDB	OD2, C_ASP_82	N, C_GLU_79	H, C_GLU_79	2.86	2.02	10.29
4F33.PDB	O, C_GLU_79	N, C_ASP_82	H, C_ASP_82	2.89	2.04	7.80
4F33.PDB	O, C_GLN_38	N, C_THR_85	H, C_THR_85	2.95	2.11	9.52
4F33.PDB	O, C_THR_102	N, C_TYR_86	H, C_TYR_86	2.85	2.02	13.04
4F33.PDB	O, C_TYR_36	N, C_TYR_87	H, C_TYR_87	2.85	2.03	14.78
4F33.PDB	O, C_TYR_32	NE1, C_TRP_91	HE1, C_TRP_91	2.75	1.98	22.25
4F33.PDB	O, D_TYR_60	NE2, C_HIS_94	HE2, C_HIS_94	2.75	2.00	24.62
4F33.PDB	O, C_ILE_3	OG1, C_THR_97	HG1, C_THR_97	2.89	2.10	13.01
4F33.PDB	O, C_CYS_88	N, C_GLY_99	H, C_GLY_99	2.82	2.00	15.41
4F33.PDB	OE1, C_GLN_7	N, C_GLY_101	H, C_GLY_101	2.82	2.04	21.32
4F33.PDB	O, C_TYR_86	N, C_THR_102	H, C_THR_102	2.90	2.08	14.65
4F33.PDB	O, C_PRO_9	OG1, C_THR_102	HG1, C_THR_102	2.73	1.96	16.75
4F33.PDB	O, C_ALA_10	N, C_LYS_103	H, C_LYS_103	2.87	2.02	9.78
4F33.PDB	O, C_ALA_84	N, C_VAL_104	H, C_VAL_104	2.85	1.99	3.00
4F33.PDB	O, C_MET_12	N, C_GLU_105	H, C_GLU_105	2.79	1.94	5.03
4F33.PDB	OE1, C_GLN_166	N, C_ILE_106	H, C_ILE_106	2.86	2.01	8.73
4F33.PDB	O, C_ALA_14	N, C_LYS_107	H, C_LYS_107	2.76	1.93	12.89
4F33.PDB	OG, C_SER_13	NZ, C_LYS_107	HZ3, C_LYS_107	2.78	1.89	2.73
4F33.PDB	O, C_THR_109	NE, C_ARG_108	HE, C_ARG_108	2.78	1.92	5.15
4F33.PDB	O, C_ASP_170	NH1, C_ARG_108	HH11, C_ARG_108	2.94	2.11	12.58
4F33.PDB	O, C_TYR_140	N, C_ALA_111	H, C_ALA_111	2.88	2.05	12.17
4F33.PDB	O, C_LEU_135	N, C_PHE_116	H, C_PHE_116	2.88	2.08	18.08
4F33.PDB	O, C_VAL_133	N, C_PHE_118	H, C_PHE_118	2.80	1.99	16.53
4F33.PDB	OG, C_SER_131	NE2, C_GLN_124	HE22, C_GLN_124	2.83	1.97	4.97
4F33.PDB	O, C_GLN_124	N, C_SER_127	H, C_SER_127	2.84	2.05	19.55
4F33.PDB	O, C_LEU_125	N, C_GLY_128	H, C_GLY_128	2.88	2.04	11.07
4F33.PDB	O, C_LEU_181	N, C_ALA_130	H, C_ALA_130	2.79	1.95	9.71
4F33.PDB	OE1, C_GLN_124	N, C_SER_131	H, C_SER_131	2.98	2.18	18.03
4F33.PDB	O, C_LEU_179	N, C_VAL_132	H, C_VAL_132	2.83	2.00	12.70
4F33.PDB	O, C_SER_177	N, C_CYS_134	H, C_CYS_134	2.82	1.97	5.76
4F33.PDB	O, C_PHE_116	N, C_LEU_135	H, C_LEU_135	2.74	1.89	9.47
4F33.PDB	O, C_LEU_175	N, C_LEU_136	H, C_LEU_136	2.76	1.91	7.00
4F33.PDB	O, C_SER_114	N, C_ASN_137	H, C_ASN_137	2.81	1.98	13.13
4F33.PDB	O, C_TYR_173	N, C_PHE_139	H, C_PHE_139	2.86	2.04	15.11
4F33.PDB	O, C_ALA_111	N, C_TYR_140	H, C_TYR_140	2.92	2.12	17.57
4F33.PDB	O, C_GLU_195	N, C_GLN_147	H, C_GLN_147	2.86	2.02	11.56
4F33.PDB	OG, C_SER_177	NE1, C_TRP_148	HE1, C_TRP_148	2.93	2.10	14.22
4F33.PDB	O, C_ALA_193	N, C_LYS_149	H, C_LYS_149	2.87	2.03	10.70
4F33.PDB	OE1, C_GLU_195	NZ, C_LYS_149	HZ2, C_LYS_149	2.67	1.88	22.11
4F33.PDB	O, C_VAL_191	N, C_ASP_151	H, C_ASP_151	2.76	1.93	12.00
4F33.PDB	O, C_VAL_150	N, C_ALA_153	H, C_ALA_153	2.82	1.97	7.87
4F33.PDB	O, C_TRP_148	N, C_GLN_155	H, C_GLN_155	2.94	2.10	11.34
4F33.PDB	OE1, C_GLN_155	ND2, C_ASN_158	HD22, C_ASN_158	2.91	2.09	15.33

4F33.PDB	O, C_SER.176	N, C_SER.162	H, C_SER.162	2.97	2.18	19.59
4F33.PDB	O, D_PRO.173	OG, C_SER.162	HG, C_SER.162	2.78	2.07	25.83
4F33.PDB	O, C_SER.174	N, C_THR.164	H, C_THR.164	2.96	2.13	12.36
4F33.PDB	O, C_SER.171	NE2, C_GLN.166	HE21, C_GLN.166	2.98	2.16	14.32
4F33.PDB	O, C_ILE.106	NE2, C_GLN.166	HE22, C_GLN.166	2.67	1.89	20.30
4F33.PDB	O, C_THR.172	N, C_ASP.167	H, C_ASP.167	2.93	2.09	7.56
4F33.PDB	OD1, C_ASP.167	N, C_LYS.169	H, C_LYS.169	2.61	1.77	10.10
4F33.PDB	OD1, C_ASP.170	N, C_THR.172	H, C_THR.172	2.87	2.04	12.16
4F33.PDB	OD1, C_ASP.170	OG1, C_THR.172	HG1, C_THR.172	2.72	1.91	5.07
4F33.PDB	O, C_PHE.139	N, C_TYR.173	H, C_TYR.173	2.83	2.00	13.92
4F33.PDB	OG1, C_THR.164	N, C_SER.174	H, C_SER.174	2.96	2.12	9.60
4F33.PDB	O, C_LEU.136	N, C_LEU.175	H, C_LEU.175	2.83	2.02	15.79
4F33.PDB	O, C_SER.162	N, C_SER.176	H, C_SER.176	2.89	2.07	14.79
4F33.PDB	O, C_CYS.134	N, C_SER.177	H, C_SER.177	2.90	2.08	14.93
4F33.PDB	O, C_GLN.160	N, C_THR.178	H, C_THR.178	2.90	2.07	13.20
4F33.PDB	O, C_VAL.132	N, C_LEU.179	H, C_LEU.179	2.84	2.04	17.52
4F33.PDB	O, C_ASN.158	N, C_THR.180	H, C_THR.180	2.93	2.09	10.99
4F33.PDB	O, C_ALA.130	N, C_LEU.181	H, C_LEU.181	2.89	2.06	12.78
4F33.PDB	O, C_GLY.128	N, C_LYS.183	H, C_LYS.183	2.87	2.02	7.20
4F33.PDB	OG, C_SER.182	N, C_ASP.185	H, C_ASP.185	2.76	1.98	21.47
4F33.PDB	O, C_SER.182	N, C_TYR.186	H, C_TYR.186	2.81	1.98	11.89
4F33.PDB	OD2, C_ASP.151	N, C_LYS.190	H, C_LYS.190	2.88	2.06	14.40
4F33.PDB	OD1, C_ASP.151	N, C_VAL.191	H, C_VAL.191	2.83	1.97	2.95
4F33.PDB	O, C_PHE.209	N, C_TYR.192	H, C_TYR.192	2.95	2.11	11.22
4F33.PDB	O, C_LYS.149	N, C_ALA.193	H, C_ALA.193	2.88	2.09	19.06
4F33.PDB	O, C_LYS.207	N, C_CYS.194	H, C_CYS.194	2.93	2.15	21.61
4F33.PDB	O, C_GLN.147	N, C_GLU.195	H, C_GLU.195	2.81	1.98	11.88
4F33.PDB	O, C_VAL.205	N, C_VAL.196	H, C_VAL.196	2.70	1.88	13.56
4F33.PDB	O, C_LYS.145	N, C_THR.197	H, C_THR.197	2.85	2.02	13.13
4F33.PDB	O, C_HIS.198	N, C_LEU.201	H, C_LEU.201	2.84	1.98	4.52
4F33.PDB	O, C_VAL.196	N, C_VAL.205	H, C_VAL.205	2.89	2.08	16.55
4F33.PDB	O, C_TYR.192	N, C_PHE.209	H, C_PHE.209	2.97	2.18	20.47
4F33.PDB	O, C_LYS.190	N, C_ARG.211	H, C_ARG.211	2.85	2.00	9.23
4F33.PDB	O, C_HIS.189	NE, C_ARG.211	HE, C_ARG.211	2.85	2.00	3.91
4F33.PDB	O, D_SER.25	N, D_GLN.3	H, D_GLN.3	2.93	2.12	15.40
4F33.PDB	O, D_LYS.23	N, D_GLN.5	H, D_GLN.5	2.87	2.02	5.59
4F33.PDB	O, D_TYR.94	NE2, D_GLN.6	HE22, D_GLN.6	2.88	2.07	16.36
4F33.PDB	O, D_PRO.114	N, D_GLU.10	H, D_GLU.10	2.90	2.11	19.09
4F33.PDB	O, D_THR.116	N, D_GLU.12	H, D_GLU.12	2.98	2.19	19.88
4F33.PDB	O, D_LEU.86	N, D_GLY.15	H, D_GLY.15	2.74	1.92	14.74
4F33.PDB	O, D_LEU.83	N, D_VAL.18	H, D_VAL.18	2.96	2.19	22.61
4F33.PDB	O, D_MET.81	N, D_ILE.20	H, D_ILE.20	2.89	2.06	12.32
4F33.PDB	OG, D_SER.7	N, D_SER.21	H, D_SER.21	2.90	2.06	8.88
4F33.PDB	O, D_ALA.79	N, D_CYS.22	H, D_CYS.22	2.83	2.09	25.29
4F33.PDB	O, D_GLN.5	N, D_LYS.23	H, D_LYS.23	2.75	1.91	10.41
4F33.PDB	O, D_SER.77	N, D_ALA.24	H, D_ALA.24	2.92	2.07	4.90
4F33.PDB	O, D_GLN.3	N, D_SER.25	H, D_SER.25	2.94	2.12	15.81
4F33.PDB	O, D_SER.28	N, D_GLY.31	H, D_GLY.31	2.96	2.11	6.44
4F33.PDB	O, D_GLY.99	N, D_THR.33	H, D_THR.33	2.96	2.15	17.63
4F33.PDB	O, D_ALA.97	N, D_ASN.35	H, D_ASN.35	2.79	1.98	15.45
4F33.PDB	O, D_PHE.95	N, D_VAL.37	H, D_VAL.37	2.84	2.04	17.56
4F33.PDB	O, D_GLU.46	N, D_LYS.38	H, D_LYS.38	2.82	2.00	14.83
4F33.PDB	O, D_GLU.89	NZ, D_LYS.38	HZ1, D_LYS.38	2.95	2.06	6.08
4F33.PDB	O, D_VAL.93	N, D_GLN.39	H, D_GLN.39	2.83	1.98	3.65
4F33.PDB	OE1, C_GLN.38	NE2, D_GLN.39	HE22, D_GLN.39	2.89	2.03	5.23
4F33.PDB	O, D_SER.40	N, D_LYS.43	H, D_LYS.43	2.91	2.09	14.92
4F33.PDB	O, D_LYS.38	N, D_GLU.46	H, D_GLU.46	2.91	2.09	16.01
4F33.PDB	O, D_TRP.36	N, D_ILE.48	H, D_ILE.48	2.86	2.02	11.41

4F33.PDB	O, D_SER_59	N, D_LEU_50	H, D_LEU_50	2.88	2.10	20.07
4F33.PDB	O, D_MET_34	N, D_ILE_51	H, D_ILE_51	2.90	2.09	16.54
4F33.PDB	O, D_ALA_57	N, D_THR_52	H, D_THR_52	2.93	2.11	14.70
4F33.PDB	O, D_THR_52	N, D_GLY_56	H, D_GLY_56	2.90	2.15	24.29
4F33.PDB	OD1, D_ASN_55	N, D_ALA_57	H, D_ALA_57	2.90	2.05	6.42
4F33.PDB	O, D_LEU_50	N, D_SER_59	H, D_SER_59	2.88	2.07	17.59
4F33.PDB	O, D_ILE_48	N, D_ASN_61	H, D_ASN_61	2.92	2.10	15.21
4F33.PDB	O, D_TRP_47	ND2, D_ASN_61	HD21, D_ASN_61	2.96	2.14	14.14
4F33.PDB	OE2, D_GLU_46	NZ, D_LYS_63	HZ3, D_LYS_63	2.60	1.76	15.82
4F33.PDB	O, D_ASN_61	N, D_PHE_64	H, D_PHE_64	2.75	1.91	9.55
4F33.PDB	OD2, D_ASP_90	NZ, D_LYS_67	HZ2, D_LYS_67	2.76	2.03	29.11
4F33.PDB	O, D_PHE_64	N, D_ALA_68	H, D_ALA_68	2.91	2.10	17.71
4F33.PDB	O, D_ASP_82	N, D_THR_69	H, D_THR_69	2.88	2.12	23.04
4F33.PDB	OH, D_TYR_60	N, D_LEU_70	H, D_LEU_70	2.83	1.99	10.08
4F33.PDB	O, D_THR_78	N, D_ASP_73	H, D_ASP_73	2.75	1.92	11.81
4F33.PDB	O, D_CYS_22	N, D_ALA_79	H, D_ALA_79	2.88	2.07	15.38
4F33.PDB	O, D_THR_71	N, D_TYR_80	H, D_TYR_80	2.77	1.92	5.85
4F33.PDB	O, D_ILE_20	N, D_MET_81	H, D_MET_81	2.97	2.15	15.01
4F33.PDB	O, D_THR_69	N, D_ASP_82	H, D_ASP_82	2.90	2.08	13.98
4F33.PDB	O, D_VAL_18	N, D_LEU_83	H, D_LEU_83	2.77	1.94	12.96
4F33.PDB	O, D_LYS_67	N, D_LEU_84	H, D_LEU_84	2.92	2.10	15.11
4F33.PDB	O, D_ALA_16	N, D_LEU_86	H, D_LEU_86	2.90	2.05	7.92
4F33.PDB	OD2, D_ASP_90	N, D_THR_87	H, D_THR_87	2.84	2.02	15.18
4F33.PDB	O, D_THR_87	N, D_ASP_90	H, D_ASP_90	2.90	2.06	10.57
4F33.PDB	O, D_SER_88	N, D_SER_91	H, D_SER_91	2.97	2.12	5.73
4F33.PDB	O, D_VAL_115	N, D_ALA_92	H, D_ALA_92	2.97	2.21	24.68
4F33.PDB	O, D_THR_113	N, D_TYR_94	H, D_TYR_94	2.85	2.00	9.44
4F33.PDB	O, D_VAL_37	N, D_PHE_95	H, D_PHE_95	2.78	1.94	9.26
4F33.PDB	O, D_ASN_35	N, D_ALA_97	H, D_ALA_97	2.87	2.11	23.35
4F33.PDB	O, D_TYR_108	N, D_ARG_98	H, D_ARG_98	2.83	2.05	21.19
4F33.PDB	OD2, D_ASP_107	NH2, D_ARG_98	HH21, D_ARG_98	2.74	1.89	7.29
4F33.PDB	O, D_THR_33	N, D_GLY_99	H, D_GLY_99	2.93	2.09	9.33
4F33.PDB	OD1, D_ASP_102	NE, D_ARG_104	HE, D_ARG_104	2.89	2.05	10.59
4F33.PDB	OD2, D_ASP_107	NH1, D_ARG_104	HH11, D_ARG_104	2.83	2.01	15.77
4F33.PDB	OD2, D_ASP_102	NH2, D_ARG_104	HH21, D_ARG_104	2.91	2.10	15.53
4F33.PDB	O, D_CYS_96	N, D_GLY_110	H, D_GLY_110	2.76	1.90	5.93
4F33.PDB	OE1, D_GLN_6	N, D_GLY_112	H, D_GLY_112	2.92	2.15	21.82
4F33.PDB	O, D_TYR_94	N, D_THR_113	H, D_THR_113	2.83	2.03	18.15
4F33.PDB	O, D_SER_7	OG1, D_THR_113	HG1, D_THR_113	2.79	2.01	15.83
4F33.PDB	O, D_ALA_92	N, D_VAL_115	H, D_VAL_115	2.80	1.95	9.13
4F33.PDB	O, D_GLU_10	N, D_THR_116	H, D_THR_116	2.95	2.12	11.31
4F33.PDB	OG, D_SER_91	N, D_VAL_117	H, D_VAL_117	2.81	1.98	11.24
4F33.PDB	O, D_GLU_12	N, D_SER_118	H, D_SER_118	2.89	2.09	17.84
4F33.PDB	O, D_PHE_152	N, D_LYS_123	H, D_LYS_123	2.79	1.97	13.96
4F33.PDB	O, D_ASP_150	NZ, D_LYS_123	HZ2, D_LYS_123	2.85	2.02	18.34
4F33.PDB	OE2, E_GLU_123	N, D_GLY_124	H, D_GLY_124	2.84	1.99	7.85
4F33.PDB	O, D_LYS_149	N, D_SER_126	H, D_SER_126	2.92	2.12	17.54
4F33.PDB	O, D_LEU_147	N, D_PHE_128	H, D_PHE_128	2.91	2.07	11.82
4F33.PDB	O, D_GLY_145	N, D_LEU_130	H, D_LEU_130	2.69	1.84	6.30
4F33.PDB	OG, D_SER_136	N, D_SER_133	H, D_SER_133	2.93	2.12	15.23
4F33.PDB	OG, D_SER_133	N, D_LYS_135	H, D_LYS_135	2.86	2.06	18.00
4F33.PDB	O, D_SER_133	OG1, D_THR_137	HG1, D_THR_137	2.93	2.22	24.93
4F33.PDB	O, D_SER_138	N, D_THR_141	H, D_THR_141	2.86	2.02	10.67
4F33.PDB	O, D_VAL_190	N, D_ALA_142	H, D_ALA_142	2.79	1.94	3.93
4F33.PDB	O, D_SER_136	N, D_ALA_143	H, D_ALA_143	2.80	1.98	13.96
4F33.PDB	O, D_VAL_188	N, D_LEU_144	H, D_LEU_144	2.99	2.17	15.33
4F33.PDB	O, D_LEU_130	N, D_GLY_145	H, D_GLY_145	2.95	2.17	22.25
4F33.PDB	O, D_PHE_128	N, D_LEU_147	H, D_LEU_147	2.85	2.01	10.25

4F33.PDB	O, D_LEU_184	N, D_VAL_148	H, D_VAL_148	2.76	1.91	9.22
4F33.PDB	O, D_SER_126	N, D_LYS_149	H, D_LYS_149	2.79	1.93	3.93
4F33.PDB	O, D_LYS_123	N, D_PHE_152	H, D_PHE_152	2.96	2.17	18.86
4F33.PDB	O, D_ASN_203	N, D_SER_159	H, D_SER_159	2.92	2.12	18.15
4F33.PDB	OG, D_SER_186	NE1, D_TRP_160	HE1, D_TRP_160	3.00	2.15	9.78
4F33.PDB	O, D_ILE_201	N, D_ASN_161	H, D_ASN_161	2.81	1.96	10.06
4F33.PDB	OD1, D_ASN_203	N, D_SER_162	H, D_SER_162	2.79	1.98	16.60
4F33.PDB	O, D_TRP_160	N, D_GLY_163	H, D_GLY_163	2.90	2.14	23.00
4F33.PDB	O, D_VAL_187	N, D_HIS_170	H, D_HIS_170	2.79	1.95	11.73
4F33.PDB	O, D_SER_185	N, D_PHE_172	H, D_PHE_172	2.98	2.14	9.15
4F33.PDB	O, D_SER_183	N, D_VAL_175	H, D_VAL_175	2.91	2.09	14.44
4F33.PDB	O, D_LEU_181	N, D_GLN_177	H, D_GLN_177	2.85	2.00	7.10
4F33.PDB	OD1, D_ASP_150	NE2, D_GLN_177	HE22, D_GLN_177	2.86	2.09	21.57
4F33.PDB	O, D_TYR_151	N, D_TYR_182	H, D_TYR_182	2.82	1.97	7.39
4F33.PDB	O, D_VAL_148	N, D_LEU_184	H, D_LEU_184	2.89	2.08	17.21
4F33.PDB	O, D_CYS_146	N, D_SER_186	H, D_SER_186	2.93	2.11	15.37
4F33.PDB	O, D_HIS_170	N, D_VAL_187	H, D_VAL_187	2.83	2.00	11.95
4F33.PDB	O, D_LEU_144	N, D_VAL_188	H, D_VAL_188	2.81	2.00	17.23
4F33.PDB	O, D_ALA_142	N, D_VAL_190	H, D_VAL_190	2.77	1.95	14.72
4F33.PDB	O, D_GLY_140	N, D_SER_192	H, D_SER_192	2.86	2.02	8.26
4F33.PDB	O, D_PRO_191	N, D_SER_194	H, D_SER_194	2.92	2.08	9.17
4F33.PDB	O, D_SER_194	N, D_GLN_198	H, D_GLN_198	2.75	1.89	2.92
4F33.PDB	OD1, D_ASN_161	N, D_ILE_201	H, D_ILE_201	2.80	1.96	10.93
4F33.PDB	O, D_LYS_215	N, D_CYS_202	H, D_CYS_202	2.93	2.15	21.05
4F33.PDB	O, D_SER_159	N, D_ASN_203	H, D_ASN_203	2.77	1.92	5.28
4F33.PDB	O, D_VAL_213	N, D_VAL_204	H, D_VAL_204	2.77	1.93	9.54
4F33.PDB	O, D_THR_157	N, D_ASN_205	H, D_ASN_205	2.87	2.02	7.57
4F33.PDB	O, D_THR_211	N, D_HIS_206	H, D_HIS_206	2.84	1.99	6.89
4F33.PDB	O, D_PRO_153	NE2, D_HIS_206	HE2, D_HIS_206	2.81	1.97	10.37
4F33.PDB	O, D_LYS_207	N, D_ASN_210	H, D_ASN_210	2.91	2.08	12.71
4F33.PDB	O, F_ASP_214	N, D_LYS_212	H, D_LYS_212	2.98	2.15	12.10
4F33.PDB	O, D_VAL_204	N, D_VAL_213	H, D_VAL_213	2.79	1.97	13.65
4F33.PDB	O, F_LYS_212	N, D_ASP_214	H, D_ASP_214	2.85	2.03	14.94
4F33.PDB	O, D_CYS_202	N, D_LYS_215	H, D_LYS_215	2.96	2.16	17.33
4F33.PDB	OE1, C_GLU_123	NZ, D_LYS_215	HZ1, D_LYS_215	2.79	1.99	22.47
4F33.PDB	OG1, F_THR_211	NZ, D_LYS_215	HZ2, D_LYS_215	2.86	1.99	10.67
4F33.PDB	O, F_ASN_210	N, D_LYS_216	H, D_LYS_216	2.98	2.16	15.42
4F33.PDB	O, D_TYR_200	N, D_VAL_217	H, D_VAL_217	2.85	2.00	8.55
4F33.PDB	OG, E_SER_27	N, E_GLU_4	H, E_GLU_4	2.92	2.11	16.14
4F33.PDB	O, E_SER_25	N, E_THR_6	H, E_THR_6	2.78	1.92	4.96
4F33.PDB	O, E_TYR_86	NE2, E_GLN_7	HE22, E_GLN_7	2.94	2.17	22.59
4F33.PDB	O, E_THR_23	N, E_SER_8	H, E_SER_8	2.92	2.12	16.81
4F33.PDB	O, E_LYS_103	N, E_MET_12	H, E_MET_12	2.82	1.98	10.01
4F33.PDB	O, E_GLU_105	N, E_ALA_14	H, E_ALA_14	2.97	2.16	16.60
4F33.PDB	OE2, E_GLU_18	N, E_SER_15	H, E_SER_15	2.79	1.94	7.58
4F33.PDB	O, E_VAL_78	N, E_GLY_17	H, E_GLY_17	2.81	2.00	17.52
4F33.PDB	OG1, E_THR_74	OG1, E_THR_21	HG1, E_THR_21	2.80	2.03	17.05
4F33.PDB	O, E_LEU_73	N, E_MET_22	H, E_MET_22	2.92	2.09	12.31
4F33.PDB	O, E_SER_8	N, E_THR_23	H, E_THR_23	2.82	1.97	8.66
4F33.PDB	O, E_TYR_71	N, E_CYS_24	H, E_CYS_24	2.67	1.82	5.57
4F33.PDB	O, E_THR_6	N, E_SER_25	H, E_SER_25	2.85	2.00	8.30
4F33.PDB	O, E_ASN_69	N, E_ALA_26	H, E_ALA_26	2.80	1.95	9.70
4F33.PDB	O, E_GLN_89	N, E_HIS_34	H, E_HIS_34	2.94	2.08	4.58
4F33.PDB	O, E_ILE_48	N, E_TRP_35	H, E_TRP_35	2.69	1.88	16.85
4F33.PDB	O, E_TYR_87	N, E_TYR_36	H, E_TYR_36	2.80	1.97	13.97
4F33.PDB	O, E_LYS_45	N, E_GLN_37	H, E_GLN_37	2.87	2.09	20.05
4F33.PDB	O, E_THR_85	N, E_GLN_38	H, E_GLN_38	2.87	2.05	13.42
4F33.PDB	O, E_THR_42	NE2, E_GLN_38	HE21, E_GLN_38	2.90	2.07	12.17

4F33.PDB	O, E_GLU_81	NZ, E_LYS_39	HZ1, E_LYS_39	2.82	1.96	12.79
4F33.PDB	O, E_ASP_83	NZ, E_LYS_39	HZ3, E_LYS_39	2.75	1.95	21.71
4F33.PDB	O, E_LYS_39	OG1, E_THR_42	HG1, E_THR_42	2.99	2.17	4.21
4F33.PDB	O, F_GLY_110	OG, E_SER_43	HG, E_SER_43	2.52	1.83	27.97
4F33.PDB	O, E_GLN_37	N, E_LYS_45	H, E_LYS_45	2.74	1.96	19.86
4F33.PDB	O, F_ARG_104	NH1, E_ARG_46	HH11, E_ARG_46	2.85	2.03	15.38
4F33.PDB	O, E_TRP_35	N, E_TRP_47	H, E_TRP_47	2.82	2.04	19.57
4F33.PDB	O, E_LYS_53	N, E_TYR_49	H, E_TYR_49	2.74	1.93	17.49
4F33.PDB	O, E_MET_33	N, E_THR_51	H, E_THR_51	2.76	1.93	12.30
4F33.PDB	O, E_ASP_50	N, E_SER_52	H, E_SER_52	2.85	2.14	29.22
4F33.PDB	O, E_TYR_49	N, E_LYS_53	H, E_LYS_53	2.87	2.09	20.53
4F33.PDB	O, E_TRP_47	N, E_ALA_55	H, E_ALA_55	2.97	2.11	5.56
4F33.PDB	OD2, E_ASP_82	NE, E_ARG_61	HE, E_ARG_61	2.93	2.08	6.42
4F33.PDB	OD1, E_ASP_82	NH2, E_ARG_61	HH21, E_ARG_61	2.82	1.98	9.42
4F33.PDB	O, E_THR_74	N, E_SER_63	H, E_SER_63	2.96	2.20	24.19
4F33.PDB	O, E_ALA_26	ND2, E_ASN_69	HD21, E_ASN_69	2.90	2.05	3.08
4F33.PDB	O, E_CYS_24	N, E_TYR_71	H, E_TYR_71	2.86	2.02	8.43
4F33.PDB	O, E_VAL_30	OH, E_TYR_71	HH, E_TYR_71	2.89	2.18	25.55
4F33.PDB	O, E_SER_65	N, E_SER_72	H, E_SER_72	2.76	1.93	12.78
4F33.PDB	O, E_SER_63	N, E_THR_74	H, E_THR_74	2.80	1.96	11.27
4F33.PDB	O, E_VAL_20	N, E_ILE_75	H, E_ILE_75	2.91	2.09	15.96
4F33.PDB	O, E_ARG_61	N, E_SER_76	H, E_SER_76	2.77	1.96	15.82
4F33.PDB	O, E_GLU_18	N, E_VAL_78	H, E_VAL_78	2.84	2.06	21.38
4F33.PDB	OD2, E_ASP_82	N, E_GLU_79	H, E_GLU_79	2.86	2.00	3.08
4F33.PDB	O, E_GLU_79	N, E_ASP_82	H, E_ASP_82	2.87	2.03	9.88
4F33.PDB	O, E_GLN_38	N, E_THR_85	H, E_THR_85	2.88	2.04	8.55
4F33.PDB	O, E_THR_102	N, E_TYR_86	H, E_TYR_86	2.86	2.02	10.02
4F33.PDB	O, E_TYR_36	N, E_TYR_87	H, E_TYR_87	2.88	2.07	16.48
4F33.PDB	OG1, E_THR_97	NE2, E_GLN_90	HE21, E_GLN_90	2.99	2.17	14.98
4F33.PDB	O, E_TYR_32	NE1, E_TRP_91	HE1, E_TRP_91	2.73	1.95	21.71
4F33.PDB	O, E_ILE_3	OG1, E_THR_97	HG1, E_THR_97	2.76	1.96	11.49
4F33.PDB	O, E_CYS_88	N, E_GLY_99	H, E_GLY_99	2.76	1.93	12.97
4F33.PDB	OE1, E_GLN_7	N, E_GLY_101	H, E_GLY_101	2.77	2.01	24.02
4F33.PDB	O, E_TYR_86	N, E_THR_102	H, E_THR_102	2.88	2.06	14.06
4F33.PDB	O, E_PRO_9	OG1, E_THR_102	HG1, E_THR_102	2.74	1.97	16.27
4F33.PDB	O, E_ALA_10	N, E_LYS_103	H, E_LYS_103	2.83	1.99	8.80
4F33.PDB	O, E_ALA_84	N, E_VAL_104	H, E_VAL_104	2.84	1.98	6.54
4F33.PDB	O, E_MET_12	N, E_GLU_105	H, E_GLU_105	2.75	1.90	5.61
4F33.PDB	OE1, E_GLN_166	N, E_ILE_106	H, E_ILE_106	2.88	2.05	11.13
4F33.PDB	O, E_ALA_14	N, E_LYS_107	H, E_LYS_107	2.77	1.92	7.71
4F33.PDB	O, E_THR_109	NE, E_ARG_108	HE, E_ARG_108	2.78	1.92	2.02
4F33.PDB	O, E_ASP_170	NH1, E_ARG_108	HH11, E_ARG_108	2.88	2.05	12.27
4F33.PDB	O, E_TYR_140	N, E_ALA_111	H, E_ALA_111	2.93	2.09	9.90
4F33.PDB	O, E_LEU_135	N, E_PHE_116	H, E_PHE_116	2.88	2.07	17.28
4F33.PDB	O, E_VAL_133	N, E_PHE_118	H, E_PHE_118	2.80	2.05	23.65
4F33.PDB	OG, E_SER_131	NE2, E_GLN_124	HE22, E_GLN_124	2.81	1.95	4.17
4F33.PDB	O, E_GLN_124	N, E_SER_127	H, E_SER_127	2.86	2.13	27.30
4F33.PDB	O, E_LEU_125	N, E_GLY_128	H, E_GLY_128	2.83	1.98	9.86
4F33.PDB	O, E_LEU_181	N, E_ALA_130	H, E_ALA_130	2.74	1.89	8.05
4F33.PDB	O, E_LEU_179	N, E_VAL_132	H, E_VAL_132	2.80	1.98	14.92
4F33.PDB	O, E_SER_177	N, E_CYS_134	H, E_CYS_134	2.85	2.00	9.73
4F33.PDB	O, E_PHE_116	N, E_LEU_135	H, E_LEU_135	2.83	1.99	7.95
4F33.PDB	O, E_LEU_175	N, E_LEU_136	H, E_LEU_136	2.79	1.94	6.94
4F33.PDB	O, E_SER_114	N, E_ASN_137	H, E_ASN_137	2.80	1.99	16.39
4F33.PDB	O, E_TYR_173	N, E_PHE_139	H, E_PHE_139	2.88	2.07	16.01
4F33.PDB	O, E_ALA_111	N, E_TYR_140	H, E_TYR_140	2.90	2.10	17.94
4F33.PDB	O, E_GLU_195	N, E_GLN_147	H, E_GLN_147	2.86	2.03	12.56
4F33.PDB	OG, E_SER_177	NE1, E_TRP_148	HE1, E_TRP_148	2.88	2.05	13.86

4F33.PDB	O, E_ALA_193	N, E_LYS_149	H, E_LYS_149	2.81	1.97	9.94
4F33.PDB	OE1, E_GLU_195	NZ, E_LYS_149	HZ2, E_LYS_149	2.77	1.97	22.37
4F33.PDB	O, E_VAL_191	N, E_ASP_151	H, E_ASP_151	2.76	1.93	11.74
4F33.PDB	O, E_VAL_150	N, E_ALA_153	H, E_ALA_153	2.93	2.08	7.11
4F33.PDB	O, E_TRP_148	N, E_GLN_155	H, E_GLN_155	2.90	2.06	11.04
4F33.PDB	OE1, E_GLN_155	ND2, E_ASN_158	HD22, E_ASN_158	2.91	2.08	12.67
4F33.PDB	O, F_LEU_176	NE2, E_GLN_160	HE22, E_GLN_160	2.93	2.08	4.21
4F33.PDB	O, E_SER_176	N, E_SER_162	H, E_SER_162	2.99	2.20	20.78
4F33.PDB	O, F_PRO_173	OG, E_SER_162	HG, E_SER_162	2.63	1.89	21.98
4F33.PDB	O, E_SER_174	N, E_THR_164	H, E_THR_164	2.96	2.13	13.63
4F33.PDB	O, E_SER_171	NE2, E_GLN_166	HE21, E_GLN_166	2.92	2.10	16.16
4F33.PDB	O, E_ILE_106	NE2, E_GLN_166	HE22, E_GLN_166	2.70	1.91	18.56
4F33.PDB	O, E_THR_172	N, E_ASP_167	H, E_ASP_167	2.96	2.11	9.67
4F33.PDB	OD1, E_ASP_170	N, E_THR_172	H, E_THR_172	2.87	2.07	17.42
4F33.PDB	OD1, E_ASP_170	OG1, E_THR_172	HG1, E_THR_172	2.66	1.85	7.41
4F33.PDB	O, E_PHE_139	N, E_TYR_173	H, E_TYR_173	2.81	1.97	10.48
4F33.PDB	OG1, E_THR_164	N, E_SER_174	H, E_SER_174	3.00	2.15	8.96
4F33.PDB	O, E_LEU_136	N, E_LEU_175	H, E_LEU_175	2.88	2.07	16.14
4F33.PDB	O, E_SER_162	N, E_SER_176	H, E_SER_176	2.95	2.12	13.93
4F33.PDB	O, E_CYS_134	N, E_SER_177	H, E_SER_177	2.89	2.07	14.26
4F33.PDB	O, E_GLN_160	N, E_THR_178	H, E_THR_178	2.90	2.07	12.50
4F33.PDB	O, E_VAL_132	N, E_LEU_179	H, E_LEU_179	2.83	2.00	13.32
4F33.PDB	O, E_ASN_158	N, E_THR_180	H, E_THR_180	2.97	2.13	9.98
4F33.PDB	O, E_ALA_130	N, E_LEU_181	H, E_LEU_181	2.88	2.04	11.81
4F33.PDB	O, E_GLY_128	N, E_LYS_183	H, E_LYS_183	2.91	2.08	11.41
4F33.PDB	OG, E_SER_182	N, E_ASP_185	H, E_ASP_185	2.89	2.05	12.49
4F33.PDB	O, E_SER_182	N, E_TYR_186	H, E_TYR_186	2.82	2.00	13.68
4F33.PDB	O, E_LYS_183	N, E_GLU_187	H, E_GLU_187	2.88	2.09	19.35
4F33.PDB	OD1, E_ASP_151	N, E_VAL_191	H, E_VAL_191	2.77	1.93	8.77
4F33.PDB	O, E_PHE_209	N, E_TYR_192	H, E_TYR_192	2.98	2.13	8.15
4F33.PDB	O, E_LYS_149	N, E_ALA_193	H, E_ALA_193	2.88	2.08	18.56
4F33.PDB	O, E_LYS_207	N, E_CYS_194	H, E_CYS_194	2.96	2.17	20.79
4F33.PDB	O, E_GLN_147	N, E_GLU_195	H, E_GLU_195	2.74	1.90	10.88
4F33.PDB	O, E_VAL_205	N, E_VAL_196	H, E_VAL_196	2.72	1.89	12.46
4F33.PDB	ND1, E_HIS_198	N, E_GLY_200	H, E_GLY_200	2.98	2.12	5.22
4F33.PDB	O, E_HIS_198	N, E_LEU_201	H, E_LEU_201	2.84	1.99	5.31
4F33.PDB	O, E_VAL_196	N, E_VAL_205	H, E_VAL_205	2.92	2.09	13.32
4F33.PDB	O, E_TYR_192	N, E_PHE_209	H, E_PHE_209	2.94	2.17	22.18
4F33.PDB	O, E_LYS_190	N, E_ARG_211	H, E_ARG_211	2.74	1.94	17.57
4F33.PDB	O, E_HIS_189	NE, E_ARG_211	HE, E_ARG_211	2.92	2.09	14.00
4F33.PDB	O, F_SER_25	N, F_GLN_3	H, F_GLN_3	2.92	2.09	11.79
4F33.PDB	O, F_LYS_23	N, F_GLN_5	H, F_GLN_5	2.85	2.00	7.55
4F33.PDB	O, F_TYR_94	NE2, F_GLN_6	HE22, F_GLN_6	2.86	2.05	16.42
4F33.PDB	O, F_PRO_114	N, F_GLU_10	H, F_GLU_10	2.96	2.18	21.47
4F33.PDB	O, F_THR_116	N, F_GLU_12	H, F_GLU_12	2.95	2.15	17.10
4F33.PDB	O, F_LEU_86	N, F_GLY_15	H, F_GLY_15	2.68	1.85	13.71
4F33.PDB	O, F_LEU_83	N, F_VAL_18	H, F_VAL_18	2.99	2.22	23.08
4F33.PDB	O, F_MET_81	N, F_ILE_20	H, F_ILE_20	2.85	2.01	12.08
4F33.PDB	OG, F_SER_7	N, F_SER_21	H, F_SER_21	2.96	2.12	10.03
4F33.PDB	O, F_GLN_5	N, F_LYS_23	H, F_LYS_23	2.77	1.93	10.80
4F33.PDB	O, F_SER_77	N, F_ALA_24	H, F_ALA_24	2.90	2.05	6.06
4F33.PDB	O, F_GLN_3	N, F_SER_25	H, F_SER_25	2.87	2.06	15.90
4F33.PDB	O, A_GLY_60	N, F_PHE_29	H, F_PHE_29	2.97	2.18	20.00
4F33.PDB	O, F_GLY_99	N, F_THR_33	H, F_THR_33	2.87	2.06	15.66
4F33.PDB	O, F_ALA_97	N, F_ASN_35	H, F_ASN_35	2.80	1.96	10.72
4F33.PDB	O, F_PHE_95	N, F_VAL_37	H, F_VAL_37	2.82	2.02	18.07
4F33.PDB	O, F_GLU_46	N, F_LYS_38	H, F_LYS_38	2.79	1.98	16.31
4F33.PDB	O, F_GLU_89	NZ, F_LYS_38	HZ1, F_LYS_38	2.88	2.00	2.60

4F33.PDB	O, F_VAL_93	N, F_GLN_39	H, F_GLN_39	2.84	1.98	5.27
4F33.PDB	OE1, E_GLN_38	NE2, F_GLN_39	HE22, F_GLN_39	2.92	2.06	5.53
4F33.PDB	O, F_SER_40	N, F_LYS_43	H, F_LYS_43	2.90	2.09	15.21
4F33.PDB	O, F_LYS_38	N, F_GLU_46	H, F_GLU_46	2.89	2.10	18.91
4F33.PDB	O, F_TRP_36	N, F_ILE_48	H, F_ILE_48	2.82	1.97	6.48
4F33.PDB	O, F_SER_59	N, F_LEU_50	H, F_LEU_50	2.90	2.11	20.04
4F33.PDB	O, F_MET_34	N, F_ILE_51	H, F_ILE_51	2.90	2.10	17.75
4F33.PDB	O, F_ALA_57	N, F_THR_52	H, F_THR_52	2.97	2.15	14.94
4F33.PDB	O, F_THR_52	N, F_GLY_56	H, F_GLY_56	2.93	2.22	29.15
4F33.PDB	OD1, F_ASN_55	N, F_ALA_57	H, F_ALA_57	2.86	2.00	3.80
4F33.PDB	O, F_LEU_50	N, F_SER_59	H, F_SER_59	2.89	2.09	17.90
4F33.PDB	O, F_ILE_48	N, F_ASN_61	H, F_ASN_61	2.97	2.17	18.69
4F33.PDB	O, F_TRP_47	ND2, F_ASN_61	HD21, F_ASN_61	2.90	2.07	11.50
4F33.PDB	OE2, F_GLU_46	NZ, F_LYS_63	HZ3, F_LYS_63	2.68	1.79	3.79
4F33.PDB	O, F_ASN_61	N, F_PHE_64	H, F_PHE_64	2.81	1.98	12.75
4F33.PDB	OD2, F_ASP_90	NZ, F_LYS_67	HZ2, F_LYS_67	2.98	2.09	4.59
4F33.PDB	O, F_LEU_84	NZ, F_LYS_67	HZ3, F_LYS_67	2.88	2.01	9.79
4F33.PDB	O, F_PHE_64	N, F_ALA_68	H, F_ALA_68	2.89	2.09	17.94
4F33.PDB	O, F_ASP_82	N, F_THR_69	H, F_THR_69	2.89	2.11	21.20
4F33.PDB	OH, F_TYR_60	N, F_LEU_70	H, F_LEU_70	2.85	2.00	7.63
4F33.PDB	O, F_THR_78	N, F_ASP_73	H, F_ASP_73	2.73	1.90	11.77
4F33.PDB	O, F_CYS_22	N, F_ALA_79	H, F_ALA_79	2.88	2.06	15.43
4F33.PDB	O, F_THR_71	N, F_TYR_80	H, F_TYR_80	2.81	1.96	9.04
4F33.PDB	O, F_ILE_20	N, F_MET_81	H, F_MET_81	2.93	2.11	15.35
4F33.PDB	O, F_THR_69	N, F_ASP_82	H, F_ASP_82	2.94	2.10	11.40
4F33.PDB	O, F_VAL_18	N, F_LEU_83	H, F_LEU_83	2.81	1.97	10.47
4F33.PDB	O, F_LYS_67	N, F_LEU_84	H, F_LEU_84	2.89	2.09	17.45
4F33.PDB	O, F_ALA_16	N, F_LEU_86	H, F_LEU_86	2.91	2.07	9.18
4F33.PDB	OD2, F_ASP_90	N, F_THR_87	H, F_THR_87	2.85	2.02	12.72
4F33.PDB	O, F_THR_87	N, F_ASP_90	H, F_ASP_90	2.83	1.99	10.62
4F33.PDB	O, F_VAL_115	N, F_ALA_92	H, F_ALA_92	2.97	2.26	28.93
4F33.PDB	O, F_THR_113	N, F_TYR_94	H, F_TYR_94	2.92	2.08	8.53
4F33.PDB	O, F_VAL_37	N, F_PHE_95	H, F_PHE_95	2.78	1.94	9.71
4F33.PDB	O, F_ASN_35	N, F_ALA_97	H, F_ALA_97	2.84	2.08	24.00
4F33.PDB	O, F_TYR_108	N, F_ARG_98	H, F_ARG_98	2.82	2.03	20.08
4F33.PDB	OD1, F_ASP_107	NE, F_ARG_98	HE, F_ARG_98	2.99	2.13	4.74
4F33.PDB	OD2, F_ASP_107	NH2, F_ARG_98	HH21, F_ARG_98	2.77	1.91	5.42
4F33.PDB	O, F_THR_33	N, F_GLY_99	H, F_GLY_99	2.97	2.13	11.08
4F33.PDB	OD1, F_ASP_102	NE, F_ARG_104	HE, F_ARG_104	2.84	1.99	7.33
4F33.PDB	OD2, F_ASP_107	NH1, F_ARG_104	HH11, F_ARG_104	2.84	2.02	14.35
4F33.PDB	OD2, F_ASP_102	NH2, F_ARG_104	HH21, F_ARG_104	2.90	2.10	17.22
4F33.PDB	OH, E_TYR_36	N, F_PHE_106	H, F_PHE_106	2.80	1.96	9.30
4F33.PDB	O, F_CYS_96	N, F_GLY_110	H, F_GLY_110	2.75	1.90	3.11
4F33.PDB	OE1, F_GLN_6	N, F_GLY_112	H, F_GLY_112	2.83	2.05	20.58
4F33.PDB	O, F_TYR_94	N, F_THR_113	H, F_THR_113	2.80	2.02	20.38
4F33.PDB	O, F_SER_7	OG1, F_THR_113	HG1, F_THR_113	2.84	2.08	18.41
4F33.PDB	O, F_ALA_92	N, F_VAL_115	H, F_VAL_115	2.82	1.98	10.24
4F33.PDB	OG, F_SER_91	N, F_VAL_117	H, F_VAL_117	2.84	2.00	11.18
4F33.PDB	O, F_GLU_12	N, F_SER_118	H, F_SER_118	2.89	2.09	17.44
4F33.PDB	O, F_PHE_152	N, F_LYS_123	H, F_LYS_123	2.81	1.98	13.07
4F33.PDB	O, F_ASP_150	NZ, F_LYS_123	HZ2, F_LYS_123	2.85	2.01	15.13
4F33.PDB	OE2, C_GLU_123	N, F_GLY_124	H, F_GLY_124	2.81	1.96	5.00
4F33.PDB	O, F_LYS_149	N, F_SER_126	H, F_SER_126	2.90	2.09	15.48
4F33.PDB	O, F_LEU_147	N, F_PHE_128	H, F_PHE_128	2.87	2.04	12.96
4F33.PDB	O, F_GLY_145	N, F_LEU_130	H, F_LEU_130	2.73	1.88	6.31
4F33.PDB	OG, F_SER_136	N, F_SER_133	H, F_SER_133	2.95	2.13	15.24
4F33.PDB	OG, F_SER_133	N, F_LYS_135	H, F_LYS_135	2.90	2.11	20.53
4F33.PDB	O, F_SER_133	OG1, F_THR_137	HG1, F_THR_137	2.95	2.23	24.52

4F33.PDB	O, F_SER_138	N, F_THR_141	H, F_THR_141	2.81	1.97	11.04
4F33.PDB	O, F_VAL_190	N, F_ALA_142	H, F_ALA_142	2.77	1.91	4.10
4F33.PDB	O, F_SER_136	N, F_ALA_143	H, F_ALA_143	2.80	1.97	12.99
4F33.PDB	O, F_LEU_130	N, F_GLY_145	H, F_GLY_145	2.92	2.16	24.09
4F33.PDB	O, F_PHE_128	N, F_LEU_147	H, F_LEU_147	2.82	1.98	9.09
4F33.PDB	O, F_LEU_184	N, F_VAL_148	H, F_VAL_148	2.76	1.91	9.03
4F33.PDB	O, F_SER_126	N, F_LYS_149	H, F_LYS_149	2.76	1.90	3.32
4F33.PDB	O, F_LYS_123	N, F_PHE_152	H, F_PHE_152	2.93	2.12	17.02
4F33.PDB	O, F_ASN_203	N, F_SER_159	H, F_SER_159	2.97	2.16	16.38
4F33.PDB	OG, F_SER_186	NE1, F_TRP_160	HE1, F_TRP_160	3.00	2.15	9.04
4F33.PDB	O, F_ILE_201	N, F_ASN_161	H, F_ASN_161	2.83	1.99	9.71
4F33.PDB	OD1, F_ASN_203	N, F_SER_162	H, F_SER_162	2.79	1.98	16.87
4F33.PDB	O, F_TRP_160	N, F_GLY_163	H, F_GLY_163	2.90	2.14	23.82
4F33.PDB	O, F_VAL_187	N, F_HIS_170	H, F_HIS_170	2.79	1.95	11.88
4F33.PDB	O, F_SER_185	N, F_PHE_172	H, F_PHE_172	2.94	2.09	4.01
4F33.PDB	O, F_SER_183	N, F_VAL_175	H, F_VAL_175	2.90	2.08	14.72
4F33.PDB	O, F_LEU_181	N, F_GLN_177	H, F_GLN_177	2.83	1.98	7.25
4F33.PDB	OD1, F_ASP_150	NE2, F_GLN_177	HE22, F_GLN_177	2.82	2.02	17.76
4F33.PDB	O, F_TYR_151	N, F_TYR_182	H, F_TYR_182	2.79	1.93	3.62
4F33.PDB	O, F_VAL_148	N, F_LEU_184	H, F_LEU_184	2.91	2.11	17.32
4F33.PDB	O, F_CYS_146	N, F_SER_186	H, F_SER_186	2.97	2.15	15.30
4F33.PDB	O, F_HIS_170	N, F_VAL_187	H, F_VAL_187	2.89	2.06	12.38
4F33.PDB	O, F_LEU_144	N, F_VAL_188	H, F_VAL_188	2.81	2.01	17.82
4F33.PDB	O, F_ALA_142	N, F_VAL_190	H, F_VAL_190	2.77	1.95	15.08
4F33.PDB	O, F_GLY_140	N, F_SER_192	H, F_SER_192	2.89	2.04	8.47
4F33.PDB	O, F_PRO_191	N, F_SER_194	H, F_SER_194	2.94	2.10	10.73
4F33.PDB	O, F_SER_194	N, F_GLN_198	H, F_GLN_198	2.74	1.88	2.67
4F33.PDB	O, F_THR_199	NE2, F_GLN_198	HE21, F_GLN_198	2.92	2.06	2.83
4F33.PDB	OD1, F_ASN_161	N, F_ILE_201	H, F_ILE_201	2.77	1.94	13.18
4F33.PDB	O, F_LYS_215	N, F_CYS_202	H, F_CYS_202	2.93	2.14	19.72
4F33.PDB	O, F_SER_159	N, F_ASN_203	H, F_ASN_203	2.82	1.96	5.68
4F33.PDB	OD1, F_ASP_214	ND2, F_ASN_203	HD21, F_ASN_203	2.95	2.10	8.40
4F33.PDB	O, F_VAL_213	N, F_VAL_204	H, F_VAL_204	2.74	1.89	7.26
4F33.PDB	O, F_THR_157	N, F_ASN_205	H, F_ASN_205	2.87	2.02	8.95
4F33.PDB	O, F_THR_211	N, F_HIS_206	H, F_HIS_206	2.87	2.02	7.60
4F33.PDB	OG, F_SER_209	ND1, F_HIS_206	HD1, F_HIS_206	2.64	1.82	13.68
4F33.PDB	O, F_PRO_153	NE2, F_HIS_206	HE2, F_HIS_206	2.81	1.97	9.86
4F33.PDB	O, F_LYS_207	N, F_ASN_210	H, F_ASN_210	2.97	2.15	14.98
4F33.PDB	O, D_ASP_214	N, F_LYS_212	H, F_LYS_212	2.94	2.11	12.64
4F33.PDB	O, F_VAL_204	N, F_VAL_213	H, F_VAL_213	2.85	2.02	13.27
4F33.PDB	O, D_LYS_212	N, F_ASP_214	H, F_ASP_214	2.84	2.02	14.84
4F33.PDB	O, F_CYS_202	N, F_LYS_215	H, F_LYS_215	2.92	2.10	15.07
4F33.PDB	OE1, E_GLU_123	NZ, F_LYS_215	HZ1, F_LYS_215	2.61	1.84	24.34
4F33.PDB	OG1, D_THR_211	NZ, F_LYS_215	HZ2, F_LYS_215	2.92	2.04	7.71
4F33.PDB	O, F_TYR_200	N, F_VAL_217	H, F_VAL_217	2.89	2.04	9.32
4F33.PDB	OG, G_SER_27	N, G_GLU_4	H, G_GLU_4	2.95	2.12	14.03
4F33.PDB	O, G_SER_25	N, G_THR_6	H, G_THR_6	2.78	1.93	4.59
4F33.PDB	O, G_TYR_86	NE2, G_GLN_7	HE22, G_GLN_7	2.90	2.13	22.62
4F33.PDB	O, G_THR_23	N, G_SER_8	H, G_SER_8	2.90	2.09	16.80
4F33.PDB	O, G_LYS_103	N, G_MET_12	H, G_MET_12	2.76	1.93	13.02
4F33.PDB	O, G_GLU_105	N, G_ALA_14	H, G_ALA_14	2.97	2.16	16.65
4F33.PDB	OE2, G_GLU_18	N, G_SER_15	H, G_SER_15	2.71	1.86	9.24
4F33.PDB	O, G_VAL_78	N, G_GLY_17	H, G_GLY_17	2.81	2.01	18.15
4F33.PDB	O, G_ILE_75	N, G_VAL_20	H, G_VAL_20	2.96	2.19	21.57
4F33.PDB	OG1, G_THR_74	OG1, G_THR_21	HG1, G_THR_21	2.73	1.97	18.47
4F33.PDB	O, G_SER_8	N, G_THR_23	H, G_THR_23	2.83	1.99	8.78
4F33.PDB	O, G_TYR_71	N, G_CYS_24	H, G_CYS_24	2.68	1.82	4.01
4F33.PDB	O, G_THR_6	N, G_SER_25	H, G_SER_25	2.81	1.96	7.25

4F33.PDB	O, G_ASN_69	N, G_ALA_26	H, G_ALA_26	2.79	1.95	9.77
4F33.PDB	O, G_GLN_89	N, G_HIS_34	H, G_HIS_34	2.98	2.11	0.46
4F33.PDB	O, G_ILE_48	N, G_TRP_35	H, G_TRP_35	2.66	1.84	13.67
4F33.PDB	O, G_TYR_87	N, G_TYR_36	H, G_TYR_36	2.77	1.96	14.84
4F33.PDB	O, G_LYS_45	N, G_GLN_37	H, G_GLN_37	2.88	2.13	24.53
4F33.PDB	O, G_THR_85	N, G_GLN_38	H, G_GLN_38	2.82	1.98	9.18
4F33.PDB	O, G_THR_42	NE2, G_GLN_38	HE21, G_GLN_38	2.88	2.05	12.56
4F33.PDB	O, G_GLU_81	NZ, G_LYS_39	HZ1, G_LYS_39	2.81	1.93	9.10
4F33.PDB	O, G_ASP_83	NZ, G_LYS_39	HZ3, G_LYS_39	2.78	1.91	11.96
4F33.PDB	O, G_GLN_37	N, G_LYS_45	H, G_LYS_45	2.77	1.97	18.28
4F33.PDB	O, G_TRP_35	N, G_TRP_47	H, G_TRP_47	2.83	2.03	17.67
4F33.PDB	O, G_LYS_53	N, G_TYR_49	H, G_TYR_49	2.75	1.94	15.45
4F33.PDB	O, G_MET_33	N, G_THR_51	H, G_THR_51	2.73	1.90	12.70
4F33.PDB	O, G_ASP_50	N, G_SER_52	H, G_SER_52	2.85	2.13	28.17
4F33.PDB	O, G_TYR_49	N, G_LYS_53	H, G_LYS_53	2.86	2.08	20.69
4F33.PDB	O, G_TRP_47	N, G_ALA_55	H, G_ALA_55	2.97	2.12	4.41
4F33.PDB	OD1, G_ASP_82	NH2, G_ARG_61	HH21, G_ARG_61	2.73	1.89	8.68
4F33.PDB	OE2, G_GLU_81	NH2, G_ARG_61	HH22, G_ARG_61	2.96	2.16	17.92
4F33.PDB	O, G_THR_74	N, G_SER_63	H, G_SER_63	2.95	2.19	22.57
4F33.PDB	O, G_ALA_26	ND2, G_ASN_69	HD21, G_ASN_69	2.91	2.05	4.65
4F33.PDB	O, G_SER_67	N, G_SER_70	H, G_SER_70	2.98	2.13	6.01
4F33.PDB	O, G_CYS_24	N, G_TYR_71	H, G_TYR_71	2.90	2.05	8.92
4F33.PDB	O, G_VAL_30	OH, G_TYR_71	HH, G_TYR_71	2.88	2.15	24.02
4F33.PDB	O, G_SER_65	N, G_SER_72	H, G_SER_72	2.77	1.93	11.28
4F33.PDB	O, G_SER_63	N, G_THR_74	H, G_THR_74	2.79	1.96	12.22
4F33.PDB	O, G_VAL_20	N, G_ILE_75	H, G_ILE_75	2.92	2.11	16.41
4F33.PDB	O, G_ARG_61	N, G_SER_76	H, G_SER_76	2.80	1.98	14.52
4F33.PDB	O, G_GLU_18	N, G_VAL_78	H, G_VAL_78	2.74	1.99	24.30
4F33.PDB	OD2, G_ASP_82	N, G_GLU_79	H, G_GLU_79	2.87	2.02	5.18
4F33.PDB	O, G_GLU_79	N, G_ASP_82	H, G_ASP_82	2.87	2.04	11.79
4F33.PDB	O, G_GLN_38	N, G_THR_85	H, G_THR_85	2.89	2.05	11.10
4F33.PDB	O, G_THR_102	N, G_TYR_86	H, G_TYR_86	2.86	2.02	10.07
4F33.PDB	O, G_TYR_36	N, G_TYR_87	H, G_TYR_87	2.88	2.07	16.64
4F33.PDB	O, G_TYR_32	NE1, G_TRP_91	HE1, G_TRP_91	2.74	1.97	22.30
4F33.PDB	OE1, G_GLN_90	N, G_LYS_93	H, G_LYS_93	2.98	2.15	12.47
4F33.PDB	O, H_TYR_60	NE2, G_HIS_94	HE2, G_HIS_94	2.97	2.17	17.68
4F33.PDB	O, G_ILE_3	OG1, G_THR_97	HG1, G_THR_97	2.79	1.99	11.42
4F33.PDB	O, G_CYS_88	N, G_GLY_99	H, G_GLY_99	2.79	1.97	13.30
4F33.PDB	OE1, G_GLN_7	N, G_GLY_101	H, G_GLY_101	2.78	2.01	21.97
4F33.PDB	O, G_TYR_86	N, G_THR_102	H, G_THR_102	2.90	2.07	12.97
4F33.PDB	O, G_PRO_9	OG1, G_THR_102	HG1, G_THR_102	2.80	2.04	18.20
4F33.PDB	O, G_ALA_10	N, G_LYS_103	H, G_LYS_103	2.82	1.98	10.32
4F33.PDB	O, G_ALA_84	N, G_VAL_104	H, G_VAL_104	2.84	1.98	2.92
4F33.PDB	O, G_MET_12	N, G_GLU_105	H, G_GLU_105	2.77	1.92	6.46
4F33.PDB	OE1, G_GLN_166	N, G_ILE_106	H, G_ILE_106	2.88	2.04	11.50
4F33.PDB	O, G_ALA_14	N, G_LYS_107	H, G_LYS_107	2.80	1.96	9.94
4F33.PDB	O, G_THR_109	NE, G_ARG_108	HE, G_ARG_108	2.74	1.88	3.40
4F33.PDB	O, G_ASP_170	NH1, G_ARG_108	HH11, G_ARG_108	2.91	2.09	13.89
4F33.PDB	O, G_TYR_140	N, G_ALA_111	H, G_ALA_111	2.91	2.07	11.81
4F33.PDB	O, G_LEU_135	N, G_PHE_116	H, G_PHE_116	2.84	2.01	14.03
4F33.PDB	O, G_VAL_133	N, G_PHE_118	H, G_PHE_118	2.82	2.01	17.24
4F33.PDB	OG, G_SER_131	NE2, G_GLN_124	HE22, G_GLN_124	2.79	1.93	5.18
4F33.PDB	O, G_GLN_124	N, G_SER_127	H, G_SER_127	2.82	2.03	19.57
4F33.PDB	O, G_LEU_125	N, G_GLY_128	H, G_GLY_128	2.86	2.03	13.69
4F33.PDB	O, G_LEU_181	N, G_ALA_130	H, G_ALA_130	2.79	1.94	9.03
4F33.PDB	O, G_LEU_179	N, G_VAL_132	H, G_VAL_132	2.82	1.99	12.45
4F33.PDB	O, G_SER_177	N, G_CYS_134	H, G_CYS_134	2.82	1.98	10.53
4F33.PDB	O, G_PHE_116	N, G_LEU_135	H, G_LEU_135	2.78	1.93	9.33

4F33.PDB	O, G_LEU_175	N, G_LEU_136	H, G_LEU_136	2.79	1.94	5.85
4F33.PDB	O, G_SER_114	N, G_ASN_137	H, G_ASN_137	2.85	2.02	14.57
4F33.PDB	O, G_TYR_173	N, G_PHE_139	H, G_PHE_139	2.87	2.06	16.25
4F33.PDB	O, G_ALA_111	N, G_TYR_140	H, G_TYR_140	2.87	2.06	17.58
4F33.PDB	O, G_GLU_195	N, G_GLN_147	H, G_GLN_147	2.86	2.03	12.62
4F33.PDB	OG, G_SER_177	NE1, G_TRP_148	HE1, G_TRP_148	2.87	2.04	13.06
4F33.PDB	O, G_ALA_193	N, G_LYS_149	H, G_LYS_149	2.82	1.98	9.73
4F33.PDB	O, G_VAL_191	N, G_ASP_151	H, G_ASP_151	2.80	1.96	11.61
4F33.PDB	O, G_VAL_150	N, G_ALA_153	H, G_ALA_153	2.97	2.12	7.09
4F33.PDB	O, G_TRP_148	N, G_GLN_155	H, G_GLN_155	2.87	2.02	6.80
4F33.PDB	OE1, G_GLN_155	ND2, G_ASN_158	HD22, G_ASN_158	2.92	2.10	14.66
4F33.PDB	O, H_LEU_176	NE2, G_GLN_160	HE22, G_GLN_160	2.89	2.04	8.42
4F33.PDB	O, G_SER_176	N, G_SER_162	H, G_SER_162	2.99	2.22	21.55
4F33.PDB	O, H_PRO_173	OG, G_SER_162	HG, G_SER_162	2.65	1.94	25.59
4F33.PDB	O, G_SER_174	N, G_THR_164	H, G_THR_164	3.00	2.17	13.79
4F33.PDB	O, G_SER_171	NE2, G_GLN_166	HE21, G_GLN_166	2.92	2.09	14.25
4F33.PDB	O, G_LE_106	NE2, G_GLN_166	HE22, G_GLN_166	2.78	2.00	21.03
4F33.PDB	O, G_THR_172	N, G_ASP_167	H, G_ASP_167	3.00	2.15	7.80
4F33.PDB	OD1, G_ASP_167	N, G_LYS_169	H, G_LYS_169	2.59	1.77	13.16
4F33.PDB	OD1, G_ASP_170	N, G_THR_172	H, G_THR_172	2.88	2.07	16.47
4F33.PDB	OD1, G_ASP_170	OG1, G_THR_172	HG1, G_THR_172	2.69	1.89	8.34
4F33.PDB	O, G_PHE_139	N, G_TYR_173	H, G_TYR_173	2.81	1.97	8.53
4F33.PDB	OG1, G_THR_164	N, G_SER_174	H, G_SER_174	2.96	2.14	13.32
4F33.PDB	O, G_LEU_136	N, G_LEU_175	H, G_LEU_175	2.80	1.99	16.36
4F33.PDB	O, G_SER_162	N, G_SER_176	H, G_SER_176	2.93	2.11	14.30
4F33.PDB	O, G_CYS_134	N, G_SER_177	H, G_SER_177	2.88	2.06	13.62
4F33.PDB	O, G_GLN_160	N, G_THR_178	H, G_THR_178	2.92	2.10	14.24
4F33.PDB	O, G_VAL_132	N, G_LEU_179	H, G_LEU_179	2.85	2.02	12.70
4F33.PDB	O, G_ASN_158	N, G_THR_180	H, G_THR_180	2.97	2.14	11.60
4F33.PDB	O, G_ALA_130	N, G_LEU_181	H, G_LEU_181	2.90	2.07	12.18
4F33.PDB	O, G_GLY_128	N, G_LYS_183	H, G_LYS_183	2.88	2.04	9.29
4F33.PDB	OG, G_SER_182	N, G_ASP_185	H, G_ASP_185	2.89	2.09	18.06
4F33.PDB	O, G_SER_182	N, G_TYR_186	H, G_TYR_186	2.85	2.00	5.00
4F33.PDB	O, G_LYS_183	N, G_GLU_187	H, G_GLU_187	2.98	2.20	20.06
4F33.PDB	O, G_ASP_185	N, G_LYS_188	H, G_LYS_188	2.67	1.90	21.28
4F33.PDB	OD2, G_ASP_151	ND1, G_HIS_189	HD1, G_HIS_189	2.86	2.09	22.44
4F33.PDB	OD1, G_ASP_151	N, G_VAL_191	H, G_VAL_191	2.83	1.98	7.69
4F33.PDB	O, G_PHE_209	N, G_TYR_192	H, G_TYR_192	2.93	2.08	7.39
4F33.PDB	O, G_LYS_149	N, G_ALA_193	H, G_ALA_193	2.92	2.11	16.65
4F33.PDB	O, G_LYS_207	N, G_CYS_194	H, G_CYS_194	2.88	2.10	20.64
4F33.PDB	O, G_GLN_147	N, G_GLU_195	H, G_GLU_195	2.75	1.91	11.05
4F33.PDB	O, G_VAL_205	N, G_VAL_196	H, G_VAL_196	2.75	1.92	11.23
4F33.PDB	ND1, G_HIS_198	N, G_GLY_200	H, G_GLY_200	2.95	2.10	7.40
4F33.PDB	O, G_HIS_198	N, G_LEU_201	H, G_LEU_201	2.95	2.09	6.07
4F33.PDB	O, G_VAL_196	N, G_VAL_205	H, G_VAL_205	2.94	2.12	15.56
4F33.PDB	O, G_TYR_192	N, G_PHE_209	H, G_PHE_209	2.97	2.19	21.65
4F33.PDB	O, G_LYS_190	N, G_ARG_211	H, G_ARG_211	2.69	1.87	14.60
4F33.PDB	O, G_HIS_189	NE, G_ARG_211	HE, G_ARG_211	2.61	1.80	15.33
4F33.PDB	O, H_SER_25	N, H_GLN_3	H, H_GLN_3	2.95	2.13	15.35
4F33.PDB	O, H_LYS_23	N, H_GLN_5	H, H_GLN_5	2.86	2.00	5.15
4F33.PDB	O, H_TYR_94	NE2, H_GLN_6	HE22, H_GLN_6	2.90	2.09	16.65
4F33.PDB	O, H_SER_21	N, H_SER_7	H, H_SER_7	2.94	2.20	26.21
4F33.PDB	O, H_PRO_114	N, H_GLU_10	H, H_GLU_10	2.90	2.11	19.39
4F33.PDB	O, H_LEU_86	N, H_GLY_15	H, H_GLY_15	2.71	1.88	13.48
4F33.PDB	O, H_LEU_83	N, H_VAL_18	H, H_VAL_18	2.99	2.23	23.20
4F33.PDB	O, H_MET_81	N, H_ILE_20	H, H_ILE_20	2.88	2.05	13.37
4F33.PDB	O, H_GLN_5	N, H_LYS_23	H, H_LYS_23	2.75	1.91	8.98
4F33.PDB	O, H_SER_77	N, H_ALA_24	H, H_ALA_24	2.91	2.05	3.04

4F33.PDB	O, H_GLN_3	N, H_SER_25	H, H_SER_25	2.89	2.07	15.25
4F33.PDB	O, C_GLY_60	N, H_PHE_29	H, H_PHE_29	2.96	2.15	17.00
4F33.PDB	O, H_SER_28	N, H_GLY_31	H, H_GLY_31	3.00	2.15	9.57
4F33.PDB	O, H_GLY_99	N, H_THR_33	H, H_THR_33	2.95	2.14	17.33
4F33.PDB	O, H_ALA_97	N, H_ASN_35	H, H_ASN_35	2.77	1.93	11.02
4F33.PDB	O, H_PHE_95	N, H_VAL_37	H, H_VAL_37	2.79	1.98	16.38
4F33.PDB	O, H_GLU_46	N, H_LYS_38	H, H_LYS_38	2.77	1.95	13.91
4F33.PDB	O, H_GLU_89	NZ, H_LYS_38	HZ1, H_LYS_38	2.83	1.95	4.26
4F33.PDB	O, H_VAL_93	N, H_GLN_39	H, H_GLN_39	2.79	1.93	3.64
4F33.PDB	O, H_SER_40	N, H_LYS_43	H, H_LYS_43	2.96	2.14	14.33
4F33.PDB	O, H_LYS_38	N, H_GLU_46	H, H_GLU_46	2.92	2.12	18.59
4F33.PDB	O, H_TRP_36	N, H_ILE_48	H, H_ILE_48	2.85	2.00	7.74
4F33.PDB	O, H_SER_59	N, H_LEU_50	H, H_LEU_50	2.90	2.12	20.46
4F33.PDB	O, H_MET_34	N, H_ILE_51	H, H_ILE_51	2.91	2.11	17.46
4F33.PDB	O, H_ALA_57	N, H_THR_52	H, H_THR_52	2.92	2.10	14.38
4F33.PDB	O, H_THR_52	N, H_GLY_56	H, H_GLY_56	2.89	2.18	28.64
4F33.PDB	OD1, H_ASN_55	N, H_ALA_57	H, H_ALA_57	2.90	2.05	3.80
4F33.PDB	O, H_LEU_50	N, H_SER_59	H, H_SER_59	2.92	2.11	17.14
4F33.PDB	O, H_ILE_48	N, H_ASN_61	H, H_ASN_61	2.88	2.05	13.78
4F33.PDB	O, H_TRP_47	ND2, H_ASN_61	HD21, H_ASN_61	2.94	2.11	13.13
4F33.PDB	OE2, H_GLU_46	NZ, H_LYS_63	HZ3, H_LYS_63	2.72	1.93	23.08
4F33.PDB	O, H_ASN_61	N, H_PHE_64	H, H_PHE_64	2.76	1.93	12.08
4F33.PDB	O, H_PHE_64	N, H_LYS_67	H, H_LYS_67	2.99	2.27	28.17
4F33.PDB	OD2, H_ASP_90	NZ, H_LYS_67	HZ2, H_LYS_67	2.82	1.98	16.29
4F33.PDB	O, H_LEU_84	NZ, H_LYS_67	HZ3, H_LYS_67	2.97	2.18	23.42
4F33.PDB	O, H_PHE_64	N, H_ALA_68	H, H_ALA_68	2.90	2.09	16.52
4F33.PDB	O, H_ASP_82	N, H_THR_69	H, H_THR_69	2.92	2.16	23.47
4F33.PDB	OH, H_TYR_60	N, H_LEU_70	H, H_LEU_70	2.87	2.03	9.16
4F33.PDB	O, H_THR_78	N, H_ASP_73	H, H_ASP_73	2.76	1.93	11.64
4F33.PDB	O, H_CYS_22	N, H_ALA_79	H, H_ALA_79	2.86	2.05	15.52
4F33.PDB	O, H_THR_71	N, H_TYR_80	H, H_TYR_80	2.82	1.96	4.65
4F33.PDB	O, H_ILE_20	N, H_MET_81	H, H_MET_81	2.94	2.11	14.01
4F33.PDB	O, H_THR_69	N, H_ASP_82	H, H_ASP_82	2.90	2.07	11.71
4F33.PDB	O, H_VAL_18	N, H_LEU_83	H, H_LEU_83	2.79	1.96	11.28
4F33.PDB	O, H_LYS_67	N, H_LEU_84	H, H_LEU_84	2.89	2.08	16.65
4F33.PDB	O, H_ALA_16	N, H_LEU_86	H, H_LEU_86	2.90	2.06	8.91
4F33.PDB	OD2, H_ASP_90	N, H_THR_87	H, H_THR_87	2.84	2.01	13.54
4F33.PDB	O, H_THR_87	N, H_ASP_90	H, H_ASP_90	2.82	1.98	9.38
4F33.PDB	O, H_SER_88	N, H_SER_91	H, H_SER_91	2.94	2.08	5.94
4F33.PDB	O, H_VAL_115	N, H_ALA_92	H, H_ALA_92	2.98	2.25	27.64
4F33.PDB	O, H_THR_113	N, H_TYR_94	H, H_TYR_94	2.93	2.08	7.56
4F33.PDB	O, H_VAL_37	N, H_PHE_95	H, H_PHE_95	2.76	1.92	9.09
4F33.PDB	O, H_ASN_35	N, H_ALA_97	H, H_ALA_97	2.85	2.09	23.41
4F33.PDB	O, H_TYR_108	N, H_ARG_98	H, H_ARG_98	2.84	2.07	21.36
4F33.PDB	OD1, H_ASP_107	NE, H_ARG_98	HE, H_ARG_98	2.95	2.15	18.92
4F33.PDB	OD2, H_ASP_107	NH2, H_ARG_98	HH21, H_ARG_98	2.79	1.95	8.93
4F33.PDB	O, H_THR_33	N, H_GLY_99	H, H_GLY_99	2.98	2.14	10.15
4F33.PDB	OD1, H_ASP_102	NE, H_ARG_104	HE, H_ARG_104	2.85	2.00	6.80
4F33.PDB	OD2, H_ASP_107	NH1, H_ARG_104	HH11, H_ARG_104	2.85	2.04	16.23
4F33.PDB	OD2, H_ASP_102	NH2, H_ARG_104	HH21, H_ARG_104	2.93	2.12	16.50
4F33.PDB	OH, G_TYR_36	N, H_PHE_106	H, H_PHE_106	2.74	1.89	7.07
4F33.PDB	O, H_CYS_96	N, H_GLY_110	H, H_GLY_110	2.73	1.87	4.66
4F33.PDB	OE1, H_GLN_6	N, H_GLY_112	H, H_GLY_112	2.84	2.08	23.08
4F33.PDB	O, H_TYR_94	N, H_THR_113	H, H_THR_113	2.79	2.00	19.33
4F33.PDB	O, H_SER_7	OG1, H_THR_113	HG1, H_THR_113	2.86	2.10	18.89
4F33.PDB	O, H_ALA_92	N, H_VAL_115	H, H_VAL_115	2.81	1.98	12.26
4F33.PDB	OG, H_SER_91	N, H_VAL_117	H, H_VAL_117	2.86	2.06	16.73
4F33.PDB	O, H_GLU_12	N, H_SER_118	H, H_SER_118	2.89	2.08	15.90

4F33.PDB	O, H_PHE.152	N, H_LYS.123	H, H_LYS.123	2.83	2.00	12.24
4F33.PDB	O, H_ASP.150	NZ, H_LYS.123	HZ2, H_LYS.123	2.81	1.95	12.86
4F33.PDB	OE2, A_GLU.123	N, H_GLY.124	H, H_GLY.124	2.97	2.12	7.35
4F33.PDB	O, H_LYS.149	N, H_SER.126	H, H_SER.126	2.87	2.05	14.54
4F33.PDB	O, H_LEU.147	N, H_PHE.128	H, H_PHE.128	2.88	2.06	14.55
4F33.PDB	O, H_GLY.145	N, H_LEU.130	H, H_LEU.130	2.75	1.90	6.63
4F33.PDB	OG, H_SER.136	N, H_SER.133	H, H_SER.133	2.96	2.15	16.37
4F33.PDB	OG, H_SER.133	N, H_LYS.135	H, H_LYS.135	2.86	2.08	20.02
4F33.PDB	O, G_SER.208	NZ, H_LYS.135	HZ3, H_LYS.135	2.85	1.99	13.05
4F33.PDB	O, H_SER.133	OG1, H_THR.137	HG1, H_THR.137	2.95	2.25	26.10
4F33.PDB	O, H_SER.138	N, H_THR.141	H, H_THR.141	2.82	1.99	10.59
4F33.PDB	O, H_VAL.190	N, H_ALA.142	H, H_ALA.142	2.80	1.95	4.86
4F33.PDB	O, H_SER.136	N, H_ALA.143	H, H_ALA.143	2.78	1.96	14.14
4F33.PDB	O, H_VAL.188	N, H_LEU.144	H, H_LEU.144	2.99	2.16	14.52
4F33.PDB	O, H_LEU.130	N, H_GLY.145	H, H_GLY.145	2.92	2.15	21.74
4F33.PDB	O, H_PHE.128	N, H_LEU.147	H, H_LEU.147	2.83	1.99	10.04
4F33.PDB	O, H_LEU.184	N, H_VAL.148	H, H_VAL.148	2.77	1.93	9.98
4F33.PDB	O, H_SER.126	N, H_LYS.149	H, H_LYS.149	2.81	1.96	4.12
4F33.PDB	O, H_LYS.123	N, H_PHE.152	H, H_PHE.152	2.92	2.12	18.54
4F33.PDB	OG, H_SER.186	NE1, H_TRP.160	HE1, H_TRP.160	2.99	2.15	10.12
4F33.PDB	O, H_ILE.201	N, H_ASN.161	H, H_ASN.161	2.75	1.91	10.53
4F33.PDB	OD1, H_ASN.203	N, H_SER.162	H, H_SER.162	2.80	1.99	16.84
4F33.PDB	O, H_TRP.160	N, H_GLY.163	H, H_GLY.163	2.91	2.16	25.30
4F33.PDB	O, H_ASN.161	N, H_ALA.164	H, H_ALA.164	2.99	2.13	5.75
4F33.PDB	O, H_VAL.187	N, H_HIS.170	H, H_HIS.170	2.76	1.93	12.16
4F33.PDB	O, H_SER.185	N, H_PHE.172	H, H_PHE.172	2.96	2.11	6.73
4F33.PDB	O, H_SER.183	N, H_VAL.175	H, H_VAL.175	2.88	2.06	12.99
4F33.PDB	O, H_LEU.181	N, H_GLN.177	H, H_GLN.177	2.85	2.00	6.78
4F33.PDB	OD1, H_ASP.150	NE2, H_GLN.177	HE22, H_GLN.177	2.83	2.04	19.22
4F33.PDB	O, H_GLN.177	N, H_GLY.180	H, H_GLY.180	2.96	2.10	4.33
4F33.PDB	O, H_TYR.151	N, H_TYR.182	H, H_TYR.182	2.83	1.98	4.16
4F33.PDB	O, H_VAL.148	N, H_LEU.184	H, H_LEU.184	2.93	2.14	19.17
4F33.PDB	O, H_CYS.146	N, H_SER.186	H, H_SER.186	2.99	2.19	16.98
4F33.PDB	O, H_HIS.170	N, H_VAL.187	H, H_VAL.187	2.86	2.03	12.28
4F33.PDB	O, H_LEU.144	N, H_VAL.188	H, H_VAL.188	2.79	1.98	17.58
4F33.PDB	O, H_ALA.142	N, H_VAL.190	H, H_VAL.190	2.80	1.99	14.89
4F33.PDB	O, H_GLY.140	N, H_SER.192	H, H_SER.192	2.85	2.00	7.56
4F33.PDB	O, H_SER.194	N, H_GLN.198	H, H_GLN.198	2.75	1.90	3.78
4F33.PDB	O, H_THR.199	NE2, H_GLN.198	HE21, H_GLN.198	2.90	2.04	2.16
4F33.PDB	OD1, H_ASN.161	N, H_ILE.201	H, H_ILE.201	2.74	1.91	10.89
4F33.PDB	O, H_LYS.215	N, H_CYS.202	H, H_CYS.202	2.98	2.20	21.56
4F33.PDB	O, H_SER.159	N, H_ASN.203	H, H_ASN.203	2.79	1.94	8.15
4F33.PDB	OD1, H_ASP.214	ND2, H_ASN.203	HD21, H_ASN.203	2.91	2.05	5.75
4F33.PDB	O, H_VAL.213	N, H_VAL.204	H, H_VAL.204	2.77	1.91	5.12
4F33.PDB	O, H_THR.157	N, H_ASN.205	H, H_ASN.205	2.86	2.02	8.69
4F33.PDB	O, H_THR.211	N, H_HIS.206	H, H_HIS.206	2.87	2.02	7.96
4F33.PDB	O, H_PRO.153	NE2, H_HIS.206	HE2, H_HIS.206	2.85	2.00	9.82
4F33.PDB	O, H_LYS.207	N, H_ASN.210	H, H_ASN.210	2.94	2.11	13.37
4F33.PDB	O, H_SER.209	OG1, H_THR.211	HG1, H_THR.211	2.98	2.28	27.00
4F33.PDB	O, H_VAL.204	N, H_VAL.213	H, H_VAL.213	2.84	2.02	14.41
4F33.PDB	O, B_LYS.212	N, H_ASP.214	H, H_ASP.214	2.71	1.89	15.00
4F33.PDB	O, H_CYS.202	N, H_LYS.215	H, H_LYS.215	2.98	2.18	17.82
4F33.PDB	OE1, G_GLU.123	NZ, H_LYS.215	HZ1, H_LYS.215	2.97	2.19	24.10
4F33.PDB	OG1, B_THR.211	NZ, H_LYS.215	HZ2, H_LYS.215	2.80	1.95	14.49
4F33.PDB	O, B_ASN.210	N, H_LYS.216	H, H_LYS.216	2.82	2.01	16.40
4F33.PDB	O, H_TYR.200	N, H_VAL.217	H, H_VAL.217	2.85	2.01	9.04
4F3F.PDB	O, A_SER.25	N, A_THR.6	H, A_THR.6	2.85	2.00	8.09
4F3F.PDB	O, A_THR.23	N, A_SER.8	H, A_SER.8	2.94	2.15	20.13

4F3F.PDB	O, A_LYS_103	N, A_MET_12	H, A_MET_12	2.79	1.97	13.63
4F3F.PDB	O, A_GLU_105	N, A_ALA_14	H, A_ALA_14	2.99	2.22	22.34
4F3F.PDB	O, A_VAL_78	N, A_GLY_17	H, A_GLY_17	2.86	2.04	14.29
4F3F.PDB	O, A_SER_15	N, A_GLU_18	H, A_GLU_18	3.00	2.16	11.55
4F3F.PDB	O, A_ILE_75	N, A_VAL_20	H, A_VAL_20	2.94	2.13	15.17
4F3F.PDB	O, A_LEU_73	N, A_MET_22	H, A_MET_22	2.83	2.00	12.74
4F3F.PDB	O, A_SER_8	N, A_THR_23	H, A_THR_23	2.79	1.94	4.31
4F3F.PDB	O, A_TYR_71	N, A_CYS_24	H, A_CYS_24	2.77	1.94	12.44
4F3F.PDB	O, A_THR_6	N, A_SER_25	H, A_SER_25	2.94	2.11	13.40
4F3F.PDB	O, A_ASN_69	N, A_ALA_26	H, A_ALA_26	2.80	1.96	8.83
4F3F.PDB	O, A_GLU_4	N, A_SER_27	H, A_SER_27	2.90	2.18	27.52
4F3F.PDB	O, A_GLN_89	N, A_HIS_34	H, A_HIS_34	2.93	2.11	13.52
4F3F.PDB	O, A_ILE_48	N, A_TRP_35	H, A_TRP_35	2.83	2.01	14.96
4F3F.PDB	O, A_TYR_87	N, A_TYR_36	H, A_TYR_36	2.88	2.12	23.08
4F3F.PDB	O, A_LYS_45	N, A_GLN_37	H, A_GLN_37	2.83	2.04	20.59
4F3F.PDB	O, A_THR_85	N, A_GLN_38	H, A_GLN_38	2.89	2.06	12.49
4F3F.PDB	O, A_THR_42	NE2, A_GLN_38	HE21, A_GLN_38	2.97	2.19	20.06
4F3F.PDB	OE1, B_GLN_39	NE2, A_GLN_38	HE22, A_GLN_38	2.88	2.04	8.75
4F3F.PDB	O, A_GLU_81	NZ, A_LYS_39	HZ1, A_LYS_39	2.81	1.98	18.05
4F3F.PDB	O, A_LYS_39	OG1, A_THR_42	HG1, A_THR_42	3.00	2.19	8.01
4F3F.PDB	O, A_GLN_37	N, A_LYS_45	H, A_LYS_45	2.76	2.04	27.53
4F3F.PDB	O, B_ARG_104	NH1, A_ARG_46	HH11, A_ARG_46	2.93	2.16	22.46
4F3F.PDB	O, A_TRP_35	N, A_TRP_47	H, A_TRP_47	2.80	1.94	4.03
4F3F.PDB	O, A_LYS_53	N, A_TYR_49	H, A_TYR_49	2.96	2.17	19.74
4F3F.PDB	ND1, A_HIS_34	N, A_ASP_50	H, A_ASP_50	2.97	2.24	27.25
4F3F.PDB	O, A_MET_33	N, A_THR_51	H, A_THR_51	2.64	1.85	18.18
4F3F.PDB	OD1, A_ASP_82	NH2, A_ARG_61	HH21, A_ARG_61	2.60	1.79	16.27
4F3F.PDB	OE2, A_GLU_81	NH2, A_ARG_61	HH22, A_ARG_61	2.95	2.12	13.66
4F3F.PDB	O, A_THR_74	N, A_SER_63	H, A_SER_63	2.85	2.05	18.09
4F3F.PDB	O, A_CYS_24	N, A_TYR_71	H, A_TYR_71	2.90	2.04	4.79
4F3F.PDB	O, A_SER_65	N, A_SER_72	H, A_SER_72	2.82	1.98	10.66
4F3F.PDB	O, A_MET_22	N, A_LEU_73	H, A_LEU_73	2.92	2.10	15.06
4F3F.PDB	O, A_SER_63	N, A_THR_74	H, A_THR_74	2.88	2.03	8.55
4F3F.PDB	OG1, A_THR_21	OG1, A_THR_74	HG1, A_THR_74	2.77	2.04	22.11
4F3F.PDB	O, A_VAL_20	N, A_ILE_75	H, A_ILE_75	2.85	2.01	11.39
4F3F.PDB	O, A_ARG_61	N, A_SER_76	H, A_SER_76	2.86	2.02	10.12
4F3F.PDB	O, A_GLU_18	N, A_VAL_78	H, A_VAL_78	2.86	2.14	28.13
4F3F.PDB	O, A_GLU_79	N, A_ASP_82	H, A_ASP_82	2.80	1.94	6.21
4F3F.PDB	O, A_GLN_38	N, A_THR_85	H, A_THR_85	2.92	2.06	3.36
4F3F.PDB	O, A_TYR_36	N, A_TYR_87	H, A_TYR_87	2.93	2.15	21.63
4F3F.PDB	O, A_LYS_93	NE2, A_GLN_90	HE22, A_GLN_90	2.99	2.13	6.87
4F3F.PDB	OE1, A_GLN_90	N, A_LYS_93	H, A_LYS_93	2.97	2.13	10.10
4F3F.PDB	OG, B_SER_59	NE2, A_HIS_94	HE2, A_HIS_94	2.82	2.03	19.68
4F3F.PDB	O, A_ILE_3	OG1, A_THR_97	HG1, A_THR_97	2.80	2.02	14.86
4F3F.PDB	O, A_CYS_88	N, A_GLY_99	H, A_GLY_99	2.99	2.20	20.16
4F3F.PDB	OE1, A_GLN_7	N, A_GLY_101	H, A_GLY_101	2.71	1.99	27.52
4F3F.PDB	O, A_TYR_86	N, A_THR_102	H, A_THR_102	2.92	2.11	15.50
4F3F.PDB	O, A_PRO_9	OG1, A_THR_102	HG1, A_THR_102	2.92	2.17	21.04
4F3F.PDB	O, A_ALA_10	N, A_LYS_103	H, A_LYS_103	2.75	1.91	11.21
4F3F.PDB	O, A_ALA_84	N, A_VAL_104	H, A_VAL_104	2.95	2.11	8.56
4F3F.PDB	O, A_MET_12	N, A_GLU_105	H, A_GLU_105	2.87	2.10	22.23
4F3F.PDB	OE1, A_GLN_166	N, A_ILE_106	H, A_ILE_106	2.99	2.18	16.49
4F3F.PDB	O, A_ALA_14	N, A_LYS_107	H, A_LYS_107	2.82	1.98	10.57
4F3F.PDB	O, A_THR_109	NE, A_ARG_108	HE, A_ARG_108	2.88	2.12	22.89
4F3F.PDB	O, A_ASP_170	NH1, A_ARG_108	HH11, A_ARG_108	2.89	2.10	20.47
4F3F.PDB	O, A_TYR_140	N, A_ALA_111	H, A_ALA_111	2.92	2.09	12.11
4F3F.PDB	O, A_LEU_135	N, A_PHE_116	H, A_PHE_116	2.90	2.08	13.90
4F3F.PDB	O, A_VAL_133	N, A_PHE_118	H, A_PHE_118	2.78	1.95	12.67

4F3F.PDB	OG, A_SER.131	NE2, A_GLN.124	HE22, A_GLN.124	2.84	2.05	19.05
4F3F.PDB	O, A_LEU.181	N, A_ALA.130	H, A_ALA.130	2.80	1.96	8.40
4F3F.PDB	O, A_LEU.179	N, A_VAL.132	H, A_VAL.132	2.96	2.17	19.13
4F3F.PDB	O, A_SER.177	N, A_CYS.134	H, A_CYS.134	2.84	2.04	17.70
4F3F.PDB	O, A_PHE.116	N, A_LEU.135	H, A_LEU.135	2.66	1.81	8.41
4F3F.PDB	O, A_LEU.175	N, A_LEU.136	H, A_LEU.136	2.88	2.03	5.32
4F3F.PDB	O, A_SER.114	N, A_ASN.137	H, A_ASN.137	2.75	1.89	4.10
4F3F.PDB	O, A_TYR.173	N, A_PHE.139	H, A_PHE.139	2.82	2.03	20.49
4F3F.PDB	O, A_ALA.111	N, A_TYR.140	H, A_TYR.140	2.95	2.18	22.48
4F3F.PDB	O, A_ALA.193	N, A_LYS.149	H, A_LYS.149	3.00	2.22	21.52
4F3F.PDB	O, A_VAL.191	N, A_ASP.151	H, A_ASP.151	2.71	1.88	11.67
4F3F.PDB	O, A_VAL.150	N, A_ALA.153	H, A_ALA.153	2.83	2.03	17.81
4F3F.PDB	O, A_TRP.148	N, A_GLN.155	H, A_GLN.155	2.92	2.17	25.11
4F3F.PDB	O, A_SER.176	N, A_SER.162	H, A_SER.162	2.98	2.24	25.07
4F3F.PDB	O, A_SER.174	N, A_THR.164	H, A_THR.164	2.92	2.10	15.13
4F3F.PDB	O, A_THR.172	N, A_ASP.167	H, A_ASP.167	2.94	2.11	11.83
4F3F.PDB	OD1, A_ASP.167	N, A_LYS.169	H, A_LYS.169	2.79	1.96	13.81
4F3F.PDB	OD1, A_ASP.170	OG1, A_THR.172	HG1, A_THR.172	2.85	2.05	10.97
4F3F.PDB	O, A_PHE.139	N, A_TYR.173	H, A_TYR.173	2.86	2.03	12.73
4F3F.PDB	O, A_SER.162	N, A_SER.176	H, A_SER.176	2.91	2.10	15.82
4F3F.PDB	O, A_CYS.134	N, A_SER.177	H, A_SER.177	2.93	2.13	19.09
4F3F.PDB	O, A_GLN.160	N, A_THR.178	H, A_THR.178	2.92	2.12	17.96
4F3F.PDB	O, A_VAL.132	N, A_LEU.179	H, A_LEU.179	2.93	2.14	19.16
4F3F.PDB	O, A_ALA.130	N, A_LEU.181	H, A_LEU.181	2.80	1.95	8.13
4F3F.PDB	O, A_SER.182	N, A_TYR.186	H, A_TYR.186	2.99	2.15	10.88
4F3F.PDB	OD1, A_ASP.151	N, A_VAL.191	H, A_VAL.191	2.94	2.11	13.49
4F3F.PDB	O, A_PHE.209	N, A_TYR.192	H, A_TYR.192	2.94	2.10	9.21
4F3F.PDB	O, A_GLN.147	N, A_GLU.195	H, A_GLU.195	2.80	1.99	16.60
4F3F.PDB	O, A_VAL.205	N, A_VAL.196	H, A_VAL.196	2.78	1.93	8.20
4F3F.PDB	ND1, A_HIS.198	N, A_GLY.200	H, A_GLY.200	2.95	2.12	12.01
4F3F.PDB	O, A_HIS.198	N, A_LEU.201	H, A_LEU.201	2.90	2.07	12.31
4F3F.PDB	O, B_TYR.94	NE2, B_GLN.6	HE22, B_GLN.6	2.92	2.11	17.10
4F3F.PDB	O, B_PRO.114	N, B_GLU.10	H, B_GLU.10	2.98	2.18	17.64
4F3F.PDB	O, B_LEU.86	N, B_GLY.15	H, B_GLY.15	2.56	1.75	16.93
4F3F.PDB	O, B_LYS.13	N, B_ALA.16	H, B_ALA.16	2.90	2.04	5.29
4F3F.PDB	O, B_LEU.83	N, B_VAL.18	H, B_VAL.18	2.95	2.18	22.39
4F3F.PDB	O, B_GLN.5	N, B_LYS.23	H, B_LYS.23	2.93	2.10	13.11
4F3F.PDB	O, B_SER.77	N, B_ALA.24	H, B_ALA.24	2.82	2.01	16.18
4F3F.PDB	O, B_GLN.3	N, B_SER.25	H, B_SER.25	3.00	2.19	16.92
4F3F.PDB	O, B_SER.28	N, B_GLY.31	H, B_GLY.31	2.71	1.95	22.79
4F3F.PDB	O, B_ALA.97	N, B_ASN.35	H, B_ASN.35	2.89	2.09	18.86
4F3F.PDB	O, B_GLY.49	N, B_TRP.36	H, B_TRP.36	3.00	2.19	17.54
4F3F.PDB	O, B_PHE.95	N, B_VAL.37	H, B_VAL.37	2.87	2.08	19.73
4F3F.PDB	O, B_GLU.46	N, B_LYS.38	H, B_LYS.38	2.87	2.05	15.48
4F3F.PDB	O, B_GLU.89	NZ, B_LYS.38	HZ1, B_LYS.38	2.93	2.08	14.15
4F3F.PDB	O, B_VAL.93	N, B_GLN.39	H, B_GLN.39	2.84	2.02	15.17
4F3F.PDB	OD1, B_ASN.35	NE1, B_TRP.47	HE1, B_TRP.47	2.99	2.19	19.59
4F3F.PDB	O, B_TRP.36	N, B_ILE.48	H, B_ILE.48	2.96	2.11	6.75
4F3F.PDB	O, B_SER.59	N, B_LEU.50	H, B_LEU.50	2.89	2.11	20.92
4F3F.PDB	O, B_MET.34	N, B_ILE.51	H, B_ILE.51	2.99	2.27	27.72
4F3F.PDB	O, B_THR.52	N, B_GLY.56	H, B_GLY.56	2.97	2.22	25.34
4F3F.PDB	OD1, B_ASN.55	N, B_ALA.57	H, B_ALA.57	2.90	2.06	10.30
4F3F.PDB	O, B_LEU.50	N, B_SER.59	H, B_SER.59	2.93	2.13	17.76
4F3F.PDB	O, B_ILE.48	N, B_ASN.61	H, B_ASN.61	2.87	2.04	12.30
4F3F.PDB	O, B_TRP.47	ND2, B_ASN.61	HD21, B_ASN.61	2.71	1.89	13.91
4F3F.PDB	O, B_ASN.61	N, B_PHE.64	H, B_PHE.64	2.78	1.97	15.06
4F3F.PDB	O, B_GLN.62	N, B_ARG.65	H, B_ARG.65	2.89	2.05	11.05
4F3F.PDB	OD2, B_ASP.90	NZ, B_LYS.67	HZ2, B_LYS.67	2.92	2.05	9.99

4F3F.PDB	O, B_PHE.64	N, B_ALA.68	H, B_ALA.68	2.96	2.20	23.34
4F3F.PDB	O, B_ASP.82	N, B_THR.69	H, B_THR.69	2.93	2.18	24.51
4F3F.PDB	O, B_THR.78	N, B_ASP.73	H, B_ASP.73	2.77	1.93	10.54
4F3F.PDB	O, B_TYR.54	NZ, B_LYS.74	HZ2, B_LYS.74	2.82	1.94	9.19
4F3F.PDB	O, B_LYS.74	N, B_SER.77	H, B_SER.77	2.92	2.08	10.24
4F3F.PDB	O, B_SER.76	OG1, B_THR.78	HG1, B_THR.78	2.88	2.12	18.89
4F3F.PDB	O, B_CYS.22	N, B_ALA.79	H, B_ALA.79	2.86	2.03	14.35
4F3F.PDB	O, B_THR.71	N, B_TYR.80	H, B_TYR.80	2.91	2.08	12.13
4F3F.PDB	O, B_ILE.20	N, B_MET.81	H, B_MET.81	2.89	2.08	15.65
4F3F.PDB	O, B_THR.69	N, B_ASP.82	H, B_ASP.82	2.91	2.07	10.66
4F3F.PDB	O, B_VAL.18	N, B_LEU.83	H, B_LEU.83	2.87	2.02	5.50
4F3F.PDB	O, B_LYS.67	N, B_LEU.84	H, B_LEU.84	2.90	2.07	12.20
4F3F.PDB	O, B_ALA.16	N, B_LEU.86	H, B_LEU.86	2.91	2.08	13.35
4F3F.PDB	OD2, B_ASP.90	N, B_THR.87	H, B_THR.87	2.74	1.92	13.61
4F3F.PDB	O, B_THR.87	N, B_ASP.90	H, B_ASP.90	2.93	2.08	9.70
4F3F.PDB	O, B_VAL.115	N, B_ALA.92	H, B_ALA.92	2.95	2.23	27.95
4F3F.PDB	O, B_THR.113	N, B_TYR.94	H, B_TYR.94	2.79	1.96	11.98
4F3F.PDB	O, B_VAL.37	N, B_PHE.95	H, B_PHE.95	2.81	2.00	16.62
4F3F.PDB	O, B_ASN.35	N, B_ALA.97	H, B_ALA.97	2.93	2.17	24.23
4F3F.PDB	O, B_TYR.108	N, B_ARG.98	H, B_ARG.98	2.77	2.02	24.77
4F3F.PDB	OD2, B_ASP.107	NH2, B_ARG.98	HH21, B_ARG.98	2.79	1.95	9.80
4F3F.PDB	O, B_GLY.105	N, B_GLY.100	H, B_GLY.100	2.89	2.13	23.94
4F3F.PDB	OE1, C_GLU.52	N, B_ASP.102	H, B_ASP.102	2.88	2.08	17.53
4F3F.PDB	O, B_GLY.103	N, B_GLY.105	H, B_GLY.105	2.80	2.09	28.59
4F3F.PDB	OH, A_TYR.36	N, B_PHE.106	H, B_PHE.106	2.71	1.88	12.56
4F3F.PDB	O, B_CYS.96	N, B_GLY.110	H, B_GLY.110	2.79	1.94	7.86
4F3F.PDB	OE1, B_GLN.6	N, B_GLY.112	H, B_GLY.112	2.83	2.12	28.70
4F3F.PDB	O, B_TYR.94	N, B_THR.113	H, B_THR.113	2.82	2.00	14.66
4F3F.PDB	O, B_SER.7	OG1, B_THR.113	HG1, B_THR.113	2.72	1.93	13.91
4F3F.PDB	O, B_ALA.92	N, B_VAL.115	H, B_VAL.115	2.81	1.96	5.43
4F3F.PDB	OG, B_SER.91	N, B_VAL.117	H, B_VAL.117	2.69	1.83	2.50
4F3F.PDB	OG, B_SER.118	N, B_ALA.120	H, B_ALA.120	2.75	2.02	26.82
4F3F.PDB	O, B_PHE.152	N, B_LYS.123	H, B_LYS.123	2.85	2.11	25.39
4F3F.PDB	O, B_LEU.147	N, B_PHE.128	H, B_PHE.128	2.79	2.01	20.40
4F3F.PDB	O, B_GLY.145	N, B_LEU.130	H, B_LEU.130	2.57	1.73	11.24
4F3F.PDB	O, B_LEU.130	N, B_GLY.145	H, B_GLY.145	2.80	2.01	19.86
4F3F.PDB	O, B_SER.186	N, B_CYS.146	H, B_CYS.146	2.73	1.98	24.62
4F3F.PDB	O, B_PHE.128	N, B_LEU.147	H, B_LEU.147	2.70	1.84	3.31
4F3F.PDB	O, B_LEU.184	N, B_VAL.148	H, B_VAL.148	2.84	2.01	12.24
4F3F.PDB	O, B_SER.126	N, B_LYS.149	H, B_LYS.149	2.81	2.00	15.44
4F3F.PDB	O, B_LYS.123	N, B_PHE.152	H, B_PHE.152	2.80	2.03	23.11
4F3F.PDB	O, B_ASN.205	N, B_THR.157	H, B_THR.157	2.70	1.85	8.13
4F3F.PDB	O, B_ILE.201	N, B_ASN.161	H, B_ASN.161	2.74	1.89	7.43
4F3F.PDB	O, B_ASN.161	N, B_ALA.164	H, B_ALA.164	2.98	2.15	14.27
4F3F.PDB	O, B_VAL.187	N, B_HIS.170	H, B_HIS.170	2.83	1.99	10.01
4F3F.PDB	OD1, A_ASN.138	NE2, B_HIS.170	HE2, B_HIS.170	2.82	2.05	21.56
4F3F.PDB	O, B_SER.185	N, B_PHE.172	H, B_PHE.172	2.99	2.14	4.25
4F3F.PDB	O, B_SER.183	N, B_VAL.175	H, B_VAL.175	2.79	1.99	18.03
4F3F.PDB	O, B_LEU.181	N, B_GLN.177	H, B_GLN.177	2.69	1.88	16.92
4F3F.PDB	OD1, B_ASP.150	NE2, B_GLN.177	HE22, B_GLN.177	2.87	2.13	25.54
4F3F.PDB	O, B_GLN.177	N, B_GLY.180	H, B_GLY.180	2.83	2.02	16.47
4F3F.PDB	O, B_TYR.151	N, B_TYR.182	H, B_TYR.182	2.87	2.02	3.69
4F3F.PDB	O, B_CYS.146	N, B_SER.186	H, B_SER.186	2.83	2.01	14.97
4F3F.PDB	O, B_HIS.170	N, B_VAL.187	H, B_VAL.187	2.77	1.93	9.44
4F3F.PDB	O, B_LEU.144	N, B_VAL.188	H, B_VAL.188	2.86	2.09	23.17
4F3F.PDB	O, B_ALA.142	N, B_VAL.190	H, B_VAL.190	2.86	2.06	18.75
4F3F.PDB	OD1, B_ASN.161	N, B_ILE.201	H, B_ILE.201	2.88	2.06	14.25
4F3F.PDB	O, B_SER.159	N, B_ASN.203	H, B_ASN.203	2.81	1.96	4.97

4F3F.PDB	O, B_VAL_213	N, B_VAL_204	H, B_VAL_204	2.70	1.90	17.22
4F3F.PDB	O, B_THR_211	N, B_HIS_206	H, B_HIS_206	2.82	2.01	16.21
4F3F.PDB	OG, B_SER_209	ND1, B_HIS_206	HD1, B_HIS_206	2.43	1.61	13.98
4F3F.PDB	O, B_PRO_153	NE2, B_HIS_206	HE2, B_HIS_206	2.65	1.82	11.74
4F3F.PDB	OE1, C_GLN_40	N, C_ILE_16	H, C_ILE_16	2.59	1.73	3.34
4F3F.PDB	OE1, C_GLU_27	N, C_LYS_24	H, C_LYS_24	2.86	2.05	15.66
4F3F.PDB	O, B_ASP_102	NZ, C_LYS_24	HZ2, C_LYS_24	2.85	2.03	18.08
4F3F.PDB	OD1, B_ASP_102	N, C_LYS_25	H, C_LYS_25	2.86	2.02	9.58
4F3F.PDB	OH, B_TYR_101	NZ, C_LYS_25	HZ3, C_LYS_25	2.87	2.11	26.18
4F3F.PDB	OH, A_TYR_32	NE1, C_TRP_26	HE1, C_TRP_26	2.97	2.17	18.16
4F3F.PDB	O, C_LYS_24	N, C_LEU_28	H, C_LEU_28	2.97	2.15	14.14
4F3F.PDB	O, C_LEU_28	N, C_CYS_31	H, C_CYS_31	2.99	2.25	25.66
4F3F.PDB	OD1, C_ASP_33	N, C_LEU_36	H, C_LEU_36	2.84	2.00	10.02
4F3F.PDB	O, C_ALA_34	N, C_ALA_38	H, C_ALA_38	2.78	1.99	18.86
4F3F.PDB	O, C_LEU_36	OG1, C_THR_39	HG1, C_THR_39	2.91	2.17	21.49
4F3F.PDB	OE2, C_GLU_15	NH2, C_ARG_43	HH21, C_ARG_43	2.88	2.04	9.30
4F3F.PDB	O, C_VAL_44	N, C_ILE_47	H, C_ILE_47	2.93	2.16	22.22
4F3F.PDB	O, C_ILE_47	N, C_PHE_49	H, C_PHE_49	2.71	1.99	27.94
4F3F.PDB	OE1, C_GLN_53	N, C_THR_50	H, C_THR_50	2.83	2.01	14.01
4F3F.PDB	O, C_TYR_23	NE2, C_GLN_53	HE21, C_GLN_53	2.91	2.11	17.04
4F3F.PDB	O, C_ILE_21	NE2, C_GLN_53	HE22, C_GLN_53	2.85	2.03	15.04
4F3F.PDB	O, C_THR_50	N, C_LEU_54	H, C_LEU_54	2.77	1.94	11.60
4F3F.PDB	O, C_TYR_51	N, C_ASP_55	H, C_ASP_55	2.90	2.12	22.28
4F3F.PDB	O, C_LEU_54	N, C_LYS_58	H, C_LYS_58	2.82	2.01	16.54
4F3F.PDB	O, C_ASP_55	N, C_HIS_59	H, C_HIS_59	2.98	2.22	24.03
4F3F.PDB	O, C_GLU_29	NZ, C_LYS_60	HZ1, C_LYS_60	2.68	1.83	14.40
4F3F.PDB	O, C_HIS_59	N, C_ASP_62	H, C_ASP_62	2.90	2.16	25.96
4F3F.PDB	O, C_HIS_59	N, C_GLU_63	H, C_GLU_63	2.98	2.18	17.58
4JAM.PDB	O, H_SER_25	N, H_GLN_3	H, H_GLN_3	2.94	2.14	17.76
4JAM.PDB	O, H_THR_23	N, H_GLN_5	H, H_GLN_5	3.00	2.20	17.90
4JAM.PDB	O, H_THR_21	N, H_SER_7	H, H_SER_7	2.81	2.01	18.59
4JAM.PDB	O, H_VAL_82C	N, H_SER_15	H, H_SER_15	2.81	1.98	12.83
4JAM.PDB	O, H_LYS_13	N, H_GLU_16	H, H_GLU_16	3.00	2.20	18.36
4JAM.PDB	O, H_LEU_82	N, H_LEU_18	H, H_LEU_18	2.84	2.06	21.67
4JAM.PDB	O, H_LEU_80	N, H_LEU_20	H, H_LEU_20	2.89	2.05	11.57
4JAM.PDB	O, H_PHE_78	N, H_CYS_22	H, H_CYS_22	2.73	1.91	13.99
4JAM.PDB	O, H_GLN_5	N, H_THR_23	H, H_THR_23	2.84	2.01	12.14
4JAM.PDB	O, H_ASP_76	N, H_VAL_24	H, H_VAL_24	2.88	2.03	6.27
4JAM.PDB	O, H_GLN_3	N, H_SER_25	H, H_SER_25	2.95	2.17	20.66
4JAM.PDB	O, H_GLY_30	OG1, H_THR_32	HG1, H_THR_32	2.84	2.06	16.49
4JAM.PDB	O, H_LEU_95	N, H_TYR_33	H, H_TYR_33	2.76	1.93	13.12
4JAM.PDB	O, H_ILE_51	N, H_TRP_34	H, H_TRP_34	2.84	2.05	18.90
4JAM.PDB	O, H_MET_29	NE1, H_TRP_34	HE1, H_TRP_34	2.94	2.08	6.03
4JAM.PDB	O, H_ALA_93	N, H_SER_35	H, H_SER_35	2.84	2.00	9.25
4JAM.PDB	O, H_GLY_49	N, H_TRP_36	H, H_TRP_36	2.94	2.10	11.93
4JAM.PDB	O, H_PHE_91	N, H_LEU_37	H, H_LEU_37	2.84	2.01	12.67
4JAM.PDB	O, H_GLU_46	N, H_ARG_38	H, H_ARG_38	2.86	2.06	18.02
4JAM.PDB	OE2, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.93	2.10	13.53
4JAM.PDB	OH, H_TYR_90	NH1, H_ARG_38	HH11, H_ARG_38	2.92	2.12	17.99
4JAM.PDB	OD1, H_ASP_86	NH1, H_ARG_38	HH12, H_ARG_38	2.91	2.07	10.41
4JAM.PDB	O, H_VAL_89	N, H_LEU_39	H, H_LEU_39	2.84	2.08	24.06
4JAM.PDB	O, H_ARG_38	N, H_GLU_46	H, H_GLU_46	2.84	2.01	13.22
4JAM.PDB	O, H_TRP_36	N, H_ILE_48	H, H_ILE_48	2.87	2.03	11.32
4JAM.PDB	O, H_ASN_58	N, H_TYR_50	H, H_TYR_50	2.84	2.06	20.47
4JAM.PDB	O, H_TRP_34	N, H_ILE_51	H, H_ILE_51	2.88	2.15	26.94
4JAM.PDB	O, H_GLU_56	N, H_PHE_52	H, H_PHE_52	2.96	2.12	11.30
4JAM.PDB	O, H_PHE_52	N, H_GLY_55	H, H_GLY_55	2.76	1.91	7.28
4JAM.PDB	O, H_TYR_50	N, H_ASN_58	H, H_ASN_58	2.98	2.17	16.49

4JAM.PDB	O, H_ILE_48	N, H_SER_60	H, H_SER_60	2.89	2.04	4.59
4JAM.PDB	O, H_LEU_63	N, H_ARG_66	H, H_ARG_66	2.96	2.10	3.45
4JAM.PDB	O, H_ARG_82A	NH1, H_ARG_66	HH11, H_ARG_66	2.94	2.15	19.87
4JAM.PDB	OD1, H_ASP_86	NH2, H_ARG_66	HH22, H_ARG_66	2.96	2.12	9.52
4JAM.PDB	O, H_ARG_81	N, H_SER_68	H, H_SER_68	2.89	2.11	20.79
4JAM.PDB	OH, H_TYR_59	N, H_ILE_69	H, H_ILE_69	2.96	2.15	16.37
4JAM.PDB	O, H_GLN_77	N, H_ASP_72	H, H_ASP_72	2.79	1.94	5.32
4JAM.PDB	OD1, H_ASP_72	N, H_SER_74	H, H_SER_74	2.98	2.20	21.77
4JAM.PDB	OD1, H_ASP_72	N, H_GLU_75	H, H_GLU_75	2.97	2.14	12.50
4JAM.PDB	O, H_CYS_22	N, H_PHE_78	H, H_PHE_78	2.92	2.11	17.57
4JAM.PDB	O, H_SER_70	N, H_SER_79	H, H_SER_79	2.91	2.12	20.02
4JAM.PDB	O, H_LEU_20	N, H_LEU_80	H, H_LEU_80	2.92	2.08	12.05
4JAM.PDB	O, H_SER_68	N, H_ARG_81	H, H_ARG_81	2.90	2.07	12.47
4JAM.PDB	O, H_LEU_18	N, H_LEU_82	H, H_LEU_82	2.90	2.10	17.80
4JAM.PDB	O, H_ARG_66	N, H_ARG_82A	H, H_ARG_82A	2.87	2.03	10.53
4JAM.PDB	OD2, H_ASP_86	N, H_THR_83	H, H_THR_83	2.93	2.14	18.89
4JAM.PDB	O, H_THR_83	N, H_ASP_86	H, H_ASP_86	2.85	2.00	7.55
4JAM.PDB	O, H_ALA_84	N, H_THR_87	H, H_THR_87	2.98	2.13	7.55
4JAM.PDB	O, H_LEU_39	N, H_VAL_89	H, H_VAL_89	2.92	2.09	11.66
4JAM.PDB	O, H_SER_107	N, H_TYR_90	H, H_TYR_90	2.92	2.07	8.56
4JAM.PDB	O, H_LEU_37	N, H_PHE_91	H, H_PHE_91	2.79	1.93	6.64
4JAM.PDB	O, H_SER_35	N, H_ALA_93	H, H_ALA_93	2.97	2.20	22.59
4JAM.PDB	O, H_ARG_101	N, H_SER_94	H, H_SER_94	2.87	2.08	19.41
4JAM.PDB	O, H_GLY_31	N, H_ARG_97	H, H_ARG_97	2.96	2.11	7.24
4JAM.PDB	O, H_LEU_100	N, H_ALA_100C	H, H_ALA_100C	3.00	2.15	9.56
4JAM.PDB	OH, L_TYR_36	N, H_PHE_100E	H, H_PHE_100E	2.85	2.03	15.20
4JAM.PDB	O, H_SER_94	N, H_ARG_101	H, H_ARG_101	2.76	1.92	10.57
4JAM.PDB	O, H_CYS_92	N, H_GLY_104	H, H_GLY_104	2.85	2.01	11.27
4JAM.PDB	O, H_TYR_90	N, H_SER_107	H, H_SER_107	2.95	2.16	20.47
4JAM.PDB	O, H_SER_7	OG, H_SER_107	HG, H_SER_107	2.70	1.93	17.20
4JAM.PDB	O, H_ALA_88	N, H_VAL_109	H, H_VAL_109	2.86	2.01	8.44
4JAM.PDB	OG1, H_THR_87	N, H_VAL_111	H, H_VAL_111	2.96	2.11	6.95
4JAM.PDB	O, H_PHE_146	N, H_LYS_117	H, H_LYS_117	2.84	2.00	10.63
4JAM.PDB	O, H_ASP_144	NZ, H_LYS_117	HZ2, H_LYS_117	2.90	2.10	21.43
4JAM.PDB	O, H_LYS_143	N, H_SER_120	H, H_SER_120	2.96	2.16	18.52
4JAM.PDB	O, H_LEU_141	N, H_PHE_122	H, H_PHE_122	2.88	2.04	12.44
4JAM.PDB	O, H_GLY_139	N, H_LEU_124	H, H_LEU_124	2.76	1.91	9.61
4JAM.PDB	OG, H_SER_127	N, H_LYS_129	H, H_LYS_129	2.99	2.25	26.12
4JAM.PDB	O, H_VAL_184	N, H_ALA_136	H, H_ALA_136	2.89	2.08	16.20
4JAM.PDB	O, H_LEU_124	N, H_GLY_139	H, H_GLY_139	2.92	2.13	20.18
4JAM.PDB	O, H_SER_180	N, H_CYS_140	H, H_CYS_140	2.84	2.07	21.53
4JAM.PDB	O, H_PHE_122	N, H_LEU_141	H, H_LEU_141	2.77	1.93	9.15
4JAM.PDB	O, H_LEU_178	N, H_VAL_142	H, H_VAL_142	2.76	1.91	9.10
4JAM.PDB	O, H_SER_120	N, H_LYS_143	H, H_LYS_143	2.77	1.92	7.28
4JAM.PDB	OD1, H_ASP_144	NZ, H_LYS_143	HZ2, H_LYS_143	3.00	2.12	8.81
4JAM.PDB	O, H_TYR_176	N, H_TYR_145	H, H_TYR_145	2.91	2.10	17.24
4JAM.PDB	O, H_LYS_117	N, H_PHE_146	H, H_PHE_146	2.94	2.14	18.10
4JAM.PDB	O, H_ASN_197	N, H_SER_153	H, H_SER_153	2.89	2.07	14.46
4JAM.PDB	OG, H_SER_180	NE1, H_TRP_154	HE1, H_TRP_154	2.95	2.10	8.20
4JAM.PDB	O, H_ILE_195	N, H_ASN_155	H, H_ASN_155	2.94	2.10	11.47
4JAM.PDB	OD1, H_ASN_197	N, H_SER_156	H, H_SER_156	2.74	1.93	17.72
4JAM.PDB	O, H_TRP_154	N, H_GLY_157	H, H_GLY_157	2.90	2.12	19.88
4JAM.PDB	O, H_VAL_181	N, H_HIS_164	H, H_HIS_164	2.85	2.02	12.88
4JAM.PDB	OG, H_SER_180	OG1, H_THR_165	HG1, H_THR_165	2.85	2.09	18.68
4JAM.PDB	O, H_SER_179	N, H_PHE_166	H, H_PHE_166	2.96	2.10	3.06
4JAM.PDB	O, H_SER_177	N, H_VAL_169	H, H_VAL_169	2.88	2.09	20.11
4JAM.PDB	O, H_LEU_175	N, H_GLN_171	H, H_GLN_171	2.88	2.02	6.22
4JAM.PDB	O, H_GLN_171	N, H_GLY_174	H, H_GLY_174	2.89	2.04	7.16

4JAM.PDB	O, H_TYR_145	N, H_TYR_176	H, H_TYR_176	2.77	1.92	3.97
4JAM.PDB	O, H_VAL_142	N, H_LEU_178	H, H_LEU_178	2.91	2.13	21.00
4JAM.PDB	O, H_CYS_140	N, H_SER_180	H, H_SER_180	3.00	2.18	15.61
4JAM.PDB	O, H_HIS_164	N, H_VAL_181	H, H_VAL_181	2.91	2.06	7.14
4JAM.PDB	O, H_LEU_138	N, H_VAL_182	H, H_VAL_182	2.78	1.95	12.87
4JAM.PDB	O, H_GLY_162	N, H_THR_183	H, H_THR_183	2.94	2.15	19.24
4JAM.PDB	O, H_GLY_134	N, H_SER_186	H, H_SER_186	2.99	2.13	1.16
4JAM.PDB	O, H_PRO_185	N, H_SER_188	H, H_SER_188	2.94	2.11	13.31
4JAM.PDB	O, H_SER_188	N, H_GLN_192	H, H_GLN_192	2.79	1.94	7.97
4JAM.PDB	OD1, H_ASN_155	N, H_ILE_195	H, H_ILE_195	2.97	2.17	18.26
4JAM.PDB	O, H_LYS_209	N, H_CYS_196	H, H_CYS_196	2.89	2.09	19.00
4JAM.PDB	O, H_SER_153	N, H_ASN_197	H, H_ASN_197	2.82	1.97	5.10
4JAM.PDB	O, H_VAL_207	N, H_VAL_198	H, H_VAL_198	2.79	1.94	6.21
4JAM.PDB	O, H_THR_151	N, H_ASN_199	H, H_ASN_199	2.92	2.08	11.31
4JAM.PDB	O, H_THR_205	N, H_HIS_200	H, H_HIS_200	2.85	1.99	2.37
4JAM.PDB	OG, H_SER_203	ND1, H_HIS_200	HD1, H_HIS_200	2.70	1.91	20.45
4JAM.PDB	O, H_PRO_147	NE2, H_HIS_200	HE2, H_HIS_200	2.80	1.96	10.13
4JAM.PDB	O, H_LYS_201	N, H_ASN_204	H, H_ASN_204	2.95	2.12	12.20
4JAM.PDB	O, H_VAL_198	N, H_VAL_207	H, H_VAL_207	2.89	2.08	17.27
4JAM.PDB	O, H_CYS_196	N, H_LYS_209	H, H_LYS_209	2.97	2.17	17.34
4JAM.PDB	O, H_TYR_194	N, H_VAL_211	H, H_VAL_211	2.86	2.01	8.16
4JAM.PDB	O, L_TYR_86	NE2, L_GLN_6	HE22, L_GLN_6	2.86	2.03	12.40
4JAM.PDB	O, L_GLN_103	N, L_VAL_11	H, L_VAL_11	2.91	2.06	8.42
4JAM.PDB	OE1, L_GLN_17	N, L_SER_14	H, L_SER_14	2.84	2.00	10.61
4JAM.PDB	O, L_ILE_75	N, L_ALA_19	H, L_ALA_19	2.99	2.17	15.72
4JAM.PDB	O, L_LEU_73	N, L_ILE_21	H, L_ILE_21	2.83	1.99	10.81
4JAM.PDB	O, L_ALA_71	N, L_CYS_23	H, L_CYS_23	2.74	2.01	26.68
4JAM.PDB	O, L_THR_5	N, L_SER_24	H, L_SER_24	2.92	2.08	11.35
4JAM.PDB	O, L_SER_69	N, L_ALA_26	H, L_ALA_26	2.89	2.06	12.83
4JAM.PDB	OD1, H_ASN_100B	ND2, L_ASN_32	HD21, L_ASN_32	2.96	2.21	25.94
4JAM.PDB	OD1, L_ASN_51	N, L_VAL_33	H, L_VAL_33	2.88	2.05	13.33
4JAM.PDB	O, L_ILE_48	N, L_TRP_35	H, L_TRP_35	2.89	2.14	24.66
4JAM.PDB	O, L_TYR_87	N, L_TYR_36	H, L_TYR_36	2.84	2.01	12.44
4JAM.PDB	O, L_GLU_45	N, L_GLN_37	H, L_GLN_37	2.80	1.97	12.63
4JAM.PDB	OH, L_TYR_86	NE2, L_GLN_37	HE21, L_GLN_37	2.92	2.07	7.82
4JAM.PDB	O, L_ASP_85	N, L_VAL_38	H, L_VAL_38	2.71	1.87	12.07
4JAM.PDB	O, L_ILE_81	NZ, L_LYS_39	HZ3, L_LYS_39	2.71	1.89	18.99
4JAM.PDB	O, L_TRP_35	N, L_VAL_47	H, L_VAL_47	2.89	2.06	14.03
4JAM.PDB	O, L_LYS_53	N, L_PHE_49	H, L_PHE_49	2.86	2.03	12.66
4JAM.PDB	O, L_VAL_33	N, L_ASN_51	H, L_ASN_51	2.91	2.07	10.53
4JAM.PDB	O, L_GLU_50	N, L_TYR_52	H, L_TYR_52	2.89	2.17	28.38
4JAM.PDB	O, L_PHE_49	N, L_LYS_53	H, L_LYS_53	2.85	2.05	18.62
4JAM.PDB	OE1, L_GLU_50	NZ, L_LYS_53	HZ1, L_LYS_53	2.81	1.96	13.53
4JAM.PDB	OD2, L_ASP_82	NE, L_ARG_61	HE, L_ARG_61	2.81	2.02	19.36
4JAM.PDB	OD1, L_ASP_82	NH2, L_ARG_61	HH21, L_ARG_61	2.93	2.10	13.29
4JAM.PDB	O, L_THR_74	N, L_SER_63	H, L_SER_63	2.92	2.09	12.30
4JAM.PDB	O, L_ALA_26	NZ, L_LYS_66	HZ1, L_LYS_66	2.91	2.11	21.70
4JAM.PDB	O, L_GLY_68	NZ, L_LYS_66	HZ3, L_LYS_66	2.98	2.22	27.29
4JAM.PDB	O, L_CYS_23	N, L_ALA_71	H, L_ALA_71	2.82	2.01	15.87
4JAM.PDB	O, L_SER_65	N, L_THR_72	H, L_THR_72	2.77	1.93	11.94
4JAM.PDB	O, L_ILE_21	N, L_LEU_73	H, L_LEU_73	2.77	1.96	15.27
4JAM.PDB	O, L_SER_63	N, L_THR_74	H, L_THR_74	2.90	2.05	4.48
4JAM.PDB	O, L_ALA_19	N, L_ILE_75	H, L_ILE_75	2.91	2.09	14.28
4JAM.PDB	OD2, L_ASP_82	N, L_GLN_79	H, L_GLN_79	2.89	2.04	5.61
4JAM.PDB	O, L_GLN_79	N, L_ASP_82	H, L_ASP_82	2.89	2.09	18.18
4JAM.PDB	O, L_VAL_38	N, L_ASP_85	H, L_ASP_85	2.90	2.08	16.10
4JAM.PDB	O, L_THR_102	N, L_TYR_86	H, L_TYR_86	2.86	2.04	14.55
4JAM.PDB	O, L_TYR_36	N, L_TYR_87	H, L_TYR_87	2.99	2.18	17.93

4JAM.PDB	O, L_VAL_97	N, L_VAL_90	H, L_VAL_90	2.92	2.09	13.43
4JAM.PDB	O, L_THR_95A	N, L_ASP_92	H, L_ASP_92	2.92	2.16	23.57
4JAM.PDB	OD1, L_ASP_92	N, L_PHE_94	H, L_PHE_94	2.87	2.09	20.85
4JAM.PDB	OD1, L_ASP_92	N, L_SER_95	H, L_SER_95	2.87	2.05	13.98
4JAM.PDB	O, L_SER_95	N, L_PHE_96	H, L_PHE_96	2.80	2.09	28.58
4JAM.PDB	O, L_VAL_90	N, L_VAL_97	H, L_VAL_97	2.88	2.03	5.98
4JAM.PDB	O, L_CYS_88	N, L_GLY_99	H, L_GLY_99	2.82	1.99	13.21
4JAM.PDB	O, L_TYR_86	N, L_THR_102	H, L_THR_102	2.90	2.13	22.21
4JAM.PDB	O, L_PRO_7	OG1, L_THR_102	HG1, L_THR_102	2.58	1.77	7.88
4JAM.PDB	O, L_PRO_8	N, L_GLN_103	H, L_GLN_103	2.91	2.06	9.20
4JAM.PDB	O, L_ALA_84	N, L_VAL_104	H, L_VAL_104	2.83	1.97	5.25
4JAM.PDB	OE1, L_GLU_83	N, L_VAL_106	H, L_VAL_106	2.88	2.04	10.37
4JAM.PDB	O, L_VAL_113	N, L_LEU_106A	H, L_LEU_106A	2.89	2.06	12.78
4JAM.PDB	OH, L_TYR_172	NH2, L_ARG_107	HH22, L_ARG_107	2.87	2.14	27.08
4JAM.PDB	O, L_ASN_170	NE2, L_GLN_108	HE22, L_GLN_108	2.96	2.17	20.42
4JAM.PDB	OE1, L_GLU_198	NZ, L_LYS_110	HZ2, L_LYS_110	2.60	1.75	13.04
4JAM.PDB	O, L_TYR_140	N, L_ALA_111	H, L_ALA_111	2.92	2.08	10.21
4JAM.PDB	O, L_SER_137	N, L_THR_114	H, L_THR_114	2.88	2.05	12.38
4JAM.PDB	O, L_LEU_135	N, L_THR_116	H, L_THR_116	2.92	2.09	14.50
4JAM.PDB	O, L_VAL_133	N, L_PHE_118	H, L_PHE_118	2.86	2.02	11.47
4JAM.PDB	O, L_SER_122	N, L_GLN_126	H, L_GLN_126	2.95	2.16	20.22
4JAM.PDB	O, L_LEU_125	N, L_ASN_128	H, L_ASN_128	2.93	2.12	17.43
4JAM.PDB	OE2, L_GLU_124	OG1, L_THR_131	HG1, L_THR_131	2.56	1.86	25.46
4JAM.PDB	O, L_LEU_178	N, L_LEU_132	H, L_LEU_132	2.88	2.05	11.45
4JAM.PDB	O, L_SER_176	N, L_CYS_134	H, L_CYS_134	2.82	1.98	10.00
4JAM.PDB	O, L_THR_116	N, L_LEU_135	H, L_LEU_135	2.80	1.96	9.63
4JAM.PDB	O, L_ALA_174	N, L_ILE_136	H, L_ILE_136	2.86	2.07	20.07
4JAM.PDB	O, L_THR_114	N, L_SER_137	H, L_SER_137	2.99	2.19	17.72
4JAM.PDB	OE1, L_GLN_167	N, L_ASP_138	H, L_ASP_138	2.84	2.00	8.06
4JAM.PDB	O, L_ALA_111	N, L_TYR_140	H, L_TYR_140	2.99	2.16	14.54
4JAM.PDB	O, L_GLN_194	N, L_ALA_147	H, L_ALA_147	2.82	1.99	11.47
4JAM.PDB	OG, L_SER_176	NE1, L_TRP_148	HE1, L_TRP_148	2.87	2.03	8.58
4JAM.PDB	O, L_SER_192	N, L_LYS_149	H, L_LYS_149	2.97	2.15	15.62
4JAM.PDB	OE1, L_GLU_203	NZ, L_LYS_149	HZ2, L_LYS_149	2.76	1.94	19.38
4JAM.PDB	O, L_SER_153	N, L_ALA_150	H, L_ALA_150	2.77	1.99	21.36
4JAM.PDB	O, L_SER_190	N, L_ASP_151	H, L_ASP_151	2.76	1.91	6.56
4JAM.PDB	O, L_ALA_150	N, L_SER_153	H, L_SER_153	2.98	2.14	10.89
4JAM.PDB	O, L_TRP_148	N, L_VAL_155	H, L_VAL_155	2.93	2.10	14.25
4JAM.PDB	O, L_TYR_177	N, L_GLU_160	H, L_GLU_160	2.98	2.18	18.13
4JAM.PDB	O, L_SER_175	N, L_THR_162	H, L_THR_162	2.83	2.01	13.96
4JAM.PDB	O, L_ALA_173	N, L_SER_165	H, L_SER_165	2.87	2.08	18.46
4JAM.PDB	O, L_LYS_171	N, L_GLN_167	H, L_GLN_167	2.72	1.88	10.56
4JAM.PDB	OD1, L_ASN_169	N, L_LYS_171	H, L_LYS_171	2.95	2.10	8.57
4JAM.PDB	O, L_PHE_139	N, L_TYR_172	H, L_TYR_172	2.85	2.06	19.58
4JAM.PDB	O, L_SER_165	N, L_ALA_173	H, L_ALA_173	2.90	2.09	17.11
4JAM.PDB	O, L_ILE_136	N, L_ALA_174	H, L_ALA_174	2.73	1.92	17.17
4JAM.PDB	OG1, L_THR_162	N, L_SER_175	H, L_SER_175	2.85	2.04	16.03
4JAM.PDB	O, L_CYS_134	N, L_SER_176	H, L_SER_176	2.90	2.09	17.03
4JAM.PDB	O, L_GLU_160	N, L_TYR_177	H, L_TYR_177	2.83	2.06	21.58
4JAM.PDB	O, L_GLY_158	N, L_SER_179	H, L_SER_179	2.81	1.99	14.68
4JAM.PDB	OE1, L_GLN_184	N, L_THR_181	H, L_THR_181	2.99	2.16	13.42
4JAM.PDB	OG1, L_THR_181	N, L_GLN_184	H, L_GLN_184	2.98	2.15	12.48
4JAM.PDB	O, L_PRO_182	N, L_LYS_186	H, L_LYS_186	2.91	2.10	17.39
4JAM.PDB	O, L_GLN_184	ND1, L_HIS_188	HD1, L_HIS_188	2.79	1.96	11.98
4JAM.PDB	O, L_VAL_206	N, L_TYR_191	H, L_TYR_191	2.94	2.12	15.63
4JAM.PDB	O, L_LYS_149	N, L_SER_192	H, L_SER_192	2.93	2.14	19.54
4JAM.PDB	O, L_LYS_204	N, L_CYS_193	H, L_CYS_193	2.94	2.17	21.83
4JAM.PDB	O, L_ALA_147	N, L_GLN_194	H, L_GLN_194	2.78	1.94	10.07

4JAM.PDB	O, L_VAL_202	N, L_VAL_195	H, L_VAL_195	2.79	1.94	8.00
4JAM.PDB	O, L_THR_145	N, L_THR_196	H, L_THR_196	2.89	2.05	11.25
4JAM.PDB	O, L_SER_200	N, L_HIS_197	H, L_HIS_197	2.89	2.06	12.19
4JAM.PDB	O, L_PRO_141	NE2, L_HIS_197	HE2, L_HIS_197	2.88	2.09	19.08
4JAM.PDB	O, L_HIS_197	N, L_SER_200	H, L_SER_200	2.90	2.08	13.58
4JAM.PDB	O, B_THR_201	N, L_THR_201	H, L_THR_201	2.84	2.04	18.18
4JAM.PDB	O, L_VAL_195	N, L_VAL_202	H, L_VAL_202	2.85	2.05	16.95
4JAM.PDB	O, B_GLY_199	N, L_GLU_203	H, L_GLU_203	2.91	2.13	21.03
4JAM.PDB	O, L_CYS_193	N, L_LYS_204	H, L_LYS_204	2.98	2.16	14.76
4JAM.PDB	OG, L_SER_192	OG1, L_THR_205	HG1, L_THR_205	2.80	2.01	12.51
4JAM.PDB	O, L_TYR_191	N, L_VAL_206	H, L_VAL_206	2.94	2.11	11.22
4JAM.PDB	O, A_SER_25	N, A_GLN_3	H, A_GLN_3	2.94	2.10	9.95
4JAM.PDB	O, A_THR_23	N, A_GLN_5	H, A_GLN_5	2.89	2.07	13.60
4JAM.PDB	O, A_THR_21	N, A_SER_7	H, A_SER_7	2.82	2.01	14.85
4JAM.PDB	O, A_SER_110	N, A_VAL_12	H, A_VAL_12	2.99	2.19	18.50
4JAM.PDB	O, A_THR_112	N, A_SER_14	H, A_SER_14	2.90	2.06	9.18
4JAM.PDB	O, A_VAL_82C	N, A_SER_15	H, A_SER_15	2.89	2.08	16.29
4JAM.PDB	O, A_LEU_82	N, A_LEU_18	H, A_LEU_18	2.70	1.88	14.19
4JAM.PDB	O, A_LEU_80	N, A_LEU_20	H, A_LEU_20	2.81	1.98	11.56
4JAM.PDB	O, A_PHE_78	N, A_CYS_22	H, A_CYS_22	2.83	2.07	24.51
4JAM.PDB	O, A_GLN_5	N, A_THR_23	H, A_THR_23	2.83	1.99	10.35
4JAM.PDB	O, A_ASP_76	N, A_VAL_24	H, A_VAL_24	2.78	1.94	10.44
4JAM.PDB	O, A_GLN_3	N, A_SER_25	H, A_SER_25	2.88	2.06	13.90
4JAM.PDB	O, A_LEU_95	N, A_TYR_33	H, A_TYR_33	2.74	1.91	11.80
4JAM.PDB	O, A_ILE_51	N, A_TRP_34	H, A_TRP_34	2.90	2.16	25.25
4JAM.PDB	OE1, A_GLU_75	NE1, A_TRP_34	HE1, A_TRP_34	2.65	1.81	8.69
4JAM.PDB	O, A_ALA_93	N, A_SER_35	H, A_SER_35	2.81	1.97	10.90
4JAM.PDB	O, A_GLY_49	N, A_TRP_36	H, A_TRP_36	2.88	2.06	14.67
4JAM.PDB	O, A_PHE_91	N, A_LEU_37	H, A_LEU_37	2.78	1.96	15.17
4JAM.PDB	O, A_GLU_46	N, A_ARG_38	H, A_ARG_38	2.85	2.04	17.56
4JAM.PDB	OH, A_TYR_90	NH1, A_ARG_38	HH11, A_ARG_38	2.87	2.07	18.01
4JAM.PDB	OD1, A_ASP_86	NH1, A_ARG_38	HH12, A_ARG_38	2.79	1.96	13.17
4JAM.PDB	O, A_VAL_89	N, A_LEU_39	H, A_LEU_39	2.82	2.05	21.84
4JAM.PDB	OG, A_SER_40	N, A_LYS_43	H, A_LYS_43	2.68	1.90	20.68
4JAM.PDB	O, A_SER_40	N, A_GLY_44	H, A_GLY_44	2.72	2.01	28.80
4JAM.PDB	O, A_ARG_38	N, A_GLU_46	H, A_GLU_46	2.77	1.99	21.09
4JAM.PDB	O, A_TRP_36	N, A_ILE_48	H, A_ILE_48	2.90	2.07	12.30
4JAM.PDB	O, A_ASN_58	N, A_TYR_50	H, A_TYR_50	2.95	2.18	21.50
4JAM.PDB	O, A_TRP_34	N, A_ILE_51	H, A_ILE_51	2.90	2.16	25.67
4JAM.PDB	O, A_GLU_56	N, A_PHE_52	H, A_PHE_52	2.91	2.08	12.28
4JAM.PDB	O, A_PHE_52	N, A_GLY_55	H, A_GLY_55	2.79	1.95	9.90
4JAM.PDB	O, A_ILE_48	N, A_SER_60	H, A_SER_60	2.88	2.02	3.37
4JAM.PDB	O, A_SER_60	N, A_LEU_63	H, A_LEU_63	2.89	2.04	9.01
4JAM.PDB	O, A_ARG_82A	NE, A_ARG_66	HE, A_ARG_66	2.88	2.02	3.98
4JAM.PDB	OD2, A_ASP_86	NH2, A_ARG_66	HH22, A_ARG_66	2.34	1.63	27.75
4JAM.PDB	O, A_ARG_81	N, A_SER_68	H, A_SER_68	2.87	2.07	18.65
4JAM.PDB	OH, A_TYR_59	N, A_ILE_69	H, A_ILE_69	2.97	2.13	12.03
4JAM.PDB	O, A_ASP_72	N, A_GLU_75	H, A_GLU_75	2.93	2.09	9.42
4JAM.PDB	O, A_CYS_22	N, A_PHE_78	H, A_PHE_78	2.92	2.13	18.49
4JAM.PDB	O, A_SER_70	N, A_SER_79	H, A_SER_79	2.85	2.07	21.83
4JAM.PDB	O, A_LEU_20	N, A_LEU_80	H, A_LEU_80	2.84	2.00	11.63
4JAM.PDB	O, A_SER_68	N, A_ARG_81	H, A_ARG_81	2.88	2.05	14.04
4JAM.PDB	O, A_LEU_18	N, A_LEU_82	H, A_LEU_82	2.75	1.94	16.17
4JAM.PDB	O, A_ARG_66	N, A_ARG_82A	H, A_ARG_82A	2.95	2.11	11.99
4JAM.PDB	OD2, A_ASP_86	N, A_THR_83	H, A_THR_83	2.96	2.22	25.50
4JAM.PDB	O, A_THR_83	N, A_ASP_86	H, A_ASP_86	2.86	2.09	22.70
4JAM.PDB	O, A_SER_107	N, A_TYR_90	H, A_TYR_90	2.85	2.01	8.55
4JAM.PDB	O, A_LEU_37	N, A_PHE_91	H, A_PHE_91	2.75	1.90	5.20

4JAM.PDB	O, A_SER_35	N, A_ALA_93	H, A_ALA_93	2.93	2.20	27.04
4JAM.PDB	O, A_TYR_33	N, A_LEU_95	H, A_LEU_95	3.00	2.25	25.86
4JAM.PDB	O, A_GLY_31	N, A_ARG_97	H, A_ARG_97	2.91	2.06	7.51
4JAM.PDB	OH, B_TYR_36	N, A_PHE_100E	H, A_PHE_100E	2.90	2.09	16.41
4JAM.PDB	O, A_CYS_92	N, A_GLY_104	H, A_GLY_104	2.77	1.93	10.11
4JAM.PDB	O, A_TYR_90	N, A_SER_107	H, A_SER_107	2.89	2.11	20.38
4JAM.PDB	O, A_SER_7	OG, A_SER_107	HG, A_SER_107	2.54	1.76	15.69
4JAM.PDB	O, A_ALA_88	N, A_VAL_109	H, A_VAL_109	2.91	2.06	7.84
4JAM.PDB	O, A_GLY_10	N, A_SER_110	H, A_SER_110	2.93	2.15	20.41
4JAM.PDB	OG1, A_THR_87	N, A_VAL_111	H, A_VAL_111	2.97	2.12	7.94
4JAM.PDB	O, A_PHE_146	N, A_LYS_117	H, A_LYS_117	2.85	2.02	10.61
4JAM.PDB	O, A_ASP_144	NZ, A_LYS_117	HZ2, A_LYS_117	2.79	1.99	21.27
4JAM.PDB	O, A_LYS_143	N, A_SER_120	H, A_SER_120	2.98	2.15	12.51
4JAM.PDB	O, A_LEU_141	N, A_PHE_122	H, A_PHE_122	2.89	2.06	12.92
4JAM.PDB	O, A_GLY_139	N, A_LEU_124	H, A_LEU_124	2.77	1.92	5.35
4JAM.PDB	O, A_THR_131	N, A_GLY_134	H, A_GLY_134	2.80	2.06	25.22
4JAM.PDB	O, A_VAL_184	N, A_ALA_136	H, A_ALA_136	2.84	2.01	14.16
4JAM.PDB	O, A_LEU_124	N, A_GLY_139	H, A_GLY_139	2.85	2.09	22.70
4JAM.PDB	O, A_SER_180	N, A_CYS_140	H, A_CYS_140	2.87	2.09	20.45
4JAM.PDB	O, A_PHE_122	N, A_LEU_141	H, A_LEU_141	2.78	1.94	10.64
4JAM.PDB	O, A_LEU_178	N, A_VAL_142	H, A_VAL_142	2.76	1.91	7.10
4JAM.PDB	O, A_SER_120	N, A_LYS_143	H, A_LYS_143	2.81	1.96	7.64
4JAM.PDB	O, A_TYR_176	N, A_TYR_145	H, A_TYR_145	2.94	2.13	16.66
4JAM.PDB	O, A_LYS_117	N, A_PHE_146	H, A_PHE_146	2.87	2.06	16.70
4JAM.PDB	O, A_ASN_199	N, A_THR_151	H, A_THR_151	2.95	2.15	18.15
4JAM.PDB	O, A_ASN_197	N, A_SER_153	H, A_SER_153	2.87	2.06	16.36
4JAM.PDB	OG, A_SER_180	NE1, A_TRP_154	HE1, A_TRP_154	2.95	2.10	7.51
4JAM.PDB	O, A_ILE_195	N, A_ASN_155	H, A_ASN_155	2.80	1.97	12.29
4JAM.PDB	O, A_THR_193	ND2, A_ASN_155	HD22, A_ASN_155	2.86	2.05	16.16
4JAM.PDB	OD1, A_ASN_197	N, A_SER_156	H, A_SER_156	2.73	1.93	18.38
4JAM.PDB	O, A_TRP_154	N, A_GLY_157	H, A_GLY_157	2.96	2.18	20.46
4JAM.PDB	O, A_VAL_181	N, A_HIS_164	H, A_HIS_164	2.77	1.93	10.79
4JAM.PDB	O, A_SER_179	N, A_PHE_166	H, A_PHE_166	2.88	2.02	6.82
4JAM.PDB	O, A_SER_177	N, A_VAL_169	H, A_VAL_169	2.89	2.12	22.70
4JAM.PDB	O, A_LEU_175	N, A_GLN_171	H, A_GLN_171	2.93	2.09	10.51
4JAM.PDB	O, A_TYR_145	N, A_TYR_176	H, A_TYR_176	2.79	1.94	7.72
4JAM.PDB	O, A_VAL_142	N, A_LEU_178	H, A_LEU_178	2.85	2.07	20.92
4JAM.PDB	O, A_HIS_164	N, A_VAL_181	H, A_VAL_181	2.86	2.02	11.33
4JAM.PDB	O, A_LEU_138	N, A_VAL_182	H, A_VAL_182	2.71	1.88	13.50
4JAM.PDB	O, A_GLY_162	N, A_THR_183	H, A_THR_183	2.84	2.03	17.10
4JAM.PDB	O, A_ALA_136	N, A_VAL_184	H, A_VAL_184	2.93	2.09	11.23
4JAM.PDB	O, A_PRO_185	N, A_SER_188	H, A_SER_188	2.84	2.02	14.21
4JAM.PDB	O, A_SER_188	N, A_GLN_192	H, A_GLN_192	2.88	2.11	21.94
4JAM.PDB	OD1, A_ASN_155	N, A_ILE_195	H, A_ILE_195	2.80	2.00	18.20
4JAM.PDB	O, A_LYS_209	N, A_CYS_196	H, A_CYS_196	2.93	2.15	20.80
4JAM.PDB	O, A_SER_153	N, A_ASN_197	H, A_ASN_197	2.73	1.88	7.40
4JAM.PDB	OD1, A_ASP_208	ND2, A_ASN_197	HD21, A_ASN_197	2.90	2.10	17.20
4JAM.PDB	O, A_VAL_207	N, A_VAL_198	H, A_VAL_198	2.77	1.91	4.34
4JAM.PDB	O, A_THR_151	N, A_ASN_199	H, A_ASN_199	2.89	2.04	9.44
4JAM.PDB	O, A_THR_205	N, A_HIS_200	H, A_HIS_200	2.91	2.05	2.97
4JAM.PDB	OG, A_SER_203	ND1, A_HIS_200	HD1, A_HIS_200	2.74	1.92	14.00
4JAM.PDB	O, A_PRO_147	NE2, A_HIS_200	HE2, A_HIS_200	2.78	1.94	11.18
4JAM.PDB	O, A_LYS_201	N, A_ASN_204	H, A_ASN_204	2.92	2.09	11.42
4JAM.PDB	O, A_VAL_198	N, A_VAL_207	H, A_VAL_207	2.80	2.00	17.03
4JAM.PDB	O, A_TYR_194	N, A_VAL_211	H, A_VAL_211	2.81	1.96	8.45
4JAM.PDB	O, B_TYR_86	NE2, B_GLN_6	HE22, B_GLN_6	2.90	2.06	9.94
4JAM.PDB	O, B_GLN_103	N, B_VAL_11	H, B_VAL_11	2.89	2.06	12.76
4JAM.PDB	O, B_THR_105	N, B_VAL_13	H, B_VAL_13	2.98	2.16	14.79

4JAM.PDB	OE1, B_GLN_17	N, B_SER_14	H, B_SER_14	2.99	2.15	10.22
4JAM.PDB	O, B_THR_78	N, B_GLY_16	H, B_GLY_16	2.84	2.02	14.85
4JAM.PDB	O, B_ILE_75	N, B_ALA_19	H, B_ALA_19	2.87	2.07	18.88
4JAM.PDB	O, B_LEU_73	N, B_ILE_21	H, B_ILE_21	2.84	2.01	13.27
4JAM.PDB	O, B_ALA_71	N, B_CYS_23	H, B_CYS_23	2.84	2.13	29.21
4JAM.PDB	O, B_THR_5	N, B_SER_24	H, B_SER_24	2.89	2.07	16.00
4JAM.PDB	O, B_SER_69	N, B_ALA_26	H, B_ALA_26	2.97	2.15	14.49
4JAM.PDB	OD1, B_ASN_51	N, B_VAL_33	H, B_VAL_33	2.90	2.09	17.62
4JAM.PDB	O, B_ILE_48	N, B_TRP_35	H, B_TRP_35	2.87	2.06	17.28
4JAM.PDB	O, B_TYR_87	N, B_TYR_36	H, B_TYR_36	2.80	1.98	15.33
4JAM.PDB	O, B_GLU_45	N, B_GLN_37	H, B_GLN_37	2.84	2.00	10.11
4JAM.PDB	O, B_ASP_85	N, B_VAL_38	H, B_VAL_38	2.74	1.98	24.01
4JAM.PDB	O, B_TRP_35	N, B_VAL_47	H, B_VAL_47	2.91	2.08	11.41
4JAM.PDB	O, B_LYS_53	N, B_PHE_49	H, B_PHE_49	2.82	2.00	15.86
4JAM.PDB	O, B_VAL_33	N, B_ASN_51	H, B_ASN_51	2.89	2.05	8.66
4JAM.PDB	O, B_PHE_49	N, B_LYS_53	H, B_LYS_53	2.88	2.08	17.59
4JAM.PDB	OE1, B_GLU_50	NZ, B_LYS_53	HZ1, B_LYS_53	2.75	1.92	17.48
4JAM.PDB	OD2, B_ASP_82	NE, B_ARG_61	HE, B_ARG_61	2.84	2.00	9.73
4JAM.PDB	OD1, B_ASP_82	NH2, B_ARG_61	HH21, B_ARG_61	2.90	2.08	13.97
4JAM.PDB	O, B_THR_74	N, B_SER_63	H, B_SER_63	2.90	2.11	18.40
4JAM.PDB	O, B_THR_72	N, B_SER_65	H, B_SER_65	2.98	2.21	22.62
4JAM.PDB	O, B_GLY_68	NZ, B_LYS_66	HZ2, B_LYS_66	2.76	1.98	23.05
4JAM.PDB	O, B_ALA_26	NZ, B_LYS_66	HZ3, B_LYS_66	2.92	2.09	18.23
4JAM.PDB	O, B_THR_70	N, B_SER_67	H, B_SER_67	2.96	2.13	11.34
4JAM.PDB	O, B_CYS_23	N, B_ALA_71	H, B_ALA_71	2.82	1.99	11.72
4JAM.PDB	O, B_SER_65	N, B_THR_72	H, B_THR_72	2.73	1.91	13.48
4JAM.PDB	O, B_ILE_21	N, B_LEU_73	H, B_LEU_73	2.73	1.91	13.67
4JAM.PDB	O, B_SER_63	N, B_THR_74	H, B_THR_74	2.81	1.96	4.99
4JAM.PDB	O, B_ALA_19	N, B_ILE_75	H, B_ILE_75	2.81	1.98	12.21
4JAM.PDB	O, B_ARG_61	N, B_ARG_76	H, B_ARG_76	2.93	2.11	14.36
4JAM.PDB	O, B_GLN_17	OG1, B_THR_78	HG1, B_THR_78	2.80	2.08	24.26
4JAM.PDB	OD2, B_ASP_82	N, B_GLN_79	H, B_GLN_79	2.86	2.01	7.86
4JAM.PDB	O, B_GLN_79	N, B_ASP_82	H, B_ASP_82	2.76	1.93	12.45
4JAM.PDB	O, B_VAL_38	N, B_ASP_85	H, B_ASP_85	2.95	2.11	9.64
4JAM.PDB	O, B_THR_102	N, B_TYR_86	H, B_TYR_86	2.85	2.02	14.13
4JAM.PDB	O, B_TYR_36	N, B_TYR_87	H, B_TYR_87	2.90	2.10	18.08
4JAM.PDB	O, B_VAL_97	N, B_VAL_90	H, B_VAL_90	2.97	2.14	13.94
4JAM.PDB	O, B_THR_95A	N, B_ASP_92	H, B_ASP_92	2.89	2.11	20.40
4JAM.PDB	OD2, B_ASP_92	N, B_PHE_94	H, B_PHE_94	3.00	2.22	21.54
4JAM.PDB	OD2, B_ASP_92	N, B_SER_95	H, B_SER_95	2.88	2.04	10.50
4JAM.PDB	O, B_CYS_88	N, B_GLY_99	H, B_GLY_99	2.86	2.06	17.89
4JAM.PDB	O, B_TYR_86	N, B_THR_102	H, B_THR_102	2.89	2.09	19.07
4JAM.PDB	O, B_PRO_7	OG1, B_THR_102	HG1, B_THR_102	2.60	1.79	5.95
4JAM.PDB	O, B_PRO_8	N, B_GLN_103	H, B_GLN_103	2.92	2.06	5.49
4JAM.PDB	O, B_ALA_84	N, B_VAL_104	H, B_VAL_104	2.91	2.06	7.09
4JAM.PDB	O, B_VAL_11	N, B_THR_105	H, B_THR_105	2.91	2.10	16.07
4JAM.PDB	OE2, B_GLU_83	N, B_VAL_106	H, B_VAL_106	2.95	2.13	15.31
4JAM.PDB	O, B_VAL_13	N, B_LEU_106A	H, B_LEU_106A	2.82	1.99	13.48
4JAM.PDB	O, B_TYR_140	N, B_ALA_111	H, B_ALA_111	2.90	2.06	11.74
4JAM.PDB	O, B_SER_137	N, B_THR_114	H, B_THR_114	2.85	2.03	14.77
4JAM.PDB	O, B_LEU_135	N, B_THR_116	H, B_THR_116	2.92	2.10	15.29
4JAM.PDB	O, B_VAL_133	N, B_PHE_118	H, B_PHE_118	2.84	2.00	12.03
4JAM.PDB	O, B_SER_122	N, B_GLN_126	H, B_GLN_126	2.94	2.16	20.43
4JAM.PDB	O, B_LEU_125	N, B_ASN_128	H, B_ASN_128	2.88	2.08	18.55
4JAM.PDB	OE2, B_GLU_124	OG1, B_THR_131	HG1, B_THR_131	2.53	1.82	24.30
4JAM.PDB	O, B_LEU_178	N, B_LEU_132	H, B_LEU_132	2.89	2.06	12.17
4JAM.PDB	O, B_SER_176	N, B_CYS_134	H, B_CYS_134	2.78	1.93	7.29
4JAM.PDB	O, B_THR_116	N, B_LEU_135	H, B_LEU_135	2.79	1.95	9.74

4JAM.PDB	O, B_ALA_174	N, B_ILE_136	H, B_ILE_136	2.88	2.07	16.56
4JAM.PDB	O, B_THR_114	N, B_SER_137	H, B_SER_137	2.91	2.10	17.42
4JAM.PDB	OE1, B_GLN_167	N, B_ASP_138	H, B_ASP_138	2.91	2.10	16.41
4JAM.PDB	O, B_ALA_111	N, B_TYR_140	H, B_TYR_140	2.91	2.10	17.01
4JAM.PDB	O, B_PRO_141	N, B_ALA_143	H, B_ALA_143	2.99	2.27	28.43
4JAM.PDB	O, B_THR_196	N, B_THR_145	H, B_THR_145	2.96	2.12	11.72
4JAM.PDB	O, B_GLN_194	N, B_ALA_147	H, B_ALA_147	2.86	2.01	7.10
4JAM.PDB	OG, B_SER_176	NE1, B_TRP_148	HE1, B_TRP_148	2.84	1.99	9.50
4JAM.PDB	O, B_SER_192	N, B_LYS_149	H, B_LYS_149	2.91	2.11	17.98
4JAM.PDB	O, B_SER_153	N, B_ALA_150	H, B_ALA_150	2.77	1.99	21.31
4JAM.PDB	O, B_SER_190	N, B_ASP_151	H, B_ASP_151	2.80	1.95	5.68
4JAM.PDB	O, B_ALA_150	N, B_SER_153	H, B_SER_153	2.93	2.09	10.65
4JAM.PDB	O, B_TRP_148	N, B_VAL_155	H, B_VAL_155	2.88	2.08	19.02
4JAM.PDB	O, B_SER_175	N, B_THR_162	H, B_THR_162	2.91	2.09	13.86
4JAM.PDB	O, B_ALA_173	N, B_SER_165	H, B_SER_165	2.90	2.11	18.23
4JAM.PDB	O, B_LYS_171	N, B_GLN_167	H, B_GLN_167	2.72	1.89	12.32
4JAM.PDB	OD1, B_ASP_138	ND2, B_ASN_169	HD22, B_ASN_169	2.93	2.14	18.27
4JAM.PDB	O, B_GLN_167	N, B_ASN_170	H, B_ASN_170	2.86	2.04	15.66
4JAM.PDB	OD1, B_ASN_169	N, B_LYS_171	H, B_LYS_171	2.94	2.09	7.42
4JAM.PDB	O, B_PHE_139	N, B_TYR_172	H, B_TYR_172	2.86	2.05	16.14
4JAM.PDB	O, B_SER_165	N, B_ALA_173	H, B_ALA_173	2.83	2.03	18.01
4JAM.PDB	O, B_ILE_136	N, B_ALA_174	H, B_ALA_174	2.80	2.00	17.84
4JAM.PDB	OG1, B_THR_162	N, B_SER_175	H, B_SER_175	2.99	2.18	15.84
4JAM.PDB	O, B_CYS_134	N, B_SER_176	H, B_SER_176	2.83	2.04	19.01
4JAM.PDB	O, B_GLU_160	N, B_TYR_177	H, B_TYR_177	2.83	2.05	21.00
4JAM.PDB	O, B_GLY_158	N, B_SER_179	H, B_SER_179	2.85	2.02	11.54
4JAM.PDB	O, B_ALA_130	N, B_LEU_180	H, B_LEU_180	2.95	2.10	4.88
4JAM.PDB	OE1, B_GLN_184	N, B_THR_181	H, B_THR_181	2.84	2.01	11.32
4JAM.PDB	O, B_PRO_182	N, B_LYS_186	H, B_LYS_186	2.96	2.16	18.74
4JAM.PDB	O, B_GLN_184	ND1, B_HIS_188	HD1, B_HIS_188	2.78	1.95	11.73
4JAM.PDB	O, B_VAL_206	N, B_TYR_191	H, B_TYR_191	2.95	2.12	13.13
4JAM.PDB	O, B_LYS_149	N, B_SER_192	H, B_SER_192	2.94	2.14	18.61
4JAM.PDB	O, B_LYS_204	N, B_CYS_193	H, B_CYS_193	2.89	2.12	22.37
4JAM.PDB	O, B_ALA_147	N, B_GLN_194	H, B_GLN_194	2.78	1.93	7.25
4JAM.PDB	O, B_VAL_202	N, B_VAL_195	H, B_VAL_195	2.76	1.91	7.42
4JAM.PDB	O, B_THR_145	N, B_THR_196	H, B_THR_196	2.80	1.97	12.47
4JAM.PDB	O, B_SER_200	N, B_HIS_197	H, B_HIS_197	2.88	2.04	11.03
4JAM.PDB	O, B_ALA_143	ND1, B_HIS_197	HD1, B_HIS_197	2.86	2.07	19.34
4JAM.PDB	O, B_TYR_140	NE2, B_HIS_197	HE2, B_HIS_197	2.99	2.21	20.59
4JAM.PDB	O, L_THR_201	N, B_THR_201	H, B_THR_201	2.77	1.96	16.15
4JAM.PDB	O, B_VAL_195	N, B_VAL_202	H, B_VAL_202	2.88	2.09	18.94
4JAM.PDB	O, L_GLY_199	N, B_GLU_203	H, B_GLU_203	2.79	1.99	17.96
4JAM.PDB	O, B_CYS_193	N, B_LYS_204	H, B_LYS_204	2.99	2.16	13.66
4JAM.PDB	OG, B_SER_192	OG1, B_THR_205	HG1, B_THR_205	2.64	1.83	8.66
4JAM.PDB	O, B_TYR_191	N, B_VAL_206	H, B_VAL_206	2.87	2.04	12.78
4JAN.PDB	O, G_LEU_369	OG1, G_THR_373	HG1, G_THR_373	2.74	1.94	9.78
4JAN.PDB	OD2, G_ASP_457	NE, G_ARG_469	HE, G_ARG_469	2.84	2.10	25.29
4JAN.PDB	O, H_LEU_82	N, H_LEU_18	H, H_LEU_18	2.99	2.15	11.38
4JAN.PDB	O, H_LEU_80	N, H_LEU_20	H, H_LEU_20	2.91	2.08	12.99
4JAN.PDB	O, H_PHE_78	N, H_CYS_22	H, H_CYS_22	2.95	2.11	8.83
4JAN.PDB	O, H_LEU_95	N, H_TYR_33	H, H_TYR_33	2.93	2.08	3.54
4JAN.PDB	O, H_ALA_93	N, H_SER_35	H, H_SER_35	2.92	2.06	5.78
4JAN.PDB	O, H_GLY_49	N, H_TRP_36	H, H_TRP_36	2.83	2.01	15.38
4JAN.PDB	OE1, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.76	1.94	14.56
4JAN.PDB	O, H_GLU_56	N, H_PHE_52	H, H_PHE_52	2.90	2.07	12.88
4JAN.PDB	O, H_ILE_48	N, H_SER_60	H, H_SER_60	2.96	2.18	20.49
4JAN.PDB	O, H_ARG_81	N, H_SER_68	H, H_SER_68	2.97	2.23	25.47
4JAN.PDB	O, H_SER_70	N, H_SER_79	H, H_SER_79	2.76	2.01	24.12

4JAN.PDB	O, H_SER_68	N, H_ARG_81	H, H_ARG_81	2.78	1.96	15.76
4JAN.PDB	O, H_LEU_18	N, H_LEU_82	H, H_LEU_82	2.84	2.03	16.49
4JAN.PDB	O, H_ARG_66	N, H_ARG_82A	H, H_ARG_82A	2.86	2.03	11.31
4JAN.PDB	OD2, H_ASP_86	N, H_THR_83	H, H_THR_83	2.81	2.03	20.96
4JAN.PDB	O, H_LEU_39	N, H_VAL_89	H, H_VAL_89	2.99	2.16	12.27
4JAN.PDB	O, H_LEU_37	N, H_PHE_91	H, H_PHE_91	2.53	1.78	23.52
4JAN.PDB	O, H_SER_35	N, H_ALA_93	H, H_ALA_93	3.00	2.21	20.09
4JAN.PDB	O, H_ARG_101	N, H_SER_94	H, H_SER_94	2.78	1.97	15.85
4JAN.PDB	OH, L_TYR_36	N, H_PHE_100E	H, H_PHE_100E	2.91	2.16	24.28
4JAN.PDB	O, H_GLY_10	N, H_SER_110	H, H_SER_110	2.97	2.13	11.49
4JAN.PDB	OG1, H_THR_87	N, H_VAL_111	H, H_VAL_111	2.78	1.99	19.23
4JAN.PDB	O, H_LYS_143	N, H_SER_120	H, H_SER_120	3.00	2.19	17.41
4JAN.PDB	O, H_GLY_139	N, H_LEU_124	H, H_LEU_124	2.67	1.88	19.71
4JAN.PDB	O, H_SER_180	N, H_CYS_140	H, H_CYS_140	2.89	2.12	21.89
4JAN.PDB	O, H_PHE_122	N, H_LEU_141	H, H_LEU_141	2.69	1.97	27.64
4JAN.PDB	O, H_LEU_178	N, H_VAL_142	H, H_VAL_142	2.93	2.19	25.68
4JAN.PDB	O, H_SER_120	N, H_LYS_143	H, H_LYS_143	2.88	2.07	16.97
4JAN.PDB	OG, H_SER_177	N, H_ASP_144	H, H_ASP_144	2.98	2.22	23.77
4JAN.PDB	O, H_TYR_176	N, H_TYR_145	H, H_TYR_145	2.92	2.12	17.16
4JAN.PDB	O, H_ASN_197	N, H_SER_153	H, H_SER_153	2.94	2.18	23.25
4JAN.PDB	OG, H_SER_180	NE1, H_TRP_154	HE1, H_TRP_154	2.82	2.02	18.56
4JAN.PDB	O, H_ILE_195	N, H_ASN_155	H, H_ASN_155	2.83	2.00	12.78
4JAN.PDB	OD2, B_ASP_92	OG, H_SER_156	HG, H_SER_156	2.50	1.78	23.90
4JAN.PDB	O, H_ASN_155	N, H_ALA_158	H, H_ALA_158	2.83	2.01	13.54
4JAN.PDB	O, H_VAL_181	N, H_HIS_164	H, H_HIS_164	2.84	2.13	28.95
4JAN.PDB	O, H_SER_179	N, H_PHE_166	H, H_PHE_166	2.95	2.11	10.08
4JAN.PDB	O, H_SER_177	N, H_VAL_169	H, H_VAL_169	2.63	1.81	14.24
4JAN.PDB	O, H_LEU_175	N, H_GLN_171	H, H_GLN_171	2.71	1.98	26.37
4JAN.PDB	O, H_GLN_171	N, H_GLY_174	H, H_GLY_174	2.90	2.07	12.23
4JAN.PDB	O, H_TYR_145	N, H_TYR_176	H, H_TYR_176	2.70	1.90	16.76
4JAN.PDB	O, H_TYR_176	OG, H_SER_177	HG, H_SER_177	2.89	2.11	14.84
4JAN.PDB	O, H_VAL_142	N, H_LEU_178	H, H_LEU_178	3.00	2.25	25.78
4JAN.PDB	O, H_LEU_138	N, H_VAL_182	H, H_VAL_182	2.90	2.08	14.87
4JAN.PDB	O, H_ALA_136	N, H_VAL_184	H, H_VAL_184	2.78	2.07	28.36
4JAN.PDB	OD1, H_ASN_155	N, H_ILE_195	H, H_ILE_195	2.84	2.00	11.14
4JAN.PDB	O, H_SER_153	N, H_ASN_197	H, H_ASN_197	2.60	1.74	3.05
4JAN.PDB	O, H_VAL_207	N, H_VAL_198	H, H_VAL_198	2.76	1.92	8.31
4JAN.PDB	O, H_THR_205	N, H_HIS_200	H, H_HIS_200	2.76	1.93	11.54
4JAN.PDB	OG, H_SER_203	ND1, H_HIS_200	HD1, H_HIS_200	2.81	1.96	7.87
4JAN.PDB	O, H_PRO_147	NE2, H_HIS_200	HE2, H_HIS_200	2.77	1.95	14.57
4JAN.PDB	OD1, H_ASN_199	NZ, H_LYS_201	HZ2, H_LYS_201	2.90	2.05	14.58
4JAN.PDB	O, H_LYS_201	N, H_ASN_204	H, H_ASN_204	2.80	1.95	7.81
4JAN.PDB	OE1, L_GLU_123	NZ, H_LYS_209	HZ1, H_LYS_209	2.89	2.13	26.71
4JAN.PDB	O, L_SER_24	N, L_THR_5	H, L_THR_5	2.90	2.04	2.68
4JAN.PDB	OG1, L_THR_102	NE2, L_GLN_6	HE21, L_GLN_6	2.82	2.05	22.18
4JAN.PDB	O, L_THR_5	N, L_SER_24	H, L_SER_24	2.97	2.16	17.64
4JAN.PDB	OD1, H_ASN_100B	ND2, L_ASN_32	HD21, L_ASN_32	2.76	1.91	6.44
4JAN.PDB	OD1, L_ASN_51	N, L_VAL_33	H, L_VAL_33	2.69	1.88	15.86
4JAN.PDB	O, L_ILE_48	N, L_TRP_35	H, L_TRP_35	2.76	1.98	21.52
4JAN.PDB	O, L_TYR_87	N, L_TYR_36	H, L_TYR_36	2.91	2.21	29.89
4JAN.PDB	O, L_GLU_45	N, L_GLN_37	H, L_GLN_37	2.95	2.11	10.30
4JAN.PDB	OH, L_TYR_86	NE2, L_GLN_37	HE21, L_GLN_37	2.95	2.09	6.42
4JAN.PDB	O, L_ASP_85	N, L_VAL_38	H, L_VAL_38	2.79	2.03	23.50
4JAN.PDB	O, L_LYS_53	N, L_PHE_49	H, L_PHE_49	2.88	2.09	19.26
4JAN.PDB	O, L_VAL_33	N, L_ASN_51	H, L_ASN_51	2.69	1.87	15.52
4JAN.PDB	O, L_GLU_50	N, L_TYR_52	H, L_TYR_52	2.84	2.11	27.26
4JAN.PDB	O, L_THR_70	N, L_SER_67	H, L_SER_67	3.00	2.15	8.93
4JAN.PDB	O, L_ILE_21	N, L_LEU_73	H, L_LEU_73	2.82	1.99	12.33

4JAN.PDB	O, L_THR_102	N, L_TYR_86	H, L_TYR_86	2.80	1.98	15.29
4JAN.PDB	O, L_TYR_36	N, L_TYR_87	H, L_TYR_87	2.98	2.17	16.36
4JAN.PDB	OE1, L_GLN_6	N, L_CYS_88	H, L_CYS_88	2.79	1.93	6.67
4JAN.PDB	O, L_CYS_34	N, L_GLN_89	H, L_GLN_89	2.97	2.18	19.32
4JAN.PDB	O, L_VAL_97	N, L_VAL_90	H, L_VAL_90	2.89	2.10	20.39
4JAN.PDB	OD2, L_ASP_92	N, L_PHE_94	H, L_PHE_94	2.63	1.85	20.98
4JAN.PDB	O, L_SER_95	N, L_PHE_96	H, L_PHE_96	2.69	1.97	28.39
4JAN.PDB	O, L_VAL_90	N, L_VAL_97	H, L_VAL_97	2.99	2.15	10.31
4JAN.PDB	O, L_CYS_88	N, L_GLY_99	H, L_GLY_99	2.82	2.06	23.88
4JAN.PDB	O, L_TYR_86	N, L_THR_102	H, L_THR_102	2.93	2.11	14.91
4JAN.PDB	O, L_PRO_7	OG1, L_THR_102	HG1, L_THR_102	2.82	2.04	15.16
4JAN.PDB	O, L_PRO_8	N, L_GLN_103	H, L_GLN_103	2.82	2.06	23.53
4JAN.PDB	O, L_TYR_140	N, L_ALA_111	H, L_ALA_111	2.97	2.14	13.46
4JAN.PDB	O, L_SER_137	N, L_THR_114	H, L_THR_114	2.99	2.13	3.09
4JAN.PDB	O, L_VAL_133	N, L_PHE_118	H, L_PHE_118	2.93	2.14	19.05
4JAN.PDB	O, L_LEU_125	N, L_ASN_128	H, L_ASN_128	2.78	1.96	14.81
4JAN.PDB	O, L_LEU_178	N, L_LEU_132	H, L_LEU_132	2.97	2.12	8.13
4JAN.PDB	O, L_SER_176	N, L_CYS_134	H, L_CYS_134	2.87	2.02	8.60
4JAN.PDB	O, L_THR_116	N, L_LEU_135	H, L_LEU_135	2.88	2.10	20.45
4JAN.PDB	O, L_ALA_174	N, L_ILE_136	H, L_ILE_136	2.97	2.14	12.22
4JAN.PDB	O, L_GLN_194	N, L_ALA_147	H, L_ALA_147	2.83	2.00	13.79
4JAN.PDB	OG, L_SER_176	NE1, L_TRP_148	HE1, L_TRP_148	2.88	2.04	9.05
4JAN.PDB	O, L_SER_192	N, L_LYS_149	H, L_LYS_149	2.99	2.18	15.44
4JAN.PDB	O, L_SER_153	N, L_ALA_150	H, L_ALA_150	2.78	2.08	29.85
4JAN.PDB	O, L_ALA_150	N, L_SER_153	H, L_SER_153	2.82	2.11	29.31
4JAN.PDB	O, L_TYR_177	N, L_GLU_160	H, L_GLU_160	2.87	2.05	14.31
4JAN.PDB	O, L_LYS_171	N, L_GLN_167	H, L_GLN_167	2.85	2.01	10.38
4JAN.PDB	O, L_ILE_136	N, L_ALA_174	H, L_ALA_174	2.73	1.95	20.72
4JAN.PDB	O, L_CYS_134	N, L_SER_176	H, L_SER_176	2.88	2.05	13.75
4JAN.PDB	O, L_GLU_160	N, L_TYR_177	H, L_TYR_177	2.73	1.90	14.38
4JAN.PDB	O, L_GLY_158	N, L_SER_179	H, L_SER_179	2.92	2.09	12.76
4JAN.PDB	O, L_ALA_130	N, L_LEU_180	H, L_LEU_180	2.75	1.90	5.66
4JAN.PDB	O, L_GLN_184	ND1, L_HIS_188	HD1, L_HIS_188	2.96	2.12	10.76
4JAN.PDB	OD1, L_ASP_151	N, L_ARG_189	H, L_ARG_189	3.00	2.16	11.57
4JAN.PDB	O, L_LYS_149	N, L_SER_192	H, L_SER_192	2.84	2.11	26.53
4JAN.PDB	O, L_LYS_204	N, L_CYS_193	H, L_CYS_193	2.87	2.03	10.09
4JAN.PDB	O, L_ALA_147	N, L_GLN_194	H, L_GLN_194	2.87	2.02	4.62
4JAN.PDB	O, L_VAL_202	N, L_VAL_195	H, L_VAL_195	2.90	2.06	10.52
4JAN.PDB	O, L_THR_145	N, L_THR_196	H, L_THR_196	2.87	2.04	12.50
4JAN.PDB	O, L_SER_200	N, L_HIS_197	H, L_HIS_197	2.86	2.00	3.42
4JAN.PDB	O, L_ASP_368	OG1, L_THR_372	HG1, L_THR_372	2.92	2.17	20.42
4JAN.PDB	O, A_THR_21	N, A_SER_7	H, A_SER_7	2.83	1.99	9.81
4JAN.PDB	O, A_THR_112	N, A_SER_14	H, A_SER_14	2.81	2.04	22.68
4JAN.PDB	O, A_LEU_80	N, A_LEU_20	H, A_LEU_20	2.96	2.16	17.44
4JAN.PDB	O, A_PHE_78	N, A_CYS_22	H, A_CYS_22	2.83	1.97	0.81
4JAN.PDB	O, A_GLN_5	N, A_THR_23	H, A_THR_23	2.99	2.16	14.12
4JAN.PDB	O, A_GLN_3	N, A_SER_25	H, A_SER_25	2.86	2.06	18.82
4JAN.PDB	O, A_LEU_95	N, A_TYR_33	H, A_TYR_33	2.88	2.02	1.62
4JAN.PDB	O, A_ILE_51	N, A_TRP_34	H, A_TRP_34	2.83	2.04	18.86
4JAN.PDB	O, A_MET_29	NE1, A_TRP_34	HE1, A_TRP_34	2.96	2.14	15.47
4JAN.PDB	O, A_ALA_93	N, A_SER_35	H, A_SER_35	2.87	2.01	0.65
4JAN.PDB	O, A_GLY_49	N, A_TRP_36	H, A_TRP_36	2.82	2.06	23.18
4JAN.PDB	O, A_GLY_44	N, A_SER_40	H, A_SER_40	2.94	2.14	17.50
4JAN.PDB	O, A_ARG_38	N, A_GLU_46	H, A_GLU_46	2.99	2.17	14.48
4JAN.PDB	O, A_TRP_36	N, A_ILE_48	H, A_ILE_48	2.86	2.04	16.32
4JAN.PDB	O, A_GLU_56	N, A_PHE_52	H, A_PHE_52	2.98	2.16	16.12
4JAN.PDB	O, A_ILE_48	N, A_SER_60	H, A_SER_60	2.99	2.18	16.95
4JAN.PDB	O, A_SER_60	N, A_LEU_63	H, A_LEU_63	2.80	1.99	16.81

4JAN.PDB	O, A_SER_68	N, A_ARG_81	H, A_ARG_81	2.93	2.10	13.34
4JAN.PDB	O, A_LEU_18	N, A_LEU_82	H, A_LEU_82	2.69	1.85	10.39
4JAN.PDB	O, A_GLU_16	N, A_VAL_82C	H, A_VAL_82C	3.00	2.21	20.36
4JAN.PDB	OD2, A_ASP_86	N, A_THR_83	H, A_THR_83	2.88	2.09	19.27
4JAN.PDB	O, A_THR_83	N, A_ASP_86	H, A_ASP_86	2.91	2.07	9.93
4JAN.PDB	O, A_SER_107	N, A_TYR_90	H, A_TYR_90	2.97	2.13	10.15
4JAN.PDB	O, A_LEU_37	N, A_PHE_91	H, A_PHE_91	2.69	1.88	17.21
4JAN.PDB	O, A_ARG_101	N, A_SER_94	H, A_SER_94	2.99	2.21	21.56
4JAN.PDB	OH, B_TYR_36	N, A_PHE_100E	H, A_PHE_100E	2.74	1.90	10.14
4JAN.PDB	OE1, A_GLU_6	N, A_GLY_106	H, A_GLY_106	2.61	1.75	6.59
4JAN.PDB	O, A_TYR_90	N, A_SER_107	H, A_SER_107	2.97	2.13	8.67
4JAN.PDB	O, A_ALA_88	N, A_VAL_109	H, A_VAL_109	2.99	2.18	17.96
4JAN.PDB	O, A_PHE_146	N, A_LYS_117	H, A_LYS_117	2.69	1.91	19.93
4JAN.PDB	O, A_LYS_143	N, A_SER_120	H, A_SER_120	2.98	2.15	12.62
4JAN.PDB	O, A_GLY_139	N, A_LEU_124	H, A_LEU_124	2.71	1.91	18.55
4JAN.PDB	O, A_SER_180	N, A_CYS_140	H, A_CYS_140	2.65	1.92	25.79
4JAN.PDB	O, A_PHE_122	N, A_LEU_141	H, A_LEU_141	2.77	1.98	18.97
4JAN.PDB	O, A_SER_120	N, A_LYS_143	H, A_LYS_143	2.80	1.94	2.87
4JAN.PDB	OG, A_SER_177	N, A_ASP_144	H, A_ASP_144	2.90	2.06	12.00
4JAN.PDB	O, A_LYS_117	N, A_PHE_146	H, A_PHE_146	2.99	2.19	18.95
4JAN.PDB	OG, A_SER_180	NE1, A_TRP_154	HE1, A_TRP_154	2.82	2.05	22.21
4JAN.PDB	O, A_ILE_195	N, A_ASN_155	H, A_ASN_155	2.74	1.91	12.38
4JAN.PDB	O, A_ASN_155	N, A_ALA_158	H, A_ALA_158	2.86	2.02	8.83
4JAN.PDB	O, A_THR_160	N, A_VAL_163	H, A_VAL_163	2.86	2.07	19.66
4JAN.PDB	O, A_VAL_181	N, A_HIS_164	H, A_HIS_164	2.90	2.04	3.65
4JAN.PDB	O, A_SER_177	N, A_VAL_169	H, A_VAL_169	2.73	1.92	17.07
4JAN.PDB	O, A_LEU_175	N, A_GLN_171	H, A_GLN_171	2.97	2.21	23.74
4JAN.PDB	O, A_TYR_145	N, A_TYR_176	H, A_TYR_176	2.83	2.03	16.73
4JAN.PDB	O, A_HIS_164	N, A_VAL_181	H, A_VAL_181	2.91	2.06	6.75
4JAN.PDB	O, A_LEU_138	N, A_VAL_182	H, A_VAL_182	2.71	1.89	15.22
4JAN.PDB	O, A_GLY_162	N, A_THR_183	H, A_THR_183	2.93	2.11	13.23
4JAN.PDB	O, A_SER_153	N, A_ASN_197	H, A_ASN_197	2.67	1.82	8.22
4JAN.PDB	O, A_VAL_207	N, A_VAL_198	H, A_VAL_198	2.88	2.07	16.65
4JAN.PDB	O, A_THR_205	N, A_HIS_200	H, A_HIS_200	2.71	1.87	10.96
4JAN.PDB	O, A_PRO_147	NE2, A_HIS_200	HE2, A_HIS_200	2.55	1.74	15.97
4JAN.PDB	O, A_LYS_201	N, A_ASN_204	H, A_ASN_204	2.88	2.07	15.76
4JAN.PDB	OG, B_SER_100	N, B_GLN_6	H, B_GLN_6	3.00	2.16	10.47
4JAN.PDB	O, B_TYR_86	NE2, B_GLN_6	HE22, B_GLN_6	2.99	2.19	18.54
4JAN.PDB	O, B_LEU_73	N, B_ILE_21	H, B_ILE_21	2.96	2.14	15.25
4JAN.PDB	O, B_SER_69	N, B_GLY_25	H, B_GLY_25	2.72	1.94	20.09
4JAN.PDB	O, I_GLY_458	ND2, B_ASN_32	HD22, B_ASN_32	2.86	2.11	24.85
4JAN.PDB	OD1, B_ASN_51	N, B_VAL_33	H, B_VAL_33	2.78	2.02	23.53
4JAN.PDB	O, B_ILE_48	N, B_TRP_35	H, B_TRP_35	2.62	1.79	12.25
4JAN.PDB	O, B_TYR_87	N, B_TYR_36	H, B_TYR_36	2.76	1.97	19.04
4JAN.PDB	O, B_GLU_45	N, B_GLN_37	H, B_GLN_37	2.98	2.12	6.36
4JAN.PDB	O, B_LYS_39	N, B_GLN_42	H, B_GLN_42	2.91	2.08	12.48
4JAN.PDB	O, B_GLN_37	N, B_GLU_45	H, B_GLU_45	2.95	2.21	25.79
4JAN.PDB	O, B_LYS_53	N, B_PHE_49	H, B_PHE_49	2.84	2.05	19.11
4JAN.PDB	O, B_VAL_33	N, B_ASN_51	H, B_ASN_51	2.74	1.89	7.92
4JAN.PDB	O, B_GLU_50	N, B_TYR_52	H, B_TYR_52	2.69	1.94	24.45
4JAN.PDB	O, B_ILE_58	NH1, B_ARG_54	HH11, B_ARG_54	2.92	2.17	24.41
4JAN.PDB	O, B_SER_65	N, B_THR_72	H, B_THR_72	2.86	2.07	20.13
4JAN.PDB	O, B_ILE_21	N, B_LEU_73	H, B_LEU_73	2.97	2.14	12.90
4JAN.PDB	O, B_SER_63	N, B_THR_74	H, B_THR_74	2.68	1.89	18.45
4JAN.PDB	O, B_ALA_19	N, B_ILE_75	H, B_ILE_75	2.83	1.99	8.89
4JAN.PDB	OD2, B_ASP_82	N, B_GLN_79	H, B_GLN_79	2.99	2.13	4.57
4JAN.PDB	O, B_GLY_77	NE2, B_GLN_79	HE21, B_GLN_79	2.96	2.14	15.90
4JAN.PDB	O, B_GLN_79	N, B_ASP_82	H, B_ASP_82	2.87	2.03	10.85

4JAN.PDB	O, B_THR_102	N, B_TYR_86	H, B_TYR_86	2.79	1.98	17.36
4JAN.PDB	O, B_TYR_36	N, B_TYR_87	H, B_TYR_87	2.95	2.16	19.18
4JAN.PDB	OE1, B_GLN_6	N, B_CYS_88	H, B_CYS_88	2.99	2.13	6.44
4JAN.PDB	O, B_VAL_97	N, B_VAL_90	H, B_VAL_90	2.92	2.10	15.26
4JAN.PDB	O, B_THR_95A	N, B_ASP_92	H, B_ASP_92	2.97	2.19	21.06
4JAN.PDB	OD1, B_ASP_92	N, B_SER_95	H, B_SER_95	2.95	2.11	10.76
4JAN.PDB	O, B_CYS_88	N, B_GLY_99	H, B_GLY_99	2.83	2.06	22.19
4JAN.PDB	O, B_PRO_7	OG1, B_THR_102	HG1, B_THR_102	2.80	2.02	16.54
4JAN.PDB	O, B_ALA_84	N, B_VAL_104	H, B_VAL_104	2.98	2.27	29.44
4JAN.PDB	O, B_SER_137	N, B_THR_114	H, B_THR_114	2.85	2.04	16.89
4JAN.PDB	O, B_LEU_135	N, B_THR_116	H, B_THR_116	2.95	2.14	16.39
4JAN.PDB	O, B_VAL_133	N, B_PHE_118	H, B_PHE_118	2.86	2.07	20.55
4JAN.PDB	O, B_LEU_125	N, B_ASN_128	H, B_ASN_128	2.72	1.91	16.63
4JAN.PDB	O, B_GLU_124	N, B_LYS_129	H, B_LYS_129	2.87	2.08	18.91
4JAN.PDB	OE2, B_GLU_124	OG1, B_THR_131	HG1, B_THR_131	2.64	1.97	29.01
4JAN.PDB	O, B_THR_116	N, B_LEU_135	H, B_LEU_135	2.75	1.97	21.41
4JAN.PDB	O, B_ALA_174	N, B_ILE_136	H, B_ILE_136	2.78	1.97	16.45
4JAN.PDB	OG, B_SER_176	NE1, B_TRP_148	HE1, B_TRP_148	2.83	1.98	7.29
4JAN.PDB	O, B_SER_192	N, B_LYS_149	H, B_LYS_149	2.90	2.11	19.36
4JAN.PDB	O, B_SER_190	N, B_ASP_151	H, B_ASP_151	2.88	2.10	21.97
4JAN.PDB	O, B_TRP_148	N, B_VAL_155	H, B_VAL_155	2.98	2.17	15.79
4JAN.PDB	O, B_SER_175	N, B_THR_162	H, B_THR_162	2.94	2.10	11.27
4JAN.PDB	O, B_ALA_173	N, B_SER_165	H, B_SER_165	2.74	1.89	5.66
4JAN.PDB	O, B_SER_165	N, B_ALA_173	H, B_ALA_173	2.84	2.14	29.64
4JAN.PDB	O, B_ILE_136	N, B_ALA_174	H, B_ALA_174	2.68	1.83	6.81
4JAN.PDB	OG1, B_THR_162	N, B_SER_175	H, B_SER_175	2.88	2.10	20.76
4JAN.PDB	O, B_CYS_134	N, B_SER_176	H, B_SER_176	2.98	2.17	16.97
4JAN.PDB	O, B_GLU_160	N, B_TYR_177	H, B_TYR_177	2.73	1.89	11.82
4JAN.PDB	O, B_GLY_158	N, B_SER_179	H, B_SER_179	2.67	1.83	10.89
4JAN.PDB	O, B_ALA_130	N, B_LEU_180	H, B_LEU_180	2.91	2.07	11.05
4JAN.PDB	O, B_GLN_184	ND1, B_HIS_188	HD1, B_HIS_188	2.88	2.12	24.08
4JAN.PDB	O, B_VAL_206	N, B_TYR_191	H, B_TYR_191	2.91	2.11	18.32
4JAN.PDB	O, B_LYS_149	N, B_SER_192	H, B_SER_192	2.92	2.08	10.84
4JAN.PDB	O, B_LYS_204	N, B_CYS_193	H, B_CYS_193	2.89	2.08	17.27
4JAN.PDB	O, B_THR_145	N, B_THR_196	H, B_THR_196	2.81	1.98	12.47
4JAN.PDB	O, B_TYR_191	N, B_VAL_206	H, B_VAL_206	2.97	2.16	15.65
4KRM.PDB	OG1, A_THR_339	N, A_LYS_311	H, A_LYS_311	2.92	2.20	28.58
4KRM.PDB	O, A_SER_340	N, A_CYS_313	H, A_CYS_313	2.94	2.14	18.43
4KRM.PDB	O, A_PHE_321	N, A_GLY_317	H, A_GLY_317	2.69	1.98	27.87
4KRM.PDB	O, A_ILE_318	N, A_PHE_321	H, A_PHE_321	2.88	2.03	7.40
4KRM.PDB	O, A_ILE_327	OG, A_SER_326	HG, A_SER_326	2.93	2.13	14.37
4KRM.PDB	O, A_HIS_346	N, A_ILE_327	H, A_ILE_327	2.90	2.07	14.21
4KRM.PDB	OD1, A_ASN_331	N, A_ASN_328	H, A_ASN_328	2.99	2.15	12.11
4KRM.PDB	OD1, A_ASN_328	N, A_ASN_331	H, A_ASN_331	2.99	2.22	23.18
4KRM.PDB	O, A_ASN_328	N, A_ILE_332	H, A_ILE_332	2.91	2.20	29.98
4KRM.PDB	O, A_LYS_311	N, A_THR_339	H, A_THR_339	2.88	2.02	6.29
4KRM.PDB	O, A_GLU_376	N, A_ILE_341	H, A_ILE_341	2.94	2.11	11.47
4KRM.PDB	O, A_CYS_313	N, A_SER_342	H, A_SER_342	2.76	1.95	16.34
4KRM.PDB	O, A_LEU_382	N, A_ILE_347	H, A_ILE_347	2.79	1.99	18.25
4KRM.PDB	OG, A_SER_326	N, A_LEU_348	H, A_LEU_348	2.83	2.02	16.65
4KRM.PDB	OE1, B_GLU_110	NH1, A_ARG_353	HH11, A_ARG_353	2.81	2.05	22.81
4KRM.PDB	O, B_GLU_110	NH1, A_ARG_353	HH12, A_ARG_353	2.55	1.85	29.89
4KRM.PDB	O, B_ALA_100	NH2, A_ARG_353	HH21, A_ARG_353	2.89	2.04	4.33
4KRM.PDB	O, A_THR_360	N, A_ASP_355	H, A_ASP_355	2.66	1.81	5.35
4KRM.PDB	OD2, A_ASP_355	OG1, A_THR_358	HG1, A_THR_358	2.65	1.94	26.40
4KRM.PDB	O, A_SER_356	N, A_HIS_359	H, A_HIS_359	2.84	2.01	13.45
4KRM.PDB	O, A_ASP_355	N, A_THR_360	H, A_THR_360	2.91	2.05	3.38
4KRM.PDB	O, A_ALA_351	N, A_LEU_363	H, A_LEU_363	2.79	2.01	20.09

4KRM.PDB	O, A_LEU_368	N, A_LEU_371	H, A_LEU_371	2.89	2.04	5.32
4KRM.PDB	O, A_CYS_338	OG1, A_THR_373	HG1, A_THR_373	2.68	1.93	22.17
4KRM.PDB	O, A_LEU_371	N, A_VAL_374	H, A_VAL_374	2.85	2.00	7.81
4KRM.PDB	O, A_THR_339	N, A_LYS_375	H, A_LYS_375	2.66	1.83	11.99
4KRM.PDB	O, A_ILE_401	N, A_ILE_377	H, A_ILE_377	2.94	2.18	24.17
4KRM.PDB	OD1, A_ASP_344	N, A_PHE_380	H, A_PHE_380	2.98	2.20	21.02
4KRM.PDB	O, A_SER_413	N, A_LEU_381	H, A_LEU_381	2.78	1.97	16.41
4KRM.PDB	O, A_LEU_345	N, A_LEU_382	H, A_LEU_382	2.88	2.02	4.02
4KRM.PDB	O, A_ALA_415	N, A_ILE_383	H, A_ILE_383	2.77	1.92	6.18
4KRM.PDB	O, A_ILE_347	N, A_GLN_384	H, A_GLN_384	2.86	2.00	5.29
4KRM.PDB	O, B_ASP_112	NE2, A_GLN_384	HE22, A_GLN_384	2.93	2.19	25.19
4KRM.PDB	O, A_ASP_392	NE1, A_TRP_386	HE1, A_TRP_386	2.99	2.28	29.76
4KRM.PDB	O, A_LEU_424	N, A_LEU_393	H, A_LEU_393	2.91	2.10	16.43
4KRM.PDB	O, A_LEU_393	N, A_PHE_396	H, A_PHE_396	2.71	1.87	10.13
4KRM.PDB	O, A_HIS_394	N, A_GLU_397	H, A_GLU_397	2.91	2.12	20.07
4KRM.PDB	O, A_LYS_372	ND2, A_ASN_398	HD22, A_ASN_398	2.93	2.13	18.65
4KRM.PDB	O, A_LYS_375	N, A_GLU_400	H, A_GLU_400	2.70	1.87	10.88
4KRM.PDB	O, A_ILE_377	N, A_ARG_403	H, A_ARG_403	2.78	1.94	11.49
4KRM.PDB	OE1, A_GLU_376	NE, A_ARG_403	HE, A_ARG_403	2.51	1.78	27.17
4KRM.PDB	O, A_THR_378	N, A_ARG_405	H, A_ARG_405	2.85	2.00	9.02
4KRM.PDB	OD1, A_ASP_434	NZ, A_LYS_407	HZ1, A_LYS_407	2.92	2.12	20.92
4KRM.PDB	O, A_PHE_412	N, A_GLN_408	H, A_GLN_408	2.63	1.80	13.69
4KRM.PDB	O, A_GLN_408	N, A_GLN_411	H, A_GLN_411	2.82	1.96	5.62
4KRM.PDB	O, A_GLN_408	N, A_PHE_412	H, A_PHE_412	2.94	2.09	8.70
4KRM.PDB	O, A_ASP_436	N, A_SER_413	H, A_SER_413	2.93	2.11	15.55
4KRM.PDB	O, A_LEU_381	N, A_ALA_415	H, A_ALA_415	2.80	1.97	12.88
4KRM.PDB	O, A_ILE_438	N, A_VAL_416	H, A_VAL_416	2.99	2.16	12.80
4KRM.PDB	O, A_ILE_383	N, A_VAL_417	H, A_VAL_417	2.95	2.13	13.97
4KRM.PDB	OD1, A_ASN_442	N, A_LEU_419	H, A_LEU_419	2.76	1.92	9.88
4KRM.PDB	O, A_THR_391	N, A_THR_422	H, A_THR_422	2.81	2.00	16.60
4KRM.PDB	O, A_GLU_400	N, A_LYS_430	H, A_LYS_430	2.90	2.04	3.76
4KRM.PDB	O, A_LEU_456	N, A_ILE_432	H, A_ILE_432	2.57	1.76	16.64
4KRM.PDB	O, A_ILE_402	N, A_SER_433	H, A_SER_433	2.90	2.16	25.97
4KRM.PDB	OE2, A_GLU_431	OG, A_SER_433	HG, A_SER_433	2.82	2.09	25.22
4KRM.PDB	O, A_GLN_411	N, A_ASP_436	H, A_ASP_436	2.93	2.08	7.26
4KRM.PDB	O, A_LYS_465	N, A_ILE_439	H, A_ILE_439	2.96	2.14	14.27
4KRM.PDB	O, A_ASN_442	N, A_LEU_445	H, A_LEU_445	2.98	2.12	2.89
4KRM.PDB	O, A_THR_422	N, A_CYS_446	H, A_CYS_446	2.97	2.11	5.38
4KRM.PDB	O, A_TYR_447	OG1, A_THR_450	HG1, A_THR_450	2.75	1.92	8.55
4KRM.PDB	O, A_TRP_453	N, A_LEU_456	H, A_LEU_456	2.93	2.12	17.80
4KRM.PDB	OE1, A_GLN_462	N, A_GLY_458	H, A_GLY_458	2.69	1.84	7.86
4KRM.PDB	OE1, A_GLN_462	N, A_THR_459	H, A_THR_459	2.99	2.16	12.73
4KRM.PDB	O, A_GLY_435	NE2, A_GLN_462	HE21, A_GLN_462	2.63	1.77	3.27
4KRM.PDB	OD1, A_ASP_436	N, A_LYS_463	H, A_LYS_463	2.91	2.06	8.47
4KRM.PDB	O, A_VAL_437	N, A_LYS_465	H, A_LYS_465	2.78	2.01	22.88
4KRM.PDB	O, A_ILE_439	ND2, A_ASN_469	HD21, A_ASN_469	2.85	2.08	21.76
4KRM.PDB	O, A_GLY_471	N, A_CYS_475	H, A_CYS_475	2.79	2.04	24.90
4KRM.PDB	O, A_GLU_472	N, A_LYS_476	H, A_LYS_476	2.77	1.94	13.13
4KRM.PDB	O, A_ASN_473	N, A_ALA_477	H, A_ALA_477	2.66	1.88	21.43
4KRM.PDB	O, A_HIS_483	N, A_CYS_486	H, A_CYS_486	2.87	2.03	10.18
4KRM.PDB	O, A_SER_501	N, A_SER_487	H, A_SER_487	2.90	2.07	12.52
4KRM.PDB	OG, A_SER_487	N, A_GLU_489	H, A_GLU_489	2.96	2.14	13.27
4KRM.PDB	OG1, A_THR_450	N, A_CYS_491	H, A_CYS_491	2.91	2.10	16.18
4KRM.PDB	O, A_ASP_498	N, A_TRP_492	H, A_TRP_492	2.86	2.05	15.11
4KRM.PDB	O, A_GLU_495	N, A_ASP_498	H, A_ASP_498	2.80	2.03	22.83
4KRM.PDB	O, A_LEU_485	N, A_ARG_503	H, A_ARG_503	2.76	1.90	4.21
4KRM.PDB	O, B_SER_25	N, B_LYS_3	H, B_LYS_3	2.91	2.07	11.33
4KRM.PDB	O, B_ALA_23	N, B_GLU_5	H, B_GLU_5	2.96	2.22	26.70

4KRM.PDB	O, B_THR_21	N, B_SER_7	H, B_SER_7	2.88	2.10	21.31
4KRM.PDB	O, B_THR_121	N, B_VAL_12	H, B_VAL_12	2.77	2.07	29.25
4KRM.PDB	O, B_SER_123	N, B_THR_14	H, B_THR_14	2.68	1.96	28.32
4KRM.PDB	O, B_SER_123	OG1, B_THR_14	HG1, B_THR_14	2.82	1.99	5.72
4KRM.PDB	O, B_LEU_86	N, B_GLY_15	H, B_GLY_15	2.91	2.05	5.95
4KRM.PDB	O, B_GLN_13	N, B_GLY_16	H, B_GLY_16	2.98	2.16	15.73
4KRM.PDB	O, B_MET_83	N, B_LEU_18	H, B_LEU_18	2.71	1.92	20.37
4KRM.PDB	OD1, B_ASP_80	NE, B_ARG_19	HE, B_ARG_19	2.67	1.85	15.03
4KRM.PDB	O, B_SER_7	N, B_THR_21	H, B_THR_21	2.89	2.05	10.43
4KRM.PDB	O, B_VAL_79	N, B_CYS_22	H, B_CYS_22	2.79	2.06	26.42
4KRM.PDB	O, B_GLU_5	N, B_ALA_23	H, B_ALA_23	2.89	2.05	11.71
4KRM.PDB	O, B_LYS_3	N, B_SER_25	H, B_SER_25	2.88	2.12	23.79
4KRM.PDB	O, B_SER_31	NH2, B_ARG_30	HH21, B_ARG_30	2.67	1.86	15.52
4KRM.PDB	O, B_ILE_51	N, B_MET_34	H, B_MET_34	2.89	2.11	20.74
4KRM.PDB	O, B_ALA_97	N, B_GLY_35	H, B_GLY_35	2.89	2.06	13.98
4KRM.PDB	O, B_SER_49	N, B_TRP_36	H, B_TRP_36	2.64	1.81	13.98
4KRM.PDB	O, B_TYR_95	N, B_PHE_37	H, B_PHE_37	2.76	1.91	6.76
4KRM.PDB	O, B_GLU_46	N, B_ARG_38	H, B_ARG_38	2.99	2.20	20.36
4KRM.PDB	OH, B_TYR_94	NH1, B_ARG_38	HH11, B_ARG_38	2.87	2.05	14.24
4KRM.PDB	OD2, B_ASP_90	NH1, B_ARG_38	HH12, B_ARG_38	2.85	2.02	12.95
4KRM.PDB	O, B_ILE_93	N, B_GLN_39	H, B_GLN_39	2.92	2.13	20.36
4KRM.PDB	O, B_ARG_38	N, B_GLU_46	H, B_GLU_46	2.95	2.11	11.02
4KRM.PDB	O, B_TRP_36	N, B_VAL_48	H, B_VAL_48	2.79	1.99	17.02
4KRM.PDB	O, B_GLY_59	OG, B_SER_49	HG, B_SER_49	3.00	2.27	25.42
4KRM.PDB	O, B_GLY_59	N, B_GLY_50	H, B_GLY_50	2.98	2.19	19.85
4KRM.PDB	O, B_MET_34	N, B_ILE_51	H, B_ILE_51	2.75	1.95	18.18
4KRM.PDB	O, B_SER_57	N, B_SER_52	H, B_SER_52	2.88	2.11	21.64
4KRM.PDB	O, B_SER_102	N, B_TRP_53	H, B_TRP_53	2.88	2.06	15.16
4KRM.PDB	O, C_LYS_310	N, B_THR_58	H, B_THR_58	2.99	2.17	13.91
4KRM.PDB	O, B_GLY_50	N, B_GLY_59	H, B_GLY_59	2.89	2.09	18.08
4KRM.PDB	O, C_GLU_308	N, B_TYR_60	H, B_TYR_60	2.75	1.96	19.67
4KRM.PDB	O, B_VAL_48	N, B_ALA_61	H, B_ALA_61	2.97	2.14	11.48
4KRM.PDB	O, B_GLN_82	N, B_THR_69	H, B_THR_69	2.86	2.07	20.15
4KRM.PDB	OH, B_TYR_60	N, B_ILE_70	H, B_ILE_70	2.77	1.93	11.16
4KRM.PDB	O, B_TYR_32	NH1, B_ARG_72	HH12, B_ARG_72	2.74	1.92	15.98
4KRM.PDB	O, B_THR_78	N, B_ASP_73	H, B_ASP_73	2.94	2.13	15.69
4KRM.PDB	O, B_TRP_53	ND2, B_ASN_74	HD21, B_ASN_74	2.77	1.97	18.80
4KRM.PDB	OD2, B_ASP_73	N, B_LYS_76	H, B_LYS_76	2.99	2.16	13.15
4KRM.PDB	O, B_CYS_22	N, B_VAL_79	H, B_VAL_79	2.99	2.26	27.32
4KRM.PDB	O, B_SER_71	N, B_ASP_80	H, B_ASP_80	2.86	2.11	25.20
4KRM.PDB	O, B_LEU_20	N, B_LEU_81	H, B_LEU_81	2.80	1.98	15.20
4KRM.PDB	O, B_THR_69	N, B_GLN_82	H, B_GLN_82	2.74	1.94	17.70
4KRM.PDB	O, B_LEU_18	N, B_MET_83	H, B_MET_83	2.77	1.93	11.70
4KRM.PDB	OD1, B_ASP_90	N, B_LYS_87	H, B_LYS_87	2.76	1.93	11.52
4KRM.PDB	O, B_LYS_87	N, B_ASP_90	H, B_ASP_90	2.96	2.12	11.27
4KRM.PDB	O, B_THR_118	N, B_TYR_94	H, B_TYR_94	2.77	1.94	12.66
4KRM.PDB	O, B_ASP_90	OH, B_TYR_94	HH, B_TYR_94	2.84	2.02	10.29
4KRM.PDB	O, B_PHE_37	N, B_TYR_95	H, B_TYR_95	2.82	2.03	20.26
4KRM.PDB	OE2, B_GLU_6	N, B_CYS_96	H, B_CYS_96	2.72	1.87	8.28
4KRM.PDB	O, B_GLY_35	N, B_ALA_97	H, B_ALA_97	2.96	2.23	26.81
4KRM.PDB	O, B_TYR_113	N, B_ALA_98	H, B_ALA_98	2.91	2.10	17.25
4KRM.PDB	O, B_GLY_33	N, B_ALA_99	H, B_ALA_99	2.85	2.03	15.87
4KRM.PDB	OD2, B_ASP_112	N, B_ALA_100	H, B_ALA_100	2.80	1.99	16.77
4KRM.PDB	OH, B_TYR_111	N, B_TYR_105	H, B_TYR_105	2.90	2.06	10.42
4KRM.PDB	O, B_TYR_105	OH, B_TYR_111	HH, B_TYR_111	2.48	1.64	3.96
4KRM.PDB	O, B_ALA_98	N, B_ASP_112	H, B_ASP_112	2.84	2.11	26.99
4KRM.PDB	O, B_CYS_96	N, B_GLY_115	H, B_GLY_115	2.90	2.14	23.95
4KRM.PDB	OE1, B_GLU_6	N, B_GLY_117	H, B_GLY_117	2.78	1.97	15.53

4KRM.PDB	O, B_ALA_92	N, B_VAL_120	H, B_VAL_120	2.95	2.13	14.97
4KRM.PDB	O, B_GLY_10	N, B_THR_121	H, B_THR_121	2.89	2.05	10.22
4KRM.PDB	O, B_VAL_12	N, B_SER_123	H, B_SER_123	2.95	2.12	14.13
4KRM.PDB	O, B_TYR_60	N, C_GLU_308	H, C_GLU_308	2.91	2.19	28.33
4KRM.PDB	O, B_THR_58	N, C_LYS_310	H, C_LYS_310	2.88	2.06	14.23
4KRM.PDB	OG1, C_THR_339	N, C_LYS_311	H, C_LYS_311	2.77	2.04	26.62
4KRM.PDB	O, B_ASP_56	N, C_VAL_312	H, C_VAL_312	2.73	1.89	9.64
4KRM.PDB	O, C_SER_340	N, C_CYS_313	H, C_CYS_313	2.90	2.07	13.28
4KRM.PDB	O, C_PHE_321	N, C_GLY_317	H, C_GLY_317	2.70	1.87	11.98
4KRM.PDB	OD1, C_ASN_331	N, C_ASN_328	H, C_ASN_328	2.83	1.99	10.78
4KRM.PDB	O, C_ASN_328	N, C_ILE_332	H, C_ILE_332	3.00	2.27	27.38
4KRM.PDB	O, C_ILE_332	N, C_PHE_335	H, C_PHE_335	2.93	2.08	7.41
4KRM.PDB	O, C_LYS_311	N, C_THR_339	H, C_THR_339	2.74	1.92	14.57
4KRM.PDB	O, C_GLU_376	N, C_ILE_341	H, C_ILE_341	2.82	2.00	14.90
4KRM.PDB	O, C_CYS_313	N, C_SER_342	H, C_SER_342	2.83	2.04	19.53
4KRM.PDB	OG1, C_THR_378	N, C_GLY_343	H, C_GLY_343	2.77	2.01	23.25
4KRM.PDB	O, C_LEU_382	N, C_ILE_347	H, C_ILE_347	2.86	2.08	21.12
4KRM.PDB	O, C_LEU_348	N, C_ALA_351	H, C_ALA_351	2.96	2.12	10.17
4KRM.PDB	OE1, D_GLU_110	NH1, C_ARG_353	HH11, C_ARG_353	2.87	2.05	16.15
4KRM.PDB	O, D_ALA_100	NH2, C_ARG_353	HH21, C_ARG_353	2.80	2.00	16.96
4KRM.PDB	O, C_VAL_350	N, C_GLY_354	H, C_GLY_354	2.77	2.02	24.08
4KRM.PDB	O, C_THR_360	N, C_ASP_355	H, C_ASP_355	2.65	1.83	13.88
4KRM.PDB	OD2, C_ASP_355	OG1, C_THR_358	HG1, C_THR_358	2.75	2.00	22.12
4KRM.PDB	O, C_SER_356	N, C_HIS_359	H, C_HIS_359	2.67	1.84	12.90
4KRM.PDB	O, C_ASP_355	N, C_THR_360	H, C_THR_360	2.84	1.99	7.14
4KRM.PDB	O, C_ALA_351	N, C_LEU_363	H, C_LEU_363	2.78	2.07	28.76
4KRM.PDB	O, C_ASP_364	N, C_GLU_367	H, C_GLU_367	2.87	2.07	17.30
4KRM.PDB	O, C_CYS_338	OG1, C_THR_373	HG1, C_THR_373	2.60	1.90	27.53
4KRM.PDB	O, C_LEU_371	N, C_VAL_374	H, C_VAL_374	3.00	2.15	9.63
4KRM.PDB	O, C_THR_339	N, C_LYS_375	H, C_LYS_375	2.73	1.87	2.04
4KRM.PDB	O, C_ILE_401	N, C_ILE_377	H, C_ILE_377	2.94	2.12	15.55
4KRM.PDB	O, C_ILE_341	N, C_THR_378	H, C_THR_378	2.99	2.14	8.37
4KRM.PDB	O, C_GLY_343	N, C_GLY_379	H, C_GLY_379	2.96	2.24	28.09
4KRM.PDB	OD1, C_ASP_344	N, C_PHE_380	H, C_PHE_380	2.87	2.06	16.59
4KRM.PDB	O, C_SER_413	N, C_LEU_381	H, C_LEU_381	2.85	2.05	18.05
4KRM.PDB	O, C_LEU_345	N, C_LEU_382	H, C_LEU_382	2.85	2.00	6.50
4KRM.PDB	O, C_ALA_415	N, C_ILE_383	H, C_ILE_383	2.86	2.06	18.11
4KRM.PDB	O, C_ILE_347	N, C_GLN_384	H, C_GLN_384	2.79	2.00	19.39
4KRM.PDB	O, C_ASP_392	NE1, C_TRP_386	HE1, C_TRP_386	2.82	2.06	23.80
4KRM.PDB	O, C_LEU_424	N, C_LEU_393	H, C_LEU_393	2.90	2.09	16.80
4KRM.PDB	O, C_LEU_393	N, C_PHE_396	H, C_PHE_396	2.95	2.11	10.22
4KRM.PDB	O, C_HIS_394	N, C_GLU_397	H, C_GLU_397	2.85	2.06	19.79
4KRM.PDB	O, C_LYS_372	ND2, C_ASN_398	HD22, C_ASN_398	2.65	1.81	9.39
4KRM.PDB	O, C_LYS_375	N, C_GLU_400	H, C_GLU_400	2.97	2.13	10.86
4KRM.PDB	O, C_GLU_431	N, C_ILE_402	H, C_ILE_402	2.98	2.16	15.59
4KRM.PDB	O, C_ILE_377	N, C_ARG_403	H, C_ARG_403	2.88	2.07	17.91
4KRM.PDB	OE1, C_GLU_376	NH1, C_ARG_403	HH11, C_ARG_403	3.00	2.18	16.51
4KRM.PDB	O, C_THR_378	N, C_ARG_405	H, C_ARG_405	2.81	1.97	9.73
4KRM.PDB	O, C_PHE_412	N, C_GLN_408	H, C_GLN_408	2.69	1.89	18.44
4KRM.PDB	O, C_GLN_408	N, C_GLN_411	H, C_GLN_411	2.85	2.01	8.79
4KRM.PDB	O, C_GLN_408	N, C_PHE_412	H, C_PHE_412	2.93	2.08	8.35
4KRM.PDB	O, C_ASP_436	N, C_SER_413	H, C_SER_413	2.81	1.98	12.74
4KRM.PDB	O, C_LEU_381	N, C_ALA_415	H, C_ALA_415	2.86	2.01	6.79
4KRM.PDB	O, C_ILE_438	N, C_VAL_416	H, C_VAL_416	2.91	2.08	11.96
4KRM.PDB	OD1, C_ASN_442	N, C_LEU_419	H, C_LEU_419	2.87	2.05	14.54
4KRM.PDB	O, C_THR_391	N, C_THR_422	H, C_THR_422	2.92	2.14	20.64
4KRM.PDB	OD1, C_ASP_498	NH2, C_ARG_427	HH21, C_ARG_427	2.43	1.69	25.29
4KRM.PDB	O, C_GLU_400	N, C_LYS_430	H, C_LYS_430	2.87	2.01	1.36

4KRM.PDB	O, C_LEU_456	N, C_ILE_432	H, C_ILE_432	2.84	1.99	8.13
4KRM.PDB	O, C_ILE_402	N, C_SER_433	H, C_SER_433	2.88	2.13	25.53
4KRM.PDB	OE2, C_GLU_431	OG, C_SER_433	HG, C_SER_433	2.86	2.06	14.79
4KRM.PDB	O, C_GLN_411	N, C_ASP_436	H, C_ASP_436	2.86	2.00	4.00
4KRM.PDB	O, C_LEU_414	N, C_ILE_438	H, C_ILE_438	2.90	2.08	13.19
4KRM.PDB	O, C_LYS_465	N, C_ILE_439	H, C_ILE_439	2.99	2.17	14.81
4KRM.PDB	OD1, C_ASN_469	N, C_ASN_442	H, C_ASN_442	2.74	1.97	21.04
4KRM.PDB	O, C_ASN_442	N, C_LEU_445	H, C_LEU_445	2.89	2.04	5.71
4KRM.PDB	O, C_TYR_447	N, C_THR_450	H, C_THR_450	2.94	2.09	7.41
4KRM.PDB	O, C_TYR_447	OG1, C_THR_450	HG1, C_THR_450	2.78	1.97	12.32
4KRM.PDB	OE1, C_GLU_489	NZ, C_LYS_455	HZ2, C_LYS_455	2.73	1.95	24.04
4KRM.PDB	O, C_TRP_453	N, C_LEU_456	H, C_LEU_456	2.87	2.15	27.86
4KRM.PDB	OE1, C_GLN_462	N, C_THR_459	H, C_THR_459	2.63	1.78	3.39
4KRM.PDB	O, C_SER_433	OG1, C_THR_459	HG1, C_THR_459	2.93	2.13	15.18
4KRM.PDB	O, C_GLY_435	NE2, C_GLN_462	HE21, C_GLN_462	2.88	2.03	7.30
4KRM.PDB	O, C_ILE_432	NE2, C_GLN_462	HE22, C_GLN_462	2.87	2.04	12.71
4KRM.PDB	OD1, C_ASP_436	N, C_LYS_463	H, C_LYS_463	2.83	1.97	7.15
4KRM.PDB	O, C_VAL_437	N, C_LYS_465	H, C_LYS_465	2.86	2.07	19.53
4KRM.PDB	O, C_ILE_439	ND2, C_ASN_469	HD21, C_ASN_469	2.82	2.06	23.01
4KRM.PDB	O, C_GLY_471	N, C_CYS_475	H, C_CYS_475	2.80	1.97	13.89
4KRM.PDB	O, C_GLU_472	N, C_LYS_476	H, C_LYS_476	2.76	1.96	18.66
4KRM.PDB	O, C_SER_501	N, C_SER_487	H, C_SER_487	2.90	2.08	13.40
4KRM.PDB	O, C_ASP_498	N, C_TRP_492	H, C_TRP_492	2.81	1.98	12.84
4KRM.PDB	O, C_PRO_496	N, C_CYS_499	H, C_CYS_499	2.91	2.08	13.02
4KRM.PDB	O, C_ALA_484	NE, C_ARG_503	HE, C_ARG_503	2.52	1.76	22.72
4KRM.PDB	O, D_SER_25	N, D_LYS_3	H, D_LYS_3	2.82	1.97	7.73
4KRM.PDB	O, D_ALA_23	N, D_GLU_5	H, D_GLU_5	2.92	2.10	13.79
4KRM.PDB	O, D_THR_121	N, D_VAL_12	H, D_VAL_12	2.95	2.18	23.16
4KRM.PDB	O, D_LEU_86	N, D_GLY_15	H, D_GLY_15	2.70	1.87	11.51
4KRM.PDB	O, D_GLN_13	N, D_GLY_16	H, D_GLY_16	2.72	1.98	26.19
4KRM.PDB	O, D_MET_83	N, D_LEU_18	H, D_LEU_18	3.00	2.20	18.58
4KRM.PDB	OE1, D_GLN_82	NH1, D_ARG_19	HH11, D_ARG_19	2.94	2.12	14.24
4KRM.PDB	O, D_LEU_81	N, D_LEU_20	H, D_LEU_20	2.98	2.19	20.30
4KRM.PDB	O, D_SER_7	N, D_THR_21	H, D_THR_21	2.83	1.99	11.71
4KRM.PDB	O, D_VAL_79	N, D_CYS_22	H, D_CYS_22	2.91	2.16	23.74
4KRM.PDB	O, D_GLU_5	N, D_ALA_23	H, D_ALA_23	2.86	2.02	10.32
4KRM.PDB	O, D_LYS_3	N, D_SER_25	H, D_SER_25	2.93	2.11	14.36
4KRM.PDB	OD2, C_ASP_355	NH1, D_ARG_30	HH12, D_ARG_30	2.45	1.63	13.53
4KRM.PDB	O, D_ALA_99	N, D_GLY_33	H, D_GLY_33	2.93	2.16	22.74
4KRM.PDB	O, D_ALA_97	N, D_GLY_35	H, D_GLY_35	2.86	2.06	17.94
4KRM.PDB	O, D_SER_49	N, D_TRP_36	H, D_TRP_36	2.77	1.94	12.95
4KRM.PDB	O, D_TYR_95	N, D_PHE_37	H, D_PHE_37	2.83	2.00	11.67
4KRM.PDB	O, D_GLU_46	N, D_ARG_38	H, D_ARG_38	2.89	2.09	17.91
4KRM.PDB	OE1, D_GLU_46	NE, D_ARG_38	HE, D_ARG_38	2.79	1.96	12.48
4KRM.PDB	O, D_ILE_93	N, D_GLN_39	H, D_GLN_39	2.91	2.12	19.63
4KRM.PDB	O, D_ARG_38	N, D_GLU_46	H, D_GLU_46	2.85	2.02	11.19
4KRM.PDB	O, D_TRP_36	N, D_VAL_48	H, D_VAL_48	2.93	2.16	21.89
4KRM.PDB	O, D_GLY_59	OG, D_SER_49	HG, D_SER_49	2.87	2.17	28.65
4KRM.PDB	O, D_GLY_59	N, D_GLY_50	H, D_GLY_50	2.97	2.17	17.64
4KRM.PDB	O, D_MET_34	N, D_ILE_51	H, D_ILE_51	2.91	2.12	20.05
4KRM.PDB	O, D_SER_102	N, D_TRP_53	H, D_TRP_53	2.83	2.01	14.56
4KRM.PDB	O, D_GLY_50	N, D_GLY_59	H, D_GLY_59	2.80	2.03	22.40
4KRM.PDB	O, E_GLU_308	N, D_TYR_60	H, D_TYR_60	2.82	2.08	26.84
4KRM.PDB	O, D_VAL_48	N, D_ALA_61	H, D_ALA_61	2.93	2.14	18.86
4KRM.PDB	O, D_GLN_82	N, D_THR_69	H, D_THR_69	2.93	2.16	22.84
4KRM.PDB	OH, D_TYR_60	N, D_ILE_70	H, D_ILE_70	2.85	2.02	13.28
4KRM.PDB	O, D_TYR_32	NH2, D_ARG_72	HH22, D_ARG_72	2.68	1.86	14.70
4KRM.PDB	O, D_TRP_53	ND2, D_ASN_74	HD21, D_ASN_74	2.93	2.13	17.25

4KRM.PDB	O, D_SER_71	N, D_ASP_80	H, D_ASP_80	2.68	1.90	20.52
4KRM.PDB	O, D_LEU_20	N, D_LEU_81	H, D_LEU_81	2.87	2.07	19.11
4KRM.PDB	O, D_THR_69	N, D_GLN_82	H, D_GLN_82	2.77	1.93	7.52
4KRM.PDB	O, D_LEU_18	N, D_MET_83	H, D_MET_83	2.74	1.89	9.04
4KRM.PDB	OD1, D_ASP_90	N, D_LYS_87	H, D_LYS_87	2.86	2.02	10.59
4KRM.PDB	O, D_THR_118	N, D_TYR_94	H, D_TYR_94	2.80	1.95	8.02
4KRM.PDB	O, D_ASP_90	OH, D_TYR_94	HH, D_TYR_94	2.74	1.90	2.03
4KRM.PDB	O, D_PHE_37	N, D_TYR_95	H, D_TYR_95	2.75	1.94	16.71
4KRM.PDB	OE2, D_GLU_6	N, D_CYS_96	H, D_CYS_96	2.74	1.90	11.31
4KRM.PDB	O, D_TYR_113	N, D_ALA_98	H, D_ALA_98	2.88	2.08	18.17
4KRM.PDB	O, D_GLY_33	N, D_ALA_99	H, D_ALA_99	2.73	1.90	13.15
4KRM.PDB	OD2, D_ASP_112	N, D_ALA_100	H, D_ALA_100	2.90	2.08	15.09
4KRM.PDB	O, D_SER_31	N, D_GLY_101	H, D_GLY_101	2.79	1.93	3.06
4KRM.PDB	O, D_TYR_105	OH, D_TYR_111	HH, D_TYR_111	2.68	1.86	10.32
4KRM.PDB	O, D_ALA_98	N, D_ASP_112	H, D_ASP_112	2.84	2.03	16.97
4KRM.PDB	O, D_ALA_92	N, D_VAL_120	H, D_VAL_120	2.94	2.12	14.83
4KRM.PDB	O, D_GLY_10	N, D_THR_121	H, D_THR_121	2.87	2.04	11.88
4KRM.PDB	OG1, D_THR_91	N, D_VAL_122	H, D_VAL_122	2.88	2.06	14.21
4KRM.PDB	O, D_THR_58	N, E_LYS_310	H, E_LYS_310	2.79	2.02	22.01
4KRM.PDB	O, E_SER_340	N, E_CYS_313	H, E_CYS_313	2.94	2.14	19.13
4KRM.PDB	O, E_PHE_321	N, E_GLY_317	H, E_GLY_317	2.77	1.95	14.36
4KRM.PDB	O, E_GLY_319	N, E_LYS_322	H, E_LYS_322	2.82	2.09	27.17
4KRM.PDB	O, E_ILE_327	OG, E_SER_326	HG, E_SER_326	2.91	2.09	10.66
4KRM.PDB	O, E_HIS_346	N, E_ILE_327	H, E_ILE_327	2.96	2.13	12.07
4KRM.PDB	OD1, E_ASN_331	N, E_ASN_328	H, E_ASN_328	2.92	2.08	11.06
4KRM.PDB	OD1, E_ASN_328	N, E_ASN_331	H, E_ASN_331	2.76	1.96	17.47
4KRM.PDB	O, E_LYS_311	N, E_THR_339	H, E_THR_339	2.88	2.04	8.53
4KRM.PDB	O, E_GLU_376	N, E_ILE_341	H, E_ILE_341	2.83	1.99	10.53
4KRM.PDB	O, E_CYS_313	N, E_SER_342	H, E_SER_342	2.81	2.01	18.67
4KRM.PDB	OG1, E_THR_378	N, E_GLY_343	H, E_GLY_343	2.67	1.96	28.18
4KRM.PDB	O, E_PHE_380	N, E_LEU_345	H, E_LEU_345	2.98	2.16	13.52
4KRM.PDB	O, E_LEU_382	N, E_ILE_347	H, E_ILE_347	2.93	2.15	21.34
4KRM.PDB	OG, E_SER_326	N, E_LEU_348	H, E_LEU_348	2.89	2.06	13.76
4KRM.PDB	O, E_LEU_348	N, E_ALA_351	H, E_ALA_351	2.93	2.15	20.83
4KRM.PDB	O, E_PRO_349	N, E_ARG_353	H, E_ARG_353	2.97	2.21	24.57
4KRM.PDB	OE1, F_GLU_110	NH1, E_ARG_353	HH11, E_ARG_353	2.85	2.03	14.34
4KRM.PDB	O, F_GLU_110	NH1, E_ARG_353	HH12, E_ARG_353	2.46	1.72	24.77
4KRM.PDB	O, F_ALA_100	NH2, E_ARG_353	HH21, E_ARG_353	2.81	1.99	15.85
4KRM.PDB	OD2, F_ASP_112	NH2, E_ARG_353	HH22, E_ARG_353	2.96	2.18	20.33
4KRM.PDB	O, E_VAL_350	N, E_GLY_354	H, E_GLY_354	2.78	1.95	14.18
4KRM.PDB	O, E_THR_360	N, E_ASP_355	H, E_ASP_355	2.77	1.92	5.02
4KRM.PDB	OD2, E_ASP_355	OG1, E_THR_358	HG1, E_THR_358	2.55	1.85	27.90
4KRM.PDB	O, E_SER_356	N, E_HIS_359	H, E_HIS_359	2.96	2.14	15.14
4KRM.PDB	O, E_ASP_355	N, E_THR_360	H, E_THR_360	2.89	2.04	8.71
4KRM.PDB	O, E_LEU_368	N, E_LEU_371	H, E_LEU_371	2.96	2.11	6.62
4KRM.PDB	O, E_CYS_338	OG1, E_THR_373	HG1, E_THR_373	2.65	1.89	21.62
4KRM.PDB	O, E_LEU_371	N, E_VAL_374	H, E_VAL_374	2.87	2.03	11.52
4KRM.PDB	O, E_THR_339	N, E_LYS_375	H, E_LYS_375	2.80	1.95	3.65
4KRM.PDB	O, E_ILE_341	N, E_THR_378	H, E_THR_378	2.99	2.16	11.77
4KRM.PDB	O, E_GLY_343	N, E_GLY_379	H, E_GLY_379	2.96	2.26	29.80
4KRM.PDB	O, E_SER_413	N, E_LEU_381	H, E_LEU_381	2.89	2.08	16.67
4KRM.PDB	O, E_LEU_345	N, E_LEU_382	H, E_LEU_382	2.95	2.10	8.54
4KRM.PDB	O, E_ALA_415	N, E_ILE_383	H, E_ILE_383	2.79	1.94	5.21
4KRM.PDB	O, F_ASP_112	NE2, E_GLN_384	HE22, E_GLN_384	2.82	2.10	28.13
4KRM.PDB	O, E_LEU_424	N, E_LEU_393	H, E_LEU_393	2.88	2.06	14.51
4KRM.PDB	O, E_LEU_393	N, E_PHE_396	H, E_PHE_396	2.99	2.16	13.86
4KRM.PDB	O, E_HIS_394	N, E_GLU_397	H, E_GLU_397	2.82	2.04	20.64
4KRM.PDB	O, E_LYS_372	ND2, E_ASN_398	HD22, E_ASN_398	2.92	2.11	15.20

4KRM.PDB	O, E.LYS.375	N, E.GLU.400	H, E.GLU.400	2.81	1.96	8.49
4KRM.PDB	O, E.ILE.377	N, E.ARG.403	H, E.ARG.403	2.94	2.11	13.50
4KRM.PDB	O, E.THR.378	N, E.ARG.405	H, E.ARG.405	2.98	2.15	12.71
4KRM.PDB	OD1, E.ASP.434	NZ, E.LYS.407	HZ1, E.LYS.407	2.65	1.88	23.95
4KRM.PDB	O, E.PHE.412	N, E.GLN.408	H, E.GLN.408	2.79	1.99	17.99
4KRM.PDB	O, E.LYS.407	N, E.GLY.410	H, E.GLY.410	2.97	2.18	18.85
4KRM.PDB	O, E.GLN.408	N, E.GLN.411	H, E.GLN.411	2.93	2.08	6.71
4KRM.PDB	O, E.ASP.436	N, E.SER.413	H, E.SER.413	2.91	2.10	16.30
4KRM.PDB	O, E.LEU.381	N, E.ALA.415	H, E.ALA.415	2.85	2.12	26.97
4KRM.PDB	O, E.ILE.383	N, E.VAL.417	H, E.VAL.417	2.90	2.05	7.33
4KRM.PDB	O, E.SER.440	N, E.SER.418	H, E.SER.418	2.92	2.12	18.48
4KRM.PDB	OD1, E.ASN.442	N, E.LEU.419	H, E.LEU.419	2.67	1.86	14.59
4KRM.PDB	O, E.THR.391	N, E.THR.422	H, E.THR.422	2.80	2.00	17.36
4KRM.PDB	O, E.LEU.456	N, E.ILE.432	H, E.ILE.432	2.68	1.84	9.53
4KRM.PDB	O, E.ILE.402	N, E.SER.433	H, E.SER.433	2.93	2.19	25.97
4KRM.PDB	OE2, E.GLU.431	OG, E.SER.433	HG, E.SER.433	2.91	2.17	23.57
4KRM.PDB	O, E.GLN.411	N, E.ASP.436	H, E.ASP.436	2.85	1.99	3.30
4KRM.PDB	O, E.LYS.465	N, E.ILE.439	H, E.ILE.439	2.87	2.04	13.60
4KRM.PDB	O, E.ASN.442	N, E.LEU.445	H, E.LEU.445	2.93	2.08	7.42
4KRM.PDB	O, E.THR.422	N, E.CYS.446	H, E.CYS.446	2.91	2.06	4.97
4KRM.PDB	O, E.TYR.447	N, E.THR.450	H, E.THR.450	2.98	2.15	11.59
4KRM.PDB	O, E.TYR.447	OG1, E.THR.450	HG1, E.THR.450	2.73	1.91	9.86
4KRM.PDB	O, E.GLU.489	N, E.ASN.452	H, E.ASN.452	2.85	2.08	22.47
4KRM.PDB	OE1, E.GLN.462	N, E.GLY.458	H, E.GLY.458	2.67	1.84	13.21
4KRM.PDB	OE1, E.GLN.462	N, E.THR.459	H, E.THR.459	2.93	2.08	6.67
4KRM.PDB	O, E.GLY.435	NE2, E.GLN.462	HE21, E.GLN.462	2.81	1.97	10.34
4KRM.PDB	OD1, E.ASP.436	N, E.LYS.463	H, E.LYS.463	2.74	1.90	10.82
4KRM.PDB	O, E.VAL.437	N, E.LYS.465	H, E.LYS.465	2.73	1.90	11.45
4KRM.PDB	O, E.ILE.439	ND2, E.ASN.469	HD21, E.ASN.469	2.99	2.18	18.20
4KRM.PDB	O, E.GLY.471	N, E.CYS.475	H, E.CYS.475	2.86	2.02	8.70
4KRM.PDB	O, E.GLU.472	N, E.LYS.476	H, E.LYS.476	2.70	1.86	10.04
4KRM.PDB	O, E.SER.501	N, E.SER.487	H, E.SER.487	2.92	2.08	12.18
4KRM.PDB	OG, E.SER.487	N, E.GLU.489	H, E.GLU.489	2.96	2.14	14.73
4KRM.PDB	OG1, E.THR.450	N, E.CYS.491	H, E.CYS.491	2.93	2.14	19.72
4KRM.PDB	O, E.ASP.498	N, E.TRP.492	H, E.TRP.492	2.80	1.98	14.94
4KRM.PDB	OD2, E.ASP.498	N, E.GLU.495	H, E.GLU.495	2.92	2.09	11.64
4KRM.PDB	O, E.GLU.495	N, E.ASP.498	H, E.ASP.498	2.98	2.18	17.73
4KRM.PDB	O, E.LEU.485	N, E.ARG.503	H, E.ARG.503	2.88	2.12	23.79
4KRM.PDB	O, F.SER.25	N, F.LYS.3	H, F.LYS.3	2.86	2.05	17.09
4KRM.PDB	O, F.THR.21	N, F.SER.7	H, F.SER.7	2.95	2.13	15.30
4KRM.PDB	O, F.SER.7	N, F.THR.21	H, F.THR.21	2.73	1.87	2.52
4KRM.PDB	O, F.LYS.3	N, F.SER.25	H, F.SER.25	2.98	2.15	11.96
4KRM.PDB	O, F.SER.31	NH2, F.ARG.30	HH21, F.ARG.30	2.61	1.79	15.83
4KRM.PDB	O, F.ALA.99	N, F.GLY.33	H, F.GLY.33	2.82	2.07	24.40
4KRM.PDB	O, F.ILE.51	N, F.MET.34	H, F.MET.34	2.93	2.11	15.70
4KRM.PDB	O, F.ALA.97	N, F.GLY.35	H, F.GLY.35	2.80	1.97	12.17
4KRM.PDB	O, F.SER.49	N, F.TRP.36	H, F.TRP.36	2.73	1.89	10.21
4KRM.PDB	O, F.TYR.95	N, F.PHE.37	H, F.PHE.37	2.81	1.97	10.88
4KRM.PDB	O, F.GLU.46	N, F.ARG.38	H, F.ARG.38	2.90	2.09	16.96
4KRM.PDB	OE1, F.GLU.46	NE, F.ARG.38	HE, F.ARG.38	2.74	1.95	18.99
4KRM.PDB	OD2, F.ASP.90	NH1, F.ARG.38	HH12, F.ARG.38	2.95	2.22	27.79
4KRM.PDB	OE1, F.GLU.46	NH2, F.ARG.38	HH21, F.ARG.38	2.97	2.26	28.90
4KRM.PDB	O, F.ILE.93	N, F.GLN.39	H, F.GLN.39	2.82	2.04	20.98
4KRM.PDB	O, F.ARG.38	N, F.GLU.46	H, F.GLU.46	2.90	2.06	10.12
4KRM.PDB	O, F.TRP.36	N, F.VAL.48	H, F.VAL.48	2.88	2.06	14.02
4KRM.PDB	O, F.GLY.59	OG, F.SER.49	HG, F.SER.49	2.88	2.11	18.96
4KRM.PDB	O, F.MET.34	N, F.ILE.51	H, F.ILE.51	2.74	1.95	19.38
4KRM.PDB	O, F.SER.57	N, F.SER.52	H, F.SER.52	2.97	2.18	19.50

4KRM.PDB	O, F_SER_102	N, F_TRP_53	H, F_TRP_53	2.81	2.02	19.56
4KRM.PDB	O, F_GLY_50	N, F_GLY_59	H, F_GLY_59	2.97	2.21	23.47
4KRM.PDB	O, F_VAL_48	N, F_ALA_61	H, F_ALA_61	2.76	1.97	19.40
4KRM.PDB	O, F_ALA_61	N, F_VAL_64	H, F_VAL_64	2.98	2.13	8.69
4KRM.PDB	O, F_GLN_82	N, F_THR_69	H, F_THR_69	2.91	2.11	18.52
4KRM.PDB	OH, F_TYR_60	N, F_ILE_70	H, F_ILE_70	2.89	2.06	11.48
4KRM.PDB	O, F_TYR_32	NH2, F_ARG_72	HH22, F_ARG_72	2.78	1.95	12.55
4KRM.PDB	O, F_THR_78	N, F_ASP_73	H, F_ASP_73	2.80	1.97	13.02
4KRM.PDB	O, F_TRP_53	ND2, F_ASN_74	HD21, F_ASN_74	2.93	2.12	16.19
4KRM.PDB	O, F_SER_71	N, F_ASP_80	H, F_ASP_80	2.70	1.92	21.61
4KRM.PDB	O, F_LEU_20	N, F_LEU_81	H, F_LEU_81	2.76	1.99	22.17
4KRM.PDB	O, F_THR_69	N, F_GLN_82	H, F_GLN_82	2.76	1.97	19.23
4KRM.PDB	O, F_LEU_18	N, F_MET_83	H, F_MET_83	2.64	1.79	6.89
4KRM.PDB	O, F_LYS_87	N, F_ASP_90	H, F_ASP_90	2.98	2.21	22.29
4KRM.PDB	O, F_VAL_120	N, F_ALA_92	H, F_ALA_92	2.97	2.23	25.76
4KRM.PDB	O, F_GLN_39	N, F_ILE_93	H, F_ILE_93	2.94	2.10	11.68
4KRM.PDB	O, F_THR_118	N, F_TYR_94	H, F_TYR_94	2.68	1.91	22.25
4KRM.PDB	O, F_PHE_37	N, F_TYR_95	H, F_TYR_95	2.61	1.83	20.76
4KRM.PDB	OE2, F_GLU_6	N, F_CYS_96	H, F_CYS_96	2.70	1.85	6.40
4KRM.PDB	O, F_TYR_113	N, F_ALA_98	H, F_ALA_98	2.93	2.11	13.82
4KRM.PDB	O, F_GLY_33	N, F_ALA_99	H, F_ALA_99	2.73	1.91	15.09
4KRM.PDB	OD2, F_ASP_112	N, F_ALA_100	H, F_ALA_100	2.76	1.94	15.63
4KRM.PDB	O, F_SER_31	N, F_GLY_101	H, F_GLY_101	2.75	1.91	9.93
4KRM.PDB	OG, F_SER_57	NE1, F_TRP_104	HE1, F_TRP_104	3.00	2.20	18.23
4KRM.PDB	OH, F_TYR_111	N, F_TYR_105	H, F_TYR_105	2.96	2.11	6.28
4KRM.PDB	O, F_TYR_105	OH, F_TYR_111	HH, F_TYR_111	2.59	1.76	7.82
4KRM.PDB	O, F_ALA_98	N, F_ASP_112	H, F_ASP_112	2.76	1.97	19.53
4KRM.PDB	O, F_ALA_92	N, F_VAL_120	H, F_VAL_120	2.87	2.04	13.51
4KRM.PDB	O, J_THR_58	N, G_LYS_310	H, G_LYS_310	2.73	1.87	4.39
4KRM.PDB	OG1, G_THR_339	N, G_LYS_311	H, G_LYS_311	2.65	1.81	9.30
4KRM.PDB	O, J_ASP_56	N, G_VAL_312	H, G_VAL_312	2.86	2.02	9.25
4KRM.PDB	O, G_SER_340	N, G_CYS_313	H, G_CYS_313	2.95	2.13	14.37
4KRM.PDB	OE2, G_GLU_320	ND2, G_ASN_314	HD22, G_ASN_314	2.93	2.08	7.68
4KRM.PDB	O, G_PHE_321	N, G_GLY_317	H, G_GLY_317	2.53	1.78	24.02
4KRM.PDB	O, G_ILE_318	N, G_PHE_321	H, G_PHE_321	2.93	2.11	15.10
4KRM.PDB	O, G_ILE_327	OG, G_SER_326	HG, G_SER_326	2.75	1.93	11.46
4KRM.PDB	OD1, G_ASN_331	N, G_ASN_328	H, G_ASN_328	2.74	1.90	10.28
4KRM.PDB	OD1, G_ASN_328	N, G_THR_330	H, G_THR_330	2.95	2.20	24.53
4KRM.PDB	O, G_LYS_311	N, G_THR_339	H, G_THR_339	2.89	2.05	9.34
4KRM.PDB	O, G_GLU_376	N, G_ILE_341	H, G_ILE_341	2.80	1.96	11.60
4KRM.PDB	O, G_CYS_313	N, G_SER_342	H, G_SER_342	2.82	1.98	11.49
4KRM.PDB	O, G_PHE_380	N, G_LEU_345	H, G_LEU_345	2.93	2.10	13.53
4KRM.PDB	O, G_LEU_382	N, G_ILE_347	H, G_ILE_347	2.70	1.92	20.05
4KRM.PDB	OD1, H_ASP_112	N, G_VAL_350	H, G_VAL_350	2.96	2.25	28.54
4KRM.PDB	O, H_GLU_110	NH1, G_ARG_353	HH12, G_ARG_353	2.56	1.83	26.87
4KRM.PDB	O, H_ALA_100	NH2, G_ARG_353	HH21, G_ARG_353	2.51	1.75	22.59
4KRM.PDB	O, G_THR_360	N, G_ASP_355	H, G_ASP_355	2.70	1.88	14.64
4KRM.PDB	OD2, G_ASP_355	OG1, G_THR_358	HG1, G_THR_358	2.44	1.73	26.83
4KRM.PDB	O, G_SER_356	N, G_HIS_359	H, G_HIS_359	2.93	2.09	11.16
4KRM.PDB	O, G_ASP_355	N, G_THR_360	H, G_THR_360	2.97	2.12	5.02
4KRM.PDB	O, G_ALA_351	N, G_LEU_363	H, G_LEU_363	2.76	1.95	17.12
4KRM.PDB	O, G_ASP_364	N, G_GLU_367	H, G_GLU_367	2.88	2.09	19.30
4KRM.PDB	O, G_CYS_338	OG1, G_THR_373	HG1, G_THR_373	2.73	2.02	27.50
4KRM.PDB	O, G_LEU_371	N, G_VAL_374	H, G_VAL_374	2.85	2.01	8.31
4KRM.PDB	O, G_THR_339	N, G_LYS_375	H, G_LYS_375	2.65	1.80	5.93
4KRM.PDB	O, G_ILE_401	N, G_ILE_377	H, G_ILE_377	2.87	2.09	20.96
4KRM.PDB	O, G_ILE_341	N, G_THR_378	H, G_THR_378	2.88	2.03	7.65
4KRM.PDB	O, G_GLY_343	N, G_GLY_379	H, G_GLY_379	2.80	2.07	27.17

4KRM.PDB	O, G_SER.413	N, G_LEU.381	H, G_LEU.381	2.90	2.12	21.15
4KRM.PDB	O, G_LEU.345	N, G_LEU.382	H, G_LEU.382	2.83	1.99	8.73
4KRM.PDB	O, G_ALA.415	N, G_ILE.383	H, G_ILE.383	2.86	2.01	8.40
4KRM.PDB	O, G_ILE.347	N, G_GLN.384	H, G_GLN.384	2.81	1.95	0.88
4KRM.PDB	O, G_LEU.424	N, G_LEU.393	H, G_LEU.393	2.77	1.94	12.00
4KRM.PDB	O, G_ASP.392	N, G_HIS.394	H, G_HIS.394	2.93	2.22	28.78
4KRM.PDB	O, G_LEU.393	N, G_PHE.396	H, G_PHE.396	2.92	2.10	14.77
4KRM.PDB	O, G_HIS.394	N, G_GLU.397	H, G_GLU.397	2.97	2.19	21.14
4KRM.PDB	O, G_LYS.372	ND2, G_ASN.398	HD22, G_ASN.398	2.84	2.00	11.57
4KRM.PDB	O, G_LYS.375	N, G_GLU.400	H, G_GLU.400	2.78	1.96	14.21
4KRM.PDB	O, G_LYS.375	N, G_ILE.401	H, G_ILE.401	2.99	2.20	20.10
4KRM.PDB	O, G_GLU.431	N, G_ILE.402	H, G_ILE.402	2.97	2.14	13.48
4KRM.PDB	O, G_ILE.377	N, G_ARG.403	H, G_ARG.403	2.93	2.11	14.81
4KRM.PDB	OE2, B_GLU.5	NZ, G_LYS.407	HZ1, G_LYS.407	2.98	2.17	20.60
4KRM.PDB	O, G_PHE.412	N, G_GLN.408	H, G_GLN.408	2.76	2.01	23.83
4KRM.PDB	O, G_LYS.407	N, G_GLY.410	H, G_GLY.410	2.94	2.22	27.68
4KRM.PDB	O, G_GLN.408	N, G_GLN.411	H, G_GLN.411	2.79	2.01	20.58
4KRM.PDB	O, G_ASP.436	N, G_SER.413	H, G_SER.413	2.85	2.07	21.98
4KRM.PDB	O, G_LEU.381	N, G_ALA.415	H, G_ALA.415	2.89	2.06	13.22
4KRM.PDB	O, G_ILE.438	N, G_VAL.416	H, G_VAL.416	2.96	2.13	13.42
4KRM.PDB	O, G_ILE.383	N, G_VAL.417	H, G_VAL.417	2.92	2.07	10.01
4KRM.PDB	O, G_SER.440	N, G_SER.418	H, G_SER.418	2.92	2.13	19.69
4KRM.PDB	OD1, G_ASN.442	N, G_LEU.419	H, G_LEU.419	2.75	1.90	7.74
4KRM.PDB	O, G_THR.391	N, G_THR.422	H, G_THR.422	2.76	1.99	22.35
4KRM.PDB	OD1, G_ASP.498	NE, G_ARG.427	HE, G_ARG.427	2.63	1.82	16.62
4KRM.PDB	O, G_GLU.400	N, G_LYS.430	H, G_LYS.430	2.83	2.00	11.28
4KRM.PDB	O, G_LEU.456	N, G_ILE.432	H, G_ILE.432	2.61	1.79	15.19
4KRM.PDB	O, G_ILE.402	N, G_SER.433	H, G_SER.433	2.83	2.10	26.95
4KRM.PDB	OE2, G_GLU.431	OG, G_SER.433	HG, G_SER.433	2.90	2.13	19.38
4KRM.PDB	O, G_GLN.411	N, G_ASP.436	H, G_ASP.436	2.84	1.99	7.12
4KRM.PDB	O, G_LEU.414	N, G_ILE.438	H, G_ILE.438	2.99	2.16	12.24
4KRM.PDB	O, G_LYS.465	N, G_ILE.439	H, G_ILE.439	2.85	2.05	16.86
4KRM.PDB	O, G_THR.422	N, G_CYS.446	H, G_CYS.446	2.95	2.09	5.98
4KRM.PDB	O, G_TYR.447	OG1, G_THR.450	HG1, G_THR.450	2.91	2.12	17.41
4KRM.PDB	O, G_TRP.453	N, G_LEU.456	H, G_LEU.456	2.82	2.02	18.78
4KRM.PDB	OE1, G_GLN.462	N, G_GLY.458	H, G_GLY.458	2.58	1.75	11.60
4KRM.PDB	OE1, G_GLN.462	N, G_THR.459	H, G_THR.459	2.66	1.85	16.39
4KRM.PDB	O, G_ILE.432	NE2, G_GLN.462	HE22, G_GLN.462	2.98	2.14	10.37
4KRM.PDB	OD2, G_ASP.436	NZ, G_LYS.463	HZ3, G_LYS.463	2.68	1.83	13.12
4KRM.PDB	O, G_VAL.437	N, G_LYS.465	H, G_LYS.465	2.68	1.91	21.58
4KRM.PDB	O, G_ILE.439	ND2, G_ASN.469	HD21, G_ASN.469	2.98	2.19	20.07
4KRM.PDB	O, G_GLY.479	N, G_VAL.481	H, G_VAL.481	2.78	2.05	26.86
4KRM.PDB	O, G_HIS.483	N, G_CYS.486	H, G_CYS.486	2.82	1.98	11.71
4KRM.PDB	O, G_SER.501	N, G_SER.487	H, G_SER.487	2.97	2.12	8.14
4KRM.PDB	OG1, G_THR.450	N, G_CYS.491	H, G_CYS.491	2.97	2.16	16.33
4KRM.PDB	O, G_ASP.498	N, G_TRP.492	H, G_TRP.492	2.74	1.91	11.68
4KRM.PDB	OD2, G_ASP.498	N, G_GLU.495	H, G_GLU.495	2.95	2.14	15.12
4KRM.PDB	O, G_GLU.495	N, G_ASP.498	H, G_ASP.498	2.86	2.09	21.75
4KRM.PDB	O, H_SER.25	N, H_LYS.3	H, H_LYS.3	2.79	1.95	8.78
4KRM.PDB	O, H_THR.121	N, H_VAL.12	H, H_VAL.12	2.78	2.06	27.37
4KRM.PDB	O, H_LEU.86	N, H_GLY.15	H, H_GLY.15	2.81	1.97	8.46
4KRM.PDB	O, H_GLN.13	N, H_GLY.16	H, H_GLY.16	2.88	2.10	20.19
4KRM.PDB	O, H_MET.83	N, H_LEU.18	H, H_LEU.18	2.86	2.12	25.13
4KRM.PDB	O, H_LEU.81	N, H_LEU.20	H, H_LEU.20	2.99	2.19	18.49
4KRM.PDB	O, H_SER.7	N, H_THR.21	H, H_THR.21	2.95	2.12	12.95
4KRM.PDB	OD1, H_ASP.80	OG1, H_THR.21	HG1, H_THR.21	2.86	2.06	13.63
4KRM.PDB	O, H_VAL.79	N, H_CYS.22	H, H_CYS.22	2.70	1.88	14.06
4KRM.PDB	O, H_GLU.5	N, H_ALA.23	H, H_ALA.23	2.89	2.06	12.94

4KRM.PDB	O, H_LYS_3	N, H_SER_25	H, H_SER_25	2.91	2.09	13.71
4KRM.PDB	O, H_GLN_1	N, H_ARG_27	H, H_ARG_27	2.48	1.77	28.35
4KRM.PDB	OD2, G_ASP_355	NH1, H_ARG_30	HH12, H_ARG_30	2.45	1.69	23.45
4KRM.PDB	O, H_SER_31	NH2, H_ARG_30	HH21, H_ARG_30	2.78	1.93	7.41
4KRM.PDB	O, H_ALA_99	N, H_GLY_33	H, H_GLY_33	2.86	2.05	16.44
4KRM.PDB	O, H_ALA_97	N, H_GLY_35	H, H_GLY_35	2.94	2.11	13.58
4KRM.PDB	O, H_SER_49	N, H_TRP_36	H, H_TRP_36	2.62	1.77	8.75
4KRM.PDB	O, H_TYR_95	N, H_PHE_37	H, H_PHE_37	2.89	2.05	9.66
4KRM.PDB	O, H_GLU_46	N, H_ARG_38	H, H_ARG_38	2.94	2.12	14.51
4KRM.PDB	OH, H_TYR_94	NH1, H_ARG_38	HH11, H_ARG_38	2.96	2.15	17.21
4KRM.PDB	OD2, H_ASP_90	NH1, H_ARG_38	HH12, H_ARG_38	2.78	1.94	11.87
4KRM.PDB	O, H_ILE_93	N, H_GLN_39	H, H_GLN_39	2.82	2.05	22.91
4KRM.PDB	O, H_ARG_38	N, H_GLU_46	H, H_GLU_46	2.85	2.00	7.03
4KRM.PDB	O, H_TRP_36	N, H_VAL_48	H, H_VAL_48	2.89	2.09	19.35
4KRM.PDB	O, H_GLY_59	OG, H_SER_49	HG, H_SER_49	2.79	2.01	17.53
4KRM.PDB	O, H_SER_57	N, H_SER_52	H, H_SER_52	2.91	2.10	15.97
4KRM.PDB	O, H_SER_102	N, H_TRP_53	H, H_TRP_53	2.86	2.06	18.40
4KRM.PDB	O, H_GLY_50	N, H_GLY_59	H, H_GLY_59	2.99	2.18	17.15
4KRM.PDB	O, H_VAL_48	N, H_ALA_61	H, H_ALA_61	2.83	2.04	18.74
4KRM.PDB	O, H_GLN_82	N, H_THR_69	H, H_THR_69	2.90	2.15	24.65
4KRM.PDB	OH, H_TYR_60	N, H_ILE_70	H, H_ILE_70	2.79	1.97	14.83
4KRM.PDB	O, H_ASP_80	N, H_SER_71	H, H_SER_71	3.00	2.23	22.57
4KRM.PDB	O, H_TRP_53	ND2, H_ASN_74	HD21, H_ASN_74	2.76	1.95	15.85
4KRM.PDB	OD2, H_ASP_73	N, H_LYS_76	H, H_LYS_76	2.90	2.09	16.51
4KRM.PDB	O, H_CYS_22	N, H_VAL_79	H, H_VAL_79	2.88	2.15	26.91
4KRM.PDB	O, H_SER_71	N, H_ASP_80	H, H_ASP_80	2.65	1.83	14.09
4KRM.PDB	O, H_LEU_20	N, H_LEU_81	H, H_LEU_81	2.81	2.00	15.97
4KRM.PDB	O, H_THR_69	N, H_GLN_82	H, H_GLN_82	2.88	2.06	13.12
4KRM.PDB	O, H_LEU_18	N, H_MET_83	H, H_MET_83	2.85	2.06	18.92
4KRM.PDB	OD1, H_ASP_90	N, H_LYS_87	H, H_LYS_87	2.94	2.18	22.86
4KRM.PDB	O, H_LYS_87	N, H_ASP_90	H, H_ASP_90	2.96	2.13	11.70
4KRM.PDB	O, H_VAL_120	N, H_ALA_92	H, H_ALA_92	2.96	2.18	20.64
4KRM.PDB	O, H_THR_118	N, H_TYR_94	H, H_TYR_94	2.81	1.97	10.96
4KRM.PDB	O, H_ASP_90	OH, H_TYR_94	HH, H_TYR_94	2.70	1.86	4.54
4KRM.PDB	O, H_PHE_37	N, H_TYR_95	H, H_TYR_95	2.58	1.73	7.75
4KRM.PDB	OE2, H_GLU_6	N, H_CYS_96	H, H_CYS_96	2.89	2.06	12.97
4KRM.PDB	O, H_TYR_113	N, H_ALA_98	H, H_ALA_98	2.83	2.01	14.92
4KRM.PDB	O, H_GLY_33	N, H_ALA_99	H, H_ALA_99	2.76	1.95	17.06
4KRM.PDB	OD2, H_ASP_112	N, H_ALA_100	H, H_ALA_100	2.90	2.11	20.56
4KRM.PDB	OH, H_TYR_111	N, H_TYR_105	H, H_TYR_105	3.00	2.17	13.07
4KRM.PDB	O, H_TYR_105	OH, H_TYR_111	HH, H_TYR_111	2.65	1.82	7.16
4KRM.PDB	O, H_ALA_98	N, H_ASP_112	H, H_ASP_112	2.68	1.89	19.59
4KRM.PDB	O, H_CYS_96	N, H_GLY_115	H, H_GLY_115	2.91	2.11	18.40
4KRM.PDB	O, H_ALA_92	N, H_VAL_120	H, H_VAL_120	2.84	1.98	5.98
4KRM.PDB	O, H_GLY_10	N, H_THR_121	H, H_THR_121	2.98	2.20	20.73
4KRM.PDB	O, H_VAL_12	N, H_SER_123	H, H_SER_123	2.98	2.16	13.88
4KRM.PDB	O, L_TYR_60	N, L_GLU_308	H, L_GLU_308	2.69	1.88	16.25
4KRM.PDB	O, L_THR_58	N, L_LYS_310	H, L_LYS_310	2.70	1.84	3.45
4KRM.PDB	OG1, L_THR_339	N, L_LYS_311	H, L_LYS_311	2.88	2.03	10.00
4KRM.PDB	O, L_ASP_56	N, L_VAL_312	H, L_VAL_312	2.83	1.98	8.53
4KRM.PDB	O, L_SER_340	N, L_CYS_313	H, L_CYS_313	2.89	2.06	11.76
4KRM.PDB	O, L_ASP_344	N, L_ILE_316	H, L_ILE_316	2.80	2.09	29.01
4KRM.PDB	O, L_PHE_321	N, L_GLY_317	H, L_GLY_317	2.73	1.96	22.99
4KRM.PDB	O, L_ILE_318	N, L_PHE_321	H, L_PHE_321	2.93	2.10	12.75
4KRM.PDB	O, L_ILE_327	OG, L_SER_326	HG, L_SER_326	2.89	2.08	11.44
4KRM.PDB	OD1, L_ASN_331	N, L_ASN_328	H, L_ASN_328	2.82	1.98	9.33
4KRM.PDB	OD1, L_ASN_328	N, L_ASN_331	H, L_ASN_331	2.99	2.20	19.62
4KRM.PDB	O, L_SER_326	ND2, L_ASN_331	HD21, L_ASN_331	2.92	2.07	8.49

4KRM.PDB	O, I.LE_332	N, I.PHE_335	H, I.PHE_335	2.95	2.11	11.07
4KRM.PDB	O, I.LYS_311	N, I.THR_339	H, I.THR_339	2.90	2.09	16.73
4KRM.PDB	O, I.GLU_376	N, I.LE_341	H, I.LE_341	2.71	1.87	11.39
4KRM.PDB	O, I.CYS_313	N, I.SER_342	H, I.SER_342	2.80	1.99	16.11
4KRM.PDB	OD1, J.ASP_112	N, I.VAL_350	H, I.VAL_350	2.88	2.05	13.27
4KRM.PDB	O, I.PRO_349	N, I.PHE_352	H, I.PHE_352	2.95	2.25	30.00
4KRM.PDB	OE1, J.GLU_110	NH1, I.ARG_353	HH11, I.ARG_353	2.86	2.07	18.90
4KRM.PDB	O, J.ALA_100	NH2, I.ARG_353	HH21, I.ARG_353	2.97	2.14	13.62
4KRM.PDB	OD2, J.ASP_112	NH2, I.ARG_353	HH22, I.ARG_353	3.00	2.19	17.61
4KRM.PDB	O, I.VAL_350	N, I.GLY_354	H, I.GLY_354	2.71	1.89	14.51
4KRM.PDB	O, I.THR_360	N, I.ASP_355	H, I.ASP_355	2.71	1.86	7.14
4KRM.PDB	O, I.SER_356	N, I.HIS_359	H, I.HIS_359	2.93	2.08	7.30
4KRM.PDB	O, I.ASP_355	N, I.THR_360	H, I.THR_360	2.86	2.01	5.45
4KRM.PDB	O, I.ALA_351	N, I.LEU_363	H, I.LEU_363	2.78	1.95	13.31
4KRM.PDB	O, I.ASP_364	N, I.GLU_367	H, I.GLU_367	2.93	2.21	27.86
4KRM.PDB	O, I.GLN_366	N, I.ASP_369	H, I.ASP_369	2.86	2.00	2.35
4KRM.PDB	O, I.CYS_338	OG1, I.THR_373	HG1, I.THR_373	2.82	2.09	25.50
4KRM.PDB	O, I.THR_339	N, I.LYS_375	H, I.LYS_375	2.71	1.85	3.93
4KRM.PDB	O, I.LE_401	N, I.LE_377	H, I.LE_377	2.89	2.07	14.58
4KRM.PDB	O, I.LE_341	N, I.THR_378	H, I.THR_378	2.93	2.08	9.23
4KRM.PDB	O, I.SER_413	N, I.LEU_381	H, I.LEU_381	2.75	1.94	16.75
4KRM.PDB	O, I.LEU_345	N, I.LEU_382	H, I.LEU_382	2.90	2.05	7.20
4KRM.PDB	O, I.ALA_415	N, I.LE_383	H, I.LE_383	2.86	2.06	17.70
4KRM.PDB	O, I.LE_347	N, I.GLN_384	H, I.GLN_384	2.86	2.01	5.31
4KRM.PDB	O, I.ASP_392	NE1, I.TRP_386	HE1, I.TRP_386	2.95	2.22	27.18
4KRM.PDB	O, I.LEU_424	N, I.LEU_393	H, I.LEU_393	2.95	2.14	17.35
4KRM.PDB	O, I.LEU_393	N, I.PHE_396	H, I.PHE_396	2.98	2.13	9.44
4KRM.PDB	O, I.HIS_394	N, I.GLU_397	H, I.GLU_397	2.79	2.02	21.70
4KRM.PDB	O, I.LYS_372	ND2, I.ASN_398	HD22, I.ASN_398	2.66	1.85	16.79
4KRM.PDB	O, I.GLU_431	N, I.LE_402	H, I.LE_402	2.98	2.16	14.32
4KRM.PDB	O, I.LE_377	N, I.ARG_403	H, I.ARG_403	2.74	1.92	14.23
4KRM.PDB	OE1, I.GLU_376	NH1, I.ARG_403	HH11, I.ARG_403	2.44	1.73	28.52
4KRM.PDB	O, I.THR_378	N, I.ARG_405	H, I.ARG_405	2.76	1.91	6.37
4KRM.PDB	O, I.PHE_412	N, I.GLN_408	H, I.GLN_408	2.70	1.95	24.36
4KRM.PDB	O, I.GLN_408	N, I.GLN_411	H, I.GLN_411	2.99	2.13	5.39
4KRM.PDB	O, I.GLN_408	N, I.PHE_412	H, I.PHE_412	2.93	2.08	4.67
4KRM.PDB	O, I.ASP_436	N, I.SER_413	H, I.SER_413	2.86	2.02	12.03
4KRM.PDB	O, I.LEU_381	N, I.ALA_415	H, I.ALA_415	2.85	2.03	14.56
4KRM.PDB	O, I.LE_438	N, I.VAL_416	H, I.VAL_416	2.89	2.05	11.42
4KRM.PDB	O, I.LE_383	N, I.VAL_417	H, I.VAL_417	2.89	2.03	5.24
4KRM.PDB	OD1, I.ASN_442	N, I.LEU_419	H, I.LEU_419	2.81	1.99	14.43
4KRM.PDB	O, I.THR_391	N, I.THR_422	H, I.THR_422	2.89	2.08	17.87
4KRM.PDB	O, I.GLU_400	N, I.LYS_430	H, I.LYS_430	2.98	2.13	8.06
4KRM.PDB	O, I.LEU_456	N, I.LE_432	H, I.LE_432	2.75	1.92	11.71
4KRM.PDB	O, I.LE_402	N, I.SER_433	H, I.SER_433	2.89	2.14	24.79
4KRM.PDB	OE2, I.GLU_431	OG, I.SER_433	HG, I.SER_433	2.91	2.09	9.73
4KRM.PDB	OD1, I.ASP_434	N, I.GLY_435	H, I.GLY_435	2.61	1.88	26.82
4KRM.PDB	O, I.GLN_411	N, I.ASP_436	H, I.ASP_436	2.81	1.95	4.03
4KRM.PDB	O, I.LEU_414	N, I.LE_438	H, I.LE_438	2.94	2.11	13.80
4KRM.PDB	OD1, I.ASN_469	ND2, I.ASN_442	HD22, I.ASN_442	2.76	1.93	12.03
4KRM.PDB	O, I.THR_422	N, I.CYS_446	H, I.CYS_446	2.73	1.88	7.27
4KRM.PDB	O, I.TYR_447	OG1, I.THR_450	HG1, I.THR_450	2.88	2.08	15.87
4KRM.PDB	OE1, I.GLN_462	N, I.GLY_458	H, I.GLY_458	2.63	1.77	6.16
4KRM.PDB	OE1, I.GLN_462	N, I.THR_459	H, I.THR_459	2.73	1.99	24.99
4KRM.PDB	O, I.LE_432	NE2, I.GLN_462	HE22, I.GLN_462	2.64	1.79	3.75
4KRM.PDB	O, I.VAL_437	N, I.LYS_465	H, I.LYS_465	2.80	2.00	17.16
4KRM.PDB	O, I.LE_439	ND2, I.ASN_469	HD21, I.ASN_469	2.82	2.04	21.05
4KRM.PDB	OD1, I.ASN_473	OG, I.SER_474	HG, I.SER_474	2.73	1.91	11.26

4KRM.PDB	O, I_GLY_479	N, I_VAL_481	H, I_VAL_481	2.96	2.25	29.56
4KRM.PDB	OG1, I_THR_450	N, I_CYS_491	H, I_CYS_491	2.81	1.99	15.75
4KRM.PDB	O, I_ASP_498	N, I_TRP_492	H, I_TRP_492	2.78	1.96	14.16
4KRM.PDB	O, I_PRO_496	N, I_CYS_499	H, I_CYS_499	2.92	2.09	12.35
4KRM.PDB	O, J_SER_25	N, J_LYS_3	H, J_LYS_3	2.85	2.01	8.57
4KRM.PDB	O, J_ALA_23	N, J_GLU_5	H, J_GLU_5	2.99	2.16	13.86
4KRM.PDB	O, J_THR_121	N, J_VAL_12	H, J_VAL_12	3.00	2.24	24.14
4KRM.PDB	O, J_LEU_86	N, J_GLY_15	H, J_GLY_15	2.66	1.81	6.69
4KRM.PDB	O, J_GLN_13	N, J_GLY_16	H, J_GLY_16	2.94	2.17	21.17
4KRM.PDB	OD1, J_ASP_80	NE, J_ARG_19	HE, J_ARG_19	2.78	1.97	16.74
4KRM.PDB	O, J_LEU_81	N, J_LEU_20	H, J_LEU_20	2.96	2.15	16.27
4KRM.PDB	O, J_SER_7	N, J_THR_21	H, J_THR_21	2.87	2.05	15.09
4KRM.PDB	O, J_VAL_79	N, J_CYS_22	H, J_CYS_22	2.95	2.23	28.38
4KRM.PDB	O, J_GLU_5	N, J_ALA_23	H, J_ALA_23	2.89	2.08	15.16
4KRM.PDB	O, J_GLN_1	N, J_ARG_27	H, J_ARG_27	2.63	1.91	27.25
4KRM.PDB	O, J_THR_28	N, J_ARG_30	H, J_ARG_30	2.80	2.09	29.22
4KRM.PDB	O, J_SER_31	NH2, J_ARG_30	HH21, J_ARG_30	2.53	1.73	17.55
4KRM.PDB	O, J_ALA_99	N, J_GLY_33	H, J_GLY_33	2.86	2.12	25.08
4KRM.PDB	O, J_ILE_51	N, J_MET_34	H, J_MET_34	2.99	2.28	29.29
4KRM.PDB	O, J_ALA_97	N, J_GLY_35	H, J_GLY_35	2.84	2.04	17.40
4KRM.PDB	O, J_SER_49	N, J_TRP_36	H, J_TRP_36	2.70	1.86	9.65
4KRM.PDB	O, J_TYR_95	N, J_PHE_37	H, J_PHE_37	2.82	1.99	12.49
4KRM.PDB	O, J_GLU_46	N, J_ARG_38	H, J_ARG_38	2.92	2.10	15.90
4KRM.PDB	OH, J_TYR_94	NH1, J_ARG_38	HH11, J_ARG_38	2.85	2.02	12.10
4KRM.PDB	OD2, J_ASP_90	NH1, J_ARG_38	HH12, J_ARG_38	2.97	2.15	14.05
4KRM.PDB	O, J_ILE_93	N, J_GLN_39	H, J_GLN_39	2.89	2.11	20.97
4KRM.PDB	O, J_ARG_38	N, J_GLU_46	H, J_GLU_46	2.86	2.02	11.35
4KRM.PDB	O, J_TRP_36	N, J_VAL_48	H, J_VAL_48	2.89	2.09	18.44
4KRM.PDB	O, J_MET_34	N, J_ILE_51	H, J_ILE_51	2.84	2.02	15.75
4KRM.PDB	O, J_SER_57	N, J_SER_52	H, J_SER_52	2.88	2.10	20.91
4KRM.PDB	O, J_SER_102	N, J_TRP_53	H, J_TRP_53	2.92	2.12	18.19
4KRM.PDB	O, J_GLY_50	N, J_GLY_59	H, J_GLY_59	2.99	2.18	16.04
4KRM.PDB	O, G_GLU_308	N, J_TYR_60	H, J_TYR_60	2.74	1.97	22.05
4KRM.PDB	O, J_VAL_48	N, J_ALA_61	H, J_ALA_61	2.78	1.94	11.47
4KRM.PDB	O, J_SER_63	NH1, J_ARG_67	HH11, J_ARG_67	2.71	1.87	10.55
4KRM.PDB	OD1, J_ASP_90	NH2, J_ARG_67	HH22, J_ARG_67	2.61	1.77	10.49
4KRM.PDB	O, J_GLN_82	N, J_THR_69	H, J_THR_69	2.92	2.13	20.56
4KRM.PDB	OH, J_TYR_60	N, J_ILE_70	H, J_ILE_70	2.83	2.01	15.28
4KRM.PDB	OD1, J_ASN_74	NE, J_ARG_72	HE, J_ARG_72	2.67	1.87	16.97
4KRM.PDB	O, J_TYR_32	NH1, J_ARG_72	HH12, J_ARG_72	2.75	1.96	19.64
4KRM.PDB	O, J_TYR_32	NH2, J_ARG_72	HH22, J_ARG_72	2.98	2.27	29.63
4KRM.PDB	O, J_TRP_53	ND2, J_ASN_74	HD21, J_ASN_74	2.64	1.92	27.41
4KRM.PDB	O, J_SER_71	N, J_ASP_80	H, J_ASP_80	2.70	1.90	17.63
4KRM.PDB	O, J_LEU_20	N, J_LEU_81	H, J_LEU_81	2.84	2.06	20.27
4KRM.PDB	O, J_THR_69	N, J_GLN_82	H, J_GLN_82	2.78	1.99	19.54
4KRM.PDB	O, J_LEU_18	N, J_MET_83	H, J_MET_83	2.71	1.90	15.45
4KRM.PDB	OD1, J_ASP_90	N, J_LYS_87	H, J_LYS_87	2.95	2.13	13.64
4KRM.PDB	O, J_LYS_87	N, J_ASP_90	H, J_ASP_90	2.61	1.76	7.15
4KRM.PDB	O, J_ASP_90	OH, J_TYR_94	HH, J_TYR_94	2.63	1.80	7.10
4KRM.PDB	O, J_PHE_37	N, J_TYR_95	H, J_TYR_95	2.62	1.79	12.04
4KRM.PDB	OE2, J_GLU_6	N, J_CYS_96	H, J_CYS_96	2.75	1.91	8.89
4KRM.PDB	O, J_TYR_113	N, J_ALA_98	H, J_ALA_98	3.00	2.20	18.29
4KRM.PDB	O, J_GLY_33	N, J_ALA_99	H, J_ALA_99	2.77	1.94	13.41
4KRM.PDB	OD2, J_ASP_112	N, J_ALA_100	H, J_ALA_100	2.99	2.17	16.23
4KRM.PDB	O, J_SER_31	N, J_GLY_101	H, J_GLY_101	2.93	2.08	6.19
4KRM.PDB	OG, J_SER_57	NE1, J_TRP_104	HE1, J_TRP_104	2.98	2.26	28.43
4KRM.PDB	OH, J_TYR_111	N, J_TYR_105	H, J_TYR_105	2.99	2.14	8.48
4KRM.PDB	O, J_TYR_105	OH, J_TYR_111	HH, J_TYR_111	2.76	1.92	3.09

4KRM.PDB	O, J_ALA_98	N, J_ASP_112	H, J_ASP_112	2.80	2.02	20.50
4KRM.PDB	OE1, J_GLU_6	N, J_GLY_117	H, J_GLY_117	2.88	2.04	11.43
4KRM.PDB	O, J_ALA_92	N, J_VAL_120	H, J_VAL_120	2.87	2.03	9.32
4KRM.PDB	O, J_GLY_10	N, J_THR_121	H, J_THR_121	2.81	1.98	11.54
4KRM.PDB	OG1, J_THR_91	N, J_VAL_122	H, J_VAL_122	2.77	1.92	7.72
4KRM.PDB	O, K_SER_340	N, K_CYS_313	H, K_CYS_313	2.84	2.01	12.83
4KRM.PDB	O, K_ASP_344	N, K_ILE_316	H, K_ILE_316	3.00	2.29	29.47
4KRM.PDB	O, K_PHE_321	N, K_GLY_317	H, K_GLY_317	2.69	1.90	19.46
4KRM.PDB	OD1, K_ASN_331	N, K_ASN_328	H, K_ASN_328	2.83	1.99	11.57
4KRM.PDB	OD1, K_ASN_328	N, K_THR_330	H, K_THR_330	2.89	2.17	28.13
4KRM.PDB	O, K_SER_326	ND2, K_ASN_331	HD21, K_ASN_331	2.93	2.14	20.17
4KRM.PDB	O, K_LYS_311	N, K_THR_339	H, K_THR_339	2.88	2.03	7.02
4KRM.PDB	O, K_GLU_376	N, K_ILE_341	H, K_ILE_341	2.75	1.92	10.64
4KRM.PDB	O, K_CYS_313	N, K_SER_342	H, K_SER_342	2.81	1.98	11.90
4KRM.PDB	O, K_PHE_380	N, K_LEU_345	H, K_LEU_345	2.95	2.14	16.87
4KRM.PDB	O, K_LEU_382	N, K_ILE_347	H, K_ILE_347	2.87	2.09	20.57
4KRM.PDB	OD1, L_ASP_112	N, K_VAL_350	H, K_VAL_350	2.89	2.07	15.44
4KRM.PDB	O, K_LEU_348	N, K_ALA_351	H, K_ALA_351	2.98	2.18	17.67
4KRM.PDB	O, K_PRO_349	N, K_PHE_352	H, K_PHE_352	2.94	2.16	21.68
4KRM.PDB	OE1, L_GLU_110	NH1, K_ARG_353	HH11, K_ARG_353	2.89	2.06	12.41
4KRM.PDB	O, L_GLU_110	NH1, K_ARG_353	HH12, K_ARG_353	2.54	1.80	24.42
4KRM.PDB	O, L_ALA_100	NH2, K_ARG_353	HH21, K_ARG_353	2.92	2.14	20.95
4KRM.PDB	OD2, L_ASP_112	NH2, K_ARG_353	HH22, K_ARG_353	2.89	2.07	13.96
4KRM.PDB	O, K_VAL_350	N, K_GLY_354	H, K_GLY_354	2.71	1.91	17.56
4KRM.PDB	O, K_THR_360	N, K_ASP_355	H, K_ASP_355	2.67	1.85	14.28
4KRM.PDB	O, K_ASP_355	N, K_THR_358	H, K_THR_358	2.95	2.19	22.97
4KRM.PDB	OD2, K_ASP_355	OG1, K_THR_358	HG1, K_THR_358	2.91	2.21	28.73
4KRM.PDB	O, K_ASP_355	N, K_THR_360	H, K_THR_360	2.96	2.12	9.53
4KRM.PDB	O, K_ALA_351	N, K_LEU_363	H, K_LEU_363	2.66	1.89	22.52
4KRM.PDB	O, K_ASP_364	N, K_GLU_367	H, K_GLU_367	2.81	1.97	10.44
4KRM.PDB	O, K_LEU_368	N, K_LEU_371	H, K_LEU_371	2.97	2.12	7.39
4KRM.PDB	O, K_THR_339	N, K_LYS_375	H, K_LYS_375	2.86	2.00	4.75
4KRM.PDB	O, K_ILE_401	N, K_ILE_377	H, K_ILE_377	2.86	2.06	18.35
4KRM.PDB	O, K_SER_413	N, K_LEU_381	H, K_LEU_381	2.86	2.05	17.20
4KRM.PDB	O, K_LEU_345	N, K_LEU_382	H, K_LEU_382	2.82	1.96	1.57
4KRM.PDB	O, K_ALA_415	N, K_ILE_383	H, K_ILE_383	2.80	1.95	7.54
4KRM.PDB	O, K_ILE_347	N, K_GLN_384	H, K_GLN_384	2.96	2.17	19.38
4KRM.PDB	O, K_LYS_375	N, K_GLU_400	H, K_GLU_400	2.90	2.08	14.24
4KRM.PDB	O, K_LYS_375	N, K_ILE_401	H, K_ILE_401	2.95	2.14	17.68
4KRM.PDB	O, K_ILE_377	N, K_ARG_403	H, K_ARG_403	2.74	1.95	18.26
4KRM.PDB	O, K_THR_378	N, K_ARG_405	H, K_ARG_405	2.74	1.91	12.90
4KRM.PDB	O, K_PHE_412	N, K_GLN_408	H, K_GLN_408	2.74	1.94	17.95
4KRM.PDB	O, K_ASP_436	N, K_SER_413	H, K_SER_413	2.84	2.02	13.83
4KRM.PDB	O, K_LEU_381	N, K_ALA_415	H, K_ALA_415	2.89	2.12	21.80
4KRM.PDB	O, K_SER_440	N, K_SER_418	H, K_SER_418	2.83	1.99	11.88
4KRM.PDB	O, K_THR_391	N, K_THR_422	H, K_THR_422	2.85	2.06	19.39
4KRM.PDB	O, K_GLU_400	N, K_LYS_430	H, K_LYS_430	2.91	2.08	12.04
4KRM.PDB	O, K_LEU_456	N, K_ILE_432	H, K_ILE_432	2.65	1.80	6.86
4KRM.PDB	OD2, K_ASP_434	N, K_GLY_435	H, K_GLY_435	2.55	1.82	26.56
4KRM.PDB	O, K_GLN_411	N, K_ASP_436	H, K_ASP_436	2.63	1.81	13.73
4KRM.PDB	O, K_LYS_465	N, K_ILE_439	H, K_ILE_439	2.92	2.09	12.95
4KRM.PDB	OD1, K_ASN_469	N, K_ASN_442	H, K_ASN_442	2.83	2.07	23.19
4KRM.PDB	O, K_THR_422	N, K_CYS_446	H, K_CYS_446	2.91	2.07	11.69
4KRM.PDB	O, K_TYR_447	OG1, K_THR_450	HG1, K_THR_450	2.66	1.87	18.01
4KRM.PDB	OE1, K_GLN_462	N, K_GLY_458	H, K_GLY_458	2.63	1.78	7.92
4KRM.PDB	OE1, K_GLN_462	N, K_THR_459	H, K_THR_459	2.89	2.13	24.15
4KRM.PDB	O, K_GLY_435	NE2, K_GLN_462	HE21, K_GLN_462	2.96	2.10	5.79
4KRM.PDB	O, K_ILE_432	NE2, K_GLN_462	HE22, K_GLN_462	2.88	2.05	10.71

4KRM.PDB	OD1, K_ASP_436	N, K_LYS_463	H, K_LYS_463	2.88	2.03	6.44
4KRM.PDB	O, K_VAL_437	N, K_LYS_465	H, K_LYS_465	2.84	2.14	29.81
4KRM.PDB	O, K_ILE_439	ND2, K_ASN_469	HD21, K_ASN_469	2.65	1.81	9.31
4KRM.PDB	O, K_HIS_483	N, K_CYS_486	H, K_CYS_486	2.95	2.11	10.23
4KRM.PDB	O, K_SER_501	N, K_SER_487	H, K_SER_487	2.75	1.90	8.02
4KRM.PDB	O, K_ASP_498	N, K_TRP_492	H, K_TRP_492	2.71	1.86	9.15
4KRM.PDB	OD2, K_ASP_498	N, K_GLU_495	H, K_GLU_495	2.88	2.09	20.84
4KRM.PDB	O, K_GLU_495	N, K_ASP_498	H, K_ASP_498	2.85	2.04	15.93
4KRM.PDB	O, L_SER_25	N, L_LYS_3	H, L_LYS_3	2.83	2.01	14.97
4KRM.PDB	O, L_THR_121	N, L_VAL_12	H, L_VAL_12	2.91	2.16	24.48
4KRM.PDB	O, L_SER_123	OG1, L_THR_14	HG1, L_THR_14	2.67	1.86	12.28
4KRM.PDB	O, L_LEU_86	N, L_GLY_15	H, L_GLY_15	2.91	2.05	2.74
4KRM.PDB	O, L_GLN_13	N, L_GLY_16	H, L_GLY_16	2.82	2.02	18.09
4KRM.PDB	O, L_MET_83	N, L_LEU_18	H, L_LEU_18	2.78	1.98	18.62
4KRM.PDB	OD1, L_ASP_80	NE, L_ARG_19	HE, L_ARG_19	2.96	2.10	5.59
4KRM.PDB	O, L_SER_7	N, L_THR_21	H, L_THR_21	2.74	1.90	9.36
4KRM.PDB	O, L_GLN_1	N, L_ARG_27	H, L_ARG_27	2.68	1.97	28.48
4KRM.PDB	OD2, K_ASP_355	NH1, L_ARG_30	HH12, L_ARG_30	2.44	1.65	18.93
4KRM.PDB	O, L_SER_31	NH2, L_ARG_30	HH21, L_ARG_30	2.82	1.99	12.91
4KRM.PDB	O, L_ALA_99	N, L_GLY_33	H, L_GLY_33	2.77	2.03	25.95
4KRM.PDB	O, L_ILE_51	N, L_MET_34	H, L_MET_34	2.99	2.20	19.18
4KRM.PDB	O, L_SER_49	N, L_TRP_36	H, L_TRP_36	2.68	1.84	10.36
4KRM.PDB	O, L_TYR_95	N, L_PHE_37	H, L_PHE_37	2.91	2.07	10.93
4KRM.PDB	O, L_GLU_46	N, L_ARG_38	H, L_ARG_38	2.90	2.07	13.98
4KRM.PDB	OE1, L_GLU_46	NE, L_ARG_38	HE, L_ARG_38	2.86	2.01	10.17
4KRM.PDB	O, L_ARG_38	N, L_GLU_46	H, L_GLU_46	2.74	1.90	10.16
4KRM.PDB	O, L_GLY_59	OG, L_SER_49	HG, L_SER_49	2.90	2.14	20.97
4KRM.PDB	O, L_MET_34	N, L_ILE_51	H, L_ILE_51	2.78	1.94	10.92
4KRM.PDB	O, L_SER_57	N, L_SER_52	H, L_SER_52	2.96	2.15	16.80
4KRM.PDB	O, L_SER_102	N, L_TRP_53	H, L_TRP_53	3.00	2.20	17.87
4KRM.PDB	O, L_LYS_310	N, L_THR_58	H, L_THR_58	2.98	2.15	12.69
4KRM.PDB	O, L_GLY_50	N, L_GLY_59	H, L_GLY_59	2.79	1.99	18.05
4KRM.PDB	O, L_GLU_308	N, L_TYR_60	H, L_TYR_60	2.75	2.02	27.31
4KRM.PDB	O, L_VAL_48	N, L_ALA_61	H, L_ALA_61	2.83	1.98	9.16
4KRM.PDB	O, L_VAL_64	N, L_ARG_67	H, L_ARG_67	3.00	2.22	21.09
4KRM.PDB	O, L_SER_63	NH1, L_ARG_67	HH11, L_ARG_67	2.44	1.68	23.68
4KRM.PDB	OD1, L_ASP_90	NH2, L_ARG_67	HH22, L_ARG_67	2.60	1.80	17.17
4KRM.PDB	O, L_GLN_82	N, L_THR_69	H, L_THR_69	2.84	2.07	22.44
4KRM.PDB	OH, L_TYR_60	N, L_ILE_70	H, L_ILE_70	2.86	2.03	11.87
4KRM.PDB	O, L_SER_71	N, L_ASP_80	H, L_ASP_80	2.67	1.93	24.67
4KRM.PDB	O, L_LEU_20	N, L_LEU_81	H, L_LEU_81	2.93	2.20	26.65
4KRM.PDB	O, L_THR_69	N, L_GLN_82	H, L_GLN_82	2.79	2.06	26.22
4KRM.PDB	O, L_LEU_18	N, L_MET_83	H, L_MET_83	2.64	1.78	5.27
4KRM.PDB	OD1, L_ASP_90	N, L_LYS_87	H, L_LYS_87	2.83	2.05	20.17
4KRM.PDB	O, L_LYS_87	N, L_ASP_90	H, L_ASP_90	2.74	1.91	10.51
4KRM.PDB	O, L_VAL_120	N, L_ALA_92	H, L_ALA_92	2.86	2.07	19.77
4KRM.PDB	O, L_THR_118	N, L_TYR_94	H, L_TYR_94	2.84	2.02	14.78
4KRM.PDB	O, L_ASP_90	OH, L_TYR_94	HH, L_TYR_94	2.64	1.81	6.78
4KRM.PDB	O, L_PHE_37	N, L_TYR_95	H, L_TYR_95	2.71	1.89	15.70
4KRM.PDB	OE2, L_GLU_6	N, L_CYS_96	H, L_CYS_96	2.72	1.88	9.52
4KRM.PDB	O, L_TYR_113	N, L_ALA_98	H, L_ALA_98	2.86	2.11	25.39
4KRM.PDB	O, L_GLY_33	N, L_ALA_99	H, L_ALA_99	2.67	1.81	5.83
4KRM.PDB	O, L_SER_31	N, L_GLY_101	H, L_GLY_101	2.99	2.14	7.82
4KRM.PDB	O, L_TYR_105	OH, L_TYR_111	HH, L_TYR_111	2.61	1.77	5.19
4KRM.PDB	O, L_ALA_98	N, L_ASP_112	H, L_ASP_112	2.77	2.00	22.02
4KRM.PDB	O, L_ALA_92	N, L_VAL_120	H, L_VAL_120	2.77	1.92	3.01
4KRM.PDB	O, L_GLY_10	N, L_THR_121	H, L_THR_121	2.92	2.12	18.79
4KRM.PDB	OG1, L_THR_91	N, L_VAL_122	H, L_VAL_122	2.76	1.92	9.29

4KRO.PDB	O, A_LYS_5	N, A_GLU_35	H, A_GLU_35	2.92	2.11	16.47
4KRO.PDB	O, A_VAL_268	N, A_TYR_261	H, A_TYR_261	2.78	2.04	26.05
4KRO.PDB	O, A_VAL_284	N, A_VAL_276	H, A_VAL_276	2.65	1.87	20.75
4KRO.PDB	O, A_SER_282	N, A_THR_278	H, A_THR_278	2.79	1.96	11.51
4KRO.PDB	OG1, A_THR_278	OG, A_SER_282	HG, A_SER_282	2.99	2.27	26.50
4KRO.PDB	O, A_SER_262	N, A_CYS_283	H, A_CYS_283	2.82	2.04	21.13
4KRO.PDB	O, A_VAL_276	N, A_VAL_284	H, A_VAL_284	2.74	2.03	29.17
4KRO.PDB	O, A_LYS_303	N, A_TYR_292	H, A_TYR_292	2.85	1.99	3.19
4KRO.PDB	O, A_LYS_301	N, A_MET_294	H, A_MET_294	2.78	1.96	14.61
4KRO.PDB	OE2, A_GLU_376	NH2, A_ARG_310	HH21, A_ARG_310	2.98	2.18	18.33
4KRO.PDB	OG1, A_THR_339	N, A_LYS_311	H, A_LYS_311	2.69	1.85	11.41
4KRO.PDB	O, A_LYS_336	NZ, A_LYS_311	HZ2, A_LYS_311	2.69	1.83	12.56
4KRO.PDB	O, A_ASP_344	N, A_ILE_316	H, A_ILE_316	2.97	2.17	18.52
4KRO.PDB	O, A_ILE_318	N, A_PHE_321	H, A_PHE_321	2.93	2.07	5.85
4KRO.PDB	OD1, A_ASN_331	N, A_ASN_328	H, A_ASN_328	2.73	1.96	22.23
4KRO.PDB	OD1, A_ASN_328	N, A_ASN_331	H, A_ASN_331	2.87	2.05	14.42
4KRO.PDB	O, A_ASN_331	N, A_HIS_334	H, A_HIS_334	2.89	2.11	21.52
4KRO.PDB	O, A_LYS_311	N, A_THR_339	H, A_THR_339	2.87	2.02	7.89
4KRO.PDB	O, A_CYS_313	N, A_SER_342	H, A_SER_342	2.88	2.10	20.40
4KRO.PDB	OG1, A_THR_378	N, A_GLY_343	H, A_GLY_343	2.79	1.97	15.18
4KRO.PDB	O, A_PHE_380	N, A_LEU_345	H, A_LEU_345	2.94	2.19	25.43
4KRO.PDB	O, A_LEU_382	N, A_ILE_347	H, A_ILE_347	2.91	2.17	26.62
4KRO.PDB	O, D_GLY_54	NH1, A_ARG_353	HH12, A_ARG_353	2.81	1.97	9.47
4KRO.PDB	O, A_VAL_350	N, A_GLY_354	H, A_GLY_354	2.70	1.97	26.74
4KRO.PDB	O, A_THR_360	N, A_ASP_355	H, A_ASP_355	2.94	2.16	20.76
4KRO.PDB	OD2, A_ASP_355	OG1, A_THR_358	HG1, A_THR_358	2.98	2.18	14.96
4KRO.PDB	O, A_SER_356	N, A_HIS_359	H, A_HIS_359	2.50	1.76	24.87
4KRO.PDB	O, A_ALA_351	N, A_LEU_363	H, A_LEU_363	2.64	1.78	3.26
4KRO.PDB	O, A_ASP_364	N, A_GLU_367	H, A_GLU_367	2.99	2.20	18.77
4KRO.PDB	O, A_LEU_368	N, A_LEU_371	H, A_LEU_371	2.92	2.07	9.49
4KRO.PDB	O, A_ASP_369	N, A_LYS_372	H, A_LYS_372	2.82	1.98	9.49
4KRO.PDB	O, A_CYS_338	OG1, A_THR_373	HG1, A_THR_373	2.91	2.20	27.34
4KRO.PDB	O, A_THR_339	N, A_LYS_375	H, A_LYS_375	2.64	1.78	1.90
4KRO.PDB	OG, B_SER_103	NZ, A_LYS_375	HZ2, A_LYS_375	2.61	1.76	15.34
4KRO.PDB	O, A_ILE_401	N, A_ILE_377	H, A_ILE_377	2.94	2.13	16.36
4KRO.PDB	OD1, A_ASP_344	N, A_PHE_380	H, A_PHE_380	2.92	2.14	21.56
4KRO.PDB	O, A_SER_413	N, A_LEU_381	H, A_LEU_381	2.80	2.00	16.89
4KRO.PDB	O, A_LEU_345	N, A_LEU_382	H, A_LEU_382	2.86	2.00	3.58
4KRO.PDB	O, A_ALA_415	N, A_ILE_383	H, A_ILE_383	2.88	2.04	11.10
4KRO.PDB	O, A_ILE_347	N, A_GLN_384	H, A_GLN_384	2.90	2.16	25.76
4KRO.PDB	OH, D_TYR_102	NE2, A_GLN_384	HE21, A_GLN_384	2.87	2.16	29.24
4KRO.PDB	O, A_LEU_424	N, A_LEU_393	H, A_LEU_393	2.79	1.95	10.09
4KRO.PDB	O, A_ASP_392	N, A_HIS_394	H, A_HIS_394	2.67	1.93	25.23
4KRO.PDB	O, A_LEU_393	N, A_PHE_396	H, A_PHE_396	2.83	1.98	8.97
4KRO.PDB	O, A_HIS_394	N, A_GLU_397	H, A_GLU_397	2.93	2.19	26.10
4KRO.PDB	O, A_LYS_375	N, A_GLU_400	H, A_GLU_400	2.79	1.95	10.25
4KRO.PDB	O, A_GLU_431	N, A_ILE_402	H, A_ILE_402	2.98	2.18	17.20
4KRO.PDB	O, A_ILE_377	N, A_ARG_403	H, A_ARG_403	2.73	1.91	14.33
4KRO.PDB	O, B_TYR_100	NH2, A_ARG_403	HH22, A_ARG_403	2.57	1.73	11.63
4KRO.PDB	O, A_GLY_379	N, A_GLY_404	H, A_GLY_404	2.93	2.20	27.61
4KRO.PDB	O, A_THR_378	N, A_ARG_405	H, A_ARG_405	2.90	2.05	8.12
4KRO.PDB	OD1, B_ASP_118	NE, A_ARG_405	HE, A_ARG_405	2.72	1.93	19.48
4KRO.PDB	O, A_PHE_412	N, A_GLN_408	H, A_GLN_408	2.80	2.00	17.98
4KRO.PDB	O, A_GLN_408	N, A_GLN_411	H, A_GLN_411	2.81	2.01	18.21
4KRO.PDB	O, A_GLN_408	N, A_PHE_412	H, A_PHE_412	2.97	2.14	13.47
4KRO.PDB	O, A_ASP_436	N, A_SER_413	H, A_SER_413	2.98	2.23	25.46
4KRO.PDB	O, A_ILE_438	N, A_VAL_416	H, A_VAL_416	2.84	2.03	15.03
4KRO.PDB	O, A_SER_440	N, A_SER_418	H, A_SER_418	2.77	2.00	21.19

4KRO.PDB	OD1, A_ASN_442	N, A_LEU_419	H, A_LEU_419	2.67	1.82	7.73
4KRO.PDB	O, A_THR_391	N, A_THR_422	H, A_THR_422	2.54	1.70	10.95
4KRO.PDB	OD1, A_ASP_498	NH2, A_ARG_427	HH21, A_ARG_427	2.62	1.82	18.67
4KRO.PDB	O, A_GLU_400	N, A_LYS_430	H, A_LYS_430	2.73	1.88	4.94
4KRO.PDB	O, A_GLN_411	N, A_ASP_436	H, A_ASP_436	2.89	2.06	12.84
4KRO.PDB	O, A_LEU_414	N, A_ILE_438	H, A_ILE_438	2.87	2.04	13.24
4KRO.PDB	O, A_LYS_465	N, A_ILE_439	H, A_ILE_439	2.84	1.99	6.10
4KRO.PDB	OD1, A_ASN_469	ND2, A_ASN_442	HD22, A_ASN_442	2.75	1.96	18.83
4KRO.PDB	O, A_THR_422	N, A_CYS_446	H, A_CYS_446	2.88	2.05	14.08
4KRO.PDB	O, A_TRP_453	N, A_LEU_456	H, A_LEU_456	2.81	2.03	20.74
4KRO.PDB	O, A_SER_433	OG1, A_THR_459	HG1, A_THR_459	2.64	1.93	27.14
4KRO.PDB	O, A_GLY_435	NE2, A_GLN_462	HE21, A_GLN_462	2.56	1.71	6.56
4KRO.PDB	OD1, A_ASP_436	N, A_LYS_463	H, A_LYS_463	2.76	1.91	6.26
4KRO.PDB	O, A_VAL_437	N, A_LYS_465	H, A_LYS_465	2.89	2.08	15.96
4KRO.PDB	O, A_ILE_439	N, A_ILE_467	H, A_ILE_467	2.90	2.11	19.76
4KRO.PDB	O, A_GLU_472	N, A_LYS_476	H, A_LYS_476	2.82	2.01	16.80
4KRO.PDB	O, A_HIS_483	N, A_CYS_486	H, A_CYS_486	3.00	2.18	14.93
4KRO.PDB	O, A_SER_501	N, A_SER_487	H, A_SER_487	2.94	2.09	7.57
4KRO.PDB	OG, A_SER_501	OG, A_SER_487	HG, A_SER_487	2.37	1.68	29.03
4KRO.PDB	OG, A_SER_487	N, A_GLU_489	H, A_GLU_489	2.96	2.12	10.12
4KRO.PDB	O, A_ASP_498	N, A_TRP_492	H, A_TRP_492	2.74	1.90	10.17
4KRO.PDB	O, A_GLY_490	N, A_VAL_500	H, A_VAL_500	2.91	2.13	19.89
4KRO.PDB	O, A_LEU_485	N, A_ARG_503	H, A_ARG_503	2.90	2.06	9.38
4KRO.PDB	OD1, A_ASN_504	NH1, A_ARG_503	HH11, A_ARG_503	2.52	1.76	23.61
4KRO.PDB	O, A_VAL_505	N, A_VAL_512	H, A_VAL_512	2.94	2.11	13.63
4KRO.PDB	OE1, A_GLU_524	N, A_ASN_516	H, A_ASN_516	2.81	1.95	3.86
4KRO.PDB	O, A_CYS_515	N, A_LEU_517	H, A_LEU_517	2.67	1.93	26.36
4KRO.PDB	O, A_LEU_517	N, A_GLU_519	H, A_GLU_519	2.78	2.04	26.41
4KRO.PDB	O, A_GLY_520	NH1, A_ARG_523	HH11, A_ARG_523	2.75	2.02	27.17
4KRO.PDB	O, A_ILE_532	N, A_PHE_525	H, A_PHE_525	2.85	2.07	20.01
4KRO.PDB	O, A_PHE_525	N, A_ILE_532	H, A_ILE_532	2.90	2.06	11.44
4KRO.PDB	O, A_ARG_523	N, A_CYS_534	H, A_CYS_534	2.64	1.78	1.35
4KRO.PDB	O, A_PRO_536	N, A_CYS_538	H, A_CYS_538	2.84	2.10	26.42
4KRO.PDB	O, A_GLN_557	N, A_LEU_539	H, A_LEU_539	2.89	2.11	20.92
4KRO.PDB	O, A_LEU_539	NE2, A_GLN_541	HE21, A_GLN_541	2.61	1.79	15.38
4KRO.PDB	O, A_ASN_554	N, A_THR_548	H, A_THR_548	2.75	1.93	14.66
4KRO.PDB	OG1, A_THR_548	ND2, A_ASN_554	HD22, A_ASN_554	2.92	2.13	19.09
4KRO.PDB	O, A_VAL_568	N, A_TYR_561	H, A_TYR_561	2.97	2.17	17.83
4KRO.PDB	O, A_GLY_458	N, B_VAL_2	H, B_VAL_2	2.76	1.93	12.61
4KRO.PDB	O, B_SER_25	N, B_GLN_3	H, B_GLN_3	2.75	1.92	13.69
4KRO.PDB	O, B_THR_77	N, B_ALA_24	H, B_ALA_24	2.76	1.99	21.77
4KRO.PDB	O, B_THR_99	N, B_ALA_33	H, B_ALA_33	2.78	2.00	21.37
4KRO.PDB	O, B_ILE_51	N, B_MET_34	H, B_MET_34	2.93	2.11	14.97
4KRO.PDB	O, B_GLY_55	N, B_TYR_57	H, B_TYR_57	2.52	1.78	25.18
4KRO.PDB	O, B_TYR_119	N, B_ALA_98	H, B_ALA_98	2.93	2.19	26.24
4KRO.PDB	O, B_SER_31	N, B_LEU_101	H, B_LEU_101	2.95	2.17	21.67
4KRO.PDB	O, B_SER_102	N, B_TYR_105	H, B_TYR_105	2.87	2.05	13.73
4KRO.PDB	O, B_PRO_114	N, B_TYR_117	H, B_TYR_117	2.95	2.10	5.45
4KRO.PDB	O, B_PRO_111	OH, B_TYR_117	HH, B_TYR_117	2.59	1.81	17.04
4KRO.PDB	O, C_ARG_24	N, C_THR_5	H, C_THR_5	2.91	2.15	23.49
4KRO.PDB	O, C_GLU_105	N, C_VAL_13	H, C_VAL_13	3.00	2.29	29.53
4KRO.PDB	O, C_LEU_73	N, C_PHE_21	H, C_PHE_21	2.68	1.86	14.19
4KRO.PDB	O, C_PHE_71	N, C_CYS_23	H, C_CYS_23	2.97	2.13	10.71
4KRO.PDB	O, C_THR_5	N, C_ARG_24	H, C_ARG_24	2.88	2.05	12.65
4KRO.PDB	O, C_THR_69	N, C_ALA_25	H, C_ALA_25	2.78	1.97	17.42
4KRO.PDB	O, C_GLY_68	N, C_ILE_29	H, C_ILE_29	2.76	1.93	13.88
4KRO.PDB	O, C_THR_31	N, C_ILE_33	H, C_ILE_33	2.83	2.11	27.53
4KRO.PDB	O, C_GLN_89	N, C_HIS_34	H, C_HIS_34	2.73	1.95	19.98

4KRO.PDB	O, C_ILE_48	N, C_TRP_35	H, C_TRP_35	2.83	2.00	11.93
4KRO.PDB	O, C_TYR_87	N, C_TYR_36	H, C_TYR_36	2.69	1.90	19.38
4KRO.PDB	OE1, C_GLN_89	OH, C_TYR_36	HH, C_TYR_36	2.63	1.80	6.46
4KRO.PDB	O, C_ARG_45	N, C_GLN_37	H, C_GLN_37	2.62	1.80	13.58
4KRO.PDB	OH, C_TYR_86	NE2, C_GLN_37	HE21, C_GLN_37	2.94	2.13	16.57
4KRO.PDB	O, C_ASP_85	N, C_GLN_38	H, C_GLN_38	2.68	1.83	9.02
4KRO.PDB	OE1, D_GLN_39	NE2, C_GLN_38	HE22, C_GLN_38	2.85	2.00	7.50
4KRO.PDB	O, C_GLN_37	N, C_ARG_45	H, C_ARG_45	2.41	1.69	27.50
4KRO.PDB	O, C_TRP_35	N, C_LEU_47	H, C_LEU_47	2.85	1.99	3.81
4KRO.PDB	O, C_GLU_53	N, C_LYS_49	H, C_LYS_49	2.98	2.17	16.10
4KRO.PDB	OD2, D_ASP_103	OH, C_TYR_50	HH, C_TYR_50	2.49	1.72	20.15
4KRO.PDB	O, C_ILE_33	N, C_ALA_51	H, C_ALA_51	2.88	2.14	26.02
4KRO.PDB	OD1, C_ASP_82	NH2, C_ARG_61	HH21, C_ARG_61	2.64	1.81	12.76
4KRO.PDB	O, C_GLY_30	N, C_GLY_68	H, C_GLY_68	2.70	1.96	25.34
4KRO.PDB	O, C_CYS_23	N, C_PHE_71	H, C_PHE_71	2.97	2.22	24.26
4KRO.PDB	O, C_SER_63	N, C_SER_74	H, C_SER_74	2.78	1.94	9.14
4KRO.PDB	O, C_VAL_19	N, C_ILE_75	H, C_ILE_75	2.80	2.05	24.74
4KRO.PDB	OD2, C_ASP_82	N, C_GLU_79	H, C_GLU_79	2.59	1.74	8.25
4KRO.PDB	O, C_GLU_79	N, C_ASP_82	H, C_ASP_82	2.82	1.98	10.41
4KRO.PDB	O, C_GLN_38	N, C_ASP_85	H, C_ASP_85	2.89	2.07	15.87
4KRO.PDB	O, C_THR_102	N, C_TYR_86	H, C_TYR_86	2.96	2.19	22.34
4KRO.PDB	O, C_ASP_82	OH, C_TYR_86	HH, C_TYR_86	2.61	1.78	7.16
4KRO.PDB	O, C_TYR_36	N, C_TYR_87	H, C_TYR_87	2.90	2.11	19.86
4KRO.PDB	O, D_TYR_104	NE2, C_GLN_89	HE22, C_GLN_89	3.00	2.19	16.80
4KRO.PDB	OD1, D_ASP_103	ND2, C_ASN_91	HD21, C_ASN_91	2.93	2.12	16.18
4KRO.PDB	OE1, C_GLN_90	N, C_ASN_92	H, C_ASN_92	2.89	2.15	26.36
4KRO.PDB	OD1, C_ASN_32	ND2, C_ASN_92	HD22, C_ASN_92	2.97	2.20	23.59
4KRO.PDB	O, A_ASN_469	N, C_TRP_94	H, C_TRP_94	2.75	1.95	19.24
4KRO.PDB	OD2, D_ASP_58	NE1, C_TRP_94	HE1, C_TRP_94	2.80	2.10	29.15
4KRO.PDB	O, C_CYS_88	N, C_GLY_99	H, C_GLY_99	2.89	2.12	21.60
4KRO.PDB	OE1, C_GLN_6	N, C_GLY_101	H, C_GLY_101	2.92	2.21	28.54
4KRO.PDB	O, C_TYR_86	N, C_THR_102	H, C_THR_102	2.97	2.19	21.52
4KRO.PDB	O, C_PRO_8	OG1, C_THR_102	HG1, C_THR_102	2.68	1.90	18.51
4KRO.PDB	O, C_VAL_9	N, C_LYS_103	H, C_LYS_103	2.98	2.14	9.34
4KRO.PDB	O, C_VAL_13	N, C_LYS_107	H, C_LYS_107	2.95	2.13	15.77
4KRO.PDB	O, C_TYR_140	N, C_ALA_111	H, C_ALA_111	2.89	2.03	3.33
4KRO.PDB	O, C_LEU_135	N, C_PHE_116	H, C_PHE_116	2.87	2.15	27.51
4KRO.PDB	O, C_VAL_133	N, C_PHE_118	H, C_PHE_118	2.79	2.04	24.19
4KRO.PDB	OG, C_SER_121	N, C_GLN_124	H, C_GLN_124	2.92	2.16	22.95
4KRO.PDB	OG, C_SER_131	NE2, C_GLN_124	HE22, C_GLN_124	2.85	2.00	6.78
4KRO.PDB	OE1, C_GLN_124	N, C_SER_131	H, C_SER_131	2.94	2.16	21.66
4KRO.PDB	O, C_LEU_179	N, C_VAL_132	H, C_VAL_132	2.76	1.90	3.17
4KRO.PDB	O, C_SER_177	N, C_CYS_134	H, C_CYS_134	2.88	2.05	12.39
4KRO.PDB	O, C_PHE_116	N, C_LEU_135	H, C_LEU_135	2.91	2.11	17.23
4KRO.PDB	O, C_LEU_175	N, C_LEU_136	H, C_LEU_136	2.87	2.05	14.62
4KRO.PDB	O, C_SER_114	N, C_ASN_137	H, C_ASN_137	2.91	2.13	21.13
4KRO.PDB	O, C_TYR_173	N, C_PHE_139	H, C_PHE_139	2.69	1.92	21.18
4KRO.PDB	O, C_ALA_111	N, C_TYR_140	H, C_TYR_140	2.84	1.99	7.77
4KRO.PDB	O, C_GLU_195	N, C_GLN_147	H, C_GLN_147	2.74	1.94	17.18
4KRO.PDB	OG, C_SER_177	NE1, C_TRP_148	HE1, C_TRP_148	2.83	2.01	15.90
4KRO.PDB	O, C_VAL_150	N, C_ALA_153	H, C_ALA_153	3.00	2.29	29.91
4KRO.PDB	O, C_TRP_148	N, C_GLN_155	H, C_GLN_155	2.90	2.07	11.42
4KRO.PDB	OE1, C_GLN_155	ND2, C_ASN_158	HD21, C_ASN_158	2.72	1.97	24.54
4KRO.PDB	O, D_LEU_176	NE2, C_GLN_160	HE22, C_GLN_160	2.74	1.92	15.89
4KRO.PDB	O, C_SER_174	N, C_THR_164	H, C_THR_164	2.94	2.12	15.62
4KRO.PDB	O, C_LEU_106	NE2, C_GLN_166	HE22, C_GLN_166	2.49	1.66	13.43
4KRO.PDB	OD1, C_ASP_167	N, C_LYS_169	H, C_LYS_169	2.54	1.73	16.83
4KRO.PDB	OD1, C_ASP_167	N, C_ASP_170	H, C_ASP_170	2.97	2.21	22.78

4KRO.PDB	OD1, C_ASP_170	OG1, C_THR_172	HG1, C_THR_172	2.68	1.86	11.97
4KRO.PDB	O, C_PHE_139	N, C_TYR_173	H, C_TYR_173	2.66	1.84	12.86
4KRO.PDB	O, C_LEU_136	N, C_LEU_175	H, C_LEU_175	2.88	2.06	14.51
4KRO.PDB	O, C_SER_162	N, C_SER_176	H, C_SER_176	2.82	2.00	14.99
4KRO.PDB	O, C_GLN_160	N, C_THR_178	H, C_THR_178	2.80	2.08	27.64
4KRO.PDB	O, C_VAL_132	N, C_LEU_179	H, C_LEU_179	2.78	2.01	22.37
4KRO.PDB	OG, C_SER_182	N, C_ASP_185	H, C_ASP_185	2.76	1.91	3.71
4KRO.PDB	O, C_SER_182	N, C_TYR_186	H, C_TYR_186	2.63	1.82	15.93
4KRO.PDB	O, C_LYS_183	N, C_GLU_187	H, C_GLU_187	2.89	2.10	19.45
4KRO.PDB	O, C_ASP_185	ND1, C_HIS_189	HD1, C_HIS_189	2.98	2.14	11.48
4KRO.PDB	O, C_TYR_186	OH, C_TYR_192	HH, C_TYR_192	2.55	1.84	27.09
4KRO.PDB	O, C_LYS_149	N, C_ALA_193	H, C_ALA_193	2.99	2.27	28.68
4KRO.PDB	O, C_GLN_147	N, C_GLU_195	H, C_GLU_195	2.80	2.05	25.03
4KRO.PDB	O, C_PRO_141	NE2, C_HIS_198	HE2, C_HIS_198	2.93	2.09	10.93
4KRO.PDB	O, D_SER_25	N, D_GLN_3	H, D_GLN_3	2.73	1.89	10.77
4KRO.PDB	O, D_THR_23	N, D_LYS_5	H, D_LYS_5	2.94	2.08	5.53
4KRO.PDB	OE1, D_GLN_111	N, D_GLN_6	H, D_GLN_6	2.70	1.86	8.92
4KRO.PDB	O, D_TYR_93	NE2, D_GLN_6	HE22, D_GLN_6	2.93	2.12	16.83
4KRO.PDB	O, D_THR_116	N, D_VAL_12	H, D_VAL_12	2.92	2.09	13.60
4KRO.PDB	O, D_LEU_85	N, D_SER_15	H, D_SER_15	2.92	2.10	15.76
4KRO.PDB	O, D_MET_82	N, D_LEU_18	H, D_LEU_18	2.86	2.03	12.27
4KRO.PDB	O, D_SER_7	N, D_THR_21	H, D_THR_21	2.91	2.14	22.32
4KRO.PDB	O, D_VAL_78	N, D_CYS_22	H, D_CYS_22	2.84	2.11	27.17
4KRO.PDB	O, D_LYS_5	N, D_THR_23	H, D_THR_23	2.75	1.97	20.91
4KRO.PDB	O, D_SER_76	N, D_VAL_24	H, D_VAL_24	2.87	2.01	5.71
4KRO.PDB	O, D_GLN_3	N, D_SER_25	H, D_SER_25	2.95	2.20	25.22
4KRO.PDB	OG, D_SER_28	N, D_THR_30	H, D_THR_30	2.84	2.00	11.38
4KRO.PDB	O, D_ALA_96	N, D_HIS_35	H, D_HIS_35	2.82	2.00	14.36
4KRO.PDB	O, D_GLY_49	N, D_TRP_36	H, D_TRP_36	2.85	2.06	19.08
4KRO.PDB	O, D_GLU_46	N, D_ARG_38	H, D_ARG_38	2.89	2.07	15.74
4KRO.PDB	OE1, D_GLU_46	NE, D_ARG_38	HE, D_ARG_38	3.00	2.22	20.92
4KRO.PDB	OH, D_TYR_93	NH1, D_ARG_38	HH11, D_ARG_38	2.92	2.15	22.16
4KRO.PDB	OE1, D_GLU_46	NH2, D_ARG_38	HH21, D_ARG_38	2.98	2.22	22.99
4KRO.PDB	O, D_ILE_92	N, D_GLN_39	H, D_GLN_39	2.94	2.21	27.13
4KRO.PDB	OE1, C_GLN_38	NE2, D_GLN_39	HE22, D_GLN_39	2.80	1.94	4.32
4KRO.PDB	OG, D_SER_40	N, D_GLY_42	H, D_GLY_42	2.92	2.07	6.19
4KRO.PDB	OG, D_SER_40	N, D_LYS_43	H, D_LYS_43	2.94	2.09	7.22
4KRO.PDB	O, D_ARG_38	N, D_GLU_46	H, D_GLU_46	2.75	1.90	6.17
4KRO.PDB	O, D_TRP_36	N, D_LEU_48	H, D_LEU_48	2.73	1.89	10.02
4KRO.PDB	O, D_ASP_58	N, D_VAL_50	H, D_VAL_50	2.87	2.09	21.92
4KRO.PDB	O, D_ASN_56	N, D_TRP_52	H, D_TRP_52	2.99	2.23	23.03
4KRO.PDB	O, D_TRP_52	N, D_GLY_55	H, D_GLY_55	2.93	2.09	9.77
4KRO.PDB	OH, D_TYR_59	OG1, D_THR_57	HG1, D_THR_57	2.96	2.15	12.78
4KRO.PDB	O, D_LEU_48	N, D_ASN_60	H, D_ASN_60	2.85	2.00	4.84
4KRO.PDB	O, D_TRP_47	ND2, D_ASN_60	HD22, D_ASN_60	2.96	2.11	6.97
4KRO.PDB	O, D_ASN_60	N, D_PHE_63	H, D_PHE_63	2.78	2.00	21.76
4KRO.PDB	O, D_ASN_83	NH1, D_ARG_66	HH11, D_ARG_66	2.85	2.14	29.21
4KRO.PDB	O, D_LYS_81	N, D_SER_68	H, D_SER_68	2.97	2.25	28.54
4KRO.PDB	OH, D_TYR_59	N, D_ILE_69	H, D_ILE_69	2.89	2.06	12.12
4KRO.PDB	O, D_SER_53	NZ, D_LYS_71	HZ1, D_LYS_71	2.91	2.02	5.81
4KRO.PDB	O, D_GLN_77	N, D_ASP_72	H, D_ASP_72	2.90	2.08	14.73
4KRO.PDB	OD1, D_ASP_72	N, D_LYS_75	H, D_LYS_75	2.48	1.64	10.83
4KRO.PDB	O, D_CYS_22	N, D_VAL_78	H, D_VAL_78	2.93	2.12	17.21
4KRO.PDB	O, D_ASN_70	N, D_PHE_79	H, D_PHE_79	2.77	1.91	3.73
4KRO.PDB	O, D_ILE_20	N, D_PHE_80	H, D_PHE_80	2.90	2.07	13.53
4KRO.PDB	O, D_ARG_66	N, D_ASN_83	H, D_ASN_83	2.97	2.16	16.89
4KRO.PDB	O, D_GLN_16	N, D_LEU_85	H, D_LEU_85	2.55	1.73	12.99
4KRO.PDB	OD2, D_ASP_89	N, D_GLN_86	H, D_GLN_86	2.43	1.70	25.84

4KRO.PDB	O, D_GLN_86	N, D_ASP_89	H, D_ASP_89	2.86	2.03	12.89
4KRO.PDB	O, D_SER_87	N, D_THR_90	H, D_THR_90	2.89	2.04	5.88
4KRO.PDB	O, D_SER_87	OG1, D_THR_90	HG1, D_THR_90	2.62	1.82	14.65
4KRO.PDB	O, D_THR_113	N, D_TYR_93	H, D_TYR_93	2.85	2.02	14.16
4KRO.PDB	O, D_ASP_89	OH, D_TYR_93	HH, D_TYR_93	2.82	1.98	1.28
4KRO.PDB	O, D_VAL_37	N, D_TYR_94	H, D_TYR_94	2.63	1.78	8.56
4KRO.PDB	OE1, D_GLN_6	N, D_CYS_95	H, D_CYS_95	2.92	2.20	28.43
4KRO.PDB	O, D_HIS_35	N, D_ALA_96	H, D_ALA_96	2.91	2.11	17.80
4KRO.PDB	O, D_TYR_108	N, D_ARG_97	H, D_ARG_97	2.79	1.98	15.74
4KRO.PDB	O, D_ALA_98	NE, D_ARG_97	HE, D_ARG_97	2.79	2.01	20.72
4KRO.PDB	O, D_ALA_98	NH2, D_ARG_97	HH21, D_ARG_97	2.94	2.23	29.79
4KRO.PDB	O, D_GLU_105	N, D_LEU_99	H, D_LEU_99	2.85	2.03	14.43
4KRO.PDB	OE1, A_GLN_408	OH, D_TYR_102	HH, D_TYR_102	2.75	1.97	18.39
4KRO.PDB	OD1, D_ASP_103	N, D_TYR_104	H, D_TYR_104	2.55	1.84	28.26
4KRO.PDB	OH, C_TYR_36	N, D_PHE_106	H, D_PHE_106	2.93	2.08	9.34
4KRO.PDB	O, D_CYS_95	N, D_GLY_110	H, D_GLY_110	2.62	1.82	17.46
4KRO.PDB	O, D_GLN_6	NE2, D_GLN_111	HE22, D_GLN_111	2.78	2.02	23.66
4KRO.PDB	O, D_TYR_93	N, D_THR_113	H, D_THR_113	2.89	2.15	25.46
4KRO.PDB	O, D_ALA_91	N, D_VAL_115	H, D_VAL_115	2.99	2.15	11.01
4KRO.PDB	OG, D_SER_118	N, D_ALA_120	H, D_ALA_120	2.76	1.99	21.72
4KRO.PDB	O, D_PHE_152	N, D_LYS_123	H, D_LYS_123	2.82	1.99	13.07
4KRO.PDB	O, D_LEU_147	N, D_PHE_128	H, D_PHE_128	2.92	2.17	24.83
4KRO.PDB	O, D_GLY_145	N, D_LEU_130	H, D_LEU_130	2.69	1.85	11.60
4KRO.PDB	O, D_VAL_190	N, D_ALA_142	H, D_ALA_142	2.67	1.84	12.02
4KRO.PDB	O, D_SER_186	N, D_CYS_146	H, D_CYS_146	2.74	1.92	15.98
4KRO.PDB	O, D_PHE_128	N, D_LEU_147	H, D_LEU_147	2.84	2.06	20.81
4KRO.PDB	O, D_LEU_184	N, D_VAL_148	H, D_VAL_148	2.86	2.09	22.97
4KRO.PDB	O, D_SER_126	N, D_LYS_149	H, D_LYS_149	2.93	2.10	12.69
4KRO.PDB	O, D_TYR_182	N, D_TYR_151	H, D_TYR_151	2.83	2.02	15.76
4KRO.PDB	O, D_LYS_123	N, D_PHE_152	H, D_PHE_152	2.93	2.11	15.98
4KRO.PDB	O, D_ASN_203	N, D_SER_159	H, D_SER_159	2.92	2.10	15.23
4KRO.PDB	O, D_ILE_201	N, D_ASN_161	H, D_ASN_161	2.76	1.94	14.37
4KRO.PDB	O, D_ASN_161	N, D_ALA_164	H, D_ALA_164	2.84	2.02	14.35
4KRO.PDB	O, D_VAL_187	N, D_HIS_170	H, D_HIS_170	2.69	1.86	10.95
4KRO.PDB	O, D_SER_185	N, D_PHE_172	H, D_PHE_172	2.85	2.00	6.56
4KRO.PDB	O, D_SER_183	N, D_VAL_175	H, D_VAL_175	2.75	1.89	4.87
4KRO.PDB	O, D_LEU_181	N, D_GLN_177	H, D_GLN_177	2.93	2.08	7.13
4KRO.PDB	O, D_TYR_151	N, D_TYR_182	H, D_TYR_182	2.50	1.65	4.99
4KRO.PDB	O, D_VAL_148	N, D_LEU_184	H, D_LEU_184	2.76	1.92	11.80
4KRO.PDB	O, D_HIS_170	N, D_VAL_187	H, D_VAL_187	2.73	1.92	16.55
4KRO.PDB	O, D_LEU_144	N, D_VAL_188	H, D_VAL_188	2.75	1.91	11.62
4KRO.PDB	O, D_ALA_142	N, D_VAL_190	H, D_VAL_190	2.86	2.04	15.25
4KRO.PDB	O, D_PRO_191	N, D_SER_194	H, D_SER_194	2.76	1.94	14.19
4KRO.PDB	O, D_PRO_191	OG, D_SER_194	HG, D_SER_194	2.46	1.63	8.00
4KRO.PDB	O, D_SER_194	N, D_GLN_198	H, D_GLN_198	2.58	1.74	10.02
4KRO.PDB	OD1, D_ASN_161	N, D_ILE_201	H, D_ILE_201	2.82	1.96	5.92
4KRO.PDB	O, D_SER_159	N, D_ASN_203	H, D_ASN_203	2.69	1.89	17.41
4KRO.PDB	O, D_VAL_213	N, D_VAL_204	H, D_VAL_204	2.66	1.81	8.41
4KRO.PDB	O, D_THR_211	N, D_HIS_206	H, D_HIS_206	2.94	2.10	11.11
4KRO.PDB	OG, D_SER_209	ND1, D_HIS_206	HD1, D_HIS_206	2.71	1.87	9.56
4KRO.PDB	O, D_PRO_153	NE2, D_HIS_206	HE2, D_HIS_206	2.79	1.99	18.14
4KRO.PDB	O, D_LYS_207	N, D_ASN_210	H, D_ASN_210	2.94	2.16	21.67
4KRO.PDB	O, D_VAL_204	N, D_VAL_213	H, D_VAL_213	2.73	1.93	18.78
4KRO.PDB	O, D_TYR_200	N, D_VAL_217	H, D_VAL_217	2.94	2.10	7.76
4KRP.PDB	OE2, A_GLU_376	NH2, A_ARG_310	HH21, A_ARG_310	2.93	2.09	9.81
4KRP.PDB	OG1, A_THR_339	N, A_LYS_311	H, A_LYS_311	2.83	2.07	23.53
4KRP.PDB	O, A_SER_340	N, A_CYS_313	H, A_CYS_313	2.79	2.04	24.55
4KRP.PDB	O, A_ILE_318	N, A_PHE_321	H, A_PHE_321	2.70	1.86	11.77

4KRP.PDB	OD1, A_ASN_331	N, A_ASN_328	H, A_ASN_328	2.72	1.98	25.49
4KRP.PDB	OD1, A_ASN_328	N, A_ASN_331	H, A_ASN_331	2.86	2.01	7.83
4KRP.PDB	O, A_SER_326	ND2, A_ASN_331	HD21, A_ASN_331	2.94	2.16	20.31
4KRP.PDB	O, A_LYS_311	N, A_THR_339	H, A_THR_339	2.82	1.97	9.55
4KRP.PDB	O, A_CYS_313	N, A_SER_342	H, A_SER_342	2.72	1.88	10.06
4KRP.PDB	O, A_PHE_380	N, A_LEU_345	H, A_LEU_345	3.00	2.26	26.76
4KRP.PDB	O, A_LEU_382	N, A_ILE_347	H, A_ILE_347	2.72	1.92	18.37
4KRP.PDB	O, A_PRO_349	N, A_PHE_352	H, A_PHE_352	2.78	2.03	24.55
4KRP.PDB	O, D_GLY_54	NH2, A_ARG_353	HH22, A_ARG_353	2.83	1.98	6.79
4KRP.PDB	O, A_VAL_350	N, A_GLY_354	H, A_GLY_354	2.64	1.84	18.31
4KRP.PDB	O, A_SER_356	N, A_HIS_359	H, A_HIS_359	2.65	1.82	11.74
4KRP.PDB	O, A_ASP_355	N, A_THR_360	H, A_THR_360	2.92	2.06	3.09
4KRP.PDB	O, A_ALA_351	N, A_LEU_363	H, A_LEU_363	2.92	2.16	23.72
4KRP.PDB	O, A_ASP_364	N, A_GLU_367	H, A_GLU_367	2.97	2.11	4.06
4KRP.PDB	O, A_LEU_368	N, A_LEU_371	H, A_LEU_371	2.87	2.01	5.39
4KRP.PDB	O, A_ASP_369	N, A_LYS_372	H, A_LYS_372	2.94	2.10	8.68
4KRP.PDB	O, A_LEU_371	N, A_VAL_374	H, A_VAL_374	2.92	2.07	7.73
4KRP.PDB	O, A_THR_339	N, A_LYS_375	H, A_LYS_375	2.78	1.92	1.18
4KRP.PDB	O, A_GLY_343	N, A_GLY_379	H, A_GLY_379	2.76	2.04	28.24
4KRP.PDB	O, A_SER_413	N, A_LEU_381	H, A_LEU_381	2.81	2.01	17.34
4KRP.PDB	O, A_LEU_345	N, A_LEU_382	H, A_LEU_382	2.80	1.94	4.00
4KRP.PDB	O, A_ILE_347	N, A_GLN_384	H, A_GLN_384	2.84	2.01	12.43
4KRP.PDB	O, A_LEU_424	N, A_LEU_393	H, A_LEU_393	2.97	2.16	16.10
4KRP.PDB	O, A_HIS_394	N, A_GLU_397	H, A_GLU_397	2.88	2.13	24.87
4KRP.PDB	O, A_LYS_375	N, A_GLU_400	H, A_GLU_400	2.71	1.87	9.05
4KRP.PDB	O, A_ILE_377	N, A_ARG_403	H, A_ARG_403	2.92	2.09	14.20
4KRP.PDB	O, A_THR_378	N, A_ARG_405	H, A_ARG_405	2.67	1.81	2.52
4KRP.PDB	OD1, B_ASP_115	NH2, A_ARG_405	HH21, A_ARG_405	2.63	1.81	15.48
4KRP.PDB	O, A_PHE_412	N, A_GLN_408	H, A_GLN_408	2.79	2.03	23.31
4KRP.PDB	O, A_LYS_407	N, A_GLY_410	H, A_GLY_410	2.86	2.05	17.53
4KRP.PDB	O, A_GLN_408	N, A_GLN_411	H, A_GLN_411	2.78	2.00	20.78
4KRP.PDB	O, A_ASP_436	N, A_SER_413	H, A_SER_413	2.87	2.07	17.71
4KRP.PDB	O, A_ILE_438	N, A_VAL_416	H, A_VAL_416	2.90	2.08	16.39
4KRP.PDB	O, A_SER_440	N, A_SER_418	H, A_SER_418	2.95	2.20	24.18
4KRP.PDB	OD1, A_ASN_442	N, A_LEU_419	H, A_LEU_419	2.73	1.91	15.19
4KRP.PDB	O, A_THR_391	N, A_THR_422	H, A_THR_422	2.73	1.88	8.32
4KRP.PDB	OD1, A_ASP_498	NE, A_ARG_427	HE, A_ARG_427	2.55	1.82	26.18
4KRP.PDB	OD1, A_ASP_498	NH2, A_ARG_427	HH21, A_ARG_427	2.59	1.89	29.61
4KRP.PDB	O, A_LEU_426	N, A_LEU_429	H, A_LEU_429	3.00	2.18	15.49
4KRP.PDB	O, A_GLU_400	N, A_LYS_430	H, A_LYS_430	2.88	2.03	9.97
4KRP.PDB	O, A_LEU_456	N, A_ILE_432	H, A_ILE_432	2.71	1.86	9.38
4KRP.PDB	OE2, A_GLU_431	OG, A_SER_433	HG, A_SER_433	2.69	1.90	15.48
4KRP.PDB	O, A_GLN_411	N, A_ASP_436	H, A_ASP_436	2.90	2.06	8.63
4KRP.PDB	O, A_LEU_414	N, A_ILE_438	H, A_ILE_438	2.88	2.06	16.00
4KRP.PDB	O, A_LYS_465	N, A_ILE_439	H, A_ILE_439	2.90	2.09	17.29
4KRP.PDB	O, A_VAL_416	N, A_SER_440	H, A_SER_440	2.97	2.14	13.77
4KRP.PDB	O, D_TYR_102	OG, A_SER_440	HG, A_SER_440	2.65	1.82	4.10
4KRP.PDB	OD1, A_ASN_469	N, A_ASN_442	H, A_ASN_442	2.97	2.19	20.16
4KRP.PDB	OD1, A_ASN_469	ND2, A_ASN_442	HD22, A_ASN_442	2.94	2.17	23.18
4KRP.PDB	OD1, D_ASP_58	NZ, A_LYS_443	HZ1, A_LYS_443	2.65	1.82	17.69
4KRP.PDB	O, A_ASN_442	N, A_LEU_445	H, A_LEU_445	2.90	2.04	7.12
4KRP.PDB	O, A_THR_422	N, A_CYS_446	H, A_CYS_446	2.71	1.90	15.25
4KRP.PDB	O, A_TYR_447	N, A_ASN_449	H, A_ASN_449	2.43	1.66	21.82
4KRP.PDB	OE1, A_GLU_489	NZ, A_LYS_455	HZ2, A_LYS_455	2.95	2.19	25.72
4KRP.PDB	O, A_TRP_453	N, A_LEU_456	H, A_LEU_456	2.87	2.09	20.64
4KRP.PDB	OE1, A_GLN_462	N, A_THR_459	H, A_THR_459	2.95	2.18	22.01
4KRP.PDB	O, A_SER_433	OG1, A_THR_459	HG1, A_THR_459	2.66	1.97	29.29
4KRP.PDB	O, A_GLY_435	NE2, A_GLN_462	HE21, A_GLN_462	2.76	1.90	2.70

4KRP.PDB	O, A_ILE.432	NE2, A_GLN.462	HE22, A_GLN.462	2.97	2.15	14.48
4KRP.PDB	O, A_VAL.437	N, A_LYS.465	H, A_LYS.465	2.75	1.95	18.20
4KRP.PDB	OD2, D_ASP.103	NZ, A_LYS.465	HZ2, A_LYS.465	2.93	2.05	5.06
4KRP.PDB	O, A_ILE.439	N, A_ILE.467	H, A_ILE.467	2.93	2.10	12.53
4KRP.PDB	OG, A_SER.474	NE, A_ARG.470	HE, A_ARG.470	2.76	1.96	18.13
4KRP.PDB	O, A_LYS.476	N, A_GLY.479	H, A_GLY.479	2.71	1.88	12.77
4KRP.PDB	O, A_CYS.475	N, A_GLN.480	H, A_GLN.480	2.77	1.95	13.73
4KRP.PDB	O, A_SER.501	N, A_SER.487	H, A_SER.487	2.89	2.04	7.18
4KRP.PDB	OG, A_SER.501	OG, A_SER.487	HG, A_SER.487	2.45	1.66	16.67
4KRP.PDB	O, A_ASP.498	N, A_TRP.492	H, A_TRP.492	2.79	1.96	13.24
4KRP.PDB	OE1, A_GLU.495	NE, A_ARG.497	HE, A_ARG.497	2.60	1.79	14.71
4KRP.PDB	O, A_GLU.495	N, A_ASP.498	H, A_ASP.498	2.96	2.15	17.44
4KRP.PDB	O, A_GLY.490	N, A_VAL.500	H, A_VAL.500	2.88	2.04	9.24
4KRP.PDB	O, A_LEU.485	N, A_ARG.503	H, A_ARG.503	2.76	1.97	19.17
4KRP.PDB	O, A_GLU.510	N, A_ARG.507	H, A_ARG.507	2.85	2.07	20.90
4KRP.PDB	OE1, A_GLU.524	NE, A_ARG.507	HE, A_ARG.507	2.83	2.04	19.78
4KRP.PDB	O, A_VAL.505	N, A_VAL.512	H, A_VAL.512	2.78	1.98	18.78
4KRP.PDB	O, A_GLY.520	NH1, A_ARG.523	HH11, A_ARG.523	2.96	2.22	25.33
4KRP.PDB	O, A_ASN.516	N, A_GLU.524	H, A_GLU.524	2.98	2.17	17.27
4KRP.PDB	O, A_ILE.532	N, A_PHE.525	H, A_PHE.525	2.83	2.06	21.15
4KRP.PDB	O, A_GLU.530	N, A_GLU.527	H, A_GLU.527	2.83	2.00	14.02
4KRP.PDB	O, A_SER.506	N, A_CYS.531	H, A_CYS.531	2.79	1.96	12.76
4KRP.PDB	O, A_PHE.525	N, A_ILE.532	H, A_ILE.532	2.70	1.90	17.86
4KRP.PDB	O, A_ARG.523	N, A_CYS.534	H, A_CYS.534	2.73	1.90	12.34
4KRP.PDB	O, A_HIS.535	N, A_CYS.538	H, A_CYS.538	2.99	2.17	14.86
4KRP.PDB	O, A_GLN.557	N, A_LEU.539	H, A_LEU.539	2.68	1.97	29.21
4KRP.PDB	O, A_LEU.539	NE2, A_GLN.541	HE21, A_GLN.541	2.85	2.01	8.93
4KRP.PDB	OD1, A_ASN.544	N, A_ILE.545	H, A_ILE.545	2.79	2.04	25.27
4KRP.PDB	OE2, A_GLU.527	NH2, A_ARG.550	HH22, A_ARG.550	2.54	1.76	21.10
4KRP.PDB	O, A_GLU.537	N, A_ALA.559	H, A_ALA.559	2.74	1.88	1.56
4KRP.PDB	O, A_ALA.559	ND1, A_HIS.560	HD1, A_HIS.560	2.61	1.91	29.44
4KRP.PDB	O, A_HIS.566	N, A_ASP.563	H, A_ASP.563	2.73	1.89	10.58
4KRP.PDB	O, A_TYR.561	N, A_VAL.568	H, A_VAL.568	2.97	2.14	13.62
4KRP.PDB	OG, C_SER.26	N, C_LEU.3	H, C_LEU.3	2.98	2.13	7.00
4KRP.PDB	O, C_ARG.24	N, C_THR.5	H, C_THR.5	2.78	1.93	4.32
4KRP.PDB	O, C_TYR.86	NE2, C_GLN.6	HE22, C_GLN.6	2.90	2.07	11.06
4KRP.PDB	O, C_SER.22	N, C_SER.7	H, C_SER.7	2.93	2.12	15.95
4KRP.PDB	O, C_LYS.103	N, C_LEU.11	H, C_LEU.11	2.74	2.00	25.88
4KRP.PDB	OE1, C_GLU.17	N, C_SER.14	H, C_SER.14	2.90	2.05	7.83
4KRP.PDB	O, C_VAL.78	N, C_GLY.16	H, C_GLY.16	2.86	2.04	14.86
4KRP.PDB	O, C_ILE.75	N, C_VAL.19	H, C_VAL.19	2.92	2.12	19.12
4KRP.PDB	O, C_LEU.73	N, C_PHE.21	H, C_PHE.21	2.85	2.02	11.22
4KRP.PDB	O, C_SER.7	N, C_SER.22	H, C_SER.22	2.96	2.13	12.93
4KRP.PDB	O, C_THR.5	N, C_ARG.24	H, C_ARG.24	2.76	1.98	20.70
4KRP.PDB	O, C_THR.69	N, C_ALA.25	H, C_ALA.25	2.58	1.76	13.74
4KRP.PDB	O, C_LEU.3	N, C_SER.26	H, C_SER.26	2.90	2.10	18.68
4KRP.PDB	O, C_GLY.68	N, C_ILE.29	H, C_ILE.29	2.84	2.01	12.74
4KRP.PDB	OD1, C_ASN.92	ND2, C_ASN.32	HD22, C_ASN.32	2.85	2.14	29.38
4KRP.PDB	O, C_THR.31	N, C_ILE.33	H, C_ILE.33	2.75	2.02	26.66
4KRP.PDB	O, C_GLN.89	N, C_HIS.34	H, C_HIS.34	2.86	2.05	15.92
4KRP.PDB	O, C_ILE.48	N, C_TRP.35	H, C_TRP.35	2.96	2.13	11.92
4KRP.PDB	O, C_TYR.87	N, C_TYR.36	H, C_TYR.36	2.77	1.96	16.47
4KRP.PDB	OE1, C_GLN.89	OH, C_TYR.36	HH, C_TYR.36	2.33	1.50	6.36
4KRP.PDB	O, C_ARG.45	N, C_GLN.37	H, C_GLN.37	2.82	2.00	14.50
4KRP.PDB	OH, C_TYR.86	NE2, C_GLN.37	HE21, C_GLN.37	2.85	2.02	13.51
4KRP.PDB	O, C_ASP.85	N, C_GLN.38	H, C_GLN.38	2.84	2.04	18.23
4KRP.PDB	OE1, D_GLN.39	NE2, C_GLN.38	HE22, C_GLN.38	2.70	1.84	6.09
4KRP.PDB	O, C_ARG.39	N, C_GLY.42	H, C_GLY.42	2.94	2.19	25.37

4KRP.PDB	O, C_GLN_37	N, C_ARG_45	H, C_ARG_45	2.51	1.81	29.63
4KRP.PDB	O, C_TRP_35	N, C_LEU_47	H, C_LEU_47	2.88	2.04	8.47
4KRP.PDB	O, C_GLU_53	N, C_LYS_49	H, C_LYS_49	2.92	2.08	11.40
4KRP.PDB	OE1, C_GLU_53	NZ, C_LYS_49	HZ3, C_LYS_49	2.81	1.93	8.64
4KRP.PDB	OD2, D_ASP_103	OH, C_TYR_50	HH, C_TYR_50	2.43	1.66	18.96
4KRP.PDB	O, C_ILE_33	N, C_ALA_51	H, C_ALA_51	2.69	1.90	19.00
4KRP.PDB	OD1, C_ASP_82	NH2, C_ARG_61	HH21, C_ARG_61	2.79	1.98	15.39
4KRP.PDB	O, C_SER_74	N, C_SER_63	H, C_SER_63	2.89	2.12	22.33
4KRP.PDB	O, C_THR_72	N, C_SER_65	H, C_SER_65	2.82	2.03	19.74
4KRP.PDB	O, C_GLY_30	N, C_GLY_68	H, C_GLY_68	2.65	1.84	16.72
4KRP.PDB	O, C_CYS_23	N, C_PHE_71	H, C_PHE_71	2.92	2.13	19.47
4KRP.PDB	O, C_SER_65	N, C_THR_72	H, C_THR_72	2.85	2.06	18.53
4KRP.PDB	O, C_SER_63	N, C_SER_74	H, C_SER_74	2.53	1.70	12.96
4KRP.PDB	O, C_VAL_19	N, C_ILE_75	H, C_ILE_75	2.98	2.18	17.84
4KRP.PDB	OD2, C_ASP_82	N, C_GLU_79	H, C_GLU_79	2.97	2.11	4.01
4KRP.PDB	O, C_GLN_38	N, C_ASP_85	H, C_ASP_85	2.96	2.14	13.68
4KRP.PDB	O, C_THR_102	N, C_TYR_86	H, C_TYR_86	2.85	2.05	17.70
4KRP.PDB	O, C_ASP_82	OH, C_TYR_86	HH, C_TYR_86	2.56	1.73	8.98
4KRP.PDB	O, C_HIS_34	N, C_GLN_89	H, C_GLN_89	2.79	2.03	23.96
4KRP.PDB	OG1, C_THR_96	NE2, C_GLN_89	HE21, C_GLN_89	2.69	1.93	23.74
4KRP.PDB	O, C_ASN_93	NE2, C_GLN_90	HE22, C_GLN_90	2.65	1.80	8.11
4KRP.PDB	O, C_ASN_32	N, C_ASN_91	H, C_ASN_91	2.95	2.16	18.97
4KRP.PDB	OD1, D_ASP_103	ND2, C_ASN_91	HD21, C_ASN_91	2.77	1.91	6.24
4KRP.PDB	OD1, C_ASN_93	ND2, C_ASN_92	HD22, C_ASN_92	2.69	1.97	27.74
4KRP.PDB	OE1, C_GLN_90	N, C_ASN_93	H, C_ASN_93	2.83	2.02	15.94
4KRP.PDB	O, A_ASN_469	N, C_TRP_94	H, C_TRP_94	2.68	1.89	19.97
4KRP.PDB	OD2, D_ASP_58	NE1, C_TRP_94	HE1, C_TRP_94	2.98	2.17	17.26
4KRP.PDB	O, C_GLN_90	OG1, C_THR_96	HG1, C_THR_96	2.81	1.98	6.89
4KRP.PDB	O, C_CYS_88	N, C_GLY_99	H, C_GLY_99	2.82	1.98	10.72
4KRP.PDB	OE1, C_GLN_6	N, C_GLY_101	H, C_GLY_101	2.99	2.26	27.03
4KRP.PDB	O, C_TYR_86	N, C_THR_102	H, C_THR_102	2.99	2.27	27.64
4KRP.PDB	O, C_PRO_8	OG1, C_THR_102	HG1, C_THR_102	2.64	1.87	19.11
4KRP.PDB	O, C_VAL_9	N, C_LYS_103	H, C_LYS_103	2.82	2.01	15.16
4KRP.PDB	OE2, C_GLU_105	NZ, C_LYS_103	HZ1, C_LYS_103	2.82	2.05	25.15
4KRP.PDB	O, C_ALA_84	N, C_LEU_104	H, C_LEU_104	2.94	2.09	2.60
4KRP.PDB	O, C_VAL_13	N, C_LYS_107	H, C_LYS_107	2.79	1.98	15.54
4KRP.PDB	O, C_TYR_140	N, C_ALA_111	H, C_ALA_111	2.77	1.92	7.65
4KRP.PDB	O, C_LEU_135	N, C_PHE_116	H, C_PHE_116	2.88	2.06	15.19
4KRP.PDB	O, C_VAL_133	N, C_PHE_118	H, C_PHE_118	2.72	1.89	12.07
4KRP.PDB	OG, C_SER_131	NE2, C_GLN_124	HE22, C_GLN_124	2.89	2.10	19.98
4KRP.PDB	O, C_GLN_124	N, C_SER_127	H, C_SER_127	2.75	2.03	27.79
4KRP.PDB	O, C_LEU_125	N, C_GLY_128	H, C_GLY_128	2.99	2.19	18.71
4KRP.PDB	O, C_LEU_179	N, C_VAL_132	H, C_VAL_132	2.64	1.85	19.72
4KRP.PDB	O, C_SER_177	N, C_CYS_134	H, C_CYS_134	2.73	1.88	7.44
4KRP.PDB	O, C_PHE_116	N, C_LEU_135	H, C_LEU_135	2.66	1.81	8.16
4KRP.PDB	O, C_LEU_175	N, C_LEU_136	H, C_LEU_136	2.74	1.88	6.29
4KRP.PDB	O, C_SER_114	N, C_ASN_137	H, C_ASN_137	2.81	1.97	10.83
4KRP.PDB	OG, C_SER_174	N, C_ASN_138	H, C_ASN_138	2.97	2.11	3.04
4KRP.PDB	O, C_TYR_173	N, C_PHE_139	H, C_PHE_139	2.73	1.95	19.51
4KRP.PDB	O, C_ALA_111	N, C_TYR_140	H, C_TYR_140	2.91	2.08	13.77
4KRP.PDB	O, C_THR_197	N, C_LYS_145	H, C_LYS_145	2.91	2.06	4.69
4KRP.PDB	O, C_GLU_195	N, C_GLN_147	H, C_GLN_147	2.81	1.96	9.38
4KRP.PDB	O, C_ALA_193	N, C_LYS_149	H, C_LYS_149	2.85	2.05	18.63
4KRP.PDB	O, C_ALA_153	NE2, C_GLN_155	HE21, C_GLN_155	2.95	2.09	2.78
4KRP.PDB	OE1, C_GLN_155	ND2, C_ASN_158	HD21, C_ASN_158	2.83	2.12	29.23
4KRP.PDB	O, D_LEU_176	NE2, C_GLN_160	HE22, C_GLN_160	2.56	1.80	22.58
4KRP.PDB	O, C_SER_176	N, C_SER_162	H, C_SER_162	2.90	2.19	29.40
4KRP.PDB	O, D_PRO_173	OG, C_SER_162	HG, C_SER_162	2.80	2.10	28.74

4KRP.PDB	O, C_SER.174	N, C_THR.164	H, C_THR.164	2.91	2.07	10.69
4KRP.PDB	O, C_LEU.106	NE2, C_GLN.166	HE22, C_GLN.166	2.63	1.89	25.54
4KRP.PDB	OD2, C_ASP.167	N, C_LYS.169	H, C_LYS.169	2.96	2.14	15.63
4KRP.PDB	OD1, C_ASP.170	N, C_THR.172	H, C_THR.172	2.88	2.10	20.13
4KRP.PDB	OD1, C_ASP.170	OG1, C_THR.172	HG1, C_THR.172	2.53	1.69	5.91
4KRP.PDB	O, C_PHE.139	N, C_TYR.173	H, C_TYR.173	2.71	1.87	11.75
4KRP.PDB	O, C_LEU.136	N, C_LEU.175	H, C_LEU.175	2.80	2.00	17.17
4KRP.PDB	O, C_SER.162	N, C_SER.176	H, C_SER.176	2.91	2.09	14.35
4KRP.PDB	O, C_CYS.134	N, C_SER.177	H, C_SER.177	2.80	1.97	12.12
4KRP.PDB	O, C_GLN.160	N, C_THR.178	H, C_THR.178	2.94	2.21	26.85
4KRP.PDB	O, C_VAL.132	N, C_LEU.179	H, C_LEU.179	2.74	1.93	15.89
4KRP.PDB	O, C_ALA.130	N, C_LEU.181	H, C_LEU.181	2.98	2.18	18.35
4KRP.PDB	O, C_SER.182	N, C_TYR.186	H, C_TYR.186	2.78	1.98	17.36
4KRP.PDB	O, C_LYS.183	N, C_GLU.187	H, C_GLU.187	2.89	2.07	14.82
4KRP.PDB	O, C_ASP.185	ND1, C_HIS.189	HD1, C_HIS.189	2.74	1.90	11.57
4KRP.PDB	OD1, C_ASP.151	N, C_VAL.191	H, C_VAL.191	2.89	2.04	6.74
4KRP.PDB	O, C_TYR.186	OH, C_TYR.192	HH, C_TYR.192	2.61	1.88	24.84
4KRP.PDB	O, C_LYS.149	N, C_ALA.193	H, C_ALA.193	2.84	2.08	22.88
4KRP.PDB	O, C_LYS.207	N, C_CYS.194	H, C_CYS.194	2.89	2.06	14.21
4KRP.PDB	O, C_GLN.147	N, C_GLU.195	H, C_GLU.195	2.73	1.87	5.27
4KRP.PDB	O, C_VAL.205	N, C_VAL.196	H, C_VAL.196	2.64	1.80	9.51
4KRP.PDB	O, C_LYS.145	N, C_THR.197	H, C_THR.197	2.81	1.98	11.85
4KRP.PDB	O, C_PRO.141	NE2, C_HIS.198	HE2, C_HIS.198	2.87	2.02	6.17
4KRP.PDB	O, C_LYS.190	N, C_ARG.211	H, C_ARG.211	2.85	2.03	15.20
4KRP.PDB	O, C_HIS.189	NE, C_ARG.211	HE, C_ARG.211	2.71	1.90	16.56
4KRP.PDB	O, D_SER.25	N, D_GLN.3	H, D_GLN.3	2.74	1.91	10.35
4KRP.PDB	O, D_THR.23	N, D_LYS.5	H, D_LYS.5	2.97	2.12	3.88
4KRP.PDB	OE1, D_GLN.111	N, D_GLN.6	H, D_GLN.6	2.91	2.08	12.88
4KRP.PDB	OG1, D_THR.113	NE2, D_GLN.6	HE21, D_GLN.6	2.88	2.03	4.76
4KRP.PDB	O, D_TYR.93	NE2, D_GLN.6	HE22, D_GLN.6	2.91	2.18	26.39
4KRP.PDB	O, D_THR.21	N, D_SER.7	H, D_SER.7	2.78	1.98	17.63
4KRP.PDB	O, D_LEU.85	N, D_SER.15	H, D_SER.15	2.66	1.85	14.89
4KRP.PDB	O, D_GLN.13	N, D_GLN.16	H, D_GLN.16	2.90	2.10	17.19
4KRP.PDB	O, D_MET.82	N, D_LEU.18	H, D_LEU.18	2.72	1.90	13.60
4KRP.PDB	O, D_SER.7	N, D_THR.21	H, D_THR.21	2.80	1.94	2.06
4KRP.PDB	O, D_VAL.78	N, D_CYS.22	H, D_CYS.22	2.79	1.97	15.13
4KRP.PDB	O, D_LYS.5	N, D_THR.23	H, D_THR.23	2.64	1.81	12.04
4KRP.PDB	O, D_SER.76	N, D_VAL.24	H, D_VAL.24	2.93	2.08	8.52
4KRP.PDB	OG, D_SER.28	N, D_THR.30	H, D_THR.30	2.95	2.11	10.64
4KRP.PDB	O, D_ALA.96	N, D_HIS.35	H, D_HIS.35	2.75	1.91	9.74
4KRP.PDB	O, D_GLY.49	N, D_TRP.36	H, D_TRP.36	2.84	2.06	19.69
4KRP.PDB	O, D_TYR.94	N, D_VAL.37	H, D_VAL.37	2.90	2.08	13.15
4KRP.PDB	O, D_GLU.46	N, D_ARG.38	H, D_ARG.38	2.87	2.05	14.44
4KRP.PDB	OH, D_TYR.93	NH1, D_ARG.38	HH11, D_ARG.38	2.96	2.18	20.80
4KRP.PDB	OD1, D_ASP.89	NH1, D_ARG.38	HH12, D_ARG.38	2.91	2.06	7.49
4KRP.PDB	OE1, C_GLN.38	NE2, D_GLN.39	HE22, D_GLN.39	2.72	1.87	5.47
4KRP.PDB	O, D_ARG.38	N, D_GLU.46	H, D_GLU.46	2.84	2.01	12.31
4KRP.PDB	O, D_TRP.36	N, D_LEU.48	H, D_LEU.48	2.81	1.97	10.41
4KRP.PDB	O, D_ASP.58	N, D_VAL.50	H, D_VAL.50	2.83	2.10	26.44
4KRP.PDB	O, D_ASN.56	N, D_TRP.52	H, D_TRP.52	2.85	2.04	16.32
4KRP.PDB	O, D_LEU.48	N, D_ASN.60	H, D_ASN.60	2.81	1.96	6.79
4KRP.PDB	O, D_TRP.47	ND2, D_ASN.60	HD22, D_ASN.60	2.84	2.05	19.17
4KRP.PDB	O, D_ASN.60	N, D_PHE.63	H, D_PHE.63	2.99	2.23	24.51
4KRP.PDB	OD1, D_ASP.89	NH2, D_ARG.66	HH22, D_ARG.66	2.59	1.74	9.60
4KRP.PDB	O, D_LYS.81	N, D_SER.68	H, D_SER.68	2.89	2.07	14.89
4KRP.PDB	OH, D_TYR.59	N, D_ILE.69	H, D_ILE.69	2.90	2.09	15.54
4KRP.PDB	O, D_CYS.22	N, D_VAL.78	H, D_VAL.78	2.72	1.92	18.23
4KRP.PDB	O, D_ASN.70	N, D_PHE.79	H, D_PHE.79	2.97	2.12	3.62

4KRP.PDB	O, D_ILE_20	N, D_PHE_80	H, D_PHE_80	2.75	1.92	12.16
4KRP.PDB	O, D_ARG_66	N, D_ASN_83	H, D_ASN_83	2.96	2.20	23.47
4KRP.PDB	O, D_GLN_16	N, D_LEU_85	H, D_LEU_85	2.88	2.04	9.71
4KRP.PDB	O, D_GLN_86	N, D_ASP_89	H, D_ASP_89	2.99	2.19	16.67
4KRP.PDB	O, D_SER_87	N, D_THR_90	H, D_THR_90	2.99	2.16	13.47
4KRP.PDB	O, D_SER_87	OG1, D_THR_90	HG1, D_THR_90	2.81	2.08	24.26
4KRP.PDB	O, D_ASP_89	OH, D_TYR_93	HH, D_TYR_93	2.65	1.83	9.74
4KRP.PDB	O, D_VAL_37	N, D_TYR_94	H, D_TYR_94	2.57	1.74	12.70
4KRP.PDB	O, D_HIS_35	N, D_ALA_96	H, D_ALA_96	2.75	1.98	21.78
4KRP.PDB	O, D_TYR_108	N, D_ARG_97	H, D_ARG_97	2.89	2.07	13.85
4KRP.PDB	O, D_ALA_98	NE, D_ARG_97	HE, D_ARG_97	2.79	1.94	9.03
4KRP.PDB	OE1, A_GLN_408	OH, D_TYR_102	HH, D_TYR_102	2.56	1.74	10.00
4KRP.PDB	OD1, D_ASP_103	N, D_TYR_104	H, D_TYR_104	2.53	1.80	26.58
4KRP.PDB	OG, A_SER_440	OH, D_TYR_104	HH, D_TYR_104	2.94	2.22	25.72
4KRP.PDB	OH, C_TYR_36	N, D_PHE_106	H, D_PHE_106	2.89	2.11	20.61
4KRP.PDB	O, D_PHE_106	NE1, D_TRP_109	HE1, D_TRP_109	2.74	2.02	27.52
4KRP.PDB	O, D_CYS_95	N, D_GLY_110	H, D_GLY_110	2.83	1.97	4.87
4KRP.PDB	O, D_TYR_93	N, D_THR_113	H, D_THR_113	2.79	2.00	19.35
4KRP.PDB	O, D_ALA_91	N, D_VAL_115	H, D_VAL_115	2.94	2.21	27.64
4KRP.PDB	O, D_GLY_10	N, D_THR_116	H, D_THR_116	2.48	1.64	10.06
4KRP.PDB	OG, D_SER_118	N, D_ALA_120	H, D_ALA_120	2.80	1.99	15.68
4KRP.PDB	O, D_PHE_152	N, D_LYS_123	H, D_LYS_123	2.61	1.84	21.89
4KRP.PDB	O, D_ASP_150	NZ, D_LYS_123	HZ2, D_LYS_123	2.97	2.10	10.97
4KRP.PDB	O, D_LYS_149	N, D_SER_126	H, D_SER_126	2.93	2.09	12.06
4KRP.PDB	O, D_LEU_147	N, D_PHE_128	H, D_PHE_128	2.93	2.14	18.89
4KRP.PDB	O, D_GLY_145	N, D_LEU_130	H, D_LEU_130	2.60	1.75	6.78
4KRP.PDB	O, D_VAL_190	N, D_ALA_142	H, D_ALA_142	2.58	1.73	8.25
4KRP.PDB	O, D_LEU_130	N, D_GLY_145	H, D_GLY_145	2.97	2.21	23.33
4KRP.PDB	O, D_SER_186	N, D_CYS_146	H, D_CYS_146	2.72	1.92	18.42
4KRP.PDB	O, D_PHE_128	N, D_LEU_147	H, D_LEU_147	2.61	1.77	10.44
4KRP.PDB	O, D_LEU_184	N, D_VAL_148	H, D_VAL_148	2.60	1.80	18.24
4KRP.PDB	O, D_TYR_182	N, D_TYR_151	H, D_TYR_151	2.99	2.17	14.93
4KRP.PDB	O, D_LYS_123	N, D_PHE_152	H, D_PHE_152	2.86	2.03	12.67
4KRP.PDB	O, D_ASN_205	N, D_THR_157	H, D_THR_157	2.80	1.97	11.71
4KRP.PDB	O, D_ILE_201	N, D_ASN_161	H, D_ASN_161	2.77	1.93	9.15
4KRP.PDB	OD1, D_ASN_203	N, D_SER_162	H, D_SER_162	2.69	1.90	19.84
4KRP.PDB	O, D_VAL_187	N, D_HIS_170	H, D_HIS_170	2.77	1.95	15.10
4KRP.PDB	O, D_SER_185	N, D_PHE_172	H, D_PHE_172	2.95	2.10	7.75
4KRP.PDB	O, D_LEU_181	N, D_GLN_177	H, D_GLN_177	2.91	2.07	9.36
4KRP.PDB	O, D_GLN_177	N, D_GLY_180	H, D_GLY_180	2.74	1.90	10.27
4KRP.PDB	OG, D_SER_179	N, D_LEU_181	H, D_LEU_181	2.98	2.17	16.32
4KRP.PDB	O, D_TYR_151	N, D_TYR_182	H, D_TYR_182	2.66	1.81	7.88
4KRP.PDB	O, D_VAL_148	N, D_LEU_184	H, D_LEU_184	2.65	1.91	24.40
4KRP.PDB	O, D_CYS_146	N, D_SER_186	H, D_SER_186	2.92	2.10	15.79
4KRP.PDB	O, D_HIS_170	N, D_VAL_187	H, D_VAL_187	2.99	2.16	13.15
4KRP.PDB	O, D_LEU_144	N, D_VAL_188	H, D_VAL_188	2.79	2.00	19.05
4KRP.PDB	O, D_ALA_142	N, D_VAL_190	H, D_VAL_190	2.74	1.92	13.51
4KRP.PDB	O, D_SER_192	N, D_SER_194	H, D_SER_194	2.72	1.97	24.52
4KRP.PDB	O, D_SER_194	N, D_THR_197	H, D_THR_197	2.83	2.02	16.59
4KRP.PDB	O, D_SER_194	N, D_GLN_198	H, D_GLN_198	2.63	1.78	8.20
4KRP.PDB	O, D_SER_159	N, D_ASN_203	H, D_ASN_203	2.84	2.01	11.39
4KRP.PDB	OD1, D_ASP_214	ND2, D_ASN_203	HD22, D_ASN_203	2.70	1.84	4.78
4KRP.PDB	O, D_VAL_213	N, D_VAL_204	H, D_VAL_204	2.74	1.92	15.13
4KRP.PDB	O, D_THR_157	N, D_ASN_205	H, D_ASN_205	2.79	1.96	11.86
4KRP.PDB	O, D_THR_211	N, D_HIS_206	H, D_HIS_206	2.93	2.14	19.62
4KRP.PDB	OG, D_SER_209	ND1, D_HIS_206	HD1, D_HIS_206	2.94	2.08	3.63
4KRP.PDB	O, D_PRO_153	NE2, D_HIS_206	HE2, D_HIS_206	2.75	1.91	8.08
4KRP.PDB	O, D_LYS_207	N, D_ASN_210	H, D_ASN_210	2.60	1.84	22.95

4KRP.PDB	OG, D_SER.209	OG1, D_THR.211	HG1, D_THR.211	2.56	1.87	28.78
4KRP.PDB	O, D_VAL.204	N, D_VAL.213	H, D_VAL.213	2.73	1.88	7.94
4KRP.PDB	O, D_TYR.200	N, D_VAL.217	H, D_VAL.217	2.90	2.06	11.80
4KRP.PDB	O, B_SER.25	N, B_GLN.3	H, B_GLN.3	2.91	2.07	9.08
4KRP.PDB	O, B_ALA.23	N, B_VAL.5	H, B_VAL.5	2.88	2.02	5.91
4KRP.PDB	OE1, A_GLU.431	OH, B_TYR.32	HH, B_TYR.32	2.59	1.78	7.49
4KRP.PDB	O, B_GLY.99	N, B_ALA.33	H, B_ALA.33	2.82	2.06	24.31
4KRP.PDB	O, B_MET.34	N, B_ILE.51	H, B_ILE.51	2.92	2.20	27.79
4KRP.PDB	O, B_SER.104	ND2, B_ASN.52	HD21, B_ASN.52	2.66	1.89	21.34
4KRP.PDB	O, B_ALA.50	N, B_TYR.59	H, B_TYR.59	2.95	2.11	9.44
4KRP.PDB	O, B_TYR.116	N, B_ALA.98	H, B_ALA.98	2.91	2.18	26.96
4KRP.PDB	OE1, A_GLU.400	OH, B_TYR.100	HH, B_TYR.100	2.94	2.13	13.29
4KRP.PDB	OE2, A_GLU.431	OH, B_TYR.116	HH, B_TYR.116	2.43	1.75	29.09
4NZR.PDB	O, H_SER.25	N, H_GLN.3	H, H_GLN.3	2.88	2.05	13.11
4NZR.PDB	O, H_THR.23	N, H_GLN.5	H, H_GLN.5	2.98	2.24	25.71
4NZR.PDB	O, H_SER.21	N, H_SER.7	H, H_SER.7	2.82	2.05	20.97
4NZR.PDB	O, H_THR.110	N, H_VAL.12	H, H_VAL.12	2.90	2.11	18.80
4NZR.PDB	OE1, H_GLU.16	N, H_LYS.13	H, H_LYS.13	2.94	2.09	8.37
4NZR.PDB	O, H_VAL.82C	N, H_SER.15	H, H_SER.15	2.76	1.92	10.81
4NZR.PDB	O, H_LEU.82	N, H_LEU.18	H, H_LEU.18	2.85	2.05	16.86
4NZR.PDB	O, H_LEU.80	N, H_LEU.20	H, H_LEU.20	2.86	2.03	13.74
4NZR.PDB	O, H_PHE.78	N, H_CYS.22	H, H_CYS.22	2.79	1.97	15.99
4NZR.PDB	O, H_GLN.5	N, H_THR.23	H, H_THR.23	2.93	2.12	16.85
4NZR.PDB	O, H_ASN.76	N, H_VAL.24	H, H_VAL.24	2.94	2.10	8.87
4NZR.PDB	O, H_GLN.3	N, H_SER.25	H, H_SER.25	2.82	1.99	12.13
4NZR.PDB	OD1, H_ASN.76	N, H_ILE.29	H, H_ILE.29	2.97	2.16	16.56
4NZR.PDB	O, H_ASP.31E	N, H_GLY.31A	H, H_GLY.31A	2.95	2.12	14.61
4NZR.PDB	O, H_GLU.31B	N, H_ASP.31E	H, H_ASP.31E	2.99	2.13	1.38
4NZR.PDB	O, H_ALA.93	N, H_GLY.35	H, H_GLY.35	2.82	1.96	6.32
4NZR.PDB	O, H_GLY.49	N, H_TRP.36	H, H_TRP.36	2.93	2.18	24.86
4NZR.PDB	O, H_PHE.91	N, H_VAL.37	H, H_VAL.37	2.89	2.07	13.63
4NZR.PDB	O, H_GLU.46	N, H_ARG.38	H, H_ARG.38	2.82	2.00	14.96
4NZR.PDB	OE1, H_GLU.46	NE, H_ARG.38	HE, H_ARG.38	2.83	2.07	23.07
4NZR.PDB	OH, H_TYR.90	NH1, H_ARG.38	HH11, H_ARG.38	2.96	2.16	17.91
4NZR.PDB	OD1, H_ASP.86	NH1, H_ARG.38	HH12, H_ARG.38	2.73	1.88	7.20
4NZR.PDB	OE1, H_GLU.46	NH2, H_ARG.38	HH21, H_ARG.38	2.78	2.02	22.98
4NZR.PDB	O, H_VAL.89	N, H_HIS.39	H, H_HIS.39	2.78	1.96	14.92
4NZR.PDB	O, H_SER.40	N, H_LYS.43	H, H_LYS.43	2.77	1.94	13.14
4NZR.PDB	O, H_ARG.38	N, H_GLU.46	H, H_GLU.46	2.92	2.12	17.91
4NZR.PDB	OG, H_SER.50	NE1, H_TRP.47	HE1, H_TRP.47	2.87	2.03	11.63
4NZR.PDB	O, H_TRP.36	N, H_ILE.48	H, H_ILE.48	2.93	2.07	4.55
4NZR.PDB	O, H_HIS.58	N, H_SER.50	H, H_SER.50	2.85	2.04	14.94
4NZR.PDB	O, H_TRP.34	N, H_ILE.51	H, H_ILE.51	2.79	1.98	16.48
4NZR.PDB	O, H_THR.56	N, H_HIS.52	H, H_HIS.52	2.85	2.01	9.46
4NZR.PDB	OD1, H_ASP.31G	NE2, H_HIS.52	HE2, H_HIS.52	2.60	1.83	22.01
4NZR.PDB	OD1, H_ASP.31G	NE1, H_TRP.53	HE1, H_TRP.53	2.92	2.20	28.43
4NZR.PDB	O, H_HIS.52	N, H_GLY.55	H, H_GLY.55	2.84	2.03	16.32
4NZR.PDB	O, H_SER.50	N, H_HIS.58	H, H_HIS.58	2.89	2.05	10.67
4NZR.PDB	O, H_ILE.48	N, H_LYS.60	H, H_LYS.60	2.87	2.02	5.64
4NZR.PDB	O, H_LYS.60	N, H_LEU.63	H, H_LEU.63	2.86	2.08	20.68
4NZR.PDB	O, H_LEU.63	N, H_ARG.66	H, H_ARG.66	2.78	1.94	10.08
4NZR.PDB	O, H_ALA.82A	NH1, H_ARG.66	HH11, H_ARG.66	2.95	2.12	13.91
4NZR.PDB	OD2, H_ASP.86	NH1, H_ARG.66	HH12, H_ARG.66	2.98	2.20	21.88
4NZR.PDB	O, H_ARG.81	N, H_SER.68	H, H_SER.68	2.95	2.16	19.71
4NZR.PDB	O, H_TRP.77	N, H_ASP.72	H, H_ASP.72	2.90	2.05	4.26
4NZR.PDB	O, H_ASP.27	ND2, H_ASN.76	HD21, H_ASN.76	2.81	2.01	17.45
4NZR.PDB	O, H_VAL.24	ND2, H_ASN.76	HD22, H_ASN.76	2.87	2.02	7.45
4NZR.PDB	O, H_SER.70	N, H_SER.79	H, H_SER.79	2.92	2.13	19.56

4NZR.PDB	O, H_LEU_20	N, H_LEU_80	H, H_LEU_80	2.88	2.05	13.30
4NZR.PDB	O, H_SER_68	N, H_ARG_81	H, H_ARG_81	2.79	1.94	8.27
4NZR.PDB	O, H_LEU_18	N, H_LEU_82	H, H_LEU_82	2.82	2.00	14.32
4NZR.PDB	O, H_ARG_66	N, H_ALA_82A	H, H_ALA_82A	2.75	1.90	8.50
4NZR.PDB	O, H_THR_83	N, H_ASP_86	H, H_ASP_86	2.82	1.97	8.78
4NZR.PDB	O, H_ALA_84	N, H_THR_87	H, H_THR_87	2.95	2.10	9.57
4NZR.PDB	O, H_HIS_39	N, H_VAL_89	H, H_VAL_89	2.90	2.08	15.32
4NZR.PDB	O, H_VAL_107	N, H_TYR_90	H, H_TYR_90	2.84	2.00	11.61
4NZR.PDB	O, H_VAL_37	N, H_PHE_91	H, H_PHE_91	2.75	1.91	10.12
4NZR.PDB	OE2, H_GLU_6	N, H_CYS_92	H, H_CYS_92	2.87	2.06	15.61
4NZR.PDB	O, H_GLY_35	N, H_ALA_93	H, H_ALA_93	2.84	2.09	24.53
4NZR.PDB	O, H_VAL_102	N, H_ARG_94	H, H_ARG_94	2.90	2.15	25.02
4NZR.PDB	OD1, H_ASP_101	NE, H_ARG_94	HE, H_ARG_94	2.90	2.05	5.79
4NZR.PDB	OD2, H_ASP_101	NH2, H_ARG_94	HH21, H_ARG_94	2.73	1.90	13.79
4NZR.PDB	O, H_HIS_33	N, H_HIS_95	H, H_HIS_95	2.85	2.00	2.84
4NZR.PDB	OG, H_SER_50	ND1, H_HIS_95	HD1, H_HIS_95	2.67	1.84	11.69
4NZR.PDB	O, H_GLY_100H	NE2, H_HIS_95	HE2, H_HIS_95	2.92	2.20	27.79
4NZR.PDB	O, H_TRP_100I	N, H_ARG_96	H, H_ARG_96	2.84	2.03	17.11
4NZR.PDB	O, H_ARG_96	N, H_GLY_100H	H, H_GLY_100H	2.83	2.09	26.32
4NZR.PDB	O, H_ARG_96	N, H_TRP_100I	H, H_TRP_100I	2.87	2.13	26.51
4NZR.PDB	OH, L_TYR_36	N, H_PHE_100J	H, H_PHE_100J	2.96	2.11	8.14
4NZR.PDB	O, H_PHE_100J	NE1, H_TRP_103	HE1, H_TRP_103	2.95	2.19	23.88
4NZR.PDB	O, H_CYS_92	N, H_GLY_104	H, H_GLY_104	2.86	2.04	15.44
4NZR.PDB	OE1, H_GLU_6	N, H_GLY_106	H, H_GLY_106	2.82	2.04	21.27
4NZR.PDB	O, H_TYR_90	N, H_VAL_107	H, H_VAL_107	2.93	2.12	16.92
4NZR.PDB	O, H_ALA_88	N, H_VAL_109	H, H_VAL_109	2.86	2.00	1.82
4NZR.PDB	O, H_GLY_10	N, H_THR_110	H, H_THR_110	2.80	1.95	8.91
4NZR.PDB	OG1, H_THR_87	N, H_VAL_111	H, H_VAL_111	2.87	2.02	10.02
4NZR.PDB	O, H_VAL_12	N, H_SER_112	H, H_SER_112	2.92	2.12	18.68
4NZR.PDB	O, H_PHE_148	N, H_LYS_117	H, H_LYS_117	2.83	1.99	10.22
4NZR.PDB	O, H_ASP_146	NZ, H_LYS_117	HZ2, H_LYS_117	2.85	2.05	22.38
4NZR.PDB	O, H_LYS_145	N, H_SER_120	H, H_SER_120	2.88	2.07	16.11
4NZR.PDB	O, H_LEU_143	N, H_PHE_122	H, H_PHE_122	2.83	2.00	12.46
4NZR.PDB	O, H_GLY_141	N, H_LEU_124	H, H_LEU_124	2.75	1.90	5.12
4NZR.PDB	O, H_VAL_193	N, H_ALA_138	H, H_ALA_138	2.76	1.91	7.40
4NZR.PDB	O, H_VAL_191	N, H_LEU_140	H, H_LEU_140	2.93	2.10	13.85
4NZR.PDB	O, H_LEU_124	N, H_GLY_141	H, H_GLY_141	2.91	2.17	26.54
4NZR.PDB	O, H_SER_189	N, H_CYS_142	H, H_CYS_142	2.86	2.07	19.75
4NZR.PDB	O, H_PHE_122	N, H_LEU_143	H, H_LEU_143	2.77	1.93	12.58
4NZR.PDB	O, H_LEU_187	N, H_VAL_144	H, H_VAL_144	2.76	1.91	5.81
4NZR.PDB	O, H_SER_120	N, H_LYS_145	H, H_LYS_145	2.83	1.98	8.06
4NZR.PDB	O, H_LYS_117	N, H_PHE_148	H, H_PHE_148	2.88	2.08	18.10
4NZR.PDB	O, H_ASN_211	N, H_THR_153	H, H_THR_153	2.86	2.04	14.37
4NZR.PDB	O, H_ASN_209	N, H_SER_156	H, H_SER_156	2.93	2.11	14.90
4NZR.PDB	O, H_ILE_207	N, H_ASN_162	H, H_ASN_162	2.83	1.99	8.33
4NZR.PDB	OD1, H_ASN_209	N, H_SER_163	H, H_SER_163	2.78	2.01	22.06
4NZR.PDB	O, H_VAL_190	N, H_HIS_172	H, H_HIS_172	2.89	2.06	13.96
4NZR.PDB	O, H_SER_188	N, H_PHE_174	H, H_PHE_174	2.98	2.13	5.13
4NZR.PDB	O, H_SER_186	N, H_VAL_177	H, H_VAL_177	2.84	2.01	12.47
4NZR.PDB	O, H_LEU_184	N, H_GLN_179	H, H_GLN_179	2.83	1.98	4.97
4NZR.PDB	OD1, H_ASP_146	NE2, H_GLN_179	HE22, H_GLN_179	2.89	2.12	22.14
4NZR.PDB	O, H_GLN_179	N, H_GLY_183	H, H_GLY_183	2.81	1.99	13.79
4NZR.PDB	O, H_TYR_147	N, H_TYR_185	H, H_TYR_185	2.76	1.91	6.87
4NZR.PDB	O, H_VAL_177	N, H_SER_186	H, H_SER_186	2.92	2.15	22.72
4NZR.PDB	O, H_VAL_144	N, H_LEU_187	H, H_LEU_187	2.86	2.05	15.45
4NZR.PDB	OG, L_SER_176	OG, H_SER_188	HG, H_SER_188	2.88	2.16	24.46
4NZR.PDB	O, H_CYS_142	N, H_SER_189	H, H_SER_189	2.99	2.16	13.39
4NZR.PDB	O, H_HIS_172	N, H_VAL_190	H, H_VAL_190	2.81	1.98	14.14

4NZR.PDB	O, H.LEU_140	N, H.VAL_191	H, H.VAL_191	2.76	1.94	15.00
4NZR.PDB	O, H.ALA_138	N, H.VAL_193	H, H.VAL_193	2.76	1.96	16.51
4NZR.PDB	O, H.GLY_136	N, H.SER_195	H, H.SER_195	2.71	1.87	10.73
4NZR.PDB	O, H.PRO_194	N, H.SER_197	H, H.SER_197	2.94	2.08	6.12
4NZR.PDB	O, H.SER_197	N, H.GLN_203	H, H.GLN_203	2.86	2.05	15.22
4NZR.PDB	OD1, H.ASN_162	N, H.ILE_207	H, H.ILE_207	2.78	1.97	16.55
4NZR.PDB	O, H.SER_156	N, H.ASN_209	H, H.ASN_209	2.81	1.96	7.21
4NZR.PDB	OD1, H.ASP_220	ND2, H.ASN_209	HD22, H.ASN_209	2.89	2.06	12.07
4NZR.PDB	O, H.VAL_219	N, H.VAL_210	H, H.VAL_210	2.75	1.90	7.71
4NZR.PDB	O, H.THR_153	N, H.ASN_211	H, H.ASN_211	2.89	2.07	14.75
4NZR.PDB	OG, H.SER_215	ND1, H.HIS_212	HD1, H.HIS_212	2.80	1.99	17.07
4NZR.PDB	O, H.PRO_149	NE2, H.HIS_212	HE2, H.HIS_212	2.62	1.78	7.68
4NZR.PDB	O, H.LYS_213	N, H.ASN_216	H, H.ASN_216	2.95	2.12	11.20
4NZR.PDB	O, H.VAL_210	N, H.VAL_219	H, H.VAL_219	2.94	2.10	10.72
4NZR.PDB	O, H.CYS_208	N, H.LYS_221	H, H.LYS_221	2.90	2.08	14.73
4NZR.PDB	OE2, L.GLU_123	NZ, H.LYS_221	HZ2, H.LYS_221	2.99	2.10	2.00
4NZR.PDB	OE2, H.GLU_226	NE, H.ARG_222	HE, H.ARG_222	2.65	1.93	27.41
4NZR.PDB	O, H.TYR_206	N, H.VAL_225	H, H.VAL_225	2.90	2.05	6.78
4NZR.PDB	OG, L.SER_26	N, L.VAL_3	H, L.VAL_3	2.89	2.07	14.71
4NZR.PDB	O, L.ARG_24	N, L.THR_5	H, L.THR_5	2.79	1.95	10.02
4NZR.PDB	OE1, L.GLN_100	N, L.GLN_6	H, L.GLN_6	2.88	2.02	5.19
4NZR.PDB	O, L.TYR_86	NE2, L.GLN_6	HE22, L.GLN_6	2.88	2.05	12.91
4NZR.PDB	O, L.LYS_103	N, L.LEU_11	H, L.LEU_11	2.85	2.09	23.33
4NZR.PDB	OE2, L.GLU_17	N, L.SER_14	H, L.SER_14	2.82	1.98	9.91
4NZR.PDB	O, M.PRO_119	OG, L.SER_14	HG, L.SER_14	2.76	2.00	18.37
4NZR.PDB	O, L.MET_78	N, L.GLY_16	H, L.GLY_16	2.77	1.93	12.23
4NZR.PDB	OG1, M.THR_110	N, L.THR_18	H, L.THR_18	2.82	2.00	15.23
4NZR.PDB	O, L.ILE_75	N, L.VAL_19	H, L.VAL_19	2.83	2.05	21.72
4NZR.PDB	O, L.LEU_73	N, L.LEU_21	H, L.LEU_21	2.87	2.02	8.50
4NZR.PDB	O, L.SER_7	N, L.SER_22	H, L.SER_22	2.89	2.05	9.28
4NZR.PDB	O, L.PHE_71	N, L.CYS_23	H, L.CYS_23	2.92	2.12	16.99
4NZR.PDB	O, L.THR_5	N, L.ARG_24	H, L.ARG_24	2.83	2.01	13.32
4NZR.PDB	O, L.THR_69	N, L.ALA_25	H, L.ALA_25	2.94	2.14	18.04
4NZR.PDB	O, L.GLY_68	N, L.ILE_29	H, L.ILE_29	2.91	2.06	8.12
4NZR.PDB	OD1, L.ASN_28	N, L.ASN_30	H, L.ASN_30	2.80	1.97	11.83
4NZR.PDB	OE1, L.GLU_92	ND2, L.ASN_30	HD22, L.ASN_30	2.94	2.10	10.05
4NZR.PDB	OH, L.TYR_52	NZ, L.LYS_31	HZ1, L.LYS_31	2.57	1.77	21.34
4NZR.PDB	O, L.ILE_29	N, L.ASN_32	H, L.ASN_32	2.86	2.02	10.39
4NZR.PDB	O, L.GLN_89	N, L.ALA_34	H, L.ALA_34	2.87	2.04	11.97
4NZR.PDB	O, L.ILE_48	N, L.TRP_35	H, L.TRP_35	2.93	2.13	19.22
4NZR.PDB	O, L.TYR_87	N, L.TYR_36	H, L.TYR_36	2.69	1.88	17.31
4NZR.PDB	O, L.ARG_45	N, L.GLN_37	H, L.GLN_37	2.90	2.09	17.34
4NZR.PDB	OH, L.TYR_86	NE2, L.GLN_37	HE21, L.GLN_37	2.96	2.11	9.58
4NZR.PDB	O, L.VAL_85	N, L.TYR_38	H, L.TYR_38	2.76	1.97	19.78
4NZR.PDB	O, L.GLN_37	N, L.ARG_45	H, L.ARG_45	2.86	2.09	21.39
4NZR.PDB	O, L.TRP_35	N, L.VAL_47	H, L.VAL_47	2.91	2.05	2.37
4NZR.PDB	O, L.SER_53	N, L.PHE_49	H, L.PHE_49	2.86	2.07	19.76
4NZR.PDB	OH, L.TYR_91	N, L.GLU_50	H, L.GLU_50	2.96	2.25	29.60
4NZR.PDB	O, L.LEU_33	N, L.THR_51	H, L.THR_51	2.80	1.96	10.12
4NZR.PDB	O, L.LYS_31	OG1, L.THR_51	HG1, L.THR_51	2.80	2.02	13.30
4NZR.PDB	O, L.GLU_50	N, L.TYR_52	H, L.TYR_52	2.75	2.01	25.67
4NZR.PDB	O, L.PHE_49	N, L.SER_53	H, L.SER_53	2.90	2.12	21.06
4NZR.PDB	OH, M.TYR_444	N, L.LYS_54	H, L.LYS_54	2.91	2.06	4.85
4NZR.PDB	OD2, L.ASP_82	NH1, L.ARG_61	HH12, L.ARG_61	2.70	1.89	15.31
4NZR.PDB	O, M.ALA_391	NH2, L.ARG_61	HH21, L.ARG_61	2.90	2.11	19.46
4NZR.PDB	OD1, L.ASP_82	NH2, L.ARG_61	HH22, L.ARG_61	2.85	2.01	9.02
4NZR.PDB	O, L.THR_74	N, L.VAL_63	H, L.VAL_63	2.91	2.08	12.21
4NZR.PDB	O, L.THR_72	N, L.SER_65	H, L.SER_65	2.90	2.08	15.21

4NZR.PDB	O, L_GLU_70	N, L_SER_67	H, L_SER_67	2.94	2.16	20.85
4NZR.PDB	O, L_CYS_23	N, L_PHE_71	H, L_PHE_71	2.88	2.14	25.90
4NZR.PDB	O, L_SER_65	N, L_THR_72	H, L_THR_72	2.94	2.11	12.62
4NZR.PDB	O, L_LEU_21	N, L_LEU_73	H, L_LEU_73	2.84	2.03	16.61
4NZR.PDB	O, L_VAL_63	N, L_THR_74	H, L_THR_74	2.76	1.90	4.94
4NZR.PDB	O, L_VAL_19	N, L_ILE_75	H, L_ILE_75	2.77	1.98	19.82
4NZR.PDB	O, L_ARG_61	ND2, L_ASN_76	HD22, L_ASN_76	2.96	2.12	12.10
4NZR.PDB	OG, M_SER_106	N, L_ASN_77	H, L_ASN_77	2.86	2.01	5.30
4NZR.PDB	O, L_GLU_17	N, L_MET_78	H, L_MET_78	2.92	2.06	6.39
4NZR.PDB	OD2, L_ASP_82	N, L_GLN_79	H, L_GLN_79	2.85	2.01	8.63
4NZR.PDB	O, L_ASN_77	NE2, L_GLN_79	HE21, L_GLN_79	2.79	1.94	9.45
4NZR.PDB	O, L_GLN_79	N, L_ASP_82	H, L_ASP_82	2.93	2.08	8.91
4NZR.PDB	O, L_TYR_38	N, L_VAL_85	H, L_VAL_85	2.95	2.10	5.38
4NZR.PDB	O, L_THR_102	N, L_TYR_86	H, L_TYR_86	2.91	2.07	11.72
4NZR.PDB	O, L_TYR_36	N, L_TYR_87	H, L_TYR_87	2.86	2.04	15.92
4NZR.PDB	O, L_THR_97	N, L_GLN_90	H, L_GLN_90	2.96	2.18	20.60
4NZR.PDB	O, H_ALA_100G	NE, L_ARG_96	HE, L_ARG_96	2.83	2.08	23.79
4NZR.PDB	O, L_GLU_93	NH1, L_ARG_96	HH11, L_ARG_96	2.92	2.18	26.23
4NZR.PDB	O, H_ALA_100G	NH2, L_ARG_96	HH21, L_ARG_96	2.80	2.05	24.03
4NZR.PDB	O, L_ILE_2	OG1, L_THR_97	HG1, L_THR_97	2.76	1.95	5.21
4NZR.PDB	O, L_CYS_88	N, L_GLY_99	H, L_GLY_99	2.96	2.18	21.78
4NZR.PDB	O, L_GLN_6	NE2, L_GLN_100	HE22, L_GLN_100	2.65	1.87	20.23
4NZR.PDB	OE1, L_GLN_6	N, L_GLY_101	H, L_GLY_101	2.96	2.20	24.19
4NZR.PDB	O, L_TYR_86	N, L_THR_102	H, L_THR_102	2.92	2.12	16.99
4NZR.PDB	O, L_PRO_8	OG1, L_THR_102	HG1, L_THR_102	2.71	2.03	28.62
4NZR.PDB	O, L_ASP_9	N, L_LYS_103	H, L_LYS_103	2.97	2.17	18.66
4NZR.PDB	O, L_ALA_84	N, L_VAL_104	H, L_VAL_104	2.92	2.09	11.20
4NZR.PDB	O, L_LEU_11	N, L_ASP_105	H, L_ASP_105	2.92	2.08	10.70
4NZR.PDB	O, L_VAL_13	N, L_LYS_107	H, L_LYS_107	2.87	2.06	16.88
4NZR.PDB	O, L_THR_109	NE, L_ARG_108	HE, L_ARG_108	2.88	2.03	6.39
4NZR.PDB	O, L_ASP_170	NH1, L_ARG_108	HH11, L_ARG_108	2.85	2.01	10.32
4NZR.PDB	O, M_ASN_177	NH2, L_ARG_108	HH22, L_ARG_108	2.82	2.05	22.21
4NZR.PDB	O, M_GLY_178	N, L_THR_109	H, L_THR_109	2.92	2.07	5.99
4NZR.PDB	O, M_GLY_178	OG1, L_THR_109	HG1, L_THR_109	2.88	2.17	26.23
4NZR.PDB	O, M_ASP_117	N, L_VAL_110	H, L_VAL_110	2.96	2.14	15.09
4NZR.PDB	O, L_TYR_140	N, L_ALA_111	H, L_ALA_111	2.82	1.99	12.32
4NZR.PDB	O, L_LEU_135	N, L_PHE_116	H, L_PHE_116	2.94	2.12	15.43
4NZR.PDB	O, L_VAL_133	N, L_PHE_118	H, L_PHE_118	2.81	1.99	14.02
4NZR.PDB	OG, L_SER_121	N, L_GLN_124	H, L_GLN_124	2.99	2.17	16.25
4NZR.PDB	OG, L_SER_131	NE2, L_GLN_124	HE22, L_GLN_124	2.90	2.04	4.21
4NZR.PDB	O, L_GLN_124	N, L_SER_127	H, L_SER_127	2.85	2.12	26.70
4NZR.PDB	O, L_LEU_125	N, L_GLY_128	H, L_GLY_128	2.99	2.18	17.68
4NZR.PDB	O, L_LEU_181	N, L_ALA_130	H, L_ALA_130	2.81	2.02	18.51
4NZR.PDB	OE1, L_GLN_124	N, L_SER_131	H, L_SER_131	2.91	2.10	17.17
4NZR.PDB	O, L_LEU_179	N, L_VAL_132	H, L_VAL_132	2.79	1.95	10.51
4NZR.PDB	O, L_SER_177	N, L_CYS_134	H, L_CYS_134	2.78	1.94	10.51
4NZR.PDB	O, L_PHE_116	N, L_LEU_135	H, L_LEU_135	2.78	1.93	7.68
4NZR.PDB	O, L_LEU_175	N, L_LEU_136	H, L_LEU_136	2.79	1.93	3.71
4NZR.PDB	O, L_SER_114	N, L_ASN_137	H, L_ASN_137	2.76	1.93	13.32
4NZR.PDB	OG, L_SER_174	N, L_ASN_138	H, L_ASN_138	2.97	2.12	9.18
4NZR.PDB	O, L_TYR_173	N, L_PHE_139	H, L_PHE_139	2.80	1.98	13.87
4NZR.PDB	O, L_ALA_111	N, L_TYR_140	H, L_TYR_140	2.94	2.14	17.85
4NZR.PDB	O, L_GLU_195	N, L_GLN_147	H, L_GLN_147	2.85	2.04	15.79
4NZR.PDB	OG, L_SER_177	NE1, L_TRP_148	HE1, L_TRP_148	2.91	2.07	10.59
4NZR.PDB	O, L_ALA_193	N, L_LYS_149	H, L_LYS_149	2.88	2.05	12.05
4NZR.PDB	O, L_VAL_191	N, L_ASP_151	H, L_ASP_151	2.81	1.98	13.22
4NZR.PDB	O, L_VAL_150	N, L_ALA_153	H, L_ALA_153	2.92	2.07	7.66
4NZR.PDB	O, L_TRP_148	N, L_GLN_155	H, L_GLN_155	2.84	2.00	9.48

4NZR.PDB	O, L_ALA_153	NE2, L_GLN_155	HE21, L_GLN_155	2.97	2.11	2.73
4NZR.PDB	OE1, L_GLN_155	ND2, L_ASN_158	HD21, L_ASN_158	2.96	2.11	9.14
4NZR.PDB	O, H_LEU_178	NE2, L_GLN_160	HE22, L_GLN_160	2.86	2.01	7.83
4NZR.PDB	O, L_SER_176	N, L_SER_162	H, L_SER_162	2.96	2.18	20.83
4NZR.PDB	O, H_PRO_175	OG, L_SER_162	HG, L_SER_162	2.79	1.98	7.14
4NZR.PDB	O, L_SER_174	N, L_THR_164	H, L_THR_164	2.96	2.15	15.87
4NZR.PDB	O, L_SER_171	NE2, L_GLN_166	HE21, L_GLN_166	2.93	2.09	7.84
4NZR.PDB	O, L_ILE_106	NE2, L_GLN_166	HE22, L_GLN_166	2.71	1.88	13.12
4NZR.PDB	O, L_THR_172	N, L_ASP_167	H, L_ASP_167	2.77	1.92	9.43
4NZR.PDB	OD1, L_ASP_167	N, L_LYS_169	H, L_LYS_169	2.86	2.01	8.70
4NZR.PDB	O, L_ASP_167	N, L_SER_171	H, L_SER_171	2.75	2.00	24.50
4NZR.PDB	OD1, L_ASP_170	OG1, L_THR_172	HG1, L_THR_172	2.70	1.89	6.41
4NZR.PDB	O, L_PHE_139	N, L_TYR_173	H, L_TYR_173	2.82	1.99	11.40
4NZR.PDB	OG1, L_THR_164	N, L_SER_174	H, L_SER_174	2.94	2.15	19.12
4NZR.PDB	O, L_LEU_136	N, L_LEU_175	H, L_LEU_175	2.89	2.12	21.67
4NZR.PDB	O, L_SER_162	N, L_SER_176	H, L_SER_176	2.97	2.14	13.36
4NZR.PDB	OG, H_SER_188	OG, L_SER_176	HG, L_SER_176	2.88	2.09	13.66
4NZR.PDB	O, L_CYS_134	N, L_SER_177	H, L_SER_177	2.86	2.02	10.25
4NZR.PDB	O, L_GLN_160	N, L_THR_178	H, L_THR_178	2.83	2.00	11.32
4NZR.PDB	O, L_VAL_132	N, L_LEU_179	H, L_LEU_179	2.78	1.96	14.30
4NZR.PDB	O, L_ASN_158	N, L_THR_180	H, L_THR_180	2.97	2.13	10.64
4NZR.PDB	O, L_ALA_130	N, L_LEU_181	H, L_LEU_181	2.88	2.04	10.13
4NZR.PDB	O, L_GLY_128	N, L_LYS_183	H, L_LYS_183	2.93	2.11	14.95
4NZR.PDB	O, L_SER_182	N, L_TYR_186	H, L_TYR_186	2.96	2.11	6.64
4NZR.PDB	O, L_LYS_183	N, L_GLU_187	H, L_GLU_187	3.00	2.19	17.62
4NZR.PDB	O, L_ASP_185	N, L_LYS_188	H, L_LYS_188	2.95	2.13	13.06
4NZR.PDB	OD2, L_ASP_151	ND1, L_HIS_189	HD1, L_HIS_189	2.85	2.11	26.53
4NZR.PDB	OD1, L_ASP_151	N, L_VAL_191	H, L_VAL_191	2.94	2.08	3.42
4NZR.PDB	O, L_PHE_209	N, L_TYR_192	H, L_TYR_192	2.93	2.08	7.61
4NZR.PDB	O, L_LYS_149	N, L_ALA_193	H, L_ALA_193	2.88	2.09	18.86
4NZR.PDB	O, L_LYS_207	N, L_CYS_194	H, L_CYS_194	2.85	2.01	12.39
4NZR.PDB	O, L_VAL_205	N, L_VAL_196	H, L_VAL_196	2.71	1.89	14.56
4NZR.PDB	O, L_LYS_145	N, L_THR_197	H, L_THR_197	2.92	2.09	11.99
4NZR.PDB	O, L_PRO_141	NE2, L_HIS_198	HE2, L_HIS_198	2.90	2.07	12.26
4NZR.PDB	ND1, L_HIS_198	N, L_GLY_200	H, L_GLY_200	2.94	2.09	6.73
4NZR.PDB	O, L_HIS_198	N, L_LEU_201	H, L_LEU_201	2.89	2.04	8.10
4NZR.PDB	O, L_VAL_196	N, L_VAL_205	H, L_VAL_205	2.92	2.14	20.36
4NZR.PDB	O, L_CYS_194	N, L_LYS_207	H, L_LYS_207	2.92	2.14	21.11
4NZR.PDB	O, L_TYR_192	N, L_PHE_209	H, L_PHE_209	2.96	2.19	21.79
4NZR.PDB	O, L_LYS_190	N, L_ARG_211	H, L_ARG_211	2.70	1.87	12.15
4NZR.PDB	O, L_HIS_189	NE, L_ARG_211	HE, L_ARG_211	2.80	2.03	21.60
4NZR.PDB	O, M_GLU_124	N, M_TYR_82	H, M_TYR_82	2.96	2.13	13.02
4NZR.PDB	O, M_SER_126	N, M_SER_84	H, M_SER_84	2.98	2.15	13.57
4NZR.PDB	O, M_LEU_128	N, M_ILE_86	H, M_ILE_86	2.86	2.05	17.30
4NZR.PDB	O, M_LYS_130	N, M_LEU_88	H, M_LEU_88	2.84	1.99	7.85
4NZR.PDB	OD1, M_ASP_87	N, M_SER_89	H, M_SER_89	2.86	2.02	8.48
4NZR.PDB	OD1, M_ASN_378	NH1, M_ARG_95	HH12, M_ARG_95	2.71	1.91	18.53
4NZR.PDB	O, M_PHE_94	N, M_PHE_98	H, M_PHE_98	2.87	2.04	11.19
4NZR.PDB	O, M_ARG_95	N, M_ARG_99	H, M_ARG_99	2.91	2.10	16.79
4NZR.PDB	O, M_PHE_98	N, M_ALA_102	H, M_ALA_102	2.82	1.99	13.59
4NZR.PDB	O, M_ARG_99	N, M_ASN_103	H, M_ASN_103	2.77	1.95	14.29
4NZR.PDB	O, M_ALA_102	N, M_SER_106	H, M_SER_106	2.84	2.02	14.09
4NZR.PDB	O, M_ASN_103	N, M_GLU_107	H, M_GLU_107	2.90	2.10	17.39
4NZR.PDB	O, M_GLU_104	N, M_ALA_108	H, M_ALA_108	2.97	2.17	17.15
4NZR.PDB	O, M_LEU_105	N, M_ILE_109	H, M_ILE_109	2.94	2.17	22.50
4NZR.PDB	O, M_SER_106	N, M_THR_110	H, M_THR_110	2.95	2.12	14.11
4NZR.PDB	O, M_SER_106	OG1, M_THR_110	HG1, M_THR_110	2.74	1.95	13.19
4NZR.PDB	O, M_GLU_107	N, M_ASN_111	H, M_ASN_111	2.94	2.16	21.46

4NZR.PDB	O, M_SER_112	NZ, M_LYS_114	HZ1, M_LYS_114	2.69	1.82	10.18
4NZR.PDB	O, M_VAL_120	N, M_GLY_115	H, M_GLY_115	2.93	2.17	24.30
4NZR.PDB	O, M_SER_156	NE, M_ARG_118	HE, M_ARG_118	3.00	2.25	25.81
4NZR.PDB	O, M_SER_156	NH2, M_ARG_118	HH21, M_ARG_118	2.85	2.07	20.58
4NZR.PDB	O, M_ARG_118	N, M_VAL_120	H, M_VAL_120	2.76	2.02	26.00
4NZR.PDB	O, M_TYR_144	N, M_ILE_125	H, M_ILE_125	2.88	2.09	19.38
4NZR.PDB	O, M_TYR_82	N, M_SER_126	H, M_SER_126	2.89	2.07	14.81
4NZR.PDB	OE2, M_GLU_124	OG, M_SER_126	HG, M_SER_126	2.49	1.81	27.79
4NZR.PDB	O, M_ALA_142	N, M_GLY_127	H, M_GLY_127	2.88	2.07	15.98
4NZR.PDB	O, M_SER_84	N, M_LEU_128	H, M_LEU_128	2.81	1.97	11.35
4NZR.PDB	O, M_PHE_140	N, M_ILE_129	H, M_ILE_129	2.77	1.91	2.60
4NZR.PDB	O, M_ILE_86	N, M_LYS_130	H, M_LYS_130	2.86	2.00	2.42
4NZR.PDB	O, M_THR_137	OG1, M_THR_131	HG1, M_THR_131	2.69	1.93	17.31
4NZR.PDB	O, M_TYR_379	N, M_ILE_136	H, M_ILE_136	2.91	2.08	13.78
4NZR.PDB	O, M_ILE_129	N, M_PHE_140	H, M_PHE_140	2.99	2.21	21.20
4NZR.PDB	OE2, M_GLU_124	NZ, M_LYS_141	HZ2, M_LYS_141	2.96	2.15	21.57
4NZR.PDB	O, M_GLY_127	N, M_ALA_142	H, M_ALA_142	2.80	1.95	6.73
4NZR.PDB	O, M_GLN_159	N, M_GLY_143	H, M_GLY_143	2.82	2.00	13.14
4NZR.PDB	O, M_ILE_125	N, M_TYR_144	H, M_TYR_144	2.80	2.04	23.22
4NZR.PDB	O, M_LEU_155	N, M_HIS_147	H, M_HIS_147	2.85	2.01	10.85
4NZR.PDB	O, M_SER_153	N, M_ALA_149	H, M_ALA_149	2.76	1.91	5.90
4NZR.PDB	O, M_ALA_149	N, M_GLY_152	H, M_GLY_152	2.79	1.94	8.29
4NZR.PDB	O, M_LEU_180	N, M_TYR_158	H, M_TYR_158	2.83	1.99	9.68
4NZR.PDB	O, M_GLY_143	N, M_GLN_159	H, M_GLN_159	2.87	2.04	13.27
4NZR.PDB	O, M_PHE_382	N, M_PHE_164	H, M_PHE_164	2.85	2.03	14.98
4NZR.PDB	O, M_TYR_338	ND2, M_ASN_165	HD21, M_ASN_165	2.81	2.03	20.49
4NZR.PDB	O, M_ASN_183	ND2, M_ASN_165	HD22, M_ASN_165	2.99	2.16	11.12
4NZR.PDB	OD1, M_ASN_335	ND2, M_ASN_166	HD22, M_ASN_166	2.95	2.13	14.03
4NZR.PDB	OD1, M_ASN_183	NE, M_ARG_167	HE, M_ARG_167	2.87	2.09	20.21
4NZR.PDB	OD1, M_ASP_339	NH2, M_ARG_167	HH22, M_ARG_167	2.84	2.05	19.40
4NZR.PDB	OE2, M_GLU_311	N, M_LEU_169	H, M_LEU_169	2.70	1.87	11.59
4NZR.PDB	OE2, M_GLU_311	N, M_MET_170	H, M_MET_170	2.91	2.07	11.26
4NZR.PDB	O, M_SER_198	N, M_LEU_173	H, M_LEU_173	2.95	2.10	5.86
4NZR.PDB	OD1, M_ASN_177	N, M_THR_179	H, M_THR_179	2.81	1.95	3.90
4NZR.PDB	OD1, M_ASN_177	OG1, M_THR_179	HG1, M_THR_179	2.75	1.94	6.81
4NZR.PDB	O, M_TYR_158	N, M_ALA_182	H, M_ALA_182	2.88	2.03	6.05
4NZR.PDB	OE1, M_GLN_174	N, M_ASN_183	H, M_ASN_183	2.83	2.00	12.26
4NZR.PDB	O, M_ASN_165	ND2, M_ASN_183	HD21, M_ASN_183	2.83	2.00	11.27
4NZR.PDB	O, M_TYR_187	N, M_PHE_191	H, M_PHE_191	2.90	2.07	12.39
4NZR.PDB	O, M_ASP_189	N, M_SER_196	H, M_SER_196	2.84	2.04	18.29
4NZR.PDB	O, M_PHE_197	N, M_TRP_200	H, M_TRP_200	2.82	1.97	10.31
4NZR.PDB	O, M_PRO_171	NE1, M_TRP_200	HE1, M_TRP_200	2.83	1.99	8.99
4NZR.PDB	O, M_PHE_222	N, M_SER_201	H, M_SER_201	2.78	1.94	12.33
4NZR.PDB	O, M_THR_203	ND2, M_ASN_202	HD22, M_ASN_202	2.86	2.06	17.05
4NZR.PDB	O, M_THR_220	N, M_THR_203	H, M_THR_203	2.86	2.05	16.26
4NZR.PDB	OD1, M_ASP_217	OG1, M_THR_207	HG1, M_THR_207	2.72	1.90	1.28
4NZR.PDB	O, M_TYR_216	N, M_VAL_208	H, M_VAL_208	2.71	1.87	8.33
4NZR.PDB	O, M_LEU_214	N, M_THR_210	H, M_THR_210	2.96	2.14	13.71
4NZR.PDB	O, M_ALA_245	N, M_ASP_217	H, M_ASP_217	2.93	2.09	9.77
4NZR.PDB	O, M_THR_206	N, M_LYS_218	H, M_LYS_218	2.92	2.13	20.21
4NZR.PDB	OG1, M_THR_203	N, M_THR_220	H, M_THR_220	2.85	2.05	18.11
4NZR.PDB	O, M_VAL_241	N, M_TYR_221	H, M_TYR_221	2.93	2.11	14.30
4NZR.PDB	O, M_SER_201	N, M_PHE_222	H, M_PHE_222	2.88	2.09	19.39
4NZR.PDB	O, M_ALA_224	N, M_SER_227	H, M_SER_227	2.86	2.03	13.10
4NZR.PDB	O, M_PRO_228	N, M_SER_232	H, M_SER_232	2.88	2.10	20.88
4NZR.PDB	O, M_LEU_229	N, M_TYR_233	H, M_TYR_233	2.92	2.16	23.55
4NZR.PDB	O, M_TYR_221	N, M_VAL_241	H, M_VAL_241	2.87	2.02	7.27
4NZR.PDB	OE1, M_GLU_261	NZ, M_LYS_242	HZ1, M_LYS_242	2.96	2.22	28.06

4NZR.PDB	O, M_GLU_261	NZ, M_LYS_242	HZ3, M_LYS_242	2.55	1.69	11.67
4NZR.PDB	O, M_TRP_219	N, M_THR_243	H, M_THR_243	2.79	1.95	10.59
4NZR.PDB	O, M_ASP_217	N, M_ALA_245	H, M_ALA_245	2.89	2.07	14.41
4NZR.PDB	O, M_ILE_267	N, M_ILE_246	H, M_ILE_246	2.96	2.14	14.76
4NZR.PDB	O, M_ARG_269	N, M_ALA_248	H, M_ALA_248	2.78	1.96	15.32
4NZR.PDB	OD1, M_ASP_247	N, M_LYS_249	H, M_LYS_249	2.95	2.10	5.78
4NZR.PDB	OD1, M_ASP_250	NZ, M_LYS_249	HZ2, M_LYS_249	2.93	2.05	7.77
4NZR.PDB	O, M_ASP_247	N, M_ASP_250	H, M_ASP_250	2.94	2.10	10.81
4NZR.PDB	O, M_ASP_250	N, M_LEU_254	H, M_LEU_254	2.89	2.16	27.92
4NZR.PDB	NE2, M_GLN_282	NZ, M_LYS_255	HZ2, M_LYS_255	2.97	2.08	5.26
4NZR.PDB	O, M_LEU_254	N, M_ILE_258	H, M_ILE_258	2.84	1.99	9.84
4NZR.PDB	O, M_THR_257	N, M_GLU_261	H, M_GLU_261	2.89	2.08	16.34
4NZR.PDB	O, M_ILE_258	N, M_LYS_262	H, M_LYS_262	2.89	2.11	21.82
4NZR.PDB	O, M_LYS_289	N, M_LEU_266	H, M_LEU_266	2.92	2.10	13.96
4NZR.PDB	O, M_LEU_244	N, M_ILE_267	H, M_ILE_267	2.88	2.03	7.52
4NZR.PDB	O, M_SER_291	N, M_ILE_268	H, M_ILE_268	2.95	2.09	5.10
4NZR.PDB	O, M_ILE_246	N, M_ARG_269	H, M_ARG_269	2.83	1.98	9.70
4NZR.PDB	OD2, M_ASP_217	NH1, M_ARG_269	HH12, M_ARG_269	2.82	1.99	14.04
4NZR.PDB	O, M_GLN_193	NH2, M_ARG_269	HH21, M_ARG_269	2.90	2.20	29.55
4NZR.PDB	O, M_TYR_293	N, M_LEU_271	H, M_LEU_271	2.91	2.07	10.40
4NZR.PDB	O, M_GLY_275	N, M_LEU_278	H, M_LEU_278	2.93	2.08	6.63
4NZR.PDB	O, M_SER_276	N, M_ASN_279	H, M_ASN_279	2.87	2.04	13.20
4NZR.PDB	O, M_LEU_278	N, M_LEU_281	H, M_LEU_281	3.00	2.14	5.40
4NZR.PDB	O, M_THR_264	N, M_LYS_288	H, M_LYS_288	2.79	2.01	19.89
4NZR.PDB	OE2, M_GLU_313	NZ, M_LYS_289	HZ1, M_LYS_289	2.70	1.96	27.41
4NZR.PDB	OE1, M_GLU_311	NZ, M_LYS_289	HZ3, M_LYS_289	2.89	2.00	2.29
4NZR.PDB	O, M_GLU_313	N, M_LEU_292	H, M_LEU_292	2.92	2.08	9.41
4NZR.PDB	O, M_ILE_268	N, M_TYR_293	H, M_TYR_293	2.81	1.96	5.69
4NZR.PDB	O, M_GLY_273	N, M_THR_297	H, M_THR_297	2.74	1.93	16.92
4NZR.PDB	O, M_ASN_274	N, M_ASN_300	H, M_ASN_300	2.77	1.96	17.19
4NZR.PDB	O, M_LEU_330	NE2, M_GLN_304	HE21, M_GLN_304	2.93	2.09	8.97
4NZR.PDB	O, M_VAL_329	N, M_PHE_306	H, M_PHE_306	2.92	2.13	19.27
4NZR.PDB	O, M_LYS_288	N, M_VAL_310	H, M_VAL_310	2.73	1.91	14.16
4NZR.PDB	O, M_ASN_335	N, M_LEU_312	H, M_LEU_312	2.83	2.09	26.31
4NZR.PDB	O, M_LEU_292	N, M_TYR_315	H, M_TYR_315	2.81	2.05	23.22
4NZR.PDB	O, M_GLY_294	N, M_THR_317	H, M_THR_317	2.77	1.95	15.24
4NZR.PDB	O, M_VAL_299	N, M_ASN_326	H, M_ASN_326	2.99	2.14	6.61
4NZR.PDB	O, M_VAL_309	OG1, M_THR_334	HG1, M_THR_334	2.89	2.12	15.85
4NZR.PDB	O, M_VAL_310	N, M_ASN_335	H, M_ASN_335	2.95	2.14	16.98
4NZR.PDB	O, M_VAL_310	ND2, M_ASN_335	HD22, M_ASN_335	2.97	2.16	17.87
4NZR.PDB	OE2, M_GLU_383	N, M_VAL_336	H, M_VAL_336	2.87	2.03	8.95
4NZR.PDB	O, M_LEU_312	N, M_ILE_337	H, M_ILE_337	2.90	2.08	14.00
4NZR.PDB	OD1, M_ASN_165	N, M_TYR_338	H, M_TYR_338	2.85	2.02	11.20
4NZR.PDB	OG, M_SER_343	N, M_ASP_339	H, M_ASP_339	2.88	2.05	13.57
4NZR.PDB	OD1, M_ASN_184	N, M_LEU_340	H, M_LEU_340	2.86	2.02	9.90
4NZR.PDB	O, M_ASP_339	N, M_SER_343	H, M_SER_343	2.85	2.02	12.90
4NZR.PDB	O, M_ALA_320	NZ, M_LYS_344	HZ1, M_LYS_344	2.76	1.89	11.48
4NZR.PDB	O, M_SER_318	NZ, M_LYS_344	HZ3, M_LYS_344	2.90	2.04	12.02
4NZR.PDB	O, M_PHE_323	N, M_THR_347	H, M_THR_347	2.86	2.04	13.38
4NZR.PDB	O, M_PHE_325	N, M_ASP_350	H, M_ASP_350	2.77	1.92	5.83
4NZR.PDB	O, M_LEU_399	N, M_LEU_351	H, M_LEU_351	2.77	1.98	19.72
4NZR.PDB	OD1, M_ASP_350	N, M_THR_352	H, M_THR_352	2.94	2.11	11.48
4NZR.PDB	OD1, M_ASP_350	OG1, M_THR_352	HG1, M_THR_352	2.69	1.93	19.00
4NZR.PDB	O, M_LEU_351	N, M_VAL_354	H, M_VAL_354	2.99	2.17	14.74
4NZR.PDB	O, M_ALA_363	N, M_ASN_358	H, M_ASN_358	2.83	2.00	12.67
4NZR.PDB	O, M_LEU_356	N, M_ASP_365	H, M_ASP_365	2.81	1.96	8.63
4NZR.PDB	O, M_GLN_357	NZ, M_LYS_368	HZ2, M_LYS_368	2.90	2.01	4.14
4NZR.PDB	O, M_ALA_366	N, M_LYS_370	H, M_LYS_370	2.94	2.09	7.76

4NZR.PDB	OE1, M_GLU_420	NZ, M_LYS_370	HZ2, M_LYS_370	2.61	1.80	20.02
4NZR.PDB	O, M_ASN_367	N, M_GLN_371	H, M_GLN_371	2.96	2.16	18.23
4NZR.PDB	OD1, M_ASP_375	NE2, M_GLN_371	HE21, M_GLN_371	2.92	2.12	18.76
4NZR.PDB	O, M_LEU_369	N, M_VAL_373	H, M_VAL_373	2.99	2.14	9.69
4NZR.PDB	O, M_LYS_370	N, M_GLY_374	H, M_GLY_374	2.80	1.98	14.26
4NZR.PDB	O, M_GLN_371	N, M_ASP_375	H, M_ASP_375	2.91	2.15	24.37
4NZR.PDB	O, M_VAL_373	N, M_ILE_376	H, M_ILE_376	2.99	2.25	26.03
4NZR.PDB	O, M_VAL_373	N, M_TYR_377	H, M_TYR_377	2.78	1.92	4.41
4NZR.PDB	O, M_GLY_374	N, M_ASN_378	H, M_ASN_378	2.88	2.07	16.83
4NZR.PDB	O, M_GLY_374	N, M_TYR_379	H, M_TYR_379	2.99	2.17	15.14
4NZR.PDB	OE1, M_GLU_383	NH1, M_ARG_380	HH11, M_ARG_380	2.65	1.84	14.74
4NZR.PDB	O, M_THR_334	NH1, M_ARG_380	HH12, M_ARG_380	2.93	2.14	19.06
4NZR.PDB	O, M_GLU_162	NH1, M_ARG_381	HH12, M_ARG_381	2.93	2.20	26.71
4NZR.PDB	OE1, M_GLU_162	NH2, M_ARG_381	HH22, M_ARG_381	3.00	2.22	21.24
4NZR.PDB	OE1, L_GLU_81	NE, M_ARG_384	HE, M_ARG_384	2.93	2.09	10.37
4NZR.PDB	O, M_GLY_388	NH1, M_ARG_384	HH12, M_ARG_384	2.81	2.01	18.07
4NZR.PDB	O, M_LYS_344	NE2, M_GLN_385	HE22, M_GLN_385	2.71	1.92	19.06
4NZR.PDB	O, M_GLU_383	N, M_PHE_386	H, M_PHE_386	2.99	2.17	16.23
4NZR.PDB	O, M_ARG_384	N, M_GLN_387	H, M_GLN_387	2.98	2.13	8.94
4NZR.PDB	O, M_ARG_381	NE2, M_GLN_387	HE21, M_GLN_387	2.77	1.96	17.54
4NZR.PDB	O, M_GLU_162	NE2, M_GLN_387	HE22, M_GLN_387	2.83	2.04	18.31
4NZR.PDB	OE1, M_GLN_387	N, M_GLY_392	H, M_GLY_392	2.78	1.95	10.56
4NZR.PDB	O, M_PHE_390	N, M_GLY_393	H, M_GLY_393	2.93	2.13	18.34
4NZR.PDB	OD1, M_ASP_396	NZ, M_LYS_397	HZ1, M_LYS_397	2.90	2.03	10.85
4NZR.PDB	O, M_TYR_437	N, M_TYR_398	H, M_TYR_398	2.93	2.11	14.24
4NZR.PDB	O, M_ILE_349	N, M_LEU_399	H, M_LEU_399	2.84	2.00	10.68
4NZR.PDB	O, M_THR_435	N, M_VAL_400	H, M_VAL_400	2.89	2.06	12.03
4NZR.PDB	OD2, M_ASP_410	ND2, M_ASN_402	HD22, M_ASN_402	2.93	2.14	18.97
4NZR.PDB	OD2, M_ASP_410	N, M_VAL_403	H, M_VAL_403	2.81	2.04	21.61
4NZR.PDB	OD1, M_ASN_404	N, M_ASN_406	H, M_ASN_406	2.87	2.04	12.77
4NZR.PDB	O, M_LYS_407	N, M_ASP_411	H, M_ASP_411	2.97	2.15	15.64
4NZR.PDB	O, M_ASP_408	N, M_ASP_412	H, M_ASP_412	2.92	2.12	19.03
4NZR.PDB	O, M_SER_409	N, M_LEU_413	H, M_LEU_413	2.93	2.10	12.24
4NZR.PDB	O, M_ASP_410	N, M_VAL_414	H, M_VAL_414	2.89	2.06	12.64
4NZR.PDB	O, M_ASP_411	N, M_TYR_415	H, M_TYR_415	2.83	1.98	9.53
4NZR.PDB	O, M_ASP_412	N, M_ARG_416	H, M_ARG_416	2.86	2.01	9.04
4NZR.PDB	OE2, M_GLU_464	NH1, M_ARG_416	HH12, M_ARG_416	2.68	1.83	5.86
4NZR.PDB	OE1, M_GLU_464	NH2, M_ARG_416	HH22, M_ARG_416	2.88	2.03	6.77
4NZR.PDB	O, M_LEU_413	N, M_SER_417	H, M_SER_417	2.88	2.05	11.51
4NZR.PDB	O, M_VAL_414	N, M_LEU_418	H, M_LEU_418	2.92	2.09	12.46
4NZR.PDB	O, M_LEU_418	N, M_LEU_421	H, M_LEU_421	2.84	2.06	20.21
4NZR.PDB	O, M_LYS_419	N, M_ASN_422	H, M_ASN_422	2.91	2.11	18.90
4NZR.PDB	O, M_LEU_418	N, M_LEU_423	H, M_LEU_423	2.97	2.13	11.14
4NZR.PDB	O, M_ASN_440	N, M_HIS_424	H, M_HIS_424	2.82	2.03	19.83
4NZR.PDB	O, M_ARG_438	N, M_GLU_426	H, M_GLU_426	2.73	1.89	8.53
4NZR.PDB	O, M_TYR_436	N, M_TYR_429	H, M_TYR_429	2.86	2.01	8.90
4NZR.PDB	OD1, M_ASP_411	NH1, M_ARG_430	HH12, M_ARG_430	2.84	2.06	21.86
4NZR.PDB	O, M_ASN_434	N, M_GLU_431	H, M_GLU_431	2.87	2.02	8.65
4NZR.PDB	O, M_VAL_400	N, M_THR_435	H, M_THR_435	2.80	1.99	16.75
4NZR.PDB	OD1, M_ASN_402	OG1, M_THR_435	HG1, M_THR_435	2.74	1.98	18.44
4NZR.PDB	O, M_TYR_429	N, M_TYR_436	H, M_TYR_436	2.75	1.91	12.60
4NZR.PDB	O, M_TYR_398	N, M_TYR_437	H, M_TYR_437	2.80	1.95	5.61
4NZR.PDB	O, M_GLU_427	N, M_ARG_438	H, M_ARG_438	2.92	2.08	10.71
4NZR.PDB	OD2, M_ASP_396	NE, M_ARG_438	HE, M_ARG_438	2.86	2.00	5.29
4NZR.PDB	O, M_ASP_396	N, M_VAL_439	H, M_VAL_439	2.78	2.00	20.99
4NZR.PDB	O, M_HIS_424	N, M_ASN_440	H, M_ASN_440	2.91	2.07	11.96
4NZR.PDB	OE2, M_GLU_426	ND2, M_ASN_440	HD22, M_ASN_440	2.87	2.05	14.71
4NZR.PDB	OH, M_TYR_394	N, M_GLU_441	H, M_GLU_441	2.91	2.08	11.38

4NZR.PDB	OD1, M_ASN_440	N, M_ASN_442	H, M_ASN_442	2.86	2.01	10.00
4NZR.PDB	O, M_GLU_426	N, M_TYR_450	H, M_TYR_450	2.94	2.10	8.91
4NZR.PDB	OG, M_SER_448	N, M_GLU_451	H, M_GLU_451	3.00	2.15	7.42
4NZR.PDB	O, M_SER_448	N, M_ASN_452	H, M_ASN_452	2.99	2.16	12.61
4NZR.PDB	O, M_GLY_446	ND2, M_ASN_452	HD22, M_ASN_452	2.95	2.14	17.61
4NZR.PDB	O, M_ILE_449	N, M_GLU_453	H, M_GLU_453	2.90	2.04	6.17
4NZR.PDB	OD1, M_ASP_412	NH1, M_ARG_454	HH12, M_ARG_454	2.79	1.98	15.66
4NZR.PDB	O, M_GLU_451	N, M_ALA_455	H, M_ALA_455	2.80	1.96	11.85
4NZR.PDB	O, M_GLU_453	NH1, M_ARG_457	HH11, M_ARG_457	2.87	2.09	20.01
4NZR.PDB	OD1, H_ASP_31E	NH1, M_ARG_457	HH12, M_ARG_457	2.96	2.12	11.27
4NZR.PDB	OD2, H_ASP_31E	NH2, M_ARG_457	HH22, M_ARG_457	2.55	1.75	17.03
4NZR.PDB	O, M_ARG_454	N, M_ASP_458	H, M_ASP_458	2.91	2.20	29.30
4NZR.PDB	O, M_ASP_458	N, M_GLN_462	H, M_GLN_462	2.90	2.06	11.58
4NZR.PDB	O, M_SER_459	N, M_ASN_463	H, M_ASN_463	2.97	2.15	14.56
4NZR.PDB	O, M_GLU_460	N, M_GLU_464	H, M_GLU_464	2.94	2.12	14.76
4NZR.PDB	O, M_PHE_461	N, M_ILE_465	H, M_ILE_465	2.92	2.11	16.00
4NZR.PDB	O, M_ASN_463	N, M_LYS_467	H, M_LYS_467	2.98	2.13	6.16
4NZR.PDB	O, M_GLU_464	N, M_ARG_468	H, M_ARG_468	2.90	2.06	11.94
4NZU.PDB	OG, L_SER_26	N, L_GLU_3	H, L_GLU_3	2.85	2.00	7.06
4NZU.PDB	O, L_GLN_24	N, L_THR_5	H, L_THR_5	2.89	2.06	12.85
4NZU.PDB	O, L_LYS_103	N, L_LEU_11	H, L_LEU_11	2.89	2.11	20.24
4NZU.PDB	O, L_GLU_105	N, L_ALA_13	H, L_ALA_13	2.97	2.15	15.91
4NZU.PDB	OD2, L_ASP_17	N, L_SER_14	H, L_SER_14	2.85	2.00	6.08
4NZU.PDB	O, L_LEU_78	N, L_GLY_16	H, L_GLY_16	2.75	1.92	11.17
4NZU.PDB	O, L_ILE_75	N, L_VAL_19	H, L_VAL_19	2.93	2.10	12.37
4NZU.PDB	O, L_PHE_73	N, L_ILE_21	H, L_ILE_21	2.89	2.06	11.61
4NZU.PDB	O, L_SER_7	N, L_THR_22	H, L_THR_22	2.86	2.01	5.56
4NZU.PDB	O, L_PHE_71	N, L_CYS_23	H, L_CYS_23	2.91	2.09	15.17
4NZU.PDB	O, L_THR_5	N, L_GLN_24	H, L_GLN_24	2.88	2.07	16.80
4NZU.PDB	O, L_THR_69	N, L_ALA_25	H, L_ALA_25	2.86	2.06	18.12
4NZU.PDB	O, L_GLY_68	N, L_ILE_29	H, L_ILE_29	2.87	2.02	6.63
4NZU.PDB	O, L_ILE_29	N, L_PHE_32	H, L_PHE_32	2.88	2.03	7.32
4NZU.PDB	O, L_GLN_89	N, L_ASP_34	H, L_ASP_34	2.88	2.05	12.07
4NZU.PDB	O, L_ILE_48	N, L_TRP_35	H, L_TRP_35	2.86	2.02	11.26
4NZU.PDB	O, L_TYR_87	N, L_TYR_36	H, L_TYR_36	2.84	2.02	14.90
4NZU.PDB	O, L_LYS_45	N, L_GLN_37	H, L_GLN_37	2.88	2.06	16.18
4NZU.PDB	O, L_VAL_85	N, L_GLN_38	H, L_GLN_38	2.81	2.00	16.84
4NZU.PDB	O, L_GLU_81	NE, L_ARG_39	HE, L_ARG_39	2.82	1.89	12.62
4NZU.PDB	O, L_ARG_39	N, L_LYS_42	H, L_LYS_42	2.98	2.17	16.62
4NZU.PDB	O, L_GLN_37	N, L_LYS_45	H, L_LYS_45	2.86	2.08	21.32
4NZU.PDB	O, L_TRP_35	N, L_LEU_47	H, L_LEU_47	2.90	2.05	4.96
4NZU.PDB	O, L_ASN_53	N, L_TYR_49	H, L_TYR_49	2.92	2.13	19.67
4NZU.PDB	O, L_LEU_33	N, L_ALA_51	H, L_ALA_51	2.73	1.91	14.91
4NZU.PDB	O, L_ASP_50	N, L_SER_52	H, L_SER_52	2.85	2.15	29.96
4NZU.PDB	O, L_TYR_49	N, L_ASN_53	H, L_ASN_53	2.95	2.12	14.12
4NZU.PDB	O, L_LEU_47	N, L_ALA_55	H, L_ALA_55	2.95	2.09	3.99
4NZU.PDB	OD2, L_ASP_82	NE, L_ARG_61	HE, L_ARG_61	2.83	2.03	27.68
4NZU.PDB	OD1, L_ASP_82	NH2, L_ARG_61	HH21, L_ARG_61	2.85	2.00	7.18
4NZU.PDB	O, L_THR_72	N, L_SER_65	H, L_SER_65	2.93	2.14	18.79
4NZU.PDB	O, L_ALA_30	N, L_GLY_68	H, L_GLY_68	2.88	2.07	17.47
4NZU.PDB	O, L_CYS_23	N, L_PHE_71	H, L_PHE_71	2.88	2.07	16.98
4NZU.PDB	O, L_SER_65	N, L_THR_72	H, L_THR_72	2.92	2.09	12.57
4NZU.PDB	O, L_ILE_21	N, L_PHE_73	H, L_PHE_73	2.91	2.08	12.35
4NZU.PDB	O, L_THR_63	N, L_THR_74	H, L_THR_74	2.88	2.05	11.92
4NZU.PDB	O, L_VAL_19	N, L_ILE_75	H, L_ILE_75	2.89	2.09	18.00
4NZU.PDB	O, L_ARG_61	N, L_SER_76	H, L_SER_76	2.83	2.03	17.44
4NZU.PDB	O, L_ASP_17	N, L_LEU_78	H, L_LEU_78	2.83	2.04	19.06
4NZU.PDB	OD2, L_ASP_82	N, L_GLN_79	H, L_GLN_79	2.91	2.07	9.01

4NZU.PDB	O, L_GLN_79	N, L_ASP_82	H, L_ASP_82	2.86	2.03	11.16
4NZU.PDB	O, L_THR_102	N, L_TYR_86	H, L_TYR_86	2.95	2.13	15.14
4NZU.PDB	O, L_TYR_36	N, L_TYR_87	H, L_TYR_87	2.92	2.11	16.96
4NZU.PDB	O, L_PHE_32	N, L_TYR_91	H, L_TYR_91	2.96	2.16	17.93
4NZU.PDB	O, L_CYS_88	N, L_GLY_99	H, L_GLY_99	2.83	2.03	18.33
4NZU.PDB	OE1, L_GLN_6	N, L_GLY_101	H, L_GLY_101	2.96	2.20	24.47
4NZU.PDB	O, L_TYR_86	N, L_THR_102	H, L_THR_102	2.91	2.10	16.25
4NZU.PDB	O, L_ALA_84	N, L_LEU_104	H, L_LEU_104	2.96	2.10	5.58
4NZU.PDB	O, L_LEU_11	N, L_GLU_105	H, L_GLU_105	2.96	2.15	17.50
4NZU.PDB	OE1, L_GLN_166	N, L_THR_106	H, L_THR_106	2.83	1.99	8.58
4NZU.PDB	O, L_ALA_13	N, L_LYS_107	H, L_LYS_107	2.88	2.05	13.69
4NZU.PDB	O, L_THR_109	NE, L_ARG_108	HE, L_ARG_108	2.81	1.86	9.52
4NZU.PDB	O, L_ASP_170	NH1, L_ARG_108	HH11, L_ARG_108	2.81	1.98	12.07
4NZU.PDB	O, L_TYR_140	N, L_ALA_111	H, L_ALA_111	2.88	2.04	11.37
4NZU.PDB	O, L_LEU_135	N, L_PHE_116	H, L_PHE_116	2.95	2.18	22.98
4NZU.PDB	O, L_VAL_133	N, L_PHE_118	H, L_PHE_118	2.80	2.00	18.01
4NZU.PDB	OG, L_SER_121	N, L_GLN_124	H, L_GLN_124	2.94	2.11	13.38
4NZU.PDB	O, L_LEU_181	N, L_ALA_130	H, L_ALA_130	2.90	2.05	9.45
4NZU.PDB	NE2, L_GLN_124	N, L_SER_131	H, L_SER_131	2.97	2.20	21.35
4NZU.PDB	O, L_LEU_179	N, L_VAL_132	H, L_VAL_132	2.90	2.07	11.76
4NZU.PDB	O, L_SER_177	N, L_CYS_134	H, L_CYS_134	2.87	2.04	13.69
4NZU.PDB	O, L_PHE_116	N, L_LEU_135	H, L_LEU_135	2.83	2.00	10.89
4NZU.PDB	O, L_LEU_175	N, L_LEU_136	H, L_LEU_136	2.84	1.99	6.57
4NZU.PDB	O, L_SER_114	N, L_ASN_137	H, L_ASN_137	2.79	1.96	12.42
4NZU.PDB	O, L_TYR_173	N, L_PHE_139	H, L_PHE_139	2.81	1.98	12.12
4NZU.PDB	O, L_ALA_111	N, L_TYR_140	H, L_TYR_140	2.98	2.17	16.59
4NZU.PDB	O, L_GLU_195	N, L_GLN_147	H, L_GLN_147	2.80	1.97	12.05
4NZU.PDB	OG, L_SER_177	NE1, L_TRP_148	HE1, L_TRP_148	2.90	1.89	11.12
4NZU.PDB	O, L_ALA_193	N, L_LYS_149	H, L_LYS_149	2.86	2.04	14.54
4NZU.PDB	O, L_VAL_191	N, L_ASP_151	H, L_ASP_151	2.81	1.98	13.30
4NZU.PDB	O, L_VAL_150	N, L_ALA_153	H, L_ALA_153	2.89	2.05	9.67
4NZU.PDB	O, L_TRP_148	N, L_GLN_155	H, L_GLN_155	2.91	2.07	10.18
4NZU.PDB	O, L_SER_176	N, L_SER_162	H, L_SER_162	2.96	2.18	20.50
4NZU.PDB	O, L_SER_174	N, L_THR_164	H, L_THR_164	2.99	2.18	16.93
4NZU.PDB	O, L_THR_172	N, L_ASP_167	H, L_ASP_167	2.80	1.96	8.83
4NZU.PDB	OD2, L_ASP_167	N, L_LYS_169	H, L_LYS_169	2.96	2.24	28.01
4NZU.PDB	OD2, L_ASP_167	N, L_ASP_170	H, L_ASP_170	2.95	2.13	14.40
4NZU.PDB	O, L_ASP_167	N, L_SER_171	H, L_SER_171	2.96	2.22	25.63
4NZU.PDB	OD1, L_ASP_170	N, L_THR_172	H, L_THR_172	2.94	2.13	16.20
4NZU.PDB	O, L_PHE_139	N, L_TYR_173	H, L_TYR_173	2.83	1.98	8.20
4NZU.PDB	O, L_LEU_136	N, L_LEU_175	H, L_LEU_175	2.85	2.05	17.53
4NZU.PDB	O, L_SER_162	N, L_SER_176	H, L_SER_176	2.96	2.14	14.63
4NZU.PDB	O, L_CYS_134	N, L_SER_177	H, L_SER_177	2.92	2.08	12.73
4NZU.PDB	O, L_GLN_160	N, L_THR_178	H, L_THR_178	2.85	2.02	12.21
4NZU.PDB	O, L_VAL_132	N, L_LEU_179	H, L_LEU_179	2.78	1.95	11.28
4NZU.PDB	O, L_ASN_158	N, L_THR_180	H, L_THR_180	2.89	2.04	7.97
4NZU.PDB	O, L_ALA_130	N, L_LEU_181	H, L_LEU_181	2.89	2.03	5.02
4NZU.PDB	O, L_GLY_128	N, L_LYS_183	H, L_LYS_183	2.93	2.08	7.57
4NZU.PDB	OG, L_SER_182	N, L_ASP_185	H, L_ASP_185	2.98	2.15	12.85
4NZU.PDB	O, L_SER_182	N, L_TYR_186	H, L_TYR_186	2.98	2.14	10.93
4NZU.PDB	O, L_LYS_183	N, L_GLU_187	H, L_GLU_187	2.86	2.03	12.51
4NZU.PDB	OD1, L_ASP_151	N, L_LYS_190	H, L_LYS_190	2.93	2.09	10.09
4NZU.PDB	OD1, L_ASP_151	N, L_VAL_191	H, L_VAL_191	2.97	2.13	9.29
4NZU.PDB	O, L_PHE_209	N, L_TYR_192	H, L_TYR_192	2.93	2.08	5.07
4NZU.PDB	O, L_LYS_149	N, L_ALA_193	H, L_ALA_193	2.96	2.16	18.28
4NZU.PDB	O, L_LYS_207	N, L_CYS_194	H, L_CYS_194	2.90	2.07	13.44
4NZU.PDB	O, L_GLN_147	N, L_GLU_195	H, L_GLU_195	2.85	2.00	7.85
4NZU.PDB	O, L_VAL_205	N, L_VAL_196	H, L_VAL_196	2.76	1.93	12.73

4NZU.PDB	O, L_LYS_145	N, L_THR_197	H, L_THR_197	2.96	2.14	13.76
4NZU.PDB	ND1, L_HIS_198	N, L_GLY_200	H, L_GLY_200	2.95	2.10	4.09
4NZU.PDB	O, L_HIS_198	N, L_LEU_201	H, L_LEU_201	2.91	2.06	7.34
4NZU.PDB	O, L_VAL_196	N, L_VAL_205	H, L_VAL_205	2.97	2.18	19.82
4NZU.PDB	O, L_TYR_192	N, L_PHE_209	H, L_PHE_209	2.95	2.17	20.95
4NZU.PDB	O, L_LYS_190	N, L_ARG_211	H, L_ARG_211	2.79	1.96	13.34
4NZU.PDB	O, L_HIS_189	NE, L_ARG_211	HE, L_ARG_211	2.83	1.95	20.09
4NZU.PDB	O, H_SER_25	N, H_SER_3	H, H_SER_3	2.94	2.15	18.68
4NZU.PDB	O, H_ALA_23	N, H_VAL_5	H, H_VAL_5	2.94	2.11	12.25
4NZU.PDB	OE1, H_GLN_105	N, H_GLU_6	H, H_GLU_6	2.88	2.02	2.55
4NZU.PDB	O, H_SER_21	N, H_SER_7	H, H_SER_7	2.91	2.11	18.23
4NZU.PDB	O, H_THR_110	N, H_VAL_12	H, H_VAL_12	2.93	2.20	26.91
4NZU.PDB	O, H_LEU_82C	N, H_GLY_15	H, H_GLY_15	2.72	1.86	1.10
4NZU.PDB	O, H_MET_82	N, H_LEU_18	H, H_LEU_18	2.87	2.07	18.95
4NZU.PDB	O, H_LEU_80	N, H_LEU_20	H, H_LEU_20	2.89	2.06	11.46
4NZU.PDB	O, H_SER_7	N, H_SER_21	H, H_SER_21	2.98	2.14	9.55
4NZU.PDB	O, H_LEU_78	N, H_CYS_22	H, H_CYS_22	2.82	2.04	21.59
4NZU.PDB	O, H_VAL_5	N, H_ALA_23	H, H_ALA_23	2.82	1.97	8.42
4NZU.PDB	O, H_ASN_76	N, H_ALA_24	H, H_ALA_24	2.93	2.07	4.56
4NZU.PDB	O, H_SER_3	N, H_SER_25	H, H_SER_25	2.99	2.20	20.90
4NZU.PDB	O, H_ALA_93	N, H_HIS_35	H, H_HIS_35	2.93	2.12	16.07
4NZU.PDB	O, H_ALA_49	N, H_TRP_36	H, H_TRP_36	2.92	2.14	21.04
4NZU.PDB	O, H_TYR_91	N, H_VAL_37	H, H_VAL_37	2.88	2.05	13.75
4NZU.PDB	O, H_GLU_46	N, H_ARG_38	H, H_ARG_38	2.81	1.97	10.17
4NZU.PDB	OE2, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.81	1.92	18.37
4NZU.PDB	OD1, H_ASP_86	NH1, H_ARG_38	HH12, H_ARG_38	2.87	2.03	8.91
4NZU.PDB	O, H_VAL_89	N, H_GLN_39	H, H_GLN_39	2.85	2.12	26.56
4NZU.PDB	O, H_ALA_40	N, H_ASP_43	H, H_ASP_43	2.95	2.13	14.09
4NZU.PDB	O, H_ARG_38	N, H_GLU_46	H, H_GLU_46	2.83	2.07	24.02
4NZU.PDB	O, H_TRP_36	N, H_VAL_48	H, H_VAL_48	2.86	2.04	15.06
4NZU.PDB	O, H_TYR_58	N, H_PHE_50	H, H_PHE_50	2.88	2.08	16.89
4NZU.PDB	O, H_PHE_34	N, H_ILE_51	H, H_ILE_51	2.88	2.05	13.34
4NZU.PDB	O, H_SER_56	N, H_SER_52	H, H_SER_52	2.92	2.10	13.95
4NZU.PDB	O, H_SER_52	N, H_GLY_54	H, H_GLY_54	2.94	2.14	17.16
4NZU.PDB	O, H_VAL_48	N, H_ALA_60	H, H_ALA_60	2.91	2.08	13.02
4NZU.PDB	O, H_SER_82B	NH1, H_ARG_66	HH11, H_ARG_66	2.99	2.16	13.59
4NZU.PDB	OD2, H_ASP_86	NH1, H_ARG_66	HH12, H_ARG_66	2.80	1.94	3.46
4NZU.PDB	O, H_GLN_81	N, H_THR_68	H, H_THR_68	2.85	2.05	17.96
4NZU.PDB	OH, H_TYR_59	N, H_ILE_69	H, H_ILE_69	2.96	2.13	12.69
4NZU.PDB	O, H_TYR_32	NH1, H_ARG_71	HH12, H_ARG_71	2.89	2.14	25.08
4NZU.PDB	O, H_TYR_32	NH2, H_ARG_71	HH22, H_ARG_71	2.94	2.22	27.85
4NZU.PDB	O, H_THR_77	N, H_ASP_72	H, H_ASP_72	2.87	2.04	12.43
4NZU.PDB	O, H_CYS_22	N, H_LEU_78	H, H_LEU_78	2.86	2.03	13.04
4NZU.PDB	O, H_SER_70	N, H_SER_79	H, H_SER_79	2.89	2.05	11.36
4NZU.PDB	O, H_LEU_20	N, H_LEU_80	H, H_LEU_80	2.94	2.13	15.87
4NZU.PDB	O, H_THR_68	N, H_GLN_81	H, H_GLN_81	2.89	2.05	10.75
4NZU.PDB	O, H_LEU_18	N, H_MET_82	H, H_MET_82	2.85	2.01	9.41
4NZU.PDB	O, H_ARG_66	N, H_ASN_82A	H, H_ASN_82A	2.85	2.04	16.30
4NZU.PDB	OD2, H_ASP_86	N, H_LYS_83	H, H_LYS_83	2.86	2.03	12.94
4NZU.PDB	O, H_LYS_83	N, H_ASP_86	H, H_ASP_86	2.84	2.02	13.61
4NZU.PDB	O, H_GLN_39	N, H_VAL_89	H, H_VAL_89	2.90	2.11	18.38
4NZU.PDB	O, H_THR_107	N, H_TYR_90	H, H_TYR_90	2.88	2.04	8.85
4NZU.PDB	O, H_VAL_37	N, H_TYR_91	H, H_TYR_91	2.73	1.88	6.70
4NZU.PDB	O, H_HIS_35	N, H_ALA_93	H, H_ALA_93	2.90	2.19	28.63
4NZU.PDB	O, H_TYR_102	N, H_ARG_94	H, H_ARG_94	2.97	2.19	21.23
4NZU.PDB	O, H_ALA_95	NE, H_ARG_94	HE, H_ARG_94	2.86	2.03	25.77
4NZU.PDB	O, H_ALA_95	NH2, H_ARG_94	HH21, H_ARG_94	2.85	2.09	22.83
4NZU.PDB	OD1, H_ASP_97	NH2, H_ARG_94	HH22, H_ARG_94	2.85	2.02	14.02

4NZU.PDB	O, H_SER_31	N, H_CYS_100C	H, H_CYS_100C	2.76	1.91	5.59
4NZU.PDB	O, H_LYS_100E	N, H_ALA_100G	H, H_ALA_100G	2.86	2.15	29.42
4NZU.PDB	OH, L_TYR_36	N, H_PHE_100H	H, H_PHE_100H	2.86	2.04	13.13
4NZU.PDB	O, H_PHE_100H	NE1, H_TRP_103	HE1, H_TRP_103	2.88	2.03	28.43
4NZU.PDB	O, H_CYS_92	N, H_GLY_104	H, H_GLY_104	2.88	2.05	13.50
4NZU.PDB	OE2, H_GLU_6	N, H_GLY_106	H, H_GLY_106	2.99	2.21	21.44
4NZU.PDB	O, H_ALA_88	N, H_VAL_109	H, H_VAL_109	2.91	2.05	3.91
4NZU.PDB	OG1, H_THR_87	N, H_VAL_111	H, H_VAL_111	2.93	2.07	3.36
4NZU.PDB	O, H_VAL_112	N, H_SER_112	H, H_SER_112	2.95	2.14	16.38
4NZU.PDB	OG, H_SER_112	N, H_ALA_114	H, H_ALA_114	2.91	2.06	8.79
4NZU.PDB	O, H_PHE_148	N, H_LYS_117	H, H_LYS_117	2.88	2.05	12.81
4NZU.PDB	O, H_LYS_145	N, H_SER_120	H, H_SER_120	2.90	2.12	21.09
4NZU.PDB	O, H_LEU_143	N, H_PHE_122	H, H_PHE_122	2.87	2.03	9.52
4NZU.PDB	O, H_GLY_141	N, H_LEU_124	H, H_LEU_124	2.81	1.96	5.22
4NZU.PDB	OG, H_SER_195	N, H_GLY_135	H, H_GLY_135	2.91	2.20	29.13
4NZU.PDB	O, H_VAL_193	N, H_ALA_138	H, H_ALA_138	2.83	2.01	14.25
4NZU.PDB	O, H_VAL_191	N, H_LEU_140	H, H_LEU_140	2.93	2.10	13.71
4NZU.PDB	O, H_LEU_124	N, H_GLY_141	H, H_GLY_141	2.82	2.09	26.80
4NZU.PDB	O, H_SER_189	N, H_CYS_142	H, H_CYS_142	2.85	2.07	19.90
4NZU.PDB	O, H_PHE_122	N, H_LEU_143	H, H_LEU_143	2.81	1.97	11.58
4NZU.PDB	O, H_LEU_187	N, H_VAL_144	H, H_VAL_144	2.71	1.85	5.98
4NZU.PDB	O, H_SER_120	N, H_LYS_145	H, H_LYS_145	2.81	1.96	5.69
4NZU.PDB	O, H_LYS_117	N, H_PHE_148	H, H_PHE_148	2.88	2.08	17.45
4NZU.PDB	O, H_ASN_209	N, H_SER_156	H, H_SER_156	2.95	2.15	17.06
4NZU.PDB	OG, H_SER_189	NE1, H_TRP_157	HE1, H_TRP_157	2.92	1.90	9.04
4NZU.PDB	O, H_ILE_207	N, H_ASN_162	H, H_ASN_162	2.83	1.99	9.99
4NZU.PDB	OD1, H_ASN_209	N, H_SER_163	H, H_SER_163	2.80	1.99	15.68
4NZU.PDB	O, H_TRP_157	N, H_GLY_164	H, H_GLY_164	2.93	2.20	26.82
4NZU.PDB	O, H_VAL_190	N, H_HIS_172	H, H_HIS_172	2.83	2.02	16.48
4NZU.PDB	O, H_SER_188	N, H_PHE_174	H, H_PHE_174	2.92	2.06	3.04
4NZU.PDB	O, H_SER_186	N, H_VAL_177	H, H_VAL_177	2.90	2.09	15.20
4NZU.PDB	O, H_LEU_184	N, H_GLN_179	H, H_GLN_179	2.86	2.01	8.15
4NZU.PDB	O, H_GLN_179	N, H_GLY_183	H, H_GLY_183	2.91	2.06	7.56
4NZU.PDB	O, H_TYR_147	N, H_TYR_185	H, H_TYR_185	2.80	1.95	8.98
4NZU.PDB	O, H_VAL_144	N, H_LEU_187	H, H_LEU_187	2.87	2.07	16.93
4NZU.PDB	O, H_CYS_142	N, H_SER_189	H, H_SER_189	2.99	2.16	14.04
4NZU.PDB	O, H_HIS_172	N, H_VAL_190	H, H_VAL_190	2.85	2.02	12.23
4NZU.PDB	O, H_LEU_140	N, H_VAL_191	H, H_VAL_191	2.86	2.05	16.60
4NZU.PDB	O, H_ALA_138	N, H_VAL_193	H, H_VAL_193	2.91	2.09	14.81
4NZU.PDB	O, H_GLY_136	N, H_SER_195	H, H_SER_195	2.96	2.15	15.58
4NZU.PDB	O, H_PRO_194	N, H_SER_197	H, H_SER_197	2.90	2.09	16.91
4NZU.PDB	OH, H_TYR_206	OG, H_BSER_197	HG, H_BSER_197	2.82	2.05	15.42
4NZU.PDB	O, H_SER_197	N, H_GLN_203	H, H_GLN_203	2.89	2.06	13.09
4NZU.PDB	OD1, H_ASN_162	N, H_ILE_207	H, H_ILE_207	2.90	2.10	18.98
4NZU.PDB	O, H_LYS_221	N, H_CYS_208	H, H_CYS_208	2.94	2.14	18.10
4NZU.PDB	O, H_SER_156	N, H_ASN_209	H, H_ASN_209	2.80	1.94	7.24
4NZU.PDB	O, H_VAL_219	N, H_VAL_210	H, H_VAL_210	2.79	1.93	4.11
4NZU.PDB	O, H_THR_153	N, H_ASN_211	H, H_ASN_211	2.98	2.16	14.35
4NZU.PDB	O, H_THR_217	N, H_HIS_212	H, H_HIS_212	2.78	1.93	6.91
4NZU.PDB	O, H_VAL_210	N, H_VAL_219	H, H_VAL_219	2.89	2.07	13.72
4NZU.PDB	O, H_CYS_208	N, H_LYS_221	H, H_LYS_221	2.90	2.08	13.19
4NZU.PDB	O, H_TYR_206	N, H_VAL_223	H, H_VAL_223	2.82	1.97	6.85
4QEX.PDB	OD2, A_ASP_414	NH2, A_ARG_349	HH21, A_ARG_349	3.00	2.26	27.00
4QEX.PDB	O, A_PHE_316	N, A_ASN_356	H, A_ASN_356	2.87	2.04	13.53
4QEX.PDB	O, H_ALA_78	N, H_CYS_22	H, H_CYS_22	2.89	2.13	23.77
4QEX.PDB	O, H_ILE_51	N, H_MET_34	H, H_MET_34	2.99	2.24	24.56
4QEX.PDB	O, H_MET_34	N, H_ILE_51	H, H_ILE_51	2.88	2.12	24.11
4QEX.PDB	O, H_VAL_37	N, H_TYR_91	H, H_TYR_91	2.94	2.16	21.47

4QEX.PDB	OD2, B.ASP_414	NH2, B.ARG_349	HH21, B.ARG_349	2.99	2.26	27.25
4QEX.PDB	O, B.PHE_316	N, B.ASN_356	H, B.ASN_356	2.87	2.04	13.77
4QEX.PDB	O, I.ALA_78	N, I.CYS_22	H, I.CYS_22	2.89	2.13	24.05
4QEX.PDB	O, I.ILE_51	N, I.MET_34	H, I.MET_34	2.98	2.23	24.63
4QEX.PDB	O, I.TYR_91	N, I.VAL_37	H, I.VAL_37	3.00	2.18	14.72
4QEX.PDB	O, I.MET_34	N, I.ILE_51	H, I.ILE_51	2.88	2.13	24.11
4QEX.PDB	O, I.VAL_37	N, I.TYR_91	H, I.TYR_91	2.96	2.15	17.39
4WUU.PDB	OD2, A.ASP_29	ND1, A.HIS_3	HD1, A.HIS_3	2.93	2.13	17.75
4WUU.PDB	O, A.TYR_99	N, A.TYR_7	H, A.TYR_7	2.76	1.92	10.35
4WUU.PDB	O, A.VAL_25	N, A.PHE_8	H, A.PHE_8	2.96	2.14	14.63
4WUU.PDB	O, A.ARG_97	N, A.PHE_9	H, A.PHE_9	2.76	2.00	23.12
4WUU.PDB	O, A.ILE_23	N, A.THR_10	H, A.THR_10	2.77	1.94	11.62
4WUU.PDB	O, A.HIS_93	N, A.SER_13	H, A.SER_13	2.94	2.18	22.69
4WUU.PDB	OG, A.SER_38	N, A.PHE_22	H, A.PHE_22	2.99	2.28	28.95
4WUU.PDB	O, A.THR_10	N, A.ILE_23	H, A.ILE_23	2.73	1.91	14.53
4WUU.PDB	O, A.PHE_36	N, A.ALA_24	H, A.ALA_24	2.98	2.17	16.88
4WUU.PDB	O, A.PHE_8	N, A.VAL_25	H, A.VAL_25	2.92	2.13	19.23
4WUU.PDB	O, A.ARG_6	N, A.TYR_27	H, A.TYR_27	2.91	2.07	7.74
4WUU.PDB	O, A.THR_31	N, A.VAL_28	H, A.VAL_28	2.84	2.03	16.38
4WUU.PDB	O, A.SER_4	N, A.ASP_29	H, A.ASP_29	2.78	1.95	12.60
4WUU.PDB	O, A.VAL_28	N, A.THR_31	H, A.THR_31	2.84	1.99	7.07
4WUU.PDB	OE1, A.GLU_46	NE, A.ARG_35	HE, A.ARG_35	2.77	1.96	15.11
4WUU.PDB	O, A.ALA_24	N, A.PHE_36	H, A.PHE_36	2.92	2.14	20.69
4WUU.PDB	O, A.PHE_22	N, A.SER_38	H, A.SER_38	2.95	2.16	19.48
4WUU.PDB	OD1, A.ASP_37	N, A.ASP_39	H, A.ASP_39	2.77	1.98	19.65
4WUU.PDB	OE2, A.GLU_46	OG, A.SER_42	HG, A.SER_42	2.85	2.07	18.95
4WUU.PDB	O, A.ARG_35	N, A.GLU_46	H, A.GLU_46	2.99	2.17	14.81
4WUU.PDB	O, A.PHE_33	N, A.ARG_48	H, A.ARG_48	2.89	2.07	14.83
4WUU.PDB	OD2, B.ASP_53	NE, A.ARG_48	HE, A.ARG_48	2.84	2.13	29.12
4WUU.PDB	OH, A.TYR_171	OH, A.TYR_59	HH, A.TYR_59	2.71	1.89	11.34
4WUU.PDB	O, A.PRO_57	N, A.ASP_61	H, A.ASP_61	2.71	1.85	6.09
4WUU.PDB	O, A.GLU_58	N, A.GLY_62	H, A.GLY_62	2.94	2.16	20.28
4WUU.PDB	O, A.TYR_59	N, A.GLU_63	H, A.GLU_63	2.86	2.00	6.81
4WUU.PDB	O, A.TRP_60	N, A.THR_64	H, A.THR_64	2.90	2.08	14.57
4WUU.PDB	OH, E.TYR_104	NZ, A.LYS_66	HZ3, A.LYS_66	2.89	2.02	10.84
4WUU.PDB	O, A.GLU_63	N, A.VAL_67	H, A.VAL_67	2.84	2.02	14.98
4WUU.PDB	O, A.ARG_65	N, A.ALA_69	H, A.ALA_69	3.00	2.14	3.72
4WUU.PDB	O, A.LYS_68	OG, A.SER_71	HG, A.SER_71	2.82	2.03	15.69
4WUU.PDB	O, A.ALA_69	OG1, A.THR_73	HG1, A.THR_73	3.00	2.20	14.54
4WUU.PDB	O, A.HIS_70	N, A.HIS_74	H, A.HIS_74	2.95	2.14	15.71
4WUU.PDB	O, A.SER_71	N, A.ARG_75	H, A.ARG_75	2.82	2.00	14.92
4WUU.PDB	O, A.THR_73	N, A.ASP_77	H, A.ASP_77	2.79	1.98	16.13
4WUU.PDB	O, A.VAL_76	N, A.THR_80	H, A.THR_80	2.88	2.08	19.21
4WUU.PDB	O, A.ASP_77	N, A.LEU_81	H, A.LEU_81	2.80	2.01	18.94
4WUU.PDB	OXT, C.LEU_9	OH, A.TYR_84	HH, A.TYR_84	2.64	1.82	12.17
4WUU.PDB	OD2, A.ASP_137	OH, A.TYR_85	HH, A.TYR_85	2.79	1.98	13.39
4WUU.PDB	O, A.SER_13	OG, A.SER_92	HG, A.SER_92	2.55	1.73	10.54
4WUU.PDB	OG, A.SER_13	N, A.HIS_93	H, A.HIS_93	2.78	1.95	13.85
4WUU.PDB	OD1, A.ASP_119	N, A.THR_94	H, A.THR_94	2.87	2.10	22.46
4WUU.PDB	O, A.SER_11	N, A.VAL_95	H, A.VAL_95	2.78	1.96	15.83
4WUU.PDB	O, A.ALA_117	N, A.GLN_96	H, A.GLN_96	2.85	2.05	18.30
4WUU.PDB	O, B.TRP_60	NE2, A.GLN_96	HE22, A.GLN_96	2.78	1.93	8.81
4WUU.PDB	O, A.PHE_9	N, A.ARG_97	H, A.ARG_97	2.92	2.14	20.57
4WUU.PDB	O, A.GLN_115	N, A.MET_98	H, A.MET_98	2.92	2.09	12.67
4WUU.PDB	O, A.MET_5	N, A.CYS_101	H, A.CYS_101	2.91	2.19	28.90
4WUU.PDB	O, A.ARG_111	N, A.ASP_102	H, A.ASP_102	2.81	1.99	13.14
4WUU.PDB	O, A.HIS_3	N, A.VAL_103	H, A.VAL_103	2.85	2.00	5.54
4WUU.PDB	O, A.ARG_108	N, A.GLY_104	H, A.GLY_104	2.96	2.19	22.29

4WUU.PDB	O, A_GLY_104	N, A_TRP_107	H, A_TRP_107	2.80	2.02	20.77
4WUU.PDB	O, A_ASP_102	N, A_LEU_110	H, A_LEU_110	2.72	1.90	14.82
4WUU.PDB	O, A_MET_98	N, A_GLN_115	H, A_GLN_115	2.70	1.87	13.07
4WUU.PDB	O, A_ILE_124	N, A_TYR_116	H, A_TYR_116	2.79	1.93	4.70
4WUU.PDB	OE1, A_GLN_87	OH, A_TYR_118	HH, A_TYR_118	2.94	2.13	11.47
4WUU.PDB	O, A_THR_94	N, A_ASP_119	H, A_ASP_119	2.71	1.87	9.67
4WUU.PDB	OG1, A_THR_143	OH, A_TYR_123	HH, A_TYR_123	2.74	1.95	17.32
4WUU.PDB	O, A_THR_134	N, A_ALA_125	H, A_ALA_125	2.79	2.07	26.99
4WUU.PDB	O, A_ALA_125	N, A_THR_134	H, A_THR_134	2.73	1.89	10.54
4WUU.PDB	O, A_ALA_140	N, A_LYS_144	H, A_LYS_144	2.66	1.82	11.78
4WUU.PDB	O, C_LEU_9	NZ, A_LYS_146	HZ3, A_LYS_146	2.76	1.90	13.68
4WUU.PDB	O, C_TYR_8	NE1, A_TRP_147	HE1, A_TRP_147	2.81	1.99	15.97
4WUU.PDB	O, A_LYS_146	N, A_ALA_150	H, A_ALA_150	2.92	2.13	20.13
4WUU.PDB	O, A_TRP_147	N, A_VAL_152	H, A_VAL_152	2.94	2.08	3.18
4WUU.PDB	O, A_VAL_152	N, A_LEU_156	H, A_LEU_156	2.97	2.15	15.29
4WUU.PDB	O, A_ALA_153	N, A_ARG_157	H, A_ARG_157	2.89	2.04	9.86
4WUU.PDB	O, C_ARG_1	OH, A_TYR_159	HH, A_TYR_159	2.86	2.02	6.39
4WUU.PDB	O, A_LEU_156	N, A_LEU_160	H, A_LEU_160	2.72	1.88	9.29
4WUU.PDB	O, A_TYR_159	N, A_CYS_164	H, A_CYS_164	2.62	1.77	6.61
4WUU.PDB	O, A_CYS_164	N, A_LEU_168	H, A_LEU_168	2.93	2.10	13.84
4WUU.PDB	O, A_VAL_165	N, A_ARG_169	H, A_ARG_169	2.89	2.05	8.58
4WUU.PDB	O, A_TRP_107	NE, A_ARG_169	HE, A_ARG_169	2.99	2.28	29.58
4WUU.PDB	O, A_TRP_107	NH2, A_ARG_169	HH21, A_ARG_169	2.90	2.19	28.46
4WUU.PDB	OE2, A_GLU_55	NE, A_ARG_170	HE, A_ARG_170	2.89	2.03	3.82
4WUU.PDB	O, A_TRP_167	N, A_TYR_171	H, A_TYR_171	2.90	2.05	5.21
4WUU.PDB	O, A_LEU_168	N, A_LEU_172	H, A_LEU_172	2.90	2.13	22.30
4WUU.PDB	O, A_ARG_170	N, A_ASN_174	H, A_ASN_174	2.98	2.15	11.94
4WUU.PDB	O, A_TYR_171	N, A_GLY_175	H, A_GLY_175	2.88	2.04	8.17
4WUU.PDB	O, A_GLY_175	N, A_LEU_179	H, A_LEU_179	2.67	1.82	8.19
4WUU.PDB	O, A_THR_178	NH2, A_ARG_181	HH21, A_ARG_181	2.71	1.91	17.26
4WUU.PDB	O, A_HIS_188	N, A_TRP_204	H, A_TRP_204	2.78	1.93	9.00
4WUU.PDB	O, A_LYS_186	N, A_LEU_206	H, A_LEU_206	2.86	2.04	15.38
4WUU.PDB	O, A_ASP_183	N, A_TYR_209	H, A_TYR_209	2.76	1.98	20.63
4WUU.PDB	O, A_ALA_245	NE1, A_TRP_217	HE1, A_TRP_217	2.84	2.09	23.84
4WUU.PDB	O, A_GLN_242	N, A_ARG_234	H, A_ARG_234	2.84	2.02	15.28
4WUU.PDB	OE1, B_GLN_8	NH1, A_ARG_234	HH11, A_ARG_234	2.79	2.07	27.49
4WUU.PDB	OE1, A_GLN_242	NH2, A_ARG_234	HH21, A_ARG_234	3.00	2.27	27.42
4WUU.PDB	O, A_THR_240	N, A_ALA_236	H, A_ALA_236	2.92	2.07	7.39
4WUU.PDB	OD1, A_ASP_238	OG1, A_THR_240	HG1, A_THR_240	2.61	1.79	8.96
4WUU.PDB	O, A_ARG_234	N, A_GLN_242	H, A_GLN_242	2.75	1.97	20.96
4WUU.PDB	O, B_HIS_31	N, B_ARG_3	H, B_ARG_3	2.86	2.03	11.56
4WUU.PDB	OG1, B_THR_86	OG1, B_THR_4	HG1, B_THR_4	2.90	2.14	21.40
4WUU.PDB	O, B_SER_28	N, B_LYS_6	H, B_LYS_6	2.87	2.05	15.60
4WUU.PDB	O, A_PRO_235	OH, B_TYR_10	HH, B_TYR_10	2.61	1.79	11.75
4WUU.PDB	O, B_PHE_22	N, B_ARG_12	H, B_ARG_12	2.79	2.03	23.74
4WUU.PDB	OD1, B_ASN_21	N, B_HIS_13	H, B_HIS_13	2.89	2.04	5.58
4WUU.PDB	O, B_PRO_72	N, B_GLY_18	H, B_GLY_18	2.92	2.11	17.66
4WUU.PDB	O, B_GLU_16	N, B_LYS_19	H, B_LYS_19	2.97	2.20	22.07
4WUU.PDB	O, B_PHE_70	N, B_ASN_21	H, B_ASN_21	2.81	2.00	16.15
4WUU.PDB	O, B_HIS_13	ND2, B_ASN_21	HD21, B_ASN_21	2.56	1.73	12.09
4WUU.PDB	OD1, B_ASN_21	N, B_PHE_22	H, B_PHE_22	2.97	2.25	28.82
4WUU.PDB	O, B_THR_68	N, B_LEU_23	H, B_LEU_23	2.82	1.98	11.92
4WUU.PDB	O, B_TYR_10	N, B_ASN_24	H, B_ASN_24	2.72	1.90	14.68
4WUU.PDB	O, A_ALA_236	ND2, B_ASN_24	HD21, B_ASN_24	2.81	2.05	22.96
4WUU.PDB	O, B_TYR_66	N, B_CYS_25	H, B_CYS_25	2.71	1.87	10.19
4WUU.PDB	O, B_GLN_8	N, B_TYR_26	H, B_TYR_26	2.86	2.05	15.75
4WUU.PDB	OE1, A_GLU_232	OH, B_TYR_26	HH, B_TYR_26	2.95	2.14	13.27
4WUU.PDB	O, B_LEU_64	N, B_VAL_27	H, B_VAL_27	2.92	2.11	17.06

4WUU.PDB	O, B_LYS_6	N, B_SER_28	H, B_SER_28	2.97	2.17	19.07
4WUU.PDB	O, B_ARG_3	N, B_HIS_31	H, B_HIS_31	2.97	2.16	15.90
4WUU.PDB	O, B_GLU_44	N, B_LYS_41	H, B_LYS_41	2.88	2.07	16.59
4WUU.PDB	O, B_GLU_77	N, B_ASN_42	H, B_ASN_42	2.51	1.66	6.56
4WUU.PDB	OD1, B_ASP_38	NE, B_ARG_45	HE, B_ARG_45	2.54	1.82	27.34
4WUU.PDB	O, B_LEU_65	N, B_SER_52	H, B_SER_52	2.79	2.01	20.88
4WUU.PDB	O, B_SER_61	N, B_SER_57	H, B_SER_57	2.89	2.12	21.85
4WUU.PDB	O, B_SER_57	N, B_TRP_60	H, B_TRP_60	2.99	2.16	14.14
4WUU.PDB	O, B_PHE_30	N, B_PHE_62	H, B_PHE_62	2.98	2.14	10.04
4WUU.PDB	OG, B_SER_52	N, B_LEU_65	H, B_LEU_65	2.96	2.16	18.95
4WUU.PDB	O, B_CYS_25	N, B_TYR_66	H, B_TYR_66	2.90	2.12	19.74
4WUU.PDB	OD1, B_ASN_42	N, B_GLU_77	H, B_GLU_77	2.71	1.88	11.42
4WUU.PDB	O, B_ASP_38	N, B_ARG_81	H, B_ARG_81	2.83	1.98	5.14
4WUU.PDB	O, B_LYS_91	N, B_VAL_82	H, B_VAL_82	2.78	1.94	11.03
4WUU.PDB	O, B_GLU_36	N, B_ASN_83	H, B_ASN_83	2.81	1.99	15.23
4WUU.PDB	O, B_PRO_32	NE2, B_HIS_84	HE2, B_HIS_84	2.79	1.94	7.34
4WUU.PDB	ND1, B_HIS_84	OG1, B_THR_86	HG1, B_THR_86	2.95	2.20	22.57
4WUU.PDB	O, B_CYS_80	N, B_VAL_93	H, B_VAL_93	2.90	2.07	14.26
4WUU.PDB	O, B_TYR_78	N, B_TRP_95	H, B_TRP_95	2.84	2.01	11.88
4WUU.PDB	OH, A_TYR_171	N, C_ARG_1	H1, C_ARG_1	2.79	2.03	25.96
4WUU.PDB	OE2, A_GLU_63	N, C_MET_2	H, C_MET_2	2.90	2.09	16.21
4WUU.PDB	O, D_TYR_87	NE2, D_GLN_6	HE22, D_GLN_6	2.71	1.90	15.76
4WUU.PDB	O, D_LYS_106	N, D_ALA_10	H, D_ALA_10	2.90	2.14	24.22
4WUU.PDB	OE1, D_GLN_16	N, D_THR_13	H, D_THR_13	2.67	1.88	19.99
4WUU.PDB	O, D_LEU_74	N, D_ILE_20	H, D_ILE_20	2.74	1.99	24.99
4WUU.PDB	O, D_THR_5	N, D_SER_23	H, D_SER_23	2.85	2.04	15.21
4WUU.PDB	O, D_THR_70	N, D_GLY_24	H, D_GLY_24	2.81	1.97	11.14
4WUU.PDB	OD1, D_ASN_28	N, D_SER_25	H, D_SER_25	2.82	2.03	19.32
4WUU.PDB	OD1, D_ASN_28	N, D_ILE_29	H, D_ILE_29	2.67	1.86	15.71
4WUU.PDB	O, D_SER_25	N, D_GLY_30	H, D_GLY_30	2.74	2.02	28.00
4WUU.PDB	OD1, D_ASN_52	N, D_VAL_34	H, D_VAL_34	2.65	1.82	10.44
4WUU.PDB	O, D_ILE_49	N, D_TRP_36	H, D_TRP_36	2.74	1.90	10.94
4WUU.PDB	O, D_TYR_88	N, D_TYR_37	H, D_TYR_37	2.74	1.93	16.60
4WUU.PDB	O, D_LYS_46	N, D_GLN_38	H, D_GLN_38	2.85	2.06	19.88
4WUU.PDB	O, D_ASP_86	N, D_GLN_39	H, D_GLN_39	2.86	2.07	20.09
4WUU.PDB	OE1, E_GLN_39	NE2, D_GLN_39	HE22, D_GLN_39	2.94	2.18	23.53
4WUU.PDB	O, D_GLN_38	N, D_LYS_46	H, D_LYS_46	2.66	1.91	24.48
4WUU.PDB	O, D_TRP_36	N, D_LEU_48	H, D_LEU_48	2.81	1.96	9.20
4WUU.PDB	O, D_VAL_34	N, D_ASN_52	H, D_ASN_52	2.71	1.91	17.51
4WUU.PDB	O, D_TYR_50	N, D_GLN_54	H, D_GLN_54	2.84	2.03	17.63
4WUU.PDB	OD2, D_ASP_83	NE, D_ARG_62	HE, D_ARG_62	2.79	2.08	28.83
4WUU.PDB	OD1, D_ASP_83	NH2, D_ARG_62	HH21, D_ARG_62	2.86	2.00	2.74
4WUU.PDB	O, D_SER_73	N, D_SER_66	H, D_SER_66	2.98	2.20	21.24
4WUU.PDB	O, D_SER_71	N, D_SER_68	H, D_SER_68	2.91	2.13	20.74
4WUU.PDB	O, D_CYS_22	N, D_ALA_72	H, D_ALA_72	2.80	1.97	12.36
4WUU.PDB	O, D_SER_64	N, D_ALA_75	H, D_ALA_75	2.67	1.84	13.24
4WUU.PDB	O, D_ARG_62	N, D_SER_77	H, D_SER_77	2.87	2.05	15.21
4WUU.PDB	O, D_GLN_16	N, D_GLY_78	H, D_GLY_78	2.83	2.06	22.13
4WUU.PDB	O, D_GLN_16	N, D_LEU_79	H, D_LEU_79	2.99	2.26	27.65
4WUU.PDB	O, D_GLY_78	NE2, D_GLN_80	HE21, D_GLN_80	2.75	1.96	20.10
4WUU.PDB	O, D_THR_105	N, D_TYR_87	H, D_TYR_87	2.90	2.13	23.52
4WUU.PDB	O, D_ASP_83	OH, D_TYR_87	HH, D_TYR_87	2.68	1.84	6.34
4WUU.PDB	O, D_TYR_37	N, D_TYR_88	H, D_TYR_88	2.89	2.07	13.58
4WUU.PDB	OE1, D_GLN_6	N, D_CYS_89	H, D_CYS_89	2.99	2.19	19.58
4WUU.PDB	O, D_GLY_98	N, D_ASP_93	H, D_ASP_93	2.75	1.89	0.36
4WUU.PDB	OD1, E_ASP_106	NE1, D_TRP_99	HE1, D_TRP_99	2.95	2.19	24.35
4WUU.PDB	O, D_ALA_91	N, D_VAL_100	H, D_VAL_100	2.97	2.13	10.77
4WUU.PDB	O, D_TYR_87	N, D_THR_105	H, D_THR_105	2.86	2.16	29.98

4WUU.PDB	O, D_PRO_7	OG1, D_THR_105	HG1, D_THR_105	2.43	1.60	5.47
4WUU.PDB	O, D_PRO_8	N, D_LYS_106	H, D_LYS_106	2.54	1.73	16.46
4WUU.PDB	O, D_ALA_10	N, D_THR_108	H, D_THR_108	2.87	2.05	14.29
4WUU.PDB	O, D_VAL_137	N, D_PHE_122	H, D_PHE_122	2.93	2.13	18.73
4WUU.PDB	O, D_ILE_140	OG, D_SER_141	HG, D_SER_141	2.39	1.64	20.74
4WUU.PDB	O, D_CYS_138	N, D_SER_180	H, D_SER_180	2.83	2.03	17.76
4WUU.PDB	OG1, D_THR_165	OG, D_SER_180	HG, D_SER_180	3.00	2.24	22.62
4WUU.PDB	O, D_GLU_164	N, D_TYR_181	H, D_TYR_181	2.94	2.09	6.97
4WUU.PDB	O, E_LYS_23	N, E_VAL_5	H, E_VAL_5	2.91	2.08	12.06
4WUU.PDB	O, E_TYR_94	NE2, E_GLN_6	HE22, E_GLN_6	2.66	1.82	10.49
4WUU.PDB	O, E_LEU_116	N, E_GLU_10	H, E_GLU_10	2.74	1.93	15.88
4WUU.PDB	O, E_THR_118	N, E_LYS_12	H, E_LYS_12	2.72	1.97	24.94
4WUU.PDB	O, E_LEU_81	N, E_ILE_20	H, E_ILE_20	2.99	2.27	27.77
4WUU.PDB	O, E_ALA_79	N, E_CYS_22	H, E_CYS_22	2.79	2.05	26.43
4WUU.PDB	O, E_VAL_5	N, E_LYS_23	H, E_LYS_23	2.85	2.00	7.51
4WUU.PDB	O, E_SER_77	N, E_GLY_24	H, E_GLY_24	2.96	2.13	14.07
4WUU.PDB	O, E_ALA_97	N, E_SER_35	H, E_SER_35	2.86	2.01	6.50
4WUU.PDB	O, E_TYR_95	N, E_VAL_37	H, E_VAL_37	2.60	1.79	15.34
4WUU.PDB	O, E_GLU_46	N, E_ARG_38	H, E_ARG_38	2.74	1.93	15.84
4WUU.PDB	O, E_MET_93	N, E_GLN_39	H, E_GLN_39	2.93	2.14	19.90
4WUU.PDB	OE1, D_GLN_39	NE2, E_GLN_39	HE22, E_GLN_39	2.55	1.73	14.29
4WUU.PDB	O, E_MET_40	N, E_LYS_43	H, E_LYS_43	2.92	2.08	8.65
4WUU.PDB	O, E_ARG_38	N, E_GLU_46	H, E_GLU_46	2.81	2.04	21.42
4WUU.PDB	O, E_TRP_36	N, E_MET_48	H, E_MET_48	2.85	2.01	9.52
4WUU.PDB	O, E_THR_59	N, E_ARG_50	H, E_ARG_50	2.92	2.11	16.22
4WUU.PDB	OE2, A_GLU_166	NH2, E_ARG_50	HH22, E_ARG_50	2.67	1.88	18.69
4WUU.PDB	O, E_ILE_34	N, E_VAL_51	H, E_VAL_51	2.91	2.10	17.37
4WUU.PDB	O, E_TYR_57	N, E_ASP_52	H, E_ASP_52	2.77	1.94	11.78
4WUU.PDB	OD1, E_ASP_52	N, E_GLY_54	H, E_GLY_54	2.93	2.22	29.55
4WUU.PDB	O, E_ILE_70	OG, E_SER_58	HG, E_SER_58	2.56	1.77	16.65
4WUU.PDB	O, E_MET_48	N, E_SER_61	H, E_SER_61	3.00	2.19	16.66
4WUU.PDB	O, E_SER_61	N, E_PHE_64	H, E_PHE_64	2.90	2.08	14.75
4WUU.PDB	O, E_GLN_82	N, E_THR_69	H, E_THR_69	2.86	2.06	17.27
4WUU.PDB	OH, E_TYR_60	N, E_ILE_70	H, E_ILE_70	2.95	2.13	13.50
4WUU.PDB	O, E_THR_78	N, E_ASP_73	H, E_ASP_73	2.72	1.95	22.66
4WUU.PDB	OD1, E_ASP_73	OG, E_SER_75	HG, E_SER_75	2.93	2.16	19.72
4WUU.PDB	O, E_CYS_22	N, E_ALA_79	H, E_ALA_79	2.74	1.89	8.78
4WUU.PDB	O, E_SER_71	N, E_TYR_80	H, E_TYR_80	2.97	2.17	17.59
4WUU.PDB	O, E_THR_69	N, E_GLN_82	H, E_GLN_82	2.93	2.22	28.66
4WUU.PDB	O, E_LEU_18	N, E_TRP_83	H, E_TRP_83	2.80	1.95	10.15
4WUU.PDB	OD2, E_ASP_90	N, E_LYS_87	H, E_LYS_87	2.81	1.97	9.45
4WUU.PDB	O, E_THR_115	N, E_TYR_94	H, E_TYR_94	2.93	2.16	22.48
4WUU.PDB	O, E_ASP_90	OH, E_TYR_94	HH, E_TYR_94	2.62	1.78	4.11
4WUU.PDB	O, E_VAL_37	N, E_TYR_95	H, E_TYR_95	2.78	2.01	21.75
4WUU.PDB	O, E_PRO_110	N, E_ARG_98	H, E_ARG_98	2.98	2.16	15.09
4WUU.PDB	OE1, A_GLU_63	OH, E_TYR_104	HH, E_TYR_104	2.59	1.76	7.82
4WUU.PDB	OE1, A_GLU_58	N, E_TYR_105	H, E_TYR_105	2.88	2.05	12.40
4WUU.PDB	OE1, A_GLU_55	OH, E_TYR_105	HH, E_TYR_105	2.47	1.79	29.86
4WUU.PDB	O, E_CYS_96	N, E_GLY_112	H, E_GLY_112	2.73	1.88	6.91
4WUU.PDB	O, E_SER_7	OG1, E_THR_115	HG1, E_THR_115	2.87	2.12	21.80
4WUU.PDB	O, E_ALA_92	N, E_VAL_117	H, E_VAL_117	2.94	2.09	9.12
4WUU.PDB	O, E_GLU_10	N, E_THR_118	H, E_THR_118	2.81	2.08	26.12
4WUU.PDB	OG1, E_THR_91	N, E_VAL_119	H, E_VAL_119	2.69	1.92	22.07
4WUU.PDB	O, E_SER_188	N, E_CYS_148	H, E_CYS_148	2.84	2.07	21.15
4WUU.PDB	O, E_PHE_130	N, E_LEU_149	H, E_LEU_149	2.81	2.09	28.03
4WUU.PDB	O, E_TYR_184	N, E_TYR_153	H, E_TYR_153	2.99	2.17	14.59
4WUU.PDB	OE1, E_GLU_156	OH, E_TYR_153	HH, E_TYR_153	2.97	2.18	16.08
4WUU.PDB	O, E_LYS_125	N, E_PHE_154	H, E_PHE_154	2.79	1.96	12.82

4WUU.PDB	O, E_TYR_153	N, E_TYR_184	H, E_TYR_184	2.70	1.85	7.96
4Z0X.PDB	O, A_ASP_25	OH, A_TYR_2	HH, A_TYR_2	2.80	1.97	6.75
4Z0X.PDB	O, A_SER_23	N, A_THR_5	H, A_THR_5	2.85	2.02	14.04
4Z0X.PDB	OG1, A_THR_101	NE2, A_GLN_6	HE21, A_GLN_6	2.98	2.23	24.64
4Z0X.PDB	O, A_TYR_85	NE2, A_GLN_6	HE22, A_GLN_6	2.80	1.95	8.09
4Z0X.PDB	O, A_THR_104	N, A_VAL_12	H, A_VAL_12	2.52	1.67	7.35
4Z0X.PDB	OG1, A_THR_77	N, A_GLY_15	H, A_GLY_15	2.67	1.88	19.17
4Z0X.PDB	OE1, A_GLN_16	OG1, A_THR_17	HG1, A_THR_17	2.97	2.23	24.46
4Z0X.PDB	O, A_LEU_72	N, A_ILE_20	H, A_ILE_20	2.77	1.96	17.57
4Z0X.PDB	O, A_ALA_70	N, A_CYS_22	H, A_CYS_22	2.77	1.99	21.67
4Z0X.PDB	O, A_THR_5	N, A_SER_23	H, A_SER_23	2.81	2.00	16.58
4Z0X.PDB	O, A_ASN_68	N, A_GLY_24	H, A_GLY_24	2.89	2.08	17.57
4Z0X.PDB	O, A_LEU_27	N, A_LYS_30	H, A_LYS_30	2.84	2.00	9.85
4Z0X.PDB	OD1, A_ASP_50	N, A_VAL_32	H, A_VAL_32	2.87	2.04	13.49
4Z0X.PDB	O, A_LEU_47	N, A_TRP_34	H, A_TRP_34	2.79	1.98	15.57
4Z0X.PDB	O, A_TYR_86	N, A_TYR_35	H, A_TYR_35	2.82	2.01	16.09
4Z0X.PDB	OE1, A_GLN_88	OH, A_TYR_35	HH, A_TYR_35	2.99	2.19	16.02
4Z0X.PDB	O, A_VAL_44	N, A_GLN_36	H, A_GLN_36	2.60	1.77	13.39
4Z0X.PDB	O, A_ASP_84	N, A_GLN_37	H, A_GLN_37	2.88	2.08	17.37
4Z0X.PDB	OE1, B_GLN_64	NE2, A_GLN_37	HE22, A_GLN_37	2.75	1.99	23.41
4Z0X.PDB	O, A_GLN_36	N, A_VAL_44	H, A_VAL_44	2.70	1.89	16.44
4Z0X.PDB	O, A_TRP_34	N, A_VAL_46	H, A_VAL_46	2.99	2.14	7.42
4Z0X.PDB	O, A_LYS_52	N, A_TYR_48	H, A_TYR_48	2.81	1.99	14.31
4Z0X.PDB	O, A_VAL_32	N, A_ASP_50	H, A_ASP_50	2.74	1.91	13.42
4Z0X.PDB	O, A_GLN_49	N, A_SER_51	H, A_SER_51	2.75	2.01	26.59
4Z0X.PDB	O, A_TYR_48	N, A_LYS_52	H, A_LYS_52	2.96	2.19	22.52
4Z0X.PDB	O, A_PHE_61	NE, A_ARG_53	HE, A_ARG_53	2.38	1.60	20.12
4Z0X.PDB	OD2, A_ASP_81	NH1, A_ARG_60	HH12, A_ARG_60	2.72	1.91	16.22
4Z0X.PDB	O, A_THR_73	N, A_SER_62	H, A_SER_62	2.83	2.01	14.05
4Z0X.PDB	O, A_THR_69	N, A_SER_66	H, A_SER_66	2.92	2.06	6.16
4Z0X.PDB	O, A_SER_66	N, A_THR_69	H, A_THR_69	2.80	1.94	3.16
4Z0X.PDB	OD1, A_ASN_68	OG1, A_THR_69	HG1, A_THR_69	2.91	2.09	9.92
4Z0X.PDB	O, A_CYS_22	N, A_ALA_70	H, A_ALA_70	2.78	1.96	14.70
4Z0X.PDB	O, A_SER_64	N, A_THR_71	H, A_THR_71	2.92	2.10	14.49
4Z0X.PDB	O, A_ILE_20	N, A_LEU_72	H, A_LEU_72	2.78	1.96	14.72
4Z0X.PDB	O, A_SER_62	N, A_THR_73	H, A_THR_73	2.73	1.87	2.53
4Z0X.PDB	O, A_ALA_18	N, A_ILE_74	H, A_ILE_74	2.71	1.87	12.36
4Z0X.PDB	O, A_ARG_60	N, A_SER_75	H, A_SER_75	2.66	1.92	25.71
4Z0X.PDB	O, A_GLN_78	N, A_ASP_81	H, A_ASP_81	2.82	2.02	19.19
4Z0X.PDB	O, A_GLN_37	N, A_ASP_84	H, A_ASP_84	2.80	1.95	9.61
4Z0X.PDB	O, A_THR_101	N, A_TYR_85	H, A_TYR_85	2.95	2.11	9.72
4Z0X.PDB	O, A_ASP_81	OH, A_TYR_85	HH, A_TYR_85	2.69	1.90	17.09
4Z0X.PDB	O, B_GLY_129	NE2, A_GLN_88	HE22, A_GLN_88	2.63	1.87	22.97
4Z0X.PDB	O, B_GLY_129	NE1, A_TRP_90	HE1, A_TRP_90	2.96	2.14	15.73
4Z0X.PDB	O, A_ALA_94	N, A_ASP_91	H, A_ASP_91	2.88	2.04	11.61
4Z0X.PDB	OH, C_TYR_443	N, A_SER_93	H, A_SER_93	2.99	2.17	13.42
4Z0X.PDB	O, A_ALA_89	N, A_VAL_96	H, A_VAL_96	2.88	2.05	11.58
4Z0X.PDB	O, A_CYS_87	N, A_GLY_98	H, A_GLY_98	2.99	2.16	12.80
4Z0X.PDB	O, A_TYR_85	N, A_THR_101	H, A_THR_101	2.96	2.16	18.49
4Z0X.PDB	O, A_PRO_7	OG1, A_THR_101	HG1, A_THR_101	2.61	1.78	9.78
4Z0X.PDB	O, A_PRO_8	N, A_LYS_102	H, A_LYS_102	2.94	2.08	5.27
4Z0X.PDB	O, A_ALA_83	N, A_LEU_103	H, A_LEU_103	2.90	2.08	13.84
4Z0X.PDB	O, A_VAL_10	N, A_THR_104	H, A_THR_104	2.88	2.05	13.22
4Z0X.PDB	O, A_VAL_12	N, A_LEU_106	H, A_LEU_106	2.44	1.64	16.67
4Z0X.PDB	O, B_LEU_139	N, B_GLU_35	H, B_GLU_35	2.78	1.95	12.53
4Z0X.PDB	O, B_LEU_111	N, B_GLY_40	H, B_GLY_40	2.87	2.06	15.69
4Z0X.PDB	O, B_LYS_38	N, B_SER_41	H, B_SER_41	2.91	2.07	11.45
4Z0X.PDB	O, B_LYS_38	OG, B_SER_41	HG, B_SER_41	2.46	1.70	19.33

4Z0X.PDB	OE2, B_GLU_107	OG, B_SER_42	HG, B_SER_42	2.96	2.17	17.40
4Z0X.PDB	O, B_MET_106	N, B_VAL_45	H, B_VAL_45	2.73	1.90	11.31
4Z0X.PDB	OE1, B_GLN_31	N, B_SER_46	H, B_SER_46	2.95	2.11	10.80
4Z0X.PDB	OE1, B_GLN_31	OG, B_SER_46	HG, B_SER_46	2.75	1.93	11.18
4Z0X.PDB	O, B_ALA_104	N, B_CYS_47	H, B_CYS_47	2.48	1.72	23.24
4Z0X.PDB	O, B_PHE_76	N, B_ILE_59	H, B_ILE_59	2.75	1.91	10.64
4Z0X.PDB	O, B_ALA_122	N, B_THR_60	H, B_THR_60	2.78	2.00	20.86
4Z0X.PDB	O, B_GLY_74	N, B_TRP_61	H, B_TRP_61	2.88	2.03	5.31
4Z0X.PDB	O, B_TYR_120	N, B_VAL_62	H, B_VAL_62	2.96	2.12	9.50
4Z0X.PDB	OE2, B_GLU_71	NE, B_ARG_63	HE, B_ARG_63	2.78	1.94	9.25
4Z0X.PDB	OD1, B_ASP_115	NH1, B_ARG_63	HH12, B_ARG_63	3.00	2.15	8.77
4Z0X.PDB	O, B_VAL_118	N, B_GLN_64	H, B_GLN_64	2.70	1.91	18.82
4Z0X.PDB	O, B_TRP_61	N, B_MET_73	H, B_MET_73	2.89	2.05	11.27
4Z0X.PDB	O, B_MET_84	N, B_GLY_75	H, B_GLY_75	2.80	2.00	19.09
4Z0X.PDB	O, B_ILE_59	N, B_PHE_76	H, B_PHE_76	2.84	2.02	13.51
4Z0X.PDB	O, B_GLY_75	N, B_MET_84	H, B_MET_84	2.91	2.08	13.54
4Z0X.PDB	OE1, B_GLN_90	NE, B_ARG_92	HE, B_ARG_92	2.75	1.97	21.20
4Z0X.PDB	OD2, B_ASP_115	NH1, B_ARG_92	HH12, B_ARG_92	2.90	2.09	15.11
4Z0X.PDB	OD1, B_ASP_115	NH2, B_ARG_92	HH22, B_ARG_92	2.68	1.87	17.08
4Z0X.PDB	O, B_GLU_107	N, B_THR_94	H, B_THR_94	2.93	2.14	19.73
4Z0X.PDB	O, B_TYR_105	N, B_THR_96	H, B_THR_96	2.98	2.17	16.27
4Z0X.PDB	O, B_SER_100	OG, B_SER_102	HG, B_SER_102	2.77	1.99	18.26
4Z0X.PDB	O, B_THR_96	N, B_TYR_105	H, B_TYR_105	2.64	1.82	13.50
4Z0X.PDB	O, B_VAL_45	N, B_MET_106	H, B_MET_106	2.83	1.98	6.79
4Z0X.PDB	O, B_THR_94	N, B_GLU_107	H, B_GLU_107	2.90	2.05	7.24
4Z0X.PDB	O, B_VAL_43	N, B_LEU_108	H, B_LEU_108	2.96	2.14	15.47
4Z0X.PDB	O, B_ARG_92	N, B_THR_109	H, B_THR_109	2.97	2.14	11.99
4Z0X.PDB	O, B_SER_41	N, B_LEU_111	H, B_LEU_111	2.94	2.09	6.29
4Z0X.PDB	OD2, B_ASP_115	N, B_ARG_112	H, B_ARG_112	2.72	1.96	22.70
4Z0X.PDB	O, B_ARG_112	N, B_ASP_115	H, B_ASP_115	2.66	1.82	10.17
4Z0X.PDB	O, B_THR_138	N, B_TYR_119	H, B_TYR_119	2.87	2.02	7.83
4Z0X.PDB	O, B_ASP_115	OH, B_TYR_119	HH, B_TYR_119	2.68	1.89	16.10
4Z0X.PDB	O, B_VAL_62	N, B_TYR_120	H, B_TYR_120	2.59	1.74	8.64
4Z0X.PDB	OE1, B_GLN_64	OH, B_TYR_120	HH, B_TYR_120	2.91	2.08	8.45
4Z0X.PDB	O, B_THR_60	N, B_ALA_122	H, B_ALA_122	2.71	1.91	17.66
4Z0X.PDB	O, B_TYR_133	N, B_ARG_123	H, B_ARG_123	2.79	1.95	10.77
4Z0X.PDB	O, B_VAL_27	NE, B_ARG_123	HE, B_ARG_123	2.62	1.82	18.21
4Z0X.PDB	O, C_LEU_441	N, B_SER_127	H, B_SER_127	2.61	1.82	19.78
4Z0X.PDB	OH, A_TYR_35	N, B_TYR_131	H, B_TYR_131	2.85	2.09	23.16
4Z0X.PDB	O, B_SER_32	OG1, B_THR_138	HG1, B_THR_138	2.51	1.69	7.93
4Z0X.PDB	O, B_ALA_117	N, B_VAL_140	H, B_VAL_140	2.85	1.99	6.27
4Z0X.PDB	O, B_GLU_35	N, B_THR_141	H, B_THR_141	2.88	2.05	13.44
4Z0X.PDB	O, C_ALA_439	N, C_TYR_443	H, C_TYR_443	2.86	2.01	7.86
5I76.PDB	OG, A_SER_26	N, A_LEU_3	H, A_LEU_3	2.93	2.11	13.63
5I76.PDB	O, A_ARG_24	N, A_THR_5	H, A_THR_5	2.85	2.02	11.85
5I76.PDB	O, A_TYR_86	NE2, A_GLN_6	HE22, A_GLN_6	2.97	2.18	18.78
5I76.PDB	O, A_LYS_103	N, A_LEU_11	H, A_LEU_11	2.81	1.99	15.02
5I76.PDB	O, A_VAL_78	N, A_GLY_16	H, A_GLY_16	2.83	1.97	5.42
5I76.PDB	OD1, A_ASN_76	NH1, A_ARG_18	HH11, A_ARG_18	2.77	1.94	12.53
5I76.PDB	O, A_ILE_75	N, A_VAL_19	H, A_VAL_19	2.92	2.11	15.94
5I76.PDB	O, A_LEU_73	N, A_PHE_21	H, A_PHE_21	2.75	1.92	12.31
5I76.PDB	O, A_PHE_71	N, A_CYS_23	H, A_CYS_23	2.97	2.12	7.46
5I76.PDB	O, A_THR_5	N, A_ARG_24	H, A_ARG_24	2.95	2.13	14.78
5I76.PDB	O, A_THR_69	N, A_ALA_25	H, A_ALA_25	2.95	2.17	21.21
5I76.PDB	O, A_GLY_68	N, A_ILE_29	H, A_ILE_29	2.89	2.05	11.68
5I76.PDB	O, A_ILE_29	N, A_ASN_32	H, A_ASN_32	2.93	2.08	6.67
5I76.PDB	O, A_THR_31	N, A_ILE_33	H, A_ILE_33	2.92	2.20	28.68
5I76.PDB	O, A_GLN_89	N, A_HIS_34	H, A_HIS_34	2.81	1.99	14.63

5I76.PDB	O, A_ILE_48	N, A_TRP_35	H, A_TRP_35	2.92	2.10	13.82
5I76.PDB	O, A_TYR_87	N, A_TYR_36	H, A_TYR_36	2.81	2.01	17.84
5I76.PDB	OE1, A_GLN_89	OH, A_TYR_36	HH, A_TYR_36	2.60	1.77	6.74
5I76.PDB	O, A_ARG_45	N, A_GLN_37	H, A_GLN_37	2.91	2.08	14.58
5I76.PDB	OH, A_TYR_86	NE2, A_GLN_37	HE21, A_GLN_37	2.93	2.09	10.63
5I76.PDB	O, A_ASP_85	N, A_GLN_38	H, A_GLN_38	2.79	1.98	15.97
5I76.PDB	OE1, B_GLN_39	NE2, A_GLN_38	HE22, A_GLN_38	2.94	2.10	10.68
5I76.PDB	O, A_ARG_39	N, A_GLY_42	H, A_GLY_42	2.91	2.09	15.47
5I76.PDB	O, B_GLY_110	OG, A_SER_43	HG, A_SER_43	2.73	2.02	27.09
5I76.PDB	O, A_TRP_35	N, A_LEU_47	H, A_LEU_47	2.79	1.93	2.43
5I76.PDB	OE1, A_GLU_53	NZ, A_LYS_49	HZ2, A_LYS_49	2.94	2.09	13.35
5I76.PDB	OD2, B_ASP_103	OH, A_TYR_50	HH, A_TYR_50	2.64	1.88	21.01
5I76.PDB	O, A_ILE_33	N, A_ALA_51	H, A_ALA_51	2.67	1.85	13.57
5I76.PDB	O, A_TYR_50	N, A_SER_52	H, A_SER_52	2.77	2.05	27.32
5I76.PDB	O, A_LYS_49	N, A_GLU_53	H, A_GLU_53	2.80	2.00	17.59
5I76.PDB	OD1, A_ASP_82	NH2, A_ARG_61	HH21, A_ARG_61	2.77	1.93	10.41
5I76.PDB	OE2, A_GLU_81	NH2, A_ARG_61	HH22, A_ARG_61	2.77	1.92	8.54
5I76.PDB	O, A_SER_74	N, A_SER_63	H, A_SER_63	2.94	2.14	18.34
5I76.PDB	O, A_THR_72	N, A_SER_65	H, A_SER_65	2.92	2.10	15.80
5I76.PDB	O, A_GLY_30	N, A_GLY_68	H, A_GLY_68	2.79	2.04	24.26
5I76.PDB	O, A_SER_65	N, A_THR_72	H, A_THR_72	2.94	2.12	13.74
5I76.PDB	O, A_PHE_21	N, A_LEU_73	H, A_LEU_73	3.00	2.22	21.96
5I76.PDB	O, A_SER_63	N, A_SER_74	H, A_SER_74	2.85	1.99	4.51
5I76.PDB	O, A_VAL_19	N, A_ILE_75	H, A_ILE_75	2.85	2.03	15.69
5I76.PDB	O, A_ARG_61	N, A_ASN_76	H, A_ASN_76	2.79	1.97	14.79
5I76.PDB	O, A_GLU_17	N, A_VAL_78	H, A_VAL_78	2.96	2.12	10.44
5I76.PDB	OD2, A_ASP_82	N, A_GLU_79	H, A_GLU_79	2.95	2.11	11.60
5I76.PDB	O, A_GLU_79	N, A_ASP_82	H, A_ASP_82	2.78	1.95	11.07
5I76.PDB	O, A_GLN_38	N, A_ASP_85	H, A_ASP_85	2.93	2.13	17.77
5I76.PDB	O, A_THR_102	N, A_TYR_86	H, A_TYR_86	2.91	2.14	23.37
5I76.PDB	O, A_ASP_82	OH, A_TYR_86	HH, A_TYR_86	2.55	1.72	9.51
5I76.PDB	O, A_TYR_36	N, A_TYR_87	H, A_TYR_87	2.89	2.08	16.03
5I76.PDB	OG1, A_THR_96	NE2, A_GLN_89	HE21, A_GLN_89	2.89	2.08	16.62
5I76.PDB	O, A_THR_97	N, A_GLN_90	H, A_GLN_90	2.93	2.15	21.05
5I76.PDB	OD1, A_ASN_93	ND2, A_ASN_92	HD22, A_ASN_92	2.89	2.06	14.53
5I76.PDB	O, A_GLN_90	OG1, A_THR_96	HG1, A_THR_96	2.66	1.94	25.05
5I76.PDB	O, A_ILE_2	OG1, A_THR_97	HG1, A_THR_97	2.88	2.08	14.12
5I76.PDB	O, A_CYS_88	N, A_GLY_99	H, A_GLY_99	2.80	1.99	16.49
5I76.PDB	OE1, A_GLN_6	N, A_GLY_101	H, A_GLY_101	2.95	2.25	29.58
5I76.PDB	O, A_TYR_86	N, A_THR_102	H, A_THR_102	2.91	2.11	17.28
5I76.PDB	O, A_PRO_8	OG1, A_THR_102	HG1, A_THR_102	2.77	2.04	24.64
5I76.PDB	O, A_VAL_9	N, A_LYS_103	H, A_LYS_103	2.97	2.12	8.09
5I76.PDB	O, A_ALA_84	N, A_LEU_104	H, A_LEU_104	2.94	2.08	1.76
5I76.PDB	O, A_LEU_11	N, A_GLU_105	H, A_GLU_105	2.78	1.93	6.87
5I76.PDB	O, A_VAL_13	N, A_LYS_107	H, A_LYS_107	2.80	1.97	11.70
5I76.PDB	OG, A_SER_12	NZ, A_LYS_107	HZ3, A_LYS_107	2.75	1.89	12.15
5I76.PDB	O, A_TYR_140	N, A_ALA_111	H, A_ALA_111	2.82	2.00	15.73
5I76.PDB	O, A_LEU_135	N, A_PHE_116	H, A_PHE_116	2.95	2.18	23.57
5I76.PDB	O, A_VAL_133	N, A_PHE_118	H, A_PHE_118	2.81	2.04	21.46
5I76.PDB	OG, A_SER_131	NE2, A_GLN_124	HE22, A_GLN_124	2.78	1.92	5.16
5I76.PDB	O, A_GLN_124	N, A_SER_127	H, A_SER_127	2.80	1.97	11.43
5I76.PDB	O, A_GLN_124	OG, A_SER_127	HG, A_SER_127	2.76	1.92	5.99
5I76.PDB	O, A_LEU_181	N, A_ALA_130	H, A_ALA_130	2.88	2.06	14.29
5I76.PDB	OE1, A_GLN_124	N, A_SER_131	H, A_SER_131	2.93	2.12	16.06
5I76.PDB	O, A_LEU_179	N, A_VAL_132	H, A_VAL_132	2.86	2.02	10.93
5I76.PDB	O, A_SER_177	N, A_CYS_134	H, A_CYS_134	2.84	1.99	8.38
5I76.PDB	O, A_PHE_116	N, A_LEU_135	H, A_LEU_135	2.80	1.96	8.13
5I76.PDB	O, A_LEU_175	N, A_LEU_136	H, A_LEU_136	2.86	2.01	4.38

5I76.PDB	O, A_SER_114	N, A_ASN_137	H, A_ASN_137	2.78	1.96	14.88
5I76.PDB	OG, A_SER_174	N, A_ASN_138	H, A_ASN_138	2.99	2.15	10.62
5I76.PDB	O, A_TYR_173	N, A_PHE_139	H, A_PHE_139	2.85	2.03	14.64
5I76.PDB	O, A_ALA_111	N, A_TYR_140	H, A_TYR_140	2.84	2.04	18.07
5I76.PDB	OE2, A_GLU_143	NZ, A_LYS_145	HZ3, A_LYS_145	2.87	2.06	20.39
5I76.PDB	O, A_GLU_195	N, A_GLN_147	H, A_GLN_147	2.83	2.01	15.29
5I76.PDB	OG, A_SER_177	NE1, A_TRP_148	HE1, A_TRP_148	2.97	2.15	13.90
5I76.PDB	O, A_ALA_193	N, A_LYS_149	H, A_LYS_149	2.89	2.04	9.43
5I76.PDB	O, A_VAL_191	N, A_ASP_151	H, A_ASP_151	2.77	1.94	12.86
5I76.PDB	O, A_TRP_148	N, A_GLN_155	H, A_GLN_155	2.81	1.97	9.99
5I76.PDB	O, A_ALA_153	NE2, A_GLN_155	HE21, A_GLN_155	2.93	2.08	7.12
5I76.PDB	O, A_THR_178	N, A_GLN_160	H, A_GLN_160	2.97	2.20	22.65
5I76.PDB	O, A_SER_176	N, A_SER_162	H, A_SER_162	2.82	2.02	18.15
5I76.PDB	O, B_PRO_173	OG, A_SER_162	HG, A_SER_162	2.48	1.79	28.75
5I76.PDB	O, A_SER_174	N, A_THR_164	H, A_THR_164	2.85	2.02	12.10
5I76.PDB	O, A_SER_171	NE2, A_GLN_166	HE21, A_GLN_166	2.90	2.05	6.30
5I76.PDB	O, A_LEU_106	NE2, A_GLN_166	HE22, A_GLN_166	2.72	1.91	17.00
5I76.PDB	O, A_THR_172	N, A_ASP_167	H, A_ASP_167	2.78	1.95	11.68
5I76.PDB	OD1, A_ASP_167	N, A_LYS_169	H, A_LYS_169	2.67	1.87	18.00
5I76.PDB	O, A_ASP_167	N, A_SER_171	H, A_SER_171	2.85	2.10	24.64
5I76.PDB	OD1, A_ASP_170	OG1, A_THR_172	HG1, A_THR_172	2.65	1.83	9.24
5I76.PDB	O, A_PHE_139	N, A_TYR_173	H, A_TYR_173	2.85	2.00	5.15
5I76.PDB	OE2, A_GLU_105	OH, A_TYR_173	HH, A_TYR_173	2.42	1.66	21.73
5I76.PDB	OG1, A_THR_164	N, A_SER_174	H, A_SER_174	2.83	2.01	15.67
5I76.PDB	O, A_LEU_136	N, A_LEU_175	H, A_LEU_175	2.85	2.05	17.34
5I76.PDB	O, A_SER_162	N, A_SER_176	H, A_SER_176	2.84	2.01	11.93
5I76.PDB	O, A_CYS_134	N, A_SER_177	H, A_SER_177	2.92	2.08	10.24
5I76.PDB	O, A_GLN_160	N, A_THR_178	H, A_THR_178	2.84	2.01	11.67
5I76.PDB	O, A_VAL_132	N, A_LEU_179	H, A_LEU_179	2.88	2.05	12.69
5I76.PDB	O, A_ALA_130	N, A_LEU_181	H, A_LEU_181	2.89	2.05	10.41
5I76.PDB	O, A_GLY_128	N, A_LYS_183	H, A_LYS_183	2.99	2.14	6.01
5I76.PDB	OG, A_SER_182	N, A_ASP_185	H, A_ASP_185	2.96	2.11	8.88
5I76.PDB	O, A_SER_182	N, A_TYR_186	H, A_TYR_186	2.77	1.92	7.00
5I76.PDB	O, A_LYS_183	N, A_GLU_187	H, A_GLU_187	2.88	2.08	18.36
5I76.PDB	O, A_ASP_185	N, A_LYS_188	H, A_LYS_188	2.97	2.19	21.73
5I76.PDB	OD1, A_ASP_151	N, A_VAL_191	H, A_VAL_191	2.98	2.13	9.38
5I76.PDB	O, A_PHE_209	N, A_TYR_192	H, A_TYR_192	2.92	2.08	9.60
5I76.PDB	O, A_LYS_149	N, A_ALA_193	H, A_ALA_193	2.91	2.19	28.01
5I76.PDB	O, A_LYS_207	N, A_CYS_194	H, A_CYS_194	2.85	2.00	8.12
5I76.PDB	O, A_GLN_147	N, A_GLU_195	H, A_GLU_195	2.84	1.99	7.10
5I76.PDB	O, A_VAL_205	N, A_VAL_196	H, A_VAL_196	2.79	2.00	20.45
5I76.PDB	O, A_LYS_145	N, A_THR_197	H, A_THR_197	2.98	2.16	15.25
5I76.PDB	O, A_PRO_141	NE2, A_HIS_198	HE2, A_HIS_198	2.94	2.11	12.28
5I76.PDB	ND1, A_HIS_198	N, A_GLY_200	H, A_GLY_200	2.85	1.99	1.58
5I76.PDB	O, A_HIS_198	N, A_LEU_201	H, A_LEU_201	2.86	2.01	7.02
5I76.PDB	O, A_CYS_194	N, A_LYS_207	H, A_LYS_207	2.92	2.10	16.09
5I76.PDB	O, A_TYR_192	N, A_PHE_209	H, A_PHE_209	2.90	2.13	22.49
5I76.PDB	O, A_LYS_190	N, A_ARG_211	H, A_ARG_211	2.76	1.93	12.12
5I76.PDB	O, A_HIS_189	NE, A_ARG_211	HE, A_ARG_211	2.68	1.86	13.91
5I76.PDB	O, B_SER_25	N, B_GLN_3	H, B_GLN_3	2.91	2.09	13.09
5I76.PDB	O, B_THR_23	N, B_LYS_5	H, B_LYS_5	2.90	2.14	23.54
5I76.PDB	OE1, B_GLN_111	N, B_GLN_6	H, B_GLN_6	2.83	2.01	14.84
5I76.PDB	O, B_TYR_93	NE2, B_GLN_6	HE22, B_GLN_6	2.84	1.99	7.48
5I76.PDB	O, B_THR_21	N, B_SER_7	H, B_SER_7	2.98	2.22	22.91
5I76.PDB	O, B_THR_116	N, B_VAL_12	H, B_VAL_12	2.86	2.03	11.02
5I76.PDB	O, B_LEU_85	N, B_SER_15	H, B_SER_15	2.72	1.87	6.27
5I76.PDB	O, B_PRO_14	OG, B_SER_15	HG, B_SER_15	2.58	1.82	21.55
5I76.PDB	O, B_GLN_13	N, B_GLN_16	H, B_GLN_16	2.98	2.13	9.97

5I76.PDB	O, B_MET_82	N, B_LEU_18	H, B_LEU_18	2.89	2.08	17.80
5I76.PDB	O, B_PHE_80	N, B_ILE_20	H, B_ILE_20	2.83	2.01	14.78
5I76.PDB	OG, B_SER_7	N, B_THR_21	H, B_THR_21	2.99	2.15	11.92
5I76.PDB	O, B_VAL_78	N, B_CYS_22	H, B_CYS_22	2.85	2.00	8.90
5I76.PDB	O, B_LYS_5	N, B_THR_23	H, B_THR_23	2.85	2.00	7.48
5I76.PDB	O, B_SER_76	N, B_VAL_24	H, B_VAL_24	2.97	2.13	10.77
5I76.PDB	O, B_GLN_3	N, B_SER_25	H, B_SER_25	2.89	2.10	18.84
5I76.PDB	O, B_SER_28	N, B_ASN_31	H, B_ASN_31	2.98	2.14	8.72
5I76.PDB	O, B_ILE_51	N, B_VAL_34	H, B_VAL_34	2.93	2.14	19.88
5I76.PDB	O, B_ALA_96	N, B_HIS_35	H, B_HIS_35	2.88	2.03	7.93
5I76.PDB	O, B_GLY_49	N, B_TRP_36	H, B_TRP_36	2.91	2.12	19.85
5I76.PDB	O, B_TYR_94	N, B_VAL_37	H, B_VAL_37	2.91	2.08	14.52
5I76.PDB	O, B_GLU_46	N, B_ARG_38	H, B_ARG_38	2.84	2.03	16.24
5I76.PDB	OD1, B_ASP_89	NH1, B_ARG_38	HH12, B_ARG_38	2.81	1.96	5.27
5I76.PDB	O, B_ILE_92	N, B_GLN_39	H, B_GLN_39	2.86	2.11	24.85
5I76.PDB	OE1, A_GLN_38	NE2, B_GLN_39	HE22, B_GLN_39	2.80	1.95	6.66
5I76.PDB	O, B_ARG_38	N, B_GLU_46	H, B_GLU_46	2.80	2.03	22.07
5I76.PDB	O, B_TRP_36	N, B_LEU_48	H, B_LEU_48	2.83	1.97	5.22
5I76.PDB	O, B_ASP_58	N, B_VAL_50	H, B_VAL_50	2.90	2.16	26.66
5I76.PDB	O, B_VAL_34	N, B_ILE_51	H, B_ILE_51	2.98	2.17	16.74
5I76.PDB	O, B_ASN_56	N, B_TRP_52	H, B_TRP_52	2.85	1.99	5.55
5I76.PDB	OD2, B_ASP_58	NE1, B_TRP_52	HE1, B_TRP_52	2.79	1.94	5.91
5I76.PDB	O, B_TRP_52	N, B_GLY_55	H, B_GLY_55	2.86	2.04	14.33
5I76.PDB	O, B_LEU_48	N, B_ASN_60	H, B_ASN_60	2.81	1.96	6.22
5I76.PDB	O, B_TRP_47	ND2, B_ASN_60	HD22, B_ASN_60	2.78	1.99	18.30
5I76.PDB	O, B_ASN_60	N, B_PHE_63	H, B_PHE_63	2.84	1.99	7.17
5I76.PDB	OD2, B_ASP_89	NH1, B_ARG_66	HH12, B_ARG_66	2.96	2.17	19.36
5I76.PDB	OD1, B_ASP_89	NH2, B_ARG_66	HH22, B_ARG_66	2.84	1.99	7.50
5I76.PDB	O, B_LYS_81	N, B_SER_68	H, B_SER_68	2.86	2.02	9.98
5I76.PDB	OH, B_TYR_59	N, B_ILE_69	H, B_ILE_69	3.00	2.17	14.31
5I76.PDB	O, B_SER_53	NZ, B_LYS_71	HZ1, B_LYS_71	2.77	1.91	12.10
5I76.PDB	O, B_GLN_77	N, B_ASP_72	H, B_ASP_72	2.80	1.95	9.05
5I76.PDB	OD1, B_ASP_72	OG, B_SER_74	HG, B_SER_74	2.49	1.80	29.35
5I76.PDB	O, B_CYS_22	N, B_VAL_78	H, B_VAL_78	2.83	1.99	12.58
5I76.PDB	O, B_ASN_70	N, B_PHE_79	H, B_PHE_79	2.80	1.94	1.15
5I76.PDB	O, B_ILE_20	N, B_PHE_80	H, B_PHE_80	2.88	2.02	3.13
5I76.PDB	O, B_SER_68	N, B_LYS_81	H, B_LYS_81	2.91	2.14	22.98
5I76.PDB	O, B_LEU_18	N, B_MET_82	H, B_MET_82	2.97	2.19	21.42
5I76.PDB	O, B_ARG_66	N, B_ASN_83	H, B_ASN_83	2.85	2.05	18.95
5I76.PDB	OD2, B_ASP_89	N, B_GLN_86	H, B_GLN_86	2.84	2.01	11.92
5I76.PDB	O, B_GLN_86	N, B_ASP_89	H, B_ASP_89	2.79	1.94	8.58
5I76.PDB	O, B_SER_87	N, B_THR_90	H, B_THR_90	2.93	2.07	2.10
5I76.PDB	O, B_GLN_39	N, B_ILE_92	H, B_ILE_92	2.94	2.12	13.61
5I76.PDB	O, B_THR_113	N, B_TYR_93	H, B_TYR_93	2.91	2.07	10.02
5I76.PDB	O, B_ASP_89	OH, B_TYR_93	HH, B_TYR_93	2.75	1.94	12.69
5I76.PDB	O, B_VAL_37	N, B_TYR_94	H, B_TYR_94	2.72	1.88	9.49
5I76.PDB	O, B_TYR_108	N, B_ARG_97	H, B_ARG_97	2.86	2.06	17.77
5I76.PDB	O, B_ALA_98	NH1, B_ARG_97	HH11, B_ARG_97	2.98	2.16	15.13
5I76.PDB	OD1, B_ASP_103	N, B_TYR_104	H, B_TYR_104	2.65	1.89	23.73
5I76.PDB	O, B_PHE_106	NE1, B_TRP_109	HE1, B_TRP_109	2.83	2.11	27.98
5I76.PDB	O, B_CYS_95	N, B_GLY_110	H, B_GLY_110	2.95	2.10	8.84
5I76.PDB	O, B_GLN_6	NE2, B_GLN_111	HE22, B_GLN_111	2.97	2.18	20.05
5I76.PDB	O, B_TYR_93	N, B_THR_113	H, B_THR_113	2.81	2.08	26.53
5I76.PDB	O, B_ALA_91	N, B_VAL_115	H, B_VAL_115	2.97	2.13	9.34
5I76.PDB	OG1, B_THR_90	N, B_VAL_117	H, B_VAL_117	2.78	1.93	4.58
5I76.PDB	O, B_PHE_152	N, B_LYS_123	H, B_LYS_123	2.83	1.99	11.39
5I76.PDB	O, B_ASP_150	NZ, B_LYS_123	HZ2, B_LYS_123	2.87	2.07	21.60
5I76.PDB	O, B_LYS_149	N, B_SER_126	H, B_SER_126	2.91	2.10	15.91

5I76.PDB	O, B_LEU_147	N, B_PHE_128	H, B_PHE_128	2.88	2.05	13.67
5I76.PDB	O, B_GLY_145	N, B_LEU_130	H, B_LEU_130	2.86	2.03	13.19
5I76.PDB	O, B_SER_134	OG1, B_THR_137	HG1, B_THR_137	2.81	2.01	14.63
5I76.PDB	O, B_VAL_190	N, B_ALA_142	H, B_ALA_142	2.82	1.97	8.01
5I76.PDB	O, B_LEU_130	N, B_GLY_145	H, B_GLY_145	2.93	2.14	20.40
5I76.PDB	O, B_SER_186	N, B_CYS_146	H, B_CYS_146	2.85	2.05	18.23
5I76.PDB	O, B_PHE_128	N, B_LEU_147	H, B_LEU_147	2.85	2.03	14.76
5I76.PDB	O, B_LEU_184	N, B_VAL_148	H, B_VAL_148	2.78	1.93	4.33
5I76.PDB	O, B_SER_126	N, B_LYS_149	H, B_LYS_149	2.80	1.95	7.51
5I76.PDB	O, B_LYS_123	N, B_PHE_152	H, B_PHE_152	2.84	2.02	15.64
5I76.PDB	O, B_ASN_205	N, B_THR_157	H, B_THR_157	2.93	2.11	15.41
5I76.PDB	O, B_ASN_203	N, B_SER_159	H, B_SER_159	2.90	2.10	17.76
5I76.PDB	OD1, B_ASN_203	OG, B_SER_159	HG, B_SER_159	2.82	2.04	17.93
5I76.PDB	OG, B_SER_186	NE1, B_TRP_160	HE1, B_TRP_160	2.99	2.15	11.06
5I76.PDB	O, B_ILE_201	N, B_ASN_161	H, B_ASN_161	2.78	1.93	9.08
5I76.PDB	OD1, B_ASN_203	N, B_SER_162	H, B_SER_162	2.79	2.01	21.54
5I76.PDB	O, B_TRP_160	N, B_GLY_163	H, B_GLY_163	2.88	2.13	24.26
5I76.PDB	O, B_ASN_161	N, B_ALA_164	H, B_ALA_164	2.99	2.14	8.06
5I76.PDB	O, B_VAL_187	N, B_HIS_170	H, B_HIS_170	2.79	1.96	12.00
5I76.PDB	O, B_SER_185	N, B_PHE_172	H, B_PHE_172	2.91	2.06	5.99
5I76.PDB	O, B_SER_183	N, B_VAL_175	H, B_VAL_175	2.87	2.03	11.83
5I76.PDB	O, B_LEU_181	N, B_GLN_177	H, B_GLN_177	2.84	2.00	8.84
5I76.PDB	OD1, B_ASP_150	NE2, B_GLN_177	HE22, B_GLN_177	2.79	2.00	19.18
5I76.PDB	O, B_GLN_177	N, B_GLY_180	H, B_GLY_180	2.82	1.98	9.91
5I76.PDB	O, B_TYR_151	N, B_TYR_182	H, B_TYR_182	2.72	1.88	9.69
5I76.PDB	O, B_VAL_148	N, B_LEU_184	H, B_LEU_184	2.84	2.03	15.91
5I76.PDB	OG, A_SER_176	OG, B_SER_185	HG, B_SER_185	2.89	2.15	23.05
5I76.PDB	O, B_CYS_146	N, B_SER_186	H, B_SER_186	2.93	2.10	13.63
5I76.PDB	O, B_HIS_170	N, B_VAL_187	H, B_VAL_187	2.94	2.11	13.31
5I76.PDB	O, B_LEU_144	N, B_VAL_188	H, B_VAL_188	2.83	2.02	16.59
5I76.PDB	O, B_ALA_142	N, B_VAL_190	H, B_VAL_190	2.85	2.05	17.07
5I76.PDB	O, B_GLY_140	N, B_SER_192	H, B_SER_192	2.92	2.09	13.75
5I76.PDB	O, B_PRO_191	OG, B_SER_194	HG, B_SER_194	2.91	2.11	15.99
5I76.PDB	O, B_SER_194	N, B_GLN_198	H, B_GLN_198	2.93	2.07	2.43
5I76.PDB	OG, B_SER_194	OH, B_TYR_200	HH, B_TYR_200	2.81	2.03	18.26
5I76.PDB	OD1, B_ASN_161	N, B_ILE_201	H, B_ILE_201	2.82	2.02	18.20
5I76.PDB	O, B_LYS_215	N, B_CYS_202	H, B_CYS_202	2.96	2.17	19.90
5I76.PDB	O, B_SER_159	N, B_ASN_203	H, B_ASN_203	2.80	1.94	5.79
5I76.PDB	OD1, B_ASP_214	ND2, B_ASN_203	HD22, B_ASN_203	2.90	2.11	19.71
5I76.PDB	O, B_VAL_213	N, B_VAL_204	H, B_VAL_204	2.78	1.92	4.35
5I76.PDB	O, B_THR_157	N, B_ASN_205	H, B_ASN_205	2.91	2.08	13.35
5I76.PDB	O, B_THR_211	N, B_HIS_206	H, B_HIS_206	2.85	2.00	6.66
5I76.PDB	O, B_LYS_207	N, B_ASN_210	H, B_ASN_210	2.96	2.11	7.92
5I76.PDB	O, B_VAL_204	N, B_VAL_213	H, B_VAL_213	2.87	2.05	15.17
5I76.PDB	O, B_CYS_202	N, B_LYS_215	H, B_LYS_215	2.91	2.13	20.69
5I76.PDB	OE1, A_GLU_123	NZ, B_LYS_215	HZ1, B_LYS_215	2.73	1.96	24.68
5I76.PDB	OE2, A_GLU_123	NZ, B_LYS_215	HZ1, B_LYS_215	2.89	2.11	24.69
5I76.PDB	OE1, B_GLU_218	NE, B_ARG_216	HE, B_ARG_216	2.64	1.90	25.25
5I76.PDB	OE1, B_GLU_218	NH2, B_ARG_216	HH21, B_ARG_216	2.69	1.98	29.12
5I76.PDB	O, B_TYR_200	N, B_VAL_217	H, B_VAL_217	2.83	1.99	10.82
5I76.PDB	O, C_ARG_24	N, C_THR_5	H, C_THR_5	2.87	2.03	8.25
5I76.PDB	O, C_TYR_86	NE2, C_GLN_6	HE22, C_GLN_6	2.86	2.05	16.89
5I76.PDB	O, C_LYS_103	N, C_LEU_11	H, C_LEU_11	2.75	1.91	12.00
5I76.PDB	O, C_GLU_105	N, C_VAL_13	H, C_VAL_13	2.98	2.20	22.09
5I76.PDB	OE1, C_GLU_17	N, C_SER_14	H, C_SER_14	3.00	2.15	7.87
5I76.PDB	O, C_VAL_78	N, C_GLY_16	H, C_GLY_16	2.98	2.12	1.61
5I76.PDB	O, C_ILE_75	N, C_VAL_19	H, C_VAL_19	2.86	2.02	11.04
5I76.PDB	O, C_LEU_73	N, C_PHE_21	H, C_PHE_21	2.77	1.93	10.26

5I76.PDB	O, C_PHE_71	N, C_CYS_23	H, C_CYS_23	2.95	2.11	10.08
5I76.PDB	O, C_THR_5	N, C_ARG_24	H, C_ARG_24	2.99	2.18	17.88
5I76.PDB	OD2, A_ASP_70	NH1, C_ARG_24	HH12, C_ARG_24	2.95	2.23	28.81
5I76.PDB	O, C_THR_69	N, C_ALA_25	H, C_ALA_25	2.74	1.96	20.09
5I76.PDB	O, C_GLY_68	N, C_ILE_29	H, C_ILE_29	2.91	2.08	12.56
5I76.PDB	O, C_ILE_29	N, C_ASN_32	H, C_ASN_32	2.96	2.11	6.37
5I76.PDB	O, C_THR_31	N, C_ILE_33	H, C_ILE_33	2.97	2.26	29.60
5I76.PDB	O, C_GLN_89	N, C_HIS_34	H, C_HIS_34	2.87	2.06	16.27
5I76.PDB	O, C_ILE_48	N, C_TRP_35	H, C_TRP_35	2.95	2.13	14.67
5I76.PDB	O, C_TYR_87	N, C_TYR_36	H, C_TYR_36	2.85	2.04	16.51
5I76.PDB	OE1, C_GLN_89	OH, C_TYR_36	HH, C_TYR_36	2.73	1.90	7.00
5I76.PDB	O, C_ARG_45	N, C_GLN_37	H, C_GLN_37	2.82	2.01	17.23
5I76.PDB	OH, C_TYR_86	NE2, C_GLN_37	HE21, C_GLN_37	2.93	2.09	9.49
5I76.PDB	O, C_ASP_85	N, C_GLN_38	H, C_GLN_38	2.82	1.99	13.89
5I76.PDB	O, C_GLY_42	NE2, C_GLN_38	HE21, C_GLN_38	3.00	2.24	24.26
5I76.PDB	O, C_ARG_39	N, C_GLY_42	H, C_GLY_42	2.88	2.09	19.43
5I76.PDB	O, D_GLY_110	OG, C_SER_43	HG, C_SER_43	2.84	2.15	29.22
5I76.PDB	O, C_GLN_37	N, C_ARG_45	H, C_ARG_45	2.65	1.95	29.24
5I76.PDB	OE1, C_GLN_37	NH1, C_ARG_45	HH11, C_ARG_45	2.96	2.15	17.42
5I76.PDB	O, C_TRP_35	N, C_LEU_47	H, C_LEU_47	2.79	1.93	2.36
5I76.PDB	O, C_GLU_53	N, C_LYS_49	H, C_LYS_49	2.99	2.18	15.56
5I76.PDB	OE1, C_GLU_53	NZ, C_LYS_49	HZ2, C_LYS_49	2.64	1.79	13.55
5I76.PDB	OD2, D_ASP_103	OH, C_TYR_50	HH, C_TYR_50	2.76	1.95	12.40
5I76.PDB	O, C_ILE_33	N, C_ALA_51	H, C_ALA_51	2.70	1.88	13.82
5I76.PDB	O, C_TYR_50	N, C_SER_52	H, C_SER_52	2.78	2.06	27.37
5I76.PDB	O, C_LYS_49	N, C_GLU_53	H, C_GLU_53	2.82	2.02	19.04
5I76.PDB	OD1, C_ASP_82	NH2, C_ARG_61	HH21, C_ARG_61	2.76	1.93	11.41
5I76.PDB	OE2, C_GLU_81	NH2, C_ARG_61	HH22, C_ARG_61	2.83	2.01	16.02
5I76.PDB	O, C_SER_74	N, C_SER_63	H, C_SER_63	2.93	2.13	17.96
5I76.PDB	O, C_THR_72	N, C_SER_65	H, C_SER_65	2.91	2.11	19.14
5I76.PDB	O, C_GLY_30	N, C_GLY_68	H, C_GLY_68	2.72	1.97	23.76
5I76.PDB	O, C_CYS_23	N, C_PHE_71	H, C_PHE_71	2.89	2.16	27.04
5I76.PDB	O, C_SER_65	N, C_THR_72	H, C_THR_72	2.94	2.10	11.42
5I76.PDB	O, C_PHE_21	N, C_LEU_73	H, C_LEU_73	2.99	2.22	23.12
5I76.PDB	O, C_SER_63	N, C_SER_74	H, C_SER_74	2.84	1.98	5.34
5I76.PDB	O, C_VAL_19	N, C_ILE_75	H, C_ILE_75	2.92	2.11	17.51
5I76.PDB	O, C_ARG_61	N, C_ASN_76	H, C_ASN_76	2.86	2.03	12.61
5I76.PDB	O, C_GLU_17	N, C_VAL_78	H, C_VAL_78	2.96	2.15	17.03
5I76.PDB	OD2, C_ASP_82	N, C_GLU_79	H, C_GLU_79	2.90	2.06	11.12
5I76.PDB	OG, C_SER_171	OG, C_SER_80	HG, C_SER_80	2.59	1.79	14.57
5I76.PDB	O, C_GLU_79	N, C_ASP_82	H, C_ASP_82	2.91	2.09	15.61
5I76.PDB	O, C_GLN_38	N, C_ASP_85	H, C_ASP_85	2.95	2.16	19.54
5I76.PDB	O, C_THR_102	N, C_TYR_86	H, C_TYR_86	2.85	2.08	22.66
5I76.PDB	O, C_ASP_82	OH, C_TYR_86	HH, C_TYR_86	2.60	1.79	11.86
5I76.PDB	O, C_TYR_36	N, C_TYR_87	H, C_TYR_87	2.91	2.10	16.52
5I76.PDB	OG1, C_THR_96	NE2, C_GLN_89	HE21, C_GLN_89	2.74	1.92	15.47
5I76.PDB	O, C_THR_97	N, C_GLN_90	H, C_GLN_90	2.85	2.07	20.66
5I76.PDB	O, C_ASN_93	NE2, C_GLN_90	HE22, C_GLN_90	2.93	2.08	7.37
5I76.PDB	OD1, C_ASN_93	ND2, C_ASN_92	HD22, C_ASN_92	2.84	2.03	16.29
5I76.PDB	O, C_GLN_90	OG1, C_THR_96	HG1, C_THR_96	2.71	1.98	25.42
5I76.PDB	O, C_ILE_2	OG1, C_THR_97	HG1, C_THR_97	2.79	1.98	12.72
5I76.PDB	O, C_CYS_88	N, C_GLY_99	H, C_GLY_99	2.86	2.07	19.65
5I76.PDB	O, C_TYR_86	N, C_THR_102	H, C_THR_102	2.98	2.17	16.60
5I76.PDB	O, C_PRO_8	OG1, C_THR_102	HG1, C_THR_102	2.70	1.91	16.81
5I76.PDB	O, C_VAL_9	N, C_LYS_103	H, C_LYS_103	2.92	2.08	9.07
5I76.PDB	O, C_ALA_84	N, C_LEU_104	H, C_LEU_104	3.00	2.14	2.26
5I76.PDB	O, C_LEU_11	N, C_GLU_105	H, C_GLU_105	2.83	1.99	8.86
5I76.PDB	O, C_VAL_13	N, C_LYS_107	H, C_LYS_107	2.70	1.85	8.61

5I76.PDB	O, C_THR_109	NE, C_ARG_108	HE, C_ARG_108	2.76	1.94	14.16
5I76.PDB	O, C_ASP_170	NH1, C_ARG_108	HH11, C_ARG_108	2.86	2.03	13.35
5I76.PDB	O, C_TYR_140	N, C_ALA_111	H, C_ALA_111	2.87	2.03	11.62
5I76.PDB	O, C_LEU_135	N, C_PHE_116	H, C_PHE_116	2.94	2.17	22.55
5I76.PDB	O, C_VAL_133	N, C_PHE_118	H, C_PHE_118	2.80	1.99	16.08
5I76.PDB	OG, C_SER_131	NE2, C_GLN_124	HE22, C_GLN_124	2.87	2.02	5.94
5I76.PDB	O, C_ASP_122	N, C_LYS_126	H, C_LYS_126	2.96	2.16	17.90
5I76.PDB	O, C_GLN_124	N, C_SER_127	H, C_SER_127	2.86	2.07	20.07
5I76.PDB	O, C_GLN_124	OG, C_SER_127	HG, C_SER_127	2.65	1.87	17.60
5I76.PDB	O, C_LEU_125	N, C_GLY_128	H, C_GLY_128	2.88	2.03	8.22
5I76.PDB	O, C_LEU_181	N, C_ALA_130	H, C_ALA_130	2.83	2.02	16.04
5I76.PDB	OE1, C_GLN_124	N, C_SER_131	H, C_SER_131	2.91	2.10	16.13
5I76.PDB	OG1, C_THR_180	OG, C_SER_131	HG, C_SER_131	2.93	2.13	14.64
5I76.PDB	O, C_LEU_179	N, C_VAL_132	H, C_VAL_132	2.79	1.93	4.92
5I76.PDB	O, C_SER_177	N, C_CYS_134	H, C_CYS_134	2.78	1.93	7.78
5I76.PDB	O, C_PHE_116	N, C_LEU_135	H, C_LEU_135	2.83	1.98	7.23
5I76.PDB	O, C_LEU_175	N, C_LEU_136	H, C_LEU_136	2.87	2.03	8.14
5I76.PDB	O, C_SER_114	N, C_ASN_137	H, C_ASN_137	2.83	1.99	9.65
5I76.PDB	O, C_TYR_173	N, C_PHE_139	H, C_PHE_139	2.81	1.98	14.22
5I76.PDB	O, C_ALA_111	N, C_TYR_140	H, C_TYR_140	2.97	2.16	16.55
5I76.PDB	OE1, C_GLU_105	OH, C_TYR_140	HH, C_TYR_140	2.89	2.14	22.51
5I76.PDB	O, C_THR_197	N, C_LYS_145	H, C_LYS_145	2.98	2.14	9.58
5I76.PDB	O, C_GLU_195	N, C_GLN_147	H, C_GLN_147	2.87	2.05	14.85
5I76.PDB	O, A_SER_202	NE2, C_GLN_147	HE22, C_GLN_147	2.78	1.96	13.33
5I76.PDB	OG, C_SER_177	NE1, C_TRP_148	HE1, C_TRP_148	2.90	2.11	19.54
5I76.PDB	O, C_ALA_193	N, C_LYS_149	H, C_LYS_149	2.90	2.07	12.57
5I76.PDB	O, C_ALA_153	N, C_VAL_150	H, C_VAL_150	2.94	2.13	15.93
5I76.PDB	O, C_VAL_191	N, C_ASP_151	H, C_ASP_151	2.91	2.07	12.19
5I76.PDB	O, C_VAL_150	N, C_ALA_153	H, C_ALA_153	2.82	1.97	8.28
5I76.PDB	O, C_TRP_148	N, C_GLN_155	H, C_GLN_155	2.85	2.01	11.31
5I76.PDB	O, C_ALA_153	NE2, C_GLN_155	HE21, C_GLN_155	2.94	2.09	9.82
5I76.PDB	OE1, C_GLN_155	ND2, C_ASN_158	HD22, C_ASN_158	2.96	2.21	25.95
5I76.PDB	O, C_THR_178	N, C_GLN_160	H, C_GLN_160	2.96	2.16	17.81
5I76.PDB	O, C_SER_176	N, C_SER_162	H, C_SER_162	2.87	2.08	18.90
5I76.PDB	O, C_SER_174	N, C_THR_164	H, C_THR_164	2.96	2.12	9.89
5I76.PDB	O, C_SER_171	NE2, C_GLN_166	HE21, C_GLN_166	2.93	2.09	11.05
5I76.PDB	O, C_LEU_106	NE2, C_GLN_166	HE22, C_GLN_166	2.76	1.97	19.15
5I76.PDB	O, C_THR_172	N, C_ASP_167	H, C_ASP_167	2.84	2.05	19.17
5I76.PDB	OD2, C_ASP_167	N, C_LYS_169	H, C_LYS_169	2.81	2.03	20.18
5I76.PDB	OD2, C_ASP_167	N, C_ASP_170	H, C_ASP_170	2.96	2.19	22.65
5I76.PDB	O, C_ASP_167	N, C_SER_171	H, C_SER_171	2.79	2.03	23.14
5I76.PDB	OD1, C_ASP_170	N, C_THR_172	H, C_THR_172	2.98	2.17	15.09
5I76.PDB	OD1, C_ASP_170	OG1, C_THR_172	HG1, C_THR_172	2.79	1.97	11.52
5I76.PDB	O, C_PHE_139	N, C_TYR_173	H, C_TYR_173	2.84	1.99	6.46
5I76.PDB	OE2, C_GLU_105	OH, C_TYR_173	HH, C_TYR_173	2.72	1.89	6.26
5I76.PDB	O, C_LEU_136	N, C_LEU_175	H, C_LEU_175	2.89	2.11	21.04
5I76.PDB	O, C_SER_162	N, C_SER_176	H, C_SER_176	2.87	2.04	12.82
5I76.PDB	O, C_CYS_134	N, C_SER_177	H, C_SER_177	2.86	2.04	15.37
5I76.PDB	O, C_GLN_160	N, C_THR_178	H, C_THR_178	2.89	2.09	17.26
5I76.PDB	O, C_VAL_132	N, C_LEU_179	H, C_LEU_179	2.86	2.02	11.05
5I76.PDB	O, C_ALA_130	N, C_LEU_181	H, C_LEU_181	2.86	2.03	12.11
5I76.PDB	O, C_SER_182	N, C_TYR_186	H, C_TYR_186	2.80	1.95	6.73
5I76.PDB	O, C_LYS_183	N, C_GLU_187	H, C_GLU_187	2.92	2.12	19.05
5I76.PDB	O, C_ASP_185	N, C_LYS_188	H, C_LYS_188	2.99	2.16	13.62
5I76.PDB	OD2, C_ASP_151	ND1, C_HIS_189	HD1, C_HIS_189	2.35	1.61	24.33
5I76.PDB	OD1, C_ASP_151	N, C_VAL_191	H, C_VAL_191	2.92	2.09	11.65
5I76.PDB	O, C_PHE_209	N, C_TYR_192	H, C_TYR_192	2.96	2.11	8.01
5I76.PDB	O, C_LYS_149	N, C_ALA_193	H, C_ALA_193	2.98	2.25	27.79

5I76.PDB	O, C_LYS_207	N, C_CYS_194	H, C_CYS_194	2.84	1.98	5.34
5I76.PDB	O, C_GLN_147	N, C_GLU_195	H, C_GLU_195	2.83	1.99	10.59
5I76.PDB	O, C_VAL_205	N, C_VAL_196	H, C_VAL_196	2.75	1.95	18.04
5I76.PDB	O, C_LYS_145	N, C_THR_197	H, C_THR_197	2.93	2.12	16.49
5I76.PDB	ND1, C_HIS_198	N, C_GLY_200	H, C_GLY_200	2.94	2.08	6.54
5I76.PDB	O, C_HIS_198	N, C_LEU_201	H, C_LEU_201	2.84	1.98	6.14
5I76.PDB	O, C_VAL_196	N, C_VAL_205	H, C_VAL_205	2.92	2.11	16.84
5I76.PDB	O, C_CYS_194	N, C_LYS_207	H, C_LYS_207	2.90	2.08	15.23
5I76.PDB	O, C_TYR_192	N, C_PHE_209	H, C_PHE_209	2.92	2.14	20.73
5I76.PDB	O, C_LYS_190	N, C_ARG_211	H, C_ARG_211	2.72	1.88	9.66
5I76.PDB	O, C_HIS_189	NE, C_ARG_211	HE, C_ARG_211	2.72	1.86	2.35
5I76.PDB	O, D_SER_25	N, D_GLN_3	H, D_GLN_3	2.94	2.11	12.93
5I76.PDB	O, D_THR_23	N, D_LYS_5	H, D_LYS_5	2.88	2.10	20.15
5I76.PDB	OE1, D_GLN_111	N, D_GLN_6	H, D_GLN_6	2.88	2.06	13.61
5I76.PDB	O, D_TYR_93	NE2, D_GLN_6	HE22, D_GLN_6	2.83	1.97	5.03
5I76.PDB	O, D_THR_21	N, D_SER_7	H, D_SER_7	2.93	2.18	24.73
5I76.PDB	O, D_THR_116	N, D_VAL_12	H, D_VAL_12	2.82	1.99	13.27
5I76.PDB	O, D_LEU_85	N, D_SER_15	H, D_SER_15	2.74	1.90	9.28
5I76.PDB	O, D_GLN_13	N, D_GLN_16	H, D_GLN_16	2.92	2.10	15.02
5I76.PDB	O, D_MET_82	N, D_LEU_18	H, D_LEU_18	2.87	2.04	11.26
5I76.PDB	O, D_PHE_80	N, D_ILE_20	H, D_ILE_20	2.93	2.12	15.50
5I76.PDB	O, D_VAL_78	N, D_CYS_22	H, D_CYS_22	2.82	1.97	8.74
5I76.PDB	O, D_LYS_5	N, D_THR_23	H, D_THR_23	2.84	2.00	7.60
5I76.PDB	O, D_SER_76	N, D_VAL_24	H, D_VAL_24	2.91	2.08	12.63
5I76.PDB	O, D_GLN_3	N, D_SER_25	H, D_SER_25	2.93	2.11	15.90
5I76.PDB	OG, D_SER_28	OG1, D_THR_30	HG1, D_THR_30	2.71	1.88	5.11
5I76.PDB	O, D_SER_28	N, D_ASN_31	H, D_ASN_31	2.99	2.14	9.76
5I76.PDB	O, D_ILE_51	N, D_VAL_34	H, D_VAL_34	2.92	2.14	20.26
5I76.PDB	O, D_ALA_96	N, D_HIS_35	H, D_HIS_35	2.85	2.01	8.24
5I76.PDB	O, D_GLY_49	N, D_TRP_36	H, D_TRP_36	2.85	2.04	16.83
5I76.PDB	O, D_TYR_94	N, D_VAL_37	H, D_VAL_37	2.97	2.15	14.15
5I76.PDB	O, D_GLU_46	N, D_ARG_38	H, D_ARG_38	2.89	2.08	16.88
5I76.PDB	OD1, D_ASP_89	NH1, D_ARG_38	HH12, D_ARG_38	2.88	2.03	7.89
5I76.PDB	O, D_ILE_92	N, D_GLN_39	H, D_GLN_39	2.87	2.14	26.90
5I76.PDB	OE1, C_GLN_38	NE2, D_GLN_39	HE22, D_GLN_39	2.85	2.01	10.98
5I76.PDB	O, D_ARG_38	N, D_GLU_46	H, D_GLU_46	2.89	2.10	19.77
5I76.PDB	O, D_TRP_36	N, D_LEU_48	H, D_LEU_48	2.71	1.86	7.08
5I76.PDB	O, D_ASP_58	N, D_VAL_50	H, D_VAL_50	2.87	2.11	23.52
5I76.PDB	O, D_VAL_34	N, D_ILE_51	H, D_ILE_51	3.00	2.19	16.46
5I76.PDB	O, D_ASN_56	N, D_TRP_52	H, D_TRP_52	2.87	2.02	5.92
5I76.PDB	OD2, D_ASP_58	NE1, D_TRP_52	HE1, D_TRP_52	2.82	1.96	3.64
5I76.PDB	O, D_TRP_52	N, D_GLY_55	H, D_GLY_55	2.86	2.03	12.93
5I76.PDB	O, D_VAL_50	N, D_ASP_58	H, D_ASP_58	2.98	2.17	16.49
5I76.PDB	O, D_LEU_48	N, D_ASN_60	H, D_ASN_60	2.77	1.91	2.03
5I76.PDB	O, D_TRP_47	ND2, D_ASN_60	HD22, D_ASN_60	2.84	2.02	13.85
5I76.PDB	O, D_ASN_60	N, D_PHE_63	H, D_PHE_63	2.84	1.99	9.46
5I76.PDB	OD2, D_ASP_89	NH1, D_ARG_66	HH12, D_ARG_66	2.85	2.02	11.59
5I76.PDB	OD1, D_ASP_89	NH2, D_ARG_66	HH22, D_ARG_66	2.74	1.89	8.51
5I76.PDB	O, D_LYS_81	N, D_SER_68	H, D_SER_68	2.88	2.06	12.89
5I76.PDB	OH, D_TYR_59	N, D_ILE_69	H, D_ILE_69	2.95	2.13	14.70
5I76.PDB	O, D_PHE_79	N, D_ASN_70	H, D_ASN_70	2.95	2.13	15.10
5I76.PDB	O, D_SER_53	NZ, D_LYS_71	HZ1, D_LYS_71	2.72	1.85	9.25
5I76.PDB	O, D_GLN_77	N, D_ASP_72	H, D_ASP_72	2.82	1.99	12.40
5I76.PDB	OD1, D_ASP_72	OG, D_SER_74	HG, D_SER_74	2.71	2.00	26.33
5I76.PDB	O, D_CYS_22	N, D_VAL_78	H, D_VAL_78	2.81	1.98	14.10
5I76.PDB	O, D_ASN_70	N, D_PHE_79	H, D_PHE_79	2.80	1.95	6.90
5I76.PDB	O, D_ILE_20	N, D_PHE_80	H, D_PHE_80	2.86	2.01	4.93
5I76.PDB	O, D_SER_68	N, D_LYS_81	H, D_LYS_81	2.90	2.09	17.14

5I76.PDB	O, D_LEU_18	N, D_MET_82	H, D_MET_82	2.95	2.17	20.62
5I76.PDB	O, D_ARG_66	N, D_ASN_83	H, D_ASN_83	2.77	1.99	20.75
5I76.PDB	OD2, D_ASP_89	N, D_GLN_86	H, D_GLN_86	2.92	2.09	12.09
5I76.PDB	O, D_GLN_86	N, D_ASP_89	H, D_ASP_89	2.77	1.93	7.75
5I76.PDB	O, D_SER_87	N, D_THR_90	H, D_THR_90	3.00	2.14	2.55
5I76.PDB	O, D_GLN_39	N, D_ILE_92	H, D_ILE_92	2.92	2.12	17.89
5I76.PDB	O, D_THR_113	N, D_TYR_93	H, D_TYR_93	2.90	2.07	10.93
5I76.PDB	O, D_ASP_89	OH, D_TYR_93	HH, D_TYR_93	2.67	1.84	7.84
5I76.PDB	O, D_VAL_37	N, D_TYR_94	H, D_TYR_94	2.74	1.91	13.14
5I76.PDB	O, D_TYR_108	N, D_ARG_97	H, D_ARG_97	2.84	2.04	16.66
5I76.PDB	O, D_GLU_105	N, D_LEU_99	H, D_LEU_99	2.74	1.99	24.80
5I76.PDB	OD1, D_ASP_103	N, D_TYR_104	H, D_TYR_104	2.78	2.02	23.34
5I76.PDB	OH, C_TYR_36	N, D_PHE_106	H, D_PHE_106	2.93	2.09	12.40
5I76.PDB	O, D_PHE_106	NE1, D_TRP_109	HE1, D_TRP_109	2.87	2.14	26.78
5I76.PDB	O, D_CYS_95	N, D_GLY_110	H, D_GLY_110	2.79	1.94	6.99
5I76.PDB	O, D_GLN_6	NE2, D_GLN_111	HE22, D_GLN_111	2.93	2.16	22.33
5I76.PDB	O, D_TYR_93	N, D_THR_113	H, D_THR_113	2.81	2.09	27.66
5I76.PDB	O, D_SER_7	OG1, D_THR_113	HG1, D_THR_113	2.96	2.26	28.05
5I76.PDB	O, D_ALA_91	N, D_VAL_115	H, D_VAL_115	2.92	2.06	1.61
5I76.PDB	OG1, D_THR_90	N, D_VAL_117	H, D_VAL_117	2.98	2.15	13.35
5I76.PDB	O, D_PHE_152	N, D_LYS_123	H, D_LYS_123	2.78	1.94	11.09
5I76.PDB	O, D_ASP_150	NZ, D_LYS_123	HZ2, D_LYS_123	2.95	2.13	19.50
5I76.PDB	O, D_LYS_149	N, D_SER_126	H, D_SER_126	2.93	2.12	16.07
5I76.PDB	O, D_LEU_147	N, D_PHE_128	H, D_PHE_128	2.86	2.04	14.01
5I76.PDB	O, D_GLY_145	N, D_LEU_130	H, D_LEU_130	2.76	1.93	12.37
5I76.PDB	O, D_VAL_190	N, D_ALA_142	H, D_ALA_142	2.84	1.99	7.81
5I76.PDB	O, D_VAL_188	N, D_LEU_144	H, D_LEU_144	2.94	2.11	12.57
5I76.PDB	O, D_LEU_130	N, D_GLY_145	H, D_GLY_145	2.87	2.09	20.87
5I76.PDB	O, D_SER_186	N, D_CYS_146	H, D_CYS_146	2.86	2.06	18.05
5I76.PDB	O, D_PHE_128	N, D_LEU_147	H, D_LEU_147	2.79	1.96	12.46
5I76.PDB	O, D_LEU_184	N, D_VAL_148	H, D_VAL_148	2.78	1.92	3.60
5I76.PDB	O, D_SER_126	N, D_LYS_149	H, D_LYS_149	2.86	2.01	8.73
5I76.PDB	OD1, D_ASP_150	NZ, D_LYS_149	HZ3, D_LYS_149	2.86	2.03	16.70
5I76.PDB	OE1, D_GLU_154	OH, D_TYR_151	HH, D_TYR_151	2.91	2.09	9.17
5I76.PDB	O, D_LYS_123	N, D_PHE_152	H, D_PHE_152	2.92	2.10	15.60
5I76.PDB	O, D_ASN_205	N, D_THR_157	H, D_THR_157	2.93	2.10	13.79
5I76.PDB	O, D_ASN_203	N, D_SER_159	H, D_SER_159	2.90	2.10	17.79
5I76.PDB	OD1, D_ASN_203	OG, D_SER_159	HG, D_SER_159	2.84	2.05	16.99
5I76.PDB	OG, D_SER_186	NE1, D_TRP_160	HE1, D_TRP_160	2.92	2.08	9.81
5I76.PDB	O, D_ILE_201	N, D_ASN_161	H, D_ASN_161	2.80	1.97	10.81
5I76.PDB	OD1, D_ASN_203	N, D_SER_162	H, D_SER_162	2.77	1.99	21.35
5I76.PDB	O, D_TRP_160	N, D_GLY_163	H, D_GLY_163	2.92	2.16	23.49
5I76.PDB	O, D_ASN_161	N, D_ALA_164	H, D_ALA_164	2.96	2.12	9.30
5I76.PDB	O, D_VAL_187	N, D_HIS_170	H, D_HIS_170	2.80	1.97	11.03
5I76.PDB	O, D_SER_185	N, D_PHE_172	H, D_PHE_172	2.92	2.07	3.58
5I76.PDB	O, D_LEU_181	N, D_GLN_177	H, D_GLN_177	2.88	2.03	5.94
5I76.PDB	OD1, D_ASP_150	NE2, D_GLN_177	HE22, D_GLN_177	2.71	1.92	19.90
5I76.PDB	O, D_GLN_177	N, D_GLY_180	H, D_GLY_180	2.92	2.07	7.88
5I76.PDB	O, D_TYR_151	N, D_TYR_182	H, D_TYR_182	2.70	1.85	9.44
5I76.PDB	O, D_VAL_148	N, D_LEU_184	H, D_LEU_184	2.93	2.12	16.08
5I76.PDB	O, D_CYS_146	N, D_SER_186	H, D_SER_186	2.93	2.10	13.35
5I76.PDB	O, D_HIS_170	N, D_VAL_187	H, D_VAL_187	2.85	2.02	13.58
5I76.PDB	O, D_LEU_144	N, D_VAL_188	H, D_VAL_188	2.84	2.04	18.13
5I76.PDB	O, D_ALA_142	N, D_VAL_190	H, D_VAL_190	2.88	2.06	15.90
5I76.PDB	O, D_GLY_140	N, D_SER_192	H, D_SER_192	2.66	1.82	10.87
5I76.PDB	O, D_PRO_191	N, D_SER_194	H, D_SER_194	2.93	2.12	17.62
5I76.PDB	O, D_PRO_191	OG, D_SER_194	HG, D_SER_194	2.78	2.01	19.83
5I76.PDB	O, D_SER_194	N, D_GLN_198	H, D_GLN_198	2.92	2.06	3.85

5I76.PDB	O, D_THR_199	NE2, D_GLN_198	HE21, D_GLN_198	2.86	2.01	0.69
5I76.PDB	OG, D_SER_194	OH, D_TYR_200	HH, D_TYR_200	2.69	1.90	16.49
5I76.PDB	OD1, D_ASN_161	N, D_ILE_201	H, D_ILE_201	2.91	2.08	13.96
5I76.PDB	O, D_LYS_215	N, D_CYS_202	H, D_CYS_202	2.93	2.15	21.14
5I76.PDB	O, D_SER_159	N, D_ASN_203	H, D_ASN_203	2.82	1.98	10.06
5I76.PDB	O, D_VAL_213	N, D_VAL_204	H, D_VAL_204	2.81	1.96	3.09
5I76.PDB	O, D_THR_157	N, D_ASN_205	H, D_ASN_205	2.91	2.08	12.09
5I76.PDB	O, D_THR_211	N, D_HIS_206	H, D_HIS_206	2.80	1.95	4.50
5I76.PDB	O, D_PRO_153	NE2, D_HIS_206	HE2, D_HIS_206	2.83	1.99	8.92
5I76.PDB	O, D_LYS_207	N, D_ASN_210	H, D_ASN_210	2.86	2.01	9.18
5I76.PDB	O, D_VAL_204	N, D_VAL_213	H, D_VAL_213	2.96	2.15	16.50
5I76.PDB	O, D_CYS_202	N, D_LYS_215	H, D_LYS_215	2.92	2.10	13.71
5I76.PDB	OE1, C_GLU_123	NZ, D_LYS_215	HZ1, D_LYS_215	2.60	1.73	11.40
5I76.PDB	O, D_TYR_200	N, D_VAL_217	H, D_VAL_217	2.83	1.98	9.45
5JO5.PDB	O, H_SER_25	N, H_GLN_3	H, H_GLN_3	2.86	2.02	10.87
5JO5.PDB	O, H_ALA_23	N, H_VAL_5	H, H_VAL_5	2.97	2.20	22.57
5JO5.PDB	O, H_SER_21	N, H_SER_7	H, H_SER_7	2.83	2.06	22.33
5JO5.PDB	OG1, H_THR_107	N, H_GLY_9	H, H_GLY_9	2.92	2.18	25.94
5JO5.PDB	O, H_THR_110	N, H_VAL_12	H, H_VAL_12	2.95	2.16	19.95
5JO5.PDB	O, H_LEU_82C	N, H_GLY_15	H, H_GLY_15	2.87	2.03	10.84
5JO5.PDB	O, H_LYS_13	N, H_GLY_16	H, H_GLY_16	2.89	2.08	16.43
5JO5.PDB	O, H_MET_82	N, H_LEU_18	H, H_LEU_18	2.85	2.08	21.54
5JO5.PDB	O, H_LEU_80	N, H_LEU_20	H, H_LEU_20	2.83	1.98	7.63
5JO5.PDB	O, H_SER_7	N, H_SER_21	H, H_SER_21	2.95	2.11	11.17
5JO5.PDB	O, H_LEU_78	N, H_CYS_22	H, H_CYS_22	2.71	1.93	21.85
5JO5.PDB	O, H_ASN_76	N, H_ALA_24	H, H_ALA_24	2.98	2.24	25.87
5JO5.PDB	O, H_GLN_3	N, H_SER_25	H, H_SER_25	2.97	2.18	20.13
5JO5.PDB	OD2, H_ASP_53	NE1, H_TRP_33	HE1, H_TRP_33	2.93	2.17	24.23
5JO5.PDB	O, H_ALA_93	N, H_SER_35	H, H_SER_35	2.89	2.05	12.04
5JO5.PDB	OG1, H_THR_95	OG, H_SER_35	HG, H_SER_35	2.68	1.99	28.91
5JO5.PDB	O, H_GLY_49	N, H_TRP_36	H, H_TRP_36	2.91	2.11	18.39
5JO5.PDB	O, H_TYR_91	N, H_VAL_37	H, H_VAL_37	2.87	2.05	15.23
5JO5.PDB	O, H_GLU_46	N, H_ARG_38	H, H_ARG_38	2.84	1.99	8.78
5JO5.PDB	OE1, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.82	2.00	14.74
5JO5.PDB	OH, H_TYR_90	NH1, H_ARG_38	HH11, H_ARG_38	2.91	2.09	14.97
5JO5.PDB	OD1, H_ASP_86	NH1, H_ARG_38	HH12, H_ARG_38	2.87	2.05	14.25
5JO5.PDB	O, H_VAL_89	N, H_GLN_39	H, H_GLN_39	2.85	2.14	29.27
5JO5.PDB	O, H_LYS_43	NE2, H_GLN_39	HE21, H_GLN_39	2.97	2.25	28.76
5JO5.PDB	OE1, L_GLN_38	NE2, H_GLN_39	HE22, H_GLN_39	2.84	2.00	9.38
5JO5.PDB	O, H_ALA_40	N, H_LYS_43	H, H_LYS_43	2.90	2.09	16.35
5JO5.PDB	O, H_ARG_38	N, H_GLU_46	H, H_GLU_46	2.79	2.02	21.68
5JO5.PDB	O, H_TRP_36	N, H_VAL_48	H, H_VAL_48	2.94	2.11	12.31
5JO5.PDB	OE1, H_GLU_100J	NE, H_ARG_50	HE, H_ARG_50	2.77	2.00	22.35
5JO5.PDB	OD2, H_ASP_58	NH2, H_ARG_50	HH22, H_ARG_50	2.84	2.00	11.12
5JO5.PDB	O, H_MET_34	N, H_ILE_51	H, H_ILE_51	2.83	2.00	12.12
5JO5.PDB	O, H_THR_56	N, H_LYS_52	H, H_LYS_52	2.88	2.07	15.53
5JO5.PDB	O, H_LYS_52B	N, H_GLY_54	H, H_GLY_54	2.98	2.13	6.95
5JO5.PDB	O, H_SER_52A	N, H_GLY_55	H, H_GLY_55	2.78	2.06	28.32
5JO5.PDB	O, H_VAL_48	N, H_ALA_60	H, H_ALA_60	2.93	2.08	7.36
5JO5.PDB	O, H_VAL_63	N, H_ARG_66	H, H_ARG_66	2.94	2.10	10.09
5JO5.PDB	OD2, H_ASP_86	NH1, H_ARG_66	HH12, H_ARG_66	2.78	1.94	11.10
5JO5.PDB	O, H_PRO_62	NH2, H_ARG_66	HH21, H_ARG_66	2.88	2.03	7.86
5JO5.PDB	O, H_GLN_81	N, H_THR_68	H, H_THR_68	2.80	1.99	17.53
5JO5.PDB	OH, H_TYR_59	N, H_ILE_69	H, H_ILE_69	2.86	2.01	7.98
5JO5.PDB	OD1, H_ASP_73	NE, H_ARG_71	HE, H_ARG_71	2.85	2.05	17.58
5JO5.PDB	O, H_ALA_32	NH1, H_ARG_71	HH12, H_ARG_71	2.86	2.11	24.42
5JO5.PDB	O, H_ALA_32	NH2, H_ARG_71	HH22, H_ARG_71	2.83	2.07	23.03
5JO5.PDB	O, H_THR_77	N, H_ASP_72	H, H_ASP_72	2.89	2.04	7.72

5JO5.PDB	OD1, H_ASP_72	OG, H_SER_74	HG, H_SER_74	2.59	1.76	4.73
5JO5.PDB	O, H_LYS_75	OG1, H_THR_77	HG1, H_THR_77	2.84	2.04	15.24
5JO5.PDB	O, H_CYS_22	N, H_LEU_78	H, H_LEU_78	2.85	2.02	12.40
5JO5.PDB	O, H_SER_70	N, H_TYR_79	H, H_TYR_79	2.84	2.00	10.37
5JO5.PDB	O, H_LEU_20	N, H_LEU_80	H, H_LEU_80	2.99	2.17	15.30
5JO5.PDB	O, H_THR_68	N, H_GLN_81	H, H_GLN_81	2.80	1.97	11.82
5JO5.PDB	O, H_LEU_18	N, H_MET_82	H, H_MET_82	2.68	1.83	6.72
5JO5.PDB	O, H_ARG_66	N, H_ASN_82A	H, H_ASN_82A	2.89	2.08	16.66
5JO5.PDB	OD2, H_ASP_86	N, H_LYS_83	H, H_LYS_83	2.83	2.01	15.00
5JO5.PDB	O, H_LYS_83	N, H_ASP_86	H, H_ASP_86	2.89	2.04	9.43
5JO5.PDB	O, H_VAL_109	N, H_ALA_88	H, H_ALA_88	2.98	2.20	21.19
5JO5.PDB	O, H_GLN_39	N, H_VAL_89	H, H_VAL_89	2.91	2.12	19.27
5JO5.PDB	O, H_THR_107	N, H_TYR_90	H, H_TYR_90	2.80	1.96	8.92
5JO5.PDB	O, H_ASP_86	OH, H_TYR_90	HH, H_TYR_90	2.72	1.89	9.52
5JO5.PDB	O, H_VAL_37	N, H_TYR_91	H, H_TYR_91	2.60	1.74	3.84
5JO5.PDB	OE2, H_GLU_6	N, H_CYS_92	H, H_CYS_92	2.73	1.88	6.94
5JO5.PDB	O, H_SER_35	N, H_ALA_93	H, H_ALA_93	2.87	2.09	21.23
5JO5.PDB	OD2, H_ASP_102	NE, H_ARG_94	HE, H_ARG_94	2.81	2.07	25.27
5JO5.PDB	OD2, H_ASP_102	NH1, H_ARG_94	HH11, H_ARG_94	2.70	1.93	22.67
5JO5.PDB	O, H_TRP_33	N, H_THR_95	H, H_THR_95	2.84	2.02	13.21
5JO5.PDB	O, H_TYR_100K	N, H_GLY_96	H, H_GLY_96	2.75	2.04	28.69
5JO5.PDB	OH, L_TYR_36	N, H_PHE_100L	H, H_PHE_100L	2.79	1.96	12.88
5JO5.PDB	O, H_ARG_94	N, H_GLN_101	H, H_GLN_101	2.75	2.02	27.16
5JO5.PDB	O, H_CYS_92	N, H_GLY_104	H, H_GLY_104	2.98	2.18	17.80
5JO5.PDB	O, L_GLY_41	NH2, H_ARG_105	HH22, H_ARG_105	2.85	2.05	18.48
5JO5.PDB	OE1, H_GLU_6	N, H_GLY_106	H, H_GLY_106	2.83	1.97	2.31
5JO5.PDB	O, H_ALA_88	N, H_VAL_109	H, H_VAL_109	2.90	2.04	1.74
5JO5.PDB	OG1, H_THR_87	N, H_VAL_111	H, H_VAL_111	2.87	2.02	7.41
5JO5.PDB	O, H_PHE_146	N, H_LYS_117	H, H_LYS_117	2.78	1.95	14.10
5JO5.PDB	O, H_ASP_144	NZ, H_LYS_117	HZ2, H_LYS_117	2.88	2.15	29.08
5JO5.PDB	O, H_LEU_141	N, H_PHE_122	H, H_PHE_122	2.87	2.06	15.46
5JO5.PDB	O, H_GLY_139	N, H_LEU_124	H, H_LEU_124	2.83	1.98	8.83
5JO5.PDB	O, H_THR_135	N, H_SER_132	H, H_SER_132	2.79	2.00	20.13
5JO5.PDB	O, H_VAL_184	N, H_ALA_136	H, H_ALA_136	2.77	1.96	15.59
5JO5.PDB	O, H_LEU_124	N, H_GLY_139	H, H_GLY_139	2.94	2.17	22.16
5JO5.PDB	O, H_SER_180	N, H_CYS_140	H, H_CYS_140	2.79	2.01	20.41
5JO5.PDB	O, H_PHE_122	N, H_LEU_141	H, H_LEU_141	2.81	1.96	8.37
5JO5.PDB	O, H_LEU_178	N, H_VAL_142	H, H_VAL_142	2.78	1.93	4.91
5JO5.PDB	O, H_SER_120	N, H_LYS_143	H, H_LYS_143	2.78	1.93	7.38
5JO5.PDB	OE2, L_GLU_124	NZ, H_LYS_143	HZ2, H_LYS_143	2.46	1.63	17.05
5JO5.PDB	O, H_TYR_176	N, H_TYR_145	H, H_TYR_145	2.93	2.12	18.01
5JO5.PDB	O, H_LYS_117	N, H_PHE_146	H, H_PHE_146	2.91	2.11	18.36
5JO5.PDB	O, H_ASN_197	N, H_SER_153	H, H_SER_153	2.98	2.17	17.36
5JO5.PDB	OD1, H_ASN_197	OG, H_SER_153	HG, H_SER_153	2.83	2.04	17.75
5JO5.PDB	OG, H_SER_180	NE1, H_TRP_154	HE1, H_TRP_154	2.93	2.09	10.13
5JO5.PDB	O, H_ILE_195	N, H_ASN_155	H, H_ASN_155	2.79	1.95	11.56
5JO5.PDB	OD1, H_ASN_197	N, H_SER_156	H, H_SER_156	2.79	1.98	16.54
5JO5.PDB	O, H_VAL_181	N, H_HIS_164	H, H_HIS_164	2.87	2.04	11.88
5JO5.PDB	O, H_SER_179	N, H_PHE_166	H, H_PHE_166	2.94	2.09	7.03
5JO5.PDB	O, H_SER_177	N, H_VAL_169	H, H_VAL_169	2.82	1.99	13.61
5JO5.PDB	O, H_LEU_175	N, H_GLN_171	H, H_GLN_171	2.90	2.04	2.90
5JO5.PDB	OD1, H_ASP_144	NE2, H_GLN_171	HE22, H_GLN_171	2.85	2.05	18.06
5JO5.PDB	O, H_GLN_171	N, H_GLY_174	H, H_GLY_174	2.76	1.91	7.94
5JO5.PDB	O, H_TYR_145	N, H_TYR_176	H, H_TYR_176	2.87	2.01	3.19
5JO5.PDB	O, H_VAL_142	N, H_LEU_178	H, H_LEU_178	2.88	2.10	20.17
5JO5.PDB	OH, L_TYR_177	OG, H_SER_179	HG, H_SER_179	2.73	2.00	25.96
5JO5.PDB	O, H_CYS_140	N, H_SER_180	H, H_SER_180	2.97	2.15	16.14
5JO5.PDB	O, H_HIS_164	N, H_VAL_181	H, H_VAL_181	2.90	2.05	10.33

5JO5.PDB	O, H.LEU.138	N, H.VAL.182	H, H.VAL.182	2.81	1.98	13.21
5JO5.PDB	O, H.ALA.136	N, H.VAL.184	H, H.VAL.184	2.93	2.09	11.13
5JO5.PDB	O, H.GLY.134	N, H.SER.186	H, H.SER.186	2.74	1.90	11.33
5JO5.PDB	O, H.PRO.185	N, H.SER.188	H, H.SER.188	2.93	2.12	16.10
5JO5.PDB	O, H.PRO.185	OG, H.SER.188	HG, H.SER.188	2.69	1.85	3.24
5JO5.PDB	O, H.SER.188	N, H.GLN.192	H, H.GLN.192	2.64	1.80	8.80
5JO5.PDB	O, H.THR.193	NE2, H.GLN.192	HE21, H.GLN.192	2.95	2.13	13.81
5JO5.PDB	OG, H.SER.188	OH, H.TYR.194	HH, H.TYR.194	2.61	1.85	20.74
5JO5.PDB	OD1, H.ASN.155	N, H.ILE.195	H, H.ILE.195	2.90	2.09	16.29
5JO5.PDB	O, H.LYS.209	N, H.CYS.196	H, H.CYS.196	2.98	2.20	20.49
5JO5.PDB	O, H.SER.153	N, H.ASN.197	H, H.ASN.197	2.76	1.91	7.31
5JO5.PDB	OD1, H.ASP.208	ND2, H.ASN.197	HD22, H.ASN.197	2.91	2.06	7.04
5JO5.PDB	O, H.VAL.207	N, H.VAL.198	H, H.VAL.198	2.73	1.88	4.89
5JO5.PDB	O, H.THR.205	N, H.HIS.200	H, H.HIS.200	2.87	2.01	1.84
5JO5.PDB	O, H.PRO.147	NE2, H.HIS.200	HE2, H.HIS.200	2.76	1.91	9.60
5JO5.PDB	O, H.LYS.201	N, H.ASN.204	H, H.ASN.204	2.99	2.16	10.85
5JO5.PDB	O, H.VAL.198	N, H.VAL.207	H, H.VAL.207	2.80	1.98	14.15
5JO5.PDB	O, H.TYR.194	N, H.VAL.211	H, H.VAL.211	2.90	2.06	10.21
5JO5.PDB	O, L.GLN.24	N, L.THR.5	H, L.THR.5	2.86	2.04	14.84
5JO5.PDB	O, L.TYR.86	NE2, L.GLN.6	HE22, L.GLN.6	2.96	2.12	10.37
5JO5.PDB	O, L.LYS.103	N, L.VAL.11	H, L.VAL.11	2.96	2.14	15.21
5JO5.PDB	O, L.THR.105	N, L.VAL.13	H, L.VAL.13	2.96	2.22	26.22
5JO5.PDB	O, L.ALA.78	N, L.GLY.16	H, L.GLY.16	2.86	2.00	4.99
5JO5.PDB	O, L.ILE.75	N, L.VAL.19	H, L.VAL.19	2.97	2.17	18.95
5JO5.PDB	O, L.LEU.73	N, L.ILE.21	H, L.ILE.21	2.80	1.96	10.07
5JO5.PDB	O, L.ALA.71	N, L.CYS.23	H, L.CYS.23	2.65	1.81	9.51
5JO5.PDB	O, L.THR.5	N, L.GLN.24	H, L.GLN.24	2.94	2.18	24.54
5JO5.PDB	O, L.ASN.69	N, L.GLY.25	H, L.GLY.25	2.97	2.14	12.74
5JO5.PDB	O, L.ARG.91	OG, L.SER.27	HG, L.SER.27	2.58	1.79	15.77
5JO5.PDB	OE1, D.GLN.24	OG, L.SER.30	HG, L.SER.30	2.84	2.07	18.45
5JO5.PDB	O, L.SER.89	N, L.SER.34	H, L.SER.34	2.96	2.20	23.71
5JO5.PDB	O, L.ILE.48	N, L.TRP.35	H, L.TRP.35	2.92	2.12	18.40
5JO5.PDB	O, L.TYR.87	N, L.TYR.36	H, L.TYR.36	2.82	2.06	23.68
5JO5.PDB	O, L.VAL.45	N, L.GLN.37	H, L.GLN.37	2.90	2.07	14.26
5JO5.PDB	OH, L.TYR.86	NE2, L.GLN.37	HE21, L.GLN.37	2.94	2.08	4.10
5JO5.PDB	O, L.ASP.85	N, L.GLN.38	H, L.GLN.38	2.78	1.99	19.05
5JO5.PDB	OE1, H.GLN.39	NE2, L.GLN.38	HE22, L.GLN.38	2.83	2.00	13.03
5JO5.PDB	O, L.LYS.39	N, L.GLN.42	H, L.GLN.42	2.99	2.18	16.76
5JO5.PDB	O, L.GLN.37	N, L.VAL.45	H, L.VAL.45	2.86	2.09	22.29
5JO5.PDB	O, L.TRP.35	N, L.VAL.47	H, L.VAL.47	2.87	2.01	3.07
5JO5.PDB	OD1, L.ASN.52	NE, L.ARG.54	HE, L.ARG.54	2.95	2.15	18.15
5JO5.PDB	OD1, L.ASP.82	NH2, L.ARG.61	HH21, L.ARG.61	2.75	1.92	13.56
5JO5.PDB	OE2, L.GLU.81	NH2, L.ARG.61	HH22, L.ARG.61	2.98	2.17	16.30
5JO5.PDB	O, L.THR.74	N, L.SER.63	H, L.SER.63	2.91	2.14	22.21
5JO5.PDB	OD1, L.ASN.52	N, L.GLY.64	H, L.GLY.64	2.74	1.93	16.44
5JO5.PDB	O, L.SER.72	N, L.SER.65	H, L.SER.65	2.99	2.21	21.03
5JO5.PDB	O, L.THR.70	N, L.SER.67	H, L.SER.67	2.96	2.13	12.51
5JO5.PDB	O, L.SER.67	N, L.THR.70	H, L.THR.70	2.95	2.13	15.77
5JO5.PDB	O, L.SER.67	OG1, L.THR.70	HG1, L.THR.70	2.76	1.95	12.31
5JO5.PDB	O, L.CYS.23	N, L.ALA.71	H, L.ALA.71	2.78	1.96	15.50
5JO5.PDB	O, L.SER.65	N, L.SER.72	H, L.SER.72	2.85	2.01	11.19
5JO5.PDB	O, L.ILE.21	N, L.LEU.73	H, L.LEU.73	2.77	1.95	14.84
5JO5.PDB	O, L.SER.63	N, L.THR.74	H, L.THR.74	2.81	1.96	6.34
5JO5.PDB	O, L.VAL.19	N, L.ILE.75	H, L.ILE.75	2.92	2.10	14.23
5JO5.PDB	O, L.ARG.61	N, L.THR.76	H, L.THR.76	3.00	2.18	15.65
5JO5.PDB	O, L.GLN.17	N, L.ALA.78	H, L.ALA.78	2.90	2.06	10.41
5JO5.PDB	OD2, L.ASP.82	N, L.GLN.79	H, L.GLN.79	2.88	2.03	7.63
5JO5.PDB	O, L.GLN.79	N, L.ASP.82	H, L.ASP.82	2.84	1.99	8.17

5JO5.PDB	O, L_GLN_38	N, L_ASP_85	H, L_ASP_85	2.85	2.02	13.72
5JO5.PDB	O, L_THR_102	N, L_TYR_86	H, L_TYR_86	2.82	2.00	14.85
5JO5.PDB	O, L_ASP_82	OH, L_TYR_86	HH, L_TYR_86	2.63	1.81	7.96
5JO5.PDB	O, L_TYR_36	N, L_TYR_87	H, L_TYR_87	2.95	2.15	18.69
5JO5.PDB	O, L_SER_34	N, L_SER_89	H, L_SER_89	2.88	2.15	26.79
5JO5.PDB	O, L_VAL_97	OG, L_SER_89	HG, L_SER_89	2.82	2.06	20.46
5JO5.PDB	OE2, H_GLU_100J	NH2, L_ARG_91	HH22, L_ARG_91	2.69	1.84	7.26
5JO5.PDB	OH, L_TYR_31	N, L_GLY_95	H, L_GLY_95	2.78	1.95	11.57
5JO5.PDB	OD1, L_ASP_92	OG, L_SER_95A	HG, L_SER_95A	2.53	1.76	19.87
5JO5.PDB	OD1, H_ASP_58	NE, L_ARG_95B	HE, L_ARG_95B	2.95	2.13	14.76
5JO5.PDB	OG, L_SER_95A	N, L_LEU_95C	H, L_LEU_95C	2.90	2.07	11.01
5JO5.PDB	O, L_SER_90	N, L_VAL_97	H, L_VAL_97	2.91	2.08	13.54
5JO5.PDB	O, L_CYS_88	N, L_GLY_99	H, L_GLY_99	2.86	2.04	15.85
5JO5.PDB	OE1, L_GLN_6	N, L_GLY_101	H, L_GLY_101	2.93	2.15	20.63
5JO5.PDB	O, L_TYR_86	N, L_THR_102	H, L_THR_102	2.83	2.05	21.30
5JO5.PDB	O, L_ASP_7	OG1, L_THR_102	HG1, L_THR_102	2.55	1.71	2.52
5JO5.PDB	O, L_PRO_8	N, L_LYS_103	H, L_LYS_103	2.89	2.05	8.92
5JO5.PDB	O, L_ALA_84	N, L_LEU_104	H, L_LEU_104	2.87	2.03	9.56
5JO5.PDB	OE2, L_GLU_83	N, L_VAL_106	H, L_VAL_106	2.95	2.18	22.86
5JO5.PDB	O, L_VAL_13	N, L_LEU_106A	H, L_LEU_106A	2.88	2.04	12.25
5JO5.PDB	OH, L_TYR_140	N, L_SER_107	H, L_SER_107	2.96	2.15	15.96
5JO5.PDB	OE1, L_GLU_198	NZ, L_LYS_110	HZ3, L_LYS_110	2.94	2.09	14.01
5JO5.PDB	O, L_TYR_140	N, L_ALA_111	H, L_ALA_111	2.75	1.91	11.65
5JO5.PDB	O, L_SER_137	N, L_SER_114	H, L_SER_114	2.88	2.08	18.09
5JO5.PDB	O, L_LEU_135	N, L_THR_116	H, L_THR_116	2.97	2.14	11.76
5JO5.PDB	O, L_VAL_133	N, L_PHE_118	H, L_PHE_118	2.81	1.95	5.47
5JO5.PDB	OE2, L_GLU_124	OG1, L_THR_131	HG1, L_THR_131	2.52	1.80	26.33
5JO5.PDB	O, L_LEU_178	N, L_LEU_132	H, L_LEU_132	2.86	2.05	15.80
5JO5.PDB	O, L_SER_176	N, L_CYS_134	H, L_CYS_134	2.82	1.97	8.12
5JO5.PDB	O, L_THR_116	N, L_LEU_135	H, L_LEU_135	2.90	2.05	8.63
5JO5.PDB	O, L_ALA_174	N, L_ILE_136	H, L_ILE_136	2.88	2.10	21.82
5JO5.PDB	O, L_SER_114	N, L_SER_137	H, L_SER_137	2.94	2.15	19.51
5JO5.PDB	OE1, L_GLN_167	N, L_ASP_138	H, L_ASP_138	2.79	2.02	21.93
5JO5.PDB	O, L_PRO_141	N, L_ALA_143	H, L_ALA_143	2.87	2.16	29.13
5JO5.PDB	O, L_GLN_194	N, L_ALA_147	H, L_ALA_147	2.86	2.03	12.40
5JO5.PDB	OG, L_SER_176	NE1, L_TRP_148	HE1, L_TRP_148	2.93	2.09	9.40
5JO5.PDB	O, L_SER_192	N, L_LYS_149	H, L_LYS_149	2.97	2.16	17.57
5JO5.PDB	O, L_SER_153	N, L_ALA_150	H, L_ALA_150	2.83	2.05	20.73
5JO5.PDB	O, L_TRP_148	N, L_VAL_155	H, L_VAL_155	2.95	2.13	15.00
5JO5.PDB	O, L_SER_175	N, L_THR_162	H, L_THR_162	2.86	2.04	15.42
5JO5.PDB	O, H_GLY_42	OG1, L_THR_163	HG1, L_THR_163	2.52	1.79	25.04
5JO5.PDB	O, L_LYS_171	N, L_GLN_167	H, L_GLN_167	2.64	1.79	5.56
5JO5.PDB	OD1, L_ASN_169	NE2, L_GLN_167	HE21, L_GLN_167	2.89	2.12	21.54
5JO5.PDB	O, L_PHE_139	N, L_TYR_172	H, L_TYR_172	2.91	2.12	19.98
5JO5.PDB	O, L_SER_165	N, L_ALA_173	H, L_ALA_173	2.99	2.18	16.79
5JO5.PDB	O, L_ILE_136	N, L_ALA_174	H, L_ALA_174	2.74	1.94	17.43
5JO5.PDB	OG1, L_THR_162	OG, L_SER_175	HG, L_SER_175	2.94	2.19	22.64
5JO5.PDB	O, L_CYS_134	N, L_SER_176	H, L_SER_176	2.92	2.13	20.19
5JO5.PDB	OG1, L_THR_161	OG, L_SER_176	HG, L_SER_176	2.79	2.07	26.34
5JO5.PDB	O, L_GLU_160	N, L_TYR_177	H, L_TYR_177	2.76	1.95	17.14
5JO5.PDB	O, L_LEU_132	N, L_LEU_178	H, L_LEU_178	2.97	2.16	15.14
5JO5.PDB	O, L_GLY_158	N, L_SER_179	H, L_SER_179	2.93	2.10	12.81
5JO5.PDB	O, L_ALA_130	N, L_LEU_180	H, L_LEU_180	2.74	1.88	1.66
5JO5.PDB	OE1, L_GLN_184	N, L_THR_181	H, L_THR_181	2.79	1.96	12.16
5JO5.PDB	O, L_LYS_149	N, L_SER_192	H, L_SER_192	2.91	2.12	19.77
5JO5.PDB	OG1, L_THR_205	OG, L_SER_192	HG, L_SER_192	2.82	2.12	28.14
5JO5.PDB	O, L_LYS_204	N, L_CYS_193	H, L_CYS_193	2.89	2.08	16.55
5JO5.PDB	O, L_ALA_147	N, L_GLN_194	H, L_GLN_194	2.74	1.89	6.08

5JO5.PDB	O, L_VAL_202	N, L_VAL_195	H, L_VAL_195	2.92	2.09	13.64
5JO5.PDB	O, L_THR_145	N, L_THR_196	H, L_THR_196	2.99	2.14	7.48
5JO5.PDB	O, L_SER_200	N, L_HIS_197	H, L_HIS_197	2.70	1.87	12.42
5JO5.PDB	O, L_PRO_141	NE2, L_HIS_197	HE2, L_HIS_197	2.84	2.04	18.51
5JO5.PDB	O, L_HIS_197	N, L_SER_200	H, L_SER_200	2.99	2.16	11.48
5JO5.PDB	OG1, L_THR_196	OG1, L_THR_201	HG1, L_THR_201	2.95	2.20	22.04
5JO5.PDB	O, L_VAL_195	N, L_VAL_202	H, L_VAL_202	2.93	2.11	14.66
5JO5.PDB	O, L_TYR_191	N, L_VAL_206	H, L_VAL_206	2.84	2.01	13.12
5JO5.PDB	O, A_SER_25	N, A_GLN_3	H, A_GLN_3	2.86	2.01	9.97
5JO5.PDB	O, A_ALA_23	N, A_VAL_5	H, A_VAL_5	3.00	2.23	23.15
5JO5.PDB	O, A_SER_21	N, A_SER_7	H, A_SER_7	2.80	2.01	19.59
5JO5.PDB	OG1, A_THR_107	N, A_GLY_9	H, A_GLY_9	2.93	2.20	27.02
5JO5.PDB	O, A_THR_110	N, A_VAL_12	H, A_VAL_12	2.89	2.09	18.23
5JO5.PDB	O, A_LEU_82C	N, A_GLY_15	H, A_GLY_15	2.79	1.96	12.62
5JO5.PDB	O, A_LYS_13	N, A_GLY_16	H, A_GLY_16	2.95	2.13	15.67
5JO5.PDB	O, A_MET_82	N, A_LEU_18	H, A_LEU_18	2.94	2.14	18.28
5JO5.PDB	O, A_LEU_80	N, A_LEU_20	H, A_LEU_20	2.82	2.00	14.35
5JO5.PDB	O, A_SER_7	N, A_SER_21	H, A_SER_21	2.92	2.08	11.20
5JO5.PDB	O, A_LEU_78	N, A_CYS_22	H, A_CYS_22	2.77	2.01	23.44
5JO5.PDB	O, A_VAL_5	N, A_ALA_23	H, A_ALA_23	2.96	2.14	16.35
5JO5.PDB	O, A_PHE_29	N, A_ALA_32	H, A_ALA_32	2.94	2.09	3.75
5JO5.PDB	OD2, A ASP_53	NE1, A_TRP_33	HE1, A_TRP_33	2.82	2.05	21.67
5JO5.PDB	O, A_ALA_93	N, A_SER_35	H, A_SER_35	2.92	2.09	13.78
5JO5.PDB	O, A_GLY_49	N, A_TRP_36	H, A_TRP_36	2.89	2.08	17.21
5JO5.PDB	O, A_TYR_91	N, A_VAL_37	H, A_VAL_37	2.83	2.00	13.43
5JO5.PDB	O, A_GLU_46	N, A_ARG_38	H, A_ARG_38	2.87	2.02	9.33
5JO5.PDB	OE1, A_GLU_46	NE, A_ARG_38	HE, A_ARG_38	2.78	1.97	16.63
5JO5.PDB	OD1, A ASP_86	NH1, A_ARG_38	HH12, A_ARG_38	2.83	2.01	14.60
5JO5.PDB	OE1, B_GLN_38	NE2, A_GLN_39	HE22, A_GLN_39	2.87	2.02	8.31
5JO5.PDB	O, A_ALA_40	N, A_LYS_43	H, A_LYS_43	2.86	2.03	13.20
5JO5.PDB	O, A_ARG_38	N, A_GLU_46	H, A_GLU_46	2.79	2.01	20.62
5JO5.PDB	O, A_TRP_36	N, A_VAL_48	H, A_VAL_48	2.91	2.08	13.09
5JO5.PDB	OE1, A_GLU_100J	NE, A_ARG_50	HE, A_ARG_50	2.88	2.11	22.13
5JO5.PDB	OE2, A_GLU_100J	NH1, A_ARG_50	HH11, A_ARG_50	2.91	2.07	11.34
5JO5.PDB	OD2, A ASP_58	NH2, A_ARG_50	HH22, A_ARG_50	2.88	2.05	13.39
5JO5.PDB	O, A_MET_34	N, A_ILE_51	H, A_ILE_51	2.86	2.02	11.89
5JO5.PDB	O, A_THR_56	N, A_LYS_52	H, A_LYS_52	2.85	2.02	13.45
5JO5.PDB	O, A_LYS_52B	N, A_GLY_54	H, A_GLY_54	2.90	2.06	8.56
5JO5.PDB	O, A_SER_52A	N, A_GLY_55	H, A_GLY_55	2.85	2.06	18.80
5JO5.PDB	O, A_VAL_48	N, A_ALA_60	H, A_ALA_60	2.97	2.12	7.83
5JO5.PDB	O, A_VAL_63	N, A_ARG_66	H, A_ARG_66	2.94	2.11	11.71
5JO5.PDB	O, A_SER_82B	NH1, A_ARG_66	HH11, A_ARG_66	2.94	2.23	29.90
5JO5.PDB	OD2, A ASP_86	NH1, A_ARG_66	HH12, A_ARG_66	2.80	1.98	14.11
5JO5.PDB	O, A_PRO_62	NH2, A_ARG_66	HH21, A_ARG_66	2.96	2.10	6.17
5JO5.PDB	O, A_GLN_81	N, A_THR_68	H, A_THR_68	2.83	2.01	13.97
5JO5.PDB	OH, A_TYR_59	N, A_ILE_69	H, A_ILE_69	2.85	2.01	8.90
5JO5.PDB	OD1, A ASP_73	NE, A_ARG_71	HE, A_ARG_71	2.86	2.09	22.09
5JO5.PDB	O, A_ALA_32	NH1, A_ARG_71	HH12, A_ARG_71	2.93	2.18	24.18
5JO5.PDB	O, A_ALA_32	NH2, A_ARG_71	HH22, A_ARG_71	2.90	2.14	22.88
5JO5.PDB	O, A_THR_77	N, A ASP_72	H, A ASP_72	2.96	2.10	6.62
5JO5.PDB	OD1, A ASP_72	OG, A_SER_74	HG, A_SER_74	2.54	1.80	22.83
5JO5.PDB	O, A_LYS_75	OG1, A_THR_77	HG1, A_THR_77	2.92	2.11	13.47
5JO5.PDB	O, A_CYS_22	N, A_LEU_78	H, A_LEU_78	2.92	2.08	10.42
5JO5.PDB	O, A_SER_70	N, A_TYR_79	H, A_TYR_79	2.88	2.05	13.41
5JO5.PDB	O, A_THR_68	N, A_GLN_81	H, A_GLN_81	2.75	1.92	12.07
5JO5.PDB	O, A_LEU_18	N, A_MET_82	H, A_MET_82	2.76	1.91	7.81
5JO5.PDB	OD2, A ASP_86	N, A_LYS_83	H, A_LYS_83	2.81	1.98	13.27
5JO5.PDB	O, A_LYS_83	N, A ASP_86	H, A ASP_86	2.81	1.98	12.37

5JO5.PDB	O, A_GLN_39	N, A_VAL_89	H, A_VAL_89	2.91	2.12	19.76
5JO5.PDB	O, A_THR_107	N, A_TYR_90	H, A_TYR_90	2.80	1.95	9.44
5JO5.PDB	O, A_ASP_86	OH, A_TYR_90	HH, A_TYR_90	2.68	1.87	12.71
5JO5.PDB	O, A_VAL_37	N, A_TYR_91	H, A_TYR_91	2.64	1.78	2.28
5JO5.PDB	OE2, A_GLU_6	N, A_CYS_92	H, A_CYS_92	2.84	2.03	15.70
5JO5.PDB	O, A_SER_35	N, A_ALA_93	H, A_ALA_93	2.90	2.14	23.25
5JO5.PDB	OD2, A_ASP_102	NE, A_ARG_94	HE, A_ARG_94	2.86	2.14	28.73
5JO5.PDB	OD2, A_ASP_102	NH1, A_ARG_94	HH11, A_ARG_94	2.58	1.79	19.06
5JO5.PDB	O, A_TRP_33	N, A_THR_95	H, A_THR_95	2.83	2.01	14.93
5JO5.PDB	O, A_TYR_100K	N, A_GLY_96	H, A_GLY_96	2.84	2.07	22.90
5JO5.PDB	O, A_GLU_100I	N, A_TYR_98	H, A_TYR_98	2.88	2.03	8.11
5JO5.PDB	O, A_GLY_96	N, A_TYR_100K	H, A_TYR_100K	2.90	2.10	17.32
5JO5.PDB	OH, B_TYR_36	N, A_PHE_100L	H, A_PHE_100L	2.86	2.06	18.12
5JO5.PDB	O, A_ARG_94	N, A_GLN_101	H, A_GLN_101	2.84	2.09	25.14
5JO5.PDB	O, B_GLY_41	NH1, A_ARG_105	HH12, A_ARG_105	2.66	1.82	9.49
5JO5.PDB	OE1, A_GLU_6	N, A_GLY_106	H, A_GLY_106	2.88	2.02	1.10
5JO5.PDB	O, A_ALA_88	N, A_VAL_109	H, A_VAL_109	2.93	2.07	3.98
5JO5.PDB	OG1, A_THR_87	N, A_VAL_111	H, A_VAL_111	2.98	2.14	10.40
5JO5.PDB	O, A_PHE_146	N, A_LYS_117	H, A_LYS_117	2.76	1.96	17.53
5JO5.PDB	O, A_ASP_144	NZ, A_LYS_117	HZ2, A_LYS_117	2.76	2.02	28.39
5JO5.PDB	O, A_LEU_141	N, A_PHE_122	H, A_PHE_122	2.89	2.09	16.71
5JO5.PDB	O, A_GLY_139	N, A_LEU_124	H, A_LEU_124	2.85	2.00	8.87
5JO5.PDB	O, A_SER_132	N, A_THR_135	H, A_THR_135	3.00	2.15	8.03
5JO5.PDB	O, A_VAL_184	N, A_ALA_136	H, A_ALA_136	2.76	1.95	16.74
5JO5.PDB	O, A_SER_180	N, A_CYS_140	H, A_CYS_140	2.83	2.05	19.65
5JO5.PDB	O, A_PHE_122	N, A_LEU_141	H, A_LEU_141	2.83	1.98	7.04
5JO5.PDB	O, A_LEU_178	N, A_VAL_142	H, A_VAL_142	2.79	1.93	5.86
5JO5.PDB	O, A_SER_120	N, A_LYS_143	H, A_LYS_143	2.78	1.93	6.54
5JO5.PDB	OE2, B_GLU_124	NZ, A_LYS_143	HZ2, A_LYS_143	2.62	1.83	23.29
5JO5.PDB	O, A_TYR_176	N, A_TYR_145	H, A_TYR_145	2.91	2.11	17.73
5JO5.PDB	O, A_LYS_117	N, A_PHE_146	H, A_PHE_146	2.93	2.13	18.00
5JO5.PDB	O, A_ASN_197	N, A_SER_153	H, A_SER_153	2.99	2.18	16.28
5JO5.PDB	OD1, A_ASN_197	OG, A_SER_153	HG, A_SER_153	2.78	2.00	18.34
5JO5.PDB	OG, A_SER_180	NE1, A_TRP_154	HE1, A_TRP_154	2.89	2.05	11.45
5JO5.PDB	O, A_ILE_195	N, A_ASN_155	H, A_ASN_155	2.78	1.95	12.63
5JO5.PDB	OD1, A_ASN_197	N, A_SER_156	H, A_SER_156	2.75	1.94	16.25
5JO5.PDB	O, A_TRP_154	N, A_GLY_157	H, A_GLY_157	2.98	2.18	18.25
5JO5.PDB	O, A_VAL_181	N, A_HIS_164	H, A_HIS_164	2.84	2.01	12.57
5JO5.PDB	O, A_SER_179	N, A_PHE_166	H, A_PHE_166	2.92	2.07	5.08
5JO5.PDB	O, A_SER_177	N, A_VAL_169	H, A_VAL_169	2.79	1.96	14.12
5JO5.PDB	O, A_LEU_175	N, A_GLN_171	H, A_GLN_171	2.92	2.06	3.13
5JO5.PDB	OD1, A_ASP_144	NE2, A_GLN_171	HE22, A_GLN_171	2.80	2.01	18.53
5JO5.PDB	O, A_GLN_171	N, A_GLY_174	H, A_GLY_174	2.84	1.99	4.07
5JO5.PDB	O, A_TYR_145	N, A_TYR_176	H, A_TYR_176	2.86	2.00	3.44
5JO5.PDB	O, A_VAL_142	N, A_LEU_178	H, A_LEU_178	2.89	2.11	20.35
5JO5.PDB	OH, B_TYR_177	OG, A_SER_179	HG, A_SER_179	2.83	2.10	25.21
5JO5.PDB	O, A_CYS_140	N, A_SER_180	H, A_SER_180	2.96	2.14	14.89
5JO5.PDB	O, A_HIS_164	N, A_VAL_181	H, A_VAL_181	2.88	2.06	14.86
5JO5.PDB	O, A_LEU_138	N, A_VAL_182	H, A_VAL_182	2.81	1.98	12.72
5JO5.PDB	O, A_ALA_136	N, A_VAL_184	H, A_VAL_184	2.85	2.03	14.13
5JO5.PDB	O, A_GLY_134	N, A_SER_186	H, A_SER_186	2.73	1.88	8.68
5JO5.PDB	O, A_PRO_185	N, A_SER_188	H, A_SER_188	2.87	2.11	23.16
5JO5.PDB	O, A_PRO_185	OG, A_SER_188	HG, A_SER_188	2.64	1.81	7.89
5JO5.PDB	O, A_SER_188	N, A_THR_191	H, A_THR_191	2.98	2.17	16.73
5JO5.PDB	O, A_SER_188	N, A_GLN_192	H, A_GLN_192	2.81	1.96	9.04
5JO5.PDB	OG, A_SER_188	OH, A_TYR_194	HH, A_TYR_194	2.69	1.94	22.27
5JO5.PDB	OD1, A_ASN_155	N, A_ILE_195	H, A_ILE_195	2.85	2.04	16.46
5JO5.PDB	O, A_LYS_209	N, A_CYS_196	H, A_CYS_196	2.97	2.19	19.93

5JO5.PDB	O, A_SER_153	N, A_ASN_197	H, A_ASN_197	2.77	1.92	7.59
5JO5.PDB	O, A_VAL_207	N, A_VAL_198	H, A_VAL_198	2.69	1.83	4.66
5JO5.PDB	OG, A_SER_203	ND1, A_HIS_200	HD1, A_HIS_200	2.79	2.03	23.43
5JO5.PDB	O, A_PRO_147	NE2, A_HIS_200	HE2, A_HIS_200	2.73	1.88	6.85
5JO5.PDB	O, A_SER_203	OG1, A_THR_205	HG1, A_THR_205	2.95	2.24	27.28
5JO5.PDB	O, A_VAL_198	N, A_VAL_207	H, A_VAL_207	2.77	1.95	15.31
5JO5.PDB	O, A_CYS_196	N, A_LYS_209	H, A_LYS_209	2.98	2.17	16.36
5JO5.PDB	OE2, B_GLU_123	NZ, A_LYS_209	HZ1, A_LYS_209	2.55	1.68	10.64
5JO5.PDB	O, A_TYR_194	N, A_VAL_211	H, A_VAL_211	2.93	2.09	10.38
5JO5.PDB	O, B_GLN_24	N, B_THR_5	H, B_THR_5	2.82	1.99	13.54
5JO5.PDB	O, B_TYR_86	NE2, B_GLN_6	HE22, B_GLN_6	2.95	2.13	14.24
5JO5.PDB	O, B_LYS_103	N, B_VAL_11	H, B_VAL_11	2.99	2.17	14.79
5JO5.PDB	O, B_THR_105	N, B_VAL_13	H, B_VAL_13	2.91	2.14	21.54
5JO5.PDB	O, B_ALA_78	N, B_GLY_16	H, B_GLY_16	2.80	1.95	6.96
5JO5.PDB	O, B_ALA_14	N, B_GLN_17	H, B_GLN_17	3.00	2.14	6.45
5JO5.PDB	O, B_ILE_75	N, B_VAL_19	H, B_VAL_19	2.94	2.13	16.92
5JO5.PDB	O, B_LEU_73	N, B_ILE_21	H, B_ILE_21	2.77	1.92	7.42
5JO5.PDB	O, B_ALA_71	N, B_CYS_23	H, B_CYS_23	2.73	1.95	21.25
5JO5.PDB	O, B_THR_5	N, B_GLN_24	H, B_GLN_24	2.88	2.15	26.17
5JO5.PDB	O, B_ASN_69	N, B_GLY_25	H, B_GLY_25	2.95	2.12	12.16
5JO5.PDB	O, B_ARG_91	OG, B_SER_27	HG, B_SER_27	2.69	1.95	23.94
5JO5.PDB	O, B_GLY_25	N, B_LEU_28	H, B_LEU_28	2.92	2.12	17.50
5JO5.PDB	O, B_SER_27	N, B_SER_30	H, B_SER_30	2.94	2.12	14.59
5JO5.PDB	O, B_SER_89	N, B_SER_34	H, B_SER_34	2.95	2.14	17.48
5JO5.PDB	O, B_ILE_48	N, B_TRP_35	H, B_TRP_35	2.82	2.01	17.71
5JO5.PDB	O, B_TYR_87	N, B_TYR_36	H, B_TYR_36	2.80	2.06	24.94
5JO5.PDB	O, B_VAL_45	N, B_GLN_37	H, B_GLN_37	2.88	2.07	16.60
5JO5.PDB	OH, B_TYR_86	NE2, B_GLN_37	HE21, B_GLN_37	2.95	2.09	5.48
5JO5.PDB	O, B_ASP_85	N, B_GLN_38	H, B_GLN_38	2.79	2.00	18.67
5JO5.PDB	OE1, A_GLN_39	NE2, B_GLN_38	HE22, B_GLN_38	2.90	2.07	12.43
5JO5.PDB	O, B_GLN_37	N, B_VAL_45	H, B_VAL_45	2.85	2.08	22.23
5JO5.PDB	O, B_TRP_35	N, B_VAL_47	H, B_VAL_47	2.80	1.94	1.50
5JO5.PDB	O, B_ASN_53	N, B_TYR_49	H, B_TYR_49	2.95	2.14	16.79
5JO5.PDB	O, B_ASP_60	NH1, B_ARG_54	HH12, B_ARG_54	2.83	2.07	22.75
5JO5.PDB	OD1, B_ASP_82	NH2, B_ARG_61	HH21, B_ARG_61	2.66	1.83	11.88
5JO5.PDB	O, B_THR_74	N, B_SER_63	H, B_SER_63	2.95	2.17	20.44
5JO5.PDB	OD1, B_ASN_52	N, B_GLY_64	H, B_GLY_64	2.76	1.93	12.24
5JO5.PDB	O, F_ARG_29	ND2, B_ASN_69	HD21, B_ASN_69	2.80	1.99	16.03
5JO5.PDB	O, B_SER_67	N, B_THR_70	H, B_THR_70	2.93	2.12	15.05
5JO5.PDB	O, B_SER_67	OG1, B_THR_70	HG1, B_THR_70	2.62	1.83	17.02
5JO5.PDB	O, B_CYS_23	N, B_ALA_71	H, B_ALA_71	2.77	1.96	16.51
5JO5.PDB	O, B_SER_65	N, B_SER_72	H, B_SER_72	2.94	2.10	12.05
5JO5.PDB	O, B_ILE_21	N, B_LEU_73	H, B_LEU_73	2.80	2.00	18.00
5JO5.PDB	O, B_SER_63	N, B_THR_74	H, B_THR_74	2.83	1.99	8.11
5JO5.PDB	O, B_VAL_19	N, B_ILE_75	H, B_ILE_75	2.88	2.05	12.36
5JO5.PDB	O, B_GLN_17	N, B_ALA_78	H, B_ALA_78	2.88	2.04	9.27
5JO5.PDB	OD2, B_ASP_82	N, B_GLN_79	H, B_GLN_79	2.90	2.05	7.32
5JO5.PDB	O, B_GLN_79	N, B_ASP_82	H, B_ASP_82	2.86	2.02	10.30
5JO5.PDB	O, B_GLN_38	N, B_ASP_85	H, B_ASP_85	2.90	2.08	13.72
5JO5.PDB	O, B_THR_102	N, B_TYR_86	H, B_TYR_86	2.83	2.01	15.48
5JO5.PDB	O, B_ASP_82	OH, B_TYR_86	HH, B_TYR_86	2.63	1.81	9.87
5JO5.PDB	O, B_TYR_36	N, B_TYR_87	H, B_TYR_87	2.92	2.12	17.35
5JO5.PDB	O, B_SER_34	N, B_SER_89	H, B_SER_89	2.90	2.16	26.65
5JO5.PDB	O, B_VAL_97	OG, B_SER_89	HG, B_SER_89	2.80	2.03	20.14
5JO5.PDB	O, A_GLY_100H	NE, B_ARG_91	HE, B_ARG_91	2.94	2.09	9.41
5JO5.PDB	OH, B_TYR_31	N, B_GLY_95	H, B_GLY_95	2.85	2.01	11.73
5JO5.PDB	OD1, B_ASP_92	OG, B_SER_95A	HG, B_SER_95A	2.47	1.67	15.14
5JO5.PDB	OG, B_SER_95A	N, B_LEU_95C	H, B_LEU_95C	2.98	2.13	6.04

5JO5.PDB	O, B_SER_90	N, B_VAL_97	H, B_VAL_97	2.93	2.11	13.52
5JO5.PDB	O, B_CYS_88	N, B_GLY_99	H, B_GLY_99	2.87	2.07	18.58
5JO5.PDB	O, B_TYR_86	N, B_THR_102	H, B_THR_102	2.85	2.06	19.16
5JO5.PDB	O, B_ASP_7	OG1, B_THR_102	HG1, B_THR_102	2.67	1.84	6.53
5JO5.PDB	O, B_PRO_8	N, B_LYS_103	H, B_LYS_103	2.86	2.01	7.04
5JO5.PDB	O, B_ALA_84	N, B_LEU_104	H, B_LEU_104	2.88	2.04	10.34
5JO5.PDB	O, B_VAL_11	N, B_THR_105	H, B_THR_105	2.98	2.17	16.12
5JO5.PDB	OE2, B_GLU_83	N, B_VAL_106	H, B_VAL_106	2.94	2.17	22.79
5JO5.PDB	O, B_VAL_13	N, B_LEU_106A	H, B_LEU_106A	2.84	2.01	13.15
5JO5.PDB	OH, B_TYR_140	N, B_SER_107	H, B_SER_107	2.96	2.17	18.24
5JO5.PDB	O, B_TYR_140	N, B_ALA_111	H, B_ALA_111	2.79	1.96	11.97
5JO5.PDB	O, B_SER_137	N, B_SER_114	H, B_SER_114	2.91	2.11	17.49
5JO5.PDB	O, B_LEU_135	N, B_THR_116	H, B_THR_116	2.96	2.13	12.67
5JO5.PDB	O, B_VAL_133	N, B_PHE_118	H, B_PHE_118	2.80	1.94	5.22
5JO5.PDB	O, B_LEU_125	N, B_ASN_128	H, B_ASN_128	2.88	2.06	15.38
5JO5.PDB	OE1, B_GLU_124	N, B_THR_131	H, B_THR_131	2.94	2.22	28.36
5JO5.PDB	OE2, B_GLU_124	OG1, B_THR_131	HG1, B_THR_131	2.59	1.86	24.88
5JO5.PDB	O, B_LEU_178	N, B_LEU_132	H, B_LEU_132	2.93	2.11	15.51
5JO5.PDB	O, B_SER_176	N, B_CYS_134	H, B_CYS_134	2.82	1.97	4.20
5JO5.PDB	O, B_THR_116	N, B_LEU_135	H, B_LEU_135	2.91	2.08	12.22
5JO5.PDB	O, B_ALA_174	N, B_ILE_136	H, B_ILE_136	2.90	2.13	23.29
5JO5.PDB	O, B_SER_114	N, B_SER_137	H, B_SER_137	2.93	2.15	21.86
5JO5.PDB	OE1, B_GLN_167	N, B_ASP_138	H, B_ASP_138	2.85	2.08	22.86
5JO5.PDB	O, B_ALA_111	N, B_TYR_140	H, B_TYR_140	2.99	2.17	16.28
5JO5.PDB	O, B_GLN_194	N, B_ALA_147	H, B_ALA_147	2.88	2.05	13.99
5JO5.PDB	OG, B_SER_176	NE1, B_TRP_148	HE1, B_TRP_148	2.89	2.05	10.46
5JO5.PDB	O, B_SER_192	N, B_LYS_149	H, B_LYS_149	2.94	2.16	21.00
5JO5.PDB	O, B_SER_153	N, B_ALA_150	H, B_ALA_150	2.80	1.98	15.92
5JO5.PDB	O, B_SER_190	N, B_ASP_151	H, B_ASP_151	2.96	2.12	10.60
5JO5.PDB	O, B_ALA_150	N, B_SER_153	H, B_SER_153	2.85	2.01	8.39
5JO5.PDB	O, B_TYR_177	N, B_GLU_160	H, B_GLU_160	2.99	2.19	18.42
5JO5.PDB	O, B_SER_175	N, B_THR_162	H, B_THR_162	2.83	2.00	12.84
5JO5.PDB	O, A_GLY_42	OG1, B_THR_163	HG1, B_THR_163	2.48	1.73	21.87
5JO5.PDB	O, B_LYS_171	N, B_GLN_167	H, B_GLN_167	2.72	1.87	6.72
5JO5.PDB	OD1, B_ASN_169	NE2, B_GLN_167	HE21, B_GLN_167	2.98	2.24	26.40
5JO5.PDB	OD1, B_ASP_138	NE2, B_GLN_167	HE22, B_GLN_167	2.99	2.14	6.65
5JO5.PDB	O, B_PHE_139	N, B_TYR_172	H, B_TYR_172	2.89	2.09	16.64
5JO5.PDB	O, B_ILE_136	N, B_ALA_174	H, B_ALA_174	2.78	1.99	18.28
5JO5.PDB	OG1, B_THR_162	N, B_SER_175	H, B_SER_175	2.97	2.18	20.62
5JO5.PDB	OG1, B_THR_162	OG, B_SER_175	HG, B_SER_175	2.87	2.11	21.53
5JO5.PDB	O, B_CYS_134	N, B_SER_176	H, B_SER_176	2.89	2.09	18.62
5JO5.PDB	OG1, B_THR_161	OG, B_SER_176	HG, B_SER_176	2.78	2.05	24.57
5JO5.PDB	O, B_GLU_160	N, B_TYR_177	H, B_TYR_177	2.74	1.95	18.78
5JO5.PDB	O, B_LEU_132	N, B_LEU_178	H, B_LEU_178	2.98	2.16	14.96
5JO5.PDB	O, B_GLY_158	N, B_SER_179	H, B_SER_179	2.79	1.95	12.09
5JO5.PDB	O, B_ALA_130	N, B_LEU_180	H, B_LEU_180	2.84	1.98	3.06
5JO5.PDB	OE1, B_GLN_184	N, B_THR_181	H, B_THR_181	2.98	2.15	11.97
5JO5.PDB	O, B_GLN_184	OG, B_SER_187	HG, B_SER_187	2.84	2.02	9.83
5JO5.PDB	OD1, B_ASP_151	N, B_ARG_189	H, B_ARG_189	2.77	1.99	21.06
5JO5.PDB	O, B_VAL_206	N, B_TYR_191	H, B_TYR_191	2.97	2.14	12.35
5JO5.PDB	O, B_LYS_149	N, B_SER_192	H, B_SER_192	2.94	2.15	19.79
5JO5.PDB	OG1, B_THR_205	OG, B_SER_192	HG, B_SER_192	2.59	1.90	29.12
5JO5.PDB	O, B_LYS_204	N, B_CYS_193	H, B_CYS_193	2.85	2.06	19.97
5JO5.PDB	O, B_ALA_147	N, B_GLN_194	H, B_GLN_194	2.76	1.91	8.07
5JO5.PDB	OE2, B_GLU_203	NE2, B_GLN_194	HE21, B_GLN_194	2.60	1.77	11.97
5JO5.PDB	O, B_VAL_202	N, B_VAL_195	H, B_VAL_195	2.87	2.03	10.67
5JO5.PDB	O, B_THR_145	N, B_THR_196	H, B_THR_196	2.94	2.09	7.84
5JO5.PDB	O, B_SER_200	N, B_HIS_197	H, B_HIS_197	2.84	2.00	11.99

5JO5.PDB	O, B.PRO_141	NE2, B.HIS_197	HE2, B.HIS_197	2.91	2.14	22.84
5JO5.PDB	OG1, B.THR_196	OG1, B.THR_201	HG1, B.THR_201	2.97	2.21	22.11
5JO5.PDB	O, B.VAL_195	N, B.VAL_202	H, B.VAL_202	2.91	2.09	14.85
5JO5.PDB	O, B.TYR_191	N, B.VAL_206	H, B.VAL_206	2.88	2.07	15.96
5JO5.PDB	O, C.SER_25	N, C.GLN_3	H, C.GLN_3	2.95	2.10	9.50
5JO5.PDB	O, C.SER_21	N, C.SER_7	H, C.SER_7	2.80	2.03	21.56
5JO5.PDB	OG1, C.THR_107	N, C.GLY_9	H, C.GLY_9	2.94	2.21	27.65
5JO5.PDB	O, C.THR_110	N, C.VAL_12	H, C.VAL_12	2.90	2.11	19.33
5JO5.PDB	O, C.LEU_82C	N, C.GLY_15	H, C.GLY_15	2.77	1.95	13.95
5JO5.PDB	O, C.LYS_13	N, C.GLY_16	H, C.GLY_16	2.93	2.13	17.72
5JO5.PDB	O, C.MET_82	N, C.LEU_18	H, C.LEU_18	2.90	2.11	18.94
5JO5.PDB	O, C.LEU_80	N, C.LEU_20	H, C.LEU_20	2.76	1.94	13.93
5JO5.PDB	O, C.SER_7	N, C.SER_21	H, C.SER_21	2.94	2.10	10.42
5JO5.PDB	O, C.LEU_78	N, C.CYS_22	H, C.CYS_22	2.73	1.95	21.22
5JO5.PDB	O, C.VAL_5	N, C.ALA_23	H, C.ALA_23	2.95	2.13	13.78
5JO5.PDB	O, C.PHE_29	N, C.ALA_32	H, C.ALA_32	2.90	2.05	5.82
5JO5.PDB	OD2, C.ASP_53	NE1, C.TRP_33	HE1, C.TRP_33	2.84	2.06	21.35
5JO5.PDB	O, C.ALA_93	N, C.SER_35	H, C.SER_35	2.93	2.11	13.64
5JO5.PDB	O, C.GLY_49	N, C.TRP_36	H, C.TRP_36	2.89	2.07	16.12
5JO5.PDB	O, C.TYR_91	N, C.VAL_37	H, C.VAL_37	2.87	2.05	13.46
5JO5.PDB	O, C.GLU_46	N, C.ARG_38	H, C.ARG_38	2.87	2.03	9.28
5JO5.PDB	OE1, C.GLU_46	NE, C.ARG_38	HE, C.ARG_38	2.77	1.97	17.97
5JO5.PDB	OH, C.TYR_90	NH1, C.ARG_38	HH11, C.ARG_38	3.00	2.18	14.70
5JO5.PDB	OD1, C.ASP_86	NH1, C.ARG_38	HH12, C.ARG_38	2.85	2.02	13.98
5JO5.PDB	OE1, D.GLN_38	NE2, C.GLN_39	HE22, C.GLN_39	2.86	2.02	9.45
5JO5.PDB	O, C.ALA_40	N, C.LYS_43	H, C.LYS_43	2.88	2.04	10.48
5JO5.PDB	O, C.ARG_38	N, C.GLU_46	H, C.GLU_46	2.77	1.99	20.78
5JO5.PDB	O, C.TRP_36	N, C.VAL_48	H, C.VAL_48	2.90	2.07	13.17
5JO5.PDB	OE1, C.GLU_100J	NE, C.ARG_50	HE, C.ARG_50	2.87	2.09	20.20
5JO5.PDB	OD2, C.ASP_58	NH1, C.ARG_50	HH12, C.ARG_50	2.77	1.94	11.94
5JO5.PDB	OE2, C.GLU_100J	NH2, C.ARG_50	HH21, C.ARG_50	2.86	2.02	10.69
5JO5.PDB	O, C.MET_34	N, C.ILE_51	H, C.ILE_51	2.83	1.99	11.56
5JO5.PDB	O, C.THR_56	N, C.LYS_52	H, C.LYS_52	2.95	2.12	13.78
5JO5.PDB	O, C.SER_52A	N, C.ASP_53	H, C.ASP_53	2.94	2.23	29.56
5JO5.PDB	O, C.LYS_52B	N, C.GLY_54	H, C.GLY_54	3.00	2.15	9.38
5JO5.PDB	O, C.SER_52A	N, C.GLY_55	H, C.GLY_55	2.78	2.00	20.47
5JO5.PDB	O, C.VAL_48	N, C.ALA_60	H, C.ALA_60	2.89	2.04	7.94
5JO5.PDB	O, C.VAL_63	N, C.ARG_66	H, C.ARG_66	2.93	2.09	10.54
5JO5.PDB	OD2, C.ASP_86	NH1, C.ARG_66	HH12, C.ARG_66	2.83	2.01	15.29
5JO5.PDB	O, C.PRO_62	NH2, C.ARG_66	HH21, C.ARG_66	2.87	2.02	7.14
5JO5.PDB	O, C.GLN_81	N, C.THR_68	H, C.THR_68	2.82	2.00	14.42
5JO5.PDB	OH, C.TYR_59	N, C.ILE_69	H, C.ILE_69	2.82	1.97	9.17
5JO5.PDB	OD1, C.ASP_73	NE, C.ARG_71	HE, C.ARG_71	2.90	2.12	21.25
5JO5.PDB	O, C.ALA_32	NH1, C.ARG_71	HH12, C.ARG_71	2.94	2.19	24.89
5JO5.PDB	O, C.ALA_32	NH2, C.ARG_71	HH22, C.ARG_71	2.89	2.13	22.77
5JO5.PDB	O, C.THR_77	N, C.ASP_72	H, C.ASP_72	2.91	2.06	7.23
5JO5.PDB	OD1, C.ASP_72	OG, C.SER_74	HG, C.SER_74	2.61	1.84	20.06
5JO5.PDB	O, C.CYS_22	N, C.LEU_78	H, C.LEU_78	2.88	2.05	11.40
5JO5.PDB	O, C.SER_70	N, C.TYR_79	H, C.TYR_79	2.85	2.00	9.09
5JO5.PDB	O, C.THR_68	N, C.GLN_81	H, C.GLN_81	2.76	1.93	12.88
5JO5.PDB	OD2, C.ASP_86	N, C.LYS_83	H, C.LYS_83	2.79	1.97	14.63
5JO5.PDB	O, C.LYS_83	N, C.ASP_86	H, C.ASP_86	2.83	2.00	13.05
5JO5.PDB	O, C.VAL_109	N, C.ALA_88	H, C.ALA_88	2.97	2.19	21.73
5JO5.PDB	O, C.GLN_39	N, C.VAL_89	H, C.VAL_89	2.92	2.12	17.72
5JO5.PDB	O, C.THR_107	N, C.TYR_90	H, C.TYR_90	2.82	1.97	9.30
5JO5.PDB	O, C.ASP_86	OH, C.TYR_90	HH, C.TYR_90	2.68	1.88	13.76
5JO5.PDB	O, C.VAL_37	N, C.TYR_91	H, C.TYR_91	2.60	1.74	2.45
5JO5.PDB	OE2, C.GLU_6	N, C.CYS_92	H, C.CYS_92	2.75	1.90	6.95

5JO5.PDB	O, C_SER_35	N, C_ALA_93	H, C_ALA_93	2.91	2.13	21.34
5JO5.PDB	OD2, C_ASP_102	NE, C_ARG_94	HE, C_ARG_94	2.79	2.08	28.98
5JO5.PDB	OD2, C_ASP_102	NH1, C_ARG_94	HH11, C_ARG_94	2.55	1.78	21.18
5JO5.PDB	O, C_TYR_100K	N, C_GLY_96	H, C_GLY_96	2.82	2.05	21.49
5JO5.PDB	O, C_GLU_100I	N, C_TYR_98	H, C_TYR_98	2.79	1.95	9.02
5JO5.PDB	O, C_GLY_96	N, C_TYR_100K	H, C_TYR_100K	2.91	2.11	17.91
5JO5.PDB	OH, D_TYR_36	N, C_PHE_100L	H, C_PHE_100L	2.87	2.08	19.05
5JO5.PDB	O, C_ARG_94	N, C_GLN_101	H, C_GLN_101	2.81	2.06	25.18
5JO5.PDB	O, C_CYS_92	N, C_GLY_104	H, C_GLY_104	2.86	2.05	16.43
5JO5.PDB	OE1, C_GLU_6	N, C_ARG_105	H, C_ARG_105	2.82	2.06	23.52
5JO5.PDB	OE1, C_GLU_6	N, C_GLY_106	H, C_GLY_106	2.82	1.96	3.31
5JO5.PDB	O, C_ALA_88	N, C_VAL_109	H, C_VAL_109	2.90	2.04	2.47
5JO5.PDB	OG1, C_THR_87	N, C_VAL_111	H, C_VAL_111	2.92	2.08	9.87
5JO5.PDB	O, C_PHE_146	N, C_LYS_117	H, C_LYS_117	2.76	1.94	13.75
5JO5.PDB	O, C_ASP_144	NZ, C_LYS_117	HZ2, C_LYS_117	2.78	2.05	29.84
5JO5.PDB	O, C_LEU_141	N, C_PHE_122	H, C_PHE_122	2.86	2.03	12.84
5JO5.PDB	O, C_GLY_139	N, C_LEU_124	H, C_LEU_124	2.85	2.00	9.59
5JO5.PDB	O, C_VAL_184	N, C_ALA_136	H, C_ALA_136	2.67	1.87	17.12
5JO5.PDB	O, C_VAL_182	N, C_LEU_138	H, C_LEU_138	2.99	2.15	10.96
5JO5.PDB	O, C_SER_180	N, C_CYS_140	H, C_CYS_140	2.84	2.06	20.26
5JO5.PDB	O, C_PHE_122	N, C_LEU_141	H, C_LEU_141	2.78	1.93	7.78
5JO5.PDB	O, C_LEU_178	N, C_VAL_142	H, C_VAL_142	2.81	1.96	6.47
5JO5.PDB	O, C_SER_120	N, C_LYS_143	H, C_LYS_143	2.82	1.98	11.11
5JO5.PDB	OE2, D_GLU_124	NZ, C_LYS_143	HZ2, C_LYS_143	2.79	1.92	10.71
5JO5.PDB	O, C_TYR_176	N, C_TYR_145	H, C_TYR_145	2.94	2.13	17.07
5JO5.PDB	O, C_LYS_117	N, C_PHE_146	H, C_PHE_146	2.94	2.13	16.66
5JO5.PDB	OD1, C_ASN_197	OG, C_SER_153	HG, C_SER_153	2.81	2.01	15.61
5JO5.PDB	OG, C_SER_180	NE1, C_TRP_154	HE1, C_TRP_154	2.96	2.13	11.76
5JO5.PDB	O, C_ILE_195	N, C_ASN_155	H, C_ASN_155	2.75	1.92	12.18
5JO5.PDB	OD1, C_ASN_197	N, C_SER_156	H, C_SER_156	2.79	1.97	14.38
5JO5.PDB	O, C_VAL_181	N, C_HIS_164	H, C_HIS_164	2.89	2.06	13.61
5JO5.PDB	O, C_SER_179	N, C_PHE_166	H, C_PHE_166	2.91	2.06	6.29
5JO5.PDB	OD1, C_ASP_144	NE2, C_GLN_171	HE22, C_GLN_171	2.92	2.12	18.22
5JO5.PDB	O, C_GLN_171	N, C_GLY_174	H, C_GLY_174	2.78	1.92	5.07
5JO5.PDB	O, C_TYR_145	N, C_TYR_176	H, C_TYR_176	2.90	2.05	5.55
5JO5.PDB	O, C_VAL_142	N, C_LEU_178	H, C_LEU_178	2.87	2.09	20.32
5JO5.PDB	OH, D_TYR_177	OG, C_SER_179	HG, C_SER_179	2.71	1.97	23.23
5JO5.PDB	O, C_HIS_164	N, C_VAL_181	H, C_VAL_181	2.89	2.06	14.17
5JO5.PDB	O, C_LEU_138	N, C_VAL_182	H, C_VAL_182	2.77	1.94	12.20
5JO5.PDB	O, C_ALA_136	N, C_VAL_184	H, C_VAL_184	2.81	1.98	13.68
5JO5.PDB	O, C_GLY_134	N, C_SER_186	H, C_SER_186	2.64	1.80	9.61
5JO5.PDB	O, C_PRO_185	OG, C_SER_188	HG, C_SER_188	2.73	1.93	15.82
5JO5.PDB	OG, C_SER_188	OH, C_TYR_194	HH, C_TYR_194	2.62	1.86	20.70
5JO5.PDB	OD1, C_ASN_155	N, C_ILE_195	H, C_ILE_195	2.85	2.02	13.84
5JO5.PDB	O, C_LYS_209	N, C_CYS_196	H, C_CYS_196	2.96	2.18	21.34
5JO5.PDB	O, C_SER_153	N, C_ASN_197	H, C_ASN_197	2.74	1.89	6.97
5JO5.PDB	OD1, C_ASP_208	ND2, C_ASN_197	HD22, C_ASN_197	2.98	2.12	6.27
5JO5.PDB	O, C_VAL_207	N, C_VAL_198	H, C_VAL_198	2.78	1.92	1.89
5JO5.PDB	OG, C_SER_203	ND1, C_HIS_200	HD1, C_HIS_200	2.85	2.10	24.59
5JO5.PDB	O, C_PRO_147	NE2, C_HIS_200	HE2, C_HIS_200	2.76	1.92	8.00
5JO5.PDB	O, C_LYS_201	N, C_ASN_204	H, C_ASN_204	2.96	2.12	10.38
5JO5.PDB	O, C_SER_203	OG1, C_THR_205	HG1, C_THR_205	2.94	2.25	29.40
5JO5.PDB	O, C_VAL_198	N, C_VAL_207	H, C_VAL_207	2.82	2.00	14.71
5JO5.PDB	O, C_CYS_196	N, C_LYS_209	H, C_LYS_209	3.00	2.20	18.19
5JO5.PDB	OE2, D_GLU_123	NZ, C_LYS_209	HZ1, C_LYS_209	2.58	1.72	11.28
5JO5.PDB	O, C_TYR_194	N, C_VAL_211	H, C_VAL_211	2.92	2.08	10.11
5JO5.PDB	O, D_LEU_4	OG, D_SER_2	HG, D_SER_2	2.63	1.95	29.82
5JO5.PDB	O, D_GLN_24	N, D_THR_5	H, D_THR_5	2.84	2.03	16.14

5JO5.PDB	O, D_TYR_86	NE2, D_GLN_6	HE22, D_GLN_6	3.00	2.19	16.22
5JO5.PDB	O, D_LYS_103	N, D_VAL_11	H, D_VAL_11	2.98	2.16	13.76
5JO5.PDB	O, D_THR_105	N, D_VAL_13	H, D_VAL_13	2.89	2.13	23.23
5JO5.PDB	O, D_ALA_78	N, D_GLY_16	H, D_GLY_16	2.84	1.98	3.58
5JO5.PDB	O, D_ILE_75	N, D_VAL_19	H, D_VAL_19	2.97	2.17	17.08
5JO5.PDB	O, D_LEU_73	N, D_ILE_21	H, D_ILE_21	2.92	2.07	8.03
5JO5.PDB	O, D_ALA_71	N, D_CYS_23	H, D_CYS_23	2.70	1.92	20.84
5JO5.PDB	O, D_THR_5	N, D_GLN_24	H, D_GLN_24	2.92	2.17	25.43
5JO5.PDB	O, D_ASN_69	N, D_GLY_25	H, D_GLY_25	2.96	2.12	12.19
5JO5.PDB	O, D_ARG_91	OG, D_SER_27	HG, D_SER_27	2.66	1.91	22.45
5JO5.PDB	O, D_GLY_25	N, D_LEU_28	H, D_LEU_28	2.92	2.11	17.85
5JO5.PDB	O, D_SER_27	N, D_SER_30	H, D_SER_30	2.96	2.14	14.55
5JO5.PDB	O, D_SER_89	N, D_SER_34	H, D_SER_34	2.92	2.12	18.05
5JO5.PDB	O, D_ILE_48	N, D_TRP_35	H, D_TRP_35	2.78	1.99	19.58
5JO5.PDB	O, D_TYR_87	N, D_TYR_36	H, D_TYR_36	2.78	2.03	24.47
5JO5.PDB	OG, D_SER_34	OH, D_TYR_36	HH, D_TYR_36	2.76	2.07	29.85
5JO5.PDB	O, D_VAL_45	N, D_GLN_37	H, D_GLN_37	2.86	2.04	14.87
5JO5.PDB	OH, D_TYR_86	NE2, D_GLN_37	HE21, D_GLN_37	2.93	2.09	8.87
5JO5.PDB	O, D_ASP_85	N, D_GLN_38	H, D_GLN_38	2.81	2.02	20.05
5JO5.PDB	OE1, C_GLN_39	NE2, D_GLN_38	HE22, D_GLN_38	2.92	2.09	12.72
5JO5.PDB	O, D_GLN_37	N, D_VAL_45	H, D_VAL_45	2.80	2.03	21.65
5JO5.PDB	O, D_TRP_35	N, D_VAL_47	H, D_VAL_47	2.89	2.03	2.23
5JO5.PDB	O, D_ASN_53	N, D_TYR_49	H, D_TYR_49	2.99	2.18	15.70
5JO5.PDB	OD1, D_ASP_82	NH2, D_ARG_61	HH21, D_ARG_61	2.88	2.03	6.97
5JO5.PDB	O, D_THR_74	N, D_SER_63	H, D_SER_63	2.94	2.16	21.20
5JO5.PDB	OD1, D_ASN_52	N, D_GLY_64	H, D_GLY_64	2.96	2.14	14.40
5JO5.PDB	O, D_SER_72	N, D_SER_65	H, D_SER_65	2.95	2.18	22.43
5JO5.PDB	O, L_ARG_29	ND2, D_ASN_69	HD21, D_ASN_69	2.86	2.03	13.06
5JO5.PDB	O, D_SER_67	N, D_THR_70	H, D_THR_70	2.94	2.12	15.68
5JO5.PDB	O, D_SER_67	OG1, D_THR_70	HG1, D_THR_70	2.67	1.87	14.98
5JO5.PDB	O, D_CYS_23	N, D_ALA_71	H, D_ALA_71	2.75	1.94	16.72
5JO5.PDB	O, D_SER_65	N, D_SER_72	H, D_SER_72	2.85	2.02	12.10
5JO5.PDB	O, D_ILE_21	N, D_LEU_73	H, D_LEU_73	2.82	2.05	22.07
5JO5.PDB	O, D_SER_63	N, D_THR_74	H, D_THR_74	2.79	1.94	10.27
5JO5.PDB	O, D_VAL_19	N, D_ILE_75	H, D_ILE_75	2.89	2.06	12.55
5JO5.PDB	O, D_GLN_17	N, D_ALA_78	H, D_ALA_78	2.90	2.06	11.54
5JO5.PDB	OD2, D_ASP_82	N, D_GLN_79	H, D_GLN_79	2.86	2.00	5.70
5JO5.PDB	O, D_GLN_79	N, D_ASP_82	H, D_ASP_82	2.84	2.00	10.08
5JO5.PDB	O, D_GLN_38	N, D_ASP_85	H, D_ASP_85	2.92	2.10	13.46
5JO5.PDB	O, D_THR_102	N, D_TYR_86	H, D_TYR_86	2.83	2.01	15.81
5JO5.PDB	O, D_ASP_82	OH, D_TYR_86	HH, D_TYR_86	2.68	1.86	10.68
5JO5.PDB	O, D_TYR_36	N, D_TYR_87	H, D_TYR_87	2.93	2.13	17.76
5JO5.PDB	O, D_SER_34	N, D_SER_89	H, D_SER_89	2.89	2.16	27.05
5JO5.PDB	O, D_VAL_97	OG, D_SER_89	HG, D_SER_89	2.81	2.05	20.40
5JO5.PDB	OH, D_TYR_31	N, D_GLY_95	H, D_GLY_95	2.87	2.05	14.54
5JO5.PDB	OD1, D_ASP_92	OG, D_SER_95A	HG, D_SER_95A	2.53	1.74	15.88
5JO5.PDB	OD1, C_ASP_58	NE, D_ARG_95B	HE, D_ARG_95B	2.94	2.10	11.64
5JO5.PDB	OG, D_SER_95A	N, D_LEU_95C	H, D_LEU_95C	2.96	2.11	7.06
5JO5.PDB	O, D_SER_90	N, D_VAL_97	H, D_VAL_97	2.96	2.13	12.85
5JO5.PDB	O, D_CYS_88	N, D_GLY_99	H, D_GLY_99	2.87	2.08	18.28
5JO5.PDB	O, D_TYR_86	N, D_THR_102	H, D_THR_102	2.86	2.06	18.86
5JO5.PDB	O, D_ASP_7	OG1, D_THR_102	HG1, D_THR_102	2.66	1.83	6.75
5JO5.PDB	O, D_PRO_8	N, D_LYS_103	H, D_LYS_103	2.88	2.03	8.03
5JO5.PDB	O, D_ALA_84	N, D_LEU_104	H, D_LEU_104	2.86	2.02	9.74
5JO5.PDB	O, D_VAL_11	N, D_THR_105	H, D_THR_105	2.94	2.13	15.68
5JO5.PDB	OE2, D_GLU_83	N, D_VAL_106	H, D_VAL_106	2.99	2.26	27.16
5JO5.PDB	O, D_VAL_13	N, D_LEU_106A	H, D_LEU_106A	2.85	2.03	13.72
5JO5.PDB	OH, D_TYR_140	N, D_SER_107	H, D_SER_107	2.99	2.19	18.62

5JO5.PDB	O, D_TYR_140	N, D_ALA_111	H, D_ALA_111	2.83	2.00	12.24
5JO5.PDB	O, D_SER_137	N, D_SER_114	H, D_SER_114	2.93	2.12	17.17
5JO5.PDB	O, D_LEU_135	N, D_THR_116	H, D_THR_116	2.99	2.15	12.62
5JO5.PDB	O, D_VAL_133	N, D_PHE_118	H, D_PHE_118	2.76	1.91	6.01
5JO5.PDB	O, D_LEU_125	N, D_ASN_128	H, D_ASN_128	3.00	2.17	13.92
5JO5.PDB	OE1, D_GLU_124	N, D_THR_131	H, D_THR_131	2.94	2.20	26.30
5JO5.PDB	OE2, D_GLU_124	OG1, D_THR_131	HG1, D_THR_131	2.53	1.79	22.99
5JO5.PDB	O, D_LEU_178	N, D_LEU_132	H, D_LEU_132	2.92	2.11	16.22
5JO5.PDB	O, D_SER_176	N, D_CYS_134	H, D_CYS_134	2.87	2.02	3.73
5JO5.PDB	O, D_THR_116	N, D_LEU_135	H, D_LEU_135	2.89	2.05	10.60
5JO5.PDB	O, D_ALA_174	N, D_ILE_136	H, D_ILE_136	2.85	2.08	22.19
5JO5.PDB	O, D_SER_114	N, D_SER_137	H, D_SER_137	2.94	2.16	20.21
5JO5.PDB	OE1, D_GLN_167	N, D_ASP_138	H, D_ASP_138	2.90	2.13	21.66
5JO5.PDB	O, D_ALA_111	N, D_TYR_140	H, D_TYR_140	2.95	2.14	16.49
5JO5.PDB	O, D_PRO_141	N, D_ALA_143	H, D_ALA_143	2.91	2.20	29.22
5JO5.PDB	O, D_GLN_194	N, D_ALA_147	H, D_ALA_147	2.87	2.05	14.86
5JO5.PDB	OG, D_SER_176	NE1, D_TRP_148	HE1, D_TRP_148	2.85	2.01	9.98
5JO5.PDB	O, D_SER_153	N, D_ALA_150	H, D_ALA_150	2.82	2.02	17.16
5JO5.PDB	O, D_SER_190	N, D_ASP_151	H, D_ASP_151	2.91	2.08	10.80
5JO5.PDB	O, D_ALA_150	N, D_SER_153	H, D_SER_153	2.91	2.07	9.74
5JO5.PDB	O, D_TYR_177	N, D_GLU_160	H, D_GLU_160	2.99	2.19	18.70
5JO5.PDB	O, D_SER_175	N, D_THR_162	H, D_THR_162	2.86	2.03	12.76
5JO5.PDB	O, C_GLY_42	OG1, D_THR_163	HG1, D_THR_163	2.56	1.81	22.64
5JO5.PDB	O, D_LYS_171	N, D_GLN_167	H, D_GLN_167	2.61	1.77	8.91
5JO5.PDB	OD1, D_ASN_169	NE2, D_GLN_167	HE21, D_GLN_167	2.91	2.12	19.40
5JO5.PDB	OD1, D_ASP_138	NE2, D_GLN_167	HE22, D_GLN_167	2.88	2.03	6.31
5JO5.PDB	O, D_GLN_167	N, D_ASN_170	H, D_ASN_170	2.90	2.07	12.77
5JO5.PDB	O, D_PHE_139	N, D_TYR_172	H, D_TYR_172	2.94	2.13	17.51
5JO5.PDB	O, D_ILE_136	N, D_ALA_174	H, D_ALA_174	2.70	1.89	16.69
5JO5.PDB	OG1, D_THR_162	N, D_SER_175	H, D_SER_175	2.99	2.19	18.15
5JO5.PDB	O, D_CYS_134	N, D_SER_176	H, D_SER_176	2.88	2.10	20.17
5JO5.PDB	OG1, D_THR_161	OG, D_SER_176	HG, D_SER_176	2.78	2.01	20.04
5JO5.PDB	O, D_GLU_160	N, D_TYR_177	H, D_TYR_177	2.73	1.94	18.28
5JO5.PDB	O, D_LEU_132	N, D_LEU_178	H, D_LEU_178	3.00	2.17	13.80
5JO5.PDB	O, D_GLY_158	N, D_SER_179	H, D_SER_179	2.79	1.96	12.81
5JO5.PDB	O, D_ALA_130	N, D_LEU_180	H, D_LEU_180	2.83	1.97	3.34
5JO5.PDB	OD2, D_ASP_151	ND1, D_HIS_188	HD1, D_HIS_188	2.67	1.86	16.19
5JO5.PDB	O, D_VAL_206	N, D_TYR_191	H, D_TYR_191	2.99	2.16	11.55
5JO5.PDB	O, D_GLN_184	OH, D_TYR_191	HH, D_TYR_191	2.98	2.21	19.53
5JO5.PDB	O, D_LYS_149	N, D_SER_192	H, D_SER_192	2.91	2.12	19.04
5JO5.PDB	OG1, D_THR_205	OG, D_SER_192	HG, D_SER_192	2.76	2.06	27.74
5JO5.PDB	O, D_LYS_204	N, D_CYS_193	H, D_CYS_193	2.83	2.03	16.94
5JO5.PDB	O, D_ALA_147	N, D_GLN_194	H, D_GLN_194	2.79	1.95	9.12
5JO5.PDB	OE2, D_GLU_203	NE2, D_GLN_194	HE21, D_GLN_194	2.41	1.67	25.54
5JO5.PDB	O, D_VAL_202	N, D_VAL_195	H, D_VAL_195	2.84	2.00	11.51
5JO5.PDB	O, D_THR_145	N, D_THR_196	H, D_THR_196	2.90	2.05	9.26
5JO5.PDB	O, D_SER_200	N, D_HIS_197	H, D_HIS_197	2.74	1.91	13.29
5JO5.PDB	O, D_PRO_141	NE2, D_HIS_197	HE2, D_HIS_197	2.94	2.17	22.03
5JO5.PDB	O, D_HIS_197	N, D_SER_200	H, D_SER_200	2.99	2.14	6.86
5JO5.PDB	O, D_VAL_195	N, D_VAL_202	H, D_VAL_202	2.92	2.09	14.26
5JO5.PDB	O, D_TYR_191	N, D_VAL_206	H, D_VAL_206	2.89	2.07	14.82
5JO5.PDB	O, E_SER_25	N, E_GLN_3	H, E_GLN_3	2.86	2.02	10.81
5JO5.PDB	O, E_SER_21	N, E_SER_7	H, E_SER_7	2.79	2.01	21.43
5JO5.PDB	OG1, E_THR_107	N, E_GLY_9	H, E_GLY_9	2.94	2.20	26.14
5JO5.PDB	O, E_THR_110	N, E_VAL_12	H, E_VAL_12	2.91	2.13	20.76
5JO5.PDB	O, E_LEU_82C	N, E_GLY_15	H, E_GLY_15	2.84	2.01	12.49
5JO5.PDB	O, E_LYS_13	N, E_GLY_16	H, E_GLY_16	2.85	2.02	13.81
5JO5.PDB	O, E_MET_82	N, E_LEU_18	H, E_LEU_18	2.89	2.11	20.71

5JO5.PDB	O, E_LEU_80	N, E_LEU_20	H, E_LEU_20	2.82	1.97	8.28
5JO5.PDB	O, E_SER_7	N, E_SER_21	H, E_SER_21	2.95	2.12	12.48
5JO5.PDB	O, E_LEU_78	N, E_CYS_22	H, E_CYS_22	2.73	1.97	22.79
5JO5.PDB	O, E_ASN_76	N, E_ALA_24	H, E_ALA_24	2.94	2.16	21.70
5JO5.PDB	O, E_GLN_3	N, E_SER_25	H, E_SER_25	2.98	2.18	19.36
5JO5.PDB	OD2, E_ASP_53	NE1, E_TRP_33	HE1, E_TRP_33	2.89	2.14	24.08
5JO5.PDB	O, E_ALA_93	N, E_SER_35	H, E_SER_35	2.93	2.11	14.57
5JO5.PDB	OG1, E_THR_95	OG, E_SER_35	HG, E_SER_35	2.65	1.97	29.96
5JO5.PDB	O, E_GLY_49	N, E_TRP_36	H, E_TRP_36	2.88	2.07	17.60
5JO5.PDB	O, E_TYR_91	N, E_VAL_37	H, E_VAL_37	2.87	2.04	13.44
5JO5.PDB	O, E_GLU_46	N, E_ARG_38	H, E_ARG_38	2.86	2.02	8.76
5JO5.PDB	OE1, E_GLU_46	NE, E_ARG_38	HE, E_ARG_38	2.75	1.95	17.65
5JO5.PDB	OH, E_TYR_90	NH1, E_ARG_38	HH11, E_ARG_38	2.94	2.11	14.05
5JO5.PDB	OD1, E_ASP_86	NH1, E_ARG_38	HH12, E_ARG_38	2.82	2.00	15.16
5JO5.PDB	O, E_LYS_43	NE2, E_GLN_39	HE21, E_GLN_39	2.97	2.27	29.74
5JO5.PDB	OE1, F_GLN_38	NE2, E_GLN_39	HE22, E_GLN_39	2.90	2.06	10.70
5JO5.PDB	O, E_ALA_40	N, E_LYS_43	H, E_LYS_43	2.91	2.07	11.48
5JO5.PDB	O, E_ARG_38	N, E_GLU_46	H, E_GLU_46	2.82	2.03	20.58
5JO5.PDB	O, E_TRP_36	N, E_VAL_48	H, E_VAL_48	2.91	2.08	12.92
5JO5.PDB	OE1, E_GLU_100J	NE, E_ARG_50	HE, E_ARG_50	2.82	2.06	22.79
5JO5.PDB	OD2, E_ASP_58	NH1, E_ARG_50	HH12, E_ARG_50	2.78	1.94	10.17
5JO5.PDB	OE2, E_GLU_100J	NH2, E_ARG_50	HH21, E_ARG_50	2.98	2.13	7.82
5JO5.PDB	O, E_MET_34	N, E_ILE_51	H, E_ILE_51	2.82	1.99	12.16
5JO5.PDB	O, E_THR_56	N, E_LYS_52	H, E_LYS_52	2.88	2.06	15.44
5JO5.PDB	O, E_SER_52A	N, E_GLY_55	H, E_GLY_55	2.77	2.05	28.25
5JO5.PDB	O, E_VAL_48	N, E_ALA_60	H, E_ALA_60	2.92	2.07	6.71
5JO5.PDB	O, E_VAL_63	N, E_ARG_66	H, E_ARG_66	2.94	2.10	9.43
5JO5.PDB	OD2, E_ASP_86	NH1, E_ARG_66	HH12, E_ARG_66	2.75	1.91	9.04
5JO5.PDB	O, E_PRO_62	NH2, E_ARG_66	HH21, E_ARG_66	2.89	2.04	7.82
5JO5.PDB	O, E_GLN_81	N, E_THR_68	H, E_THR_68	2.78	1.96	15.96
5JO5.PDB	OH, E_TYR_59	N, E_ILE_69	H, E_ILE_69	2.86	2.02	8.94
5JO5.PDB	OD1, E_ASP_73	NE, E_ARG_71	HE, E_ARG_71	2.89	2.11	20.53
5JO5.PDB	O, E_ALA_32	NH1, E_ARG_71	HH12, E_ARG_71	2.87	2.12	24.62
5JO5.PDB	O, E_ALA_32	NH2, E_ARG_71	HH22, E_ARG_71	2.83	2.06	22.60
5JO5.PDB	O, E_THR_77	N, E_ASP_72	H, E_ASP_72	2.94	2.10	9.13
5JO5.PDB	OD1, E_ASP_72	OG, E_SER_74	HG, E_SER_74	2.60	1.77	6.90
5JO5.PDB	O, E_ASP_72	N, E_LYS_75	H, E_LYS_75	2.92	2.11	15.84
5JO5.PDB	O, E_LYS_75	OG1, E_THR_77	HG1, E_THR_77	2.87	2.06	11.81
5JO5.PDB	O, E_CYS_22	N, E_LEU_78	H, E_LEU_78	2.84	2.01	12.18
5JO5.PDB	O, E_SER_70	N, E_TYR_79	H, E_TYR_79	2.79	1.96	14.25
5JO5.PDB	O, E_LEU_20	N, E_LEU_80	H, E_LEU_80	2.96	2.14	14.05
5JO5.PDB	O, E_THR_68	N, E_GLN_81	H, E_GLN_81	2.80	1.97	12.32
5JO5.PDB	O, E_LEU_18	N, E_MET_82	H, E_MET_82	2.73	1.87	5.04
5JO5.PDB	O, E_ARG_66	N, E_ASN_82A	H, E_ASN_82A	2.93	2.10	12.92
5JO5.PDB	OD2, E_ASP_86	N, E_LYS_83	H, E_LYS_83	2.87	2.04	12.63
5JO5.PDB	O, E_LYS_83	N, E_ASP_86	H, E_ASP_86	2.88	2.03	9.99
5JO5.PDB	O, E_VAL_109	N, E_ALA_88	H, E_ALA_88	3.00	2.22	22.40
5JO5.PDB	O, E_GLN_39	N, E_VAL_89	H, E_VAL_89	2.94	2.14	17.80
5JO5.PDB	O, E_THR_107	N, E_TYR_90	H, E_TYR_90	2.81	1.97	10.34
5JO5.PDB	O, E_ASP_86	OH, E_TYR_90	HH, E_TYR_90	2.76	1.94	9.78
5JO5.PDB	O, E_VAL_37	N, E_TYR_91	H, E_TYR_91	2.62	1.76	3.70
5JO5.PDB	OE2, E_GLU_6	N, E_CYS_92	H, E_CYS_92	2.83	2.01	14.83
5JO5.PDB	O, E_SER_35	N, E_ALA_93	H, E_ALA_93	2.90	2.13	22.60
5JO5.PDB	OD2, E_ASP_102	NE, E_ARG_94	HE, E_ARG_94	2.83	2.08	25.07
5JO5.PDB	OD2, E_ASP_102	NH2, E_ARG_94	HH21, E_ARG_94	2.73	1.97	23.25
5JO5.PDB	O, E_TRP_33	N, E_THR_95	H, E_THR_95	2.81	1.99	14.28
5JO5.PDB	O, E_TYR_100K	N, E_GLY_96	H, E_GLY_96	2.75	2.03	27.94
5JO5.PDB	O, E_GLY_96	N, E_TYR_100K	H, E_TYR_100K	2.92	2.10	14.59

5JO5.PDB	OH, F_TYR_36	N, E_PHE_100L	H, E_PHE_100L	2.79	1.96	13.04
5JO5.PDB	O, E_ARG_94	N, E_GLN_101	H, E_GLN_101	2.75	2.03	27.51
5JO5.PDB	O, F_GLY_41	NH2, E_ARG_105	HH22, E_ARG_105	2.92	2.13	19.96
5JO5.PDB	OE1, E_GLU_6	N, E_GLY_106	H, E_GLY_106	2.88	2.02	0.89
5JO5.PDB	O, E_ALA_88	N, E_VAL_109	H, E_VAL_109	2.88	2.03	1.87
5JO5.PDB	OG1, E_THR_87	N, E_VAL_111	H, E_VAL_111	2.92	2.06	5.86
5JO5.PDB	O, E_VAL_12	N, E_SER_112	H, E_SER_112	2.97	2.21	23.58
5JO5.PDB	O, E_PHE_146	N, E_LYS_117	H, E_LYS_117	2.75	1.93	13.93
5JO5.PDB	O, E_ASP_144	NZ, E_LYS_117	HZ2, E_LYS_117	2.91	2.14	25.25
5JO5.PDB	O, E_LEU_141	N, E_PHE_122	H, E_PHE_122	2.90	2.08	14.62
5JO5.PDB	O, E_GLY_139	N, E_LEU_124	H, E_LEU_124	2.87	2.02	7.60
5JO5.PDB	O, E_VAL_184	N, E_ALA_136	H, E_ALA_136	2.71	1.90	16.68
5JO5.PDB	O, E_LEU_124	N, E_GLY_139	H, E_GLY_139	2.98	2.20	21.04
5JO5.PDB	O, E_SER_180	N, E_CYS_140	H, E_CYS_140	2.80	2.01	20.63
5JO5.PDB	O, E_PHE_122	N, E_LEU_141	H, E_LEU_141	2.82	1.97	5.54
5JO5.PDB	O, E_LEU_178	N, E_VAL_142	H, E_VAL_142	2.80	1.95	6.99
5JO5.PDB	O, E_SER_120	N, E_LYS_143	H, E_LYS_143	2.77	1.93	10.34
5JO5.PDB	OE2, F_GLU_124	NZ, E_LYS_143	HZ2, E_LYS_143	2.55	1.75	21.57
5JO5.PDB	O, E_TYR_176	N, E_TYR_145	H, E_TYR_145	2.90	2.11	20.23
5JO5.PDB	O, E_LYS_117	N, E_PHE_146	H, E_PHE_146	2.89	2.08	16.85
5JO5.PDB	O, E_ASN_197	N, E_SER_153	H, E_SER_153	2.97	2.16	17.92
5JO5.PDB	OD1, E_ASN_197	OG, E_SER_153	HG, E_SER_153	2.80	2.02	18.49
5JO5.PDB	OG, E_SER_180	NE1, E_TRP_154	HE1, E_TRP_154	2.96	2.13	12.27
5JO5.PDB	O, E_ILE_195	N, E_ASN_155	H, E_ASN_155	2.72	1.89	11.94
5JO5.PDB	OD1, E_ASN_197	N, E_SER_156	H, E_SER_156	2.66	1.84	15.32
5JO5.PDB	O, E_VAL_181	N, E_HIS_164	H, E_HIS_164	2.85	2.02	11.29
5JO5.PDB	O, E_SER_179	N, E_PHE_166	H, E_PHE_166	2.89	2.04	5.07
5JO5.PDB	O, E_SER_177	N, E_VAL_169	H, E_VAL_169	2.81	2.02	19.59
5JO5.PDB	OD1, E_ASP_144	NE2, E_GLN_171	HE22, E_GLN_171	2.83	2.02	16.42
5JO5.PDB	O, E_GLN_171	N, E_GLY_174	H, E_GLY_174	2.76	1.91	5.26
5JO5.PDB	O, E_TYR_145	N, E_TYR_176	H, E_TYR_176	2.86	2.00	3.93
5JO5.PDB	O, E_VAL_142	N, E_LEU_178	H, E_LEU_178	2.85	2.07	21.31
5JO5.PDB	OH, F_TYR_177	OG, E_SER_179	HG, E_SER_179	2.58	1.87	27.02
5JO5.PDB	O, E_CYS_140	N, E_SER_180	H, E_SER_180	2.98	2.17	15.74
5JO5.PDB	O, E_HIS_164	N, E_VAL_181	H, E_VAL_181	2.86	2.02	9.16
5JO5.PDB	O, E_LEU_138	N, E_VAL_182	H, E_VAL_182	2.76	1.93	11.92
5JO5.PDB	O, E_ALA_136	N, E_VAL_184	H, E_VAL_184	2.83	2.00	12.03
5JO5.PDB	O, E_GLY_134	N, E_SER_186	H, E_SER_186	2.88	2.03	8.01
5JO5.PDB	O, E_GLY_133	OG, E_SER_186	HG, E_SER_186	2.97	2.22	21.72
5JO5.PDB	O, E_PRO_185	N, E_SER_188	H, E_SER_188	2.97	2.20	23.16
5JO5.PDB	O, E_PRO_185	OG, E_SER_188	HG, E_SER_188	2.59	1.76	5.13
5JO5.PDB	O, E_SER_188	N, E_THR_191	H, E_THR_191	2.90	2.15	24.49
5JO5.PDB	O, E_SER_188	N, E_GLN_192	H, E_GLN_192	2.68	1.83	7.38
5JO5.PDB	OG, E_SER_188	OH, E_TYR_194	HH, E_TYR_194	2.65	1.91	23.44
5JO5.PDB	OD1, E_ASN_155	N, E_ILE_195	H, E_ILE_195	2.79	1.96	12.66
5JO5.PDB	O, E_LYS_209	N, E_CYS_196	H, E_CYS_196	2.95	2.16	19.80
5JO5.PDB	O, E_SER_153	N, E_ASN_197	H, E_ASN_197	2.69	1.84	6.11
5JO5.PDB	OD1, E_ASP_208	ND2, E_ASN_197	HD22, E_ASN_197	2.93	2.08	6.74
5JO5.PDB	O, E_VAL_207	N, E_VAL_198	H, E_VAL_198	2.75	1.89	4.70
5JO5.PDB	O, E_THR_151	N, E_ASN_199	H, E_ASN_199	2.87	2.02	5.85
5JO5.PDB	O, E_THR_205	N, E_HIS_200	H, E_HIS_200	2.87	2.01	4.48
5JO5.PDB	O, E_PRO_147	NE2, E_HIS_200	HE2, E_HIS_200	2.80	1.96	10.29
5JO5.PDB	O, E_LYS_201	N, E_ASN_204	H, E_ASN_204	2.97	2.13	10.21
5JO5.PDB	O, E_SER_203	OG1, E_THR_205	HG1, E_THR_205	2.99	2.30	29.09
5JO5.PDB	O, E_VAL_198	N, E_VAL_207	H, E_VAL_207	2.77	1.95	14.33
5JO5.PDB	OE2, F_GLU_123	NZ, E_LYS_209	HZ1, E_LYS_209	2.57	1.74	17.62
5JO5.PDB	O, E_TYR_194	N, E_VAL_211	H, E_VAL_211	2.91	2.07	9.99
5JO5.PDB	O, F_GLN_24	N, F_THR_5	H, F_THR_5	2.85	2.04	16.07

5JO5.PDB	O, F_TYR_86	NE2, F_GLN_6	HE22, F_GLN_6	2.95	2.11	10.68
5JO5.PDB	O, F_LYS_103	N, F_VAL_11	H, F_VAL_11	2.95	2.12	12.95
5JO5.PDB	O, F_THR_105	N, F_VAL_13	H, F_VAL_13	2.93	2.19	26.75
5JO5.PDB	O, F_ALA_78	N, F_GLY_16	H, F_GLY_16	2.88	2.02	3.27
5JO5.PDB	O, F_ALA_14	N, F_GLN_17	H, F_GLN_17	2.98	2.13	8.18
5JO5.PDB	O, F_ILE_75	N, F_VAL_19	H, F_VAL_19	2.97	2.17	17.62
5JO5.PDB	O, F_LEU_73	N, F_ILE_21	H, F_ILE_21	2.79	1.95	9.82
5JO5.PDB	O, F_ALA_71	N, F_CYS_23	H, F_CYS_23	2.65	1.81	10.82
5JO5.PDB	O, F_THR_5	N, F_GLN_24	H, F_GLN_24	2.96	2.22	25.96
5JO5.PDB	O, F_ASN_69	N, F_GLY_25	H, F_GLY_25	2.99	2.16	12.96
5JO5.PDB	O, F_ARG_91	OG, F_SER_27	HG, F_SER_27	2.61	1.83	18.13
5JO5.PDB	O, F_SER_27	N, F_SER_30	H, F_SER_30	2.99	2.17	15.08
5JO5.PDB	OE1, B_GLN_24	OG, F_SER_30	HG, F_SER_30	2.88	2.11	20.15
5JO5.PDB	O, F_SER_89	N, F_SER_34	H, F_SER_34	2.96	2.19	21.82
5JO5.PDB	O, F_ILE_48	N, F_TRP_35	H, F_TRP_35	2.86	2.07	19.30
5JO5.PDB	O, F_TYR_87	N, F_TYR_36	H, F_TYR_36	2.85	2.11	26.39
5JO5.PDB	O, F_VAL_45	N, F_GLN_37	H, F_GLN_37	2.90	2.07	14.11
5JO5.PDB	OH, F_TYR_86	NE2, F_GLN_37	HE21, F_GLN_37	2.98	2.12	5.01
5JO5.PDB	O, F_ASP_85	N, F_GLN_38	H, F_GLN_38	2.82	2.06	22.85
5JO5.PDB	OE1, E_GLN_39	NE2, F_GLN_38	HE22, F_GLN_38	2.85	2.02	12.75
5JO5.PDB	O, F_GLN_37	N, F_VAL_45	H, F_VAL_45	2.82	2.05	21.93
5JO5.PDB	OD2, F_ASP_82	NE, F_ARG_61	HE, F_ARG_61	2.99	2.15	12.18
5JO5.PDB	OD1, F_ASP_82	NH2, F_ARG_61	HH21, F_ARG_61	2.81	1.97	11.97
5JO5.PDB	O, F_THR_74	N, F_SER_63	H, F_SER_63	2.98	2.21	22.42
5JO5.PDB	OD1, F_ASN_52	N, F_GLY_64	H, F_GLY_64	2.75	1.92	12.61
5JO5.PDB	O, F_SER_72	N, F_SER_65	H, F_SER_65	2.99	2.19	19.46
5JO5.PDB	O, F_THR_70	N, F_SER_67	H, F_SER_67	2.97	2.14	12.81
5JO5.PDB	O, F_SER_67	N, F_THR_70	H, F_THR_70	2.94	2.14	18.28
5JO5.PDB	O, F_SER_67	OG1, F_THR_70	HG1, F_THR_70	2.69	1.87	11.09
5JO5.PDB	O, F_CYS_23	N, F_ALA_71	H, F_ALA_71	2.78	1.96	15.69
5JO5.PDB	O, F_SER_65	N, F_SER_72	H, F_SER_72	2.89	2.05	10.31
5JO5.PDB	O, F_ILE_21	N, F_LEU_73	H, F_LEU_73	2.79	1.97	15.26
5JO5.PDB	O, F_SER_63	N, F_THR_74	H, F_THR_74	2.85	2.00	6.83
5JO5.PDB	O, F_VAL_19	N, F_ILE_75	H, F_ILE_75	2.91	2.08	12.77
5JO5.PDB	O, F_GLN_17	N, F_ALA_78	H, F_ALA_78	2.92	2.08	9.70
5JO5.PDB	OD2, F_ASP_82	N, F_GLN_79	H, F_GLN_79	2.94	2.10	8.41
5JO5.PDB	O, F_GLN_79	N, F_ASP_82	H, F_ASP_82	2.82	1.98	9.27
5JO5.PDB	O, F_GLN_38	N, F_ASP_85	H, F_ASP_85	2.86	2.02	11.88
5JO5.PDB	O, F_THR_102	N, F_TYR_86	H, F_TYR_86	2.82	2.01	15.14
5JO5.PDB	O, F_ASP_82	OH, F_TYR_86	HH, F_TYR_86	2.63	1.82	11.29
5JO5.PDB	O, F_TYR_36	N, F_TYR_87	H, F_TYR_87	2.95	2.15	18.80
5JO5.PDB	O, F_SER_34	N, F_SER_89	H, F_SER_89	2.90	2.17	27.32
5JO5.PDB	O, F_VAL_97	OG, F_SER_89	HG, F_SER_89	2.78	2.02	20.17
5JO5.PDB	OE2, E_GLU_100J	NH2, F_ARG_91	HH22, F_ARG_91	2.72	1.87	5.99
5JO5.PDB	OH, F_TYR_31	N, F_GLY_95	H, F_GLY_95	2.74	1.89	6.32
5JO5.PDB	OD1, F_ASP_92	OG, F_SER_95A	HG, F_SER_95A	2.58	1.83	23.06
5JO5.PDB	OD1, E_ASP_58	NE, F_ARG_95B	HE, F_ARG_95B	2.92	2.09	12.47
5JO5.PDB	OG, F_SER_95A	N, F_LEU_95C	H, F_LEU_95C	2.90	2.05	9.93
5JO5.PDB	O, F_SER_90	N, F_VAL_97	H, F_VAL_97	2.91	2.09	15.13
5JO5.PDB	O, F_CYS_88	N, F_GLY_99	H, F_GLY_99	2.87	2.06	15.92
5JO5.PDB	OE1, F_GLN_6	N, F_GLY_101	H, F_GLY_101	2.94	2.16	20.91
5JO5.PDB	O, F_TYR_86	N, F_THR_102	H, F_THR_102	2.82	2.02	18.81
5JO5.PDB	O, F_ASP_7	OG1, F_THR_102	HG1, F_THR_102	2.62	1.78	2.80
5JO5.PDB	O, F_PRO_8	N, F_LYS_103	H, F_LYS_103	2.89	2.04	8.00
5JO5.PDB	O, F_ALA_84	N, F_LEU_104	H, F_LEU_104	2.87	2.02	9.37
5JO5.PDB	O, F_VAL_11	N, F_THR_105	H, F_THR_105	2.99	2.16	14.54
5JO5.PDB	OE2, F_GLU_83	N, F_VAL_106	H, F_VAL_106	3.00	2.24	24.21
5JO5.PDB	O, F_VAL_13	N, F_LEU_106A	H, F_LEU_106A	2.87	2.04	14.03

5JO5.PDB	OH, F_TYR_140	N, F_SER_107	H, F_SER_107	2.93	2.11	14.82
5JO5.PDB	OE1, F_GLU_198	NZ, F_LYS_110	HZ3, F_LYS_110	2.97	2.11	10.79
5JO5.PDB	O, F_TYR_140	N, F_ALA_111	H, F_ALA_111	2.81	1.99	13.38
5JO5.PDB	O, F_SER_137	N, F_SER_114	H, F_SER_114	2.87	2.06	17.12
5JO5.PDB	O, F_LEU_135	N, F_THR_116	H, F_THR_116	2.97	2.14	11.95
5JO5.PDB	O, F_VAL_133	N, F_PHE_118	H, F_PHE_118	2.79	1.95	9.20
5JO5.PDB	O, F_LEU_125	N, F_ASN_128	H, F_ASN_128	2.88	2.07	17.11
5JO5.PDB	OE1, F_GLU_124	N, F_THR_131	H, F_THR_131	2.94	2.22	28.54
5JO5.PDB	OE2, F_GLU_124	OG1, F_THR_131	HG1, F_THR_131	2.49	1.76	24.10
5JO5.PDB	O, F_LEU_178	N, F_LEU_132	H, F_LEU_132	2.91	2.08	13.23
5JO5.PDB	O, F_SER_176	N, F_CYS_134	H, F_CYS_134	2.83	1.97	3.69
5JO5.PDB	O, F_THR_116	N, F_LEU_135	H, F_LEU_135	2.88	2.04	11.11
5JO5.PDB	O, F_ALA_174	N, F_ILE_136	H, F_ILE_136	2.89	2.10	19.87
5JO5.PDB	O, F_SER_114	N, F_SER_137	H, F_SER_137	2.91	2.12	19.22
5JO5.PDB	OE1, F_GLN_167	N, F_ASP_138	H, F_ASP_138	2.81	2.05	22.81
5JO5.PDB	O, F_PRO_141	N, F_ALA_143	H, F_ALA_143	2.90	2.19	29.08
5JO5.PDB	O, F_GLN_194	N, F_ALA_147	H, F_ALA_147	2.81	1.99	13.22
5JO5.PDB	OG, F_SER_176	NE1, F_TRP_148	HE1, F_TRP_148	2.88	2.03	9.94
5JO5.PDB	O, F_SER_192	N, F_LYS_149	H, F_LYS_149	2.88	2.06	15.62
5JO5.PDB	O, F_SER_153	N, F_ALA_150	H, F_ALA_150	2.80	1.99	15.96
5JO5.PDB	O, F_SER_190	N, F_ASP_151	H, F_ASP_151	2.90	2.06	10.54
5JO5.PDB	O, F_TRP_148	N, F_VAL_155	H, F_VAL_155	2.94	2.14	18.31
5JO5.PDB	O, F_TYR_177	N, F_GLU_160	H, F_GLU_160	2.97	2.17	17.39
5JO5.PDB	O, F_SER_175	N, F_THR_162	H, F_THR_162	2.87	2.04	13.17
5JO5.PDB	O, E_GLY_42	OG1, F_THR_163	HG1, F_THR_163	2.55	1.80	22.10
5JO5.PDB	O, F_ALA_173	N, F_SER_165	H, F_SER_165	2.89	2.07	14.19
5JO5.PDB	O, F_LYS_171	N, F_GLN_167	H, F_GLN_167	2.66	1.81	8.80
5JO5.PDB	OD1, F_ASN_169	NE2, F_GLN_167	HE21, F_GLN_167	2.87	2.13	25.80
5JO5.PDB	OD1, F_ASP_138	NE2, F_GLN_167	HE22, F_GLN_167	2.86	2.01	8.07
5JO5.PDB	OD1, F_ASN_169	N, F_LYS_171	H, F_LYS_171	2.94	2.09	6.57
5JO5.PDB	O, F_PHE_139	N, F_TYR_172	H, F_TYR_172	2.89	2.07	14.51
5JO5.PDB	O, F_SER_165	N, F_ALA_173	H, F_ALA_173	2.87	2.08	18.80
5JO5.PDB	O, F_ILE_136	N, F_ALA_174	H, F_ALA_174	2.75	1.95	16.67
5JO5.PDB	O, F_CYS_134	N, F_SER_176	H, F_SER_176	2.88	2.10	19.67
5JO5.PDB	OG1, F_THR_161	OG, F_SER_176	HG, F_SER_176	2.84	2.06	17.97
5JO5.PDB	O, F_GLU_160	N, F_TYR_177	H, F_TYR_177	2.70	1.88	14.68
5JO5.PDB	O, F_LEU_132	N, F_LEU_178	H, F_LEU_178	2.95	2.12	12.77
5JO5.PDB	O, F_GLY_158	N, F_SER_179	H, F_SER_179	2.85	2.02	11.91
5JO5.PDB	O, F_ALA_130	N, F_LEU_180	H, F_LEU_180	2.77	1.91	5.50
5JO5.PDB	OE1, F_GLN_184	N, F_THR_181	H, F_THR_181	2.91	2.08	13.75
5JO5.PDB	OG1, F_THR_181	N, F_GLN_184	H, F_GLN_184	2.92	2.09	12.10
5JO5.PDB	O, F_THR_181	N, F_TRP_185	H, F_TRP_185	2.95	2.13	14.97
5JO5.PDB	O, F_GLN_184	OG, F_SER_187	HG, F_SER_187	2.92	2.14	19.66
5JO5.PDB	OD1, F_ASP_151	N, F_ARG_189	H, F_ARG_189	2.70	1.97	26.16
5JO5.PDB	O, F_VAL_206	N, F_TYR_191	H, F_TYR_191	2.98	2.14	9.84
5JO5.PDB	O, F_GLN_184	OH, F_TYR_191	HH, F_TYR_191	2.85	2.14	27.44
5JO5.PDB	O, F_LYS_149	N, F_SER_192	H, F_SER_192	2.93	2.14	18.88
5JO5.PDB	O, F_LYS_204	N, F_CYS_193	H, F_CYS_193	2.94	2.14	19.38
5JO5.PDB	O, F_ALA_147	N, F_GLN_194	H, F_GLN_194	2.69	1.84	5.08
5JO5.PDB	OE2, F_GLU_203	NE2, F_GLN_194	HE21, F_GLN_194	2.48	1.75	26.23
5JO5.PDB	O, F_VAL_202	N, F_VAL_195	H, F_VAL_195	2.88	2.05	13.06
5JO5.PDB	O, F_THR_145	N, F_THR_196	H, F_THR_196	2.95	2.10	7.48
5JO5.PDB	O, F_SER_200	N, F_HIS_197	H, F_HIS_197	2.74	1.91	11.69
5JO5.PDB	O, F_PRO_141	NE2, F_HIS_197	HE2, F_HIS_197	2.87	2.10	22.42
5JO5.PDB	O, F_HIS_197	N, F_SER_200	H, F_SER_200	2.97	2.13	8.27
5JO5.PDB	O, F_VAL_195	N, F_VAL_202	H, F_VAL_202	2.91	2.07	12.06
5JO5.PDB	O, F_TYR_191	N, F_VAL_206	H, F_VAL_206	2.91	2.09	15.37
5JR1.PDB	O, H_SER_21	N, H_SER_7	H, H_SER_7	2.87	2.09	21.13

5JR1.PDB	O, H_THR_110	N, H_VAL_12	H, H_VAL_12	2.96	2.15	17.17
5JR1.PDB	O, H_LEU_82C	N, H_GLY_15	H, H_GLY_15	2.79	1.94	9.64
5JR1.PDB	O, H_LYS_13	N, H_GLY_16	H, H_GLY_16	2.88	2.07	16.51
5JR1.PDB	O, H_MET_82	N, H_LEU_18	H, H_LEU_18	2.78	2.00	19.93
5JR1.PDB	O, H_LEU_80	N, H_LEU_20	H, H_LEU_20	2.79	1.95	10.03
5JR1.PDB	O, H_LEU_78	N, H_CYS_22	H, H_CYS_22	2.73	2.00	26.48
5JR1.PDB	O, H_ASN_76	N, H_ALA_24	H, H_ALA_24	2.94	2.10	11.00
5JR1.PDB	O, H_PHE_29	N, H_ALA_32	H, H_ALA_32	2.90	2.05	7.28
5JR1.PDB	O, H_ALA_93	N, H_SER_35	H, H_SER_35	2.81	1.99	14.30
5JR1.PDB	O, H_GLY_49	N, H_TRP_36	H, H_TRP_36	2.95	2.15	18.51
5JR1.PDB	O, H_TYR_91	N, H_VAL_37	H, H_VAL_37	2.90	2.08	14.88
5JR1.PDB	O, H_GLU_46	N, H_ARG_38	H, H_ARG_38	2.79	1.96	12.39
5JR1.PDB	OE2, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.66	1.91	24.18
5JR1.PDB	OH, H_TYR_90	NH1, H_ARG_38	HH11, H_ARG_38	2.93	2.12	16.05
5JR1.PDB	OD1, H_ASP_86	NH1, H_ARG_38	HH12, H_ARG_38	2.94	2.11	12.77
5JR1.PDB	OE2, H_GLU_46	NH2, H_ARG_38	HH21, H_ARG_38	2.68	1.95	27.48
5JR1.PDB	O, H_VAL_89	N, H_GLN_39	H, H_GLN_39	2.80	2.04	23.21
5JR1.PDB	O, H_ALA_40	N, H_LYS_43	H, H_LYS_43	2.97	2.14	12.77
5JR1.PDB	O, H_TRP_36	N, H_VAL_48	H, H_VAL_48	2.78	1.94	10.30
5JR1.PDB	O, H_ASP_58	N, H_ARG_50	H, H_ARG_50	2.97	2.19	21.36
5JR1.PDB	O, H_MET_34	N, H_ILE_51	H, H_ILE_51	2.89	2.08	16.37
5JR1.PDB	O, H_THR_56	N, H_LYS_52	H, H_LYS_52	2.98	2.15	12.98
5JR1.PDB	OD1, H_ASP_53	N, H_GLY_54	H, H_GLY_54	2.21	1.48	25.64
5JR1.PDB	O, H_VAL_48	N, H_ALA_60	H, H_ALA_60	2.91	2.06	6.87
5JR1.PDB	OD2, H_ASP_86	NH1, H_ARG_66	HH12, H_ARG_66	2.72	1.87	9.50
5JR1.PDB	O, H_PRO_62	NH2, H_ARG_66	HH21, H_ARG_66	2.78	1.93	7.41
5JR1.PDB	O, H_GLN_81	N, H_THR_68	H, H_THR_68	2.82	2.01	16.76
5JR1.PDB	OH, H_TYR_59	N, H_ILE_69	H, H_ILE_69	2.78	1.93	7.40
5JR1.PDB	OD1, H_ASP_73	NE, H_ARG_71	HE, H_ARG_71	2.99	2.20	19.01
5JR1.PDB	O, H_ALA_32	NH1, H_ARG_71	HH12, H_ARG_71	2.98	2.22	23.48
5JR1.PDB	O, H_ALA_32	NH2, H_ARG_71	HH22, H_ARG_71	2.99	2.24	24.05
5JR1.PDB	O, H_THR_77	N, H_ASP_72	H, H_ASP_72	2.92	2.10	14.47
5JR1.PDB	OD1, H_ASP_72	OG, H_SER_74	HG, H_SER_74	2.50	1.70	14.47
5JR1.PDB	O, H_LYS_75	OG1, H_THR_77	HG1, H_THR_77	2.91	2.09	10.97
5JR1.PDB	O, H_CYS_22	N, H_LEU_78	H, H_LEU_78	2.87	2.04	11.82
5JR1.PDB	O, H_SER_70	N, H_TYR_79	H, H_TYR_79	2.85	2.00	9.75
5JR1.PDB	O, H_LEU_20	N, H_LEU_80	H, H_LEU_80	2.93	2.12	16.09
5JR1.PDB	O, H_THR_68	N, H_GLN_81	H, H_GLN_81	2.82	1.98	10.53
5JR1.PDB	O, H_LEU_18	N, H_MET_82	H, H_MET_82	2.76	1.92	9.12
5JR1.PDB	OD2, H_ASP_86	N, H_LYS_83	H, H_LYS_83	2.82	1.96	6.84
5JR1.PDB	O, H_LYS_83	N, H_ASP_86	H, H_ASP_86	2.64	1.79	6.68
5JR1.PDB	O, H_VAL_109	N, H_ALA_88	H, H_ALA_88	2.98	2.19	19.05
5JR1.PDB	O, H_GLN_39	N, H_VAL_89	H, H_VAL_89	2.83	2.04	19.63
5JR1.PDB	O, H_THR_107	N, H_TYR_90	H, H_TYR_90	2.85	2.00	7.31
5JR1.PDB	O, H_ASP_86	OH, H_TYR_90	HH, H_TYR_90	2.69	1.86	8.47
5JR1.PDB	O, H_VAL_37	N, H_TYR_91	H, H_TYR_91	2.66	1.80	1.80
5JR1.PDB	OE2, H_GLU_6	N, H_CYS_92	H, H_CYS_92	2.70	1.87	12.64
5JR1.PDB	O, H_SER_35	N, H_ALA_93	H, H_ALA_93	2.93	2.15	21.88
5JR1.PDB	O, H_ASP_102	N, H_ARG_94	H, H_ARG_94	2.91	2.18	27.54
5JR1.PDB	O, H_TRP_33	N, H_THR_95	H, H_THR_95	2.98	2.15	11.92
5JR1.PDB	O, H_TYR_100K	N, H_GLY_96	H, H_GLY_96	2.88	2.07	15.19
5JR1.PDB	O, H_GLU_100I	N, H_TYR_98	H, H_TYR_98	2.97	2.17	18.39
5JR1.PDB	O, H_TYR_98	N, H_GLU_100I	H, H_GLU_100I	2.76	1.96	17.68
5JR1.PDB	O, H_GLY_96	N, H_TYR_100K	H, H_TYR_100K	2.85	2.09	23.20
5JR1.PDB	OH, L_TYR_36	N, H_PHE_100L	H, H_PHE_100L	2.93	2.14	18.24
5JR1.PDB	O, H_ARG_94	N, H_GLN_101	H, H_GLN_101	2.77	2.05	27.74
5JR1.PDB	O, L_GLY_41	NH1, H_ARG_105	HH11, H_ARG_105	2.58	1.82	23.25
5JR1.PDB	OE1, H_GLU_6	N, H_GLY_106	H, H_GLY_106	2.84	2.01	12.28

5JR1.PDB	O, H_TYR_90	N, H_THR_107	H, H_THR_107	2.99	2.28	29.77
5JR1.PDB	O, H_ALA_88	N, H_VAL_109	H, H_VAL_109	2.92	2.07	7.11
5JR1.PDB	OG1, H_THR_87	N, H_BVAL_111	H, H_BVAL_111	3.00	2.15	5.58
5JR1.PDB	O, H_PHE_146	N, H_LYS_117	H, H_LYS_117	2.82	1.99	13.52
5JR1.PDB	O, H_ASP_144	NZ, H_LYS_117	HZ2, H_LYS_117	2.92	2.10	18.09
5JR1.PDB	O, H_LYS_143	N, H_SER_120	H, H_SER_120	2.94	2.13	15.86
5JR1.PDB	O, H_LEU_141	N, H_PHE_122	H, H_PHE_122	2.88	2.05	12.08
5JR1.PDB	O, H_GLY_139	N, H_LEU_124	H, H_LEU_124	2.79	1.94	8.07
5JR1.PDB	O, H_VAL_184	N, H_ALA_136	H, H_ALA_136	2.78	1.96	15.67
5JR1.PDB	O, H_LEU_124	N, H_GLY_139	H, H_GLY_139	2.92	2.11	16.29
5JR1.PDB	O, H_SER_180	N, H_CYS_140	H, H_CYS_140	2.94	2.15	19.79
5JR1.PDB	O, H_PHE_122	N, H_LEU_141	H, H_LEU_141	2.84	1.99	9.59
5JR1.PDB	O, H_LEU_178	N, H_VAL_142	H, H_VAL_142	2.76	1.90	4.75
5JR1.PDB	O, H_SER_120	N, H_LYS_143	H, H_LYS_143	2.77	1.93	8.90
5JR1.PDB	O, H_TYR_176	N, H_TYR_145	H, H_TYR_145	2.95	2.14	16.52
5JR1.PDB	O, H_LYS_117	N, H_PHE_146	H, H_PHE_146	2.89	2.08	16.28
5JR1.PDB	O, H_ASN_199	N, H_THR_151	H, H_THR_151	2.93	2.09	11.48
5JR1.PDB	O, H_ASN_197	N, H_SER_153	H, H_SER_153	2.90	2.09	17.08
5JR1.PDB	OD1, H_ASN_197	OG, H_SER_153	HG, H_SER_153	2.85	2.04	12.85
5JR1.PDB	OG, H_SER_180	NE1, H_TRP_154	HE1, H_TRP_154	2.87	2.02	7.55
5JR1.PDB	O, H_ILE_195	N, H_ASN_155	H, H_ASN_155	2.82	1.98	10.05
5JR1.PDB	OD1, H_ASN_197	N, H_SER_156	H, H_SER_156	2.76	1.96	17.23
5JR1.PDB	O, H_VAL_181	N, H_HIS_164	H, H_HIS_164	2.82	1.99	11.94
5JR1.PDB	O, H_SER_179	N, H_PHE_166	H, H_PHE_166	2.91	2.06	3.95
5JR1.PDB	O, H_SER_177	N, H_VAL_169	H, H_VAL_169	2.84	2.03	16.11
5JR1.PDB	O, H_LEU_175	N, H_GLN_171	H, H_GLN_171	2.92	2.06	5.15
5JR1.PDB	OD1, H_ASP_144	NE2, H_GLN_171	HE22, H_GLN_171	2.73	1.95	20.99
5JR1.PDB	O, H_GLN_171	N, H_GLY_174	H, H_GLY_174	2.88	2.05	12.35
5JR1.PDB	O, H_TYR_145	N, H_TYR_176	H, H_TYR_176	2.81	1.96	8.57
5JR1.PDB	OE1, H_GLN_171	OG, H_SER_177	HG, H_SER_177	2.71	1.98	25.79
5JR1.PDB	O, H_VAL_142	N, H_LEU_178	H, H_LEU_178	2.91	2.11	17.70
5JR1.PDB	OH, L_TYR_178	OG, H_SER_179	HG, H_SER_179	2.83	2.03	15.88
5JR1.PDB	O, H_HIS_164	N, H_VAL_181	H, H_VAL_181	2.79	1.96	12.10
5JR1.PDB	O, H_LEU_138	N, H_VAL_182	H, H_VAL_182	2.82	2.00	14.39
5JR1.PDB	O, H_ALA_136	N, H_VAL_184	H, H_VAL_184	2.80	1.97	12.21
5JR1.PDB	O, H_GLY_134	N, H_SER_186	H, H_SER_186	2.82	1.97	7.53
5JR1.PDB	O, H_PRO_185	OG, H_SER_188	HG, H_SER_188	2.70	1.86	3.21
5JR1.PDB	O, H_SER_188	N, H_GLN_192	H, H_GLN_192	2.88	2.04	10.77
5JR1.PDB	OG, H_SER_188	OH, H_TYR_194	HH, H_TYR_194	2.70	1.94	20.59
5JR1.PDB	OD1, H_ASN_155	N, H_ILE_195	H, H_ILE_195	2.86	2.03	13.39
5JR1.PDB	O, H_LYS_209	N, H_CYS_196	H, H_CYS_196	2.96	2.17	19.83
5JR1.PDB	O, H_SER_153	N, H_ASN_197	H, H_ASN_197	2.79	1.95	7.76
5JR1.PDB	O, H_VAL_207	N, H_VAL_198	H, H_VAL_198	2.80	1.97	13.81
5JR1.PDB	O, H_THR_151	N, H_ASN_199	H, H_ASN_199	2.88	2.05	14.08
5JR1.PDB	O, H_THR_205	N, H_HIS_200	H, H_HIS_200	2.87	2.03	10.85
5JR1.PDB	O, H_PRO_147	NE2, H_HIS_200	HE2, H_HIS_200	2.86	2.02	11.05
5JR1.PDB	O, H_LYS_201	N, H_ASN_204	H, H_ASN_204	2.97	2.13	9.90
5JR1.PDB	O, H_VAL_198	N, H_VAL_207	H, H_VAL_207	2.90	2.09	16.74
5JR1.PDB	O, H_CYS_196	N, H_LYS_209	H, H_LYS_209	2.83	2.04	19.23
5JR1.PDB	OE2, H_GLU_212	NE, H_BARG_210	HE, H_BARG_210	2.40	1.64	22.83
5JR1.PDB	O, H_TYR_194	N, H_VAL_211	H, H_VAL_211	2.98	2.15	13.77
5JR1.PDB	O, L_ARG_24	N, L_THR_5	H, L_THR_5	2.88	2.05	12.05
5JR1.PDB	O, L_TYR_86	NE2, L_GLN_6	HE22, L_GLN_6	2.95	2.16	19.38
5JR1.PDB	O, L_LYS_103	N, L_VAL_11	H, L_VAL_11	2.92	2.11	16.33
5JR1.PDB	O, L_ALA_78	N, L_GLY_16	H, L_GLY_16	2.86	2.01	7.27
5JR1.PDB	O, L_LEU_73	N, L_ILE_21	H, L_ILE_21	2.79	1.95	10.20
5JR1.PDB	O, L_ALA_71	N, L_CYS_23	H, L_CYS_23	2.79	1.94	9.36
5JR1.PDB	O, L_THR_5	N, L_ARG_24	H, L_ARG_24	2.91	2.12	20.30

5JR1.PDB	O, L_GLY_25	N, L_LEU_28	H, L_LEU_28	2.91	2.14	22.06
5JR1.PDB	O, L_SER_89	N, L_SER_34	H, L_SER_34	2.85	2.04	16.48
5JR1.PDB	O, L_PHE_48	N, L_TRP_35	H, L_TRP_35	2.89	2.09	17.65
5JR1.PDB	O, L_TYR_87	N, L_TYR_36	H, L_TYR_36	2.89	2.07	15.48
5JR1.PDB	N, H_PHE_100L	OH, L_TYR_36	HH, L_TYR_36	2.93	2.21	26.41
5JR1.PDB	O, L_ILE_45	N, L_GLN_37	H, L_GLN_37	2.91	2.11	18.13
5JR1.PDB	OH, L_TYR_86	NE2, L_GLN_37	HE21, L_GLN_37	2.92	2.08	10.60
5JR1.PDB	O, L_GLU_85	N, L_LYS_38	H, L_LYS_38	2.75	1.91	11.42
5JR1.PDB	O, L_GLN_37	N, L_ILE_45	H, L_ILE_45	2.81	1.99	14.72
5JR1.PDB	O, L_TRP_35	N, L_LEU_47	H, L_LEU_47	2.80	1.95	7.57
5JR1.PDB	O, L_ASN_53	N, L_TYR_49	H, L_TYR_49	2.89	2.10	19.62
5JR1.PDB	O, L_PHE_62	NE, L_ARG_54	HE, L_ARG_54	2.79	2.02	21.45
5JR1.PDB	O, L_PHE_62	NH2, L_ARG_54	HH21, L_ARG_54	2.91	2.19	28.02
5JR1.PDB	OD2, L_ASP_82	NE, L_ARG_61	HE, L_ARG_61	2.81	2.00	15.72
5JR1.PDB	OD1, L_ASP_82	NH2, L_ARG_61	HH21, L_ARG_61	2.74	1.90	11.09
5JR1.PDB	O, L_THR_74	N, L_SER_63	H, L_SER_63	2.98	2.19	19.40
5JR1.PDB	O, L_SER_72	N, L_SER_65	H, L_SER_65	2.90	2.12	21.18
5JR1.PDB	O, L_SER_67	N, L_ARG_70	H, L_ARG_70	2.86	2.02	9.85
5JR1.PDB	O, L_CYS_23	N, L_ALA_71	H, L_ALA_71	2.91	2.10	16.23
5JR1.PDB	O, L_SER_65	N, L_SER_72	H, L_SER_72	2.84	2.01	12.34
5JR1.PDB	O, L_ILE_21	N, L_LEU_73	H, L_LEU_73	2.78	1.95	12.54
5JR1.PDB	O, L_SER_63	N, L_THR_74	H, L_THR_74	2.78	1.93	7.21
5JR1.PDB	OG1, L_THR_20	OG1, L_THR_74	HG1, L_THR_74	2.96	2.15	13.12
5JR1.PDB	O, L_VAL_19	N, L_ILE_75	H, L_ILE_75	2.80	1.99	13.64
5JR1.PDB	O, L_ARG_61	N, L_SER_76	H, L_SER_76	2.98	2.17	14.63
5JR1.PDB	O, L_ARG_17	N, L_ALA_78	H, L_ALA_78	2.83	2.04	17.38
5JR1.PDB	OD2, L_ASP_82	N, L_GLN_79	H, L_GLN_79	2.91	2.06	9.01
5JR1.PDB	O, L_GLN_79	N, L_ASP_82	H, L_ASP_82	2.90	2.05	8.33
5JR1.PDB	O, L_LYS_38	N, L_GLU_85	H, L_GLU_85	2.91	2.07	8.57
5JR1.PDB	O, L_THR_102	N, L_TYR_86	H, L_TYR_86	2.84	2.05	20.14
5JR1.PDB	O, L_ASP_82	OH, L_TYR_86	HH, L_TYR_86	2.65	1.82	8.64
5JR1.PDB	O, L_TYR_36	N, L_TYR_87	H, L_TYR_87	2.94	2.12	15.76
5JR1.PDB	O, L_VAL_97	OG, L_SER_89	HG, L_SER_89	2.81	2.07	23.50
5JR1.PDB	O, L_TYR_32	OG, L_SER_90	HG, L_SER_90	2.84	2.07	19.10
5JR1.PDB	O, L_SER_95A	NE, L_ARG_91	HE, L_ARG_91	2.92	2.13	19.73
5JR1.PDB	O, L_GLY_95	NH1, L_ARG_91	HH11, L_ARG_91	2.58	1.80	19.50
5JR1.PDB	O, H_PRO_100F	NH1, L_ARG_91	HH12, L_ARG_91	2.89	2.18	29.36
5JR1.PDB	O, H_PRO_100F	NH2, L_ARG_91	HH22, L_ARG_91	2.82	2.09	26.91
5JR1.PDB	O, L_LEU_95C	N, L_ASP_92	H, L_ASP_92	2.85	2.03	14.49
5JR1.PDB	OD2, L_ASP_92	N, L_SER_94	H, L_SER_94	2.66	1.84	13.82
5JR1.PDB	OD2, L_ASP_92	OG, L_SER_94	HG, L_SER_94	2.41	1.66	21.72
5JR1.PDB	O, L_ASP_92	N, L_GLY_95	H, L_GLY_95	2.95	2.09	5.43
5JR1.PDB	OD2, H_ASP_58	NH2, L_ARG_95B	HH22, L_ARG_95B	2.47	1.67	16.99
5JR1.PDB	O, L_SER_90	N, L_VAL_97	H, L_VAL_97	2.83	1.98	7.91
5JR1.PDB	O, L_CYS_88	N, L_GLY_99	H, L_GLY_99	2.88	2.08	16.95
5JR1.PDB	O, L_TYR_86	N, L_THR_102	H, L_THR_102	2.89	2.09	17.99
5JR1.PDB	O, L_GLU_7	OG1, L_THR_102	HG1, L_THR_102	2.75	1.92	9.86
5JR1.PDB	O, L_THR_8	N, L_LYS_103	H, L_LYS_103	2.87	2.02	7.49
5JR1.PDB	O, L_ALA_84	N, L_LEU_104	H, L_LEU_104	2.86	2.02	10.37
5JR1.PDB	O, L_VAL_11	N, L_THR_105	H, L_THR_105	2.95	2.12	13.22
5JR1.PDB	OD1, L_ASP_83	N, L_VAL_106	H, L_VAL_106	2.52	1.67	7.56
5JR1.PDB	O, L_VAL_13	N, L_LEU_106A	H, L_LEU_106A	2.86	2.04	13.99
5JR1.PDB	OH, L_TYR_141	N, L_SER_107	H, L_SER_107	2.98	2.19	19.63
5JR1.PDB	OE1, L_GLU_199	NZ, L_LYS_110	HZ3, L_LYS_110	2.77	1.91	11.53
5JR1.PDB	O, L_TYR_141	N, L_ALA_111	H, L_ALA_111	2.82	1.98	10.35
5JR1.PDB	O, L_SER_138	N, L_SER_114	H, L_SER_114	2.83	1.98	5.37
5JR1.PDB	O, L_LEU_136	N, L_THR_116	H, L_THR_116	2.93	2.12	15.66
5JR1.PDB	O, L_VAL_134	N, L_PHE_118	H, L_PHE_118	2.82	1.99	11.01

5JR1.PDB	O, L.SER.122	N, L.LEU.126	H, L.LEU.126	2.98	2.14	8.64
5JR1.PDB	O, L.LEU.126	N, L.ASN.129	H, L.ASN.129	2.85	2.04	16.99
5JR1.PDB	OE2, L.GLU.125	OG1, L.THR.132	HG1, L.THR.132	2.53	1.79	23.02
5JR1.PDB	O, L.LEU.179	N, L.LEU.133	H, L.LEU.133	2.87	2.06	17.19
5JR1.PDB	O, L.SER.177	N, L.CYS.135	H, L.CYS.135	2.87	2.01	4.08
5JR1.PDB	O, L.THR.116	N, L.LEU.136	H, L.LEU.136	2.82	1.96	6.02
5JR1.PDB	O, L.ALA.175	N, L.ILE.137	H, L.ILE.137	2.93	2.15	21.12
5JR1.PDB	O, L.SER.114	N, L.SER.138	H, L.SER.138	2.87	2.07	19.40
5JR1.PDB	OE1, L.GLN.168	N, L.ASP.139	H, L.ASP.139	2.93	2.12	16.63
5JR1.PDB	O, L.ALA.111	N, L.TYR.141	H, L.TYR.141	2.90	2.08	15.02
5JR1.PDB	O, L.GLN.195	N, L.ALA.148	H, L.ALA.148	2.93	2.11	16.11
5JR1.PDB	OG, L.SER.177	NE1, L.TRP.149	HE1, L.TRP.149	2.84	1.99	9.64
5JR1.PDB	O, L.SER.193	N, L.LYS.150	H, L.LYS.150	2.91	2.10	16.78
5JR1.PDB	OE1, L.GLN.195	NZ, L.LYS.150	HZ3, L.LYS.150	2.79	1.91	7.52
5JR1.PDB	O, L.SER.154	N, L.ALA.151	H, L.ALA.151	2.97	2.15	14.89
5JR1.PDB	O, L.ALA.151	N, L.SER.154	H, L.SER.154	2.85	2.01	8.48
5JR1.PDB	O, L.TRP.149	N, L.VAL.156	H, L.VAL.156	2.98	2.14	8.84
5JR1.PDB	O, L.TYR.178	N, L.GLU.161	H, L.GLU.161	2.96	2.15	17.71
5JR1.PDB	O, L.SER.176	N, L.THR.163	H, L.THR.163	2.91	2.08	11.01
5JR1.PDB	O, L.ALA.174	N, L.SER.166	H, L.SER.166	2.98	2.16	14.11
5JR1.PDB	O, L.LYS.172	N, L.GLN.168	H, L.GLN.168	2.54	1.68	1.19
5JR1.PDB	OD1, L.ASN.170	NE2, L.GLN.168	HE21, L.GLN.168	2.60	1.77	13.13
5JR1.PDB	OD1, L.ASP.139	NE2, L.GLN.168	HE22, L.GLN.168	2.73	1.87	5.77
5JR1.PDB	O, L.GLN.168	N, L.ASN.171	H, L.ASN.171	2.91	2.08	14.01
5JR1.PDB	O, L.PHE.140	N, L.TYR.173	H, L.TYR.173	2.88	2.05	13.43
5JR1.PDB	O, L.SER.166	N, L.ALA.174	H, L.ALA.174	2.94	2.15	19.09
5JR1.PDB	O, L.ILE.137	N, L.ALA.175	H, L.ALA.175	2.81	2.00	16.74
5JR1.PDB	O, L.CYS.135	N, L.SER.177	H, L.SER.177	2.92	2.12	17.27
5JR1.PDB	O, L.GLU.161	N, L.TYR.178	H, L.TYR.178	2.78	1.97	16.16
5JR1.PDB	O, L.LEU.133	N, L.LEU.179	H, L.LEU.179	2.98	2.17	15.29
5JR1.PDB	O, L.GLY.159	N, L.SER.180	H, L.SER.180	2.73	1.89	11.54
5JR1.PDB	O, L.ALA.131	N, L.LEU.181	H, L.LEU.181	2.95	2.10	6.67
5JR1.PDB	OE1, L.GLN.185	N, L.THR.182	H, L.THR.182	2.93	2.10	11.07
5JR1.PDB	OG1, L.THR.182	N, L.GLN.185	H, L.GLN.185	2.88	2.04	12.03
5JR1.PDB	O, L.THR.182	N, L.TRP.186	H, L.TRP.186	2.96	2.13	12.66
5JR1.PDB	O, L.VAL.207	N, L.TYR.192	H, L.TYR.192	2.92	2.08	9.44
5JR1.PDB	O, L.LYS.150	N, L.SER.193	H, L.SER.193	2.81	1.99	15.01
5JR1.PDB	O, L.LYS.205	N, L.CYS.194	H, L.CYS.194	2.96	2.17	19.17
5JR1.PDB	O, L.ALA.148	N, L.GLN.195	H, L.GLN.195	2.75	1.89	4.07
5JR1.PDB	OE2, L.GLU.204	NE2, L.GLN.195	HE21, L.GLN.195	2.95	2.12	11.81
5JR1.PDB	O, L.VAL.203	N, L.VAL.196	H, L.VAL.196	2.75	1.89	4.95
5JR1.PDB	O, L.THR.146	N, L.THR.197	H, L.THR.197	2.80	1.96	10.45
5JR1.PDB	O, L.SER.201	N, L.HIS.198	H, L.HIS.198	2.87	2.03	9.19
5JR1.PDB	O, L.PRO.142	NE2, L.HIS.198	HE2, L.HIS.198	2.88	2.11	21.70
5JR1.PDB	O, L.HIS.198	N, L.SER.201	H, L.SER.201	2.99	2.18	15.98
5JR1.PDB	OG1, L.THR.197	OG1, L.THR.202	HG1, L.THR.202	2.77	1.97	14.73
5JR1.PDB	O, L.VAL.196	N, L.VAL.203	H, L.VAL.203	2.77	1.92	8.70
5JR1.PDB	O, L.TYR.192	N, L.VAL.207	H, L.VAL.207	2.92	2.11	16.47
5JUE.PDB	OG, L.SER.26	N, L.VAL.3	H, L.VAL.3	2.98	2.17	16.79
5JUE.PDB	O, L.ARG.24	N, L.THR.5	H, L.THR.5	2.79	1.95	8.65
5JUE.PDB	O, L.TYR.86	NE2, L.GLN.6	HE22, L.GLN.6	2.67	1.82	7.14
5JUE.PDB	O, L.LYS.103	N, L.LEU.11	H, L.LEU.11	2.83	2.02	15.60
5JUE.PDB	O, L.ASP.105	N, L.VAL.13	H, L.VAL.13	2.59	1.84	24.65
5JUE.PDB	O, L.VAL.78	N, L.GLY.16	H, L.GLY.16	2.91	2.08	13.41
5JUE.PDB	O, L.ILE.75	N, L.ALA.19	H, L.ALA.19	2.83	2.04	19.69
5JUE.PDB	O, L.LEU.73	N, L.ILE.21	H, L.ILE.21	2.80	1.97	12.30
5JUE.PDB	O, L.PHE.71	N, L.CYS.23	H, L.CYS.23	2.87	2.07	17.94
5JUE.PDB	O, L.THR.5	N, L.ARG.24	H, L.ARG.24	2.84	2.02	16.32

5JUE.PDB	O, L_THR_69	N, L_SER_25	H, L_SER_25	2.87	2.09	20.67
5JUE.PDB	O, L_GLY_68	N, L_LEU_27B	H, L_LEU_27B	2.95	2.09	6.56
5JUE.PDB	O, L_ASN_30	N, L_HIS_27D	H, L_HIS_27D	2.78	1.95	11.98
5JUE.PDB	O, L_HIS_27D	N, L_GLY_29	H, L_GLY_29	2.92	2.07	9.18
5JUE.PDB	OD1, L_ASN_28	N, L_ASN_30	H, L_ASN_30	2.82	1.98	7.63
5JUE.PDB	O, L_SER_89	N, L_HIS_34	H, L_HIS_34	2.90	2.08	14.05
5JUE.PDB	O, L_ILE_48	N, L_TRP_35	H, L_TRP_35	2.88	2.05	13.75
5JUE.PDB	O, L_PHE_87	N, L_TYR_36	H, L_TYR_36	2.82	2.02	18.65
5JUE.PDB	O, H_MET_100E	OH, L_TYR_36	HH, L_TYR_36	2.57	1.73	1.94
5JUE.PDB	O, L_IYS_45	N, L_LEU_37	H, L_LEU_37	2.94	2.13	17.21
5JUE.PDB	O, L_VAL_85	N, L_GLN_38	H, L_GLN_38	2.76	1.91	8.75
5JUE.PDB	OH, H_TYR_91	NE2, L_GLN_38	HE22, L_GLN_38	2.57	1.77	17.09
5JUE.PDB	O, L_LEU_37	N, L_IYS_45	H, L_IYS_45	2.82	2.01	16.77
5JUE.PDB	O, L_TRP_35	N, L_LEU_47	H, L_LEU_47	2.92	2.07	6.45
5JUE.PDB	O, L_ASN_53	N, L_TYR_49	H, L_TYR_49	2.77	1.96	16.15
5JUE.PDB	O, L_LEU_33	N, L_VAL_51	H, L_VAL_51	2.73	1.88	3.35
5JUE.PDB	O, L_IYS_50	N, L_SER_52	H, L_SER_52	2.82	2.09	27.26
5JUE.PDB	O, L_TYR_49	N, L_ASN_53	H, L_ASN_53	2.91	2.09	15.10
5JUE.PDB	O, L_LEU_47	N, L_PHE_55	H, L_PHE_55	2.94	2.09	7.35
5JUE.PDB	OD1, L_ASP_82	NH1, L_ARG_61	HH12, L_ARG_61	2.84	1.98	1.66
5JUE.PDB	OD2, L_ASP_82	NH2, L_ARG_61	HH22, L_ARG_61	2.58	1.76	15.54
5JUE.PDB	O, L_IYS_74	N, L_SER_63	H, L_SER_63	2.99	2.17	15.39
5JUE.PDB	O, L_THR_72	N, L_SER_65	H, L_SER_65	2.99	2.19	17.98
5JUE.PDB	O, L_CYS_23	N, L_PHE_71	H, L_PHE_71	2.91	2.13	20.93
5JUE.PDB	O, L_SER_65	N, L_THR_72	H, L_THR_72	3.00	2.17	13.38
5JUE.PDB	O, L_ILE_21	N, L_LEU_73	H, L_LEU_73	2.72	1.90	13.66
5JUE.PDB	O, L_SER_63	N, L_IYS_74	H, L_IYS_74	2.85	1.99	5.09
5JUE.PDB	O, L_ALA_19	N, L_ILE_75	H, L_ILE_75	2.85	2.02	11.67
5JUE.PDB	O, L_ARG_61	N, L_SER_76	H, L_SER_76	2.90	2.06	8.87
5JUE.PDB	OD2, L_ASP_82	N, L_GLU_79	H, L_GLU_79	2.91	2.07	10.58
5JUE.PDB	O, L_GLN_38	N, L_VAL_85	H, L_VAL_85	2.89	2.03	2.65
5JUE.PDB	O, L_THR_102	N, L_TYR_86	H, L_TYR_86	2.84	1.99	9.23
5JUE.PDB	O, L_ASP_82	OH, L_TYR_86	HH, L_TYR_86	2.44	1.73	27.01
5JUE.PDB	O, L_HIS_34	N, L_SER_89	H, L_SER_89	2.89	2.13	24.06
5JUE.PDB	O, L_HIS_93	NE2, L_GLN_90	HE22, L_GLN_90	2.99	2.13	3.59
5JUE.PDB	O, L_LEU_27B	OG1, L_THR_92	HG1, L_THR_92	2.74	1.96	18.74
5JUE.PDB	OE1, L_GLN_90	N, L_HIS_93	H, L_HIS_93	2.98	2.13	5.06
5JUE.PDB	O, L_VAL_2	OG1, L_THR_97	HG1, L_THR_97	2.62	1.84	18.25
5JUE.PDB	O, L_CYS_88	N, L_GLY_99	H, L_GLY_99	2.87	2.05	14.91
5JUE.PDB	OE1, L_GLN_6	N, L_GLY_101	H, L_GLY_101	2.93	2.15	21.08
5JUE.PDB	O, L_TYR_86	N, L_THR_102	H, L_THR_102	2.79	2.00	18.87
5JUE.PDB	O, L_PRO_8	OG1, L_THR_102	HG1, L_THR_102	2.72	1.95	19.56
5JUE.PDB	O, L_LEU_9	N, L_IYS_103	H, L_IYS_103	2.97	2.12	8.91
5JUE.PDB	O, L_LEU_11	N, L_ASP_105	H, L_ASP_105	2.72	1.89	12.81
5JUE.PDB	OE1, L_GLN_166	N, L_ILE_106	H, L_ILE_106	2.97	2.13	9.61
5JUE.PDB	O, L_VAL_13	N, L_IYS_107	H, L_IYS_107	2.92	2.11	17.64
5JUE.PDB	O, L_ALA_109	NE, L_ARG_108	HE, L_ARG_108	2.71	1.88	11.79
5JUE.PDB	O, L_ASP_170	NH1, L_ARG_108	HH11, L_ARG_108	2.89	2.05	10.58
5JUE.PDB	O, L_TYR_140	N, L_ALA_111	H, L_ALA_111	2.90	2.07	11.29
5JUE.PDB	O, L_ASN_137	N, L_THR_114	H, L_THR_114	2.87	2.02	7.17
5JUE.PDB	O, L_VAL_133	N, L_PHE_118	H, L_PHE_118	2.73	1.99	26.03
5JUE.PDB	OG, L_SER_121	N, L_GLN_124	H, L_GLN_124	2.96	2.13	13.41
5JUE.PDB	OG, L_SER_131	NE2, L_GLN_124	HE22, L_GLN_124	2.87	2.01	1.74
5JUE.PDB	O, L_SER_122	N, L_THR_126	H, L_THR_126	2.98	2.17	17.04
5JUE.PDB	OE1, L_GLN_124	N, L_SER_131	H, L_SER_131	2.85	2.11	26.16
5JUE.PDB	O, L_LEU_179	N, L_VAL_132	H, L_VAL_132	2.77	1.93	11.31
5JUE.PDB	O, L_SER_177	N, L_CYS_134	H, L_CYS_134	2.80	1.98	14.40
5JUE.PDB	O, L_SER_116	N, L_PHE_135	H, L_PHE_135	2.88	2.09	19.24

5JUE.PDB	O, L_MET.175	N, L_LEU.136	H, L_LEU.136	2.81	1.96	4.25
5JUE.PDB	O, L_THR.114	N, L_ASN.137	H, L_ASN.137	2.86	2.04	14.67
5JUE.PDB	O, L_TYR.173	N, L_PHE.139	H, L_PHE.139	2.85	2.03	14.35
5JUE.PDB	OD2, L_ASP.105	OH, L_TYR.140	HH, L_TYR.140	2.73	1.90	9.39
5JUE.PDB	O, L_GLU.195	N, L_LYS.147	H, L_LYS.147	2.84	2.04	18.72
5JUE.PDB	OG, L_SER.177	NE1, L_TRP.148	HE1, L_TRP.148	2.84	1.99	8.07
5JUE.PDB	O, L_THR.193	N, L_LYS.149	H, L_LYS.149	2.96	2.16	18.02
5JUE.PDB	OE2, L_GLU.195	NZ, L_LYS.149	HZ1, L_LYS.149	2.94	2.11	18.07
5JUE.PDB	O, L_SER.153	N, L_ILE.150	H, L_ILE.150	2.87	2.09	21.73
5JUE.PDB	O, L_SER.191	N, L_ASP.151	H, L_ASP.151	2.80	1.96	9.61
5JUE.PDB	O, L_ILE.150	N, L_SER.153	H, L_SER.153	2.88	2.02	3.01
5JUE.PDB	O, L_TRP.148	N, L_ARG.155	H, L_ARG.155	2.83	2.02	17.08
5JUE.PDB	OE1, L_GLU.185	NH1, L_ARG.155	HH12, L_ARG.155	2.98	2.13	8.18
5JUE.PDB	O, L_THR.178	N, L_LEU.160	H, L_LEU.160	2.89	2.07	14.30
5JUE.PDB	O, L_SER.176	N, L_SER.162	H, L_SER.162	2.89	2.09	18.60
5JUE.PDB	O, H_PRO.167	OG, L_SER.162	HG, L_SER.162	2.70	1.95	22.84
5JUE.PDB	O, L_SER.174	N, L_THR.164	H, L_THR.164	2.96	2.13	11.82
5JUE.PDB	O, L_ILE.106	NE2, L_GLN.166	HE22, L_GLN.166	2.89	2.10	19.76
5JUE.PDB	O, L_THR.172	N, L_ASP.167	H, L_ASP.167	2.82	1.99	14.34
5JUE.PDB	OD2, L_ASP.167	N, L_ASP.170	H, L_ASP.170	2.89	2.09	18.48
5JUE.PDB	O, L_ASP.167	N, L_SER.171	H, L_SER.171	2.91	2.19	28.73
5JUE.PDB	OD1, L_ASP.170	N, L_THR.172	H, L_THR.172	2.88	2.05	13.18
5JUE.PDB	OD1, L_ASP.170	OG1, L_THR.172	HG1, L_THR.172	2.65	1.84	10.43
5JUE.PDB	O, L_PHE.139	N, L_TYR.173	H, L_TYR.173	2.81	1.98	12.09
5JUE.PDB	OD1, L_ASP.105	OH, L_TYR.173	HH, L_TYR.173	2.53	1.79	22.81
5JUE.PDB	O, L_LEU.136	N, L_MET.175	H, L_MET.175	2.80	2.04	23.93
5JUE.PDB	O, L_SER.162	N, L_SER.176	H, L_SER.176	2.85	2.01	10.71
5JUE.PDB	OG, H_SER.178	OG, L_SER.176	HG, L_SER.176	2.78	1.94	3.13
5JUE.PDB	O, L_CYS.134	N, L_SER.177	H, L_SER.177	2.87	2.03	11.31
5JUE.PDB	OD1, L_ASN.161	OG, L_SER.177	HG, L_SER.177	2.61	1.88	24.46
5JUE.PDB	O, L_LEU.160	N, L_THR.178	H, L_THR.178	2.82	1.98	12.12
5JUE.PDB	O, L_VAL.132	N, L_LEU.179	H, L_LEU.179	2.82	2.00	15.30
5JUE.PDB	O, L_GLY.158	N, L_THR.180	H, L_THR.180	2.90	2.06	10.37
5JUE.PDB	O, L_ALA.130	N, L_LEU.181	H, L_LEU.181	2.87	2.02	8.71
5JUE.PDB	OG1, L_THR.182	N, L_GLU.185	H, L_GLU.185	2.89	2.08	16.50
5JUE.PDB	O, L_THR.182	N, L_TYR.186	H, L_TYR.186	2.88	2.04	12.09
5JUE.PDB	O, L_LYS.183	N, L_GLU.187	H, L_GLU.187	2.97	2.16	17.18
5JUE.PDB	OD1, L_ASP.184	NE, L_ARG.188	HE, L_ARG.188	2.70	1.93	22.77
5JUE.PDB	OD1, L_ASP.151	N, L_SER.191	H, L_SER.191	2.84	1.99	8.55
5JUE.PDB	OG, L_SER.208	OG1, L_THR.193	HG1, L_THR.193	2.92	2.19	25.67
5JUE.PDB	O, L_LYS.207	N, L_CYS.194	H, L_CYS.194	2.90	2.07	13.15
5JUE.PDB	O, L_LYS.147	N, L_GLU.195	H, L_GLU.195	2.80	2.03	21.10
5JUE.PDB	O, L_ILE.205	N, L_ALA.196	H, L_ALA.196	2.77	1.93	11.01
5JUE.PDB	O, L_ASN.145	N, L_THR.197	H, L_THR.197	2.81	1.97	10.17
5JUE.PDB	ND1, L_HIS.198	OG1, L_THR.200	HG1, L_THR.200	2.88	2.17	27.29
5JUE.PDB	O, L_HIS.198	N, L_SER.201	H, L_SER.201	2.99	2.13	4.28
5JUE.PDB	O, L_ALA.196	N, L_ILE.205	H, L_ILE.205	2.89	2.16	26.61
5JUE.PDB	O, L_CYS.194	N, L_LYS.207	H, L_LYS.207	2.98	2.13	8.08
5JUE.PDB	O, L_TYR.192	OG, L_SER.208	HG, L_SER.208	2.94	2.25	29.37
5JUE.PDB	O, L_TYR.192	N, L_PHE.209	H, L_PHE.209	2.97	2.18	20.14
5JUE.PDB	O, L_ASN.190	N, L_ARG.211	H, L_ARG.211	2.82	2.02	17.54
5JUE.PDB	O, L_HIS.189	NH1, L_ARG.211	HH11, L_ARG.211	2.81	2.00	16.77
5JUE.PDB	O, H_LYS.23	N, H_GLN.5	H, H_GLN.5	2.85	2.00	7.87
5JUE.PDB	OE1, H_GLN.105	N, H_GLU.6	H, H_GLU.6	2.79	1.93	4.85
5JUE.PDB	O, H_THR.108	N, H_GLU.10	H, H_GLU.10	2.90	2.06	10.22
5JUE.PDB	O, H_THR.110	N, H_VAL.12	H, H_VAL.12	2.87	2.05	14.20
5JUE.PDB	O, H_LEU.82C	N, H_GLY.15	H, H_GLY.15	2.69	1.84	3.78
5JUE.PDB	O, H_PHE.82	N, H_VAL.18	H, H_VAL.18	2.89	2.15	25.49

5JUE.PDB	O, H_MET_80	N, H_ILE_20	H, H_ILE_20	2.88	2.05	14.33
5JUE.PDB	OG, H_SER_7	N, H_SER_21	H, H_SER_21	2.95	2.10	6.39
5JUE.PDB	O, H_GLN_5	N, H_LYS_23	H, H_LYS_23	2.86	2.01	5.12
5JUE.PDB	O, H_SER_76	N, H_ALA_24	H, H_ALA_24	2.79	1.93	3.59
5JUE.PDB	O, H_LEU_95	N, H_TYR_33	H, H_TYR_33	2.75	1.97	21.10
5JUE.PDB	O, H_ILE_51	N, H_ILE_34	H, H_ILE_34	2.95	2.13	14.74
5JUE.PDB	O, H_ALA_93	N, H_HIS_35	H, H_HIS_35	2.70	1.87	12.64
5JUE.PDB	O, H_GLY_49	N, H_TRP_36	H, H_TRP_36	2.96	2.14	14.80
5JUE.PDB	O, H_TYR_91	N, H_VAL_37	H, H_VAL_37	2.90	2.12	21.72
5JUE.PDB	O, H_GLU_46	N, H_LYS_38	H, H_LYS_38	2.77	1.91	6.07
5JUE.PDB	O, H_GLU_85	NZ, H_LYS_38	HZ3, H_LYS_38	2.96	2.18	24.16
5JUE.PDB	O, H_VAL_89	N, H_GLN_39	H, H_GLN_39	2.71	1.95	22.82
5JUE.PDB	O, H_LYS_38	N, H_GLU_46	H, H_GLU_46	2.82	2.03	19.41
5JUE.PDB	ND1, H_HIS_35	NE1, H_TRP_47	HE1, H_TRP_47	2.93	2.15	20.72
5JUE.PDB	O, H_TRP_36	N, H_ILE_48	H, H_ILE_48	2.82	1.97	8.50
5JUE.PDB	O, H_PHE_58	N, H_PHE_50	H, H_PHE_50	2.95	2.18	21.32
5JUE.PDB	O, H_ILE_34	N, H_ILE_51	H, H_ILE_51	2.91	2.08	13.15
5JUE.PDB	O, H_ALA_56	N, H_SER_52	H, H_SER_52	2.80	1.98	14.65
5JUE.PDB	O, H_TYR_32	N, H_CYS_52A	H, H_CYS_52A	2.96	2.15	16.57
5JUE.PDB	O, H_SER_52	N, H_GLY_55	H, H_GLY_55	2.82	2.07	24.44
5JUE.PDB	O, H_ILE_48	N, H_ASN_60	H, H_ASN_60	2.84	2.02	15.39
5JUE.PDB	O, H_TRP_47	ND2, H_ASN_60	HD22, H_ASN_60	2.96	2.15	16.53
5JUE.PDB	O, H_ASN_60	N, H_PHE_63	H, H_PHE_63	2.69	1.86	13.05
5JUE.PDB	O, H_PHE_63	N, H_LYS_66	H, H_LYS_66	2.88	2.11	21.18
5JUE.PDB	OD2, H_ASP_86	NZ, H_LYS_66	HZ1, H_LYS_66	2.76	1.87	4.19
5JUE.PDB	O, H_LYS_81	N, H_THR_68	H, H_THR_68	2.79	2.01	20.33
5JUE.PDB	OH, H_TYR_59	N, H_PHE_69	H, H_PHE_69	2.85	2.00	6.71
5JUE.PDB	O, H_THR_77	N, H_ASP_72	H, H_ASP_72	2.79	1.96	13.59
5JUE.PDB	O, H_SER_75	OG1, H_THR_77	HG1, H_THR_77	2.86	2.10	21.30
5JUE.PDB	O, H_CYS_22	N, H_ALA_78	H, H_ALA_78	2.84	2.01	12.71
5JUE.PDB	O, H_THR_70	N, H_TYR_79	H, H_TYR_79	2.81	1.97	11.04
5JUE.PDB	O, H_ILE_20	N, H_MET_80	H, H_MET_80	2.90	2.08	15.24
5JUE.PDB	O, H_THR_68	N, H_LYS_81	H, H_LYS_81	2.77	1.92	8.40
5JUE.PDB	O, H_VAL_18	N, H_PHE_82	H, H_PHE_82	2.76	1.93	11.48
5JUE.PDB	O, H_ALA_16	N, H_LEU_82C	H, H_LEU_82C	2.95	2.10	6.09
5JUE.PDB	OD2, H_ASP_86	N, H_THR_83	H, H_THR_83	2.87	2.09	20.55
5JUE.PDB	O, H_THR_83	N, H_ASP_86	H, H_ASP_86	2.75	1.95	17.05
5JUE.PDB	O, H_PHE_84	N, H_SER_87	H, H_SER_87	2.98	2.14	9.08
5JUE.PDB	O, H_GLN_39	N, H_VAL_89	H, H_VAL_89	2.93	2.09	11.76
5JUE.PDB	O, H_THR_107	N, H_TYR_90	H, H_TYR_90	2.88	2.04	10.67
5JUE.PDB	O, H_ASP_86	OH, H_TYR_90	HH, H_TYR_90	2.63	1.81	11.12
5JUE.PDB	O, H_VAL_37	N, H_TYR_91	H, H_TYR_91	2.79	1.95	9.11
5JUE.PDB	OE1, H_GLN_39	OH, H_TYR_91	HH, H_TYR_91	2.83	2.02	11.19
5JUE.PDB	O, H_HIS_35	N, H_ALA_93	H, H_ALA_93	2.84	2.10	26.47
5JUE.PDB	O, H_TYR_102	N, H_ARG_94	H, H_ARG_94	2.91	2.11	17.26
5JUE.PDB	OD1, H_ASP_101	NE, H_ARG_94	HE, H_ARG_94	2.72	1.88	8.15
5JUE.PDB	OD2, H_ASP_101	NH2, H_ARG_94	HH21, H_ARG_94	2.85	2.02	12.42
5JUE.PDB	O, H_TYR_33	N, H_LEU_95	H, H_LEU_95	2.78	2.01	21.79
5JUE.PDB	O, H_CYS_92	N, H_GLY_104	H, H_GLY_104	2.87	2.02	8.85
5JUE.PDB	O, H_GLU_6	NE2, H_GLN_105	HE22, H_GLN_105	2.95	2.22	27.22
5JUE.PDB	OE1, H_GLU_6	N, H_GLY_106	H, H_GLY_106	2.94	2.16	21.03
5JUE.PDB	O, H_TYR_90	N, H_THR_107	H, H_THR_107	2.85	2.05	17.16
5JUE.PDB	O, H_SER_7	OG1, H_THR_107	HG1, H_THR_107	2.75	1.97	19.56
5JUE.PDB	O, H_ALA_88	N, H_VAL_109	H, H_VAL_109	2.87	2.01	4.42
5JUE.PDB	O, H_GLU_10	N, H_THR_110	H, H_THR_110	2.93	2.09	10.96
5JUE.PDB	OG, H_SER_87	N, H_VAL_111	H, H_VAL_111	2.90	2.07	12.94
5JUE.PDB	OG, H_SER_112	N, H_ALA_114	H, H_ALA_114	2.93	2.07	5.78
5JUE.PDB	O, H_PHE_146	N, H_THR_117	H, H_THR_117	2.86	2.04	14.00

5JUE.PDB	O, H_LYS_115	OG1, H_THR_117	HG1, H_THR_117	2.86	2.06	13.74
5JUE.PDB	O, H_LYS_143	N, H_SER_120	H, H_SER_120	2.92	2.10	14.44
5JUE.PDB	O, H_LEU_141	N, H_TYR_122	H, H_TYR_122	2.78	1.95	12.46
5JUE.PDB	O, H_GLY_139	N, H_LEU_124	H, H_LEU_124	2.76	1.94	15.50
5JUE.PDB	O, H_VAL_183	N, H_VAL_136	H, H_VAL_136	2.78	1.97	15.84
5JUE.PDB	O, H_VAL_181	N, H_LEU_138	H, H_LEU_138	2.83	1.98	9.69
5JUE.PDB	O, H_LEU_124	N, H_GLY_139	H, H_GLY_139	2.92	2.12	17.53
5JUE.PDB	O, H_SER_179	N, H_CYS_140	H, H_CYS_140	2.90	2.16	25.88
5JUE.PDB	O, H_TYR_122	N, H_LEU_141	H, H_LEU_141	2.90	2.05	9.18
5JUE.PDB	O, H_LEU_177	N, H_VAL_142	H, H_VAL_142	2.80	1.96	9.80
5JUE.PDB	O, H_SER_120	N, H_LYS_143	H, H_LYS_143	2.83	1.99	8.41
5JUE.PDB	OE2, H_GLU_148	OH, H_TYR_145	HH, H_TYR_145	2.72	1.89	3.03
5JUE.PDB	O, H_THR_117	N, H_PHE_146	H, H_PHE_146	2.99	2.19	18.30
5JUE.PDB	O, H_ALA_198	N, H_THR_151	H, H_THR_151	2.83	2.01	15.90
5JUE.PDB	O, H_ASN_196	N, H_THR_153	H, H_THR_153	2.83	2.02	15.46
5JUE.PDB	OD1, H_ASN_196	OG1, H_THR_153	HG1, H_THR_153	2.74	1.98	20.12
5JUE.PDB	O, H_THR_194	N, H_ASN_155	H, H_ASN_155	2.82	1.98	9.66
5JUE.PDB	OD1, H_ASN_196	N, H_SER_156	H, H_SER_156	2.76	1.93	12.37
5JUE.PDB	O, H_ASN_155	N, H_SER_158	H, H_SER_158	2.96	2.12	11.60
5JUE.PDB	O, H_SER_180	N, H_HIS_164	H, H_HIS_164	2.88	2.06	15.45
5JUE.PDB	O, H_SER_178	N, H_PHE_166	H, H_PHE_166	2.91	2.05	0.92
5JUE.PDB	O, H_THR_176	N, H_VAL_169	H, H_VAL_169	2.91	2.09	14.10
5JUE.PDB	O, H_LEU_174	N, H_GLN_171	H, H_GLN_171	2.86	2.02	11.81
5JUE.PDB	O, H_TYR_145	N, H_TYR_175	H, H_TYR_175	2.78	1.92	3.54
5JUE.PDB	O, H_VAL_169	N, H_THR_176	H, H_THR_176	2.91	2.13	21.19
5JUE.PDB	O, H_VAL_142	N, H_LEU_177	H, H_LEU_177	2.89	2.07	15.29
5JUE.PDB	O, H_CYS_140	N, H_SER_179	H, H_SER_179	2.96	2.18	21.41
5JUE.PDB	O, H_HIS_164	N, H_SER_180	H, H_SER_180	2.77	1.97	17.64
5JUE.PDB	O, H_LEU_138	N, H_VAL_181	H, H_VAL_181	2.85	2.04	16.39
5JUE.PDB	O, H_GLY_162	N, H_THR_182	H, H_THR_182	2.95	2.18	23.27
5JUE.PDB	OG1, H_THR_137	OG1, H_THR_182	HG1, H_THR_182	2.77	2.00	20.14
5JUE.PDB	O, H_VAL_136	N, H_VAL_183	H, H_VAL_183	2.99	2.18	15.82
5JUE.PDB	O, H_SER_134	N, H_SER_185	H, H_SER_185	2.84	2.01	11.66
5JUE.PDB	O, H_THR_184	N, H_THR_187	H, H_THR_187	2.89	2.07	14.43
5JUE.PDB	OG1, H_THR_184	OG1, H_THR_187	HG1, H_THR_187	2.67	1.90	19.94
5JUE.PDB	O, H_THR_187	N, H_GLN_191	H, H_GLN_191	2.84	2.07	22.35
5JUE.PDB	OD1, H_ASN_155	N, H_THR_194	H, H_THR_194	2.84	2.06	20.75
5JUE.PDB	O, H_LYS_208	N, H_CYS_195	H, H_CYS_195	2.98	2.17	16.43
5JUE.PDB	O, H_THR_153	N, H_ASN_196	H, H_ASN_196	2.77	1.92	6.43
5JUE.PDB	O, H_VAL_206	N, H_VAL_197	H, H_VAL_197	2.87	2.03	11.32
5JUE.PDB	O, H_THR_151	N, H_ALA_198	H, H_ALA_198	2.82	2.00	15.03
5JUE.PDB	ND1, H_HIS_199	OG, H_SER_202	HG, H_SER_202	2.87	2.13	24.10
5JUE.PDB	O, H_PRO_200	N, H_SER_203	H, H_SER_203	2.74	1.98	23.65
5JUE.PDB	O, H_VAL_197	N, H_VAL_206	H, H_VAL_206	2.85	2.02	12.25
5JUE.PDB	O, H_CYS_195	N, H_LYS_208	H, H_LYS_208	2.96	2.13	13.25
5JUE.PDB	OE1, L_GLU_123	NZ, H_LYS_208	HZ1, H_LYS_208	2.81	1.98	17.66
5JUE.PDB	O, H_ILE_193	N, H_ILE_210	H, H_ILE_210	2.91	2.05	5.10
5JUE.PDB	O, H_ALA_125	NE, H_ARG_213	HE, H_ARG_213	2.97	2.21	22.96
5JUE.PDB	O, H_ALA_125	NH1, H_ARG_213	HH11, H_ARG_213	2.91	2.14	23.09
5JUE.PDB	O, L_PRO_119	NH1, H_ARG_213	HH12, H_ARG_213	2.84	2.13	29.21
5JUE.PDB	O, L_PRO_120	NH2, H_ARG_213	HH22, H_ARG_213	2.94	2.13	15.93
5JXA.PDB	OE1, H_GLN_105	N, H_GLN_6	H, H_GLN_6	2.84	1.98	2.17
5JXA.PDB	O, H_TYR_90	NE2, H_GLN_6	HE22, H_GLN_6	2.90	2.05	7.37
5JXA.PDB	O, H_VAL_110	N, H_LYS_12	H, H_LYS_12	2.83	2.00	13.73
5JXA.PDB	O, H_LEU_82C	N, H_GLY_15	H, H_GLY_15	2.72	1.89	11.76
5JXA.PDB	O, H_THR_13	OG, H_SER_16	HG, H_SER_16	2.64	1.85	16.20
5JXA.PDB	O, H_PHE_82	N, H_VAL_18	H, H_VAL_18	3.00	2.19	17.49
5JXA.PDB	O, H_MET_80	N, H_ILE_20	H, H_ILE_20	2.90	2.05	7.33

5JXA.PDB	O, H_ALA_78	N, H_CYS_22	H, H_CYS_22	2.76	2.06	29.69
5JXA.PDB	O, H_GLY_76G	N, H_ALA_24	H, H_ALA_24	2.81	1.96	7.69
5JXA.PDB	OD1, H_ASN_28	N, H_ARG_30	H, H_ARG_30	2.98	2.23	24.67
5JXA.PDB	O, H_SER_74	NH2, H_ARG_30	HH22, H_ARG_30	2.90	2.07	12.90
5JXA.PDB	O, H_ASN_28	N, H_ASP_31	H, H_ASP_31	2.98	2.13	8.21
5JXA.PDB	O, H_ILE_51	N, H_ILE_34	H, H_ILE_34	2.89	2.08	16.53
5JXA.PDB	O, H_GLY_49	N, H_TRP_36	H, H_TRP_36	2.93	2.16	21.63
5JXA.PDB	O, H_PHE_91	N, H_VAL_37	H, H_VAL_37	3.00	2.19	17.03
5JXA.PDB	O, H_GLU_46	N, H_ARG_38	H, H_ARG_38	2.95	2.12	11.49
5JXA.PDB	OE1, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.80	2.04	23.29
5JXA.PDB	OD1, H_ASP_86	NH1, H_ARG_38	HH12, H_ARG_38	2.74	1.88	4.26
5JXA.PDB	OE1, H_GLU_46	NH2, H_ARG_38	HH21, H_ARG_38	2.76	2.00	23.95
5JXA.PDB	O, H_GLU_89	N, H_LEU_39	H, H_LEU_39	2.77	1.93	11.85
5JXA.PDB	O, H_GLY_44	N, H_ILE_40	H, H_ILE_40	2.91	2.05	5.76
5JXA.PDB	O, H_ILE_40	N, H_GLY_44	H, H_GLY_44	2.97	2.17	18.25
5JXA.PDB	O, H_ARG_38	N, H_GLU_46	H, H_GLU_46	2.79	2.00	19.09
5JXA.PDB	O, H_TRP_36	N, H_ILE_48	H, H_ILE_48	2.83	1.98	7.19
5JXA.PDB	O, H_SER_58	N, H_TRP_50	H, H_TRP_50	2.83	2.05	20.31
5JXA.PDB	O, H_ILE_34	N, H_ILE_51	H, H_ILE_51	2.86	2.05	16.90
5JXA.PDB	O, H_ALA_56	N, H_LYS_52	H, H_LYS_52	2.85	2.02	13.26
5JXA.PDB	O, H_TRP_50	N, H_SER_58	H, H_SER_58	2.99	2.19	18.18
5JXA.PDB	O, H_ILE_48	N, H_ALA_60	H, H_ALA_60	2.91	2.07	7.65
5JXA.PDB	OE2, H_GLU_46	NE2, H_GLN_62	HE21, H_GLN_62	2.86	2.00	1.72
5JXA.PDB	O, H_ALA_60	N, H_LEU_63	H, H_LEU_63	2.91	2.10	16.09
5JXA.PDB	O, H_LEU_63	N, H_ARG_66	H, H_ARG_66	2.89	2.06	11.35
5JXA.PDB	OD1, H_ASP_86	NH2, H_ARG_66	HH22, H_ARG_66	2.96	2.11	6.31
5JXA.PDB	O, H_GLU_81	N, H_SER_68	H, H_SER_68	2.87	2.09	21.34
5JXA.PDB	OH, H_TYR_59	N, H_MET_69	H, H_MET_69	2.89	2.04	7.98
5JXA.PDB	O, H_PRO_52A	NE, H_ARG_71	HE, H_ARG_71	2.75	1.92	12.12
5JXA.PDB	O, H_ASP_76C	OG, H_SER_74	HG, H_SER_74	2.75	1.97	16.95
5JXA.PDB	OD1, H_ASP_76	N, H_ASP_76B	H, H_ASP_76B	2.44	1.62	14.02
5JXA.PDB	O, H_ASP_76	N, H_ASP_76C	H, H_ASP_76C	2.97	2.14	13.17
5JXA.PDB	OD2, H_ASP_76C	NE1, H_TRP_76F	HE1, H_TRP_76F	2.87	2.15	28.04
5JXA.PDB	O, H_CYS_22	N, H_ALA_78	H, H_ALA_78	2.89	2.05	10.11
5JXA.PDB	O, H_THR_70	N, H_TYR_79	H, H_TYR_79	2.80	1.95	8.03
5JXA.PDB	O, H_SER_68	N, H_GLU_81	H, H_GLU_81	2.76	1.90	6.10
5JXA.PDB	O, H_VAL_18	N, H_PHE_82	H, H_PHE_82	2.84	2.03	16.50
5JXA.PDB	O, H_ARG_66	N, H_SER_82A	H, H_SER_82A	2.80	1.99	17.15
5JXA.PDB	OD2, H_ASP_86	N, H_THR_83	H, H_THR_83	2.91	2.10	15.72
5JXA.PDB	O, H_THR_83	N, H_ASP_86	H, H_ASP_86	2.85	2.00	7.33
5JXA.PDB	O, H_THR_107	N, H_TYR_90	H, H_TYR_90	2.86	2.00	7.75
5JXA.PDB	O, H_VAL_37	N, H_PHE_91	H, H_PHE_91	2.82	1.95	8.59
5JXA.PDB	O, H_HIS_35	N, H_VAL_93	H, H_VAL_93	2.91	2.05	12.82
5JXA.PDB	O, H_TYR_102	N, H_ARG_94	H, H_ARG_94	2.93	2.09	18.47
5JXA.PDB	O, H_GLY_96	NE, H_ARG_95	HE, H_ARG_95	2.87	2.08	18.29
5JXA.PDB	O, H_GLY_96	NH2, H_ARG_95	HH21, H_ARG_95	2.95	2.20	24.49
5JXA.PDB	OD1, H_ASP_99	NH2, H_ARG_95	HH22, H_ARG_95	2.95	2.09	5.23
5JXA.PDB	OD2, L_ASP_50	OH, H_TYR_100	HH, H_TYR_100	2.57	1.75	11.76
5JXA.PDB	OH, L_TYR_36	N, H_TRP_100F	H, H_TRP_100F	2.85	2.00	7.52
5JXA.PDB	O, H_CYS_92	N, H_GLY_104	H, H_GLY_104	2.82	1.96	4.16
5JXA.PDB	O, H_GLN_6	NE2, H_GLN_105	HE22, H_GLN_105	2.97	2.19	21.71
5JXA.PDB	O, H_TYR_90	N, H_THR_107	H, H_THR_107	2.79	2.05	25.50
5JXA.PDB	O, H_SER_7	OG1, H_THR_107	HG1, H_THR_107	2.82	2.10	26.24
5JXA.PDB	O, H_ALA_88	N, H_VAL_109	H, H_VAL_109	2.99	2.13	5.29
5JXA.PDB	OG1, H_THR_87	N, H_VAL_111	H, H_VAL_111	2.97	2.11	2.98
5JXA.PDB	O, H_LYS_12	N, H_SER_112	H, H_SER_112	2.81	2.01	17.72
5JXA.PDB	OG, H_SER_112	N, H_ALA_114	H, H_ALA_114	2.92	2.06	5.24
5JXA.PDB	O, H_PHE_146	N, H_LYS_117	H, H_LYS_117	2.81	2.00	15.52

5JXA.PDB	O, H_ASP_144	NZ, H_LYS_117	HZ2, H_LYS_117	2.76	2.00	26.54
5JXA.PDB	O, H_LYS_143	N, H_SER_120	H, H_SER_120	2.88	2.02	13.76
5JXA.PDB	O, H_LEU_141	N, H_PHE_122	H, H_PHE_122	2.87	2.05	13.14
5JXA.PDB	O, H_GLY_139	N, H_LEU_124	H, H_LEU_124	2.78	1.93	6.72
5JXA.PDB	O, H_VAL_184	N, H_ALA_136	H, H_ALA_136	2.62	1.77	9.09
5JXA.PDB	O, H_LEU_124	N, H_GLY_139	H, H_GLY_139	2.90	2.16	25.91
5JXA.PDB	O, H_SER_180	N, H_CYS_140	H, H_CYS_140	2.84	2.03	17.78
5JXA.PDB	O, H_PHE_122	N, H_LEU_141	H, H_LEU_141	2.80	1.96	10.45
5JXA.PDB	O, H_LEU_178	N, H_VAL_142	H, H_VAL_142	2.71	1.86	8.75
5JXA.PDB	O, H_SER_120	N, H_LYS_143	H, H_LYS_143	2.86	2.01	6.05
5JXA.PDB	OD1, H_ASP_144	NZ, H_LYS_143	HZ3, H_LYS_143	2.92	2.12	22.30
5JXA.PDB	O, H_LYS_117	N, H_PHE_146	H, H_PHE_146	2.93	2.11	14.00
5JXA.PDB	O, H_ASN_199	N, H_THR_151	H, H_THR_151	2.95	2.12	13.67
5JXA.PDB	O, H_ASN_197	N, H_SER_153	H, H_SER_153	2.94	2.13	16.37
5JXA.PDB	OD1, H_ASN_197	OG, H_SER_153	HG, H_SER_153	2.75	1.96	17.62
5JXA.PDB	OG, H_SER_180	NE1, H_TRP_154	HE1, H_TRP_154	2.96	2.12	10.70
5JXA.PDB	O, H_ILE_195	N, H_ASN_155	H, H_ASN_155	2.75	1.91	9.52
5JXA.PDB	OD1, H_ASN_197	N, H_SER_156	H, H_SER_156	2.77	1.96	16.97
5JXA.PDB	O, H_VAL_181	N, H_HIS_164	H, H_HIS_164	2.83	2.00	13.86
5JXA.PDB	O, H_SER_179	N, H_PHE_166	H, H_PHE_166	3.00	2.16	10.32
5JXA.PDB	O, H_SER_177	N, H_VAL_169	H, H_VAL_169	2.97	2.15	15.76
5JXA.PDB	O, H_LEU_175	N, H_GLN_171	H, H_GLN_171	2.96	2.12	8.09
5JXA.PDB	O, H_LEU_175	NE2, H_GLN_171	HE21, H_GLN_171	2.90	2.06	9.29
5JXA.PDB	OD1, H_ASP_144	NE2, H_GLN_171	HE22, H_GLN_171	2.86	2.05	16.31
5JXA.PDB	O, H_GLN_171	N, H_GLY_174	H, H_GLY_174	2.95	2.10	7.88
5JXA.PDB	O, H_TYR_145	N, H_TYR_176	H, H_TYR_176	2.75	1.91	10.32
5JXA.PDB	O, H_VAL_142	N, H_LEU_178	H, H_LEU_178	2.89	2.08	16.18
5JXA.PDB	O, H_CYS_140	N, H_SER_180	H, H_SER_180	2.89	2.07	14.12
5JXA.PDB	O, H_HIS_164	N, H_VAL_181	H, H_VAL_181	2.89	2.06	12.60
5JXA.PDB	O, H_LEU_138	N, H_VAL_182	H, H_VAL_182	2.88	2.09	18.88
5JXA.PDB	O, H_ALA_136	N, H_VAL_184	H, H_VAL_184	2.85	2.04	16.24
5JXA.PDB	O, H_GLY_134	N, H_SER_186	H, H_SER_186	2.13	1.27	5.45
5JXA.PDB	O, H_PRO_185	OG, H_SER_188	HG, H_SER_188	2.58	1.75	4.20
5JXA.PDB	O, H_SER_188	N, H_GLN_192	H, H_GLN_192	2.82	1.97	8.59
5JXA.PDB	O, H_THR_193	NE2, H_GLN_192	HE21, H_GLN_192	2.91	2.09	13.40
5JXA.PDB	OG, H_SER_188	OH, H_TYR_194	HH, H_TYR_194	2.92	2.22	28.67
5JXA.PDB	OD1, H_ASN_155	N, H_ILE_195	H, H_ILE_195	2.81	2.00	16.75
5JXA.PDB	O, H_LYS_209	N, H_CYS_196	H, H_CYS_196	2.97	2.21	23.72
5JXA.PDB	O, H_SER_153	N, H_ASN_197	H, H_ASN_197	2.71	1.87	7.78
5JXA.PDB	O, H_VAL_207	N, H_VAL_198	H, H_VAL_198	2.72	1.86	4.76
5JXA.PDB	O, H_THR_151	N, H_ASN_199	H, H_ASN_199	2.95	2.11	11.96
5JXA.PDB	O, H_THR_205	N, H_HIS_200	H, H_HIS_200	2.85	2.00	9.64
5JXA.PDB	O, H_PRO_147	NE2, H_HIS_200	HE2, H_HIS_200	2.71	1.87	10.25
5JXA.PDB	ND1, H_HIS_200	OG, H_SER_203	HG, H_SER_203	2.82	2.10	26.44
5JXA.PDB	O, H_LYS_201	N, H_ASN_204	H, H_ASN_204	2.83	2.01	13.96
5JXA.PDB	O, H_VAL_198	N, H_VAL_207	H, H_VAL_207	2.84	2.02	14.35
5JXA.PDB	O, H_CYS_196	N, H_LYS_209	H, H_LYS_209	2.96	2.14	15.80
5JXA.PDB	O, H_TYR_194	N, H_VAL_211	H, H_VAL_211	2.90	2.05	6.52
5JXA.PDB	OG, L_SER_26	N, L_VAL_3	H, L_VAL_3	2.90	2.06	10.44
5JXA.PDB	O, L_LYS_24	N, L_THR_5	H, L_THR_5	2.81	1.98	12.20
5JXA.PDB	O, L_TYR_86	NE2, L_GLN_6	HE22, L_GLN_6	2.89	2.07	15.63
5JXA.PDB	O, L_GLU_103	N, L_LEU_11	H, L_LEU_11	2.77	1.93	11.05
5JXA.PDB	OE1, L_GLU_17	N, L_SER_14	H, L_SER_14	2.78	1.95	10.28
5JXA.PDB	O, L_LEU_78	N, L_GLY_16	H, L_GLY_16	2.83	2.05	20.59
5JXA.PDB	O, L_SER_14	N, L_GLU_17	H, L_GLU_17	2.99	2.14	6.52
5JXA.PDB	O, L_ILE_75	N, L_ALA_19	H, L_ALA_19	2.95	2.13	15.15
5JXA.PDB	O, L_LEU_73	N, L_LEU_21	H, L_LEU_21	2.85	2.01	11.82
5JXA.PDB	O, L_SER_7	N, L_PHE_22	H, L_PHE_22	2.93	2.08	9.65

5JXA.PDB	O, L_PHE.71	N, L_CYS.23	H, L_CYS.23	2.86	2.02	10.81
5JXA.PDB	O, L_THR.5	N, L_LYS.24	H, L_LYS.24	2.95	2.10	7.38
5JXA.PDB	O, L_THR.69	N, L_ALA.25	H, L_ALA.25	2.83	2.00	12.63
5JXA.PDB	O, L_ILE.48	N, L_TRP.35	H, L_TRP.35	2.93	2.10	13.22
5JXA.PDB	O, L_TYR.87	N, L_TYR.36	H, L_TYR.36	2.78	1.95	13.00
5JXA.PDB	OE1, L_GLN.89	OH, L_TYR.36	HH, L_TYR.36	2.71	1.91	14.07
5JXA.PDB	O, L_ARG.45	N, L_GLN.37	H, L_GLN.37	2.89	2.06	13.47
5JXA.PDB	OH, L_TYR.86	NE2, L_GLN.37	HE21, L_GLN.37	2.99	2.15	10.29
5JXA.PDB	O, L_VAL.85	N, L_LYS.38	H, L_LYS.38	2.75	1.89	4.40
5JXA.PDB	O, L_GLN.42	NZ, L_LYS.38	HZ3, L_LYS.38	2.71	1.90	27.32
5JXA.PDB	O, L_GLU.81	NE, L_ARG.39	HE, L_ARG.39	2.78	1.86	16.81
5JXA.PDB	O, L_ARG.39	N, L_GLN.42	H, L_GLN.42	2.96	2.14	14.42
5JXA.PDB	O, L_GLN.37	N, L_ARG.45	H, L_ARG.45	2.85	2.09	23.31
5JXA.PDB	O, L_TRP.35	N, L_LEU.47	H, L_LEU.47	2.90	2.06	9.03
5JXA.PDB	O, L_ARG.53	N, L_TYR.49	H, L_TYR.49	2.87	2.07	17.25
5JXA.PDB	O, L_MET.33	N, L_THR.51	H, L_THR.51	2.75	1.91	11.49
5JXA.PDB	O, L_TYR.49	N, L_ARG.53	H, L_ARG.53	2.88	2.10	22.06
5JXA.PDB	OH, H_TYR.100	NH2, L_ARG.53	HH21, L_ARG.53	2.89	2.07	18.12
5JXA.PDB	O, L_LEU.47	N, L_ALA.55	H, L_ALA.55	2.99	2.14	7.32
5JXA.PDB	OD2, L_ASP.82	NE, L_ARG.61	HE, L_ARG.61	2.88	2.15	27.19
5JXA.PDB	OD1, L_ASP.82	NH2, L_ARG.61	HH21, L_ARG.61	2.84	1.98	2.45
5JXA.PDB	O, L_THR.74	N, L_VAL.63	H, L_VAL.63	2.82	1.99	13.39
5JXA.PDB	O, L_PHE.72	N, L_SER.65	H, L_SER.65	2.91	2.10	15.27
5JXA.PDB	OD1, L_ASP.70	OG1, L_THR.69	HG1, L_THR.69	2.92	2.09	7.50
5JXA.PDB	O, L_CYS.23	N, L_PHE.71	H, L_PHE.71	2.96	2.17	20.10
5JXA.PDB	O, L_SER.65	N, L_PHE.72	H, L_PHE.72	2.92	2.09	12.41
5JXA.PDB	O, L_LEU.21	N, L_LEU.73	H, L_LEU.73	2.92	2.12	19.36
5JXA.PDB	O, L_VAL.63	N, L_THR.74	H, L_THR.74	2.86	2.00	5.29
5JXA.PDB	O, L_ALA.19	N, L_ILE.75	H, L_ILE.75	2.87	2.05	14.95
5JXA.PDB	O, L_ARG.61	N, L_ASN.76	H, L_ASN.76	2.88	2.03	8.54
5JXA.PDB	O, L_GLU.17	N, L_LEU.78	H, L_LEU.78	2.83	2.01	13.81
5JXA.PDB	OD2, L_ASP.82	N, L_ASP.79	H, L_ASP.79	2.65	1.79	5.80
5JXA.PDB	OD2, L_ASP.79	N, L_GLU.81	H, L_GLU.81	2.94	2.08	2.69
5JXA.PDB	O, L_ASP.79	N, L_ASP.82	H, L_ASP.82	2.79	1.95	7.93
5JXA.PDB	O, L_SER.102	N, L_TYR.86	H, L_TYR.86	2.86	2.03	12.51
5JXA.PDB	O, L_ASP.82	OH, L_TYR.86	HH, L_TYR.86	2.60	1.79	10.99
5JXA.PDB	O, L_TYR.36	N, L_TYR.87	H, L_TYR.87	2.95	2.13	15.47
5JXA.PDB	O, L_THR.34	N, L_GLN.89	H, L_GLN.89	2.89	2.18	29.17
5JXA.PDB	O, L_PHE.97	N, L_GLN.90	H, L_GLN.90	2.95	2.17	21.39
5JXA.PDB	O, L_GLN.90	N, L_PHE.97	H, L_PHE.97	2.85	2.03	15.63
5JXA.PDB	O, L_CYS.88	N, L_GLY.99	H, L_GLY.99	2.94	2.12	17.39
5JXA.PDB	OE1, L_GLN.6	N, L_GLY.101	H, L_GLY.101	2.89	2.15	26.61
5JXA.PDB	O, L_TYR.86	N, L_SER.102	H, L_SER.102	2.89	2.08	16.76
5JXA.PDB	O, L_PRO.8	OG, L_SER.102	HG, L_SER.102	2.69	2.00	29.55
5JXA.PDB	O, L_GLY.9	N, L_GLU.103	H, L_GLU.103	2.89	2.04	6.77
5JXA.PDB	O, L_ALA.84	N, L_LEU.104	H, L_LEU.104	2.88	2.04	11.59
5JXA.PDB	O, L_LEU.11	N, L_GLU.105	H, L_GLU.105	2.90	2.07	12.41
5JXA.PDB	OE1, L_GLN.166	N, L_VAL.106	H, L_VAL.106	2.98	2.12	4.21
5JXA.PDB	O, L_LEU.13	N, L_HIS.107	H, L_HIS.107	2.92	2.09	12.00
5JXA.PDB	O, L_THR.109	NE, L_ARG.108	HE, L_ARG.108	2.85	2.02	11.20
5JXA.PDB	O, L_ASP.170	NH1, L_ARG.108	HH11, L_ARG.108	2.90	2.05	7.50
5JXA.PDB	O, L_TYR.140	N, L_ALA.111	H, L_ALA.111	2.88	2.04	11.67
5JXA.PDB	O, L_LEU.135	N, L_PHE.116	H, L_PHE.116	2.95	2.16	18.98
5JXA.PDB	O, L_VAL.133	N, L_PHE.118	H, L_PHE.118	2.79	1.99	17.84
5JXA.PDB	OG, L_SER.131	NE2, L_GLN.124	HE22, L_GLN.124	2.80	1.95	4.80
5JXA.PDB	O, L_GLN.124	N, L_SER.127	H, L_SER.127	2.78	1.98	17.11
5JXA.PDB	O, L_LEU.125	N, L_GLY.128	H, L_GLY.128	2.90	2.04	5.48
5JXA.PDB	O, L_LEU.181	N, L_ALA.130	H, L_ALA.130	2.76	1.92	10.28

5JXA.PDB	OE1, L_GLN_124	N, L_SER_131	H, L_SER_131	3.00	2.18	14.97
5JXA.PDB	O, L_LEU_179	N, L_VAL_132	H, L_VAL_132	2.83	1.99	9.70
5JXA.PDB	O, L_SER_177	N, L_CYS_134	H, L_CYS_134	2.84	2.01	12.61
5JXA.PDB	O, L_PHE_116	N, L_LEU_135	H, L_LEU_135	2.76	1.91	8.80
5JXA.PDB	O, L_LEU_175	N, L_LEU_136	H, L_LEU_136	2.76	1.91	4.29
5JXA.PDB	O, L_SER_114	N, L_ASN_137	H, L_ASN_137	2.86	2.06	16.81
5JXA.PDB	O, L_TYR_173	N, L_PHE_139	H, L_PHE_139	2.83	2.00	12.08
5JXA.PDB	O, L_ALA_111	N, L_TYR_140	H, L_TYR_140	2.95	2.14	16.31
5JXA.PDB	OE1, L_GLU_105	OH, L_TYR_140	HH, L_TYR_140	2.43	1.65	17.73
5JXA.PDB	OE1, L_GLU_103	NH1, L_ARG_142	HH12, L_ARG_142	2.87	2.05	14.46
5JXA.PDB	OH, L_TYR_173	NH2, L_ARG_142	HH21, L_ARG_142	2.84	2.07	21.88
5JXA.PDB	OE2, L_GLU_103	NH2, L_ARG_142	HH22, L_ARG_142	2.79	1.94	8.50
5JXA.PDB	O, L_THR_197	N, L_LYS_145	H, L_LYS_145	2.95	2.11	9.81
5JXA.PDB	O, L_GLU_195	N, L_GLN_147	H, L_GLN_147	2.80	1.97	13.47
5JXA.PDB	O, L_TRP_148	NE2, L_GLN_147	HE21, L_GLN_147	2.90	2.05	7.67
5JXA.PDB	OG, L_SER_177	NE1, L_TRP_148	HE1, L_TRP_148	2.86	2.05	17.07
5JXA.PDB	O, L_ALA_193	N, L_LYS_149	H, L_LYS_149	2.88	2.05	13.32
5JXA.PDB	O, L_ALA_153	N, L_VAL_150	H, L_VAL_150	3.00	2.18	15.98
5JXA.PDB	O, L_VAL_191	N, L_ASP_151	H, L_ASP_151	2.79	1.95	10.19
5JXA.PDB	O, L_VAL_150	N, L_ALA_153	H, L_ALA_153	2.90	2.07	13.09
5JXA.PDB	O, L_TRP_148	N, L_GLN_155	H, L_GLN_155	2.93	2.09	9.40
5JXA.PDB	OE1, L_GLN_155	ND2, L_ASN_158	HD21, L_ASN_158	2.94	2.10	10.59
5JXA.PDB	O, H_LEU_170	NE2, L_GLN_160	HE22, L_GLN_160	2.84	1.99	4.55
5JXA.PDB	O, L_SER_176	N, L_SER_162	H, L_SER_162	2.98	2.19	20.08
5JXA.PDB	O, H_PRO_167	OG, L_SER_162	HG, L_SER_162	2.69	1.94	23.37
5JXA.PDB	O, L_SER_171	NE2, L_GLN_166	HE21, L_GLN_166	2.90	2.05	9.75
5JXA.PDB	O, L_VAL_106	NE2, L_GLN_166	HE22, L_GLN_166	2.89	2.10	19.46
5JXA.PDB	O, L_THR_172	N, L_ASP_167	H, L_ASP_167	2.83	2.01	13.03
5JXA.PDB	OD2, L_ASP_167	N, L_LYS_169	H, L_LYS_169	2.81	2.02	19.97
5JXA.PDB	OD2, L_ASP_167	N, L_ASP_170	H, L_ASP_170	2.85	2.02	14.37
5JXA.PDB	O, L_ASP_167	N, L_SER_171	H, L_SER_171	2.99	2.25	26.24
5JXA.PDB	OD1, L_ASP_170	N, L_THR_172	H, L_THR_172	2.91	2.07	10.06
5JXA.PDB	OD1, L_ASP_170	OG1, L_THR_172	HG1, L_THR_172	2.69	1.87	10.60
5JXA.PDB	O, L_PHE_139	N, L_TYR_173	H, L_TYR_173	2.81	1.97	11.11
5JXA.PDB	OE2, L_GLU_105	OH, L_TYR_173	HH, L_TYR_173	2.63	1.83	14.46
5JXA.PDB	OG1, L_THR_164	N, L_SER_174	H, L_SER_174	2.99	2.15	10.27
5JXA.PDB	O, L_LEU_136	N, L_LEU_175	H, L_LEU_175	2.81	2.01	18.94
5JXA.PDB	O, L_SER_162	N, L_SER_176	H, L_SER_176	2.93	2.11	14.73
5JXA.PDB	O, L_CYS_134	N, L_SER_177	H, L_SER_177	2.85	2.03	14.72
5JXA.PDB	O, L_GLN_160	N, L_THR_178	H, L_THR_178	2.87	2.05	14.07
5JXA.PDB	O, L_VAL_132	N, L_LEU_179	H, L_LEU_179	2.77	1.94	12.42
5JXA.PDB	O, L_ALA_130	N, L_LEU_181	H, L_LEU_181	2.90	2.06	10.98
5JXA.PDB	O, L_GLY_128	N, L_LYS_183	H, L_LYS_183	2.84	2.03	16.09
5JXA.PDB	O, L_SER_182	N, L_TYR_186	H, L_TYR_186	2.88	2.05	12.31
5JXA.PDB	O, L_LYS_183	N, L_GLU_187	H, L_GLU_187	2.94	2.15	20.11
5JXA.PDB	OD1, L_ASP_185	NZ, L_LYS_188	HZ2, L_LYS_188	2.85	2.03	19.98
5JXA.PDB	OD1, L_ASP_151	N, L_VAL_191	H, L_VAL_191	2.74	1.89	7.60
5JXA.PDB	O, L_PHE_209	N, L_TYR_192	H, L_TYR_192	2.93	2.07	4.78
5JXA.PDB	O, L_LYS_149	N, L_ALA_193	H, L_ALA_193	2.95	2.14	18.10
5JXA.PDB	O, L_LYS_207	N, L_CYS_194	H, L_CYS_194	2.83	1.98	9.36
5JXA.PDB	O, L_GLN_147	N, L_GLU_195	H, L_GLU_195	2.80	1.95	6.91
5JXA.PDB	O, L_VAL_205	N, L_VAL_196	H, L_VAL_196	2.78	1.95	10.55
5JXA.PDB	O, L_LYS_145	N, L_THR_197	H, L_THR_197	2.82	1.99	11.86
5JXA.PDB	O, L_PRO_141	NE2, L_HIS_198	HE2, L_HIS_198	2.88	2.05	12.53
5JXA.PDB	ND1, L_HIS_198	N, L_GLY_200	H, L_GLY_200	2.95	2.09	3.68
5JXA.PDB	O, L_HIS_198	N, L_LEU_201	H, L_LEU_201	2.92	2.08	9.11
5JXA.PDB	O, L_TYR_192	N, L_PHE_209	H, L_PHE_209	2.96	2.19	22.81
5JXA.PDB	OE2, L_GLU_213	ND2, L_ASN_210	HD22, L_ASN_210	2.76	1.93	12.84

5JXA.PDB	O, L_LYS_190	N, L_ARG_211	H, L_ARG_211	2.77	1.93	11.49
5JXA.PDB	O, L_HIS_189	NE, L_ARG_211	HE, L_ARG_211	2.81	1.95	5.90
5JXA.PDB	O, L_ASN_210	N, L_GLU_213	H, L_GLU_213	2.99	2.18	16.84
5M2C.PDB	OD1, A_ASN_115	N, A_GLN_118	H, A_GLN_118	2.65	1.88	23.04
5M2C.PDB	O, A_LYS_116	N, A_ALA_120	H, A_ALA_120	2.80	1.94	5.96
5M2C.PDB	O, A_ASP_117	N, A_LYS_121	H, A_LYS_121	2.93	2.08	6.70
5M2C.PDB	O, A_GLN_118	N, A_ASP_122	H, A_ASP_122	2.87	2.05	16.09
5M2C.PDB	O, A_ILE_119	N, A_VAL_123	H, A_VAL_123	2.90	2.07	12.20
5M2C.PDB	O, A_ALA_120	N, A_LYS_124	H, A_LYS_124	2.89	2.06	12.17
5M2C.PDB	OD1, A_ASP_195	NZ, A_LYS_124	HZ1, A_LYS_124	2.99	2.26	29.03
5M2C.PDB	O, A_LYS_121	N, A_GLN_125	H, A_GLN_125	2.83	2.00	12.74
5M2C.PDB	O, A_ASP_122	N, A_PHE_126	H, A_PHE_126	2.85	2.04	15.29
5M2C.PDB	O, A_VAL_123	N, A_TYR_127	H, A_TYR_127	2.79	1.94	7.39
5M2C.PDB	O, A_LYS_124	N, A_ASP_128	H, A_ASP_128	2.86	2.06	18.46
5M2C.PDB	O, A_TYR_127	N, A_LEU_131	H, A_LEU_131	2.86	2.03	12.22
5M2C.PDB	O, A_ALA_130	N, A_ALA_134	H, A_ALA_134	2.83	2.04	19.67
5M2C.PDB	O, A_ASN_142	N, A_VAL_146	H, A_VAL_146	2.94	2.13	15.93
5M2C.PDB	O, A_ALA_143	N, A_VAL_147	H, A_VAL_147	2.90	2.05	6.08
5M2C.PDB	O, A_LYS_144	N, A_LYS_148	H, A_LYS_148	2.93	2.10	12.46
5M2C.PDB	O, A_VAL_146	N, A_PHE_150	H, A_PHE_150	2.92	2.07	6.77
5M2C.PDB	O, A_VAL_147	N, A_HIS_151	H, A_HIS_151	2.88	2.04	10.85
5M2C.PDB	O, A_LEU_174	ND1, A_HIS_151	HD1, A_HIS_151	2.73	1.92	15.82
5M2C.PDB	OH, A_TYR_127	NE2, A_HIS_151	HE2, A_HIS_151	2.61	1.77	12.06
5M2C.PDB	O, A_LYS_148	N, A_GLU_152	H, A_GLU_152	2.86	2.05	15.70
5M2C.PDB	O, A_THR_149	N, A_THR_153	H, A_THR_153	2.91	2.10	16.77
5M2C.PDB	O, A_THR_149	OG1, A_THR_153	HG1, A_THR_153	2.64	1.94	28.18
5M2C.PDB	O, A_PHE_150	N, A_LEU_154	H, A_LEU_154	2.87	2.06	17.25
5M2C.PDB	OG1, A_THR_163	N, A_SER_160	H, A_SER_160	2.95	2.16	19.89
5M2C.PDB	OG, A_SER_159	OG1, A_THR_163	HG1, A_THR_163	2.88	2.07	13.51
5M2C.PDB	O, A_SER_160	N, A_ALA_164	H, A_ALA_164	2.88	2.08	17.84
5M2C.PDB	O, A_THR_163	N, A_THR_167	H, A_THR_167	3.00	2.16	10.84
5M2C.PDB	O, A_THR_163	OG1, A_THR_167	HG1, A_THR_167	2.60	1.83	18.83
5M2C.PDB	O, A_ALA_164	N, A_SER_168	H, A_SER_168	2.91	2.11	17.88
5M2C.PDB	O, A_LEU_165	N, A_VAL_169	H, A_VAL_169	2.99	2.26	28.05
5M2C.PDB	O, A_THR_166	N, A_LEU_170	H, A_LEU_170	2.75	1.89	5.46
5M2C.PDB	O, A_THR_167	N, A_LYS_171	H, A_LYS_171	2.68	1.86	14.38
5M2C.PDB	O, A_LYS_171	N, A_LEU_174	H, A_LEU_174	2.89	2.03	5.60
5M2C.PDB	O, A_ASN_172	N, A_CYS_175	H, A_CYS_175	2.92	2.11	15.91
5M2C.PDB	O, A_PRO_176	N, A_SER_179	H, A_SER_179	2.98	2.16	15.63
5M2C.PDB	O, A_PRO_176	OG, A_SER_179	HG, A_SER_179	2.63	1.93	27.89
5M2C.PDB	OG, A_SER_183	N, A_ASN_180	H, A_ASN_180	2.83	2.08	25.30
5M2C.PDB	O, A_ASN_180	N, A_ASN_184	H, A_ASN_184	2.95	2.10	7.28
5M2C.PDB	OG, A_SER_179	ND2, A_ASN_184	HD21, A_ASN_184	2.93	2.13	18.24
5M2C.PDB	O, A_SER_183	N, A_PHE_186	H, A_PHE_186	2.77	1.95	13.31
5M2C.PDB	O, A_GLY_158	N, A_CYS_190	H, A_CYS_190	2.73	1.87	5.91
5M2C.PDB	OD2, A_ASP_128	NE2, A_HIS_191	HE2, A_HIS_191	2.69	1.84	6.13
5M2C.PDB	OD2, A_ASP_189	N, A_GLN_192	H, A_GLN_192	2.84	2.00	11.08
5M2C.PDB	O, A_CYS_190	N, A_ILE_194	H, A_ILE_194	2.93	2.11	15.42
5M2C.PDB	O, A_HIS_191	N, A_ASP_195	H, A_ASP_195	2.87	2.03	10.69
5M2C.PDB	O, A_GLN_192	N, A_ASP_196	H, A_ASP_196	2.80	2.05	24.04
5M2C.PDB	O, A_LYS_193	N, A_LEU_197	H, A_LEU_197	2.95	2.18	21.85
5M2C.PDB	O, A_ASP_195	OG, A_SER_199	HG, A_SER_199	2.79	2.04	23.21
5M2C.PDB	O, A_ASP_196	N, A_LYS_201	H, A_LYS_201	2.85	2.04	17.50
5M2C.PDB	OD1, B_ASN_115	N, B_GLN_118	H, B_GLN_118	2.50	1.70	17.47
5M2C.PDB	O, B_LYS_116	N, B_ALA_120	H, B_ALA_120	2.85	2.00	7.33
5M2C.PDB	O, B_ASP_117	N, B_LYS_121	H, B_LYS_121	2.86	2.01	8.98
5M2C.PDB	O, B_GLN_118	N, B_ASP_122	H, B_ASP_122	2.84	2.03	16.46
5M2C.PDB	O, B_ILE_119	N, B_VAL_123	H, B_VAL_123	2.89	2.07	14.86

5M2C.PDB	O, B_ALA_120	N, B_LYS_124	H, B_LYS_124	2.93	2.08	10.04
5M2C.PDB	O, B_LYS_121	N, B_GLN_125	H, B_GLN_125	2.84	2.01	12.48
5M2C.PDB	O, B_ASP_122	N, B_PHE_126	H, B_PHE_126	2.86	2.06	18.89
5M2C.PDB	O, B_VAL_123	N, B_TYR_127	H, B_TYR_127	2.81	1.97	10.19
5M2C.PDB	O, B_LYS_124	N, B_ASP_128	H, B_ASP_128	2.88	2.10	21.63
5M2C.PDB	O, B_TYR_127	N, B_LEU_131	H, B_LEU_131	2.85	2.02	11.94
5M2C.PDB	O, B_ALA_130	N, B_ALA_134	H, B_ALA_134	2.90	2.12	20.23
5M2C.PDB	O, B_ASN_142	N, B_VAL_146	H, B_VAL_146	2.99	2.15	11.45
5M2C.PDB	O, B_ALA_143	N, B_VAL_147	H, B_VAL_147	2.91	2.05	3.26
5M2C.PDB	O, B_LYS_144	N, B_LYS_148	H, B_LYS_148	2.96	2.14	15.99
5M2C.PDB	O, B_ALA_145	N, B_THR_149	H, B_THR_149	2.98	2.21	21.80
5M2C.PDB	O, B_ALA_145	OG1, B_THR_149	HG1, B_THR_149	2.78	1.99	18.17
5M2C.PDB	O, B_VAL_146	N, B_PHE_150	H, B_PHE_150	2.91	2.07	8.81
5M2C.PDB	O, B_VAL_147	N, B_HIS_151	H, B_HIS_151	2.89	2.07	14.41
5M2C.PDB	O, B_LEU_174	ND1, B_HIS_151	HD1, B_HIS_151	2.73	1.93	16.98
5M2C.PDB	OH, B_TYR_127	NE2, B_HIS_151	HE2, B_HIS_151	2.61	1.78	13.01
5M2C.PDB	O, B_LYS_148	N, B_GLU_152	H, B_GLU_152	2.84	2.02	14.19
5M2C.PDB	O, B_THR_149	N, B_THR_153	H, B_THR_153	2.90	2.09	15.77
5M2C.PDB	O, B_PHE_150	N, B_LEU_154	H, B_LEU_154	2.88	2.08	18.38
5M2C.PDB	O, B_SER_160	N, B_ALA_164	H, B_ALA_164	2.89	2.09	18.03
5M2C.PDB	O, B_THR_163	N, B_THR_167	H, B_THR_167	2.99	2.16	11.49
5M2C.PDB	O, B_THR_163	OG1, B_THR_167	HG1, B_THR_167	2.57	1.79	17.65
5M2C.PDB	O, B_ALA_164	N, B_SER_168	H, B_SER_168	2.89	2.09	18.74
5M2C.PDB	O, B_LEU_165	N, B_VAL_169	H, B_VAL_169	2.94	2.15	19.39
5M2C.PDB	O, B_THR_166	N, B_LEU_170	H, B_LEU_170	2.77	1.92	7.49
5M2C.PDB	O, B_THR_167	N, B_LYS_171	H, B_LYS_171	2.70	1.89	16.35
5M2C.PDB	O, B_LYS_171	N, B_LEU_174	H, B_LEU_174	2.94	2.09	4.41
5M2C.PDB	O, B_ASN_172	N, B_CYS_175	H, B_CYS_175	2.97	2.15	14.80
5M2C.PDB	O, B_PRO_176	OG, B_SER_179	HG, B_SER_179	2.63	1.92	26.26
5M2C.PDB	OG, B_SER_183	N, B_ASN_180	H, B_ASN_180	2.76	1.98	21.29
5M2C.PDB	O, B_ASN_180	N, B_ASN_184	H, B_ASN_184	2.89	2.04	8.95
5M2C.PDB	OG, B_SER_179	ND2, B_ASN_184	HD21, B_ASN_184	2.89	2.10	19.97
5M2C.PDB	O, B_SER_183	N, B_PHE_186	H, B_PHE_186	2.92	2.09	13.99
5M2C.PDB	O, B_GLY_158	N, B_CYS_190	H, B_CYS_190	2.71	1.85	3.39
5M2C.PDB	OD2, B_ASP_128	NE2, B_HIS_191	HE2, B_HIS_191	2.71	1.86	7.63
5M2C.PDB	OD2, B_ASP_189	N, B_GLN_192	H, B_GLN_192	2.90	2.07	13.53
5M2C.PDB	O, B_CYS_190	N, B_ILE_194	H, B_ILE_194	2.91	2.10	17.50
5M2C.PDB	O, B_HIS_191	N, B_ASP_195	H, B_ASP_195	2.87	2.03	11.04
5M2C.PDB	O, B_GLN_192	N, B_ASP_196	H, B_ASP_196	2.81	2.05	23.43
5M2C.PDB	O, B_ASP_195	N, B_SER_199	H, B_SER_199	2.98	2.26	28.48
5M2C.PDB	O, B_ASP_195	OG, B_SER_199	HG, B_SER_199	2.85	2.13	27.00
5M2C.PDB	O, B_ASP_196	N, B_LYS_201	H, B_LYS_201	2.97	2.16	15.75
5M33.PDB	O, A_GLU_110	N, A_PHE_113	H, A_PHE_113	2.89	2.13	23.34
5M33.PDB	OD1, A_ASN_115	N, A_GLN_118	H, A_GLN_118	2.87	2.05	15.86
5M33.PDB	OD1, A_ASP_122	NE2, A_GLN_118	HE21, A_GLN_118	2.92	2.20	28.21
5M33.PDB	O, A_GLN_118	N, A_ASP_122	H, A_ASP_122	2.91	2.09	14.98
5M33.PDB	O, A_ILE_119	N, A_VAL_123	H, A_VAL_123	2.90	2.08	14.75
5M33.PDB	O, A_ALA_120	N, A_LYS_124	H, A_LYS_124	2.97	2.13	9.03
5M33.PDB	OD1, A_ASP_195	NZ, A_LYS_124	HZ3, A_LYS_124	2.81	2.00	20.18
5M33.PDB	O, A_LYS_121	N, A_GLN_125	H, A_GLN_125	2.95	2.14	15.95
5M33.PDB	O, A_ASP_122	N, A_PHE_126	H, A_PHE_126	2.85	2.02	12.96
5M33.PDB	O, A_VAL_123	N, A_TYR_127	H, A_TYR_127	2.90	2.06	8.97
5M33.PDB	NE2, A_HIS_151	OH, A_TYR_127	HH, A_TYR_127	2.74	1.90	5.54
5M33.PDB	O, A_LYS_124	N, A_ASP_128	H, A_ASP_128	2.96	2.14	15.35
5M33.PDB	O, A_GLN_125	N, A_GLN_129	H, A_GLN_129	2.89	2.05	10.97
5M33.PDB	O, A_TYR_127	N, A_LEU_131	H, A_LEU_131	2.85	2.03	13.94
5M33.PDB	O, A_ALA_130	N, A_ALA_134	H, A_ALA_134	2.84	2.03	15.90
5M33.PDB	O, A_GLN_133	N, A_ASP_137	H, A_ASP_137	2.89	2.12	21.46

5M33.PDB	O, A_ASP_139	N, A_ASN_141	H, A_ASN_141	2.85	2.12	27.58
5M33.PDB	O, A_ALA_140	N, A_LYS_144	H, A_LYS_144	2.99	2.14	7.21
5M33.PDB	O, A_ALA_134	NZ, A_LYS_144	HZ1, A_LYS_144	2.63	1.88	27.02
5M33.PDB	O, A_ASN_142	N, A_VAL_146	H, A_VAL_146	2.83	2.01	15.56
5M33.PDB	O, A_LYS_144	N, A_LYS_148	H, A_LYS_148	2.98	2.13	8.41
5M33.PDB	O, A_ALA_145	N, A_THR_149	H, A_THR_149	2.97	2.14	13.99
5M33.PDB	O, A_ALA_145	OG1, A_THR_149	HG1, A_THR_149	2.90	2.10	14.64
5M33.PDB	O, A_VAL_146	N, A_PHE_150	H, A_PHE_150	2.90	2.07	12.70
5M33.PDB	O, A_VAL_147	N, A_HIS_151	H, A_HIS_151	2.86	2.03	12.68
5M33.PDB	O, A_LEU_174	ND1, A_HIS_151	HD1, A_HIS_151	2.74	1.89	6.51
5M33.PDB	O, A_LYS_148	N, A_GLU_152	H, A_GLU_152	2.94	2.12	14.44
5M33.PDB	O, A_THR_149	N, A_THR_153	H, A_THR_153	2.89	2.04	7.79
5M33.PDB	O, A_PHE_150	N, A_LEU_154	H, A_LEU_154	2.88	2.05	10.83
5M33.PDB	OD2, A_ASP_189	N, A_SER_160	H, A_SER_160	2.83	2.06	21.68
5M33.PDB	O, A_LEU_162	N, A_LEU_165	H, A_LEU_165	2.91	2.09	16.07
5M33.PDB	O, A_LEU_165	N, A_VAL_169	H, A_VAL_169	2.92	2.13	19.68
5M33.PDB	O, A_THR_166	N, A_LEU_170	H, A_LEU_170	2.91	2.09	13.68
5M33.PDB	O, A_PRO_176	N, A_SER_179	H, A_SER_179	2.93	2.10	12.30
5M33.PDB	O, A_ASN_180	N, A_ASN_184	H, A_ASN_184	2.90	2.08	14.21
5M33.PDB	O, A_CYS_157	ND2, A_ASN_184	HD21, A_ASN_184	2.88	2.04	11.64
5M33.PDB	OD1, A_ASP_155	NZ, A_LYS_187	HZ1, A_LYS_187	2.82	1.95	10.61
5M33.PDB	O, A_GLY_158	N, A_CYS_190	H, A_CYS_190	2.93	2.07	4.56
5M33.PDB	OD2, A_ASP_189	N, A_HIS_191	H, A_HIS_191	2.98	2.19	19.93
5M33.PDB	OD2, A_ASP_128	NE2, A_HIS_191	HE2, A_HIS_191	2.76	2.00	23.16
5M33.PDB	OD1, A_ASP_196	NE2, A_GLN_192	HE21, A_GLN_192	2.98	2.18	18.41
5M33.PDB	OE1, A_GLU_188	NZ, A_LYS_193	HZ2, A_LYS_193	2.93	2.07	12.47
5M33.PDB	O, A_CYS_190	N, A_ILE_194	H, A_ILE_194	2.89	2.07	15.58
5M33.PDB	O, A_HIS_191	N, A_ASP_195	H, A_ASP_195	2.97	2.13	8.98
5M33.PDB	O, A_GLN_192	N, A_ASP_196	H, A_ASP_196	2.88	2.06	14.98
5M33.PDB	O, A_ASP_195	N, A_SER_199	H, A_SER_199	2.93	2.19	25.46
5M33.PDB	O, A_ASP_196	N, A_LYS_201	H, A_LYS_201	2.86	2.03	14.10
5M33.PDB	OE1, A_GLN_129	N, B_VAL_114	H, B_VAL_114	2.67	1.84	13.32
5M33.PDB	OD1, B_ASN_115	N, B_GLN_118	H, B_GLN_118	2.98	2.19	19.82
5M33.PDB	OD1, B_ASP_122	NE2, B_GLN_118	HE21, B_GLN_118	2.96	2.19	23.61
5M33.PDB	O, B_GLN_118	N, B_ASP_122	H, B_ASP_122	2.94	2.12	14.74
5M33.PDB	O, B_ILE_119	N, B_VAL_123	H, B_VAL_123	2.92	2.09	14.21
5M33.PDB	O, B_ALA_120	N, B_LYS_124	H, B_LYS_124	2.95	2.13	13.05
5M33.PDB	O, B_LYS_121	N, B_GLN_125	H, B_GLN_125	2.97	2.15	14.67
5M33.PDB	O, B_ASP_122	N, B_PHE_126	H, B_PHE_126	2.83	2.02	16.58
5M33.PDB	O, B_VAL_123	N, B_TYR_127	H, B_TYR_127	2.90	2.05	7.34
5M33.PDB	NE2, B_HIS_151	OH, B_TYR_127	HH, B_TYR_127	2.78	1.94	5.42
5M33.PDB	O, B_LYS_124	N, B_ASP_128	H, B_ASP_128	2.88	2.07	15.69
5M33.PDB	O, B_GLN_125	N, B_GLN_129	H, B_GLN_129	3.00	2.18	15.70
5M33.PDB	OE1, B_GLN_133	NE2, B_GLN_129	HE22, B_GLN_129	2.83	2.06	21.87
5M33.PDB	O, B_TYR_127	N, B_LEU_131	H, B_LEU_131	2.88	2.05	11.48
5M33.PDB	O, B_GLN_129	N, B_GLN_133	H, B_GLN_133	2.98	2.15	12.11
5M33.PDB	O, B_ALA_130	N, B_ALA_134	H, B_ALA_134	2.83	2.07	24.03
5M33.PDB	O, B_ALA_134	NZ, B_LYS_144	HZ2, B_LYS_144	2.73	1.99	28.33
5M33.PDB	O, B_ALA_143	N, B_VAL_147	H, B_VAL_147	2.84	1.99	5.95
5M33.PDB	O, B_LYS_144	N, B_LYS_148	H, B_LYS_148	2.93	2.08	9.25
5M33.PDB	O, B_ALA_145	N, B_THR_149	H, B_THR_149	2.93	2.11	14.19
5M33.PDB	O, B_ALA_145	OG1, B_THR_149	HG1, B_THR_149	2.85	2.11	23.29
5M33.PDB	O, B_VAL_146	N, B_PHE_150	H, B_PHE_150	2.93	2.09	9.45
5M33.PDB	O, B_VAL_147	N, B_HIS_151	H, B_HIS_151	2.93	2.09	11.38
5M33.PDB	O, B_LEU_174	ND1, B_HIS_151	HD1, B_HIS_151	2.74	1.90	9.06
5M33.PDB	O, B_LYS_148	N, B_GLU_152	H, B_GLU_152	2.91	2.08	12.10
5M33.PDB	O, B_THR_149	N, B_THR_153	H, B_THR_153	2.90	2.07	12.38
5M33.PDB	O, B_PHE_150	N, B_LEU_154	H, B_LEU_154	2.87	2.02	7.88

5M33.PDB	OD1, B_ASP_189	N, B_SER_160	H, B_SER_160	2.83	1.97	1.56
5M33.PDB	OD1, B_ASP_189	OG, B_SER_160	HG, B_SER_160	2.86	2.13	25.03
5M33.PDB	O, B_SER_159	N, B_LEU_162	H, B_LEU_162	2.96	2.12	9.23
5M33.PDB	O, B_LEU_162	OG1, B_THR_166	HG1, B_THR_166	2.89	2.08	13.11
5M33.PDB	O, B_THR_163	N, B_THR_167	H, B_THR_167	2.93	2.11	14.74
5M33.PDB	O, B_LEU_165	N, B_VAL_169	H, B_VAL_169	2.98	2.16	14.43
5M33.PDB	O, B_THR_167	N, B_LYS_171	H, B_LYS_171	2.99	2.26	27.58
5M33.PDB	O, B_SER_179	N, B_SER_183	H, B_SER_183	2.82	1.97	7.48
5M33.PDB	O, B_GLY_158	N, B_CYS_190	H, B_CYS_190	2.96	2.12	9.28
5M33.PDB	OD2, B_ASP_128	NE2, B_HIS_191	HE2, B_HIS_191	2.69	1.83	4.41
5M33.PDB	OD2, B_ASP_189	N, B_GLN_192	H, B_GLN_192	2.97	2.16	16.91
5M33.PDB	OD1, B_ASP_196	NE2, B_GLN_192	HE21, B_GLN_192	2.92	2.12	17.81
5M33.PDB	O, B_CYS_190	N, B_ILE_194	H, B_ILE_194	2.95	2.13	14.36
5M33.PDB	O, B_HIS_191	N, B_ASP_195	H, B_ASP_195	2.95	2.10	7.27
5M33.PDB	O, B_GLN_192	N, B_ASP_196	H, B_ASP_196	2.83	2.01	15.81
5M33.PDB	O, B_LYS_193	N, B_LEU_197	H, B_LEU_197	2.94	2.16	20.67
5M33.PDB	O, B_ASP_195	N, B_SER_199	H, B_SER_199	2.93	2.22	28.83
5M33.PDB	O, B_ASP_196	N, B_LYS_201	H, B_LYS_201	2.98	2.26	27.91
5M3D.PDB	O, A_ASP_117	N, A_LYS_121	H, A_LYS_121	2.91	2.07	9.22
5M3D.PDB	O, A_GLN_118	N, A_ASP_122	H, A_ASP_122	2.83	1.99	10.35
5M3D.PDB	O, A_ILE_119	N, A_VAL_123	H, A_VAL_123	2.80	2.00	16.75
5M3D.PDB	O, A_ALA_120	N, A_LYS_124	H, A_LYS_124	2.87	2.02	7.87
5M3D.PDB	OD2, A_ASP_195	NZ, A_LYS_124	HZ1, A_LYS_124	2.68	1.86	18.64
5M3D.PDB	O, A_LYS_121	N, A_GLN_125	H, A_GLN_125	2.82	1.99	11.95
5M3D.PDB	O, A_ASP_122	N, A_PHE_126	H, A_PHE_126	2.97	2.13	10.05
5M3D.PDB	O, A_VAL_123	N, A_TYR_127	H, A_TYR_127	2.86	2.04	15.68
5M3D.PDB	NE2, A_HIS_151	OH, A_TYR_127	HH, A_TYR_127	2.90	2.07	7.76
5M3D.PDB	O, A_LYS_124	N, A_ASP_128	H, A_ASP_128	2.81	1.97	10.20
5M3D.PDB	O, A_TYR_127	N, A_LEU_131	H, A_LEU_131	2.85	2.06	19.33
5M3D.PDB	O, A_ASP_128	N, A_GLN_132	H, A_GLN_132	2.90	2.05	6.60
5M3D.PDB	O, A_ALA_130	N, A_ALA_134	H, A_ALA_134	2.87	2.13	25.45
5M3D.PDB	O, A_LEU_131	N, A_VAL_135	H, A_VAL_135	2.91	2.18	26.93
5M3D.PDB	O, A_ALA_143	N, A_VAL_147	H, A_VAL_147	2.83	1.97	0.49
5M3D.PDB	O, A_LYS_144	N, A_LYS_148	H, A_LYS_148	2.78	1.93	2.97
5M3D.PDB	O, A_ALA_145	N, A_THR_149	H, A_THR_149	2.94	2.20	26.27
5M3D.PDB	O, A_VAL_146	N, A_PHE_150	H, A_PHE_150	2.81	1.96	8.90
5M3D.PDB	O, A_VAL_147	N, A_HIS_151	H, A_HIS_151	2.83	2.03	18.07
5M3D.PDB	O, A_LEU_174	ND1, A_HIS_151	HD1, A_HIS_151	2.54	1.70	10.32
5M3D.PDB	O, A_LYS_148	N, A_GLU_152	H, A_GLU_152	2.91	2.05	3.90
5M3D.PDB	O, A_THR_149	N, A_THR_153	H, A_THR_153	2.94	2.14	17.42
5M3D.PDB	O, A_THR_149	OG1, A_THR_153	HG1, A_THR_153	2.71	1.99	26.30
5M3D.PDB	O, A_PHE_150	N, A_LEU_154	H, A_LEU_154	2.82	2.01	16.30
5M3D.PDB	OG1, A_THR_163	N, A_SER_160	H, A_SER_160	2.68	1.93	24.41
5M3D.PDB	OG, A_SER_159	OG1, A_THR_163	HG1, A_THR_163	2.65	1.81	3.28
5M3D.PDB	O, A_SER_160	N, A_ALA_164	H, A_ALA_164	2.68	1.86	13.35
5M3D.PDB	O, A_LEU_162	N, A_THR_166	H, A_THR_166	2.92	2.11	17.03
5M3D.PDB	O, A_THR_163	N, A_THR_167	H, A_THR_167	2.80	1.97	12.32
5M3D.PDB	O, A_THR_163	OG1, A_THR_167	HG1, A_THR_167	2.52	1.70	11.15
5M3D.PDB	O, A_ALA_164	N, A_SER_168	H, A_SER_168	2.89	2.05	8.46
5M3D.PDB	O, A_LEU_165	OG, A_SER_168	HG, A_SER_168	2.61	1.86	22.97
5M3D.PDB	O, A_THR_166	N, A_LEU_170	H, A_LEU_170	2.78	1.95	12.52
5M3D.PDB	O, A_THR_167	N, A_LYS_171	H, A_LYS_171	2.87	2.05	15.75
5M3D.PDB	O, A_ASN_172	N, A_CYS_175	H, A_CYS_175	2.95	2.10	9.28
5M3D.PDB	OE2, A_GLU_152	N, A_SER_177	H, A_SER_177	2.77	2.02	24.92
5M3D.PDB	O, A_PRO_176	N, A_SER_179	H, A_SER_179	2.91	2.14	22.27
5M3D.PDB	O, A_GLY_158	N, A_CYS_190	H, A_CYS_190	2.75	1.91	12.01
5M3D.PDB	OD2, A_ASP_128	NE2, A_HIS_191	HE2, A_HIS_191	2.68	1.84	10.19
5M3D.PDB	OD2, A_ASP_189	N, A_GLN_192	H, A_GLN_192	2.94	2.11	13.24

5M3D.PDB	O, A_CYS_190	N, A_ILE_194	H, A_ILE_194	2.85	2.02	12.94
5M3D.PDB	O, A_GLN_192	N, A_ASP_196	H, A_ASP_196	2.98	2.19	20.53
5M3D.PDB	O, A_LYS_193	N, A_LEU_197	H, A_LEU_197	2.95	2.19	23.68
5M3D.PDB	O, A_ASP_196	N, A_GLY_200	H, A_GLY_200	2.84	2.13	29.15
5M3D.PDB	O, A_ASP_196	N, A_LYS_201	H, A_LYS_201	2.79	1.95	11.59
5M3D.PDB	O, B_ASP_117	N, B_LYS_121	H, B_LYS_121	2.91	2.06	7.49
5M3D.PDB	O, B_GLN_118	N, B_ASP_122	H, B_ASP_122	2.85	2.04	15.98
5M3D.PDB	O, B_ILE_119	N, B_VAL_123	H, B_VAL_123	2.79	2.02	22.71
5M3D.PDB	O, B_ALA_120	N, B_LYS_124	H, B_LYS_124	2.98	2.14	9.81
5M3D.PDB	O, B_LYS_121	N, B_GLN_125	H, B_GLN_125	2.85	2.02	12.96
5M3D.PDB	O, B_VAL_123	N, B_TYR_127	H, B_TYR_127	2.75	1.92	13.65
5M3D.PDB	O, B_LYS_124	N, B_ASP_128	H, B_ASP_128	2.78	1.96	14.20
5M3D.PDB	O, B_TYR_127	N, B_LEU_131	H, B_LEU_131	2.91	2.12	19.44
5M3D.PDB	O, B_ASP_128	N, B_GLN_132	H, B_GLN_132	2.94	2.09	6.13
5M3D.PDB	O, B_LEU_131	N, B_VAL_135	H, B_VAL_135	2.87	2.11	24.04
5M3D.PDB	O, B_GLN_133	N, B_ASP_137	H, B_ASP_137	2.97	2.23	25.98
5M3D.PDB	O, B_ALA_140	N, B_LYS_144	H, B_LYS_144	2.98	2.14	8.88
5M3D.PDB	O, B_ALA_143	N, B_VAL_147	H, B_VAL_147	2.86	2.01	7.67
5M3D.PDB	O, B_LYS_144	N, B_LYS_148	H, B_LYS_148	2.88	2.04	10.53
5M3D.PDB	O, B_ALA_145	N, B_THR_149	H, B_THR_149	2.92	2.16	24.76
5M3D.PDB	O, B_ALA_145	OG1, B_THR_149	HG1, B_THR_149	2.92	2.10	9.10
5M3D.PDB	O, B_VAL_146	N, B_PHE_150	H, B_PHE_150	2.87	2.03	11.14
5M3D.PDB	O, B_VAL_147	N, B_HIS_151	H, B_HIS_151	2.90	2.05	8.21
5M3D.PDB	O, B_LEU_174	ND1, B_HIS_151	HD1, B_HIS_151	2.69	1.87	15.29
5M3D.PDB	O, B_LYS_148	N, B_GLU_152	H, B_GLU_152	2.90	2.06	9.45
5M3D.PDB	O, B_THR_149	N, B_THR_153	H, B_THR_153	2.76	1.95	16.27
5M3D.PDB	O, B_THR_149	OG1, B_THR_153	HG1, B_THR_153	2.68	1.93	21.92
5M3D.PDB	O, B_PHE_150	N, B_LEU_154	H, B_LEU_154	2.72	1.93	19.17
5M3D.PDB	OG1, B_THR_163	N, B_SER_160	H, B_SER_160	2.60	1.81	18.90
5M3D.PDB	O, B_SER_160	N, B_ALA_164	H, B_ALA_164	2.64	1.86	20.55
5M3D.PDB	O, B_LEU_162	N, B_THR_166	H, B_THR_166	2.88	2.06	14.51
5M3D.PDB	O, B_THR_163	N, B_THR_167	H, B_THR_167	2.95	2.11	9.70
5M3D.PDB	O, B_THR_163	OG1, B_THR_167	HG1, B_THR_167	2.62	1.82	14.83
5M3D.PDB	O, B_ALA_164	N, B_SER_168	H, B_SER_168	2.95	2.12	11.19
5M3D.PDB	O, B_LEU_165	N, B_VAL_169	H, B_VAL_169	2.95	2.20	25.38
5M3D.PDB	O, B_THR_166	N, B_LEU_170	H, B_LEU_170	2.72	1.93	19.91
5M3D.PDB	O, B_THR_167	N, B_LYS_171	H, B_LYS_171	2.71	1.87	9.68
5M3D.PDB	O, B_LYS_171	N, B_LEU_174	H, B_LEU_174	2.95	2.14	16.60
5M3D.PDB	O, B_PRO_176	OG, B_SER_179	HG, B_SER_179	2.60	1.81	16.72
5M3D.PDB	O, B_ILE_181	N, B_ASN_184	H, B_ASN_184	2.99	2.21	20.02
5M3D.PDB	O, B_ILE_182	N, B_LEU_185	H, B_LEU_185	2.82	1.98	10.54
5M3D.PDB	O, B_GLY_158	N, B_CYS_190	H, B_CYS_190	2.80	1.94	4.10
5M3D.PDB	OD2, B_ASP_128	NE2, B_HIS_191	HE2, B_HIS_191	2.60	1.78	15.29
5M3D.PDB	OD2, B_ASP_189	N, B_GLN_192	H, B_GLN_192	2.93	2.11	13.82
5M3D.PDB	O, B_CYS_190	N, B_ILE_194	H, B_ILE_194	2.95	2.12	12.39
5M3D.PDB	O, B_GLN_192	N, B_ASP_196	H, B_ASP_196	2.84	2.02	14.80
5M3D.PDB	O, B_LYS_193	N, B_LEU_197	H, B_LEU_197	2.93	2.17	22.99
5M3D.PDB	O, B_ASP_195	N, B_SER_199	H, B_SER_199	2.86	2.15	29.72
5M3D.PDB	O, B_ASP_195	OG, B_SER_199	HG, B_SER_199	2.55	1.74	13.09
5M3D.PDB	O, B_ASP_196	N, B_LYS_201	H, B_LYS_201	2.86	2.06	19.17
5M3D.PDB	OD1, C_ASN_115	N, C_ASP_117	H, C_ASP_117	2.96	2.17	19.69
5M3D.PDB	O, C_ILE_119	N, C_VAL_123	H, C_VAL_123	2.94	2.22	28.48
5M3D.PDB	O, C_ALA_120	N, C_LYS_124	H, C_LYS_124	2.91	2.07	9.91
5M3D.PDB	O, C_LYS_121	N, C_GLN_125	H, C_GLN_125	2.85	2.05	17.95
5M3D.PDB	O, C_VAL_123	N, C_TYR_127	H, C_TYR_127	2.85	2.00	5.96
5M3D.PDB	O, C_LYS_124	N, C_ASP_128	H, C_ASP_128	2.86	2.05	16.00
5M3D.PDB	O, C_GLN_125	N, C_GLN_129	H, C_GLN_129	2.82	2.03	19.59
5M3D.PDB	O, C_TYR_127	N, C_LEU_131	H, C_LEU_131	2.81	1.98	13.11

5M3D.PDB	O, C_ASP_128	N, C_GLN_132	H, C_GLN_132	2.89	2.04	7.47
5M3D.PDB	O, C_ALA_130	N, C_ALA_134	H, C_ALA_134	2.74	1.97	21.94
5M3D.PDB	O, C_LEU_131	N, C_VAL_135	H, C_VAL_135	2.89	2.05	11.04
5M3D.PDB	O, C_ALA_134	N, C_ASP_137	H, C_ASP_137	2.88	2.05	12.98
5M3D.PDB	O, C_ASP_139	N, C_ASN_142	H, C_ASN_142	2.98	2.16	15.52
5M3D.PDB	O, C_ALA_143	N, C_VAL_147	H, C_VAL_147	2.88	2.05	12.04
5M3D.PDB	O, C_ALA_145	N, C_THR_149	H, C_THR_149	2.76	1.97	19.10
5M3D.PDB	O, C_ALA_145	OG1, C_THR_149	HG1, C_THR_149	2.85	2.04	10.77
5M3D.PDB	O, C_VAL_146	N, C_PHE_150	H, C_PHE_150	2.86	2.02	10.98
5M3D.PDB	O, C_VAL_147	N, C_HIS_151	H, C_HIS_151	2.93	2.10	13.09
5M3D.PDB	O, C_LEU_174	ND1, C_HIS_151	HD1, C_HIS_151	2.77	1.93	9.75
5M3D.PDB	OH, C_TYR_127	NE2, C_HIS_151	HE2, C_HIS_151	2.47	1.64	11.96
5M3D.PDB	O, C_LYS_148	N, C_GLU_152	H, C_GLU_152	2.93	2.07	6.86
5M3D.PDB	O, C_THR_149	N, C_THR_153	H, C_THR_153	2.90	2.09	16.64
5M3D.PDB	O, C_THR_149	OG1, C_THR_153	HG1, C_THR_153	2.82	2.11	26.57
5M3D.PDB	O, C_PHE_150	N, C_LEU_154	H, C_LEU_154	2.84	2.09	25.26
5M3D.PDB	O, C_SER_160	N, C_ALA_164	H, C_ALA_164	2.77	1.96	15.47
5M3D.PDB	O, C_THR_161	N, C_LEU_165	H, C_LEU_165	2.92	2.11	16.78
5M3D.PDB	O, C_LEU_162	N, C_THR_166	H, C_THR_166	2.96	2.13	14.34
5M3D.PDB	O, C_LEU_162	OG1, C_THR_166	HG1, C_THR_166	2.66	1.88	17.50
5M3D.PDB	O, C_THR_163	N, C_THR_167	H, C_THR_167	2.83	2.02	16.33
5M3D.PDB	O, C_ALA_164	N, C_SER_168	H, C_SER_168	2.89	2.05	9.74
5M3D.PDB	O, C_LEU_165	N, C_VAL_169	H, C_VAL_169	2.92	2.16	23.23
5M3D.PDB	O, C_THR_166	N, C_LEU_170	H, C_LEU_170	2.78	2.00	20.88
5M3D.PDB	O, C_THR_167	N, C_LYS_171	H, C_LYS_171	2.57	1.75	15.04
5M3D.PDB	O, C_LYS_171	N, C_LEU_174	H, C_LEU_174	2.84	1.99	6.87
5M3D.PDB	OE2, C_GLU_152	N, C_SER_177	H, C_SER_177	2.69	1.86	11.04
5M3D.PDB	O, C_PRO_176	N, C_SER_179	H, C_SER_179	2.93	2.13	18.85
5M3D.PDB	O, C_SER_183	N, C_LYS_187	H, C_LYS_187	2.80	1.94	3.39
5M3D.PDB	O, C_GLY_158	N, C_CYS_190	H, C_CYS_190	2.73	1.88	7.85
5M3D.PDB	OD2, C_ASP_128	NE2, C_HIS_191	HE2, C_HIS_191	2.54	1.74	17.73
5M3D.PDB	OD2, C_ASP_189	N, C_GLN_192	H, C_GLN_192	2.80	1.97	13.12
5M3D.PDB	O, C_CYS_190	N, C_ILE_194	H, C_ILE_194	2.91	2.07	10.39
5M3D.PDB	O, C_GLN_192	N, C_ASP_196	H, C_ASP_196	3.00	2.18	15.71
5M3D.PDB	O, C_LYS_193	N, C_LEU_197	H, C_LEU_197	2.84	2.09	24.23
5M3D.PDB	O, C_ILE_194	N, C_PHE_198	H, C_PHE_198	2.99	2.20	19.69
5M3D.PDB	O, C_ASP_195	N, C_SER_199	H, C_SER_199	2.70	2.00	29.60
5M3D.PDB	O, C_ASP_196	N, C_GLY_200	H, C_GLY_200	2.91	2.19	27.12
5M3D.PDB	O, C_ASP_196	N, C_LYS_201	H, C_LYS_201	2.94	2.12	15.69
5M3D.PDB	O, D_LYS_116	N, D_ALA_120	H, D_ALA_120	2.96	2.12	9.84
5M3D.PDB	O, D_ASP_117	N, D_LYS_121	H, D_LYS_121	2.91	2.07	10.71
5M3D.PDB	O, D_GLN_118	N, D_ASP_122	H, D_ASP_122	2.91	2.16	24.90
5M3D.PDB	O, D_ILE_119	N, D_VAL_123	H, D_VAL_123	2.93	2.21	28.37
5M3D.PDB	O, D_LYS_121	N, D_GLN_125	H, D_GLN_125	2.91	2.11	17.36
5M3D.PDB	O, D_ASP_122	N, D_PHE_126	H, D_PHE_126	2.97	2.18	20.39
5M3D.PDB	O, D_VAL_123	N, D_TYR_127	H, D_TYR_127	2.77	1.93	9.04
5M3D.PDB	O, D_LYS_124	N, D_ASP_128	H, D_ASP_128	2.88	2.02	2.98
5M3D.PDB	O, D_GLN_125	N, D_GLN_129	H, D_GLN_129	2.86	2.07	19.17
5M3D.PDB	O, D_TYR_127	N, D_LEU_131	H, D_LEU_131	2.78	1.93	8.17
5M3D.PDB	O, D_ASP_128	N, D_GLN_132	H, D_GLN_132	2.90	2.06	10.99
5M3D.PDB	O, D_ALA_130	N, D_ALA_134	H, D_ALA_134	2.62	1.92	29.22
5M3D.PDB	O, D_ALA_134	N, D_ASP_137	H, D_ASP_137	2.77	1.92	5.77
5M3D.PDB	OD1, D_ASP_139	N, D_LYS_144	H, D_LYS_144	2.75	1.89	6.98
5M3D.PDB	O, D_ALA_143	N, D_VAL_147	H, D_VAL_147	2.90	2.06	10.59
5M3D.PDB	O, D_ALA_145	N, D_THR_149	H, D_THR_149	2.80	2.05	24.05
5M3D.PDB	O, D_ALA_145	OG1, D_THR_149	HG1, D_THR_149	2.76	1.96	14.72
5M3D.PDB	O, D_VAL_146	N, D_PHE_150	H, D_PHE_150	2.91	2.07	9.79
5M3D.PDB	O, D_VAL_147	N, D_HIS_151	H, D_HIS_151	2.81	1.99	13.17

5M3D.PDB	O, D_LEU_174	ND1, D_HIS_151	HD1, D_HIS_151	2.86	2.05	15.14
5M3D.PDB	O, D_THR_149	N, D_THR_153	H, D_THR_153	2.95	2.11	9.66
5M3D.PDB	O, D_THR_149	OG1, D_THR_153	HG1, D_THR_153	2.80	2.08	26.61
5M3D.PDB	O, D_PHE_150	N, D_LEU_154	H, D_LEU_154	2.86	2.05	16.07
5M3D.PDB	O, D_SER_160	N, D_ALA_164	H, D_ALA_164	2.69	1.86	12.75
5M3D.PDB	O, D_THR_161	N, D_LEU_165	H, D_LEU_165	2.89	2.08	15.84
5M3D.PDB	O, D_LEU_162	N, D_THR_166	H, D_THR_166	2.90	2.06	10.23
5M3D.PDB	O, D_THR_163	N, D_THR_167	H, D_THR_167	2.74	1.91	11.96
5M3D.PDB	O, D_THR_163	OG1, D_THR_167	HG1, D_THR_167	2.95	2.24	27.05
5M3D.PDB	O, D_ALA_164	N, D_SER_168	H, D_SER_168	2.84	2.03	16.52
5M3D.PDB	O, D_LEU_165	N, D_VAL_169	H, D_VAL_169	2.95	2.18	22.42
5M3D.PDB	O, D_THR_166	N, D_LEU_170	H, D_LEU_170	2.84	2.04	17.12
5M3D.PDB	O, D_THR_167	N, D_LYS_171	H, D_LYS_171	2.56	1.77	19.83
5M3D.PDB	O, D_LYS_171	N, D_LEU_174	H, D_LEU_174	2.77	1.92	4.36
5M3D.PDB	O, D_PRO_176	OG, D_SER_179	HG, D_SER_179	2.66	1.84	11.66
5M3D.PDB	O, D_ASN_180	OG, D_SER_183	HG, D_SER_183	2.86	2.12	23.28
5M3D.PDB	O, D_ILE_182	N, D_LEU_185	H, D_LEU_185	2.97	2.13	11.47
5M3D.PDB	O, D_SER_183	N, D_LYS_187	H, D_LYS_187	2.96	2.10	3.55
5M3D.PDB	OE1, D_GLN_192	N, D_ASP_189	H, D_ASP_189	2.76	1.94	13.89
5M3D.PDB	O, D_GLY_158	N, D_CYS_190	H, D_CYS_190	2.79	1.94	7.19
5M3D.PDB	OD2, D_ASP_128	NE2, D_HIS_191	HE2, D_HIS_191	2.53	1.71	14.84
5M3D.PDB	OD2, D_ASP_189	N, D_GLN_192	H, D_GLN_192	2.82	1.99	12.15
5M3D.PDB	O, D_CYS_190	N, D_ILE_194	H, D_ILE_194	2.85	2.03	13.91
5M3D.PDB	O, D_GLN_192	N, D_ASP_196	H, D_ASP_196	2.90	2.15	24.84
5M3D.PDB	O, D_LYS_193	N, D_LEU_197	H, D_LEU_197	2.84	2.06	21.13
5M3D.PDB	O, D_ASP_196	N, D_GLY_200	H, D_GLY_200	2.79	2.05	26.33
5M3D.PDB	O, D_ASP_196	N, D_LYS_201	H, D_LYS_201	2.96	2.14	14.32
5M3T.PDB	O, A_ASN_115	N, A_ILE_119	H, A_ILE_119	2.94	2.13	16.30
5M3T.PDB	O, A_GLN_118	N, A_ASP_122	H, A_ASP_122	2.97	2.19	21.02
5M3T.PDB	O, A_ILE_119	N, A_VAL_123	H, A_VAL_123	2.95	2.14	16.63
5M3T.PDB	O, A_ASP_122	N, A_PHE_126	H, A_PHE_126	2.88	2.06	13.64
5M3T.PDB	O, A_VAL_123	N, A_TYR_127	H, A_TYR_127	2.88	2.09	19.10
5M3T.PDB	NE2, A_HIS_151	OH, A_TYR_127	HH, A_TYR_127	2.73	1.92	14.40
5M3T.PDB	O, A_LYS_124	N, A_ASP_128	H, A_ASP_128	2.86	2.07	18.62
5M3T.PDB	O, A_GLN_125	N, A_GLN_129	H, A_GLN_129	2.97	2.16	16.06
5M3T.PDB	O, A_TYR_127	N, A_LEU_131	H, A_LEU_131	2.89	2.07	15.58
5M3T.PDB	O, A_ALA_130	N, A_ALA_134	H, A_ALA_134	2.77	2.03	25.75
5M3T.PDB	O, A_ALA_140	N, A_LYS_144	H, A_LYS_144	2.98	2.17	17.68
5M3T.PDB	O, A_ASN_142	N, A_VAL_146	H, A_VAL_146	2.80	1.98	15.12
5M3T.PDB	O, A_ALA_143	N, A_VAL_147	H, A_VAL_147	2.84	1.99	7.75
5M3T.PDB	O, A_LYS_144	N, A_LYS_148	H, A_LYS_148	2.91	2.07	11.07
5M3T.PDB	O, A_ALA_145	N, A_THR_149	H, A_THR_149	2.85	2.06	19.94
5M3T.PDB	O, A_ALA_145	OG1, A_THR_149	HG1, A_THR_149	2.69	1.91	17.48
5M3T.PDB	O, A_VAL_146	N, A_PHE_150	H, A_PHE_150	2.91	2.08	11.96
5M3T.PDB	O, A_VAL_147	N, A_HIS_151	H, A_HIS_151	2.93	2.10	13.01
5M3T.PDB	O, A_LEU_174	ND1, A_HIS_151	HD1, A_HIS_151	2.75	1.93	15.38
5M3T.PDB	O, A_LYS_148	N, A_GLU_152	H, A_GLU_152	2.97	2.16	17.30
5M3T.PDB	O, A_THR_149	N, A_THR_153	H, A_THR_153	2.89	2.07	15.13
5M3T.PDB	O, A_THR_149	OG1, A_THR_153	HG1, A_THR_153	2.85	2.15	27.69
5M3T.PDB	O, A_GLU_188	N, A_CYS_157	H, A_CYS_157	2.99	2.17	14.35
5M3T.PDB	OD2, A_ASP_189	N, A_SER_160	H, A_SER_160	2.80	1.94	2.42
5M3T.PDB	OG, A_SER_159	OG1, A_THR_161	HG1, A_THR_161	2.93	2.10	8.83
5M3T.PDB	O, A_SER_159	N, A_LEU_162	H, A_LEU_162	3.00	2.15	8.92
5M3T.PDB	O, A_LEU_162	N, A_THR_166	H, A_THR_166	2.96	2.13	13.96
5M3T.PDB	O, A_LEU_162	OG1, A_THR_166	HG1, A_THR_166	2.89	2.11	19.45
5M3T.PDB	O, A_THR_163	N, A_THR_167	H, A_THR_167	2.97	2.15	13.47
5M3T.PDB	O, A_LEU_165	N, A_VAL_169	H, A_VAL_169	2.96	2.14	13.88
5M3T.PDB	O, A_THR_166	N, A_LEU_170	H, A_LEU_170	2.99	2.16	12.64

5M3T.PDB	O, A_VAL.169	N, A_LEU.174	H, A_LEU.174	2.96	2.11	5.74
5M3T.PDB	O, A_ILE.182	N, A_PHE.186	H, A_PHE.186	2.70	1.92	20.08
5M3T.PDB	O, A_GLY.158	N, A_CYS.190	H, A_CYS.190	2.89	2.03	5.47
5M3T.PDB	OD1, A_ASP.189	N, A_HIS.191	H, A_HIS.191	2.81	2.03	20.34
5M3T.PDB	OD1, A_ASP.128	NE2, A_HIS.191	HE2, A_HIS.191	2.70	1.84	4.47
5M3T.PDB	O, A_ASP.189	N, A_LYS.193	H, A_LYS.193	3.00	2.19	17.82
5M3T.PDB	O, A_ASP.155	NZ, A_LYS.193	HZ1, A_LYS.193	2.94	2.21	29.02
5M3T.PDB	O, A_CYS.190	N, A_ILE.194	H, A_ILE.194	2.88	2.04	11.45
5M3T.PDB	O, A_HIS.191	N, A_ASP.195	H, A_ASP.195	2.95	2.12	14.00
5M3T.PDB	O, A_GLN.192	N, A_ASP.196	H, A_ASP.196	2.79	2.00	19.02
5M3T.PDB	O, A_LYS.193	N, A_LEU.197	H, A_LEU.197	2.95	2.23	28.39
5M3T.PDB	O, B_ILE.119	N, B_VAL.123	H, B_VAL.123	2.98	2.18	17.74
5M3T.PDB	OD2, B_ASP.195	NZ, B_LYS.124	HZ1, B_LYS.124	2.94	2.15	23.24
5M3T.PDB	O, B_ASP.122	N, B_PHE.126	H, B_PHE.126	2.88	2.07	16.55
5M3T.PDB	O, B_VAL.123	N, B_TYR.127	H, B_TYR.127	2.81	1.99	15.05
5M3T.PDB	NE2, B_HIS.151	OH, B_TYR.127	HH, B_TYR.127	2.86	2.03	6.62
5M3T.PDB	O, B_LYS.124	N, B_ASP.128	H, B_ASP.128	2.79	1.96	14.44
5M3T.PDB	O, B_TYR.127	N, B_LEU.131	H, B_LEU.131	2.74	1.91	11.63
5M3T.PDB	O, B_ASP.128	N, B_GLN.132	H, B_GLN.132	2.93	2.08	4.43
5M3T.PDB	O, B_ALA.130	N, B_ALA.134	H, B_ALA.134	2.82	2.01	17.03
5M3T.PDB	O, B_LEU.131	N, B_VAL.135	H, B_VAL.135	2.93	2.13	18.76
5M3T.PDB	O, B_ALA.140	N, B_LYS.144	H, B_LYS.144	2.99	2.13	5.84
5M3T.PDB	O, B_ASN.142	N, B_VAL.146	H, B_VAL.146	2.82	1.98	10.01
5M3T.PDB	O, B_ALA.143	N, B_VAL.147	H, B_VAL.147	2.79	1.96	12.14
5M3T.PDB	O, B_LYS.144	N, B_LYS.148	H, B_LYS.148	2.86	2.03	12.94
5M3T.PDB	O, B_CYS.175	NZ, B_LYS.148	HZ1, B_LYS.148	2.54	1.78	25.33
5M3T.PDB	O, B_ASN.173	NZ, B_LYS.148	HZ2, B_LYS.148	2.88	2.03	13.59
5M3T.PDB	O, B_ALA.145	N, B_THR.149	H, B_THR.149	2.96	2.15	16.07
5M3T.PDB	O, B_ALA.145	OG1, B_THR.149	HG1, B_THR.149	2.88	2.12	22.32
5M3T.PDB	O, B_VAL.146	N, B_PHE.150	H, B_PHE.150	2.92	2.09	12.17
5M3T.PDB	O, B_VAL.147	N, B_HIS.151	H, B_HIS.151	2.86	2.03	12.60
5M3T.PDB	O, B_LEU.174	ND1, B_HIS.151	HD1, B_HIS.151	2.62	1.77	9.06
5M3T.PDB	O, B_LYS.148	N, B_GLU.152	H, B_GLU.152	2.91	2.09	13.59
5M3T.PDB	O, B_THR.149	N, B_THR.153	H, B_THR.153	2.94	2.11	13.14
5M3T.PDB	O, B_THR.149	OG1, B_THR.153	HG1, B_THR.153	2.80	2.10	28.85
5M3T.PDB	O, B_PHE.150	N, B_LEU.154	H, B_LEU.154	2.95	2.15	17.32
5M3T.PDB	OG1, B_THR.163	N, B_SER.160	H, B_SER.160	2.86	2.05	16.20
5M3T.PDB	O, B_SER.160	N, B_ALA.164	H, B_ALA.164	2.90	2.11	19.32
5M3T.PDB	O, B_THR.161	N, B_LEU.165	H, B_LEU.165	2.94	2.12	14.02
5M3T.PDB	O, B_LEU.162	N, B_THR.166	H, B_THR.166	2.99	2.17	13.93
5M3T.PDB	O, B_LEU.162	OG1, B_THR.166	HG1, B_THR.166	2.94	2.16	18.55
5M3T.PDB	O, B_THR.163	N, B_THR.167	H, B_THR.167	2.90	2.06	9.78
5M3T.PDB	O, B_THR.163	OG1, B_THR.167	HG1, B_THR.167	2.66	1.89	19.90
5M3T.PDB	O, B_ALA.164	N, B_SER.168	H, B_SER.168	2.96	2.19	22.50
5M3T.PDB	O, B_LEU.165	OG, B_SER.168	HG, B_SER.168	2.85	2.06	16.49
5M3T.PDB	O, B_THR.166	N, B_LEU.170	H, B_LEU.170	2.88	2.10	19.82
5M3T.PDB	O, B_THR.167	N, B_LYS.171	H, B_LYS.171	2.76	1.95	17.26
5M3T.PDB	O, B_SER.168	ND2, B_ASN.172	HD21, B_ASN.172	2.93	2.11	14.38
5M3T.PDB	O, B_ASN.172	N, B_CYS.175	H, B_CYS.175	2.85	2.01	8.34
5M3T.PDB	O, B_ILE.181	N, B_ASN.184	H, B_ASN.184	2.85	2.05	18.46
5M3T.PDB	O, B_SER.183	N, B_LYS.187	H, B_LYS.187	2.83	2.00	12.69
5M3T.PDB	OE1, B_GLN.192	N, B_ASP.189	H, B_ASP.189	2.94	2.14	17.48
5M3T.PDB	O, B_GLY.158	N, B_CYS.190	H, B_CYS.190	2.83	1.97	6.16
5M3T.PDB	OD1, B_ASP.128	NE2, B_HIS.191	HE2, B_HIS.191	2.76	1.92	11.16
5M3T.PDB	OD1, B_ASP.189	N, B_GLN.192	H, B_GLN.192	2.85	2.02	14.15
5M3T.PDB	O, B_LEU.154	NZ, B_LYS.193	HZ2, B_LYS.193	2.66	1.92	28.24
5M3T.PDB	O, B_CYS.190	N, B_ILE.194	H, B_ILE.194	2.86	2.09	22.77
5M3T.PDB	O, B_HIS.191	N, B_ASP.195	H, B_ASP.195	2.99	2.18	15.97

5M3T.PDB	O, B_GLN_192	N, B_ASP_196	H, B_ASP_196	2.98	2.18	17.63
5M3T.PDB	O, B_ASP_195	OG, B_SER_199	HG, B_SER_199	2.82	2.09	24.74
5M4R.PDB	OG1, A_THR_163	N, A_SER_160	H, A_SER_160	2.97	2.12	8.70
5M4R.PDB	OG, A_SER_159	OG1, A_THR_163	HG1, A_THR_163	2.93	2.14	15.31
5M4R.PDB	O, A_SER_160	N, A_ALA_164	H, A_ALA_164	2.56	1.75	15.32
5M4R.PDB	O, A_GLY_158	N, A_CYS_190	H, A_CYS_190	2.82	1.96	5.83
5M4R.PDB	OD2, A_ASP_128	NE2, A_HIS_191	HE2, A_HIS_191	2.54	1.73	17.27
5M4R.PDB	O, A_CYS_190	N, A_ILE_194	H, A_ILE_194	2.79	2.00	18.71
5M4R.PDB	O, A_HIS_191	N, A_ASP_195	H, A_ASP_195	2.85	2.00	5.80
5M4R.PDB	O, B_LYS_121	N, B_GLN_125	H, B_GLN_125	2.88	2.03	8.53
5M4R.PDB	O, B_LYS_124	N, B_ASP_128	H, B_ASP_128	2.83	1.99	10.44
5M4R.PDB	O, B_VAL_146	N, B_PHE_150	H, B_PHE_150	2.87	2.04	11.41
5M4R.PDB	O, B_VAL_147	N, B_HIS_151	H, B_HIS_151	2.85	2.02	12.74
5M4R.PDB	O, B_LYS_148	N, B_GLU_152	H, B_GLU_152	2.83	2.00	11.22
5M4R.PDB	O, B_THR_149	N, B_THR_153	H, B_THR_153	2.76	1.93	11.52
5M4R.PDB	O, B_THR_149	OG1, B_THR_153	HG1, B_THR_153	2.73	2.03	28.15
5M4R.PDB	OG1, B_THR_163	N, B_SER_160	H, B_SER_160	2.82	2.01	15.84
5M4R.PDB	OG, B_SER_159	OG1, B_THR_163	HG1, B_THR_163	2.85	2.02	5.63
5M4R.PDB	O, B_SER_160	N, B_ALA_164	H, B_ALA_164	2.76	2.02	25.53
5M4R.PDB	O, B_THR_161	N, B_LEU_165	H, B_LEU_165	2.85	2.00	9.07
5M4R.PDB	O, B_LEU_162	N, B_THR_166	H, B_THR_166	2.80	1.95	8.30
5M4R.PDB	O, B_LEU_162	OG1, B_THR_166	HG1, B_THR_166	2.92	2.11	12.23
5M4R.PDB	O, B_THR_163	N, B_THR_167	H, B_THR_167	2.81	1.99	13.82
5M4R.PDB	O, B_ALA_164	N, B_SER_168	H, B_SER_168	2.85	2.04	17.78
5M4R.PDB	O, B_LEU_165	N, B_VAL_169	H, B_VAL_169	2.67	1.97	29.59
5M4R.PDB	O, C_ASP_117	N, C_LYS_121	H, C_LYS_121	2.88	2.04	8.52
5M4R.PDB	O, C_ALA_120	N, C_LYS_124	H, C_LYS_124	2.90	2.05	8.18
5M4R.PDB	O, C_LYS_121	N, C_GLN_125	H, C_GLN_125	2.88	2.04	12.44
5M4R.PDB	O, C_ASP_122	N, C_PHE_126	H, C_PHE_126	2.84	1.99	7.74
5M4R.PDB	O, C_VAL_123	N, C_TYR_127	H, C_TYR_127	2.85	2.01	7.89
5M4R.PDB	O, C_LYS_124	N, C_ASP_128	H, C_ASP_128	2.85	2.01	11.99
5M4R.PDB	O, C_GLN_125	N, C_GLN_129	H, C_GLN_129	2.90	2.06	10.04
5M4R.PDB	O, C_PHE_126	N, C_ALA_130	H, C_ALA_130	2.92	2.07	6.44
5M4R.PDB	O, C_TYR_127	N, C_LEU_131	H, C_LEU_131	2.76	1.97	18.98
5M4R.PDB	O, C_ASP_128	N, C_GLN_132	H, C_GLN_132	2.86	2.01	6.65
5M4R.PDB	O, C_LEU_131	N, C_VAL_135	H, C_VAL_135	2.86	2.02	10.05
5M4R.PDB	O, C_ALA_143	N, C_VAL_147	H, C_VAL_147	2.83	1.98	7.24
5M4R.PDB	O, C_ALA_145	N, C_THR_149	H, C_THR_149	2.85	2.02	12.51
5M4R.PDB	O, C_VAL_146	N, C_PHE_150	H, C_PHE_150	2.86	2.02	10.77
5M4R.PDB	O, C_VAL_147	N, C_HIS_151	H, C_HIS_151	2.82	2.00	14.15
5M4R.PDB	O, C_THR_149	OG1, C_THR_153	HG1, C_THR_153	2.74	2.04	29.05
5M4R.PDB	O, C_PHE_150	N, C_LEU_154	H, C_LEU_154	2.89	2.07	13.98
5M4R.PDB	OG1, C_THR_163	N, C_SER_160	H, C_SER_160	2.80	1.95	7.20
5M4R.PDB	OG, C_SER_159	OG1, C_THR_163	HG1, C_THR_163	2.95	2.12	7.91
5M4R.PDB	O, C_SER_160	N, C_ALA_164	H, C_ALA_164	2.84	2.04	18.04
5M4R.PDB	O, C_THR_161	N, C_LEU_165	H, C_LEU_165	2.77	1.94	14.09
5M4R.PDB	O, C_LEU_162	OG1, C_THR_166	HG1, C_THR_166	2.73	1.97	21.05
5M4R.PDB	O, C_THR_163	N, C_THR_167	H, C_THR_167	2.86	2.02	10.18
5M4R.PDB	O, C_THR_163	OG1, C_THR_167	HG1, C_THR_167	2.56	1.86	28.52
5M4R.PDB	O, C_LEU_165	N, C_VAL_169	H, C_VAL_169	2.81	2.04	22.87
5M4R.PDB	OD2, C_ASP_189	N, C_GLN_192	H, C_GLN_192	2.75	1.90	7.52
5M4R.PDB	O, C_CYS_190	N, C_ILE_194	H, C_ILE_194	2.79	1.99	17.52
5M4R.PDB	O, C_HIS_191	N, C_ASP_195	H, C_ASP_195	2.83	1.98	6.12
5M4R.PDB	O, C_GLN_192	N, C_ASP_196	H, C_ASP_196	2.81	1.97	12.51
5M4R.PDB	O, C_LYS_193	N, C_LEU_197	H, C_LEU_197	2.74	1.99	24.89
5M4R.PDB	O, D_THR_149	N, D_THR_153	H, D_THR_153	2.76	1.94	13.90
5M4R.PDB	O, D_CYS_190	N, D_ILE_194	H, D_ILE_194	2.80	1.98	16.24
5M4R.PDB	O, D_ILE_194	N, D_PHE_198	H, D_PHE_198	2.90	2.07	14.01

5M4R.PDB	O, E_ALA.145	N, E_THR.149	H, E_THR.149	2.84	2.01	12.20
5M4R.PDB	O, E_VAL.147	N, E_HIS.151	H, E_HIS.151	2.82	1.99	11.67
5M4R.PDB	O, E_LYS.148	N, E_GLU.152	H, E_GLU.152	2.81	1.99	14.86
5M4R.PDB	O, E_THR.149	N, E_THR.153	H, E_THR.153	2.77	1.95	13.19
5M4R.PDB	O, E_THR.149	OG1, E_THR.153	HG1, E_THR.153	2.73	2.03	28.19
5M4R.PDB	O, E_PHE.150	N, E_LEU.154	H, E_LEU.154	2.88	2.06	14.16
5M4R.PDB	OG1, E_THR.163	N, E_SER.160	H, E_SER.160	2.70	1.88	13.56
5M4R.PDB	O, E_SER.160	N, E_ALA.164	H, E_ALA.164	2.73	1.96	22.03
5M4R.PDB	OD2, E_ASP.128	NE2, E_HIS.191	HE2, E_HIS.191	2.53	1.73	17.17
5M4R.PDB	O, E_CYS.190	N, E_ILE.194	H, E_ILE.194	2.78	1.97	15.37
5T6P.PDB	OG, A_SER.26	N, A_LEU.3	H, A_LEU.3	2.84	1.99	5.70
5T6P.PDB	O, A_ARG.24	N, A_THR.5	H, A_THR.5	2.80	1.96	9.75
5T6P.PDB	O, A_TYR.91	NE2, A_GLN.6	HE22, A_GLN.6	2.77	1.91	5.02
5T6P.PDB	O, A_SER.22	N, A_THR.7	H, A_THR.7	2.80	1.98	15.63
5T6P.PDB	O, A_LYS.108	N, A_LEU.11	H, A_LEU.11	2.86	2.14	28.05
5T6P.PDB	O, A_GLU.110	N, A_VAL.13	H, A_VAL.13	2.92	2.18	25.74
5T6P.PDB	O, A_ILE.80	N, A_ALA.19	H, A_ALA.19	2.98	2.15	13.33
5T6P.PDB	O, A_LEU.78	N, A_ILE.21	H, A_ILE.21	2.78	1.94	11.87
5T6P.PDB	O, A_THR.7	N, A_SER.22	H, A_SER.22	2.67	1.82	5.62
5T6P.PDB	O, A_PHE.76	N, A_CYS.23	H, A_CYS.23	2.67	1.84	13.46
5T6P.PDB	O, A_THR.5	N, A_ARG.24	H, A_ARG.24	2.81	2.01	17.15
5T6P.PDB	OD1, A_ASP.75	NE, A_ARG.24	HE, A_ARG.24	2.87	2.06	16.15
5T6P.PDB	O, A_THR.74	N, A_SER.25	H, A_SER.25	2.92	2.15	21.71
5T6P.PDB	O, A_LYS.35	N, A_HIS.31	H, A_HIS.31	2.71	1.85	5.88
5T6P.PDB	O, A_HIS.31	N, A_GLY.34	H, A_GLY.34	2.72	1.87	7.51
5T6P.PDB	OD1, A_ASN.33	N, A_LYS.35	H, A_LYS.35	2.79	1.96	11.94
5T6P.PDB	O, A_PHE.94	N, A_GLU.39	H, A_GLU.39	2.82	1.99	13.41
5T6P.PDB	O, A_ILE.53	N, A_TRP.40	H, A_TRP.40	2.93	2.13	18.35
5T6P.PDB	O, A_TYR.92	N, A_TYR.41	H, A_TYR.41	2.73	1.89	11.55
5T6P.PDB	O, A_LYS.50	N, A_LEU.42	H, A_LEU.42	2.88	2.08	18.93
5T6P.PDB	O, A_VAL.90	N, A_GLN.43	H, A_GLN.43	2.78	1.94	8.75
5T6P.PDB	O, A_GLN.47	NE2, A_GLN.43	HE21, A_GLN.43	2.91	2.07	10.44
5T6P.PDB	O, B_GLY.107	OG, A_SER.48	HG, A_SER.48	2.52	1.72	14.73
5T6P.PDB	O, A_LEU.42	N, A_LYS.50	H, A_LYS.50	2.76	2.01	25.02
5T6P.PDB	O, A_TRP.40	N, A_LEU.52	H, A_LEU.52	2.89	2.04	6.78
5T6P.PDB	O, A_LYS.58	N, A_TYR.54	H, A_TYR.54	2.88	2.08	17.82
5T6P.PDB	O, A_ILE.36	NE, A_ARG.55	HE, A_ARG.55	2.95	2.12	13.12
5T6P.PDB	O, A_LEU.38	N, A_VAL.56	H, A_VAL.56	2.81	1.97	8.99
5T6P.PDB	O, A_ARG.55	N, A_SER.57	H, A_SER.57	2.79	2.06	26.54
5T6P.PDB	O, A_TYR.54	N, A_LYS.58	H, A_LYS.58	2.92	2.13	19.37
5T6P.PDB	O, A_LEU.52	N, A_PHE.60	H, A_PHE.60	2.86	2.00	6.63
5T6P.PDB	OD1, A_ASP.87	NH2, A_ARG.66	HH22, A_ARG.66	2.87	2.03	10.92
5T6P.PDB	O, A_LYS.79	N, A_SER.68	H, A_SER.68	2.87	2.04	13.46
5T6P.PDB	O, A_CYS.23	N, A_PHE.76	H, A_PHE.76	2.81	1.99	14.73
5T6P.PDB	O, A_SER.70	N, A_THR.77	H, A_THR.77	2.96	2.14	16.18
5T6P.PDB	O, A_ILE.21	N, A_LEU.78	H, A_LEU.78	2.87	2.08	19.36
5T6P.PDB	O, A_SER.68	N, A_LYS.79	H, A_LYS.79	2.72	1.88	9.62
5T6P.PDB	O, A_ALA.19	N, A_ILE.80	H, A_ILE.80	2.82	1.98	10.03
5T6P.PDB	O, A_GLN.43	N, A_VAL.90	H, A_VAL.90	2.99	2.16	12.00
5T6P.PDB	O, A_THR.107	N, A_TYR.91	H, A_TYR.91	2.97	2.12	9.83
5T6P.PDB	O, A_ASP.87	OH, A_TYR.91	HH, A_TYR.91	2.67	1.98	29.62
5T6P.PDB	O, A_TYR.41	N, A_TYR.92	H, A_TYR.92	2.76	1.93	13.16
5T6P.PDB	OE1, A_GLN.6	N, A_CYS.93	H, A_CYS.93	2.94	2.12	14.92
5T6P.PDB	O, A_THR.102	N, A_GLN.95	H, A_GLN.95	2.94	2.13	17.40
5T6P.PDB	O, A_HIS.98	NE2, A_GLN.95	HE22, A_GLN.95	2.68	1.87	14.95
5T6P.PDB	O, A_TYR.37	N, A_GLY.96	H, A_GLY.96	2.73	1.90	11.23
5T6P.PDB	O, A_ILE.29	OG, A_SER.97	HG, A_SER.97	2.65	1.82	7.55
5T6P.PDB	OE1, A_GLN.95	N, A_HIS.98	H, A_HIS.98	2.88	2.02	3.19

5T6P.PDB	O, A_VAL_2	OG1, A_THR_102	HG1, A_THR_102	2.83	2.02	12.78
5T6P.PDB	O, A_CYS_93	N, A_GLY_104	H, A_GLY_104	2.64	1.79	9.16
5T6P.PDB	O, A_TYR_91	N, A_THR_107	H, A_THR_107	2.98	2.24	26.12
5T6P.PDB	O, A_PRO_8	OG1, A_THR_107	HG1, A_THR_107	2.63	1.91	24.93
5T6P.PDB	O, A_GLY_89	N, A_LEU_109	H, A_LEU_109	2.81	1.95	2.82
5T6P.PDB	O, A_VAL_13	N, A_LYS_112	H, A_LYS_112	2.81	1.97	10.01
5T6P.PDB	O, A_TYR_145	N, A_ALA_116	H, A_ALA_116	2.79	1.99	17.20
5T6P.PDB	O, A_ASN_142	N, A_THR_119	H, A_THR_119	2.97	2.14	12.03
5T6P.PDB	O, A_VAL_138	N, A_PHE_123	H, A_PHE_123	2.88	2.11	21.78
5T6P.PDB	OG, A_SER_136	NE2, A_GLN_129	HE22, A_GLN_129	2.81	1.96	6.44
5T6P.PDB	O, A_GLN_129	OG, A_SER_132	HG, A_SER_132	2.72	1.92	13.31
5T6P.PDB	O, A_LEU_130	N, A_GLY_133	H, A_GLY_133	2.98	2.20	21.49
5T6P.PDB	OE1, A_GLN_129	N, A_SER_136	H, A_SER_136	2.79	1.94	7.05
5T6P.PDB	O, A_LEU_184	N, A_VAL_137	H, A_VAL_137	2.71	1.87	10.57
5T6P.PDB	O, A_SER_182	N, A_CYS_139	H, A_CYS_139	2.76	2.04	28.21
5T6P.PDB	O, A_SER_121	N, A_PHE_140	H, A_PHE_140	2.76	1.97	19.62
5T6P.PDB	O, A_MET_180	N, A_LEU_141	H, A_LEU_141	2.79	1.94	5.89
5T6P.PDB	OG, A_SER_179	N, A_ASN_143	H, A_ASN_143	2.90	2.08	15.40
5T6P.PDB	O, A_TYR_178	N, A_PHE_144	H, A_PHE_144	2.81	1.97	9.66
5T6P.PDB	O, A_ALA_116	N, A_TYR_145	H, A_TYR_145	2.97	2.15	15.15
5T6P.PDB	O, A_GLU_200	N, A_LYS_152	H, A_LYS_152	2.97	2.17	16.98
5T6P.PDB	OG, A_SER_182	NE1, A_TRP_153	HE1, A_TRP_153	2.84	2.00	11.05
5T6P.PDB	O, A_THR_198	N, A_LYS_154	H, A_LYS_154	2.71	1.93	21.47
5T6P.PDB	O, A_SER_196	N, A_ASP_156	H, A_ASP_156	2.70	1.86	10.47
5T6P.PDB	O, A_TRP_153	N, A_ARG_160	H, A_ARG_160	2.85	2.08	22.60
5T6P.PDB	O, A_SER_181	N, A_SER_167	H, A_SER_167	2.92	2.15	23.07
5T6P.PDB	O, B_PRO_170	OG, A_SER_167	HG, A_SER_167	2.98	2.14	3.80
5T6P.PDB	O, A_LYS_147	NE1, A_TRP_168	HE1, A_TRP_168	2.99	2.28	29.51
5T6P.PDB	O, A_SER_179	N, A_THR_169	H, A_THR_169	2.77	1.93	8.31
5T6P.PDB	O, A_ASP_170	OG1, A_THR_169	HG1, A_THR_169	2.93	2.19	24.31
5T6P.PDB	O, A_THR_177	N, A_ASP_172	H, A_ASP_172	2.83	2.02	16.18
5T6P.PDB	OD1, A_ASP_172	N, A_LYS_174	H, A_LYS_174	2.80	1.97	12.91
5T6P.PDB	O, A_ASP_172	N, A_SER_176	H, A_SER_176	2.74	2.02	27.29
5T6P.PDB	OD1, A_ASP_175	OG1, A_THR_177	HG1, A_THR_177	2.59	1.78	13.64
5T6P.PDB	O, A_PHE_144	N, A_TYR_178	H, A_TYR_178	2.77	1.93	7.97
5T6P.PDB	O, A_LEU_141	N, A_MET_180	H, A_MET_180	2.77	1.96	16.22
5T6P.PDB	O, A_SER_167	N, A_SER_181	H, A_SER_181	2.83	2.04	19.51
5T6P.PDB	O, A_CYS_139	N, A_SER_182	H, A_SER_182	2.79	1.96	11.39
5T6P.PDB	OD1, A_ASN_166	OG, A_SER_182	HG, A_SER_182	2.54	1.72	9.61
5T6P.PDB	O, A_LEU_165	N, A_THR_183	H, A_THR_183	2.87	2.06	15.52
5T6P.PDB	O, A_VAL_137	N, A_LEU_184	H, A_LEU_184	2.77	1.97	18.32
5T6P.PDB	O, A_GLY_163	N, A_THR_185	H, A_THR_185	2.97	2.14	12.81
5T6P.PDB	O, A_ALA_135	N, A_LEU_186	H, A_LEU_186	2.78	1.96	13.71
5T6P.PDB	O, A_GLY_133	N, A_LYS_188	H, A_LYS_188	2.86	2.01	2.28
5T6P.PDB	OG1, A_THR_187	N, A_GLU_190	H, A_GLU_190	2.92	2.08	10.76
5T6P.PDB	O, A_THR_187	N, A_TYR_191	H, A_TYR_191	2.82	1.98	9.18
5T6P.PDB	OD1, A_ASP_156	N, A_SER_196	H, A_SER_196	2.91	2.06	3.81
5T6P.PDB	O, A_LYS_152	N, A_GLU_200	H, A_GLU_200	2.95	2.17	21.10
5T6P.PDB	O, A_ILE_210	N, A_ALA_201	H, A_ALA_201	2.76	1.98	21.19
5T6P.PDB	O, A_ASN_150	N, A_THR_202	H, A_THR_202	2.73	1.90	13.59
5T6P.PDB	OG, A_SER_206	N, A_SER_208	H, A_SER_208	2.93	2.13	18.20
5T6P.PDB	O, A_ALA_201	N, A_ILE_210	H, A_ILE_210	2.83	2.04	19.01
5T6P.PDB	O, B_SER_25	N, B_LYS_3	H, B_LYS_3	2.92	2.08	9.95
5T6P.PDB	O, B_ALA_23	N, B_VAL_5	H, B_VAL_5	2.98	2.21	22.28
5T6P.PDB	O, B_SER_21	N, B_SER_7	H, B_SER_7	2.97	2.22	25.31
5T6P.PDB	O, B_THR_113	N, B_VAL_12	H, B_VAL_12	2.78	2.02	23.72
5T6P.PDB	O, B_LEU_86	N, B_GLY_15	H, B_GLY_15	2.71	1.85	6.92
5T6P.PDB	O, B_ALA_13	N, B_GLY_16	H, B_GLY_16	2.97	2.19	21.44

5T6P.PDB	O, B_LEU_81	N, B_LEU_20	H, B_LEU_20	2.89	2.07	14.31
5T6P.PDB	O, B_VAL_5	N, B_ALA_23	H, B_ALA_23	2.70	1.89	15.98
5T6P.PDB	O, B_LYS_3	N, B_SER_25	H, B_SER_25	2.98	2.28	29.57
5T6P.PDB	O, B_ILE_51	N, B_MET_34	H, B_MET_34	2.95	2.13	15.81
5T6P.PDB	O, B_ALA_49	N, B_TRP_36	H, B_TRP_36	2.99	2.18	18.20
5T6P.PDB	O, B_GLU_46	N, B_ARG_38	H, B_ARG_38	2.93	2.09	10.53
5T6P.PDB	OE1, B_GLU_46	NE, B_ARG_38	HE, B_ARG_38	2.70	1.96	26.33
5T6P.PDB	O, B_ILE_93	N, B_GLN_39	H, B_GLN_39	2.73	1.94	18.82
5T6P.PDB	OE1, A_GLN_43	NE2, B_GLN_39	HE22, B_GLN_39	2.71	1.86	5.14
5T6P.PDB	O, B_ARG_44	N, B_THR_40	H, B_THR_40	2.94	2.13	17.68
5T6P.PDB	O, B_THR_40	N, B_LYS_43	H, B_LYS_43	2.81	1.99	15.16
5T6P.PDB	O, B_ARG_38	N, B_GLU_46	H, B_GLU_46	2.91	2.09	13.32
5T6P.PDB	O, B_TYR_59	N, B_TYR_50	H, B_TYR_50	2.85	2.14	28.28
5T6P.PDB	O, B_MET_34	N, B_ILE_51	H, B_ILE_51	3.00	2.23	23.58
5T6P.PDB	O, B_GLY_56	N, B_ASN_52	H, B_ASN_52	2.85	1.99	5.44
5T6P.PDB	O, B_ASN_52	N, B_GLY_55	H, B_GLY_55	2.99	2.14	4.85
5T6P.PDB	OD1, B_ASN_52	N, B_GLY_56	H, B_GLY_56	2.63	1.80	11.54
5T6P.PDB	O, F_PRO_8	ND2, B_ASN_57	HD21, B_ASN_57	2.91	2.07	9.74
5T6P.PDB	O, B_TYR_50	N, B_TYR_59	H, B_TYR_59	2.93	2.14	20.03
5T6P.PDB	O, B_GLN_82	N, B_THR_69	H, B_THR_69	2.67	1.94	26.83
5T6P.PDB	OD1, B_ASN_74	NE, B_ARG_72	HE, B_ARG_72	2.87	2.14	26.22
5T6P.PDB	O, B_THR_78	N, B_ASP_73	H, B_ASP_73	2.91	2.10	15.58
5T6P.PDB	O, B_LYS_76	OG1, B_THR_78	HG1, B_THR_78	2.86	2.09	20.72
5T6P.PDB	O, B_SER_71	N, B_TYR_80	H, B_TYR_80	2.84	1.99	6.51
5T6P.PDB	O, B_THR_69	N, B_GLN_82	H, B_GLN_82	2.81	1.97	9.07
5T6P.PDB	O, B_LEU_18	N, B_MET_83	H, B_MET_83	2.79	1.99	17.97
5T6P.PDB	O, B_ARG_67	OG, B_SER_84	HG, B_SER_84	2.97	2.16	13.27
5T6P.PDB	O, B_GLN_39	N, B_ILE_93	H, B_ILE_93	2.90	2.11	19.97
5T6P.PDB	O, B_THR_110	N, B_TYR_94	H, B_TYR_94	2.94	2.08	2.28
5T6P.PDB	O, B_ASP_90	OH, B_TYR_94	HH, B_TYR_94	2.68	1.86	11.38
5T6P.PDB	O, B_VAL_37	N, B_TYR_95	H, B_TYR_95	2.64	1.79	3.58
5T6P.PDB	O, B_PRO_33	N, B_GLN_99	H, B_GLN_99	2.96	2.14	14.24
5T6P.PDB	O, B_GLY_102	N, B_TYR_100	H, B_TYR_100	2.99	2.25	25.89
5T6P.PDB	OD1, B_ASP_104	N, B_GLY_102	H, B_GLY_102	2.80	1.95	8.41
5T6P.PDB	O, B_PHE_103	NE1, B_TRP_106	HE1, B_TRP_106	2.96	2.22	25.91
5T6P.PDB	O, B_CYS_96	N, B_GLY_107	H, B_GLY_107	2.84	2.03	15.83
5T6P.PDB	OE1, B_GLU_6	N, B_GLY_109	H, B_GLY_109	2.80	1.98	13.61
5T6P.PDB	O, B_ALA_92	N, B_LEU_112	H, B_LEU_112	2.89	2.04	9.43
5T6P.PDB	O, B_GLY_10	N, B_THR_113	H, B_THR_113	2.91	2.09	14.72
5T6P.PDB	O, B_VAL_12	N, B_SER_115	H, B_SER_115	2.80	2.05	24.92
5T6P.PDB	O, B_PHE_149	N, B_THR_120	H, B_THR_120	2.75	1.91	11.84
5T6P.PDB	O, B_LEU_144	N, B_TYR_125	H, B_TYR_125	2.91	2.10	16.22
5T6P.PDB	O, B_VAL_186	N, B_VAL_139	H, B_VAL_139	2.78	1.95	11.66
5T6P.PDB	O, B_VAL_184	N, B_LEU_141	H, B_LEU_141	2.63	1.79	9.20
5T6P.PDB	O, B_SER_182	N, B_CYS_143	H, B_CYS_143	2.65	1.86	19.42
5T6P.PDB	O, B_TYR_125	N, B_LEU_144	H, B_LEU_144	2.95	2.09	2.74
5T6P.PDB	O, B_LEU_180	N, B_VAL_145	H, B_VAL_145	2.75	1.91	7.82
5T6P.PDB	O, B_TYR_178	N, B_TYR_148	H, B_TYR_148	2.98	2.19	19.53
5T6P.PDB	O, B_THR_120	N, B_PHE_149	H, B_PHE_149	2.83	2.02	15.93
5T6P.PDB	O, B_ALA_201	N, B_THR_154	H, B_THR_154	2.97	2.17	18.38
5T6P.PDB	O, B_ASN_199	N, B_THR_156	H, B_THR_156	2.88	2.07	16.23
5T6P.PDB	O, B_THR_197	N, B_ASN_158	H, B_ASN_158	2.90	2.09	16.11
5T6P.PDB	O, B_SER_181	N, B_PHE_169	H, B_PHE_169	2.91	2.06	6.94
5T6P.PDB	O, B_LEU_177	N, B_GLN_174	H, B_GLN_174	2.84	1.98	4.57
5T6P.PDB	O, B_GLN_174	N, B_LEU_177	H, B_LEU_177	2.93	2.14	19.22
5T6P.PDB	O, B_TYR_148	N, B_TYR_178	H, B_TYR_178	2.71	1.85	6.27
5T6P.PDB	O, B_VAL_145	N, B_LEU_180	H, B_LEU_180	2.86	2.04	15.49
5T6P.PDB	O, B_CYS_143	N, B_SER_182	H, B_SER_182	2.70	1.91	18.91

5T6P.PDB	O, B_LEU_141	N, B_VAL_184	H, B_VAL_184	2.73	1.88	7.12
5T6P.PDB	O, B_VAL_139	N, B_VAL_186	H, B_VAL_186	2.85	2.02	12.50
5T6P.PDB	OD1, B_ASN_158	N, B_THR_197	H, B_THR_197	2.89	2.12	22.97
5T6P.PDB	O, B_LYS_211	N, B_CYS_198	H, B_CYS_198	2.83	2.00	11.79
5T6P.PDB	O, B_THR_156	N, B_ASN_199	H, B_ASN_199	2.83	1.97	3.18
5T6P.PDB	O, B_VAL_209	N, B_VAL_200	H, B_VAL_200	2.85	2.02	12.35
5T6P.PDB	O, B_THR_154	N, B_ALA_201	H, B_ALA_201	2.90	2.12	21.54
5T6P.PDB	O, B_PRO_150	NE2, B_HIS_202	HE2, B_HIS_202	2.71	1.86	4.81
5T6P.PDB	O, B_VAL_200	N, B_VAL_209	H, B_VAL_209	2.85	2.04	16.15
5T6P.PDB	O, B_CYS_198	N, B_LYS_211	H, B_LYS_211	2.86	2.05	16.75
5T6P.PDB	O, B_VAL_196	N, B_ILE_213	H, B_ILE_213	2.82	1.97	6.68
5T6P.PDB	OG, C_SER_26	N, C_LEU_3	H, C_LEU_3	2.79	1.93	4.03
5T6P.PDB	O, C_ARG_24	N, C_THR_5	H, C_THR_5	2.86	2.03	11.46
5T6P.PDB	O, C_TYR_91	NE2, C_GLN_6	HE22, C_GLN_6	2.75	1.89	3.04
5T6P.PDB	O, C_SER_22	N, C_THR_7	H, C_THR_7	2.88	2.06	14.16
5T6P.PDB	O, C_LYS_108	N, C_LEU_11	H, C_LEU_11	2.88	2.16	28.19
5T6P.PDB	O, C_GLU_110	N, C_VAL_13	H, C_VAL_13	2.97	2.24	26.82
5T6P.PDB	O, C_ILE_80	N, C_ALA_19	H, C_ALA_19	3.00	2.17	14.18
5T6P.PDB	O, C_LEU_78	N, C_ILE_21	H, C_ILE_21	2.76	1.92	12.06
5T6P.PDB	O, C_THR_7	N, C_SER_22	H, C_SER_22	2.70	1.85	6.95
5T6P.PDB	O, C_PHE_76	N, C_CYS_23	H, C_CYS_23	2.70	1.86	10.98
5T6P.PDB	O, C_THR_5	N, C_ARG_24	H, C_ARG_24	2.81	2.00	15.67
5T6P.PDB	OD1, C_ASP_75	NE, C_ARG_24	HE, C_ARG_24	2.92	2.14	20.59
5T6P.PDB	OD1, C_ASP_75	NH2, C_ARG_24	HH21, C_ARG_24	2.94	2.18	23.70
5T6P.PDB	O, C_HIS_31	N, C_GLY_34	H, C_GLY_34	2.90	2.04	3.71
5T6P.PDB	OD1, C_ASN_33	N, C_LYS_35	H, C_LYS_35	2.76	1.93	12.01
5T6P.PDB	O, C_PHE_94	N, C_GLU_39	H, C_GLU_39	2.84	2.01	13.22
5T6P.PDB	O, C_ILE_53	N, C_TRP_40	H, C_TRP_40	2.81	2.01	18.58
5T6P.PDB	O, C_TYR_92	N, C_TYR_41	H, C_TYR_41	2.76	1.92	9.44
5T6P.PDB	O, C_LYS_50	N, C_LEU_42	H, C_LEU_42	2.99	2.19	18.71
5T6P.PDB	O, C_VAL_90	N, C_GLN_43	H, C_GLN_43	2.75	1.90	8.01
5T6P.PDB	OE1, D_GLN_39	NE2, C_GLN_43	HE22, C_GLN_43	3.00	2.17	12.88
5T6P.PDB	O, D_GLY_107	OG, C_SER_48	HG, C_SER_48	2.66	1.94	25.38
5T6P.PDB	O, C_LEU_42	N, C_LYS_50	H, C_LYS_50	2.87	2.11	23.73
5T6P.PDB	O, C_TRP_40	N, C_LEU_52	H, C_LEU_52	2.81	1.96	6.06
5T6P.PDB	O, C_LYS_58	N, C_TYR_54	H, C_TYR_54	2.92	2.10	15.01
5T6P.PDB	O, C_LEU_38	N, C_VAL_56	H, C_VAL_56	2.88	2.04	8.48
5T6P.PDB	O, C_ARG_55	N, C_SER_57	H, C_SER_57	2.66	1.91	24.23
5T6P.PDB	O, C_TYR_54	N, C_LYS_58	H, C_LYS_58	2.91	2.14	22.42
5T6P.PDB	O, C_LEU_52	N, C_PHE_60	H, C_PHE_60	2.93	2.07	3.44
5T6P.PDB	O, C_LYS_79	N, C_SER_68	H, C_SER_68	2.83	1.99	10.51
5T6P.PDB	O, C_CYS_23	N, C_PHE_76	H, C_PHE_76	2.93	2.11	14.43
5T6P.PDB	O, C_ILE_21	N, C_LEU_78	H, C_LEU_78	2.76	1.99	21.57
5T6P.PDB	O, C_SER_68	N, C_LYS_79	H, C_LYS_79	2.78	1.92	4.56
5T6P.PDB	O, C_ALA_19	N, C_ILE_80	H, C_ILE_80	2.92	2.08	10.76
5T6P.PDB	O, C_GLN_43	N, C_VAL_90	H, C_VAL_90	2.95	2.12	13.12
5T6P.PDB	O, C_THR_107	N, C_TYR_91	H, C_TYR_91	2.80	1.96	9.61
5T6P.PDB	O, C_TYR_41	N, C_TYR_92	H, C_TYR_92	2.74	1.93	15.61
5T6P.PDB	O, C_HIS_98	NE2, C_GLN_95	HE22, C_GLN_95	2.72	1.90	15.32
5T6P.PDB	O, C_TYR_37	N, C_GLY_96	H, C_GLY_96	2.80	1.96	11.65
5T6P.PDB	O, C_ILE_29	OG, C_SER_97	HG, C_SER_97	2.80	1.98	12.04
5T6P.PDB	OE1, C_GLN_95	N, C_HIS_98	H, C_HIS_98	2.87	2.02	5.84
5T6P.PDB	O, C_VAL_2	OG1, C_THR_102	HG1, C_THR_102	2.71	1.89	10.27
5T6P.PDB	O, C_CYS_93	N, C_GLY_104	H, C_GLY_104	2.76	1.92	10.56
5T6P.PDB	OE1, C_GLN_6	N, C_GLY_106	H, C_GLY_106	2.99	2.28	28.82
5T6P.PDB	O, C_TYR_91	N, C_THR_107	H, C_THR_107	2.87	2.11	24.01
5T6P.PDB	O, C_PRO_8	OG1, C_THR_107	HG1, C_THR_107	2.74	2.02	25.98
5T6P.PDB	O, C_GLY_89	N, C_LEU_109	H, C_LEU_109	2.77	1.92	5.68

5T6P.PDB	OE1, C_GLN_171	N, C_ILE_111	H, C_ILE_111	2.98	2.15	12.64
5T6P.PDB	O, C_VAL_13	N, C_LYS_112	H, C_LYS_112	2.85	2.02	11.60
5T6P.PDB	O, C_ASP_175	NE, C_ARG_113	HE, C_ARG_113	2.48	1.76	27.03
5T6P.PDB	O, C_TYR_145	N, C_ALA_116	H, C_ALA_116	2.84	2.04	18.21
5T6P.PDB	O, C_ASN_142	N, C_THR_119	H, C_THR_119	2.93	2.10	12.42
5T6P.PDB	O, C_VAL_138	N, C_PHE_123	H, C_PHE_123	2.72	1.95	21.08
5T6P.PDB	OG, C_SER_136	NE2, C_GLN_129	HE22, C_GLN_129	2.79	1.95	11.34
5T6P.PDB	O, C_SER_127	N, C_THR_131	H, C_THR_131	2.98	2.17	16.75
5T6P.PDB	O, C_SER_127	OG1, C_THR_131	HG1, C_THR_131	2.92	2.09	7.67
5T6P.PDB	O, C_GLN_129	OG, C_SER_132	HG, C_SER_132	2.59	1.78	13.08
5T6P.PDB	O, C_LEU_130	N, C_GLY_133	H, C_GLY_133	2.95	2.18	22.40
5T6P.PDB	O, C_LEU_184	N, C_VAL_137	H, C_VAL_137	2.75	1.91	11.06
5T6P.PDB	O, C_SER_182	N, C_CYS_139	H, C_CYS_139	2.88	2.16	27.24
5T6P.PDB	O, C_SER_121	N, C_PHE_140	H, C_PHE_140	2.80	2.02	21.09
5T6P.PDB	O, C_MET_180	N, C_LEU_141	H, C_LEU_141	2.85	2.01	8.82
5T6P.PDB	OG, C_SER_179	N, C_ASN_143	H, C_ASN_143	2.94	2.10	9.85
5T6P.PDB	O, C_TYR_178	N, C_PHE_144	H, C_PHE_144	2.77	1.92	8.13
5T6P.PDB	OG, C_SER_182	NE1, C_TRP_153	HE1, C_TRP_153	2.89	2.07	15.50
5T6P.PDB	O, C_THR_198	N, C_LYS_154	H, C_LYS_154	2.75	1.96	18.48
5T6P.PDB	O, C_SER_196	N, C_ASP_156	H, C_ASP_156	2.70	1.86	10.78
5T6P.PDB	O, C_TRP_153	N, C_ARG_160	H, C_ARG_160	2.72	1.94	21.43
5T6P.PDB	O, C_SER_181	N, C_SER_167	H, C_SER_167	2.91	2.15	22.92
5T6P.PDB	O, C_LYS_147	NE1, C_TRP_168	HE1, C_TRP_168	3.00	2.28	28.07
5T6P.PDB	O, C_SER_179	N, C_THR_169	H, C_THR_169	2.70	1.86	8.97
5T6P.PDB	O, C_ASP_170	OG1, C_THR_169	HG1, C_THR_169	2.94	2.20	24.83
5T6P.PDB	O, C_SER_176	NE2, C_GLN_171	HE21, C_GLN_171	2.89	2.05	12.01
5T6P.PDB	O, C_ILE_111	NE2, C_GLN_171	HE22, C_GLN_171	2.85	2.04	15.54
5T6P.PDB	O, C_THR_177	N, C_ASP_172	H, C_ASP_172	2.94	2.12	14.22
5T6P.PDB	OD1, C_ASP_172	N, C_LYS_174	H, C_LYS_174	2.89	2.05	10.44
5T6P.PDB	O, C_ASP_172	N, C_SER_176	H, C_SER_176	2.80	2.08	27.25
5T6P.PDB	OD1, C_ASP_175	N, C_THR_177	H, C_THR_177	2.99	2.17	14.08
5T6P.PDB	OD1, C_ASP_175	OG1, C_THR_177	HG1, C_THR_177	2.69	1.86	7.21
5T6P.PDB	O, C_PHE_144	N, C_TYR_178	H, C_TYR_178	2.70	1.84	4.46
5T6P.PDB	O, C_LEU_141	N, C_MET_180	H, C_MET_180	2.84	2.02	15.41
5T6P.PDB	O, C_SER_167	N, C_SER_181	H, C_SER_181	2.79	2.00	19.18
5T6P.PDB	O, C_CYS_139	N, C_SER_182	H, C_SER_182	2.88	2.03	8.59
5T6P.PDB	OD1, C_ASN_166	OG, C_SER_182	HG, C_SER_182	2.45	1.64	11.11
5T6P.PDB	O, C_VAL_137	N, C_LEU_184	H, C_LEU_184	2.79	1.98	16.51
5T6P.PDB	O, C_ALA_135	N, C_LEU_186	H, C_LEU_186	2.93	2.10	13.93
5T6P.PDB	O, C_GLY_133	N, C_LYS_188	H, C_LYS_188	2.95	2.12	12.53
5T6P.PDB	O, C_THR_187	N, C_TYR_191	H, C_TYR_191	2.98	2.13	6.59
5T6P.PDB	OD1, C_ASP_156	N, C_SER_196	H, C_SER_196	2.87	2.02	6.00
5T6P.PDB	OG, C_SER_213	OG1, C_THR_198	HG1, C_THR_198	3.00	2.20	14.46
5T6P.PDB	O, C_ILE_210	N, C_ALA_201	H, C_ALA_201	2.94	2.14	17.24
5T6P.PDB	O, C_ASN_150	N, C_THR_202	H, C_THR_202	2.84	2.03	16.39
5T6P.PDB	O, C_ALA_201	N, C_ILE_210	H, C_ILE_210	2.99	2.24	25.62
5T6P.PDB	O, D_SER_25	N, D_LYS_3	H, D_LYS_3	2.88	2.06	14.17
5T6P.PDB	O, D_THR_113	N, D_VAL_12	H, D_VAL_12	2.73	1.95	21.29
5T6P.PDB	O, D_LEU_86	N, D_GLY_15	H, D_GLY_15	2.72	1.86	4.08
5T6P.PDB	O, D_ALA_13	N, D_GLY_16	H, D_GLY_16	2.92	2.16	22.99
5T6P.PDB	O, D_MET_83	N, D_LEU_18	H, D_LEU_18	2.98	2.18	18.81
5T6P.PDB	O, D_LEU_81	N, D_LEU_20	H, D_LEU_20	2.99	2.15	11.31
5T6P.PDB	O, D_VAL_5	N, D_ALA_23	H, D_ALA_23	2.75	1.94	16.20
5T6P.PDB	O, D_LYS_3	N, D_SER_25	H, D_SER_25	2.97	2.23	25.58
5T6P.PDB	O, D_ILE_51	N, D_MET_34	H, D_MET_34	2.96	2.14	15.76
5T6P.PDB	O, D_GLU_46	N, D_ARG_38	H, D_ARG_38	2.85	2.01	11.39
5T6P.PDB	O, D_ILE_93	N, D_GLN_39	H, D_GLN_39	2.72	1.93	19.22
5T6P.PDB	OE1, C_GLN_43	NE2, D_GLN_39	HE22, D_GLN_39	2.79	1.94	7.20

5T6P.PDB	O, D_THR_40	N, D_LYS_43	H, D_LYS_43	2.74	1.92	14.91
5T6P.PDB	O, D_ARG_38	N, D_GLU_46	H, D_GLU_46	2.87	2.03	9.75
5T6P.PDB	O, D_GLY_56	N, D_ASN_52	H, D_ASN_52	2.87	2.01	5.61
5T6P.PDB	OD1, D_ASN_52	N, D_GLY_56	H, D_GLY_56	2.70	1.88	14.82
5T6P.PDB	O, D_VAL_64	N, D_ARG_67	H, D_ARG_67	2.94	2.10	10.62
5T6P.PDB	O, D_GLN_82	N, D_THR_69	H, D_THR_69	2.84	2.13	29.43
5T6P.PDB	OD1, D_ASN_74	NE, D_ARG_72	HE, D_ARG_72	2.79	2.07	27.15
5T6P.PDB	O, D_TYR_32	NH2, D_ARG_72	HH22, D_ARG_72	3.00	2.24	24.48
5T6P.PDB	O, D_THR_78	N, D_ASP_73	H, D_ASP_73	2.80	1.97	14.04
5T6P.PDB	O, D_ASN_53	ND2, D_ASN_74	HD21, D_ASN_74	3.00	2.17	13.41
5T6P.PDB	O, D_LYS_76	OG1, D_THR_78	HG1, D_THR_78	2.82	2.06	20.07
5T6P.PDB	O, D_SER_71	N, D_TYR_80	H, D_TYR_80	2.80	1.95	7.50
5T6P.PDB	O, D_THR_69	N, D_GLN_82	H, D_GLN_82	2.94	2.10	10.42
5T6P.PDB	O, D_LEU_18	N, D_MET_83	H, D_MET_83	2.78	1.94	10.80
5T6P.PDB	O, D_ARG_67	OG, D_SER_84	HG, D_SER_84	2.89	2.11	18.15
5T6P.PDB	O, D_GLN_39	N, D_ILE_93	H, D_ILE_93	2.95	2.17	20.82
5T6P.PDB	O, D_ASP_90	OH, D_TYR_94	HH, D_TYR_94	2.82	2.01	12.26
5T6P.PDB	O, D_VAL_37	N, D_TYR_95	H, D_TYR_95	2.61	1.75	6.47
5T6P.PDB	O, D_TYR_105	N, D_ARG_98	H, D_ARG_98	2.94	2.21	27.44
5T6P.PDB	OD1, D_ASP_104	N, D_GLY_102	H, D_GLY_102	2.73	1.88	6.65
5T6P.PDB	OH, C_TYR_41	N, D_PHE_103	H, D_PHE_103	2.95	2.09	5.85
5T6P.PDB	O, D_PHE_103	NE1, D_TRP_106	HE1, D_TRP_106	2.89	2.15	26.36
5T6P.PDB	O, D_CYS_96	N, D_GLY_107	H, D_GLY_107	2.78	1.98	18.45
5T6P.PDB	OE1, D_GLU_6	N, D_GLY_109	H, D_GLY_109	2.82	1.98	11.29
5T6P.PDB	O, D_ALA_92	N, D_LEU_112	H, D_LEU_112	2.91	2.08	13.48
5T6P.PDB	O, D_GLY_10	N, D_THR_113	H, D_THR_113	2.98	2.16	15.81
5T6P.PDB	O, D_VAL_12	N, D_SER_115	H, D_SER_115	2.63	1.84	18.22
5T6P.PDB	OG, D_SER_115	N, D_ALA_117	H, D_ALA_117	2.99	2.16	13.20
5T6P.PDB	O, D_PHE_149	N, D_THR_120	H, D_THR_120	2.64	1.82	13.09
5T6P.PDB	O, D_LEU_144	N, D_TYR_125	H, D_TYR_125	2.84	2.03	17.31
5T6P.PDB	O, D_GLY_142	N, D_LEU_127	H, D_LEU_127	2.66	1.91	24.44
5T6P.PDB	O, D_VAL_184	N, D_LEU_141	H, D_LEU_141	2.71	1.86	8.53
5T6P.PDB	O, D_LEU_127	N, D_GLY_142	H, D_GLY_142	2.95	2.21	25.85
5T6P.PDB	O, D_SER_182	N, D_CYS_143	H, D_CYS_143	2.92	2.13	19.17
5T6P.PDB	O, D_TYR_125	N, D_LEU_144	H, D_LEU_144	2.68	1.83	6.73
5T6P.PDB	O, D_LEU_180	N, D_VAL_145	H, D_VAL_145	2.89	2.05	11.52
5T6P.PDB	O, D_TYR_178	N, D_GLY_147	H, D_GLY_147	2.78	2.07	29.34
5T6P.PDB	O, D_THR_120	N, D_PHE_149	H, D_PHE_149	2.69	1.86	13.14
5T6P.PDB	O, D_ASN_199	N, D_THR_156	H, D_THR_156	2.86	2.04	16.17
5T6P.PDB	OG, D_SER_182	NE1, D_TRP_157	HE1, D_TRP_157	2.97	2.13	11.56
5T6P.PDB	O, D_THR_197	N, D_ASN_158	H, D_ASN_158	2.80	1.97	13.62
5T6P.PDB	OD1, D_ASN_199	N, D_SER_159	H, D_SER_159	2.76	1.93	12.39
5T6P.PDB	O, D_SER_181	N, D_PHE_169	H, D_PHE_169	2.92	2.06	6.74
5T6P.PDB	O, D_LEU_177	N, D_GLN_174	H, D_GLN_174	2.90	2.05	9.77
5T6P.PDB	O, D_VAL_145	N, D_LEU_180	H, D_LEU_180	2.92	2.09	12.70
5T6P.PDB	O, D_CYS_143	N, D_SER_182	H, D_SER_182	2.99	2.18	17.49
5T6P.PDB	O, D_LEU_141	N, D_VAL_184	H, D_VAL_184	2.83	2.00	11.08
5T6P.PDB	O, D_VAL_139	N, D_VAL_186	H, D_VAL_186	2.98	2.17	17.79
5T6P.PDB	N, D_MET_138	OG, D_SER_188	HG, D_SER_188	2.81	2.08	24.12
5T6P.PDB	O, D_LYS_211	N, D_CYS_198	H, D_CYS_198	2.89	2.04	10.05
5T6P.PDB	O, D_THR_156	N, D_ASN_199	H, D_ASN_199	2.84	1.98	3.08
5T6P.PDB	O, D_THR_207	N, D_HIS_202	H, D_HIS_202	2.87	2.08	19.72
5T6P.PDB	O, D_PRO_150	NE2, D_HIS_202	HE2, D_HIS_202	2.50	1.66	9.39
5T6P.PDB	O, D_PRO_203	N, D_SER_206	H, D_SER_206	3.00	2.24	23.51
5T6P.PDB	O, D_HIS_202	N, D_THR_207	H, D_THR_207	2.78	1.92	6.54
5T6P.PDB	O, D_VAL_200	N, D_VAL_209	H, D_VAL_209	2.88	2.09	19.68
5T6P.PDB	O, D_CYS_198	N, D_LYS_211	H, D_LYS_211	2.87	2.05	13.61
5T6P.PDB	OE1, C_GLU_39	NE, E_ARG_5	HE, E_ARG_5	2.86	2.02	10.72

5T78.PDB	OD1, C_ASN_150	N, A_ASP_1	H1, A_ASP_1	2.85	2.07	23.76
5T78.PDB	OG, A_SER_26	N, A_LEU_3	H, A_LEU_3	2.77	1.92	5.16
5T78.PDB	O, A_ARG_24	N, A_THR_5	H, A_THR_5	2.76	1.94	14.03
5T78.PDB	O, A_SER_22	N, A_THR_7	H, A_THR_7	2.99	2.18	17.34
5T78.PDB	O, A_LYS_108	N, A_LEU_11	H, A_LEU_11	2.88	2.17	29.09
5T78.PDB	O, A_VAL_83	N, A_GLY_16	H, A_GLY_16	2.89	2.04	7.22
5T78.PDB	O, A_LEU_78	N, A_ILE_21	H, A_ILE_21	2.93	2.10	12.51
5T78.PDB	O, A_THR_7	N, A_SER_22	H, A_SER_22	2.70	1.84	3.93
5T78.PDB	O, A_PHE_76	N, A_CYS_23	H, A_CYS_23	2.77	1.99	20.04
5T78.PDB	O, A_THR_5	N, A_ARG_24	H, A_ARG_24	2.73	1.95	21.00
5T78.PDB	O, A_THR_74	N, A_SER_25	H, A_SER_25	2.93	2.13	18.34
5T78.PDB	O, A_LYS_35	N, A_HIS_31	H, A_HIS_31	2.86	2.05	16.92
5T78.PDB	O, A_HIS_31	N, A_GLY_34	H, A_GLY_34	2.98	2.13	5.88
5T78.PDB	OD1, A_ASN_33	N, A_LYS_35	H, A_LYS_35	2.95	2.11	11.40
5T78.PDB	O, A_PHE_94	N, A_GLU_39	H, A_GLU_39	2.67	1.85	14.17
5T78.PDB	O, A_ILE_53	N, A_TRP_40	H, A_TRP_40	2.80	1.98	14.47
5T78.PDB	O, A_TYR_92	N, A_TYR_41	H, A_TYR_41	2.83	2.00	12.62
5T78.PDB	O, A_LYS_50	N, A_LEU_42	H, A_LEU_42	2.94	2.12	15.79
5T78.PDB	O, A_VAL_90	N, A_GLN_43	H, A_GLN_43	2.75	1.91	9.96
5T78.PDB	O, A_GLN_47	NE2, A_GLN_43	HE21, A_GLN_43	2.87	2.05	14.69
5T78.PDB	OE1, B_GLN_39	NE2, A_GLN_43	HE22, A_GLN_43	2.92	2.08	9.79
5T78.PDB	O, A_LYS_44	N, A_GLN_47	H, A_GLN_47	2.88	2.11	22.48
5T78.PDB	O, B_GLY_107	OG, A_SER_48	HG, A_SER_48	2.44	1.64	14.53
5T78.PDB	O, A_LEU_42	N, A_LYS_50	H, A_LYS_50	2.92	2.18	25.97
5T78.PDB	O, A_TRP_40	N, A_LEU_52	H, A_LEU_52	2.90	2.04	3.31
5T78.PDB	O, A_LYS_58	N, A_TYR_54	H, A_TYR_54	2.94	2.12	16.14
5T78.PDB	O, A_LEU_38	N, A_VAL_56	H, A_VAL_56	2.99	2.14	9.64
5T78.PDB	O, A_ARG_55	N, A_SER_57	H, A_SER_57	2.65	1.91	25.85
5T78.PDB	O, A_TYR_54	N, A_LYS_58	H, A_LYS_58	2.90	2.09	16.26
5T78.PDB	O, A_LEU_52	N, A_PHE_60	H, A_PHE_60	2.85	2.03	15.54
5T78.PDB	OD2, A_ASP_87	NH1, A_ARG_66	HH12, A_ARG_66	2.55	1.80	24.29
5T78.PDB	OD1, A_ASP_87	NH2, A_ARG_66	HH22, A_ARG_66	2.87	2.03	11.23
5T78.PDB	O, A_LYS_79	N, A_SER_68	H, A_SER_68	2.94	2.13	16.71
5T78.PDB	O, A_THR_77	N, A_SER_70	H, A_SER_70	2.85	2.11	25.59
5T78.PDB	O, A_CYS_23	N, A_PHE_76	H, A_PHE_76	2.95	2.11	10.95
5T78.PDB	O, A_SER_70	N, A_THR_77	H, A_THR_77	2.83	2.03	18.36
5T78.PDB	O, A_ILE_21	N, A_LEU_78	H, A_LEU_78	2.90	2.07	13.51
5T78.PDB	O, A_SER_68	N, A_LYS_79	H, A_LYS_79	2.71	1.87	11.82
5T78.PDB	O, A_ALA_19	N, A_ILE_80	H, A_ILE_80	2.96	2.14	14.84
5T78.PDB	OD2, A_ASP_87	N, A_GLU_84	H, A_GLU_84	2.82	1.98	8.50
5T78.PDB	O, A_GLU_84	N, A_ASP_87	H, A_ASP_87	2.85	2.00	6.16
5T78.PDB	O, A_GLN_43	N, A_VAL_90	H, A_VAL_90	2.81	1.97	10.43
5T78.PDB	O, A_THR_107	N, A_TYR_91	H, A_TYR_91	2.77	1.92	8.36
5T78.PDB	O, A_ASP_87	OH, A_TYR_91	HH, A_TYR_91	2.69	1.98	27.33
5T78.PDB	O, A_TYR_41	N, A_TYR_92	H, A_TYR_92	2.75	1.92	13.82
5T78.PDB	O, B_LYS_43	OH, A_TYR_92	HH, A_TYR_92	2.74	2.03	27.20
5T78.PDB	O, A_HIS_98	NE2, A_GLN_95	HE22, A_GLN_95	2.92	2.12	18.53
5T78.PDB	O, A_TYR_37	N, A_GLY_96	H, A_GLY_96	2.69	1.89	17.50
5T78.PDB	O, A_ILE_29	OG, A_SER_97	HG, A_SER_97	2.60	1.77	8.73
5T78.PDB	OE1, A_GLN_95	N, A_HIS_98	H, A_HIS_98	2.98	2.13	5.45
5T78.PDB	O, A_VAL_2	OG1, A_THR_102	HG1, A_THR_102	2.90	2.09	13.47
5T78.PDB	O, A_CYS_93	N, A_GLY_104	H, A_GLY_104	2.80	1.97	11.96
5T78.PDB	O, A_TYR_91	N, A_THR_107	H, A_THR_107	2.90	2.14	23.68
5T78.PDB	O, A_PRO_8	OG1, A_THR_107	HG1, A_THR_107	2.83	2.13	28.32
5T78.PDB	O, A_GLY_89	N, A_LEU_109	H, A_LEU_109	2.84	2.00	8.45
5T78.PDB	O, A_LEU_11	N, A_GLU_110	H, A_GLU_110	2.89	2.03	4.85
5T78.PDB	OE1, A_GLN_171	N, A_ILE_111	H, A_ILE_111	2.97	2.14	12.35
5T78.PDB	O, A_VAL_13	N, A_LYS_112	H, A_LYS_112	2.85	2.01	10.13

5T78.PDB	O, A_ASP_175	NE, A_ARG_113	HE, A_ARG_113	2.74	2.03	29.28
5T78.PDB	O, A_TYR_145	N, A_ALA_116	H, A_ALA_116	2.81	1.98	12.42
5T78.PDB	O, A_ASN_142	N, A_THR_119	H, A_THR_119	2.97	2.16	15.94
5T78.PDB	O, A_VAL_138	N, A_PHE_123	H, A_PHE_123	2.72	1.95	21.36
5T78.PDB	OG, A_SER_136	NE2, A_GLN_129	HE22, A_GLN_129	2.86	2.01	3.70
5T78.PDB	OE1, A_GLN_129	N, A_SER_136	H, A_SER_136	2.91	2.06	8.11
5T78.PDB	O, A_LEU_184	N, A_VAL_137	H, A_VAL_137	2.77	1.93	11.05
5T78.PDB	O, A_SER_182	N, A_CYS_139	H, A_CYS_139	2.88	2.10	21.11
5T78.PDB	O, A_SER_121	N, A_PHE_140	H, A_PHE_140	2.83	2.07	23.10
5T78.PDB	O, A_MET_180	N, A_LEU_141	H, A_LEU_141	2.79	1.93	5.17
5T78.PDB	OG, A_SER_179	N, A_ASN_143	H, A_ASN_143	2.98	2.18	18.51
5T78.PDB	O, A_TYR_178	N, A_PHE_144	H, A_PHE_144	2.83	2.00	10.95
5T78.PDB	O, A_GLU_200	N, A_LYS_152	H, A_LYS_152	2.93	2.13	17.83
5T78.PDB	OG, A_SER_182	NE1, A_TRP_153	HE1, A_TRP_153	2.68	1.86	12.79
5T78.PDB	O, A_THR_198	N, A_LYS_154	H, A_LYS_154	2.86	2.06	17.77
5T78.PDB	O, A_SER_158	N, A_ILE_155	H, A_ILE_155	2.71	1.89	15.55
5T78.PDB	O, A_SER_196	N, A_ASP_156	H, A_ASP_156	2.87	2.03	11.28
5T78.PDB	O, A_THR_183	N, A_LEU_165	H, A_LEU_165	2.87	2.15	28.15
5T78.PDB	O, A_SER_181	N, A_SER_167	H, A_SER_167	2.88	2.13	24.95
5T78.PDB	O, B_PRO_170	OG, A_SER_167	HG, A_SER_167	2.91	2.11	14.54
5T78.PDB	O, A_SER_179	N, A_THR_169	H, A_THR_169	2.90	2.06	10.39
5T78.PDB	O, A_ASP_170	OG1, A_THR_169	HG1, A_THR_169	2.92	2.23	29.63
5T78.PDB	O, A_ILE_111	NE2, A_GLN_171	HE22, A_GLN_171	2.73	1.91	15.69
5T78.PDB	O, A_THR_177	N, A_ASP_172	H, A_ASP_172	2.80	1.95	9.74
5T78.PDB	OD1, A_ASP_172	N, A_LYS_174	H, A_LYS_174	2.78	1.98	17.25
5T78.PDB	OD1, A_ASP_175	N, A_THR_177	H, A_THR_177	2.96	2.13	13.21
5T78.PDB	OD1, A_ASP_175	OG1, A_THR_177	HG1, A_THR_177	2.57	1.74	7.68
5T78.PDB	O, A_PHE_144	N, A_TYR_178	H, A_TYR_178	2.78	1.93	4.54
5T78.PDB	O, A_LEU_141	N, A_MET_180	H, A_MET_180	2.83	2.03	17.69
5T78.PDB	O, A_SER_167	N, A_SER_181	H, A_SER_181	2.92	2.13	19.33
5T78.PDB	O, A_CYS_139	N, A_SER_182	H, A_SER_182	2.91	2.07	11.51
5T78.PDB	OD1, A_ASN_166	OG, A_SER_182	HG, A_SER_182	2.63	1.89	23.17
5T78.PDB	O, A_LEU_165	N, A_THR_183	H, A_THR_183	2.82	2.01	15.88
5T78.PDB	O, A_VAL_137	N, A_LEU_184	H, A_LEU_184	2.80	1.99	16.92
5T78.PDB	O, A_GLY_163	N, A_THR_185	H, A_THR_185	2.94	2.10	11.69
5T78.PDB	O, A_ALA_135	N, A_LEU_186	H, A_LEU_186	2.79	1.97	14.73
5T78.PDB	O, A_GLY_133	N, A_LYS_188	H, A_LYS_188	2.91	2.08	12.09
5T78.PDB	OD2, A_ASP_156	ND1, A_HIS_194	HD1, A_HIS_194	2.73	1.92	16.43
5T78.PDB	O, A_LYS_154	N, A_THR_198	H, A_THR_198	2.92	2.19	26.56
5T78.PDB	O, A_LYS_152	N, A_GLU_200	H, A_GLU_200	2.90	2.08	15.52
5T78.PDB	O, A_ILE_210	N, A_ALA_201	H, A_ALA_201	2.96	2.16	17.21
5T78.PDB	O, A_ASN_150	N, A_THR_202	H, A_THR_202	2.72	1.89	13.21
5T78.PDB	ND1, A_HIS_203	OG1, A_THR_205	HG1, A_THR_205	2.99	2.26	25.09
5T78.PDB	O, A_ALA_201	N, A_ILE_210	H, A_ILE_210	2.84	2.02	14.61
5T78.PDB	OG1, A_THR_198	OG, A_SER_213	HG, A_SER_213	2.76	1.99	20.46
5T78.PDB	O, B_SER_21	N, B_SER_7	H, B_SER_7	2.89	2.16	26.40
5T78.PDB	O, B_THR_113	N, B_VAL_12	H, B_VAL_12	2.88	2.08	18.22
5T78.PDB	O, B_LEU_86	N, B_GLY_15	H, B_GLY_15	2.82	1.98	8.23
5T78.PDB	O, B_LEU_81	N, B_LEU_20	H, B_LEU_20	2.77	1.95	14.38
5T78.PDB	O, B_VAL_5	N, B_ALA_23	H, B_ALA_23	2.79	1.96	12.99
5T78.PDB	O, B_ASN_77	N, B_ALA_24	H, B_ALA_24	2.95	2.10	5.61
5T78.PDB	O, B_ILE_97	N, B_SER_35	H, B_SER_35	3.00	2.17	14.65
5T78.PDB	O, B_ALA_49	N, B_TRP_36	H, B_TRP_36	2.97	2.18	20.26
5T78.PDB	O, B_GLU_46	N, B_ARG_38	H, B_ARG_38	2.72	1.88	9.22
5T78.PDB	OE1, B_GLU_46	NE, B_ARG_38	HE, B_ARG_38	2.94	2.16	20.63
5T78.PDB	OH, B_TYR_94	NH1, B_ARG_38	HH11, B_ARG_38	2.90	2.09	15.42
5T78.PDB	OD1, B_ASP_90	NH1, B_ARG_38	HH12, B_ARG_38	2.89	2.09	17.62
5T78.PDB	O, B_ILE_93	N, B_GLN_39	H, B_GLN_39	2.78	1.98	17.72

5T78.PDB	OE1, A_GLN_43	NE2, B_GLN_39	HE22, B_GLN_39	2.63	1.78	5.56
5T78.PDB	O, B_THR_40	N, B_LYS_43	H, B_LYS_43	2.64	1.83	15.69
5T78.PDB	O, B_ARG_38	N, B_GLU_46	H, B_GLU_46	2.78	1.95	11.59
5T78.PDB	O, B_TRP_36	N, B_VAL_48	H, B_VAL_48	2.96	2.11	4.39
5T78.PDB	O, B_GLN_82	N, B_THR_69	H, B_THR_69	2.84	2.05	19.71
5T78.PDB	OH, B_TYR_60	N, B_ILE_70	H, B_ILE_70	2.81	2.01	18.63
5T78.PDB	OD1, B_ASN_74	NE, B_ARG_72	HE, B_ARG_72	2.69	1.95	25.68
5T78.PDB	O, B_THR_78	N, B_ASP_73	H, B_ASP_73	3.00	2.15	8.98
5T78.PDB	O, B_CYS_22	N, B_LEU_79	H, B_LEU_79	2.95	2.15	18.76
5T78.PDB	O, B_SER_71	N, B_TYR_80	H, B_TYR_80	2.82	1.97	8.86
5T78.PDB	O, B_LEU_20	N, B_LEU_81	H, B_LEU_81	2.97	2.19	21.07
5T78.PDB	O, B_THR_69	N, B_GLN_82	H, B_GLN_82	2.85	2.05	17.58
5T78.PDB	O, B_LEU_18	N, B_MET_83	H, B_MET_83	2.74	1.98	23.26
5T78.PDB	OD2, B_ASP_90	N, B_LYS_87	H, B_LYS_87	2.78	1.92	2.04
5T78.PDB	O, B_GLN_39	N, B_ILE_93	H, B_ILE_93	2.84	2.04	18.32
5T78.PDB	O, B_THR_110	N, B_TYR_94	H, B_TYR_94	2.77	1.91	3.39
5T78.PDB	O, B_ASP_90	OH, B_TYR_94	HH, B_TYR_94	2.74	1.93	12.66
5T78.PDB	O, B_VAL_37	N, B_TYR_95	H, B_TYR_95	2.67	1.82	4.17
5T78.PDB	OE1, B_GLN_39	OH, B_TYR_95	HH, B_TYR_95	2.91	2.11	14.46
5T78.PDB	OE2, B_GLU_6	N, B_CYS_96	H, B_CYS_96	2.65	1.81	8.49
5T78.PDB	OD1, B_ASP_104	N, B_GLY_102	H, B_GLY_102	2.93	2.09	9.46
5T78.PDB	OH, A_TYR_41	N, B_PHE_103	H, B_PHE_103	2.85	2.00	5.24
5T78.PDB	O, B_PHE_103	NE1, B_TRP_106	HE1, B_TRP_106	2.89	2.16	27.37
5T78.PDB	O, B_CYS_96	N, B_GLY_107	H, B_GLY_107	2.88	2.05	11.81
5T78.PDB	O, B_ALA_92	N, B_LEU_112	H, B_LEU_112	2.91	2.10	16.63
5T78.PDB	OG1, B_THR_91	N, B_VAL_114	H, B_VAL_114	2.84	1.98	4.39
5T78.PDB	O, B_PHE_149	N, B_THR_120	H, B_THR_120	2.84	2.00	10.54
5T78.PDB	O, B_LYS_146	N, B_SER_123	H, B_SER_123	2.99	2.18	17.27
5T78.PDB	O, B_LEU_144	N, B_TYR_125	H, B_TYR_125	2.88	2.07	16.65
5T78.PDB	O, B_GLY_142	N, B_LEU_127	H, B_LEU_127	2.85	2.06	19.67
5T78.PDB	O, B_VAL_186	N, B_VAL_139	H, B_VAL_139	2.76	1.90	4.98
5T78.PDB	OG1, B_THR_185	OG1, B_THR_140	HG1, B_THR_140	2.97	2.14	5.19
5T78.PDB	O, B_VAL_184	N, B_LEU_141	H, B_LEU_141	2.73	1.89	10.61
5T78.PDB	O, B_SER_182	N, B_CYS_143	H, B_CYS_143	2.99	2.23	23.48
5T78.PDB	O, B_TYR_125	N, B_LEU_144	H, B_LEU_144	2.79	1.95	10.28
5T78.PDB	O, B_LEU_180	N, B_VAL_145	H, B_VAL_145	2.91	2.07	9.52
5T78.PDB	O, B_SER_123	N, B_LYS_146	H, B_LYS_146	2.85	2.01	7.84
5T78.PDB	O, B_THR_120	N, B_PHE_149	H, B_PHE_149	2.90	2.09	17.04
5T78.PDB	O, B_ALA_201	N, B_THR_154	H, B_THR_154	3.00	2.21	19.88
5T78.PDB	O, B_ASN_199	N, B_THR_156	H, B_THR_156	2.81	1.98	11.68
5T78.PDB	O, B_THR_197	N, B_ASN_158	H, B_ASN_158	2.82	1.98	10.92
5T78.PDB	OD1, B_ASN_199	N, B_SER_159	H, B_SER_159	2.70	1.89	14.93
5T78.PDB	O, B_TRP_157	N, B_GLY_160	H, B_GLY_160	2.98	2.17	16.73
5T78.PDB	O, B_SER_181	N, B_PHE_169	H, B_PHE_169	2.81	1.96	6.40
5T78.PDB	O, B_LEU_177	N, B_GLN_174	H, B_GLN_174	2.94	2.10	10.35
5T78.PDB	O, B_TYR_148	N, B_TYR_178	H, B_TYR_178	2.83	1.97	1.07
5T78.PDB	O, B_VAL_172	N, B_THR_179	H, B_THR_179	2.95	2.19	24.45
5T78.PDB	O, B_VAL_145	N, B_LEU_180	H, B_LEU_180	2.94	2.12	15.28
5T78.PDB	O, B_HIS_167	N, B_SER_183	H, B_SER_183	2.99	2.13	4.09
5T78.PDB	O, B_LEU_141	N, B_VAL_184	H, B_VAL_184	2.95	2.11	9.47
5T78.PDB	O, B_GLY_165	N, B_THR_185	H, B_THR_185	2.86	2.16	29.53
5T78.PDB	O, B_VAL_139	N, B_VAL_186	H, B_VAL_186	2.86	2.08	20.52
5T78.PDB	OD1, B_ASN_158	N, B_THR_197	H, B_THR_197	2.72	1.93	18.91
5T78.PDB	O, B_LYS_211	N, B_CYS_198	H, B_CYS_198	2.79	1.94	3.58
5T78.PDB	O, B_THR_156	N, B_ASN_199	H, B_ASN_199	2.75	1.89	4.63
5T78.PDB	O, B_VAL_209	N, B_VAL_200	H, B_VAL_200	2.85	2.01	8.95
5T78.PDB	O, B_THR_154	N, B_ALA_201	H, B_ALA_201	2.91	2.08	12.90
5T78.PDB	O, B_THR_207	N, B_HIS_202	H, B_HIS_202	2.79	1.94	7.70

5T78.PDB	O, B.PRO_150	NE2, B.HIS_202	HE2, B.HIS_202	2.74	1.92	14.58
5T78.PDB	O, B.PRO_203	N, B.SER_206	H, B.SER_206	2.79	2.01	21.34
5T78.PDB	O, B.VAL_200	N, B.VAL_209	H, B.VAL_209	2.83	2.00	12.26
5T78.PDB	O, B.CYS_198	N, B.LYS_211	H, B.LYS_211	2.91	2.09	14.58
5T78.PDB	O, B.VAL_196	N, B.ILE_213	H, B.ILE_213	2.98	2.13	8.16
5T78.PDB	OE1, A.GLU_39	NH1, F.ARG_5	HH11, F.ARG_5	2.68	1.83	9.33
5T78.PDB	OG, C.SER_26	N, C.LEU_3	H, C.LEU_3	2.73	1.88	4.61
5T78.PDB	O, C.ARG_24	N, C.THR_5	H, C.THR_5	2.78	1.95	10.72
5T78.PDB	O, C.TYR_91	NE2, C.GLN_6	HE22, C.GLN_6	2.96	2.13	12.54
5T78.PDB	O, C.SER_22	N, C.THR_7	H, C.THR_7	2.88	2.10	19.87
5T78.PDB	O, C.LYS_108	N, C.LEU_11	H, C.LEU_11	2.84	2.11	26.95
5T78.PDB	O, C.VAL_83	N, C.GLY_16	H, C.GLY_16	2.91	2.06	6.60
5T78.PDB	O, C.ILE_80	N, C.ALA_19	H, C.ALA_19	2.84	2.03	15.95
5T78.PDB	O, C.LEU_78	N, C.ILE_21	H, C.ILE_21	2.99	2.16	13.69
5T78.PDB	O, C.THR_7	N, C.SER_22	H, C.SER_22	2.73	1.88	3.18
5T78.PDB	O, C.PHE_76	N, C.CYS_23	H, C.CYS_23	2.75	1.96	19.40
5T78.PDB	O, C.THR_5	N, C.ARG_24	H, C.ARG_24	2.63	1.83	18.67
5T78.PDB	OD1, C.ASP_75	NE, C.ARG_24	HE, C.ARG_24	2.96	2.16	17.61
5T78.PDB	O, C.THR_74	N, C.SER_25	H, C.SER_25	2.94	2.15	19.26
5T78.PDB	O, C.LYS_35	N, C.HIS_31	H, C.HIS_31	2.92	2.13	19.70
5T78.PDB	OH, C.TYR_37	ND2, C.ASN_33	HD21, C.ASN_33	2.96	2.18	21.06
5T78.PDB	O, C.HIS_31	N, C.GLY_34	H, C.GLY_34	3.00	2.15	8.88
5T78.PDB	OD1, C.ASN_33	N, C.LYS_35	H, C.LYS_35	2.89	2.07	15.44
5T78.PDB	O, C.PHE_94	N, C.GLU_39	H, C.GLU_39	2.80	1.97	13.19
5T78.PDB	O, C.ILE_53	N, C.TRP_40	H, C.TRP_40	2.85	2.04	17.58
5T78.PDB	O, C.TYR_92	N, C.TYR_41	H, C.TYR_41	2.86	2.04	13.58
5T78.PDB	O, C.LYS_50	N, C.LEU_42	H, C.LEU_42	2.96	2.15	16.18
5T78.PDB	O, C.VAL_90	N, C.GLN_43	H, C.GLN_43	2.84	2.01	10.96
5T78.PDB	O, C.LYS_44	N, C.GLN_47	H, C.GLN_47	2.91	2.11	19.11
5T78.PDB	O, D.GLY_107	OG, C.SER_48	HG, C.SER_48	2.59	1.80	15.22
5T78.PDB	O, C.LEU_42	N, C.LYS_50	H, C.LYS_50	2.85	2.10	25.26
5T78.PDB	O, C.TRP_40	N, C.LEU_52	H, C.LEU_52	2.91	2.06	6.20
5T78.PDB	O, C.LYS_58	N, C.TYR_54	H, C.TYR_54	2.95	2.13	15.51
5T78.PDB	O, C.LEU_38	N, C.VAL_56	H, C.VAL_56	2.84	1.99	9.09
5T78.PDB	O, C.ARG_55	N, C.SER_57	H, C.SER_57	2.67	1.95	28.00
5T78.PDB	O, C.TYR_54	N, C.LYS_58	H, C.LYS_58	2.92	2.10	14.52
5T78.PDB	O, C.LEU_52	N, C.PHE_60	H, C.PHE_60	2.96	2.14	14.24
5T78.PDB	OD2, C.ASP_87	NH1, C.ARG_66	HH12, C.ARG_66	2.35	1.56	19.31
5T78.PDB	O, C.LYS_79	N, C.SER_68	H, C.SER_68	2.84	2.06	20.21
5T78.PDB	O, C.THR_77	N, C.SER_70	H, C.SER_70	2.99	2.25	25.43
5T78.PDB	O, C.CYS_23	N, C.PHE_76	H, C.PHE_76	2.98	2.15	10.91
5T78.PDB	O, C.SER_70	N, C.THR_77	H, C.THR_77	2.95	2.14	16.22
5T78.PDB	O, C.ILE_21	N, C.LEU_78	H, C.LEU_78	2.92	2.09	12.26
5T78.PDB	O, C.SER_68	N, C.LYS_79	H, C.LYS_79	2.69	1.86	12.12
5T78.PDB	O, C.ALA_19	N, C.ILE_80	H, C.ILE_80	2.92	2.10	14.89
5T78.PDB	O, C.ASP_17	N, C.VAL_83	H, C.VAL_83	2.96	2.10	6.35
5T78.PDB	O, C.GLU_84	N, C.ASP_87	H, C.ASP_87	2.96	2.11	8.35
5T78.PDB	O, C.GLN_43	N, C.VAL_90	H, C.VAL_90	2.89	2.05	10.76
5T78.PDB	O, C.THR_107	N, C.TYR_91	H, C.TYR_91	2.71	1.86	8.50
5T78.PDB	O, C.ASP_87	OH, C.TYR_91	HH, C.TYR_91	2.69	1.94	21.91
5T78.PDB	O, C.TYR_41	N, C.TYR_92	H, C.TYR_92	2.85	2.03	14.75
5T78.PDB	O, D.LYS_43	OH, C.TYR_92	HH, C.TYR_92	2.90	2.21	29.37
5T78.PDB	O, C.HIS_98	NE2, C.GLN_95	HE22, C.GLN_95	2.74	1.90	10.22
5T78.PDB	O, C.TYR_37	N, C.GLY_96	H, C.GLY_96	2.72	1.93	19.30
5T78.PDB	O, C.ILE_29	OG, C.SER_97	HG, C.SER_97	2.56	1.73	9.58
5T78.PDB	O, C.VAL_2	OG1, C.THR_102	HG1, C.THR_102	2.90	2.09	14.58
5T78.PDB	O, C.CYS_93	N, C.GLY_104	H, C.GLY_104	2.78	1.94	9.79
5T78.PDB	O, C.TYR_91	N, C.THR_107	H, C.THR_107	2.86	2.08	22.08

5T78.PDB	O, C_PRO_8	OG1, C_THR_107	HG1, C_THR_107	2.85	2.11	24.36
5T78.PDB	O, C_GLY_89	N, C_LEU_109	H, C_LEU_109	2.72	1.88	8.68
5T78.PDB	O, C_LEU_11	N, C_GLU_110	H, C_GLU_110	2.94	2.09	6.48
5T78.PDB	OE1, C_GLN_171	N, C_ILE_111	H, C_ILE_111	2.92	2.08	10.11
5T78.PDB	O, C_VAL_13	N, C_LYS_112	H, C_LYS_112	2.91	2.09	13.64
5T78.PDB	O, C_ASP_175	NE, C_ARG_113	HE, C_ARG_113	2.82	2.03	19.01
5T78.PDB	O, C_TYR_145	N, C_ALA_116	H, C_ALA_116	2.82	1.99	13.51
5T78.PDB	O, C_ASN_142	N, C_THR_119	H, C_THR_119	2.98	2.18	17.98
5T78.PDB	O, C_VAL_138	N, C_PHE_123	H, C_PHE_123	2.72	1.94	20.98
5T78.PDB	O, C_GLN_129	OG, C_SER_132	HG, C_SER_132	2.70	1.96	24.09
5T78.PDB	OE1, C_GLN_129	N, C_SER_136	H, C_SER_136	2.96	2.13	13.97
5T78.PDB	O, C_LEU_184	N, C_VAL_137	H, C_VAL_137	2.85	2.01	9.76
5T78.PDB	O, C_SER_182	N, C_CYS_139	H, C_CYS_139	2.88	2.10	20.35
5T78.PDB	O, C_SER_121	N, C_PHE_140	H, C_PHE_140	2.89	2.10	20.29
5T78.PDB	O, C_MET_180	N, C_LEU_141	H, C_LEU_141	2.83	1.97	5.00
5T78.PDB	OG, C_SER_179	N, C_ASN_143	H, C_ASN_143	2.76	1.98	21.20
5T78.PDB	O, C_TYR_178	N, C_PHE_144	H, C_PHE_144	2.82	2.00	13.31
5T78.PDB	OG, C_SER_182	NE1, C_TRP_153	HE1, C_TRP_153	2.84	2.01	13.01
5T78.PDB	O, C_THR_198	N, C_LYS_154	H, C_LYS_154	2.79	1.99	17.84
5T78.PDB	O, C_SER_158	N, C_ILE_155	H, C_ILE_155	2.77	1.97	16.65
5T78.PDB	O, C_SER_196	N, C_ASP_156	H, C_ASP_156	2.85	2.02	12.83
5T78.PDB	O, A_SER_26	N, C_ASN_166	H, C_ASN_166	2.63	1.86	20.95
5T78.PDB	O, D_PRO_170	OG, C_SER_167	HG, C_SER_167	2.87	2.05	10.83
5T78.PDB	O, C_LYS_147	NE1, C_TRP_168	HE1, C_TRP_168	2.87	2.16	29.23
5T78.PDB	O, C_SER_179	N, C_THR_169	H, C_THR_169	2.97	2.13	10.91
5T78.PDB	O, C_ILE_111	NE2, C_GLN_171	HE22, C_GLN_171	2.61	1.79	14.42
5T78.PDB	O, C_THR_177	N, C_ASP_172	H, C_ASP_172	2.84	2.00	11.78
5T78.PDB	OD1, C_ASP_175	OG1, C_THR_177	HG1, C_THR_177	2.53	1.70	9.09
5T78.PDB	O, C_PHE_144	N, C_TYR_178	H, C_TYR_178	2.83	1.97	6.87
5T78.PDB	O, C_LEU_141	N, C_MET_180	H, C_MET_180	2.81	2.01	18.22
5T78.PDB	O, C_SER_167	N, C_SER_181	H, C_SER_181	3.00	2.20	18.36
5T78.PDB	O, C_CYS_139	N, C_SER_182	H, C_SER_182	2.90	2.06	10.20
5T78.PDB	OD1, C_ASN_166	OG, C_SER_182	HG, C_SER_182	2.85	2.09	21.73
5T78.PDB	O, C_LEU_165	N, C_THR_183	H, C_THR_183	2.96	2.12	11.56
5T78.PDB	O, C_VAL_137	N, C_LEU_184	H, C_LEU_184	2.88	2.07	16.37
5T78.PDB	O, C_ALA_135	N, C_LEU_186	H, C_LEU_186	2.77	1.93	10.86
5T78.PDB	O, C_GLY_133	N, C_LYS_188	H, C_LYS_188	2.96	2.15	17.19
5T78.PDB	OG1, C_THR_187	N, C_GLU_190	H, C_GLU_190	2.96	2.14	14.63
5T78.PDB	OD2, C_ASP_156	ND1, C_HIS_194	HD1, C_HIS_194	2.58	1.78	18.23
5T78.PDB	O, C_LYS_152	N, C_GLU_200	H, C_GLU_200	2.99	2.19	18.60
5T78.PDB	O, C_ILE_210	N, C_ALA_201	H, C_ALA_201	2.91	2.11	18.88
5T78.PDB	O, C_ASN_150	N, C_THR_202	H, C_THR_202	2.79	1.96	11.41
5T78.PDB	O, C_PRO_146	NE2, C_HIS_203	HE2, C_HIS_203	2.99	2.15	9.93
5T78.PDB	ND1, C_HIS_203	OG1, C_THR_205	HG1, C_THR_205	3.00	2.26	23.83
5T78.PDB	O, C_ALA_201	N, C_ILE_210	H, C_ILE_210	2.84	2.01	13.72
5T78.PDB	O, C_ASN_195	N, C_ARG_216	H, C_ARG_216	2.82	2.00	14.32
5T78.PDB	O, D_SER_25	N, D_LYS_3	H, D_LYS_3	2.88	2.06	16.00
5T78.PDB	O, D_SER_21	N, D_SER_7	H, D_SER_7	2.77	2.07	29.94
5T78.PDB	O, D_THR_113	N, D_VAL_12	H, D_VAL_12	2.94	2.15	19.31
5T78.PDB	O, D_LEU_86	N, D_GLY_15	H, D_GLY_15	2.80	1.95	6.77
5T78.PDB	O, D_ALA_13	N, D_GLY_16	H, D_GLY_16	2.96	2.14	15.77
5T78.PDB	O, D_MET_83	N, D_LEU_18	H, D_LEU_18	2.98	2.18	18.13
5T78.PDB	O, D_LEU_81	N, D_LEU_20	H, D_LEU_20	2.82	2.00	15.18
5T78.PDB	O, D_VAL_5	N, D_ALA_23	H, D_ALA_23	2.89	2.09	16.85
5T78.PDB	O, D_ASN_77	N, D_ALA_24	H, D_ALA_24	2.81	1.96	7.81
5T78.PDB	O, D_ILE_97	N, D_SER_35	H, D_SER_35	2.90	2.09	16.41
5T78.PDB	O, D_ALA_49	N, D_TRP_36	H, D_TRP_36	2.96	2.19	21.68
5T78.PDB	O, D_GLU_46	N, D_ARG_38	H, D_ARG_38	2.84	1.99	7.93

5T78.PDB	OE1, D_GLU_46	NE, D_ARG_38	HE, D_ARG_38	2.65	1.91	25.36
5T78.PDB	OH, D_TYR_94	NH1, D_ARG_38	HH11, D_ARG_38	2.88	2.06	14.14
5T78.PDB	OD1, D_ASP_90	NH1, D_ARG_38	HH12, D_ARG_38	2.85	2.05	16.93
5T78.PDB	O, D_ILE_93	N, D_GLN_39	H, D_GLN_39	2.73	1.94	19.04
5T78.PDB	OE1, C_GLN_43	NE2, D_GLN_39	HE22, D_GLN_39	2.72	1.87	5.23
5T78.PDB	O, D_ARG_44	N, D_THR_40	H, D_THR_40	2.98	2.18	19.30
5T78.PDB	O, D_THR_40	N, D_LYS_43	H, D_LYS_43	2.67	1.84	13.85
5T78.PDB	O, D_ARG_38	N, D_GLU_46	H, D_GLU_46	2.84	2.01	12.67
5T78.PDB	O, D_TRP_36	N, D_VAL_48	H, D_VAL_48	2.98	2.12	3.28
5T78.PDB	O, D_MET_34	N, D_ILE_51	H, D_ILE_51	2.95	2.17	21.24
5T78.PDB	OD1, D_ASN_52	N, D_GLY_56	H, D_GLY_56	2.75	1.95	18.27
5T78.PDB	O, D_GLN_82	N, D_THR_69	H, D_THR_69	2.80	2.05	24.68
5T78.PDB	OH, D_TYR_60	N, D_ILE_70	H, D_ILE_70	2.81	2.01	18.25
5T78.PDB	OD1, D_ASN_74	NE, D_ARG_72	HE, D_ARG_72	2.71	2.01	29.42
5T78.PDB	O, D_TYR_32	NH1, D_ARG_72	HH12, D_ARG_72	2.98	2.17	17.20
5T78.PDB	O, D_CYS_22	N, D_LEU_79	H, D_LEU_79	2.88	2.07	17.29
5T78.PDB	O, D_SER_71	N, D_TYR_80	H, D_TYR_80	2.89	2.04	9.91
5T78.PDB	O, D_LEU_20	N, D_LEU_81	H, D_LEU_81	2.95	2.20	24.69
5T78.PDB	O, D_THR_69	N, D_GLN_82	H, D_GLN_82	2.94	2.12	15.46
5T78.PDB	O, D_LEU_18	N, D_MET_83	H, D_MET_83	2.79	2.00	20.15
5T78.PDB	OD2, D_ASP_90	N, D_LYS_87	H, D_LYS_87	2.89	2.04	6.02
5T78.PDB	O, D_LEU_112	N, D_ALA_92	H, D_ALA_92	2.85	2.07	20.10
5T78.PDB	O, D_GLN_39	N, D_ILE_93	H, D_ILE_93	2.93	2.16	22.14
5T78.PDB	O, D_THR_110	N, D_TYR_94	H, D_TYR_94	2.81	1.96	2.19
5T78.PDB	O, D_ASP_90	OH, D_TYR_94	HH, D_TYR_94	2.65	1.83	8.83
5T78.PDB	O, D_VAL_37	N, D_TYR_95	H, D_TYR_95	2.63	1.78	4.62
5T78.PDB	OE1, D_GLN_39	OH, D_TYR_95	HH, D_TYR_95	2.98	2.17	11.35
5T78.PDB	OE2, D_GLU_6	N, D_CYS_96	H, D_CYS_96	2.78	1.93	7.90
5T78.PDB	OD1, D_ASP_104	N, D_GLY_102	H, D_GLY_102	2.77	1.92	7.47
5T78.PDB	OH, C_TYR_41	N, D_PHE_103	H, D_PHE_103	2.85	2.00	7.54
5T78.PDB	O, D_CYS_96	N, D_GLY_107	H, D_GLY_107	2.94	2.10	10.44
5T78.PDB	OE1, D_GLU_6	N, D_GLY_109	H, D_GLY_109	2.82	1.99	12.53
5T78.PDB	O, D_ALA_92	N, D_LEU_112	H, D_LEU_112	2.76	1.94	15.02
5T78.PDB	OG1, D_THR_91	N, D_VAL_114	H, D_VAL_114	2.86	2.01	6.88
5T78.PDB	O, D_PHE_149	N, D_THR_120	H, D_THR_120	2.81	1.96	9.17
5T78.PDB	O, D_LYS_146	N, D_SER_123	H, D_SER_123	2.97	2.17	17.75
5T78.PDB	O, D_LEU_144	N, D_TYR_125	H, D_TYR_125	2.89	2.08	16.53
5T78.PDB	O, D_GLY_142	N, D_LEU_127	H, D_LEU_127	2.90	2.13	23.33
5T78.PDB	O, D_VAL_186	N, D_VAL_139	H, D_VAL_139	2.83	1.97	3.34
5T78.PDB	O, D_VAL_184	N, D_LEU_141	H, D_LEU_141	2.81	1.99	15.70
5T78.PDB	O, D_SER_182	N, D_CYS_143	H, D_CYS_143	2.95	2.18	22.37
5T78.PDB	O, D_TYR_125	N, D_LEU_144	H, D_LEU_144	2.93	2.09	9.92
5T78.PDB	O, D_LEU_180	N, D_VAL_145	H, D_VAL_145	2.81	1.97	7.59
5T78.PDB	O, D_SER_123	N, D_LYS_146	H, D_LYS_146	2.94	2.10	9.29
5T78.PDB	O, D_THR_120	N, D_PHE_149	H, D_PHE_149	2.90	2.10	18.43
5T78.PDB	O, D_ASN_199	N, D_THR_156	H, D_THR_156	2.94	2.10	10.47
5T78.PDB	OG, D_SER_182	NE1, D_TRP_157	HE1, D_TRP_157	2.99	2.19	18.03
5T78.PDB	O, D_THR_197	N, D_ASN_158	H, D_ASN_158	2.89	2.04	8.58
5T78.PDB	OD1, D_ASN_199	N, D_SER_159	H, D_SER_159	2.73	1.89	10.93
5T78.PDB	O, D_TRP_157	N, D_GLY_160	H, D_GLY_160	2.79	1.98	17.29
5T78.PDB	OD1, C_ASN_142	NE2, D_HIS_167	HE2, D_HIS_167	2.85	2.00	9.68
5T78.PDB	O, D_SER_181	N, D_PHE_169	H, D_PHE_169	2.91	2.06	5.50
5T78.PDB	O, D_THR_179	N, D_VAL_172	H, D_VAL_172	2.97	2.16	16.66
5T78.PDB	O, D_LEU_177	N, D_GLN_174	H, D_GLN_174	2.91	2.06	7.53
5T78.PDB	OD2, A_ASP_75	N, D_SER_175	H, D_SER_175	2.84	2.00	10.93
5T78.PDB	O, D_TYR_148	N, D_TYR_178	H, D_TYR_178	2.82	1.96	2.75
5T78.PDB	O, D_VAL_172	N, D_THR_179	H, D_THR_179	2.97	2.22	24.34
5T78.PDB	O, D_VAL_145	N, D_LEU_180	H, D_LEU_180	2.85	2.03	14.78

5T78.PDB	O, D_CYS.143	N, D_SER.182	H, D_SER.182	2.99	2.19	18.10
5T78.PDB	O, D_HIS.167	N, D_SER.183	H, D_SER.183	2.87	2.01	1.62
5T78.PDB	O, D_LEU.141	N, D_VAL.184	H, D_VAL.184	2.93	2.08	8.26
5T78.PDB	O, D_VAL.139	N, D_VAL.186	H, D_VAL.186	2.97	2.19	20.48
5T78.PDB	OD1, D_ASN.158	N, D_THR.197	H, D_THR.197	2.81	2.01	18.23
5T78.PDB	O, D_LYS.211	N, D_CYS.198	H, D_CYS.198	2.82	1.96	5.03
5T78.PDB	O, D_THR.156	N, D_ASN.199	H, D_ASN.199	2.88	2.02	1.38
5T78.PDB	O, D_VAL.209	N, D_VAL.200	H, D_VAL.200	2.81	1.96	8.46
5T78.PDB	O, D_THR.154	N, D_ALA.201	H, D_ALA.201	2.98	2.16	13.25
5T78.PDB	O, D_THR.207	N, D_HIS.202	H, D_HIS.202	2.80	1.95	7.22
5T78.PDB	O, D_PRO.150	NE2, D_HIS.202	HE2, D_HIS.202	2.66	1.84	14.06
5T78.PDB	O, D_PRO.203	N, D_SER.206	H, D_SER.206	2.91	2.12	19.46
5T78.PDB	O, D_VAL.200	N, D_VAL.209	H, D_VAL.209	2.85	2.03	14.24
5T78.PDB	O, D_CYS.198	N, D_LYS.211	H, D_LYS.211	2.85	2.05	18.38
5T78.PDB	OE1, C_GLU.39	NH1, E_ARG.5	HH11, E_ARG.5	2.69	1.87	13.16
5U3J.PDB	O, H_LEU.82C	N, H_GLY.15	H, H_GLY.15	2.68	1.83	3.74
5U3J.PDB	O, H_LYS.13	N, H_GLY.16	H, H_GLY.16	2.99	2.15	12.62
5U3J.PDB	O, H_MET.82	N, H_LEU.18	H, H_LEU.18	2.68	1.88	17.05
5U3J.PDB	OE1, H_GLN.81	NE, H_ARG.19	HE, H_ARG.19	2.98	2.21	22.79
5U3J.PDB	O, H_LEU.80	N, H_LEU.20	H, H_LEU.20	2.96	2.14	16.12
5U3J.PDB	O, H_LEU.78	N, H_CYS.22	H, H_CYS.22	2.77	1.97	17.66
5U3J.PDB	O, H_THR.28	OG1, H_THR.32	HG1, H_THR.32	2.71	2.00	27.44
5U3J.PDB	OD2, H_ASP.53	NE1, H_TRP.33	HE1, H_TRP.33	2.97	2.22	24.73
5U3J.PDB	O, H_THR.93	N, H_SER.35	H, H_SER.35	2.87	2.05	14.77
5U3J.PDB	O, H_GLY.49	N, H_TRP.36	H, H_TRP.36	2.81	1.99	15.09
5U3J.PDB	O, H_PHE.91	N, H_VAL.37	H, H_VAL.37	2.90	2.06	9.69
5U3J.PDB	OE1, H_GLU.46	NE, H_ARG.38	HE, H_ARG.38	2.88	2.05	13.82
5U3J.PDB	OD1, H_ASP.86	NH1, H_ARG.38	HH12, H_ARG.38	2.85	2.09	23.00
5U3J.PDB	OG, H_SER.35	NE1, H_TRP.47	HE1, H_TRP.47	2.44	1.73	27.73
5U3J.PDB	O, H_TRP.36	N, H_VAL.48	H, H_VAL.48	2.91	2.09	13.49
5U3J.PDB	O, H_GLU.58	N, H_ARG.50	H, H_ARG.50	2.88	2.07	16.55
5U3J.PDB	OE1, H_GLU.58	NE, H_ARG.50	HE, H_ARG.50	2.83	2.12	29.07
5U3J.PDB	OE1, H_GLU.58	NH2, H_ARG.50	HH21, H_ARG.50	2.79	2.08	29.38
5U3J.PDB	O, H_MET.34	N, H_ILE.51	H, H_ILE.51	2.70	1.90	17.80
5U3J.PDB	O, H_ASN.52B	N, H_GLY.54	H, H_GLY.54	2.97	2.17	18.44
5U3J.PDB	O, H_VAL.48	N, H_ALA.60	H, H_ALA.60	2.71	1.92	19.22
5U3J.PDB	O, H_VAL.63	N, H_ARG.66	H, H_ARG.66	2.99	2.15	10.50
5U3J.PDB	OD2, H_ASP.86	NH1, H_ARG.66	HH12, H_ARG.66	2.57	1.73	9.26
5U3J.PDB	OD1, H_ASP.86	NH2, H_ARG.66	HH22, H_ARG.66	2.89	2.04	5.32
5U3J.PDB	O, H_GLN.81	N, H_THR.68	H, H_THR.68	2.98	2.27	28.87
5U3J.PDB	OH, H_TYR.59	N, H_ILE.69	H, H_ILE.69	2.88	2.05	11.11
5U3J.PDB	O, H_THR.32	NH1, H_ARG.71	HH12, H_ARG.71	2.85	2.04	17.00
5U3J.PDB	O, H_THR.77	N, H_ASP.72	H, H_ASP.72	2.83	2.04	19.14
5U3J.PDB	O, H_ASP.72	N, H_ARG.75	H, H_ARG.75	2.96	2.12	10.52
5U3J.PDB	O, H_ARG.75	OG1, H_THR.77	HG1, H_THR.77	2.85	2.06	17.00
5U3J.PDB	O, H_CYS.22	N, H_LEU.78	H, H_LEU.78	2.84	2.02	14.17
5U3J.PDB	O, H_SER.70	N, H_TYR.79	H, H_TYR.79	2.89	2.05	10.03
5U3J.PDB	O, H_THR.68	N, H_GLN.81	H, H_GLN.81	2.76	1.91	9.85
5U3J.PDB	O, H_LEU.18	N, H_MET.82	H, H_MET.82	2.72	1.89	13.44
5U3J.PDB	O, H_ARG.66	OG1, H_THR.82A	HG1, H_THR.82A	2.74	1.94	14.02
5U3J.PDB	O, H_GLY.16	N, H_LEU.82C	H, H_LEU.82C	2.98	2.20	20.11
5U3J.PDB	OD2, H_ASP.86	N, H_LYS.83	H, H_LYS.83	2.93	2.08	5.84
5U3J.PDB	O, H_GLN.39	N, H_ARG.89	H, H_ARG.89	2.74	1.90	10.05
5U3J.PDB	O, H_THR.107	N, H_TYR.90	H, H_TYR.90	2.95	2.11	11.30
5U3J.PDB	O, H_ASP.86	OH, H_TYR.90	HH, H_TYR.90	2.53	1.71	8.74
5U3J.PDB	O, H_VAL.37	N, H_PHE.91	H, H_PHE.91	2.51	1.68	10.84
5U3J.PDB	OE2, H_GLU.6	N, H_CYS.92	H, H_CYS.92	2.75	1.89	6.53
5U3J.PDB	O, H_TRP.33	N, H_ASP.95	H, H_ASP.95	2.77	1.92	6.84

5U3J.PDB	O, H_TYR_100K	N, H_GLU_98	H, H_GLU_98	2.94	2.22	28.79
5U3J.PDB	O, H_PHE_100D	N, H_TRP_100G	H, H_TRP_100G	2.86	2.01	6.48
5U3J.PDB	O, H_GLU_100F	OG, H_SER_100I	HG, H_SER_100I	2.76	1.95	12.70
5U3J.PDB	O, H_GLU_98	N, H_TYR_100K	H, H_TYR_100K	2.86	2.12	25.47
5U3J.PDB	OD1, L_ASP_31	OH, H_TYR_100K	HH, H_TYR_100K	2.88	2.04	5.22
5U3J.PDB	OH, L_TYR_36	N, H_MET_100N	H, H_MET_100N	2.75	1.92	13.09
5U3J.PDB	OE1, H_GLU_6	N, H_GLY_106	H, H_GLY_106	2.94	2.10	10.69
5U3J.PDB	O, H_GLY_88	N, H_VAL_109	H, H_VAL_109	2.80	1.95	8.22
5U3J.PDB	O, H_GLY_10	N, H_THR_110	H, H_THR_110	2.98	2.17	17.31
5U3J.PDB	OG, H_SER_87	N, H_VAL_111	H, H_VAL_111	2.79	1.95	7.31
5U3J.PDB	O, H_PHE_146	N, H_LYS_117	H, H_LYS_117	2.94	2.12	14.80
5U3J.PDB	O, H_LYS_143	N, H_SER_120	H, H_SER_120	2.97	2.12	7.20
5U3J.PDB	O, H_LEU_141	N, H_PHE_122	H, H_PHE_122	2.79	2.02	22.59
5U3J.PDB	O, H_GLY_139	N, H_LEU_124	H, H_LEU_124	2.74	1.98	23.31
5U3J.PDB	O, H_SER_130	N, H_ALA_137	H, H_ALA_137	2.87	2.16	29.44
5U3J.PDB	O, H_SER_180	N, H_CYS_140	H, H_CYS_140	2.63	1.85	19.83
5U3J.PDB	O, H_PHE_122	N, H_LEU_141	H, H_LEU_141	2.71	1.86	7.01
5U3J.PDB	O, H_LEU_178	N, H_VAL_142	H, H_VAL_142	2.96	2.22	26.19
5U3J.PDB	O, H_LYS_117	N, H_PHE_146	H, H_PHE_146	2.97	2.25	28.41
5U3J.PDB	O, H_ASN_197	N, H_SER_153	H, H_SER_153	2.96	2.15	16.40
5U3J.PDB	OG, H_SER_180	NE1, H_TRP_154	HE1, H_TRP_154	2.98	2.15	12.85
5U3J.PDB	O, H_SER_177	N, H_VAL_169	H, H_VAL_169	2.87	2.08	18.96
5U3J.PDB	O, H_LEU_175	N, H_GLN_171	H, H_GLN_171	2.85	2.01	9.90
5U3J.PDB	O, H_GLN_171	N, H_GLY_174	H, H_GLY_174	2.81	1.98	10.98
5U3J.PDB	O, H_TYR_145	N, H_TYR_176	H, H_TYR_176	2.90	2.05	6.56
5U3J.PDB	O, H_VAL_142	N, H_LEU_178	H, H_LEU_178	2.95	2.16	18.81
5U3J.PDB	O, H_HIS_164	N, H_VAL_181	H, H_VAL_181	2.91	2.08	14.09
5U3J.PDB	O, H_LEU_138	N, H_VAL_182	H, H_VAL_182	2.66	1.85	17.24
5U3J.PDB	OD1, H_ASN_155	N, H_ILE_195	H, H_ILE_195	2.70	1.88	13.20
5U3J.PDB	O, H_SER_153	N, H_ASN_197	H, H_ASN_197	2.90	2.15	24.53
5U3J.PDB	O, H_VAL_207	N, H_VAL_198	H, H_VAL_198	2.82	1.98	9.42
5U3J.PDB	O, H_PRO_147	NE2, H_HIS_200	HE2, H_HIS_200	2.98	2.14	11.71
5U3J.PDB	O, H_VAL_198	N, H_VAL_207	H, H_VAL_207	2.90	2.10	17.28
5U3J.PDB	O, L_TYR_86	NE2, L_GLN_6	HE22, L_GLN_6	2.61	1.91	29.28
5U3J.PDB	O, L_ILE_29	N, L_TYR_32	H, L_TYR_32	2.94	2.08	3.56
5U3J.PDB	OE1, H_GLU_100F	OH, L_TYR_32	HH, L_TYR_32	2.62	1.91	27.84
5U3J.PDB	O, L_ILE_48	N, L_TRP_35	H, L_TRP_35	2.59	1.80	18.85
5U3J.PDB	O, L_TYR_87	N, L_TYR_36	H, L_TYR_36	2.81	2.00	16.97
5U3J.PDB	OE1, L_GLN_89	OH, L_TYR_36	HH, L_TYR_36	2.74	1.93	13.79
5U3J.PDB	O, L_LYS_45	N, L_GLN_37	H, L_GLN_37	2.91	2.10	17.84
5U3J.PDB	OE1, H_GLN_39	NE2, L_GLN_38	HE22, L_GLN_38	2.66	1.83	12.57
5U3J.PDB	O, L_GLN_37	N, L_LYS_45	H, L_LYS_45	2.58	1.77	16.56
5U3J.PDB	O, L_LYS_53	N, L_TYR_49	H, L_TYR_49	2.83	2.07	23.24
5U3J.PDB	O, L_ASP_82	OH, L_TYR_86	HH, L_TYR_86	2.92	2.16	22.19
5U3J.PDB	O, L_ASN_34	N, L_GLN_89	H, L_GLN_89	2.94	2.19	25.35
5U3J.PDB	O, L_VAL_133	N, L_PHE_118	H, L_PHE_118	2.97	2.15	14.78
5U3J.PDB	OG, L_SER_131	NE2, L_GLN_124	HE22, L_GLN_124	2.67	1.82	7.69
5U3J.PDB	O, L_LEU_181	N, L_ALA_130	H, L_ALA_130	2.68	1.95	26.74
5U3J.PDB	O, L_LEU_179	N, L_VAL_132	H, L_VAL_132	2.84	2.01	12.36
5U3J.PDB	O, L_GLU_195	N, L_GLN_147	H, L_GLN_147	2.91	2.06	7.51
5U3J.PDB	OG, L_SER_177	NE1, L_TRP_148	HE1, L_TRP_148	2.81	2.02	19.92
5U3J.PDB	O, L_TRP_148	N, L_GLN_155	H, L_GLN_155	2.85	2.01	10.26
5U3J.PDB	O, H_PRO_167	OG, L_SER_162	HG, L_SER_162	2.90	2.16	24.21
5U3J.PDB	O, L_LEU_136	N, L_LEU_175	H, L_LEU_175	2.78	2.04	25.99
5U3J.PDB	O, L_SER_162	N, L_SER_176	H, L_SER_176	2.81	2.07	25.43
5U3J.PDB	O, L_GLN_160	N, L_THR_178	H, L_THR_178	2.90	2.05	9.65
5U3J.PDB	O, L_VAL_132	N, L_LEU_179	H, L_LEU_179	2.58	1.74	8.42
5U3J.PDB	O, L_ALA_130	N, L_LEU_181	H, L_LEU_181	2.90	2.18	27.62

5U3J.PDB	O, L.SER_182	N, L.TYR_186	H, L.TYR_186	2.73	1.97	23.20
5U3J.PDB	O, L.LYS_183	N, L.GLU_187	H, L.GLU_187	2.87	2.13	25.64
5U3J.PDB	O, L.VAL_205	N, L.VAL_196	H, L.VAL_196	2.92	2.06	3.44
5U3J.PDB	O, A.PHE_673	OG1, A.THR_676	HG1, A.THR_676	2.55	1.85	27.32
5U3J.PDB	O, A.ASP_674	N, A.TRP_678	H, A.TRP_678	2.96	2.23	26.81
5U3J.PDB	O, A.ILE_675	N, A.LEU_679	H, A.LEU_679	2.98	2.15	11.89
5U3J.PDB	O, A.THR_676	N, A.TRP_680	H, A.TRP_680	2.90	2.12	20.48
5U3J.PDB	O, A.ASN_677	N, A.TYR_681	H, A.TYR_681	2.74	1.96	21.09
5U3J.PDB	O, A.TRP_678	N, A.ILE_682	H, A.ILE_682	2.63	1.81	13.86
5U3N.PDB	O, H.VAL_23	N, H.VAL_5	H, H.VAL_5	2.91	2.06	7.34
5U3N.PDB	O, H.TYR_90	NE2, H.GLN_6	HE22, H.GLN_6	2.83	2.00	12.08
5U3N.PDB	O, H.LEU_82C	N, H.GLY_15	H, H.GLY_15	2.69	1.84	5.70
5U3N.PDB	O, H.LYS_13	N, H.GLY_16	H, H.GLY_16	2.84	2.03	16.66
5U3N.PDB	O, H.MET_82	N, H.LEU_18	H, H.LEU_18	2.86	2.07	19.50
5U3N.PDB	OG, H.SER_7	N, H.SER_21	H, H.SER_21	2.86	2.03	12.74
5U3N.PDB	O, H.VAL_5	N, H.VAL_23	H, H.VAL_23	2.81	1.99	14.35
5U3N.PDB	O, H.ASN_76	N, H.THR_24	H, H.THR_24	2.94	2.15	18.71
5U3N.PDB	O, H.GLN_3	N, H.SER_25	H, H.SER_25	2.99	2.20	19.07
5U3N.PDB	O, H.THR_28	OG1, H.THR_32	HG1, H.THR_32	2.86	2.15	27.61
5U3N.PDB	O, H.ILE_51	N, H.MET_34	H, H.MET_34	2.95	2.12	13.00
5U3N.PDB	O, H.ALA_49	N, H.TRP_36	H, H.TRP_36	2.81	2.02	19.03
5U3N.PDB	O, H.TYR_91	N, H.VAL_37	H, H.VAL_37	2.87	2.04	12.29
5U3N.PDB	O, H.GLU_46	N, H.ARG_38	H, H.ARG_38	2.84	1.99	7.64
5U3N.PDB	OE1, H.GLU_46	NE, H.ARG_38	HE, H.ARG_38	2.91	2.07	9.07
5U3N.PDB	OH, H.TYR_90	NH1, H.ARG_38	HH11, H.ARG_38	3.00	2.21	20.04
5U3N.PDB	O, H.VAL_89	N, H.GLN_39	H, H.GLN_39	2.83	2.04	20.47
5U3N.PDB	O, H.ARG_38	N, H.GLU_46	H, H.GLU_46	2.85	2.12	27.26
5U3N.PDB	O, H.TRP_36	N, H.VAL_48	H, H.VAL_48	2.79	1.97	13.99
5U3N.PDB	OD2, H.ASP_58	NE, H.ARG_50	HE, H.ARG_50	2.78	1.98	18.36
5U3N.PDB	O, H.MET_34	N, H.ILE_51	H, H.ILE_51	2.79	1.99	18.29
5U3N.PDB	O, H.ILE_56	N, H.SER_52	H, H.SER_52	2.99	2.26	27.62
5U3N.PDB	OD2, A.ASP_674	NH1, H.ARG_52A	HH12, H.ARG_52A	3.00	2.24	24.41
5U3N.PDB	OD1, H.ASP_53	NH2, H.ARG_52A	HH21, H.ARG_52A	2.93	2.18	25.35
5U3N.PDB	O, H.ARG_52A	N, H.ASP_53	H, H.ASP_53	2.99	2.21	21.52
5U3N.PDB	OG, H.SER_52	N, H.ILE_56	H, H.ILE_56	2.80	2.06	25.80
5U3N.PDB	O, H.VAL_48	N, H.ALA_60	H, H.ALA_60	2.80	1.95	7.61
5U3N.PDB	O, H.VAL_63	N, H.ARG_66	H, H.ARG_66	3.00	2.17	13.97
5U3N.PDB	OD2, H.ASP_86	NH1, H.ARG_66	HH12, H.ARG_66	2.73	1.91	14.46
5U3N.PDB	O, H.PRO_62	NH2, H.ARG_66	HH21, H.ARG_66	2.95	2.10	7.27
5U3N.PDB	O, H.HIS_81	N, H.ILE_68	H, H.ILE_68	2.90	2.10	18.72
5U3N.PDB	OH, H.TYR_59	N, H.ILE_69	H, H.ILE_69	2.92	2.12	19.11
5U3N.PDB	OD1, H.ASP_73	NE, H.ARG_71	HE, H.ARG_71	2.93	2.13	17.92
5U3N.PDB	O, H.THR_32	NH1, H.ARG_71	HH12, H.ARG_71	2.85	2.04	16.27
5U3N.PDB	O, H.THR_77	N, H.ASP_72	H, H.ASP_72	2.83	1.99	11.84
5U3N.PDB	O, H.CYS_22	N, H.LEU_78	H, H.LEU_78	2.84	2.00	10.39
5U3N.PDB	O, H.SER_70	N, H.PHE_79	H, H.PHE_79	2.80	1.94	3.12
5U3N.PDB	O, H.ILE_68	N, H.HIS_81	H, H.HIS_81	2.75	1.95	17.72
5U3N.PDB	O, H.LEU_18	N, H.MET_82	H, H.MET_82	2.59	1.75	10.08
5U3N.PDB	OD2, H.ASP_86	N, H.LYS_83	H, H.LYS_83	2.93	2.12	15.88
5U3N.PDB	O, H.LYS_83	N, H.ASP_86	H, H.ASP_86	2.78	1.94	11.41
5U3N.PDB	O, H.THR_107	N, H.TYR_90	H, H.TYR_90	2.72	1.88	9.30
5U3N.PDB	O, H.ASP_86	OH, H.TYR_90	HH, H.TYR_90	2.67	1.88	16.73
5U3N.PDB	O, H.VAL_37	N, H.TYR_91	H, H.TYR_91	2.62	1.77	5.09
5U3N.PDB	O, H.SER_35	N, H.THR_93	H, H.THR_93	2.88	2.10	21.23
5U3N.PDB	O, H.TRP_33	N, H.ASP_95	H, H.ASP_95	2.83	1.98	5.13
5U3N.PDB	O, H.TYR_100L	N, H.GLU_96	H, H.GLU_96	2.96	2.15	16.42
5U3N.PDB	O, H.ASN_100J	N, H.ALA_98	H, H.ALA_98	2.86	2.02	10.29
5U3N.PDB	OE1, H.GLU_100E	NE, H.ARG_100B	HE, H.ARG_100B	2.83	1.97	4.42

5U3N.PDB	OE2, H_GLU_100E	NH2, H_ARG_100B	HH21, H_ARG_100B	2.91	2.08	12.18
5U3N.PDB	OD1, L_ASP_31	NH2, H_ARG_100B	HH22, H_ARG_100B	2.97	2.15	14.50
5U3N.PDB	O, H_ARG_100B	N, H_GLU_100E	H, H_GLU_100E	2.83	2.05	20.60
5U3N.PDB	O, H_PHE_100C	N, H_TRP_100F	H, H_TRP_100F	2.93	2.08	6.81
5U3N.PDB	O, H_LEU_100A	NE1, H_TRP_100F	HE1, H_TRP_100F	2.88	2.10	19.92
5U3N.PDB	O, H_GLU_100E	N, H_TYR_100H	H, H_TYR_100H	2.96	2.12	9.41
5U3N.PDB	O, H_ALA_98	N, H_ASN_100J	H, H_ASN_100J	2.93	2.10	13.13
5U3N.PDB	OD1, L_ASN_34	ND2, H_ASN_100J	HD21, H_ASN_100J	2.72	1.86	2.61
5U3N.PDB	O, H_GLU_96	N, H_TYR_100L	H, H_TYR_100L	2.88	2.05	12.56
5U3N.PDB	OH, L_TYR_36	N, H_MET_100M	H, H_MET_100M	2.99	2.13	5.54
5U3N.PDB	O, H_ALA_94	N, H_ASP_101	H, H_ASP_101	2.74	1.99	25.37
5U3N.PDB	O, H_CYS_92	N, H_GLY_104	H, H_GLY_104	2.82	1.98	9.77
5U3N.PDB	OE1, H_GLN_6	N, H_GLY_106	H, H_GLY_106	2.96	2.22	25.98
5U3N.PDB	O, H_TYR_90	N, H_THR_107	H, H_THR_107	2.85	2.08	22.78
5U3N.PDB	O, H_ALA_88	N, H_VAL_109	H, H_VAL_109	2.88	2.03	6.16
5U3N.PDB	O, H_GLY_10	N, H_ILE_110	H, H_ILE_110	2.94	2.09	6.89
5U3N.PDB	OG1, H_THR_87	N, H_VAL_111	H, H_VAL_111	2.89	2.03	4.98
5U3N.PDB	O, H_VAL_12	N, H_SER_112	H, H_SER_112	2.98	2.17	17.21
5U3N.PDB	O, H_PHE_146	N, H_LYS_117	H, H_LYS_117	2.78	1.97	16.03
5U3N.PDB	O, H_GLY_139	N, H_LEU_124	H, H_LEU_124	2.86	2.00	5.63
5U3N.PDB	O, H_VAL_184	N, H_ALA_136	H, H_ALA_136	2.84	1.99	5.94
5U3N.PDB	O, H_LEU_124	N, H_GLY_139	H, H_GLY_139	3.00	2.25	25.48
5U3N.PDB	O, H_SER_180	N, H_CYS_140	H, H_CYS_140	2.82	2.02	17.61
5U3N.PDB	O, H_PHE_122	N, H_LEU_141	H, H_LEU_141	2.79	1.95	10.76
5U3N.PDB	O, H_LEU_178	N, H_VAL_142	H, H_VAL_142	2.71	1.86	7.20
5U3N.PDB	O, H_SER_120	N, H_LYS_143	H, H_LYS_143	2.84	1.99	7.21
5U3N.PDB	O, H_LYS_117	N, H_PHE_146	H, H_PHE_146	2.94	2.13	16.41
5U3N.PDB	O, H_ASN_199	N, H_THR_151	H, H_THR_151	3.00	2.17	12.79
5U3N.PDB	OG, H_SER_180	NE1, H_TRP_154	HE1, H_TRP_154	2.95	2.11	9.10
5U3N.PDB	O, H_ILE_195	N, H_ASN_155	H, H_ASN_155	2.79	1.95	11.06
5U3N.PDB	OD1, H_ASN_197	N, H_SER_156	H, H_SER_156	2.62	1.82	17.28
5U3N.PDB	O, H_TRP_154	N, H_GLY_157	H, H_GLY_157	2.98	2.26	27.93
5U3N.PDB	OD1, L_ASN_138	NE2, H_HIS_164	HE2, H_HIS_164	2.92	2.21	29.54
5U3N.PDB	O, H_SER_179	N, H_PHE_166	H, H_PHE_166	2.96	2.11	6.98
5U3N.PDB	O, H_SER_177	N, H_VAL_169	H, H_VAL_169	2.89	2.05	12.11
5U3N.PDB	O, H_LEU_175	N, H_GLN_171	H, H_GLN_171	2.79	1.96	11.18
5U3N.PDB	O, H_LEU_175	NE2, H_GLN_171	HE21, H_GLN_171	2.95	2.10	7.82
5U3N.PDB	OD1, H_ASP_144	NE2, H_GLN_171	HE22, H_GLN_171	2.99	2.19	18.08
5U3N.PDB	O, H_GLN_171	N, H_GLY_174	H, H_GLY_174	2.89	2.04	7.78
5U3N.PDB	O, H_TYR_145	N, H_TYR_176	H, H_TYR_176	2.81	1.96	5.90
5U3N.PDB	O, H_VAL_169	N, H_SER_177	H, H_SER_177	2.98	2.23	24.19
5U3N.PDB	O, H_VAL_142	N, H_LEU_178	H, H_LEU_178	2.86	2.04	15.63
5U3N.PDB	O, H_HIS_164	N, H_VAL_181	H, H_VAL_181	2.83	1.99	10.90
5U3N.PDB	O, H_LEU_138	N, H_VAL_182	H, H_VAL_182	2.84	2.03	16.03
5U3N.PDB	O, H_ALA_136	N, H_VAL_184	H, H_VAL_184	2.89	2.08	16.51
5U3N.PDB	O, H_GLY_134	N, H_SER_186	H, H_SER_186	2.89	2.05	9.68
5U3N.PDB	O, H_PRO_185	N, H_SER_188	H, H_SER_188	2.86	2.07	20.15
5U3N.PDB	O, H_SER_188	N, H_GLN_192	H, H_GLN_192	2.98	2.15	13.47
5U3N.PDB	OD1, H_ASN_155	N, H_ILE_195	H, H_ILE_195	2.89	2.08	15.15
5U3N.PDB	O, H_LYS_209	N, H_CYS_196	H, H_CYS_196	2.96	2.17	20.77
5U3N.PDB	O, H_SER_153	N, H_ASN_197	H, H_ASN_197	2.66	1.82	9.65
5U3N.PDB	O, H_VAL_207	N, H_VAL_198	H, H_VAL_198	2.77	1.91	0.90
5U3N.PDB	O, H_THR_205	N, H_HIS_200	H, H_HIS_200	2.79	1.93	4.87
5U3N.PDB	O, H_PRO_147	NE2, H_HIS_200	HE2, H_HIS_200	2.62	1.78	9.36
5U3N.PDB	O, H_VAL_198	N, H_VAL_207	H, H_VAL_207	2.91	2.08	14.15
5U3N.PDB	O, H_TYR_194	N, H_AVAL_211	H, H_AVAL_211	2.89	2.05	9.34
5U3N.PDB	O, H_TYR_194	N, H_BVAL_211	H, H_BVAL_211	2.89	2.05	9.13
5U3N.PDB	O, H_PRO_126	N, H_LYS_214	H, H_LYS_214	2.98	2.16	14.79

5U3N.PDB	OG, L_SER_26	N, L_ARG_3	H, L_ARG_3	2.86	2.02	10.52
5U3N.PDB	O, L_ARG_24	N, L_THR_5	H, L_THR_5	2.80	1.98	16.09
5U3N.PDB	O, L_TYR_86	NE2, L_GLN_6	HE22, L_GLN_6	2.86	2.00	3.53
5U3N.PDB	O, L_LYS_103	N, L_LEU_11	H, L_LEU_11	2.90	2.11	18.99
5U3N.PDB	OH, L_TYR_140	OG, L_SER_12	HG, L_SER_12	2.60	1.87	23.71
5U3N.PDB	O, L_ASP_105	N, L_ALA_13	H, L_ALA_13	2.97	2.13	11.36
5U3N.PDB	OD2, L_ASP_17	N, L_SER_14	H, L_SER_14	2.75	1.96	18.71
5U3N.PDB	O, L_LEU_78	N, L_GLY_16	H, L_GLY_16	2.68	1.90	20.67
5U3N.PDB	O, L_ILE_75	N, L_ILE_19	H, L_ILE_19	2.79	1.95	9.47
5U3N.PDB	O, L_LEU_73	N, L_ILE_21	H, L_ILE_21	2.95	2.11	10.95
5U3N.PDB	O, L_PHE_71	N, L_CYS_23	H, L_CYS_23	2.87	2.04	13.33
5U3N.PDB	O, L_THR_5	N, L_ARG_24	H, L_ARG_24	2.75	1.90	7.83
5U3N.PDB	O, L_SER_69	N, L_ALA_25	H, L_ALA_25	2.85	2.03	14.92
5U3N.PDB	O, L_ARG_3	N, L_SER_26	H, L_SER_26	2.91	2.13	20.77
5U3N.PDB	O, L_GLY_68	N, L_ILE_29	H, L_ILE_29	2.69	1.85	10.61
5U3N.PDB	O, L_ILE_29	N, L_TYR_32	H, L_TYR_32	2.96	2.12	12.33
5U3N.PDB	O, L_ASP_31	N, L_LEU_33	H, L_LEU_33	2.77	2.05	28.04
5U3N.PDB	O, L_GLN_89	N, L_ASN_34	H, L_ASN_34	2.83	2.03	18.28
5U3N.PDB	OE1, L_GLN_89	ND2, L_ASN_34	HD22, L_ASN_34	2.99	2.18	18.14
5U3N.PDB	O, L_ILE_48	N, L_TRP_35	H, L_TRP_35	2.81	1.99	14.14
5U3N.PDB	O, L_TYR_87	N, L_TYR_36	H, L_TYR_36	2.79	1.96	13.76
5U3N.PDB	OE1, L_GLN_89	OH, L_TYR_36	HH, L_TYR_36	2.64	1.80	1.88
5U3N.PDB	O, L_LYS_45	N, L_LYS_37	H, L_LYS_37	2.84	2.01	13.10
5U3N.PDB	O, L_THR_85	N, L_HIS_38	H, L_HIS_38	2.80	2.03	21.49
5U3N.PDB	O, L_LYS_37	N, L_LYS_45	H, L_LYS_45	2.88	2.10	20.13
5U3N.PDB	O, L_TRP_35	N, L_LEU_47	H, L_LEU_47	2.79	1.93	3.84
5U3N.PDB	O, L_LYS_53	N, L_TYR_49	H, L_TYR_49	2.82	2.01	15.81
5U3N.PDB	OD1, L_ASN_34	N, L_SER_50	H, L_SER_50	2.96	2.18	21.09
5U3N.PDB	O, L_LEU_33	N, L_ALA_51	H, L_ALA_51	2.71	1.90	16.24
5U3N.PDB	O, L_TYR_49	N, L_LYS_53	H, L_LYS_53	2.83	2.03	18.60
5U3N.PDB	O, L_THR_72	N, L_SER_65	H, L_SER_65	2.95	2.15	18.23
5U3N.PDB	O, L_LYS_30	N, L_GLY_68	H, L_GLY_68	2.91	2.07	11.47
5U3N.PDB	O, L_CYS_23	N, L_PHE_71	H, L_PHE_71	2.92	2.08	10.20
5U3N.PDB	O, L_SER_65	N, L_THR_72	H, L_THR_72	2.89	2.07	15.08
5U3N.PDB	O, L_ILE_21	N, L_LEU_73	H, L_LEU_73	2.84	2.01	12.13
5U3N.PDB	O, L_SER_63	N, L_THR_74	H, L_THR_74	2.80	1.97	11.07
5U3N.PDB	O, L_ILE_19	N, L_ILE_75	H, L_ILE_75	2.86	2.08	19.78
5U3N.PDB	O, L_ARG_61	N, L_SER_76	H, L_SER_76	2.96	2.19	23.24
5U3N.PDB	O, L_ASP_17	N, L_LEU_78	H, L_LEU_78	2.72	1.92	19.04
5U3N.PDB	OD2, L_ASP_82	N, L_GLN_79	H, L_GLN_79	3.00	2.14	4.35
5U3N.PDB	O, L_GLN_79	N, L_ASP_82	H, L_ASP_82	2.83	1.99	10.16
5U3N.PDB	O, L_THR_102	N, L_TYR_86	H, L_TYR_86	2.90	2.10	17.67
5U3N.PDB	O, L_ASP_82	OH, L_TYR_86	HH, L_TYR_86	2.60	1.78	10.78
5U3N.PDB	O, L_TYR_36	N, L_TYR_87	H, L_TYR_87	2.92	2.10	15.56
5U3N.PDB	OE2, L_GLU_90	N, L_TYR_92	H, L_TYR_92	2.85	2.02	13.73
5U3N.PDB	O, L_CYS_88	N, L_GLY_99	H, L_GLY_99	2.82	2.02	16.99
5U3N.PDB	O, L_TYR_86	N, L_THR_102	H, L_THR_102	2.93	2.13	18.82
5U3N.PDB	O, L_PRO_8	OG1, L_THR_102	HG1, L_THR_102	2.67	1.96	27.26
5U3N.PDB	O, L_ALA_84	N, L_VAL_104	H, L_VAL_104	2.83	1.97	3.89
5U3N.PDB	O, L_LEU_11	N, L_ASP_105	H, L_ASP_105	2.98	2.15	13.92
5U3N.PDB	O, L_ALA_13	N, L_LYS_107	H, L_LYS_107	2.81	1.99	14.79
5U3N.PDB	O, L_THR_109	NE, L_ARG_108	HE, L_ARG_108	2.80	1.97	12.49
5U3N.PDB	O, L_ASP_170	NH1, L_ARG_108	HH11, L_ARG_108	2.97	2.15	15.13
5U3N.PDB	O, L_TYR_140	N, L_ALA_111	H, L_ALA_111	2.86	2.03	12.00
5U3N.PDB	O, L_LEU_135	N, L_PHE_116	H, L_PHE_116	2.88	2.09	19.79
5U3N.PDB	O, L_VAL_133	N, L_PHE_118	H, L_PHE_118	2.74	1.97	21.45
5U3N.PDB	OG, L_SER_131	NE2, L_GLN_124	HE22, L_GLN_124	2.80	1.94	3.81
5U3N.PDB	O, L_GLN_124	N, L_SER_127	H, L_SER_127	2.78	1.95	13.25

5U3N.PDB	O, L_GLN_124	OG, L_SER_127	HG, L_SER_127	2.63	1.79	4.63
5U3N.PDB	O, L_LEU_181	N, L_ALA_130	H, L_ALA_130	2.78	1.96	14.77
5U3N.PDB	OE1, L_GLN_124	N, L_SER_131	H, L_SER_131	2.94	2.15	18.69
5U3N.PDB	O, L_LEU_179	N, L_VAL_132	H, L_VAL_132	2.83	2.00	12.34
5U3N.PDB	O, L_SER_177	N, L_CYS_134	H, L_CYS_134	2.80	1.96	9.76
5U3N.PDB	O, L_PHE_116	N, L_LEU_135	H, L_LEU_135	2.72	1.88	11.53
5U3N.PDB	O, L_LEU_175	N, L_LEU_136	H, L_LEU_136	2.80	1.95	6.87
5U3N.PDB	O, L_SER_114	N, L_ASN_137	H, L_ASN_137	2.88	2.07	16.62
5U3N.PDB	OG, L_SER_174	N, L_ASN_138	H, L_ASN_138	2.99	2.16	12.45
5U3N.PDB	O, L_TYR_173	N, L_PHE_139	H, L_PHE_139	2.79	1.97	14.75
5U3N.PDB	O, L_ALA_111	N, L_TYR_140	H, L_TYR_140	2.87	2.08	18.95
5U3N.PDB	OD1, L_ASP_105	OH, L_TYR_140	HH, L_TYR_140	2.61	1.87	24.55
5U3N.PDB	O, L_GLU_195	N, L_GLN_147	H, L_GLN_147	2.84	2.01	12.00
5U3N.PDB	OG, L_SER_177	NE1, L_TRP_148	HE1, L_TRP_148	2.84	2.01	13.43
5U3N.PDB	O, L_ALA_193	N, L_LYS_149	H, L_LYS_149	2.84	2.00	9.94
5U3N.PDB	O, L_ALA_153	N, L_VAL_150	H, L_VAL_150	2.99	2.18	15.96
5U3N.PDB	O, L_AVAL_191	N, L_ASP_151	H, L_ASP_151	2.86	2.04	14.13
5U3N.PDB	O, L_BVAL_191	N, L_ASP_151	H, L_ASP_151	2.89	2.08	16.42
5U3N.PDB	O, L_VAL_150	N, L_ALA_153	H, L_ALA_153	2.90	2.05	8.35
5U3N.PDB	O, L_TRP_148	N, L_GLN_155	H, L_GLN_155	2.90	2.06	8.61
5U3N.PDB	O, L_ALA_153	NE2, L_GLN_155	HE21, L_GLN_155	2.97	2.12	8.23
5U3N.PDB	O, L_SER_176	N, L_SER_162	H, L_SER_162	2.95	2.15	17.97
5U3N.PDB	O, H_PRO_167	OG, L_SER_162	HG, L_SER_162	2.77	1.98	17.29
5U3N.PDB	O, L_SER_174	N, L_THR_164	H, L_THR_164	2.94	2.11	13.10
5U3N.PDB	O, L_SER_171	NE2, L_GLN_166	HE21, L_GLN_166	2.97	2.12	7.09
5U3N.PDB	O, L_LEU_106	NE2, L_GLN_166	HE22, L_GLN_166	2.79	2.02	22.69
5U3N.PDB	O, L_THR_172	N, L_ASP_167	H, L_ASP_167	2.90	2.10	16.69
5U3N.PDB	OD1, L_ASP_170	N, L_THR_172	H, L_THR_172	2.98	2.17	16.32
5U3N.PDB	OD1, L_ASP_170	OG1, L_THR_172	HG1, L_THR_172	2.63	1.80	7.71
5U3N.PDB	O, L_PHE_139	N, L_TYR_173	H, L_TYR_173	2.80	1.96	11.34
5U3N.PDB	OD2, L_ASP_105	OH, L_TYR_173	HH, L_TYR_173	2.66	1.88	16.93
5U3N.PDB	OG1, L_THR_164	N, L_SER_174	H, L_SER_174	2.99	2.17	14.48
5U3N.PDB	O, L_LEU_136	N, L_LEU_175	H, L_LEU_175	2.82	2.02	18.65
5U3N.PDB	O, L_SER_162	N, L_SER_176	H, L_SER_176	2.90	2.07	13.04
5U3N.PDB	O, L_CYS_134	N, L_SER_177	H, L_SER_177	2.88	2.05	10.58
5U3N.PDB	O, L_GLN_160	N, L_THR_178	H, L_THR_178	2.93	2.10	13.26
5U3N.PDB	O, L_VAL_132	N, L_LEU_179	H, L_LEU_179	2.72	1.91	15.62
5U3N.PDB	O, L_ASN_158	N, L_ATHR_180	H, L_ATHR_180	2.96	2.10	5.76
5U3N.PDB	O, L_ASN_158	N, L_BTHR_180	H, L_BTHR_180	2.98	2.13	8.23
5U3N.PDB	O, L_GLY_128	N, L_LYS_183	H, L_LYS_183	2.89	2.05	8.75
5U3N.PDB	O, L_SER_182	N, L_TYR_186	H, L_TYR_186	2.90	2.05	6.90
5U3N.PDB	O, L_LYS_183	N, L_GLU_187	H, L_GLU_187	2.91	2.12	19.43
5U3N.PDB	O, L_ASP_185	ND1, L_HIS_189	HD1, L_HIS_189	2.98	2.23	25.25
5U3N.PDB	OD1, L_ASP_151	N, L_BVAL_191	H, L_BVAL_191	3.00	2.14	6.33
5U3N.PDB	O, L_LYS_149	N, L_ALA_193	H, L_ALA_193	2.88	2.14	25.73
5U3N.PDB	O, L_LYS_207	N, L_CYS_194	H, L_CYS_194	2.96	2.16	18.86
5U3N.PDB	O, L_GLN_147	N, L_GLU_195	H, L_GLU_195	2.72	1.89	12.68
5U3N.PDB	O, L_VAL_205	N, L_VAL_196	H, L_VAL_196	2.76	1.95	15.71
5U3N.PDB	O, L_PRO_141	NE2, L_HIS_198	HE2, L_HIS_198	2.82	1.99	12.93
5U3N.PDB	O, L_HIS_198	N, L_LEU_201	H, L_LEU_201	2.79	1.94	8.84
5U3N.PDB	O, L_VAL_196	N, L_VAL_205	H, L_VAL_205	2.95	2.17	20.32
5U3N.PDB	O, L_TYR_192	N, L_PHE_209	H, L_PHE_209	2.95	2.17	22.09
5U3N.PDB	O, L_LYS_190	N, L_ARG_211	H, L_ARG_211	2.79	1.98	15.41
5U3N.PDB	O, L_HIS_189	NE, L_ARG_211	HE, L_ARG_211	2.72	1.88	11.65
5U3N.PDB	OD1, A_ASP_664	N, A_TRP_666	H, A_TRP_666	2.85	1.99	5.09
5U3N.PDB	OD2, A_ASP_674	N, A_ASN_671	H, A_ASN_671	2.89	2.10	19.70
5U3N.PDB	O, A_ASP_674	N, A_TRP_678	H, A_TRP_678	2.91	2.12	19.94
5U3N.PDB	O, A_ILE_675	N, A_LEU_679	H, A_LEU_679	2.85	2.02	12.95

5U3N.PDB	O, A_THR_676	N, A_TRP_680	H, A_TRP_680	2.88	2.03	5.54
5U3N.PDB	O, A_ASN_677	N, A_TYR_681	H, A_TYR_681	2.92	2.08	9.34
5U3N.PDB	O, A_TRP_678	N, A_ILE_682	H, A_ILE_682	2.84	2.11	26.86
5U3N.PDB	O, A_TRP_680	N, A_LYS_684	H, A_LYS_684	2.96	2.10	3.54
5UCB.PDB	O, H_SER_25	N, H_GLN_3	H, H_GLN_3	2.99	2.18	16.58
5UCB.PDB	O, H_SER_21	N, H_SER_7	H, H_SER_7	2.88	2.10	20.32
5UCB.PDB	O, H_THR_110	N, H_VAL_12	H, H_VAL_12	2.93	2.15	21.18
5UCB.PDB	O, H_LEU_82C	N, H_GLY_15	H, H_GLY_15	2.80	1.96	10.79
5UCB.PDB	O, H_GLN_13	N, H_GLY_16	H, H_GLY_16	2.96	2.13	13.46
5UCB.PDB	O, H_MET_82	N, H_LEU_18	H, H_LEU_18	2.96	2.17	20.10
5UCB.PDB	O, H_LEU_80	N, H_LEU_20	H, H_LEU_20	2.83	2.01	13.56
5UCB.PDB	O, H_SER_7	N, H_SER_21	H, H_SER_21	2.92	2.09	11.91
5UCB.PDB	O, H_ALA_78	N, H_CYS_22	H, H_CYS_22	2.76	2.02	25.89
5UCB.PDB	O, H_VAL_5	N, H_ALA_23	H, H_ALA_23	2.98	2.15	12.17
5UCB.PDB	O, H_GLN_3	N, H_SER_25	H, H_SER_25	2.87	2.02	8.54
5UCB.PDB	OD1, H_ASN_76	N, H_VAL_29	H, H_VAL_29	2.79	1.95	9.36
5UCB.PDB	OD1, H_ASN_28	N, H_SER_30	H, H_SER_30	2.95	2.10	6.39
5UCB.PDB	O, H_ALA_93	N, H_HIS_35	H, H_HIS_35	2.87	2.12	24.96
5UCB.PDB	OG, H_SER_33	NE2, H_HIS_35	HE2, H_HIS_35	2.88	2.09	19.50
5UCB.PDB	O, H_ALA_49	N, H_TRP_36	H, H_TRP_36	2.86	2.03	11.66
5UCB.PDB	O, H_TYR_91	N, H_VAL_37	H, H_VAL_37	2.92	2.10	13.93
5UCB.PDB	O, H_GLU_46	N, H_ARG_38	H, H_ARG_38	2.80	1.96	9.03
5UCB.PDB	OE1, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.85	2.03	15.54
5UCB.PDB	OH, H_TYR_90	NH1, H_ARG_38	HH11, H_ARG_38	2.94	2.12	15.88
5UCB.PDB	OD1, H_ASP_86	NH1, H_ARG_38	HH12, H_ARG_38	2.88	2.08	18.54
5UCB.PDB	O, H_VAL_89	N, H_GLN_39	H, H_GLN_39	2.83	2.10	26.74
5UCB.PDB	O, H_LYS_43	NE2, H_GLN_39	HE21, H_GLN_39	2.97	2.21	23.38
5UCB.PDB	OE1, L_GLN_38	NE2, H_GLN_39	HE22, H_GLN_39	2.96	2.12	9.92
5UCB.PDB	O, H_ALA_40	N, H_LYS_43	H, H_LYS_43	2.94	2.10	10.79
5UCB.PDB	O, H_ARG_38	N, H_GLU_46	H, H_GLU_46	2.82	2.01	15.90
5UCB.PDB	OG, H_SER_50	NE1, H_TRP_47	HE1, H_TRP_47	2.72	1.98	25.90
5UCB.PDB	O, H_TRP_36	N, H_VAL_48	H, H_VAL_48	2.90	2.07	12.31
5UCB.PDB	O, H_SER_58	N, H_SER_50	H, H_SER_50	2.91	2.11	18.26
5UCB.PDB	O, H_ILE_34	N, H_ILE_51	H, H_ILE_51	2.92	2.10	14.85
5UCB.PDB	O, H_SER_56	N, H_TYR_52	H, H_TYR_52	2.91	2.14	22.03
5UCB.PDB	O, B_LEU_5	OH, H_TYR_53	HH, H_TYR_53	2.73	1.99	23.03
5UCB.PDB	O, H_PRO_52A	N, H_TYR_54	H, H_TYR_54	2.76	2.01	24.37
5UCB.PDB	O, H_SER_50	N, H_SER_58	H, H_SER_58	2.97	2.16	17.28
5UCB.PDB	O, H_VAL_48	N, H_ALA_60	H, H_ALA_60	2.97	2.12	8.58
5UCB.PDB	O, H_VAL_63	N, H_ARG_66	H, H_ARG_66	2.93	2.10	10.67
5UCB.PDB	O, H_SER_82B	NH1, H_ARG_66	HH11, H_ARG_66	2.96	2.19	22.84
5UCB.PDB	OD2, H_ASP_86	NH1, H_ARG_66	HH12, H_ARG_66	2.75	1.90	5.99
5UCB.PDB	O, H_SER_62	NH2, H_ARG_66	HH21, H_ARG_66	2.91	2.06	4.12
5UCB.PDB	O, H_GLN_81	N, H_THR_68	H, H_THR_68	2.89	2.10	19.31
5UCB.PDB	OH, H_TYR_59	N, H_ILE_69	H, H_ILE_69	2.89	2.08	15.94
5UCB.PDB	O, H_THR_77	N, H_ASP_72	H, H_ASP_72	2.91	2.07	9.90
5UCB.PDB	OD1, H_ASP_72	OG, H_SER_74	HG, H_SER_74	2.60	1.83	20.07
5UCB.PDB	O, H_PHE_27	ND2, H_ASN_76	HD21, H_ASN_76	2.86	2.00	2.63
5UCB.PDB	O, H_LYS_75	OG1, H_THR_77	HG1, H_THR_77	2.96	2.13	8.72
5UCB.PDB	O, H_CYS_22	N, H_ALA_78	H, H_ALA_78	2.91	2.09	14.01
5UCB.PDB	O, H_SER_70	N, H_TYR_79	H, H_TYR_79	2.82	2.01	17.30
5UCB.PDB	O, H_LEU_20	N, H_LEU_80	H, H_LEU_80	2.93	2.12	15.92
5UCB.PDB	O, H_THR_68	N, H_GLN_81	H, H_GLN_81	2.85	2.03	14.25
5UCB.PDB	O, H_LEU_18	N, H_MET_82	H, H_MET_82	2.76	1.91	5.48
5UCB.PDB	OD2, H_ASP_86	N, H_ARG_83	H, H_ARG_83	2.84	2.02	15.13
5UCB.PDB	O, H_ARG_83	N, H_ASP_86	H, H_ASP_86	2.85	2.00	6.49
5UCB.PDB	O, H_GLN_39	N, H_VAL_89	H, H_VAL_89	2.94	2.15	19.65
5UCB.PDB	O, H_THR_107	N, H_TYR_90	H, H_TYR_90	2.82	1.97	6.43

5UCB.PDB	O, H_ASP_86	OH, H_TYR_90	HH, H_TYR_90	2.71	1.87	3.56
5UCB.PDB	O, H_VAL_37	N, H_TYR_91	H, H_TYR_91	2.75	1.90	8.79
5UCB.PDB	OE2, H_GLU_6	N, H_CYS_92	H, H_CYS_92	2.86	2.03	11.54
5UCB.PDB	O, H_HIS_35	N, H_ALA_93	H, H_ALA_93	2.82	2.03	19.85
5UCB.PDB	O, H_TYR_102	N, H_ARG_94	H, H_ARG_94	2.90	2.09	15.76
5UCB.PDB	O, H_SER_33	N, H_GLY_95	H, H_GLY_95	2.82	1.97	6.39
5UCB.PDB	O, H_ALA_99	N, H_TYR_96	H, H_TYR_96	2.79	1.94	8.94
5UCB.PDB	O, B_VAL_145	N, H_GLY_97	H, H_GLY_97	2.90	2.05	8.98
5UCB.PDB	O, H_TYR_96	N, H_ALA_99	H, H_ALA_99	2.86	2.03	11.06
5UCB.PDB	O, H_ARG_94	N, H_ASP_101	H, H_ASP_101	2.97	2.22	25.01
5UCB.PDB	O, H_CYS_92	N, H_GLY_104	H, H_GLY_104	2.92	2.08	11.62
5UCB.PDB	OE1, H_GLU_6	N, H_GLY_106	H, H_GLY_106	2.84	2.01	12.83
5UCB.PDB	O, H_TYR_90	N, H_THR_107	H, H_THR_107	2.95	2.15	17.03
5UCB.PDB	O, H_ALA_88	N, H_VAL_109	H, H_VAL_109	2.93	2.08	2.47
5UCB.PDB	OG1, H_THR_87	N, H_VAL_111	H, H_VAL_111	2.96	2.11	5.78
5UCB.PDB	O, H_VAL_12	N, H_PHE_112	H, H_PHE_112	2.91	2.15	23.15
5UCB.PDB	O, H_PHE_146	N, H_LYS_116	H, H_LYS_116	2.86	2.03	11.25
5UCB.PDB	O, H_LYS_143	N, H_SER_120	H, H_SER_120	2.97	2.14	12.13
5UCB.PDB	O, H_LEU_141	N, H_PHE_122	H, H_PHE_122	2.87	2.04	11.40
5UCB.PDB	O, H_GLY_139	N, H_LEU_124	H, H_LEU_124	2.78	1.92	6.23
5UCB.PDB	OG, H_SER_127	N, H_LYS_129	H, H_LYS_129	2.96	2.13	12.32
5UCB.PDB	O, L_SER_208	NZ, H_LYS_129	HZ2, H_LYS_129	2.83	2.06	25.53
5UCB.PDB	O, H_SER_127	N, H_SER_130	H, H_SER_130	2.91	2.06	7.11
5UCB.PDB	O, H_SER_132	N, H_THR_135	H, H_THR_135	2.95	2.10	8.67
5UCB.PDB	O, H_VAL_184	N, H_ALA_136	H, H_ALA_136	2.78	1.98	18.51
5UCB.PDB	O, H_SER_130	N, H_ALA_137	H, H_ALA_137	2.85	2.03	15.53
5UCB.PDB	O, H_VAL_182	N, H_LEU_138	H, H_LEU_138	2.99	2.18	16.62
5UCB.PDB	O, H_LEU_124	N, H_GLY_139	H, H_GLY_139	2.94	2.17	22.56
5UCB.PDB	O, H_SER_180	N, H_CYS_140	H, H_CYS_140	2.83	2.03	18.28
5UCB.PDB	O, H_PHE_122	N, H_LEU_141	H, H_LEU_141	2.79	1.94	8.33
5UCB.PDB	O, H_LEU_178	N, H_VAL_142	H, H_VAL_142	2.74	1.88	4.14
5UCB.PDB	O, H_SER_120	N, H_LYS_143	H, H_LYS_143	2.78	1.93	5.09
5UCB.PDB	O, H_LYS_116	N, H_PHE_146	H, H_PHE_146	2.95	2.14	16.58
5UCB.PDB	O, H_ASN_199	N, H_THR_151	H, H_THR_151	2.98	2.16	14.61
5UCB.PDB	O, H_ASN_197	N, H_SER_153	H, H_SER_153	2.95	2.14	16.54
5UCB.PDB	OD1, H_ASN_197	OG, H_SER_153	HG, H_SER_153	2.85	2.06	15.76
5UCB.PDB	OG, H_SER_180	NE1, H_TRP_154	HE1, H_TRP_154	2.92	2.07	7.16
5UCB.PDB	O, H_ILE_195	N, H_ASN_155	H, H_ASN_155	2.78	1.94	9.76
5UCB.PDB	OD1, H_ASN_197	N, H_SER_156	H, H_SER_156	2.74	1.94	17.37
5UCB.PDB	O, H_TRP_154	N, H_GLY_157	H, H_GLY_157	2.95	2.22	27.37
5UCB.PDB	O, H_VAL_181	N, H_HIS_164	H, H_HIS_164	2.82	1.99	13.79
5UCB.PDB	O, H_SER_179	N, H_PHE_166	H, H_PHE_166	2.94	2.09	6.35
5UCB.PDB	O, H_SER_177	N, H_VAL_169	H, H_VAL_169	2.90	2.07	11.28
5UCB.PDB	O, H_LEU_175	N, H_GLN_171	H, H_GLN_171	2.90	2.06	8.51
5UCB.PDB	OD1, H_ASP_144	NE2, H_GLN_171	HE22, H_GLN_171	2.78	1.99	18.86
5UCB.PDB	O, H_GLN_171	N, H_GLY_174	H, H_GLY_174	2.86	2.01	8.15
5UCB.PDB	O, H_TYR_145	N, H_TYR_176	H, H_TYR_176	2.86	2.01	5.39
5UCB.PDB	O, H_VAL_142	N, H_LEU_178	H, H_LEU_178	2.87	2.06	16.64
5UCB.PDB	O, H_HIS_164	N, H_VAL_181	H, H_VAL_181	2.87	2.03	11.87
5UCB.PDB	O, H_LEU_138	N, H_VAL_182	H, H_VAL_182	2.82	2.02	16.97
5UCB.PDB	O, H_ALA_136	N, H_VAL_184	H, H_VAL_184	2.90	2.07	12.53
5UCB.PDB	O, H_GLY_134	N, H_SER_186	H, H_SER_186	2.94	2.10	11.37
5UCB.PDB	O, H_PRO_185	N, H_SER_188	H, H_SER_188	2.97	2.14	13.02
5UCB.PDB	O, H_PRO_185	OG, H_SER_188	HG, H_SER_188	2.68	1.85	4.71
5UCB.PDB	O, H_THR_193	NE2, H_GLN_192	HE21, H_GLN_192	2.94	2.08	2.24
5UCB.PDB	OG, H_SER_188	OH, H_TYR_194	HH, H_TYR_194	2.72	1.90	9.93
5UCB.PDB	OD1, H_ASN_155	N, H_ILE_195	H, H_ILE_195	2.82	2.03	19.24
5UCB.PDB	O, H_LYS_209	N, H_CYS_196	H, H_CYS_196	2.98	2.19	20.71

5UCB.PDB	O, H_SER_153	N, H_ASN_197	H, H_ASN_197	2.75	1.90	8.02
5UCB.PDB	OD1, H_ASP_208	ND2, H_ASN_197	HD22, H_ASN_197	2.80	1.95	7.44
5UCB.PDB	O, H_VAL_207	N, H_VAL_198	H, H_VAL_198	2.80	1.95	7.37
5UCB.PDB	O, H_THR_151	N, H_ASN_199	H, H_ASN_199	2.96	2.13	12.40
5UCB.PDB	O, H_THR_205	N, H_HIS_200	H, H_HIS_200	2.86	2.02	9.86
5UCB.PDB	O, H_PRO_147	NE2, H_HIS_200	HE2, H_HIS_200	2.80	1.97	12.02
5UCB.PDB	O, H_VAL_198	N, H_VAL_207	H, H_VAL_207	2.86	2.03	11.55
5UCB.PDB	O, H_CYS_196	N, H_LYS_209	H, H_LYS_209	2.99	2.16	13.99
5UCB.PDB	O, H_TYR_194	N, H_VAL_211	H, H_VAL_211	2.90	2.04	4.78
5UCB.PDB	O, L_TYR_86	NE2, L_GLN_6	HE22, L_GLN_6	2.81	2.01	17.50
5UCB.PDB	O, L_LYS_103	N, L_LEU_11	H, L_LEU_11	2.85	2.05	18.74
5UCB.PDB	O, L_GLU_105	N, L_ALA_13	H, L_ALA_13	2.91	2.12	19.40
5UCB.PDB	OD2, L_ASP_17	N, L_SER_14	H, L_SER_14	2.85	2.00	7.52
5UCB.PDB	O, L_LEU_78	N, L_GLY_16	H, L_GLY_16	2.86	2.04	14.88
5UCB.PDB	O, L_SER_14	N, L_ASP_17	H, L_ASP_17	2.92	2.09	12.95
5UCB.PDB	O, L_LEU_73	N, L_ILE_21	H, L_ILE_21	2.89	2.08	16.55
5UCB.PDB	O, L_TYR_71	N, L_CYS_23	H, L_CYS_23	2.80	1.98	13.36
5UCB.PDB	O, L_THR_5	N, L_ARG_24	H, L_ARG_24	2.82	2.03	19.90
5UCB.PDB	O, L_THR_69	N, L_ALA_25	H, L_ALA_25	2.83	1.98	7.34
5UCB.PDB	OE1, L_GLN_3	OG, L_SER_26	HG, L_SER_26	2.61	1.78	7.17
5UCB.PDB	OD2, B_ASP_51	OG, L_SER_30	HG, L_SER_30	2.58	1.81	20.19
5UCB.PDB	O, L_ILE_48	N, L_TRP_35	H, L_TRP_35	2.89	2.09	17.06
5UCB.PDB	O, L_TYR_87	N, L_TYR_36	H, L_TYR_36	2.82	2.03	19.85
5UCB.PDB	OE1, L_GLN_89	OH, L_TYR_36	HH, L_TYR_36	2.64	1.84	15.57
5UCB.PDB	O, L_LYS_45	N, L_GLN_37	H, L_GLN_37	2.91	2.09	14.54
5UCB.PDB	OH, L_TYR_86	NE2, L_GLN_37	HE21, L_GLN_37	2.99	2.15	9.80
5UCB.PDB	O, L_THR_85	N, L_GLN_38	H, L_GLN_38	2.74	1.93	16.51
5UCB.PDB	O, L_LYS_42	NE2, L_GLN_38	HE21, L_GLN_38	2.88	2.08	17.97
5UCB.PDB	OE1, H_GLN_39	NE2, L_GLN_38	HE22, L_GLN_38	2.95	2.13	14.86
5UCB.PDB	O, L_GLU_81	NZ, L_LYS_39	HZ1, L_LYS_39	2.69	1.90	22.19
5UCB.PDB	O, L_GLN_37	N, L_LYS_45	H, L_LYS_45	2.84	2.05	19.57
5UCB.PDB	O, L_TRP_35	N, L_LEU_47	H, L_LEU_47	2.82	1.97	5.85
5UCB.PDB	O, L_SER_53	N, L_TYR_49	H, L_TYR_49	2.87	2.07	17.59
5UCB.PDB	O, L_VAL_33	N, L_ALA_51	H, L_ALA_51	2.85	2.02	11.41
5UCB.PDB	O, L_TYR_49	N, L_SER_53	H, L_SER_53	2.93	2.12	15.91
5UCB.PDB	O, L_LEU_47	N, L_TYR_55	H, L_TYR_55	2.94	2.08	2.44
5UCB.PDB	OD2, L_ASP_82	NE, L_ARG_61	HE, L_ARG_61	2.82	2.01	16.79
5UCB.PDB	OD1, L_ASP_82	NH2, L_ARG_61	HH21, L_ARG_61	2.85	1.99	4.65
5UCB.PDB	O, L_THR_74	N, L_SER_63	H, L_SER_63	2.97	2.19	19.92
5UCB.PDB	O, L_THR_72	N, L_SER_65	H, L_SER_65	2.97	2.20	22.80
5UCB.PDB	O, B_SER_47	NH1, L_ARG_66	HH12, L_ARG_66	2.77	1.99	21.64
5UCB.PDB	O, B_SER_47	NH2, L_ARG_66	HH22, L_ARG_66	2.89	2.16	27.12
5UCB.PDB	O, L_ASP_70	N, L_SER_67	H, L_SER_67	2.84	2.01	11.95
5UCB.PDB	O, B_ARG_48	N, L_GLY_68	H, L_GLY_68	2.79	1.95	9.02
5UCB.PDB	O, L_SER_67	N, L_ASP_70	H, L_ASP_70	2.95	2.11	10.96
5UCB.PDB	O, L_CYS_23	N, L_TYR_71	H, L_TYR_71	2.85	2.00	7.89
5UCB.PDB	O, L_SER_65	N, L_THR_72	H, L_THR_72	2.92	2.09	12.93
5UCB.PDB	OG1, L_THR_22	OG1, L_THR_72	HG1, L_THR_72	2.96	2.18	19.19
5UCB.PDB	O, L_ILE_21	N, L_LEU_73	H, L_LEU_73	2.82	2.02	18.31
5UCB.PDB	O, L_SER_63	N, L_THR_74	H, L_THR_74	2.88	2.03	7.94
5UCB.PDB	O, L_VAL_19	N, L_ILE_75	H, L_ILE_75	2.85	2.02	13.35
5UCB.PDB	O, L_ARG_61	N, L_SER_76	H, L_SER_76	2.93	2.12	17.13
5UCB.PDB	O, L_ASP_17	N, L_LEU_78	H, L_LEU_78	2.83	2.04	19.24
5UCB.PDB	OD2, L_ASP_82	N, L_GLN_79	H, L_GLN_79	2.81	1.95	4.90
5UCB.PDB	O, L_GLN_79	N, L_ASP_82	H, L_ASP_82	2.94	2.09	7.96
5UCB.PDB	O, L_GLN_38	N, L_THR_85	H, L_THR_85	2.95	2.11	8.28
5UCB.PDB	O, L_THR_102	N, L_TYR_86	H, L_TYR_86	2.88	2.06	15.79
5UCB.PDB	O, L_ASP_82	OH, L_TYR_86	HH, L_TYR_86	2.68	1.86	10.64

5UCB.PDB	O, L_TYR_36	N, L_TYR_87	H, L_TYR_87	2.88	2.06	15.19
5UCB.PDB	O, L_ALA_32	N, L_ASP_91	H, L_ASP_91	2.84	1.99	7.27
5UCB.PDB	O, L_LEU_95	N, L_GLY_92	H, L_GLY_92	2.81	2.01	17.89
5UCB.PDB	O, L_GLN_90	N, L_THR_97	H, L_THR_97	2.89	2.07	13.99
5UCB.PDB	O, L_CYS_88	N, L_GLY_99	H, L_GLY_99	2.87	2.06	16.05
5UCB.PDB	O, L_GLN_6	NE2, L_GLN_100	HE21, L_GLN_100	2.96	2.10	3.33
5UCB.PDB	O, L_TYR_86	N, L_THR_102	H, L_THR_102	2.91	2.11	19.06
5UCB.PDB	O, L_PRO_8	OG1, L_THR_102	HG1, L_THR_102	2.64	1.82	9.17
5UCB.PDB	O, L_SER_9	N, L_LYS_103	H, L_LYS_103	2.86	2.02	9.83
5UCB.PDB	OE1, L_GLU_165	NZ, L_LYS_103	HZ3, L_LYS_103	2.77	1.90	9.89
5UCB.PDB	O, L_ALA_84	N, L_VAL_104	H, L_VAL_104	2.92	2.06	4.48
5UCB.PDB	O, L_LEU_11	N, L_GLU_105	H, L_GLU_105	2.83	1.98	7.22
5UCB.PDB	OE1, L_GLN_166	N, L_ILE_106	H, L_ILE_106	2.97	2.14	12.29
5UCB.PDB	O, L_ALA_13	N, L_LYS_107	H, L_LYS_107	2.94	2.14	17.97
5UCB.PDB	O, L_THR_109	NE, L_ARG_108	HE, L_ARG_108	2.81	1.98	12.46
5UCB.PDB	O, L_ASP_170	NH1, L_ARG_108	HH11, L_ARG_108	2.96	2.13	10.72
5UCB.PDB	O, L_TYR_140	N, L_ALA_111	H, L_ALA_111	2.86	2.03	12.05
5UCB.PDB	O, L_LEU_135	N, L_PHE_116	H, L_PHE_116	2.91	2.10	16.52
5UCB.PDB	O, L_VAL_133	N, L_PHE_118	H, L_PHE_118	2.84	2.06	20.95
5UCB.PDB	OG, L_SER_131	NE2, L_GLN_124	HE22, L_GLN_124	2.73	1.87	2.66
5UCB.PDB	O, L_GLN_124	N, L_SER_127	H, L_SER_127	2.84	2.11	27.03
5UCB.PDB	O, L_GLN_124	OG, L_SER_127	HG, L_SER_127	2.54	1.72	9.22
5UCB.PDB	O, L_LEU_125	N, L_GLY_128	H, L_GLY_128	2.90	2.09	16.29
5UCB.PDB	O, L_LEU_181	N, L_ALA_130	H, L_ALA_130	2.86	2.04	14.78
5UCB.PDB	OE1, L_GLN_124	N, L_SER_131	H, L_SER_131	2.91	2.10	16.27
5UCB.PDB	O, L_LEU_179	N, L_VAL_132	H, L_VAL_132	2.80	1.95	9.72
5UCB.PDB	O, L_SER_177	N, L_CYS_134	H, L_CYS_134	2.81	1.97	8.89
5UCB.PDB	O, L_PHE_116	N, L_LEU_135	H, L_LEU_135	2.84	2.00	9.91
5UCB.PDB	O, L_LEU_175	N, L_LEU_136	H, L_LEU_136	2.82	1.97	6.91
5UCB.PDB	O, L_SER_114	N, L_ASN_137	H, L_ASN_137	2.82	2.00	13.64
5UCB.PDB	OG, L_SER_174	N, L_ASN_138	H, L_ASN_138	3.00	2.18	14.73
5UCB.PDB	O, L_TYR_173	N, L_PHE_139	H, L_PHE_139	2.80	1.98	15.50
5UCB.PDB	O, L_ALA_111	N, L_TYR_140	H, L_TYR_140	2.92	2.11	16.50
5UCB.PDB	O, L_GLU_195	N, L_GLN_147	H, L_GLN_147	2.87	2.02	9.88
5UCB.PDB	OG, L_SER_177	NE1, L_TRP_148	HE1, L_TRP_148	2.92	2.09	12.30
5UCB.PDB	O, L_ALA_193	N, L_LYS_149	H, L_LYS_149	2.92	2.09	12.63
5UCB.PDB	O, L_ALA_153	N, L_VAL_150	H, L_VAL_150	2.98	2.16	16.04
5UCB.PDB	O, L_VAL_191	N, L_ASP_151	H, L_ASP_151	2.74	1.90	10.65
5UCB.PDB	O, L_VAL_150	N, L_ALA_153	H, L_ALA_153	2.91	2.06	8.01
5UCB.PDB	O, L_TRP_148	N, L_GLN_155	H, L_GLN_155	2.94	2.12	14.17
5UCB.PDB	O, L_ALA_153	NE2, L_GLN_155	HE21, L_GLN_155	2.97	2.12	7.54
5UCB.PDB	OE1, L_GLN_155	ND2, L_ASN_158	HD21, L_ASN_158	2.98	2.15	12.35
5UCB.PDB	O, H_LEU_170	NE2, L_GLN_160	HE22, L_GLN_160	2.99	2.13	5.75
5UCB.PDB	O, L_SER_176	N, L_SER_162	H, L_SER_162	2.95	2.16	19.90
5UCB.PDB	O, H_PRO_167	OG, L_SER_162	HG, L_SER_162	2.68	1.94	24.13
5UCB.PDB	O, L_SER_174	N, L_THR_164	H, L_THR_164	2.94	2.12	14.57
5UCB.PDB	O, L_SER_171	NE2, L_GLN_166	HE21, L_GLN_166	2.94	2.17	23.45
5UCB.PDB	O, L_ILE_106	NE2, L_GLN_166	HE22, L_GLN_166	2.80	1.96	9.36
5UCB.PDB	O, L_THR_172	N, L_ASP_167	H, L_ASP_167	2.83	2.01	14.08
5UCB.PDB	OD2, L_ASP_167	N, L_ASP_170	H, L_ASP_170	2.95	2.15	18.34
5UCB.PDB	O, L_ASP_167	N, L_SER_171	H, L_SER_171	2.83	2.10	27.38
5UCB.PDB	OD1, L_ASP_170	N, L_THR_172	H, L_THR_172	2.93	2.09	9.94
5UCB.PDB	OD1, L_ASP_170	OG1, L_THR_172	HG1, L_THR_172	2.71	1.89	8.99
5UCB.PDB	O, L_PHE_139	N, L_TYR_173	H, L_TYR_173	2.82	1.97	6.86
5UCB.PDB	OE2, L_GLU_105	OH, L_TYR_173	HH, L_TYR_173	2.61	1.81	15.35
5UCB.PDB	O, L_LEU_136	N, L_LEU_175	H, L_LEU_175	2.88	2.08	17.16
5UCB.PDB	O, L_SER_162	N, L_SER_176	H, L_SER_176	2.94	2.12	15.24
5UCB.PDB	O, L_CYS_134	N, L_SER_177	H, L_SER_177	2.86	2.02	11.18

5UCB.PDB	O, L_GLN_160	N, L_THR_178	H, L_THR_178	2.87	2.04	12.63
5UCB.PDB	O, L_VAL_132	N, L_LEU_179	H, L_LEU_179	2.79	1.97	14.56
5UCB.PDB	O, L_ASN_158	N, L_THR_180	H, L_THR_180	2.97	2.12	9.36
5UCB.PDB	O, L_ALA_130	N, L_LEU_181	H, L_LEU_181	2.88	2.04	9.45
5UCB.PDB	OG, L_SER_182	N, L_ASP_185	H, L_ASP_185	3.00	2.15	7.40
5UCB.PDB	O, L_SER_182	N, L_TYR_186	H, L_TYR_186	2.90	2.06	11.13
5UCB.PDB	O, L_LYS_183	N, L_GLU_187	H, L_GLU_187	2.89	2.04	6.84
5UCB.PDB	OD1, L_ASP_151	N, L_VAL_191	H, L_VAL_191	2.90	2.05	6.39
5UCB.PDB	O, L_PHE_209	N, L_TYR_192	H, L_TYR_192	2.96	2.11	7.95
5UCB.PDB	O, L_LYS_149	N, L_ALA_193	H, L_ALA_193	2.91	2.10	16.38
5UCB.PDB	O, L_LYS_207	N, L_CYS_194	H, L_CYS_194	2.82	1.97	8.63
5UCB.PDB	O, L_GLN_147	N, L_GLU_195	H, L_GLU_195	2.82	1.97	7.58
5UCB.PDB	O, L_VAL_205	N, L_VAL_196	H, L_VAL_196	2.73	1.91	15.27
5UCB.PDB	O, L_LYS_145	N, L_THR_197	H, L_THR_197	2.87	2.03	10.61
5UCB.PDB	O, L_PRO_141	NE2, L_HIS_198	HE2, L_HIS_198	2.90	2.07	14.06
5UCB.PDB	ND1, L_HIS_198	N, L_GLY_200	H, L_GLY_200	2.97	2.11	4.92
5UCB.PDB	O, L_HIS_198	N, L_LEU_201	H, L_LEU_201	2.92	2.08	10.11
5UCB.PDB	O, L_VAL_196	N, L_VAL_205	H, L_VAL_205	2.94	2.22	28.63
5UCB.PDB	O, L_CYS_194	N, L_LYS_207	H, L_LYS_207	2.89	2.07	14.81
5UCB.PDB	O, L_TYR_192	N, L_PHE_209	H, L_PHE_209	2.96	2.17	21.00
5UCB.PDB	O, L_LYS_190	N, L_ARG_211	H, L_ARG_211	2.83	2.11	27.52
5UCB.PDB	O, B_GLU_28	N, B_SER_4	H, B_SER_4	2.92	2.10	13.37
5UCB.PDB	O, B_THR_26	N, B_LEU_6	H, B_LEU_6	2.81	1.99	15.67
5UCB.PDB	O, B_GLU_24	N, B_LYS_9	H, B_LYS_9	2.95	2.17	21.44
5UCB.PDB	O, B_GLU_22	N, B_LEU_11	H, B_LEU_11	2.84	1.99	8.95
5UCB.PDB	O, B_PRO_20	ND2, B_ASN_12	HD21, B_ASN_12	2.86	2.03	12.12
5UCB.PDB	O, B_ILE_138	ND2, B_ASN_13	HD21, B_ASN_13	2.86	2.13	26.24
5UCB.PDB	O, B_ARG_136	N, B_ALA_15	H, B_ALA_15	3.00	2.19	16.91
5UCB.PDB	OD1, B_ASP_132	NZ, B_LYS_16	HZ1, B_LYS_16	2.90	2.15	27.66
5UCB.PDB	O, B_ILE_134	N, B_PHE_17	H, B_PHE_17	2.94	2.10	10.85
5UCB.PDB	O, B_LYS_16	N, B_ASP_19	H, B_ASP_19	2.97	2.13	10.34
5UCB.PDB	O, B_ALA_75	N, B_TYR_21	H, B_TYR_21	2.82	2.02	17.42
5UCB.PDB	O, B_PHE_73	N, B_PHE_23	H, B_PHE_23	2.94	2.09	7.26
5UCB.PDB	O, B_LYS_9	N, B_GLU_24	H, B_GLU_24	2.80	1.98	14.46
5UCB.PDB	O, B_PHE_71	N, B_ILE_25	H, B_ILE_25	2.84	1.99	6.56
5UCB.PDB	O, B_GLY_7	N, B_THR_26	H, B_THR_26	2.95	2.10	4.53
5UCB.PDB	O, B_ASN_69	N, B_PHE_27	H, B_PHE_27	2.94	2.11	13.13
5UCB.PDB	O, B_SER_4	N, B_GLU_28	H, B_GLU_28	2.91	2.10	17.54
5UCB.PDB	O, B_GLY_67	N, B_CYS_29	H, B_CYS_29	2.96	2.14	15.57
5UCB.PDB	O, B_ILE_2	N, B_LEU_30	H, B_LEU_30	2.83	2.00	11.91
5UCB.PDB	OD2, B_ASP_153	N, B_LYS_34	H, B_LYS_34	2.94	2.14	18.44
5UCB.PDB	OH, B_TYR_100	N, B_HIS_35	H, B_HIS_35	2.93	2.15	21.81
5UCB.PDB	O, B_VAL_61	N, B_LEU_37	H, B_LEU_37	2.93	2.13	18.65
5UCB.PDB	O, B_ILE_59	N, B_TRP_39	H, B_TRP_39	2.91	2.12	19.76
5UCB.PDB	O, B_SER_97	N, B_LYS_40	H, B_LYS_40	2.88	2.06	15.75
5UCB.PDB	O, B_LEU_95	N, B_THR_42	H, B_THR_42	2.88	2.09	19.90
5UCB.PDB	O, B_GLN_54	N, B_TYR_43	H, B_TYR_43	2.83	2.01	14.02
5UCB.PDB	OE2, B_GLU_87	OH, B_TYR_43	HH, B_TYR_43	2.72	1.91	12.68
5UCB.PDB	O, B_VAL_93	N, B_VAL_44	H, B_VAL_44	2.93	2.08	6.15
5UCB.PDB	O, B_HIS_52	N, B_GLY_45	H, B_GLY_45	2.82	1.98	9.81
5UCB.PDB	OD1, B_ASP_51	OG, B_SER_46	HG, B_SER_46	2.83	2.02	12.78
5UCB.PDB	O, B_LEU_50	N, B_SER_47	H, B_SER_47	2.94	2.21	27.12
5UCB.PDB	OE1, B_GLU_87	OG, B_SER_47	HG, B_SER_47	2.62	1.82	14.05
5UCB.PDB	O, B_GLY_45	N, B_HIS_52	H, B_HIS_52	2.75	1.95	17.98
5UCB.PDB	O, B_TYR_43	N, B_GLN_54	H, B_GLN_54	2.99	2.21	20.44
5UCB.PDB	O, B_LEU_41	N, B_LEU_56	H, B_LEU_56	2.80	2.03	22.15
5UCB.PDB	O, B_TRP_39	N, B_ILE_59	H, B_ILE_59	2.85	2.07	20.70
5UCB.PDB	O, B_LEU_37	N, B_VAL_61	H, B_VAL_61	2.83	1.99	11.73

5UCB.PDB	O, B_CYS_29	N, B_GLY_67	H, B_GLY_67	2.83	1.97	6.62
5UCB.PDB	O, B_PHE_27	N, B_ASN_69	H, B_ASN_69	2.76	1.99	22.57
5UCB.PDB	O, B_PHE_23	N, B_PHE_73	H, B_PHE_73	2.79	1.98	16.10
5UCB.PDB	O, B_TYR_21	N, B_ALA_75	H, B_ALA_75	2.81	1.98	12.45
5UCB.PDB	OD2, B_ASP_57	N, B_ASP_76	H, B_ASP_76	2.88	2.07	15.78
5UCB.PDB	OE1, B_GLN_54	N, B_SER_79	H, B_SER_79	2.94	2.10	11.73
5UCB.PDB	O, B_ALA_80	N, B_ILE_83	H, B_ILE_83	3.00	2.16	12.13
5UCB.PDB	O, B_PRO_84	N, B_GLU_87	H, B_GLU_87	2.81	2.08	26.69
5UCB.PDB	O, B_GLU_87	OG, B_SER_90	HG, B_SER_90	2.87	2.04	8.25
5UCB.PDB	O, B_VAL_112	N, B_THR_92	H, B_THR_92	2.86	2.03	12.64
5UCB.PDB	O, B_THR_42	N, B_LEU_95	H, B_LEU_95	2.81	2.01	16.51
5UCB.PDB	O, B_VAL_108	N, B_LEU_96	H, B_LEU_96	2.80	1.97	10.47
5UCB.PDB	O, B_LYS_40	N, B_SER_97	H, B_SER_97	2.90	2.07	12.23
5UCB.PDB	O, B_GLU_38	N, B_SER_99	H, B_SER_99	2.90	2.12	21.40
5UCB.PDB	O, B_ARG_103	N, B_TYR_100	H, B_TYR_100	2.86	2.06	17.81
5UCB.PDB	OD1, B_ASP_153	OH, B_TYR_100	HH, B_TYR_100	2.55	1.73	8.75
5UCB.PDB	O, B_TYR_100	N, B_ARG_103	H, B_ARG_103	2.90	2.08	14.68
5UCB.PDB	O, B_VAL_151	NE, B_ARG_103	HE, B_ARG_103	2.81	2.01	18.23
5UCB.PDB	OD2, B_ASP_101	NH1, B_ARG_103	HH12, B_ARG_103	2.89	2.11	20.47
5UCB.PDB	O, B_THR_146	N, B_ARG_107	H, B_ARG_107	2.85	2.07	20.33
5UCB.PDB	OE2, B_GLU_104	NE, B_ARG_107	HE, B_ARG_107	2.91	2.05	4.26
5UCB.PDB	O, B_LEU_96	N, B_VAL_108	H, B_VAL_108	2.68	1.84	10.31
5UCB.PDB	O, B_ARG_144	N, B_GLY_109	H, B_GLY_109	2.80	1.96	9.36
5UCB.PDB	O, B_ILE_94	N, B_TYR_110	H, B_TYR_110	2.92	2.13	18.74
5UCB.PDB	O, L_ASP_91	OH, B_TYR_111	HH, B_TYR_111	2.57	1.75	11.11
5UCB.PDB	O, B_THR_92	N, B_VAL_112	H, B_VAL_112	2.87	2.09	21.11
5UCB.PDB	O, B_ASN_137	N, B_ASN_113	H, B_ASN_113	2.89	2.05	9.00
5UCB.PDB	O, B_SER_90	ND2, B_ASN_114	HD22, B_ASN_114	2.97	2.13	9.19
5UCB.PDB	O, B_GLU_118	N, B_ARG_122	H, B_ARG_122	2.99	2.17	14.84
5UCB.PDB	O, B_TYR_116	NH1, B_ARG_122	HH11, B_ARG_122	2.93	2.10	12.81
5UCB.PDB	O, B_GLU_120	N, B_ASN_124	H, B_ASN_124	2.98	2.27	29.44
5UCB.PDB	O, B_VAL_129	NZ, B_LYS_128	HZ2, B_LYS_128	2.82	1.95	9.37
5UCB.PDB	O, B_GLN_130	N, B_HIS_133	H, B_HIS_133	2.98	2.14	9.05
5UCB.PDB	OD1, B_ASP_117	ND1, B_HIS_133	HD1, B_HIS_133	2.95	2.15	18.23
5UCB.PDB	O, B_GLU_115	N, B_VAL_135	H, B_VAL_135	2.83	1.97	4.10
5UCB.PDB	O, B_ALA_15	N, B_ARG_136	H, B_ARG_136	2.79	1.98	17.55
5UCB.PDB	O, B_ASP_19	NH1, B_ARG_136	HH12, B_ARG_136	2.88	2.07	16.59
5UCB.PDB	O, B_ASN_113	N, B_ASN_137	H, B_ASN_137	2.81	2.02	19.05
5UCB.PDB	OD1, B_ASN_13	N, B_ILE_138	H, B_ILE_138	2.88	2.04	12.14
5UCB.PDB	O, B_TYR_111	N, B_LEU_139	H, B_LEU_139	2.86	2.01	7.51
5UCB.PDB	OG, H_SER_58	NZ, B_LYS_142	HZ3, B_LYS_142	2.83	1.96	8.82
5UCB.PDB	O, B_GLY_109	N, B_ARG_144	H, B_ARG_144	2.81	1.96	8.55
5UCB.PDB	O, B_LYS_142	NH1, B_ARG_144	HH11, B_ARG_144	2.91	2.12	19.24
5UCB.PDB	OD1, L_ASP_91	NH2, B_ARG_144	HH21, B_ARG_144	2.84	2.03	16.18
5UCB.PDB	O, B_ARG_107	N, B_THR_146	H, B_THR_146	2.81	1.98	11.97
5UCB.PDB	O, B_PHE_105	N, B_PHE_148	H, B_PHE_148	2.97	2.13	9.82
5UJZ.PDB	OD2, B_ASP_612	N, B_PHE_503	H, B_PHE_503	2.82	1.98	9.98
5UJZ.PDB	OE1, B_GLU_574	N, B_ASN_571	H, B_ASN_571	2.73	1.96	22.10
5UJZ.PDB	OD1, B_ASN_571	N, B_LEU_573	H, B_LEU_573	2.86	2.10	22.42
5UJZ.PDB	O, B_ARG_575	N, B_ASN_579	H, B_ASN_579	2.92	2.06	2.26
5UJZ.PDB	O, B_ARG_576	N, B_LEU_580	H, B_LEU_580	2.88	2.06	14.57
5UJZ.PDB	O, B_MET_577	N, B_ASN_581	H, B_ASN_581	2.87	2.02	8.14
5UJZ.PDB	O, B_GLU_578	N, B_LYS_582	H, B_LYS_582	2.88	2.03	6.05
5UJZ.PDB	O, B_ASN_579	N, B_LYS_583	H, B_LYS_583	2.96	2.20	23.30
5UJZ.PDB	O, B_LEU_580	N, B_VAL_584	H, B_VAL_584	2.77	1.95	12.45
5UJZ.PDB	O, B_LYS_583	N, B_GLY_587	H, B_GLY_587	2.90	2.12	21.34
5UJZ.PDB	O, B_VAL_584	N, B_PHE_588	H, B_PHE_588	2.97	2.16	15.91
5UJZ.PDB	O, B_PHE_588	N, B_TRP_592	H, B_TRP_592	2.95	2.10	7.22

5UJZ.PDB	O, B_ASP_590	N, B_TYR_594	H, B_TYR_594	2.86	2.06	18.30
5UJZ.PDB	O, B_ILE_591	N, B_ASN_595	H, B_ASN_595	2.96	2.11	4.50
5UJZ.PDB	O, B_TRP_592	N, B_ALA_596	H, B_ALA_596	2.92	2.09	14.14
5UJZ.PDB	O, B_THR_593	N, B_GLU_597	H, B_GLU_597	2.94	2.13	17.13
5UJZ.PDB	O, B_ASN_595	N, B_LEU_599	H, B_LEU_599	2.92	2.21	29.47
5UJZ.PDB	O, B_ALA_596	N, B_VAL_600	H, B_VAL_600	2.90	2.16	25.76
5UJZ.PDB	O, B_LEU_598	N, B_LEU_602	H, B_LEU_602	2.89	2.04	6.88
5UJZ.PDB	O, B_LEU_599	N, B_GLU_603	H, B_GLU_603	2.89	2.05	10.08
5UJZ.PDB	O, B_VAL_600	N, B_ASN_604	H, B_ASN_604	2.99	2.17	14.45
5UJZ.PDB	O, B_LEU_602	N, B_ARG_606	H, B_ARG_606	2.86	2.03	11.15
5UJZ.PDB	O, B_ASN_604	N, B_LEU_608	H, B_LEU_608	2.98	2.16	15.31
5UJZ.PDB	O, B_LEU_608	N, B_ASP_612	H, B_ASP_612	2.95	2.10	4.89
5UJZ.PDB	OE1, D_GLU_574	N, D_ASN_571	H, D_ASN_571	2.73	1.96	22.20
5UJZ.PDB	OD1, D_ASN_571	N, D_LEU_573	H, D_LEU_573	2.86	2.10	22.20
5UJZ.PDB	O, D_ARG_575	N, D_ASN_579	H, D_ASN_579	2.92	2.06	2.09
5UJZ.PDB	O, D_ARG_576	N, D_LEU_580	H, D_LEU_580	2.88	2.06	14.50
5UJZ.PDB	O, D_MET_577	N, D_ASN_581	H, D_ASN_581	2.87	2.02	7.86
5UJZ.PDB	O, D_GLU_578	N, D_LYS_582	H, D_LYS_582	2.88	2.03	5.99
5UJZ.PDB	O, D_ASN_579	N, D_LYS_583	H, D_LYS_583	2.96	2.20	23.42
5UJZ.PDB	O, D_LEU_580	N, D_VAL_584	H, D_VAL_584	2.77	1.95	12.36
5UJZ.PDB	O, D_ASN_581	N, D_ASP_585	H, D_ASP_585	2.93	2.09	8.97
5UJZ.PDB	O, D_LYS_583	N, D_GLY_587	H, D_GLY_587	2.90	2.12	21.44
5UJZ.PDB	O, D_VAL_584	N, D_PHE_588	H, D_PHE_588	2.97	2.16	15.92
5UJZ.PDB	O, D_ASP_585	N, D_ILE_589	H, D_ILE_589	2.87	2.03	9.83
5UJZ.PDB	O, D_PHE_588	N, D_TRP_592	H, D_TRP_592	2.95	2.10	7.33
5UJZ.PDB	O, D_TRP_592	N, D_ALA_596	H, D_ALA_596	2.92	2.09	14.04
5UJZ.PDB	O, D_ASN_595	N, D_LEU_599	H, D_LEU_599	2.91	2.21	29.48
5UJZ.PDB	OE1, F_GLU_574	N, F_ASN_571	H, F_ASN_571	2.73	1.96	22.15
5UJZ.PDB	OD1, F_ASN_571	N, F_LEU_573	H, F_LEU_573	2.86	2.10	22.13
5UJZ.PDB	O, F_ARG_575	N, F_ASN_579	H, F_ASN_579	2.92	2.05	1.88
5UJZ.PDB	O, F_ARG_576	N, F_LEU_580	H, F_LEU_580	2.88	2.06	14.64
5UJZ.PDB	O, F_MET_577	N, F_ASN_581	H, F_ASN_581	2.87	2.02	7.56
5UJZ.PDB	O, F_GLU_578	N, F_LYS_582	H, F_LYS_582	2.88	2.03	5.84
5UJZ.PDB	O, F_ASN_579	N, F_LYS_583	H, F_LYS_583	2.96	2.20	23.60
5UJZ.PDB	O, F_LEU_580	N, F_VAL_584	H, F_VAL_584	2.77	1.95	12.39
5UJZ.PDB	O, F_ASN_581	N, F_ASP_585	H, F_ASP_585	2.93	2.09	8.86
5UJZ.PDB	O, F_LYS_582	N, F_ASP_586	H, F_ASP_586	2.90	2.06	8.24
5UJZ.PDB	O, F_LYS_583	N, F_GLY_587	H, F_GLY_587	2.90	2.12	21.41
5UJZ.PDB	O, F_VAL_584	N, F_PHE_588	H, F_PHE_588	2.97	2.16	15.90
5UJZ.PDB	O, F_ASP_585	N, F_ILE_589	H, F_ILE_589	2.87	2.03	9.71
5UJZ.PDB	O, F_ASP_586	N, F_ASP_590	H, F_ASP_590	2.94	2.13	16.67
5UJZ.PDB	O, F_PHE_588	N, F_TRP_592	H, F_TRP_592	2.95	2.10	7.36
5UJZ.PDB	O, F_ILE_589	N, F_THR_593	H, F_THR_593	2.94	2.15	21.05
5UJZ.PDB	O, F_ASP_590	N, F_TYR_594	H, F_TYR_594	2.86	2.06	18.69
5UJZ.PDB	O, F_ILE_591	N, F_ASN_595	H, F_ASN_595	2.96	2.11	4.41
5UJZ.PDB	O, F_TRP_592	N, F_ALA_596	H, F_ALA_596	2.92	2.09	13.92
5UK0.PDB	O, A_THR_235	N, A_VAL_178	H, A_VAL_178	3.00	2.15	9.10
5UK0.PDB	O, A_TYR_233	N, A_TRP_180	H, A_TRP_180	2.83	2.06	22.85
5UK0.PDB	O, A_HIS_98	N, A_TYR_232	H, A_TYR_232	2.76	1.93	13.46
5UK0.PDB	O, A_TRP_180	N, A_TYR_233	H, A_TYR_233	2.86	2.01	7.16
5UK0.PDB	O, A_ALA_100	NE1, A_TRP_234	HE1, A_TRP_234	2.75	1.95	17.16
5UK0.PDB	O, A_VAL_178	N, A_THR_235	H, A_THR_235	2.96	2.15	14.92
5UK0.PDB	OD2, B_ASP_612	N, B_PHE_503	H, B_PHE_503	2.70	1.87	11.32
5UK0.PDB	O, B_ALA_505	N, B_GLY_508	H, B_GLY_508	2.62	1.89	25.83
5UK0.PDB	O, B_GLY_504	N, B_PHE_509	H, B_PHE_509	2.72	1.93	19.32
5UK0.PDB	O, B_ALA_535	N, B_TYR_524	H, B_TYR_524	2.87	2.06	16.06
5UK0.PDB	O, B_GLY_533	N, B_HIS_526	H, B_HIS_526	2.86	2.15	29.56
5UK0.PDB	O, B_TYR_524	N, B_ALA_535	H, B_ALA_535	2.96	2.18	21.03

5UK0.PDB	O, B_TYR_522	N, B_ASP_537	H, B_ASP_537	2.88	2.08	16.70
5UK0.PDB	O, B_GLN_538	N, B_GLN_542	H, B_GLN_542	2.87	2.06	16.85
5UK0.PDB	O, B_LYS_539	N, B_ASN_543	H, B_ASN_543	2.98	2.18	18.23
5UK0.PDB	O, B_SER_540	N, B_ALA_544	H, B_ALA_544	2.92	2.10	14.62
5UK0.PDB	O, B_THR_541	N, B_ILE_545	H, B_ILE_545	2.93	2.14	18.92
5UK0.PDB	O, B_GLN_542	N, B_ASN_546	H, B_ASN_546	2.90	2.07	13.85
5UK0.PDB	O, B_ILE_545	N, B_THR_549	H, B_THR_549	2.91	2.09	13.10
5UK0.PDB	O, B_ASN_546	N, B_ASN_550	H, B_ASN_550	2.97	2.16	16.74
5UK0.PDB	O, B_GLY_547	N, B_LYS_551	H, B_LYS_551	2.90	2.15	24.65
5UK0.PDB	O, B_ILE_548	N, B_VAL_552	H, B_VAL_552	2.98	2.14	11.61
5UK0.PDB	O, B_THR_549	N, B_ASN_553	H, B_ASN_553	2.96	2.10	2.11
5UK0.PDB	O, B_ASN_550	N, B_SER_554	H, B_SER_554	2.98	2.23	25.37
5UK0.PDB	O, B_VAL_552	N, B_ILE_556	H, B_ILE_556	2.99	2.17	15.52
5UK0.PDB	OD1, F_ASP_590	ND2, B_ASN_560	HD22, B_ASN_560	2.72	1.94	19.72
5UK0.PDB	O, B_GLU_574	N, B_GLU_578	H, B_GLU_578	2.95	2.23	28.27
5UK0.PDB	O, B_ARG_575	N, B_ASN_579	H, B_ASN_579	2.86	2.00	5.28
5UK0.PDB	O, B_ARG_576	N, B_LEU_580	H, B_LEU_580	2.90	2.08	14.14
5UK0.PDB	O, B_MET_577	N, B_ASN_581	H, B_ASN_581	2.90	2.05	9.42
5UK0.PDB	O, B_GLU_578	N, B_LYS_582	H, B_LYS_582	2.89	2.04	6.59
5UK0.PDB	O, B_ASN_579	N, B_LYS_583	H, B_LYS_583	2.99	2.19	17.96
5UK0.PDB	O, B_LEU_580	N, B_VAL_584	H, B_VAL_584	2.79	1.97	14.76
5UK0.PDB	O, B_ASN_581	N, B_ASP_585	H, B_ASP_585	2.96	2.12	8.51
5UK0.PDB	O, B_LYS_582	N, B_ASP_586	H, B_ASP_586	2.88	2.03	6.06
5UK0.PDB	O, B_LYS_583	N, B_GLY_587	H, B_GLY_587	2.88	2.11	21.69
5UK0.PDB	O, B_ASP_585	N, B_ILE_589	H, B_ILE_589	2.91	2.09	14.38
5UK0.PDB	O, B_ASP_586	N, B_ASP_590	H, B_ASP_590	2.91	2.09	14.55
5UK0.PDB	O, B_PHE_588	N, B_TRP_592	H, B_TRP_592	2.93	2.08	6.61
5UK0.PDB	O, B_ILE_589	N, B_THR_593	H, B_THR_593	2.96	2.20	24.14
5UK0.PDB	O, B_ASP_590	N, B_TYR_594	H, B_TYR_594	2.90	2.12	20.32
5UK0.PDB	O, B_ILE_591	N, B_ASN_595	H, B_ASN_595	2.98	2.13	3.96
5UK0.PDB	O, B_TRP_592	N, B_ALA_596	H, B_ALA_596	2.89	2.07	14.01
5UK0.PDB	O, B_THR_593	N, B_GLU_597	H, B_GLU_597	2.94	2.15	19.17
5UK0.PDB	O, B_ASN_595	N, B_LEU_599	H, B_LEU_599	2.94	2.22	27.64
5UK0.PDB	O, B_ALA_596	N, B_VAL_600	H, B_VAL_600	2.93	2.19	26.06
5UK0.PDB	O, B_LEU_598	N, B_LEU_602	H, B_LEU_602	2.93	2.09	10.30
5UK0.PDB	O, B_LEU_599	N, B_GLU_603	H, B_GLU_603	2.87	2.04	13.58
5UK0.PDB	O, B_VAL_600	N, B_ASN_604	H, B_ASN_604	2.99	2.17	14.76
5UK0.PDB	O, B_LEU_601	N, B_GLU_605	H, B_GLU_605	2.98	2.18	18.00
5UK0.PDB	O, B_LEU_602	N, B_ARG_606	H, B_ARG_606	2.85	2.01	10.65
5UK0.PDB	O, B_ASN_604	N, B_LEU_608	H, B_LEU_608	2.96	2.16	17.86
5UK0.PDB	O, B_GLU_605	N, B_ASP_609	H, B_ASP_609	2.94	2.14	18.33
5UK0.PDB	O, B_THR_607	N, B_HIS_611	H, B_HIS_611	2.95	2.15	17.84
5UK0.PDB	O, B_LEU_608	N, B_ASP_612	H, B_ASP_612	2.94	2.09	8.40
5UK0.PDB	O, B_ASP_609	N, B_SER_613	H, B_SER_613	2.89	2.09	18.36
5UK0.PDB	O, B_HIS_611	N, B_VAL_615	H, B_VAL_615	2.99	2.17	12.43
5UK0.PDB	O, B_SER_613	N, B_ASN_617	H, B_ASN_617	2.86	2.04	15.11
5UK0.PDB	O, F_LEU_502	ND2, B_ASN_617	HD22, B_ASN_617	2.60	1.80	16.74
5UK0.PDB	O, B_ASN_614	N, B_LEU_618	H, B_LEU_618	2.97	2.17	18.23
5UK0.PDB	O, B_VAL_615	N, B_TYR_619	H, B_TYR_619	2.89	2.08	17.73
5UK0.PDB	O, B_ASN_617	N, B_LYS_621	H, B_LYS_621	2.91	2.19	28.31
5UK0.PDB	O, B_LEU_618	N, B_VAL_622	H, B_VAL_622	2.91	2.12	20.36
5UK0.PDB	O, B_TYR_619	N, B_LYS_623	H, B_LYS_623	2.95	2.14	15.77
5UK0.PDB	O, B_GLU_639	N, B_LYS_631	H, B_LYS_631	2.93	2.13	17.90
5UK0.PDB	OD1, C_ASN_231	N, C_HIS_98	H, C_HIS_98	2.89	2.08	15.31
5UK0.PDB	O, C_ASP_101	N, C_LEU_105	H, C_LEU_105	2.95	2.14	16.91
5UK0.PDB	O, C_LEU_105	N, C_LEU_109	H, C_LEU_109	2.87	2.07	17.71
5UK0.PDB	O, C_THR_131	N, C_THR_155	H, C_THR_155	2.70	1.87	11.80
5UK0.PDB	O, C_THR_235	N, C_VAL_178	H, C_VAL_178	2.99	2.15	8.93

5UK0.PDB	O, C_TYR_233	N, C_TRP_180	H, C_TRP_180	2.83	2.06	22.92
5UK0.PDB	O, C_ILE_252	N, C_GLY_181	H, C_GLY_181	2.96	2.20	23.53
5UK0.PDB	O, C_ASN_231	N, C_VAL_182	H, C_VAL_182	2.94	2.21	26.92
5UK0.PDB	O, C_ASN_250	N, C_HIS_183	H, C_HIS_183	2.90	2.10	17.87
5UK0.PDB	O, C_HIS_98	N, C_TYR_232	H, C_TYR_232	2.75	1.93	13.38
5UK0.PDB	O, C_TRP_180	N, C_TYR_233	H, C_TYR_233	2.86	2.01	7.20
5UK0.PDB	O, C_ALA_100	NE1, C_TRP_234	HE1, C_TRP_234	2.75	1.95	17.15
5UK0.PDB	O, C_VAL_178	N, C_THR_235	H, C_THR_235	2.96	2.15	14.97
5UK0.PDB	O, C_VAL_176	N, C_LEU_237	H, C_LEU_237	2.90	2.14	23.70
5UK0.PDB	O, C_GLY_181	N, C_ILE_252	H, C_ILE_252	2.86	2.07	19.19
5UK0.PDB	OD1, D_ASP_586	NH2, C_ARG_311	HH22, C_ARG_311	2.98	2.20	18.56
5UK0.PDB	OD2, D_ASP_612	N, D_PHE_503	H, D_PHE_503	2.70	1.87	11.03
5UK0.PDB	O, D_ALA_505	N, D_GLY_508	H, D_GLY_508	2.63	1.89	25.56
5UK0.PDB	O, D_GLY_504	N, D_PHE_509	H, D_PHE_509	2.72	1.93	19.19
5UK0.PDB	O, D_ALA_535	N, D_TYR_524	H, D_TYR_524	2.87	2.06	15.73
5UK0.PDB	O, D_TYR_524	N, D_ALA_535	H, D_ALA_535	2.96	2.18	21.51
5UK0.PDB	O, D_TYR_522	N, D_ASP_537	H, D_ASP_537	2.88	2.07	16.56
5UK0.PDB	O, D_GLN_538	N, D_GLN_542	H, D_GLN_542	2.87	2.06	16.50
5UK0.PDB	O, D_LYS_539	N, D_ASN_543	H, D_ASN_543	2.98	2.18	18.20
5UK0.PDB	O, D_SER_540	N, D_ALA_544	H, D_ALA_544	2.93	2.11	14.85
5UK0.PDB	O, D_THR_541	N, D_ILE_545	H, D_ILE_545	2.93	2.14	18.87
5UK0.PDB	O, D_GLN_542	N, D_ASN_546	H, D_ASN_546	2.90	2.07	13.58
5UK0.PDB	O, D_ILE_545	N, D_THR_549	H, D_THR_549	2.91	2.09	12.94
5UK0.PDB	O, D_ASN_546	N, D_ASN_550	H, D_ASN_550	2.97	2.16	16.37
5UK0.PDB	O, D_GLY_547	N, D_LYS_551	H, D_LYS_551	2.90	2.15	24.73
5UK0.PDB	O, D_ILE_548	N, D_VAL_552	H, D_VAL_552	2.98	2.14	11.77
5UK0.PDB	O, D_THR_549	N, D_ASN_553	H, D_ASN_553	2.96	2.10	2.11
5UK0.PDB	O, D_ASN_550	N, D_SER_554	H, D_SER_554	2.98	2.23	25.34
5UK0.PDB	O, D_VAL_552	N, D_ILE_556	H, D_ILE_556	2.99	2.17	15.75
5UK0.PDB	OD1, B_ASP_590	ND2, D_ASN_560	HD22, D_ASN_560	2.73	1.95	20.06
5UK0.PDB	O, D_GLU_574	N, D_GLU_578	H, D_GLU_578	2.95	2.23	28.68
5UK0.PDB	O, D_ARG_575	N, D_ASN_579	H, D_ASN_579	2.86	2.00	3.72
5UK0.PDB	O, D_ARG_576	N, D_LEU_580	H, D_LEU_580	2.90	2.07	13.93
5UK0.PDB	O, D_MET_577	N, D_ASN_581	H, D_ASN_581	2.90	2.05	9.24
5UK0.PDB	O, D_GLU_578	N, D_LYS_582	H, D_LYS_582	2.89	2.04	7.42
5UK0.PDB	O, D_ASN_579	N, D_LYS_583	H, D_LYS_583	2.99	2.19	18.48
5UK0.PDB	O, D_LEU_580	N, D_VAL_584	H, D_VAL_584	2.79	1.97	14.60
5UK0.PDB	O, D_ASN_581	N, D_ASP_585	H, D_ASP_585	2.96	2.12	8.30
5UK0.PDB	O, D_LYS_582	N, D_ASP_586	H, D_ASP_586	2.88	2.03	7.07
5UK0.PDB	O, D_LYS_583	N, D_GLY_587	H, D_GLY_587	2.88	2.11	21.76
5UK0.PDB	O, D_ASP_585	N, D_ILE_589	H, D_ILE_589	2.91	2.09	14.41
5UK0.PDB	O, D_ASP_586	N, D_ASP_590	H, D_ASP_590	2.91	2.09	15.63
5UK0.PDB	O, D_PHE_588	N, D_TRP_592	H, D_TRP_592	2.93	2.08	6.27
5UK0.PDB	O, D_ILE_589	N, D_THR_593	H, D_THR_593	2.96	2.21	24.62
5UK0.PDB	O, D_ASP_590	N, D_TYR_594	H, D_TYR_594	2.90	2.12	21.14
5UK0.PDB	O, D_ILE_591	N, D_ASN_595	H, D_ASN_595	2.98	2.12	3.15
5UK0.PDB	O, D_TRP_592	N, D_ALA_596	H, D_ALA_596	2.89	2.07	14.15
5UK0.PDB	O, D_THR_593	N, D_GLU_597	H, D_GLU_597	2.94	2.15	19.89
5UK0.PDB	O, D_ASN_595	N, D_LEU_599	H, D_LEU_599	2.94	2.21	26.82
5UK0.PDB	O, D_ALA_596	N, D_VAL_600	H, D_VAL_600	2.93	2.19	25.78
5UK0.PDB	O, D_LEU_598	N, D_LEU_602	H, D_LEU_602	2.93	2.09	10.12
5UK0.PDB	O, D_LEU_599	N, D_GLU_603	H, D_GLU_603	2.86	2.04	13.30
5UK0.PDB	O, D_VAL_600	N, D_ASN_604	H, D_ASN_604	2.99	2.17	15.08
5UK0.PDB	O, D_LEU_601	N, D_GLU_605	H, D_GLU_605	2.98	2.18	18.56
5UK0.PDB	O, D_LEU_602	N, D_ARG_606	H, D_ARG_606	2.85	2.01	10.50
5UK0.PDB	O, D_ASN_604	N, D_LEU_608	H, D_LEU_608	2.96	2.16	18.11
5UK0.PDB	O, D_GLU_605	N, D_ASP_609	H, D_ASP_609	2.94	2.14	18.44
5UK0.PDB	O, D_THR_607	N, D_HIS_611	H, D_HIS_611	2.95	2.15	17.74

5UK0.PDB	O, D_LEU_608	N, D_ASP_612	H, D_ASP_612	2.94	2.09	8.59
5UK0.PDB	O, D_ASP_609	N, D_SER_613	H, D_SER_613	2.89	2.09	18.51
5UK0.PDB	O, D_HIS_611	N, D_VAL_615	H, D_VAL_615	2.99	2.17	12.24
5UK0.PDB	O, D_SER_613	N, D_ASN_617	H, D_ASN_617	2.86	2.05	15.31
5UK0.PDB	O, B_LEU_502	ND2, D_ASN_617	HD22, D_ASN_617	2.62	1.80	13.03
5UK0.PDB	O, D_ASN_614	N, D_LEU_618	H, D_LEU_618	2.97	2.17	17.99
5UK0.PDB	O, D_VAL_615	N, D_TYR_619	H, D_TYR_619	2.89	2.08	17.58
5UK0.PDB	O, D_ASN_617	N, D_LYS_621	H, D_LYS_621	2.91	2.19	28.69
5UK0.PDB	O, D_LEU_618	N, D_VAL_622	H, D_VAL_622	2.91	2.12	19.99
5UK0.PDB	O, D_TYR_619	N, D_LYS_623	H, D_LYS_623	2.95	2.14	15.66
5UK0.PDB	OH, D_TYR_659	ND2, D_ASN_628	HD22, D_ASN_628	2.78	1.98	17.11
5UK0.PDB	O, D_GLU_639	N, D_LYS_631	H, D_LYS_631	2.93	2.13	17.74
5UK0.PDB	OD1, E_ASN_231	N, E_HIS_98	H, E_HIS_98	2.89	2.08	15.58
5UK0.PDB	O, E_ASP_101	N, E_LEU_105	H, E_LEU_105	2.95	2.14	17.24
5UK0.PDB	O, E_ALA_253	N, E_LEU_152	H, E_LEU_152	2.92	2.19	27.06
5UK0.PDB	O, E_THR_235	N, E_VAL_178	H, E_VAL_178	2.99	2.15	9.16
5UK0.PDB	O, E_TYR_233	N, E_TRP_180	H, E_TRP_180	2.83	2.07	23.11
5UK0.PDB	O, E_ILE_252	N, E_GLY_181	H, E_GLY_181	2.96	2.20	23.58
5UK0.PDB	O, E_ASN_231	N, E_VAL_182	H, E_VAL_182	2.94	2.21	26.82
5UK0.PDB	O, E_ASN_250	N, E_HIS_183	H, E_HIS_183	2.90	2.10	17.70
5UK0.PDB	O, E_HIS_98	N, E_TYR_232	H, E_TYR_232	2.75	1.93	13.43
5UK0.PDB	O, E_TRP_180	N, E_TYR_233	H, E_TYR_233	2.86	2.01	7.32
5UK0.PDB	O, E_ALA_100	NE1, E_TRP_234	HE1, E_TRP_234	2.75	1.95	17.13
5UK0.PDB	O, E_VAL_178	N, E_THR_235	H, E_THR_235	2.96	2.15	14.95
5UK0.PDB	O, E_GLY_181	N, E_ILE_252	H, E_ILE_252	2.86	2.06	19.00
5UK0.PDB	O, E_LEU_152	N, E_ALA_253	H, E_ALA_253	2.98	2.15	13.22
5UK0.PDB	OD2, F_ASP_612	N, F_PHE_503	H, F_PHE_503	2.70	1.87	11.30
5UK0.PDB	O, F_ALA_505	N, F_GLY_508	H, F_GLY_508	2.62	1.89	25.82
5UK0.PDB	O, F_GLY_504	N, F_PHE_509	H, F_PHE_509	2.72	1.93	19.29
5UK0.PDB	O, F_TYR_522	N, F_ASP_537	H, F_ASP_537	2.88	2.08	16.77
5UK0.PDB	O, F_GLN_538	N, F_GLN_542	H, F_GLN_542	2.87	2.06	16.85
5UK0.PDB	O, F_LYS_539	N, F_ASN_543	H, F_ASN_543	2.98	2.18	18.15
5UK0.PDB	O, F_SER_540	N, F_ALA_544	H, F_ALA_544	2.92	2.10	14.52
5UK0.PDB	O, F_THR_541	N, F_ILE_545	H, F_ILE_545	2.93	2.14	19.01
5UK0.PDB	O, F_GLN_542	N, F_ASN_546	H, F_ASN_546	2.90	2.07	13.91
5UK0.PDB	O, F_ILE_545	N, F_THR_549	H, F_THR_549	2.91	2.09	13.20
5UK0.PDB	O, F_GLY_547	N, F_LYS_551	H, F_LYS_551	2.90	2.15	24.70
5UK0.PDB	O, F_ILE_548	N, F_VAL_552	H, F_VAL_552	2.98	2.14	11.60
5UK0.PDB	O, F_THR_549	N, F_ASN_553	H, F_ASN_553	2.96	2.10	2.17
5UK0.PDB	O, F_GLU_574	N, F_GLU_578	H, F_GLU_578	2.95	2.23	28.18
5UK0.PDB	O, F_ARG_575	N, F_ASN_579	H, F_ASN_579	2.86	2.00	5.11
5UK0.PDB	O, F_ARG_576	N, F_LEU_580	H, F_LEU_580	2.90	2.08	14.08
5UK0.PDB	O, F_MET_577	N, F_ASN_581	H, F_ASN_581	2.90	2.05	9.26
5UK0.PDB	O, F_GLU_578	N, F_LYS_582	H, F_LYS_582	2.89	2.04	6.55
5UK0.PDB	O, F_ASN_579	N, F_LYS_583	H, F_LYS_583	2.99	2.19	17.94
5UK0.PDB	O, F_LEU_580	N, F_VAL_584	H, F_VAL_584	2.79	1.97	14.87
5UK0.PDB	O, F_ASN_581	N, F_ASP_585	H, F_ASP_585	2.96	2.12	8.36
5UK0.PDB	O, F_LYS_582	N, F_ASP_586	H, F_ASP_586	2.88	2.03	6.16
5UK0.PDB	O, F_LYS_583	N, F_GLY_587	H, F_GLY_587	2.88	2.11	21.80
5UK0.PDB	O, F_ASP_585	N, F_ILE_589	H, F_ILE_589	2.91	2.09	14.50
5UK0.PDB	O, F_ASP_586	N, F_ASP_590	H, F_ASP_590	2.91	2.09	14.81
5UK0.PDB	O, F_PHE_588	N, F_TRP_592	H, F_TRP_592	2.93	2.08	6.51
5UK0.PDB	O, F_ILE_589	N, F_THR_593	H, F_THR_593	2.96	2.20	24.02
5UK0.PDB	O, F_ASP_590	N, F_TYR_594	H, F_TYR_594	2.90	2.12	20.53
5UK0.PDB	O, F_ILE_591	N, F_ASN_595	H, F_ASN_595	2.98	2.13	3.84
5UK0.PDB	O, F_TRP_592	N, F_ALA_596	H, F_ALA_596	2.89	2.07	13.98
5UK0.PDB	O, F_THR_593	N, F_GLU_597	H, F_GLU_597	2.94	2.15	19.04
5UK0.PDB	O, F_ASN_595	N, F_LEU_599	H, F_LEU_599	2.94	2.22	27.60

5UK0.PDB	O, F_ALA_596	N, F_VAL_600	H, F_VAL_600	2.93	2.19	26.00
5UK0.PDB	O, F_LEU_598	N, F_LEU_602	H, F_LEU_602	2.93	2.09	10.36
5UK0.PDB	O, F_LEU_599	N, F_GLU_603	H, F_GLU_603	2.87	2.04	13.60
5UK0.PDB	O, F_VAL_600	N, F_ASN_604	H, F_ASN_604	2.99	2.17	14.81
5UK0.PDB	O, F_LEU_601	N, F_GLU_605	H, F_GLU_605	2.98	2.18	18.18
5UK0.PDB	O, F_LEU_602	N, F_ARG_606	H, F_ARG_606	2.84	2.01	10.64
5UK0.PDB	O, F_ASN_604	N, F_LEU_608	H, F_LEU_608	2.96	2.16	17.90
5UK0.PDB	O, F_GLU_605	N, F_ASP_609	H, F_ASP_609	2.94	2.14	18.42
5UK0.PDB	O, F_THR_607	N, F_HIS_611	H, F_HIS_611	2.95	2.15	17.79
5UK0.PDB	O, F_LEU_608	N, F_ASP_612	H, F_ASP_612	2.94	2.09	8.54
5UK0.PDB	O, F_ASP_609	N, F_SER_613	H, F_SER_613	2.89	2.09	18.54
5UK0.PDB	O, F_HIS_611	N, F_VAL_615	H, F_VAL_615	2.99	2.17	12.51
5UK0.PDB	O, F_SER_613	N, F_ASN_617	H, F_ASN_617	2.86	2.04	15.17
5UK0.PDB	O, D_LEU_502	ND2, F_ASN_617	HD22, F_ASN_617	2.71	1.89	14.40
5UK0.PDB	O, F_ASN_614	N, F_LEU_618	H, F_LEU_618	2.97	2.17	18.13
5UK0.PDB	O, F_VAL_615	N, F_TYR_619	H, F_TYR_619	2.89	2.08	17.81
5UK0.PDB	O, F_ASN_617	N, F_LYS_621	H, F_LYS_621	2.91	2.19	28.37
5UK0.PDB	O, F_LEU_618	N, F_VAL_622	H, F_VAL_622	2.91	2.12	20.33
5UK0.PDB	O, F_TYR_619	N, F_LYS_623	H, F_LYS_623	2.95	2.14	15.82
5UK1.PDB	O, D_VAL_552	N, D_ILE_556	H, D_ILE_556	2.96	2.12	11.93
5UK1.PDB	OE1, F_GLU_574	N, F_ASN_571	H, F_ASN_571	2.86	2.03	13.31
5UK1.PDB	O, F_GLU_574	N, F_GLU_578	H, F_GLU_578	2.94	2.20	25.93
5UK1.PDB	O, F_ARG_575	N, F_ASN_579	H, F_ASN_579	2.86	2.00	2.72
5UK1.PDB	O, F_ARG_576	N, F_LEU_580	H, F_LEU_580	2.81	1.99	13.05
5UK1.PDB	O, F_MET_577	N, F_ASN_581	H, F_ASN_581	2.86	2.02	9.83
5UK1.PDB	O, F_GLU_578	N, F_LYS_582	H, F_LYS_582	2.87	2.01	5.13
5UK1.PDB	O, F_ASN_579	N, F_LYS_583	H, F_LYS_583	2.94	2.18	22.71
5UK1.PDB	O, F_LEU_580	N, F_VAL_584	H, F_VAL_584	2.76	1.97	18.59
5UK1.PDB	O, F_ASN_581	N, F_ASP_585	H, F_ASP_585	2.97	2.13	10.07
5UK1.PDB	O, F_VAL_584	N, F_PHE_588	H, F_PHE_588	2.96	2.20	23.32
5UK2.PDB	O, A_ALA_100	NE1, A_TRP_234	HE1, A_TRP_234	2.78	1.96	13.46
5UK2.PDB	OE1, B_GLU_574	N, B_ASN_571	H, B_ASN_571	2.96	2.16	19.53
5UK2.PDB	OD1, B_ASN_571	N, B_LEU_573	H, B_LEU_573	2.85	2.08	22.03
5UK2.PDB	O, B_ARG_575	N, B_ASN_579	H, B_ASN_579	2.99	2.13	2.73
5UK2.PDB	O, B_ARG_576	N, B_LEU_580	H, B_LEU_580	2.91	2.11	18.12
5UK2.PDB	O, B_MET_577	N, B_ASN_581	H, B_ASN_581	2.88	2.04	8.65
5UK2.PDB	O, B_GLU_578	N, B_LYS_582	H, B_LYS_582	2.97	2.11	2.97
5UK2.PDB	O, B_ASN_579	N, B_LYS_583	H, B_LYS_583	2.97	2.22	23.65
5UK2.PDB	O, B_LEU_580	N, B_VAL_584	H, B_VAL_584	2.78	1.98	15.70
5UK2.PDB	O, B_ASN_581	N, B_ASP_585	H, B_ASP_585	2.99	2.14	7.89
5UK2.PDB	O, B_LYS_583	N, B_GLY_587	H, B_GLY_587	2.91	2.15	22.85
5UK2.PDB	O, B_VAL_584	N, B_PHE_588	H, B_PHE_588	2.97	2.15	13.63
5UK2.PDB	O, B_ASP_585	N, B_ILE_589	H, B_ILE_589	2.86	2.03	12.99
5UK2.PDB	O, B_PHE_588	N, B_TRP_592	H, B_TRP_592	2.95	2.11	9.98
5UK2.PDB	O, B_ILE_589	N, B_THR_593	H, B_THR_593	2.97	2.20	23.17
5UK2.PDB	O, B_ASP_590	N, B_TYR_594	H, B_TYR_594	2.88	2.12	22.46
5UK2.PDB	O, B_ILE_591	N, B_ASN_595	H, B_ASN_595	2.96	2.11	4.99
5UK2.PDB	O, B_TRP_592	N, B_ALA_596	H, B_ALA_596	2.93	2.11	15.16
5UK2.PDB	OE1, F_GLU_574	N, F_ASN_571	H, F_ASN_571	2.96	2.16	19.49
5UK2.PDB	OD1, F_ASN_571	N, F_LEU_573	H, F_LEU_573	2.85	2.08	21.74
5UK2.PDB	O, F_ARG_575	N, F_ASN_579	H, F_ASN_579	2.99	2.13	2.69
5UK2.PDB	O, F_ARG_576	N, F_LEU_580	H, F_LEU_580	2.91	2.11	18.05
5UK2.PDB	O, F_MET_577	N, F_ASN_581	H, F_ASN_581	2.88	2.04	8.63
5UK2.PDB	O, F_ASN_579	N, F_LYS_583	H, F_LYS_583	2.97	2.22	23.60
5UK2.PDB	O, F_LEU_580	N, F_VAL_584	H, F_VAL_584	2.78	1.98	15.73
5UK2.PDB	O, F_VAL_584	N, F_PHE_588	H, F_PHE_588	2.97	2.15	13.56
5VXJ.PDB	O, A_VAL_41	N, A_THR_45	H, A_THR_45	2.85	2.03	14.33
5VXJ.PDB	O, A_SER_43	N, A_LEU_47	H, A_LEU_47	2.92	2.09	14.12

5VXJ.PDB	O, A_MET.46	N, A_THR.50	H, A_THR.50	2.71	1.87	10.48
5VXJ.PDB	O, A_MET.46	OG1, A_THR.50	HG1, A_THR.50	2.73	1.96	20.05
5VXJ.PDB	O, A_LEU.47	N, A_LEU.51	H, A_LEU.51	2.75	1.90	3.64
5VXJ.PDB	OD2, A_ASP.309	NH2, A_ARG.55	HH21, A_ARG.55	2.90	2.12	21.39
5VXJ.PDB	O, A_ASN.53	N, A_THR.57	H, A_THR.57	2.92	2.09	13.03
5VXJ.PDB	O, A_ILE.54	N, A_ASN.58	H, A_ASN.58	2.76	1.94	14.78
5VXJ.PDB	O, A_THR.57	N, A_LEU.61	H, A_LEU.61	2.95	2.16	20.24
5VXJ.PDB	O, A_ASN.58	N, A_LYS.62	H, A_LYS.62	2.92	2.08	10.15
5VXJ.PDB	OG, A_SER.302	NZ, A_LYS.62	HZ2, A_LYS.62	2.77	1.91	12.44
5VXJ.PDB	OG, A_SER.306	NZ, A_LYS.62	HZ3, A_LYS.62	2.75	1.92	16.95
5VXJ.PDB	O, A_LEU.61	N, A_LEU.65	H, A_LEU.65	2.88	2.04	11.05
5VXJ.PDB	O, A_THR.73	N, A_GLU.77	H, A_GLU.77	2.92	2.15	21.99
5VXJ.PDB	O, A_SER.74	N, A_ILE.78	H, A_ILE.78	2.84	1.99	6.65
5VXJ.PDB	O, A_GLU.77	N, A_HIS.81	H, A_HIS.81	2.96	2.12	10.84
5VXJ.PDB	O, A_ILE.78	N, A_SER.82	H, A_SER.82	2.74	1.89	4.58
5VXJ.PDB	O, A_ALA.79	N, A_SER.83	H, A_SER.83	2.95	2.13	16.02
5VXJ.PDB	O, A_LEU.80	N, A_GLN.84	H, A_GLN.84	2.97	2.17	18.25
5VXJ.PDB	O, A_HIS.81	N, A_ILE.85	H, A_ILE.85	2.84	2.00	10.73
5VXJ.PDB	O, A_SER.82	N, A_SER.86	H, A_SER.86	2.95	2.09	3.63
5VXJ.PDB	O, A_SER.83	N, A_MET.87	H, A_MET.87	2.90	2.08	16.45
5VXJ.PDB	O, A_ILE.85	N, A_VAL.89	H, A_VAL.89	2.68	1.83	6.60
5VXJ.PDB	O, A_SER.86	N, A_ASN.90	H, A_ASN.90	2.83	2.04	19.63
5VXJ.PDB	O, A_ASP.88	N, A_SER.92	H, A_SER.92	2.88	2.03	7.69
5VXJ.PDB	O, A_VAL.89	N, A_ALA.93	H, A_ALA.93	2.95	2.14	16.09
5VXJ.PDB	O, A_LYS.91	N, A_LEU.95	H, A_LEU.95	2.93	2.12	16.80
5VXJ.PDB	O, A_SER.92	N, A_LEU.96	H, A_LEU.96	2.83	1.97	3.74
5VXJ.PDB	O, A_ALA.93	N, A_ASP.97	H, A_ASP.97	2.81	2.03	20.86
5VXJ.PDB	O, A_LEU.96	N, A_SER.100	H, A_SER.100	2.98	2.27	29.77
5VXJ.PDB	O, A_ARG.132	OG, A_SER.100	HG, A_SER.100	2.62	1.84	18.43
5VXJ.PDB	OD2, A_ASP.97	NE, A_ARG.101	HE, A_ARG.101	2.80	1.97	13.39
5VXJ.PDB	O, A_ILE.98	N, A_ASN.102	H, A_ASN.102	2.95	2.11	10.28
5VXJ.PDB	O, A_SER.100	N, A_GLU.103	H, A_GLU.103	2.99	2.22	22.55
5VXJ.PDB	O, A_LEU.99	N, A_TYR.104	H, A_TYR.104	2.95	2.14	17.03
5VXJ.PDB	O, A_ILE.129	NH1, A_ARG.111	HH12, A_ARG.111	2.61	1.80	16.87
5VXJ.PDB	O, A_LEU.113	N, A_SER.116	H, A_SER.116	2.99	2.17	13.81
5VXJ.PDB	O, A_LEU.114	N, A_ALA.117	H, A_ALA.117	2.91	2.07	9.65
5VXJ.PDB	O, A_LYS.119	N, A_GLU.122	H, A_GLU.122	2.96	2.17	19.32
5VXJ.PDB	O, A_SER.130	N, A_LEU.134	H, A_LEU.134	2.99	2.20	18.86
5VXJ.PDB	O, A_TYR.104	NE1, A_TRP.135	HE1, A_TRP.135	2.84	2.08	23.47
5VXJ.PDB	O, A_GLU.133	N, A_LYS.137	H, A_LYS.137	2.97	2.16	17.73
5VXJ.PDB	O, A_LEU.134	N, A_ILE.138	H, A_ILE.138	2.93	2.16	21.74
5VXJ.PDB	O, A_TRP.135	N, A_ALA.139	H, A_ALA.139	2.99	2.16	12.41
5VXJ.PDB	O, A_ALA.136	N, A_ASN.140	H, A_ASN.140	2.89	2.04	5.99
5VXJ.PDB	O, A_LYS.137	N, A_SER.141	H, A_SER.141	2.86	2.11	24.60
5VXJ.PDB	O, A_ALA.121	OG, A_SER.141	HG, A_SER.141	2.90	2.17	24.63
5VXJ.PDB	O, A_ILE.138	N, A_ILE.142	H, A_ILE.142	2.98	2.14	10.65
5VXJ.PDB	O, A_ASN.140	N, A_ASP.144	H, A_ASP.144	2.74	1.94	18.04
5VXJ.PDB	O, A_SER.141	N, A_ILE.145	H, A_ILE.145	2.97	2.12	7.63
5VXJ.PDB	O, A_ASP.144	N, A_GLN.148	H, A_GLN.148	2.73	1.88	8.38
5VXJ.PDB	O, A_ILE.145	N, A_LEU.150	H, A_LEU.150	2.96	2.11	7.42
5VXJ.PDB	O, A_ASN.146	N, A_LYS.151	H, A_LYS.151	2.96	2.16	18.68
5VXJ.PDB	OE2, A_GLU.229	OH, A_TYR.153	HH, A_TYR.153	2.70	1.94	21.05
5VXJ.PDB	O, A_GLU.154	N, A_SER.158	H, A_SER.158	2.90	2.09	15.89
5VXJ.PDB	O, A_HIS.155	N, A_SER.159	H, A_SER.159	2.80	1.96	9.42
5VXJ.PDB	O, A_VAL.157	N, A_THR.161	H, A_THR.161	2.82	1.98	11.00
5VXJ.PDB	O, A_VAL.157	OG1, A_THR.161	HG1, A_THR.161	2.60	1.90	27.90
5VXJ.PDB	O, A_TYR.160	N, A_TYR.164	H, A_TYR.164	2.91	2.09	14.34
5VXJ.PDB	OD1, A_ASP.287	OH, A_TYR.164	HH, A_TYR.164	2.72	1.96	22.05

5VXJ.PDB	O, A_THR_161	N, A_GLN_165	H, A_GLN_165	2.84	2.05	19.22
5VXJ.PDB	O, A_GLN_162	N, A_ASP_166	H, A_ASP_166	2.94	2.09	8.93
5VXJ.PDB	O, A_MET_163	N, A_PHE_167	H, A_PHE_167	2.91	2.10	17.54
5VXJ.PDB	O, A_TYR_164	N, A_SER_168	H, A_SER_168	2.81	2.03	20.85
5VXJ.PDB	O, A_TYR_164	OG, A_SER_168	HG, A_SER_168	2.89	2.09	13.52
5VXJ.PDB	O, A_SER_168	N, A_SER_172	H, A_SER_172	2.98	2.21	21.86
5VXJ.PDB	O, A_LEU_174	N, A_TRP_177	H, A_TRP_177	2.99	2.26	27.17
5VXJ.PDB	OD1, A_ASP_184	N, A_ASN_186	H, A_ASN_186	2.76	1.91	7.29
5VXJ.PDB	O, A_LEU_271	N, A_VAL_188	H, A_VAL_188	2.87	2.09	19.88
5VXJ.PDB	O, A_SER_179	N, A_LYS_189	H, A_LYS_189	2.61	1.75	6.27
5VXJ.PDB	O, A_VAL_269	N, A_LEU_190	H, A_LEU_190	2.84	2.02	14.05
5VXJ.PDB	O, A_TRP_177	N, A_GLN_191	H, A_GLN_191	2.95	2.15	19.06
5VXJ.PDB	OE2, A_GLU_268	NE2, A_GLN_191	HE22, A_GLN_191	2.93	2.12	16.99
5VXJ.PDB	O, A_VAL_192	N, A_LYS_196	H, A_LYS_196	2.67	1.82	7.56
5VXJ.PDB	O, A_ASN_193	N, A_LYS_197	H, A_LYS_197	2.75	1.93	14.74
5VXJ.PDB	O, A_LYS_196	N, A_GLU_200	H, A_GLU_200	2.98	2.16	13.97
5VXJ.PDB	O, A_ALA_198	N, A_LEU_202	H, A_LEU_202	2.92	2.14	21.59
5VXJ.PDB	OD1, A_ASP_254	NZ, A_LYS_203	HZ2, A_LYS_203	2.48	1.62	10.37
5VXJ.PDB	O, A_GLU_201	N, A_LYS_205	H, A_LYS_205	2.84	2.05	19.85
5VXJ.PDB	OD2, A_ASP_166	NZ, A_LYS_205	HZ2, A_LYS_205	2.60	1.73	10.82
5VXJ.PDB	OD2, A_ASP_166	OH, A_TYR_206	HH, A_TYR_206	2.59	1.78	13.29
5VXJ.PDB	O, A_TYR_244	N, A_VAL_218	H, A_VAL_218	2.97	2.15	14.20
5VXJ.PDB	OG, A_SER_219	N, A_GLN_222	H, A_GLN_222	2.99	2.14	8.32
5VXJ.PDB	O, A_SER_219	N, A_ALA_223	H, A_ALA_223	2.98	2.15	10.83
5VXJ.PDB	O, A_GLN_220	N, A_ASN_224	H, A_ASN_224	2.96	2.18	20.88
5VXJ.PDB	O, A_ALA_223	N, A_LEU_227	H, A_LEU_227	2.92	2.16	24.23
5VXJ.PDB	O, A_TRP_226	N, A_LEU_230	H, A_LEU_230	2.82	1.96	5.43
5VXJ.PDB	O, A_LEU_227	N, A_GLY_231	H, A_GLY_231	2.79	1.94	7.11
5VXJ.PDB	O, A_VAL_245	N, A_SER_238	H, A_SER_238	2.93	2.14	18.31
5VXJ.PDB	O, A_SER_238	N, A_VAL_245	H, A_VAL_245	2.90	2.09	17.18
5VXJ.PDB	O, A_TYR_212	N, A_VAL_246	H, A_VAL_246	2.63	1.77	2.37
5VXJ.PDB	O, A_LYS_236	N, A_SER_247	H, A_SER_247	2.73	1.99	25.54
5VXJ.PDB	O, A_ILE_234	N, A_ASN_249	H, A_ASN_249	2.99	2.14	5.52
5VXJ.PDB	OD1, A_ASN_249	N, A_THR_251	H, A_THR_251	2.98	2.14	12.09
5VXJ.PDB	OD1, A_ASN_249	OG1, A_THR_251	HG1, A_THR_251	2.61	1.88	24.99
5VXJ.PDB	O, A_THR_251	N, A_ASN_255	H, A_ASN_255	2.72	1.90	15.38
5VXJ.PDB	O, A_PRO_252	N, A_MET_256	H, A_MET_256	2.93	2.09	10.06
5VXJ.PDB	O, A_ILE_253	N, A_LEU_257	H, A_LEU_257	2.89	2.11	21.11
5VXJ.PDB	O, A_ASP_254	N, A_LYS_258	H, A_LYS_258	2.89	2.05	10.53
5VXJ.PDB	O, A_ASN_255	N, A_SER_259	H, A_SER_259	2.85	2.05	18.21
5VXJ.PDB	O, A_MET_256	N, A_LEU_260	H, A_LEU_260	2.88	2.06	15.58
5VXJ.PDB	O, A_LEU_260	N, A_LEU_263	H, A_LEU_263	2.93	2.08	8.28
5VXJ.PDB	O, A_VAL_188	N, A_LEU_271	H, A_LEU_271	2.79	1.96	13.97
5VXJ.PDB	OD1, A_ASP_272	N, A_LYS_275	H, A_LYS_275	2.71	1.87	8.42
5VXJ.PDB	O, A_ASP_272	N, A_TYR_276	H, A_TYR_276	2.96	2.18	20.66
5VXJ.PDB	O, A_ASN_273	N, A_GLN_277	H, A_GLN_277	2.93	2.09	9.71
5VXJ.PDB	O, A_ALA_274	N, A_ALA_278	H, A_ALA_278	2.97	2.14	12.65
5VXJ.PDB	O, A_TYR_276	N, A_ASN_280	H, A_ASN_280	2.81	1.95	2.97
5VXJ.PDB	O, A_GLN_277	N, A_ALA_281	H, A_ALA_281	2.86	2.07	19.09
5VXJ.PDB	O, A_TRP_279	N, A_PHE_283	H, A_PHE_283	2.88	2.07	15.81
5VXJ.PDB	O, A_ASN_280	N, A_SER_284	H, A_SER_284	2.76	1.91	8.04
5VXJ.PDB	O, A_ASN_280	OG, A_SER_284	HG, A_SER_284	2.99	2.26	24.82
5VXJ.PDB	O, A_ALA_281	N, A_ALA_285	H, A_ALA_285	2.96	2.19	22.09
5VXJ.PDB	O, A_SER_284	N, A_GLU_288	H, A_GLU_288	2.97	2.15	15.81
5VXJ.PDB	O, A_ALA_285	N, A_THR_289	H, A_THR_289	2.87	2.12	24.45
5VXJ.PDB	O, A_ALA_285	OG1, A_THR_289	HG1, A_THR_289	2.86	2.03	7.57
5VXJ.PDB	O, A_ASP_287	N, A_LYS_291	H, A_LYS_291	2.93	2.09	9.56
5VXJ.PDB	O, A_GLU_288	N, A_ASN_292	H, A_ASN_292	2.87	2.05	14.52

5VXJ.PDB	O, A_THR_289	N, A_ASN_293	H, A_ASN_293	2.90	2.09	17.21
5VXJ.PDB	O, A_MET_290	N, A_LEU_294	H, A_LEU_294	2.92	2.07	7.82
5VXJ.PDB	O, A_LYS_291	N, A_GLN_295	H, A_GLN_295	2.99	2.14	9.97
5VXJ.PDB	O, A_ASN_292	N, A_THR_296	H, A_THR_296	2.84	2.08	24.09
5VXJ.PDB	O, A_LEU_294	N, A_VAL_298	H, A_VAL_298	2.91	2.08	13.79
5VXJ.PDB	O, A_LEU_297	N, A_TYR_301	H, A_TYR_301	2.90	2.05	7.11
5VXJ.PDB	O, A_VAL_298	N, A_SER_302	H, A_SER_302	2.79	1.95	9.28
5VXJ.PDB	O, A_GLN_299	N, A_ASN_303	H, A_ASN_303	2.74	1.90	10.18
5VXJ.PDB	O, A_LYS_300	N, A_ALA_304	H, A_ALA_304	2.86	2.05	16.63
5VXJ.PDB	O, A_TYR_301	N, A_ASN_305	H, A_ASN_305	2.97	2.18	19.72
5VXJ.PDB	OD1, A_ASN_58	ND2, A_ASN_305	HD21, A_ASN_305	2.96	2.14	16.38
5VXJ.PDB	O, A_ALA_304	N, A_PHE_308	H, A_PHE_308	2.88	2.04	10.22
5VXJ.PDB	O, A_ASN_305	N, A_ASP_309	H, A_ASP_309	2.74	1.94	18.74
5VXJ.PDB	O, A_SER_306	N, A_ASN_310	H, A_ASN_310	2.77	1.99	20.96
5VXJ.PDB	O, A_ASP_309	N, A_LYS_313	H, A_LYS_313	2.88	2.04	10.21
5VXJ.PDB	O, A_ASN_310	N, A_VAL_314	H, A_VAL_314	2.93	2.11	13.42
5VXJ.PDB	O, A_LEU_311	N, A_LEU_315	H, A_LEU_315	2.74	1.89	8.56
5VXJ.PDB	N, A_VAL_312	N, A_SER_316	H, A_SER_316	2.85	2.04	14.90
5VXJ.PDB	O, A_VAL_314	OG1, A_THR_318	HG1, A_THR_318	2.99	2.16	6.68
5VXJ.PDB	O, A_LEU_315	N, A_ILE_319	H, A_ILE_319	2.97	2.18	20.05
5VXJ.PDB	O, A_SER_316	N, A_SER_320	H, A_SER_320	3.00	2.17	14.20
5VXJ.PDB	O, A_THR_318	OG, A_SER_322	HG, A_SER_322	2.97	2.21	21.62
5VXJ.PDB	O, B_SER_25	N, B_GLN_3	H, B_GLN_3	2.86	2.03	13.37
5VXJ.PDB	O, B_ALA_23	N, B_ALA_5	H, B_ALA_5	2.95	2.16	20.65
5VXJ.PDB	O, B_GLN_114	N, B_GLY_10	H, B_GLY_10	2.78	1.93	4.26
5VXJ.PDB	O, B_THR_116	N, B_ALA_12	H, B_ALA_12	2.97	2.27	29.86
5VXJ.PDB	O, B_LEU_86	N, B_GLY_15	H, B_GLY_15	2.80	1.97	12.25
5VXJ.PDB	O, B_GLN_13	N, B_GLY_16	H, B_GLY_16	2.89	2.07	14.89
5VXJ.PDB	O, B_MET_83	N, B_LEU_18	H, B_LEU_18	2.81	2.01	18.59
5VXJ.PDB	OE1, B_GLN_82	NE, B_ARG_19	HE, B_ARG_19	2.47	1.66	15.76
5VXJ.PDB	O, B_THR_7	N, B_SER_21	H, B_SER_21	2.89	2.13	23.79
5VXJ.PDB	O, B_VAL_79	N, B_CYS_22	H, B_CYS_22	2.97	2.22	24.17
5VXJ.PDB	O, B_ALA_5	N, B_ALA_23	H, B_ALA_23	2.85	2.01	10.80
5VXJ.PDB	O, B_ASN_77	N, B_ALA_24	H, B_ALA_24	2.89	2.04	8.57
5VXJ.PDB	O, B_THR_28	N, B_ARG_31	H, B_ARG_31	2.95	2.13	14.81
5VXJ.PDB	O, B_GLY_99	N, B_VAL_33	H, B_VAL_33	2.85	2.06	20.75
5VXJ.PDB	O, B_ASN_97	N, B_ASN_35	H, B_ASN_35	2.73	1.92	16.35
5VXJ.PDB	O, B_VAL_95	N, B_TYR_37	H, B_TYR_37	2.74	1.89	6.02
5VXJ.PDB	OE2, B_GLU_46	NE, B_ARG_38	HE, B_ARG_38	2.93	2.12	17.64
5VXJ.PDB	OH, B_TYR_94	NH1, B_ARG_38	HH11, B_ARG_38	2.80	1.98	13.19
5VXJ.PDB	OD1, B_ASP_90	NH1, B_ARG_38	HH12, B_ARG_38	2.76	1.91	7.08
5VXJ.PDB	O, B_ARG_38	N, B_GLU_46	H, B_GLU_46	2.92	2.08	10.18
5VXJ.PDB	O, B_TRP_36	N, B_VAL_48	H, B_VAL_48	2.83	2.04	19.58
5VXJ.PDB	OD1, B_ASN_35	NE, B_ARG_50	HE, B_ARG_50	2.65	1.82	11.22
5VXJ.PDB	OE1, I_GLU_200	NH1, B_ARG_50	HH12, B_ARG_50	2.92	2.07	7.25
5VXJ.PDB	O, B_SER_30	OH, B_TYR_52	HH, B_TYR_52	2.72	1.93	15.55
5VXJ.PDB	OD1, B_ASP_53	N, B_GLY_55	H, B_GLY_55	2.72	1.91	16.35
5VXJ.PDB	O, B_ARG_50	N, B_SER_59	H, B_SER_59	2.55	1.72	12.05
5VXJ.PDB	O, B_VAL_48	N, B_ALA_61	H, B_ALA_61	2.78	1.92	5.65
5VXJ.PDB	OD2, B_ASP_90	NH1, B_ARG_67	HH12, B_ARG_67	2.82	2.01	16.67
5VXJ.PDB	OD1, B_ASP_90	NH2, B_ARG_67	HH22, B_ARG_67	2.96	2.12	11.06
5VXJ.PDB	O, B_VAL_64	N, B_PHE_68	H, B_PHE_68	2.90	2.06	11.49
5VXJ.PDB	O, B_GLN_82	N, B_THR_69	H, B_THR_69	2.99	2.19	17.88
5VXJ.PDB	O, B_HIS_80	N, B_SER_71	H, B_SER_71	2.98	2.19	19.14
5VXJ.PDB	O, B_ALA_32	NH2, B_ARG_72	HH22, B_ARG_72	2.73	1.87	6.16
5VXJ.PDB	O, B_THR_78	N, B_ASP_73	H, B_ASP_73	2.88	2.03	8.84
5VXJ.PDB	O, B_SER_71	N, B_HIS_80	H, B_HIS_80	2.94	2.16	21.65
5VXJ.PDB	O, B_LEU_20	N, B_LEU_81	H, B_LEU_81	2.93	2.12	17.56

5VXJ.PDB	O, B_THR_69	N, B_GLN_82	H, B_GLN_82	2.77	2.03	25.51
5VXJ.PDB	OD1, B_ASN_84	NE2, B_GLN_82	HE21, B_GLN_82	2.95	2.09	2.81
5VXJ.PDB	O, B_LEU_18	N, B_MET_83	H, B_MET_83	2.63	1.77	6.35
5VXJ.PDB	O, B_LYS_87	N, B_ASP_90	H, B_ASP_90	2.82	2.01	16.00
5VXJ.PDB	O, B_THR_113	N, B_TYR_94	H, B_TYR_94	2.87	2.08	19.12
5VXJ.PDB	O, B_ASP_90	OH, B_TYR_94	HH, B_TYR_94	2.68	1.86	10.06
5VXJ.PDB	O, B_TYR_37	N, B_VAL_95	H, B_VAL_95	3.00	2.17	13.97
5VXJ.PDB	O, B_ASN_35	N, B_ASN_97	H, B_ASN_97	2.80	2.07	26.52
5VXJ.PDB	OG1, B_THR_107	ND2, B_ASN_97	HD21, B_ASN_97	2.64	1.86	19.39
5VXJ.PDB	O, B_VAL_33	N, B_GLY_99	H, B_GLY_99	2.75	1.91	8.60
5VXJ.PDB	O, B_ARG_106	N, B_ILE_100	H, B_ILE_100	2.81	1.95	1.78
5VXJ.PDB	O, B_ASN_104	N, B_ASP_102	H, B_ASP_102	2.92	2.07	4.41
5VXJ.PDB	OE1, I_GLU_201	OH, B_TYR_105	HH, B_TYR_105	2.51	1.70	12.69
5VXJ.PDB	O, B_ALA_98	OG1, B_THR_107	HG1, B_THR_107	2.89	2.18	28.04
5VXJ.PDB	OE1, B_GLU_6	N, B_GLY_112	H, B_GLY_112	2.87	2.05	14.11
5VXJ.PDB	O, B_TYR_94	N, B_THR_113	H, B_THR_113	2.58	1.76	13.84
5VXJ.PDB	O, B_GLY_10	N, B_THR_116	H, B_THR_116	2.97	2.14	11.68
5VXJ.PDB	O, C_THR_45	N, C_ASP_49	H, C_ASP_49	3.00	2.16	11.23
5VXJ.PDB	O, C_MET_46	N, C_THR_50	H, C_THR_50	2.75	1.93	15.42
5VXJ.PDB	O, C_MET_46	OG1, C_THR_50	HG1, C_THR_50	2.84	2.05	16.87
5VXJ.PDB	O, C_LEU_47	N, C_LEU_51	H, C_LEU_51	2.66	1.82	9.17
5VXJ.PDB	OD2, C_ASP_309	NH2, C_ARG_55	HH21, C_ARG_55	2.97	2.17	18.00
5VXJ.PDB	O, C_HIS_52	N, C_THR_56	H, C_THR_56	2.83	2.00	14.10
5VXJ.PDB	O, C_ASN_53	N, C_THR_57	H, C_THR_57	2.88	2.05	12.91
5VXJ.PDB	O, C_ILE_54	N, C_ASN_58	H, C_ASN_58	2.78	2.03	23.87
5VXJ.PDB	O, C_THR_57	N, C_LEU_61	H, C_LEU_61	2.97	2.16	17.22
5VXJ.PDB	O, C_ASN_58	N, C_LYS_62	H, C_LYS_62	2.91	2.07	10.71
5VXJ.PDB	OG, C_SER_302	NZ, C_LYS_62	HZ2, C_LYS_62	2.61	1.73	6.54
5VXJ.PDB	O, C_THR_73	N, C_GLU_77	H, C_GLU_77	2.89	2.05	10.72
5VXJ.PDB	O, C_SER_74	N, C_ILE_78	H, C_ILE_78	2.75	1.91	9.49
5VXJ.PDB	O, C_LEU_75	N, C_ALA_79	H, C_ALA_79	2.88	2.03	7.76
5VXJ.PDB	O, C_GLU_76	N, C_LEU_80	H, C_LEU_80	2.83	1.99	11.70
5VXJ.PDB	O, C_GLU_77	N, C_HIS_81	H, C_HIS_81	2.88	2.03	8.46
5VXJ.PDB	O, C_ILE_78	N, C_SER_82	H, C_SER_82	2.83	2.00	12.85
5VXJ.PDB	OE2, C_GLU_154	OG, C_SER_82	HG, C_SER_82	2.58	1.81	19.25
5VXJ.PDB	O, C_ALA_79	N, C_SER_83	H, C_SER_83	2.82	1.99	12.64
5VXJ.PDB	O, C_HIS_81	N, C_ILE_85	H, C_ILE_85	2.92	2.10	14.49
5VXJ.PDB	O, C_SER_82	N, C_SER_86	H, C_SER_86	2.94	2.09	6.22
5VXJ.PDB	O, C_SER_83	N, C_MET_87	H, C_MET_87	2.90	2.13	22.48
5VXJ.PDB	O, C_ILE_85	N, C_VAL_89	H, C_VAL_89	2.71	1.95	23.99
5VXJ.PDB	O, C_SER_86	N, C_ASN_90	H, C_ASN_90	2.95	2.14	17.73
5VXJ.PDB	O, C_ASP_88	OG, C_SER_92	HG, C_SER_92	2.81	2.10	26.84
5VXJ.PDB	O, C_VAL_89	N, C_ALA_93	H, C_ALA_93	2.99	2.18	16.35
5VXJ.PDB	O, C_ASN_90	N, C_GLN_94	H, C_GLN_94	2.93	2.09	10.71
5VXJ.PDB	O, C_LYS_91	N, C_LEU_95	H, C_LEU_95	2.99	2.16	11.86
5VXJ.PDB	O, C_SER_92	N, C_LEU_96	H, C_LEU_96	2.76	1.91	4.52
5VXJ.PDB	O, C_ALA_93	N, C_ASP_97	H, C_ASP_97	2.67	1.87	17.34
5VXJ.PDB	O, C_GLN_94	N, C_ILE_98	H, C_ILE_98	2.93	2.20	27.48
5VXJ.PDB	O, C_LEU_95	N, C_LEU_99	H, C_LEU_99	2.86	2.06	16.81
5VXJ.PDB	O, C_LEU_96	N, C_SER_100	H, C_SER_100	2.97	2.19	20.79
5VXJ.PDB	O, C_ARG_132	OG, C_SER_100	HG, C_SER_100	2.62	1.83	15.07
5VXJ.PDB	OD2, C_ASP_97	NE, C_ARG_101	HE, C_ARG_101	2.84	2.03	16.71
5VXJ.PDB	O, C_ILE_98	N, C_ASN_102	H, C_ASN_102	2.93	2.10	11.46
5VXJ.PDB	OD1, C_ASN_107	N, C_ALA_110	H, C_ALA_110	2.74	1.90	11.07
5VXJ.PDB	O, C_ILE_106	NE, C_ARG_111	HE, C_ARG_111	2.84	2.08	23.05
5VXJ.PDB	O, C_ILE_129	NH1, C_ARG_111	HH12, C_ARG_111	2.70	1.99	28.89
5VXJ.PDB	O, C_ILE_129	NH2, C_ARG_111	HH22, C_ARG_111	2.67	1.95	27.54
5VXJ.PDB	O, C_LEU_113	N, C_SER_116	H, C_SER_116	2.74	1.92	13.94

5VXJ.PDB	O, C_PRO.118	N, C_ALA.121	H, C_ALA.121	2.93	2.09	9.05
5VXJ.PDB	O, C_LYS.119	N, C_GLU.122	H, C_GLU.122	2.93	2.12	17.73
5VXJ.PDB	O, D_GLY.56	NH2, C_ARG.132	HH22, C_ARG.132	2.97	2.20	22.55
5VXJ.PDB	O, C_SER.130	N, C_LEU.134	H, C_LEU.134	2.95	2.18	22.13
5VXJ.PDB	O, C_HIS.131	N, C_TRP.135	H, C_TRP.135	2.90	2.05	5.85
5VXJ.PDB	O, C_TYR.104	NE1, C_TRP.135	HE1, C_TRP.135	2.72	1.92	17.01
5VXJ.PDB	O, C_TRP.135	N, C_ALA.139	H, C_ALA.139	2.83	1.99	9.11
5VXJ.PDB	O, C_ALA.136	N, C_ASN.140	H, C_ASN.140	2.88	2.08	18.03
5VXJ.PDB	O, C_LYS.137	N, C_SER.141	H, C_SER.141	2.84	2.09	25.00
5VXJ.PDB	O, C_ALA.121	OG, C_SER.141	HG, C_SER.141	2.69	1.99	27.96
5VXJ.PDB	O, C_ASN.140	N, C_ASP.144	H, C_ASP.144	2.68	1.84	11.11
5VXJ.PDB	O, C_SER.141	N, C_ILE.145	H, C_ILE.145	2.98	2.16	13.90
5VXJ.PDB	O, C_ASP.144	N, C_GLN.148	H, C_GLN.148	2.81	1.97	10.25
5VXJ.PDB	O, C_ILE.145	N, C_LEU.150	H, C_LEU.150	2.99	2.16	11.96
5VXJ.PDB	O, C_ASN.146	N, C_LYS.151	H, C_LYS.151	2.89	2.07	15.50
5VXJ.PDB	O, C_TYR.153	N, C_VAL.157	H, C_VAL.157	2.98	2.14	11.48
5VXJ.PDB	O, C_GLU.154	N, C_SER.158	H, C_SER.158	2.91	2.10	16.58
5VXJ.PDB	O, C_HIS.155	N, C_SER.159	H, C_SER.159	2.84	2.04	18.93
5VXJ.PDB	O, C_VAL.157	N, C_THR.161	H, C_THR.161	2.84	2.01	12.19
5VXJ.PDB	O, C_TYR.160	N, C_TYR.164	H, C_TYR.164	2.88	2.06	13.58
5VXJ.PDB	OD1, C_ASP.287	OH, C_TYR.164	HH, C_TYR.164	2.77	1.96	12.03
5VXJ.PDB	O, C_THR.161	N, C_GLN.165	H, C_GLN.165	2.79	1.97	15.66
5VXJ.PDB	O, C_TYR.164	N, C_SER.168	H, C_SER.168	2.76	1.95	16.85
5VXJ.PDB	O, C_TYR.164	OG, C_SER.168	HG, C_SER.168	2.78	1.96	10.71
5VXJ.PDB	O, C_PHE.167	N, C_LEU.171	H, C_LEU.171	2.81	2.03	19.93
5VXJ.PDB	O, C_SER.168	N, C_SER.172	H, C_SER.172	2.88	2.13	25.56
5VXJ.PDB	O, C_LEU.271	N, C_VAL.188	H, C_VAL.188	2.99	2.14	7.19
5VXJ.PDB	O, C_SER.179	N, C_LYS.189	H, C_LYS.189	2.75	1.90	6.70
5VXJ.PDB	O, C_VAL.269	N, C_LEU.190	H, C_LEU.190	2.85	2.06	18.77
5VXJ.PDB	O, C_TRP.177	N, C_GLN.191	H, C_GLN.191	2.92	2.10	14.50
5VXJ.PDB	OE2, C_GLU.268	NE2, C_GLN.191	HE22, C_GLN.191	2.80	1.97	12.09
5VXJ.PDB	O, C_VAL.192	N, C_LYS.196	H, C_LYS.196	2.64	1.80	8.82
5VXJ.PDB	O, C_ASN.193	N, C_LYS.197	H, C_LYS.197	2.77	1.95	14.40
5VXJ.PDB	OE1, C_GLU.201	NZ, C_LYS.197	HZ3, C_LYS.197	2.59	1.85	27.46
5VXJ.PDB	O, C_LYS.196	N, C_GLU.200	H, C_GLU.200	2.98	2.14	10.98
5VXJ.PDB	O, C_ALA.198	N, C_LEU.202	H, C_LEU.202	2.84	2.10	25.29
5VXJ.PDB	OD1, C_ASP.254	NZ, C_LYS.203	HZ2, C_LYS.203	2.69	1.87	19.49
5VXJ.PDB	O, C_GLU.201	N, C_LYS.205	H, C_LYS.205	2.93	2.15	21.77
5VXJ.PDB	OD2, C_ASP.166	NZ, C_LYS.205	HZ2, C_LYS.205	2.85	1.99	12.15
5VXJ.PDB	OD2, C_ASP.166	OH, C_TYR.206	HH, C_TYR.206	2.58	1.76	10.37
5VXJ.PDB	O, C_TYR.244	N, C_VAL.218	H, C_VAL.218	2.89	2.05	9.55
5VXJ.PDB	O, C_SER.219	N, C_ALA.223	H, C_ALA.223	2.91	2.08	14.53
5VXJ.PDB	O, C_GLN.220	N, C_ASN.224	H, C_ASN.224	2.98	2.12	5.55
5VXJ.PDB	O, C_GLN.220	ND2, C_ASN.224	HD22, C_ASN.224	2.76	2.00	23.07
5VXJ.PDB	O, C_GLU.221	N, C_LYS.225	H, C_LYS.225	2.88	2.10	20.87
5VXJ.PDB	O, C_ALA.223	N, C_LEU.227	H, C_LEU.227	2.84	2.04	17.85
5VXJ.PDB	O, C_TRP.226	N, C_LEU.230	H, C_LEU.230	2.93	2.16	22.32
5VXJ.PDB	O, C_LEU.227	N, C_GLY.231	H, C_GLY.231	2.79	1.97	15.24
5VXJ.PDB	O, C_SER.247	N, C_LYS.236	H, C_LYS.236	2.90	2.15	23.83
5VXJ.PDB	O, C_VAL.245	N, C_SER.238	H, C_SER.238	2.96	2.16	18.06
5VXJ.PDB	O, C_SER.238	N, C_VAL.245	H, C_VAL.245	2.79	1.99	18.55
5VXJ.PDB	O, C_TYR.212	N, C_VAL.246	H, C_VAL.246	2.73	1.88	6.99
5VXJ.PDB	O, C_ILE.234	N, C_ASN.249	H, C_ASN.249	2.93	2.08	8.15
5VXJ.PDB	OD1, C_ASN.249	N, C_THR.251	H, C_THR.251	2.83	2.01	13.51
5VXJ.PDB	OD1, C_ASN.249	OG1, C_THR.251	HG1, C_THR.251	2.56	1.78	18.84
5VXJ.PDB	O, C_MET.250	N, C_ASP.254	H, C_ASP.254	2.97	2.14	14.27
5VXJ.PDB	O, C_THR.251	N, C_ASN.255	H, C_ASN.255	2.90	2.11	19.57
5VXJ.PDB	O, C_ASN.255	N, C_SER.259	H, C_SER.259	2.82	1.98	10.57

5VXJ.PDB	O, C_LEU_257	N, C_ASP_261	H, C_ASP_261	2.89	2.05	9.73
5VXJ.PDB	O, C_VAL_188	N, C_LEU_271	H, C_LEU_271	2.72	1.88	10.23
5VXJ.PDB	OD1, C_ASP_272	N, C_LYS_275	H, C_LYS_275	2.76	1.96	18.08
5VXJ.PDB	O, C_ASP_272	N, C_TYR_276	H, C_TYR_276	2.98	2.15	12.87
5VXJ.PDB	O, C_ASN_273	N, C_GLN_277	H, C_GLN_277	2.97	2.12	5.77
5VXJ.PDB	O, C_LYS_275	N, C_TRP_279	H, C_TRP_279	3.00	2.19	17.09
5VXJ.PDB	O, C_TYR_276	N, C_ASN_280	H, C_ASN_280	2.84	2.00	8.68
5VXJ.PDB	O, C_GLN_277	N, C_ALA_281	H, C_ALA_281	2.95	2.16	19.58
5VXJ.PDB	O, C_TRP_279	N, C_PHE_283	H, C_PHE_283	2.80	1.97	11.54
5VXJ.PDB	O, C_ASN_280	N, C_SER_284	H, C_SER_284	2.86	2.05	17.29
5VXJ.PDB	O, C_ALA_281	N, C_ALA_285	H, C_ALA_285	2.97	2.22	25.52
5VXJ.PDB	O, C_SER_284	N, C_GLU_288	H, C_GLU_288	2.90	2.09	16.06
5VXJ.PDB	O, C_ASP_287	N, C_LYS_291	H, C_LYS_291	2.96	2.16	17.42
5VXJ.PDB	O, C_GLU_288	N, C_ASN_292	H, C_ASN_292	2.78	1.93	7.30
5VXJ.PDB	O, C_MET_290	N, C_LEU_294	H, C_LEU_294	2.96	2.14	14.65
5VXJ.PDB	O, C_LYS_291	N, C_GLN_295	H, C_GLN_295	2.93	2.08	7.49
5VXJ.PDB	O, C_ASN_292	N, C_THR_296	H, C_THR_296	2.81	1.96	6.25
5VXJ.PDB	O, C_ASN_293	N, C_LEU_297	H, C_LEU_297	2.87	2.03	9.84
5VXJ.PDB	O, C_LEU_294	N, C_VAL_298	H, C_VAL_298	2.89	2.07	16.24
5VXJ.PDB	O, C_GLN_295	N, C_GLN_299	H, C_GLN_299	2.96	2.18	20.39
5VXJ.PDB	O, C_THR_296	N, C_LYS_300	H, C_LYS_300	2.95	2.12	12.60
5VXJ.PDB	O, C_VAL_298	N, C_SER_302	H, C_SER_302	2.91	2.17	26.05
5VXJ.PDB	O, C_GLN_299	N, C_ASN_303	H, C_ASN_303	2.83	2.01	12.96
5VXJ.PDB	O, C_LYS_300	N, C_ALA_304	H, C_ALA_304	2.95	2.16	19.44
5VXJ.PDB	OD1, C_ASN_58	ND2, C_ASN_305	HD21, C_ASN_305	2.84	2.04	17.79
5VXJ.PDB	O, C_ALA_304	N, C_PHE_308	H, C_PHE_308	2.91	2.07	9.64
5VXJ.PDB	O, C_ASN_305	N, C_ASP_309	H, C_ASP_309	2.81	2.07	26.01
5VXJ.PDB	O, C_SER_306	N, C_ASN_310	H, C_ASN_310	2.67	1.91	23.54
5VXJ.PDB	O, C_ASP_309	N, C_LYS_313	H, C_LYS_313	2.90	2.07	12.85
5VXJ.PDB	O, C_ASN_310	N, C_VAL_314	H, C_VAL_314	2.90	2.06	10.88
5VXJ.PDB	O, C_LEU_311	N, C_LEU_315	H, C_LEU_315	2.75	1.90	6.64
5VXJ.PDB	O, C_VAL_312	N, C_SER_316	H, C_SER_316	2.93	2.11	14.92
5VXJ.PDB	O, C_VAL_314	OG, C_SER_317	HG, C_SER_317	2.65	1.90	22.58
5VXJ.PDB	O, C_LEU_315	OG1, C_THR_318	HG1, C_THR_318	2.63	1.83	14.36
5VXJ.PDB	O, D_SER_25	N, D_GLN_3	H, D_GLN_3	2.83	2.04	19.53
5VXJ.PDB	O, D_ALA_23	N, D_ALA_5	H, D_ALA_5	2.92	2.12	17.92
5VXJ.PDB	O, D_SER_21	N, D_THR_7	H, D_THR_7	2.92	2.12	17.84
5VXJ.PDB	O, D_GLN_114	N, D_GLY_10	H, D_GLY_10	2.92	2.10	13.53
5VXJ.PDB	O, D_THR_116	N, D_ALA_12	H, D_ALA_12	2.90	2.14	23.36
5VXJ.PDB	O, D_LEU_86	N, D_GLY_15	H, D_GLY_15	2.64	1.81	11.28
5VXJ.PDB	O, D_GLN_13	N, D_GLY_16	H, D_GLY_16	2.82	2.06	23.83
5VXJ.PDB	O, D_MET_83	N, D_LEU_18	H, D_LEU_18	2.89	2.09	18.27
5VXJ.PDB	OD1, C_ASN_140	NE, D_ARG_19	HE, D_ARG_19	2.55	1.80	23.66
5VXJ.PDB	OE1, D_GLN_82	NH1, D_ARG_19	HH11, D_ARG_19	2.94	2.14	18.04
5VXJ.PDB	O, D_THR_7	N, D_SER_21	H, D_SER_21	2.99	2.14	7.08
5VXJ.PDB	O, D_ALA_5	N, D_ALA_23	H, D_ALA_23	2.87	2.03	10.49
5VXJ.PDB	O, D_ASN_77	N, D_ALA_24	H, D_ALA_24	2.92	2.08	9.76
5VXJ.PDB	O, D_THR_28	N, D_ARG_31	H, D_ARG_31	2.98	2.15	11.20
5VXJ.PDB	O, D_GLY_99	N, D_VAL_33	H, D_VAL_33	2.95	2.15	17.67
5VXJ.PDB	O, D_ASN_97	N, D_ASN_35	H, D_ASN_35	2.69	1.87	14.00
5VXJ.PDB	O, D_VAL_95	N, D_TYR_37	H, D_TYR_37	2.62	1.77	8.93
5VXJ.PDB	O, D_GLU_46	N, D_ARG_38	H, D_ARG_38	2.97	2.17	18.09
5VXJ.PDB	OE2, D_GLU_46	NE, D_ARG_38	HE, D_ARG_38	2.46	1.69	20.96
5VXJ.PDB	OD1, D_ASP_90	NH1, D_ARG_38	HH12, D_ARG_38	2.86	2.04	15.32
5VXJ.PDB	O, D_ARG_38	N, D_GLU_46	H, D_GLU_46	2.89	2.05	10.29
5VXJ.PDB	O, D_TRP_36	N, D_VAL_48	H, D_VAL_48	2.77	1.94	12.94
5VXJ.PDB	OD1, D_ASN_35	NE, D_ARG_50	HE, D_ARG_50	2.89	2.08	17.01
5VXJ.PDB	O, D_SER_30	OH, D_TYR_52	HH, D_TYR_52	2.65	1.82	6.70

5VXJ.PDB	OD1, D_ASP_53	N, D_GLY_55	H, D_GLY_55	2.89	2.10	19.66
5VXJ.PDB	O, D_ASP_53	N, D_GLY_56	H, D_GLY_56	2.97	2.13	9.23
5VXJ.PDB	O, D_ARG_50	N, D_SER_59	H, D_SER_59	2.64	1.81	11.93
5VXJ.PDB	O, D_VAL_48	N, D_ALA_61	H, D_ALA_61	2.74	1.98	23.42
5VXJ.PDB	OD2, D_ASP_90	NH1, D_ARG_67	HH12, D_ARG_67	2.76	1.94	14.49
5VXJ.PDB	OD1, D_ASP_90	NH2, D_ARG_67	HH22, D_ARG_67	2.92	2.07	6.62
5VXJ.PDB	O, D_VAL_64	N, D_PHE_68	H, D_PHE_68	2.99	2.19	16.85
5VXJ.PDB	O, D_GLN_82	N, D_THR_69	H, D_THR_69	2.99	2.18	16.88
5VXJ.PDB	O, D_HIS_80	N, D_SER_71	H, D_SER_71	2.95	2.13	13.86
5VXJ.PDB	OD1, D_ASN_74	NE, D_ARG_72	HE, D_ARG_72	2.76	1.91	6.10
5VXJ.PDB	O, D_THR_78	N, D_ASP_73	H, D_ASP_73	2.97	2.14	12.70
5VXJ.PDB	OD1, D_ASP_73	N, D_LYS_76	H, D_LYS_76	2.99	2.16	13.54
5VXJ.PDB	O, D_LEU_20	N, D_LEU_81	H, D_LEU_81	2.96	2.19	22.26
5VXJ.PDB	OD1, D_ASN_84	NE2, D_GLN_82	HE21, D_GLN_82	2.80	1.94	4.20
5VXJ.PDB	O, D_LEU_18	N, D_MET_83	H, D_MET_83	2.68	1.83	7.86
5VXJ.PDB	O, D_ARG_67	N, D_ASN_84	H, D_ASN_84	2.94	2.13	15.75
5VXJ.PDB	O, D_LYS_87	N, D_ASP_90	H, D_ASP_90	2.78	1.93	7.73
5VXJ.PDB	O, D_VAL_115	N, D_ALA_92	H, D_ALA_92	2.97	2.20	22.44
5VXJ.PDB	O, D_THR_113	N, D_TYR_94	H, D_TYR_94	2.96	2.15	16.57
5VXJ.PDB	O, D_ASP_90	OH, D_TYR_94	HH, D_TYR_94	2.94	2.12	10.43
5VXJ.PDB	O, D_TYR_37	N, D_VAL_95	H, D_VAL_95	2.83	2.02	15.84
5VXJ.PDB	O, D_ASN_35	N, D_ASN_97	H, D_ASN_97	2.86	2.07	19.41
5VXJ.PDB	OG1, D_THR_107	ND2, D_ASN_97	HD21, D_ASN_97	2.71	1.91	17.78
5VXJ.PDB	O, D_VAL_33	N, D_GLY_99	H, D_GLY_99	2.78	1.95	12.57
5VXJ.PDB	O, D_ARG_106	N, D_ILE_100	H, D_ILE_100	2.91	2.05	5.49
5VXJ.PDB	O, D_ARG_31	N, D_PHE_101	H, D_PHE_101	2.74	1.90	10.09
5VXJ.PDB	OE1, E_GLU_201	OH, D_TYR_105	HH, D_TYR_105	2.53	1.70	8.84
5VXJ.PDB	O, D_ALA_98	OG1, D_THR_107	HG1, D_THR_107	2.97	2.23	23.46
5VXJ.PDB	O, D_TYR_94	N, D_THR_113	H, D_THR_113	2.79	1.97	15.52
5VXJ.PDB	O, D_GLY_8	OG1, D_THR_113	HG1, D_THR_113	2.58	1.83	22.66
5VXJ.PDB	O, D_ALA_92	N, D_VAL_115	H, D_VAL_115	2.94	2.08	3.33
5VXJ.PDB	O, D_ALA_12	N, D_SER_118	H, D_SER_118	2.88	2.09	19.39
5VXJ.PDB	O, E_SER_42	OG1, E_THR_45	HG1, E_THR_45	2.81	2.08	25.17
5VXJ.PDB	O, E_SER_43	N, E_LEU_47	H, E_LEU_47	2.99	2.22	22.05
5VXJ.PDB	O, E_LEU_44	N, E_ASN_48	H, E_ASN_48	2.99	2.18	16.94
5VXJ.PDB	O, E_LEU_47	N, E_LEU_51	H, E_LEU_51	2.95	2.10	6.68
5VXJ.PDB	O, E_ASP_49	N, E_ASN_53	H, E_ASN_53	2.84	2.02	14.73
5VXJ.PDB	O, E_THR_50	N, E_ILE_54	H, E_ILE_54	2.90	2.13	22.19
5VXJ.PDB	OD2, E_ASP_309	NH2, E_ARG_55	HH21, E_ARG_55	2.82	2.06	24.28
5VXJ.PDB	O, E_HIS_52	N, E_THR_56	H, E_THR_56	2.95	2.14	17.58
5VXJ.PDB	O, E_ILE_54	N, E_ASN_58	H, E_ASN_58	2.86	2.04	14.78
5VXJ.PDB	O, E_THR_57	N, E_LEU_61	H, E_LEU_61	2.88	2.07	15.00
5VXJ.PDB	O, E_ASN_58	N, E_LYS_62	H, E_LYS_62	2.72	1.87	6.56
5VXJ.PDB	OG, E_SER_306	NZ, E_LYS_62	HZ1, E_LYS_62	2.46	1.61	13.80
5VXJ.PDB	O, E_GLN_59	N, E_LYS_63	H, E_LYS_63	2.92	2.13	20.33
5VXJ.PDB	OG, E_SER_74	N, E_THR_71	H, E_THR_71	2.92	2.17	24.42
5VXJ.PDB	O, E_THR_73	N, E_GLU_77	H, E_GLU_77	2.99	2.15	11.35
5VXJ.PDB	O, E_LEU_75	N, E_ALA_79	H, E_ALA_79	2.96	2.12	10.44
5VXJ.PDB	O, E_GLU_76	N, E_LEU_80	H, E_LEU_80	2.99	2.17	14.62
5VXJ.PDB	O, E_GLU_77	N, E_HIS_81	H, E_HIS_81	2.87	2.01	3.03
5VXJ.PDB	O, E_ILE_78	N, E_SER_82	H, E_SER_82	2.71	1.88	13.72
5VXJ.PDB	O, E_ALA_79	N, E_SER_83	H, E_SER_83	2.74	1.90	10.07
5VXJ.PDB	O, E_LEU_80	N, E_GLN_84	H, E_GLN_84	2.86	2.13	27.19
5VXJ.PDB	O, E_HIS_81	N, E_ILE_85	H, E_ILE_85	2.94	2.14	18.50
5VXJ.PDB	O, E_ILE_85	N, E_VAL_89	H, E_VAL_89	2.68	1.84	9.90
5VXJ.PDB	O, E_SER_86	N, E_ASN_90	H, E_ASN_90	2.92	2.12	17.55
5VXJ.PDB	O, E_ASP_88	N, E_SER_92	H, E_SER_92	2.75	1.92	13.99
5VXJ.PDB	O, E_VAL_89	N, E_ALA_93	H, E_ALA_93	2.83	2.00	12.43

5VXJ.PDB	O, E_ASN_90	N, E_GLN_94	H, E_GLN_94	2.83	2.00	12.46
5VXJ.PDB	O, E_LYS_91	N, E_LEU_95	H, E_LEU_95	2.99	2.16	12.05
5VXJ.PDB	O, E_SER_92	N, E_LEU_96	H, E_LEU_96	2.76	1.90	1.16
5VXJ.PDB	O, E_ALA_93	N, E_ASP_97	H, E_ASP_97	2.76	2.00	23.32
5VXJ.PDB	O, E_ARG_132	OG, E_SER_100	HG, E_SER_100	2.69	1.91	17.95
5VXJ.PDB	O, E_ILE_98	N, E_ASN_102	H, E_ASN_102	2.86	2.01	8.88
5VXJ.PDB	O, E_SER_100	N, E_GLU_103	H, E_GLU_103	2.97	2.19	21.11
5VXJ.PDB	O, E_LEU_99	N, E_TYR_104	H, E_TYR_104	2.98	2.17	15.50
5VXJ.PDB	OD1, E_ASN_107	N, E_ALA_110	H, E_ALA_110	2.69	1.84	7.11
5VXJ.PDB	O, E_ILE_106	NE, E_ARG_111	HE, E_ARG_111	2.78	2.02	23.50
5VXJ.PDB	O, E_LEU_113	OG, E_SER_116	HG, E_SER_116	2.58	1.78	13.78
5VXJ.PDB	O, E_LEU_114	N, E_ALA_117	H, E_ALA_117	2.86	2.02	11.54
5VXJ.PDB	O, E_PRO_118	N, E_ALA_121	H, E_ALA_121	2.98	2.15	11.22
5VXJ.PDB	O, E_LYS_119	N, E_GLU_122	H, E_GLU_122	2.92	2.14	21.73
5VXJ.PDB	O, E_TYR_104	NE1, E_TRP_135	HE1, E_TRP_135	2.71	1.94	22.95
5VXJ.PDB	O, E_GLU_133	N, E_LYS_137	H, E_LYS_137	2.86	2.07	19.63
5VXJ.PDB	OD2, F_ASP_73	NZ, E_LYS_137	HZ2, E_LYS_137	2.77	1.96	20.15
5VXJ.PDB	O, E_LEU_134	N, E_ILE_138	H, E_ILE_138	2.98	2.17	17.01
5VXJ.PDB	O, E_TRP_135	N, E_ALA_139	H, E_ALA_139	2.97	2.13	10.92
5VXJ.PDB	O, E_ALA_136	N, E_ASN_140	H, E_ASN_140	2.93	2.08	7.93
5VXJ.PDB	O, E_LYS_137	N, E_SER_141	H, E_SER_141	2.81	2.07	25.81
5VXJ.PDB	O, E_ALA_121	OG, E_SER_141	HG, E_SER_141	2.98	2.28	28.49
5VXJ.PDB	O, E_ASN_140	N, E_ASP_144	H, E_ASP_144	2.69	1.88	16.68
5VXJ.PDB	O, E_SER_141	N, E_ILE_145	H, E_ILE_145	2.84	2.00	9.07
5VXJ.PDB	O, E_ASP_144	N, E_GLN_148	H, E_GLN_148	2.78	1.95	12.00
5VXJ.PDB	O, E_ILE_145	N, E_LEU_150	H, E_LEU_150	2.93	2.08	9.20
5VXJ.PDB	O, E_ASN_146	N, E_LYS_151	H, E_LYS_151	2.91	2.08	12.08
5VXJ.PDB	O, E_TYR_153	N, E_VAL_157	H, E_VAL_157	2.91	2.06	8.11
5VXJ.PDB	O, E_GLU_154	N, E_SER_158	H, E_SER_158	2.80	1.95	8.74
5VXJ.PDB	O, E_HIS_155	N, E_SER_159	H, E_SER_159	2.71	1.87	11.62
5VXJ.PDB	O, E_ALA_156	N, E_TYR_160	H, E_TYR_160	2.93	2.08	7.60
5VXJ.PDB	O, E_VAL_157	N, E_THR_161	H, E_THR_161	2.81	1.98	13.79
5VXJ.PDB	O, E_VAL_157	OG1, E_THR_161	HG1, E_THR_161	2.55	1.80	22.47
5VXJ.PDB	O, E_TYR_160	N, E_TYR_164	H, E_TYR_164	3.00	2.18	15.88
5VXJ.PDB	OD1, E_ASP_287	OH, E_TYR_164	HH, E_TYR_164	2.85	2.09	21.13
5VXJ.PDB	O, E_THR_161	N, E_GLN_165	H, E_GLN_165	2.75	1.91	9.80
5VXJ.PDB	O, E_LEU_70	NE2, E_GLN_165	HE21, E_GLN_165	2.84	2.05	19.77
5VXJ.PDB	O, E_GLN_162	N, E_ASP_166	H, E_ASP_166	2.97	2.14	14.36
5VXJ.PDB	O, E_MET_163	N, E_PHE_167	H, E_PHE_167	2.92	2.13	18.67
5VXJ.PDB	O, E_TYR_164	N, E_SER_168	H, E_SER_168	2.77	1.96	15.85
5VXJ.PDB	O, E_TYR_164	OG, E_SER_168	HG, E_SER_168	2.89	2.07	10.15
5VXJ.PDB	O, E_PHE_167	N, E_LEU_171	H, E_LEU_171	2.80	2.00	18.45
5VXJ.PDB	O, E_SER_168	N, E_SER_172	H, E_SER_172	2.82	2.04	21.33
5VXJ.PDB	O, D_TYR_105	OG, E_SER_173	HG, E_SER_173	2.87	2.17	28.40
5VXJ.PDB	O, E_LEU_271	N, E_VAL_188	H, E_VAL_188	2.72	1.89	11.17
5VXJ.PDB	O, E_SER_179	N, E_LYS_189	H, E_LYS_189	2.74	1.89	6.16
5VXJ.PDB	O, E_VAL_269	N, E_LEU_190	H, E_LEU_190	2.84	2.05	20.49
5VXJ.PDB	O, E_TRP_177	N, E_GLN_191	H, E_GLN_191	2.94	2.12	14.86
5VXJ.PDB	O, E_VAL_192	N, E_LYS_196	H, E_LYS_196	2.75	1.91	8.80
5VXJ.PDB	O, E_ASN_193	N, E_LYS_197	H, E_LYS_197	2.71	1.85	6.12
5VXJ.PDB	OD1, D_ASN_97	NZ, E_LYS_197	HZ1, E_LYS_197	2.80	1.95	14.72
5VXJ.PDB	OE2, E_GLU_201	NZ, E_LYS_197	HZ3, E_LYS_197	2.47	1.71	25.42
5VXJ.PDB	O, E_LEU_195	N, E_LEU_199	H, E_LEU_199	3.00	2.17	13.11
5VXJ.PDB	O, E_LYS_196	N, E_GLU_200	H, E_GLU_200	2.76	1.92	10.71
5VXJ.PDB	O, E_ALA_198	N, E_LEU_202	H, E_LEU_202	2.95	2.17	21.29
5VXJ.PDB	OD1, E_ASP_254	NZ, E_LYS_203	HZ2, E_LYS_203	2.55	1.67	5.69
5VXJ.PDB	O, E_GLU_201	N, E_LYS_205	H, E_LYS_205	2.76	2.01	23.93
5VXJ.PDB	OD2, E_ASP_166	NZ, E_LYS_205	HZ2, E_LYS_205	2.79	1.95	15.80

5VXJ.PDB	OD2, E_ASP_166	OH, E_TYR_206	HH, E_TYR_206	2.80	1.99	13.17
5VXJ.PDB	O, F_GLY_112	ND2, E_ASN_216	HD21, E_ASN_216	2.68	1.91	21.74
5VXJ.PDB	O, E_TYR_244	N, E_VAL_218	H, E_VAL_218	2.90	2.07	12.38
5VXJ.PDB	O, E_SER_219	N, E_ALA_223	H, E_ALA_223	2.85	2.02	12.36
5VXJ.PDB	O, E_GLN_220	N, E_ASN_224	H, E_ASN_224	2.92	2.12	17.22
5VXJ.PDB	O, E_GLU_221	N, E_LYS_225	H, E_LYS_225	2.83	2.07	23.55
5VXJ.PDB	O, E_ALA_223	N, E_LEU_227	H, E_LEU_227	2.90	2.08	14.99
5VXJ.PDB	O, E_TRP_226	N, E_LEU_230	H, E_LEU_230	2.79	1.93	5.43
5VXJ.PDB	O, E_SER_247	N, E_LYS_236	H, E_LYS_236	2.89	2.18	29.32
5VXJ.PDB	O, E_GLY_243	N, E_LYS_240	H, E_LYS_240	2.92	2.06	6.86
5VXJ.PDB	O, E_VAL_218	N, E_TYR_244	H, E_TYR_244	2.83	2.10	27.72
5VXJ.PDB	O, E_SER_238	N, E_VAL_245	H, E_VAL_245	2.99	2.17	14.78
5VXJ.PDB	O, E_TYR_212	N, E_VAL_246	H, E_VAL_246	2.78	1.92	1.28
5VXJ.PDB	O, E_ILE_234	N, E_ASN_249	H, E_ASN_249	2.95	2.10	8.04
5VXJ.PDB	OD1, E_ASN_249	N, E_THR_251	H, E_THR_251	2.92	2.09	11.77
5VXJ.PDB	OD1, E_ASN_249	OG1, E_THR_251	HG1, E_THR_251	2.55	1.84	26.63
5VXJ.PDB	O, E_MET_250	N, E_ASP_254	H, E_ASP_254	2.99	2.17	15.41
5VXJ.PDB	O, E_THR_251	N, E_ASN_255	H, E_ASN_255	2.75	1.94	15.61
5VXJ.PDB	O, E_MET_256	N, E_LEU_260	H, E_LEU_260	2.96	2.20	24.13
5VXJ.PDB	O, E_LYS_258	N, E_ASN_262	H, E_ASN_262	2.93	2.19	25.85
5VXJ.PDB	O, E_VAL_188	N, E_LEU_271	H, E_LEU_271	2.71	1.86	9.01
5VXJ.PDB	O, E_ASN_273	N, E_GLN_277	H, E_GLN_277	2.93	2.08	8.17
5VXJ.PDB	O, E_LYS_275	N, E_TRP_279	H, E_TRP_279	2.94	2.10	8.60
5VXJ.PDB	O, E_TYR_276	N, E_ASN_280	H, E_ASN_280	2.69	1.83	1.86
5VXJ.PDB	O, E_TRP_279	N, E_PHE_283	H, E_PHE_283	2.90	2.06	8.44
5VXJ.PDB	O, E_GLU_288	N, E_ASN_292	H, E_ASN_292	2.93	2.09	10.24
5VXJ.PDB	O, E_THR_289	N, E_ASN_293	H, E_ASN_293	2.93	2.09	10.01
5VXJ.PDB	O, E_MET_290	N, E_LEU_294	H, E_LEU_294	2.94	2.11	13.11
5VXJ.PDB	O, E_LYS_291	N, E_GLN_295	H, E_GLN_295	2.83	1.98	7.53
5VXJ.PDB	O, E_ASN_292	N, E_THR_296	H, E_THR_296	2.78	2.01	22.46
5VXJ.PDB	O, E_LEU_294	N, E_VAL_298	H, E_VAL_298	2.95	2.10	6.64
5VXJ.PDB	O, E_THR_296	N, E_LYS_300	H, E_LYS_300	2.96	2.14	14.74
5VXJ.PDB	O, E_LEU_297	N, E_TYR_301	H, E_TYR_301	2.79	1.94	8.70
5VXJ.PDB	O, E_VAL_298	N, E_SER_302	H, E_SER_302	2.84	2.02	14.64
5VXJ.PDB	O, E_GLN_299	N, E_ASN_303	H, E_ASN_303	2.93	2.07	5.66
5VXJ.PDB	O, E_LYS_300	N, E_ALA_304	H, E_ALA_304	2.85	2.08	22.30
5VXJ.PDB	OD1, E_ASN_58	ND2, E_ASN_305	HD21, E_ASN_305	2.80	1.98	14.83
5VXJ.PDB	O, E_ALA_304	N, E_PHE_308	H, E_PHE_308	2.93	2.09	11.91
5VXJ.PDB	O, E_ASN_305	N, E_ASP_309	H, E_ASP_309	2.75	1.92	13.10
5VXJ.PDB	O, E_SER_306	N, E_ASN_310	H, E_ASN_310	2.83	2.05	20.17
5VXJ.PDB	O, E_LEU_311	N, E_LEU_315	H, E_LEU_315	2.80	1.98	13.54
5VXJ.PDB	O, E_VAL_312	N, E_SER_316	H, E_SER_316	2.92	2.08	10.70
5VXJ.PDB	O, E_LYS_313	OG, E_SER_316	HG, E_SER_316	2.95	2.17	17.14
5VXJ.PDB	O, E_VAL_314	N, E_THR_318	H, E_THR_318	2.84	2.03	16.20
5VXJ.PDB	O, E_LEU_315	N, E_ILE_319	H, E_ILE_319	2.87	2.09	21.51
5VXJ.PDB	O, E_SER_316	OG, E_SER_320	HG, E_SER_320	2.93	2.11	9.97
5VXJ.PDB	O, F_SER_25	N, F_GLN_3	H, F_GLN_3	2.86	2.05	17.85
5VXJ.PDB	O, F_ALA_23	N, F_ALA_5	H, F_ALA_5	2.98	2.24	26.74
5VXJ.PDB	O, F_SER_21	N, F_THR_7	H, F_THR_7	2.94	2.17	21.96
5VXJ.PDB	O, F_GLN_114	N, F_GLY_10	H, F_GLY_10	2.72	1.87	6.47
5VXJ.PDB	O, F_THR_116	N, F_ALA_12	H, F_ALA_12	2.88	2.15	27.23
5VXJ.PDB	O, F_LEU_86	N, F_GLY_15	H, F_GLY_15	2.89	2.06	12.09
5VXJ.PDB	O, F_GLN_13	N, F_GLY_16	H, F_GLY_16	2.90	2.06	10.07
5VXJ.PDB	O, F_MET_83	N, F_LEU_18	H, F_LEU_18	2.85	2.06	20.12
5VXJ.PDB	OE1, F_GLN_82	NE, F_ARG_19	HE, F_ARG_19	2.82	1.96	3.39
5VXJ.PDB	O, F_THR_7	N, F_SER_21	H, F_SER_21	2.85	2.05	18.37
5VXJ.PDB	O, F_VAL_79	N, F_CYS_22	H, F_CYS_22	2.95	2.15	19.55
5VXJ.PDB	O, F_ALA_5	N, F_ALA_23	H, F_ALA_23	2.80	1.96	10.17

5VXJ.PDB	O, F_ASN_77	N, F_ALA_24	H, F_ALA_24	2.80	1.95	4.41
5VXJ.PDB	O, F_GLY_99	N, F_VAL_33	H, F_VAL_33	2.72	1.90	15.23
5VXJ.PDB	O, F_ASN_97	N, F_ASN_35	H, F_ASN_35	2.71	1.87	10.04
5VXJ.PDB	OD1, F_ASN_97	ND2, F_ASN_35	HD22, F_ASN_35	2.86	2.08	21.21
5VXJ.PDB	O, F_ALA_49	N, F_TRP_36	H, F_TRP_36	2.90	2.07	13.72
5VXJ.PDB	O, F_VAL_95	N, F_TYR_37	H, F_TYR_37	2.88	2.02	2.78
5VXJ.PDB	OD1, F_ASP_90	NH1, F_ARG_38	HH12, F_ARG_38	2.92	2.20	28.14
5VXJ.PDB	OE2, F_GLU_46	NH2, F_ARG_38	HH21, F_ARG_38	2.73	1.93	18.99
5VXJ.PDB	OE1, F_GLU_44	N, F_ARG_45	H, F_ARG_45	2.62	1.85	20.92
5VXJ.PDB	O, F_ARG_38	N, F_GLU_46	H, F_GLU_46	2.92	2.09	11.31
5VXJ.PDB	O, F_TRP_36	N, F_VAL_48	H, F_VAL_48	2.74	1.91	14.11
5VXJ.PDB	O, F_SER_59	N, F_ARG_50	H, F_ARG_50	2.88	2.09	20.53
5VXJ.PDB	OE1, G_GLU_200	NH2, F_ARG_50	HH22, F_ARG_50	2.70	1.89	15.49
5VXJ.PDB	O, F_SER_30	OH, F_TYR_52	HH, F_TYR_52	2.69	1.86	8.38
5VXJ.PDB	OD1, F_ASP_53	N, F_GLY_55	H, F_GLY_55	2.61	1.87	25.39
5VXJ.PDB	O, F_ARG_50	N, F_SER_59	H, F_SER_59	2.82	2.00	14.71
5VXJ.PDB	O, F_SER_85	NH1, F_ARG_67	HH11, F_ARG_67	2.83	2.08	24.34
5VXJ.PDB	OD2, F_ASP_90	NH1, F_ARG_67	HH12, F_ARG_67	2.83	1.99	10.41
5VXJ.PDB	OD1, F_ASN_74	NE, F_ARG_72	HE, F_ARG_72	2.72	1.88	10.50
5VXJ.PDB	O, F_ALA_32	NH1, F_ARG_72	HH12, F_ARG_72	2.99	2.18	16.73
5VXJ.PDB	O, F_LEU_18	N, F_MET_83	H, F_MET_83	2.56	1.71	7.06
5VXJ.PDB	OD2, F_ASP_90	N, F_LYS_87	H, F_LYS_87	2.92	2.15	21.40
5VXJ.PDB	O, F_LYS_87	N, F_ASP_90	H, F_ASP_90	2.85	2.01	12.44
5VXJ.PDB	O, F_PRO_88	N, F_THR_91	H, F_THR_91	2.99	2.14	6.98
5VXJ.PDB	O, F_VAL_115	N, F_ALA_92	H, F_ALA_92	2.99	2.23	23.19
5VXJ.PDB	O, F_GLN_39	N, F_MET_93	H, F_MET_93	2.76	1.90	4.39
5VXJ.PDB	O, F_THR_113	N, F_TYR_94	H, F_TYR_94	2.89	2.09	17.19
5VXJ.PDB	O, F_ASP_90	OH, F_TYR_94	HH, F_TYR_94	2.65	1.83	9.35
5VXJ.PDB	OE2, F_GLU_6	N, F_CYS_96	H, F_CYS_96	2.48	1.64	10.12
5VXJ.PDB	O, F_ASN_35	N, F_ASN_97	H, F_ASN_97	2.96	2.17	18.94
5VXJ.PDB	OG1, F_THR_107	ND2, F_ASN_97	HD21, F_ASN_97	2.73	1.95	21.26
5VXJ.PDB	O, F_VAL_33	N, F_GLY_99	H, F_GLY_99	2.77	1.92	6.76
5VXJ.PDB	O, F_ARG_106	N, F_ILE_100	H, F_ILE_100	2.81	1.97	10.04
5VXJ.PDB	O, F_ARG_31	N, F_PHE_101	H, F_PHE_101	2.72	1.87	8.92
5VXJ.PDB	OE1, G_GLU_201	OH, F_TYR_105	HH, F_TYR_105	2.57	1.75	11.97
5VXJ.PDB	O, F_CYS_96	N, F_GLY_110	H, F_GLY_110	2.87	2.09	20.49
5VXJ.PDB	O, E_THR_217	NE2, F_GLN_111	HE22, F_GLN_111	2.98	2.12	6.26
5VXJ.PDB	OE1, F_GLU_6	N, F_GLY_112	H, F_GLY_112	2.49	1.66	12.35
5VXJ.PDB	O, F_TYR_94	N, F_THR_113	H, F_THR_113	2.80	1.99	17.44
5VXJ.PDB	O, F_ALA_92	N, F_VAL_115	H, F_VAL_115	2.94	2.08	6.59
5VXJ.PDB	OG1, F_THR_91	N, F_VAL_117	H, F_VAL_117	2.91	2.05	1.59
5VXJ.PDB	O, G_LEU_47	N, G_LEU_51	H, G_LEU_51	2.82	2.00	14.56
5VXJ.PDB	O, G_ASP_49	N, G_ASN_53	H, G_ASN_53	2.43	1.60	12.48
5VXJ.PDB	O, G_HIS_52	N, G_THR_56	H, G_THR_56	2.92	2.09	13.87
5VXJ.PDB	O, G_ARG_55	N, G_THR_57	H, G_THR_57	2.92	2.19	26.60
5VXJ.PDB	O, G_THR_57	N, G_LEU_61	H, G_LEU_61	2.82	1.99	11.74
5VXJ.PDB	O, G_ASN_58	N, G_LYS_62	H, G_LYS_62	2.82	1.97	8.16
5VXJ.PDB	O, G_LEU_61	N, G_LEU_65	H, G_LEU_65	2.93	2.16	22.32
5VXJ.PDB	O, G_LYS_62	OG, G_SER_66	HG, G_SER_66	2.76	1.97	15.54
5VXJ.PDB	O, G_ALA_79	N, G_SER_83	H, G_SER_83	2.87	2.11	23.33
5VXJ.PDB	O, G_LEU_80	N, G_GLN_84	H, G_GLN_84	2.88	2.12	24.02
5VXJ.PDB	O, G_HIS_81	N, G_ILE_85	H, G_ILE_85	2.98	2.19	19.61
5VXJ.PDB	O, G_ILE_85	N, G_VAL_89	H, G_VAL_89	2.81	2.00	16.83
5VXJ.PDB	O, G_ASP_88	N, G_SER_92	H, G_SER_92	2.63	1.80	11.22
5VXJ.PDB	O, G_ASP_88	OG, G_SER_92	HG, G_SER_92	2.83	2.07	20.88
5VXJ.PDB	O, G_VAL_89	N, G_ALA_93	H, G_ALA_93	2.81	1.99	14.69
5VXJ.PDB	O, G_SER_92	N, G_LEU_96	H, G_LEU_96	2.87	2.02	7.93
5VXJ.PDB	O, G_ALA_93	N, G_ASP_97	H, G_ASP_97	2.78	1.96	13.95

5VXJ.PDB	O, G_GLN_94	N, G_ILE_98	H, G_ILE_98	2.75	1.95	17.07
5VXJ.PDB	O, G_LEU_95	N, G_LEU_99	H, G_LEU_99	2.95	2.15	17.03
5VXJ.PDB	O, G_LEU_96	N, G_SER_100	H, G_SER_100	2.90	2.14	23.00
5VXJ.PDB	O, G_ARG_132	OG, G_SER_100	HG, G_SER_100	2.76	1.96	15.44
5VXJ.PDB	O, G_ASP_97	N, G_ARG_101	H, G_ARG_101	2.92	2.09	13.45
5VXJ.PDB	OD2, G_ASP_97	NE, G_ARG_101	HE, G_ARG_101	2.67	1.82	7.54
5VXJ.PDB	O, G_ILE_98	N, G_ASN_102	H, G_ASN_102	2.95	2.14	17.00
5VXJ.PDB	O, G_LEU_113	OG, G_SER_116	HG, G_SER_116	2.49	1.72	19.82
5VXJ.PDB	O, G_PRO_118	N, G_ALA_121	H, G_ALA_121	2.99	2.21	20.79
5VXJ.PDB	O, G_LYS_119	N, G_GLU_122	H, G_GLU_122	2.97	2.13	11.69
5VXJ.PDB	O, H_GLY_56	NH2, G_ARG_132	HH22, G_ARG_132	2.94	2.20	26.37
5VXJ.PDB	O, G_TYR_104	NE1, G_TRP_135	HE1, G_TRP_135	2.73	1.97	23.31
5VXJ.PDB	O, G_GLU_133	N, G_LYS_137	H, G_LYS_137	2.98	2.20	21.62
5VXJ.PDB	O, G_LEU_134	N, G_ILE_138	H, G_ILE_138	2.96	2.21	25.46
5VXJ.PDB	O, G_TRP_135	N, G_ALA_139	H, G_ALA_139	2.77	1.93	7.72
5VXJ.PDB	O, G_ALA_136	N, G_ASN_140	H, G_ASN_140	2.82	1.97	8.22
5VXJ.PDB	O, G_LYS_137	N, G_SER_141	H, G_SER_141	3.00	2.27	27.08
5VXJ.PDB	O, G_ALA_121	OG, G_SER_141	HG, G_SER_141	2.84	2.05	16.77
5VXJ.PDB	O, G_ASN_140	N, G_ASP_144	H, G_ASP_144	2.65	1.83	15.34
5VXJ.PDB	O, G_SER_141	N, G_ILE_145	H, G_ILE_145	2.98	2.15	13.01
5VXJ.PDB	O, G_ASP_144	N, G_GLN_148	H, G_GLN_148	2.87	2.03	9.64
5VXJ.PDB	O, G_ILE_145	N, G_LEU_150	H, G_LEU_150	2.93	2.09	11.15
5VXJ.PDB	O, G_ASN_146	N, G_LYS_151	H, G_LYS_151	2.69	1.86	11.46
5VXJ.PDB	O, G_LYS_151	N, G_HIS_155	H, G_HIS_155	2.94	2.14	18.38
5VXJ.PDB	O, G_VAL_152	N, G_ALA_156	H, G_ALA_156	2.99	2.15	9.93
5VXJ.PDB	O, G_TYR_153	N, G_VAL_157	H, G_VAL_157	2.97	2.12	8.52
5VXJ.PDB	O, G_GLU_154	N, G_SER_158	H, G_SER_158	2.89	2.07	14.41
5VXJ.PDB	O, G_HIS_155	N, G_SER_159	H, G_SER_159	2.67	1.82	8.29
5VXJ.PDB	O, G_ALA_156	N, G_TYR_160	H, G_TYR_160	2.95	2.09	4.91
5VXJ.PDB	O, G_VAL_157	N, G_THR_161	H, G_THR_161	2.89	2.06	12.73
5VXJ.PDB	O, G_VAL_157	OG1, G_THR_161	HG1, G_THR_161	2.73	2.03	28.26
5VXJ.PDB	O, G_TYR_160	N, G_TYR_164	H, G_TYR_164	2.94	2.13	15.80
5VXJ.PDB	OD1, G_ASP_287	OH, G_TYR_164	HH, G_TYR_164	2.79	1.99	15.03
5VXJ.PDB	O, G_THR_161	N, G_GLN_165	H, G_GLN_165	2.71	1.89	15.11
5VXJ.PDB	O, G_GLN_162	N, G_ASP_166	H, G_ASP_166	2.86	2.02	10.34
5VXJ.PDB	O, G_MET_163	N, G_PHE_167	H, G_PHE_167	2.94	2.13	15.85
5VXJ.PDB	O, G_TYR_164	N, G_SER_168	H, G_SER_168	2.76	1.96	17.74
5VXJ.PDB	O, G_PHE_167	N, G_LEU_171	H, G_LEU_171	2.92	2.14	21.89
5VXJ.PDB	O, F_TYR_105	OG, G_SER_173	HG, G_SER_173	2.88	2.16	26.33
5VXJ.PDB	OD1, I_ASN_292	N, G_GLY_176	H, G_GLY_176	2.76	2.01	25.37
5VXJ.PDB	O, G_LYS_189	N, G_SER_179	H, G_SER_179	2.93	2.15	21.27
5VXJ.PDB	O, G_SER_187	N, G_GLY_181	H, G_GLY_181	2.82	1.96	3.25
5VXJ.PDB	O, G_LEU_271	N, G_VAL_188	H, G_VAL_188	2.64	1.80	10.40
5VXJ.PDB	O, G_SER_179	N, G_LYS_189	H, G_LYS_189	2.74	1.88	0.48
5VXJ.PDB	O, G_VAL_269	N, G_LEU_190	H, G_LEU_190	2.94	2.10	11.59
5VXJ.PDB	O, G_TRP_177	N, G_GLN_191	H, G_GLN_191	2.89	2.06	12.28
5VXJ.PDB	O, G_VAL_192	N, G_LYS_196	H, G_LYS_196	2.73	1.88	6.19
5VXJ.PDB	O, G_ASN_193	N, G_LYS_197	H, G_LYS_197	2.77	1.93	12.03
5VXJ.PDB	OE2, G_GLU_201	NZ, G_LYS_197	HZ3, G_LYS_197	2.59	1.86	28.64
5VXJ.PDB	O, G_LYS_196	N, G_GLU_200	H, G_GLU_200	2.89	2.03	3.65
5VXJ.PDB	O, G_ALA_198	N, G_LEU_202	H, G_LEU_202	2.82	2.06	23.29
5VXJ.PDB	OD1, G_ASP_254	NZ, G_LYS_203	HZ2, G_LYS_203	2.49	1.62	9.92
5VXJ.PDB	O, G_GLU_201	N, G_LYS_205	H, G_LYS_205	2.90	2.17	27.16
5VXJ.PDB	OD2, G_ASP_166	NZ, G_LYS_205	HZ2, G_LYS_205	2.82	1.96	12.05
5VXJ.PDB	OD2, G_ASP_166	OH, G_TYR_206	HH, G_TYR_206	2.52	1.70	11.57
5VXJ.PDB	OE1, H_GLN_111	OG1, G_THR_217	HG1, G_THR_217	2.86	2.17	29.58
5VXJ.PDB	O, G_TYR_244	N, G_VAL_218	H, G_VAL_218	2.86	2.06	17.78
5VXJ.PDB	O, G_SER_219	N, G_ALA_223	H, G_ALA_223	2.97	2.15	15.26

5VXJ.PDB	O, G_ALA_223	N, G_LEU_227	H, G_LEU_227	2.91	2.13	21.40
5VXJ.PDB	O, G_ASN_224	N, G_THR_228	H, G_THR_228	2.94	2.09	5.59
5VXJ.PDB	O, G_TRP_226	N, G_LEU_230	H, G_LEU_230	2.80	1.99	15.37
5VXJ.PDB	O, G_SER_247	N, G_LYS_236	H, G_LYS_236	2.91	2.21	29.46
5VXJ.PDB	O, G_GLY_243	N, G_LYS_240	H, G_LYS_240	2.93	2.08	7.36
5VXJ.PDB	O, G_VAL_218	N, G_TYR_244	H, G_TYR_244	2.68	1.96	27.92
5VXJ.PDB	O, G_TYR_212	N, G_VAL_246	H, G_VAL_246	2.69	1.84	4.47
5VXJ.PDB	O, G_ILE_234	N, G_ASN_249	H, G_ASN_249	2.98	2.13	6.76
5VXJ.PDB	OD1, G_ASN_249	N, G_THR_251	H, G_THR_251	2.80	1.95	8.59
5VXJ.PDB	O, G_MET_250	N, G_ASP_254	H, G_ASP_254	2.98	2.15	13.88
5VXJ.PDB	O, G_THR_251	N, G_ASN_255	H, G_ASN_255	2.80	1.98	15.19
5VXJ.PDB	O, G_ILE_253	N, G_LEU_257	H, G_LEU_257	2.98	2.19	19.77
5VXJ.PDB	O, G_ASP_254	N, G_LYS_258	H, G_LYS_258	2.96	2.13	13.32
5VXJ.PDB	O, G_ASN_255	N, G_SER_259	H, G_SER_259	2.97	2.13	11.23
5VXJ.PDB	O, G_MET_256	N, G_LEU_260	H, G_LEU_260	2.98	2.17	16.38
5VXJ.PDB	O, G_LEU_257	N, G_ASP_261	H, G_ASP_261	2.95	2.11	10.36
5VXJ.PDB	O, G_VAL_188	N, G_LEU_271	H, G_LEU_271	2.72	1.88	11.49
5VXJ.PDB	OD1, G_ASP_272	N, G_LYS_275	H, G_LYS_275	2.67	1.82	9.36
5VXJ.PDB	O, G_ASN_273	N, G_GLN_277	H, G_GLN_277	2.90	2.04	4.56
5VXJ.PDB	O, G_TYR_276	N, G_ASN_280	H, G_ASN_280	2.80	1.95	8.62
5VXJ.PDB	O, G_TRP_279	N, G_PHE_283	H, G_PHE_283	2.87	2.07	17.67
5VXJ.PDB	O, G_ASN_280	N, G_SER_284	H, G_SER_284	2.95	2.13	14.24
5VXJ.PDB	O, G_ASN_280	OG, G_SER_284	HG, G_SER_284	2.97	2.24	25.76
5VXJ.PDB	O, G_SER_284	N, G_GLU_288	H, G_GLU_288	2.91	2.15	23.37
5VXJ.PDB	O, G_GLU_288	N, G_ASN_292	H, G_ASN_292	2.83	1.99	8.91
5VXJ.PDB	O, G_THR_289	N, G_ASN_293	H, G_ASN_293	2.94	2.09	6.63
5VXJ.PDB	O, G_LYS_291	N, G_GLN_295	H, G_GLN_295	2.97	2.14	12.50
5VXJ.PDB	O, G_ASN_292	N, G_THR_296	H, G_THR_296	2.78	1.97	17.22
5VXJ.PDB	O, G_ASN_293	N, G_LEU_297	H, G_LEU_297	2.97	2.15	14.27
5VXJ.PDB	O, G_LEU_294	N, G_VAL_298	H, G_VAL_298	2.94	2.10	8.59
5VXJ.PDB	O, G_THR_296	N, G_LYS_300	H, G_LYS_300	2.93	2.11	14.54
5VXJ.PDB	O, G_LEU_297	N, G_TYR_301	H, G_TYR_301	2.79	1.93	5.96
5VXJ.PDB	O, G_VAL_298	N, G_SER_302	H, G_SER_302	2.92	2.18	25.79
5VXJ.PDB	O, G_GLN_299	N, G_ASN_303	H, G_ASN_303	2.89	2.06	11.76
5VXJ.PDB	O, G_LYS_300	N, G_ALA_304	H, G_ALA_304	2.91	2.09	15.09
5VXJ.PDB	O, G_ASN_305	N, G_ASP_309	H, G_ASP_309	2.86	2.10	23.50
5VXJ.PDB	O, G_ASN_310	N, G_VAL_314	H, G_VAL_314	2.93	2.09	9.81
5VXJ.PDB	O, G_LEU_311	N, G_LEU_315	H, G_LEU_315	2.80	1.98	14.79
5VXJ.PDB	O, G_VAL_312	N, G_SER_316	H, G_SER_316	2.85	2.00	7.85
5VXJ.PDB	O, G_VAL_314	OG, G_SER_317	HG, G_SER_317	2.91	2.15	20.46
5VXJ.PDB	OE1, H_GLN_1	N, H_VAL_2	H, H_VAL_2	2.95	2.22	27.04
5VXJ.PDB	O, H_SER_25	N, H_GLN_3	H, H_GLN_3	2.91	2.09	16.25
5VXJ.PDB	O, H_ALA_23	N, H_ALA_5	H, H_ALA_5	2.99	2.18	17.17
5VXJ.PDB	O, H_SER_21	N, H_THR_7	H, H_THR_7	2.88	2.14	25.14
5VXJ.PDB	O, H_GLN_114	N, H_GLY_10	H, H_GLY_10	2.91	2.07	10.18
5VXJ.PDB	O, H_THR_116	N, H_ALA_12	H, H_ALA_12	2.81	2.11	29.16
5VXJ.PDB	O, H_LEU_86	N, H_GLY_15	H, H_GLY_15	2.89	2.09	19.18
5VXJ.PDB	O, H_GLN_13	N, H_GLY_16	H, H_GLY_16	2.90	2.08	13.33
5VXJ.PDB	O, H_MET_83	N, H_LEU_18	H, H_LEU_18	2.94	2.15	20.85
5VXJ.PDB	OE1, H_GLN_82	NE, H_ARG_19	HE, H_ARG_19	2.76	1.91	8.69
5VXJ.PDB	O, H_LEU_81	N, H_LEU_20	H, H_LEU_20	2.81	2.00	16.24
5VXJ.PDB	O, H_THR_7	N, H_SER_21	H, H_SER_21	2.81	2.01	17.25
5VXJ.PDB	O, H_VAL_79	N, H_CYS_22	H, H_CYS_22	2.93	2.10	13.46
5VXJ.PDB	O, H_ALA_5	N, H_ALA_23	H, H_ALA_23	2.89	2.09	18.03
5VXJ.PDB	O, H_ASN_77	N, H_ALA_24	H, H_ALA_24	2.87	2.01	2.06
5VXJ.PDB	O, H_THR_28	N, H_ARG_31	H, H_ARG_31	2.95	2.12	13.87
5VXJ.PDB	O, H_GLY_99	N, H_VAL_33	H, H_VAL_33	2.75	1.93	14.82
5VXJ.PDB	O, H_ASN_97	N, H_ASN_35	H, H_ASN_35	2.70	1.89	16.43

5VXJ.PDB	OD1, H_ASN_97	ND2, H_ASN_35	HD22, H_ASN_35	2.85	2.10	23.91
5VXJ.PDB	O, H_ALA_49	N, H_TRP_36	H, H_TRP_36	2.96	2.13	12.43
5VXJ.PDB	O, H_VAL_95	N, H_TYR_37	H, H_TYR_37	2.93	2.07	4.40
5VXJ.PDB	O, H_GLU_46	N, H_ARG_38	H, H_ARG_38	3.00	2.20	19.46
5VXJ.PDB	OD1, H_ASP_90	NH1, H_ARG_38	HH12, H_ARG_38	3.00	2.16	12.34
5VXJ.PDB	O, H_LYS_43	NE2, H_GLN_39	HE21, H_GLN_39	2.90	2.07	12.82
5VXJ.PDB	O, H_ALA_40	N, H_LYS_43	H, H_LYS_43	2.85	2.05	18.19
5VXJ.PDB	O, H_TRP_36	N, H_VAL_48	H, H_VAL_48	2.81	1.99	14.82
5VXJ.PDB	OD1, H_ASN_35	NE, H_ARG_50	HE, H_ARG_50	2.75	1.93	14.53
5VXJ.PDB	O, H_SER_30	OH, H_TYR_52	HH, H_TYR_52	2.54	1.73	12.01
5VXJ.PDB	O, H_ARG_50	N, H_SER_59	H, H_SER_59	2.65	1.83	14.48
5VXJ.PDB	O, H_VAL_48	N, H_ALA_61	H, H_ALA_61	2.92	2.06	6.45
5VXJ.PDB	OD2, H_ASP_90	NH1, H_ARG_67	HH12, H_ARG_67	2.89	2.05	9.62
5VXJ.PDB	O, H_VAL_64	N, H_PHE_68	H, H_PHE_68	2.94	2.11	12.01
5VXJ.PDB	O, H_GLN_82	N, H_THR_69	H, H_THR_69	2.98	2.17	16.65
5VXJ.PDB	O, H_HIS_80	N, H_SER_71	H, H_SER_71	2.96	2.17	19.86
5VXJ.PDB	OD1, H_ASN_74	NE, H_ARG_72	HE, H_ARG_72	2.76	1.95	17.61
5VXJ.PDB	O, H_THR_78	N, H_ASP_73	H, H_ASP_73	2.94	2.10	8.61
5VXJ.PDB	OD1, H_ASP_73	N, H_ALA_75	H, H_ALA_75	2.98	2.24	26.47
5VXJ.PDB	O, H_LEU_20	N, H_LEU_81	H, H_LEU_81	2.92	2.17	25.39
5VXJ.PDB	O, H_THR_69	N, H_GLN_82	H, H_GLN_82	2.80	2.01	19.49
5VXJ.PDB	OD1, H_ASN_84	NE2, H_GLN_82	HE21, H_GLN_82	2.86	2.05	16.57
5VXJ.PDB	O, H_LEU_18	N, H_MET_83	H, H_MET_83	2.73	1.88	6.75
5VXJ.PDB	OD2, H_ASP_90	N, H_LYS_87	H, H_LYS_87	2.78	1.93	8.81
5VXJ.PDB	O, H_LYS_87	N, H_ASP_90	H, H_ASP_90	2.91	2.12	18.68
5VXJ.PDB	O, H_PRO_88	OG1, H_THR_91	HG1, H_THR_91	2.87	2.17	28.10
5VXJ.PDB	O, H_GLN_39	N, H_MET_93	H, H_MET_93	2.94	2.08	2.62
5VXJ.PDB	O, H_THR_113	N, H_TYR_94	H, H_TYR_94	2.90	2.08	15.59
5VXJ.PDB	O, H_ASP_90	OH, H_TYR_94	HH, H_TYR_94	2.76	1.93	4.55
5VXJ.PDB	OE2, H_GLU_6	N, H_CYS_96	H, H_CYS_96	2.77	1.93	11.06
5VXJ.PDB	O, H_ASN_35	N, H_ASN_97	H, H_ASN_97	3.00	2.18	14.80
5VXJ.PDB	OG1, H_THR_107	ND2, H_ASN_97	HD21, H_ASN_97	2.53	1.81	26.67
5VXJ.PDB	O, H_VAL_33	N, H_GLY_99	H, H_GLY_99	2.83	1.97	3.41
5VXJ.PDB	O, H_ARG_31	N, H_PHE_101	H, H_PHE_101	2.92	2.07	4.69
5VXJ.PDB	O, H_ALA_98	OG1, H_THR_107	HG1, H_THR_107	2.78	2.00	18.25
5VXJ.PDB	O, H_TYR_94	N, H_THR_113	H, H_THR_113	2.71	1.88	13.43
5VXJ.PDB	O, H_ALA_92	N, H_VAL_115	H, H_VAL_115	2.99	2.14	8.76
5VXJ.PDB	O, I_HIS_52	N, I_THR_56	H, I_THR_56	3.00	2.25	25.56
5VXJ.PDB	O, I_ILE_54	N, I_ASN_58	H, I_ASN_58	2.85	2.04	16.92
5VXJ.PDB	OD1, I_ASP_309	ND2, I_ASN_58	HD22, I_ASN_58	2.73	1.88	5.94
5VXJ.PDB	O, I_THR_57	N, I_LEU_61	H, I_LEU_61	2.75	1.93	14.25
5VXJ.PDB	O, I_SER_74	N, I_ILE_78	H, I_ILE_78	2.96	2.17	19.05
5VXJ.PDB	O, I_ILE_78	N, I_SER_82	H, I_SER_82	2.89	2.03	4.23
5VXJ.PDB	OE1, I_GLU_154	OG, I_SER_82	HG, I_SER_82	2.52	1.79	24.33
5VXJ.PDB	O, I_ALA_79	N, I_SER_83	H, I_SER_83	2.97	2.17	18.99
5VXJ.PDB	O, I_LEU_80	N, I_GLN_84	H, I_GLN_84	2.85	2.09	23.46
5VXJ.PDB	O, I_HIS_81	N, I_ILE_85	H, I_ILE_85	2.91	2.07	9.50
5VXJ.PDB	O, I_SER_82	N, I_SER_86	H, I_SER_86	2.96	2.13	13.40
5VXJ.PDB	O, I_ILE_85	N, I_VAL_89	H, I_VAL_89	2.75	1.92	11.99
5VXJ.PDB	O, I_SER_86	N, I_ASN_90	H, I_ASN_90	2.87	2.05	14.01
5VXJ.PDB	O, I_ASP_88	N, I_SER_92	H, I_SER_92	2.88	2.08	18.99
5VXJ.PDB	O, I_VAL_89	N, I_ALA_93	H, I_ALA_93	2.77	1.96	17.15
5VXJ.PDB	O, I_SER_92	N, I_LEU_96	H, I_LEU_96	2.85	1.99	1.66
5VXJ.PDB	O, I_ALA_93	N, I_ASP_97	H, I_ASP_97	2.73	1.95	20.17
5VXJ.PDB	O, I_ARG_132	OG, I_SER_100	HG, I_SER_100	2.62	1.86	20.59
5VXJ.PDB	OD2, I_ASP_97	NE, I_ARG_101	HE, I_ARG_101	2.83	2.07	23.56
5VXJ.PDB	O, I_ILE_98	N, I_ASN_102	H, I_ASN_102	2.91	2.10	16.45
5VXJ.PDB	O, I_ILE_129	NH2, I_ARG_111	HH22, I_ARG_111	2.55	1.83	26.80

5VXJ.PDB	O, I.GLU.112	N, I.HIS.115	H, I.HIS.115	2.95	2.18	22.09
5VXJ.PDB	O, I.LEU.113	N, I.SER.116	H, I.SER.116	2.82	1.99	12.68
5VXJ.PDB	O, I.LEU.114	N, I.ALA.117	H, I.ALA.117	2.81	1.96	7.97
5VXJ.PDB	O, I.HIS.131	N, I.TRP.135	H, I.TRP.135	2.86	2.01	6.63
5VXJ.PDB	O, I.TYR.104	NE1, I.TRP.135	HE1, I.TRP.135	2.77	2.01	23.99
5VXJ.PDB	OD2, J.ASP.73	NZ, I.LYS.137	HZ3, I.LYS.137	2.90	2.17	29.52
5VXJ.PDB	O, I.TRP.135	N, I.ALA.139	H, I.ALA.139	2.88	2.02	5.33
5VXJ.PDB	O, I.ALA.136	N, I.ASN.140	H, I.ASN.140	2.79	1.94	7.31
5VXJ.PDB	O, I.ASN.140	N, I.ASP.144	H, I.ASP.144	2.67	1.82	9.22
5VXJ.PDB	O, I.SER.141	N, I.ILE.145	H, I.ILE.145	2.92	2.09	14.16
5VXJ.PDB	O, I.ASP.144	N, I.GLN.148	H, I.GLN.148	2.87	2.03	10.58
5VXJ.PDB	O, I.ASN.146	N, I.LYS.151	H, I.LYS.151	2.96	2.13	13.63
5VXJ.PDB	O, I.GLU.154	N, I.SER.158	H, I.SER.158	2.91	2.08	12.92
5VXJ.PDB	O, I.HIS.155	N, I.SER.159	H, I.SER.159	2.86	2.02	8.08
5VXJ.PDB	O, I.VAL.157	N, I.THR.161	H, I.THR.161	2.74	1.90	11.36
5VXJ.PDB	O, I.SER.158	N, I.GLN.162	H, I.GLN.162	2.99	2.14	8.77
5VXJ.PDB	O, I.TYR.160	N, I.TYR.164	H, I.TYR.164	2.94	2.12	14.36
5VXJ.PDB	OD1, I.ASP.287	OH, I.TYR.164	HH, I.TYR.164	2.95	2.16	17.45
5VXJ.PDB	O, I.THR.161	N, I.GLN.165	H, I.GLN.165	2.73	1.92	16.54
5VXJ.PDB	O, I.GLN.162	N, I.ASP.166	H, I.ASP.166	2.98	2.15	13.40
5VXJ.PDB	O, I.MET.163	N, I.PHE.167	H, I.PHE.167	2.92	2.10	14.46
5VXJ.PDB	O, I.TYR.164	N, I.SER.168	H, I.SER.168	2.79	1.99	18.69
5VXJ.PDB	O, I.TYR.164	OG, I.SER.168	HG, I.SER.168	2.84	2.02	10.56
5VXJ.PDB	O, I.PHE.167	N, I.LEU.171	H, I.LEU.171	2.88	2.09	18.97
5VXJ.PDB	O, I.SER.168	N, I.SER.172	H, I.SER.172	2.93	2.14	20.32
5VXJ.PDB	O, I.LEU.171	N, I.LEU.174	H, I.LEU.174	2.98	2.15	13.51
5VXJ.PDB	O, I.LYS.189	N, I.SER.179	H, I.SER.179	2.95	2.20	24.93
5VXJ.PDB	O, I.SER.187	N, I.GLY.181	H, I.GLY.181	2.71	1.95	23.30
5VXJ.PDB	O, I.LEU.271	N, I.VAL.188	H, I.VAL.188	2.51	1.65	3.63
5VXJ.PDB	O, I.SER.179	N, I.LYS.189	H, I.LYS.189	2.57	1.72	7.44
5VXJ.PDB	O, I.VAL.269	N, I.LEU.190	H, I.LEU.190	2.88	2.08	17.76
5VXJ.PDB	O, I.TRP.177	N, I.GLN.191	H, I.GLN.191	2.84	2.00	11.79
5VXJ.PDB	O, I.VAL.192	N, I.LYS.196	H, I.LYS.196	2.80	1.94	4.24
5VXJ.PDB	O, I.ASN.193	N, I.LYS.197	H, I.LYS.197	2.85	2.02	13.07
5VXJ.PDB	OD1, B.ASN.97	NZ, I.LYS.197	HZ1, I.LYS.197	2.68	1.88	21.92
5VXJ.PDB	O, I.LEU.195	N, I.LEU.199	H, I.LEU.199	3.00	2.18	15.17
5VXJ.PDB	O, I.LYS.196	N, I.GLU.200	H, I.GLU.200	2.81	1.96	9.14
5VXJ.PDB	O, I.LYS.197	N, I.GLU.201	H, I.GLU.201	2.97	2.16	16.25
5VXJ.PDB	O, I.ALA.198	N, I.LEU.202	H, I.LEU.202	3.00	2.21	19.76
5VXJ.PDB	OD1, I.ASP.254	NZ, I.LYS.203	HZ2, I.LYS.203	2.60	1.74	12.72
5VXJ.PDB	O, I.GLU.201	N, I.LYS.205	H, I.LYS.205	2.75	1.96	18.48
5VXJ.PDB	OD2, I.ASP.166	NZ, I.LYS.205	HZ2, I.LYS.205	2.77	1.91	10.79
5VXJ.PDB	OD2, I.ASP.166	OH, I.TYR.206	HH, I.TYR.206	2.50	1.67	8.28
5VXJ.PDB	O, I.VAL.246	N, I.LEU.211	H, I.LEU.211	2.81	2.10	28.98
5VXJ.PDB	O, I.SER.219	N, I.ALA.223	H, I.ALA.223	2.88	2.07	17.36
5VXJ.PDB	O, I.GLN.220	N, I.ASN.224	H, I.ASN.224	2.91	2.06	6.82
5VXJ.PDB	O, I.GLU.221	N, I.LYS.225	H, I.LYS.225	2.94	2.21	26.90
5VXJ.PDB	O, I.ALA.223	N, I.LEU.227	H, I.LEU.227	2.90	2.08	14.48
5VXJ.PDB	O, I.TRP.226	N, I.LEU.230	H, I.LEU.230	2.81	1.97	9.92
5VXJ.PDB	O, I.GLY.231	N, I.ILE.234	H, I.ILE.234	2.96	2.14	14.73
5VXJ.PDB	O, I.VAL.245	N, I.SER.238	H, I.SER.238	2.98	2.16	15.04
5VXJ.PDB	O, I.TYR.212	N, I.VAL.246	H, I.VAL.246	2.76	1.90	2.08
5VXJ.PDB	O, I.ILE.234	N, I.ASN.249	H, I.ASN.249	2.85	2.02	12.88
5VXJ.PDB	OD1, I.ASN.249	N, I.THR.251	H, I.THR.251	2.98	2.14	10.78
5VXJ.PDB	OD1, I.ASN.249	OG1, I.THR.251	HG1, I.THR.251	2.69	1.98	27.82
5VXJ.PDB	O, I.THR.251	N, I.ASN.255	H, I.ASN.255	2.72	1.91	16.03
5VXJ.PDB	O, I.PRO.252	N, I.MET.256	H, I.MET.256	2.98	2.15	12.95
5VXJ.PDB	O, I.ILE.253	N, I.LEU.257	H, I.LEU.257	2.86	2.03	13.56

5VXJ.PDB	O, I.ASP_254	N, I.LYS_258	H, I.LYS_258	2.91	2.07	10.53
5VXJ.PDB	O, I.ASN_255	N, I.SER_259	H, I.SER_259	2.91	2.10	16.35
5VXJ.PDB	O, I.MET_256	N, I.LEU_260	H, I.LEU_260	2.77	2.06	28.49
5VXJ.PDB	O, I.LEU_257	N, I.ASP_261	H, I.ASP_261	2.89	2.05	10.23
5VXJ.PDB	O, I.VAL_188	N, I.LEU_271	H, I.LEU_271	2.63	1.80	11.88
5VXJ.PDB	O, I.LYS_275	N, I.TRP_279	H, I.TRP_279	2.89	2.08	15.60
5VXJ.PDB	O, I.TYR_276	N, I.ASN_280	H, I.ASN_280	2.72	1.88	10.70
5VXJ.PDB	O, I.TRP_279	N, I.PHE_283	H, I.PHE_283	2.84	1.99	5.52
5VXJ.PDB	O, I.ASN_280	N, I.SER_284	H, I.SER_284	2.88	2.09	19.38
5VXJ.PDB	O, I.ASN_280	OG, I.SER_284	HG, I.SER_284	2.54	1.77	19.23
5VXJ.PDB	O, I.ALA_281	N, I.ALA_285	H, I.ALA_285	2.96	2.25	29.29
5VXJ.PDB	O, I.SER_284	N, I.GLU_288	H, I.GLU_288	2.89	2.11	20.80
5VXJ.PDB	O, I.THR_289	N, I.ASN_293	H, I.ASN_293	2.83	2.00	11.34
5VXJ.PDB	O, I.MET_290	N, I.LEU_294	H, I.LEU_294	2.91	2.07	11.98
5VXJ.PDB	O, I.ASN_292	N, I.THR_296	H, I.THR_296	2.91	2.10	15.19
5VXJ.PDB	O, I.LEU_294	N, I.VAL_298	H, I.VAL_298	2.97	2.13	11.40
5VXJ.PDB	O, I.GLN_295	N, I.GLN_299	H, I.GLN_299	2.67	1.83	9.61
5VXJ.PDB	O, I.THR_296	N, I.LYS_300	H, I.LYS_300	2.79	1.96	13.56
5VXJ.PDB	O, I.LEU_297	N, I.TYR_301	H, I.TYR_301	2.86	2.02	11.85
5VXJ.PDB	O, I.VAL_298	N, I.SER_302	H, I.SER_302	2.89	2.10	19.67
5VXJ.PDB	O, I.ASN_303	N, I.ILE_307	H, I.ILE_307	2.99	2.15	10.86
5VXJ.PDB	O, I.ALA_304	N, I.PHE_308	H, I.PHE_308	2.90	2.15	24.75
5VXJ.PDB	O, I.ASN_305	N, I.ASP_309	H, I.ASP_309	2.79	2.00	19.69
5VXJ.PDB	O, I.SER_306	N, I.ASN_310	H, I.ASN_310	2.75	1.93	13.59
5VXJ.PDB	O, I.ASP_309	N, I.LYS_313	H, I.LYS_313	2.84	2.05	19.66
5VXJ.PDB	O, I.LEU_311	N, I.LEU_315	H, I.LEU_315	2.80	1.96	10.49
5VXJ.PDB	O, I.VAL_312	N, I.SER_316	H, I.SER_316	3.00	2.19	16.29
5VXJ.PDB	O, I.LEU_315	OG1, I.THR_318	HG1, I.THR_318	2.75	2.04	26.52
5VXJ.PDB	O, I.LEU_315	N, I.ILE_319	H, I.ILE_319	2.98	2.22	23.66
5VXJ.PDB	O, J.SER_25	N, J.GLN_3	H, J.GLN_3	2.93	2.12	17.29
5VXJ.PDB	O, J.ALA_23	N, J.ALA_5	H, J.ALA_5	2.99	2.25	25.24
5VXJ.PDB	O, J.SER_21	N, J.THR_7	H, J.THR_7	2.92	2.17	25.75
5VXJ.PDB	O, J.GLN_114	N, J.GLY_10	H, J.GLY_10	2.89	2.04	6.92
5VXJ.PDB	O, J.THR_116	N, J.ALA_12	H, J.ALA_12	2.87	2.12	24.55
5VXJ.PDB	O, J.LEU_86	N, J.GLY_15	H, J.GLY_15	2.84	2.02	14.92
5VXJ.PDB	O, J.GLN_13	N, J.GLY_16	H, J.GLY_16	2.95	2.13	13.71
5VXJ.PDB	O, J.MET_83	N, J.LEU_18	H, J.LEU_18	2.83	2.07	23.77
5VXJ.PDB	OE1, J.GLN_82	NE, J.ARG_19	HE, J.ARG_19	2.52	1.72	17.43
5VXJ.PDB	O, J.THR_7	N, J.SER_21	H, J.SER_21	2.88	2.09	20.19
5VXJ.PDB	O, J.ASN_77	N, J.ALA_24	H, J.ALA_24	2.97	2.12	7.90
5VXJ.PDB	O, J.GLY_99	N, J.VAL_33	H, J.VAL_33	2.92	2.10	15.57
5VXJ.PDB	O, J.ASN_97	N, J.ASN_35	H, J.ASN_35	2.70	1.87	12.63
5VXJ.PDB	OD1, J.ASN_97	ND2, J.ASN_35	HD22, J.ASN_35	3.00	2.21	19.94
5VXJ.PDB	O, J.ALA_49	N, J.TRP_36	H, J.TRP_36	2.88	2.04	12.12
5VXJ.PDB	O, J.VAL_95	N, J.TYR_37	H, J.TYR_37	2.66	1.81	6.37
5VXJ.PDB	OD1, J.ASP_90	NH1, J.ARG_38	HH12, J.ARG_38	2.89	2.13	23.59
5VXJ.PDB	OE2, J.GLU_46	NH2, J.ARG_38	HH21, J.ARG_38	2.77	1.96	16.80
5VXJ.PDB	O, J.ARG_38	N, J.GLU_46	H, J.GLU_46	2.68	1.85	12.20
5VXJ.PDB	O, J.TRP_36	N, J.VAL_48	H, J.VAL_48	2.83	2.01	13.87
5VXJ.PDB	O, J.SER_59	N, J.ARG_50	H, J.ARG_50	2.92	2.18	25.84
5VXJ.PDB	OD1, J.ASN_35	NE, J.ARG_50	HE, J.ARG_50	2.74	1.91	11.68
5VXJ.PDB	O, J.SER_30	OH, J.TYR_52	HH, J.TYR_52	2.67	1.83	3.11
5VXJ.PDB	OD1, J.ASP_53	N, J.GLY_55	H, J.GLY_55	2.81	1.99	15.68
5VXJ.PDB	O, J.ARG_50	N, J.SER_59	H, J.SER_59	2.68	1.87	16.27
5VXJ.PDB	O, J.VAL_48	N, J.ALA_61	H, J.ALA_61	2.84	2.03	16.19
5VXJ.PDB	O, J.VAL_64	N, J.ARG_67	H, J.ARG_67	2.97	2.13	10.41
5VXJ.PDB	O, J.SER_85	NH1, J.ARG_67	HH11, J.ARG_67	2.90	2.16	26.24
5VXJ.PDB	OD2, J.ASP_90	NH1, J.ARG_67	HH12, J.ARG_67	2.55	1.74	16.72

5VXJ.PDB	OD1, J_ASP_90	NH2, J_ARG_67	HH22, J_ARG_67	2.84	1.98	5.11
5VXJ.PDB	O, J_VAL_64	N, J_PHE_68	H, J_PHE_68	2.99	2.15	10.61
5VXJ.PDB	O, J_HIS_80	N, J_SER_71	H, J_SER_71	2.98	2.20	21.12
5VXJ.PDB	O, J_ALA_32	NH2, J_ARG_72	HH22, J_ARG_72	2.52	1.69	13.12
5VXJ.PDB	O, J_THR_78	N, J_ASP_73	H, J_ASP_73	2.84	2.00	9.78
5VXJ.PDB	O, J_SER_71	N, J_HIS_80	H, J_HIS_80	2.97	2.18	20.55
5VXJ.PDB	O, J_THR_69	N, J_GLN_82	H, J_GLN_82	2.81	2.10	29.71
5VXJ.PDB	OD1, J_ASN_84	NE2, J_GLN_82	HE21, J_GLN_82	2.94	2.08	3.32
5VXJ.PDB	O, J_LEU_18	N, J_MET_83	H, J_MET_83	2.68	1.83	7.41
5VXJ.PDB	OD2, J_ASP_90	N, J_LYS_87	H, J_LYS_87	2.89	2.11	21.60
5VXJ.PDB	O, J_GLN_39	N, J_MET_93	H, J_MET_93	2.84	2.02	15.68
5VXJ.PDB	O, J_THR_113	N, J_TYR_94	H, J_TYR_94	2.95	2.11	9.77
5VXJ.PDB	O, J_ASP_90	OH, J_TYR_94	HH, J_TYR_94	2.90	2.08	7.74
5VXJ.PDB	O, J_ASN_35	N, J_ASN_97	H, J_ASN_97	2.69	1.93	22.73
5VXJ.PDB	OG1, J_THR_107	ND2, J_ASN_97	HD21, J_ASN_97	2.57	1.77	17.56
5VXJ.PDB	O, J_VAL_33	N, J_GLY_99	H, J_GLY_99	2.77	1.92	8.58
5VXJ.PDB	O, J_ARG_106	N, J_ILE_100	H, J_ILE_100	2.88	2.03	4.95
5VXJ.PDB	O, J_ARG_31	N, J_PHE_101	H, J_PHE_101	2.81	1.97	10.82
5VXJ.PDB	O, J_ALA_98	OG1, J_THR_107	HG1, J_THR_107	2.84	2.12	25.86
5VXJ.PDB	O, I_THR_217	NE2, J_GLN_111	HE22, J_GLN_111	2.92	2.11	16.33
5VXJ.PDB	OE1, J_GLU_6	N, J_GLY_112	H, J_GLY_112	2.94	2.09	6.96
5VXJ.PDB	O, J_TYR_94	N, J_THR_113	H, J_THR_113	2.80	1.97	13.72
5VXJ.PDB	OG1, J_THR_91	N, J_VAL_117	H, J_VAL_117	2.75	1.90	8.09
5VXK.PDB	O, B_SER_21	N, B_SER_7	H, B_SER_7	2.86	2.13	26.17
5VXK.PDB	O, B_GLN_13	N, B_GLY_16	H, B_GLY_16	2.95	2.16	18.88
5VXK.PDB	O, B_MET_83	N, B_LEU_18	H, B_LEU_18	2.96	2.15	15.77
5VXK.PDB	O, B_LEU_81	N, B_LEU_20	H, B_LEU_20	2.96	2.23	26.63
5VXK.PDB	O, B_VAL_79	N, B_CYS_22	H, B_CYS_22	2.62	1.80	13.05
5VXK.PDB	O, B_VAL_5	N, B_ALA_23	H, B_ALA_23	2.80	1.94	5.13
5VXK.PDB	OD1, B_ASN_77	N, B_LEU_29	H, B_LEU_29	2.87	2.10	22.34
5VXK.PDB	O, B_SER_49	N, B_TRP_36	H, B_TRP_36	2.81	1.99	12.98
5VXK.PDB	O, B_TYR_95	N, B_PHE_37	H, B_PHE_37	2.70	1.90	18.05
5VXK.PDB	O, B_GLU_46	N, B_ARG_38	H, B_ARG_38	2.93	2.12	16.27
5VXK.PDB	O, B_ARG_38	N, B_GLU_46	H, B_GLU_46	2.99	2.14	5.94
5VXK.PDB	O, B_TRP_36	N, B_VAL_48	H, B_VAL_48	2.67	1.86	15.37
5VXK.PDB	O, B_SER_59	N, B_CYS_50	H, B_CYS_50	2.88	2.12	22.90
5VXK.PDB	O, B_ILE_34	N, B_ILE_51	H, B_ILE_51	2.91	2.11	17.59
5VXK.PDB	O, B_THR_57	N, B_SER_52	H, B_SER_52	2.96	2.19	22.56
5VXK.PDB	O, B_GLN_106	OG1, B_THR_57	HG1, B_THR_57	2.72	2.03	28.93
5VXK.PDB	O, B_CYS_50	N, B_SER_59	H, B_SER_59	2.94	2.13	16.19
5VXK.PDB	O, B_VAL_48	N, B_SER_61	H, B_SER_61	2.73	1.90	12.27
5VXK.PDB	OD2, B_ASP_90	NH2, B_ARG_67	HH22, B_ARG_67	2.27	1.58	28.79
5VXK.PDB	OH, B_TYR_60	N, B_ILE_70	H, B_ILE_70	2.93	2.10	13.23
5VXK.PDB	O, B_SER_52	NH1, B_ARG_72	HH11, B_ARG_72	2.49	1.76	25.78
5VXK.PDB	O, B_ARG_78	N, B_ASP_73	H, B_ASP_73	2.58	1.73	6.46
5VXK.PDB	O, B_ASP_73	N, B_ARG_78	H, B_ARG_78	2.89	2.11	20.69
5VXK.PDB	O, B_CYS_22	N, B_VAL_79	H, B_VAL_79	2.94	2.14	17.09
5VXK.PDB	O, B_LEU_20	N, B_LEU_81	H, B_LEU_81	2.95	2.13	15.57
5VXK.PDB	O, B_THR_69	N, B_GLN_82	H, B_GLN_82	2.72	1.89	13.34
5VXK.PDB	O, B_LEU_18	N, B_MET_83	H, B_MET_83	2.84	2.03	16.84
5VXK.PDB	O, B_VAL_124	N, B_ALA_92	H, B_ALA_92	2.95	2.21	25.44
5VXK.PDB	O, B_PHE_37	N, B_TYR_95	H, B_TYR_95	2.71	1.89	14.49
5VXK.PDB	O, B_ALA_35	N, B_ALA_97	H, B_ALA_97	2.83	2.02	15.30
5VXK.PDB	O, B_VAL_117	N, B_ALA_98	H, B_ALA_98	2.99	2.21	21.08
5VXK.PDB	OD1, A_ASN_280	N, B_SER_103	H, B_SER_103	2.64	1.78	2.03
5VXK.PDB	OD1, A_ASN_280	N, B_VAL_104	H, B_VAL_104	2.84	2.01	12.48
5VXK.PDB	OG, A_SER_168	NE2, B_GLN_106	HE21, B_GLN_106	2.99	2.23	24.43
5VXK.PDB	OD2, A_ASP_287	NE2, B_GLN_106	HE22, B_GLN_106	2.77	1.94	12.81

5VXK.PDB	O, B_ILE_111	ND1, B_HIS_115	HD1, B_HIS_115	2.77	2.01	23.21
5VXK.PDB	O, B_GLY_113	NE, B_ARG_116	HE, B_ARG_116	2.86	2.06	17.67
5VXK.PDB	O, B_HIS_115	NE1, B_TRP_118	HE1, B_TRP_118	2.75	1.99	22.39
5VXK.PDB	OE1, B_GLU_6	N, B_GLY_121	H, B_GLY_121	2.76	1.92	11.78
5VXK.PDB	O, B_ALA_92	N, B_VAL_124	H, B_VAL_124	2.96	2.14	13.72
5VXK.PDB	OG1, B_THR_91	N, B_VAL_126	H, B_VAL_126	2.92	2.13	18.63
5VXK.PDB	O, A_LEU_44	N, A_ASN_48	H, A_ASN_48	2.73	1.91	14.91
5VXK.PDB	O, A_MET_46	N, A_THR_50	H, A_THR_50	2.82	1.97	7.12
5VXK.PDB	O, A_MET_46	OG1, A_THR_50	HG1, A_THR_50	2.68	1.85	7.57
5VXK.PDB	O, A_LEU_47	N, A_LEU_51	H, A_LEU_51	2.82	2.05	22.07
5VXK.PDB	O, A_ASP_49	N, A_ASN_53	H, A_ASN_53	2.90	2.05	9.25
5VXK.PDB	O, A_ASN_53	OG1, A_THR_57	HG1, A_THR_57	2.98	2.23	23.33
5VXK.PDB	O, A_ILE_54	N, A_ASN_58	H, A_ASN_58	2.93	2.11	14.43
5VXK.PDB	O, A_THR_56	N, A_ALA_60	H, A_ALA_60	2.98	2.15	13.11
5VXK.PDB	O, A_THR_57	N, A_LEU_61	H, A_LEU_61	2.94	2.13	16.68
5VXK.PDB	O, A_THR_71	N, A_LEU_75	H, A_LEU_75	2.95	2.14	16.00
5VXK.PDB	O, A_SER_74	N, A_ILE_78	H, A_ILE_78	2.92	2.06	5.83
5VXK.PDB	O, A_LEU_75	N, A_ALA_79	H, A_ALA_79	2.85	2.04	15.25
5VXK.PDB	O, A_GLU_77	N, A_HIS_81	H, A_HIS_81	2.98	2.14	8.61
5VXK.PDB	O, A_HIS_81	N, A_ILE_85	H, A_ILE_85	2.94	2.14	17.36
5VXK.PDB	O, A_SER_82	N, A_SER_86	H, A_SER_86	2.95	2.11	11.27
5VXK.PDB	O, A_SER_83	N, A_MET_87	H, A_MET_87	2.97	2.19	21.87
5VXK.PDB	O, A_ILE_85	N, A_VAL_89	H, A_VAL_89	2.79	2.01	20.21
5VXK.PDB	O, A_SER_86	N, A_ASN_90	H, A_ASN_90	2.99	2.14	5.84
5VXK.PDB	O, A_ASP_88	N, A_SER_92	H, A_SER_92	2.74	1.93	15.12
5VXK.PDB	O, A_ASP_88	OG, A_SER_92	HG, A_SER_92	3.00	2.29	28.37
5VXK.PDB	O, A_VAL_89	N, A_ALA_93	H, A_ALA_93	2.64	1.84	17.64
5VXK.PDB	O, A_SER_92	N, A_LEU_96	H, A_LEU_96	2.92	2.12	17.09
5VXK.PDB	O, A_LEU_96	N, A_SER_100	H, A_SER_100	2.70	1.93	21.92
5VXK.PDB	O, A_ARG_132	OG, A_SER_100	HG, A_SER_100	2.56	1.76	14.48
5VXK.PDB	O, A_ILE_98	N, A_ASN_102	H, A_ASN_102	2.91	2.05	5.88
5VXK.PDB	O, A_ILE_129	NH1, A_ARG_111	HH12, A_ARG_111	2.59	1.79	17.96
5VXK.PDB	O, A_ARG_111	N, A_LEU_114	H, A_LEU_114	2.85	2.05	18.01
5VXK.PDB	O, A_LEU_114	N, A_ALA_117	H, A_ALA_117	2.88	2.04	10.22
5VXK.PDB	O, A_TYR_104	NE1, A_TRP_135	HE1, A_TRP_135	2.54	1.70	9.79
5VXK.PDB	O, A_GLU_133	N, A_LYS_137	H, A_LYS_137	2.56	1.75	16.84
5VXK.PDB	O, A_LEU_134	N, A_ILE_138	H, A_ILE_138	2.73	1.96	22.76
5VXK.PDB	O, A_ALA_136	N, A_ASN_140	H, A_ASN_140	2.97	2.13	10.71
5VXK.PDB	O, A_ASN_140	N, A_ASP_144	H, A_ASP_144	2.65	1.81	8.85
5VXK.PDB	O, A_ASN_143	N, A_GLU_147	H, A_GLU_147	2.75	1.98	21.76
5VXK.PDB	O, A_ASP_144	N, A_GLN_148	H, A_GLN_148	2.72	1.87	4.64
5VXK.PDB	O, A_ASN_146	N, A_LYS_151	H, A_LYS_151	2.89	2.03	2.48
5VXK.PDB	O, A_LEU_150	N, A_GLU_154	H, A_GLU_154	2.80	1.99	16.19
5VXK.PDB	O, A_TYR_153	N, A_VAL_157	H, A_VAL_157	2.98	2.12	4.91
5VXK.PDB	O, A_HIS_155	N, A_SER_159	H, A_SER_159	2.74	1.89	9.23
5VXK.PDB	O, A_ALA_156	N, A_TYR_160	H, A_TYR_160	2.93	2.08	2.62
5VXK.PDB	O, A_VAL_157	N, A_THR_161	H, A_THR_161	2.80	1.98	15.42
5VXK.PDB	O, A_VAL_157	OG1, A_THR_161	HG1, A_THR_161	2.57	1.86	27.02
5VXK.PDB	O, A_SER_158	N, A_GLN_162	H, A_GLN_162	2.99	2.13	2.67
5VXK.PDB	O, A_TYR_160	N, A_TYR_164	H, A_TYR_164	2.84	2.00	11.73
5VXK.PDB	OD2, A_ASP_287	OH, A_TYR_164	HH, A_TYR_164	2.91	2.21	28.15
5VXK.PDB	O, A_THR_161	N, A_GLN_165	H, A_GLN_165	2.79	1.96	12.75
5VXK.PDB	O, A_MET_163	N, A_PHE_167	H, A_PHE_167	2.79	1.98	16.43
5VXK.PDB	O, A_TYR_164	N, A_SER_168	H, A_SER_168	2.63	1.79	8.68
5VXK.PDB	O, A_GLN_165	N, A_ALA_169	H, A_ALA_169	2.96	2.21	24.63
5VXK.PDB	O, A_SER_168	N, A_SER_172	H, A_SER_172	2.96	2.20	23.46
5VXK.PDB	O, A_LYS_189	N, A_SER_179	H, A_SER_179	2.81	2.06	25.54
5VXK.PDB	O, A_LEU_271	N, A_VAL_188	H, A_VAL_188	2.72	1.94	20.48

5VXK.PDB	O, A_SER_179	N, A_LYS_189	H, A_LYS_189	2.77	1.93	11.30
5VXK.PDB	O, A_VAL_269	N, A_LEU_190	H, A_LEU_190	2.98	2.14	11.69
5VXK.PDB	O, A_TRP_177	N, A_GLN_191	H, A_GLN_191	2.79	1.96	11.53
5VXK.PDB	O, A_GLN_191	N, A_LEU_195	H, A_LEU_195	2.98	2.12	0.40
5VXK.PDB	O, A_VAL_192	N, A_LYS_196	H, A_LYS_196	2.70	1.92	21.14
5VXK.PDB	OD2, A_ASP_261	NZ, A_LYS_196	HZ3, A_LYS_196	2.74	1.87	9.57
5VXK.PDB	O, A_ASN_193	N, A_LYS_197	H, A_LYS_197	2.84	1.99	8.82
5VXK.PDB	O, A_SER_194	N, A_ALA_198	H, A_ALA_198	2.95	2.12	13.78
5VXK.PDB	O, A_LYS_196	N, A_GLU_200	H, A_GLU_200	2.92	2.18	26.73
5VXK.PDB	O, A_LYS_197	N, A_GLU_201	H, A_GLU_201	2.99	2.17	14.72
5VXK.PDB	O, A_GLU_200	N, A_GLU_204	H, A_GLU_204	2.87	2.03	10.71
5VXK.PDB	O, A_VAL_246	N, A_LEU_211	H, A_LEU_211	2.69	1.92	21.70
5VXK.PDB	O, A_SER_219	N, A_ALA_223	H, A_ALA_223	2.87	2.01	6.41
5VXK.PDB	O, A_GLN_222	N, A_TRP_226	H, A_TRP_226	2.85	2.07	21.25
5VXK.PDB	O, A_ASN_224	N, A_THR_228	H, A_THR_228	2.67	1.85	13.34
5VXK.PDB	O, A_GLY_231	N, A_THR_233	H, A_THR_233	2.55	1.79	23.98
5VXK.PDB	O, A_SER_247	N, A_LYS_236	H, A_LYS_236	2.76	1.98	20.26
5VXK.PDB	O, A_VAL_245	N, A_SER_238	H, A_SER_238	2.92	2.13	19.88
5VXK.PDB	O, A_TYR_212	N, A_VAL_246	H, A_VAL_246	2.83	1.98	7.21
5VXK.PDB	O, A_LYS_236	N, A_SER_247	H, A_SER_247	2.77	1.95	15.51
5VXK.PDB	O, A_ILE_234	N, A_ASN_249	H, A_ASN_249	2.90	2.07	12.40
5VXK.PDB	OD1, A_ASN_249	N, A_THR_251	H, A_THR_251	2.95	2.10	9.19
5VXK.PDB	O, A_MET_250	N, A_ASP_254	H, A_ASP_254	2.78	1.96	13.63
5VXK.PDB	O, A_THR_251	N, A_ASN_255	H, A_ASN_255	2.70	1.89	17.04
5VXK.PDB	O, A_ASP_254	N, A_LYS_258	H, A_LYS_258	2.95	2.18	22.11
5VXK.PDB	O, A_ASN_255	N, A_SER_259	H, A_SER_259	2.99	2.21	21.36
5VXK.PDB	O, A_MET_256	OG, A_SER_259	HG, A_SER_259	2.72	1.88	2.53
5VXK.PDB	O, A_LEU_257	N, A_ASP_261	H, A_ASP_261	2.96	2.15	15.35
5VXK.PDB	O, A_LYS_258	N, A_ASN_262	H, A_ASN_262	3.00	2.20	18.58
5VXK.PDB	O, A_VAL_188	N, A_LEU_271	H, A_LEU_271	2.82	1.97	7.95
5VXK.PDB	O, A_ASN_186	N, A_ASN_273	H, A_ASN_273	2.88	2.14	26.01
5VXK.PDB	O, A_ASP_272	N, A_TYR_276	H, A_TYR_276	2.84	2.01	12.24
5VXK.PDB	OG1, B_THR_102	OH, A_TYR_276	HH, A_TYR_276	2.57	1.73	6.50
5VXK.PDB	O, A_ASN_273	N, A_GLN_277	H, A_GLN_277	2.84	2.02	14.45
5VXK.PDB	O, A_LYS_275	N, A_TRP_279	H, A_TRP_279	2.92	2.06	3.36
5VXK.PDB	O, A_TYR_276	N, A_ASN_280	H, A_ASN_280	2.71	1.86	7.15
5VXK.PDB	O, A_GLN_277	N, A_ALA_281	H, A_ALA_281	2.91	2.11	18.24
5VXK.PDB	O, A_ALA_281	N, A_ALA_285	H, A_ALA_285	2.89	2.13	23.89
5VXK.PDB	O, A_ASP_287	N, A_LYS_291	H, A_LYS_291	2.81	1.95	4.20
5VXK.PDB	O, A_GLU_288	N, A_ASN_292	H, A_ASN_292	2.77	1.96	17.31
5VXK.PDB	O, A_THR_289	N, A_ASN_293	H, A_ASN_293	2.79	1.96	12.40
5VXK.PDB	OH, A_TYR_160	ND2, A_ASN_293	HD22, A_ASN_293	2.77	1.97	18.05
5VXK.PDB	O, A_MET_290	N, A_LEU_294	H, A_LEU_294	2.88	2.05	13.48
5VXK.PDB	O, A_ASN_292	N, A_THR_296	H, A_THR_296	2.98	2.19	19.74
5VXK.PDB	O, A_LEU_294	N, A_VAL_298	H, A_VAL_298	2.93	2.09	11.47
5VXK.PDB	O, A_GLN_295	N, A_GLN_299	H, A_GLN_299	2.92	2.19	26.68
5VXK.PDB	O, A_THR_296	N, A_LYS_300	H, A_LYS_300	2.95	2.12	13.38
5VXK.PDB	O, A_LEU_297	N, A_TYR_301	H, A_TYR_301	2.89	2.06	12.10
5VXK.PDB	O, A_VAL_298	N, A_SER_302	H, A_SER_302	2.77	1.95	14.37
5VXK.PDB	O, A_GLN_299	N, A_ASN_303	H, A_ASN_303	2.69	1.84	7.73
5VXK.PDB	O, A_ALA_304	N, A_PHE_308	H, A_PHE_308	2.91	2.07	9.74
5VXK.PDB	O, A_ASN_305	N, A_ASP_309	H, A_ASP_309	2.69	1.83	5.55
5VXK.PDB	O, A_SER_306	N, A_ASN_310	H, A_ASN_310	2.96	2.11	5.89
5VXK.PDB	O, A_PHE_308	N, A_VAL_312	H, A_VAL_312	2.89	2.04	4.79
5VXK.PDB	O, A_ASP_309	N, A_LYS_313	H, A_LYS_313	2.99	2.14	4.76
5VXK.PDB	O, A_LEU_311	N, A_LEU_315	H, A_LEU_315	2.77	1.95	15.34
5VXK.PDB	O, A_VAL_312	N, A_SER_316	H, A_SER_316	2.86	2.04	13.60
5VXK.PDB	O, A_VAL_314	N, A_THR_318	H, A_THR_318	2.93	2.12	16.50

5VXK.PDB	O, A_LEU_315	N, A_ILE_319	H, A_ILE_319	2.77	1.92	6.38
5VXK.PDB	O, A_SER_316	N, A_SER_320	H, A_SER_320	2.83	1.98	7.77
5VXK.PDB	O, A_SER_316	OG, A_SER_320	HG, A_SER_320	2.92	2.19	24.37
5VXK.PDB	O, A_SER_317	OG, A_SER_321	HG, A_SER_321	2.91	2.13	18.92
5VXL.PDB	O, A_SER_42	N, A_MET_46	H, A_MET_46	2.87	2.01	3.50
5VXL.PDB	O, A_LEU_44	N, A_ASN_48	H, A_ASN_48	2.76	1.92	10.16
5VXL.PDB	O, A_THR_45	N, A_ASP_49	H, A_ASP_49	2.99	2.15	12.53
5VXL.PDB	O, A_MET_46	OG1, A_THR_50	HG1, A_THR_50	2.62	1.82	14.28
5VXL.PDB	O, A_LEU_47	N, A_LEU_51	H, A_LEU_51	2.90	2.10	17.57
5VXL.PDB	O, A_HIS_52	N, A_THR_56	H, A_THR_56	2.90	2.15	24.51
5VXL.PDB	O, A_ILE_54	N, A_ASN_58	H, A_ASN_58	2.71	1.88	13.56
5VXL.PDB	OD1, A_ASP_309	ND2, A_ASN_58	HD22, A_ASN_58	2.92	2.09	13.70
5VXL.PDB	O, A_THR_57	N, A_LEU_61	H, A_LEU_61	2.89	2.12	22.63
5VXL.PDB	O, A_THR_73	N, A_GLU_77	H, A_GLU_77	2.82	2.00	14.04
5VXL.PDB	O, A_SER_74	N, A_ILE_78	H, A_ILE_78	2.96	2.13	11.95
5VXL.PDB	OE1, A_GLU_154	OG, A_SER_82	HG, A_SER_82	2.52	1.77	21.68
5VXL.PDB	O, A_ALA_79	N, A_SER_83	H, A_SER_83	2.92	2.10	15.30
5VXL.PDB	O, A_LEU_80	N, A_GLN_84	H, A_GLN_84	2.91	2.12	19.31
5VXL.PDB	OD2, A_ASP_88	NE2, A_GLN_84	HE21, A_GLN_84	2.89	2.16	27.92
5VXL.PDB	O, A_HIS_81	N, A_ILE_85	H, A_ILE_85	2.85	2.01	10.10
5VXL.PDB	O, A_SER_82	N, A_SER_86	H, A_SER_86	2.94	2.14	18.49
5VXL.PDB	O, A_SER_82	OG, A_SER_86	HG, A_SER_86	2.79	1.98	12.76
5VXL.PDB	O, A_GLN_84	N, A_ASP_88	H, A_ASP_88	2.93	2.10	13.48
5VXL.PDB	O, A_ILE_85	N, A_VAL_89	H, A_VAL_89	2.78	1.95	11.84
5VXL.PDB	O, A_ASP_88	N, A_SER_92	H, A_SER_92	2.92	2.08	10.89
5VXL.PDB	O, A_ASP_88	OG, A_SER_92	HG, A_SER_92	2.87	2.05	11.00
5VXL.PDB	O, A_VAL_89	N, A_ALA_93	H, A_ALA_93	2.95	2.11	11.37
5VXL.PDB	O, A_LYS_91	N, A_LEU_95	H, A_LEU_95	2.97	2.17	17.92
5VXL.PDB	O, A_SER_92	N, A_LEU_96	H, A_LEU_96	2.63	1.78	7.72
5VXL.PDB	O, A_ALA_93	N, A_ASP_97	H, A_ASP_97	2.67	1.89	19.80
5VXL.PDB	O, A_SER_100	N, A_GLU_103	H, A_GLU_103	2.79	2.00	19.85
5VXL.PDB	O, A_PRO_118	N, A_ALA_121	H, A_ALA_121	2.84	2.03	15.32
5VXL.PDB	O, A_TYR_104	NE1, A_TRP_135	HE1, A_TRP_135	2.90	2.05	6.79
5VXL.PDB	O, A_GLU_133	N, A_LYS_137	H, A_LYS_137	2.91	2.15	23.30
5VXL.PDB	O, A_ALA_136	ND2, A_ASN_140	HD22, A_ASN_140	2.52	1.69	13.57
5VXL.PDB	O, A_ILE_138	N, A_ILE_142	H, A_ILE_142	2.68	1.84	10.96
5VXL.PDB	O, A_ASN_140	N, A_ASP_144	H, A_ASP_144	2.65	1.82	12.29
5VXL.PDB	O, A_SER_141	N, A_ILE_145	H, A_ILE_145	2.85	2.02	11.93
5VXL.PDB	O, A_ILE_145	N, A_LEU_150	H, A_LEU_150	2.86	2.08	21.09
5VXL.PDB	O, A_ASN_146	N, A_LYS_151	H, A_LYS_151	2.72	1.87	8.33
5VXL.PDB	O, A_TYR_153	N, A_VAL_157	H, A_VAL_157	2.99	2.14	9.15
5VXL.PDB	O, A_HIS_155	OG, A_SER_158	HG, A_SER_158	2.93	2.15	19.18
5VXL.PDB	O, A_HIS_155	N, A_SER_159	H, A_SER_159	2.66	1.80	3.85
5VXL.PDB	O, A_HIS_155	OG, A_SER_159	HG, A_SER_159	2.90	2.17	24.99
5VXL.PDB	O, A_ALA_156	N, A_TYR_160	H, A_TYR_160	2.93	2.09	8.00
5VXL.PDB	O, A_VAL_157	N, A_THR_161	H, A_THR_161	2.60	1.78	15.33
5VXL.PDB	O, A_VAL_157	OG1, A_THR_161	HG1, A_THR_161	2.46	1.70	20.64
5VXL.PDB	O, A_SER_158	N, A_GLN_162	H, A_GLN_162	2.84	1.98	1.63
5VXL.PDB	O, A_TYR_160	N, A_TYR_164	H, A_TYR_164	2.84	2.00	8.81
5VXL.PDB	O, A_THR_161	N, A_GLN_165	H, A_GLN_165	2.72	1.90	14.74
5VXL.PDB	O, A_TYR_164	N, A_SER_168	H, A_SER_168	2.87	2.04	11.91
5VXL.PDB	O, A_TYR_164	OG, A_SER_168	HG, A_SER_168	2.96	2.15	13.58
5VXL.PDB	O, A_PHE_167	N, A_LEU_171	H, A_LEU_171	2.92	2.16	23.19
5VXL.PDB	O, A_SER_168	N, A_SER_172	H, A_SER_172	2.92	2.12	18.79
5VXL.PDB	O, A_LYS_189	N, A_SER_179	H, A_SER_179	2.93	2.11	16.24
5VXL.PDB	O, A_SER_187	N, A_GLY_181	H, A_GLY_181	2.88	2.06	15.19
5VXL.PDB	O, A_SER_179	N, A_LYS_189	H, A_LYS_189	2.63	1.86	21.36
5VXL.PDB	O, A_VAL_269	N, A_LEU_190	H, A_LEU_190	2.66	1.92	26.28

5VXL.PDB	O, A_TRP_177	N, A_GLN_191	H, A_GLN_191	2.89	2.06	12.45
5VXL.PDB	O, A_VAL_192	N, A_LYS_196	H, A_LYS_196	2.82	1.98	9.06
5VXL.PDB	O, A_ASN_193	N, A_LYS_197	H, A_LYS_197	2.99	2.13	1.38
5VXL.PDB	O, A_LEU_195	N, A_LEU_199	H, A_LEU_199	2.96	2.13	13.84
5VXL.PDB	O, A_LYS_196	N, A_GLU_200	H, A_GLU_200	2.68	1.83	8.42
5VXL.PDB	O, A_LYS_197	N, A_GLU_201	H, A_GLU_201	2.99	2.18	15.98
5VXL.PDB	OD1, A_ASP_254	NZ, A_LYS_203	HZ3, A_LYS_203	2.55	1.71	15.49
5VXL.PDB	O, A_GLU_201	N, A_LYS_205	H, A_LYS_205	2.94	2.16	21.06
5VXL.PDB	OD2, B_ASP_52	NZ, A_LYS_205	HZ1, A_LYS_205	3.00	2.13	10.69
5VXL.PDB	OD2, A_ASP_166	OH, A_TYR_206	HH, A_TYR_206	2.43	1.61	11.33
5VXL.PDB	O, A_SER_219	N, A_ALA_223	H, A_ALA_223	2.65	1.81	10.36
5VXL.PDB	O, A_GLN_220	N, A_ASN_224	H, A_ASN_224	2.69	1.83	3.86
5VXL.PDB	OE1, A_GLN_148	NE1, A_TRP_226	HE1, A_TRP_226	2.87	2.02	9.28
5VXL.PDB	O, A_ALA_223	N, A_LEU_227	H, A_LEU_227	2.81	2.00	17.07
5VXL.PDB	O, A_TRP_226	N, A_LEU_230	H, A_LEU_230	2.94	2.11	10.97
5VXL.PDB	O, A_LEU_227	N, A_GLY_231	H, A_GLY_231	2.69	1.85	9.90
5VXL.PDB	O, A_GLY_243	N, A_LYS_240	H, A_LYS_240	2.98	2.14	10.92
5VXL.PDB	O, A_VAL_218	N, A_TYR_244	H, A_TYR_244	2.96	2.11	6.92
5VXL.PDB	O, A_SER_238	N, A_VAL_245	H, A_VAL_245	2.99	2.26	27.20
5VXL.PDB	O, A_TYR_212	N, A_VAL_246	H, A_VAL_246	2.52	1.74	20.61
5VXL.PDB	O, A_ILE_234	N, A_ASN_249	H, A_ASN_249	2.93	2.09	9.83
5VXL.PDB	OD1, A_ASN_249	N, A_THR_251	H, A_THR_251	2.75	1.91	9.14
5VXL.PDB	O, A_MET_250	N, A_ASP_254	H, A_ASP_254	2.85	2.02	11.68
5VXL.PDB	O, A_THR_251	N, A_ASN_255	H, A_ASN_255	2.77	1.94	13.53
5VXL.PDB	OE2, A_GLU_286	ND2, A_ASN_255	HD22, A_ASN_255	2.74	1.94	17.54
5VXL.PDB	O, A_ILE_253	N, A_LEU_257	H, A_LEU_257	2.98	2.15	14.50
5VXL.PDB	O, A_ASP_254	N, A_LYS_258	H, A_LYS_258	2.99	2.17	14.91
5VXL.PDB	O, A_ASN_255	N, A_SER_259	H, A_SER_259	2.97	2.14	13.88
5VXL.PDB	O, A_MET_256	N, A_LEU_260	H, A_LEU_260	2.88	2.07	16.61
5VXL.PDB	O, A_LEU_257	N, A_ASP_261	H, A_ASP_261	2.97	2.13	9.61
5VXL.PDB	O, A_LEU_260	N, A_LEU_263	H, A_LEU_263	2.99	2.27	28.32
5VXL.PDB	O, A_LEU_190	N, A_VAL_269	H, A_VAL_269	2.90	2.08	13.99
5VXL.PDB	O, A_VAL_188	N, A_LEU_271	H, A_LEU_271	2.85	2.02	11.38
5VXL.PDB	OD1, A_ASP_272	N, A_ASN_273	H, A_ASN_273	2.65	1.95	29.16
5VXL.PDB	O, A_TYR_276	N, A_ASN_280	H, A_ASN_280	2.86	2.01	4.96
5VXL.PDB	O, A_TRP_279	N, A_PHE_283	H, A_PHE_283	2.89	2.08	16.09
5VXL.PDB	O, A_ASN_280	N, A_SER_284	H, A_SER_284	2.73	1.94	20.02
5VXL.PDB	O, A_ASN_280	OG, A_SER_284	HG, A_SER_284	2.71	1.94	20.16
5VXL.PDB	O, A_ALA_281	N, A_ALA_285	H, A_ALA_285	2.78	2.01	22.25
5VXL.PDB	O, A_ALA_285	N, A_THR_289	H, A_THR_289	2.98	2.16	14.81
5VXL.PDB	O, A_ASP_287	N, A_LYS_291	H, A_LYS_291	2.89	2.06	14.03
5VXL.PDB	O, A_GLU_288	N, A_ASN_292	H, A_ASN_292	2.65	1.85	17.95
5VXL.PDB	O, A_THR_289	N, A_ASN_293	H, A_ASN_293	2.72	1.88	9.66
5VXL.PDB	O, A_MET_290	N, A_LEU_294	H, A_LEU_294	2.92	2.12	18.98
5VXL.PDB	O, A_ASN_292	N, A_THR_296	H, A_THR_296	2.80	2.02	20.58
5VXL.PDB	O, A_ASN_292	OG1, A_THR_296	HG1, A_THR_296	2.92	2.11	12.62
5VXL.PDB	O, A_LEU_294	N, A_VAL_298	H, A_VAL_298	2.97	2.14	12.75
5VXL.PDB	O, A_THR_296	N, A_LYS_300	H, A_LYS_300	2.96	2.11	7.04
5VXL.PDB	O, A_LEU_297	N, A_TYR_301	H, A_TYR_301	2.75	2.04	28.78
5VXL.PDB	O, A_VAL_298	N, A_SER_302	H, A_SER_302	2.75	1.91	8.45
5VXL.PDB	O, A_GLN_299	N, A_ASN_303	H, A_ASN_303	2.84	2.01	12.17
5VXL.PDB	O, A_TYR_301	N, A_ASN_305	H, A_ASN_305	2.82	2.10	28.03
5VXL.PDB	O, A_SER_302	N, A_SER_306	H, A_SER_306	2.92	2.14	21.23
5VXL.PDB	O, A_ASN_303	N, A_ILE_307	H, A_ILE_307	2.92	2.13	18.78
5VXL.PDB	O, A_ASN_305	N, A_ASP_309	H, A_ASP_309	2.71	1.93	21.31
5VXL.PDB	O, A_ILE_307	N, A_LEU_311	H, A_LEU_311	2.89	2.07	14.43
5VXL.PDB	O, A_ASP_309	N, A_LYS_313	H, A_LYS_313	2.80	1.99	16.36
5VXL.PDB	O, A_ASN_310	N, A_VAL_314	H, A_VAL_314	2.86	2.01	5.31

5VXL.PDB	O, A_VAL_312	N, A_SER_316	H, A_SER_316	2.63	1.77	5.33
5VXL.PDB	O, A_VAL_314	OG1, A_THR_318	HG1, A_THR_318	2.55	1.72	7.64
5VXL.PDB	O, B_SER_25	N, B_GLN_3	H, B_GLN_3	2.70	1.85	6.65
5VXL.PDB	O, B_SER_21	N, B_SER_7	H, B_SER_7	2.62	1.81	16.40
5VXL.PDB	O, B_THR_114	N, B_VAL_12	H, B_VAL_12	2.86	2.04	13.69
5VXL.PDB	O, B_LEU_87	N, B_GLY_15	H, B_GLY_15	2.66	1.82	8.14
5VXL.PDB	O, B_GLN_13	N, B_GLY_16	H, B_GLY_16	2.79	1.96	12.54
5VXL.PDB	O, B_MET_84	N, B_LEU_18	H, B_LEU_18	2.84	2.08	22.47
5VXL.PDB	O, B_LEU_18	NH1, B_ARG_19	HH11, B_ARG_19	2.76	1.99	23.14
5VXL.PDB	O, B_SER_7	N, B_SER_21	H, B_SER_21	2.79	1.97	15.64
5VXL.PDB	O, B_VAL_80	N, B_CYS_22	H, B_CYS_22	2.67	1.84	12.31
5VXL.PDB	O, B_GLN_3	N, B_SER_25	H, B_SER_25	2.94	2.16	21.35
5VXL.PDB	O, B_ILE_51	N, B_MET_34	H, B_MET_34	2.85	2.13	28.16
5VXL.PDB	O, B_ASN_98	N, B_GLY_35	H, B_GLY_35	2.93	2.19	27.03
5VXL.PDB	O, B_TYR_96	N, B_TYR_37	H, B_TYR_37	2.76	1.92	10.99
5VXL.PDB	O, B_GLU_46	N, B_ARG_38	H, B_ARG_38	2.91	2.11	17.69
5VXL.PDB	OD1, B_ASP_91	NH1, B_ARG_38	HH12, B_ARG_38	2.97	2.23	26.01
5VXL.PDB	O, B_MET_34	N, B_ILE_51	H, B_ILE_51	2.82	1.98	9.96
5VXL.PDB	O, B_ILE_30	N, B_TYR_54	H, B_TYR_54	2.87	2.10	22.14
5VXL.PDB	O, A_ALA_198	OH, B_TYR_54	HH, B_TYR_54	2.38	1.67	27.03
5VXL.PDB	OD1, A_ASP_166	N, B_SER_55	H, B_SER_55	2.91	2.18	28.04
5VXL.PDB	OD1, A_ASP_166	OG, B_SER_55	HG, B_SER_55	2.56	1.73	4.68
5VXL.PDB	O, B_ALA_62	N, B_VAL_65	H, B_VAL_65	2.93	2.21	29.05
5VXL.PDB	OD2, B_ASP_91	NH1, B_ARG_68	HH12, B_ARG_68	2.83	2.06	22.74
5VXL.PDB	O, B_SER_64	NH2, B_ARG_68	HH21, B_ARG_68	2.89	2.07	15.16
5VXL.PDB	OD1, B_ASN_75	NE, B_ARG_73	HE, B_ARG_73	2.98	2.26	28.00
5VXL.PDB	O, B_TYR_32	NH1, B_ARG_73	HH12, B_ARG_73	2.99	2.21	21.42
5VXL.PDB	O, B_ARG_79	N, B_ASP_74	H, B_ASP_74	2.83	1.98	9.00
5VXL.PDB	OH, B_TYR_81	NE, B_ARG_79	HE, B_ARG_79	2.96	2.14	13.15
5VXL.PDB	O, B_CYS_22	N, B_VAL_80	H, B_VAL_80	2.66	1.84	14.02
5VXL.PDB	O, B_SER_72	N, B_TYR_81	H, B_TYR_81	2.82	1.97	3.12
5VXL.PDB	O, B_LEU_20	N, B_LEU_82	H, B_LEU_82	2.80	2.00	19.11
5VXL.PDB	O, B_LEU_18	N, B_MET_84	H, B_MET_84	2.92	2.06	5.88
5VXL.PDB	O, B_ARG_68	N, B_ASN_85	H, B_ASN_85	2.99	2.16	13.78
5VXL.PDB	O, B_GLY_16	N, B_LEU_87	H, B_LEU_87	2.89	2.07	14.28
5VXL.PDB	OD2, B_ASP_91	N, B_LYS_88	H, B_LYS_88	2.92	2.07	3.13
5VXL.PDB	O, B_LYS_88	N, B_ASP_91	H, B_ASP_91	2.90	2.09	15.76
5VXL.PDB	O, B_PRO_89	N, B_THR_92	H, B_THR_92	2.97	2.23	25.58
5VXL.PDB	O, B_VAL_113	N, B_ALA_93	H, B_ALA_93	2.99	2.24	25.85
5VXL.PDB	O, B_THR_111	N, B_TYR_95	H, B_TYR_95	2.79	2.00	19.66
5VXL.PDB	O, B_ASP_91	OH, B_TYR_95	HH, B_TYR_95	2.70	1.86	0.59
5VXL.PDB	O, B_TYR_37	N, B_TYR_96	H, B_TYR_96	2.76	2.02	25.56
5VXL.PDB	OE2, B_GLU_6	N, B_CYS_97	H, B_CYS_97	2.88	2.07	15.37
5VXL.PDB	O, B_GLY_35	N, B_ASN_98	H, B_ASN_98	2.73	1.91	13.08
5VXL.PDB	O, B_TYR_106	N, B_ALA_99	H, B_ALA_99	2.92	2.09	12.87
5VXL.PDB	O, B_ASN_33	N, B_ASN_100	H, B_ASN_100	2.79	2.01	20.69
5VXL.PDB	O, B_ASN_104	N, B_LEU_101	H, B_LEU_101	2.93	2.12	16.88
5VXL.PDB	OE2, A_GLU_201	NH2, B_ARG_102	HH22, B_ARG_102	2.87	2.08	20.03
5VXL.PDB	O, B_LEU_101	N, B_ASN_104	H, B_ASN_104	2.99	2.18	16.70
5VXL.PDB	O, B_ALA_99	N, B_TYR_106	H, B_TYR_106	2.85	2.08	22.40
5VXL.PDB	OE1, B_GLU_6	N, B_GLY_110	H, B_GLY_110	2.56	1.79	21.05
5VXL.PDB	O, B_ALA_93	N, B_VAL_113	H, B_VAL_113	2.86	2.05	16.79
5VXM.PDB	O, A_SER_43	N, A_LEU_47	H, A_LEU_47	2.98	2.17	15.99
5VXM.PDB	O, A_THR_45	N, A_ASP_49	H, A_ASP_49	2.87	2.12	24.84
5VXM.PDB	O, A_LEU_47	N, A_LEU_51	H, A_LEU_51	2.78	1.93	8.20
5VXM.PDB	O, A_ASN_48	N, A_HIS_52	H, A_HIS_52	2.97	2.22	25.09
5VXM.PDB	O, A_HIS_52	OG1, A_THR_56	HG1, A_THR_56	2.93	2.14	17.08
5VXM.PDB	O, A_ILE_54	N, A_ASN_58	H, A_ASN_58	2.67	1.83	11.82

5VXM.PDB	OD1, A_ASP_309	ND2, A_ASN_58	HD22, A_ASN_58	2.74	1.89	5.63
5VXM.PDB	O, A_ARG_55	N, A_GLN_59	H, A_GLN_59	2.87	2.11	23.42
5VXM.PDB	O, A_THR_57	N, A_LEU_61	H, A_LEU_61	2.81	1.96	8.36
5VXM.PDB	O, A_ASN_58	N, A_LYS_62	H, A_LYS_62	2.92	2.12	18.24
5VXM.PDB	O, A_LYS_63	OG, A_SER_66	HG, A_SER_66	2.80	2.08	26.74
5VXM.PDB	O, A_THR_71	N, A_LEU_75	H, A_LEU_75	2.95	2.16	20.11
5VXM.PDB	O, A_SER_74	N, A_ILE_78	H, A_ILE_78	2.99	2.18	16.60
5VXM.PDB	O, A_LEU_75	N, A_ALA_79	H, A_ALA_79	2.89	2.06	11.29
5VXM.PDB	O, A_ILE_78	N, A_SER_82	H, A_SER_82	2.98	2.13	10.08
5VXM.PDB	O, A_ILE_78	OG, A_SER_82	HG, A_SER_82	2.83	2.02	14.46
5VXM.PDB	O, A_ALA_79	N, A_SER_83	H, A_SER_83	2.84	2.05	18.67
5VXM.PDB	O, A_LEU_80	N, A_GLN_84	H, A_GLN_84	2.64	1.80	8.82
5VXM.PDB	OD1, A_ASP_88	NE2, A_GLN_84	HE21, A_GLN_84	2.60	1.75	9.62
5VXM.PDB	O, A_HIS_81	N, A_ILE_85	H, A_ILE_85	2.65	1.82	12.85
5VXM.PDB	O, A_SER_82	OG, A_SER_86	HG, A_SER_86	2.97	2.14	6.66
5VXM.PDB	O, A_ILE_85	N, A_VAL_89	H, A_VAL_89	2.86	2.05	15.94
5VXM.PDB	O, A_MET_87	N, A_LYS_91	H, A_LYS_91	2.99	2.19	17.82
5VXM.PDB	O, A_ASP_88	N, A_SER_92	H, A_SER_92	2.77	1.94	12.57
5VXM.PDB	O, A_ILE_145	N, A_LEU_150	H, A_LEU_150	2.92	2.12	18.38
5VXM.PDB	O, A_ASN_146	N, A_LYS_151	H, A_LYS_151	2.86	2.02	9.54
5VXM.PDB	O, A_LEU_150	N, A_GLU_154	H, A_GLU_154	2.97	2.16	16.91
5VXM.PDB	O, A_VAL_152	N, A_ALA_156	H, A_ALA_156	2.98	2.13	8.33
5VXM.PDB	O, A_TYR_153	N, A_VAL_157	H, A_VAL_157	2.93	2.11	15.35
5VXM.PDB	O, A_GLU_154	N, A_SER_158	H, A_SER_158	2.98	2.18	17.97
5VXM.PDB	O, A_HIS_155	N, A_SER_159	H, A_SER_159	2.95	2.10	8.74
5VXM.PDB	O, A_VAL_157	N, A_THR_161	H, A_THR_161	2.89	2.06	13.47
5VXM.PDB	O, A_VAL_157	OG1, A_THR_161	HG1, A_THR_161	2.43	1.69	23.26
5VXM.PDB	O, A_SER_158	N, A_GLN_162	H, A_GLN_162	2.97	2.13	9.45
5VXM.PDB	O, A_SER_159	N, A_MET_163	H, A_MET_163	2.98	2.14	9.28
5VXM.PDB	O, A_TYR_160	N, A_TYR_164	H, A_TYR_164	2.84	2.00	11.12
5VXM.PDB	OD1, A_ASP_287	OH, A_TYR_164	HH, A_TYR_164	2.66	1.84	11.86
5VXM.PDB	O, A_THR_161	N, A_GLN_165	H, A_GLN_165	2.81	1.96	8.47
5VXM.PDB	O, A_LEU_70	NE2, A_GLN_165	HE21, A_GLN_165	2.72	1.96	23.75
5VXM.PDB	O, A_GLN_162	N, A_ASP_166	H, A_ASP_166	2.96	2.12	10.69
5VXM.PDB	O, A_MET_163	N, A_PHE_167	H, A_PHE_167	2.81	2.01	18.58
5VXM.PDB	O, A_TYR_164	N, A_SER_168	H, A_SER_168	2.79	2.00	19.99
5VXM.PDB	O, A_TYR_164	OG, A_SER_168	HG, A_SER_168	2.87	2.02	0.77
5VXM.PDB	O, A_SER_168	N, A_SER_172	H, A_SER_172	2.86	2.05	16.01
5VXM.PDB	O, A_LEU_171	N, A_LEU_174	H, A_LEU_174	2.94	2.11	13.11
5VXM.PDB	O, A_LEU_174	N, A_TRP_177	H, A_TRP_177	2.78	1.95	10.80
5VXM.PDB	OE2, B_GLU_111	NE1, A_TRP_177	HE1, A_TRP_177	2.76	1.97	19.61
5VXM.PDB	O, A_SER_187	N, A_GLY_181	H, A_GLY_181	2.97	2.17	18.19
5VXM.PDB	O, A_LEU_271	N, A_VAL_188	H, A_VAL_188	2.81	1.98	12.86
5VXM.PDB	O, A_SER_179	N, A_LYS_189	H, A_LYS_189	2.57	1.73	10.12
5VXM.PDB	O, A_VAL_269	N, A_LEU_190	H, A_LEU_190	2.87	2.05	15.09
5VXM.PDB	O, A_TRP_177	N, A_GLN_191	H, A_GLN_191	2.93	2.13	18.42
5VXM.PDB	O, A_VAL_192	N, A_LYS_196	H, A_LYS_196	2.81	1.97	10.63
5VXM.PDB	O, A_ASN_193	N, A_LYS_197	H, A_LYS_197	2.96	2.10	4.46
5VXM.PDB	O, A_LYS_196	N, A_GLU_200	H, A_GLU_200	2.84	2.04	17.32
5VXM.PDB	O, A_LEU_199	N, A_LYS_203	H, A_LYS_203	2.98	2.17	15.17
5VXM.PDB	O, A_GLU_200	N, A_GLU_204	H, A_GLU_204	2.89	2.04	8.12
5VXM.PDB	O, A_GLU_201	N, A_LYS_205	H, A_LYS_205	2.81	2.04	22.11
5VXM.PDB	OD2, A_ASP_166	NZ, A_LYS_205	HZ3, A_LYS_205	2.79	1.92	8.41
5VXM.PDB	OD2, A_ASP_166	OH, A_TYR_206	HH, A_TYR_206	2.53	1.73	14.26
5VXM.PDB	O, A_TYR_244	N, A_VAL_218	H, A_VAL_218	2.98	2.15	13.66
5VXM.PDB	O, A_SER_219	N, A_ALA_223	H, A_ALA_223	2.76	1.93	12.38
5VXM.PDB	O, A_GLN_220	ND2, A_ASN_224	HD22, A_ASN_224	2.78	1.96	13.87
5VXM.PDB	O, A_GLU_221	N, A_LYS_225	H, A_LYS_225	2.92	2.09	12.89

5VXM.PDB	O, A_ALA_223	N, A_LEU_227	H, A_LEU_227	2.97	2.23	26.22
5VXM.PDB	O, A_TRP_226	N, A_LEU_230	H, A_LEU_230	2.84	2.13	28.15
5VXM.PDB	O, A_LEU_227	N, A_GLY_231	H, A_GLY_231	2.67	1.83	9.65
5VXM.PDB	O, A_SER_247	N, A_LYS_236	H, A_LYS_236	2.94	2.17	23.09
5VXM.PDB	O, A_VAL_245	N, A_SER_238	H, A_SER_238	2.82	2.00	14.23
5VXM.PDB	O, A_GLY_243	N, A_LYS_240	H, A_LYS_240	2.90	2.05	7.30
5VXM.PDB	O, A_VAL_218	N, A_TYR_244	H, A_TYR_244	2.94	2.13	17.51
5VXM.PDB	O, A_TYR_212	N, A_VAL_246	H, A_VAL_246	2.67	1.83	9.46
5VXM.PDB	O, A_LYS_236	N, A_SER_247	H, A_SER_247	2.73	1.97	23.18
5VXM.PDB	O, A_ILE_234	N, A_ASN_249	H, A_ASN_249	2.66	1.81	8.12
5VXM.PDB	O, A_GLY_232	ND2, A_ASN_249	HD22, A_ASN_249	2.93	2.16	22.59
5VXM.PDB	OD1, A_ASN_249	N, A_THR_251	H, A_THR_251	2.92	2.07	8.88
5VXM.PDB	O, A_MET_250	N, A_ASP_254	H, A_ASP_254	2.82	1.99	10.70
5VXM.PDB	O, A_THR_251	N, A_ASN_255	H, A_ASN_255	2.65	1.83	15.00
5VXM.PDB	O, A_ILE_253	N, A_LEU_257	H, A_LEU_257	2.90	2.05	9.48
5VXM.PDB	O, A_ASP_254	N, A_LYS_258	H, A_LYS_258	2.93	2.08	4.06
5VXM.PDB	O, A_ASN_255	OG, A_SER_259	HG, A_SER_259	2.90	2.14	20.43
5VXM.PDB	O, A_MET_256	N, A_LEU_260	H, A_LEU_260	2.87	2.06	16.67
5VXM.PDB	O, A_LEU_257	N, A_ASP_261	H, A_ASP_261	2.90	2.07	12.51
5VXM.PDB	O, A_VAL_188	N, A_LEU_271	H, A_LEU_271	2.70	1.86	11.12
5VXM.PDB	O, A_TYR_276	N, A_ASN_280	H, A_ASN_280	2.79	1.94	7.45
5VXM.PDB	O, A_ALA_278	N, A_GLY_282	H, A_GLY_282	2.93	2.21	27.83
5VXM.PDB	O, A_TRP_279	N, A_PHE_283	H, A_PHE_283	2.71	1.90	16.14
5VXM.PDB	O, A_ALA_281	N, A_ALA_285	H, A_ALA_285	2.95	2.16	20.45
5VXM.PDB	O, A_GLY_282	N, A_GLU_286	H, A_GLU_286	2.89	2.04	9.37
5VXM.PDB	O, A_ALA_285	N, A_THR_289	H, A_THR_289	2.85	2.02	13.32
5VXM.PDB	O, A_GLU_286	N, A_MET_290	H, A_MET_290	2.99	2.16	12.67
5VXM.PDB	O, A_ASP_287	N, A_LYS_291	H, A_LYS_291	2.81	1.96	6.90
5VXM.PDB	OE2, A_GLU_288	NZ, A_LYS_291	HZ1, A_LYS_291	2.70	1.90	22.27
5VXM.PDB	O, A_GLU_288	N, A_ASN_292	H, A_ASN_292	2.85	2.03	14.40
5VXM.PDB	O, A_THR_289	N, A_ASN_293	H, A_ASN_293	2.86	2.04	14.91
5VXM.PDB	O, A_MET_290	N, A_LEU_294	H, A_LEU_294	2.98	2.18	17.50
5VXM.PDB	O, A_LYS_291	N, A_GLN_295	H, A_GLN_295	2.91	2.06	10.25
5VXM.PDB	O, A_ASN_292	N, A_THR_296	H, A_THR_296	2.99	2.15	11.78
5VXM.PDB	O, A_ASN_292	OG1, A_THR_296	HG1, A_THR_296	2.95	2.17	19.47
5VXM.PDB	O, A_LEU_294	N, A_VAL_298	H, A_VAL_298	2.79	1.95	9.51
5VXM.PDB	O, A_GLN_295	N, A_GLN_299	H, A_GLN_299	2.83	2.05	20.38
5VXM.PDB	O, A_VAL_298	N, A_SER_302	H, A_SER_302	2.97	2.12	8.83
5VXM.PDB	O, A_GLN_299	N, A_ASN_303	H, A_ASN_303	2.91	2.08	12.38
5VXM.PDB	O, A_LYS_300	N, A_ALA_304	H, A_ALA_304	2.94	2.10	8.88
5VXM.PDB	O, A_TYR_301	N, A_ASN_305	H, A_ASN_305	2.83	2.00	12.81
5VXM.PDB	O, A_SER_302	N, A_SER_306	H, A_SER_306	2.82	2.09	26.84
5VXM.PDB	O, A_ASN_303	N, A_ILE_307	H, A_ILE_307	2.93	2.12	16.79
5VXM.PDB	O, A_ALA_304	N, A_PHE_308	H, A_PHE_308	2.85	2.02	14.30
5VXM.PDB	O, A_ASN_305	N, A_ASP_309	H, A_ASP_309	2.84	2.05	19.19
5VXM.PDB	O, A_ASP_309	N, A_LYS_313	H, A_LYS_313	2.76	1.93	13.42
5VXM.PDB	O, B_SER_25	N, B_GLN_3	H, B_GLN_3	2.54	1.70	8.57
5VXM.PDB	O, B_SER_21	N, B_SER_7	H, B_SER_7	2.84	2.04	16.92
5VXM.PDB	O, B_LEU_86	N, B_GLY_15	H, B_GLY_15	2.69	1.85	9.47
5VXM.PDB	O, B_GLN_13	N, B_GLY_16	H, B_GLY_16	2.77	1.93	10.62
5VXM.PDB	O, B_MET_83	N, B_LEU_18	H, B_LEU_18	2.79	2.00	18.93
5VXM.PDB	O, B_LEU_81	N, B_LEU_20	H, B_LEU_20	2.91	2.09	14.06
5VXM.PDB	O, B_SER_7	N, B_SER_21	H, B_SER_21	2.77	1.94	13.53
5VXM.PDB	O, B_VAL_79	N, B_CYS_22	H, B_CYS_22	2.80	2.05	25.06
5VXM.PDB	O, B_VAL_5	N, B_ALA_23	H, B_ALA_23	2.85	2.03	14.23
5VXM.PDB	O, B_ASN_77	N, B_VAL_24	H, B_VAL_24	2.90	2.04	1.76
5VXM.PDB	O, B_GLN_3	N, B_SER_25	H, B_SER_25	2.84	2.00	10.15
5VXM.PDB	O, B_ALA_97	N, B_GLY_35	H, B_GLY_35	2.79	1.95	10.70

5VXM.PDB	O, B_SER_49	N, B_TRP_36	H, B_TRP_36	2.71	1.90	16.74
5VXM.PDB	O, B_PHE_95	N, B_PHE_37	H, B_PHE_37	2.88	2.07	17.02
5VXM.PDB	O, B_GLU_46	N, B_ARG_38	H, B_ARG_38	2.87	2.06	16.90
5VXM.PDB	OH, B_TYR_94	NH1, B_ARG_38	HH11, B_ARG_38	2.95	2.12	12.47
5VXM.PDB	OD1, B_ASP_90	NH1, B_ARG_38	HH12, B_ARG_38	2.77	1.97	17.13
5VXM.PDB	O, B_VAL_93	N, B_GLN_39	H, B_GLN_39	2.84	2.06	21.66
5VXM.PDB	O, B_ARG_38	N, B_GLU_46	H, B_GLU_46	2.82	2.11	29.28
5VXM.PDB	O, B_TRP_36	N, B_VAL_48	H, B_VAL_48	2.81	2.02	19.40
5VXM.PDB	O, B_ARG_59	OG, B_SER_49	HG, B_SER_49	2.90	2.19	27.71
5VXM.PDB	O, B_ARG_59	N, B_CYS_50	H, B_CYS_50	2.95	2.17	21.36
5VXM.PDB	O, B_ILE_34	N, B_ILE_51	H, B_ILE_51	2.96	2.19	22.03
5VXM.PDB	O, B_ASN_52	N, B_GLY_55	H, B_GLY_55	2.92	2.12	17.73
5VXM.PDB	OD1, B_ASP_54	OG, B_SER_56	HG, B_SER_56	2.63	1.84	17.09
5VXM.PDB	O, B_CYS_50	N, B_ARG_59	H, B_ARG_59	2.78	1.95	11.90
5VXM.PDB	O, B_VAL_48	N, B_ALA_61	H, B_ALA_61	2.94	2.11	11.33
5VXM.PDB	O, B_ALA_61	N, B_VAL_64	H, B_VAL_64	2.99	2.14	7.44
5VXM.PDB	OD2, B_ASP_90	NH1, B_ARG_67	HH12, B_ARG_67	2.75	1.92	11.95
5VXM.PDB	O, B_SER_63	NH2, B_ARG_67	HH21, B_ARG_67	2.79	1.93	1.60
5VXM.PDB	O, B_GLN_82	N, B_THR_69	H, B_THR_69	2.89	2.14	25.06
5VXM.PDB	OH, B_TYR_60	N, B_ILE_70	H, B_ILE_70	2.83	1.99	10.74
5VXM.PDB	O, B_THR_78	N, B_ASP_73	H, B_ASP_73	2.82	1.98	10.27
5VXM.PDB	O, B_LYS_76	OG1, B_THR_78	HG1, B_THR_78	2.89	2.13	21.00
5VXM.PDB	O, B_SER_71	N, B_TYR_80	H, B_TYR_80	2.70	1.86	9.68
5VXM.PDB	O, B_LEU_20	N, B_LEU_81	H, B_LEU_81	2.93	2.11	15.49
5VXM.PDB	O, B_THR_69	N, B_GLN_82	H, B_GLN_82	2.76	1.95	17.35
5VXM.PDB	OD1, B_ASN_84	NE2, B_GLN_82	HE21, B_GLN_82	2.81	1.97	10.38
5VXM.PDB	O, B_LEU_18	N, B_MET_83	H, B_MET_83	2.67	1.83	10.89
5VXM.PDB	OD2, B_ASP_90	N, B_LYS_87	H, B_LYS_87	2.82	1.98	12.23
5VXM.PDB	O, B_LYS_87	N, B_ASP_90	H, B_ASP_90	2.83	2.00	13.54
5VXM.PDB	O, B_VAL_121	N, B_ALA_92	H, B_ALA_92	2.97	2.16	16.91
5VXM.PDB	O, B_THR_119	N, B_TYR_94	H, B_TYR_94	2.86	2.01	6.10
5VXM.PDB	O, B_ASP_90	OH, B_TYR_94	HH, B_TYR_94	2.85	2.04	12.05
5VXM.PDB	O, B_PHE_37	N, B_PHE_95	H, B_PHE_95	2.68	1.84	10.79
5VXM.PDB	OE2, B_GLU_6	N, B_CYS_96	H, B_CYS_96	2.76	1.91	7.11
5VXM.PDB	O, B_GLY_35	N, B_ALA_97	H, B_ALA_97	2.99	2.18	17.54
5VXM.PDB	O, B_SER_114	N, B_ALA_98	H, B_ALA_98	2.98	2.19	20.00
5VXM.PDB	O, B_ALA_33	N, B_LYS_99	H, B_LYS_99	2.92	2.09	12.04
5VXM.PDB	O, B_CYS_104	NZ, B_LYS_99	HZ2, B_LYS_99	2.88	2.13	28.17
5VXM.PDB	O, B_PHE_103	NZ, B_LYS_99	HZ3, B_LYS_99	2.88	2.06	19.18
5VXM.PDB	O, A_ASP_166	NE1, B_TRP_102	HE1, B_TRP_102	2.92	2.09	13.88
5VXM.PDB	OE2, A_GLU_201	N, B_CYS_104	H, B_CYS_104	2.85	2.02	10.45
5VXM.PDB	OE1, A_GLU_201	N, B_SER_105	H, B_SER_105	2.58	1.74	9.22
5VXM.PDB	O, B_ALA_98	N, B_ASN_113	H, B_ASN_113	2.61	1.89	26.80
5VXM.PDB	O, B_CYS_96	N, B_GLY_116	H, B_GLY_116	2.83	2.02	17.26
5VXM.PDB	O, B_TYR_94	N, B_THR_119	H, B_THR_119	2.94	2.16	20.89
5VXM.PDB	O, B_ALA_92	N, B_VAL_121	H, B_VAL_121	2.99	2.14	5.92
5VXM.PDB	O, B_GLY_10	N, B_THR_122	H, B_THR_122	2.99	2.17	15.52
5VXM.PDB	OG1, B_THR_91	N, B_VAL_123	H, B_VAL_123	2.86	2.00	4.07
5VXR.PDB	O, H_THR_25	N, H_GLN_3	H, H_GLN_3	2.92	1.95	14.37
5VXR.PDB	O, H_THR_21	N, H_SER_7	H, H_SER_7	2.88	2.02	26.36
5VXR.PDB	O, H_THR_116	N, H_VAL_12	H, H_VAL_12	2.94	2.01	19.87
5VXR.PDB	O, H_VAL_85	N, H_SER_15	H, H_SER_15	2.75	1.75	7.98
5VXR.PDB	O, H_LEU_82	N, H_LEU_18	H, H_LEU_18	2.86	1.91	16.47
5VXR.PDB	O, H_LEU_80	N, H_LEU_20	H, H_LEU_20	2.86	1.87	11.91
5VXR.PDB	O, H_SER_7	N, H_THR_21	H, H_THR_21	2.94	1.94	9.22
5VXR.PDB	O, H_TYR_78	N, H_CYS_22	H, H_CYS_22	2.74	1.74	4.96
5VXR.PDB	O, H_GLN_5	N, H_SER_23	H, H_SER_23	2.92	1.94	11.80
5VXR.PDB	O, H_GLN_3	N, H_THR_25	H, H_THR_25	2.97	2.00	12.94

5VXR.PDB	OD1, H_ASN_76	N, H_ILE_29	H, H_ILE_29	2.90	1.95	16.89
5VXR.PDB	OH, H_TYR_100	N, H_GLY_32	H, H_GLY_32	2.89	1.92	12.65
5VXR.PDB	O, H_MET_98	N, H_TYR_33	H, H_TYR_33	2.88	1.88	9.69
5VXR.PDB	O, H_ILE_51	N, H_TRP_34	H, H_TRP_34	2.94	1.99	17.07
5VXR.PDB	O, H_SER_31	NE1, H_TRP_34	HE1, H_TRP_34	2.87	2.00	25.22
5VXR.PDB	O, H_ALA_96	N, H_ASN_35	H, H_ASN_35	2.84	1.89	16.00
5VXR.PDB	O, H_ALA_96	ND2, H_ASN_35	HD22, H_ASN_35	2.93	1.96	14.02
5VXR.PDB	O, H_GLY_49	N, H_TRP_36	H, H_TRP_36	2.83	1.89	18.36
5VXR.PDB	O, H_TYR_94	N, H_ILE_37	H, H_ILE_37	2.90	1.96	17.84
5VXR.PDB	O, H_GLU_46	N, H_ARG_38	H, H_ARG_38	2.92	1.95	13.24
5VXR.PDB	OE1, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.74	1.86	23.26
5VXR.PDB	OH, H_TYR_93	NH1, H_ARG_38	HH11, H_ARG_38	2.95	1.99	15.54
5VXR.PDB	OD1, H_ASP_89	NH1, H_ARG_38	HH12, H_ARG_38	2.81	1.80	4.81
5VXR.PDB	OE1, H_GLU_46	NH2, H_ARG_38	HH21, H_ARG_38	2.83	2.01	29.32
5VXR.PDB	O, H_THR_92	N, H_LYS_39	H, H_LYS_39	2.79	1.85	17.39
5VXR.PDB	OE1, L_GLN_38	NZ, H_LYS_39	HZ2, H_LYS_39	2.72	1.76	14.94
5VXR.PDB	O, H_LYS_44	N, H_PHE_40	H, H_PHE_40	2.95	2.01	17.78
5VXR.PDB	O, H_ARG_38	N, H_GLU_46	H, H_GLU_46	2.82	1.86	15.19
5VXR.PDB	OD1, H_ASN_35	OH, H_TYR_47	HH, H_TYR_47	2.72	1.74	8.88
5VXR.PDB	O, H_TRP_36	N, H_VAL_48	H, H_VAL_48	2.92	1.97	16.43
5VXR.PDB	O, H_TYR_58	N, H_TYR_50	H, H_TYR_50	2.82	1.91	21.30
5VXR.PDB	OD1, P_ASN_415	OH, H_TYR_50	HH, H_TYR_50	2.71	1.82	21.79
5VXR.PDB	O, H_TRP_34	N, H_ILE_51	H, H_ILE_51	2.89	1.95	17.36
5VXR.PDB	O, H_ASP_56	N, H_SER_52	H, H_SER_52	2.72	1.75	13.95
5VXR.PDB	O, H_SER_52	N, H_GLY_55	H, H_GLY_55	2.89	1.89	5.97
5VXR.PDB	O, H_VAL_48	N, H_ASN_60	H, H_ASN_60	2.87	1.86	4.40
5VXR.PDB	O, H_TYR_47	ND2, H_ASN_60	HD22, H_ASN_60	2.79	1.80	10.72
5VXR.PDB	OD1, H_ASN_60	N, H_SER_62	H, H_SER_62	2.94	2.03	22.09
5VXR.PDB	O, H_ASN_60	N, H_LEU_63	H, H_LEU_63	2.95	1.98	13.61
5VXR.PDB	O, H_LEU_63	N, H_ARG_66	H, H_ARG_66	2.91	1.93	12.44
5VXR.PDB	O, H_ASN_83	NH1, H_ARG_66	HH11, H_ARG_66	2.95	1.98	13.74
5VXR.PDB	OD1, H_ASP_89	NH2, H_ARG_66	HH22, H_ARG_66	2.99	1.98	4.54
5VXR.PDB	O, H_GLN_81	N, H_SER_68	H, H_SER_68	2.99	2.08	21.53
5VXR.PDB	O, H_TYR_53	NH1, H_ARG_71	HH12, H_ARG_71	2.89	2.01	24.28
5VXR.PDB	O, H_GLN_77	N, H_ASP_72	H, H_ASP_72	2.86	1.87	9.03
5VXR.PDB	O, H_ASP_27	ND2, H_ASN_76	HD21, H_ASN_76	2.65	1.73	19.67
5VXR.PDB	O, H_ASN_35	OH, H_TYR_78	HH, H_TYR_78	2.85	1.87	7.07
5VXR.PDB	O, H_THR_70	N, H_TYR_79	H, H_TYR_79	2.84	1.90	18.23
5VXR.PDB	OE1, H_GLN_77	OH, H_TYR_79	HH, H_TYR_79	2.72	1.76	12.10
5VXR.PDB	O, H_LEU_20	N, H_LEU_80	H, H_LEU_80	2.93	1.97	15.68
5VXR.PDB	O, H_SER_68	N, H_GLN_81	H, H_GLN_81	2.89	1.91	12.77
5VXR.PDB	O, H_LEU_18	N, H_LEU_82	H, H_LEU_82	2.90	1.93	13.50
5VXR.PDB	O, H_ARG_66	N, H_ASN_83	H, H_ASN_83	2.85	1.86	10.37
5VXR.PDB	O, H_THR_86	N, H_ASP_89	H, H_ASP_89	2.84	1.84	7.21
5VXR.PDB	O, H_LYS_39	N, H_THR_92	H, H_THR_92	2.80	1.83	13.98
5VXR.PDB	O, H_THR_113	N, H_TYR_93	H, H_TYR_93	2.85	1.85	8.50
5VXR.PDB	O, H_ASP_89	OH, H_TYR_93	HH, H_TYR_93	2.69	1.71	5.93
5VXR.PDB	O, H_ILE_37	N, H_TYR_94	H, H_TYR_94	2.75	1.75	6.84
5VXR.PDB	OE2, H_GLU_6	N, H_CYS_95	H, H_CYS_95	2.78	1.84	17.15
5VXR.PDB	O, H_SER_108	N, H_ARG_97	H, H_ARG_97	2.83	1.90	18.04
5VXR.PDB	O, H_TYR_33	N, H_MET_98	H, H_MET_98	2.92	1.95	14.04
5VXR.PDB	O, H_TYR_100	N, H_GLN_103	H, H_GLN_103	2.92	2.02	21.61
5VXR.PDB	OH, L_TYR_36	N, H_PHE_106	H, H_PHE_106	2.92	1.92	7.59
5VXR.PDB	O, H_CYS_95	N, H_GLY_110	H, H_GLY_110	2.91	1.93	12.29
5VXR.PDB	OE1, H_GLU_6	N, H_GLY_112	H, H_GLY_112	2.87	1.90	13.05
5VXR.PDB	O, H_TYR_93	N, H_THR_113	H, H_THR_113	2.95	2.02	20.05
5VXR.PDB	O, H_ALA_91	N, H_VAL_115	H, H_VAL_115	2.97	1.97	6.59
5VXR.PDB	O, H_SER_10	N, H_THR_116	H, H_THR_116	2.95	1.96	9.99

5VXR.PDB	OG1, H_THR_90	N, H_VAL_117	H, H_VAL_117	2.94	1.93	5.04
5VXR.PDB	O, H_VAL_12	N, H_SER_118	H, H_SER_118	2.98	2.10	24.14
5VXR.PDB	OG, H_SER_118	N, H_ALA_120	H, H_ALA_120	2.97	2.00	14.42
5VXR.PDB	O, H_PHE_152	N, H_THR_123	H, H_THR_123	2.88	1.92	15.25
5VXR.PDB	O, H_LYS_149	N, H_SER_126	H, H_SER_126	2.81	1.84	13.35
5VXR.PDB	O, H_LEU_147	N, H_TYR_128	H, H_TYR_128	2.83	1.83	9.66
5VXR.PDB	O, H_GLY_145	N, H_LEU_130	H, H_LEU_130	2.83	1.90	19.03
5VXR.PDB	O, H_VAL_189	N, H_VAL_142	H, H_VAL_142	2.94	1.98	15.04
5VXR.PDB	O, H_VAL_187	N, H_LEU_144	H, H_LEU_144	2.89	1.92	13.91
5VXR.PDB	O, H_LEU_130	N, H_GLY_145	H, H_GLY_145	2.93	2.02	21.14
5VXR.PDB	O, H_SER_185	N, H_CYS_146	H, H_CYS_146	2.89	1.97	20.23
5VXR.PDB	O, H_TYR_128	N, H_LEU_147	H, H_LEU_147	2.91	1.92	10.17
5VXR.PDB	O, H_MET_183	N, H_VAL_148	H, H_VAL_148	2.86	1.85	4.57
5VXR.PDB	O, H_SER_126	N, H_LYS_149	H, H_LYS_149	2.87	1.88	10.16
5VXR.PDB	OE2, H_GLU_154	OH, H_TYR_151	HH, H_TYR_151	2.81	1.83	6.84
5VXR.PDB	O, H_THR_123	N, H_PHE_152	H, H_PHE_152	2.98	2.05	18.35
5VXR.PDB	O, H_SER_202	N, H_THR_159	H, H_THR_159	2.91	1.94	14.94
5VXR.PDB	OG, H_SER_185	NE1, H_TRP_160	HE1, H_TRP_160	2.93	1.93	7.21
5VXR.PDB	O, H_THR_188	OG, H_SER_168	HG, H_SER_168	2.72	1.82	20.67
5VXR.PDB	O, H_SER_186	N, H_HIS_170	H, H_HIS_170	2.94	2.01	18.18
5VXR.PDB	OD1, L_ASN_138	NE2, H_HIS_170	HE2, H_HIS_170	2.89	1.98	20.57
5VXR.PDB	O, H_SER_184	N, H_PHE_172	H, H_PHE_172	2.89	1.89	7.85
5VXR.PDB	O, H_THR_182	N, H_LEU_175	H, H_LEU_175	2.96	2.01	16.29
5VXR.PDB	O, H_GLN_177	OG, H_SER_178	HG, H_SER_178	2.93	2.03	20.61
5VXR.PDB	O, H_TYR_151	N, H_TYR_181	H, H_TYR_181	2.81	1.80	4.32
5VXR.PDB	O, H_VAL_148	N, H_MET_183	H, H_MET_183	2.89	1.92	13.39
5VXR.PDB	O, H_LEU_144	N, H_VAL_187	H, H_VAL_187	2.82	1.86	14.30
5VXR.PDB	OG1, H_THR_143	OG1, H_THR_188	HG1, H_THR_188	2.81	1.84	10.15
5VXR.PDB	O, H_GLY_139	OG, H_ASER_191	HG, H_ASER_191	2.77	1.88	20.92
5VXR.PDB	O, H_GLY_139	OG, H_BSER_191	HG, H_BSER_191	2.77	1.86	19.71
5VXR.PDB	O, H_PRO_190	N, H_THR_193	H, H_THR_193	2.87	1.87	5.97
5VXR.PDB	O, H_THR_193	N, H_GLN_197	H, H_GLN_197	2.93	2.07	26.39
5VXR.PDB	OD1, H_ASN_161	N, H_THR_200	H, H_THR_200	2.97	2.02	17.18
5VXR.PDB	O, H_THR_159	N, H_SER_202	H, H_SER_202	2.75	1.75	5.74
5VXR.PDB	O, H_VAL_212	N, H_VAL_203	H, H_VAL_203	2.81	1.81	7.96
5VXR.PDB	O, H_THR_157	N, H_ALA_204	H, H_ALA_204	2.86	1.90	13.85
5VXR.PDB	O, H_THR_210	N, H_HIS_205	H, H_HIS_205	2.82	1.84	11.68
5VXR.PDB	O, H_PRO_153	NE2, H_HIS_205	HE2, H_HIS_205	2.81	1.82	9.76
5VXR.PDB	O, H_PRO_206	N, H_SER_209	H, H_SER_209	2.98	2.02	13.76
5VXR.PDB	O, H_SER_208	OG1, H_THR_210	HG1, H_THR_210	2.87	2.03	26.51
5VXR.PDB	O, H_VAL_203	N, H_VAL_212	H, H_VAL_212	2.95	2.00	16.98
5VXR.PDB	O, H_CYS_201	N, H_LYS_214	H, H_LYS_214	2.91	2.01	22.37
5VXR.PDB	OE2, L_GLU_123	NZ, H_LYS_214	HZ1, H_LYS_214	2.93	1.98	15.97
5VXR.PDB	O, H_VAL_199	N, H_LEU_216	H, H_LEU_216	2.90	1.89	4.43
5VXR.PDB	OG, L_SER_26	N, L_VAL_3	H, L_VAL_3	2.91	1.91	7.32
5VXR.PDB	O, L_ARG_24	N, L_THR_5	H, L_THR_5	2.78	1.77	4.90
5VXR.PDB	O, L_TYR_86	NE2, L_GLN_6	HE22, L_GLN_6	2.89	1.89	8.04
5VXR.PDB	O, L_SER_22	N, L_SER_7	H, L_SER_7	2.95	2.03	19.63
5VXR.PDB	O, L_LYS_103	N, L_LEU_11	H, L_LEU_11	2.93	2.01	19.94
5VXR.PDB	O, L_GLU_105	N, L_VAL_13	H, L_VAL_13	2.91	1.98	18.79
5VXR.PDB	O, L_VAL_78	N, L_GLY_16	H, L_GLY_16	2.93	1.93	8.01
5VXR.PDB	O, L_ILE_75	N, L_ALA_19	H, L_ALA_19	2.83	1.83	8.13
5VXR.PDB	O, L_SER_7	N, L_SER_22	H, L_SER_22	2.84	1.82	1.96
5VXR.PDB	O, L_PHE_71	N, L_CYS_23	H, L_CYS_23	2.89	1.92	13.55
5VXR.PDB	O, L_THR_5	N, L_ARG_24	H, L_ARG_24	2.90	1.89	4.93
5VXR.PDB	OD1, L_ASP_70	NE, L_ARG_24	HE, L_ARG_24	2.94	2.08	26.80
5VXR.PDB	O, L_THR_69	N, L_ALA_25	H, L_ALA_25	2.84	1.89	15.97
5VXR.PDB	O, L_LYS_30	N, L_SER_27D	H, L_SER_27D	2.97	2.06	21.07

5VXR.PDB	OD1, L_ASN_92	OG, L_SER_27D	HG, L_SER_27D	2.79	1.83	11.69
5VXR.PDB	O, L_SER_27D	N, L_LYS_30	H, L_LYS_30	3.00	2.02	13.12
5VXR.PDB	O, H_GLY_101	NZ, L_LYS_30	HZ1, L_LYS_30	2.83	1.85	13.06
5VXR.PDB	O, L_GLN_89	N, L_HIS_34	H, L_HIS_34	2.88	1.90	13.39
5VXR.PDB	OD1, L_ASN_91	NE2, L_HIS_34	HE2, L_HIS_34	2.77	1.79	12.93
5VXR.PDB	O, L_ILE_48	N, L_TRP_35	H, L_TRP_35	2.81	1.84	13.58
5VXR.PDB	O, L_TYR_87	N, L_TYR_36	H, L_TYR_36	2.86	1.93	18.12
5VXR.PDB	OE1, L_GLN_89	OH, L_TYR_36	HH, L_TYR_36	2.69	1.74	13.43
5VXR.PDB	O, L_LYS_45	N, L_GLN_37	H, L_GLN_37	2.88	1.93	17.34
5VXR.PDB	OH, L_TYR_86	NE2, L_GLN_37	HE21, L_GLN_37	2.98	1.98	9.70
5VXR.PDB	O, L_THR_85	N, L_GLN_38	H, L_GLN_38	2.78	1.82	15.10
5VXR.PDB	O, L_GLN_42	NE2, L_GLN_38	HE21, L_GLN_38	2.91	1.92	11.28
5VXR.PDB	O, L_ASP_81	NZ, L_LYS_39	HZ3, L_LYS_39	2.63	1.68	15.29
5VXR.PDB	O, L_GLN_37	N, L_LYS_45	H, L_LYS_45	2.79	1.86	19.53
5VXR.PDB	O, L_TRP_35	N, L_LEU_47	H, L_LEU_47	2.83	1.83	6.37
5VXR.PDB	O, L_ASN_53	N, L_TYR_49	H, L_TYR_49	2.88	1.93	17.74
5VXR.PDB	O, L_LEU_33	N, L_ALA_51	H, L_ALA_51	2.80	1.87	18.75
5VXR.PDB	O, L_TYR_49	N, L_ASN_53	H, L_ASN_53	2.90	1.93	14.40
5VXR.PDB	O, L_LEU_47	N, L_GLU_55	H, L_GLU_55	2.95	1.94	3.22
5VXR.PDB	O, L_PRO_59	N, L_ARG_61	H, L_ARG_61	2.78	1.96	29.25
5VXR.PDB	O, L_PRO_77	NH1, L_ARG_61	HH11, L_ARG_61	2.81	1.92	23.49
5VXR.PDB	OD2, L_ASP_82	NH1, L_ARG_61	HH12, L_ARG_61	2.75	1.79	15.16
5VXR.PDB	OD1, L_ASP_82	NH2, L_ARG_61	HH22, L_ARG_61	2.82	1.82	7.27
5VXR.PDB	O, L_THR_74	N, L_SER_63	H, L_SER_63	2.98	2.05	19.15
5VXR.PDB	O, L_THR_72	N, L_SER_65	H, L_SER_65	2.96	2.02	18.59
5VXR.PDB	OD1, L_ASP_27C	N, L_ARG_68	H, L_ARG_68	2.98	2.08	21.58
5VXR.PDB	O, L_CYS_23	N, L_PHE_71	H, L_PHE_71	2.90	2.01	23.31
5VXR.PDB	O, L_SER_65	N, L_THR_72	H, L_THR_72	2.91	1.95	14.63
5VXR.PDB	O, L_ILE_21	N, L_LEU_73	H, L_LEU_73	2.86	1.89	14.64
5VXR.PDB	O, L_SER_63	N, L_THR_74	H, L_THR_74	2.84	1.84	5.95
5VXR.PDB	O, L_ALA_19	N, L_ILE_75	H, L_ILE_75	2.86	1.89	14.39
5VXR.PDB	O, L_ARG_61	N, L_ASP_76	H, L_ASP_76	2.76	1.80	14.69
5VXR.PDB	O, L_GLN_17	N, L_VAL_78	H, L_VAL_78	2.93	1.95	13.22
5VXR.PDB	OD2, L_ASP_82	N, L_GLU_79	H, L_GLU_79	2.85	1.85	8.34
5VXR.PDB	O, L_GLU_79	N, L_ASP_82	H, L_ASP_82	2.97	1.97	6.55
5VXR.PDB	O, L_THR_102	N, L_TYR_86	H, L_TYR_86	2.91	1.93	13.41
5VXR.PDB	O, L_ASP_82	OH, L_TYR_86	HH, L_TYR_86	2.70	1.78	16.73
5VXR.PDB	O, L_TYR_36	N, L_TYR_87	H, L_TYR_87	2.90	1.95	16.78
5VXR.PDB	O, L_THR_97	N, L_HIS_90	H, L_HIS_90	2.99	2.05	18.83
5VXR.PDB	O, P_GLY_418	NE1, L_TRP_96	HE1, L_TRP_96	2.88	1.87	5.74
5VXR.PDB	O, L_ILE_2	OG1, L_THR_97	HG1, L_THR_97	2.97	2.02	14.29
5VXR.PDB	O, L_CYS_88	N, L_GLY_99	H, L_GLY_99	2.83	1.83	7.30
5VXR.PDB	O, L_TYR_86	N, L_THR_102	H, L_THR_102	2.94	2.03	21.75
5VXR.PDB	O, L_PRO_8	OG1, L_THR_102	HG1, L_THR_102	2.75	1.79	11.72
5VXR.PDB	O, L_ALA_84	N, L_LEU_104	H, L_LEU_104	2.91	1.89	2.60
5VXR.PDB	OE1, L_GLN_166	N, L_ILE_106	H, L_ILE_106	2.84	1.85	9.18
5VXR.PDB	O, L_VAL_13	N, L_LYS_107	H, L_LYS_107	2.81	1.82	9.46
5VXR.PDB	O, L_ALA_109	NE, L_ARG_108	HE, L_ARG_108	2.87	1.86	6.94
5VXR.PDB	O, L_ASP_170	NH1, L_ARG_108	HH11, L_ARG_108	2.81	1.81	8.28
5VXR.PDB	O, L_TYR_140	N, L_ALA_111	H, L_ALA_111	2.89	1.90	8.41
5VXR.PDB	O, L_ASN_137	N, L_THR_114	H, L_THR_114	2.87	1.88	8.25
5VXR.PDB	O, L_PHE_135	N, L_SER_116	H, L_SER_116	2.96	2.02	17.37
5VXR.PDB	O, L_VAL_133	N, L_PHE_118	H, L_PHE_118	2.78	1.90	24.38
5VXR.PDB	OG, L_SER_131	NE2, L_GLN_124	HE22, L_GLN_124	2.92	1.91	5.03
5VXR.PDB	O, L_SER_122	N, L_THR_126	H, L_THR_126	2.91	1.96	16.41
5VXR.PDB	O, L_GLN_124	OG, L_SER_127	HG, L_SER_127	2.77	1.86	18.69
5VXR.PDB	O, L_LEU_181	N, L_ALA_130	H, L_ALA_130	2.92	2.02	22.78
5VXR.PDB	OE1, L_GLN_124	N, L_SER_131	H, L_SER_131	2.86	1.94	21.02

5VXR.PDB	O, L_LEU_179	N, L_VAL_132	H, L_VAL_132	2.84	1.88	14.58
5VXR.PDB	O, L_SER_116	N, L_PHE_135	H, L_PHE_135	2.89	1.98	20.99
5VXR.PDB	O, L_MET_175	N, L_LEU_136	H, L_LEU_136	2.88	1.87	5.63
5VXR.PDB	O, L_THR_114	N, L_ASN_137	H, L_ASN_137	2.89	1.90	10.32
5VXR.PDB	OG, L_SER_174	N, L_ASN_138	H, L_ASN_138	2.95	1.98	14.50
5VXR.PDB	O, L_TYR_173	N, L_PHE_139	H, L_PHE_139	2.83	1.84	11.10
5VXR.PDB	O, L_ALA_111	N, L_TYR_140	H, L_TYR_140	2.94	1.98	15.41
5VXR.PDB	O, L_GLU_195	N, L_LYS_147	H, L_LYS_147	2.93	1.98	16.97
5VXR.PDB	OG, L_SER_177	NE1, L_TRP_148	HE1, L_TRP_148	2.80	1.85	16.41
5VXR.PDB	O, L_THR_193	N, L_LYS_149	H, L_LYS_149	2.85	1.88	14.14
5VXR.PDB	O, L_SER_153	N, L_ILE_150	H, L_ILE_150	2.93	1.98	15.57
5VXR.PDB	O, L_SER_191	N, L_ASP_151	H, L_ASP_151	2.78	1.80	12.18
5VXR.PDB	O, L_ILE_150	N, L_SER_153	H, L_SER_153	2.99	1.99	4.98
5VXR.PDB	O, L_TRP_148	N, L_ARG_155	H, L_ARG_155	2.93	1.99	17.51
5VXR.PDB	O, L_THR_178	N, L_LEU_160	H, L_LEU_160	2.91	1.98	18.71
5VXR.PDB	O, L_SER_176	N, L_SER_162	H, L_SER_162	2.83	1.87	15.71
5VXR.PDB	O, L_SER_174	N, L_THR_164	H, L_THR_164	2.88	1.88	8.76
5VXR.PDB	O, L_SER_171	NE2, L_GLN_166	HE21, L_GLN_166	2.83	1.86	12.46
5VXR.PDB	O, L_ILE_106	NE2, L_GLN_166	HE22, L_GLN_166	2.77	1.85	20.51
5VXR.PDB	O, L_THR_172	N, L_ASP_167	H, L_ASP_167	2.85	1.85	9.35
5VXR.PDB	OD2, L_ASP_167	N, L_LYS_169	H, L_LYS_169	2.90	1.99	21.19
5VXR.PDB	OD2, L_ASP_167	N, L_ASP_170	H, L_ASP_170	2.84	1.89	16.19
5VXR.PDB	OD1, L_ASP_170	N, L_THR_172	H, L_THR_172	2.96	2.00	16.34
5VXR.PDB	OD1, L_ASP_170	OG1, L_THR_172	HG1, L_THR_172	2.70	1.76	15.44
5VXR.PDB	O, L_PHE_139	N, L_TYR_173	H, L_TYR_173	2.85	1.84	7.73
5VXR.PDB	O, L_LEU_136	N, L_MET_175	H, L_MET_175	2.84	1.91	18.20
5VXR.PDB	O, L_SER_162	N, L_SER_176	H, L_SER_176	2.88	1.94	17.54
5VXR.PDB	OG, H_SER_184	OG, L_SER_176	HG, L_SER_176	2.79	1.86	17.30
5VXR.PDB	O, L_CYS_134	N, L_SER_177	H, L_SER_177	2.91	1.91	10.22
5VXR.PDB	OD1, L_ASN_161	OG, L_SER_177	HG, L_SER_177	2.64	1.73	19.24
5VXR.PDB	O, L_LEU_160	N, L_THR_178	H, L_THR_178	2.85	1.91	18.48
5VXR.PDB	O, L_VAL_132	N, L_LEU_179	H, L_LEU_179	2.78	1.81	13.39
5VXR.PDB	O, L_GLY_158	N, L_THR_180	H, L_THR_180	2.83	1.86	14.32
5VXR.PDB	OG, L_SER_131	OG1, L_THR_180	HG1, L_THR_180	2.88	2.00	21.77
5VXR.PDB	O, L_ALA_130	N, L_LEU_181	H, L_LEU_181	2.83	1.84	9.97
5VXR.PDB	O, L_GLY_128	N, L_LYS_183	H, L_LYS_183	2.94	1.97	12.73
5VXR.PDB	O, L_THR_182	N, L_TYR_186	H, L_TYR_186	2.95	1.95	8.11
5VXR.PDB	O, L_LYS_183	N, L_GLU_187	H, L_GLU_187	3.00	2.08	21.03
5VXR.PDB	OD2, L_ASP_151	ND1, L_HIS_189	HD1, L_HIS_189	2.73	1.79	17.03
5VXR.PDB	OD1, L_ASP_151	N, L_SER_191	H, L_SER_191	2.90	1.90	6.70
5VXR.PDB	O, L_PHE_209	N, L_TYR_192	H, L_TYR_192	2.97	1.97	6.50
5VXR.PDB	O, L_LYS_149	N, L_THR_193	H, L_THR_193	2.96	2.06	22.36
5VXR.PDB	O, L_LYS_147	N, L_GLU_195	H, L_GLU_195	2.79	1.85	17.75
5VXR.PDB	O, L_ILE_205	N, L_ALA_196	H, L_ALA_196	2.78	1.81	13.90
5VXR.PDB	O, L_ASN_145	N, L_THR_197	H, L_THR_197	2.84	1.85	9.75
5VXR.PDB	O, L_PRO_141	NE2, L_HIS_198	HE2, L_HIS_198	2.90	1.90	7.27
5VXR.PDB	ND1, L_HIS_198	OG1, L_THR_200	HG1, L_THR_200	2.74	1.84	20.28
5VXR.PDB	O, L_SER_203	OG, L_SER_201	HG, L_SER_201	2.73	1.78	13.42
5VXR.PDB	O, L_ALA_196	N, L_ILE_205	H, L_ILE_205	2.98	2.07	22.00
5VXR.PDB	O, L_ASN_190	N, L_ARG_211	H, L_ARG_211	2.77	1.80	14.86
5VXR.PDB	O, L_HIS_189	NE, L_ARG_211	HE, L_ARG_211	2.85	1.85	8.53
5VXR.PDB	O, P_HIS_421	N, P_ILE_414	H, P_ILE_414	2.99	2.01	11.82
5VXR.PDB	OH, H_TYR_33	N, P_ASN_415	H, P_ASN_415	2.82	1.94	24.20
5VXR.PDB	O, P_SER_419	N, P_THR_416	H, P_THR_416	2.88	1.93	15.75
5VXR.PDB	NE2, P_HIS_421	OG1, P_THR_416	HG1, P_THR_416	2.72	1.87	24.94
5VXR.PDB	O, L_ASN_91	NE1, P_TRP_420	HE1, P_TRP_420	2.80	1.97	28.78
5VXR.PDB	O, P_ILE_414	N, P_HIS_421	H, P_HIS_421	2.91	2.04	25.40
5WKQ.PDB	O, A_ASN_74	N, A_GLN_78	H, A_GLN_78	2.98	2.14	9.16

5WKQ.PDB	O, A_ALA_75	N, A_LEU_79	H, A_LEU_79	2.93	2.08	8.87
5WKQ.PDB	O, A_SER_76	OG1, A_THR_80	HG1, A_THR_80	2.93	2.13	16.27
5WKQ.PDB	O, A_GLN_78	N, A_LEU_82	H, A_LEU_82	2.82	2.00	15.52
5WKQ.PDB	O, A_LEU_79	N, A_ILE_83	H, A_ILE_83	2.90	2.05	7.59
5WKQ.PDB	O, A_LEU_81	N, A_ASN_85	H, A_ASN_85	2.92	2.07	7.63
5WKQ.PDB	O, A_ILE_83	N, A_ILE_87	H, A_ILE_87	2.92	2.08	9.62
5WKQ.PDB	O, A_LEU_86	N, A_LEU_90	H, A_LEU_90	2.92	2.07	6.38
5WKQ.PDB	O, A_ILE_87	N, A_GLY_91	H, A_GLY_91	2.97	2.16	15.88
5WKQ.PDB	O, A_GLY_91	OG, A_SER_94	HG, A_SER_94	2.98	2.17	13.97
5WKQ.PDB	O, A_LEU_95	N, A_THR_99	H, A_THR_99	2.87	2.01	5.83
5WKQ.PDB	O, A_THR_96	N, A_ASN_100	H, A_ASN_100	2.93	2.14	18.75
5WKQ.PDB	O, A_LEU_98	N, A_ILE_102	H, A_ILE_102	2.87	2.09	20.92
5WKQ.PDB	O, A_THR_99	N, A_THR_103	H, A_THR_103	2.97	2.15	15.29
5WKQ.PDB	O, A_LYS_101	N, A_TRP_105	H, A_TRP_105	2.97	2.17	18.38
5WKQ.PDB	OG1, A_THR_80	NZ, A_LYS_106	HZ1, A_LYS_106	2.47	1.72	27.03
5WKQ.PDB	O, A_ALA_104	N, A_GLN_108	H, A_GLN_108	2.95	2.11	11.57
5WKQ.PDB	O, A_TRP_105	N, A_GLN_109	H, A_GLN_109	2.89	2.04	3.84
5WKQ.PDB	O, A_LYS_106	N, A_GLN_110	H, A_GLN_110	2.89	2.05	11.19
5WKQ.PDB	O, A_SER_107	N, A_ALA_111	H, A_ALA_111	3.00	2.17	13.35
5WKQ.PDB	O, A_GLN_108	N, A_ARG_112	H, A_ARG_112	2.98	2.16	14.92
5WKQ.PDB	O, A_GLN_109	N, A_GLN_113	H, A_GLN_113	2.94	2.10	9.80
5WKQ.PDB	O, A_ARG_112	N, A_ASN_116	H, A_ASN_116	2.83	1.99	11.00
5WKQ.PDB	O, A_GLN_113	N, A_LEU_117	H, A_LEU_117	2.99	2.18	16.36
5WKQ.PDB	O, A_LYS_115	N, A_PHE_119	H, A_PHE_119	2.80	1.98	13.76
5WKQ.PDB	O, A_ASN_116	N, A_SER_120	H, A_SER_120	2.81	1.97	9.85
5WKQ.PDB	O, A_PHE_119	N, A_ILE_123	H, A_ILE_123	2.99	2.14	9.43
5WKQ.PDB	O, A_SER_120	N, A_ASN_124	H, A_ASN_124	2.97	2.14	13.74
5WKQ.PDB	O, A_ILE_123	N, A_LEU_127	H, A_LEU_127	2.86	2.03	12.46
5WKQ.PDB	O, A_THR_125	N, A_GLU_129	H, A_GLU_129	2.89	2.06	14.27
5WKQ.PDB	O, A_LEU_126	N, A_THR_130	H, A_THR_130	2.85	2.02	13.06
5WKQ.PDB	O, A_LEU_127	N, A_GLU_131	H, A_GLU_131	2.91	2.07	8.81
5WKQ.PDB	O, A_SER_128	N, A_GLY_132	H, A_GLY_132	2.95	2.11	11.67
5WKQ.PDB	O, A_THR_130	N, A_THR_134	H, A_THR_134	2.86	2.03	13.70
5WKQ.PDB	O, A_THR_130	OG1, A_THR_134	HG1, A_THR_134	2.90	2.17	24.55
5WKQ.PDB	O, A_GLU_131	N, A_ARG_135	H, A_ARG_135	2.96	2.15	15.46
5WKQ.PDB	OG, B_SER_208	NH2, A_ARG_135	HH21, A_ARG_135	2.89	2.06	11.87
5WKQ.PDB	O, A_LEU_133	N, A_TYR_137	H, A_TYR_137	2.86	2.07	19.86
5WKQ.PDB	O, A_THR_134	N, A_GLU_138	H, A_GLU_138	2.82	1.98	11.30
5WKQ.PDB	O, A_TYR_137	N, A_ILE_141	H, A_ILE_141	2.92	2.07	6.24
5WKQ.PDB	O, A_GLN_140	N, A_LEU_144	H, A_LEU_144	2.76	1.98	19.80
5WKQ.PDB	O, A_ILE_141	N, A_LYS_145	H, A_LYS_145	2.95	2.17	21.49
5WKQ.PDB	O, A_LYS_143	N, A_ALA_147	H, A_ALA_147	2.98	2.17	16.58
5WKQ.PDB	O, A_LEU_144	N, A_ASP_148	H, A_ASP_148	2.92	2.09	13.80
5WKQ.PDB	O, A_ALA_147	N, A_ILE_151	H, A_ILE_151	3.00	2.18	14.31
5WKQ.PDB	O, A_SER_149	N, A_ASP_153	H, A_ASP_153	2.97	2.14	11.92
5WKQ.PDB	O, A_ILE_151	N, A_GLU_155	H, A_GLU_155	2.91	2.05	3.54
5WKQ.PDB	O, A_LYS_152	N, A_ASN_156	H, A_ASN_156	2.94	2.16	21.59
5WKQ.PDB	O, A_ASP_153	N, A_LYS_157	H, A_LYS_157	2.91	2.13	20.82
5WKQ.PDB	O, A_LEU_154	N, A_ILE_158	H, A_ILE_158	2.88	2.06	14.11
5WKQ.PDB	O, A_GLU_155	N, A_ASN_159	H, A_ASN_159	2.95	2.11	10.87
5WKQ.PDB	O, A_LYS_157	N, A_ILE_161	H, A_ILE_161	2.96	2.13	11.39
5WKQ.PDB	O, A_ILE_158	N, A_GLN_162	H, A_GLN_162	2.96	2.16	19.47
5WKQ.PDB	OE2, A_GLU_182	NE2, A_GLN_162	HE21, A_GLN_162	2.71	1.89	15.15
5WKQ.PDB	O, A_ILE_161	N, A_LEU_165	H, A_LEU_165	2.83	2.01	14.76
5WKQ.PDB	O, A_THR_163	OG, A_SER_166	HG, A_SER_166	2.82	1.99	6.15
5WKQ.PDB	O, A_ARG_164	N, A_GLU_167	H, A_GLU_167	2.98	2.16	15.01
5WKQ.PDB	O, A_LYS_175	N, A_SER_179	H, A_SER_179	2.81	1.95	0.77
5WKQ.PDB	O, A_LYS_177	N, A_GLU_181	H, A_GLU_181	2.97	2.17	18.02

5WKQ.PDB	O, A_LEU_178	N, A_GLU_182	H, A_GLU_182	2.79	1.97	15.96
5WKQ.PDB	O, A_SER_179	N, A_ILE_183	H, A_ILE_183	2.86	2.03	12.39
5WKQ.PDB	O, A_GLU_182	N, A_THR_186	H, A_THR_186	2.96	2.16	17.62
5WKQ.PDB	O, A_GLU_182	OG1, A_THR_186	HG1, A_THR_186	2.95	2.25	28.98
5WKQ.PDB	O, A_LEU_185	N, A_LYS_189	H, A_LYS_189	2.81	2.00	16.47
5WKQ.PDB	O, A_THR_186	N, A_ASP_190	H, A_ASP_190	2.80	1.95	5.67
5WKQ.PDB	O, A_LYS_188	N, A_ALA_192	H, A_ALA_192	2.92	2.13	19.91
5WKQ.PDB	O, A_LYS_189	N, A_VAL_193	H, A_VAL_193	2.85	2.05	18.34
5WKQ.PDB	O, A_ALA_192	N, A_ARG_196	H, A_ARG_196	2.85	2.00	8.33
5WKQ.PDB	O, A_ASP_195	N, A_ILE_199	H, A_ILE_199	2.97	2.14	13.27
5WKQ.PDB	O, A_ARG_196	N, A_GLU_200	H, A_GLU_200	2.87	2.01	4.50
5WKQ.PDB	O, A_LEU_198	N, A_LYS_202	H, A_LYS_202	2.90	2.10	18.39
5WKQ.PDB	O, A_ILE_199	N, A_THR_203	H, A_THR_203	2.80	1.96	10.08
5WKQ.PDB	O, A_ILE_199	OG1, A_THR_203	HG1, A_THR_203	2.97	2.24	25.20
5WKQ.PDB	O, A_LEU_204	N, A_SER_208	H, A_SER_208	2.96	2.20	23.33
5WKQ.PDB	O, A_ILE_206	N, A_LEU_210	H, A_LEU_210	2.92	2.12	17.69
5WKQ.PDB	O, A_HIS_207	N, A_THR_211	H, A_THR_211	3.00	2.23	23.43
5WKQ.PDB	O, A_SER_208	N, A_ASP_212	H, A_ASP_212	2.86	2.05	16.07
5WKQ.PDB	O, A_LYS_209	N, A_LYS_213	H, A_LYS_213	2.99	2.21	20.73
5WKQ.PDB	O, A_LEU_210	N, A_SER_214	H, A_SER_214	2.99	2.17	15.42
5WKQ.PDB	O, A_THR_211	OG, A_SER_214	HG, A_SER_214	2.74	1.93	13.01
5WKQ.PDB	O, A_ASP_212	N, A_GLN_216	H, A_GLN_216	2.85	2.04	17.18
5WKQ.PDB	O, A_LYS_213	N, A_LEU_217	H, A_LEU_217	2.82	1.99	14.07
5WKQ.PDB	O, A_MET_215	N, A_LYS_219	H, A_LYS_219	2.99	2.17	15.70
5WKQ.PDB	O, A_LEU_217	N, A_ILE_221	H, A_ILE_221	3.00	2.19	17.23
5WKQ.PDB	O, A_GLU_218	N, A_ASP_222	H, A_ASP_222	2.93	2.08	8.56
5WKQ.PDB	O, A_LYS_219	N, A_SER_223	H, A_SER_223	2.82	2.02	17.93
5WKQ.PDB	O, A_GLU_220	N, A_PHE_224	H, A_PHE_224	2.96	2.16	19.24
5WKQ.PDB	O, A_ILE_221	N, A_SER_225	H, A_SER_225	2.98	2.15	11.85
5WKQ.PDB	O, A_ASP_222	N, A_ALA_226	H, A_ALA_226	2.92	2.10	14.82
5WKQ.PDB	O, A_PHE_224	N, A_SER_228	H, A_SER_228	2.81	1.98	13.22
5WKQ.PDB	O, A_SER_225	N, A_ASN_229	H, A_ASN_229	2.97	2.17	18.32
5WKQ.PDB	O, A_ALA_226	OG1, A_THR_230	HG1, A_THR_230	3.00	2.17	9.26
5WKQ.PDB	O, A_SER_228	NE2, A_GLN_235	HE22, A_GLN_235	2.83	2.08	24.75
5WKQ.PDB	O, B_ALA_75	N, B_LEU_79	H, B_LEU_79	2.76	1.93	13.13
5WKQ.PDB	O, B_SER_76	N, B_THR_80	H, B_THR_80	3.00	2.21	19.48
5WKQ.PDB	O, B_GLN_78	N, B_LEU_82	H, B_LEU_82	2.90	2.10	19.38
5WKQ.PDB	O, B_LEU_79	N, B_ILE_83	H, B_ILE_83	2.90	2.06	11.95
5WKQ.PDB	O, B_LEU_81	N, B_ASN_85	H, B_ASN_85	2.99	2.16	14.14
5WKQ.PDB	O, B_LEU_82	N, B_LEU_86	H, B_LEU_86	2.93	2.11	15.27
5WKQ.PDB	O, B_ILE_83	N, B_ILE_87	H, B_ILE_87	2.80	1.97	13.54
5WKQ.PDB	O, B_GLY_84	N, B_GLN_88	H, B_GLN_88	2.92	2.15	21.64
5WKQ.PDB	O, B_LEU_86	N, B_LEU_90	H, B_LEU_90	2.83	1.98	8.98
5WKQ.PDB	O, B_ILE_87	N, B_GLY_91	H, B_GLY_91	2.92	2.09	13.90
5WKQ.PDB	O, B_LEU_95	N, B_THR_99	H, B_THR_99	2.78	1.92	3.48
5WKQ.PDB	O, B_THR_96	N, B_ASN_100	H, B_ASN_100	2.89	2.06	14.47
5WKQ.PDB	O, B_ALA_97	N, B_LYS_101	H, B_LYS_101	2.94	2.10	8.27
5WKQ.PDB	O, B_LEU_98	N, B_ILE_102	H, B_ILE_102	2.87	2.10	23.41
5WKQ.PDB	O, B_THR_99	N, B_THR_103	H, B_THR_103	2.98	2.14	12.40
5WKQ.PDB	O, B_LYS_101	N, B_TRP_105	H, B_TRP_105	2.85	2.02	12.87
5WKQ.PDB	O, B_ILE_102	N, B_LYS_106	H, B_LYS_106	2.89	2.08	17.14
5WKQ.PDB	O, B_TRP_105	N, B_GLN_109	H, B_GLN_109	2.93	2.12	16.73
5WKQ.PDB	O, B_LYS_106	N, B_GLN_110	H, B_GLN_110	2.89	2.09	18.27
5WKQ.PDB	O, B_SER_107	N, B_ALA_111	H, B_ALA_111	2.92	2.12	17.32
5WKQ.PDB	O, B_GLN_108	N, B_ARG_112	H, B_ARG_112	2.99	2.14	6.98
5WKQ.PDB	O, B_GLN_109	N, B_GLN_113	H, B_GLN_113	2.90	2.09	16.25
5WKQ.PDB	O, B_GLN_110	N, B_GLN_114	H, B_GLN_114	2.91	2.09	15.83
5WKQ.PDB	O, B_ALA_111	N, B_LYS_115	H, B_LYS_115	2.90	2.07	13.13

5WKQ.PDB	O, B_ARG_112	N, B_ASN_116	H, B_ASN_116	2.85	2.03	15.38
5WKQ.PDB	O, B_GLN_114	N, B_GLU_118	H, B_GLU_118	2.95	2.12	11.18
5WKQ.PDB	O, B_LYS_115	N, B_PHE_119	H, B_PHE_119	2.93	2.08	7.47
5WKQ.PDB	O, B_ASN_116	N, B_SER_120	H, B_SER_120	2.96	2.11	7.40
5WKQ.PDB	O, B_LEU_117	N, B_ASP_121	H, B_ASP_121	2.93	2.09	10.56
5WKQ.PDB	O, B_GLU_118	N, B_LYS_122	H, B_LYS_122	2.95	2.15	18.53
5WKQ.PDB	O, B_PHE_119	N, B_ILE_123	H, B_ILE_123	2.84	2.00	11.79
5WKQ.PDB	O, B_LYS_122	N, B_LEU_126	H, B_LEU_126	2.94	2.08	4.26
5WKQ.PDB	O, B_ILE_123	N, B_LEU_127	H, B_LEU_127	2.80	2.00	17.69
5WKQ.PDB	O, B_THR_125	N, B_GLU_129	H, B_GLU_129	2.91	2.08	11.09
5WKQ.PDB	O, B_LEU_126	N, B_THR_130	H, B_THR_130	2.83	2.00	12.55
5WKQ.PDB	O, B_LEU_127	N, B_GLU_131	H, B_GLU_131	2.89	2.05	10.95
5WKQ.PDB	O, B_THR_130	N, B_THR_134	H, B_THR_134	2.79	1.98	16.24
5WKQ.PDB	O, B_THR_130	OG1, B_THR_134	HG1, B_THR_134	2.99	2.22	19.25
5WKQ.PDB	O, B_GLY_132	N, B_ASP_136	H, B_ASP_136	2.99	2.18	16.20
5WKQ.PDB	O, B_LEU_133	N, B_TYR_137	H, B_TYR_137	2.84	2.01	13.19
5WKQ.PDB	O, B_THR_134	N, B_GLU_138	H, B_GLU_138	2.98	2.16	14.73
5WKQ.PDB	O, B_TYR_137	N, B_ILE_141	H, B_ILE_141	2.98	2.19	19.03
5WKQ.PDB	O, B_GLN_140	N, B_LEU_144	H, B_LEU_144	2.86	2.11	25.33
5WKQ.PDB	O, B_ILE_141	N, B_LYS_145	H, B_LYS_145	2.89	2.08	15.46
5WKQ.PDB	O, B_LYS_143	N, B_ALA_147	H, B_ALA_147	2.95	2.16	20.04
5WKQ.PDB	O, B_LEU_144	N, B_ASP_148	H, B_ASP_148	2.84	1.99	5.61
5WKQ.PDB	O, B_LYS_145	N, B_SER_149	H, B_SER_149	2.97	2.17	18.50
5WKQ.PDB	O, B_ASN_146	N, B_LYS_150	H, B_LYS_150	2.94	2.13	17.77
5WKQ.PDB	O, B_ALA_147	N, B_ILE_151	H, B_ILE_151	2.98	2.16	14.66
5WKQ.PDB	O, B_ASP_148	N, B_LYS_152	H, B_LYS_152	2.91	2.07	10.46
5WKQ.PDB	O, B_ILE_151	N, B_GLU_155	H, B_GLU_155	2.85	2.01	9.24
5WKQ.PDB	O, B_LYS_152	N, B_ASN_156	H, B_ASN_156	2.87	2.10	22.12
5WKQ.PDB	O, B_LEU_154	N, B_ILE_158	H, B_ILE_158	2.84	2.00	9.55
5WKQ.PDB	O, B_ASN_156	N, B_GLN_160	H, B_GLN_160	2.98	2.15	12.59
5WKQ.PDB	O, B_LYS_157	N, B_ILE_161	H, B_ILE_161	2.99	2.17	15.50
5WKQ.PDB	OE2, B_GLU_182	NE2, B_GLN_162	HE21, B_GLN_162	2.63	1.85	20.38
5WKQ.PDB	O, B_ASN_159	N, B_THR_163	H, B_THR_163	2.97	2.13	11.47
5WKQ.PDB	O, B_GLN_160	N, B_ARG_164	H, B_ARG_164	2.79	1.95	8.04
5WKQ.PDB	O, B_ILE_161	N, B_LEU_165	H, B_LEU_165	2.73	1.95	20.16
5WKQ.PDB	O, B_THR_163	OG, B_SER_166	HG, B_SER_166	2.84	2.00	2.60
5WKQ.PDB	O, B_GLU_182	N, B_THR_186	H, B_THR_186	2.91	2.09	14.89
5WKQ.PDB	O, B_LEU_185	N, B_LYS_189	H, B_LYS_189	2.88	2.10	21.13
5WKQ.PDB	O, B_THR_186	N, B_ASP_190	H, B_ASP_190	2.94	2.09	7.09
5WKQ.PDB	O, B_LYS_189	N, B_VAL_193	H, B_VAL_193	2.86	2.07	19.28
5WKQ.PDB	O, B_ALA_191	N, B_ASP_195	H, B_ASP_195	2.76	1.92	9.36
5WKQ.PDB	O, B_ALA_192	N, B_ARG_196	H, B_ARG_196	2.80	2.02	20.33
5WKQ.PDB	OD1, B_ASP_148	NH1, B_ARG_196	HH11, B_ARG_196	2.87	2.13	25.83
5WKQ.PDB	O, B_VAL_193	N, B_THR_197	H, B_THR_197	2.86	2.02	10.23
5WKQ.PDB	O, B_ARG_196	N, B_GLU_200	H, B_GLU_200	2.88	2.05	12.74
5WKQ.PDB	O, B_THR_197	N, B_GLN_201	H, B_GLN_201	2.89	2.05	8.57
5WKQ.PDB	O, B_ILE_199	N, B_THR_203	H, B_THR_203	2.92	2.14	20.25
5WKQ.PDB	O, B_ILE_199	OG1, B_THR_203	HG1, B_THR_203	2.75	2.02	24.53
5WKQ.PDB	O, B_GLU_200	N, B_LEU_204	H, B_LEU_204	2.93	2.09	11.16
5WKQ.PDB	O, B_THR_203	N, B_HIS_207	H, B_HIS_207	2.92	2.07	7.74
5WKQ.PDB	OE2, A_GLU_131	ND1, B_HIS_207	HD1, B_HIS_207	2.65	1.88	22.26
5WKQ.PDB	O, B_LEU_204	N, B_SER_208	H, B_SER_208	2.87	2.08	18.92
5WKQ.PDB	O, B_SER_205	N, B_LYS_209	H, B_LYS_209	2.90	2.09	16.81
5WKQ.PDB	O, B_ILE_206	N, B_LEU_210	H, B_LEU_210	2.88	2.10	21.93
5WKQ.PDB	O, B_HIS_207	N, B_THR_211	H, B_THR_211	2.88	2.05	12.96
5WKQ.PDB	OE1, A_GLU_131	OG1, B_THR_211	HG1, B_THR_211	2.63	1.86	19.68
5WKQ.PDB	O, B_SER_208	N, B_ASP_212	H, B_ASP_212	2.88	2.08	18.34
5WKQ.PDB	O, B_LYS_209	N, B_LYS_213	H, B_LYS_213	2.97	2.19	21.54

5WKQ.PDB	O, B_THR_211	OG, B_SER_214	HG, B_SER_214	2.63	1.88	22.05
5WKQ.PDB	O, B_ASP_212	N, B_GLN_216	H, B_GLN_216	2.92	2.09	13.17
5WKQ.PDB	O, B_LYS_213	N, B_LEU_217	H, B_LEU_217	2.89	2.06	14.20
5WKQ.PDB	O, B_MET_215	N, B_LYS_219	H, B_LYS_219	2.89	2.07	14.81
5WKQ.PDB	O, B_GLN_216	N, B_GLU_220	H, B_GLU_220	2.97	2.15	14.12
5WKQ.PDB	O, B_LEU_217	N, B_ILE_221	H, B_ILE_221	2.90	2.10	17.72
5WKQ.PDB	O, B_GLU_218	N, B_ASP_222	H, B_ASP_222	2.89	2.07	14.28
5WKQ.PDB	O, B_LYS_219	N, B_SER_223	H, B_SER_223	2.87	2.04	11.53
5WKQ.PDB	O, B_ASP_222	N, B_ALA_226	H, B_ALA_226	2.87	2.09	21.47
5WKQ.PDB	O, B_SER_223	N, B_PHE_227	H, B_PHE_227	2.88	2.09	20.68
5WN9.PDB	OE1, H_GLN_1	NE2, H_GLN_3	HE21, H_GLN_3	2.70	1.88	14.43
5WN9.PDB	O, H_LYS_23	N, H_VAL_5	H, H_VAL_5	2.93	2.10	13.33
5WN9.PDB	OE1, H_GLN_116	N, H_GLN_6	H, H_GLN_6	2.83	1.97	4.77
5WN9.PDB	O, H_TYR_94	NE2, H_GLN_6	HE22, H_GLN_6	2.87	2.09	20.35
5WN9.PDB	O, H_LEU_119	N, H_GLU_10	H, H_GLU_10	2.95	2.12	13.96
5WN9.PDB	O, H_THR_121	N, H_LYS_12	H, H_LYS_12	2.90	2.09	16.60
5WN9.PDB	O, H_LEU_86	N, H_GLY_15	H, H_GLY_15	2.76	1.92	11.25
5WN9.PDB	O, H_LEU_83	N, H_VAL_18	H, H_VAL_18	2.97	2.16	16.04
5WN9.PDB	O, H_MET_81	N, H_LEU_20	H, H_LEU_20	2.76	1.92	9.07
5WN9.PDB	O, H_VAL_5	N, H_LYS_23	H, H_LYS_23	2.84	1.99	8.74
5WN9.PDB	O, H_ASN_77	N, H_ALA_24	H, H_ALA_24	2.85	2.00	2.73
5WN9.PDB	O, H_GLN_3	N, H_SER_25	H, H_SER_25	2.91	2.11	19.22
5WN9.PDB	O, H_GLY_97	N, H_SER_35	H, H_SER_35	2.98	2.16	11.85
5WN9.PDB	O, H_TYR_95	N, H_VAL_37	H, H_VAL_37	2.89	2.08	15.19
5WN9.PDB	O, H_GLU_46	N, H_ARG_38	H, H_ARG_38	2.88	2.07	17.27
5WN9.PDB	OE1, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.78	2.00	20.76
5WN9.PDB	OH, H_TYR_94	NH2, H_ARG_38	HH21, H_ARG_38	2.96	2.17	18.48
5WN9.PDB	OD1, H_ASP_90	NH2, H_ARG_38	HH22, H_ARG_38	2.91	2.07	9.36
5WN9.PDB	O, H_VAL_93	N, H_GLN_39	H, H_GLN_39	2.85	2.11	25.52
5WN9.PDB	OE1, H_GLN_182	NE2, H_GLN_39	HE22, H_GLN_39	2.96	2.11	8.81
5WN9.PDB	O, H_ARG_38	N, H_GLU_46	H, H_GLU_46	2.90	2.11	19.48
5WN9.PDB	O, H_TRP_36	N, H_MET_48	H, H_MET_48	2.86	2.02	9.08
5WN9.PDB	O, H_TYR_59	N, H_TRP_50	H, H_TRP_50	2.87	2.08	18.82
5WN9.PDB	O, H_ALA_106	NE1, H_TRP_50	HE1, H_TRP_50	2.91	2.13	20.34
5WN9.PDB	O, H_VAL_34	N, H_SER_51	H, H_SER_51	2.88	2.09	18.45
5WN9.PDB	O, H_VAL_34	OG, H_SER_51	HG, H_SER_51	2.85	2.13	25.31
5WN9.PDB	O, H_ASN_57	N, H_SER_52	H, H_SER_52	2.90	2.09	17.84
5WN9.PDB	O, H_SER_52	N, H_GLY_56	H, H_GLY_56	2.91	2.13	21.69
5WN9.PDB	OD1, H_ASN_55	N, H_ASN_57	H, H_ASN_57	2.95	2.11	6.76
5WN9.PDB	O, H_TRP_50	N, H_TYR_59	H, H_TYR_59	2.96	2.17	19.00
5WN9.PDB	O, H_MET_48	N, H_ALA_61	H, H_ALA_61	2.91	2.07	8.09
5WN9.PDB	O, H_ALA_61	N, H_LEU_64	H, H_LEU_64	2.94	2.13	15.81
5WN9.PDB	O, H_LEU_64	N, H_ARG_67	H, H_ARG_67	2.91	2.19	28.27
5WN9.PDB	OD2, H_ASP_90	NH1, H_ARG_67	HH12, H_ARG_67	2.27	1.51	22.67
5WN9.PDB	O, H_GLU_82	N, H_THR_69	H, H_THR_69	2.97	2.19	21.04
5WN9.PDB	OH, H_TYR_60	N, H_MET_70	H, H_MET_70	2.89	2.04	9.93
5WN9.PDB	O, H_THR_78	N, H_ASP_73	H, H_ASP_73	2.77	1.94	12.50
5WN9.PDB	OD1, H_ASP_73	N, H_SER_75	H, H_SER_75	2.97	2.21	23.09
5WN9.PDB	OD1, H_ASP_73	OG, H_SER_75	HG, H_SER_75	2.58	1.79	16.04
5WN9.PDB	O, H_CYS_22	N, H_ALA_79	H, H_ALA_79	2.83	1.99	10.49
5WN9.PDB	O, H_THR_71	N, H_TYR_80	H, H_TYR_80	2.85	2.01	11.64
5WN9.PDB	O, H_LEU_20	N, H_MET_81	H, H_MET_81	2.95	2.14	16.70
5WN9.PDB	O, H_THR_69	N, H_GLU_82	H, H_GLU_82	2.85	2.02	12.09
5WN9.PDB	O, H_VAL_18	N, H_LEU_83	H, H_LEU_83	2.91	2.12	19.85
5WN9.PDB	O, H_ARG_67	N, H_ARG_84	H, H_ARG_84	2.80	1.98	15.10
5WN9.PDB	OG1, H_THR_69	NH1, H_ARG_84	HH12, H_ARG_84	2.83	2.06	21.62
5WN9.PDB	O, H_ALA_66	NH2, H_ARG_84	HH21, H_ARG_84	2.99	2.24	24.04
5WN9.PDB	O, H_ALA_16	N, H_LEU_86	H, H_LEU_86	2.99	2.14	2.07

5WN9.PDB	OD2, H_ASP_90	N, H_ARG_87	H, H_ARG_87	2.89	2.10	17.07
5WN9.PDB	O, H_SER_85	NH1, H_ARG_87	HH11, H_ARG_87	2.78	2.03	24.21
5WN9.PDB	O, H_ARG_87	N, H_ASP_90	H, H_ASP_90	2.92	2.07	9.16
5WN9.PDB	O, H_GLN_39	N, H_VAL_93	H, H_VAL_93	2.93	2.14	19.95
5WN9.PDB	O, H_THR_118	N, H_TYR_94	H, H_TYR_94	2.77	1.92	7.11
5WN9.PDB	O, H_ASP_90	OH, H_TYR_94	HH, H_TYR_94	2.64	1.81	7.80
5WN9.PDB	O, H_VAL_37	N, H_TYR_95	H, H_TYR_95	2.71	1.86	4.49
5WN9.PDB	O, H_SER_35	N, H_GLY_97	H, H_GLY_97	2.90	2.14	23.59
5WN9.PDB	O, H_SER_113	N, H_ARG_98	H, H_ARG_98	2.91	2.10	16.03
5WN9.PDB	OD1, H_ASP_112	NE, H_ARG_98	HE, H_ARG_98	2.94	2.13	15.87
5WN9.PDB	OD2, H_ASP_112	NH1, H_ARG_98	HH11, H_ARG_98	2.84	2.01	13.12
5WN9.PDB	O, H_PRO_110	N, H_MET_100	H, H_MET_100	2.87	2.05	15.00
5WN9.PDB	OD1, H_ASP_99	N, H_GLY_109	H, H_GLY_109	2.84	2.01	13.27
5WN9.PDB	OH, H_TYR_180	N, H_PHE_111	H, H_PHE_111	2.98	2.20	19.41
5WN9.PDB	O, H_CYS_96	N, H_GLY_115	H, H_GLY_115	2.86	2.02	9.77
5WN9.PDB	O, H_GLN_6	NE2, H_GLN_116	HE22, H_GLN_116	2.88	2.05	14.44
5WN9.PDB	OE1, H_GLN_6	N, H_GLY_117	H, H_GLY_117	2.99	2.25	25.16
5WN9.PDB	O, H_TYR_94	N, H_THR_118	H, H_THR_118	2.78	1.97	14.98
5WN9.PDB	O, H_SER_7	OG1, H_THR_118	HG1, H_THR_118	2.77	2.03	24.19
5WN9.PDB	O, H_ALA_92	N, H_VAL_120	H, H_VAL_120	2.95	2.10	8.42
5WN9.PDB	O, H_GLU_10	N, H_THR_121	H, H_THR_121	2.91	2.06	8.28
5WN9.PDB	OG1, H_THR_91	N, H_VAL_122	H, H_VAL_122	2.90	2.05	5.63
5WN9.PDB	O, H_LYS_12	N, H_SER_123	H, H_SER_123	2.75	1.94	16.31
5WN9.PDB	O, H_ARG_168	N, H_THR_149	H, H_THR_149	2.97	2.13	11.46
5WN9.PDB	O, H_TYR_230	NE2, H_GLN_150	HE22, H_GLN_150	2.99	2.13	4.72
5WN9.PDB	O, H_SER_166	N, H_SER_151	H, H_SER_151	2.95	2.15	17.82
5WN9.PDB	O, H_LYS_247	N, H_VAL_155	H, H_VAL_155	2.96	2.17	20.07
5WN9.PDB	O, H_GLU_249	N, H_ALA_157	H, H_ALA_157	2.97	2.20	22.22
5WN9.PDB	OD2, H_ASP_161	N, H_SER_158	H, H_SER_158	2.85	2.00	7.54
5WN9.PDB	O, H_LEU_222	N, H_GLY_160	H, H_GLY_160	2.71	1.90	15.63
5WN9.PDB	OG1, H_THR_218	NH2, H_ARG_162	HH21, H_ARG_162	2.83	2.04	19.79
5WN9.PDB	O, H_LEU_217	N, H_ILE_165	H, H_ILE_165	2.79	1.95	8.96
5WN9.PDB	O, H_SER_151	N, H_SER_166	H, H_SER_166	2.82	1.97	7.02
5WN9.PDB	O, H_PHE_215	N, H_CYS_167	H, H_CYS_167	2.89	2.04	8.23
5WN9.PDB	O, H_THR_149	N, H_ARG_168	H, H_ARG_168	2.89	2.06	13.39
5WN9.PDB	O, H_THR_213	N, H_ALA_169	H, H_ALA_169	2.83	2.01	14.31
5WN9.PDB	O, H_GLY_212	N, H_ILE_173	H, H_ILE_173	2.92	2.09	10.87
5WN9.PDB	O, H_ILE_173	N, H_SER_176	H, H_SER_176	2.94	2.08	5.22
5WN9.PDB	O, H_GLN_233	N, H_ALA_178	H, H_ALA_178	2.89	2.06	12.90
5WN9.PDB	O, H_ILE_192	N, H_TRP_179	H, H_TRP_179	2.88	2.07	16.13
5WN9.PDB	O, H_TYR_231	N, H_TYR_180	H, H_TYR_180	2.81	2.00	16.41
5WN9.PDB	OE1, H_GLN_233	OH, H_TYR_180	HH, H_TYR_180	2.70	1.87	8.37
5WN9.PDB	O, H_GLN_189	N, H_GLN_181	H, H_GLN_181	2.87	2.05	15.50
5WN9.PDB	O, H_THR_229	N, H_GLN_182	H, H_GLN_182	2.73	1.91	15.73
5WN9.PDB	O, H_LYS_186	NE2, H_GLN_182	HE21, H_GLN_182	2.95	2.15	17.69
5WN9.PDB	OE1, H_GLN_39	NE2, H_GLN_182	HE22, H_GLN_182	2.85	2.00	9.41
5WN9.PDB	O, H_GLN_181	N, H_GLN_189	H, H_GLN_189	2.76	1.98	20.74
5WN9.PDB	O, H_TRP_179	N, H_LEU_191	H, H_LEU_191	2.80	1.95	5.76
5WN9.PDB	O, H_SER_197	N, H_TYR_193	H, H_TYR_193	2.93	2.13	18.06
5WN9.PDB	O, H_LEU_177	N, H_ALA_195	H, H_ALA_195	2.82	2.00	13.79
5WN9.PDB	O, H_GLY_208	OG, H_BSER_196	HG, H_BSER_196	2.95	2.19	21.28
5WN9.PDB	O, H_TYR_193	N, H_SER_197	H, H_SER_197	2.88	2.08	19.19
5WN9.PDB	O, H_LEU_191	N, H_GLN_199	H, H_GLN_199	2.93	2.07	0.47
5WN9.PDB	OD2, H_ASP_226	NE, H_ARG_205	HE, H_ARG_205	2.80	1.99	17.36
5WN9.PDB	OD1, H_ASP_226	NH1, H_ARG_205	HH11, H_ARG_205	2.89	2.03	4.48
5WN9.PDB	O, H_THR_216	N, H_SER_209	H, H_SER_209	3.00	2.21	19.73
5WN9.PDB	O, H_SER_174	N, H_GLY_212	H, H_GLY_212	2.91	2.07	9.42
5WN9.PDB	O, H_CYS_167	N, H_PHE_215	H, H_PHE_215	2.93	2.12	15.69

5WN9.PDB	O, H_ILE_165	N, H_LEU_217	H, H_LEU_217	2.91	2.09	15.07
5WN9.PDB	O, H_SER_207	N, H_THR_218	H, H_THR_218	2.92	2.08	10.72
5WN9.PDB	OG1, H_THR_164	OG1, H_THR_218	HG1, H_THR_218	2.96	2.26	28.62
5WN9.PDB	O, H_VAL_163	N, H_ILE_219	H, H_ILE_219	2.79	1.97	14.91
5WN9.PDB	O, H_ARG_205	N, H_SER_220	H, H_SER_220	2.99	2.21	20.02
5WN9.PDB	O, H_ASP_161	N, H_LEU_222	H, H_LEU_222	2.76	1.97	18.80
5WN9.PDB	OD2, H_ASP_226	N, H_GLN_223	H, H_GLN_223	2.93	2.08	7.95
5WN9.PDB	O, H_GLN_223	N, H_ASP_226	H, H_ASP_226	2.82	1.98	8.91
5WN9.PDB	O, H_THR_246	N, H_TYR_230	H, H_TYR_230	2.87	2.06	16.33
5WN9.PDB	O, H_ASP_226	OH, H_TYR_230	HH, H_TYR_230	2.62	1.80	10.05
5WN9.PDB	O, H_TYR_180	N, H_TYR_231	H, H_TYR_231	2.93	2.12	16.57
5WN9.PDB	O, H_THR_241	N, H_GLN_234	H, H_GLN_234	2.95	2.18	23.47
5WN9.PDB	O, H_THR_146	OG1, H_THR_241	HG1, H_THR_241	2.72	1.91	13.19
5WN9.PDB	O, H_CYS_232	N, H_GLY_243	H, H_GLY_243	2.91	2.11	17.20
5WN9.PDB	O, H_TYR_230	N, H_THR_246	H, H_THR_246	2.86	2.08	20.56
5WN9.PDB	O, H_PRO_152	OG1, H_THR_246	HG1, H_THR_246	2.65	1.95	28.58
5WN9.PDB	O, H_SER_153	N, H_LYS_247	H, H_LYS_247	2.96	2.15	15.87
5WN9.PDB	O, H_ALA_228	N, H_VAL_248	H, H_VAL_248	2.90	2.04	3.82
5WN9.PDB	O, H_VAL_155	N, H_GLU_249	H, H_GLU_249	2.87	2.03	10.19
5WN9.PDB	O, A_LYS_187	N, A_CYS_173	H, A_CYS_173	2.97	2.18	19.66
5WN9.PDB	O, A_CYS_176	N, A_ASN_179	H, A_ASN_179	2.99	2.15	7.83
5WN9.PDB	O, A_SER_177	NE1, A_TRP_183	HE1, A_TRP_183	2.88	2.03	4.80
5WN9.PDB	O, A_VAL_171	N, A_LYS_187	H, A_LYS_187	2.85	2.04	15.74
5WN9.PDB	OD1, H_ASN_57	NE, A_ARG_188	HE, A_ARG_188	2.58	1.61	2.15

Table 5: The side chain and main chain hydrogen bonding networks of all experimentally determined antigen-antibody-related structures. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1A14.PDB	OG, H.SER.25	NE2, H.GLN.5	HE21, H.GLN.5	2.94	2.02	15.87
1A14.PDB	OE1, L.GLN.38	NE2, H.GLN.39	HE21, H.GLN.39	2.62	1.69	9.24
1A14.PDB	OG1, H.THR.77	OG, H.SER.75	HG, H.SER.75	2.86	2.04	27.11
1A14.PDB	OE2, H.GLU.85	OG, H.SER.84	HG, H.SER.84	2.91	1.99	12.42
1A14.PDB	OD2, H.ASP.101	NH2, H.ARG.94	HH21, H.ARG.94	2.75	1.83	16.91
1E6J.PDB	OH, L.TYR.85	NE2, L.GLN.36	HE21, L.GLN.36	2.83	1.87	8.49
1E6J.PDB	OE1, H.GLN.39	NE2, L.GLN.37	HE22, L.GLN.37	2.69	1.84	23.98
1E6J.PDB	OG, L.SER.129	NE2, L.GLN.122	HE22, L.GLN.122	2.94	2.00	13.76
1F3R.PDB	OD1, B.ASN.83	OG1, B.THR.17	HG1, B.THR.17	2.73	1.80	13.32
1F3R.PDB	NE1, A.TRP.67	OG, B.SER.61	HG, B.SER.61	2.86	1.89	6.31
1F3R.PDB	OG1, B.THR.212	OG1, B.THR.158	HG1, B.THR.158	2.80	1.87	11.10
1F3R.PDB	OD1, B.ASP.220	NH1, B.ARG.199	HH12, B.ARG.199	2.89	1.98	22.15
1F3R.PDB	OE1, B.GLN.217	OG, B.SER.215	HG, B.SER.215	2.66	1.72	13.57
1F3R.PDB	NE1, B.TRP.47	OH, B.TYR.227	HH, B.TYR.227	2.99	2.20	29.73
1F3R.PDB	OD1, B.ASN.188	OH, B.TYR.229	HH, B.TYR.229	2.66	1.70	7.44
1HCV.PDB	OE2, A.GLU.46	NE, A.ARG.38	HE, A.ARG.38	2.98	2.01	4.47
1HCV.PDB	OH, A.TYR.90	NH1, A.ARG.38	HH11, A.ARG.38	2.93	1.98	14.34
1HCV.PDB	OD1, A.ASP.86	NH1, A.ARG.38	HH12, A.ARG.38	2.86	1.90	11.61
1HGD.PDB	OE2, B.GLU.97	NZ, A.LYS.27	HZ1, A.LYS.27	2.80	1.78	9.95
1HGD.PDB	OD2, A.ASP.275	NZ, A.LYS.50	HZ1, A.LYS.50	2.70	1.79	23.99
1HGD.PDB	OD1, A.ASP.73	ND1, A.HIS.75	HD1, A.HIS.75	2.82	1.92	19.21
1HGD.PDB	OD1, A.ASP.60	NE, A.ARG.90	HE, A.ARG.90	2.88	1.91	7.55
1HGD.PDB	OD2, A.ASP.60	NH2, A.ARG.90	HH21, A.ARG.90	2.80	1.82	10.07
1HGD.PDB	OD1, A.ASP.271	OG, A.SER.91	HG, A.SER.91	2.93	2.12	28.00
1HGD.PDB	OD2, A.ASP.271	OG, A.SER.91	HG, A.SER.91	2.81	1.91	17.78
1HGD.PDB	OD2, A.ASP.68	OG, A.SER.95	HG, A.SER.95	2.92	1.99	16.11
1HGD.PDB	OD1, A.ASP.68	OH, A.TYR.100	HH, A.TYR.100	2.88	1.90	0.98
1HGD.PDB	OD2, A.ASP.104	OG, A.SER.107	HG, A.SER.107	2.86	1.96	19.52
1HGD.PDB	OE2, B.GLU.67	NH2, A.ARG.109	HH21, A.ARG.109	2.83	1.84	13.41
1HGD.PDB	OD2, F.ASP.79	OG, A.SER.110	HG, A.SER.110	2.92	1.96	11.03
1HGD.PDB	OE2, A.GLU.119	OG1, A.THR.117	HG1, A.THR.117	2.87	1.92	9.92
1HGD.PDB	OD1, A.ASN.137	NZ, A.LYS.140	HZ2, A.LYS.140	2.76	1.82	19.96
1HGD.PDB	OD2, A.ASP.77	NE, A.ARG.141	HE, A.ARG.141	2.80	1.97	26.87
1HGD.PDB	OD1, A.ASP.77	NH2, A.ARG.141	HH21, A.ARG.141	2.86	1.95	21.98
1HGD.PDB	OD2, A.ASP.77	NH2, A.ARG.141	HH21, A.ARG.141	2.74	1.86	23.87
1HGD.PDB	OH, A.TYR.195	NE1, A.TRP.153	HE1, A.TRP.153	2.81	1.92	20.45
1HGD.PDB	OE2, A.GLU.123	NZ, A.LYS.176	HZ2, A.LYS.176	2.69	1.80	25.20
1HGD.PDB	OE1, A.GLU.123	OH, A.TYR.178	HH, A.TYR.178	2.75	1.82	12.48
1HGD.PDB	OG1, A.THR.235	NE1, A.TRP.180	HE1, A.TRP.180	2.94	1.95	4.39
1HGD.PDB	OG, A.SER.231	NE2, A.HIS.184	HE2, A.HIS.184	2.78	1.93	25.06
1HGD.PDB	OD1, A.ASN.246	NH2, A.ARG.201	HH21, A.ARG.201	2.59	1.75	26.83
1HGD.PDB	OG1, A.THR.206	OG, A.SER.209	HG, A.SER.209	2.90	1.96	11.12
1HGD.PDB	OD1, E.ASP.101	NE2, A.GLN.210	HE22, A.GLN.210	3.00	2.15	26.33
1HGD.PDB	OG1, A.THR.203	OG1, A.THR.212	HG1, A.THR.212	2.90	1.94	6.68
1HGD.PDB	OE1, C.GLN.210	NH2, A.ARG.220	HH21, A.ARG.220	2.78	1.86	19.99
1HGD.PDB	OE2, A.GLU.190	OG, A.SER.228	HG, A.SER.228	2.98	2.00	5.61
1HGD.PDB	OD1, A.ASP.101	OG, A.SER.231	HG, A.SER.231	2.84	1.88	8.92
1HGD.PDB	OE1, F.GLU.72	NZ, A.LYS.238	HZ3, A.LYS.238	2.93	1.92	13.44
1HGD.PDB	OD1, A.ASN.165	ND2, A.ASN.246	HD22, A.ASN.246	2.92	1.97	12.69
1HGD.PDB	OE1, A.GLN.191	ND2, A.ASN.250	HD21, A.ASN.250	2.94	1.98	9.96
1HGD.PDB	OD1, A.ASN.133	NH2, A.ARG.255	HH22, A.ARG.255	2.53	1.69	26.82
1HGD.PDB	OE2, A.GLU.119	NH1, A.ARG.261	HH12, A.ARG.261	2.65	1.81	27.93
1HGD.PDB	OE1, A.GLU.119	NH2, A.ARG.261	HH22, A.ARG.261	2.88	1.97	22.77
1HGD.PDB	OD2, A.ASP.85	NZ, A.LYS.264	HZ3, A.LYS.264	2.85	1.86	16.67
1HGD.PDB	OE1, A.GLN.44	NZ, A.LYS.292	HZ1, A.LYS.292	2.71	1.70	11.58
1HGD.PDB	OD2, A.ASP.291	NZ, A.LYS.292	HZ3, A.LYS.292	2.78	1.85	22.68
1HGD.PDB	OD1, A.ASN.285	ND2, A.ASN.298	HD22, A.ASN.298	2.98	2.04	13.52

1HGD.PDB	OE1, A_GLU_41	NZ, A_LYS_315	HZ3, A_LYS_315	2.76	1.81	20.40
1HGD.PDB	OE2, A_GLU_35	ND2, A_ASN_322	HD22, A_ASN_322	2.84	1.97	23.40
1HGD.PDB	OE1, B_GLN_34	NE, B_ARG_25	HE, B_ARG_25	2.65	1.77	20.51
1HGD.PDB	OD1, B ASP_46	NE2, B_GLN_42	HE22, B_GLN_42	2.84	1.95	20.63
1HGD.PDB	OG1, B_THR_107	NZ, B_LYS_51	HZ1, B_LYS_51	2.96	1.97	16.32
1HGD.PDB	OE1, B_GLU_103	NZ, B_LYS_51	HZ2, B_LYS_51	2.73	1.71	9.93
1HGD.PDB	ND1, B_HIS_106	NZ, B_LYS_51	HZ3, B_LYS_51	2.75	1.79	17.84
1HGD.PDB	OE1, B_GLU_57	NH1, B_ARG_54	HH11, B_ARG_54	2.86	1.87	11.55
1HGD.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.77	1.80	12.79
1HGD.PDB	OE2, B_GLU_61	NZ, B_LYS_58	HZ2, B_LYS_58	2.91	1.88	11.49
1HGD.PDB	OD2, F ASP_86	NZ, B_LYS_62	HZ1, B_LYS_62	2.61	1.78	29.53
1HGD.PDB	OD2, F ASP_90	NZ, B_LYS_62	HZ3, B_LYS_62	2.73	1.84	25.56
1HGD.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.96	2.01	12.34
1HGD.PDB	OE2, B_GLU_85	NZ, B_LYS_68	HZ2, B_LYS_68	2.76	1.74	9.73
1HGD.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.88	1.91	8.67
1HGD.PDB	OE2, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.84	1.82	2.51
1HGD.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.71	1.71	6.80
1HGD.PDB	OE1, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.75	1.75	3.21
1HGD.PDB	OE1, B_GLU_74	NE2, B_GLN_78	HE22, B_GLN_78	2.92	1.97	11.55
1HGD.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.65	1.81	23.27
1HGD.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.76	1.72	5.59
1HGD.PDB	OE2, B_GLU_120	NH1, B_ARG_123	HH11, B_ARG_123	2.79	1.91	24.17
1HGD.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.83	2.02	28.17
1HGD.PDB	OE2, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.88	2.01	22.00
1HGD.PDB	OH, B_TYR_157	ND2, B_ASN_129	HD22, B_ASN_129	2.78	1.83	11.22
1HGD.PDB	OE2, B_GLU_150	ND2, B_ASN_154	HD21, B_ASN_154	2.98	2.09	22.34
1HGD.PDB	OD1, B_ASN_154	OG1, B_THR_156	HG1, B_THR_156	2.75	1.84	16.14
1HGD.PDB	OE2, B_GLU_131	NH1, B_ARG_170	HH11, B_ARG_170	2.78	1.79	7.42
1HGD.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.80	1.77	7.54
1HGD.PDB	OD2, C ASP_275	NZ, C_LYS_50	HZ1, C_LYS_50	2.66	1.78	25.77
1HGD.PDB	OD1, C ASP_73	ND1, C_HIS_75	HD1, C_HIS_75	2.77	1.87	19.67
1HGD.PDB	OD1, C ASP_60	NE, C_ARG_90	HE, C_ARG_90	2.86	1.89	9.66
1HGD.PDB	OD2, C ASP_60	NH2, C_ARG_90	HH21, C_ARG_90	2.78	1.79	10.49
1HGD.PDB	OD1, C ASP_271	OG, C_SER_91	HG, C_SER_91	2.93	2.11	26.93
1HGD.PDB	OD2, C ASP_271	OG, C_SER_91	HG, C_SER_91	2.86	1.96	18.80
1HGD.PDB	OD2, C ASP_68	OG, C_SER_95	HG, C_SER_95	2.88	1.96	15.18
1HGD.PDB	OD1, C ASP_68	OH, C_TYR_100	HH, C_TYR_100	2.89	1.96	14.39
1HGD.PDB	OD2, C ASP_104	OG, C_SER_107	HG, C_SER_107	2.91	2.00	17.92
1HGD.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.87	1.88	13.44
1HGD.PDB	OD2, B ASP_79	OG, C_SER_110	HG, C_SER_110	2.73	1.84	19.59
1HGD.PDB	OE2, C_GLU_119	OG1, C_THR_117	HG1, C_THR_117	2.86	1.93	10.42
1HGD.PDB	OD1, C_ASN_137	NZ, C_LYS_140	HZ2, C_LYS_140	2.78	1.84	20.52
1HGD.PDB	OD2, C ASP_77	NE, C_ARG_141	HE, C_ARG_141	2.80	1.97	27.06
1HGD.PDB	OD1, C ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.87	1.96	21.76
1HGD.PDB	OD2, C ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.75	1.86	23.93
1HGD.PDB	OD1, C_ASN_137	OG, C_SER_145	HG, C_SER_145	2.98	2.13	22.87
1HGD.PDB	OH, C_TYR_195	NE1, C_TRP_153	HE1, C_TRP_153	2.80	1.95	24.25
1HGD.PDB	OE2, C_GLU_123	NZ, C_LYS_176	HZ2, C_LYS_176	2.69	1.80	25.35
1HGD.PDB	OE1, C_GLU_123	OH, C_TYR_178	HH, C_TYR_178	2.73	1.80	13.21
1HGD.PDB	OG1, C_THR_235	NE1, C_TRP_180	HE1, C_TRP_180	2.91	1.93	2.97
1HGD.PDB	OG, C_SER_231	NE2, C_HIS_184	HE2, C_HIS_184	2.75	1.91	25.20
1HGD.PDB	OD1, C_ASN_250	NE2, C_GLN_191	HE21, C_GLN_191	2.98	2.02	9.43
1HGD.PDB	OD1, C_ASN_246	NH2, C_ARG_201	HH21, C_ARG_201	2.60	1.77	27.30
1HGD.PDB	OG1, C_THR_212	OG1, C_THR_203	HG1, C_THR_203	2.89	1.96	13.30
1HGD.PDB	OD2, C ASP_241	NE, C_ARG_208	HE, C_ARG_208	2.97	2.08	21.42
1HGD.PDB	OG1, C_THR_206	OG, C_SER_209	HG, C_SER_209	2.92	1.98	10.99
1HGD.PDB	OD1, A ASP_101	NE2, C_GLN_210	HE22, C_GLN_210	2.97	2.13	27.21
1HGD.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.69	1.80	23.00

1HGD.PDB	OE2, C_GLU_190	OG, C_SER_228	HG, C_SER_228	3.00	2.02	4.69
1HGD.PDB	OD1, C_ASP_101	OG, C_SER_231	HG, C_SER_231	2.87	1.90	8.39
1HGD.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.80	1.83	17.68
1HGD.PDB	OD1, C_ASN_165	ND2, C_ASN_246	HD22, C_ASN_246	2.91	1.96	13.56
1HGD.PDB	OE1, C_GLN_191	ND2, C_ASN_250	HD21, C_ASN_250	2.90	1.95	10.99
1HGD.PDB	OD1, C_ASN_133	NH2, C_ARG_255	HH22, C_ARG_255	2.52	1.69	27.35
1HGD.PDB	OE2, C_GLU_119	NH1, C_ARG_261	HH12, C_ARG_261	2.66	1.83	27.96
1HGD.PDB	OE1, C_GLU_119	NH2, C_ARG_261	HH22, C_ARG_261	2.90	2.00	23.32
1HGD.PDB	OD2, C_ASP_85	NZ, C_LYS_264	HZ3, C_LYS_264	2.82	1.84	16.88
1HGD.PDB	OE1, C_GLN_44	NZ, C_LYS_292	HZ1, C_LYS_292	2.73	1.73	12.00
1HGD.PDB	OD2, C_ASP_291	NZ, C_LYS_292	HZ3, C_LYS_292	2.79	1.88	23.81
1HGD.PDB	OD1, C_ASN_285	ND2, C_ASN_298	HD22, C_ASN_298	2.96	2.02	13.09
1HGD.PDB	OE1, C_GLU_41	NZ, C_LYS_315	HZ3, C_LYS_315	2.78	1.84	20.99
1HGD.PDB	OE2, C_GLU_35	ND2, C_ASN_322	HD22, C_ASN_322	2.83	1.94	21.17
1HGD.PDB	OE1, D_GLU_15	NZ, C_LYS_326	HZ1, C_LYS_326	2.78	1.77	11.96
1HGD.PDB	OXT, C_THR_328	NE2, C_GLN_327	HE22, C_GLN_327	2.97	2.03	15.01
1HGD.PDB	OE1, D_GLN_34	NE, D_ARG_25	HE, D_ARG_25	2.61	1.77	24.43
1HGD.PDB	OD1, D_ASN_146	ND2, D_ASN_28	HD21, D_ASN_28	3.00	2.03	9.16
1HGD.PDB	OD2, D_ASP_37	OG, D_SER_40	HG, D_SER_40	2.86	1.96	18.80
1HGD.PDB	OD1, D_ASP_46	NE2, D_GLN_42	HE22, D_GLN_42	2.84	1.95	20.82
1HGD.PDB	OG1, D_THR_107	NZ, D_LYS_51	HZ1, D_LYS_51	2.96	1.98	16.97
1HGD.PDB	OE1, D_GLU_103	NZ, D_LYS_51	HZ2, D_LYS_51	2.74	1.72	8.47
1HGD.PDB	ND1, D_HIS_106	NZ, D_LYS_51	HZ3, D_LYS_51	2.74	1.78	16.91
1HGD.PDB	OE1, D_GLU_57	NH1, D_ARG_54	HH11, D_ARG_54	2.85	1.86	12.06
1HGD.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.79	1.82	13.03
1HGD.PDB	OE2, D_GLU_61	NZ, D_LYS_58	HZ2, D_LYS_58	2.90	1.87	10.86
1HGD.PDB	OD2, B_ASP_90	NZ, D_LYS_62	HZ3, D_LYS_62	2.62	1.79	29.99
1HGD.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.96	1.98	5.65
1HGD.PDB	OE2, D_GLU_85	NZ, D_LYS_68	HZ2, D_LYS_68	2.78	1.76	10.92
1HGD.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.83	1.87	10.56
1HGD.PDB	OE2, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.78	1.77	3.14
1HGD.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.65	1.67	9.42
1HGD.PDB	OE1, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.69	1.70	6.24
1HGD.PDB	OE1, D_GLU_74	NE2, D_GLN_78	HE22, D_GLN_78	2.94	1.97	10.43
1HGD.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.57	1.79	29.87
1HGD.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.76	1.72	5.75
1HGD.PDB	OE2, D_GLU_120	NH1, D_ARG_123	HH11, D_ARG_123	2.80	1.92	24.08
1HGD.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.80	2.01	29.31
1HGD.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.82	1.95	21.73
1HGD.PDB	OH, D_TYR_157	ND2, D_ASN_129	HD22, D_ASN_129	2.79	1.82	6.93
1HGD.PDB	OE2, D_GLU_150	ND2, D_ASN_154	HD21, D_ASN_154	2.88	2.05	27.54
1HGD.PDB	OD1, D_ASN_154	OG1, D_THR_156	HG1, D_THR_156	2.79	1.83	8.53
1HGD.PDB	NE2, D_HIS_142	OH, D_TYR_157	HH, D_TYR_157	2.78	1.89	18.65
1HGD.PDB	OE2, D_GLU_131	NH1, D_ARG_170	HH11, D_ARG_170	2.77	1.78	7.65
1HGD.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.79	1.77	8.77
1HGD.PDB	OD2, E_ASP_275	NZ, E_LYS_50	HZ1, E_LYS_50	2.69	1.80	25.14
1HGD.PDB	OD1, E_ASP_73	ND1, E_HIS_75	HD1, E_HIS_75	2.79	1.88	18.25
1HGD.PDB	OD1, E_ASP_60	NE, E_ARG_90	HE, E_ARG_90	2.88	1.91	7.90
1HGD.PDB	OD2, E_ASP_60	NH2, E_ARG_90	HH21, E_ARG_90	2.82	1.83	10.15
1HGD.PDB	OD1, E_ASP_271	OG, E_SER_91	HG, E_SER_91	2.94	2.13	28.39
1HGD.PDB	OD2, E_ASP_271	OG, E_SER_91	HG, E_SER_91	2.84	1.93	17.47
1HGD.PDB	OD2, E_ASP_68	OG, E_SER_95	HG, E_SER_95	2.91	1.98	14.66
1HGD.PDB	OD1, E_ASP_68	OH, E_TYR_100	HH, E_TYR_100	2.86	1.93	14.06
1HGD.PDB	OD2, E_ASP_104	OG, E_SER_107	HG, E_SER_107	2.90	1.98	16.44
1HGD.PDB	OE2, F_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.82	1.85	14.73
1HGD.PDB	OD2, D_ASP_79	OG, E_SER_110	HG, E_SER_110	2.81	1.89	15.50
1HGD.PDB	OE2, E_GLU_119	OG1, E_THR_117	HG1, E_THR_117	2.90	1.95	9.79
1HGD.PDB	OD1, E_ASN_137	NZ, E_LYS_140	HZ2, E_LYS_140	2.79	1.84	19.51

1HGD.PDB	OD2, E_ASP_77	NE, E_ARG_141	HE, E_ARG_141	2.82	1.98	26.95
1HGD.PDB	OD1, E_ASP_77	NH2, E_ARG_141	HH21, E_ARG_141	2.88	1.95	21.13
1HGD.PDB	OD2, E_ASP_77	NH2, E_ARG_141	HH21, E_ARG_141	2.75	1.86	24.62
1HGD.PDB	OH, E_TYR_195	NE1, E_TRP_153	HE1, E_TRP_153	2.82	1.91	19.17
1HGD.PDB	OE2, E_GLU_123	NZ, E_LYS_176	HZ2, E_LYS_176	2.69	1.80	25.12
1HGD.PDB	OE1, E_GLU_123	OH, E_TYR_178	HH, E_TYR_178	2.75	1.83	13.46
1HGD.PDB	OG1, E_THR_235	NE1, E_TRP_180	HE1, E_TRP_180	2.93	1.94	3.75
1HGD.PDB	OG, E_SER_231	NE2, E_HIS_184	HE2, E_HIS_184	2.80	1.95	25.42
1HGD.PDB	OD1, E_ASN_246	NH2, E_ARG_201	HH21, E_ARG_201	2.60	1.77	27.54
1HGD.PDB	OG1, E_THR_212	OG1, E_THR_203	HG1, E_THR_203	2.93	1.99	12.22
1HGD.PDB	OG1, E_THR_206	OG, E_SER_209	HG, E_SER_209	2.91	1.97	11.26
1HGD.PDB	OD1, C_ASP_101	NE2, E_GLN_210	HE22, E_GLN_210	2.98	2.14	27.07
1HGD.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.77	1.90	25.11
1HGD.PDB	OE2, E_GLU_190	OG, E_SER_228	HG, E_SER_228	2.96	1.98	4.78
1HGD.PDB	OD1, E_ASP_101	OG, E_SER_231	HG, E_SER_231	2.85	1.91	13.25
1HGD.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ3, E_LYS_238	2.87	1.86	13.40
1HGD.PDB	OD1, E_ASN_165	ND2, E_ASN_246	HD22, E_ASN_246	2.91	1.96	12.66
1HGD.PDB	OE1, E_GLN_191	ND2, E_ASN_250	HD21, E_ASN_250	2.95	1.99	9.92
1HGD.PDB	OD1, E_ASN_133	NH2, E_ARG_255	HH22, E_ARG_255	2.52	1.69	27.28
1HGD.PDB	OE2, E_GLU_119	NH1, E_ARG_261	HH12, E_ARG_261	2.64	1.81	27.92
1HGD.PDB	OE1, E_GLU_119	NH2, E_ARG_261	HH22, E_ARG_261	2.88	1.97	22.94
1HGD.PDB	OD2, E_ASP_85	NZ, E_LYS_264	HZ3, E_LYS_264	2.87	1.88	16.50
1HGD.PDB	OE1, E_GLN_44	NZ, E_LYS_292	HZ1, E_LYS_292	2.70	1.70	12.87
1HGD.PDB	OD2, E_ASP_291	NZ, E_LYS_292	HZ3, E_LYS_292	2.83	1.91	23.60
1HGD.PDB	OD1, E_ASN_285	ND2, E_ASN_298	HD22, E_ASN_298	2.95	2.01	14.15
1HGD.PDB	OE1, E_GLU_41	NZ, E_LYS_315	HZ3, E_LYS_315	2.76	1.83	22.10
1HGD.PDB	OE2, E_GLU_35	ND2, E_ASN_322	HD22, E_ASN_322	2.82	1.95	23.13
1HGD.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.97	1.97	16.19
1HGD.PDB	OE1, F_GLN_34	NE, F_ARG_25	HE, F_ARG_25	2.93	2.07	24.69
1HGD.PDB	OE1, F_GLN_34	NH2, F_ARG_25	HH21, F_ARG_25	2.80	1.89	20.31
1HGD.PDB	OD1, F_ASN_146	ND2, F_ASN_28	HD21, F_ASN_28	2.81	1.89	15.27
1HGD.PDB	OD2, F_ASP_37	OG, F_SER_40	HG, F_SER_40	2.84	1.98	23.42
1HGD.PDB	OD1, F_ASP_46	NE2, F_GLN_42	HE22, F_GLN_42	2.83	1.94	21.51
1HGD.PDB	OE1, F_GLU_103	NZ, F_LYS_51	HZ2, F_LYS_51	2.72	1.70	8.28
1HGD.PDB	ND1, F_HIS_106	NZ, F_LYS_51	HZ3, F_LYS_51	2.73	1.76	16.89
1HGD.PDB	OE1, F_GLU_57	NH1, F_ARG_54	HH11, F_ARG_54	2.86	1.85	10.37
1HGD.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.72	1.75	12.85
1HGD.PDB	OE2, F_GLU_61	NZ, F_LYS_58	HZ2, F_LYS_58	2.92	1.89	10.22
1HGD.PDB	OD2, D_ASP_90	NZ, F_LYS_62	HZ3, F_LYS_62	2.71	1.86	28.09
1HGD.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.95	1.98	9.92
1HGD.PDB	OE2, F_GLU_85	NZ, F_LYS_68	HZ2, F_LYS_68	2.72	1.77	19.94
1HGD.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.86	1.90	10.66
1HGD.PDB	OE2, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.77	1.75	1.42
1HGD.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.64	1.65	5.37
1HGD.PDB	OE1, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.71	1.72	7.42
1HGD.PDB	OE1, F_GLU_74	NE2, F_GLN_78	HE22, F_GLN_78	2.96	1.99	9.91
1HGD.PDB	OE1, B_GLU_85	OH, F_TYR_83	HH, F_TYR_83	2.53	1.75	27.84
1HGD.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.67	1.66	8.83
1HGD.PDB	OE2, F_GLU_120	NH1, F_ARG_123	HH11, F_ARG_123	2.77	1.88	23.82
1HGD.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.96	2.14	28.71
1HGD.PDB	OE2, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.94	2.05	20.84
1HGD.PDB	OH, F_TYR_157	ND2, F_ASN_129	HD22, F_ASN_129	2.80	1.85	12.13
1HGD.PDB	OE2, F_GLU_131	NH1, F_ARG_170	HH11, F_ARG_170	2.76	1.77	6.97
1HGE.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.80	1.78	10.14
1HGE.PDB	OD2, A_ASP_275	NZ, A_LYS_50	HZ1, A_LYS_50	2.75	1.80	21.09
1HGE.PDB	OD1, A_ASP_73	ND1, A_HIS_75	HD1, A_HIS_75	2.80	1.89	17.62
1HGE.PDB	OD1, A_ASP_60	NE, A_ARG_90	HE, A_ARG_90	2.85	1.89	7.94
1HGE.PDB	OD2, A_ASP_60	NH2, A_ARG_90	HH21, A_ARG_90	2.79	1.80	8.90

1HGE.PDB	OD2, A_ASP_271	OG, A_SER_91	HG, A_SER_91	2.81	1.90	18.10
1HGE.PDB	OD2, A_ASP_68	OG, A_SER_95	HG, A_SER_95	2.90	1.97	15.50
1HGE.PDB	OD1, A_ASP_68	OH, A_TYR_100	HH, A_TYR_100	2.91	1.93	2.88
1HGE.PDB	OD2, A_ASP_104	OG, A_SER_107	HG, A_SER_107	2.86	1.94	16.59
1HGE.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.74	1.75	12.19
1HGE.PDB	OD2, F_ASP_79	OG, A_SER_110	HG, A_SER_110	2.90	1.95	11.19
1HGE.PDB	OE2, A_GLU_119	OG1, A_THR_117	HG1, A_THR_117	2.90	1.95	8.88
1HGE.PDB	OD1, A_ASN_137	NZ, A_LYS_140	HZ2, A_LYS_140	2.81	1.83	16.67
1HGE.PDB	OD2, A_ASP_77	NE, A_ARG_141	HE, A_ARG_141	2.81	1.97	26.71
1HGE.PDB	OD1, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.89	1.98	21.76
1HGE.PDB	OD2, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.75	1.86	23.90
1HGE.PDB	OH, A_TYR_195	NE1, A_TRP_153	HE1, A_TRP_153	2.88	1.99	20.14
1HGE.PDB	OE2, A_GLU_123	NZ, A_LYS_176	HZ1, A_LYS_176	2.71	1.79	22.78
1HGE.PDB	OE1, A_GLU_123	OH, A_TYR_178	HH, A_TYR_178	2.75	1.82	10.80
1HGE.PDB	OG1, A_THR_235	NE1, A_TRP_180	HE1, A_TRP_180	2.92	1.93	3.33
1HGE.PDB	OG, A_SER_231	NE2, A_HIS_184	HE2, A_HIS_184	2.72	1.88	25.40
1HGE.PDB	OD1, A_ASN_246	NH2, A_ARG_201	HH21, A_ARG_201	2.60	1.73	24.24
1HGE.PDB	OG1, A_THR_206	OG, A_SER_209	HG, A_SER_209	2.97	2.03	10.25
1HGE.PDB	OD1, E_ASP_101	NE2, A_GLN_210	HE22, A_GLN_210	2.91	2.05	24.48
1HGE.PDB	OG1, A_THR_203	OG1, A_THR_212	HG1, A_THR_212	2.85	1.89	3.04
1HGE.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.71	1.78	19.14
1HGE.PDB	OD1, A_ASP_101	OG, A_SER_231	HG, A_SER_231	2.85	1.89	7.16
1HGE.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.91	1.89	11.73
1HGE.PDB	OD1, A_ASN_165	ND2, A_ASN_246	HD22, A_ASN_246	2.88	1.94	13.15
1HGE.PDB	OE1, A_GLN_191	ND2, A_ASN_250	HD21, A_ASN_250	2.94	1.97	8.25
1HGE.PDB	OD1, A_ASN_133	NH2, A_ARG_255	HH22, A_ARG_255	2.48	1.67	28.93
1HGE.PDB	OE2, A_GLU_119	NH1, A_ARG_261	HH12, A_ARG_261	2.64	1.81	27.97
1HGE.PDB	OE1, A_GLU_119	NH2, A_ARG_261	HH22, A_ARG_261	2.84	1.95	24.23
1HGE.PDB	OD2, A_ASP_85	NZ, A_LYS_264	HZ3, A_LYS_264	2.77	1.79	16.96
1HGE.PDB	OE1, A_GLN_44	NZ, A_LYS_292	HZ1, A_LYS_292	2.69	1.69	12.67
1HGE.PDB	OD2, A_ASP_291	NZ, A_LYS_292	HZ3, A_LYS_292	2.82	1.86	19.03
1HGE.PDB	OE1, A_GLU_41	NZ, A_LYS_315	HZ3, A_LYS_315	2.82	1.87	21.00
1HGE.PDB	OE2, A_GLU_35	ND2, A_ASN_322	HD22, A_ASN_322	2.88	1.99	21.26
1HGE.PDB	OE1, A_GLU_325	NZ, A_LYS_326	HZ3, A_LYS_326	2.85	1.86	15.04
1HGE.PDB	OE1, B_GLN_34	NE, B_ARG_25	HE, B_ARG_25	2.59	1.77	25.60
1HGE.PDB	OG1, B_THR_32	NE2, B_GLN_27	HE22, B_GLN_27	2.99	2.08	18.28
1HGE.PDB	OD1, B_ASP_46	NE2, B_GLN_42	HE22, B_GLN_42	2.87	1.96	19.05
1HGE.PDB	OG1, B_THR_107	NZ, B_LYS_51	HZ1, B_LYS_51	2.97	1.99	17.16
1HGE.PDB	OE1, B_GLU_103	NZ, B_LYS_51	HZ2, B_LYS_51	2.76	1.73	6.92
1HGE.PDB	ND1, B_HIS_106	NZ, B_LYS_51	HZ3, B_LYS_51	2.73	1.78	18.14
1HGE.PDB	OE1, B_GLU_57	NH1, B_ARG_54	HH11, B_ARG_54	2.83	1.84	12.19
1HGE.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.84	1.86	12.76
1HGE.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ1, B_LYS_62	2.60	1.76	28.82
1HGE.PDB	OD2, F_ASP_90	NZ, B_LYS_62	HZ3, B_LYS_62	2.69	1.82	26.81
1HGE.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.97	2.02	12.36
1HGE.PDB	OE2, B_GLU_85	NZ, B_LYS_68	HZ2, B_LYS_68	2.78	1.76	9.50
1HGE.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.87	1.91	11.56
1HGE.PDB	OE2, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.84	1.83	5.81
1HGE.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.70	1.70	6.45
1HGE.PDB	OE1, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.79	1.79	3.91
1HGE.PDB	OE1, B_GLU_74	NE2, B_GLN_78	HE22, B_GLN_78	2.97	2.00	7.88
1HGE.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.65	1.81	24.86
1HGE.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.75	1.71	5.62
1HGE.PDB	OE2, B_GLU_120	NH1, B_ARG_123	HH11, B_ARG_123	2.84	1.95	23.29
1HGE.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.80	1.98	27.36
1HGE.PDB	OE2, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.94	2.06	21.65
1HGE.PDB	OH, B_TYR_157	ND2, B_ASN_129	HD22, B_ASN_129	2.79	1.85	12.68
1HGE.PDB	OD2, B_ASP_145	NZ, B_LYS_143	HZ1, B_LYS_143	2.79	1.94	29.42

1HGE.PDB	OE2, B_GLU_150	ND2, B_ASN_154	HD21, B_ASN_154	2.93	2.05	22.48
1HGE.PDB	OD1, B_ASN_154	OG1, B_THR_156	HG1, B_THR_156	2.71	1.82	17.99
1HGE.PDB	OE2, B_GLU_131	NH1, B_ARG_170	HH11, B_ARG_170	2.80	1.80	6.47
1HGE.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.79	1.77	8.74
1HGE.PDB	OD2, C_ASP_275	NZ, C_LYS_50	HZ1, C_LYS_50	2.70	1.77	22.15
1HGE.PDB	OD1, C_ASP_73	ND1, C_HIS_75	HD1, C_HIS_75	2.76	1.85	18.20
1HGE.PDB	OD1, C_ASP_60	NE, C_ARG_90	HE, C_ARG_90	2.84	1.88	10.34
1HGE.PDB	OD2, C_ASP_60	NH2, C_ARG_90	HH21, C_ARG_90	2.77	1.78	9.61
1HGE.PDB	OD2, C_ASP_271	OG, C_SER_91	HG, C_SER_91	2.80	1.91	19.19
1HGE.PDB	OD2, C_ASP_68	OG, C_SER_95	HG, C_SER_95	2.88	1.95	14.90
1HGE.PDB	OD1, C_ASP_68	OH, C_TYR_100	HH, C_TYR_100	2.89	1.97	15.01
1HGE.PDB	OD2, C_ASP_104	OG, C_SER_107	HG, C_SER_107	2.88	1.96	15.70
1HGE.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.78	1.79	11.19
1HGE.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.78	1.86	15.09
1HGE.PDB	OE2, C_GLU_119	OG1, C_THR_117	HG1, C_THR_117	2.89	1.94	9.29
1HGE.PDB	OD1, C_ASN_137	NZ, C_LYS_140	HZ2, C_LYS_140	2.83	1.86	16.66
1HGE.PDB	OD2, C_ASP_77	NE, C_ARG_141	HE, C_ARG_141	2.80	1.97	26.96
1HGE.PDB	OD1, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.88	1.96	21.42
1HGE.PDB	OD2, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.74	1.86	24.30
1HGE.PDB	OH, C_TYR_195	NE1, C_TRP_153	HE1, C_TRP_153	2.85	1.98	22.78
1HGE.PDB	OE2, C_GLU_123	NZ, C_LYS_176	HZ1, C_LYS_176	2.71	1.80	23.44
1HGE.PDB	OE1, C_GLU_123	OH, C_TYR_178	HH, C_TYR_178	2.73	1.80	12.29
1HGE.PDB	OG1, C_THR_235	NE1, C_TRP_180	HE1, C_TRP_180	2.92	1.93	1.68
1HGE.PDB	OG, C_SER_231	NE2, C_HIS_184	HE2, C_HIS_184	2.71	1.87	25.48
1HGE.PDB	OD1, C_ASN_250	NE2, C_GLN_191	HE21, C_GLN_191	3.00	2.03	7.73
1HGE.PDB	OD1, C_ASN_246	NH2, C_ARG_201	HH21, C_ARG_201	2.62	1.75	24.53
1HGE.PDB	OG1, C_THR_212	OG1, C_THR_203	HG1, C_THR_203	2.89	1.94	9.07
1HGE.PDB	OG1, C_THR_206	OG, C_SER_209	HG, C_SER_209	2.98	2.03	9.68
1HGE.PDB	OD1, A_ASP_101	NE2, C_GLN_210	HE22, C_GLN_210	2.93	2.07	24.92
1HGE.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.64	1.76	23.09
1HGE.PDB	OD1, C_ASP_101	OG, C_SER_231	HG, C_SER_231	2.89	1.93	7.03
1HGE.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.78	1.80	16.75
1HGE.PDB	OD1, C_ASN_165	ND2, C_ASN_246	HD22, C_ASN_246	2.89	1.94	13.09
1HGE.PDB	OE1, C_GLN_191	ND2, C_ASN_250	HD21, C_ASN_250	2.89	1.93	9.19
1HGE.PDB	OD1, C_ASN_133	NH2, C_ARG_255	HH22, C_ARG_255	2.48	1.68	29.46
1HGE.PDB	OE2, C_GLU_119	NH1, C_ARG_261	HH12, C_ARG_261	2.65	1.82	27.69
1HGE.PDB	OE1, C_GLU_119	NH2, C_ARG_261	HH22, C_ARG_261	2.84	1.95	24.41
1HGE.PDB	OD2, C_ASP_85	NZ, C_LYS_264	HZ3, C_LYS_264	2.77	1.79	16.79
1HGE.PDB	OE1, C_GLN_44	NZ, C_LYS_292	HZ1, C_LYS_292	2.72	1.72	12.77
1HGE.PDB	OD2, C_ASP_291	NZ, C_LYS_292	HZ3, C_LYS_292	2.84	1.88	19.72
1HGE.PDB	OD1, C_ASN_285	ND2, C_ASN_298	HD22, C_ASN_298	2.99	2.05	12.60
1HGE.PDB	OE1, C_GLU_41	NZ, C_LYS_315	HZ3, C_LYS_315	2.82	1.88	21.70
1HGE.PDB	OE2, C_GLU_35	ND2, C_ASN_322	HD22, C_ASN_322	2.89	2.00	20.86
1HGE.PDB	OE1, D_GLU_15	NZ, C_LYS_326	HZ1, C_LYS_326	2.74	1.73	12.73
1HGE.PDB	OXT, C_THR_328	NE2, C_GLN_327	HE22, C_GLN_327	2.97	2.01	12.27
1HGE.PDB	OE1, D_GLN_34	NE, D_ARG_25	HE, D_ARG_25	2.56	1.76	28.50
1HGE.PDB	OD2, D_ASP_37	OG, D_SER_40	HG, D_SER_40	2.78	1.93	24.10
1HGE.PDB	OD1, D_ASP_46	NE2, D_GLN_42	HE22, D_GLN_42	2.87	1.96	19.33
1HGE.PDB	OE2, D_GLU_114	NE2, D_GLN_47	HE21, D_GLN_47	2.99	2.06	16.53
1HGE.PDB	OG1, D_THR_107	NZ, D_LYS_51	HZ1, D_LYS_51	2.96	1.98	16.83
1HGE.PDB	OE1, D_GLU_103	NZ, D_LYS_51	HZ2, D_LYS_51	2.76	1.73	6.47
1HGE.PDB	ND1, D_HIS_106	NZ, D_LYS_51	HZ3, D_LYS_51	2.77	1.82	18.39
1HGE.PDB	OE1, D_GLU_57	NH1, D_ARG_54	HH11, D_ARG_54	2.82	1.84	12.42
1HGE.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.87	1.89	12.82
1HGE.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.96	1.98	6.23
1HGE.PDB	OE2, D_GLU_85	NZ, D_LYS_68	HZ2, D_LYS_68	2.80	1.78	10.75
1HGE.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.79	1.85	14.06
1HGE.PDB	OE2, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.78	1.78	7.91

1HGE.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.63	1.67	11.36
1HGE.PDB	OE1, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.74	1.75	7.04
1HGE.PDB	OE1, D_GLU_74	NE2, D_GLN_78	HE22, D_GLN_78	2.96	1.99	8.03
1HGE.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.58	1.80	29.40
1HGE.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.71	1.68	6.52
1HGE.PDB	OE2, D_GLU_120	NH1, D_ARG_123	HH11, D_ARG_123	2.83	1.93	23.01
1HGE.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.78	1.98	28.90
1HGE.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.90	2.01	20.41
1HGE.PDB	OH, D_TYR_157	ND2, D_ASN_129	HD22, D_ASN_129	2.81	1.85	9.24
1HGE.PDB	OD1, D_ASN_154	OG1, D_THR_156	HG1, D_THR_156	2.74	1.81	12.51
1HGE.PDB	NE2, D_HIS_142	OH, D_TYR_157	HH, D_TYR_157	2.73	1.86	21.01
1HGE.PDB	OE2, D_GLU_131	NH1, D_ARG_170	HH11, D_ARG_170	2.79	1.79	6.83
1HGE.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.79	1.77	9.75
1HGE.PDB	OD2, E_ASP_275	NZ, E_LYS_50	HZ1, E_LYS_50	2.73	1.80	21.86
1HGE.PDB	OD1, E_ASP_73	ND1, E_HIS_75	HD1, E_HIS_75	2.77	1.85	16.90
1HGE.PDB	OD1, E_ASP_60	NE, E_ARG_90	HE, E_ARG_90	2.88	1.91	8.59
1HGE.PDB	OD2, E_ASP_60	NH2, E_ARG_90	HH21, E_ARG_90	2.80	1.80	8.94
1HGE.PDB	OD2, E_ASP_271	OG, E_SER_91	HG, E_SER_91	2.83	1.92	17.26
1HGE.PDB	OD2, E_ASP_68	OG, E_SER_95	HG, E_SER_95	2.91	1.97	13.28
1HGE.PDB	OD1, E_ASP_68	OH, E_TYR_100	HH, E_TYR_100	2.88	1.95	14.25
1HGE.PDB	OD2, E_ASP_104	OG, E_SER_107	HG, E_SER_107	2.86	1.93	15.15
1HGE.PDB	OE2, F_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.78	1.79	11.63
1HGE.PDB	OD2, D_ASP_79	OG, E_SER_110	HG, E_SER_110	2.82	1.89	14.19
1HGE.PDB	OE2, E_GLU_119	OG1, E_THR_117	HG1, E_THR_117	2.93	1.97	8.29
1HGE.PDB	OD1, E_ASN_137	NZ, E_LYS_140	HZ2, E_LYS_140	2.84	1.86	16.83
1HGE.PDB	OD2, E_ASP_77	NE, E_ARG_141	HE, E_ARG_141	2.80	1.96	26.48
1HGE.PDB	OD1, E_ASP_77	NH2, E_ARG_141	HH21, E_ARG_141	2.91	2.00	21.55
1HGE.PDB	OD2, E_ASP_77	NH2, E_ARG_141	HH21, E_ARG_141	2.75	1.87	24.36
1HGE.PDB	OD1, E_ASP_77	OG, E_SER_149	HG, E_SER_149	2.99	2.14	24.93
1HGE.PDB	OH, E_TYR_195	NE1, E_TRP_153	HE1, E_TRP_153	2.90	1.99	18.82
1HGE.PDB	OE2, E_GLU_123	NZ, E_LYS_176	HZ1, E_LYS_176	2.73	1.81	23.24
1HGE.PDB	OE1, E_GLU_123	OH, E_TYR_178	HH, E_TYR_178	2.75	1.82	12.06
1HGE.PDB	OG1, E_THR_235	NE1, E_TRP_180	HE1, E_TRP_180	2.93	1.94	2.48
1HGE.PDB	OG, E_SER_231	NE2, E_HIS_184	HE2, E_HIS_184	2.75	1.91	25.72
1HGE.PDB	OD1, E_ASN_246	NH2, E_ARG_201	HH21, E_ARG_201	2.61	1.75	25.36
1HGE.PDB	OG1, E_THR_212	OG1, E_THR_203	HG1, E_THR_203	2.89	1.95	10.14
1HGE.PDB	OG1, E_THR_206	OG, E_SER_209	HG, E_SER_209	2.98	2.04	10.06
1HGE.PDB	OD1, C_ASP_101	NE2, E_GLN_210	HE22, E_GLN_210	2.89	2.04	25.02
1HGE.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.74	1.87	25.04
1HGE.PDB	OD1, E_ASP_101	OG, E_SER_231	HG, E_SER_231	2.87	1.92	12.10
1HGE.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ3, E_LYS_238	2.85	1.84	12.25
1HGE.PDB	OD1, E_ASN_165	ND2, E_ASN_246	HD22, E_ASN_246	2.88	1.93	12.25
1HGE.PDB	OE1, E_GLN_191	ND2, E_ASN_250	HD21, E_ASN_250	2.94	1.97	8.28
1HGE.PDB	OD1, E_ASN_133	NH2, E_ARG_255	HH22, E_ARG_255	2.49	1.68	28.65
1HGE.PDB	OE2, E_GLU_119	NH1, E_ARG_261	HH12, E_ARG_261	2.65	1.81	27.82
1HGE.PDB	OE1, E_GLU_119	NH2, E_ARG_261	HH22, E_ARG_261	2.83	1.95	24.52
1HGE.PDB	OD2, E_ASP_85	NZ, E_LYS_264	HZ3, E_LYS_264	2.81	1.83	16.30
1HGE.PDB	OE1, E_GLN_44	NZ, E_LYS_292	HZ1, E_LYS_292	2.72	1.72	11.93
1HGE.PDB	OD2, E_ASP_291	NZ, E_LYS_292	HZ3, E_LYS_292	2.84	1.89	19.87
1HGE.PDB	OD1, E_ASN_285	ND2, E_ASN_298	HD22, E_ASN_298	2.98	2.04	13.10
1HGE.PDB	OD1, F_ASP_86	NZ, E_LYS_310	HZ3, E_LYS_310	2.86	2.02	29.64
1HGE.PDB	OE1, E_GLU_41	NZ, E_LYS_315	HZ3, E_LYS_315	2.80	1.87	22.54
1HGE.PDB	OE2, E_GLU_35	ND2, E_ASN_322	HD22, E_ASN_322	2.87	1.98	21.90
1HGE.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.99	2.00	17.08
1HGE.PDB	OE1, F_GLN_34	NE, F_ARG_25	HE, F_ARG_25	2.92	2.07	24.83
1HGE.PDB	OE1, F_GLN_34	NH2, F_ARG_25	HH21, F_ARG_25	2.81	1.90	20.25
1HGE.PDB	OD1, F_ASN_146	ND2, F_ASN_28	HD21, F_ASN_28	2.81	1.89	15.75
1HGE.PDB	OD2, F_ASP_37	OG, F_SER_40	HG, F_SER_40	2.76	1.94	26.96

1HGE.PDB	OD1, F_ASP_46	NE2, F_GLN_42	HE22, F_GLN_42	2.86	1.96	19.38
1HGE.PDB	OE2, F_GLU_114	NE2, F_GLN_47	HE21, F_GLN_47	3.00	2.09	17.78
1HGE.PDB	OG1, F_THR_107	NZ, F_LYS_51	HZ1, F_LYS_51	2.97	2.00	18.12
1HGE.PDB	OE1, F_GLU_103	NZ, F_LYS_51	HZ2, F_LYS_51	2.77	1.74	6.40
1HGE.PDB	ND1, F_HIS_106	NZ, F_LYS_51	HZ3, F_LYS_51	2.74	1.79	17.89
1HGE.PDB	OE1, F_GLU_57	NH1, F_ARG_54	HH11, F_ARG_54	2.82	1.83	11.59
1HGE.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.80	1.82	12.52
1HGE.PDB	OD2, D_ASP_90	NZ, F_LYS_62	HZ2, F_LYS_62	2.67	1.83	29.15
1HGE.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.94	1.97	9.11
1HGE.PDB	OE2, F_GLU_85	NZ, F_LYS_68	HZ2, F_LYS_68	2.75	1.78	18.51
1HGE.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.85	1.89	11.64
1HGE.PDB	OE2, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.73	1.73	6.19
1HGE.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.65	1.66	5.51
1HGE.PDB	OE1, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.70	1.73	9.07
1HGE.PDB	OE1, F_GLU_74	NE2, F_GLN_78	HE22, F_GLN_78	2.96	1.99	8.87
1HGE.PDB	OE1, B_GLU_85	OH, F_TYR_83	HH, F_TYR_83	2.51	1.76	30.00
1HGE.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.67	1.65	8.34
1HGE.PDB	OE2, F_GLU_120	NH1, F_ARG_123	HH11, F_ARG_123	2.81	1.92	23.28
1HGE.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.92	2.09	27.36
1HGE.PDB	OH, F_TYR_157	ND2, F_ASN_129	HD22, F_ASN_129	2.80	1.87	15.30
1HGE.PDB	OE2, F_GLU_131	NH1, F_ARG_170	HH11, F_ARG_170	2.78	1.79	6.04
1HGF.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.79	1.86	21.55
1HGF.PDB	OD2, A_ASP_275	NZ, A_LYS_50	HZ2, A_LYS_50	2.91	1.91	15.13
1HGF.PDB	OD1, A_ASP_73	ND1, A_HIS_75	HD1, A_HIS_75	2.84	1.91	15.59
1HGF.PDB	OD1, A_ASP_60	NE, A_ARG_90	HE, A_ARG_90	2.77	1.85	16.11
1HGF.PDB	OD2, A_ASP_60	NH2, A_ARG_90	HH21, A_ARG_90	2.84	1.84	8.73
1HGF.PDB	OD2, A_ASP_271	OG, A_SER_91	HG, A_SER_91	2.85	1.91	12.59
1HGF.PDB	OD2, A_ASP_104	OG, A_SER_107	HG, A_SER_107	2.89	1.97	16.55
1HGF.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.92	1.92	10.51
1HGF.PDB	OD2, F_ASP_79	OG, A_SER_110	HG, A_SER_110	2.82	1.90	15.87
1HGF.PDB	OE2, A_GLU_119	OG1, A_THR_117	HG1, A_THR_117	2.95	1.98	3.95
1HGF.PDB	ND2, A_ASN_152	NE2, A_GLN_132	HE21, A_GLN_132	2.94	2.00	10.26
1HGF.PDB	OD2, A_ASP_77	NE, A_ARG_141	HE, A_ARG_141	2.91	2.06	25.46
1HGF.PDB	OD1, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.84	1.97	26.05
1HGF.PDB	OD2, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.78	1.86	20.91
1HGF.PDB	OH, A_TYR_195	NE1, A_TRP_153	HE1, A_TRP_153	2.84	1.90	13.02
1HGF.PDB	OE2, A_GLU_123	NZ, A_LYS_176	HZ1, A_LYS_176	2.72	1.80	23.85
1HGF.PDB	OG1, A_THR_235	NE1, A_TRP_180	HE1, A_TRP_180	2.87	1.89	5.46
1HGF.PDB	OH, A_TYR_98	NE2, A_HIS_183	HE2, A_HIS_183	2.90	1.98	15.32
1HGF.PDB	OG, A_SER_231	NE2, A_HIS_184	HE2, A_HIS_184	2.68	1.88	29.05
1HGF.PDB	OD1, A_ASN_250	NE2, A_GLN_191	HE22, A_GLN_191	2.90	1.94	8.27
1HGF.PDB	OG1, A_THR_203	OG1, A_THR_212	HG1, A_THR_212	2.83	1.91	15.11
1HGF.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.64	1.76	23.62
1HGF.PDB	OD1, A_ASP_101	OG, A_SER_231	HG, A_SER_231	2.83	1.87	7.29
1HGF.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ2, A_LYS_238	2.85	1.85	14.58
1HGF.PDB	OD1, A_ASN_165	ND2, A_ASN_246	HD21, A_ASN_246	2.93	2.03	19.92
1HGF.PDB	OE1, A_GLN_191	ND2, A_ASN_250	HD22, A_ASN_250	2.86	1.90	9.57
1HGF.PDB	OD1, A_ASN_133	NH2, A_ARG_255	HH22, A_ARG_255	2.49	1.67	28.52
1HGF.PDB	OE1, A_GLU_119	NH2, A_ARG_261	HH22, A_ARG_261	2.74	1.90	27.76
1HGF.PDB	OE1, A_GLN_44	NZ, A_LYS_292	HZ1, A_LYS_292	2.87	1.83	0.68
1HGF.PDB	OD1, A_ASP_291	NZ, A_LYS_292	HZ2, A_LYS_292	2.86	1.83	8.47
1HGF.PDB	OE1, A_GLU_41	OG1, A_THR_313	HG1, A_THR_313	2.68	1.87	27.57
1HGF.PDB	OG1, A_THR_313	NZ, A_LYS_315	HZ2, A_LYS_315	2.95	2.00	20.61
1HGF.PDB	OE2, A_GLU_35	ND2, A_ASN_322	HD21, A_ASN_322	2.76	1.93	26.44
1HGF.PDB	OE1, B_GLN_34	NE, B_ARG_25	HE, B_ARG_25	2.64	1.77	20.89
1HGF.PDB	OE1, B_GLN_34	NH2, B_ARG_25	HH21, B_ARG_25	2.81	1.99	28.67
1HGF.PDB	OE2, A_GLU_325	NH2, B_ARG_25	HH22, B_ARG_25	2.99	2.04	16.52
1HGF.PDB	OD1, B_ASP_46	NE2, B_GLN_42	HE21, B_GLN_42	2.87	1.99	22.40

1HGF.PDB	OE1, B_GLU_103	NZ, B_LYS_51	HZ1, B_LYS_51	2.74	1.70	5.26
1HGF.PDB	ND1, B_HIS_106	NZ, B_LYS_51	HZ3, B_LYS_51	2.67	1.72	18.38
1HGF.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.83	1.86	13.50
1HGF.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ2, B_LYS_62	2.71	1.70	11.44
1HGF.PDB	OD2, F_ASP_90	NZ, B_LYS_62	HZ3, B_LYS_62	2.77	1.82	20.37
1HGF.PDB	OG, A_SER_266	ND1, B_HIS_64	HD1, B_HIS_64	2.66	1.79	20.68
1HGF.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.89	1.92	10.70
1HGF.PDB	OE2, B_GLU_85	NZ, B_LYS_68	HZ1, B_LYS_68	2.67	1.75	22.44
1HGF.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.92	1.92	2.47
1HGF.PDB	OE1, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.86	1.84	3.80
1HGF.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.73	1.74	10.29
1HGF.PDB	OE2, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.75	1.74	3.91
1HGF.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.57	1.80	29.66
1HGF.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.72	1.70	9.91
1HGF.PDB	OE2, B_GLU_120	NH1, B_ARG_123	HH11, B_ARG_123	2.78	1.93	26.74
1HGF.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.80	1.86	13.00
1HGF.PDB	OH, B_TYR_157	ND2, B_ASN_129	HD21, B_ASN_129	2.81	1.86	11.58
1HGF.PDB	OD1, B_ASN_154	OG1, B_THR_156	HG1, B_THR_156	2.68	1.80	19.09
1HGF.PDB	OE1, F_GLU_131	NH2, B_ARG_163	HH21, B_ARG_163	2.74	1.86	24.20
1HGF.PDB	OE2, B_GLU_131	NH1, B_ARG_170	HH11, B_ARG_170	2.84	1.84	5.96
1HGF.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.81	1.85	19.93
1HGF.PDB	OD2, C_ASP_275	NZ, C_LYS_50	HZ2, C_LYS_50	2.88	1.87	13.71
1HGF.PDB	OD1, C_ASP_73	ND1, C_HIS_75	HD1, C_HIS_75	2.84	1.90	12.73
1HGF.PDB	OD1, C_ASP_60	NE, C_ARG_90	HE, C_ARG_90	2.76	1.85	16.46
1HGF.PDB	OD2, C_ASP_60	NH2, C_ARG_90	HH21, C_ARG_90	2.84	1.85	9.99
1HGF.PDB	OD1, C_ASP_271	OG, C_SER_91	HG, C_SER_91	2.91	2.11	29.01
1HGF.PDB	OD2, C_ASP_271	OG, C_SER_91	HG, C_SER_91	2.86	1.95	16.65
1HGF.PDB	OD1, C_ASP_68	OH, C_TYR_100	HH, C_TYR_100	2.97	2.03	12.15
1HGF.PDB	OD2, C_ASP_104	OG, C_SER_107	HG, C_SER_107	2.91	1.98	14.76
1HGF.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.91	1.92	11.49
1HGF.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.69	1.85	25.37
1HGF.PDB	OE2, C_GLU_119	OG1, C_THR_117	HG1, C_THR_117	2.97	2.00	2.16
1HGF.PDB	ND2, C_ASN_152	NE2, C_GLN_132	HE21, C_GLN_132	2.94	2.00	12.42
1HGF.PDB	OD2, C_ASP_77	NE, C_ARG_141	HE, C_ARG_141	2.91	2.05	25.56
1HGF.PDB	OD1, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.84	1.98	26.48
1HGF.PDB	OD2, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.79	1.86	20.63
1HGF.PDB	OH, C_TYR_195	NE1, C_TRP_153	HE1, C_TRP_153	2.82	1.92	18.47
1HGF.PDB	OE2, C_GLU_123	NZ, C_LYS_176	HZ1, C_LYS_176	2.72	1.80	22.47
1HGF.PDB	OG1, C_THR_235	NE1, C_TRP_180	HE1, C_TRP_180	2.86	1.88	3.91
1HGF.PDB	OH, C_TYR_98	NE2, C_HIS_183	HE2, C_HIS_183	2.89	1.99	18.89
1HGF.PDB	OG, C_SER_231	NE2, C_HIS_184	HE2, C_HIS_184	2.67	1.86	27.83
1HGF.PDB	OD1, C_ASN_250	NE2, C_GLN_191	HE22, C_GLN_191	2.91	1.94	7.66
1HGF.PDB	OG1, C_THR_212	OG1, C_THR_203	HG1, C_THR_203	2.82	1.90	14.76
1HGF.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.56	1.72	26.72
1HGF.PDB	OD1, C_ASP_101	OG, C_SER_231	HG, C_SER_231	2.86	1.89	4.34
1HGF.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ2, C_LYS_238	2.75	1.78	18.48
1HGF.PDB	OD1, C_ASN_165	ND2, C_ASN_246	HD21, C_ASN_246	2.93	2.04	21.38
1HGF.PDB	OE1, C_GLN_191	ND2, C_ASN_250	HD22, C_ASN_250	2.84	1.89	10.62
1HGF.PDB	OD1, C_ASN_133	NH2, C_ARG_255	HH22, C_ARG_255	2.47	1.67	28.90
1HGF.PDB	OE1, C_GLU_119	NH2, C_ARG_261	HH22, C_ARG_261	2.72	1.88	28.14
1HGF.PDB	OE1, C_GLN_44	NZ, C_LYS_292	HZ1, C_LYS_292	2.89	1.84	2.00
1HGF.PDB	OD1, C_ASP_291	NZ, C_LYS_292	HZ2, C_LYS_292	2.88	1.85	8.89
1HGF.PDB	OE1, C_GLU_41	OG1, C_THR_313	HG1, C_THR_313	2.66	1.87	29.10
1HGF.PDB	OG1, C_THR_313	NZ, C_LYS_315	HZ2, C_LYS_315	2.92	1.98	21.54
1HGF.PDB	OE2, C_GLU_35	ND2, C_ASN_322	HD21, C_ASN_322	2.77	1.93	25.57
1HGF.PDB	OXT, C_THR_328	NE2, C_GLN_327	HE21, C_GLN_327	2.93	2.09	26.28
1HGF.PDB	OE1, D_GLN_34	NE, D_ARG_25	HE, D_ARG_25	2.69	1.78	17.17
1HGF.PDB	OD1, D_ASN_146	ND2, D_ASN_28	HD22, D_ASN_28	2.89	1.97	17.31

1HGF.PDB	OD2, D_ASP_37	OG, D_SER_40	HG, D_SER_40	2.85	1.95	18.29
1HGF.PDB	OD1, D_ASP_46	NE2, D_GLN_42	HE21, D_GLN_42	2.85	1.97	22.40
1HGF.PDB	OE1, D_GLU_103	NZ, D_LYS_51	HZ1, D_LYS_51	2.74	1.71	5.53
1HGF.PDB	ND1, D_HIS_106	NZ, D_LYS_51	HZ3, D_LYS_51	2.69	1.73	17.89
1HGF.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.84	1.86	12.74
1HGF.PDB	OD2, B_ASP_86	NZ, D_LYS_62	HZ2, D_LYS_62	2.69	1.69	13.49
1HGF.PDB	OD2, B_ASP_90	NZ, D_LYS_62	HZ3, D_LYS_62	2.68	1.77	22.81
1HGF.PDB	OG, C_SER_266	ND1, D_HIS_64	HD1, D_HIS_64	2.64	1.83	27.58
1HGF.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.90	1.92	7.33
1HGF.PDB	OE2, D_GLU_85	NZ, D_LYS_68	HZ1, D_LYS_68	2.73	1.78	19.48
1HGF.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.82	1.85	5.34
1HGF.PDB	OE1, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.79	1.78	3.81
1HGF.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.64	1.68	12.43
1HGF.PDB	OE2, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.70	1.71	7.38
1HGF.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.58	1.80	29.87
1HGF.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.68	1.69	13.85
1HGF.PDB	OE2, D_GLU_120	NH1, D_ARG_123	HH11, D_ARG_123	2.79	1.92	25.71
1HGF.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.79	1.88	16.40
1HGF.PDB	OH, D_TYR_157	ND2, D_ASN_129	HD21, D_ASN_129	2.81	1.84	5.39
1HGF.PDB	OG, D_SER_29	NZ, D_LYS_143	HZ1, D_LYS_143	2.83	1.89	20.16
1HGF.PDB	OD1, D_ASN_154	OG1, D_THR_156	HG1, D_THR_156	2.72	1.80	12.72
1HGF.PDB	NE2, D_HIS_142	OH, D_TYR_157	HH, D_TYR_157	2.72	1.85	19.75
1HGF.PDB	OE1, B_GLU_131	NH2, D_ARG_163	HH21, D_ARG_163	2.70	1.83	24.43
1HGF.PDB	OE2, D_GLU_131	NH1, D_ARG_170	HH11, D_ARG_170	2.84	1.84	5.29
1HGF.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.75	1.83	22.30
1HGF.PDB	OD2, E_ASP_275	NZ, E_LYS_50	HZ2, E_LYS_50	2.90	1.90	14.56
1HGF.PDB	OD1, E_ASP_73	ND1, E_HIS_75	HD1, E_HIS_75	2.85	1.91	12.17
1HGF.PDB	OD1, E_ASP_60	NE, E_ARG_90	HE, E_ARG_90	2.80	1.85	10.51
1HGF.PDB	OD2, E_ASP_60	NH2, E_ARG_90	HH21, E_ARG_90	2.88	1.89	10.22
1HGF.PDB	OD2, E_ASP_104	OG, E_SER_107	HG, E_SER_107	2.88	1.94	12.45
1HGF.PDB	OE2, F_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.88	1.88	11.28
1HGF.PDB	OD2, D_ASP_79	OG, E_SER_110	HG, E_SER_110	2.78	1.90	21.69
1HGF.PDB	OE2, E_GLU_119	OG1, E_THR_117	HG1, E_THR_117	2.96	1.99	6.08
1HGF.PDB	ND2, E_ASN_152	NE2, E_GLN_132	HE21, E_GLN_132	2.95	2.01	11.55
1HGF.PDB	OD2, E_ASP_77	NE, E_ARG_141	HE, E_ARG_141	2.92	2.06	25.46
1HGF.PDB	OD1, E_ASP_77	NH2, E_ARG_141	HH21, E_ARG_141	2.83	1.96	25.41
1HGF.PDB	OD2, E_ASP_77	NH2, E_ARG_141	HH21, E_ARG_141	2.77	1.86	21.24
1HGF.PDB	OH, E_TYR_195	NE1, E_TRP_153	HE1, E_TRP_153	2.83	1.89	12.15
1HGF.PDB	OE2, E_GLU_123	NZ, E_LYS_176	HZ1, E_LYS_176	2.76	1.80	18.44
1HGF.PDB	OE1, E_GLU_123	OH, E_TYR_178	HH, E_TYR_178	2.88	1.93	11.71
1HGF.PDB	OG1, E_THR_235	NE1, E_TRP_180	HE1, E_TRP_180	2.85	1.87	2.94
1HGF.PDB	OH, E_TYR_98	NE2, E_HIS_183	HE2, E_HIS_183	2.91	1.99	15.99
1HGF.PDB	OG, E_SER_231	NE2, E_HIS_184	HE2, E_HIS_184	2.70	1.89	28.56
1HGF.PDB	OD1, E_ASN_250	NE2, E_GLN_191	HE22, E_GLN_191	2.96	1.99	7.90
1HGF.PDB	OG1, E_THR_212	OG1, E_THR_203	HG1, E_THR_203	2.89	1.95	9.70
1HGF.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.65	1.79	25.97
1HGF.PDB	OD1, E_ASP_101	OG, E_SER_231	HG, E_SER_231	2.82	1.90	15.36
1HGF.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ2, E_LYS_238	2.83	1.84	16.42
1HGF.PDB	OD1, E_ASN_165	ND2, E_ASN_246	HD21, E_ASN_246	2.93	2.02	19.67
1HGF.PDB	OE1, E_GLN_191	ND2, E_ASN_250	HD22, E_ASN_250	2.87	1.91	8.14
1HGF.PDB	OD1, E_ASN_133	NH2, E_ARG_255	HH22, E_ARG_255	2.47	1.67	29.09
1HGF.PDB	OE1, E_GLU_119	NH2, E_ARG_261	HH22, E_ARG_261	2.73	1.89	28.16
1HGF.PDB	OE1, E_GLN_44	NZ, E_LYS_292	HZ1, E_LYS_292	2.90	1.86	1.40
1HGF.PDB	OD1, E_ASP_291	NZ, E_LYS_292	HZ2, E_LYS_292	2.87	1.84	9.03
1HGF.PDB	OE1, E_GLU_41	OG1, E_THR_313	HG1, E_THR_313	2.68	1.89	29.15
1HGF.PDB	OG1, E_THR_313	NZ, E_LYS_315	HZ2, E_LYS_315	2.94	2.00	21.30
1HGF.PDB	OE2, E_GLU_35	ND2, E_ASN_322	HD21, E_ASN_322	2.77	1.93	26.11
1HGF.PDB	OE1, F_GLN_34	NE, F_ARG_25	HE, F_ARG_25	2.89	2.02	23.18

1HGF.PDB	OE1, F_GLN_34	NH2, F_ARG_25	HH21, F_ARG_25	2.91	2.03	24.46
1HGF.PDB	OD1, F_ASN_146	ND2, F_ASN_28	HD22, F_ASN_28	2.88	2.02	23.75
1HGF.PDB	OD1, F_ASP_46	NE2, F_GLN_42	HE21, F_GLN_42	2.86	1.99	23.71
1HGF.PDB	OE1, F_GLU_103	NZ, F_LYS_51	HZ1, F_LYS_51	2.72	1.69	6.79
1HGF.PDB	ND1, F_HIS_106	NZ, F_LYS_51	HZ3, F_LYS_51	2.66	1.70	17.89
1HGF.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.79	1.81	11.74
1HGF.PDB	OD2, D_ASP_86	NZ, F_LYS_62	HZ2, F_LYS_62	2.67	1.68	13.64
1HGF.PDB	OD2, D_ASP_90	NZ, F_LYS_62	HZ3, F_LYS_62	2.75	1.81	20.23
1HGF.PDB	OG, E_SER_266	ND1, F_HIS_64	HD1, F_HIS_64	2.65	1.77	20.25
1HGF.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.89	1.92	9.46
1HGF.PDB	OE2, F_GLU_85	NZ, F_LYS_68	HZ1, F_LYS_68	2.64	1.77	26.62
1HGF.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.86	1.88	5.84
1HGF.PDB	OE1, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.78	1.77	1.59
1HGF.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.69	1.70	7.61
1HGF.PDB	OE2, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.71	1.73	8.88
1HGF.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.55	1.63	21.75
1HGF.PDB	OE2, F_GLU_120	NH1, F_ARG_123	HH11, F_ARG_123	2.79	1.92	25.30
1HGF.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.90	1.96	15.73
1HGF.PDB	OH, F_TYR_157	ND2, F_ASN_129	HD21, F_ASN_129	2.83	1.89	13.44
1HGF.PDB	OE1, D_GLU_131	NH2, F_ARG_163	HH21, F_ARG_163	2.69	1.84	27.00
1HGF.PDB	OE2, F_GLU_131	NH1, F_ARG_170	HH11, F_ARG_170	2.85	1.84	3.96
1HGG.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.90	1.87	9.15
1HGG.PDB	OD2, A_ASP_275	NZ, A_LYS_50	HZ1, A_LYS_50	2.71	1.78	22.40
1HGG.PDB	OD1, A_ASP_73	ND1, A_HIS_75	HD1, A_HIS_75	2.77	1.87	17.99
1HGG.PDB	OD1, A_ASP_60	NE, A_ARG_90	HE, A_ARG_90	2.94	1.96	6.92
1HGG.PDB	OD2, A_ASP_60	NH2, A_ARG_90	HH21, A_ARG_90	2.79	1.81	10.63
1HGG.PDB	OD1, A_ASP_271	OG, A_SER_91	HG, A_SER_91	2.86	2.03	25.78
1HGG.PDB	OD2, A_ASP_271	OG, A_SER_91	HG, A_SER_91	2.85	1.97	21.46
1HGG.PDB	OD2, A_ASP_68	OG, A_SER_95	HG, A_SER_95	2.94	1.99	11.26
1HGG.PDB	OD1, A_ASP_68	OH, A_TYR_100	HH, A_TYR_100	2.94	1.99	11.28
1HGG.PDB	OD2, A_ASP_104	OG, A_SER_107	HG, A_SER_107	2.84	1.92	16.45
1HGG.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.84	1.86	14.43
1HGG.PDB	OD2, F_ASP_79	OG, A_SER_110	HG, A_SER_110	2.88	1.95	14.29
1HGG.PDB	OE2, A_GLU_119	OG1, A_THR_117	HG1, A_THR_117	2.88	1.93	9.58
1HGG.PDB	OD1, A_ASN_137	NZ, A_LYS_140	HZ2, A_LYS_140	2.76	1.76	13.87
1HGG.PDB	OD2, A_ASP_77	NE, A_ARG_141	HE, A_ARG_141	2.89	2.07	28.91
1HGG.PDB	OD1, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.76	1.85	22.03
1HGG.PDB	OD2, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.76	1.87	24.00
1HGG.PDB	OH, A_TYR_195	NE1, A_TRP_153	HE1, A_TRP_153	2.91	1.96	13.96
1HGG.PDB	OE2, A_GLU_123	NZ, A_LYS_176	HZ1, A_LYS_176	2.65	1.77	25.92
1HGG.PDB	OE1, A_GLU_123	OH, A_TYR_178	HH, A_TYR_178	2.78	1.83	8.16
1HGG.PDB	OG1, A_THR_235	NE1, A_TRP_180	HE1, A_TRP_180	2.92	1.93	2.35
1HGG.PDB	OG, A_SER_231	NE2, A_HIS_184	HE2, A_HIS_184	2.80	1.92	21.87
1HGG.PDB	OD1, A_ASN_246	NH2, A_ARG_201	HH21, A_ARG_201	2.65	1.72	18.81
1HGG.PDB	OD2, A_ASP_241	NE, A_ARG_208	HE, A_ARG_208	2.96	2.06	20.34
1HGG.PDB	OG1, A_THR_206	OG, A_SER_209	HG, A_SER_209	2.95	2.03	14.98
1HGG.PDB	OD1, E_ASP_101	NE2, A_GLN_210	HE22, A_GLN_210	2.99	2.07	17.95
1HGG.PDB	OG1, A_THR_203	OG1, A_THR_212	HG1, A_THR_212	2.88	1.92	6.20
1HGG.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.73	1.78	15.93
1HGG.PDB	OD1, A_ASP_101	OG, A_SER_231	HG, A_SER_231	2.88	1.92	8.82
1HGG.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.93	1.93	14.31
1HGG.PDB	OE2, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.74	1.91	29.92
1HGG.PDB	OD1, A_ASN_165	ND2, A_ASN_246	HD22, A_ASN_246	2.90	1.98	17.02
1HGG.PDB	OE1, A_GLN_191	ND2, A_ASN_250	HD21, A_ASN_250	2.92	1.96	11.11
1HGG.PDB	OD1, A_ASN_133	NH2, A_ARG_255	HH22, A_ARG_255	2.52	1.66	24.50
1HGG.PDB	OE2, A_GLU_119	NH1, A_ARG_261	HH12, A_ARG_261	2.68	1.87	29.79
1HGG.PDB	OE1, A_GLU_119	NH2, A_ARG_261	HH22, A_ARG_261	2.74	1.88	26.75
1HGG.PDB	OH, A_TYR_302	NZ, A_LYS_264	HZ1, A_LYS_264	2.93	1.98	19.58

1HGG.PDB	ND1, A_HIS_56	NZ, A_LYS_264	HZ2, A_LYS_264	2.66	1.73	19.87
1HGG.PDB	OD2, A_ASP_85	NZ, A_LYS_264	HZ3, A_LYS_264	2.83	1.83	12.74
1HGG.PDB	OE1, B_GLU_67	NH1, A_ARG_269	HH12, A_ARG_269	2.69	1.86	28.34
1HGG.PDB	OE1, A_GLN_44	NZ, A_LYS_292	HZ1, A_LYS_292	2.74	1.73	11.51
1HGG.PDB	OD2, A_ASP_291	NZ, A_LYS_292	HZ3, A_LYS_292	2.77	1.90	27.56
1HGG.PDB	OD1, A_ASN_285	ND2, A_ASN_298	HD22, A_ASN_298	2.97	2.01	11.28
1HGG.PDB	OD1, B_ASP_90	NZ, A_LYS_310	HZ2, A_LYS_310	2.70	1.74	18.08
1HGG.PDB	OE1, A_GLU_41	NZ, A_LYS_315	HZ3, A_LYS_315	2.73	1.81	23.14
1HGG.PDB	OE2, A_GLU_35	ND2, A_ASN_322	HD22, A_ASN_322	2.81	1.95	25.01
1HGG.PDB	OE2, B_GLU_15	NZ, A_LYS_326	HZ1, A_LYS_326	2.83	1.89	21.04
1HGG.PDB	OE1, A_GLU_325	NZ, A_LYS_326	HZ3, A_LYS_326	2.82	1.86	18.51
1HGG.PDB	OE1, B_GLN_34	NE, B_ARG_25	HE, B_ARG_25	2.80	1.89	18.36
1HGG.PDB	OE1, B_GLN_34	NH2, B_ARG_25	HH21, B_ARG_25	2.91	2.04	24.97
1HGG.PDB	OE2, A_GLU_325	NH2, B_ARG_25	HH22, B_ARG_25	2.94	1.96	12.23
1HGG.PDB	OD2, B_ASP_37	OG, B_SER_40	HG, B_SER_40	2.80	1.93	21.69
1HGG.PDB	OD1, B_ASP_46	NE2, B_GLN_42	HE22, B_GLN_42	2.83	1.95	21.37
1HGG.PDB	OE2, B_GLU_114	NE2, B_GLN_47	HE21, B_GLN_47	2.96	2.05	17.92
1HGG.PDB	OG1, B_THR_107	NZ, B_LYS_51	HZ1, B_LYS_51	2.97	2.00	18.19
1HGG.PDB	OE1, B_GLU_103	NZ, B_LYS_51	HZ2, B_LYS_51	2.76	1.73	5.86
1HGG.PDB	ND1, B_HIS_106	NZ, B_LYS_51	HZ3, B_LYS_51	2.77	1.79	14.96
1HGG.PDB	OE1, B_GLU_57	NH1, B_ARG_54	HH11, B_ARG_54	2.86	1.86	11.23
1HGG.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.75	1.76	9.96
1HGG.PDB	OE2, B_GLU_61	NZ, B_LYS_58	HZ3, B_LYS_58	2.94	1.92	12.53
1HGG.PDB	OD2, F_ASP_90	NZ, B_LYS_62	HZ2, B_LYS_62	2.65	1.82	29.87
1HGG.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ3, B_LYS_62	2.64	1.73	23.35
1HGG.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.90	1.96	14.63
1HGG.PDB	OE2, B_GLU_85	NZ, B_LYS_68	HZ2, B_LYS_68	2.75	1.72	7.06
1HGG.PDB	OE2, B_GLU_72	OG, B_SER_71	HG, B_SER_71	2.84	2.03	27.31
1HGG.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.94	1.96	10.47
1HGG.PDB	OE1, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.88	1.89	10.69
1HGG.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.73	1.73	5.91
1HGG.PDB	OE2, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.82	1.82	7.26
1HGG.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.68	1.80	19.99
1HGG.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.77	1.73	5.14
1HGG.PDB	OE2, B_GLU_120	NH1, B_ARG_123	HH11, B_ARG_123	2.73	1.87	25.50
1HGG.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.84	1.98	22.96
1HGG.PDB	OE2, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.81	1.98	25.54
1HGG.PDB	OH, B_TYR_157	ND2, B_ASN_129	HD22, B_ASN_129	2.80	1.86	13.18
1HGG.PDB	OD1, B_ASN_154	OG1, B_THR_156	HG1, B_THR_156	2.71	1.81	17.64
1HGG.PDB	OE2, B_GLU_131	NH1, B_ARG_170	HH11, B_ARG_170	2.85	1.85	6.28
1HGG.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.94	1.91	8.28
1HGG.PDB	OD2, C_ASP_275	NZ, C_LYS_50	HZ1, C_LYS_50	2.68	1.77	23.74
1HGG.PDB	OE1, C_GLU_82	NH2, C_ARG_57	HH21, C_ARG_57	2.59	1.77	28.22
1HGG.PDB	OD1, C_ASP_73	ND1, C_HIS_75	HD1, C_HIS_75	2.72	1.84	20.87
1HGG.PDB	OD1, C_ASP_60	NE, C_ARG_90	HE, C_ARG_90	2.93	1.95	8.71
1HGG.PDB	OD2, C_ASP_60	NH2, C_ARG_90	HH21, C_ARG_90	2.79	1.80	9.72
1HGG.PDB	OD1, C_ASP_271	OG, C_SER_91	HG, C_SER_91	2.89	2.06	25.85
1HGG.PDB	OD2, C_ASP_271	OG, C_SER_91	HG, C_SER_91	2.90	2.02	21.44
1HGG.PDB	OD2, C_ASP_68	OG, C_SER_95	HG, C_SER_95	2.90	1.95	11.80
1HGG.PDB	OD1, C_ASP_68	OH, C_TYR_100	HH, C_TYR_100	2.93	1.98	11.50
1HGG.PDB	OD2, C_ASP_104	OG, C_SER_107	HG, C_SER_107	2.88	1.95	15.82
1HGG.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.85	1.88	14.56
1HGG.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.76	1.86	17.83
1HGG.PDB	OE2, C_GLU_119	OG1, C_THR_117	HG1, C_THR_117	2.92	1.97	8.69
1HGG.PDB	OD1, C_ASN_137	NZ, C_LYS_140	HZ2, C_LYS_140	2.78	1.78	13.21
1HGG.PDB	OD2, C_ASP_77	NE, C_ARG_141	HE, C_ARG_141	2.87	2.06	29.23
1HGG.PDB	OD1, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.76	1.85	22.10
1HGG.PDB	OD2, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.74	1.86	24.28

1HGG.PDB	OD1, C_ASN_137	OG, C_SER_145	HG, C_SER_145	2.90	2.03	20.82
1HGG.PDB	OH, C_TYR_195	NE1, C_TRP_153	HE1, C_TRP_153	2.90	1.98	17.08
1HGG.PDB	OE2, C_GLU_123	NZ, C_LYS_176	HZ1, C_LYS_176	2.63	1.76	26.89
1HGG.PDB	OE1, C_GLU_123	OH, C_TYR_178	HH, C_TYR_178	2.78	1.82	5.18
1HGG.PDB	OG1, C_THR_235	NE1, C_TRP_180	HE1, C_TRP_180	2.92	1.93	1.99
1HGG.PDB	OG, C_SER_231	NE2, C_HIS_184	HE2, C_HIS_184	2.79	1.91	21.48
1HGG.PDB	OD1, C_ASN_250	NE2, C_GLN_191	HE21, C_GLN_191	2.95	1.99	11.16
1HGG.PDB	OD1, C_ASN_246	NH2, C_ARG_201	HH21, C_ARG_201	2.66	1.74	19.39
1HGG.PDB	OG1, C_THR_212	OG1, C_THR_203	HG1, C_THR_203	2.83	1.91	13.70
1HGG.PDB	OD2, C_ASP_241	NE, C_ARG_208	HE, C_ARG_208	2.93	2.03	20.59
1HGG.PDB	OG1, C_THR_206	OG, C_SER_209	HG, C_SER_209	2.99	2.06	14.06
1HGG.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.61	1.71	21.26
1HGG.PDB	OD1, C_ASP_101	OG, C_SER_231	HG, C_SER_231	2.91	1.95	9.20
1HGG.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.83	1.86	17.18
1HGG.PDB	OE2, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.70	1.87	29.85
1HGG.PDB	OD1, C_ASN_165	ND2, C_ASN_246	HD22, C_ASN_246	2.88	1.97	17.94
1HGG.PDB	OE1, C_GLN_191	ND2, C_ASN_250	HD21, C_ASN_250	2.88	1.93	11.32
1HGG.PDB	OD1, C_ASN_133	NH2, C_ARG_255	HH22, C_ARG_255	2.54	1.68	24.43
1HGG.PDB	OE2, C_GLU_119	NH1, C_ARG_261	HH12, C_ARG_261	2.67	1.86	29.79
1HGG.PDB	OE1, C_GLU_119	NH2, C_ARG_261	HH22, C_ARG_261	2.73	1.87	26.76
1HGG.PDB	OH, C_TYR_302	NZ, C_LYS_264	HZ1, C_LYS_264	2.88	1.92	18.77
1HGG.PDB	ND1, C_HIS_56	NZ, C_LYS_264	HZ2, C_LYS_264	2.66	1.73	19.57
1HGG.PDB	OD2, C_ASP_85	NZ, C_LYS_264	HZ3, C_LYS_264	2.85	1.83	11.83
1HGG.PDB	OE1, D_GLU_67	NH1, C_ARG_269	HH12, C_ARG_269	2.69	1.85	27.75
1HGG.PDB	OE1, C_GLN_44	NZ, C_LYS_292	HZ1, C_LYS_292	2.77	1.76	11.69
1HGG.PDB	OD2, C_ASP_291	NZ, C_LYS_292	HZ3, C_LYS_292	2.78	1.91	27.51
1HGG.PDB	OD1, C_ASN_285	ND2, C_ASN_298	HD22, C_ASN_298	2.95	2.00	10.88
1HGG.PDB	OD1, D_ASP_90	NZ, C_LYS_310	HZ2, C_LYS_310	2.65	1.73	21.74
1HGG.PDB	OE1, C_GLU_41	NZ, C_LYS_315	HZ3, C_LYS_315	2.73	1.82	23.48
1HGG.PDB	OE2, C_GLU_35	ND2, C_ASN_322	HD22, C_ASN_322	2.82	1.96	24.18
1HGG.PDB	OXT, C_THR_328	NE2, C_GLN_327	HE22, C_GLN_327	2.99	2.05	16.22
1HGG.PDB	OE1, D_GLN_34	NE, D_ARG_25	HE, D_ARG_25	2.69	1.81	20.51
1HGG.PDB	OE1, D_GLN_34	NH2, D_ARG_25	HH21, D_ARG_25	2.92	2.08	27.66
1HGG.PDB	OD1, D_ASN_146	ND2, D_ASN_28	HD21, D_ASN_28	2.95	1.98	8.75
1HGG.PDB	OD2, D_ASP_37	OG, D_SER_40	HG, D_SER_40	2.77	1.93	24.58
1HGG.PDB	OD1, D_ASP_46	NE2, D_GLN_42	HE22, D_GLN_42	2.85	1.96	21.08
1HGG.PDB	OE2, D_GLU_114	NE2, D_GLN_47	HE21, D_GLN_47	2.97	2.05	17.17
1HGG.PDB	OG1, D_THR_107	NZ, D_LYS_51	HZ1, D_LYS_51	2.98	2.00	17.66
1HGG.PDB	OE1, D_GLU_103	NZ, D_LYS_51	HZ2, D_LYS_51	2.77	1.73	6.39
1HGG.PDB	ND1, D_HIS_106	NZ, D_LYS_51	HZ3, D_LYS_51	2.76	1.78	15.09
1HGG.PDB	OE1, D_GLU_57	NH1, D_ARG_54	HH11, D_ARG_54	2.86	1.86	11.12
1HGG.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.76	1.78	10.56
1HGG.PDB	OE2, D_GLU_61	NZ, D_LYS_58	HZ3, D_LYS_58	2.91	1.89	12.30
1HGG.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.86	1.90	9.42
1HGG.PDB	OE2, D_GLU_85	NZ, D_LYS_68	HZ2, D_LYS_68	2.77	1.74	6.59
1HGG.PDB	OE2, D_GLU_72	OG, D_SER_71	HG, D_SER_71	2.82	2.00	26.77
1HGG.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.86	1.89	9.57
1HGG.PDB	OE1, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.78	1.80	12.10
1HGG.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.67	1.68	6.66
1HGG.PDB	OE2, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.74	1.75	9.29
1HGG.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.59	1.78	26.83
1HGG.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.73	1.70	8.35
1HGG.PDB	OE2, D_GLU_120	NH1, D_ARG_123	HH11, D_ARG_123	2.73	1.87	25.59
1HGG.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.86	2.00	22.57
1HGG.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.78	1.96	26.12
1HGG.PDB	OH, D_TYR_157	ND2, D_ASN_129	HD22, D_ASN_129	2.80	1.84	10.50
1HGG.PDB	OD1, D_ASN_154	OG1, D_THR_156	HG1, D_THR_156	2.73	1.82	15.46
1HGG.PDB	NE2, D_HIS_142	OH, D_TYR_157	HH, D_TYR_157	2.72	1.85	20.87

1HGG.PDB	OE2, D_GLU_131	NH1, D_ARG_170	HH11, D_ARG_170	2.85	1.86	6.70
1HGG.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.91	1.88	8.89
1HGG.PDB	OD2, E_ASP_275	NZ, E_LYS_50	HZ1, E_LYS_50	2.68	1.77	24.10
1HGG.PDB	OD1, E_ASP_73	ND1, E_HIS_75	HD1, E_HIS_75	2.75	1.85	17.34
1HGG.PDB	OD1, E_ASP_60	NE, E_ARG_90	HE, E_ARG_90	2.91	1.94	9.27
1HGG.PDB	OD2, E_ASP_60	NH2, E_ARG_90	HH21, E_ARG_90	2.83	1.84	9.64
1HGG.PDB	OD1, E_ASP_271	OG, E_SER_91	HG, E_SER_91	2.92	2.07	24.79
1HGG.PDB	OD2, E_ASP_271	OG, E_SER_91	HG, E_SER_91	2.93	2.06	22.08
1HGG.PDB	OD2, E_ASP_68	OG, E_SER_95	HG, E_SER_95	2.93	1.98	13.19
1HGG.PDB	OD1, E_ASP_68	OH, E_TYR_100	HH, E_TYR_100	2.92	1.96	10.90
1HGG.PDB	OD2, E_ASP_104	OG, E_SER_107	HG, E_SER_107	2.85	1.93	15.56
1HGG.PDB	OE2, F_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.88	1.90	14.20
1HGG.PDB	OD2, D_ASP_79	OG, E_SER_110	HG, E_SER_110	2.79	1.88	16.48
1HGG.PDB	OE2, E_GLU_119	OG1, E_THR_117	HG1, E_THR_117	2.95	1.99	7.33
1HGG.PDB	OD1, E_ASN_137	NZ, E_LYS_140	HZ2, E_LYS_140	2.76	1.76	13.40
1HGG.PDB	OD2, E_ASP_77	NE, E_ARG_141	HE, E_ARG_141	2.90	2.09	29.10
1HGG.PDB	OD1, E_ASP_77	NH2, E_ARG_141	HH21, E_ARG_141	2.80	1.90	22.17
1HGG.PDB	OD2, E_ASP_77	NH2, E_ARG_141	HH21, E_ARG_141	2.74	1.86	23.74
1HGG.PDB	OD1, E_ASN_137	OG, E_SER_145	HG, E_SER_145	2.95	2.08	20.42
1HGG.PDB	OH, E_TYR_195	NE1, E_TRP_153	HE1, E_TRP_153	2.91	1.97	14.69
1HGG.PDB	OE2, E_GLU_123	NZ, E_LYS_176	HZ1, E_LYS_176	2.65	1.78	26.50
1HGG.PDB	OE1, E_GLU_123	OH, E_TYR_178	HH, E_TYR_178	2.80	1.84	8.47
1HGG.PDB	OG1, E_THR_235	NE1, E_TRP_180	HE1, E_TRP_180	2.93	1.94	2.01
1HGG.PDB	OG, E_SER_231	NE2, E_HIS_184	HE2, E_HIS_184	2.81	1.94	22.49
1HGG.PDB	OD1, E_ASN_246	NH2, E_ARG_201	HH21, E_ARG_201	2.66	1.74	20.08
1HGG.PDB	OG1, E_THR_212	OG1, E_THR_203	HG1, E_THR_203	2.88	1.95	13.34
1HGG.PDB	OD2, E_ASP_241	NE, E_ARG_208	HE, E_ARG_208	2.96	2.05	19.90
1HGG.PDB	OG1, E_THR_206	OG, E_SER_209	HG, E_SER_209	2.99	2.07	14.54
1HGG.PDB	OD1, C_ASP_101	NE2, E_GLN_210	HE22, E_GLN_210	2.96	2.04	17.70
1HGG.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.72	1.80	20.26
1HGG.PDB	OD1, E_ASP_101	OG, E_SER_231	HG, E_SER_231	2.91	1.96	10.31
1HGG.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ1, E_LYS_238	2.89	1.89	13.93
1HGG.PDB	OD1, E_ASN_165	ND2, E_ASN_246	HD22, E_ASN_246	2.88	1.96	17.66
1HGG.PDB	OE1, E_GLN_191	ND2, E_ASN_250	HD21, E_ASN_250	2.89	1.94	10.20
1HGG.PDB	OD1, E_ASN_133	NH2, E_ARG_255	HH22, E_ARG_255	2.55	1.68	24.24
1HGG.PDB	OE2, E_GLU_119	NH1, E_ARG_261	HH12, E_ARG_261	2.69	1.87	29.29
1HGG.PDB	OE1, E_GLU_119	NH2, E_ARG_261	HH22, E_ARG_261	2.74	1.88	26.67
1HGG.PDB	OH, E_TYR_302	NZ, E_LYS_264	HZ1, E_LYS_264	2.90	1.93	18.14
1HGG.PDB	ND1, E_HIS_56	NZ, E_LYS_264	HZ2, E_LYS_264	2.66	1.73	20.09
1HGG.PDB	OD2, E_ASP_85	NZ, E_LYS_264	HZ3, E_LYS_264	2.85	1.83	11.84
1HGG.PDB	OE1, F_GLU_67	NH1, E_ARG_269	HH12, E_ARG_269	2.69	1.85	27.32
1HGG.PDB	OE1, E_GLN_44	NZ, E_LYS_292	HZ1, E_LYS_292	2.77	1.75	10.61
1HGG.PDB	OD2, E_ASP_291	NZ, E_LYS_292	HZ3, E_LYS_292	2.76	1.90	27.94
1HGG.PDB	OD1, E_ASN_285	ND2, E_ASN_298	HD22, E_ASN_298	2.95	2.00	11.31
1HGG.PDB	OD1, F_ASP_90	NZ, E_LYS_310	HZ2, E_LYS_310	2.64	1.72	22.12
1HGG.PDB	OE1, E_GLU_41	NZ, E_LYS_315	HZ3, E_LYS_315	2.68	1.80	26.22
1HGG.PDB	OE2, E_GLU_35	ND2, E_ASN_322	HD22, E_ASN_322	2.79	1.94	25.02
1HGG.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.98	1.97	15.13
1HGG.PDB	OD2, F_ASP_37	OG, F_SER_40	HG, F_SER_40	2.74	1.92	26.19
1HGG.PDB	OD1, F_ASP_46	NE2, F_GLN_42	HE22, F_GLN_42	2.82	1.94	21.99
1HGG.PDB	OE2, F_GLU_114	NE2, F_GLN_47	HE21, F_GLN_47	2.97	2.06	18.05
1HGG.PDB	OG1, F_THR_107	NZ, F_LYS_51	HZ1, F_LYS_51	2.98	2.02	18.55
1HGG.PDB	OE1, F_GLU_103	NZ, F_LYS_51	HZ2, F_LYS_51	2.79	1.76	6.25
1HGG.PDB	ND1, F_HIS_106	NZ, F_LYS_51	HZ3, F_LYS_51	2.72	1.74	15.22
1HGG.PDB	OE1, F_GLU_57	NH1, F_ARG_54	HH11, F_ARG_54	2.85	1.85	10.83
1HGG.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.73	1.74	10.16
1HGG.PDB	OE2, F_GLU_61	NZ, F_LYS_58	HZ3, F_LYS_58	2.94	1.92	12.48
1HGG.PDB	OD2, D_ASP_86	NZ, F_LYS_62	HZ3, F_LYS_62	2.58	1.75	29.01

1HGG.PDB	OG, E_SER.110	NE2, F_HIS.64	HE2, F_HIS.64	2.87	1.91	10.03
1HGG.PDB	OE2, F_GLU.85	NZ, F_LYS.68	HZ2, F_LYS.68	2.75	1.74	10.05
1HGG.PDB	OE2, F_GLU.72	OG, F_SER.71	HG, F_SER.71	2.86	2.03	26.49
1HGG.PDB	OE2, B_GLU.81	NE, F_ARG.76	HE, F_ARG.76	2.88	1.92	11.44
1HGG.PDB	OE1, B_GLU.74	NH1, F_ARG.76	HH12, F_ARG.76	2.75	1.76	9.13
1HGG.PDB	OE1, B_GLU.81	NH2, F_ARG.76	HH21, F_ARG.76	2.67	1.68	1.99
1HGG.PDB	OE2, B_GLU.74	NH2, F_ARG.76	HH22, F_ARG.76	2.79	1.81	10.64
1HGG.PDB	OH, D_TYR.83	NZ, F_LYS.88	HZ1, F_LYS.88	2.68	1.67	10.46
1HGG.PDB	OE2, F_GLU.120	NH1, F_ARG.123	HH11, F_ARG.123	2.72	1.86	25.68
1HGG.PDB	OE1, D_GLU.132	NE, F_ARG.124	HE, F_ARG.124	2.96	2.09	22.59
1HGG.PDB	OE2, D_GLU.132	NE, F_ARG.124	HE, F_ARG.124	2.87	2.01	24.00
1HGG.PDB	OH, F_TYR.157	ND2, F_ASN.129	HD22, F_ASN.129	2.79	1.86	14.20
1HGG.PDB	OE2, F_GLU.131	NH1, F_ARG.170	HH11, F_ARG.170	2.84	1.84	6.38
1HGH.PDB	OE2, B_GLU.97	NZ, A_LYS.27	HZ1, A_LYS.27	2.78	1.76	9.03
1HGH.PDB	OD2, A_ASP.275	NZ, A_LYS.50	HZ1, A_LYS.50	2.79	1.83	19.36
1HGH.PDB	OD1, A_ASP.73	ND1, A_HIS.75	HD1, A_HIS.75	2.74	1.85	19.20
1HGH.PDB	OD1, A_ASP.60	NE, A_ARG.90	HE, A_ARG.90	2.85	1.88	8.50
1HGH.PDB	OD2, A_ASP.60	NH2, A_ARG.90	HH21, A_ARG.90	2.79	1.80	9.33
1HGH.PDB	OD2, A_ASP.271	OG, A_SER.91	HG, A_SER.91	2.76	1.89	21.30
1HGH.PDB	OD2, A_ASP.68	OG, A_SER.95	HG, A_SER.95	2.83	1.95	21.96
1HGH.PDB	OD1, A_ASP.68	OH, A_TYR.100	HH, A_TYR.100	2.95	2.07	21.37
1HGH.PDB	OD2, A_ASP.104	OG, A_SER.107	HG, A_SER.107	2.88	1.94	14.34
1HGH.PDB	OE2, B_GLU.67	NH2, A_ARG.109	HH21, A_ARG.109	2.86	1.88	13.48
1HGH.PDB	OD2, F_ASP.79	OG, A_SER.110	HG, A_SER.110	2.97	2.01	11.65
1HGH.PDB	OE2, A_GLU.119	OG1, A_THR.117	HG1, A_THR.117	2.86	1.91	8.00
1HGH.PDB	OD1, A_ASN.137	NZ, A_LYS.140	HZ2, A_LYS.140	2.74	1.73	12.09
1HGH.PDB	OD2, A_ASP.77	NE, A_ARG.141	HE, A_ARG.141	2.85	2.03	27.72
1HGH.PDB	OD1, A_ASP.77	NH2, A_ARG.141	HH21, A_ARG.141	2.86	1.95	21.78
1HGH.PDB	OD2, A_ASP.77	NH2, A_ARG.141	HH21, A_ARG.141	2.74	1.85	23.60
1HGH.PDB	OH, A_TYR.195	NE1, A_TRP.153	HE1, A_TRP.153	2.96	2.05	18.96
1HGH.PDB	OE2, A_GLU.123	NZ, A_LYS.176	HZ1, A_LYS.176	2.68	1.79	24.70
1HGH.PDB	OE1, A_GLU.123	OH, A_TYR.178	HH, A_TYR.178	2.75	1.81	10.37
1HGH.PDB	OG1, A_THR.235	NE1, A_TRP.180	HE1, A_TRP.180	2.89	1.90	1.65
1HGH.PDB	OG, A_SER.231	NE2, A_HIS.184	HE2, A_HIS.184	2.74	1.90	25.48
1HGH.PDB	OD1, A_ASN.250	NE2, A_GLN.191	HE21, A_GLN.191	2.96	2.00	8.72
1HGH.PDB	OD1, A_ASN.246	NH2, A_ARG.201	HH21, A_ARG.201	2.63	1.71	19.32
1HGH.PDB	OG1, A_THR.206	OG, A_SER.209	HG, A_SER.209	2.93	1.98	8.14
1HGH.PDB	OD1, E_ASP.101	NE2, A_GLN.210	HE22, A_GLN.210	2.97	2.14	27.61
1HGH.PDB	OG1, A_THR.203	OG1, A_THR.212	HG1, A_THR.212	2.93	1.98	7.92
1HGH.PDB	OE1, C_GLN.210	NH2, A_ARG.220	HH21, A_ARG.220	2.66	1.73	18.15
1HGH.PDB	OD1, A_ASP.101	OG, A_SER.231	HG, A_SER.231	2.86	1.91	11.01
1HGH.PDB	OE1, F_GLU.72	NZ, A_LYS.238	HZ3, A_LYS.238	2.92	1.93	15.64
1HGH.PDB	OD1, A_ASN.165	ND2, A_ASN.246	HD22, A_ASN.246	2.95	1.98	10.57
1HGH.PDB	OE1, A_GLN.191	ND2, A_ASN.250	HD21, A_ASN.250	2.87	1.90	5.96
1HGH.PDB	OE2, A_GLU.119	NH1, A_ARG.261	HH12, A_ARG.261	2.62	1.81	29.53
1HGH.PDB	OE1, A_GLU.119	NH2, A_ARG.261	HH22, A_ARG.261	2.87	1.97	23.64
1HGH.PDB	OD2, A_ASP.85	NZ, A_LYS.264	HZ3, A_LYS.264	2.81	1.82	15.33
1HGH.PDB	OE1, A_GLN.44	NZ, A_LYS.292	HZ1, A_LYS.292	2.68	1.67	11.56
1HGH.PDB	OD2, A_ASP.291	NZ, A_LYS.292	HZ3, A_LYS.292	2.82	1.85	18.01
1HGH.PDB	OD1, B_ASP.86	NZ, A_LYS.310	HZ2, A_LYS.310	2.71	1.84	27.09
1HGH.PDB	OE1, A_GLU.41	NZ, A_LYS.315	HZ3, A_LYS.315	2.87	1.90	18.83
1HGH.PDB	OE2, A_GLU.35	ND2, A_ASN.322	HD22, A_ASN.322	2.83	1.93	20.02
1HGH.PDB	OE1, A_GLU.325	NZ, A_LYS.326	HZ3, A_LYS.326	2.84	1.87	17.61
1HGH.PDB	OE1, B_GLN.34	NE, B_ARG.25	HE, B_ARG.25	2.67	1.79	21.37
1HGH.PDB	OE1, B_GLN.34	NH2, B_ARG.25	HH21, B_ARG.25	2.91	2.10	29.24
1HGH.PDB	OD1, B_ASP.46	NE2, B_GLN.42	HE22, B_GLN.42	2.86	1.97	20.47
1HGH.PDB	OE1, B_GLU.103	NZ, B_LYS.51	HZ1, B_LYS.51	2.79	1.76	7.63
1HGH.PDB	ND1, B_HIS.106	NZ, B_LYS.51	HZ2, B_LYS.51	2.80	1.85	18.51

1HGH.PDB	OG1, B.THR.107	NZ, B.LYS.51	HZ3, B.LYS.51	2.89	1.91	15.99
1HGH.PDB	OE1, B.GLU.57	NH1, B.ARG.54	HH11, B.ARG.54	2.86	1.87	11.36
1HGH.PDB	OE2, F.GLU.97	NH2, B.ARG.54	HH22, B.ARG.54	2.82	1.86	15.60
1HGH.PDB	OD2, F.ASP.86	NZ, B.LYS.62	HZ1, B.LYS.62	2.66	1.80	27.71
1HGH.PDB	OD2, F.ASP.90	NZ, B.LYS.62	HZ3, B.LYS.62	2.68	1.82	27.13
1HGH.PDB	OG, A.SER.110	NE2, B.HIS.64	HE2, B.HIS.64	2.87	1.91	11.96
1HGH.PDB	OE2, B.GLU.85	NZ, B.LYS.68	HZ2, B.LYS.68	2.73	1.71	6.94
1HGH.PDB	OE2, D.GLU.81	NE, B.ARG.76	HE, B.ARG.76	2.87	1.90	9.70
1HGH.PDB	OE2, D.GLU.74	NH1, B.ARG.76	HH12, B.ARG.76	2.91	1.90	8.45
1HGH.PDB	OE1, D.GLU.81	NH2, B.ARG.76	HH21, B.ARG.76	2.77	1.76	5.47
1HGH.PDB	OE1, D.GLU.74	NH2, B.ARG.76	HH22, B.ARG.76	2.89	1.87	2.83
1HGH.PDB	OE1, B.GLU.74	NE2, B.GLN.78	HE22, B.GLN.78	2.91	1.95	10.12
1HGH.PDB	OE1, D.GLU.85	OH, B.TYR.83	HH, B.TYR.83	2.69	1.84	23.96
1HGH.PDB	OH, F.TYR.83	NZ, B.LYS.88	HZ1, B.LYS.88	2.74	1.71	7.44
1HGH.PDB	OE2, B.GLU.120	NH1, B.ARG.123	HH11, B.ARG.123	2.74	1.85	22.74
1HGH.PDB	OE1, F.GLU.132	NE, B.ARG.124	HE, B.ARG.124	2.76	1.94	26.47
1HGH.PDB	OE2, F.GLU.132	NE, B.ARG.124	HE, B.ARG.124	2.83	1.98	23.62
1HGH.PDB	OH, B.TYR.157	ND2, B.ASN.129	HD22, B.ASN.129	2.83	1.87	11.09
1HGH.PDB	OE2, B.GLU.150	ND2, B.ASN.154	HD21, B.ASN.154	2.97	2.10	23.74
1HGH.PDB	OD1, B.ASN.154	OG1, B.THR.156	HG1, B.THR.156	2.66	1.78	19.28
1HGH.PDB	OE2, B.GLU.131	NH1, B.ARG.170	HH11, B.ARG.170	2.83	1.83	5.81
1HGH.PDB	OE2, D.GLU.97	NZ, C.LYS.27	HZ1, C.LYS.27	2.82	1.78	7.61
1HGH.PDB	OD2, C.ASP.275	NZ, C.LYS.50	HZ1, C.LYS.50	2.77	1.81	19.74
1HGH.PDB	OD1, C.ASP.73	ND1, C.HIS.75	HD1, C.HIS.75	2.71	1.84	22.23
1HGH.PDB	OD1, C.ASP.60	NE, C.ARG.90	HE, C.ARG.90	2.80	1.87	15.44
1HGH.PDB	OD2, C.ASP.60	NH2, C.ARG.90	HH21, C.ARG.90	2.76	1.77	8.79
1HGH.PDB	OD2, C.ASP.271	OG, C.SER.91	HG, C.SER.91	2.80	1.87	12.62
1HGH.PDB	OD2, C.ASP.68	OG, C.SER.95	HG, C.SER.95	2.83	1.92	18.04
1HGH.PDB	OD1, C.ASP.68	OH, C.TYR.100	HH, C.TYR.100	2.94	2.01	15.20
1HGH.PDB	OD2, C.ASP.104	OG, C.SER.107	HG, C.SER.107	2.88	1.96	17.02
1HGH.PDB	OE2, D.GLU.67	NH2, C.ARG.109	HH21, C.ARG.109	2.86	1.88	13.66
1HGH.PDB	OD2, B.ASP.79	OG, C.SER.110	HG, C.SER.110	2.78	1.85	13.87
1HGH.PDB	OE2, C.GLU.119	OG1, C.THR.117	HG1, C.THR.117	2.87	1.92	8.14
1HGH.PDB	OD1, C.ASN.137	NZ, C.LYS.140	HZ2, C.LYS.140	2.76	1.74	10.11
1HGH.PDB	OD2, C.ASP.77	NE, C.ARG.141	HE, C.ARG.141	2.85	2.02	26.86
1HGH.PDB	OD1, C.ASP.77	NH2, C.ARG.141	HH21, C.ARG.141	2.88	1.98	22.59
1HGH.PDB	OD2, C.ASP.77	NH2, C.ARG.141	HH21, C.ARG.141	2.75	1.86	23.43
1HGH.PDB	OD1, C.ASN.137	OG, C.SER.145	HG, C.SER.145	2.89	2.04	23.42
1HGH.PDB	OH, C.TYR.195	NE1, C.TRP.153	HE1, C.TRP.153	2.92	2.00	17.94
1HGH.PDB	OE2, C.GLU.123	NZ, C.LYS.176	HZ1, C.LYS.176	2.65	1.80	28.51
1HGH.PDB	OE1, C.GLU.123	OH, C.TYR.178	HH, C.TYR.178	2.74	1.81	11.36
1HGH.PDB	OG1, C.THR.235	NE1, C.TRP.180	HE1, C.TRP.180	2.88	1.89	0.71
1HGH.PDB	OG, C.SER.231	NE2, C.HIS.184	HE2, C.HIS.184	2.77	1.92	24.69
1HGH.PDB	OD1, C.ASN.250	NE2, C.GLN.191	HE21, C.GLN.191	2.95	1.99	9.46
1HGH.PDB	OD1, C.ASN.246	NH2, C.ARG.201	HH21, C.ARG.201	2.65	1.73	20.02
1HGH.PDB	OG1, C.THR.212	OG1, C.THR.203	HG1, C.THR.203	2.92	1.98	11.43
1HGH.PDB	OD2, C.ASP.241	NE, C.ARG.208	HE, C.ARG.208	2.97	2.08	22.63
1HGH.PDB	OG1, C.THR.206	OG, C.SER.209	HG, C.SER.209	2.95	2.00	8.11
1HGH.PDB	OD1, A.ASP.101	NE2, C.GLN.210	HE22, C.GLN.210	2.93	2.07	24.87
1HGH.PDB	OE1, E.GLN.210	NH2, C.ARG.220	HH21, C.ARG.220	2.57	1.72	26.03
1HGH.PDB	OD1, C.ASP.101	OG, C.SER.231	HG, C.SER.231	2.86	1.92	12.68
1HGH.PDB	OE1, B.GLU.72	NZ, C.LYS.238	HZ1, C.LYS.238	2.71	1.80	22.72
1HGH.PDB	OD1, C.ASN.165	ND2, C.ASN.246	HD22, C.ASN.246	2.97	2.00	10.03
1HGH.PDB	OE1, C.GLN.191	ND2, C.ASN.250	HD21, C.ASN.250	2.86	1.89	6.98
1HGH.PDB	OE2, C.GLU.119	NH1, C.ARG.261	HH12, C.ARG.261	2.64	1.82	29.37
1HGH.PDB	OE1, C.GLU.119	NH2, C.ARG.261	HH22, C.ARG.261	2.85	1.97	24.44
1HGH.PDB	OD2, C.ASP.85	NZ, C.LYS.264	HZ3, C.LYS.264	2.79	1.81	15.90
1HGH.PDB	OE1, C.GLN.44	NZ, C.LYS.292	HZ1, C.LYS.292	2.68	1.68	11.00

1HGH.PDB	OD2, C_ASP_291	NZ, C_LYS_292	HZ3, C_LYS_292	2.82	1.84	17.38
1HGH.PDB	OD1, C_ASN_285	ND2, C_ASN_298	HD22, C_ASN_298	2.99	2.06	14.92
1HGH.PDB	OD1, D_ASP_86	NZ, C_LYS_310	HZ2, C_LYS_310	2.73	1.85	26.20
1HGH.PDB	OE1, C_GLU_41	NZ, C_LYS_315	HZ3, C_LYS_315	2.87	1.91	19.47
1HGH.PDB	OE2, C_GLU_35	ND2, C_ASN_322	HD22, C_ASN_322	2.82	1.91	18.57
1HGH.PDB	OE1, D_GLU_15	NZ, C_LYS_326	HZ1, C_LYS_326	2.77	1.75	11.00
1HGH.PDB	OXT, C_THR_328	NE2, C_GLN_327	HE22, C_GLN_327	2.93	1.99	14.57
1HGH.PDB	OE1, D_GLN_34	NE, D_ARG_25	HE, D_ARG_25	2.91	1.96	12.36
1HGH.PDB	OD2, D_ASP_37	OG, D_SER_40	HG, D_SER_40	2.74	1.93	27.28
1HGH.PDB	OD1, D_ASP_46	NE2, D_GLN_42	HE22, D_GLN_42	2.87	1.96	19.71
1HGH.PDB	OE1, D_GLU_103	NZ, D_LYS_51	HZ1, D_LYS_51	2.74	1.72	7.43
1HGH.PDB	ND1, D_HIS_106	NZ, D_LYS_51	HZ2, D_LYS_51	2.80	1.84	18.41
1HGH.PDB	OG1, D_THR_107	NZ, D_LYS_51	HZ3, D_LYS_51	2.90	1.93	16.98
1HGH.PDB	OE1, D_GLU_57	NH1, D_ARG_54	HH11, D_ARG_54	2.86	1.86	11.45
1HGH.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.80	1.85	16.64
1HGH.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.84	1.88	10.18
1HGH.PDB	OE2, D_GLU_85	NZ, D_LYS_68	HZ2, D_LYS_68	2.75	1.73	9.37
1HGH.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.79	1.84	10.45
1HGH.PDB	OE2, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.77	1.77	10.38
1HGH.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.70	1.70	6.41
1HGH.PDB	OE1, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.75	1.75	5.88
1HGH.PDB	OE1, D_GLU_74	NE2, D_GLN_78	HE22, D_GLN_78	2.92	1.96	9.79
1HGH.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.59	1.81	29.86
1HGH.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.66	1.64	7.83
1HGH.PDB	OE2, D_GLU_120	NH1, D_ARG_123	HH11, D_ARG_123	2.77	1.87	22.36
1HGH.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.80	1.98	26.35
1HGH.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.84	1.99	23.38
1HGH.PDB	OH, D_TYR_157	ND2, D_ASN_129	HD22, D_ASN_129	2.83	1.87	7.67
1HGH.PDB	OD1, D_ASN_154	OG1, D_THR_156	HG1, D_THR_156	2.69	1.80	16.96
1HGH.PDB	NE2, D_HIS_142	OH, D_TYR_157	HH, D_TYR_157	2.68	1.87	26.02
1HGH.PDB	OE2, D_GLU_131	NH1, D_ARG_170	HH11, D_ARG_170	2.83	1.83	5.85
1HGH.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.77	1.74	8.08
1HGH.PDB	OD2, E_ASP_275	NZ, E_LYS_50	HZ1, E_LYS_50	2.78	1.83	20.38
1HGH.PDB	OD1, E_ASP_73	ND1, E_HIS_75	HD1, E_HIS_75	2.70	1.83	21.52
1HGH.PDB	OD1, E_ASP_60	NE, E_ARG_90	HE, E_ARG_90	2.82	1.87	13.57
1HGH.PDB	OD2, E_ASP_60	NH2, E_ARG_90	HH21, E_ARG_90	2.82	1.82	8.69
1HGH.PDB	OD2, E_ASP_271	OG, E_SER_91	HG, E_SER_91	2.81	1.88	14.87
1HGH.PDB	OD2, E_ASP_68	OG, E_SER_95	HG, E_SER_95	2.88	1.94	13.28
1HGH.PDB	OD1, E_ASP_68	OH, E_TYR_100	HH, E_TYR_100	2.91	1.97	12.96
1HGH.PDB	OD2, E_ASP_104	OG, E_SER_107	HG, E_SER_107	2.88	1.97	18.12
1HGH.PDB	OE2, F_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.88	1.90	13.56
1HGH.PDB	OD2, D_ASP_79	OG, E_SER_110	HG, E_SER_110	2.90	1.94	9.49
1HGH.PDB	OE2, E_GLU_119	OG1, E_THR_117	HG1, E_THR_117	2.88	1.94	11.16
1HGH.PDB	OD1, E_ASN_137	NZ, E_LYS_140	HZ2, E_LYS_140	2.75	1.75	11.91
1HGH.PDB	OD2, E_ASP_77	NE, E_ARG_141	HE, E_ARG_141	2.85	2.01	27.16
1HGH.PDB	OD1, E_ASP_77	NH2, E_ARG_141	HH21, E_ARG_141	2.89	1.99	22.46
1HGH.PDB	OD2, E_ASP_77	NH2, E_ARG_141	HH21, E_ARG_141	2.74	1.84	23.25
1HGH.PDB	OD1, E_ASN_137	OG, E_SER_145	HG, E_SER_145	2.98	2.07	15.03
1HGH.PDB	OH, E_TYR_195	NE1, E_TRP_153	HE1, E_TRP_153	2.94	2.03	18.49
1HGH.PDB	OE2, E_GLU_123	NZ, E_LYS_176	HZ1, E_LYS_176	2.69	1.82	26.87
1HGH.PDB	OE1, E_GLU_123	OH, E_TYR_178	HH, E_TYR_178	2.77	1.82	8.79
1HGH.PDB	OG1, E_THR_235	NE1, E_TRP_180	HE1, E_TRP_180	2.88	1.89	0.99
1HGH.PDB	OG, E_SER_231	NE2, E_HIS_184	HE2, E_HIS_184	2.78	1.93	25.10
1HGH.PDB	OD1, E_ASN_250	NE2, E_GLN_191	HE21, E_GLN_191	2.99	2.02	8.22
1HGH.PDB	OD1, E_ASN_246	NH2, E_ARG_201	HH21, E_ARG_201	2.64	1.73	21.41
1HGH.PDB	OG1, E_THR_212	OG1, E_THR_203	HG1, E_THR_203	2.98	2.08	17.30
1HGH.PDB	OG1, E_THR_206	OG, E_SER_209	HG, E_SER_209	2.95	2.00	8.64
1HGH.PDB	OD1, C_ASP_101	NE2, E_GLN_210	HE22, E_GLN_210	2.95	2.09	25.33

1HGH.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.68	1.79	22.30
1HGH.PDB	OD1, E_ASP_101	OG, E_SER_231	HG, E_SER_231	2.86	1.91	11.78
1HGH.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ3, E_LYS_238	2.87	1.88	15.42
1HGH.PDB	OD1, E_ASN_165	ND2, E_ASN_246	HD22, E_ASN_246	2.98	2.01	10.13
1HGH.PDB	OE1, E_GLN_191	ND2, E_ASN_250	HD21, E_ASN_250	2.89	1.92	6.88
1HGH.PDB	OE2, E_GLU_119	NH1, E_ARG_261	HH12, E_ARG_261	2.63	1.81	29.30
1HGH.PDB	OE1, E_GLU_119	NH2, E_ARG_261	HH22, E_ARG_261	2.85	1.96	24.42
1HGH.PDB	OD2, E_ASP_85	NZ, E_LYS_264	HZ3, E_LYS_264	2.81	1.82	14.94
1HGH.PDB	OE1, F_GLU_67	NH1, E_ARG_269	HH12, E_ARG_269	2.71	1.88	29.19
1HGH.PDB	OE1, E_GLN_44	NZ, E_LYS_292	HZ1, E_LYS_292	2.67	1.66	10.24
1HGH.PDB	OD2, E_ASP_291	NZ, E_LYS_292	HZ3, E_LYS_292	2.84	1.86	17.36
1HGH.PDB	OD1, F_ASP_86	NZ, E_LYS_310	HZ2, E_LYS_310	2.74	1.87	26.77
1HGH.PDB	OE1, E_GLU_41	NZ, E_LYS_315	HZ3, E_LYS_315	2.85	1.89	19.70
1HGH.PDB	OE2, E_GLU_35	ND2, E_ASN_322	HD22, E_ASN_322	2.80	1.90	19.14
1HGH.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.90	1.89	12.96
1HGH.PDB	OE1, F_GLN_34	NH2, F_ARG_25	HH21, F_ARG_25	2.92	2.03	23.48
1HGH.PDB	OD1, F_ASN_146	ND2, F_ASN_28	HD21, F_ASN_28	2.91	1.96	12.69
1HGH.PDB	OD2, F_ASP_37	OG, F_SER_40	HG, F_SER_40	2.73	1.92	26.94
1HGH.PDB	OD1, F_ASP_46	NE2, F_GLN_42	HE22, F_GLN_42	2.85	1.95	20.25
1HGH.PDB	OE2, F_GLU_114	NE2, F_GLN_47	HE21, F_GLN_47	2.99	2.08	19.28
1HGH.PDB	OE1, F_GLU_103	NZ, F_LYS_51	HZ1, F_LYS_51	2.75	1.72	7.02
1HGH.PDB	ND1, F_HIS_106	NZ, F_LYS_51	HZ2, F_LYS_51	2.77	1.82	19.11
1HGH.PDB	OG1, F_THR_107	NZ, F_LYS_51	HZ3, F_LYS_51	2.93	1.96	17.40
1HGH.PDB	OE1, F_GLU_57	NH1, F_ARG_54	HH11, F_ARG_54	2.88	1.88	10.86
1HGH.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.72	1.77	15.67
1HGH.PDB	OD2, D_ASP_90	NZ, F_LYS_62	HZ2, F_LYS_62	2.68	1.83	28.02
1HGH.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.87	1.91	9.23
1HGH.PDB	OE2, F_GLU_85	NZ, F_LYS_68	HZ2, F_LYS_68	2.73	1.74	15.07
1HGH.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.84	1.87	10.72
1HGH.PDB	OE2, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.73	1.73	5.34
1HGH.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.71	1.70	1.21
1HGH.PDB	OE1, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.78	1.78	7.19
1HGH.PDB	OE1, F_GLU_74	NE2, F_GLN_78	HE22, F_GLN_78	2.92	1.95	8.97
1HGH.PDB	OE1, B_GLU_85	OH, F_TYR_83	HH, F_TYR_83	2.53	1.74	27.23
1HGH.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.65	1.63	9.88
1HGH.PDB	OE2, F_GLU_120	NH1, F_ARG_123	HH11, F_ARG_123	2.74	1.84	22.63
1HGH.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.89	2.06	26.55
1HGH.PDB	OE2, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.92	2.03	21.52
1HGH.PDB	OH, F_TYR_157	ND2, F_ASN_129	HD22, F_ASN_129	2.82	1.88	14.11
1HGH.PDB	OE2, F_GLU_131	NH1, F_ARG_170	HH11, F_ARG_170	2.84	1.84	5.40
1HGI.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.90	1.86	7.66
1HGI.PDB	OD2, A_ASP_275	NZ, A_LYS_50	HZ1, A_LYS_50	2.71	1.78	22.79
1HGI.PDB	OD1, A_ASP_73	ND1, A_HIS_75	HD1, A_HIS_75	2.90	1.96	15.34
1HGI.PDB	OD1, A_ASP_60	NE, A_ARG_90	HE, A_ARG_90	2.89	1.91	4.93
1HGI.PDB	OD2, A_ASP_60	NH2, A_ARG_90	HH21, A_ARG_90	2.83	1.85	11.60
1HGI.PDB	OD1, A_ASP_271	OG, A_SER_91	HG, A_SER_91	2.93	2.10	25.86
1HGI.PDB	OD2, A_ASP_271	OG, A_SER_91	HG, A_SER_91	2.80	1.92	20.51
1HGI.PDB	OD2, A_ASP_68	OG, A_SER_95	HG, A_SER_95	2.89	1.96	14.00
1HGI.PDB	OD1, A_ASP_68	OH, A_TYR_100	HH, A_TYR_100	2.99	2.05	13.08
1HGI.PDB	OD2, A_ASP_104	OG, A_SER_107	HG, A_SER_107	2.89	1.96	15.23
1HGI.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.80	1.81	13.24
1HGI.PDB	OE2, A_GLU_119	OG1, A_THR_117	HG1, A_THR_117	2.93	2.01	15.43
1HGI.PDB	OD1, A_ASN_137	NZ, A_LYS_140	HZ2, A_LYS_140	2.79	1.79	13.01
1HGI.PDB	OD2, A_ASP_77	NE, A_ARG_141	HE, A_ARG_141	2.82	2.01	29.43
1HGI.PDB	OD1, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.93	2.01	20.43
1HGI.PDB	OD2, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.69	1.82	24.99
1HGI.PDB	OH, A_TYR_195	NE1, A_TRP_153	HE1, A_TRP_153	2.87	1.98	21.02
1HGI.PDB	OG1, A_THR_131	OG, A_SER_157	HG, A_SER_157	2.97	2.02	9.12

1HGI.PDB	OE2, A_GLU_123	NZ, A_LYS_176	HZ1, A_LYS_176	2.68	1.79	25.50
1HGI.PDB	OE1, A_GLU_123	OH, A_TYR_178	HH, A_TYR_178	2.78	1.82	7.33
1HGI.PDB	OG1, A_THR_235	NE1, A_TRP_180	HE1, A_TRP_180	2.85	1.87	3.02
1HGI.PDB	OG, A_SER_231	NE2, A_HIS_184	HE2, A_HIS_184	2.81	1.93	22.19
1HGI.PDB	OD1, A_ASN_250	NE2, A_GLN_191	HE21, A_GLN_191	2.93	1.97	11.19
1HGI.PDB	OD1, A_ASN_246	NH2, A_ARG_201	HH21, A_ARG_201	2.54	1.71	26.99
1HGI.PDB	OD2, A_ASP_241	NE, A_ARG_208	HE, A_ARG_208	2.96	2.05	19.55
1HGI.PDB	OG1, A_THR_203	OG1, A_THR_212	HG1, A_THR_212	2.96	2.00	2.15
1HGI.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.65	1.73	18.55
1HGI.PDB	OD1, A_ASP_101	OG, A_SER_231	HG, A_SER_231	2.96	2.01	11.74
1HGI.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.85	1.85	15.00
1HGI.PDB	OE1, A_GLN_191	ND2, A_ASN_250	HD21, A_ASN_250	2.89	1.93	10.00
1HGI.PDB	OE2, A_GLU_119	NH1, A_ARG_261	HH12, A_ARG_261	2.66	1.83	28.46
1HGI.PDB	OE1, A_GLU_119	NH2, A_ARG_261	HH22, A_ARG_261	2.85	1.99	27.12
1HGI.PDB	OD2, A_ASP_85	NZ, A_LYS_264	HZ3, A_LYS_264	2.82	1.85	17.23
1HGI.PDB	OE1, A_GLN_44	NZ, A_LYS_292	HZ1, A_LYS_292	2.74	1.74	11.73
1HGI.PDB	OD2, A_ASP_291	NZ, A_LYS_292	HZ3, A_LYS_292	2.81	1.89	23.33
1HGI.PDB	OD1, B_ASP_86	NZ, A_LYS_310	HZ3, A_LYS_310	2.76	1.92	29.34
1HGI.PDB	OE1, A_GLU_41	NZ, A_LYS_315	HZ3, A_LYS_315	2.77	1.82	19.86
1HGI.PDB	OE2, A_GLU_35	ND2, A_ASN_322	HD22, A_ASN_322	2.93	1.97	12.34
1HGI.PDB	OE2, B_GLU_15	NZ, A_LYS_326	HZ1, A_LYS_326	2.79	1.93	27.33
1HGI.PDB	OE1, A_GLU_325	NZ, A_LYS_326	HZ3, A_LYS_326	2.91	1.94	17.77
1HGI.PDB	OE1, B_GLN_34	NE, B_ARG_25	HE, B_ARG_25	2.60	1.78	26.17
1HGI.PDB	OE1, B_GLN_34	NH2, B_ARG_25	HH21, B_ARG_25	2.75	1.92	27.98
1HGI.PDB	OE2, A_GLU_325	NH2, B_ARG_25	HH22, B_ARG_25	2.93	1.95	13.46
1HGI.PDB	OD1, B_ASP_46	NE2, B_GLN_42	HE22, B_GLN_42	2.89	2.02	23.36
1HGI.PDB	OG1, B_THR_107	NZ, B_LYS_51	HZ1, B_LYS_51	2.96	1.97	15.88
1HGI.PDB	OE1, B_GLU_103	NZ, B_LYS_51	HZ2, B_LYS_51	2.82	1.78	6.88
1HGI.PDB	ND1, B_HIS_106	NZ, B_LYS_51	HZ3, B_LYS_51	2.81	1.87	19.52
1HGI.PDB	OE1, B_GLU_57	NH1, B_ARG_54	HH11, B_ARG_54	2.86	1.87	11.02
1HGI.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.81	1.84	14.63
1HGI.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ1, B_LYS_62	2.67	1.78	25.75
1HGI.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.87	1.89	8.13
1HGI.PDB	OE2, B_GLU_85	NZ, B_LYS_68	HZ2, B_LYS_68	2.79	1.75	2.13
1HGI.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.86	1.89	7.04
1HGI.PDB	OE2, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.92	1.89	1.72
1HGI.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.71	1.72	8.42
1HGI.PDB	OE1, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.86	1.86	6.93
1HGI.PDB	OE1, B_GLU_74	NE2, B_GLN_78	HE22, B_GLN_78	2.94	1.97	8.23
1HGI.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.78	1.84	13.46
1HGI.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.65	1.64	9.94
1HGI.PDB	OE2, B_GLU_120	NH1, B_ARG_123	HH11, B_ARG_123	2.84	1.97	25.22
1HGI.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.81	1.96	23.50
1HGI.PDB	OE2, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.86	2.02	24.92
1HGI.PDB	OH, B_TYR_157	ND2, B_ASN_129	HD22, B_ASN_129	2.81	1.86	9.72
1HGI.PDB	OE2, B_GLU_150	ND2, B_ASN_154	HD21, B_ASN_154	2.84	2.01	27.47
1HGI.PDB	OD1, B_ASN_154	OG1, B_THR_156	HG1, B_THR_156	2.64	1.78	21.15
1HGI.PDB	OE2, B_GLU_131	NH1, B_ARG_170	HH11, B_ARG_170	2.77	1.77	6.54
1HGI.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.88	1.83	6.58
1HGI.PDB	OD2, C_ASP_275	NZ, C_LYS_50	HZ1, C_LYS_50	2.68	1.77	23.91
1HGI.PDB	OD1, C_ASP_73	ND1, C_HIS_75	HD1, C_HIS_75	2.88	1.94	15.46
1HGI.PDB	OD1, C_ASP_60	NE, C_ARG_90	HE, C_ARG_90	2.83	1.88	11.13
1HGI.PDB	OD2, C_ASP_60	NH2, C_ARG_90	HH21, C_ARG_90	2.77	1.79	11.02
1HGI.PDB	OD1, C_ASP_271	OG, C_SER_91	HG, C_SER_91	2.95	2.13	27.22
1HGI.PDB	OD2, C_ASP_271	OG, C_SER_91	HG, C_SER_91	2.83	1.94	19.64
1HGI.PDB	OD2, C_ASP_68	OG, C_SER_95	HG, C_SER_95	2.89	1.96	14.85
1HGI.PDB	OD1, C_ASP_68	OH, C_TYR_100	HH, C_TYR_100	2.94	1.99	10.92
1HGI.PDB	OD2, C_ASP_104	OG, C_SER_107	HG, C_SER_107	2.90	1.96	13.90

1HGI.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.82	1.84	15.02
1HGI.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.85	1.90	11.29
1HGI.PDB	OE2, C_GLU_119	OG1, C_THR_117	HG1, C_THR_117	2.95	2.03	14.67
1HGI.PDB	OD1, C_ASN_137	NZ, C_LYS_140	HZ2, C_LYS_140	2.83	1.83	12.62
1HGI.PDB	OD2, C_ASP_77	NE, C_ARG_141	HE, C_ARG_141	2.83	2.02	29.40
1HGI.PDB	OD1, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.93	2.01	20.50
1HGI.PDB	OD2, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.70	1.83	25.10
1HGI.PDB	OH, C_TYR_195	NE1, C_TRP_153	HE1, C_TRP_153	2.82	1.96	22.98
1HGI.PDB	OE2, C_GLU_123	NZ, C_LYS_176	HZ1, C_LYS_176	2.68	1.80	26.11
1HGI.PDB	OE1, C_GLU_123	OH, C_TYR_178	HH, C_TYR_178	2.75	1.80	7.25
1HGI.PDB	OG1, C_THR_235	NE1, C_TRP_180	HE1, C_TRP_180	2.84	1.86	3.22
1HGI.PDB	OG, C_SER_231	NE2, C_HIS_184	HE2, C_HIS_184	2.81	1.93	22.34
1HGI.PDB	OD1, C_ASN_250	NE2, C_GLN_191	HE21, C_GLN_191	2.86	1.91	10.94
1HGI.PDB	OD1, C_ASN_246	NH2, C_ARG_201	HH21, C_ARG_201	2.55	1.72	27.61
1HGI.PDB	OG1, C_THR_212	OG1, C_THR_203	HG1, C_THR_203	2.94	2.00	11.06
1HGI.PDB	OD2, C_ASP_241	NE, C_ARG_208	HE, C_ARG_208	2.92	2.01	19.66
1HGI.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.62	1.75	23.70
1HGI.PDB	OD1, C_ASP_101	OG, C_SER_231	HG, C_SER_231	2.97	2.02	12.14
1HGI.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.67	1.77	23.68
1HGI.PDB	OE1, C_GLN_191	ND2, C_ASN_250	HD21, C_ASN_250	2.87	1.92	11.00
1HGI.PDB	OE2, C_GLU_119	NH1, C_ARG_261	HH12, C_ARG_261	2.66	1.84	29.01
1HGI.PDB	OE1, C_GLU_119	NH2, C_ARG_261	HH22, C_ARG_261	2.84	1.99	27.78
1HGI.PDB	OD2, C_ASP_85	NZ, C_LYS_264	HZ3, C_LYS_264	2.83	1.86	17.28
1HGI.PDB	OE1, C_GLN_44	NZ, C_LYS_292	HZ1, C_LYS_292	2.75	1.75	12.02
1HGI.PDB	OD2, C_ASP_291	NZ, C_LYS_292	HZ3, C_LYS_292	2.82	1.90	23.36
1HGI.PDB	OD1, C_ASN_285	ND2, C_ASN_298	HD22, C_ASN_298	3.00	2.03	7.73
1HGI.PDB	OD1, D_ASP_86	NZ, C_LYS_310	HZ3, C_LYS_310	2.77	1.93	29.51
1HGI.PDB	OE1, C_GLU_41	NZ, C_LYS_315	HZ3, C_LYS_315	2.75	1.80	20.43
1HGI.PDB	OE2, C_GLU_35	ND2, C_ASN_322	HD22, C_ASN_322	2.90	1.95	11.70
1HGI.PDB	OE1, D_GLU_15	NZ, C_LYS_326	HZ1, C_LYS_326	2.83	1.84	16.25
1HGI.PDB	OE1, D_GLN_34	NE, D_ARG_25	HE, D_ARG_25	2.62	1.78	23.70
1HGI.PDB	OD1, D_ASN_146	ND2, D_ASN_28	HD21, D_ASN_28	2.93	1.98	12.39
1HGI.PDB	OD2, D_ASP_37	OG, D_SER_40	HG, D_SER_40	2.78	1.93	23.19
1HGI.PDB	OD1, D_ASP_46	NE2, D_GLN_42	HE22, D_GLN_42	2.88	2.01	23.38
1HGI.PDB	OE1, D_GLU_103	NZ, D_LYS_51	HZ2, D_LYS_51	2.81	1.77	5.89
1HGI.PDB	ND1, D_HIS_106	NZ, D_LYS_51	HZ3, D_LYS_51	2.78	1.83	18.78
1HGI.PDB	OE1, D_GLU_57	NH1, D_ARG_54	HH11, D_ARG_54	2.85	1.86	11.80
1HGI.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.81	1.85	15.40
1HGI.PDB	OE2, D_GLU_61	NZ, D_LYS_58	HZ2, D_LYS_58	3.00	2.01	17.14
1HGI.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.83	1.85	2.78
1HGI.PDB	OE2, D_GLU_85	NZ, D_LYS_68	HZ2, D_LYS_68	2.81	1.76	2.16
1HGI.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.80	1.82	5.40
1HGI.PDB	OE2, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.78	1.76	4.18
1HGI.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.61	1.67	15.38
1HGI.PDB	OE1, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.76	1.77	8.75
1HGI.PDB	OE1, D_GLU_74	NE2, D_GLN_78	HE22, D_GLN_78	2.92	1.95	8.47
1HGI.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.69	1.81	20.41
1HGI.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.66	1.64	7.30
1HGI.PDB	OE2, D_GLU_120	NH1, D_ARG_123	HH11, D_ARG_123	2.83	1.97	25.69
1HGI.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.84	1.98	23.95
1HGI.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.88	2.03	24.96
1HGI.PDB	OH, D_TYR_157	ND2, D_ASN_129	HD22, D_ASN_129	2.81	1.84	5.40
1HGI.PDB	OD1, D_ASN_154	OG1, D_THR_156	HG1, D_THR_156	2.68	1.79	17.62
1HGI.PDB	NE2, D_HIS_142	OH, D_TYR_157	HH, D_TYR_157	2.72	1.85	20.80
1HGI.PDB	OE2, D_GLU_131	NH1, D_ARG_170	HH11, D_ARG_170	2.77	1.78	6.80
1HGI.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.86	1.82	7.44
1HGI.PDB	OD2, E_ASP_275	NZ, E_LYS_50	HZ1, E_LYS_50	2.70	1.78	22.89
1HGI.PDB	OD1, E_ASP_73	ND1, E_HIS_75	HD1, E_HIS_75	2.87	1.94	15.26

1HGI.PDB	OD1, E_ASP_60	NE, E_ARG_90	HE, E_ARG_90	2.89	1.92	8.33
1HGI.PDB	OD2, E_ASP_60	NH2, E_ARG_90	HH21, E_ARG_90	2.84	1.85	10.04
1HGI.PDB	OD1, E_ASP_271	OG, E_SER_91	HG, E_SER_91	2.94	2.11	26.21
1HGI.PDB	OD2, E_ASP_271	OG, E_SER_91	HG, E_SER_91	2.82	1.93	20.43
1HGI.PDB	OD2, E_ASP_68	OG, E_SER_95	HG, E_SER_95	2.90	1.96	13.54
1HGI.PDB	OD1, E_ASP_68	OH, E_TYR_100	HH, E_TYR_100	2.94	1.98	8.32
1HGI.PDB	OD2, E_ASP_104	OG, E_SER_107	HG, E_SER_107	2.91	1.98	14.52
1HGI.PDB	OE2, F_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.78	1.80	14.37
1HGI.PDB	OD2, D_ASP_79	OG, E_SER_110	HG, E_SER_110	2.90	1.94	10.08
1HGI.PDB	OE2, E_GLU_119	OG1, E_THR_117	HG1, E_THR_117	2.98	2.05	12.54
1HGI.PDB	OD1, E_ASN_137	NZ, E_LYS_140	HZ2, E_LYS_140	2.83	1.82	12.93
1HGI.PDB	OD2, E_ASP_77	NE, E_ARG_141	HE, E_ARG_141	2.83	2.01	29.05
1HGI.PDB	OD1, E_ASP_77	NH2, E_ARG_141	HH21, E_ARG_141	2.94	2.01	20.45
1HGI.PDB	OD2, E_ASP_77	NH2, E_ARG_141	HH21, E_ARG_141	2.70	1.83	24.80
1HGI.PDB	OD1, E_ASN_137	OG, E_SER_145	HG, E_SER_145	2.92	2.15	29.94
1HGI.PDB	OH, E_TYR_195	NE1, E_TRP_153	HE1, E_TRP_153	2.87	1.98	20.67
1HGI.PDB	OE2, E_GLU_123	NZ, E_LYS_176	HZ1, E_LYS_176	2.69	1.80	25.89
1HGI.PDB	OE1, E_GLU_123	OH, E_TYR_178	HH, E_TYR_178	2.77	1.82	8.27
1HGI.PDB	OG1, E_THR_235	NE1, E_TRP_180	HE1, E_TRP_180	2.85	1.87	2.03
1HGI.PDB	OG, E_SER_231	NE2, E_HIS_184	HE2, E_HIS_184	2.81	1.95	23.57
1HGI.PDB	OD1, E_ASN_250	NE2, E_GLN_191	HE21, E_GLN_191	2.93	1.97	10.64
1HGI.PDB	OD1, E_ASN_246	NH2, E_ARG_201	HH21, E_ARG_201	2.57	1.74	27.51
1HGI.PDB	OD2, E_ASP_241	NE, E_ARG_208	HE, E_ARG_208	2.98	2.07	19.52
1HGI.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.69	1.80	23.03
1HGI.PDB	OD1, E_ASP_101	OG, E_SER_231	HG, E_SER_231	2.99	2.05	12.53
1HGI.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ3, E_LYS_238	2.80	1.81	15.90
1HGI.PDB	OE1, E_GLN_191	ND2, E_ASN_250	HD21, E_ASN_250	2.90	1.94	10.02
1HGI.PDB	OE2, E_GLU_119	NH1, E_ARG_261	HH12, E_ARG_261	2.65	1.83	28.50
1HGI.PDB	OE1, E_GLU_119	NH2, E_ARG_261	HH22, E_ARG_261	2.84	1.99	27.52
1HGI.PDB	OD2, E_ASP_85	NZ, E_LYS_264	HZ3, E_LYS_264	2.86	1.87	16.39
1HGI.PDB	OE1, E_GLN_44	NZ, E_LYS_292	HZ1, E_LYS_292	2.73	1.72	12.13
1HGI.PDB	OD2, E_ASP_291	NZ, E_LYS_292	HZ3, E_LYS_292	2.87	1.94	23.09
1HGI.PDB	OD1, E_ASN_285	ND2, E_ASN_298	HD22, E_ASN_298	2.97	2.00	7.97
1HGI.PDB	OD1, F_ASP_86	NZ, E_LYS_310	HZ3, E_LYS_310	2.76	1.91	29.16
1HGI.PDB	OE1, E_GLU_41	NZ, E_LYS_315	HZ3, E_LYS_315	2.74	1.81	21.50
1HGI.PDB	OE2, E_GLU_35	ND2, E_ASN_322	HD22, E_ASN_322	2.92	1.96	12.59
1HGI.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.88	1.86	11.05
1HGI.PDB	OE1, F_GLN_34	NH2, F_ARG_25	HH21, F_ARG_25	2.91	1.98	18.85
1HGI.PDB	OD1, F_ASN_146	ND2, F_ASN_28	HD21, F_ASN_28	2.93	2.01	16.48
1HGI.PDB	OD2, F_ASP_37	OG, F_SER_40	HG, F_SER_40	2.76	1.92	24.70
1HGI.PDB	OD1, F_ASP_46	NE2, F_GLN_42	HE22, F_GLN_42	2.86	1.99	23.93
1HGI.PDB	OE1, F_GLU_103	NZ, F_LYS_51	HZ2, F_LYS_51	2.80	1.76	5.82
1HGI.PDB	ND1, F_HIS_106	NZ, F_LYS_51	HZ3, F_LYS_51	2.75	1.80	19.60
1HGI.PDB	OE1, F_GLU_57	NH1, F_ARG_54	HH11, F_ARG_54	2.83	1.84	11.68
1HGI.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.75	1.79	14.82
1HGI.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.84	1.87	3.62
1HGI.PDB	OE2, F_GLU_85	NZ, F_LYS_68	HZ2, F_LYS_68	2.74	1.72	8.70
1HGI.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.85	1.88	7.37
1HGI.PDB	OE2, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.77	1.76	3.93
1HGI.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.64	1.66	4.79
1HGI.PDB	OE1, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.76	1.78	10.40
1HGI.PDB	OE1, F_GLU_74	NE2, F_GLN_78	HE22, F_GLN_78	2.95	1.98	8.40
1HGI.PDB	OE1, B_GLU_85	OH, F_TYR_83	HH, F_TYR_83	2.58	1.75	24.06
1HGI.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.61	1.62	12.49
1HGI.PDB	OE2, F_GLU_120	NH1, F_ARG_123	HH11, F_ARG_123	2.81	1.95	25.91
1HGI.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.96	2.09	23.50
1HGI.PDB	OE2, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.96	2.09	23.34
1HGI.PDB	OH, F_TYR_157	ND2, F_ASN_129	HD22, F_ASN_129	2.81	1.86	11.53

1HGI.PDB	OE2, D_GLU_131	NH2, F_ARG_163	HH22, F_ARG_163	2.69	1.85	26.81
1HGI.PDB	OE2, F_GLU_131	NH1, F_ARG_170	HH11, F_ARG_170	2.75	1.76	6.67
1HGJ.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.81	1.78	9.30
1HGJ.PDB	OD2, A_ASP_275	NZ, A_LYS_50	HZ1, A_LYS_50	2.74	1.82	22.91
1HGJ.PDB	OD1, A_ASP_73	ND1, A_HIS_75	HD1, A_HIS_75	2.83	1.91	17.40
1HGJ.PDB	OD1, A_ASP_60	NE, A_ARG_90	HE, A_ARG_90	2.88	1.91	7.56
1HGJ.PDB	OD2, A_ASP_60	NH2, A_ARG_90	HH21, A_ARG_90	2.81	1.82	10.05
1HGJ.PDB	OD1, A_ASP_271	OG, A_SER_91	HG, A_SER_91	2.98	2.13	24.27
1HGJ.PDB	OD2, A_ASP_271	OG, A_SER_91	HG, A_SER_91	2.78	1.90	20.01
1HGJ.PDB	OD2, A_ASP_68	OG, A_SER_95	HG, A_SER_95	2.95	2.05	19.19
1HGJ.PDB	OD2, A_ASP_104	OG, A_SER_107	HG, A_SER_107	2.84	1.95	18.85
1HGJ.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.75	1.77	12.07
1HGJ.PDB	OD2, F_ASP_79	OG, A_SER_110	HG, A_SER_110	2.94	1.98	10.39
1HGJ.PDB	OE2, A_GLU_119	OG1, A_THR_117	HG1, A_THR_117	2.87	1.94	12.44
1HGJ.PDB	OD1, A_ASN_137	NZ, A_LYS_140	HZ2, A_LYS_140	2.70	1.70	13.62
1HGJ.PDB	OD2, A_ASP_77	NE, A_ARG_141	HE, A_ARG_141	2.82	1.99	27.09
1HGJ.PDB	OD1, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.82	1.90	21.48
1HGJ.PDB	OD2, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.75	1.86	24.28
1HGJ.PDB	OH, A_TYR_195	NE1, A_TRP_153	HE1, A_TRP_153	2.85	1.94	18.91
1HGJ.PDB	OE2, A_GLU_123	NZ, A_LYS_176	HZ1, A_LYS_176	2.68	1.78	24.65
1HGJ.PDB	OE1, A_GLU_123	OH, A_TYR_178	HH, A_TYR_178	2.79	1.84	8.91
1HGJ.PDB	OG1, A_THR_235	NE1, A_TRP_180	HE1, A_TRP_180	2.92	1.93	4.44
1HGJ.PDB	OG, A_SER_231	NE2, A_HIS_184	HE2, A_HIS_184	2.75	1.92	26.36
1HGJ.PDB	OD1, A_ASN_246	NH2, A_ARG_201	HH21, A_ARG_201	2.58	1.73	25.49
1HGJ.PDB	OG1, A_THR_206	OG, A_SER_209	HG, A_SER_209	3.00	2.04	8.15
1HGJ.PDB	OG1, A_THR_203	OG1, A_THR_212	HG1, A_THR_212	2.89	1.93	3.12
1HGJ.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.67	1.78	22.50
1HGJ.PDB	OD1, A_ASP_101	OG, A_SER_231	HG, A_SER_231	2.87	1.91	9.73
1HGJ.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.90	1.90	13.91
1HGJ.PDB	OD1, A_ASN_165	ND2, A_ASN_246	HD22, A_ASN_246	2.91	1.95	11.26
1HGJ.PDB	OD1, A_ASN_133	NH2, A_ARG_255	HH22, A_ARG_255	2.53	1.70	27.52
1HGJ.PDB	OE2, A_GLU_119	NH1, A_ARG_261	HH12, A_ARG_261	2.65	1.82	28.35
1HGJ.PDB	OE1, A_GLU_119	NH2, A_ARG_261	HH22, A_ARG_261	2.90	1.99	23.18
1HGJ.PDB	OD2, A_ASP_85	NZ, A_LYS_264	HZ3, A_LYS_264	2.84	1.85	15.53
1HGJ.PDB	OE1, A_GLN_44	NZ, A_LYS_292	HZ1, A_LYS_292	2.71	1.70	11.30
1HGJ.PDB	OD2, A_ASP_291	NZ, A_LYS_292	HZ3, A_LYS_292	2.80	1.82	17.27
1HGJ.PDB	OE1, A_GLU_41	NZ, A_LYS_315	HZ3, A_LYS_315	2.85	1.90	20.12
1HGJ.PDB	OE2, A_GLU_35	ND2, A_ASN_322	HD22, A_ASN_322	2.88	1.99	20.96
1HGJ.PDB	OE1, A_GLU_325	NZ, A_LYS_326	HZ3, A_LYS_326	2.92	1.93	15.95
1HGJ.PDB	OE1, B_GLN_34	NE, B_ARG_25	HE, B_ARG_25	2.57	1.79	29.34
1HGJ.PDB	OE2, A_GLU_325	NH2, B_ARG_25	HH22, B_ARG_25	2.97	2.01	15.94
1HGJ.PDB	OD1, B_ASP_46	NE2, B_GLN_42	HE22, B_GLN_42	2.81	1.92	21.14
1HGJ.PDB	OE2, B_GLU_114	NE2, B_GLN_47	HE21, B_GLN_47	2.96	2.05	17.93
1HGJ.PDB	OG1, B_THR_107	NZ, B_LYS_51	HZ1, B_LYS_51	2.96	1.99	17.76
1HGJ.PDB	OE1, B_GLU_103	NZ, B_LYS_51	HZ2, B_LYS_51	2.78	1.74	6.16
1HGJ.PDB	ND1, B_HIS_106	NZ, B_LYS_51	HZ3, B_LYS_51	2.79	1.82	16.46
1HGJ.PDB	OE1, B_GLU_57	NH1, B_ARG_54	HH11, B_ARG_54	2.87	1.87	9.43
1HGJ.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.77	1.81	15.09
1HGJ.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ1, B_LYS_62	2.65	1.75	23.55
1HGJ.PDB	OD2, F_ASP_90	NZ, B_LYS_62	HZ3, B_LYS_62	2.74	1.89	28.52
1HGJ.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.89	1.93	11.21
1HGJ.PDB	OE2, B_GLU_85	NZ, B_LYS_68	HZ2, B_LYS_68	2.78	1.76	8.72
1HGJ.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.90	1.93	10.80
1HGJ.PDB	OE2, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.88	1.87	5.28
1HGJ.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.72	1.72	3.64
1HGJ.PDB	OE1, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.85	1.84	3.19
1HGJ.PDB	OE1, B_GLU_74	NE2, B_GLN_78	HE22, B_GLN_78	2.90	1.95	12.93
1HGJ.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.67	1.83	24.12

1HGJ.PDB	OH, F.TYR.83	NZ, B.LYS.88	HZ1, B.LYS.88	2.78	1.75	7.42
1HGJ.PDB	OE2, B.GLU.120	NH1, B.ARG.123	HH11, B.ARG.123	2.74	1.86	23.95
1HGJ.PDB	OE1, F.GLU.132	NE, B.ARG.124	HE, B.ARG.124	2.82	2.00	27.29
1HGJ.PDB	OE2, F.GLU.132	NE, B.ARG.124	HE, B.ARG.124	2.91	2.02	20.91
1HGJ.PDB	OH, B.TYR.157	ND2, B.ASN.129	HD22, B.ASN.129	2.77	1.84	15.18
1HGJ.PDB	OE2, B.GLU.150	ND2, B.ASN.154	HD21, B.ASN.154	2.81	2.00	28.55
1HGJ.PDB	OD1, B.ASN.154	OG1, B.THR.156	HG1, B.THR.156	2.67	1.80	19.98
1HGJ.PDB	OE2, B.GLU.131	NH1, B.ARG.170	HH11, B.ARG.170	2.80	1.80	6.39
1HGJ.PDB	OE2, D.GLU.97	NZ, C.LYS.27	HZ1, C.LYS.27	2.82	1.80	8.63
1HGJ.PDB	OD2, C.ASP.275	NZ, C.LYS.50	HZ1, C.LYS.50	2.74	1.82	22.76
1HGJ.PDB	OD1, C.ASP.73	ND1, C.HIS.75	HD1, C.HIS.75	2.80	1.89	17.49
1HGJ.PDB	OD1, C.ASP.60	NE, C.ARG.90	HE, C.ARG.90	2.88	1.91	9.03
1HGJ.PDB	OD2, C.ASP.60	NH2, C.ARG.90	HH21, C.ARG.90	2.78	1.79	9.66
1HGJ.PDB	OD1, C.ASP.271	OG, C.SER.91	HG, C.SER.91	2.99	2.16	26.38
1HGJ.PDB	OD2, C.ASP.271	OG, C.SER.91	HG, C.SER.91	2.81	1.92	18.67
1HGJ.PDB	OD2, C.ASP.68	OG, C.SER.95	HG, C.SER.95	2.93	1.99	14.68
1HGJ.PDB	OD1, C.ASP.68	OH, C.TYR.100	HH, C.TYR.100	2.88	1.95	14.58
1HGJ.PDB	OD2, C.ASP.104	OG, C.SER.107	HG, C.SER.107	2.90	1.99	17.96
1HGJ.PDB	OE2, D.GLU.67	NH2, C.ARG.109	HH21, C.ARG.109	2.76	1.78	13.33
1HGJ.PDB	OD2, B.ASP.79	OG, C.SER.110	HG, C.SER.110	2.79	1.87	14.95
1HGJ.PDB	OE2, C.GLU.119	OG1, C.THR.117	HG1, C.THR.117	2.88	1.94	11.85
1HGJ.PDB	OD1, C.ASN.137	NZ, C.LYS.140	HZ2, C.LYS.140	2.71	1.72	13.24
1HGJ.PDB	OD2, C.ASP.77	NE, C.ARG.141	HE, C.ARG.141	2.82	1.99	27.42
1HGJ.PDB	OD1, C.ASP.77	NH2, C.ARG.141	HH21, C.ARG.141	2.81	1.89	21.37
1HGJ.PDB	OD2, C.ASP.77	NH2, C.ARG.141	HH21, C.ARG.141	2.74	1.86	24.47
1HGJ.PDB	OD1, C.ASN.137	OG, C.SER.145	HG, C.SER.145	2.92	2.08	24.33
1HGJ.PDB	OH, C.TYR.195	NE1, C.TRP.153	HE1, C.TRP.153	2.84	1.96	21.72
1HGJ.PDB	OE2, C.GLU.123	NZ, C.LYS.176	HZ1, C.LYS.176	2.69	1.80	24.96
1HGJ.PDB	OE1, C.GLU.123	OH, C.TYR.178	HH, C.TYR.178	2.77	1.82	8.51
1HGJ.PDB	OG1, C.THR.235	NE1, C.TRP.180	HE1, C.TRP.180	2.91	1.92	4.72
1HGJ.PDB	OG, C.SER.231	NE2, C.HIS.184	HE2, C.HIS.184	2.74	1.91	26.34
1HGJ.PDB	OD1, C.ASN.250	NE2, C.GLN.191	HE21, C.GLN.191	2.99	2.02	8.22
1HGJ.PDB	OD1, C.ASN.246	NH2, C.ARG.201	HH21, C.ARG.201	2.59	1.74	25.86
1HGJ.PDB	OG1, C.THR.212	OG1, C.THR.203	HG1, C.THR.203	2.89	1.94	9.95
1HGJ.PDB	OE1, E.GLN.210	NH2, C.ARG.220	HH21, C.ARG.220	2.66	1.82	26.85
1HGJ.PDB	OD1, C.ASP.101	OG, C.SER.231	HG, C.SER.231	2.91	1.95	9.37
1HGJ.PDB	OE1, B.GLU.72	NZ, C.LYS.238	HZ1, C.LYS.238	2.75	1.79	18.67
1HGJ.PDB	OD1, C.ASN.165	ND2, C.ASN.246	HD22, C.ASN.246	2.89	1.93	12.15
1HGJ.PDB	OD1, C.ASN.133	NH2, C.ARG.255	HH22, C.ARG.255	2.54	1.71	27.08
1HGJ.PDB	OE2, C.GLU.119	NH1, C.ARG.261	HH12, C.ARG.261	2.65	1.83	28.56
1HGJ.PDB	OE1, C.GLU.119	NH2, C.ARG.261	HH22, C.ARG.261	2.92	2.03	23.97
1HGJ.PDB	OD2, C.ASP.85	NZ, C.LYS.264	HZ3, C.LYS.264	2.82	1.83	14.94
1HGJ.PDB	OE1, C.GLN.44	NZ, C.LYS.292	HZ1, C.LYS.292	2.73	1.72	10.59
1HGJ.PDB	OD2, C.ASP.291	NZ, C.LYS.292	HZ3, C.LYS.292	2.82	1.84	16.66
1HGJ.PDB	OD1, D.ASP.86	NZ, C.LYS.310	HZ3, C.LYS.310	2.94	2.10	29.37
1HGJ.PDB	OE1, C.GLU.41	NZ, C.LYS.315	HZ3, C.LYS.315	2.86	1.91	20.22
1HGJ.PDB	OE2, C.GLU.35	ND2, C.ASN.322	HD22, C.ASN.322	2.88	1.97	19.99
1HGJ.PDB	OE1, D.GLU.15	NZ, C.LYS.326	HZ1, C.LYS.326	2.91	1.86	5.48
1HGJ.PDB	OE1, D.GLN.34	NE, D.ARG.25	HE, D.ARG.25	2.65	1.80	23.08
1HGJ.PDB	OD1, D.ASN.146	ND2, D.ASN.28	HD21, D.ASN.28	2.98	2.03	11.81
1HGJ.PDB	OD2, D.ASP.37	OG, D.SER.40	HG, D.SER.40	2.82	1.96	22.49
1HGJ.PDB	OD1, D.ASP.46	NE2, D.GLN.42	HE22, D.GLN.42	2.81	1.92	21.12
1HGJ.PDB	OE2, D.GLU.114	NE2, D.GLN.47	HE21, D.GLN.47	2.94	2.03	18.44
1HGJ.PDB	OG1, D.THR.107	NZ, D.LYS.51	HZ1, D.LYS.51	2.97	1.99	16.18
1HGJ.PDB	OE1, D.GLU.103	NZ, D.LYS.51	HZ2, D.LYS.51	2.80	1.76	6.89
1HGJ.PDB	ND1, D.HIS.106	NZ, D.LYS.51	HZ3, D.LYS.51	2.79	1.82	16.80
1HGJ.PDB	OE1, D.GLU.57	NH1, D.ARG.54	HH11, D.ARG.54	2.87	1.86	9.17
1HGJ.PDB	OE2, B.GLU.97	NH2, D.ARG.54	HH22, D.ARG.54	2.84	1.88	15.58

1HGJ.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.89	1.91	5.59
1HGJ.PDB	OE2, D_GLU_85	NZ, D_LYS_68	HZ2, D_LYS_68	2.82	1.80	11.23
1HGJ.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.85	1.89	10.87
1HGJ.PDB	OE2, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.76	1.76	7.89
1HGJ.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.68	1.69	5.65
1HGJ.PDB	OE1, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.71	1.72	5.59
1HGJ.PDB	OE1, D_GLU_74	NE2, D_GLN_78	HE22, D_GLN_78	2.88	1.94	14.79
1HGJ.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.63	1.81	25.72
1HGJ.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.75	1.72	7.31
1HGJ.PDB	OE2, D_GLU_120	NH1, D_ARG_123	HH11, D_ARG_123	2.74	1.85	23.39
1HGJ.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.80	1.98	27.33
1HGJ.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.87	2.00	21.99
1HGJ.PDB	OH, B_TYR_141	NH1, D_ARG_127	HH12, D_ARG_127	2.99	2.02	12.89
1HGJ.PDB	OH, D_TYR_157	ND2, D_ASN_129	HD22, D_ASN_129	2.79	1.84	10.20
1HGJ.PDB	OD1, D_ASN_154	OG1, D_THR_156	HG1, D_THR_156	2.71	1.81	16.75
1HGJ.PDB	NE2, D_HIS_142	OH, D_TYR_157	HH, D_TYR_157	2.78	1.88	18.06
1HGJ.PDB	OE2, D_GLU_131	NH1, D_ARG_170	HH11, D_ARG_170	2.79	1.80	6.55
1HGJ.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.81	1.79	8.50
1HGJ.PDB	OD2, E_ASP_275	NZ, E_LYS_50	HZ1, E_LYS_50	2.74	1.82	22.90
1HGJ.PDB	OD1, E_ASP_73	ND1, E_HIS_75	HD1, E_HIS_75	2.80	1.88	17.19
1HGJ.PDB	OD1, E_ASP_60	NE, E_ARG_90	HE, E_ARG_90	2.91	1.94	8.87
1HGJ.PDB	OD2, E_ASP_60	NH2, E_ARG_90	HH21, E_ARG_90	2.83	1.83	8.62
1HGJ.PDB	OD1, E_ASP_271	OG, E_SER_91	HG, E_SER_91	2.99	2.15	25.95
1HGJ.PDB	OD2, E_ASP_271	OG, E_SER_91	HG, E_SER_91	2.82	1.92	18.47
1HGJ.PDB	OD2, E_ASP_68	OG, E_SER_95	HG, E_SER_95	2.94	2.00	13.81
1HGJ.PDB	OD1, E_ASP_68	OH, E_TYR_100	HH, E_TYR_100	2.88	1.94	12.28
1HGJ.PDB	OD2, E_ASP_104	OG, E_SER_107	HG, E_SER_107	2.85	1.94	18.67
1HGJ.PDB	OE2, F_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.76	1.77	12.82
1HGJ.PDB	OD2, D_ASP_79	OG, E_SER_110	HG, E_SER_110	2.79	1.87	15.96
1HGJ.PDB	OE2, E_GLU_119	OG1, E_THR_117	HG1, E_THR_117	2.91	1.96	10.96
1HGJ.PDB	OD1, E_ASN_137	NZ, E_LYS_140	HZ2, E_LYS_140	2.71	1.72	13.56
1HGJ.PDB	OD2, E_ASP_77	NE, E_ARG_141	HE, E_ARG_141	2.84	2.00	27.31
1HGJ.PDB	OD1, E_ASP_77	NH2, E_ARG_141	HH21, E_ARG_141	2.84	1.92	21.35
1HGJ.PDB	OD2, E_ASP_77	NH2, E_ARG_141	HH21, E_ARG_141	2.75	1.86	24.32
1HGJ.PDB	OD1, E_ASN_137	OG, E_SER_145	HG, E_SER_145	2.96	2.12	24.46
1HGJ.PDB	OH, E_TYR_195	NE1, E_TRP_153	HE1, E_TRP_153	2.83	1.93	19.26
1HGJ.PDB	OE2, E_GLU_123	NZ, E_LYS_176	HZ1, E_LYS_176	2.69	1.80	25.95
1HGJ.PDB	OE1, E_GLU_123	OH, E_TYR_178	HH, E_TYR_178	2.77	1.83	11.08
1HGJ.PDB	OG1, E_THR_235	NE1, E_TRP_180	HE1, E_TRP_180	2.94	1.96	4.45
1HGJ.PDB	OG, E_SER_231	NE2, E_HIS_184	HE2, E_HIS_184	2.75	1.92	26.56
1HGJ.PDB	OD1, E_ASN_246	NH2, E_ARG_201	HH21, E_ARG_201	2.59	1.74	26.30
1HGJ.PDB	OG1, E_THR_212	OG1, E_THR_203	HG1, E_THR_203	2.93	1.99	12.00
1HGJ.PDB	OD1, C_ASP_101	NE2, E_GLN_210	HE22, E_GLN_210	2.94	2.10	26.45
1HGJ.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.69	1.86	28.41
1HGJ.PDB	OD1, E_ASP_101	OG, E_SER_231	HG, E_SER_231	2.90	1.95	11.36
1HGJ.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ3, E_LYS_238	2.87	1.86	13.82
1HGJ.PDB	OD1, E_ASN_165	ND2, E_ASN_246	HD22, E_ASN_246	2.89	1.94	11.88
1HGJ.PDB	OD1, E_ASN_133	NH2, E_ARG_255	HH22, E_ARG_255	2.55	1.71	26.62
1HGJ.PDB	OE2, E_GLU_119	NH1, E_ARG_261	HH12, E_ARG_261	2.65	1.82	28.15
1HGJ.PDB	OE1, E_GLU_119	NH2, E_ARG_261	HH22, E_ARG_261	2.91	2.01	23.66
1HGJ.PDB	OD2, E_ASP_85	NZ, E_LYS_264	HZ3, E_LYS_264	2.86	1.86	15.01
1HGJ.PDB	OE1, E_GLN_44	NZ, E_LYS_292	HZ1, E_LYS_292	2.72	1.70	10.33
1HGJ.PDB	OD2, E_ASP_291	NZ, E_LYS_292	HZ3, E_LYS_292	2.83	1.86	17.49
1HGJ.PDB	OD1, F_ASP_86	NZ, E_LYS_310	HZ3, E_LYS_310	2.93	2.08	29.22
1HGJ.PDB	OE1, E_GLU_41	NZ, E_LYS_315	HZ3, E_LYS_315	2.86	1.91	20.65
1HGJ.PDB	OE2, E_GLU_35	ND2, E_ASN_322	HD22, E_ASN_322	2.86	1.96	20.74
1HGJ.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.87	1.86	12.83
1HGJ.PDB	OE1, F_GLN_34	NE, F_ARG_25	HE, F_ARG_25	2.86	2.05	28.42

1HGJ.PDB	OE1, F_GLN_34	NH2, F_ARG_25	HH21, F_ARG_25	2.64	1.73	20.69
1HGJ.PDB	OD1, F_ASN_146	ND2, F_ASN_28	HD21, F_ASN_28	2.81	1.89	16.64
1HGJ.PDB	OD2, F_ASP_37	OG, F_SER_40	HG, F_SER_40	2.80	1.95	24.06
1HGJ.PDB	OD1, F_ASP_46	NE2, F_GLN_42	HE22, F_GLN_42	2.80	1.92	21.18
1HGJ.PDB	OE2, F_GLU_114	NE2, F_GLN_47	HE21, F_GLN_47	2.95	2.04	18.06
1HGJ.PDB	OE1, F_GLU_103	NZ, F_LYS_51	HZ2, F_LYS_51	2.79	1.75	5.77
1HGJ.PDB	ND1, F_HIS_106	NZ, F_LYS_51	HZ3, F_LYS_51	2.75	1.79	17.21
1HGJ.PDB	OE1, F_GLU_57	NH1, F_ARG_54	HH11, F_ARG_54	2.86	1.86	9.70
1HGJ.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.77	1.81	14.54
1HGJ.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.90	1.93	7.02
1HGJ.PDB	OE2, F_GLU_85	NZ, F_LYS_68	HZ2, F_LYS_68	2.74	1.77	18.09
1HGJ.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.85	1.89	12.57
1HGJ.PDB	OE2, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.70	1.70	4.55
1HGJ.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.65	1.66	2.84
1HGJ.PDB	OE1, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.72	1.73	7.95
1HGJ.PDB	OE1, F_GLU_74	NE2, F_GLN_78	HE22, F_GLN_78	2.92	1.97	13.10
1HGJ.PDB	OE1, B_GLU_85	OH, F_TYR_83	HH, F_TYR_83	2.53	1.75	28.54
1HGJ.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.70	1.68	8.19
1HGJ.PDB	OE2, F_GLU_120	NH1, F_ARG_123	HH11, F_ARG_123	2.73	1.86	24.44
1HGJ.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.92	2.09	27.65
1HGJ.PDB	OE2, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.96	2.06	20.98
1HGJ.PDB	OH, F_TYR_157	ND2, F_ASN_129	HD22, F_ASN_129	2.75	1.85	17.65
1HGJ.PDB	OE2, F_GLU_131	NH1, F_ARG_170	HH11, F_ARG_170	2.79	1.80	6.77
1OSP.PDB	OE1, L_GLN_89	OH, L_TYR_36	HH, L_TYR_36	2.81	1.86	10.05
1OSP.PDB	OG1, L_THR_97	NE2, L_GLN_90	HE22, L_GLN_90	3.00	2.06	15.72
1OSP.PDB	OE1, L_GLU_105	OH, L_TYR_140	HH, L_TYR_140	2.90	2.03	21.23
1OSP.PDB	OG, L_SER_177	NE1, L_TRP_148	HE1, L_TRP_148	2.94	1.97	6.03
1OSP.PDB	OG, L_SER_131	OG1, L_THR_180	HG1, L_THR_180	2.85	1.92	11.66
1OSP.PDB	OD2, L_ASP_110	NZ, L_LYS_199	HZ3, L_LYS_199	2.64	1.82	29.88
1OSP.PDB	OD1, H_ASN_83	OG1, H_THR_17	HG1, H_THR_17	2.79	1.95	24.49
1OSP.PDB	OE1, H_GLU_46	NH1, H_ARG_38	HH11, H_ARG_38	2.77	1.80	9.20
1OSP.PDB	OH, H_TYR_93	NH2, H_ARG_38	HH21, H_ARG_38	2.83	1.87	12.82
1OSP.PDB	OD1, H_ASP_89	NH2, H_ARG_38	HH22, H_ARG_38	2.83	1.91	19.07
1OSP.PDB	OD2, L_ASP_1	OG, H_SER_62	HG, H_SER_62	2.98	2.17	26.53
1OSP.PDB	OG, H_SER_186	NE1, H_TRP_161	HE1, H_TRP_161	2.94	1.96	6.92
1OSP.PDB	OG, L_SER_176	OG, H_SER_185	HG, H_SER_185	2.74	1.91	24.72
1OSP.PDB	OG, H_SER_209	ND1, H_HIS_206	HD1, H_HIS_206	2.73	1.88	25.05
1OSP.PDB	OE1, L_GLU_123	NZ, H_LYS_215	HZ2, H_LYS_215	2.78	1.85	20.53
1OSP.PDB	OD1, O_ASP_33	NZ, O_LYS_39	HZ2, O_LYS_39	2.81	1.85	17.76
1OSP.PDB	OG1, O_THR_143	NH1, O_ARG_139	HH11, O_ARG_139	2.73	1.78	14.74
1OSP.PDB	OE2, O_GLU_160	NH2, O_ARG_139	HH22, O_ARG_139	2.96	2.05	19.95
1OSP.PDB	OE1, O_GLU_160	NZ, O_LYS_189	HZ1, O_LYS_189	2.95	1.93	9.44
1OSP.PDB	OG, O_SER_198	ND2, O_ASN_190	HD22, O_ASN_190	2.97	2.02	11.75
1OSP.PDB	OD1, O_ASP_234	OG1, O_THR_224	HG1, O_THR_224	2.71	1.92	27.50
1OSP.PDB	OD1, O_ASP_234	OH, O_TYR_248	HH, O_TYR_248	2.73	1.90	24.06
1PSK.PDB	OG, L_SER_176	NE1, L_TRP_147	HE1, L_TRP_147	2.73	1.78	10.14
1PSK.PDB	OD1, L_ASN_160	OG, L_SER_176	HG, L_SER_176	2.79	1.87	14.99
1PSK.PDB	NE1, H_TRP_47	ND1, H_HIS_35	HD1, H_HIS_35	2.92	2.03	20.19
1PSK.PDB	OG1, H_THR_78	OG, H_SER_76	HG, H_SER_76	2.94	2.03	16.27
1PSK.PDB	OH, H_TYR_27	OG, H_SER_98	HG, H_SER_98	2.95	2.06	19.06
1R21-1.PDB	OG1, A_THR_69	ND2, A_ASN_62	HD21, A_ASN_62	2.86	1.99	21.79
1R21-10.PDB	OG1, A_THR_69	ND2, A_ASN_62	HD21, A_ASN_62	2.90	2.06	25.22
1R21-11.PDB	OG, A_SER_64	ND2, A_ASN_62	HD22, A_ASN_62	2.35	1.48	21.77
1R21-12.PDB	OD1, A_ASN_67	OG1, A_THR_66	HG1, A_THR_66	2.34	1.38	3.67
1R21-13.PDB	OG1, A_THR_69	ND2, A_ASN_62	HD22, A_ASN_62	2.50	1.62	19.65
1R21-13.PDB	OH, A_TYR_97	ND2, A_ASN_99	HD21, A_ASN_99	2.51	1.54	7.69
1R21-14.PDB	OG1, A_THR_69	ND2, A_ASN_62	HD21, A_ASN_62	2.52	1.57	12.09
1R21-14.PDB	OE1, A_GLU_57	NE, A_ARG_81	HE, A_ARG_81	2.82	2.02	29.06

1R21-14.PDB	OE2, A_GLU_57	NH2, A_ARG_81	HH21, A_ARG_81	2.46	1.50	12.90
1R21-14.PDB	OH, A_TYR_97	ND2, A_ASN_99	HD22, A_ASN_99	2.66	1.70	8.32
1R21-16.PDB	OE1, A_GLU_57	NE, A_ARG_81	HE, A_ARG_81	2.43	1.60	25.79
1R21-17.PDB	ND2, A_ASN_99	NE, A_ARG_5	HE, A_ARG_5	2.79	1.84	10.87
1R21-17.PDB	OG, A_SER_94	OG1, A_THR_89	HG1, A_THR_89	2.85	1.94	16.35
1R21-18.PDB	OD1, A_ASN_67	OG1, A_THR_66	HG1, A_THR_66	2.60	1.66	10.07
1R21-18.PDB	OE2, A_GLU_100	NE2, A_HIS_84	HE2, A_HIS_84	2.44	1.60	25.14
1R21-19.PDB	OE2, A_GLU_34	NE2, A_GLN_47	HE21, A_GLN_47	2.80	1.93	22.82
1R21-19.PDB	OG1, A_THR_69	ND2, A_ASN_62	HD21, A_ASN_62	2.83	2.03	29.57
1R21-2.PDB	OE2, A_GLU_34	NE2, A_GLN_47	HE21, A_GLN_47	2.62	1.65	7.42
1R21-2.PDB	OG1, A_THR_69	ND2, A_ASN_62	HD21, A_ASN_62	2.81	1.92	20.56
1R21-2.PDB	OG, A_SER_64	ND2, A_ASN_62	HD22, A_ASN_62	2.42	1.53	18.22
1R21-2.PDB	OG, A_SER_94	OG1, A_THR_89	HG1, A_THR_89	2.98	2.02	6.58
1R21-2.PDB	OD2, A_ASP_16	NH1, A_ARG_96	HH12, A_ARG_96	2.71	1.87	26.03
1R21-22.PDB	OG, A_SER_64	ND2, A_ASN_62	HD22, A_ASN_62	2.37	1.45	16.21
1R21-23.PDB	OE1, A_GLU_57	NE, A_ARG_81	HE, A_ARG_81	2.65	1.70	11.54
1R21-3.PDB	OD1, A_ASP_16	NE2, A_HIS_19	HE2, A_HIS_19	2.71	1.85	23.51
1R21-3.PDB	OE2, A_GLU_34	NE2, A_GLN_47	HE22, A_GLN_47	2.72	1.92	29.24
1R21-3.PDB	OG1, A_THR_69	ND2, A_ASN_62	HD21, A_ASN_62	2.87	2.01	23.40
1R21-4.PDB	OD1, A_ASN_67	OG1, A_THR_66	HG1, A_THR_66	2.40	1.45	5.76
1R21-4.PDB	OE1, A_GLU_57	NE, A_ARG_81	HE, A_ARG_81	2.76	1.87	19.46
1R21-4.PDB	OE1, A_GLU_57	NH2, A_ARG_81	HH21, A_ARG_81	2.93	2.10	27.48
1R21-5.PDB	OG1, A_THR_69	ND2, A_ASN_62	HD22, A_ASN_62	2.62	1.75	21.48
1R21-6.PDB	OG1, A_THR_69	ND2, A_ASN_62	HD21, A_ASN_62	2.81	1.95	22.23
1R21-6.PDB	OD1, A_ASN_67	OG1, A_THR_66	HG1, A_THR_66	2.30	1.42	18.29
1R21-7.PDB	OD1, A_ASN_67	OG1, A_THR_66	HG1, A_THR_66	2.91	2.05	21.54
1R21-9.PDB	OG1, A_THR_69	ND2, A_ASN_62	HD21, A_ASN_62	2.59	1.65	13.02
1VFB.PDB	OE1, A_GLN_89	OH, A_TYR_36	HH, A_TYR_36	2.84	2.00	25.31
1VFB.PDB	OD2, A_ASP_82	NE, A_ARG_61	HE, A_ARG_61	2.88	1.96	15.15
1VFB.PDB	OD1, A_ASP_82	NH2, A_ARG_61	HH21, A_ARG_61	2.85	1.87	9.42
1VFB.PDB	OE1, B_GLU_98	NH1, A_ARG_96	HH12, A_ARG_96	2.82	1.84	8.38
1VFB.PDB	OE2, B_GLU_98	NH2, A_ARG_96	HH22, A_ARG_96	2.81	1.85	10.74
1VFB.PDB	OG, B_SER_28	OG1, B_THR_30	HG1, B_THR_30	2.97	2.08	19.82
1VFB.PDB	OE1, B_GLU_98	ND2, B_ASN_35	HD21, B_ASN_35	2.85	2.00	23.37
1VFB.PDB	OD1, B_ASP_89	NH1, B_ARG_38	HH12, B_ARG_38	3.00	2.07	17.31
1VFB.PDB	OE1, A_GLN_38	NE2, B_GLN_39	HE21, B_GLN_39	2.95	1.98	8.04
1VFB.PDB	OD1, B_ASN_35	NE1, B_TRP_47	HE1, B_TRP_47	2.80	1.83	5.78
1VFB.PDB	OD2, B_ASP_89	NH1, B_ARG_66	HH12, B_ARG_66	2.89	1.97	19.13
1VFB.PDB	OD1, B_ASP_89	NH2, B_ARG_66	HH22, B_ARG_66	2.93	1.93	3.85
1VFB.PDB	OD1, B_ASN_73	NZ, B_LYS_71	HZ1, B_LYS_71	2.93	2.08	28.65
1VFB.PDB	OG, B_SER_70	NZ, B_LYS_81	HZ2, B_LYS_81	2.92	2.05	26.58
1VFB.PDB	OD1, B_ASN_83	OG, B_SER_84	HG, B_SER_84	2.99	2.04	8.51
1VFB.PDB	OD1, B_ASP_104	NE, B_ARG_97	HE, B_ARG_97	2.99	2.02	4.50
1VFB.PDB	OD2, B_ASP_104	NH2, B_ARG_97	HH21, B_ARG_97	2.86	1.87	3.52
1VFB.PDB	OG1, C_THR_89	NE2, C_HIS_15	HE2, C_HIS_15	2.84	1.94	19.37
1VFB.PDB	OE1, C_GLN_41	OG1, C_THR_40	HG1, C_THR_40	2.88	1.98	18.75
1VFB.PDB	OG1, C_THR_69	OG, C_SER_60	HG, C_SER_60	2.78	1.84	10.98
1VFB.PDB	OD1, C_ASN_27	NE1, C_TRP_111	HE1, C_TRP_111	2.95	2.01	14.04
1VFB.PDB	OE1, C_GLN_121	NH1, C_ARG_125	HH11, C_ARG_125	2.96	2.02	16.36
2MKL-1.PDB	OXT, C_ALA_105	NZ, C_LYS_13	HZ3, C_LYS_13	2.65	1.63	10.83
2MKL-1.PDB	OG1, C_ASP_80	OG1, C_THR_21	HG1, C_THR_21	2.65	1.79	22.35
2MKL-1.PDB	OD2, C_ASP_80	NE2, C_GLN_22	HE21, C_GLN_22	2.86	1.96	18.61
2MKL-1.PDB	OG, C_SER_34	NZ, C_LYS_65	HZ2, C_LYS_65	2.81	1.84	16.47
2MKL-1.PDB	OE1, C_GLU_78	OG1, C_THR_83	HG1, C_THR_83	2.66	1.70	8.48
2MKL-1.PDB	OD1, C_ASP_80	NZ, C_LYS_104	HZ1, C_LYS_104	2.72	1.78	20.43
2MKL-10.PDB	OE2, C_GLU_90	NZ, C_LYS_40	HZ2, C_LYS_40	2.58	1.67	23.06
2MKL-10.PDB	OG, C_SER_62	OG1, C_THR_67	HG1, C_THR_67	2.83	1.88	6.13
2MKL-10.PDB	OXT, C_ALA_105	NZ, C_LYS_104	HZ3, C_LYS_104	2.68	1.72	17.77

2MKL-2.PDB	OXT, C_ALA_105	NZ, C_LYS_13	HZ3, C_LYS_13	2.61	1.67	20.57
2MKL-2.PDB	OD1, C_ASP_35	OG, C_SER_34	HG, C_SER_34	2.77	1.81	5.76
2MKL-2.PDB	OH, C_TYR_85	NH1, C_ARG_50	HH11, C_ARG_50	2.66	1.70	14.67
2MKL-2.PDB	OE2, C_GLU_78	NH1, C_ARG_50	HH12, C_ARG_50	2.73	1.79	17.34
2MKL-2.PDB	OE1, C_GLU_55	NZ, C_LYS_71	HZ1, C_LYS_71	2.72	1.71	11.97
2MKL-2.PDB	OD1, C_ASN_46	OG1, C_THR_83	HG1, C_THR_83	2.72	1.91	26.52
2MKL-3.PDB	OE1, C_GLU_93	NH1, C_ARG_3	HH12, C_ARG_3	2.68	1.70	11.24
2MKL-3.PDB	OXT, C_ALA_105	NZ, C_LYS_13	HZ1, C_LYS_13	2.67	1.72	19.52
2MKL-3.PDB	OG, C_SER_34	NZ, C_LYS_65	HZ3, C_LYS_65	2.80	1.76	6.92
2MKL-3.PDB	OE2, C_GLU_55	NZ, C_LYS_71	HZ1, C_LYS_71	2.64	1.59	1.73
2MKL-3.PDB	OG1, C_THR_26	NZ, C_LYS_71	HZ3, C_LYS_71	2.86	1.95	23.23
2MKL-3.PDB	OD1, C_ASN_46	OG1, C_THR_83	HG1, C_THR_83	2.91	1.97	11.57
2MKL-3.PDB	OD1, C_ASP_80	NZ, C_LYS_104	HZ2, C_LYS_104	2.61	1.56	1.39
2MKL-4.PDB	OE1, C_GLU_17	NE1, C_TRP_20	HE1, C_TRP_20	2.69	1.70	6.61
2MKL-4.PDB	OE1, C_GLU_37	ND2, C_ASN_38	HD21, C_ASN_38	2.75	1.84	18.89
2MKL-4.PDB	OE1, C_GLU_84	ND2, C_ASN_46	HD21, C_ASN_46	2.79	1.87	17.49
2MKL-4.PDB	OH, C_TYR_85	NE, C_ARG_50	HE, C_ARG_50	2.95	2.07	22.98
2MKL-4.PDB	OE1, C_GLU_78	NH2, C_ARG_50	HH21, C_ARG_50	2.70	1.74	15.78
2MKL-4.PDB	OE2, C_GLU_55	NZ, C_LYS_71	HZ1, C_LYS_71	2.65	1.66	15.29
2MKL-5.PDB	OG1, C_THR_5	NE2, C_GLN_4	HE21, C_GLN_4	2.80	1.92	21.71
2MKL-5.PDB	OD1, C_ASP_35	OG, C_SER_34	HG, C_SER_34	2.85	1.91	12.30
2MKL-5.PDB	OE1, C_GLU_78	NH2, C_ARG_50	HH22, C_ARG_50	2.76	1.81	16.18
2MKL-5.PDB	OD2, C_ASP_6	NZ, C_LYS_65	HZ2, C_LYS_65	2.68	1.69	14.66
2MKL-5.PDB	OE2, C_GLU_78	OG1, C_THR_83	HG1, C_THR_83	2.81	1.87	12.01
2MKL-5.PDB	OXT, C_ALA_105	NZ, C_LYS_104	HZ2, C_LYS_104	2.74	1.74	13.81
2MKL-6.PDB	OXT, C_ALA_105	NZ, C_LYS_13	HZ2, C_LYS_13	2.64	1.69	18.78
2MKL-6.PDB	OE2, C_GLU_17	NZ, C_LYS_13	HZ3, C_LYS_13	2.63	1.59	5.83
2MKL-6.PDB	OE1, C_GLU_84	ND2, C_ASN_46	HD21, C_ASN_46	2.90	1.97	15.36
2MKL-6.PDB	OE2, C_GLU_78	NH2, C_ARG_50	HH22, C_ARG_50	2.72	1.70	3.73
2MKL-6.PDB	OD2, C_ASP_6	NZ, C_LYS_65	HZ3, C_LYS_65	2.59	1.63	17.95
2MKL-6.PDB	OE2, C_GLU_55	NZ, C_LYS_71	HZ1, C_LYS_71	2.70	1.72	16.34
2MKL-6.PDB	OD1, C_ASN_46	OG1, C_THR_83	HG1, C_THR_83	2.65	1.71	11.83
2MKL-6.PDB	OD1, C_ASP_80	NZ, C_LYS_104	HZ1, C_LYS_104	2.64	1.71	20.84
2MKL-7.PDB	OD1, C_ASP_6	NE, C_ARG_3	HE, C_ARG_3	2.80	1.90	20.83
2MKL-7.PDB	OD2, C_ASP_6	NE, C_ARG_3	HE, C_ARG_3	2.95	2.13	27.86
2MKL-7.PDB	OD2, C_ASP_6	NH2, C_ARG_3	HH21, C_ARG_3	2.72	1.79	18.49
2MKL-7.PDB	OD1, C_ASP_6	NZ, C_LYS_65	HZ2, C_LYS_65	2.61	1.57	4.07
2MKL-7.PDB	OG1, C_THR_24	NZ, C_LYS_73	HZ1, C_LYS_73	2.79	1.84	19.74
2MKL-7.PDB	OE2, C_GLU_78	OG1, C_THR_83	HG1, C_THR_83	2.59	1.64	9.74
2MKL-8.PDB	OG, C_SER_70	NE1, C_TRP_43	HE1, C_TRP_43	2.82	1.83	2.10
2MKL-8.PDB	OE2, C_GLU_78	NH1, C_ARG_50	HH12, C_ARG_50	2.63	1.62	3.58
2MKL-8.PDB	OD2, C_ASP_6	NZ, C_LYS_65	HZ3, C_LYS_65	2.64	1.68	18.41
2MKL-8.PDB	OD1, C_ASP_80	NZ, C_LYS_104	HZ1, C_LYS_104	2.61	1.59	9.01
2MKL-9.PDB	OE2, C_GLU_78	NH2, C_ARG_50	HH22, C_ARG_50	2.68	1.69	8.63
2MKL-9.PDB	OD2, C_ASP_6	NZ, C_LYS_65	HZ2, C_LYS_65	2.75	1.71	7.05
2MKL-9.PDB	OE2, C_GLU_37	OG, C_SER_92	HG, C_SER_92	3.00	2.20	28.49
3SE8.PDB	OE2, G_GLU_91	NE1, G_TRP_45	HE1, G_TRP_45	2.78	2.03	24.08
3SE8.PDB	OE2, G_GLU_64	ND1, G_HIS_66	HD1, G_HIS_66	2.82	1.98	11.41
3SE8.PDB	OE1, G_GLU_64	ND2, G_ASN_67	HD22, G_ASN_67	2.82	2.00	14.84
3SE8.PDB	OD1, G_ASN_99	NE2, G_GLN_103	HE22, G_GLN_103	2.99	2.17	14.68
3SE8.PDB	OE2, G_GLU_381	NZ, G_LYS_207	HZ2, G_LYS_207	2.74	1.86	4.82
3SE8.PDB	OE2, G_GLU_83	OG, G_SER_243	HG, G_SER_243	2.64	1.83	7.57
3SE8.PDB	OH, G_TYR_486	ND1, G_HIS_249	HD1, G_HIS_249	2.64	1.81	12.83
3SE8.PDB	OE1, G_GLU_482	NE2, G_HIS_249	HE2, G_HIS_249	3.00	2.16	9.93
3SE8.PDB	OE2, G_GLU_269	NZ, G_LYS_348	HZ1, G_LYS_348	2.90	2.14	25.94
3SE8.PDB	OE1, G_GLU_351	NZ, G_LYS_348	HZ3, G_LYS_348	2.96	2.10	14.00
3SE8.PDB	OD1, G_ASN_295	ND2, G_ASN_444	HD21, G_ASN_444	2.87	2.12	25.11
3SE8.PDB	OG1, G_THR_297	ND2, G_ASN_444	HD22, G_ASN_444	2.77	1.99	20.73

3SE8.PDB	OD2, G.ASP.457	NE, G.ARG.469	HE, G.ARG.469	2.90	2.06	8.93
3SE8.PDB	OD1, G.ASP.457	NH2, G.ARG.469	HH21, G.ARG.469	2.93	2.11	16.29
3SE8.PDB	OE1, G.GLN.105	NE1, G.TRP.479	HE1, G.TRP.479	2.68	1.92	22.70
3SE8.PDB	OE1, G.GLU.91	NZ, G.LYS.487	HZ1, G.LYS.487	2.58	1.77	20.55
3SE8.PDB	OD1, G.ASP.47	NZ, G.LYS.487	HZ2, G.LYS.487	2.90	2.08	19.02
3SE8.PDB	OE1, H.GLU.46	NH1, H.ARG.38	HH11, H.ARG.38	2.64	1.78	1.94
3SE8.PDB	OH, H.TYR.90	NH2, H.ARG.38	HH21, H.ARG.38	2.79	1.95	9.66
3SE8.PDB	OD1, H.ASP.86	NH2, H.ARG.38	HH22, H.ARG.38	2.67	1.83	8.41
3SE8.PDB	OD1, G.ASN.280	NE1, H.TRP.50	HE1, H.TRP.50	3.00	2.21	20.49
3SE8.PDB	OE2, H.GLU.46	NE2, H.GLN.62	HE21, H.GLN.62	2.91	2.06	7.60
3SE8.PDB	OD1, G.ASP.457	NE2, H.GLN.64	HE22, H.GLN.64	2.94	2.12	14.23
3SE8.PDB	OD2, H.ASP.86	NH2, H.ARG.66	HH22, H.ARG.66	2.60	1.84	23.72
3SE8.PDB	OD2, G.ASP.368	NH2, H.ARG.71	HH22, H.ARG.71	2.91	2.05	6.24
3SE8.PDB	OG, H.SER.180	NE1, H.TRP.154	HE1, H.TRP.154	2.94	2.09	7.62
3SE8.PDB	OD1, H.ASP.144	NE2, H.GLN.171	HE22, H.GLN.171	2.79	1.98	16.20
3SE8.PDB	OG, H.SER.203	ND1, H.HIS.200	HD1, H.HIS.200	2.45	1.61	10.75
3SE8.PDB	OD1, L.ASP.70	NZ, L.LYS.24	HZ3, L.LYS.24	2.62	1.80	18.41
3SE8.PDB	OH, L.TYR.86	NE2, L.GLN.37	HE21, L.GLN.37	2.98	2.15	12.85
3SE8.PDB	OD2, L.ASP.50	NE, L.ARG.53	HE, L.ARG.53	2.87	2.02	8.47
3SE8.PDB	OD2, L.ASP.82	NE, L.ARG.61	HE, L.ARG.61	2.91	2.18	26.35
3SE8.PDB	OD1, L.ASP.82	NH2, L.ARG.61	HH21, L.ARG.61	2.77	1.91	2.48
3SE8.PDB	OG, L.SER.131	NE2, L.GLN.124	HE22, L.GLN.124	2.53	1.70	11.07
3SE8.PDB	OE2, L.GLU.103	NH2, L.ARG.142	HH22, L.ARG.142	2.84	2.00	11.39
3SE8.PDB	OE1, L.GLU.195	NE2, L.GLN.147	HE21, L.GLN.147	2.66	1.93	26.32
3SE8.PDB	OG, L.SER.177	NE1, L.TRP.148	HE1, L.TRP.148	2.88	2.08	18.18
3SE8.PDB	OD1, L.ASP.170	OG1, L.THR.172	HG1, L.THR.172	2.49	1.68	7.38
3SE9.PDB	OE2, G.GLU.64	ND1, G.HIS.66	HD1, G.HIS.66	2.73	1.88	8.47
3SE9.PDB	OE1, G.GLU.64	ND2, G.ASN.67	HD21, G.ASN.67	2.83	2.01	14.03
3SE9.PDB	OD1, G.ASN.99	NE2, G.GLN.103	HE21, G.GLN.103	2.75	1.96	19.57
3SE9.PDB	OE1, G.GLN.117	NZ, G.LYS.121	HZ3, G.LYS.121	2.58	1.83	27.32
3SE9.PDB	OE2, G.GLU.83	OG, G.SER.243	HG, G.SER.243	2.65	1.89	17.63
3SE9.PDB	OH, G.TYR.486	ND1, G.HIS.249	HD1, G.HIS.249	2.73	1.91	13.84
3SE9.PDB	OE1, G.GLN.422	NH1, G.ARG.327	HH11, G.ARG.327	2.62	1.84	19.91
3SE9.PDB	OE1, G.GLU.370	ND2, G.ASN.425	HD21, G.ASN.425	2.86	2.02	9.78
3SE9.PDB	OD1, G.ASN.295	ND2, G.ASN.444	HD21, G.ASN.444	2.93	2.17	24.18
3SE9.PDB	OG1, G.THR.297	ND2, G.ASN.444	HD22, G.ASN.444	2.97	2.23	26.41
3SE9.PDB	OE2, G.GLU.466	NH1, G.ARG.456	HH11, G.ARG.456	2.71	1.88	12.87
3SE9.PDB	OE1, G.GLN.105	NE1, G.TRP.479	HE1, G.TRP.479	2.69	1.89	17.56
3SE9.PDB	OE1, G.GLU.91	NZ, G.LYS.487	HZ3, G.LYS.487	2.63	1.86	24.78
3SE9.PDB	OD1, H.ASP.81	NE, H.ARG.19	HE, H.ARG.19	2.75	1.91	10.76
3SE9.PDB	OH, H.TYR.90	NH1, H.ARG.38	HH11, H.ARG.38	2.99	2.21	21.73
3SE9.PDB	OD1, H.ASP.86	NH1, H.ARG.38	HH12, H.ARG.38	2.86	2.03	12.66
3SE9.PDB	OD1, G.ASN.280	NE1, H.TRP.50	HE1, H.TRP.50	2.86	2.03	11.46
3SE9.PDB	OG, G.SER.365	NH1, H.ARG.64	HH11, H.ARG.64	2.81	2.04	21.79
3SE9.PDB	OD2, H.ASP.86	NH2, H.ARG.66	HH22, H.ARG.66	2.37	1.62	23.34
3SE9.PDB	OD2, G.ASP.368	NH1, H.ARG.71	HH12, H.ARG.71	2.77	1.92	7.25
3SE9.PDB	OG, H.SER.21	ND1, H.HIS.79	HD1, H.HIS.79	2.69	1.93	23.16
3SE9.PDB	OG, H.SER.68	NH1, H.ARG.82A	HH12, H.ARG.82A	2.84	2.02	15.25
3SE9.PDB	OD1, H.ASP.101	NH2, H.ARG.94	HH21, H.ARG.94	2.74	1.90	10.49
3SE9.PDB	OH, H.TYR.100E	NE2, H.GLN.100B	HE22, H.GLN.100B	2.88	2.05	12.80
3SE9.PDB	OD1, G.ASN.279	NE1, H.TRP.100D	HE1, H.TRP.100D	2.86	2.13	26.83
3SE9.PDB	OG, H.SER.180	NE1, H.TRP.154	HE1, H.TRP.154	2.83	2.00	12.34
3SE9.PDB	OD1, L.ASN.138	NE2, H.HIS.164	HE2, H.HIS.164	2.87	2.10	22.18
3SE9.PDB	OD1, H.ASP.144	NE2, H.GLN.171	HE22, H.GLN.171	2.70	1.89	15.22
3SE9.PDB	OD1, H.ASP.208	ND2, H.ASN.197	HD21, H.ASN.197	2.90	2.07	13.74
3SE9.PDB	OG, H.SER.203	ND1, H.HIS.200	HD1, H.HIS.200	2.68	1.84	9.59
3SE9.PDB	OG, L.SER.131	NE2, L.GLN.124	HE21, L.GLN.124	2.87	2.02	8.09
3SE9.PDB	OG, L.SER.177	NE1, L.TRP.148	HE1, L.TRP.148	2.88	2.05	13.01

3SE9.PDB	OD1, L_ASP_170	OG1, L_THR_172	HG1, L_THR_172	2.48	1.71	16.29
3SE9.PDB	OE1, L_GLU_187	NZ, L_LYS_183	HZ3, L_LYS_183	2.82	2.09	29.82
3SE9.PDB	OD2, L_ASP_151	ND1, L_HIS_189	HD1, L_HIS_189	2.89	2.18	29.99
3THM.PDB	OD1, L_ASP_93	ND2, L_ASN_28	HD21, L_ASN_28	2.85	2.01	9.28
3THM.PDB	OH, L_TYR_87	NE2, L_GLN_38	HE21, L_GLN_38	2.86	2.05	16.36
3THM.PDB	OD1, L_ASP_83	NE, L_ARG_62	HE, L_ARG_62	2.86	2.03	12.52
3THM.PDB	OD2, L_ASP_83	NH2, L_ARG_62	HH21, L_ARG_62	2.63	1.79	10.74
3THM.PDB	OD2, L_ASP_78	NH1, L_ARG_77	HH11, L_ARG_77	2.79	2.00	19.01
3THM.PDB	OG, L_SER_180	NE1, L_TRP_152	HE1, L_TRP_152	2.84	1.99	7.64
3THM.PDB	OD1, L_ASP_142	NE2, L_GLN_171	HE22, L_GLN_171	2.87	2.03	8.80
3THM.PDB	OD1, L_ASP_155	ND1, L_HIS_192	HD1, L_HIS_192	2.84	1.98	0.83
3THM.PDB	OG1, L_THR_205	OG1, L_THR_200	HG1, L_THR_200	2.83	2.04	14.40
3THM.PDB	OE1, H_GLU_48	NE, H_ARG_40	HE, H_ARG_40	2.92	2.11	16.36
3THM.PDB	OD1, H_ASP_96	NH1, H_ARG_40	HH12, H_ARG_40	2.76	1.92	9.45
3THM.PDB	OE1, L_GLN_39	NE2, H_GLN_41	HE22, H_GLN_41	2.98	2.14	9.35
3THM.PDB	OG, H_SER_52	NE1, H_TRP_49	HE1, H_TRP_49	2.98	2.27	29.23
3THM.PDB	OD1, H_ASP_96	NH2, H_ARG_73	HH22, H_ARG_73	2.91	2.05	3.20
3THM.PDB	OD1, H_ASP_120	NE, H_ARG_104	HE, H_ARG_104	2.94	2.10	9.96
3THM.PDB	OD2, H_ASP_120	NH2, H_ARG_104	HH21, H_ARG_104	2.75	2.00	25.31
3THM.PDB	OD2, H_ASP_110	OG1, H_THR_112	HG1, H_THR_112	2.76	1.95	7.38
3THM.PDB	OD1, H_ASP_109	NE2, H_GLN_115	HE21, H_GLN_115	2.80	1.96	11.40
3THM.PDB	OG, L_SER_183	NZ, H_LYS_162	HZ1, H_LYS_162	2.77	1.97	21.34
3THM.PDB	OG1, L_THR_135	NZ, H_LYS_162	HZ2, H_LYS_162	2.85	2.02	17.75
3THM.PDB	OG, H_SER_199	NE1, H_TRP_173	HE1, H_TRP_173	3.00	2.15	7.78
3THM.PDB	OD1, H_ASP_227	ND2, H_ASN_216	HD22, H_ASN_216	2.86	2.03	14.19
3THM.PDB	OG, H_SER_222	ND1, H_HIS_219	HD1, H_HIS_219	2.82	2.08	24.90
3THM.PDB	OD2, F_ASP_56	ND1, F_HIS_38	HD1, F_HIS_38	2.77	1.98	19.59
3THM.PDB	OH, H_TYR_35	ND1, F_HIS_44	HD1, F_HIS_44	2.69	1.83	5.98
3THM.PDB	OG, H_SER_63	NE2, F_HIS_44	HE2, F_HIS_44	2.83	2.07	23.36
3TJE.PDB	OD1, L_ASP_93	ND2, L_ASN_28	HD21, L_ASN_28	2.73	1.89	10.95
3TJE.PDB	OD1, L_ASP_94	NH1, L_ARG_31	HH11, L_ARG_31	2.81	2.04	22.49
3TJE.PDB	OH, L_TYR_87	NE2, L_GLN_38	HE21, L_GLN_38	2.91	2.10	17.00
3TJE.PDB	OD2, L_ASP_83	NH1, L_ARG_62	HH12, L_ARG_62	2.77	1.98	19.25
3TJE.PDB	OD1, L_ASP_83	NH2, L_ARG_62	HH22, L_ARG_62	2.87	2.01	3.19
3TJE.PDB	OD2, L_ASP_78	NH1, L_ARG_77	HH11, L_ARG_77	2.74	1.93	16.91
3TJE.PDB	OE2, L_GLU_128	OG1, L_THR_135	HG1, L_THR_135	2.52	1.76	18.95
3TJE.PDB	OG, L_SER_180	NE1, L_TRP_152	HE1, L_TRP_152	2.95	2.10	8.91
3TJE.PDB	OD1, L_ASP_142	NE2, L_GLN_171	HE21, L_GLN_171	2.80	1.98	15.09
3TJE.PDB	OG1, L_THR_205	OG1, L_THR_200	HG1, L_THR_200	2.75	1.97	15.90
3TJE.PDB	OE1, H_GLU_48	NE, H_ARG_40	HE, H_ARG_40	2.72	1.90	14.58
3TJE.PDB	OD1, H_ASP_96	NH1, H_ARG_40	HH12, H_ARG_40	2.84	2.01	12.94
3TJE.PDB	OE1, L_GLN_39	NE2, H_GLN_41	HE21, H_GLN_41	2.98	2.15	10.85
3TJE.PDB	OD2, H_ASP_96	NH1, H_ARG_73	HH12, H_ARG_73	2.84	2.09	24.31
3TJE.PDB	OD1, H_ASP_96	NH2, H_ARG_73	HH22, H_ARG_73	2.94	2.09	3.77
3TJE.PDB	OD2, H_ASP_79	OG, H_SER_81	HG, H_SER_81	2.85	2.15	27.35
3TJE.PDB	OD1, H_ASP_120	NE, H_ARG_104	HE, H_ARG_104	2.87	2.06	15.55
3TJE.PDB	OD2, H_ASP_120	NH2, H_ARG_104	HH21, H_ARG_104	2.68	1.96	27.63
3TJE.PDB	OG, H_SER_199	NE1, H_TRP_173	HE1, H_TRP_173	2.95	2.10	8.21
3TJE.PDB	OD1, H_ASP_163	NE2, H_GLN_190	HE21, H_GLN_190	2.74	1.93	16.43
3TJE.PDB	OD1, H_ASP_227	ND2, H_ASN_216	HD22, H_ASN_216	2.79	1.98	17.28
3TJE.PDB	OG, H_SER_222	OG1, H_THR_224	HG1, H_THR_224	2.65	1.92	22.20
3TJE.PDB	OH, H_TYR_35	ND1, F_HIS_44	HD1, F_HIS_44	2.56	1.70	3.69
3TJE.PDB	OE2, F_GLU_98	NE, F_ARG_112	HE, F_ARG_112	2.97	2.20	22.98
3U2S.PDB	OE1, H_GLU_95	NE2, H_HIS_35	HE2, H_HIS_35	2.64	1.80	11.05
3U2S.PDB	OE2, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.80	2.01	18.34
3U2S.PDB	OD1, H_ASP_86	NH1, H_ARG_38	HH12, H_ARG_38	2.84	2.00	11.28
3U2S.PDB	OE2, H_GLU_46	NH2, H_ARG_38	HH21, H_ARG_38	2.92	2.18	25.81
3U2S.PDB	OE1, L_GLN_38	NE2, H_GLN_39	HE22, H_GLN_39	2.89	2.04	8.55

3U2S.PDB	OE1, H_GLU_46	OG, H_SER_62	HG, H_SER_62	2.75	1.94	7.42
3U2S.PDB	OD2, H_ASP_86	NH1, H_ARG_66	HH12, H_ARG_66	2.53	1.74	19.65
3U2S.PDB	OD1, H_ASP_86	NH2, H_ARG_66	HH22, H_ARG_66	2.93	2.08	7.53
3U2S.PDB	OD1, H_ASN_73	NE, H_ARG_71	HE, H_ARG_71	2.77	1.98	19.66
3U2S.PDB	OD1, H_ASP_101	NE, H_ARG_94	HE, H_ARG_94	2.95	2.09	2.87
3U2S.PDB	OD2, H_ASP_101	NH2, H_ARG_94	HH21, H_ARG_94	2.85	2.03	14.60
3U2S.PDB	OG, H_SER_180	NE1, H_TRP_154	HE1, H_TRP_154	2.93	2.08	7.46
3U2S.PDB	OG, L_SER_165	NE2, H_HIS_164	HE2, H_HIS_164	2.93	2.12	16.97
3U2S.PDB	OD2, H_ASP_144	NE2, H_GLN_171	HE22, H_GLN_171	2.87	2.09	20.57
3U2S.PDB	OD2, H_ASP_208	ND2, H_ASN_197	HD21, H_ASN_197	2.76	1.92	10.02
3U2S.PDB	OG, H_SER_203	ND1, H_HIS_200	HD1, H_HIS_200	2.77	1.92	6.39
3U2S.PDB	OG1, L_THR_74	OG1, L_THR_20	HG1, L_THR_20	2.83	2.11	23.78
3U2S.PDB	OD2, L_ASP_27B	OG1, L_THR_26	HG1, L_THR_26	2.86	2.11	19.40
3U2S.PDB	OH, L_TYR_86	NE2, L_GLN_37	HE21, L_GLN_37	2.82	1.97	2.95
3U2S.PDB	OE1, H_GLN_39	NE2, L_GLN_38	HE22, L_GLN_38	2.91	2.09	13.75
3U2S.PDB	OD2, L_ASP_50	NZ, L_LYS_53	HZ2, L_LYS_53	2.84	1.96	4.63
3U2S.PDB	OD2, C_ASP_167	ND2, L_ASN_60	HD22, L_ASN_60	2.90	2.14	22.76
3U2S.PDB	OD2, L_ASP_82	NH1, L_ARG_61	HH12, L_ARG_61	2.86	2.09	21.77
3U2S.PDB	OD1, L_ASP_82	NH2, L_ARG_61	HH22, L_ARG_61	2.97	2.11	4.14
3U2S.PDB	OE2, L_GLU_31	NZ, L_LYS_66	HZ1, L_LYS_66	2.99	2.15	15.69
3U2S.PDB	OD1, H_ASP_61	NH2, L_ARG_95A	HH22, L_ARG_95A	2.34	1.58	22.53
3U2S.PDB	OE2, H_GLU_95	NH2, L_ARG_96	HH21, L_ARG_96	2.87	2.05	15.72
3U2S.PDB	OE2, L_GLU_124	OG1, L_THR_131	HG1, L_THR_131	2.54	1.83	25.31
3U2S.PDB	OG, L_SER_176	NE1, L_TRP_148	HE1, L_TRP_148	2.93	2.09	11.15
3U2S.PDB	OD1, L_ASP_138	NE2, L_GLN_167	HE22, L_GLN_167	2.82	2.00	15.99
3U2S.PDB	OD1, L_ASP_138	ND2, L_ASN_169	HD22, L_ASN_169	2.92	2.10	15.30
3U2S.PDB	OG1, L_THR_201	OG1, L_THR_196	HG1, L_THR_196	2.99	2.20	12.41
3U2S.PDB	OH, H_TYR_100K	ND2, G_ASN_173	HD21, G_ASN_173	2.97	2.13	8.87
3U2S.PDB	OE1, A_GLN_81	NH1, A_ARG_19	HH11, A_ARG_19	2.87	2.10	22.03
3U2S.PDB	OE1, A_GLU_95	NE2, A_HIS_35	HE2, A_HIS_35	2.70	1.86	8.94
3U2S.PDB	OE2, A_GLU_46	NE, A_ARG_38	HE, A_ARG_38	2.74	1.98	23.65
3U2S.PDB	OH, A_TYR_90	NH1, A_ARG_38	HH11, A_ARG_38	2.88	2.07	17.44
3U2S.PDB	OD1, A_ASP_86	NH1, A_ARG_38	HH12, A_ARG_38	2.89	2.04	8.28
3U2S.PDB	OE2, A_GLU_46	NH2, A_ARG_38	HH21, A_ARG_38	2.90	2.18	27.83
3U2S.PDB	OE1, B_GLN_38	NE2, A_GLN_39	HE22, A_GLN_39	2.92	2.07	7.34
3U2S.PDB	OD2, A_ASP_86	NH1, A_ARG_66	HH12, A_ARG_66	2.48	1.66	13.42
3U2S.PDB	OD1, A_ASN_73	NE, A_ARG_71	HE, A_ARG_71	2.81	2.03	20.92
3U2S.PDB	OE1, A_GLU_85	NH1, A_ARG_83	HH11, A_ARG_83	2.91	2.14	21.39
3U2S.PDB	OD1, A_ASP_101	NE, A_ARG_94	HE, A_ARG_94	2.84	1.98	4.74
3U2S.PDB	OD2, A_ASP_101	NH2, A_ARG_94	HH21, A_ARG_94	2.90	2.12	20.79
3U2S.PDB	OG1, B_THR_131	NZ, A_LYS_143	HZ2, A_LYS_143	2.41	1.67	27.35
3U2S.PDB	OD2, A_ASP_144	NE2, A_GLN_171	HE22, A_GLN_171	2.82	1.98	10.06
3U2S.PDB	OG, A_SER_203	ND1, A_HIS_200	HD1, A_HIS_200	2.63	1.78	5.16
3U2S.PDB	OG1, B_THR_74	OG1, B_THR_20	HG1, B_THR_20	2.88	2.16	24.36
3U2S.PDB	OD2, B_ASP_27B	OG1, B_THR_26	HG1, B_THR_26	2.89	2.14	20.81
3U2S.PDB	OH, B_TYR_86	NE2, B_GLN_37	HE21, B_GLN_37	2.88	2.02	1.18
3U2S.PDB	OE1, A_GLN_39	NE2, B_GLN_38	HE22, B_GLN_38	2.92	2.08	10.61
3U2S.PDB	OD2, B_ASP_50	NZ, B_LYS_53	HZ2, B_LYS_53	2.75	1.88	8.80
3U2S.PDB	OD2, B_ASP_82	NH1, B_ARG_61	HH12, B_ARG_61	2.78	1.98	19.10
3U2S.PDB	OD1, B_ASP_82	NH2, B_ARG_61	HH22, B_ARG_61	2.93	2.07	0.82
3U2S.PDB	OD1, A_ASP_61	NH1, B_ARG_95A	HH12, B_ARG_95A	2.63	1.91	26.97
3U2S.PDB	OE2, A_GLU_95	NH2, B_ARG_96	HH21, B_ARG_96	2.98	2.16	13.77
3U2S.PDB	OG, B_SER_176	NE1, B_TRP_148	HE1, B_TRP_148	2.87	2.03	9.65
3U2S.PDB	OD1, B_ASN_169	NE2, B_GLN_167	HE21, B_GLN_167	2.93	2.16	22.14
3U2S.PDB	OD1, B_ASP_138	NE2, B_GLN_167	HE22, B_GLN_167	2.75	1.90	7.18
3U2S.PDB	OG1, B_THR_201	OG1, B_THR_196	HG1, B_THR_196	2.79	1.99	11.66
3UYR.PDB	OE1, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.84	2.03	16.92
3UYR.PDB	OD1, H_ASN_50	NE1, H_TRP_47	HE1, H_TRP_47	2.95	2.18	22.72

3UYR.PDB	OD1, H_ASP_105	NE, H_ARG_98	HE, H_ARG_98	2.98	2.16	14.38
3UYR.PDB	OD2, H_ASP_105	NH2, H_ARG_98	HH21, H_ARG_98	2.92	2.07	8.84
3UYR.PDB	OG, H_SER_183	NE1, H_TRP_158	HE1, H_TRP_158	2.93	2.08	7.42
3UYR.PDB	OG, H_SER_206	ND1, H_HIS_203	HD1, H_HIS_203	2.81	2.06	24.47
3UYR.PDB	OE2, L_GLU_127	NZ, H_LYS_212	HZ3, H_LYS_212	2.87	2.08	23.12
3UYR.PDB	OD2, L_ASP_87	NH1, L_ARG_66	HH12, L_ARG_66	2.92	2.12	17.99
3UYR.PDB	OG, L_SER_135	NE2, L_GLN_128	HE22, L_GLN_128	2.97	2.12	5.23
3UYR.PDB	OD1, L_ASP_174	OG1, L_THR_176	HG1, L_THR_176	2.78	1.97	7.90
3UYR.PDB	OD2, L_ASP_155	ND1, L_HIS_193	HD1, L_HIS_193	2.93	2.16	21.52
3UYR.PDB	ND2, L_ASN_216	ND2, L_ASN_194	HD22, L_ASN_194	2.90	2.18	28.48
3UYR.PDB	OG1, L_THR_204	ND1, L_HIS_202	HD1, L_HIS_202	2.78	1.93	6.06
3UYR.PDB	OD1, H_ASN_101	NE2, P_GLN_48	HE22, P_GLN_48	2.57	1.87	29.89
3X0E.PDB	OD1, A_ASP_122	NE2, A_GLN_118	HE21, A_GLN_118	2.93	2.22	29.07
3X0E.PDB	OD2, A_ASP_195	NZ, A_LYS_124	HZ1, A_LYS_124	3.00	2.19	21.32
3X0E.PDB	OD2, A_ASP_128	OG1, A_THR_161	HG1, A_THR_161	2.92	2.13	12.66
3X0E.PDB	OD1, A_ASP_155	NZ, A_LYS_187	HZ1, A_LYS_187	2.84	2.07	26.10
3X0E.PDB	OD1, B_ASP_195	NZ, B_LYS_124	HZ1, B_LYS_124	2.75	2.02	29.74
3X0E.PDB	OG, B_SER_159	OG1, B_THR_161	HG1, B_THR_161	2.79	1.98	7.89
3X0E.PDB	OD1, B_ASP_128	NE2, B_HIS_191	HE2, B_HIS_191	2.68	1.83	6.07
3X0F.PDB	OD1, A_ASP_195	NZ, A_LYS_124	HZ3, A_LYS_124	2.91	2.03	6.30
3X0F.PDB	OG, A_SER_159	OG1, A_THR_163	HG1, A_THR_163	2.77	1.96	7.35
3X0F.PDB	OD1, A_ASP_128	NE2, A_HIS_191	HE2, A_HIS_191	2.65	1.83	14.50
3X0F.PDB	OH, B_TYR_127	NE2, B_HIS_151	HE2, B_HIS_151	2.81	2.02	19.67
3X0F.PDB	OG1, B_THR_163	OG, B_SER_159	HG, B_SER_159	2.96	2.16	10.94
3X0F.PDB	OD1, B_ASP_128	NE2, B_HIS_191	HE2, B_HIS_191	2.69	1.83	1.74
4F33.PDB	OE1, B_GLN_39	NE2, A_GLN_38	HE22, A_GLN_38	2.96	2.13	12.75
4F33.PDB	OD2, A_ASP_82	NE, A_ARG_61	HE, A_ARG_61	2.81	2.09	28.09
4F33.PDB	OD1, A_ASP_82	NH2, A_ARG_61	HH21, A_ARG_61	2.71	1.85	4.82
4F33.PDB	OG1, A_THR_21	OG1, A_THR_74	HG1, A_THR_74	2.73	1.99	21.82
4F33.PDB	OG1, A_THR_97	NE2, A_GLN_90	HE21, A_GLN_90	2.97	2.15	14.62
4F33.PDB	OG, A_SER_13	NZ, A_LYS_107	HZ3, A_LYS_107	2.94	2.07	9.78
4F33.PDB	OG, A_SER_131	NE2, A_GLN_124	HE22, A_GLN_124	2.81	1.96	5.54
4F33.PDB	OG, A_SER_177	NE1, A_TRP_148	HE1, A_TRP_148	2.91	2.09	14.52
4F33.PDB	OE1, A_GLU_195	NZ, A_LYS_149	HZ2, A_LYS_149	2.59	1.85	28.21
4F33.PDB	OE1, A_GLN_155	ND2, A_ASN_158	HD22, A_ASN_158	2.89	2.06	12.00
4F33.PDB	OD1, A_ASP_170	OG1, A_THR_172	HG1, A_THR_172	2.68	1.86	4.02
4F33.PDB	OE1, A_GLN_38	NE2, B_GLN_39	HE22, B_GLN_39	2.82	1.97	5.31
4F33.PDB	OE2, B_GLU_46	NZ, B_LYS_63	HZ3, B_LYS_63	2.70	1.89	19.35
4F33.PDB	OD2, B_ASP_90	NZ, B_LYS_67	HZ2, B_LYS_67	2.73	1.86	7.48
4F33.PDB	OD2, B_ASP_107	NH2, B_ARG_98	HH21, B_ARG_98	2.74	1.88	6.50
4F33.PDB	OD1, B_ASP_102	NE, B_ARG_104	HE, B_ARG_104	2.87	2.03	8.81
4F33.PDB	OD2, B_ASP_107	NH1, B_ARG_104	HH11, B_ARG_104	2.78	1.96	13.74
4F33.PDB	OD2, B_ASP_102	NH2, B_ARG_104	HH21, B_ARG_104	2.87	2.08	19.19
4F33.PDB	OG, B_SER_186	NE1, B_TRP_160	HE1, B_TRP_160	2.97	2.13	10.43
4F33.PDB	OD1, B_ASP_150	NE2, B_GLN_177	HE22, B_GLN_177	2.84	2.07	21.15
4F33.PDB	OD1, B_ASP_214	ND2, B_ASN_203	HD21, B_ASN_203	2.97	2.12	8.15
4F33.PDB	OG, B_SER_209	ND1, B_HIS_206	HD1, B_HIS_206	2.61	1.78	12.57
4F33.PDB	OE1, A_GLU_123	NZ, B_LYS_215	HZ1, B_LYS_215	2.68	1.82	12.44
4F33.PDB	OG1, H_THR_211	NZ, B_LYS_215	HZ2, B_LYS_215	2.83	1.95	7.37
4F33.PDB	OD2, C_ASP_82	NE, C_ARG_61	HE, C_ARG_61	2.88	2.06	14.32
4F33.PDB	OD1, C_ASP_82	NH2, C_ARG_61	HH21, C_ARG_61	2.91	2.08	14.25
4F33.PDB	OG1, C_THR_21	OG1, C_THR_74	HG1, C_THR_74	2.68	1.93	19.90
4F33.PDB	OG, C_SER_13	NZ, C_LYS_107	HZ3, C_LYS_107	2.78	1.89	2.73
4F33.PDB	OG, C_SER_131	NE2, C_GLN_124	HE22, C_GLN_124	2.83	1.97	4.97
4F33.PDB	OG, C_SER_177	NE1, C_TRP_148	HE1, C_TRP_148	2.93	2.10	14.22
4F33.PDB	OE1, C_GLU_195	NZ, C_LYS_149	HZ2, C_LYS_149	2.67	1.88	22.11
4F33.PDB	OE1, C_GLN_155	ND2, C_ASN_158	HD22, C_ASN_158	2.91	2.09	15.33
4F33.PDB	OD1, C_ASP_170	OG1, C_THR_172	HG1, C_THR_172	2.72	1.91	5.07

4F33.PDB	OE1, C_GLN_38	NE2, D_GLN_39	HE22, D_GLN_39	2.89	2.03	5.23
4F33.PDB	OE2, D_GLU_46	NZ, D_LYS_63	HZ3, D_LYS_63	2.60	1.76	15.82
4F33.PDB	OD2, D_ASP_90	NZ, D_LYS_67	HZ2, D_LYS_67	2.76	2.03	29.11
4F33.PDB	OD2, D_ASP_107	NH2, D_ARG_98	HH21, D_ARG_98	2.74	1.89	7.29
4F33.PDB	OD1, D_ASP_102	NE, D_ARG_104	HE, D_ARG_104	2.89	2.05	10.59
4F33.PDB	OD2, D_ASP_107	NH1, D_ARG_104	HH11, D_ARG_104	2.83	2.01	15.77
4F33.PDB	OD2, D_ASP_102	NH2, D_ARG_104	HH21, D_ARG_104	2.91	2.10	15.53
4F33.PDB	OG, D_SER_186	NE1, D_TRP_160	HE1, D_TRP_160	3.00	2.15	9.78
4F33.PDB	OD1, D_ASP_150	NE2, D_GLN_177	HE22, D_GLN_177	2.86	2.09	21.57
4F33.PDB	OE1, C_GLU_123	NZ, D_LYS_215	HZ1, D_LYS_215	2.79	1.99	22.47
4F33.PDB	OG1, F_THR_211	NZ, D_LYS_215	HZ2, D_LYS_215	2.86	1.99	10.67
4F33.PDB	OG1, E_THR_74	OG1, E_THR_21	HG1, E_THR_21	2.80	2.03	17.05
4F33.PDB	OD2, E_ASP_82	NE, E_ARG_61	HE, E_ARG_61	2.93	2.08	6.42
4F33.PDB	OD1, E_ASP_82	NH2, E_ARG_61	HH21, E_ARG_61	2.82	1.98	9.42
4F33.PDB	OG1, E_THR_97	NE2, E_GLN_90	HE21, E_GLN_90	2.99	2.17	14.98
4F33.PDB	OG, E_SER_131	NE2, E_GLN_124	HE22, E_GLN_124	2.81	1.95	4.17
4F33.PDB	OG, E_SER_177	NE1, E_TRP_148	HE1, E_TRP_148	2.88	2.05	13.86
4F33.PDB	OE1, E_GLU_195	NZ, E_LYS_149	HZ2, E_LYS_149	2.77	1.97	22.37
4F33.PDB	OE1, E_GLN_155	ND2, E_ASN_158	HD22, E_ASN_158	2.91	2.08	12.67
4F33.PDB	OD1, E_ASP_170	OG1, E_THR_172	HG1, E_THR_172	2.66	1.85	7.41
4F33.PDB	OE1, E_GLN_38	NE2, F_GLN_39	HE22, F_GLN_39	2.92	2.06	5.53
4F33.PDB	OE2, F_GLU_46	NZ, F_LYS_63	HZ3, F_LYS_63	2.68	1.79	3.79
4F33.PDB	OD2, F_ASP_90	NZ, F_LYS_67	HZ2, F_LYS_67	2.98	2.09	4.59
4F33.PDB	OD1, F_ASP_107	NE, F_ARG_98	HE, F_ARG_98	2.99	2.13	4.74
4F33.PDB	OD2, F_ASP_107	NH2, F_ARG_98	HH21, F_ARG_98	2.77	1.91	5.42
4F33.PDB	OD1, F_ASP_102	NE, F_ARG_104	HE, F_ARG_104	2.84	1.99	7.33
4F33.PDB	OD2, F_ASP_107	NH1, F_ARG_104	HH11, F_ARG_104	2.84	2.02	14.35
4F33.PDB	OD2, F_ASP_102	NH2, F_ARG_104	HH21, F_ARG_104	2.90	2.10	17.22
4F33.PDB	OG, F_SER_186	NE1, F_TRP_160	HE1, F_TRP_160	3.00	2.15	9.04
4F33.PDB	OD1, F_ASP_150	NE2, F_GLN_177	HE22, F_GLN_177	2.82	2.02	17.76
4F33.PDB	OD1, F_ASP_214	ND2, F_ASN_203	HD21, F_ASN_203	2.95	2.10	8.40
4F33.PDB	OG, F_SER_209	ND1, F_HIS_206	HD1, F_HIS_206	2.64	1.82	13.68
4F33.PDB	OE1, E_GLU_123	NZ, F_LYS_215	HZ1, F_LYS_215	2.61	1.84	24.34
4F33.PDB	OG1, D_THR_211	NZ, F_LYS_215	HZ2, F_LYS_215	2.92	2.04	7.71
4F33.PDB	OG1, G_THR_74	OG1, G_THR_21	HG1, G_THR_21	2.73	1.97	18.47
4F33.PDB	OD1, G_ASP_82	NH2, G_ARG_61	HH21, G_ARG_61	2.73	1.89	8.68
4F33.PDB	OE2, G_GLU_81	NH2, G_ARG_61	HH22, G_ARG_61	2.96	2.16	17.92
4F33.PDB	OG, G_SER_131	NE2, G_GLN_124	HE22, G_GLN_124	2.79	1.93	5.18
4F33.PDB	OG, G_SER_177	NE1, G_TRP_148	HE1, G_TRP_148	2.87	2.04	13.06
4F33.PDB	OE1, G_GLN_155	ND2, G_ASN_158	HD22, G_ASN_158	2.92	2.10	14.66
4F33.PDB	OD1, G_ASP_170	OG1, G_THR_172	HG1, G_THR_172	2.69	1.89	8.34
4F33.PDB	OD2, G_ASP_151	ND1, G_HIS_189	HD1, G_HIS_189	2.86	2.09	22.44
4F33.PDB	OE2, H_GLU_46	NZ, H_LYS_63	HZ3, H_LYS_63	2.72	1.93	23.08
4F33.PDB	OD2, H_ASP_90	NZ, H_LYS_67	HZ2, H_LYS_67	2.82	1.98	16.29
4F33.PDB	OD1, H_ASP_107	NE, H_ARG_98	HE, H_ARG_98	2.95	2.15	18.92
4F33.PDB	OD2, H_ASP_107	NH2, H_ARG_98	HH21, H_ARG_98	2.79	1.95	8.93
4F33.PDB	OD1, H_ASP_102	NE, H_ARG_104	HE, H_ARG_104	2.85	2.00	6.80
4F33.PDB	OD2, H_ASP_107	NH1, H_ARG_104	HH11, H_ARG_104	2.85	2.04	16.23
4F33.PDB	OD2, H_ASP_102	NH2, H_ARG_104	HH21, H_ARG_104	2.93	2.12	16.50
4F33.PDB	OG, H_SER_186	NE1, H_TRP_160	HE1, H_TRP_160	2.99	2.15	10.12
4F33.PDB	OD1, H_ASP_150	NE2, H_GLN_177	HE22, H_GLN_177	2.83	2.04	19.22
4F33.PDB	OD1, H_ASP_214	ND2, H_ASN_203	HD21, H_ASN_203	2.91	2.05	5.75
4F33.PDB	OE1, G_GLU_123	NZ, H_LYS_215	HZ1, H_LYS_215	2.97	2.19	24.10
4F33.PDB	OG1, B_THR_211	NZ, H_LYS_215	HZ2, H_LYS_215	2.80	1.95	14.49
4F3F.PDB	OE1, B_GLN_39	NE2, A_GLN_38	HE22, A_GLN_38	2.88	2.04	8.75
4F3F.PDB	OD1, A_ASP_82	NH2, A_ARG_61	HH21, A_ARG_61	2.60	1.79	16.27
4F3F.PDB	OE2, A_GLU_81	NH2, A_ARG_61	HH22, A_ARG_61	2.95	2.12	13.66
4F3F.PDB	OG1, A_THR_21	OG1, A_THR_74	HG1, A_THR_74	2.77	2.04	22.11

4F3F.PDB	OG, B.SER.59	NE2, A.HIS.94	HE2, A.HIS.94	2.82	2.03	19.68
4F3F.PDB	OG, A.SER.131	NE2, A.GLN.124	HE22, A.GLN.124	2.84	2.05	19.05
4F3F.PDB	OD1, A.ASP.170	OG1, A.THR.172	HG1, A.THR.172	2.85	2.05	10.97
4F3F.PDB	OD1, B.ASN.35	NE1, B.TRP.47	HE1, B.TRP.47	2.99	2.19	19.59
4F3F.PDB	OD2, B.ASP.90	NZ, B.LYS.67	HZ2, B.LYS.67	2.92	2.05	9.99
4F3F.PDB	OD2, B.ASP.107	NH2, B.ARG.98	HH21, B.ARG.98	2.79	1.95	9.80
4F3F.PDB	OD1, A.ASN.138	NE2, B.HIS.170	HE2, B.HIS.170	2.82	2.05	21.56
4F3F.PDB	OD1, B.ASP.150	NE2, B.GLN.177	HE22, B.GLN.177	2.87	2.13	25.54
4F3F.PDB	OG, B.SER.209	ND1, B.HIS.206	HD1, B.HIS.206	2.43	1.61	13.98
4F3F.PDB	OH, B.TYR.101	NZ, C.LYS.25	HZ3, C.LYS.25	2.87	2.11	26.18
4F3F.PDB	OH, A.TYR.32	NE1, C.TRP.26	HE1, C.TRP.26	2.97	2.17	18.16
4F3F.PDB	OE2, C.GLU.15	NH2, C.ARG.43	HH21, C.ARG.43	2.88	2.04	9.30
4JAM.PDB	OE2, H.GLU.46	NE, H.ARG.38	HE, H.ARG.38	2.93	2.10	13.53
4JAM.PDB	OH, H.TYR.90	NH1, H.ARG.38	HH11, H.ARG.38	2.92	2.12	17.99
4JAM.PDB	OD1, H.ASP.86	NH1, H.ARG.38	HH12, H.ARG.38	2.91	2.07	10.41
4JAM.PDB	OD1, H.ASP.86	NH2, H.ARG.66	HH22, H.ARG.66	2.96	2.12	9.52
4JAM.PDB	OD1, H.ASP.144	NZ, H.LYS.143	HZ2, H.LYS.143	3.00	2.12	8.81
4JAM.PDB	OG, H.SER.180	NE1, H.TRP.154	HE1, H.TRP.154	2.95	2.10	8.20
4JAM.PDB	OG, H.SER.180	OG1, H.THR.165	HG1, H.THR.165	2.85	2.09	18.68
4JAM.PDB	OG, H.SER.203	ND1, H.HIS.200	HD1, H.HIS.200	2.70	1.91	20.45
4JAM.PDB	OD1, H.ASN.100B	ND2, L.ASN.32	HD21, L.ASN.32	2.96	2.21	25.94
4JAM.PDB	OH, L.TYR.86	NE2, L.GLN.37	HE21, L.GLN.37	2.92	2.07	7.82
4JAM.PDB	OE1, L.GLU.50	NZ, L.LYS.53	HZ1, L.LYS.53	2.81	1.96	13.53
4JAM.PDB	OD2, L.ASP.82	NE, L.ARG.61	HE, L.ARG.61	2.81	2.02	19.36
4JAM.PDB	OD1, L.ASP.82	NH2, L.ARG.61	HH21, L.ARG.61	2.93	2.10	13.29
4JAM.PDB	OH, L.TYR.172	NH2, L.ARG.107	HH22, L.ARG.107	2.87	2.14	27.08
4JAM.PDB	OE1, L.GLU.198	NZ, L.LYS.110	HZ2, L.LYS.110	2.60	1.75	13.04
4JAM.PDB	OE2, L.GLU.124	OG1, L.THR.131	HG1, L.THR.131	2.56	1.86	25.46
4JAM.PDB	OG, L.SER.176	NE1, L.TRP.148	HE1, L.TRP.148	2.87	2.03	8.58
4JAM.PDB	OE1, L.GLU.203	NZ, L.LYS.149	HZ2, L.LYS.149	2.76	1.94	19.38
4JAM.PDB	OG, L.SER.192	OG1, L.THR.205	HG1, L.THR.205	2.80	2.01	12.51
4JAM.PDB	OE1, A.GLU.75	NE1, A.TRP.34	HE1, A.TRP.34	2.65	1.81	8.69
4JAM.PDB	OH, A.TYR.90	NH1, A.ARG.38	HH11, A.ARG.38	2.87	2.07	18.01
4JAM.PDB	OD1, A.ASP.86	NH1, A.ARG.38	HH12, A.ARG.38	2.79	1.96	13.17
4JAM.PDB	OD2, A.ASP.86	NH2, A.ARG.66	HH22, A.ARG.66	2.34	1.63	27.75
4JAM.PDB	OG, A.SER.180	NE1, A.TRP.154	HE1, A.TRP.154	2.95	2.10	7.51
4JAM.PDB	OD1, A.ASP.208	ND2, A.ASN.197	HD21, A.ASN.197	2.90	2.10	17.20
4JAM.PDB	OG, A.SER.203	ND1, A.HIS.200	HD1, A.HIS.200	2.74	1.92	14.00
4JAM.PDB	OE1, B.GLU.50	NZ, B.LYS.53	HZ1, B.LYS.53	2.75	1.92	17.48
4JAM.PDB	OD2, B.ASP.82	NE, B.ARG.61	HE, B.ARG.61	2.84	2.00	9.73
4JAM.PDB	OD1, B.ASP.82	NH2, B.ARG.61	HH21, B.ARG.61	2.90	2.08	13.97
4JAM.PDB	OE2, B.GLU.124	OG1, B.THR.131	HG1, B.THR.131	2.53	1.82	24.30
4JAM.PDB	OG, B.SER.176	NE1, B.TRP.148	HE1, B.TRP.148	2.84	1.99	9.50
4JAM.PDB	OD1, B.ASP.138	ND2, B.ASN.169	HD22, B.ASN.169	2.93	2.14	18.27
4JAM.PDB	OG, B.SER.192	OG1, B.THR.205	HG1, B.THR.205	2.64	1.83	8.66
4JAN.PDB	OD2, G.ASP.457	NE, G.ARG.469	HE, G.ARG.469	2.84	2.10	25.29
4JAN.PDB	OE1, H.GLU.46	NE, H.ARG.38	HE, H.ARG.38	2.76	1.94	14.56
4JAN.PDB	OG, H.SER.180	NE1, H.TRP.154	HE1, H.TRP.154	2.82	2.02	18.56
4JAN.PDB	OD2, B.ASP.92	OG, H.SER.156	HG, H.SER.156	2.50	1.78	23.90
4JAN.PDB	OG, H.SER.203	ND1, H.HIS.200	HD1, H.HIS.200	2.81	1.96	7.87
4JAN.PDB	OD1, H.ASN.199	NZ, H.LYS.201	HZ2, H.LYS.201	2.90	2.05	14.58
4JAN.PDB	OE1, L.GLU.123	NZ, H.LYS.209	HZ1, H.LYS.209	2.89	2.13	26.71
4JAN.PDB	OG1, L.THR.102	NE2, L.GLN.6	HE21, L.GLN.6	2.82	2.05	22.18
4JAN.PDB	OD1, H.ASN.100B	ND2, L.ASN.32	HD21, L.ASN.32	2.76	1.91	6.44
4JAN.PDB	OH, L.TYR.86	NE2, L.GLN.37	HE21, L.GLN.37	2.95	2.09	6.42
4JAN.PDB	OG, L.SER.176	NE1, L.TRP.148	HE1, L.TRP.148	2.88	2.04	9.05
4JAN.PDB	OG, A.SER.180	NE1, A.TRP.154	HE1, A.TRP.154	2.82	2.05	22.21
4JAN.PDB	OE2, B.GLU.124	OG1, B.THR.131	HG1, B.THR.131	2.64	1.97	29.01

4JAN.PDB	OG, B_SER_176	NE1, B_TRP_148	HE1, B_TRP_148	2.83	1.98	7.29
4KRM.PDB	OE1, B_GLU_110	NH1, A_ARG_353	HH11, A_ARG_353	2.81	2.05	22.81
4KRM.PDB	OD2, A_ASP_355	OG1, A_THR_358	HG1, A_THR_358	2.65	1.94	26.40
4KRM.PDB	OE1, A_GLU_376	NE, A_ARG_403	HE, A_ARG_403	2.51	1.78	27.17
4KRM.PDB	OD1, A_ASP_434	NZ, A_LYS_407	HZ1, A_LYS_407	2.92	2.12	20.92
4KRM.PDB	OE2, A_GLU_431	OG, A_SER_433	HG, A_SER_433	2.82	2.09	25.22
4KRM.PDB	OD1, B_ASP_80	NE, B_ARG_19	HE, B_ARG_19	2.67	1.85	15.03
4KRM.PDB	OH, B_TYR_94	NH1, B_ARG_38	HH11, B_ARG_38	2.87	2.05	14.24
4KRM.PDB	OD2, B_ASP_90	NH1, B_ARG_38	HH12, B_ARG_38	2.85	2.02	12.95
4KRM.PDB	OE1, D_GLU_110	NH1, C_ARG_353	HH11, C_ARG_353	2.87	2.05	16.15
4KRM.PDB	OD2, C_ASP_355	OG1, C_THR_358	HG1, C_THR_358	2.75	2.00	22.12
4KRM.PDB	OE1, C_GLU_376	NH1, C_ARG_403	HH11, C_ARG_403	3.00	2.18	16.51
4KRM.PDB	OD1, C_ASP_498	NH2, C_ARG_427	HH21, C_ARG_427	2.43	1.69	25.29
4KRM.PDB	OE2, C_GLU_431	OG, C_SER_433	HG, C_SER_433	2.86	2.06	14.79
4KRM.PDB	OE1, C_GLU_489	NZ, C_LYS_455	HZ2, C_LYS_455	2.73	1.95	24.04
4KRM.PDB	OE1, D_GLN_82	NH1, D_ARG_19	HH11, D_ARG_19	2.94	2.12	14.24
4KRM.PDB	OD2, C_ASP_355	NH1, D_ARG_30	HH12, D_ARG_30	2.45	1.63	13.53
4KRM.PDB	OE1, D_GLU_46	NE, D_ARG_38	HE, D_ARG_38	2.79	1.96	12.48
4KRM.PDB	OE1, F_GLU_110	NH1, E_ARG_353	HH11, E_ARG_353	2.85	2.03	14.34
4KRM.PDB	OD2, F_ASP_112	NH2, E_ARG_353	HH22, E_ARG_353	2.96	2.18	20.33
4KRM.PDB	OD2, E_ASP_355	OG1, E_THR_358	HG1, E_THR_358	2.55	1.85	27.90
4KRM.PDB	OD1, E_ASP_434	NZ, E_LYS_407	HZ1, E_LYS_407	2.65	1.88	23.95
4KRM.PDB	OE2, E_GLU_431	OG, E_SER_433	HG, E_SER_433	2.91	2.17	23.57
4KRM.PDB	OE1, F_GLU_46	NE, F_ARG_38	HE, F_ARG_38	2.74	1.95	18.99
4KRM.PDB	OD2, F_ASP_90	NH1, F_ARG_38	HH12, F_ARG_38	2.95	2.22	27.79
4KRM.PDB	OE1, F_GLU_46	NH2, F_ARG_38	HH21, F_ARG_38	2.97	2.26	28.90
4KRM.PDB	OG, F_SER_57	NE1, F_TRP_104	HE1, F_TRP_104	3.00	2.20	18.23
4KRM.PDB	OE2, G_GLU_320	ND2, G_ASN_314	HD22, G_ASN_314	2.93	2.08	7.68
4KRM.PDB	OD2, G_ASP_355	OG1, G_THR_358	HG1, G_THR_358	2.44	1.73	26.83
4KRM.PDB	OE2, B_GLU_5	NZ, G_LYS_407	HZ1, G_LYS_407	2.98	2.17	20.60
4KRM.PDB	OD1, G_ASP_498	NE, G_ARG_427	HE, G_ARG_427	2.63	1.82	16.62
4KRM.PDB	OE2, G_GLU_431	OG, G_SER_433	HG, G_SER_433	2.90	2.13	19.38
4KRM.PDB	OD2, G_ASP_436	NZ, G_LYS_463	HZ3, G_LYS_463	2.68	1.83	13.12
4KRM.PDB	OD1, H_ASP_80	OG1, H_THR_21	HG1, H_THR_21	2.86	2.06	13.63
4KRM.PDB	OD2, G_ASP_355	NH1, H_ARG_30	HH12, H_ARG_30	2.45	1.69	23.45
4KRM.PDB	OH, H_TYR_94	NH1, H_ARG_38	HH11, H_ARG_38	2.96	2.15	17.21
4KRM.PDB	OD2, H_ASP_90	NH1, H_ARG_38	HH12, H_ARG_38	2.78	1.94	11.87
4KRM.PDB	OE1, J_GLU_110	NH1, I_ARG_353	HH11, I_ARG_353	2.86	2.07	18.90
4KRM.PDB	OD2, J_ASP_112	NH2, I_ARG_353	HH22, I_ARG_353	3.00	2.19	17.61
4KRM.PDB	OE1, I_GLU_376	NH1, I_ARG_403	HH11, I_ARG_403	2.44	1.73	28.52
4KRM.PDB	OE2, I_GLU_431	OG, I_SER_433	HG, I_SER_433	2.91	2.09	9.73
4KRM.PDB	OD1, I_ASN_469	ND2, I_ASN_442	HD22, I_ASN_442	2.76	1.93	12.03
4KRM.PDB	OD1, I_ASN_473	OG, I_SER_474	HG, I_SER_474	2.73	1.91	11.26
4KRM.PDB	OD1, J_ASP_80	NE, J_ARG_19	HE, J_ARG_19	2.78	1.97	16.74
4KRM.PDB	OH, J_TYR_94	NH1, J_ARG_38	HH11, J_ARG_38	2.85	2.02	12.10
4KRM.PDB	OD2, J_ASP_90	NH1, J_ARG_38	HH12, J_ARG_38	2.97	2.15	14.05
4KRM.PDB	OD1, J_ASP_90	NH2, J_ARG_67	HH22, J_ARG_67	2.61	1.77	10.49
4KRM.PDB	OD1, J_ASN_74	NE, J_ARG_72	HE, J_ARG_72	2.67	1.87	16.97
4KRM.PDB	OG, J_SER_57	NE1, J_TRP_104	HE1, J_TRP_104	2.98	2.26	28.43
4KRM.PDB	OE1, L_GLU_110	NH1, K_ARG_353	HH11, K_ARG_353	2.89	2.06	12.41
4KRM.PDB	OD2, L_ASP_112	NH2, K_ARG_353	HH22, K_ARG_353	2.89	2.07	13.96
4KRM.PDB	OD2, K_ASP_355	OG1, K_THR_358	HG1, K_THR_358	2.91	2.21	28.73
4KRM.PDB	OD1, L_ASP_80	NE, L_ARG_19	HE, L_ARG_19	2.96	2.10	5.59
4KRM.PDB	OD2, K_ASP_355	NH1, L_ARG_30	HH12, L_ARG_30	2.44	1.65	18.93
4KRM.PDB	OE1, L_GLU_46	NE, L_ARG_38	HE, L_ARG_38	2.86	2.01	10.17
4KRM.PDB	OD1, L_ASP_90	NH2, L_ARG_67	HH22, L_ARG_67	2.60	1.80	17.17
4KRO.PDB	OG1, A_THR_278	OG, A_SER_282	HG, A_SER_282	2.99	2.27	26.50
4KRO.PDB	OE2, A_GLU_376	NH2, A_ARG_310	HH21, A_ARG_310	2.98	2.18	18.33

4KRO.PDB	OD2, A_ASP_355	OG1, A_THR_358	HG1, A_THR_358	2.98	2.18	14.96
4KRO.PDB	OG, B_SER_103	NZ, A_LYS_375	HZ2, A_LYS_375	2.61	1.76	15.34
4KRO.PDB	OH, D_TYR_102	NE2, A_GLN_384	HE21, A_GLN_384	2.87	2.16	29.24
4KRO.PDB	OD1, B_ASP_118	NE, A_ARG_405	HE, A_ARG_405	2.72	1.93	19.48
4KRO.PDB	OD1, A_ASP_498	NH2, A_ARG_427	HH21, A_ARG_427	2.62	1.82	18.67
4KRO.PDB	OD1, A_ASN_469	ND2, A_ASN_442	HD22, A_ASN_442	2.75	1.96	18.83
4KRO.PDB	OG, A_SER_501	OG, A_SER_487	HG, A_SER_487	2.37	1.68	29.03
4KRO.PDB	OD1, A_ASN_504	NH1, A_ARG_503	HH11, A_ARG_503	2.52	1.76	23.61
4KRO.PDB	OG1, A_THR_548	ND2, A_ASN_554	HD22, A_ASN_554	2.92	2.13	19.09
4KRO.PDB	OE1, C_GLN_89	OH, C_TYR_36	HH, C_TYR_36	2.63	1.80	6.46
4KRO.PDB	OH, C_TYR_86	NE2, C_GLN_37	HE21, C_GLN_37	2.94	2.13	16.57
4KRO.PDB	OE1, D_GLN_39	NE2, C_GLN_38	HE22, C_GLN_38	2.85	2.00	7.50
4KRO.PDB	OD2, D_ASP_103	OH, C_TYR_50	HH, C_TYR_50	2.49	1.72	20.15
4KRO.PDB	OD1, C_ASP_82	NH2, C_ARG_61	HH21, C_ARG_61	2.64	1.81	12.76
4KRO.PDB	OD1, D_ASP_103	ND2, C_ASN_91	HD21, C_ASN_91	2.93	2.12	16.18
4KRO.PDB	OD1, C_ASN_32	ND2, C_ASN_92	HD22, C_ASN_92	2.97	2.20	23.59
4KRO.PDB	OD2, D_ASP_58	NE1, C_TRP_94	HE1, C_TRP_94	2.80	2.10	29.15
4KRO.PDB	OG, C_SER_131	NE2, C_GLN_124	HE22, C_GLN_124	2.85	2.00	6.78
4KRO.PDB	OG, C_SER_177	NE1, C_TRP_148	HE1, C_TRP_148	2.83	2.01	15.90
4KRO.PDB	OE1, C_GLN_155	ND2, C_ASN_158	HD21, C_ASN_158	2.72	1.97	24.54
4KRO.PDB	OD1, C_ASP_170	OG1, C_THR_172	HG1, C_THR_172	2.68	1.86	11.97
4KRO.PDB	OE1, D_GLU_46	NE, D_ARG_38	HE, D_ARG_38	3.00	2.22	20.92
4KRO.PDB	OH, D_TYR_93	NH1, D_ARG_38	HH11, D_ARG_38	2.92	2.15	22.16
4KRO.PDB	OE1, D_GLU_46	NH2, D_ARG_38	HH21, D_ARG_38	2.98	2.22	22.99
4KRO.PDB	OE1, C_GLN_38	NE2, D_GLN_39	HE22, D_GLN_39	2.80	1.94	4.32
4KRO.PDB	OH, D_TYR_59	OG1, D_THR_57	HG1, D_THR_57	2.96	2.15	12.78
4KRO.PDB	OE1, A_GLN_408	OH, D_TYR_102	HH, D_TYR_102	2.75	1.97	18.39
4KRO.PDB	OG, D_SER_209	ND1, D_HIS_206	HD1, D_HIS_206	2.71	1.87	9.56
4KRP.PDB	OE2, A_GLU_376	NH2, A_ARG_310	HH21, A_ARG_310	2.93	2.09	9.81
4KRP.PDB	OD1, B_ASP_115	NH2, A_ARG_405	HH21, A_ARG_405	2.63	1.81	15.48
4KRP.PDB	OD1, A_ASP_498	NE, A_ARG_427	HE, A_ARG_427	2.55	1.82	26.18
4KRP.PDB	OD1, A_ASP_498	NH2, A_ARG_427	HH21, A_ARG_427	2.59	1.89	29.61
4KRP.PDB	OE2, A_GLU_431	OG, A_SER_433	HG, A_SER_433	2.69	1.90	15.48
4KRP.PDB	OD1, A_ASN_469	ND2, A_ASN_442	HD22, A_ASN_442	2.94	2.17	23.18
4KRP.PDB	OD1, D_ASP_58	NZ, A_LYS_443	HZ1, A_LYS_443	2.65	1.82	17.69
4KRP.PDB	OE1, A_GLU_489	NZ, A_LYS_455	HZ2, A_LYS_455	2.95	2.19	25.72
4KRP.PDB	OD2, D_ASP_103	NZ, A_LYS_465	HZ2, A_LYS_465	2.93	2.05	5.06
4KRP.PDB	OG, A_SER_474	NE, A_ARG_470	HE, A_ARG_470	2.76	1.96	18.13
4KRP.PDB	OG, A_SER_501	OG, A_SER_487	HG, A_SER_487	2.45	1.66	16.67
4KRP.PDB	OE1, A_GLU_495	NE, A_ARG_497	HE, A_ARG_497	2.60	1.79	14.71
4KRP.PDB	OE1, A_GLU_524	NE, A_ARG_507	HE, A_ARG_507	2.83	2.04	19.78
4KRP.PDB	OE2, A_GLU_527	NH2, A_ARG_550	HH22, A_ARG_550	2.54	1.76	21.10
4KRP.PDB	OD1, C_ASN_92	ND2, C_ASN_32	HD22, C_ASN_32	2.85	2.14	29.38
4KRP.PDB	OE1, C_GLN_89	OH, C_TYR_36	HH, C_TYR_36	2.33	1.50	6.36
4KRP.PDB	OH, C_TYR_86	NE2, C_GLN_37	HE21, C_GLN_37	2.85	2.02	13.51
4KRP.PDB	OE1, D_GLN_39	NE2, C_GLN_38	HE22, C_GLN_38	2.70	1.84	6.09
4KRP.PDB	OE1, C_GLU_53	NZ, C_LYS_49	HZ3, C_LYS_49	2.81	1.93	8.64
4KRP.PDB	OD2, D_ASP_103	OH, C_TYR_50	HH, C_TYR_50	2.43	1.66	18.96
4KRP.PDB	OD1, C_ASP_82	NH2, C_ARG_61	HH21, C_ARG_61	2.79	1.98	15.39
4KRP.PDB	OG1, C_THR_96	NE2, C_GLN_89	HE21, C_GLN_89	2.69	1.93	23.74
4KRP.PDB	OD1, D_ASP_103	ND2, C_ASN_91	HD21, C_ASN_91	2.77	1.91	6.24
4KRP.PDB	OD1, C_ASN_93	ND2, C_ASN_92	HD22, C_ASN_92	2.69	1.97	27.74
4KRP.PDB	OD2, D_ASP_58	NE1, C_TRP_94	HE1, C_TRP_94	2.98	2.17	17.26
4KRP.PDB	OE2, C_GLU_105	NZ, C_LYS_103	HZ1, C_LYS_103	2.82	2.05	25.15
4KRP.PDB	OG, C_SER_131	NE2, C_GLN_124	HE22, C_GLN_124	2.89	2.10	19.98
4KRP.PDB	OE1, C_GLN_155	ND2, C_ASN_158	HD21, C_ASN_158	2.83	2.12	29.23
4KRP.PDB	OD1, C_ASP_170	OG1, C_THR_172	HG1, C_THR_172	2.53	1.69	5.91
4KRP.PDB	OG1, D_THR_113	NE2, D_GLN_6	HE21, D_GLN_6	2.88	2.03	4.76

4KRP.PDB	OH, D_TYR_93	NH1, D_ARG_38	HH11, D_ARG_38	2.96	2.18	20.80
4KRP.PDB	OD1, D_ASP_89	NH1, D_ARG_38	HH12, D_ARG_38	2.91	2.06	7.49
4KRP.PDB	OE1, C_GLN_38	NE2, D_GLN_39	HE22, D_GLN_39	2.72	1.87	5.47
4KRP.PDB	OD1, D_ASP_89	NH2, D_ARG_66	HH22, D_ARG_66	2.59	1.74	9.60
4KRP.PDB	OE1, A_GLN_408	OH, D_TYR_102	HH, D_TYR_102	2.56	1.74	10.00
4KRP.PDB	OG, A_SER_440	OH, D_TYR_104	HH, D_TYR_104	2.94	2.22	25.72
4KRP.PDB	OD1, D_ASP_214	ND2, D_ASN_203	HD22, D_ASN_203	2.70	1.84	4.78
4KRP.PDB	OG, D_SER_209	ND1, D_HIS_206	HD1, D_HIS_206	2.94	2.08	3.63
4KRP.PDB	OG, D_SER_209	OG1, D_THR_211	HG1, D_THR_211	2.56	1.87	28.78
4KRP.PDB	OE1, A_GLU_431	OH, B_TYR_32	HH, B_TYR_32	2.59	1.78	7.49
4KRP.PDB	OE1, A_GLU_400	OH, B_TYR_100	HH, B_TYR_100	2.94	2.13	13.29
4KRP.PDB	OE2, A_GLU_431	OH, B_TYR_116	HH, B_TYR_116	2.43	1.75	29.09
4NZR.PDB	OE1, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.83	2.07	23.07
4NZR.PDB	OH, H_TYR_90	NH1, H_ARG_38	HH11, H_ARG_38	2.96	2.16	17.91
4NZR.PDB	OD1, H_ASP_86	NH1, H_ARG_38	HH12, H_ARG_38	2.73	1.88	7.20
4NZR.PDB	OE1, H_GLU_46	NH2, H_ARG_38	HH21, H_ARG_38	2.78	2.02	22.98
4NZR.PDB	OG, H_SER_50	NE1, H_TRP_47	HE1, H_TRP_47	2.87	2.03	11.63
4NZR.PDB	OD1, H_ASP_31G	NE2, H_HIS_52	HE2, H_HIS_52	2.60	1.83	22.01
4NZR.PDB	OD1, H_ASP_31G	NE1, H_TRP_53	HE1, H_TRP_53	2.92	2.20	28.43
4NZR.PDB	OD2, H_ASP_86	NH1, H_ARG_66	HH12, H_ARG_66	2.98	2.20	21.88
4NZR.PDB	OD1, H_ASP_101	NE, H_ARG_94	HE, H_ARG_94	2.90	2.05	5.79
4NZR.PDB	OD2, H_ASP_101	NH2, H_ARG_94	HH21, H_ARG_94	2.73	1.90	13.79
4NZR.PDB	OG, H_SER_50	ND1, H_HIS_95	HD1, H_HIS_95	2.67	1.84	11.69
4NZR.PDB	OD1, H_ASP_146	NE2, H_GLN_179	HE22, H_GLN_179	2.89	2.12	22.14
4NZR.PDB	OG, L_SER_176	OG, H_SER_188	HG, H_SER_188	2.88	2.16	24.46
4NZR.PDB	OD1, H_ASP_220	ND2, H_ASN_209	HD22, H_ASN_209	2.89	2.06	12.07
4NZR.PDB	OG, H_SER_215	ND1, H_HIS_212	HD1, H_HIS_212	2.80	1.99	17.07
4NZR.PDB	OE2, L_GLU_123	NZ, H_LYS_221	HZ2, H_LYS_221	2.99	2.10	2.00
4NZR.PDB	OE2, H_GLU_226	NE, H_ARG_222	HE, H_ARG_222	2.65	1.93	27.41
4NZR.PDB	OE1, L_GLU_92	ND2, L_ASN_30	HD22, L_ASN_30	2.94	2.10	10.05
4NZR.PDB	OH, L_TYR_52	NZ, L_LYS_31	HZ1, L_LYS_31	2.57	1.77	21.34
4NZR.PDB	OH, L_TYR_86	NE2, L_GLN_37	HE21, L_GLN_37	2.96	2.11	9.58
4NZR.PDB	OD2, L_ASP_82	NH1, L_ARG_61	HH12, L_ARG_61	2.70	1.89	15.31
4NZR.PDB	OD1, L_ASP_82	NH2, L_ARG_61	HH22, L_ARG_61	2.85	2.01	9.02
4NZR.PDB	OG, L_SER_131	NE2, L_GLN_124	HE22, L_GLN_124	2.90	2.04	4.21
4NZR.PDB	OG, L_SER_177	NE1, L_TRP_148	HE1, L_TRP_148	2.91	2.07	10.59
4NZR.PDB	OE1, L_GLN_155	ND2, L_ASN_158	HD21, L_ASN_158	2.96	2.11	9.14
4NZR.PDB	OD1, L_ASP_170	OG1, L_THR_172	HG1, L_THR_172	2.70	1.89	6.41
4NZR.PDB	OG, H_SER_188	OG, L_SER_176	HG, L_SER_176	2.88	2.09	13.66
4NZR.PDB	OD2, L_ASP_151	ND1, L_HIS_189	HD1, L_HIS_189	2.85	2.11	26.53
4NZR.PDB	OD1, M_ASN_378	NH1, M_ARG_95	HH12, M_ARG_95	2.71	1.91	18.53
4NZR.PDB	OE2, M_GLU_124	OG, M_SER_126	HG, M_SER_126	2.49	1.81	27.79
4NZR.PDB	OE2, M_GLU_124	NZ, M_LYS_141	HZ2, M_LYS_141	2.96	2.15	21.57
4NZR.PDB	OD1, M_ASN_335	ND2, M_ASN_166	HD22, M_ASN_166	2.95	2.13	14.03
4NZR.PDB	OD1, M_ASN_183	NE, M_ARG_167	HE, M_ARG_167	2.87	2.09	20.21
4NZR.PDB	OD1, M_ASP_339	NH2, M_ARG_167	HH22, M_ARG_167	2.84	2.05	19.40
4NZR.PDB	OD1, M_ASN_177	OG1, M_THR_179	HG1, M_THR_179	2.75	1.94	6.81
4NZR.PDB	OD1, M_ASP_217	OG1, M_THR_207	HG1, M_THR_207	2.72	1.90	1.28
4NZR.PDB	OE1, M_GLU_261	NZ, M_LYS_242	HZ1, M_LYS_242	2.96	2.22	28.06
4NZR.PDB	OD1, M_ASP_250	NZ, M_LYS_249	HZ2, M_LYS_249	2.93	2.05	7.77
4NZR.PDB	NE2, M_GLN_282	NZ, M_LYS_255	HZ2, M_LYS_255	2.97	2.08	5.26
4NZR.PDB	OD2, M_ASP_217	NH1, M_ARG_269	HH12, M_ARG_269	2.82	1.99	14.04
4NZR.PDB	OE2, M_GLU_313	NZ, M_LYS_289	HZ1, M_LYS_289	2.70	1.96	27.41
4NZR.PDB	OE1, M_GLU_311	NZ, M_LYS_289	HZ3, M_LYS_289	2.89	2.00	2.29
4NZR.PDB	OD1, M_ASP_350	OG1, M_THR_352	HG1, M_THR_352	2.69	1.93	19.00
4NZR.PDB	OE1, M_GLU_420	NZ, M_LYS_370	HZ2, M_LYS_370	2.61	1.80	20.02
4NZR.PDB	OD1, M_ASP_375	NE2, M_GLN_371	HE21, M_GLN_371	2.92	2.12	18.76
4NZR.PDB	OE1, M_GLU_383	NH1, M_ARG_380	HH11, M_ARG_380	2.65	1.84	14.74

4NZR.PDB	OE1, M_GLU_162	NH2, M_ARG_381	HH22, M_ARG_381	3.00	2.22	21.24
4NZR.PDB	OE1, L_GLU_81	NE, M_ARG_384	HE, M_ARG_384	2.93	2.09	10.37
4NZR.PDB	OD1, M_ASP_396	NZ, M_LYS_397	HZ1, M_LYS_397	2.90	2.03	10.85
4NZR.PDB	OD2, M_ASP_410	ND2, M_ASN_402	HD22, M_ASN_402	2.93	2.14	18.97
4NZR.PDB	OE2, M_GLU_464	NH1, M_ARG_416	HH12, M_ARG_416	2.68	1.83	5.86
4NZR.PDB	OE1, M_GLU_464	NH2, M_ARG_416	HH22, M_ARG_416	2.88	2.03	6.77
4NZR.PDB	OD1, M_ASP_411	NH1, M_ARG_430	HH12, M_ARG_430	2.84	2.06	21.86
4NZR.PDB	OD1, M_ASN_402	OG1, M_THR_435	HG1, M_THR_435	2.74	1.98	18.44
4NZR.PDB	OD2, M_ASP_396	NE, M_ARG_438	HE, M_ARG_438	2.86	2.00	5.29
4NZR.PDB	OE2, M_GLU_426	ND2, M_ASN_440	HD22, M_ASN_440	2.87	2.05	14.71
4NZR.PDB	OD1, M_ASP_412	NH1, M_ARG_454	HH12, M_ARG_454	2.79	1.98	15.66
4NZR.PDB	OD1, H_ASP_31E	NH1, M_ARG_457	HH12, M_ARG_457	2.96	2.12	11.27
4NZR.PDB	OD2, H_ASP_31E	NH2, M_ARG_457	HH22, M_ARG_457	2.55	1.75	17.03
4NZU.PDB	OD2, L_ASP_82	NE, L_ARG_61	HE, L_ARG_61	2.83	2.03	27.68
4NZU.PDB	OD1, L_ASP_82	NH2, L_ARG_61	HH21, L_ARG_61	2.85	2.00	7.18
4NZU.PDB	OG, L_SER_177	NE1, L_TRP_148	HE1, L_TRP_148	2.90	1.89	11.12
4NZU.PDB	OE2, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.81	1.92	18.37
4NZU.PDB	OD1, H_ASP_86	NH1, H_ARG_38	HH12, H_ARG_38	2.87	2.03	8.91
4NZU.PDB	OD2, H_ASP_86	NH1, H_ARG_66	HH12, H_ARG_66	2.80	1.94	3.46
4NZU.PDB	OD1, H_ASP_97	NH2, H_ARG_94	HH22, H_ARG_94	2.85	2.02	14.02
4NZU.PDB	OG, H_SER_189	NE1, H_TRP_157	HE1, H_TRP_157	2.92	1.90	9.04
4NZU.PDB	OH, H_TYR_206	OG, H_BSER_197	HG, H_BSER_197	2.82	2.05	15.42
4QEX.PDB	OD2, A_ASP_414	NH2, A_ARG_349	HH21, A_ARG_349	3.00	2.26	27.00
4QEX.PDB	OD2, B_ASP_414	NH2, B_ARG_349	HH21, B_ARG_349	2.99	2.26	27.25
4WUU.PDB	OD2, A_ASP_29	ND1, A_HIS_3	HD1, A_HIS_3	2.93	2.13	17.75
4WUU.PDB	OE1, A_GLU_46	NE, A_ARG_35	HE, A_ARG_35	2.77	1.96	15.11
4WUU.PDB	OE2, A_GLU_46	OG, A_SER_42	HG, A_SER_42	2.85	2.07	18.95
4WUU.PDB	OD2, B_ASP_53	NE, A_ARG_48	HE, A_ARG_48	2.84	2.13	29.12
4WUU.PDB	OH, A_TYR_171	OH, A_TYR_59	HH, A_TYR_59	2.71	1.89	11.34
4WUU.PDB	OH, E_TYR_104	NZ, A_LYS_66	HZ3, A_LYS_66	2.89	2.02	10.84
4WUU.PDB	OXT, C_LEU_9	OH, A_TYR_84	HH, A_TYR_84	2.64	1.82	12.17
4WUU.PDB	OD2, A_ASP_137	OH, A_TYR_85	HH, A_TYR_85	2.79	1.98	13.39
4WUU.PDB	OE1, A_GLN_87	OH, A_TYR_118	HH, A_TYR_118	2.94	2.13	11.47
4WUU.PDB	OG1, A_THR_143	OH, A_TYR_123	HH, A_TYR_123	2.74	1.95	17.32
4WUU.PDB	OE2, A_GLU_55	NE, A_ARG_170	HE, A_ARG_170	2.89	2.03	3.82
4WUU.PDB	OE1, B_GLN_8	NH1, A_ARG_234	HH11, A_ARG_234	2.79	2.07	27.49
4WUU.PDB	OE1, A_GLN_242	NH2, A_ARG_234	HH21, A_ARG_234	3.00	2.27	27.42
4WUU.PDB	OD1, A_ASP_238	OG1, A_THR_240	HG1, A_THR_240	2.61	1.79	8.96
4WUU.PDB	OG1, B_THR_86	OG1, B_THR_4	HG1, B_THR_4	2.90	2.14	21.40
4WUU.PDB	OE1, A_GLU_232	OH, B_TYR_26	HH, B_TYR_26	2.95	2.14	13.27
4WUU.PDB	OD1, B_ASP_38	NE, B_ARG_45	HE, B_ARG_45	2.54	1.82	27.34
4WUU.PDB	ND1, B_HIS_84	OG1, B_THR_86	HG1, B_THR_86	2.95	2.20	22.57
4WUU.PDB	OE1, E_GLN_39	NE2, D_GLN_39	HE22, D_GLN_39	2.94	2.18	23.53
4WUU.PDB	OD2, D_ASP_83	NE, D_ARG_62	HE, D_ARG_62	2.79	2.08	28.83
4WUU.PDB	OD1, D_ASP_83	NH2, D_ARG_62	HH21, D_ARG_62	2.86	2.00	2.74
4WUU.PDB	OD1, E_ASP_106	NE1, D_TRP_99	HE1, D_TRP_99	2.95	2.19	24.35
4WUU.PDB	OG1, D_THR_165	OG, D_SER_180	HG, D_SER_180	3.00	2.24	22.62
4WUU.PDB	OE1, D_GLN_39	NE2, E_GLN_39	HE22, E_GLN_39	2.55	1.73	14.29
4WUU.PDB	OE2, A_GLU_166	NH2, E_ARG_50	HH22, E_ARG_50	2.67	1.88	18.69
4WUU.PDB	OD1, E_ASP_73	OG, E_SER_75	HG, E_SER_75	2.93	2.16	19.72
4WUU.PDB	OE1, A_GLU_63	OH, E_TYR_104	HH, E_TYR_104	2.59	1.76	7.82
4WUU.PDB	OE1, A_GLU_55	OH, E_TYR_105	HH, E_TYR_105	2.47	1.79	29.86
4WUU.PDB	OE1, E_GLU_156	OH, E_TYR_153	HH, E_TYR_153	2.97	2.18	16.08
4Z0X.PDB	OG1, A_THR_101	NE2, A_GLN_6	HE21, A_GLN_6	2.98	2.23	24.64
4Z0X.PDB	OE1, A_GLN_16	OG1, A_THR_17	HG1, A_THR_17	2.97	2.23	24.46
4Z0X.PDB	OE1, A_GLN_88	OH, A_TYR_35	HH, A_TYR_35	2.99	2.19	16.02
4Z0X.PDB	OE1, B_GLN_64	NE2, A_GLN_37	HE22, A_GLN_37	2.75	1.99	23.41
4Z0X.PDB	OD2, A_ASP_81	NH1, A_ARG_60	HH12, A_ARG_60	2.72	1.91	16.22

4Z0X.PDB	OD1, A.ASN.68	OG1, A.THR.69	HG1, A.THR.69	2.91	2.09	9.92
4Z0X.PDB	OE2, B.GLU.107	OG, B.SER.42	HG, B.SER.42	2.96	2.17	17.40
4Z0X.PDB	OE1, B.GLN.31	OG, B.SER.46	HG, B.SER.46	2.75	1.93	11.18
4Z0X.PDB	OE2, B.GLU.71	NE, B.ARG.63	HE, B.ARG.63	2.78	1.94	9.25
4Z0X.PDB	OD1, B.ASP.115	NH1, B.ARG.63	HH12, B.ARG.63	3.00	2.15	8.77
4Z0X.PDB	OE1, B.GLN.90	NE, B.ARG.92	HE, B.ARG.92	2.75	1.97	21.20
4Z0X.PDB	OD2, B.ASP.115	NH1, B.ARG.92	HH12, B.ARG.92	2.90	2.09	15.11
4Z0X.PDB	OD1, B.ASP.115	NH2, B.ARG.92	HH22, B.ARG.92	2.68	1.87	17.08
4Z0X.PDB	OE1, B.GLN.64	OH, B.TYR.120	HH, B.TYR.120	2.91	2.08	8.45
5I76.PDB	OD1, A.ASN.76	NH1, A.ARG.18	HH11, A.ARG.18	2.77	1.94	12.53
5I76.PDB	OE1, A.GLN.89	OH, A.TYR.36	HH, A.TYR.36	2.60	1.77	6.74
5I76.PDB	OH, A.TYR.86	NE2, A.GLN.37	HE21, A.GLN.37	2.93	2.09	10.63
5I76.PDB	OE1, B.GLN.39	NE2, A.GLN.38	HE22, A.GLN.38	2.94	2.10	10.68
5I76.PDB	OE1, A.GLU.53	NZ, A.LYS.49	HZ2, A.LYS.49	2.94	2.09	13.35
5I76.PDB	OD2, B.ASP.103	OH, A.TYR.50	HH, A.TYR.50	2.64	1.88	21.01
5I76.PDB	OD1, A.ASP.82	NH2, A.ARG.61	HH21, A.ARG.61	2.77	1.93	10.41
5I76.PDB	OE2, A.GLU.81	NH2, A.ARG.61	HH22, A.ARG.61	2.77	1.92	8.54
5I76.PDB	OG1, A.THR.96	NE2, A.GLN.89	HE21, A.GLN.89	2.89	2.08	16.62
5I76.PDB	OD1, A.ASN.93	ND2, A.ASN.92	HD22, A.ASN.92	2.89	2.06	14.53
5I76.PDB	OG, A.SER.12	NZ, A.LYS.107	HZ3, A.LYS.107	2.75	1.89	12.15
5I76.PDB	OG, A.SER.131	NE2, A.GLN.124	HE22, A.GLN.124	2.78	1.92	5.16
5I76.PDB	OE2, A.GLU.143	NZ, A.LYS.145	HZ3, A.LYS.145	2.87	2.06	20.39
5I76.PDB	OG, A.SER.177	NE1, A.TRP.148	HE1, A.TRP.148	2.97	2.15	13.90
5I76.PDB	OD1, A.ASP.170	OG1, A.THR.172	HG1, A.THR.172	2.65	1.83	9.24
5I76.PDB	OE2, A.GLU.105	OH, A.TYR.173	HH, A.TYR.173	2.42	1.66	21.73
5I76.PDB	OD1, B.ASP.89	NH1, B.ARG.38	HH12, B.ARG.38	2.81	1.96	5.27
5I76.PDB	OE1, A.GLN.38	NE2, B.GLN.39	HE22, B.GLN.39	2.80	1.95	6.66
5I76.PDB	OD2, B.ASP.58	NE1, B.TRP.52	HE1, B.TRP.52	2.79	1.94	5.91
5I76.PDB	OD2, B.ASP.89	NH1, B.ARG.66	HH12, B.ARG.66	2.96	2.17	19.36
5I76.PDB	OD1, B.ASP.89	NH2, B.ARG.66	HH22, B.ARG.66	2.84	1.99	7.50
5I76.PDB	OD1, B.ASP.72	OG, B.SER.74	HG, B.SER.74	2.49	1.80	29.35
5I76.PDB	OD1, B.ASN.203	OG, B.SER.159	HG, B.SER.159	2.82	2.04	17.93
5I76.PDB	OG, B.SER.186	NE1, B.TRP.160	HE1, B.TRP.160	2.99	2.15	11.06
5I76.PDB	OD1, B.ASP.150	NE2, B.GLN.177	HE22, B.GLN.177	2.79	2.00	19.18
5I76.PDB	OG, A.SER.176	OG, B.SER.185	HG, B.SER.185	2.89	2.15	23.05
5I76.PDB	OG, B.SER.194	OH, B.TYR.200	HH, B.TYR.200	2.81	2.03	18.26
5I76.PDB	OD1, B.ASP.214	ND2, B.ASN.203	HD22, B.ASN.203	2.90	2.11	19.71
5I76.PDB	OE1, A.GLU.123	NZ, B.LYS.215	HZ1, B.LYS.215	2.73	1.96	24.68
5I76.PDB	OE2, A.GLU.123	NZ, B.LYS.215	HZ1, B.LYS.215	2.89	2.11	24.69
5I76.PDB	OE1, B.GLU.218	NE, B.ARG.216	HE, B.ARG.216	2.64	1.90	25.25
5I76.PDB	OE1, B.GLU.218	NH2, B.ARG.216	HH21, B.ARG.216	2.69	1.98	29.12
5I76.PDB	OD2, A.ASP.70	NH1, C.ARG.24	HH12, C.ARG.24	2.95	2.23	28.81
5I76.PDB	OE1, C.GLN.89	OH, C.TYR.36	HH, C.TYR.36	2.73	1.90	7.00
5I76.PDB	OH, C.TYR.86	NE2, C.GLN.37	HE21, C.GLN.37	2.93	2.09	9.49
5I76.PDB	OE1, C.GLN.37	NH1, C.ARG.45	HH11, C.ARG.45	2.96	2.15	17.42
5I76.PDB	OE1, C.GLU.53	NZ, C.LYS.49	HZ2, C.LYS.49	2.64	1.79	13.55
5I76.PDB	OD2, D.ASP.103	OH, C.TYR.50	HH, C.TYR.50	2.76	1.95	12.40
5I76.PDB	OD1, C.ASP.82	NH2, C.ARG.61	HH21, C.ARG.61	2.76	1.93	11.41
5I76.PDB	OE2, C.GLU.81	NH2, C.ARG.61	HH22, C.ARG.61	2.83	2.01	16.02
5I76.PDB	OG, C.SER.171	OG, C.SER.80	HG, C.SER.80	2.59	1.79	14.57
5I76.PDB	OG1, C.THR.96	NE2, C.GLN.89	HE21, C.GLN.89	2.74	1.92	15.47
5I76.PDB	OD1, C.ASN.93	ND2, C.ASN.92	HD22, C.ASN.92	2.84	2.03	16.29
5I76.PDB	OG, C.SER.131	NE2, C.GLN.124	HE22, C.GLN.124	2.87	2.02	5.94
5I76.PDB	OG1, C.THR.180	OG, C.SER.131	HG, C.SER.131	2.93	2.13	14.64
5I76.PDB	OE1, C.GLU.105	OH, C.TYR.140	HH, C.TYR.140	2.89	2.14	22.51
5I76.PDB	OG, C.SER.177	NE1, C.TRP.148	HE1, C.TRP.148	2.90	2.11	19.54
5I76.PDB	OE1, C.GLN.155	ND2, C.ASN.158	HD22, C.ASN.158	2.96	2.21	25.95
5I76.PDB	OD1, C.ASP.170	OG1, C.THR.172	HG1, C.THR.172	2.79	1.97	11.52

5I76.PDB	OE2, C_GLU_105	OH, C_TYR_173	HH, C_TYR_173	2.72	1.89	6.26
5I76.PDB	OD2, C_ASP_151	ND1, C_HIS_189	HD1, C_HIS_189	2.35	1.61	24.33
5I76.PDB	OG, D_SER_28	OG1, D_THR_30	HG1, D_THR_30	2.71	1.88	5.11
5I76.PDB	OD1, D_ASP_89	NH1, D_ARG_38	HH12, D_ARG_38	2.88	2.03	7.89
5I76.PDB	OE1, C_GLN_38	NE2, D_GLN_39	HE22, D_GLN_39	2.85	2.01	10.98
5I76.PDB	OD2, D_ASP_58	NE1, D_TRP_52	HE1, D_TRP_52	2.82	1.96	3.64
5I76.PDB	OD2, D_ASP_89	NH1, D_ARG_66	HH12, D_ARG_66	2.85	2.02	11.59
5I76.PDB	OD1, D_ASP_89	NH2, D_ARG_66	HH22, D_ARG_66	2.74	1.89	8.51
5I76.PDB	OD1, D_ASP_72	OG, D_SER_74	HG, D_SER_74	2.71	2.00	26.33
5I76.PDB	OD1, D_ASP_150	NZ, D_LYS_149	HZ3, D_LYS_149	2.86	2.03	16.70
5I76.PDB	OE1, D_GLU_154	OH, D_TYR_151	HH, D_TYR_151	2.91	2.09	9.17
5I76.PDB	OD1, D_ASN_203	OG, D_SER_159	HG, D_SER_159	2.84	2.05	16.99
5I76.PDB	OG, D_SER_186	NE1, D_TRP_160	HE1, D_TRP_160	2.92	2.08	9.81
5I76.PDB	OD1, D_ASP_150	NE2, D_GLN_177	HE22, D_GLN_177	2.71	1.92	19.90
5I76.PDB	OG, D_SER_194	OH, D_TYR_200	HH, D_TYR_200	2.69	1.90	16.49
5I76.PDB	OE1, C_GLU_123	NZ, D_LYS_215	HZ1, D_LYS_215	2.60	1.73	11.40
5JO5.PDB	OD2, H_ASP_53	NE1, H_TRP_33	HE1, H_TRP_33	2.93	2.17	24.23
5JO5.PDB	OG1, H_THR_95	OG, H_SER_35	HG, H_SER_35	2.68	1.99	28.91
5JO5.PDB	OE1, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.82	2.00	14.74
5JO5.PDB	OH, H_TYR_90	NH1, H_ARG_38	HH11, H_ARG_38	2.91	2.09	14.97
5JO5.PDB	OD1, H_ASP_86	NH1, H_ARG_38	HH12, H_ARG_38	2.87	2.05	14.25
5JO5.PDB	OE1, L_GLN_38	NE2, H_GLN_39	HE22, H_GLN_39	2.84	2.00	9.38
5JO5.PDB	OE1, H_GLU_100J	NE, H_ARG_50	HE, H_ARG_50	2.77	2.00	22.35
5JO5.PDB	OD2, H_ASP_58	NH2, H_ARG_50	HH22, H_ARG_50	2.84	2.00	11.12
5JO5.PDB	OD2, H_ASP_86	NH1, H_ARG_66	HH12, H_ARG_66	2.78	1.94	11.10
5JO5.PDB	OD1, H_ASP_73	NE, H_ARG_71	HE, H_ARG_71	2.85	2.05	17.58
5JO5.PDB	OD1, H_ASP_72	OG, H_SER_74	HG, H_SER_74	2.59	1.76	4.73
5JO5.PDB	OD2, H_ASP_102	NE, H_ARG_94	HE, H_ARG_94	2.81	2.07	25.27
5JO5.PDB	OD2, H_ASP_102	NH1, H_ARG_94	HH11, H_ARG_94	2.70	1.93	22.67
5JO5.PDB	OE2, L_GLU_124	NZ, H_LYS_143	HZ2, H_LYS_143	2.46	1.63	17.05
5JO5.PDB	OD1, H_ASN_197	OG, H_SER_153	HG, H_SER_153	2.83	2.04	17.75
5JO5.PDB	OG, H_SER_180	NE1, H_TRP_154	HE1, H_TRP_154	2.93	2.09	10.13
5JO5.PDB	OD1, H_ASP_144	NE2, H_GLN_171	HE22, H_GLN_171	2.85	2.05	18.06
5JO5.PDB	OH, L_TYR_177	OG, H_SER_179	HG, H_SER_179	2.73	2.00	25.96
5JO5.PDB	OG, H_SER_188	OH, H_TYR_194	HH, H_TYR_194	2.61	1.85	20.74
5JO5.PDB	OD1, H_ASP_208	ND2, H_ASN_197	HD22, H_ASN_197	2.91	2.06	7.04
5JO5.PDB	OE1, D_GLN_24	OG, L_SER_30	HG, L_SER_30	2.84	2.07	18.45
5JO5.PDB	OH, L_TYR_86	NE2, L_GLN_37	HE21, L_GLN_37	2.94	2.08	4.10
5JO5.PDB	OE1, H_GLN_39	NE2, L_GLN_38	HE22, L_GLN_38	2.83	2.00	13.03
5JO5.PDB	OD1, L_ASN_52	NE, L_ARG_54	HE, L_ARG_54	2.95	2.15	18.15
5JO5.PDB	OD1, L_ASP_82	NH2, L_ARG_61	HH21, L_ARG_61	2.75	1.92	13.56
5JO5.PDB	OE2, L_GLU_81	NH2, L_ARG_61	HH22, L_ARG_61	2.98	2.17	16.30
5JO5.PDB	OE2, H_GLU_100J	NH2, L_ARG_91	HH22, L_ARG_91	2.69	1.84	7.26
5JO5.PDB	OD1, L_ASP_92	OG, L_SER_95A	HG, L_SER_95A	2.53	1.76	19.87
5JO5.PDB	OD1, H_ASP_58	NE, L_ARG_95B	HE, L_ARG_95B	2.95	2.13	14.76
5JO5.PDB	OE1, L_GLU_198	NZ, L_LYS_110	HZ3, L_LYS_110	2.94	2.09	14.01
5JO5.PDB	OE2, L_GLU_124	OG1, L_THR_131	HG1, L_THR_131	2.52	1.80	26.33
5JO5.PDB	OG, L_SER_176	NE1, L_TRP_148	HE1, L_TRP_148	2.93	2.09	9.40
5JO5.PDB	OD1, L_ASN_169	NE2, L_GLN_167	HE21, L_GLN_167	2.89	2.12	21.54
5JO5.PDB	OG1, L_THR_162	OG, L_SER_175	HG, L_SER_175	2.94	2.19	22.64
5JO5.PDB	OG1, L_THR_161	OG, L_SER_176	HG, L_SER_176	2.79	2.07	26.34
5JO5.PDB	OG1, L_THR_205	OG, L_SER_192	HG, L_SER_192	2.82	2.12	28.14
5JO5.PDB	OG1, L_THR_196	OG1, L_THR_201	HG1, L_THR_201	2.95	2.20	22.04
5JO5.PDB	OD2, A_ASP_53	NE1, A_TRP_33	HE1, A_TRP_33	2.82	2.05	21.67
5JO5.PDB	OE1, A_GLU_46	NE, A_ARG_38	HE, A_ARG_38	2.78	1.97	16.63
5JO5.PDB	OD1, A_ASP_86	NH1, A_ARG_38	HH12, A_ARG_38	2.83	2.01	14.60
5JO5.PDB	OE1, B_GLN_38	NE2, A_GLN_39	HE22, A_GLN_39	2.87	2.02	8.31
5JO5.PDB	OE1, A_GLU_100J	NE, A_ARG_50	HE, A_ARG_50	2.88	2.11	22.13

5JO5.PDB	OE2, A_GLU_100J	NH1, A_ARG_50	HH11, A_ARG_50	2.91	2.07	11.34
5JO5.PDB	OD2, A_ASP_58	NH2, A_ARG_50	HH22, A_ARG_50	2.88	2.05	13.39
5JO5.PDB	OD2, A_ASP_86	NH1, A_ARG_66	HH12, A_ARG_66	2.80	1.98	14.11
5JO5.PDB	OD1, A_ASP_73	NE, A_ARG_71	HE, A_ARG_71	2.86	2.09	22.09
5JO5.PDB	OD1, A_ASP_72	OG, A_SER_74	HG, A_SER_74	2.54	1.80	22.83
5JO5.PDB	OD2, A_ASP_102	NE, A_ARG_94	HE, A_ARG_94	2.86	2.14	28.73
5JO5.PDB	OD2, A_ASP_102	NH1, A_ARG_94	HH11, A_ARG_94	2.58	1.79	19.06
5JO5.PDB	OE2, B_GLU_124	NZ, A_LYS_143	HZ2, A_LYS_143	2.62	1.83	23.29
5JO5.PDB	OD1, A_ASN_197	OG, A_SER_153	HG, A_SER_153	2.78	2.00	18.34
5JO5.PDB	OG, A_SER_180	NE1, A_TRP_154	HE1, A_TRP_154	2.89	2.05	11.45
5JO5.PDB	OD1, A_ASP_144	NE2, A_GLN_171	HE22, A_GLN_171	2.80	2.01	18.53
5JO5.PDB	OH, B_TYR_177	OG, A_SER_179	HG, A_SER_179	2.83	2.10	25.21
5JO5.PDB	OG, A_SER_188	OH, A_TYR_194	HH, A_TYR_194	2.69	1.94	22.27
5JO5.PDB	OG, A_SER_203	ND1, A_HIS_200	HD1, A_HIS_200	2.79	2.03	23.43
5JO5.PDB	OE2, B_GLU_123	NZ, A_LYS_209	HZ1, A_LYS_209	2.55	1.68	10.64
5JO5.PDB	OH, B_TYR_86	NE2, B_GLN_37	HE21, B_GLN_37	2.95	2.09	5.48
5JO5.PDB	OE1, A_GLN_39	NE2, B_GLN_38	HE22, B_GLN_38	2.90	2.07	12.43
5JO5.PDB	OD1, B_ASP_82	NH2, B_ARG_61	HH21, B_ARG_61	2.66	1.83	11.88
5JO5.PDB	OD1, B_ASP_92	OG, B_SER_95A	HG, B_SER_95A	2.47	1.67	15.14
5JO5.PDB	OE2, B_GLU_124	OG1, B_THR_131	HG1, B_THR_131	2.59	1.86	24.88
5JO5.PDB	OG, B_SER_176	NE1, B_TRP_148	HE1, B_TRP_148	2.89	2.05	10.46
5JO5.PDB	OD1, B_ASN_169	NE2, B_GLN_167	HE21, B_GLN_167	2.98	2.24	26.40
5JO5.PDB	OD1, B_ASP_138	NE2, B_GLN_167	HE22, B_GLN_167	2.99	2.14	6.65
5JO5.PDB	OG1, B_THR_162	OG, B_SER_175	HG, B_SER_175	2.87	2.11	21.53
5JO5.PDB	OG1, B_THR_161	OG, B_SER_176	HG, B_SER_176	2.78	2.05	24.57
5JO5.PDB	OG1, B_THR_205	OG, B_SER_192	HG, B_SER_192	2.59	1.90	29.12
5JO5.PDB	OE2, B_GLU_203	NE2, B_GLN_194	HE21, B_GLN_194	2.60	1.77	11.97
5JO5.PDB	OG1, B_THR_196	OG1, B_THR_201	HG1, B_THR_201	2.97	2.21	22.11
5JO5.PDB	OD2, C_ASP_53	NE1, C_TRP_33	HE1, C_TRP_33	2.84	2.06	21.35
5JO5.PDB	OE1, C_GLU_46	NE, C_ARG_38	HE, C_ARG_38	2.77	1.97	17.97
5JO5.PDB	OH, C_TYR_90	NH1, C_ARG_38	HH11, C_ARG_38	3.00	2.18	14.70
5JO5.PDB	OD1, C_ASP_86	NH1, C_ARG_38	HH12, C_ARG_38	2.85	2.02	13.98
5JO5.PDB	OE1, D_GLN_38	NE2, C_GLN_39	HE22, C_GLN_39	2.86	2.02	9.45
5JO5.PDB	OE1, C_GLU_100J	NE, C_ARG_50	HE, C_ARG_50	2.87	2.09	20.20
5JO5.PDB	OD2, C_ASP_58	NH1, C_ARG_50	HH12, C_ARG_50	2.77	1.94	11.94
5JO5.PDB	OE2, C_GLU_100J	NH2, C_ARG_50	HH21, C_ARG_50	2.86	2.02	10.69
5JO5.PDB	OD2, C_ASP_86	NH1, C_ARG_66	HH12, C_ARG_66	2.83	2.01	15.29
5JO5.PDB	OD1, C_ASP_73	NE, C_ARG_71	HE, C_ARG_71	2.90	2.12	21.25
5JO5.PDB	OD1, C_ASP_72	OG, C_SER_74	HG, C_SER_74	2.61	1.84	20.06
5JO5.PDB	OD2, C_ASP_102	NE, C_ARG_94	HE, C_ARG_94	2.79	2.08	28.98
5JO5.PDB	OD2, C_ASP_102	NH1, C_ARG_94	HH11, C_ARG_94	2.55	1.78	21.18
5JO5.PDB	OE2, D_GLU_124	NZ, C_LYS_143	HZ2, C_LYS_143	2.79	1.92	10.71
5JO5.PDB	OD1, C_ASN_197	OG, C_SER_153	HG, C_SER_153	2.81	2.01	15.61
5JO5.PDB	OG, C_SER_180	NE1, C_TRP_154	HE1, C_TRP_154	2.96	2.13	11.76
5JO5.PDB	OD1, C_ASP_144	NE2, C_GLN_171	HE22, C_GLN_171	2.92	2.12	18.22
5JO5.PDB	OH, D_TYR_177	OG, C_SER_179	HG, C_SER_179	2.71	1.97	23.23
5JO5.PDB	OG, C_SER_188	OH, C_TYR_194	HH, C_TYR_194	2.62	1.86	20.70
5JO5.PDB	OD1, C_ASP_208	ND2, C_ASN_197	HD22, C_ASN_197	2.98	2.12	6.27
5JO5.PDB	OG, C_SER_203	ND1, C_HIS_200	HD1, C_HIS_200	2.85	2.10	24.59
5JO5.PDB	OE2, D_GLU_123	NZ, C_LYS_209	HZ1, C_LYS_209	2.58	1.72	11.28
5JO5.PDB	OG, D_SER_34	OH, D_TYR_36	HH, D_TYR_36	2.76	2.07	29.85
5JO5.PDB	OH, D_TYR_86	NE2, D_GLN_37	HE21, D_GLN_37	2.93	2.09	8.87
5JO5.PDB	OE1, C_GLN_39	NE2, D_GLN_38	HE22, D_GLN_38	2.92	2.09	12.72
5JO5.PDB	OD1, D_ASP_82	NH2, D_ARG_61	HH21, D_ARG_61	2.88	2.03	6.97
5JO5.PDB	OD1, D_ASP_92	OG, D_SER_95A	HG, D_SER_95A	2.53	1.74	15.88
5JO5.PDB	OD1, C_ASP_58	NE, D_ARG_95B	HE, D_ARG_95B	2.94	2.10	11.64
5JO5.PDB	OE2, D_GLU_124	OG1, D_THR_131	HG1, D_THR_131	2.53	1.79	22.99
5JO5.PDB	OG, D_SER_176	NE1, D_TRP_148	HE1, D_TRP_148	2.85	2.01	9.98

5JO5.PDB	OD1, D_ASN_169	NE2, D_GLN_167	HE21, D_GLN_167	2.91	2.12	19.40
5JO5.PDB	OD1, D_ASP_138	NE2, D_GLN_167	HE22, D_GLN_167	2.88	2.03	6.31
5JO5.PDB	OG1, D_THR_161	OG, D_SER_176	HG, D_SER_176	2.78	2.01	20.04
5JO5.PDB	OD2, D_ASP_151	ND1, D_HIS_188	HD1, D_HIS_188	2.67	1.86	16.19
5JO5.PDB	OG1, D_THR_205	OG, D_SER_192	HG, D_SER_192	2.76	2.06	27.74
5JO5.PDB	OE2, D_GLU_203	NE2, D_GLN_194	HE21, D_GLN_194	2.41	1.67	25.54
5JO5.PDB	OD2, E_ASP_53	NE1, E_TRP_33	HE1, E_TRP_33	2.89	2.14	24.08
5JO5.PDB	OG1, E_THR_95	OG, E_SER_35	HG, E_SER_35	2.65	1.97	29.96
5JO5.PDB	OE1, E_GLU_46	NE, E_ARG_38	HE, E_ARG_38	2.75	1.95	17.65
5JO5.PDB	OH, E_TYR_90	NH1, E_ARG_38	HH11, E_ARG_38	2.94	2.11	14.05
5JO5.PDB	OD1, E_ASP_86	NH1, E_ARG_38	HH12, E_ARG_38	2.82	2.00	15.16
5JO5.PDB	OE1, F_GLN_38	NE2, E_GLN_39	HE22, E_GLN_39	2.90	2.06	10.70
5JO5.PDB	OE1, E_GLU_100J	NE, E_ARG_50	HE, E_ARG_50	2.82	2.06	22.79
5JO5.PDB	OD2, E_ASP_58	NH1, E_ARG_50	HH12, E_ARG_50	2.78	1.94	10.17
5JO5.PDB	OE2, E_GLU_100J	NH2, E_ARG_50	HH21, E_ARG_50	2.98	2.13	7.82
5JO5.PDB	OD2, E_ASP_86	NH1, E_ARG_66	HH12, E_ARG_66	2.75	1.91	9.04
5JO5.PDB	OD1, E_ASP_73	NE, E_ARG_71	HE, E_ARG_71	2.89	2.11	20.53
5JO5.PDB	OD1, E_ASP_72	OG, E_SER_74	HG, E_SER_74	2.60	1.77	6.90
5JO5.PDB	OD2, E_ASP_102	NE, E_ARG_94	HE, E_ARG_94	2.83	2.08	25.07
5JO5.PDB	OD2, E_ASP_102	NH2, E_ARG_94	HH21, E_ARG_94	2.73	1.97	23.25
5JO5.PDB	OE2, F_GLU_124	NZ, E_LYS_143	HZ2, E_LYS_143	2.55	1.75	21.57
5JO5.PDB	OD1, E_ASN_197	OG, E_SER_153	HG, E_SER_153	2.80	2.02	18.49
5JO5.PDB	OG, E_SER_180	NE1, E_TRP_154	HE1, E_TRP_154	2.96	2.13	12.27
5JO5.PDB	OD1, E_ASP_144	NE2, E_GLN_171	HE22, E_GLN_171	2.83	2.02	16.42
5JO5.PDB	OH, F_TYR_177	OG, E_SER_179	HG, E_SER_179	2.58	1.87	27.02
5JO5.PDB	OG, E_SER_188	OH, E_TYR_194	HH, E_TYR_194	2.65	1.91	23.44
5JO5.PDB	OD1, E_ASP_208	ND2, E_ASN_197	HD22, E_ASN_197	2.93	2.08	6.74
5JO5.PDB	OE2, F_GLU_123	NZ, E_LYS_209	HZ1, E_LYS_209	2.57	1.74	17.62
5JO5.PDB	OE1, B_GLN_24	OG, F_SER_30	HG, F_SER_30	2.88	2.11	20.15
5JO5.PDB	OH, F_TYR_86	NE2, F_GLN_37	HE21, F_GLN_37	2.98	2.12	5.01
5JO5.PDB	OE1, E_GLN_39	NE2, F_GLN_38	HE22, F_GLN_38	2.85	2.02	12.75
5JO5.PDB	OD2, F_ASP_82	NE, F_ARG_61	HE, F_ARG_61	2.99	2.15	12.18
5JO5.PDB	OD1, F_ASP_82	NH2, F_ARG_61	HH21, F_ARG_61	2.81	1.97	11.97
5JO5.PDB	OE2, E_GLU_100J	NH2, F_ARG_91	HH22, F_ARG_91	2.72	1.87	5.99
5JO5.PDB	OD1, F_ASP_92	OG, F_SER_95A	HG, F_SER_95A	2.58	1.83	23.06
5JO5.PDB	OD1, E_ASP_58	NE, F_ARG_95B	HE, F_ARG_95B	2.92	2.09	12.47
5JO5.PDB	OE1, F_GLU_198	NZ, F_LYS_110	HZ3, F_LYS_110	2.97	2.11	10.79
5JO5.PDB	OE2, F_GLU_124	OG1, F_THR_131	HG1, F_THR_131	2.49	1.76	24.10
5JO5.PDB	OG, F_SER_176	NE1, F_TRP_148	HE1, F_TRP_148	2.88	2.03	9.94
5JO5.PDB	OD1, F_ASN_169	NE2, F_GLN_167	HE21, F_GLN_167	2.87	2.13	25.80
5JO5.PDB	OD1, F_ASP_138	NE2, F_GLN_167	HE22, F_GLN_167	2.86	2.01	8.07
5JO5.PDB	OG1, F_THR_161	OG, F_SER_176	HG, F_SER_176	2.84	2.06	17.97
5JO5.PDB	OE2, F_GLU_203	NE2, F_GLN_194	HE21, F_GLN_194	2.48	1.75	26.23
5JR1.PDB	OE2, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.66	1.91	24.18
5JR1.PDB	OH, H_TYR_90	NH1, H_ARG_38	HH11, H_ARG_38	2.93	2.12	16.05
5JR1.PDB	OD1, H_ASP_86	NH1, H_ARG_38	HH12, H_ARG_38	2.94	2.11	12.77
5JR1.PDB	OE2, H_GLU_46	NH2, H_ARG_38	HH21, H_ARG_38	2.68	1.95	27.48
5JR1.PDB	OD2, H_ASP_86	NH1, H_ARG_66	HH12, H_ARG_66	2.72	1.87	9.50
5JR1.PDB	OD1, H_ASP_73	NE, H_ARG_71	HE, H_ARG_71	2.99	2.20	19.01
5JR1.PDB	OD1, H_ASP_72	OG, H_SER_74	HG, H_SER_74	2.50	1.70	14.47
5JR1.PDB	OD1, H_ASN_197	OG, H_SER_153	HG, H_SER_153	2.85	2.04	12.85
5JR1.PDB	OG, H_SER_180	NE1, H_TRP_154	HE1, H_TRP_154	2.87	2.02	7.55
5JR1.PDB	OD1, H_ASP_144	NE2, H_GLN_171	HE22, H_GLN_171	2.73	1.95	20.99
5JR1.PDB	OE1, H_GLN_171	OG, H_SER_177	HG, H_SER_177	2.71	1.98	25.79
5JR1.PDB	OH, L_TYR_178	OG, H_SER_179	HG, H_SER_179	2.83	2.03	15.88
5JR1.PDB	OG, H_SER_188	OH, H_TYR_194	HH, H_TYR_194	2.70	1.94	20.59
5JR1.PDB	OE2, H_GLU_212	NE, H_BARG_210	HE, H_BARG_210	2.40	1.64	22.83
5JR1.PDB	OH, L_TYR_86	NE2, L_GLN_37	HE21, L_GLN_37	2.92	2.08	10.60

5JR1.PDB	OD2, L_ASP_82	NE, L_ARG_61	HE, L_ARG_61	2.81	2.00	15.72
5JR1.PDB	OD1, L_ASP_82	NH2, L_ARG_61	HH21, L_ARG_61	2.74	1.90	11.09
5JR1.PDB	OG1, L_THR_20	OG1, L_THR_74	HG1, L_THR_74	2.96	2.15	13.12
5JR1.PDB	OD2, L_ASP_92	OG, L_SER_94	HG, L_SER_94	2.41	1.66	21.72
5JR1.PDB	OD2, H_ASP_58	NH2, L_ARG_95B	HH22, L_ARG_95B	2.47	1.67	16.99
5JR1.PDB	OE1, L_GLU_199	NZ, L_LYS_110	HZ3, L_LYS_110	2.77	1.91	11.53
5JR1.PDB	OE2, L_GLU_125	OG1, L_THR_132	HG1, L_THR_132	2.53	1.79	23.02
5JR1.PDB	OG, L_SER_177	NE1, L_TRP_149	HE1, L_TRP_149	2.84	1.99	9.64
5JR1.PDB	OE1, L_GLN_195	NZ, L_LYS_150	HZ3, L_LYS_150	2.79	1.91	7.52
5JR1.PDB	OD1, L_ASN_170	NE2, L_GLN_168	HE21, L_GLN_168	2.60	1.77	13.13
5JR1.PDB	OD1, L_ASP_139	NE2, L_GLN_168	HE22, L_GLN_168	2.73	1.87	5.77
5JR1.PDB	OE2, L_GLU_204	NE2, L_GLN_195	HE21, L_GLN_195	2.95	2.12	11.81
5JR1.PDB	OG1, L_THR_197	OG1, L_THR_202	HG1, L_THR_202	2.77	1.97	14.73
5JUE.PDB	OH, H_TYR_91	NE2, L_GLN_38	HE22, L_GLN_38	2.57	1.77	17.09
5JUE.PDB	OD1, L_ASP_82	NH1, L_ARG_61	HH12, L_ARG_61	2.84	1.98	1.66
5JUE.PDB	OD2, L_ASP_82	NH2, L_ARG_61	HH22, L_ARG_61	2.58	1.76	15.54
5JUE.PDB	OG, L_SER_131	NE2, L_GLN_124	HE22, L_GLN_124	2.87	2.01	1.74
5JUE.PDB	OD2, L_ASP_105	OH, L_TYR_140	HH, L_TYR_140	2.73	1.90	9.39
5JUE.PDB	OG, L_SER_177	NE1, L_TRP_148	HE1, L_TRP_148	2.84	1.99	8.07
5JUE.PDB	OE2, L_GLU_195	NZ, L_LYS_149	HZ1, L_LYS_149	2.94	2.11	18.07
5JUE.PDB	OE1, L_GLU_185	NH1, L_ARG_155	HH12, L_ARG_155	2.98	2.13	8.18
5JUE.PDB	OD1, L_ASP_170	OG1, L_THR_172	HG1, L_THR_172	2.65	1.84	10.43
5JUE.PDB	OD1, L_ASP_105	OH, L_TYR_173	HH, L_TYR_173	2.53	1.79	22.81
5JUE.PDB	OG, H_SER_178	OG, L_SER_176	HG, L_SER_176	2.78	1.94	3.13
5JUE.PDB	OD1, L_ASN_161	OG, L_SER_177	HG, L_SER_177	2.61	1.88	24.46
5JUE.PDB	OD1, L_ASP_184	NE, L_ARG_188	HE, L_ARG_188	2.70	1.93	22.77
5JUE.PDB	OG, L_SER_208	OG1, L_THR_193	HG1, L_THR_193	2.92	2.19	25.67
5JUE.PDB	ND1, L_HIS_198	OG1, L_THR_200	HG1, L_THR_200	2.88	2.17	27.29
5JUE.PDB	ND1, H_HIS_35	NE1, H_TRP_47	HE1, H_TRP_47	2.93	2.15	20.72
5JUE.PDB	OD2, H_ASP_86	NZ, H_LYS_66	HZ1, H_LYS_66	2.76	1.87	4.19
5JUE.PDB	OE1, H_GLN_39	OH, H_TYR_91	HH, H_TYR_91	2.83	2.02	11.19
5JUE.PDB	OD1, H_ASP_101	NE, H_ARG_94	HE, H_ARG_94	2.72	1.88	8.15
5JUE.PDB	OD2, H_ASP_101	NH2, H_ARG_94	HH21, H_ARG_94	2.85	2.02	12.42
5JUE.PDB	OE2, H_GLU_148	OH, H_TYR_145	HH, H_TYR_145	2.72	1.89	3.03
5JUE.PDB	OD1, H_ASN_196	OG1, H_THR_153	HG1, H_THR_153	2.74	1.98	20.12
5JUE.PDB	OG1, H_THR_137	OG1, H_THR_182	HG1, H_THR_182	2.77	2.00	20.14
5JUE.PDB	OG1, H_THR_184	OG1, H_THR_187	HG1, H_THR_187	2.67	1.90	19.94
5JUE.PDB	ND1, H_HIS_199	OG, H_SER_202	HG, H_SER_202	2.87	2.13	24.10
5JUE.PDB	OE1, L_GLU_123	NZ, H_LYS_208	HZ1, H_LYS_208	2.81	1.98	17.66
5JXA.PDB	OE1, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.80	2.04	23.29
5JXA.PDB	OD1, H_ASP_86	NH1, H_ARG_38	HH12, H_ARG_38	2.74	1.88	4.26
5JXA.PDB	OE1, H_GLU_46	NH2, H_ARG_38	HH21, H_ARG_38	2.76	2.00	23.95
5JXA.PDB	OE2, H_GLU_46	NE2, H_GLN_62	HE21, H_GLN_62	2.86	2.00	1.72
5JXA.PDB	OD1, H_ASP_86	NH2, H_ARG_66	HH22, H_ARG_66	2.96	2.11	6.31
5JXA.PDB	OD2, H_ASP_76C	NE1, H_TRP_76F	HE1, H_TRP_76F	2.87	2.15	28.04
5JXA.PDB	OD1, H_ASP_99	NH2, H_ARG_95	HH22, H_ARG_95	2.95	2.09	5.23
5JXA.PDB	OD2, L_ASP_50	OH, H_TYR_100	HH, H_TYR_100	2.57	1.75	11.76
5JXA.PDB	OD1, H_ASP_144	NZ, H_LYS_143	HZ3, H_LYS_143	2.92	2.12	22.30
5JXA.PDB	OD1, H_ASN_197	OG, H_SER_153	HG, H_SER_153	2.75	1.96	17.62
5JXA.PDB	OG, H_SER_180	NE1, H_TRP_154	HE1, H_TRP_154	2.96	2.12	10.70
5JXA.PDB	OD1, H_ASP_144	NE2, H_GLN_171	HE22, H_GLN_171	2.86	2.05	16.31
5JXA.PDB	OG, H_SER_188	OH, H_TYR_194	HH, H_TYR_194	2.92	2.22	28.67
5JXA.PDB	ND1, H_HIS_200	OG, H_SER_203	HG, H_SER_203	2.82	2.10	26.44
5JXA.PDB	OE1, L_GLN_89	OH, L_TYR_36	HH, L_TYR_36	2.71	1.91	14.07
5JXA.PDB	OH, L_TYR_86	NE2, L_GLN_37	HE21, L_GLN_37	2.99	2.15	10.29
5JXA.PDB	OH, H_TYR_100	NH2, L_ARG_53	HH21, L_ARG_53	2.89	2.07	18.12
5JXA.PDB	OD2, L_ASP_82	NE, L_ARG_61	HE, L_ARG_61	2.88	2.15	27.19
5JXA.PDB	OD1, L_ASP_82	NH2, L_ARG_61	HH21, L_ARG_61	2.84	1.98	2.45

5JXA.PDB	OD1, L_ASP_70	OG1, L_THR_69	HG1, L_THR_69	2.92	2.09	7.50
5JXA.PDB	OG, L_SER_131	NE2, L_GLN_124	HE22, L_GLN_124	2.80	1.95	4.80
5JXA.PDB	OE1, L_GLU_105	OH, L_TYR_140	HH, L_TYR_140	2.43	1.65	17.73
5JXA.PDB	OE1, L_GLU_103	NH1, L_ARG_142	HH12, L_ARG_142	2.87	2.05	14.46
5JXA.PDB	OH, L_TYR_173	NH2, L_ARG_142	HH21, L_ARG_142	2.84	2.07	21.88
5JXA.PDB	OE2, L_GLU_103	NH2, L_ARG_142	HH22, L_ARG_142	2.79	1.94	8.50
5JXA.PDB	OG, L_SER_177	NE1, L_TRP_148	HE1, L_TRP_148	2.86	2.05	17.07
5JXA.PDB	OE1, L_GLN_155	ND2, L_ASN_158	HD21, L_ASN_158	2.94	2.10	10.59
5JXA.PDB	OD1, L_ASP_170	OG1, L_THR_172	HG1, L_THR_172	2.69	1.87	10.60
5JXA.PDB	OE2, L_GLU_105	OH, L_TYR_173	HH, L_TYR_173	2.63	1.83	14.46
5JXA.PDB	OD1, L_ASP_185	NZ, L_LYS_188	HZ2, L_LYS_188	2.85	2.03	19.98
5JXA.PDB	OE2, L_GLU_213	ND2, L_ASN_210	HD22, L_ASN_210	2.76	1.93	12.84
5M2C.PDB	OD1, A_ASP_195	NZ, A_LYS_124	HZ1, A_LYS_124	2.99	2.26	29.03
5M2C.PDB	OH, A_TYR_127	NE2, A_HIS_151	HE2, A_HIS_151	2.61	1.77	12.06
5M2C.PDB	OG, A_SER_159	OG1, A_THR_163	HG1, A_THR_163	2.88	2.07	13.51
5M2C.PDB	OG, A_SER_179	ND2, A_ASN_184	HD21, A_ASN_184	2.93	2.13	18.24
5M2C.PDB	OD2, A_ASP_128	NE2, A_HIS_191	HE2, A_HIS_191	2.69	1.84	6.13
5M2C.PDB	OH, B_TYR_127	NE2, B_HIS_151	HE2, B_HIS_151	2.61	1.78	13.01
5M2C.PDB	OG, B_SER_179	ND2, B_ASN_184	HD21, B_ASN_184	2.89	2.10	19.97
5M2C.PDB	OD2, B_ASP_128	NE2, B_HIS_191	HE2, B_HIS_191	2.71	1.86	7.63
5M33.PDB	OD1, A_ASP_122	NE2, A_GLN_118	HE21, A_GLN_118	2.92	2.20	28.21
5M33.PDB	OD1, A_ASP_195	NZ, A_LYS_124	HZ3, A_LYS_124	2.81	2.00	20.18
5M33.PDB	NE2, A_HIS_151	OH, A_TYR_127	HH, A_TYR_127	2.74	1.90	5.54
5M33.PDB	OD1, A_ASP_155	NZ, A_LYS_187	HZ1, A_LYS_187	2.82	1.95	10.61
5M33.PDB	OD2, A_ASP_128	NE2, A_HIS_191	HE2, A_HIS_191	2.76	2.00	23.16
5M33.PDB	OD1, A_ASP_196	NE2, A_GLN_192	HE21, A_GLN_192	2.98	2.18	18.41
5M33.PDB	OE1, A_GLU_188	NZ, A_LYS_193	HZ2, A_LYS_193	2.93	2.07	12.47
5M33.PDB	OD1, B_ASP_122	NE2, B_GLN_118	HE21, B_GLN_118	2.96	2.19	23.61
5M33.PDB	NE2, B_HIS_151	OH, B_TYR_127	HH, B_TYR_127	2.78	1.94	5.42
5M33.PDB	OE1, B_GLN_133	NE2, B_GLN_129	HE22, B_GLN_129	2.83	2.06	21.87
5M33.PDB	OD1, B_ASP_189	OG, B_SER_160	HG, B_SER_160	2.86	2.13	25.03
5M33.PDB	OD2, B_ASP_128	NE2, B_HIS_191	HE2, B_HIS_191	2.69	1.83	4.41
5M33.PDB	OD1, B_ASP_196	NE2, B_GLN_192	HE21, B_GLN_192	2.92	2.12	17.81
5M3D.PDB	OD2, A_ASP_195	NZ, A_LYS_124	HZ1, A_LYS_124	2.68	1.86	18.64
5M3D.PDB	NE2, A_HIS_151	OH, A_TYR_127	HH, A_TYR_127	2.90	2.07	7.76
5M3D.PDB	OG, A_SER_159	OG1, A_THR_163	HG1, A_THR_163	2.65	1.81	3.28
5M3D.PDB	OD2, A_ASP_128	NE2, A_HIS_191	HE2, A_HIS_191	2.68	1.84	10.19
5M3D.PDB	OD2, B_ASP_128	NE2, B_HIS_191	HE2, B_HIS_191	2.60	1.78	15.29
5M3D.PDB	OH, C_TYR_127	NE2, C_HIS_151	HE2, C_HIS_151	2.47	1.64	11.96
5M3D.PDB	OD2, C_ASP_128	NE2, C_HIS_191	HE2, C_HIS_191	2.54	1.74	17.73
5M3D.PDB	OD2, D_ASP_128	NE2, D_HIS_191	HE2, D_HIS_191	2.53	1.71	14.84
5M3T.PDB	NE2, A_HIS_151	OH, A_TYR_127	HH, A_TYR_127	2.73	1.92	14.40
5M3T.PDB	OG, A_SER_159	OG1, A_THR_161	HG1, A_THR_161	2.93	2.10	8.83
5M3T.PDB	OD1, A_ASP_128	NE2, A_HIS_191	HE2, A_HIS_191	2.70	1.84	4.47
5M3T.PDB	OD2, B_ASP_195	NZ, B_LYS_124	HZ1, B_LYS_124	2.94	2.15	23.24
5M3T.PDB	NE2, B_HIS_151	OH, B_TYR_127	HH, B_TYR_127	2.86	2.03	6.62
5M3T.PDB	OD1, B_ASP_128	NE2, B_HIS_191	HE2, B_HIS_191	2.76	1.92	11.16
5M4R.PDB	OG, A_SER_159	OG1, A_THR_163	HG1, A_THR_163	2.93	2.14	15.31
5M4R.PDB	OD2, A_ASP_128	NE2, A_HIS_191	HE2, A_HIS_191	2.54	1.73	17.27
5M4R.PDB	OG, B_SER_159	OG1, B_THR_163	HG1, B_THR_163	2.85	2.02	5.63
5M4R.PDB	OG, C_SER_159	OG1, C_THR_163	HG1, C_THR_163	2.95	2.12	7.91
5M4R.PDB	OD2, E_ASP_128	NE2, E_HIS_191	HE2, E_HIS_191	2.53	1.73	17.17
5T6P.PDB	OD1, A_ASP_75	NE, A_ARG_24	HE, A_ARG_24	2.87	2.06	16.15
5T6P.PDB	OD1, A_ASP_87	NH2, A_ARG_66	HH22, A_ARG_66	2.87	2.03	10.92
5T6P.PDB	OG, A_SER_136	NE2, A_GLN_129	HE22, A_GLN_129	2.81	1.96	6.44
5T6P.PDB	OG, A_SER_182	NE1, A_TRP_153	HE1, A_TRP_153	2.84	2.00	11.05
5T6P.PDB	OD1, A_ASP_175	OG1, A_THR_177	HG1, A_THR_177	2.59	1.78	13.64
5T6P.PDB	OD1, A_ASN_166	OG, A_SER_182	HG, A_SER_182	2.54	1.72	9.61

5T6P.PDB	OE1, B_GLU_46	NE, B_ARG_38	HE, B_ARG_38	2.70	1.96	26.33
5T6P.PDB	OE1, A_GLN_43	NE2, B_GLN_39	HE22, B_GLN_39	2.71	1.86	5.14
5T6P.PDB	OD1, B_ASN_74	NE, B_ARG_72	HE, B_ARG_72	2.87	2.14	26.22
5T6P.PDB	OD1, C_ASP_75	NE, C_ARG_24	HE, C_ARG_24	2.92	2.14	20.59
5T6P.PDB	OD1, C_ASP_75	NH2, C_ARG_24	HH21, C_ARG_24	2.94	2.18	23.70
5T6P.PDB	OE1, D_GLN_39	NE2, C_GLN_43	HE22, C_GLN_43	3.00	2.17	12.88
5T6P.PDB	OG, C_SER_136	NE2, C_GLN_129	HE22, C_GLN_129	2.79	1.95	11.34
5T6P.PDB	OG, C_SER_182	NE1, C_TRP_153	HE1, C_TRP_153	2.89	2.07	15.50
5T6P.PDB	OD1, C_ASP_175	OG1, C_THR_177	HG1, C_THR_177	2.69	1.86	7.21
5T6P.PDB	OD1, C_ASN_166	OG, C_SER_182	HG, C_SER_182	2.45	1.64	11.11
5T6P.PDB	OG, C_SER_213	OG1, C_THR_198	HG1, C_THR_198	3.00	2.20	14.46
5T6P.PDB	OE1, C_GLN_43	NE2, D_GLN_39	HE22, D_GLN_39	2.79	1.94	7.20
5T6P.PDB	OD1, D_ASN_74	NE, D_ARG_72	HE, D_ARG_72	2.79	2.07	27.15
5T6P.PDB	OG, D_SER_182	NE1, D_TRP_157	HE1, D_TRP_157	2.97	2.13	11.56
5T6P.PDB	OE1, C_GLU_39	NE, E_ARG_5	HE, E_ARG_5	2.86	2.02	10.72
5T78.PDB	OE1, B_GLN_39	NE2, A_GLN_43	HE22, A_GLN_43	2.92	2.08	9.79
5T78.PDB	OD2, A_ASP_87	NH1, A_ARG_66	HH12, A_ARG_66	2.55	1.80	24.29
5T78.PDB	OD1, A_ASP_87	NH2, A_ARG_66	HH22, A_ARG_66	2.87	2.03	11.23
5T78.PDB	OG, A_SER_136	NE2, A_GLN_129	HE22, A_GLN_129	2.86	2.01	3.70
5T78.PDB	OG, A_SER_182	NE1, A_TRP_153	HE1, A_TRP_153	2.68	1.86	12.79
5T78.PDB	OD1, A_ASP_175	OG1, A_THR_177	HG1, A_THR_177	2.57	1.74	7.68
5T78.PDB	OD1, A_ASN_166	OG, A_SER_182	HG, A_SER_182	2.63	1.89	23.17
5T78.PDB	OD2, A_ASP_156	ND1, A_HIS_194	HD1, A_HIS_194	2.73	1.92	16.43
5T78.PDB	ND1, A_HIS_203	OG1, A_THR_205	HG1, A_THR_205	2.99	2.26	25.09
5T78.PDB	OG1, A_THR_198	OG, A_SER_213	HG, A_SER_213	2.76	1.99	20.46
5T78.PDB	OE1, B_GLU_46	NE, B_ARG_38	HE, B_ARG_38	2.94	2.16	20.63
5T78.PDB	OH, B_TYR_94	NH1, B_ARG_38	HH11, B_ARG_38	2.90	2.09	15.42
5T78.PDB	OD1, B_ASP_90	NH1, B_ARG_38	HH12, B_ARG_38	2.89	2.09	17.62
5T78.PDB	OE1, A_GLN_43	NE2, B_GLN_39	HE22, B_GLN_39	2.63	1.78	5.56
5T78.PDB	OD1, B_ASN_74	NE, B_ARG_72	HE, B_ARG_72	2.69	1.95	25.68
5T78.PDB	OE1, B_GLN_39	OH, B_TYR_95	HH, B_TYR_95	2.91	2.11	14.46
5T78.PDB	OG1, B_THR_185	OG1, B_THR_140	HG1, B_THR_140	2.97	2.14	5.19
5T78.PDB	OE1, A_GLU_39	NH1, F_ARG_5	HH11, F_ARG_5	2.68	1.83	9.33
5T78.PDB	OD1, C_ASP_75	NE, C_ARG_24	HE, C_ARG_24	2.96	2.16	17.61
5T78.PDB	OH, C_TYR_37	ND2, C_ASN_33	HD21, C_ASN_33	2.96	2.18	21.06
5T78.PDB	OD2, C_ASP_87	NH1, C_ARG_66	HH12, C_ARG_66	2.35	1.56	19.31
5T78.PDB	OG, C_SER_182	NE1, C_TRP_153	HE1, C_TRP_153	2.84	2.01	13.01
5T78.PDB	OD1, C_ASP_175	OG1, C_THR_177	HG1, C_THR_177	2.53	1.70	9.09
5T78.PDB	OD1, C_ASN_166	OG, C_SER_182	HG, C_SER_182	2.85	2.09	21.73
5T78.PDB	OD2, C_ASP_156	ND1, C_HIS_194	HD1, C_HIS_194	2.58	1.78	18.23
5T78.PDB	ND1, C_HIS_203	OG1, C_THR_205	HG1, C_THR_205	3.00	2.26	23.83
5T78.PDB	OE1, D_GLU_46	NE, D_ARG_38	HE, D_ARG_38	2.65	1.91	25.36
5T78.PDB	OH, D_TYR_94	NH1, D_ARG_38	HH11, D_ARG_38	2.88	2.06	14.14
5T78.PDB	OD1, D_ASP_90	NH1, D_ARG_38	HH12, D_ARG_38	2.85	2.05	16.93
5T78.PDB	OE1, C_GLN_43	NE2, D_GLN_39	HE22, D_GLN_39	2.72	1.87	5.23
5T78.PDB	OD1, D_ASN_74	NE, D_ARG_72	HE, D_ARG_72	2.71	2.01	29.42
5T78.PDB	OE1, D_GLN_39	OH, D_TYR_95	HH, D_TYR_95	2.98	2.17	11.35
5T78.PDB	OG, D_SER_182	NE1, D_TRP_157	HE1, D_TRP_157	2.99	2.19	18.03
5T78.PDB	OD1, C_ASN_142	NE2, D_HIS_167	HE2, D_HIS_167	2.85	2.00	9.68
5T78.PDB	OE1, C_GLU_39	NH1, E_ARG_5	HH11, E_ARG_5	2.69	1.87	13.16
5U3J.PDB	OE1, H_GLN_81	NE, H_ARG_19	HE, H_ARG_19	2.98	2.21	22.79
5U3J.PDB	OD2, H_ASP_53	NE1, H_TRP_33	HE1, H_TRP_33	2.97	2.22	24.73
5U3J.PDB	OE1, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.88	2.05	13.82
5U3J.PDB	OD1, H_ASP_86	NH1, H_ARG_38	HH12, H_ARG_38	2.85	2.09	23.00
5U3J.PDB	OG, H_SER_35	NE1, H_TRP_47	HE1, H_TRP_47	2.44	1.73	27.73
5U3J.PDB	OE1, H_GLU_58	NE, H_ARG_50	HE, H_ARG_50	2.83	2.12	29.07
5U3J.PDB	OE1, H_GLU_58	NH2, H_ARG_50	HH21, H_ARG_50	2.79	2.08	29.38
5U3J.PDB	OD2, H_ASP_86	NH1, H_ARG_66	HH12, H_ARG_66	2.57	1.73	9.26

5U3J.PDB	OD1, H_ASP_86	NH2, H_ARG_66	HH22, H_ARG_66	2.89	2.04	5.32
5U3J.PDB	OD1, L_ASP_31	OH, H_TYR_100K	HH, H_TYR_100K	2.88	2.04	5.22
5U3J.PDB	OG, H_SER_180	NE1, H_TRP_154	HE1, H_TRP_154	2.98	2.15	12.85
5U3J.PDB	OE1, H_GLU_100F	OH, L_TYR_32	HH, L_TYR_32	2.62	1.91	27.84
5U3J.PDB	OE1, L_GLN_89	OH, L_TYR_36	HH, L_TYR_36	2.74	1.93	13.79
5U3J.PDB	OE1, H_GLN_39	NE2, L_GLN_38	HE22, L_GLN_38	2.66	1.83	12.57
5U3J.PDB	OG, L_SER_131	NE2, L_GLN_124	HE22, L_GLN_124	2.67	1.82	7.69
5U3J.PDB	OG, L_SER_177	NE1, L_TRP_148	HE1, L_TRP_148	2.81	2.02	19.92
5U3N.PDB	OE1, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.91	2.07	9.07
5U3N.PDB	OH, H_TYR_90	NH1, H_ARG_38	HH11, H_ARG_38	3.00	2.21	20.04
5U3N.PDB	OD2, H_ASP_58	NE, H_ARG_50	HE, H_ARG_50	2.78	1.98	18.36
5U3N.PDB	OD2, A_ASP_674	NH1, H_ARG_52A	HH12, H_ARG_52A	3.00	2.24	24.41
5U3N.PDB	OD1, H_ASP_53	NH2, H_ARG_52A	HH21, H_ARG_52A	2.93	2.18	25.35
5U3N.PDB	OD2, H_ASP_86	NH1, H_ARG_66	HH12, H_ARG_66	2.73	1.91	14.46
5U3N.PDB	OD1, H_ASP_73	NE, H_ARG_71	HE, H_ARG_71	2.93	2.13	17.92
5U3N.PDB	OE1, H_GLU_100E	NE, H_ARG_100B	HE, H_ARG_100B	2.83	1.97	4.42
5U3N.PDB	OE2, H_GLU_100E	NH2, H_ARG_100B	HH21, H_ARG_100B	2.91	2.08	12.18
5U3N.PDB	OD1, L_ASP_31	NH2, H_ARG_100B	HH22, H_ARG_100B	2.97	2.15	14.50
5U3N.PDB	OD1, L_ASN_34	ND2, H_ASN_100J	HD21, H_ASN_100J	2.72	1.86	2.61
5U3N.PDB	OG, H_SER_180	NE1, H_TRP_154	HE1, H_TRP_154	2.95	2.11	9.10
5U3N.PDB	OD1, L_ASN_138	NE2, H_HIS_164	HE2, H_HIS_164	2.92	2.21	29.54
5U3N.PDB	OD1, H_ASP_144	NE2, H_GLN_171	HE22, H_GLN_171	2.99	2.19	18.08
5U3N.PDB	OH, L_TYR_140	OG, L_SER_12	HG, L_SER_12	2.60	1.87	23.71
5U3N.PDB	OE1, L_GLN_89	ND2, L_ASN_34	HD22, L_ASN_34	2.99	2.18	18.14
5U3N.PDB	OE1, L_GLN_89	OH, L_TYR_36	HH, L_TYR_36	2.64	1.80	1.88
5U3N.PDB	OG, L_SER_131	NE2, L_GLN_124	HE22, L_GLN_124	2.80	1.94	3.81
5U3N.PDB	OD1, L_ASP_105	OH, L_TYR_140	HH, L_TYR_140	2.61	1.87	24.55
5U3N.PDB	OG, L_SER_177	NE1, L_TRP_148	HE1, L_TRP_148	2.84	2.01	13.43
5U3N.PDB	OD1, L_ASP_170	OG1, L_THR_172	HG1, L_THR_172	2.63	1.80	7.71
5U3N.PDB	OD2, L_ASP_105	OH, L_TYR_173	HH, L_TYR_173	2.66	1.88	16.93
5UCB.PDB	OG, H_SER_33	NE2, H_HIS_35	HE2, H_HIS_35	2.88	2.09	19.50
5UCB.PDB	OE1, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.85	2.03	15.54
5UCB.PDB	OH, H_TYR_90	NH1, H_ARG_38	HH11, H_ARG_38	2.94	2.12	15.88
5UCB.PDB	OD1, H_ASP_86	NH1, H_ARG_38	HH12, H_ARG_38	2.88	2.08	18.54
5UCB.PDB	OE1, L_GLN_38	NE2, H_GLN_39	HE22, H_GLN_39	2.96	2.12	9.92
5UCB.PDB	OG, H_SER_50	NE1, H_TRP_47	HE1, H_TRP_47	2.72	1.98	25.90
5UCB.PDB	OD2, H_ASP_86	NH1, H_ARG_66	HH12, H_ARG_66	2.75	1.90	5.99
5UCB.PDB	OD1, H_ASP_72	OG, H_SER_74	HG, H_SER_74	2.60	1.83	20.07
5UCB.PDB	OD1, H_ASN_197	OG1, H_SER_153	HG, H_SER_153	2.85	2.06	15.76
5UCB.PDB	OG, H_SER_180	NE1, H_TRP_154	HE1, H_TRP_154	2.92	2.07	7.16
5UCB.PDB	OD1, H_ASP_144	NE2, H_GLN_171	HE22, H_GLN_171	2.78	1.99	18.86
5UCB.PDB	OG, H_SER_188	OH, H_TYR_194	HH, H_TYR_194	2.72	1.90	9.93
5UCB.PDB	OD1, H_ASP_208	ND2, H_ASN_197	HD22, H_ASN_197	2.80	1.95	7.44
5UCB.PDB	OE1, L_GLN_3	OG, L_SER_26	HG, L_SER_26	2.61	1.78	7.17
5UCB.PDB	OD2, B_ASP_51	OG, L_SER_30	HG, L_SER_30	2.58	1.81	20.19
5UCB.PDB	OE1, L_GLN_89	OH, L_TYR_36	HH, L_TYR_36	2.64	1.84	15.57
5UCB.PDB	OH, L_TYR_86	NE2, L_GLN_37	HE21, L_GLN_37	2.99	2.15	9.80
5UCB.PDB	OE1, H_GLN_39	NE2, L_GLN_38	HE22, L_GLN_38	2.95	2.13	14.86
5UCB.PDB	OD2, L_ASP_82	NE, L_ARG_61	HE, L_ARG_61	2.82	2.01	16.79
5UCB.PDB	OD1, L_ASP_82	NH2, L_ARG_61	HH21, L_ARG_61	2.85	1.99	4.65
5UCB.PDB	OG1, L_THR_22	OG1, L_THR_72	HG1, L_THR_72	2.96	2.18	19.19
5UCB.PDB	OE1, L_GLU_165	NZ, L_LYS_103	HZ3, L_LYS_103	2.77	1.90	9.89
5UCB.PDB	OG, L_SER_131	NE2, L_GLN_124	HE22, L_GLN_124	2.73	1.87	2.66
5UCB.PDB	OG, L_SER_177	NE1, L_TRP_148	HE1, L_TRP_148	2.92	2.09	12.30
5UCB.PDB	OE1, L_GLN_155	ND2, L_ASN_158	HD21, L_ASN_158	2.98	2.15	12.35
5UCB.PDB	OD1, L_ASP_170	OG1, L_THR_172	HG1, L_THR_172	2.71	1.89	8.99
5UCB.PDB	OE2, L_GLU_105	OH, L_TYR_173	HH, L_TYR_173	2.61	1.81	15.35
5UCB.PDB	OD1, B_ASP_132	NZ, B_LYS_16	HZ1, B_LYS_16	2.90	2.15	27.66

5UCB.PDB	OE2, B_GLU_87	OH, B_TYR_43	HH, B_TYR_43	2.72	1.91	12.68
5UCB.PDB	OD1, B_ASP_51	OG, B_SER_46	HG, B_SER_46	2.83	2.02	12.78
5UCB.PDB	OE1, B_GLU_87	OG, B_SER_47	HG, B_SER_47	2.62	1.82	14.05
5UCB.PDB	OD1, B_ASP_153	OH, B_TYR_100	HH, B_TYR_100	2.55	1.73	8.75
5UCB.PDB	OD2, B_ASP_101	NH1, B_ARG_103	HH12, B_ARG_103	2.89	2.11	20.47
5UCB.PDB	OE2, B_GLU_104	NE, B_ARG_107	HE, B_ARG_107	2.91	2.05	4.26
5UCB.PDB	OD1, B_ASP_117	ND1, B_HIS_133	HD1, B_HIS_133	2.95	2.15	18.23
5UCB.PDB	OG, H_SER_58	NZ, B_LYS_142	HZ3, B_LYS_142	2.83	1.96	8.82
5UCB.PDB	OD1, L_ASP_91	NH2, B_ARG_144	HH21, B_ARG_144	2.84	2.03	16.18
5UK0.PDB	OD1, F_ASP_590	ND2, B_ASN_560	HD22, B_ASN_560	2.72	1.94	19.72
5UK0.PDB	OD1, D_ASP_586	NH2, C_ARG_311	HH22, C_ARG_311	2.98	2.20	18.56
5UK0.PDB	OD1, B_ASP_590	ND2, D_ASN_560	HD22, D_ASN_560	2.73	1.95	20.06
5UK0.PDB	OH, D_TYR_659	ND2, D_ASN_628	HD22, D_ASN_628	2.78	1.98	17.11
5VXJ.PDB	OD2, A_ASP_309	NH2, A_ARG_55	HH21, A_ARG_55	2.90	2.12	21.39
5VXJ.PDB	OG, A_SER_302	NZ, A_LYS_62	HZ2, A_LYS_62	2.77	1.91	12.44
5VXJ.PDB	OG, A_SER_306	NZ, A_LYS_62	HZ3, A_LYS_62	2.75	1.92	16.95
5VXJ.PDB	OD2, A_ASP_97	NE, A_ARG_101	HE, A_ARG_101	2.80	1.97	13.39
5VXJ.PDB	OE2, A_GLU_229	OH, A_TYR_153	HH, A_TYR_153	2.70	1.94	21.05
5VXJ.PDB	OD1, A_ASP_287	OH, A_TYR_164	HH, A_TYR_164	2.72	1.96	22.05
5VXJ.PDB	OE2, A_GLU_268	NE2, A_GLN_191	HE22, A_GLN_191	2.93	2.12	16.99
5VXJ.PDB	OD1, A_ASP_254	NZ, A_LYS_203	HZ2, A_LYS_203	2.48	1.62	10.37
5VXJ.PDB	OD2, A_ASP_166	NZ, A_LYS_205	HZ2, A_LYS_205	2.60	1.73	10.82
5VXJ.PDB	OD2, A_ASP_166	OH, A_TYR_206	HH, A_TYR_206	2.59	1.78	13.29
5VXJ.PDB	OD1, A_ASN_249	OG1, A_THR_251	HG1, A_THR_251	2.61	1.88	24.99
5VXJ.PDB	OD1, A_ASN_58	ND2, A_ASN_305	HD21, A_ASN_305	2.96	2.14	16.38
5VXJ.PDB	OE1, B_GLN_82	NE, B_ARG_19	HE, B_ARG_19	2.47	1.66	15.76
5VXJ.PDB	OE2, B_GLU_46	NE, B_ARG_38	HE, B_ARG_38	2.93	2.12	17.64
5VXJ.PDB	OH, B_TYR_94	NH1, B_ARG_38	HH11, B_ARG_38	2.80	1.98	13.19
5VXJ.PDB	OD1, B_ASP_90	NH1, B_ARG_38	HH12, B_ARG_38	2.76	1.91	7.08
5VXJ.PDB	OD1, B_ASN_35	NE, B_ARG_50	HE, B_ARG_50	2.65	1.82	11.22
5VXJ.PDB	OE1, I_GLU_200	NH1, B_ARG_50	HH12, B_ARG_50	2.92	2.07	7.25
5VXJ.PDB	OD2, B_ASP_90	NH1, B_ARG_67	HH12, B_ARG_67	2.82	2.01	16.67
5VXJ.PDB	OD1, B_ASP_90	NH2, B_ARG_67	HH22, B_ARG_67	2.96	2.12	11.06
5VXJ.PDB	OD1, B_ASN_84	NE2, B_GLN_82	HE21, B_GLN_82	2.95	2.09	2.81
5VXJ.PDB	OG1, B_THR_107	ND2, B_ASN_97	HD21, B_ASN_97	2.64	1.86	19.39
5VXJ.PDB	OE1, I_GLU_201	OH, B_TYR_105	HH, B_TYR_105	2.51	1.70	12.69
5VXJ.PDB	OD2, C_ASP_309	NH2, C_ARG_55	HH21, C_ARG_55	2.97	2.17	18.00
5VXJ.PDB	OG, C_SER_302	NZ, C_LYS_62	HZ2, C_LYS_62	2.61	1.73	6.54
5VXJ.PDB	OE2, C_GLU_154	OG, C_SER_82	HG, C_SER_82	2.58	1.81	19.25
5VXJ.PDB	OD2, C_ASP_97	NE, C_ARG_101	HE, C_ARG_101	2.84	2.03	16.71
5VXJ.PDB	OD1, C_ASP_287	OH, C_TYR_164	HH, C_TYR_164	2.77	1.96	12.03
5VXJ.PDB	OE2, C_GLU_268	NE2, C_GLN_191	HE22, C_GLN_191	2.80	1.97	12.09
5VXJ.PDB	OE1, C_GLU_201	NZ, C_LYS_197	HZ3, C_LYS_197	2.59	1.85	27.46
5VXJ.PDB	OD1, C_ASP_254	NZ, C_LYS_203	HZ2, C_LYS_203	2.69	1.87	19.49
5VXJ.PDB	OD2, C_ASP_166	NZ, C_LYS_205	HZ2, C_LYS_205	2.85	1.99	12.15
5VXJ.PDB	OD2, C_ASP_166	OH, C_TYR_206	HH, C_TYR_206	2.58	1.76	10.37
5VXJ.PDB	OD1, C_ASN_249	OG1, C_THR_251	HG1, C_THR_251	2.56	1.78	18.84
5VXJ.PDB	OD1, C_ASN_58	ND2, C_ASN_305	HD21, C_ASN_305	2.84	2.04	17.79
5VXJ.PDB	OD1, C_ASN_140	NE, D_ARG_19	HE, D_ARG_19	2.55	1.80	23.66
5VXJ.PDB	OE1, D_GLN_82	NH1, D_ARG_19	HH11, D_ARG_19	2.94	2.14	18.04
5VXJ.PDB	OE2, D_GLU_46	NE, D_ARG_38	HE, D_ARG_38	2.46	1.69	20.96
5VXJ.PDB	OD1, D_ASP_90	NH1, D_ARG_38	HH12, D_ARG_38	2.86	2.04	15.32
5VXJ.PDB	OD1, D_ASN_35	NE, D_ARG_50	HE, D_ARG_50	2.89	2.08	17.01
5VXJ.PDB	OD2, D_ASP_90	NH1, D_ARG_67	HH12, D_ARG_67	2.76	1.94	14.49
5VXJ.PDB	OD1, D_ASP_90	NH2, D_ARG_67	HH22, D_ARG_67	2.92	2.07	6.62
5VXJ.PDB	OD1, D_ASN_74	NE, D_ARG_72	HE, D_ARG_72	2.76	1.91	6.10
5VXJ.PDB	OD1, D_ASN_84	NE2, D_GLN_82	HE21, D_GLN_82	2.80	1.94	4.20
5VXJ.PDB	OG1, D_THR_107	ND2, D_ASN_97	HD21, D_ASN_97	2.71	1.91	17.78

5VXJ.PDB	OE1, E_GLU_201	OH, D_TYR_105	HH, D_TYR_105	2.53	1.70	8.84
5VXJ.PDB	OD2, E_ASP_309	NH2, E_ARG_55	HH21, E_ARG_55	2.82	2.06	24.28
5VXJ.PDB	OG, E_SER_306	NZ, E_LYS_62	HZ1, E_LYS_62	2.46	1.61	13.80
5VXJ.PDB	OD2, F_ASP_73	NZ, E_LYS_137	HZ2, E_LYS_137	2.77	1.96	20.15
5VXJ.PDB	OD1, E_ASP_287	OH, E_TYR_164	HH, E_TYR_164	2.85	2.09	21.13
5VXJ.PDB	OD1, D_ASN_97	NZ, E_LYS_197	HZ1, E_LYS_197	2.80	1.95	14.72
5VXJ.PDB	OE2, E_GLU_201	NZ, E_LYS_197	HZ3, E_LYS_197	2.47	1.71	25.42
5VXJ.PDB	OD1, E_ASP_254	NZ, E_LYS_203	HZ2, E_LYS_203	2.55	1.67	5.69
5VXJ.PDB	OD2, E_ASP_166	NZ, E_LYS_205	HZ2, E_LYS_205	2.79	1.95	15.80
5VXJ.PDB	OD2, E_ASP_166	OH, E_TYR_206	HH, E_TYR_206	2.80	1.99	13.17
5VXJ.PDB	OD1, E_ASN_249	OG1, E_THR_251	HG1, E_THR_251	2.55	1.84	26.63
5VXJ.PDB	OD1, E_ASN_58	ND2, E_ASN_305	HD21, E_ASN_305	2.80	1.98	14.83
5VXJ.PDB	OE1, F_GLN_82	NE, F_ARG_19	HE, F_ARG_19	2.82	1.96	3.39
5VXJ.PDB	OD1, F_ASN_97	ND2, F_ASN_35	HD22, F_ASN_35	2.86	2.08	21.21
5VXJ.PDB	OD1, F_ASP_90	NH1, F_ARG_38	HH12, F_ARG_38	2.92	2.20	28.14
5VXJ.PDB	OE2, F_GLU_46	NH2, F_ARG_38	HH21, F_ARG_38	2.73	1.93	18.99
5VXJ.PDB	OE1, G_GLU_200	NH2, F_ARG_50	HH22, F_ARG_50	2.70	1.89	15.49
5VXJ.PDB	OD2, F_ASP_90	NH1, F_ARG_67	HH12, F_ARG_67	2.83	1.99	10.41
5VXJ.PDB	OD1, F_ASN_74	NE, F_ARG_72	HE, F_ARG_72	2.72	1.88	10.50
5VXJ.PDB	OG1, F_THR_107	ND2, F_ASN_97	HD21, F_ASN_97	2.73	1.95	21.26
5VXJ.PDB	OE1, G_GLU_201	OH, F_TYR_105	HH, F_TYR_105	2.57	1.75	11.97
5VXJ.PDB	OD2, G_ASP_97	NE, G_ARG_101	HE, G_ARG_101	2.67	1.82	7.54
5VXJ.PDB	OD1, G_ASP_287	OH, G_TYR_164	HH, G_TYR_164	2.79	1.99	15.03
5VXJ.PDB	OE2, G_GLU_201	NZ, G_LYS_197	HZ3, G_LYS_197	2.59	1.86	28.64
5VXJ.PDB	OD1, G_ASP_254	NZ, G_LYS_203	HZ2, G_LYS_203	2.49	1.62	9.92
5VXJ.PDB	OD2, G_ASP_166	NZ, G_LYS_205	HZ2, G_LYS_205	2.82	1.96	12.05
5VXJ.PDB	OD2, G_ASP_166	OH, G_TYR_206	HH, G_TYR_206	2.52	1.70	11.57
5VXJ.PDB	OE1, H_GLN_111	OG1, G_THR_217	HG1, G_THR_217	2.86	2.17	29.58
5VXJ.PDB	OE1, H_GLN_82	NE, H_ARG_19	HE, H_ARG_19	2.76	1.91	8.69
5VXJ.PDB	OD1, H_ASN_97	ND2, H_ASN_35	HD22, H_ASN_35	2.85	2.10	23.91
5VXJ.PDB	OD1, H_ASP_90	NH1, H_ARG_38	HH12, H_ARG_38	3.00	2.16	12.34
5VXJ.PDB	OD1, H_ASN_35	NE, H_ARG_50	HE, H_ARG_50	2.75	1.93	14.53
5VXJ.PDB	OD2, H_ASP_90	NH1, H_ARG_67	HH12, H_ARG_67	2.89	2.05	9.62
5VXJ.PDB	OD1, H_ASN_74	NE, H_ARG_72	HE, H_ARG_72	2.76	1.95	17.61
5VXJ.PDB	OD1, H_ASN_84	NE2, H_GLN_82	HE21, H_GLN_82	2.86	2.05	16.57
5VXJ.PDB	OG1, H_THR_107	ND2, H_ASN_97	HD21, H_ASN_97	2.53	1.81	26.67
5VXJ.PDB	OD1, I_ASP_309	ND2, I_ASN_58	HD22, I_ASN_58	2.73	1.88	5.94
5VXJ.PDB	OE1, I_GLU_154	OG, I_SER_82	HG, I_SER_82	2.52	1.79	24.33
5VXJ.PDB	OD2, I_ASP_97	NE, I_ARG_101	HE, I_ARG_101	2.83	2.07	23.56
5VXJ.PDB	OD2, J_ASP_73	NZ, I_LYS_137	HZ3, I_LYS_137	2.90	2.17	29.52
5VXJ.PDB	OD1, I_ASP_287	OH, I_TYR_164	HH, I_TYR_164	2.95	2.16	17.45
5VXJ.PDB	OD1, B_ASN_97	NZ, I_LYS_197	HZ1, I_LYS_197	2.68	1.88	21.92
5VXJ.PDB	OD1, I_ASP_254	NZ, I_LYS_203	HZ2, I_LYS_203	2.60	1.74	12.72
5VXJ.PDB	OD2, I_ASP_166	NZ, I_LYS_205	HZ2, I_LYS_205	2.77	1.91	10.79
5VXJ.PDB	OD2, I_ASP_166	OH, I_TYR_206	HH, I_TYR_206	2.50	1.67	8.28
5VXJ.PDB	OD1, I_ASN_249	OG1, I_THR_251	HG1, I_THR_251	2.69	1.98	27.82
5VXJ.PDB	OE1, J_GLN_82	NE, J_ARG_19	HE, J_ARG_19	2.52	1.72	17.43
5VXJ.PDB	OD1, J_ASN_97	ND2, J_ASN_35	HD22, J_ASN_35	3.00	2.21	19.94
5VXJ.PDB	OD1, J_ASP_90	NH1, J_ARG_38	HH12, J_ARG_38	2.89	2.13	23.59
5VXJ.PDB	OE2, J_GLU_46	NH2, J_ARG_38	HH21, J_ARG_38	2.77	1.96	16.80
5VXJ.PDB	OD1, J_ASN_35	NE, J_ARG_50	HE, J_ARG_50	2.74	1.91	11.68
5VXJ.PDB	OD2, J_ASP_90	NH1, J_ARG_67	HH12, J_ARG_67	2.55	1.74	16.72
5VXJ.PDB	OD1, J_ASP_90	NH2, J_ARG_67	HH22, J_ARG_67	2.84	1.98	5.11
5VXJ.PDB	OD1, J_ASN_84	NE2, J_GLN_82	HE21, J_GLN_82	2.94	2.08	3.32
5VXJ.PDB	OG1, J_THR_107	ND2, J_ASN_97	HD21, J_ASN_97	2.57	1.77	17.56
5VXK.PDB	OD2, B_ASP_90	NH2, B_ARG_67	HH22, B_ARG_67	2.27	1.58	28.79
5VXK.PDB	OG, A_SER_168	NE2, B_GLN_106	HE21, B_GLN_106	2.99	2.23	24.43
5VXK.PDB	OD2, A_ASP_287	NE2, B_GLN_106	HE22, B_GLN_106	2.77	1.94	12.81

5VXK.PDB	OD2, A_ASP_287	OH, A_TYR_164	HH, A_TYR_164	2.91	2.21	28.15
5VXK.PDB	OD2, A_ASP_261	NZ, A_LYS_196	HZ3, A_LYS_196	2.74	1.87	9.57
5VXK.PDB	OG1, B_THR_102	OH, A_TYR_276	HH, A_TYR_276	2.57	1.73	6.50
5VXK.PDB	OH, A_TYR_160	ND2, A_ASN_293	HD22, A_ASN_293	2.77	1.97	18.05
5VXL.PDB	OD1, A_ASP_309	ND2, A_ASN_58	HD22, A_ASN_58	2.92	2.09	13.70
5VXL.PDB	OE1, A_GLU_154	OG, A_SER_82	HG, A_SER_82	2.52	1.77	21.68
5VXL.PDB	OD2, A_ASP_88	NE2, A_GLN_84	HE21, A_GLN_84	2.89	2.16	27.92
5VXL.PDB	OD1, A_ASP_254	NZ, A_LYS_203	HZ3, A_LYS_203	2.55	1.71	15.49
5VXL.PDB	OD2, B_ASP_52	NZ, A_LYS_205	HZ1, A_LYS_205	3.00	2.13	10.69
5VXL.PDB	OD2, A_ASP_166	OH, A_TYR_206	HH, A_TYR_206	2.43	1.61	11.33
5VXL.PDB	OE1, A_GLN_148	NE1, A_TRP_226	HE1, A_TRP_226	2.87	2.02	9.28
5VXL.PDB	OE2, A_GLU_286	ND2, A_ASN_255	HD22, A_ASN_255	2.74	1.94	17.54
5VXL.PDB	OD1, B_ASP_91	NH1, B_ARG_38	HH12, B_ARG_38	2.97	2.23	26.01
5VXL.PDB	OD1, A_ASP_166	OG, B_SER_55	HG, B_SER_55	2.56	1.73	4.68
5VXL.PDB	OD2, B_ASP_91	NH1, B_ARG_68	HH12, B_ARG_68	2.83	2.06	22.74
5VXL.PDB	OD1, B_ASN_75	NE, B_ARG_73	HE, B_ARG_73	2.98	2.26	28.00
5VXL.PDB	OH, B_TYR_81	NE, B_ARG_79	HE, B_ARG_79	2.96	2.14	13.15
5VXL.PDB	OE2, A_GLU_201	NH2, B_ARG_102	HH22, B_ARG_102	2.87	2.08	20.03
5VXM.PDB	OD1, A_ASP_309	ND2, A_ASN_58	HD22, A_ASN_58	2.74	1.89	5.63
5VXM.PDB	OD1, A_ASP_88	NE2, A_GLN_84	HE21, A_GLN_84	2.60	1.75	9.62
5VXM.PDB	OD1, A_ASP_287	OH, A_TYR_164	HH, A_TYR_164	2.66	1.84	11.86
5VXM.PDB	OE2, B_GLU_111	NE1, A_TRP_177	HE1, A_TRP_177	2.76	1.97	19.61
5VXM.PDB	OD2, A_ASP_166	NZ, A_LYS_205	HZ3, A_LYS_205	2.79	1.92	8.41
5VXM.PDB	OD2, A_ASP_166	OH, A_TYR_206	HH, A_TYR_206	2.53	1.73	14.26
5VXM.PDB	OE2, A_GLU_288	NZ, A_LYS_291	HZ1, A_LYS_291	2.70	1.90	22.27
5VXM.PDB	OH, B_TYR_94	NH1, B_ARG_38	HH11, B_ARG_38	2.95	2.12	12.47
5VXM.PDB	OD1, B_ASP_90	NH1, B_ARG_38	HH12, B_ARG_38	2.77	1.97	17.13
5VXM.PDB	OD1, B_ASP_54	OG, B_SER_56	HG, B_SER_56	2.63	1.84	17.09
5VXM.PDB	OD2, B_ASP_90	NH1, B_ARG_67	HH12, B_ARG_67	2.75	1.92	11.95
5VXM.PDB	OD1, B_ASN_84	NE2, B_GLN_82	HE21, B_GLN_82	2.81	1.97	10.38
5VXR.PDB	OE1, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.74	1.86	23.26
5VXR.PDB	OH, H_TYR_93	NH1, H_ARG_38	HH11, H_ARG_38	2.95	1.99	15.54
5VXR.PDB	OD1, H_ASP_89	NH1, H_ARG_38	HH12, H_ARG_38	2.81	1.80	4.81
5VXR.PDB	OE1, H_GLU_46	NH2, H_ARG_38	HH21, H_ARG_38	2.83	2.01	29.32
5VXR.PDB	OE1, L_GLN_38	NZ, H_LYS_39	HZ2, H_LYS_39	2.72	1.76	14.94
5VXR.PDB	OD1, H_ASN_35	OH, H_TYR_47	HH, H_TYR_47	2.72	1.74	8.88
5VXR.PDB	OD1, P_ASN_415	OH, H_TYR_50	HH, H_TYR_50	2.71	1.82	21.79
5VXR.PDB	OD1, H_ASP_89	NH2, H_ARG_66	HH22, H_ARG_66	2.99	1.98	4.54
5VXR.PDB	OE1, H_GLN_77	OH, H_TYR_79	HH, H_TYR_79	2.72	1.76	12.10
5VXR.PDB	OE2, H_GLU_154	OH, H_TYR_151	HH, H_TYR_151	2.81	1.83	6.84
5VXR.PDB	OG, H_SER_185	NE1, H_TRP_160	HE1, H_TRP_160	2.93	1.93	7.21
5VXR.PDB	OD1, L_ASN_138	NE2, H_HIS_170	HE2, H_HIS_170	2.89	1.98	20.57
5VXR.PDB	OG1, H_THR_143	OG1, H_THR_188	HG1, H_THR_188	2.81	1.84	10.15
5VXR.PDB	OE2, L_GLU_123	NZ, H_LYS_214	HZ1, H_LYS_214	2.93	1.98	15.97
5VXR.PDB	OD1, L_ASP_70	NE, L_ARG_24	HE, L_ARG_24	2.94	2.08	26.80
5VXR.PDB	OD1, L_ASN_92	OG, L_SER_27D	HG, L_SER_27D	2.79	1.83	11.69
5VXR.PDB	OD1, L_ASN_91	NE2, L_HIS_34	HE2, L_HIS_34	2.77	1.79	12.93
5VXR.PDB	OE1, L_GLN_89	OH, L_TYR_36	HH, L_TYR_36	2.69	1.74	13.43
5VXR.PDB	OH, L_TYR_86	NE2, L_GLN_37	HE21, L_GLN_37	2.98	1.98	9.70
5VXR.PDB	OD2, L_ASP_82	NH1, L_ARG_61	HH12, L_ARG_61	2.75	1.79	15.16
5VXR.PDB	OD1, L_ASP_82	NH2, L_ARG_61	HH22, L_ARG_61	2.82	1.82	7.27
5VXR.PDB	OG, L_SER_131	NE2, L_GLN_124	HE22, L_GLN_124	2.92	1.91	5.03
5VXR.PDB	OG, L_SER_177	NE1, L_TRP_148	HE1, L_TRP_148	2.80	1.85	16.41
5VXR.PDB	OD1, L_ASP_170	OG1, L_THR_172	HG1, L_THR_172	2.70	1.76	15.44
5VXR.PDB	OG, H_SER_184	OG, L_SER_176	HG, L_SER_176	2.79	1.86	17.30
5VXR.PDB	OD1, L_ASN_161	OG, L_SER_177	HG, L_SER_177	2.64	1.73	19.24
5VXR.PDB	OG, L_SER_131	OG1, L_THR_180	HG1, L_THR_180	2.88	2.00	21.77
5VXR.PDB	OD2, L_ASP_151	ND1, L_HIS_189	HD1, L_HIS_189	2.73	1.79	17.03

5VXR.PDB	ND1, L_HIS_198	OG1, L_THR_200	HG1, L_THR_200	2.74	1.84	20.28
5VXR.PDB	NE2, P_HIS_421	OG1, P_THR_416	HG1, P_THR_416	2.72	1.87	24.94
5WKQ.PDB	OG1, A_THR_80	NZ, A_LYS_106	HZ1, A_LYS_106	2.47	1.72	27.03
5WKQ.PDB	OG, B_SER_208	NH2, A_ARG_135	HH21, A_ARG_135	2.89	2.06	11.87
5WKQ.PDB	OE2, A_GLU_182	NE2, A_GLN_162	HE21, A_GLN_162	2.71	1.89	15.15
5WKQ.PDB	OE2, B_GLU_182	NE2, B_GLN_162	HE21, B_GLN_162	2.63	1.85	20.38
5WKQ.PDB	OD1, B_ASP_148	NH1, B_ARG_196	HH11, B_ARG_196	2.87	2.13	25.83
5WKQ.PDB	OE2, A_GLU_131	ND1, B_HIS_207	HD1, B_HIS_207	2.65	1.88	22.26
5WKQ.PDB	OE1, A_GLU_131	OG1, B_THR_211	HG1, B_THR_211	2.63	1.86	19.68
5WN9.PDB	OE1, H_GLN_1	NE2, H_GLN_3	HE21, H_GLN_3	2.70	1.88	14.43
5WN9.PDB	OE1, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.78	2.00	20.76
5WN9.PDB	OH, H_TYR_94	NH2, H_ARG_38	HH21, H_ARG_38	2.96	2.17	18.48
5WN9.PDB	OD1, H_ASP_90	NH2, H_ARG_38	HH22, H_ARG_38	2.91	2.07	9.36
5WN9.PDB	OE1, H_GLN_182	NE2, H_GLN_39	HE22, H_GLN_39	2.96	2.11	8.81
5WN9.PDB	OD2, H_ASP_90	NH1, H_ARG_67	HH12, H_ARG_67	2.27	1.51	22.67
5WN9.PDB	OD1, H_ASP_73	OG, H_SER_75	HG, H_SER_75	2.58	1.79	16.04
5WN9.PDB	OG1, H_THR_69	NH1, H_ARG_84	HH12, H_ARG_84	2.83	2.06	21.62
5WN9.PDB	OD1, H_ASP_112	NE, H_ARG_98	HE, H_ARG_98	2.94	2.13	15.87
5WN9.PDB	OD2, H_ASP_112	NH1, H_ARG_98	HH11, H_ARG_98	2.84	2.01	13.12
5WN9.PDB	OG1, H_THR_218	NH2, H_ARG_162	HH21, H_ARG_162	2.83	2.04	19.79
5WN9.PDB	OE1, H_GLN_233	OH, H_TYR_180	HH, H_TYR_180	2.70	1.87	8.37
5WN9.PDB	OE1, H_GLN_39	NE2, H_GLN_182	HE22, H_GLN_182	2.85	2.00	9.41
5WN9.PDB	OD2, H_ASP_226	NE, H_ARG_205	HE, H_ARG_205	2.80	1.99	17.36
5WN9.PDB	OD1, H_ASP_226	NH1, H_ARG_205	HH11, H_ARG_205	2.89	2.03	4.48
5WN9.PDB	OG1, H_THR_164	OG1, H_THR_218	HG1, H_THR_218	2.96	2.26	28.62
5WN9.PDB	OD1, H_ASN_57	NE, A_ARG_188	HE, A_ARG_188	2.58	1.61	2.15

Table 6: The side chain hydrogen bonding networks of all experimentally determined antigen-antibody-related structures. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1A14.PDB	OE1, L_GLN_38	NE2, H_GLN_39	HE21, H_GLN_39	2.62	1.69	9.24
1A14.PDB	OH, L_TYR_36	N, H_PHE_100E	H, H_PHE_100E	2.73	1.81	13.85
1E6J.PDB	OE1, H_GLN_39	NE2, L_GLN_37	HE22, L_GLN_37	2.69	1.84	23.98
1F3R.PDB	O, B_ASN_230	OH, A_TYR_72	HH, A_TYR_72	2.67	1.70	2.56
1F3R.PDB	O, A_GLY_70	NH2, B_ARG_50	HH21, B_ARG_50	2.81	1.79	6.29
1F3R.PDB	NE1, A_TRP_67	OG, B_SER_61	HG, B_SER_61	2.86	1.89	6.31
1F3R.PDB	O, A_ILE_75	OH, B_TYR_170	HH, B_TYR_170	2.72	1.77	10.88
1F3R.PDB	O, A_ASP_71	OH, B_TYR_233	HH, B_TYR_233	2.71	1.89	25.38
1HGD.PDB	O, B_ILE_140	N, A_ALA_11	H, A_ALA_11	2.90	2.03	23.17
1HGD.PDB	O, B_PHE_138	N, A_LEU_13	H, A_LEU_13	2.95	2.00	13.08
1HGD.PDB	O, B_ARG_25	N, A_CYS_14	H, A_CYS_14	2.89	1.92	6.63
1HGD.PDB	O, B_GLY_136	N, A_LEU_15	H, A_LEU_15	2.87	1.90	8.68
1HGD.PDB	O, B_GLY_23	N, A_GLY_16	H, A_GLY_16	2.93	2.02	18.64
1HGD.PDB	O, B_TRP_21	N, A_HIS_18	H, A_HIS_18	2.86	2.01	24.44
1HGD.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.80	1.78	9.95
1HGD.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.83	1.84	13.41
1HGD.PDB	OD2, F_ASP_79	OG, A_SER_110	HG, A_SER_110	2.92	1.96	11.03
1HGD.PDB	OD1, E_ASP_101	NE2, A_GLN_210	HE22, A_GLN_210	3.00	2.15	26.33
1HGD.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.78	1.86	19.99
1HGD.PDB	O, F_SER_71	NZ, A_LYS_238	HZ2, A_LYS_238	2.63	1.73	23.20
1HGD.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.93	1.92	13.44
1HGD.PDB	O, B_LYS_68	NZ, A_LYS_299	HZ2, A_LYS_299	2.96	1.95	12.60
1HGD.PDB	O, B_LYS_62	N, A_GLY_303	H, A_GLY_303	2.91	1.96	9.72
1HGD.PDB	OG, B_SER_93	N, A_LYS_310	H, A_LYS_310	2.92	1.97	11.29
1HGD.PDB	OD1, B_ASN_104	N, A_ALA_317	H, A_ALA_317	2.78	1.85	14.55
1HGD.PDB	O, A_VAL_323	N, B_GLY_13	H, B_GLY_13	2.71	1.77	11.58
1HGD.PDB	O, A_HIS_17	N, B_TRP_14	H, B_TRP_14	2.85	1.93	15.85
1HGD.PDB	O, A_GLY_16	N, B_GLY_23	H, B_GLY_23	2.92	1.99	15.76
1HGD.PDB	O, A_CYS_14	N, B_ARG_25	H, B_ARG_25	2.96	2.02	13.01
1HGD.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.77	1.80	12.79
1HGD.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ1, B_LYS_62	2.61	1.78	29.53
1HGD.PDB	OD2, F_ASP_90	NZ, B_LYS_62	HZ3, B_LYS_62	2.73	1.84	25.56
1HGD.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.96	2.01	12.34
1HGD.PDB	O, A_LYS_299	NZ, B_LYS_68	HZ1, B_LYS_68	2.92	1.90	10.17
1HGD.PDB	OG, C_SER_107	N, B_ARG_76	H, B_ARG_76	2.80	1.86	12.47
1HGD.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.88	1.91	8.67
1HGD.PDB	OE2, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.84	1.82	2.51
1HGD.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.71	1.71	6.80
1HGD.PDB	OE1, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.75	1.75	3.21
1HGD.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.65	1.81	23.27
1HGD.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.76	1.72	5.59
1HGD.PDB	O, A_LYS_27	ND2, B_ASN_104	HD22, B_ASN_104	2.94	1.98	9.01
1HGD.PDB	O, F_LEU_2	OG, B_SER_113	HG, B_SER_113	2.69	1.91	29.59
1HGD.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.83	2.02	28.17
1HGD.PDB	OE2, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.88	2.01	22.00
1HGD.PDB	O, A_LEU_13	N, B_PHE_138	H, B_PHE_138	2.71	1.82	20.20
1HGD.PDB	O, A_ALA_11	N, B_ILE_140	H, B_ILE_140	2.81	1.89	16.38
1HGD.PDB	O, F_ARG_170	NH1, B_ARG_163	HH12, B_ARG_163	2.75	1.79	14.15
1HGD.PDB	O, D_ILE_140	N, C_ALA_11	H, C_ALA_11	2.91	2.01	19.96
1HGD.PDB	O, D_GLN_27	N, C_THR_12	H, C_THR_12	2.92	1.96	10.52
1HGD.PDB	O, D_PHE_138	N, C_LEU_13	H, C_LEU_13	2.98	2.02	9.60
1HGD.PDB	O, D_ARG_25	N, C_CYS_14	H, C_CYS_14	2.74	1.84	19.68
1HGD.PDB	O, D_GLY_136	N, C_LEU_15	H, C_LEU_15	2.88	1.91	5.44
1HGD.PDB	O, D_GLY_23	N, C_GLY_16	H, C_GLY_16	2.97	2.07	19.04
1HGD.PDB	O, D_TRP_21	N, C_HIS_18	H, C_HIS_18	2.85	1.99	23.00
1HGD.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.80	1.77	7.54
1HGD.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.87	1.88	13.44

1HGD.PDB	OD2, B.ASP.79	OG, C.SER.110	HG, C.SER.110	2.73	1.84	19.59
1HGD.PDB	OD1, A.ASP.101	NE2, C.GLN.210	HE22, C.GLN.210	2.97	2.13	27.21
1HGD.PDB	OE1, E.GLN.210	NH2, C.ARG.220	HH21, C.ARG.220	2.69	1.80	23.00
1HGD.PDB	OE1, B.GLU.72	NZ, C.LYS.238	HZ1, C.LYS.238	2.80	1.83	17.68
1HGD.PDB	O, B.SER.71	NZ, C.LYS.238	HZ3, C.LYS.238	2.57	1.67	23.33
1HGD.PDB	O, D.LYS.68	NZ, C.LYS.299	HZ2, C.LYS.299	2.97	1.97	13.11
1HGD.PDB	O, D.LYS.62	N, C.GLY.303	H, C.GLY.303	2.92	1.97	11.11
1HGD.PDB	OG, D.SER.93	N, C.LYS.310	H, C.LYS.310	2.96	2.01	12.70
1HGD.PDB	OD1, D.ASN.104	N, C.ALA.317	H, C.ALA.317	2.76	1.81	11.23
1HGD.PDB	OE1, D.GLU.15	NZ, C.LYS.326	HZ1, C.LYS.326	2.78	1.77	11.96
1HGD.PDB	O, C.VAL.323	N, D.GLY.13	H, D.GLY.13	2.70	1.78	14.49
1HGD.PDB	O, C.HIS.17	N, D.TRP.14	H, D.TRP.14	2.85	1.91	13.36
1HGD.PDB	O, C.GLY.16	N, D.GLY.23	H, D.GLY.23	2.93	2.01	16.45
1HGD.PDB	O, C.CYS.14	N, D.ARG.25	H, D.ARG.25	2.91	1.95	9.92
1HGD.PDB	O, C.THR.12	N, D.GLN.27	H, D.GLN.27	2.91	1.98	16.00
1HGD.PDB	O, A.THR.28	NE, D.ARG.54	HE, D.ARG.54	3.00	2.06	13.94
1HGD.PDB	OE2, B.GLU.97	NH2, D.ARG.54	HH22, D.ARG.54	2.79	1.82	13.03
1HGD.PDB	OD2, B.ASP.90	NZ, D.LYS.62	HZ3, D.LYS.62	2.62	1.79	29.99
1HGD.PDB	OG, C.SER.110	NE2, D.HIS.64	HE2, D.HIS.64	2.96	1.98	5.65
1HGD.PDB	O, C.LYS.299	NZ, D.LYS.68	HZ1, D.LYS.68	2.93	1.92	12.36
1HGD.PDB	OG, E.SER.107	N, D.ARG.76	H, D.ARG.76	2.86	1.90	9.40
1HGD.PDB	OE2, F.GLU.81	NE, D.ARG.76	HE, D.ARG.76	2.83	1.87	10.56
1HGD.PDB	OE2, F.GLU.74	NH1, D.ARG.76	HH12, D.ARG.76	2.78	1.77	3.14
1HGD.PDB	OE1, F.GLU.81	NH2, D.ARG.76	HH21, D.ARG.76	2.65	1.67	9.42
1HGD.PDB	OE1, F.GLU.74	NH2, D.ARG.76	HH22, D.ARG.76	2.69	1.70	6.24
1HGD.PDB	OE1, F.GLU.85	OH, D.TYR.83	HH, D.TYR.83	2.57	1.79	29.87
1HGD.PDB	OH, B.TYR.83	NZ, D.LYS.88	HZ1, D.LYS.88	2.76	1.72	5.75
1HGD.PDB	O, C.LYS.27	ND2, D.ASN.104	HD22, D.ASN.104	2.96	2.00	10.74
1HGD.PDB	OE1, B.GLU.132	NE, D.ARG.124	HE, D.ARG.124	2.80	2.01	29.31
1HGD.PDB	OE2, B.GLU.132	NE, D.ARG.124	HE, D.ARG.124	2.82	1.95	21.73
1HGD.PDB	O, C.LEU.13	N, D.PHE.138	H, D.PHE.138	2.74	1.85	19.25
1HGD.PDB	O, C.ALA.11	N, D.ILE.140	H, D.ILE.140	2.85	1.94	17.95
1HGD.PDB	O, B.ARG.170	NH1, D.ARG.163	HH12, D.ARG.163	2.77	1.79	12.64
1HGD.PDB	O, F.ILE.140	N, E.ALA.11	H, E.ALA.11	2.92	2.03	20.36
1HGD.PDB	O, F.GLN.27	N, E.THR.12	H, E.THR.12	2.97	2.03	14.03
1HGD.PDB	O, F.PHE.138	N, E.LEU.13	H, E.LEU.13	2.98	2.02	11.10
1HGD.PDB	O, F.ARG.25	N, E.CYS.14	H, E.CYS.14	2.65	1.79	21.42
1HGD.PDB	O, F.GLY.136	N, E.LEU.15	H, E.LEU.15	2.85	1.88	5.88
1HGD.PDB	O, F.GLY.23	N, E.GLY.16	H, E.GLY.16	2.93	2.04	20.98
1HGD.PDB	O, F.TRP.21	N, E.HIS.18	H, E.HIS.18	2.83	1.98	25.03
1HGD.PDB	OE2, F.GLU.97	NZ, E.LYS.27	HZ1, E.LYS.27	2.79	1.77	8.77
1HGD.PDB	OE2, F.GLU.67	NH2, E.ARG.109	HH21, E.ARG.109	2.82	1.85	14.73
1HGD.PDB	OD2, D.ASP.79	OG, E.SER.110	HG, E.SER.110	2.81	1.89	15.50
1HGD.PDB	OD1, C.ASP.101	NE2, E.GLN.210	HE22, E.GLN.210	2.98	2.14	27.07
1HGD.PDB	OE1, A.GLN.210	NH2, E.ARG.220	HH21, E.ARG.220	2.77	1.90	25.11
1HGD.PDB	O, D.SER.71	NZ, E.LYS.238	HZ2, E.LYS.238	2.73	1.80	21.39
1HGD.PDB	OE1, D.GLU.72	NZ, E.LYS.238	HZ3, E.LYS.238	2.87	1.86	13.40
1HGD.PDB	O, F.LYS.68	NZ, E.LYS.299	HZ1, E.LYS.299	2.98	1.98	14.54
1HGD.PDB	O, F.LYS.62	N, E.GLY.303	H, E.GLY.303	2.94	1.98	8.87
1HGD.PDB	OG, F.SER.93	N, E.LYS.310	H, E.LYS.310	2.95	2.00	12.05
1HGD.PDB	OD1, F.ASN.104	N, E.ALA.317	H, E.ALA.317	2.79	1.84	10.01
1HGD.PDB	OE2, F.GLU.15	N, E.GLU.325	H, E.GLU.325	2.91	2.10	28.29
1HGD.PDB	OE1, F.GLU.15	NZ, E.LYS.326	HZ3, E.LYS.326	2.97	1.97	16.19
1HGD.PDB	O, E.VAL.323	N, F.GLY.13	H, F.GLY.13	2.71	1.79	15.38
1HGD.PDB	O, E.HIS.17	N, F.TRP.14	H, F.TRP.14	2.87	1.92	12.04
1HGD.PDB	O, E.GLY.16	N, F.GLY.23	H, F.GLY.23	2.91	2.00	17.89
1HGD.PDB	O, E.CYS.14	N, F.ARG.25	H, F.ARG.25	2.88	1.94	13.26
1HGD.PDB	O, E.THR.12	N, F.GLN.27	H, F.GLN.27	2.97	2.04	16.25

1HGD.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.72	1.75	12.85
1HGD.PDB	OD2, D_ASP_90	NZ, F_LYS_62	HZ3, F_LYS_62	2.71	1.86	28.09
1HGD.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.95	1.98	9.92
1HGD.PDB	O, E_LYS_299	NZ, F_LYS_68	HZ1, F_LYS_68	2.97	1.94	5.85
1HGD.PDB	OG, A_SER_107	N, F_ARG_76	H, F_ARG_76	2.82	1.86	9.34
1HGD.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.86	1.90	10.66
1HGD.PDB	OE2, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.77	1.75	1.42
1HGD.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.64	1.65	5.37
1HGD.PDB	OE1, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.71	1.72	7.42
1HGD.PDB	OE1, B_GLU_85	OH, F_TYR_83	HH, F_TYR_83	2.53	1.75	27.84
1HGD.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.67	1.66	8.83
1HGD.PDB	O, E_LYS_27	ND2, F_ASN_104	HD22, F_ASN_104	2.95	1.99	8.95
1HGD.PDB	O, D_LEU_2	OG, F_SER_113	HG, F_SER_113	2.74	1.91	25.98
1HGD.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.96	2.14	28.71
1HGD.PDB	OE2, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.94	2.05	20.84
1HGD.PDB	O, E_LEU_13	N, F_PHE_138	H, F_PHE_138	2.72	1.85	21.62
1HGD.PDB	O, E_ALA_11	N, F_ILE_140	H, F_ILE_140	2.82	1.92	18.45
1HGD.PDB	O, D_ARG_170	NH1, F_ARG_163	HH12, F_ARG_163	2.94	1.98	14.11
1HGE.PDB	O, B_ILE_140	N, A_ALA_11	H, A_ALA_11	2.81	1.93	21.75
1HGE.PDB	O, B_PHE_138	N, A_LEU_13	H, A_LEU_13	2.99	2.04	13.41
1HGE.PDB	O, B_ARG_25	N, A_CYS_14	H, A_CYS_14	2.88	1.92	6.83
1HGE.PDB	O, B_GLY_136	N, A_LEU_15	H, A_LEU_15	2.86	1.90	7.71
1HGE.PDB	O, B_GLY_23	N, A_GLY_16	H, A_GLY_16	2.95	2.03	17.76
1HGE.PDB	O, B_TRP_21	N, A_HIS_18	H, A_HIS_18	2.85	1.97	21.20
1HGE.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.80	1.78	10.14
1HGE.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.74	1.75	12.19
1HGE.PDB	OD2, F_ASP_79	OG, A_SER_110	HG, A_SER_110	2.90	1.95	11.19
1HGE.PDB	OD1, E_ASP_101	NE2, A_GLN_210	HE22, A_GLN_210	2.91	2.05	24.48
1HGE.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.71	1.78	19.14
1HGE.PDB	O, F_SER_71	NZ, A_LYS_238	HZ2, A_LYS_238	2.67	1.73	19.84
1HGE.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.91	1.89	11.73
1HGE.PDB	O, B_LYS_68	NZ, A_LYS_299	HZ2, A_LYS_299	2.95	1.93	10.27
1HGE.PDB	O, B_LYS_62	N, A_GLY_303	H, A_GLY_303	2.95	1.98	8.88
1HGE.PDB	OG, B_SER_93	N, A_LYS_310	H, A_LYS_310	2.91	1.95	10.06
1HGE.PDB	OD1, B_ASN_104	N, A_ALA_317	H, A_ALA_317	2.72	1.81	16.15
1HGE.PDB	O, A_VAL_323	N, B_GLY_13	H, B_GLY_13	2.72	1.79	12.30
1HGE.PDB	O, A_HIS_17	N, B_TRP_14	H, B_TRP_14	2.85	1.92	15.18
1HGE.PDB	O, A_GLY_16	N, B_GLY_23	H, B_GLY_23	2.92	2.01	18.67
1HGE.PDB	O, A_CYS_14	N, B_ARG_25	H, B_ARG_25	3.00	2.06	13.87
1HGE.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.84	1.86	12.76
1HGE.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ1, B_LYS_62	2.60	1.76	28.82
1HGE.PDB	OD2, F_ASP_90	NZ, B_LYS_62	HZ3, B_LYS_62	2.69	1.82	26.81
1HGE.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.97	2.02	12.36
1HGE.PDB	O, A_LYS_299	NZ, B_LYS_68	HZ1, B_LYS_68	2.93	1.92	11.15
1HGE.PDB	OG, C_SER_107	N, B_ARG_76	H, B_ARG_76	2.82	1.86	9.28
1HGE.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.87	1.91	11.56
1HGE.PDB	OE2, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.84	1.83	5.81
1HGE.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.70	1.70	6.45
1HGE.PDB	OE1, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.79	1.79	3.91
1HGE.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.65	1.81	24.86
1HGE.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.75	1.71	5.62
1HGE.PDB	O, A_LYS_27	ND2, B_ASN_104	HD22, B_ASN_104	2.93	1.97	10.25
1HGE.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.80	1.98	27.36
1HGE.PDB	OE2, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.94	2.06	21.65
1HGE.PDB	O, A_LEU_13	N, B_PHE_138	H, B_PHE_138	2.71	1.84	21.33
1HGE.PDB	O, A_ALA_11	N, B_ILE_140	H, B_ILE_140	2.75	1.86	18.72
1HGE.PDB	O, F_ARG_170	NH1, B_ARG_163	HH12, B_ARG_163	2.78	1.81	13.88
1HGE.PDB	O, D_ILE_140	N, C_ALA_11	H, C_ALA_11	2.80	1.91	19.98

1HGE.PDB	O, D_PHE_138	N, C_LEU_13	H, C_LEU_13	2.99	2.04	12.20
1HGE.PDB	O, D_ARG_25	N, C_CYS_14	H, C_CYS_14	2.73	1.82	16.85
1HGE.PDB	O, D_GLY_136	N, C_LEU_15	H, C_LEU_15	2.89	1.92	5.03
1HGE.PDB	O, D_GLY_23	N, C_GLY_16	H, C_GLY_16	2.98	2.07	18.60
1HGE.PDB	O, D_TRP_21	N, C_HIS_18	H, C_HIS_18	2.85	1.96	19.89
1HGE.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.79	1.77	8.74
1HGE.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.78	1.79	11.19
1HGE.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.78	1.86	15.09
1HGE.PDB	OD1, A_ASP_101	NE2, C_GLN_210	HE22, C_GLN_210	2.93	2.07	24.92
1HGE.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.64	1.76	23.09
1HGE.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.78	1.80	16.75
1HGE.PDB	O, B_SER_71	NZ, C_LYS_238	HZ3, C_LYS_238	2.65	1.71	19.56
1HGE.PDB	O, D_LYS_68	NZ, C_LYS_299	HZ2, C_LYS_299	2.96	1.94	10.83
1HGE.PDB	O, D_LYS_62	N, C_GLY_303	H, C_GLY_303	2.94	1.98	10.89
1HGE.PDB	OG, D_SER_93	N, C_LYS_310	H, C_LYS_310	2.92	1.96	11.23
1HGE.PDB	OD1, D_ASN_104	N, C_ALA_317	H, C_ALA_317	2.73	1.80	14.37
1HGE.PDB	OE1, D_GLU_15	NZ, C_LYS_326	HZ1, C_LYS_326	2.74	1.73	12.73
1HGE.PDB	O, C_VAL_323	N, D_GLY_13	H, D_GLY_13	2.71	1.79	14.79
1HGE.PDB	O, C_HIS_17	N, D_TRP_14	H, D_TRP_14	2.88	1.94	13.07
1HGE.PDB	O, C_GLY_16	N, D_GLY_23	H, D_GLY_23	2.94	2.04	19.95
1HGE.PDB	O, C_CYS_14	N, D_ARG_25	H, D_ARG_25	2.94	1.98	9.40
1HGE.PDB	O, C_THR_12	N, D_GLN_27	H, D_GLN_27	2.86	1.95	18.04
1HGE.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.87	1.89	12.82
1HGE.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.96	1.98	6.23
1HGE.PDB	O, C_LYS_299	NZ, D_LYS_68	HZ1, D_LYS_68	2.92	1.91	12.00
1HGE.PDB	OG, E_SER_107	N, D_ARG_76	H, D_ARG_76	2.87	1.90	6.58
1HGE.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.79	1.85	14.06
1HGE.PDB	OE2, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.78	1.78	7.91
1HGE.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.63	1.67	11.36
1HGE.PDB	OE1, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.74	1.75	7.04
1HGE.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.58	1.80	29.40
1HGE.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.71	1.68	6.52
1HGE.PDB	O, C_LYS_27	ND2, D_ASN_104	HD22, D_ASN_104	2.96	2.00	10.88
1HGE.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.78	1.98	28.90
1HGE.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.90	2.01	20.41
1HGE.PDB	O, C_LEU_13	N, D_PHE_138	H, D_PHE_138	2.74	1.87	21.30
1HGE.PDB	O, C_ALA_11	N, D_ILE_140	H, D_ILE_140	2.78	1.88	18.97
1HGE.PDB	O, B_ARG_170	NH1, D_ARG_163	HH12, D_ARG_163	2.79	1.82	14.16
1HGE.PDB	O, F_ILE_140	N, E_ALA_11	H, E_ALA_11	2.82	1.93	19.79
1HGE.PDB	O, F_GLN_27	N, E_THR_12	H, E_THR_12	2.91	1.97	12.43
1HGE.PDB	O, F_PHE_138	N, E_LEU_13	H, E_LEU_13	2.98	2.03	12.93
1HGE.PDB	O, F_ARG_25	N, E_CYS_14	H, E_CYS_14	2.61	1.80	26.88
1HGE.PDB	O, F_GLY_136	N, E_LEU_15	H, E_LEU_15	2.88	1.90	5.56
1HGE.PDB	O, F_GLY_23	N, E_GLY_16	H, E_GLY_16	2.95	2.06	19.95
1HGE.PDB	O, F_TRP_21	N, E_HIS_18	H, E_HIS_18	2.85	1.97	21.43
1HGE.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.79	1.77	9.75
1HGE.PDB	OE2, F_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.78	1.79	11.63
1HGE.PDB	OD2, D_ASP_79	OG, E_SER_110	HG, E_SER_110	2.82	1.89	14.19
1HGE.PDB	OD1, C_ASP_101	NE2, E_GLN_210	HE22, E_GLN_210	2.89	2.04	25.02
1HGE.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.74	1.87	25.04
1HGE.PDB	O, D_SER_71	NZ, E_LYS_238	HZ2, E_LYS_238	2.75	1.79	18.19
1HGE.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ3, E_LYS_238	2.85	1.84	12.25
1HGE.PDB	O, F_LYS_68	NZ, E_LYS_299	HZ2, E_LYS_299	2.95	1.93	11.73
1HGE.PDB	O, F_LYS_62	N, E_GLY_303	H, E_GLY_303	2.95	1.98	8.29
1HGE.PDB	OG, F_SER_93	N, E_LYS_310	H, E_LYS_310	2.93	1.97	10.15
1HGE.PDB	OD1, F_ASP_86	NZ, E_LYS_310	HZ3, E_LYS_310	2.86	2.02	29.64
1HGE.PDB	OD1, F_ASN_104	N, E_ALA_317	H, E_ALA_317	2.73	1.80	13.22
1HGE.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.99	2.00	17.08

1HGE.PDB	O, E_VAL_323	N, F_GLY_13	H, F_GLY_13	2.72	1.79	12.93
1HGE.PDB	O, E_HIS_17	N, F_TRP_14	H, F_TRP_14	2.85	1.91	12.63
1HGE.PDB	O, E_GLY_16	N, F_GLY_23	H, F_GLY_23	2.91	2.01	19.90
1HGE.PDB	O, E_CYS_14	N, F_ARG_25	H, F_ARG_25	2.88	1.93	12.79
1HGE.PDB	O, E_THR_12	N, F_GLN_27	H, F_GLN_27	2.82	1.90	16.16
1HGE.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.80	1.82	12.52
1HGE.PDB	OD2, D_ASP_90	NZ, F_LYS_62	HZ2, F_LYS_62	2.67	1.83	29.15
1HGE.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.94	1.97	9.11
1HGE.PDB	O, E_LYS_299	NZ, F_LYS_68	HZ1, F_LYS_68	2.97	1.93	4.62
1HGE.PDB	OG, A_SER_107	N, F_ARG_76	H, F_ARG_76	2.81	1.83	4.38
1HGE.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.85	1.89	11.64
1HGE.PDB	OE2, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.73	1.73	6.19
1HGE.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.65	1.66	5.51
1HGE.PDB	OE1, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.70	1.73	9.07
1HGE.PDB	OE1, B_GLU_85	OH, F_TYR_83	HH, F_TYR_83	2.51	1.76	30.00
1HGE.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.67	1.65	8.34
1HGE.PDB	O, E_LYS_27	ND2, F_ASN_104	HD22, F_ASN_104	2.94	1.99	10.01
1HGE.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.92	2.09	27.36
1HGE.PDB	O, E_LEU_13	N, F_PHE_138	H, F_PHE_138	2.73	1.86	22.03
1HGE.PDB	O, E_ALA_11	N, F_ILE_140	H, F_ILE_140	2.75	1.87	19.65
1HGE.PDB	O, D_ARG_170	NH1, F_ARG_163	HH12, F_ARG_163	2.95	1.99	14.32
1HGF.PDB	O, B_ILE_140	N, A_ALA_11	H, A_ALA_11	2.90	2.03	22.48
1HGF.PDB	O, B_PHE_138	N, A_LEU_13	H, A_LEU_13	2.96	1.99	8.07
1HGF.PDB	O, B_ARG_25	N, A_CYS_14	H, A_CYS_14	2.98	2.02	8.89
1HGF.PDB	O, B_GLY_136	N, A_LEU_15	H, A_LEU_15	2.92	1.95	7.83
1HGF.PDB	O, B_GLY_23	N, A_GLY_16	H, A_GLY_16	2.92	2.03	19.80
1HGF.PDB	O, B_TRP_21	N, A_HIS_18	H, A_HIS_18	2.92	2.01	18.08
1HGF.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.79	1.86	21.55
1HGF.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.92	1.92	10.51
1HGF.PDB	OD2, F_ASP_79	OG, A_SER_110	HG, A_SER_110	2.82	1.90	15.87
1HGF.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.64	1.76	23.62
1HGF.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ2, A_LYS_238	2.85	1.85	14.58
1HGF.PDB	O, F_SER_71	NZ, A_LYS_238	HZ3, A_LYS_238	2.63	1.67	16.71
1HGF.PDB	O, B_LYS_62	N, A_GLY_303	H, A_GLY_303	2.90	1.93	4.88
1HGF.PDB	OG, B_SER_93	N, A_LYS_310	H, A_LYS_310	2.89	1.97	16.03
1HGF.PDB	OD1, B_ASN_104	N, A_ALA_317	H, A_ALA_317	2.74	1.82	15.07
1HGF.PDB	O, A_VAL_323	N, B_GLY_13	H, B_GLY_13	2.74	1.86	21.47
1HGF.PDB	O, A_HIS_17	N, B_TRP_14	H, B_TRP_14	2.87	1.97	19.18
1HGF.PDB	O, A_CYS_14	N, B_ARG_25	H, B_ARG_25	2.97	2.03	13.73
1HGF.PDB	OE2, A_GLU_325	NH2, B_ARG_25	HH22, B_ARG_25	2.99	2.04	16.52
1HGF.PDB	O, E_THR_28	NE, B_ARG_54	HE, B_ARG_54	2.92	1.94	6.13
1HGF.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.83	1.86	13.50
1HGF.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ2, B_LYS_62	2.71	1.70	11.44
1HGF.PDB	OD2, F_ASP_90	NZ, B_LYS_62	HZ3, B_LYS_62	2.77	1.82	20.37
1HGF.PDB	OG, A_SER_266	ND1, B_HIS_64	HD1, B_HIS_64	2.66	1.79	20.68
1HGF.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.89	1.92	10.70
1HGF.PDB	O, A_LYS_299	NZ, B_LYS_68	HZ2, B_LYS_68	2.93	1.89	4.53
1HGF.PDB	OG, C_SER_107	N, B_ARG_76	H, B_ARG_76	2.84	1.90	13.38
1HGF.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.92	1.92	2.47
1HGF.PDB	OE1, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.86	1.84	3.80
1HGF.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.73	1.74	10.29
1HGF.PDB	OE2, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.75	1.74	3.91
1HGF.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.57	1.80	29.66
1HGF.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.72	1.70	9.91
1HGF.PDB	O, A_LYS_27	ND2, B_ASN_104	HD21, B_ASN_104	2.88	1.94	13.97
1HGF.PDB	O, F_LEU_2	OG, B_SER_113	HG, B_SER_113	2.68	1.90	29.80
1HGF.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.80	1.86	13.00
1HGF.PDB	O, A_LEU_13	N, B_PHE_138	H, B_PHE_138	2.73	1.88	23.58

1HGF.PDB	O, A_ALA_11	N, B_ILE_140	H, B_ILE_140	2.80	1.87	14.66
1HGF.PDB	O, F_ARG_170	NH1, B_ARG_163	HH12, B_ARG_163	2.79	1.78	1.27
1HGF.PDB	OE1, F_GLU_131	NH2, B_ARG_163	HH21, B_ARG_163	2.74	1.86	24.20
1HGF.PDB	O, D_ILE_140	N, C_ALA_11	H, C_ALA_11	2.89	2.00	20.42
1HGF.PDB	O, D_GLN_27	N, C_THR_12	H, C_THR_12	2.90	1.96	12.68
1HGF.PDB	O, D_PHE_138	N, C_LEU_13	H, C_LEU_13	2.97	1.99	7.01
1HGF.PDB	O, D_ARG_25	N, C_CYS_14	H, C_CYS_14	2.79	1.86	15.57
1HGF.PDB	O, D_GLY_136	N, C_LEU_15	H, C_LEU_15	2.95	1.97	3.72
1HGF.PDB	O, D_GLY_23	N, C_GLY_16	H, C_GLY_16	2.95	2.05	18.06
1HGF.PDB	O, D_TRP_21	N, C_HIS_18	H, C_HIS_18	2.91	2.01	18.40
1HGF.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.81	1.85	19.93
1HGF.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.91	1.92	11.49
1HGF.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.69	1.85	25.37
1HGF.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.56	1.72	26.72
1HGF.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ2, C_LYS_238	2.75	1.78	18.48
1HGF.PDB	O, B_SER_71	NZ, C_LYS_238	HZ3, C_LYS_238	2.61	1.62	12.67
1HGF.PDB	O, D_LYS_62	N, C_GLY_303	H, C_GLY_303	2.91	1.95	8.09
1HGF.PDB	OG, D_SER_93	N, C_LYS_310	H, C_LYS_310	2.89	1.98	17.69
1HGF.PDB	OD1, D_ASN_104	N, C_ALA_317	H, C_ALA_317	2.78	1.83	11.25
1HGF.PDB	O, C_VAL_323	N, D_GLY_13	H, D_GLY_13	2.72	1.85	21.39
1HGF.PDB	O, C_HIS_17	N, D_TRP_14	H, D_TRP_14	2.87	1.96	16.75
1HGF.PDB	O, C_CYS_14	N, D_ARG_25	H, D_ARG_25	2.90	1.93	7.59
1HGF.PDB	O, C_THR_12	N, D_GLN_27	H, D_GLN_27	2.86	1.94	17.23
1HGF.PDB	O, A_THR_28	NE, D_ARG_54	HE, D_ARG_54	2.88	1.90	8.46
1HGF.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.84	1.86	12.74
1HGF.PDB	OD2, B_ASP_86	NZ, D_LYS_62	HZ2, D_LYS_62	2.69	1.69	13.49
1HGF.PDB	OD2, B_ASP_90	NZ, D_LYS_62	HZ3, D_LYS_62	2.68	1.77	22.81
1HGF.PDB	OG, C_SER_266	ND1, D_HIS_64	HD1, D_HIS_64	2.64	1.83	27.58
1HGF.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.90	1.92	7.33
1HGF.PDB	O, C_LYS_299	NZ, D_LYS_68	HZ2, D_LYS_68	2.93	1.89	4.98
1HGF.PDB	OG, E_SER_107	N, D_ARG_76	H, D_ARG_76	2.91	1.94	7.76
1HGF.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.82	1.85	5.34
1HGF.PDB	OE1, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.79	1.78	3.81
1HGF.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.64	1.68	12.43
1HGF.PDB	OE2, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.70	1.71	7.38
1HGF.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.58	1.80	29.87
1HGF.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.68	1.69	13.85
1HGF.PDB	O, C_LYS_27	ND2, D_ASN_104	HD21, D_ASN_104	2.89	1.96	15.72
1HGF.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.79	1.88	16.40
1HGF.PDB	O, C_LEU_13	N, D_PHE_138	H, D_PHE_138	2.75	1.91	24.76
1HGF.PDB	O, C_ALA_11	N, D_ILE_140	H, D_ILE_140	2.82	1.90	15.68
1HGF.PDB	O, B_ARG_170	NH1, D_ARG_163	HH12, D_ARG_163	2.84	1.83	3.71
1HGF.PDB	OE1, B_GLU_131	NH2, D_ARG_163	HH21, D_ARG_163	2.70	1.83	24.43
1HGF.PDB	O, F_ILE_140	N, E_ALA_11	H, E_ALA_11	2.95	2.06	20.63
1HGF.PDB	O, F_GLN_27	N, E_THR_12	H, E_THR_12	2.87	1.93	12.24
1HGF.PDB	O, F_PHE_138	N, E_LEU_13	H, E_LEU_13	2.96	1.99	8.43
1HGF.PDB	O, F_ARG_25	N, E_CYS_14	H, E_CYS_14	2.65	1.83	26.13
1HGF.PDB	O, F_GLY_136	N, E_LEU_15	H, E_LEU_15	2.91	1.93	3.45
1HGF.PDB	O, F_GLY_23	N, E_GLY_16	H, E_GLY_16	2.94	2.06	22.45
1HGF.PDB	O, F_TRP_21	N, E_HIS_18	H, E_HIS_18	2.91	2.00	17.81
1HGF.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.75	1.83	22.30
1HGF.PDB	OE2, F_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.88	1.88	11.28
1HGF.PDB	OD2, D_ASP_79	OG, E_SER_110	HG, E_SER_110	2.78	1.90	21.69
1HGF.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.65	1.79	25.97
1HGF.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ2, E_LYS_238	2.83	1.84	16.42
1HGF.PDB	O, D_SER_71	NZ, E_LYS_238	HZ3, E_LYS_238	2.74	1.75	13.85
1HGF.PDB	O, F_LYS_62	N, E_GLY_303	H, E_GLY_303	2.90	1.93	6.18
1HGF.PDB	OG, F_SER_93	N, E_LYS_310	H, E_LYS_310	2.86	1.93	14.59

1HGF.PDB	OD1, F_ASN_104	N, E_ALA_317	H, E_ALA_317	2.72	1.78	10.77
1HGF.PDB	O, E_VAL_323	N, F_GLY_13	H, F_GLY_13	2.75	1.85	19.07
1HGF.PDB	O, E_HIS_17	N, F_TRP_14	H, F_TRP_14	2.87	1.96	16.52
1HGF.PDB	O, E_CYS_14	N, F_ARG_25	H, F_ARG_25	2.91	1.94	8.25
1HGF.PDB	O, E_THR_12	N, F_GLN_27	H, F_GLN_27	3.00	2.08	17.91
1HGF.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.79	1.81	11.74
1HGF.PDB	OD2, D_ASP_86	NZ, F_LYS_62	HZ2, F_LYS_62	2.67	1.68	13.64
1HGF.PDB	OD2, D_ASP_90	NZ, F_LYS_62	HZ3, F_LYS_62	2.75	1.81	20.23
1HGF.PDB	OG, E_SER_266	ND1, F_HIS_64	HD1, F_HIS_64	2.65	1.77	20.25
1HGF.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.89	1.92	9.46
1HGF.PDB	O, E_LYS_299	NZ, F_LYS_68	HZ2, F_LYS_68	2.97	1.95	8.70
1HGF.PDB	OG, A_SER_107	N, F_ARG_76	H, F_ARG_76	2.83	1.87	9.12
1HGF.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.86	1.88	5.84
1HGF.PDB	OE1, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.78	1.77	1.59
1HGF.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.69	1.70	7.61
1HGF.PDB	OE2, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.71	1.73	8.88
1HGF.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.55	1.63	21.75
1HGF.PDB	O, E_LYS_27	ND2, F_ASN_104	HD21, F_ASN_104	2.91	1.99	15.12
1HGF.PDB	O, D_LEU_2	OG, F_SER_113	HG, F_SER_113	2.73	1.92	27.40
1HGF.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.90	1.96	15.73
1HGF.PDB	O, E_LEU_13	N, F_PHE_138	H, F_PHE_138	2.75	1.92	26.04
1HGF.PDB	O, E_ALA_11	N, F_ILE_140	H, F_ILE_140	2.82	1.90	16.36
1HGF.PDB	OE1, D_GLU_131	NH2, F_ARG_163	HH21, F_ARG_163	2.69	1.84	27.00
1HGG.PDB	O, B_ILE_140	N, A_ALA_11	H, A_ALA_11	2.90	1.98	16.87
1HGG.PDB	O, B_PHE_138	N, A_LEU_13	H, A_LEU_13	2.97	2.01	10.10
1HGG.PDB	O, B_ARG_25	N, A_CYS_14	H, A_CYS_14	2.92	1.97	11.02
1HGG.PDB	O, B_GLY_136	N, A_LEU_15	H, A_LEU_15	2.86	1.89	7.78
1HGG.PDB	O, B_GLY_23	N, A_GLY_16	H, A_GLY_16	2.90	2.00	20.11
1HGG.PDB	O, B_TRP_21	N, A_HIS_18	H, A_HIS_18	2.90	1.99	17.50
1HGG.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.90	1.87	9.15
1HGG.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.84	1.86	14.43
1HGG.PDB	OD2, F_ASP_79	OG, A_SER_110	HG, A_SER_110	2.88	1.95	14.29
1HGG.PDB	OD1, E_ASP_101	NE2, A_GLN_210	HE22, A_GLN_210	2.99	2.07	17.95
1HGG.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.73	1.78	15.93
1HGG.PDB	O, F_SER_71	NZ, A_LYS_238	HZ2, A_LYS_238	2.70	1.77	20.55
1HGG.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.93	1.93	14.31
1HGG.PDB	OE2, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.74	1.91	29.92
1HGG.PDB	OE1, B_GLU_67	NH1, A_ARG_269	HH12, A_ARG_269	2.69	1.86	28.34
1HGG.PDB	O, B_LYS_68	NZ, A_LYS_299	HZ1, A_LYS_299	2.91	1.88	9.16
1HGG.PDB	O, B_LYS_62	N, A_GLY_303	H, A_GLY_303	2.91	1.94	6.06
1HGG.PDB	OG, B_SER_93	N, A_LYS_310	H, A_LYS_310	2.89	1.96	14.59
1HGG.PDB	OD1, B_ASP_90	NZ, A_LYS_310	HZ2, A_LYS_310	2.70	1.74	18.08
1HGG.PDB	OD1, B_ASN_104	N, A_ALA_317	H, A_ALA_317	2.79	1.88	16.20
1HGG.PDB	OE2, B_GLU_15	NZ, A_LYS_326	HZ1, A_LYS_326	2.83	1.89	21.04
1HGG.PDB	O, A_VAL_323	N, B_GLY_13	H, B_GLY_13	2.71	1.78	13.00
1HGG.PDB	O, A_HIS_17	N, B_TRP_14	H, B_TRP_14	2.79	1.88	17.76
1HGG.PDB	O, A_GLY_16	N, B_GLY_23	H, B_GLY_23	2.99	2.09	20.32
1HGG.PDB	OE2, A_GLU_325	NH2, B_ARG_25	HH22, B_ARG_25	2.94	1.96	12.23
1HGG.PDB	O, E_THR_28	NE, B_ARG_54	HE, B_ARG_54	2.94	1.97	7.82
1HGG.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.75	1.76	9.96
1HGG.PDB	OD2, F_ASP_90	NZ, B_LYS_62	HZ2, B_LYS_62	2.65	1.82	29.87
1HGG.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ3, B_LYS_62	2.64	1.73	23.35
1HGG.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.90	1.96	14.63
1HGG.PDB	O, A_LYS_299	NZ, B_LYS_68	HZ1, B_LYS_68	2.86	1.83	9.73
1HGG.PDB	OG, C_SER_107	N, B_ARG_76	H, B_ARG_76	2.77	1.82	10.45
1HGG.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.94	1.96	10.47
1HGG.PDB	OE1, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.88	1.89	10.69
1HGG.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.73	1.73	5.91

1HGG.PDB	OE2, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.82	1.82	7.26
1HGG.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.68	1.80	19.99
1HGG.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.77	1.73	5.14
1HGG.PDB	O, A_LYS_27	ND2, B_ASN_104	HD22, B_ASN_104	2.88	1.95	14.60
1HGG.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.84	1.98	22.96
1HGG.PDB	OE2, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.81	1.98	25.54
1HGG.PDB	O, A_LEU_13	N, B_PHE_138	H, B_PHE_138	2.70	1.86	24.49
1HGG.PDB	O, A_ALA_11	N, B_ILE_140	H, B_ILE_140	2.77	1.86	18.05
1HGG.PDB	O, F_ARG_170	NH1, B_ARG_163	HH12, B_ARG_163	2.76	1.82	18.13
1HGG.PDB	O, D_ILE_140	N, C_ALA_11	H, C_ALA_11	2.88	1.96	16.67
1HGG.PDB	O, D_PHE_138	N, C_LEU_13	H, C_LEU_13	3.00	2.04	10.72
1HGG.PDB	O, D_ARG_25	N, C_CYS_14	H, C_CYS_14	2.73	1.80	13.70
1HGG.PDB	O, D_GLY_136	N, C_LEU_15	H, C_LEU_15	2.90	1.94	8.49
1HGG.PDB	O, D_GLY_23	N, C_GLY_16	H, C_GLY_16	2.91	2.01	20.14
1HGG.PDB	O, D_TRP_21	N, C_HIS_18	H, C_HIS_18	2.90	2.00	17.75
1HGG.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.94	1.91	8.28
1HGG.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.85	1.88	14.56
1HGG.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.76	1.86	17.83
1HGG.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.61	1.71	21.26
1HGG.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.83	1.86	17.18
1HGG.PDB	OE2, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.70	1.87	29.85
1HGG.PDB	O, B_SER_71	NZ, C_LYS_238	HZ3, C_LYS_238	2.64	1.71	20.39
1HGG.PDB	OE1, D_GLU_67	NH1, C_ARG_269	HH12, C_ARG_269	2.69	1.85	27.75
1HGG.PDB	O, D_LYS_68	NZ, C_LYS_299	HZ1, C_LYS_299	2.94	1.91	9.55
1HGG.PDB	O, D_LYS_62	N, C_GLY_303	H, C_GLY_303	2.91	1.94	5.10
1HGG.PDB	OG, D_SER_93	N, C_LYS_310	H, C_LYS_310	2.89	1.96	14.95
1HGG.PDB	OD1, D_ASP_90	NZ, C_LYS_310	HZ2, C_LYS_310	2.65	1.73	21.74
1HGG.PDB	OD1, D_ASN_104	N, C_ALA_317	H, C_ALA_317	2.78	1.87	17.02
1HGG.PDB	O, C_VAL_323	N, D_GLY_13	H, D_GLY_13	2.71	1.79	13.39
1HGG.PDB	O, C_HIS_17	N, D_TRP_14	H, D_TRP_14	2.80	1.89	17.21
1HGG.PDB	O, C_GLY_16	N, D_GLY_23	H, D_GLY_23	2.99	2.09	20.18
1HGG.PDB	O, C_CYS_14	N, D_ARG_25	H, D_ARG_25	2.94	1.98	8.24
1HGG.PDB	O, A_THR_28	NE, D_ARG_54	HE, D_ARG_54	2.88	1.91	8.15
1HGG.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.76	1.78	10.56
1HGG.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.86	1.90	9.42
1HGG.PDB	O, C_LYS_299	NZ, D_LYS_68	HZ1, D_LYS_68	2.84	1.83	12.46
1HGG.PDB	OG, E_SER_107	N, D_ARG_76	H, D_ARG_76	2.84	1.88	7.98
1HGG.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.86	1.89	9.57
1HGG.PDB	OE1, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.78	1.80	12.10
1HGG.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.67	1.68	6.66
1HGG.PDB	OE2, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.74	1.75	9.29
1HGG.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.59	1.78	26.83
1HGG.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.73	1.70	8.35
1HGG.PDB	O, C_LYS_27	ND2, D_ASN_104	HD22, D_ASN_104	2.86	1.93	13.53
1HGG.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.86	2.00	22.57
1HGG.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.78	1.96	26.12
1HGG.PDB	O, C_LEU_13	N, D_PHE_138	H, D_PHE_138	2.73	1.88	23.87
1HGG.PDB	O, C_ALA_11	N, D_ILE_140	H, D_ILE_140	2.80	1.89	17.21
1HGG.PDB	O, B_ARG_170	NH1, D_ARG_163	HH12, D_ARG_163	2.79	1.85	17.60
1HGG.PDB	O, F_ILE_140	N, E_ALA_11	H, E_ALA_11	2.91	1.98	15.76
1HGG.PDB	O, F_GLN_27	N, E_THR_12	H, E_THR_12	2.92	1.99	15.18
1HGG.PDB	O, F_PHE_138	N, E_LEU_13	H, E_LEU_13	2.97	2.01	11.10
1HGG.PDB	O, F_ARG_25	N, E_CYS_14	H, E_CYS_14	2.71	1.83	19.57
1HGG.PDB	O, F_GLY_136	N, E_LEU_15	H, E_LEU_15	2.87	1.90	6.84
1HGG.PDB	O, F_GLY_23	N, E_GLY_16	H, E_GLY_16	2.91	2.01	19.19
1HGG.PDB	O, F_TRP_21	N, E_HIS_18	H, E_HIS_18	2.89	1.99	18.05
1HGG.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.91	1.88	8.89
1HGG.PDB	OE2, F_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.88	1.90	14.20

1HGG.PDB	OD2, D-ASP.79	OG, E-SER.110	HG, E-SER.110	2.79	1.88	16.48
1HGG.PDB	OD1, C-ASP.101	NE2, E-GLN.210	HE22, E-GLN.210	2.96	2.04	17.70
1HGG.PDB	OE1, A-GLN.210	NH2, E-ARG.220	HH21, E-ARG.220	2.72	1.80	20.26
1HGG.PDB	OE1, D-GLU.72	NZ, E-LYS.238	HZ1, E-LYS.238	2.89	1.89	13.93
1HGG.PDB	O, D-SER.71	NZ, E-LYS.238	HZ3, E-LYS.238	2.80	1.86	20.00
1HGG.PDB	OE1, F-GLU.67	NH1, E-ARG.269	HH12, E-ARG.269	2.69	1.85	27.32
1HGG.PDB	O, F-LYS.68	NZ, E-LYS.299	HZ1, E-LYS.299	2.93	1.91	9.86
1HGG.PDB	O, F-LYS.62	N, E-GLY.303	H, E-GLY.303	2.92	1.95	6.71
1HGG.PDB	OG, F-SER.93	N, E-LYS.310	H, E-LYS.310	2.89	1.95	15.34
1HGG.PDB	OD1, F-ASP.90	NZ, E-LYS.310	HZ2, E-LYS.310	2.64	1.72	22.12
1HGG.PDB	OD1, F-ASN.104	N, E-ALA.317	H, E-ALA.317	2.80	1.89	16.99
1HGG.PDB	OE2, F-GLU.15	N, E-GLU.325	H, E-GLU.325	2.88	2.08	28.79
1HGG.PDB	OE1, F-GLU.15	NZ, E-LYS.326	HZ3, E-LYS.326	2.98	1.97	15.13
1HGG.PDB	O, E-VAL.323	N, F-GLY.13	H, F-GLY.13	2.73	1.78	9.21
1HGG.PDB	O, E-HIS.17	N, F-TRP.14	H, F-TRP.14	2.81	1.90	18.17
1HGG.PDB	O, E-GLY.16	N, F-GLY.23	H, F-GLY.23	2.97	2.08	20.37
1HGG.PDB	O, E-CYS.14	N, F-ARG.25	H, F-ARG.25	2.99	2.04	12.72
1HGG.PDB	O, E-THR.12	N, F-GLN.27	H, F-GLN.27	2.98	2.05	15.41
1HGG.PDB	OE2, D-GLU.97	NH2, F-ARG.54	HH22, F-ARG.54	2.73	1.74	10.16
1HGG.PDB	OD2, D-ASP.86	NZ, F-LYS.62	HZ3, F-LYS.62	2.58	1.75	29.01
1HGG.PDB	OG, E-SER.110	NE2, F-HIS.64	HE2, F-HIS.64	2.87	1.91	10.03
1HGG.PDB	O, E-LYS.299	NZ, F-LYS.68	HZ1, F-LYS.68	2.85	1.83	8.63
1HGG.PDB	OG, A-SER.107	N, F-ARG.76	H, F-ARG.76	2.79	1.82	4.90
1HGG.PDB	OE2, B-GLU.81	NE, F-ARG.76	HE, F-ARG.76	2.88	1.92	11.44
1HGG.PDB	OE1, B-GLU.74	NH1, F-ARG.76	HH12, F-ARG.76	2.75	1.76	9.13
1HGG.PDB	OE1, B-GLU.81	NH2, F-ARG.76	HH21, F-ARG.76	2.67	1.68	1.99
1HGG.PDB	OE2, B-GLU.74	NH2, F-ARG.76	HH22, F-ARG.76	2.79	1.81	10.64
1HGG.PDB	OH, D-TYR.83	NZ, F-LYS.88	HZ1, F-LYS.88	2.68	1.67	10.46
1HGG.PDB	O, E-LYS.27	ND2, F-ASN.104	HD22, F-ASN.104	2.91	1.98	14.98
1HGG.PDB	OE1, D-GLU.132	NE, F-ARG.124	HE, F-ARG.124	2.96	2.09	22.59
1HGG.PDB	OE2, D-GLU.132	NE, F-ARG.124	HE, F-ARG.124	2.87	2.01	24.00
1HGG.PDB	O, E-LEU.13	N, F-PHE.138	H, F-PHE.138	2.72	1.87	23.38
1HGG.PDB	O, E-ALA.11	N, F-ILE.140	H, F-ILE.140	2.79	1.89	17.86
1HGG.PDB	O, D-ARG.170	NH1, F-ARG.163	HH12, F-ARG.163	2.94	2.00	17.69
1HGH.PDB	O, B-ILE.140	N, A-ALA.11	H, A-ALA.11	2.91	2.03	21.75
1HGH.PDB	O, B-PHE.138	N, A-LEU.13	H, A-LEU.13	2.96	1.99	9.24
1HGH.PDB	O, B-ARG.25	N, A-CYS.14	H, A-CYS.14	2.90	1.93	6.13
1HGH.PDB	O, B-GLY.136	N, A-LEU.15	H, A-LEU.15	2.89	1.92	5.59
1HGH.PDB	O, B-GLY.23	N, A-GLY.16	H, A-GLY.16	2.92	2.07	24.71
1HGH.PDB	O, B-TRP.21	N, A-HIS.18	H, A-HIS.18	2.92	2.03	20.10
1HGH.PDB	OE2, B-GLU.97	NZ, A-LYS.27	HZ1, A-LYS.27	2.78	1.76	9.03
1HGH.PDB	OE2, B-GLU.67	NH2, A-ARG.109	HH21, A-ARG.109	2.86	1.88	13.48
1HGH.PDB	OD2, F-ASP.79	OG, A-SER.110	HG, A-SER.110	2.97	2.01	11.65
1HGH.PDB	OD1, E-ASP.101	NE2, A-GLN.210	HE22, A-GLN.210	2.97	2.14	27.61
1HGH.PDB	OE1, C-GLN.210	NH2, A-ARG.220	HH21, A-ARG.220	2.66	1.73	18.15
1HGH.PDB	O, F-SER.71	NZ, A-LYS.238	HZ2, A-LYS.238	2.69	1.74	19.56
1HGH.PDB	OE1, F-GLU.72	NZ, A-LYS.238	HZ3, A-LYS.238	2.92	1.93	15.64
1HGH.PDB	O, B-LYS.68	NZ, A-LYS.299	HZ1, A-LYS.299	2.98	1.97	13.59
1HGH.PDB	O, B-LYS.62	N, A-GLY.303	H, A-GLY.303	3.00	2.03	6.35
1HGH.PDB	OG, B-SER.93	N, A-LYS.310	H, A-LYS.310	2.90	1.94	8.41
1HGH.PDB	OD1, B-ASP.86	NZ, A-LYS.310	HZ2, A-LYS.310	2.71	1.84	27.09
1HGH.PDB	OD1, B-ASN.104	N, A-ALA.317	H, A-ALA.317	2.74	1.80	10.38
1HGH.PDB	O, A-VAL.323	N, B-GLY.13	H, B-GLY.13	2.69	1.78	16.40
1HGH.PDB	O, A-HIS.17	N, B-TRP.14	H, B-TRP.14	2.80	1.87	14.18
1HGH.PDB	O, A-GLY.16	N, B-GLY.23	H, B-GLY.23	2.92	2.01	18.42
1HGH.PDB	O, A-CYS.14	N, B-ARG.25	H, B-ARG.25	2.97	2.02	12.29
1HGH.PDB	OE2, F-GLU.97	NH2, B-ARG.54	HH22, B-ARG.54	2.82	1.86	15.60
1HGH.PDB	OD2, F-ASP.86	NZ, B-LYS.62	HZ1, B-LYS.62	2.66	1.80	27.71

1HGH.PDB	OD2, F_ASP_90	NZ, B_LYS_62	HZ3, B_LYS_62	2.68	1.82	27.13
1HGH.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.87	1.91	11.96
1HGH.PDB	O, A_LYS_299	NZ, B_LYS_68	HZ1, B_LYS_68	2.89	1.86	6.42
1HGH.PDB	OG, C_SER_107	N, B_ARG_76	H, B_ARG_76	2.88	1.92	9.13
1HGH.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.87	1.90	9.70
1HGH.PDB	OE2, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.91	1.90	8.45
1HGH.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.77	1.76	5.47
1HGH.PDB	OE1, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.89	1.87	2.83
1HGH.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.69	1.84	23.96
1HGH.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.74	1.71	7.44
1HGH.PDB	O, A_LYS_27	ND2, B_ASN_104	HD22, B_ASN_104	2.88	1.93	11.07
1HGH.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.76	1.94	26.47
1HGH.PDB	OE2, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.83	1.98	23.62
1HGH.PDB	O, A_LEU_13	N, B_PHE_138	H, B_PHE_138	2.71	1.82	19.17
1HGH.PDB	O, A_ALA_11	N, B_ILE_140	H, B_ILE_140	2.77	1.85	16.34
1HGH.PDB	O, F_ARG_170	NH1, B_ARG_163	HH12, B_ARG_163	2.69	1.71	10.72
1HGH.PDB	O, D_ILE_140	N, C_ALA_11	H, C_ALA_11	2.90	2.02	21.17
1HGH.PDB	O, D_GLN_27	N, C_THR_12	H, C_THR_12	2.94	1.99	10.37
1HGH.PDB	O, D_PHE_138	N, C_LEU_13	H, C_LEU_13	2.98	2.01	8.63
1HGH.PDB	O, D_ARG_25	N, C_CYS_14	H, C_CYS_14	2.74	1.80	11.01
1HGH.PDB	O, D_GLY_136	N, C_LEU_15	H, C_LEU_15	2.92	1.95	6.34
1HGH.PDB	O, D_GLY_23	N, C_GLY_16	H, C_GLY_16	2.95	2.08	23.40
1HGH.PDB	O, D_TRP_21	N, C_HIS_18	H, C_HIS_18	2.93	2.04	20.66
1HGH.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.82	1.78	7.61
1HGH.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.86	1.88	13.66
1HGH.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.78	1.85	13.87
1HGH.PDB	OD1, A_ASP_101	NE2, C_GLN_210	HE22, C_GLN_210	2.93	2.07	24.87
1HGH.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.57	1.72	26.03
1HGH.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.71	1.80	22.72
1HGH.PDB	O, B_SER_71	NZ, C_LYS_238	HZ3, C_LYS_238	2.68	1.75	20.57
1HGH.PDB	OG, D_SER_93	N, C_LYS_310	H, C_LYS_310	2.93	1.96	8.29
1HGH.PDB	OD1, D_ASP_86	NZ, C_LYS_310	HZ2, C_LYS_310	2.73	1.85	26.20
1HGH.PDB	OD1, D_ASN_104	N, C_ALA_317	H, C_ALA_317	2.74	1.81	14.42
1HGH.PDB	OE1, D_GLU_15	NZ, C_LYS_326	HZ1, C_LYS_326	2.77	1.75	11.00
1HGH.PDB	O, C_VAL_323	N, D_GLY_13	H, D_GLY_13	2.68	1.77	15.36
1HGH.PDB	O, C_HIS_17	N, D_TRP_14	H, D_TRP_14	2.80	1.87	13.64
1HGH.PDB	O, C_GLY_16	N, D_GLY_23	H, D_GLY_23	2.92	2.01	18.18
1HGH.PDB	O, C_CYS_14	N, D_ARG_25	H, D_ARG_25	2.90	1.94	10.42
1HGH.PDB	O, C_THR_12	N, D_GLN_27	H, D_GLN_27	2.91	1.98	14.85
1HGH.PDB	O, A_THR_28	NE, D_ARG_54	HE, D_ARG_54	2.96	1.98	3.97
1HGH.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.80	1.85	16.64
1HGH.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.84	1.88	10.18
1HGH.PDB	O, C_LYS_299	NZ, D_LYS_68	HZ1, D_LYS_68	2.88	1.85	6.67
1HGH.PDB	OG, E_SER_107	N, D_ARG_76	H, D_ARG_76	2.91	1.94	8.23
1HGH.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.79	1.84	10.45
1HGH.PDB	OE2, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.77	1.77	10.38
1HGH.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.70	1.70	6.41
1HGH.PDB	OE1, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.75	1.75	5.88
1HGH.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.59	1.81	29.86
1HGH.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.66	1.64	7.83
1HGH.PDB	O, C_LYS_27	ND2, D_ASN_104	HD22, D_ASN_104	2.89	1.94	11.70
1HGH.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.80	1.98	26.35
1HGH.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.84	1.99	23.38
1HGH.PDB	O, C_LEU_13	N, D_PHE_138	H, D_PHE_138	2.75	1.85	18.05
1HGH.PDB	O, C_ALA_11	N, D_ILE_140	H, D_ILE_140	2.83	1.90	15.57
1HGH.PDB	O, B_ARG_170	NH1, D_ARG_163	HH12, D_ARG_163	2.75	1.77	10.76
1HGH.PDB	O, F_ILE_140	N, E_ALA_11	H, E_ALA_11	2.92	2.02	19.53
1HGH.PDB	O, F_PHE_138	N, E_LEU_13	H, E_LEU_13	2.96	1.99	9.34

1HGH.PDB	O, F_ARG_25	N, E_CYS_14	H, E_CYS_14	2.64	1.78	21.59
1HGH.PDB	O, F_GLY_136	N, E_LEU_15	H, E_LEU_15	2.90	1.93	5.74
1HGH.PDB	O, F_GLY_23	N, E_GLY_16	H, E_GLY_16	2.92	2.05	22.72
1HGH.PDB	O, F_TRP_21	N, E_HIS_18	H, E_HIS_18	2.92	2.03	19.54
1HGH.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.77	1.74	8.08
1HGH.PDB	OE2, F_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.88	1.90	13.56
1HGH.PDB	OD2, D_ASP_79	OG, E_SER_110	HG, E_SER_110	2.90	1.94	9.49
1HGH.PDB	OD1, C_ASP_101	NE2, E_GLN_210	HE22, E_GLN_210	2.95	2.09	25.33
1HGH.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.68	1.79	22.30
1HGH.PDB	O, D_SER_71	NZ, E_LYS_238	HZ2, E_LYS_238	2.84	1.88	19.22
1HGH.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ3, E_LYS_238	2.87	1.88	15.42
1HGH.PDB	OE1, F_GLU_67	NH1, E_ARG_269	HH12, E_ARG_269	2.71	1.88	29.19
1HGH.PDB	O, F_LYS_62	N, E_GLY_303	H, E_GLY_303	2.98	2.01	7.92
1HGH.PDB	OG, F_SER_93	N, E_LYS_310	H, E_LYS_310	2.93	1.97	10.42
1HGH.PDB	OD1, F_ASP_86	NZ, E_LYS_310	HZ2, E_LYS_310	2.74	1.87	26.77
1HGH.PDB	O, F_SER_93	NE2, E_GLN_311	HE21, E_GLN_311	2.99	2.02	4.65
1HGH.PDB	OD1, F_ASN_104	N, E_ALA_317	H, E_ALA_317	2.75	1.81	11.69
1HGH.PDB	OE2, F_GLU_15	N, E_GLU_325	H, E_GLU_325	2.97	2.16	28.37
1HGH.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.90	1.89	12.96
1HGH.PDB	O, E_VAL_323	N, F_GLY_13	H, F_GLY_13	2.70	1.77	11.97
1HGH.PDB	O, E_HIS_17	N, F_TRP_14	H, F_TRP_14	2.81	1.87	12.50
1HGH.PDB	O, E_GLY_16	N, F_GLY_23	H, F_GLY_23	2.91	2.00	17.53
1HGH.PDB	O, E_CYS_14	N, F_ARG_25	H, F_ARG_25	2.90	1.98	16.77
1HGH.PDB	O, E_THR_12	N, F_GLN_27	H, F_GLN_27	2.91	2.03	20.46
1HGH.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.72	1.77	15.67
1HGH.PDB	OD2, D_ASP_90	NZ, F_LYS_62	HZ2, F_LYS_62	2.68	1.83	28.02
1HGH.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.87	1.91	9.23
1HGH.PDB	O, E_LYS_299	NZ, F_LYS_68	HZ1, F_LYS_68	2.91	1.87	1.37
1HGH.PDB	OG, A_SER_107	N, F_ARG_76	H, F_ARG_76	2.80	1.83	4.45
1HGH.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.84	1.87	10.72
1HGH.PDB	OE2, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.73	1.73	5.34
1HGH.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.71	1.70	1.21
1HGH.PDB	OE1, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.78	1.78	7.19
1HGH.PDB	OE1, B_GLU_85	OH, F_TYR_83	HH, F_TYR_83	2.53	1.74	27.23
1HGH.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.65	1.63	9.88
1HGH.PDB	O, E_LYS_27	ND2, F_ASN_104	HD22, F_ASN_104	2.90	1.95	12.28
1HGH.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.89	2.06	26.55
1HGH.PDB	OE2, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.92	2.03	21.52
1HGH.PDB	O, E_LEU_13	N, F_PHE_138	H, F_PHE_138	2.71	1.82	18.02
1HGH.PDB	O, E_ALA_11	N, F_ILE_140	H, F_ILE_140	2.79	1.87	15.45
1HGH.PDB	O, D_ARG_170	NH1, F_ARG_163	HH12, F_ARG_163	2.89	1.90	10.67
1HGI.PDB	O, B_ILE_140	N, A_ALA_11	H, A_ALA_11	2.84	1.92	15.59
1HGI.PDB	O, B_PHE_138	N, A_LEU_13	H, A_LEU_13	3.00	2.03	9.98
1HGI.PDB	O, B_ARG_25	N, A_CYS_14	H, A_CYS_14	2.96	2.03	15.50
1HGI.PDB	O, B_GLY_136	N, A_LEU_15	H, A_LEU_15	2.93	1.96	7.25
1HGI.PDB	O, B_GLY_23	N, A_GLY_16	H, A_GLY_16	2.98	2.12	23.40
1HGI.PDB	O, B_TRP_21	N, A_HIS_18	H, A_HIS_18	2.89	1.98	18.40
1HGI.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.90	1.86	7.66
1HGI.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.80	1.81	13.24
1HGI.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.65	1.73	18.55
1HGI.PDB	OE1, F_SER_71	NZ, A_LYS_238	HZ2, A_LYS_238	2.65	1.80	28.67
1HGI.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.85	1.85	15.00
1HGI.PDB	O, B_LYS_62	N, A_GLY_303	H, A_GLY_303	2.96	1.99	7.07
1HGI.PDB	OG, B_SER_93	N, A_LYS_310	H, A_LYS_310	2.98	2.05	15.58
1HGI.PDB	OD1, B_ASP_86	NZ, A_LYS_310	HZ3, A_LYS_310	2.76	1.92	29.34
1HGI.PDB	OD1, B_ASN_104	N, A_ALA_317	H, A_ALA_317	2.74	1.83	15.76
1HGI.PDB	OE2, B_GLU_15	NZ, A_LYS_326	HZ1, A_LYS_326	2.79	1.93	27.33
1HGI.PDB	OE1, B_GLU_15	N, A_THR_328	H, A_THR_328	2.87	1.93	12.65

1HGI.PDB	O, A_VAL_323	N, B_GLY_13	H, B_GLY_13	2.68	1.79	18.45
1HGI.PDB	O, A_HIS_17	N, B_TRP_14	H, B_TRP_14	2.78	1.88	17.65
1HGI.PDB	O, A_GLY_16	N, B_GLY_23	H, B_GLY_23	2.97	2.06	17.58
1HGI.PDB	OE2, A_GLU_325	NH2, B_ARG_25	HH22, B_ARG_25	2.93	1.95	13.46
1HGI.PDB	O, E_THR_28	NE, B_ARG_54	HE, B_ARG_54	2.88	1.92	10.21
1HGI.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.81	1.84	14.63
1HGI.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ1, B_LYS_62	2.67	1.78	25.75
1HGI.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.87	1.89	8.13
1HGI.PDB	O, A_LYS_299	NZ, B_LYS_68	HZ1, B_LYS_68	2.81	1.78	9.15
1HGI.PDB	OG, C_SER_107	N, B_ARG_76	H, B_ARG_76	2.85	1.90	10.66
1HGI.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.86	1.89	7.04
1HGI.PDB	OE2, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.92	1.89	1.72
1HGI.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.71	1.72	8.42
1HGI.PDB	OE1, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.86	1.86	6.93
1HGI.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.78	1.84	13.46
1HGI.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.65	1.64	9.94
1HGI.PDB	O, A_LYS_27	ND2, B_ASN_104	HD22, B_ASN_104	2.86	1.90	10.00
1HGI.PDB	O, F_LEU_2	OG, B_SER_113	HG, B_SER_113	2.77	1.90	22.05
1HGI.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.81	1.96	23.50
1HGI.PDB	OE2, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.86	2.02	24.92
1HGI.PDB	O, A_LEU_13	N, B_PHE_138	H, B_PHE_138	2.74	1.89	23.78
1HGI.PDB	O, A_ALA_11	N, B_ILE_140	H, B_ILE_140	2.77	1.87	18.46
1HGI.PDB	O, F_ARG_170	NH1, B_ARG_163	HH12, B_ARG_163	2.73	1.76	13.86
1HGI.PDB	O, D_ILE_140	N, C_ALA_11	H, C_ALA_11	2.86	1.93	15.33
1HGI.PDB	O, D_GLN_27	N, C_THR_12	H, C_THR_12	2.98	2.01	4.69
1HGI.PDB	O, D_PHE_138	N, C_LEU_13	H, C_LEU_13	2.99	2.03	9.93
1HGI.PDB	O, D_ARG_25	N, C_CYS_14	H, C_CYS_14	2.67	1.83	24.75
1HGI.PDB	O, D_GLY_136	N, C_LEU_15	H, C_LEU_15	2.95	1.98	7.51
1HGI.PDB	O, D_GLY_23	N, C_GLY_16	H, C_GLY_16	2.99	2.12	22.96
1HGI.PDB	O, D_TRP_21	N, C_HIS_18	H, C_HIS_18	2.88	1.97	18.12
1HGI.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.88	1.83	6.58
1HGI.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.82	1.84	15.02
1HGI.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.85	1.90	11.29
1HGI.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.62	1.75	23.70
1HGI.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.67	1.77	23.68
1HGI.PDB	O, B_SER_71	NZ, C_LYS_238	HZ3, C_LYS_238	2.57	1.73	28.43
1HGI.PDB	O, D_LYS_62	N, C_GLY_303	H, C_GLY_303	2.97	2.00	7.92
1HGI.PDB	OD1, D_ASP_86	NZ, C_LYS_310	HZ3, C_LYS_310	2.77	1.93	29.51
1HGI.PDB	OD1, D_ASN_104	N, C_ALA_317	H, C_ALA_317	2.74	1.83	16.29
1HGI.PDB	OE1, D_GLU_15	NZ, C_LYS_326	HZ1, C_LYS_326	2.83	1.84	16.25
1HGI.PDB	O, C_VAL_323	N, D_GLY_13	H, D_GLY_13	2.65	1.77	19.23
1HGI.PDB	O, C_HIS_17	N, D_TRP_14	H, D_TRP_14	2.83	1.92	16.86
1HGI.PDB	O, C_GLY_16	N, D_GLY_23	H, D_GLY_23	2.94	2.02	16.89
1HGI.PDB	O, C_CYS_14	N, D_ARG_25	H, D_ARG_25	2.88	1.94	13.44
1HGI.PDB	O, C_THR_12	N, D_GLN_27	H, D_GLN_27	2.95	2.00	13.47
1HGI.PDB	O, A_THR_28	NE, D_ARG_54	HE, D_ARG_54	2.83	1.87	10.21
1HGI.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.81	1.85	15.40
1HGI.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.83	1.85	2.78
1HGI.PDB	O, C_LYS_299	NZ, D_LYS_68	HZ1, D_LYS_68	2.79	1.78	10.55
1HGI.PDB	OG, E_SER_107	N, D_ARG_76	H, D_ARG_76	2.89	1.92	9.17
1HGI.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.80	1.82	5.40
1HGI.PDB	OE2, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.78	1.76	4.18
1HGI.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.61	1.67	15.38
1HGI.PDB	OE1, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.76	1.77	8.75
1HGI.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.69	1.81	20.41
1HGI.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.66	1.64	7.30
1HGI.PDB	O, C_LYS_27	ND2, D_ASN_104	HD22, D_ASN_104	2.83	1.88	11.60
1HGI.PDB	O, B_LEU_2	OG, D_SER_113	HG, D_SER_113	2.77	1.91	22.96

1HGI.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.84	1.98	23.95
1HGI.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.88	2.03	24.96
1HGI.PDB	O, C_LEU_13	N, D_PHE_138	H, D_PHE_138	2.79	1.92	22.46
1HGI.PDB	O, C_ALA_11	N, D_ILE_140	H, D_ILE_140	2.81	1.91	18.30
1HGI.PDB	O, B_ARG_170	NH1, D_ARG_163	HH12, D_ARG_163	2.80	1.83	13.94
1HGI.PDB	O, F_ILE_140	N, E_ALA_11	H, E_ALA_11	2.89	1.95	14.83
1HGI.PDB	O, F_GLN_27	N, E_THR_12	H, E_THR_12	2.94	2.00	13.31
1HGI.PDB	O, F_PHE_138	N, E_LEU_13	H, E_LEU_13	2.97	2.02	11.46
1HGI.PDB	O, F_ARG_25	N, E_CYS_14	H, E_CYS_14	2.66	1.84	26.53
1HGI.PDB	O, F_GLY_136	N, E_LEU_15	H, E_LEU_15	2.92	1.95	6.28
1HGI.PDB	O, F_GLY_23	N, E_GLY_16	H, E_GLY_16	2.99	2.12	22.78
1HGI.PDB	O, F_TRP_21	N, E_HIS_18	H, E_HIS_18	2.89	1.99	19.14
1HGI.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.86	1.82	7.44
1HGI.PDB	OE2, F_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.78	1.80	14.37
1HGI.PDB	OD2, D_ASP_79	OG, E_SER_110	HG, E_SER_110	2.90	1.94	10.08
1HGI.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.69	1.80	23.03
1HGI.PDB	O, D_SER_71	NZ, E_LYS_238	HZ2, E_LYS_238	2.75	1.87	26.62
1HGI.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ3, E_LYS_238	2.80	1.81	15.90
1HGI.PDB	O, F_LYS_62	N, E_GLY_303	H, E_GLY_303	2.93	1.96	6.65
1HGI.PDB	OG, F_SER_93	N, E_LYS_310	H, E_LYS_310	2.99	2.05	13.79
1HGI.PDB	OD1, F_ASP_86	NZ, E_LYS_310	HZ3, E_LYS_310	2.76	1.91	29.16
1HGI.PDB	OD1, F_ASN_104	N, E_ALA_317	H, E_ALA_317	2.72	1.81	15.78
1HGI.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.88	1.86	11.05
1HGI.PDB	O, E_VAL_323	N, F_GLY_13	H, F_GLY_13	2.66	1.77	18.62
1HGI.PDB	O, E_HIS_17	N, F_TRP_14	H, F_TRP_14	2.84	1.93	16.42
1HGI.PDB	O, E_GLY_16	N, F_GLY_23	H, F_GLY_23	2.97	2.05	16.89
1HGI.PDB	O, E_CYS_14	N, F_ARG_25	H, F_ARG_25	2.91	2.04	22.96
1HGI.PDB	O, E_THR_12	N, F_GLN_27	H, F_GLN_27	2.93	1.99	14.92
1HGI.PDB	O, C_THR_28	NE, F_ARG_54	HE, F_ARG_54	2.95	1.99	9.70
1HGI.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.75	1.79	14.82
1HGI.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.84	1.87	3.62
1HGI.PDB	O, E_LYS_299	NZ, F_LYS_68	HZ1, F_LYS_68	2.80	1.76	2.37
1HGI.PDB	OG, A_SER_107	N, F_ARG_76	H, F_ARG_76	2.79	1.83	7.22
1HGI.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.85	1.88	7.37
1HGI.PDB	OE2, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.77	1.76	3.93
1HGI.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.64	1.66	4.79
1HGI.PDB	OE1, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.76	1.78	10.40
1HGI.PDB	OE1, B_GLU_85	OH, F_TYR_83	HH, F_TYR_83	2.58	1.75	24.06
1HGI.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.61	1.62	12.49
1HGI.PDB	O, E_LYS_27	ND2, F_ASN_104	HD22, F_ASN_104	2.88	1.93	10.77
1HGI.PDB	O, D_LEU_2	OG, F_SER_113	HG, F_SER_113	2.78	1.94	24.17
1HGI.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.96	2.09	23.50
1HGI.PDB	OE2, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.96	2.09	23.34
1HGI.PDB	O, E_LEU_13	N, F_PHE_138	H, F_PHE_138	2.75	1.89	22.82
1HGI.PDB	O, E_ALA_11	N, F_ILE_140	H, F_ILE_140	2.78	1.89	18.92
1HGI.PDB	O, D_ARG_170	NH1, F_ARG_163	HH12, F_ARG_163	2.92	1.95	13.55
1HGI.PDB	OE2, D_GLU_131	NH2, F_ARG_163	HH22, F_ARG_163	2.69	1.85	26.81
1HGJ.PDB	O, B_ILE_140	N, A_ALA_11	H, A_ALA_11	2.85	1.95	18.97
1HGJ.PDB	O, B_PHE_138	N, A_LEU_13	H, A_LEU_13	2.97	2.00	8.62
1HGJ.PDB	O, B_ARG_25	N, A_CYS_14	H, A_CYS_14	2.88	1.94	12.89
1HGJ.PDB	O, B_GLY_136	N, A_LEU_15	H, A_LEU_15	2.93	1.95	2.37
1HGJ.PDB	O, B_GLY_23	N, A_GLY_16	H, A_GLY_16	2.86	1.96	18.97
1HGJ.PDB	O, B_TRP_21	N, A_HIS_18	H, A_HIS_18	2.85	1.98	21.54
1HGJ.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.81	1.78	9.30
1HGJ.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.75	1.77	12.07
1HGJ.PDB	OD2, F_ASP_79	OG, A_SER_110	HG, A_SER_110	2.94	1.98	10.39
1HGJ.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.67	1.78	22.50
1HGJ.PDB	O, F_SER_71	NZ, A_LYS_238	HZ2, A_LYS_238	2.62	1.72	23.44

1HGJ.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.90	1.90	13.91
1HGJ.PDB	O, B_LYS_68	NZ, A_LYS_299	HZ2, A_LYS_299	2.95	1.96	14.91
1HGJ.PDB	O, B_LYS_62	N, A_GLY_303	H, A_GLY_303	2.93	1.97	8.41
1HGJ.PDB	OD1, B_ASN_104	N, A_ALA_317	H, A_ALA_317	2.74	1.81	13.01
1HGJ.PDB	OE1, B_GLU_15	N, A_THR_328	H, A_THR_328	2.99	2.03	9.44
1HGJ.PDB	O, A_VAL_323	N, B_GLY_13	H, B_GLY_13	2.69	1.76	11.68
1HGJ.PDB	O, A_HIS_17	N, B_TRP_14	H, B_TRP_14	2.84	1.89	12.22
1HGJ.PDB	O, A_GLY_16	N, B_GLY_23	H, B_GLY_23	2.94	2.02	17.07
1HGJ.PDB	O, A_CYS_14	N, B_ARG_25	H, B_ARG_25	2.98	2.05	15.51
1HGJ.PDB	OE2, A_GLU_325	NH2, B_ARG_25	HH22, B_ARG_25	2.97	2.01	15.94
1HGJ.PDB	O, E_THR_28	NE, B_ARG_54	HE, B_ARG_54	3.00	2.04	10.82
1HGJ.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.77	1.81	15.09
1HGJ.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ1, B_LYS_62	2.65	1.75	23.55
1HGJ.PDB	OD2, F_ASP_90	NZ, B_LYS_62	HZ3, B_LYS_62	2.74	1.89	28.52
1HGJ.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.89	1.93	11.21
1HGJ.PDB	O, A_LYS_299	NZ, B_LYS_68	HZ1, B_LYS_68	2.90	1.89	11.39
1HGJ.PDB	OG, C_SER_107	N, B_ARG_76	H, B_ARG_76	2.84	1.89	10.24
1HGJ.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.90	1.93	10.80
1HGJ.PDB	OE2, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.88	1.87	5.28
1HGJ.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.72	1.72	3.64
1HGJ.PDB	OE1, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.85	1.84	3.19
1HGJ.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.67	1.83	24.12
1HGJ.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.78	1.75	7.42
1HGJ.PDB	O, A_LYS_27	ND2, B_ASN_104	HD22, B_ASN_104	2.89	1.94	10.52
1HGJ.PDB	O, F_LEU_2	OG, B_SER_113	HG, B_SER_113	2.74	1.91	25.16
1HGJ.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.82	2.00	27.29
1HGJ.PDB	OE2, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.91	2.02	20.91
1HGJ.PDB	O, A_LEU_13	N, B_PHE_138	H, B_PHE_138	2.71	1.86	23.78
1HGJ.PDB	O, A_ALA_11	N, B_ILE_140	H, B_ILE_140	2.77	1.86	16.77
1HGJ.PDB	O, F_ARG_170	NH1, B_ARG_163	HH12, B_ARG_163	2.72	1.75	12.61
1HGJ.PDB	O, D_ILE_140	N, C_ALA_11	H, C_ALA_11	2.85	1.95	19.06
1HGJ.PDB	O, D_GLN_27	N, C_THR_12	H, C_THR_12	2.99	2.03	8.05
1HGJ.PDB	O, D_PHE_138	N, C_LEU_13	H, C_LEU_13	2.99	2.02	7.89
1HGJ.PDB	O, D_ARG_25	N, C_CYS_14	H, C_CYS_14	2.76	1.85	16.80
1HGJ.PDB	O, D_GLY_136	N, C_LEU_15	H, C_LEU_15	2.95	1.97	3.95
1HGJ.PDB	O, D_GLY_23	N, C_GLY_16	H, C_GLY_16	2.89	1.98	18.54
1HGJ.PDB	O, D_TRP_21	N, C_HIS_18	H, C_HIS_18	2.86	1.97	20.63
1HGJ.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.82	1.80	8.63
1HGJ.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.76	1.78	13.33
1HGJ.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.79	1.87	14.95
1HGJ.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.66	1.82	26.85
1HGJ.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.75	1.79	18.67
1HGJ.PDB	O, B_SER_71	NZ, C_LYS_238	HZ3, C_LYS_238	2.55	1.67	24.42
1HGJ.PDB	O, D_LYS_68	NZ, C_LYS_299	HZ2, C_LYS_299	2.96	1.96	14.80
1HGJ.PDB	O, D_LYS_62	N, C_GLY_303	H, C_GLY_303	2.93	1.98	10.54
1HGJ.PDB	OG, D_SER_93	N, C_LYS_310	H, C_LYS_310	3.00	2.04	11.61
1HGJ.PDB	OD1, D_ASP_86	NZ, C_LYS_310	HZ3, C_LYS_310	2.94	2.10	29.37
1HGJ.PDB	OD1, D_ASN_104	N, C_ALA_317	H, C_ALA_317	2.74	1.82	13.77
1HGJ.PDB	OE1, D_GLU_15	NZ, C_LYS_326	HZ1, C_LYS_326	2.91	1.86	5.48
1HGJ.PDB	O, C_VAL_323	N, D_GLY_13	H, D_GLY_13	2.70	1.77	13.01
1HGJ.PDB	O, C_HIS_17	N, D_TRP_14	H, D_TRP_14	2.84	1.88	10.47
1HGJ.PDB	O, C_GLY_16	N, D_GLY_23	H, D_GLY_23	2.95	2.03	16.60
1HGJ.PDB	O, C_CYS_14	N, D_ARG_25	H, D_ARG_25	2.96	2.03	15.69
1HGJ.PDB	O, C_THR_12	N, D_GLN_27	H, D_GLN_27	2.96	2.04	16.68
1HGJ.PDB	O, A_THR_28	NE, D_ARG_54	HE, D_ARG_54	2.94	1.98	10.71
1HGJ.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.84	1.88	15.58
1HGJ.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.89	1.91	5.59
1HGJ.PDB	O, C_LYS_299	NZ, D_LYS_68	HZ1, D_LYS_68	2.93	1.91	11.63

1HGJ.PDB	OG, E_SER_107	N, D_ARG_76	H, D_ARG_76	2.86	1.90	9.67
1HGJ.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.85	1.89	10.87
1HGJ.PDB	OE2, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.76	1.76	7.89
1HGJ.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.68	1.69	5.65
1HGJ.PDB	OE1, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.71	1.72	5.59
1HGJ.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.63	1.81	25.72
1HGJ.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.75	1.72	7.31
1HGJ.PDB	O, C_LYS_27	ND2, D_ASN_104	HD22, D_ASN_104	2.90	1.94	10.67
1HGJ.PDB	O, B_LEU_2	OG, D_SER_113	HG, D_SER_113	2.68	1.87	27.58
1HGJ.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.80	1.98	27.33
1HGJ.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.87	2.00	21.99
1HGJ.PDB	OH, B_TYR_141	NH1, D_ARG_127	HH12, D_ARG_127	2.99	2.02	12.89
1HGJ.PDB	O, C_LEU_13	N, D_PHE_138	H, D_PHE_138	2.74	1.87	22.25
1HGJ.PDB	O, C_ALA_11	N, D_ILE_140	H, D_ILE_140	2.80	1.87	15.19
1HGJ.PDB	O, B_ARG_170	NH1, D_ARG_163	HH12, D_ARG_163	2.74	1.76	11.80
1HGJ.PDB	O, F_ILE_140	N, E_ALA_11	H, E_ALA_11	2.86	1.96	18.18
1HGJ.PDB	O, F_GLN_27	N, E_THR_12	H, E_THR_12	2.93	2.00	15.55
1HGJ.PDB	O, F_PHE_138	N, E_LEU_13	H, E_LEU_13	2.96	1.99	8.56
1HGJ.PDB	O, F_ARG_25	N, E_CYS_14	H, E_CYS_14	2.66	1.82	24.90
1HGJ.PDB	O, F_GLY_136	N, E_LEU_15	H, E_LEU_15	2.91	1.94	3.68
1HGJ.PDB	O, F_GLY_23	N, E_GLY_16	H, E_GLY_16	2.87	1.96	18.32
1HGJ.PDB	O, F_TRP_21	N, E_HIS_18	H, E_HIS_18	2.83	1.96	22.19
1HGJ.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.81	1.79	8.50
1HGJ.PDB	OE2, F_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.76	1.77	12.82
1HGJ.PDB	OD2, D_ASP_79	OG, E_SER_110	HG, E_SER_110	2.79	1.87	15.96
1HGJ.PDB	OD1, C_ASP_101	NE2, E_GLN_210	HE22, E_GLN_210	2.94	2.10	26.45
1HGJ.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.69	1.86	28.41
1HGJ.PDB	O, D_SER_71	NZ, E_LYS_238	HZ2, E_LYS_238	2.65	1.73	22.71
1HGJ.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ3, E_LYS_238	2.87	1.86	13.82
1HGJ.PDB	O, F_LYS_68	NZ, E_LYS_299	HZ1, E_LYS_299	2.94	1.95	15.31
1HGJ.PDB	O, F_LYS_62	N, E_GLY_303	H, E_GLY_303	2.92	1.96	9.12
1HGJ.PDB	OG, F_SER_93	N, E_LYS_310	H, E_LYS_310	2.99	2.03	10.38
1HGJ.PDB	OD1, F_ASP_86	NZ, E_LYS_310	HZ3, E_LYS_310	2.93	2.08	29.22
1HGJ.PDB	OD1, F_ASN_104	N, E_ALA_317	H, E_ALA_317	2.73	1.80	11.35
1HGJ.PDB	OE2, F_GLU_15	N, E_GLU_325	H, E_GLU_325	2.88	2.08	29.65
1HGJ.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.87	1.86	12.83
1HGJ.PDB	O, E_VAL_323	N, F_GLY_13	H, F_GLY_13	2.69	1.76	10.96
1HGJ.PDB	O, E_HIS_17	N, F_TRP_14	H, F_TRP_14	2.84	1.89	11.67
1HGJ.PDB	O, E_GLY_16	N, F_GLY_23	H, F_GLY_23	2.93	2.01	16.90
1HGJ.PDB	O, E_CYS_14	N, F_ARG_25	H, F_ARG_25	2.87	1.99	20.85
1HGJ.PDB	O, E_THR_12	N, F_GLN_27	H, F_GLN_27	2.89	1.97	15.73
1HGJ.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.77	1.81	14.54
1HGJ.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.90	1.93	7.02
1HGJ.PDB	O, E_LYS_299	NZ, F_LYS_68	HZ1, F_LYS_68	2.93	1.90	4.77
1HGJ.PDB	OG, A_SER_107	N, F_ARG_76	H, F_ARG_76	2.85	1.88	6.29
1HGJ.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.85	1.89	12.57
1HGJ.PDB	OE2, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.70	1.70	4.55
1HGJ.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.65	1.66	2.84
1HGJ.PDB	OE1, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.72	1.73	7.95
1HGJ.PDB	OE1, B_GLU_85	OH, F_TYR_83	HH, F_TYR_83	2.53	1.75	28.54
1HGJ.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.70	1.68	8.19
1HGJ.PDB	O, E_LYS_27	ND2, F_ASN_104	HD22, F_ASN_104	2.91	1.96	11.78
1HGJ.PDB	O, D_LEU_2	OG, F_SER_113	HG, F_SER_113	2.74	1.92	26.51
1HGJ.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.92	2.09	27.65
1HGJ.PDB	OE2, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.96	2.06	20.98
1HGJ.PDB	O, E_LEU_13	N, F_PHE_138	H, F_PHE_138	2.73	1.87	22.18
1HGJ.PDB	O, E_ALA_11	N, F_ILE_140	H, F_ILE_140	2.78	1.87	17.89
1HGJ.PDB	O, D_ARG_170	NH1, F_ARG_163	HH12, F_ARG_163	2.89	1.91	11.37

1OSP.PDB	O, O_LYS_44	NH1, L_ARG_32	HH12, L_ARG_32	2.98	2.09	22.73
1OSP.PDB	O, O_SER_43	NH2, L_ARG_32	HH22, L_ARG_32	2.91	1.93	9.19
1OSP.PDB	OD2, L_ASP_1	OG, H_SER_62	HG, H_SER_62	2.98	2.17	26.53
1OSP.PDB	O, O_ASP_93	N, H_TYR_101	H, H_TYR_101	2.96	2.00	9.88
1OSP.PDB	OH, L_TYR_36	N, H_PHE_107	H, H_PHE_107	2.90	1.92	4.68
1OSP.PDB	OG, L_SER_176	OG, H_SER_185	HG, H_SER_185	2.74	1.91	24.72
1OSP.PDB	OE1, L_GLU_123	NZ, H_LYS_215	HZ2, H_LYS_215	2.78	1.85	20.53
1PSK.PDB	O, H_PRO_168	OG, L_SER_161	HG, L_SER_161	2.76	1.90	22.64
1VFB.PDB	OE1, C_GLN_121	N, A_SER_93	H, A_SER_93	2.89	1.92	8.17
1VFB.PDB	OE1, B_GLU_98	NH1, A_ARG_96	HH12, A_ARG_96	2.82	1.84	8.38
1VFB.PDB	OE2, B_GLU_98	NH2, A_ARG_96	HH22, A_ARG_96	2.81	1.85	10.74
1VFB.PDB	OE1, A_GLN_38	NE2, B_GLN_39	HE21, B_GLN_39	2.95	1.98	8.04
1VFB.PDB	O, C_GLY_22	NH1, B_ARG_102	HH12, B_ARG_102	2.82	1.90	18.81
1VFB.PDB	OD2, B_ASP_100	N, C_SER_24	H, C_SER_24	2.91	2.09	27.47
1VFB.PDB	O, A_PHE_91	NE2, C_GLN_121	HE21, C_GLN_121	2.82	1.88	14.37
3SE8.PDB	O, H_TRP_54	N, G_ASP_368	H, G_ASP_368	2.75	1.91	10.72
3SE8.PDB	OE2, L_GLU_96	N, G_GLY_459	H, G_GLY_459	2.81	1.99	15.35
3SE8.PDB	OD1, G_ASN_280	NE1, H_TRP_50	HE1, H_TRP_50	3.00	2.21	20.49
3SE8.PDB	O, G_GLY_473	NE1, H_TRP_54	HE1, H_TRP_54	2.82	1.98	10.03
3SE8.PDB	O, G_GLY_458	N, H_ARG_61	H, H_ARG_61	2.91	2.08	12.24
3SE8.PDB	OD1, G_ASP_457	NE2, H_GLN_64	HE22, H_GLN_64	2.94	2.12	14.23
3SE8.PDB	OD2, G_ASP_368	NH2, H_ARG_71	HH22, H_ARG_71	2.91	2.05	6.24
3SE8.PDB	OH, L_TYR_36	N, H_TRP_100F	H, H_TRP_100F	2.89	2.04	6.32
3SE8.PDB	OE1, H_GLN_101	N, L_SER_56	H, L_SER_56	2.97	2.12	7.63
3SE8.PDB	O, H_PRO_167	OG, L_SER_162	HG, L_SER_162	2.71	1.98	23.05
3SE9.PDB	O, H_THR_53	N, G_ASP_368	H, G_ASP_368	2.97	2.15	15.24
3SE9.PDB	OD1, G_ASN_280	NE1, H_TRP_50	HE1, H_TRP_50	2.86	2.03	11.46
3SE9.PDB	O, G_ARG_456	ND2, H_ASN_57	HD22, H_ASN_57	2.82	1.98	10.42
3SE9.PDB	OG, G_SER_365	NH1, H_ARG_64	HH11, H_ARG_64	2.81	2.04	21.79
3SE9.PDB	OD2, G_ASP_368	NH1, H_ARG_71	HH12, H_ARG_71	2.77	1.92	7.25
3SE9.PDB	O, G_GLY_429	NH1, H_ARG_73	HH12, H_ARG_73	2.99	2.23	23.32
3SE9.PDB	OD1, G_ASN_279	NE1, H_TRP_100D	HE1, H_TRP_100D	2.86	2.13	26.83
3SE9.PDB	OH, L_TYR_36	N, H_PHE_100F	H, H_PHE_100F	2.88	2.05	11.59
3SE9.PDB	OD1, L_ASN_138	NE2, H_HIS_164	HE2, H_HIS_164	2.87	2.10	22.18
3SE9.PDB	O, H_PRO_167	OG, L_SER_162	HG, L_SER_162	2.60	1.89	25.20
3THM.PDB	O, H_ALA_117	ND2, L_ASN_35	HD21, L_ASN_35	2.77	1.97	17.79
3THM.PDB	OE1, L_GLN_39	NE2, H_GLN_41	HE22, H_GLN_41	2.98	2.14	9.35
3THM.PDB	O, F_CYS_43	NH1, H_ARG_105	HH12, H_ARG_105	2.85	2.05	18.46
3THM.PDB	OG, L_SER_183	NZ, H_LYS_162	HZ1, H_LYS_162	2.77	1.97	21.34
3THM.PDB	OG1, L_THR_135	NZ, H_LYS_162	HZ2, H_LYS_162	2.85	2.02	17.75
3THM.PDB	OH, H_TYR_35	ND1, F_HIS_44	HD1, F_HIS_44	2.69	1.83	5.98
3THM.PDB	OG, H_SER_63	NE2, F_HIS_44	HE2, F_HIS_44	2.83	2.07	23.36
3THM.PDB	O, L_SER_51	NZ, F_LYS_78	HZ2, F_LYS_78	3.00	2.15	15.09
3TJE.PDB	O, H_ALA_117	ND2, L_ASN_35	HD21, L_ASN_35	2.81	2.01	17.88
3TJE.PDB	OE1, L_GLN_39	NE2, H_GLN_41	HE21, H_GLN_41	2.98	2.15	10.85
3TJE.PDB	O, F_CYS_43	NH1, H_ARG_105	HH12, H_ARG_105	2.85	2.08	23.11
3TJE.PDB	OH, L_TYR_37	N, H_PHE_119	H, H_PHE_119	2.96	2.10	4.74
3TJE.PDB	OH, H_TYR_35	ND1, F_HIS_44	HD1, F_HIS_44	2.56	1.70	3.69
3U2S.PDB	OE1, L_GLN_38	NE2, H_GLN_39	HE22, H_GLN_39	2.89	2.04	8.55
3U2S.PDB	OH, L_TYR_36	N, H_MET_100T	H, H_MET_100T	2.95	2.15	18.41
3U2S.PDB	OG, L_SER_165	NE2, H_HIS_164	HE2, H_HIS_164	2.93	2.12	16.97
3U2S.PDB	OE1, H_GLN_39	NE2, L_GLN_38	HE22, L_GLN_38	2.91	2.09	13.75
3U2S.PDB	OD2, C_ASP_167	ND2, L_ASN_60	HD22, L_ASN_60	2.90	2.14	22.76
3U2S.PDB	OD1, H_ASP_61	NH2, L_ARG_95A	HH22, L_ARG_95A	2.34	1.58	22.53
3U2S.PDB	OE2, H_GLU_95	NH2, L_ARG_96	HH21, L_ARG_96	2.87	2.05	15.72
3U2S.PDB	O, H_ASN_100F	N, G_LYS_169	H, G_LYS_169	2.84	1.99	7.68
3U2S.PDB	OH, H_TYR_100K	ND2, G_ASN_173	HD21, G_ASN_173	2.97	2.13	8.87
3U2S.PDB	OE1, B_GLN_38	NE2, A_GLN_39	HE22, A_GLN_39	2.92	2.07	7.34

3U2S.PDB	O, C_ASP_167	N, A_ASN_100F	H, A_ASN_100F	2.97	2.14	14.21
3U2S.PDB	OG1, B_THR_131	NZ, A_LYS_143	HZ2, A_LYS_143	2.41	1.67	27.35
3U2S.PDB	OE1, A_GLN_39	NE2, B_GLN_38	HE22, B_GLN_38	2.92	2.08	10.61
3U2S.PDB	OG1, H_THR_160	N, B_ALA_80	H, B_ALA_80	2.90	2.08	14.44
3U2S.PDB	OD1, A_ASP_61	NH1, B_ARG_95A	HH12, B_ARG_95A	2.63	1.91	26.97
3U2S.PDB	OE2, A_GLU_95	NH2, B_ARG_96	HH21, B_ARG_96	2.98	2.16	13.77
3U2S.PDB	O, A_ASN_100F	N, C_LYS_169	H, C_LYS_169	2.91	2.08	13.24
3UYR.PDB	OE1, P_GLN_48	N, H_ASN_101	H, H_ASN_101	2.90	2.08	14.57
3UYR.PDB	OH, L_TYR_41	N, H_LEU_104	H, H_LEU_104	2.91	2.05	4.02
3UYR.PDB	OE2, L_GLU_127	NZ, H_LYS_212	HZ3, H_LYS_212	2.87	2.08	23.12
3UYR.PDB	O, P_PRO_50	NE2, L_HIS_31	HE2, L_HIS_31	2.91	2.13	21.00
3UYR.PDB	O, H_PRO_171	OG, L_SER_166	HG, L_SER_166	2.72	1.97	20.46
3UYR.PDB	OD1, H_ASN_101	NE2, P_GLN_48	HE22, P_GLN_48	2.57	1.87	29.89
4F33.PDB	OE1, B_GLN_39	NE2, A_GLN_38	HE22, A_GLN_38	2.96	2.13	12.75
4F33.PDB	O, B_GLY_110	OG, A_SER_43	HG, A_SER_43	2.65	1.95	25.99
4F33.PDB	O, B_ARG_104	NH1, A_ARG_46	HH11, A_ARG_46	2.62	1.83	18.99
4F33.PDB	O, B_PRO_173	OG, A_SER_162	HG, A_SER_162	2.76	2.03	23.18
4F33.PDB	OE1, A_GLN_38	NE2, B_GLN_39	HE22, B_GLN_39	2.82	1.97	5.31
4F33.PDB	OH, A_TYR_36	N, B_PHE_106	H, B_PHE_106	2.97	2.12	7.79
4F33.PDB	OE2, G_GLU_123	N, B_GLY_124	H, B_GLY_124	2.73	1.87	2.75
4F33.PDB	O, H_ASP_214	N, B_LYS_212	H, B_LYS_212	2.81	2.00	15.02
4F33.PDB	O, H_LYS_212	N, B_ASP_214	H, B_ASP_214	2.84	2.02	15.98
4F33.PDB	OE1, A_GLU_123	NZ, B_LYS_215	HZ1, B_LYS_215	2.68	1.82	12.44
4F33.PDB	OG1, H_THR_211	NZ, B_LYS_215	HZ2, B_LYS_215	2.83	1.95	7.37
4F33.PDB	O, D_GLY_110	OG, C_SER_43	HG, C_SER_43	2.70	1.98	23.76
4F33.PDB	O, D_ARG_104	NH1, C_ARG_46	HH11, C_ARG_46	2.70	1.92	20.25
4F33.PDB	O, D_TYR_60	NE2, C_HIS_94	HE2, C_HIS_94	2.75	2.00	24.62
4F33.PDB	O, D_PRO_173	OG, C_SER_162	HG, C_SER_162	2.78	2.07	25.83
4F33.PDB	OE1, C_GLN_38	NE2, D_GLN_39	HE22, D_GLN_39	2.89	2.03	5.23
4F33.PDB	OE2, E_GLU_123	N, D_GLY_124	H, D_GLY_124	2.84	1.99	7.85
4F33.PDB	O, F_ASP_214	N, D_LYS_212	H, D_LYS_212	2.98	2.15	12.10
4F33.PDB	O, F_LYS_212	N, D_ASP_214	H, D_ASP_214	2.85	2.03	14.94
4F33.PDB	OE1, C_GLU_123	NZ, D_LYS_215	HZ1, D_LYS_215	2.79	1.99	22.47
4F33.PDB	OG1, F_THR_211	NZ, D_LYS_215	HZ2, D_LYS_215	2.86	1.99	10.67
4F33.PDB	O, F_ASN_210	N, D_LYS_216	H, D_LYS_216	2.98	2.16	15.42
4F33.PDB	O, F_GLY_110	OG, E_SER_43	HG, E_SER_43	2.52	1.83	27.97
4F33.PDB	O, F_ARG_104	NH1, E_ARG_46	HH11, E_ARG_46	2.85	2.03	15.38
4F33.PDB	O, F_LEU_176	NE2, E_GLN_160	HE22, E_GLN_160	2.93	2.08	4.21
4F33.PDB	O, F_PRO_173	OG, E_SER_162	HG, E_SER_162	2.63	1.89	21.98
4F33.PDB	O, A_GLY_60	N, F_PHE_29	H, F_PHE_29	2.97	2.18	20.00
4F33.PDB	OE1, E_GLN_38	NE2, F_GLN_39	HE22, F_GLN_39	2.92	2.06	5.53
4F33.PDB	OH, E_TYR_36	N, F_PHE_106	H, F_PHE_106	2.80	1.96	9.30
4F33.PDB	OE2, C_GLU_123	N, F_GLY_124	H, F_GLY_124	2.81	1.96	5.00
4F33.PDB	O, D_ASP_214	N, F_LYS_212	H, F_LYS_212	2.94	2.11	12.64
4F33.PDB	O, D_LYS_212	N, F_ASP_214	H, F_ASP_214	2.84	2.02	14.84
4F33.PDB	OE1, E_GLU_123	NZ, F_LYS_215	HZ1, F_LYS_215	2.61	1.84	24.34
4F33.PDB	OG1, D_THR_211	NZ, F_LYS_215	HZ2, F_LYS_215	2.92	2.04	7.71
4F33.PDB	O, H_TYR_60	NE2, G_HIS_94	HE2, G_HIS_94	2.97	2.17	17.68
4F33.PDB	O, H_LEU_176	NE2, G_GLN_160	HE22, G_GLN_160	2.89	2.04	8.42
4F33.PDB	O, H_PRO_173	OG, G_SER_162	HG, G_SER_162	2.65	1.94	25.59
4F33.PDB	O, C_GLY_60	N, H_PHE_29	H, H_PHE_29	2.96	2.15	17.00
4F33.PDB	OH, G_TYR_36	N, H_PHE_106	H, H_PHE_106	2.74	1.89	7.07
4F33.PDB	OE2, A_GLU_123	N, H_GLY_124	H, H_GLY_124	2.97	2.12	7.35
4F33.PDB	O, G_SER_208	NZ, H_LYS_135	HZ3, H_LYS_135	2.85	1.99	13.05
4F33.PDB	O, B_LYS_212	N, H_ASP_214	H, H_ASP_214	2.71	1.89	15.00
4F33.PDB	OE1, G_GLU_123	NZ, H_LYS_215	HZ1, H_LYS_215	2.97	2.19	24.10
4F33.PDB	OG1, B_THR_211	NZ, H_LYS_215	HZ2, H_LYS_215	2.80	1.95	14.49
4F33.PDB	O, B_ASN_210	N, H_LYS_216	H, H_LYS_216	2.82	2.01	16.40

4F3F.PDB	OE1, B_GLN_39	NE2, A_GLN_38	HE22, A_GLN_38	2.88	2.04	8.75
4F3F.PDB	O, B_ARG_104	NH1, A_ARG_46	HH11, A_ARG_46	2.93	2.16	22.46
4F3F.PDB	OG, B_SER_59	NE2, A_HIS_94	HE2, A_HIS_94	2.82	2.03	19.68
4F3F.PDB	OE1, C_GLU_52	N, B_ASP_102	H, B_ASP_102	2.88	2.08	17.53
4F3F.PDB	OH, A_TYR_36	N, B_PHE_106	H, B_PHE_106	2.71	1.88	12.56
4F3F.PDB	OD1, A_ASN_138	NE2, B_HIS_170	HE2, B_HIS_170	2.82	2.05	21.56
4F3F.PDB	O, B_ASP_102	NZ, C_LYS_24	HZ2, C_LYS_24	2.85	2.03	18.08
4F3F.PDB	OD1, B_ASP_102	N, C_LYS_25	H, C_LYS_25	2.86	2.02	9.58
4F3F.PDB	OH, B_TYR_101	NZ, C_LYS_25	HZ3, C_LYS_25	2.87	2.11	26.18
4F3F.PDB	OH, A_TYR_32	NE1, C_TRP_26	HE1, C_TRP_26	2.97	2.17	18.16
4JAM.PDB	OH, L_TYR_36	N, H_PHE_100E	H, H_PHE_100E	2.85	2.03	15.20
4JAM.PDB	OD1, H_ASN_100B	ND2, L_ASN_32	HD21, L_ASN_32	2.96	2.21	25.94
4JAM.PDB	O, B_THR_201	N, L_THR_201	H, L_THR_201	2.84	2.04	18.18
4JAM.PDB	O, B_GLY_199	N, L_GLU_203	H, L_GLU_203	2.91	2.13	21.03
4JAM.PDB	OH, B_TYR_36	N, A_PHE_100E	H, A_PHE_100E	2.90	2.09	16.41
4JAM.PDB	O, L_THR_201	N, B_THR_201	H, B_THR_201	2.77	1.96	16.15
4JAM.PDB	O, L_GLY_199	N, B_GLU_203	H, B_GLU_203	2.79	1.99	17.96
4JAN.PDB	OH, L_TYR_36	N, H_PHE_100E	H, H_PHE_100E	2.91	2.16	24.28
4JAN.PDB	OD2, B_ASP_92	OG, H_SER_156	HG, H_SER_156	2.50	1.78	23.90
4JAN.PDB	OE1, L_GLU_123	NZ, H_LYS_209	HZ1, H_LYS_209	2.89	2.13	26.71
4JAN.PDB	OD1, H_ASN_100B	ND2, L_ASN_32	HD21, L_ASN_32	2.76	1.91	6.44
4JAN.PDB	OH, B_TYR_36	N, A_PHE_100E	H, A_PHE_100E	2.74	1.90	10.14
4JAN.PDB	O, I_GLY_458	ND2, B_ASN_32	HD22, B_ASN_32	2.86	2.11	24.85
4KRM.PDB	OE1, B_GLU_110	NH1, A_ARG_353	HH11, A_ARG_353	2.81	2.05	22.81
4KRM.PDB	O, B_GLU_110	NH1, A_ARG_353	HH12, A_ARG_353	2.55	1.85	29.89
4KRM.PDB	O, B_ALA_100	NH2, A_ARG_353	HH21, A_ARG_353	2.89	2.04	4.33
4KRM.PDB	O, B_ASP_112	NE2, A_GLN_384	HE22, A_GLN_384	2.93	2.19	25.19
4KRM.PDB	O, C_LYS_310	N, B_THR_58	H, B_THR_58	2.99	2.17	13.91
4KRM.PDB	O, C_GLU_308	N, B_TYR_60	H, B_TYR_60	2.75	1.96	19.67
4KRM.PDB	O, B_TYR_60	N, C_GLU_308	H, C_GLU_308	2.91	2.19	28.33
4KRM.PDB	O, B_THR_58	N, C_LYS_310	H, C_LYS_310	2.88	2.06	14.23
4KRM.PDB	O, B_ASP_56	N, C_VAL_312	H, C_VAL_312	2.73	1.89	9.64
4KRM.PDB	OE1, D_GLU_110	NH1, C_ARG_353	HH11, C_ARG_353	2.87	2.05	16.15
4KRM.PDB	O, D_ALA_100	NH2, C_ARG_353	HH21, C_ARG_353	2.80	2.00	16.96
4KRM.PDB	OD2, C_ASP_355	NH1, D_ARG_30	HH12, D_ARG_30	2.45	1.63	13.53
4KRM.PDB	O, E_GLU_308	N, D_TYR_60	H, D_TYR_60	2.82	2.08	26.84
4KRM.PDB	O, D_THR_58	N, E_LYS_310	H, E_LYS_310	2.79	2.02	22.01
4KRM.PDB	OE1, F_GLU_110	NH1, E_ARG_353	HH11, E_ARG_353	2.85	2.03	14.34
4KRM.PDB	O, F_GLU_110	NH1, E_ARG_353	HH12, E_ARG_353	2.46	1.72	24.77
4KRM.PDB	O, F_ALA_100	NH2, E_ARG_353	HH21, E_ARG_353	2.81	1.99	15.85
4KRM.PDB	OD2, F_ASP_112	NH2, E_ARG_353	HH22, E_ARG_353	2.96	2.18	20.33
4KRM.PDB	O, F_ASP_112	NE2, E_GLN_384	HE22, E_GLN_384	2.82	2.10	28.13
4KRM.PDB	O, J_THR_58	N, G_LYS_310	H, G_LYS_310	2.73	1.87	4.39
4KRM.PDB	O, J_ASP_56	N, G_VAL_312	H, G_VAL_312	2.86	2.02	9.25
4KRM.PDB	OD1, H_ASP_112	N, G_VAL_350	H, G_VAL_350	2.96	2.25	28.54
4KRM.PDB	O, H_GLU_110	NH1, G_ARG_353	HH12, G_ARG_353	2.56	1.83	26.87
4KRM.PDB	O, H_ALA_100	NH2, G_ARG_353	HH21, G_ARG_353	2.51	1.75	22.59
4KRM.PDB	OE2, B_GLU_5	NZ, G_LYS_407	HZ1, G_LYS_407	2.98	2.17	20.60
4KRM.PDB	OD2, G_ASP_355	NH1, H_ARG_30	HH12, H_ARG_30	2.45	1.69	23.45
4KRM.PDB	O, L_TYR_60	N, I_GLU_308	H, I_GLU_308	2.69	1.88	16.25
4KRM.PDB	O, L_THR_58	N, I_LYS_310	H, I_LYS_310	2.70	1.84	3.45
4KRM.PDB	O, L_ASP_56	N, I_VAL_312	H, I_VAL_312	2.83	1.98	8.53
4KRM.PDB	OD1, J_ASP_112	N, I_VAL_350	H, I_VAL_350	2.88	2.05	13.27
4KRM.PDB	OE1, J_GLU_110	NH1, I_ARG_353	HH11, I_ARG_353	2.86	2.07	18.90
4KRM.PDB	O, J_ALA_100	NH2, I_ARG_353	HH21, I_ARG_353	2.97	2.14	13.62
4KRM.PDB	OD2, J_ASP_112	NH2, I_ARG_353	HH22, I_ARG_353	3.00	2.19	17.61
4KRM.PDB	O, G_GLU_308	N, J_TYR_60	H, J_TYR_60	2.74	1.97	22.05
4KRM.PDB	OD1, L_ASP_112	N, K_VAL_350	H, K_VAL_350	2.89	2.07	15.44

4KRM.PDB	OE1, L_GLU_110	NH1, K_ARG_353	HH11, K_ARG_353	2.89	2.06	12.41
4KRM.PDB	O, L_GLU_110	NH1, K_ARG_353	HH12, K_ARG_353	2.54	1.80	24.42
4KRM.PDB	O, L_ALA_100	NH2, K_ARG_353	HH21, K_ARG_353	2.92	2.14	20.95
4KRM.PDB	OD2, L_ASP_112	NH2, K_ARG_353	HH22, K_ARG_353	2.89	2.07	13.96
4KRM.PDB	OD2, K_ASP_355	NH1, L_ARG_30	HH12, L_ARG_30	2.44	1.65	18.93
4KRM.PDB	O, L_LYS_310	N, L_THR_58	H, L_THR_58	2.98	2.15	12.69
4KRM.PDB	O, L_GLU_308	N, L_TYR_60	H, L_TYR_60	2.75	2.02	27.31
4KRO.PDB	O, D_GLY_54	NH1, A_ARG_353	HH12, A_ARG_353	2.81	1.97	9.47
4KRO.PDB	OG, B_SER_103	NZ, A_LYS_375	HZ2, A_LYS_375	2.61	1.76	15.34
4KRO.PDB	OH, D_TYR_102	NE2, A_GLN_384	HE21, A_GLN_384	2.87	2.16	29.24
4KRO.PDB	O, B_TYR_100	NH2, A_ARG_403	HH22, A_ARG_403	2.57	1.73	11.63
4KRO.PDB	OD1, B_ASP_118	NE, A_ARG_405	HE, A_ARG_405	2.72	1.93	19.48
4KRO.PDB	O, A_GLY_458	N, B_VAL_2	H, B_VAL_2	2.76	1.93	12.61
4KRO.PDB	OE1, D_GLN_39	NE2, C_GLN_38	HE22, C_GLN_38	2.85	2.00	7.50
4KRO.PDB	OD2, D_ASP_103	OH, C_TYR_50	HH, C_TYR_50	2.49	1.72	20.15
4KRO.PDB	O, D_TYR_104	NE2, C_GLN_89	HE22, C_GLN_89	3.00	2.19	16.80
4KRO.PDB	OD1, D_ASP_103	ND2, C_ASN_91	HD21, C_ASN_91	2.93	2.12	16.18
4KRO.PDB	O, A_ASN_469	N, C_TRP_94	H, C_TRP_94	2.75	1.95	19.24
4KRO.PDB	OD2, D_ASP_58	NE1, C_TRP_94	HE1, C_TRP_94	2.80	2.10	29.15
4KRO.PDB	O, D_LEU_176	NE2, C_GLN_160	HE22, C_GLN_160	2.74	1.92	15.89
4KRO.PDB	OE1, C_GLN_38	NE2, D_GLN_39	HE22, D_GLN_39	2.80	1.94	4.32
4KRO.PDB	OE1, A_GLN_408	OH, D_TYR_102	HH, D_TYR_102	2.75	1.97	18.39
4KRO.PDB	OH, C_TYR_36	N, D_PHE_106	H, D_PHE_106	2.93	2.08	9.34
4KRP.PDB	O, D_GLY_54	NH2, A_ARG_353	HH22, A_ARG_353	2.83	1.98	6.79
4KRP.PDB	OD1, B_ASP_115	NH2, A_ARG_405	HH21, A_ARG_405	2.63	1.81	15.48
4KRP.PDB	O, D_TYR_102	OG, A_SER_440	HG, A_SER_440	2.65	1.82	4.10
4KRP.PDB	OD1, D_ASP_58	NZ, A_LYS_443	HZ1, A_LYS_443	2.65	1.82	17.69
4KRP.PDB	OD2, D_ASP_103	NZ, A_LYS_465	HZ2, A_LYS_465	2.93	2.05	5.06
4KRP.PDB	OE1, D_GLN_39	NE2, C_GLN_38	HE22, C_GLN_38	2.70	1.84	6.09
4KRP.PDB	OD2, D_ASP_103	OH, C_TYR_50	HH, C_TYR_50	2.43	1.66	18.96
4KRP.PDB	OD1, D_ASP_103	ND2, C_ASN_91	HD21, C_ASN_91	2.77	1.91	6.24
4KRP.PDB	O, A_ASN_469	N, C_TRP_94	H, C_TRP_94	2.68	1.89	19.97
4KRP.PDB	OD2, D_ASP_58	NE1, C_TRP_94	HE1, C_TRP_94	2.98	2.17	17.26
4KRP.PDB	O, D_LEU_176	NE2, C_GLN_160	HE22, C_GLN_160	2.56	1.80	22.58
4KRP.PDB	O, D_PRO_173	OG, C_SER_162	HG, C_SER_162	2.80	2.10	28.74
4KRP.PDB	OE1, C_GLN_38	NE2, D_GLN_39	HE22, D_GLN_39	2.72	1.87	5.47
4KRP.PDB	OE1, A_GLN_408	OH, D_TYR_102	HH, D_TYR_102	2.56	1.74	10.00
4KRP.PDB	OG, A_SER_440	OH, D_TYR_104	HH, D_TYR_104	2.94	2.22	25.72
4KRP.PDB	OH, C_TYR_36	N, D_PHE_106	H, D_PHE_106	2.89	2.11	20.61
4KRP.PDB	OE1, A_GLU_431	OH, B_TYR_32	HH, B_TYR_32	2.59	1.78	7.49
4KRP.PDB	OE1, A_GLU_400	OH, B_TYR_100	HH, B_TYR_100	2.94	2.13	13.29
4KRP.PDB	OE2, A_GLU_431	OH, B_TYR_116	HH, B_TYR_116	2.43	1.75	29.09
4NZR.PDB	OH, L_TYR_36	N, H_PHE_100J	H, H_PHE_100J	2.96	2.11	8.14
4NZR.PDB	OG, L_SER_176	OG, H_SER_188	HG, H_SER_188	2.88	2.16	24.46
4NZR.PDB	OE2, L_GLU_123	NZ, H_LYS_221	HZ2, H_LYS_221	2.99	2.10	2.00
4NZR.PDB	O, M_PRO_119	OG, L_SER_14	HG, L_SER_14	2.76	2.00	18.37
4NZR.PDB	OG1, M_THR_110	N, L_THR_18	H, L_THR_18	2.82	2.00	15.23
4NZR.PDB	OH, M_TYR_444	N, L_LYS_54	H, L_LYS_54	2.91	2.06	4.85
4NZR.PDB	O, M_ALA_391	NH2, L_ARG_61	HH21, L_ARG_61	2.90	2.11	19.46
4NZR.PDB	OG, M_SER_106	N, L_ASN_77	H, L_ASN_77	2.86	2.01	5.30
4NZR.PDB	O, H_ALA_100G	NE, L_ARG_96	HE, L_ARG_96	2.83	2.08	23.79
4NZR.PDB	O, H_ALA_100G	NH2, L_ARG_96	HH21, L_ARG_96	2.80	2.05	24.03
4NZR.PDB	O, M_ASN_177	NH2, L_ARG_108	HH22, L_ARG_108	2.82	2.05	22.21
4NZR.PDB	O, M_GLY_178	N, L_THR_109	H, L_THR_109	2.92	2.07	5.99
4NZR.PDB	O, M_GLY_178	OG1, L_THR_109	HG1, L_THR_109	2.88	2.17	26.23
4NZR.PDB	O, M_ASP_117	N, L_VAL_110	H, L_VAL_110	2.96	2.14	15.09
4NZR.PDB	O, H_LEU_178	NE2, L_GLN_160	HE22, L_GLN_160	2.86	2.01	7.83
4NZR.PDB	O, H_PRO_175	OG, L_SER_162	HG, L_SER_162	2.79	1.98	7.14

4NZR.PDB	OG, H_SER_188	OG, L_SER_176	HG, L_SER_176	2.88	2.09	13.66
4NZR.PDB	OE1, L_GLU_81	NE, M_ARG_384	HE, M_ARG_384	2.93	2.09	10.37
4NZR.PDB	OD1, H_ASP_31E	NH1, M_ARG_457	HH12, M_ARG_457	2.96	2.12	11.27
4NZR.PDB	OD2, H_ASP_31E	NH2, M_ARG_457	HH22, M_ARG_457	2.55	1.75	17.03
4NZU.PDB	OH, L_TYR_36	N, H_PHE_100H	H, H_PHE_100H	2.86	2.04	13.13
4WUU.PDB	OD2, B_ASP_53	NE, A_ARG_48	HE, A_ARG_48	2.84	2.13	29.12
4WUU.PDB	OH, E_TYR_104	NZ, A_LYS_66	HZ3, A_LYS_66	2.89	2.02	10.84
4WUU.PDB	OXT, C_LEU_9	OH, A_TYR_84	HH, A_TYR_84	2.64	1.82	12.17
4WUU.PDB	O, B_TRP_60	NE2, A_GLN_96	HE22, A_GLN_96	2.78	1.93	8.81
4WUU.PDB	O, C_LEU_9	NZ, A_LYS_146	HZ3, A_LYS_146	2.76	1.90	13.68
4WUU.PDB	O, C_TYR_8	NE1, A_TRP_147	HE1, A_TRP_147	2.81	1.99	15.97
4WUU.PDB	O, C_ARG_1	OH, A_TYR_159	HH, A_TYR_159	2.86	2.02	6.39
4WUU.PDB	OE1, B_GLN_8	NH1, A_ARG_234	HH11, A_ARG_234	2.79	2.07	27.49
4WUU.PDB	O, A_PRO_235	OH, B_TYR_10	HH, B_TYR_10	2.61	1.79	11.75
4WUU.PDB	O, A_ALA_236	ND2, B_ASN_24	HD21, B_ASN_24	2.81	2.05	22.96
4WUU.PDB	OE1, A_GLU_232	OH, B_TYR_26	HH, B_TYR_26	2.95	2.14	13.27
4WUU.PDB	OH, A_TYR_171	N, C_ARG_1	H1, C_ARG_1	2.79	2.03	25.96
4WUU.PDB	OE2, A_GLU_63	N, C_MET_2	H, C_MET_2	2.90	2.09	16.21
4WUU.PDB	OE1, E_GLN_39	NE2, D_GLN_39	HE22, D_GLN_39	2.94	2.18	23.53
4WUU.PDB	OD1, E_ASP_106	NE1, D_TRP_99	HE1, D_TRP_99	2.95	2.19	24.35
4WUU.PDB	OE1, D_GLN_39	NE2, E_GLN_39	HE22, E_GLN_39	2.55	1.73	14.29
4WUU.PDB	OE2, A_GLU_166	NH2, E_ARG_50	HH22, E_ARG_50	2.67	1.88	18.69
4WUU.PDB	OE1, A_GLU_63	OH, E_TYR_104	HH, E_TYR_104	2.59	1.76	7.82
4WUU.PDB	OE1, A_GLU_58	N, E_TYR_105	H, E_TYR_105	2.88	2.05	12.40
4WUU.PDB	OE1, A_GLU_55	OH, E_TYR_105	HH, E_TYR_105	2.47	1.79	29.86
4Z0X.PDB	OE1, B_GLN_64	NE2, A_GLN_37	HE22, A_GLN_37	2.75	1.99	23.41
4Z0X.PDB	O, B_GLY_129	NE2, A_GLN_88	HE22, A_GLN_88	2.63	1.87	22.97
4Z0X.PDB	O, B_GLY_129	NE1, A_TRP_90	HE1, A_TRP_90	2.96	2.14	15.73
4Z0X.PDB	OH, C_TYR_443	N, A_SER_93	H, A_SER_93	2.99	2.17	13.42
4Z0X.PDB	O, C_LEU_441	N, B_SER_127	H, B_SER_127	2.61	1.82	19.78
4Z0X.PDB	OH, A_TYR_35	N, B_TYR_131	H, B_TYR_131	2.85	2.09	23.16
5I76.PDB	OE1, B_GLN_39	NE2, A_GLN_38	HE22, A_GLN_38	2.94	2.10	10.68
5I76.PDB	O, B_GLY_110	OG, A_SER_43	HG, A_SER_43	2.73	2.02	27.09
5I76.PDB	OD2, B_ASP_103	OH, A_TYR_50	HH, A_TYR_50	2.64	1.88	21.01
5I76.PDB	O, B_PRO_173	OG, A_SER_162	HG, A_SER_162	2.48	1.79	28.75
5I76.PDB	OE1, A_GLN_38	NE2, B_GLN_39	HE22, B_GLN_39	2.80	1.95	6.66
5I76.PDB	OG, A_SER_176	OG, B_SER_185	HG, B_SER_185	2.89	2.15	23.05
5I76.PDB	OE1, A_GLU_123	NZ, B_LYS_215	HZ1, B_LYS_215	2.73	1.96	24.68
5I76.PDB	OE2, A_GLU_123	NZ, B_LYS_215	HZ1, B_LYS_215	2.89	2.11	24.69
5I76.PDB	OD2, A_ASP_70	NH1, C_ARG_24	HH12, C_ARG_24	2.95	2.23	28.81
5I76.PDB	O, D_GLY_110	OG, C_SER_43	HG, C_SER_43	2.84	2.15	29.22
5I76.PDB	OD2, D_ASP_103	OH, C_TYR_50	HH, C_TYR_50	2.76	1.95	12.40
5I76.PDB	O, A_SER_202	NE2, C_GLN_147	HE22, C_GLN_147	2.78	1.96	13.33
5I76.PDB	OE1, C_GLN_38	NE2, D_GLN_39	HE22, D_GLN_39	2.85	2.01	10.98
5I76.PDB	OH, C_TYR_36	N, D_PHE_106	H, D_PHE_106	2.93	2.09	12.40
5I76.PDB	OE1, C_GLU_123	NZ, D_LYS_215	HZ1, D_LYS_215	2.60	1.73	11.40
5JO5.PDB	OE1, L_GLN_38	NE2, H_GLN_39	HE22, H_GLN_39	2.84	2.00	9.38
5JO5.PDB	OH, L_TYR_36	N, H_PHE_100L	H, H_PHE_100L	2.79	1.96	12.88
5JO5.PDB	O, L_GLY_41	NH2, H_ARG_105	HH22, H_ARG_105	2.85	2.05	18.48
5JO5.PDB	OE2, L_GLU_124	NZ, H_LYS_143	HZ2, H_LYS_143	2.46	1.63	17.05
5JO5.PDB	OH, L_TYR_177	OG, H_SER_179	HG, H_SER_179	2.73	2.00	25.96
5JO5.PDB	OE1, D_GLN_24	OG, L_SER_30	HG, L_SER_30	2.84	2.07	18.45
5JO5.PDB	OE1, H_GLN_39	NE2, L_GLN_38	HE22, L_GLN_38	2.83	2.00	13.03
5JO5.PDB	OE2, H_GLU_100J	NH2, L_ARG_91	HH22, L_ARG_91	2.69	1.84	7.26
5JO5.PDB	OD1, H_ASP_58	NE, L_ARG_95B	HE, L_ARG_95B	2.95	2.13	14.76
5JO5.PDB	O, H_GLY_42	OG1, L_THR_163	HG1, L_THR_163	2.52	1.79	25.04
5JO5.PDB	OE1, B_GLN_38	NE2, A_GLN_39	HE22, A_GLN_39	2.87	2.02	8.31
5JO5.PDB	OH, B_TYR_36	N, A_PHE_100L	H, A_PHE_100L	2.86	2.06	18.12

5JO5.PDB	O, B_GLY_41	NH1, A_ARG_105	HH12, A_ARG_105	2.66	1.82	9.49
5JO5.PDB	OE2, B_GLU_124	NZ, A_LYS_143	HZ2, A_LYS_143	2.62	1.83	23.29
5JO5.PDB	OH, B_TYR_177	OG, A_SER_179	HG, A_SER_179	2.83	2.10	25.21
5JO5.PDB	OE2, B_GLU_123	NZ, A_LYS_209	HZ1, A_LYS_209	2.55	1.68	10.64
5JO5.PDB	OE1, A_GLN_39	NE2, B_GLN_38	HE22, B_GLN_38	2.90	2.07	12.43
5JO5.PDB	O, F_ARG_29	ND2, B_ASN_69	HD21, B_ASN_69	2.80	1.99	16.03
5JO5.PDB	O, A_GLY_100H	NE, B_ARG_91	HE, B_ARG_91	2.94	2.09	9.41
5JO5.PDB	O, A_GLY_42	OG1, B_THR_163	HG1, B_THR_163	2.48	1.73	21.87
5JO5.PDB	OE1, D_GLN_38	NE2, C_GLN_39	HE22, C_GLN_39	2.86	2.02	9.45
5JO5.PDB	OH, D_TYR_36	N, C_PHE_100L	H, C_PHE_100L	2.87	2.08	19.05
5JO5.PDB	OE2, D_GLU_124	NZ, C_LYS_143	HZ2, C_LYS_143	2.79	1.92	10.71
5JO5.PDB	OH, D_TYR_177	OG, C_SER_179	HG, C_SER_179	2.71	1.97	23.23
5JO5.PDB	OE2, D_GLU_123	NZ, C_LYS_209	HZ1, C_LYS_209	2.58	1.72	11.28
5JO5.PDB	OE1, C_GLN_39	NE2, D_GLN_38	HE22, D_GLN_38	2.92	2.09	12.72
5JO5.PDB	O, L_ARG_29	ND2, D_ASN_69	HD21, D_ASN_69	2.86	2.03	13.06
5JO5.PDB	OD1, C_ASP_58	NE, D_ARG_95B	HE, D_ARG_95B	2.94	2.10	11.64
5JO5.PDB	O, C_GLY_42	OG1, D_THR_163	HG1, D_THR_163	2.56	1.81	22.64
5JO5.PDB	OE1, F_GLN_38	NE2, E_GLN_39	HE22, E_GLN_39	2.90	2.06	10.70
5JO5.PDB	OH, F_TYR_36	N, E_PHE_100L	H, E_PHE_100L	2.79	1.96	13.04
5JO5.PDB	O, F_GLY_41	NH2, E_ARG_105	HH22, E_ARG_105	2.92	2.13	19.96
5JO5.PDB	OE2, F_GLU_124	NZ, E_LYS_143	HZ2, E_LYS_143	2.55	1.75	21.57
5JO5.PDB	OH, F_TYR_177	OG, E_SER_179	HG, E_SER_179	2.58	1.87	27.02
5JO5.PDB	OE2, F_GLU_123	NZ, E_LYS_209	HZ1, E_LYS_209	2.57	1.74	17.62
5JO5.PDB	OE1, B_GLN_24	OG, F_SER_30	HG, F_SER_30	2.88	2.11	20.15
5JO5.PDB	OE1, E_GLN_39	NE2, F_GLN_38	HE22, F_GLN_38	2.85	2.02	12.75
5JO5.PDB	OE2, E_GLU_100J	NH2, F_ARG_91	HH22, F_ARG_91	2.72	1.87	5.99
5JO5.PDB	OD1, E_ASP_58	NE, F_ARG_95B	HE, F_ARG_95B	2.92	2.09	12.47
5JO5.PDB	O, E_GLY_42	OG1, F_THR_163	HG1, F_THR_163	2.55	1.80	22.10
5JR1.PDB	OH, L_TYR_36	N, H_PHE_100L	H, H_PHE_100L	2.93	2.14	18.24
5JR1.PDB	O, L_GLY_41	NH1, H_ARG_105	HH11, H_ARG_105	2.58	1.82	23.25
5JR1.PDB	OH, L_TYR_178	OG, H_SER_179	HG, H_SER_179	2.83	2.03	15.88
5JR1.PDB	N, H_PHE_100L	OH, L_TYR_36	HH, L_TYR_36	2.93	2.21	26.41
5JR1.PDB	O, H_PRO_100F	NH1, L_ARG_91	HH12, L_ARG_91	2.89	2.18	29.36
5JR1.PDB	O, H_PRO_100F	NH2, L_ARG_91	HH22, L_ARG_91	2.82	2.09	26.91
5JR1.PDB	OD2, H_ASP_58	NH2, L_ARG_95B	HH22, L_ARG_95B	2.47	1.67	16.99
5JUE.PDB	O, H_MET_100E	OH, L_TYR_36	HH, L_TYR_36	2.57	1.73	1.94
5JUE.PDB	OH, H_TYR_91	NE2, L_GLN_38	HE22, L_GLN_38	2.57	1.77	17.09
5JUE.PDB	O, H_PRO_167	OG, L_SER_162	HG, L_SER_162	2.70	1.95	22.84
5JUE.PDB	OG, H_SER_178	OG, L_SER_176	HG, L_SER_176	2.78	1.94	3.13
5JUE.PDB	OE1, L_GLU_123	NZ, H_LYS_208	HZ1, H_LYS_208	2.81	1.98	17.66
5JUE.PDB	O, L_PRO_119	NH1, H_ARG_213	HH12, H_ARG_213	2.84	2.13	29.21
5JUE.PDB	O, L_PRO_120	NH2, H_ARG_213	HH22, H_ARG_213	2.94	2.13	15.93
5JXA.PDB	OD2, L_ASP_50	OH, H_TYR_100	HH, H_TYR_100	2.57	1.75	11.76
5JXA.PDB	OH, L_TYR_36	N, H_TRP_100F	H, H_TRP_100F	2.85	2.00	7.52
5JXA.PDB	OH, H_TYR_100	NH2, L_ARG_53	HH21, L_ARG_53	2.89	2.07	18.12
5JXA.PDB	O, H_LEU_170	NE2, L_GLN_160	HE22, L_GLN_160	2.84	1.99	4.55
5JXA.PDB	O, H_PRO_167	OG, L_SER_162	HG, L_SER_162	2.69	1.94	23.37
5M33.PDB	OE1, A_GLN_129	N, B_VAL_114	H, B_VAL_114	2.67	1.84	13.32
5T6P.PDB	O, B_GLY_107	OG, A_SER_48	HG, A_SER_48	2.52	1.72	14.73
5T6P.PDB	O, B_PRO_170	OG, A_SER_167	HG, A_SER_167	2.98	2.14	3.80
5T6P.PDB	OE1, A_GLN_43	NE2, B_GLN_39	HE22, B_GLN_39	2.71	1.86	5.14
5T6P.PDB	O, F_PRO_8	ND2, B_ASN_57	HD21, B_ASN_57	2.91	2.07	9.74
5T6P.PDB	OE1, D_GLN_39	NE2, C_GLN_43	HE22, C_GLN_43	3.00	2.17	12.88
5T6P.PDB	O, D_GLY_107	OG, C_SER_48	HG, C_SER_48	2.66	1.94	25.38
5T6P.PDB	OE1, C_GLN_43	NE2, D_GLN_39	HE22, D_GLN_39	2.79	1.94	7.20
5T6P.PDB	OH, C_TYR_41	N, D_PHE_103	H, D_PHE_103	2.95	2.09	5.85
5T6P.PDB	OE1, C_GLU_39	NE, E_ARG_5	HE, E_ARG_5	2.86	2.02	10.72
5T78.PDB	OD1, C_ASN_150	N, A_ASP_1	H1, A_ASP_1	2.85	2.07	23.76

5T78.PDB	OE1, B_GLN_39	NE2, A_GLN_43	HE22, A_GLN_43	2.92	2.08	9.79
5T78.PDB	O, B_GLY_107	OG, A_SER_48	HG, A_SER_48	2.44	1.64	14.53
5T78.PDB	O, B_LYS_43	OH, A_TYR_92	HH, A_TYR_92	2.74	2.03	27.20
5T78.PDB	O, B_PRO_170	OG, A_SER_167	HG, A_SER_167	2.91	2.11	14.54
5T78.PDB	OE1, A_GLN_43	NE2, B_GLN_39	HE22, B_GLN_39	2.63	1.78	5.56
5T78.PDB	OH, A_TYR_41	N, B_PHE_103	H, B_PHE_103	2.85	2.00	5.24
5T78.PDB	OE1, A_GLU_39	NH1, F_ARG_5	HH11, F_ARG_5	2.68	1.83	9.33
5T78.PDB	O, D_GLY_107	OG, C_SER_48	HG, C_SER_48	2.59	1.80	15.22
5T78.PDB	O, D_LYS_43	OH, C_TYR_92	HH, C_TYR_92	2.90	2.21	29.37
5T78.PDB	O, A_SER_26	N, C_ASN_166	H, C_ASN_166	2.63	1.86	20.95
5T78.PDB	O, D_PRO_170	OG, C_SER_167	HG, C_SER_167	2.87	2.05	10.83
5T78.PDB	OE1, C_GLN_43	NE2, D_GLN_39	HE22, D_GLN_39	2.72	1.87	5.23
5T78.PDB	OH, C_TYR_41	N, D_PHE_103	H, D_PHE_103	2.85	2.00	7.54
5T78.PDB	OD1, C_ASN_142	NE2, D_HIS_167	HE2, D_HIS_167	2.85	2.00	9.68
5T78.PDB	OD2, A_ASP_75	N, D_SER_175	H, D_SER_175	2.84	2.00	10.93
5T78.PDB	OE1, C_GLU_39	NH1, E_ARG_5	HH11, E_ARG_5	2.69	1.87	13.16
5U3J.PDB	OD1, L_ASP_31	OH, H_TYR_100K	HH, H_TYR_100K	2.88	2.04	5.22
5U3J.PDB	OH, L_TYR_36	N, H_MET_100N	H, H_MET_100N	2.75	1.92	13.09
5U3J.PDB	OE1, H_GLU_100F	OH, L_TYR_32	HH, L_TYR_32	2.62	1.91	27.84
5U3J.PDB	OE1, H_GLN_39	NE2, L_GLN_38	HE22, L_GLN_38	2.66	1.83	12.57
5U3J.PDB	O, H_PRO_167	OG, L_SER_162	HG, L_SER_162	2.90	2.16	24.21
5U3N.PDB	OD2, A_ASP_674	NH1, H_ARG_52A	HH12, H_ARG_52A	3.00	2.24	24.41
5U3N.PDB	OD1, L_ASP_31	NH2, H_ARG_100B	HH22, H_ARG_100B	2.97	2.15	14.50
5U3N.PDB	OD1, L_ASN_34	ND2, H_ASN_100J	HD21, H_ASN_100J	2.72	1.86	2.61
5U3N.PDB	OH, L_TYR_36	N, H_MET_100M	H, H_MET_100M	2.99	2.13	5.54
5U3N.PDB	OD1, L_ASN_138	NE2, H_HIS_164	HE2, H_HIS_164	2.92	2.21	29.54
5U3N.PDB	O, H_PRO_167	OG, L_SER_162	HG, L_SER_162	2.77	1.98	17.29
5UCB.PDB	OE1, L_GLN_38	NE2, H_GLN_39	HE22, H_GLN_39	2.96	2.12	9.92
5UCB.PDB	O, B_LEU_5	OH, H_TYR_53	HH, H_TYR_53	2.73	1.99	23.03
5UCB.PDB	O, B_VAL_145	N, H_GLY_97	H, H_GLY_97	2.90	2.05	8.98
5UCB.PDB	O, L_SER_208	NZ, H_LYS_129	HZ2, H_LYS_129	2.83	2.06	25.53
5UCB.PDB	OD2, B_ASP_51	OG, L_SER_30	HG, L_SER_30	2.58	1.81	20.19
5UCB.PDB	OE1, H_GLN_39	NE2, L_GLN_38	HE22, L_GLN_38	2.95	2.13	14.86
5UCB.PDB	O, B_SER_47	NH1, L_ARG_66	HH12, L_ARG_66	2.77	1.99	21.64
5UCB.PDB	O, B_SER_47	NH2, L_ARG_66	HH22, L_ARG_66	2.89	2.16	27.12
5UCB.PDB	O, B_ARG_48	N, L_GLY_68	H, L_GLY_68	2.79	1.95	9.02
5UCB.PDB	O, H_LEU_170	NE2, L_GLN_160	HE22, L_GLN_160	2.99	2.13	5.75
5UCB.PDB	O, H_PRO_167	OG, L_SER_162	HG, L_SER_162	2.68	1.94	24.13
5UCB.PDB	O, L_ASP_91	OH, B_TYR_111	HH, B_TYR_111	2.57	1.75	11.11
5UCB.PDB	OG, H_SER_58	NZ, B_LYS_142	HZ3, B_LYS_142	2.83	1.96	8.82
5UCB.PDB	OD1, L_ASP_91	NH2, B_ARG_144	HH21, B_ARG_144	2.84	2.03	16.18
5UK0.PDB	OD1, F_ASP_590	ND2, B_ASN_560	HD22, B_ASN_560	2.72	1.94	19.72
5UK0.PDB	O, F_LEU_502	ND2, B_ASN_617	HD22, B_ASN_617	2.60	1.80	16.74
5UK0.PDB	OD1, D_ASP_586	NH2, C_ARG_311	HH22, C_ARG_311	2.98	2.20	18.56
5UK0.PDB	OD1, B_ASP_590	ND2, D_ASN_560	HD22, D_ASN_560	2.73	1.95	20.06
5UK0.PDB	O, B_LEU_502	ND2, D_ASN_617	HD22, D_ASN_617	2.62	1.80	13.03
5UK0.PDB	O, D_LEU_502	ND2, F_ASN_617	HD22, F_ASN_617	2.71	1.89	14.40
5VXJ.PDB	OE1, I_GLU_200	NH1, B_ARG_50	HH12, B_ARG_50	2.92	2.07	7.25
5VXJ.PDB	OE1, I_GLU_201	OH, B_TYR_105	HH, B_TYR_105	2.51	1.70	12.69
5VXJ.PDB	O, D_GLY_56	NH2, C_ARG_132	HH22, C_ARG_132	2.97	2.20	22.55
5VXJ.PDB	OD1, C_ASN_140	NE, D_ARG_19	HE, D_ARG_19	2.55	1.80	23.66
5VXJ.PDB	OE1, E_GLU_201	OH, D_TYR_105	HH, D_TYR_105	2.53	1.70	8.84
5VXJ.PDB	OD2, F_ASP_73	NZ, E_LYS_137	HZ2, E_LYS_137	2.77	1.96	20.15
5VXJ.PDB	O, D_TYR_105	OG, E_SER_173	HG, E_SER_173	2.87	2.17	28.40
5VXJ.PDB	OD1, D_ASN_97	NZ, E_LYS_197	HZ1, E_LYS_197	2.80	1.95	14.72
5VXJ.PDB	O, F_GLY_112	ND2, E_ASN_216	HD21, E_ASN_216	2.68	1.91	21.74
5VXJ.PDB	OE1, G_GLU_200	NH2, F_ARG_50	HH22, F_ARG_50	2.70	1.89	15.49
5VXJ.PDB	OE1, G_GLU_201	OH, F_TYR_105	HH, F_TYR_105	2.57	1.75	11.97

5VXJ.PDB	O, E_THR_217	NE2, F_GLN_111	HE22, F_GLN_111	2.98	2.12	6.26
5VXJ.PDB	O, H_GLY_56	NH2, G_ARG_132	HH22, G_ARG_132	2.94	2.20	26.37
5VXJ.PDB	O, F_TYR_105	OG, G_SER_173	HG, G_SER_173	2.88	2.16	26.33
5VXJ.PDB	OD1, L_ASN_292	N, G_GLY_176	H, G_GLY_176	2.76	2.01	25.37
5VXJ.PDB	OE1, H_GLN_111	OG1, G_THR_217	HG1, G_THR_217	2.86	2.17	29.58
5VXJ.PDB	OD2, J_ASP_73	NZ, L_LYS_137	HZ3, L_LYS_137	2.90	2.17	29.52
5VXJ.PDB	OD1, B_ASN_97	NZ, L_LYS_197	HZ1, L_LYS_197	2.68	1.88	21.92
5VXJ.PDB	O, L_THR_217	NE2, J_GLN_111	HE22, J_GLN_111	2.92	2.11	16.33
5VXK.PDB	OD1, A_ASN_280	N, B_SER_103	H, B_SER_103	2.64	1.78	2.03
5VXK.PDB	OD1, A_ASN_280	N, B_VAL_104	H, B_VAL_104	2.84	2.01	12.48
5VXK.PDB	OG, A_SER_168	NE2, B_GLN_106	HE21, B_GLN_106	2.99	2.23	24.43
5VXK.PDB	OD2, A_ASP_287	NE2, B_GLN_106	HE22, B_GLN_106	2.77	1.94	12.81
5VXK.PDB	OG1, B_THR_102	OH, A_TYR_276	HH, A_TYR_276	2.57	1.73	6.50
5VXL.PDB	OD2, B_ASP_52	NZ, A_LYS_205	HZ1, A_LYS_205	3.00	2.13	10.69
5VXL.PDB	O, A_ALA_198	OH, B_TYR_54	HH, B_TYR_54	2.38	1.67	27.03
5VXL.PDB	OD1, A_ASP_166	N, B_SER_55	H, B_SER_55	2.91	2.18	28.04
5VXL.PDB	OD1, A_ASP_166	OG, B_SER_55	HG, B_SER_55	2.56	1.73	4.68
5VXL.PDB	OE2, A_GLU_201	NH2, B_ARG_102	HH22, B_ARG_102	2.87	2.08	20.03
5VXM.PDB	OE2, B_GLU_111	NE1, A_TRP_177	HE1, A_TRP_177	2.76	1.97	19.61
5VXM.PDB	O, A_ASP_166	NE1, B_TRP_102	HE1, B_TRP_102	2.92	2.09	13.88
5VXM.PDB	OE2, A_GLU_201	N, B_CYS_104	H, B_CYS_104	2.85	2.02	10.45
5VXM.PDB	OE1, A_GLU_201	N, B_SER_105	H, B_SER_105	2.58	1.74	9.22
5VXR.PDB	OE1, L_GLN_38	NZ, H_LYS_39	HZ2, H_LYS_39	2.72	1.76	14.94
5VXR.PDB	OD1, P_ASN_415	OH, H_TYR_50	HH, H_TYR_50	2.71	1.82	21.79
5VXR.PDB	OH, L_TYR_36	N, H_PHE_106	H, H_PHE_106	2.92	1.92	7.59
5VXR.PDB	OD1, L_ASN_138	NE2, H_HIS_170	HE2, H_HIS_170	2.89	1.98	20.57
5VXR.PDB	OE2, L_GLU_123	NZ, H_LYS_214	HZ1, H_LYS_214	2.93	1.98	15.97
5VXR.PDB	O, H_GLY_101	NZ, L_LYS_30	HZ1, L_LYS_30	2.83	1.85	13.06
5VXR.PDB	O, P_GLY_418	NE1, L_TRP_96	HE1, L_TRP_96	2.88	1.87	5.74
5VXR.PDB	OG, H_SER_184	OG, L_SER_176	HG, L_SER_176	2.79	1.86	17.30
5VXR.PDB	OH, H_TYR_33	N, P_ASN_415	H, P_ASN_415	2.82	1.94	24.20
5VXR.PDB	O, L_ASN_91	NE1, P_TRP_420	HE1, P_TRP_420	2.80	1.97	28.78
5WKQ.PDB	OG, B_SER_208	NH2, A_ARG_135	HH21, A_ARG_135	2.89	2.06	11.87
5WKQ.PDB	OE2, A_GLU_131	ND1, B_HIS_207	HD1, B_HIS_207	2.65	1.88	22.26
5WKQ.PDB	OE1, A_GLU_131	OG1, B_THR_211	HG1, B_THR_211	2.63	1.86	19.68
5WN9.PDB	OD1, H_ASN_57	NE, A_ARG_188	HE, A_ARG_188	2.58	1.61	2.15

Table 7: Interfacial side chain and main chain hydrogen bonding networks of all experimentally determined antigen-antibody-related structures. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1A14.PDB	OE1, L_GLN_38	NE2, H_GLN_39	HE21, H_GLN_39	2.62	1.69	9.24
1E6J.PDB	OE1, H_GLN_39	NE2, L_GLN_37	HE22, L_GLN_37	2.69	1.84	23.98
1F3R.PDB	NE1, A_TRP_67	OG, B_SER_61	HG, B_SER_61	2.86	1.89	6.31
1HGD.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.80	1.78	9.95
1HGD.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.83	1.84	13.41
1HGD.PDB	OD2, F_ASP_79	OG, A_SER_110	HG, A_SER_110	2.92	1.96	11.03
1HGD.PDB	OD1, E_ASP_101	NE2, A_GLN_210	HE22, A_GLN_210	3.00	2.15	26.33
1HGD.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.78	1.86	19.99
1HGD.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.93	1.92	13.44
1HGD.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.77	1.80	12.79
1HGD.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ1, B_LYS_62	2.61	1.78	29.53
1HGD.PDB	OD2, F_ASP_90	NZ, B_LYS_62	HZ3, B_LYS_62	2.73	1.84	25.56
1HGD.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.96	2.01	12.34
1HGD.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.88	1.91	8.67
1HGD.PDB	OE2, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.84	1.82	2.51
1HGD.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.71	1.71	6.80
1HGD.PDB	OE1, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.75	1.75	3.21
1HGD.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.65	1.81	23.27
1HGD.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.76	1.72	5.59
1HGD.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.83	2.02	28.17
1HGD.PDB	OE2, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.88	2.01	22.00
1HGD.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.80	1.77	7.54
1HGD.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.87	1.88	13.44
1HGD.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.73	1.84	19.59
1HGD.PDB	OD1, A_ASP_101	NE2, C_GLN_210	HE22, C_GLN_210	2.97	2.13	27.21
1HGD.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.69	1.80	23.00
1HGD.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.80	1.83	17.68
1HGD.PDB	OE1, D_GLU_15	NZ, C_LYS_326	HZ1, C_LYS_326	2.78	1.77	11.96
1HGD.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.79	1.82	13.03
1HGD.PDB	OD2, B_ASP_90	NZ, D_LYS_62	HZ3, D_LYS_62	2.62	1.79	29.99
1HGD.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.96	1.98	5.65
1HGD.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.83	1.87	10.56
1HGD.PDB	OE2, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.78	1.77	3.14
1HGD.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.65	1.67	9.42
1HGD.PDB	OE1, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.69	1.70	6.24
1HGD.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.57	1.79	29.87
1HGD.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.76	1.72	5.75
1HGD.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.80	2.01	29.31
1HGD.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.82	1.95	21.73
1HGD.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.79	1.77	8.77
1HGD.PDB	OE2, F_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.82	1.85	14.73
1HGD.PDB	OD2, D_ASP_79	OG, E_SER_110	HG, E_SER_110	2.81	1.89	15.50
1HGD.PDB	OD1, C_ASP_101	NE2, E_GLN_210	HE22, E_GLN_210	2.98	2.14	27.07
1HGD.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.77	1.90	25.11
1HGD.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ3, E_LYS_238	2.87	1.86	13.40
1HGD.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.97	1.97	16.19
1HGD.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.72	1.75	12.85
1HGD.PDB	OD2, D_ASP_90	NZ, F_LYS_62	HZ3, F_LYS_62	2.71	1.86	28.09
1HGD.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.95	1.98	9.92
1HGD.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.86	1.90	10.66
1HGD.PDB	OE2, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.77	1.75	1.42
1HGD.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.64	1.65	5.37
1HGD.PDB	OE1, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.71	1.72	7.42
1HGD.PDB	OE1, B_GLU_85	OH, F_TYR_83	HH, F_TYR_83	2.53	1.75	27.84
1HGD.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.67	1.66	8.83
1HGD.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.96	2.14	28.71
1HGD.PDB	OE2, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.94	2.05	20.84

1HGE.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.80	1.78	10.14
1HGE.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.74	1.75	12.19
1HGE.PDB	OD2, F_ASP_79	OG, A_SER_110	HG, A_SER_110	2.90	1.95	11.19
1HGE.PDB	OD1, E_ASP_101	NE2, A_GLN_210	HE22, A_GLN_210	2.91	2.05	24.48
1HGE.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.71	1.78	19.14
1HGE.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.91	1.89	11.73
1HGE.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.84	1.86	12.76
1HGE.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ1, B_LYS_62	2.60	1.76	28.82
1HGE.PDB	OD2, F_ASP_90	NZ, B_LYS_62	HZ3, B_LYS_62	2.69	1.82	26.81
1HGE.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.97	2.02	12.36
1HGE.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.87	1.91	11.56
1HGE.PDB	OE2, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.84	1.83	5.81
1HGE.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.70	1.70	6.45
1HGE.PDB	OE1, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.79	1.79	3.91
1HGE.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.65	1.81	24.86
1HGE.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.75	1.71	5.62
1HGE.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.80	1.98	27.36
1HGE.PDB	OE2, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.94	2.06	21.65
1HGE.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.79	1.77	8.74
1HGE.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.78	1.79	11.19
1HGE.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.78	1.86	15.09
1HGE.PDB	OD1, A_ASP_101	NE2, C_GLN_210	HE22, C_GLN_210	2.93	2.07	24.92
1HGE.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.64	1.76	23.09
1HGE.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.78	1.80	16.75
1HGE.PDB	OE1, D_GLU_15	NZ, C_LYS_326	HZ1, C_LYS_326	2.74	1.73	12.73
1HGE.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.87	1.89	12.82
1HGE.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.96	1.98	6.23
1HGE.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.79	1.85	14.06
1HGE.PDB	OE2, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.78	1.78	7.91
1HGE.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.63	1.67	11.36
1HGE.PDB	OE1, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.74	1.75	7.04
1HGE.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.58	1.80	29.40
1HGE.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.71	1.68	6.52
1HGE.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.78	1.98	28.90
1HGE.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.90	2.01	20.41
1HGE.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.79	1.77	9.75
1HGE.PDB	OE2, F_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.78	1.79	11.63
1HGE.PDB	OD2, D_ASP_79	OG, E_SER_110	HG, E_SER_110	2.82	1.89	14.19
1HGE.PDB	OD1, C_ASP_101	NE2, E_GLN_210	HE22, E_GLN_210	2.89	2.04	25.02
1HGE.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.74	1.87	25.04
1HGE.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ3, E_LYS_238	2.85	1.84	12.25
1HGE.PDB	OD1, F_ASP_86	NZ, E_LYS_310	HZ3, E_LYS_310	2.86	2.02	29.64
1HGE.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.99	2.00	17.08
1HGE.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.80	1.82	12.52
1HGE.PDB	OD2, D_ASP_90	NZ, F_LYS_62	HZ2, F_LYS_62	2.67	1.83	29.15
1HGE.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.94	1.97	9.11
1HGE.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.85	1.89	11.64
1HGE.PDB	OE2, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.73	1.73	6.19
1HGE.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.65	1.66	5.51
1HGE.PDB	OE1, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.70	1.73	9.07
1HGE.PDB	OE1, B_GLU_85	OH, F_TYR_83	HH, F_TYR_83	2.51	1.76	30.00
1HGE.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.67	1.65	8.34
1HGE.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.92	2.09	27.36
1HGF.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.79	1.86	21.55
1HGF.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.92	1.92	10.51
1HGF.PDB	OD2, F_ASP_79	OG, A_SER_110	HG, A_SER_110	2.82	1.90	15.87
1HGF.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.64	1.76	23.62
1HGF.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ2, A_LYS_238	2.85	1.85	14.58

1HGF.PDB	OE2, A_GLU_325	NH2, B_ARG_25	HH22, B_ARG_25	2.99	2.04	16.52
1HGF.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.83	1.86	13.50
1HGF.PDB	OD2, F ASP_86	NZ, B_LYS_62	HZ2, B_LYS_62	2.71	1.70	11.44
1HGF.PDB	OD2, F ASP_90	NZ, B_LYS_62	HZ3, B_LYS_62	2.77	1.82	20.37
1HGF.PDB	OG, A_SER_266	ND1, B_HIS_64	HD1, B_HIS_64	2.66	1.79	20.68
1HGF.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.89	1.92	10.70
1HGF.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.92	1.92	2.47
1HGF.PDB	OE1, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.86	1.84	3.80
1HGF.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.73	1.74	10.29
1HGF.PDB	OE2, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.75	1.74	3.91
1HGF.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.57	1.80	29.66
1HGF.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.72	1.70	9.91
1HGF.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.80	1.86	13.00
1HGF.PDB	OE1, F_GLU_131	NH2, B_ARG_163	HH21, B_ARG_163	2.74	1.86	24.20
1HGF.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.81	1.85	19.93
1HGF.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.91	1.92	11.49
1HGF.PDB	OD2, B ASP_79	OG, C_SER_110	HG, C_SER_110	2.69	1.85	25.37
1HGF.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.56	1.72	26.72
1HGF.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ2, C_LYS_238	2.75	1.78	18.48
1HGF.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.84	1.86	12.74
1HGF.PDB	OD2, B ASP_86	NZ, D_LYS_62	HZ2, D_LYS_62	2.69	1.69	13.49
1HGF.PDB	OD2, B ASP_90	NZ, D_LYS_62	HZ3, D_LYS_62	2.68	1.77	22.81
1HGF.PDB	OG, C_SER_266	ND1, D_HIS_64	HD1, D_HIS_64	2.64	1.83	27.58
1HGF.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.90	1.92	7.33
1HGF.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.82	1.85	5.34
1HGF.PDB	OE1, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.79	1.78	3.81
1HGF.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.64	1.68	12.43
1HGF.PDB	OE2, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.70	1.71	7.38
1HGF.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.58	1.80	29.87
1HGF.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.68	1.69	13.85
1HGF.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.79	1.88	16.40
1HGF.PDB	OE1, B_GLU_131	NH2, D_ARG_163	HH21, D_ARG_163	2.70	1.83	24.43
1HGF.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.75	1.83	22.30
1HGF.PDB	OE2, F_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.88	1.88	11.28
1HGF.PDB	OD2, D ASP_79	OG, E_SER_110	HG, E_SER_110	2.78	1.90	21.69
1HGF.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.65	1.79	25.97
1HGF.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ2, E_LYS_238	2.83	1.84	16.42
1HGF.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.79	1.81	11.74
1HGF.PDB	OD2, D ASP_86	NZ, F_LYS_62	HZ2, F_LYS_62	2.67	1.68	13.64
1HGF.PDB	OD2, D ASP_90	NZ, F_LYS_62	HZ3, F_LYS_62	2.75	1.81	20.23
1HGF.PDB	OG, E_SER_266	ND1, F_HIS_64	HD1, F_HIS_64	2.65	1.77	20.25
1HGF.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.89	1.92	9.46
1HGF.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.86	1.88	5.84
1HGF.PDB	OE1, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.78	1.77	1.59
1HGF.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.69	1.70	7.61
1HGF.PDB	OE2, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.71	1.73	8.88
1HGF.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.55	1.63	21.75
1HGF.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.90	1.96	15.73
1HGF.PDB	OE1, D_GLU_131	NH2, F_ARG_163	HH21, F_ARG_163	2.69	1.84	27.00
1HGG.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.90	1.87	9.15
1HGG.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.84	1.86	14.43
1HGG.PDB	OD2, F ASP_79	OG, A_SER_110	HG, A_SER_110	2.88	1.95	14.29
1HGG.PDB	OD1, E ASP_101	NE2, A_GLN_210	HE22, A_GLN_210	2.99	2.07	17.95
1HGG.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.73	1.78	15.93
1HGG.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.93	1.93	14.31
1HGG.PDB	OE2, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.74	1.91	29.92
1HGG.PDB	OE1, B_GLU_67	NH1, A_ARG_269	HH12, A_ARG_269	2.69	1.86	28.34
1HGG.PDB	OD1, B ASP_90	NZ, A_LYS_310	HZ2, A_LYS_310	2.70	1.74	18.08

1HGG.PDB	OE2, B_GLU_15	NZ, A_LYS_326	HZ1, A_LYS_326	2.83	1.89	21.04
1HGG.PDB	OE2, A_GLU_325	NH2, B_ARG_25	HH22, B_ARG_25	2.94	1.96	12.23
1HGG.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.75	1.76	9.96
1HGG.PDB	OD2, F_ASP_90	NZ, B_LYS_62	HZ2, B_LYS_62	2.65	1.82	29.87
1HGG.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ3, B_LYS_62	2.64	1.73	23.35
1HGG.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.90	1.96	14.63
1HGG.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.94	1.96	10.47
1HGG.PDB	OE1, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.88	1.89	10.69
1HGG.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.73	1.73	5.91
1HGG.PDB	OE2, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.82	1.82	7.26
1HGG.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.68	1.80	19.99
1HGG.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.77	1.73	5.14
1HGG.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.84	1.98	22.96
1HGG.PDB	OE2, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.81	1.98	25.54
1HGG.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.94	1.91	8.28
1HGG.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.85	1.88	14.56
1HGG.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.76	1.86	17.83
1HGG.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.61	1.71	21.26
1HGG.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.83	1.86	17.18
1HGG.PDB	OE2, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.70	1.87	29.85
1HGG.PDB	OE1, D_GLU_67	NH1, C_ARG_269	HH12, C_ARG_269	2.69	1.85	27.75
1HGG.PDB	OD1, D_ASP_90	NZ, C_LYS_310	HZ2, C_LYS_310	2.65	1.73	21.74
1HGG.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.76	1.78	10.56
1HGG.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.86	1.90	9.42
1HGG.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.86	1.89	9.57
1HGG.PDB	OE1, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.78	1.80	12.10
1HGG.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.67	1.68	6.66
1HGG.PDB	OE2, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.74	1.75	9.29
1HGG.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.59	1.78	26.83
1HGG.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.73	1.70	8.35
1HGG.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.86	2.00	22.57
1HGG.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.78	1.96	26.12
1HGG.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.91	1.88	8.89
1HGG.PDB	OE2, F_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.88	1.90	14.20
1HGG.PDB	OD2, D_ASP_79	OG, E_SER_110	HG, E_SER_110	2.79	1.88	16.48
1HGG.PDB	OD1, C_ASP_101	NE2, E_GLN_210	HE22, E_GLN_210	2.96	2.04	17.70
1HGG.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.72	1.80	20.26
1HGG.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ1, E_LYS_238	2.89	1.89	13.93
1HGG.PDB	OE1, F_GLU_67	NH1, E_ARG_269	HH12, E_ARG_269	2.69	1.85	27.32
1HGG.PDB	OD1, F_ASP_90	NZ, E_LYS_310	HZ2, E_LYS_310	2.64	1.72	22.12
1HGG.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.98	1.97	15.13
1HGG.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.73	1.74	10.16
1HGG.PDB	OD2, D_ASP_86	NZ, F_LYS_62	HZ3, F_LYS_62	2.58	1.75	29.01
1HGG.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.87	1.91	10.03
1HGG.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.88	1.92	11.44
1HGG.PDB	OE1, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.75	1.76	9.13
1HGG.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.67	1.68	1.99
1HGG.PDB	OE2, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.79	1.81	10.64
1HGG.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.68	1.67	10.46
1HGG.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.96	2.09	22.59
1HGG.PDB	OE2, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.87	2.01	24.00
1HGH.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.78	1.76	9.03
1HGH.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.86	1.88	13.48
1HGH.PDB	OD2, F_ASP_79	OG, A_SER_110	HG, A_SER_110	2.97	2.01	11.65
1HGH.PDB	OD1, E_ASP_101	NE2, A_GLN_210	HE22, A_GLN_210	2.97	2.14	27.61
1HGH.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.66	1.73	18.15
1HGH.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.92	1.93	15.64
1HGH.PDB	OD1, B_ASP_86	NZ, A_LYS_310	HZ2, A_LYS_310	2.71	1.84	27.09

1HGH.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.82	1.86	15.60
1HGH.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ1, B_LYS_62	2.66	1.80	27.71
1HGH.PDB	OD2, F_ASP_90	NZ, B_LYS_62	HZ3, B_LYS_62	2.68	1.82	27.13
1HGH.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.87	1.91	11.96
1HGH.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.87	1.90	9.70
1HGH.PDB	OE2, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.91	1.90	8.45
1HGH.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.77	1.76	5.47
1HGH.PDB	OE1, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.89	1.87	2.83
1HGH.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.69	1.84	23.96
1HGH.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.74	1.71	7.44
1HGH.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.76	1.94	26.47
1HGH.PDB	OE2, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.83	1.98	23.62
1HGH.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.82	1.78	7.61
1HGH.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.86	1.88	13.66
1HGH.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.78	1.85	13.87
1HGH.PDB	OD1, A_ASP_101	NE2, C_GLN_210	HE22, C_GLN_210	2.93	2.07	24.87
1HGH.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.57	1.72	26.03
1HGH.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.71	1.80	22.72
1HGH.PDB	OD1, D_ASP_86	NZ, C_LYS_310	HZ2, C_LYS_310	2.73	1.85	26.20
1HGH.PDB	OE1, D_GLU_15	NZ, C_LYS_326	HZ1, C_LYS_326	2.77	1.75	11.00
1HGH.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.80	1.85	16.64
1HGH.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.84	1.88	10.18
1HGH.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.79	1.84	10.45
1HGH.PDB	OE2, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.77	1.77	10.38
1HGH.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.70	1.70	6.41
1HGH.PDB	OE1, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.75	1.75	5.88
1HGH.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.59	1.81	29.86
1HGH.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.66	1.64	7.83
1HGH.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.80	1.98	26.35
1HGH.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.84	1.99	23.38
1HGH.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.77	1.74	8.08
1HGH.PDB	OE2, F_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.88	1.90	13.56
1HGH.PDB	OD2, D_ASP_79	OG, E_SER_110	HG, E_SER_110	2.90	1.94	9.49
1HGH.PDB	OD1, C_ASP_101	NE2, E_GLN_210	HE22, E_GLN_210	2.95	2.09	25.33
1HGH.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.68	1.79	22.30
1HGH.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ3, E_LYS_238	2.87	1.88	15.42
1HGH.PDB	OE1, F_GLU_67	NH1, E_ARG_269	HH12, E_ARG_269	2.71	1.88	29.19
1HGH.PDB	OD1, F_ASP_86	NZ, E_LYS_310	HZ2, E_LYS_310	2.74	1.87	26.77
1HGH.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.90	1.89	12.96
1HGH.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.72	1.77	15.67
1HGH.PDB	OD2, D_ASP_90	NZ, F_LYS_62	HZ2, F_LYS_62	2.68	1.83	28.02
1HGH.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.87	1.91	9.23
1HGH.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.84	1.87	10.72
1HGH.PDB	OE2, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.73	1.73	5.34
1HGH.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.71	1.70	1.21
1HGH.PDB	OE1, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.78	1.78	7.19
1HGH.PDB	OE1, B_GLU_85	OH, F_TYR_83	HH, F_TYR_83	2.53	1.74	27.23
1HGH.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.65	1.63	9.88
1HGH.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.89	2.06	26.55
1HGH.PDB	OE2, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.92	2.03	21.52
1HGI.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.90	1.86	7.66
1HGI.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.80	1.81	13.24
1HGI.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.65	1.73	18.55
1HGI.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.85	1.85	15.00
1HGI.PDB	OD1, B_ASP_86	NZ, A_LYS_310	HZ3, A_LYS_310	2.76	1.92	29.34
1HGI.PDB	OE2, B_GLU_15	NZ, A_LYS_326	HZ1, A_LYS_326	2.79	1.93	27.33
1HGI.PDB	OE2, A_GLU_325	NH2, B_ARG_25	HH22, B_ARG_25	2.93	1.95	13.46
1HGI.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.81	1.84	14.63

1HGI.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ1, B_LYS_62	2.67	1.78	25.75
1HGI.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.87	1.89	8.13
1HGI.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.86	1.89	7.04
1HGI.PDB	OE2, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.92	1.89	1.72
1HGI.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.71	1.72	8.42
1HGI.PDB	OE1, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.86	1.86	6.93
1HGI.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.78	1.84	13.46
1HGI.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.65	1.64	9.94
1HGI.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.81	1.96	23.50
1HGI.PDB	OE2, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.86	2.02	24.92
1HGI.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.88	1.83	6.58
1HGI.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.82	1.84	15.02
1HGI.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.85	1.90	11.29
1HGI.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.62	1.75	23.70
1HGI.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.67	1.77	23.68
1HGI.PDB	OD1, D_ASP_86	NZ, C_LYS_310	HZ3, C_LYS_310	2.77	1.93	29.51
1HGI.PDB	OE1, D_GLU_15	NZ, C_LYS_326	HZ1, C_LYS_326	2.83	1.84	16.25
1HGI.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.81	1.85	15.40
1HGI.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.83	1.85	2.78
1HGI.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.80	1.82	5.40
1HGI.PDB	OE2, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.78	1.76	4.18
1HGI.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.61	1.67	15.38
1HGI.PDB	OE1, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.76	1.77	8.75
1HGI.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.69	1.81	20.41
1HGI.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.66	1.64	7.30
1HGI.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.84	1.98	23.95
1HGI.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.88	2.03	24.96
1HGI.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.86	1.82	7.44
1HGI.PDB	OE2, F_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.78	1.80	14.37
1HGI.PDB	OD2, D_ASP_79	OG, E_SER_110	HG, E_SER_110	2.90	1.94	10.08
1HGI.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.69	1.80	23.03
1HGI.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ3, E_LYS_238	2.80	1.81	15.90
1HGI.PDB	OD1, F_ASP_86	NZ, E_LYS_310	HZ3, E_LYS_310	2.76	1.91	29.16
1HGI.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.88	1.86	11.05
1HGI.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.75	1.79	14.82
1HGI.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.84	1.87	3.62
1HGI.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.85	1.88	7.37
1HGI.PDB	OE2, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.77	1.76	3.93
1HGI.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.64	1.66	4.79
1HGI.PDB	OE1, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.76	1.78	10.40
1HGI.PDB	OE1, B_GLU_85	OH, F_TYR_83	HH, F_TYR_83	2.58	1.75	24.06
1HGI.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.61	1.62	12.49
1HGI.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.96	2.09	23.50
1HGI.PDB	OE2, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.96	2.09	23.34
1HGI.PDB	OE2, D_GLU_131	NH2, F_ARG_163	HH22, F_ARG_163	2.69	1.85	26.81
1HGJ.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.81	1.78	9.30
1HGJ.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.75	1.77	12.07
1HGJ.PDB	OD2, F_ASP_79	OG, A_SER_110	HG, A_SER_110	2.94	1.98	10.39
1HGJ.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.67	1.78	22.50
1HGJ.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.90	1.90	13.91
1HGJ.PDB	OE2, A_GLU_325	NH2, B_ARG_25	HH22, B_ARG_25	2.97	2.01	15.94
1HGJ.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.77	1.81	15.09
1HGJ.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ1, B_LYS_62	2.65	1.75	23.55
1HGJ.PDB	OD2, F_ASP_90	NZ, B_LYS_62	HZ3, B_LYS_62	2.74	1.89	28.52
1HGJ.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.89	1.93	11.21
1HGJ.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.90	1.93	10.80
1HGJ.PDB	OE2, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.88	1.87	5.28
1HGJ.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.72	1.72	3.64

1HGJ.PDB	OE1, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.85	1.84	3.19
1HGJ.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.67	1.83	24.12
1HGJ.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.78	1.75	7.42
1HGJ.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.82	2.00	27.29
1HGJ.PDB	OE2, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.91	2.02	20.91
1HGJ.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.82	1.80	8.63
1HGJ.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.76	1.78	13.33
1HGJ.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.79	1.87	14.95
1HGJ.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.66	1.82	26.85
1HGJ.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.75	1.79	18.67
1HGJ.PDB	OD1, D_ASP_86	NZ, C_LYS_310	HZ3, C_LYS_310	2.94	2.10	29.37
1HGJ.PDB	OE1, D_GLU_15	NZ, C_LYS_326	HZ1, C_LYS_326	2.91	1.86	5.48
1HGJ.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.84	1.88	15.58
1HGJ.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.89	1.91	5.59
1HGJ.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.85	1.89	10.87
1HGJ.PDB	OE2, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.76	1.76	7.89
1HGJ.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.68	1.69	5.65
1HGJ.PDB	OE1, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.71	1.72	5.59
1HGJ.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.63	1.81	25.72
1HGJ.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.75	1.72	7.31
1HGJ.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.80	1.98	27.33
1HGJ.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.87	2.00	21.99
1HGJ.PDB	OH, B_TYR_141	NH1, D_ARG_127	HH12, D_ARG_127	2.99	2.02	12.89
1HGJ.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.81	1.79	8.50
1HGJ.PDB	OE2, F_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.76	1.77	12.82
1HGJ.PDB	OD2, D_ASP_79	OG, E_SER_110	HG, E_SER_110	2.79	1.87	15.96
1HGJ.PDB	OD1, C_ASP_101	NE2, E_GLN_210	HE22, E_GLN_210	2.94	2.10	26.45
1HGJ.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.69	1.86	28.41
1HGJ.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ3, E_LYS_238	2.87	1.86	13.82
1HGJ.PDB	OD1, F_ASP_86	NZ, E_LYS_310	HZ3, E_LYS_310	2.93	2.08	29.22
1HGJ.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.87	1.86	12.83
1HGJ.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.77	1.81	14.54
1HGJ.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.90	1.93	7.02
1HGJ.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.85	1.89	12.57
1HGJ.PDB	OE2, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.70	1.70	4.55
1HGJ.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.65	1.66	2.84
1HGJ.PDB	OE1, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.72	1.73	7.95
1HGJ.PDB	OE1, B_GLU_85	OH, F_TYR_83	HH, F_TYR_83	2.53	1.75	28.54
1HGJ.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.70	1.68	8.19
1HGJ.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.92	2.09	27.65
1HGJ.PDB	OE2, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.96	2.06	20.98
1OSP.PDB	OD2, L_ASP_1	OG, H_SER_62	HG, H_SER_62	2.98	2.17	26.53
1OSP.PDB	OG, L_SER_176	OG, H_SER_185	HG, H_SER_185	2.74	1.91	24.72
1OSP.PDB	OE1, L_GLU_123	NZ, H_LYS_215	HZ2, H_LYS_215	2.78	1.85	20.53
1VFB.PDB	OE1, B_GLU_98	NH1, A_ARG_96	HH12, A_ARG_96	2.82	1.84	8.38
1VFB.PDB	OE2, B_GLU_98	NH2, A_ARG_96	HH22, A_ARG_96	2.81	1.85	10.74
1VFB.PDB	OE1, A_GLN_38	NE2, B_GLN_39	HE21, B_GLN_39	2.95	1.98	8.04
3SE8.PDB	OD1, G_ASN_280	NE1, H_TRP_50	HE1, H_TRP_50	3.00	2.21	20.49
3SE8.PDB	OD1, G_ASP_457	NE2, H_GLN_64	HE22, H_GLN_64	2.94	2.12	14.23
3SE8.PDB	OD2, G_ASP_368	NH2, H_ARG_71	HH22, H_ARG_71	2.91	2.05	6.24
3SE9.PDB	OD1, G_ASN_280	NE1, H_TRP_50	HE1, H_TRP_50	2.86	2.03	11.46
3SE9.PDB	OG, G_SER_365	NH1, H_ARG_64	HH11, H_ARG_64	2.81	2.04	21.79
3SE9.PDB	OD2, G_ASP_368	NH1, H_ARG_71	HH12, H_ARG_71	2.77	1.92	7.25
3SE9.PDB	OD1, G_ASN_279	NE1, H_TRP_100D	HE1, H_TRP_100D	2.86	2.13	26.83
3SE9.PDB	OD1, L_ASN_138	NE2, H_HIS_164	HE2, H_HIS_164	2.87	2.10	22.18
3THM.PDB	OE1, L_GLN_39	NE2, H_GLN_41	HE22, H_GLN_41	2.98	2.14	9.35
3THM.PDB	OG, L_SER_183	NZ, H_LYS_162	HZ1, H_LYS_162	2.77	1.97	21.34
3THM.PDB	OG1, L_THR_135	NZ, H_LYS_162	HZ2, H_LYS_162	2.85	2.02	17.75

3THM.PDB	OH, H_TYR_35	ND1, F_HIS_44	HD1, F_HIS_44	2.69	1.83	5.98
3THM.PDB	OG, H_SER_63	NE2, F_HIS_44	HE2, F_HIS_44	2.83	2.07	23.36
3TJE.PDB	OE1, L_GLN_39	NE2, H_GLN_41	HE21, H_GLN_41	2.98	2.15	10.85
3TJE.PDB	OH, H_TYR_35	ND1, F_HIS_44	HD1, F_HIS_44	2.56	1.70	3.69
3U2S.PDB	OE1, L_GLN_38	NE2, H_GLN_39	HE22, H_GLN_39	2.89	2.04	8.55
3U2S.PDB	OG, L_SER_165	NE2, H_HIS_164	HE2, H_HIS_164	2.93	2.12	16.97
3U2S.PDB	OE1, H_GLN_39	NE2, L_GLN_38	HE22, L_GLN_38	2.91	2.09	13.75
3U2S.PDB	OD2, C_ASP_167	ND2, L_ASN_60	HD22, L_ASN_60	2.90	2.14	22.76
3U2S.PDB	OD1, H_ASP_61	NH2, L_ARG_95A	HH22, L_ARG_95A	2.34	1.58	22.53
3U2S.PDB	OE2, H_GLU_95	NH2, L_ARG_96	HH21, L_ARG_96	2.87	2.05	15.72
3U2S.PDB	OH, H_TYR_100K	ND2, G_ASN_173	HD21, G_ASN_173	2.97	2.13	8.87
3U2S.PDB	OE1, B_GLN_38	NE2, A_GLN_39	HE22, A_GLN_39	2.92	2.07	7.34
3U2S.PDB	OG1, B_THR_131	NZ, A_LYS_143	HZ2, A_LYS_143	2.41	1.67	27.35
3U2S.PDB	OE1, A_GLN_39	NE2, B_GLN_38	HE22, B_GLN_38	2.92	2.08	10.61
3U2S.PDB	OD1, A_ASP_61	NH1, B_ARG_95A	HH12, B_ARG_95A	2.63	1.91	26.97
3U2S.PDB	OE2, A_GLU_95	NH2, B_ARG_96	HH21, B_ARG_96	2.98	2.16	13.77
3UYR.PDB	OE2, L_GLU_127	NZ, H_LYS_212	HZ3, H_LYS_212	2.87	2.08	23.12
3UYR.PDB	OD1, H_ASN_101	NE2, P_GLN_48	HE22, P_GLN_48	2.57	1.87	29.89
4F33.PDB	OE1, B_GLN_39	NE2, A_GLN_38	HE22, A_GLN_38	2.96	2.13	12.75
4F33.PDB	OE1, A_GLN_38	NE2, B_GLN_39	HE22, B_GLN_39	2.82	1.97	5.31
4F33.PDB	OE1, A_GLU_123	NZ, B_LYS_215	HZ1, B_LYS_215	2.68	1.82	12.44
4F33.PDB	OG1, H_THR_211	NZ, B_LYS_215	HZ2, B_LYS_215	2.83	1.95	7.37
4F33.PDB	OE1, C_GLN_38	NE2, D_GLN_39	HE22, D_GLN_39	2.89	2.03	5.23
4F33.PDB	OE1, C_GLU_123	NZ, D_LYS_215	HZ1, D_LYS_215	2.79	1.99	22.47
4F33.PDB	OG1, F_THR_211	NZ, D_LYS_215	HZ2, D_LYS_215	2.86	1.99	10.67
4F33.PDB	OE1, E_GLN_38	NE2, F_GLN_39	HE22, F_GLN_39	2.92	2.06	5.53
4F33.PDB	OE1, E_GLU_123	NZ, F_LYS_215	HZ1, F_LYS_215	2.61	1.84	24.34
4F33.PDB	OG1, D_THR_211	NZ, F_LYS_215	HZ2, F_LYS_215	2.92	2.04	7.71
4F33.PDB	OE1, G_GLU_123	NZ, H_LYS_215	HZ1, H_LYS_215	2.97	2.19	24.10
4F33.PDB	OG1, B_THR_211	NZ, H_LYS_215	HZ2, H_LYS_215	2.80	1.95	14.49
4F3F.PDB	OE1, B_GLN_39	NE2, A_GLN_38	HE22, A_GLN_38	2.88	2.04	8.75
4F3F.PDB	OG, B_SER_59	NE2, A_HIS_94	HE2, A_HIS_94	2.82	2.03	19.68
4F3F.PDB	OD1, A_ASN_138	NE2, B_HIS_170	HE2, B_HIS_170	2.82	2.05	21.56
4F3F.PDB	OH, B_TYR_101	NZ, C_LYS_25	HZ3, C_LYS_25	2.87	2.11	26.18
4F3F.PDB	OH, A_TYR_32	NE1, C_TRP_26	HE1, C_TRP_26	2.97	2.17	18.16
4JAM.PDB	OD1, H_ASN_100B	ND2, L_ASN_32	HD21, L_ASN_32	2.96	2.21	25.94
4JAN.PDB	OD2, B_ASP_92	OG, H_SER_156	HG, H_SER_156	2.50	1.78	23.90
4JAN.PDB	OE1, L_GLU_123	NZ, H_LYS_209	HZ1, H_LYS_209	2.89	2.13	26.71
4JAN.PDB	OD1, H_ASN_100B	ND2, L_ASN_32	HD21, L_ASN_32	2.76	1.91	6.44
4KRM.PDB	OE1, B_GLU_110	NH1, A_ARG_353	HH11, A_ARG_353	2.81	2.05	22.81
4KRM.PDB	OE1, D_GLU_110	NH1, C_ARG_353	HH11, C_ARG_353	2.87	2.05	16.15
4KRM.PDB	OD2, C_ASP_355	NH1, D_ARG_30	HH12, D_ARG_30	2.45	1.63	13.53
4KRM.PDB	OE1, F_GLU_110	NH1, E_ARG_353	HH11, E_ARG_353	2.85	2.03	14.34
4KRM.PDB	OD2, F_ASP_112	NH2, E_ARG_353	HH22, E_ARG_353	2.96	2.18	20.33
4KRM.PDB	OE2, B_GLU_5	NZ, G_LYS_407	HZ1, G_LYS_407	2.98	2.17	20.60
4KRM.PDB	OD2, G_ASP_355	NH1, H_ARG_30	HH12, H_ARG_30	2.45	1.69	23.45
4KRM.PDB	OE1, J_GLU_110	NH1, I_ARG_353	HH11, I_ARG_353	2.86	2.07	18.90
4KRM.PDB	OD2, J_ASP_112	NH2, I_ARG_353	HH22, I_ARG_353	3.00	2.19	17.61
4KRM.PDB	OE1, L_GLU_110	NH1, K_ARG_353	HH11, K_ARG_353	2.89	2.06	12.41
4KRM.PDB	OD2, L_ASP_112	NH2, K_ARG_353	HH22, K_ARG_353	2.89	2.07	13.96
4KRM.PDB	OD2, K_ASP_355	NH1, L_ARG_30	HH12, L_ARG_30	2.44	1.65	18.93
4KRO.PDB	OG, B_SER_103	NZ, A_LYS_375	HZ2, A_LYS_375	2.61	1.76	15.34
4KRO.PDB	OH, D_TYR_102	NE2, A_GLN_384	HE21, A_GLN_384	2.87	2.16	29.24
4KRO.PDB	OD1, B_ASP_118	NE, A_ARG_405	HE, A_ARG_405	2.72	1.93	19.48
4KRO.PDB	OE1, D_GLN_39	NE2, C_GLN_38	HE22, C_GLN_38	2.85	2.00	7.50
4KRO.PDB	OD2, D_ASP_103	OH, C_TYR_50	HH, C_TYR_50	2.49	1.72	20.15
4KRO.PDB	OD1, D_ASP_103	ND2, C_ASN_91	HD21, C_ASN_91	2.93	2.12	16.18
4KRO.PDB	OD2, D_ASP_58	NE1, C_TRP_94	HE1, C_TRP_94	2.80	2.10	29.15

4KRO.PDB	OE1, C_GLN_38	NE2, D_GLN_39	HE22, D_GLN_39	2.80	1.94	4.32
4KRO.PDB	OE1, A_GLN_408	OH, D_TYR_102	HH, D_TYR_102	2.75	1.97	18.39
4KRP.PDB	OD1, B_ASP_115	NH2, A_ARG_405	HH21, A_ARG_405	2.63	1.81	15.48
4KRP.PDB	OD1, D_ASP_58	NZ, A_LYS_443	HZ1, A_LYS_443	2.65	1.82	17.69
4KRP.PDB	OD2, D_ASP_103	NZ, A_LYS_465	HZ2, A_LYS_465	2.93	2.05	5.06
4KRP.PDB	OE1, D_GLN_39	NE2, C_GLN_38	HE22, C_GLN_38	2.70	1.84	6.09
4KRP.PDB	OD2, D_ASP_103	OH, C_TYR_50	HH, C_TYR_50	2.43	1.66	18.96
4KRP.PDB	OD1, D_ASP_103	ND2, C_ASN_91	HD21, C_ASN_91	2.77	1.91	6.24
4KRP.PDB	OD2, D_ASP_58	NE1, C_TRP_94	HE1, C_TRP_94	2.98	2.17	17.26
4KRP.PDB	OE1, C_GLN_38	NE2, D_GLN_39	HE22, D_GLN_39	2.72	1.87	5.47
4KRP.PDB	OE1, A_GLN_408	OH, D_TYR_102	HH, D_TYR_102	2.56	1.74	10.00
4KRP.PDB	OG, A_SER_440	OH, D_TYR_104	HH, D_TYR_104	2.94	2.22	25.72
4KRP.PDB	OE1, A_GLU_431	OH, B_TYR_32	HH, B_TYR_32	2.59	1.78	7.49
4KRP.PDB	OE1, A_GLU_400	OH, B_TYR_100	HH, B_TYR_100	2.94	2.13	13.29
4KRP.PDB	OE2, A_GLU_431	OH, B_TYR_116	HH, B_TYR_116	2.43	1.75	29.09
4NZR.PDB	OG, L_SER_176	OG, H_SER_188	HG, H_SER_188	2.88	2.16	24.46
4NZR.PDB	OE2, L_GLU_123	NZ, H_LYS_221	HZ2, H_LYS_221	2.99	2.10	2.00
4NZR.PDB	OG, H_SER_188	OG, L_SER_176	HG, L_SER_176	2.88	2.09	13.66
4NZR.PDB	OE1, L_GLU_81	NE, M_ARG_384	HE, M_ARG_384	2.93	2.09	10.37
4NZR.PDB	OD1, H_ASP_31E	NH1, M_ARG_457	HH12, M_ARG_457	2.96	2.12	11.27
4NZR.PDB	OD2, H_ASP_31E	NH2, M_ARG_457	HH22, M_ARG_457	2.55	1.75	17.03
4WUU.PDB	OD2, B_ASP_53	NE, A_ARG_48	HE, A_ARG_48	2.84	2.13	29.12
4WUU.PDB	OH, E_TYR_104	NZ, A_LYS_66	HZ3, A_LYS_66	2.89	2.02	10.84
4WUU.PDB	OXT, C_LEU_9	OH, A_TYR_84	HH, A_TYR_84	2.64	1.82	12.17
4WUU.PDB	OE1, B_GLN_8	NH1, A_ARG_234	HH11, A_ARG_234	2.79	2.07	27.49
4WUU.PDB	OE1, A_GLU_232	OH, B_TYR_26	HH, B_TYR_26	2.95	2.14	13.27
4WUU.PDB	OE1, E_GLN_39	NE2, D_GLN_39	HE22, D_GLN_39	2.94	2.18	23.53
4WUU.PDB	OD1, E_ASP_106	NE1, D_TRP_99	HE1, D_TRP_99	2.95	2.19	24.35
4WUU.PDB	OE1, D_GLN_39	NE2, E_GLN_39	HE22, E_GLN_39	2.55	1.73	14.29
4WUU.PDB	OE2, A_GLU_166	NH2, E_ARG_50	HH22, E_ARG_50	2.67	1.88	18.69
4WUU.PDB	OE1, A_GLU_63	OH, E_TYR_104	HH, E_TYR_104	2.59	1.76	7.82
4WUU.PDB	OE1, A_GLU_55	OH, E_TYR_105	HH, E_TYR_105	2.47	1.79	29.86
4Z0X.PDB	OE1, B_GLN_64	NE2, A_GLN_37	HE22, A_GLN_37	2.75	1.99	23.41
5I76.PDB	OE1, B_GLN_39	NE2, A_GLN_38	HE22, A_GLN_38	2.94	2.10	10.68
5I76.PDB	OD2, B_ASP_103	OH, A_TYR_50	HH, A_TYR_50	2.64	1.88	21.01
5I76.PDB	OE1, A_GLN_38	NE2, B_GLN_39	HE22, B_GLN_39	2.80	1.95	6.66
5I76.PDB	OG, A_SER_176	OG, B_SER_185	HG, B_SER_185	2.89	2.15	23.05
5I76.PDB	OE1, A_GLU_123	NZ, B_LYS_215	HZ1, B_LYS_215	2.73	1.96	24.68
5I76.PDB	OE2, A_GLU_123	NZ, B_LYS_215	HZ1, B_LYS_215	2.89	2.11	24.69
5I76.PDB	OD2, A_ASP_70	NH1, C_ARG_24	HH12, C_ARG_24	2.95	2.23	28.81
5I76.PDB	OD2, D_ASP_103	OH, C_TYR_50	HH, C_TYR_50	2.76	1.95	12.40
5I76.PDB	OE1, C_GLN_38	NE2, D_GLN_39	HE22, D_GLN_39	2.85	2.01	10.98
5I76.PDB	OE1, C_GLU_123	NZ, D_LYS_215	HZ1, D_LYS_215	2.60	1.73	11.40
5JO5.PDB	OE1, L_GLN_38	NE2, H_GLN_39	HE22, H_GLN_39	2.84	2.00	9.38
5JO5.PDB	OE2, L_GLU_124	NZ, H_LYS_143	HZ2, H_LYS_143	2.46	1.63	17.05
5JO5.PDB	OH, L_TYR_177	OG, H_SER_179	HG, H_SER_179	2.73	2.00	25.96
5JO5.PDB	OE1, D_GLN_24	OG, L_SER_30	HG, L_SER_30	2.84	2.07	18.45
5JO5.PDB	OE1, H_GLN_39	NE2, L_GLN_38	HE22, L_GLN_38	2.83	2.00	13.03
5JO5.PDB	OE2, H_GLU_100J	NH2, L_ARG_91	HH22, L_ARG_91	2.69	1.84	7.26
5JO5.PDB	OD1, H_ASP_58	NE, L_ARG_95B	HE, L_ARG_95B	2.95	2.13	14.76
5JO5.PDB	OE1, B_GLN_38	NE2, A_GLN_39	HE22, A_GLN_39	2.87	2.02	8.31
5JO5.PDB	OE2, B_GLU_124	NZ, A_LYS_143	HZ2, A_LYS_143	2.62	1.83	23.29
5JO5.PDB	OH, B_TYR_177	OG, A_SER_179	HG, A_SER_179	2.83	2.10	25.21
5JO5.PDB	OE2, B_GLU_123	NZ, A_LYS_209	HZ1, A_LYS_209	2.55	1.68	10.64
5JO5.PDB	OE1, A_GLN_39	NE2, B_GLN_38	HE22, B_GLN_38	2.90	2.07	12.43
5JO5.PDB	OE1, D_GLN_38	NE2, C_GLN_39	HE22, C_GLN_39	2.86	2.02	9.45
5JO5.PDB	OE2, D_GLU_124	NZ, C_LYS_143	HZ2, C_LYS_143	2.79	1.92	10.71
5JO5.PDB	OH, D_TYR_177	OG, C_SER_179	HG, C_SER_179	2.71	1.97	23.23

5JO5.PDB	OE2, D_GLU_123	NZ, C_LYS_209	HZ1, C_LYS_209	2.58	1.72	11.28
5JO5.PDB	OE1, C_GLN_39	NE2, D_GLN_38	HE22, D_GLN_38	2.92	2.09	12.72
5JO5.PDB	OD1, C_ASP_58	NE, D_ARG_95B	HE, D_ARG_95B	2.94	2.10	11.64
5JO5.PDB	OE1, F_GLN_38	NE2, E_GLN_39	HE22, E_GLN_39	2.90	2.06	10.70
5JO5.PDB	OE2, F_GLU_124	NZ, E_LYS_143	HZ2, E_LYS_143	2.55	1.75	21.57
5JO5.PDB	OH, F_TYR_177	OG, E_SER_179	HG, E_SER_179	2.58	1.87	27.02
5JO5.PDB	OE2, F_GLU_123	NZ, E_LYS_209	HZ1, E_LYS_209	2.57	1.74	17.62
5JO5.PDB	OE1, B_GLN_24	OG, F_SER_30	HG, F_SER_30	2.88	2.11	20.15
5JO5.PDB	OE1, E_GLN_39	NE2, F_GLN_38	HE22, F_GLN_38	2.85	2.02	12.75
5JO5.PDB	OE2, E_GLU_100J	NH2, F_ARG_91	HH22, F_ARG_91	2.72	1.87	5.99
5JO5.PDB	OD1, E_ASP_58	NE, F_ARG_95B	HE, F_ARG_95B	2.92	2.09	12.47
5JR1.PDB	OH, L_TYR_178	OG, H_SER_179	HG, H_SER_179	2.83	2.03	15.88
5JR1.PDB	OD2, H_ASP_58	NH2, L_ARG_95B	HH22, L_ARG_95B	2.47	1.67	16.99
5JUE.PDB	OH, H_TYR_91	NE2, L_GLN_38	HE22, L_GLN_38	2.57	1.77	17.09
5JUE.PDB	OG, H_SER_178	OG, L_SER_176	HG, L_SER_176	2.78	1.94	3.13
5JUE.PDB	OE1, L_GLU_123	NZ, H_LYS_208	HZ1, H_LYS_208	2.81	1.98	17.66
5JXA.PDB	OD2, L_ASP_50	OH, H_TYR_100	HH, H_TYR_100	2.57	1.75	11.76
5JXA.PDB	OH, H_TYR_100	NH2, L_ARG_53	HH21, L_ARG_53	2.89	2.07	18.12
5T6P.PDB	OE1, A_GLN_43	NE2, B_GLN_39	HE22, B_GLN_39	2.71	1.86	5.14
5T6P.PDB	OE1, D_GLN_39	NE2, C_GLN_43	HE22, C_GLN_43	3.00	2.17	12.88
5T6P.PDB	OE1, C_GLN_43	NE2, D_GLN_39	HE22, D_GLN_39	2.79	1.94	7.20
5T6P.PDB	OE1, C_GLU_39	NE, E_ARG_5	HE, E_ARG_5	2.86	2.02	10.72
5T78.PDB	OE1, B_GLN_39	NE2, A_GLN_43	HE22, A_GLN_43	2.92	2.08	9.79
5T78.PDB	OE1, A_GLN_43	NE2, B_GLN_39	HE22, B_GLN_39	2.63	1.78	5.56
5T78.PDB	OE1, A_GLU_39	NH1, F_ARG_5	HH11, F_ARG_5	2.68	1.83	9.33
5T78.PDB	OE1, C_GLN_43	NE2, D_GLN_39	HE22, D_GLN_39	2.72	1.87	5.23
5T78.PDB	OD1, C_ASN_142	NE2, D_HIS_167	HE2, D_HIS_167	2.85	2.00	9.68
5T78.PDB	OE1, C_GLU_39	NH1, E_ARG_5	HH11, E_ARG_5	2.69	1.87	13.16
5U3J.PDB	OD1, L_ASP_31	OH, H_TYR_100K	HH, H_TYR_100K	2.88	2.04	5.22
5U3J.PDB	OE1, H_GLU_100F	OH, L_TYR_32	HH, L_TYR_32	2.62	1.91	27.84
5U3J.PDB	OE1, H_GLN_39	NE2, L_GLN_38	HE22, L_GLN_38	2.66	1.83	12.57
5U3N.PDB	OD2, A_ASP_674	NH1, H_ARG_52A	HH12, H_ARG_52A	3.00	2.24	24.41
5U3N.PDB	OD1, L_ASP_31	NH2, H_ARG_100B	HH22, H_ARG_100B	2.97	2.15	14.50
5U3N.PDB	OD1, L_ASN_34	ND2, H_ASN_100J	HD21, H_ASN_100J	2.72	1.86	2.61
5U3N.PDB	OD1, L_ASN_138	NE2, H_HIS_164	HE2, H_HIS_164	2.92	2.21	29.54
5UCB.PDB	OE1, L_GLN_38	NE2, H_GLN_39	HE22, H_GLN_39	2.96	2.12	9.92
5UCB.PDB	OD2, B_ASP_51	OG, L_SER_30	HG, L_SER_30	2.58	1.81	20.19
5UCB.PDB	OE1, H_GLN_39	NE2, L_GLN_38	HE22, L_GLN_38	2.95	2.13	14.86
5UCB.PDB	OG, H_SER_58	NZ, B_LYS_142	HZ3, B_LYS_142	2.83	1.96	8.82
5UCB.PDB	OD1, L_ASP_91	NH2, B_ARG_144	HH21, B_ARG_144	2.84	2.03	16.18
5UK0.PDB	OD1, F_ASP_590	ND2, B_ASN_560	HD22, B_ASN_560	2.72	1.94	19.72
5UK0.PDB	OD1, D_ASP_586	NH2, C_ARG_311	HH22, C_ARG_311	2.98	2.20	18.56
5UK0.PDB	OD1, B_ASP_590	ND2, D_ASN_560	HD22, D_ASN_560	2.73	1.95	20.06
5VXJ.PDB	OE1, I_GLU_200	NH1, B_ARG_50	HH12, B_ARG_50	2.92	2.07	7.25
5VXJ.PDB	OE1, I_GLU_201	OH, B_TYR_105	HH, B_TYR_105	2.51	1.70	12.69
5VXJ.PDB	OD1, C_ASN_140	NE, D_ARG_19	HE, D_ARG_19	2.55	1.80	23.66
5VXJ.PDB	OE1, E_GLU_201	OH, D_TYR_105	HH, D_TYR_105	2.53	1.70	8.84
5VXJ.PDB	OD2, F_ASP_73	NZ, E_LYS_137	HZ2, E_LYS_137	2.77	1.96	20.15
5VXJ.PDB	OD1, D_ASN_97	NZ, E_LYS_197	HZ1, E_LYS_197	2.80	1.95	14.72
5VXJ.PDB	OE1, G_GLU_200	NH2, F_ARG_50	HH22, F_ARG_50	2.70	1.89	15.49
5VXJ.PDB	OE1, G_GLU_201	OH, F_TYR_105	HH, F_TYR_105	2.57	1.75	11.97
5VXJ.PDB	OE1, H_GLN_111	OG1, G_THR_217	HG1, G_THR_217	2.86	2.17	29.58
5VXJ.PDB	OD2, J_ASP_73	NZ, I_LYS_137	HZ3, I_LYS_137	2.90	2.17	29.52
5VXJ.PDB	OD1, B_ASN_97	NZ, I_LYS_197	HZ1, I_LYS_197	2.68	1.88	21.92
5VXK.PDB	OG, A_SER_168	NE2, B_GLN_106	HE21, B_GLN_106	2.99	2.23	24.43
5VXK.PDB	OD2, A_ASP_287	NE2, B_GLN_106	HE22, B_GLN_106	2.77	1.94	12.81
5VXK.PDB	OG1, B_THR_102	OH, A_TYR_276	HH, A_TYR_276	2.57	1.73	6.50
5VXL.PDB	OD2, B_ASP_52	NZ, A_LYS_205	HZ1, A_LYS_205	3.00	2.13	10.69

5VXL.PDB	OD1, A_ASP_166	OG, B_SER_55	HG, B_SER_55	2.56	1.73	4.68
5VXL.PDB	OE2, A_GLU_201	NH2, B_ARG_102	HH22, B_ARG_102	2.87	2.08	20.03
5VXM.PDB	OE2, B_GLU_111	NE1, A_TRP_177	HE1, A_TRP_177	2.76	1.97	19.61
5VXR.PDB	OE1, L_GLN_38	NZ, H_LYS_39	HZ2, H_LYS_39	2.72	1.76	14.94
5VXR.PDB	OD1, P_ASN_415	OH, H_TYR_50	HH, H_TYR_50	2.71	1.82	21.79
5VXR.PDB	OD1, L_ASN_138	NE2, H_HIS_170	HE2, H_HIS_170	2.89	1.98	20.57
5VXR.PDB	OE2, L_GLU_123	NZ, H_LYS_214	HZ1, H_LYS_214	2.93	1.98	15.97
5VXR.PDB	OG, H_SER_184	OG, L_SER_176	HG, L_SER_176	2.79	1.86	17.30
5WKQ.PDB	OG, B_SER_208	NH2, A_ARG_135	HH21, A_ARG_135	2.89	2.06	11.87
5WKQ.PDB	OE2, A_GLU_131	ND1, B_HIS_207	HD1, B_HIS_207	2.65	1.88	22.26
5WKQ.PDB	OE1, A_GLU_131	OG1, B_THR_211	HG1, B_THR_211	2.63	1.86	19.68
5WN9.PDB	OD1, H_ASN_57	NE, A_ARG_188	HE, A_ARG_188	2.58	1.61	2.15

Table 8: Interfacial side chain hydrogen bonding networks of all experimentally determined antigen-antibody-related structures. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

Residue-specific analysis of the interfacial electrostatic features of all experimentally determined antigen-antibody-related structures

[1A14', 1A2Y', 1A7L', 1A7N', 1A7O', 1A7P', 1A7Q', 1A7R', 1ADQ', 1BJ1', 1BLN', 1BQL', 1BVK', 1C08', 1C12', 1CE1', 1CFS', 1CFT', 1CG9', 1CLO', 1CLY', 1CLZ', 1CS9-1', 1CS9-3', 1CS9-6', 1CT6-1', 1CT6-7', 1CZ8', 1DBJ', 1DBK', 1DBM', 1DEE', 1DLF', 1DQD', 1DQJ', 1DQM', 1DQQ', 1DVF', 1DZB', 1E4W', 1E4X', 1E6J', 1E6O', 1EJO', 1EMT', 1ETZ', 1F11', 1F2X', 1F3R', 1F4W', 1F4X', 1F4Y', 1F8T', 1F90', 1FBI', 1FCC', 1FDL', 1FJ1', 1FRG', 1FUJ', 1FVC', 1FVD', 1FVE', 1G6V', 1G7H', 1G7I', 1G7J', 1G7L', 1G7M', 1G8Q', 1G9M', 1G9N', 1GC1', 1GGB', 1GGC', 1GGI', 1GPO', 1HCV', 1HEZ', 1HGD', 1HGE', 1HGF', 1HGG', 1HGH', 1HGI', 1HGI', 1HGI', 1HGI', 1HIL', 1HIM', 1HIN', 1I8I', 1I8K', 1I8M', 1IC4', 1IC5', 1IC7', 1IFH', 1IGF', 1IND', 1INE', 1IQW', 1IT9', 1J05', 1J1O', 1J1P', 1J1X', 1JFQ', 1JHL', 1JP5', 1JPS', 1JPT', 1JRH', 1JTO', 1JTP', 1JTT', 1JV5', 1K6Q', 1KB5', 1KC5', 1KCR', 1KCS', 1KIP', 1KIQ', 1KIR', 1KTR', 1L7I', 1LK3', 1M71', 1M7D', 1M7I', 1MCO', 1MEL', 1MFA', 1MFB', 1MFC', 1MHH', 1MLB', 1MLC', 1N64', 1NBY', 1NBZ', 1NDG', 1NDM', 1NGW', 1NGX', 1NGY', 1NGZ', 1NLB', 1NMC', 1OB1', 1OP9', 1OSP', 1OW0', 1P2C', 1P4B', 1P7K', 1PG7', 1PSK', 1PZ5', 1Q9K', 1Q9L', 1Q9O', 1Q9W', 1QBL', 1QBM', 1QGC', 1QKZ', 1QOK', 1R21-1', 1R21-10', 1R21-11', 1R21-12', 1R21-13', 1R21-14', 1R21-15', 1R21-16', 1R21-17', 1R21-18', 1R21-19', 1R21-2', 1R21-20', 1R21-21', 1R21-22', 1R21-23', 1R21-3', 1R21-4', 1R21-5', 1R21-6', 1R21-7', 1R21-8', 1R21-9', 1RZJ', 1RZK', 1S3K', 1S5I', 1S78', 1SM3', 1SQ2', 1SVZ', 1T2Q', 1T6V', 1TYE', 1TZH', 1TZI', 1U6A', 1UA6', 1UAC', 1UCB', 1UJ3', 1UWX', 1UZ6', 1UZ8', 1V7M', 1V7N', 1VER', 1VES', 1VFA', 1VFB', 1W72', 1WEJ', 1WZ1', 1XF2', 1XGY', 1XIW', 1YC7', 1YC8', 1YEI', 1YEJ', 1YEK', 1YNT', 1YQV', 1YYL', 1YYM', 1YZZ', 1ZEA', 1ZMY', 2AAB', 2ARJ', 2B2X', 2B4C', 2BDN', 2BJM', 2BRR', 2COQ', 2D03', 2DBL', 2DLF', 2DQC', 2DQD', 2DQE', 2DQF', 2DQG', 2DQH', 2DQI', 2DQJ', 2DQT', 2DQU', 2FB4', 2FD6', 2FR4', 2H32', 2H9G', 2HFG', 2HKF', 2HMG', 2HQ6', 2HRP', 2I24', 2I25', 2I26', 2I27', 2I5Y', 2I60', 2IFF', 2IG2', 2IGF', 2IHL', 2J4W', 2J5L', 2JB6', 2JEL', 2MCP', 2MKL-1', 2MKL-10', 2MKL-2', 2MKL-3', 2MKL-4', 2MKL-5', 2MKL-6', 2MKL-7', 2MKL-8',

'2MKL-9', '2MTW', '2NXY', '2NXZ', '2NY0', '2NY1', '2NY2', '2NY3', '2NY4', '2NY5',
 '2NY6', '2NY7', '2OR9', '2ORB', '2OSL', '2OTU', '2OTW', '2P8L', '2P8M', '2P8P', '2PR4',
 '2Q8A', '2Q8B', '2QAD', '2QQI', '2QQM', '2QQN', '2R29', '2R69', '2UYL', '2VC2', '2VDK',
 '2VDL', '2VDM', '2VDN', '2VDO', '2VDP', '2VDQ', '2VDR', '2VIR', '2VIS', '2VIT', '2VIU',
 '2VXS', '2VXT', '2VXU', '2VXV', '2XEF', '2XEG', '2XEI', '2XEJ', '2XZQ', '2Y06', '2Y07',
 '2Y36', '2Y7S', '2YPV', '2YWY', '2YWZ', '2ZCH', '2ZCK', '2ZCL', '2ZNW', '2ZNX', '2ZPK',
 '32C2', '3A67', '3A6B', '3A6C', '3AUV', '3B9K', '3BDY', '3BE1', '3BGF', '3BIK', '3BIS',
 '3BKY', '3BO8', '3BT2', '3BZ4', '3C09', '3C5S', '3C6S', '3CVH', '3CXD', '3D0L', '3D0V',
 '3D9A', '3DRO', '3DRQ', '3DSF', '3EBA', '3EOA', '3EOB', '3ESU', '3ESV', '3ET9', '3ETB',
 '3EYV', '3FMG', '3G39', '3G3A', '3G3B', '3GGW', '3GHB', '3GHE', '3GJF', '3GNM', '3GO1',
 '3HAE', '3HFM', '3HI6', '3HMG', '3HZK', '3HZM', '3HZV', '3HZY', '3I02', '3I9G', '3IET',
 '3IF1', '3IJH', '3IJS', '3IJY', '3IKC', '3IU3', '3IU4', '3IVK', '3J5M', '3J70', '3JCC', '3KS0',
 '3L7E', '3LZF', '3M18', '3M19', '3MLR', '3MLS', '3MLT', '3MLU', '3MLV', '3MLW', '3MLX',
 '3MLY', '3MLZ', '3NFP', '3NGB', '3NH7', '3NZ8', '3O2D', '3O41', '3O45', '3OJD', '3P0V',
 '3P0Y', '3P11', '3PGF', '3PNW', '3PP4', '3Q3G', '3QA3', '3QG6', '3QG7', '3QO1', '3QUM',
 '3R08', '3SE8', '3SE9', '3SGD', '3SKJ', '3SY0', '3T4Y', '3T65', '3T77', '3THM', '3TJE',
 '3U1S', '3U2S', '3U36', '3UBX', '3UJI', '3UJJ', '3UJT', '3UO1', '3UYR', '3V4P', '3V4U',
 '3V4V', '3V52', '3V6F', '3WIH', '3WN5', '3X0E', '3X0F', '4A6Y', '4AG4', '4B50', '4BH7',
 '4BH8', '4C83', '4CJD', '4DAG', '4DGV', '4DGY', '4E9O', '4EBQ', '4EDW', '4EDX', '4ETQ',
 '4F33', '4F3F', '4FFV', '4FFW', '4FQH', '4FQI', '4G6A', '4G6F', '4GMT', '4GXU', '4GXV',
 '4GXX', '4H0G', '4H0H', '4H0I', '4H8W', '4HF5', '4HGK', '4HH9', '4HHA', '4HIE', '4HIH',
 '4HII', '4HIJ', '4HK0', '4HK3', '4HKB', '4HKX', '4HLZ', '4HMG', '4HWB', '4HXA', '4HXB',
 '4I2X', '4I3R', '4I3S', '4JAM', '4JAN', '4JHA', '4JHW', '4JO1', '4JO2', '4JO3', '4JO4', '4K24',
 '4K2U', '4KI5', '4KJY', '4KPH', '4KRL', '4KRM', '4KRO', '4KRP', '4KV5', '4KXZ', '4LQF',
 '4LSS', '4LST', '4LU5', '4M1D', '4M1G', '4M3J', '4M3K', '4M5Y', '4M7J', '4M7Z', '4M93',
 '4MA1', '4N0Y', '4N1H', '4NBX', '4NBY', '4NBZ', '4NC0', '4NC1', '4NC2', '4NGH', '4NHC',
 '4NIK', '4NZR', '4NZT', '4NZU', '4O5L', '4OLU', '4OLV', '4OLW', '4OLX', '4OLY', '4OLZ',
 '4OM0', '4OM1', '4OT1', '4OTX', '4P49', '4P9H', '4PTT', '4PTU', '4Q6I', '4Q97', '4Q9B',
 '4Q9C', '4QEX', '4QHU', '4QTI', '4QXG', '4R2G', '4R4H', '4R7D', '4R7N', '4R9Y', '4RAU',
 '4RRP', '4TRP', '4TUJ', '4TUK', '4TUL', '4TUO', '4U0Q', '4U3X', '4U6G', '4U6V', '4UAO',

'4UV6', '4WEU', '4WHT', '4WHY', '4WUU', '4XVJ', '4YHP', '4YHY', '4YHZ', '4YNY',
 '4YO0', '4Z0X', '4ZD3', '4ZFF', '4ZFG', '4ZFO', '4ZH7', '5A2I', '5A2J', '5A2K', '5A2L',
 '5A7X', '5A8H', '5AZE', '5BW7', '5CMA', '5CP3', '5CP7', '5DFV', '5DFW', '5DMI', '5DMJ',
 '5DWU', '5ERW', '5EZI', '5EZJ', '5EZL', '5EZN', '5EZO', '5GGV', '5GKR', '5GKS', '5HDQ',
 '5HMG', '5I4F', '5I76', '5IHL', '5ITB', '5J3D', '5JO5', '5JOF', '5JR1', '5JUE', '5JXA', '5KZP',
 '5LDN', '5M2C', '5M33', '5M3D', '5M3T', '5M4R', '5MO9', '5N2B', '5N4J', '5N7B', '5N7W',
 '5N88', '5NPH', '5NPI', '5NPJ', '5NST', '5NUZ', '5O14', '5O1R', '5OLM', '5OPY', '5OWP',
 '5SV3', '5SV4', '5T6P', '5T78', '5TCX', '5TIH', '5TIK', '5TL5', '5TLJ', '5TLK', '5TRU',
 '5TZ2', '5TZT', '5TZU', '5U3J', '5U3N', '5UCB', '5UEA', '5UEK', '5UG0', '5UJZ', '5UK0',
 '5UK1', '5UK2', '5UR8', '5VF2', '5VL3', '5VN8', '5VXJ', '5VXK', '5VXL', '5VXM', '5VXR',
 '5VZR', '5W2B', '5W9H', '5W9I', '5W9J', '5W9K', '5W9L', '5W9M', '5W9N', '5W9O',
 '5W9P', '5WK4', '5WKQ', '5WN9', '5WNA', '5WNB', '5XBM', '5XCQ', '5XCR', '5XCS',
 '5XCT', '5XCU', '5XCV', '5XJ3', '5XRT', '5XWD', '5YC5', '5ZV3', '6A3V', '6A3W', '6A76',
 '6A77', '6A78', '6A79', '6AL5', '6ANA', '6AND', '6ANI', '6AQ7', '6ATT', '6AZZ', '6B08',
 '6B0A', '6B0E', '6B0G', '6B0H', '6BE2', '6BE3', '6BE4', '6BIT', '6BRB', '6BXA', '6BXC',
 '6BXD', '6BXE', '6BZU', '6BZV', '6BZW', '6BZY', '6C5H', '6C5I', '6C5J', '6C5K', '6C6X',
 '6C6Y', '6C6Z', '6CUJ', '6DC3', '6DC4', '6DC5', '6DCV', '6DCW', '6DDM', '6DDR', '6DDV',
 '6DFG', '6DFH', '6DG2', '6E62', '6E63', '6E64', '6E65', '6E8V', '6E9G', '6E9H', '6E9I',
 '6E9K', '6E9Q', '6E9U', '6EDU', '6EJG', '6EJM', '6EK2', '6EUN', '6EUP', '6EV1', '6EV2',
 '6EWB', '6FAB', '6FAX', '6FN1', '6FN4', '6FRJ', '6GK7', '6GK8', '6H2Y', '6I3Z', '6I9J',
 '6IAP', '6JMQ', '6JMR', '6K4Z', '6K7O', '6KN9', '6MH2', '6MHR', '6MI2', '6MN7', '6MPG',
 '6MPH', '6MQC', '6MQE', '6MQM', '6MQR', '6MQS', '6N16', '6N1V', '6N1W', '6N5B',
 '6N5D', '6N5E', '6N6B', '6NB5', '6NB8', '6NC2', '6NC3', '6NEX', '6NF2', '6NF5', '6NFC',
 '6NMR', '6NMS', '6NMT', '6NMU', '6NMV', '6O9B', '6O9C', '6OGX', '6OKM', '6OKN',
 '6OOR', '6OSY', '6OT1', '6P62', '6P65', '6PE8', '6PE9', '6PHB', '6PHC', '6PHD', '6PHF',
 '6PHG', '6PHH', '6PI7', '6PYC', '6PYD', '6PZW', '6RPS', '6S3T', '6U02', '6U1T', '6U59',
 '6UG7', '6UG8', '6UG9', '6UGA']

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1A14	N_ARG_82	NH1	N_ASP_127	OD2	3.377
1A14	N_ARG_82	NH2	N_ASP_127	OD2	3.103
1A14	N_ARG_118	NH1	N_GLU_119	OE2	3.614
1A14	N_ARG_118	NH2	N_GLU_425	OE1	2.718
1A14	N_ARG_118	NH2	N_GLU_425	OE2	3.457
1A14	N_ARG_130	NH1	N_GLU_128	OE2	3.346
1A14	N_ARG_141	NH1	N_GLU_110	OE2	2.663
1A14	N_ARG_156	NH1	N_GLU_119	OE1	3.576
1A14	N_ARG_156	NH2	N_GLU_119	OE1	3.307
1A14	N_ARG_172	NH1	N_GLU_174	OE1	3.579
1A14	N_ARG_172	NH1	N_GLU_174	OE2	2.688
1A14	N_ARG_189	NH1	N_ASP_125	OD1	2.993
1A14	N_ARG_209	NH2	N_GLU_174	OE1	2.647
1A14	N_ARG_224	NH1	N_GLU_276	OE1	3.468
1A14	N_ARG_224	NH1	N_GLU_276	OE2	2.449
1A14	N_ARG_224	NH2	N_GLU_276	OE2	3.362
1A14	N_HIS_274	ND1	N_GLU_276	OE2	3.981
1A14	N_HIS_274	NE2	N_GLU_276	OE2	3.658
1A14	N_ARG_292	NH2	N_GLU_277	OE1	3.076
1A14	N_ARG_292	NH2	N_GLU_277	OE2	3.834
1A14	N_ARG_300	NH1	N_ASP_324	OD1	3.224
1A14	N_ARG_300	NH2	N_ASP_324	OD1	3.465
1A14	N_ARG_304	NH1	N_GLU_286	OE2	3.487
1A14	N_HIS_312	ND1	N_GLU_266	OE1	3.839
1A14	N_HIS_312	ND1	N_GLU_266	OE2	2.824
1A14	N_ARG_364	NH1	N_ASP_330	OD2	3.955
1A14	N_ARG_364	NH1	N_GLU_375	OE2	2.918
1A14	N_ARG_364	NH2	N_ASP_330	OD1	2.939
1A14	N_ARG_364	NH2	N_ASP_330	OD2	2.852
1A14	N_LYS_387	NZ	N_ASP_386	OD1	2.949
1A14	N_LYS_387	NZ	N_ASP_386	OD2	3.684
1A14	N_ARG_428	NH1	N_ASP_460	OD2	2.670
1A14	N_ARG_428	NH2	N_GLU_433	OE1	3.485
1A14	N_ARG_428	NH2	N_GLU_433	OE2	2.572
1A14	N_LYS_432	NZ	H_ASP_56	OD1	3.071
1A14	H_LYS_38	NZ	H_ASP_86	OD1	3.927
1A14	H_LYS_66	NZ	H_ASP_86	OD1	3.084
1A14	H_LYS_66	NZ	H_ASP_86	OD2	3.096
1A14	H_ARG_94	NH2	H_ASP_101	OD2	2.754
1A14	H_ARG_100	NH1	H_ASP_100B	OD1	2.852
1A14	H_ARG_100	NH1	H_ASP_100B	OD2	3.179
1A14	L_ARG_61	NH1	L_GLU_79	OE1	3.189
1A14	L_ARG_61	NH1	L_GLU_79	OE2	3.942
1A14	L_ARG_61	NH2	L_GLU_79	OE1	3.107
1A14	L_ARG_61	NH2	L_ASP_82	OD1	2.650
1A14	L_ARG_61	NH2	L_ASP_82	OD2	3.122

Table 9: 1A14-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1A2Y	A_ARG_61	NH2	A_GLU_81	OE2	3.299
1A2Y	A_ARG_61	NH2	A_ASP_82	OD1	2.783
1A2Y	A_ARG_61	NH2	A_ASP_82	OD2	3.405
1A2Y	A_ARG_96	NH1	B_GLU_98	OE1	2.846
1A2Y	A_ARG_96	NH1	B_GLU_98	OE2	3.664
1A2Y	A_ARG_96	NH2	B_GLU_98	OE1	3.545
1A2Y	A_ARG_96	NH2	B_GLU_98	OE2	2.882
1A2Y	B_ARG_38	NH1	B_ASP_89	OD1	3.030
1A2Y	B_ARG_38	NH2	B_GLU_46	OE1	3.122
1A2Y	B_ARG_38	NH2	B_ASP_89	OD1	3.828
1A2Y	B_ARG_66	NH1	B_ASP_89	OD1	3.898
1A2Y	B_ARG_66	NH1	B_ASP_89	OD2	3.063
1A2Y	B_ARG_66	NH2	B_ASP_89	OD1	3.023
1A2Y	B_ARG_66	NH2	B_ASP_89	OD2	3.441
1A2Y	B_ARG_97	NH2	B_ASP_104	OD1	3.891
1A2Y	B_ARG_97	NH2	B_ASP_104	OD2	2.921
1A2Y	B_ARG_102	NH1	B_ASP_100	OD2	3.378
1A2Y	C_ARG_61	NH1	C_ASP_48	OD1	2.641
1A2Y	C_ARG_68	NH1	C_ASP_66	OD2	3.417
1A2Y	C_ARG_125	NH1	C_ASP_119	OD1	3.449
1A2Y	C_ARG_125	NH1	C_ASP_119	OD2	3.142
1A2Y	C_ARG_125	NH2	C_ASP_119	OD2	3.057

Table 10: 1A2Y-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1A7L	A_LYS_15	NZ	A_GLU_111	OE1	3.415
1A7L	A_LYS_15	NZ	A_GLU_111	OE2	2.711
1A7L	A_LYS_83	NZ	A_ASP_87	OD1	3.030
1A7L	A_LYS_83	NZ	A_ASP_87	OD2	3.304
1A7L	A_LYS_140	NZ	A_ASP_136	OD1	3.902
1A7L	A_LYS_140	NZ	A_ASP_136	OD2	2.755
1A7L	A_LYS_170	NZ	A_ASP_180	OD2	2.887
1A7L	A_LYS_189	NZ	A_ASP_358	OD2	2.997
1A7L	A_HIS_203	ND1	A_ASP_136	OD2	2.891
1A7L	A_LYS_219	NZ	B_GLU_131	OE1	3.835
1A7L	A_LYS_251	NZ	A_ASP_164	OD2	3.413
1A7L	A_ARG_316	NH1	A_ASP_236	OD2	3.471
1A7L	A_ARG_316	NH2	A_ASP_314	OD2	2.893
1A7L	A_ARG_344	NH2	A_GLU_153	OE1	2.800
1A7L	A_ARG_344	NH2	A_GLU_153	OE2	3.001
1A7L	A_ARG_135E	NH2	A_ASP_133E	OD1	3.683
1A7L	A_ARG_135E	NH2	A_ASP_133E	OD2	3.429
1A7L	B_LYS_15	NZ	B_GLU_111	OE1	3.377
1A7L	B_LYS_15	NZ	B_GLU_111	OE2	3.759
1A7L	B_LYS_42	NZ	B_GLU_44	OE2	3.460
1A7L	B_LYS_42	NZ	B_GLU_45	OE2	3.115
1A7L	B_LYS_140	NZ	B_ASP_136	OD2	3.464
1A7L	B_LYS_170	NZ	B_ASP_180	OD2	3.114
1A7L	B_LYS_189	NZ	B_ASP_358	OD2	3.685
1A7L	B_HIS_203	ND1	B_ASP_136	OD2	2.601
1A7L	B_LYS_251	NZ	B_ASP_164	OD2	3.639
1A7L	B_LYS_277	NZ	B_GLU_281	OE1	3.203
1A7L	B_LYS_277	NZ	B_GLU_281	OE2	2.832
1A7L	B_ARG_316	NH1	B_ASP_236	OD1	3.944
1A7L	B_ARG_316	NH1	B_ASP_236	OD2	3.485
1A7L	B_ARG_316	NH2	B_ASP_314	OD2	3.346
1A7L	B_LYS_326	NZ	B_GLU_322	OE2	3.744
1A7L	B_ARG_344	NH2	B_GLU_153	OE1	2.942
1A7L	B_ARG_344	NH2	B_GLU_153	OE2	3.765
1A7L	C_LYS_29	NZ	C_GLU_28	OE2	3.650
1A7L	C_LYS_83	NZ	C_ASP_87	OD1	3.169
1A7L	C_LYS_83	NZ	C_ASP_87	OD2	3.327
1A7L	C_LYS_102	NZ	C_GLU_78	OE1	3.945
1A7L	C_LYS_140	NZ	C_ASP_136	OD1	2.897
1A7L	C_LYS_140	NZ	C_ASP_136	OD2	3.618
1A7L	C_LYS_170	NZ	C_GLU_172	OE2	3.002
1A7L	C_LYS_189	NZ	C_ASP_184	OD1	3.860
1A7L	C_LYS_189	NZ	C_ASP_358	OD2	3.399
1A7L	C_HIS_203	ND1	C_ASP_136	OD1	2.895
1A7L	C_LYS_219	NZ	C_GLU_221	OE2	3.817
1A7L	C_LYS_277	NZ	C_GLU_281	OE1	3.148
1A7L	C_LYS_277	NZ	C_GLU_281	OE2	3.283
1A7L	C_LYS_295	NZ	C_GLU_291	OE2	3.540
1A7L	C_ARG_316	NH1	C_ASP_236	OD2	3.877
1A7L	C_ARG_316	NH2	C_ASP_314	OD2	3.048
1A7L	C_LYS_326	NZ	C_GLU_322	OE2	3.201
1A7L	C_ARG_344	NH1	C_GLU_153	OE1	3.865
1A7L	C_ARG_344	NH1	C_GLU_153	OE2	2.640
1A7L	C_ARG_344	NH2	C_GLU_153	OE1	2.933
1A7L	C_ARG_344	NH2	C_GLU_153	OE2	3.058
1A7L	C_LYS_362	NZ	C_ASP_363	OD1	3.768

Table 11: 1A7L-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1A7N	L_ARG_61	NH2	L_ASP_81	OD2	3.125
1A7N	L_ARG_61	NH2	L_ASP_82	OD1	2.727
1A7N	L_ARG_61	NH2	L_ASP_82	OD2	3.246
1A7N	L_ARG_96	NH1	H_GLU_298	OE1	2.957
1A7N	L_ARG_96	NH1	H_GLU_298	OE2	3.249
1A7N	L_ARG_96	NH2	H_GLU_298	OE2	3.297
1A7N	L_LYS_107	NZ	L_GLU_17	OE2	2.821
1A7N	H_ARG_238	NH1	H_ASP_289	OD1	2.802
1A7N	H_ARG_238	NH2	H_GLU_246	OE1	3.463
1A7N	H_ARG_238	NH2	H_GLU_246	OE2	3.781
1A7N	H_ARG_238	NH2	H_ASP_289	OD1	3.741
1A7N	H_ARG_266	NH1	H_ASP_289	OD1	3.782
1A7N	H_ARG_266	NH1	H_ASP_289	OD2	2.637
1A7N	H_ARG_266	NH2	H_ASP_289	OD1	3.006
1A7N	H_ARG_266	NH2	H_ASP_289	OD2	3.237
1A7N	H_LYS_275	NZ	H_ASP_272	OD2	3.739
1A7N	H_ARG_297	NH2	H_ASP_304	OD1	3.472
1A7N	H_ARG_297	NH2	H_ASP_304	OD2	2.559
1A7N	H_ARG_302	NH1	H_ASP_300	OD1	2.938

Table 12: 1A7N-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID residue name residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1A7O	L_ARG_61	NH2	L_ASP_81	OD2	3.044
1A7O	L_ARG_61	NH2	L_ASP_82	OD1	2.765
1A7O	L_ARG_61	NH2	L_ASP_82	OD2	3.549
1A7O	L_LYS_107	NZ	L_GLU_17	OE2	3.441
1A7O	H_ARG_238	NH1	H_ASP_289	OD1	2.721
1A7O	H_ARG_238	NH2	H_GLU_246	OE1	3.298
1A7O	H_ARG_238	NH2	H_GLU_246	OE2	3.986
1A7O	H_ARG_238	NH2	H_ASP_289	OD1	3.845
1A7O	H_ARG_266	NH1	H_ASP_289	OD1	3.739
1A7O	H_ARG_266	NH1	H_ASP_289	OD2	2.614
1A7O	H_ARG_266	NH2	H_ASP_289	OD1	2.654
1A7O	H_ARG_266	NH2	H_ASP_289	OD2	2.979
1A7O	H_ARG_297	NH2	H_ASP_304	OD1	3.602
1A7O	H_ARG_297	NH2	H_ASP_304	OD2	2.696

Table 13: 1A7O-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1A7P	L_ARG_61	NH2	L_ASP_81	OD2	3.219
1A7P	L_ARG_61	NH2	L_ASP_82	OD1	2.851
1A7P	L_ARG_61	NH2	L_ASP_82	OD2	3.384
1A7P	L_ARG_96	NH2	H_GLU_298	OE1	3.845
1A7P	L_ARG_96	NH2	H_GLU_298	OE2	2.867
1A7P	L_LYS_107	NZ	L_GLU_17	OE2	2.919
1A7P	H_ARG_238	NH1	H_ASP_289	OD1	2.885
1A7P	H_ARG_238	NH2	H_GLU_246	OE1	3.234
1A7P	H_ARG_238	NH2	H_GLU_246	OE2	3.868
1A7P	H_ARG_238	NH2	H_ASP_289	OD1	3.785
1A7P	H_ARG_266	NH1	H_ASP_289	OD1	3.679
1A7P	H_ARG_266	NH1	H_ASP_289	OD2	2.508
1A7P	H_ARG_266	NH2	H_ASP_289	OD1	2.957
1A7P	H_ARG_266	NH2	H_ASP_289	OD2	3.253
1A7P	H_ARG_297	NH2	H_ASP_304	OD1	3.629
1A7P	H_ARG_297	NH2	H_ASP_304	OD2	2.709

Table 14: 1A7P-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1A7Q	L_ARG_96	NH1	H_GLU_298	OE1	2.615
1A7Q	L_ARG_96	NH1	H_GLU_298	OE2	3.239
1A7Q	L_ARG_96	NH2	H_GLU_298	OE1	3.431
1A7Q	L_ARG_96	NH2	H_GLU_298	OE2	2.621
1A7Q	H_ARG_238	NH1	H_ASP_289	OD1	2.800
1A7Q	H_ARG_238	NH2	H_GLU_246	OE1	3.193
1A7Q	H_ARG_238	NH2	H_GLU_246	OE2	3.915
1A7Q	H_ARG_238	NH2	H_ASP_289	OD1	3.788
1A7Q	H_ARG_266	NH1	H_ASP_289	OD1	3.820
1A7Q	H_ARG_266	NH1	H_ASP_289	OD2	2.595
1A7Q	H_ARG_266	NH2	H_ASP_289	OD1	2.974
1A7Q	H_ARG_266	NH2	H_ASP_289	OD2	3.211
1A7Q	H_ARG_297	NH2	H_ASP_304	OD1	3.728
1A7Q	H_ARG_297	NH2	H_ASP_304	OD2	2.870
1A7Q	H_ARG_299	NH1	H_ASP_304	OD2	3.412
1A7Q	H_ARG_302	NH1	H_ASP_300	OD2	3.990

Table 15: 1A7Q-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1A7R	L_ARG_61	NH2	L_ASP_81	OD2	3.198
1A7R	L_ARG_61	NH2	L_ASP_82	OD1	2.615
1A7R	L_ARG_61	NH2	L_ASP_82	OD2	3.098
1A7R	L_ARG_96	NH1	H_GLU_298	OE1	2.658
1A7R	L_ARG_96	NH1	H_GLU_298	OE2	3.535
1A7R	L_ARG_96	NH2	H_GLU_298	OE1	3.614
1A7R	L_ARG_96	NH2	H_GLU_298	OE2	2.905
1A7R	L_LYS_107	NZ	L_GLU_17	OE2	3.377
1A7R	H_ARG_238	NH1	H_ASP_289	OD1	2.846
1A7R	H_ARG_238	NH2	H_GLU_246	OE1	3.349
1A7R	H_ARG_238	NH2	H_GLU_246	OE2	3.834
1A7R	H_ARG_238	NH2	H_ASP_289	OD1	3.880
1A7R	H_ARG_266	NH1	H_ASP_289	OD1	3.623
1A7R	H_ARG_266	NH1	H_ASP_289	OD2	2.578
1A7R	H_ARG_266	NH2	H_ASP_289	OD1	2.893
1A7R	H_ARG_266	NH2	H_ASP_289	OD2	3.226
1A7R	H_LYS_275	NZ	H_ASP_272	OD2	3.976
1A7R	H_ARG_297	NH2	H_ASP_304	OD1	3.559
1A7R	H_ARG_297	NH2	H_ASP_304	OD2	2.633

Table 16: 1A7R-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID residue name residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1ADQ	A_LYS_248	NZ	A_GLU_380	OE2	3.226
1ADQ	A_ARG_255	NH1	A_ASP_249	OD1	3.987
1ADQ	A_ARG_255	NH2	H_ASP_31	OD2	2.929
1ADQ	A_LYS_320	NZ	A_GLU_333	OE1	3.855
1ADQ	A_LYS_320	NZ	A_GLU_333	OE2	3.755
1ADQ	A_LYS_326	NZ	A_ASP_270	OD1	3.273
1ADQ	A_LYS_326	NZ	A_ASP_270	OD2	3.723
1ADQ	A_LYS_338	NZ	A_GLU_430	OE1	3.031
1ADQ	A_LYS_338	NZ	A_GLU_430	OE2	2.803
1ADQ	A_ARG_344	NH1	A_ASP_401	OD2	3.235
1ADQ	A_ARG_416	NH1	A_GLU_388	OE1	3.926
1ADQ	A_ARG_416	NH1	A_GLU_388	OE2	3.113
1ADQ	A_ARG_416	NH2	A_GLU_388	OE1	3.507
1ADQ	A_ARG_416	NH2	A_GLU_388	OE2	2.923
1ADQ	A_HIS_433	NE2	L_ASP_50	OD1	3.394
1ADQ	A_HIS_433	NE2	L_ASP_50	OD2	3.883
1ADQ	L_LYS_31	NZ	L_ASP_92	OD1	3.026
1ADQ	L_ARG_61	NH2	L_GLU_79	OE1	3.104
1ADQ	L_ARG_61	NH2	L_ASP_82	OD1	3.715
1ADQ	L_ARG_61	NH2	L_ASP_82	OD2	3.959
1ADQ	L_HIS_95B	NE2	H_ASP_61	OD2	3.425
1ADQ	L_LYS_149	NZ	L_GLU_206	OE1	3.712
1ADQ	H_ARG_38	NH1	H_ASP_86	OD1	3.336
1ADQ	H_ARG_66	NH1	H_ASP_86	OD1	3.600
1ADQ	H_ARG_66	NH1	H_ASP_86	OD2	2.617
1ADQ	H_ARG_66	NH2	H_ASP_86	OD1	2.939
1ADQ	H_ARG_66	NH2	H_ASP_86	OD2	3.254
1ADQ	H_LYS_158	NZ	H_GLU_220	OE1	3.150
1ADQ	H_LYS_184	NZ	H_ASP_146	OD2	3.128
1ADQ	H_LYS_221	NZ	H_ASP_222	OD2	3.919

Table 17: 1ADQ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1BJ1	L_ARG_61	NH2	L_GLU_81	OE2	3.689
1BJ1	L_ARG_61	NH2	L_ASP_82	OD1	2.770
1BJ1	L_ARG_61	NH2	L_ASP_82	OD2	3.181
1BJ1	L_LYS_103	NZ	L_GLU_165	OE2	3.052
1BJ1	L_ARG_142	NH2	L_GLU_105	OE2	3.352
1BJ1	L_LYS_188	NZ	L_ASP_185	OD1	3.571
1BJ1	H_ARG_38	NH1	H_ASP_90	OD1	3.092
1BJ1	H_ARG_38	NH2	H_GLU_46	OE1	3.575
1BJ1	H_ARG_38	NH2	H_ASP_90	OD1	3.916
1BJ1	H_ARG_67	NH1	H_ASP_90	OD2	2.757
1BJ1	H_ARG_67	NH2	H_ASP_90	OD1	3.333
1BJ1	H_ARG_67	NH2	H_ASP_90	OD2	3.289
1BJ1	H_ARG_87	NH1	H_GLU_89	OE2	3.150
1BJ1	H_LYS_153	NZ	H_ASP_154	OD1	3.946
1BJ1	H_LYS_219	NZ	L_GLU_123	OE1	2.948
1BJ1	H_LYS_220	NZ	H_GLU_222	OE1	3.519
1BJ1	H_LYS_224	NZ	L_ASP_122	OD2	2.691
1BJ1	V_ARG_23	NH1	W_GLU_30	OE1	3.305
1BJ1	V_ARG_56	NH2	V_GLU_38	OE1	3.031
1BJ1	V_ARG_82	NH1	V_GLU_42	OE1	3.483
1BJ1	V_ARG_82	NH2	V_GLU_42	OE1	2.954
1BJ1	V_HIS_99	NE2	V_GLU_73	OE2	3.634
1BJ1	V_LYS_107	NZ	V_GLU_64	OE1	3.520
1BJ1	W_ARG_23	NH1	V_GLU_30	OE1	3.351
1BJ1	W_ARG_56	NH2	W_GLU_38	OE1	3.008
1BJ1	W_ARG_82	NH1	W_GLU_42	OE2	3.753
1BJ1	W_ARG_82	NH2	W_GLU_42	OE2	2.675
1BJ1	W_HIS_99	NE2	W_GLU_73	OE2	3.679
1BJ1	W_ARG_105	NH1	W_GLU_103	OE1	3.917
1BJ1	W_ARG_105	NH2	W_GLU_103	OE1	2.651
1BJ1	W_LYS_107	NZ	W_GLU_64	OE1	3.656
1BJ1	J_ARG_61	NH2	J_GLU_81	OE2	3.502
1BJ1	J_ARG_61	NH2	J_ASP_82	OD1	2.721
1BJ1	J_ARG_61	NH2	J_ASP_82	OD2	3.272
1BJ1	J_LYS_103	NZ	J_GLU_165	OE2	3.042
1BJ1	J_LYS_126	NZ	J_GLU_123	OE2	3.084
1BJ1	J_LYS_145	NZ	J_GLU_195	OE2	3.741
1BJ1	J_LYS_188	NZ	J_ASP_185	OD1	3.653
1BJ1	K_ARG_38	NH1	K_ASP_90	OD1	3.157
1BJ1	K_ARG_38	NH2	K_GLU_46	OE1	3.735
1BJ1	K_ARG_38	NH2	K_ASP_90	OD1	3.789
1BJ1	K_ARG_67	NH1	K_ASP_90	OD2	2.824
1BJ1	K_ARG_67	NH2	K_ASP_90	OD1	3.565
1BJ1	K_ARG_67	NH2	K_ASP_90	OD2	3.500
1BJ1	K_ARG_87	NH1	K_GLU_89	OE2	3.633
1BJ1	K_LYS_127	NZ	K_ASP_154	OD2	3.373
1BJ1	K_LYS_220	NZ	K_GLU_222	OE1	3.843

Table 18: 1BJ1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1BLN	A_ARG_24	NH1	A_ASP_70	OD1	2.713
1BLN	A_LYS_39	NZ	A_GLU_81	OE1	3.030
1BLN	A_LYS_39	NZ	A_GLU_81	OE2	2.665
1BLN	A_ARG_54	NH1	A_ASP_60	OD1	3.451
1BLN	A_ARG_54	NH1	A_ASP_60	OD2	2.737
1BLN	A_ARG_54	NH2	A_ASP_60	OD1	3.686
1BLN	A_ARG_61	NH1	A_GLU_79	OE1	3.238
1BLN	A_ARG_61	NH1	A_GLU_79	OE2	2.929
1BLN	A_ARG_61	NH2	A_GLU_79	OE1	2.868
1BLN	A_ARG_61	NH2	A_ASP_82	OD1	2.719
1BLN	A_ARG_61	NH2	A_ASP_82	OD2	2.933
1BLN	A_LYS_103	NZ	A_ASP_165	OD1	2.680
1BLN	A_LYS_103	NZ	A_ASP_165	OD2	2.779
1BLN	A_LYS_149	NZ	A_GLU_195	OE1	2.904
1BLN	A_LYS_149	NZ	A_GLU_195	OE2	2.718
1BLN	A_LYS_169	NZ	A_ASP_167	OD1	3.151
1BLN	A_LYS_169	NZ	A_ASP_167	OD2	2.577
1BLN	A_LYS_169	NZ	A_ASP_170	OD2	3.534
1BLN	A_LYS_183	NZ	A_ASP_184	OD1	3.490
1BLN	A_LYS_183	NZ	A_ASP_184	OD2	2.917
1BLN	A_ARG_188	NH1	A_GLU_185	OE2	2.624
1BLN	A_ARG_188	NH2	A_GLU_185	OE1	3.741
1BLN	A_ARG_188	NH2	A_GLU_185	OE2	2.727
1BLN	A_HIS_189	ND1	A_ASP_151	OD2	2.822
1BLN	A_HIS_189	NE2	A_GLU_154	OE1	3.457
1BLN	A_HIS_189	NE2	A_GLU_154	OE2	3.510
1BLN	A_ARG_211	NH1	A_GLU_213	OE2	3.546
1BLN	B_ARG_38	NH1	B_GLU_46	OE1	2.899
1BLN	B_ARG_38	NH2	B_ASP_86	OD1	2.861
1BLN	B_LYS_64	NZ	B_ASP_61	OD1	2.441
1BLN	B_ARG_66	NH1	B_ASP_86	OD1	3.791
1BLN	B_ARG_66	NH1	B_ASP_86	OD2	2.687
1BLN	B_ARG_66	NH2	B_GLU_85	OE2	2.818
1BLN	B_ARG_66	NH2	B_ASP_86	OD1	2.906
1BLN	B_ARG_66	NH2	B_ASP_86	OD2	3.348
1BLN	B_LYS_75	NZ	B_ASP_72	OD1	2.753
1BLN	B_LYS_75	NZ	B_ASP_72	OD2	2.989
1BLN	B_ARG_83	NH2	B_GLU_85	OE1	2.930
1BLN	B_ARG_83	NH2	B_GLU_85	OE2	2.872
1BLN	B_LYS_218	NZ	B_ASP_220	OD1	2.783
1BLN	B_LYS_218	NZ	B_ASP_220	OD2	2.601
1BLN	B_LYS_221	NZ	A_GLU_123	OE2	2.688
1BLN	B_LYS_222	NZ	B_GLU_226	OE1	2.622
1BLN	B_LYS_222	NZ	B_GLU_226	OE2	2.602
1BLN	C_ARG_24	NH1	C_ASP_70	OD1	3.436
1BLN	C_ARG_24	NH1	C_ASP_70	OD2	2.560
1BLN	C_LYS_39	NZ	C_GLU_81	OE1	2.548
1BLN	C_LYS_39	NZ	C_GLU_81	OE2	2.754
1BLN	C_ARG_54	NH1	C_ASP_60	OD2	3.393
1BLN	C_ARG_61	NH1	C_GLU_79	OE1	3.333
1BLN	C_ARG_61	NH1	C_GLU_79	OE2	2.726
1BLN	C_ARG_61	NH2	C_GLU_79	OE1	3.200
1BLN	C_ARG_61	NH2	C_ASP_82	OD1	2.668
1BLN	C_ARG_61	NH2	C_ASP_82	OD2	3.423
1BLN	C_LYS_103	NZ	C_GLU_105	OE2	2.790
1BLN	C_LYS_103	NZ	C_ASP_165	OD1	3.363
1BLN	C_LYS_103	NZ	C_ASP_165	OD2	3.568

1BLN	C_LYS_149	NZ	C_GLU_195	OE1	2.899
1BLN	C_LYS_149	NZ	C_GLU_195	OE2	2.725
1BLN	C_LYS_169	NZ	C_ASP_167	OD1	3.137
1BLN	C_LYS_169	NZ	C_ASP_167	OD2	2.563
1BLN	C_LYS_169	NZ	C_ASP_170	OD2	3.533
1BLN	C_LYS_183	NZ	C_ASP_184	OD1	3.499
1BLN	C_LYS_183	NZ	C_ASP_184	OD2	2.904
1BLN	C_ARG_188	NH1	C_GLU_185	OE2	2.652
1BLN	C_ARG_188	NH2	C_GLU_185	OE1	3.758
1BLN	C_ARG_188	NH2	C_GLU_185	OE2	2.730
1BLN	C_HIS_189	ND1	C_ASP_151	OD2	2.783
1BLN	C_HIS_189	NE2	C_GLU_154	OE1	3.449
1BLN	C_HIS_189	NE2	C_GLU_154	OE2	3.510
1BLN	C_ARG_211	NH1	C_GLU_213	OE2	3.540
1BLN	D_ARG_38	NH1	D_ASP_86	OD1	2.873
1BLN	D_ARG_38	NH2	D_GLU_46	OE1	2.870
1BLN	D_ARG_38	NH2	D_ASP_86	OD1	3.962
1BLN	D_LYS_64	NZ	D_ASP_61	OD1	2.496
1BLN	D_ARG_66	NH1	D_ASP_86	OD1	3.322
1BLN	D_ARG_66	NH1	D_ASP_86	OD2	3.365
1BLN	D_ARG_66	NH2	D_ASP_86	OD1	3.949
1BLN	D_ARG_66	NH2	D_ASP_86	OD2	2.588
1BLN	D_LYS_75	NZ	D_ASP_72	OD1	2.846
1BLN	D_LYS_75	NZ	D_ASP_72	OD2	2.946
1BLN	D_ARG_83	NH2	D_GLU_85	OE2	2.754
1BLN	D_LYS_218	NZ	D_ASP_220	OD1	2.806
1BLN	D_LYS_218	NZ	D_ASP_220	OD2	2.614
1BLN	D_LYS_221	NZ	C_GLU_123	OE2	2.694
1BLN	D_LYS_222	NZ	D_GLU_226	OE1	2.616
1BLN	D_LYS_222	NZ	D_GLU_226	OE2	2.583

Table 19: 1BLN-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1BQL	L_LYS_44	NZ	H_ASP_104	OD1	3.995
1BQL	L_ARG_45	NH2	H_ASP_104	OD2	3.212
1BQL	L_ARG_60	NH2	L_ASP_81	OD1	2.877
1BQL	L_ARG_106	NH2	L_ASP_168	OD1	2.775
1BQL	L_ARG_106	NH2	L_ASP_168	OD2	3.565
1BQL	L_LYS_147	NZ	L_GLU_193	OE1	3.381
1BQL	L_LYS_147	NZ	L_GLU_193	OE2	3.056
1BQL	L_LYS_167	NZ	L_ASP_165	OD1	3.577
1BQL	L_ARG_186	NH2	L_ASP_182	OD2	3.759
1BQL	L_HIS_187	ND1	L_ASP_149	OD2	3.204
1BQL	H_LYS_38	NZ	H_GLU_46	OE2	3.708
1BQL	H_LYS_67	NZ	H_ASP_90	OD1	3.576
1BQL	H_LYS_67	NZ	H_ASP_90	OD2	2.891
1BQL	H_LYS_208	NZ	H_ASP_210	OD1	3.394
1BQL	H_LYS_211	NZ	L_GLU_121	OE1	2.714
1BQL	H_LYS_211	NZ	L_GLU_121	OE2	2.963
1BQL	Y_LYS_1	NZ	Y_GLU_7	OE1	2.931
1BQL	Y_LYS_1	NZ	Y_GLU_7	OE2	3.316
1BQL	Y_LYS_13	NZ	Y_ASP_18	OD2	3.337
1BQL	Y_ARG_45	NH1	H_GLU_50	OE1	3.800
1BQL	Y_ARG_45	NH1	H_GLU_50	OE2	2.920
1BQL	Y_LYS_68	NZ	H_GLU_50	OE1	3.561
1BQL	Y_LYS_97	NZ	Y_ASP_101	OD1	2.891
1BQL	Y_ARG_125	NH2	Y_ASP_119	OD2	2.588

Table 20: 1BQL-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1BVK	A_ARG_24	NH1	A_ASP_70	OD1	2.987
1BVK	A_ARG_61	NH2	A_GLU_81	OE1	3.459
1BVK	A_ARG_61	NH2	A_ASP_82	OD1	2.453
1BVK	A_ARG_61	NH2	A_ASP_82	OD2	3.255
1BVK	A_ARG_96	NH2	B_GLU_98	OE1	2.978
1BVK	A_ARG_96	NH2	B_GLU_98	OE2	2.932
1BVK	B_ARG_38	NH1	B_ASP_89	OD1	2.858
1BVK	B_ARG_38	NH2	B_GLU_46	OE1	3.400
1BVK	B_ARG_38	NH2	B_GLU_46	OE2	3.917
1BVK	B_ARG_38	NH2	B_ASP_89	OD1	3.415
1BVK	B_ARG_66	NH1	B_ASP_89	OD1	3.789
1BVK	B_ARG_66	NH1	B_ASP_89	OD2	2.919
1BVK	B_ARG_66	NH2	B_ASP_89	OD1	2.669
1BVK	B_ARG_66	NH2	B_ASP_89	OD2	3.080
1BVK	B_ARG_97	NH2	B_ASP_104	OD1	3.302
1BVK	B_ARG_97	NH2	B_ASP_104	OD2	3.220
1BVK	B_ARG_102	NH1	B_ASP_100	OD2	3.508
1BVK	B_ARG_102	NH2	B_ASP_100	OD2	3.959
1BVK	C_ARG_61	NH1	C_ASP_48	OD2	2.726
1BVK	C_ARG_68	NH1	C_ASP_66	OD2	3.814
1BVK	C_ARG_125	NH1	C_ASP_119	OD2	3.413
1BVK	C_ARG_125	NH2	C_ASP_119	OD2	2.659
1BVK	D_ARG_24	NH1	D_ASP_70	OD1	3.898
1BVK	D_ARG_24	NH1	D_ASP_70	OD2	3.517
1BVK	D_ARG_61	NH1	D_GLU_81	OE1	3.485
1BVK	D_ARG_61	NH1	D_GLU_81	OE2	3.564
1BVK	D_ARG_61	NH2	D_GLU_81	OE1	2.809
1BVK	D_ARG_61	NH2	D_GLU_81	OE2	3.799
1BVK	D_ARG_61	NH2	D_ASP_82	OD1	2.873
1BVK	D_ARG_61	NH2	D_ASP_82	OD2	3.655
1BVK	D_ARG_96	NH2	E_GLU_98	OE1	2.525
1BVK	D_ARG_96	NH2	E_GLU_98	OE2	2.753
1BVK	E_ARG_38	NH1	E_ASP_89	OD1	3.089
1BVK	E_ARG_38	NH2	E_GLU_46	OE1	3.613
1BVK	E_ARG_38	NH2	E_GLU_46	OE2	3.594
1BVK	E_ARG_38	NH2	E_ASP_89	OD1	3.476
1BVK	E_ARG_66	NH1	E_ASP_89	OD1	3.924
1BVK	E_ARG_66	NH1	E_ASP_89	OD2	2.743
1BVK	E_ARG_66	NH2	E_ASP_89	OD1	3.027
1BVK	E_ARG_66	NH2	E_ASP_89	OD2	3.167
1BVK	E_ARG_97	NH2	E_ASP_104	OD1	3.359
1BVK	E_ARG_97	NH2	E_ASP_104	OD2	2.447
1BVK	E_ARG_102	NH1	E_ASP_100	OD2	3.374
1BVK	E_ARG_102	NH2	E_ASP_100	OD2	3.788
1BVK	F_LYS_1	NZ	F_GLU_7	OE2	2.724
1BVK	F_LYS_13	NZ	F_ASP_18	OD2	3.816
1BVK	F_ARG_61	NH1	F_ASP_48	OD2	3.232
1BVK	F_ARG_125	NH1	F_ASP_119	OD1	3.126
1BVK	F_ARG_125	NH1	F_ASP_119	OD2	2.577
1BVK	F_ARG_125	NH2	F_ASP_119	OD2	2.733

Table 21: 1BVK-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1C08	A_ARG_61	NH1	A_GLU_79	OE1	3.359
1C08	A_ARG_61	NH1	A_GLU_79	OE2	3.299
1C08	A_ARG_61	NH2	A_GLU_79	OE1	3.600
1C08	A_ARG_61	NH2	A_GLU_81	OE2	3.058
1C08	A_ARG_61	NH2	A_ASP_82	OD1	2.615
1C08	A_ARG_61	NH2	A_ASP_82	OD2	3.483
1C08	A_LYS_103	NZ	A_GLU_105	OE2	3.843
1C08	B_ARG_38	NH1	B_ASP_89	OD1	2.821
1C08	B_ARG_38	NH2	B_GLU_46	OE1	2.693
1C08	B_ARG_38	NH2	B_ASP_89	OD1	3.615
1C08	B_ARG_66	NH1	B_ASP_89	OD1	3.916
1C08	B_ARG_66	NH1	B_ASP_89	OD2	3.160
1C08	B_ARG_66	NH2	B_ASP_89	OD1	3.080
1C08	B_ARG_66	NH2	B_ASP_89	OD2	3.629
1C08	B_LYS_75	NZ	B_ASP_72	OD2	2.822
1C08	C_LYS_1	NZ	C_GLU_7	OE1	3.861
1C08	C_LYS_1	NZ	C_GLU_7	OE2	2.619
1C08	C_ARG_61	NH1	C_ASP_48	OD2	2.684
1C08	C_ARG_61	NH2	C_ASP_48	OD2	3.901
1C08	C_LYS_97	NZ	B_ASP_32	OD1	2.620
1C08	C_LYS_97	NZ	B_ASP_32	OD2	3.999
1C08	C_LYS_97	NZ	B_ASP_99	OD2	2.365
1C08	C_ARG_125	NH1	C_ASP_119	OD2	3.458
1C08	C_ARG_125	NH2	C_ASP_119	OD1	3.749
1C08	C_ARG_125	NH2	C_ASP_119	OD2	3.808

Table 22: 1C08-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1C12	A_ARG_61	NH1	A_GLU_79	OE1	3.872
1C12	A_ARG_61	NH1	A_GLU_79	OE2	3.629
1C12	A_ARG_61	NH1	A_GLU_81	OE2	3.588
1C12	A_ARG_61	NH1	A_ASP_82	OD1	3.976
1C12	A_ARG_61	NH2	A_ASP_82	OD1	2.627
1C12	A_ARG_61	NH2	A_ASP_82	OD2	3.162
1C12	A_LYS_103	NZ	A_ASP_85	OD1	2.711
1C12	A_LYS_103	NZ	A_ASP_85	OD2	3.993
1C12	A_LYS_147	NZ	A_GLU_154	OE2	3.218
1C12	A_LYS_149	NZ	A_GLU_154	OE1	3.689
1C12	A_ARG_155	NH1	A_GLU_185	OE1	3.418
1C12	A_ARG_155	NH2	A_GLU_185	OE1	3.302
1C12	A_LYS_169	NZ	A_ASP_167	OD1	3.892
1C12	A_ARG_188	NH1	A_ASP_184	OD1	3.647
1C12	A_ARG_188	NH1	A_ASP_184	OD2	3.352
1C12	A_HIS_189	ND1	A_ASP_151	OD2	3.592
1C12	A_LYS_199	NZ	A_ASP_143	OD2	3.366
1C12	A_ARG_211	NH2	A_GLU_187	OE2	3.347
1C12	B_ARG_338	NH1	B_GLU_346	OE2	2.575
1C12	B_ARG_338	NH2	B_ASP_386	OD1	2.668
1C12	B_ARG_366	NH1	B_ASP_386	OD1	2.858
1C12	B_ARG_366	NH1	B_ASP_386	OD2	3.220
1C12	B_ARG_366	NH2	B_ASP_386	OD1	3.966
1C12	B_ARG_366	NH2	B_ASP_386	OD2	2.872
1C12	B_LYS_508	NZ	A_GLU_123	OE2	3.314

Table 23: 1C12-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1CE1	L_ARG_61	NH2	L_GLU_81	OE1	3.727
1CE1	L_ARG_61	NH2	L_ASP_82	OD1	2.705
1CE1	L_ARG_61	NH2	L_ASP_82	OD2	3.700
1CE1	L_ARG_94	NH2	H_GLU_61	OE2	3.979
1CE1	L_ARG_96	NH1	H_GLU_101	OE1	2.707
1CE1	L_ARG_96	NH1	H_GLU_101	OE2	3.562
1CE1	L_ARG_96	NH2	H_GLU_101	OE1	3.509
1CE1	L_ARG_96	NH2	H_GLU_101	OE2	2.787
1CE1	L_LYS_103	NZ	L_GLU_105	OE1	3.913
1CE1	L_LYS_149	NZ	L_GLU_195	OE2	3.867
1CE1	L_LYS_188	NZ	L_ASP_185	OD1	3.892
1CE1	H_ARG_38	NH1	H_ASP_92	OD1	2.855
1CE1	H_ARG_38	NH2	H_GLU_46	OE1	2.954
1CE1	H_ARG_38	NH2	H_ASP_92	OD1	3.724
1CE1	H_ARG_52	NH1	H_GLU_61	OE2	3.297
1CE1	H_ARG_52	NH2	H_GLU_61	OE2	2.740
1CE1	H_ARG_52	NH2	P_ASP_7	OD1	3.481
1CE1	H_LYS_56	NZ	P_ASP_7	OD2	2.951
1CE1	H_ARG_69	NH1	H_ASP_92	OD1	3.674
1CE1	H_ARG_69	NH1	H_ASP_92	OD2	2.964
1CE1	H_ARG_69	NH2	H_ASP_92	OD1	2.906
1CE1	H_ARG_69	NH2	H_ASP_92	OD2	3.491
1CE1	H_ARG_100	NH2	H_ASP_109	OD1	3.721
1CE1	H_ARG_100	NH2	H_ASP_109	OD2	2.688
1CE1	H_LYS_218	NZ	H_GLU_220	OE2	3.210

Table 24: 1CE1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1CFS	A_ARG_61	NH1	A_GLU_79	OE1	3.782
1CFS	A_ARG_61	NH1	A_ASP_82	OD1	2.689
1CFS	A_ARG_61	NH1	A_ASP_82	OD2	2.385
1CFS	A_ARG_61	NH2	A_GLU_79	OE1	3.368
1CFS	A_LYS_147	NZ	A_GLU_154	OE2	3.751
1CFS	A_LYS_149	NZ	A_GLU_195	OE1	3.919
1CFS	A_LYS_149	NZ	A_GLU_195	OE2	2.427
1CFS	A_HIS_189	ND1	A_ASP_151	OD2	3.201
1CFS	A_LYS_199	NZ	A_ASP_110	OD2	2.468
1CFS	A_ARG_211	NH2	A_GLU_187	OE2	3.817
1CFS	B_LYS_19	NZ	B_GLU_82	OE1	2.420
1CFS	B_LYS_19	NZ	B_GLU_82	OE2	3.235
1CFS	B_HIS_35	NE2	B_GLU_33	OE1	3.092
1CFS	B_LYS_38	NZ	B_ASP_90	OD1	3.977
1CFS	B_LYS_63	NZ	B_GLU_46	OE2	2.435
1CFS	B_LYS_67	NZ	B_ASP_90	OD2	3.258
1CFS	B_ARG_98	NH1	B_ASP_100	OD1	3.172
1CFS	B_ARG_98	NH1	B_ASP_100	OD2	2.621
1CFS	B_LYS_99	NZ	B_GLU_33	OE1	3.391
1CFS	B_LYS_207	NZ	A_GLU_123	OE1	3.526
1CFS	B_ARG_212	NH2	B_GLU_210	OE1	3.742

Table 25: 1CFS-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1CFT	A_ARG.61	NH1	A_GLU.79	OE1	3.018
1CFT	A_ARG.61	NH1	A_GLU.79	OE2	2.933
1CFT	A_ARG.61	NH1	A_ASP.82	OD1	3.900
1CFT	A_ARG.61	NH1	A_ASP.82	OD2	3.509
1CFT	A_ARG.61	NH2	A_ASP.82	OD1	3.453
1CFT	A_LYS.103	NZ	A_ASP.105	OD1	3.879
1CFT	A_LYS.103	NZ	A_ASP.105	OD2	3.379
1CFT	A_LYS.149	NZ	A_GLU.195	OE1	3.740
1CFT	A_LYS.149	NZ	A_GLU.195	OE2	2.938
1CFT	A_ARG.155	NH1	A_GLU.185	OE2	3.873
1CFT	A_ARG.155	NH2	A_GLU.185	OE1	3.494
1CFT	A_ARG.155	NH2	A_GLU.185	OE2	2.450
1CFT	A_LYS.183	NZ	A_GLU.187	OE1	3.152
1CFT	A_LYS.183	NZ	A_GLU.187	OE2	3.103
1CFT	A_HIS.189	ND1	A_ASP.151	OD2	2.935
1CFT	B_HIS.35	NE2	B_GLU.33	OE1	2.890
1CFT	B_LYS.38	NZ	B_ASP.90	OD1	3.646
1CFT	B_LYS.63	NZ	B_GLU.46	OE1	3.173
1CFT	B_LYS.63	NZ	B_GLU.46	OE2	3.453
1CFT	B_LYS.67	NZ	B_ASP.90	OD1	3.866
1CFT	B_LYS.67	NZ	B_ASP.90	OD2	2.897
1CFT	B_ARG.98	NH2	B_ASP.100	OD1	3.436
1CFT	B_ARG.98	NH2	B_ASP.100	OD2	2.735
1CFT	B_LYS.99	NZ	B_GLU.33	OE1	2.555
1CFT	B_LYS.204	NZ	B_ASP.206	OD2	3.553
1CFT	B_LYS.207	NZ	A_GLU.123	OE1	2.550
1CFT	B_LYS.208	NZ	B_GLU.210	OE2	2.675
1CFT	C_LYS.2	NZ	A_ASP.92	OD1	2.682

Table 26: 1CFT-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1CG9	A_HIS_3	ND1	A_ASP_29	OD2	2.918
1CG9	A_ARG_6	NH1	A_ASP_102	OD1	3.165
1CG9	A_ARG_6	NH2	A_ASP_102	OD1	2.958
1CG9	A_ARG_6	NH2	A_ASP_102	OD2	3.809
1CG9	A_ARG_14	NH1	A_ASP_39	OD1	3.895
1CG9	A_ARG_14	NH1	A_ASP_39	OD2	3.383
1CG9	A_ARG_14	NH2	A_ASP_39	OD1	2.876
1CG9	A_ARG_14	NH2	A_ASP_39	OD2	3.696
1CG9	A_ARG_17	NH1	B_ASP_35	OD2	3.201
1CG9	A_ARG_17	NH2	B_ASP_35	OD1	3.038
1CG9	A_ARG_17	NH2	B_ASP_35	OD2	3.401
1CG9	A_ARG_21	NH2	A_ASP_37	OD1	3.415
1CG9	A_ARG_21	NH2	A_ASP_37	OD2	2.852
1CG9	A_ARG_35	NH1	A_GLU_46	OE1	3.005
1CG9	A_ARG_35	NH1	A_GLU_46	OE2	3.637
1CG9	A_ARG_35	NH2	A_ASP_37	OD2	3.660
1CG9	A_ARG_44	NH2	A_GLU_46	OE2	3.936
1CG9	A_ARG_48	NH1	A_GLU_46	OE1	3.350
1CG9	A_ARG_48	NH2	A_GLU_46	OE1	3.509
1CG9	A_ARG_48	NH2	B_ASP_54	OD1	3.456
1CG9	A_ARG_48	NH2	B_ASP_54	OD2	3.762
1CG9	A_ARG_82	NH1	A_GLU_89	OE1	2.878
1CG9	A_ARG_82	NH1	A_GLU_89	OE2	2.767
1CG9	A_HIS_93	ND1	A_ASP_119	OD1	3.615
1CG9	A_HIS_93	ND1	A_ASP_119	OD2	2.882
1CG9	A_ARG_111	NH2	A_ASP_102	OD2	3.428
1CG9	A_HIS_113	NE2	A_ASP_102	OD2	2.935
1CG9	A_ARG_151	NH2	A_GLU_154	OE1	3.687
1CG9	A_ARG_151	NH2	A_GLU_154	OE2	3.160
1CG9	A_ARG_169	NH2	A_GLU_166	OE1	3.233
1CG9	A_ARG_170	NH2	A_GLU_166	OE2	3.714
1CG9	A_HIS_191	NE2	A_GLU_254	OE1	3.499
1CG9	A_HIS_191	NE2	A_GLU_254	OE2	3.158
1CG9	A_HIS_192	ND1	B_ASP_99	OD2	3.812
1CG9	A_ARG_256	NH1	A_ASP_220	OD2	2.755
1CG9	A_ARG_256	NH2	A_GLU_253	OE1	2.835
1CG9	B_LYS_7	NZ	A_GLU_232	OE1	3.887
1CG9	B_ARG_46	NH1	B_GLU_48	OE2	3.451
1CG9	B_ARG_82	NH2	B_ASP_39	OD2	3.296

Table 27: 1CG9-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1CLO	L_ARG_61	NH2	L_GLU_81	OE2	3.507
1CLO	L_ARG_61	NH2	L_ASP_82	OD1	2.686
1CLO	L_ARG_61	NH2	L_ASP_82	OD2	3.628
1CLO	L_LYS_107	NZ	L_GLU_17	OE2	3.193
1CLO	L_LYS_147	NZ	L_GLU_154	OE1	2.893
1CLO	L_LYS_149	NZ	L_GLU_195	OE1	2.730
1CLO	L_LYS_183	NZ	L_GLU_187	OE1	3.637
1CLO	L_ARG_188	NH2	L_ASP_184	OD2	3.790
1CLO	L_HIS_189	ND1	L_ASP_151	OD2	3.698
1CLO	L_HIS_189	NE2	L_GLU_185	OE1	3.878
1CLO	L_HIS_189	NE2	L_GLU_185	OE2	3.586
1CLO	L_LYS_199	NZ	L_ASP_110	OD1	3.988
1CLO	H_ARG_38	NH1	H_ASP_86	OD1	2.756
1CLO	H_ARG_38	NH2	H_GLU_46	OE1	3.383
1CLO	H_ARG_38	NH2	H_GLU_46	OE2	3.812
1CLO	H_ARG_38	NH2	H_ASP_86	OD1	3.644
1CLO	H_ARG_66	NH1	H_ASP_86	OD1	3.875
1CLO	H_ARG_66	NH1	H_ASP_86	OD2	3.046
1CLO	H_ARG_66	NH2	H_ASP_86	OD1	2.884
1CLO	H_ARG_66	NH2	H_ASP_86	OD2	3.391
1CLO	H_ARG_94	NH2	H_ASP_101	OD1	3.855
1CLO	H_ARG_94	NH2	H_ASP_101	OD2	2.771
1CLO	H_ARG_99	NH2	H_GLU_58	OE1	2.867
1CLO	H_ARG_99	NH2	H_GLU_58	OE2	3.927

Table 28: 1CLO-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1CLY	L_ARG_24	NH2	L_ASP_70	OD1	3.806
1CLY	L_ARG_24	NH2	L_ASP_70	OD2	2.805
1CLY	L_ARG_54	NH2	L_ASP_60	OD1	3.787
1CLY	L_ARG_61	NH1	L_ASP_82	OD1	2.802
1CLY	L_ARG_61	NH1	L_ASP_82	OD2	3.085
1CLY	L_LYS_188	NZ	L_ASP_185	OD1	3.969
1CLY	L_HIS_189	ND1	L_ASP_151	OD2	3.439
1CLY	H_ARG_38	NH1	H_ASP_86	OD1	2.869
1CLY	H_ARG_38	NH2	H_GLU_46	OE1	3.344
1CLY	H_ARG_38	NH2	H_ASP_86	OD1	3.797
1CLY	H_LYS_64	NZ	H_ASP_58	OD1	2.930
1CLY	H_ARG_66	NH1	H_ASP_86	OD1	3.905
1CLY	H_ARG_66	NH1	H_ASP_86	OD2	2.752
1CLY	H_ARG_66	NH2	H_ASP_86	OD1	2.793
1CLY	H_ARG_66	NH2	H_ASP_86	OD2	3.024
1CLY	H_LYS_83	NZ	H_GLU_85	OE2	3.267

Table 29: 1CLY-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1CLZ	L_ARG_24	NH1	L_ASP_70	OD1	3.101
1CLZ	L_ARG_24	NH1	L_ASP_70	OD2	3.153
1CLZ	L_ARG_54	NH2	L_ASP_60	OD2	3.723
1CLZ	L_ARG_61	NH1	L_GLU_81	OE2	2.935
1CLZ	L_ARG_61	NH1	L_ASP_82	OD1	2.614
1CLZ	L_ARG_61	NH1	L_ASP_82	OD2	2.847
1CLZ	L_ARG_61	NH2	L_GLU_81	OE2	2.838
1CLZ	L_ARG_155	NH1	L_GLU_195	OE1	3.513
1CLZ	L_ARG_155	NH1	L_GLU_195	OE2	2.873
1CLZ	L_ARG_155	NH2	L_GLU_195	OE2	3.852
1CLZ	L_LYS_183	NZ	L_ASP_184	OD1	3.131
1CLZ	L_LYS_183	NZ	L_ASP_184	OD2	3.972
1CLZ	L_LYS_199	NZ	L_ASP_110	OD1	3.811
1CLZ	L_LYS_207	NZ	H_ASP_130	OD1	3.119
1CLZ	L_LYS_207	NZ	H_ASP_130	OD2	3.445
1CLZ	H_ARG_38	NH1	H_GLU_85	OE2	3.982
1CLZ	H_ARG_38	NH1	H_ASP_86	OD1	2.887
1CLZ	H_ARG_38	NH2	H_GLU_46	OE1	2.799
1CLZ	H_ARG_38	NH2	H_GLU_46	OE2	3.386
1CLZ	H_ARG_38	NH2	H_GLU_85	OE2	3.329
1CLZ	H_LYS_64	NZ	H_ASP_61	OD1	3.149
1CLZ	H_ARG_66	NH1	H_ASP_86	OD2	2.828
1CLZ	H_ARG_66	NH2	H_ASP_86	OD1	3.003
1CLZ	H_ARG_66	NH2	H_ASP_86	OD2	2.860
1CLZ	H_LYS_75	NZ	H_ASP_72	OD1	3.567
1CLZ	H_LYS_75	NZ	H_ASP_72	OD2	3.842
1CLZ	H_ARG_172	NH1	L_ASP_170	OD2	3.885
1CLZ	H_ARG_172	NH2	L_ASP_170	OD2	3.384
1CLZ	H_LYS_221	NZ	L_GLU_123	OE1	3.750
1CLZ	H_LYS_221	NZ	L_GLU_123	OE2	2.509

Table 30: 1CLZ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1CS9-1	A_ARG_5	NH1	A_GLU_7	OE1	3.450
1CS9-1	A_ARG_5	NH2	A_GLU_7	OE1	3.678

Table 31: 1CS9-1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1CS9-3	A_ARG_5	NH1	A_GLU_7	OE2	3.468
1CS9-3	A_ARG_5	NH2	A_GLU_7	OE1	3.563
1CS9-3	A_ARG_5	NH2	A_GLU_7	OE2	3.412

Table 32: 1CS9-3-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1CS9-6	A_ARG_5	NH2	A_GLU_7	OE1	3.965
1CS9-6	A_ARG_5	NH2	A_GLU_7	OE2	3.461

Table 33: 1CS9-6-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1CT6-1	A_ARG_5	NH2	A_GLU_7	OE2	3.406

Table 34: 1CT6-1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1CT6-7	A_ARG_5	NH1	A_GLU_7	OE1	3.406
1CT6-7	A_ARG_5	NH2	A_GLU_7	OE1	3.280

Table 35: 1CT6-7-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1CZ8	V_ARG_23	NH1	W_GLU_30	OE1	3.162
1CZ8	V_ARG_23	NH1	W_GLU_30	OE2	3.558
1CZ8	V_ARG_56	NH1	V_GLU_38	OE1	2.977
1CZ8	V_ARG_56	NH1	V_GLU_38	OE2	3.581
1CZ8	V_ARG_56	NH2	V_GLU_38	OE1	3.435
1CZ8	V_ARG_82	NH1	V_GLU_42	OE1	3.541
1CZ8	V_ARG_82	NH1	V_GLU_42	OE2	3.530
1CZ8	V_ARG_82	NH2	V_GLU_42	OE1	2.378
1CZ8	V_ARG_82	NH2	V_GLU_42	OE2	3.778
1CZ8	V_LYS_84	NZ	V_GLU_44	OE1	3.578
1CZ8	V_HIS_99	NE2	V_GLU_73	OE2	3.799
1CZ8	W_ARG_23	NH1	V_GLU_30	OE1	3.011
1CZ8	W_ARG_23	NH1	V_GLU_30	OE2	3.663
1CZ8	W_ARG_56	NH1	W_GLU_38	OE1	3.539
1CZ8	W_ARG_56	NH2	W_GLU_38	OE1	2.665
1CZ8	W_ARG_82	NH1	W_GLU_42	OE1	3.515
1CZ8	W_ARG_82	NH1	W_GLU_42	OE2	3.352
1CZ8	W_ARG_82	NH2	W_GLU_42	OE1	2.236
1CZ8	W_ARG_82	NH2	W_GLU_42	OE2	3.471
1CZ8	W_LYS_84	NZ	W_GLU_44	OE1	3.728
1CZ8	W_HIS_99	NE2	W_GLU_73	OE2	3.726
1CZ8	W_ARG_105	NH1	W_GLU_103	OE1	3.814
1CZ8	W_ARG_105	NH2	W_GLU_103	OE1	3.500
1CZ8	L_ARG_61	NH2	L_GLU_81	OE1	3.328
1CZ8	L_ARG_61	NH2	L_ASP_82	OD1	3.668
1CZ8	L_ARG_61	NH2	L_ASP_82	OD2	2.923
1CZ8	L_LYS_103	NZ	L_GLU_165	OE1	3.942
1CZ8	L_LYS_103	NZ	L_GLU_165	OE2	3.656
1CZ8	L_ARG_142	NH1	L_GLU_105	OE1	3.981
1CZ8	L_ARG_142	NH2	L_GLU_105	OE1	2.514
1CZ8	L_LYS_188	NZ	L_ASP_185	OD1	3.914
1CZ8	H_HIS_31	NE2	H_ASP_28	OD1	3.613
1CZ8	H_HIS_31	NE2	H_ASP_28	OD2	3.218
1CZ8	H_ARG_38	NH1	H_ASP_90	OD1	2.960
1CZ8	H_ARG_38	NH2	H_GLU_46	OE2	3.234
1CZ8	H_ARG_67	NH1	H_ASP_90	OD1	3.710
1CZ8	H_ARG_67	NH1	H_ASP_90	OD2	2.499
1CZ8	H_ARG_67	NH2	H_ASP_90	OD1	2.930
1CZ8	H_ARG_67	NH2	H_ASP_90	OD2	3.145
1CZ8	H_ARG_87	NH1	H_GLU_89	OE2	3.671
1CZ8	H_LYS_98	NZ	H_ASP_111	OD1	3.604
1CZ8	H_LYS_153	NZ	H_ASP_154	OD1	3.169
1CZ8	H_LYS_153	NZ	H_ASP_154	OD2	3.317
1CZ8	H_LYS_219	NZ	L_GLU_123	OE1	3.027
1CZ8	H_LYS_224	NZ	L_ASP_122	OD1	2.846
1CZ8	H_LYS_224	NZ	L_ASP_122	OD2	3.185
1CZ8	X_ARG_61	NH2	X_GLU_81	OE1	2.956
1CZ8	X_ARG_61	NH2	X_ASP_82	OD1	3.979
1CZ8	X_ARG_61	NH2	X_ASP_82	OD2	3.064
1CZ8	X_LYS_103	NZ	X_GLU_165	OE1	3.796
1CZ8	X_LYS_103	NZ	X_GLU_165	OE2	3.476
1CZ8	X_LYS_183	NZ	X_GLU_187	OE1	3.233
1CZ8	X_HIS_189	ND1	X_ASP_151	OD2	2.531
1CZ8	X_ARG_211	NH1	X_GLU_187	OE2	3.961
1CZ8	X_ARG_211	NH2	X_GLU_187	OE2	3.336
1CZ8	Y_HIS_31	NE2	Y_ASP_28	OD2	2.704
1CZ8	Y_ARG_38	NH1	Y_ASP_90	OD1	2.984

1CZ8	Y_ARG_38	NH2	Y_GLU_46	OE2	3.050
1CZ8	Y_ARG_67	NH1	Y_ASP_90	OD1	3.758
1CZ8	Y_ARG_67	NH1	Y_ASP_90	OD2	2.753
1CZ8	Y_ARG_67	NH2	Y_ASP_90	OD1	3.089
1CZ8	Y_ARG_67	NH2	Y_ASP_90	OD2	3.481
1CZ8	Y_ARG_87	NH1	Y_GLU_89	OE2	3.919
1CZ8	Y_LYS_98	NZ	Y_ASP_111	OD1	3.728
1CZ8	Y_LYS_153	NZ	Y_ASP_154	OD1	3.924
1CZ8	Y_LYS_219	NZ	X_GLU_123	OE2	3.832

Table 36: 1CZ8-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1DBJ	L_ARG_61	NH1	L_ASP_82	OD1	2.891
1DBJ	L_ARG_61	NH1	L_ASP_82	OD2	2.924
1DBJ	L_LYS_149	NZ	L_GLU_195	OE2	2.903
1DBJ	L_ARG_155	NH2	L_GLU_185	OE1	3.640
1DBJ	L_LYS_183	NZ	L_GLU_187	OE1	3.039
1DBJ	L_LYS_183	NZ	L_GLU_187	OE2	3.038
1DBJ	L_ARG_188	NH1	L_GLU_185	OE1	2.980
1DBJ	L_ARG_188	NH1	L_GLU_185	OE2	3.840
1DBJ	L_HIS_189	ND1	L_ASP_151	OD1	3.098
1DBJ	L_HIS_189	ND1	L_ASP_151	OD2	3.952
1DBJ	L_HIS_189	NE2	L_GLU_185	OE2	3.171
1DBJ	H_LYS_13	NZ	H_GLU_16	OE1	3.105
1DBJ	H_LYS_46	NZ	H_ASP_62	OD2	3.771
1DBJ	H_ARG_66	NH1	H_ASP_86	OD2	2.961
1DBJ	H_ARG_66	NH2	H_ASP_86	OD1	3.477
1DBJ	H_ARG_66	NH2	H_ASP_86	OD2	3.338
1DBJ	H_LYS_83	NZ	H_GLU_85	OE1	3.571
1DBJ	H_LYS_83	NZ	H_GLU_85	OE2	3.324
1DBJ	H_ARG_94	NH2	H_ASP_101	OD1	3.264
1DBJ	H_ARG_94	NH2	H_ASP_101	OD2	2.951
1DBJ	H_LYS_221	NZ	L_GLU_123	OE1	3.386
1DBJ	H_LYS_221	NZ	L_GLU_123	OE2	2.770

Table 37: 1DBJ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1DBK	L_LYS_39	NZ	L_GLU_81	OE2	2.712
1DBK	L_ARG_61	NH1	L_ASP_82	OD1	2.915
1DBK	L_ARG_61	NH1	L_ASP_82	OD2	2.731
1DBK	L_ARG_61	NH2	L_GLU_79	OE1	3.019
1DBK	L_ARG_61	NH2	L_ASP_82	OD1	2.792
1DBK	L_ARG_61	NH2	L_ASP_82	OD2	3.954
1DBK	L_LYS_149	NZ	L_GLU_195	OE1	3.811
1DBK	L_LYS_149	NZ	L_GLU_195	OE2	3.034
1DBK	L_ARG_155	NH2	L_GLU_185	OE2	2.794
1DBK	L_LYS_169	NZ	L_ASP_167	OD1	2.955
1DBK	L_LYS_169	NZ	L_ASP_167	OD2	3.539
1DBK	L_HIS_189	ND1	L_ASP_151	OD1	3.187
1DBK	L_HIS_189	NE2	L_GLU_185	OE1	3.126
1DBK	L_HIS_189	NE2	L_GLU_185	OE2	3.082
1DBK	H_LYS_12	NZ	H_GLU_16	OE2	3.384
1DBK	H_LYS_46	NZ	H_ASP_62	OD2	3.857
1DBK	H_ARG_66	NH1	H_ASP_86	OD1	3.550
1DBK	H_ARG_66	NH2	H_ASP_86	OD1	3.122
1DBK	H_ARG_66	NH2	H_ASP_86	OD2	2.683
1DBK	H_ARG_94	NH2	H_ASP_101	OD2	3.605
1DBK	H_HIS_172	ND1	L_ASP_167	OD2	3.619
1DBK	H_LYS_221	NZ	L_GLU_123	OE2	3.030

Table 38: 1DBK-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1DBM	L_ARG_61	NH1	L_ASP_82	OD1	2.913
1DBM	L_ARG_61	NH1	L_ASP_82	OD2	3.927
1DBM	L_LYS_103	NZ	L_GLU_105	OE1	2.993
1DBM	L_LYS_142	NZ	L_GLU_105	OE1	2.864
1DBM	L_LYS_147	NZ	L_GLU_154	OE2	3.864
1DBM	L_LYS_149	NZ	L_GLU_195	OE1	3.140
1DBM	L_LYS_149	NZ	L_GLU_195	OE2	3.919
1DBM	L_ARG_155	NH2	L_GLU_185	OE2	2.959
1DBM	L_LYS_183	NZ	L_GLU_187	OE1	3.017
1DBM	L_LYS_183	NZ	L_GLU_187	OE2	2.825
1DBM	L_HIS_189	ND1	L_ASP_151	OD1	3.307
1DBM	L_HIS_189	ND1	L_ASP_151	OD2	3.881
1DBM	L_HIS_189	NE2	L_ASP_151	OD1	3.334
1DBM	L_HIS_189	NE2	L_ASP_151	OD2	2.747
1DBM	L_LYS_199	NZ	L_ASP_110	OD1	3.963
1DBM	L_LYS_199	NZ	L_ASP_110	OD2	3.388
1DBM	H_LYS_12	NZ	H_GLU_16	OE1	3.842
1DBM	H_LYS_46	NZ	H_ASP_62	OD1	3.760
1DBM	H_LYS_46	NZ	H_ASP_62	OD2	2.943
1DBM	H_ARG_66	NH2	H_ASP_86	OD1	2.873
1DBM	H_ARG_66	NH2	H_ASP_86	OD2	2.647
1DBM	H_ARG_94	NH1	H_ASP_101	OD1	3.264
1DBM	H_ARG_94	NH1	H_ASP_101	OD2	2.957
1DBM	H_LYS_218	NZ	H_ASP_220	OD1	2.773
1DBM	H_LYS_218	NZ	H_ASP_220	OD2	3.444
1DBM	H_LYS_221	NZ	L_GLU_123	OE2	3.277

Table 39: 1DBM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1DEE	A_ARG_24	NH1	D_GLU_1555	OE1	3.510
1DEE	A_ARG_24	NH2	A_ASP_70	OD2	3.825
1DEE	A_ARG_61	NH1	A_GLU_81	OE2	3.998
1DEE	A_ARG_61	NH2	A_GLU_81	OE2	3.015
1DEE	A_ARG_61	NH2	A_ASP_82	OD1	2.929
1DEE	A_ARG_61	NH2	A_ASP_82	OD2	3.738
1DEE	A_ARG_142	NH1	A_GLU_105	OE2	3.645
1DEE	A_ARG_142	NH2	A_GLU_105	OE2	3.806
1DEE	A_LYS_149	NZ	A_GLU_195	OE1	3.119
1DEE	A_LYS_183	NZ	A_GLU_187	OE1	3.333
1DEE	A_LYS_183	NZ	A_GLU_187	OE2	3.384
1DEE	A_HIS_189	ND1	A_ASP_151	OD2	3.212
1DEE	B_ARG_538	NH1	B_ASP_590	OD1	2.876
1DEE	B_ARG_538	NH2	B_GLU_546	OE1	3.449
1DEE	B_ARG_538	NH2	B_ASP_590	OD1	3.533
1DEE	B_ARG_567	NH1	B_ASP_590	OD1	3.757
1DEE	B_ARG_567	NH1	B_ASP_590	OD2	2.653
1DEE	B_ARG_567	NH2	B_ASP_590	OD1	2.770
1DEE	B_ARG_567	NH2	B_ASP_590	OD2	3.245
1DEE	B_ARG_587	NH2	B_GLU_589	OE2	3.287
1DEE	B_ARG_587	NH2	B_ASP_590	OD1	3.980
1DEE	B_LYS_598	NZ	B_ASP_609	OD1	3.328
1DEE	B_LYS_598	NZ	B_ASP_609	OD2	2.849
1DEE	B_LYS_663	NZ	B_ASP_669	OD1	2.882
1DEE	B_LYS_663	NZ	B_ASP_669	OD2	3.035
1DEE	B_LYS_665	NZ	B_GLU_704	OE1	2.806
1DEE	B_LYS_665	NZ	B_GLU_704	OE2	3.764
1DEE	B_ARG_674	NH1	A_ASP_167	OD2	3.579
1DEE	B_LYS_684	NZ	B_ASP_652	OD2	3.529
1DEE	B_HIS_705	NE2	B_ASP_720	OD2	3.635
1DEE	B_LYS_719	NZ	A_GLU_123	OE1	2.730
1DEE	B_LYS_719	NZ	A_GLU_123	OE2	3.113
1DEE	C_ARG_1024	NH1	C_ASP_1070	OD1	3.035
1DEE	C_ARG_1024	NH1	C_ASP_1070	OD2	3.310
1DEE	C_ARG_1061	NH2	C_GLU_1081	OE2	3.124
1DEE	C_ARG_1061	NH2	C_ASP_1082	OD1	2.857
1DEE	C_ARG_1061	NH2	C_ASP_1082	OD2	3.774
1DEE	C_LYS_1103	NZ	C_GLU_1165	OE1	3.566
1DEE	C_LYS_1103	NZ	C_GLU_1165	OE2	2.924
1DEE	C_LYS_1107	NZ	C_ASP_1017	OD2	3.997
1DEE	C_LYS_1149	NZ	C_GLU_1195	OE1	3.072
1DEE	C_LYS_1183	NZ	C_GLU_1187	OE2	3.540
1DEE	C_LYS_1188	NZ	C_ASP_1185	OD2	3.897
1DEE	C_HIS_1189	ND1	C_ASP_1151	OD2	2.785
1DEE	D_ARG_1519	NH1	G_ASP_1834	OD1	3.122
1DEE	D_ARG_1519	NH1	G_ASP_1834	OD2	3.064
1DEE	D_ARG_1519	NH2	G_ASP_1834	OD1	3.684
1DEE	D_ARG_1519	NH2	G_ASP_1834	OD2	2.875
1DEE	D_ARG_1538	NH1	D_ASP_1590	OD1	2.724
1DEE	D_ARG_1538	NH2	D_GLU_1546	OE1	3.584
1DEE	D_ARG_1538	NH2	D_GLU_1546	OE2	3.849
1DEE	D_ARG_1538	NH2	D_ASP_1590	OD1	3.421
1DEE	D_LYS_1565	NZ	D_ASP_1562	OD1	2.918
1DEE	D_ARG_1567	NH1	D_ASP_1590	OD1	3.432
1DEE	D_ARG_1567	NH2	D_ASP_1590	OD1	2.922
1DEE	D_ARG_1567	NH2	D_ASP_1590	OD2	2.448
1DEE	D_LYS_1576	NZ	D_ASP_1573	OD2	3.953

1DEE	D_ARG.1587	NH1	D_GLU.1589	OE2	3.755
1DEE	D_ARG.1587	NH2	D_GLU.1589	OE2	2.965
1DEE	D_LYS.1598	NZ	D_ASP.1609	OD1	3.236
1DEE	D_LYS.1598	NZ	D_ASP.1609	OD2	3.057
1DEE	D_LYS.1663	NZ	D_ASP.1669	OD1	3.393
1DEE	D_LYS.1663	NZ	D_ASP.1669	OD2	3.077
1DEE	D_LYS.1665	NZ	D_GLU.1704	OE1	2.915
1DEE	D_ARG.1674	NH1	C_ASP.1167	OD2	3.619
1DEE	D_HIS.1705	NE2	D_ASP.1720	OD2	3.228
1DEE	D_LYS.1719	NZ	C_GLU.1123	OE1	3.687
1DEE	D_LYS.1719	NZ	C_GLU.1123	OE2	2.890
1DEE	E_ARG.2024	NH1	E_ASP.2070	OD1	3.455
1DEE	E_ARG.2024	NH1	E_ASP.2070	OD2	3.446
1DEE	E_ARG.2024	NH2	E_ASP.2070	OD2	3.331
1DEE	E_ARG.2061	NH2	E_GLU.2081	OE2	3.103
1DEE	E_ARG.2061	NH2	E_ASP.2082	OD1	3.070
1DEE	E_ARG.2061	NH2	E_ASP.2082	OD2	3.805
1DEE	E_ARG.2142	NH1	E_GLU.2165	OE2	3.927
1DEE	E_LYS.2149	NZ	E_GLU.2195	OE1	2.878
1DEE	E_LYS.2149	NZ	E_GLU.2195	OE2	3.165
1DEE	E_LYS.2183	NZ	E_GLU.2187	OE1	2.894
1DEE	E_LYS.2183	NZ	E_GLU.2187	OE2	3.210
1DEE	E_HIS.2189	ND1	E_ASP.2151	OD2	3.099
1DEE	F_ARG.2519	NH1	H_ASP.2834	OD1	3.463
1DEE	F_ARG.2519	NH1	H_ASP.2834	OD2	2.731
1DEE	F_ARG.2519	NH2	H_ASP.2834	OD1	3.523
1DEE	F_ARG.2519	NH2	H_ASP.2834	OD2	3.444
1DEE	F_ARG.2538	NH1	F_ASP.2590	OD1	2.942
1DEE	F_ARG.2538	NH2	F_GLU.2546	OE1	3.386
1DEE	F_ARG.2538	NH2	F_GLU.2546	OE2	3.004
1DEE	F_LYS.2565	NZ	F_ASP.2562	OD1	3.402
1DEE	F_ARG.2567	NH1	F_ASP.2590	OD1	3.677
1DEE	F_ARG.2567	NH2	F_ASP.2590	OD1	2.797
1DEE	F_ARG.2567	NH2	F_ASP.2590	OD2	2.401
1DEE	F_ARG.2587	NH2	F_GLU.2589	OE2	3.479
1DEE	F_LYS.2598	NZ	F_ASP.2609	OD1	3.297
1DEE	F_LYS.2598	NZ	F_ASP.2609	OD2	2.926
1DEE	F_LYS.2663	NZ	F_ASP.2669	OD1	3.683
1DEE	F_LYS.2663	NZ	F_ASP.2669	OD2	2.643
1DEE	F_LYS.2665	NZ	F_GLU.2704	OE1	3.853
1DEE	F_LYS.2665	NZ	F_GLU.2704	OE2	3.766
1DEE	F_ARG.2674	NH1	E_ASP.2167	OD2	3.989
1DEE	F_HIS.2705	ND1	F_ASP.2720	OD2	3.943
1DEE	F_HIS.2705	NE2	F_ASP.2720	OD2	2.896
1DEE	F_LYS.2719	NZ	E_GLU.2123	OE1	2.882
1DEE	F_LYS.2719	NZ	E_GLU.2123	OE2	3.779
1DEE	G_LYS.1848	NZ	G_GLU.1845	OE1	3.421
1DEE	G_LYS.1848	NZ	G_GLU.1845	OE2	3.954
1DEE	H_ARG.2825	NH1	H_GLU.2822	OE2	2.870

Table 40: 1DEE-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1DLF	L_ARG_61	NH1	L_GLU_79	OE2	3.180
1DLF	L_ARG_61	NH1	L_GLU_81	OE2	3.784
1DLF	L_ARG_61	NH2	L_GLU_79	OE1	3.855
1DLF	L_ARG_61	NH2	L_GLU_79	OE2	3.835
1DLF	L_ARG_61	NH2	L_GLU_81	OE2	2.913
1DLF	L_ARG_61	NH2	L_ASP_82	OD1	2.721
1DLF	L_ARG_61	NH2	L_ASP_82	OD2	3.431
1DLF	L_LYS_103	NZ	L_GLU_105	OE1	3.806
1DLF	H_ARG_38	NH1	H_GLU_85	OE2	3.709
1DLF	H_ARG_38	NH1	H_ASP_86	OD1	2.859
1DLF	H_ARG_38	NH2	H_GLU_46	OE2	3.187
1DLF	H_ARG_38	NH2	H_GLU_85	OE2	2.874
1DLF	H_ARG_38	NH2	H_ASP_86	OD1	3.920
1DLF	H_HIS_55	NE2	H_ASP_73	OD2	3.282
1DLF	H_ARG_66	NH1	H_ASP_86	OD1	3.873
1DLF	H_ARG_66	NH1	H_ASP_86	OD2	2.756
1DLF	H_ARG_66	NH2	H_GLU_85	OE2	3.284
1DLF	H_ARG_66	NH2	H_ASP_86	OD1	3.045
1DLF	H_ARG_66	NH2	H_ASP_86	OD2	3.370
1DLF	H_ARG_71	NH2	H_ASP_73	OD1	3.603

Table 41: 1DLF-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1DQD	L_ARG_60	NH2	L_GLU_80	OE1	2.987
1DQD	L_ARG_60	NH2	L_ASP_81	OD1	3.630
1DQD	L_ARG_60	NH2	L_ASP_81	OD2	2.547
1DQD	L_LYS_146	NZ	L_GLU_153	OE2	3.290
1DQD	L_LYS_148	NZ	L_GLU_194	OE1	2.964
1DQD	L_LYS_148	NZ	L_GLU_194	OE2	3.564
1DQD	L_ARG_154	NH2	L_GLU_184	OE1	2.744
1DQD	L_ARG_154	NH2	L_GLU_184	OE2	3.605
1DQD	L_ARG_187	NH1	L_ASP_183	OD1	2.725
1DQD	L_ARG_187	NH2	L_ASP_183	OD1	3.759
1DQD	L_HIS_188	ND1	L_ASP_150	OD2	2.488
1DQD	L_ARG_210	NH2	L_GLU_186	OE1	3.748
1DQD	H_ARG_38	NH1	H_GLU_46	OE2	2.968
1DQD	H_ARG_38	NH1	H_ASP_89	OD2	3.490
1DQD	H_ARG_38	NH2	H_ASP_89	OD2	2.519
1DQD	H_ARG_66	NH1	H_ASP_89	OD1	3.667
1DQD	H_ARG_66	NH1	H_ASP_89	OD2	3.034
1DQD	H_ARG_66	NH2	H_ASP_89	OD1	3.179
1DQD	H_ARG_66	NH2	H_ASP_89	OD2	3.557
1DQD	H_ARG_75	NH1	H_ASP_72	OD2	3.952
1DQD	H_LYS_217	NZ	L_GLU_122	OE2	3.953

Table 42: 1DQD-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1DQJ	A_ARG_24	NH2	A_ASP_70	OD1	3.733
1DQJ	A_ARG_61	NH2	A_GLU_81	OE1	3.324
1DQJ	A_ARG_61	NH2	A_ASP_82	OD1	2.881
1DQJ	A_ARG_61	NH2	A_ASP_82	OD2	3.607
1DQJ	A_ARG_155	NH1	A_GLU_185	OE2	3.740
1DQJ	A_ARG_155	NH2	A_GLU_185	OE2	3.256
1DQJ	A_LYS_199	NZ	A_ASP_110	OD2	3.573
1DQJ	B_ARG_38	NH1	B_GLU_46	OE1	2.669
1DQJ	B_ARG_38	NH1	B_ASP_89	OD1	3.653
1DQJ	B_ARG_38	NH2	B_ASP_89	OD1	2.527
1DQJ	B_ARG_66	NH1	B_ASP_89	OD1	3.044
1DQJ	B_ARG_66	NH1	B_ASP_89	OD2	3.584
1DQJ	B_ARG_66	NH2	B_ASP_89	OD1	3.713
1DQJ	B_ARG_66	NH2	B_ASP_89	OD2	2.977
1DQJ	B_LYS_216	NZ	B_ASP_218	OD2	3.941
1DQJ	B_LYS_219	NZ	A_GLU_123	OE2	2.598
1DQJ	C_LYS_1	NZ	C_GLU_7	OE1	3.940
1DQJ	C_LYS_1	NZ	C_GLU_7	OE2	2.753
1DQJ	C_LYS_97	NZ	B_ASP_32	OD2	2.665
1DQJ	C_ARG_125	NH2	C_ASP_119	OD1	3.333
1DQJ	C_ARG_125	NH2	C_ASP_119	OD2	2.489

Table 43: 1DQJ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1DQM	L_ARG_61	NH1	L_GLU_81	OE2	3.595
1DQM	L_ARG_61	NH1	L_ASP_82	OD1	2.747
1DQM	L_ARG_61	NH1	L_ASP_82	OD2	3.200
1DQM	L_ARG_61	NH2	L_GLU_81	OE2	3.902
1DQM	L_LYS_147	NZ	L_GLU_154	OE1	3.964
1DQM	L_LYS_147	NZ	L_GLU_195	OE2	3.903
1DQM	L_LYS_149	NZ	L_GLU_195	OE1	3.696
1DQM	L_ARG_155	NH1	L_GLU_185	OE2	3.981
1DQM	L_ARG_188	NH2	L_ASP_184	OD1	3.190
1DQM	L_HIS_189	ND1	L_ASP_151	OD2	3.171
1DQM	L_LYS_199	NZ	L_ASP_110	OD2	3.862
1DQM	L_LYS_207	NZ	H_ASP_130	OD1	3.491
1DQM	L_LYS_207	NZ	H_ASP_130	OD2	3.782
1DQM	H_ARG_38	NH1	H_GLU_46	OE1	2.699
1DQM	H_ARG_38	NH1	H_ASP_89	OD1	3.926
1DQM	H_ARG_38	NH2	H_ASP_89	OD1	2.730
1DQM	H_ARG_66	NH1	H_ASP_89	OD1	3.559
1DQM	H_ARG_66	NH1	H_ASP_89	OD2	2.987
1DQM	H_ARG_66	NH2	H_ASP_89	OD1	3.082
1DQM	H_ARG_66	NH2	H_ASP_89	OD2	3.726

Table 44: 1DQM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1DQQ	A_ARG.24	NH1	A_ASP.70	OD2	3.225
1DQQ	A_LYS.49	NZ	B_ASP.101	OD1	2.957
1DQQ	A_ARG.61	NH1	A_ASP.82	OD1	2.631
1DQQ	A_ARG.61	NH1	A_ASP.82	OD2	2.802
1DQQ	A_ARG.61	NH2	A_GLU.79	OE1	3.923
1DQQ	A_ARG.61	NH2	A_GLU.79	OE2	3.136
1DQQ	A_ARG.61	NH2	A_GLU.81	OE2	3.324
1DQQ	A_ARG.61	NH2	A_ASP.82	OD1	3.627
1DQQ	A_LYS.147	NZ	A_GLU.154	OE1	3.318
1DQQ	A_LYS.147	NZ	A_GLU.154	OE2	3.055
1DQQ	A_LYS.149	NZ	A_GLU.195	OE1	3.522
1DQQ	A_LYS.149	NZ	A_GLU.195	OE2	3.885
1DQQ	A_ARG.155	NH1	A_GLU.185	OE2	3.911
1DQQ	A_ARG.155	NH2	A_GLU.185	OE2	3.794
1DQQ	A_ARG.188	NH2	A_ASP.184	OD1	2.977
1DQQ	A_LYS.199	NZ	A_ASP.110	OD1	3.108
1DQQ	A_LYS.199	NZ	A_ASP.110	OD2	3.095
1DQQ	B_ARG.38	NH1	B_GLU.46	OE1	2.694
1DQQ	B_ARG.38	NH1	B_ASP.89	OD1	3.867
1DQQ	B_ARG.38	NH2	B_ASP.89	OD1	2.625
1DQQ	B_ARG.66	NH1	B_ASP.89	OD1	3.469
1DQQ	B_ARG.66	NH1	B_ASP.89	OD2	2.954
1DQQ	B_ARG.66	NH2	B_ASP.89	OD1	2.959
1DQQ	B_ARG.66	NH2	B_ASP.89	OD2	3.690
1DQQ	B_LYS.216	NZ	D_ASP.218	OD1	2.965
1DQQ	B_LYS.219	NZ	A_GLU.123	OE2	2.763
1DQQ	C_LYS.49	NZ	D_ASP.101	OD1	3.456
1DQQ	C_LYS.49	NZ	D_ASP.101	OD2	3.943
1DQQ	C_LYS.147	NZ	C_GLU.154	OE2	3.726
1DQQ	C_LYS.149	NZ	C_GLU.195	OE1	3.353
1DQQ	C_ARG.155	NH2	C_GLU.185	OE2	3.704
1DQQ	C_ARG.188	NH2	C_ASP.184	OD1	2.882
1DQQ	C_ARG.188	NH2	C_ASP.184	OD2	3.940
1DQQ	C_HIS.189	ND1	C_ASP.151	OD2	2.642
1DQQ	C_LYS.199	NZ	C_ASP.110	OD2	3.094
1DQQ	C_ARG.211	NH2	C_GLU.187	OE2	2.769
1DQQ	D_ARG.38	NH1	D_GLU.46	OE1	2.831
1DQQ	D_ARG.38	NH1	D_ASP.89	OD1	3.780
1DQQ	D_ARG.38	NH2	D_ASP.89	OD1	2.692
1DQQ	D_ARG.66	NH1	D_ASP.89	OD1	3.708
1DQQ	D_ARG.66	NH2	D_ASP.89	OD1	3.416
1DQQ	D_ARG.66	NH2	D_ASP.89	OD2	2.649
1DQQ	D_LYS.216	NZ	D_ASP.218	OD1	2.953
1DQQ	D_LYS.216	NZ	D_ASP.218	OD2	2.618
1DQQ	D_LYS.219	NZ	C_GLU.123	OE1	3.088

Table 45: 1DQQ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1DVF	A_ARG_61	NH2	A_GLU_81	OE2	3.091
1DVF	A_ARG_61	NH2	A_ASP_82	OD1	2.772
1DVF	A_ARG_61	NH2	A_ASP_82	OD2	3.277
1DVF	A_ARG_96	NH1	B_GLU_98	OE1	2.616
1DVF	A_ARG_96	NH1	B_GLU_98	OE2	3.746
1DVF	A_ARG_96	NH2	B_GLU_98	OE1	3.400
1DVF	A_ARG_96	NH2	B_GLU_98	OE2	2.958
1DVF	A_LYS_103	NZ	A_GLU_105	OE2	3.937
1DVF	B_ARG_38	NH1	B_ASP_89	OD1	2.871
1DVF	B_ARG_38	NH2	B_GLU_46	OE1	3.990
1DVF	B_ARG_38	NH2	B_GLU_46	OE2	3.805
1DVF	B_ARG_38	NH2	B_ASP_89	OD1	3.345
1DVF	B_ARG_66	NH1	B_ASP_89	OD1	3.908
1DVF	B_ARG_66	NH1	B_ASP_89	OD2	3.826
1DVF	B_ARG_66	NH2	B_ASP_89	OD1	3.644
1DVF	B_ARG_66	NH2	B_ASP_89	OD2	2.583
1DVF	B_LYS_75	NZ	B_ASP_72	OD2	2.871
1DVF	B_HIS_86	ND1	B_ASP_88	OD2	3.353
1DVF	B_ARG_97	NH2	B_ASP_104	OD1	3.629
1DVF	B_ARG_97	NH2	B_ASP_104	OD2	2.634
1DVF	B_ARG_102	NH1	B_ASP_100	OD2	2.926
1DVF	C_ARG_61	NH1	C_ASP_82	OD1	3.565
1DVF	C_ARG_61	NH1	C_ASP_82	OD2	2.521
1DVF	C_ARG_61	NH2	C_GLU_79	OE2	3.798
1DVF	C_ARG_61	NH2	C_GLU_81	OE2	3.578
1DVF	C_ARG_61	NH2	C_ASP_82	OD1	2.671
1DVF	C_ARG_61	NH2	C_ASP_82	OD2	3.084
1DVF	C_LYS_103	NZ	C_GLU_105	OE2	3.563
1DVF	D_HIS_33	NE2	B_ASP_100	OD1	3.569
1DVF	D_HIS_33	NE2	B_ASP_100	OD2	3.052
1DVF	D_HIS_33	NE2	D_ASP_52	OD2	3.296
1DVF	D_LYS_62	NZ	D_GLU_46	OE1	3.985
1DVF	D_LYS_66	NZ	D_ASP_86	OD1	3.906
1DVF	D_LYS_66	NZ	D_ASP_86	OD2	2.839

Table 46: 1DVF-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1DZB	A_LYS_38	NZ	A_ASP_90	OD1	3.686
1DZB	A_ARG_40	NH2	A_GLU_46	OE1	3.204
1DZB	A_ARG_40	NH2	A_GLU_46	OE2	2.668
1DZB	A_LYS_63	NZ	B_GLU_89	OE1	3.983
1DZB	A_LYS_67	NZ	B_ASP_90	OD2	3.792
1DZB	A_ARG_234	NH2	A_ASP_104	OD1	2.721
1DZB	A_ARG_234	NH2	A_ASP_104	OD2	3.895
1DZB	A_ARG_261	NH1	A_GLU_279	OE1	3.537
1DZB	B_LYS_38	NZ	B_ASP_90	OD1	3.512
1DZB	B_ARG_40	NH2	B_GLU_46	OE1	3.754
1DZB	B_ARG_40	NH2	B_GLU_46	OE2	3.419
1DZB	B_LYS_63	NZ	B_GLU_46	OE1	3.854
1DZB	B_LYS_67	NZ	B_ASP_90	OD1	3.833
1DZB	B_ARG_234	NH2	B_ASP_104	OD1	2.732
1DZB	B_ARG_234	NH2	B_ASP_104	OD2	3.591
1DZB	B_ARG_261	NH1	B_GLU_279	OE2	3.580
1DZB	X_LYS_1	NZ	X_GLU_7	OE1	3.363
1DZB	X_LYS_1	NZ	X_GLU_7	OE2	3.292
1DZB	X_ARG_61	NH2	A_ASP_256	OD2	3.887
1DZB	X_LYS_73	NZ	A_ASP_256	OD1	3.412
1DZB	X_LYS_73	NZ	A_ASP_256	OD2	3.290
1DZB	X_ARG_112	NH2	A_ASP_31	OD2	3.878
1DZB	X_ARG_125	NH2	X_ASP_119	OD2	3.529
1DZB	Y_LYS_73	NZ	B_ASP_256	OD1	3.559

Table 47: 1DZB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1E4W	H_HIS_35	ND1	H_GLU_50	OE1	3.798
1E4W	H_HIS_35	NE2	H_GLU_50	OE1	3.250
1E4W	H_ARG_40	NH1	H_GLU_85	OE1	2.990
1E4W	H_ARG_40	NH1	H_GLU_85	OE2	3.128
1E4W	H_ARG_40	NH2	H_GLU_85	OE1	3.469
1E4W	H_LYS_62	NZ	H_GLU_46	OE1	2.859
1E4W	H_LYS_62	NZ	H_GLU_46	OE2	3.777
1E4W	H_LYS_64	NZ	H_GLU_61	OE2	3.986
1E4W	H_LYS_66	NZ	H_ASP_86	OD1	3.553
1E4W	H_LYS_66	NZ	H_ASP_86	OD2	2.752
1E4W	H_LYS_205	NZ	L_GLU_123	OE1	3.384
1E4W	H_LYS_205	NZ	L_GLU_123	OE2	3.066
1E4W	L_ARG_24	NH2	L_ASP_70	OD1	2.921
1E4W	L_ARG_24	NH2	L_ASP_70	OD2	2.509
1E4W	L_ARG_61	NH1	L_GLU_79	OE2	3.003
1E4W	L_ARG_61	NH2	L_GLU_79	OE2	3.488
1E4W	L_ARG_61	NH2	L_GLU_81	OE2	2.874
1E4W	L_ARG_61	NH2	L_ASP_82	OD1	2.888
1E4W	L_ARG_61	NH2	L_ASP_82	OD2	3.583
1E4W	L_LYS_103	NZ	L_ASP_165	OD1	3.413
1E4W	L_LYS_147	NZ	L_GLU_154	OE1	3.975
1E4W	L_LYS_149	NZ	L_GLU_195	OE1	3.539
1E4W	L_LYS_149	NZ	L_GLU_195	OE2	2.744
1E4W	L_ARG_155	NH1	L_GLU_185	OE1	3.875
1E4W	L_ARG_155	NH1	L_GLU_185	OE2	2.836
1E4W	L_ARG_155	NH2	L_GLU_185	OE1	3.575
1E4W	L_ARG_155	NH2	L_GLU_185	OE2	3.879
1E4W	L_LYS_183	NZ	L_GLU_187	OE2	2.427
1E4W	P_HIS_2	ND1	P_GLU_5	OE1	3.603
1E4W	P_HIS_2	ND1	P_GLU_5	OE2	2.765

Table 48: 1E4W-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1E4X	H_HIS_35	ND1	H_GLU_50	OE1	3.676
1E4X	H_HIS_35	NE2	H_GLU_50	OE1	3.169
1E4X	H_ARG_40	NH1	H_GLU_85	OE1	3.357
1E4X	H_LYS_62	NZ	H_GLU_46	OE1	2.577
1E4X	H_LYS_62	NZ	H_GLU_46	OE2	3.834
1E4X	H_LYS_64	NZ	H_GLU_61	OE1	2.708
1E4X	H_LYS_64	NZ	H_GLU_61	OE2	3.973
1E4X	H_LYS_66	NZ	H_ASP_86	OD1	3.625
1E4X	H_LYS_66	NZ	H_ASP_86	OD2	3.022
1E4X	I_HIS_35	ND1	I_GLU_50	OE1	3.895
1E4X	I_HIS_35	NE2	I_GLU_50	OE1	3.180
1E4X	I_ARG_40	NH1	I_GLU_85	OE1	2.650
1E4X	I_ARG_40	NH2	I_GLU_46	OE1	3.611
1E4X	I_LYS_62	NZ	I_GLU_46	OE2	2.935
1E4X	I_LYS_64	NZ	I_GLU_61	OE1	2.622
1E4X	I_LYS_66	NZ	I_ASP_86	OD1	3.395
1E4X	I_LYS_66	NZ	I_ASP_86	OD2	2.825
1E4X	I_LYS_205	NZ	M_GLU_123	OE1	2.874
1E4X	I_LYS_205	NZ	M_GLU_123	OE2	3.751
1E4X	L_ARG_24	NH1	L_ASP_70	OD1	2.619
1E4X	L_ARG_24	NH1	L_ASP_70	OD2	3.556
1E4X	L_ARG_24	NH2	L_ASP_70	OD1	3.060
1E4X	L_ARG_24	NH2	L_ASP_70	OD2	2.776
1E4X	L_ARG_61	NH2	L_GLU_81	OE2	3.067
1E4X	L_ARG_61	NH2	L_ASP_82	OD1	2.814
1E4X	L_ARG_61	NH2	L_ASP_82	OD2	3.641
1E4X	L_LYS_147	NZ	L_GLU_154	OE1	3.971
1E4X	L_LYS_149	NZ	L_GLU_195	OE1	3.274
1E4X	L_LYS_149	NZ	L_GLU_195	OE2	2.560
1E4X	L_ARG_155	NH1	L_GLU_185	OE1	3.930
1E4X	L_ARG_155	NH1	L_GLU_185	OE2	2.776
1E4X	L_ARG_155	NH2	L_GLU_185	OE1	3.867
1E4X	L_ARG_155	NH2	L_GLU_185	OE2	3.813
1E4X	L_LYS_183	NZ	L_GLU_187	OE1	2.722
1E4X	L_LYS_183	NZ	L_GLU_187	OE2	2.806
1E4X	L_HIS_189	ND1	L_ASP_151	OD2	2.526
1E4X	L_LYS_199	NZ	L_ASP_110	OD1	3.989
1E4X	L_LYS_199	NZ	L_ASP_110	OD2	2.510
1E4X	M_ARG_24	NH1	M_ASP_70	OD1	2.588
1E4X	M_ARG_24	NH1	M_ASP_70	OD2	3.544
1E4X	M_ARG_61	NH2	M_GLU_81	OE2	2.997
1E4X	M_ARG_61	NH2	M_ASP_82	OD1	2.719
1E4X	M_ARG_61	NH2	M_ASP_82	OD2	3.382
1E4X	M_LYS_147	NZ	M_GLU_195	OE1	3.439
1E4X	M_LYS_149	NZ	M_GLU_195	OE1	3.962
1E4X	M_LYS_149	NZ	M_GLU_195	OE2	3.421
1E4X	M_ARG_155	NH1	M_GLU_185	OE1	3.714
1E4X	M_ARG_155	NH1	M_GLU_185	OE2	2.851
1E4X	M_ARG_155	NH2	M_GLU_185	OE1	3.119
1E4X	M_ARG_155	NH2	M_GLU_185	OE2	3.643
1E4X	M_LYS_183	NZ	M_GLU_187	OE1	3.326
1E4X	M_LYS_183	NZ	M_GLU_187	OE2	2.734
1E4X	M_HIS_189	ND1	M_ASP_151	OD2	2.418
1E4X	M_LYS_199	NZ	M_ASP_110	OD2	3.890
1E4X	P_HIS_4	ND1	P_ASP_7	OD1	3.911
1E4X	P_HIS_4	ND1	P_ASP_7	OD2	2.895
1E4X	Q_HIS_4	ND1	Q_ASP_7	OD1	3.489

1E4X	Q_HIS_4	ND1	Q_ASP_7	OD2	2.725
1E4X	Q_HIS_4	NE2	I_ASP_98	OD2	3.960

Table 49: 1E4X-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1E6J	H_LYS_38	NZ	H_ASP_90	OD1	3.507
1E6J	H_ARG_40	NH2	H_GLU_89	OE1	3.271
1E6J	H_LYS_63	NZ	H_GLU_46	OE1	2.880
1E6J	H_LYS_63	NZ	H_GLU_46	OE2	3.429
1E6J	H_LYS_67	NZ	H_ASP_90	OD1	3.890
1E6J	H_LYS_67	NZ	H_ASP_90	OD2	2.857
1E6J	H_ARG_102	NH1	H_ASP_108	OD1	3.654
1E6J	H_ARG_102	NH1	H_ASP_108	OD2	3.188
1E6J	H_ARG_102	NH2	H_ASP_108	OD2	3.453
1E6J	H_LYS_215	NZ	L_GLU_121	OE1	3.273
1E6J	H_LYS_215	NZ	L_GLU_121	OE2	3.199
1E6J	L_LYS_52	NZ	L_GLU_49	OE1	2.788
1E6J	L_ARG_60	NH1	L_GLU_78	OE1	3.448
1E6J	L_ARG_60	NH1	L_GLU_78	OE2	3.377
1E6J	L_ARG_60	NH2	L_GLU_80	OE1	3.435
1E6J	L_ARG_60	NH2	L_GLU_80	OE2	3.837
1E6J	L_ARG_60	NH2	L_ASP_81	OD1	3.036
1E6J	L_ARG_60	NH2	L_ASP_81	OD2	3.778
1E6J	L_LYS_101	NZ	L_GLU_103	OE2	3.191
1E6J	L_LYS_101	NZ	L_ASP_163	OD1	3.381
1E6J	L_LYS_101	NZ	L_ASP_163	OD2	3.618
1E6J	L_LYS_140	NZ	L_GLU_103	OE1	3.034
1E6J	L_LYS_140	NZ	L_GLU_103	OE2	3.715
1E6J	L_LYS_147	NZ	L_GLU_193	OE1	3.705
1E6J	L_LYS_147	NZ	L_GLU_193	OE2	3.642
1E6J	L_ARG_153	NH2	L_GLU_183	OE2	3.850
1E6J	L_LYS_181	NZ	L_GLU_185	OE1	2.925
1E6J	L_LYS_181	NZ	L_GLU_185	OE2	3.102
1E6J	L_HIS_187	ND1	L_ASP_149	OD2	3.110
1E6J	L_LYS_197	NZ	L_ASP_108	OD1	3.404
1E6J	L_LYS_197	NZ	L_ASP_108	OD2	3.535
1E6J	P_LYS_25	NZ	P_GLU_28	OE1	3.310
1E6J	P_LYS_30	NZ	P_GLU_35	OE1	3.279
1E6J	P_LYS_30	NZ	P_GLU_35	OE2	3.714
1E6J	P_ARG_82	NH2	P_GLU_79	OE1	3.880
1E6J	P_ARG_82	NH2	P_GLU_79	OE2	2.977
1E6J	P_ARG_97	NH1	P_ASP_103	OD1	3.867
1E6J	P_ARG_97	NH1	P_ASP_103	OD2	2.872
1E6J	P_ARG_97	NH2	P_ASP_103	OD2	2.992
1E6J	P_ARG_97	NH2	P_GLU_113	OE1	3.011
1E6J	P_ARG_97	NH2	P_GLU_113	OE2	2.907
1E6J	P_LYS_131	NZ	P_GLU_128	OE2	3.566
1E6J	P_LYS_140	NZ	P_GLU_75	OE1	3.007
1E6J	P_ARG_162	NH2	P_ASP_166	OD1	2.737
1E6J	P_ARG_162	NH2	P_ASP_166	OD2	3.737
1E6J	P_ARG_167	NH2	P_GLU_159	OE1	3.117
1E6J	P_ARG_167	NH2	P_GLU_159	OE2	3.307

Table 50: 1E6J-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1E6O	H_ARG_40	NH1	H_GLU_89	OE1	3.448
1E6O	H_ARG_40	NH2	H_GLU_89	OE1	2.779
1E6O	H_LYS_63	NZ	H_GLU_46	OE1	3.050
1E6O	H_LYS_67	NZ	H_ASP_90	OD1	3.728
1E6O	H_LYS_67	NZ	H_ASP_90	OD2	2.754
1E6O	H_ARG_98	NH2	H_ASP_108	OD1	3.003
1E6O	H_ARG_98	NH2	H_ASP_108	OD2	3.258
1E6O	H_LYS_215	NZ	L_GLU_121	OE1	2.731
1E6O	H_LYS_215	NZ	L_GLU_121	OE2	3.094
1E6O	L_LYS_52	NZ	L_GLU_49	OE1	2.480
1E6O	L_ARG_60	NH1	L_GLU_78	OE1	3.734
1E6O	L_ARG_60	NH1	L_GLU_78	OE2	3.517
1E6O	L_ARG_60	NH2	L_GLU_78	OE1	3.763
1E6O	L_ARG_60	NH2	L_GLU_80	OE1	3.787
1E6O	L_ARG_60	NH2	L_GLU_80	OE2	3.444
1E6O	L_ARG_60	NH2	L_ASP_81	OD1	2.714
1E6O	L_ARG_60	NH2	L_ASP_81	OD2	3.690
1E6O	L_LYS_101	NZ	L_GLU_103	OE2	2.711
1E6O	L_LYS_101	NZ	L_ASP_163	OD1	2.813
1E6O	L_LYS_101	NZ	L_ASP_163	OD2	3.565
1E6O	L_LYS_140	NZ	L_GLU_103	OE1	2.639
1E6O	L_LYS_140	NZ	L_GLU_103	OE2	3.651
1E6O	L_LYS_147	NZ	L_GLU_193	OE1	3.537
1E6O	L_LYS_147	NZ	L_GLU_193	OE2	3.485
1E6O	L_LYS_181	NZ	L_GLU_185	OE1	3.457
1E6O	L_LYS_181	NZ	L_GLU_185	OE2	2.602
1E6O	L_HIS_187	ND1	L_ASP_149	OD2	2.973
1E6O	L_LYS_197	NZ	L_ASP_108	OD1	3.626
1E6O	L_LYS_197	NZ	L_ASP_108	OD2	2.685

Table 51: 1E6O-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1EJO	L.HIS_2038	NE2	H.ASP_2603	OD1	3.217
1EJO	L.ARG_2065	NH1	L.ASP_2085	OD1	3.884
1EJO	L.ARG_2065	NH1	L.ASP_2085	OD2	3.751
1EJO	L.ARG_2065	NH1	L.ASP_2086	OD1	3.789
1EJO	L.ARG_2065	NH1	L.ASP_2086	OD2	2.949
1EJO	L.ARG_2065	NH2	L.GLU_2083	OE2	3.437
1EJO	L.LYS_2107	NZ	L.ASP_2169	OD1	3.608
1EJO	L.LYS_2153	NZ	L.GLU_2199	OE2	3.964
1EJO	L.ARG_2159	NH2	L.GLU_2189	OE1	2.792
1EJO	L.ARG_2159	NH2	L.GLU_2189	OE2	2.939
1EJO	L.LYS_2187	NZ	L.ASP_2188	OD1	3.810
1EJO	H.ARG_2537	NH1	H.ASP_2589	OD1	2.793
1EJO	H.ARG_2537	NH2	H.GLU_2545	OE1	3.422
1EJO	H.ARG_2537	NH2	H.ASP_2589	OD1	3.718
1EJO	H.ARG_2543	NH1	H.GLU_2545	OE1	3.893
1EJO	H.ARG_2543	NH1	H.GLU_2545	OE2	2.876
1EJO	H.ARG_2543	NH2	H.GLU_2541	OE1	3.189
1EJO	H.ARG_2566	NH1	H.ASP_2589	OD2	2.850
1EJO	H.ARG_2566	NH2	H.ASP_2589	OD1	3.228
1EJO	H.ARG_2566	NH2	H.ASP_2589	OD2	3.243
1EJO	H.ARG_2598	NH1	H.ASP_2603	OD1	3.142
1EJO	H.ARG_2598	NH1	H.ASP_2603	OD2	3.978
1EJO	H.ARG_2598	NH2	H.ASP_2603	OD1	3.242
1EJO	H.ARG_2598	NH2	H.ASP_2603	OD2	2.790
1EJO	H.ARG_2598	NH2	P.ASP_3143	OD1	3.795
1EJO	H.ARG_2598	NH2	P.ASP_3143	OD2	2.982
1EJO	H.LYS_2714	NZ	L.GLU_2127	OE1	2.933
1EJO	H.LYS_2714	NZ	L.GLU_2127	OE2	3.046
1EJO	P.ARG_3141	NH1	L.GLU_2027	OE2	3.696
1EJO	P.ARG_3141	NH1	L.GLU_2097	OE1	2.675
1EJO	P.ARG_3141	NH2	L.GLU_2027	OE2	3.441

Table 52: 1EJO-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1EMT	L_LYS_39	NZ	L_GLU_81	OE1	2.666
1EMT	L_LYS_39	NZ	L_GLU_81	OE2	3.409
1EMT	L_ARG_61	NH1	L_ASP_82	OD1	2.890
1EMT	L_ARG_61	NH2	L_ASP_82	OD1	2.955
1EMT	L_ARG_61	NH2	L_ASP_82	OD2	2.766
1EMT	L_LYS_147	NZ	L_GLU_154	OE2	3.689
1EMT	L_LYS_149	NZ	L_GLU_195	OE2	3.241
1EMT	L_LYS_183	NZ	L_GLU_187	OE1	2.782
1EMT	L_LYS_183	NZ	L_GLU_187	OE2	3.826
1EMT	L_ARG_188	NH2	L_GLU_185	OE1	3.057
1EMT	L_ARG_188	NH2	L_GLU_185	OE2	3.248
1EMT	L_HIS_189	ND1	L_GLU_185	OE2	3.669
1EMT	L_HIS_189	NE2	L_GLU_185	OE2	3.443
1EMT	H_LYS_63	NZ	L_ASP_1	OD1	3.310
1EMT	H_LYS_67	NZ	H_ASP_90	OD1	2.648
1EMT	H_LYS_67	NZ	H_ASP_90	OD2	3.672
1EMT	H_LYS_211	NZ	L_GLU_123	OE1	2.945
1EMT	H_LYS_211	NZ	L_GLU_123	OE2	2.554

Table 53: 1EMT-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1ETZ	L_ARG_23	NH2	L_ASP_71	OD2	3.806
1ETZ	L_ARG_63	NH2	L_GLU_83	OE2	3.283
1ETZ	L_ARG_63	NH2	L_ASP_84	OD1	2.986
1ETZ	L_ARG_63	NH2	L_ASP_84	OD2	3.556
1ETZ	L_LYS_113	NZ	L_GLU_201	OE1	3.231
1ETZ	L_ARG_186	NH1	B_GLU_48	OE1	2.771
1ETZ	L_ARG_186	NH1	B_GLU_48	OE2	3.248
1ETZ	L_ARG_190	NH1	L_GLU_189	OE2	3.584
1ETZ	L_ARG_190	NH2	L_GLU_189	OE2	3.089
1ETZ	L_ARG_190	NH2	B_GLU_48	OE2	3.331
1ETZ	H_ARG_40	NH1	H_ASP_91	OD1	2.907
1ETZ	H_ARG_40	NH2	H_GLU_48	OE1	3.221
1ETZ	H_ARG_40	NH2	H_ASP_91	OD1	3.222
1ETZ	H_ARG_68	NH2	H_ASP_91	OD1	3.774
1ETZ	H_ARG_68	NH2	H_ASP_91	OD2	2.733
1ETZ	H_LYS_73	NZ	H_ASP_57	OD1	3.834
1ETZ	H_ARG_99	NH1	H_ASP_114	OD1	2.968
1ETZ	H_ARG_99	NH1	H_ASP_114	OD2	3.185
1ETZ	H_ARG_100	NH1	H_ASP_52	OD1	3.260
1ETZ	H_ARG_100	NH1	H_ASP_52	OD2	2.758
1ETZ	H_LYS_156	NZ	L_GLU_127	OE2	3.377
1ETZ	H_LYS_221	NZ	L_GLU_126	OE1	3.184
1ETZ	A_ARG_23	NH1	A_ASP_71	OD2	2.921
1ETZ	A_ARG_23	NH2	A_ASP_71	OD2	2.821
1ETZ	A_ARG_63	NH2	A_GLU_83	OE2	3.430
1ETZ	A_ARG_63	NH2	A_ASP_84	OD1	2.842
1ETZ	A_ARG_63	NH2	A_ASP_84	OD2	3.406
1ETZ	A_LYS_113	NZ	A_GLU_201	OE1	2.940
1ETZ	A_ARG_186	NH1	H_GLU_45	OE2	3.236
1ETZ	A_ARG_186	NH2	H_GLU_48	OE1	3.518
1ETZ	B_ARG_40	NH1	B_ASP_91	OD1	3.069
1ETZ	B_ARG_40	NH2	B_GLU_48	OE1	3.077
1ETZ	B_ARG_40	NH2	B_ASP_91	OD1	3.733
1ETZ	B_LYS_59	NZ	B_ASP_57	OD1	3.243
1ETZ	B_LYS_59	NZ	B_ASP_57	OD2	3.017
1ETZ	B_ARG_68	NH1	B_ASP_91	OD1	3.924
1ETZ	B_ARG_68	NH2	B_ASP_91	OD1	3.185
1ETZ	B_ARG_68	NH2	B_ASP_91	OD2	2.598
1ETZ	B_LYS_73	NZ	B_ASP_57	OD1	2.975
1ETZ	B_ARG_99	NH1	B_ASP_114	OD1	2.870
1ETZ	B_ARG_99	NH1	B_ASP_114	OD2	3.787
1ETZ	B_ARG_100	NH1	B_ASP_52	OD1	2.947
1ETZ	B_ARG_100	NH1	B_ASP_52	OD2	2.788
1ETZ	B_LYS_156	NZ	A_GLU_127	OE2	2.979
1ETZ	B_LYS_221	NZ	A_GLU_126	OE1	3.572
1ETZ	B_LYS_222	NZ	B_GLU_224	OE1	3.556

Table 54: 1ETZ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1F11	A_ARG_61	NH1	A_GLU_79	OE2	3.870
1F11	A_ARG_61	NH1	A_GLU_81	OE1	3.780
1F11	A_ARG_61	NH2	A_GLU_81	OE1	3.819
1F11	A_ARG_61	NH2	A_ASP_82	OD1	2.589
1F11	A_ARG_61	NH2	A_ASP_82	OD2	2.998
1F11	A_LYS_147	NZ	A_GLU_154	OE1	3.554
1F11	A_LYS_149	NZ	A_GLU_195	OE1	2.800
1F11	A_LYS_149	NZ	A_GLU_195	OE2	3.495
1F11	A_ARG_155	NH2	A_GLU_185	OE2	3.833
1F11	A_LYS_183	NZ	A_ASP_184	OD1	3.227
1F11	A_LYS_183	NZ	A_ASP_184	OD2	3.413
1F11	A_HIS_189	NE2	A_ASP_151	OD2	3.960
1F11	A_ARG_211	NH1	A_GLU_187	OE1	3.379
1F11	B_LYS_35	NZ	B_ASP_50	OD2	2.899
1F11	B_LYS_62	NZ	B_GLU_46	OE1	3.878
1F11	B_LYS_62	NZ	B_GLU_46	OE2	3.017
1F11	B_LYS_66	NZ	B_ASP_86	OD1	3.898
1F11	B_LYS_66	NZ	B_ASP_86	OD2	2.909
1F11	B_LYS_218	NZ	B_ASP_220	OD1	3.293
1F11	B_LYS_221	NZ	A_GLU_123	OE2	3.880
1F11	C_ARG_61	NH1	C_GLU_79	OE2	3.820
1F11	C_ARG_61	NH1	C_GLU_81	OE1	3.765
1F11	C_ARG_61	NH2	C_GLU_81	OE1	3.827
1F11	C_ARG_61	NH2	C_ASP_82	OD1	2.588
1F11	C_ARG_61	NH2	C_ASP_82	OD2	2.920
1F11	C_LYS_147	NZ	C_GLU_154	OE1	3.496
1F11	C_LYS_149	NZ	C_GLU_195	OE1	2.803
1F11	C_LYS_149	NZ	C_GLU_195	OE2	3.539
1F11	C_ARG_155	NH2	C_GLU_185	OE2	3.909
1F11	C_LYS_183	NZ	C_ASP_184	OD1	3.200
1F11	C_LYS_183	NZ	C_ASP_184	OD2	3.469
1F11	C_ARG_211	NH1	C_GLU_187	OE1	3.266
1F11	D_LYS_35	NZ	D_ASP_50	OD2	2.846
1F11	D_LYS_62	NZ	D_GLU_46	OE1	3.912
1F11	D_LYS_62	NZ	D_GLU_46	OE2	3.130
1F11	D_LYS_66	NZ	D_ASP_86	OD1	3.943
1F11	D_LYS_66	NZ	D_ASP_86	OD2	2.885
1F11	D_LYS_218	NZ	D_ASP_220	OD1	3.381
1F11	D_LYS_221	NZ	C_GLU_123	OE2	3.786

Table 55: 1F11-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1F2X	K_ARG_838	NH1	K_ASP_888	OD1	2.859
1F2X	K_ARG_838	NH2	K_GLU_846	OE2	2.923
1F2X	K_ARG_865	NH1	K_ASP_888	OD1	3.794
1F2X	K_ARG_865	NH1	K_ASP_888	OD2	2.763
1F2X	K_ARG_865	NH2	K_ASP_888	OD1	3.027
1F2X	K_ARG_865	NH2	K_ASP_888	OD2	3.447
1F2X	K_LYS_874	NZ	K_ASP_871	OD1	3.294
1F2X	K_ARG_909	NH2	K_ASP_912	OD1	2.589
1F2X	K_ARG_909	NH2	K_ASP_912	OD2	3.255
1F2X	L_ARG_1038	NH1	L_ASP_1088	OD1	2.834
1F2X	L_ARG_1038	NH2	L_GLU_1046	OE2	3.098
1F2X	L_ARG_1038	NH2	L_ASP_1088	OD1	3.939
1F2X	L_ARG_1065	NH1	L_ASP_1088	OD1	3.834
1F2X	L_ARG_1065	NH1	L_ASP_1088	OD2	2.618
1F2X	L_ARG_1065	NH2	L_ASP_1088	OD1	3.165
1F2X	L_ARG_1065	NH2	L_ASP_1088	OD2	3.405
1F2X	L_ARG_1109	NH2	L_ASP_1112	OD1	3.166
1F2X	L_ARG_1109	NH2	L_ASP_1112	OD2	2.892

Table 56: 1F2X-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1F3R	B_ARG_38	NH1	B_ASP_89	OD2	2.997
1F3R	B_ARG_38	NH2	B_GLU_46	OE1	3.068
1F3R	B_ARG_50	NH1	B_ASP_98	OD1	3.532
1F3R	B_ARG_66	NH1	B_ASP_89	OD1	3.017
1F3R	B_ARG_66	NH2	B_ASP_89	OD1	3.057
1F3R	B_ARG_97	NH1	B_ASP_111	OD1	3.327
1F3R	B_ARG_97	NH1	B_ASP_111	OD2	3.427
1F3R	B_ARG_97	NH2	B_ASP_111	OD1	3.187
1F3R	B_ARG_97	NH2	B_ASP_111	OD2	3.419
1F3R	B_LYS_177	NZ	B_GLU_180	OE1	3.798
1F3R	B_LYS_177	NZ	B_GLU_180	OE2	3.027
1F3R	B_ARG_199	NH1	B_ASP_220	OD1	2.891
1F3R	B_ARG_199	NH1	B_ASP_220	OD2	3.346
1F3R	B_ARG_199	NH2	B_GLU_219	OE1	3.171
1F3R	B_LYS_244	NZ	B_GLU_242	OE2	3.193
1F3R	B_LYS_249	NZ	B_GLU_247	OE1	3.078

Table 57: 1F3R-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1F4W	L_ARG_63	NH2	L_GLU_83	OE2	3.740
1F4W	L_ARG_63	NH2	L_ASP_84	OD1	3.103
1F4W	L_ARG_63	NH2	L_ASP_84	OD2	3.558
1F4W	L_LYS_113	NZ	L_GLU_201	OE1	2.889
1F4W	L_LYS_169	NZ	L_GLU_85	OE2	3.500
1F4W	H_ARG_38	NH1	H_ASP_90	OD1	2.942
1F4W	H_ARG_38	NH2	H_GLU_46	OE1	2.644
1F4W	H_ARG_67	NH1	H_ASP_90	OD1	3.871
1F4W	H_ARG_67	NH1	H_ASP_90	OD2	2.697
1F4W	H_ARG_67	NH2	H_ASP_90	OD1	3.052
1F4W	H_ARG_67	NH2	H_ASP_90	OD2	3.253
1F4W	H_ARG_72	NH2	H_ASP_74	OD1	3.561
1F4W	H_LYS_76	NZ	H_ASP_73	OD2	3.208
1F4W	H_ARG_98	NH1	H_ASP_105	OD1	3.445
1F4W	H_ARG_98	NH1	H_ASP_105	OD2	2.877
1F4W	H_LYS_147	NZ	L_GLU_127	OE2	2.611
1F4W	H_LYS_212	NZ	L_GLU_126	OE1	2.614
1F4W	H_LYS_212	NZ	L_GLU_126	OE2	2.379

Table 58: 1F4W-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1F4X	L_HIS_44	ND1	L_GLU_40	OE2	3.729
1F4X	L_ARG_63	NH2	L_ASP_84	OD1	3.061
1F4X	L_ARG_63	NH2	L_ASP_84	OD2	3.605
1F4X	L_LYS_113	NZ	L_GLU_201	OE1	3.012
1F4X	L_LYS_169	NZ	L_GLU_85	OE2	3.678
1F4X	H_ARG_38	NH1	H_ASP_90	OD1	2.949
1F4X	H_ARG_38	NH2	H_GLU_46	OE1	2.849
1F4X	H_ARG_38	NH2	H_ASP_90	OD1	3.913
1F4X	H_ARG_67	NH1	H_ASP_90	OD1	3.808
1F4X	H_ARG_67	NH1	H_ASP_90	OD2	2.538
1F4X	H_ARG_67	NH2	H_ASP_90	OD1	3.205
1F4X	H_ARG_67	NH2	H_ASP_90	OD2	3.358
1F4X	H_ARG_72	NH2	H_ASP_74	OD1	3.580
1F4X	H_LYS_76	NZ	H_ASP_73	OD2	2.862
1F4X	H_ARG_98	NH1	H_ASP_105	OD1	3.356
1F4X	H_ARG_98	NH1	H_ASP_105	OD2	2.740
1F4X	H_LYS_147	NZ	L_GLU_127	OE2	2.699
1F4X	H_LYS_212	NZ	L_GLU_126	OE1	2.421
1F4X	H_LYS_212	NZ	L_GLU_126	OE2	2.990

Table 59: 1F4X-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID** **residue name** **residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1F4Y	L_ARG_63	NH2	L_ASP_84	OD1	3.366
1F4Y	L_LYS_105	NZ	L_GLU_85	OE1	3.158
1F4Y	H_ARG_38	NH1	H_ASP_90	OD1	3.048
1F4Y	H_ARG_38	NH2	H_GLU_46	OE1	2.579
1F4Y	H_LYS_65	NZ	H_ASP_62	OD1	3.084
1F4Y	H_LYS_65	NZ	H_ASP_62	OD2	3.693
1F4Y	H_ARG_67	NH1	H_ASP_90	OD1	3.760
1F4Y	H_ARG_67	NH1	H_ASP_90	OD2	2.465
1F4Y	H_ARG_67	NH2	H_ASP_90	OD1	2.587
1F4Y	H_ARG_67	NH2	H_ASP_90	OD2	2.864
1F4Y	H_ARG_98	NH1	H_ASP_105	OD1	3.675
1F4Y	H_ARG_98	NH1	H_ASP_105	OD2	3.275
1F4Y	H_LYS_212	NZ	L_GLU_126	OE2	3.609

Table 60: 1F4Y-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1F8T	L_ARG_46	NH2	L_ASP_55	OD1	2.680
1F8T	L_ARG_46	NH2	L_ASP_55	OD2	3.749
1F8T	L_ARG_61	NH1	L_GLU_79	OE1	3.213
1F8T	L_ARG_61	NH2	L_GLU_79	OE1	3.750
1F8T	L_ARG_61	NH2	L_ASP_82	OD1	2.713
1F8T	L_ARG_61	NH2	L_ASP_82	OD2	3.022
1F8T	L_ARG_77	NH1	L_GLU_79	OE2	2.715
1F8T	L_ARG_77	NH2	L_GLU_79	OE2	3.752
1F8T	L_ARG_96	NH1	H_ASP_97	OD1	3.105
1F8T	L_ARG_96	NH1	H_ASP_97	OD2	3.586
1F8T	L_ARG_96	NH2	H_ASP_97	OD1	3.395
1F8T	L_ARG_96	NH2	H_ASP_97	OD2	2.424
1F8T	L_LYS_	NZ	L_GLU_	OE1	3.476
1F8T	L_LYS_	NZ	L_GLU_	OE1	3.068
1F8T	L_LYS_	NZ	L_GLU_	OE2	3.947
1F8T	L_ARG_	NH2	L_GLU_	OE1	3.027
1F8T	L_ARG_	NH2	L_GLU_	OE2	2.531
1F8T	L_LYS_	NZ	L_GLU_	OE2	3.307
1F8T	L_HIS_	ND1	L_ASP_	OD2	2.855
1F8T	L_LYS_199	NZ	L_ASP_110	OD2	3.253
1F8T	H_ARG_38	NH1	H_ASP_86	OD1	2.940
1F8T	H_ARG_38	NH2	H_GLU_46	OE1	2.881
1F8T	H_ARG_38	NH2	H_ASP_86	OD1	3.828
1F8T	H_ARG_66	NH1	H_ASP_86	OD1	3.709
1F8T	H_ARG_66	NH1	H_ASP_86	OD2	3.187
1F8T	H_ARG_66	NH2	H_ASP_86	OD1	2.923
1F8T	H_ARG_66	NH2	H_ASP_86	OD2	3.622
1F8T	H_LYS_221	NZ	L_GLU_123	OE1	3.087

Table 61: 1F8T-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1F90	L_LYS_30	NZ	E_GLU_4	OE1	2.620
1F90	L_LYS_30	NZ	E_GLU_4	OE2	2.679
1F90	L_ARG_46	NH2	L_ASP_55	OD1	2.495
1F90	L_ARG_46	NH2	L_ASP_55	OD2	3.861
1F90	L_ARG_61	NH1	L_GLU_79	OE2	3.045
1F90	L_ARG_61	NH2	L_GLU_79	OE2	3.948
1F90	L_ARG_61	NH2	L_GLU_81	OE1	3.955
1F90	L_ARG_61	NH2	L_ASP_82	OD1	2.600
1F90	L_ARG_61	NH2	L_ASP_82	OD2	2.843
1F90	L_ARG_77	NH1	L_GLU_79	OE1	2.895
1F90	L_ARG_77	NH1	L_GLU_79	OE2	3.695
1F90	L_ARG_96	NH2	H_ASP_97	OD1	2.720
1F90	L_ARG_96	NH2	H_ASP_97	OD2	2.722
1F90	L_LYS_103	NZ	L_GLU_105	OE1	3.749
1F90	L_LYS_103	NZ	L_ASP_165	OD1	3.843
1F90	L_LYS_149	NZ	L_GLU_195	OE1	3.370
1F90	L_LYS_149	NZ	L_GLU_195	OE2	3.504
1F90	L_ARG_188	NH1	L_GLU_185	OE2	2.963
1F90	L_ARG_188	NH2	L_GLU_185	OE2	3.164
1F90	L_HIS_189	ND1	L_ASP_151	OD2	3.004
1F90	L_HIS_189	NE2	L_GLU_185	OE2	2.903
1F90	H_ARG_38	NH1	H_ASP_86	OD1	3.080
1F90	H_ARG_38	NH2	H_GLU_46	OE1	3.030
1F90	H_ARG_38	NH2	H_ASP_86	OD1	3.543
1F90	H_ARG_66	NH1	H_ASP_86	OD1	3.378
1F90	H_ARG_66	NH1	H_ASP_86	OD2	3.136
1F90	H_ARG_66	NH2	H_ASP_86	OD1	2.890
1F90	H_ARG_66	NH2	H_ASP_86	OD2	3.648
1F90	H_LYS_221	NZ	L_GLU_123	OE2	3.675
1F90	E_LYS_1	NZ	E_GLU_5	OE1	3.986
1F90	E_LYS_1	NZ	E_GLU_5	OE2	3.901

Table 62: 1F90-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1FBI	L_ARG_61	NH1	L_ASP_82	OD1	3.634
1FBI	L_ARG_61	NH1	L_ASP_82	OD2	2.723
1FBI	L_ARG_61	NH2	L_ASP_82	OD1	3.289
1FBI	L_ARG_61	NH2	L_ASP_82	OD2	3.818
1FBI	L_LYS_147	NZ	L_GLU_195	OE2	3.806
1FBI	L_LYS_149	NZ	L_GLU_195	OE1	2.895
1FBI	L_LYS_149	NZ	L_GLU_195	OE2	3.340
1FBI	L_ARG_155	NH1	L_GLU_185	OE2	3.988
1FBI	L_ARG_155	NH2	L_GLU_185	OE1	3.443
1FBI	L_ARG_155	NH2	L_GLU_185	OE2	3.420
1FBI	L_LYS_183	NZ	L_GLU_187	OE1	3.147
1FBI	L_LYS_183	NZ	L_GLU_187	OE2	3.215
1FBI	L_HIS_189	ND1	L_ASP_151	OD2	3.770
1FBI	L_LYS_199	NZ	L_ASP_110	OD1	2.851
1FBI	L_LYS_199	NZ	L_ASP_110	OD2	3.860
1FBI	H_HIS_35	ND1	H_GLU_50	OE2	3.933
1FBI	H_HIS_35	NE2	H_GLU_50	OE2	3.486
1FBI	H_LYS_38	NZ	H_ASP_90	OD1	3.514
1FBI	H_LYS_38	NZ	H_ASP_90	OD2	3.031
1FBI	H_LYS_63	NZ	L_ASP_1	OD1	2.933
1FBI	H_LYS_63	NZ	L_ASP_1	OD2	2.804
1FBI	H_LYS_65	NZ	H_GLU_62	OE1	2.904
1FBI	H_LYS_67	NZ	H_ASP_90	OD1	3.905
1FBI	H_LYS_217	NZ	L_GLU_123	OE1	3.667
1FBI	X_LYS_1	NZ	X_GLU_7	OE2	3.145
1FBI	X_HIS_15	ND1	H_ASP_55	OD1	3.190
1FBI	X_HIS_15	ND1	H_ASP_55	OD2	3.649
1FBI	X_ARG_61	NH1	X_ASP_48	OD1	3.808
1FBI	X_ARG_61	NH1	X_ASP_48	OD2	3.628
1FBI	X_ARG_61	NH2	X_ASP_48	OD1	3.862
1FBI	X_LYS_96	NZ	H_ASP_52	OD2	2.922
1FBI	X_LYS_97	NZ	H_GLU_50	OE1	3.586
1FBI	X_LYS_97	NZ	H_GLU_50	OE2	2.898
1FBI	X_ARG_121	NH1	X_ASP_119	OD1	3.058
1FBI	P_ARG_24	NH2	P_ASP_70	OD1	3.358
1FBI	P_ARG_61	NH1	P_GLU_79	OE2	3.500
1FBI	P_ARG_61	NH2	P_ASP_82	OD2	2.619
1FBI	P_LYS_149	NZ	P_GLU_195	OE1	3.522
1FBI	P_LYS_149	NZ	P_GLU_195	OE2	3.273
1FBI	P_LYS_183	NZ	P_GLU_187	OE1	3.943
1FBI	P_HIS_189	ND1	P_ASP_151	OD2	3.620
1FBI	P_HIS_189	NE2	P_GLU_185	OE1	3.397
1FBI	P_HIS_189	NE2	P_GLU_185	OE2	3.570
1FBI	P_LYS_199	NZ	P_ASP_110	OD2	3.380
1FBI	P_ARG_211	NH2	P_GLU_187	OE1	3.763
1FBI	Q_HIS_35	NE2	Q_GLU_50	OE2	3.940
1FBI	Q_LYS_63	NZ	P_ASP_1	OD1	3.020
1FBI	Q_LYS_63	NZ	P_ASP_1	OD2	3.850
1FBI	Q_LYS_65	NZ	Q_GLU_62	OE1	2.725
1FBI	Q_LYS_65	NZ	Q_GLU_62	OE2	3.529
1FBI	Y_HIS_15	ND1	Q_ASP_55	OD1	3.335
1FBI	Y_HIS_15	ND1	Q_ASP_55	OD2	3.838
1FBI	Y_LYS_96	NZ	Q_ASP_52	OD2	2.727
1FBI	Y_LYS_97	NZ	Q_GLU_50	OE1	2.828
1FBI	Y_LYS_97	NZ	Q_GLU_50	OE2	3.159

Table 63: 1FBI-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1FCC	A_LYS_248	NZ	A_GLU_380	OE2	2.872
1FCC	A_ARG_255	NH1	A_ASP_249	OD1	3.810
1FCC	A_LYS_317	NZ	A_ASP_280	OD2	3.593
1FCC	A_LYS_320	NZ	A_GLU_333	OE2	2.861
1FCC	A_LYS_322	NZ	A_GLU_333	OE2	3.431
1FCC	A_LYS_338	NZ	A_GLU_430	OE1	3.073
1FCC	A_LYS_338	NZ	A_GLU_430	OE2	2.873
1FCC	A_LYS_370	NZ	B_GLU_357	OE2	2.948
1FCC	A_LYS_409	NZ	B_ASP_399	OD2	2.859
1FCC	A_ARG_416	NH1	A_GLU_388	OE1	2.663
1FCC	A_ARG_416	NH1	A_GLU_388	OE2	2.822
1FCC	A_ARG_416	NH2	A_GLU_388	OE1	3.781
1FCC	A_ARG_416	NH2	A_GLU_388	OE2	2.901
1FCC	A_LYS_439	NZ	B_GLU_356	OE1	3.550
1FCC	A_LYS_439	NZ	B_GLU_356	OE2	3.522
1FCC	C_LYS_4	NZ	C_GLU_15	OE1	3.955
1FCC	C_LYS_4	NZ	C_GLU_15	OE2	3.020
1FCC	C_LYS_28	NZ	A_GLU_380	OE1	2.730
1FCC	C_LYS_28	NZ	A_GLU_380	OE2	3.982
1FCC	C_LYS_28	NZ	A_GLU_382	OE1	3.879
1FCC	C_LYS_28	NZ	A_GLU_382	OE2	2.866
1FCC	C_LYS_31	NZ	C_GLU_27	OE2	2.693
1FCC	B_LYS_248	NZ	B_GLU_380	OE2	2.873
1FCC	B_ARG_255	NH1	B_ASP_249	OD1	3.810
1FCC	B_LYS_317	NZ	B_ASP_280	OD2	3.592
1FCC	B_LYS_320	NZ	B_GLU_333	OE2	2.862
1FCC	B_LYS_322	NZ	B_GLU_333	OE2	3.430
1FCC	B_LYS_338	NZ	B_GLU_430	OE1	3.074
1FCC	B_LYS_338	NZ	B_GLU_430	OE2	2.873
1FCC	B_LYS_370	NZ	A_GLU_357	OE2	2.633
1FCC	B_LYS_409	NZ	A_ASP_399	OD2	3.360
1FCC	B_ARG_416	NH1	B_GLU_388	OE1	2.663
1FCC	B_ARG_416	NH1	B_GLU_388	OE2	2.823
1FCC	B_ARG_416	NH2	B_GLU_388	OE1	3.781
1FCC	B_ARG_416	NH2	B_GLU_388	OE2	2.902
1FCC	B_LYS_439	NZ	A_GLU_356	OE1	3.166
1FCC	B_LYS_439	NZ	A_GLU_356	OE2	3.295
1FCC	D_LYS_4	NZ	D_GLU_15	OE1	3.955
1FCC	D_LYS_4	NZ	D_GLU_15	OE2	3.020
1FCC	D_LYS_28	NZ	B_GLU_380	OE1	2.730
1FCC	D_LYS_28	NZ	B_GLU_380	OE2	3.982
1FCC	D_LYS_28	NZ	B_GLU_382	OE1	3.879
1FCC	D_LYS_28	NZ	B_GLU_382	OE2	2.865
1FCC	D_LYS_31	NZ	D_GLU_27	OE2	2.693

Table 64: 1FCC-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1FDL	L_ARG_61	NH1	L_GLU_81	OE2	3.900
1FDL	L_ARG_61	NH1	L_ASP_82	OD1	2.792
1FDL	L_ARG_61	NH1	L_ASP_82	OD2	2.681
1FDL	L_ARG_61	NH2	L_GLU_81	OE2	3.608
1FDL	L_ARG_96	NH1	H_GLU_98	OE1	3.307
1FDL	L_ARG_96	NH1	H_GLU_98	OE2	2.802
1FDL	L_ARG_96	NH2	H_GLU_98	OE1	2.754
1FDL	L_ARG_96	NH2	H_GLU_98	OE2	3.656
1FDL	L_LYS_107	NZ	L_GLU_17	OE1	3.380
1FDL	L_LYS_149	NZ	L_GLU_195	OE1	3.099
1FDL	L_LYS_149	NZ	L_GLU_195	OE2	3.490
1FDL	L_ARG_155	NH2	L_GLU_185	OE1	3.454
1FDL	L_ARG_155	NH2	L_GLU_185	OE2	3.567
1FDL	L_LYS_183	NZ	L_GLU_187	OE1	2.772
1FDL	L_LYS_183	NZ	L_GLU_187	OE2	2.921
1FDL	L_HIS_189	ND1	L_ASP_151	OD2	3.048
1FDL	L_LYS_199	NZ	L_ASP_110	OD1	2.959
1FDL	L_LYS_199	NZ	L_ASP_110	OD2	3.198
1FDL	H_ARG_38	NH1	H_ASP_89	OD2	3.284
1FDL	H_ARG_38	NH2	H_GLU_46	OE1	3.064
1FDL	H_ARG_38	NH2	H_ASP_89	OD2	3.961
1FDL	H_ARG_66	NH1	H_ASP_89	OD2	3.688
1FDL	H_ARG_66	NH2	H_ASP_89	OD1	2.978
1FDL	H_ARG_66	NH2	H_ASP_89	OD2	3.755
1FDL	H_ARG_97	NH2	H_ASP_104	OD1	2.804
1FDL	H_ARG_97	NH2	H_ASP_104	OD2	2.688
1FDL	H_ARG_102	NH1	H_ASP_100	OD1	3.620
1FDL	H_LYS_211	NZ	L_GLU_123	OE1	2.896
1FDL	H_LYS_211	NZ	L_GLU_123	OE2	3.291
1FDL	Y_LYS_1	NZ	Y_GLU_7	OE2	3.281
1FDL	Y_ARG_61	NH1	Y_ASP_48	OD2	3.796
1FDL	Y_ARG_61	NH2	Y_ASP_48	OD2	3.093
1FDL	Y_ARG_125	NH1	Y_ASP_119	OD1	3.041
1FDL	Y_ARG_125	NH1	Y_ASP_119	OD2	3.285
1FDL	Y_ARG_125	NH2	Y_ASP_119	OD1	3.894
1FDL	Y_ARG_125	NH2	Y_ASP_119	OD2	2.759

Table 65: 1FDL-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1FJ1	A_LYS_24	NZ	A_ASP_70	OD1	3.672
1FJ1	A_LYS_24	NZ	A_ASP_70	OD2	2.846
1FJ1	A_ARG_61	NH2	A_ASP_82	OD1	2.576
1FJ1	A_ARG_61	NH2	A_ASP_82	OD2	2.776
1FJ1	A_LYS_103	NZ	A_GLU_105	OE2	3.775
1FJ1	A_LYS_147	NZ	A_GLU_154	OE2	3.963
1FJ1	A_LYS_149	NZ	A_GLU_195	OE2	2.928
1FJ1	A_ARG_155	NH1	A_GLU_185	OE2	3.662
1FJ1	A_ARG_155	NH2	A_GLU_185	OE1	2.919
1FJ1	A_ARG_155	NH2	A_GLU_185	OE2	3.026
1FJ1	A_ARG_188	NH2	E_GLU_196	OE2	3.475
1FJ1	A_HIS_189	ND1	E_GLU_196	OE1	3.723
1FJ1	A_HIS_189	NE2	E_GLU_196	OE1	3.502
1FJ1	A_LYS_199	NZ	A_ASP_110	OD1	3.803
1FJ1	A_LYS_199	NZ	A_ASP_110	OD2	3.857
1FJ1	B_ARG_47	NH1	A_ASP_1	OD1	3.251
1FJ1	B_ARG_47	NH2	A_ASP_1	OD1	2.492
1FJ1	B_LYS_65	NZ	B_ASP_62	OD1	3.433
1FJ1	B_ARG_67	NH1	B_ASP_90	OD1	2.927
1FJ1	B_ARG_67	NH1	B_ASP_90	OD2	3.891
1FJ1	B_ARG_67	NH2	B_ASP_90	OD1	3.450
1FJ1	B_ARG_67	NH2	B_ASP_90	OD2	3.269
1FJ1	B_ARG_98	NH2	B_ASP_101	OD1	3.026
1FJ1	B_ARG_98	NH2	B_ASP_101	OD2	3.672
1FJ1	B_LYS_209	NZ	B_GLU_211	OE1	3.349
1FJ1	B_LYS_209	NZ	B_GLU_211	OE2	3.845
1FJ1	C_LYS_24	NZ	C_ASP_70	OD1	3.574
1FJ1	C_LYS_24	NZ	C_ASP_70	OD2	2.777
1FJ1	C_ARG_61	NH2	C_ASP_82	OD1	2.572
1FJ1	C_ARG_61	NH2	C_ASP_82	OD2	2.742
1FJ1	C_LYS_103	NZ	C_GLU_105	OE2	3.738
1FJ1	C_LYS_147	NZ	C_GLU_154	OE2	3.995
1FJ1	C_LYS_149	NZ	C_GLU_195	OE2	2.876
1FJ1	C_ARG_155	NH1	C_GLU_185	OE2	3.699
1FJ1	C_ARG_155	NH2	C_GLU_185	OE1	2.898
1FJ1	C_ARG_155	NH2	C_GLU_185	OE2	3.006
1FJ1	C_HIS_189	NE2	F_GLU_196	OE1	3.808
1FJ1	C_LYS_199	NZ	C_ASP_110	OD1	3.817
1FJ1	C_LYS_199	NZ	C_ASP_110	OD2	3.838
1FJ1	D_ARG_47	NH1	C_ASP_1	OD1	3.296
1FJ1	D_ARG_47	NH2	C_ASP_1	OD1	2.800
1FJ1	D_LYS_65	NZ	D_ASP_62	OD1	3.432
1FJ1	D_ARG_67	NH1	D_ASP_90	OD1	2.939
1FJ1	D_ARG_67	NH1	D_ASP_90	OD2	3.923
1FJ1	D_ARG_67	NH2	D_ASP_90	OD1	3.458
1FJ1	D_ARG_67	NH2	D_ASP_90	OD2	3.292
1FJ1	D_ARG_98	NH2	D_ASP_101	OD1	3.012
1FJ1	D_ARG_98	NH2	D_ASP_101	OD2	3.702
1FJ1	D_LYS_209	NZ	D_GLU_211	OE1	3.891
1FJ1	E_LYS_117	NZ	E_ASP_118	OD1	3.779
1FJ1	E_ARG_139	NH1	E_GLU_160	OE2	3.349
1FJ1	E_ARG_139	NH2	E_GLU_160	OE2	3.249
1FJ1	E_ARG_144	NH1	E_GLU_146	OE2	2.339
1FJ1	E_ARG_144	NH2	E_GLU_146	OE2	3.724
1FJ1	E_LYS_157	NZ	E_GLU_168	OE2	3.224
1FJ1	E_LYS_159	NZ	E_GLU_168	OE2	3.688
1FJ1	E_LYS_175	NZ	E_GLU_174	OE1	3.503

1FJ1	E_LYS_189	NZ	E_GLU_160	OE1	2.964
1FJ1	E_LYS_189	NZ	E_GLU_160	OE2	3.493
1FJ1	E_LYS_212	NZ	E_ASP_203	OD2	3.853
1FJ1	F_LYS_117	NZ	F_ASP_118	OD1	3.790
1FJ1	F_ARG_139	NH1	F_GLU_160	OE2	3.340
1FJ1	F_ARG_139	NH2	F_GLU_160	OE2	3.235
1FJ1	F_ARG_144	NH1	F_GLU_146	OE2	2.359
1FJ1	F_ARG_144	NH2	F_GLU_146	OE2	3.733
1FJ1	F_LYS_157	NZ	F_GLU_168	OE2	3.244
1FJ1	F_LYS_159	NZ	F_GLU_168	OE2	3.700
1FJ1	F_LYS_175	NZ	F_GLU_174	OE1	3.506
1FJ1	F_LYS_189	NZ	F_GLU_160	OE1	2.954
1FJ1	F_LYS_189	NZ	F_GLU_160	OE2	3.524
1FJ1	F_LYS_212	NZ	F_ASP_203	OD2	3.830

Table 66: 1FJ1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1FRG	L_LYS_24	NZ	L_ASP_76	OD2	3.234
1FRG	L_ARG_67	NH2	L_GLU_87	OE2	3.036
1FRG	L_ARG_67	NH2	L_ASP_88	OD1	2.765
1FRG	L_ARG_67	NH2	L_ASP_88	OD2	3.277
1FRG	L_LYS_109	NZ	L_ASP_171	OD1	2.782
1FRG	L_LYS_109	NZ	L_ASP_171	OD2	3.487
1FRG	L_LYS_113	NZ	L_GLU_17	OE2	3.158
1FRG	L_LYS_148	NZ	L_GLU_111	OE2	3.465
1FRG	L_LYS_155	NZ	L_GLU_201	OE1	3.359
1FRG	L_LYS_155	NZ	L_GLU_201	OE2	3.552
1FRG	L_ARG_161	NH2	L_GLU_191	OE1	3.188
1FRG	L_ARG_161	NH2	L_GLU_191	OE2	2.743
1FRG	L_LYS_175	NZ	L_ASP_176	OD2	3.335
1FRG	L_ARG_194	NH2	L_ASP_190	OD2	3.738
1FRG	L_LYS_205	NZ	L_ASP_116	OD1	2.961
1FRG	L_LYS_205	NZ	L_ASP_116	OD2	3.132
1FRG	L_LYS_213	NZ	H_ASP_354	OD1	3.324
1FRG	L_ARG_217	NH2	L_GLU_193	OE1	3.045
1FRG	H_ARG_255	NH1	H_GLU_263	OE1	2.874
1FRG	H_ARG_255	NH2	H_ASP_307	OD1	2.867
1FRG	H_LYS_282	NZ	H_ASP_279	OD1	3.750
1FRG	H_LYS_282	NZ	H_ASP_279	OD2	3.157
1FRG	H_ARG_284	NH1	H_ASP_307	OD1	3.863
1FRG	H_ARG_284	NH1	H_ASP_307	OD2	2.813
1FRG	H_ARG_284	NH2	H_ASP_307	OD1	2.826
1FRG	H_ARG_284	NH2	H_ASP_307	OD2	3.114
1FRG	H_LYS_304	NZ	H_GLU_306	OE2	3.614
1FRG	H_ARG_315	NH1	H_GLU_317	OE1	2.677
1FRG	H_ARG_315	NH1	H_GLU_317	OE2	3.312
1FRG	H_ARG_316	NH1	L_ASP_97	OD1	2.879
1FRG	H_ARG_316	NH2	L_ASP_97	OD1	3.078
1FRG	H_ARG_316	NH2	P_ASP_5	OD2	2.959
1FRG	H_LYS_322	NZ	L_GLU_61	OE1	2.861
1FRG	H_LYS_322	NZ	L_GLU_61	OE2	3.997
1FRG	H_LYS_432	NZ	L_GLU_129	OE1	3.086
1FRG	H_LYS_432	NZ	L_GLU_129	OE2	3.769

Table 67: 1FRG-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1FUJ	A_HIS_20	NE2	A_GLU_157	OE2	3.467
1FUJ	A_ARG_27	NH2	A_GLU_157	OE1	3.676
1FUJ	A_ARG_27	NH2	A_GLU_157	OE2	3.673
1FUJ	A_HIS_57	ND1	A_ASP_102	OD1	3.496
1FUJ	A_HIS_57	ND1	A_ASP_102	OD2	2.542
1FUJ	A_HIS_71	NE2	A_GLU_21	OE2	2.398
1FUJ	A_LYS_187	NZ	B_GLU_97	OE1	3.506
1FUJ	B_ARG_27	NH1	B_GLU_157	OE1	2.690
1FUJ	B_ARG_27	NH1	B_GLU_157	OE2	2.783
1FUJ	B_HIS_57	ND1	B_ASP_102	OD1	3.393
1FUJ	B_HIS_57	ND1	B_ASP_102	OD2	2.604
1FUJ	B_HIS_71	NE2	B_GLU_21	OE2	2.397
1FUJ	B_ARG_143	NH1	A_ASP_61	OD2	3.455
1FUJ	B_LYS_187	NZ	A_GLU_97	OE1	3.870
1FUJ	C_HIS_20	ND1	C_GLU_157	OE2	3.974
1FUJ	C_HIS_20	NE2	C_GLU_157	OE2	3.570
1FUJ	C_ARG_27	NH2	C_GLU_157	OE1	2.756
1FUJ	C_ARG_27	NH2	C_GLU_157	OE2	3.280
1FUJ	C_HIS_57	ND1	C_ASP_102	OD1	3.598
1FUJ	C_HIS_57	ND1	C_ASP_102	OD2	2.742
1FUJ	C_ARG_60	NH2	C_ASP_61	OD1	3.164
1FUJ	C_HIS_71	NE2	C_GLU_21	OE2	2.759
1FUJ	C_ARG_143	NH2	D_ASP_61	OD1	3.394
1FUJ	C_ARG_143	NH2	D_ASP_61	OD2	3.428
1FUJ	C_LYS_187	NZ	D_GLU_97	OE2	2.917
1FUJ	D_HIS_20	NE2	D_GLU_157	OE2	3.668
1FUJ	D_ARG_27	NH1	D_GLU_157	OE1	2.572
1FUJ	D_ARG_27	NH1	D_GLU_157	OE2	3.950
1FUJ	D_HIS_57	ND1	D_ASP_102	OD1	3.325
1FUJ	D_HIS_57	ND1	D_ASP_102	OD2	2.459
1FUJ	D_HIS_71	NE2	D_GLU_21	OE2	2.398
1FUJ	D_HIS_147	ND1	C_GLU_97	OE1	3.734
1FUJ	D_LYS_187	NZ	C_GLU_97	OE1	3.930

Table 68: 1FUJ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1FVC	A_ARG_24	NH1	A_ASP_70	OD1	3.629
1FVC	A_ARG_24	NH1	A_ASP_70	OD2	3.125
1FVC	A_ARG_24	NH2	A_ASP_70	OD2	3.258
1FVC	A_ARG_61	NH2	A_GLU_81	OE2	3.238
1FVC	A_ARG_61	NH2	A_ASP_82	OD1	2.827
1FVC	A_ARG_61	NH2	A_ASP_82	OD2	3.397
1FVC	A_LYS_107	NZ	A_ASP_17	OD2	3.723
1FVC	B_LYS_30	NZ	B_ASP_31	OD1	2.864
1FVC	B_ARG_38	NH1	B_ASP_90	OD1	3.106
1FVC	B_ARG_38	NH2	B_GLU_46	OE1	3.355
1FVC	B_ARG_38	NH2	B_ASP_90	OD1	3.972
1FVC	B_ARG_67	NH1	B_ASP_90	OD1	3.826
1FVC	B_ARG_67	NH1	B_ASP_90	OD2	2.865
1FVC	B_ARG_67	NH2	B_ASP_90	OD1	2.815
1FVC	B_ARG_67	NH2	B_ASP_90	OD2	3.370
1FVC	B_LYS_76	NZ	B_ASP_73	OD2	3.296
1FVC	B_ARG_98	NH1	B_ASP_108	OD1	3.172
1FVC	B_ARG_98	NH1	B_ASP_108	OD2	2.880
1FVC	C_ARG_61	NH1	C_GLU_81	OE2	3.955
1FVC	C_ARG_61	NH2	C_GLU_81	OE2	3.336
1FVC	C_ARG_61	NH2	C_ASP_82	OD1	2.944
1FVC	C_ARG_61	NH2	C_ASP_82	OD2	3.489
1FVC	C_ARG_66	NH2	C_ASP_28	OD1	3.198
1FVC	D_ARG_38	NH1	D_ASP_90	OD1	3.684
1FVC	D_ARG_38	NH2	D_GLU_46	OE1	3.562
1FVC	D_ARG_67	NH1	D_ASP_90	OD1	3.498
1FVC	D_ARG_67	NH1	D_ASP_90	OD2	2.863
1FVC	D_ARG_67	NH2	D_ASP_90	OD1	3.039
1FVC	D_ARG_67	NH2	D_ASP_90	OD2	3.182
1FVC	D_ARG_98	NH1	D_ASP_108	OD1	3.384
1FVC	D_ARG_98	NH1	D_ASP_108	OD2	2.939

Table 69: 1FVC-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1FVD	A_ARG_18	NH1	C_ASP_70	OD2	3.361
1FVD	A_ARG_24	NH2	A_ASP_70	OD1	3.049
1FVD	A_ARG_24	NH2	A_ASP_70	OD2	3.841
1FVD	A_ARG_61	NH2	A_GLU_81	OE2	3.219
1FVD	A_ARG_61	NH2	A_ASP_82	OD1	3.298
1FVD	A_ARG_61	NH2	A_ASP_82	OD2	3.528
1FVD	A_ARG_66	NH2	A_ASP_28	OD1	3.272
1FVD	A_LYS_103	NZ	A_GLU_165	OE2	2.750
1FVD	A_ARG_142	NH1	A_GLU_105	OE1	3.252
1FVD	A_ARG_142	NH1	A_GLU_105	OE2	3.136
1FVD	A_ARG_142	NH2	A_GLU_105	OE1	2.987
1FVD	A_ARG_142	NH2	A_GLU_105	OE2	3.986
1FVD	A_LYS_183	NZ	A_GLU_187	OE2	3.983
1FVD	A_LYS_188	NZ	A_ASP_185	OD1	3.689
1FVD	B_ARG_38	NH1	B_ASP_90	OD1	2.959
1FVD	B_ARG_38	NH2	B_GLU_46	OE1	3.651
1FVD	B_ARG_38	NH2	B_ASP_90	OD1	3.403
1FVD	B_LYS_65	NZ	B_ASP_62	OD1	3.297
1FVD	B_ARG_67	NH1	B_ASP_90	OD2	3.358
1FVD	B_ARG_67	NH2	B_ASP_90	OD1	3.444
1FVD	B_ARG_67	NH2	B_ASP_90	OD2	3.537
1FVD	B_LYS_76	NZ	B_ASP_73	OD2	3.292
1FVD	B_ARG_98	NH2	B_ASP_108	OD1	3.885
1FVD	B_ARG_98	NH2	B_ASP_108	OD2	2.828
1FVD	B_LYS_150	NZ	B_ASP_151	OD1	3.971
1FVD	B_LYS_150	NZ	B_ASP_151	OD2	3.685
1FVD	B_LYS_216	NZ	A_GLU_123	OE2	3.426
1FVD	C_ARG_18	NH1	A_ASP_70	OD2	3.065
1FVD	C_ARG_24	NH1	C_ASP_70	OD1	3.877
1FVD	C_ARG_24	NH2	C_ASP_70	OD1	3.499
1FVD	C_ARG_24	NH2	C_ASP_70	OD2	3.062
1FVD	C_ARG_61	NH2	C_GLU_81	OE2	3.791
1FVD	C_ARG_61	NH2	C_ASP_82	OD1	2.871
1FVD	C_ARG_61	NH2	C_ASP_82	OD2	3.205
1FVD	C_ARG_66	NH2	C_ASP_28	OD1	3.599
1FVD	C_LYS_103	NZ	C_GLU_165	OE1	3.456
1FVD	C_ARG_142	NH1	C_GLU_105	OE1	3.866
1FVD	D_ARG_38	NH1	D_ASP_90	OD1	2.804
1FVD	D_ARG_38	NH2	D_GLU_46	OE1	3.405
1FVD	D_ARG_38	NH2	D_ASP_90	OD1	3.854
1FVD	D_ARG_67	NH1	D_ASP_90	OD1	3.794
1FVD	D_ARG_67	NH1	D_ASP_90	OD2	2.754
1FVD	D_ARG_67	NH2	D_ASP_90	OD1	2.991
1FVD	D_ARG_67	NH2	D_ASP_90	OD2	3.196
1FVD	D_LYS_76	NZ	D_ASP_73	OD2	3.310
1FVD	D_ARG_87	NH1	D_GLU_89	OE1	3.906
1FVD	D_ARG_87	NH2	D_GLU_89	OE1	3.896
1FVD	D_ARG_87	NH2	D_ASP_90	OD1	3.754
1FVD	D_ARG_98	NH1	D_ASP_108	OD1	3.545
1FVD	D_ARG_98	NH1	D_ASP_108	OD2	3.091
1FVD	D_LYS_150	NZ	D_ASP_151	OD1	3.457
1FVD	D_LYS_150	NZ	D_ASP_151	OD2	3.794
1FVD	D_LYS_213	NZ	D_ASP_215	OD1	2.673
1FVD	D_LYS_216	NZ	C_GLU_123	OE1	2.737

Table 70: 1FVD-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1FVE	A_ARG_18	NH1	C_ASP_70	OD1	3.613
1FVE	A_ARG_18	NH1	C_ASP_70	OD2	3.316
1FVE	A_ARG_24	NH2	A_ASP_70	OD1	3.581
1FVE	A_ARG_24	NH2	A_ASP_70	OD2	3.679
1FVE	A_ARG_61	NH2	A_GLU_81	OE2	3.047
1FVE	A_ARG_61	NH2	A_ASP_82	OD1	3.215
1FVE	A_ARG_61	NH2	A_ASP_82	OD2	3.538
1FVE	A_ARG_66	NH2	A_ASP_28	OD1	3.900
1FVE	A_LYS_103	NZ	A_GLU_105	OE1	3.573
1FVE	A_LYS_103	NZ	A_GLU_105	OE2	3.185
1FVE	A_LYS_103	NZ	A_GLU_165	OE1	2.869
1FVE	A_LYS_103	NZ	A_GLU_165	OE2	3.988
1FVE	A_ARG_142	NH2	A_GLU_105	OE1	3.848
1FVE	A_ARG_142	NH2	A_GLU_105	OE2	3.667
1FVE	A_ARG_142	NH2	A_GLU_165	OE2	3.452
1FVE	A_LYS_149	NZ	A_GLU_195	OE1	2.902
1FVE	A_LYS_169	NZ	A_ASP_167	OD2	3.928
1FVE	A_LYS_169	NZ	A_ASP_170	OD2	3.977
1FVE	B_ARG_38	NH1	B_ASP_90	OD1	3.055
1FVE	B_ARG_38	NH2	B_GLU_46	OE2	3.767
1FVE	B_ARG_38	NH2	B_ASP_90	OD1	3.522
1FVE	B_ARG_67	NH1	B_ASP_90	OD2	3.077
1FVE	B_ARG_67	NH2	B_ASP_90	OD1	3.046
1FVE	B_ARG_67	NH2	B_ASP_90	OD2	3.273
1FVE	B_LYS_76	NZ	B_ASP_73	OD2	3.045
1FVE	B_ARG_87	NH1	B_GLU_89	OE2	3.292
1FVE	B_ARG_98	NH2	B_ASP_108	OD2	3.050
1FVE	B_LYS_150	NZ	B_ASP_151	OD1	3.911
1FVE	B_LYS_150	NZ	B_ASP_151	OD2	3.600
1FVE	B_LYS_216	NZ	A_GLU_123	OE2	3.328
1FVE	B_LYS_217	NZ	B_GLU_219	OE1	3.280
1FVE	C_ARG_61	NH2	C_GLU_81	OE2	3.092
1FVE	C_ARG_61	NH2	C_ASP_82	OD1	2.991
1FVE	C_ARG_61	NH2	C_ASP_82	OD2	3.500
1FVE	C_LYS_103	NZ	C_GLU_165	OE1	3.377
1FVE	C_LYS_103	NZ	C_GLU_165	OE2	3.755
1FVE	C_ARG_142	NH2	C_GLU_105	OE1	3.256
1FVE	C_HIS_189	ND1	C_ASP_151	OD2	3.275
1FVE	C_LYS_190	NZ	C_ASP_151	OD1	3.284
1FVE	C_LYS_190	NZ	C_ASP_151	OD2	3.663
1FVE	D_ARG_38	NH1	D_GLU_46	OE1	3.179
1FVE	D_ARG_38	NH1	D_GLU_46	OE2	3.488
1FVE	D_ARG_38	NH2	D_ASP_90	OD1	2.634
1FVE	D_ARG_67	NH1	D_ASP_90	OD1	3.960
1FVE	D_ARG_67	NH1	D_ASP_90	OD2	2.712
1FVE	D_ARG_67	NH2	D_ASP_90	OD1	2.924
1FVE	D_ARG_67	NH2	D_ASP_90	OD2	3.109
1FVE	D_LYS_76	NZ	D_ASP_73	OD2	3.266
1FVE	D_ARG_87	NH1	D_GLU_89	OE2	3.190
1FVE	D_ARG_87	NH2	D_ASP_90	OD1	3.371
1FVE	D_ARG_98	NH1	D_ASP_108	OD1	3.433
1FVE	D_ARG_98	NH1	D_ASP_108	OD2	2.999
1FVE	D_LYS_150	NZ	D_ASP_151	OD1	3.818
1FVE	D_LYS_150	NZ	D_ASP_151	OD2	3.688

Table 71: 1FVE-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1G6V	A_HIS_4	NE2	A_ASP_19	OD2	3.118
1G6V	A_HIS_15	NE2	A_GLU_14	OE1	3.258
1G6V	A_ARG_58	NH1	A_GLU_69	OE1	3.110
1G6V	A_ARG_58	NH1	A_GLU_69	OE2	2.848
1G6V	A_LYS_76	NZ	A_ASP_71	OD2	3.042
1G6V	A_ARG_89	NH2	A_ASP_75	OD1	3.650
1G6V	A_ARG_89	NH2	A_ASP_75	OD2	3.835
1G6V	A_HIS_96	ND1	A_GLU_106	OE2	3.452
1G6V	A_HIS_96	NE2	A_GLU_106	OE1	3.503
1G6V	A_HIS_96	NE2	A_GLU_106	OE2	3.870
1G6V	A_HIS_107	ND1	A_GLU_117	OE1	3.817
1G6V	A_HIS_107	ND1	A_GLU_117	OE2	3.100
1G6V	A_HIS_119	NE2	A_GLU_117	OE2	2.477
1G6V	A_LYS_127	NZ	A_ASP_139	OD1	3.129
1G6V	A_LYS_168	NZ	A_GLU_238	OE1	3.560
1G6V	A_ARG_182	NH1	A_ASP_180	OD1	3.589
1G6V	A_ARG_182	NH1	A_ASP_180	OD2	3.216
1G6V	A_ARG_182	NH2	A_ASP_180	OD2	2.890
1G6V	A_LYS_225	NZ	A_ASP_165	OD1	3.680
1G6V	A_LYS_225	NZ	A_ASP_165	OD2	3.357
1G6V	A_ARG_227	NH1	A_ASP_101	OD2	3.543
1G6V	A_ARG_227	NH2	A_ASP_101	OD2	3.620
1G6V	A_LYS_228	NZ	A_GLU_238	OE1	3.937
1G6V	A_LYS_257	NZ	A_ASP_41	OD1	3.993
1G6V	K_ARG_838	NH1	K_GLU_887	OE1	3.646
1G6V	K_ARG_838	NH1	K_ASP_888	OD1	3.042
1G6V	K_ARG_838	NH2	K_GLU_846	OE1	3.505
1G6V	K_ARG_838	NH2	K_GLU_846	OE2	3.350
1G6V	K_ARG_838	NH2	K_GLU_887	OE1	3.576
1G6V	K_ARG_838	NH2	K_GLU_887	OE2	3.967
1G6V	K_ARG_865	NH1	K_ASP_888	OD2	3.258
1G6V	K_ARG_865	NH2	K_ASP_888	OD1	2.941
1G6V	K_ARG_865	NH2	K_ASP_888	OD2	3.106
1G6V	K_LYS_885	NZ	K_GLU_887	OE2	3.937
1G6V	K_ARG_907	NH1	A_GLU_187	OE2	2.962
1G6V	K_ARG_909	NH1	A_GLU_187	OE1	3.909
1G6V	K_ARG_909	NH2	A_GLU_187	OE1	3.477
1G6V	K_ARG_909	NH2	K_ASP_912	OD1	3.915

Table 72: 1G6V-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1G7H	A_ARG_61	NH1	A_GLU_81	OE2	3.037
1G7H	A_ARG_61	NH1	A_ASP_82	OD1	3.527
1G7H	A_ARG_61	NH1	A_ASP_82	OD2	2.782
1G7H	A_ARG_96	NH1	B_GLU_98	OE1	2.788
1G7H	A_ARG_96	NH1	B_GLU_98	OE2	3.317
1G7H	A_ARG_96	NH2	B_GLU_98	OE1	3.736
1G7H	A_ARG_96	NH2	B_GLU_98	OE2	2.819
1G7H	A_LYS_107	NZ	A_GLU_17	OE1	3.055
1G7H	A_LYS_107	NZ	A_GLU_17	OE2	3.162
1G7H	B_ARG_38	NH1	B_GLU_46	OE1	3.731
1G7H	B_ARG_38	NH1	B_GLU_46	OE2	3.064
1G7H	B_ARG_38	NH1	B_ASP_89	OD1	3.653
1G7H	B_ARG_38	NH2	B_ASP_89	OD1	3.025
1G7H	B_ARG_66	NH1	B_ASP_89	OD1	2.763
1G7H	B_ARG_66	NH1	B_ASP_89	OD2	2.968
1G7H	B_ARG_66	NH2	B_ASP_89	OD1	3.934
1G7H	B_ARG_66	NH2	B_ASP_89	OD2	2.612
1G7H	B_LYS_75	NZ	B_ASP_72	OD1	2.977
1G7H	B_ARG_97	NH1	B_ASP_104	OD1	3.709
1G7H	B_ARG_97	NH1	B_ASP_104	OD2	2.680
1G7H	B_ARG_102	NH2	B_ASP_100	OD1	3.012
1G7H	C_LYS_1	NZ	C_GLU_7	OE1	3.565
1G7H	C_ARG_61	NH2	C_ASP_48	OD2	3.173
1G7H	C_ARG_125	NH1	C_ASP_119	OD2	2.772
1G7H	C_ARG_125	NH2	C_ASP_119	OD1	3.386
1G7H	C_ARG_125	NH2	C_ASP_119	OD2	3.194

Table 73: 1G7H-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1G7I	A_ARG_61	NH1	A_GLU_81	OE2	2.718
1G7I	A_ARG_61	NH1	A_ASP_82	OD1	3.562
1G7I	A_ARG_61	NH1	A_ASP_82	OD2	2.822
1G7I	A_ARG_96	NH1	B_GLU_98	OE1	2.881
1G7I	A_ARG_96	NH1	B_GLU_98	OE2	3.589
1G7I	A_ARG_96	NH2	B_GLU_98	OE1	3.599
1G7I	A_ARG_96	NH2	B_GLU_98	OE2	2.841
1G7I	A_LYS_107	NZ	A_GLU_17	OE1	2.870
1G7I	A_LYS_107	NZ	A_GLU_17	OE2	3.799
1G7I	B_ARG_38	NH1	B_GLU_46	OE2	3.033
1G7I	B_ARG_38	NH1	B_ASP_89	OD1	3.781
1G7I	B_ARG_38	NH2	B_ASP_89	OD1	3.005
1G7I	B_ARG_66	NH1	B_ASP_89	OD1	2.745
1G7I	B_ARG_66	NH1	B_ASP_89	OD2	3.417
1G7I	B_ARG_66	NH2	B_ASP_89	OD1	3.758
1G7I	B_ARG_66	NH2	B_ASP_89	OD2	2.954
1G7I	B_ARG_97	NH1	B_ASP_104	OD1	3.710
1G7I	B_ARG_97	NH1	B_ASP_104	OD2	2.883
1G7I	B_ARG_102	NH2	B_ASP_100	OD1	3.310
1G7I	C_LYS_1	NZ	C_GLU_7	OE1	3.016
1G7I	C_LYS_1	NZ	C_GLU_7	OE2	3.596
1G7I	C_ARG_61	NH2	C_ASP_48	OD1	3.373
1G7I	C_ARG_68	NH2	C_ASP_66	OD2	3.145
1G7I	C_ARG_125	NH1	C_ASP_119	OD2	2.952
1G7I	C_ARG_125	NH2	C_ASP_119	OD1	3.392
1G7I	C_ARG_125	NH2	C_ASP_119	OD2	2.970

Table 74: 1G7I-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1G7J	A_ARG_61	NH1	A_GLU_81	OE2	3.122
1G7J	A_ARG_61	NH1	A_ASP_82	OD1	3.459
1G7J	A_ARG_61	NH1	A_ASP_82	OD2	2.826
1G7J	A_ARG_96	NH1	B_GLU_98	OE1	2.834
1G7J	A_ARG_96	NH1	B_GLU_98	OE2	3.535
1G7J	A_ARG_96	NH2	B_GLU_98	OE1	3.524
1G7J	A_ARG_96	NH2	B_GLU_98	OE2	2.694
1G7J	A_LYS_107	NZ	A_GLU_17	OE1	3.323
1G7J	A_LYS_107	NZ	A_GLU_17	OE2	2.601
1G7J	B_ARG_38	NH1	B_GLU_46	OE1	3.932
1G7J	B_ARG_38	NH1	B_GLU_46	OE2	2.970
1G7J	B_ARG_38	NH1	B_ASP_89	OD1	3.769
1G7J	B_ARG_38	NH2	B_ASP_89	OD1	2.824
1G7J	B_ARG_66	NH1	B_ASP_89	OD1	2.871
1G7J	B_ARG_66	NH1	B_ASP_89	OD2	3.276
1G7J	B_ARG_66	NH2	B_ASP_89	OD1	3.824
1G7J	B_ARG_66	NH2	B_ASP_89	OD2	2.793
1G7J	B_HIS_86	NE2	B_ASP_88	OD1	3.358
1G7J	B_HIS_86	NE2	B_ASP_88	OD2	3.564
1G7J	B_ARG_97	NH1	B_ASP_104	OD1	3.791
1G7J	B_ARG_97	NH1	B_ASP_104	OD2	2.737
1G7J	B_ARG_102	NH2	B_ASP_100	OD1	3.301
1G7J	C_LYS_1	NZ	C_GLU_7	OE1	2.740
1G7J	C_ARG_61	NH1	C_ASP_48	OD2	3.771
1G7J	C_ARG_125	NH1	C_ASP_119	OD2	3.004
1G7J	C_ARG_125	NH2	C_ASP_119	OD1	3.354
1G7J	C_ARG_125	NH2	C_ASP_119	OD2	3.147

Table 75: 1G7J-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1G7L	A_ARG_61	NH1	A_GLU_81	OE2	3.595
1G7L	A_ARG_61	NH1	A_ASP_82	OD1	3.389
1G7L	A_ARG_61	NH1	A_ASP_82	OD2	2.780
1G7L	A_ARG_96	NH1	B_GLU_98	OE1	2.744
1G7L	A_ARG_96	NH1	B_GLU_98	OE2	3.483
1G7L	A_ARG_96	NH2	B_GLU_98	OE1	3.535
1G7L	A_ARG_96	NH2	B_GLU_98	OE2	2.761
1G7L	A_LYS_107	NZ	A_GLU_17	OE1	3.286
1G7L	A_LYS_107	NZ	A_GLU_17	OE2	2.822
1G7L	B_ARG_38	NH1	B_GLU_46	OE2	3.105
1G7L	B_ARG_38	NH1	B_ASP_89	OD1	3.832
1G7L	B_ARG_38	NH2	B_ASP_89	OD1	2.874
1G7L	B_ARG_66	NH1	B_ASP_89	OD1	3.004
1G7L	B_ARG_66	NH1	B_ASP_89	OD2	3.786
1G7L	B_ARG_66	NH2	B_ASP_89	OD1	3.392
1G7L	B_ARG_66	NH2	B_ASP_89	OD2	2.877
1G7L	B_ARG_97	NH1	B_ASP_104	OD1	3.584
1G7L	B_ARG_97	NH1	B_ASP_104	OD2	2.551
1G7L	B_ARG_102	NH2	B_ASP_100	OD1	3.204
1G7L	C_LYS_1	NZ	C_GLU_7	OE1	2.763
1G7L	C_HIS_15	NE2	C_ASP_87	OD2	3.997
1G7L	C_ARG_61	NH2	C_ASP_48	OD2	2.882
1G7L	C_ARG_125	NH1	C_ASP_119	OD2	2.762
1G7L	C_ARG_125	NH2	C_ASP_119	OD1	3.327
1G7L	C_ARG_125	NH2	C_ASP_119	OD2	2.838

Table 76: 1G7L-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1G7M	A_ARG_61	NH1	A_GLU_81	OE2	3.936
1G7M	A_ARG_61	NH1	A_ASP_82	OD1	3.601
1G7M	A_ARG_61	NH1	A_ASP_82	OD2	2.851
1G7M	A_ARG_96	NH1	B_GLU_98	OE1	2.792
1G7M	A_ARG_96	NH1	B_GLU_98	OE2	3.493
1G7M	A_ARG_96	NH2	B_GLU_98	OE1	3.544
1G7M	A_ARG_96	NH2	B_GLU_98	OE2	2.732
1G7M	B_ARG_38	NH1	B_GLU_46	OE1	3.743
1G7M	B_ARG_38	NH1	B_GLU_46	OE2	3.134
1G7M	B_ARG_38	NH1	B_ASP_89	OD1	3.885
1G7M	B_ARG_38	NH2	B_ASP_89	OD1	2.901
1G7M	B_ARG_66	NH1	B_ASP_89	OD1	3.117
1G7M	B_ARG_66	NH1	B_ASP_89	OD2	3.721
1G7M	B_ARG_66	NH2	B_ASP_89	OD1	3.761
1G7M	B_ARG_66	NH2	B_ASP_89	OD2	2.897
1G7M	B_LYS_75	NZ	B_ASP_72	OD1	3.993
1G7M	B_ARG_97	NH1	B_ASP_104	OD1	3.720
1G7M	B_ARG_97	NH1	B_ASP_104	OD2	2.732
1G7M	B_ARG_102	NH2	B_ASP_100	OD1	3.308
1G7M	C_LYS_1	NZ	C_GLU_7	OE1	2.835
1G7M	C_ARG_61	NH2	C_ASP_48	OD2	3.861
1G7M	C_ARG_125	NH1	C_ASP_119	OD2	2.991
1G7M	C_ARG_125	NH2	C_ASP_119	OD1	3.407
1G7M	C_ARG_125	NH2	C_ASP_119	OD2	3.048

Table 77: 1G7M-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1G8Q	A_LYS_121	NZ	A_ASP_122	OD1	2.599
1G8Q	A_LYS_121	NZ	A_ASP_122	OD2	3.460
1G8Q	A_LYS_124	NZ	A_ASP_195	OD1	3.016
1G8Q	A_LYS_124	NZ	A_ASP_195	OD2	3.072
1G8Q	A_LYS_187	NZ	A_ASP_155	OD2	2.795
1G8Q	A_HIS_191	NE2	A_ASP_128	OD1	3.354
1G8Q	A_HIS_191	NE2	A_ASP_128	OD2	2.859
1G8Q	A_LYS_193	NZ	A_ASP_155	OD1	3.991
1G8Q	B_LYS_224	NZ	B_ASP_295	OD1	2.542
1G8Q	B_LYS_224	NZ	B_ASP_295	OD2	3.203
1G8Q	B_HIS_291	NE2	B_ASP_228	OD1	2.670
1G8Q	B_HIS_291	NE2	B_ASP_228	OD2	3.342
1G8Q	B_LYS_293	NZ	B_GLU_288	OE2	2.739

Table 78: 1G8Q-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1G9M	G_LYS_207	NZ	G_GLU_381	OE1	3.792
1G9M	G_LYS_207	NZ	G_GLU_381	OE2	2.500
1G9M	G_LYS_231	NZ	G_GLU_268	OE2	3.144
1G9M	G_HIS_249	NE2	G_GLU_482	OE1	3.558
1G9M	G_HIS_249	NE2	G_GLU_482	OE2	3.514
1G9M	G_LYS_337	NZ	G_GLU_293	OE2	3.954
1G9M	G_LYS_348	NZ	G_GLU_269	OE2	2.920
1G9M	G_LYS_348	NZ	G_GLU_351	OE2	3.765
1G9M	G_LYS_357	NZ	G_GLU_466	OE1	3.174
1G9M	G_ARG_419	NH1	H_GLU_103	OE2	3.773
1G9M	G_ARG_419	NH2	H_GLU_103	OE2	2.762
1G9M	G_ARG_419	NH2	H_GLU_108	OE2	3.794
1G9M	G_ARG_456	NH2	G_GLU_466	OE1	3.727
1G9M	G_ARG_456	NH2	G_GLU_466	OE2	3.003
1G9M	G_ARG_469	NH2	G_ASP_457	OD1	3.290
1G9M	G_ARG_476	NH1	G_ASP_474	OD1	2.906
1G9M	G_ARG_480	NH1	G_ASP_477	OD1	2.553
1G9M	G_LYS_487	NZ	G_GLU_91	OE1	3.951
1G9M	G_LYS_487	NZ	G_GLU_91	OE2	2.923
1G9M	C_LYS_8	NZ	C_GLU_119	OE1	2.848
1G9M	C_HIS_27	NE2	C_GLU_85	OE1	2.711
1G9M	C_LYS_29	NZ	G_ASP_279	OD2	3.077
1G9M	C_LYS_29	NZ	C_GLU_85	OE1	2.735
1G9M	C_LYS_29	NZ	C_GLU_85	OE2	3.809
1G9M	C_LYS_46	NZ	C_ASP_56	OD1	3.759
1G9M	C_ARG_54	NH1	C_ASP_78	OD1	3.768
1G9M	C_ARG_54	NH1	C_ASP_78	OD2	2.778
1G9M	C_ARG_54	NH2	C_ASP_78	OD1	2.931
1G9M	C_ARG_54	NH2	C_ASP_78	OD2	3.434
1G9M	C_ARG_59	NH1	G_ASP_368	OD1	3.576
1G9M	C_ARG_59	NH1	G_ASP_368	OD2	3.197
1G9M	C_ARG_59	NH2	G_ASP_368	OD1	2.550
1G9M	C_ARG_59	NH2	G_ASP_368	OD2	3.360
1G9M	C_ARG_134	NH2	C_ASP_153	OD1	3.987
1G9M	L_ARG_24	NH2	L_GLU_3	OE2	3.072
1G9M	L_ARG_61	NH2	L_GLU_81	OE2	3.403
1G9M	L_ARG_61	NH2	L_ASP_82	OD1	2.707
1G9M	L_ARG_61	NH2	L_ASP_82	OD2	3.381
1G9M	L_LYS_151	NZ	L_GLU_197	OE1	3.157
1G9M	L_LYS_151	NZ	L_GLU_197	OE2	3.538
1G9M	L_HIS_191	ND1	L_ASP_153	OD2	3.573
1G9M	H_LYS_12	NZ	H_GLU_10	OE1	3.811
1G9M	H_LYS_19	NZ	H_GLU_82	OE2	2.937
1G9M	H_ARG_31	NH2	H_GLU_103	OE1	3.557
1G9M	H_ARG_31	NH2	H_ASP_105	OD1	3.841
1G9M	H_ARG_31	NH2	H_ASP_105	OD2	3.073
1G9M	H_ARG_38	NH1	H_GLU_46	OE1	3.715
1G9M	H_ARG_38	NH1	H_GLU_46	OE2	2.917
1G9M	H_ARG_38	NH2	H_ASP_90	OD2	2.688
1G9M	H_ARG_50	NH2	H_GLU_101	OE2	2.484
1G9M	H_HIS_63	NE2	H_GLU_46	OE1	3.776
1G9M	H_HIS_63	NE2	H_GLU_46	OE2	2.782
1G9M	H_ARG_67	NH1	H_ASP_90	OD1	2.916
1G9M	H_ARG_67	NH1	H_ASP_90	OD2	3.928
1G9M	H_ARG_67	NH2	H_ASP_90	OD1	3.114
1G9M	H_ARG_67	NH2	H_ASP_90	OD2	2.646
1G9M	H_LYS_74	NZ	H_ASP_56	OD1	3.247

1G9M	H_LYS_74	NZ	H_ASP_56	OD2	3.751
1G9M	H_ARG_84	NH2	H_GLU_82	OE1	2.803
1G9M	H_ARG_110	NH2	H_GLU_108	OE1	3.721
1G9M	H_LYS_158	NZ	H_ASP_159	OD1	2.791
1G9M	H_LYS_158	NZ	H_ASP_159	OD2	2.929

Table 79: 1G9M-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1G9N	G_LYS_121	NZ	G_GLU_429	OE1	2.598
1G9N	G_LYS_121	NZ	G_GLU_429	OE2	3.835
1G9N	G_LYS_207	NZ	G_GLU_381	OE1	3.761
1G9N	G_LYS_207	NZ	G_GLU_381	OE2	3.069
1G9N	G_HIS_249	NE2	G_GLU_482	OE1	3.588
1G9N	G_LYS_282	NZ	G_GLU_275	OE1	3.728
1G9N	G_LYS_282	NZ	G_GLU_275	OE2	2.699
1G9N	G_LYS_348	NZ	G_GLU_269	OE2	3.322
1G9N	G_LYS_348	NZ	G_GLU_351	OE1	3.879
1G9N	G_LYS_348	NZ	G_GLU_351	OE2	3.198
1G9N	G_LYS_350	NZ	G_ASP_395	OD1	3.491
1G9N	G_LYS_357	NZ	G_GLU_466	OE1	3.697
1G9N	G_ARG_419	NH1	H_GLU_106	OE1	2.930
1G9N	G_ARG_419	NH1	H_GLU_106	OE2	3.665
1G9N	G_ARG_419	NH2	H_GLU_103	OE1	2.300
1G9N	G_ARG_419	NH2	H_GLU_106	OE2	3.990
1G9N	G_ARG_456	NH2	G_GLU_466	OE1	3.622
1G9N	G_ARG_456	NH2	G_GLU_466	OE2	3.509
1G9N	G_ARG_469	NH2	G_ASP_457	OD1	3.668
1G9N	G_ARG_476	NH1	G_ASP_474	OD1	3.685
1G9N	G_ARG_476	NH2	G_GLU_102	OE1	3.192
1G9N	G_ARG_476	NH2	G_GLU_102	OE2	2.740
1G9N	G_ARG_480	NH1	G_ASP_477	OD1	3.994
1G9N	G_LYS_487	NZ	G_GLU_91	OE2	3.841
1G9N	G_LYS_490	NZ	G_GLU_492	OE1	3.571
1G9N	C_LYS_29	NZ	C_GLU_85	OE1	3.106
1G9N	C_LYS_29	NZ	C_GLU_85	OE2	3.864
1G9N	C_LYS_35	NZ	G_ASP_457	OD2	3.608
1G9N	C_ARG_54	NH1	C_ASP_78	OD1	3.979
1G9N	C_ARG_54	NH1	C_ASP_78	OD2	2.754
1G9N	C_ARG_54	NH2	C_ASP_78	OD1	2.744
1G9N	C_ARG_54	NH2	C_ASP_78	OD2	3.015
1G9N	C_ARG_59	NH1	G_ASP_368	OD1	3.032
1G9N	C_ARG_59	NH1	G_ASP_368	OD2	3.045
1G9N	C_ARG_59	NH2	G_ASP_368	OD1	2.609
1G9N	C_ARG_59	NH2	G_ASP_368	OD2	3.355
1G9N	C_HIS_107	ND1	C_ASP_105	OD1	2.754
1G9N	C_HIS_107	ND1	C_ASP_105	OD2	3.107
1G9N	C_ARG_134	NH2	C_ASP_153	OD1	3.650
1G9N	C_LYS_136	NZ	C_GLU_150	OE2	3.852
1G9N	C_LYS_136	NZ	C_ASP_153	OD1	3.794
1G9N	C_LYS_136	NZ	C_ASP_153	OD2	2.773
1G9N	C_LYS_171	NZ	C_GLU_169	OE1	3.972
1G9N	C_LYS_171	NZ	C_GLU_169	OE2	2.770
1G9N	L_ARG_61	NH2	L_GLU_81	OE1	3.113
1G9N	L_ARG_61	NH2	L_ASP_82	OD1	3.659
1G9N	L_ARG_97	NH2	L_GLU_1	OE1	3.685
1G9N	L_ARG_97	NH2	L_GLU_1	OE2	2.961
1G9N	L_HIS_191	ND1	L_ASP_153	OD2	2.588
1G9N	L_HIS_191	NE2	L_ASP_187	OD2	2.897
1G9N	L_ARG_213	NH1	L_GLU_189	OE1	3.830
1G9N	H_ARG_31	NH2	H_ASP_105	OD1	3.178
1G9N	H_ARG_31	NH2	H_ASP_105	OD2	3.436
1G9N	H_ARG_38	NH1	H_GLU_46	OE1	2.711
1G9N	H_ARG_38	NH1	H_GLU_46	OE2	3.252
1G9N	H_ARG_38	NH2	H_ASP_90	OD2	2.680
1G9N	H_ARG_50	NH2	H_GLU_101	OE2	2.305

1G9N	H_ARG_67	NH1	H_ASP_90	OD1	3.457
1G9N	H_ARG_67	NH2	H_ASP_90	OD1	2.540
1G9N	H_ARG_67	NH2	H_ASP_90	OD2	2.635
1G9N	H_LYS_74	NZ	H_ASP_56	OD2	2.889
1G9N	H_ARG_84	NH2	H_GLU_82	OE1	3.161
1G9N	H_ARG_110	NH1	H_GLU_108	OE1	3.833
1G9N	H_ARG_110	NH2	H_GLU_108	OE1	3.692
1G9N	H_LYS_158	NZ	H_ASP_159	OD1	2.649
1G9N	H_LYS_158	NZ	H_ASP_159	OD2	3.459
1G9N	H_LYS_224	NZ	L_GLU_125	OE1	3.507
1G9N	H_LYS_224	NZ	L_GLU_125	OE2	3.538
1G9N	H_LYS_229	NZ	L_ASP_124	OD2	3.557

Table 80: 1G9N-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1GC1	G_LYS_207	NZ	G_GLU_381	OE1	3.546
1GC1	G_LYS_207	NZ	G_GLU_381	OE2	2.763
1GC1	G_LYS_231	NZ	G_GLU_268	OE1	2.870
1GC1	G_HIS_249	NE2	G_GLU_482	OE1	2.874
1GC1	G_LYS_282	NZ	G_ASP_279	OD2	2.766
1GC1	G_ARG_335	NH1	G_ASP_412	OD1	2.680
1GC1	G_ARG_335	NH1	G_ASP_412	OD2	3.973
1GC1	G_ARG_335	NH2	G_ASP_412	OD1	3.328
1GC1	G_LYS_337	NZ	G_GLU_293	OE1	2.668
1GC1	G_LYS_357	NZ	G_GLU_466	OE2	3.400
1GC1	G_ARG_419	NH1	H_GLU_106	OE1	2.761
1GC1	G_ARG_419	NH2	H_GLU_106	OE1	2.942
1GC1	G_ARG_419	NH2	H_GLU_108	OE1	3.887
1GC1	G_ARG_419	NH2	H_GLU_108	OE2	3.401
1GC1	G_ARG_456	NH2	G_GLU_466	OE1	2.736
1GC1	G_ARG_456	NH2	G_GLU_466	OE2	3.604
1GC1	G_ARG_469	NH2	G_ASP_457	OD1	3.571
1GC1	G_ARG_469	NH2	G_ASP_457	OD2	2.956
1GC1	G_ARG_476	NH1	G_ASP_474	OD1	3.210
1GC1	G_ARG_480	NH1	G_ASP_477	OD1	3.075
1GC1	C_LYS_1	NZ	C_GLU_92	OE1	2.611
1GC1	C_LYS_7	NZ	C_ASP_10	OD1	3.825
1GC1	C_LYS_7	NZ	C_ASP_10	OD2	2.811
1GC1	C_LYS_8	NZ	C_GLU_119	OE1	2.599
1GC1	C_HIS_27	ND1	C_GLU_85	OE1	2.734
1GC1	C_LYS_29	NZ	G_ASP_279	OD1	2.748
1GC1	C_LYS_29	NZ	C_GLU_85	OE1	2.817
1GC1	C_LYS_29	NZ	C_GLU_85	OE2	3.379
1GC1	C_LYS_46	NZ	C_ASP_56	OD2	2.852
1GC1	C_LYS_50	NZ	C_GLU_77	OE1	2.464
1GC1	C_LYS_50	NZ	C_GLU_77	OE2	3.327
1GC1	C_ARG_54	NH1	C_ASP_78	OD1	3.681
1GC1	C_ARG_54	NH1	C_ASP_78	OD2	2.523
1GC1	C_ARG_54	NH2	C_ASP_78	OD1	2.648
1GC1	C_ARG_54	NH2	C_ASP_78	OD2	3.132
1GC1	C_ARG_59	NH1	G_ASP_368	OD1	2.780
1GC1	C_ARG_59	NH1	G_ASP_368	OD2	3.645
1GC1	C_ARG_59	NH2	G_ASP_368	OD1	3.062
1GC1	C_ARG_59	NH2	G_ASP_368	OD2	2.481
1GC1	C_LYS_90	NZ	C_GLU_85	OE2	3.366
1GC1	C_ARG_134	NH2	C_ASP_153	OD1	3.312
1GC1	C_ARG_134	NH2	C_ASP_153	OD2	3.071
1GC1	C_LYS_167	NZ	C_GLU_169	OE1	3.179
1GC1	L_ARG_24	NH1	L_GLU_3	OE1	2.728
1GC1	L_ARG_24	NH2	L_GLU_3	OE1	3.024
1GC1	L_ARG_24	NH2	L_GLU_3	OE2	3.874
1GC1	L_ARG_61	NH1	L_GLU_81	OE2	3.374
1GC1	L_ARG_61	NH1	L_ASP_82	OD1	2.506
1GC1	L_ARG_61	NH1	L_ASP_82	OD2	2.919
1GC1	L_ARG_61	NH2	L_GLU_81	OE2	3.159
1GC1	L_LYS_128	NZ	L_ASP_124	OD1	2.735
1GC1	L_LYS_185	NZ	L_GLU_189	OE1	3.492
1GC1	L_LYS_185	NZ	L_GLU_189	OE2	3.997
1GC1	L_HIS_191	ND1	L_ASP_153	OD2	3.341
1GC1	L_HIS_191	NE2	L_ASP_187	OD1	2.956
1GC1	L_HIS_191	NE2	L_ASP_187	OD2	3.839
1GC1	H_LYS_12	NZ	H_GLU_10	OE1	2.918

1GC1	H_LYS_19	NZ	H_GLU_82	OE1	2.992
1GC1	H_ARG_31	NH1	H_GLU_106	OE2	2.532
1GC1	H_ARG_38	NH1	H_GLU_46	OE2	2.989
1GC1	H_ARG_38	NH1	H_ASP_90	OD1	3.814
1GC1	H_ARG_38	NH2	H_ASP_90	OD1	2.619
1GC1	H_ARG_50	NH2	H_GLU_101	OE2	2.957
1GC1	H_HIS_63	NE2	H_GLU_46	OE1	3.828
1GC1	H_HIS_63	NE2	H_GLU_46	OE2	2.878
1GC1	H_ARG_67	NH1	H_ASP_90	OD1	3.587
1GC1	H_ARG_67	NH1	H_ASP_90	OD2	2.706
1GC1	H_ARG_67	NH2	H_ASP_90	OD1	2.708
1GC1	H_ARG_67	NH2	H_ASP_90	OD2	3.261
1GC1	H_ARG_84	NH2	H_GLU_82	OE2	2.925
1GC1	H_LYS_158	NZ	H_ASP_159	OD1	2.936
1GC1	H_LYS_158	NZ	H_ASP_159	OD2	3.481
1GC1	H_LYS_224	NZ	L_GLU_125	OE1	2.581
1GC1	H_LYS_224	NZ	L_GLU_125	OE2	3.963

Table 81: 1GC1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1GGB	L_LYS_39	NZ	L_ASP_81	OD1	3.691
1GGB	L_ARG_61	NH2	L_ASP_82	OD1	3.069
1GGB	L_ARG_61	NH2	L_ASP_82	OD2	3.921
1GGB	L_LYS_149	NZ	L_GLU_195	OE1	3.055
1GGB	L_LYS_149	NZ	L_GLU_195	OE2	3.602
1GGB	L_ARG_155	NH1	L_GLU_185	OE1	3.649
1GGB	L_ARG_155	NH2	L_GLU_185	OE1	2.814
1GGB	L_HIS_189	ND1	L_ASP_151	OD2	3.149
1GGB	L_ARG_211	NH2	L_GLU_187	OE2	3.888
1GGB	H_ARG_38	NH1	H_ASP_86	OD1	3.008
1GGB	H_ARG_38	NH2	H_GLU_46	OE1	3.247
1GGB	H_ARG_38	NH2	H_ASP_86	OD1	3.365
1GGB	H_ARG_58	NH1	L_ASP_94	OD1	3.623
1GGB	H_ARG_58	NH2	L_ASP_94	OD1	2.873
1GGB	H_ARG_66	NH1	H_ASP_83	OD1	3.682
1GGB	H_ARG_66	NH1	H_ASP_86	OD1	3.167
1GGB	H_ARG_66	NH1	H_ASP_86	OD2	3.895
1GGB	H_ARG_66	NH2	H_ASP_83	OD1	3.328
1GGB	H_ARG_66	NH2	H_ASP_86	OD1	3.262
1GGB	H_ARG_66	NH2	H_ASP_86	OD2	2.539
1GGB	H_LYS_221	NZ	L_GLU_123	OE1	2.690
1GGB	H_LYS_221	NZ	L_GLU_123	OE2	3.205
1GGB	H_LYS_222	NZ	H_GLU_226	OE2	3.191

Table 82: 1GGB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1GGC	L_ARG_61	NH1	L_GLU_79	OE2	3.692
1GGC	L_ARG_61	NH1	L_ASP_82	OD1	3.115
1GGC	L_ARG_61	NH1	L_ASP_82	OD2	2.752
1GGC	L_ARG_61	NH2	L_GLU_79	OE1	3.661
1GGC	L_ARG_61	NH2	L_GLU_79	OE2	3.675
1GGC	L_ARG_61	NH2	L_ASP_82	OD1	3.438
1GGC	L_LYS_149	NZ	L_GLU_195	OE2	3.691
1GGC	L_ARG_155	NH2	L_GLU_185	OE2	2.870
1GGC	L_LYS_183	NZ	L_GLU_187	OE1	3.373
1GGC	L_LYS_183	NZ	L_GLU_187	OE2	3.046
1GGC	L_LYS_199	NZ	L_ASP_110	OD1	3.437
1GGC	L_LYS_199	NZ	L_ASP_110	OD2	2.666
1GGC	H_ARG_38	NH1	H_ASP_86	OD1	3.206
1GGC	H_ARG_38	NH2	H_GLU_46	OE1	3.183
1GGC	H_ARG_38	NH2	H_ASP_86	OD1	3.921
1GGC	H_ARG_58	NH2	L_ASP_94	OD1	3.221
1GGC	H_ARG_66	NH1	H_ASP_86	OD1	3.876
1GGC	H_ARG_66	NH2	H_ASP_86	OD1	2.865
1GGC	H_ARG_66	NH2	H_ASP_86	OD2	2.907
1GGC	H_LYS_218	NZ	H_ASP_220	OD1	3.849
1GGC	H_LYS_221	NZ	L_GLU_123	OE1	2.942

Table 83: 1GGC-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1GGI	L_LYS_39	NZ	L_ASP_81	OD2	3.200
1GGI	L_ARG_61	NH2	L_ASP_82	OD1	3.494
1GGI	L_ARG_61	NH2	L_ASP_82	OD2	3.194
1GGI	L_LYS_142	NZ	L_GLU_105	OE1	3.057
1GGI	L_LYS_149	NZ	L_GLU_195	OE1	3.085
1GGI	L_LYS_149	NZ	L_GLU_195	OE2	2.765
1GGI	L_ARG_155	NH2	L_GLU_185	OE1	2.906
1GGI	L_ARG_155	NH2	L_GLU_185	OE2	3.331
1GGI	L_LYS_183	NZ	L_GLU_187	OE1	2.955
1GGI	L_LYS_183	NZ	L_GLU_187	OE2	3.308
1GGI	H_ARG_38	NH1	H_GLU_46	OE1	2.813
1GGI	H_ARG_38	NH2	H_ASP_86	OD1	2.641
1GGI	H_HIS_50	NE2	H_GLU_95	OE1	3.102
1GGI	H_ARG_58	NH1	H_ASP_56	OD1	3.338
1GGI	H_ARG_58	NH1	H_ASP_56	OD2	3.571
1GGI	H_ARG_58	NH2	L_ASP_94	OD2	3.749
1GGI	H_ARG_66	NH1	H_ASP_86	OD1	3.518
1GGI	H_ARG_66	NH1	H_ASP_86	OD2	3.473
1GGI	H_ARG_66	NH2	H_ASP_86	OD1	3.109
1GGI	H_ARG_66	NH2	H_ASP_86	OD2	2.810
1GGI	H_LYS_221	NZ	L_GLU_123	OE2	3.900
1GGI	P_LYS_312	NZ	H_ASP_54	OD1	2.914
1GGI	P_LYS_312	NZ	H_ASP_54	OD2	3.188
1GGI	P_LYS_312	NZ	H_ASP_56	OD1	2.830
1GGI	P_LYS_312	NZ	H_ASP_56	OD2	3.728
1GGI	M_ARG_24	NH1	M_ASP_70	OD1	2.935
1GGI	M_ARG_24	NH1	M_ASP_70	OD2	3.520
1GGI	M_ARG_61	NH1	M_ASP_82	OD1	2.935
1GGI	M_ARG_61	NH1	M_ASP_82	OD2	2.776
1GGI	M_ARG_61	NH2	M_ASP_82	OD1	3.065
1GGI	M_LYS_142	NZ	M_GLU_105	OE1	3.711
1GGI	M_LYS_142	NZ	M_GLU_105	OE2	2.989
1GGI	M_ARG_155	NH1	M_GLU_185	OE2	3.862
1GGI	M_ARG_155	NH2	M_GLU_185	OE1	2.644
1GGI	M_ARG_155	NH2	M_GLU_185	OE2	3.063
1GGI	M_LYS_183	NZ	M_GLU_187	OE1	3.427
1GGI	M_LYS_183	NZ	M_GLU_187	OE2	3.848
1GGI	M_HIS_189	ND1	M_ASP_151	OD2	3.374
1GGI	M_LYS_199	NZ	M_ASP_110	OD1	3.172
1GGI	M_LYS_199	NZ	M_ASP_110	OD2	3.326
1GGI	J_ARG_38	NH1	J_ASP_86	OD1	2.716
1GGI	J_ARG_38	NH2	J_ASP_86	OD1	3.121
1GGI	J_HIS_50	NE2	J_GLU_95	OE1	2.732
1GGI	J_ARG_58	NH1	J_ASP_56	OD2	2.535
1GGI	J_ARG_58	NH2	M_ASP_94	OD2	3.966
1GGI	J_ARG_66	NH1	J_ASP_86	OD1	3.627
1GGI	J_ARG_66	NH2	J_ASP_86	OD1	3.502
1GGI	J_ARG_66	NH2	J_ASP_86	OD2	2.746
1GGI	J_HIS_172	NE2	M_ASP_167	OD2	3.287
1GGI	J_LYS_221	NZ	M_GLU_123	OE1	3.528
1GGI	J_LYS_221	NZ	M_GLU_123	OE2	3.781
1GGI	Q_LYS_312	NZ	J_ASP_54	OD1	3.299
1GGI	Q_LYS_312	NZ	J_ASP_54	OD2	2.967
1GGI	Q_LYS_312	NZ	J_ASP_56	OD1	3.964
1GGI	Q_LYS_312	NZ	J_ASP_56	OD2	3.120

Table 84: 1GGI-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1GPO	L_LYS_54	NZ	H_ASP_101	OD1	2.768
1GPO	L_LYS_54	NZ	H_ASP_101	OD2	3.525
1GPO	L_ARG_66	NH2	L_GLU_86	OE2	3.655
1GPO	L_ARG_66	NH2	L_ASP_87	OD1	2.651
1GPO	L_ARG_66	NH2	L_ASP_87	OD2	3.453
1GPO	L_LYS_147	NZ	L_ASP_148	OD1	3.371
1GPO	L_LYS_152	NZ	L_GLU_159	OE2	2.707
1GPO	L_LYS_154	NZ	L_GLU_200	OE2	3.219
1GPO	L_ARG_160	NH1	L_GLU_190	OE2	3.906
1GPO	L_ARG_193	NH2	L_ASP_189	OD1	3.683
1GPO	L_ARG_193	NH2	L_ASP_189	OD2	2.940
1GPO	L_HIS_194	NE2	L_GLU_190	OE2	3.215
1GPO	L_LYS_204	NZ	L_ASP_115	OD1	3.884
1GPO	L_LYS_204	NZ	L_ASP_115	OD2	2.884
1GPO	H_ARG_38	NH1	H_ASP_89	OD1	3.025
1GPO	H_ARG_38	NH2	H_GLU_46	OE1	2.836
1GPO	H_ARG_38	NH2	H_ASP_89	OD1	3.663
1GPO	H_ARG_66	NH1	H_ASP_89	OD1	3.859
1GPO	H_ARG_66	NH1	H_ASP_89	OD2	3.366
1GPO	H_ARG_66	NH2	H_ASP_89	OD1	3.032
1GPO	H_ARG_66	NH2	H_ASP_89	OD2	3.658
1GPO	H_LYS_208	NZ	L_GLU_128	OE2	3.848
1GPO	M_ARG_24	NH1	M_ASP_75	OD1	3.059
1GPO	M_LYS_44	NZ	M_GLU_86	OE1	3.993
1GPO	M_LYS_54	NZ	L_ASP_101	OD1	3.704
1GPO	M_ARG_66	NH2	M_GLU_86	OE2	3.739
1GPO	M_ARG_66	NH2	M_ASP_87	OD1	2.836
1GPO	M_ARG_66	NH2	M_ASP_87	OD2	3.679
1GPO	M_LYS_108	NZ	M_GLU_110	OE1	2.976
1GPO	M_LYS_108	NZ	M_GLU_110	OE2	3.953
1GPO	M_LYS_154	NZ	M_GLU_200	OE1	3.791
1GPO	M_LYS_154	NZ	M_GLU_200	OE2	3.297
1GPO	M_HIS_194	ND1	M_ASP_156	OD2	3.167
1GPO	M_HIS_194	NE2	M_GLU_190	OE2	3.816
1GPO	I_ARG_38	NH1	I_ASP_89	OD1	2.915
1GPO	I_ARG_38	NH2	I_GLU_46	OE1	3.130
1GPO	I_ARG_38	NH2	I_GLU_46	OE2	3.937
1GPO	I_ARG_38	NH2	I_ASP_89	OD1	3.560
1GPO	I_ARG_66	NH1	I_ASP_89	OD1	3.810
1GPO	I_ARG_66	NH1	I_ASP_89	OD2	3.000
1GPO	I_ARG_66	NH2	I_ASP_89	OD1	3.073
1GPO	I_ARG_66	NH2	I_ASP_89	OD2	3.643
1GPO	I_LYS_208	NZ	M_GLU_128	OE2	3.367

Table 85: 1GPO-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1HCV	A_ARG_38	NH1	A_ASP_86	OD1	2.863
1HCV	A_ARG_38	NH2	A_GLU_46	OE2	3.573
1HCV	A_ARG_38	NH2	A_ASP_86	OD1	3.820
1HCV	A_ARG_66	NH2	A_ASP_86	OD1	3.579
1HCV	A_ARG_66	NH2	A_ASP_86	OD2	2.581

Table 86: 1HCV-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1HEZ	A_ARG_24	NH1	C_ASP_70	OD1	3.567
1HEZ	A_ARG_24	NH1	C_ASP_70	OD2	3.209
1HEZ	A_ARG_24	NH2	A_ASP_70	OD1	3.267
1HEZ	A_ARG_24	NH2	A_ASP_70	OD2	3.046
1HEZ	A_ARG_61	NH2	A_GLU_81	OE1	2.928
1HEZ	A_ARG_61	NH2	A_ASP_82	OD1	2.762
1HEZ	A_ARG_61	NH2	A_ASP_82	OD2	3.538
1HEZ	A_LYS_103	NZ	A_GLU_165	OE2	3.539
1HEZ	A_LYS_145	NZ	A_GLU_143	OE1	3.528
1HEZ	A_LYS_145	NZ	A_GLU_143	OE2	2.903
1HEZ	A_LYS_149	NZ	A_GLU_195	OE1	2.775
1HEZ	B_ARG_38	NH1	B_ASP_90	OD1	3.118
1HEZ	B_ARG_38	NH2	B_GLU_46	OE1	2.692
1HEZ	B_ARG_38	NH2	B_GLU_46	OE2	3.888
1HEZ	B_ARG_67	NH1	B_ASP_90	OD1	3.575
1HEZ	B_ARG_67	NH1	B_ASP_90	OD2	3.985
1HEZ	B_ARG_67	NH2	B_ASP_90	OD1	3.231
1HEZ	B_ARG_67	NH2	B_ASP_90	OD2	2.419
1HEZ	B_LYS_98	NZ	B_ASP_109	OD1	3.274
1HEZ	B_LYS_98	NZ	B_ASP_109	OD2	3.047
1HEZ	B_HIS_205	NE2	B_ASP_220	OD2	3.169
1HEZ	B_LYS_219	NZ	A_GLU_123	OE1	2.923
1HEZ	B_LYS_219	NZ	A_GLU_123	OE2	2.722
1HEZ	C_ARG_24	NH1	E_ASP_855	OD1	2.717
1HEZ	C_ARG_61	NH2	C_GLU_81	OE1	3.663
1HEZ	C_ARG_61	NH2	C_GLU_81	OE2	3.949
1HEZ	C_ARG_61	NH2	C_ASP_82	OD1	2.937
1HEZ	C_ARG_61	NH2	C_ASP_82	OD2	3.542
1HEZ	C_LYS_103	NZ	C_GLU_165	OE1	2.714
1HEZ	C_LYS_107	NZ	E_ASP_867	OD1	2.620
1HEZ	C_LYS_149	NZ	C_GLU_195	OE2	3.147
1HEZ	C_LYS_169	NZ	C_ASP_167	OD1	3.018
1HEZ	C_LYS_169	NZ	C_ASP_167	OD2	3.798
1HEZ	C_LYS_183	NZ	C_GLU_187	OE1	3.073
1HEZ	C_LYS_183	NZ	C_GLU_187	OE2	3.001
1HEZ	C_LYS_190	NZ	C_GLU_213	OE1	3.539
1HEZ	D_ARG_38	NH1	D_ASP_90	OD1	2.991
1HEZ	D_ARG_38	NH2	D_GLU_46	OE1	3.960
1HEZ	D_ARG_38	NH2	D_GLU_46	OE2	3.492
1HEZ	D_ARG_38	NH2	D_ASP_90	OD1	3.798
1HEZ	D_ARG_67	NH1	D_ASP_90	OD1	3.763
1HEZ	D_ARG_67	NH1	D_ASP_90	OD2	2.714
1HEZ	D_ARG_67	NH2	D_ASP_90	OD1	2.942
1HEZ	D_ARG_67	NH2	D_ASP_90	OD2	3.444
1HEZ	D_LYS_76	NZ	D_ASP_73	OD1	3.956
1HEZ	D_LYS_76	NZ	D_ASP_73	OD2	3.200
1HEZ	D_LYS_98	NZ	D_ASP_109	OD1	2.982
1HEZ	D_LYS_98	NZ	D_ASP_109	OD2	3.292
1HEZ	D_LYS_163	NZ	D_ASP_169	OD1	2.707
1HEZ	D_LYS_163	NZ	D_ASP_169	OD2	2.741
1HEZ	D_HIS_205	NE2	D_ASP_220	OD1	3.150
1HEZ	D_HIS_205	NE2	D_ASP_220	OD2	3.664
1HEZ	E_ARG_852	NH1	E_GLU_849	OE1	2.953
1HEZ	E_ARG_852	NH1	E_GLU_849	OE2	2.803
1HEZ	E_ARG_852	NH2	E_GLU_849	OE2	3.099
1HEZ	E_HIS_874	NE2	E_GLU_869	OE2	3.386

Table 87: 1HEZ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1HGD	A_LYS_27	NZ	B_GLU_97	OE1	2.787
1HGD	A_LYS_27	NZ	B_GLU_97	OE2	2.801
1HGD	A_LYS_50	NZ	A_ASP_275	OD1	3.503
1HGD	A_LYS_50	NZ	A_ASP_275	OD2	2.699
1HGD	A_ARG_57	NH2	A_GLU_82	OE1	2.541
1HGD	A_ARG_57	NH2	A_GLU_82	OE2	3.602
1HGD	A_HIS_75	ND1	A_ASP_73	OD1	2.825
1HGD	A_HIS_75	ND1	A_ASP_73	OD2	3.404
1HGD	A_HIS_75	NE2	A_ASP_63	OD1	3.503
1HGD	A_ARG_90	NH2	A_ASP_60	OD1	3.606
1HGD	A_ARG_90	NH2	A_ASP_60	OD2	2.804
1HGD	A_ARG_109	NH1	A_GLU_89	OE1	2.520
1HGD	A_ARG_109	NH1	A_GLU_89	OE2	3.261
1HGD	A_ARG_109	NH2	B_GLU_67	OE1	3.474
1HGD	A_ARG_109	NH2	B_GLU_67	OE2	2.826
1HGD	A_ARG_141	NH2	A_ASP_77	OD1	2.863
1HGD	A_ARG_141	NH2	A_ASP_77	OD2	2.743
1HGD	A_LYS_176	NZ	A_GLU_123	OE2	2.689
1HGD	A_HIS_183	NE2	A_GLU_190	OE2	3.734
1HGD	A_LYS_238	NZ	F_GLU_72	OE1	2.925
1HGD	A_LYS_238	NZ	F_GLU_72	OE2	2.815
1HGD	A_ARG_261	NH1	A_GLU_119	OE2	2.647
1HGD	A_ARG_261	NH2	A_GLU_119	OE1	2.879
1HGD	A_ARG_261	NH2	A_GLU_119	OE2	2.926
1HGD	A_LYS_264	NZ	A_ASP_85	OD1	3.573
1HGD	A_LYS_264	NZ	A_ASP_85	OD2	2.845
1HGD	A_ARG_269	NH1	B_GLU_67	OE1	2.758
1HGD	A_ARG_269	NH2	B_GLU_67	OE1	3.754
1HGD	A_LYS_292	NZ	A_ASP_291	OD1	2.852
1HGD	A_LYS_292	NZ	A_ASP_291	OD2	2.779
1HGD	A_LYS_299	NZ	B_GLU_69	OE2	2.769
1HGD	A_LYS_310	NZ	B_ASP_86	OD1	2.861
1HGD	A_LYS_310	NZ	B_ASP_90	OD1	2.569
1HGD	A_LYS_315	NZ	A_GLU_41	OE1	2.760
1HGD	A_LYS_326	NZ	A_GLU_325	OE1	3.012
1HGD	A_LYS_326	NZ	B_GLU_15	OE1	3.037
1HGD	A_LYS_326	NZ	B_GLU_15	OE2	2.743
1HGD	B_ARG_25	NH1	A_GLU_325	OE2	3.743
1HGD	B_ARG_25	NH2	A_GLU_325	OE2	3.016
1HGD	B_LYS_51	NZ	B_GLU_103	OE1	2.725
1HGD	B_ARG_54	NH1	B_GLU_57	OE1	2.860
1HGD	B_ARG_54	NH1	B_GLU_57	OE2	2.845
1HGD	B_ARG_54	NH1	F_GLU_97	OE2	3.275
1HGD	B_ARG_54	NH2	F_GLU_97	OE2	2.774
1HGD	B_LYS_58	NZ	B_GLU_61	OE2	2.905
1HGD	B_LYS_62	NZ	F_ASP_86	OD1	2.852
1HGD	B_LYS_62	NZ	F_ASP_86	OD2	2.612
1HGD	B_LYS_62	NZ	F_ASP_90	OD1	3.620
1HGD	B_LYS_62	NZ	F_ASP_90	OD2	2.727
1HGD	B_LYS_68	NZ	B_GLU_85	OE1	3.140
1HGD	B_LYS_68	NZ	B_GLU_85	OE2	2.759
1HGD	B_ARG_76	NH1	D_GLU_74	OE1	3.558
1HGD	B_ARG_76	NH1	D_GLU_74	OE2	2.838
1HGD	B_ARG_76	NH2	D_GLU_74	OE1	2.751
1HGD	B_ARG_76	NH2	D_GLU_74	OE2	3.529
1HGD	B_ARG_76	NH2	D_GLU_81	OE1	2.707
1HGD	B_ARG_76	NH2	D_GLU_81	OE2	3.498

1HGD	B_LYS_117	NZ	B_GLU_114	OE1	2.958
1HGD	B_LYS_117	NZ	B_GLU_114	OE2	2.520
1HGD	B_ARG_123	NH1	B_GLU_120	OE1	2.589
1HGD	B_ARG_123	NH1	B_GLU_120	OE2	2.787
1HGD	B_ARG_123	NH2	F_GLU_132	OE1	3.169
1HGD	B_ARG_124	NH1	B_GLU_120	OE1	3.722
1HGD	B_ARG_124	NH2	F_GLU_132	OE1	3.011
1HGD	B_ARG_124	NH2	F_GLU_132	OE2	3.294
1HGD	B_ARG_127	NH1	F_GLU_131	OE1	2.471
1HGD	B_LYS_143	NZ	B_ASP_145	OD2	2.849
1HGD	B_ARG_153	NH1	B_GLU_150	OE1	2.627
1HGD	B_HIS_159	NE2	B_ASP_160	OD2	3.135
1HGD	B_ARG_163	NH2	F_GLU_131	OE1	2.583
1HGD	B_ARG_163	NH2	F_GLU_131	OE2	2.596
1HGD	B_ARG_170	NH1	B_GLU_131	OE2	2.779
1HGD	B_ARG_170	NH1	D_GLU_128	OE1	3.354
1HGD	B_ARG_170	NH1	D_GLU_128	OE2	3.628
1HGD	B_ARG_170	NH2	B_GLU_128	OE2	2.668
1HGD	B_LYS_174	NZ	D_ASP_164	OD1	2.787
1HGD	B_LYS_174	NZ	D_ASP_164	OD2	2.517
1HGD	C_LYS_27	NZ	D_GLU_97	OE1	2.760
1HGD	C_LYS_27	NZ	D_GLU_97	OE2	2.799
1HGD	C_LYS_50	NZ	C_ASP_275	OD1	3.482
1HGD	C_LYS_50	NZ	C_ASP_275	OD2	2.664
1HGD	C_ARG_57	NH2	C_GLU_82	OE1	2.562
1HGD	C_ARG_57	NH2	C_GLU_82	OE2	3.993
1HGD	C_HIS_75	ND1	C_ASP_73	OD1	2.767
1HGD	C_HIS_75	ND1	C_ASP_73	OD2	3.384
1HGD	C_HIS_75	NE2	C_ASP_63	OD1	3.497
1HGD	C_ARG_90	NH2	C_ASP_60	OD1	3.613
1HGD	C_ARG_90	NH2	C_ASP_60	OD2	2.775
1HGD	C_ARG_109	NH1	C_GLU_89	OE1	2.543
1HGD	C_ARG_109	NH1	C_GLU_89	OE2	3.286
1HGD	C_ARG_109	NH2	D_GLU_67	OE1	3.480
1HGD	C_ARG_109	NH2	D_GLU_67	OE2	2.867
1HGD	C_ARG_141	NH2	C_ASP_77	OD1	2.873
1HGD	C_ARG_141	NH2	C_ASP_77	OD2	2.747
1HGD	C_LYS_176	NZ	C_GLU_123	OE2	2.693
1HGD	C_HIS_183	NE2	C_GLU_190	OE2	3.721
1HGD	C_LYS_238	NZ	B_GLU_72	OE1	2.801
1HGD	C_LYS_238	NZ	B_GLU_72	OE2	2.746
1HGD	C_ARG_261	NH1	C_GLU_119	OE2	2.657
1HGD	C_ARG_261	NH2	C_GLU_119	OE1	2.896
1HGD	C_ARG_261	NH2	C_GLU_119	OE2	2.924
1HGD	C_LYS_264	NZ	C_ASP_85	OD1	3.582
1HGD	C_LYS_264	NZ	C_ASP_85	OD2	2.818
1HGD	C_ARG_269	NH1	D_GLU_67	OE1	2.720
1HGD	C_ARG_269	NH2	D_GLU_67	OE1	3.733
1HGD	C_LYS_292	NZ	C_ASP_291	OD1	2.883
1HGD	C_LYS_292	NZ	C_ASP_291	OD2	2.789
1HGD	C_LYS_299	NZ	D_GLU_69	OE2	2.796
1HGD	C_LYS_310	NZ	D_ASP_86	OD1	2.878
1HGD	C_LYS_310	NZ	D_ASP_90	OD1	2.526
1HGD	C_LYS_315	NZ	C_GLU_41	OE1	2.785
1HGD	C_LYS_326	NZ	D_GLU_15	OE1	2.784
1HGD	C_LYS_326	NZ	D_GLU_15	OE2	3.881
1HGD	D_LYS_51	NZ	D_GLU_103	OE1	2.736
1HGD	D_ARG_54	NH1	B_GLU_97	OE2	3.293

1HGD	D_ARG_54	NH1	D_GLU_57	OE1	2.846
1HGD	D_ARG_54	NH1	D_GLU_57	OE2	2.834
1HGD	D_ARG_54	NH2	B_GLU_97	OE2	2.793
1HGD	D_LYS_58	NZ	D_GLU_61	OE2	2.900
1HGD	D_LYS_62	NZ	B_ASP_86	OD1	2.884
1HGD	D_LYS_62	NZ	B_ASP_86	OD2	2.567
1HGD	D_LYS_62	NZ	B_ASP_90	OD1	3.576
1HGD	D_LYS_62	NZ	B_ASP_90	OD2	2.617
1HGD	D_LYS_68	NZ	D_GLU_85	OE1	3.140
1HGD	D_LYS_68	NZ	D_GLU_85	OE2	2.777
1HGD	D_ARG_76	NH1	F_GLU_74	OE1	3.379
1HGD	D_ARG_76	NH1	F_GLU_74	OE2	2.785
1HGD	D_ARG_76	NH2	F_GLU_74	OE1	2.687
1HGD	D_ARG_76	NH2	F_GLU_74	OE2	3.593
1HGD	D_ARG_76	NH2	F_GLU_81	OE1	2.649
1HGD	D_ARG_76	NH2	F_GLU_81	OE2	3.537
1HGD	D_LYS_117	NZ	D_GLU_114	OE1	3.015
1HGD	D_LYS_117	NZ	D_GLU_114	OE2	2.569
1HGD	D_ARG_123	NH1	D_GLU_120	OE1	2.582
1HGD	D_ARG_123	NH1	D_GLU_120	OE2	2.804
1HGD	D_ARG_123	NH2	B_GLU_132	OE1	3.120
1HGD	D_ARG_124	NH1	D_GLU_120	OE1	3.720
1HGD	D_ARG_124	NH2	B_GLU_132	OE1	2.998
1HGD	D_ARG_124	NH2	B_GLU_132	OE2	3.261
1HGD	D_ARG_127	NH1	B_GLU_131	OE1	2.513
1HGD	D_LYS_143	NZ	D_ASP_145	OD2	2.863
1HGD	D_ARG_153	NH1	D_GLU_150	OE1	2.616
1HGD	D_HIS_159	NE2	D_ASP_160	OD2	3.164
1HGD	D_ARG_163	NH2	B_GLU_131	OE1	2.583
1HGD	D_ARG_163	NH2	B_GLU_131	OE2	2.616
1HGD	D_ARG_170	NH1	D_GLU_131	OE2	2.771
1HGD	D_ARG_170	NH1	F_GLU_128	OE1	3.487
1HGD	D_ARG_170	NH1	F_GLU_128	OE2	3.741
1HGD	D_ARG_170	NH2	D_GLU_128	OE2	2.697
1HGD	D_LYS_174	NZ	F_ASP_164	OD1	2.806
1HGD	D_LYS_174	NZ	F_ASP_164	OD2	2.686
1HGD	E_LYS_27	NZ	F_GLU_97	OE1	2.794
1HGD	E_LYS_27	NZ	F_GLU_97	OE2	2.792
1HGD	E_LYS_50	NZ	E_ASP_275	OD1	3.496
1HGD	E_LYS_50	NZ	E_ASP_275	OD2	2.695
1HGD	E_ARG_57	NH2	E_GLU_82	OE1	2.588
1HGD	E_HIS_75	ND1	E_ASP_73	OD1	2.791
1HGD	E_HIS_75	ND1	E_ASP_73	OD2	3.377
1HGD	E_HIS_75	NE2	E_ASP_63	OD1	3.540
1HGD	E_ARG_90	NH2	E_ASP_60	OD1	3.606
1HGD	E_ARG_90	NH2	E_ASP_60	OD2	2.820
1HGD	E_ARG_109	NH1	E_GLU_89	OE1	2.520
1HGD	E_ARG_109	NH1	E_GLU_89	OE2	3.279
1HGD	E_ARG_109	NH2	F_GLU_67	OE1	3.474
1HGD	E_ARG_109	NH2	F_GLU_67	OE2	2.818
1HGD	E_ARG_141	NH2	E_ASP_77	OD1	2.875
1HGD	E_ARG_141	NH2	E_ASP_77	OD2	2.746
1HGD	E_LYS_176	NZ	E_GLU_123	OE2	2.694
1HGD	E_HIS_183	NE2	E_GLU_190	OE2	3.738
1HGD	E_LYS_238	NZ	D_GLU_72	OE1	2.872
1HGD	E_LYS_238	NZ	D_GLU_72	OE2	2.843
1HGD	E_ARG_261	NH1	E_GLU_119	OE2	2.644
1HGD	E_ARG_261	NH2	E_GLU_119	OE1	2.878

1HGD	E_ARG_261	NH2	E_GLU_119	OE2	2.908
1HGD	E_LYS_264	NZ	E_ASP_85	OD1	3.622
1HGD	E_LYS_264	NZ	E_ASP_85	OD2	2.868
1HGD	E_ARG_269	NH1	F_GLU_67	OE1	2.732
1HGD	E_ARG_269	NH2	F_GLU_67	OE1	3.760
1HGD	E_LYS_292	NZ	E_ASP_291	OD1	2.887
1HGD	E_LYS_292	NZ	E_ASP_291	OD2	2.826
1HGD	E_LYS_299	NZ	F_GLU_69	OE2	2.767
1HGD	E_LYS_310	NZ	F_ASP_86	OD1	2.884
1HGD	E_LYS_310	NZ	F_ASP_90	OD1	2.533
1HGD	E_LYS_315	NZ	E_GLU_41	OE1	2.761
1HGD	E_LYS_326	NZ	F_GLU_15	OE1	2.967
1HGD	E_LYS_326	NZ	F_GLU_15	OE2	3.203
1HGD	F_LYS_51	NZ	F_GLU_103	OE1	2.718
1HGD	F_ARG_54	NH1	D_GLU_97	OE2	3.306
1HGD	F_ARG_54	NH1	F_GLU_57	OE1	2.855
1HGD	F_ARG_54	NH1	F_GLU_57	OE2	2.837
1HGD	F_ARG_54	NH2	D_GLU_97	OE2	2.719
1HGD	F_LYS_58	NZ	F_GLU_61	OE2	2.922
1HGD	F_LYS_62	NZ	D_ASP_86	OD1	2.854
1HGD	F_LYS_62	NZ	D_ASP_86	OD2	2.590
1HGD	F_LYS_62	NZ	D_ASP_90	OD1	3.656
1HGD	F_LYS_62	NZ	D_ASP_90	OD2	2.713
1HGD	F_HIS_64	NE2	D_ASP_79	OD2	3.996
1HGD	F_LYS_68	NZ	F_GLU_85	OE1	3.116
1HGD	F_LYS_68	NZ	F_GLU_85	OE2	2.719
1HGD	F_ARG_76	NH1	B_GLU_74	OE1	3.419
1HGD	F_ARG_76	NH1	B_GLU_74	OE2	2.766
1HGD	F_ARG_76	NH2	B_GLU_74	OE1	2.711
1HGD	F_ARG_76	NH2	B_GLU_74	OE2	3.568
1HGD	F_ARG_76	NH2	B_GLU_81	OE1	2.637
1HGD	F_ARG_76	NH2	B_GLU_81	OE2	3.557
1HGD	F_LYS_117	NZ	F_GLU_114	OE1	3.015
1HGD	F_LYS_117	NZ	F_GLU_114	OE2	2.552
1HGD	F_ARG_123	NH1	F_GLU_120	OE1	2.598
1HGD	F_ARG_123	NH1	F_GLU_120	OE2	2.770
1HGD	F_ARG_123	NH2	D_GLU_132	OE1	3.156
1HGD	F_ARG_124	NH1	F_GLU_120	OE1	3.728
1HGD	F_ARG_124	NH2	D_GLU_132	OE1	3.098
1HGD	F_ARG_124	NH2	D_GLU_132	OE2	3.292
1HGD	F_ARG_127	NH1	D_GLU_131	OE1	2.558
1HGD	F_LYS_143	NZ	F_ASP_145	OD2	2.843
1HGD	F_ARG_153	NH1	F_GLU_150	OE2	2.541
1HGD	F_HIS_159	NE2	F_ASP_160	OD2	3.168
1HGD	F_ARG_163	NH2	D_GLU_131	OE1	2.583
1HGD	F_ARG_163	NH2	D_GLU_131	OE2	2.699
1HGD	F_ARG_170	NH1	B_GLU_128	OE1	3.398
1HGD	F_ARG_170	NH1	B_GLU_128	OE2	3.736
1HGD	F_ARG_170	NH1	F_GLU_131	OE2	2.763
1HGD	F_ARG_170	NH2	F_GLU_128	OE2	2.704
1HGD	F_LYS_174	NZ	B_ASP_164	OD1	2.545
1HGD	F_LYS_174	NZ	B_ASP_164	OD2	2.838

Table 88: 1HGD-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1HGE	A_LYS_27	NZ	B_GLU_97	OE1	2.881
1HGE	A_LYS_27	NZ	B_GLU_97	OE2	2.803
1HGE	A_LYS_50	NZ	A_ASP_275	OD1	3.562
1HGE	A_LYS_50	NZ	A_ASP_275	OD2	2.748
1HGE	A_ARG_57	NH2	A_GLU_82	OE1	2.500
1HGE	A_ARG_57	NH2	A_GLU_82	OE2	3.546
1HGE	A_HIS_75	ND1	A_ASP_73	OD1	2.802
1HGE	A_HIS_75	ND1	A_ASP_73	OD2	3.532
1HGE	A_HIS_75	NE2	A_ASP_63	OD1	3.437
1HGE	A_ARG_90	NH2	A_ASP_60	OD1	3.553
1HGE	A_ARG_90	NH2	A_ASP_60	OD2	2.793
1HGE	A_ARG_109	NH1	A_GLU_89	OE1	2.487
1HGE	A_ARG_109	NH1	A_GLU_89	OE2	3.213
1HGE	A_ARG_109	NH2	B_GLU_67	OE1	3.666
1HGE	A_ARG_109	NH2	B_GLU_67	OE2	2.737
1HGE	A_ARG_141	NH2	A_ASP_77	OD1	2.893
1HGE	A_ARG_141	NH2	A_ASP_77	OD2	2.750
1HGE	A_LYS_176	NZ	A_GLU_123	OE2	2.715
1HGE	A_HIS_183	NE2	A_GLU_190	OE2	3.843
1HGE	A_LYS_238	NZ	F_GLU_72	OE1	2.915
1HGE	A_LYS_238	NZ	F_GLU_72	OE2	2.732
1HGE	A_ARG_261	NH1	A_GLU_119	OE2	2.640
1HGE	A_ARG_261	NH2	A_GLU_119	OE1	2.839
1HGE	A_ARG_261	NH2	A_GLU_119	OE2	2.928
1HGE	A_LYS_264	NZ	A_ASP_85	OD1	3.662
1HGE	A_LYS_264	NZ	A_ASP_85	OD2	2.767
1HGE	A_ARG_269	NH1	B_GLU_67	OE1	2.727
1HGE	A_ARG_269	NH2	B_GLU_67	OE1	3.813
1HGE	A_LYS_292	NZ	A_ASP_291	OD1	2.918
1HGE	A_LYS_292	NZ	A_ASP_291	OD2	2.823
1HGE	A_LYS_299	NZ	B_GLU_69	OE2	2.765
1HGE	A_LYS_310	NZ	B_ASP_86	OD1	2.860
1HGE	A_LYS_310	NZ	B_ASP_90	OD1	2.586
1HGE	A_LYS_310	NZ	B_ASP_90	OD2	3.982
1HGE	A_LYS_315	NZ	A_GLU_41	OE1	2.816
1HGE	A_LYS_326	NZ	A_GLU_325	OE1	2.847
1HGE	A_LYS_326	NZ	B_GLU_15	OE1	3.112
1HGE	A_LYS_326	NZ	B_GLU_15	OE2	2.788
1HGE	B_ARG_25	NH1	A_GLU_325	OE2	3.901
1HGE	B_ARG_25	NH2	A_GLU_325	OE2	3.058
1HGE	B_LYS_51	NZ	B_GLU_103	OE1	2.764
1HGE	B_ARG_54	NH1	B_GLU_57	OE1	2.831
1HGE	B_ARG_54	NH1	B_GLU_57	OE2	2.867
1HGE	B_ARG_54	NH1	F_GLU_97	OE2	3.352
1HGE	B_ARG_54	NH2	F_GLU_97	OE2	2.840
1HGE	B_LYS_58	NZ	B_GLU_61	OE2	3.128
1HGE	B_LYS_62	NZ	F_ASP_86	OD1	2.965
1HGE	B_LYS_62	NZ	F_ASP_86	OD2	2.602
1HGE	B_LYS_62	NZ	F_ASP_90	OD1	3.562
1HGE	B_LYS_62	NZ	F_ASP_90	OD2	2.691
1HGE	B_LYS_68	NZ	B_GLU_85	OE1	3.200
1HGE	B_LYS_68	NZ	B_GLU_85	OE2	2.780
1HGE	B_ARG_76	NH1	D_GLU_74	OE1	3.487
1HGE	B_ARG_76	NH1	D_GLU_74	OE2	2.838
1HGE	B_ARG_76	NH2	D_GLU_74	OE1	2.788
1HGE	B_ARG_76	NH2	D_GLU_74	OE2	3.585
1HGE	B_ARG_76	NH2	D_GLU_81	OE1	2.698

1HGE	B_ARG_76	NH2	D_GLU_81	OE2	3.486
1HGE	B_LYS_117	NZ	B_GLU_114	OE1	3.021
1HGE	B_LYS_117	NZ	B_GLU_114	OE2	2.593
1HGE	B_ARG_123	NH1	B_GLU_120	OE1	2.560
1HGE	B_ARG_123	NH1	B_GLU_120	OE2	2.842
1HGE	B_ARG_123	NH2	F_GLU_132	OE1	3.159
1HGE	B_ARG_124	NH1	B_GLU_120	OE1	3.659
1HGE	B_ARG_124	NH2	F_GLU_132	OE1	3.028
1HGE	B_ARG_124	NH2	F_GLU_132	OE2	3.444
1HGE	B_ARG_127	NH1	F_GLU_131	OE1	2.492
1HGE	B_LYS_143	NZ	B_ASP_145	OD2	2.791
1HGE	B_ARG_153	NH1	B_GLU_150	OE1	2.552
1HGE	B_HIS_159	NE2	B_ASP_160	OD2	2.984
1HGE	B_ARG_163	NH2	F_GLU_131	OE1	2.609
1HGE	B_ARG_163	NH2	F_GLU_131	OE2	2.622
1HGE	B_ARG_170	NH1	B_GLU_131	OE2	2.795
1HGE	B_ARG_170	NH1	D_GLU_128	OE1	3.351
1HGE	B_ARG_170	NH1	D_GLU_128	OE2	3.595
1HGE	B_ARG_170	NH2	B_GLU_128	OE2	2.691
1HGE	B_LYS_174	NZ	D_ASP_164	OD1	2.542
1HGE	B_LYS_174	NZ	D_ASP_164	OD2	2.784
1HGE	C_LYS_27	NZ	D_GLU_97	OE1	2.850
1HGE	C_LYS_27	NZ	D_GLU_97	OE2	2.792
1HGE	C_LYS_50	NZ	C_ASP_275	OD1	3.553
1HGE	C_LYS_50	NZ	C_ASP_275	OD2	2.700
1HGE	C_ARG_57	NH2	C_GLU_82	OE1	2.538
1HGE	C_ARG_57	NH2	C_GLU_82	OE2	3.923
1HGE	C_HIS_75	ND1	C_ASP_73	OD1	2.756
1HGE	C_HIS_75	ND1	C_ASP_73	OD2	3.513
1HGE	C_HIS_75	NE2	C_ASP_63	OD1	3.447
1HGE	C_ARG_90	NH2	C_ASP_60	OD1	3.557
1HGE	C_ARG_90	NH2	C_ASP_60	OD2	2.770
1HGE	C_ARG_109	NH1	C_GLU_89	OE1	2.521
1HGE	C_ARG_109	NH1	C_GLU_89	OE2	3.282
1HGE	C_ARG_109	NH2	D_GLU_67	OE1	3.673
1HGE	C_ARG_109	NH2	D_GLU_67	OE2	2.784
1HGE	C_ARG_141	NH2	C_ASP_77	OD1	2.880
1HGE	C_ARG_141	NH2	C_ASP_77	OD2	2.743
1HGE	C_LYS_176	NZ	C_GLU_123	OE2	2.713
1HGE	C_HIS_183	NE2	C_GLU_190	OE2	3.847
1HGE	C_LYS_238	NZ	B_GLU_72	OE1	2.779
1HGE	C_LYS_238	NZ	B_GLU_72	OE2	2.668
1HGE	C_ARG_261	NH1	C_GLU_119	OE2	2.652
1HGE	C_ARG_261	NH2	C_GLU_119	OE1	2.839
1HGE	C_ARG_261	NH2	C_GLU_119	OE2	2.930
1HGE	C_LYS_264	NZ	C_ASP_85	OD1	3.674
1HGE	C_LYS_264	NZ	C_ASP_85	OD2	2.771
1HGE	C_ARG_269	NH1	D_GLU_67	OE1	2.720
1HGE	C_ARG_269	NH2	D_GLU_67	OE1	3.811
1HGE	C_LYS_292	NZ	C_ASP_291	OD1	2.950
1HGE	C_LYS_292	NZ	C_ASP_291	OD2	2.836
1HGE	C_LYS_299	NZ	D_GLU_69	OE2	2.808
1HGE	C_LYS_310	NZ	D_ASP_86	OD1	2.890
1HGE	C_LYS_310	NZ	D_ASP_90	OD1	2.566
1HGE	C_LYS_310	NZ	D_ASP_90	OD2	3.955
1HGE	C_LYS_315	NZ	C_GLU_41	OE1	2.819
1HGE	C_LYS_326	NZ	D_GLU_15	OE1	2.739
1HGE	C_LYS_326	NZ	D_GLU_15	OE2	3.731

1HGE	D_LYS_51	NZ	D_GLU_103	OE1	2.765
1HGE	D_ARG_54	NH1	B_GLU_97	OE2	3.383
1HGE	D_ARG_54	NH1	D_GLU_57	OE1	2.823
1HGE	D_ARG_54	NH1	D_GLU_57	OE2	2.877
1HGE	D_ARG_54	NH2	B_GLU_97	OE2	2.866
1HGE	D_LYS_58	NZ	D_GLU_61	OE2	3.115
1HGE	D_LYS_62	NZ	B_ASP_86	OD1	3.023
1HGE	D_LYS_62	NZ	B_ASP_86	OD2	2.550
1HGE	D_LYS_62	NZ	B_ASP_90	OD1	3.565
1HGE	D_LYS_62	NZ	B_ASP_90	OD2	2.627
1HGE	D_LYS_68	NZ	D_GLU_85	OE1	3.196
1HGE	D_LYS_68	NZ	D_GLU_85	OE2	2.796
1HGE	D_ARG_76	NH1	F_GLU_74	OE1	3.355
1HGE	D_ARG_76	NH1	F_GLU_74	OE2	2.783
1HGE	D_ARG_76	NH2	F_GLU_74	OE1	2.745
1HGE	D_ARG_76	NH2	F_GLU_74	OE2	3.636
1HGE	D_ARG_76	NH2	F_GLU_81	OE1	2.634
1HGE	D_ARG_76	NH2	F_GLU_81	OE2	3.497
1HGE	D_LYS_117	NZ	D_GLU_114	OE1	3.039
1HGE	D_LYS_117	NZ	D_GLU_114	OE2	2.617
1HGE	D_ARG_123	NH1	D_GLU_120	OE1	2.560
1HGE	D_ARG_123	NH1	D_GLU_120	OE2	2.826
1HGE	D_ARG_123	NH2	B_GLU_132	OE1	3.118
1HGE	D_ARG_124	NH1	D_GLU_120	OE1	3.700
1HGE	D_ARG_124	NH2	B_GLU_132	OE1	3.002
1HGE	D_ARG_124	NH2	B_GLU_132	OE2	3.417
1HGE	D_ARG_127	NH1	B_GLU_131	OE1	2.524
1HGE	D_LYS_143	NZ	D_ASP_145	OD2	2.817
1HGE	D_ARG_153	NH1	D_GLU_150	OE2	2.568
1HGE	D_HIS_159	NE2	D_ASP_160	OD2	3.004
1HGE	D_ARG_163	NH2	B_GLU_131	OE1	2.587
1HGE	D_ARG_163	NH2	B_GLU_131	OE2	2.600
1HGE	D_ARG_170	NH1	D_GLU_131	OE2	2.790
1HGE	D_ARG_170	NH1	F_GLU_128	OE1	3.477
1HGE	D_ARG_170	NH1	F_GLU_128	OE2	3.701
1HGE	D_ARG_170	NH2	D_GLU_128	OE2	2.719
1HGE	D_LYS_174	NZ	F_ASP_164	OD1	2.678
1HGE	D_LYS_174	NZ	F_ASP_164	OD2	2.785
1HGE	E_LYS_27	NZ	F_GLU_97	OE1	2.844
1HGE	E_LYS_27	NZ	F_GLU_97	OE2	2.791
1HGE	E_LYS_50	NZ	E_ASP_275	OD1	3.556
1HGE	E_LYS_50	NZ	E_ASP_275	OD2	2.730
1HGE	E_ARG_57	NH2	E_GLU_82	OE1	2.607
1HGE	E_ARG_57	NH2	E_GLU_82	OE2	3.970
1HGE	E_HIS_75	ND1	E_ASP_73	OD1	2.770
1HGE	E_HIS_75	ND1	E_ASP_73	OD2	3.474
1HGE	E_HIS_75	NE2	E_ASP_63	OD1	3.473
1HGE	E_ARG_90	NH2	E_ASP_60	OD1	3.571
1HGE	E_ARG_90	NH2	E_ASP_60	OD2	2.802
1HGE	E_ARG_109	NH1	E_GLU_89	OE1	2.498
1HGE	E_ARG_109	NH1	E_GLU_89	OE2	3.250
1HGE	E_ARG_109	NH2	F_GLU_67	OE1	3.658
1HGE	E_ARG_109	NH2	F_GLU_67	OE2	2.776
1HGE	E_ARG_141	NH2	E_ASP_77	OD1	2.913
1HGE	E_ARG_141	NH2	E_ASP_77	OD2	2.749
1HGE	E_LYS_176	NZ	E_GLU_123	OE2	2.730
1HGE	E_HIS_183	NE2	E_GLU_190	OE2	3.836
1HGE	E_LYS_238	NZ	D_GLU_72	OE1	2.851

1HGE	E_LYS_238	NZ	D_GLU_72	OE2	2.740
1HGE	E_ARG_261	NH1	E_GLU_119	OE2	2.647
1HGE	E_ARG_261	NH2	E_GLU_119	OE1	2.833
1HGE	E_ARG_261	NH2	E_GLU_119	OE2	2.933
1HGE	E_LYS_264	NZ	E_ASP_85	OD1	3.706
1HGE	E_LYS_264	NZ	E_ASP_85	OD2	2.812
1HGE	E_ARG_269	NH1	F_GLU_67	OE1	2.696
1HGE	E_ARG_269	NH2	F_GLU_67	OE1	3.784
1HGE	E_LYS_292	NZ	E_ASP_291	OD1	2.975
1HGE	E_LYS_292	NZ	E_ASP_291	OD2	2.845
1HGE	E_LYS_299	NZ	F_GLU_69	OE2	2.768
1HGE	E_LYS_310	NZ	F_ASP_86	OD1	2.863
1HGE	E_LYS_310	NZ	F_ASP_90	OD1	2.577
1HGE	E_LYS_310	NZ	F_ASP_90	OD2	3.952
1HGE	E_LYS_315	NZ	E_GLU_41	OE1	2.801
1HGE	E_LYS_326	NZ	F_GLU_15	OE1	2.987
1HGE	E_LYS_326	NZ	F_GLU_15	OE2	3.095
1HGE	F_LYS_51	NZ	F_GLU_103	OE1	2.773
1HGE	F_ARG_54	NH1	D_GLU_97	OE2	3.384
1HGE	F_ARG_54	NH1	F_GLU_57	OE1	2.822
1HGE	F_ARG_54	NH1	F_GLU_57	OE2	2.866
1HGE	F_ARG_54	NH2	D_GLU_97	OE2	2.800
1HGE	F_LYS_58	NZ	F_GLU_61	OE2	3.128
1HGE	F_LYS_62	NZ	D_ASP_86	OD1	2.945
1HGE	F_LYS_62	NZ	D_ASP_86	OD2	2.535
1HGE	F_LYS_62	NZ	D_ASP_90	OD1	3.592
1HGE	F_LYS_62	NZ	D_ASP_90	OD2	2.671
1HGE	F_LYS_68	NZ	F_GLU_85	OE1	3.151
1HGE	F_LYS_68	NZ	F_GLU_85	OE2	2.745
1HGE	F_ARG_76	NH1	B_GLU_74	OE1	3.326
1HGE	F_ARG_76	NH1	B_GLU_74	OE2	2.732
1HGE	F_ARG_76	NH2	B_GLU_74	OE1	2.705
1HGE	F_ARG_76	NH2	B_GLU_74	OE2	3.590
1HGE	F_ARG_76	NH2	B_GLU_81	OE1	2.650
1HGE	F_ARG_76	NH2	B_GLU_81	OE2	3.592
1HGE	F_LYS_117	NZ	F_GLU_114	OE1	3.064
1HGE	F_LYS_117	NZ	F_GLU_114	OE2	2.613
1HGE	F_ARG_123	NH1	F_GLU_120	OE1	2.576
1HGE	F_ARG_123	NH1	F_GLU_120	OE2	2.810
1HGE	F_ARG_123	NH2	D_GLU_132	OE1	3.161
1HGE	F_ARG_124	NH1	F_GLU_120	OE1	3.667
1HGE	F_ARG_124	NH2	D_GLU_132	OE1	3.085
1HGE	F_ARG_124	NH2	D_GLU_132	OE2	3.468
1HGE	F_ARG_127	NH1	D_GLU_131	OE1	2.578
1HGE	F_LYS_143	NZ	F_ASP_145	OD2	2.798
1HGE	F_ARG_153	NH1	F_GLU_150	OE2	2.492
1HGE	F_HIS_159	NE2	F_ASP_160	OD2	3.030
1HGE	F_ARG_163	NH2	D_GLU_131	OE1	2.628
1HGE	F_ARG_163	NH2	D_GLU_131	OE2	2.698
1HGE	F_ARG_170	NH1	B_GLU_128	OE1	3.389
1HGE	F_ARG_170	NH1	B_GLU_128	OE2	3.679
1HGE	F_ARG_170	NH1	F_GLU_131	OE2	2.783
1HGE	F_ARG_170	NH2	F_GLU_128	OE2	2.721
1HGE	F_LYS_174	NZ	B_ASP_164	OD1	2.537
1HGE	F_LYS_174	NZ	B_ASP_164	OD2	2.796

Table 89: 1HGE-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1HGF	A_LYS_27	NZ	B_GLU_97	OE1	2.809
1HGF	A_LYS_27	NZ	B_GLU_97	OE2	2.791
1HGF	A_LYS_50	NZ	A_ASP_275	OD2	2.912
1HGF	A_ARG_57	NH2	A_GLU_82	OE1	2.650
1HGF	A_ARG_57	NH2	A_GLU_82	OE2	3.590
1HGF	A_HIS_75	ND1	A_ASP_73	OD1	2.838
1HGF	A_HIS_75	ND1	A_ASP_73	OD2	3.347
1HGF	A_HIS_75	NE2	A_ASP_63	OD1	3.455
1HGF	A_ARG_90	NH2	A_ASP_60	OD1	3.473
1HGF	A_ARG_90	NH2	A_ASP_60	OD2	2.841
1HGF	A_ARG_109	NH1	A_GLU_89	OE1	2.536
1HGF	A_ARG_109	NH1	A_GLU_89	OE2	2.889
1HGF	A_ARG_109	NH2	B_GLU_67	OE1	3.699
1HGF	A_ARG_109	NH2	B_GLU_67	OE2	2.917
1HGF	A_ARG_141	NH2	A_ASP_77	OD1	2.837
1HGF	A_ARG_141	NH2	A_ASP_77	OD2	2.783
1HGF	A_LYS_176	NZ	A_GLU_123	OE2	2.716
1HGF	A_LYS_176	NZ	A_ASP_172	OD1	3.709
1HGF	A_HIS_183	NE2	A_GLU_190	OE2	3.660
1HGF	A_LYS_238	NZ	F_GLU_72	OE1	2.852
1HGF	A_LYS_238	NZ	F_GLU_72	OE2	2.778
1HGF	A_ARG_261	NH1	A_GLU_119	OE1	3.779
1HGF	A_ARG_261	NH1	A_GLU_119	OE2	2.603
1HGF	A_ARG_261	NH2	A_GLU_119	OE1	2.742
1HGF	A_ARG_261	NH2	A_GLU_119	OE2	3.168
1HGF	A_LYS_264	NZ	A_ASP_85	OD2	3.310
1HGF	A_ARG_269	NH1	B_GLU_67	OE1	2.939
1HGF	A_LYS_292	NZ	A_ASP_291	OD1	2.863
1HGF	A_LYS_292	NZ	A_ASP_291	OD2	3.511
1HGF	A_LYS_299	NZ	B_GLU_69	OE2	3.681
1HGF	A_LYS_310	NZ	B_ASP_86	OD1	2.820
1HGF	A_LYS_310	NZ	B_ASP_90	OD1	2.555
1HGF	A_LYS_310	NZ	B_ASP_90	OD2	3.978
1HGF	A_LYS_315	NZ	A_GLU_41	OE1	3.740
1HGF	A_LYS_326	NZ	A_GLU_325	OE1	2.712
1HGF	A_LYS_326	NZ	B_GLU_15	OE1	3.851
1HGF	A_LYS_326	NZ	B_GLU_15	OE2	3.863
1HGF	B_ARG_25	NH1	A_GLU_325	OE2	3.563
1HGF	B_ARG_25	NH2	A_GLU_325	OE2	2.989
1HGF	B_LYS_51	NZ	B_GLU_103	OE1	2.735
1HGF	B_ARG_54	NH1	B_GLU_57	OE1	3.296
1HGF	B_ARG_54	NH1	F_GLU_97	OE2	3.282
1HGF	B_ARG_54	NH2	F_GLU_97	OE2	2.831
1HGF	B_LYS_62	NZ	F_ASP_86	OD1	3.116
1HGF	B_LYS_62	NZ	F_ASP_86	OD2	2.708
1HGF	B_LYS_62	NZ	F_ASP_90	OD1	3.733
1HGF	B_LYS_62	NZ	F_ASP_90	OD2	2.767
1HGF	B_LYS_68	NZ	B_GLU_85	OE1	3.045
1HGF	B_LYS_68	NZ	B_GLU_85	OE2	2.673
1HGF	B_ARG_76	NH1	D_GLU_74	OE1	2.859
1HGF	B_ARG_76	NH1	D_GLU_74	OE2	3.561
1HGF	B_ARG_76	NH2	D_GLU_74	OE1	3.524
1HGF	B_ARG_76	NH2	D_GLU_74	OE2	2.746
1HGF	B_ARG_76	NH2	D_GLU_81	OE1	2.726
1HGF	B_ARG_76	NH2	D_GLU_81	OE2	3.662
1HGF	B_LYS_117	NZ	B_GLU_114	OE1	3.311
1HGF	B_LYS_117	NZ	B_GLU_114	OE2	2.558

1HGF	B_ARG_123	NH1	B_GLU_120	OE1	2.618
1HGF	B_ARG_123	NH1	B_GLU_120	OE2	2.780
1HGF	B_ARG_123	NH2	F_GLU_132	OE1	3.495
1HGF	B_ARG_124	NH2	F_GLU_132	OE1	3.111
1HGF	B_ARG_124	NH2	F_GLU_132	OE2	3.495
1HGF	B_ARG_127	NH1	F_GLU_131	OE1	2.468
1HGF	B_ARG_153	NH1	B_GLU_150	OE1	2.531
1HGF	B_HIS_159	NE2	B_ASP_160	OD2	3.002
1HGF	B_ARG_163	NH2	F_GLU_131	OE1	2.740
1HGF	B_ARG_163	NH2	F_GLU_131	OE2	2.533
1HGF	B_ARG_170	NH1	B_GLU_131	OE2	2.840
1HGF	B_ARG_170	NH1	D_GLU_128	OE1	3.455
1HGF	B_ARG_170	NH1	D_GLU_128	OE2	3.294
1HGF	B_ARG_170	NH2	B_GLU_128	OE2	2.821
1HGF	B_LYS_174	NZ	D_ASP_164	OD2	3.813
1HGF	C_LYS_27	NZ	D_GLU_97	OE1	2.824
1HGF	C_LYS_27	NZ	D_GLU_97	OE2	2.808
1HGF	C_LYS_50	NZ	C_ASP_275	OD2	2.881
1HGF	C_ARG_57	NH2	C_GLU_82	OE1	2.589
1HGF	C_ARG_57	NH2	C_GLU_82	OE2	3.890
1HGF	C_HIS_75	ND1	C_ASP_73	OD1	2.839
1HGF	C_HIS_75	ND1	C_ASP_73	OD2	3.334
1HGF	C_HIS_75	NE2	C_ASP_63	OD1	3.432
1HGF	C_ARG_90	NH2	C_ASP_60	OD1	3.494
1HGF	C_ARG_90	NH2	C_ASP_60	OD2	2.843
1HGF	C_ARG_109	NH1	C_GLU_89	OE1	2.579
1HGF	C_ARG_109	NH1	C_GLU_89	OE2	2.919
1HGF	C_ARG_109	NH2	D_GLU_67	OE1	3.698
1HGF	C_ARG_109	NH2	D_GLU_67	OE2	2.914
1HGF	C_ARG_141	NH2	C_ASP_77	OD1	2.838
1HGF	C_ARG_141	NH2	C_ASP_77	OD2	2.786
1HGF	C_LYS_176	NZ	C_GLU_123	OE2	2.724
1HGF	C_LYS_176	NZ	C_ASP_172	OD1	3.678
1HGF	C_HIS_183	NE2	C_GLU_190	OE2	3.665
1HGF	C_LYS_238	NZ	B_GLU_72	OE1	2.746
1HGF	C_LYS_238	NZ	B_GLU_72	OE2	2.727
1HGF	C_ARG_261	NH1	C_GLU_119	OE1	3.774
1HGF	C_ARG_261	NH1	C_GLU_119	OE2	2.592
1HGF	C_ARG_261	NH2	C_GLU_119	OE1	2.721
1HGF	C_ARG_261	NH2	C_GLU_119	OE2	3.119
1HGF	C_LYS_264	NZ	C_ASP_85	OD2	3.303
1HGF	C_ARG_269	NH1	D_GLU_67	OE1	2.900
1HGF	C_LYS_292	NZ	C_ASP_291	OD1	2.883
1HGF	C_LYS_292	NZ	C_ASP_291	OD2	3.545
1HGF	C_LYS_299	NZ	D_GLU_69	OE2	3.732
1HGF	C_LYS_310	NZ	D_ASP_86	OD1	2.839
1HGF	C_LYS_310	NZ	D_ASP_90	OD1	2.507
1HGF	C_LYS_310	NZ	D_ASP_90	OD2	3.941
1HGF	C_LYS_315	NZ	C_GLU_41	OE1	3.725
1HGF	C_LYS_326	NZ	D_GLU_15	OE1	3.713
1HGF	D_LYS_51	NZ	D_GLU_103	OE1	2.742
1HGF	D_ARG_54	NH1	B_GLU_97	OE2	3.314
1HGF	D_ARG_54	NH1	D_GLU_57	OE1	3.296
1HGF	D_ARG_54	NH2	B_GLU_97	OE2	2.840
1HGF	D_LYS_62	NZ	B_ASP_86	OD1	3.122
1HGF	D_LYS_62	NZ	B_ASP_86	OD2	2.686
1HGF	D_LYS_62	NZ	B_ASP_90	OD1	3.703
1HGF	D_LYS_62	NZ	B_ASP_90	OD2	2.682

1HGF	D_LYS_68	NZ	D_GLU_85	OE1	3.023
1HGF	D_LYS_68	NZ	D_GLU_85	OE2	2.732
1HGF	D_ARG_76	NH1	F_GLU_74	OE1	2.790
1HGF	D_ARG_76	NH1	F_GLU_74	OE2	3.379
1HGF	D_ARG_76	NH2	F_GLU_74	OE1	3.594
1HGF	D_ARG_76	NH2	F_GLU_74	OE2	2.697
1HGF	D_ARG_76	NH2	F_GLU_81	OE1	2.644
1HGF	D_ARG_76	NH2	F_GLU_81	OE2	3.691
1HGF	D_LYS_117	NZ	D_GLU_114	OE1	3.303
1HGF	D_LYS_117	NZ	D_GLU_114	OE2	2.574
1HGF	D_ARG_123	NH1	D_GLU_120	OE1	2.580
1HGF	D_ARG_123	NH1	D_GLU_120	OE2	2.788
1HGF	D_ARG_123	NH2	B_GLU_132	OE1	3.407
1HGF	D_ARG_124	NH2	B_GLU_132	OE1	3.100
1HGF	D_ARG_124	NH2	B_GLU_132	OE2	3.442
1HGF	D_ARG_127	NH1	B_GLU_131	OE1	2.516
1HGF	D_ARG_153	NH1	D_GLU_150	OE1	2.657
1HGF	D_HIS_159	NE2	D_ASP_160	OD2	3.002
1HGF	D_ARG_163	NH2	B_GLU_131	OE1	2.704
1HGF	D_ARG_163	NH2	B_GLU_131	OE2	2.556
1HGF	D_ARG_170	NH1	D_GLU_131	OE2	2.839
1HGF	D_ARG_170	NH1	F_GLU_128	OE1	3.604
1HGF	D_ARG_170	NH1	F_GLU_128	OE2	3.428
1HGF	D_ARG_170	NH2	D_GLU_128	OE2	2.843
1HGF	E_LYS_27	NZ	F_GLU_97	OE1	2.793
1HGF	E_LYS_27	NZ	F_GLU_97	OE2	2.754
1HGF	E_LYS_50	NZ	E_ASP_275	OD2	2.903
1HGF	E_ARG_57	NH2	E_GLU_82	OE1	2.780
1HGF	E_HIS_75	ND1	E_ASP_73	OD1	2.855
1HGF	E_HIS_75	ND1	E_ASP_73	OD2	3.339
1HGF	E_HIS_75	NE2	E_ASP_63	OD1	3.444
1HGF	E_ARG_90	NH2	E_ASP_60	OD1	3.506
1HGF	E_ARG_90	NH2	E_ASP_60	OD2	2.882
1HGF	E_ARG_109	NH1	E_GLU_89	OE1	2.522
1HGF	E_ARG_109	NH1	E_GLU_89	OE2	2.887
1HGF	E_ARG_109	NH2	F_GLU_67	OE1	3.694
1HGF	E_ARG_109	NH2	F_GLU_67	OE2	2.878
1HGF	E_ARG_141	NH2	E_ASP_77	OD1	2.834
1HGF	E_ARG_141	NH2	E_ASP_77	OD2	2.773
1HGF	E_LYS_176	NZ	E_GLU_123	OE2	2.761
1HGF	E_LYS_176	NZ	E_ASP_172	OD1	3.700
1HGF	E_HIS_183	NE2	E_GLU_190	OE2	3.673
1HGF	E_LYS_238	NZ	D_GLU_72	OE1	2.831
1HGF	E_LYS_238	NZ	D_GLU_72	OE2	2.834
1HGF	E_ARG_261	NH1	E_GLU_119	OE1	3.764
1HGF	E_ARG_261	NH1	E_GLU_119	OE2	2.590
1HGF	E_ARG_261	NH2	E_GLU_119	OE1	2.729
1HGF	E_ARG_261	NH2	E_GLU_119	OE2	3.139
1HGF	E_LYS_264	NZ	E_ASP_85	OD2	3.295
1HGF	E_ARG_269	NH1	F_GLU_67	OE1	2.906
1HGF	E_LYS_292	NZ	E_ASP_291	OD1	2.871
1HGF	E_LYS_292	NZ	E_ASP_291	OD2	3.523
1HGF	E_LYS_299	NZ	F_GLU_69	OE2	3.655
1HGF	E_LYS_310	NZ	F_ASP_86	OD1	2.832
1HGF	E_LYS_310	NZ	F_ASP_90	OD1	2.514
1HGF	E_LYS_310	NZ	F_ASP_90	OD2	3.973
1HGF	E_LYS_315	NZ	E_GLU_41	OE1	3.726
1HGF	E_LYS_326	NZ	F_GLU_15	OE1	3.652

1HGF	E_LYS_326	NZ	F_GLU_15	OE2	3.771
1HGF	F_LYS_51	NZ	F_GLU_103	OE1	2.723
1HGF	F_ARG_54	NH1	D_GLU_97	OE2	3.368
1HGF	F_ARG_54	NH1	F_GLU_57	OE1	3.280
1HGF	F_ARG_54	NH2	D_GLU_97	OE2	2.791
1HGF	F_LYS_62	NZ	D_ASP_86	OD1	3.076
1HGF	F_LYS_62	NZ	D_ASP_86	OD2	2.672
1HGF	F_LYS_62	NZ	D_ASP_90	OD1	3.773
1HGF	F_LYS_62	NZ	D_ASP_90	OD2	2.752
1HGF	F_LYS_68	NZ	F_GLU_85	OE1	3.011
1HGF	F_LYS_68	NZ	F_GLU_85	OE2	2.638
1HGF	F_ARG_76	NH1	B_GLU_74	OE1	2.779
1HGF	F_ARG_76	NH1	B_GLU_74	OE2	3.420
1HGF	F_ARG_76	NH2	B_GLU_74	OE1	3.542
1HGF	F_ARG_76	NH2	B_GLU_74	OE2	2.707
1HGF	F_ARG_76	NH2	B_GLU_81	OE1	2.689
1HGF	F_ARG_76	NH2	B_GLU_81	OE2	3.716
1HGF	F_LYS_117	NZ	F_GLU_114	OE1	3.348
1HGF	F_LYS_117	NZ	F_GLU_114	OE2	2.589
1HGF	F_ARG_123	NH1	F_GLU_120	OE1	2.596
1HGF	F_ARG_123	NH1	F_GLU_120	OE2	2.789
1HGF	F_ARG_123	NH2	D_GLU_132	OE1	3.469
1HGF	F_ARG_124	NH2	D_GLU_132	OE1	3.198
1HGF	F_ARG_124	NH2	D_GLU_132	OE2	3.522
1HGF	F_ARG_127	NH1	D_GLU_131	OE1	2.568
1HGF	F_HIS_159	NE2	F_ASP_160	OD2	3.032
1HGF	F_ARG_163	NH2	D_GLU_131	OE1	2.689
1HGF	F_ARG_163	NH2	D_GLU_131	OE2	2.644
1HGF	F_ARG_170	NH1	B_GLU_128	OE1	3.432
1HGF	F_ARG_170	NH1	B_GLU_128	OE2	3.366
1HGF	F_ARG_170	NH1	F_GLU_131	OE2	2.852
1HGF	F_ARG_170	NH2	F_GLU_128	OE2	2.847
1HGF	F_LYS_174	NZ	B_ASP_164	OD2	3.837

Table 90: 1HGF-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1HGG	A_LYS_27	NZ	B_GLU_97	OE1	2.679
1HGG	A_LYS_27	NZ	B_GLU_97	OE2	2.904
1HGG	A_LYS_50	NZ	A_ASP_275	OD1	3.658
1HGG	A_LYS_50	NZ	A_ASP_275	OD2	2.711
1HGG	A_ARG_57	NH2	A_GLU_82	OE1	2.519
1HGG	A_ARG_57	NH2	A_GLU_82	OE2	3.336
1HGG	A_HIS_75	ND1	A_ASP_73	OD1	2.772
1HGG	A_HIS_75	ND1	A_ASP_73	OD2	3.336
1HGG	A_HIS_75	NE2	A_ASP_63	OD1	3.694
1HGG	A_ARG_90	NH2	A_ASP_60	OD1	3.622
1HGG	A_ARG_90	NH2	A_ASP_60	OD2	2.794
1HGG	A_ARG_109	NH1	A_GLU_89	OE1	2.517
1HGG	A_ARG_109	NH1	A_GLU_89	OE2	3.003
1HGG	A_ARG_109	NH2	B_GLU_67	OE1	3.854
1HGG	A_ARG_109	NH2	B_GLU_67	OE2	2.838
1HGG	A_ARG_141	NH2	A_ASP_77	OD1	2.758
1HGG	A_ARG_141	NH2	A_ASP_77	OD2	2.757
1HGG	A_LYS_176	NZ	A_GLU_123	OE2	2.648
1HGG	A_HIS_183	NE2	A_GLU_190	OE2	3.990
1HGG	A_LYS_238	NZ	F_GLU_72	OE1	2.931
1HGG	A_LYS_238	NZ	F_GLU_72	OE2	2.744
1HGG	A_ARG_261	NH1	A_GLU_119	OE1	3.988
1HGG	A_ARG_261	NH1	A_GLU_119	OE2	2.685
1HGG	A_ARG_261	NH2	A_GLU_119	OE1	2.738
1HGG	A_ARG_261	NH2	A_GLU_119	OE2	2.969
1HGG	A_LYS_264	NZ	A_ASP_85	OD1	3.326
1HGG	A_LYS_264	NZ	A_ASP_85	OD2	2.834
1HGG	A_ARG_269	NH1	B_GLU_67	OE1	2.694
1HGG	A_ARG_269	NH2	B_GLU_67	OE1	3.814
1HGG	A_LYS_292	NZ	A_ASP_291	OD1	2.980
1HGG	A_LYS_292	NZ	A_ASP_291	OD2	2.773
1HGG	A_LYS_299	NZ	B_GLU_69	OE2	2.915
1HGG	A_LYS_310	NZ	B_ASP_86	OD1	2.852
1HGG	A_LYS_310	NZ	B_ASP_90	OD1	2.700
1HGG	A_LYS_310	NZ	B_ASP_90	OD2	3.923
1HGG	A_LYS_315	NZ	A_GLU_41	OE1	2.731
1HGG	A_LYS_326	NZ	A_GLU_325	OE1	2.817
1HGG	A_LYS_326	NZ	B_GLU_15	OE1	3.039
1HGG	A_LYS_326	NZ	B_GLU_15	OE2	2.830
1HGG	B_ARG_25	NH1	A_GLU_325	OE2	3.770
1HGG	B_ARG_25	NH2	A_GLU_325	OE2	2.944
1HGG	B_LYS_51	NZ	B_GLU_103	OE1	2.759
1HGG	B_ARG_54	NH1	B_GLU_57	OE1	2.857
1HGG	B_ARG_54	NH1	B_GLU_57	OE2	2.882
1HGG	B_ARG_54	NH1	F_GLU_97	OE2	3.410
1HGG	B_ARG_54	NH2	F_GLU_97	OE2	2.750
1HGG	B_LYS_58	NZ	B_GLU_61	OE2	2.938
1HGG	B_LYS_62	NZ	F_ASP_86	OD1	2.889
1HGG	B_LYS_62	NZ	F_ASP_86	OD2	2.639
1HGG	B_LYS_62	NZ	F_ASP_90	OD1	3.716
1HGG	B_LYS_62	NZ	F_ASP_90	OD2	2.650
1HGG	B_LYS_68	NZ	B_GLU_85	OE1	3.149
1HGG	B_LYS_68	NZ	B_GLU_85	OE2	2.746
1HGG	B_ARG_76	NH1	D_GLU_74	OE1	2.882
1HGG	B_ARG_76	NH1	D_GLU_74	OE2	3.580
1HGG	B_ARG_76	NH2	D_GLU_74	OE1	3.459
1HGG	B_ARG_76	NH2	D_GLU_74	OE2	2.820

1HGG	B_ARG_76	NH2	D_GLU_81	OE1	2.731
1HGG	B_ARG_76	NH2	D_GLU_81	OE2	3.473
1HGG	B_LYS_117	NZ	B_GLU_114	OE1	3.037
1HGG	B_LYS_117	NZ	B_GLU_114	OE2	2.573
1HGG	B_ARG_123	NH1	B_GLU_120	OE1	2.615
1HGG	B_ARG_123	NH1	B_GLU_120	OE2	2.734
1HGG	B_ARG_123	NH2	F_GLU_132	OE1	2.827
1HGG	B_ARG_124	NH1	B_GLU_120	OE1	3.704
1HGG	B_ARG_124	NH2	F_GLU_132	OE1	3.221
1HGG	B_ARG_124	NH2	F_GLU_132	OE2	3.297
1HGG	B_ARG_127	NH1	F_GLU_131	OE1	2.465
1HGG	B_LYS_143	NZ	B_ASP_145	OD2	2.940
1HGG	B_ARG_153	NH1	B_GLU_150	OE1	2.632
1HGG	B_HIS_159	NE2	B_ASP_160	OD2	3.121
1HGG	B_ARG_163	NH2	B_GLU_128	OE1	3.737
1HGG	B_ARG_163	NH2	F_GLU_131	OE1	2.594
1HGG	B_ARG_163	NH2	F_GLU_131	OE2	2.562
1HGG	B_ARG_170	NH1	B_GLU_131	OE2	2.846
1HGG	B_ARG_170	NH1	D_GLU_128	OE1	3.236
1HGG	B_ARG_170	NH1	D_GLU_128	OE2	3.289
1HGG	B_ARG_170	NH2	B_GLU_128	OE2	2.890
1HGG	B_LYS_174	NZ	D_ASP_164	OD1	2.736
1HGG	B_LYS_174	NZ	D_ASP_164	OD2	2.575
1HGG	C_LYS_27	NZ	D_GLU_97	OE1	2.683
1HGG	C_LYS_27	NZ	D_GLU_97	OE2	2.941
1HGG	C_LYS_50	NZ	C_ASP_275	OD1	3.663
1HGG	C_LYS_50	NZ	C_ASP_275	OD2	2.681
1HGG	C_ARG_57	NH2	C_GLU_82	OE1	2.593
1HGG	C_ARG_57	NH2	C_GLU_82	OE2	3.431
1HGG	C_HIS_75	ND1	C_ASP_73	OD1	2.715
1HGG	C_HIS_75	ND1	C_ASP_73	OD2	3.305
1HGG	C_HIS_75	NE2	C_ASP_63	OD1	3.698
1HGG	C_ARG_90	NH2	C_ASP_60	OD1	3.640
1HGG	C_ARG_90	NH2	C_ASP_60	OD2	2.792
1HGG	C_ARG_109	NH1	C_GLU_89	OE1	2.511
1HGG	C_ARG_109	NH1	C_GLU_89	OE2	3.012
1HGG	C_ARG_109	NH2	D_GLU_67	OE1	3.869
1HGG	C_ARG_109	NH2	D_GLU_67	OE2	2.853
1HGG	C_ARG_141	NH2	C_ASP_77	OD1	2.758
1HGG	C_ARG_141	NH2	C_ASP_77	OD2	2.737
1HGG	C_LYS_176	NZ	C_GLU_123	OE2	2.629
1HGG	C_HIS_183	NE2	C_GLU_190	OE2	3.969
1HGG	C_LYS_238	NZ	B_GLU_72	OE1	2.830
1HGG	C_LYS_238	NZ	B_GLU_72	OE2	2.699
1HGG	C_ARG_261	NH1	C_GLU_119	OE1	3.989
1HGG	C_ARG_261	NH1	C_GLU_119	OE2	2.670
1HGG	C_ARG_261	NH2	C_GLU_119	OE1	2.730
1HGG	C_ARG_261	NH2	C_GLU_119	OE2	2.933
1HGG	C_LYS_264	NZ	C_ASP_85	OD1	3.356
1HGG	C_LYS_264	NZ	C_ASP_85	OD2	2.849
1HGG	C_ARG_269	NH1	D_GLU_67	OE1	2.688
1HGG	C_ARG_269	NH2	D_GLU_67	OE1	3.820
1HGG	C_LYS_292	NZ	C_ASP_291	OD1	3.021
1HGG	C_LYS_292	NZ	C_ASP_291	OD2	2.777
1HGG	C_LYS_299	NZ	D_GLU_69	OE2	2.932
1HGG	C_LYS_310	NZ	D_ASP_86	OD1	2.859
1HGG	C_LYS_310	NZ	D_ASP_90	OD1	2.651
1HGG	C_LYS_310	NZ	D_ASP_90	OD2	3.858

1HGG	C_LYS_315	NZ	C_GLU_41	OE1	2.732
1HGG	C_LYS_326	NZ	D_GLU_15	OE1	2.591
1HGG	C_LYS_326	NZ	D_GLU_15	OE2	3.450
1HGG	D_LYS_51	NZ	D_GLU_103	OE1	2.765
1HGG	D_ARG_54	NH1	B_GLU_97	OE2	3.442
1HGG	D_ARG_54	NH1	D_GLU_57	OE1	2.855
1HGG	D_ARG_54	NH1	D_GLU_57	OE2	2.880
1HGG	D_ARG_54	NH2	B_GLU_97	OE2	2.764
1HGG	D_LYS_58	NZ	D_GLU_61	OE2	2.913
1HGG	D_LYS_62	NZ	B_ASP_86	OD1	2.924
1HGG	D_LYS_62	NZ	B_ASP_86	OD2	2.567
1HGG	D_LYS_62	NZ	B_ASP_90	OD1	3.695
1HGG	D_LYS_62	NZ	B_ASP_90	OD2	2.575
1HGG	D_LYS_68	NZ	D_GLU_85	OE1	3.169
1HGG	D_LYS_68	NZ	D_GLU_85	OE2	2.772
1HGG	D_ARG_76	NH1	F_GLU_74	OE1	2.783
1HGG	D_ARG_76	NH1	F_GLU_74	OE2	3.379
1HGG	D_ARG_76	NH2	F_GLU_74	OE1	3.480
1HGG	D_ARG_76	NH2	F_GLU_74	OE2	2.737
1HGG	D_ARG_76	NH2	F_GLU_81	OE1	2.674
1HGG	D_ARG_76	NH2	F_GLU_81	OE2	3.521
1HGG	D_LYS_117	NZ	D_GLU_114	OE1	3.041
1HGG	D_LYS_117	NZ	D_GLU_114	OE2	2.574
1HGG	D_ARG_123	NH1	D_GLU_120	OE1	2.613
1HGG	D_ARG_123	NH1	D_GLU_120	OE2	2.730
1HGG	D_ARG_123	NH2	B_GLU_132	OE1	2.793
1HGG	D_ARG_124	NH1	D_GLU_120	OE1	3.717
1HGG	D_ARG_124	NH2	B_GLU_132	OE1	3.241
1HGG	D_ARG_124	NH2	B_GLU_132	OE2	3.297
1HGG	D_ARG_127	NH1	B_GLU_131	OE1	2.475
1HGG	D_LYS_143	NZ	D_ASP_145	OD2	2.930
1HGG	D_ARG_153	NH1	D_GLU_150	OE1	2.636
1HGG	D_HIS_159	NE2	D_ASP_160	OD2	3.127
1HGG	D_ARG_163	NH2	B_GLU_131	OE1	2.580
1HGG	D_ARG_163	NH2	B_GLU_131	OE2	2.598
1HGG	D_ARG_163	NH2	D_GLU_128	OE1	3.766
1HGG	D_ARG_170	NH1	D_GLU_131	OE2	2.855
1HGG	D_ARG_170	NH1	F_GLU_128	OE1	3.365
1HGG	D_ARG_170	NH1	F_GLU_128	OE2	3.390
1HGG	D_ARG_170	NH2	D_GLU_128	OE2	2.921
1HGG	D_LYS_174	NZ	F_ASP_164	OD1	2.763
1HGG	D_LYS_174	NZ	F_ASP_164	OD2	2.711
1HGG	E_LYS_27	NZ	F_GLU_97	OE1	2.689
1HGG	E_LYS_27	NZ	F_GLU_97	OE2	2.909
1HGG	E_LYS_50	NZ	E_ASP_275	OD1	3.653
1HGG	E_LYS_50	NZ	E_ASP_275	OD2	2.678
1HGG	E_ARG_57	NH2	E_GLU_82	OE1	2.569
1HGG	E_ARG_57	NH2	E_GLU_82	OE2	3.845
1HGG	E_HIS_75	ND1	E_ASP_73	OD1	2.755
1HGG	E_HIS_75	ND1	E_ASP_73	OD2	3.285
1HGG	E_HIS_75	NE2	E_ASP_63	OD1	3.700
1HGG	E_ARG_90	NH2	E_ASP_60	OD1	3.616
1HGG	E_ARG_90	NH2	E_ASP_60	OD2	2.834
1HGG	E_ARG_109	NH1	E_GLU_89	OE1	2.488
1HGG	E_ARG_109	NH1	E_GLU_89	OE2	2.947
1HGG	E_ARG_109	NH2	F_GLU_67	OE1	3.891
1HGG	E_ARG_109	NH2	F_GLU_67	OE2	2.876
1HGG	E_ARG_141	NH2	E_ASP_77	OD1	2.801

1HGG	E_ARG_141	NH2	E_ASP_77	OD2	2.744
1HGG	E_LYS_176	NZ	E_GLU_123	OE2	2.653
1HGG	E_HIS_183	NE2	E_GLU_190	OE2	3.980
1HGG	E_LYS_238	NZ	D_GLU_72	OE1	2.893
1HGG	E_LYS_238	NZ	D_GLU_72	OE2	2.782
1HGG	E_ARG_261	NH1	E_GLU_119	OE1	3.984
1HGG	E_ARG_261	NH1	E_GLU_119	OE2	2.694
1HGG	E_ARG_261	NH2	E_GLU_119	OE1	2.738
1HGG	E_ARG_261	NH2	E_GLU_119	OE2	2.981
1HGG	E_LYS_264	NZ	E_ASP_85	OD1	3.369
1HGG	E_LYS_264	NZ	E_ASP_85	OD2	2.847
1HGG	E_ARG_269	NH1	F_GLU_67	OE1	2.691
1HGG	E_ARG_269	NH2	F_GLU_67	OE1	3.830
1HGG	E_LYS_292	NZ	E_ASP_291	OD1	2.996
1HGG	E_LYS_292	NZ	E_ASP_291	OD2	2.759
1HGG	E_LYS_299	NZ	F_GLU_69	OE2	2.920
1HGG	E_LYS_310	NZ	F_ASP_86	OD1	2.871
1HGG	E_LYS_310	NZ	F_ASP_90	OD1	2.639
1HGG	E_LYS_310	NZ	F_ASP_90	OD2	3.900
1HGG	E_LYS_315	NZ	E_GLU_41	OE1	2.684
1HGG	E_LYS_326	NZ	F_GLU_15	OE1	2.975
1HGG	E_LYS_326	NZ	F_GLU_15	OE2	3.000
1HGG	F_LYS_51	NZ	F_GLU_103	OE1	2.794
1HGG	F_ARG_54	NH1	D_GLU_97	OE2	3.483
1HGG	F_ARG_54	NH1	F_GLU_57	OE1	2.848
1HGG	F_ARG_54	NH1	F_GLU_57	OE2	2.863
1HGG	F_ARG_54	NH2	D_GLU_97	OE2	2.727
1HGG	F_LYS_58	NZ	F_GLU_61	OE2	2.938
1HGG	F_LYS_62	NZ	D_ASP_86	OD1	2.904
1HGG	F_LYS_62	NZ	D_ASP_86	OD2	2.582
1HGG	F_LYS_62	NZ	D_ASP_90	OD1	3.752
1HGG	F_LYS_62	NZ	D_ASP_90	OD2	2.595
1HGG	F_LYS_68	NZ	F_GLU_85	OE1	3.147
1HGG	F_LYS_68	NZ	F_GLU_85	OE2	2.755
1HGG	F_ARG_76	NH1	B_GLU_74	OE1	2.750
1HGG	F_ARG_76	NH1	B_GLU_74	OE2	3.432
1HGG	F_ARG_76	NH2	B_GLU_74	OE1	3.456
1HGG	F_ARG_76	NH2	B_GLU_74	OE2	2.786
1HGG	F_ARG_76	NH2	B_GLU_81	OE1	2.674
1HGG	F_ARG_76	NH2	B_GLU_81	OE2	3.545
1HGG	F_LYS_117	NZ	F_GLU_114	OE1	3.063
1HGG	F_LYS_117	NZ	F_GLU_114	OE2	2.581
1HGG	F_ARG_123	NH1	F_GLU_120	OE1	2.640
1HGG	F_ARG_123	NH1	F_GLU_120	OE2	2.718
1HGG	F_ARG_123	NH2	D_GLU_132	OE1	2.843
1HGG	F_ARG_124	NH1	F_GLU_120	OE1	3.721
1HGG	F_ARG_124	NH2	D_GLU_132	OE1	3.317
1HGG	F_ARG_124	NH2	D_GLU_132	OE2	3.342
1HGG	F_ARG_127	NH1	D_GLU_131	OE1	2.523
1HGG	F_LYS_143	NZ	F_ASP_145	OD2	2.914
1HGG	F_ARG_153	NH1	F_GLU_150	OE2	2.532
1HGG	F_HIS_159	NE2	F_ASP_160	OD2	3.162
1HGG	F_ARG_163	NH2	D_GLU_131	OE1	2.589
1HGG	F_ARG_163	NH2	D_GLU_131	OE2	2.640
1HGG	F_ARG_163	NH2	F_GLU_128	OE1	3.754
1HGG	F_ARG_170	NH1	B_GLU_128	OE1	3.237
1HGG	F_ARG_170	NH1	B_GLU_128	OE2	3.354
1HGG	F_ARG_170	NH1	F_GLU_131	OE2	2.835

1HGG	F_ARG_170	NH2	F_GLU_128	OE2	2.924
1HGG	F_LYS_174	NZ	B_ASP_164	OD1	2.757
1HGG	F_LYS_174	NZ	B_ASP_164	OD2	2.547

Table 91: 1HGG-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1HGH	A_LYS_27	NZ	B_GLU_97	OE1	2.856
1HGH	A_LYS_27	NZ	B_GLU_97	OE2	2.781
1HGH	A_LYS_50	NZ	A_ASP_275	OD1	3.680
1HGH	A_LYS_50	NZ	A_ASP_275	OD2	2.788
1HGH	A_ARG_57	NH2	A_GLU_82	OE1	2.548
1HGH	A_ARG_57	NH2	A_GLU_82	OE2	3.398
1HGH	A_HIS_75	ND1	A_ASP_73	OD1	2.741
1HGH	A_HIS_75	ND1	A_ASP_73	OD2	3.401
1HGH	A_HIS_75	NE2	A_ASP_63	OD1	3.595
1HGH	A_ARG_90	NH2	A_ASP_60	OD1	3.580
1HGH	A_ARG_90	NH2	A_ASP_60	OD2	2.788
1HGH	A_ARG_109	NH1	A_GLU_89	OE1	2.475
1HGH	A_ARG_109	NH1	A_GLU_89	OE2	3.343
1HGH	A_ARG_109	NH2	B_GLU_67	OE1	3.697
1HGH	A_ARG_109	NH2	B_GLU_67	OE2	2.864
1HGH	A_ARG_141	NH2	A_ASP_77	OD1	2.863
1HGH	A_ARG_141	NH2	A_ASP_77	OD2	2.744
1HGH	A_LYS_176	NZ	A_GLU_123	OE2	2.684
1HGH	A_HIS_183	NE2	A_GLU_190	OE2	3.803
1HGH	A_LYS_238	NZ	F_GLU_72	OE1	2.921
1HGH	A_LYS_238	NZ	F_GLU_72	OE2	2.736
1HGH	A_ARG_261	NH1	A_GLU_119	OE2	2.623
1HGH	A_ARG_261	NH2	A_GLU_119	OE1	2.866
1HGH	A_ARG_261	NH2	A_GLU_119	OE2	2.801
1HGH	A_LYS_264	NZ	A_ASP_85	OD1	3.600
1HGH	A_LYS_264	NZ	A_ASP_85	OD2	2.814
1HGH	A_ARG_269	NH1	B_GLU_67	OE1	2.720
1HGH	A_ARG_269	NH2	B_GLU_67	OE1	3.718
1HGH	A_LYS_292	NZ	A_ASP_291	OD1	3.015
1HGH	A_LYS_292	NZ	A_ASP_291	OD2	2.819
1HGH	A_LYS_299	NZ	B_GLU_69	OE2	2.918
1HGH	A_LYS_310	NZ	B_ASP_86	OD1	2.712
1HGH	A_LYS_310	NZ	B_ASP_90	OD1	2.578
1HGH	A_LYS_310	NZ	B_ASP_90	OD2	3.975
1HGH	A_LYS_315	NZ	A_GLU_41	OE1	2.869
1HGH	A_LYS_326	NZ	A_GLU_325	OE1	2.838
1HGH	A_LYS_326	NZ	B_GLU_15	OE1	3.092
1HGH	A_LYS_326	NZ	B_GLU_15	OE2	2.707
1HGH	B_ARG_25	NH1	A_GLU_325	OE2	3.971
1HGH	B_ARG_25	NH2	A_GLU_325	OE2	3.017
1HGH	B_LYS_51	NZ	B_GLU_103	OE1	2.789
1HGH	B_ARG_54	NH1	B_GLU_57	OE1	2.865
1HGH	B_ARG_54	NH1	B_GLU_57	OE2	2.969
1HGH	B_ARG_54	NH1	F_GLU_97	OE2	3.285
1HGH	B_ARG_54	NH2	F_GLU_97	OE2	2.823
1HGH	B_LYS_58	NZ	B_GLU_61	OE2	3.237
1HGH	B_LYS_62	NZ	F_ASP_86	OD1	3.064
1HGH	B_LYS_62	NZ	F_ASP_86	OD2	2.661
1HGH	B_LYS_62	NZ	F_ASP_90	OD1	3.547
1HGH	B_LYS_62	NZ	F_ASP_90	OD2	2.683
1HGH	B_LYS_68	NZ	B_GLU_85	OE1	3.132
1HGH	B_LYS_68	NZ	B_GLU_85	OE2	2.734
1HGH	B_ARG_76	NH1	D_GLU_74	OE1	3.707
1HGH	B_ARG_76	NH1	D_GLU_74	OE2	2.912
1HGH	B_ARG_76	NH2	D_GLU_74	OE1	2.889
1HGH	B_ARG_76	NH2	D_GLU_74	OE2	3.526
1HGH	B_ARG_76	NH2	D_GLU_81	OE1	2.765

1HGH	B_ARG_76	NH2	D_GLU_81	OE2	3.411
1HGH	B_LYS_117	NZ	B_GLU_114	OE1	3.139
1HGH	B_LYS_117	NZ	B_GLU_114	OE2	2.561
1HGH	B_ARG_123	NH1	B_GLU_120	OE1	2.569
1HGH	B_ARG_123	NH1	B_GLU_120	OE2	2.742
1HGH	B_ARG_123	NH2	F_GLU_132	OE1	3.134
1HGH	B_ARG_124	NH1	B_GLU_120	OE1	3.740
1HGH	B_ARG_124	NH2	F_GLU_132	OE1	3.005
1HGH	B_ARG_124	NH2	F_GLU_132	OE2	3.302
1HGH	B_ARG_127	NH1	F_GLU_131	OE1	2.524
1HGH	B_LYS_143	NZ	B_ASP_145	OD2	2.787
1HGH	B_ARG_153	NH1	B_GLU_150	OE1	2.556
1HGH	B_HIS_159	NE2	B_ASP_160	OD2	3.003
1HGH	B_ARG_163	NH2	F_GLU_131	OE1	2.607
1HGH	B_ARG_163	NH2	F_GLU_131	OE2	2.538
1HGH	B_ARG_170	NH1	B_GLU_131	OE2	2.832
1HGH	B_ARG_170	NH1	D_GLU_128	OE1	3.253
1HGH	B_ARG_170	NH1	D_GLU_128	OE2	3.577
1HGH	B_ARG_170	NH2	B_GLU_128	OE2	2.706
1HGH	B_LYS_174	NZ	D_ASP_164	OD1	2.767
1HGH	B_LYS_174	NZ	D_ASP_164	OD2	2.573
1HGH	C_LYS_27	NZ	D_GLU_97	OE1	2.897
1HGH	C_LYS_27	NZ	D_GLU_97	OE2	2.815
1HGH	C_LYS_50	NZ	C_ASP_275	OD1	3.681
1HGH	C_LYS_50	NZ	C_ASP_275	OD2	2.765
1HGH	C_ARG_57	NH2	C_GLU_82	OE1	2.537
1HGH	C_ARG_57	NH2	C_GLU_82	OE2	3.720
1HGH	C_HIS_75	ND1	C_ASP_73	OD1	2.705
1HGH	C_HIS_75	ND1	C_ASP_73	OD2	3.403
1HGH	C_HIS_75	NE2	C_ASP_63	OD1	3.580
1HGH	C_ARG_90	NH2	C_ASP_60	OD1	3.561
1HGH	C_ARG_90	NH2	C_ASP_60	OD2	2.760
1HGH	C_ARG_109	NH1	C_GLU_89	OE1	2.510
1HGH	C_ARG_109	NH1	C_GLU_89	OE2	3.378
1HGH	C_ARG_109	NH2	D_GLU_67	OE1	3.686
1HGH	C_ARG_109	NH2	D_GLU_67	OE2	2.856
1HGH	C_ARG_141	NH2	C_ASP_77	OD1	2.881
1HGH	C_ARG_141	NH2	C_ASP_77	OD2	2.750
1HGH	C_LYS_176	NZ	C_GLU_123	OE2	2.654
1HGH	C_HIS_183	NE2	C_GLU_190	OE2	3.784
1HGH	C_LYS_238	NZ	B_GLU_72	OE1	2.713
1HGH	C_LYS_238	NZ	B_GLU_72	OE2	2.597
1HGH	C_ARG_261	NH1	C_GLU_119	OE2	2.638
1HGH	C_ARG_261	NH2	C_GLU_119	OE1	2.853
1HGH	C_ARG_261	NH2	C_GLU_119	OE2	2.786
1HGH	C_LYS_264	NZ	C_ASP_85	OD1	3.599
1HGH	C_LYS_264	NZ	C_ASP_85	OD2	2.793
1HGH	C_ARG_269	NH1	D_GLU_67	OE1	2.732
1HGH	C_ARG_269	NH2	D_GLU_67	OE1	3.725
1HGH	C_LYS_292	NZ	C_ASP_291	OD1	3.012
1HGH	C_LYS_292	NZ	C_ASP_291	OD2	2.815
1HGH	C_LYS_299	NZ	D_GLU_69	OE2	2.939
1HGH	C_LYS_310	NZ	D_ASP_86	OD1	2.734
1HGH	C_LYS_310	NZ	D_ASP_90	OD1	2.551
1HGH	C_LYS_310	NZ	D_ASP_90	OD2	3.913
1HGH	C_LYS_315	NZ	C_GLU_41	OE1	2.867
1HGH	C_LYS_326	NZ	D_GLU_15	OE1	2.774
1HGH	C_LYS_326	NZ	D_GLU_15	OE2	3.676

1HGH	D_LYS_51	NZ	D_GLU_103	OE1	2.742
1HGH	D_ARG_54	NH1	B_GLU_97	OE2	3.277
1HGH	D_ARG_54	NH1	D_GLU_57	OE1	2.856
1HGH	D_ARG_54	NH1	D_GLU_57	OE2	2.958
1HGH	D_ARG_54	NH2	B_GLU_97	OE2	2.797
1HGH	D_LYS_58	NZ	D_GLU_61	OE2	3.225
1HGH	D_LYS_62	NZ	B_ASP_86	OD1	3.011
1HGH	D_LYS_62	NZ	B_ASP_86	OD2	2.510
1HGH	D_LYS_62	NZ	B_ASP_90	OD1	3.543
1HGH	D_LYS_62	NZ	B_ASP_90	OD2	2.589
1HGH	D_LYS_68	NZ	D_GLU_85	OE1	3.123
1HGH	D_LYS_68	NZ	D_GLU_85	OE2	2.750
1HGH	D_ARG_76	NH1	F_GLU_74	OE1	3.430
1HGH	D_ARG_76	NH1	F_GLU_74	OE2	2.765
1HGH	D_ARG_76	NH2	F_GLU_74	OE1	2.747
1HGH	D_ARG_76	NH2	F_GLU_74	OE2	3.553
1HGH	D_ARG_76	NH2	F_GLU_81	OE1	2.698
1HGH	D_ARG_76	NH2	F_GLU_81	OE2	3.487
1HGH	D_LYS_117	NZ	D_GLU_114	OE1	3.179
1HGH	D_LYS_117	NZ	D_GLU_114	OE2	2.579
1HGH	D_ARG_123	NH1	D_GLU_120	OE1	2.573
1HGH	D_ARG_123	NH1	D_GLU_120	OE2	2.771
1HGH	D_ARG_123	NH2	B_GLU_132	OE1	3.141
1HGH	D_ARG_124	NH1	D_GLU_120	OE1	3.722
1HGH	D_ARG_124	NH2	B_GLU_132	OE1	3.050
1HGH	D_ARG_124	NH2	B_GLU_132	OE2	3.354
1HGH	D_ARG_127	NH1	B_GLU_131	OE1	2.536
1HGH	D_LYS_143	NZ	D_ASP_145	OD2	2.793
1HGH	D_ARG_153	NH1	D_GLU_150	OE2	2.554
1HGH	D_HIS_159	NE2	D_ASP_160	OD2	3.042
1HGH	D_ARG_163	NH2	B_GLU_131	OE1	2.609
1HGH	D_ARG_163	NH2	B_GLU_131	OE2	2.570
1HGH	D_ARG_170	NH1	D_GLU_131	OE2	2.834
1HGH	D_ARG_170	NH1	F_GLU_128	OE1	3.352
1HGH	D_ARG_170	NH1	F_GLU_128	OE2	3.641
1HGH	D_ARG_170	NH2	D_GLU_128	OE2	2.742
1HGH	D_LYS_174	NZ	F_ASP_164	OD1	2.863
1HGH	D_LYS_174	NZ	F_ASP_164	OD2	2.724
1HGH	E_LYS_27	NZ	F_GLU_97	OE1	2.917
1HGH	E_LYS_27	NZ	F_GLU_97	OE2	2.767
1HGH	E_LYS_50	NZ	E_ASP_275	OD1	3.706
1HGH	E_LYS_50	NZ	E_ASP_275	OD2	2.783
1HGH	E_ARG_57	NH2	E_GLU_82	OE1	2.543
1HGH	E_ARG_57	NH2	E_GLU_82	OE2	3.770
1HGH	E_HIS_75	ND1	E_ASP_73	OD1	2.703
1HGH	E_HIS_75	ND1	E_ASP_73	OD2	3.377
1HGH	E_HIS_75	NE2	E_ASP_63	OD1	3.572
1HGH	E_ARG_90	NH2	E_ASP_60	OD1	3.573
1HGH	E_ARG_90	NH2	E_ASP_60	OD2	2.816
1HGH	E_ARG_109	NH1	E_GLU_89	OE1	2.463
1HGH	E_ARG_109	NH1	E_GLU_89	OE2	3.357
1HGH	E_ARG_109	NH2	F_GLU_67	OE1	3.698
1HGH	E_ARG_109	NH2	F_GLU_67	OE2	2.878
1HGH	E_ARG_141	NH2	E_ASP_77	OD1	2.892
1HGH	E_ARG_141	NH2	E_ASP_77	OD2	2.736
1HGH	E_LYS_176	NZ	E_GLU_123	OE2	2.692
1HGH	E_HIS_183	NE2	E_GLU_190	OE2	3.780
1HGH	E_LYS_238	NZ	D_GLU_72	OE1	2.870

1HGH	E_LYS_238	NZ	D_GLU_72	OE2	2.766
1HGH	E_ARG_261	NH1	E_GLU_119	OE2	2.629
1HGH	E_ARG_261	NH2	E_GLU_119	OE1	2.852
1HGH	E_ARG_261	NH2	E_GLU_119	OE2	2.789
1HGH	E_LYS_264	NZ	E_ASP_85	OD1	3.620
1HGH	E_LYS_264	NZ	E_ASP_85	OD2	2.815
1HGH	E_ARG_269	NH1	F_GLU_67	OE1	2.705
1HGH	E_ARG_269	NH2	F_GLU_67	OE1	3.715
1HGH	E_LYS_292	NZ	E_ASP_291	OD1	3.036
1HGH	E_LYS_292	NZ	E_ASP_291	OD2	2.839
1HGH	E_LYS_299	NZ	F_GLU_69	OE2	2.896
1HGH	E_LYS_310	NZ	F_ASP_86	OD1	2.740
1HGH	E_LYS_310	NZ	F_ASP_90	OD1	2.571
1HGH	E_LYS_310	NZ	F_ASP_90	OD2	3.948
1HGH	E_LYS_315	NZ	E_GLU_41	OE1	2.853
1HGH	E_LYS_326	NZ	F_GLU_15	OE1	2.900
1HGH	E_LYS_326	NZ	F_GLU_15	OE2	3.072
1HGH	F_LYS_51	NZ	F_GLU_103	OE1	2.753
1HGH	F_ARG_54	NH1	D_GLU_97	OE2	3.293
1HGH	F_ARG_54	NH1	F_GLU_57	OE1	2.877
1HGH	F_ARG_54	NH1	F_GLU_57	OE2	2.968
1HGH	F_ARG_54	NH2	D_GLU_97	OE2	2.723
1HGH	F_LYS_58	NZ	F_GLU_61	OE2	3.244
1HGH	F_LYS_62	NZ	D_ASP_86	OD1	3.012
1HGH	F_LYS_62	NZ	D_ASP_86	OD2	2.546
1HGH	F_LYS_62	NZ	D_ASP_90	OD1	3.612
1HGH	F_LYS_62	NZ	D_ASP_90	OD2	2.682
1HGH	F_LYS_68	NZ	F_GLU_85	OE1	3.145
1HGH	F_LYS_68	NZ	F_GLU_85	OE2	2.728
1HGH	F_ARG_76	NH1	B_GLU_74	OE1	3.509
1HGH	F_ARG_76	NH1	B_GLU_74	OE2	2.732
1HGH	F_ARG_76	NH2	B_GLU_74	OE1	2.780
1HGH	F_ARG_76	NH2	B_GLU_74	OE2	3.488
1HGH	F_ARG_76	NH2	B_GLU_81	OE1	2.709
1HGH	F_ARG_76	NH2	B_GLU_81	OE2	3.513
1HGH	F_LYS_117	NZ	F_GLU_114	OE1	3.171
1HGH	F_LYS_117	NZ	F_GLU_114	OE2	2.578
1HGH	F_ARG_123	NH1	F_GLU_120	OE1	2.557
1HGH	F_ARG_123	NH1	F_GLU_120	OE2	2.739
1HGH	F_ARG_123	NH2	D_GLU_132	OE1	3.148
1HGH	F_ARG_124	NH1	F_GLU_120	OE1	3.713
1HGH	F_ARG_124	NH2	D_GLU_132	OE1	3.099
1HGH	F_ARG_124	NH2	D_GLU_132	OE2	3.356
1HGH	F_ARG_127	NH1	D_GLU_131	OE1	2.577
1HGH	F_LYS_143	NZ	F_ASP_145	OD2	2.769
1HGH	F_ARG_153	NH1	F_GLU_150	OE2	2.536
1HGH	F_HIS_159	NE2	F_ASP_160	OD2	3.043
1HGH	F_ARG_163	NH2	D_GLU_131	OE1	2.600
1HGH	F_ARG_163	NH2	D_GLU_131	OE2	2.611
1HGH	F_ARG_170	NH1	B_GLU_128	OE1	3.225
1HGH	F_ARG_170	NH1	B_GLU_128	OE2	3.576
1HGH	F_ARG_170	NH1	F_GLU_131	OE2	2.843
1HGH	F_ARG_170	NH2	F_GLU_128	OE2	2.737
1HGH	F_LYS_174	NZ	B_ASP_164	OD1	2.776
1HGH	F_LYS_174	NZ	B_ASP_164	OD2	2.495

Table 92: 1HGH-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1HGI	A.LYS_27	NZ	B.GLU_97	OE1	2.940
1HGI	A.LYS_27	NZ	B.GLU_97	OE2	2.900
1HGI	A.LYS_50	NZ	A.ASP_275	OD1	3.608
1HGI	A.LYS_50	NZ	A.ASP_275	OD2	2.707
1HGI	A.ARG_57	NH2	A.GLU_82	OE1	2.526
1HGI	A.ARG_57	NH2	A.GLU_82	OE2	3.433
1HGI	A.HIS_75	ND1	A.ASP_73	OD1	2.896
1HGI	A.HIS_75	ND1	A.ASP_73	OD2	3.177
1HGI	A.HIS_75	NE2	A.ASP_63	OD1	3.557
1HGI	A.ARG_90	NH2	A.ASP_60	OD1	3.597
1HGI	A.ARG_90	NH2	A.ASP_60	OD2	2.834
1HGI	A.ARG_109	NH1	A.GLU_89	OE1	2.511
1HGI	A.ARG_109	NH1	A.GLU_89	OE2	3.252
1HGI	A.ARG_109	NH2	B.GLU_67	OE1	3.638
1HGI	A.ARG_109	NH2	B.GLU_67	OE2	2.797
1HGI	A.ARG_141	NH2	A.ASP_77	OD1	2.933
1HGI	A.ARG_141	NH2	A.ASP_77	OD2	2.691
1HGI	A.LYS_176	NZ	A.GLU_123	OE2	2.677
1HGI	A.LYS_238	NZ	F.GLU_72	OE1	2.849
1HGI	A.LYS_238	NZ	F.GLU_72	OE2	2.839
1HGI	A.ARG_261	NH1	A.GLU_119	OE2	2.655
1HGI	A.ARG_261	NH2	A.GLU_119	OE1	2.852
1HGI	A.ARG_261	NH2	A.GLU_119	OE2	2.888
1HGI	A.LYS_264	NZ	A.ASP_85	OD1	3.460
1HGI	A.LYS_264	NZ	A.ASP_85	OD2	2.825
1HGI	A.ARG_269	NH1	B.GLU_67	OE1	2.748
1HGI	A.ARG_269	NH2	B.GLU_67	OE1	3.823
1HGI	A.LYS_292	NZ	A.ASP_291	OD1	2.954
1HGI	A.LYS_292	NZ	A.ASP_291	OD2	2.810
1HGI	A.LYS_299	NZ	B.GLU_69	OE2	2.728
1HGI	A.LYS_310	NZ	B.ASP_86	OD1	2.759
1HGI	A.LYS_310	NZ	B.ASP_90	OD1	2.527
1HGI	A.LYS_315	NZ	A.GLU_41	OE1	2.774
1HGI	A.LYS_326	NZ	A.GLU_325	OE1	2.913
1HGI	A.LYS_326	NZ	B.GLU_15	OE1	3.374
1HGI	A.LYS_326	NZ	B.GLU_15	OE2	2.794
1HGI	B.ARG_25	NH1	A.GLU_325	OE2	3.734
1HGI	B.ARG_25	NH2	A.GLU_325	OE2	2.929
1HGI	B.LYS_51	NZ	B.GLU_103	OE1	2.815
1HGI	B.ARG_54	NH1	B.GLU_57	OE1	2.860
1HGI	B.ARG_54	NH1	B.GLU_57	OE2	2.893
1HGI	B.ARG_54	NH1	F.GLU_97	OE2	3.222
1HGI	B.ARG_54	NH2	F.GLU_97	OE2	2.806
1HGI	B.LYS_58	NZ	B.GLU_61	OE2	3.021
1HGI	B.LYS_62	NZ	F.ASP_86	OD1	2.942
1HGI	B.LYS_62	NZ	F.ASP_86	OD2	2.668
1HGI	B.LYS_62	NZ	F.ASP_90	OD1	3.332
1HGI	B.LYS_62	NZ	F.ASP_90	OD2	2.667
1HGI	B.LYS_68	NZ	B.GLU_85	OE1	3.269
1HGI	B.LYS_68	NZ	B.GLU_85	OE2	2.791
1HGI	B.ARG_76	NH1	D.GLU_74	OE1	3.625
1HGI	B.ARG_76	NH1	D.GLU_74	OE2	2.918
1HGI	B.ARG_76	NH2	D.GLU_74	OE1	2.861
1HGI	B.ARG_76	NH2	D.GLU_74	OE2	3.621
1HGI	B.ARG_76	NH2	D.GLU_81	OE1	2.708
1HGI	B.ARG_76	NH2	D.GLU_81	OE2	3.474
1HGI	B.LYS_117	NZ	B.GLU_114	OE1	3.138

1HGI	B_LYS_117	NZ	B_GLU_114	OE2	2.563
1HGI	B_ARG_123	NH1	B_GLU_120	OE1	2.571
1HGI	B_ARG_123	NH1	B_GLU_120	OE2	2.840
1HGI	B_ARG_123	NH2	F_GLU_132	OE1	3.105
1HGI	B_ARG_124	NH1	B_GLU_120	OE1	3.733
1HGI	B_ARG_124	NH2	F_GLU_132	OE1	3.081
1HGI	B_ARG_124	NH2	F_GLU_132	OE2	3.356
1HGI	B_ARG_127	NH1	F_GLU_131	OE1	2.493
1HGI	B_LYS_143	NZ	B_ASP_145	OD2	2.749
1HGI	B_ARG_153	NH1	B_GLU_150	OE1	2.584
1HGI	B_HIS_159	NE2	B_ASP_160	OD2	3.012
1HGI	B_ARG_163	NH2	B_GLU_128	OE1	3.957
1HGI	B_ARG_163	NH2	F_GLU_131	OE1	2.586
1HGI	B_ARG_163	NH2	F_GLU_131	OE2	2.598
1HGI	B_ARG_170	NH1	B_GLU_131	OE2	2.767
1HGI	B_ARG_170	NH1	D_GLU_128	OE1	3.640
1HGI	B_ARG_170	NH1	D_GLU_128	OE2	3.301
1HGI	B_ARG_170	NH2	B_GLU_128	OE2	2.947
1HGI	B_LYS_174	NZ	D_ASP_164	OD1	2.745
1HGI	B_LYS_174	NZ	D_ASP_164	OD2	2.560
1HGI	C_LYS_27	NZ	D_GLU_97	OE1	2.951
1HGI	C_LYS_27	NZ	D_GLU_97	OE2	2.876
1HGI	C_LYS_50	NZ	C_ASP_275	OD1	3.635
1HGI	C_LYS_50	NZ	C_ASP_275	OD2	2.676
1HGI	C_ARG_57	NH2	C_GLU_82	OE1	2.525
1HGI	C_ARG_57	NH2	C_GLU_82	OE2	3.836
1HGI	C_HIS_75	ND1	C_ASP_73	OD1	2.875
1HGI	C_HIS_75	ND1	C_ASP_73	OD2	3.155
1HGI	C_HIS_75	NE2	C_ASP_63	OD1	3.544
1HGI	C_ARG_90	NH2	C_ASP_60	OD1	3.575
1HGI	C_ARG_90	NH2	C_ASP_60	OD2	2.774
1HGI	C_ARG_109	NH1	C_GLU_89	OE1	2.522
1HGI	C_ARG_109	NH1	C_GLU_89	OE2	3.270
1HGI	C_ARG_109	NH2	D_GLU_67	OE1	3.637
1HGI	C_ARG_109	NH2	D_GLU_67	OE2	2.819
1HGI	C_ARG_141	NH2	C_ASP_77	OD1	2.934
1HGI	C_ARG_141	NH2	C_ASP_77	OD2	2.703
1HGI	C_LYS_176	NZ	C_GLU_123	OE2	2.678
1HGI	C_LYS_238	NZ	B_GLU_72	OE1	2.671
1HGI	C_LYS_238	NZ	B_GLU_72	OE2	2.721
1HGI	C_ARG_261	NH1	C_GLU_119	OE2	2.664
1HGI	C_ARG_261	NH2	C_GLU_119	OE1	2.844
1HGI	C_ARG_261	NH2	C_GLU_119	OE2	2.850
1HGI	C_LYS_264	NZ	C_ASP_85	OD1	3.489
1HGI	C_LYS_264	NZ	C_ASP_85	OD2	2.832
1HGI	C_ARG_269	NH1	D_GLU_67	OE1	2.753
1HGI	C_ARG_269	NH2	D_GLU_67	OE1	3.850
1HGI	C_LYS_292	NZ	C_ASP_291	OD1	2.977
1HGI	C_LYS_292	NZ	C_ASP_291	OD2	2.816
1HGI	C_LYS_299	NZ	D_GLU_69	OE2	2.739
1HGI	C_LYS_310	NZ	D_ASP_86	OD1	2.772
1HGI	C_LYS_310	NZ	D_ASP_90	OD1	2.525
1HGI	C_LYS_315	NZ	C_GLU_41	OE1	2.748
1HGI	C_LYS_326	NZ	D_GLU_15	OE1	2.825
1HGI	C_LYS_326	NZ	D_GLU_15	OE2	3.570
1HGI	D_LYS_51	NZ	D_GLU_103	OE1	2.810
1HGI	D_ARG_54	NH1	B_GLU_97	OE2	3.254
1HGI	D_ARG_54	NH1	D_GLU_57	OE1	2.846

1HGI	D_ARG_54	NH1	D_GLU_57	OE2	2.899
1HGI	D_ARG_54	NH2	B_GLU_97	OE2	2.808
1HGI	D_LYS_58	NZ	D_GLU_61	OE2	2.998
1HGI	D_LYS_62	NZ	B_ASP_86	OD1	2.962
1HGI	D_LYS_62	NZ	B_ASP_86	OD2	2.570
1HGI	D_LYS_62	NZ	B_ASP_90	OD1	3.335
1HGI	D_LYS_62	NZ	B_ASP_90	OD2	2.541
1HGI	D_LYS_68	NZ	D_GLU_85	OE1	3.268
1HGI	D_LYS_68	NZ	D_GLU_85	OE2	2.807
1HGI	D_ARG_76	NH1	F_GLU_74	OE1	3.375
1HGI	D_ARG_76	NH1	F_GLU_74	OE2	2.776
1HGI	D_ARG_76	NH2	F_GLU_74	OE1	2.760
1HGI	D_ARG_76	NH2	F_GLU_74	OE2	3.657
1HGI	D_ARG_76	NH2	F_GLU_81	OE1	2.608
1HGI	D_ARG_76	NH2	F_GLU_81	OE2	3.506
1HGI	D_LYS_117	NZ	D_GLU_114	OE1	3.195
1HGI	D_LYS_117	NZ	D_GLU_114	OE2	2.582
1HGI	D_ARG_123	NH1	D_GLU_120	OE1	2.549
1HGI	D_ARG_123	NH1	D_GLU_120	OE2	2.835
1HGI	D_ARG_123	NH2	B_GLU_132	OE1	3.093
1HGI	D_ARG_124	NH1	D_GLU_120	OE1	3.750
1HGI	D_ARG_124	NH2	B_GLU_132	OE1	3.096
1HGI	D_ARG_124	NH2	B_GLU_132	OE2	3.377
1HGI	D_ARG_127	NH1	B_GLU_131	OE1	2.513
1HGI	D_LYS_143	NZ	D_ASP_145	OD2	2.778
1HGI	D_ARG_153	NH1	D_GLU_150	OE2	2.550
1HGI	D_HIS_159	NE2	D_ASP_160	OD2	3.012
1HGI	D_ARG_163	NH2	B_GLU_131	OE1	2.590
1HGI	D_ARG_163	NH2	B_GLU_131	OE2	2.616
1HGI	D_ARG_163	NH2	D_GLU_128	OE1	3.999
1HGI	D_ARG_170	NH1	D_GLU_131	OE2	2.771
1HGI	D_ARG_170	NH1	F_GLU_128	OE1	3.797
1HGI	D_ARG_170	NH1	F_GLU_128	OE2	3.417
1HGI	D_ARG_170	NH2	D_GLU_128	OE2	2.974
1HGI	D_LYS_174	NZ	F_ASP_164	OD1	2.814
1HGI	D_LYS_174	NZ	F_ASP_164	OD2	2.727
1HGI	E_LYS_27	NZ	F_GLU_97	OE1	2.961
1HGI	E_LYS_27	NZ	F_GLU_97	OE2	2.862
1HGI	E_LYS_50	NZ	E_ASP_275	OD1	3.624
1HGI	E_LYS_50	NZ	E_ASP_275	OD2	2.698
1HGI	E_ARG_57	NH2	E_GLU_82	OE1	2.652
1HGI	E_ARG_57	NH2	E_GLU_82	OE2	3.886
1HGI	E_HIS_75	ND1	E_ASP_73	OD1	2.868
1HGI	E_HIS_75	ND1	E_ASP_73	OD2	3.142
1HGI	E_HIS_75	NE2	E_ASP_63	OD1	3.556
1HGI	E_ARG_90	NH2	E_ASP_60	OD1	3.607
1HGI	E_ARG_90	NH2	E_ASP_60	OD2	2.841
1HGI	E_ARG_109	NH1	E_GLU_89	OE1	2.478
1HGI	E_ARG_109	NH1	E_GLU_89	OE2	3.260
1HGI	E_ARG_109	NH2	F_GLU_67	OE1	3.649
1HGI	E_ARG_109	NH2	F_GLU_67	OE2	2.781
1HGI	E_ARG_141	NH2	E_ASP_77	OD1	2.937
1HGI	E_ARG_141	NH2	E_ASP_77	OD2	2.703
1HGI	E_LYS_176	NZ	E_GLU_123	OE2	2.685
1HGI	E_LYS_238	NZ	D_GLU_72	OE1	2.803
1HGI	E_LYS_238	NZ	D_GLU_72	OE2	2.859
1HGI	E_ARG_261	NH1	E_GLU_119	OE2	2.651
1HGI	E_ARG_261	NH2	E_GLU_119	OE1	2.844

1HGI	E_ARG_261	NH2	E_GLU_119	OE2	2.870
1HGI	E_LYS_264	NZ	E_ASP_85	OD1	3.485
1HGI	E_LYS_264	NZ	E_ASP_85	OD2	2.858
1HGI	E_ARG_269	NH1	F_GLU_67	OE1	2.720
1HGI	E_ARG_269	NH2	F_GLU_67	OE1	3.815
1HGI	E_LYS_292	NZ	E_ASP_291	OD1	2.984
1HGI	E_LYS_292	NZ	E_ASP_291	OD2	2.865
1HGI	E_LYS_299	NZ	F_GLU_69	OE2	2.715
1HGI	E_LYS_310	NZ	F_ASP_86	OD1	2.757
1HGI	E_LYS_310	NZ	F_ASP_90	OD1	2.523
1HGI	E_LYS_315	NZ	E_GLU_41	OE1	2.741
1HGI	E_LYS_326	NZ	F_GLU_15	OE1	2.882
1HGI	E_LYS_326	NZ	F_GLU_15	OE2	3.090
1HGI	F_LYS_51	NZ	F_GLU_103	OE1	2.800
1HGI	F_ARG_54	NH1	D_GLU_97	OE2	3.254
1HGI	F_ARG_54	NH1	F_GLU_57	OE1	2.835
1HGI	F_ARG_54	NH1	F_GLU_57	OE2	2.892
1HGI	F_ARG_54	NH2	D_GLU_97	OE2	2.750
1HGI	F_LYS_58	NZ	F_GLU_61	OE2	3.021
1HGI	F_LYS_62	NZ	D_ASP_86	OD1	2.884
1HGI	F_LYS_62	NZ	D_ASP_86	OD2	2.563
1HGI	F_LYS_62	NZ	D_ASP_90	OD1	3.358
1HGI	F_LYS_62	NZ	D_ASP_90	OD2	2.609
1HGI	F_LYS_68	NZ	F_GLU_85	OE1	3.264
1HGI	F_LYS_68	NZ	F_GLU_85	OE2	2.739
1HGI	F_ARG_76	NH1	B_GLU_74	OE1	3.420
1HGI	F_ARG_76	NH1	B_GLU_74	OE2	2.771
1HGI	F_ARG_76	NH2	B_GLU_74	OE1	2.763
1HGI	F_ARG_76	NH2	B_GLU_74	OE2	3.604
1HGI	F_ARG_76	NH2	B_GLU_81	OE1	2.645
1HGI	F_ARG_76	NH2	B_GLU_81	OE2	3.592
1HGI	F_LYS_117	NZ	F_GLU_114	OE1	3.182
1HGI	F_LYS_117	NZ	F_GLU_114	OE2	2.543
1HGI	F_ARG_123	NH1	F_GLU_120	OE1	2.586
1HGI	F_ARG_123	NH1	F_GLU_120	OE2	2.812
1HGI	F_ARG_123	NH2	D_GLU_132	OE1	3.144
1HGI	F_ARG_124	NH1	F_GLU_120	OE1	3.763
1HGI	F_ARG_124	NH2	D_GLU_132	OE1	3.185
1HGI	F_ARG_124	NH2	D_GLU_132	OE2	3.386
1HGI	F_ARG_127	NH1	D_GLU_131	OE1	2.561
1HGI	F_LYS_143	NZ	F_ASP_145	OD2	2.731
1HGI	F_ARG_153	NH1	F_GLU_150	OE2	2.577
1HGI	F_HIS_159	NE2	F_ASP_160	OD2	3.055
1HGI	F_ARG_163	NH2	D_GLU_131	OE1	2.567
1HGI	F_ARG_163	NH2	D_GLU_131	OE2	2.692
1HGI	F_ARG_163	NH2	F_GLU_128	OE1	3.975
1HGI	F_ARG_170	NH1	B_GLU_128	OE1	3.621
1HGI	F_ARG_170	NH1	B_GLU_128	OE2	3.345
1HGI	F_ARG_170	NH1	F_GLU_131	OE2	2.754
1HGI	F_ARG_170	NH2	F_GLU_128	OE2	2.972
1HGI	F_LYS_174	NZ	B_ASP_164	OD1	2.789
1HGI	F_LYS_174	NZ	B_ASP_164	OD2	2.521

Table 93: 1HGI-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1HGJ	A_LYS_27	NZ	B_GLU_97	OE1	2.775
1HGJ	A_LYS_27	NZ	B_GLU_97	OE2	2.807
1HGJ	A_LYS_50	NZ	A_ASP_275	OD1	3.487
1HGJ	A_LYS_50	NZ	A_ASP_275	OD2	2.742
1HGJ	A_ARG_57	NH2	A_GLU_82	OE1	2.521
1HGJ	A_ARG_57	NH2	A_GLU_82	OE2	3.796
1HGJ	A_HIS_75	ND1	A_ASP_73	OD1	2.831
1HGJ	A_HIS_75	ND1	A_ASP_73	OD2	3.407
1HGJ	A_HIS_75	NE2	A_ASP_63	OD1	3.353
1HGJ	A_ARG_90	NH2	A_ASP_60	OD1	3.662
1HGJ	A_ARG_90	NH2	A_ASP_60	OD2	2.811
1HGJ	A_ARG_109	NH1	A_GLU_89	OE1	2.528
1HGJ	A_ARG_109	NH1	A_GLU_89	OE2	3.223
1HGJ	A_ARG_109	NH2	B_GLU_67	OE1	3.648
1HGJ	A_ARG_109	NH2	B_GLU_67	OE2	2.748
1HGJ	A_ARG_141	NH2	A_ASP_77	OD1	2.818
1HGJ	A_ARG_141	NH2	A_ASP_77	OD2	2.748
1HGJ	A_LYS_176	NZ	A_GLU_123	OE2	2.680
1HGJ	A_HIS_183	NE2	A_GLU_190	OE2	3.316
1HGJ	A_LYS_238	NZ	F_GLU_72	OE1	2.903
1HGJ	A_LYS_238	NZ	F_GLU_72	OE2	2.788
1HGJ	A_ARG_261	NH1	A_GLU_119	OE2	2.647
1HGJ	A_ARG_261	NH2	A_GLU_119	OE1	2.898
1HGJ	A_ARG_261	NH2	A_GLU_119	OE2	2.927
1HGJ	A_LYS_264	NZ	A_ASP_85	OD1	3.715
1HGJ	A_LYS_264	NZ	A_ASP_85	OD2	2.840
1HGJ	A_ARG_269	NH1	B_GLU_67	OE1	2.736
1HGJ	A_ARG_269	NH2	B_GLU_67	OE1	3.791
1HGJ	A_LYS_292	NZ	A_ASP_291	OD1	2.856
1HGJ	A_LYS_292	NZ	A_ASP_291	OD2	2.799
1HGJ	A_LYS_299	NZ	B_GLU_69	OE2	2.821
1HGJ	A_LYS_310	NZ	B_ASP_86	OD1	2.922
1HGJ	A_LYS_310	NZ	B_ASP_90	OD1	2.569
1HGJ	A_LYS_315	NZ	A_GLU_41	OE1	2.855
1HGJ	A_LYS_326	NZ	A_GLU_325	OE1	2.919
1HGJ	A_LYS_326	NZ	B_GLU_15	OE1	3.187
1HGJ	A_LYS_326	NZ	B_GLU_15	OE2	2.826
1HGJ	B_ARG_25	NH1	A_GLU_325	OE2	3.775
1HGJ	B_ARG_25	NH2	A_GLU_325	OE2	2.974
1HGJ	B_LYS_51	NZ	B_GLU_103	OE1	2.778
1HGJ	B_ARG_54	NH1	B_GLU_57	OE1	2.874
1HGJ	B_ARG_54	NH1	B_GLU_57	OE2	2.925
1HGJ	B_ARG_54	NH1	F_GLU_97	OE2	3.272
1HGJ	B_ARG_54	NH2	F_GLU_97	OE2	2.774
1HGJ	B_LYS_58	NZ	B_GLU_61	OE2	3.374
1HGJ	B_LYS_62	NZ	F_ASP_86	OD1	2.863
1HGJ	B_LYS_62	NZ	F_ASP_86	OD2	2.651
1HGJ	B_LYS_62	NZ	F_ASP_90	OD1	3.453
1HGJ	B_LYS_62	NZ	F_ASP_90	OD2	2.738
1HGJ	B_LYS_68	NZ	B_GLU_85	OE1	3.167
1HGJ	B_LYS_68	NZ	B_GLU_85	OE2	2.782
1HGJ	B_ARG_76	NH1	D_GLU_74	OE1	3.648
1HGJ	B_ARG_76	NH1	D_GLU_74	OE2	2.885
1HGJ	B_ARG_76	NH2	D_GLU_74	OE1	2.846
1HGJ	B_ARG_76	NH2	D_GLU_74	OE2	3.547
1HGJ	B_ARG_76	NH2	D_GLU_81	OE1	2.721
1HGJ	B_ARG_76	NH2	D_GLU_81	OE2	3.500

1HGJ	B_LYS_117	NZ	B_GLU_114	OE1	3.054
1HGJ	B_LYS_117	NZ	B_GLU_114	OE2	2.578
1HGJ	B_ARG_123	NH1	B_GLU_120	OE1	2.614
1HGJ	B_ARG_123	NH1	B_GLU_120	OE2	2.737
1HGJ	B_ARG_123	NH2	F_GLU_132	OE1	3.120
1HGJ	B_ARG_124	NH1	B_GLU_120	OE1	3.704
1HGJ	B_ARG_124	NH2	F_GLU_132	OE1	3.095
1HGJ	B_ARG_124	NH2	F_GLU_132	OE2	3.375
1HGJ	B_ARG_127	NH1	F_GLU_131	OE1	2.484
1HGJ	B_LYS_143	NZ	B_ASP_145	OD2	2.863
1HGJ	B_ARG_153	NH1	B_GLU_150	OE1	2.677
1HGJ	B_HIS_159	NE2	B_ASP_160	OD2	3.106
1HGJ	B_ARG_163	NH2	F_GLU_131	OE1	2.591
1HGJ	B_ARG_163	NH2	F_GLU_131	OE2	2.571
1HGJ	B_ARG_170	NH1	B_GLU_131	OE2	2.795
1HGJ	B_ARG_170	NH1	D_GLU_128	OE1	3.291
1HGJ	B_ARG_170	NH1	D_GLU_128	OE2	3.706
1HGJ	B_ARG_170	NH2	B_GLU_128	OE2	2.712
1HGJ	B_LYS_174	NZ	D_ASP_164	OD1	2.810
1HGJ	B_LYS_174	NZ	D_ASP_164	OD2	2.550
1HGJ	C_LYS_27	NZ	D_GLU_97	OE1	2.755
1HGJ	C_LYS_27	NZ	D_GLU_97	OE2	2.824
1HGJ	C_LYS_50	NZ	C_ASP_275	OD1	3.494
1HGJ	C_LYS_50	NZ	C_ASP_275	OD2	2.741
1HGJ	C_ARG_57	NH2	C_GLU_82	OE1	2.545
1HGJ	C_ARG_57	NH2	C_GLU_82	OE2	3.939
1HGJ	C_HIS_75	ND1	C_ASP_73	OD1	2.800
1HGJ	C_HIS_75	ND1	C_ASP_73	OD2	3.368
1HGJ	C_HIS_75	NE2	C_ASP_63	OD1	3.332
1HGJ	C_ARG_90	NH2	C_ASP_60	OD1	3.676
1HGJ	C_ARG_90	NH2	C_ASP_60	OD2	2.784
1HGJ	C_ARG_109	NH1	C_GLU_89	OE1	2.558
1HGJ	C_ARG_109	NH1	C_GLU_89	OE2	3.226
1HGJ	C_ARG_109	NH2	D_GLU_67	OE1	3.638
1HGJ	C_ARG_109	NH2	D_GLU_67	OE2	2.758
1HGJ	C_ARG_141	NH2	C_ASP_77	OD1	2.808
1HGJ	C_ARG_141	NH2	C_ASP_77	OD2	2.737
1HGJ	C_LYS_176	NZ	C_GLU_123	OE2	2.691
1HGJ	C_HIS_183	NE2	C_GLU_190	OE2	3.331
1HGJ	C_LYS_238	NZ	B_GLU_72	OE1	2.749
1HGJ	C_LYS_238	NZ	B_GLU_72	OE2	2.713
1HGJ	C_ARG_261	NH1	C_GLU_119	OE2	2.654
1HGJ	C_ARG_261	NH2	C_GLU_119	OE1	2.921
1HGJ	C_ARG_261	NH2	C_GLU_119	OE2	2.914
1HGJ	C_LYS_264	NZ	C_ASP_85	OD1	3.727
1HGJ	C_LYS_264	NZ	C_ASP_85	OD2	2.825
1HGJ	C_ARG_269	NH1	D_GLU_67	OE1	2.708
1HGJ	C_ARG_269	NH2	D_GLU_67	OE1	3.781
1HGJ	C_LYS_292	NZ	C_ASP_291	OD1	2.908
1HGJ	C_LYS_292	NZ	C_ASP_291	OD2	2.818
1HGJ	C_LYS_299	NZ	D_GLU_69	OE2	2.827
1HGJ	C_LYS_310	NZ	D_ASP_86	OD1	2.943
1HGJ	C_LYS_310	NZ	D_ASP_90	OD1	2.532
1HGJ	C_LYS_315	NZ	C_GLU_41	OE1	2.864
1HGJ	C_LYS_326	NZ	D_GLU_15	OE1	2.911
1HGJ	C_LYS_326	NZ	D_GLU_15	OE2	3.904
1HGJ	D_LYS_51	NZ	D_GLU_103	OE1	2.796
1HGJ	D_ARG_54	NH1	B_GLU_97	OE2	3.338

1HGJ	D_ARG_54	NH1	D_GLU_57	OE1	2.865
1HGJ	D_ARG_54	NH1	D_GLU_57	OE2	2.909
1HGJ	D_ARG_54	NH2	B_GLU_97	OE2	2.835
1HGJ	D_LYS_58	NZ	D_GLU_61	OE2	3.356
1HGJ	D_LYS_62	NZ	B_ASP_86	OD1	2.910
1HGJ	D_LYS_62	NZ	B_ASP_86	OD2	2.574
1HGJ	D_LYS_62	NZ	B_ASP_90	OD1	3.419
1HGJ	D_LYS_62	NZ	B_ASP_90	OD2	2.622
1HGJ	D_LYS_68	NZ	D_GLU_85	OE1	3.144
1HGJ	D_LYS_68	NZ	D_GLU_85	OE2	2.820
1HGJ	D_ARG_76	NH1	F_GLU_74	OE1	3.424
1HGJ	D_ARG_76	NH1	F_GLU_74	OE2	2.763
1HGJ	D_ARG_76	NH2	F_GLU_74	OE1	2.714
1HGJ	D_ARG_76	NH2	F_GLU_74	OE2	3.550
1HGJ	D_ARG_76	NH2	F_GLU_81	OE1	2.684
1HGJ	D_ARG_76	NH2	F_GLU_81	OE2	3.574
1HGJ	D_LYS_117	NZ	D_GLU_114	OE1	3.086
1HGJ	D_LYS_117	NZ	D_GLU_114	OE2	2.611
1HGJ	D_ARG_123	NH1	D_GLU_120	OE1	2.598
1HGJ	D_ARG_123	NH1	D_GLU_120	OE2	2.741
1HGJ	D_ARG_123	NH2	B_GLU_132	OE1	3.075
1HGJ	D_ARG_124	NH1	D_GLU_120	OE1	3.708
1HGJ	D_ARG_124	NH2	B_GLU_132	OE1	3.055
1HGJ	D_ARG_124	NH2	B_GLU_132	OE2	3.342
1HGJ	D_ARG_127	NH1	B_GLU_131	OE1	2.514
1HGJ	D_LYS_143	NZ	D_ASP_145	OD2	2.897
1HGJ	D_ARG_153	NH1	D_GLU_150	OE1	2.604
1HGJ	D_HIS_159	NE2	D_ASP_160	OD2	3.102
1HGJ	D_ARG_163	NH2	B_GLU_131	OE1	2.599
1HGJ	D_ARG_163	NH2	B_GLU_131	OE2	2.594
1HGJ	D_ARG_170	NH1	D_GLU_131	OE2	2.793
1HGJ	D_ARG_170	NH1	F_GLU_128	OE1	3.405
1HGJ	D_ARG_170	NH1	F_GLU_128	OE2	3.769
1HGJ	D_ARG_170	NH2	D_GLU_128	OE2	2.726
1HGJ	D_LYS_174	NZ	F_ASP_164	OD1	2.824
1HGJ	D_LYS_174	NZ	F_ASP_164	OD2	2.673
1HGJ	E_LYS_27	NZ	F_GLU_97	OE1	2.779
1HGJ	E_LYS_27	NZ	F_GLU_97	OE2	2.813
1HGJ	E_LYS_50	NZ	E_ASP_275	OD1	3.506
1HGJ	E_LYS_50	NZ	E_ASP_275	OD2	2.739
1HGJ	E_ARG_57	NH2	E_GLU_82	OE1	2.663
1HGJ	E_HIS_75	ND1	E_ASP_73	OD1	2.798
1HGJ	E_HIS_75	ND1	E_ASP_73	OD2	3.347
1HGJ	E_HIS_75	NE2	E_ASP_63	OD1	3.371
1HGJ	E_ARG_90	NH2	E_ASP_60	OD1	3.683
1HGJ	E_ARG_90	NH2	E_ASP_60	OD2	2.826
1HGJ	E_ARG_109	NH1	E_GLU_89	OE1	2.541
1HGJ	E_ARG_109	NH1	E_GLU_89	OE2	3.205
1HGJ	E_ARG_109	NH2	F_GLU_67	OE1	3.635
1HGJ	E_ARG_109	NH2	F_GLU_67	OE2	2.759
1HGJ	E_ARG_141	NH2	E_ASP_77	OD1	2.840
1HGJ	E_ARG_141	NH2	E_ASP_77	OD2	2.747
1HGJ	E_LYS_176	NZ	E_GLU_123	OE2	2.685
1HGJ	E_HIS_183	NE2	E_GLU_190	OE2	3.333
1HGJ	E_LYS_238	NZ	D_GLU_72	OE1	2.865
1HGJ	E_LYS_238	NZ	D_GLU_72	OE2	2.804
1HGJ	E_ARG_261	NH1	E_GLU_119	OE2	2.651
1HGJ	E_ARG_261	NH2	E_GLU_119	OE1	2.905

1HGJ	E_ARG_261	NH2	E_GLU_119	OE2	2.913
1HGJ	E_LYS_264	NZ	E_ASP_85	OD1	3.746
1HGJ	E_LYS_264	NZ	E_ASP_85	OD2	2.856
1HGJ	E_ARG_269	NH1	F_GLU_67	OE1	2.691
1HGJ	E_ARG_269	NH2	F_GLU_67	OE1	3.759
1HGJ	E_LYS_292	NZ	E_ASP_291	OD1	2.893
1HGJ	E_LYS_292	NZ	E_ASP_291	OD2	2.833
1HGJ	E_LYS_299	NZ	F_GLU_69	OE2	2.806
1HGJ	E_LYS_310	NZ	F_ASP_86	OD1	2.930
1HGJ	E_LYS_310	NZ	F_ASP_90	OD1	2.553
1HGJ	E_LYS_315	NZ	E_GLU_41	OE1	2.860
1HGJ	E_LYS_326	NZ	F_GLU_15	OE1	2.874
1HGJ	E_LYS_326	NZ	F_GLU_15	OE2	3.254
1HGJ	F_LYS_51	NZ	F_GLU_103	OE1	2.791
1HGJ	F_ARG_54	NH1	D_GLU_97	OE2	3.349
1HGJ	F_ARG_54	NH1	F_GLU_57	OE1	2.862
1HGJ	F_ARG_54	NH1	F_GLU_57	OE2	2.926
1HGJ	F_ARG_54	NH2	D_GLU_97	OE2	2.771
1HGJ	F_LYS_58	NZ	F_GLU_61	OE2	3.370
1HGJ	F_LYS_62	NZ	D_ASP_86	OD1	2.846
1HGJ	F_LYS_62	NZ	D_ASP_86	OD2	2.568
1HGJ	F_LYS_62	NZ	D_ASP_90	OD1	3.467
1HGJ	F_LYS_62	NZ	D_ASP_90	OD2	2.658
1HGJ	F_LYS_68	NZ	F_GLU_85	OE1	3.136
1HGJ	F_LYS_68	NZ	F_GLU_85	OE2	2.737
1HGJ	F_ARG_76	NH1	B_GLU_74	OE1	3.383
1HGJ	F_ARG_76	NH1	B_GLU_74	OE2	2.704
1HGJ	F_ARG_76	NH2	B_GLU_74	OE1	2.715
1HGJ	F_ARG_76	NH2	B_GLU_74	OE2	3.551
1HGJ	F_ARG_76	NH2	B_GLU_81	OE1	2.654
1HGJ	F_ARG_76	NH2	B_GLU_81	OE2	3.611
1HGJ	F_LYS_117	NZ	F_GLU_114	OE1	3.106
1HGJ	F_LYS_117	NZ	F_GLU_114	OE2	2.590
1HGJ	F_ARG_123	NH1	F_GLU_120	OE1	2.625
1HGJ	F_ARG_123	NH1	F_GLU_120	OE2	2.732
1HGJ	F_ARG_123	NH2	D_GLU_132	OE1	3.110
1HGJ	F_ARG_124	NH1	F_GLU_120	OE1	3.711
1HGJ	F_ARG_124	NH2	D_GLU_132	OE1	3.125
1HGJ	F_ARG_124	NH2	D_GLU_132	OE2	3.360
1HGJ	F_ARG_127	NH1	D_GLU_131	OE1	2.554
1HGJ	F_LYS_143	NZ	F_ASP_145	OD2	2.873
1HGJ	F_ARG_153	NH1	F_GLU_150	OE2	2.597
1HGJ	F_HIS_159	NE2	F_ASP_160	OD2	3.139
1HGJ	F_ARG_163	NH2	D_GLU_131	OE1	2.636
1HGJ	F_ARG_163	NH2	D_GLU_131	OE2	2.696
1HGJ	F_ARG_170	NH1	B_GLU_128	OE1	3.311
1HGJ	F_ARG_170	NH1	B_GLU_128	OE2	3.766
1HGJ	F_ARG_170	NH1	F_GLU_131	OE2	2.790
1HGJ	F_ARG_170	NH2	F_GLU_128	OE2	2.737
1HGJ	F_LYS_174	NZ	B_ASP_164	OD1	2.859
1HGJ	F_LYS_174	NZ	B_ASP_164	OD2	2.554

Table 94: 1HGJ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1HIL	A_LYS_28	NZ	B_ASP_99	OD1	3.388
1HIL	A_LYS_28	NZ	B_ASP_99	OD2	3.371
1HIL	A_LYS_30	NZ	B_ASP_99	OD2	3.991
1HIL	A_ARG_61	NH2	A_GLU_81	OE2	3.453
1HIL	A_ARG_61	NH2	A_ASP_82	OD1	2.803
1HIL	A_ARG_61	NH2	A_ASP_82	OD2	3.572
1HIL	A_LYS_142	NZ	A_GLU_105	OE1	3.449
1HIL	A_LYS_147	NZ	A_GLU_154	OE1	3.856
1HIL	A_LYS_147	NZ	A_GLU_154	OE2	3.602
1HIL	A_LYS_149	NZ	A_GLU_195	OE2	3.175
1HIL	A_ARG_155	NH2	A_GLU_185	OE1	3.376
1HIL	A_ARG_155	NH2	A_GLU_185	OE2	2.897
1HIL	A_LYS_169	NZ	A_ASP_170	OD2	2.962
1HIL	A_LYS_183	NZ	A_GLU_187	OE1	2.919
1HIL	A_LYS_183	NZ	A_GLU_187	OE2	3.001
1HIL	A_ARG_188	NH1	A_ASP_184	OD1	2.997
1HIL	A_ARG_188	NH2	A_ASP_184	OD1	2.719
1HIL	A_HIS_189	ND1	A_ASP_151	OD2	2.887
1HIL	A_HIS_189	NE2	A_GLU_185	OE2	3.281
1HIL	A_LYS_199	NZ	A_ASP_110	OD1	3.849
1HIL	A_LYS_199	NZ	A_ASP_110	OD2	2.611
1HIL	B_ARG_38	NH1	B_ASP_86	OD1	2.872
1HIL	B_ARG_38	NH2	B_GLU_46	OE1	2.814
1HIL	B_ARG_38	NH2	B_ASP_86	OD1	3.831
1HIL	B_ARG_44	NH1	B_ASP_42	OD2	3.962
1HIL	B_ARG_44	NH2	B_ASP_42	OD2	2.795
1HIL	B_ARG_66	NH1	B_ASP_86	OD1	3.878
1HIL	B_ARG_66	NH1	B_ASP_86	OD2	2.766
1HIL	B_ARG_66	NH2	B_ASP_86	OD1	2.971
1HIL	B_ARG_66	NH2	B_ASP_86	OD2	3.323
1HIL	B_ARG_94	NH2	B_GLU_96	OE1	2.937
1HIL	B_ARG_94	NH2	B_GLU_96	OE2	3.442
1HIL	B_ARG_95	NH1	A_ASP_91	OD1	2.828
1HIL	B_ARG_95	NH1	A_ASP_91	OD2	3.804
1HIL	B_ARG_95	NH2	A_ASP_91	OD1	3.160
1HIL	B_ARG_95	NH2	A_ASP_91	OD2	3.904
1HIL	B_HIS_172	NE2	A_ASP_167	OD2	3.701
1HIL	B_LYS_221	NZ	A_GLU_123	OE1	2.980
1HIL	B_LYS_222	NZ	B_GLU_226	OE2	3.471
1HIL	C_LYS_28	NZ	D_ASP_99	OD1	3.565
1HIL	C_LYS_28	NZ	D_ASP_99	OD2	3.509
1HIL	C_ARG_61	NH2	C_GLU_81	OE1	3.959
1HIL	C_ARG_61	NH2	C_GLU_81	OE2	3.333
1HIL	C_ARG_61	NH2	C_ASP_82	OD1	2.824
1HIL	C_ARG_61	NH2	C_ASP_82	OD2	3.820
1HIL	C_LYS_149	NZ	C_GLU_195	OE1	2.867
1HIL	C_LYS_149	NZ	C_GLU_195	OE2	3.545
1HIL	C_ARG_155	NH1	C_GLU_185	OE2	3.376
1HIL	C_LYS_183	NZ	C_GLU_187	OE1	2.913
1HIL	C_LYS_183	NZ	C_GLU_187	OE2	2.922
1HIL	C_ARG_188	NH2	C_ASP_184	OD2	3.681
1HIL	C_HIS_189	ND1	C_ASP_151	OD2	2.657
1HIL	C_LYS_199	NZ	C_ASP_110	OD1	3.869
1HIL	C_LYS_199	NZ	C_ASP_110	OD2	3.718
1HIL	D_ARG_38	NH1	D_GLU_85	OE2	3.765
1HIL	D_ARG_38	NH1	D_ASP_86	OD1	2.811
1HIL	D_ARG_38	NH2	D_GLU_46	OE1	2.914

1HIL	D_ARG_38	NH2	D_GLU_85	OE1	3.376
1HIL	D_ARG_38	NH2	D_GLU_85	OE2	2.939
1HIL	D_ARG_38	NH2	D_ASP_86	OD1	3.843
1HIL	D_LYS_64	NZ	D_ASP_61	OD1	3.347
1HIL	D_ARG_66	NH1	D_ASP_86	OD2	2.825
1HIL	D_ARG_66	NH2	D_GLU_85	OE2	3.393
1HIL	D_ARG_66	NH2	D_ASP_86	OD1	3.008
1HIL	D_ARG_66	NH2	D_ASP_86	OD2	3.234
1HIL	D_ARG_94	NH2	D_GLU_96	OE1	3.117
1HIL	D_ARG_94	NH2	D_GLU_96	OE2	3.597
1HIL	D_ARG_95	NH1	C_ASP_91	OD1	2.906
1HIL	D_ARG_95	NH1	C_ASP_91	OD2	3.993
1HIL	D_ARG_95	NH2	C_ASP_91	OD1	3.045
1HIL	D_ARG_95	NH2	C_ASP_91	OD2	3.822
1HIL	D_LYS_221	NZ	C_GLU_123	OE1	2.896
1HIL	D_LYS_221	NZ	C_GLU_123	OE2	3.091

Table 95: 1HIL-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1HIM	H_ARG_54	NH1	H_ASP_60	OD1	3.270
1HIM	H_ARG_61	NH1	H_ASP_82	OD1	2.766
1HIM	H_ARG_61	NH1	H_ASP_82	OD2	2.580
1HIM	H_ARG_61	NH2	H_GLU_81	OE1	3.629
1HIM	H_ARG_61	NH2	H_GLU_81	OE2	3.486
1HIM	H_LYS_103	NZ	H_GLU_105	OE1	2.947
1HIM	H_LYS_103	NZ	H_GLU_105	OE2	3.074
1HIM	H_LYS_103	NZ	H_ASP_165	OD1	2.840
1HIM	H_LYS_103	NZ	H_ASP_165	OD2	2.960
1HIM	H_ARG_108	NH2	H_ASP_170	OD1	3.527
1HIM	H_LYS_142	NZ	H_GLU_105	OE2	3.186
1HIM	H_LYS_149	NZ	H_GLU_195	OE1	3.565
1HIM	H_ARG_155	NH1	H_GLU_185	OE1	3.606
1HIM	H_ARG_155	NH2	H_GLU_185	OE1	3.185
1HIM	H_LYS_183	NZ	H_GLU_187	OE1	3.388
1HIM	H_ARG_188	NH1	H_ASP_184	OD2	3.229
1HIM	H_ARG_188	NH2	H_ASP_184	OD2	3.788
1HIM	H_ARG_188	NH2	H_GLU_185	OE2	3.216
1HIM	H_HIS_189	ND1	H_ASP_151	OD2	3.238
1HIM	H_HIS_189	NE2	H_GLU_185	OE1	3.139
1HIM	H_HIS_189	NE2	H_GLU_185	OE2	2.919
1HIM	H_LYS_199	NZ	H_ASP_110	OD1	3.999
1HIM	H_LYS_199	NZ	H_ASP_110	OD2	3.600
1HIM	H_ARG_211	NH2	H_GLU_187	OE2	3.728
1HIM	L_ARG_38	NH1	L_GLU_46	OE1	2.537
1HIM	L_ARG_38	NH2	L_ASP_86	OD1	2.913
1HIM	L_ARG_44	NH1	L_ASP_42	OD2	3.518
1HIM	L_ARG_44	NH2	L_ASP_42	OD2	2.772
1HIM	L_LYS_64	NZ	L_ASP_61	OD1	3.754
1HIM	L_ARG_66	NH2	L_ASP_86	OD1	3.439
1HIM	L_ARG_66	NH2	L_ASP_86	OD2	2.636
1HIM	L_ARG_94	NH2	L_GLU_96	OE1	2.855
1HIM	L_ARG_94	NH2	L_GLU_96	OE2	2.784
1HIM	L_ARG_95	NH1	H_ASP_91	OD1	3.100
1HIM	L_ARG_95	NH2	H_ASP_91	OD1	3.427
1HIM	L_ARG_95	NH2	P_ASP_104	OD1	3.909
1HIM	L_ARG_95	NH2	P_ASP_104	OD2	3.079
1HIM	L_LYS_218	NZ	L_ASP_220	OD1	2.947
1HIM	L_LYS_218	NZ	L_ASP_220	OD2	3.790
1HIM	L_LYS_221	NZ	H_GLU_123	OE1	3.486
1HIM	L_LYS_221	NZ	H_GLU_123	OE2	2.924
1HIM	L_LYS_222	NZ	L_GLU_226	OE1	3.594
1HIM	L_LYS_222	NZ	L_GLU_226	OE2	3.507
1HIM	J_LYS_28	NZ	M_GLU_100	OE1	3.991
1HIM	J_LYS_28	NZ	M_GLU_100	OE2	3.433
1HIM	J_ARG_54	NH1	J_ASP_60	OD1	3.053
1HIM	J_ARG_61	NH1	J_GLU_81	OE1	2.794
1HIM	J_ARG_61	NH1	J_ASP_82	OD1	2.566
1HIM	J_ARG_61	NH1	J_ASP_82	OD2	2.940
1HIM	J_ARG_61	NH2	J_GLU_81	OE1	2.977
1HIM	J_ARG_61	NH2	J_GLU_81	OE2	3.767
1HIM	J_LYS_103	NZ	J_GLU_105	OE1	3.363
1HIM	J_LYS_103	NZ	J_GLU_105	OE2	3.574
1HIM	J_LYS_103	NZ	J_ASP_165	OD1	2.834
1HIM	J_LYS_103	NZ	J_ASP_165	OD2	3.265
1HIM	J_ARG_108	NH1	J_ASP_170	OD2	3.737
1HIM	J_LYS_142	NZ	J_GLU_105	OE2	3.350

1HIM	J_LYS_147	NZ	J_GLU_154	OE1	3.824
1HIM	J_LYS_149	NZ	J_GLU_195	OE1	2.922
1HIM	J_ARG_155	NH1	J_GLU_185	OE2	2.780
1HIM	J_ARG_155	NH2	J_GLU_185	OE2	2.860
1HIM	J_LYS_183	NZ	J_GLU_187	OE1	3.132
1HIM	J_LYS_183	NZ	J_GLU_187	OE2	3.144
1HIM	J_ARG_188	NH1	J_GLU_185	OE1	3.001
1HIM	J_ARG_188	NH2	J_GLU_185	OE1	3.202
1HIM	J_HIS_189	ND1	J_ASP_151	OD2	3.228
1HIM	J_HIS_189	NE2	J_GLU_185	OE1	3.040
1HIM	J_HIS_189	NE2	J_GLU_185	OE2	3.204
1HIM	J_LYS_199	NZ	J_ASP_110	OD1	2.949
1HIM	J_LYS_199	NZ	J_ASP_110	OD2	3.017
1HIM	M_ARG_38	NH1	M_ASP_86	OD1	2.851
1HIM	M_ARG_38	NH2	M_GLU_46	OE1	3.834
1HIM	M_ARG_38	NH2	M_ASP_86	OD1	3.546
1HIM	M_LYS_64	NZ	M_ASP_61	OD1	3.375
1HIM	M_LYS_64	NZ	M_ASP_61	OD2	3.721
1HIM	M_ARG_66	NH1	M_ASP_86	OD2	2.851
1HIM	M_ARG_66	NH2	M_ASP_86	OD1	3.649
1HIM	M_ARG_66	NH2	M_ASP_86	OD2	3.020
1HIM	M_LYS_75	NZ	M_ASP_72	OD2	3.415
1HIM	M_LYS_83	NZ	M_GLU_85	OE2	3.803
1HIM	M_LYS_83	NZ	M_ASP_86	OD1	2.818
1HIM	M_LYS_83	NZ	M_ASP_86	OD2	3.385
1HIM	M_ARG_94	NH2	M_GLU_96	OE1	2.883
1HIM	M_ARG_94	NH2	M_GLU_96	OE2	2.984
1HIM	M_ARG_95	NH1	J_ASP_91	OD1	2.854
1HIM	M_ARG_95	NH2	J_ASP_91	OD1	3.712
1HIM	M_ARG_95	NH2	R_ASP_104	OD1	2.834
1HIM	M_ARG_95	NH2	R_ASP_104	OD2	3.540
1HIM	M_LYS_222	NZ	M_GLU_226	OE2	2.900

Table 96: 1HIM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1HIN	L_LYS_28	NZ	H_GLU_100	OE2	2.975
1HIN	L_ARG_54	NH1	L_ASP_60	OD1	2.976
1HIN	L_ARG_54	NH2	L_ASP_60	OD1	3.006
1HIN	L_ARG_61	NH2	L_ASP_82	OD1	3.350
1HIN	L_LYS_103	NZ	L_GLU_105	OE1	3.163
1HIN	L_LYS_103	NZ	L_GLU_105	OE2	2.963
1HIN	L_LYS_103	NZ	L_ASP_165	OD1	3.325
1HIN	L_LYS_107	NZ	L_GLU_17	OE1	3.860
1HIN	L_LYS_147	NZ	L_GLU_195	OE2	3.604
1HIN	L_LYS_183	NZ	L_GLU_187	OE1	3.063
1HIN	L_LYS_183	NZ	L_GLU_187	OE2	2.809
1HIN	L_ARG_188	NH1	L_GLU_185	OE1	3.655
1HIN	L_HIS_189	ND1	L_ASP_151	OD2	2.920
1HIN	L_HIS_189	NE2	L_GLU_185	OE2	2.966
1HIN	H_ARG_38	NH1	H_ASP_86	OD1	2.756
1HIN	H_ARG_38	NH2	H_GLU_46	OE2	3.346
1HIN	H_ARG_38	NH2	H_ASP_86	OD1	3.928
1HIN	H_ARG_44	NH1	H_ASP_42	OD1	3.927
1HIN	H_ARG_44	NH1	H_ASP_42	OD2	3.226
1HIN	H_ARG_44	NH2	H_ASP_42	OD1	3.335
1HIN	H_ARG_66	NH1	H_ASP_86	OD1	3.830
1HIN	H_ARG_66	NH1	H_ASP_86	OD2	3.068
1HIN	H_ARG_66	NH2	H_ASP_86	OD1	3.938
1HIN	H_LYS_83	NZ	H_ASP_86	OD1	3.978
1HIN	H_ARG_94	NH2	H_GLU_96	OE1	2.995
1HIN	H_ARG_94	NH2	H_GLU_96	OE2	3.965
1HIN	H_ARG_95	NH1	L_ASP_91	OD1	3.169
1HIN	H_ARG_95	NH1	P_ASP_104	OD1	3.889
1HIN	H_ARG_95	NH2	L_ASP_91	OD1	2.746

Table 97: 1HIN-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1I8I	A_ARG_22	NH2	A_ASP_70	OD2	3.152
1I8I	A_ARG_61	NH1	A_GLU_81	OE1	3.598
1I8I	A_ARG_61	NH2	A_GLU_81	OE1	2.756
1I8I	A_ARG_61	NH2	A_ASP_82	OD1	2.774
1I8I	B_ARG_338	NH1	B_ASP_390	OD1	3.395
1I8I	B_ARG_338	NH2	B_GLU_346	OE1	3.519
1I8I	B_ARG_338	NH2	B_GLU_346	OE2	3.077
1I8I	B_LYS_343	NZ	A_ASP_85	OD1	3.777
1I8I	B_ARG_367	NH1	B_ASP_390	OD1	3.777
1I8I	B_ARG_367	NH1	B_ASP_390	OD2	2.803
1I8I	B_ARG_367	NH2	B_ASP_390	OD1	2.832
1I8I	B_ARG_367	NH2	B_ASP_390	OD2	3.335
1I8I	B_ARG_398	NH1	B_ASP_408	OD1	2.704
1I8I	B_ARG_398	NH1	B_ASP_408	OD2	3.295
1I8I	C_LYS_502	NZ	A_GLU_50	OE1	3.673
1I8I	C_LYS_502	NZ	A_GLU_50	OE2	3.232

Table 98: 1I8I-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1I8K	A_ARG_61	NH1	A_GLU_81	OE1	3.901
1I8K	A_ARG_61	NH2	A_GLU_81	OE1	2.704
1I8K	A_ARG_61	NH2	A_ASP_82	OD1	2.775
1I8K	A_ARG_61	NH2	A_ASP_82	OD2	3.582
1I8K	A_LYS_103	NZ	A_GLU_105	OE1	3.849
1I8K	A_LYS_103	NZ	A_GLU_105	OE2	3.265
1I8K	B_ARG_338	NH1	B_ASP_390	OD1	2.955
1I8K	B_ARG_338	NH2	B_GLU_346	OE2	2.897
1I8K	B_LYS_343	NZ	A_ASP_85	OD1	3.688
1I8K	B_LYS_343	NZ	A_ASP_85	OD2	2.833
1I8K	B_LYS_365	NZ	B_ASP_362	OD1	3.025
1I8K	B_ARG_367	NH1	B_ASP_390	OD1	3.793
1I8K	B_ARG_367	NH1	B_ASP_390	OD2	2.806
1I8K	B_ARG_367	NH2	B_ASP_390	OD1	2.921
1I8K	B_ARG_367	NH2	B_ASP_390	OD2	3.420
1I8K	B_ARG_398	NH1	B_ASP_408	OD1	3.548
1I8K	B_ARG_398	NH1	B_ASP_408	OD2	2.958
1I8K	C_LYS_502	NZ	A_GLU_50	OE1	3.381
1I8K	C_LYS_502	NZ	A_GLU_50	OE2	3.653

Table 99: 1I8K-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID residue name residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1I8M	L_ARG_61	NH2	L_GLU_81	OE2	3.348
1I8M	L_ARG_61	NH2	L_ASP_82	OD1	2.791
1I8M	L_ARG_61	NH2	L_ASP_82	OD2	3.473
1I8M	L_LYS_149	NZ	L_GLU_195	OE1	2.669
1I8M	L_ARG_155	NH1	L_GLU_185	OE1	3.608
1I8M	L_ARG_155	NH1	L_GLU_185	OE2	3.044
1I8M	L_ARG_155	NH2	L_GLU_185	OE1	2.570
1I8M	L_ARG_155	NH2	L_GLU_185	OE2	3.578
1I8M	L_ARG_188	NH1	L_GLU_185	OE1	3.999
1I8M	L_HIS_189	ND1	L_ASP_151	OD2	2.965
1I8M	L_HIS_189	NE2	L_GLU_185	OE1	3.384
1I8M	L_ARG_211	NH1	L_GLU_187	OE1	3.084
1I8M	H_LYS_62	NZ	H_GLU_46	OE2	2.992
1I8M	H_LYS_66	NZ	H_ASP_86	OD1	2.668
1I8M	H_LYS_66	NZ	H_ASP_86	OD2	3.680
1I8M	H_ARG_94	NH2	H_ASP_101	OD1	3.336
1I8M	H_ARG_94	NH2	H_ASP_101	OD2	3.003
1I8M	H_LYS_208	NZ	L_GLU_123	OE1	2.918
1I8M	A_ARG_61	NH1	A_GLU_81	OE2	3.331
1I8M	A_ARG_61	NH1	A_ASP_82	OD1	2.710
1I8M	A_ARG_61	NH1	A_ASP_82	OD2	3.466
1I8M	A_LYS_147	NZ	A_GLU_195	OE1	3.288
1I8M	A_LYS_149	NZ	A_GLU_195	OE1	3.797
1I8M	A_LYS_149	NZ	A_GLU_195	OE2	2.770
1I8M	A_ARG_155	NH1	A_GLU_185	OE1	2.722
1I8M	A_ARG_155	NH2	A_GLU_185	OE1	3.688
1I8M	A_LYS_183	NZ	A_GLU_187	OE1	3.381
1I8M	A_HIS_189	ND1	A_ASP_151	OD2	2.740
1I8M	A_LYS_199	NZ	A_ASP_110	OD2	3.951
1I8M	A_ARG_211	NH1	A_GLU_187	OE2	3.834
1I8M	B_LYS_66	NZ	B_ASP_86	OD1	2.796
1I8M	B_LYS_66	NZ	B_ASP_86	OD2	3.783
1I8M	B_ARG_94	NH2	B_ASP_101	OD1	3.715
1I8M	B_ARG_94	NH2	B_ASP_101	OD2	2.888
1I8M	B_LYS_208	NZ	A_GLU_123	OE2	2.887

Table 100: 1I8M-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1IC4	L_ARG_61	NH1	L_GLU_81	OE1	2.751
1IC4	L_ARG_61	NH1	L_ASP_82	OD1	2.563
1IC4	L_ARG_61	NH1	L_ASP_82	OD2	3.173
1IC4	L_ARG_61	NH2	L_GLU_79	OE1	3.626
1IC4	L_ARG_61	NH2	L_GLU_81	OE1	3.608
1IC4	H_ARG_38	NH1	H_ASP_89	OD1	2.935
1IC4	H_ARG_38	NH2	H_GLU_46	OE1	2.745
1IC4	H_ARG_38	NH2	H_ASP_89	OD1	3.350
1IC4	H_ARG_66	NH1	H_ASP_89	OD2	3.087
1IC4	H_ARG_66	NH2	H_ASP_89	OD1	3.196
1IC4	H_ARG_66	NH2	H_ASP_89	OD2	3.495
1IC4	H_LYS_75	NZ	H_ASP_72	OD2	2.682
1IC4	Y_LYS_1	NZ	Y_GLU_7	OE1	3.619
1IC4	Y_LYS_1	NZ	Y_GLU_7	OE2	2.535
1IC4	Y_LYS_13	NZ	Y_ASP_18	OD2	3.711
1IC4	Y_ARG_61	NH2	Y_ASP_48	OD1	3.871
1IC4	Y_ARG_68	NH2	Y_ASP_66	OD2	2.848
1IC4	Y_LYS_97	NZ	H_ASP_99	OD1	2.657
1IC4	Y_LYS_97	NZ	H_ASP_99	OD2	3.938
1IC4	Y_ARG_125	NH1	Y_ASP_119	OD1	3.300
1IC4	Y_ARG_125	NH1	Y_ASP_119	OD2	3.023
1IC4	Y_ARG_125	NH2	Y_ASP_119	OD2	3.490

Table 101: 1IC4-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1IC5	L_LYS_39	NZ	L_GLU_42	OE1	3.119
1IC5	L_ARG_61	NH1	L_GLU_79	OE1	3.450
1IC5	L_ARG_61	NH1	L_GLU_81	OE1	2.953
1IC5	L_ARG_61	NH1	L_ASP_82	OD1	2.717
1IC5	L_ARG_61	NH1	L_ASP_82	OD2	3.546
1IC5	L_ARG_61	NH2	L_GLU_79	OE1	3.079
1IC5	L_ARG_61	NH2	L_GLU_79	OE2	3.755
1IC5	L_LYS_103	NZ	L_GLU_105	OE2	3.954
1IC5	H_ARG_38	NH1	H_ASP_89	OD1	2.839
1IC5	H_ARG_38	NH2	H_GLU_46	OE1	2.758
1IC5	H_ARG_38	NH2	H_ASP_89	OD1	3.693
1IC5	H_ARG_66	NH1	H_ASP_89	OD1	3.998
1IC5	H_ARG_66	NH1	H_ASP_89	OD2	3.250
1IC5	H_ARG_66	NH2	H_ASP_89	OD1	3.110
1IC5	H_ARG_66	NH2	H_ASP_89	OD2	3.644
1IC5	H_LYS_75	NZ	H_ASP_72	OD2	3.897
1IC5	Y_LYS_1	NZ	Y_GLU_7	OE1	3.768
1IC5	Y_LYS_1	NZ	Y_GLU_7	OE2	2.582
1IC5	Y_ARG_61	NH2	Y_ASP_48	OD1	3.930
1IC5	Y_LYS_97	NZ	H_ASP_32	OD1	2.694
1IC5	Y_ARG_125	NH1	Y_ASP_119	OD1	3.569
1IC5	Y_ARG_125	NH1	Y_ASP_119	OD2	3.500
1IC5	Y_ARG_125	NH2	Y_ASP_119	OD1	3.857
1IC5	Y_ARG_125	NH2	Y_ASP_119	OD2	2.635

Table 102: 1IC5-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1IC7	L_ARG_45	NH2	L_GLU_42	OE1	3.451
1IC7	L_ARG_61	NH1	L_GLU_79	OE1	3.604
1IC7	L_ARG_61	NH1	L_GLU_81	OE2	3.867
1IC7	L_ARG_61	NH2	L_GLU_81	OE2	2.625
1IC7	L_ARG_61	NH2	L_ASP_82	OD1	2.810
1IC7	L_ARG_61	NH2	L_ASP_82	OD2	3.484
1IC7	L_LYS_103	NZ	L_GLU_105	OE2	2.664
1IC7	H_ARG_38	NH1	H_ASP_89	OD1	2.659
1IC7	H_ARG_38	NH2	H_GLU_46	OE1	2.814
1IC7	H_ARG_38	NH2	H_ASP_89	OD1	3.507
1IC7	H_ARG_66	NH1	H_ASP_89	OD1	3.777
1IC7	H_ARG_66	NH1	H_ASP_89	OD2	2.821
1IC7	H_ARG_66	NH2	H_ASP_89	OD1	3.054
1IC7	H_ARG_66	NH2	H_ASP_89	OD2	3.478
1IC7	Y_LYS_1	NZ	Y_GLU_7	OE1	3.641
1IC7	Y_LYS_1	NZ	Y_GLU_7	OE2	2.660
1IC7	Y_ARG_125	NH2	Y_ASP_119	OD1	3.644
1IC7	Y_ARG_125	NH2	Y_ASP_119	OD2	2.585

Table 103: 1IC7-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1IFH	L_ARG_54	NH1	L_ASP_60	OD1	3.414
1IFH	L_ARG_54	NH1	L_ASP_60	OD2	3.205
1IFH	L_ARG_61	NH1	L_ASP_82	OD1	2.658
1IFH	L_ARG_61	NH1	L_ASP_82	OD2	3.079
1IFH	L_ARG_61	NH2	L_GLU_81	OE2	3.987
1IFH	L_LYS_149	NZ	L_GLU_195	OE1	3.474
1IFH	L_LYS_149	NZ	L_GLU_195	OE2	3.400
1IFH	L_ARG_155	NH1	L_GLU_185	OE1	3.273
1IFH	L_ARG_155	NH2	L_GLU_185	OE2	3.721
1IFH	L_ARG_188	NH1	L_ASP_184	OD1	3.900
1IFH	L_ARG_188	NH2	L_ASP_184	OD1	3.145
1IFH	L_HIS_189	ND1	L_ASP_151	OD2	3.236
1IFH	L_LYS_199	NZ	L_ASP_110	OD1	3.492
1IFH	L_LYS_199	NZ	L_ASP_110	OD2	3.178
1IFH	H_ARG_38	NH1	H_ASP_86	OD1	3.355
1IFH	H_ARG_38	NH2	H_GLU_46	OE1	3.340
1IFH	H_ARG_38	NH2	H_ASP_86	OD1	3.860
1IFH	H_ARG_66	NH1	H_ASP_86	OD1	3.538
1IFH	H_ARG_66	NH2	H_ASP_86	OD1	3.023
1IFH	H_ARG_66	NH2	H_ASP_86	OD2	2.605
1IFH	H_ARG_94	NH2	H_GLU_96	OE1	2.733
1IFH	H_ARG_95	NH1	L_ASP_91	OD1	2.782
1IFH	H_ARG_95	NH2	P_ASP_104	OD1	2.974
1IFH	H_ARG_95	NH2	P_ASP_104	OD2	2.813
1IFH	H_LYS_221	NZ	L_GLU_123	OE1	3.267
1IFH	H_LYS_221	NZ	L_GLU_123	OE2	2.926
1IFH	H_LYS_222	NZ	H_GLU_226	OE2	3.617

Table 104: 1IFH-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1IGF	L_LYS_50	NZ	H_ASP_98	OD2	3.036
1IGF	L_ARG_61	NH1	L_GLU_79	OE1	3.608
1IGF	L_ARG_61	NH1	L_GLU_79	OE2	3.209
1IGF	L_ARG_61	NH2	L_ASP_82	OD1	2.804
1IGF	L_ARG_61	NH2	L_ASP_82	OD2	2.709
1IGF	L_LYS_142	NZ	L_ASP_143	OD1	3.847
1IGF	L_LYS_142	NZ	L_ASP_143	OD2	3.953
1IGF	L_LYS_149	NZ	L_GLU_195	OE1	3.005
1IGF	L_HIS_189	ND1	L_GLU_185	OE1	3.423
1IGF	L_HIS_189	ND1	L_GLU_185	OE2	3.814
1IGF	L_HIS_189	NE2	L_GLU_154	OE1	3.930
1IGF	L_HIS_189	NE2	L_GLU_154	OE2	2.963
1IGF	L_HIS_189	NE2	L_GLU_185	OE1	3.959
1IGF	L_LYS_199	NZ	L_ASP_110	OD1	2.851
1IGF	L_LYS_199	NZ	L_ASP_110	OD2	3.161
1IGF	H_ARG_38	NH1	H_GLU_46	OE1	2.875
1IGF	H_ARG_38	NH1	H_GLU_46	OE2	3.277
1IGF	H_ARG_38	NH2	H_ASP_86	OD1	2.708
1IGF	H_LYS_64	NZ	H_ASP_61	OD1	3.360
1IGF	H_ARG_66	NH1	H_ASP_86	OD1	3.532
1IGF	H_ARG_66	NH1	H_ASP_86	OD2	2.901
1IGF	H_ARG_66	NH2	H_ASP_86	OD1	3.011
1IGF	H_ARG_66	NH2	H_ASP_86	OD2	3.582
1IGF	H_ARG_83	NH2	H_GLU_85	OE2	3.398
1IGF	H_ARG_94	NH1	H_ASP_101	OD1	2.803
1IGF	H_ARG_94	NH1	H_ASP_101	OD2	2.950
1IGF	H_LYS_221	NZ	L_GLU_123	OE1	3.549
1IGF	M_ARG_61	NH1	M_ASP_82	OD1	3.656
1IGF	M_ARG_61	NH2	M_GLU_79	OE1	3.684
1IGF	M_ARG_61	NH2	M_GLU_79	OE2	3.861
1IGF	M_ARG_61	NH2	M_ASP_82	OD1	3.256
1IGF	M_ARG_61	NH2	M_ASP_82	OD2	2.603
1IGF	M_LYS_149	NZ	M_GLU_195	OE1	3.495
1IGF	M_LYS_183	NZ	M_GLU_187	OE2	2.898
1IGF	M_LYS_199	NZ	M_ASP_110	OD2	3.163
1IGF	J_ARG_38	NH1	J_ASP_86	OD1	3.058
1IGF	J_ARG_38	NH2	J_GLU_46	OE1	2.898
1IGF	J_ARG_38	NH2	J_GLU_85	OE2	3.952
1IGF	J_LYS_64	NZ	J_ASP_61	OD1	3.146
1IGF	J_LYS_64	NZ	J_ASP_61	OD2	3.948
1IGF	J_ARG_66	NH1	J_GLU_85	OE2	3.586
1IGF	J_ARG_66	NH1	J_ASP_86	OD1	3.108
1IGF	J_ARG_66	NH1	J_ASP_86	OD2	3.486
1IGF	J_ARG_66	NH2	J_ASP_86	OD1	3.509
1IGF	J_ARG_66	NH2	J_ASP_86	OD2	2.722
1IGF	J_ARG_83	NH1	J_GLU_85	OE1	3.819
1IGF	J_ARG_83	NH2	J_GLU_85	OE1	3.702
1IGF	J_ARG_83	NH2	J_GLU_85	OE2	3.508
1IGF	J_ARG_94	NH2	J_ASP_101	OD1	2.994
1IGF	J_ARG_94	NH2	J_ASP_101	OD2	2.766
1IGF	J_LYS_218	NZ	J_ASP_220	OD1	3.151
1IGF	J_LYS_221	NZ	M_GLU_123	OE1	3.800
1IGF	J_LYS_221	NZ	M_GLU_123	OE2	3.750

Table 105: 1IGF-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1IND	L_LYS_41	NZ	L_GLU_83	OE1	3.721
1IND	L_ARG_63	NH2	L_GLU_83	OE2	3.365
1IND	L_ARG_63	NH2	L_ASP_84	OD1	2.728
1IND	L_ARG_63	NH2	L_ASP_84	OD2	3.765
1IND	L_LYS_72	NZ	L_ASP_71	OD1	3.764
1IND	L_LYS_113	NZ	L_GLU_201	OE1	3.425
1IND	L_ARG_186	NH2	L_GLU_189	OE1	2.887
1IND	L_ARG_186	NH2	L_GLU_189	OE2	2.679
1IND	L_HIS_191	ND1	L_ASP_154	OD2	3.038
1IND	H_ARG_38	NH1	H_GLU_46	OE1	3.013
1IND	H_ARG_38	NH2	H_ASP_90	OD1	2.950
1IND	H_ARG_67	NH1	H_ASP_90	OD1	3.223
1IND	H_ARG_67	NH2	H_ASP_90	OD1	3.035
1IND	H_ARG_67	NH2	H_ASP_90	OD2	2.402
1IND	H_ARG_87	NH2	H_GLU_89	OE1	2.860
1IND	H_HIS_106	ND1	H_GLU_6	OE1	3.067
1IND	H_LYS_143	NZ	L_GLU_127	OE2	2.765
1IND	H_HIS_164	NE2	L_ASP_141	OD1	3.891

Table 106: 1IND-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1INE	L_ARG_63	NH1	L_ASP_84	OD1	3.522
1INE	L_ARG_63	NH1	L_ASP_84	OD2	3.841
1INE	L_LYS_113	NZ	L_GLU_201	OE1	3.453
1INE	L_LYS_152	NZ	L_GLU_206	OE1	3.945
1INE	L_ARG_186	NH2	L_GLU_189	OE1	3.738
1INE	L_ARG_186	NH2	L_GLU_189	OE2	2.847
1INE	L_HIS_191	ND1	L_ASP_154	OD2	2.790
1INE	H_ARG_38	NH1	H_GLU_46	OE1	3.495
1INE	H_ARG_38	NH1	H_GLU_46	OE2	3.232
1INE	H_ARG_38	NH2	H_ASP_90	OD1	2.602
1INE	H_ARG_67	NH2	H_ASP_90	OD1	3.249
1INE	H_ARG_67	NH2	H_ASP_90	OD2	2.823
1INE	H_ARG_87	NH2	H_GLU_89	OE1	2.822
1INE	H_LYS_143	NZ	L_GLU_127	OE2	2.920
1INE	H_HIS_164	NE2	L_ASP_141	OD2	3.817

Table 107: 1INE-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1IQW	L_LYS_24	NZ	L_ASP_74	OD1	3.077
1IQW	L_LYS_24	NZ	L_ASP_74	OD2	3.598
1IQW	L_ARG_65	NH1	L_GLU_83	OE2	3.811
1IQW	L_ARG_65	NH1	L_GLU_85	OE2	3.948
1IQW	L_ARG_65	NH2	L_GLU_85	OE2	2.881
1IQW	L_ARG_65	NH2	L_ASP_86	OD1	2.853
1IQW	L_ARG_65	NH2	L_ASP_86	OD2	3.630
1IQW	L_ARG_100	NH1	L_ASP_98	OD2	3.926
1IQW	L_ARG_100	NH2	L_ASP_98	OD2	3.900
1IQW	L_ARG_100	NH2	H_GLU_50	OE1	2.572
1IQW	L_ARG_100	NH2	H_GLU_50	OE2	2.799
1IQW	L_ARG_112	NH1	L_ASP_174	OD1	3.939
1IQW	L_LYS_146	NZ	L_GLU_109	OE1	3.307
1IQW	L_LYS_151	NZ	L_GLU_158	OE1	3.903
1IQW	L_LYS_151	NZ	L_GLU_158	OE2	3.426
1IQW	L_LYS_153	NZ	L_GLU_199	OE1	2.679
1IQW	L_LYS_153	NZ	L_GLU_199	OE2	3.687
1IQW	L_ARG_159	NH1	L_GLU_189	OE1	2.786
1IQW	L_ARG_159	NH2	L_GLU_189	OE1	3.653
1IQW	L_LYS_187	NZ	L_GLU_191	OE1	3.905
1IQW	L_HIS_193	ND1	L_ASP_155	OD2	3.111
1IQW	L_LYS_203	NZ	L_ASP_114	OD1	2.895
1IQW	L_LYS_203	NZ	L_ASP_114	OD2	3.727
1IQW	H_LYS_67	NZ	H_ASP_90	OD1	3.551
1IQW	H_ARG_98	NH2	H_ASP_109	OD1	2.686
1IQW	H_ARG_98	NH2	H_ASP_109	OD2	3.835
1IQW	H_ARG_100	NH1	H_ASP_109	OD1	3.614
1IQW	H_HIS_172	NE2	L_ASP_171	OD1	3.594

Table 108: 1IQW-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1IT9	L_ARG_65	NH1	L_GLU_85	OE1	3.637
1IT9	L_ARG_65	NH2	L_GLU_85	OE1	2.628
1IT9	L_ARG_65	NH2	L_ASP_86	OD1	2.793
1IT9	L_ARG_65	NH2	L_ASP_86	OD2	3.255
1IT9	L_ARG_100	NH1	L_ASP_98	OD2	3.522
1IT9	L_ARG_100	NH2	L_ASP_98	OD2	3.953
1IT9	L_ARG_100	NH2	H_GLU_50	OE2	3.105
1IT9	L_LYS_153	NZ	L_GLU_199	OE1	3.686
1IT9	L_LYS_187	NZ	L_GLU_191	OE2	3.697
1IT9	L_LYS_192	NZ	L_ASP_189	OD1	3.604
1IT9	H_LYS_63	NZ	H_GLU_46	OE1	3.197
1IT9	H_LYS_67	NZ	H_ASP_90	OD1	3.421
1IT9	H_LYS_67	NZ	H_ASP_90	OD2	2.822
1IT9	H_ARG_98	NH1	H_ASP_109	OD1	3.442
1IT9	H_ARG_98	NH1	H_ASP_109	OD2	2.634
1IT9	H_LYS_217	NZ	L_GLU_127	OE1	3.545
1IT9	H_LYS_217	NZ	L_GLU_127	OE2	3.302

Table 109: 1IT9-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1J05	L_ARG_18	NH1	L_ASP_76	OD2	2.833
1J05	L_LYS_103	NZ	L_GLU_105	OE2	3.967
1J05	H_ARG_40	NH1	H_GLU_85	OE1	3.148
1J05	H_ARG_40	NH2	H_GLU_85	OE1	2.682
1J05	H_LYS_58	NZ	L_ASP_94	OD2	2.663
1J05	H_LYS_62	NZ	H_GLU_46	OE2	2.498
1J05	H_LYS_66	NZ	H_ASP_86	OD1	3.951
1J05	H_LYS_66	NZ	H_ASP_86	OD2	2.776
1J05	A_ARG_18	NH2	A_ASP_76	OD2	3.093
1J05	A_ARG_61	NH2	A_ASP_81	OD1	3.469
1J05	A_ARG_61	NH2	A_ASP_82	OD1	2.736
1J05	A_ARG_61	NH2	A_ASP_82	OD2	3.685
1J05	B_LYS_58	NZ	A_ASP_94	OD2	2.870
1J05	B_LYS_62	NZ	B_GLU_46	OE1	3.609
1J05	B_LYS_66	NZ	B_ASP_86	OD1	3.619
1J05	B_LYS_66	NZ	B_ASP_86	OD2	2.721

Table 110: 1J05-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1J1O	L_ARG_61	NH2	L_ASP_82	OD1	2.910
1J1O	L_ARG_61	NH2	L_ASP_82	OD2	3.568
1J1O	L_LYS_103	NZ	L_GLU_105	OE2	3.101
1J1O	H_ARG_38	NH1	H_ASP_89	OD1	2.830
1J1O	H_ARG_38	NH2	H_GLU_46	OE1	2.878
1J1O	H_ARG_38	NH2	H_ASP_89	OD1	3.468
1J1O	H_ARG_66	NH1	H_ASP_89	OD1	3.734
1J1O	H_ARG_66	NH1	H_ASP_89	OD2	3.001
1J1O	H_ARG_66	NH2	H_ASP_89	OD1	3.010
1J1O	H_ARG_66	NH2	H_ASP_89	OD2	3.624
1J1O	H_LYS_75	NZ	H_ASP_72	OD1	3.670
1J1O	H_LYS_75	NZ	H_ASP_72	OD2	2.565
1J1O	Y_LYS_1	NZ	Y_GLU_7	OE2	2.858
1J1O	Y_LYS_13	NZ	Y_ASP_18	OD1	3.427
1J1O	Y_LYS_13	NZ	Y_ASP_18	OD2	3.311
1J1O	Y_ARG_61	NH1	Y_ASP_48	OD2	2.936
1J1O	Y_ARG_61	NH2	Y_ASP_48	OD2	3.586
1J1O	Y_ARG_68	NH2	Y_ASP_66	OD2	3.730
1J1O	Y_LYS_97	NZ	H_ASP_32	OD1	2.636
1J1O	Y_LYS_97	NZ	H_ASP_32	OD2	3.985
1J1O	Y_LYS_97	NZ	H_ASP_99	OD1	3.590
1J1O	Y_LYS_97	NZ	H_ASP_99	OD2	2.896
1J1O	Y_ARG_125	NH1	Y_ASP_119	OD2	3.446
1J1O	Y_ARG_125	NH2	Y_ASP_119	OD1	3.689
1J1O	Y_ARG_125	NH2	Y_ASP_119	OD2	3.547

Table 111: 1J1O-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1J1P	L_ARG_61	NH2	L_ASP_82	OD1	2.811
1J1P	L_ARG_61	NH2	L_ASP_82	OD2	3.464
1J1P	L_LYS_103	NZ	L_GLU_105	OE2	2.960
1J1P	H_ARG_38	NH1	H_ASP_89	OD1	2.854
1J1P	H_ARG_38	NH2	H_GLU_46	OE1	2.924
1J1P	H_ARG_38	NH2	H_ASP_89	OD1	3.457
1J1P	H_ARG_66	NH1	H_ASP_89	OD1	3.754
1J1P	H_ARG_66	NH1	H_ASP_89	OD2	3.009
1J1P	H_ARG_66	NH2	H_ASP_89	OD1	2.987
1J1P	H_ARG_66	NH2	H_ASP_89	OD2	3.600
1J1P	H_LYS_75	NZ	H_ASP_72	OD1	3.943
1J1P	H_LYS_75	NZ	H_ASP_72	OD2	2.743
1J1P	Y_LYS_1	NZ	Y_GLU_7	OE2	2.945
1J1P	Y_ARG_61	NH1	Y_ASP_48	OD1	3.659
1J1P	Y_ARG_61	NH1	Y_ASP_48	OD2	2.763
1J1P	Y_ARG_61	NH2	Y_ASP_48	OD2	3.923
1J1P	Y_ARG_68	NH2	Y_ASP_66	OD2	3.805
1J1P	Y_LYS_97	NZ	H_ASP_32	OD1	2.700
1J1P	Y_LYS_97	NZ	H_ASP_99	OD1	3.721
1J1P	Y_LYS_97	NZ	H_ASP_99	OD2	2.595
1J1P	Y_ARG_125	NH1	Y_ASP_119	OD1	3.879
1J1P	Y_ARG_125	NH1	Y_ASP_119	OD2	2.802
1J1P	Y_ARG_125	NH2	Y_ASP_119	OD1	3.068
1J1P	Y_ARG_125	NH2	Y_ASP_119	OD2	3.059

Table 112: 1J1P-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1J1X	L_ARG_61	NH1	L_GLU_81	OE2	3.955
1J1X	L_ARG_61	NH2	L_GLU_81	OE2	2.869
1J1X	L_ARG_61	NH2	L_ASP_82	OD1	2.807
1J1X	L_ARG_61	NH2	L_ASP_82	OD2	3.443
1J1X	L_LYS_103	NZ	L_GLU_105	OE2	3.635
1J1X	H_ARG_38	NH1	H_ASP_89	OD1	2.839
1J1X	H_ARG_38	NH2	H_GLU_46	OE1	2.984
1J1X	H_ARG_38	NH2	H_ASP_89	OD1	3.410
1J1X	H_ARG_66	NH1	H_ASP_89	OD1	3.723
1J1X	H_ARG_66	NH1	H_ASP_89	OD2	3.043
1J1X	H_ARG_66	NH2	H_ASP_89	OD1	3.064
1J1X	H_ARG_66	NH2	H_ASP_89	OD2	3.686
1J1X	Y_LYS_1	NZ	Y_GLU_7	OE2	2.973
1J1X	Y_ARG_61	NH1	Y_ASP_48	OD2	2.934
1J1X	Y_ARG_68	NH2	Y_ASP_66	OD2	3.707
1J1X	Y_LYS_97	NZ	H_ASP_32	OD1	2.655
1J1X	Y_LYS_97	NZ	H_ASP_32	OD2	3.935
1J1X	Y_LYS_97	NZ	H_ASP_99	OD1	3.479
1J1X	Y_LYS_97	NZ	H_ASP_99	OD2	2.956
1J1X	Y_ARG_125	NH1	Y_ASP_119	OD1	3.927
1J1X	Y_ARG_125	NH1	Y_ASP_119	OD2	3.825
1J1X	Y_ARG_125	NH2	Y_ASP_119	OD2	2.717

Table 113: 1J1X-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1JFQ	L_ARG_61	NH2	L_GLU_81	OE2	3.034
1JFQ	L_ARG_61	NH2	L_ASP_82	OD1	2.626
1JFQ	L_ARG_61	NH2	L_ASP_82	OD2	3.469
1JFQ	L_LYS_147	NZ	L_GLU_154	OE2	3.134
1JFQ	L_LYS_149	NZ	L_GLU_195	OE1	3.635
1JFQ	L_LYS_149	NZ	L_GLU_195	OE2	2.808
1JFQ	L_LYS_169	NZ	L_ASP_167	OD1	3.763
1JFQ	L_LYS_169	NZ	L_ASP_167	OD2	3.427
1JFQ	L_LYS_183	NZ	L_GLU_187	OE2	3.965
1JFQ	L_ARG_188	NH1	L_ASP_184	OD1	2.482
1JFQ	L_ARG_188	NH1	L_ASP_184	OD2	3.747
1JFQ	L_ARG_188	NH2	L_GLU_185	OE2	3.747
1JFQ	L_HIS_189	NE2	L_GLU_185	OE2	3.915
1JFQ	L_LYS_199	NZ	L_ASP_110	OD1	3.726
1JFQ	L_LYS_199	NZ	L_ASP_110	OD2	2.782
1JFQ	H_LYS_363	NZ	H_GLU_346	OE1	2.893
1JFQ	H_LYS_367	NZ	H_ASP_390	OD2	3.164
1JFQ	H_ARG_398	NH2	H_ASP_409	OD1	3.741
1JFQ	H_ARG_398	NH2	H_ASP_409	OD2	2.842
1JFQ	H_LYS_516	NZ	L_GLU_123	OE1	3.003
1JFQ	H_LYS_516	NZ	L_GLU_123	OE2	3.095

Table 114: 1JFQ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1JHL	L_ARG_61	NH2	L_ASP_82	OD2	2.857
1JHL	L_LYS_107	NZ	L_GLU_17	OE1	3.758
1JHL	H_LYS_63	NZ	H_GLU_46	OE1	2.911
1JHL	H_LYS_63	NZ	H_GLU_46	OE2	3.457
1JHL	H_ARG_98	NH1	H_ASP_106	OD1	3.193
1JHL	H_ARG_98	NH1	H_ASP_106	OD2	2.879
1JHL	A_LYS_1	NZ	A_GLU_7	OE2	2.890
1JHL	A_ARG_112	NH1	H_ASP_55	OD1	3.828
1JHL	A_ARG_112	NH1	H_ASP_55	OD2	3.112
1JHL	A_LYS_116	NZ	H_ASP_99	OD1	3.763
1JHL	A_LYS_116	NZ	H_ASP_99	OD2	3.232
1JHL	A_ARG_125	NH2	A_ASP_119	OD2	3.005

Table 115: 1JHL-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID** **residue name** **residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1JP5	A_ARG_24	NH1	A_ASP_75	OD1	3.622
1JP5	A_ARG_24	NH1	A_ASP_75	OD2	2.930
1JP5	A_ARG_24	NH2	A_ASP_75	OD1	2.789
1JP5	A_ARG_24	NH2	A_ASP_75	OD2	3.224
1JP5	A_ARG_66	NH1	A_GLU_84	OE2	3.961
1JP5	A_ARG_66	NH2	A_GLU_86	OE1	3.649
1JP5	A_ARG_66	NH2	A_ASP_87	OD1	2.642
1JP5	A_ARG_66	NH2	A_ASP_87	OD2	2.495
1JP5	A_ARG_82	NH1	A_GLU_84	OE2	3.359
1JP5	A_HIS_162	NE2	A_ASP_226	OD1	3.329
1JP5	A_HIS_162	NE2	A_ASP_226	OD2	3.666
1JP5	A_LYS_173	NZ	A_ASP_190	OD2	2.916
1JP5	A_LYS_192	NZ	A_ASP_189	OD1	2.549
1JP5	A_ARG_194	NH1	A_GLU_216	OE2	3.691
1JP5	A_ARG_194	NH1	A_ASP_217	OD1	3.483
1JP5	A_ARG_194	NH1	A_ASP_217	OD2	3.993
1JP5	A_ARG_194	NH2	A_ASP_217	OD1	3.125
1JP5	A_ARG_194	NH2	A_ASP_217	OD2	2.288
1JP5	A_ARG_227	NH1	A_GLU_232	OE1	3.878
1JP5	A_ARG_227	NH1	A_GLU_232	OE2	3.876
1JP5	A_HIS_228	ND1	A_ASP_226	OD1	3.183
1JP5	A_HIS_228	ND1	A_ASP_226	OD2	3.924
1JP5	B_ARG_24	NH1	B_ASP_75	OD1	3.589
1JP5	B_ARG_24	NH1	B_ASP_75	OD2	2.884
1JP5	B_ARG_24	NH2	B_ASP_75	OD1	2.786
1JP5	B_ARG_24	NH2	B_ASP_75	OD2	3.283
1JP5	B_ARG_66	NH2	B_GLU_86	OE1	3.667
1JP5	B_ARG_66	NH2	B_ASP_87	OD1	2.594
1JP5	B_ARG_66	NH2	B_ASP_87	OD2	2.543
1JP5	B_ARG_82	NH1	B_GLU_84	OE2	3.388
1JP5	B_LYS_139	NZ	B_GLU_137	OE1	3.932
1JP5	B_HIS_162	NE2	B_ASP_226	OD1	3.248
1JP5	B_HIS_162	NE2	B_ASP_226	OD2	3.774
1JP5	B_LYS_173	NZ	B_ASP_190	OD2	3.014
1JP5	B_LYS_192	NZ	B_ASP_189	OD1	2.617
1JP5	B_ARG_194	NH1	B_GLU_216	OE2	3.383
1JP5	B_ARG_194	NH1	B_ASP_217	OD1	2.811
1JP5	B_ARG_194	NH1	B_ASP_217	OD2	3.494
1JP5	B_ARG_194	NH2	B_ASP_217	OD1	3.744
1JP5	B_ARG_194	NH2	B_ASP_217	OD2	2.928
1JP5	B_ARG_227	NH1	B_GLU_232	OE1	3.968
1JP5	B_ARG_227	NH1	B_GLU_232	OE2	3.830
1JP5	B_HIS_228	ND1	B_ASP_226	OD1	3.260
1JP5	B_HIS_228	ND1	B_ASP_226	OD2	3.862

Table 116: 1JP5-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1JPS	L_ARG_24	NH1	L_ASP_70	OD2	3.616
1JPS	L_ARG_27	NH2	L_GLU_93	OE1	3.147
1JPS	L_ARG_61	NH2	L_GLU_81	OE2	3.693
1JPS	L_ARG_61	NH2	L_ASP_82	OD1	2.870
1JPS	L_ARG_61	NH2	L_ASP_82	OD2	3.637
1JPS	L_LYS_103	NZ	L_GLU_165	OE1	2.915
1JPS	L_LYS_126	NZ	L_GLU_123	OE1	3.492
1JPS	L_ARG_142	NH2	L_GLU_105	OE2	3.364
1JPS	L_LYS_149	NZ	L_GLU_195	OE2	3.272
1JPS	L_LYS_188	NZ	L_ASP_185	OD1	3.281
1JPS	H_LYS_30	NZ	H_GLU_54	OE1	3.726
1JPS	H_HIS_35	NE2	H_ASP_99	OD2	2.904
1JPS	H_ARG_38	NH1	H_ASP_90	OD1	2.795
1JPS	H_ARG_38	NH2	H_GLU_46	OE2	3.099
1JPS	H_ARG_38	NH2	H_ASP_90	OD1	3.661
1JPS	H_LYS_63	NZ	H_ASP_61	OD1	2.512
1JPS	H_LYS_63	NZ	H_ASP_61	OD2	3.231
1JPS	H_ARG_67	NH1	H_ASP_90	OD1	3.087
1JPS	H_ARG_67	NH1	H_ASP_90	OD2	3.639
1JPS	H_ARG_67	NH2	H_ASP_90	OD1	3.450
1JPS	H_ARG_67	NH2	H_ASP_90	OD2	2.676
1JPS	H_ARG_98	NH2	H_ASP_105	OD1	3.651
1JPS	H_ARG_98	NH2	H_ASP_105	OD2	2.801
1JPS	H_LYS_147	NZ	H_ASP_148	OD1	3.289
1JPS	H_LYS_214	NZ	H_GLU_216	OE2	3.681
1JPS	T_LYS_15	NZ	T_GLU_24	OE2	3.265
1JPS	T_LYS_20	NZ	T_ASP_58	OD2	3.975
1JPS	T_LYS_46	NZ	T_GLU_62	OE2	3.654
1JPS	T_LYS_48	NZ	T_GLU_62	OE2	2.510
1JPS	T_LYS_65	NZ	T_GLU_62	OE1	3.161
1JPS	T_LYS_65	NZ	T_GLU_62	OE2	3.595
1JPS	T_LYS_122	NZ	T_ASP_178	OD1	2.673
1JPS	T_LYS_122	NZ	T_ASP_178	OD2	3.856
1JPS	T_LYS_159	NZ	T_ASP_180	OD2	2.746
1JPS	T_LYS_201	NZ	H_ASP_52	OD1	2.781

Table 117: 1JPS-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1JPT	L_ARG_24	NH2	L_ASP_70	OD1	3.381
1JPT	L_ARG_24	NH2	L_ASP_70	OD2	2.823
1JPT	L_ARG_27	NH2	L_GLU_93	OE1	2.552
1JPT	L_ARG_61	NH2	L_GLU_81	OE2	3.592
1JPT	L_ARG_61	NH2	L_ASP_82	OD1	2.733
1JPT	L_ARG_61	NH2	L_ASP_82	OD2	3.583
1JPT	L_LYS_149	NZ	L_GLU_195	OE1	3.445
1JPT	L_HIS_189	ND1	L_ASP_151	OD2	2.609
1JPT	L_ARG_211	NH1	L_GLU_187	OE1	3.952
1JPT	H_LYS_30	NZ	H_GLU_54	OE1	3.750
1JPT	H_HIS_35	NE2	H_ASP_99	OD2	2.901
1JPT	H_ARG_38	NH1	H_ASP_90	OD1	2.806
1JPT	H_ARG_38	NH2	H_GLU_46	OE2	3.279
1JPT	H_ARG_38	NH2	H_ASP_90	OD1	3.559
1JPT	H_LYS_63	NZ	H_GLU_46	OE1	2.705
1JPT	H_LYS_63	NZ	H_ASP_61	OD1	3.701
1JPT	H_ARG_67	NH1	H_ASP_90	OD1	3.340
1JPT	H_ARG_67	NH1	H_ASP_90	OD2	3.607
1JPT	H_ARG_67	NH2	H_ASP_90	OD1	3.600
1JPT	H_ARG_67	NH2	H_ASP_90	OD2	2.497
1JPT	H_ARG_87	NH2	H_GLU_89	OE1	3.851
1JPT	H_ARG_98	NH2	H_ASP_105	OD1	3.572
1JPT	H_ARG_98	NH2	H_ASP_105	OD2	2.539
1JPT	H_LYS_147	NZ	H_ASP_148	OD1	3.107
1JPT	H_LYS_147	NZ	H_ASP_148	OD2	3.168
1JPT	H_LYS_213	NZ	L_GLU_123	OE1	3.226
1JPT	H_LYS_213	NZ	L_GLU_123	OE2	3.740

Table 118: 1JPT-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1JRH	L_ARG_61	NH2	L_ASP_82	OD1	3.229
1JRH	L_ARG_61	NH2	L_ASP_82	OD2	3.948
1JRH	L_LYS_103	NZ	L_ASP_165	OD2	3.995
1JRH	H_ARG_38	NH1	H_GLU_46	OE1	2.881
1JRH	H_ARG_38	NH1	H_GLU_46	OE2	3.879
1JRH	H_ARG_38	NH2	H_ASP_86	OD2	3.530
1JRH	H_LYS_57	NZ	H_ASP_55	OD2	3.070
1JRH	H_ARG_66	NH1	H_ASP_86	OD1	3.819
1JRH	H_ARG_66	NH1	H_ASP_86	OD2	3.178
1JRH	H_ARG_66	NH2	H_ASP_86	OD1	3.486
1JRH	H_ARG_66	NH2	H_ASP_86	OD2	2.963
1JRH	H_LYS_71	NZ	H_ASP_55	OD1	3.729
1JRH	H_ARG_75	NH2	H_ASP_72	OD2	2.739
1JRH	H_ARG_94	NH2	H_ASP_101	OD2	2.863
1JRH	I_LYS_52	NZ	H_ASP_54	OD1	3.471
1JRH	I_LYS_52	NZ	H_ASP_54	OD2	2.819
1JRH	I_LYS_52	NZ	H_ASP_56	OD2	2.824
1JRH	I_HIS_73	NE2	I_ASP_72	OD1	3.994
1JRH	I_HIS_73	NE2	I_ASP_72	OD2	3.992
1JRH	I_ARG_84	NH1	I_GLU_45	OE1	2.869
1JRH	I_ARG_84	NH1	I_GLU_45	OE2	3.093
1JRH	I_ARG_84	NH2	L_GLU_27	OE1	3.652
1JRH	I_ARG_84	NH2	L_GLU_27	OE2	3.984
1JRH	I_LYS_86	NZ	I_GLU_93	OE1	3.237
1JRH	I_LYS_86	NZ	I_GLU_93	OE2	3.629

Table 119: 1JRH-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1JTO	A_ARG_38	NH1	A_ASP_90	OD2	2.989
1JTO	A_ARG_38	NH2	A_GLU_46	OE1	3.765
1JTO	A_ARG_38	NH2	A_GLU_46	OE2	3.163
1JTO	A_ARG_38	NH2	A_ASP_90	OD2	3.961
1JTO	A_ARG_67	NH1	A_ASP_90	OD1	2.656
1JTO	A_ARG_67	NH1	A_ASP_90	OD2	3.690
1JTO	A_ARG_67	NH2	A_ASP_90	OD1	3.432
1JTO	A_ARG_67	NH2	A_ASP_90	OD2	2.929
1JTO	B_ARG_38	NH1	B_ASP_90	OD2	2.804
1JTO	B_ARG_38	NH2	B_GLU_46	OE1	3.744
1JTO	B_ARG_38	NH2	B_ASP_90	OD2	3.904
1JTO	B_LYS_65	NZ	B_ASP_62	OD1	3.988
1JTO	B_ARG_67	NH1	B_ASP_90	OD1	2.582
1JTO	B_ARG_67	NH1	B_ASP_90	OD2	4.000
1JTO	B_ARG_67	NH2	B_ASP_90	OD1	3.081
1JTO	B_ARG_67	NH2	B_ASP_90	OD2	2.986
1JTO	L_LYS_1	NZ	L_GLU_7	OE2	3.834
1JTO	L_LYS_13	NZ	L_ASP_18	OD2	2.997
1JTO	L_ARG_61	NH2	L_ASP_48	OD1	3.510
1JTO	L_LYS_97	NZ	L_ASP_101	OD1	2.937
1JTO	L_ARG_125	NH1	L_ASP_119	OD2	3.230
1JTO	L_ARG_125	NH2	L_ASP_119	OD1	3.769
1JTO	L_ARG_125	NH2	L_ASP_119	OD2	3.012
1JTO	M_LYS_1	NZ	M_GLU_7	OE1	3.717
1JTO	M_LYS_1	NZ	M_GLU_7	OE2	2.519
1JTO	M_ARG_61	NH2	M_ASP_48	OD1	3.874
1JTO	M_ARG_125	NH1	M_ASP_119	OD2	2.938
1JTO	M_ARG_125	NH2	M_ASP_119	OD1	3.078
1JTO	M_ARG_125	NH2	M_ASP_119	OD2	3.152

Table 120: 1JTO-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1JTP	A_ARG_38	NH1	A_ASP_90	OD1	2.844
1JTP	A_ARG_38	NH2	A_GLU_46	OE1	2.990
1JTP	A_ARG_38	NH2	A_ASP_90	OD1	3.872
1JTP	A_LYS_65	NZ	A_ASP_62	OD1	3.073
1JTP	A_ARG_67	NH1	A_GLU_87	OE1	3.833
1JTP	A_ARG_67	NH1	A_ASP_90	OD1	3.796
1JTP	A_ARG_67	NH1	A_ASP_90	OD2	2.836
1JTP	A_ARG_67	NH2	A_GLU_87	OE2	3.971
1JTP	A_ARG_67	NH2	A_ASP_90	OD1	3.167
1JTP	A_ARG_67	NH2	A_ASP_90	OD2	3.669
1JTP	B_ARG_38	NH1	B_ASP_90	OD1	3.088
1JTP	B_ARG_38	NH2	B_GLU_46	OE1	3.231
1JTP	B_ARG_38	NH2	B_GLU_46	OE2	3.901
1JTP	B_LYS_65	NZ	B_ASP_62	OD1	2.767
1JTP	B_ARG_67	NH1	B_ASP_90	OD1	3.639
1JTP	B_ARG_67	NH1	B_ASP_90	OD2	2.730
1JTP	B_ARG_67	NH2	B_ASP_90	OD1	2.941
1JTP	B_ARG_67	NH2	B_ASP_90	OD2	3.599
1JTP	L_LYS_1	NZ	L_GLU_7	OE1	3.651
1JTP	L_LYS_1	NZ	L_GLU_7	OE2	2.871
1JTP	L_LYS_13	NZ	L_ASP_18	OD2	2.822
1JTP	L_ARG_61	NH2	L_ASP_48	OD2	3.676
1JTP	L_ARG_125	NH2	L_ASP_119	OD2	3.456
1JTP	M_LYS_1	NZ	M_GLU_7	OE1	3.807
1JTP	M_LYS_1	NZ	M_GLU_7	OE2	2.795
1JTP	M_LYS_13	NZ	M_ASP_18	OD2	3.184
1JTP	M_ARG_61	NH2	M_ASP_48	OD2	3.928
1JTP	M_ARG_125	NH1	M_ASP_119	OD1	3.405
1JTP	M_ARG_125	NH1	M_ASP_119	OD2	2.529
1JTP	M_ARG_125	NH2	M_ASP_119	OD1	2.657
1JTP	M_ARG_125	NH2	M_ASP_119	OD2	3.292

Table 121: 1JTP-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1JTT	A_ARG_38	NH1	A_ASP_90	OD1	2.882
1JTT	A_ARG_38	NH2	A_GLU_46	OE2	2.917
1JTT	A_LYS_65	NZ	A_ASP_62	OD2	2.806
1JTT	A_ARG_67	NH1	A_ASP_90	OD1	3.707
1JTT	A_ARG_67	NH1	A_ASP_90	OD2	2.718
1JTT	A_ARG_67	NH2	A_ASP_90	OD1	3.006
1JTT	A_ARG_67	NH2	A_ASP_90	OD2	3.559
1JTT	L_LYS_1	NZ	L_GLU_7	OE2	2.871
1JTT	L_ARG_61	NH2	L_ASP_48	OD2	3.382
1JTT	L_ARG_125	NH1	L_ASP_119	OD1	3.528
1JTT	L_ARG_125	NH1	L_ASP_119	OD2	3.412
1JTT	L_ARG_125	NH2	L_ASP_119	OD1	3.866
1JTT	L_ARG_125	NH2	L_ASP_119	OD2	2.346

Table 122: 1JTT-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1JV5	A_ARG_61	NH1	A_GLU_81	OE1	3.715
1JV5	A_ARG_61	NH1	A_ASP_82	OD1	3.734
1JV5	A_ARG_61	NH2	A_ASP_82	OD1	2.672
1JV5	A_ARG_61	NH2	A_ASP_82	OD2	3.335
1JV5	B_LYS_363	NZ	B_GLU_346	OE1	3.710
1JV5	B_LYS_367	NZ	B_ASP_390	OD1	2.564
1JV5	B_LYS_367	NZ	B_ASP_390	OD2	3.314

Table 123: 1JV5-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1K6Q	L_LYS_3	NZ	L_ASP_1	OD1	3.247
1K6Q	L_LYS_3	NZ	L_ASP_1	OD2	3.989
1K6Q	L_ARG_27	NH1	L_GLU_93	OE1	3.087
1K6Q	L_ARG_27	NH2	L_GLU_93	OE1	3.061
1K6Q	L_ARG_27	NH2	L_GLU_93	OE2	3.535
1K6Q	L_ARG_61	NH1	L_GLU_79	OE2	3.467
1K6Q	L_ARG_61	NH2	L_GLU_79	OE1	3.569
1K6Q	L_ARG_61	NH2	L_GLU_79	OE2	3.481
1K6Q	L_ARG_61	NH2	L_ASP_81	OD1	3.557
1K6Q	L_ARG_61	NH2	L_ASP_82	OD1	2.902
1K6Q	L_ARG_61	NH2	L_ASP_82	OD2	3.306
1K6Q	L_LYS_149	NZ	L_GLU_195	OE1	3.892
1K6Q	L_LYS_149	NZ	L_GLU_195	OE2	2.797
1K6Q	L_ARG_188	NH1	L_GLU_185	OE1	3.503
1K6Q	L_ARG_188	NH2	L_GLU_185	OE1	2.593
1K6Q	L_ARG_188	NH2	L_GLU_185	OE2	3.878
1K6Q	L_HIS_189	ND1	L_ASP_151	OD2	2.798
1K6Q	H_LYS_30	NZ	H_GLU_54	OE1	3.652
1K6Q	H_HIS_35	NE2	H_ASP_99	OD2	3.337
1K6Q	H_ARG_40	NH1	H_GLU_89	OE2	2.763
1K6Q	H_ARG_40	NH2	H_GLU_89	OE2	2.831
1K6Q	H_LYS_63	NZ	H_GLU_46	OE1	3.998
1K6Q	H_LYS_67	NZ	H_ASP_90	OD1	3.649
1K6Q	H_LYS_67	NZ	H_ASP_90	OD2	3.070
1K6Q	H_ARG_98	NH2	H_ASP_105	OD1	3.693
1K6Q	H_ARG_98	NH2	H_ASP_105	OD2	2.580
1K6Q	H_HIS_168	NE2	L_ASP_167	OD1	3.896

Table 124: 1K6Q-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1KB5	A_ARG_4	NH1	A_GLU_25	OE1	3.756
1KB5	A_ARG_4	NH1	A_GLU_25	OE2	3.640
1KB5	A_ARG_4	NH2	A_GLU_25	OE1	2.650
1KB5	A_ARG_4	NH2	A_GLU_25	OE2	3.717
1KB5	A_ARG_61	NH1	A_ASP_84	OD1	3.434
1KB5	A_ARG_61	NH1	A_ASP_84	OD2	2.899
1KB5	A_ARG_61	NH2	A_ASP_84	OD1	2.515
1KB5	A_ARG_61	NH2	A_ASP_84	OD2	3.185
1KB5	A_LYS_72	NZ	A_GLU_70	OE1	3.823
1KB5	A_ARG_93	NH1	B_GLU_105	OE1	2.975
1KB5	A_ARG_93	NH1	B_GLU_105	OE2	3.412
1KB5	A_ARG_101	NH2	H_ASP_98	OD1	2.690
1KB5	B_ARG_22	NH2	B_GLU_74	OE2	3.622
1KB5	B_LYS_26	NZ	B_GLU_5	OE1	2.619
1KB5	B_ARG_50	NH2	B_ASP_72	OD1	3.832
1KB5	L_LYS_27	NZ	B_ASP_54	OD1	3.460
1KB5	L_ARG_61	NH1	L_ASP_82	OD1	3.130
1KB5	L_ARG_61	NH1	L_ASP_82	OD2	2.318
1KB5	L_ARG_61	NH2	L_GLU_81	OE2	3.530
1KB5	L_ARG_61	NH2	L_ASP_82	OD1	2.659
1KB5	L_ARG_61	NH2	L_ASP_82	OD2	3.409
1KB5	L_LYS_149	NZ	L_GLU_195	OE1	3.078
1KB5	L_ARG_155	NH2	L_GLU_185	OE1	2.951
1KB5	L_ARG_155	NH2	L_GLU_185	OE2	3.151
1KB5	L_ARG_188	NH1	L_GLU_185	OE2	3.844
1KB5	L_ARG_188	NH2	L_ASP_184	OD1	3.621
1KB5	L_HIS_189	NE2	L_ASP_151	OD2	3.476
1KB5	H_LYS_62	NZ	H_GLU_46	OE2	3.773
1KB5	H_ARG_66	NH1	H_ASP_86	OD2	3.354
1KB5	H_ARG_94	NH1	H_ASP_101	OD1	3.952
1KB5	H_ARG_94	NH1	H_ASP_101	OD2	2.472
1KB5	H_ARG_94	NH2	H_ASP_101	OD2	2.694
1KB5	H_ARG_96	NH1	A_ASP_26	OD1	2.599
1KB5	H_ARG_96	NH1	A_ASP_26	OD2	2.834
1KB5	H_ARG_96	NH2	L_GLU_56	OE2	2.981
1KB5	H_ARG_96	NH2	H_ASP_101	OD1	3.517
1KB5	H_ARG_96	NH2	H_ASP_101	OD2	3.239
1KB5	H_LYS_209	NZ	H_GLU_211	OE1	3.539
1KB5	H_LYS_209	NZ	H_GLU_211	OE2	3.472

Table 125: 1KB5-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1KC5	L_ARG_54	NH1	L_ASP_60	OD1	2.682
1KC5	L_ARG_61	NH1	L_ASP_82	OD1	2.395
1KC5	L_ARG_61	NH1	L_ASP_82	OD2	2.703
1KC5	L_ARG_61	NH2	L_ASP_82	OD1	3.920
1KC5	L_LYS_107	NZ	L_GLU_17	OE2	3.192
1KC5	L_LYS_142	NZ	L_GLU_105	OE2	3.861
1KC5	L_LYS_147	NZ	L_GLU_154	OE1	3.049
1KC5	L_LYS_147	NZ	L_GLU_154	OE2	3.591
1KC5	L_LYS_149	NZ	L_GLU_195	OE1	2.716
1KC5	L_LYS_149	NZ	L_GLU_195	OE2	3.100
1KC5	L_ARG_155	NH1	L_GLU_185	OE1	3.442
1KC5	L_LYS_169	NZ	L_ASP_167	OD1	3.457
1KC5	L_LYS_169	NZ	L_ASP_167	OD2	3.411
1KC5	L_ARG_188	NH1	L_GLU_185	OE2	3.469
1KC5	L_HIS_189	ND1	L_ASP_151	OD2	3.918
1KC5	L_HIS_189	NE2	L_GLU_185	OE1	3.880
1KC5	L_LYS_199	NZ	L_ASP_110	OD2	2.858
1KC5	H_ARG_39	NH1	H_ASP_90	OD1	3.033
1KC5	H_ARG_39	NH2	H_GLU_47	OE1	2.994
1KC5	H_ARG_67	NH2	H_ASP_90	OD1	3.361
1KC5	H_ARG_67	NH2	H_ASP_90	OD2	2.772
1KC5	H_ARG_98	NH1	H_ASP_104	OD2	2.421
1KC5	H_LYS_211	NZ	L_GLU_123	OE2	2.759

Table 126: 1KC5-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1KCR	L_ARG_61	NH1	L_ASP_82	OD1	3.167
1KCR	L_ARG_61	NH1	L_ASP_82	OD2	3.442
1KCR	L_LYS_146	NZ	L_GLU_153	OE1	3.602
1KCR	L_LYS_146	NZ	L_GLU_153	OE2	3.503
1KCR	L_LYS_148	NZ	L_GLU_194	OE1	3.325
1KCR	L_ARG_154	NH2	L_GLU_184	OE1	3.047
1KCR	L_ARG_154	NH2	L_GLU_184	OE2	3.767
1KCR	L_HIS_188	ND1	L_ASP_150	OD2	3.289
1KCR	H_ARG_39	NH1	H_ASP_90	OD1	2.787
1KCR	H_ARG_39	NH2	H_GLU_47	OE1	3.186
1KCR	H_ARG_39	NH2	H_ASP_90	OD1	2.864
1KCR	H_ARG_67	NH1	H_ASP_90	OD1	3.439
1KCR	H_ARG_67	NH1	H_ASP_90	OD2	3.339
1KCR	H_ARG_67	NH2	H_ASP_90	OD1	3.781
1KCR	H_ARG_67	NH2	H_ASP_90	OD2	2.578
1KCR	H_LYS_76	NZ	H_ASP_73	OD2	3.906

Table 127: 1KCR-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1KCS	L_LYS_24	NZ	L_ASP_70	OD1	3.278
1KCS	L_ARG_54	NH1	L_ASP_60	OD1	3.351
1KCS	L_ARG_61	NH1	L_ASP_82	OD1	3.132
1KCS	L_ARG_61	NH1	L_ASP_82	OD2	3.710
1KCS	L_LYS_103	NZ	L_ASP_85	OD2	3.830
1KCS	L_LYS_149	NZ	L_GLU_195	OE1	3.249
1KCS	L_LYS_149	NZ	L_GLU_195	OE2	3.257
1KCS	L_HIS_189	ND1	L_ASP_151	OD2	2.813
1KCS	L_LYS_199	NZ	L_ASP_110	OD1	3.476
1KCS	L_LYS_199	NZ	L_ASP_110	OD2	3.643
1KCS	H_ARG_39	NH1	H_ASP_90	OD1	2.811
1KCS	H_ARG_39	NH2	H_GLU_47	OE1	2.833
1KCS	H_ARG_39	NH2	H_ASP_90	OD1	3.463
1KCS	H_ARG_67	NH1	H_ASP_90	OD1	3.415
1KCS	H_ARG_67	NH1	H_ASP_90	OD2	3.871
1KCS	H_ARG_67	NH2	H_ASP_90	OD1	2.423
1KCS	H_ARG_67	NH2	H_ASP_90	OD2	2.528
1KCS	H_LYS_211	NZ	L_GLU_123	OE1	3.340
1KCS	H_LYS_211	NZ	L_GLU_123	OE2	2.904
1KCS	H_LYS_212	NZ	H_GLU_214	OE2	2.957

Table 128: 1KCS-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1KIP	A_ARG_61	NH2	A_GLU_81	OE2	3.479
1KIP	A_ARG_61	NH2	A_ASP_82	OD1	2.597
1KIP	A_ARG_61	NH2	A_ASP_82	OD2	3.338
1KIP	A_ARG_96	NH1	B_GLU_98	OE1	2.773
1KIP	A_ARG_96	NH1	B_GLU_98	OE2	3.817
1KIP	A_ARG_96	NH2	B_GLU_98	OE1	3.280
1KIP	A_ARG_96	NH2	B_GLU_98	OE2	2.802
1KIP	A_LYS_107	NZ	A_GLU_17	OE1	3.197
1KIP	A_LYS_107	NZ	A_GLU_17	OE2	2.849
1KIP	B_ARG_38	NH1	B_ASP_89	OD1	3.191
1KIP	B_ARG_38	NH2	B_GLU_46	OE1	3.093
1KIP	B_ARG_38	NH2	B_GLU_46	OE2	3.933
1KIP	B_ARG_38	NH2	B_ASP_89	OD1	3.743
1KIP	B_ARG_66	NH1	B_ASP_89	OD1	3.854
1KIP	B_ARG_66	NH1	B_ASP_89	OD2	2.776
1KIP	B_ARG_66	NH2	B_ASP_89	OD1	2.725
1KIP	B_ARG_66	NH2	B_ASP_89	OD2	3.126
1KIP	B_ARG_97	NH2	B_ASP_104	OD1	3.837
1KIP	B_ARG_97	NH2	B_ASP_104	OD2	2.804
1KIP	B_ARG_102	NH1	B_ASP_100	OD2	3.276
1KIP	C_LYS_1	NZ	C_GLU_7	OE2	3.468
1KIP	C_ARG_61	NH1	C_ASP_48	OD1	3.721
1KIP	C_ARG_125	NH1	C_ASP_119	OD1	3.514
1KIP	C_ARG_125	NH1	C_ASP_119	OD2	3.062
1KIP	C_ARG_125	NH2	C_ASP_119	OD2	3.245

Table 129: 1KIP-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1KIQ	A_ARG.61	NH2	A_GLU.81	OE2	3.197
1KIQ	A_ARG.61	NH2	A_ASP.82	OD1	2.691
1KIQ	A_ARG.61	NH2	A_ASP.82	OD2	3.415
1KIQ	A_ARG.96	NH1	B_GLU.98	OE1	2.812
1KIQ	A_ARG.96	NH1	B_GLU.98	OE2	3.589
1KIQ	A_ARG.96	NH2	B_GLU.98	OE1	3.677
1KIQ	A_ARG.96	NH2	B_GLU.98	OE2	2.919
1KIQ	A_LYS.103	NZ	A_GLU.105	OE1	2.805
1KIQ	A_LYS.103	NZ	A_GLU.105	OE2	3.912
1KIQ	A_LYS.107	NZ	A_GLU.17	OE1	3.881
1KIQ	A_LYS.107	NZ	A_GLU.17	OE2	2.784
1KIQ	B_ARG.38	NH1	B_ASP.89	OD1	2.893
1KIQ	B_ARG.38	NH2	B_GLU.46	OE1	3.199
1KIQ	B_ARG.38	NH2	B_GLU.46	OE2	3.778
1KIQ	B_ARG.38	NH2	B_ASP.89	OD1	3.733
1KIQ	B_ARG.66	NH1	B_ASP.89	OD1	3.789
1KIQ	B_ARG.66	NH1	B_ASP.89	OD2	2.815
1KIQ	B_ARG.66	NH2	B_ASP.89	OD1	2.856
1KIQ	B_ARG.66	NH2	B_ASP.89	OD2	3.346
1KIQ	B_LYS.75	NZ	B_ASP.72	OD2	3.652
1KIQ	B_ARG.97	NH2	B_ASP.104	OD1	3.671
1KIQ	B_ARG.97	NH2	B_ASP.104	OD2	2.756
1KIQ	B_ARG.102	NH1	B_ASP.100	OD2	3.299
1KIQ	C_LYS.1	NZ	C_GLU.7	OE1	3.271
1KIQ	C_LYS.1	NZ	C_GLU.7	OE2	3.227
1KIQ	C_LYS.13	NZ	C_ASP.18	OD2	3.514
1KIQ	C_ARG.68	NH1	C_ASP.66	OD2	2.812
1KIQ	C_ARG.125	NH1	C_ASP.119	OD1	3.267
1KIQ	C_ARG.125	NH1	C_ASP.119	OD2	3.095
1KIQ	C_ARG.125	NH2	C_ASP.119	OD2	3.062

Table 130: 1KIQ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1KIR	A_ARG_61	NH2	A_GLU_81	OE2	3.612
1KIR	A_ARG_61	NH2	A_ASP_82	OD1	2.646
1KIR	A_ARG_61	NH2	A_ASP_82	OD2	3.502
1KIR	A_ARG_96	NH1	B_GLU_98	OE1	2.757
1KIR	A_ARG_96	NH1	B_GLU_98	OE2	3.582
1KIR	A_ARG_96	NH2	B_GLU_98	OE1	3.625
1KIR	A_ARG_96	NH2	B_GLU_98	OE2	2.980
1KIR	A_LYS_107	NZ	A_GLU_17	OE2	2.685
1KIR	B_ARG_38	NH1	B_ASP_89	OD1	3.082
1KIR	B_ARG_38	NH2	B_GLU_46	OE1	3.138
1KIR	B_ARG_38	NH2	B_GLU_46	OE2	3.860
1KIR	B_ARG_38	NH2	B_ASP_89	OD1	3.771
1KIR	B_ARG_66	NH1	B_ASP_89	OD2	2.949
1KIR	B_ARG_66	NH2	B_ASP_89	OD1	2.669
1KIR	B_ARG_66	NH2	B_ASP_89	OD2	2.955
1KIR	B_LYS_75	NZ	B_ASP_72	OD2	3.972
1KIR	B_ARG_97	NH2	B_ASP_104	OD1	3.914
1KIR	B_ARG_97	NH2	B_ASP_104	OD2	2.816
1KIR	B_ARG_102	NH1	B_ASP_100	OD2	3.339
1KIR	C_LYS_1	NZ	C_GLU_7	OE1	3.936
1KIR	C_LYS_1	NZ	C_GLU_7	OE2	3.274
1KIR	C_ARG_68	NH1	C_ASP_66	OD2	3.347
1KIR	C_ARG_125	NH1	C_ASP_119	OD1	3.220
1KIR	C_ARG_125	NH1	C_ASP_119	OD2	2.967
1KIR	C_ARG_125	NH2	C_ASP_119	OD2	3.129

Table 131: 1KIR-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1KTR	L_ARG_24	NH2	L_ASP_75	OD1	3.305
1KTR	L_ARG_24	NH2	L_ASP_75	OD2	3.234
1KTR	L_ARG_66	NH1	L_ASP_87	OD1	3.908
1KTR	L_ARG_66	NH1	L_ASP_87	OD2	2.898
1KTR	L_ARG_66	NH2	L_GLU_84	OE1	3.858
1KTR	L_ARG_66	NH2	L_GLU_84	OE2	3.876
1KTR	L_ARG_66	NH2	L_ASP_87	OD1	2.818
1KTR	L_ARG_66	NH2	L_ASP_87	OD2	3.123
1KTR	L_LYS_108	NZ	L_GLU_110	OE2	3.290
1KTR	L_ARG_200	NH1	L_ASP_223	OD1	3.461
1KTR	L_ARG_200	NH1	L_ASP_223	OD2	3.017
1KTR	L_ARG_200	NH2	L_ASP_223	OD1	2.813
1KTR	L_ARG_200	NH2	L_ASP_223	OD2	3.629
1KTR	P_HIS_4	NE2	L_ASP_183	OD1	3.445
1KTR	P_HIS_4	NE2	L_ASP_183	OD2	2.673
1KTR	P_HIS_6	ND1	L_GLU_39	OE1	3.223
1KTR	P_HIS_6	ND1	L_GLU_39	OE2	2.811
1KTR	P_HIS_6	NE2	L_GLU_230	OE1	3.040
1KTR	P_HIS_6	NE2	L_GLU_230	OE2	3.199

Table 132: 1KTR-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID** **residue name** **residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1L7I	L_LYS_24	NZ	L_ASP_70	OD1	3.450
1L7I	L_LYS_24	NZ	L_ASP_70	OD2	2.756
1L7I	L_ARG_61	NH2	L_GLU_81	OE1	3.159
1L7I	L_ARG_61	NH2	L_ASP_82	OD1	2.832
1L7I	L_ARG_61	NH2	L_ASP_82	OD2	3.810
1L7I	L_LYS_149	NZ	L_GLU_195	OE1	3.108
1L7I	L_LYS_149	NZ	L_GLU_195	OE2	3.606
1L7I	L_HIS_189	ND1	L_ASP_151	OD2	3.427
1L7I	H_ARG_38	NH1	H_ASP_86	OD1	2.914
1L7I	H_ARG_38	NH2	H_GLU_46	OE1	3.005
1L7I	H_ARG_62	NH2	H_GLU_46	OE1	3.101
1L7I	H_ARG_62	NH2	H_GLU_46	OE2	2.791
1L7I	H_ARG_66	NH1	H_ASP_86	OD1	2.927
1L7I	H_ARG_66	NH1	H_ASP_86	OD2	3.600
1L7I	H_ARG_94	NH2	H_ASP_101	OD1	3.112
1L7I	H_LYS_143	NZ	H_ASP_144	OD1	3.173
1L7I	H_LYS_143	NZ	H_ASP_144	OD2	3.234
1L7I	H_LYS_209	NZ	L_GLU_123	OE1	2.718
1L7I	H_LYS_210	NZ	H_GLU_212	OE2	3.013

Table 133: 1L7I-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID residue name residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1LK3	A_ARG_27	NH1	A_GLU_151	OE1	3.162
1LK3	A_ARG_27	NH1	A_GLU_151	OE2	3.248
1LK3	A_ARG_27	NH2	A_GLU_151	OE2	2.810
1LK3	A_LYS_99	NZ	A_GLU_96	OE2	3.379
1LK3	A_LYS_125	NZ	A_GLU_122	OE2	3.974
1LK3	A_LYS_130	NZ	L_ASP_1	OD1	2.906
1LK3	L_ARG_31	NH1	A_GLU_133	OE1	2.703
1LK3	L_ARG_60	NH1	L_GLU_78	OE1	3.757
1LK3	L_ARG_60	NH1	L_ASP_81	OD1	3.577
1LK3	L_ARG_60	NH1	L_ASP_81	OD2	2.703
1LK3	L_ARG_60	NH2	L_GLU_78	OE1	3.450
1LK3	L_ARG_60	NH2	L_GLU_78	OE2	3.792
1LK3	L_ARG_60	NH2	L_ASP_81	OD1	2.902
1LK3	L_ARG_60	NH2	L_ASP_81	OD2	3.590
1LK3	L_LYS_146	NZ	L_GLU_153	OE2	2.870
1LK3	L_LYS_148	NZ	L_GLU_194	OE1	2.968
1LK3	L_LYS_148	NZ	L_GLU_194	OE2	3.177
1LK3	L_ARG_154	NH1	L_ASP_184	OD1	3.134
1LK3	L_ARG_154	NH1	L_ASP_184	OD2	3.607
1LK3	L_ARG_154	NH2	L_ASP_184	OD1	3.715
1LK3	L_ARG_154	NH2	L_ASP_184	OD2	2.806
1LK3	L_ARG_155	NH1	L_GLU_153	OE2	2.979
1LK3	L_LYS_182	NZ	L_GLU_186	OE2	3.604
1LK3	L_HIS_188	ND1	L_ASP_150	OD2	3.740
1LK3	L_HIS_188	NE2	L_ASP_184	OD1	3.222
1LK3	H_LYS_13	NZ	H_GLU_121	OE2	2.581
1LK3	H_LYS_23	NZ	I_GLU_121	OE2	2.800
1LK3	H_LYS_65	NZ	H_GLU_62	OE1	3.360
1LK3	H_LYS_67	NZ	H_ASP_90	OD1	3.589
1LK3	H_LYS_67	NZ	H_ASP_90	OD2	2.874
1LK3	H_LYS_214	NZ	L_GLU_122	OE1	2.517
1LK3	B_ARG_27	NH1	B_GLU_151	OE1	2.917
1LK3	B_ARG_27	NH2	B_GLU_151	OE1	3.090
1LK3	B_ARG_27	NH2	B_GLU_151	OE2	3.902
1LK3	B_LYS_88	NZ	B_GLU_81	OE2	3.290
1LK3	B_LYS_99	NZ	B_GLU_96	OE1	3.193
1LK3	B_LYS_99	NZ	B_GLU_96	OE2	3.913
1LK3	B_LYS_125	NZ	B_GLU_122	OE2	3.816
1LK3	B_LYS_130	NZ	M_ASP_1	OD1	2.851
1LK3	M_LYS_23	NZ	M_ASP_69	OD1	2.916
1LK3	M_LYS_23	NZ	M_ASP_69	OD2	3.739
1LK3	M_ARG_31	NH1	B_GLU_133	OE1	2.693
1LK3	M_LYS_38	NZ	M_ASP_80	OD1	3.251
1LK3	M_LYS_38	NZ	M_ASP_80	OD2	3.163
1LK3	M_ARG_60	NH1	M_ASP_81	OD1	3.524
1LK3	M_ARG_60	NH1	M_ASP_81	OD2	2.748
1LK3	M_ARG_60	NH2	M_GLU_78	OE1	3.446
1LK3	M_ARG_60	NH2	M_GLU_78	OE2	3.705
1LK3	M_ARG_60	NH2	M_ASP_81	OD1	2.992
1LK3	M_ARG_60	NH2	M_ASP_81	OD2	3.699
1LK3	M_LYS_148	NZ	M_GLU_194	OE1	3.154
1LK3	M_LYS_148	NZ	M_GLU_194	OE2	2.891
1LK3	M_ARG_154	NH1	M_ASP_184	OD1	3.102
1LK3	M_ARG_154	NH1	M_ASP_184	OD2	3.559
1LK3	M_ARG_154	NH2	M_ASP_184	OD1	3.772
1LK3	M_ARG_154	NH2	M_ASP_184	OD2	2.866
1LK3	M_ARG_155	NH1	M_GLU_153	OE2	2.799

1LK3	M_LYS_182	NZ	M_GLU_186	OE1	2.894
1LK3	M_LYS_182	NZ	M_GLU_186	OE2	3.921
1LK3	M_HIS_188	ND1	M_ASP_150	OD2	3.800
1LK3	M_HIS_188	NE2	M_ASP_184	OD1	3.004
1LK3	M_LYS_198	NZ	M_ASP_109	OD1	3.702
1LK3	M_LYS_198	NZ	M_ASP_109	OD2	3.602
1LK3	I_LYS_13	NZ	I_GLU_121	OE1	2.774
1LK3	I_LYS_63	NZ	M_ASP_1	OD2	3.881
1LK3	I_LYS_67	NZ	I_ASP_90	OD1	3.913
1LK3	I_LYS_67	NZ	I_ASP_90	OD2	2.939
1LK3	I_LYS_214	NZ	M_GLU_122	OE2	2.753

Table 134: 1LK3-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1M71	A_ARG_14	NH1	A_ASP_17	OD1	3.710
1M71	A_HIS_27D	ND1	A_ASP_28	OD1	3.392
1M71	A_HIS_27D	ND1	A_ASP_28	OD2	2.865
1M71	A_LYS_39	NZ	A_GLU_81	OE1	2.866
1M71	A_ARG_61	NH1	A_GLU_79	OE1	3.543
1M71	A_ARG_61	NH2	A_ASP_82	OD1	2.481
1M71	A_ARG_61	NH2	A_ASP_82	OD2	2.894
1M71	A_LYS_149	NZ	A_GLU_195	OE2	3.376
1M71	A_LYS_183	NZ	A_GLU_187	OE1	2.685
1M71	A_ARG_188	NH1	A_GLU_185	OE1	3.609
1M71	A_ARG_188	NH2	A_ASP_184	OD1	3.517
1M71	A_HIS_189	ND1	A_ASP_151	OD1	3.287
1M71	A_LYS_199	NZ	A_ASP_110	OD1	2.781
1M71	A_LYS_199	NZ	A_ASP_110	OD2	3.508
1M71	B_ARG_38	NH1	B_GLU_46	OE1	2.911
1M71	B_ARG_38	NH1	B_GLU_46	OE2	3.780
1M71	B_ARG_38	NH2	B_ASP_86	OD1	3.068
1M71	B_ARG_52	NH1	B_GLU_50	OE2	2.697
1M71	B_HIS_58	ND1	B_GLU_50	OE2	3.091
1M71	B_ARG_66	NH1	B_ASP_86	OD1	3.230
1M71	B_ARG_66	NH1	B_ASP_86	OD2	3.124
1M71	B_ARG_66	NH2	B_ASP_86	OD1	3.143
1M71	B_ARG_66	NH2	B_ASP_86	OD2	3.298
1M71	B_ARG_71	NH1	B_ASP_73	OD2	3.433
1M71	B_LYS_75	NZ	B_ASP_72	OD2	3.881
1M71	B_ARG_83	NH1	B_GLU_85	OE2	3.022
1M71	B_ARG_83	NH2	B_GLU_85	OE2	2.413
1M71	B_ARG_94	NH1	B_ASP_101	OD1	3.346
1M71	B_ARG_94	NH1	B_ASP_101	OD2	3.346
1M71	B_ARG_164	NH1	A_ASP_167	OD2	3.246
1M71	B_ARG_164	NH1	A_ASP_170	OD1	3.912
1M71	B_ARG_164	NH2	A_ASP_167	OD2	2.886
1M71	B_LYS_208	NZ	A_GLU_123	OE1	2.546
1M71	B_LYS_208	NZ	A_GLU_123	OE2	3.594

Table 135: 1M71-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1M7D	A_ARG_24	NH1	A_ASP_70	OD1	3.427
1M7D	A_HIS_27D	ND1	A_ASP_28	OD1	3.488
1M7D	A_HIS_27D	ND1	A_ASP_28	OD2	3.058
1M7D	A_LYS_39	NZ	A_GLU_81	OE1	2.802
1M7D	A_ARG_61	NH1	A_ASP_82	OD1	2.789
1M7D	A_ARG_61	NH1	A_ASP_82	OD2	3.838
1M7D	A_ARG_61	NH2	A_ASP_82	OD1	3.397
1M7D	A_ARG_61	NH2	A_ASP_82	OD2	2.952
1M7D	A_LYS_103	NZ	A_ASP_165	OD1	3.651
1M7D	A_LYS_149	NZ	A_GLU_195	OE1	2.888
1M7D	A_LYS_149	NZ	A_GLU_195	OE2	3.877
1M7D	A_ARG_188	NH1	A_GLU_185	OE1	2.963
1M7D	A_ARG_188	NH2	A_ASP_184	OD1	3.464
1M7D	A_HIS_189	ND1	A_ASP_151	OD1	2.856
1M7D	A_HIS_189	NE2	A_GLU_185	OE2	2.728
1M7D	A_LYS_199	NZ	A_ASP_110	OD1	3.424
1M7D	B_ARG_38	NH1	B_GLU_46	OE1	3.681
1M7D	B_ARG_38	NH1	B_GLU_46	OE2	3.270
1M7D	B_ARG_38	NH2	B_ASP_86	OD1	3.018
1M7D	B_ARG_52	NH1	B_GLU_50	OE2	3.410
1M7D	B_HIS_58	ND1	B_GLU_50	OE2	3.864
1M7D	B_ARG_66	NH1	B_ASP_86	OD1	3.193
1M7D	B_ARG_66	NH1	B_ASP_86	OD2	3.613
1M7D	B_ARG_66	NH2	B_ASP_86	OD1	3.775
1M7D	B_ARG_66	NH2	B_ASP_86	OD2	2.708
1M7D	B_ARG_71	NH1	B_ASP_73	OD2	2.991
1M7D	B_LYS_75	NZ	B_ASP_72	OD1	3.686
1M7D	B_ARG_94	NH1	B_ASP_101	OD1	3.533
1M7D	B_ARG_94	NH1	B_ASP_101	OD2	2.689
1M7D	B_ARG_164	NH1	A_ASP_167	OD2	3.313
1M7D	B_ARG_164	NH1	A_ASP_170	OD1	3.795
1M7D	B_ARG_164	NH2	A_ASP_167	OD2	3.482
1M7D	B_LYS_208	NZ	A_GLU_123	OE1	2.586
1M7D	B_LYS_208	NZ	A_GLU_123	OE2	3.420

Table 136: 1M7D-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1M7I	A_ARG_14	NH1	A_ASP_17	OD1	3.105
1M7I	A_ARG_14	NH1	A_ASP_17	OD2	3.058
1M7I	A_ARG_24	NH1	A_ASP_70	OD1	3.369
1M7I	A_ARG_24	NH1	A_ASP_70	OD2	3.708
1M7I	A_HIS_27D	ND1	A_ASP_28	OD1	3.271
1M7I	A_HIS_27D	ND1	A_ASP_28	OD2	2.955
1M7I	A_LYS_39	NZ	A_GLU_81	OE1	3.102
1M7I	A_ARG_61	NH1	A_ASP_82	OD1	2.522
1M7I	A_ARG_61	NH1	A_ASP_82	OD2	3.863
1M7I	A_ARG_61	NH2	A_GLU_79	OE2	3.752
1M7I	A_ARG_61	NH2	A_ASP_82	OD1	2.961
1M7I	A_ARG_61	NH2	A_ASP_82	OD2	2.695
1M7I	A_LYS_103	NZ	A_ASP_165	OD1	3.427
1M7I	A_LYS_147	NZ	A_GLU_154	OE1	3.983
1M7I	A_LYS_149	NZ	A_GLU_195	OE1	2.955
1M7I	A_LYS_183	NZ	A_GLU_187	OE1	3.069
1M7I	A_LYS_183	NZ	A_GLU_187	OE2	2.718
1M7I	A_ARG_188	NH1	A_GLU_185	OE1	2.765
1M7I	A_ARG_188	NH1	A_GLU_185	OE2	3.812
1M7I	A_ARG_188	NH2	A_ASP_184	OD1	3.546
1M7I	A_HIS_189	ND1	A_ASP_151	OD1	2.633
1M7I	A_HIS_189	NE2	A_GLU_185	OE2	3.470
1M7I	A_LYS_199	NZ	A_ASP_110	OD1	3.401
1M7I	A_LYS_199	NZ	A_ASP_110	OD2	3.942
1M7I	B_LYS_3	NZ	B_GLU_5	OE1	3.875
1M7I	B_ARG_38	NH1	B_GLU_46	OE1	3.661
1M7I	B_ARG_38	NH1	B_GLU_46	OE2	3.487
1M7I	B_ARG_38	NH2	B_ASP_86	OD1	2.988
1M7I	B_ARG_52	NH1	B_GLU_50	OE2	3.454
1M7I	B_LYS_64	NZ	B_GLU_61	OE1	3.621
1M7I	B_ARG_66	NH1	B_ASP_86	OD1	3.442
1M7I	B_ARG_66	NH2	B_ASP_86	OD1	3.524
1M7I	B_ARG_66	NH2	B_ASP_86	OD2	3.046
1M7I	B_ARG_71	NH1	B_ASP_73	OD2	3.013
1M7I	B_ARG_83	NH2	B_GLU_85	OE2	3.534
1M7I	B_ARG_94	NH1	B_ASP_101	OD1	3.458
1M7I	B_ARG_94	NH1	B_ASP_101	OD2	2.750
1M7I	B_ARG_164	NH1	A_ASP_167	OD2	3.340
1M7I	B_ARG_164	NH1	A_ASP_170	OD1	3.884
1M7I	B_ARG_164	NH2	A_ASP_167	OD2	3.473
1M7I	B_LYS_208	NZ	A_GLU_123	OE1	3.031
1M7I	B_LYS_208	NZ	A_GLU_123	OE2	3.016

Table 137: 1M7I-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1MCO	L_LYS_55	NZ	L_GLU_52	OE1	3.257
1MCO	L_LYS_55	NZ	L_GLU_52	OE2	2.994
1MCO	L_ARG_63	NH1	L_GLU_83	OE1	3.878
1MCO	L_ARG_63	NH1	L_ASP_84	OD1	3.777
1MCO	L_ARG_63	NH1	L_ASP_84	OD2	3.204
1MCO	L_ARG_63	NH2	L_GLU_83	OE1	2.986
1MCO	L_LYS_153	NZ	L_GLU_207	OE1	3.930
1MCO	L_HIS_192	ND1	L_ASP_155	OD1	3.857
1MCO	L_HIS_192	ND1	L_ASP_155	OD2	3.328
1MCO	H_ARG_40	NH1	H_ASP_91	OD2	3.601
1MCO	H_ARG_40	NH2	H_GLU_48	OE1	3.700
1MCO	H_ARG_68	NH1	H_ASP_91	OD2	3.621
1MCO	H_ARG_68	NH2	H_ASP_91	OD2	3.951
1MCO	H_ARG_99	NH1	H_ASP_27	OD1	3.647
1MCO	H_ARG_99	NH1	H_ASP_27	OD2	2.797
1MCO	H_LYS_302	NZ	H_ASP_265	OD1	3.759
1MCO	H_LYS_302	NZ	H_ASP_265	OD2	3.098
1MCO	H_LYS_305	NZ	H_GLU_318	OE1	3.587
1MCO	H_LYS_305	NZ	H_GLU_318	OE2	3.377
1MCO	H_ARG_329	NH1	H_ASP_386	OD1	3.691
1MCO	H_ARG_401	NH1	H_GLU_373	OE1	3.230
1MCO	H_ARG_401	NH1	H_GLU_373	OE2	3.498
1MCO	H_ARG_401	NH2	H_GLU_373	OE1	3.949
1MCO	H_ARG_401	NH2	H_GLU_373	OE2	3.117

Table 138: 1MCO-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1MEL	A_ARG_38	NH1	A_ASP_90	OD1	3.059
1MEL	A_ARG_38	NH2	A_GLU_46	OE1	3.526
1MEL	A_ARG_38	NH2	A_GLU_46	OE2	3.673
1MEL	A_ARG_38	NH2	A_ASP_90	OD1	3.839
1MEL	A_ARG_67	NH1	A_ASP_90	OD1	3.797
1MEL	A_ARG_67	NH1	A_ASP_90	OD2	2.991
1MEL	A_ARG_67	NH2	A_ASP_90	OD1	2.893
1MEL	A_ARG_67	NH2	A_ASP_90	OD2	3.367
1MEL	B_ARG_38	NH1	B_ASP_90	OD1	3.033
1MEL	B_ARG_38	NH2	B_GLU_46	OE2	2.855
1MEL	B_ARG_38	NH2	B_ASP_90	OD1	3.939
1MEL	B_LYS_65	NZ	B_ASP_62	OD1	3.615
1MEL	B_ARG_67	NH1	B_ASP_90	OD2	2.997
1MEL	B_ARG_67	NH2	B_ASP_90	OD1	2.985
1MEL	B_ARG_67	NH2	B_ASP_90	OD2	2.943
1MEL	B_HIS_111	NE2	B_GLU_108	OE1	3.372
1MEL	L_LYS_1	NZ	L_GLU_7	OE1	3.475
1MEL	L_LYS_1	NZ	L_GLU_7	OE2	3.097
1MEL	L_HIS_15	NE2	L_ASP_87	OD1	3.885
1MEL	L_ARG_61	NH2	L_ASP_48	OD2	3.045
1MEL	L_LYS_97	NZ	L_ASP_101	OD2	2.722
1MEL	L_ARG_125	NH2	L_ASP_119	OD1	3.620
1MEL	L_ARG_125	NH2	L_ASP_119	OD2	2.816
1MEL	M_LYS_1	NZ	M_GLU_7	OE1	3.630
1MEL	M_LYS_1	NZ	M_GLU_7	OE2	2.907
1MEL	M_ARG_61	NH2	M_ASP_48	OD2	3.828
1MEL	M_ARG_125	NH1	M_ASP_119	OD2	3.053
1MEL	M_ARG_125	NH2	M_ASP_119	OD1	3.215
1MEL	M_ARG_125	NH2	M_ASP_119	OD2	3.106

Table 139: 1MEL-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1MFA	L_HIS_34	ND1	L_ASP_52	OD1	2.763
1MFA	L_ARG_63	NH2	L_ASP_84	OD1	2.796
1MFA	L_ARG_63	NH2	L_ASP_84	OD2	3.671
1MFA	H_LYS_313	NZ	H_GLU_296	OE1	3.001
1MFA	H_LYS_313	NZ	H_GLU_296	OE2	3.675
1MFA	H_LYS_317	NZ	H_ASP_340	OD1	3.252
1MFA	H_LYS_317	NZ	H_ASP_340	OD2	2.782
1MFA	H_ARG_348	NH2	H_ASP_356	OD1	3.621
1MFA	H_ARG_348	NH2	H_ASP_356	OD2	2.864

Table 140: 1MFA-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1MFB	L_HIS_34	ND1	L_ASP_52	OD1	2.852
1MFB	L_HIS_44	ND1	L_GLU_40	OE2	3.943
1MFB	L_ARG_63	NH2	L_GLU_83	OE2	3.681
1MFB	L_ARG_63	NH2	L_ASP_84	OD1	2.962
1MFB	L_ARG_63	NH2	L_ASP_84	OD2	3.489
1MFB	L_LYS_113	NZ	L_GLU_201	OE1	3.004
1MFB	L_LYS_169	NZ	L_GLU_85	OE2	3.323
1MFB	L_HIS_191	ND1	L_ASP_154	OD2	3.623
1MFB	H_LYS_313	NZ	H_GLU_296	OE1	3.225
1MFB	H_LYS_313	NZ	H_GLU_296	OE2	3.887
1MFB	H_LYS_317	NZ	H_ASP_340	OD1	3.570
1MFB	H_LYS_317	NZ	H_ASP_340	OD2	2.807
1MFB	H_ARG_348	NH1	H_ASP_356	OD1	3.475
1MFB	H_ARG_348	NH1	H_ASP_356	OD2	3.034
1MFB	H_LYS_398	NZ	L_GLU_127	OE2	2.924
1MFB	H_LYS_463	NZ	L_GLU_126	OE1	3.780

Table 141: 1MFB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1MFC	L_HIS_34	ND1	L_ASP_52	OD1	2.788
1MFC	L_ARG_63	NH2	L_GLU_83	OE2	3.733
1MFC	L_ARG_63	NH2	L_ASP_84	OD1	2.943
1MFC	L_ARG_63	NH2	L_ASP_84	OD2	3.639
1MFC	L_LYS_72	NZ	L_ASP_71	OD1	3.757
1MFC	L_LYS_113	NZ	L_GLU_201	OE1	2.885
1MFC	L_LYS_169	NZ	L_GLU_85	OE2	2.931
1MFC	L_HIS_191	ND1	L_ASP_154	OD2	3.170
1MFC	H_LYS_313	NZ	H_GLU_296	OE1	3.268
1MFC	H_LYS_313	NZ	H_GLU_296	OE2	3.847
1MFC	H_LYS_317	NZ	H_ASP_340	OD1	3.122
1MFC	H_LYS_317	NZ	H_ASP_340	OD2	2.805
1MFC	H_ARG_348	NH1	H_ASP_356	OD1	3.435
1MFC	H_ARG_348	NH1	H_ASP_356	OD2	2.938
1MFC	H_LYS_398	NZ	L_GLU_127	OE2	2.815
1MFC	H_LYS_463	NZ	L_GLU_126	OE1	3.807

Table 142: 1MFC-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1MHH	A_ARG_61	NH1	A_GLU_81	OE1	3.842
1MHH	A_ARG_61	NH2	A_GLU_81	OE1	2.895
1MHH	A_ARG_61	NH2	A_ASP_82	OD1	2.685
1MHH	A_ARG_61	NH2	A_ASP_82	OD2	3.421
1MHH	A_LYS_103	NZ	A_GLU_105	OE1	3.375
1MHH	A_LYS_103	NZ	A_GLU_105	OE2	3.766
1MHH	A_LYS_142	NZ	A_GLU_105	OE1	3.319
1MHH	A_LYS_142	NZ	A_GLU_105	OE2	2.969
1MHH	A_LYS_147	NZ	A_GLU_195	OE2	3.944
1MHH	A_LYS_149	NZ	A_GLU_195	OE1	2.919
1MHH	A_LYS_149	NZ	A_GLU_195	OE2	3.626
1MHH	A_ARG_155	NH2	A_GLU_185	OE2	3.327
1MHH	A_LYS_183	NZ	A_GLU_187	OE1	2.817
1MHH	A_LYS_183	NZ	A_GLU_187	OE2	3.387
1MHH	A_HIS_189	ND1	A_ASP_151	OD2	2.738
1MHH	A_LYS_199	NZ	A_ASP_110	OD2	3.962
1MHH	B_LYS_64	NZ	B_ASP_61	OD1	3.336
1MHH	B_ARG_66	NH1	B_ASP_86	OD1	3.761
1MHH	B_ARG_66	NH1	B_ASP_86	OD2	2.813
1MHH	B_ARG_66	NH2	B_ASP_86	OD1	3.094
1MHH	B_ARG_66	NH2	B_ASP_86	OD2	3.485
1MHH	B_ARG_94	NH2	B_ASP_101	OD1	2.684
1MHH	B_ARG_94	NH2	B_ASP_101	OD2	3.615
1MHH	B_LYS_208	NZ	A_GLU_123	OE2	3.019
1MHH	C_LYS_24	NZ	C_ASP_70	OD1	3.911
1MHH	C_ARG_61	NH1	C_GLU_81	OE2	3.375
1MHH	C_ARG_61	NH1	C_ASP_82	OD1	2.924
1MHH	C_ARG_61	NH1	C_ASP_82	OD2	3.294
1MHH	C_ARG_61	NH2	C_ASP_82	OD1	3.459
1MHH	C_ARG_61	NH2	C_ASP_82	OD2	2.571
1MHH	C_LYS_147	NZ	C_GLU_195	OE1	3.060
1MHH	C_LYS_149	NZ	C_GLU_195	OE2	3.143
1MHH	C_ARG_155	NH1	C_GLU_185	OE1	3.912
1MHH	C_ARG_155	NH1	C_GLU_185	OE2	3.653
1MHH	C_ARG_155	NH2	C_GLU_185	OE1	2.731
1MHH	C_ARG_155	NH2	C_GLU_185	OE2	3.507
1MHH	C_LYS_183	NZ	C_GLU_187	OE1	2.713
1MHH	C_ARG_188	NH1	E_ASP_831	OD2	3.196
1MHH	C_ARG_188	NH2	E_ASP_831	OD2	3.360
1MHH	C_HIS_189	ND1	C_ASP_151	OD1	2.633
1MHH	C_LYS_199	NZ	C_ASP_110	OD2	2.558
1MHH	D_ARG_66	NH1	D_ASP_86	OD1	3.829
1MHH	D_ARG_66	NH1	D_ASP_86	OD2	2.884
1MHH	D_ARG_66	NH2	D_ASP_86	OD1	2.828
1MHH	D_ARG_66	NH2	D_ASP_86	OD2	3.264
1MHH	D_ARG_94	NH2	D_ASP_101	OD1	3.655
1MHH	D_ARG_94	NH2	D_ASP_101	OD2	2.611
1MHH	E_LYS_833	NZ	C_GLU_185	OE2	2.489
1MHH	E_LYS_840	NZ	E_GLU_838	OE1	3.866
1MHH	E_HIS_874	NE2	E_GLU_869	OE2	3.707
1MHH	E_LYS_878	NZ	E_ASP_867	OD2	2.644
1MHH	F_LYS_1833	NZ	C_GLU_17	OE1	3.798

Table 143: 1MHH-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1MLB	A_ARG_61	NH1	A_ASP_82	OD1	2.159
1MLB	A_ARG_61	NH1	A_ASP_82	OD2	2.329
1MLB	A_ARG_61	NH2	A_GLU_79	OE1	3.872
1MLB	A_ARG_61	NH2	A_GLU_81	OE2	3.099
1MLB	A_LYS_147	NZ	A_GLU_154	OE1	3.634
1MLB	A_LYS_147	NZ	A_GLU_154	OE2	2.438
1MLB	A_LYS_149	NZ	A_GLU_195	OE1	3.556
1MLB	A_LYS_149	NZ	A_GLU_195	OE2	3.786
1MLB	A_ARG_155	NH1	A_GLU_185	OE2	2.511
1MLB	A_ARG_155	NH2	A_GLU_185	OE1	3.793
1MLB	A_ARG_155	NH2	A_GLU_185	OE2	2.918
1MLB	A_HIS_189	ND1	A_ASP_151	OD2	2.937
1MLB	A_LYS_199	NZ	A_ASP_110	OD2	2.869
1MLB	B_ARG_40	NH1	B_GLU_89	OE2	3.375
1MLB	B_ARG_40	NH2	B_GLU_89	OE2	3.648
1MLB	B_LYS_63	NZ	B_GLU_46	OE1	3.279
1MLB	B_LYS_67	NZ	B_ASP_90	OD1	2.983
1MLB	B_LYS_67	NZ	B_ASP_90	OD2	2.383
1MLB	B_ARG_98	NH2	B_ASP_100	OD1	3.092
1MLB	B_ARG_98	NH2	B_ASP_100	OD2	2.647
1MLB	B_LYS_211	NZ	A_GLU_123	OE1	3.556

Table 144: 1MLB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1MLC	A_ARG.61	NH1	A_ASP.82	OD1	2.951
1MLC	A_ARG.61	NH1	A_ASP.82	OD2	2.608
1MLC	A_LYS.149	NZ	A_GLU.195	OE1	3.271
1MLC	A_LYS.149	NZ	A_GLU.195	OE2	2.595
1MLC	A_ARG.155	NH2	A_GLU.185	OE1	2.706
1MLC	A_ARG.155	NH2	A_GLU.185	OE2	3.006
1MLC	A_LYS.183	NZ	A_GLU.187	OE1	2.465
1MLC	A_LYS.183	NZ	A_GLU.187	OE2	2.957
1MLC	A_HIS.189	ND1	A_ASP.151	OD2	3.264
1MLC	A_HIS.189	NE2	A_GLU.185	OE2	3.846
1MLC	A_LYS.199	NZ	A_ASP.110	OD1	3.804
1MLC	A_LYS.199	NZ	A_ASP.110	OD2	2.246
1MLC	B_LYS.38	NZ	B_ASP.90	OD1	3.791
1MLC	B_ARG.40	NH2	B_GLU.89	OE1	3.285
1MLC	B_LYS.63	NZ	B_GLU.46	OE2	3.505
1MLC	B_LYS.67	NZ	B_ASP.90	OD1	3.662
1MLC	B_LYS.67	NZ	B_ASP.90	OD2	2.412
1MLC	B_ARG.98	NH2	B_ASP.100	OD1	2.914
1MLC	B_ARG.98	NH2	B_ASP.100	OD2	3.525
1MLC	C_ARG.61	NH1	C_ASP.82	OD1	3.434
1MLC	C_ARG.61	NH1	C_ASP.82	OD2	2.291
1MLC	C_ARG.61	NH2	C_ASP.82	OD1	2.696
1MLC	C_ARG.61	NH2	C_ASP.82	OD2	3.196
1MLC	C_ARG.155	NH2	C_GLU.185	OE2	3.214
1MLC	C_LYS.183	NZ	C_GLU.187	OE1	2.976
1MLC	C_LYS.183	NZ	C_GLU.187	OE2	3.623
1MLC	C_ARG.188	NH1	C_GLU.185	OE1	3.888
1MLC	C_HIS.189	ND1	C_ASP.151	OD2	3.300
1MLC	C_HIS.189	NE2	C_GLU.185	OE1	2.956
1MLC	C_LYS.199	NZ	C_ASP.110	OD2	3.357
1MLC	D_LYS.63	NZ	D_GLU.46	OE2	2.938
1MLC	D_LYS.67	NZ	D_ASP.90	OD1	3.041
1MLC	D_LYS.67	NZ	D_ASP.90	OD2	2.752
1MLC	D_ARG.98	NH2	D_ASP.100	OD1	3.684
1MLC	D_ARG.98	NH2	D_ASP.100	OD2	2.571
1MLC	E_LYS.1	NZ	E_GLU.7	OE2	3.616
1MLC	E_ARG.45	NH2	B_GLU.50	OE2	3.032
1MLC	E_ARG.68	NH1	B_GLU.50	OE2	3.781
1MLC	E_ARG.68	NH2	B_GLU.35	OE2	2.927
1MLC	E_ARG.68	NH2	B_GLU.50	OE1	2.510
1MLC	E_ARG.68	NH2	B_GLU.50	OE2	3.189
1MLC	F_LYS.1	NZ	F_GLU.7	OE2	3.323
1MLC	F_ARG.45	NH2	D_GLU.50	OE2	2.431
1MLC	F_ARG.68	NH2	D_GLU.35	OE2	3.266
1MLC	F_ARG.68	NH2	D_GLU.50	OE1	2.710
1MLC	F_ARG.68	NH2	D_GLU.50	OE2	3.606
1MLC	F_ARG.125	NH1	F_ASP.119	OD2	3.464
1MLC	F_ARG.125	NH2	F_ASP.119	OD2	2.213

Table 145: 1MLC-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1N64	L_LYS_24	NZ	L_ASP_70	OD2	3.651
1N64	L_ARG_54	NH2	L_ASP_60	OD2	3.449
1N64	L_ARG_61	NH1	L_GLU_81	OE1	3.429
1N64	L_ARG_61	NH1	L_ASP_82	OD1	2.971
1N64	L_ARG_61	NH1	L_ASP_82	OD2	2.992
1N64	L_LYS_142	NZ	L_GLU_105	OE2	3.590
1N64	L_LYS_149	NZ	L_GLU_195	OE1	3.534
1N64	L_ARG_155	NH2	L_GLU_185	OE2	3.243
1N64	L_LYS_183	NZ	L_GLU_187	OE2	2.697
1N64	L_HIS_189	ND1	L_ASP_151	OD2	3.116
1N64	L_ARG_211	NH2	L_GLU_187	OE1	3.018
1N64	H_LYS_12	NZ	H_GLU_16	OE1	3.976
1N64	H_LYS_64	NZ	H_ASP_61	OD1	2.775
1N64	H_ARG_66	NH1	H_ASP_86	OD1	3.467
1N64	H_ARG_66	NH1	H_ASP_86	OD2	3.004
1N64	H_ARG_66	NH2	H_ASP_86	OD1	2.824
1N64	H_ARG_66	NH2	H_ASP_86	OD2	3.196
1N64	H_ARG_94	NH1	H_ASP_101	OD1	2.581
1N64	H_ARG_94	NH1	H_ASP_101	OD2	3.313
1N64	H_LYS_208	NZ	L_GLU_123	OE1	3.752

Table 146: 1N64-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1NBY	A_ARG.61	NH2	A_GLU.81	OE1	3.423
1NBY	A_ARG.61	NH2	A_ASP.82	OD1	2.821
1NBY	A_ARG.61	NH2	A_ASP.82	OD2	3.549
1NBY	A_LYS.103	NZ	A_GLU.105	OE2	3.768
1NBY	A_LYS.147	NZ	A_GLU.154	OE2	3.844
1NBY	A_LYS.149	NZ	A_GLU.195	OE1	3.898
1NBY	A_LYS.149	NZ	A_GLU.195	OE2	3.414
1NBY	A_ARG.155	NH2	A_GLU.185	OE2	3.438
1NBY	A_LYS.169	NZ	A_ASP.167	OD1	3.633
1NBY	A_LYS.169	NZ	A_ASP.167	OD2	2.995
1NBY	B_ARG.338	NH1	B_ASP.389	OD1	2.811
1NBY	B_ARG.338	NH2	B_GLU.346	OE1	2.861
1NBY	B_ARG.338	NH2	B_ASP.389	OD1	3.519
1NBY	B_ARG.366	NH1	B_ASP.389	OD1	3.031
1NBY	B_ARG.366	NH1	B_ASP.389	OD2	3.595
1NBY	B_ARG.366	NH2	B_ASP.389	OD1	3.673
1NBY	B_ARG.366	NH2	B_ASP.389	OD2	2.895
1NBY	B_LYS.508	NZ	A_GLU.123	OE1	2.458
1NBY	B_LYS.508	NZ	A_GLU.123	OE2	3.274
1NBY	C_LYS.601	NZ	C_GLU.607	OE2	2.838
1NBY	C_LYS.613	NZ	C_ASP.618	OD1	3.678
1NBY	C_LYS.697	NZ	B_ASP.332	OD1	3.949
1NBY	C_LYS.697	NZ	B_ASP.332	OD2	2.515
1NBY	C_ARG.725	NH1	C_ASP.719	OD1	3.590
1NBY	C_ARG.725	NH1	C_ASP.719	OD2	3.913
1NBY	C_ARG.725	NH2	C_ASP.719	OD1	3.444
1NBY	C_ARG.725	NH2	C_ASP.719	OD2	3.368

Table 147: 1NBY-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1NBZ	A_ARG_24	NH2	A_ASP_70	OD1	2.834
1NBZ	A_ARG_61	NH1	A_GLU_79	OE2	3.336
1NBZ	A_ARG_61	NH2	A_GLU_79	OE2	3.126
1NBZ	A_ARG_61	NH2	A_GLU_81	OE1	3.673
1NBZ	A_ARG_61	NH2	A_ASP_82	OD1	2.933
1NBZ	A_ARG_61	NH2	A_ASP_82	OD2	3.530
1NBZ	A_LYS_147	NZ	A_GLU_154	OE1	3.461
1NBZ	A_LYS_149	NZ	A_GLU_195B	OE1	3.640
1NBZ	A_ARG_155	NH1	A_GLU_185	OE2	3.835
1NBZ	A_ARG_155	NH2	A_GLU_185	OE2	3.081
1NBZ	B_ARG_338	NH1	B_GLU_346	OE1	2.666
1NBZ	B_ARG_338	NH1	B_ASP_389	OD1	3.713
1NBZ	B_ARG_338	NH2	B_ASP_389	OD1	2.601
1NBZ	B_ARG_366	NH1	B_ASP_389	OD1	3.099
1NBZ	B_ARG_366	NH1	B_ASP_389	OD2	3.734
1NBZ	B_ARG_366	NH2	B_ASP_389	OD1	3.577
1NBZ	B_ARG_366	NH2	B_ASP_389	OD2	2.894
1NBZ	C_LYS_601	NZ	C_GLU_607	OE2	3.226
1NBZ	C_ARG_661	NH1	C_ASP_648	OD1	3.578
1NBZ	C_ARG_661	NH1	C_ASP_648	OD2	3.756

Table 148: 1NBZ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1NDG	A_ARG_61	NH2	A_GLU_81	OE1	3.007
1NDG	A_ARG_61	NH2	A_ASP_82	OD1	2.723
1NDG	A_ARG_61	NH2	A_ASP_82	OD2	3.409
1NDG	A_LYS_147	NZ	A_GLU_154	OE1	3.627
1NDG	A_LYS_149	NZ	A_GLU_195	OE1	3.917
1NDG	A_LYS_149	NZ	A_GLU_195	OE2	3.737
1NDG	A_ARG_155	NH2	A_GLU_185	OE2	3.269
1NDG	A_LYS_199	NZ	A_ASP_110	OD2	3.863
1NDG	B_ARG_338	NH1	B_GLU_346	OE1	2.782
1NDG	B_ARG_338	NH1	B_ASP_389	OD1	3.738
1NDG	B_ARG_338	NH2	B_ASP_389	OD1	2.639
1NDG	B_HIS_360	NE2	A_ASP_1	OD2	3.716
1NDG	B_ARG_366	NH1	B_ASP_389	OD1	3.027
1NDG	B_ARG_366	NH1	B_ASP_389	OD2	3.618
1NDG	B_ARG_366	NH2	B_ASP_389	OD1	3.672
1NDG	B_ARG_366	NH2	B_ASP_389	OD2	2.903
1NDG	B_LYS_519	NZ	A_GLU_123	OE2	2.645
1NDG	C_LYS_601	NZ	C_GLU_607	OE1	3.948
1NDG	C_LYS_601	NZ	C_GLU_607	OE2	3.018
1NDG	C_LYS_613	NZ	C_ASP_618	OD2	3.695
1NDG	C_ARG_668	NH1	C_ASP_666	OD2	3.998
1NDG	C_LYS_697	NZ	B_ASP_332	OD1	3.996
1NDG	C_LYS_697	NZ	B_ASP_332	OD2	2.706
1NDG	C_LYS_697	NZ	B_ASP_399	OD1	2.922
1NDG	C_LYS_697	NZ	B_ASP_399	OD2	3.579
1NDG	C_ARG_725	NH2	C_ASP_719	OD1	3.484
1NDG	C_ARG_725	NH2	C_ASP_719	OD2	2.665

Table 149: 1NDG-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1NDM	A_ARG_24	NH2	A_ASP_70	OD1	3.107
1NDM	A_ARG_61	NH1	A_GLU_79	OE1	3.684
1NDM	A_ARG_61	NH1	A_GLU_79	OE2	2.866
1NDM	A_ARG_61	NH2	A_GLU_79	OE1	3.477
1NDM	A_ARG_61	NH2	A_GLU_79	OE2	3.744
1NDM	A_ARG_61	NH2	A_GLU_81	OE1	3.172
1NDM	A_ARG_61	NH2	A_ASP_82	OD1	2.876
1NDM	A_ARG_61	NH2	A_ASP_82	OD2	3.578
1NDM	A_LYS_149	NZ	A_GLU_195	OE1	3.953
1NDM	A_LYS_149	NZ	A_GLU_195	OE2	3.016
1NDM	A_ARG_155	NH1	A_GLU_185	OE1	3.939
1NDM	A_ARG_155	NH2	A_GLU_185	OE1	3.970
1NDM	A_ARG_188	NH2	A_ASP_184	OD1	3.023
1NDM	A_LYS_199	NZ	A_ASP_110	OD2	3.562
1NDM	B_ARG_338	NH1	B_GLU_346	OE1	2.753
1NDM	B_ARG_338	NH1	B_ASP_389	OD1	3.746
1NDM	B_ARG_338	NH2	B_ASP_389	OD1	2.687
1NDM	B_ARG_366	NH1	B_ASP_389	OD1	3.863
1NDM	B_ARG_366	NH2	B_ASP_389	OD1	3.499
1NDM	B_ARG_366	NH2	B_ASP_389	OD2	2.806
1NDM	B_ARG_397	NH1	B_ASP_332	OD1	3.700
1NDM	B_ARG_397	NH2	B_ASP_401	OD1	2.798
1NDM	B_ARG_397	NH2	B_ASP_401	OD2	3.696
1NDM	B_LYS_519	NZ	A_GLU_123	OE1	3.184
1NDM	C_LYS_601	NZ	C_GLU_607	OE1	3.751
1NDM	C_LYS_601	NZ	C_GLU_607	OE2	2.713
1NDM	C_ARG_668	NH1	C_ASP_666	OD2	3.599
1NDM	C_LYS_697	NZ	B_ASP_332	OD1	3.954
1NDM	C_LYS_697	NZ	B_ASP_332	OD2	2.468
1NDM	C_LYS_697	NZ	B_GLU_399	OE1	2.743

Table 150: 1NDM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1NGW	L_LYS_24	NZ	L_ASP_70	OD1	3.381
1NGW	L_ARG_61	NH1	L_ASP_82	OD1	2.889
1NGW	L_ARG_61	NH1	L_ASP_82	OD2	3.061
1NGW	L_LYS_103	NZ	L_GLU_165	OE1	3.834
1NGW	L_LYS_103	NZ	L_GLU_165	OE2	3.110
1NGW	L_LYS_149	NZ	L_GLU_195	OE1	2.871
1NGW	L_LYS_183	NZ	L_GLU_187	OE1	3.850
1NGW	L_LYS_183	NZ	L_GLU_187	OE2	2.603
1NGW	L_LYS_188	NZ	L_ASP_185	OD1	3.745
1NGW	H_LYS_38	NZ	H_GLU_89	OE1	3.916
1NGW	H_LYS_38	NZ	H_GLU_89	OE2	3.046
1NGW	H_ARG_40	NH1	H_GLU_89	OE2	3.692
1NGW	H_LYS_63	NZ	H_GLU_46	OE1	3.487
1NGW	H_LYS_67	NZ	H_GLU_89	OE1	3.643
1NGW	H_LYS_67	NZ	H_ASP_90	OD1	2.985
1NGW	H_LYS_67	NZ	H_ASP_90	OD2	3.338
1NGW	H_ARG_98	NH1	H_ASP_102	OD1	3.333
1NGW	H_ARG_99	NH2	H_ASP_100	OD1	3.884
1NGW	H_ARG_99	NH2	H_ASP_100	OD2	3.152
1NGW	H_LYS_144	NZ	H_ASP_145	OD1	3.933
1NGW	H_LYS_144	NZ	H_ASP_145	OD2	3.556
1NGW	H_HIS_165	NE2	L_ASP_167	OD1	3.771
1NGW	H_LYS_210	NZ	L_GLU_123	OE1	3.544
1NGW	H_LYS_210	NZ	L_GLU_123	OE2	3.092
1NGW	A_LYS_24	NZ	A_ASP_70	OD1	3.412
1NGW	A_ARG_61	NH1	A_ASP_82	OD1	2.833
1NGW	A_ARG_61	NH1	A_ASP_82	OD2	3.020
1NGW	A_LYS_103	NZ	A_GLU_165	OE2	3.226
1NGW	A_LYS_149	NZ	A_GLU_195	OE1	2.874
1NGW	A_LYS_183	NZ	A_GLU_187	OE1	3.842
1NGW	A_LYS_183	NZ	A_GLU_187	OE2	2.592
1NGW	A_LYS_188	NZ	A_ASP_185	OD1	3.777
1NGW	B_LYS_38	NZ	B_GLU_89	OE1	3.908
1NGW	B_LYS_38	NZ	B_GLU_89	OE2	3.066
1NGW	B_ARG_40	NH1	B_GLU_89	OE2	3.715
1NGW	B_LYS_63	NZ	B_GLU_46	OE1	3.549
1NGW	B_LYS_67	NZ	B_GLU_89	OE1	3.643
1NGW	B_LYS_67	NZ	B_ASP_90	OD1	2.988
1NGW	B_LYS_67	NZ	B_ASP_90	OD2	3.345
1NGW	B_ARG_98	NH1	B_ASP_102	OD1	3.321
1NGW	B_ARG_99	NH2	B_ASP_100	OD1	3.865
1NGW	B_ARG_99	NH2	B_ASP_100	OD2	3.174
1NGW	B_LYS_144	NZ	B_ASP_145	OD1	3.893
1NGW	B_LYS_144	NZ	B_ASP_145	OD2	3.494
1NGW	B_HIS_165	NE2	A_ASP_167	OD1	3.804
1NGW	B_LYS_210	NZ	A_GLU_123	OE1	3.662
1NGW	B_LYS_210	NZ	A_GLU_123	OE2	3.240

Table 151: 1NGW-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1NGX	A_LYS_24	NZ	A_ASP_70	OD1	3.081
1NGX	A_LYS_24	NZ	A_ASP_70	OD2	3.994
1NGX	A_ARG_61	NH2	A_ASP_82	OD1	2.985
1NGX	A_ARG_61	NH2	A_ASP_82	OD2	2.969
1NGX	A_LYS_149	NZ	A_GLU_195	OE1	3.396
1NGX	A_LYS_149	NZ	A_GLU_195	OE2	3.345
1NGX	A_LYS_188	NZ	A_ASP_185	OD2	3.626
1NGX	B_ARG_40	NH1	B_GLU_46	OE2	3.949
1NGX	B_ARG_40	NH2	B_GLU_89	OE1	3.668
1NGX	B_ARG_40	NH2	B_GLU_89	OE2	3.900
1NGX	B_LYS_65	NZ	B_GLU_62	OE1	3.589
1NGX	B_LYS_65	NZ	B_GLU_62	OE2	2.814
1NGX	B_ARG_98	NH1	B_GLU_6	OE1	3.105
1NGX	B_ARG_98	NH1	B_GLU_6	OE2	3.939
1NGX	B_ARG_98	NH2	B_GLU_6	OE1	3.343
1NGX	B_ARG_98	NH2	B_GLU_6	OE2	2.833
1NGX	B_LYS_210	NZ	A_GLU_123	OE1	3.994
1NGX	L_LYS_24	NZ	L_ASP_70	OD1	3.096
1NGX	L_LYS_24	NZ	L_ASP_70	OD2	3.994
1NGX	L_LYS_45	NZ	H_ASP_102	OD2	3.800
1NGX	L_ARG_61	NH2	L_ASP_82	OD1	2.986
1NGX	L_ARG_61	NH2	L_ASP_82	OD2	2.973
1NGX	L_LYS_149	NZ	L_GLU_195	OE1	3.398
1NGX	L_LYS_149	NZ	L_GLU_195	OE2	3.336
1NGX	L_LYS_188	NZ	L_ASP_185	OD2	3.617
1NGX	H_ARG_40	NH1	H_GLU_46	OE2	3.939
1NGX	H_ARG_40	NH2	H_GLU_89	OE1	3.665
1NGX	H_ARG_40	NH2	H_GLU_89	OE2	3.888
1NGX	H_LYS_65	NZ	H_GLU_62	OE1	3.585
1NGX	H_LYS_65	NZ	H_GLU_62	OE2	2.810
1NGX	H_ARG_98	NH1	H_GLU_6	OE1	3.117
1NGX	H_ARG_98	NH1	H_GLU_6	OE2	3.962
1NGX	H_ARG_98	NH2	H_GLU_6	OE1	3.326
1NGX	H_ARG_98	NH2	H_GLU_6	OE2	2.854
1NGX	H_LYS_210	NZ	L_GLU_123	OE1	3.804

Table 152: 1NGX-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1NGY	A_ARG_18	NH1	A_ASP_17	OD2	3.594
1NGY	A_LYS_24	NZ	A_ASP_70	OD2	3.919
1NGY	A_ARG_61	NH2	A_ASP_82	OD1	2.968
1NGY	A_ARG_61	NH2	A_ASP_82	OD2	3.529
1NGY	A_LYS_103	NZ	A_ASP_85	OD1	3.853
1NGY	A_LYS_103	NZ	A_ASP_85	OD2	3.272
1NGY	A_LYS_188	NZ	A_ASP_185	OD2	2.771
1NGY	A_HIS_189	ND1	A_ASP_151	OD1	3.054
1NGY	B_LYS_67	NZ	B_ASP_90	OD1	3.731
1NGY	B_LYS_67	NZ	B_ASP_90	OD2	2.958
1NGY	B_ARG_98	NH1	B_ASP_102	OD1	3.607
1NGY	B_ARG_98	NH1	B_ASP_102	OD2	3.510
1NGY	B_ARG_99	NH2	B_ASP_100	OD2	3.858
1NGY	B_LYS_144	NZ	B_ASP_145	OD1	3.371
1NGY	B_LYS_144	NZ	B_ASP_145	OD2	3.636
1NGY	B_LYS_211	NZ	B_GLU_213	OE2	3.805
1NGY	B_LYS_215	NZ	A_ASP_122	OD1	3.713
1NGY	B_LYS_215	NZ	A_ASP_122	OD2	3.325

Table 153: 1NGY-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1NGZ	A_ARG_	NH1	A_ASP_	OD1	3.637
1NGZ	A_ARG_	NH1	A_ASP_	OD2	2.596
1NGZ	A_ARG_	NH2	A_GLU_	OE1	3.959
1NGZ	A_ARG_	NH2	A_ASP_	OD1	3.037
1NGZ	A_ARG_	NH2	A_ASP_	OD2	3.356
1NGZ	A_LYS_	NZ	A_GLU_	OE1	2.828
1NGZ	A_LYS_	NZ	A_GLU_	OE2	3.489
1NGZ	A_LYS_	NZ	A_GLU_	OE1	3.044
1NGZ	A_LYS_	NZ	A_GLU_	OE1	3.604
1NGZ	A_HIS_	ND1	A_ASP_	OD1	3.223
1NGZ	B_LYS_	NZ	B_GLU_	OE1	2.735
1NGZ	B_ARG_	NH2	B_ASP_	OD2	3.084
1NGZ	B_LYS_	NZ	B_ASP_	OD1	3.293
1NGZ	B_LYS_	NZ	A_GLU_	OE2	3.517
1NGZ	B_LYS_	NZ	B_GLU_	OE2	3.319

Table 154: 1NGZ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1NLB	L_ARG_61	NH1	L_GLU_81	OE1	3.945
1NLB	L_ARG_61	NH1	L_ASP_82	OD1	3.512
1NLB	L_ARG_61	NH1	L_ASP_82	OD2	2.842
1NLB	L_ARG_61	NH2	L_ASP_82	OD1	2.825
1NLB	L_ARG_61	NH2	L_ASP_82	OD2	3.519
1NLB	L_LYS_103	NZ	L_GLU_105	OE1	2.975
1NLB	L_LYS_149	NZ	L_GLU_195	OE1	2.997
1NLB	L_LYS_149	NZ	L_GLU_195	OE2	3.428
1NLB	L_ARG_155	NH1	L_GLU_185	OE1	3.426
1NLB	L_ARG_155	NH1	L_GLU_185	OE2	3.047
1NLB	L_HIS_189	ND1	L_ASP_151	OD2	2.936
1NLB	L_LYS_199	NZ	L_ASP_110	OD1	3.501
1NLB	H_LYS_64	NZ	H_ASP_61	OD2	2.732
1NLB	H_ARG_66	NH1	H_ASP_86	OD1	3.711
1NLB	H_ARG_66	NH1	H_ASP_86	OD2	2.788
1NLB	H_ARG_66	NH2	H_ASP_86	OD1	2.985
1NLB	H_ARG_66	NH2	H_ASP_86	OD2	3.410
1NLB	H_ARG_94	NH1	H_ASP_101	OD1	2.645
1NLB	H_ARG_94	NH1	H_ASP_101	OD2	3.679
1NLB	H_LYS_115	NZ	H_ASP_173	OD2	3.346
1NLB	H_LYS_205	NZ	H_ASP_207	OD1	3.946
1NLB	H_LYS_205	NZ	H_ASP_207	OD2	2.901
1NLB	H_LYS_208	NZ	L_GLU_123	OE1	3.572

Table 155: 1NLB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1NMC	N_ARG_118	NH1	N_GLU_119	OE2	3.499
1NMC	N_ARG_118	NH2	N_GLU_119	OE2	3.987
1NMC	N_ARG_118	NH2	N_GLU_425	OE1	2.873
1NMC	N_ARG_118	NH2	N_GLU_425	OE2	3.183
1NMC	N_ARG_130	NH1	N_GLU_128	OE1	3.693
1NMC	N_ARG_130	NH1	N_GLU_128	OE2	3.810
1NMC	N_ARG_141	NH1	N_GLU_110	OE2	2.793
1NMC	N_ARG_152	NH2	N_ASP_151	OD1	3.884
1NMC	N_ARG_156	NH1	N_GLU_119	OE1	3.978
1NMC	N_ARG_156	NH2	N_GLU_119	OE1	3.322
1NMC	N_ARG_172	NH1	N_GLU_174	OE2	2.630
1NMC	N_ARG_189	NH2	N_ASP_125	OD1	2.838
1NMC	N_ARG_209	NH1	N_GLU_174	OE1	3.221
1NMC	N_ARG_209	NH1	N_GLU_174	OE2	3.350
1NMC	N_ARG_209	NH2	N_GLU_174	OE1	3.641
1NMC	N_ARG_209	NH2	N_GLU_174	OE2	3.567
1NMC	N_ARG_224	NH2	N_GLU_276	OE1	3.973
1NMC	N_ARG_224	NH2	N_GLU_276	OE2	2.790
1NMC	N_LYS_264	NZ	N_GLU_266	OE1	3.220
1NMC	N_LYS_273	NZ	N_ASP_339	OD1	3.418
1NMC	N_HIS_274	NE2	N_GLU_276	OE2	3.907
1NMC	N_ARG_292	NH1	N_GLU_277	OE1	2.656
1NMC	N_ARG_292	NH1	N_GLU_277	OE2	3.466
1NMC	N_ARG_300	NH1	N_ASP_324	OD2	3.693
1NMC	N_ARG_300	NH2	N_ASP_324	OD1	3.980
1NMC	N_ARG_304	NH1	N_GLU_286	OE2	2.662
1NMC	N_HIS_312	ND1	N_GLU_266	OE2	2.860
1NMC	N_ARG_364	NH1	N_GLU_375	OE2	2.972
1NMC	N_ARG_364	NH2	N_ASP_330	OD1	3.061
1NMC	N_ARG_364	NH2	N_ASP_330	OD2	2.772
1NMC	N_ARG_428	NH1	N_ASP_460	OD2	2.607
1NMC	N_ARG_428	NH2	N_GLU_433	OE1	3.420
1NMC	N_ARG_428	NH2	N_GLU_433	OE2	2.884
1NMC	N_LYS_432	NZ	H_ASP_56	OD1	2.750
1NMC	H_LYS_62	NZ	H_GLU_46	OE1	2.874
1NMC	H_LYS_62	NZ	H_GLU_46	OE2	3.520
1NMC	H_LYS_66	NZ	H_ASP_86	OD2	3.403
1NMC	H_ARG_94	NH2	H_ASP_101	OD1	3.582
1NMC	H_ARG_94	NH2	H_ASP_101	OD2	2.789
1NMC	H_ARG_100	NH1	H_ASP_100B	OD1	2.808
1NMC	H_ARG_100	NH1	H_ASP_100B	OD2	2.674
1NMC	H_ARG_100	NH2	H_ASP_100B	OD1	3.142
1NMC	L_ARG_61	NH1	L_GLU_79	OE1	3.308
1NMC	L_ARG_61	NH2	L_GLU_79	OE1	3.314
1NMC	L_ARG_61	NH2	L_ASP_82	OD1	2.650
1NMC	L_ARG_61	NH2	L_ASP_82	OD2	3.093
1NMC	L_ARG_107	NH2	L_ASP_108	OD2	3.871
1NMC	A_ARG_118	NH1	A_GLU_119	OE2	3.500
1NMC	A_ARG_118	NH2	A_GLU_119	OE2	3.987
1NMC	A_ARG_118	NH2	A_GLU_425	OE1	2.872
1NMC	A_ARG_118	NH2	A_GLU_425	OE2	3.182
1NMC	A_ARG_130	NH1	A_GLU_128	OE1	3.693
1NMC	A_ARG_130	NH1	A_GLU_128	OE2	3.809
1NMC	A_ARG_141	NH1	A_GLU_110	OE2	2.794
1NMC	A_ARG_152	NH2	A_ASP_151	OD1	3.884
1NMC	A_ARG_156	NH1	A_GLU_119	OE1	3.979
1NMC	A_ARG_156	NH2	A_GLU_119	OE1	3.323

1NMC	A_ARG_172	NH1	A_GLU_174	OE2	2.630
1NMC	A_ARG_189	NH2	A_ASP_125	OD1	2.839
1NMC	A_ARG_209	NH1	A_GLU_174	OE1	3.221
1NMC	A_ARG_209	NH1	A_GLU_174	OE2	3.350
1NMC	A_ARG_209	NH2	A_GLU_174	OE1	3.641
1NMC	A_ARG_209	NH2	A_GLU_174	OE2	3.567
1NMC	A_ARG_224	NH2	A_GLU_276	OE1	3.973
1NMC	A_ARG_224	NH2	A_GLU_276	OE2	2.791
1NMC	A_LYS_264	NZ	A_GLU_266	OE1	3.220
1NMC	A_LYS_273	NZ	A_ASP_339	OD1	3.419
1NMC	A_HIS_274	NE2	A_GLU_276	OE2	3.907
1NMC	A_ARG_292	NH1	A_GLU_277	OE1	2.655
1NMC	A_ARG_292	NH1	A_GLU_277	OE2	3.465
1NMC	A_ARG_300	NH1	A_ASP_324	OD2	3.694
1NMC	A_ARG_300	NH2	A_ASP_324	OD1	3.980
1NMC	A_ARG_304	NH1	A_GLU_286	OE2	2.663
1NMC	A_HIS_312	ND1	A_GLU_266	OE2	2.860
1NMC	A_ARG_364	NH1	A_GLU_375	OE2	2.972
1NMC	A_ARG_364	NH2	A_ASP_330	OD1	3.062
1NMC	A_ARG_364	NH2	A_ASP_330	OD2	2.772
1NMC	A_ARG_428	NH1	A_ASP_460	OD2	2.606
1NMC	A_ARG_428	NH2	A_GLU_433	OE1	3.421
1NMC	A_ARG_428	NH2	A_GLU_433	OE2	2.883
1NMC	A_LYS_432	NZ	B_ASP_56	OD1	2.750
1NMC	B_LYS_62	NZ	B_GLU_46	OE1	2.874
1NMC	B_LYS_62	NZ	B_GLU_46	OE2	3.520
1NMC	B_LYS_66	NZ	B_ASP_86	OD2	3.404
1NMC	B_ARG_94	NH2	B_ASP_101	OD1	3.582
1NMC	B_ARG_94	NH2	B_ASP_101	OD2	2.789
1NMC	B_ARG_100	NH1	B_ASP_100B	OD1	2.808
1NMC	B_ARG_100	NH1	B_ASP_100B	OD2	2.675
1NMC	B_ARG_100	NH2	B_ASP_100B	OD1	3.142
1NMC	C_ARG_61	NH1	C_GLU_79	OE1	3.308
1NMC	C_ARG_61	NH2	C_GLU_79	OE1	3.313
1NMC	C_ARG_61	NH2	C_ASP_82	OD1	2.649
1NMC	C_ARG_61	NH2	C_ASP_82	OD2	3.094
1NMC	C_ARG_107	NH2	C_ASP_108	OD2	3.871

Table 156: 1NMC-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1OB1	A_ARG_61	NH1	A_GLU_81	OE2	3.808
1OB1	A_ARG_61	NH1	A_ASP_82	OD1	2.619
1OB1	A_ARG_61	NH1	A_ASP_82	OD2	2.877
1OB1	A_ARG_61	NH2	A_GLU_81	OE2	3.763
1OB1	A_ARG_61	NH2	F_ASP_59	OD1	3.421
1OB1	A_ARG_61	NH2	F_ASP_59	OD2	2.223
1OB1	A_LYS_103	NZ	A_GLU_105	OE1	3.763
1OB1	A_ARG_154	NH2	A_GLU_184	OE2	2.981
1OB1	A_LYS_182	NZ	A_ASP_183	OD1	3.727
1OB1	A_LYS_182	NZ	A_GLU_186	OE1	3.077
1OB1	A_HIS_188	NE2	A_GLU_184	OE2	3.652
1OB1	A_ARG_210	NH2	A_GLU_186	OE2	3.268
1OB1	B_LYS_13	NZ	B_GLU_16	OE2	3.100
1OB1	B_ARG_66	NH1	B_ASP_86	OD1	3.867
1OB1	B_ARG_66	NH2	B_ASP_86	OD1	2.818
1OB1	B_ARG_66	NH2	B_ASP_86	OD2	3.197
1OB1	B_ARG_94	NH1	B_ASP_101	OD1	3.340
1OB1	B_ARG_94	NH1	B_ASP_101	OD2	2.759
1OB1	B_HIS_164	NE2	A_ASP_166	OD2	3.671
1OB1	B_LYS_205	NZ	B_ASP_207	OD1	3.102
1OB1	B_LYS_205	NZ	B_ASP_207	OD2	2.900
1OB1	B_LYS_209	NZ	B_GLU_211	OE1	3.918
1OB1	B_LYS_209	NZ	B_GLU_211	OE2	3.120
1OB1	C_LYS_9	NZ	C_GLU_24	OE2	3.557
1OB1	C_LYS_9	NZ	C_GLU_26	OE2	3.148
1OB1	C_LYS_10	NZ	B_ASP_100	OD1	2.437
1OB1	C_ARG_20	NH1	C_GLU_24	OE1	3.737
1OB1	C_ARG_20	NH2	C_GLU_24	OE1	2.454
1OB1	C_ARG_20	NH2	C_GLU_24	OE2	3.232
1OB1	C_HIS_21	NE2	C_GLU_27	OE2	2.879
1OB1	C_LYS_80	NZ	D_GLU_79	OE1	3.373
1OB1	C_LYS_80	NZ	D_GLU_81	OE1	3.553
1OB1	C_LYS_80	NZ	D_GLU_81	OE2	2.714
1OB1	D_ARG_61	NH1	D_GLU_81	OE2	3.991
1OB1	D_ARG_61	NH1	D_ASP_82	OD1	2.474
1OB1	D_ARG_61	NH1	D_ASP_82	OD2	2.804
1OB1	D_ARG_61	NH2	C_ASP_59	OD1	3.599
1OB1	D_ARG_61	NH2	C_ASP_59	OD2	2.460
1OB1	D_ARG_61	NH2	D_GLU_81	OE2	3.779
1OB1	D_LYS_103	NZ	D_GLU_105	OE1	3.861
1OB1	D_ARG_154	NH2	D_GLU_184	OE2	2.971
1OB1	D_LYS_182	NZ	D_ASP_183	OD1	3.753
1OB1	D_LYS_182	NZ	D_GLU_186	OE1	3.086
1OB1	D_HIS_188	NE2	D_GLU_184	OE2	3.651
1OB1	D_ARG_210	NH2	D_GLU_186	OE2	3.229
1OB1	E_LYS_13	NZ	E_GLU_16	OE2	3.102
1OB1	E_LYS_46	NZ	E_ASP_44	OD2	3.971
1OB1	E_ARG_66	NH1	E_ASP_86	OD1	3.843
1OB1	E_ARG_66	NH2	E_ASP_86	OD1	2.795
1OB1	E_ARG_66	NH2	E_ASP_86	OD2	3.186
1OB1	E_ARG_94	NH1	E_ASP_101	OD1	3.270
1OB1	E_ARG_94	NH1	E_ASP_101	OD2	2.697
1OB1	E_ARG_98	NH1	F_ASP_39	OD1	2.706
1OB1	E_HIS_164	NE2	D_ASP_166	OD2	3.790
1OB1	E_LYS_205	NZ	E_ASP_207	OD1	3.032
1OB1	E_LYS_205	NZ	E_ASP_207	OD2	2.849
1OB1	E_LYS_209	NZ	E_GLU_211	OE1	3.962

1OB1	E_LYS_209	NZ	E_GLU_211	OE2	3.194
1OB1	F_LYS_9	NZ	F_GLU_24	OE2	3.571
1OB1	F_LYS_9	NZ	F_GLU_26	OE2	3.085
1OB1	F_LYS_10	NZ	E_ASP_100	OD1	2.524
1OB1	F_ARG_20	NH1	F_GLU_24	OE1	3.734
1OB1	F_ARG_20	NH2	F_GLU_24	OE1	2.432
1OB1	F_ARG_20	NH2	F_GLU_24	OE2	3.245
1OB1	F_HIS_21	NE2	F_GLU_27	OE2	2.859
1OB1	F_LYS_80	NZ	A_GLU_79	OE1	3.743
1OB1	F_LYS_80	NZ	A_GLU_81	OE1	3.454
1OB1	F_LYS_80	NZ	A_GLU_81	OE2	2.796
1OB1	F_HIS_96	NE2	A_GLU_79	OE1	3.773

Table 157: 1OB1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1OP9	A_ARG_35	NH1	A_ASP_87	OD1	2.983
1OP9	A_ARG_35	NH2	A_GLU_43	OE2	2.955
1OP9	A_ARG_49	NH1	A_ASP_52	OD1	2.941
1OP9	A_ARG_49	NH1	A_ASP_52	OD2	3.907
1OP9	A_ARG_64	NH1	A_ASP_87	OD1	3.965
1OP9	A_ARG_64	NH1	A_ASP_87	OD2	2.867
1OP9	A_ARG_64	NH2	A_ASP_87	OD1	3.040
1OP9	A_ARG_64	NH2	A_ASP_87	OD2	3.424
1OP9	B_LYS_1	NZ	B_GLU_7	OE2	2.875
1OP9	B_LYS_97	NZ	A_GLU_97	OE1	2.570
1OP9	B_ARG_98	NH1	B_ASP_102	OD1	2.828
1OP9	B_ARG_98	NH1	B_ASP_102	OD2	3.807
1OP9	B_ARG_101	NH1	A_ASP_109	OD1	3.213
1OP9	B_ARG_101	NH1	A_ASP_109	OD2	2.829
1OP9	B_ARG_101	NH2	A_ASP_109	OD1	2.793
1OP9	B_ARG_101	NH2	A_ASP_109	OD2	3.765
1OP9	B_ARG_122	NH1	B_ASP_120	OD1	3.408

Table 158: 1OP9-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1OSP	L_ARG_61	NH1	L_GLU_81	OE2	3.794
1OSP	L_ARG_61	NH1	L_ASP_82	OD1	2.742
1OSP	L_ARG_61	NH1	L_ASP_82	OD2	3.281
1OSP	L_LYS_69	NZ	L_ASP_70	OD2	3.957
1OSP	L_LYS_147	NZ	L_GLU_154	OE1	3.795
1OSP	L_LYS_149	NZ	L_GLU_195	OE1	3.168
1OSP	L_LYS_149	NZ	L_GLU_195	OE2	3.070
1OSP	L_ARG_155	NH2	L_GLU_185	OE1	3.054
1OSP	L_ARG_155	NH2	L_GLU_185	OE2	3.470
1OSP	L_ARG_188	NH2	L_GLU_185	OE2	3.854
1OSP	L_LYS_199	NZ	L_ASP_110	OD1	3.945
1OSP	L_LYS_199	NZ	L_ASP_110	OD2	2.639
1OSP	L_ARG_211	NH1	L_GLU_187	OE2	3.387
1OSP	L_ARG_211	NH2	L_GLU_187	OE2	3.391
1OSP	H_ARG_38	NH1	H_GLU_46	OE1	2.774
1OSP	H_ARG_38	NH2	H_ASP_89	OD1	2.825
1OSP	H_ARG_97	NH2	H_GLU_27	OE1	3.273
1OSP	H_ARG_99	NH1	L_GLU_55	OE1	3.970
1OSP	H_ARG_99	NH1	L_GLU_55	OE2	2.686
1OSP	H_ARG_99	NH2	O_ASP_92	OD1	3.355
1OSP	H_ARG_99	NH2	O_ASP_92	OD2	2.514
1OSP	H_LYS_215	NZ	L_GLU_123	OE1	2.783
1OSP	H_LYS_215	NZ	L_GLU_123	OE2	3.079
1OSP	O_LYS_39	NZ	O_ASP_33	OD1	2.809
1OSP	O_LYS_46	NZ	L_ASP_66	OD2	3.087
1OSP	O_LYS_69	NZ	O_ASP_92	OD1	3.769
1OSP	O_LYS_103	NZ	O_GLU_128	OE2	3.115
1OSP	O_LYS_113	NZ	O_GLU_123	OE1	3.755
1OSP	O_LYS_129	NZ	O_GLU_131	OE1	3.327
1OSP	O_ARG_139	NH1	O_GLU_160	OE2	3.268
1OSP	O_ARG_139	NH2	O_GLU_160	OE2	2.962
1OSP	O_ARG_144	NH1	O_GLU_146	OE1	3.930
1OSP	O_ARG_144	NH1	O_GLU_146	OE2	2.637
1OSP	O_LYS_159	NZ	O_GLU_168	OE2	3.915
1OSP	O_LYS_175	NZ	O_GLU_174	OE2	3.895
1OSP	O_LYS_189	NZ	O_GLU_160	OE1	2.949
1OSP	O_LYS_189	NZ	O_GLU_160	OE2	3.302

Table 159: 1OSP-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1OW0	A_ARG_250	NH1	A_ASP_378	OD1	2.566
1OW0	A_ARG_250	NH1	A_ASP_378	OD2	3.422
1OW0	A_ARG_250	NH1	A_GLU_437	OE1	2.982
1OW0	A_ARG_250	NH2	A_ASP_378	OD1	3.947
1OW0	A_ARG_250	NH2	A_GLU_437	OE1	2.644
1OW0	A_ARG_372	NH1	A_GLU_403	OE1	2.406
1OW0	A_ARG_372	NH1	A_GLU_403	OE2	2.605
1OW0	A_ARG_372	NH2	A_GLU_403	OE1	3.805
1OW0	B_ARG_250	NH1	B_ASP_378	OD1	2.587
1OW0	B_ARG_250	NH1	B_ASP_378	OD2	3.428
1OW0	B_ARG_250	NH1	B_GLU_437	OE1	2.993
1OW0	B_ARG_250	NH2	B_ASP_378	OD1	3.931
1OW0	B_ARG_250	NH2	B_GLU_437	OE1	2.615
1OW0	B_ARG_372	NH1	B_GLU_403	OE1	2.384
1OW0	B_ARG_372	NH1	B_GLU_403	OE2	2.617
1OW0	B_ARG_372	NH2	B_GLU_403	OE1	3.789
1OW0	C_LYS_13	NZ	C_GLU_63	OE2	3.686
1OW0	C_ARG_52	NH2	C_GLU_49	OE1	2.995
1OW0	C_ARG_52	NH2	C_GLU_49	OE2	3.667
1OW0	C_LYS_55	NZ	C_GLU_59	OE1	3.649
1OW0	C_LYS_55	NZ	C_GLU_59	OE2	3.759
1OW0	C_HIS_68	ND1	C_ASP_21	OD2	3.825
1OW0	C_HIS_68	NE2	C_ASP_21	OD2	3.915
1OW0	C_LYS_139	NZ	C_GLU_142	OE2	3.692
1OW0	C_ARG_171	NH1	C_GLU_140	OE2	3.418
1OW0	C_ARG_171	NH2	C_GLU_140	OE2	3.168
1OW0	D_LYS_13	NZ	D_GLU_63	OE2	3.662
1OW0	D_ARG_52	NH2	D_GLU_49	OE1	3.006
1OW0	D_ARG_52	NH2	D_GLU_49	OE2	3.670
1OW0	D_LYS_55	NZ	D_GLU_59	OE1	3.602
1OW0	D_LYS_55	NZ	D_GLU_59	OE2	3.741
1OW0	D_HIS_68	ND1	D_ASP_21	OD2	3.833
1OW0	D_HIS_68	NE2	D_ASP_21	OD2	3.920
1OW0	D_LYS_139	NZ	D_GLU_142	OE2	3.692
1OW0	D_ARG_171	NH1	D_GLU_140	OE2	3.423
1OW0	D_ARG_171	NH2	D_GLU_140	OE2	3.181

Table 160: 1OW0-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1P2C	A_ARG_24	NH2	A_ASP_70	OD1	3.561
1P2C	A_ARG_24	NH2	A_ASP_70	OD2	3.968
1P2C	A_ARG_61	NH1	A_GLU_79	OE1	3.212
1P2C	A_ARG_61	NH1	A_ASP_82	OD1	3.355
1P2C	A_ARG_61	NH1	A_ASP_82	OD2	2.848
1P2C	A_ARG_61	NH2	A_GLU_79	OE1	2.589
1P2C	A_ARG_61	NH2	A_GLU_79	OE2	3.654
1P2C	A_LYS_149	NZ	A_GLU_195	OE1	3.222
1P2C	A_LYS_149	NZ	A_GLU_195	OE2	3.909
1P2C	A_ARG_155	NH1	A_GLU_185	OE1	3.712
1P2C	A_ARG_155	NH1	A_GLU_185	OE2	3.813
1P2C	A_ARG_155	NH2	A_GLU_185	OE1	3.966
1P2C	A_ARG_155	NH2	A_GLU_185	OE2	2.811
1P2C	A_LYS_183	NZ	A_GLU_187	OE2	2.959
1P2C	A_ARG_188	NH2	F_ASP_1518	OD1	2.778
1P2C	A_HIS_189	ND1	A_ASP_151	OD2	2.583
1P2C	A_LYS_199	NZ	A_ASP_110	OD1	2.789
1P2C	B_ARG_340	NH1	B_GLU_389	OE1	3.429
1P2C	B_LYS_363	NZ	B_GLU_346	OE1	3.861
1P2C	B_LYS_367	NZ	B_ASP_390	OD1	2.706
1P2C	B_LYS_367	NZ	B_ASP_390	OD2	3.064
1P2C	B_ARG_398	NH2	B_ASP_400	OD1	2.942
1P2C	B_ARG_398	NH2	B_ASP_400	OD2	3.446
1P2C	B_LYS_511	NZ	A_GLU_123	OE1	3.498
1P2C	C_LYS_601	NZ	C_GLU_607	OE1	2.618
1P2C	C_ARG_645	NH2	B_GLU_350	OE1	2.980
1P2C	C_ARG_668	NH1	B_GLU_350	OE1	3.355
1P2C	C_ARG_668	NH1	B_GLU_350	OE2	3.681
1P2C	C_ARG_668	NH2	B_GLU_335	OE2	3.090
1P2C	C_ARG_668	NH2	B_GLU_350	OE1	3.316
1P2C	C_ARG_668	NH2	B_GLU_350	OE2	2.404
1P2C	C_ARG_725	NH2	C_ASP_719	OD1	2.463
1P2C	C_ARG_725	NH2	C_ASP_719	OD2	3.674
1P2C	D_ARG_924	NH2	D_ASP_970	OD2	3.311
1P2C	D_ARG_961	NH1	D_GLU_981	OE2	3.455
1P2C	D_ARG_961	NH1	D_ASP_982	OD1	3.476
1P2C	D_ARG_961	NH1	D_ASP_982	OD2	3.040
1P2C	D_LYS_1049	NZ	D_GLU_1095	OE1	3.108
1P2C	D_ARG_1055	NH1	D_GLU_1085	OE1	3.789
1P2C	D_ARG_1055	NH1	D_GLU_1085	OE2	2.663
1P2C	D_ARG_1055	NH2	D_GLU_1085	OE2	2.728
1P2C	D_HIS_1089	ND1	D_ASP_1051	OD1	2.579
1P2C	D_LYS_1099	NZ	D_ASP_1010	OD2	2.865
1P2C	D_ARG_1111	NH1	D_GLU_1087	OE2	3.738
1P2C	E_LYS_1263	NZ	E_GLU_1246	OE2	3.563
1P2C	E_LYS_1267	NZ	E_ASP_1290	OD2	2.785
1P2C	E_ARG_1298	NH2	E_ASP_1300	OD1	2.640
1P2C	E_ARG_1298	NH2	E_ASP_1300	OD2	3.489
1P2C	E_LYS_1411	NZ	D_GLU_1023	OE1	3.897
1P2C	F_LYS_1501	NZ	F_GLU_1507	OE1	2.851
1P2C	F_ARG_1545	NH2	E_GLU_1250	OE1	2.861
1P2C	F_ARG_1561	NH1	F_ASP_1548	OD2	3.292
1P2C	F_ARG_1568	NH1	E_GLU_1250	OE1	3.580
1P2C	F_ARG_1568	NH1	E_GLU_1250	OE2	3.708
1P2C	F_ARG_1568	NH2	E_GLU_1235	OE2	2.833
1P2C	F_ARG_1568	NH2	E_GLU_1250	OE1	3.551
1P2C	F_ARG_1568	NH2	E_GLU_1250	OE2	2.418

1P2C	F_ARG_1625	NH2	F_ASP_1619	OD1	3.266
1P2C	F_ARG_1625	NH2	F_ASP_1619	OD2	3.611

Table 161: 1P2C-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1P4B	L_ARG_77	NH2	L_GLU_99	OE2	3.709
1P4B	L_ARG_77	NH2	L_ASP_100	OD1	2.914
1P4B	L_ARG_77	NH2	L_ASP_100	OD2	3.654
1P4B	H_ARG_45	NH1	H_ASP_100	OD1	2.724
1P4B	H_ARG_45	NH2	H_GLU_53	OE1	3.936
1P4B	H_ARG_45	NH2	H_GLU_53	OE2	3.140
1P4B	H_ARG_45	NH2	H_ASP_100	OD1	3.840
1P4B	H_ARG_77	NH1	H_ASP_100	OD1	3.338
1P4B	H_ARG_77	NH1	H_ASP_100	OD2	2.557
1P4B	H_ARG_77	NH2	H_ASP_100	OD1	3.920
1P4B	H_LYS_86	NZ	H_ASP_83	OD1	3.623
1P4B	P_HIS_2	NE2	H_ASP_65	OD1	3.248
1P4B	P_HIS_2	NE2	H_ASP_65	OD2	3.747
1P4B	P_ARG_9	NH1	H_ASP_137	OD1	2.804
1P4B	P_ARG_9	NH1	H_ASP_137	OD2	3.838
1P4B	P_ARG_9	NH2	H_ASP_137	OD1	3.399
1P4B	P_ARG_9	NH2	H_ASP_137	OD2	3.080
1P4B	P_ARG_9	NH2	P_GLU_6	OE1	3.138

Table 162: 1P4B-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1P7K	L_ARG_61	NH2	L_GLU_81	OE2	2.946
1P7K	L_ARG_61	NH2	L_ASP_82	OD1	2.757
1P7K	L_ARG_61	NH2	L_ASP_82	OD2	3.505
1P7K	L_LYS_149	NZ	L_GLU_195	OE1	3.555
1P7K	L_LYS_149	NZ	L_GLU_195	OE2	3.346
1P7K	L_ARG_155	NH1	L_GLU_185	OE2	3.215
1P7K	L_ARG_155	NH2	L_GLU_185	OE2	2.646
1P7K	H_LYS_40	NZ	H_GLU_85	OE1	3.931
1P7K	H_LYS_62	NZ	L_GLU_1	OE2	3.723
1P7K	H_LYS_66	NZ	H_ASP_86	OD1	2.877
1P7K	H_LYS_66	NZ	H_ASP_86	OD2	3.789
1P7K	H_ARG_94	NH2	H_ASP_101	OD1	3.280
1P7K	H_ARG_94	NH2	H_ASP_101	OD2	3.021
1P7K	H_LYS_208	NZ	L_GLU_123	OE1	3.517
1P7K	H_LYS_208	NZ	L_GLU_123	OE2	2.802
1P7K	A_ARG_61	NH2	A_ASP_82	OD1	2.829
1P7K	A_ARG_61	NH2	A_ASP_82	OD2	3.548
1P7K	A_LYS_103	NZ	A_ASP_165	OD1	3.013
1P7K	A_LYS_103	NZ	A_ASP_165	OD2	3.850
1P7K	A_LYS_149	NZ	A_GLU_195	OE2	3.766
1P7K	A_ARG_155	NH1	A_GLU_185	OE2	3.343
1P7K	A_ARG_155	NH2	A_GLU_185	OE2	3.044
1P7K	A_HIS_189	ND1	A_ASP_151	OD2	3.542
1P7K	A_LYS_199	NZ	A_ASP_110	OD1	3.716
1P7K	A_LYS_199	NZ	A_ASP_110	OD2	2.490
1P7K	B_LYS_62	NZ	A_GLU_1	OE2	2.848
1P7K	B_LYS_66	NZ	B_ASP_86	OD1	2.903
1P7K	B_LYS_66	NZ	B_ASP_86	OD2	3.739
1P7K	B_ARG_94	NH2	B_ASP_101	OD1	3.555
1P7K	B_ARG_94	NH2	B_ASP_101	OD2	2.792

Table 163: 1P7K-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1PG7	H_HIS_35	NE2	H_ASP_95	OD2	2.988
1PG7	H_ARG_38	NH1	H_ASP_86	OD1	2.891
1PG7	H_ARG_38	NH2	H_GLU_46	OE1	2.886
1PG7	H_ARG_38	NH2	H_GLU_46	OE2	3.488
1PG7	H_ARG_38	NH2	H_ASP_86	OD1	3.755
1PG7	H_LYS_62	NZ	H_GLU_46	OE1	3.013
1PG7	H_LYS_62	NZ	H_ASP_60	OD2	3.697
1PG7	H_ARG_66	NH2	H_ASP_86	OD1	3.366
1PG7	H_ARG_66	NH2	H_ASP_86	OD2	2.811
1PG7	H_ARG_83	NH1	H_GLU_85	OE2	3.159
1PG7	H_ARG_94	NH2	H_ASP_101	OD1	3.671
1PG7	H_ARG_94	NH2	H_ASP_101	OD2	2.700
1PG7	H_LYS_143	NZ	H_ASP_144	OD1	3.667
1PG7	H_LYS_209	NZ	L_GLU_123	OE1	2.828
1PG7	H_LYS_209	NZ	L_GLU_123	OE2	3.697
1PG7	L_HIS_35	NE2	L_ASP_95	OD2	2.860
1PG7	L_ARG_38	NH1	L_ASP_86	OD1	3.016
1PG7	L_ARG_38	NH2	L_GLU_46	OE1	3.146
1PG7	L_ARG_38	NH2	L_GLU_46	OE2	3.649
1PG7	L_ARG_38	NH2	L_GLU_85	OE2	3.601
1PG7	L_ARG_38	NH2	L_ASP_86	OD1	3.900
1PG7	L_ARG_66	NH2	L_ASP_86	OD1	3.391
1PG7	L_ARG_66	NH2	L_ASP_86	OD2	2.626
1PG7	L_ARG_83	NH2	L_GLU_85	OE1	3.938
1PG7	L_ARG_94	NH2	L_ASP_101	OD1	3.654
1PG7	L_ARG_94	NH2	L_ASP_101	OD2	2.818
1PG7	L_LYS_143	NZ	L_ASP_144	OD1	3.370
1PG7	L_LYS_209	NZ	M_GLU_123	OE1	2.829
1PG7	L_LYS_209	NZ	M_GLU_123	OE2	3.963
1PG7	L_LYS_210	NZ	L_GLU_212	OE1	3.335
1PG7	L_LYS_210	NZ	L_GLU_212	OE2	3.997
1PG7	L_LYS_30	NZ	X_GLU_95	OE1	3.476
1PG7	L_LYS_30	NZ	X_GLU_95	OE2	2.795
1PG7	L_ARG_61	NH2	L_ASP_82	OD1	3.019
1PG7	L_ARG_61	NH2	L_ASP_82	OD2	3.567
1PG7	L_LYS_149	NZ	L_GLU_195	OE1	3.477
1PG7	L_LYS_149	NZ	L_GLU_195	OE2	3.023
1PG7	L_LYS_183	NZ	L_GLU_187	OE2	2.996
1PG7	L_HIS_189	ND1	L_ASP_151	OD2	3.757
1PG7	M_ARG_24	NH2	M_ASP_70	OD1	3.617
1PG7	M_ARG_24	NH2	M_ASP_70	OD2	2.951
1PG7	M_ARG_27	NH1	M_GLU_93	OE2	3.544
1PG7	M_LYS_30	NZ	Z_GLU_95	OE2	3.166
1PG7	M_ARG_61	NH2	M_GLU_81	OE2	3.691
1PG7	M_ARG_61	NH2	M_ASP_82	OD1	3.010
1PG7	M_ARG_61	NH2	M_ASP_82	OD2	3.569
1PG7	M_LYS_149	NZ	M_GLU_195	OE1	2.679
1PG7	M_LYS_183	NZ	M_GLU_187	OE1	3.114
1PG7	M_LYS_183	NZ	M_GLU_187	OE2	2.640
1PG7	M_LYS_188	NZ	M_ASP_185	OD1	3.378
1PG7	M_HIS_189	ND1	M_ASP_151	OD2	3.163
1PG7	W_ARG_24	NH2	W_ASP_69	OD1	2.965
1PG7	W_HIS_42	ND1	W_GLU_38	OE2	3.572
1PG7	W_ARG_61	NH2	W_ASP_82	OD1	2.800
1PG7	W_ARG_61	NH2	W_ASP_82	OD2	3.379
1PG7	W_LYS_111	NZ	W_GLU_197	OE1	3.487
1PG7	W_LYS_111	NZ	W_GLU_197	OE2	3.605

1PG7	W_LYS_150	NZ	W_GLU_202	OE1	3.697
1PG7	W_LYS_150	NZ	W_GLU_202	OE2	2.961
1PG7	W_HIS_193	NE2	W_GLU_202	OE1	2.915
1PG7	W_HIS_193	NE2	W_GLU_202	OE2	3.635
1PG7	X_HIS_32	NE2	X_ASP_96	OD1	3.692
1PG7	X_LYS_62	NZ	X_GLU_46	OE2	3.660
1PG7	X_LYS_64	NZ	X_ASP_65	OD2	3.444
1PG7	X_LYS_66	NZ	X_ASP_86	OD1	2.694
1PG7	X_LYS_66	NZ	X_ASP_86	OD2	3.927
1PG7	X_ARG_94	NH1	H_GLU_53	OE1	3.386
1PG7	X_ARG_94	NH1	H_GLU_53	OE2	3.321
1PG7	X_ARG_94	NH2	H_GLU_53	OE1	3.937
1PG7	X_ARG_94	NH2	H_GLU_53	OE2	2.866
1PG7	X_ARG_94	NH2	X_ASP_101	OD1	3.743
1PG7	X_ARG_94	NH2	X_ASP_101	OD2	2.609
1PG7	X_ARG_98	NH2	H_ASP_95	OD1	2.990
1PG7	X_ARG_98	NH2	H_ASP_95	OD2	3.561
1PG7	X_HIS_100	NE2	X_ASP_96	OD1	3.548
1PG7	X_HIS_100	NE2	X_ASP_96	OD2	3.817
1PG7	X_LYS_143	NZ	W_GLU_125	OE2	2.675
1PG7	X_HIS_164	NE2	W_GLU_139	OE2	3.801
1PG7	X_LYS_208	NZ	W_GLU_124	OE2	2.927
1PG7	Y_ARG_24	NH1	Y_ASP_69	OD2	3.633
1PG7	Y_HIS_42	ND1	Y_GLU_38	OE2	2.936
1PG7	Y_ARG_61	NH2	Y_GLU_81	OE1	3.193
1PG7	Y_ARG_61	NH2	Y_ASP_82	OD1	2.746
1PG7	Y_ARG_61	NH2	Y_ASP_82	OD2	3.675
1PG7	Y_LYS_111	NZ	Y_GLU_197	OE1	3.272
1PG7	Y_LYS_111	NZ	Y_GLU_197	OE2	2.744
1PG7	Y_LYS_150	NZ	Y_GLU_202	OE2	3.486
1PG7	Y_LYS_170	NZ	Y_GLU_139	OE1	3.781
1PG7	Y_HIS_193	NE2	Y_GLU_202	OE1	3.285
1PG7	Y_HIS_193	NE2	Y_GLU_202	OE2	3.532
1PG7	Z_LYS_66	NZ	Z_ASP_86	OD2	2.953
1PG7	Z_ARG_94	NH1	I_GLU_53	OE1	3.259
1PG7	Z_ARG_94	NH1	I_GLU_53	OE2	3.931
1PG7	Z_ARG_94	NH1	Z_ASP_101	OD1	3.771
1PG7	Z_ARG_94	NH1	Z_ASP_101	OD2	2.810
1PG7	Z_ARG_94	NH2	I_GLU_53	OE1	2.918
1PG7	Z_ARG_94	NH2	I_GLU_53	OE2	2.525
1PG7	Z_ARG_98	NH2	I_ASP_95	OD1	3.168
1PG7	Z_ARG_98	NH2	I_ASP_95	OD2	3.781
1PG7	Z_HIS_100	NE2	Z_ASP_96	OD1	3.911
1PG7	Z_HIS_100	NE2	Z_ASP_96	OD2	3.774
1PG7	Z_LYS_143	NZ	Y_GLU_125	OE2	2.901
1PG7	Z_LYS_208	NZ	Y_GLU_124	OE2	3.302

Table 164: 1PG7-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1PSK	L_ARG_60	NH1	L_GLU_80	OE1	3.760
1PSK	L_ARG_60	NH1	L_GLU_80	OE2	3.891
1PSK	L_ARG_60	NH1	L_ASP_81	OD2	3.537
1PSK	L_ARG_60	NH2	L_GLU_80	OE1	3.568
1PSK	L_ARG_60	NH2	L_GLU_80	OE2	3.225
1PSK	L_ARG_60	NH2	L_ASP_81	OD1	3.069
1PSK	L_ARG_60	NH2	L_ASP_81	OD2	3.788
1PSK	L_LYS_141	NZ	L_ASP_142	OD2	3.990
1PSK	L_LYS_148	NZ	L_GLU_194	OE2	2.802
1PSK	L_ARG_154	NH2	L_GLU_184	OE1	3.691
1PSK	L_HIS_188	ND1	L_ASP_150	OD2	2.717
1PSK	L_LYS_198	NZ	L_ASP_142	OD2	3.973
1PSK	H_LYS_38	NZ	H_ASP_90	OD1	3.879
1PSK	H_ARG_84	NH1	H_GLU_82	OE1	3.149
1PSK	H_ARG_84	NH2	H_GLU_82	OE1	3.059
1PSK	H_ARG_84	NH2	H_GLU_82	OE2	3.244
1PSK	H_LYS_99	NZ	H_ASP_102	OD2	3.135

Table 165: 1PSK-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1PZ5	A_ARG_24	NH1	A_ASP_70	OD1	3.050
1PZ5	A_ARG_24	NH1	A_ASP_70	OD2	3.589
1PZ5	A_HIS_27D	ND1	A_ASP_28	OD1	3.297
1PZ5	A_HIS_27D	ND1	A_ASP_28	OD2	3.192
1PZ5	A_HIS_27D	NE2	C_ASP_2	OD1	2.720
1PZ5	A_LYS_39	NZ	A_GLU_81	OE1	3.469
1PZ5	A_ARG_61	NH1	A_ASP_82	OD1	2.720
1PZ5	A_ARG_61	NH1	A_ASP_82	OD2	3.796
1PZ5	A_ARG_61	NH2	A_GLU_79	OE1	3.814
1PZ5	A_ARG_61	NH2	A_GLU_79	OE2	3.855
1PZ5	A_ARG_61	NH2	A_ASP_82	OD1	3.374
1PZ5	A_ARG_61	NH2	A_ASP_82	OD2	2.955
1PZ5	A_ARG_77	NH1	A_ASP_60	OD2	3.886
1PZ5	A_LYS_147	NZ	A_GLU_154	OE1	3.998
1PZ5	A_LYS_149	NZ	A_GLU_195	OE1	2.953
1PZ5	A_LYS_149	NZ	A_GLU_195	OE2	3.630
1PZ5	A_LYS_183	NZ	A_GLU_187	OE1	2.839
1PZ5	A_LYS_183	NZ	A_GLU_187	OE2	2.663
1PZ5	A_ARG_188	NH1	A_ASP_184	OD1	3.586
1PZ5	A_ARG_188	NH1	A_GLU_185	OE1	3.143
1PZ5	A_ARG_188	NH2	A_ASP_184	OD1	2.987
1PZ5	A_HIS_189	ND1	A_ASP_151	OD1	3.048
1PZ5	A_HIS_189	NE2	A_GLU_185	OE2	2.825
1PZ5	A_LYS_199	NZ	A_ASP_110	OD1	3.069
1PZ5	A_LYS_199	NZ	A_ASP_110	OD2	3.840
1PZ5	B_ARG_38	NH1	B_GLU_46	OE2	2.914
1PZ5	B_ARG_38	NH1	B_ASP_86	OD1	3.910
1PZ5	B_ARG_38	NH2	B_ASP_86	OD1	2.823
1PZ5	B_ARG_52	NH1	B_GLU_50	OE2	2.848
1PZ5	B_HIS_58	ND1	B_GLU_50	OE2	3.633
1PZ5	B_ARG_66	NH1	B_ASP_86	OD1	3.057
1PZ5	B_ARG_66	NH1	B_ASP_86	OD2	3.525
1PZ5	B_ARG_66	NH2	B_ASP_86	OD1	3.778
1PZ5	B_ARG_66	NH2	B_ASP_86	OD2	2.847
1PZ5	B_ARG_71	NH1	B_ASP_73	OD2	3.288
1PZ5	B_ARG_94	NH1	B_ASP_101	OD1	3.495
1PZ5	B_ARG_94	NH1	B_ASP_101	OD2	2.627
1PZ5	B_ARG_164	NH1	A_ASP_167	OD2	3.218
1PZ5	B_ARG_164	NH2	A_ASP_167	OD2	3.712
1PZ5	B_LYS_208	NZ	A_GLU_123	OE1	2.648
1PZ5	B_LYS_208	NZ	A_GLU_123	OE2	3.713

Table 166: 1PZ5-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1Q9K	A_ARG_54	NH2	A_ASP_60	OD2	3.319
1Q9K	A_ARG_61	NH1	A_ASP_82	OD1	2.801
1Q9K	A_ARG_61	NH1	A_ASP_82	OD2	3.363
1Q9K	A_ARG_61	NH2	A_GLU_81	OE1	3.964
1Q9K	A_ARG_95	NH2	B_ASP_95	OD1	3.932
1Q9K	A_ARG_95	NH2	B_ASP_95	OD2	3.226
1Q9K	A_LYS_146	NZ	A_GLU_153	OE1	3.709
1Q9K	A_LYS_148	NZ	A_GLU_194	OE1	3.150
1Q9K	A_LYS_148	NZ	A_GLU_194	OE2	3.820
1Q9K	A_LYS_168	NZ	A_ASP_166	OD1	2.237
1Q9K	A_LYS_168	NZ	A_ASP_166	OD2	3.163
1Q9K	A_HIS_188	ND1	A_ASP_150	OD2	2.831
1Q9K	A_LYS_198	NZ	A_ASP_109	OD1	3.804
1Q9K	A_LYS_198	NZ	A_ASP_109	OD2	3.067
1Q9K	B_ARG_38	NH1	B_ASP_86	OD2	2.774
1Q9K	B_ARG_38	NH2	B_GLU_46	OE1	3.263
1Q9K	B_ARG_38	NH2	B_ASP_86	OD2	3.827
1Q9K	B_ARG_52	NH1	B_GLU_56	OE2	3.179
1Q9K	B_ARG_52	NH2	B_GLU_56	OE2	2.529
1Q9K	B_ARG_64	NH1	B_ASP_86	OD1	2.817
1Q9K	B_ARG_64	NH1	B_ASP_86	OD2	3.706
1Q9K	B_ARG_64	NH2	B_ASP_86	OD1	3.623
1Q9K	B_ARG_64	NH2	B_ASP_86	OD2	3.040
1Q9K	B_HIS_162	NE2	A_ASP_166	OD1	3.847

Table 167: 1Q9K-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1Q9L	B_ARG_38	NH1	B_ASP_86	OD2	2.938
1Q9L	B_ARG_38	NH2	B_GLU_46	OE1	3.214
1Q9L	B_ARG_38	NH2	B_GLU_46	OE2	3.981
1Q9L	B_ARG_38	NH2	B_ASP_86	OD2	3.814
1Q9L	B_ARG_52	NH1	B_GLU_56	OE2	3.639
1Q9L	B_ARG_52	NH2	B_GLU_56	OE2	2.657
1Q9L	B_ARG_64	NH1	B_ASP_86	OD1	2.799
1Q9L	B_ARG_64	NH2	B_ASP_86	OD1	3.122
1Q9L	B_ARG_64	NH2	B_ASP_86	OD2	2.942
1Q9L	B_HIS_96	ND1	B_ASP_97	OD2	2.998
1Q9L	B_LYS_113	NZ	B_ASP_171	OD2	3.940
1Q9L	B_LYS_206	NZ	A_GLU_122	OE2	3.242
1Q9L	D_ARG_38	NH1	D_ASP_86	OD2	3.041
1Q9L	D_ARG_38	NH2	D_GLU_46	OE1	2.944
1Q9L	D_ARG_38	NH2	D_GLU_46	OE2	3.965
1Q9L	D_ARG_52	NH1	D_GLU_56	OE2	3.147
1Q9L	D_ARG_52	NH2	D_GLU_56	OE2	2.760
1Q9L	D_ARG_64	NH1	D_ASP_86	OD1	2.602
1Q9L	D_ARG_64	NH1	D_ASP_86	OD2	3.534
1Q9L	D_ARG_64	NH2	D_ASP_86	OD1	3.533
1Q9L	D_ARG_64	NH2	D_ASP_86	OD2	2.877
1Q9L	D_HIS_96	ND1	D_ASP_97	OD2	3.015
1Q9L	D_HIS_96	NE2	D_ASP_97	OD2	3.962
1Q9L	D_ARG_100B	NH1	B_GLU_85	OE1	3.618
1Q9L	D_ARG_100B	NH1	B_GLU_85	OE2	3.115
1Q9L	D_HIS_162	NE2	C_ASP_166	OD1	3.172
1Q9L	A_LYS_24	NZ	A_ASP_70	OD2	3.888
1Q9L	A_LYS_39	NZ	A_GLU_81	OE2	3.778
1Q9L	A_ARG_54	NH2	A_ASP_60	OD2	3.464
1Q9L	A_ARG_61	NH1	A_ASP_82	OD1	3.170
1Q9L	A_ARG_61	NH1	A_ASP_82	OD2	2.681
1Q9L	A_ARG_61	NH2	A_GLU_81	OE1	3.824
1Q9L	A_ARG_95	NH2	B_ASP_95	OD2	3.284
1Q9L	A_LYS_102	NZ	A_GLU_104	OE2	2.656
1Q9L	A_LYS_146	NZ	A_GLU_194	OE2	3.634
1Q9L	A_LYS_148	NZ	A_GLU_194	OE1	3.229
1Q9L	A_LYS_148	NZ	A_GLU_194	OE2	3.316
1Q9L	A_ARG_154	NH2	A_GLU_184	OE1	2.873
1Q9L	A_LYS_168	NZ	A_ASP_166	OD1	3.711
1Q9L	A_LYS_168	NZ	A_ASP_166	OD2	3.118
1Q9L	A_ARG_187	NH1	A_GLU_184	OE2	2.612
1Q9L	A_HIS_188	ND1	A_ASP_150	OD2	2.879
1Q9L	A_HIS_188	NE2	A_GLU_184	OE1	3.087
1Q9L	A_HIS_188	NE2	A_GLU_184	OE2	3.294
1Q9L	A_LYS_198	NZ	A_ASP_109	OD2	3.680
1Q9L	C_LYS_39	NZ	C_GLU_81	OE1	3.843
1Q9L	C_ARG_54	NH2	C_ASP_60	OD2	2.952
1Q9L	C_ARG_61	NH1	C_ASP_82	OD1	2.562
1Q9L	C_ARG_61	NH1	C_ASP_82	OD2	2.760
1Q9L	C_ARG_95	NH2	D_ASP_95	OD2	3.309
1Q9L	C_LYS_102	NZ	C_GLU_104	OE2	3.348
1Q9L	C_LYS_148	NZ	C_GLU_194	OE1	2.541
1Q9L	C_LYS_148	NZ	C_GLU_194	OE2	3.918
1Q9L	C_ARG_154	NH1	C_GLU_184	OE1	3.911
1Q9L	C_LYS_168	NZ	C_ASP_166	OD1	2.581
1Q9L	C_LYS_168	NZ	C_ASP_166	OD2	2.492
1Q9L	C_ARG_187	NH1	C_GLU_184	OE2	2.720

1Q9L	C_HIS_188	ND1	C_ASP_150	OD2	2.739
1Q9L	C_HIS_188	NE2	C_GLU_184	OE1	3.004
1Q9L	C_HIS_188	NE2	C_GLU_184	OE2	3.759

Table 168: 1Q9L-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1Q9O	B_ARG_38	NH1	B_GLU_46	OE1	3.016
1Q9O	B_ARG_38	NH1	B_GLU_46	OE2	3.916
1Q9O	B_ARG_38	NH1	B_ASP_86	OD2	3.956
1Q9O	B_ARG_38	NH2	B_ASP_86	OD2	2.860
1Q9O	B_ARG_52	NH1	B_GLU_56	OE2	2.831
1Q9O	B_ARG_52	NH2	B_GLU_56	OE2	3.407
1Q9O	B_ARG_64	NH1	B_ASP_86	OD1	3.248
1Q9O	B_ARG_64	NH1	B_ASP_86	OD2	2.899
1Q9O	B_ARG_64	NH2	B_ASP_86	OD1	2.692
1Q9O	B_ARG_64	NH2	B_ASP_86	OD2	3.771
1Q9O	B_ARG_83	NH2	B_GLU_85	OE1	2.612
1Q9O	B_ARG_94	NH1	B_ASP_100D	OD1	3.613
1Q9O	B_ARG_94	NH1	B_ASP_100D	OD2	2.755
1Q9O	B_ARG_100	NH1	A_GLU_55	OE1	3.447
1Q9O	B_ARG_100	NH1	A_GLU_55	OE2	3.466
1Q9O	B_ARG_100	NH2	A_GLU_55	OE1	3.378
1Q9O	B_ARG_100	NH2	A_GLU_55	OE2	2.999
1Q9O	B_LYS_206	NZ	A_GLU_122	OE2	3.964
1Q9O	D_ARG_38	NH1	D_ASP_86	OD2	2.888
1Q9O	D_ARG_38	NH2	D_GLU_46	OE1	3.098
1Q9O	D_ARG_38	NH2	D_ASP_86	OD2	3.945
1Q9O	D_ARG_52	NH1	D_GLU_56	OE2	3.504
1Q9O	D_ARG_52	NH2	D_GLU_56	OE2	3.047
1Q9O	D_ARG_64	NH1	D_ASP_86	OD1	2.898
1Q9O	D_ARG_64	NH1	D_ASP_86	OD2	3.621
1Q9O	D_ARG_64	NH2	D_ASP_86	OD1	3.767
1Q9O	D_ARG_64	NH2	D_ASP_86	OD2	3.117
1Q9O	D_ARG_83	NH2	D_GLU_85	OE1	3.293
1Q9O	D_ARG_83	NH2	D_GLU_85	OE2	3.082
1Q9O	D_ARG_94	NH2	D_ASP_100D	OD1	2.763
1Q9O	D_ARG_94	NH2	D_ASP_100D	OD2	3.701
1Q9O	D_ARG_100	NH1	C_GLU_55	OE1	3.493
1Q9O	D_ARG_100	NH1	C_GLU_55	OE2	3.040
1Q9O	D_ARG_100	NH2	C_GLU_55	OE1	3.391
1Q9O	D_ARG_100	NH2	C_GLU_55	OE2	3.047
1Q9O	A_ARG_54	NH1	A_ASP_60	OD2	3.439
1Q9O	A_ARG_61	NH1	A_ASP_82	OD1	3.512
1Q9O	A_ARG_61	NH1	A_ASP_82	OD2	2.892
1Q9O	A_ARG_61	NH2	A_GLU_81	OE1	3.882
1Q9O	A_ARG_61	NH2	A_ASP_82	OD1	2.949
1Q9O	A_ARG_61	NH2	A_ASP_82	OD2	3.770
1Q9O	A_ARG_95	NH2	B_ASP_95	OD1	2.958
1Q9O	A_ARG_95	NH2	B_ASP_95	OD2	3.717
1Q9O	A_LYS_102	NZ	A_GLU_104	OE1	2.779
1Q9O	A_LYS_146	NZ	A_GLU_194	OE2	2.676
1Q9O	A_LYS_148	NZ	A_GLU_194	OE1	3.510
1Q9O	A_LYS_182	NZ	A_GLU_186	OE1	2.761
1Q9O	A_LYS_182	NZ	A_GLU_186	OE2	3.253
1Q9O	A_HIS_188	ND1	A_ASP_150	OD2	2.674
1Q9O	A_LYS_198	NZ	A_ASP_109	OD1	3.691
1Q9O	A_LYS_198	NZ	A_ASP_109	OD2	3.683
1Q9O	C_ARG_61	NH1	C_ASP_82	OD1	2.516
1Q9O	C_ARG_61	NH1	C_ASP_82	OD2	3.228
1Q9O	C_ARG_61	NH2	C_GLU_81	OE2	3.883
1Q9O	C_ARG_95	NH2	D_ASP_95	OD1	3.672
1Q9O	C_ARG_95	NH2	D_ASP_95	OD2	2.974
1Q9O	C_LYS_102	NZ	C_GLU_104	OE1	3.839

1Q9O	C_LYS_148	NZ	C_GLU_194	OE1	2.914
1Q9O	C_LYS_148	NZ	C_GLU_194	OE2	3.816

Table 169: 1Q9O-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1Q9W	A_ARG_61	NH2	A_ASP_82	OD1	2.327
1Q9W	A_ARG_61	NH2	A_ASP_82	OD2	2.627
1Q9W	A_ARG_95	NH2	B_ASP_95	OD1	2.949
1Q9W	A_ARG_95	NH2	B_ASP_95	OD2	3.845
1Q9W	A_LYS_102	NZ	A_GLU_104	OE1	3.845
1Q9W	A_LYS_146	NZ	A_GLU_153	OE2	3.713
1Q9W	A_LYS_148	NZ	A_GLU_194	OE1	2.859
1Q9W	A_ARG_154	NH1	A_GLU_184	OE1	3.813
1Q9W	A_ARG_154	NH2	A_GLU_184	OE1	3.493
1Q9W	A_ARG_154	NH2	A_GLU_184	OE2	2.753
1Q9W	A_ARG_187	NH1	A_GLU_184	OE2	3.961
1Q9W	A_ARG_187	NH2	A_GLU_184	OE2	2.743
1Q9W	A_HIS_188	ND1	A_ASP_150	OD2	2.924
1Q9W	B_ARG_38	NH1	B_ASP_86	OD2	2.826
1Q9W	B_ARG_38	NH2	B_GLU_46	OE1	3.067
1Q9W	B_ARG_38	NH2	B_ASP_86	OD2	3.866
1Q9W	B_ARG_52	NH1	B_GLU_56	OE2	3.024
1Q9W	B_ARG_52	NH2	B_GLU_56	OE2	3.531
1Q9W	B_ARG_64	NH1	B_ASP_86	OD1	2.680
1Q9W	B_ARG_64	NH1	B_ASP_86	OD2	3.618
1Q9W	B_ARG_64	NH2	B_ASP_86	OD1	3.562
1Q9W	B_ARG_64	NH2	B_ASP_86	OD2	3.048
1Q9W	B_ARG_83	NH2	B_GLU_85	OE1	3.148
1Q9W	B_ARG_83	NH2	B_GLU_85	OE2	3.088
1Q9W	B_ARG_94	NH2	B_ASP_100D	OD1	2.686
1Q9W	B_ARG_94	NH2	B_ASP_100D	OD2	3.453
1Q9W	B_ARG_100	NH1	A_GLU_55	OE1	2.615
1Q9W	B_ARG_100	NH1	A_GLU_55	OE2	3.657
1Q9W	B_ARG_100	NH2	A_GLU_55	OE1	2.891
1Q9W	B_ARG_100	NH2	A_GLU_55	OE2	3.820
1Q9W	C_LYS_24	NZ	C_ASP_70	OD1	3.583
1Q9W	C_ARG_61	NH2	C_ASP_82	OD1	2.769
1Q9W	C_ARG_61	NH2	C_ASP_82	OD2	3.531
1Q9W	C_ARG_95	NH2	D_ASP_95	OD1	2.929
1Q9W	C_ARG_95	NH2	D_ASP_95	OD2	3.831
1Q9W	C_LYS_106	NZ	C_GLU_17	OE1	2.879
1Q9W	C_LYS_148	NZ	C_GLU_194	OE1	2.881
1Q9W	C_LYS_148	NZ	C_GLU_194	OE2	3.569
1Q9W	C_ARG_154	NH2	C_GLU_184	OE1	2.757
1Q9W	C_LYS_168	NZ	C_ASP_166	OD1	3.032
1Q9W	C_LYS_168	NZ	C_ASP_166	OD2	2.758
1Q9W	C_ARG_187	NH1	C_GLU_184	OE2	2.691
1Q9W	C_ARG_187	NH2	C_GLU_184	OE2	2.833
1Q9W	D_ARG_38	NH1	D_ASP_86	OD2	2.855
1Q9W	D_ARG_38	NH2	D_GLU_46	OE1	3.105
1Q9W	D_ARG_38	NH2	D_ASP_86	OD2	3.747
1Q9W	D_ARG_52	NH1	D_GLU_56	OE2	3.012
1Q9W	D_ARG_52	NH2	D_GLU_56	OE2	3.725
1Q9W	D_ARG_64	NH1	D_ASP_86	OD1	3.569
1Q9W	D_ARG_64	NH1	D_ASP_86	OD2	3.180
1Q9W	D_ARG_94	NH2	D_ASP_100D	OD1	2.639
1Q9W	D_ARG_94	NH2	D_ASP_100D	OD2	3.620
1Q9W	D_ARG_100	NH1	C_GLU_55	OE1	3.356
1Q9W	D_ARG_100	NH1	C_GLU_55	OE2	3.002
1Q9W	D_ARG_100	NH2	C_GLU_55	OE1	3.373
1Q9W	D_ARG_100	NH2	C_GLU_55	OE2	3.045

Table 170: 1Q9W-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1QBL	L_ARG_61	NH2	L_ASP_82	OD1	2.786
1QBL	L_ARG_61	NH2	L_ASP_82	OD2	3.721
1QBL	L_LYS_147	NZ	L_GLU_154	OE1	3.338
1QBL	L_LYS_149	NZ	L_GLU_195	OE1	3.827
1QBL	L_LYS_149	NZ	L_GLU_195	OE2	2.952
1QBL	L_ARG_155	NH1	L_GLU_185	OE1	3.191
1QBL	L_ARG_155	NH1	L_GLU_185	OE2	3.323
1QBL	L_ARG_155	NH2	L_GLU_185	OE1	3.979
1QBL	L_ARG_155	NH2	L_GLU_185	OE2	2.777
1QBL	L_HIS_189	ND1	L_ASP_151	OD2	2.720
1QBL	L_HIS_189	NE2	L_GLU_185	OE2	3.448
1QBL	L_LYS_199	NZ	L_ASP_110	OD2	3.257
1QBL	H_LYS_63	NZ	H_GLU_46	OE1	3.796
1QBL	H_LYS_67	NZ	H_ASP_90	OD2	3.852
1QBL	H_LYS_212	NZ	L_GLU_123	OE1	3.581

Table 171: 1QBL-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1QBM	L_ARG_61	NH2	L_GLU_81	OE2	2.739
1QBM	L_ARG_61	NH2	L_ASP_82	OD1	2.797
1QBM	L_ARG_61	NH2	L_ASP_82	OD2	3.689
1QBM	L_LYS_107	NZ	L_GLU_17	OE1	3.352
1QBM	L_LYS_107	NZ	L_GLU_17	OE2	3.277
1QBM	L_LYS_142	NZ	L_ASP_143	OD1	3.711
1QBM	L_LYS_147	NZ	L_GLU_154	OE2	2.702
1QBM	L_LYS_149	NZ	L_GLU_195	OE1	3.463
1QBM	L_LYS_149	NZ	L_GLU_195	OE2	3.031
1QBM	L_ARG_155	NH1	L_GLU_185	OE1	3.258
1QBM	L_ARG_155	NH1	L_GLU_185	OE2	2.899
1QBM	L_ARG_155	NH2	L_GLU_185	OE2	2.603
1QBM	L_HIS_189	ND1	L_ASP_151	OD2	2.710
1QBM	H_LYS_63	NZ	H_GLU_46	OE1	3.520
1QBM	H_LYS_67	NZ	H_ASP_90	OD1	3.236
1QBM	H_LYS_67	NZ	H_ASP_90	OD2	3.485
1QBM	H_LYS_212	NZ	L_GLU_123	OE1	2.762
1QBM	H_LYS_212	NZ	L_GLU_123	OE2	3.773

Table 172: 1QBM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1QGC	1_LYS_41	NZ	1_GLU_175	OE2	3.394
1QGC	1_HIS_57	NE2	1_ASP_59	OD2	3.737
1QGC	1_ARG_114	NH2	1_GLU_77	OE2	2.895
1QGC	1_ARG_124	NH1	2_ASP_41	OD1	3.642
1QGC	1_ARG_124	NH1	2_ASP_41	OD2	2.877
1QGC	1_ARG_124	NH2	2_ASP_41	OD1	3.740
1QGC	1_ARG_179	NH1	1_ASP_37	OD1	3.088
1QGC	1_ARG_179	NH2	1_ASP_37	OD1	3.997
1QGC	1_ARG_179	NH2	1_GLU_77	OE2	3.665
1QGC	1_LYS_181	NZ	1_ASP_37	OD1	3.047
1QGC	1_LYS_181	NZ	1_ASP_37	OD2	3.465
1QGC	1_LYS_181	NZ	1_GLU_77	OE2	3.717
1QGC	2_ARG_54	NH1	2_GLU_59	OE1	3.984
1QGC	2_ARG_54	NH1	2_GLU_59	OE2	3.432
1QGC	2_ARG_54	NH2	2_GLU_59	OE1	3.031
1QGC	2_ARG_54	NH2	2_GLU_59	OE2	3.842
1QGC	2_LYS_88	NZ	2_GLU_86	OE1	3.903
1QGC	2_ARG_102	NH1	2_GLU_40	OE1	2.629
1QGC	2_ARG_102	NH2	2_ASP_41	OD1	2.799
1QGC	2_ARG_102	NH2	2_ASP_41	OD2	3.402
1QGC	2_HIS_157	NE2	2_ASP_106	OD1	2.653
1QGC	2_HIS_157	NE2	2_ASP_106	OD2	3.740
1QGC	2_ARG_167	NH2	3_ASP_166	OD1	2.757
1QGC	2_ARG_167	NH2	3_ASP_166	OD2	2.777
1QGC	2_HIS_174	ND1	2_ASP_169	OD1	3.562
1QGC	2_HIS_174	ND1	2_ASP_169	OD2	2.877
1QGC	2_HIS_174	NE2	2_GLU_128	OE1	2.739
1QGC	2_HIS_174	NE2	2_GLU_128	OE2	3.273
1QGC	2_LYS_198	NZ	2_ASP_68	OD1	3.053
1QGC	2_LYS_198	NZ	2_ASP_68	OD2	3.315
1QGC	3_LYS_20	NZ	3_ASP_18	OD2	2.699
1QGC	3_ARG_120	NH1	3_GLU_146	OE2	2.906
1QGC	3_ARG_120	NH2	3_ASP_148	OD2	2.596
1QGC	3_LYS_193	NZ	3_ASP_116	OD2	3.610
1QGC	3_LYS_207	NZ	3_GLU_49	OE1	3.193
1QGC	4_ARG_18	NH1	4_ASP_80	OD2	2.980
1QGC	4_ARG_18	NH2	4_ASP_80	OD2	3.279
1QGC	4_ARG_24	NH1	4_ASP_74	OD2	3.755
1QGC	4_ARG_24	NH2	4_ASP_74	OD1	3.361
1QGC	4_ARG_24	NH2	4_ASP_74	OD2	2.753
1QGC	4_ARG_65	NH1	4_ASP_86	OD1	3.995
1QGC	4_ARG_65	NH1	4_ASP_86	OD2	2.787
1QGC	4_ARG_65	NH2	4_ASP_85	OD2	3.117
1QGC	4_ARG_65	NH2	4_ASP_86	OD1	3.250
1QGC	4_ARG_65	NH2	4_ASP_86	OD2	3.419
1QGC	4_LYS_107	NZ	4_ASP_109	OD1	3.987
1QGC	4_LYS_107	NZ	4_ASP_169	OD1	3.205
1QGC	4_LYS_153	NZ	4_GLU_199	OE1	3.327
1QGC	4_ARG_159	NH1	4_GLU_189	OE1	3.473
1QGC	4_LYS_173	NZ	4_ASP_171	OD1	3.263
1QGC	4_LYS_173	NZ	4_ASP_171	OD2	3.461
1QGC	4_LYS_187	NZ	4_GLU_191	OE1	2.654
1QGC	4_LYS_203	NZ	4_ASP_114	OD1	3.911
1QGC	4_LYS_203	NZ	4_ASP_114	OD2	3.518
1QGC	A_ARG_38	NH1	A_ASP_90	OD1	3.118
1QGC	A_ARG_38	NH2	A_GLU_46	OE1	3.211
1QGC	A_ARG_38	NH2	A_ASP_90	OD1	3.660

1QGC	A_ARG_67	NH1	A_ASP_90	OD1	3.761
1QGC	A_ARG_67	NH1	A_ASP_90	OD2	2.866
1QGC	A_ARG_67	NH2	A_ASP_90	OD1	3.418
1QGC	A_ARG_67	NH2	A_ASP_90	OD2	3.559
1QGC	A_ARG_98	NH1	A_ASP_101	OD1	3.353
1QGC	A_ARG_98	NH1	A_ASP_101	OD2	3.278
1QGC	A_ARG_98	NH2	A_ASP_101	OD1	3.317
1QGC	A_ARG_98	NH2	A_ASP_101	OD2	3.911
1QGC	A_ARG_99	NH1	A_ASP_104	OD1	2.799
1QGC	A_ARG_99	NH2	A_ASP_104	OD1	2.841
1QGC	A_ARG_99	NH2	A_ASP_104	OD2	3.281
1QGC	A_ARG_99	NH2	5_ASP_143	OD1	3.483
1QGC	A_LYS_215	NZ	4_GLU_127	OE2	3.716

Table 173: 1QGC-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1QKZ	A.LYS_15	NZ	A.GLU_61	OE1	3.616
1QKZ	A.LYS_36	NZ	A.GLU_32	OE2	3.573
1QKZ	H.ARG_38	NH1	H.ASP_86	OD1	2.872
1QKZ	H.ARG_38	NH2	H.GLU_46	OE1	2.843
1QKZ	H.ARG_38	NH2	H.GLU_46	OE2	3.701
1QKZ	H.ARG_38	NH2	H.ASP_86	OD1	3.867
1QKZ	H.LYS_64	NZ	H.ASP_61	OD1	2.866
1QKZ	H.ARG_66	NH2	H.ASP_86	OD1	3.410
1QKZ	H.ARG_66	NH2	H.ASP_86	OD2	2.614
1QKZ	H.LYS_83	NZ	H.GLU_85	OE1	3.867
1QKZ	H.ARG_94	NH2	H.ASP_101	OD1	3.649
1QKZ	H.ARG_94	NH2	H.ASP_101	OD2	2.613
1QKZ	H.LYS_208	NZ	L.GLU_123	OE2	2.582
1QKZ	L.ARG_61	NH1	L.ASP_82	OD1	3.436
1QKZ	L.ARG_61	NH1	L.ASP_82	OD2	2.498
1QKZ	L.ARG_61	NH2	L.GLU_79	OE1	3.597
1QKZ	L.ARG_61	NH2	L.ASP_82	OD1	2.782
1QKZ	L.ARG_61	NH2	L.ASP_82	OD2	3.478
1QKZ	L.ARG_77	NH2	L.GLU_79	OE2	3.903
1QKZ	L.LYS_103	NZ	L.GLU_105	OE1	3.233
1QKZ	L.LYS_147	NZ	L.GLU_154	OE1	3.920
1QKZ	L.LYS_147	NZ	L.GLU_154	OE2	2.870
1QKZ	L.LYS_149	NZ	L.GLU_195	OE1	2.933
1QKZ	L.LYS_149	NZ	L.GLU_195	OE2	3.912
1QKZ	L.ARG_155	NH1	L.GLU_185	OE1	3.847
1QKZ	L.ARG_155	NH1	L.GLU_185	OE2	2.779
1QKZ	L.ARG_155	NH2	L.GLU_185	OE2	3.332
1QKZ	L.LYS_183	NZ	L.GLU_187	OE1	3.886
1QKZ	L.LYS_183	NZ	L.GLU_187	OE2	2.674
1QKZ	L.HIS_189	ND1	L.ASP_151	OD2	2.784
1QKZ	L.LYS_199	NZ	L.ASP_110	OD2	2.613

Table 174: 1QKZ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1QOK	A_ARG_64	NH1	A_GLU_72	OE2	2.857
1QOK	A_ARG_64	NH2	A_ASP_116	OD1	2.731
1QOK	A_LYS_89	NZ	A_GLU_72	OE1	3.015
1QOK	A_LYS_89	NZ	A_GLU_72	OE2	3.466
1QOK	A_LYS_93	NZ	A_ASP_116	OD1	3.171
1QOK	A_LYS_93	NZ	A_ASP_116	OD2	2.764
1QOK	A_ARG_221	NH2	A_GLU_241	OE1	3.500
1QOK	A_ARG_221	NH2	A_GLU_241	OE2	3.768
1QOK	A_ARG_221	NH2	A_ASP_242	OD1	2.782
1QOK	A_ARG_221	NH2	A_ASP_242	OD2	3.516
1QOK	A_LYS_263	NZ	A_GLU_265	OE2	3.711
1QOK	A_LYS_267	NZ	A_GLU_178	OE1	3.144
1QOK	A_LYS_267	NZ	A_GLU_178	OE2	3.767

Table 175: 1QOK-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1R21-1	A_HIS_54	NE2	A_GLU_52	OE2	3.592
1R21-1	A_HIS_61	NE2	A_GLU_52	OE1	3.344
1R21-1	A_ARG_96	NH1	A_ASP_16	OD1	3.366
1R21-1	A_ARG_96	NH2	A_GLU_98	OE2	3.736
1R21-10	A_HIS_54	NE2	A_GLU_52	OE1	3.820
1R21-10	A_HIS_54	NE2	A_GLU_52	OE2	3.819
1R21-10	A_HIS_61	NE2	A_GLU_52	OE1	3.243
1R21-11	A_LYS_50	NZ	A_GLU_52	OE1	3.980
1R21-11	A_HIS_54	NE2	A_GLU_52	OE1	3.682
1R21-11	A_HIS_54	NE2	A_GLU_52	OE2	3.726
1R21-11	A_HIS_61	NE2	A_GLU_52	OE1	3.099
1R21-11	A_ARG_81	NH2	A_GLU_57	OE1	3.622
1R21-11	A_ARG_81	NH2	A_GLU_57	OE2	3.877
1R21-12	A_ARG_6	NH2	A_GLU_98	OE2	3.220
1R21-12	A_LYS_50	NZ	A_GLU_52	OE2	3.513
1R21-12	A_HIS_54	ND1	A_GLU_55	OE1	3.706
1R21-12	A_HIS_61	NE2	A_GLU_52	OE1	3.484
1R21-12	A_HIS_61	NE2	A_GLU_52	OE2	3.957
1R21-12	A_LYS_83	NZ	A_ASP_86	OD1	3.921
1R21-12	A_ARG_96	NH1	A_ASP_16	OD1	2.338
1R21-12	A_ARG_96	NH2	A_ASP_16	OD1	3.435
1R21-13	A_LYS_50	NZ	A_GLU_52	OE2	3.811
1R21-13	A_HIS_61	NE2	A_GLU_52	OE1	3.018
1R21-13	A_HIS_61	NE2	A_GLU_52	OE2	3.663
1R21-13	A_ARG_96	NH1	A_ASP_16	OD1	2.697
1R21-13	A_ARG_96	NH2	A_GLU_98	OE2	3.649
1R21-14	A_HIS_61	ND1	A_GLU_52	OE2	3.472
1R21-14	A_HIS_61	NE2	A_GLU_52	OE1	2.859
1R21-14	A_HIS_61	NE2	A_GLU_52	OE2	3.106
1R21-14	A_ARG_81	NH2	A_GLU_57	OE1	3.503
1R21-14	A_ARG_81	NH2	A_GLU_57	OE2	2.460
1R21-14	A_ARG_96	NH2	A_GLU_98	OE2	2.878
1R21-15	A_ARG_6	NH2	A_GLU_100	OE1	2.871
1R21-15	A_ARG_6	NH2	A_GLU_100	OE2	3.726
1R21-15	A_HIS_54	NE2	A_GLU_52	OE1	3.410
1R21-15	A_HIS_54	NE2	A_GLU_52	OE2	3.502
1R21-15	A_HIS_61	NE2	A_GLU_52	OE1	3.119
1R21-15	A_ARG_81	NH2	A_GLU_57	OE1	3.147
1R21-16	A_HIS_54	NE2	A_GLU_52	OE1	3.412
1R21-16	A_HIS_54	NE2	A_GLU_52	OE2	3.663
1R21-16	A_HIS_61	NE2	A_GLU_52	OE1	2.774
1R21-16	A_ARG_81	NH2	A_GLU_57	OE1	2.662
1R21-16	A_ARG_81	NH2	A_GLU_57	OE2	3.500
1R21-16	A_ARG_96	NH2	A_GLU_98	OE2	3.655
1R21-17	A_HIS_19	NE2	A_ASP_16	OD1	2.979
1R21-17	A_LYS_50	NZ	A_GLU_52	OE1	3.597
1R21-17	A_HIS_54	NE2	A_GLU_52	OE1	3.729
1R21-17	A_HIS_54	NE2	A_GLU_52	OE2	3.299
1R21-17	A_HIS_61	NE2	A_GLU_52	OE1	3.150
1R21-17	A_ARG_96	NH1	A_ASP_16	OD1	3.990
1R21-17	A_ARG_96	NH1	A_ASP_16	OD2	3.847
1R21-18	A_HIS_54	NE2	A_GLU_52	OE2	3.726
1R21-18	A_HIS_61	NE2	A_GLU_52	OE1	3.370
1R21-18	A_HIS_84	NE2	A_GLU_100	OE2	2.435
1R21-18	A_ARG_96	NH2	A_GLU_98	OE2	3.170
1R21-19	A_HIS_54	NE2	A_GLU_52	OE2	3.585
1R21-19	A_HIS_61	NE2	A_GLU_52	OE1	3.355

1R21-19	A_ARG_96	NH2	A_GLU_98	OE2	2.978
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Table 176: 1R21-1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1R21-10	A_HIS_54	NE2	A_GLU_52	OE1	3.820
1R21-10	A_HIS_54	NE2	A_GLU_52	OE2	3.819
1R21-10	A_HIS_61	NE2	A_GLU_52	OE1	3.243

Table 177: 1R21-10-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1R21-11	A_LYS_50	NZ	A_GLU_52	OE1	3.980
1R21-11	A_HIS_54	NE2	A_GLU_52	OE1	3.682
1R21-11	A_HIS_54	NE2	A_GLU_52	OE2	3.726
1R21-11	A_HIS_61	NE2	A_GLU_52	OE1	3.099
1R21-11	A_ARG_81	NH2	A_GLU_57	OE1	3.622
1R21-11	A_ARG_81	NH2	A_GLU_57	OE2	3.877

Table 178: 1R21-11-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1R21-12	A_ARG_6	NH2	A_GLU_98	OE2	3.220
1R21-12	A_LYS_50	NZ	A_GLU_52	OE2	3.513
1R21-12	A_HIS_54	ND1	A_GLU_55	OE1	3.706
1R21-12	A_HIS_61	NE2	A_GLU_52	OE1	3.484
1R21-12	A_HIS_61	NE2	A_GLU_52	OE2	3.957
1R21-12	A_LYS_83	NZ	A_ASP_86	OD1	3.921
1R21-12	A_ARG_96	NH1	A_ASP_16	OD1	2.338
1R21-12	A_ARG_96	NH2	A_ASP_16	OD1	3.435

Table 179: 1R21-12-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1R21-13	A_LYS_50	NZ	A_GLU_52	OE2	3.811
1R21-13	A_HIS_61	NE2	A_GLU_52	OE1	3.018
1R21-13	A_HIS_61	NE2	A_GLU_52	OE2	3.663
1R21-13	A_ARG_96	NH1	A_ASP_16	OD1	2.697
1R21-13	A_ARG_96	NH2	A_GLU_98	OE2	3.649

Table 180: 1R21-13-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1R21-14	A_HIS_61	ND1	A_GLU_52	OE2	3.472
1R21-14	A_HIS_61	NE2	A_GLU_52	OE1	2.859
1R21-14	A_HIS_61	NE2	A_GLU_52	OE2	3.106
1R21-14	A_ARG_81	NH2	A_GLU_57	OE1	3.503
1R21-14	A_ARG_81	NH2	A_GLU_57	OE2	2.460
1R21-14	A_ARG_96	NH2	A_GLU_98	OE2	2.878

Table 181: 1R21-14-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1R21-15	A_ARG_6	NH2	A_GLU_100	OE1	2.871
1R21-15	A_ARG_6	NH2	A_GLU_100	OE2	3.726
1R21-15	A_HIS_54	NE2	A_GLU_52	OE1	3.410
1R21-15	A_HIS_54	NE2	A_GLU_52	OE2	3.502
1R21-15	A_HIS_61	NE2	A_GLU_52	OE1	3.119
1R21-15	A_ARG_81	NH2	A_GLU_57	OE1	3.147

Table 182: 1R21-15-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1R21-16	A_HIS_54	NE2	A_GLU_52	OE1	3.412
1R21-16	A_HIS_54	NE2	A_GLU_52	OE2	3.663
1R21-16	A_HIS_61	NE2	A_GLU_52	OE1	2.774
1R21-16	A_ARG_81	NH2	A_GLU_57	OE1	2.662
1R21-16	A_ARG_81	NH2	A_GLU_57	OE2	3.500
1R21-16	A_ARG_96	NH2	A_GLU_98	OE2	3.655

Table 183: 1R21-16-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1R21-17	A_HIS_19	NE2	A_ASP_16	OD1	2.979
1R21-17	A_LYS_50	NZ	A_GLU_52	OE1	3.597
1R21-17	A_HIS_54	NE2	A_GLU_52	OE1	3.729
1R21-17	A_HIS_54	NE2	A_GLU_52	OE2	3.299
1R21-17	A_HIS_61	NE2	A_GLU_52	OE1	3.150
1R21-17	A_ARG_96	NH1	A_ASP_16	OD1	3.990
1R21-17	A_ARG_96	NH1	A_ASP_16	OD2	3.847

Table 184: 1R21-17-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1R21-18	A_HIS_54	NE2	A_GLU_52	OE2	3.726
1R21-18	A_HIS_61	NE2	A_GLU_52	OE1	3.370
1R21-18	A_HIS_84	NE2	A_GLU_100	OE2	2.435
1R21-18	A_ARG_96	NH2	A_GLU_98	OE2	3.170

Table 185: 1R21-18-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1R21-19	A_HIS_54	NE2	A_GLU_52	OE2	3.585
1R21-19	A_HIS_61	NE2	A_GLU_52	OE1	3.355
1R21-19	A_ARG_96	NH2	A_GLU_98	OE2	2.978

Table 186: 1R21-19-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1R21-2	A_HIS_54	NE2	A_GLU_52	OE1	3.826
1R21-2	A_HIS_54	NE2	A_GLU_52	OE2	2.948
1R21-2	A_HIS_61	NE2	A_GLU_52	OE1	3.312
1R21-2	A_ARG_96	NH1	A_ASP_16	OD1	2.740
1R21-2	A_ARG_96	NH1	A_ASP_16	OD2	2.714
1R21-2	A_ARG_96	NH2	A_ASP_16	OD1	3.323
1R21-20	A_HIS_54	NE2	A_GLU_52	OE2	3.415
1R21-20	A_HIS_61	NE2	A_GLU_52	OE1	3.170
1R21-20	A_HIS_84	NE2	A_GLU_100	OE2	3.227
1R21-20	A_ARG_96	NH1	A_ASP_16	OD1	3.434
1R21-20	A_ARG_96	NH1	A_ASP_16	OD2	3.592
1R21-21	A_ARG_6	NH2	A_GLU_98	OE1	3.967
1R21-21	A_HIS_19	NE2	A_ASP_16	OD2	3.709
1R21-21	A_HIS_61	NE2	A_GLU_52	OE1	3.030
1R21-22	A_HIS_54	NE2	A_GLU_52	OE1	3.543
1R21-22	A_HIS_54	NE2	A_GLU_52	OE2	3.368
1R21-22	A_HIS_61	NE2	A_GLU_52	OE1	3.436
1R21-22	A_ARG_96	NH1	A_ASP_16	OD1	3.702
1R21-22	A_ARG_96	NH1	A_ASP_16	OD2	3.090
1R21-23	A_ARG_6	NH1	A_GLU_98	OE1	2.790
1R21-23	A_HIS_61	NE2	A_GLU_52	OE1	3.027
1R21-23	A_ARG_81	NH2	A_GLU_57	OE1	3.135
1R21-23	A_ARG_96	NH1	A_ASP_16	OD1	2.357
1R21-23	A_ARG_96	NH1	A_ASP_16	OD2	3.412
1R21-23	A_ARG_96	NH2	A_GLU_98	OE2	3.160

Table 187: 1R21-2-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1R21-20	A_HIS_54	NE2	A_GLU_52	OE2	3.415
1R21-20	A_HIS_61	NE2	A_GLU_52	OE1	3.170
1R21-20	A_HIS_84	NE2	A_GLU_100	OE2	3.227
1R21-20	A_ARG_96	NH1	A_ASP_16	OD1	3.434
1R21-20	A_ARG_96	NH1	A_ASP_16	OD2	3.592

Table 188: 1R21-20-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1R21-21	A_ARG_6	NH2	A_GLU_98	OE1	3.967
1R21-21	A_HIS_19	NE2	A_ASP_16	OD2	3.709
1R21-21	A_HIS_61	NE2	A_GLU_52	OE1	3.030

Table 189: 1R21-21-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1R21-22	A_HIS_54	NE2	A_GLU_52	OE1	3.543
1R21-22	A_HIS_54	NE2	A_GLU_52	OE2	3.368
1R21-22	A_HIS_61	NE2	A_GLU_52	OE1	3.436
1R21-22	A_ARG_96	NH1	A_ASP_16	OD1	3.702
1R21-22	A_ARG_96	NH1	A_ASP_16	OD2	3.090

Table 190: 1R21-22-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1R21-23	A_ARG_6	NH1	A_GLU_98	OE1	2.790
1R21-23	A_HIS_61	NE2	A_GLU_52	OE1	3.027
1R21-23	A_ARG_81	NH2	A_GLU_57	OE1	3.135
1R21-23	A_ARG_96	NH1	A_ASP_16	OD1	2.357
1R21-23	A_ARG_96	NH1	A_ASP_16	OD2	3.412
1R21-23	A_ARG_96	NH2	A_GLU_98	OE2	3.160

Table 191: 1R21-23-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1R21-3	A_HIS_19	NE2	A_ASP_16	OD1	2.708
1R21-3	A_HIS_19	NE2	A_ASP_16	OD2	3.092
1R21-3	A_LYS_50	NZ	A_GLU_52	OE2	3.328
1R21-3	A_HIS_61	NE2	A_GLU_52	OE1	3.178
1R21-3	A_HIS_61	NE2	A_GLU_52	OE2	3.637
1R21-3	A_ARG_81	NH2	A_GLU_57	OE1	3.507
1R21-3	A_ARG_81	NH2	A_GLU_57	OE2	2.346
1R21-3	A_ARG_96	NH1	A_GLU_98	OE1	3.034
1R21-3	A_ARG_96	NH2	A_GLU_98	OE1	3.009

Table 192: 1R21-3-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1R21-4	A_HIS_61	ND1	A_GLU_52	OE2	3.789
1R21-4	A_HIS_61	NE2	A_GLU_52	OE1	2.749
1R21-4	A_HIS_61	NE2	A_GLU_52	OE2	3.111
1R21-4	A_ARG_81	NH2	A_GLU_57	OE1	2.933
1R21-4	A_ARG_96	NH1	A_GLU_98	OE1	3.705
1R21-4	A_ARG_96	NH1	A_GLU_98	OE2	3.277
1R21-4	A_ARG_96	NH2	A_GLU_98	OE2	2.612

Table 193: 1R21-4-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1R21-5	A_ARG_6	NH1	A_GLU_100	OE2	3.869
1R21-5	A_ARG_6	NH2	A_GLU_100	OE2	2.476
1R21-5	A_HIS_54	NE2	A_GLU_52	OE1	3.312
1R21-5	A_HIS_54	NE2	A_GLU_52	OE2	3.040
1R21-5	A_HIS_61	NE2	A_GLU_52	OE1	2.875
1R21-5	A_ARG_96	NH2	A_GLU_98	OE2	3.021

Table 194: 1R21-5-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1R21-6	A_HIS_19	NE2	A_ASP_16	OD2	3.980
1R21-6	A_HIS_54	NE2	A_GLU_52	OE1	3.369
1R21-6	A_HIS_54	NE2	A_GLU_52	OE2	3.405
1R21-6	A_HIS_61	NE2	A_GLU_52	OE1	3.317

Table 195: 1R21-6-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1R21-7	A_HIS_19	NE2	A_ASP_16	OD1	3.586
1R21-7	A_HIS_19	NE2	A_ASP_16	OD2	3.080
1R21-7	A_HIS_61	NE2	A_GLU_52	OE1	3.436
1R21-7	A_ARG_81	NH2	A_GLU_57	OE2	3.637

Table 196: 1R21-7-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1R21-8	A_ARG_6	NH2	A_GLU_98	OE1	3.720
1R21-8	A_HIS_54	NE2	A_GLU_52	OE1	3.655
1R21-8	A_HIS_54	NE2	A_GLU_52	OE2	3.218
1R21-8	A_HIS_61	NE2	A_GLU_52	OE1	3.063
1R21-8	A_ARG_96	NH2	A_GLU_98	OE2	3.712

Table 197: 1R21-8-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1R21-9	A_HIS_54	ND1	A_GLU_55	OE1	2.611
1R21-9	A_HIS_61	NE2	A_GLU_52	OE1	3.068
1R21-9	A_ARG_96	NH2	A_GLU_98	OE2	3.654

Table 198: 1R21-9-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1RZJ	G.LYS.207	NZ	G.GLU.381	OE1	3.995
1RZJ	G.LYS.207	NZ	G.GLU.381	OE2	2.764
1RZJ	G.LYS.231	NZ	G.GLU.268	OE2	3.358
1RZJ	G.HIS.249	NE2	G.GLU.482	OE1	3.036
1RZJ	G.LYS.348	NZ	G.GLU.269	OE2	2.716
1RZJ	G.LYS.357	NZ	G.GLU.466	OE1	3.793
1RZJ	G.ARG.419	NH2	H.GLU.99	OE2	2.591
1RZJ	G.ARG.456	NH2	G.GLU.466	OE1	3.427
1RZJ	G.ARG.456	NH2	G.GLU.466	OE2	2.814
1RZJ	G.ARG.469	NH2	G.ASP.457	OD1	2.972
1RZJ	G.ARG.476	NH1	G.ASP.474	OD1	2.853
1RZJ	G.ARG.480	NH1	G.ASP.477	OD1	2.656
1RZJ	G.LYS.487	NZ	G.GLU.91	OE1	3.654
1RZJ	G.LYS.487	NZ	G.GLU.91	OE2	2.711
1RZJ	C.LYS.8	NZ	C.GLU.119	OE1	2.627
1RZJ	C.LYS.8	NZ	C.GLU.119	OE2	3.972
1RZJ	C.HIS.27	NE2	C.GLU.85	OE1	2.626
1RZJ	C.LYS.29	NZ	G.ASP.279	OD2	3.209
1RZJ	C.LYS.29	NZ	C.GLU.85	OE1	3.520
1RZJ	C.LYS.35	NZ	G.ASP.457	OD2	3.838
1RZJ	C.LYS.46	NZ	C.ASP.56	OD1	3.928
1RZJ	C.ARG.54	NH1	C.ASP.78	OD2	3.656
1RZJ	C.ARG.54	NH2	C.ASP.78	OD1	2.906
1RZJ	C.ARG.54	NH2	C.ASP.78	OD2	3.632
1RZJ	C.ARG.58	NH1	C.GLU.13	OE1	2.664
1RZJ	C.ARG.59	NH1	G.ASP.368	OD1	3.788
1RZJ	C.ARG.59	NH1	G.ASP.368	OD2	3.342
1RZJ	C.ARG.59	NH2	G.ASP.368	OD1	2.531
1RZJ	C.ARG.59	NH2	G.ASP.368	OD2	3.174
1RZJ	C.LYS.90	NZ	C.GLU.85	OE2	3.877
1RZJ	C.LYS.171	NZ	C.GLU.169	OE1	3.508
1RZJ	L.ARG.61	NH2	L.GLU.81	OE2	3.350
1RZJ	L.ARG.61	NH2	L.ASP.82	OD1	2.670
1RZJ	L.ARG.61	NH2	L.ASP.82	OD2	3.090
1RZJ	L.LYS.149	NZ	L.GLU.195	OE1	2.951
1RZJ	L.LYS.149	NZ	L.GLU.195	OE2	3.523
1RZJ	L.HIS.189	ND1	L.ASP.151	OD2	3.250
1RZJ	H.LYS.12	NZ	H.GLU.10	OE1	3.962
1RZJ	H.LYS.19	NZ	H.GLU.81	OE2	3.444
1RZJ	H.ARG.31	NH2	H.ASP.100A	OD1	3.714
1RZJ	H.ARG.31	NH2	H.ASP.100A	OD2	2.889
1RZJ	H.ARG.38	NH1	H.GLU.46	OE1	3.693
1RZJ	H.ARG.38	NH1	H.GLU.46	OE2	2.534
1RZJ	H.ARG.38	NH2	H.ASP.86	OD2	2.669
1RZJ	H.ARG.50	NH2	H.GLU.97	OE2	2.721
1RZJ	H.HIS.62	NE2	H.GLU.46	OE1	3.941
1RZJ	H.HIS.62	NE2	H.GLU.46	OE2	3.006
1RZJ	H.ARG.66	NH1	H.ASP.86	OD1	2.823
1RZJ	H.ARG.66	NH1	H.ASP.86	OD2	3.878
1RZJ	H.ARG.66	NH2	H.ASP.86	OD1	3.045
1RZJ	H.ARG.66	NH2	H.ASP.86	OD2	2.664
1RZJ	H.ARG.82A	NH1	H.GLU.81	OE1	2.688
1RZJ	H.LYS.101	NZ	H.GLU.1	OE1	3.982
1RZJ	H.HIS.102	NE2	H.GLU.1	OE1	3.443
1RZJ	H.LYS.143	NZ	H.ASP.144	OD1	3.134
1RZJ	H.LYS.143	NZ	H.ASP.144	OD2	3.259
1RZJ	H.LYS.209	NZ	L.GLU.123	OE1	3.812

Table 199: 1RZJ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1RZK	G.LYS.121	NZ	G.GLU.429	OE1	2.734
1RZK	G.LYS.121	NZ	G.GLU.429	OE2	3.567
1RZK	G.LYS.207	NZ	G.GLU.381	OE1	3.945
1RZK	G.LYS.207	NZ	G.GLU.381	OE2	3.126
1RZK	G.LYS.232	NZ	G.GLU.351	OE1	3.994
1RZK	G.HIS.249	NE2	G.GLU.482	OE1	3.525
1RZK	G.LYS.282	NZ	G.GLU.275	OE1	3.953
1RZK	G.LYS.282	NZ	G.GLU.275	OE2	2.642
1RZK	G.LYS.348	NZ	G.GLU.269	OE2	3.206
1RZK	G.LYS.348	NZ	G.GLU.351	OE1	3.941
1RZK	G.LYS.348	NZ	G.GLU.351	OE2	3.259
1RZK	G.LYS.350	NZ	G.ASP.395	OD1	3.580
1RZK	G.LYS.357	NZ	G.GLU.466	OE1	3.719
1RZK	G.ARG.419	NH1	H.GLU.100B	OE1	2.999
1RZK	G.ARG.419	NH1	H.GLU.100B	OE2	3.674
1RZK	G.ARG.419	NH2	H.GLU.99	OE1	2.292
1RZK	G.ARG.419	NH2	H.GLU.100B	OE2	3.969
1RZK	G.ARG.456	NH2	G.GLU.466	OE1	3.468
1RZK	G.ARG.456	NH2	G.GLU.466	OE2	3.536
1RZK	G.ARG.469	NH2	G.ASP.457	OD1	3.234
1RZK	G.ARG.476	NH1	G.ASP.474	OD1	3.441
1RZK	G.ARG.476	NH2	G.GLU.102	OE1	3.296
1RZK	G.ARG.476	NH2	G.GLU.102	OE2	3.010
1RZK	G.LYS.487	NZ	G.GLU.91	OE2	3.524
1RZK	G.LYS.490	NZ	G.GLU.492	OE1	3.300
1RZK	C.LYS.29	NZ	C.GLU.85	OE1	2.833
1RZK	C.LYS.29	NZ	C.GLU.85	OE2	3.848
1RZK	C.LYS.35	NZ	G.ASP.457	OD2	3.741
1RZK	C.ARG.54	NH1	C.ASP.78	OD1	3.987
1RZK	C.ARG.54	NH1	C.ASP.78	OD2	2.755
1RZK	C.ARG.54	NH2	C.ASP.78	OD1	2.666
1RZK	C.ARG.54	NH2	C.ASP.78	OD2	2.988
1RZK	C.ARG.59	NH1	G.ASP.368	OD1	3.343
1RZK	C.ARG.59	NH1	G.ASP.368	OD2	3.154
1RZK	C.ARG.59	NH2	G.ASP.368	OD1	2.433
1RZK	C.ARG.59	NH2	G.ASP.368	OD2	2.977
1RZK	C.HIS.107	ND1	C.ASP.105	OD1	2.891
1RZK	C.HIS.107	ND1	C.ASP.105	OD2	3.166
1RZK	C.ARG.134	NH2	C.ASP.153	OD1	3.766
1RZK	C.LYS.136	NZ	C.GLU.150	OE2	3.884
1RZK	C.LYS.136	NZ	C.ASP.153	OD1	3.936
1RZK	C.LYS.136	NZ	C.ASP.153	OD2	2.987
1RZK	C.LYS.171	NZ	C.GLU.169	OE2	2.874
1RZK	L.ARG.61	NH2	L.GLU.81	OE1	3.127
1RZK	L.ARG.61	NH2	L.ASP.82	OD1	3.576
1RZK	L.ARG.95B	NH2	L.ASP.1	OD2	2.985
1RZK	L.HIS.189	ND1	L.ASP.151	OD2	2.585
1RZK	L.HIS.189	NE2	L.ASP.185	OD1	3.599
1RZK	L.HIS.189	NE2	L.ASP.185	OD2	2.802
1RZK	L.ARG.211	NH1	L.GLU.187	OE1	3.851
1RZK	H.ARG.31	NH2	H.ASP.100A	OD1	3.070
1RZK	H.ARG.31	NH2	H.ASP.100A	OD2	3.614
1RZK	H.ARG.38	NH1	H.GLU.46	OE1	2.779
1RZK	H.ARG.38	NH1	H.GLU.46	OE2	3.342
1RZK	H.ARG.38	NH2	H.ASP.86	OD2	2.684
1RZK	H.ARG.50	NH2	H.GLU.97	OE2	2.332
1RZK	H.ARG.66	NH1	H.ASP.86	OD1	3.598

1RZK	H_ARG_66	NH2	H_ASP_86	OD1	2.415
1RZK	H_ARG_66	NH2	H_ASP_86	OD2	2.739
1RZK	H_LYS_73	NZ	H_ASP_55	OD2	2.968
1RZK	H_ARG_82A	NH2	H_GLU_81	OE1	3.271
1RZK	H_LYS_143	NZ	H_ASP_144	OD1	2.615
1RZK	H_LYS_143	NZ	H_ASP_144	OD2	3.235
1RZK	H_HIS_164	NE2	L_ASP_167	OD1	3.880
1RZK	H_HIS_164	NE2	L_ASP_167	OD2	2.505
1RZK	H_LYS_206	NZ	H_ASP_208	OD2	3.965
1RZK	H_LYS_209	NZ	L_GLU_123	OE1	3.513
1RZK	H_LYS_209	NZ	L_GLU_123	OE2	3.584

Table 200: 1RZK-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1S3K	L_ARG_66	NH2	L_GLU_86	OE2	3.884
1S3K	L_ARG_66	NH2	L_ASP_87	OD1	2.838
1S3K	L_ARG_66	NH2	L_ASP_87	OD2	3.885
1S3K	L_LYS_108	NZ	L_GLU_170	OE2	3.919
1S3K	L_HIS_194	ND1	L_ASP_156	OD2	2.733
1S3K	H_ARG_38	NH1	H_ASP_90	OD1	2.899
1S3K	H_ARG_38	NH2	H_GLU_46	OE2	3.185
1S3K	H_ARG_38	NH2	H_ASP_90	OD1	3.935
1S3K	H_LYS_65	NZ	H_ASP_59	OD1	3.006
1S3K	H_ARG_67	NH1	H_ASP_90	OD1	3.672
1S3K	H_ARG_67	NH1	H_ASP_90	OD2	2.699
1S3K	H_ARG_67	NH2	H_ASP_90	OD1	2.977
1S3K	H_ARG_67	NH2	H_ASP_90	OD2	3.482
1S3K	H_ARG_101	NH1	H_ASP_31	OD2	3.352
1S3K	H_LYS_149	NZ	H_ASP_150	OD1	3.589

Table 201: 1S3K-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1S5I	L_ARG_46	NH2	L_ASP_55	OD1	2.460
1S5I	L_ARG_46	NH2	L_ASP_55	OD2	3.856
1S5I	L_ARG_61	NH1	L_GLU_79	OE1	3.126
1S5I	L_ARG_61	NH1	L_GLU_81	OE2	3.788
1S5I	L_ARG_61	NH2	L_GLU_79	OE1	3.704
1S5I	L_ARG_61	NH2	L_ASP_82	OD1	2.499
1S5I	L_ARG_61	NH2	L_ASP_82	OD2	2.521
1S5I	L_ARG_77	NH1	L_GLU_79	OE2	3.348
1S5I	L_ARG_96	NH1	H_ASP_97	OD1	3.601
1S5I	L_ARG_96	NH2	H_ASP_97	OD1	2.496
1S5I	L_ARG_96	NH2	H_ASP_97	OD2	2.511
1S5I	L_LYS_147	NZ	L_GLU_154	OE1	3.415
1S5I	L_LYS_149	NZ	L_GLU_195	OE1	2.811
1S5I	L_LYS_149	NZ	L_GLU_195	OE2	3.034
1S5I	L_ARG_155	NH1	L_GLU_185	OE1	2.637
1S5I	L_ARG_155	NH2	L_GLU_185	OE1	3.738
1S5I	L_ARG_188	NH2	L_GLU_185	OE2	2.926
1S5I	L_HIS_189	ND1	L_ASP_151	OD2	2.858
1S5I	L_HIS_189	NE2	L_GLU_185	OE1	2.459
1S5I	L_HIS_189	NE2	L_GLU_185	OE2	3.318
1S5I	H_ARG_38	NH1	H_ASP_86	OD1	2.668
1S5I	H_ARG_38	NH2	H_GLU_46	OE1	2.890
1S5I	H_ARG_38	NH2	H_ASP_86	OD1	3.667
1S5I	H_ARG_66	NH1	H_ASP_86	OD1	3.962
1S5I	H_ARG_66	NH1	H_ASP_86	OD2	3.293
1S5I	H_ARG_66	NH2	H_ASP_86	OD1	3.251
1S5I	H_ARG_66	NH2	H_ASP_86	OD2	3.537
1S5I	H_LYS_75	NZ	H_ASP_72	OD1	3.618
1S5I	H_LYS_75	NZ	H_ASP_72	OD2	2.868
1S5I	H_HIS_172	NE2	L_ASP_167	OD2	3.741
1S5I	H_LYS_218	NZ	H_ASP_220	OD1	3.717
1S5I	H_LYS_221	NZ	L_GLU_123	OE2	3.213

Table 202: 1S5I-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1S78	A_ARG_25	NH2	A_ASP_22	OD2	3.377
1S78	A_HIS_26	NE2	A_ASP_22	OD1	3.860
1S78	A_HIS_26	NE2	A_ASP_22	OD2	3.677
1S78	A_ARG_76	NH1	A_ASP_54	OD1	3.940
1S78	A_ARG_81	NH2	A_GLU_57	OE1	3.403
1S78	A_ARG_81	NH2	A_GLU_57	OE2	3.079
1S78	A_ARG_121	NH1	A_GLU_188	OE1	2.989
1S78	A_ARG_121	NH2	A_GLU_188	OE1	3.618
1S78	A_ARG_121	NH2	A_ASP_189	OD1	3.441
1S78	A_ARG_121	NH2	A_ASP_189	OD2	3.303
1S78	A_ARG_135	NH2	A_ASP_96	OD1	3.677
1S78	A_ARG_135	NH2	A_ASP_96	OD2	3.036
1S78	A_HIS_152	NE2	A_GLU_125	OE1	3.976
1S78	A_ARG_166	NH2	A_ASP_143	OD1	3.122
1S78	A_ARG_204	NH1	A_ASP_149	OD1	3.810
1S78	A_ARG_204	NH2	A_GLU_125	OE2	2.685
1S78	A_LYS_206	NZ	A_ASP_212	OD2	3.591
1S78	A_HIS_238	ND1	A_GLU_243	OE1	3.574
1S78	A_HIS_238	ND1	A_GLU_243	OE2	2.921
1S78	A_ARG_308	NH2	A_GLU_310	OE2	3.285
1S78	A_LYS_311	NZ	A_ASP_285	OD2	3.743
1S78	A_HIS_327	NE2	A_GLU_341	OE1	2.783
1S78	A_HIS_327	NE2	A_GLU_341	OE2	2.983
1S78	A_ARG_332	NH1	A_GLU_357	OE2	3.575
1S78	A_ARG_332	NH2	A_GLU_357	OE1	3.867
1S78	A_ARG_332	NH2	A_GLU_357	OE2	2.955
1S78	A_LYS_347	NZ	A_GLU_299	OE2	2.643
1S78	A_LYS_347	NZ	A_GLU_383	OE1	3.238
1S78	A_ARG_410	NH2	A_GLU_383	OE1	3.550
1S78	A_ARG_410	NH2	A_GLU_383	OE2	3.659
1S78	A_ARG_412	NH1	A_GLU_299	OE1	3.168
1S78	A_ARG_412	NH1	A_GLU_299	OE2	3.462
1S78	A_ARG_412	NH2	A_GLU_299	OE2	3.187
1S78	A_ARG_437	NH1	A_GLU_438	OE1	3.837
1S78	A_ARG_465	NH1	A_GLU_438	OE1	2.796
1S78	A_ARG_465	NH1	A_GLU_438	OE2	3.955
1S78	A_ARG_477	NH1	A_GLU_485	OE1	2.683
1S78	A_ARG_477	NH2	A_GLU_481	OE2	3.214
1S78	A_ARG_477	NH2	A_GLU_485	OE1	3.223
1S78	A_ARG_514	NH1	A_GLU_531	OE2	2.772
1S78	A_ARG_523	NH1	A_GLU_531	OE1	3.483
1S78	A_ARG_523	NH1	A_GLU_531	OE2	3.476
1S78	B_ARG_25	NH2	B_ASP_22	OD2	3.334
1S78	B_HIS_26	NE2	B_ASP_22	OD1	3.990
1S78	B_HIS_26	NE2	B_ASP_22	OD2	3.840
1S78	B_ARG_76	NH1	B_ASP_54	OD1	3.948
1S78	B_ARG_81	NH2	B_GLU_57	OE1	3.380
1S78	B_ARG_81	NH2	B_GLU_57	OE2	3.017
1S78	B_ARG_121	NH1	B_GLU_188	OE1	2.787
1S78	B_ARG_121	NH2	B_GLU_188	OE1	3.424
1S78	B_ARG_121	NH2	B_ASP_189	OD1	3.468
1S78	B_ARG_121	NH2	B_ASP_189	OD2	3.329
1S78	B_ARG_135	NH2	B_ASP_96	OD1	3.610
1S78	B_ARG_135	NH2	B_ASP_96	OD2	2.916
1S78	B_HIS_152	NE2	B_GLU_125	OE1	3.902
1S78	B_ARG_166	NH2	B_ASP_143	OD1	3.128
1S78	B_ARG_204	NH1	B_ASP_149	OD1	3.952

1S78	B_ARG_204	NH2	B_GLU_125	OE2	2.608
1S78	B_LYS_206	NZ	B_ASP_212	OD2	3.574
1S78	B_HIS_238	ND1	B_GLU_243	OE1	3.602
1S78	B_HIS_238	ND1	B_GLU_243	OE2	2.978
1S78	B_ARG_308	NH2	B_GLU_310	OE2	3.284
1S78	B_LYS_311	NZ	B_ASP_285	OD2	3.757
1S78	B_HIS_327	NE2	B_GLU_341	OE1	2.772
1S78	B_HIS_327	NE2	B_GLU_341	OE2	2.972
1S78	B_ARG_332	NH1	B_GLU_357	OE2	3.726
1S78	B_ARG_332	NH2	B_GLU_357	OE1	3.938
1S78	B_ARG_332	NH2	B_GLU_357	OE2	2.990
1S78	B_LYS_347	NZ	B_GLU_299	OE2	2.672
1S78	B_LYS_347	NZ	B_GLU_383	OE1	3.084
1S78	B_LYS_347	NZ	B_GLU_383	OE2	3.934
1S78	B_ARG_410	NH2	B_GLU_383	OE1	3.602
1S78	B_ARG_410	NH2	B_GLU_383	OE2	3.759
1S78	B_ARG_412	NH1	B_GLU_299	OE1	3.217
1S78	B_ARG_412	NH1	B_GLU_299	OE2	3.556
1S78	B_ARG_412	NH2	B_GLU_299	OE2	3.170
1S78	B_ARG_465	NH1	B_GLU_438	OE1	2.881
1S78	B_ARG_477	NH1	B_GLU_485	OE1	2.617
1S78	B_ARG_477	NH1	B_GLU_485	OE2	3.941
1S78	B_ARG_477	NH2	B_GLU_481	OE2	3.169
1S78	B_ARG_477	NH2	B_GLU_485	OE1	3.166
1S78	B_ARG_514	NH1	B_GLU_531	OE1	3.612
1S78	B_ARG_514	NH1	B_GLU_531	OE2	2.336
1S78	B_ARG_523	NH1	B_GLU_531	OE1	3.374
1S78	B_ARG_523	NH1	B_GLU_531	OE2	3.242
1S78	B_HIS_567	ND1	B_GLU_544	OE1	3.248
1S78	B_HIS_567	ND1	B_GLU_544	OE2	3.019
1S78	C_LYS_24	NZ	C_ASP_70	OD1	3.323
1S78	C_ARG_61	NH2	C_ASP_82	OD1	2.646
1S78	C_ARG_61	NH2	C_ASP_82	OD2	3.273
1S78	C_LYS_103	NZ	C_GLU_165	OE1	3.918
1S78	C_LYS_103	NZ	C_GLU_165	OE2	2.759
1S78	C_LYS_149	NZ	C_GLU_195	OE2	3.249
1S78	C_HIS_189	ND1	C_ASP_151	OD2	3.312
1S78	C_ARG_211	NH1	C_GLU_187	OE2	3.367
1S78	D_ARG_38	NH1	D_ASP_86	OD1	3.229
1S78	D_ARG_38	NH2	D_GLU_46	OE1	2.855
1S78	D_ARG_62	NH1	D_GLU_85	OE1	3.019
1S78	D_ARG_62	NH2	D_GLU_46	OE1	3.024
1S78	D_ARG_62	NH2	D_GLU_46	OE2	3.448
1S78	D_ARG_66	NH1	D_ASP_86	OD1	3.283
1S78	D_ARG_66	NH1	D_ASP_86	OD2	2.439
1S78	D_ARG_66	NH2	D_ASP_86	OD1	3.573
1S78	D_ARG_94	NH2	D_ASP_101	OD1	3.501
1S78	D_ARG_94	NH2	D_ASP_101	OD2	2.662
1S78	D_LYS_143	NZ	D_ASP_144	OD2	3.814
1S78	D_HIS_164	NE2	C_ASP_167	OD1	3.839
1S78	D_LYS_209	NZ	C_GLU_123	OE1	3.290
1S78	D_LYS_214	NZ	C_ASP_122	OD1	3.484
1S78	E_LYS_24	NZ	E_ASP_70	OD1	3.695
1S78	E_LYS_24	NZ	E_ASP_70	OD2	3.318
1S78	E_ARG_61	NH2	E_GLU_81	OE1	3.985
1S78	E_ARG_61	NH2	E_GLU_81	OE2	3.655
1S78	E_ARG_61	NH2	E_ASP_82	OD1	2.822
1S78	E_ARG_61	NH2	E_ASP_82	OD2	3.506

1S78	E_LYS_103	NZ	E_GLU_165	OE1	2.948
1S78	E_LYS_103	NZ	E_GLU_165	OE2	3.258
1S78	E_HIS_189	ND1	E_ASP_151	OD2	2.704
1S78	F_ARG_38	NH1	F_ASP_86	OD1	3.191
1S78	F_ARG_38	NH2	F_GLU_46	OE1	2.976
1S78	F_ARG_38	NH2	F_ASP_86	OD1	3.546
1S78	F_ARG_66	NH1	F_ASP_86	OD1	2.849
1S78	F_ARG_66	NH1	F_ASP_86	OD2	2.628
1S78	F_ARG_83	NH1	F_GLU_85	OE1	3.280
1S78	F_ARG_83	NH1	F_GLU_85	OE2	3.676
1S78	F_ARG_94	NH2	F_ASP_101	OD1	3.456
1S78	F_ARG_94	NH2	F_ASP_101	OD2	2.584

Table 203: 1S78-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1SM3	L_HIS_42	ND1	L_GLU_38	OE2	3.552
1SM3	L_ARG_61	NH2	L_GLU_81	OE2	2.761
1SM3	L_ARG_61	NH2	L_ASP_82	OD1	2.739
1SM3	L_ARG_61	NH2	L_ASP_82	OD2	3.626
1SM3	L_LYS_110	NZ	L_GLU_198	OE2	2.701
1SM3	L_HIS_188	ND1	L_ASP_151	OD2	2.837
1SM3	H_ARG_38	NH1	H_ASP_86	OD1	2.991
1SM3	H_ARG_38	NH2	H_GLU_46	OE1	3.308
1SM3	H_ARG_38	NH2	H_GLU_46	OE2	3.468
1SM3	H_ARG_38	NH2	H_ASP_86	OD1	3.893
1SM3	H_LYS_43	NZ	H_GLU_46	OE1	3.090
1SM3	H_ARG_52	NH1	H_GLU_50	OE2	2.647
1SM3	H_HIS_58	ND1	H_GLU_50	OE2	2.597
1SM3	H_ARG_66	NH1	H_ASP_86	OD1	3.622
1SM3	H_ARG_66	NH2	H_ASP_86	OD1	3.305
1SM3	H_ARG_66	NH2	H_ASP_86	OD2	2.417
1SM3	H_ARG_71	NH2	H_ASP_73	OD1	3.453
1SM3	H_LYS_143	NZ	L_GLU_124	OE2	2.757

Table 204: 1SM3-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1SQ2	L_LYS_1	NZ	L_GLU_7	OE1	3.597
1SQ2	L_LYS_1	NZ	L_GLU_7	OE2	2.720
1SQ2	L_ARG_61	NH1	L_ASP_48	OD2	3.006
1SQ2	L_ARG_73	NH2	N_ASP_93	OD1	3.549
1SQ2	L_ARG_73	NH2	N_ASP_93	OD2	3.002
1SQ2	L_ARG_125	NH1	L_ASP_119	OD2	3.203
1SQ2	L_ARG_125	NH2	L_ASP_119	OD1	3.605
1SQ2	L_ARG_125	NH2	L_ASP_119	OD2	2.909
1SQ2	N_ARG_2	NH1	N_ASP_26	OD2	3.782
1SQ2	N_ARG_2	NH2	N_ASP_4	OD1	3.667
1SQ2	N_ARG_2	NH2	N_ASP_4	OD2	3.350
1SQ2	N_ARG_8	NH1	N_ASP_106	OD1	3.394
1SQ2	N_ARG_38	NH1	N_ASP_77	OD1	3.866
1SQ2	N_LYS_39	NZ	N_GLU_46	OE1	3.723
1SQ2	N_LYS_51	NZ	N_GLU_57	OE1	2.817
1SQ2	N_LYS_51	NZ	N_GLU_57	OE2	3.620
1SQ2	N_ARG_54	NH1	N_ASP_77	OD1	3.089
1SQ2	N_ARG_54	NH1	N_ASP_77	OD2	3.597
1SQ2	N_ARG_54	NH2	N_ASP_77	OD1	3.562
1SQ2	N_ARG_54	NH2	N_ASP_77	OD2	2.591
1SQ2	N_ARG_82	NH1	N_GLU_46	OE2	3.823
1SQ2	N_ARG_100	NH1	L_ASP_52	OD1	3.032
1SQ2	N_ARG_100	NH1	L_ASP_52	OD2	3.454
1SQ2	N_ARG_100	NH2	L_ASP_52	OD1	3.561
1SQ2	N_ARG_100	NH2	L_ASP_52	OD2	3.218

Table 205: 1SQ2-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1SVZ	A_ARG_24	NH2	A_ASP_75	OD1	2.929
1SVZ	A_ARG_66	NH1	A_ASP_87	OD1	3.870
1SVZ	A_ARG_66	NH1	A_ASP_87	OD2	2.678
1SVZ	A_ARG_66	NH2	A_GLU_84	OE1	3.931
1SVZ	A_ARG_66	NH2	A_GLU_86	OE2	3.128
1SVZ	A_ARG_66	NH2	A_ASP_87	OD1	3.084
1SVZ	A_ARG_66	NH2	A_ASP_87	OD2	3.325
1SVZ	A_LYS_139	NZ	A_GLU_137	OE1	3.533
1SVZ	A_HIS_162	NE2	A_ASP_226	OD2	2.871
1SVZ	A_LYS_173	NZ	A_ASP_190	OD2	3.311
1SVZ	A_LYS_192	NZ	A_ASP_189	OD1	2.477
1SVZ	A_ARG_194	NH1	A_ASP_217	OD1	3.731
1SVZ	A_ARG_194	NH1	A_ASP_217	OD2	2.724
1SVZ	A_ARG_194	NH2	A_ASP_217	OD1	2.551
1SVZ	A_ARG_194	NH2	A_ASP_217	OD2	2.852
1SVZ	A_ARG_227	NH2	A_GLU_232	OE1	3.187
1SVZ	A_ARG_227	NH2	A_GLU_232	OE2	2.728
1SVZ	A_HIS_228	ND1	A_ASP_226	OD1	2.644
1SVZ	B_ARG_24	NH2	B_ASP_75	OD1	3.400
1SVZ	B_ARG_24	NH2	B_ASP_75	OD2	3.186
1SVZ	B_ARG_66	NH1	B_GLU_84	OE2	3.553
1SVZ	B_ARG_66	NH2	B_GLU_86	OE2	2.747
1SVZ	B_ARG_66	NH2	B_ASP_87	OD1	3.046
1SVZ	B_ARG_66	NH2	B_ASP_87	OD2	3.702
1SVZ	B_LYS_139	NZ	B_GLU_143	OE1	3.577
1SVZ	B_HIS_162	NE2	B_ASP_226	OD2	2.989
1SVZ	B_LYS_165	NZ	B_GLU_216	OE2	2.834
1SVZ	B_LYS_173	NZ	B_ASP_190	OD1	3.857
1SVZ	B_LYS_173	NZ	B_ASP_190	OD2	3.237
1SVZ	B_LYS_192	NZ	B_ASP_189	OD1	3.974
1SVZ	B_ARG_194	NH2	B_ASP_217	OD1	3.693
1SVZ	B_ARG_194	NH2	B_ASP_217	OD2	2.595
1SVZ	B_ARG_227	NH1	B_GLU_232	OE1	3.056
1SVZ	B_ARG_227	NH1	B_GLU_232	OE2	3.538
1SVZ	B_HIS_228	ND1	B_ASP_226	OD1	2.570
1SVZ	B_HIS_228	ND1	B_ASP_226	OD2	3.901

Table 206: 1SVZ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1T2Q	L_ARG_25	NH2	L_ASP_76	OD1	3.792
1T2Q	L_ARG_60	NH2	L_ASP_66	OD1	3.739
1T2Q	L_ARG_67	NH1	L_GLU_85	OE1	3.406
1T2Q	L_ARG_67	NH2	L_GLU_85	OE1	3.629
1T2Q	L_ARG_67	NH2	L_GLU_87	OE2	3.632
1T2Q	L_ARG_67	NH2	L_ASP_88	OD1	2.658
1T2Q	L_ARG_67	NH2	L_ASP_88	OD2	3.450
1T2Q	L_LYS_109	NZ	L_ASP_171	OD1	3.845
1T2Q	L_LYS_148	NZ	L_GLU_111	OE2	3.401
1T2Q	L_LYS_155	NZ	L_GLU_201	OE1	3.097
1T2Q	L_LYS_155	NZ	L_GLU_201	OE2	2.790
1T2Q	L_ARG_194	NH2	L_ASP_190	OD2	2.982
1T2Q	L_HIS_195	ND1	L_ASP_157	OD2	2.589
1T2Q	H_ARG_39	NH1	H_ASP_90	OD1	2.798
1T2Q	H_ARG_39	NH2	H_GLU_47	OE1	2.910
1T2Q	H_ARG_39	NH2	H_GLU_47	OE2	3.823
1T2Q	H_ARG_39	NH2	H_ASP_90	OD1	3.822
1T2Q	H_LYS_44	NZ	H_ASP_89	OD2	3.291
1T2Q	H_ARG_67	NH1	H_ASP_90	OD1	3.874
1T2Q	H_ARG_67	NH1	H_ASP_90	OD2	2.949
1T2Q	H_ARG_67	NH2	H_ASP_90	OD1	2.874
1T2Q	H_ARG_67	NH2	H_ASP_90	OD2	3.246
1T2Q	H_LYS_76	NZ	H_ASP_73	OD2	3.621
1T2Q	H_ARG_98	NH2	H_ASP_107	OD1	3.528
1T2Q	H_ARG_98	NH2	H_ASP_107	OD2	2.637

Table 207: 1T2Q-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1T6V	L_LYS.1	NZ	L_GLU.7	OE1	3.814
1T6V	L_LYS.1	NZ	L_GLU.7	OE2	2.661
1T6V	L_ARG.61	NH1	L_ASP.48	OD2	3.269
1T6V	L_ARG.73	NH1	N_ASP.93	OD2	3.564
1T6V	L_ARG.73	NH2	N_ASP.93	OD1	3.874
1T6V	L_ARG.73	NH2	N_ASP.93	OD2	2.603
1T6V	L_ARG.125	NH1	L_ASP.119	OD2	3.001
1T6V	L_ARG.125	NH2	L_ASP.119	OD1	3.584
1T6V	L_ARG.125	NH2	L_ASP.119	OD2	2.767
1T6V	N_ARG.2	NH2	N_ASP.4	OD1	3.696
1T6V	N_ARG.2	NH2	N_ASP.4	OD2	3.005
1T6V	N_ARG.25	NH1	N_ASP.4	OD2	2.946
1T6V	N_ARG.38	NH2	N_GLU.47	OE1	3.551
1T6V	N_LYS.40	NZ	N_GLU.76	OE1	3.049
1T6V	N_LYS.51	NZ	N_GLU.57	OE1	2.788
1T6V	N_LYS.51	NZ	N_GLU.57	OE2	3.528
1T6V	N_ARG.54	NH1	N_ASP.77	OD1	2.809
1T6V	N_ARG.54	NH1	N_ASP.77	OD2	3.785
1T6V	N_ARG.54	NH2	N_ASP.77	OD1	3.326
1T6V	N_ARG.54	NH2	N_ASP.77	OD2	2.873
1T6V	N_ARG.100	NH1	L_ASP.52	OD1	2.973
1T6V	N_ARG.100	NH1	L_ASP.52	OD2	3.510
1T6V	N_ARG.100	NH2	L_ASP.52	OD1	3.501
1T6V	N_ARG.100	NH2	L_ASP.52	OD2	3.094
1T6V	M_LYS.1	NZ	M_GLU.7	OE1	3.728
1T6V	M_LYS.1	NZ	M_GLU.7	OE2	2.757
1T6V	M_ARG.61	NH1	M_ASP.48	OD1	3.656
1T6V	M_ARG.61	NH1	M_ASP.48	OD2	3.383
1T6V	M_ARG.73	NH2	O_ASP.93	OD1	3.734
1T6V	M_ARG.73	NH2	O_ASP.93	OD2	2.904
1T6V	M_LYS.97	NZ	N_ASP.106	OD1	3.749
1T6V	M_LYS.97	NZ	N_ASP.106	OD2	2.853
1T6V	M_ARG.125	NH1	M_ASP.119	OD2	2.764
1T6V	M_ARG.125	NH2	M_ASP.119	OD1	3.456
1T6V	M_ARG.125	NH2	M_ASP.119	OD2	3.061
1T6V	O_ARG.2	NH1	O_ASP.26	OD2	3.626
1T6V	O_ARG.2	NH2	O_ASP.4	OD1	3.686
1T6V	O_ARG.2	NH2	O_ASP.4	OD2	2.970
1T6V	O_ARG.8	NH1	O_ASP.106	OD1	3.002
1T6V	O_ARG.8	NH2	O_ASP.106	OD1	3.850
1T6V	O_LYS.51	NZ	O_GLU.57	OE1	2.819
1T6V	O_LYS.51	NZ	O_GLU.57	OE2	3.551
1T6V	O_ARG.54	NH1	O_ASP.77	OD1	3.107
1T6V	O_ARG.54	NH1	O_ASP.77	OD2	3.912
1T6V	O_ARG.54	NH2	O_ASP.77	OD1	3.448
1T6V	O_ARG.54	NH2	O_ASP.77	OD2	2.988
1T6V	O_ARG.82	NH1	O_GLU.46	OE1	3.614
1T6V	O_ARG.82	NH1	O_GLU.46	OE2	3.761
1T6V	O_ARG.100	NH1	M_ASP.52	OD1	3.232
1T6V	O_ARG.100	NH1	M_ASP.52	OD2	2.872
1T6V	O_ARG.100	NH2	M_ASP.52	OD1	3.920
1T6V	O_ARG.100	NH2	M_ASP.52	OD2	2.990

Table 208: 1T6V-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1TYE	A_HIS_30	ND1	A_GLU_136	OE2	3.797
1TYE	A_HIS_30	ND1	E_ASP_429	OD2	3.896
1TYE	A_HIS_30	NE2	A_GLU_136	OE2	3.547
1TYE	A_ARG_32	NH1	E_ASP_429	OD1	3.657
1TYE	A_ARG_32	NH1	E_ASP_429	OD2	2.825
1TYE	A_ARG_73	NH1	C_ASP_71	OD1	3.528
1TYE	A_ARG_73	NH1	C_ASP_71	OD2	3.396
1TYE	A_ARG_73	NH2	A_ASP_71	OD1	3.946
1TYE	A_ARG_73	NH2	A_ASP_71	OD2	3.781
1TYE	A_ARG_73	NH2	C_ASP_71	OD2	2.714
1TYE	A_ARG_73	NH2	C_GLU_75	OE1	3.907
1TYE	A_LYS_88	NZ	A_ASP_71	OD1	3.924
1TYE	A_LYS_88	NZ	A_GLU_75	OE1	3.696
1TYE	A_ARG_90	NH2	A_GLU_49	OE1	3.556
1TYE	A_ARG_147	NH1	A_GLU_142	OE2	3.894
1TYE	A_ARG_147	NH2	A_GLU_142	OE2	3.182
1TYE	A_ARG_153	NH1	A_GLU_157	OE2	3.772
1TYE	A_ARG_153	NH2	A_GLU_120	OE1	3.065
1TYE	A_ARG_153	NH2	A_GLU_120	OE2	3.052
1TYE	A_ARG_165	NH1	A_ASP_163	OD1	2.964
1TYE	A_ARG_165	NH1	A_ASP_163	OD2	2.782
1TYE	A_ARG_165	NH2	A_GLU_123	OE1	2.740
1TYE	A_ARG_165	NH2	A_GLU_123	OE2	3.080
1TYE	A_ARG_279	NH2	A_GLU_268	OE2	3.715
1TYE	A_ARG_327	NH1	A_GLU_283	OE1	2.906
1TYE	A_ARG_335	NH1	A_ASP_301	OD1	3.950
1TYE	A_ARG_335	NH1	A_ASP_301	OD2	2.979
1TYE	A_ARG_335	NH2	A_ASP_301	OD1	3.045
1TYE	A_ARG_335	NH2	A_ASP_301	OD2	3.119
1TYE	A_ARG_422	NH1	A_ASP_24	OD1	3.230
1TYE	B_ARG_91	NH1	B_GLU_60	OE1	3.253
1TYE	B_ARG_91	NH2	B_ASP_432	OD2	3.964
1TYE	B_ARG_105	NH1	B_ASP_71	OD1	3.549
1TYE	B_LYS_159	NZ	B_ASP_224	OD1	3.816
1TYE	B_LYS_159	NZ	B_ASP_224	OD2	2.677
1TYE	B_LYS_209	NZ	B_GLU_206	OE1	3.537
1TYE	B_LYS_209	NZ	B_GLU_206	OE2	3.891
1TYE	B_ARG_216	NH1	A_GLU_123	OE1	2.702
1TYE	B_ARG_239	NH1	B_ASP_113	OD1	2.627
1TYE	B_LYS_253	NZ	A_ASP_232	OD2	3.290
1TYE	B_HIS_255	ND1	B_ASP_259	OD2	3.030
1TYE	B_HIS_255	NE2	B_ASP_158	OD2	3.791
1TYE	B_HIS_255	NE2	B_ASP_217	OD1	3.796
1TYE	B_HIS_255	NE2	B_ASP_217	OD2	2.660
1TYE	B_HIS_274	NE2	B_ASP_270	OD1	3.163
1TYE	B_HIS_274	NE2	B_ASP_270	OD2	2.921
1TYE	B_HIS_280	ND1	B_ASP_278	OD2	3.747
1TYE	B_LYS_298	NZ	B_GLU_297	OE2	3.673
1TYE	B_LYS_302	NZ	B_ASP_233	OD1	3.013
1TYE	B_LYS_302	NZ	B_ASP_233	OD2	3.373
1TYE	B_LYS_354	NZ	B_GLU_356	OE1	3.389
1TYE	B_LYS_390	NZ	B_ASP_393	OD2	3.994
1TYE	B_ARG_404	NH2	B_GLU_364	OE2	2.885
1TYE	B_LYS_410	NZ	B_ASP_434	OD1	3.437
1TYE	C_ARG_73	NH1	A_ASP_71	OD1	3.491
1TYE	C_ARG_73	NH2	A_ASP_71	OD1	3.688
1TYE	C_ARG_73	NH2	A_ASP_71	OD2	3.197

1TYE	C_ARG_73	NH2	C_ASP_71	OD1	3.681
1TYE	C_ARG_73	NH2	C_ASP_71	OD2	3.705
1TYE	C_LYS_88	NZ	C_ASP_71	OD1	3.778
1TYE	C_LYS_88	NZ	C_GLU_75	OE2	3.812
1TYE	C_ARG_90	NH1	C_GLU_49	OE1	2.673
1TYE	C_ARG_90	NH1	C_GLU_49	OE2	3.918
1TYE	C_LYS_118	NZ	C_GLU_117	OE2	3.898
1TYE	C_ARG_147	NH1	C_GLU_142	OE2	3.614
1TYE	C_ARG_147	NH2	C_GLU_142	OE2	3.566
1TYE	C_ARG_153	NH2	C_GLU_120	OE1	3.220
1TYE	C_ARG_153	NH2	C_GLU_120	OE2	3.597
1TYE	C_ARG_165	NH1	C_ASP_163	OD1	3.313
1TYE	C_ARG_165	NH1	C_ASP_163	OD2	2.716
1TYE	C_ARG_165	NH2	C_GLU_123	OE1	3.193
1TYE	C_ARG_165	NH2	C_GLU_123	OE2	3.129
1TYE	C_ARG_279	NH2	C_GLU_268	OE2	3.615
1TYE	C_ARG_281	NH2	C_GLU_229	OE2	3.746
1TYE	C_ARG_327	NH1	C_GLU_283	OE2	2.647
1TYE	C_ARG_422	NH1	C_ASP_24	OD1	2.911
1TYE	C_ARG_422	NH1	C_ASP_24	OD2	3.921
1TYE	D_LYS_46	NZ	D_ASP_47	OD2	3.909
1TYE	D_ARG_62	NH2	D_GLU_60	OE1	3.320
1TYE	D_ARG_91	NH1	D_ASP_432	OD2	3.976
1TYE	D_ARG_91	NH2	D_ASP_432	OD1	3.669
1TYE	D_ARG_91	NH2	D_ASP_432	OD2	3.225
1TYE	D_ARG_105	NH1	D_ASP_71	OD1	3.673
1TYE	D_LYS_159	NZ	D_ASP_224	OD1	3.999
1TYE	D_LYS_159	NZ	D_ASP_224	OD2	2.881
1TYE	D_LYS_209	NZ	D_GLU_206	OE2	3.266
1TYE	D_ARG_216	NH1	C_GLU_123	OE1	2.914
1TYE	D_ARG_216	NH1	C_GLU_123	OE2	3.969
1TYE	D_ARG_239	NH1	D_ASP_113	OD1	2.677
1TYE	D_HIS_244	NE2	D_ASP_113	OD2	3.772
1TYE	D_LYS_253	NZ	C_ASP_232	OD2	3.400
1TYE	D_HIS_255	ND1	D_ASP_259	OD2	2.788
1TYE	D_HIS_255	NE2	D_ASP_158	OD2	3.582
1TYE	D_HIS_255	NE2	D_ASP_217	OD1	3.881
1TYE	D_HIS_255	NE2	D_ASP_217	OD2	2.918
1TYE	D_HIS_274	NE2	D_ASP_270	OD1	3.141
1TYE	D_HIS_274	NE2	D_ASP_270	OD2	2.980
1TYE	D_HIS_280	ND1	D_ASP_278	OD2	3.600
1TYE	D_LYS_298	NZ	D_GLU_297	OE2	3.766
1TYE	D_LYS_302	NZ	D_ASP_233	OD1	3.683
1TYE	D_LYS_302	NZ	D_ASP_233	OD2	3.005
1TYE	D_LYS_354	NZ	D_GLU_356	OE1	3.054
1TYE	D_LYS_354	NZ	D_GLU_356	OE2	3.182
1TYE	D_ARG_360	NH1	D_GLU_358	OE2	2.869
1TYE	E_HIS_30	NE2	E_GLU_136	OE2	3.296
1TYE	E_ARG_32	NH2	E_ASP_28	OD2	3.193
1TYE	E_ARG_73	NH2	E_ASP_71	OD2	3.212
1TYE	E_LYS_88	NZ	E_GLU_75	OE1	3.717
1TYE	E_ARG_90	NH1	E_GLU_49	OE1	3.580
1TYE	E_ARG_153	NH1	E_GLU_157	OE2	3.995
1TYE	E_ARG_153	NH2	E_GLU_120	OE1	3.767
1TYE	E_ARG_165	NH1	E_ASP_163	OD1	3.534
1TYE	E_ARG_165	NH1	E_ASP_163	OD2	2.834
1TYE	E_ARG_165	NH2	E_GLU_123	OE1	2.970
1TYE	E_ARG_165	NH2	E_GLU_123	OE2	3.167

1TYE	E_ARG_279	NH2	E_GLU_268	OE2	3.525
1TYE	E_ARG_281	NH2	E_GLU_229	OE2	3.697
1TYE	E_ARG_327	NH1	E_GLU_283	OE2	2.691
1TYE	E_ARG_355	NH1	E_GLU_324	OE2	3.503
1TYE	E_ARG_368	NH2	A_ASP_429	OD2	3.921
1TYE	E_ARG_422	NH1	E_ASP_24	OD1	3.604
1TYE	E_ARG_422	NH1	E_ASP_24	OD2	3.672
1TYE	F_ARG_67	NH2	F_GLU_65	OE1	3.259
1TYE	F_ARG_91	NH1	F_GLU_60	OE2	2.911
1TYE	F_ARG_91	NH2	F_ASP_432	OD2	2.722
1TYE	F_LYS_159	NZ	F_ASP_224	OD2	2.976
1TYE	F_LYS_209	NZ	F_GLU_206	OE1	3.424
1TYE	F_ARG_214	NH2	F_ASP_179	OD2	2.925
1TYE	F_ARG_216	NH1	E_GLU_123	OE1	2.938
1TYE	F_ARG_216	NH1	E_GLU_123	OE2	3.244
1TYE	F_ARG_239	NH1	F_ASP_113	OD1	2.831
1TYE	F_ARG_239	NH1	F_ASP_113	OD2	3.398
1TYE	F_HIS_244	NE2	F_ASP_113	OD2	3.408
1TYE	F_LYS_253	NZ	E_ASP_232	OD2	3.394
1TYE	F_HIS_255	ND1	F_ASP_259	OD2	2.813
1TYE	F_HIS_255	NE2	F_ASP_158	OD2	3.756
1TYE	F_HIS_255	NE2	F_ASP_217	OD1	3.834
1TYE	F_HIS_255	NE2	F_ASP_217	OD2	2.822
1TYE	F_HIS_274	NE2	F_ASP_270	OD1	3.189
1TYE	F_HIS_274	NE2	F_ASP_270	OD2	2.810
1TYE	F_HIS_280	ND1	F_ASP_278	OD2	3.328
1TYE	F_LYS_298	NZ	F_GLU_297	OE2	3.779
1TYE	F_LYS_302	NZ	F_ASP_233	OD2	2.915
1TYE	F_LYS_354	NZ	F_GLU_356	OE2	3.665
1TYE	F_ARG_360	NH1	F_GLU_358	OE2	2.965

Table 209: 1TYE-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1TZH	V_ARG_23	NH1	W_GLU_30	OE2	3.100
1TZH	V_ARG_56	NH1	V_GLU_38	OE2	3.313
1TZH	V_ARG_56	NH2	V_GLU_38	OE1	3.086
1TZH	V_ARG_56	NH2	V_GLU_38	OE2	3.428
1TZH	V_ARG_82	NH2	V_GLU_42	OE1	2.933
1TZH	V_LYS_84	NZ	V_GLU_44	OE2	3.642
1TZH	V_HIS_90	NE2	H_ASP_33	OD1	2.826
1TZH	V_HIS_90	NE2	H_ASP_33	OD2	2.524
1TZH	V_ARG_105	NH2	V_GLU_103	OE1	3.855
1TZH	W_ARG_23	NH1	V_GLU_30	OE1	3.346
1TZH	W_ARG_56	NH1	W_GLU_38	OE2	3.335
1TZH	W_ARG_56	NH2	W_GLU_38	OE1	3.077
1TZH	W_ARG_56	NH2	W_GLU_38	OE2	3.382
1TZH	W_ARG_82	NH2	W_GLU_42	OE2	2.977
1TZH	W_HIS_90	NE2	B_ASP_33	OD1	3.121
1TZH	W_HIS_90	NE2	B_ASP_33	OD2	2.585
1TZH	W_HIS_99	NE2	W_GLU_73	OE2	3.842
1TZH	W_ARG_105	NH2	W_GLU_103	OE1	3.129
1TZH	W_LYS_107	NZ	W_GLU_67	OE1	3.188
1TZH	W_LYS_107	NZ	W_GLU_67	OE2	3.161
1TZH	A_ARG_24	NH1	A_ASP_70	OD2	3.886
1TZH	A_ARG_61	NH2	A_GLU_81	OE1	3.363
1TZH	A_ARG_61	NH2	A_ASP_82	OD1	3.162
1TZH	A_ARG_61	NH2	A_ASP_82	OD2	3.912
1TZH	A_LYS_103	NZ	A_GLU_165	OE1	2.800
1TZH	A_LYS_103	NZ	A_GLU_165	OE2	3.540
1TZH	A_LYS_149	NZ	A_GLU_195	OE1	3.634
1TZH	A_LYS_149	NZ	A_GLU_195	OE2	2.910
1TZH	A_LYS_183	NZ	A_GLU_187	OE1	3.287
1TZH	A_LYS_183	NZ	A_GLU_187	OE2	2.651
1TZH	A_LYS_188	NZ	A_ASP_185	OD1	3.831
1TZH	A_HIS_189	ND1	A_ASP_151	OD2	2.992
1TZH	B_ARG_38	NH1	B_ASP_86	OD1	3.008
1TZH	B_ARG_38	NH2	B_GLU_46	OE1	3.146
1TZH	B_ARG_38	NH2	B_GLU_46	OE2	3.677
1TZH	B_ARG_38	NH2	B_ASP_86	OD1	3.681
1TZH	B_ARG_66	NH1	B_ASP_86	OD1	3.515
1TZH	B_ARG_66	NH1	B_ASP_86	OD2	2.745
1TZH	B_ARG_66	NH2	B_ASP_86	OD1	3.270
1TZH	B_ARG_66	NH2	B_ASP_86	OD2	3.900
1TZH	B_ARG_94	NH2	B_ASP_32	OD1	3.304
1TZH	B_ARG_94	NH2	B_ASP_32	OD2	3.875
1TZH	B_LYS_143	NZ	B_ASP_144	OD1	2.731
1TZH	B_LYS_143	NZ	B_ASP_144	OD2	3.209
1TZH	B_LYS_209	NZ	A_GLU_123	OE2	3.903
1TZH	L_ARG_24	NH2	L_ASP_70	OD2	3.428
1TZH	L_ARG_61	NH2	L_GLU_81	OE1	3.330
1TZH	L_ARG_61	NH2	L_ASP_82	OD1	3.040
1TZH	L_ARG_61	NH2	L_ASP_82	OD2	3.443
1TZH	L_LYS_103	NZ	L_GLU_105	OE2	3.246
1TZH	L_LYS_103	NZ	L_GLU_165	OE1	3.341
1TZH	L_LYS_103	NZ	L_GLU_165	OE2	3.547
1TZH	L_ARG_142	NH2	L_GLU_165	OE1	3.821
1TZH	L_LYS_183	NZ	L_GLU_187	OE2	3.055
1TZH	L_ARG_211	NH2	L_GLU_187	OE1	3.313
1TZH	H_ARG_38	NH1	H_ASP_86	OD1	3.223
1TZH	H_ARG_38	NH2	H_GLU_46	OE1	3.456

1TZH	H_ARG_38	NH2	H_ASP_86	OD1	3.593
1TZH	H_ARG_66	NH1	H_ASP_86	OD2	3.197
1TZH	H_ARG_66	NH2	H_ASP_86	OD1	2.884
1TZH	H_ARG_66	NH2	H_ASP_86	OD2	3.307
1TZH	H_ARG_94	NH2	H_ASP_32	OD1	3.594
1TZH	H_ARG_94	NH2	H_ASP_32	OD2	2.870
1TZH	H_LYS_143	NZ	H_ASP_144	OD1	3.985
1TZH	H_LYS_143	NZ	H_ASP_144	OD2	3.661
1TZH	H_HIS_164	NE2	L_ASP_167	OD1	3.495
1TZH	H_LYS_209	NZ	L_GLU_123	OE1	2.754
1TZH	H_LYS_209	NZ	L_GLU_123	OE2	3.404

Table 210: 1TZH-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1TZI	A_ARG_24	NH1	A_ASP_70	OD1	3.345
1TZI	A_ARG_61	NH2	A_GLU_81	OE2	3.484
1TZI	A_ARG_61	NH2	A_ASP_82	OD1	3.184
1TZI	A_LYS_103	NZ	A_GLU_165	OE2	3.341
1TZI	A_LYS_149	NZ	A_GLU_195	OE2	3.678
1TZI	B_HIS_35	NE2	B_ASP_33	OD1	3.655
1TZI	B_HIS_35	NE2	B_ASP_33	OD2	3.046
1TZI	B_HIS_35	NE2	B_ASP_50	OD2	3.907
1TZI	B_ARG_38	NH1	B_ASP_86	OD1	3.155
1TZI	B_ARG_38	NH2	B_GLU_46	OE1	3.042
1TZI	B_ARG_38	NH2	B_GLU_46	OE2	3.847
1TZI	B_ARG_38	NH2	B_ASP_86	OD1	3.843
1TZI	B_LYS_64	NZ	B_ASP_61	OD1	3.600
1TZI	B_LYS_64	NZ	B_ASP_61	OD2	3.744
1TZI	B_ARG_66	NH1	B_ASP_86	OD2	3.093
1TZI	B_ARG_66	NH2	B_ASP_86	OD1	3.082
1TZI	B_ARG_66	NH2	B_ASP_86	OD2	3.244
1TZI	B_ARG_94	NH2	B_ASP_101	OD1	3.674
1TZI	B_ARG_94	NH2	B_ASP_101	OD2	2.631
1TZI	B_LYS_143	NZ	B_ASP_144	OD1	3.643
1TZI	B_LYS_143	NZ	B_ASP_144	OD2	3.293
1TZI	B_LYS_209	NZ	A_GLU_123	OE2	3.786
1TZI	V_ARG_56	NH1	V_GLU_38	OE1	3.287
1TZI	V_ARG_56	NH1	V_GLU_38	OE2	3.396
1TZI	V_ARG_56	NH2	V_GLU_38	OE2	3.863
1TZI	V_HIS_99	NE2	V_GLU_73	OE2	3.539

Table 211: 1TZI-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1U6A	L_ARG_24	NH2	L_ASP_70	OD2	3.902
1U6A	L_ARG_61	NH1	L_GLU_79	OE2	3.901
1U6A	L_ARG_61	NH2	L_GLU_81	OE2	3.590
1U6A	L_ARG_61	NH2	L_ASP_82	OD1	2.937
1U6A	L_ARG_61	NH2	L_ASP_82	OD2	3.603
1U6A	L_LYS_149	NZ	L_GLU_195	OE1	2.946
1U6A	L_LYS_149	NZ	L_GLU_195	OE2	3.367
1U6A	L_LYS_188	NZ	L_ASP_185	OD1	3.941
1U6A	L_HIS_189	ND1	L_ASP_151	OD2	2.371
1U6A	L_ARG_211	NH1	L_GLU_187	OE1	2.862
1U6A	H_ARG_38	NH1	H_ASP_86	OD1	2.883
1U6A	H_ARG_38	NH2	H_ASP_86	OD1	3.710
1U6A	H_ARG_66	NH1	H_ASP_86	OD1	3.475
1U6A	H_ARG_66	NH1	H_ASP_86	OD2	2.761
1U6A	H_ARG_66	NH2	H_ASP_86	OD1	2.683
1U6A	H_ARG_66	NH2	H_ASP_86	OD2	3.375
1U6A	H_LYS_143	NZ	H_ASP_144	OD1	3.705
1U6A	H_LYS_143	NZ	H_ASP_144	OD2	3.600
1U6A	H_HIS_164	NE2	L_ASP_167	OD1	3.994
1U6A	H_LYS_210	NZ	H_GLU_212	OE2	3.157

Table 212: 1U6A-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1UA6	L_ARG_61	NH1	L_GLU_81	OE2	3.789
1UA6	L_ARG_61	NH2	L_GLU_81	OE2	2.779
1UA6	L_ARG_61	NH2	L_ASP_82	OD1	2.629
1UA6	L_ARG_61	NH2	L_ASP_82	OD2	3.362
1UA6	L_LYS_103	NZ	L_GLU_105	OE2	3.651
1UA6	H_ARG_38	NH1	H_ASP_89	OD2	2.881
1UA6	H_ARG_38	NH2	H_GLU_46	OE1	2.829
1UA6	H_ARG_38	NH2	H_ASP_89	OD2	3.526
1UA6	H_ARG_66	NH1	H_ASP_89	OD1	3.005
1UA6	H_ARG_66	NH1	H_ASP_89	OD2	3.836
1UA6	H_ARG_66	NH2	H_ASP_89	OD1	3.531
1UA6	H_ARG_66	NH2	H_ASP_89	OD2	2.947
1UA6	Y_LYS_1	NZ	Y_GLU_7	OE2	3.070
1UA6	Y_LYS_13	NZ	Y_ASP_18	OD2	2.985
1UA6	Y_LYS_97	NZ	H_ASP_32	OD1	2.722
1UA6	Y_LYS_97	NZ	H_ASP_99	OD2	2.674
1UA6	Y_ARG_125	NH1	Y_ASP_119	OD1	3.848
1UA6	Y_ARG_125	NH1	Y_ASP_119	OD2	3.662
1UA6	Y_ARG_125	NH2	Y_ASP_119	OD2	2.731

Table 213: 1UA6-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID residue name residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1UAC	L_ARG_45	NH2	L_GLU_42	OE1	3.506
1UAC	L_ARG_61	NH1	L_GLU_79	OE1	3.446
1UAC	L_ARG_61	NH1	L_GLU_79	OE2	3.988
1UAC	L_ARG_61	NH2	L_GLU_79	OE1	3.597
1UAC	L_ARG_61	NH2	L_GLU_81	OE2	2.939
1UAC	L_ARG_61	NH2	L_ASP_82	OD1	3.382
1UAC	L_ARG_61	NH2	L_ASP_82	OD2	3.786
1UAC	H_ARG_38	NH1	H_ASP_89	OD1	2.495
1UAC	H_ARG_38	NH2	H_GLU_46	OE1	2.848
1UAC	H_ARG_38	NH2	H_ASP_89	OD1	3.590
1UAC	H_ARG_66	NH1	H_ASP_89	OD1	3.633
1UAC	H_ARG_66	NH1	H_ASP_89	OD2	2.604
1UAC	H_ARG_66	NH2	H_ASP_89	OD1	3.226
1UAC	H_ARG_66	NH2	H_ASP_89	OD2	3.547
1UAC	Y_LYS_1	NZ	Y_GLU_7	OE2	3.056
1UAC	Y_LYS_13	NZ	Y_ASP_18	OD2	3.156
1UAC	Y_LYS_97	NZ	H_ASP_32	OD1	2.750
1UAC	Y_LYS_97	NZ	H_ASP_32	OD2	3.845
1UAC	Y_LYS_97	NZ	H_ASP_99	OD2	2.749
1UAC	Y_HIS_121	ND1	Y_ASP_119	OD1	3.781
1UAC	Y_HIS_121	NE2	Y_ASP_119	OD1	3.474
1UAC	Y_ARG_125	NH1	Y_ASP_119	OD1	3.237
1UAC	Y_ARG_125	NH1	Y_ASP_119	OD2	3.553
1UAC	Y_ARG_125	NH2	Y_ASP_119	OD1	3.403
1UAC	Y_ARG_125	NH2	Y_ASP_119	OD2	2.499

Table 214: 1UAC-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1UCB	L_ARG_24	NH1	L_ASP_70	OD1	3.292
1UCB	L_ARG_24	NH1	L_ASP_70	OD2	3.887
1UCB	L_ARG_24	NH2	L_ASP_70	OD1	3.839
1UCB	L_ARG_24	NH2	L_ASP_70	OD2	3.203
1UCB	L_LYS_50	NZ	H_ASP_98	OD1	3.160
1UCB	L_ARG_61	NH1	L_ASP_82	OD2	2.752
1UCB	L_ARG_61	NH2	L_GLU_81	OE2	3.557
1UCB	L_ARG_61	NH2	L_ASP_82	OD1	2.863
1UCB	L_ARG_61	NH2	L_ASP_82	OD2	2.961
1UCB	L_ARG_77	NH2	L_GLU_79	OE1	3.741
1UCB	L_ARG_77	NH2	L_GLU_79	OE2	2.900
1UCB	L_LYS_103	NZ	L_GLU_165	OE1	3.505
1UCB	L_LYS_103	NZ	L_GLU_165	OE2	3.935
1UCB	L_ARG_142	NH2	L_GLU_165	OE1	3.407
1UCB	L_LYS_188	NZ	L_ASP_185	OD2	3.372
1UCB	L_HIS_189	ND1	L_ASP_151	OD2	3.021
1UCB	L_ARG_211	NH2	L_GLU_187	OE1	3.809
1UCB	H_ARG_38	NH1	H_ASP_86	OD1	2.991
1UCB	H_ARG_38	NH2	H_GLU_46	OE1	3.160
1UCB	H_LYS_64	NZ	H_ASP_61	OD1	2.788
1UCB	H_LYS_64	NZ	H_ASP_61	OD2	3.139
1UCB	H_ARG_66	NH1	H_ASP_86	OD1	3.656
1UCB	H_ARG_66	NH1	H_ASP_86	OD2	2.889
1UCB	H_ARG_66	NH2	H_ASP_86	OD1	3.058
1UCB	H_ARG_66	NH2	H_ASP_86	OD2	3.202
1UCB	H_LYS_75	NZ	H_ASP_72	OD2	3.809
1UCB	H_LYS_221	NZ	L_GLU_123	OE1	3.128
1UCB	H_ARG_222	NH1	H_GLU_226	OE1	3.921
1UCB	H_ARG_222	NH1	H_GLU_226	OE2	3.794
1UCB	H_ARG_222	NH2	H_GLU_226	OE2	3.739

Table 215: 1UCB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1UJ3	A_ARG.61	NH2	A_GLU.81	OE2	3.553
1UJ3	A_ARG.61	NH2	A_ASP.82	OD1	2.902
1UJ3	A_ARG.61	NH2	A_ASP.82	OD2	3.527
1UJ3	A_HIS.91	NE2	B_ASP.399	OD1	3.708
1UJ3	A_HIS.91	NE2	B_ASP.399	OD2	2.884
1UJ3	A_LYS.103	NZ	A_GLU.165	OE1	3.612
1UJ3	A_LYS.103	NZ	A_GLU.165	OE2	3.641
1UJ3	A_LYS.107	NZ	A_ASP.17	OD2	3.650
1UJ3	A_LYS.149	NZ	A_GLU.195	OE1	2.640
1UJ3	A_LYS.149	NZ	A_GLU.195	OE2	3.439
1UJ3	A_LYS.183	NZ	A_GLU.187	OE1	3.625
1UJ3	A_LYS.183	NZ	A_GLU.187	OE2	3.082
1UJ3	A_LYS.188	NZ	A_ASP.185	OD1	3.389
1UJ3	B_HIS.335	NE2	B_ASP.399	OD1	3.715
1UJ3	B_LYS.363	NZ	B_ASP.361	OD1	2.797
1UJ3	B_LYS.363	NZ	B_ASP.361	OD2	3.526
1UJ3	B_ARG.367	NH1	B_ASP.390	OD1	3.568
1UJ3	B_ARG.367	NH1	B_ASP.390	OD2	2.817
1UJ3	B_ARG.367	NH2	B_ASP.390	OD1	2.726
1UJ3	B_ARG.367	NH2	B_ASP.390	OD2	3.364
1UJ3	B_ARG.398	NH2	B_ASP.405	OD1	3.535
1UJ3	B_ARG.398	NH2	B_ASP.405	OD2	2.642
1UJ3	B_ARG.433	NH2	B_GLU.516	OE2	3.825
1UJ3	B_LYS.447	NZ	B_ASP.448	OD1	3.091
1UJ3	B_LYS.447	NZ	B_ASP.448	OD2	2.878
1UJ3	B_LYS.513	NZ	A_GLU.123	OE1	3.554
1UJ3	B_LYS.513	NZ	A_GLU.123	OE2	3.075
1UJ3	B_ARG.514	NH2	B_GLU.516	OE1	3.640
1UJ3	C_LYS.615	NZ	C_GLU.624	OE1	2.927
1UJ3	C_LYS.646	NZ	C_GLU.662	OE2	3.280
1UJ3	C_LYS.648	NZ	C_GLU.662	OE2	3.204
1UJ3	C_LYS.665	NZ	C_GLU.662	OE1	3.069
1UJ3	C_LYS.665	NZ	C_GLU.662	OE2	3.168
1UJ3	C_LYS.722	NZ	C_ASP.778	OD1	2.825
1UJ3	C_LYS.722	NZ	C_ASP.778	OD2	3.467
1UJ3	C_LYS.759	NZ	C_ASP.780	OD2	2.414
1UJ3	C_LYS.766	NZ	A_ASP.1	OD1	3.997
1UJ3	C_LYS.769	NZ	B_ASP.399	OD1	2.791
1UJ3	C_LYS.769	NZ	B_ASP.399	OD2	3.372
1UJ3	C_LYS.801	NZ	B_ASP.352	OD1	2.774
1UJ3	C_LYS.801	NZ	B_ASP.352	OD2	3.632

Table 216: 1UJ3-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1UWX	A.LYS_36	NZ	A.GLU_32	OE1	2.824
1UWX	B.LYS_36	NZ	B.GLU_32	OE2	2.807
1UWX	H.LYS_12	NZ	H.GLU_10	OE1	3.100
1UWX	H.LYS_64	NZ	H.ASP_61	OD1	3.798
1UWX	H.ARG_66	NH1	H.ASP_86	OD1	2.454
1UWX	H.ARG_66	NH1	H.ASP_86	OD2	2.896
1UWX	H.ARG_94	NH2	H.ASP_101	OD1	2.904
1UWX	H.ARG_94	NH2	H.ASP_101	OD2	3.891
1UWX	H.HIS_164	NE2	L.ASP_168	OD2	3.899
1UWX	H.LYS_208	NZ	L.GLU_124	OE2	2.744
1UWX	H.LYS_209	NZ	H.GLU_211	OE2	3.816
1UWX	K.ARG_63	NH1	K.ASP_84	OD1	3.154
1UWX	K.ARG_63	NH1	K.ASP_84	OD2	2.158
1UWX	K.ARG_63	NH2	K.ASP_84	OD1	3.226
1UWX	K.ARG_63	NH2	K.ASP_84	OD2	3.623
1UWX	K.LYS_150	NZ	K.GLU_196	OE1	3.737
1UWX	K.LYS_150	NZ	K.GLU_196	OE2	3.159
1UWX	K.ARG_156	NH1	K.GLU_186	OE1	2.610
1UWX	K.ARG_156	NH1	K.GLU_186	OE2	3.937
1UWX	K.ARG_156	NH2	K.GLU_186	OE1	3.178
1UWX	K.ARG_156	NH2	K.GLU_186	OE2	2.975
1UWX	K.LYS_184	NZ	K.GLU_188	OE1	3.993
1UWX	K.HIS_190	ND1	K.ASP_152	OD2	2.933
1UWX	K.LYS_200	NZ	K.ASP_111	OD2	3.114
1UWX	K.ARG_212	NH1	K.GLU_188	OE2	3.245
1UWX	L.ARG_63	NH1	L.ASP_84	OD1	3.321
1UWX	L.ARG_63	NH1	L.ASP_84	OD2	2.266
1UWX	L.ARG_63	NH2	L.ASP_84	OD1	3.278
1UWX	L.ARG_63	NH2	L.ASP_84	OD2	3.625
1UWX	L.LYS_150	NZ	L.GLU_196	OE1	3.639
1UWX	L.LYS_150	NZ	L.GLU_196	OE2	3.224
1UWX	L.ARG_156	NH1	L.GLU_186	OE1	2.635
1UWX	L.ARG_156	NH1	L.GLU_186	OE2	3.963
1UWX	L.ARG_156	NH2	L.GLU_186	OE1	3.120
1UWX	L.ARG_156	NH2	L.GLU_186	OE2	2.947
1UWX	L.LYS_184	NZ	L.GLU_188	OE1	3.917
1UWX	L.HIS_190	ND1	L.ASP_152	OD2	2.931
1UWX	L.LYS_200	NZ	L.ASP_111	OD2	3.029
1UWX	L.ARG_212	NH1	L.GLU_188	OE2	3.191
1UWX	M.LYS_12	NZ	M.GLU_10	OE1	3.235
1UWX	M.LYS_64	NZ	M.ASP_61	OD1	3.798
1UWX	M.ARG_66	NH1	M.ASP_86	OD1	2.526
1UWX	M.ARG_66	NH1	M.ASP_86	OD2	2.861
1UWX	M.ARG_94	NH2	M.ASP_101	OD1	2.895
1UWX	M.ARG_94	NH2	M.ASP_101	OD2	3.832
1UWX	M.LYS_208	NZ	K.GLU_124	OE2	2.705
1UWX	M.LYS_209	NZ	M.GLU_211	OE1	3.750

Table 217: 1UWX-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1UZ6	E_ARG_24	NH1	E_ASP_70	OD2	3.187
1UZ6	E_LYS_39	NZ	E_GLU_81	OE1	3.464
1UZ6	E_ARG_61	NH1	E_ASP_82	OD1	3.736
1UZ6	E_ARG_61	NH1	E_ASP_82	OD2	2.887
1UZ6	E_ARG_61	NH2	E_GLU_79	OE1	3.920
1UZ6	E_ARG_61	NH2	E_GLU_79	OE2	3.989
1UZ6	E_ARG_61	NH2	E_ASP_82	OD1	3.165
1UZ6	E_ARG_61	NH2	E_ASP_82	OD2	3.643
1UZ6	E_LYS_103	NZ	E_ASP_164	OD1	3.599
1UZ6	E_ARG_154	NH2	E_GLU_184	OE1	3.820
1UZ6	E_ARG_154	NH2	E_GLU_184	OE2	3.327
1UZ6	E_LYS_182	NZ	E_ASP_183	OD1	3.722
1UZ6	E_ARG_210	NH1	E_GLU_186	OE1	3.231
1UZ6	F_ARG_38	NH1	F_ASP_86	OD1	2.903
1UZ6	F_ARG_38	NH2	F_GLU_46	OE1	2.942
1UZ6	F_ARG_38	NH2	F_ASP_86	OD1	3.966
1UZ6	F_LYS_66	NZ	F_ASP_86	OD1	3.610
1UZ6	F_LYS_66	NZ	F_ASP_86	OD2	2.606
1UZ6	F_ARG_164	NH1	E_ASP_166	OD1	3.662
1UZ6	F_ARG_164	NH2	E_ASP_166	OD1	3.708
1UZ6	F_ARG_164	NH2	E_ASP_169	OD2	3.554
1UZ6	F_LYS_208	NZ	E_GLU_122	OE1	3.883
1UZ6	F_ARG_209	NH1	E_GLU_122	OE2	3.531
1UZ6	H_ARG_38	NH1	H_ASP_86	OD1	2.872
1UZ6	H_ARG_38	NH2	H_GLU_46	OE1	3.043
1UZ6	H_ARG_38	NH2	H_ASP_86	OD1	3.674
1UZ6	H_LYS_66	NZ	H_GLU_85	OE2	3.660
1UZ6	H_LYS_66	NZ	H_ASP_86	OD1	3.366
1UZ6	H_LYS_66	NZ	H_ASP_86	OD2	2.666
1UZ6	H_ARG_164	NH1	L_ASP_166	OD1	3.603
1UZ6	H_ARG_164	NH2	L_ASP_166	OD1	3.557
1UZ6	H_ARG_164	NH2	L_ASP_169	OD2	3.746
1UZ6	H_LYS_208	NZ	L_GLU_122	OE1	3.795
1UZ6	H_ARG_209	NH1	L_GLU_122	OE2	3.180
1UZ6	L_ARG_24	NH1	L_ASP_70	OD2	3.991
1UZ6	L_LYS_27	NZ	L_GLU_93	OE1	3.534
1UZ6	L_LYS_27	NZ	L_GLU_93	OE2	2.676
1UZ6	L_ARG_61	NH1	L_ASP_82	OD1	3.953
1UZ6	L_ARG_61	NH1	L_ASP_82	OD2	2.962
1UZ6	L_ARG_61	NH2	L_GLU_79	OE1	3.473
1UZ6	L_ARG_61	NH2	L_GLU_79	OE2	3.740
1UZ6	L_ARG_61	NH2	L_ASP_82	OD1	3.090
1UZ6	L_ARG_61	NH2	L_ASP_82	OD2	3.270
1UZ6	L_LYS_103	NZ	L_ASP_164	OD1	3.480
1UZ6	L_LYS_146	NZ	L_GLU_194	OE1	3.535
1UZ6	L_LYS_148	NZ	L_GLU_194	OE1	3.899
1UZ6	L_ARG_154	NH2	L_GLU_184	OE2	3.580
1UZ6	L_LYS_182	NZ	L_ASP_183	OD1	3.739
1UZ6	L_HIS_188	ND1	L_ASP_150	OD2	3.153
1UZ6	L_ARG_210	NH1	L_GLU_186	OE1	3.084
1UZ6	M_ARG_61	NH1	M_ASP_82	OD1	3.933
1UZ6	M_ARG_61	NH1	M_ASP_82	OD2	3.129
1UZ6	M_ARG_61	NH2	M_GLU_79	OE1	3.335
1UZ6	M_ARG_61	NH2	M_GLU_79	OE2	3.866
1UZ6	M_ARG_61	NH2	M_ASP_82	OD1	3.049
1UZ6	M_ARG_61	NH2	M_ASP_82	OD2	3.623
1UZ6	M_LYS_148	NZ	M_GLU_194	OE2	3.095

1UZ6	M_ARG_187	NH2	M_ASP_183	OD2	3.819
1UZ6	M_ARG_210	NH1	M_GLU_186	OE1	3.314
1UZ6	P_ARG_38	NH1	P_ASP_86	OD1	3.091
1UZ6	P_ARG_38	NH2	P_GLU_46	OE1	3.209
1UZ6	P_LYS_66	NZ	P_GLU_85	OE2	3.456
1UZ6	P_LYS_66	NZ	P_ASP_86	OD1	3.180
1UZ6	P_LYS_66	NZ	P_ASP_86	OD2	2.816
1UZ6	P_ARG_164	NH1	M_ASP_166	OD1	3.636
1UZ6	P_ARG_164	NH2	M_ASP_166	OD1	3.666
1UZ6	P_ARG_164	NH2	M_ASP_166	OD2	3.901
1UZ6	P_ARG_164	NH2	M_ASP_169	OD2	3.942
1UZ6	P_LYS_208	NZ	M_GLU_122	OE1	3.361
1UZ6	V_ARG_24	NH1	V_ASP_70	OD1	3.878
1UZ6	V_ARG_61	NH1	V_GLU_79	OE2	3.911
1UZ6	V_ARG_61	NH1	V_ASP_82	OD1	3.899
1UZ6	V_ARG_61	NH1	V_ASP_82	OD2	2.935
1UZ6	V_ARG_61	NH2	V_GLU_79	OE1	3.307
1UZ6	V_ARG_61	NH2	V_GLU_79	OE2	3.400
1UZ6	V_ARG_61	NH2	V_ASP_82	OD1	3.022
1UZ6	V_ARG_61	NH2	V_ASP_82	OD2	3.415
1UZ6	V_ARG_210	NH1	V_GLU_186	OE1	3.469
1UZ6	W_ARG_38	NH1	W_ASP_86	OD1	2.995
1UZ6	W_ARG_38	NH2	W_GLU_46	OE1	3.152
1UZ6	W_ARG_38	NH2	W_ASP_86	OD1	3.942
1UZ6	W_LYS_66	NZ	W_ASP_86	OD1	3.438
1UZ6	W_LYS_66	NZ	W_ASP_86	OD2	2.729
1UZ6	W_ARG_164	NH2	V_ASP_166	OD1	3.892
1UZ6	W_LYS_208	NZ	V_GLU_122	OE1	3.069

Table 218: 1UZ6-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1UZ8	A_LYS_27	NZ	A_GLU_93	OE1	3.391
1UZ8	A_LYS_27	NZ	A_GLU_93	OE2	2.682
1UZ8	A_ARG_61	NH1	A_ASP_82	OD1	3.976
1UZ8	A_ARG_61	NH1	A_ASP_82	OD2	2.909
1UZ8	A_ARG_61	NH2	A_GLU_79	OE1	3.289
1UZ8	A_ARG_61	NH2	A_GLU_79	OE2	3.601
1UZ8	A_ARG_61	NH2	A_ASP_82	OD1	3.343
1UZ8	A_ARG_61	NH2	A_ASP_82	OD2	3.539
1UZ8	A_LYS_146	NZ	A_GLU_153	OE1	3.641
1UZ8	A_LYS_148	NZ	A_GLU_194	OE1	3.715
1UZ8	A_LYS_148	NZ	A_GLU_194	OE2	3.109
1UZ8	A_ARG_154	NH2	A_GLU_184	OE2	3.405
1UZ8	A_LYS_198	NZ	A_ASP_109	OD2	3.179
1UZ8	B_ARG_38	NH1	B_ASP_86	OD1	2.828
1UZ8	B_ARG_38	NH2	B_GLU_46	OE1	2.788
1UZ8	B_ARG_38	NH2	B_ASP_86	OD1	3.820
1UZ8	B_ARG_164	NH1	A_ASP_166	OD1	3.299
1UZ8	B_ARG_164	NH2	A_ASP_166	OD1	3.745
1UZ8	B_ARG_164	NH2	A_ASP_169	OD2	3.660
1UZ8	H_ARG_38	NH1	H_ASP_86	OD1	2.763
1UZ8	H_ARG_38	NH2	H_GLU_46	OE1	2.922
1UZ8	H_ARG_38	NH2	H_GLU_46	OE2	3.999
1UZ8	H_ARG_38	NH2	H_ASP_86	OD1	3.765
1UZ8	H_LYS_66	NZ	H_ASP_86	OD1	3.706
1UZ8	H_LYS_66	NZ	H_ASP_86	OD2	2.911
1UZ8	H_ARG_83	NH1	H_GLU_85	OE1	3.092
1UZ8	H_ARG_164	NH1	L_ASP_166	OD1	3.385
1UZ8	H_ARG_164	NH2	L_ASP_166	OD1	3.573
1UZ8	H_ARG_164	NH2	L_ASP_169	OD2	3.234
1UZ8	H_ARG_209	NH1	H_GLU_211	OE2	3.154
1UZ8	L_ARG_24	NH1	L_ASP_70	OD1	2.826
1UZ8	L_ARG_24	NH1	L_ASP_70	OD2	3.113
1UZ8	L_ARG_24	NH2	L_ASP_70	OD1	3.329
1UZ8	L_LYS_27	NZ	L_GLU_93	OE2	2.774
1UZ8	L_ARG_61	NH1	L_ASP_82	OD1	3.829
1UZ8	L_ARG_61	NH1	L_ASP_82	OD2	2.912
1UZ8	L_ARG_61	NH2	L_GLU_79	OE1	3.480
1UZ8	L_ARG_61	NH2	L_GLU_79	OE2	3.414
1UZ8	L_ARG_61	NH2	L_ASP_82	OD1	3.012
1UZ8	L_ARG_61	NH2	L_ASP_82	OD2	3.357
1UZ8	L_LYS_148	NZ	L_GLU_194	OE1	3.195
1UZ8	L_LYS_148	NZ	L_GLU_194	OE2	2.816
1UZ8	L_LYS_168	NZ	L_ASP_169	OD2	3.822
1UZ8	L_ARG_187	NH1	L_ASP_183	OD1	2.762
1UZ8	L_ARG_187	NH1	L_ASP_183	OD2	3.197
1UZ8	L_ARG_187	NH2	L_ASP_183	OD2	3.876
1UZ8	L_HIS_188	ND1	L_ASP_150	OD2	3.610
1UZ8	L_LYS_198	NZ	L_ASP_109	OD2	3.897

Table 219: 1UZ8-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1V7M	L_ARG_60	NH1	L_GLU_80	OE2	3.088
1V7M	L_ARG_60	NH1	L_ASP_81	OD1	3.052
1V7M	L_ARG_60	NH1	L_ASP_81	OD2	3.141
1V7M	L_ARG_60	NH2	L_GLU_80	OE2	3.221
1V7M	L_ARG_95	NH1	H_GLU_50	OE1	3.532
1V7M	L_LYS_106	NZ	L_GLU_17	OE1	3.130
1V7M	L_LYS_106	NZ	L_GLU_17	OE2	3.699
1V7M	L_LYS_148	NZ	L_GLU_194	OE2	3.477
1V7M	L_ARG_154	NH1	L_GLU_184	OE1	3.773
1V7M	L_HIS_188	ND1	L_ASP_150	OD2	2.800
1V7M	H_ARG_38	NH1	H_GLU_46	OE1	2.783
1V7M	H_ARG_38	NH1	H_GLU_46	OE2	2.898
1V7M	H_ARG_38	NH2	H_ASP_92	OD1	2.675
1V7M	H_ARG_52	NH1	H_GLU_50	OE2	3.445
1V7M	H_LYS_54	NZ	H_ASP_76	OD2	3.910
1V7M	H_HIS_58	NE2	H_ASP_76	OD2	3.340
1V7M	H_LYS_67	NZ	H_GLU_64	OE2	3.635
1V7M	H_ARG_69	NH1	H_ASP_92	OD1	3.860
1V7M	H_ARG_69	NH2	H_ASP_92	OD1	3.348
1V7M	H_ARG_69	NH2	H_ASP_92	OD2	2.369
1V7M	H_ARG_74	NH2	H_ASP_76	OD1	3.636
1V7M	V_LYS_14	NZ	V_ASP_18	OD1	3.648
1V7M	V_ARG_98	NH2	H_ASP_31	OD1	3.697
1V7M	M_ARG_60	NH1	M_GLU_80	OE2	3.752
1V7M	M_ARG_60	NH1	M_ASP_81	OD1	2.835
1V7M	M_ARG_60	NH1	M_ASP_81	OD2	3.333
1V7M	M_ARG_60	NH2	M_GLU_80	OE2	3.575
1V7M	M_ARG_95	NH1	L_GLU_50	OE1	3.801
1V7M	M_LYS_102	NZ	M_GLU_104	OE1	2.649
1V7M	M_LYS_106	NZ	M_GLU_17	OE1	2.876
1V7M	M_LYS_148	NZ	M_GLU_194	OE2	3.647
1V7M	M_ARG_154	NH1	M_GLU_184	OE1	3.586
1V7M	M_ARG_154	NH1	M_GLU_184	OE2	3.164
1V7M	M_LYS_182	NZ	M_GLU_186	OE1	2.598
1V7M	M_LYS_182	NZ	M_GLU_186	OE2	3.298
1V7M	M_ARG_187	NH2	M_ASP_183	OD1	3.583
1V7M	M_HIS_188	ND1	M_ASP_150	OD2	3.144
1V7M	M_HIS_188	NE2	M_GLU_184	OE1	3.787
1V7M	L_LYS_3	NZ	L_GLU_1	OE1	3.725
1V7M	L_LYS_3	NZ	L_GLU_1	OE2	3.237
1V7M	L_ARG_38	NH1	L_GLU_46	OE1	2.802
1V7M	L_ARG_38	NH1	L_GLU_46	OE2	3.233
1V7M	L_ARG_38	NH2	L_ASP_92	OD1	2.882
1V7M	L_ARG_52	NH1	L_GLU_50	OE2	3.907
1V7M	L_HIS_58	NE2	L_ASP_76	OD2	3.052
1V7M	L_LYS_67	NZ	L_GLU_64	OE2	3.990
1V7M	L_ARG_69	NH1	L_ASP_92	OD1	3.419
1V7M	L_ARG_69	NH2	L_ASP_92	OD1	2.654
1V7M	L_ARG_69	NH2	L_ASP_92	OD2	2.603
1V7M	L_ARG_74	NH2	L_ASP_76	OD1	3.380
1V7M	X_LYS_14	NZ	X_ASP_18	OD1	3.674
1V7M	X_HIS_33	ND1	X_GLU_31	OE2	3.284
1V7M	X_LYS_59	NZ	X_GLU_56	OE2	3.569
1V7M	X_ARG_98	NH2	L_ASP_31	OD1	3.214
1V7M	X_ARG_117	NH1	X_ASP_45	OD1	3.802
1V7M	X_ARG_117	NH1	X_ASP_45	OD2	3.906

Table 220: 1V7M-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1V7N	L_ARG_60	NH1	L_ASP_81	OD1	2.332
1V7N	L_ARG_60	NH1	L_ASP_81	OD2	3.010
1V7N	L_ARG_60	NH2	L_GLU_80	OE2	2.836
1V7N	L_ARG_95	NH1	H_GLU_50	OE1	3.194
1V7N	L_LYS_102	NZ	L_ASP_164	OD1	2.653
1V7N	L_ARG_107	NH1	L_ASP_169	OD2	2.613
1V7N	L_ARG_107	NH1	O_GLU_78	OE2	3.587
1V7N	L_ARG_107	NH2	O_GLU_78	OE1	3.844
1V7N	L_ARG_107	NH2	O_GLU_78	OE2	2.214
1V7N	L_LYS_148	NZ	L_GLU_194	OE2	3.869
1V7N	L_ARG_154	NH2	L_GLU_184	OE1	2.591
1V7N	L_ARG_154	NH2	L_GLU_184	OE2	3.206
1V7N	L_LYS_182	NZ	L_GLU_186	OE2	3.250
1V7N	L_HIS_188	ND1	L_ASP_150	OD2	2.542
1V7N	L_LYS_198	NZ	L_ASP_109	OD2	2.675
1V7N	H_LYS_3	NZ	H_GLU_5	OE1	3.106
1V7N	H_ARG_38	NH1	H_GLU_46	OE1	2.776
1V7N	H_ARG_38	NH1	H_GLU_46	OE2	3.676
1V7N	H_ARG_38	NH1	H_ASP_92	OD1	3.973
1V7N	H_ARG_38	NH2	H_ASP_92	OD1	3.183
1V7N	H_LYS_43	NZ	H_GLU_46	OE2	3.925
1V7N	H_LYS_54	NZ	H_ASP_76	OD2	3.243
1V7N	H_HIS_58	NE2	H_ASP_76	OD1	3.889
1V7N	H_HIS_58	NE2	H_ASP_76	OD2	2.715
1V7N	H_LYS_67	NZ	H_GLU_64	OE2	2.803
1V7N	H_ARG_69	NH1	H_ASP_92	OD1	3.102
1V7N	H_ARG_69	NH1	H_ASP_92	OD2	3.339
1V7N	H_ARG_69	NH2	H_ASP_92	OD1	3.121
1V7N	H_ARG_69	NH2	H_ASP_92	OD2	2.212
1V7N	H_ARG_74	NH2	H_ASP_76	OD1	3.408
1V7N	H_LYS_78	NZ	H_ASP_75	OD2	3.016
1V7N	H_ARG_216	NH1	H_ASP_217	OD2	3.146
1V7N	H_ARG_216	NH2	Z_ASP_123	OD2	3.997
1V7N	M_ARG_60	NH1	M_ASP_81	OD1	2.547
1V7N	M_ARG_60	NH1	M_ASP_81	OD2	2.256
1V7N	M_ARG_60	NH2	M_GLU_80	OE2	3.293
1V7N	M_ARG_60	NH2	M_ASP_81	OD1	3.559
1V7N	M_ARG_95	NH1	L_GLU_50	OE1	2.984
1V7N	M_LYS_102	NZ	M_ASP_164	OD1	3.198
1V7N	M_ARG_107	NH1	M_ASP_169	OD2	3.983
1V7N	M_ARG_107	NH1	N_GLU_78	OE2	3.960
1V7N	M_ARG_107	NH2	N_GLU_78	OE1	3.607
1V7N	M_ARG_107	NH2	N_GLU_78	OE2	2.132
1V7N	M_ARG_154	NH1	M_GLU_184	OE1	3.775
1V7N	M_ARG_154	NH1	M_GLU_184	OE2	3.880
1V7N	M_ARG_154	NH2	M_GLU_184	OE1	2.821
1V7N	M_HIS_188	ND1	M_ASP_150	OD2	2.789
1V7N	M_LYS_198	NZ	M_ASP_109	OD1	2.627
1V7N	M_LYS_198	NZ	M_ASP_109	OD2	3.022
1V7N	L_LYS_3	NZ	L_GLU_5	OE1	2.717
1V7N	L_ARG_38	NH1	L_GLU_46	OE1	2.490
1V7N	L_ARG_38	NH1	L_GLU_46	OE2	3.766
1V7N	L_ARG_38	NH2	L_ASP_92	OD1	2.898
1V7N	L_ARG_52	NH1	L_GLU_50	OE2	3.407
1V7N	L_LYS_54	NZ	L_ASP_76	OD2	3.877
1V7N	L_HIS_58	NE2	L_ASP_76	OD2	3.223
1V7N	L_LYS_67	NZ	L_GLU_64	OE2	2.515

1V7N	L_ARG_69	NH1	L_ASP_92	OD1	3.853
1V7N	L_ARG_69	NH1	L_ASP_92	OD2	3.813
1V7N	L_ARG_69	NH2	L_ASP_92	OD1	3.126
1V7N	L_ARG_69	NH2	L_ASP_92	OD2	2.285
1V7N	L_ARG_74	NH2	L_ASP_76	OD1	3.069
1V7N	L_LYS_78	NZ	L_ASP_75	OD2	3.595
1V7N	L_ARG_216	NH1	L_ASP_217	OD1	3.402
1V7N	N_ARG_60	NH1	N_GLU_80	OE2	3.770
1V7N	N_ARG_60	NH1	N_ASP_81	OD1	3.278
1V7N	N_ARG_60	NH1	N_ASP_81	OD2	2.829
1V7N	N_ARG_60	NH2	N_GLU_80	OE2	3.679
1V7N	N_ARG_95	NH1	J_GLU_50	OE1	3.631
1V7N	N_LYS_102	NZ	N_GLU_104	OE1	3.217
1V7N	N_LYS_102	NZ	N_ASP_164	OD1	2.603
1V7N	N_ARG_107	NH1	N_ASP_169	OD2	2.506
1V7N	N_ARG_107	NH2	M_GLU_78	OE1	2.980
1V7N	N_ARG_107	NH2	M_GLU_78	OE2	2.369
1V7N	N_LYS_148	NZ	N_GLU_194	OE1	3.525
1V7N	N_LYS_148	NZ	N_GLU_194	OE2	3.387
1V7N	N_ARG_154	NH1	N_GLU_184	OE1	3.587
1V7N	N_ARG_154	NH2	N_GLU_184	OE1	2.367
1V7N	N_HIS_188	ND1	N_ASP_150	OD2	2.601
1V7N	N_LYS_198	NZ	N_ASP_109	OD1	3.661
1V7N	N_LYS_198	NZ	N_ASP_109	OD2	2.822
1V7N	J_LYS_3	NZ	J_GLU_5	OE1	2.975
1V7N	J_LYS_3	NZ	J_GLU_5	OE2	2.953
1V7N	J_ARG_38	NH1	J_GLU_46	OE1	2.786
1V7N	J_ARG_38	NH2	J_ASP_92	OD1	2.704
1V7N	J_LYS_43	NZ	J_GLU_46	OE1	2.811
1V7N	J_ARG_52	NH1	J_GLU_50	OE2	3.959
1V7N	J_HIS_61	NE2	J_GLU_50	OE2	3.467
1V7N	J_LYS_67	NZ	J_GLU_64	OE2	2.606
1V7N	J_ARG_69	NH2	J_ASP_92	OD1	2.762
1V7N	J_ARG_69	NH2	J_ASP_92	OD2	3.189
1V7N	J_ARG_74	NH2	J_ASP_76	OD1	2.889
1V7N	J_LYS_78	NZ	J_ASP_75	OD2	3.061
1V7N	J_ARG_216	NH2	J_ASP_217	OD1	3.973
1V7N	J_ARG_216	NH2	X_ASP_123	OD2	3.982
1V7N	O_ARG_60	NH1	O_ASP_81	OD1	2.582
1V7N	O_ARG_60	NH1	O_ASP_81	OD2	2.736
1V7N	O_ARG_95	NH1	K_GLU_50	OE1	2.735
1V7N	O_LYS_102	NZ	O_ASP_164	OD1	3.384
1V7N	O_ARG_107	NH1	L_GLU_78	OE1	3.650
1V7N	O_ARG_107	NH1	L_GLU_78	OE2	3.114
1V7N	O_ARG_107	NH1	O_ASP_169	OD2	3.206
1V7N	O_ARG_107	NH2	L_GLU_78	OE2	2.402
1V7N	O_ARG_154	NH1	O_GLU_184	OE1	2.811
1V7N	O_ARG_154	NH1	O_GLU_184	OE2	2.989
1V7N	O_ARG_154	NH2	O_GLU_184	OE1	2.352
1V7N	O_ARG_154	NH2	O_GLU_184	OE2	3.668
1V7N	O_HIS_188	ND1	O_ASP_150	OD2	2.853
1V7N	O_LYS_198	NZ	O_ASP_109	OD1	3.907
1V7N	O_LYS_198	NZ	O_ASP_109	OD2	2.580
1V7N	K_LYS_3	NZ	K_GLU_5	OE1	3.714
1V7N	K_LYS_3	NZ	K_GLU_5	OE2	3.152
1V7N	K_ARG_38	NH1	K_GLU_46	OE1	2.302
1V7N	K_ARG_38	NH1	K_GLU_46	OE2	3.483
1V7N	K_ARG_38	NH2	K_ASP_92	OD1	3.795

1V7N	K_ARG_38	NH2	K_ASP_92	OD2	3.370
1V7N	K_LYS_43	NZ	K_GLU_46	OE2	2.793
1V7N	K_ARG_52	NH1	K_GLU_50	OE2	3.501
1V7N	K_HIS_58	NE2	K_ASP_76	OD2	3.479
1V7N	K_ARG_69	NH1	K_ASP_92	OD2	3.967
1V7N	K_ARG_69	NH2	K_ASP_92	OD1	3.583
1V7N	K_ARG_69	NH2	K_ASP_92	OD2	2.311
1V7N	K_ARG_74	NH2	K_ASP_76	OD1	3.141
1V7N	K_ARG_74	NH2	K_ASP_76	OD2	3.766
1V7N	K_LYS_78	NZ	K_ASP_75	OD2	2.815
1V7N	K_ARG_216	NH1	K_ASP_217	OD1	2.786
1V7N	V_LYS_59	NZ	V_GLU_56	OE2	3.100
1V7N	V_ARG_98	NH2	H_ASP_31	OD1	3.580
1V7N	V_LYS_138	NZ	V_ASP_62	OD2	2.822
1V7N	X_LYS_59	NZ	X_GLU_56	OE2	2.913
1V7N	X_ARG_98	NH2	I_ASP_31	OD1	3.389
1V7N	X_ARG_117	NH2	X_ASP_45	OD1	3.524
1V7N	X_HIS_121	ND1	J_ASP_217	OD1	2.619
1V7N	X_HIS_121	NE2	J_ASP_217	OD1	3.422
1V7N	X_LYS_138	NZ	X_ASP_62	OD2	3.394
1V7N	Y_HIS_20	ND1	H_ASP_217	OD1	3.368
1V7N	Y_HIS_20	ND1	H_ASP_217	OD2	3.116
1V7N	Y_HIS_20	NE2	H_ASP_217	OD1	3.862
1V7N	Y_HIS_33	NE2	Y_GLU_31	OE1	3.707
1V7N	Y_LYS_59	NZ	Y_GLU_56	OE1	3.270
1V7N	Y_LYS_59	NZ	Y_GLU_56	OE2	2.783
1V7N	Y_HIS_121	ND1	I_ASP_217	OD1	3.108
1V7N	Y_HIS_133	ND1	Y_ASP_45	OD1	3.752
1V7N	Y_LYS_138	NZ	Y_ASP_45	OD2	3.882
1V7N	Z_HIS_33	ND1	Z_GLU_31	OE1	3.839
1V7N	Z_HIS_33	NE2	Z_GLU_31	OE1	3.105
1V7N	Z_LYS_59	NZ	Z_GLU_56	OE1	3.900
1V7N	Z_LYS_59	NZ	Z_GLU_56	OE2	3.150
1V7N	Z_ARG_98	NH2	K_ASP_31	OD1	3.622
1V7N	Z_HIS_133	NE2	Z_ASP_45	OD2	3.937
1V7N	Z_LYS_138	NZ	Z_ASP_45	OD1	2.983
1V7N	Z_ARG_140	NH2	M_GLU_212	OE1	3.768

Table 221: 1V7N-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1VER	A_ARG_25	NH1	A_ASP_4	OD1	3.368
1VER	A_LYS_40	NZ	A_GLU_76	OE2	2.714
1VER	A_ARG_54	NH1	A_ASP_77	OD2	3.441
1VER	A_ARG_54	NH2	A_ASP_77	OD1	3.240
1VER	A_ARG_54	NH2	A_ASP_77	OD2	3.161
1VER	A_ARG_74	NH1	A_ASP_72	OD2	2.935
1VER	A_LYS_102	NZ	A_GLU_46	OE1	3.941
1VER	A_LYS_102	NZ	A_GLU_46	OE2	3.470

Table 222: 1VER-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1VES	A_ARG_25	NH1	A_ASP_4	OD2	3.079
1VES	A_ARG_25	NH1	B_ASP_4	OD1	3.636
1VES	A_ARG_25	NH1	B_ASP_4	OD2	2.836
1VES	A_ARG_25	NH2	B_ASP_4	OD1	2.879
1VES	A_ARG_25	NH2	B_ASP_4	OD2	3.552
1VES	A_LYS_32	NZ	A_GLU_30	OE2	2.725
1VES	A_ARG_38	NH2	A_ASP_77	OD1	3.118
1VES	A_ARG_54	NH1	A_ASP_77	OD1	3.920
1VES	A_ARG_54	NH1	A_ASP_77	OD2	2.727
1VES	A_ARG_54	NH2	A_ASP_77	OD1	3.109
1VES	A_ARG_54	NH2	A_ASP_77	OD2	3.297
1VES	A_ARG_74	NH1	A_GLU_76	OE2	3.745
1VES	A_LYS_104	NZ	A_GLU_46	OE1	2.629
1VES	A_LYS_104	NZ	A_GLU_46	OE2	3.276
1VES	B_ARG_25	NH1	A_ASP_4	OD1	3.762
1VES	B_ARG_25	NH1	A_ASP_4	OD2	2.782
1VES	B_ARG_25	NH1	B_ASP_4	OD2	3.050
1VES	B_ARG_25	NH2	A_ASP_4	OD1	3.070
1VES	B_ARG_25	NH2	A_ASP_4	OD2	3.548
1VES	B_ARG_38	NH2	B_ASP_77	OD1	3.081
1VES	B_ARG_54	NH1	B_ASP_77	OD2	2.889
1VES	B_ARG_54	NH2	B_ASP_77	OD1	3.186
1VES	B_ARG_54	NH2	B_ASP_77	OD2	3.405
1VES	B_ARG_74	NH1	B_GLU_76	OE1	3.458
1VES	B_ARG_74	NH2	B_GLU_76	OE1	3.401
1VES	B_LYS_104	NZ	B_GLU_46	OE1	2.701
1VES	B_LYS_104	NZ	B_GLU_46	OE2	2.906

Table 223: 1VES-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1VFA	A_ARG_61	NH2	A_GLU_81	OE2	3.353
1VFA	A_ARG_61	NH2	A_ASP_82	OD1	2.725
1VFA	A_ARG_61	NH2	A_ASP_82	OD2	3.247
1VFA	A_ARG_96	NH1	B_GLU_98	OE1	2.794
1VFA	A_ARG_96	NH1	B_GLU_98	OE2	3.600
1VFA	A_ARG_96	NH2	B_GLU_98	OE1	3.537
1VFA	A_ARG_96	NH2	B_GLU_98	OE2	2.928
1VFA	A_LYS_103	NZ	A_GLU_105	OE1	2.845
1VFA	B_ARG_38	NH1	B_ASP_89	OD1	2.914
1VFA	B_ARG_38	NH2	B_GLU_46	OE1	2.995
1VFA	B_ARG_38	NH2	B_GLU_46	OE2	3.956
1VFA	B_ARG_38	NH2	B_ASP_89	OD1	3.945
1VFA	B_ARG_66	NH1	B_ASP_89	OD1	3.137
1VFA	B_ARG_66	NH1	B_ASP_89	OD2	3.571
1VFA	B_ARG_66	NH2	B_ASP_89	OD1	3.559
1VFA	B_ARG_66	NH2	B_ASP_89	OD2	2.619
1VFA	B_ARG_97	NH2	B_ASP_104	OD1	3.679
1VFA	B_ARG_97	NH2	B_ASP_104	OD2	2.862
1VFA	B_ARG_99	NH1	B_ASP_104	OD2	3.881
1VFA	B_ARG_99	NH2	B_ASP_100	OD2	3.016

Table 224: 1VFA-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1VFB	A_ARG_61	NH2	A_GLU_81	OE2	3.736
1VFB	A_ARG_61	NH2	A_ASP_82	OD1	2.846
1VFB	A_ARG_61	NH2	A_ASP_82	OD2	3.553
1VFB	A_ARG_96	NH1	B_GLU_98	OE1	2.821
1VFB	A_ARG_96	NH1	B_GLU_98	OE2	3.695
1VFB	A_ARG_96	NH2	B_GLU_98	OE1	3.393
1VFB	A_ARG_96	NH2	B_GLU_98	OE2	2.813
1VFB	A_LYS_107	NZ	A_GLU_17	OE2	3.099
1VFB	B_ARG_38	NH1	B_ASP_89	OD1	3.000
1VFB	B_ARG_38	NH2	B_GLU_46	OE1	3.296
1VFB	B_ARG_38	NH2	B_GLU_46	OE2	3.076
1VFB	B_ARG_38	NH2	B_ASP_89	OD1	3.911
1VFB	B_ARG_66	NH1	B_ASP_89	OD1	3.700
1VFB	B_ARG_66	NH1	B_ASP_89	OD2	2.886
1VFB	B_ARG_66	NH2	B_ASP_89	OD1	2.927
1VFB	B_ARG_66	NH2	B_ASP_89	OD2	3.546
1VFB	B_LYS_75	NZ	B_ASP_72	OD2	3.347
1VFB	B_ARG_97	NH2	B_ASP_104	OD1	3.680
1VFB	B_ARG_97	NH2	B_ASP_104	OD2	2.861
1VFB	B_ARG_102	NH1	B_ASP_100	OD2	3.203
1VFB	C_LYS_1	NZ	C_GLU_7	OE2	3.235
1VFB	C_ARG_61	NH1	C_ASP_48	OD2	3.212
1VFB	C_ARG_125	NH1	C_ASP_119	OD1	3.267
1VFB	C_ARG_125	NH1	C_ASP_119	OD2	3.059
1VFB	C_ARG_125	NH2	C_ASP_119	OD2	3.016

Table 225: 1VFB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1W72	A_HIS_3	ND1	A_ASP_29	OD1	3.652
1W72	A_HIS_3	ND1	A_ASP_29	OD2	2.584
1W72	A_ARG_6	NH1	A_ASP_102	OD1	2.915
1W72	A_ARG_6	NH2	A_ASP_102	OD1	2.976
1W72	A_ARG_6	NH2	A_ASP_102	OD2	3.593
1W72	A_ARG_14	NH1	A_ASP_39	OD1	3.691
1W72	A_ARG_14	NH1	A_ASP_39	OD2	2.979
1W72	A_ARG_14	NH2	A_ASP_39	OD1	3.402
1W72	A_ARG_21	NH1	A_ASP_37	OD1	3.986
1W72	A_ARG_21	NH2	A_ASP_37	OD1	3.181
1W72	A_ARG_21	NH2	A_ASP_37	OD2	2.787
1W72	A_ARG_35	NH1	B_ASP_53	OD1	2.945
1W72	A_ARG_35	NH2	A_GLU_46	OE2	3.408
1W72	A_LYS_44	NZ	A_ASP_61	OD1	3.998
1W72	A_ARG_48	NH1	B_ASP_53	OD2	3.978
1W72	A_ARG_48	NH2	B_ASP_53	OD1	3.455
1W72	A_ARG_48	NH2	B_ASP_53	OD2	2.916
1W72	A_ARG_65	NH1	H_ASP_30	OD1	3.409
1W72	A_ARG_65	NH1	H_ASP_31	OD1	2.977
1W72	A_HIS_70	NE2	A_ASP_74	OD1	3.569
1W72	A_HIS_70	NE2	A_ASP_74	OD2	2.953
1W72	A_ARG_75	NH1	A_GLU_19	OE1	3.767
1W72	A_HIS_93	ND1	A_ASP_119	OD1	3.369
1W72	A_HIS_93	ND1	A_ASP_119	OD2	2.599
1W72	A_ARG_114	NH1	C_ASP_3	OD2	3.999
1W72	A_LYS_144	NZ	A_GLU_148	OE1	3.900
1W72	A_LYS_144	NZ	A_GLU_148	OE2	2.626
1W72	A_LYS_146	NZ	L_ASP_95A	OD1	3.112
1W72	A_LYS_146	NZ	L_ASP_95A	OD2	3.996
1W72	A_ARG_156	NH1	C_ASP_3	OD1	3.704
1W72	A_ARG_156	NH1	C_ASP_3	OD2	2.953
1W72	A_ARG_163	NH1	C_GLU_1	OE1	3.400
1W72	A_ARG_163	NH2	C_GLU_1	OE1	3.293
1W72	A_ARG_163	NH2	C_GLU_1	OE2	3.482
1W72	A_ARG_170	NH1	C_GLU_1	OE2	3.205
1W72	A_ARG_170	NH2	A_GLU_55	OE1	3.864
1W72	A_ARG_170	NH2	A_GLU_55	OE2	3.639
1W72	A_ARG_170	NH2	C_GLU_1	OE2	2.677
1W72	A_LYS_176	NZ	A_GLU_173	OE2	3.940
1W72	A_HIS_191	NE2	A_GLU_254	OE2	3.120
1W72	A_HIS_192	NE2	B_ASP_98	OD1	3.224
1W72	A_HIS_192	NE2	B_ASP_98	OD2	2.823
1W72	A_ARG_202	NH2	A_GLU_229	OE1	3.772
1W72	A_ARG_219	NH1	A_ASP_220	OD2	3.707
1W72	A_ARG_256	NH1	A_GLU_253	OE1	3.148
1W72	A_ARG_256	NH2	A_ASP_220	OD1	3.691
1W72	A_ARG_256	NH2	A_ASP_220	OD2	2.725
1W72	B_LYS_6	NZ	A_GLU_232	OE1	3.881
1W72	B_LYS_41	NZ	B_ASP_76	OD1	3.260
1W72	B_LYS_41	NZ	B_ASP_76	OD2	2.923
1W72	B_ARG_45	NH1	B_GLU_47	OE1	3.217
1W72	B_ARG_45	NH2	B_ASP_38	OD1	3.659
1W72	B_HIS_51	ND1	B_GLU_50	OE2	3.875
1W72	B_ARG_81	NH2	B_ASP_38	OD2	3.262
1W72	D_HIS_3	ND1	D_ASP_29	OD1	3.695
1W72	D_HIS_3	ND1	D_ASP_29	OD2	2.674
1W72	D_ARG_6	NH1	D_ASP_102	OD1	2.917

1W72	D_ARG_6	NH2	D_ASP_102	OD1	2.831
1W72	D_ARG_6	NH2	D_ASP_102	OD2	3.484
1W72	D_ARG_14	NH1	D_ASP_39	OD1	3.609
1W72	D_ARG_14	NH1	D_ASP_39	OD2	3.105
1W72	D_ARG_14	NH2	D_ASP_39	OD1	3.305
1W72	D_ARG_21	NH1	D_ASP_39	OD2	3.364
1W72	D_ARG_21	NH2	D_ASP_37	OD1	3.519
1W72	D_ARG_21	NH2	D_ASP_37	OD2	2.786
1W72	D_ARG_35	NH1	D_GLU_46	OE1	3.132
1W72	D_ARG_35	NH2	D_ASP_37	OD2	3.650
1W72	D_ARG_35	NH2	E_ASP_53	OD1	3.761
1W72	D_ARG_48	NH1	D_GLU_46	OE2	3.543
1W72	D_ARG_65	NH1	I_ASP_30	OD1	2.970
1W72	D_ARG_65	NH1	I_ASP_31	OD1	3.035
1W72	D_HIS_70	NE2	D_ASP_74	OD1	3.533
1W72	D_HIS_70	NE2	D_ASP_74	OD2	3.234
1W72	D_ARG_75	NH1	D_GLU_19	OE1	3.532
1W72	D_ARG_75	NH2	D_GLU_19	OE1	3.186
1W72	D_HIS_93	ND1	D_ASP_119	OD1	3.233
1W72	D_HIS_93	ND1	D_ASP_119	OD2	2.484
1W72	D_LYS_144	NZ	D_GLU_148	OE2	2.839
1W72	D_LYS_146	NZ	M_ASP_95A	OD2	3.397
1W72	D_ARG_156	NH1	F_ASP_3	OD1	3.644
1W72	D_ARG_156	NH1	F_ASP_3	OD2	3.082
1W72	D_ARG_157	NH2	D_GLU_154	OE2	3.289
1W72	D_ARG_163	NH1	F_GLU_1	OE1	3.609
1W72	D_ARG_163	NH1	F_GLU_1	OE2	3.022
1W72	D_ARG_163	NH2	D_ASP_166	OD2	3.278
1W72	D_ARG_170	NH2	D_GLU_55	OE1	3.599
1W72	D_ARG_170	NH2	D_GLU_55	OE2	3.371
1W72	D_HIS_191	NE2	D_GLU_254	OE2	2.873
1W72	D_HIS_192	NE2	E_ASP_98	OD2	3.123
1W72	D_ARG_219	NH1	D_ASP_220	OD2	3.836
1W72	D_ARG_256	NH1	D_ASP_220	OD2	3.881
1W72	D_ARG_256	NH2	D_GLU_253	OE1	3.311
1W72	E_LYS_6	NZ	D_GLU_232	OE2	2.863
1W72	E_LYS_41	NZ	E_ASP_76	OD1	3.809
1W72	E_LYS_41	NZ	E_ASP_76	OD2	3.639
1W72	E_ARG_45	NH1	E_ASP_38	OD1	3.708
1W72	E_ARG_81	NH1	E_ASP_38	OD2	3.844
1W72	H_ARG_38	NH1	H_ASP_86	OD1	3.015
1W72	H_ARG_38	NH2	H_GLU_46	OE1	3.060
1W72	H_ARG_38	NH2	H_GLU_46	OE2	3.921
1W72	H_ARG_38	NH2	H_ASP_86	OD1	3.932
1W72	H_ARG_66	NH1	H_ASP_86	OD1	3.676
1W72	H_ARG_66	NH1	H_ASP_86	OD2	2.720
1W72	H_ARG_66	NH2	H_ASP_86	OD1	3.173
1W72	H_ARG_66	NH2	H_ASP_86	OD2	3.657
1W72	H_ARG_83	NH1	H_GLU_85	OE1	3.964
1W72	H_ARG_94	NH2	H_ASP_101	OD1	3.551
1W72	H_ARG_94	NH2	H_ASP_101	OD2	2.836
1W72	H_LYS_145	NZ	L_GLU_124	OE2	2.720
1W72	H_LYS_221	NZ	L_GLU_123	OE1	2.737
1W72	H_LYS_221	NZ	L_GLU_123	OE2	3.946
1W72	H_LYS_222	NZ	H_GLU_226	OE2	2.721
1W72	I_ARG_38	NH1	I_ASP_86	OD1	3.126
1W72	I_ARG_38	NH2	I_GLU_46	OE1	3.128
1W72	I_ARG_38	NH2	I_GLU_46	OE2	3.763

1W72	L_ARG_38	NH2	L_ASP_86	OD1	3.826
1W72	L_LYS_64	NZ	L_ASP_61	OD1	2.896
1W72	L_ARG_66	NH1	L_ASP_86	OD1	3.873
1W72	L_ARG_66	NH1	L_ASP_86	OD2	2.731
1W72	L_ARG_66	NH2	L_ASP_86	OD1	3.149
1W72	L_ARG_66	NH2	L_ASP_86	OD2	3.465
1W72	L_ARG_94	NH2	L_ASP_101	OD1	3.478
1W72	L_ARG_94	NH2	L_ASP_101	OD2	2.930
1W72	L_ARG_96	NH1	L_ASP_101	OD2	3.483
1W72	L_LYS_145	NZ	M_GLU_124	OE2	2.470
1W72	L_LYS_222	NZ	L_GLU_226	OE2	3.445
1W72	L_LYS_228	NZ	M_GLU_123	OE2	3.514
1W72	L_ARG_31	NH2	L_ASP_92	OD2	2.894
1W72	L_ARG_61	NH1	L_ASP_82	OD1	3.611
1W72	L_ARG_61	NH1	L_ASP_82	OD2	2.785
1W72	L_ARG_61	NH2	L_GLU_79	OE1	2.992
1W72	L_ARG_61	NH2	L_ASP_82	OD1	3.068
1W72	L_ARG_61	NH2	L_ASP_82	OD2	3.602
1W72	L_LYS_166	NZ	L_GLU_83	OE2	2.718
1W72	L_HIS_189	ND1	L_ASP_151	OD2	2.787
1W72	M_ARG_31	NH2	M_ASP_92	OD2	3.047
1W72	M_ARG_61	NH1	M_ASP_82	OD1	3.754
1W72	M_ARG_61	NH1	M_ASP_82	OD2	2.671
1W72	M_ARG_61	NH2	M_GLU_79	OE1	3.828
1W72	M_ARG_61	NH2	M_GLU_79	OE2	3.741
1W72	M_ARG_61	NH2	M_ASP_82	OD1	2.860
1W72	M_ARG_61	NH2	M_ASP_82	OD2	3.245
1W72	M_HIS_95B	NE2	L_ASP_61	OD2	3.924
1W72	M_LYS_166	NZ	M_GLU_83	OE2	2.783
1W72	M_HIS_189	ND1	M_ASP_151	OD2	2.728

Table 226: 1W72-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1WEJ	L_HIS_30	ND1	F_GLU_104	OE1	2.984
1WEJ	L_HIS_30	ND1	F_GLU_104	OE2	2.758
1WEJ	L_ARG_61	NH2	L_GLU_81	OE2	3.867
1WEJ	L_ARG_61	NH2	L_ASP_82	OD1	2.963
1WEJ	L_ARG_61	NH2	L_ASP_82	OD2	3.742
1WEJ	L_LYS_142	NZ	L_ASP_143	OD1	3.329
1WEJ	L_LYS_147	NZ	L_GLU_154	OE1	2.866
1WEJ	L_LYS_149	NZ	L_GLU_195	OE1	3.636
1WEJ	L_LYS_149	NZ	L_GLU_195	OE2	3.035
1WEJ	L_ARG_155	NH1	L_GLU_185	OE1	3.455
1WEJ	L_ARG_155	NH1	L_GLU_185	OE2	3.112
1WEJ	L_ARG_155	NH2	L_GLU_185	OE2	2.727
1WEJ	L_HIS_189	ND1	L_ASP_151	OD2	3.628
1WEJ	L_HIS_189	NE2	L_GLU_185	OE2	3.295
1WEJ	L_LYS_199	NZ	L_ASP_110	OD2	3.451
1WEJ	H_ARG_40	NH2	H_GLU_89	OE2	3.626
1WEJ	H_ARG_50	NH1	F_GLU_62	OE2	3.319
1WEJ	H_ARG_50	NH2	F_GLU_62	OE2	2.823
1WEJ	H_LYS_67	NZ	H_ASP_90	OD1	3.685
1WEJ	H_LYS_67	NZ	H_ASP_90	OD2	2.798
1WEJ	H_LYS_212	NZ	L_GLU_123	OE2	3.963
1WEJ	F_LYS_60	NZ	H_ASP_100	OD2	3.322
1WEJ	F_LYS_87	NZ	F_GLU_90	OE2	3.504
1WEJ	F_LYS_88	NZ	F_GLU_92	OE2	3.066
1WEJ	F_LYS_99	NZ	F_GLU_61	OE2	2.733

Table 227: 1WEJ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1WZ1	L_ARG_24	NH1	L_ASP_75	OD2	3.952
1WZ1	L_ARG_66	NH1	L_GLU_84	OE1	3.457
1WZ1	L_ARG_66	NH1	L_GLU_84	OE2	3.613
1WZ1	L_ARG_66	NH2	L_GLU_84	OE2	3.590
1WZ1	L_ARG_66	NH2	L_GLU_86	OE2	2.822
1WZ1	L_ARG_66	NH2	L_ASP_87	OD1	2.607
1WZ1	L_ARG_66	NH2	L_ASP_87	OD2	3.494
1WZ1	H_ARG_38	NH1	H_GLU_46	OE1	3.212
1WZ1	H_ARG_38	NH1	H_GLU_46	OE2	3.069
1WZ1	H_ARG_38	NH2	H_ASP_92	OD2	2.708
1WZ1	H_ARG_52	NH1	H_GLU_50	OE2	3.191
1WZ1	H_HIS_58	NE2	H_ASP_76	OD2	3.006
1WZ1	H_ARG_69	NH1	H_ASP_92	OD1	3.703
1WZ1	H_ARG_69	NH1	H_ASP_92	OD2	3.712
1WZ1	H_ARG_69	NH2	H_ASP_92	OD1	2.195
1WZ1	H_ARG_69	NH2	H_ASP_92	OD2	3.555
1WZ1	H_ARG_74	NH2	H_ASP_76	OD1	3.331

Table 228: 1WZ1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1XF2	L_ARG_61	NH2	L_GLU_81	OE2	3.419
1XF2	L_ARG_61	NH2	L_ASP_82	OD1	3.006
1XF2	L_ARG_61	NH2	L_ASP_82	OD2	3.455
1XF2	L_LYS_149	NZ	L_GLU_195	OE1	3.344
1XF2	L_ARG_155	NH1	L_GLU_185	OE2	3.754
1XF2	L_ARG_155	NH2	L_GLU_185	OE2	2.954
1XF2	L_ARG_188	NH1	L_GLU_185	OE1	2.837
1XF2	L_HIS_189	ND1	L_ASP_151	OD2	3.000
1XF2	L_HIS_189	NE2	L_GLU_185	OE2	3.246
1XF2	L_ARG_211	NH1	L_GLU_187	OE1	3.085
1XF2	H_LYS_66	NZ	H_ASP_86	OD1	2.700
1XF2	H_LYS_66	NZ	H_ASP_86	OD2	3.586
1XF2	H_ARG_94	NH2	H_ASP_101	OD1	3.923
1XF2	H_ARG_94	NH2	H_ASP_101	OD2	3.252
1XF2	H_LYS_208	NZ	L_GLU_123	OE1	3.369
1XF2	H_LYS_208	NZ	L_GLU_123	OE2	2.577
1XF2	A_ARG_61	NH1	A_GLU_81	OE2	3.119
1XF2	A_ARG_61	NH1	A_ASP_82	OD1	2.988
1XF2	A_ARG_61	NH1	A_ASP_82	OD2	3.665
1XF2	A_LYS_149	NZ	A_GLU_195	OE2	3.121
1XF2	A_ARG_155	NH1	A_GLU_185	OE1	3.880
1XF2	A_ARG_155	NH1	A_GLU_185	OE2	2.861
1XF2	A_ARG_155	NH2	A_GLU_185	OE2	2.971
1XF2	A_ARG_188	NH2	A_GLU_185	OE1	3.702
1XF2	A_HIS_189	ND1	A_ASP_151	OD2	2.794
1XF2	A_LYS_199	NZ	A_ASP_110	OD2	3.768
1XF2	A_ARG_211	NH1	A_GLU_187	OE2	3.554
1XF2	B_LYS_66	NZ	B_ASP_86	OD1	2.668
1XF2	B_LYS_66	NZ	B_ASP_86	OD2	3.588
1XF2	B_ARG_94	NH2	B_ASP_101	OD1	3.898
1XF2	B_ARG_94	NH2	B_ASP_101	OD2	2.974
1XF2	B_LYS_208	NZ	A_GLU_123	OE2	2.913

Table 229: 1XF2-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1XGY	L.LYS_27	NZ	L.GLU_93	OE1	3.138
1XGY	L.LYS_27	NZ	L.GLU_93	OE2	3.725
1XGY	L.ARG_50	NH2	P.GLU_6	OE1	2.621
1XGY	L.ARG_61	NH1	L.ASP_82	OD1	2.794
1XGY	L.ARG_61	NH1	L.ASP_82	OD2	2.267
1XGY	L.ARG_61	NH2	L.GLU_79	OE1	3.265
1XGY	L.ARG_61	NH2	L.GLU_79	OE2	3.639
1XGY	L.ARG_61	NH2	L.GLU_81	OE2	3.975
1XGY	L.ARG_61	NH2	L.ASP_82	OD1	3.476
1XGY	L.ARG_61	NH2	L.ASP_82	OD2	3.700
1XGY	L.LYS_142	NZ	L.GLU_105	OE1	3.607
1XGY	L.LYS_147	NZ	L.GLU_195	OE1	2.404
1XGY	L.LYS_149	NZ	L.GLU_195	OE1	3.987
1XGY	L.LYS_149	NZ	L.GLU_195	OE2	2.719
1XGY	L.ARG_155	NH1	L.GLU_185	OE2	3.616
1XGY	L.ARG_155	NH2	L.GLU_185	OE2	2.613
1XGY	L.HIS_189	ND1	L.ASP_151	OD2	3.191
1XGY	L.LYS_199	NZ	L.ASP_110	OD1	2.374
1XGY	L.LYS_199	NZ	L.ASP_110	OD2	2.995
1XGY	H.ARG_40	NH1	H.GLU_85	OE1	3.102
1XGY	H.LYS_66	NZ	H.ASP_86	OD1	3.962
1XGY	H.LYS_66	NZ	H.ASP_86	OD2	2.962
1XGY	H.LYS_205	NZ	H.ASP_207	OD1	3.695
1XGY	H.LYS_208	NZ	L.GLU_123	OE2	3.768
1XGY	M.LYS_27	NZ	M.GLU_93	OE1	2.941
1XGY	M.LYS_27	NZ	M.GLU_93	OE2	3.832
1XGY	M.ARG_50	NH2	Q.GLU_6	OE1	3.022
1XGY	M.ARG_61	NH1	M.ASP_82	OD1	3.884
1XGY	M.ARG_61	NH1	M.ASP_82	OD2	2.768
1XGY	M.ARG_61	NH2	M.GLU_79	OE1	3.581
1XGY	M.ARG_61	NH2	M.GLU_79	OE2	3.865
1XGY	M.ARG_61	NH2	M.ASP_82	OD1	3.106
1XGY	M.ARG_61	NH2	M.ASP_82	OD2	3.415
1XGY	M.ARG_77	NH1	M.GLU_79	OE2	3.806
1XGY	M.LYS_142	NZ	M.GLU_105	OE1	2.680
1XGY	M.LYS_147	NZ	M.GLU_154	OE1	3.126
1XGY	M.LYS_147	NZ	M.GLU_154	OE2	3.008
1XGY	M.LYS_149	NZ	M.GLU_195	OE1	3.612
1XGY	M.LYS_149	NZ	M.GLU_195	OE2	2.488
1XGY	M.ARG_155	NH1	M.GLU_185	OE2	3.086
1XGY	M.ARG_155	NH2	M.GLU_185	OE1	3.630
1XGY	M.ARG_155	NH2	M.GLU_185	OE2	2.772
1XGY	M.HIS_189	ND1	M.ASP_151	OD2	3.229
1XGY	M.LYS_199	NZ	M.ASP_110	OD1	2.140
1XGY	M.LYS_199	NZ	M.ASP_110	OD2	2.774
1XGY	I.ARG_40	NH1	I.GLU_85	OE2	3.888
1XGY	I.LYS_66	NZ	I.ASP_86	OD1	3.839
1XGY	I.LYS_66	NZ	I.ASP_86	OD2	2.661
1XGY	I.LYS_205	NZ	I.ASP_207	OD1	3.293
1XGY	I.LYS_208	NZ	M.GLU_123	OE2	3.551

Table 230: 1XGY-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1XIW	A_LYS_52	NZ	A_ASP_48	OD1	3.395
1XIW	A_HIS_60	ND1	A_ASP_59	OD1	3.757
1XIW	A_HIS_60	NE2	A_ASP_59	OD1	3.245
1XIW	A_ARG_80	NH1	D_ASP_106	OD2	2.879
1XIW	A_ARG_80	NH2	A_GLU_35	OE1	3.061
1XIW	A_ARG_80	NH2	A_GLU_35	OE2	3.325
1XIW	A_ARG_94	NH1	A_GLU_68	OE2	2.956
1XIW	A_ARG_94	NH2	A_GLU_68	OE2	3.474
1XIW	A_ARG_94	NH2	B_GLU_7	OE1	3.648
1XIW	A_ARG_94	NH2	B_GLU_7	OE2	2.974
1XIW	B_LYS_2	NZ	A_ASP_42	OD1	3.017
1XIW	B_LYS_2	NZ	A_ASP_42	OD2	2.678
1XIW	B_ARG_11	NH1	B_ASP_38	OD1	3.352
1XIW	B_ARG_11	NH1	B_ASP_38	OD2	3.240
1XIW	B_ARG_36	NH2	B_GLU_6	OE1	3.782
1XIW	B_ARG_36	NH2	B_GLU_6	OE2	2.940
1XIW	B_ARG_42	NH1	B_GLU_7	OE2	2.789
1XIW	B_ARG_47	NH2	B_ASP_45	OD2	3.150
1XIW	C_ARG_25	NH1	C_ASP_71	OD1	2.681
1XIW	C_ARG_25	NH1	C_ASP_71	OD2	3.457
1XIW	C_ARG_31	NH1	A_ASP_86	OD1	2.919
1XIW	C_ARG_31	NH1	A_ASP_86	OD2	3.491
1XIW	C_ARG_31	NH2	A_ASP_86	OD1	3.709
1XIW	C_ARG_31	NH2	A_ASP_86	OD2	2.755
1XIW	C_ARG_54	NH1	F_GLU_6	OE1	2.951
1XIW	C_ARG_54	NH2	F_GLU_6	OE1	3.193
1XIW	C_ARG_54	NH2	F_GLU_6	OE2	3.073
1XIW	C_HIS_56	ND1	F_GLU_9	OE1	3.139
1XIW	C_HIS_56	ND1	F_GLU_9	OE2	2.963
1XIW	C_LYS_62	NZ	C_GLU_80	OE1	2.741
1XIW	C_LYS_62	NZ	C_ASP_83	OD1	3.773
1XIW	C_LYS_62	NZ	C_ASP_83	OD2	2.726
1XIW	D_LYS_55	NZ	A_ASP_57	OD1	3.690
1XIW	D_LYS_63	NZ	D_GLU_46	OE1	2.923
1XIW	D_LYS_63	NZ	D_GLU_46	OE2	3.778
1XIW	D_LYS_67	NZ	D_ASP_90	OD1	3.837
1XIW	D_LYS_67	NZ	D_ASP_90	OD2	2.934
1XIW	D_ARG_98	NH2	D_ASP_110	OD1	3.519
1XIW	D_ARG_98	NH2	D_ASP_110	OD2	2.851
1XIW	E_HIS_60	ND1	E_ASP_59	OD1	3.485
1XIW	E_HIS_60	NE2	E_ASP_59	OD1	2.909
1XIW	E_ARG_80	NH1	H_ASP_106	OD2	2.741
1XIW	E_ARG_80	NH2	E_GLU_35	OE1	3.223
1XIW	E_ARG_80	NH2	E_GLU_35	OE2	2.970
1XIW	E_ARG_94	NH1	E_GLU_68	OE2	3.220
1XIW	E_ARG_94	NH2	E_GLU_68	OE2	2.578
1XIW	E_ARG_94	NH2	F_GLU_7	OE2	3.577
1XIW	F_LYS_2	NZ	E_ASP_42	OD1	3.079
1XIW	F_LYS_2	NZ	E_ASP_42	OD2	3.491
1XIW	F_ARG_11	NH1	F_ASP_38	OD1	3.262
1XIW	F_ARG_11	NH1	F_ASP_38	OD2	3.138
1XIW	F_ARG_36	NH2	F_GLU_6	OE1	3.809
1XIW	F_ARG_36	NH2	F_GLU_6	OE2	2.975
1XIW	F_ARG_42	NH2	F_GLU_7	OE2	3.760
1XIW	F_ARG_47	NH2	F_ASP_45	OD2	3.702
1XIW	G_ARG_31	NH1	E_ASP_86	OD1	3.076
1XIW	G_ARG_31	NH1	E_ASP_86	OD2	3.219

1XIW	G_ARG_31	NH2	E_ASP_86	OD2	2.817
1XIW	G_ARG_54	NH1	B_GLU_6	OE1	2.839
1XIW	G_ARG_54	NH2	B_GLU_6	OE1	3.146
1XIW	G_ARG_54	NH2	B_GLU_6	OE2	3.222
1XIW	G_HIS_56	ND1	B_GLU_9	OE1	2.509
1XIW	G_HIS_56	ND1	B_GLU_9	OE2	3.961
1XIW	G_LYS_62	NZ	G_GLU_80	OE1	2.856
1XIW	G_LYS_62	NZ	G_ASP_83	OD1	3.394
1XIW	G_LYS_62	NZ	G_ASP_83	OD2	2.415
1XIW	H_LYS_67	NZ	H_ASP_90	OD1	3.722
1XIW	H_LYS_67	NZ	H_ASP_90	OD2	3.068
1XIW	H_ARG_98	NH2	H_ASP_110	OD1	3.520
1XIW	H_ARG_98	NH2	H_ASP_110	OD2	2.683

Table 231: 1XIW-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1YC7	A_ARG_38	NH1	A_ASP_89	OD1	2.902
1YC7	A_ARG_38	NH2	A_GLU_46	OE2	3.097
1YC7	A_ARG_38	NH2	A_ASP_89	OD1	3.949
1YC7	A_LYS_64	NZ	A_ASP_61	OD1	2.723
1YC7	A_LYS_64	NZ	A_ASP_61	OD2	3.957
1YC7	A_ARG_66	NH1	A_ASP_89	OD1	2.987
1YC7	A_ARG_66	NH1	A_ASP_89	OD2	3.524
1YC7	A_ARG_66	NH2	A_ASP_89	OD1	3.641
1YC7	A_ARG_66	NH2	A_ASP_89	OD2	2.704
1YC7	B_ARG_38	NH1	B_ASP_89	OD1	2.874
1YC7	B_ARG_38	NH2	B_GLU_46	OE2	3.356
1YC7	B_ARG_38	NH2	B_ASP_89	OD1	3.943
1YC7	B_ARG_66	NH1	B_ASP_89	OD1	3.049
1YC7	B_ARG_66	NH1	B_ASP_89	OD2	3.521
1YC7	B_ARG_66	NH2	B_ASP_89	OD1	3.788
1YC7	B_ARG_66	NH2	B_ASP_89	OD2	2.754

Table 232: 1YC7-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1YC8	A_ARG_38	NH1	A_ASP_89	OD1	2.913
1YC8	A_ARG_38	NH2	A_GLU_46	OE1	3.560
1YC8	A_ARG_38	NH2	A_GLU_46	OE2	3.758
1YC8	A_LYS_64	NZ	A_ASP_61	OD1	3.092
1YC8	A_ARG_66	NH1	A_ASP_89	OD1	2.701
1YC8	A_ARG_66	NH1	A_ASP_89	OD2	3.515
1YC8	A_ARG_66	NH2	A_ASP_89	OD1	3.553
1YC8	A_ARG_66	NH2	A_ASP_89	OD2	2.766
1YC8	B_ARG_38	NH1	B_ASP_89	OD1	2.947
1YC8	B_ARG_38	NH2	B_GLU_46	OE1	3.738
1YC8	B_ARG_38	NH2	B_GLU_46	OE2	3.326
1YC8	B_ARG_38	NH2	B_ASP_89	OD1	3.942
1YC8	B_LYS_64	NZ	B_ASP_61	OD1	2.743
1YC8	B_ARG_66	NH1	B_ASP_89	OD1	2.596
1YC8	B_ARG_66	NH1	B_ASP_89	OD2	2.980
1YC8	B_ARG_66	NH2	B_ASP_89	OD1	3.764
1YC8	B_ARG_66	NH2	B_ASP_89	OD2	2.564

Table 233: 1YC8-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1YEI	L_LYS_24	NZ	L_ASP_70	OD1	3.938
1YEI	L_LYS_30	NZ	H_GLU_100B	OE1	2.979
1YEI	L_LYS_45	NZ	H_ASP_101	OD1	2.746
1YEI	L_LYS_45	NZ	H_ASP_101	OD2	3.891
1YEI	L_ARG_46	NH2	L_ASP_55	OD1	3.728
1YEI	L_ARG_46	NH2	L_ASP_55	OD2	2.823
1YEI	L_ARG_46	NH2	H_ASP_101	OD1	3.707
1YEI	L_HIS_49	ND1	L_ASP_55	OD1	2.748
1YEI	L_HIS_49	ND1	L_ASP_55	OD2	3.813
1YEI	L_HIS_49	NE2	H_ASP_100C	OD1	3.542
1YEI	L_ARG_61	NH1	L_ASP_82	OD1	3.376
1YEI	L_ARG_61	NH1	L_ASP_82	OD2	2.794
1YEI	L_ARG_61	NH2	L_ASP_82	OD1	3.026
1YEI	L_ARG_61	NH2	L_ASP_82	OD2	3.859
1YEI	L_ARG_77	NH1	L_GLU_79	OE2	2.773
1YEI	L_LYS_103	NZ	L_ASP_165	OD1	3.211
1YEI	L_LYS_149	NZ	L_GLU_195	OE1	3.290
1YEI	L_LYS_149	NZ	L_GLU_195	OE2	3.378
1YEI	L_ARG_155	NH1	L_GLU_185	OE1	3.467
1YEI	L_ARG_155	NH1	L_GLU_185	OE2	2.801
1YEI	L_ARG_155	NH2	L_GLU_185	OE1	2.921
1YEI	L_ARG_155	NH2	L_GLU_185	OE2	3.794
1YEI	L_LYS_183	NZ	L_GLU_187	OE1	2.856
1YEI	L_LYS_183	NZ	L_GLU_187	OE2	3.649
1YEI	L_HIS_189	ND1	L_ASP_151	OD2	3.711
1YEI	L_HIS_189	NE2	L_GLU_185	OE2	2.707
1YEI	L_LYS_199	NZ	L_ASP_110	OD1	3.088
1YEI	L_LYS_199	NZ	L_ASP_110	OD2	3.565
1YEI	H_LYS_62	NZ	H_GLU_46	OE1	2.847
1YEI	H_LYS_62	NZ	H_GLU_46	OE2	3.937
1YEI	H_LYS_64	NZ	H_GLU_61	OE1	2.773
1YEI	H_LYS_66	NZ	H_ASP_86	OD1	3.924
1YEI	H_LYS_66	NZ	H_ASP_86	OD2	2.870
1YEI	H_LYS_216	NZ	H_ASP_218	OD1	3.297
1YEI	H_LYS_216	NZ	H_ASP_218	OD2	3.256

Table 234: 1YEI-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1YEJ	L_LYS_24	NZ	L_ASP_70	OD1	3.770
1YEJ	L_LYS_45	NZ	H_ASP_101	OD1	2.790
1YEJ	L_LYS_45	NZ	H_ASP_101	OD2	3.988
1YEJ	L_ARG_46	NH2	L_ASP_55	OD1	3.922
1YEJ	L_ARG_46	NH2	L_ASP_55	OD2	2.854
1YEJ	L_ARG_46	NH2	H_ASP_101	OD1	3.745
1YEJ	L_HIS_49	ND1	L_ASP_55	OD1	2.776
1YEJ	L_HIS_49	ND1	L_ASP_55	OD2	3.660
1YEJ	L_HIS_49	NE2	H_ASP_100C	OD1	3.536
1YEJ	L_LYS_53	NZ	H_ASP_100C	OD1	3.377
1YEJ	L_LYS_53	NZ	H_ASP_100C	OD2	3.298
1YEJ	L_ARG_61	NH1	L_ASP_82	OD1	3.561
1YEJ	L_ARG_61	NH1	L_ASP_82	OD2	2.867
1YEJ	L_ARG_61	NH2	L_ASP_82	OD1	3.034
1YEJ	L_ARG_61	NH2	L_ASP_82	OD2	3.799
1YEJ	L_ARG_77	NH1	L_GLU_79	OE2	2.713
1YEJ	L_LYS_103	NZ	L_ASP_165	OD1	3.615
1YEJ	L_LYS_149	NZ	L_GLU_195	OE1	3.131
1YEJ	L_LYS_149	NZ	L_GLU_195	OE2	3.063
1YEJ	L_ARG_155	NH1	L_GLU_185	OE1	3.833
1YEJ	L_ARG_155	NH1	L_GLU_185	OE2	2.788
1YEJ	L_ARG_155	NH2	L_GLU_185	OE1	2.959
1YEJ	L_ARG_155	NH2	L_GLU_185	OE2	3.459
1YEJ	L_LYS_183	NZ	L_ASP_184	OD1	3.622
1YEJ	L_LYS_183	NZ	L_GLU_187	OE1	2.703
1YEJ	L_LYS_183	NZ	L_GLU_187	OE2	3.871
1YEJ	L_HIS_189	ND1	L_ASP_151	OD2	3.584
1YEJ	L_HIS_189	NE2	L_GLU_185	OE2	2.940
1YEJ	L_LYS_199	NZ	L_ASP_110	OD1	3.252
1YEJ	L_LYS_199	NZ	L_ASP_110	OD2	3.582
1YEJ	L_ARG_211	NH2	L_GLU_213	OE2	3.445
1YEJ	H_LYS_62	NZ	H_GLU_46	OE1	3.693
1YEJ	H_LYS_62	NZ	H_GLU_46	OE2	2.771
1YEJ	H_LYS_64	NZ	H_GLU_61	OE1	2.970
1YEJ	H_LYS_66	NZ	H_ASP_86	OD1	3.807
1YEJ	H_LYS_66	NZ	H_ASP_86	OD2	2.899
1YEJ	H_LYS_220	NZ	H_GLU_222	OE2	3.507

Table 235: 1YEJ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1YEK	L_LYS_30	NZ	H_GLU_100B	OE1	2.464
1YEK	L_LYS_45	NZ	H_ASP_101	OD1	2.830
1YEK	L_ARG_46	NH2	L_ASP_55	OD1	3.853
1YEK	L_ARG_46	NH2	L_ASP_55	OD2	2.868
1YEK	L_ARG_46	NH2	H_ASP_101	OD1	3.853
1YEK	L_HIS_49	ND1	L_ASP_55	OD1	2.761
1YEK	L_HIS_49	ND1	L_ASP_55	OD2	3.901
1YEK	L_HIS_49	NE2	H_ASP_100C	OD1	3.610
1YEK	L_ARG_61	NH1	L_ASP_82	OD1	3.781
1YEK	L_ARG_61	NH1	L_ASP_82	OD2	2.826
1YEK	L_ARG_61	NH2	L_ASP_82	OD1	2.807
1YEK	L_ARG_61	NH2	L_ASP_82	OD2	3.333
1YEK	L_ARG_77	NH1	L_GLU_79	OE1	3.282
1YEK	L_ARG_77	NH1	L_GLU_79	OE2	3.016
1YEK	L_LYS_103	NZ	L_ASP_165	OD1	3.840
1YEK	L_LYS_149	NZ	L_GLU_195	OE1	3.270
1YEK	L_LYS_149	NZ	L_GLU_195	OE2	3.257
1YEK	L_ARG_155	NH1	L_GLU_185	OE1	3.905
1YEK	L_ARG_155	NH1	L_GLU_185	OE2	2.816
1YEK	L_ARG_155	NH2	L_GLU_185	OE1	3.007
1YEK	L_ARG_155	NH2	L_GLU_185	OE2	3.425
1YEK	L_LYS_169	NZ	L_ASP_167	OD1	3.838
1YEK	L_LYS_183	NZ	L_ASP_184	OD1	3.851
1YEK	L_LYS_183	NZ	L_GLU_187	OE1	2.883
1YEK	L_HIS_189	ND1	L_ASP_151	OD2	3.477
1YEK	L_HIS_189	NE2	L_GLU_185	OE2	2.892
1YEK	L_LYS_199	NZ	L_ASP_110	OD1	3.770
1YEK	L_LYS_199	NZ	L_ASP_110	OD2	3.854
1YEK	L_ARG_211	NH2	L_GLU_213	OE1	3.144
1YEK	L_ARG_211	NH2	L_GLU_213	OE2	3.561
1YEK	H_LYS_62	NZ	H_GLU_46	OE1	3.791
1YEK	H_LYS_62	NZ	H_GLU_46	OE2	2.855
1YEK	H_LYS_64	NZ	H_GLU_61	OE1	2.862
1YEK	H_LYS_66	NZ	H_ASP_86	OD1	3.789
1YEK	H_LYS_66	NZ	H_ASP_86	OD2	2.810
1YEK	H_LYS_216	NZ	H_ASP_218	OD1	2.879
1YEK	H_LYS_216	NZ	H_ASP_218	OD2	3.161
1YEK	H_LYS_220	NZ	H_GLU_222	OE1	3.196
1YEK	H_LYS_220	NZ	H_GLU_222	OE2	3.085

Table 236: 1YEK-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1YNT	A_ARG_24	NH1	A_ASP_70	OD1	3.062
1YNT	A_ARG_24	NH1	C_ASP_1070	OD2	3.114
1YNT	A_ARG_24	NH2	C_ASP_1070	OD2	3.728
1YNT	A_ARG_61	NH1	A_ASP_82	OD1	3.482
1YNT	A_ARG_61	NH1	A_ASP_82	OD2	2.608
1YNT	A_ARG_61	NH2	A_ASP_82	OD1	2.789
1YNT	A_ARG_61	NH2	A_ASP_82	OD2	2.940
1YNT	A_LYS_142	NZ	A_GLU_105	OE1	3.414
1YNT	A_LYS_142	NZ	A_GLU_105	OE2	3.809
1YNT	A_LYS_149	NZ	A_GLU_195	OE1	3.930
1YNT	A_LYS_149	NZ	A_GLU_195	OE2	3.328
1YNT	A_ARG_155	NH1	A_GLU_185	OE1	3.418
1YNT	A_ARG_155	NH2	A_GLU_185	OE1	2.764
1YNT	A_ARG_155	NH2	A_GLU_185	OE2	3.917
1YNT	A_LYS_183	NZ	A_GLU_187	OE1	3.129
1YNT	A_LYS_183	NZ	A_GLU_187	OE2	2.879
1YNT	A_LYS_199	NZ	A_ASP_110	OD1	3.520
1YNT	A_LYS_199	NZ	A_ASP_110	OD2	2.749
1YNT	B_LYS_538	NZ	B_ASP_590	OD1	3.512
1YNT	B_LYS_563	NZ	A_ASP_1	OD1	2.935
1YNT	B_LYS_563	NZ	A_ASP_1	OD2	3.384
1YNT	B_ARG_598	NH1	B_ASP_606	OD1	3.368
1YNT	B_ARG_598	NH1	B_ASP_606	OD2	3.829
1YNT	B_LYS_713	NZ	A_GLU_123	OE1	3.645
1YNT	B_LYS_714	NZ	B_GLU_716	OE1	2.761
1YNT	B_LYS_714	NZ	B_GLU_716	OE2	3.569
1YNT	C_ARG_1024	NH1	A_ASP_70	OD2	3.173
1YNT	C_ARG_1024	NH1	C_ASP_1070	OD1	3.033
1YNT	C_ARG_1024	NH2	A_ASP_70	OD2	3.802
1YNT	C_ARG_1061	NH1	C_ASP_1082	OD1	3.503
1YNT	C_ARG_1061	NH1	C_ASP_1082	OD2	2.533
1YNT	C_ARG_1061	NH2	C_ASP_1082	OD1	2.790
1YNT	C_ARG_1061	NH2	C_ASP_1082	OD2	2.886
1YNT	C_LYS_1107	NZ	E_GLU_869	OE1	3.719
1YNT	C_LYS_1142	NZ	C_GLU_1105	OE1	3.297
1YNT	C_LYS_1142	NZ	C_GLU_1105	OE2	3.821
1YNT	C_LYS_1149	NZ	C_GLU_1195	OE2	3.387
1YNT	C_ARG_1155	NH1	C_GLU_1185	OE1	3.385
1YNT	C_ARG_1155	NH2	C_GLU_1185	OE1	2.679
1YNT	C_ARG_1155	NH2	C_GLU_1185	OE2	3.830
1YNT	C_LYS_1183	NZ	C_GLU_1187	OE1	3.084
1YNT	C_LYS_1183	NZ	C_GLU_1187	OE2	2.801
1YNT	C_LYS_1199	NZ	C_ASP_1110	OD1	3.564
1YNT	C_LYS_1199	NZ	C_ASP_1110	OD2	2.804
1YNT	D_LYS_1538	NZ	D_ASP_1590	OD1	3.573
1YNT	D_LYS_1563	NZ	C_ASP_1001	OD1	2.913
1YNT	D_LYS_1563	NZ	C_ASP_1001	OD2	3.385
1YNT	D_ARG_1598	NH1	D_ASP_1606	OD1	3.332
1YNT	D_ARG_1598	NH1	D_ASP_1606	OD2	3.789
1YNT	D_LYS_1713	NZ	C_GLU_1123	OE1	3.557
1YNT	D_LYS_1714	NZ	D_GLU_1716	OE1	2.757
1YNT	D_LYS_1714	NZ	D_GLU_1716	OE2	3.550
1YNT	E_LYS_824	NZ	A_ASP_143	OD1	3.012
1YNT	E_LYS_824	NZ	A_ASP_143	OD2	3.238
1YNT	E_LYS_833	NZ	A_ASP_17	OD2	3.941
1YNT	E_ARG_852	NH1	E_GLU_845	OE1	3.602
1YNT	E_ARG_852	NH1	E_GLU_849	OE2	3.768

1YNT	E.LYS.878	NZ	E.ASP.867	OD2	2.972
1YNT	F.LYS.2036	NZ	F.ASP.2089	OD2	3.981
1YNT	F.ARG.2051	NH1	F.ASP.2078	OD1	3.866
1YNT	F.LYS.2115	NZ	F.ASP.2014	OD1	3.292
1YNT	F.ARG.2141	NH2	F.GLU.2100	OE2	3.866
1YNT	F.LYS.2154	NZ	F.GLU.2252	OE1	3.701
1YNT	F.LYS.2154	NZ	F.GLU.2252	OE2	3.571
1YNT	F.LYS.2169	NZ	F.ASP.2214	OD1	3.970
1YNT	F.LYS.2231	NZ	F.GLU.2229	OE2	3.851
1YNT	F.HIS.2245	NE2	F.GLU.2243	OE2	3.227
1YNT	F.HIS.2246	ND1	F.ASP.2147	OD1	3.500
1YNT	G.ARG.3051	NH1	G.ASP.3078	OD1	3.903
1YNT	G.LYS.3115	NZ	G.ASP.3014	OD1	3.279
1YNT	G.ARG.3141	NH2	G.GLU.3100	OE2	3.839
1YNT	G.LYS.3169	NZ	G.ASP.3214	OD1	3.964
1YNT	G.LYS.3231	NZ	G.GLU.3229	OE2	3.832
1YNT	G.HIS.3245	NE2	G.GLU.3243	OE2	3.216
1YNT	G.HIS.3246	ND1	G.ASP.3147	OD1	3.543

Table 237: 1YNT-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1YQV	L_ARG_46	NH2	H_ASP_101	OD2	3.072
1YQV	L_ARG_61	NH2	L_GLU_81	OE2	3.786
1YQV	L_ARG_61	NH2	L_ASP_82	OD1	2.822
1YQV	L_ARG_61	NH2	L_ASP_82	OD2	3.604
1YQV	L_LYS_103	NZ	L_GLU_105	OE2	2.814
1YQV	L_LYS_147	NZ	L_GLU_154	OE1	3.872
1YQV	L_LYS_149	NZ	L_GLU_195	OE1	3.292
1YQV	L_LYS_149	NZ	L_GLU_195	OE2	3.231
1YQV	L_ARG_155	NH1	L_GLU_185	OE2	3.246
1YQV	L_ARG_155	NH2	L_GLU_185	OE1	3.852
1YQV	L_ARG_155	NH2	L_GLU_185	OE2	3.444
1YQV	L_LYS_183	NZ	L_GLU_187	OE1	3.191
1YQV	L_LYS_183	NZ	L_GLU_187	OE2	2.706
1YQV	L_ARG_188	NH2	L_ASP_184	OD2	3.511
1YQV	L_HIS_189	ND1	L_ASP_151	OD2	2.829
1YQV	L_LYS_199	NZ	L_ASP_110	OD2	3.414
1YQV	H_ARG_40	NH1	H_GLU_85	OE1	3.131
1YQV	H_ARG_40	NH2	H_GLU_46	OE1	3.444
1YQV	H_ARG_62	NH1	H_GLU_46	OE2	2.704
1YQV	H_ARG_62	NH2	H_GLU_46	OE1	3.964
1YQV	H_ARG_62	NH2	H_GLU_46	OE2	2.670
1YQV	H_LYS_66	NZ	H_ASP_86	OD1	3.613
1YQV	H_LYS_66	NZ	H_ASP_86	OD2	2.967
1YQV	H_LYS_221	NZ	L_GLU_123	OE1	3.123
1YQV	H_LYS_221	NZ	L_GLU_123	OE2	2.724
1YQV	Y_LYS_1	NZ	Y_GLU_7	OE1	3.896
1YQV	Y_LYS_1	NZ	Y_GLU_7	OE2	2.890
1YQV	Y_LYS_13	NZ	Y_ASP_18	OD2	3.870
1YQV	Y_ARG_45	NH1	H_GLU_50	OE1	3.514
1YQV	Y_ARG_45	NH1	H_GLU_50	OE2	2.957
1YQV	Y_ARG_68	NH1	H_GLU_50	OE1	2.746
1YQV	Y_ARG_68	NH1	H_GLU_50	OE2	3.759
1YQV	Y_ARG_68	NH2	H_GLU_50	OE1	3.492
1YQV	Y_ARG_68	NH2	H_GLU_50	OE2	2.963
1YQV	Y_ARG_125	NH1	Y_ASP_119	OD2	3.693
1YQV	Y_ARG_125	NH2	Y_ASP_119	OD1	3.830
1YQV	Y_ARG_125	NH2	Y_ASP_119	OD2	2.874

Table 238: 1YQV-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1YYL	G.LYS_121	NZ	G.GLU_429	OE2	3.711
1YYL	G.HIS_249	NE2	G.GLU_482	OE1	2.847
1YYL	G.LYS_282	NZ	G.GLU_275	OE1	2.882
1YYL	G.LYS_348	NZ	G.GLU_269	OE1	2.580
1YYL	G.LYS_357	NZ	G.GLU_466	OE2	3.616
1YYL	G.ARG_419	NH1	H.GLU_100D	OE2	3.749
1YYL	G.ARG_419	NH2	H.GLU_99	OE2	2.852
1YYL	G.ARG_419	NH2	H.GLU_100D	OE1	3.510
1YYL	G.ARG_419	NH2	H.GLU_100D	OE2	2.773
1YYL	G.ARG_456	NH1	G.GLU_466	OE1	3.131
1YYL	G.ARG_469	NH2	G.ASP_457	OD1	3.629
1YYL	G.ARG_469	NH2	G.ASP_457	OD2	3.271
1YYL	G.ARG_476	NH1	G.GLU_102	OE1	3.069
1YYL	G.ARG_476	NH1	G.GLU_102	OE2	3.149
1YYL	G.ARG_476	NH2	G.ASP_474	OD1	3.673
1YYL	G.ARG_476	NH2	G.ASP_474	OD2	3.290
1YYL	G.ARG_480	NH1	G.ASP_477	OD1	2.475
1YYL	L.ARG_24	NH1	L.GLU_70	OE2	3.902
1YYL	L.ARG_24	NH2	L.GLU_70	OE2	2.664
1YYL	L.ARG_61	NH2	L.GLU_81	OE1	2.377
1YYL	L.ARG_61	NH2	L.ASP_82	OD1	2.888
1YYL	L.ARG_61	NH2	L.ASP_82	OD2	3.800
1YYL	L.LYS_149	NZ	L.GLU_195	OE1	3.064
1YYL	L.HIS_189	ND1	L.ASP_151	OD2	2.706
1YYL	H.ARG_31	NH2	H.ASP_100A	OD1	2.948
1YYL	H.ARG_31	NH2	H.ASP_100A	OD2	3.167
1YYL	H.ARG_38	NH1	H.GLU_46	OE1	3.897
1YYL	H.ARG_38	NH1	H.GLU_46	OE2	2.772
1YYL	H.ARG_38	NH2	H.ASP_86	OD2	3.486
1YYL	H.ARG_50	NH2	H.GLU_97	OE1	3.557
1YYL	H.ARG_50	NH2	H.GLU_97	OE2	2.825
1YYL	H.ARG_66	NH1	H.ASP_86	OD1	3.071
1YYL	H.ARG_66	NH2	H.ASP_86	OD1	3.527
1YYL	H.ARG_66	NH2	H.ASP_86	OD2	3.411
1YYL	H.ARG_82A	NH2	H.GLU_81	OE1	2.703
1YYL	H.ARG_83	NH2	H.ASP_85	OD1	3.539
1YYL	H.ARG_83	NH2	H.ASP_85	OD2	3.994
1YYL	H.LYS_143	NZ	H.ASP_144	OD1	3.315
1YYL	H.LYS_209	NZ	L.GLU_123	OE1	2.745
1YYL	H.LYS_209	NZ	L.GLU_123	OE2	3.202
1YYL	H.LYS_210	NZ	H.GLU_212	OE2	3.491
1YYL	P.LYS_1121	NZ	P.GLU_1429	OE1	3.348
1YYL	P.LYS_1207	NZ	P.GLU_1381	OE1	3.416
1YYL	P.LYS_1207	NZ	P.GLU_1381	OE2	2.566
1YYL	P.LYS_1232	NZ	P.GLU_1351	OE2	3.532
1YYL	P.HIS_1249	NE2	P.GLU_1482	OE1	3.004
1YYL	P.LYS_1282	NZ	P.GLU_1275	OE1	2.887
1YYL	P.LYS_1348	NZ	P.GLU_1269	OE1	3.461
1YYL	P.LYS_1348	NZ	P.GLU_1351	OE1	3.495
1YYL	P.LYS_1357	NZ	P.GLU_1466	OE1	3.122
1YYL	P.ARG_1419	NH1	R.GLU_1100B	OE1	3.247
1YYL	P.ARG_1419	NH2	R.GLU_1099	OE1	2.456
1YYL	P.ARG_1419	NH2	R.GLU_1100D	OE1	3.853
1YYL	P.ARG_1456	NH1	P.GLU_1466	OE1	3.752
1YYL	P.ARG_1456	NH1	P.GLU_1466	OE2	3.112
1YYL	P.ARG_1469	NH2	P.ASP_1457	OD1	3.096
1YYL	P.ARG_1476	NH1	P.GLU_1102	OE2	2.557

1YYL	P_ARG_1476	NH2	P_ASP_1474	OD2	3.225
1YYL	P_LYS_1487	NZ	P_GLU_1091	OE2	3.909
1YYL	Q_ARG_1061	NH2	Q_GLU_1081	OE1	3.180
1YYL	Q_ARG_1061	NH2	Q_ASP_1082	OD1	3.173
1YYL	Q_ARG_1061	NH2	Q_ASP_1082	OD2	3.802
1YYL	Q_ARG_1095B	NH2	Q_ASP_1001	OD1	3.399
1YYL	Q_ARG_1095B	NH2	Q_ASP_1001	OD2	3.231
1YYL	Q_LYS_1149	NZ	Q_GLU_1195	OE1	2.952
1YYL	Q_LYS_1183	NZ	Q_GLU_1187	OE1	3.809
1YYL	Q_LYS_1183	NZ	Q_GLU_1187	OE2	3.019
1YYL	Q_HIS_1189	ND1	Q_ASP_1151	OD2	3.098
1YYL	R_ARG_1031	NH1	R_GLU_1099	OE2	3.928
1YYL	R_ARG_1031	NH2	R_GLU_1099	OE2	3.597
1YYL	R_ARG_1031	NH2	R_ASP_1100A	OD1	3.501
1YYL	R_ARG_1038	NH1	R_GLU_1046	OE2	3.535
1YYL	R_ARG_1038	NH1	R_ASP_1086	OD2	3.751
1YYL	R_ARG_1038	NH2	R_ASP_1086	OD2	2.896
1YYL	R_ARG_1050	NH2	R_GLU_1097	OE2	3.268
1YYL	R_ARG_1066	NH1	R_ASP_1086	OD1	3.056
1YYL	R_ARG_1066	NH2	R_ASP_1086	OD1	3.383
1YYL	R_ARG_1066	NH2	R_ASP_1086	OD2	3.344
1YYL	R_ARG_1082A	NH2	R_GLU_1081	OE1	2.841
1YYL	R_ARG_1083	NH2	R_ASP_1085	OD1	3.521
1YYL	R_ARG_1083	NH2	R_ASP_1085	OD2	3.389
1YYL	R_LYS_1143	NZ	R_ASP_1144	OD2	3.941
1YYL	R_LYS_1201	NZ	H_GLU_10	OE1	3.633
1YYL	R_LYS_1209	NZ	Q_GLU_1123	OE2	3.934
1YYL	R_LYS_1210	NZ	R_GLU_1212	OE2	3.311
1YYL	S_ARG_1009	NH1	P_ASP_1368	OD2	3.204
1YYL	S_ARG_1009	NH2	P_ASP_1368	OD2	2.930

Table 239: 1YYL-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1YYM	G.LYS_207	NZ	G.GLU_381	OE2	3.762
1YYM	G.HIS_249	NE2	G.GLU_482	OE1	2.851
1YYM	G.LYS_282	NZ	G.GLU_275	OE1	2.507
1YYM	G.LYS_348	NZ	G.GLU_269	OE1	2.728
1YYM	G.LYS_348	NZ	G.GLU_351	OE1	3.554
1YYM	G.LYS_348	NZ	G.GLU_351	OE2	3.474
1YYM	G.LYS_350	NZ	G.ASP_395	OD2	3.297
1YYM	G.ARG_419	NH2	H.GLU_99	OE2	2.868
1YYM	G.ARG_419	NH2	H.GLU_100D	OE1	3.511
1YYM	G.ARG_456	NH1	G.GLU_466	OE1	3.106
1YYM	G.ARG_469	NH2	G.ASP_457	OD2	3.063
1YYM	G.ARG_476	NH1	G.GLU_102	OE1	3.223
1YYM	G.ARG_476	NH1	G.GLU_102	OE2	3.388
1YYM	G.ARG_476	NH2	G.ASP_474	OD1	3.743
1YYM	G.ARG_476	NH2	G.ASP_474	OD2	2.651
1YYM	G.ARG_480	NH1	G.ASP_477	OD1	2.715
1YYM	L.ARG_61	NH2	L.GLU_81	OE1	2.791
1YYM	L.ARG_61	NH2	L.ASP_82	OD1	3.065
1YYM	L.ARG_61	NH2	L.ASP_82	OD2	3.869
1YYM	L.LYS_183	NZ	L.GLU_187	OE1	3.511
1YYM	L.HIS_189	ND1	L.ASP_151	OD2	2.884
1YYM	H.LYS_12	NZ	H.GLU_10	OE1	3.907
1YYM	H.ARG_31	NH2	H.ASP_100A	OD1	3.488
1YYM	H.ARG_31	NH2	H.ASP_100A	OD2	3.551
1YYM	H.ARG_38	NH1	H.GLU_46	OE2	3.168
1YYM	H.ARG_38	NH2	H.ASP_86	OD2	3.293
1YYM	H.ARG_50	NH2	H.GLU_97	OE2	2.832
1YYM	H.ARG_66	NH1	H.ASP_86	OD1	3.105
1YYM	H.ARG_66	NH1	H.ASP_86	OD2	3.982
1YYM	H.ARG_66	NH2	H.ASP_86	OD1	3.852
1YYM	H.ARG_66	NH2	H.ASP_86	OD2	3.349
1YYM	H.ARG_82A	NH2	H.GLU_81	OE1	3.100
1YYM	H.ARG_83	NH2	H.ASP_85	OD1	3.328
1YYM	H.ARG_83	NH2	H.ASP_85	OD2	3.453
1YYM	H.LYS_143	NZ	H.ASP_144	OD1	3.488
1YYM	H.LYS_143	NZ	H.ASP_144	OD2	3.824
1YYM	H.LYS_209	NZ	L.GLU_123	OE1	2.715
1YYM	H.LYS_209	NZ	L.GLU_123	OE2	2.976
1YYM	H.LYS_210	NZ	H.GLU_212	OE2	3.803
1YYM	P.LYS_1097	NZ	P.GLU_1275	OE2	3.820
1YYM	P.LYS_1207	NZ	P.GLU_1381	OE1	3.711
1YYM	P.LYS_1207	NZ	P.GLU_1381	OE2	2.708
1YYM	P.HIS_1249	NE2	P.GLU_1482	OE1	3.026
1YYM	P.LYS_1282	NZ	P.GLU_1275	OE1	3.159
1YYM	P.LYS_1348	NZ	P.GLU_1269	OE1	3.365
1YYM	P.LYS_1348	NZ	P.GLU_1351	OE1	3.721
1YYM	P.LYS_1357	NZ	P.GLU_1466	OE1	3.358
1YYM	P.ARG_1419	NH1	R.GLU_1100B	OE1	2.635
1YYM	P.ARG_1419	NH2	R.GLU_1099	OE1	3.192
1YYM	P.ARG_1456	NH1	P.GLU_1466	OE2	3.024
1YYM	P.ARG_1469	NH2	P.ASP_1457	OD1	3.346
1YYM	P.ARG_1476	NH1	P.GLU_1102	OE2	3.088
1YYM	P.ARG_1476	NH2	P.ASP_1474	OD1	3.920
1YYM	P.ARG_1476	NH2	P.ASP_1474	OD2	3.018
1YYM	P.ARG_1480	NH1	P.ASP_1477	OD1	3.891
1YYM	Q.ARG_1061	NH2	Q.GLU_1081	OE1	3.918
1YYM	Q.ARG_1061	NH2	Q.ASP_1082	OD1	2.770

1YYM	Q_ARG_1061	NH2	Q_ASP_1082	OD2	3.285
1YYM	Q_ARG_1095B	NH2	Q_ASP_1001	OD1	3.276
1YYM	Q_ARG_1095B	NH2	Q_ASP_1001	OD2	3.393
1YYM	Q_LYS_1149	NZ	Q_GLU_1195	OE1	3.456
1YYM	Q_LYS_1183	NZ	Q_GLU_1187	OE1	3.987
1YYM	Q_LYS_1183	NZ	Q_GLU_1187	OE2	2.753
1YYM	Q_HIS_1189	ND1	Q_ASP_1151	OD2	2.971
1YYM	R_ARG_1031	NH2	R_GLU_1099	OE2	2.952
1YYM	R_ARG_1031	NH2	R_ASP_1100A	OD1	3.903
1YYM	R_ARG_1038	NH1	R_GLU_1046	OE2	3.211
1YYM	R_ARG_1038	NH2	R_ASP_1086	OD2	2.820
1YYM	R_ARG_1050	NH2	R_GLU_1097	OE2	2.957
1YYM	R_ARG_1066	NH1	R_ASP_1086	OD1	2.623
1YYM	R_ARG_1066	NH1	R_ASP_1086	OD2	3.373
1YYM	R_ARG_1066	NH2	R_ASP_1086	OD1	3.663
1YYM	R_ARG_1066	NH2	R_ASP_1086	OD2	2.872
1YYM	R_ARG_1082A	NH2	R_GLU_1081	OE1	2.831
1YYM	R_ARG_1083	NH1	R_ASP_1085	OD1	3.896
1YYM	R_ARG_1083	NH1	R_ASP_1085	OD2	3.741
1YYM	R_ARG_1083	NH2	R_ASP_1085	OD1	3.214
1YYM	R_ARG_1083	NH2	R_ASP_1085	OD2	2.624
1YYM	R_LYS_1210	NZ	R_GLU_1212	OE2	3.428
1YYM	S_ARG_1009	NH1	P_ASP_1368	OD2	3.572
1YYM	S_ARG_1009	NH2	P_ASP_1368	OD2	2.725

Table 240: 1YYM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1YZZ	A_ARG_38	NH1	A_ASP_89	OD1	2.737
1YZZ	A_ARG_38	NH2	A_GLU_46	OE2	3.110
1YZZ	A_ARG_38	NH2	A_ASP_89	OD1	3.687
1YZZ	A_ARG_66	NH1	A_ASP_89	OD1	3.398
1YZZ	A_ARG_66	NH1	A_ASP_89	OD2	3.558
1YZZ	A_ARG_66	NH2	A_ASP_89	OD2	2.939
1YZZ	B_ARG_38	NH1	B_ASP_89	OD1	2.975
1YZZ	B_ARG_38	NH2	B_GLU_46	OE2	3.058
1YZZ	B_LYS_64	NZ	B_ASP_61	OD1	2.623
1YZZ	B_ARG_66	NH1	B_ASP_89	OD1	2.532
1YZZ	B_ARG_66	NH1	B_ASP_89	OD2	3.353
1YZZ	B_ARG_66	NH2	B_ASP_89	OD1	3.279
1YZZ	B_ARG_66	NH2	B_ASP_89	OD2	2.407

Table 241: 1YZZ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1ZEA	L.LYS_24	NZ	L.ASP_70	OD1	2.669
1ZEA	L.LYS_24	NZ	L.ASP_70	OD2	2.887
1ZEA	L.LYS_39	NZ	L.GLU_81	OE1	3.641
1ZEA	L.ARG_61	NH1	L.ASP_82	OD1	3.651
1ZEA	L.ARG_61	NH1	L.ASP_82	OD2	2.744
1ZEA	L.ARG_61	NH2	L.GLU_79	OE1	3.732
1ZEA	L.ARG_61	NH2	L.ASP_82	OD1	3.003
1ZEA	L.ARG_61	NH2	L.ASP_82	OD2	3.574
1ZEA	L.ARG_77	NH2	L.ASP_60	OD2	3.436
1ZEA	L.LYS_149	NZ	L.GLU_195	OE1	2.851
1ZEA	L.LYS_149	NZ	L.GLU_195	OE2	3.548
1ZEA	L.LYS_169	NZ	L.GLU_81	OE2	3.652
1ZEA	L.ARG_188	NH2	L.ASP_184	OD1	2.975
1ZEA	L.HIS_189	ND1	L.ASP_151	OD2	2.735
1ZEA	L.LYS_199	NZ	L.ASP_110	OD2	3.834
1ZEA	H.LYS_46	NZ	H.ASP_62	OD2	2.871
1ZEA	H.LYS_64	NZ	H.ASP_61	OD1	3.284
1ZEA	H.ARG_66	NH1	H.ASP_86	OD1	3.918
1ZEA	H.ARG_66	NH1	H.ASP_86	OD2	2.875
1ZEA	H.ARG_66	NH2	H.ASP_86	OD1	2.957
1ZEA	H.ARG_66	NH2	H.ASP_86	OD2	3.243
1ZEA	H.ARG_94	NH2	H.ASP_101	OD1	3.691
1ZEA	H.ARG_94	NH2	H.ASP_101	OD2	2.853
1ZEA	H.ARG_95	NH1	L.GLU_34	OE1	2.842
1ZEA	H.ARG_95	NH1	L.GLU_34	OE2	3.642
1ZEA	H.ARG_95	NH2	L.GLU_34	OE1	3.613
1ZEA	H.ARG_95	NH2	L.GLU_34	OE2	2.859
1ZEA	H.LYS_143	NZ	H.ASP_173	OD2	3.046
1ZEA	H.LYS_205	NZ	H.ASP_207	OD1	2.729
1ZEA	H.LYS_205	NZ	H.ASP_207	OD2	3.512
1ZEA	H.LYS_208	NZ	L.GLU_123	OE2	2.817

Table 242: 1ZEA-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1ZMY	A_ARG_38	NH1	A_ASP_90	OD2	2.840
1ZMY	A_ARG_38	NH2	A_GLU_46	OE2	3.583
1ZMY	A_ARG_38	NH2	A_ASP_90	OD2	3.677
1ZMY	A_LYS_65	NZ	A_ASP_62	OD1	3.540
1ZMY	A_ARG_67	NH1	A_ASP_90	OD1	2.500
1ZMY	A_ARG_67	NH1	A_ASP_90	OD2	3.775
1ZMY	A_ARG_67	NH2	A_ASP_90	OD1	3.202
1ZMY	A_ARG_67	NH2	A_ASP_90	OD2	3.068
1ZMY	L_LYS_1	NZ	L_GLU_7	OE2	2.765
1ZMY	L_LYS_13	NZ	L_ASP_18	OD2	3.088
1ZMY	L_ARG_61	NH2	L_ASP_48	OD2	3.432
1ZMY	M_LYS_1	NZ	M_GLU_7	OE1	3.919
1ZMY	M_LYS_1	NZ	M_GLU_7	OE2	2.657
1ZMY	M_LYS_13	NZ	M_ASP_18	OD2	3.984

Table 243: 1ZMY-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2AAB	L_ARG_24	NH1	L_ASP_70	OD1	3.378
2AAB	L_ARG_24	NH1	L_ASP_70	OD2	3.076
2AAB	L_ARG_61	NH1	L_GLU_79	OE1	3.401
2AAB	L_ARG_61	NH1	L_ASP_82	OD1	2.799
2AAB	L_ARG_61	NH1	L_ASP_82	OD2	3.081
2AAB	L_ARG_61	NH2	L_GLU_79	OE1	3.087
2AAB	L_LYS_93	NZ	L_GLU_27	OE1	2.856
2AAB	L_LYS_103	NZ	L_GLU_105	OE2	3.933
2AAB	L_LYS_149	NZ	L_GLU_195	OE1	2.658
2AAB	L_LYS_149	NZ	L_GLU_195	OE2	3.769
2AAB	L_ARG_155	NH1	L_GLU_185	OE1	3.205
2AAB	L_ARG_155	NH2	L_GLU_185	OE1	3.657
2AAB	L_ARG_155	NH2	L_GLU_185	OE2	3.891
2AAB	L_HIS_189	ND1	L_ASP_151	OD2	2.588
2AAB	H_ARG_38	NH1	H_ASP_86	OD1	2.796
2AAB	H_ARG_38	NH2	H_GLU_46	OE1	2.650
2AAB	H_ARG_38	NH2	H_GLU_46	OE2	3.853
2AAB	H_ARG_38	NH2	H_ASP_86	OD1	3.953
2AAB	H_LYS_64	NZ	H_ASP_61	OD2	3.741
2AAB	H_ARG_66	NH1	H_ASP_86	OD1	3.938
2AAB	H_ARG_66	NH1	H_ASP_86	OD2	2.836
2AAB	H_ARG_66	NH2	H_ASP_86	OD1	3.107
2AAB	H_ARG_66	NH2	H_ASP_86	OD2	3.400
2AAB	H_ARG_83	NH1	H_GLU_85	OE1	3.354
2AAB	H_ARG_83	NH2	H_GLU_85	OE1	3.065
2AAB	H_ARG_94	NH2	H_ASP_101	OD1	3.332
2AAB	H_ARG_94	NH2	H_ASP_101	OD2	3.671
2AAB	H_LYS_208	NZ	L_GLU_123	OE1	3.545

Table 244: 2AAB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2ARJ	L_ARG_61	NH1	L_ASP_82	OD1	2.599
2ARJ	L_ARG_61	NH1	L_ASP_82	OD2	2.529
2ARJ	L_LYS_103	NZ	L_GLU_105	OE2	2.787
2ARJ	L_LYS_147	NZ	L_GLU_154	OE1	3.563
2ARJ	L_LYS_147	NZ	L_GLU_154	OE2	3.021
2ARJ	L_LYS_149	NZ	L_GLU_195	OE1	3.558
2ARJ	L_ARG_156	NH1	L_GLU_154	OE1	3.520
2ARJ	L_ARG_156	NH1	L_GLU_154	OE2	3.250
2ARJ	L_LYS_183	NZ	L_GLU_187	OE1	3.507
2ARJ	L_HIS_189	ND1	L_ASP_151	OD2	3.253
2ARJ	L_HIS_189	NE2	L_GLU_185	OE2	2.888
2ARJ	L_LYS_199	NZ	L_ASP_110	OD1	3.590
2ARJ	L_LYS_199	NZ	L_ASP_110	OD2	2.881
2ARJ	H_ARG_38	NH1	H_ASP_86	OD1	2.915
2ARJ	H_ARG_38	NH2	H_GLU_46	OE2	3.238
2ARJ	H_ARG_38	NH2	H_ASP_86	OD1	3.950
2ARJ	H_ARG_66	NH1	H_ASP_86	OD2	3.425
2ARJ	H_ARG_66	NH2	H_ASP_86	OD1	2.734
2ARJ	H_ARG_66	NH2	H_ASP_86	OD2	2.913
2ARJ	H_HIS_172	NE2	H_ASP_169	OD1	3.945
2ARJ	A_ARG_61	NH1	A_ASP_82	OD1	2.811
2ARJ	A_ARG_61	NH1	A_ASP_82	OD2	2.467
2ARJ	A_ARG_61	NH2	A_ASP_81	OD2	3.853
2ARJ	A_LYS_103	NZ	A_GLU_105	OE2	3.414
2ARJ	A_LYS_147	NZ	A_GLU_154	OE2	2.780
2ARJ	A_LYS_149	NZ	A_GLU_195	OE1	3.948
2ARJ	A_LYS_149	NZ	A_GLU_195	OE2	3.695
2ARJ	A_ARG_156	NH1	A_GLU_154	OE1	2.977
2ARJ	A_ARG_156	NH1	A_GLU_154	OE2	3.024
2ARJ	A_ARG_156	NH2	A_GLU_154	OE1	3.339
2ARJ	A_LYS_183	NZ	A_GLU_187	OE1	3.790
2ARJ	A_HIS_189	ND1	A_ASP_151	OD2	3.869
2ARJ	A_HIS_189	NE2	A_GLU_185	OE2	2.726
2ARJ	A_LYS_199	NZ	A_ASP_110	OD1	3.226
2ARJ	A_LYS_199	NZ	A_ASP_110	OD2	2.734
2ARJ	B_ARG_38	NH1	B_ASP_86	OD1	2.957
2ARJ	B_ARG_38	NH2	B_GLU_46	OE1	3.840
2ARJ	B_ARG_38	NH2	B_GLU_46	OE2	3.335
2ARJ	B_ARG_38	NH2	B_ASP_86	OD1	3.960
2ARJ	B_ARG_66	NH1	B_ASP_86	OD2	3.486
2ARJ	B_ARG_66	NH2	B_ASP_86	OD1	2.770
2ARJ	B_ARG_66	NH2	B_ASP_86	OD2	2.899
2ARJ	R_LYS_21	NZ	R_ASP_23	OD2	3.940
2ARJ	R_LYS_68	NZ	R_ASP_66	OD2	3.453
2ARJ	Q_LYS_21	NZ	Q_ASP_23	OD1	3.938
2ARJ	Q_LYS_21	NZ	Q_ASP_23	OD2	3.026
2ARJ	Q_LYS_68	NZ	Q_ASP_66	OD2	2.542
2ARJ	Q_LYS_121	NZ	Q_GLU_17	OE1	3.957
2ARJ	Q_LYS_121	NZ	Q_GLU_17	OE2	3.774

Table 245: 2ARJ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2B2X	A_LYS_174	NZ	A_ASP_171	OD1	3.646
2B2X	A_ARG_175	NH1	A_ASP_171	OD1	2.653
2B2X	A_ARG_175	NH2	A_ASP_171	OD1	3.756
2B2X	A_HIS_196	NE2	A_GLU_236	OE1	2.662
2B2X	A_ARG_219	NH2	A_GLU_197	OE2	3.539
2B2X	A_ARG_222	NH2	A_GLU_192	OE1	3.578
2B2X	A_ARG_222	NH2	A_GLU_192	OE2	3.205
2B2X	A_ARG_234	NH1	A_ASP_231	OD1	2.877
2B2X	A_ARG_234	NH2	A_ASP_231	OD1	3.527
2B2X	A_ARG_234	NH2	A_ASP_272	OD1	3.389
2B2X	A_LYS_235	NZ	A_ASP_231	OD2	2.623
2B2X	A_ARG_242	NH2	A_GLU_236	OE1	3.815
2B2X	A_ARG_245	NH2	A_ASP_148	OD2	2.857
2B2X	A_ARG_246	NH2	A_GLU_240	OE1	3.473
2B2X	A_LYS_250	NZ	A_GLU_276	OE2	3.894
2B2X	A_HIS_261	NE2	H_ASP_101	OD2	3.121
2B2X	A_ARG_265	NH2	A_ASP_231	OD2	3.021
2B2X	A_ARG_280	NH1	A_GLU_274	OE1	3.434
2B2X	A_ARG_280	NH2	A_GLU_274	OE1	2.884
2B2X	A_HIS_288	NE2	A_ASP_257	OD2	3.303
2B2X	A_LYS_329	NZ	A_GLU_333	OE1	2.878
2B2X	A_LYS_329	NZ	A_GLU_333	OE2	3.222
2B2X	H_ARG_38	NH1	H_GLU_46	OE1	2.704
2B2X	H_ARG_38	NH2	H_ASP_89	OD2	2.877
2B2X	H_ARG_66	NH1	H_ASP_89	OD1	2.835
2B2X	H_ARG_66	NH1	H_ASP_89	OD2	3.848
2B2X	H_ARG_66	NH2	H_ASP_89	OD1	3.615
2B2X	H_ARG_66	NH2	H_ASP_89	OD2	3.196
2B2X	H_ARG_97	NH2	H_ASP_106	OD1	3.043
2B2X	H_ARG_97	NH2	H_ASP_106	OD2	3.052
2B2X	H_HIS_169	NE2	L_ASP_171	OD2	3.832
2B2X	H_LYS_213	NZ	L_GLU_127	OE1	2.709
2B2X	H_LYS_213	NZ	L_GLU_127	OE2	3.416
2B2X	L_HIS_31	NE2	A_GLU_259	OE2	3.821
2B2X	L_ARG_60	NH2	L_ASP_81	OD1	2.811
2B2X	L_ARG_60	NH2	L_ASP_81	OD2	3.437
2B2X	L_LYS_102	NZ	L_ASP_169	OD1	3.045
2B2X	L_LYS_153	NZ	L_GLU_199	OE2	2.862
2B2X	L_ARG_159	NH2	L_GLU_189	OE1	3.544
2B2X	L_LYS_187	NZ	L_GLU_191	OE1	3.187
2B2X	L_LYS_187	NZ	L_GLU_191	OE2	3.179
2B2X	L_HIS_193	ND1	L_ASP_155	OD2	3.401
2B2X	B_LYS_174	NZ	B_ASP_171	OD1	3.653
2B2X	B_LYS_174	NZ	B_ASP_171	OD2	3.858
2B2X	B_HIS_196	NE2	B_GLU_236	OE1	2.785
2B2X	B_ARG_219	NH1	B_GLU_197	OE1	3.424
2B2X	B_ARG_219	NH1	B_GLU_197	OE2	2.578
2B2X	B_ARG_222	NH2	B_GLU_192	OE1	3.396
2B2X	B_ARG_222	NH2	B_GLU_192	OE2	3.088
2B2X	B_ARG_234	NH1	B_ASP_231	OD1	2.739
2B2X	B_ARG_234	NH1	B_ASP_231	OD2	3.550
2B2X	B_ARG_234	NH2	B_ASP_231	OD1	3.736
2B2X	B_ARG_234	NH2	B_ASP_272	OD1	3.791
2B2X	B_LYS_235	NZ	B_ASP_231	OD2	2.860
2B2X	B_ARG_245	NH2	B_ASP_148	OD1	3.373
2B2X	B_HIS_261	NE2	L_ASP_101	OD2	3.107
2B2X	B_ARG_280	NH1	B_GLU_274	OE1	3.062

2B2X	B_ARG_280	NH1	B_GLU_274	OE2	3.945
2B2X	B_ARG_280	NH2	B_GLU_274	OE1	3.114
2B2X	B_HIS_288	ND1	B_ASP_257	OD2	3.336
2B2X	B_LYS_329	NZ	B_GLU_333	OE1	3.450
2B2X	B_LYS_329	NZ	B_GLU_333	OE2	3.053
2B2X	I_ARG_38	NH1	I_GLU_46	OE1	2.780
2B2X	I_ARG_38	NH2	I_ASP_89	OD2	2.859
2B2X	I_ARG_66	NH1	I_ASP_89	OD1	2.954
2B2X	I_ARG_66	NH1	I_ASP_89	OD2	3.737
2B2X	I_ARG_66	NH2	I_ASP_89	OD1	3.772
2B2X	I_ARG_66	NH2	I_ASP_89	OD2	3.121
2B2X	I_ARG_97	NH2	I_ASP_106	OD1	3.823
2B2X	I_ARG_97	NH2	I_ASP_106	OD2	2.979
2B2X	I_HIS_169	NE2	M_ASP_171	OD2	3.874
2B2X	I_LYS_213	NZ	M_GLU_127	OE2	3.245
2B2X	M_HIS_31	NE2	B_GLU_259	OE2	3.848
2B2X	M_ARG_60	NH2	M_GLU_80	OE2	3.305
2B2X	M_ARG_60	NH2	M_ASP_81	OD1	2.985
2B2X	M_ARG_60	NH2	M_ASP_81	OD2	3.811
2B2X	M_LYS_102	NZ	M_ASP_169	OD1	3.157
2B2X	M_LYS_146	NZ	M_GLU_104	OE1	3.183
2B2X	M_LYS_151	NZ	M_GLU_158	OE1	3.453
2B2X	M_LYS_187	NZ	M_GLU_191	OE1	2.648
2B2X	M_LYS_187	NZ	M_GLU_191	OE2	3.145
2B2X	M_HIS_193	ND1	M_ASP_155	OD2	3.516

Table 246: 2B2X-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2B4C	G_LYS_	NZ	G_ASP_	OD1	3.338
2B4C	G_LYS_	NZ	G_ASP_	OD1	3.491
2B4C	G_ARG_	NH1	H_ASP_	OD2	3.237
2B4C	G_ARG_	NH2	H_ASP_	OD2	2.859
2B4C	G_LYS_	NZ	G_GLU_	OE2	3.048
2B4C	G_LYS_	NZ	G_GLU_	OE1	3.552
2B4C	G_LYS_	NZ	G_GLU_	OE2	3.954
2B4C	G_ARG_	NH2	G_GLU_	OE1	3.957
2B4C	G_LYS_	NZ	G_GLU_	OE1	3.503
2B4C	G_ARG_	NH1	G_ASP_	OD1	3.623
2B4C	G_LYS_	NZ	H_ASP_	OD2	2.598
2B4C	G_ARG_	NH1	G_GLU_	OE2	3.070
2B4C	G_ARG_	NH1	G_ASP_	OD1	3.468
2B4C	G_ARG_	NH2	G_GLU_	OE2	3.385
2B4C	C_LYS_	NZ	C_GLU_	OE1	3.632
2B4C	C_LYS_	NZ	C_GLU_	OE1	3.382
2B4C	C_LYS_	NZ	C_GLU_	OE2	3.763
2B4C	C_LYS_	NZ	C_ASP_	OD1	3.946
2B4C	C_ARG_	NH1	C_ASP_	OD2	3.370
2B4C	C_ARG_	NH2	C_ASP_	OD1	2.876
2B4C	C_ARG_	NH2	C_ASP_	OD2	3.161
2B4C	C_ARG_	NH1	H_GLU_	OE2	3.957
2B4C	C_ARG_	NH2	H_GLU_	OE2	3.405
2B4C	C_ARG_	NH1	G_ASP_	OD1	2.937
2B4C	C_ARG_	NH1	G_ASP_	OD2	3.245
2B4C	L_LYS_39	NZ	L_GLU_81	OE1	3.785
2B4C	L_LYS_39	NZ	L_GLU_81	OE2	3.605
2B4C	L_ARG_61	NH1	L_GLU_79	OE1	2.769
2B4C	L_ARG_61	NH1	L_ASP_82	OD1	3.180
2B4C	L_ARG_61	NH2	L_GLU_79	OE1	3.620
2B4C	L_ARG_61	NH2	L_ASP_82	OD1	3.064
2B4C	L_ARG_61	NH2	L_ASP_82	OD2	2.938
2B4C	L_LYS_103	NZ	L_GLU_165	OE1	3.532
2B4C	L_LYS_103	NZ	L_GLU_165	OE2	3.078
2B4C	L_LYS_149	NZ	L_GLU_195	OE1	2.786
2B4C	L_LYS_149	NZ	L_GLU_195	OE2	3.526
2B4C	L_ARG_169	NH2	L_ASP_170	OD2	3.503
2B4C	L_HIS_189	ND1	L_ASP_151	OD1	3.907
2B4C	L_HIS_189	NE2	L_ASP_185	OD2	3.165
2B4C	L_ARG_211	NH1	L_GLU_187	OE1	3.570
2B4C	H_ARG_	NH1	H_ASP_	OD2	3.124
2B4C	H_ARG_	NH2	H_GLU_	OE2	3.384
2B4C	H_LYS_	NZ	L_GLU_	OE1	3.365
2B4C	H_ARG_	NH1	H_ASP_	OD1	2.883
2B4C	H_ARG_	NH1	H_ASP_	OD2	3.887
2B4C	H_ARG_	NH2	H_ASP_	OD1	3.707
2B4C	H_ARG_	NH2	H_ASP_	OD2	3.345
2B4C	H_ARG_	NH1	H_ASP_	OD2	3.458
2B4C	H_ARG_	NH2	H_ASP_	OD2	2.912
2B4C	H_LYS_143	NZ	H_ASP_144	OD2	3.642
2B4C	H_LYS_209	NZ	L_GLU_123	OE2	3.837
2B4C	H_LYS_210	NZ	H_GLU_212	OE2	3.952

Table 247: 2B4C-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2BDN	A_ARG_29	NH2	A_GLU_50	OE1	2.816
2BDN	A_LYS_56	NZ	H_ASP_52	OD1	2.539
2BDN	A_LYS_56	NZ	H_ASP_52	OD2	3.792
2BDN	A_LYS_58	NZ	A_ASP_62	OD1	3.823
2BDN	A_LYS_58	NZ	A_ASP_62	OD2	3.097
2BDN	L_LYS_24	NZ	L_ASP_70	OD1	2.861
2BDN	L_ARG_32	NH1	A_ASP_65	OD1	3.196
2BDN	L_ARG_32	NH1	A_ASP_68	OD1	2.578
2BDN	L_ARG_32	NH2	A_ASP_65	OD1	2.774
2BDN	L_ARG_61	NH2	L_GLU_81	OE2	3.319
2BDN	L_ARG_61	NH2	L_ASP_82	OD1	2.963
2BDN	L_ARG_61	NH2	L_ASP_82	OD2	3.256
2BDN	L_LYS_147	NZ	L_GLU_154	OE1	3.710
2BDN	L_LYS_147	NZ	L_GLU_154	OE2	3.490
2BDN	L_LYS_149	NZ	L_GLU_195	OE1	3.088
2BDN	L_LYS_149	NZ	L_GLU_195	OE2	3.458
2BDN	L_ARG_155	NH1	L_GLU_185	OE2	3.304
2BDN	L_ARG_155	NH2	L_GLU_185	OE2	3.205
2BDN	L_LYS_183	NZ	L_GLU_187	OE1	3.602
2BDN	L_LYS_183	NZ	L_GLU_187	OE2	3.004
2BDN	L_ARG_188	NH1	L_GLU_185	OE1	3.733
2BDN	L_HIS_189	ND1	L_GLU_185	OE1	3.536
2BDN	L_LYS_199	NZ	L_ASP_110	OD1	2.836
2BDN	L_LYS_199	NZ	L_ASP_110	OD2	3.459
2BDN	H_ARG_40	NH1	H_GLU_89	OE1	3.907
2BDN	H_ARG_40	NH2	H_GLU_46	OE2	3.172
2BDN	H_LYS_67	NZ	H_ASP_90	OD1	3.376
2BDN	H_LYS_67	NZ	H_ASP_90	OD2	2.583
2BDN	H_ARG_98	NH1	A_GLU_39	OE2	3.155
2BDN	H_ARG_98	NH2	H_ASP_105	OD1	2.453
2BDN	H_ARG_98	NH2	H_ASP_105	OD2	3.385
2BDN	H_LYS_212	NZ	L_GLU_123	OE2	3.177

Table 248: 2BDN-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2BJM	H_LYS_67	NZ	H_ASP_90	OD2	3.645
2BJM	L_ARG_63	NH2	L_ASP_84	OD1	2.452
2BJM	L_ARG_63	NH2	L_ASP_84	OD2	2.754

Table 249: 2BJM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2BRR	H_LYS_46	NZ	H_ASP_62	OD2	2.761
2BRR	H_LYS_64	NZ	H_ASP_61	OD1	3.587
2BRR	H_ARG_66	NH1	H_ASP_86	OD1	3.672
2BRR	H_ARG_66	NH1	H_ASP_86	OD2	2.665
2BRR	H_ARG_66	NH2	H_ASP_86	OD1	2.817
2BRR	H_ARG_66	NH2	H_ASP_86	OD2	3.203
2BRR	H_ARG_94	NH2	H_ASP_101	OD1	3.717
2BRR	H_ARG_94	NH2	H_ASP_101	OD2	2.794
2BRR	H_ARG_213	NH1	L_GLU_123	OE1	2.600
2BRR	H_ARG_213	NH1	L_GLU_123	OE2	3.932
2BRR	H_ARG_213	NH2	L_GLU_123	OE1	3.110
2BRR	H_ARG_213	NH2	L_GLU_123	OE2	3.029
2BRR	L_ARG_61	NH1	L_GLU_79	OE1	3.644
2BRR	L_ARG_61	NH1	L_GLU_79	OE2	3.599
2BRR	L_ARG_61	NH1	L_GLU_81	OE2	3.861
2BRR	L_ARG_61	NH2	L_GLU_79	OE1	3.852
2BRR	L_ARG_61	NH2	L_GLU_81	OE2	2.730
2BRR	L_ARG_61	NH2	L_ASP_82	OD1	2.665
2BRR	L_ARG_61	NH2	L_ASP_82	OD2	3.473
2BRR	L_LYS_149	NZ	L_GLU_195	OE1	3.904
2BRR	L_LYS_149	NZ	L_GLU_195	OE2	3.270
2BRR	L_ARG_155	NH2	L_GLU_185	OE1	3.742
2BRR	L_LYS_183	NZ	L_ASP_184	OD1	3.014
2BRR	L_HIS_189	ND1	L_ASP_151	OD2	2.911
2BRR	L_ARG_211	NH2	L_GLU_187	OE1	3.989
2BRR	P_LYS_7	NZ	H_ASP_95	OD1	3.067
2BRR	P_LYS_7	NZ	H_ASP_95	OD2	2.549
2BRR	P_HIS_11	ND1	Y_ASP_95	OD2	2.841
2BRR	X_ARG_61	NH1	X_GLU_79	OE1	3.351
2BRR	X_ARG_61	NH1	X_GLU_79	OE2	3.765
2BRR	X_ARG_61	NH1	X_GLU_81	OE2	3.529
2BRR	X_ARG_61	NH2	X_GLU_79	OE1	3.617
2BRR	X_ARG_61	NH2	X_GLU_81	OE2	2.522
2BRR	X_ARG_61	NH2	X_ASP_82	OD1	2.621
2BRR	X_ARG_61	NH2	X_ASP_82	OD2	3.589
2BRR	X_LYS_103	NZ	X_GLU_105	OE2	3.852
2BRR	X_LYS_149	NZ	X_GLU_195	OE1	3.717
2BRR	X_LYS_149	NZ	X_GLU_195	OE2	3.215
2BRR	X_ARG_155	NH1	X_GLU_185	OE2	2.695
2BRR	X_ARG_155	NH2	X_GLU_185	OE2	3.654
2BRR	X_LYS_183	NZ	X_ASP_184	OD1	3.269
2BRR	Y_LYS_46	NZ	Y_ASP_62	OD2	3.113
2BRR	Y_LYS_64	NZ	Y_ASP_61	OD1	3.329
2BRR	Y_ARG_66	NH1	Y_ASP_86	OD1	3.748
2BRR	Y_ARG_66	NH1	Y_ASP_86	OD2	2.611
2BRR	Y_ARG_66	NH2	Y_GLU_85	OE2	3.661
2BRR	Y_ARG_66	NH2	Y_ASP_86	OD1	2.891
2BRR	Y_ARG_66	NH2	Y_ASP_86	OD2	3.154
2BRR	Y_ARG_94	NH2	Y_ASP_101	OD1	3.703
2BRR	Y_ARG_94	NH2	Y_ASP_101	OD2	2.789
2BRR	Y_LYS_208	NZ	X_GLU_123	OE2	3.359
2BRR	Y_ARG_213	NH1	X_GLU_123	OE1	2.523
2BRR	Y_ARG_213	NH1	X_GLU_123	OE2	3.327
2BRR	Y_ARG_213	NH2	X_GLU_123	OE1	3.468
2BRR	Y_ARG_213	NH2	X_GLU_123	OE2	2.546

Table 250: 2BRR-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2COQ	A_ARG_25	NH1	A_ASP_4	OD1	2.687
2COQ	A_ARG_25	NH1	A_ASP_4	OD2	3.796
2COQ	A_ARG_25	NH2	A_ASP_4	OD1	3.959
2COQ	A_ARG_54	NH1	A_ASP_77	OD1	2.737
2COQ	A_ARG_54	NH1	A_ASP_77	OD2	3.255
2COQ	A_ARG_54	NH2	A_ASP_77	OD1	3.769
2COQ	A_ARG_54	NH2	A_ASP_77	OD2	2.959
2COQ	A_ARG_74	NH1	A_ASP_72	OD2	2.997
2COQ	A_LYS_84	NZ	A_GLU_99	OE1	2.795

Table 251: 2COQ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2D03	L_ARG_67	NH1	L_GLU_85	OE1	3.502
2D03	L_ARG_67	NH2	L_GLU_85	OE1	3.293
2D03	L_ARG_67	NH2	L_ASP_88	OD1	2.725
2D03	L_ARG_67	NH2	L_ASP_88	OD2	3.706
2D03	L_LYS_148	NZ	L_GLU_111	OE2	3.675
2D03	L_LYS_155	NZ	L_GLU_201	OE1	3.930
2D03	L_LYS_155	NZ	L_GLU_201	OE2	2.490
2D03	L_ARG_194	NH1	L_ASP_190	OD2	3.257
2D03	L_HIS_195	ND1	L_ASP_157	OD2	2.581
2D03	L_ARG_217	NH1	L_GLU_193	OE2	3.351
2D03	H_ARG_39	NH1	H_ASP_90	OD1	2.887
2D03	H_ARG_39	NH2	H_GLU_47	OE1	3.007
2D03	H_ARG_39	NH2	H_ASP_90	OD1	3.668
2D03	H_LYS_44	NZ	H_ASP_89	OD2	2.726
2D03	H_ARG_67	NH1	H_ASP_90	OD1	3.817
2D03	H_ARG_67	NH1	H_ASP_90	OD2	2.856
2D03	H_ARG_67	NH2	H_ASP_90	OD1	2.855
2D03	H_ARG_67	NH2	H_ASP_90	OD2	3.320
2D03	H_ARG_98	NH2	H_ASP_107	OD1	3.817
2D03	H_ARG_98	NH2	H_ASP_107	OD2	2.632
2D03	H_ARG_100	NH1	H_ASP_107	OD2	3.028

Table 252: 2D03-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2DBL	L_ARG_24	NH1	L_ASP_70	OD1	3.462
2DBL	L_ARG_61	NH1	L_ASP_82	OD1	3.576
2DBL	L_ARG_61	NH1	L_ASP_82	OD2	3.889
2DBL	L_ARG_61	NH2	L_GLU_81	OE2	3.218
2DBL	L_ARG_61	NH2	L_ASP_82	OD1	2.842
2DBL	L_ARG_61	NH2	L_ASP_82	OD2	3.577
2DBL	L_LYS_149	NZ	L_GLU_195	OE1	3.270
2DBL	L_LYS_149	NZ	L_GLU_195	OE2	2.656
2DBL	L_LYS_169	NZ	L_ASP_167	OD1	3.936
2DBL	L_LYS_183	NZ	L_GLU_187	OE2	3.658
2DBL	L_ARG_188	NH1	L_GLU_185	OE1	3.115
2DBL	L_ARG_188	NH1	L_GLU_185	OE2	3.486
2DBL	L_ARG_188	NH2	L_GLU_185	OE1	3.398
2DBL	L_HIS_189	ND1	L_ASP_151	OD2	2.678
2DBL	L_HIS_189	NE2	L_GLU_185	OE2	3.450
2DBL	L_LYS_199	NZ	L_ASP_110	OD2	2.951
2DBL	H_LYS_12	NZ	H_GLU_16	OE1	3.932
2DBL	H_LYS_46	NZ	H_ASP_62	OD2	3.919
2DBL	H_ARG_66	NH2	H_ASP_86	OD1	2.889
2DBL	H_ARG_66	NH2	H_ASP_86	OD2	2.859
2DBL	H_ARG_94	NH1	H_ASP_101	OD1	3.455
2DBL	H_ARG_94	NH1	H_ASP_101	OD2	2.558
2DBL	H_LYS_221	NZ	L_GLU_123	OE2	3.660

Table 253: 2DBL-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2DLF	L_ARG_24	NH1	L_ASP_70	OD1	2.656
2DLF	L_ARG_24	NH2	L_ASP_70	OD1	3.467
2DLF	L_ARG_61	NH1	L_ASP_82	OD1	3.387
2DLF	L_ARG_61	NH1	L_ASP_82	OD2	2.663
2DLF	L_ARG_61	NH2	L_GLU_79	OE1	3.785
2DLF	L_ARG_61	NH2	L_GLU_79	OE2	3.705
2DLF	L_ARG_61	NH2	L_ASP_82	OD1	2.886
2DLF	L_ARG_61	NH2	L_ASP_82	OD2	3.503
2DLF	H_ARG_38	NH1	H_ASP_86	OD2	2.865
2DLF	H_ARG_38	NH2	H_GLU_46	OE2	3.124
2DLF	H_ARG_38	NH2	H_ASP_86	OD2	3.931
2DLF	H_HIS_55	NE2	H_ASP_73	OD1	3.901
2DLF	H_HIS_55	NE2	H_ASP_73	OD2	3.007
2DLF	H_ARG_66	NH1	H_ASP_86	OD1	2.819
2DLF	H_ARG_66	NH1	H_ASP_86	OD2	3.911
2DLF	H_ARG_66	NH2	H_ASP_86	OD1	3.370
2DLF	H_ARG_66	NH2	H_ASP_86	OD2	3.052
2DLF	H_ARG_71	NH2	H_ASP_73	OD1	3.380
2DLF	H_LYS_75	NZ	H_ASP_72	OD1	3.168

Table 254: 2DLF-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID residue name residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2DQC	L_ARG_61	NH2	L_GLU_81	OE2	2.947
2DQC	L_ARG_61	NH2	L_ASP_82	OD1	2.824
2DQC	L_ARG_61	NH2	L_ASP_82	OD2	3.557
2DQC	L_LYS_103	NZ	L_GLU_105	OE1	3.912
2DQC	H_ARG_38	NH1	H_ASP_89	OD1	2.829
2DQC	H_ARG_38	NH2	H_GLU_46	OE1	2.957
2DQC	H_ARG_38	NH2	H_ASP_89	OD1	3.436
2DQC	H_ARG_66	NH1	H_ASP_89	OD1	3.729
2DQC	H_ARG_66	NH1	H_ASP_89	OD2	3.006
2DQC	H_ARG_66	NH2	H_ASP_89	OD1	3.000
2DQC	H_ARG_66	NH2	H_ASP_89	OD2	3.596
2DQC	H_LYS_75	NZ	H_ASP_72	OD1	3.870
2DQC	H_LYS_75	NZ	H_ASP_72	OD2	2.592
2DQC	Y_LYS_1	NZ	Y_GLU_7	OE1	3.856
2DQC	Y_LYS_1	NZ	Y_GLU_7	OE2	2.924
2DQC	Y_LYS_13	NZ	Y_ASP_18	OD2	3.571
2DQC	Y_ARG_61	NH1	Y_ASP_48	OD2	2.731
2DQC	Y_ARG_61	NH2	Y_ASP_48	OD2	3.603
2DQC	Y_ARG_68	NH2	Y_ASP_66	OD2	3.942
2DQC	Y_LYS_97	NZ	H_ASP_32	OD1	2.612
2DQC	Y_LYS_97	NZ	H_ASP_32	OD2	3.998
2DQC	Y_LYS_97	NZ	H_ASP_99	OD1	3.500
2DQC	Y_LYS_97	NZ	H_ASP_99	OD2	2.637
2DQC	Y_ARG_125	NH1	Y_ASP_119	OD2	3.978
2DQC	Y_ARG_125	NH2	Y_ASP_119	OD1	3.933
2DQC	Y_ARG_125	NH2	Y_ASP_119	OD2	2.677

Table 255: 2DQC-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2DQD	L_ARG_61	NH1	L_GLU_79	OE1	3.706
2DQD	L_ARG_61	NH1	L_GLU_79	OE2	2.828
2DQD	L_ARG_61	NH1	L_GLU_81	OE2	3.927
2DQD	L_ARG_61	NH2	L_GLU_79	OE1	3.771
2DQD	L_ARG_61	NH2	L_GLU_79	OE2	3.992
2DQD	L_ARG_61	NH2	L_GLU_81	OE2	2.897
2DQD	L_ARG_61	NH2	L_ASP_82	OD1	2.786
2DQD	L_ARG_61	NH2	L_ASP_82	OD2	3.531
2DQD	H_ARG_38	NH1	H_ASP_89	OD1	2.878
2DQD	H_ARG_38	NH2	H_GLU_46	OE1	2.790
2DQD	H_ARG_38	NH2	H_ASP_89	OD1	3.572
2DQD	H_ARG_66	NH1	H_ASP_89	OD1	3.626
2DQD	H_ARG_66	NH1	H_ASP_89	OD2	2.940
2DQD	H_ARG_66	NH2	H_ASP_89	OD1	2.871
2DQD	H_ARG_66	NH2	H_ASP_89	OD2	3.563
2DQD	H_LYS_75	NZ	H_ASP_72	OD1	3.653
2DQD	H_LYS_75	NZ	H_ASP_72	OD2	2.566
2DQD	Y_LYS_1	NZ	Y_GLU_7	OE1	3.745
2DQD	Y_LYS_1	NZ	Y_GLU_7	OE2	2.721
2DQD	Y_ARG_61	NH2	Y_ASP_48	OD2	3.731
2DQD	Y_LYS_97	NZ	H_ASP_32	OD1	2.767
2DQD	Y_LYS_97	NZ	H_ASP_32	OD2	3.965
2DQD	Y_LYS_97	NZ	H_ASP_99	OD1	3.334
2DQD	Y_LYS_97	NZ	H_ASP_99	OD2	3.048
2DQD	Y_ARG_125	NH1	Y_ASP_119	OD2	3.233
2DQD	Y_ARG_125	NH2	Y_ASP_119	OD1	3.581
2DQD	Y_ARG_125	NH2	Y_ASP_119	OD2	3.417

Table 256: 2DQD-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2DQE	L_ARG_61	NH2	L_GLU_81	OE2	2.959
2DQE	L_ARG_61	NH2	L_ASP_82	OD1	2.845
2DQE	L_ARG_61	NH2	L_ASP_82	OD2	3.487
2DQE	L_LYS_103	NZ	L_GLU_105	OE2	3.264
2DQE	H_ARG_38	NH1	H_ASP_89	OD1	2.861
2DQE	H_ARG_38	NH2	H_GLU_46	OE1	2.782
2DQE	H_ARG_38	NH2	H_ASP_89	OD1	3.510
2DQE	H_ARG_66	NH1	H_ASP_89	OD1	3.735
2DQE	H_ARG_66	NH1	H_ASP_89	OD2	2.920
2DQE	H_ARG_66	NH2	H_ASP_89	OD1	2.982
2DQE	H_ARG_66	NH2	H_ASP_89	OD2	3.570
2DQE	Y_LYS_1	NZ	Y_GLU_7	OE2	2.773
2DQE	Y_ARG_61	NH1	Y_ASP_48	OD2	3.262
2DQE	Y_ARG_61	NH2	Y_ASP_48	OD2	3.792
2DQE	Y_LYS_97	NZ	H_ASP_32	OD1	2.650
2DQE	Y_LYS_97	NZ	H_ASP_99	OD1	3.314
2DQE	Y_LYS_97	NZ	H_ASP_99	OD2	2.899
2DQE	Y_ARG_125	NH1	Y_ASP_119	OD2	3.515
2DQE	Y_ARG_125	NH2	Y_ASP_119	OD1	3.565
2DQE	Y_ARG_125	NH2	Y_ASP_119	OD2	3.316

Table 257: 2DQE-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2DQF	A_ARG_24	NH1	A_ASP_70	OD1	2.550
2DQF	A_ARG_24	NH1	A_ASP_70	OD2	3.744
2DQF	A_LYS_39	NZ	A_GLU_81	OE2	2.959
2DQF	A_ARG_45	NH1	E_ASP_1	OD2	3.511
2DQF	A_LYS_49	NZ	B_ASP_99	OD1	3.470
2DQF	A_ARG_61	NH1	A_GLU_79	OE1	3.872
2DQF	A_ARG_61	NH1	A_GLU_79	OE2	2.799
2DQF	A_ARG_61	NH1	E_ASP_27	OD1	3.814
2DQF	A_ARG_61	NH2	A_GLU_79	OE1	3.614
2DQF	A_ARG_61	NH2	A_GLU_79	OE2	3.760
2DQF	A_ARG_61	NH2	A_ASP_82	OD1	2.799
2DQF	A_ARG_61	NH2	A_ASP_82	OD2	3.265
2DQF	A_LYS_103	NZ	A_GLU_105	OE2	3.654
2DQF	B_ARG_38	NH1	B_ASP_89	OD1	2.770
2DQF	B_ARG_38	NH2	B_GLU_46	OE1	2.742
2DQF	B_ARG_38	NH2	B_ASP_89	OD1	3.406
2DQF	B_ARG_66	NH1	B_ASP_89	OD1	3.473
2DQF	B_ARG_66	NH1	B_ASP_89	OD2	2.668
2DQF	B_ARG_66	NH2	B_ASP_89	OD1	2.704
2DQF	B_ARG_66	NH2	B_ASP_89	OD2	3.223
2DQF	C_LYS_1	NZ	C_GLU_7	OE1	3.699
2DQF	C_LYS_1	NZ	C_GLU_7	OE2	2.773
2DQF	C_LYS_97	NZ	B_ASP_99	OD1	3.543
2DQF	C_LYS_97	NZ	B_ASP_99	OD2	2.851
2DQF	C_ARG_125	NH1	C_ASP_119	OD2	3.803
2DQF	C_ARG_125	NH2	C_ASP_119	OD1	3.819
2DQF	C_ARG_125	NH2	C_ASP_119	OD2	3.276
2DQF	D_LYS_39	NZ	B_ASP_1	OD1	3.005
2DQF	D_LYS_39	NZ	D_GLU_42	OE2	3.387
2DQF	D_LYS_39	NZ	D_GLU_81	OE2	3.094
2DQF	D_ARG_61	NH1	B_ASP_27	OD1	3.581
2DQF	D_ARG_61	NH1	D_GLU_79	OE1	3.632
2DQF	D_ARG_61	NH1	D_GLU_79	OE2	2.878
2DQF	D_ARG_61	NH2	D_GLU_79	OE1	3.547
2DQF	D_ARG_61	NH2	D_GLU_79	OE2	3.942
2DQF	D_ARG_61	NH2	D_ASP_82	OD1	2.591
2DQF	D_ARG_61	NH2	D_ASP_82	OD2	3.479
2DQF	E_ARG_38	NH1	E_ASP_89	OD1	2.707
2DQF	E_ARG_38	NH2	E_GLU_46	OE1	2.703
2DQF	E_ARG_38	NH2	E_ASP_89	OD1	3.576
2DQF	E_ARG_66	NH1	E_ASP_89	OD1	3.354
2DQF	E_ARG_66	NH1	E_ASP_89	OD2	2.779
2DQF	E_ARG_66	NH2	E_ASP_89	OD1	2.920
2DQF	E_ARG_66	NH2	E_ASP_89	OD2	3.732
2DQF	E_LYS_75	NZ	E_ASP_72	OD1	3.480
2DQF	E_LYS_75	NZ	E_ASP_72	OD2	3.040
2DQF	F_LYS_1	NZ	F_GLU_7	OE1	3.776
2DQF	F_LYS_1	NZ	F_GLU_7	OE2	2.553
2DQF	F_ARG_61	NH1	F_ASP_48	OD1	3.965
2DQF	F_ARG_61	NH1	F_ASP_48	OD2	3.568
2DQF	F_LYS_97	NZ	E_ASP_99	OD2	3.165
2DQF	F_ARG_125	NH2	F_ASP_119	OD2	3.151

Table 258: 2DQF-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2DQG	L_ARG_24	NH1	L_ASP_70	OD2	2.455
2DQG	L_ARG_24	NH2	L_ASP_70	OD2	2.946
2DQG	L_ARG_61	NH1	L_GLU_81	OE1	3.776
2DQG	L_ARG_61	NH1	L_GLU_81	OE2	3.040
2DQG	L_ARG_61	NH1	L_ASP_82	OD1	2.735
2DQG	L_ARG_61	NH1	L_ASP_82	OD2	3.392
2DQG	L_ARG_61	NH2	L_GLU_81	OE2	3.998
2DQG	H_ARG_38	NH1	H_ASP_89	OD1	2.997
2DQG	H_ARG_38	NH2	H_GLU_46	OE1	2.883
2DQG	H_ARG_38	NH2	H_ASP_89	OD1	3.559
2DQG	H_ARG_66	NH1	H_ASP_89	OD1	3.739
2DQG	H_ARG_66	NH1	H_ASP_89	OD2	2.946
2DQG	H_ARG_66	NH2	H_ASP_89	OD1	2.769
2DQG	H_ARG_66	NH2	H_ASP_89	OD2	3.415
2DQG	Y_LYS_1	NZ	Y_GLU_7	OE1	2.718
2DQG	Y_ARG_61	NH1	Y_ASP_48	OD1	3.819
2DQG	Y_ARG_61	NH2	Y_ASP_48	OD1	3.754
2DQG	Y_LYS_97	NZ	H_ASP_32	OD1	3.992
2DQG	Y_LYS_97	NZ	H_ASP_32	OD2	2.695
2DQG	Y_LYS_97	NZ	H_ASP_99	OD1	3.156
2DQG	Y_LYS_97	NZ	H_ASP_99	OD2	3.019
2DQG	Y_ARG_125	NH2	Y_ASP_119	OD1	3.345
2DQG	Y_ARG_125	NH2	Y_ASP_119	OD2	2.899

Table 259: 2DQG-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2DQH	L_ARG_61	NH1	L_GLU_81	OE2	3.943
2DQH	L_ARG_61	NH2	L_GLU_81	OE2	2.998
2DQH	L_ARG_61	NH2	L_ASP_82	OD1	2.603
2DQH	L_ARG_61	NH2	L_ASP_82	OD2	3.284
2DQH	L_LYS_103	NZ	L_GLU_105	OE2	3.440
2DQH	H_ARG_38	NH1	H_ASP_89	OD1	3.065
2DQH	H_ARG_38	NH2	H_GLU_46	OE1	2.818
2DQH	H_ARG_38	NH2	H_ASP_89	OD1	3.616
2DQH	H_ARG_66	NH1	H_ASP_89	OD1	3.542
2DQH	H_ARG_66	NH1	H_ASP_89	OD2	2.882
2DQH	H_ARG_66	NH2	H_ASP_89	OD1	2.810
2DQH	H_ARG_66	NH2	H_ASP_89	OD2	3.639
2DQH	Y_LYS_1	NZ	Y_GLU_7	OE1	3.804
2DQH	Y_LYS_1	NZ	Y_GLU_7	OE2	2.722
2DQH	Y_LYS_13	NZ	Y_ASP_18	OD1	3.180
2DQH	Y_ARG_61	NH1	Y_ASP_48	OD2	3.913
2DQH	Y_ARG_68	NH2	Y_ASP_66	OD2	3.732
2DQH	Y_LYS_97	NZ	H_ASP_32	OD1	2.777
2DQH	Y_LYS_97	NZ	H_ASP_99	OD1	3.694
2DQH	Y_LYS_97	NZ	H_ASP_99	OD2	2.635
2DQH	Y_ARG_125	NH1	Y_ASP_119	OD2	3.546
2DQH	Y_ARG_125	NH2	Y_ASP_119	OD1	3.902
2DQH	Y_ARG_125	NH2	Y_ASP_119	OD2	3.500

Table 260: 2DQH-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2DQI	L_LYS_49	NZ	H_ASP_99	OD1	2.843
2DQI	L_LYS_49	NZ	H_ASP_101	OD1	3.541
2DQI	L_LYS_49	NZ	H_ASP_101	OD2	3.285
2DQI	L_ARG_61	NH2	L_GLU_81	OE2	2.840
2DQI	L_ARG_61	NH2	L_ASP_82	OD1	2.897
2DQI	L_ARG_61	NH2	L_ASP_82	OD2	3.427
2DQI	L_LYS_103	NZ	L_GLU_105	OE2	3.837
2DQI	H_ARG_38	NH1	H_ASP_89	OD1	2.893
2DQI	H_ARG_38	NH2	H_GLU_46	OE1	2.861
2DQI	H_ARG_38	NH2	H_ASP_89	OD1	3.612
2DQI	H_ARG_66	NH1	H_ASP_89	OD1	3.831
2DQI	H_ARG_66	NH1	H_ASP_89	OD2	3.064
2DQI	H_ARG_66	NH2	H_ASP_89	OD1	3.099
2DQI	H_ARG_66	NH2	H_ASP_89	OD2	3.699
2DQI	H_LYS_75	NZ	H_ASP_72	OD2	2.738
2DQI	Y_LYS_1	NZ	Y_GLU_7	OE2	3.385
2DQI	Y_LYS_97	NZ	H_ASP_32	OD1	2.729
2DQI	Y_ARG_125	NH1	Y_ASP_119	OD2	3.366
2DQI	Y_ARG_125	NH2	Y_ASP_119	OD1	3.841
2DQI	Y_ARG_125	NH2	Y_ASP_119	OD2	3.842

Table 261: 2DQI-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2DQJ	L_ARG_61	NH2	L_GLU_81	OE2	2.931
2DQJ	L_ARG_61	NH2	L_ASP_82	OD1	2.808
2DQJ	L_ARG_61	NH2	L_ASP_82	OD2	3.434
2DQJ	L_LYS_103	NZ	L_GLU_105	OE2	3.227
2DQJ	H_ARG_38	NH1	H_ASP_89	OD1	2.842
2DQJ	H_ARG_38	NH2	H_GLU_46	OE1	2.847
2DQJ	H_ARG_38	NH2	H_ASP_89	OD1	3.505
2DQJ	H_ARG_66	NH1	H_ASP_89	OD1	3.735
2DQJ	H_ARG_66	NH1	H_ASP_89	OD2	3.036
2DQJ	H_ARG_66	NH2	H_ASP_89	OD1	3.031
2DQJ	H_ARG_66	NH2	H_ASP_89	OD2	3.659
2DQJ	Y_LYS_1	NZ	Y_GLU_7	OE2	2.929
2DQJ	Y_ARG_61	NH1	Y_ASP_48	OD2	3.313
2DQJ	Y_ARG_61	NH2	Y_ASP_48	OD2	3.891
2DQJ	Y_ARG_68	NH2	Y_ASP_66	OD2	3.769
2DQJ	Y_LYS_97	NZ	H_ASP_32	OD1	2.638
2DQJ	Y_LYS_97	NZ	H_ASP_32	OD2	3.939
2DQJ	Y_LYS_97	NZ	H_ASP_99	OD1	3.482
2DQJ	Y_LYS_97	NZ	H_ASP_99	OD2	2.865
2DQJ	Y_ARG_125	NH1	Y_ASP_119	OD2	3.846
2DQJ	Y_ARG_125	NH2	Y_ASP_119	OD1	3.702
2DQJ	Y_ARG_125	NH2	Y_ASP_119	OD2	3.192

Table 262: 2DQJ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2DQT	L_LYS_50	NZ	L_ASP_30	OD2	2.780
2DQT	L_LYS_50	NZ	H_ASP_100C	OD1	3.056
2DQT	L_ARG_61	NH1	L_GLU_79	OE1	3.616
2DQT	L_ARG_61	NH2	L_GLU_81	OE1	3.572
2DQT	L_ARG_61	NH2	L_ASP_82	OD1	2.662
2DQT	L_ARG_61	NH2	L_ASP_82	OD2	3.115
2DQT	L_ARG_77	NH1	L_GLU_79	OE2	3.435
2DQT	L_LYS_103	NZ	L_GLU_105	OE2	3.442
2DQT	L_LYS_149	NZ	L_GLU_195	OE1	3.095
2DQT	L_LYS_149	NZ	L_GLU_195	OE2	3.166
2DQT	L_ARG_155	NH1	L_GLU_185	OE1	3.261
2DQT	L_ARG_155	NH1	L_GLU_185	OE2	3.888
2DQT	L_ARG_155	NH2	L_GLU_185	OE1	3.596
2DQT	L_ARG_155	NH2	L_GLU_185	OE2	2.765
2DQT	L_LYS_183	NZ	L_GLU_187	OE1	3.433
2DQT	L_LYS_183	NZ	L_GLU_187	OE2	2.630
2DQT	L_ARG_188	NH1	L_ASP_184	OD2	2.854
2DQT	L_HIS_189	ND1	L_ASP_151	OD2	2.914
2DQT	L_HIS_189	NE2	L_GLU_185	OE2	3.113
2DQT	L_LYS_199	NZ	L_ASP_110	OD2	3.558
2DQT	H_ARG_38	NH1	H_GLU_46	OE1	2.794
2DQT	H_ARG_38	NH2	H_ASP_86	OD1	2.704
2DQT	H_LYS_64	NZ	H_ASP_61	OD1	2.620
2DQT	H_ARG_66	NH1	H_ASP_86	OD1	3.819
2DQT	H_ARG_66	NH1	H_ASP_86	OD2	2.700
2DQT	H_ARG_66	NH2	H_ASP_86	OD1	2.983
2DQT	H_ARG_66	NH2	H_ASP_86	OD2	3.389
2DQT	H_ARG_83	NH2	H_GLU_85	OE1	3.980
2DQT	H_ARG_83	NH2	H_GLU_85	OE2	3.275
2DQT	H_ARG_94	NH2	H_ASP_101	OD1	3.570
2DQT	H_ARG_94	NH2	H_ASP_101	OD2	2.733
2DQT	H_ARG_100B	NH2	L_ASP_30	OD1	3.486
2DQT	H_ARG_100B	NH2	L_ASP_30	OD2	3.745

Table 263: 2DQT-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2DQU	L_ARG_24	NH1	L_ASP_70	OD1	3.427
2DQU	L_LYS_50	NZ	H_ASP_100C	OD1	2.628
2DQU	L_LYS_50	NZ	H_ASP_100C	OD2	3.616
2DQU	L_ARG_61	NH2	L_GLU_79	OE1	2.958
2DQU	L_LYS_147	NZ	L_GLU_154	OE1	3.676
2DQU	L_LYS_147	NZ	L_GLU_154	OE2	2.961
2DQU	L_LYS_147	NZ	L_GLU_195	OE2	3.938
2DQU	L_LYS_149	NZ	L_GLU_195	OE1	2.875
2DQU	L_LYS_149	NZ	L_GLU_195	OE2	3.568
2DQU	L_LYS_183	NZ	L_GLU_187	OE2	3.122
2DQU	L_HIS_189	ND1	L_ASP_151	OD2	3.386
2DQU	L_HIS_189	NE2	L_GLU_185	OE2	2.712
2DQU	L_LYS_199	NZ	L_ASP_110	OD2	3.230
2DQU	H_ARG_38	NH1	H_GLU_46	OE1	2.604
2DQU	H_ARG_38	NH1	H_ASP_86	OD1	3.950
2DQU	H_ARG_38	NH2	H_ASP_86	OD1	2.687
2DQU	H_ARG_44	NH2	H_GLU_46	OE1	2.549
2DQU	H_ARG_44	NH2	H_GLU_46	OE2	2.851
2DQU	H_ARG_66	NH1	H_ASP_86	OD1	3.787
2DQU	H_ARG_66	NH1	H_ASP_86	OD2	2.695
2DQU	H_ARG_66	NH2	H_ASP_86	OD1	2.995
2DQU	H_ARG_66	NH2	H_ASP_86	OD2	3.363
2DQU	H_ARG_94	NH2	H_ASP_101	OD1	3.556
2DQU	H_ARG_94	NH2	H_ASP_101	OD2	2.729
2DQU	H_ARG_100B	NH2	L_ASP_30	OD2	2.721
2DQU	H_LYS_208	NZ	L_GLU_123	OE2	2.915
2DQU	H_ARG_213	NH1	L_GLU_123	OE1	3.471

Table 264: 2DQU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2FB4	L_ARG_53	NH1	L_ASP_59	OD2	3.714
2FB4	L_ARG_53	NH2	L_ASP_59	OD1	3.808
2FB4	L_ARG_60	NH1	L_GLU_80	OE2	3.376
2FB4	L_ARG_60	NH2	L_GLU_80	OE2	2.766
2FB4	L_ARG_60	NH2	L_ASP_81	OD1	3.071
2FB4	L_ARG_60	NH2	L_ASP_81	OD2	2.621
2FB4	L_LYS_104	NZ	L_ASP_84	OD1	3.495
2FB4	L_LYS_104	NZ	L_ASP_84	OD2	2.981
2FB4	L_HIS_190	ND1	L_ASP_153	OD1	2.983
2FB4	H_ARG_38	NH1	H_ASP_90	OD1	2.997
2FB4	H_ARG_38	NH2	H_GLU_46	OE1	3.277
2FB4	H_ARG_38	NH2	H_GLU_46	OE2	3.164
2FB4	H_ARG_38	NH2	H_ASP_90	OD1	3.798
2FB4	H_HIS_59	NE2	H_ASP_57	OD1	3.817
2FB4	H_ARG_67	NH1	H_ASP_90	OD1	3.916
2FB4	H_ARG_67	NH1	H_ASP_90	OD2	2.836
2FB4	H_ARG_67	NH2	H_ASP_90	OD1	2.913
2FB4	H_ARG_67	NH2	H_ASP_90	OD2	3.297
2FB4	H_ARG_72	NH2	H_ASP_74	OD2	3.188
2FB4	H_ARG_98	NH2	H_ASP_106	OD1	2.760
2FB4	H_ARG_98	NH2	H_ASP_106	OD2	3.392
2FB4	H_LYS_148	NZ	L_GLU_126	OE2	2.805
2FB4	H_LYS_214	NZ	L_GLU_125	OE1	3.053
2FB4	H_LYS_214	NZ	L_GLU_125	OE2	2.759

Table 265: 2FB4-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2FD6	A_HIS_29	NE2	A_ASP_12	OD1	3.017
2FD6	A_HIS_29	NE2	A_ASP_12	OD2	3.253
2FD6	A_HIS_41	NE2	A_ASP_12	OD1	2.670
2FD6	A_HIS_41	NE2	A_ASP_12	OD2	3.732
2FD6	A_ARG_69	NH2	A_ASP_65	OD2	2.800
2FD6	A_HIS_87	ND1	U_ASP_11	OD2	3.705
2FD6	A_ARG_88	NH1	A_ASP_90	OD1	3.269
2FD6	A_ARG_88	NH1	A_ASP_90	OD2	2.893
2FD6	L_LYS_53	NZ	L_GLU_50	OE1	2.800
2FD6	L_ARG_61	NH1	L_GLU_79	OE1	3.611
2FD6	L_ARG_61	NH1	L_GLU_79	OE2	3.439
2FD6	L_ARG_61	NH2	L_GLU_79	OE1	3.617
2FD6	L_ARG_61	NH2	L_GLU_81	OE2	2.650
2FD6	L_ARG_61	NH2	L_ASP_82	OD1	2.824
2FD6	L_ARG_61	NH2	L_ASP_82	OD2	3.518
2FD6	L_LYS_103	NZ	L_ASP_164	OD1	3.838
2FD6	L_LYS_146	NZ	L_GLU_153	OE1	3.751
2FD6	L_LYS_148	NZ	L_GLU_194	OE1	2.730
2FD6	L_LYS_148	NZ	L_GLU_194	OE2	2.883
2FD6	L_ARG_154	NH1	L_GLU_184	OE1	3.569
2FD6	L_ARG_154	NH1	L_GLU_184	OE2	3.359
2FD6	L_ARG_154	NH2	L_GLU_184	OE1	2.421
2FD6	L_ARG_154	NH2	L_GLU_184	OE2	3.540
2FD6	L_ARG_187	NH1	L_ASP_183	OD1	3.359
2FD6	L_HIS_188	ND1	L_ASP_150	OD2	2.696
2FD6	H_ARG_40	NH1	H_GLU_85	OE1	2.850
2FD6	H_ARG_40	NH2	H_GLU_85	OE1	3.358
2FD6	H_LYS_64	NZ	H_GLU_61	OE1	3.156
2FD6	H_LYS_66	NZ	H_ASP_86	OD1	3.700
2FD6	H_LYS_66	NZ	H_ASP_86	OD2	2.976
2FD6	H_ARG_94	NH2	H_ASP_101	OD1	3.603
2FD6	H_ARG_94	NH2	H_ASP_101	OD2	2.621
2FD6	H_HIS_98	ND1	L_GLU_50	OE1	3.050
2FD6	H_HIS_98	ND1	L_GLU_50	OE2	3.997
2FD6	H_LYS_203	NZ	L_GLU_122	OE2	2.585
2FD6	U_ARG_2	NH2	U_ASP_74	OD1	3.037
2FD6	U_ARG_2	NH2	U_ASP_74	OD2	3.628
2FD6	U_ARG_25	NH1	U_GLU_42	OE2	3.105
2FD6	U_ARG_25	NH2	U_GLU_42	OE2	2.986
2FD6	U_ARG_30	NH2	U_GLU_39	OE1	3.610
2FD6	U_LYS_50	NZ	U_ASP_254	OD1	3.179
2FD6	U_ARG_53	NH1	U_ASP_254	OD1	3.463
2FD6	U_ARG_53	NH1	U_ASP_254	OD2	2.584
2FD6	U_ARG_53	NH2	U_ASP_254	OD2	3.352
2FD6	U_HIS_128	NE2	U_GLU_183	OE1	2.860
2FD6	U_HIS_143	NE2	U_GLU_183	OE1	3.388
2FD6	U_HIS_143	NE2	U_GLU_183	OE2	2.574
2FD6	U_ARG_145	NH2	U_ASP_124	OD2	3.333
2FD6	U_LYS_175	NZ	U_GLU_94	OE2	3.307
2FD6	U_ARG_192	NH1	H_GLU_58	OE2	2.359
2FD6	U_ARG_192	NH2	H_GLU_58	OE2	3.898
2FD6	U_HIS_260	NE2	U_ASP_262	OD1	3.106
2FD6	U_HIS_260	NE2	U_ASP_262	OD2	3.788

Table 266: 2FD6-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2FR4	L_ARG_61	NH2	L_ASP_82	OD1	2.807
2FR4	L_ARG_61	NH2	L_ASP_82	OD2	3.787
2FR4	L_LYS_142	NZ	L_GLU_105	OE1	2.764
2FR4	L_LYS_142	NZ	L_GLU_105	OE2	3.125
2FR4	L_ARG_155	NH2	L_GLU_185	OE1	3.754
2FR4	L_ARG_155	NH2	L_GLU_185	OE2	3.022
2FR4	L_LYS_183	NZ	L_GLU_187	OE1	3.253
2FR4	L_LYS_183	NZ	L_GLU_187	OE2	3.697
2FR4	L_HIS_189	ND1	L_ASP_151	OD2	3.437
2FR4	L_HIS_189	NE2	L_GLU_185	OE1	3.779
2FR4	H_LYS_38	NZ	H_GLU_85	OE1	3.892
2FR4	H_LYS_64	NZ	H_GLU_61	OE1	2.978
2FR4	H_LYS_66	NZ	H_ASP_86	OD1	2.719
2FR4	H_LYS_66	NZ	H_ASP_86	OD2	3.742
2FR4	H_ARG_94	NH2	H_ASP_101	OD1	3.962
2FR4	H_ARG_94	NH2	H_ASP_101	OD2	2.959
2FR4	H_LYS_208	NZ	L_GLU_123	OE2	3.199
2FR4	A_ARG_61	NH2	A_ASP_82	OD1	3.363
2FR4	A_LYS_142	NZ	A_ASP_143	OD1	3.736
2FR4	A_LYS_142	NZ	A_ASP_143	OD2	3.296
2FR4	A_LYS_169	NZ	A_ASP_167	OD1	3.777
2FR4	A_LYS_183	NZ	A_GLU_187	OE1	2.836
2FR4	A_LYS_183	NZ	A_GLU_187	OE2	3.027
2FR4	A_HIS_189	ND1	A_ASP_151	OD2	3.087
2FR4	B_LYS_40	NZ	B_GLU_85	OE1	3.845
2FR4	B_LYS_62	NZ	B_GLU_46	OE2	3.403
2FR4	B_LYS_64	NZ	B_GLU_61	OE2	2.733
2FR4	B_LYS_66	NZ	B_ASP_86	OD1	2.762
2FR4	B_LYS_66	NZ	B_ASP_86	OD2	3.704
2FR4	B_ARG_94	NH2	B_ASP_101	OD1	3.630
2FR4	B_ARG_94	NH2	B_ASP_101	OD2	2.755
2FR4	B_LYS_208	NZ	A_GLU_123	OE1	2.539

Table 267: 2FR4-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2H32	A_ARG_25	NH2	A_ASP_27	OD1	3.505
2H32	A_ARG_25	NH2	A_ASP_27	OD2	3.293
2H32	A_HIS_28	NE2	A_ASP_27	OD2	3.559
2H32	A_ARG_51	NH1	A_ASP_57	OD1	3.175
2H32	A_ARG_51	NH2	A_ASP_57	OD1	2.596
2H32	A_ARG_67	NH1	A_ASP_90	OD1	3.374
2H32	A_ARG_67	NH1	A_ASP_90	OD2	2.396
2H32	A_ARG_67	NH2	A_ASP_90	OD1	2.457
2H32	A_ARG_67	NH2	A_ASP_90	OD2	3.234
2H32	A_ARG_110	NH2	A_GLU_109	OE1	3.763
2H32	B_ARG_153	NH1	B_ASP_115	OD1	3.775
2H32	H_LYS_12	NZ	H_GLU_16	OE1	3.609
2H32	H_LYS_13	NZ	H_GLU_16	OE2	3.581
2H32	H_ARG_38	NH1	H_GLU_46	OE1	3.487
2H32	H_ARG_38	NH1	H_GLU_46	OE2	2.617
2H32	H_ARG_59	NH1	A_GLU_106	OE1	3.937
2H32	H_ARG_59	NH1	A_GLU_106	OE2	3.372
2H32	H_ARG_59	NH2	A_GLU_106	OE2	3.412
2H32	H_ARG_98	NH1	H_ASP_107	OD1	3.509
2H32	H_ARG_98	NH1	H_ASP_107	OD2	3.182
2H32	H_LYS_162	NZ	H_ASP_168	OD1	2.915
2H32	H_LYS_162	NZ	H_ASP_168	OD2	3.888
2H32	H_LYS_183	NZ	H_ASP_151	OD1	3.157
2H32	H_LYS_183	NZ	H_ASP_151	OD2	3.441
2H32	H_HIS_204	ND1	H_GLU_203	OE1	3.406
2H32	H_HIS_204	ND1	H_GLU_203	OE2	2.840

Table 268: 2H32-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2H9G	A_ARG_24	NH1	A_ASP_70	OD1	3.267
2H9G	A_ARG_61	NH2	A_GLU_81	OE1	3.875
2H9G	A_ARG_61	NH2	A_ASP_82	OD1	3.215
2H9G	A_ARG_61	NH2	A_ASP_82	OD2	3.850
2H9G	A_LYS_103	NZ	A_GLU_105	OE2	3.674
2H9G	A_LYS_103	NZ	A_GLU_165	OE1	2.740
2H9G	A_LYS_103	NZ	A_GLU_165	OE2	3.762
2H9G	A_ARG_142	NH1	A_GLU_105	OE1	3.505
2H9G	A_ARG_142	NH2	A_GLU_105	OE1	3.340
2H9G	A_ARG_142	NH2	A_GLU_105	OE2	3.102
2H9G	A_LYS_149	NZ	A_GLU_195	OE2	3.684
2H9G	A_LYS_183	NZ	A_GLU_187	OE1	2.832
2H9G	A_LYS_183	NZ	A_GLU_187	OE2	3.382
2H9G	B_ARG_38	NH1	B_ASP_86	OD1	2.752
2H9G	B_ARG_38	NH2	B_GLU_46	OE1	3.198
2H9G	B_ARG_38	NH2	B_GLU_46	OE2	3.634
2H9G	B_ARG_38	NH2	B_ASP_86	OD1	3.743
2H9G	B_HIS_53	ND1	R_GLU_36	OE2	3.471
2H9G	B_ARG_66	NH1	B_ASP_86	OD2	2.729
2H9G	B_ARG_66	NH2	B_ASP_86	OD1	3.172
2H9G	B_ARG_66	NH2	B_ASP_86	OD2	3.302
2H9G	B_ARG_94	NH2	B_ASP_101	OD2	3.035
2H9G	B_LYS_143	NZ	B_ASP_144	OD1	3.273
2H9G	B_LYS_143	NZ	B_ASP_144	OD2	3.261
2H9G	B_LYS_209	NZ	A_GLU_123	OE1	2.713
2H9G	R_ARG_39	NH2	R_ASP_37	OD2	2.798
2H9G	R_ARG_104	NH1	R_ASP_122	OD2	3.726
2H9G	L_ARG_24	NH1	L_ASP_70	OD1	2.993
2H9G	L_ARG_24	NH2	L_ASP_70	OD1	3.108
2H9G	L_ARG_24	NH2	L_ASP_70	OD2	3.776
2H9G	L_ARG_61	NH2	L_GLU_81	OE1	3.703
2H9G	L_ARG_61	NH2	L_ASP_82	OD1	3.174
2H9G	L_ARG_61	NH2	L_ASP_82	OD2	3.885
2H9G	L_LYS_103	NZ	L_GLU_165	OE1	2.850
2H9G	L_LYS_103	NZ	L_GLU_165	OE2	3.736
2H9G	L_LYS_149	NZ	L_GLU_195	OE2	3.720
2H9G	L_LYS_183	NZ	L_GLU_187	OE1	2.899
2H9G	L_LYS_183	NZ	L_GLU_187	OE2	2.665
2H9G	H_ARG_38	NH1	H_ASP_86	OD1	2.962
2H9G	H_ARG_38	NH2	H_GLU_46	OE1	3.123
2H9G	H_ARG_38	NH2	H_GLU_46	OE2	3.981
2H9G	H_ARG_38	NH2	H_ASP_86	OD1	3.869
2H9G	H_LYS_64	NZ	H_ASP_61	OD1	3.096
2H9G	H_ARG_66	NH1	H_ASP_86	OD1	3.877
2H9G	H_ARG_66	NH1	H_ASP_86	OD2	2.818
2H9G	H_ARG_66	NH2	H_ASP_86	OD1	3.235
2H9G	H_ARG_66	NH2	H_ASP_86	OD2	3.633
2H9G	H_ARG_94	NH2	H_ASP_101	OD2	3.129
2H9G	H_LYS_143	NZ	H_ASP_144	OD1	3.284
2H9G	H_LYS_143	NZ	H_ASP_144	OD2	3.199
2H9G	H_LYS_209	NZ	L_GLU_123	OE1	2.570

Table 269: 2H9G-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2HFG	L_ARG_61	NH2	L_GLU_81	OE2	3.934
2HFG	L_ARG_61	NH2	L_ASP_82	OD1	2.654
2HFG	L_ARG_61	NH2	L_ASP_82	OD2	3.306
2HFG	L_LYS_148	NZ	L_GLU_194	OE2	2.762
2HFG	L_LYS_168	NZ	L_ASP_166	OD1	2.951
2HFG	L_LYS_168	NZ	L_ASP_166	OD2	3.686
2HFG	L_LYS_182	NZ	L_GLU_186	OE1	3.789
2HFG	H_ARG_38	NH1	H_ASP_86	OD1	3.062
2HFG	H_ARG_38	NH2	H_GLU_46	OE1	2.864
2HFG	H_ARG_38	NH2	H_GLU_46	OE2	3.710
2HFG	H_LYS_64	NZ	H_ASP_61	OD1	3.871
2HFG	H_ARG_66	NH1	H_ASP_86	OD1	3.665
2HFG	H_ARG_66	NH1	H_ASP_86	OD2	2.735
2HFG	H_ARG_66	NH2	H_ASP_86	OD1	3.183
2HFG	H_ARG_66	NH2	H_ASP_86	OD2	3.738
2HFG	H_ARG_83	NH1	H_GLU_85	OE2	3.672
2HFG	H_ARG_94	NH2	H_ASP_101	OD1	3.612
2HFG	H_ARG_94	NH2	H_ASP_101	OD2	2.745
2HFG	H_ARG_95	NH2	R_ASP_26	OD1	2.783
2HFG	H_ARG_95	NH2	R_ASP_26	OD2	3.667
2HFG	H_LYS_143	NZ	H_ASP_144	OD1	3.062
2HFG	H_LYS_143	NZ	H_ASP_144	OD2	2.650
2HFG	H_LYS_209	NZ	L_GLU_122	OE1	3.336
2HFG	H_LYS_209	NZ	L_GLU_122	OE2	2.886

Table 270: 2HFG-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2HKF	L_ARG_24	NH2	L_ASP_75	OD2	3.672
2HKF	L_LYS_44	NZ	L_GLU_86	OE2	3.798
2HKF	L_LYS_55	NZ	P_ASP_6	OD1	2.651
2HKF	L_ARG_66	NH1	L_GLU_84	OE1	2.688
2HKF	L_ARG_66	NH1	L_GLU_84	OE2	3.893
2HKF	L_ARG_66	NH2	L_GLU_84	OE1	3.861
2HKF	L_ARG_66	NH2	L_GLU_84	OE2	3.865
2HKF	L_ARG_66	NH2	L_GLU_86	OE1	3.229
2HKF	L_ARG_66	NH2	L_ASP_87	OD1	2.449
2HKF	L_ARG_66	NH2	L_ASP_87	OD2	3.580
2HKF	L_LYS_152	NZ	L_GLU_159	OE1	3.074
2HKF	L_LYS_152	NZ	L_GLU_159	OE2	3.333
2HKF	L_LYS_154	NZ	L_GLU_200	OE1	3.172
2HKF	L_LYS_154	NZ	L_GLU_200	OE2	3.401
2HKF	L_ARG_160	NH1	L_GLU_190	OE1	2.551
2HKF	L_ARG_160	NH2	L_GLU_190	OE1	2.732
2HKF	L_ARG_160	NH2	L_GLU_190	OE2	3.200
2HKF	L_ARG_193	NH1	L_ASP_189	OD1	2.634
2HKF	L_ARG_193	NH1	L_ASP_189	OD2	3.330
2HKF	L_ARG_193	NH2	L_ASP_189	OD1	3.591
2HKF	L_LYS_204	NZ	L_ASP_115	OD2	3.829
2HKF	H_ARG_38	NH1	H_ASP_92	OD1	2.875
2HKF	H_ARG_38	NH2	H_GLU_46	OE1	3.030
2HKF	H_ARG_38	NH2	H_GLU_46	OE2	3.901
2HKF	H_ARG_38	NH2	H_ASP_92	OD1	3.900
2HKF	H_ARG_50	NH2	P_GLU_5	OE1	3.869
2HKF	H_ARG_50	NH2	P_GLU_5	OE2	2.886
2HKF	H_ARG_52	NH2	P_GLU_5	OE1	3.116
2HKF	H_ARG_69	NH1	H_ASP_92	OD1	3.597
2HKF	H_ARG_69	NH1	H_ASP_92	OD2	2.654
2HKF	H_ARG_69	NH2	H_ASP_92	OD1	2.988
2HKF	H_ARG_69	NH2	H_ASP_92	OD2	3.598
2HKF	H_ARG_74	NH1	H_ASP_76	OD1	3.578
2HKF	H_LYS_214	NZ	L_GLU_128	OE2	2.891

Table 271: 2HKF-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2HMG	A_LYS_27	NZ	B_GLU_97	OE1	2.762
2HMG	A_LYS_27	NZ	B_GLU_97	OE2	3.001
2HMG	A_ARG_57	NH1	A_GLU_82	OE1	2.651
2HMG	A_ARG_57	NH1	A_GLU_82	OE2	3.908
2HMG	A_HIS_75	ND1	A_ASP_73	OD1	3.346
2HMG	A_HIS_75	ND1	A_ASP_73	OD2	2.800
2HMG	A_HIS_75	NE2	A_ASP_63	OD1	3.583
2HMG	A_ARG_90	NH1	A_ASP_60	OD1	2.824
2HMG	A_ARG_90	NH1	A_ASP_60	OD2	3.456
2HMG	A_ARG_109	NH1	B_GLU_67	OE1	3.634
2HMG	A_ARG_109	NH1	B_GLU_67	OE2	2.959
2HMG	A_ARG_109	NH2	A_GLU_89	OE1	3.190
2HMG	A_ARG_109	NH2	A_GLU_89	OE2	2.530
2HMG	A_ARG_141	NH1	A_ASP_77	OD1	3.112
2HMG	A_ARG_141	NH1	A_ASP_77	OD2	2.766
2HMG	A_ARG_141	NH2	A_ASP_146	OD1	2.729
2HMG	A_LYS_176	NZ	A_GLU_123	OE1	2.634
2HMG	A_LYS_176	NZ	A_GLU_123	OE2	3.933
2HMG	A_HIS_183	NE2	A_GLU_190	OE1	3.669
2HMG	A_ARG_208	NH2	A_ASP_241	OD2	2.864
2HMG	A_ARG_261	NH1	A_GLU_119	OE1	2.807
2HMG	A_ARG_261	NH1	A_GLU_119	OE2	2.727
2HMG	A_ARG_261	NH2	A_GLU_119	OE1	2.881
2HMG	A_LYS_264	NZ	A_ASP_85	OD1	3.585
2HMG	A_LYS_264	NZ	A_ASP_85	OD2	2.732
2HMG	A_ARG_269	NH2	B_GLU_67	OE1	2.999
2HMG	A_LYS_292	NZ	A_ASP_291	OD1	3.659
2HMG	A_LYS_299	NZ	B_GLU_69	OE1	3.169
2HMG	B_LYS_51	NZ	B_GLU_103	OE2	3.601
2HMG	B_ARG_54	NH1	F_GLU_97	OE1	2.721
2HMG	B_ARG_54	NH2	B_GLU_57	OE1	2.859
2HMG	B_ARG_54	NH2	B_GLU_57	OE2	3.200
2HMG	B_ARG_54	NH2	F_GLU_97	OE1	3.280
2HMG	B_LYS_62	NZ	F_ASP_86	OD1	3.023
2HMG	B_LYS_62	NZ	F_ASP_86	OD2	2.718
2HMG	B_LYS_62	NZ	F_ASP_90	OD1	3.256
2HMG	B_LYS_62	NZ	F_ASP_90	OD2	2.780
2HMG	B_HIS_64	NE2	F_ASP_79	OD2	3.863
2HMG	B_LYS_68	NZ	B_GLU_85	OE1	3.214
2HMG	B_LYS_68	NZ	B_GLU_85	OE2	2.698
2HMG	B_ARG_76	NH1	D_GLU_74	OE1	3.508
2HMG	B_ARG_76	NH1	D_GLU_74	OE2	2.816
2HMG	B_ARG_76	NH1	D_GLU_81	OE1	2.774
2HMG	B_ARG_76	NH1	D_GLU_81	OE2	3.655
2HMG	B_ARG_76	NH2	D_GLU_74	OE1	2.915
2HMG	B_ARG_76	NH2	D_GLU_74	OE2	3.598
2HMG	B_LYS_88	NZ	B_GLU_85	OE1	3.844
2HMG	B_LYS_117	NZ	B_GLU_114	OE1	2.609
2HMG	B_LYS_117	NZ	B_GLU_114	OE2	3.322
2HMG	B_ARG_123	NH1	F_GLU_132	OE2	3.122
2HMG	B_ARG_123	NH2	B_GLU_120	OE1	2.604
2HMG	B_ARG_123	NH2	B_GLU_120	OE2	2.778
2HMG	B_ARG_124	NH1	F_GLU_132	OE1	3.544
2HMG	B_ARG_124	NH1	F_GLU_132	OE2	3.040
2HMG	B_ARG_127	NH2	F_GLU_131	OE1	2.502
2HMG	B_ARG_153	NH2	B_GLU_150	OE2	2.575
2HMG	B_HIS_159	NE2	B_ASP_160	OD1	3.987

2HMG	B_HIS_159	NE2	B_ASP_160	OD2	3.070
2HMG	B_ARG_163	NH1	F_GLU_131	OE1	2.668
2HMG	B_ARG_163	NH1	F_GLU_131	OE2	2.605
2HMG	B_ARG_170	NH1	B_GLU_128	OE1	3.667
2HMG	B_ARG_170	NH1	D_GLU_128	OE1	3.860
2HMG	B_ARG_170	NH2	B_GLU_131	OE2	2.770
2HMG	B_ARG_170	NH2	D_GLU_128	OE1	2.750
2HMG	B_ARG_170	NH2	D_GLU_128	OE2	3.837
2HMG	C_LYS_27	NZ	D_GLU_97	OE1	2.819
2HMG	C_LYS_27	NZ	D_GLU_97	OE2	3.060
2HMG	C_ARG_57	NH1	C_GLU_82	OE1	2.635
2HMG	C_ARG_57	NH1	C_GLU_82	OE2	3.911
2HMG	C_HIS_75	ND1	C_ASP_73	OD1	3.326
2HMG	C_HIS_75	ND1	C_ASP_73	OD2	2.769
2HMG	C_HIS_75	NE2	C_ASP_63	OD1	3.558
2HMG	C_ARG_90	NH1	C_ASP_60	OD1	2.831
2HMG	C_ARG_90	NH1	C_ASP_60	OD2	3.485
2HMG	C_ARG_109	NH1	D_GLU_67	OE1	3.653
2HMG	C_ARG_109	NH1	D_GLU_67	OE2	2.947
2HMG	C_ARG_109	NH2	C_GLU_89	OE1	3.184
2HMG	C_ARG_109	NH2	C_GLU_89	OE2	2.523
2HMG	C_ARG_141	NH1	C_ASP_77	OD1	3.115
2HMG	C_ARG_141	NH1	C_ASP_77	OD2	2.775
2HMG	C_ARG_141	NH2	C_ASP_146	OD1	2.729
2HMG	C_LYS_176	NZ	C_GLU_123	OE1	2.643
2HMG	C_LYS_176	NZ	C_GLU_123	OE2	3.924
2HMG	C_HIS_183	NE2	C_GLU_190	OE1	3.657
2HMG	C_ARG_208	NH2	C_ASP_241	OD2	2.844
2HMG	C_ARG_261	NH1	C_GLU_119	OE1	2.785
2HMG	C_ARG_261	NH1	C_GLU_119	OE2	2.729
2HMG	C_ARG_261	NH2	C_GLU_119	OE1	2.874
2HMG	C_LYS_264	NZ	C_ASP_85	OD1	3.649
2HMG	C_LYS_264	NZ	C_ASP_85	OD2	2.789
2HMG	C_ARG_269	NH2	D_GLU_67	OE1	2.972
2HMG	C_LYS_292	NZ	C_ASP_291	OD1	3.718
2HMG	C_LYS_299	NZ	D_GLU_69	OE1	3.147
2HMG	D_LYS_51	NZ	D_GLU_103	OE2	3.620
2HMG	D_ARG_54	NH1	B_GLU_97	OE1	2.735
2HMG	D_ARG_54	NH2	B_GLU_97	OE1	3.312
2HMG	D_ARG_54	NH2	D_GLU_57	OE1	2.829
2HMG	D_ARG_54	NH2	D_GLU_57	OE2	3.186
2HMG	D_LYS_62	NZ	B_ASP_86	OD1	3.037
2HMG	D_LYS_62	NZ	B_ASP_86	OD2	2.683
2HMG	D_LYS_62	NZ	B_ASP_90	OD1	3.222
2HMG	D_LYS_62	NZ	B_ASP_90	OD2	2.673
2HMG	D_HIS_64	NE2	B_ASP_79	OD2	3.737
2HMG	D_LYS_68	NZ	D_GLU_85	OE1	3.177
2HMG	D_LYS_68	NZ	D_GLU_85	OE2	2.694
2HMG	D_ARG_76	NH1	F_GLU_74	OE1	3.549
2HMG	D_ARG_76	NH1	F_GLU_74	OE2	2.731
2HMG	D_ARG_76	NH1	F_GLU_81	OE1	2.698
2HMG	D_ARG_76	NH1	F_GLU_81	OE2	3.690
2HMG	D_ARG_76	NH2	F_GLU_74	OE1	2.828
2HMG	D_ARG_76	NH2	F_GLU_74	OE2	3.390
2HMG	D_LYS_88	NZ	D_GLU_85	OE1	3.822
2HMG	D_LYS_117	NZ	D_GLU_114	OE1	2.665
2HMG	D_LYS_117	NZ	D_GLU_114	OE2	3.347
2HMG	D_ARG_123	NH1	B_GLU_132	OE2	3.058

2HMG	D_ARG_123	NH2	D_GLU_120	OE1	2.590
2HMG	D_ARG_123	NH2	D_GLU_120	OE2	2.762
2HMG	D_ARG_124	NH1	B_GLU_132	OE1	3.508
2HMG	D_ARG_124	NH1	B_GLU_132	OE2	3.040
2HMG	D_ARG_127	NH2	B_GLU_131	OE1	2.517
2HMG	D_ARG_153	NH2	D_GLU_150	OE1	2.574
2HMG	D_HIS_159	NE2	D_ASP_160	OD2	3.088
2HMG	D_ARG_163	NH1	B_GLU_131	OE1	2.667
2HMG	D_ARG_163	NH1	B_GLU_131	OE2	2.648
2HMG	D_ARG_170	NH1	D_GLU_128	OE1	3.661
2HMG	D_ARG_170	NH1	F_GLU_128	OE1	3.974
2HMG	D_ARG_170	NH2	D_GLU_131	OE2	2.792
2HMG	D_ARG_170	NH2	F_GLU_128	OE1	2.843
2HMG	E_LYS_27	NZ	F_GLU_97	OE1	2.743
2HMG	E_LYS_27	NZ	F_GLU_97	OE2	3.029
2HMG	E_ARG_57	NH1	E_GLU_82	OE1	2.650
2HMG	E_ARG_57	NH1	E_GLU_82	OE2	3.908
2HMG	E_HIS_75	ND1	E_ASP_73	OD1	3.328
2HMG	E_HIS_75	ND1	E_ASP_73	OD2	2.787
2HMG	E_HIS_75	NE2	E_ASP_63	OD1	3.573
2HMG	E_ARG_90	NH1	E_ASP_60	OD1	2.857
2HMG	E_ARG_90	NH1	E_ASP_60	OD2	3.460
2HMG	E_ARG_109	NH1	F_GLU_67	OE1	3.629
2HMG	E_ARG_109	NH1	F_GLU_67	OE2	2.891
2HMG	E_ARG_109	NH2	E_GLU_89	OE1	3.184
2HMG	E_ARG_109	NH2	E_GLU_89	OE2	2.485
2HMG	E_ARG_141	NH1	E_ASP_77	OD1	3.113
2HMG	E_ARG_141	NH1	E_ASP_77	OD2	2.782
2HMG	E_ARG_141	NH2	E_ASP_146	OD1	2.726
2HMG	E_LYS_176	NZ	E_GLU_123	OE1	2.651
2HMG	E_LYS_176	NZ	E_GLU_123	OE2	3.954
2HMG	E_HIS_183	NE2	E_GLU_190	OE1	3.654
2HMG	E_ARG_208	NH2	E_ASP_241	OD2	2.863
2HMG	E_ARG_261	NH1	E_GLU_119	OE1	2.815
2HMG	E_ARG_261	NH1	E_GLU_119	OE2	2.721
2HMG	E_ARG_261	NH2	E_GLU_119	OE1	2.908
2HMG	E_LYS_264	NZ	E_ASP_85	OD1	3.640
2HMG	E_LYS_264	NZ	E_ASP_85	OD2	2.756
2HMG	E_ARG_269	NH2	F_GLU_67	OE1	2.967
2HMG	E_LYS_292	NZ	E_ASP_291	OD1	3.670
2HMG	E_LYS_299	NZ	F_GLU_69	OE1	3.127
2HMG	F_LYS_51	NZ	F_GLU_103	OE2	3.629
2HMG	F_ARG_54	NH1	D_GLU_97	OE1	2.701
2HMG	F_ARG_54	NH2	D_GLU_97	OE1	3.310
2HMG	F_ARG_54	NH2	F_GLU_57	OE1	2.831
2HMG	F_ARG_54	NH2	F_GLU_57	OE2	3.190
2HMG	F_LYS_62	NZ	D_ASP_86	OD1	2.945
2HMG	F_LYS_62	NZ	D_ASP_86	OD2	2.624
2HMG	F_LYS_62	NZ	D_ASP_90	OD1	3.290
2HMG	F_LYS_62	NZ	D_ASP_90	OD2	2.741
2HMG	F_HIS_64	NE2	D_ASP_79	OD2	3.679
2HMG	F_LYS_68	NZ	F_GLU_85	OE1	3.184
2HMG	F_LYS_68	NZ	F_GLU_85	OE2	2.666
2HMG	F_ARG_76	NH1	B_GLU_74	OE1	3.499
2HMG	F_ARG_76	NH1	B_GLU_74	OE2	2.732
2HMG	F_ARG_76	NH1	B_GLU_81	OE1	2.710
2HMG	F_ARG_76	NH1	B_GLU_81	OE2	3.754
2HMG	F_ARG_76	NH2	B_GLU_74	OE1	2.743

2HMG	F_ARG_76	NH2	B_GLU_74	OE2	3.373
2HMG	F_LYS_88	NZ	F_GLU_85	OE1	3.793
2HMG	F_LYS_117	NZ	F_GLU_114	OE1	2.621
2HMG	F_LYS_117	NZ	F_GLU_114	OE2	3.345
2HMG	F_ARG_123	NH1	D_GLU_132	OE2	3.112
2HMG	F_ARG_123	NH2	F_GLU_120	OE1	2.606
2HMG	F_ARG_123	NH2	F_GLU_120	OE2	2.778
2HMG	F_ARG_124	NH1	D_GLU_132	OE1	3.531
2HMG	F_ARG_124	NH1	D_GLU_132	OE2	3.090
2HMG	F_ARG_127	NH2	D_GLU_131	OE1	2.569
2HMG	F_HIS_159	NE2	F_ASP_160	OD2	3.079
2HMG	F_ARG_163	NH1	D_GLU_131	OE1	2.672
2HMG	F_ARG_163	NH1	D_GLU_131	OE2	2.717
2HMG	F_ARG_170	NH1	B_GLU_128	OE1	3.849
2HMG	F_ARG_170	NH1	F_GLU_128	OE1	3.672
2HMG	F_ARG_170	NH2	B_GLU_128	OE1	2.798
2HMG	F_ARG_170	NH2	B_GLU_128	OE2	3.855
2HMG	F_ARG_170	NH2	F_GLU_131	OE2	2.792

Table 272: 2HMG-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2HQ6	A_LYS_14	NZ	A_ASP_25	OD1	2.679
2HQ6	A_LYS_14	NZ	A_ASP_25	OD2	3.183
2HQ6	A_LYS_14	NZ	A_GLU_27	OE2	3.336
2HQ6	A_LYS_18	NZ	A_GLU_165	OE1	3.585
2HQ6	A_ARG_56	NH2	A_GLU_153	OE1	3.553
2HQ6	A_ARG_95	NH2	A_GLU_8	OE1	3.484
2HQ6	A_ARG_95	NH2	A_GLU_8	OE2	3.029
2HQ6	A_HIS_107	ND1	A_ASP_85	OD2	3.517
2HQ6	A_ARG_119	NH2	A_ASP_121	OD1	2.931
2HQ6	A_ARG_119	NH2	A_ASP_121	OD2	3.815
2HQ6	A_LYS_132	NZ	A_GLU_27	OE1	3.975

Table 273: 2HQ6-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2HRP	L_ARG_24	NH1	L_ASP_70	OD1	2.572
2HRP	L_ARG_24	NH1	L_ASP_70	OD2	3.000
2HRP	L_ARG_24	NH2	L_ASP_70	OD1	3.375
2HRP	L_ARG_24	NH2	L_ASP_70	OD2	3.315
2HRP	L_LYS_30	NZ	H_ASP_100B	OD2	3.323
2HRP	L_ARG_61	NH1	L_GLU_79	OE1	3.245
2HRP	L_ARG_61	NH1	L_GLU_79	OE2	3.462
2HRP	L_ARG_61	NH1	M_GLU_79	OE1	2.692
2HRP	L_ARG_61	NH1	M_GLU_79	OE2	2.607
2HRP	L_ARG_61	NH2	L_ASP_82	OD1	2.560
2HRP	L_ARG_61	NH2	L_ASP_82	OD2	3.088
2HRP	L_ARG_108	NH1	N_ASP_1	OD1	3.613
2HRP	L_ARG_108	NH1	N_ASP_1	OD2	2.869
2HRP	L_ARG_108	NH2	N_ASP_1	OD1	3.306
2HRP	L_ARG_108	NH2	N_ASP_1	OD2	3.988
2HRP	L_LYS_149	NZ	L_GLU_195	OE1	3.493
2HRP	L_ARG_155	NH1	L_GLU_185	OE2	3.630
2HRP	L_LYS_183	NZ	L_ASP_184	OD1	3.230
2HRP	L_LYS_183	NZ	L_GLU_187	OE1	3.035
2HRP	L_LYS_183	NZ	L_GLU_187	OE2	3.729
2HRP	L_ARG_188	NH1	L_GLU_185	OE1	2.934
2HRP	L_HIS_189	ND1	L_GLU_185	OE1	3.671
2HRP	L_HIS_189	ND1	L_GLU_185	OE2	3.948
2HRP	L_HIS_189	NE2	L_GLU_185	OE1	3.865
2HRP	L_LYS_199	NZ	L_ASP_110	OD2	2.970
2HRP	H_ARG_38	NH1	H_ASP_86	OD1	2.821
2HRP	H_ARG_38	NH2	H_GLU_46	OE1	3.156
2HRP	H_ARG_38	NH2	H_ASP_86	OD1	3.790
2HRP	H_ARG_66	NH1	H_ASP_86	OD1	3.830
2HRP	H_ARG_66	NH1	H_ASP_86	OD2	2.641
2HRP	H_ARG_66	NH2	H_ASP_86	OD1	2.914
2HRP	H_ARG_66	NH2	H_ASP_86	OD2	3.262
2HRP	H_ARG_83	NH1	H_GLU_85	OE1	2.871
2HRP	H_ARG_83	NH1	H_GLU_85	OE2	3.696
2HRP	H_ARG_94	NH1	H_ASP_101	OD1	3.338
2HRP	H_ARG_94	NH1	H_ASP_101	OD2	2.708
2HRP	H_ARG_100	NH1	H_ASP_100B	OD1	2.631
2HRP	H_ARG_100	NH1	H_ASP_100B	OD2	2.982
2HRP	H_LYS_205	NZ	N_ASP_207	OD2	3.339
2HRP	H_LYS_208	NZ	L_GLU_123	OE1	2.834
2HRP	M_ARG_24	NH1	M_ASP_70	OD2	3.391
2HRP	M_ARG_24	NH2	M_ASP_70	OD2	3.532
2HRP	M_LYS_30	NZ	N_ASP_100B	OD2	3.922
2HRP	M_ARG_61	NH1	L_GLU_79	OE1	2.827
2HRP	M_ARG_61	NH1	L_GLU_79	OE2	2.489
2HRP	M_ARG_61	NH1	M_GLU_79	OE1	3.762
2HRP	M_ARG_61	NH1	M_GLU_79	OE2	3.462
2HRP	M_ARG_61	NH2	L_GLU_79	OE1	3.658
2HRP	M_ARG_61	NH2	M_GLU_79	OE1	3.939
2HRP	M_ARG_61	NH2	M_ASP_82	OD1	2.828
2HRP	M_ARG_61	NH2	M_ASP_82	OD2	3.440
2HRP	M_LYS_92	NZ	M_GLU_93	OE2	2.546
2HRP	M_ARG_108	NH1	H_ASP_1	OD2	3.449
2HRP	M_ARG_108	NH1	M_ASP_170	OD2	3.998
2HRP	M_LYS_149	NZ	M_GLU_195	OE1	3.803
2HRP	M_LYS_149	NZ	M_GLU_195	OE2	2.914
2HRP	M_ARG_155	NH2	M_GLU_185	OE1	2.687

2HRP	M_ARG_155	NH2	M_GLU_185	OE2	3.383
2HRP	N_ARG_38	NH1	N_ASP_86	OD1	2.969
2HRP	N_ARG_38	NH2	N_GLU_46	OE1	3.031
2HRP	N_ARG_38	NH2	N_ASP_86	OD1	3.858
2HRP	N_LYS_43	NZ	N_GLU_46	OE1	3.283
2HRP	N_LYS_64	NZ	N_ASP_61	OD1	3.922
2HRP	N_ARG_66	NH1	N_ASP_86	OD1	3.805
2HRP	N_ARG_66	NH1	N_ASP_86	OD2	2.812
2HRP	N_ARG_66	NH2	N_ASP_86	OD1	2.794
2HRP	N_ARG_66	NH2	N_ASP_86	OD2	3.248
2HRP	N_ARG_83	NH1	N_GLU_85	OE2	3.361
2HRP	N_ARG_94	NH2	N_ASP_101	OD1	3.720
2HRP	N_ARG_94	NH2	N_ASP_101	OD2	2.978
2HRP	N_LYS_208	NZ	M_GLU_123	OE1	2.875
2HRP	N_LYS_208	NZ	M_GLU_123	OE2	3.117

Table 274: 2HRP-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2I24	N_ARG_2	NH1	N_ASP_26	OD2	2.648
2I24	N_ARG_2	NH2	N_ASP_4	OD1	3.932
2I24	N_ARG_2	NH2	N_ASP_4	OD2	2.968
2I24	N_ARG_28	NH2	N_ASP_93	OD1	2.817
2I24	N_ARG_28	NH2	N_ASP_93	OD2	3.512
2I24	N_ARG_54	NH1	N_ASP_77	OD1	3.458
2I24	N_ARG_54	NH1	N_ASP_77	OD2	2.886
2I24	N_ARG_54	NH2	N_ASP_77	OD1	2.870
2I24	N_ARG_54	NH2	N_ASP_77	OD2	3.606
2I24	N_ARG_82	NH2	N_GLU_46	OE1	2.871
2I24	N_ARG_82	NH2	N_GLU_46	OE2	3.583

Table 275: 2I24-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2I25	N_ARG_2	NH2	N_ASP_4	OD1	2.643
2I25	N_ARG_2	NH2	N_ASP_4	OD2	3.217
2I25	N_ARG_25	NH1	O_ASP_101	OD1	3.459
2I25	N_ARG_25	NH1	O_ASP_101	OD2	3.204
2I25	N_ARG_25	NH2	N_ASP_4	OD2	2.988
2I25	N_ARG_25	NH2	O_ASP_101	OD1	2.762
2I25	N_ARG_25	NH2	O_ASP_101	OD2	3.967
2I25	N_ARG_28	NH2	N_ASP_26	OD1	2.978
2I25	N_ARG_54	NH1	N_ASP_77	OD1	3.557
2I25	N_ARG_54	NH1	N_ASP_77	OD2	2.836
2I25	N_ARG_54	NH2	N_ASP_77	OD1	2.859
2I25	N_ARG_54	NH2	N_ASP_77	OD2	3.514
2I25	N_ARG_82	NH2	N_GLU_46	OE1	3.665
2I25	N_ARG_82	NH2	N_GLU_46	OE2	2.763
2I25	N_ARG_88	NH1	N_GLU_86	OE2	2.745
2I25	N_ARG_88	NH2	L_ASP_101	OD1	2.875
2I25	N_ARG_88	NH2	L_ASP_101	OD2	3.303
2I25	L_LYS_1	NZ	L_GLU_7	OE2	3.014
2I25	L_ARG_61	NH1	L_ASP_48	OD2	3.041
2I25	L_ARG_61	NH2	N_ASP_101	OD2	3.227
2I25	L_ARG_73	NH1	N_GLU_86	OE1	3.764
2I25	L_ARG_73	NH1	N_GLU_86	OE2	2.771
2I25	L_ARG_112	NH2	N_ASP_93	OD1	2.693
2I25	O_ARG_25	NH1	O_ASP_4	OD2	2.746
2I25	O_ARG_28	NH2	O_ASP_26	OD1	3.729
2I25	O_ARG_28	NH2	O_ASP_26	OD2	3.922
2I25	O_ARG_44	NH2	N_GLU_57	OE1	3.011
2I25	O_ARG_54	NH1	O_ASP_77	OD1	3.402
2I25	O_ARG_54	NH1	O_ASP_77	OD2	2.888
2I25	O_ARG_54	NH2	O_ASP_77	OD1	2.865
2I25	O_ARG_54	NH2	O_ASP_77	OD2	3.679
2I25	O_ARG_82	NH2	O_GLU_46	OE1	3.734
2I25	O_ARG_82	NH2	O_GLU_46	OE2	2.820
2I25	O_ARG_88	NH1	O_GLU_86	OE2	2.786
2I25	O_ARG_88	NH2	M_ASP_101	OD1	2.850
2I25	O_ARG_88	NH2	M_ASP_101	OD2	3.440
2I25	M_LYS_1	NZ	M_GLU_7	OE1	3.922
2I25	M_LYS_1	NZ	M_GLU_7	OE2	2.669
2I25	M_ARG_61	NH1	M_ASP_48	OD2	3.015
2I25	M_ARG_61	NH2	O_ASP_101	OD2	2.975
2I25	M_ARG_73	NH1	O_GLU_86	OE1	3.850
2I25	M_ARG_73	NH1	O_GLU_86	OE2	2.851
2I25	M_ARG_112	NH1	O_ASP_93	OD1	3.660
2I25	M_ARG_112	NH2	O_ASP_93	OD1	3.176
2I25	M_ARG_125	NH1	M_ASP_119	OD1	3.683
2I25	M_ARG_125	NH1	M_ASP_119	OD2	2.977
2I25	M_ARG_125	NH2	M_ASP_119	OD1	3.282
2I25	M_ARG_125	NH2	M_ASP_119	OD2	3.843

Table 276: 2I25-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2I26	N_ARG_2	NH1	N_ASP_4	OD2	3.516
2I26	N_ARG_2	NH2	N_ASP_4	OD1	3.612
2I26	N_ARG_2	NH2	N_ASP_4	OD2	3.274
2I26	N_ARG_38	NH2	N_GLU_47	OE2	3.790
2I26	N_LYS_51	NZ	N_GLU_57	OE1	3.254
2I26	N_LYS_51	NZ	N_GLU_57	OE2	3.781
2I26	N_ARG_54	NH1	N_ASP_77	OD1	3.540
2I26	N_ARG_54	NH1	N_ASP_77	OD2	3.097
2I26	N_ARG_54	NH2	N_ASP_77	OD1	2.953
2I26	N_ARG_54	NH2	N_ASP_77	OD2	3.934
2I26	N_ARG_82	NH2	N_GLU_46	OE1	3.207
2I26	N_ARG_82	NH2	N_GLU_46	OE2	3.809
2I26	N_ARG_88	NH1	N_GLU_86	OE2	2.847
2I26	N_ARG_88	NH2	L_ASP_101	OD1	3.268
2I26	N_ARG_88	NH2	L_ASP_101	OD2	3.652
2I26	L_LYS_1	NZ	L_GLU_7	OE2	3.495
2I26	L_ARG_73	NH1	N_GLU_86	OE2	3.511
2I26	L_ARG_73	NH2	N_GLU_86	OE1	3.590
2I26	L_ARG_73	NH2	N_GLU_86	OE2	3.542
2I26	L_ARG_112	NH1	N_ASP_93	OD2	3.838
2I26	L_ARG_112	NH2	N_ASP_93	OD2	3.391
2I26	O_LYS_12	NZ	O_GLU_16	OE1	2.500
2I26	O_LYS_12	NZ	O_GLU_16	OE2	3.336
2I26	O_ARG_25	NH2	O_ASP_4	OD1	3.978
2I26	O_ARG_38	NH1	O_ASP_77	OD1	3.853
2I26	O_LYS_51	NZ	O_GLU_57	OE1	2.746
2I26	O_LYS_51	NZ	O_GLU_57	OE2	3.677
2I26	O_ARG_54	NH1	O_ASP_77	OD1	3.513
2I26	O_ARG_54	NH1	O_ASP_77	OD2	3.061
2I26	O_ARG_54	NH2	O_ASP_77	OD1	3.014
2I26	O_ARG_82	NH2	O_GLU_46	OE1	3.607
2I26	O_ARG_82	NH2	O_GLU_46	OE2	2.938
2I26	O_ARG_88	NH1	M_ASP_101	OD1	2.648
2I26	O_ARG_88	NH1	M_ASP_101	OD2	2.840
2I26	O_ARG_88	NH2	O_GLU_86	OE2	3.407
2I26	M_LYS_1	NZ	M_GLU_7	OE2	2.378
2I26	M_ARG_61	NH1	M_ASP_48	OD2	3.000
2I26	M_ARG_73	NH1	O_GLU_86	OE1	2.832
2I26	M_ARG_73	NH1	O_GLU_86	OE2	3.677
2I26	M_ARG_112	NH1	O_ASP_93	OD2	3.127
2I26	M_ARG_112	NH2	O_ASP_93	OD2	3.198
2I26	P_ARG_2	NH1	P_ASP_4	OD2	3.455
2I26	P_ARG_25	NH1	P_ASP_4	OD2	3.288
2I26	P_ARG_38	NH1	P_ASP_77	OD1	3.296
2I26	P_ARG_38	NH2	P_GLU_47	OE2	3.357
2I26	P_LYS_51	NZ	P_GLU_57	OE1	2.842
2I26	P_LYS_51	NZ	P_GLU_57	OE2	3.265
2I26	P_ARG_54	NH1	P_ASP_77	OD1	3.557
2I26	P_ARG_54	NH1	P_ASP_77	OD2	3.011
2I26	P_ARG_54	NH2	P_ASP_77	OD1	2.936
2I26	P_ARG_54	NH2	P_ASP_77	OD2	3.842
2I26	P_ARG_82	NH2	P_GLU_46	OE1	3.185
2I26	P_ARG_82	NH2	P_GLU_46	OE2	3.977
2I26	P_ARG_88	NH1	Q_ASP_101	OD1	3.139
2I26	P_ARG_88	NH1	Q_ASP_101	OD2	3.016
2I26	P_ARG_88	NH2	P_GLU_86	OE2	3.489
2I26	Q_LYS_1	NZ	Q_GLU_7	OE1	3.316

2I26	Q_LYS_1	NZ	Q_GLU_7	OE2	2.614
2I26	Q_ARG_61	NH1	Q_ASP_48	OD2	2.954
2I26	Q_ARG_61	NH2	P_ASP_101	OD2	3.115
2I26	Q_ARG_73	NH1	P_GLU_86	OE2	2.623
2I26	Q_ARG_112	NH1	P_ASP_93	OD2	3.805
2I26	Q_ARG_112	NH2	P_ASP_93	OD2	3.685

Table 277: 2I26-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2I27	N_ARG_2	NH1	N_ASP_26	OD2	2.576
2I27	N_ARG_2	NH2	N_ASP_4	OD1	3.448
2I27	N_ARG_2	NH2	N_ASP_4	OD2	2.863
2I27	N_ARG_2	NH2	N_ASP_26	OD2	3.218
2I27	N_ARG_25	NH1	N_ASP_4	OD2	2.953
2I27	N_ARG_25	NH2	O_GLU_46	OE2	3.350
2I27	N_ARG_38	NH1	N_ASP_77	OD1	3.382
2I27	N_ARG_38	NH2	N_GLU_47	OE2	3.845
2I27	N_LYS_40	NZ	N_GLU_47	OE1	3.628
2I27	N_LYS_40	NZ	N_GLU_47	OE2	3.547
2I27	N_LYS_51	NZ	N_GLU_57	OE1	2.697
2I27	N_LYS_51	NZ	N_GLU_57	OE2	3.720
2I27	N_ARG_54	NH1	N_ASP_77	OD2	3.203
2I27	N_ARG_54	NH2	N_ASP_77	OD1	3.149
2I27	N_ARG_54	NH2	N_ASP_77	OD2	3.554
2I27	N_ARG_82	NH2	N_GLU_46	OE1	3.563
2I27	N_ARG_82	NH2	N_GLU_46	OE2	3.008
2I27	N_LYS_84	NZ	N_GLU_86	OE2	3.122
2I27	O_ARG_2	NH1	O_ASP_4	OD1	3.181
2I27	O_ARG_2	NH1	O_ASP_4	OD2	2.592
2I27	O_ARG_2	NH1	O_ASP_26	OD1	3.779
2I27	O_ARG_25	NH1	O_ASP_4	OD2	2.830
2I27	O_ARG_38	NH1	O_ASP_77	OD1	3.942
2I27	O_ARG_38	NH2	O_GLU_47	OE1	3.232
2I27	O_LYS_51	NZ	O_GLU_57	OE1	2.589
2I27	O_LYS_51	NZ	O_GLU_57	OE2	3.473
2I27	O_ARG_54	NH1	O_ASP_77	OD1	3.892
2I27	O_ARG_54	NH1	O_ASP_77	OD2	2.920
2I27	O_ARG_54	NH2	O_ASP_77	OD1	2.998
2I27	O_ARG_54	NH2	O_ASP_77	OD2	3.435
2I27	O_ARG_82	NH2	O_GLU_46	OE1	3.189
2I27	O_ARG_82	NH2	O_GLU_46	OE2	3.126
2I27	O_LYS_84	NZ	O_GLU_86	OE2	2.951

Table 278: 2I27-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2I5Y	G.LYS.121	NZ	G.GLU.429	OE2	3.126
2I5Y	G.LYS.207	NZ	G.GLU.381	OE2	3.637
2I5Y	G.HIS.249	NE2	G.GLU.482	OE1	2.873
2I5Y	G.LYS.282	NZ	G.GLU.275	OE1	2.722
2I5Y	G.LYS.348	NZ	G.GLU.269	OE1	2.750
2I5Y	G.LYS.348	NZ	G.GLU.351	OE1	3.311
2I5Y	G.LYS.348	NZ	G.GLU.351	OE2	3.874
2I5Y	G.ARG.419	NH1	H.GLU.100B	OE1	3.248
2I5Y	G.ARG.419	NH2	H.GLU.99	OE2	3.146
2I5Y	G.ARG.419	NH2	H.GLU.100D	OE2	2.601
2I5Y	G.ARG.456	NH1	G.GLU.466	OE1	2.646
2I5Y	G.ARG.469	NH2	G.ASP.457	OD1	3.980
2I5Y	G.ARG.469	NH2	G.ASP.457	OD2	2.626
2I5Y	G.ARG.476	NH1	G.GLU.102	OE2	2.957
2I5Y	G.ARG.476	NH2	G.ASP.474	OD1	3.611
2I5Y	G.ARG.476	NH2	G.ASP.474	OD2	2.800
2I5Y	G.ARG.480	NH2	G.ASP.477	OD1	3.599
2I5Y	L.ARG.24	NH1	L.GLU.70	OE1	3.407
2I5Y	L.ARG.24	NH2	L.GLU.70	OE1	3.609
2I5Y	L.ARG.24	NH2	L.GLU.70	OE2	2.932
2I5Y	L.ARG.61	NH2	L.GLU.81	OE2	2.667
2I5Y	L.ARG.61	NH2	L.ASP.82	OD1	2.958
2I5Y	L.ARG.61	NH2	L.ASP.82	OD2	3.675
2I5Y	L.LYS.149	NZ	L.GLU.195	OE1	3.958
2I5Y	L.LYS.183	NZ	L.GLU.187	OE1	2.546
2I5Y	L.HIS.189	ND1	L.ASP.151	OD2	2.886
2I5Y	H.ARG.31	NH2	H.ASP.100A	OD1	3.028
2I5Y	H.ARG.31	NH2	H.ASP.100A	OD2	3.251
2I5Y	H.ARG.38	NH2	H.ASP.86	OD2	3.623
2I5Y	H.ARG.50	NH2	H.GLU.97	OE1	2.885
2I5Y	H.ARG.66	NH1	H.ASP.86	OD1	2.818
2I5Y	H.ARG.66	NH1	H.ASP.86	OD2	3.645
2I5Y	H.ARG.66	NH2	H.ASP.86	OD1	3.819
2I5Y	H.ARG.66	NH2	H.ASP.86	OD2	3.195
2I5Y	H.LYS.73	NZ	H.ASP.55	OD2	3.789
2I5Y	H.ARG.82A	NH2	H.GLU.81	OE1	3.762
2I5Y	H.ARG.83	NH2	H.ASP.85	OD1	3.770
2I5Y	H.ARG.83	NH2	H.ASP.85	OD2	3.930
2I5Y	H.LYS.143	NZ	H.ASP.144	OD1	3.144
2I5Y	H.LYS.143	NZ	H.ASP.144	OD2	3.616
2I5Y	H.LYS.201	NZ	R.GLU.10	OE2	3.615
2I5Y	H.LYS.209	NZ	L.GLU.123	OE1	2.531
2I5Y	H.LYS.209	NZ	L.GLU.123	OE2	3.403
2I5Y	H.LYS.210	NZ	H.GLU.212	OE2	3.232
2I5Y	P.LYS.117	NZ	P.ASP.113	OD2	3.200
2I5Y	P.LYS.121	NZ	P.GLU.429	OE1	3.512
2I5Y	P.LYS.207	NZ	P.GLU.381	OE1	3.955
2I5Y	P.LYS.207	NZ	P.GLU.381	OE2	2.682
2I5Y	P.LYS.231	NZ	P.GLU.268	OE2	3.227
2I5Y	P.LYS.232	NZ	P.GLU.269	OE2	3.441
2I5Y	P.HIS.249	NE2	P.GLU.482	OE1	2.831
2I5Y	P.LYS.282	NZ	P.GLU.275	OE1	2.851
2I5Y	P.LYS.348	NZ	P.GLU.269	OE2	2.858
2I5Y	P.LYS.357	NZ	P.GLU.466	OE1	3.584
2I5Y	P.ARG.419	NH1	R.GLU.99	OE2	3.800
2I5Y	P.ARG.419	NH1	R.GLU.100D	OE1	2.563
2I5Y	P.ARG.419	NH1	R.GLU.100D	OE2	3.898

2I5Y	P_ARG_456	NH1	P_GLU_466	OE1	3.726
2I5Y	P_ARG_456	NH1	P_GLU_466	OE2	3.233
2I5Y	P_ARG_469	NH2	P_ASP_457	OD1	3.175
2I5Y	P_ARG_476	NH1	P_ASP_474	OD1	3.001
2I5Y	P_ARG_480	NH1	P_ASP_477	OD1	3.430
2I5Y	P_LYS_487	NZ	P_GLU_91	OE2	3.288
2I5Y	Q_ARG_24	NH1	Q_GLU_70	OE2	3.564
2I5Y	Q_ARG_61	NH2	Q_GLU_81	OE1	2.900
2I5Y	Q_ARG_61	NH2	Q_ASP_82	OD1	2.991
2I5Y	Q_ARG_61	NH2	Q_ASP_82	OD2	3.633
2I5Y	Q_ARG_95B	NH2	Q_ASP_1	OD2	3.695
2I5Y	Q_LYS_149	NZ	Q_GLU_195	OE1	3.615
2I5Y	Q_LYS_149	NZ	Q_GLU_195	OE2	3.356
2I5Y	Q_LYS_183	NZ	Q_GLU_187	OE1	3.007
2I5Y	Q_LYS_183	NZ	Q_GLU_187	OE2	3.247
2I5Y	Q_HIS_189	ND1	Q_ASP_151	OD1	2.992
2I5Y	R_LYS_12	NZ	R_GLU_10	OE2	3.536
2I5Y	R_ARG_31	NH2	R_ASP_100A	OD1	3.101
2I5Y	R_ARG_38	NH1	R_GLU_46	OE2	3.641
2I5Y	R_ARG_38	NH2	R_ASP_86	OD2	2.978
2I5Y	R_ARG_50	NH2	R_GLU_97	OE2	2.640
2I5Y	R_ARG_66	NH1	R_ASP_86	OD1	3.507
2I5Y	R_ARG_66	NH2	R_ASP_86	OD1	3.587
2I5Y	R_ARG_66	NH2	R_ASP_86	OD2	3.055
2I5Y	R_ARG_83	NH2	R_ASP_85	OD1	3.357
2I5Y	R_ARG_83	NH2	R_ASP_85	OD2	2.690
2I5Y	R_LYS_209	NZ	Q_GLU_123	OE2	3.373
2I5Y	R_LYS_210	NZ	R_GLU_212	OE1	3.854
2I5Y	S_ARG_9	NH1	P_ASP_368	OD2	2.853
2I5Y	S_ARG_9	NH2	P_ASP_368	OD2	3.453

Table 279: 2I5Y-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2I60	G_LYS_85	NZ	G_GLU_87	OE1	2.991
2I60	G_LYS_97	NZ	G_GLU_275	OE2	3.907
2I60	G_LYS_121	NZ	G_GLU_429	OE2	3.453
2I60	G_LYS_207	NZ	G_GLU_381	OE2	3.877
2I60	G_LYS_231	NZ	G_GLU_268	OE1	3.768
2I60	G_HIS_249	NE2	G_GLU_482	OE1	2.855
2I60	G_LYS_282	NZ	G_GLU_275	OE1	2.727
2I60	G_LYS_348	NZ	G_GLU_269	OE1	3.168
2I60	G_LYS_350	NZ	G_ASP_395	OD2	3.640
2I60	G_ARG_419	NH2	H_GLU_99	OE1	3.736
2I60	G_ARG_419	NH2	H_GLU_99	OE2	2.767
2I60	G_ARG_419	NH2	H_GLU_100D	OE2	3.611
2I60	G_ARG_456	NH1	G_GLU_466	OE1	2.710
2I60	G_ARG_456	NH1	G_GLU_466	OE2	3.759
2I60	G_ARG_469	NH2	G_ASP_457	OD1	2.579
2I60	G_ARG_469	NH2	G_ASP_457	OD2	3.789
2I60	G_ARG_476	NH1	G_GLU_102	OE1	3.422
2I60	G_ARG_476	NH2	G_ASP_474	OD1	3.929
2I60	G_ARG_476	NH2	G_ASP_474	OD2	2.677
2I60	G_ARG_480	NH1	G_ASP_477	OD1	3.717
2I60	L_ARG_24	NH1	L_GLU_70	OE2	3.278
2I60	L_ARG_24	NH2	L_GLU_70	OE2	2.910
2I60	L_ARG_61	NH2	L_GLU_81	OE2	2.838
2I60	L_ARG_61	NH2	L_ASP_82	OD1	2.837
2I60	L_ARG_61	NH2	L_ASP_82	OD2	3.354
2I60	L_LYS_149	NZ	L_GLU_195	OE1	3.670
2I60	H_ARG_31	NH2	H_ASP_100A	OD1	3.164
2I60	H_ARG_31	NH2	H_ASP_100A	OD2	3.397
2I60	H_ARG_38	NH1	H_GLU_46	OE2	3.054
2I60	H_ARG_38	NH2	H_ASP_86	OD2	3.336
2I60	H_ARG_50	NH2	H_GLU_97	OE2	3.134
2I60	H_ARG_66	NH1	H_ASP_86	OD1	3.041
2I60	H_ARG_66	NH1	H_ASP_86	OD2	3.960
2I60	H_ARG_66	NH2	H_ASP_86	OD1	3.627
2I60	H_ARG_66	NH2	H_ASP_86	OD2	3.212
2I60	H_ARG_82A	NH2	H_GLU_81	OE2	3.855
2I60	H_ARG_83	NH1	H_ASP_85	OD1	3.248
2I60	H_ARG_83	NH1	H_ASP_85	OD2	3.416
2I60	H_LYS_143	NZ	H_ASP_144	OD1	3.384
2I60	H_LYS_209	NZ	L_GLU_123	OE1	3.997
2I60	H_LYS_210	NZ	H_GLU_212	OE2	3.501
2I60	P_LYS_121	NZ	P_GLU_429	OE1	3.897
2I60	P_LYS_207	NZ	P_GLU_381	OE1	3.463
2I60	P_LYS_207	NZ	P_GLU_381	OE2	2.996
2I60	P_HIS_249	NE2	P_GLU_482	OE1	2.831
2I60	P_LYS_282	NZ	P_GLU_275	OE1	2.805
2I60	P_LYS_348	NZ	P_GLU_269	OE1	2.586
2I60	P_LYS_357	NZ	P_GLU_466	OE2	3.512
2I60	P_ARG_419	NH1	R_GLU_100B	OE1	3.610
2I60	P_ARG_419	NH2	R_GLU_99	OE1	3.892
2I60	P_ARG_456	NH1	P_GLU_466	OE1	2.943
2I60	P_ARG_456	NH1	P_GLU_466	OE2	3.500
2I60	P_ARG_469	NH2	P_ASP_457	OD1	3.419
2I60	P_ARG_476	NH1	P_GLU_102	OE1	3.696
2I60	P_ARG_476	NH1	P_GLU_102	OE2	2.989
2I60	P_ARG_476	NH2	P_ASP_474	OD2	3.307
2I60	P_ARG_480	NH1	P_ASP_477	OD1	3.241

2I60	Q_ARG_24	NH1	Q_GLU_70	OE2	3.297
2I60	Q_ARG_61	NH2	Q_GLU_81	OE1	3.836
2I60	Q_ARG_61	NH2	Q_ASP_82	OD1	3.255
2I60	Q_ARG_61	NH2	Q_ASP_82	OD2	3.646
2I60	Q_LYS_183	NZ	Q_GLU_187	OE1	3.479
2I60	Q_LYS_183	NZ	Q_GLU_187	OE2	3.280
2I60	Q_HIS_189	ND1	Q_ASP_151	OD1	3.866
2I60	R_ARG_31	NH2	R_ASP_100A	OD1	3.967
2I60	R_ARG_31	NH2	R_ASP_100A	OD2	2.823
2I60	R_ARG_38	NH1	R_GLU_46	OE2	2.939
2I60	R_ARG_38	NH2	R_ASP_86	OD2	3.162
2I60	R_ARG_50	NH2	R_GLU_97	OE2	2.924
2I60	R_ARG_66	NH1	R_ASP_86	OD1	3.520
2I60	R_ARG_66	NH1	R_ASP_86	OD2	3.317
2I60	R_ARG_66	NH2	R_ASP_86	OD1	3.743
2I60	R_ARG_66	NH2	R_ASP_86	OD2	3.021
2I60	R_ARG_82A	NH2	R_GLU_81	OE1	3.453
2I60	R_ARG_83	NH2	R_ASP_85	OD1	3.280
2I60	R_LYS_143	NZ	R_ASP_144	OD1	3.244
2I60	R_LYS_143	NZ	R_ASP_144	OD2	3.755
2I60	R_LYS_209	NZ	Q_GLU_123	OE2	3.485
2I60	S_ARG_9	NH1	P_ASP_368	OD2	3.268
2I60	S_ARG_9	NH2	P_ASP_368	OD1	3.938
2I60	S_ARG_9	NH2	P_ASP_368	OD2	2.664

Table 280: 2I60-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2IFF	L_LYS_44	NZ	H_ASP_104	OD1	2.935
2IFF	L_ARG_45	NH2	H_ASP_104	OD2	3.348
2IFF	L_ARG_60	NH2	L_ASP_81	OD1	2.794
2IFF	L_ARG_60	NH2	L_ASP_81	OD2	3.163
2IFF	L_LYS_101	NZ	L_ASP_163	OD1	3.641
2IFF	L_LYS_105	NZ	L_GLU_17	OE1	3.700
2IFF	L_LYS_105	NZ	L_GLU_17	OE2	3.218
2IFF	L_ARG_106	NH2	L_ASP_168	OD1	2.967
2IFF	L_ARG_106	NH2	L_ASP_168	OD2	3.027
2IFF	L_LYS_147	NZ	L_GLU_193	OE1	3.478
2IFF	L_LYS_147	NZ	L_GLU_193	OE2	3.002
2IFF	L_LYS_181	NZ	L_GLU_185	OE1	2.942
2IFF	L_LYS_181	NZ	L_GLU_185	OE2	3.794
2IFF	L_ARG_186	NH2	L_ASP_182	OD2	3.027
2IFF	L_HIS_187	ND1	L_ASP_149	OD2	3.188
2IFF	L_HIS_196	ND1	L_ASP_141	OD1	3.647
2IFF	H_HIS_43	ND1	H_GLU_46	OE1	3.306
2IFF	H_HIS_43	ND1	H_GLU_46	OE2	3.465
2IFF	H_HIS_43	NE2	H_GLU_46	OE2	3.940
2IFF	H_LYS_65	NZ	H_GLU_62	OE2	3.927
2IFF	H_LYS_67	NZ	H_ASP_90	OD1	3.416
2IFF	H_LYS_67	NZ	H_ASP_90	OD2	3.000
2IFF	H_LYS_208	NZ	H_ASP_210	OD1	3.142
2IFF	H_LYS_208	NZ	H_ASP_210	OD2	3.455
2IFF	H_LYS_211	NZ	L_GLU_121	OE1	3.040
2IFF	H_LYS_211	NZ	L_GLU_121	OE2	2.921
2IFF	Y_LYS_1	NZ	Y_GLU_7	OE1	2.914
2IFF	Y_LYS_1	NZ	Y_GLU_7	OE2	3.893
2IFF	Y_LYS_13	NZ	Y_ASP_18	OD2	3.220
2IFF	Y_ARG_45	NH1	H_GLU_50	OE1	3.425
2IFF	Y_ARG_45	NH1	H_GLU_50	OE2	2.959
2IFF	Y_LYS_97	NZ	Y_ASP_101	OD1	2.879
2IFF	Y_ARG_125	NH1	Y_ASP_119	OD2	3.485
2IFF	Y_ARG_125	NH2	Y_ASP_119	OD1	3.655
2IFF	Y_ARG_125	NH2	Y_ASP_119	OD2	2.761

Table 281: 2IFF-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2IG2	L_ARG_60	NH1	L_GLU_80	OE1	3.431
2IG2	L_ARG_60	NH2	L_GLU_80	OE1	2.806
2IG2	L_ARG_60	NH2	L_ASP_81	OD1	3.509
2IG2	L_ARG_60	NH2	L_ASP_81	OD2	2.584
2IG2	L_LYS_104	NZ	L_ASP_84	OD1	3.314
2IG2	L_LYS_104	NZ	L_ASP_84	OD2	2.687
2IG2	L_LYS_112	NZ	L_GLU_200	OE2	3.492
2IG2	H_ARG_38	NH1	H_ASP_90	OD2	3.025
2IG2	H_ARG_38	NH2	H_GLU_46	OE1	3.194
2IG2	H_ARG_38	NH2	H_GLU_46	OE2	3.026
2IG2	H_ARG_67	NH1	H_ASP_90	OD1	2.773
2IG2	H_ARG_67	NH2	H_ASP_90	OD1	2.946
2IG2	H_ARG_67	NH2	H_ASP_90	OD2	2.843
2IG2	H_ARG_72	NH1	H_ASP_74	OD2	3.016
2IG2	H_ARG_98	NH2	H_ASP_106	OD1	2.603
2IG2	H_ARG_98	NH2	H_ASP_106	OD2	3.320
2IG2	H_LYS_148	NZ	L_GLU_126	OE2	2.854
2IG2	H_LYS_214	NZ	L_GLU_125	OE1	3.816
2IG2	H_LYS_214	NZ	L_GLU_125	OE2	2.866
2IG2	H_ARG_215	NH1	H_GLU_217	OE1	2.857
2IG2	H_ARG_215	NH1	H_GLU_217	OE2	3.431
2IG2	H_HIS_225	ND1	H_ASP_222	OD1	2.822
2IG2	H_HIS_225	ND1	H_ASP_222	OD2	3.302

Table 282: 2IG2-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2IGF	L_LYS_50	NZ	L_ASP_30	OD1	3.055
2IGF	L_LYS_50	NZ	L_ASP_30	OD2	3.465
2IGF	L_ARG_61	NH1	L_GLU_79	OE2	3.565
2IGF	L_ARG_61	NH2	L_ASP_82	OD1	2.974
2IGF	L_ARG_61	NH2	L_ASP_82	OD2	2.588
2IGF	L_LYS_149	NZ	L_GLU_195	OE2	3.389
2IGF	L_HIS_189	ND1	L_ASP_151	OD2	3.248
2IGF	L_ARG_211	NH1	L_GLU_187	OE1	2.780
2IGF	H_ARG_38	NH1	H_GLU_46	OE1	3.128
2IGF	H_ARG_38	NH1	H_GLU_46	OE2	2.803
2IGF	H_ARG_38	NH2	H_GLU_46	OE2	3.695
2IGF	H_ARG_38	NH2	H_ASP_86	OD1	3.966
2IGF	H_ARG_44	NH1	H_GLU_46	OE1	3.519
2IGF	H_ARG_44	NH2	H_GLU_46	OE1	3.195
2IGF	H_ARG_66	NH1	H_ASP_86	OD2	3.364
2IGF	H_ARG_66	NH2	H_ASP_86	OD1	2.723
2IGF	H_ARG_66	NH2	H_ASP_86	OD2	3.057
2IGF	H_ARG_94	NH1	H_ASP_101	OD1	2.615
2IGF	H_ARG_94	NH1	H_ASP_101	OD2	2.615
2IGF	H_LYS_221	NZ	L_GLU_123	OE1	3.203
2IGF	P_LYS_75	NZ	L_ASP_28	OD1	3.253
2IGF	P_LYS_75	NZ	L_ASP_28	OD2	2.849
2IGF	P_LYS_75	NZ	L_ASP_30	OD2	3.458

Table 283: 2IGF-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2IHL	A_LYS_1	NZ	A_GLU_7	OE1	3.817
2IHL	A_LYS_1	NZ	A_GLU_7	OE2	2.767
2IHL	A_LYS_19	NZ	A_ASP_18	OD2	3.871
2IHL	A_ARG_125	NH1	A_ASP_119	OD2	2.708
2IHL	A_ARG_125	NH2	A_ASP_119	OD1	3.281
2IHL	A_ARG_125	NH2	A_ASP_119	OD2	2.935

Table 284: 2IHL-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2J4W	D_LYS_427	NZ	D_GLU_435	OE2	3.034
2J4W	D_LYS_427	NZ	H_ASP_52A	OD1	3.478
2J4W	D_LYS_427	NZ	H_ASP_52A	OD2	2.864
2J4W	H_ARG_38	NH1	H_ASP_86	OD1	2.975
2J4W	H_ARG_38	NH2	H_GLU_46	OE1	3.139
2J4W	H_LYS_64	NZ	H_ASP_61	OD1	3.371
2J4W	H_ARG_66	NH1	H_ASP_86	OD1	3.417
2J4W	H_ARG_66	NH1	H_ASP_86	OD2	3.943
2J4W	H_ARG_66	NH2	H_ASP_86	OD1	3.210
2J4W	H_ARG_66	NH2	H_ASP_86	OD2	2.467
2J4W	H_LYS_221	NZ	L_GLU_123	OE1	3.280
2J4W	H_LYS_221	NZ	L_GLU_123	OE2	3.313
2J4W	L_ARG_61	NH1	L_GLU_79	OE1	3.729
2J4W	L_ARG_61	NH1	L_GLU_79	OE2	3.488
2J4W	L_ARG_61	NH2	L_GLU_79	OE1	3.516
2J4W	L_ARG_61	NH2	L_GLU_81	OE1	2.766
2J4W	L_ARG_61	NH2	L_ASP_82	OD1	2.774
2J4W	L_ARG_61	NH2	L_ASP_82	OD2	3.759
2J4W	L_LYS_142	NZ	L_GLU_105	OE1	3.490
2J4W	L_LYS_142	NZ	L_GLU_105	OE2	3.345
2J4W	L_LYS_149	NZ	L_GLU_195	OE1	3.192
2J4W	L_LYS_149	NZ	L_GLU_195	OE2	3.504
2J4W	L_LYS_183	NZ	L_GLU_187	OE1	3.405
2J4W	L_HIS_189	ND1	L_ASP_151	OD2	3.005
2J4W	L_LYS_199	NZ	L_ASP_110	OD1	3.337
2J4W	L_LYS_199	NZ	L_ASP_110	OD2	2.705

Table 285: 2J4W-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2J5L	A_LYS_485	NZ	A_ASP_493	OD2	3.126
2J5L	A_LYS_485	NZ	C_ASP_52A	OD1	3.476
2J5L	A_LYS_485	NZ	C_ASP_52A	OD2	3.193
2J5L	B_ARG_61	NH1	B_GLU_79	OE1	3.650
2J5L	B_ARG_61	NH1	B_GLU_81	OE1	3.873
2J5L	B_ARG_61	NH2	B_GLU_79	OE1	3.530
2J5L	B_ARG_61	NH2	B_GLU_81	OE1	2.133
2J5L	B_ARG_61	NH2	B_ASP_82	OD1	3.268
2J5L	B_ARG_61	NH2	B_ASP_82	OD2	3.063
2J5L	B_LYS_107	NZ	B_GLU_17	OE1	3.863
2J5L	B_LYS_142	NZ	B_GLU_105	OE2	3.802
2J5L	B_LYS_149	NZ	B_GLU_195	OE1	3.695
2J5L	B_LYS_149	NZ	B_GLU_195	OE2	3.425
2J5L	B_LYS_183	NZ	B_GLU_187	OE1	3.637
2J5L	B_HIS_	ND1	B_ASP_	OD1	3.873
2J5L	B_HIS_	ND1	B_ASP_	OD2	2.683
2J5L	B_LYS_199	NZ	B_ASP_110	OD1	3.371
2J5L	B_LYS_199	NZ	B_ASP_110	OD2	3.451
2J5L	B_ARG_	NH2	B_GLU_187	OE2	3.792
2J5L	C_LYS_13	NZ	C_GLU_113	OE2	3.785
2J5L	C_ARG_38	NH1	C_ASP_86	OD1	3.392
2J5L	C_ARG_38	NH2	C_GLU_46	OE1	3.226
2J5L	C_ARG_38	NH2	C_ASP_86	OD1	3.787
2J5L	C_LYS_64	NZ	C_ASP_61	OD1	2.837
2J5L	C_ARG_66	NH2	C_ASP_86	OD1	3.420
2J5L	C_ARG_66	NH2	C_ASP_86	OD2	2.859

Table 286: 2J5L-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2JB6	A_ARG_63	NH1	A_ASP_84	OD1	3.533
2JB6	A_ARG_63	NH1	A_ASP_84	OD2	2.728
2JB6	A_ARG_63	NH2	A_GLU_83	OE2	3.226
2JB6	A_ARG_63	NH2	A_ASP_84	OD1	2.862
2JB6	A_ARG_63	NH2	A_ASP_84	OD2	3.549
2JB6	A_LYS_115	NZ	A_GLU_203	OE1	3.724
2JB6	A_LYS_115	NZ	A_GLU_203	OE2	2.595
2JB6	A_LYS_171	NZ	A_GLU_85	OE2	2.779
2JB6	A_LYS_176	NZ	A_ASP_143	OD2	3.821
2JB6	B_ARG_38	NH1	B_GLU_46	OE2	3.287
2JB6	B_ARG_38	NH2	B_ASP_90	OD1	2.735
2JB6	B_LYS_63	NZ	B_GLU_46	OE1	3.460
2JB6	B_LYS_63	NZ	B_GLU_46	OE2	2.655
2JB6	B_ARG_67	NH1	B_ASP_90	OD1	2.699
2JB6	B_ARG_67	NH1	B_ASP_90	OD2	3.291
2JB6	B_ARG_67	NH2	B_ASP_90	OD2	3.389
2JB6	B_ARG_87	NH2	B_ASP_90	OD1	3.736
2JB6	B_LYS_150	NZ	B_ASP_151	OD2	3.447
2JB6	B_LYS_216	NZ	A_GLU_128	OE2	3.078
2JB6	H_LYS_19	NZ	H_GLU_82	OE2	3.873
2JB6	H_ARG_38	NH1	H_ASP_90	OD1	3.271
2JB6	H_ARG_38	NH2	H_GLU_46	OE2	3.202
2JB6	H_LYS_63	NZ	H_GLU_46	OE1	3.407
2JB6	H_LYS_63	NZ	H_GLU_46	OE2	3.102
2JB6	H_ARG_67	NH1	H_ASP_90	OD1	2.780
2JB6	H_ARG_67	NH1	H_ASP_90	OD2	2.831
2JB6	H_ARG_67	NH2	H_ASP_90	OD1	3.259
2JB6	H_LYS_150	NZ	H_ASP_151	OD1	3.864
2JB6	L_ARG_63	NH1	L_ASP_84	OD1	3.793
2JB6	L_ARG_63	NH1	L_ASP_84	OD2	2.807
2JB6	L_ARG_63	NH2	L_ASP_84	OD1	2.677
2JB6	L_ARG_63	NH2	L_ASP_84	OD2	3.231
2JB6	L_LYS_115	NZ	L_GLU_203	OE2	3.325
2JB6	L_LYS_154	NZ	L_GLU_208	OE2	3.249
2JB6	L_LYS_171	NZ	L_GLU_85	OE2	2.744

Table 287: 2JB6-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2JEL	L_ARG_24	NH2	L_ASP_70	OD1	3.600
2JEL	L_ARG_24	NH2	L_ASP_70	OD2	3.545
2JEL	L_LYS_50	NZ	H_GLU_98	OE1	2.874
2JEL	L_LYS_50	NZ	P_GLU_66	OE1	3.050
2JEL	L_LYS_50	NZ	P_GLU_66	OE2	3.051
2JEL	L_ARG_54	NH2	L_ASP_60	OD1	2.887
2JEL	L_ARG_61	NH1	L_ASP_82	OD1	3.350
2JEL	L_ARG_61	NH1	L_ASP_82	OD2	2.775
2JEL	L_ARG_61	NH2	L_GLU_81	OE2	3.253
2JEL	L_ARG_61	NH2	L_ASP_82	OD1	3.113
2JEL	L_ARG_61	NH2	L_ASP_82	OD2	3.996
2JEL	L_ARG_77	NH1	L_GLU_79	OE2	3.110
2JEL	L_LYS_103	NZ	L_ASP_165	OD1	2.863
2JEL	L_LYS_142	NZ	L_ASP_143	OD1	3.795
2JEL	L_LYS_142	NZ	L_ASP_143	OD2	3.573
2JEL	L_LYS_149	NZ	L_GLU_195	OE1	3.417
2JEL	L_LYS_149	NZ	L_GLU_195	OE2	3.269
2JEL	L_HIS_189	ND1	L_ASP_152	OD1	3.014
2JEL	L_LYS_199	NZ	L_ASP_110	OD2	2.782
2JEL	H_LYS_62	NZ	H_GLU_46	OE1	3.175
2JEL	H_LYS_62	NZ	H_GLU_46	OE2	3.429
2JEL	H_LYS_66	NZ	H_ASP_86	OD1	3.906
2JEL	H_LYS_66	NZ	H_ASP_86	OD2	2.853
2JEL	H_ARG_94	NH2	H_ASP_101	OD2	2.854
2JEL	H_LYS_218	NZ	H_ASP_220	OD1	3.234
2JEL	P_LYS_79	NZ	P_GLU_75	OE2	2.896

Table 288: 2JEL-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2MCP	L_ARG_67	NH1	L_ASP_88	OD1	3.540
2MCP	L_ARG_67	NH1	L_ASP_88	OD2	2.647
2MCP	L_ARG_67	NH2	L_GLU_87	OE1	3.416
2MCP	L_ARG_67	NH2	L_ASP_88	OD1	2.658
2MCP	L_ARG_67	NH2	L_ASP_88	OD2	3.318
2MCP	L_LYS_109	NZ	L_ASP_171	OD1	3.858
2MCP	L_LYS_148	NZ	L_ASP_149	OD1	3.270
2MCP	L_LYS_148	NZ	L_ASP_149	OD2	2.997
2MCP	L_LYS_155	NZ	L_GLU_201	OE2	2.618
2MCP	L_ARG_194	NH1	L_GLU_191	OE2	3.915
2MCP	L_HIS_195	ND1	L_ASP_157	OD1	3.712
2MCP	L_LYS_205	NZ	L_ASP_116	OD2	3.742
2MCP	H_ARG_38	NH1	H_ASP_92	OD2	3.060
2MCP	H_ARG_38	NH2	H_GLU_46	OE1	3.610
2MCP	H_ARG_38	NH2	H_GLU_46	OE2	2.688
2MCP	H_ARG_52	NH2	H_GLU_61	OE1	2.754
2MCP	H_ARG_69	NH1	H_ASP_92	OD2	3.561
2MCP	H_ARG_69	NH2	H_ASP_92	OD1	2.431
2MCP	H_ARG_69	NH2	H_ASP_92	OD2	2.824
2MCP	H_ARG_89	NH2	H_GLU_91	OE1	3.538
2MCP	H_ARG_89	NH2	H_GLU_91	OE2	3.717
2MCP	H_ARG_100	NH1	H_ASP_110	OD1	2.497
2MCP	H_ARG_100	NH1	H_ASP_110	OD2	2.947
2MCP	H_ARG_126	NH1	H_ASP_152	OD2	3.242
2MCP	H_ARG_184	NH1	H_ASP_152	OD1	2.420
2MCP	H_ARG_184	NH1	H_ASP_152	OD2	2.976
2MCP	H_LYS_205	NZ	H_ASP_219	OD1	3.027
2MCP	H_LYS_205	NZ	H_ASP_219	OD2	3.236

Table 289: 2MCP-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2MKL-1	C_ARG_50	NH1	C_GLU_49	OE2	3.937
2MKL-1	C_ARG_50	NH2	C_GLU_49	OE2	3.687
2MKL-1	C_LYS_52	NZ	C_GLU_55	OE1	2.974
2MKL-1	C_LYS_104	NZ	C_ASP_80	OD1	2.719
2MKL-10	C_LYS_40	NZ	C_GLU_90	OE1	3.590
2MKL-10	C_LYS_40	NZ	C_GLU_90	OE2	2.585
2MKL-10	C_ARG_50	NH2	C_GLU_49	OE2	3.606
2MKL-10	C_LYS_65	NZ	C_ASP_6	OD1	3.508
2MKL-10	C_LYS_71	NZ	C_GLU_55	OE2	3.851
2MKL-10	C_LYS_104	NZ	C_ASP_80	OD1	3.644

Table 290: 2MKL-1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2MKL-10	C_LYS_40	NZ	C_GLU_90	OE1	3.590
2MKL-10	C_LYS_40	NZ	C_GLU_90	OE2	2.585
2MKL-10	C_ARG_50	NH2	C_GLU_49	OE2	3.606
2MKL-10	C_LYS_65	NZ	C_ASP_6	OD1	3.508
2MKL-10	C_LYS_71	NZ	C_GLU_55	OE2	3.851
2MKL-10	C_LYS_104	NZ	C_ASP_80	OD1	3.644

Table 291: 2MKL-10-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2MKL-2	C_ARG_50	NH1	C_GLU_78	OE1	3.157
2MKL-2	C_ARG_50	NH1	C_GLU_78	OE2	2.728
2MKL-2	C_LYS_65	NZ	C_ASP_6	OD2	3.453
2MKL-2	C_LYS_71	NZ	C_GLU_55	OE1	2.717
2MKL-2	C_LYS_104	NZ	C_ASP_80	OD1	3.607

Table 292: 2MKL-2-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2MKL-3	C_ARG_3	NH1	C_GLU_93	OE1	2.682
2MKL-3	C_ARG_3	NH2	C_GLU_93	OE1	3.724
2MKL-3	C_LYS_65	NZ	C_ASP_6	OD2	3.268
2MKL-3	C_LYS_71	NZ	C_GLU_55	OE2	2.641
2MKL-3	C_LYS_104	NZ	C_ASP_80	OD1	2.606

Table 293: 2MKL-3-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2MKL-4	C_ARG_50	NH2	C_GLU_78	OE1	2.697
2MKL-4	C_ARG_50	NH2	C_GLU_78	OE2	3.554
2MKL-4	C_LYS_71	NZ	C_GLU_55	OE2	2.650

Table 294: 2MKL-4-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2MKL-5	C_ARG_50	NH1	C_GLU_78	OE1	3.904
2MKL-5	C_ARG_50	NH2	C_GLU_78	OE1	2.759
2MKL-5	C_LYS_65	NZ	C_ASP_6	OD2	2.680
2MKL-5	C_LYS_104	NZ	C_ASP_80	OD1	2.921

Table 295: 2MKL-5-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2MKL-6	C_LYS_13	NZ	C_GLU_17	OE1	3.559
2MKL-6	C_LYS_13	NZ	C_GLU_17	OE2	2.627
2MKL-6	C_ARG_50	NH1	C_GLU_78	OE2	3.662
2MKL-6	C_ARG_50	NH2	C_GLU_78	OE2	2.716
2MKL-6	C_LYS_65	NZ	C_ASP_6	OD2	2.594
2MKL-6	C_LYS_71	NZ	C_GLU_55	OE2	2.698
2MKL-6	C_LYS_104	NZ	C_ASP_80	OD1	2.644

Table 296: 2MKL-6-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2MKL-7	C_ARG_3	NH2	C_ASP_6	OD1	3.888
2MKL-7	C_ARG_3	NH2	C_ASP_6	OD2	2.720
2MKL-7	C_LYS_52	NZ	C_GLU_55	OE1	3.242
2MKL-7	C_LYS_52	NZ	C_GLU_55	OE2	2.760
2MKL-7	C_LYS_65	NZ	C_ASP_6	OD1	2.615

Table 297: 2MKL-7-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2MKL-8	C_ARG_50	NH1	C_GLU_78	OE1	3.617
2MKL-8	C_ARG_50	NH1	C_GLU_78	OE2	2.634
2MKL-8	C_ARG_50	NH2	C_GLU_78	OE1	3.131
2MKL-8	C_ARG_50	NH2	C_GLU_78	OE2	3.571
2MKL-8	C_LYS_65	NZ	C_ASP_6	OD1	3.884
2MKL-8	C_LYS_65	NZ	C_ASP_6	OD2	2.638
2MKL-8	C_LYS_104	NZ	C_ASP_80	OD1	2.614

Table 298: 2MKL-8-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2MKL-9	C_ARG_50	NH1	C_GLU_78	OE2	3.771
2MKL-9	C_ARG_50	NH2	C_GLU_78	OE2	2.683
2MKL-9	C_LYS_65	NZ	C_ASP_6	OD1	2.835
2MKL-9	C_LYS_65	NZ	C_ASP_6	OD2	2.746

Table 299: 2MKL-9-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2MTW	A_LYS_16	NZ	A_ASP_13	OD2	3.436

Table 300: 2MTW-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2NXY	A.LYS.207	NZ	A.GLU.381	OE1	3.502
2NXY	A.LYS.207	NZ	A.GLU.381	OE2	2.666
2NXY	A.LYS.231	NZ	A.GLU.267	OE1	3.733
2NXY	A.HIS.249	NE2	A.GLU.482	OE1	2.788
2NXY	A.LYS.348	NZ	A.GLU.269	OE2	2.765
2NXY	A.LYS.348	NZ	A.GLU.351	OE1	3.417
2NXY	A.LYS.348	NZ	A.GLU.351	OE2	3.879
2NXY	A.LYS.357	NZ	A.GLU.464	OE1	3.655
2NXY	A.LYS.357	NZ	A.GLU.464	OE2	2.914
2NXY	A.ARG.419	NH1	D.GLU.3103	OE2	3.305
2NXY	A.ARG.419	NH2	D.GLU.3103	OE2	2.288
2NXY	A.ARG.456	NH2	A.GLU.466	OE1	3.797
2NXY	A.ARG.456	NH2	A.GLU.466	OE2	3.132
2NXY	A.ARG.469	NH2	A.ASP.457	OD1	2.896
2NXY	A.ARG.469	NH2	A.ASP.457	OD2	3.967
2NXY	A.ARG.476	NH1	A.ASP.474	OD1	2.903
2NXY	A.ARG.476	NH1	A.ASP.474	OD2	3.603
2NXY	A.ARG.480	NH1	A.ASP.477	OD1	2.733
2NXY	A.LYS.487	NZ	A.GLU.91	OE2	2.870
2NXY	B.LYS.1008	NZ	B.GLU.1119	OE1	3.058
2NXY	B.LYS.1029	NZ	A.ASP.279	OD2	2.892
2NXY	B.LYS.1029	NZ	B.GLU.1085	OE1	3.597
2NXY	B.LYS.1029	NZ	B.GLU.1085	OE2	3.802
2NXY	B.ARG.1054	NH1	B.ASP.1078	OD1	3.769
2NXY	B.ARG.1054	NH1	B.ASP.1078	OD2	2.694
2NXY	B.ARG.1054	NH2	B.ASP.1078	OD1	2.766
2NXY	B.ARG.1054	NH2	B.ASP.1078	OD2	3.269
2NXY	B.ARG.1058	NH1	B.GLU.1013	OE1	3.012
2NXY	B.ARG.1058	NH1	B.GLU.1013	OE2	3.108
2NXY	B.ARG.1058	NH2	B.GLU.1013	OE2	2.848
2NXY	B.ARG.1059	NH1	A.ASP.368	OD1	3.350
2NXY	B.ARG.1059	NH1	A.ASP.368	OD2	2.835
2NXY	B.ARG.1059	NH2	A.ASP.368	OD1	2.856
2NXY	B.ARG.1059	NH2	A.ASP.368	OD2	3.647
2NXY	B.LYS.1171	NZ	B.GLU.1169	OE1	3.367
2NXY	C.ARG.2061	NH2	C.GLU.2081	OE2	3.328
2NXY	C.ARG.2061	NH2	C.ASP.2082	OD1	2.675
2NXY	C.ARG.2061	NH2	C.ASP.2082	OD2	3.402
2NXY	C.LYS.2185	NZ	C.GLU.2189	OE2	3.692
2NXY	C.LYS.2190	NZ	C.ASP.2187	OD1	3.154
2NXY	C.HIS.2191	ND1	C.ASP.2153	OD2	3.374
2NXY	D.ARG.3031	NH2	D.GLU.3103	OE1	3.976
2NXY	D.ARG.3031	NH2	D.ASP.3105	OD1	3.526
2NXY	D.ARG.3031	NH2	D.ASP.3105	OD2	3.213
2NXY	D.ARG.3038	NH1	D.ASP.3090	OD2	2.829
2NXY	D.ARG.3038	NH2	D.GLU.3046	OE2	2.946
2NXY	D.ARG.3038	NH2	D.ASP.3090	OD2	3.771
2NXY	D.ARG.3050	NH2	D.GLU.3101	OE2	2.808
2NXY	D.HIS.3063	NE2	D.GLU.3046	OE1	3.857
2NXY	D.HIS.3063	NE2	D.GLU.3046	OE2	2.872
2NXY	D.ARG.3067	NH1	D.ASP.3090	OD1	2.854
2NXY	D.ARG.3067	NH1	D.ASP.3090	OD2	3.874
2NXY	D.ARG.3067	NH2	D.ASP.3090	OD1	3.263
2NXY	D.ARG.3067	NH2	D.ASP.3090	OD2	2.885
2NXY	D.ARG.3084	NH1	D.GLU.3082	OE1	2.798
2NXY	D.LYS.3158	NZ	D.ASP.3159	OD1	3.389
2NXY	D.LYS.3158	NZ	D.ASP.3159	OD2	3.068

2NXY	D_LYS_3224	NZ	C_GLU_2125	OE2	3.113
2NXY	D_LYS_3225	NZ	D_GLU_3227	OE2	3.652

Table 301: 2NXY-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2NXZ	A.LYS.207	NZ	A.GLU.381	OE1	3.614
2NXZ	A.LYS.207	NZ	A.GLU.381	OE2	2.716
2NXZ	A.HIS.249	NE2	A.GLU.482	OE1	3.015
2NXZ	A.LYS.348	NZ	A.GLU.269	OE2	2.534
2NXZ	A.LYS.348	NZ	A.GLU.351	OE2	3.687
2NXZ	A.ARG.419	NH1	D.GLU.3103	OE2	3.647
2NXZ	A.ARG.419	NH2	D.GLU.3103	OE2	2.536
2NXZ	A.ARG.456	NH2	A.GLU.466	OE1	3.919
2NXZ	A.ARG.456	NH2	A.GLU.466	OE2	3.186
2NXZ	A.ARG.469	NH2	A.ASP.457	OD1	2.972
2NXZ	A.ARG.469	NH2	A.ASP.457	OD2	3.979
2NXZ	A.ARG.476	NH1	A.ASP.474	OD1	2.887
2NXZ	A.ARG.476	NH1	A.ASP.474	OD2	3.798
2NXZ	A.ARG.480	NH1	A.ASP.477	OD1	2.702
2NXZ	A.LYS.487	NZ	A.GLU.91	OE2	2.923
2NXZ	B.LYS.1008	NZ	B.GLU.1119	OE1	2.808
2NXZ	B.LYS.1029	NZ	A.ASP.279	OD2	3.046
2NXZ	B.LYS.1029	NZ	B.GLU.1085	OE1	3.780
2NXZ	B.ARG.1054	NH1	B.ASP.1078	OD1	3.891
2NXZ	B.ARG.1054	NH1	B.ASP.1078	OD2	2.802
2NXZ	B.ARG.1054	NH2	B.ASP.1078	OD1	2.919
2NXZ	B.ARG.1054	NH2	B.ASP.1078	OD2	3.323
2NXZ	B.ARG.1058	NH1	B.GLU.1013	OE1	3.851
2NXZ	B.ARG.1058	NH1	B.GLU.1013	OE2	3.822
2NXZ	B.ARG.1058	NH2	B.GLU.1013	OE1	3.720
2NXZ	B.ARG.1058	NH2	B.GLU.1013	OE2	2.745
2NXZ	B.ARG.1059	NH1	A.ASP.368	OD1	3.623
2NXZ	B.ARG.1059	NH1	A.ASP.368	OD2	3.029
2NXZ	B.ARG.1059	NH2	A.ASP.368	OD1	2.916
2NXZ	B.ARG.1059	NH2	A.ASP.368	OD2	3.612
2NXZ	B.LYS.1171	NZ	B.GLU.1169	OE1	2.773
2NXZ	C.ARG.2024	NH2	C.GLU.2070	OE2	3.227
2NXZ	C.ARG.2061	NH2	C.GLU.2081	OE2	3.424
2NXZ	C.ARG.2061	NH2	C.ASP.2082	OD1	2.628
2NXZ	C.ARG.2061	NH2	C.ASP.2082	OD2	3.308
2NXZ	C.LYS.2185	NZ	C.GLU.2189	OE2	3.904
2NXZ	C.LYS.2190	NZ	C.ASP.2187	OD1	3.130
2NXZ	C.HIS.2191	ND1	C.ASP.2153	OD2	3.486
2NXZ	D.ARG.3031	NH2	D.GLU.3103	OE1	3.879
2NXZ	D.ARG.3031	NH2	D.ASP.3105	OD1	3.392
2NXZ	D.ARG.3031	NH2	D.ASP.3105	OD2	3.171
2NXZ	D.ARG.3038	NH1	D.ASP.3090	OD2	2.879
2NXZ	D.ARG.3038	NH2	D.GLU.3046	OE1	3.581
2NXZ	D.ARG.3038	NH2	D.GLU.3046	OE2	3.314
2NXZ	D.ARG.3038	NH2	D.ASP.3090	OD2	3.776
2NXZ	D.ARG.3050	NH2	D.GLU.3101	OE2	2.731
2NXZ	D.ARG.3067	NH1	D.ASP.3090	OD1	2.950
2NXZ	D.ARG.3067	NH1	D.ASP.3090	OD2	3.870
2NXZ	D.ARG.3067	NH2	D.ASP.3090	OD1	3.342
2NXZ	D.ARG.3067	NH2	D.ASP.3090	OD2	2.876
2NXZ	D.ARG.3084	NH1	D.GLU.3082	OE1	2.896
2NXZ	D.ARG.3087	NH2	D.ASP.3089	OD2	3.888
2NXZ	D.HIS.3117	NE2	D.GLU.3001	OE1	3.258
2NXZ	D.LYS.3158	NZ	D.ASP.3159	OD1	3.552
2NXZ	D.LYS.3158	NZ	D.ASP.3159	OD2	3.527
2NXZ	D.HIS.3179	NE2	C.ASP.2169	OD2	3.986
2NXZ	D.LYS.3224	NZ	C.GLU.2125	OE1	3.503

2NXZ	D_LYS_3224	NZ	C_GLU_2125	OE2	2.801
2NXZ	D_LYS_3225	NZ	D_GLU_3227	OE2	3.804

Table 302: 2NXZ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2NY0	A.LYS.207	NZ	A.GLU.381	OE1	3.809
2NY0	A.LYS.207	NZ	A.GLU.381	OE2	2.857
2NY0	A.HIS.249	NE2	A.GLU.482	OE1	2.815
2NY0	A.LYS.337	NZ	A.GLU.293	OE1	3.033
2NY0	A.LYS.337	NZ	A.GLU.293	OE2	3.370
2NY0	A.LYS.348	NZ	A.GLU.269	OE2	2.803
2NY0	A.LYS.348	NZ	A.GLU.351	OE1	3.817
2NY0	A.LYS.348	NZ	A.GLU.351	OE2	3.477
2NY0	A.ARG.419	NH1	D.GLU.3103	OE2	3.320
2NY0	A.ARG.419	NH2	D.GLU.3103	OE2	2.328
2NY0	A.ARG.456	NH2	A.GLU.466	OE1	3.843
2NY0	A.ARG.456	NH2	A.GLU.466	OE2	3.172
2NY0	A.ARG.469	NH2	A.ASP.457	OD1	3.138
2NY0	A.ARG.469	NH2	A.ASP.457	OD2	3.931
2NY0	A.ARG.476	NH1	A.ASP.474	OD1	3.150
2NY0	A.ARG.476	NH1	A.ASP.474	OD2	3.157
2NY0	A.ARG.480	NH1	A.ASP.477	OD1	2.991
2NY0	A.LYS.487	NZ	A.GLU.91	OE2	3.787
2NY0	B.LYS.1008	NZ	B.GLU.1119	OE1	2.749
2NY0	B.LYS.1029	NZ	A.ASP.279	OD2	2.858
2NY0	B.LYS.1029	NZ	B.GLU.1085	OE1	3.146
2NY0	B.LYS.1029	NZ	B.GLU.1085	OE2	3.532
2NY0	B.ARG.1054	NH1	B.ASP.1078	OD1	3.780
2NY0	B.ARG.1054	NH1	B.ASP.1078	OD2	2.599
2NY0	B.ARG.1054	NH2	B.ASP.1078	OD1	2.962
2NY0	B.ARG.1054	NH2	B.ASP.1078	OD2	3.339
2NY0	B.ARG.1058	NH1	B.GLU.1013	OE1	3.138
2NY0	B.ARG.1058	NH1	B.GLU.1013	OE2	3.075
2NY0	B.ARG.1058	NH2	B.GLU.1013	OE2	3.481
2NY0	B.ARG.1059	NH1	A.ASP.368	OD1	3.389
2NY0	B.ARG.1059	NH1	A.ASP.368	OD2	2.874
2NY0	B.ARG.1059	NH2	A.ASP.368	OD1	2.859
2NY0	B.ARG.1059	NH2	A.ASP.368	OD2	3.661
2NY0	B.LYS.1171	NZ	B.GLU.1169	OE1	3.740
2NY0	C.ARG.2024	NH2	C.GLU.2070	OE2	3.845
2NY0	C.ARG.2061	NH2	C.GLU.2081	OE2	3.765
2NY0	C.ARG.2061	NH2	C.ASP.2082	OD1	2.698
2NY0	C.ARG.2061	NH2	C.ASP.2082	OD2	3.430
2NY0	C.LYS.2151	NZ	C.GLU.2197	OE1	3.031
2NY0	C.HIS.2191	ND1	C.ASP.2153	OD2	3.524
2NY0	D.LYS.3012	NZ	D.GLU.3010	OE1	3.853
2NY0	D.ARG.3031	NH2	D.ASP.3105	OD1	3.446
2NY0	D.ARG.3031	NH2	D.ASP.3105	OD2	3.463
2NY0	D.ARG.3038	NH1	D.ASP.3090	OD2	2.827
2NY0	D.ARG.3038	NH2	D.GLU.3046	OE2	2.883
2NY0	D.ARG.3038	NH2	D.ASP.3090	OD2	3.849
2NY0	D.ARG.3050	NH2	D.GLU.3101	OE2	2.918
2NY0	D.HIS.3063	NE2	D.GLU.3046	OE2	3.738
2NY0	D.ARG.3067	NH1	D.ASP.3090	OD1	2.827
2NY0	D.ARG.3067	NH1	D.ASP.3090	OD2	3.838
2NY0	D.ARG.3067	NH2	D.ASP.3090	OD1	3.421
2NY0	D.ARG.3067	NH2	D.ASP.3090	OD2	3.091
2NY0	D.ARG.3084	NH1	D.GLU.3082	OE1	2.595
2NY0	D.ARG.3087	NH2	D.ASP.3089	OD2	3.920
2NY0	D.HIS.3117	NE2	D.GLU.3001	OE1	3.721
2NY0	D.HIS.3117	NE2	D.GLU.3001	OE2	3.707
2NY0	D.LYS.3158	NZ	D.ASP.3159	OD1	3.309

2NY0	D_LYS_3158	NZ	D_ASP_3159	OD2	2.901
2NY0	D_LYS_3224	NZ	C_GLU_2125	OE2	3.518
2NY0	D_LYS_3225	NZ	D_GLU_3227	OE2	3.771

Table 303: 2NY0-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2NY1	A.LYS.207	NZ	A.GLU.381	OE1	3.601
2NY1	A.LYS.207	NZ	A.GLU.381	OE2	2.693
2NY1	A.LYS.231	NZ	A.GLU.268	OE2	3.557
2NY1	A.HIS.249	NE2	A.GLU.482	OE1	2.972
2NY1	A.LYS.348	NZ	A.GLU.269	OE2	2.629
2NY1	A.LYS.348	NZ	A.GLU.351	OE1	3.454
2NY1	A.LYS.348	NZ	A.GLU.351	OE2	3.942
2NY1	A.LYS.357	NZ	A.GLU.466	OE1	2.761
2NY1	A.ARG.419	NH1	D.GLU.3103	OE2	3.396
2NY1	A.ARG.419	NH2	D.GLU.3103	OE1	3.789
2NY1	A.ARG.419	NH2	D.GLU.3103	OE2	2.363
2NY1	A.ARG.456	NH2	A.GLU.466	OE2	3.471
2NY1	A.ARG.469	NH2	A.ASP.457	OD1	3.038
2NY1	A.ARG.476	NH1	A.ASP.474	OD1	2.963
2NY1	A.ARG.476	NH1	A.ASP.474	OD2	3.170
2NY1	A.LYS.487	NZ	A.GLU.91	OE1	2.543
2NY1	B.LYS.1007	NZ	B.ASP.1010	OD2	3.969
2NY1	B.LYS.1008	NZ	B.GLU.1119	OE1	3.276
2NY1	B.LYS.1029	NZ	A.ASP.279	OD2	3.031
2NY1	B.LYS.1029	NZ	B.GLU.1085	OE1	3.492
2NY1	B.LYS.1029	NZ	B.GLU.1085	OE2	3.928
2NY1	B.ARG.1054	NH1	B.ASP.1078	OD1	3.747
2NY1	B.ARG.1054	NH1	B.ASP.1078	OD2	2.698
2NY1	B.ARG.1054	NH2	B.ASP.1078	OD1	2.961
2NY1	B.ARG.1054	NH2	B.ASP.1078	OD2	3.434
2NY1	B.ARG.1058	NH1	B.GLU.1013	OE1	3.860
2NY1	B.ARG.1058	NH1	B.GLU.1013	OE2	3.051
2NY1	B.ARG.1058	NH2	B.GLU.1013	OE2	3.952
2NY1	B.ARG.1059	NH1	A.ASP.368	OD1	3.481
2NY1	B.ARG.1059	NH1	A.ASP.368	OD2	3.131
2NY1	B.ARG.1059	NH2	A.ASP.368	OD1	2.526
2NY1	B.ARG.1059	NH2	A.ASP.368	OD2	3.458
2NY1	B.LYS.1171	NZ	B.GLU.1169	OE1	2.799
2NY1	C.ARG.2024	NH1	C.GLU.2070	OE1	3.232
2NY1	C.ARG.2061	NH2	C.GLU.2081	OE2	3.250
2NY1	C.ARG.2061	NH2	C.ASP.2082	OD1	2.692
2NY1	C.ARG.2061	NH2	C.ASP.2082	OD2	3.384
2NY1	C.LYS.2190	NZ	C.ASP.2187	OD1	3.137
2NY1	C.HIS.2191	ND1	C.ASP.2153	OD2	3.008
2NY1	D.ARG.3031	NH2	D.GLU.3103	OE1	3.623
2NY1	D.ARG.3031	NH2	D.ASP.3105	OD1	3.228
2NY1	D.ARG.3031	NH2	D.ASP.3105	OD2	3.278
2NY1	D.ARG.3038	NH1	D.GLU.3046	OE1	3.615
2NY1	D.ARG.3038	NH1	D.GLU.3046	OE2	3.409
2NY1	D.ARG.3038	NH1	D.ASP.3090	OD2	3.757
2NY1	D.ARG.3038	NH2	D.ASP.3090	OD2	2.650
2NY1	D.ARG.3050	NH2	D.GLU.3101	OE2	2.827
2NY1	D.HIS.3063	ND1	D.GLU.3046	OE2	3.810
2NY1	D.HIS.3063	NE2	D.GLU.3046	OE2	2.146
2NY1	D.ARG.3067	NH1	D.ASP.3090	OD1	2.855
2NY1	D.ARG.3067	NH1	D.ASP.3090	OD2	3.809
2NY1	D.ARG.3067	NH2	D.ASP.3090	OD1	3.381
2NY1	D.ARG.3067	NH2	D.ASP.3090	OD2	3.002
2NY1	D.ARG.3084	NH1	D.GLU.3082	OE1	2.758
2NY1	D.HIS.3117	NE2	D.GLU.3001	OE1	3.822
2NY1	D.LYS.3158	NZ	D.ASP.3159	OD1	3.295
2NY1	D.LYS.3158	NZ	D.ASP.3159	OD2	2.966

2NY1	D_LYS_3224	NZ	C_GLU_2125	OE1	3.100
2NY1	D_LYS_3224	NZ	C_GLU_2125	OE2	3.945

Table 304: 2NY1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2NY2	A.LYS.207	NZ	A.GLU.381	OE1	3.598
2NY2	A.LYS.207	NZ	A.GLU.381	OE2	2.704
2NY2	A.HIS.249	NE2	A.GLU.482	OE1	3.019
2NY2	A.LYS.337	NZ	A.GLU.293	OE1	2.850
2NY2	A.LYS.337	NZ	A.GLU.293	OE2	3.461
2NY2	A.LYS.348	NZ	A.GLU.269	OE2	2.783
2NY2	A.LYS.348	NZ	A.GLU.351	OE1	3.652
2NY2	A.LYS.348	NZ	A.GLU.351	OE2	3.603
2NY2	A.LYS.357	NZ	A.GLU.466	OE1	3.351
2NY2	A.ARG.419	NH1	D.GLU.3103	OE2	2.325
2NY2	A.ARG.419	NH2	D.GLU.3103	OE2	3.124
2NY2	A.ARG.456	NH2	A.GLU.466	OE1	3.779
2NY2	A.ARG.456	NH2	A.GLU.466	OE2	3.231
2NY2	A.ARG.469	NH2	A.ASP.457	OD1	2.829
2NY2	A.ARG.469	NH2	A.ASP.457	OD2	3.887
2NY2	A.ARG.476	NH2	A.ASP.474	OD1	3.619
2NY2	A.ARG.476	NH2	A.ASP.474	OD2	3.356
2NY2	A.ARG.480	NH2	A.ASP.477	OD1	3.946
2NY2	A.LYS.487	NZ	A.GLU.91	OE2	3.417
2NY2	B.LYS.1008	NZ	B.GLU.1119	OE1	3.204
2NY2	B.LYS.1029	NZ	A.ASP.279	OD2	2.981
2NY2	B.LYS.1029	NZ	B.GLU.1085	OE1	3.198
2NY2	B.LYS.1029	NZ	B.GLU.1085	OE2	3.665
2NY2	B.ARG.1054	NH1	B.ASP.1078	OD1	3.894
2NY2	B.ARG.1054	NH1	B.ASP.1078	OD2	2.718
2NY2	B.ARG.1054	NH2	B.ASP.1078	OD1	2.960
2NY2	B.ARG.1054	NH2	B.ASP.1078	OD2	3.298
2NY2	B.ARG.1058	NH1	B.GLU.1013	OE1	3.281
2NY2	B.ARG.1058	NH1	B.GLU.1013	OE2	2.757
2NY2	B.ARG.1058	NH2	B.GLU.1013	OE2	3.611
2NY2	B.ARG.1059	NH1	A.ASP.368	OD1	3.464
2NY2	B.ARG.1059	NH1	A.ASP.368	OD2	2.895
2NY2	B.ARG.1059	NH2	A.ASP.368	OD1	2.934
2NY2	B.ARG.1059	NH2	A.ASP.368	OD2	3.638
2NY2	B.LYS.1171	NZ	B.GLU.1169	OE1	3.055
2NY2	C.ARG.2024	NH1	C.GLU.2070	OE2	3.499
2NY2	C.ARG.2061	NH2	C.GLU.2081	OE2	3.670
2NY2	C.ARG.2061	NH2	C.ASP.2082	OD1	2.785
2NY2	C.ARG.2061	NH2	C.ASP.2082	OD2	3.417
2NY2	C.LYS.2151	NZ	C.GLU.2197	OE1	3.471
2NY2	C.LYS.2185	NZ	C.GLU.2189	OE2	3.651
2NY2	C.LYS.2190	NZ	C.ASP.2187	OD1	3.182
2NY2	C.HIS.2191	ND1	C.ASP.2153	OD2	3.206
2NY2	D.ARG.3031	NH2	D.GLU.3103	OE1	3.751
2NY2	D.ARG.3031	NH2	D.ASP.3105	OD1	3.389
2NY2	D.ARG.3031	NH2	D.ASP.3105	OD2	3.283
2NY2	D.ARG.3038	NH1	D.ASP.3090	OD2	2.806
2NY2	D.ARG.3038	NH2	D.GLU.3046	OE1	3.191
2NY2	D.ARG.3038	NH2	D.GLU.3046	OE2	3.670
2NY2	D.ARG.3038	NH2	D.ASP.3090	OD2	3.755
2NY2	D.ARG.3050	NH2	D.GLU.3101	OE1	3.994
2NY2	D.ARG.3050	NH2	D.GLU.3101	OE2	2.680
2NY2	D.ARG.3067	NH1	D.ASP.3090	OD1	2.784
2NY2	D.ARG.3067	NH1	D.ASP.3090	OD2	3.789
2NY2	D.ARG.3067	NH2	D.ASP.3090	OD1	3.313
2NY2	D.ARG.3067	NH2	D.ASP.3090	OD2	2.881
2NY2	D.ARG.3084	NH1	D.GLU.3082	OE1	2.941

2NY2	D_LYS_3158	NZ	D_ASP_3159	OD1	3.305
2NY2	D_LYS_3158	NZ	D_ASP_3159	OD2	3.053
2NY2	D_LYS_3224	NZ	C_GLU_2125	OE2	2.721
2NY2	D_LYS_3225	NZ	D_GLU_3227	OE2	3.413

Table 305: 2NY2-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2NY3	A.LYS.207	NZ	A.GLU.381	OE1	3.708
2NY3	A.LYS.207	NZ	A.GLU.381	OE2	2.801
2NY3	A.HIS.249	NE2	A.GLU.482	OE1	3.056
2NY3	A.LYS.348	NZ	A.GLU.269	OE2	2.607
2NY3	A.LYS.348	NZ	A.GLU.351	OE2	3.538
2NY3	A.LYS.357	NZ	A.GLU.466	OE1	3.160
2NY3	A.ARG.419	NH1	D.GLU.3103	OE2	3.671
2NY3	A.ARG.419	NH2	D.GLU.3103	OE1	3.681
2NY3	A.ARG.419	NH2	D.GLU.3103	OE2	2.058
2NY3	A.ARG.456	NH2	A.GLU.466	OE1	3.768
2NY3	A.ARG.456	NH2	A.GLU.466	OE2	3.134
2NY3	A.ARG.469	NH2	A.ASP.457	OD1	2.972
2NY3	A.ARG.476	NH1	A.ASP.474	OD1	2.845
2NY3	A.ARG.476	NH1	A.ASP.474	OD2	3.451
2NY3	A.ARG.480	NH1	A.ASP.477	OD1	2.886
2NY3	A.LYS.487	NZ	A.GLU.91	OE2	3.142
2NY3	B.LYS.1008	NZ	B.GLU.1119	OE1	3.194
2NY3	B.LYS.1029	NZ	A.ASP.279	OD2	3.124
2NY3	B.LYS.1029	NZ	B.GLU.1085	OE1	3.294
2NY3	B.LYS.1029	NZ	B.GLU.1085	OE2	3.406
2NY3	B.ARG.1054	NH1	B.ASP.1078	OD1	3.826
2NY3	B.ARG.1054	NH1	B.ASP.1078	OD2	2.678
2NY3	B.ARG.1054	NH2	B.ASP.1078	OD1	2.943
2NY3	B.ARG.1054	NH2	B.ASP.1078	OD2	3.308
2NY3	B.ARG.1058	NH1	B.GLU.1013	OE1	3.406
2NY3	B.ARG.1058	NH1	B.GLU.1013	OE2	3.310
2NY3	B.ARG.1059	NH1	A.ASP.368	OD1	2.775
2NY3	B.ARG.1059	NH1	A.ASP.368	OD2	3.550
2NY3	B.ARG.1059	NH2	A.ASP.368	OD1	3.449
2NY3	B.ARG.1059	NH2	A.ASP.368	OD2	2.862
2NY3	B.LYS.1171	NZ	B.GLU.1169	OE1	2.751
2NY3	B.LYS.1171	NZ	B.GLU.1169	OE2	3.911
2NY3	C.ARG.2024	NH1	C.GLU.2070	OE2	3.678
2NY3	C.ARG.2061	NH2	C.GLU.2081	OE2	3.396
2NY3	C.ARG.2061	NH2	C.ASP.2082	OD1	2.625
2NY3	C.ARG.2061	NH2	C.ASP.2082	OD2	3.244
2NY3	C.ARG.2097	NH1	C.ASP.2001	OD1	3.924
2NY3	C.ARG.2097	NH1	C.ASP.2001	OD2	3.626
2NY3	C.LYS.2185	NZ	C.GLU.2189	OE2	3.801
2NY3	C.LYS.2190	NZ	C.ASP.2187	OD1	3.285
2NY3	C.HIS.2191	ND1	C.ASP.2153	OD2	3.220
2NY3	D.ARG.3031	NH2	D.GLU.3103	OE1	3.899
2NY3	D.ARG.3031	NH2	D.ASP.3105	OD1	3.267
2NY3	D.ARG.3031	NH2	D.ASP.3105	OD2	3.028
2NY3	D.ARG.3038	NH1	D.GLU.3046	OE1	3.243
2NY3	D.ARG.3038	NH1	D.GLU.3046	OE2	3.575
2NY3	D.ARG.3038	NH1	D.ASP.3090	OD2	3.960
2NY3	D.ARG.3038	NH2	D.ASP.3090	OD2	2.751
2NY3	D.ARG.3050	NH2	D.GLU.3101	OE2	2.844
2NY3	D.ARG.3067	NH1	D.ASP.3090	OD1	2.783
2NY3	D.ARG.3067	NH1	D.ASP.3090	OD2	3.729
2NY3	D.ARG.3067	NH2	D.ASP.3090	OD1	3.344
2NY3	D.ARG.3067	NH2	D.ASP.3090	OD2	2.833
2NY3	D.ARG.3084	NH1	D.GLU.3082	OE1	2.996
2NY3	D.HIS.3117	NE2	D.GLU.3001	OE1	3.405
2NY3	D.LYS.3158	NZ	D.ASP.3159	OD1	3.506
2NY3	D.LYS.3158	NZ	D.ASP.3159	OD2	3.209

2NY3	D_LYS_3224	NZ	C_GLU_2125	OE1	3.624
2NY3	D_LYS_3224	NZ	C_GLU_2125	OE2	2.832
2NY3	D_LYS_3225	NZ	D_GLU_3227	OE2	3.573

Table 306: 2NY3-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2NY4	A.LYS.207	NZ	A.GLU.381	OE1	3.731
2NY4	A.LYS.207	NZ	A.GLU.381	OE2	2.708
2NY4	A.HIS.249	NE2	A.GLU.482	OE1	2.936
2NY4	A.LYS.348	NZ	A.GLU.269	OE2	2.582
2NY4	A.LYS.348	NZ	A.GLU.351	OE2	3.483
2NY4	A.ARG.419	NH1	D.GLU.3103	OE2	3.167
2NY4	A.ARG.419	NH2	D.GLU.3103	OE2	2.562
2NY4	A.ARG.456	NH2	A.GLU.466	OE1	3.845
2NY4	A.ARG.456	NH2	A.GLU.466	OE2	3.077
2NY4	A.ARG.469	NH2	A.ASP.457	OD1	2.967
2NY4	A.ARG.476	NH1	A.ASP.474	OD1	3.082
2NY4	A.ARG.476	NH1	A.ASP.474	OD2	3.721
2NY4	A.ARG.480	NH2	A.ASP.477	OD1	3.706
2NY4	A.LYS.487	NZ	A.GLU.91	OE2	2.555
2NY4	B.LYS.1008	NZ	B.GLU.1119	OE1	3.022
2NY4	B.LYS.1029	NZ	A.ASP.279	OD2	3.126
2NY4	B.LYS.1029	NZ	B.GLU.1085	OE2	3.736
2NY4	B.ARG.1054	NH1	B.ASP.1078	OD1	3.885
2NY4	B.ARG.1054	NH1	B.ASP.1078	OD2	2.724
2NY4	B.ARG.1054	NH2	B.ASP.1078	OD1	2.927
2NY4	B.ARG.1054	NH2	B.ASP.1078	OD2	3.270
2NY4	B.ARG.1058	NH2	B.GLU.1013	OE1	3.510
2NY4	B.ARG.1058	NH2	B.GLU.1013	OE2	2.959
2NY4	B.ARG.1059	NH1	A.ASP.368	OD1	3.376
2NY4	B.ARG.1059	NH1	A.ASP.368	OD2	2.816
2NY4	B.ARG.1059	NH2	A.ASP.368	OD1	2.784
2NY4	B.ARG.1059	NH2	A.ASP.368	OD2	3.537
2NY4	B.LYS.1171	NZ	B.GLU.1169	OE1	2.831
2NY4	C.ARG.2024	NH2	C.GLU.2070	OE2	3.822
2NY4	C.ARG.2061	NH2	C.GLU.2081	OE2	3.356
2NY4	C.ARG.2061	NH2	C.ASP.2082	OD1	2.733
2NY4	C.ARG.2061	NH2	C.ASP.2082	OD2	3.375
2NY4	C.LYS.2151	NZ	C.GLU.2197	OE1	3.803
2NY4	C.LYS.2190	NZ	C.ASP.2187	OD1	3.227
2NY4	C.HIS.2191	ND1	C.ASP.2153	OD2	3.008
2NY4	D.ARG.3031	NH2	D.ASP.3105	OD1	3.479
2NY4	D.ARG.3031	NH2	D.ASP.3105	OD2	2.910
2NY4	D.ARG.3038	NH1	D.ASP.3090	OD2	2.802
2NY4	D.ARG.3038	NH2	D.GLU.3046	OE1	3.197
2NY4	D.ARG.3038	NH2	D.GLU.3046	OE2	3.685
2NY4	D.ARG.3038	NH2	D.ASP.3090	OD2	3.711
2NY4	D.ARG.3050	NH2	D.GLU.3101	OE2	2.802
2NY4	D.HIS.3063	ND1	D.GLU.3046	OE2	2.743
2NY4	D.HIS.3063	NE2	D.GLU.3046	OE2	3.513
2NY4	D.ARG.3067	NH1	D.ASP.3090	OD1	2.775
2NY4	D.ARG.3067	NH1	D.ASP.3090	OD2	3.804
2NY4	D.ARG.3067	NH2	D.ASP.3090	OD1	3.309
2NY4	D.ARG.3067	NH2	D.ASP.3090	OD2	2.883
2NY4	D.ARG.3084	NH1	D.GLU.3082	OE1	3.001
2NY4	D.HIS.3117	NE2	D.GLU.3001	OE2	3.655
2NY4	D.LYS.3158	NZ	D.ASP.3159	OD1	3.252
2NY4	D.LYS.3158	NZ	D.ASP.3159	OD2	2.781
2NY4	D.LYS.3224	NZ	C.GLU.2125	OE1	3.625
2NY4	D.LYS.3224	NZ	C.GLU.2125	OE2	3.179
2NY4	D.LYS.3225	NZ	D.GLU.3227	OE2	3.815

Table 307: 2NY4-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2NY5	G.LYS.207	NZ	G.GLU.381	OE1	3.510
2NY5	G.LYS.207	NZ	G.GLU.381	OE2	2.865
2NY5	G.HIS.249	NE2	G.GLU.482	OE1	2.564
2NY5	G.LYS.348	NZ	G.GLU.269	OE2	2.724
2NY5	G.LYS.348	NZ	G.GLU.351	OE1	3.888
2NY5	G.LYS.357	NZ	G.GLU.466	OE1	3.541
2NY5	G.ARG.419	NH2	H.GLU.3103	OE2	3.818
2NY5	G.ARG.456	NH2	G.GLU.466	OE2	3.080
2NY5	G.ARG.469	NH2	G.ASP.457	OD1	3.091
2NY5	G.ARG.469	NH2	G.ASP.457	OD2	3.726
2NY5	G.ARG.476	NH1	G.ASP.474	OD1	2.768
2NY5	G.ARG.476	NH1	G.ASP.474	OD2	3.024
2NY5	G.ARG.480	NH2	G.ASP.477	OD1	2.981
2NY5	G.LYS.487	NZ	G.GLU.91	OE2	2.768
2NY5	C.LYS.1008	NZ	C.GLU.1119	OE1	3.207
2NY5	C.LYS.1029	NZ	G.ASP.279	OD2	3.358
2NY5	C.LYS.1029	NZ	C.GLU.1085	OE1	3.759
2NY5	C.ARG.1054	NH1	C.ASP.1078	OD1	3.454
2NY5	C.ARG.1054	NH1	C.ASP.1078	OD2	3.024
2NY5	C.ARG.1054	NH2	C.ASP.1078	OD1	2.904
2NY5	C.ARG.1054	NH2	C.ASP.1078	OD2	3.790
2NY5	C.ARG.1058	NH1	C.GLU.1013	OE1	2.971
2NY5	C.ARG.1058	NH1	C.GLU.1013	OE2	3.085
2NY5	C.ARG.1058	NH2	C.GLU.1013	OE2	3.977
2NY5	C.ARG.1059	NH1	G.ASP.368	OD1	3.253
2NY5	C.ARG.1059	NH1	G.ASP.368	OD2	2.656
2NY5	C.ARG.1059	NH2	G.ASP.368	OD1	2.825
2NY5	C.ARG.1059	NH2	G.ASP.368	OD2	3.554
2NY5	L.ARG.2024	NH1	L.GLU.2070	OE2	3.011
2NY5	L.ARG.2061	NH2	L.ASP.2082	OD1	2.513
2NY5	L.ARG.2061	NH2	L.ASP.2082	OD2	3.250
2NY5	L.LYS.2151	NZ	L.GLU.2197	OE1	3.120
2NY5	L.LYS.2151	NZ	L.GLU.2197	OE2	3.898
2NY5	L.LYS.2185	NZ	L.GLU.2189	OE2	3.201
2NY5	L.LYS.2190	NZ	L.ASP.2187	OD1	3.698
2NY5	L.HIS.2191	ND1	L.ASP.2153	OD2	3.806
2NY5	H.LYS.3012	NZ	H.GLU.3010	OE1	3.934
2NY5	H.LYS.3019	NZ	H.GLU.3082	OE2	3.776
2NY5	H.ARG.3031	NH2	H.ASP.3105	OD1	3.319
2NY5	H.ARG.3031	NH2	H.ASP.3105	OD2	3.589
2NY5	H.ARG.3038	NH1	H.ASP.3090	OD2	2.958
2NY5	H.ARG.3038	NH2	H.GLU.3046	OE1	3.774
2NY5	H.ARG.3038	NH2	H.GLU.3046	OE2	3.269
2NY5	H.ARG.3038	NH2	H.ASP.3090	OD2	3.880
2NY5	H.ARG.3050	NH2	H.GLU.3101	OE2	2.904
2NY5	H.HIS.3063	NE2	H.GLU.3046	OE2	2.714
2NY5	H.ARG.3067	NH1	H.ASP.3090	OD1	2.954
2NY5	H.ARG.3067	NH1	H.ASP.3090	OD2	3.690
2NY5	H.ARG.3067	NH2	H.ASP.3090	OD1	3.799
2NY5	H.ARG.3067	NH2	H.ASP.3090	OD2	3.231
2NY5	H.ARG.3084	NH1	H.GLU.3082	OE1	2.806
2NY5	H.ARG.3087	NH2	H.ASP.3089	OD2	3.608
2NY5	H.HIS.3117	NE2	H.GLU.3001	OE2	3.918
2NY5	H.LYS.3158	NZ	H.ASP.3159	OD1	3.923
2NY5	H.LYS.3158	NZ	H.ASP.3159	OD2	3.240
2NY5	H.LYS.3224	NZ	L.GLU.2125	OE1	3.285
2NY5	H.LYS.3224	NZ	L.GLU.2125	OE2	3.364

Table 308: 2NY5-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2NY6	A.LYS.207	NZ	A.GLU.381	OE1	3.730
2NY6	A.LYS.207	NZ	A.GLU.381	OE2	2.822
2NY6	A.HIS.249	NE2	A.GLU.482	OE2	3.456
2NY6	A.LYS.337	NZ	A.GLU.293	OE1	3.079
2NY6	A.LYS.337	NZ	A.GLU.293	OE2	3.670
2NY6	A.LYS.348	NZ	A.GLU.269	OE2	3.288
2NY6	A.LYS.357	NZ	A.GLU.466	OE1	2.793
2NY6	A.ARG.419	NH2	D.GLU.3103	OE1	3.563
2NY6	A.ARG.419	NH2	D.GLU.3103	OE2	2.589
2NY6	A.ARG.456	NH2	A.GLU.466	OE1	3.680
2NY6	A.ARG.456	NH2	A.GLU.466	OE2	3.058
2NY6	A.ARG.469	NH2	A.ASP.457	OD1	2.900
2NY6	A.ARG.469	NH2	A.ASP.457	OD2	3.561
2NY6	A.ARG.476	NH1	A.ASP.474	OD1	2.511
2NY6	A.ARG.476	NH1	A.ASP.474	OD2	2.768
2NY6	A.ARG.480	NH2	A.ASP.477	OD1	2.891
2NY6	A.LYS.487	NZ	A.GLU.91	OE2	3.003
2NY6	B.LYS.1008	NZ	B.GLU.1119	OE1	2.791
2NY6	B.LYS.1029	NZ	A.ASP.279	OD2	3.061
2NY6	B.LYS.1029	NZ	B.GLU.1085	OE1	3.222
2NY6	B.ARG.1054	NH1	B.ASP.1078	OD1	3.684
2NY6	B.ARG.1054	NH1	B.ASP.1078	OD2	3.346
2NY6	B.ARG.1054	NH2	B.ASP.1078	OD1	2.747
2NY6	B.ARG.1054	NH2	B.ASP.1078	OD2	3.402
2NY6	B.ARG.1058	NH1	B.GLU.1013	OE1	3.563
2NY6	B.ARG.1058	NH2	B.GLU.1013	OE1	2.875
2NY6	B.ARG.1058	NH2	B.GLU.1013	OE2	2.875
2NY6	B.ARG.1059	NH1	A.ASP.368	OD1	2.945
2NY6	B.ARG.1059	NH1	A.ASP.368	OD2	2.767
2NY6	B.ARG.1059	NH2	A.ASP.368	OD1	3.097
2NY6	B.LYS.1090	NZ	B.GLU.1085	OE2	3.439
2NY6	B.LYS.1171	NZ	B.GLU.1169	OE1	3.858
2NY6	C.ARG.2024	NH1	C.GLU.2070	OE2	3.729
2NY6	C.ARG.2061	NH2	C.GLU.2081	OE2	3.042
2NY6	C.ARG.2061	NH2	C.ASP.2082	OD1	2.719
2NY6	C.ARG.2061	NH2	C.ASP.2082	OD2	3.011
2NY6	C.ARG.2105	NH1	C.GLU.2107	OE2	3.132
2NY6	C.LYS.2151	NZ	C.GLU.2197	OE1	3.256
2NY6	C.LYS.2151	NZ	C.GLU.2197	OE2	3.632
2NY6	C.LYS.2185	NZ	C.GLU.2189	OE2	3.738
2NY6	C.LYS.2190	NZ	C.ASP.2187	OD1	3.524
2NY6	D.LYS.3012	NZ	D.GLU.3010	OE1	3.730
2NY6	D.ARG.3031	NH2	D.ASP.3105	OD1	3.047
2NY6	D.ARG.3031	NH2	D.ASP.3105	OD2	3.789
2NY6	D.ARG.3038	NH1	D.ASP.3090	OD2	3.061
2NY6	D.ARG.3038	NH2	D.GLU.3046	OE2	3.246
2NY6	D.ARG.3038	NH2	D.ASP.3090	OD2	3.492
2NY6	D.ARG.3050	NH2	D.GLU.3101	OE2	2.217
2NY6	D.HIS.3063	ND1	D.GLU.3046	OE1	3.616
2NY6	D.HIS.3063	NE2	D.GLU.3046	OE1	2.623
2NY6	D.ARG.3067	NH1	D.ASP.3090	OD1	2.710
2NY6	D.ARG.3067	NH2	D.ASP.3090	OD1	3.291
2NY6	D.ARG.3067	NH2	D.ASP.3090	OD2	3.292
2NY6	D.LYS.3074	NZ	D.ASP.3056	OD2	3.513
2NY6	D.ARG.3084	NH1	D.GLU.3082	OE1	2.898
2NY6	D.ARG.3087	NH2	D.ASP.3089	OD2	3.510
2NY6	D.HIS.3117	ND1	D.GLU.3001	OE1	3.967

2NY6	D_HIS_3117	NE2	D_GLU_3001	OE1	3.266
2NY6	D_LYS_3158	NZ	D_ASP_3159	OD1	3.626
2NY6	D_LYS_3158	NZ	D_ASP_3159	OD2	2.711
2NY6	D_LYS_3224	NZ	C_GLU_2125	OE1	3.158
2NY6	D_LYS_3224	NZ	C_GLU_2125	OE2	2.701

Table 309: 2NY6-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2NY7	G_LYS_117	NZ	G_GLU_211	OE1	2.565
2NY7	G_LYS_117	NZ	G_GLU_211	OE2	3.261
2NY7	G_LYS_231	NZ	G_GLU_267	OE1	3.791
2NY7	G_LYS_231	NZ	G_GLU_267	OE2	3.613
2NY7	G_HIS_249	NE2	G_GLU_482	OE2	3.021
2NY7	G_LYS_337	NZ	G_GLU_293	OE1	3.715
2NY7	G_LYS_348	NZ	G_GLU_269	OE1	3.162
2NY7	G_LYS_348	NZ	G_GLU_269	OE2	3.975
2NY7	G_LYS_348	NZ	G_GLU_351	OE1	3.003
2NY7	G_LYS_357	NZ	G_GLU_466	OE1	2.755
2NY7	G_ARG_456	NH1	G_GLU_466	OE1	3.969
2NY7	G_ARG_456	NH1	G_GLU_466	OE2	3.127
2NY7	G_ARG_469	NH2	G_ASP_457	OD2	2.950
2NY7	G_ARG_480	NH1	G_ASP_99	OD2	3.193
2NY7	G_ARG_480	NH1	G_ASP_474	OD1	3.425
2NY7	G_ARG_480	NH2	G_ASP_474	OD1	2.783
2NY7	G_ARG_480	NH2	G_ASP_477	OD2	2.839
2NY7	G_LYS_487	NZ	G_GLU_91	OE2	2.858
2NY7	H_ARG_38	NH1	H_GLU_46	OE1	2.977
2NY7	H_ARG_38	NH2	H_ASP_86	OD1	2.526
2NY7	H_ARG_66	NH1	H_ASP_86	OD1	3.144
2NY7	H_ARG_66	NH1	H_ASP_86	OD2	3.436
2NY7	H_ARG_66	NH2	H_ASP_86	OD1	3.533
2NY7	H_ARG_66	NH2	H_ASP_86	OD2	2.282
2NY7	H_ARG_94	NH2	H_ASP_101	OD2	2.976
2NY7	H_LYS_145	NZ	H_ASP_146	OD1	3.590
2NY7	H_LYS_145	NZ	H_ASP_146	OD2	3.675
2NY7	H_LYS_221	NZ	L_GLU_123	OE1	3.153
2NY7	L_ARG_32	NH1	H_ASP_100F	OD2	2.962
2NY7	L_ARG_61	NH1	L_ASP_82	OD1	3.480
2NY7	L_ARG_61	NH1	L_ASP_82	OD2	2.630
2NY7	L_ARG_61	NH2	L_GLU_81	OE2	3.843
2NY7	L_ARG_61	NH2	L_ASP_82	OD1	3.037
2NY7	L_ARG_61	NH2	L_ASP_82	OD2	3.695
2NY7	L_ARG_77	NH1	L_GLU_79	OE2	3.409
2NY7	L_LYS_149	NZ	L_GLU_195	OE2	2.771

Table 310: 2NY7-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2OR9	L.LYS_39	NZ	L.ASP_81	OD1	2.675
2OR9	L.LYS_39	NZ	L.ASP_81	OD2	2.850
2OR9	L.ARG_61	NH1	L.GLU_79	OE1	3.065
2OR9	L.ARG_61	NH1	L.ASP_82	OD1	3.876
2OR9	L.ARG_61	NH2	L.GLU_79	OE1	3.933
2OR9	L.ARG_61	NH2	L.ASP_82	OD1	2.452
2OR9	L.ARG_61	NH2	L.ASP_82	OD2	2.431
2OR9	L.LYS_103	NZ	L.ASP_165	OD1	3.314
2OR9	L.LYS_147	NZ	L.GLU_154	OE1	3.105
2OR9	L.LYS_149	NZ	L.GLU_195	OE1	2.901
2OR9	L.LYS_149	NZ	L.GLU_195	OE2	3.775
2OR9	L.ARG_155	NH2	L.GLU_185	OE1	2.944
2OR9	L.HIS_189	ND1	L.ASP_151	OD2	3.316
2OR9	L.LYS_199	NZ	L.ASP_110	OD2	2.936
2OR9	H.ARG_38	NH1	H.ASP_86	OD1	2.712
2OR9	H.ARG_38	NH2	H.GLU_46	OE1	2.757
2OR9	H.ARG_38	NH2	H.ASP_86	OD1	3.623
2OR9	H.ARG_53	NH2	P.GLU_8	OE2	3.967
2OR9	H.ARG_66	NH2	H.ASP_86	OD1	2.780
2OR9	H.ARG_66	NH2	H.ASP_86	OD2	2.470
2OR9	H.ARG_94	NH2	H.ASP_101	OD1	3.716
2OR9	H.ARG_94	NH2	H.ASP_101	OD2	2.813
2OR9	H.ARG_95	NH2	H.GLU_97	OE1	3.064
2OR9	H.ARG_95	NH2	H.GLU_97	OE2	2.977
2OR9	M.LYS_39	NZ	M.ASP_81	OD1	2.510
2OR9	M.LYS_39	NZ	M.ASP_81	OD2	2.625
2OR9	M.ARG_61	NH1	M.GLU_79	OE1	3.146
2OR9	M.ARG_61	NH1	M.ASP_82	OD1	3.834
2OR9	M.ARG_61	NH2	M.GLU_79	OE1	3.978
2OR9	M.ARG_61	NH2	M.ASP_82	OD1	2.403
2OR9	M.ARG_61	NH2	M.ASP_82	OD2	2.459
2OR9	M.LYS_92	NZ	M.GLU_93	OE2	3.399
2OR9	M.LYS_147	NZ	M.GLU_154	OE1	3.668
2OR9	M.LYS_149	NZ	M.GLU_195	OE1	3.660
2OR9	M.LYS_149	NZ	M.GLU_195	OE2	3.945
2OR9	M.ARG_155	NH2	M.GLU_185	OE1	2.980
2OR9	M.HIS_189	ND1	M.ASP_151	OD2	2.969
2OR9	M.LYS_199	NZ	M.ASP_110	OD2	2.911
2OR9	I.HIS_3	NE2	I.GLU_1	OE1	2.704
2OR9	I.HIS_3	NE2	I.GLU_1	OE2	3.924
2OR9	I.ARG_38	NH1	I.ASP_86	OD1	2.804
2OR9	I.ARG_38	NH2	I.GLU_46	OE1	2.738
2OR9	I.ARG_38	NH2	I.ASP_86	OD1	3.727
2OR9	I.ARG_66	NH2	I.ASP_86	OD1	2.548
2OR9	I.ARG_66	NH2	I.ASP_86	OD2	2.491
2OR9	I.ARG_94	NH2	I.ASP_101	OD1	3.025
2OR9	I.ARG_94	NH2	I.ASP_101	OD2	2.934
2OR9	I.ARG_95	NH2	I.GLU_97	OE1	3.211
2OR9	I.LYS_208	NZ	M.GLU_123	OE2	3.803

Table 311: 2OR9-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2ORB	L_LYS_39	NZ	L_ASP_81	OD1	3.102
2ORB	L_LYS_39	NZ	L_ASP_81	OD2	2.922
2ORB	L_ARG_61	NH1	L_GLU_79	OE1	3.405
2ORB	L_ARG_61	NH1	L_GLU_79	OE2	3.954
2ORB	L_ARG_61	NH2	L_GLU_79	OE1	3.851
2ORB	L_ARG_61	NH2	L_ASP_82	OD1	2.602
2ORB	L_ARG_61	NH2	L_ASP_82	OD2	3.319
2ORB	L_LYS_92	NZ	L_GLU_93	OE2	2.584
2ORB	L_LYS_103	NZ	L_ASP_165	OD1	3.225
2ORB	L_LYS_149	NZ	L_GLU_195	OE1	3.600
2ORB	L_ARG_155	NH1	L_GLU_185	OE1	3.207
2ORB	L_ARG_155	NH2	L_GLU_185	OE1	2.465
2ORB	L_ARG_155	NH2	L_GLU_185	OE2	3.749
2ORB	L_LYS_183	NZ	L_ASP_184	OD2	3.348
2ORB	L_ARG_211	NH1	L_GLU_187	OE1	3.744
2ORB	H_HIS_3	ND1	H_GLU_1	OE1	3.990
2ORB	H_HIS_3	NE2	H_GLU_1	OE1	3.016
2ORB	H_ARG_38	NH1	H_GLU_46	OE1	3.421
2ORB	H_ARG_38	NH1	H_GLU_46	OE2	2.892
2ORB	H_ARG_38	NH2	H_ASP_86	OD1	2.745
2ORB	H_LYS_64	NZ	H_ASP_61	OD1	2.825
2ORB	H_ARG_66	NH1	H_ASP_86	OD2	2.863
2ORB	H_ARG_66	NH2	H_ASP_86	OD1	3.152
2ORB	H_ARG_66	NH2	H_ASP_86	OD2	3.464
2ORB	H_ARG_94	NH2	H_ASP_101	OD2	2.967
2ORB	M_LYS_39	NZ	M_ASP_81	OD1	3.035
2ORB	M_LYS_39	NZ	M_ASP_81	OD2	2.955
2ORB	M_ARG_61	NH1	M_GLU_79	OE1	3.351
2ORB	M_ARG_61	NH1	M_GLU_79	OE2	3.951
2ORB	M_ARG_61	NH2	M_GLU_79	OE1	3.841
2ORB	M_ARG_61	NH2	M_ASP_82	OD1	2.637
2ORB	M_ARG_61	NH2	M_ASP_82	OD2	3.364
2ORB	M_LYS_103	NZ	M_ASP_165	OD1	3.221
2ORB	M_LYS_149	NZ	M_GLU_195	OE1	3.434
2ORB	M_ARG_155	NH1	M_GLU_185	OE1	3.183
2ORB	M_ARG_155	NH2	M_GLU_185	OE1	2.497
2ORB	M_ARG_155	NH2	M_GLU_185	OE2	3.779
2ORB	M_LYS_183	NZ	M_ASP_184	OD2	3.320
2ORB	M_ARG_211	NH1	M_GLU_187	OE1	3.810
2ORB	I_HIS_3	NE2	I_GLU_1	OE1	2.997
2ORB	I_ARG_38	NH1	I_GLU_46	OE1	3.408
2ORB	I_ARG_38	NH1	I_GLU_46	OE2	2.958
2ORB	I_ARG_38	NH2	I_ASP_86	OD1	2.616
2ORB	I_LYS_64	NZ	I_ASP_61	OD1	2.889
2ORB	I_ARG_66	NH1	I_ASP_86	OD1	3.960
2ORB	I_ARG_66	NH1	I_ASP_86	OD2	2.821
2ORB	I_ARG_66	NH2	I_ASP_86	OD1	2.981
2ORB	I_ARG_66	NH2	I_ASP_86	OD2	3.330
2ORB	I_ARG_94	NH2	I_ASP_101	OD1	3.695
2ORB	I_ARG_94	NH2	I_ASP_101	OD2	3.090

Table 312: 2ORB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2OSL	L_HIS_33	NE2	H_ASP_105	OD1	3.260
2OSL	L_HIS_33	NE2	H_ASP_105	OD2	2.885
2OSL	L_ARG_60	NH1	L_GLU_78	OE2	2.907
2OSL	L_ARG_60	NH2	L_ASP_81	OD1	2.573
2OSL	L_ARG_60	NH2	L_ASP_81	OD2	2.599
2OSL	L_LYS_102	NZ	L_GLU_164	OE1	3.278
2OSL	L_LYS_102	NZ	L_GLU_164	OE2	3.140
2OSL	L_ARG_107	NH2	B_GLU_194	OE2	3.976
2OSL	L_LYS_187	NZ	L_ASP_184	OD1	2.734
2OSL	L_LYS_187	NZ	L_ASP_184	OD2	3.949
2OSL	L_HIS_188	ND1	L_ASP_150	OD2	2.901
2OSL	H_LYS_63	NZ	H_GLU_46	OE1	3.906
2OSL	H_LYS_63	NZ	H_GLU_46	OE2	2.831
2OSL	H_LYS_67	NZ	H_ASP_90	OD1	3.942
2OSL	H_LYS_67	NZ	H_ASP_90	OD2	2.944
2OSL	H_LYS_151	NZ	H_ASP_152	OD1	3.605
2OSL	H_LYS_151	NZ	H_ASP_152	OD2	2.970
2OSL	B_HIS_33	ND1	A_ASP_105	OD2	3.615
2OSL	B_HIS_33	NE2	A_ASP_105	OD2	3.957
2OSL	B_ARG_60	NH1	B_GLU_78	OE1	3.239
2OSL	B_ARG_60	NH1	B_GLU_78	OE2	3.966
2OSL	B_ARG_60	NH2	B_ASP_81	OD1	2.569
2OSL	B_ARG_60	NH2	B_ASP_81	OD2	3.261
2OSL	B_ARG_76	NH2	B_GLU_78	OE1	3.595
2OSL	B_LYS_102	NZ	B_GLU_104	OE1	3.425
2OSL	B_ARG_141	NH2	B_GLU_160	OE1	3.816
2OSL	B_HIS_188	ND1	B_ASP_150	OD2	3.233
2OSL	A_LYS_63	NZ	A_GLU_46	OE1	2.696
2OSL	A_LYS_67	NZ	A_ASP_90	OD1	2.936
2OSL	A_LYS_67	NZ	A_ASP_90	OD2	2.944
2OSL	A_LYS_151	NZ	A_ASP_152	OD1	3.042
2OSL	A_LYS_151	NZ	A_ASP_152	OD2	3.081
2OSL	A_LYS_217	NZ	B_GLU_122	OE1	2.793

Table 313: 2OSL-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2OTU	A_ARG_65	NH1	A_ASP_86	OD1	3.180
2OTU	A_ARG_65	NH1	A_ASP_86	OD2	2.487
2OTU	A_ARG_65	NH2	A_ASP_86	OD1	3.397
2OTU	A_ARG_65	NH2	A_ASP_86	OD2	3.745
2OTU	B_ARG_38	NH1	B_ASP_90	OD1	2.946
2OTU	B_ARG_38	NH2	B_GLU_46	OE1	2.919
2OTU	B_LYS_65	NZ	B_ASP_62	OD1	3.442
2OTU	B_ARG_67	NH1	B_ASP_90	OD1	3.744
2OTU	B_ARG_67	NH1	B_ASP_90	OD2	2.752
2OTU	B_ARG_67	NH2	B_ASP_90	OD1	2.959
2OTU	B_ARG_67	NH2	B_ASP_90	OD2	3.506
2OTU	B_LYS_87	NZ	F_ASP_31	OD1	3.793
2OTU	B_LYS_87	NZ	F_ASP_31	OD2	2.711
2OTU	C_ARG_65	NH1	C_ASP_86	OD1	3.191
2OTU	C_ARG_65	NH1	C_ASP_86	OD2	2.444
2OTU	C_ARG_65	NH2	C_GLU_85	OE1	3.930
2OTU	C_ARG_65	NH2	C_ASP_86	OD1	3.938
2OTU	C_ARG_65	NH2	C_ASP_86	OD2	3.948
2OTU	D_ARG_38	NH1	D_ASP_90	OD1	2.961
2OTU	D_ARG_38	NH2	D_GLU_46	OE1	2.890
2OTU	D_ARG_38	NH2	D_GLU_46	OE2	3.975
2OTU	D_ARG_38	NH2	D_ASP_90	OD1	3.915
2OTU	D_ARG_67	NH1	D_ASP_90	OD1	3.940
2OTU	D_ARG_67	NH1	D_ASP_90	OD2	2.837
2OTU	D_ARG_67	NH2	D_ASP_90	OD1	2.974
2OTU	D_ARG_67	NH2	D_ASP_90	OD2	3.349
2OTU	E_ARG_65	NH1	E_ASP_86	OD1	3.707
2OTU	E_ARG_65	NH1	E_ASP_86	OD2	2.736
2OTU	E_ARG_65	NH2	E_ASP_86	OD1	3.658
2OTU	E_ARG_65	NH2	E_ASP_86	OD2	3.976
2OTU	F_ARG_38	NH1	F_ASP_90	OD1	2.925
2OTU	F_ARG_38	NH2	F_GLU_46	OE1	2.898
2OTU	F_ARG_38	NH2	F_ASP_90	OD1	3.956
2OTU	F_LYS_65	NZ	F_ASP_62	OD1	3.608
2OTU	F_ARG_67	NH1	F_ASP_90	OD1	3.636
2OTU	F_ARG_67	NH1	F_ASP_90	OD2	2.694
2OTU	F_ARG_67	NH2	F_ASP_90	OD1	2.962
2OTU	F_ARG_67	NH2	F_ASP_90	OD2	3.544
2OTU	F_LYS_76	NZ	F_ASP_73	OD1	3.979
2OTU	F_ARG_100	NH1	E_ASP_60	OD1	3.255
2OTU	F_ARG_100	NH1	E_ASP_60	OD2	3.915
2OTU	G_ARG_65	NH1	G_ASP_86	OD1	3.029
2OTU	G_ARG_65	NH1	G_ASP_86	OD2	2.451
2OTU	G_ARG_65	NH2	G_GLU_85	OE2	3.992
2OTU	G_ARG_65	NH2	G_ASP_86	OD1	2.757
2OTU	G_ARG_65	NH2	G_ASP_86	OD2	3.075
2OTU	H_ARG_38	NH1	H_ASP_90	OD1	2.927
2OTU	H_ARG_38	NH2	H_GLU_46	OE2	3.512
2OTU	H_ARG_44	NH1	C_ASP_60	OD1	3.017
2OTU	H_ARG_44	NH1	C_ASP_60	OD2	3.518
2OTU	H_ARG_44	NH2	C_ASP_60	OD1	3.945
2OTU	H_ARG_44	NH2	C_ASP_60	OD2	3.013
2OTU	H_ARG_67	NH1	H_ASP_90	OD1	3.843
2OTU	H_ARG_67	NH1	H_ASP_90	OD2	2.748
2OTU	H_ARG_67	NH2	H_ASP_90	OD1	3.051
2OTU	H_ARG_67	NH2	H_ASP_90	OD2	3.464
2OTU	H_LYS_87	NZ	D_ASP_31	OD1	3.910

2OTU	H.LYS_87	NZ	D.ASP_31	OD2	2.759
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Table 314: 2OTU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2OTW	A_ARG_65	NH1	A_ASP_86	OD1	2.815
2OTW	A_ARG_65	NH1	A_ASP_86	OD2	2.356
2OTW	A_ARG_65	NH2	A_GLU_85	OE2	3.711
2OTW	A_ARG_65	NH2	A_ASP_86	OD1	2.988
2OTW	A_ARG_65	NH2	A_ASP_86	OD2	3.514
2OTW	B_ARG_38	NH1	B_ASP_90	OD1	3.114
2OTW	B_ARG_38	NH2	B_GLU_46	OE1	3.177
2OTW	B_ARG_38	NH2	B_GLU_46	OE2	3.352
2OTW	B_LYS_65	NZ	B_ASP_62	OD1	3.341
2OTW	B_ARG_67	NH1	B_ASP_90	OD1	3.557
2OTW	B_ARG_67	NH1	B_ASP_90	OD2	2.723
2OTW	B_ARG_67	NH2	B_ASP_90	OD1	3.013
2OTW	B_ARG_67	NH2	B_ASP_90	OD2	3.717
2OTW	B_LYS_87	NZ	D_ASP_31	OD1	3.659
2OTW	B_LYS_87	NZ	D_ASP_31	OD2	2.671
2OTW	B_ARG_100	NH1	A_ASP_60	OD1	3.223
2OTW	B_ARG_100	NH1	A_ASP_60	OD2	3.943
2OTW	C_ARG_65	NH1	C_ASP_86	OD1	2.692
2OTW	C_ARG_65	NH1	C_ASP_86	OD2	2.598
2OTW	D_ARG_38	NH1	D_ASP_90	OD1	2.989
2OTW	D_ARG_38	NH2	D_GLU_46	OE1	2.871
2OTW	D_ARG_38	NH2	D_GLU_46	OE2	3.541
2OTW	D_ARG_44	NH2	D_GLU_42	OE1	3.918
2OTW	D_ARG_67	NH1	D_ASP_90	OD1	3.886
2OTW	D_ARG_67	NH1	D_ASP_90	OD2	2.722
2OTW	D_ARG_67	NH2	D_ASP_90	OD1	2.979
2OTW	D_ARG_67	NH2	D_ASP_90	OD2	3.322
2OTW	D_ARG_100	NH1	C_ASP_60	OD1	3.882
2OTW	D_ARG_100	NH1	C_ASP_60	OD2	3.653

Table 315: 2OTW-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2P8L	A_ARG_24	NH2	A_GLU_70	OE2	3.694
2P8L	A_ARG_37	NH1	A_ASP_82	OD1	2.662
2P8L	A_ARG_61	NH2	A_ASP_82	OD1	3.178
2P8L	A_ARG_61	NH2	A_ASP_82	OD2	3.399
2P8L	A_HIS_96	NE2	C_ASP_5	OD1	2.766
2P8L	A_LYS_149	NZ	A_GLU_195	OE1	3.348
2P8L	A_LYS_149	NZ	A_GLU_195	OE2	2.911
2P8L	A_LYS_183	NZ	A_GLU_187	OE1	3.209
2P8L	A_LYS_183	NZ	A_GLU_187	OE2	3.403
2P8L	B_ARG_38	NH1	B_GLU_46	OE1	2.804
2P8L	B_ARG_38	NH1	B_GLU_46	OE2	3.681
2P8L	B_ARG_38	NH2	B_ASP_86	OD1	2.496
2P8L	B_LYS_57	NZ	B_ASP_55	OD2	3.457
2P8L	B_ARG_58	NH1	C_GLU_3	OE1	1.911
2P8L	B_ARG_58	NH1	C_GLU_3	OE2	3.223
2P8L	B_ARG_58	NH2	B_ASP_56	OD1	3.758
2P8L	B_ARG_58	NH2	B_ASP_56	OD2	3.029
2P8L	B_ARG_58	NH2	C_GLU_3	OE1	3.943
2P8L	B_ARG_66	NH1	B_ASP_86	OD1	3.620
2P8L	B_ARG_66	NH1	B_ASP_86	OD2	3.879
2P8L	B_ARG_66	NH2	B_ASP_86	OD1	3.123
2P8L	B_ARG_66	NH2	B_ASP_86	OD2	2.431
2P8L	B_LYS_71	NZ	B_ASP_55	OD1	3.582
2P8L	B_HIS_94	ND1	B_ASP_101	OD1	2.660
2P8L	B_HIS_94	ND1	B_ASP_101	OD2	3.511
2P8L	B_ARG_95	NH1	C_ASP_5	OD1	2.951
2P8L	B_ARG_95	NH1	C_ASP_5	OD2	3.619
2P8L	B_ARG_95	NH2	C_ASP_5	OD1	3.420
2P8L	B_ARG_95	NH2	C_ASP_5	OD2	2.971
2P8L	B_ARG_96	NH1	A_GLU_55	OE1	3.236
2P8L	B_ARG_96	NH1	A_GLU_55	OE2	3.320
2P8L	B_ARG_96	NH1	B_ASP_101	OD2	3.133
2P8L	B_ARG_96	NH2	A_GLU_55	OE1	3.018
2P8L	B_LYS_143	NZ	B_ASP_144	OD1	3.794
2P8L	B_LYS_209	NZ	A_GLU_123	OE1	3.743
2P8L	B_ARG_210	NH1	B_GLU_212	OE1	2.518
2P8L	B_ARG_210	NH1	B_GLU_212	OE2	2.702
2P8L	B_ARG_210	NH2	B_GLU_212	OE1	2.760
2P8L	C_LYS_6	NZ	B_ASP_54	OD1	3.641
2P8L	C_LYS_6	NZ	B_ASP_54	OD2	3.025
2P8L	C_LYS_6	NZ	B_ASP_56	OD1	2.878

Table 316: 2P8L-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2P8M	A_ARG_37	NH1	A_ASP_82	OD1	2.839
2P8M	A_ARG_61	NH2	A_ASP_82	OD1	2.944
2P8M	A_ARG_61	NH2	A_ASP_82	OD2	3.371
2P8M	A_HIS_96	NE2	C_ASP_3	OD2	2.613
2P8M	A_LYS_149	NZ	A_GLU_193	OE1	3.222
2P8M	A_LYS_149	NZ	A_GLU_195	OE1	3.752
2P8M	A_LYS_183	NZ	A_GLU_187	OE2	2.931
2P8M	A_LYS_190	NZ	A_GLU_213	OE2	3.479
2P8M	B_ARG_1	NH2	A_GLU_55	OE2	3.915
2P8M	B_ARG_38	NH1	B_GLU_46	OE1	2.460
2P8M	B_ARG_38	NH1	B_GLU_46	OE2	3.000
2P8M	B_ARG_38	NH2	B_ASP_86	OD1	2.567
2P8M	B_LYS_57	NZ	B_ASP_55	OD1	3.800
2P8M	B_LYS_57	NZ	B_ASP_55	OD2	3.375
2P8M	B_ARG_58	NH1	B_ASP_56	OD1	2.812
2P8M	B_ARG_58	NH2	C_GLU_1	OE1	2.510
2P8M	B_ARG_66	NH1	B_ASP_86	OD1	3.550
2P8M	B_ARG_66	NH2	B_ASP_86	OD1	3.137
2P8M	B_ARG_66	NH2	B_ASP_86	OD2	2.617
2P8M	B_HIS_94	ND1	B_ASP_101	OD1	2.569
2P8M	B_HIS_94	ND1	B_ASP_101	OD2	3.296
2P8M	B_ARG_95	NH1	C_ASP_3	OD1	2.973
2P8M	B_ARG_95	NH1	C_ASP_3	OD2	3.042
2P8M	B_ARG_95	NH2	C_ASP_3	OD1	3.169
2P8M	B_ARG_96	NH1	A_GLU_55	OE1	3.351
2P8M	B_ARG_96	NH1	A_GLU_55	OE2	3.448
2P8M	B_ARG_96	NH1	B_ASP_101	OD2	3.545
2P8M	B_ARG_96	NH2	A_GLU_55	OE1	3.393
2P8M	B_LYS_143	NZ	B_ASP_144	OD1	3.820
2P8M	B_LYS_143	NZ	B_ASP_144	OD2	3.945
2P8M	B_LYS_209	NZ	A_GLU_123	OE1	3.649
2P8M	B_ARG_210	NH2	B_GLU_212	OE1	2.714
2P8M	B_ARG_210	NH2	B_GLU_212	OE2	3.508
2P8M	C_LYS_4	NZ	B_ASP_54	OD1	2.903
2P8M	C_LYS_4	NZ	B_ASP_54	OD2	2.371
2P8M	C_LYS_4	NZ	B_ASP_56	OD2	3.183

Table 317: 2P8M-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2P8P	A_ARG_24	NH1	A_GLU_70	OE2	3.886
2P8P	A_ARG_24	NH2	A_GLU_70	OE2	2.623
2P8P	A_ARG_37	NH1	A_GLU_81	OE1	3.668
2P8P	A_ARG_37	NH1	A_GLU_81	OE2	3.049
2P8P	A_ARG_37	NH1	A_ASP_82	OD1	3.193
2P8P	A_ARG_37	NH2	A_GLU_81	OE1	3.421
2P8P	A_LYS_39	NZ	A_GLU_81	OE1	3.598
2P8P	A_ARG_61	NH2	A_GLU_81	OE2	2.595
2P8P	A_ARG_61	NH2	A_ASP_82	OD1	3.431
2P8P	A_HIS_96	NE2	C_ASP_3	OD1	3.214
2P8P	A_LYS_149	NZ	A_GLU_195	OE1	3.534
2P8P	A_LYS_183	NZ	A_GLU_187	OE1	2.848
2P8P	A_LYS_183	NZ	A_GLU_187	OE2	3.221
2P8P	A_LYS_188	NZ	A_ASP_185	OD1	2.922
2P8P	B_ARG_38	NH1	B_ASP_86	OD1	2.794
2P8P	B_ARG_38	NH2	B_GLU_46	OE1	3.420
2P8P	B_ARG_38	NH2	B_GLU_46	OE2	3.340
2P8P	B_ARG_38	NH2	B_ASP_86	OD1	3.738
2P8P	B_LYS_57	NZ	B_ASP_55	OD1	3.547
2P8P	B_LYS_57	NZ	B_ASP_55	OD2	2.954
2P8P	B_ARG_58	NH1	B_ASP_56	OD1	2.448
2P8P	B_ARG_58	NH1	B_ASP_56	OD2	3.762
2P8P	B_ARG_58	NH2	B_ASP_56	OD1	3.457
2P8P	B_ARG_58	NH2	B_ASP_56	OD2	3.922
2P8P	B_ARG_58	NH2	C_GLU_1	OE2	3.147
2P8P	B_ARG_66	NH1	B_ASP_86	OD1	3.503
2P8P	B_ARG_66	NH1	B_ASP_86	OD2	3.962
2P8P	B_ARG_66	NH2	B_ASP_86	OD1	3.025
2P8P	B_ARG_66	NH2	B_ASP_86	OD2	2.685
2P8P	B_LYS_71	NZ	B_ASP_55	OD1	3.926
2P8P	B_HIS_94	ND1	B_ASP_101	OD1	2.554
2P8P	B_HIS_94	ND1	B_ASP_101	OD2	3.579
2P8P	B_ARG_95	NH1	C_ASP_3	OD1	2.805
2P8P	B_ARG_95	NH1	C_ASP_3	OD2	3.510
2P8P	B_ARG_95	NH2	C_ASP_3	OD1	3.459
2P8P	B_ARG_95	NH2	C_ASP_3	OD2	2.629
2P8P	B_ARG_96	NH1	A_GLU_55	OE1	3.239
2P8P	B_ARG_96	NH1	A_GLU_55	OE2	3.518
2P8P	B_ARG_96	NH1	B_ASP_101	OD2	2.782
2P8P	B_ARG_96	NH2	A_GLU_55	OE1	3.128
2P8P	B_LYS_144	NZ	B_ASP_145	OD1	3.635
2P8P	B_LYS_144	NZ	B_ASP_145	OD2	3.553
2P8P	B_LYS_210	NZ	A_GLU_123	OE1	3.349
2P8P	B_LYS_210	NZ	A_GLU_123	OE2	3.192
2P8P	B_ARG_211	NH1	B_GLU_213	OE1	3.506
2P8P	B_ARG_211	NH1	B_GLU_213	OE2	3.532
2P8P	B_ARG_211	NH2	B_GLU_213	OE1	2.609
2P8P	B_ARG_211	NH2	B_GLU_213	OE2	3.996
2P8P	C_LYS_4	NZ	B_ASP_54	OD1	3.623
2P8P	C_LYS_4	NZ	B_ASP_54	OD2	3.010
2P8P	C_LYS_4	NZ	B_ASP_56	OD2	2.836

Table 318: 2P8P-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2PR4	L_ARG_37	NH1	L_ASP_82	OD1	3.024
2PR4	L_ARG_61	NH2	L_ASP_82	OD1	2.716
2PR4	L_ARG_61	NH2	L_ASP_82	OD2	3.445
2PR4	L_ARG_108	NH1	L_ASP_170	OD1	3.583
2PR4	L_LYS_149	NZ	L_GLU_195	OE1	3.734
2PR4	L_LYS_183	NZ	L_GLU_187	OE2	2.711
2PR4	L_LYS_190	NZ	L_ASP_151	OD1	3.274
2PR4	H_ARG_40	NH1	H_GLU_48	OE1	3.002
2PR4	H_ARG_40	NH1	H_ASP_91	OD1	3.704
2PR4	H_ARG_40	NH2	H_ASP_91	OD1	2.605
2PR4	H_ARG_60	NH1	H_ASP_58	OD1	3.465
2PR4	H_ARG_60	NH1	H_ASP_58	OD2	3.213
2PR4	H_ARG_68	NH1	H_ASP_91	OD1	3.656
2PR4	H_ARG_68	NH1	H_ASP_91	OD2	3.886
2PR4	H_ARG_68	NH2	H_ASP_91	OD1	3.393
2PR4	H_ARG_68	NH2	H_ASP_91	OD2	2.646
2PR4	H_HIS_99	ND1	H_ASP_120	OD1	2.785
2PR4	H_HIS_99	ND1	H_ASP_120	OD2	3.650
2PR4	H_ARG_101	NH1	L_GLU_55	OE1	3.296
2PR4	H_ARG_101	NH1	L_GLU_55	OE2	3.376
2PR4	H_ARG_101	NH1	H_ASP_120	OD2	3.802
2PR4	H_ARG_101	NH2	L_GLU_55	OE1	3.286
2PR4	H_LYS_162	NZ	H_ASP_163	OD1	3.519
2PR4	H_LYS_228	NZ	L_GLU_123	OE1	3.151
2PR4	H_ARG_229	NH1	H_GLU_231	OE2	3.222
2PR4	H_ARG_229	NH2	H_GLU_231	OE1	3.609
2PR4	H_ARG_229	NH2	H_GLU_231	OE2	2.833

Table 319: 2PR4-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2Q8A	A_ARG_128	NH1	A_GLU_343	OE2	2.727
2Q8A	A_ARG_128	NH2	A_GLU_256	OE1	2.979
2Q8A	A_ARG_128	NH2	A_GLU_256	OE2	2.971
2Q8A	A_LYS_203	NZ	L_ASP_32	OD1	3.044
2Q8A	A_LYS_203	NZ	L_ASP_32	OD2	2.513
2Q8A	A_LYS_245	NZ	A_GLU_213	OE2	3.921
2Q8A	A_LYS_245	NZ	A_ASP_242	OD1	3.383
2Q8A	A_LYS_245	NZ	A_ASP_242	OD2	2.933
2Q8A	A_ARG_270	NH1	A_ASP_178	OD1	2.638
2Q8A	A_ARG_270	NH1	A_ASP_178	OD2	3.624
2Q8A	A_LYS_292	NZ	A_GLU_133	OE2	2.672
2Q8A	A_ARG_304	NH1	A_GLU_436	OE1	3.883
2Q8A	A_ARG_304	NH1	A_GLU_436	OE2	2.055
2Q8A	A_ARG_304	NH2	A_GLU_436	OE1	3.764
2Q8A	A_ARG_304	NH2	A_GLU_436	OE2	3.204
2Q8A	A_LYS_311	NZ	A_ASP_322	OD1	2.775
2Q8A	A_LYS_311	NZ	A_ASP_322	OD2	3.906
2Q8A	A_LYS_339	NZ	A_GLU_336	OE1	3.158
2Q8A	A_LYS_339	NZ	A_GLU_336	OE2	3.923
2Q8A	A_LYS_364	NZ	A_GLU_361	OE1	3.383
2Q8A	A_LYS_364	NZ	A_GLU_361	OE2	3.258
2Q8A	A_LYS_368	NZ	A_ASP_227	OD1	2.672
2Q8A	A_LYS_368	NZ	A_ASP_227	OD2	3.440
2Q8A	A_LYS_391	NZ	A_ASP_134	OD2	2.727
2Q8A	A_HIS_433	NE2	A_GLU_436	OE1	3.631
2Q8A	L_ARG_54	NH1	L_ASP_60	OD1	3.683
2Q8A	L_ARG_61	NH1	L_ASP_82	OD1	2.388
2Q8A	L_ARG_61	NH1	L_ASP_82	OD2	3.063
2Q8A	L_ARG_61	NH2	L_GLU_81	OE2	3.801
2Q8A	L_ARG_96	NH1	A_ASP_204	OD1	2.971
2Q8A	L_ARG_96	NH1	A_ASP_204	OD2	2.580
2Q8A	L_ARG_96	NH2	A_ASP_204	OD1	2.882
2Q8A	L_ARG_96	NH2	A_ASP_204	OD2	3.927
2Q8A	L_ARG_96	NH2	H_GLU_59	OE2	3.755
2Q8A	L_LYS_103	NZ	L_ASP_165	OD1	3.929
2Q8A	L_HIS_189	ND1	L_ASP_151	OD2	2.903
2Q8A	L_LYS_199	NZ	L_ASP_110	OD2	2.695
2Q8A	H_HIS_35	NE2	A_ASP_204	OD2	3.930
2Q8A	H_ARG_50	NH1	H_ASP_52	OD2	3.087
2Q8A	H_ARG_50	NH2	H_GLU_59	OE2	3.157
2Q8A	H_LYS_63	NZ	H_GLU_46	OE1	3.799
2Q8A	H_LYS_67	NZ	H_ASP_90	OD1	3.906
2Q8A	H_LYS_67	NZ	H_ASP_90	OD2	3.028

Table 320: 2Q8A-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2Q8B	A_ARG_128	NH1	A_GLU_256	OE1	3.040
2Q8B	A_ARG_128	NH1	A_GLU_256	OE2	3.000
2Q8B	A_ARG_128	NH2	A_GLU_256	OE1	3.059
2Q8B	A_LYS_203	NZ	L_ASP_32	OD1	3.779
2Q8B	A_LYS_203	NZ	L_ASP_32	OD2	2.847
2Q8B	A_LYS_245	NZ	A_GLU_213	OE2	2.777
2Q8B	A_LYS_245	NZ	A_ASP_242	OD2	3.887
2Q8B	A_LYS_292	NZ	A_GLU_133	OE1	3.902
2Q8B	A_LYS_292	NZ	A_GLU_133	OE2	2.733
2Q8B	A_ARG_304	NH1	A_GLU_436	OE1	3.770
2Q8B	A_ARG_304	NH1	A_GLU_436	OE2	2.007
2Q8B	A_ARG_304	NH2	A_GLU_436	OE2	3.545
2Q8B	A_LYS_311	NZ	A_ASP_322	OD1	2.853
2Q8B	A_LYS_311	NZ	A_ASP_322	OD2	3.778
2Q8B	A_LYS_339	NZ	A_GLU_336	OE1	2.983
2Q8B	A_LYS_339	NZ	A_GLU_336	OE2	3.511
2Q8B	A_LYS_351	NZ	A_GLU_343	OE2	2.663
2Q8B	A_LYS_391	NZ	A_ASP_134	OD1	3.749
2Q8B	A_LYS_391	NZ	A_ASP_134	OD2	2.808
2Q8B	A_LYS_391	NZ	A_ASP_388	OD1	3.545
2Q8B	A_HIS_433	NE2	A_GLU_436	OE1	3.672
2Q8B	L_LYS_24	NZ	L_ASP_70	OD1	3.418
2Q8B	L_LYS_24	NZ	L_ASP_70	OD2	3.406
2Q8B	L_ARG_61	NH1	L_ASP_82	OD1	2.518
2Q8B	L_ARG_61	NH1	L_ASP_82	OD2	3.346
2Q8B	L_ARG_96	NH1	A_ASP_204	OD1	3.458
2Q8B	L_ARG_96	NH1	A_ASP_204	OD2	2.952
2Q8B	L_ARG_96	NH2	A_ASP_204	OD1	2.667
2Q8B	L_ARG_96	NH2	A_ASP_204	OD2	3.462
2Q8B	L_ARG_188	NH1	L_GLU_185	OE1	3.851
2Q8B	L_ARG_188	NH1	L_GLU_185	OE2	2.847
2Q8B	L_ARG_188	NH2	L_GLU_185	OE2	3.891
2Q8B	L_HIS_189	ND1	L_GLU_185	OE2	3.560
2Q8B	L_LYS_199	NZ	L_ASP_110	OD2	3.181
2Q8B	H_ARG_40	NH1	H_GLU_89	OE2	2.969
2Q8B	H_ARG_40	NH2	H_GLU_89	OE2	3.558
2Q8B	H_ARG_50	NH2	H_GLU_59	OE2	2.874
2Q8B	H_LYS_63	NZ	H_GLU_46	OE1	2.715
2Q8B	H_LYS_67	NZ	H_ASP_90	OD1	3.762
2Q8B	H_LYS_67	NZ	H_ASP_90	OD2	3.011

Table 321: 2Q8B-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2QAD	A.LYS.207	NZ	A.GLU.381	OE1	3.156
2QAD	A.LYS.207	NZ	A.GLU.381	OE2	2.751
2QAD	A.LYS.231	NZ	A.GLU.268	OE2	3.310
2QAD	A.LYS.232	NZ	A.GLU.269	OE2	3.594
2QAD	A.LYS.282	NZ	A.GLU.275	OE2	3.989
2QAD	A.LYS.348	NZ	A.GLU.269	OE1	3.722
2QAD	A.LYS.348	NZ	A.GLU.269	OE2	3.126
2QAD	A.ARG.419	NH1	A.ASP.325	OD2	2.671
2QAD	A.ARG.419	NH2	A.ASP.325	OD2	3.673
2QAD	A.ARG.456	NH2	A.GLU.466	OE2	3.254
2QAD	A.ARG.469	NH2	A.ASP.457	OD2	3.733
2QAD	A.ARG.476	NH1	A.ASP.474	OD1	2.798
2QAD	A.ARG.476	NH2	A.GLU.102	OE2	3.950
2QAD	A.ARG.480	NH2	A.ASP.477	OD1	3.412
2QAD	A.LYS.487	NZ	A.GLU.91	OE1	3.356
2QAD	A.LYS.487	NZ	A.GLU.91	OE2	3.914
2QAD	A.LYS.490	NZ	A.GLU.492	OE2	3.426
2QAD	B.ARG.54	NH1	B.ASP.78	OD2	3.526
2QAD	B.ARG.54	NH2	B.GLU.77	OE2	3.474
2QAD	B.ARG.54	NH2	B.ASP.78	OD2	3.454
2QAD	B.ARG.59	NH1	A.ASP.368	OD1	3.394
2QAD	B.ARG.59	NH1	A.ASP.368	OD2	2.749
2QAD	B.ARG.59	NH2	A.ASP.368	OD1	3.764
2QAD	B.LYS.72	NZ	B.ASP.56	OD2	3.172
2QAD	B.HIS.107	ND1	B.ASP.105	OD2	3.915
2QAD	C.LYS.39	NZ	C.ASP.81	OD1	3.751
2QAD	C.LYS.50	NZ	D.GLU.100F	OE2	2.989
2QAD	C.LYS.55	NZ	D.ASP.101	OD1	3.312
2QAD	C.LYS.55	NZ	D.ASP.101	OD2	3.736
2QAD	C.ARG.61	NH2	C.ASP.82	OD1	3.983
2QAD	C.ARG.61	NH2	C.ASP.82	OD2	3.945
2QAD	C.LYS.103	NZ	C.GLU.165	OE1	3.299
2QAD	C.LYS.103	NZ	C.GLU.165	OE2	3.201
2QAD	C.LYS.183	NZ	C.GLU.187	OE2	3.769
2QAD	C.LYS.188	NZ	C.ASP.185	OD1	3.463
2QAD	C.HIS.189	ND1	C.ASP.151	OD1	3.214
2QAD	C.HIS.189	ND1	C.ASP.151	OD2	3.260
2QAD	D.ARG.38	NH1	D.GLU.46	OE1	3.492
2QAD	D.ARG.38	NH1	D.GLU.46	OE2	3.474
2QAD	D.ARG.62	NH1	D.GLU.46	OE1	2.887
2QAD	D.ARG.62	NH1	D.GLU.46	OE2	2.924
2QAD	D.ARG.62	NH2	D.GLU.46	OE2	3.357
2QAD	D.LYS.143	NZ	D.ASP.144	OD1	2.885
2QAD	D.LYS.143	NZ	D.ASP.144	OD2	3.634
2QAD	D.LYS.206	NZ	D.ASP.208	OD1	3.117
2QAD	D.LYS.209	NZ	D.GLU.212	OE1	3.727
2QAD	D.LYS.210	NZ	D.GLU.212	OE2	3.492
2QAD	E.LYS.207	NZ	E.GLU.381	OE1	3.059
2QAD	E.LYS.207	NZ	E.GLU.381	OE2	2.916
2QAD	E.LYS.231	NZ	E.GLU.268	OE2	3.647
2QAD	E.LYS.282	NZ	E.GLU.275	OE1	3.736
2QAD	E.LYS.282	NZ	E.GLU.275	OE2	3.761
2QAD	E.LYS.348	NZ	E.GLU.269	OE1	3.968
2QAD	E.LYS.348	NZ	E.GLU.269	OE2	3.504
2QAD	E.ARG.419	NH1	E.ASP.325	OD2	2.690
2QAD	E.ARG.419	NH2	E.ASP.325	OD2	3.727
2QAD	E.ARG.456	NH2	E.GLU.466	OE2	3.894

2QAD	E_ARG_476	NH1	E_ASP_474	OD1	3.116
2QAD	E_ARG_476	NH2	E_GLU_102	OE1	3.845
2QAD	E_ARG_476	NH2	E_GLU_102	OE2	3.739
2QAD	E_ARG_480	NH2	E_ASP_477	OD1	3.576
2QAD	E_LYS_487	NZ	E_GLU_91	OE1	3.899
2QAD	E_LYS_487	NZ	E_GLU_91	OE2	3.462
2QAD	E_LYS_490	NZ	E_GLU_492	OE2	3.971
2QAD	F_LYS_1	NZ	F_GLU_92	OE1	3.829
2QAD	F_LYS_29	NZ	F_GLU_85	OE1	3.902
2QAD	F_ARG_54	NH1	F_ASP_78	OD2	3.625
2QAD	F_ARG_54	NH2	F_GLU_77	OE2	3.363
2QAD	F_ARG_54	NH2	F_ASP_78	OD2	3.440
2QAD	F_ARG_59	NH1	E_ASP_368	OD1	2.855
2QAD	F_ARG_59	NH1	E_ASP_368	OD2	2.624
2QAD	F_ARG_59	NH2	E_ASP_368	OD1	3.681
2QAD	F_LYS_72	NZ	F_ASP_56	OD2	3.168
2QAD	F_LYS_90	NZ	F_GLU_85	OE2	3.437
2QAD	F_ARG_134	NH1	F_GLU_150	OE1	3.188
2QAD	F_ARG_134	NH2	F_GLU_150	OE1	2.761
2QAD	F_ARG_134	NH2	F_ASP_153	OD1	2.906
2QAD	G_LYS_39	NZ	G_ASP_81	OD1	3.605
2QAD	G_LYS_50	NZ	H_GLU_100F	OE2	3.151
2QAD	G_LYS_55	NZ	H_ASP_101	OD1	3.191
2QAD	G_LYS_55	NZ	H_ASP_101	OD2	3.496
2QAD	G_ARG_61	NH2	G_ASP_82	OD1	3.464
2QAD	G_ARG_61	NH2	G_ASP_82	OD2	3.576
2QAD	G_LYS_103	NZ	G_GLU_165	OE1	3.223
2QAD	G_LYS_103	NZ	G_GLU_165	OE2	3.176
2QAD	G_LYS_183	NZ	G_GLU_187	OE2	2.926
2QAD	G_LYS_188	NZ	G_ASP_185	OD1	3.437
2QAD	G_HIS_189	ND1	G_ASP_151	OD1	3.455
2QAD	G_HIS_189	ND1	G_ASP_151	OD2	2.830
2QAD	H_ARG_62	NH1	H_GLU_46	OE1	2.833
2QAD	H_ARG_62	NH1	H_GLU_46	OE2	2.981
2QAD	H_ARG_62	NH2	H_GLU_46	OE1	3.733
2QAD	H_ARG_62	NH2	H_GLU_46	OE2	3.274
2QAD	H_ARG_83	NH2	H_ASP_86	OD1	3.458
2QAD	H_ARG_83	NH2	H_ASP_86	OD2	2.513
2QAD	H_LYS_143	NZ	H_ASP_144	OD1	2.852
2QAD	H_LYS_143	NZ	H_ASP_144	OD2	3.707
2QAD	H_LYS_206	NZ	H_ASP_208	OD1	2.954
2QAD	H_LYS_209	NZ	H_GLU_212	OE1	3.668

Table 322: 2QAD-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2QQI	A_ARG_305	NH1	A_GLU_312	OE2	3.025
2QQI	A_ARG_305	NH2	A_GLU_312	OE2	3.597
2QQI	A_LYS_347	NZ	A_GLU_312	OE1	3.337
2QQI	A_ARG_402	NH2	A_ASP_329	OD1	3.538
2QQI	A_ARG_402	NH2	A_ASP_329	OD2	2.925
2QQI	A_LYS_407	NZ	A_ASP_361	OD1	3.110
2QQI	A_LYS_407	NZ	A_ASP_361	OD2	2.901
2QQI	A_ARG_463	NH2	A_ASP_444	OD1	2.807
2QQI	A_ARG_513	NH2	A_GLU_483	OE1	3.254
2QQI	A_LYS_527	NZ	A_ASP_525	OD1	2.652
2QQI	A_LYS_527	NZ	A_ASP_525	OD2	3.292
2QQI	A_ARG_552	NH1	A_GLU_550	OE1	3.271
2QQI	A_ARG_552	NH2	A_GLU_550	OE1	2.899
2QQI	A_ARG_560	NH2	A_ASP_488	OD1	3.697
2QQI	A_ARG_560	NH2	A_ASP_488	OD2	3.358

Table 323: 2QQI-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2QQM	A_ARG_207	NH2	A_ASP_197	OD1	2.822
2QQM	A_ARG_207	NH2	A_ASP_197	OD2	3.844
2QQM	A_HIS_223	NE2	A_GLU_212	OE1	2.681
2QQM	A_ARG_226	NH2	A_GLU_212	OE2	3.329
2QQM	A_ARG_235	NH2	A_GLU_188	OE2	3.062
2QQM	A_ARG_237	NH1	A_GLU_285	OE2	2.734
2QQM	A_ARG_237	NH2	A_GLU_184	OE2	3.025
2QQM	A_ARG_237	NH2	A_GLU_285	OE2	3.428
2QQM	A_HIS_287	ND1	A_ASP_289	OD1	3.807
2QQM	A_HIS_287	ND1	A_ASP_289	OD2	3.593
2QQM	A_ARG_305	NH1	A_GLU_312	OE1	2.993
2QQM	A_ARG_305	NH2	A_GLU_312	OE1	3.753
2QQM	A_ARG_334	NH1	A_GLU_184	OE1	2.860
2QQM	A_ARG_334	NH2	A_GLU_184	OE1	3.414
2QQM	A_ARG_334	NH2	A_GLU_184	OE2	3.144
2QQM	A_LYS_347	NZ	A_GLU_312	OE2	3.827
2QQM	A_LYS_356	NZ	A_GLU_412	OE1	3.925
2QQM	A_ARG_402	NH2	A_ASP_329	OD1	3.702
2QQM	A_ARG_402	NH2	A_ASP_329	OD2	3.069
2QQM	A_LYS_407	NZ	A_ASP_361	OD1	2.925
2QQM	A_LYS_407	NZ	A_ASP_361	OD2	3.013
2QQM	A_ARG_463	NH2	A_ASP_444	OD1	2.977
2QQM	A_LYS_504	NZ	A_ASP_368	OD2	3.089
2QQM	A_ARG_513	NH1	A_GLU_541	OE1	3.868
2QQM	A_ARG_513	NH2	A_GLU_541	OE1	3.920
2QQM	A_LYS_514	NZ	A_GLU_541	OE1	3.415
2QQM	A_LYS_514	NZ	A_GLU_541	OE2	3.311
2QQM	A_LYS_536	NZ	A_ASP_531	OD2	3.748
2QQM	A_ARG_552	NH1	A_GLU_550	OE1	3.256
2QQM	A_ARG_552	NH2	A_GLU_550	OE1	3.455
2QQM	A_ARG_560	NH2	A_ASP_488	OD1	3.975
2QQM	A_ARG_560	NH2	A_ASP_488	OD2	3.187

Table 324: 2QQM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2QQN	A_ARG_305	NH1	A_GLU_312	OE1	3.596
2QQN	A_LYS_347	NZ	A_GLU_312	OE1	3.909
2QQN	A_LYS_356	NZ	A_GLU_412	OE1	3.215
2QQN	A_ARG_402	NH2	A_ASP_329	OD1	3.587
2QQN	A_ARG_402	NH2	A_ASP_329	OD2	3.150
2QQN	A_LYS_407	NZ	A_ASP_361	OD1	3.212
2QQN	A_LYS_407	NZ	A_ASP_361	OD2	2.958
2QQN	H_ARG_38	NH1	H_ASP_86	OD1	2.933
2QQN	H_ARG_38	NH2	H_GLU_46	OE1	3.167
2QQN	H_ARG_38	NH2	H_ASP_86	OD1	3.865
2QQN	H_ARG_66	NH1	H_ASP_86	OD1	3.782
2QQN	H_ARG_66	NH1	H_ASP_86	OD2	2.772
2QQN	H_ARG_66	NH2	H_ASP_86	OD1	3.232
2QQN	H_ARG_66	NH2	H_ASP_86	OD2	3.638
2QQN	H_LYS_75	NZ	H_ASP_72	OD2	3.885
2QQN	H_ARG_94	NH2	H_ASP_101	OD1	3.705
2QQN	H_ARG_94	NH2	H_ASP_101	OD2	2.999
2QQN	H_LYS_143	NZ	H_ASP_144	OD1	3.148
2QQN	H_LYS_143	NZ	H_ASP_144	OD2	2.751
2QQN	H_LYS_206	NZ	H_ASP_208	OD1	3.934
2QQN	H_LYS_209	NZ	L_GLU_123	OE1	2.782
2QQN	H_LYS_209	NZ	L_GLU_123	OE2	3.506
2QQN	H_LYS_210	NZ	H_GLU_212	OE1	3.071
2QQN	H_LYS_210	NZ	H_GLU_212	OE2	3.673
2QQN	H_LYS_214	NZ	L_ASP_122	OD1	3.854
2QQN	L_ARG_61	NH2	L_GLU_81	OE2	3.892
2QQN	L_ARG_61	NH2	L_ASP_82	OD1	2.963
2QQN	L_ARG_61	NH2	L_ASP_82	OD2	3.635
2QQN	L_LYS_103	NZ	L_GLU_105	OE2	3.304
2QQN	L_LYS_103	NZ	L_GLU_165	OE1	2.460
2QQN	L_LYS_103	NZ	L_GLU_165	OE2	3.133
2QQN	L_ARG_142	NH1	L_GLU_105	OE2	2.892
2QQN	L_ARG_142	NH2	L_GLU_165	OE2	3.206
2QQN	L_LYS_149	NZ	L_GLU_195	OE1	2.720
2QQN	L_LYS_183	NZ	L_GLU_187	OE1	3.367
2QQN	L_LYS_183	NZ	L_GLU_187	OE2	3.373
2QQN	L_LYS_188	NZ	L_ASP_185	OD1	3.017

Table 325: 2QQN-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2R29	A_LYS_307	NZ	A_GLU_327	OE2	3.953
2R29	A_LYS_307	NZ	H_ASP_99	OD1	2.956
2R29	A_LYS_307	NZ	L_GLU_59	OE1	3.335
2R29	A_LYS_310	NZ	H_ASP_52	OD1	3.449
2R29	A_LYS_310	NZ	H_ASP_52	OD2	2.764
2R29	A_ARG_323	NH2	A_GLU_311	OE2	3.982
2R29	A_ARG_350	NH1	A_GLU_370	OE1	2.411
2R29	H_ARG_40	NH2	H_GLU_46	OE2	3.642
2R29	H_LYS_59	NZ	L_ASP_98	OD2	3.485
2R29	H_LYS_67	NZ	H_ASP_90	OD1	3.208
2R29	H_LYS_67	NZ	H_ASP_90	OD2	3.049
2R29	L_ARG_54	NH2	H_GLU_101	OE1	3.814
2R29	L_ARG_54	NH2	H_GLU_101	OE2	3.270
2R29	L_LYS_107	NZ	H_GLU_42	OE1	3.937
2R29	L_LYS_151	NZ	L_GLU_199	OE1	2.854
2R29	L_LYS_151	NZ	L_GLU_199	OE2	3.268
2R29	L_ARG_159	NH2	L_GLU_189	OE1	3.854
2R29	L_HIS_193	ND1	L_ASP_155	OD2	2.763
2R29	L_HIS_193	NE2	L_GLU_189	OE1	3.126

Table 326: 2R29-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID residue name residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2R69	A_LYS_307	NZ	H_ASP_99	OD2	3.631
2R69	A_HIS_317	NE2	A_GLU_368	OE2	3.012
2R69	A_LYS_344	NZ	A_GLU_338	OE1	3.172
2R69	A_ARG_345	NH1	A_ASP_341	OD2	3.802
2R69	H_LYS_38	NZ	H_ASP_90	OD1	2.910
2R69	H_LYS_38	NZ	H_ASP_90	OD2	2.994
2R69	H_ARG_40	NH2	H_GLU_46	OE2	3.388
2R69	H_LYS_59	NZ	L_ASP_98	OD2	3.723
2R69	H_LYS_67	NZ	H_ASP_90	OD1	3.247
2R69	H_LYS_67	NZ	H_ASP_90	OD2	3.994
2R69	H_LYS_211	NZ	L_GLU_127	OE1	3.695
2R69	H_LYS_211	NZ	L_GLU_127	OE2	3.159
2R69	L_ARG_31	NH2	A_GLU_311	OE2	3.151
2R69	L_LYS_43	NZ	L_ASP_85	OD1	2.285
2R69	L_LYS_43	NZ	L_ASP_85	OD2	3.990
2R69	L_ARG_54	NH2	H_GLU_101	OE1	2.992
2R69	L_ARG_54	NH2	H_GLU_101	OE2	2.911
2R69	L_ARG_72	NH2	L_ASP_74	OD2	3.950
2R69	L_ARG_112	NH2	L_ASP_174	OD1	3.901
2R69	L_LYS_151	NZ	L_GLU_158	OE1	2.692
2R69	L_LYS_151	NZ	L_GLU_158	OE2	3.692
2R69	L_LYS_153	NZ	L_GLU_199	OE1	2.500
2R69	L_LYS_153	NZ	L_GLU_199	OE2	3.634
2R69	L_ARG_159	NH2	L_GLU_189	OE1	3.888
2R69	L_ARG_159	NH2	L_GLU_189	OE2	3.776
2R69	L_HIS_193	NE2	L_GLU_189	OE1	3.028

Table 327: 2R69-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2UYL	A_ARG_24	NH2	A_ASP_75	OD2	3.541
2UYL	A_LYS_44	NZ	A_GLU_86	OE1	3.928
2UYL	A_LYS_55	NZ	A_ASP_35	OD1	3.890
2UYL	A_ARG_66	NH1	A_GLU_84	OE2	3.593
2UYL	A_ARG_66	NH2	A_GLU_84	OE2	3.108
2UYL	A_ARG_66	NH2	A_GLU_86	OE2	3.573
2UYL	A_ARG_66	NH2	A_ASP_87	OD1	2.859
2UYL	A_ARG_66	NH2	A_ASP_87	OD2	3.807
2UYL	A_ARG_101	NH1	B_GLU_99	OE1	3.183
2UYL	A_ARG_101	NH1	B_GLU_99	OE2	3.530
2UYL	A_ARG_101	NH2	B_GLU_99	OE2	3.803
2UYL	A_LYS_152	NZ	A_GLU_159	OE2	3.364
2UYL	A_LYS_154	NZ	A_GLU_200	OE1	3.299
2UYL	A_ARG_160	NH2	A_GLU_190	OE1	2.667
2UYL	A_ARG_160	NH2	A_GLU_190	OE2	3.767
2UYL	A_LYS_188	NZ	A_GLU_192	OE1	3.100
2UYL	A_HIS_194	ND1	A_ASP_156	OD2	3.217
2UYL	B_ARG_40	NH1	B_GLU_46	OE2	3.963
2UYL	B_ARG_40	NH2	B_ASP_89	OD1	3.905
2UYL	B_LYS_63	NZ	B_GLU_46	OE1	2.751
2UYL	B_LYS_63	NZ	B_GLU_46	OE2	3.738
2UYL	B_LYS_67	NZ	B_ASP_90	OD1	2.822
2UYL	B_LYS_67	NZ	B_ASP_90	OD2	3.465
2UYL	B_ARG_98	NH2	B_GLU_100	OE2	3.144
2UYL	M_ARG_24	NH1	M_ASP_75	OD1	3.039
2UYL	M_ARG_24	NH1	M_ASP_75	OD2	2.784
2UYL	M_ARG_24	NH2	M_ASP_75	OD2	3.872
2UYL	M_ARG_66	NH1	M_GLU_84	OE1	3.248
2UYL	M_ARG_66	NH1	M_GLU_84	OE2	3.722
2UYL	M_ARG_66	NH2	M_GLU_84	OE2	3.790
2UYL	M_ARG_66	NH2	M_GLU_86	OE1	3.569
2UYL	M_ARG_66	NH2	M_GLU_86	OE2	3.070
2UYL	M_ARG_66	NH2	M_ASP_87	OD1	3.037
2UYL	M_ARG_66	NH2	M_ASP_87	OD2	3.967
2UYL	M_ARG_101	NH1	N_GLU_99	OE1	3.058
2UYL	M_ARG_101	NH1	N_GLU_99	OE2	3.775
2UYL	M_ARG_101	NH2	N_GLU_99	OE2	3.923
2UYL	M_LYS_108	NZ	M_GLU_110	OE1	3.809
2UYL	M_LYS_152	NZ	M_GLU_159	OE2	3.798
2UYL	M_LYS_154	NZ	M_GLU_200	OE1	2.830
2UYL	M_ARG_160	NH1	M_GLU_190	OE1	3.456
2UYL	M_ARG_160	NH2	M_GLU_190	OE1	2.573
2UYL	M_ARG_160	NH2	M_GLU_190	OE2	3.199
2UYL	M_LYS_188	NZ	M_GLU_192	OE2	3.865
2UYL	M_HIS_194	ND1	M_ASP_156	OD2	2.773
2UYL	N_LYS_63	NZ	N_GLU_46	OE1	2.897
2UYL	N_LYS_67	NZ	N_ASP_90	OD1	2.827
2UYL	N_LYS_67	NZ	N_ASP_90	OD2	3.442
2UYL	N_ARG_98	NH2	N_GLU_100	OE1	2.786
2UYL	N_ARG_98	NH2	N_GLU_100	OE2	3.617
2UYL	N_HIS_170	NE2	M_ASP_172	OD1	3.811
2UYL	V_ARG_24	NH1	V_ASP_75	OD1	3.803
2UYL	V_ARG_24	NH2	V_ASP_75	OD1	2.930
2UYL	V_ARG_24	NH2	V_ASP_75	OD2	3.669
2UYL	V_LYS_44	NZ	V_GLU_86	OE1	2.905
2UYL	V_LYS_55	NZ	V_ASP_35	OD2	3.201
2UYL	V_ARG_66	NH1	V_GLU_84	OE1	3.900

2UYL	V_ARG_66	NH2	V_GLU_84	OE2	3.992
2UYL	V_ARG_66	NH2	V_GLU_86	OE2	3.799
2UYL	V_ARG_66	NH2	V_ASP_87	OD1	2.834
2UYL	V_ARG_66	NH2	V_ASP_87	OD2	3.258
2UYL	V_ARG_101	NH1	W_GLU_99	OE1	2.958
2UYL	V_ARG_101	NH1	W_GLU_99	OE2	3.417
2UYL	V_ARG_101	NH2	W_GLU_99	OE2	3.369
2UYL	V_LYS_108	NZ	V_ASP_170	OD1	3.736
2UYL	V_LYS_154	NZ	V_GLU_200	OE1	2.621
2UYL	V_LYS_154	NZ	V_GLU_200	OE2	3.889
2UYL	V_ARG_160	NH1	V_GLU_190	OE1	3.166
2UYL	V_ARG_160	NH2	V_GLU_190	OE1	3.294
2UYL	V_ARG_160	NH2	V_GLU_190	OE2	3.839
2UYL	V_HIS_194	ND1	V_ASP_156	OD2	2.891
2UYL	V_LYS_204	NZ	V_ASP_115	OD1	3.190
2UYL	W_LYS_63	NZ	W_GLU_46	OE1	2.810
2UYL	W_LYS_63	NZ	W_GLU_46	OE2	3.935
2UYL	W_LYS_67	NZ	W_ASP_90	OD1	3.006
2UYL	W_LYS_67	NZ	W_ASP_90	OD2	3.683
2UYL	W_ARG_98	NH2	W_GLU_100	OE2	3.033
2UYL	X_ARG_24	NH1	X_ASP_75	OD1	3.584
2UYL	X_ARG_24	NH2	X_ASP_75	OD1	3.267
2UYL	X_LYS_55	NZ	X_ASP_35	OD2	3.064
2UYL	X_ARG_66	NH1	X_GLU_84	OE1	3.245
2UYL	X_ARG_66	NH1	X_GLU_84	OE2	3.798
2UYL	X_ARG_66	NH2	X_GLU_84	OE1	3.726
2UYL	X_ARG_66	NH2	X_GLU_84	OE2	3.244
2UYL	X_ARG_66	NH2	X_GLU_86	OE1	3.815
2UYL	X_ARG_66	NH2	X_GLU_86	OE2	2.779
2UYL	X_ARG_101	NH1	Y_GLU_99	OE1	2.789
2UYL	X_ARG_101	NH1	Y_GLU_99	OE2	3.483
2UYL	X_ARG_101	NH2	Y_GLU_99	OE2	3.405
2UYL	X_LYS_152	NZ	X_GLU_200	OE2	3.544
2UYL	X_LYS_154	NZ	X_GLU_200	OE1	3.293
2UYL	X_LYS_188	NZ	X_GLU_192	OE1	3.104
2UYL	X_LYS_188	NZ	X_GLU_192	OE2	3.213
2UYL	X_HIS_194	ND1	X_ASP_156	OD2	3.029
2UYL	X_LYS_204	NZ	X_ASP_115	OD1	2.823
2UYL	X_LYS_204	NZ	X_ASP_115	OD2	3.875
2UYL	Y_LYS_63	NZ	Y_GLU_46	OE1	3.237
2UYL	Y_LYS_63	NZ	Y_GLU_46	OE2	3.539
2UYL	Y_LYS_67	NZ	Y_ASP_90	OD1	2.881
2UYL	Y_LYS_67	NZ	Y_ASP_90	OD2	3.582
2UYL	Y_ARG_98	NH2	Y_GLU_100	OE1	2.856
2UYL	Y_ARG_98	NH2	Y_GLU_100	OE2	3.603

Table 328: 2UYL-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2VC2	A_HIS_30	ND1	A_GLU_136	OE1	3.993
2VC2	A_ARG_77	NH1	H_ASP_102	OD1	3.536
2VC2	A_ARG_77	NH1	H_ASP_102	OD2	3.007
2VC2	A_ARG_77	NH2	H_ASP_102	OD1	2.794
2VC2	A_ARG_77	NH2	H_ASP_102	OD2	3.630
2VC2	A_LYS_88	NZ	A_ASP_71	OD2	3.044
2VC2	A_LYS_88	NZ	A_GLU_75	OE2	3.709
2VC2	A_ARG_153	NH1	A_GLU_157	OE1	3.976
2VC2	A_ARG_153	NH1	A_GLU_157	OE2	3.374
2VC2	A_ARG_153	NH2	A_GLU_120	OE1	3.288
2VC2	A_ARG_153	NH2	A_GLU_120	OE2	3.798
2VC2	A_ARG_165	NH1	A_GLU_123	OE2	3.067
2VC2	A_ARG_165	NH2	A_ASP_163	OD1	2.956
2VC2	A_ARG_165	NH2	A_ASP_163	OD2	3.881
2VC2	A_ARG_279	NH2	A_GLU_268	OE2	3.656
2VC2	A_ARG_303	NH2	A_ASP_301	OD2	3.119
2VC2	A_ARG_327	NH1	A_GLU_283	OE1	3.141
2VC2	A_ARG_327	NH1	A_GLU_283	OE2	3.525
2VC2	A_ARG_422	NH1	A_ASP_24	OD1	2.995
2VC2	A_ARG_422	NH1	A_ASP_24	OD2	3.442
2VC2	B_ARG_67	NH1	B_GLU_65	OE1	3.348
2VC2	B_LYS_72	NZ	B_ASP_109	OD1	2.615
2VC2	B_LYS_72	NZ	B_ASP_109	OD2	3.592
2VC2	B_ARG_87	NH2	B_GLU_65	OE2	3.439
2VC2	B_ARG_105	NH1	B_ASP_71	OD1	3.409
2VC2	B_LYS_159	NZ	B_ASP_224	OD1	3.836
2VC2	B_LYS_159	NZ	B_ASP_224	OD2	2.792
2VC2	B_LYS_209	NZ	B_GLU_206	OE2	3.718
2VC2	B_ARG_214	NH1	B_ASP_179	OD1	3.968
2VC2	B_ARG_214	NH1	B_ASP_179	OD2	2.988
2VC2	B_ARG_214	NH2	B_ASP_179	OD1	3.866
2VC2	B_ARG_214	NH2	B_ASP_179	OD2	3.629
2VC2	B_ARG_216	NH2	A_GLU_123	OE2	3.081
2VC2	B_ARG_239	NH2	B_ASP_113	OD2	3.274
2VC2	B_HIS_244	NE2	B_ASP_113	OD1	3.820
2VC2	B_LYS_253	NZ	A_ASP_232	OD2	2.805
2VC2	B_HIS_255	ND1	B_ASP_259	OD2	2.957
2VC2	B_HIS_255	NE2	B_ASP_158	OD2	3.335
2VC2	B_HIS_255	NE2	B_ASP_217	OD1	3.717
2VC2	B_HIS_255	NE2	B_ASP_217	OD2	2.761
2VC2	B_HIS_274	NE2	B_ASP_270	OD1	2.976
2VC2	B_HIS_274	NE2	B_ASP_270	OD2	2.687
2VC2	B_LYS_298	NZ	B_GLU_297	OE2	3.182
2VC2	B_LYS_302	NZ	B_ASP_233	OD1	3.549
2VC2	B_LYS_302	NZ	B_ASP_233	OD2	3.146
2VC2	B_LYS_354	NZ	B_GLU_356	OE1	3.116
2VC2	B_ARG_360	NH2	B_GLU_358	OE2	3.412
2VC2	B_ARG_404	NH1	B_GLU_364	OE2	3.062
2VC2	B_ARG_404	NH2	B_GLU_364	OE2	3.029
2VC2	B_LYS_412	NZ	B_GLU_365	OE1	2.695
2VC2	B_LYS_412	NZ	B_GLU_365	OE2	3.221
2VC2	H_LYS_38	NZ	H_ASP_90	OD1	3.582
2VC2	H_ARG_40	NH2	H_GLU_46	OE1	3.291
2VC2	H_ARG_40	NH2	H_GLU_46	OE2	3.920
2VC2	H_LYS_67	NZ	H_ASP_90	OD2	2.912
2VC2	H_LYS_214	NZ	L_GLU_123	OE2	3.240
2VC2	H_LYS_215	NZ	H_GLU_217	OE1	3.925

2VC2	L_HIS_24	ND1	L_ASP_70	OD1	2.720
2VC2	L_HIS_24	ND1	L_ASP_70	OD2	3.328
2VC2	L_LYS_39	NZ	L_GLU_81	OE2	3.318
2VC2	L_ARG_61	NH2	L_ASP_82	OD1	3.251
2VC2	L_ARG_61	NH2	L_ASP_82	OD2	3.737
2VC2	L_LYS_103	NZ	L_ASP_85	OD1	2.978
2VC2	L_LYS_103	NZ	L_ASP_85	OD2	2.787
2VC2	L_LYS_149	NZ	L_GLU_195	OE1	2.774
2VC2	L_LYS_149	NZ	L_GLU_195	OE2	3.388
2VC2	L_ARG_155	NH1	L_GLU_185	OE1	3.167
2VC2	L_ARG_155	NH1	L_GLU_185	OE2	3.736
2VC2	L_ARG_155	NH2	L_GLU_185	OE2	3.256
2VC2	L_HIS_189	ND1	L_ASP_151	OD1	2.726
2VC2	L_LYS_199	NZ	L_ASP_110	OD2	3.011

Table 329: 2VC2-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2VDK	A_HIS_30	ND1	A_GLU_136	OE1	3.867
2VDK	A_ARG_77	NH1	H_ASP_102	OD1	3.535
2VDK	A_ARG_77	NH1	H_ASP_102	OD2	3.168
2VDK	A_ARG_77	NH2	H_ASP_102	OD1	2.738
2VDK	A_ARG_77	NH2	H_ASP_102	OD2	3.673
2VDK	A_LYS_88	NZ	A_ASP_71	OD1	3.934
2VDK	A_LYS_88	NZ	A_GLU_75	OE2	3.775
2VDK	A_ARG_153	NH1	A_GLU_157	OE1	3.920
2VDK	A_ARG_153	NH1	A_GLU_157	OE2	3.540
2VDK	A_ARG_153	NH2	A_GLU_120	OE1	3.575
2VDK	A_ARG_153	NH2	A_GLU_120	OE2	3.437
2VDK	A_ARG_165	NH1	A_GLU_123	OE1	3.551
2VDK	A_ARG_165	NH1	A_GLU_123	OE2	3.025
2VDK	A_ARG_165	NH2	A_ASP_163	OD1	2.867
2VDK	A_ARG_165	NH2	A_ASP_163	OD2	3.841
2VDK	A_ARG_279	NH2	A_GLU_268	OE2	3.830
2VDK	A_ARG_317	NH2	A_GLU_315	OE1	3.703
2VDK	A_ARG_327	NH1	A_GLU_283	OE1	2.969
2VDK	A_ARG_327	NH1	A_GLU_283	OE2	3.151
2VDK	A_ARG_422	NH1	A_ASP_24	OD1	2.982
2VDK	A_ARG_422	NH1	A_ASP_24	OD2	3.550
2VDK	B_ARG_62	NH2	B_GLU_60	OE2	3.869
2VDK	B_ARG_67	NH1	B_GLU_65	OE1	3.128
2VDK	B_LYS_72	NZ	B_ASP_109	OD1	2.883
2VDK	B_LYS_72	NZ	B_ASP_109	OD2	3.231
2VDK	B_ARG_87	NH2	B_GLU_65	OE2	3.747
2VDK	B_ARG_105	NH1	B_ASP_71	OD1	3.501
2VDK	B_LYS_159	NZ	B_ASP_224	OD1	3.871
2VDK	B_LYS_159	NZ	B_ASP_224	OD2	2.724
2VDK	B_LYS_209	NZ	B_GLU_206	OE2	3.427
2VDK	B_ARG_214	NH1	B_ASP_179	OD1	2.883
2VDK	B_ARG_214	NH1	B_ASP_179	OD2	3.837
2VDK	B_ARG_214	NH2	B_ASP_179	OD1	3.373
2VDK	B_ARG_214	NH2	B_ASP_179	OD2	3.883
2VDK	B_ARG_216	NH2	A_GLU_123	OE2	3.072
2VDK	B_ARG_239	NH2	B_ASP_113	OD2	2.945
2VDK	B_HIS_244	NE2	B_ASP_113	OD1	3.799
2VDK	B_LYS_253	NZ	A_ASP_232	OD2	2.921
2VDK	B_HIS_255	ND1	B_ASP_259	OD2	2.885
2VDK	B_HIS_255	NE2	B_ASP_158	OD2	3.290
2VDK	B_HIS_255	NE2	B_ASP_217	OD1	3.718
2VDK	B_HIS_255	NE2	B_ASP_217	OD2	2.719
2VDK	B_HIS_274	NE2	B_ASP_270	OD1	3.028
2VDK	B_HIS_274	NE2	B_ASP_270	OD2	2.677
2VDK	B_LYS_298	NZ	B_GLU_297	OE2	3.464
2VDK	B_LYS_302	NZ	B_ASP_233	OD1	3.247
2VDK	B_LYS_302	NZ	B_ASP_233	OD2	2.825
2VDK	B_LYS_354	NZ	B_GLU_356	OE1	2.748
2VDK	B_LYS_354	NZ	B_GLU_356	OE2	3.777
2VDK	B_ARG_360	NH2	B_GLU_358	OE1	3.701
2VDK	B_ARG_360	NH2	B_GLU_358	OE2	3.427
2VDK	B_ARG_404	NH1	B_GLU_364	OE2	3.192
2VDK	B_ARG_404	NH2	B_GLU_364	OE2	3.127
2VDK	B_LYS_412	NZ	B_GLU_365	OE1	2.671
2VDK	B_LYS_412	NZ	B_GLU_365	OE2	3.186
2VDK	H_LYS_38	NZ	H_GLU_46	OE1	3.930
2VDK	H_ARG_40	NH2	H_GLU_46	OE1	3.206

2VDK	H_ARG_40	NH2	H_GLU_46	OE2	3.861
2VDK	H_LYS_67	NZ	H_ASP_90	OD1	3.807
2VDK	H_LYS_67	NZ	H_ASP_90	OD2	2.831
2VDK	H_LYS_214	NZ	L_GLU_123	OE2	3.461
2VDK	H_LYS_215	NZ	H_GLU_217	OE1	3.919
2VDK	L_HIS_24	ND1	L_ASP_70	OD1	2.714
2VDK	L_HIS_24	ND1	L_ASP_70	OD2	3.907
2VDK	L_LYS_39	NZ	L_GLU_81	OE2	3.076
2VDK	L_ARG_61	NH2	L_ASP_82	OD1	3.150
2VDK	L_ARG_61	NH2	L_ASP_82	OD2	3.695
2VDK	L_LYS_103	NZ	L_ASP_85	OD1	3.316
2VDK	L_LYS_103	NZ	L_ASP_85	OD2	3.639
2VDK	L_LYS_147	NZ	L_GLU_154	OE1	3.768
2VDK	L_LYS_147	NZ	L_GLU_154	OE2	3.469
2VDK	L_LYS_149	NZ	L_GLU_195	OE1	3.051
2VDK	L_LYS_149	NZ	L_GLU_195	OE2	3.550
2VDK	L_ARG_155	NH1	L_GLU_185	OE1	3.070
2VDK	L_ARG_155	NH1	L_GLU_185	OE2	3.757
2VDK	L_ARG_155	NH2	L_GLU_185	OE1	3.874
2VDK	L_ARG_155	NH2	L_GLU_185	OE2	3.166
2VDK	L_HIS_189	ND1	L_ASP_151	OD1	2.842
2VDK	L_LYS_199	NZ	L_ASP_110	OD2	3.918

Table 330: 2VDK-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2VDL	A_HIS_30	ND1	A_GLU_136	OE1	3.983
2VDL	A_ARG_77	NH1	H_ASP_102	OD1	3.566
2VDL	A_ARG_77	NH1	H_ASP_102	OD2	3.106
2VDL	A_ARG_77	NH2	H_ASP_102	OD1	2.722
2VDL	A_ARG_77	NH2	H_ASP_102	OD2	3.538
2VDL	A_LYS_88	NZ	A_ASP_71	OD2	3.901
2VDL	A_LYS_88	NZ	A_GLU_75	OE2	3.727
2VDL	A_ARG_153	NH2	A_GLU_120	OE1	3.211
2VDL	A_ARG_153	NH2	A_GLU_120	OE2	3.450
2VDL	A_ARG_165	NH1	A_GLU_123	OE1	3.959
2VDL	A_ARG_165	NH1	A_GLU_123	OE2	2.984
2VDL	A_ARG_165	NH2	A_ASP_163	OD1	2.925
2VDL	A_ARG_165	NH2	A_ASP_163	OD2	3.806
2VDL	A_ARG_279	NH2	A_GLU_268	OE2	3.603
2VDL	A_ARG_317	NH2	A_GLU_315	OE1	3.612
2VDL	A_ARG_327	NH1	A_GLU_283	OE1	2.900
2VDL	A_ARG_327	NH1	A_GLU_283	OE2	3.367
2VDL	A_ARG_422	NH1	A_ASP_24	OD1	2.923
2VDL	A_ARG_422	NH1	A_ASP_24	OD2	3.362
2VDL	B_ARG_62	NH2	B_GLU_60	OE2	3.680
2VDL	B_ARG_67	NH1	B_GLU_65	OE1	3.332
2VDL	B_LYS_72	NZ	B_ASP_109	OD1	2.951
2VDL	B_LYS_72	NZ	B_ASP_109	OD2	3.006
2VDL	B_ARG_105	NH1	B_ASP_71	OD1	3.378
2VDL	B_LYS_159	NZ	B_ASP_224	OD1	3.910
2VDL	B_LYS_159	NZ	B_ASP_224	OD2	2.697
2VDL	B_ARG_214	NH1	B_ASP_179	OD1	3.402
2VDL	B_ARG_214	NH1	B_ASP_179	OD2	3.426
2VDL	B_ARG_214	NH2	B_ASP_179	OD1	3.763
2VDL	B_ARG_214	NH2	B_ASP_179	OD2	3.522
2VDL	B_ARG_216	NH2	A_GLU_123	OE2	3.160
2VDL	B_ARG_239	NH2	B_ASP_113	OD2	2.965
2VDL	B_HIS_244	NE2	B_ASP_113	OD1	3.758
2VDL	B_LYS_253	NZ	A_ASP_232	OD2	2.886
2VDL	B_HIS_255	ND1	B_ASP_259	OD2	2.838
2VDL	B_HIS_255	NE2	B_ASP_158	OD2	3.301
2VDL	B_HIS_255	NE2	B_ASP_217	OD1	3.748
2VDL	B_HIS_255	NE2	B_ASP_217	OD2	2.696
2VDL	B_HIS_274	NE2	B_ASP_270	OD1	3.004
2VDL	B_HIS_274	NE2	B_ASP_270	OD2	2.721
2VDL	B_LYS_298	NZ	B_GLU_297	OE2	3.472
2VDL	B_LYS_302	NZ	B_ASP_233	OD1	3.054
2VDL	B_LYS_302	NZ	B_ASP_233	OD2	3.066
2VDL	B_LYS_354	NZ	B_GLU_356	OE1	2.717
2VDL	B_ARG_360	NH2	B_GLU_358	OE1	3.910
2VDL	B_ARG_360	NH2	B_GLU_358	OE2	3.469
2VDL	B_ARG_404	NH1	B_GLU_364	OE2	3.049
2VDL	B_ARG_404	NH2	B_GLU_364	OE2	3.073
2VDL	B_LYS_417	NZ	B_GLU_358	OE2	3.933
2VDL	H_ARG_40	NH2	H_GLU_46	OE1	3.013
2VDL	H_ARG_40	NH2	H_GLU_46	OE2	3.976
2VDL	H_LYS_59	NZ	A_GLU_117	OE2	3.964
2VDL	H_LYS_67	NZ	H_ASP_90	OD1	3.729
2VDL	H_LYS_67	NZ	H_ASP_90	OD2	2.693
2VDL	H_LYS_214	NZ	L_GLU_123	OE2	3.400
2VDL	L_HIS_24	ND1	L_ASP_70	OD1	2.670
2VDL	L_HIS_24	ND1	L_ASP_70	OD2	3.843

2VDL	L_ARG_61	NH2	L_ASP_82	OD1	3.133
2VDL	L_ARG_61	NH2	L_ASP_82	OD2	3.618
2VDL	L_LYS_103	NZ	L_ASP_85	OD1	3.222
2VDL	L_LYS_103	NZ	L_ASP_85	OD2	3.662
2VDL	L_LYS_147	NZ	L_GLU_154	OE1	3.870
2VDL	L_LYS_149	NZ	L_GLU_195	OE1	3.028
2VDL	L_LYS_149	NZ	L_GLU_195	OE2	3.950
2VDL	L_ARG_155	NH1	L_GLU_185	OE1	3.118
2VDL	L_ARG_155	NH1	L_GLU_185	OE2	3.879
2VDL	L_ARG_155	NH2	L_GLU_185	OE1	3.756
2VDL	L_ARG_155	NH2	L_GLU_185	OE2	3.072
2VDL	L_HIS_189	ND1	L_ASP_151	OD1	2.876
2VDL	L_LYS_199	NZ	L_ASP_110	OD2	3.382

Table 331: 2VDL-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2VDM	A_HIS_30	ND1	A_GLU_136	OE1	3.623
2VDM	A_ARG_77	NH1	H_ASP_102	OD1	3.512
2VDM	A_ARG_77	NH1	H_ASP_102	OD2	3.196
2VDM	A_ARG_77	NH2	H_ASP_102	OD1	2.762
2VDM	A_ARG_77	NH2	H_ASP_102	OD2	3.757
2VDM	A_LYS_88	NZ	A_ASP_71	OD1	3.506
2VDM	A_LYS_88	NZ	A_GLU_75	OE2	3.717
2VDM	A_ARG_153	NH1	A_GLU_157	OE2	3.526
2VDM	A_ARG_153	NH2	A_GLU_120	OE1	3.629
2VDM	A_ARG_153	NH2	A_GLU_120	OE2	3.472
2VDM	A_ARG_165	NH1	A_GLU_123	OE1	3.954
2VDM	A_ARG_165	NH1	A_GLU_123	OE2	2.915
2VDM	A_ARG_165	NH2	A_ASP_163	OD1	2.984
2VDM	A_ARG_279	NH2	A_GLU_268	OE2	3.711
2VDM	A_ARG_317	NH2	A_GLU_315	OE1	3.553
2VDM	A_ARG_327	NH1	A_GLU_283	OE1	3.196
2VDM	A_ARG_327	NH1	A_GLU_283	OE2	3.335
2VDM	A_ARG_422	NH1	A_ASP_24	OD1	2.877
2VDM	A_ARG_422	NH1	A_ASP_24	OD2	3.314
2VDM	B_ARG_62	NH2	B_GLU_60	OE2	3.866
2VDM	B_LYS_72	NZ	B_ASP_109	OD1	2.865
2VDM	B_LYS_72	NZ	B_ASP_109	OD2	3.109
2VDM	B_ARG_91	NH2	B_GLU_60	OE1	3.150
2VDM	B_ARG_105	NH1	B_ASP_71	OD1	3.646
2VDM	B_LYS_159	NZ	B_ASP_224	OD1	3.821
2VDM	B_LYS_159	NZ	B_ASP_224	OD2	2.737
2VDM	B_LYS_209	NZ	B_GLU_206	OE2	3.484
2VDM	B_ARG_214	NH1	B_ASP_179	OD2	3.120
2VDM	B_ARG_216	NH2	A_GLU_123	OE2	2.982
2VDM	B_ARG_239	NH2	B_ASP_113	OD2	3.117
2VDM	B_HIS_244	NE2	B_ASP_113	OD1	3.810
2VDM	B_LYS_253	NZ	A_ASP_232	OD2	3.306
2VDM	B_HIS_255	ND1	B_ASP_259	OD2	2.883
2VDM	B_HIS_255	NE2	B_ASP_158	OD2	3.162
2VDM	B_HIS_255	NE2	B_ASP_217	OD1	3.723
2VDM	B_HIS_255	NE2	B_ASP_217	OD2	2.768
2VDM	B_HIS_274	NE2	B_ASP_270	OD1	3.033
2VDM	B_HIS_274	NE2	B_ASP_270	OD2	2.759
2VDM	B_HIS_280	ND1	B_ASP_278	OD2	3.990
2VDM	B_LYS_298	NZ	B_GLU_297	OE2	3.783
2VDM	B_LYS_302	NZ	B_ASP_233	OD1	3.512
2VDM	B_LYS_302	NZ	B_ASP_233	OD2	3.089
2VDM	B_LYS_354	NZ	B_GLU_356	OE1	2.934
2VDM	B_LYS_354	NZ	B_GLU_356	OE2	3.448
2VDM	B_ARG_360	NH2	B_GLU_358	OE2	3.602
2VDM	B_LYS_390	NZ	B_ASP_393	OD1	3.190
2VDM	B_ARG_404	NH1	B_GLU_364	OE2	3.379
2VDM	B_ARG_404	NH2	B_GLU_364	OE2	3.556
2VDM	B_LYS_412	NZ	B_GLU_365	OE1	2.778
2VDM	B_LYS_412	NZ	B_GLU_365	OE2	3.744
2VDM	B_LYS_417	NZ	B_GLU_358	OE2	3.687
2VDM	H_ARG_40	NH2	H_GLU_46	OE1	3.139
2VDM	H_LYS_67	NZ	H_ASP_90	OD1	3.953
2VDM	H_LYS_67	NZ	H_ASP_90	OD2	2.810
2VDM	H_LYS_214	NZ	L_GLU_123	OE2	3.334
2VDM	H_LYS_215	NZ	H_GLU_217	OE1	3.652
2VDM	L_HIS_24	ND1	L_ASP_70	OD1	2.661

2VDM	L_HIS_24	ND1	L_ASP_70	OD2	3.812
2VDM	L_LYS_39	NZ	L_GLU_81	OE2	3.325
2VDM	L_ARG_61	NH2	L_ASP_79	OD1	3.812
2VDM	L_ARG_61	NH2	L_ASP_82	OD1	3.292
2VDM	L_ARG_61	NH2	L_ASP_82	OD2	3.719
2VDM	L_LYS_103	NZ	L_ASP_85	OD1	2.836
2VDM	L_LYS_103	NZ	L_ASP_85	OD2	3.351
2VDM	L_LYS_147	NZ	L_GLU_154	OE1	3.824
2VDM	L_LYS_147	NZ	L_GLU_154	OE2	3.630
2VDM	L_LYS_149	NZ	L_GLU_195	OE1	3.194
2VDM	L_LYS_149	NZ	L_GLU_195	OE2	3.563
2VDM	L_ARG_155	NH1	L_GLU_185	OE1	3.186
2VDM	L_ARG_155	NH2	L_GLU_185	OE1	3.687
2VDM	L_ARG_155	NH2	L_GLU_185	OE2	3.288
2VDM	L_HIS_189	ND1	L_ASP_151	OD1	2.728
2VDM	L_LYS_199	NZ	L_ASP_110	OD2	3.757

Table 332: 2VDM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2VDN	A_HIS_30	ND1	A_GLU_136	OE1	3.948
2VDN	A_ARG_77	NH1	H_ASP_102	OD1	3.491
2VDN	A_ARG_77	NH1	H_ASP_102	OD2	3.169
2VDN	A_ARG_77	NH2	H_ASP_102	OD1	2.808
2VDN	A_ARG_77	NH2	H_ASP_102	OD2	3.762
2VDN	A_LYS_88	NZ	A_ASP_71	OD1	3.146
2VDN	A_LYS_88	NZ	A_GLU_75	OE2	3.755
2VDN	A_ARG_153	NH1	A_GLU_157	OE2	3.732
2VDN	A_ARG_153	NH2	A_GLU_120	OE1	3.385
2VDN	A_ARG_153	NH2	A_GLU_120	OE2	3.434
2VDN	A_ARG_165	NH1	A_GLU_123	OE1	3.564
2VDN	A_ARG_165	NH1	A_GLU_123	OE2	3.322
2VDN	A_ARG_165	NH2	A_ASP_163	OD1	2.897
2VDN	A_ARG_165	NH2	A_ASP_163	OD2	3.963
2VDN	A_ARG_317	NH2	A_GLU_315	OE1	3.869
2VDN	A_ARG_327	NH1	A_GLU_283	OE1	3.115
2VDN	A_ARG_327	NH1	A_GLU_283	OE2	3.543
2VDN	A_ARG_422	NH1	A_ASP_24	OD1	2.918
2VDN	A_ARG_422	NH1	A_ASP_24	OD2	3.024
2VDN	A_ARG_422	NH2	A_ASP_24	OD2	3.873
2VDN	B_ARG_62	NH2	B_GLU_60	OE1	3.892
2VDN	B_ARG_62	NH2	B_GLU_60	OE2	3.874
2VDN	B_ARG_67	NH1	B_GLU_65	OE1	3.311
2VDN	B_LYS_72	NZ	B_ASP_109	OD1	2.643
2VDN	B_LYS_72	NZ	B_ASP_109	OD2	3.617
2VDN	B_ARG_87	NH2	B_GLU_65	OE2	3.986
2VDN	B_ARG_91	NH1	B_GLU_60	OE2	3.487
2VDN	B_ARG_91	NH2	B_GLU_60	OE2	3.817
2VDN	B_ARG_105	NH1	B_ASP_71	OD1	3.631
2VDN	B_LYS_159	NZ	B_ASP_224	OD1	3.745
2VDN	B_LYS_159	NZ	B_ASP_224	OD2	2.600
2VDN	B_LYS_209	NZ	B_GLU_206	OE2	3.458
2VDN	B_ARG_214	NH1	B_ASP_179	OD2	2.971
2VDN	B_ARG_214	NH2	B_ASP_179	OD2	3.917
2VDN	B_ARG_216	NH2	A_GLU_123	OE2	2.995
2VDN	B_ARG_239	NH2	B_ASP_113	OD2	3.167
2VDN	B_HIS_244	NE2	B_ASP_113	OD1	3.751
2VDN	B_HIS_255	ND1	B_ASP_259	OD2	2.831
2VDN	B_HIS_255	NE2	B_ASP_158	OD2	3.236
2VDN	B_HIS_255	NE2	B_ASP_217	OD1	3.761
2VDN	B_HIS_255	NE2	B_ASP_217	OD2	2.725
2VDN	B_HIS_274	NE2	B_ASP_270	OD1	3.136
2VDN	B_HIS_274	NE2	B_ASP_270	OD2	2.767
2VDN	B_HIS_280	ND1	B_ASP_278	OD2	3.961
2VDN	B_LYS_302	NZ	B_ASP_233	OD1	3.616
2VDN	B_LYS_302	NZ	B_ASP_233	OD2	3.020
2VDN	B_LYS_354	NZ	B_GLU_356	OE1	2.617
2VDN	B_ARG_360	NH2	B_GLU_358	OE2	3.301
2VDN	B_LYS_390	NZ	B_ASP_393	OD1	3.452
2VDN	B_ARG_404	NH1	B_GLU_364	OE2	3.371
2VDN	B_ARG_404	NH2	B_GLU_364	OE2	2.851
2VDN	B_LYS_412	NZ	B_GLU_365	OE1	2.766
2VDN	B_LYS_412	NZ	B_GLU_365	OE2	3.273
2VDN	B_LYS_412	NZ	B_GLU_409	OE2	3.840
2VDN	B_LYS_417	NZ	B_GLU_358	OE2	3.820
2VDN	H_ARG_40	NH2	H_GLU_46	OE1	3.092
2VDN	H_LYS_67	NZ	H_ASP_90	OD1	3.750

2VDN	H_LYS_67	NZ	H_ASP_90	OD2	2.688
2VDN	H_LYS_214	NZ	L_GLU_123	OE2	3.685
2VDN	H_LYS_215	NZ	H_GLU_217	OE1	3.744
2VDN	L_HIS_24	ND1	L_ASP_70	OD1	2.783
2VDN	L_LYS_39	NZ	L_GLU_81	OE2	3.138
2VDN	L_ARG_61	NH2	L_ASP_82	OD1	3.159
2VDN	L_ARG_61	NH2	L_ASP_82	OD2	3.820
2VDN	L_LYS_103	NZ	L_ASP_85	OD1	3.058
2VDN	L_LYS_103	NZ	L_ASP_85	OD2	3.355
2VDN	L_LYS_147	NZ	L_GLU_154	OE1	3.309
2VDN	L_LYS_147	NZ	L_GLU_154	OE2	3.600
2VDN	L_LYS_149	NZ	L_GLU_195	OE1	3.164
2VDN	L_LYS_149	NZ	L_GLU_195	OE2	3.705
2VDN	L_ARG_155	NH1	L_GLU_185	OE1	3.044
2VDN	L_ARG_155	NH1	L_GLU_185	OE2	3.873
2VDN	L_ARG_155	NH2	L_GLU_185	OE1	3.640
2VDN	L_ARG_155	NH2	L_GLU_185	OE2	3.207
2VDN	L_LYS_199	NZ	L_ASP_110	OD2	3.394

Table 333: 2VDN-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2VDO	A_HIS_30	ND1	A_GLU_136	OE1	3.920
2VDO	A_ARG_77	NH1	H_ASP_102	OD1	3.703
2VDO	A_ARG_77	NH1	H_ASP_102	OD2	3.042
2VDO	A_ARG_77	NH2	H_ASP_102	OD1	2.789
2VDO	A_ARG_77	NH2	H_ASP_102	OD2	3.375
2VDO	A_LYS_88	NZ	A_GLU_75	OE2	3.810
2VDO	A_ARG_153	NH1	A_GLU_157	OE2	3.784
2VDO	A_ARG_153	NH2	A_GLU_120	OE1	3.533
2VDO	A_ARG_153	NH2	A_GLU_120	OE2	3.754
2VDO	A_ARG_165	NH1	A_GLU_123	OE1	3.613
2VDO	A_ARG_165	NH1	A_GLU_123	OE2	3.354
2VDO	A_ARG_165	NH2	A_ASP_163	OD1	2.853
2VDO	A_ARG_165	NH2	A_ASP_163	OD2	3.749
2VDO	A_ARG_279	NH2	A_GLU_268	OE2	3.621
2VDO	A_ARG_303	NH2	A_ASP_301	OD2	3.328
2VDO	A_ARG_317	NH2	A_GLU_315	OE1	3.691
2VDO	A_ARG_327	NH1	A_GLU_283	OE1	3.064
2VDO	A_ARG_327	NH1	A_GLU_283	OE2	3.315
2VDO	A_ARG_422	NH1	A_ASP_24	OD1	3.045
2VDO	A_ARG_422	NH1	A_ASP_24	OD2	3.220
2VDO	A_ARG_422	NH2	A_ASP_24	OD2	3.964
2VDO	B_LYS_72	NZ	B_ASP_109	OD1	2.524
2VDO	B_LYS_72	NZ	B_ASP_109	OD2	3.663
2VDO	B_ARG_91	NH1	B_GLU_60	OE1	3.543
2VDO	B_ARG_105	NH1	B_ASP_71	OD1	3.285
2VDO	B_LYS_159	NZ	B_ASP_224	OD1	3.842
2VDO	B_LYS_159	NZ	B_ASP_224	OD2	2.647
2VDO	B_LYS_209	NZ	B_GLU_206	OE2	3.221
2VDO	B_ARG_214	NH1	B_ASP_179	OD1	3.754
2VDO	B_ARG_214	NH1	B_ASP_179	OD2	2.724
2VDO	B_ARG_216	NH2	A_GLU_123	OE2	3.092
2VDO	B_ARG_239	NH2	B_ASP_113	OD2	2.947
2VDO	B_HIS_244	NE2	B_ASP_113	OD1	3.778
2VDO	B_LYS_253	NZ	A_ASP_232	OD2	2.836
2VDO	B_HIS_255	ND1	B_ASP_259	OD2	2.644
2VDO	B_HIS_255	NE2	B_ASP_158	OD2	3.337
2VDO	B_HIS_255	NE2	B_ASP_217	OD1	3.680
2VDO	B_HIS_255	NE2	B_ASP_217	OD2	2.699
2VDO	B_HIS_274	NE2	B_ASP_270	OD1	3.105
2VDO	B_HIS_274	NE2	B_ASP_270	OD2	2.754
2VDO	B_HIS_280	ND1	B_ASP_278	OD2	3.796
2VDO	B_LYS_298	NZ	B_GLU_297	OE2	3.249
2VDO	B_LYS_302	NZ	B_ASP_233	OD1	3.475
2VDO	B_LYS_302	NZ	B_ASP_233	OD2	3.319
2VDO	B_LYS_354	NZ	B_GLU_356	OE1	2.694
2VDO	B_LYS_390	NZ	B_ASP_393	OD1	2.830
2VDO	B_LYS_390	NZ	B_ASP_393	OD2	3.993
2VDO	B_ARG_404	NH1	B_GLU_364	OE2	3.382
2VDO	B_ARG_404	NH2	B_GLU_364	OE2	2.912
2VDO	C_LYS_406	NZ	A_ASP_224	OD1	2.673
2VDO	C_LYS_406	NZ	A_ASP_224	OD2	3.263
2VDO	H_ARG_40	NH2	H_GLU_46	OE1	3.274
2VDO	H_LYS_67	NZ	H_ASP_90	OD1	3.624
2VDO	H_LYS_67	NZ	H_ASP_90	OD2	2.582
2VDO	L_HIS_24	ND1	L_ASP_70	OD1	2.820
2VDO	L_HIS_24	ND1	L_ASP_70	OD2	3.898
2VDO	L_LYS_39	NZ	L_GLU_81	OE1	3.127

2VDO	L_ARG_61	NH2	L_ASP_82	OD1	3.036
2VDO	L_ARG_61	NH2	L_ASP_82	OD2	3.553
2VDO	L_LYS_103	NZ	L_ASP_85	OD1	3.186
2VDO	L_LYS_103	NZ	L_ASP_85	OD2	3.792
2VDO	L_LYS_147	NZ	L_GLU_154	OE1	3.276
2VDO	L_LYS_147	NZ	L_GLU_154	OE2	3.435
2VDO	L_LYS_149	NZ	L_GLU_195	OE1	3.199
2VDO	L_LYS_149	NZ	L_GLU_195	OE2	3.780
2VDO	L_HIS_189	ND1	L_ASP_151	OD1	2.775
2VDO	L_LYS_199	NZ	L_ASP_110	OD2	3.339

Table 334: 2VDO-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2VDP	A_HIS_30	ND1	A_GLU_136	OE1	3.660
2VDP	A_ARG_77	NH1	H_ASP_102	OD1	3.519
2VDP	A_ARG_77	NH1	H_ASP_102	OD2	3.089
2VDP	A_ARG_77	NH2	H_ASP_102	OD1	2.733
2VDP	A_ARG_77	NH2	H_ASP_102	OD2	3.585
2VDP	A_LYS_88	NZ	A_ASP_71	OD1	3.039
2VDP	A_LYS_88	NZ	A_GLU_75	OE2	3.920
2VDP	A_ARG_153	NH1	A_GLU_157	OE1	3.962
2VDP	A_ARG_153	NH1	A_GLU_157	OE2	3.572
2VDP	A_ARG_153	NH2	A_GLU_120	OE1	3.448
2VDP	A_ARG_153	NH2	A_GLU_120	OE2	3.842
2VDP	A_ARG_165	NH1	A_GLU_123	OE2	2.955
2VDP	A_ARG_165	NH2	A_ASP_163	OD1	2.890
2VDP	A_ARG_165	NH2	A_ASP_163	OD2	3.894
2VDP	A_ARG_279	NH2	A_GLU_268	OE2	3.568
2VDP	A_ARG_303	NH2	A_ASP_301	OD2	3.133
2VDP	A_ARG_317	NH2	A_GLU_315	OE1	3.662
2VDP	A_ARG_327	NH1	A_GLU_283	OE1	3.008
2VDP	A_ARG_327	NH1	A_GLU_283	OE2	3.186
2VDP	A_ARG_422	NH1	A_ASP_24	OD1	3.204
2VDP	A_ARG_422	NH1	A_ASP_24	OD2	3.337
2VDP	B_LYS_72	NZ	B_ASP_109	OD1	2.827
2VDP	B_LYS_72	NZ	B_ASP_109	OD2	3.031
2VDP	B_ARG_105	NH1	B_ASP_71	OD1	3.982
2VDP	B_LYS_159	NZ	B_ASP_224	OD1	3.737
2VDP	B_LYS_159	NZ	B_ASP_224	OD2	2.652
2VDP	B_ARG_214	NH1	B_ASP_179	OD1	3.890
2VDP	B_ARG_214	NH1	B_ASP_179	OD2	2.793
2VDP	B_ARG_214	NH2	B_ASP_179	OD1	3.782
2VDP	B_ARG_214	NH2	B_ASP_179	OD2	3.940
2VDP	B_ARG_216	NH2	A_GLU_123	OE2	3.038
2VDP	B_ARG_239	NH2	B_ASP_113	OD2	3.143
2VDP	B_HIS_244	NE2	B_ASP_113	OD1	3.933
2VDP	B_LYS_253	NZ	A_ASP_232	OD2	2.914
2VDP	B_HIS_255	ND1	B_ASP_259	OD2	2.924
2VDP	B_HIS_255	NE2	B_ASP_158	OD2	3.261
2VDP	B_HIS_255	NE2	B_ASP_217	OD1	3.670
2VDP	B_HIS_255	NE2	B_ASP_217	OD2	2.811
2VDP	B_HIS_274	NE2	B_ASP_270	OD1	2.909
2VDP	B_HIS_274	NE2	B_ASP_270	OD2	2.812
2VDP	B_HIS_280	ND1	B_ASP_278	OD2	3.653
2VDP	B_LYS_298	NZ	B_GLU_297	OE2	3.585
2VDP	B_LYS_302	NZ	B_ASP_233	OD1	3.588
2VDP	B_LYS_302	NZ	B_ASP_233	OD2	3.086
2VDP	B_LYS_354	NZ	B_GLU_356	OE1	2.651
2VDP	B_ARG_360	NH2	B_GLU_358	OE2	3.559
2VDP	B_LYS_390	NZ	B_ASP_393	OD1	2.846
2VDP	B_LYS_412	NZ	B_GLU_365	OE1	2.691
2VDP	B_LYS_412	NZ	B_GLU_365	OE2	3.358
2VDP	C_LYS_406	NZ	A_ASP_224	OD1	2.604
2VDP	C_LYS_406	NZ	A_ASP_224	OD2	3.297
2VDP	H_ARG_40	NH2	H_GLU_46	OE1	3.121
2VDP	H_LYS_67	NZ	H_ASP_90	OD1	3.700
2VDP	H_LYS_67	NZ	H_ASP_90	OD2	2.763
2VDP	H_LYS_214	NZ	L_GLU_123	OE2	3.425
2VDP	L_HIS_24	ND1	L_ASP_70	OD1	2.731
2VDP	L_HIS_24	ND1	L_ASP_70	OD2	3.759

2VDP	L_LYS_39	NZ	L_GLU_81	OE1	3.012
2VDP	L_ARG_61	NH2	L_ASP_82	OD1	3.212
2VDP	L_ARG_61	NH2	L_ASP_82	OD2	3.647
2VDP	L_LYS_103	NZ	L_ASP_85	OD1	3.404
2VDP	L_LYS_103	NZ	L_ASP_85	OD2	3.147
2VDP	L_LYS_147	NZ	L_GLU_154	OE1	3.927
2VDP	L_LYS_147	NZ	L_GLU_154	OE2	3.984
2VDP	L_LYS_149	NZ	L_GLU_195	OE1	3.337
2VDP	L_LYS_149	NZ	L_GLU_195	OE2	3.651
2VDP	L_ARG_155	NH1	L_GLU_185	OE1	3.124
2VDP	L_ARG_155	NH1	L_GLU_185	OE2	3.854
2VDP	L_ARG_155	NH2	L_GLU_185	OE1	3.803
2VDP	L_ARG_155	NH2	L_GLU_185	OE2	3.129
2VDP	L_HIS_189	ND1	L_ASP_151	OD1	3.064
2VDP	L_LYS_199	NZ	L_ASP_110	OD2	3.415

Table 335: 2VDP-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2VDQ	A_ARG_77	NH1	H_ASP_102	OD1	3.603
2VDQ	A_ARG_77	NH1	H_ASP_102	OD2	3.057
2VDQ	A_ARG_77	NH2	H_ASP_102	OD1	2.765
2VDQ	A_ARG_77	NH2	H_ASP_102	OD2	3.398
2VDQ	A_LYS_88	NZ	A_GLU_75	OE2	3.857
2VDQ	A_ARG_153	NH1	A_GLU_157	OE2	3.540
2VDQ	A_ARG_153	NH2	A_GLU_120	OE1	3.469
2VDQ	A_ARG_153	NH2	A_GLU_120	OE2	3.910
2VDQ	A_ARG_165	NH1	A_GLU_123	OE1	3.775
2VDQ	A_ARG_165	NH1	A_GLU_123	OE2	3.560
2VDQ	A_ARG_165	NH2	A_ASP_163	OD1	2.874
2VDQ	A_ARG_165	NH2	A_ASP_163	OD2	3.776
2VDQ	A_ARG_279	NH2	A_GLU_268	OE2	3.474
2VDQ	A_ARG_317	NH2	A_GLU_315	OE1	3.631
2VDQ	A_ARG_327	NH1	A_GLU_283	OE1	3.069
2VDQ	A_ARG_327	NH1	A_GLU_283	OE2	3.317
2VDQ	A_ARG_422	NH1	A_ASP_24	OD1	2.959
2VDQ	A_ARG_422	NH1	A_ASP_24	OD2	3.217
2VDQ	B_ARG_67	NH1	B_GLU_65	OE1	3.626
2VDQ	B_LYS_72	NZ	B_ASP_109	OD1	2.465
2VDQ	B_LYS_72	NZ	B_ASP_109	OD2	3.694
2VDQ	B_ARG_91	NH1	B_GLU_60	OE1	3.580
2VDQ	B_ARG_91	NH2	B_GLU_60	OE1	2.967
2VDQ	B_ARG_105	NH1	B_ASP_71	OD1	3.573
2VDQ	B_LYS_159	NZ	B_ASP_224	OD1	3.868
2VDQ	B_LYS_159	NZ	B_ASP_224	OD2	2.786
2VDQ	B_LYS_209	NZ	B_GLU_206	OE2	3.302
2VDQ	B_ARG_214	NH1	B_ASP_179	OD1	3.942
2VDQ	B_ARG_214	NH1	B_ASP_179	OD2	2.723
2VDQ	B_ARG_216	NH2	A_GLU_123	OE2	2.900
2VDQ	B_ARG_239	NH2	B_ASP_113	OD2	2.900
2VDQ	B_HIS_244	NE2	B_ASP_113	OD1	3.769
2VDQ	B_LYS_253	NZ	A_ASP_232	OD2	3.522
2VDQ	B_HIS_255	ND1	B_ASP_259	OD2	2.795
2VDQ	B_HIS_255	NE2	B_ASP_158	OD2	3.253
2VDQ	B_HIS_255	NE2	B_ASP_217	OD1	3.618
2VDQ	B_HIS_255	NE2	B_ASP_217	OD2	2.719
2VDQ	B_HIS_274	NE2	B_ASP_270	OD1	3.015
2VDQ	B_HIS_274	NE2	B_ASP_270	OD2	2.786
2VDQ	B_HIS_280	ND1	B_ASP_278	OD2	3.936
2VDQ	B_LYS_298	NZ	B_GLU_297	OE2	3.339
2VDQ	B_LYS_302	NZ	B_ASP_233	OD1	3.182
2VDQ	B_LYS_302	NZ	B_ASP_233	OD2	3.177
2VDQ	B_LYS_354	NZ	B_GLU_356	OE1	2.632
2VDQ	B_ARG_360	NH2	B_GLU_358	OE2	3.805
2VDQ	B_LYS_390	NZ	B_ASP_393	OD1	2.810
2VDQ	B_LYS_390	NZ	B_ASP_393	OD2	3.977
2VDQ	B_ARG_404	NH1	B_GLU_364	OE2	3.193
2VDQ	B_ARG_404	NH2	B_GLU_364	OE2	3.023
2VDQ	B_ARG_447	NH2	B_GLU_442	OE1	3.552
2VDQ	C_ARG_408	NH1	A_ASP_224	OD1	3.059
2VDQ	C_ARG_408	NH1	A_ASP_224	OD2	3.490
2VDQ	C_ARG_408	NH2	A_ASP_224	OD1	3.054
2VDQ	C_ARG_408	NH2	A_ASP_224	OD2	3.761
2VDQ	H_ARG_40	NH2	H_GLU_46	OE1	3.061
2VDQ	H_LYS_59	NZ	A_GLU_117	OE2	3.921
2VDQ	H_LYS_67	NZ	H_ASP_90	OD1	3.616

2VDQ	H_LYS_67	NZ	H_ASP_90	OD2	2.592
2VDQ	H_LYS_214	NZ	L_GLU_123	OE2	3.223
2VDQ	L_HIS_24	ND1	L_ASP_70	OD1	2.751
2VDQ	L_HIS_24	ND1	L_ASP_70	OD2	3.828
2VDQ	L_LYS_39	NZ	L_GLU_81	OE2	3.151
2VDQ	L_ARG_61	NH2	L_ASP_82	OD1	2.929
2VDQ	L_ARG_61	NH2	L_ASP_82	OD2	3.560
2VDQ	L_LYS_103	NZ	L_ASP_85	OD1	3.020
2VDQ	L_LYS_103	NZ	L_ASP_85	OD2	3.466
2VDQ	L_LYS_149	NZ	L_GLU_195	OE1	3.063
2VDQ	L_LYS_149	NZ	L_GLU_195	OE2	3.588
2VDQ	L_HIS_189	ND1	L_ASP_151	OD1	2.754
2VDQ	L_LYS_199	NZ	L_ASP_110	OD2	3.557

Table 336: 2VDQ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID** **residue name** **residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2VDR	A_HIS_30	ND1	A_GLU_136	OE1	3.834
2VDR	A_ARG_77	NH1	H_ASP_102	OD1	3.703
2VDR	A_ARG_77	NH1	H_ASP_102	OD2	3.091
2VDR	A_ARG_77	NH2	H_ASP_102	OD1	2.791
2VDR	A_ARG_77	NH2	H_ASP_102	OD2	3.414
2VDR	A_LYS_88	NZ	A_GLU_75	OE2	3.555
2VDR	A_ARG_153	NH1	A_GLU_157	OE2	3.722
2VDR	A_ARG_153	NH2	A_GLU_120	OE1	3.592
2VDR	A_ARG_153	NH2	A_GLU_120	OE2	3.473
2VDR	A_ARG_165	NH1	A_GLU_123	OE1	3.684
2VDR	A_ARG_165	NH1	A_GLU_123	OE2	3.385
2VDR	A_ARG_165	NH2	A_ASP_163	OD1	2.924
2VDR	A_ARG_165	NH2	A_ASP_163	OD2	3.830
2VDR	A_ARG_279	NH2	A_GLU_268	OE2	3.601
2VDR	A_ARG_303	NH2	A_ASP_301	OD2	3.138
2VDR	A_ARG_317	NH2	A_GLU_315	OE1	3.881
2VDR	A_ARG_327	NH1	A_GLU_283	OE1	2.937
2VDR	A_ARG_327	NH1	A_GLU_283	OE2	3.446
2VDR	A_ARG_422	NH1	A_ASP_24	OD1	3.228
2VDR	A_ARG_422	NH1	A_ASP_24	OD2	3.380
2VDR	A_ARG_422	NH2	A_ASP_24	OD1	3.926
2VDR	A_ARG_422	NH2	A_ASP_24	OD2	3.754
2VDR	B_LYS_72	NZ	B_ASP_109	OD1	2.563
2VDR	B_ARG_91	NH1	B_GLU_60	OE1	3.916
2VDR	B_ARG_91	NH2	B_GLU_60	OE1	2.976
2VDR	B_ARG_105	NH1	B_ASP_71	OD1	3.494
2VDR	B_LYS_159	NZ	B_ASP_224	OD1	3.854
2VDR	B_LYS_159	NZ	B_ASP_224	OD2	2.660
2VDR	B_LYS_209	NZ	B_GLU_206	OE2	3.062
2VDR	B_ARG_214	NH1	B_ASP_179	OD2	2.701
2VDR	B_ARG_216	NH2	A_GLU_123	OE2	2.956
2VDR	B_ARG_239	NH2	B_ASP_113	OD2	2.921
2VDR	B_HIS_244	NE2	B_ASP_113	OD1	3.852
2VDR	B_LYS_253	NZ	A_ASP_232	OD2	3.191
2VDR	B_HIS_255	ND1	B_ASP_259	OD2	2.853
2VDR	B_HIS_255	NE2	B_ASP_158	OD2	3.204
2VDR	B_HIS_255	NE2	B_ASP_217	OD1	3.553
2VDR	B_HIS_255	NE2	B_ASP_217	OD2	2.706
2VDR	B_HIS_274	NE2	B_ASP_270	OD1	3.093
2VDR	B_HIS_274	NE2	B_ASP_270	OD2	2.677
2VDR	B_HIS_280	ND1	B_ASP_278	OD2	3.699
2VDR	B_LYS_298	NZ	B_GLU_297	OE2	3.371
2VDR	B_LYS_302	NZ	B_ASP_233	OD1	3.473
2VDR	B_LYS_302	NZ	B_ASP_233	OD2	2.921
2VDR	B_LYS_354	NZ	B_GLU_356	OE1	2.603
2VDR	B_ARG_360	NH2	B_GLU_358	OE2	3.500
2VDR	B_LYS_390	NZ	B_ASP_393	OD1	2.719
2VDR	B_ARG_404	NH1	B_GLU_364	OE2	3.173
2VDR	B_ARG_404	NH2	B_GLU_364	OE2	3.177
2VDR	C_ARG_408	NH1	A_ASP_224	OD1	3.062
2VDR	C_ARG_408	NH1	A_ASP_224	OD2	3.850
2VDR	C_ARG_408	NH2	A_ASP_224	OD1	3.028
2VDR	C_ARG_408	NH2	A_ASP_224	OD2	3.839
2VDR	H_ARG_40	NH2	H_GLU_46	OE1	3.176
2VDR	H_LYS_67	NZ	H_ASP_90	OD1	3.584
2VDR	H_LYS_67	NZ	H_ASP_90	OD2	2.527
2VDR	H_LYS_214	NZ	L_GLU_123	OE2	3.860

2VDR	L_HIS_24	ND1	L_ASP_70	OD1	2.825
2VDR	L_HIS_24	ND1	L_ASP_70	OD2	3.852
2VDR	L_ARG_61	NH2	L_ASP_82	OD1	2.979
2VDR	L_ARG_61	NH2	L_ASP_82	OD2	3.650
2VDR	L_LYS_103	NZ	L_ASP_85	OD1	3.110
2VDR	L_LYS_103	NZ	L_ASP_85	OD2	3.591
2VDR	L_LYS_149	NZ	L_GLU_195	OE1	2.973
2VDR	L_LYS_149	NZ	L_GLU_195	OE2	3.700
2VDR	L_ARG_155	NH1	L_GLU_185	OE1	3.211
2VDR	L_ARG_155	NH1	L_GLU_185	OE2	3.858
2VDR	L_ARG_155	NH2	L_GLU_185	OE1	3.840
2VDR	L_ARG_155	NH2	L_GLU_185	OE2	3.062
2VDR	L_HIS_189	ND1	L_ASP_151	OD1	2.610
2VDR	L_LYS_199	NZ	L_ASP_110	OD2	3.796

Table 337: 2VDR-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2VIR	A_ARG_	NH2	A_GLU_	OE2	3.607
2VIR	A_ARG_	NH2	A_ASP_	OD1	3.333
2VIR	A_ARG_	NH2	A_ASP_	OD2	3.123
2VIR	A_LYS_152	NZ	A_GLU_206	OE1	3.754
2VIR	A_HIS_191	ND1	A_ASP_154	OD2	2.799
2VIR	B_HIS_	NE2	B_ASP_	OD1	3.115
2VIR	B_ARG_	NH1	B_GLU_	OE1	2.667
2VIR	B_ARG_	NH2	B_ASP_	OD1	2.935
2VIR	B_ARG_	NH1	B_ASP_	OD1	3.962
2VIR	B_ARG_	NH2	B_ASP_	OD1	3.249
2VIR	B_ARG_	NH2	B_ASP_	OD2	2.668
2VIR	B_LYS_	NZ	B_ASP_	OD1	3.397
2VIR	B_LYS_	NZ	B_ASP_	OD2	3.134
2VIR	B_ARG_	NH2	B_ASP_	OD1	3.596
2VIR	B_ARG_	NH2	B_ASP_	OD2	2.875
2VIR	B_LYS_	NZ	A_GLU_127	OE2	3.017
2VIR	B_HIS_173	NE2	A_ASP_141	OD1	3.726
2VIR	B_HIS_173	NE2	A_ASP_141	OD2	3.076
2VIR	B_LYS_217	NZ	A_GLU_126	OE2	3.903
2VIR	C_LYS_	NZ	C_ASP_	OD1	3.597
2VIR	C_LYS_	NZ	C_ASP_	OD2	3.554
2VIR	C_HIS_	NE2	C_GLU_	OE1	3.437
2VIR	C_HIS_	NE2	C_GLU_	OE2	2.908
2VIR	C_ARG_	NH1	C_GLU_	OE2	3.901
2VIR	C_ARG_	NH2	C_GLU_	OE2	2.550
2VIR	C_HIS_	ND1	C_ASP_	OD1	2.834
2VIR	C_HIS_	NE2	C_ASP_	OD1	3.558
2VIR	C_ARG_	NH2	C_ASP_	OD1	3.792
2VIR	C_ARG_	NH2	C_ASP_	OD2	2.918
2VIR	C_LYS_	NZ	C_ASP_	OD1	2.776
2VIR	C_ARG_	NH1	C_GLU_	OE1	2.706
2VIR	C_ARG_	NH1	C_GLU_	OE2	2.891
2VIR	C_ARG_	NH2	C_GLU_	OE1	3.747
2VIR	C_ARG_	NH2	C_ASP_	OD1	2.621
2VIR	C_ARG_	NH2	C_ASP_	OD2	3.048
2VIR	C_LYS_	NZ	C_GLU_	OE2	3.095
2VIR	C_LYS_	NZ	C_ASP_	OD1	3.929
2VIR	C_ARG_	NH2	C_ASP_	OD2	3.709
2VIR	C_LYS_	NZ	C_ASP_	OD1	3.380
2VIR	C_LYS_	NZ	C_ASP_	OD2	2.593
2VIR	C_ARG_	NH1	C_GLU_	OE1	3.911
2VIR	C_ARG_	NH2	C_GLU_	OE1	3.735
2VIR	C_LYS_	NZ	C_ASP_	OD1	3.157

Table 338: 2VIR-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2VIS	A_ARG_	NH2	A_GLU_	OE2	3.528
2VIS	A_ARG_	NH2	A_ASP_	OD1	3.225
2VIS	A_ARG_	NH2	A_ASP_	OD2	3.101
2VIS	A_LYS_152	NZ	A_GLU_206	OE1	3.762
2VIS	A_HIS_191	ND1	A_ASP_154	OD2	2.830
2VIS	B_HIS_	NE2	B_ASP_	OD1	3.059
2VIS	B_ARG_	NH1	B_GLU_	OE1	2.654
2VIS	B_ARG_	NH2	B_ASP_	OD1	3.129
2VIS	B_ARG_	NH1	B_ASP_	OD1	3.798
2VIS	B_ARG_	NH2	B_ASP_	OD1	3.126
2VIS	B_ARG_	NH2	B_ASP_	OD2	2.566
2VIS	B_LYS_	NZ	B_ASP_	OD1	3.701
2VIS	B_LYS_	NZ	B_ASP_	OD2	3.019
2VIS	B_ARG_	NH2	B_ASP_	OD1	3.616
2VIS	B_ARG_	NH2	B_ASP_	OD2	2.750
2VIS	B_LYS_	NZ	A_GLU_127	OE2	2.999
2VIS	B_HIS_173	NE2	A_ASP_141	OD1	3.763
2VIS	B_HIS_173	NE2	A_ASP_141	OD2	3.158
2VIS	B_LYS_217	NZ	A_GLU_126	OE2	3.709
2VIS	C_LYS_	NZ	C_ASP_	OD1	3.551
2VIS	C_LYS_	NZ	C_ASP_	OD2	3.585
2VIS	C_HIS_	NE2	C_GLU_	OE1	3.359
2VIS	C_HIS_	NE2	C_GLU_	OE2	2.830
2VIS	C_ARG_	NH1	C_GLU_	OE2	3.968
2VIS	C_ARG_	NH2	C_GLU_	OE2	2.722
2VIS	C_HIS_	ND1	C_ASP_	OD1	2.788
2VIS	C_HIS_	NE2	C_ASP_	OD1	3.544
2VIS	C_ARG_	NH2	C_ASP_	OD1	3.769
2VIS	C_ARG_	NH2	C_ASP_	OD2	2.897
2VIS	C_LYS_	NZ	C_ASP_	OD1	2.890
2VIS	C_ARG_	NH1	C_GLU_	OE1	2.736
2VIS	C_ARG_	NH1	C_GLU_	OE2	2.823
2VIS	C_ARG_	NH2	C_GLU_	OE1	3.753
2VIS	C_ARG_	NH2	C_ASP_	OD1	2.729
2VIS	C_ARG_	NH2	C_ASP_	OD2	2.980
2VIS	C_LYS_	NZ	C_GLU_	OE2	3.175
2VIS	C_LYS_	NZ	C_ASP_	OD1	3.910
2VIS	C_HIS_	NE2	C_GLU_	OE2	3.842
2VIS	C_ARG_	NH2	C_ASP_	OD2	3.593
2VIS	C_LYS_	NZ	C_ASP_	OD1	3.401
2VIS	C_LYS_	NZ	C_ASP_	OD2	2.618
2VIS	C_LYS_	NZ	C_ASP_	OD1	3.801
2VIS	C_ARG_	NH1	C_GLU_	OE1	3.717
2VIS	C_ARG_	NH2	C_GLU_	OE1	3.508
2VIS	C_LYS_	NZ	C_ASP_	OD1	3.060
2VIS	C_LYS_	NZ	C_ASP_	OD2	3.941

Table 339: 2VIS-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2VIT	A_ARG_	NH1	A_ASP_	OD2	3.967
2VIT	A_ARG_	NH2	A_GLU_	OE2	3.548
2VIT	A_ARG_	NH2	A_ASP_	OD1	3.241
2VIT	A_ARG_	NH2	A_ASP_	OD2	3.098
2VIT	A_LYS_152	NZ	A_GLU_206	OE1	3.712
2VIT	A_HIS_191	ND1	A_ASP_154	OD2	2.838
2VIT	B_HIS_	NE2	B_ASP_	OD1	2.907
2VIT	B_ARG_	NH1	B_GLU_	OE1	2.629
2VIT	B_ARG_	NH2	B_ASP_	OD1	2.987
2VIT	B_ARG_	NH1	B_ASP_	OD1	3.943
2VIT	B_ARG_	NH2	B_ASP_	OD1	3.230
2VIT	B_ARG_	NH2	B_ASP_	OD2	2.635
2VIT	B_LYS_	NZ	B_ASP_	OD1	3.471
2VIT	B_LYS_	NZ	B_ASP_	OD2	3.207
2VIT	B_ARG_	NH2	B_ASP_	OD1	3.554
2VIT	B_ARG_	NH2	B_ASP_	OD2	2.686
2VIT	B_LYS_	NZ	A_GLU_127	OE2	2.939
2VIT	B_HIS_173	NE2	A_ASP_141	OD1	3.614
2VIT	B_HIS_173	NE2	A_ASP_141	OD2	3.333
2VIT	B_LYS_217	NZ	A_GLU_126	OE2	3.872
2VIT	C_LYS_	NZ	C_ASP_	OD1	3.503
2VIT	C_LYS_	NZ	C_ASP_	OD2	3.623
2VIT	C_HIS_	NE2	C_GLU_	OE1	3.344
2VIT	C_HIS_	NE2	C_GLU_	OE2	2.697
2VIT	C_ARG_	NH2	C_GLU_	OE2	2.611
2VIT	C_HIS_	ND1	C_ASP_	OD1	2.743
2VIT	C_HIS_	ND1	C_ASP_	OD2	3.981
2VIT	C_HIS_	NE2	C_ASP_	OD1	3.636
2VIT	C_ARG_	NH2	C_ASP_	OD1	3.818
2VIT	C_ARG_	NH2	C_ASP_	OD2	2.935
2VIT	C_LYS_	NZ	C_ASP_	OD1	2.814
2VIT	C_ARG_	NH1	C_GLU_	OE1	2.724
2VIT	C_ARG_	NH1	C_GLU_	OE2	3.066
2VIT	C_ARG_	NH2	C_GLU_	OE1	3.650
2VIT	C_ARG_	NH2	C_ASP_	OD1	2.732
2VIT	C_ARG_	NH2	C_ASP_	OD2	2.999
2VIT	C_LYS_	NZ	C_GLU_	OE2	3.169
2VIT	C_LYS_	NZ	C_ASP_	OD1	3.896
2VIT	C_ARG_	NH2	C_ASP_	OD2	3.650
2VIT	C_LYS_	NZ	C_ASP_	OD1	3.387
2VIT	C_LYS_	NZ	C_ASP_	OD2	2.696
2VIT	C_ARG_	NH2	C_GLU_	OE1	3.981
2VIT	C_LYS_	NZ	C_ASP_	OD1	3.143

Table 340: 2VIT-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2VIU	A_LYS_27	NZ	B_GLU_97	OE1	3.686
2VIU	A_LYS_27	NZ	B_GLU_97	OE2	2.721
2VIU	A_ARG_57	NH1	A_GLU_82	OE1	3.419
2VIU	A_ARG_57	NH2	A_GLU_82	OE1	2.696
2VIU	A_ARG_57	NH2	A_GLU_82	OE2	3.793
2VIU	A_HIS_75	ND1	A_ASP_73	OD1	2.756
2VIU	A_HIS_75	ND1	A_ASP_73	OD2	3.587
2VIU	A_HIS_75	NE2	A_ASP_63	OD1	3.916
2VIU	A_ARG_90	NH2	A_ASP_60	OD1	3.851
2VIU	A_ARG_90	NH2	A_ASP_60	OD2	3.197
2VIU	A_ARG_109	NH1	B_GLU_67	OE1	3.978
2VIU	A_ARG_109	NH1	B_GLU_67	OE2	3.053
2VIU	A_ARG_109	NH2	A_GLU_89	OE1	2.928
2VIU	A_ARG_141	NH2	A_ASP_77	OD1	2.769
2VIU	A_ARG_141	NH2	A_ASP_77	OD2	2.741
2VIU	A_LYS_176	NZ	A_GLU_123	OE2	2.681
2VIU	A_HIS_183	NE2	A_GLU_190	OE2	3.745
2VIU	A_ARG_207	NH1	A_ASP_241	OD1	3.937
2VIU	A_ARG_208	NH1	A_ASP_241	OD2	3.116
2VIU	A_LYS_238	NZ	A_ASP_175	OD2	3.292
2VIU	A_ARG_261	NH2	A_GLU_119	OE1	3.027
2VIU	A_ARG_261	NH2	A_GLU_119	OE2	2.600
2VIU	A_LYS_264	NZ	A_ASP_85	OD1	3.975
2VIU	A_LYS_264	NZ	A_ASP_85	OD2	3.658
2VIU	A_ARG_269	NH1	B_GLU_67	OE1	2.986
2VIU	A_LYS_292	NZ	A_ASP_291	OD2	3.041
2VIU	A_LYS_310	NZ	B_ASP_90	OD1	2.868
2VIU	A_LYS_315	NZ	A_GLU_41	OE1	3.081
2VIU	B_LYS_51	NZ	B_GLU_103	OE1	2.786
2VIU	B_LYS_68	NZ	B_GLU_85	OE1	3.467
2VIU	B_LYS_68	NZ	B_GLU_85	OE2	2.818
2VIU	B_LYS_117	NZ	B_GLU_114	OE1	3.690
2VIU	B_LYS_117	NZ	B_GLU_114	OE2	2.769
2VIU	B_ARG_123	NH1	B_GLU_120	OE1	2.873
2VIU	B_ARG_123	NH1	B_GLU_120	OE2	3.282
2VIU	B_ARG_153	NH2	B_GLU_150	OE1	2.715
2VIU	B_HIS_159	NE2	B_ASP_160	OD1	3.760
2VIU	B_HIS_159	NE2	B_ASP_160	OD2	3.318
2VIU	B_ARG_170	NH1	B_GLU_128	OE1	2.843
2VIU	B_ARG_170	NH2	B_GLU_128	OE1	3.875
2VIU	B_ARG_170	NH2	B_GLU_131	OE2	3.472

Table 341: 2VIU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2VXS	A_ARG_55	NH2	A_GLU_57	OE2	3.745
2VXS	A_HIS_86	ND1	A_ASP_84	OD1	2.794
2VXS	A_HIS_86	ND1	A_ASP_84	OD2	3.861
2VXS	B_ARG_46	NH1	B_ASP_42	OD2	2.944
2VXS	B_ARG_55	NH2	B_GLU_57	OE2	2.792
2VXS	B_HIS_86	ND1	B_ASP_84	OD1	3.029
2VXS	B_HIS_86	ND1	B_ASP_84	OD2	3.887
2VXS	C_HIS_86	ND1	C_ASP_84	OD1	2.647
2VXS	C_HIS_86	ND1	C_ASP_84	OD2	3.590
2VXS	C_LYS_114	NZ	C_GLU_95	OE2	3.592
2VXS	D_ARG_46	NH1	D_ASP_42	OD2	3.642
2VXS	D_ARG_55	NH2	D_GLU_57	OE2	3.715
2VXS	D_ARG_61	NH1	D_ASP_58	OD2	3.553
2VXS	D_ARG_61	NH2	D_ASP_58	OD2	2.803
2VXS	D_HIS_86	ND1	D_ASP_84	OD1	2.787
2VXS	D_HIS_86	ND1	D_ASP_84	OD2	3.565
2VXS	H_ARG_38	NH1	H_ASP_86	OD1	3.009
2VXS	H_ARG_38	NH2	H_GLU_46	OE1	3.046
2VXS	H_ARG_38	NH2	H_GLU_46	OE2	3.669
2VXS	H_ARG_38	NH2	H_ASP_86	OD1	3.964
2VXS	H_LYS_64	NZ	H_ASP_61	OD1	3.737
2VXS	H_ARG_66	NH1	H_ASP_86	OD1	3.951
2VXS	H_ARG_66	NH1	H_ASP_86	OD2	2.759
2VXS	H_ARG_66	NH2	H_ASP_86	OD1	3.290
2VXS	H_ARG_66	NH2	H_ASP_86	OD2	3.569
2VXS	H_LYS_143	NZ	L_GLU_125	OE2	2.772
2VXS	L_ARG_38	NH1	L_ASP_86	OD1	3.106
2VXS	L_ARG_38	NH2	L_GLU_46	OE1	3.024
2VXS	L_ARG_38	NH2	L_GLU_46	OE2	3.297
2VXS	L_ARG_38	NH2	L_ASP_86	OD1	3.845
2VXS	L_LYS_64	NZ	L_ASP_61	OD1	3.015
2VXS	L_ARG_66	NH1	L_ASP_86	OD1	3.881
2VXS	L_ARG_66	NH1	L_ASP_86	OD2	2.775
2VXS	L_ARG_66	NH2	L_ASP_86	OD1	2.818
2VXS	L_ARG_66	NH2	L_ASP_86	OD2	3.215
2VXS	L_LYS_143	NZ	L_ASP_144	OD1	3.889
2VXS	L_LYS_210	NZ	L_GLU_212	OE1	2.766
2VXS	L_LYS_214	NZ	M_GLU_124	OE1	3.186
2VXS	J_ARG_	NH1	J_ASP_	OD1	2.755
2VXS	J_ARG_	NH2	J_GLU_	OE1	3.312
2VXS	J_ARG_	NH2	J_GLU_	OE2	3.407
2VXS	J_ARG_	NH2	J_ASP_	OD1	3.826
2VXS	J_LYS_64	NZ	J_ASP_	OD1	3.275
2VXS	J_ARG_	NH1	J_ASP_	OD1	3.912
2VXS	J_ARG_	NH1	J_ASP_	OD2	2.751
2VXS	J_ARG_	NH2	J_ASP_	OD1	3.250
2VXS	J_ARG_	NH2	J_ASP_	OD2	3.560
2VXS	J_LYS_	NZ	J_ASP_	OD1	3.641
2VXS	J_LYS_206	NZ	J_ASP_208	OD1	3.503
2VXS	J_LYS_	NZ	N_GLU_	OE1	2.922
2VXS	K_ARG_38	NH1	K_ASP_86	OD1	3.239
2VXS	K_ARG_38	NH2	K_GLU_46	OE1	3.227
2VXS	K_ARG_38	NH2	K_GLU_46	OE2	3.826
2VXS	K_ARG_38	NH2	K_ASP_86	OD1	3.916
2VXS	K_LYS_64	NZ	K_ASP_61	OD1	3.799
2VXS	K_ARG_66	NH1	K_ASP_86	OD1	3.713
2VXS	K_ARG_66	NH1	K_ASP_86	OD2	2.833

2VXS	K_ARG_66	NH2	K_ASP_86	OD1	2.845
2VXS	K_ARG_66	NH2	K_ASP_86	OD2	3.489
2VXS	K_LYS_210	NZ	K_GLU_212	OE1	3.930
2VXS	K_LYS_214	NZ	O_GLU_124	OE1	3.391
2VXS	L_ARG_54	NH1	L_ASP_60	OD1	3.471
2VXS	L_ARG_61	NH2	L_ASP_82	OD1	2.601
2VXS	L_ARG_61	NH2	L_ASP_82	OD2	2.642
2VXS	L_LYS_103	NZ	L_ASP_85	OD1	3.412
2VXS	L_LYS_167	NZ	L_GLU_83	OE1	3.289
2VXS	L_LYS_172	NZ	L_ASP_139	OD1	3.795
2VXS	L_HIS_189	ND1	L_ASP_152	OD2	2.849
2VXS	M_ARG_61	NH1	M_ASP_82	OD1	3.983
2VXS	M_ARG_61	NH2	M_ASP_82	OD1	2.482
2VXS	M_ARG_61	NH2	M_ASP_82	OD2	2.420
2VXS	M_LYS_103	NZ	M_ASP_85	OD1	3.469
2VXS	M_LYS_167	NZ	M_GLU_83	OE1	2.810
2VXS	M_HIS_189	ND1	M_ASP_152	OD2	3.666
2VXS	M_HIS_198	NE2	M_GLU_199	OE2	3.892
2VXS	N_ARG_61	NH2	N_ASP_	OD1	2.670
2VXS	N_ARG_61	NH2	N_ASP_	OD2	2.989
2VXS	N_LYS_	NZ	N_ASP_	OD1	3.427
2VXS	N_LYS_	NZ	J_ASP_	OD2	3.949
2VXS	N_LYS_	NZ	N_GLU_	OE1	2.677
2VXS	N_HIS_	ND1	N_ASP_	OD2	3.568
2VXS	O_ARG_61	NH2	O_ASP_82	OD1	2.574
2VXS	O_ARG_61	NH2	O_ASP_82	OD2	2.733
2VXS	O_LYS_103	NZ	O_ASP_85	OD1	2.839
2VXS	O_LYS_103	NZ	O_ASP_85	OD2	3.719
2VXS	O_LYS_167	NZ	O_GLU_83	OE1	3.622
2VXS	O_LYS_167	NZ	O_GLU_83	OE2	3.743
2VXS	O_HIS_189	ND1	O_ASP_152	OD2	3.412
2VXS	O_HIS_198	NE2	O_GLU_199	OE2	3.877

Table 342: 2VXS-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2VXT	H.LYS_62	NZ	H.GLU_46	OE1	3.909
2VXT	H.LYS_62	NZ	H.GLU_46	OE2	2.756
2VXT	H.LYS_66	NZ	H.ASP_86	OD1	3.652
2VXT	H.LYS_66	NZ	H.ASP_86	OD2	2.674
2VXT	H.ARG_94	NH2	I.GLU_179	OE1	2.816
2VXT	H.ARG_94	NH2	I.GLU_179	OE2	3.466
2VXT	H.ARG_101	NH1	I.GLU_179	OE1	2.914
2VXT	H.LYS_208	NZ	L.GLU_123	OE2	2.940
2VXT	I.LYS_44	NZ	I.GLU_42	OE1	3.741
2VXT	I.ARG_49	NH2	I.ASP_71	OD1	3.048
2VXT	I.LYS_106	NZ	I.GLU_121	OE1	3.321
2VXT	I.HIS_145	NE2	H.ASP_50	OD1	2.753
2VXT	I.LYS_148	NZ	H.ASP_56	OD2	2.664
2VXT	I.LYS_175	NZ	I.ASP_182	OD1	3.559
2VXT	I.LYS_175	NZ	I.ASP_182	OD2	2.678
2VXT	L.ARG_46	NH2	L.ASP_55	OD1	2.847
2VXT	L.ARG_46	NH2	L.ASP_55	OD2	3.641
2VXT	L.ARG_61	NH1	L.GLU_79	OE2	3.449
2VXT	L.ARG_61	NH2	L.GLU_81	OE2	3.316
2VXT	L.ARG_61	NH2	L.ASP_82	OD1	2.855
2VXT	L.ARG_61	NH2	L.ASP_82	OD2	3.570
2VXT	L.ARG_66	NH2	L.ASP_28	OD1	3.957
2VXT	L.ARG_155	NH1	L.GLU_185	OE1	3.695
2VXT	L.ARG_155	NH1	L.GLU_185	OE2	2.926
2VXT	L.ARG_155	NH2	L.GLU_185	OE1	3.294
2VXT	L.ARG_155	NH2	L.GLU_185	OE2	3.952
2VXT	L.LYS_199	NZ	L.ASP_110	OD1	3.760
2VXT	L.LYS_199	NZ	L.ASP_110	OD2	2.706

Table 343: 2VXT-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2VXU	H.LYS_43	NZ	L.ASP_85	OD1	3.097
2VXU	H.LYS_62	NZ	H.GLU_46	OE1	3.879
2VXU	H.LYS_62	NZ	H.GLU_46	OE2	2.639
2VXU	H.LYS_66	NZ	H.ASP_86	OD2	3.095
2VXU	I.LYS_62	NZ	I.GLU_46	OE1	3.778
2VXU	I.LYS_62	NZ	I.GLU_46	OE2	2.481
2VXU	I.LYS_66	NZ	I.ASP_86	OD1	3.703
2VXU	I.LYS_66	NZ	I.ASP_86	OD2	2.733
2VXU	I.LYS_208	NZ	M.GLU_123	OE1	2.734
2VXU	I.LYS_208	NZ	M.GLU_123	OE2	2.893
2VXU	L.ARG_24	NH2	L.ASP_70	OD1	3.272
2VXU	L.ARG_24	NH2	L.ASP_70	OD2	2.791
2VXU	L.ARG_46	NH2	L.ASP_55	OD1	2.844
2VXU	L.ARG_46	NH2	L.ASP_55	OD2	3.772
2VXU	L.ARG_61	NH2	L.GLU_81	OE2	3.219
2VXU	L.ARG_61	NH2	L.ASP_82	OD1	3.151
2VXU	L.ARG_61	NH2	L.ASP_82	OD2	3.745
2VXU	L.ARG_66	NH2	L.ASP_28	OD1	3.861
2VXU	L.LYS_142	NZ	L.ASP_143	OD1	3.748
2VXU	L.LYS_199	NZ	L.ASP_110	OD2	3.400
2VXU	M.ARG_24	NH2	M.ASP_70	OD1	3.639
2VXU	M.ARG_24	NH2	M.ASP_70	OD2	3.054
2VXU	M.ARG_46	NH2	M.ASP_55	OD1	2.799
2VXU	M.ARG_46	NH2	M.ASP_55	OD2	3.746
2VXU	M.ARG_61	NH1	M.GLU_79	OE2	3.549
2VXU	M.ARG_61	NH2	M.GLU_81	OE2	3.079
2VXU	M.ARG_61	NH2	M.ASP_82	OD1	2.801
2VXU	M.ARG_61	NH2	M.ASP_82	OD2	3.460
2VXU	M.ARG_66	NH2	M.ASP_28	OD1	3.960
2VXU	M.LYS_107	NZ	M.GLU_17	OE1	3.246
2VXU	M.LYS_107	NZ	M.GLU_17	OE2	2.558
2VXU	M.LYS_142	NZ	M.ASP_143	OD1	3.635
2VXU	M.ARG_155	NH1	M.GLU_185	OE1	3.951
2VXU	M.ARG_155	NH1	M.GLU_185	OE2	2.762
2VXU	M.ARG_155	NH2	M.GLU_185	OE1	3.497
2VXU	M.ARG_155	NH2	M.GLU_185	OE2	3.662
2VXU	M.HIS_189	ND1	M.ASP_151	OD2	2.958

Table 344: 2VXU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2VXV	H_ARG_38	NH2	H_GLU_46	OE1	2.913
2VXV	H_ARG_38	NH2	H_GLU_46	OE2	3.297
2VXV	H_ARG_58	NH2	H_GLU_56	OE2	2.796
2VXV	H_ARG_94	NH2	H_ASP_101	OD1	3.566
2VXV	H_ARG_94	NH2	H_ASP_101	OD2	2.867
2VXV	H_LYS_143	NZ	H_ASP_144	OD1	3.484
2VXV	H_LYS_214	NZ	L_ASP_122	OD1	3.721
2VXV	H_LYS_214	NZ	L_ASP_122	OD2	2.868
2VXV	L_ARG_61	NH2	L_GLU_81	OE2	3.747
2VXV	L_ARG_61	NH2	L_ASP_82	OD1	2.862
2VXV	L_ARG_61	NH2	L_ASP_82	OD2	3.507
2VXV	L_HIS_189	ND1	L_ASP_151	OD2	2.974

Table 345: 2VXV-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID** **residue name** **residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2XEF	A_HIS_56	NE2	A_GLU_408	OE2	2.799
2XEF	A_LYS_59	NZ	A_ASP_63	OD1	3.841
2XEF	A_LYS_59	NZ	A_ASP_63	OD2	3.009
2XEF	A_ARG_181	NH1	A_GLU_183	OE2	3.625
2XEF	A_ARG_181	NH2	A_ASP_184	OD1	2.949
2XEF	A_ARG_181	NH2	A_ASP_184	OD2	3.602
2XEF	A_ARG_190	NH1	A_ASP_714	OD1	2.918
2XEF	A_ARG_190	NH1	A_ASP_714	OD2	3.597
2XEF	A_ARG_190	NH2	A_ASP_714	OD1	3.579
2XEF	A_ARG_190	NH2	A_ASP_714	OD2	2.730
2XEF	A_ARG_204	NH1	A_ASP_233	OD2	3.163
2XEF	A_ARG_255	NH1	A_GLU_145	OE1	2.685
2XEF	A_ARG_255	NH2	A_GLU_145	OE1	2.757
2XEF	A_LYS_341	NZ	A_ASP_173	OD1	3.395
2XEF	A_LYS_341	NZ	A_ASP_173	OD2	3.841
2XEF	A_LYS_343	NZ	A_GLU_171	OE1	2.875
2XEF	A_HIS_345	ND1	A_GLU_137	OE2	3.926
2XEF	A_HIS_345	NE2	A_GLU_137	OE1	3.980
2XEF	A_HIS_345	NE2	A_GLU_137	OE2	3.120
2XEF	A_ARG_354	NH2	A_ASP_114	OD1	3.536
2XEF	A_ARG_354	NH2	A_ASP_114	OD2	2.909
2XEF	A_ARG_363	NH2	A_ASP_106	OD1	3.752
2XEF	A_ARG_370	NH1	A_ASP_369	OD1	3.987
2XEF	A_ARG_370	NH1	A_ASP_369	OD2	3.614
2XEF	A_ARG_370	NH2	A_ASP_666	OD1	2.894
2XEF	A_ARG_370	NH2	A_ASP_666	OD2	3.631
2XEF	A_HIS_377	ND1	A_ASP_379	OD1	2.940
2XEF	A_HIS_377	ND1	A_GLU_424	OE1	3.983
2XEF	A_HIS_377	NE2	A_ASP_387	OD1	3.185
2XEF	A_HIS_377	NE2	A_GLU_424	OE1	3.244
2XEF	A_HIS_377	NE2	A_GLU_425	OE2	3.914
2XEF	A_HIS_377	NE2	A_ASP_453	OD1	3.247
2XEF	A_HIS_377	NE2	A_ASP_453	OD2	3.086
2XEF	A_ARG_378	NH2	A_ASP_422	OD1	3.926
2XEF	A_ARG_378	NH2	A_ASP_422	OD2	3.342
2XEF	A_ARG_400	NH1	A_GLU_64	OE2	3.095
2XEF	A_ARG_400	NH1	A_GLU_397	OE1	3.701
2XEF	A_ARG_400	NH1	A_GLU_397	OE2	2.838
2XEF	A_ARG_400	NH2	A_GLU_64	OE2	2.882
2XEF	A_LYS_406	NZ	A_ASP_106	OD1	3.218
2XEF	A_ARG_411	NH1	A_ASP_106	OD1	3.513
2XEF	A_ARG_411	NH1	A_ASP_106	OD2	2.703
2XEF	A_ARG_411	NH2	A_ASP_106	OD1	2.830
2XEF	A_ARG_411	NH2	A_ASP_106	OD2	3.623
2XEF	A_ARG_413	NH2	A_GLU_367	OE2	3.405
2XEF	A_ARG_414	NH2	A_GLU_367	OE2	3.182
2XEF	A_ARG_463	NH1	A_GLU_457	OE1	3.344
2XEF	A_ARG_463	NH1	A_GLU_457	OE2	3.045
2XEF	A_ARG_463	NH2	A_ASP_465	OD2	2.862
2XEF	A_LYS_491	NZ	A_GLU_495	OE2	3.112
2XEF	A_LYS_500	NZ	A_ASP_485	OD2	2.872
2XEF	A_ARG_527	NH1	A_GLU_436	OE1	2.777
2XEF	A_ARG_527	NH2	A_GLU_436	OE1	2.984
2XEF	A_ARG_536	NH1	A_GLU_457	OE1	2.900
2XEF	A_HIS_553	NE2	A_ASP_387	OD2	2.946
2XEF	A_HIS_553	NE2	A_GLU_425	OE1	3.142
2XEF	A_HIS_553	NE2	A_GLU_425	OE2	3.233

2XEF	A_HIS_573	ND1	A_ASP_567	OD2	2.719
2XEF	A_ARG_598	NH2	A_ASP_596	OD1	3.762
2XEF	A_ARG_598	NH2	A_ASP_596	OD2	2.978
2XEF	A_LYS_606	NZ	A_GLU_505	OE1	3.281
2XEF	A_LYS_606	NZ	A_GLU_505	OE2	3.681
2XEF	A_LYS_610	NZ	A_GLU_703	OE2	2.847
2XEF	A_HIS_618	NE2	A_GLU_716	OE1	3.725
2XEF	A_LYS_637	NZ	A_GLU_641	OE1	3.067
2XEF	A_LYS_637	NZ	A_GLU_641	OE2	3.880
2XEF	A_ARG_684	NH2	A_ASP_710	OD2	3.381
2XEF	A_HIS_689	NE2	A_GLU_672	OE2	2.802
2XEF	A_ARG_730	NH2	A_GLU_727	OE1	3.848
2XEF	A_ARG_730	NH2	A_GLU_727	OE2	3.085

Table 346: 2XEF-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2XEG	A_HIS_56	ND1	A_GLU_408	OE2	3.766
2XEG	A_HIS_56	NE2	A_GLU_408	OE2	3.847
2XEG	A_LYS_59	NZ	A_ASP_63	OD1	3.760
2XEG	A_LYS_59	NZ	A_ASP_63	OD2	2.920
2XEG	A_ARG_181	NH1	A_GLU_183	OE2	3.616
2XEG	A_ARG_181	NH2	A_ASP_184	OD1	2.935
2XEG	A_ARG_181	NH2	A_ASP_184	OD2	3.536
2XEG	A_ARG_190	NH1	A_ASP_714	OD1	2.995
2XEG	A_ARG_190	NH1	A_ASP_714	OD2	3.628
2XEG	A_ARG_190	NH2	A_ASP_714	OD1	3.604
2XEG	A_ARG_190	NH2	A_ASP_714	OD2	2.717
2XEG	A_ARG_204	NH1	A_ASP_233	OD1	3.945
2XEG	A_ARG_204	NH1	A_ASP_233	OD2	3.115
2XEG	A_ARG_255	NH1	A_GLU_145	OE1	2.705
2XEG	A_ARG_255	NH2	A_GLU_145	OE1	2.760
2XEG	A_LYS_341	NZ	A_ASP_173	OD1	3.295
2XEG	A_LYS_341	NZ	A_ASP_173	OD2	3.942
2XEG	A_HIS_345	ND1	A_GLU_137	OE2	3.875
2XEG	A_HIS_345	NE2	A_GLU_137	OE2	3.207
2XEG	A_ARG_354	NH2	A_ASP_114	OD1	3.519
2XEG	A_ARG_354	NH2	A_ASP_114	OD2	2.914
2XEG	A_ARG_363	NH2	A_ASP_106	OD1	3.705
2XEG	A_ARG_370	NH1	A_ASP_369	OD1	3.956
2XEG	A_ARG_370	NH1	A_ASP_369	OD2	3.628
2XEG	A_ARG_370	NH2	A_ASP_666	OD1	2.842
2XEG	A_ARG_370	NH2	A_ASP_666	OD2	3.618
2XEG	A_HIS_377	ND1	A_ASP_379	OD1	2.925
2XEG	A_HIS_377	NE2	A_ASP_387	OD1	3.241
2XEG	A_HIS_377	NE2	A_GLU_424	OE1	3.209
2XEG	A_HIS_377	NE2	A_GLU_425	OE2	3.926
2XEG	A_HIS_377	NE2	A_ASP_453	OD1	3.264
2XEG	A_HIS_377	NE2	A_ASP_453	OD2	3.104
2XEG	A_ARG_378	NH2	A_ASP_422	OD1	3.876
2XEG	A_ARG_378	NH2	A_ASP_422	OD2	3.238
2XEG	A_ARG_400	NH1	A_GLU_64	OE2	3.039
2XEG	A_ARG_400	NH1	A_GLU_397	OE1	3.703
2XEG	A_ARG_400	NH1	A_GLU_397	OE2	2.812
2XEG	A_ARG_400	NH2	A_GLU_64	OE2	2.850
2XEG	A_LYS_406	NZ	A_ASP_106	OD1	3.308
2XEG	A_ARG_411	NH1	A_ASP_106	OD1	3.560
2XEG	A_ARG_411	NH1	A_ASP_106	OD2	2.790
2XEG	A_ARG_411	NH2	A_ASP_106	OD1	2.807
2XEG	A_ARG_411	NH2	A_ASP_106	OD2	3.629
2XEG	A_ARG_413	NH2	A_GLU_367	OE2	3.344
2XEG	A_ARG_414	NH2	A_GLU_367	OE2	3.206
2XEG	A_LYS_491	NZ	A_GLU_495	OE2	3.175
2XEG	A_LYS_500	NZ	A_ASP_485	OD2	2.873
2XEG	A_ARG_527	NH1	A_GLU_436	OE1	2.787
2XEG	A_ARG_527	NH2	A_GLU_436	OE1	2.964
2XEG	A_ARG_536	NH1	A_GLU_457	OE1	2.897
2XEG	A_HIS_553	NE2	A_ASP_387	OD2	2.992
2XEG	A_HIS_553	NE2	A_GLU_425	OE1	3.084
2XEG	A_HIS_553	NE2	A_GLU_425	OE2	3.216
2XEG	A_HIS_573	ND1	A_ASP_567	OD2	2.723
2XEG	A_ARG_598	NH2	A_ASP_596	OD1	3.731
2XEG	A_ARG_598	NH2	A_ASP_596	OD2	2.927
2XEG	A_LYS_606	NZ	A_GLU_505	OE1	3.338

2XEG	A_LYS_606	NZ	A_GLU_505	OE2	3.829
2XEG	A_HIS_618	NE2	A_GLU_716	OE1	3.759
2XEG	A_LYS_637	NZ	A_GLU_641	OE1	2.943
2XEG	A_LYS_637	NZ	A_GLU_641	OE2	3.902
2XEG	A_ARG_684	NH2	A_ASP_710	OD2	3.396
2XEG	A_HIS_689	NE2	A_GLU_672	OE2	2.814

Table 347: 2XEG-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2XEI	A_HIS_56	NE2	A_GLU_408	OE2	2.969
2XEI	A_LYS_59	NZ	A_ASP_63	OD2	2.953
2XEI	A_ARG_181	NH1	A_GLU_183	OE2	3.722
2XEI	A_ARG_181	NH2	A_ASP_184	OD1	2.939
2XEI	A_ARG_181	NH2	A_ASP_184	OD2	3.606
2XEI	A_LYS_187	NZ	A_ASP_316	OD2	3.720
2XEI	A_ARG_190	NH1	A_ASP_714	OD1	2.931
2XEI	A_ARG_190	NH1	A_ASP_714	OD2	3.551
2XEI	A_ARG_190	NH2	A_ASP_714	OD1	3.589
2XEI	A_ARG_190	NH2	A_ASP_714	OD2	2.720
2XEI	A_ARG_204	NH1	A_ASP_233	OD1	3.976
2XEI	A_ARG_204	NH1	A_ASP_233	OD2	3.187
2XEI	A_ARG_255	NH1	A_GLU_145	OE1	2.647
2XEI	A_ARG_255	NH2	A_GLU_145	OE1	2.713
2XEI	A_LYS_304	NZ	A_GLU_307	OE2	3.381
2XEI	A_LYS_341	NZ	A_ASP_173	OD1	3.842
2XEI	A_LYS_343	NZ	A_GLU_171	OE1	3.105
2XEI	A_HIS_345	NE2	A_GLU_137	OE1	3.939
2XEI	A_HIS_345	NE2	A_GLU_137	OE2	2.664
2XEI	A_ARG_354	NH2	A_ASP_114	OD1	3.459
2XEI	A_ARG_354	NH2	A_ASP_114	OD2	2.831
2XEI	A_ARG_363	NH2	A_ASP_106	OD1	3.622
2XEI	A_ARG_370	NH1	A_ASP_369	OD2	3.552
2XEI	A_ARG_370	NH2	A_ASP_666	OD1	2.830
2XEI	A_ARG_370	NH2	A_ASP_666	OD2	3.553
2XEI	A_HIS_377	ND1	A_ASP_379	OD1	2.915
2XEI	A_HIS_377	ND1	A_GLU_424	OE1	3.971
2XEI	A_HIS_377	NE2	A_ASP_387	OD1	3.175
2XEI	A_HIS_377	NE2	A_GLU_424	OE1	3.231
2XEI	A_HIS_377	NE2	A_GLU_425	OE2	3.821
2XEI	A_HIS_377	NE2	A_ASP_453	OD1	3.238
2XEI	A_HIS_377	NE2	A_ASP_453	OD2	3.140
2XEI	A_ARG_378	NH2	A_ASP_422	OD1	3.870
2XEI	A_ARG_378	NH2	A_ASP_422	OD2	3.255
2XEI	A_ARG_400	NH1	A_GLU_64	OE2	2.965
2XEI	A_ARG_400	NH1	A_GLU_397	OE1	3.705
2XEI	A_ARG_400	NH1	A_GLU_397	OE2	2.906
2XEI	A_ARG_400	NH2	A_GLU_64	OE2	2.816
2XEI	A_LYS_406	NZ	A_ASP_106	OD1	3.048
2XEI	A_ARG_411	NH1	A_ASP_106	OD1	3.535
2XEI	A_ARG_411	NH1	A_ASP_106	OD2	2.723
2XEI	A_ARG_411	NH2	A_ASP_106	OD1	2.835
2XEI	A_ARG_411	NH2	A_ASP_106	OD2	3.617
2XEI	A_ARG_413	NH2	A_GLU_367	OE2	3.221
2XEI	A_ARG_414	NH2	A_GLU_367	OE2	3.265
2XEI	A_ARG_463	NH1	A_GLU_457	OE1	3.475
2XEI	A_ARG_463	NH1	A_GLU_457	OE2	3.028
2XEI	A_ARG_463	NH2	A_ASP_465	OD1	3.828
2XEI	A_ARG_463	NH2	A_ASP_465	OD2	2.781
2XEI	A_LYS_491	NZ	A_GLU_495	OE2	3.533
2XEI	A_LYS_500	NZ	A_ASP_485	OD2	2.834
2XEI	A_ARG_527	NH1	A_GLU_436	OE1	2.782
2XEI	A_ARG_527	NH2	A_GLU_436	OE1	2.914
2XEI	A_ARG_536	NH2	A_GLU_457	OE1	2.981
2XEI	A_HIS_553	NE2	A_ASP_387	OD2	2.945
2XEI	A_HIS_553	NE2	A_GLU_425	OE1	3.184
2XEI	A_HIS_553	NE2	A_GLU_425	OE2	3.250

2XEI	A_HIS_573	ND1	A_ASP_567	OD2	2.635
2XEI	A_ARG_598	NH2	A_ASP_596	OD1	3.686
2XEI	A_ARG_598	NH2	A_ASP_596	OD2	2.928
2XEI	A_LYS_606	NZ	A_GLU_505	OE2	2.921
2XEI	A_LYS_610	NZ	A_GLU_703	OE2	2.865
2XEI	A_LYS_637	NZ	A_GLU_641	OE1	2.954
2XEI	A_LYS_637	NZ	A_GLU_641	OE2	3.988
2XEI	A_ARG_684	NH2	A_ASP_710	OD2	3.374
2XEI	A_HIS_689	NE2	A_GLU_672	OE2	2.779
2XEI	A_ARG_730	NH2	A_GLU_727	OE1	3.881
2XEI	A_ARG_730	NH2	A_GLU_727	OE2	3.068

Table 348: 2XEI-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2XEJ	A_HIS_56	ND1	A_GLU_408	OE2	3.595
2XEJ	A_HIS_56	NE2	A_GLU_408	OE2	3.649
2XEJ	A_LYS_59	NZ	A_ASP_63	OD1	3.833
2XEJ	A_LYS_59	NZ	A_ASP_63	OD2	3.161
2XEJ	A_ARG_181	NH1	A_GLU_183	OE2	3.636
2XEJ	A_ARG_181	NH2	A_ASP_184	OD1	3.044
2XEJ	A_ARG_181	NH2	A_ASP_184	OD2	3.609
2XEJ	A_ARG_190	NH1	A_ASP_714	OD1	2.993
2XEJ	A_ARG_190	NH1	A_ASP_714	OD2	3.604
2XEJ	A_ARG_190	NH2	A_ASP_714	OD1	3.611
2XEJ	A_ARG_190	NH2	A_ASP_714	OD2	2.731
2XEJ	A_ARG_204	NH1	A_ASP_233	OD1	3.963
2XEJ	A_ARG_204	NH1	A_ASP_233	OD2	3.162
2XEJ	A_ARG_255	NH1	A_GLU_145	OE1	2.709
2XEJ	A_ARG_255	NH2	A_GLU_145	OE1	2.779
2XEJ	A_LYS_304	NZ	A_GLU_307	OE2	3.882
2XEJ	A_LYS_341	NZ	A_ASP_173	OD1	3.630
2XEJ	A_HIS_345	NE2	A_GLU_137	OE1	3.939
2XEJ	A_HIS_345	NE2	A_GLU_137	OE2	3.101
2XEJ	A_ARG_354	NH2	A_ASP_114	OD1	3.439
2XEJ	A_ARG_354	NH2	A_ASP_114	OD2	2.884
2XEJ	A_ARG_363	NH2	A_ASP_106	OD1	3.838
2XEJ	A_ARG_370	NH1	A_ASP_369	OD1	3.947
2XEJ	A_ARG_370	NH1	A_ASP_369	OD2	3.540
2XEJ	A_ARG_370	NH2	A_ASP_666	OD1	2.915
2XEJ	A_ARG_370	NH2	A_ASP_666	OD2	3.607
2XEJ	A_HIS_377	ND1	A_ASP_379	OD1	2.947
2XEJ	A_HIS_377	ND1	A_GLU_424	OE1	3.959
2XEJ	A_HIS_377	NE2	A_ASP_387	OD1	3.198
2XEJ	A_HIS_377	NE2	A_GLU_424	OE1	3.200
2XEJ	A_HIS_377	NE2	A_GLU_425	OE2	3.909
2XEJ	A_HIS_377	NE2	A_ASP_453	OD1	3.288
2XEJ	A_HIS_377	NE2	A_ASP_453	OD2	3.106
2XEJ	A_ARG_378	NH2	A_ASP_422	OD1	3.906
2XEJ	A_ARG_378	NH2	A_ASP_422	OD2	3.305
2XEJ	A_ARG_400	NH1	A_GLU_64	OE2	3.030
2XEJ	A_ARG_400	NH1	A_GLU_397	OE1	3.701
2XEJ	A_ARG_400	NH1	A_GLU_397	OE2	2.808
2XEJ	A_ARG_400	NH2	A_GLU_64	OE2	2.879
2XEJ	A_LYS_406	NZ	A_ASP_106	OD1	3.327
2XEJ	A_ARG_411	NH1	A_ASP_106	OD1	3.525
2XEJ	A_ARG_411	NH1	A_ASP_106	OD2	2.766
2XEJ	A_ARG_411	NH2	A_ASP_106	OD1	2.901
2XEJ	A_ARG_411	NH2	A_ASP_106	OD2	3.711
2XEJ	A_ARG_413	NH2	A_GLU_367	OE2	3.406
2XEJ	A_ARG_414	NH2	A_GLU_367	OE2	3.157
2XEJ	A_ARG_463	NH1	A_GLU_457	OE1	3.276
2XEJ	A_ARG_463	NH1	A_GLU_457	OE2	3.003
2XEJ	A_ARG_463	NH2	A_ASP_465	OD1	3.986
2XEJ	A_ARG_463	NH2	A_ASP_465	OD2	2.863
2XEJ	A_LYS_491	NZ	A_GLU_495	OE2	3.392
2XEJ	A_LYS_500	NZ	A_ASP_485	OD2	2.873
2XEJ	A_ARG_527	NH1	A_GLU_436	OE1	2.804
2XEJ	A_ARG_527	NH2	A_GLU_436	OE1	3.018
2XEJ	A_ARG_536	NH1	A_GLU_457	OE1	2.942
2XEJ	A_HIS_553	NE2	A_ASP_387	OD2	2.982
2XEJ	A_HIS_553	NE2	A_GLU_425	OE1	3.077

2XEJ	A_HIS_553	NE2	A_GLU_425	OE2	3.221
2XEJ	A_HIS_573	ND1	A_ASP_567	OD2	2.723
2XEJ	A_ARG_598	NH2	A_ASP_596	OD1	3.718
2XEJ	A_ARG_598	NH2	A_ASP_596	OD2	2.988
2XEJ	A_LYS_606	NZ	A_GLU_505	OE1	3.097
2XEJ	A_LYS_606	NZ	A_GLU_505	OE2	3.795
2XEJ	A_LYS_610	NZ	A_GLU_703	OE2	2.940
2XEJ	A_HIS_618	NE2	A_GLU_716	OE1	3.742
2XEJ	A_LYS_637	NZ	A_GLU_641	OE1	2.900
2XEJ	A_LYS_637	NZ	A_GLU_641	OE2	3.785
2XEJ	A_ARG_684	NH2	A_ASP_710	OD2	3.390
2XEJ	A_HIS_689	NE2	A_GLU_672	OE2	2.745

Table 349: 2XEJ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2XZQ	H_ARG_40	NH1	H_GLU_89	OE2	3.454
2XZQ	H_ARG_40	NH2	H_GLU_89	OE2	2.650
2XZQ	H_LYS_65	NZ	H_GLU_62	OE1	2.508
2XZQ	H_LYS_65	NZ	H_GLU_62	OE2	3.892
2XZQ	H_LYS_67	NZ	H_ASP_90	OD1	3.800
2XZQ	H_LYS_67	NZ	H_ASP_90	OD2	3.016
2XZQ	H_ARG_98	NH1	H_ASP_108	OD1	3.377
2XZQ	H_ARG_98	NH1	H_ASP_108	OD2	2.748
2XZQ	H_LYS_150	NZ	L_GLU_127	OE2	3.822
2XZQ	H_LYS_212	NZ	H_ASP_214	OD1	3.314
2XZQ	H_LYS_215	NZ	L_GLU_126	OE2	2.689
2XZQ	L_ARG_23	NH1	L_ASP_71	OD1	3.290
2XZQ	L_ARG_23	NH1	L_ASP_71	OD2	3.939
2XZQ	L_ARG_23	NH2	L_ASP_71	OD1	2.856
2XZQ	L_ARG_23	NH2	L_ASP_71	OD2	3.986
2XZQ	L_HIS_44	ND1	L_GLU_40	OE2	3.471
2XZQ	L_ARG_63	NH2	L_ASP_84	OD1	2.551
2XZQ	L_ARG_63	NH2	L_ASP_84	OD2	3.490
2XZQ	L_LYS_105	NZ	L_GLU_85	OE2	3.885
2XZQ	L_LYS_113	NZ	L_GLU_201	OE1	2.868

Table 350: 2XZQ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2Y06	H_LYS_63	NZ	H_GLU_46	OE1	3.321
2Y06	H_LYS_63	NZ	H_GLU_46	OE2	2.855
2Y06	H_LYS_67	NZ	H_ASP_90	OD2	3.290
2Y06	H_ARG_98	NH1	H_ASP_108	OD1	3.019
2Y06	H_ARG_98	NH1	H_ASP_108	OD2	3.194
2Y06	H_LYS_215	NZ	L_GLU_126	OE2	2.373
2Y06	L_ARG_23	NH1	L_ASP_71	OD1	3.453
2Y06	L_ARG_23	NH2	L_ASP_71	OD1	2.764
2Y06	L_ARG_63	NH2	L_ASP_84	OD1	2.907
2Y06	L_ARG_63	NH2	L_ASP_84	OD2	3.632
2Y06	L_LYS_113	NZ	L_GLU_201	OE1	3.332
2Y06	L_LYS_169	NZ	L_GLU_85	OE2	3.628

Table 351: 2Y06-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID** **residue name** **residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2Y07	H_LYS_67	NZ	H_ASP_90	OD1	3.687
2Y07	H_LYS_67	NZ	H_ASP_90	OD2	2.861
2Y07	H_ARG_98	NH1	H_ASP_108	OD1	3.962
2Y07	H_ARG_98	NH1	H_ASP_108	OD2	2.823
2Y07	H_LYS_215	NZ	L_GLU_126	OE2	2.390
2Y07	L_ARG_23	NH1	L_ASP_71	OD1	3.698
2Y07	L_ARG_23	NH1	L_ASP_71	OD2	3.356
2Y07	L_ARG_23	NH2	L_ASP_71	OD1	2.962
2Y07	L_ARG_23	NH2	L_ASP_71	OD2	2.784
2Y07	L_ARG_63	NH2	L_GLU_82	OE2	3.307
2Y07	L_ARG_63	NH2	L_ASP_83	OD1	2.727
2Y07	L_ARG_63	NH2	L_ASP_83	OD2	3.778
2Y07	L_LYS_113	NZ	L_GLU_201	OE1	3.255
2Y07	L_LYS_113	NZ	L_GLU_201	OE2	3.532
2Y07	L_HIS_200	NE2	L_GLU_201	OE1	3.946
2Y07	L_ARG_211	NH1	L_GLU_189	OE1	3.826

Table 352: 2Y07-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2Y36	H_ARG_40	NH1	H_GLU_89	OE1	3.909
2Y36	H_ARG_40	NH1	H_GLU_89	OE2	3.356
2Y36	H_ARG_40	NH2	H_GLU_89	OE2	2.875
2Y36	H_LYS_65	NZ	H_GLU_62	OE1	2.983
2Y36	H_LYS_67	NZ	H_ASP_90	OD2	3.261
2Y36	H_ARG_98	NH1	H_ASP_108	OD1	3.408
2Y36	H_ARG_98	NH1	H_ASP_108	OD2	2.494
2Y36	H_LYS_150	NZ	L_GLU_127	OE2	3.849
2Y36	H_LYS_215	NZ	L_GLU_126	OE2	2.707
2Y36	L_ARG_23	NH1	L_ASP_71	OD2	3.674
2Y36	L_ARG_23	NH2	L_ASP_71	OD1	3.148
2Y36	L_ARG_23	NH2	L_ASP_71	OD2	3.652
2Y36	L_ARG_63	NH2	L_GLU_83	OE2	3.566
2Y36	L_ARG_63	NH2	L_ASP_84	OD1	2.616
2Y36	L_ARG_63	NH2	L_ASP_84	OD2	3.443
2Y36	L_LYS_113	NZ	L_GLU_201	OE1	3.248
2Y36	L_HIS_191	NE2	L_ASP_154	OD2	3.845

Table 353: 2Y36-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2Y7S	A_LYS_27	NZ	A_ASP_25	OD2	3.076
2Y7S	A_LYS_45	NZ	A_GLU_83	OE1	2.864
2Y7S	A_LYS_47	NZ	A_GLU_54	OE1	3.042
2Y7S	A_LYS_67	NZ	A_ASP_28	OD1	3.289
2Y7S	A_LYS_67	NZ	A_ASP_28	OD2	2.809
2Y7S	A_ARG_75	NH1	A_GLU_95	OE1	2.862
2Y7S	A_ARG_75	NH1	A_GLU_95	OE2	3.954
2Y7S	A_ARG_80	NH1	A_GLU_44	OE1	2.923
2Y7S	A_ARG_80	NH1	A_GLU_44	OE2	3.022
2Y7S	A_ARG_80	NH2	A_GLU_92	OE1	3.248
2Y7S	A_ARG_127	NH1	A_ASP_159	OD1	3.706
2Y7S	A_ARG_127	NH1	A_ASP_159	OD2	2.895
2Y7S	A_ARG_127	NH1	B_GLU_118	OE1	3.457
2Y7S	A_ARG_127	NH2	A_GLU_112	OE1	3.963
2Y7S	A_ARG_127	NH2	A_GLU_112	OE2	2.936
2Y7S	A_ARG_127	NH2	A_ASP_159	OD1	2.847
2Y7S	A_ARG_127	NH2	A_ASP_159	OD2	3.582
2Y7S	A_ARG_130	NH1	A_GLU_92	OE1	3.851
2Y7S	A_ARG_130	NH1	A_GLU_92	OE2	3.019
2Y7S	A_ARG_130	NH2	A_GLU_92	OE1	3.136
2Y7S	A_ARG_130	NH2	A_GLU_92	OE2	3.650
2Y7S	A_ARG_152	NH1	A_GLU_150	OE1	3.228
2Y7S	A_ARG_152	NH2	A_GLU_150	OE1	3.600
2Y7S	A_LYS_179	NZ	A_GLU_181	OE1	3.798
2Y7S	A_LYS_179	NZ	A_GLU_181	OE2	3.366
2Y7S	A_LYS_218	NZ	A_GLU_216	OE1	3.816
2Y7S	A_LYS_218	NZ	B_ASP_85	OD1	3.014
2Y7S	A_LYS_240	NZ	A_GLU_217	OE1	3.163
2Y7S	A_LYS_240	NZ	A_GLU_217	OE2	3.626
2Y7S	A_LYS_253	NZ	A_ASP_71	OD1	3.458
2Y7S	A_LYS_253	NZ	A_ASP_71	OD2	2.809
2Y7S	B_ARG_41	NH2	A_GLU_238	OE2	2.757
2Y7S	B_LYS_42	NZ	B_ASP_37	OD1	3.966
2Y7S	B_LYS_47	NZ	B_GLU_54	OE1	3.576
2Y7S	B_LYS_47	NZ	B_GLU_54	OE2	3.620
2Y7S	B_LYS_67	NZ	B_ASP_28	OD1	3.186
2Y7S	B_LYS_67	NZ	B_ASP_28	OD2	3.425
2Y7S	B_ARG_75	NH1	B_GLU_95	OE2	2.817
2Y7S	B_ARG_80	NH1	B_GLU_44	OE1	3.002
2Y7S	B_ARG_80	NH1	B_GLU_44	OE2	3.573
2Y7S	B_ARG_80	NH2	B_GLU_92	OE1	2.824
2Y7S	B_HIS_103	ND1	B_GLU_137	OE1	2.807
2Y7S	B_HIS_119	NE2	B_ASP_116	OD2	3.821
2Y7S	B_LYS_122	NZ	B_ASP_116	OD2	3.879
2Y7S	B_ARG_127	NH1	B_ASP_159	OD1	3.795
2Y7S	B_ARG_127	NH1	B_ASP_159	OD2	2.884
2Y7S	B_ARG_127	NH2	B_GLU_112	OE1	3.910
2Y7S	B_ARG_127	NH2	B_GLU_112	OE2	2.774
2Y7S	B_ARG_127	NH2	B_ASP_159	OD1	2.931
2Y7S	B_ARG_127	NH2	B_ASP_159	OD2	3.540
2Y7S	B_ARG_130	NH1	B_GLU_92	OE1	3.502
2Y7S	B_ARG_130	NH1	B_GLU_92	OE2	2.814
2Y7S	B_ARG_130	NH2	B_GLU_92	OE1	3.119
2Y7S	B_ARG_130	NH2	B_GLU_92	OE2	3.783
2Y7S	B_LYS_148	NZ	B_ASP_170	OD2	3.415
2Y7S	B_ARG_152	NH1	B_GLU_150	OE1	2.822
2Y7S	B_ARG_152	NH2	B_GLU_150	OE1	3.268

2Y7S	B_LYS_173	NZ	B_ASP_170	OD2	3.896
2Y7S	B_LYS_179	NZ	B_GLU_181	OE1	3.992
2Y7S	B_LYS_179	NZ	B_GLU_181	OE2	3.341
2Y7S	B_LYS_198	NZ	B_GLU_196	OE1	3.898
2Y7S	B_HIS_204	ND1	B_ASP_200	OD2	3.949
2Y7S	B_ARG_212	NH2	B_ASP_210	OD2	3.869
2Y7S	B_LYS_218	NZ	B_GLU_187	OE1	3.745
2Y7S	B_LYS_218	NZ	B_GLU_216	OE2	3.499
2Y7S	B_LYS_253	NZ	B_ASP_71	OD1	3.851
2Y7S	B_LYS_253	NZ	B_ASP_71	OD2	3.059

Table 354: 2Y7S-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2YPV	A_HIS_26	ND1	A_ASP_25	OD1	3.615
2YPV	A_LYS_47	NZ	A_GLU_54	OE2	3.265
2YPV	A_LYS_67	NZ	A_ASP_28	OD1	3.119
2YPV	A_LYS_67	NZ	A_ASP_28	OD2	2.907
2YPV	A_ARG_80	NH1	A_GLU_44	OE1	3.085
2YPV	A_ARG_80	NH1	A_GLU_44	OE2	3.642
2YPV	A_ARG_80	NH2	A_GLU_92	OE2	3.509
2YPV	A_HIS_103	ND1	A_GLU_137	OE1	2.799
2YPV	A_HIS_103	ND1	A_GLU_137	OE2	3.510
2YPV	A_ARG_127	NH1	A_ASP_160	OD1	3.664
2YPV	A_ARG_127	NH1	A_ASP_160	OD2	2.748
2YPV	A_ARG_127	NH2	A_GLU_112	OE1	3.713
2YPV	A_ARG_127	NH2	A_GLU_112	OE2	2.780
2YPV	A_ARG_127	NH2	A_ASP_160	OD1	2.809
2YPV	A_ARG_127	NH2	A_ASP_160	OD2	3.468
2YPV	A_ARG_130	NH2	L_ASP_92	OD1	2.916
2YPV	A_ARG_149	NH2	A_ASP_171	OD2	2.711
2YPV	A_LYS_180	NZ	A_GLU_182	OE1	3.802
2YPV	A_LYS_180	NZ	A_GLU_182	OE2	3.312
2YPV	A_ARG_204	NH2	A_ASP_142	OD1	2.851
2YPV	A_ARG_204	NH2	A_ASP_142	OD2	3.577
2YPV	A_HIS_205	ND1	A_ASP_201	OD2	3.920
2YPV	A_LYS_219	NZ	H_ASP_52	OD2	3.469
2YPV	A_LYS_241	NZ	H_ASP_99	OD2	2.741
2YPV	A_ARG_247	NH1	A_GLU_188	OE2	3.707
2YPV	A_LYS_254	NZ	A_ASP_71	OD1	3.594
2YPV	A_LYS_254	NZ	A_ASP_71	OD2	2.807
2YPV	H_LYS_54	NZ	H_ASP_31	OD1	2.744
2YPV	H_LYS_67	NZ	H_ASP_90	OD1	3.738
2YPV	H_LYS_67	NZ	H_ASP_90	OD2	2.816
2YPV	H_LYS_214	NZ	L_GLU_123	OE1	2.788
2YPV	H_LYS_214	NZ	L_GLU_123	OE2	2.975
2YPV	L_HIS_30	ND1	L_ASP_28	OD1	3.934
2YPV	L_HIS_30	ND1	L_ASP_92	OD1	3.607
2YPV	L_HIS_30	ND1	L_ASP_92	OD2	2.797
2YPV	L_HIS_30	NE2	L_ASP_28	OD2	3.772
2YPV	L_ARG_50	NH2	A_GLU_239	OE1	3.110
2YPV	L_ARG_50	NH2	A_GLU_239	OE2	3.975
2YPV	L_ARG_61	NH1	L_GLU_79	OE1	3.426
2YPV	L_ARG_61	NH1	L_GLU_81	OE2	3.737
2YPV	L_ARG_61	NH1	L_ASP_82	OD1	2.772
2YPV	L_ARG_61	NH1	L_ASP_82	OD2	3.085
2YPV	L_ARG_61	NH2	L_GLU_79	OE1	2.918
2YPV	L_ARG_61	NH2	L_GLU_79	OE2	3.335
2YPV	L_ARG_61	NH2	L_GLU_81	OE2	3.973
2YPV	L_LYS_149	NZ	L_GLU_195	OE1	2.918
2YPV	L_LYS_149	NZ	L_GLU_195	OE2	3.889
2YPV	L_HIS_189	ND1	L_ASP_151	OD2	2.963
2YPV	L_LYS_199	NZ	L_ASP_110	OD2	3.962

Table 355: 2YPV-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2YWY	A_ARG_33	NH2	A_ASP_35	OD1	3.217
2YWY	A_LYS_48	NZ	A_ASP_35	OD1	3.576
2YWY	A_LYS_48	NZ	A_ASP_35	OD2	2.413
2YWY	A_LYS_48	NZ	B_GLU_32	OE1	3.306
2YWY	A_LYS_48	NZ	B_GLU_32	OE2	2.998
2YWY	A_ARG_54	NH1	A_ASP_77	OD1	3.047
2YWY	A_ARG_54	NH1	A_ASP_77	OD2	3.216
2YWY	A_ARG_54	NH2	A_ASP_77	OD1	3.942
2YWY	A_ARG_54	NH2	A_ASP_77	OD2	2.619
2YWY	A_LYS_61	NZ	B_GLU_57	OE1	2.550
2YWY	A_LYS_61	NZ	B_GLU_57	OE2	3.211
2YWY	A_LYS_82	NZ	C_ASP_89	OD1	3.260
2YWY	A_LYS_102	NZ	A_GLU_46	OE1	2.844
2YWY	A_LYS_102	NZ	A_GLU_46	OE2	2.777
2YWY	B_LYS_25	NZ	B_ASP_4	OD1	3.823
2YWY	B_ARG_33	NH2	A_GLU_32	OE1	3.506
2YWY	B_ARG_33	NH2	B_ASP_35	OD1	3.061
2YWY	B_ARG_33	NH2	B_ASP_35	OD2	3.585
2YWY	B_ARG_38	NH2	B_ASP_77	OD1	2.791
2YWY	B_LYS_48	NZ	A_GLU_32	OE1	3.520
2YWY	B_LYS_48	NZ	A_GLU_32	OE2	2.757
2YWY	B_ARG_54	NH1	B_ASP_77	OD2	3.038
2YWY	B_ARG_54	NH2	B_ASP_77	OD1	2.760
2YWY	B_ARG_54	NH2	B_ASP_77	OD2	2.618
2YWY	B_LYS_61	NZ	A_GLU_57	OE1	3.086
2YWY	B_LYS_102	NZ	B_GLU_46	OE1	3.457
2YWY	C_LYS_12	NZ	C_GLU_16	OE2	3.484
2YWY	C_ARG_33	NH2	C_ASP_35	OD1	3.627
2YWY	C_LYS_48	NZ	C_ASP_35	OD2	3.144
2YWY	C_LYS_48	NZ	D_GLU_32	OE1	2.723
2YWY	C_LYS_48	NZ	D_GLU_32	OE2	3.404
2YWY	C_ARG_54	NH1	C_ASP_77	OD1	2.958
2YWY	C_ARG_54	NH1	C_ASP_77	OD2	3.216
2YWY	C_ARG_54	NH2	C_ASP_77	OD1	3.555
2YWY	C_ARG_54	NH2	C_ASP_77	OD2	2.224
2YWY	C_LYS_61	NZ	D_GLU_57	OE1	2.801
2YWY	C_LYS_61	NZ	D_GLU_57	OE2	3.948
2YWY	C_ARG_74	NH1	C_ASP_77	OD2	3.935
2YWY	C_LYS_102	NZ	C_GLU_46	OE1	3.626
2YWY	D_ARG_33	NH2	D_ASP_35	OD1	3.658
2YWY	D_ARG_38	NH2	D_ASP_77	OD1	2.919
2YWY	D_LYS_48	NZ	C_GLU_32	OE1	3.239
2YWY	D_LYS_48	NZ	C_GLU_32	OE2	2.447
2YWY	D_ARG_54	NH1	D_ASP_77	OD1	3.877
2YWY	D_ARG_54	NH1	D_ASP_77	OD2	2.884
2YWY	D_ARG_54	NH2	D_ASP_77	OD1	2.689
2YWY	D_ARG_54	NH2	D_ASP_77	OD2	3.195
2YWY	D_LYS_61	NZ	C_GLU_57	OE1	2.837
2YWY	D_LYS_61	NZ	C_GLU_57	OE2	3.637
2YWY	D_ARG_71	NH1	D_ASP_72	OD1	2.537
2YWY	D_ARG_71	NH1	D_ASP_72	OD2	3.727
2YWY	D_ARG_71	NH2	D_ASP_72	OD1	3.924
2YWY	D_LYS_102	NZ	D_GLU_46	OE1	3.940

Table 356: 2YWY-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2YWZ	A_ARG_8	NH1	A_ASP_4	OD2	3.114
2YWZ	A_LYS_25	NZ	A_ASP_4	OD1	3.407
2YWZ	A_ARG_54	NH1	A_ASP_77	OD1	3.632
2YWZ	A_ARG_54	NH1	A_ASP_77	OD2	2.888
2YWZ	A_ARG_54	NH2	A_ASP_77	OD1	3.024
2YWZ	A_ARG_54	NH2	A_ASP_77	OD2	3.599
2YWZ	A_ARG_74	NH1	A_ASP_72	OD2	2.842
2YWZ	A_LYS_82	NZ	A_GLU_46	OE1	3.217
2YWZ	A_LYS_82	NZ	A_GLU_46	OE2	3.322
2YWZ	A_LYS_82	NZ	A_GLU_102	OE1	3.820
2YWZ	A_LYS_82	NZ	A_GLU_102	OE2	3.005

Table 357: 2YWZ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2ZCH	P_HIS.57	ND1	P_ASP.102	OD1	3.188
2ZCH	P_HIS.57	ND1	P_ASP.102	OD2	2.701
2ZCH	P_HIS.70	NE2	P_GLU.21	OE1	3.047
2ZCH	P_LYS.119	NZ	P_ASP.116	OD1	3.130
2ZCH	P_LYS.178	NZ	H_ASP.96	OD1	3.502
2ZCH	P_LYS.178	NZ	H_ASP.96	OD2	3.400
2ZCH	P_ARG.185	NH2	P_ASP.159	OD1	3.236
2ZCH	P_ARG.185	NH2	P_ASP.159	OD2	3.391
2ZCH	P_LYS.188	NZ	P_ASP.159	OD2	3.769
2ZCH	P_LYS.230	NZ	P_GLU.129	OE1	3.520
2ZCH	P_LYS.230	NZ	P_GLU.129	OE2	2.924
2ZCH	P_ARG.235	NH1	L_ASP.28	OD2	2.443
2ZCH	P_ARG.235	NH2	L_ASP.28	OD2	3.166
2ZCH	P_LYS.236	NZ	H_GLU.100C	OE2	3.089
2ZCH	P_LYS.239	NZ	P_ASP.240	OD1	3.042
2ZCH	L_LYS.24	NZ	L_ASP.70	OD1	3.285
2ZCH	L_LYS.24	NZ	L_ASP.70	OD2	3.649
2ZCH	L_ARG.61	NH1	L_ASP.82	OD2	2.822
2ZCH	L_ARG.61	NH2	L_GLU.79	OE1	3.619
2ZCH	L_ARG.61	NH2	L_GLU.81	OE2	3.092
2ZCH	L_ARG.61	NH2	L_ASP.82	OD1	3.377
2ZCH	L_ARG.61	NH2	L_ASP.82	OD2	3.215
2ZCH	L_LYS.103	NZ	L_ASP.165	OD1	2.730
2ZCH	L_LYS.147	NZ	L_GLU.195	OE1	3.268
2ZCH	L_ARG.155	NH1	L_GLU.185	OE2	3.338
2ZCH	L_HIS.189	ND1	L_GLU.185	OE1	3.822
2ZCH	L_LYS.199	NZ	L_ASP.110	OD1	3.298
2ZCH	L_ARG.211	NH2	L_GLU.187	OE2	2.494
2ZCH	H_ARG.38	NH1	H_GLU.46	OE1	3.046
2ZCH	H_ARG.38	NH2	H_ASP.86	OD1	3.480
2ZCH	H_ARG.40	NH1	H_GLU.85	OE2	3.170
2ZCH	H_ARG.40	NH2	H_GLU.85	OE2	3.818
2ZCH	H_ARG.50	NH1	H_GLU.100C	OE1	3.902
2ZCH	H_ARG.50	NH2	L_ASP.94	OD1	2.658
2ZCH	H_ARG.50	NH2	L_ASP.94	OD2	2.887
2ZCH	H_LYS.66	NZ	H_ASP.86	OD1	3.386
2ZCH	H_ARG.94	NH2	H_ASP.101	OD1	3.421
2ZCH	H_ARG.94	NH2	H_ASP.101	OD2	2.694
2ZCH	H_LYS.208	NZ	L_GLU.123	OE1	3.921
2ZCH	H_LYS.208	NZ	L_GLU.123	OE2	3.396

Table 358: 2ZCH-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2ZCK	P_HIS_25	NE2	P_GLU_77	OE2	3.078
2ZCK	P_HIS_57	ND1	P_ASP_102	OD1	3.235
2ZCK	P_HIS_57	ND1	P_ASP_102	OD2	2.810
2ZCK	P_ARG_69	NH2	P_GLU_77	OE1	3.765
2ZCK	P_HIS_70	NE2	P_GLU_21	OE1	3.922
2ZCK	P_ARG_95G	NH2	P_GLU_218	OE2	2.834
2ZCK	P_LYS_178	NZ	H_ASP_96	OD1	3.892
2ZCK	P_LYS_178	NZ	H_ASP_96	OD2	3.060
2ZCK	P_ARG_185	NH2	P_ASP_159	OD1	2.897
2ZCK	P_ARG_185	NH2	P_ASP_159	OD2	3.599
2ZCK	P_LYS_188	NZ	P_ASP_159	OD2	3.306
2ZCK	P_LYS_231	NZ	P_GLU_129	OE1	3.939
2ZCK	P_ARG_236	NH2	L_ASP_28	OD1	3.496
2ZCK	P_LYS_240	NZ	P_ASP_241	OD1	3.131
2ZCK	L_ARG_61	NH1	L_ASP_82	OD1	3.643
2ZCK	L_ARG_61	NH1	L_ASP_82	OD2	2.898
2ZCK	L_ARG_61	NH2	L_GLU_79	OE1	3.648
2ZCK	L_ARG_61	NH2	L_GLU_81	OE2	3.878
2ZCK	L_ARG_61	NH2	L_ASP_82	OD1	3.492
2ZCK	L_LYS_103	NZ	L_ASP_165	OD1	3.500
2ZCK	L_LYS_183	NZ	L_GLU_187	OE1	3.434
2ZCK	L_LYS_183	NZ	L_GLU_187	OE2	3.899
2ZCK	L_ARG_188	NH1	L_GLU_185	OE2	3.774
2ZCK	L_ARG_188	NH2	L_ASP_184	OD1	3.893
2ZCK	L_HIS_189	ND1	L_GLU_185	OE1	3.762
2ZCK	L_HIS_189	ND1	L_GLU_185	OE2	3.555
2ZCK	H_ARG_38	NH1	H_GLU_46	OE1	3.860
2ZCK	H_ARG_38	NH1	H_GLU_46	OE2	3.777
2ZCK	H_ARG_38	NH2	H_ASP_86	OD1	2.988
2ZCK	H_ARG_50	NH2	L_ASP_94	OD1	3.095
2ZCK	H_ARG_50	NH2	L_ASP_94	OD2	2.679
2ZCK	H_ARG_94	NH2	H_ASP_101	OD1	3.492
2ZCK	H_ARG_94	NH2	H_ASP_101	OD2	2.952
2ZCK	H_LYS_208	NZ	L_GLU_123	OE2	2.731
2ZCK	H_ARG_213	NH1	H_ASP_214	OD2	3.175
2ZCK	H_ARG_213	NH2	H_ASP_214	OD2	2.814

Table 359: 2ZCK-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2ZCL	P_HIS_57	ND1	P_ASP_102	OD1	3.443
2ZCL	P_HIS_57	ND1	P_ASP_102	OD2	2.832
2ZCL	P_HIS_70	ND1	P_GLU_77	OE2	3.941
2ZCL	P_HIS_70	NE2	P_GLU_21	OE2	3.315
2ZCL	P_LYS_175	NZ	P_ASP_98	OD1	2.885
2ZCL	P_LYS_178	NZ	H_ASP_96	OD1	3.272
2ZCL	P_LYS_178	NZ	H_ASP_96	OD2	2.771
2ZCL	P_ARG_185	NH1	P_ASP_159	OD1	3.520
2ZCL	P_ARG_185	NH1	P_ASP_159	OD2	3.828
2ZCL	P_ARG_235	NH2	L_ASP_28	OD1	3.392
2ZCL	P_LYS_239	NZ	P_ASP_240	OD1	3.379
2ZCL	L_LYS_24	NZ	L_ASP_70	OD1	3.131
2ZCL	L_LYS_24	NZ	L_ASP_70	OD2	3.129
2ZCL	L_ARG_61	NH1	L_ASP_82	OD2	2.822
2ZCL	L_ARG_61	NH2	L_GLU_79	OE1	3.403
2ZCL	L_ARG_61	NH2	L_GLU_81	OE2	3.290
2ZCL	L_ARG_61	NH2	L_ASP_82	OD1	3.751
2ZCL	L_ARG_61	NH2	L_ASP_82	OD2	3.541
2ZCL	L_LYS_103	NZ	L_ASP_165	OD1	3.980
2ZCL	L_ARG_108	NH1	L_ASP_170	OD2	3.834
2ZCL	L_HIS_189	ND1	L_GLU_185	OE1	2.939
2ZCL	L_LYS_199	NZ	L_ASP_110	OD2	3.830
2ZCL	L_ARG_211	NH1	L_GLU_187	OE1	2.851
2ZCL	H_ARG_38	NH2	H_ASP_86	OD2	3.902
2ZCL	H_ARG_50	NH2	L_ASP_94	OD1	3.155
2ZCL	H_ARG_50	NH2	L_ASP_94	OD2	2.864
2ZCL	H_LYS_64	NZ	H_GLU_61	OE1	3.636
2ZCL	H_ARG_94	NH2	H_ASP_101	OD1	3.425
2ZCL	H_ARG_94	NH2	H_ASP_101	OD2	2.661

Table 360: 2ZCL-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2ZNW	A_ARG_61	NH1	A_GLU_81	OE2	3.724
2ZNW	A_ARG_61	NH2	A_GLU_81	OE1	3.857
2ZNW	A_ARG_61	NH2	A_GLU_81	OE2	2.689
2ZNW	A_ARG_61	NH2	A_ASP_82	OD1	2.714
2ZNW	A_ARG_61	NH2	A_ASP_82	OD2	3.434
2ZNW	A_LYS_103	NZ	A_GLU_105	OE1	2.950
2ZNW	A_LYS_103	NZ	A_GLU_105	OE2	3.174
2ZNW	A_ARG_160	NH1	A_ASP_211	OD1	2.916
2ZNW	A_ARG_160	NH2	A_GLU_168	OE1	2.840
2ZNW	A_ARG_160	NH2	A_ASP_211	OD1	3.551
2ZNW	A_ARG_188	NH1	A_ASP_211	OD1	3.826
2ZNW	A_ARG_188	NH1	A_ASP_211	OD2	3.091
2ZNW	A_ARG_188	NH2	A_ASP_211	OD1	3.128
2ZNW	A_ARG_188	NH2	A_ASP_211	OD2	3.623
2ZNW	A_LYS_197	NZ	A_ASP_194	OD2	3.664
2ZNW	Y_LYS_1	NZ	Y_GLU_7	OE2	2.868
2ZNW	Y_ARG_61	NH2	Y_ASP_48	OD2	3.340
2ZNW	Y_LYS_97	NZ	A_ASP_154	OD1	2.612
2ZNW	Y_LYS_97	NZ	A_ASP_154	OD2	3.786
2ZNW	Y_LYS_97	NZ	A_ASP_221	OD1	3.143
2ZNW	Y_LYS_97	NZ	A_ASP_221	OD2	3.719
2ZNW	Y_LYS_116	NZ	B_ASP_203	OD1	2.664
2ZNW	Y_ARG_125	NH1	Y_ASP_119	OD2	2.994
2ZNW	Y_ARG_125	NH2	Y_ASP_119	OD1	3.200
2ZNW	Y_ARG_125	NH2	Y_ASP_119	OD2	3.148
2ZNW	B_LYS_39	NZ	B_GLU_81	OE1	2.664
2ZNW	B_ARG_45	NH2	B_GLU_42	OE1	3.967
2ZNW	B_ARG_61	NH1	B_GLU_79	OE1	2.886
2ZNW	B_ARG_61	NH1	B_GLU_81	OE2	3.684
2ZNW	B_ARG_61	NH2	B_GLU_79	OE1	3.980
2ZNW	B_ARG_61	NH2	B_GLU_81	OE2	2.740
2ZNW	B_ARG_61	NH2	B_ASP_82	OD1	2.575
2ZNW	B_ARG_61	NH2	B_ASP_82	OD2	3.124
2ZNW	B_LYS_103	NZ	B_GLU_105	OE2	3.056
2ZNW	B_ARG_160	NH1	B_ASP_211	OD1	2.739
2ZNW	B_ARG_160	NH2	B_GLU_168	OE1	2.827
2ZNW	B_ARG_160	NH2	B_ASP_211	OD1	3.579
2ZNW	B_ARG_188	NH1	B_ASP_211	OD2	3.191
2ZNW	B_ARG_188	NH2	B_ASP_211	OD1	3.246
2ZNW	B_ARG_188	NH2	B_ASP_211	OD2	3.554
2ZNW	Z_LYS_1	NZ	Z_GLU_7	OE2	2.784
2ZNW	Z_ARG_61	NH1	Z_ASP_48	OD2	2.495
2ZNW	Z_ARG_61	NH2	Z_ASP_48	OD2	3.711
2ZNW	Z_ARG_68	NH2	Z_ASP_66	OD2	2.978
2ZNW	Z_LYS_97	NZ	B_ASP_154	OD1	3.042
2ZNW	Z_LYS_97	NZ	B_ASP_221	OD1	2.782
2ZNW	Z_LYS_97	NZ	B_ASP_221	OD2	3.319
2ZNW	Z_LYS_116	NZ	A_ASP_203	OD1	2.989
2ZNW	Z_ARG_125	NH1	Z_ASP_119	OD2	3.101
2ZNW	Z_ARG_125	NH2	Z_ASP_119	OD1	3.435
2ZNW	Z_ARG_125	NH2	Z_ASP_119	OD2	3.343

Table 361: 2ZNW-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2ZNX	A_ARG_61	NH2	A_GLU_81	OE1	3.274
2ZNX	A_ARG_61	NH2	A_GLU_81	OE2	3.380
2ZNX	A_ARG_61	NH2	A_ASP_82	OD1	2.710
2ZNX	A_ARG_61	NH2	A_ASP_82	OD2	3.576
2ZNX	A_ARG_160	NH1	A_ASP_211	OD1	2.745
2ZNX	A_ARG_160	NH2	A_GLU_168	OE1	2.794
2ZNX	A_ARG_160	NH2	A_ASP_211	OD1	3.557
2ZNX	A_ARG_188	NH1	A_ASP_211	OD1	3.903
2ZNX	A_ARG_188	NH1	A_ASP_211	OD2	3.003
2ZNX	A_ARG_188	NH2	A_ASP_211	OD1	3.102
2ZNX	A_ARG_188	NH2	A_ASP_211	OD2	3.513
2ZNX	A_LYS_197	NZ	A_ASP_194	OD2	3.759
2ZNX	Y_LYS_1	NZ	Y_GLU_7	OE2	2.738
2ZNX	Y_ARG_61	NH2	Y_ASP_48	OD2	3.990
2ZNX	Y_LYS_97	NZ	A_ASP_154	OD1	2.701
2ZNX	Y_LYS_97	NZ	A_ASP_221	OD1	2.716
2ZNX	Y_LYS_97	NZ	A_ASP_221	OD2	3.355
2ZNX	Y_LYS_116	NZ	B_ASP_203	OD1	3.871
2ZNX	Y_LYS_116	NZ	B_ASP_203	OD2	2.956
2ZNX	Y_ARG_125	NH1	Y_ASP_119	OD2	3.017
2ZNX	Y_ARG_125	NH2	Y_ASP_119	OD1	3.028
2ZNX	Y_ARG_125	NH2	Y_ASP_119	OD2	3.017
2ZNX	B_LYS_39	NZ	B_GLU_81	OE1	3.694
2ZNX	B_LYS_39	NZ	B_GLU_81	OE2	3.627
2ZNX	B_ARG_61	NH1	B_GLU_79	OE1	3.548
2ZNX	B_ARG_61	NH1	B_GLU_79	OE2	3.265
2ZNX	B_ARG_61	NH2	B_GLU_81	OE1	3.903
2ZNX	B_ARG_61	NH2	B_GLU_81	OE2	3.625
2ZNX	B_ARG_61	NH2	B_ASP_82	OD1	2.303
2ZNX	B_ARG_61	NH2	B_ASP_82	OD2	3.001
2ZNX	B_LYS_103	NZ	B_GLU_105	OE1	3.986
2ZNX	B_LYS_103	NZ	B_GLU_105	OE2	2.781
2ZNX	B_LYS_135	NZ	Y_ASP_119	OD2	3.744
2ZNX	B_ARG_160	NH1	B_ASP_211	OD1	2.901
2ZNX	B_ARG_160	NH2	B_GLU_168	OE1	2.918
2ZNX	B_ARG_160	NH2	B_ASP_211	OD1	3.424
2ZNX	B_ARG_188	NH1	B_ASP_211	OD1	3.668
2ZNX	B_ARG_188	NH1	B_ASP_211	OD2	2.960
2ZNX	B_ARG_188	NH2	B_ASP_211	OD1	2.965
2ZNX	B_ARG_188	NH2	B_ASP_211	OD2	3.589
2ZNX	Z_LYS_1	NZ	Z_GLU_7	OE2	2.717
2ZNX	Z_ARG_68	NH2	Z_ASP_66	OD2	2.870
2ZNX	Z_LYS_97	NZ	B_ASP_154	OD1	2.804
2ZNX	Z_LYS_97	NZ	B_ASP_221	OD1	3.005
2ZNX	Z_LYS_97	NZ	B_ASP_221	OD2	3.520
2ZNX	Z_LYS_116	NZ	A_ASP_203	OD1	3.699
2ZNX	Z_LYS_116	NZ	A_ASP_203	OD2	3.427
2ZNX	Z_ARG_125	NH1	Z_ASP_119	OD2	3.079
2ZNX	Z_ARG_125	NH2	Z_ASP_119	OD1	3.710
2ZNX	Z_ARG_125	NH2	Z_ASP_119	OD2	3.679

Table 362: 2ZNX-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2ZPK	L_ARG_61	NH2	L_GLU_81	OE2	3.597
2ZPK	L_ARG_61	NH2	L_ASP_82	OD1	2.750
2ZPK	L_ARG_61	NH2	L_ASP_82	OD2	3.576
2ZPK	L_HIS_95	NE2	H_ASP_62	OD1	3.977
2ZPK	L_LYS_111	NZ	L_GLU_199	OE1	3.322
2ZPK	L_HIS_189	ND1	L_ASP_152	OD2	2.821
2ZPK	H_LYS_64	NZ	H_GLU_61	OE1	2.974
2ZPK	H_ARG_66	NH1	H_ASP_86	OD1	3.749
2ZPK	H_ARG_66	NH1	H_ASP_86	OD2	2.760
2ZPK	H_ARG_66	NH2	H_ASP_86	OD1	2.842
2ZPK	H_ARG_66	NH2	H_ASP_86	OD2	3.335
2ZPK	H_LYS_143	NZ	L_GLU_125	OE2	2.882
2ZPK	H_LYS_208	NZ	L_GLU_124	OE2	3.548
2ZPK	M_LYS_39	NZ	M_GLU_81	OE2	3.913
2ZPK	M_HIS_42	ND1	M_GLU_38	OE2	3.014
2ZPK	M_ARG_61	NH2	M_GLU_81	OE1	3.031
2ZPK	M_ARG_61	NH2	M_ASP_82	OD1	2.872
2ZPK	M_ARG_61	NH2	M_ASP_82	OD2	3.561
2ZPK	I_LYS_46	NZ	I_ASP_62	OD1	3.734
2ZPK	I_ARG_66	NH1	I_ASP_86	OD1	3.902
2ZPK	I_ARG_66	NH1	I_ASP_86	OD2	2.665
2ZPK	I_ARG_66	NH2	I_ASP_86	OD1	2.915
2ZPK	I_ARG_66	NH2	I_ASP_86	OD2	3.188
2ZPK	I_LYS_143	NZ	M_GLU_125	OE2	2.672
2ZPK	I_LYS_208	NZ	M_GLU_124	OE2	3.137

Table 363: 2ZPK-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
32C2	A_ARG_24	NH1	A_ASP_74	OD2	3.409
32C2	A_ARG_65	NH1	A_GLU_83	OE1	3.875
32C2	A_ARG_65	NH1	A_ASP_86	OD1	3.841
32C2	A_ARG_65	NH1	A_ASP_86	OD2	3.487
32C2	A_ARG_65	NH2	A_GLU_83	OE1	2.370
32C2	A_ARG_65	NH2	A_GLU_83	OE2	3.913
32C2	A_ARG_65	NH2	A_ASP_86	OD1	3.622
32C2	A_LYS_106	NZ	A_GLU_108	OE2	3.990
32C2	A_LYS_152	NZ	A_GLU_198	OE1	2.795
32C2	A_LYS_152	NZ	A_GLU_198	OE2	3.245
32C2	A_ARG_158	NH2	A_GLU_188	OE2	2.691
32C2	A_LYS_186	NZ	A_GLU_190	OE1	3.548
32C2	A_HIS_192	NE2	A_ASP_154	OD2	3.916
32C2	A_LYS_202	NZ	A_ASP_113	OD1	3.644
32C2	A_LYS_202	NZ	A_ASP_113	OD2	3.444
32C2	B_ARG_39	NH1	B_ASP_90	OD1	2.671
32C2	B_ARG_39	NH2	B_GLU_47	OE1	3.125
32C2	B_ARG_39	NH2	B_ASP_90	OD1	3.482
32C2	B_ARG_67	NH1	B_ASP_90	OD1	3.556
32C2	B_ARG_67	NH1	B_ASP_90	OD2	3.694
32C2	B_ARG_67	NH2	B_ASP_90	OD1	3.933
32C2	B_ARG_67	NH2	B_ASP_90	OD2	2.676
32C2	B_LYS_76	NZ	B_ASP_73	OD1	3.680
32C2	B_LYS_76	NZ	B_ASP_73	OD2	2.879
32C2	B_LYS_214	NZ	A_GLU_126	OE1	3.056
32C2	B_LYS_214	NZ	A_GLU_126	OE2	3.702

Table 364: 32C2-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3A67	L_ARG_61	NH2	L_GLU_81	OE2	2.941
3A67	L_ARG_61	NH2	L_ASP_82	OD1	2.851
3A67	L_ARG_61	NH2	L_ASP_82	OD2	3.509
3A67	L_LYS_103	NZ	L_GLU_105	OE2	3.056
3A67	H_ARG_38	NH1	H_ASP_89	OD1	2.872
3A67	H_ARG_38	NH2	H_GLU_46	OE1	2.908
3A67	H_ARG_38	NH2	H_ASP_89	OD1	3.548
3A67	H_ARG_66	NH1	H_ASP_89	OD1	3.735
3A67	H_ARG_66	NH1	H_ASP_89	OD2	3.043
3A67	H_ARG_66	NH2	H_ASP_89	OD1	2.999
3A67	H_ARG_66	NH2	H_ASP_89	OD2	3.634
3A67	Y_LYS_1	NZ	Y_GLU_7	OE2	3.083
3A67	Y_ARG_61	NH2	Y_ASP_48	OD2	3.340
3A67	Y_ARG_68	NH2	Y_ASP_66	OD2	3.751
3A67	Y_LYS_96	NZ	L_ASP_31	OD1	2.774
3A67	Y_LYS_96	NZ	L_ASP_31	OD2	3.727
3A67	Y_LYS_97	NZ	H_ASP_32	OD1	2.657
3A67	Y_LYS_97	NZ	H_ASP_99	OD1	3.291
3A67	Y_LYS_97	NZ	H_ASP_99	OD2	2.885
3A67	Y_ARG_125	NH1	Y_ASP_119	OD2	2.827
3A67	Y_ARG_125	NH2	Y_ASP_119	OD1	3.106
3A67	Y_ARG_125	NH2	Y_ASP_119	OD2	3.044

Table 365: 3A67-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3A6B	L_ARG_61	NH2	L_GLU_81	OE2	2.699
3A6B	L_ARG_61	NH2	L_ASP_82	OD1	2.827
3A6B	L_ARG_61	NH2	L_ASP_82	OD2	3.489
3A6B	L_LYS_103	NZ	L_GLU_105	OE2	2.854
3A6B	H_ARG_38	NH1	H_ASP_89	OD1	2.881
3A6B	H_ARG_38	NH2	H_GLU_46	OE1	2.870
3A6B	H_ARG_38	NH2	H_ASP_89	OD1	3.597
3A6B	H_ARG_66	NH1	H_ASP_89	OD1	3.690
3A6B	H_ARG_66	NH1	H_ASP_89	OD2	3.008
3A6B	H_ARG_66	NH2	H_ASP_89	OD1	2.915
3A6B	H_ARG_66	NH2	H_ASP_89	OD2	3.568
3A6B	Y_LYS_1	NZ	Y_GLU_7	OE2	3.049
3A6B	Y_ARG_61	NH1	Y_ASP_48	OD1	3.308
3A6B	Y_ARG_61	NH1	Y_ASP_48	OD2	2.807
3A6B	Y_ARG_61	NH2	Y_ASP_48	OD2	3.969
3A6B	Y_LYS_96	NZ	L_ASP_32	OD1	2.734
3A6B	Y_LYS_97	NZ	H_ASP_32	OD1	2.700
3A6B	Y_LYS_97	NZ	H_ASP_32	OD2	3.941
3A6B	Y_LYS_97	NZ	H_ASP_99	OD1	2.956
3A6B	Y_LYS_97	NZ	H_ASP_99	OD2	3.259
3A6B	Y_ARG_125	NH1	Y_ASP_119	OD2	3.668
3A6B	Y_ARG_125	NH2	Y_ASP_119	OD1	3.613
3A6B	Y_ARG_125	NH2	Y_ASP_119	OD2	3.218

Table 366: 3A6B-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3A6C	L_ARG_61	NH1	L_GLU_81	OE2	3.920
3A6C	L_ARG_61	NH2	L_GLU_81	OE2	2.707
3A6C	L_ARG_61	NH2	L_ASP_82	OD1	2.812
3A6C	L_ARG_61	NH2	L_ASP_82	OD2	3.543
3A6C	L_LYS_103	NZ	L_GLU_105	OE2	3.380
3A6C	H_ARG_38	NH1	H_ASP_89	OD1	2.907
3A6C	H_ARG_38	NH2	H_GLU_46	OE1	2.827
3A6C	H_ARG_38	NH2	H_ASP_89	OD1	3.601
3A6C	H_ARG_66	NH1	H_ASP_89	OD1	3.604
3A6C	H_ARG_66	NH1	H_ASP_89	OD2	2.873
3A6C	H_ARG_66	NH2	H_ASP_89	OD1	2.870
3A6C	H_ARG_66	NH2	H_ASP_89	OD2	3.526
3A6C	Y_LYS_1	NZ	Y_GLU_7	OE1	3.880
3A6C	Y_LYS_1	NZ	Y_GLU_7	OE2	2.870
3A6C	Y_ARG_61	NH1	Y_ASP_48	OD2	2.954
3A6C	Y_ARG_61	NH2	Y_ASP_48	OD2	3.848
3A6C	Y_ARG_68	NH2	Y_ASP_66	OD2	3.805
3A6C	Y_LYS_97	NZ	H_ASP_32	OD1	2.672
3A6C	Y_LYS_97	NZ	H_ASP_32	OD2	3.916
3A6C	Y_LYS_97	NZ	H_ASP_99	OD1	2.965
3A6C	Y_LYS_97	NZ	H_ASP_99	OD2	3.291
3A6C	Y_ARG_125	NH1	Y_ASP_119	OD2	3.478
3A6C	Y_ARG_125	NH2	Y_ASP_119	OD1	3.773
3A6C	Y_ARG_125	NH2	Y_ASP_119	OD2	3.566

Table 367: 3A6C-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3AUV	A_ARG_72	NH2	A_GLU_92	OE2	3.439
3AUV	A_ARG_72	NH2	A_ASP_93	OD1	2.723
3AUV	A_ARG_72	NH2	A_ASP_93	OD2	3.631
3AUV	A_LYS_114	NZ	A_GLU_116	OE1	3.774
3AUV	A_LYS_114	NZ	A_GLU_116	OE2	3.679
3AUV	A_ARG_172	NH1	A_ASP_224	OD2	2.750
3AUV	A_ARG_172	NH2	A_GLU_180	OE1	2.793
3AUV	A_ARG_172	NH2	A_GLU_180	OE2	3.594
3AUV	A_ARG_172	NH2	A_ASP_224	OD2	3.992
3AUV	A_ARG_201	NH1	A_ASP_224	OD1	2.699
3AUV	A_ARG_201	NH1	A_ASP_224	OD2	3.899
3AUV	A_ARG_201	NH2	A_ASP_224	OD1	3.500
3AUV	A_ARG_201	NH2	A_ASP_224	OD2	3.246
3AUV	A_ARG_232	NH2	A_ASP_242	OD1	2.869
3AUV	A_ARG_232	NH2	A_ASP_242	OD2	3.766
3AUV	B_ARG_72	NH2	B_GLU_92	OE2	3.579
3AUV	B_ARG_72	NH2	B_ASP_93	OD1	2.590
3AUV	B_ARG_72	NH2	B_ASP_93	OD2	3.569
3AUV	B_LYS_114	NZ	B_GLU_116	OE1	3.722
3AUV	B_LYS_114	NZ	B_GLU_116	OE2	3.387
3AUV	B_ARG_172	NH1	B_ASP_224	OD2	2.806
3AUV	B_ARG_172	NH2	B_GLU_180	OE1	2.717
3AUV	B_ARG_172	NH2	B_GLU_180	OE2	3.567
3AUV	B_ARG_201	NH1	B_ASP_224	OD1	2.684
3AUV	B_ARG_201	NH1	B_ASP_224	OD2	3.823
3AUV	B_ARG_201	NH2	B_ASP_224	OD1	3.593
3AUV	B_ARG_201	NH2	B_ASP_224	OD2	3.291
3AUV	B_LYS_210	NZ	B_ASP_207	OD1	3.963
3AUV	B_ARG_232	NH2	B_ASP_242	OD1	2.862
3AUV	B_ARG_232	NH2	B_ASP_242	OD2	3.702
3AUV	C_ARG_72	NH2	C_GLU_92	OE2	3.470
3AUV	C_ARG_72	NH2	C_ASP_93	OD1	2.695
3AUV	C_ARG_72	NH2	C_ASP_93	OD2	3.642
3AUV	C_LYS_114	NZ	C_GLU_116	OE1	3.676
3AUV	C_LYS_114	NZ	C_GLU_116	OE2	3.581
3AUV	C_ARG_172	NH1	C_ASP_224	OD2	2.837
3AUV	C_ARG_172	NH2	C_GLU_180	OE1	2.666
3AUV	C_ARG_172	NH2	C_GLU_180	OE2	3.575
3AUV	C_ARG_201	NH1	C_ASP_224	OD1	2.642
3AUV	C_ARG_201	NH1	C_ASP_224	OD2	3.881
3AUV	C_ARG_201	NH2	C_ASP_224	OD1	3.488
3AUV	C_ARG_201	NH2	C_ASP_224	OD2	3.269
3AUV	C_ARG_232	NH2	C_ASP_242	OD1	2.909
3AUV	C_ARG_232	NH2	C_ASP_242	OD2	3.643
3AUV	D_ARG_72	NH2	D_GLU_92	OE2	3.526
3AUV	D_ARG_72	NH2	D_ASP_93	OD1	2.640
3AUV	D_ARG_72	NH2	D_ASP_93	OD2	3.608
3AUV	D_LYS_114	NZ	D_GLU_116	OE1	3.727
3AUV	D_LYS_114	NZ	D_GLU_116	OE2	3.600
3AUV	D_ARG_172	NH1	D_ASP_224	OD2	2.810
3AUV	D_ARG_172	NH2	D_GLU_180	OE1	2.707
3AUV	D_ARG_172	NH2	D_GLU_180	OE2	3.528
3AUV	D_ARG_201	NH1	D_ASP_224	OD1	2.734
3AUV	D_ARG_201	NH1	D_ASP_224	OD2	3.954
3AUV	D_ARG_201	NH2	D_ASP_224	OD1	3.560
3AUV	D_ARG_201	NH2	D_ASP_224	OD2	3.357
3AUV	D_ARG_232	NH2	D_ASP_242	OD1	2.882

3AUV	D_ARG_232	NH2	D_ASP_242	OD2	3.743
3AUV	E_ARG_72	NH2	E_GLU_92	OE2	3.531
3AUV	E_ARG_72	NH2	E_ASP_93	OD1	2.643
3AUV	E_ARG_72	NH2	E_ASP_93	OD2	3.543
3AUV	E_LYS_114	NZ	E_GLU_116	OE1	3.794
3AUV	E_LYS_114	NZ	E_GLU_116	OE2	3.627
3AUV	E_ARG_172	NH1	E_ASP_224	OD2	2.874
3AUV	E_ARG_172	NH2	E_GLU_180	OE1	2.698
3AUV	E_ARG_172	NH2	E_GLU_180	OE2	3.466
3AUV	E_ARG_201	NH1	E_ASP_224	OD1	2.747
3AUV	E_ARG_201	NH1	E_ASP_224	OD2	3.871
3AUV	E_ARG_201	NH2	E_ASP_224	OD1	3.622
3AUV	E_ARG_201	NH2	E_ASP_224	OD2	3.262
3AUV	E_ARG_232	NH2	E_ASP_242	OD1	2.876
3AUV	E_ARG_232	NH2	E_ASP_242	OD2	3.697
3AUV	F_ARG_72	NH2	F_GLU_92	OE2	3.450
3AUV	F_ARG_72	NH2	F_ASP_93	OD1	2.646
3AUV	F_ARG_72	NH2	F_ASP_93	OD2	3.561
3AUV	F_LYS_114	NZ	F_GLU_116	OE1	3.643
3AUV	F_LYS_114	NZ	F_GLU_116	OE2	3.465
3AUV	F_ARG_172	NH1	F_ASP_224	OD2	2.862
3AUV	F_ARG_172	NH2	F_GLU_180	OE1	2.639
3AUV	F_ARG_172	NH2	F_GLU_180	OE2	3.493
3AUV	F_ARG_201	NH1	F_ASP_224	OD1	2.716
3AUV	F_ARG_201	NH2	F_ASP_224	OD1	3.519
3AUV	F_ARG_201	NH2	F_ASP_224	OD2	3.349
3AUV	F_LYS_210	NZ	F_ASP_207	OD1	3.959
3AUV	F_ARG_232	NH2	F_ASP_242	OD1	2.985
3AUV	F_ARG_232	NH2	F_ASP_242	OD2	3.837

Table 368: 3AUV-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3B9K	L_ARG_61	NH1	L_GLU_81	OE2	3.453
3B9K	L_ARG_61	NH1	L_ASP_82	OD1	2.335
3B9K	L_ARG_61	NH1	L_ASP_82	OD2	3.046
3B9K	L_ARG_61	NH2	L_GLU_81	OE2	2.771
3B9K	L_LYS_149	NZ	L_GLU_195	OE1	3.690
3B9K	L_LYS_149	NZ	L_GLU_195	OE2	2.757
3B9K	L_HIS_189	ND1	L_ASP_151	OD2	2.589
3B9K	L_LYS_199	NZ	L_ASP_110	OD1	3.618
3B9K	H_ARG_38	NH1	H_ASP_86	OD1	2.944
3B9K	H_ARG_38	NH2	H_GLU_46	OE1	3.373
3B9K	H_ARG_38	NH2	H_ASP_86	OD1	3.659
3B9K	H_ARG_66	NH1	H_ASP_86	OD1	3.550
3B9K	H_ARG_66	NH2	H_ASP_86	OD1	3.185
3B9K	H_ARG_66	NH2	H_ASP_86	OD2	2.639
3B9K	H_HIS_172	NE2	H_ASP_167	OD1	3.568
3B9K	H_LYS_221	NZ	L_GLU_123	OE1	2.886
3B9K	A_ARG_8	NH1	A_GLU_6	OE2	3.916
3B9K	A_LYS_13	NZ	B_ASP_42	OD2	3.894
3B9K	B_LYS_17	NZ	B_GLU_72	OE1	3.264
3B9K	B_LYS_27	NZ	H_ASP_32	OD1	2.409
3B9K	B_ARG_35	NH2	B_ASP_92	OD2	2.954
3B9K	B_ARG_37	NH1	B_ASP_39	OD1	3.890
3B9K	B_ARG_37	NH2	B_GLU_46	OE1	3.384
3B9K	B_ARG_37	NH2	B_GLU_46	OE2	3.762
3B9K	B_ARG_37	NH2	B_ASP_64	OD1	3.954
3B9K	B_ARG_37	NH2	B_ASP_64	OD2	3.329
3B9K	B_LYS_43	NZ	B_GLU_36	OE2	3.566
3B9K	B_ARG_77	NH1	B_GLU_21	OE2	3.466
3B9K	B_ARG_77	NH2	L_ASP_92	OD1	3.184
3B9K	B_ARG_77	NH2	B_GLU_21	OE2	3.014
3B9K	B_ARG_78	NH2	L_ASP_92	OD1	2.834
3B9K	B_LYS_103	NZ	A_ASP_66	OD1	3.058
3B9K	C_ARG_	NH1	C_GLU_81	OE2	3.400
3B9K	C_ARG_	NH1	C_ASP_82	OD1	2.519
3B9K	C_ARG_	NH1	C_ASP_	OD2	2.958
3B9K	C_ARG_	NH2	C_GLU_81	OE2	2.927
3B9K	C_LYS_149	NZ	C_GLU_195	OE2	3.057
3B9K	C_LYS_183	NZ	C_GLU_187	OE1	2.738
3B9K	C_HIS_189	ND1	C_ASP_151	OD1	3.967
3B9K	C_HIS_189	ND1	C_ASP_151	OD2	2.217
3B9K	C_LYS_	NZ	C_ASP_	OD1	3.537
3B9K	C_LYS_	NZ	C_ASP_	OD2	2.778
3B9K	D_ARG_38	NH1	D_ASP_86	OD1	2.985
3B9K	D_ARG_38	NH2	D_GLU_46	OE1	3.027
3B9K	D_ARG_38	NH2	D_ASP_86	OD1	3.686
3B9K	D_ARG_66	NH1	D_ASP_86	OD1	3.146
3B9K	D_ARG_66	NH1	D_ASP_86	OD2	3.512
3B9K	D_ARG_66	NH2	D_ASP_86	OD1	3.576
3B9K	D_ARG_66	NH2	D_ASP_86	OD2	2.412
3B9K	D_ARG_96	NH1	D_GLU_97	OE2	2.918
3B9K	D_ARG_96	NH2	D_GLU_97	OE2	3.934
3B9K	D_HIS_172	NE2	D_ASP_167	OD1	2.867
3B9K	D_LYS_221	NZ	C_GLU_123	OE1	3.178
3B9K	E_ARG_8	NH1	E_GLU_27	OE1	3.719
3B9K	E_ARG_8	NH2	E_GLU_27	OE1	3.635
3B9K	E_LYS_	NZ	E_ASP_23	OD1	3.889
3B9K	F_LYS_27	NZ	D_ASP_32	OD1	2.318

3B9K	F_ARG_35	NH2	F_ASP_39	OD2	3.634
3B9K	F_ARG_35	NH2	F_ASP_92	OD2	2.801
3B9K	F_ARG_37	NH1	F_ASP_39	OD2	3.691
3B9K	F_ARG_37	NH2	F_GLU_46	OE1	3.350
3B9K	F_ARG_77	NH1	F_GLU_21	OE2	3.321
3B9K	F_ARG_77	NH2	C_ASP_92	OD1	2.984
3B9K	F_ARG_77	NH2	F_GLU_21	OE2	3.185
3B9K	F_ARG_78	NH2	C_ASP_92	OD1	3.141
3B9K	F_ARG_78	NH2	C_ASP_92	OD2	3.951
3B9K	F_LYS_103	NZ	E_ASP_	OD1	3.044

Table 369: 3B9K-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3BDY	H_ARG_38	NH1	H_ASP_86	OD1	2.999
3BDY	H_ARG_38	NH2	H_GLU_46	OE1	2.808
3BDY	H_ARG_38	NH2	H_GLU_46	OE2	3.622
3BDY	H_ARG_66	NH1	H_ASP_86	OD1	3.951
3BDY	H_ARG_66	NH1	H_ASP_86	OD2	3.006
3BDY	H_ARG_66	NH2	H_ASP_86	OD1	3.023
3BDY	H_ARG_66	NH2	H_ASP_86	OD2	3.512
3BDY	H_ARG_94	NH2	H_ASP_103	OD1	3.777
3BDY	H_ARG_94	NH2	H_ASP_103	OD2	3.008
3BDY	H_LYS_145	NZ	H_ASP_146	OD1	3.125
3BDY	H_LYS_145	NZ	H_ASP_146	OD2	3.665
3BDY	H_LYS_211	NZ	L_GLU_123	OE2	2.706
3BDY	L_ARG_24	NH1	L_ASP_70	OD1	2.932
3BDY	L_ARG_24	NH1	L_ASP_70	OD2	3.729
3BDY	L_ARG_27D	NH2	L_ASP_70	OD2	3.711
3BDY	L_ARG_61	NH2	L_GLU_81	OE1	3.501
3BDY	L_ARG_61	NH2	L_ASP_82	OD1	2.848
3BDY	L_ARG_61	NH2	L_ASP_82	OD2	3.523
3BDY	L_HIS_189	ND1	L_ASP_151	OD2	2.958
3BDY	V_ARG_56	NH1	V_GLU_38	OE1	3.008
3BDY	V_ARG_56	NH1	V_GLU_38	OE2	3.618
3BDY	V_ARG_56	NH2	V_GLU_38	OE1	3.690
3BDY	V_ARG_82	NH2	V_GLU_42	OE1	3.019
3BDY	V_ARG_82	NH2	V_GLU_42	OE2	3.920
3BDY	V_LYS_84	NZ	V_GLU_44	OE2	3.490
3BDY	V_LYS_	NZ	V_GLU_	OE1	2.740
3BDY	V_ARG_	NH1	V_GLU_	OE1	3.312
3BDY	V_ARG_	NH1	V_GLU_	OE2	3.557

Table 370: 3BDY-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3BE1	A_ARG_25	NH2	A_ASP_22	OD1	3.635
3BE1	A_ARG_25	NH2	A_ASP_22	OD2	3.334
3BE1	A_HIS_66	NE2	A_ASP_96	OD2	3.628
3BE1	A_ARG_81	NH2	A_GLU_57	OE1	3.307
3BE1	A_ARG_121	NH1	A_ASP_189	OD1	2.843
3BE1	A_ARG_121	NH1	A_ASP_189	OD2	3.507
3BE1	A_ARG_135	NH2	A_ASP_96	OD1	3.481
3BE1	A_ARG_135	NH2	A_ASP_96	OD2	3.295
3BE1	A_ARG_166	NH1	A_ASP_143	OD2	3.604
3BE1	A_ARG_166	NH2	A_ASP_143	OD1	3.395
3BE1	A_ARG_166	NH2	A_ASP_143	OD2	3.597
3BE1	A_HIS_171	ND1	A_GLU_185	OE1	2.686
3BE1	A_ARG_204	NH1	A_ASP_149	OD2	3.810
3BE1	A_ARG_204	NH2	A_GLU_125	OE1	3.119
3BE1	A_ARG_204	NH2	A_GLU_125	OE2	3.480
3BE1	A_HIS_215	ND1	A_GLU_216	OE2	3.902
3BE1	A_HIS_238	ND1	A_GLU_243	OE1	2.848
3BE1	A_HIS_238	ND1	A_GLU_243	OE2	3.970
3BE1	A_ARG_308	NH2	A_ASP_285	OD1	3.913
3BE1	A_HIS_327	NE2	A_GLU_341	OE2	3.469
3BE1	A_ARG_332	NH2	A_GLU_357	OE2	2.835
3BE1	A_LYS_346	NZ	A_GLU_382	OE1	3.395
3BE1	A_LYS_346	NZ	A_GLU_382	OE2	3.325
3BE1	A_LYS_347	NZ	A_GLU_299	OE1	3.844
3BE1	A_LYS_347	NZ	A_GLU_383	OE1	2.990
3BE1	A_LYS_347	NZ	A_GLU_383	OE2	3.026
3BE1	A_ARG_410	NH1	A_GLU_438	OE2	3.687
3BE1	A_ARG_410	NH2	A_GLU_383	OE1	3.367
3BE1	A_ARG_410	NH2	A_GLU_383	OE2	3.274
3BE1	A_ARG_412	NH1	A_GLU_299	OE1	3.591
3BE1	A_ARG_412	NH1	A_GLU_299	OE2	3.484
3BE1	A_ARG_437	NH1	A_GLU_438	OE1	3.301
3BE1	A_ARG_465	NH2	A_GLU_438	OE1	3.503
3BE1	A_ARG_477	NH1	A_GLU_485	OE1	3.451
3BE1	A_ARG_477	NH2	A_GLU_481	OE1	3.986
3BE1	A_ARG_477	NH2	A_GLU_485	OE1	3.615
3BE1	A_ARG_477	NH2	A_GLU_485	OE2	3.180
3BE1	A_ARG_514	NH2	A_GLU_531	OE1	3.183
3BE1	A_ARG_523	NH1	A_GLU_531	OE1	3.371
3BE1	A_ARG_523	NH1	A_GLU_531	OE2	3.636
3BE1	A_LYS_593	NZ	A_ASP_570	OD1	2.769
3BE1	A_LYS_593	NZ	A_ASP_570	OD2	2.849
3BE1	H_ARG_38	NH1	H_ASP_86	OD1	3.053
3BE1	H_ARG_38	NH2	H_GLU_46	OE1	3.297
3BE1	H_ARG_38	NH2	H_ASP_86	OD1	3.486
3BE1	H_ARG_50	NH1	A_ASP_560	OD2	3.215
3BE1	H_ARG_50	NH2	A_GLU_558	OE1	3.092
3BE1	H_ARG_50	NH2	A_GLU_558	OE2	3.263
3BE1	H_ARG_50	NH2	A_ASP_560	OD1	3.492
3BE1	H_ARG_50	NH2	A_ASP_560	OD2	3.175
3BE1	H_ARG_66	NH1	H_ASP_86	OD2	3.082
3BE1	H_ARG_66	NH2	H_ASP_86	OD1	3.252
3BE1	H_ARG_66	NH2	H_ASP_86	OD2	3.284
3BE1	H_ARG_94	NH2	H_ASP_103	OD1	3.969
3BE1	H_ARG_94	NH2	H_ASP_103	OD2	3.289
3BE1	L_ARG_24	NH1	L_ASP_70	OD1	3.044
3BE1	L_ARG_61	NH2	L_GLU_81	OE1	3.206

3BE1	L_ARG_61	NH2	L_ASP_82	OD1	2.979
3BE1	L_ARG_61	NH2	L_ASP_82	OD2	3.663
3BE1	L_LYS_149	NZ	L_GLU_195	OE2	2.739
3BE1	L_LYS_183	NZ	L_GLU_187	OE2	3.540
3BE1	L_LYS_188	NZ	L_ASP_185	OD1	3.780
3BE1	L_HIS_189	ND1	L_ASP_151	OD1	3.324
3BE1	L_HIS_189	ND1	L_ASP_151	OD2	2.626
3BE1	L_ARG_211	NH2	L_GLU_187	OE1	3.516

Table 371: 3BE1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3BGF	S_ARG_342	NH2	S_ASP_385	OD1	3.676
3BGF	S_ARG_342	NH2	S_ASP_385	OD2	3.162
3BGF	S_ARG_426	NH1	H_ASP_56	OD1	3.504
3BGF	S_ARG_426	NH1	H_ASP_56	OD2	2.403
3BGF	S_LYS_439	NZ	S_ASP_480	OD1	3.797
3BGF	S_LYS_439	NZ	A_ASP_480	OD2	3.161
3BGF	S_ARG_441	NH2	S_ASP_454	OD1	2.963
3BGF	S_ARG_444	NH2	S_GLU_452	OE2	3.267
3BGF	S_ARG_444	NH2	S_ASP_454	OD2	3.815
3BGF	S_LYS_447	NZ	S_ASP_407	OD1	3.987
3BGF	S_LYS_447	NZ	S_ASP_407	OD2	3.876
3BGF	S_ARG_449	NH2	S_GLU_452	OE1	3.535
3BGF	S_ARG_495	NH2	S_ASP_429	OD1	3.362
3BGF	S_ARG_495	NH2	S_ASP_429	OD2	3.615
3BGF	A_ARG_342	NH2	A_ASP_385	OD1	3.423
3BGF	A_ARG_342	NH2	A_ASP_385	OD2	2.961
3BGF	A_LYS_390	NZ	A_ASP_393	OD1	3.583
3BGF	A_LYS_390	NZ	A_ASP_393	OD2	3.966
3BGF	A_LYS_439	NZ	S_ASP_480	OD2	2.520
3BGF	A_LYS_439	NZ	A_ASP_480	OD1	3.180
3BGF	A_ARG_441	NH2	A_ASP_454	OD1	3.440
3BGF	A_ARG_444	NH2	A_GLU_452	OE2	3.371
3BGF	A_ARG_444	NH2	A_ASP_454	OD2	3.730
3BGF	A_LYS_447	NZ	A_ASP_407	OD1	2.877
3BGF	A_LYS_447	NZ	A_ASP_407	OD2	2.805
3BGF	A_ARG_495	NH2	A_ASP_429	OD1	3.108
3BGF	A_ARG_495	NH2	A_ASP_429	OD2	2.922
3BGF	L_ARG_24	NH2	L_ASP_70	OD1	3.258
3BGF	L_ARG_24	NH2	L_ASP_70	OD2	2.893
3BGF	L_ARG_46	NH1	L_ASP_55	OD1	3.016
3BGF	L_ARG_46	NH1	L_ASP_55	OD2	3.557
3BGF	L_ARG_61	NH1	L_GLU_79	OE1	3.984
3BGF	L_ARG_61	NH1	L_GLU_79	OE2	3.405
3BGF	L_ARG_61	NH2	L_ASP_82	OD1	2.650
3BGF	L_ARG_61	NH2	L_ASP_82	OD2	2.907
3BGF	L_ARG_66	NH2	L_GLU_28	OE2	2.738
3BGF	L_LYS_149	NZ	L_GLU_195	OE1	3.683
3BGF	L_LYS_149	NZ	L_GLU_195	OE2	3.129
3BGF	L_HIS_189	ND1	L_ASP_151	OD1	2.696
3BGF	H_ARG_33	NH1	H_ASP_56	OD2	3.848
3BGF	H_HIS_35	NE2	H_GLU_95	OE1	2.884
3BGF	H_LYS_38	NZ	H_ASP_86	OD1	3.661
3BGF	H_LYS_62	NZ	H_GLU_46	OE1	2.635
3BGF	H_LYS_62	NZ	H_GLU_46	OE2	3.712
3BGF	H_LYS_66	NZ	H_ASP_86	OD1	3.553
3BGF	H_LYS_66	NZ	H_ASP_86	OD2	2.671
3BGF	H_ARG_94	NH1	H_ASP_101	OD1	2.347
3BGF	H_ARG_94	NH1	H_ASP_101	OD2	3.381
3BGF	H_LYS_210	NZ	L_GLU_123	OE1	3.997
3BGF	H_LYS_211	NZ	H_GLU_213	OE2	3.764
3BGF	C_ARG_24	NH2	C_ASP_70	OD1	3.766
3BGF	C_ARG_46	NH1	C_ASP_55	OD1	2.965
3BGF	C_ARG_61	NH1	C_GLU_79	OE1	3.352
3BGF	C_ARG_61	NH1	C_GLU_79	OE2	3.278
3BGF	C_ARG_61	NH2	C_GLU_81	OE2	3.045
3BGF	C_ARG_61	NH2	C_ASP_82	OD1	2.379
3BGF	C_ARG_61	NH2	C_ASP_82	OD2	2.905

3BGF	C_ARG_66	NH2	C_GLU_28	OE1	3.607
3BGF	C_ARG_66	NH2	C_GLU_28	OE2	2.938
3BGF	C_LYS_142	NZ	C_GLU_105	OE1	3.341
3BGF	C_LYS_149	NZ	C_GLU_195	OE1	3.352
3BGF	C_LYS_149	NZ	C_GLU_195	OE2	3.898
3BGF	C_ARG_155	NH2	C_GLU_185	OE2	3.481
3BGF	C_LYS_199	NZ	C_ASP_110	OD2	3.825
3BGF	B_HIS_35	NE2	B_GLU_95	OE1	2.642
3BGF	B_LYS_38	NZ	B_ASP_86	OD1	3.591
3BGF	B_LYS_62	NZ	B_GLU_46	OE1	2.547
3BGF	B_LYS_62	NZ	B_GLU_46	OE2	3.280
3BGF	B_LYS_66	NZ	B_ASP_86	OD1	3.814
3BGF	B_LYS_66	NZ	B_ASP_86	OD2	2.805
3BGF	B_ARG_94	NH1	B_ASP_101	OD1	2.357
3BGF	B_ARG_94	NH1	B_ASP_101	OD2	2.930
3BGF	B_ARG_100B	NH1	B_ASP_101	OD1	3.816

Table 372: 3BGF-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3BIK	A_ARG_84	NH1	A_ASP_108	OD1	2.911
3BIK	A_ARG_84	NH1	A_ASP_108	OD2	3.517
3BIK	A_ARG_84	NH2	A_ASP_108	OD1	3.587
3BIK	A_ARG_84	NH2	A_ASP_108	OD2	2.826
3BIK	A_LYS_105	NZ	A_ASP_103	OD2	3.863
3BIK	A_ARG_113	NH2	B_GLU_136	OE2	3.149
3BIK	A_LYS_124	NZ	A_ASP_122	OD1	3.019
3BIK	A_LYS_124	NZ	A_ASP_122	OD2	3.912
3BIK	A_ARG_125	NH2	B_GLU_136	OE1	3.033
3BIK	A_ARG_125	NH2	B_GLU_136	OE2	3.001
3BIK	A_ARG_198	NH1	A_GLU_152	OE1	3.772
3BIK	A_ARG_198	NH2	A_GLU_152	OE1	3.590
3BIK	A_ARG_213	NH1	A_GLU_218	OE2	3.954
3BIK	A_ARG_213	NH2	A_GLU_218	OE1	3.723
3BIK	A_ARG_213	NH2	A_GLU_218	OE2	3.505
3BIK	A_HIS_220	NE2	A_GLU_218	OE1	3.627
3BIK	A_HIS_220	NE2	A_GLU_218	OE2	3.391
3BIK	B_ARG_33	NH1	B_GLU_135	OE2	3.354
3BIK	B_ARG_94	NH1	B_ASP_117	OD1	3.896
3BIK	B_ARG_94	NH1	B_ASP_117	OD2	2.841
3BIK	B_ARG_94	NH2	B_ASP_92	OD2	2.969
3BIK	B_ARG_94	NH2	B_ASP_117	OD1	3.201
3BIK	B_ARG_94	NH2	B_ASP_117	OD2	3.582
3BIK	B_ARG_103	NH2	B_GLU_61	OE1	3.685
3BIK	B_HIS_104	NE2	B_ASP_105	OD1	3.734
3BIK	C_ARG_33	NH2	C_GLU_135	OE2	3.450
3BIK	C_ARG_94	NH1	C_ASP_117	OD1	3.747
3BIK	C_ARG_94	NH1	C_ASP_117	OD2	2.682
3BIK	C_ARG_94	NH2	C_ASP_92	OD2	3.003
3BIK	C_ARG_94	NH2	C_ASP_117	OD1	2.982
3BIK	C_ARG_94	NH2	C_ASP_117	OD2	3.409
3BIK	C_HIS_104	ND1	C_ASP_105	OD1	2.573
3BIK	C_HIS_104	ND1	C_ASP_105	OD2	3.992
3BIK	C_ARG_114	NH1	C_ASP_92	OD2	3.856
3BIK	C_ARG_115	NH1	C_GLU_146	OE1	3.596
3BIK	C_HIS_129	NE2	C_ASP_62	OD1	3.754

Table 373: 3BIK-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3BIS	A_ARG_84	NH1	A_ASP_108	OD1	2.733
3BIS	A_ARG_84	NH1	A_ASP_108	OD2	3.411
3BIS	A_ARG_84	NH2	A_ASP_108	OD1	3.339
3BIS	A_ARG_84	NH2	A_ASP_108	OD2	2.608
3BIS	A_LYS_105	NZ	A_GLU_187	OE1	3.664
3BIS	A_LYS_124	NZ	A_ASP_122	OD1	3.773
3BIS	A_ARG_140	NH2	A_GLU_152	OE1	3.939
3BIS	A_ARG_186	NH1	A_GLU_158	OE1	2.989
3BIS	A_ARG_186	NH1	A_GLU_158	OE2	3.114
3BIS	A_LYS_189	NZ	A_GLU_188	OE1	3.362
3BIS	A_ARG_198	NH1	A_GLU_150	OE1	3.697
3BIS	A_ARG_198	NH1	A_GLU_150	OE2	2.793
3BIS	A_ARG_198	NH2	A_GLU_152	OE2	2.965
3BIS	A_ARG_212	NH2	A_GLU_217	OE1	3.792
3BIS	A_HIS_220	NE2	A_GLU_218	OE1	2.735
3BIS	B_ARG_84	NH1	B_ASP_108	OD1	3.434
3BIS	B_ARG_84	NH1	B_ASP_108	OD2	3.455
3BIS	B_ARG_84	NH2	B_ASP_108	OD2	2.983
3BIS	B_LYS_105	NZ	B_GLU_188	OE2	3.684
3BIS	B_ARG_113	NH2	B_GLU_58	OE1	3.749
3BIS	B_LYS_124	NZ	B_ASP_122	OD1	3.846
3BIS	B_ARG_140	NH2	B_GLU_152	OE2	3.790
3BIS	B_ARG_198	NH1	B_GLU_150	OE1	2.555
3BIS	B_ARG_212	NH2	B_GLU_164	OE1	3.367
3BIS	B_ARG_213	NH2	B_GLU_218	OE2	3.315

Table 374: 3BIS-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3BKY	H_LYS_38	NZ	H_ASP_90	OD1	3.615
3BKY	H_LYS_63	NZ	H_GLU_46	OE1	3.943
3BKY	H_LYS_63	NZ	H_GLU_46	OE2	3.735
3BKY	H_LYS_67	NZ	H_ASP_90	OD2	2.780
3BKY	H_ARG_98	NH1	H_ASP_110	OD1	3.350
3BKY	H_ARG_98	NH2	H_ASP_110	OD1	3.826
3BKY	H_LYS_138	NZ	L_GLU_212	OE2	2.743
3BKY	H_LYS_152	NZ	H_ASP_153	OD1	3.472
3BKY	H_LYS_152	NZ	H_ASP_153	OD2	3.466
3BKY	L_ARG_60	NH2	L_GLU_80	OE2	3.597
3BKY	L_ARG_60	NH2	L_ASP_81	OD1	2.516
3BKY	L_ARG_60	NH2	L_ASP_81	OD2	3.432
3BKY	L_ARG_76	NH1	L_GLU_78	OE1	2.817
3BKY	L_LYS_102	NZ	L_GLU_164	OE1	3.978
3BKY	L_LYS_182	NZ	L_GLU_186	OE1	3.284
3BKY	L_LYS_187	NZ	L_ASP_184	OD1	3.336
3BKY	L_HIS_188	ND1	L_ASP_150	OD2	2.994

Table 375: 3BKY-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3BO8	A_HIS_3	ND1	A_ASP_29	OD1	3.478
3BO8	A_HIS_3	ND1	A_ASP_29	OD2	2.703
3BO8	A_ARG_6	NH1	A_ASP_102	OD1	2.861
3BO8	A_ARG_6	NH2	A_ASP_102	OD1	2.772
3BO8	A_ARG_6	NH2	A_ASP_102	OD2	3.556
3BO8	A_ARG_14	NH1	A_ASP_39	OD1	3.690
3BO8	A_ARG_14	NH1	A_ASP_39	OD2	2.892
3BO8	A_ARG_14	NH2	A_ASP_39	OD1	3.076
3BO8	A_ARG_14	NH2	A_ASP_39	OD2	3.735
3BO8	A_ARG_21	NH1	A_ASP_39	OD2	3.805
3BO8	A_ARG_21	NH2	A_ASP_37	OD1	3.686
3BO8	A_ARG_21	NH2	A_ASP_37	OD2	2.860
3BO8	A_ARG_35	NH1	A_ASP_37	OD2	3.901
3BO8	A_ARG_35	NH1	B_ASP_53	OD1	3.541
3BO8	A_ARG_35	NH2	A_GLU_46	OE2	3.239
3BO8	A_ARG_48	NH1	B_ASP_53	OD1	3.101
3BO8	A_ARG_48	NH1	B_ASP_53	OD2	3.041
3BO8	A_ARG_48	NH2	B_ASP_53	OD1	3.771
3BO8	A_ARG_48	NH2	B_ASP_53	OD2	3.368
3BO8	A_HIS_70	NE2	A_ASP_74	OD1	3.486
3BO8	A_HIS_70	NE2	A_ASP_74	OD2	3.411
3BO8	A_ARG_75	NH1	A_GLU_19	OE1	2.819
3BO8	A_HIS_93	ND1	A_ASP_119	OD1	3.501
3BO8	A_HIS_93	ND1	A_ASP_119	OD2	2.724
3BO8	A_ARG_111	NH2	A_GLU_128	OE1	3.927
3BO8	A_ARG_114	NH2	A_ASP_116	OD1	3.531
3BO8	A_ARG_114	NH2	A_ASP_116	OD2	3.063
3BO8	A_LYS_144	NZ	A_GLU_148	OE1	3.974
3BO8	A_LYS_144	NZ	A_GLU_148	OE2	2.691
3BO8	A_ARG_156	NH1	C_ASP_3	OD1	3.842
3BO8	A_ARG_156	NH1	C_ASP_3	OD2	2.711
3BO8	A_ARG_163	NH1	A_ASP_166	OD2	3.922
3BO8	A_ARG_163	NH2	C_GLU_1	OE1	3.484
3BO8	A_ARG_163	NH2	C_GLU_1	OE2	2.848
3BO8	A_ARG_170	NH1	C_GLU_1	OE2	2.801
3BO8	A_ARG_170	NH2	A_GLU_55	OE1	3.555
3BO8	A_ARG_170	NH2	A_GLU_55	OE2	3.453
3BO8	A_ARG_170	NH2	C_GLU_1	OE2	3.023
3BO8	A_LYS_176	NZ	A_GLU_173	OE2	3.954
3BO8	A_HIS_191	NE2	A_GLU_254	OE2	2.780
3BO8	A_HIS_192	NE2	B_ASP_98	OD1	3.566
3BO8	A_HIS_192	NE2	B_ASP_98	OD2	3.950
3BO8	A_ARG_256	NH1	A_GLU_253	OE1	2.918
3BO8	A_ARG_256	NH2	A_ASP_220	OD1	3.803
3BO8	A_ARG_256	NH2	A_ASP_220	OD2	2.636
3BO8	B_LYS_75	NZ	B_GLU_74	OE1	3.603
3BO8	B_ARG_81	NH2	B_ASP_38	OD2	2.762

Table 376: 3BO8-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3BT2	A_HIS_29	NE2	A_ASP_12	OD1	2.667
3BT2	A_HIS_29	NE2	A_ASP_12	OD2	2.134
3BT2	A_HIS_41	NE2	A_ASP_12	OD1	3.088
3BT2	A_HIS_41	NE2	A_ASP_12	OD2	2.030
3BT2	A_ARG_69	NH2	A_ASP_65	OD2	3.423
3BT2	A_HIS_87	ND1	U_ASP_11	OD2	3.629
3BT2	A_ARG_88	NH1	A_ASP_90	OD1	3.618
3BT2	A_ARG_88	NH1	A_ASP_90	OD2	3.108
3BT2	A_ARG_108	NH1	A_ASP_106	OD1	3.445
3BT2	A_ARG_108	NH1	A_ASP_106	OD2	2.718
3BT2	A_ARG_108	NH2	A_ASP_106	OD2	3.817
3BT2	A_ARG_110	NH2	A_GLU_125	OE1	3.432
3BT2	L_LYS_53	NZ	L_GLU_50	OE1	2.553
3BT2	L_ARG_61	NH1	L_GLU_79	OE1	2.871
3BT2	L_ARG_61	NH1	L_GLU_79	OE2	3.194
3BT2	L_ARG_61	NH2	L_GLU_79	OE1	3.460
3BT2	L_ARG_61	NH2	L_GLU_81	OE2	3.022
3BT2	L_ARG_61	NH2	L_ASP_82	OD1	3.009
3BT2	L_ARG_61	NH2	L_ASP_82	OD2	3.824
3BT2	L_LYS_103	NZ	L_ASP_164	OD1	3.404
3BT2	L_LYS_148	NZ	L_GLU_194	OE1	3.204
3BT2	L_LYS_148	NZ	L_GLU_194	OE2	3.996
3BT2	L_ARG_154	NH1	L_GLU_184	OE1	3.573
3BT2	L_ARG_154	NH1	L_GLU_184	OE2	2.970
3BT2	L_ARG_154	NH2	L_GLU_184	OE1	2.853
3BT2	L_ARG_154	NH2	L_GLU_184	OE2	3.786
3BT2	L_ARG_187	NH1	L_ASP_183	OD1	3.352
3BT2	L_HIS_188	ND1	L_ASP_150	OD2	2.836
3BT2	H_ARG_40	NH1	H_GLU_85	OE1	3.704
3BT2	H_ARG_40	NH2	H_GLU_85	OE2	3.856
3BT2	H_LYS_64	NZ	H_GLU_61	OE1	2.698
3BT2	H_LYS_64	NZ	H_GLU_61	OE2	3.977
3BT2	H_LYS_66	NZ	H_ASP_86	OD1	3.311
3BT2	H_LYS_66	NZ	H_ASP_86	OD2	2.587
3BT2	H_ARG_94	NH2	H_ASP_101	OD1	3.593
3BT2	H_ARG_94	NH2	H_ASP_101	OD2	2.737
3BT2	H_HIS_98	ND1	L_GLU_50	OE1	2.845
3BT2	H_HIS_98	ND1	L_GLU_50	OE2	2.191
3BT2	H_HIS_98	NE2	L_GLU_50	OE1	3.301
3BT2	H_HIS_98	NE2	L_GLU_50	OE2	3.904
3BT2	H_LYS_203	NZ	L_GLU_122	OE2	3.715
3BT2	U_ARG_2	NH2	U_ASP_74	OD2	3.379
3BT2	U_LYS_7	NZ	U_ASP_11	OD1	3.738
3BT2	U_ARG_25	NH1	U_GLU_42	OE2	3.052
3BT2	U_ARG_25	NH2	U_GLU_42	OE2	3.321
3BT2	U_LYS_50	NZ	U_ASP_254	OD2	2.962
3BT2	U_ARG_53	NH1	U_ASP_254	OD2	3.811
3BT2	U_ARG_91	NH1	B_ASP_22	OD1	3.502
3BT2	U_ARG_91	NH1	B_ASP_22	OD2	3.574
3BT2	U_ARG_91	NH2	B_ASP_22	OD1	3.066
3BT2	U_HIS_128	ND1	U_GLU_183	OE1	3.844
3BT2	U_HIS_128	ND1	U_GLU_183	OE2	3.947
3BT2	U_HIS_128	NE2	U_GLU_183	OE1	2.249
3BT2	U_HIS_128	NE2	U_GLU_183	OE2	1.923
3BT2	U_HIS_143	NE2	U_GLU_183	OE1	3.609
3BT2	U_HIS_143	NE2	U_GLU_183	OE2	1.958
3BT2	U_ARG_145	NH2	U_ASP_124	OD2	3.397

3BT2	U_LYS_175	NZ	U_GLU_94	OE1	3.795
3BT2	U_ARG_192	NH1	H_GLU_58	OE2	2.836
3BT2	U_HIS_260	ND1	U_ASP_262	OD1	3.731

Table 377: 3BT2-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3BZ4	A_LYS_27	NZ	E_ASP_1	OD1	3.348
3BZ4	A_LYS_27	NZ	E_ASP_1	OD2	3.551
3BZ4	A_HIS_27D	ND1	A_ASP_28	OD1	3.339
3BZ4	A_HIS_27D	ND1	A_ASP_28	OD2	3.472
3BZ4	A_ARG_61	NH1	A_ASP_82	OD1	3.791
3BZ4	A_ARG_61	NH1	A_ASP_82	OD2	2.748
3BZ4	A_ARG_61	NH2	A_GLU_79	OE1	3.444
3BZ4	A_ARG_61	NH2	A_GLU_81	OE2	3.683
3BZ4	A_ARG_61	NH2	A_ASP_82	OD1	2.925
3BZ4	A_ARG_61	NH2	A_ASP_82	OD2	3.346
3BZ4	A_ARG_96	NH2	B_GLU_50	OE1	3.591
3BZ4	A_ARG_96	NH2	B_GLU_50	OE2	2.914
3BZ4	A_LYS_147	NZ	A_GLU_154	OE1	3.729
3BZ4	A_LYS_149	NZ	A_GLU_195	OE1	3.803
3BZ4	A_LYS_149	NZ	A_GLU_195	OE2	2.957
3BZ4	A_ARG_155	NH1	A_GLU_185	OE1	3.022
3BZ4	A_ARG_188	NH2	A_ASP_184	OD1	2.966
3BZ4	A_ARG_188	NH2	A_ASP_184	OD2	3.794
3BZ4	A_HIS_189	ND1	A_ASP_151	OD2	3.568
3BZ4	B_ARG_38	NH1	B_ASP_86	OD1	2.836
3BZ4	B_ARG_38	NH2	B_GLU_46	OE1	3.315
3BZ4	B_ARG_38	NH2	B_GLU_46	OE2	3.392
3BZ4	B_ARG_38	NH2	B_ASP_86	OD1	3.736
3BZ4	B_ARG_52	NH2	B_GLU_50	OE2	2.961
3BZ4	B_LYS_64	NZ	B_GLU_61	OE1	2.578
3BZ4	B_LYS_64	NZ	B_GLU_61	OE2	3.962
3BZ4	B_LYS_66	NZ	B_ASP_86	OD1	3.832
3BZ4	B_LYS_66	NZ	B_ASP_86	OD2	2.772
3BZ4	B_ARG_71	NH2	B_ASP_73	OD1	3.536
3BZ4	B_LYS_75	NZ	B_ASP_72	OD2	3.736
3BZ4	B_LYS_210	NZ	A_GLU_123	OE2	2.839
3BZ4	C_LYS_27	NZ	C_GLU_93	OE1	2.862
3BZ4	C_LYS_27	NZ	C_GLU_93	OE2	3.387
3BZ4	C_HIS_27D	ND1	C_ASP_28	OD1	3.351
3BZ4	C_HIS_27D	ND1	C_ASP_28	OD2	3.496
3BZ4	C_LYS_39	NZ	C_GLU_81	OE2	3.178
3BZ4	C_ARG_61	NH1	C_ASP_82	OD1	3.875
3BZ4	C_ARG_61	NH1	C_ASP_82	OD2	2.759
3BZ4	C_ARG_61	NH2	C_GLU_79	OE1	3.734
3BZ4	C_ARG_61	NH2	C_GLU_79	OE2	3.949
3BZ4	C_ARG_61	NH2	C_ASP_82	OD1	3.042
3BZ4	C_ARG_61	NH2	C_ASP_82	OD2	3.345
3BZ4	C_ARG_96	NH2	D_GLU_50	OE1	3.615
3BZ4	C_ARG_96	NH2	D_GLU_50	OE2	2.938
3BZ4	C_LYS_103	NZ	C_ASP_165	OD1	3.993
3BZ4	C_LYS_147	NZ	C_GLU_195	OE1	3.076
3BZ4	C_LYS_149	NZ	C_GLU_195	OE2	2.853
3BZ4	C_ARG_155	NH1	C_GLU_185	OE2	3.198
3BZ4	C_ARG_155	NH2	C_GLU_185	OE1	2.972
3BZ4	C_ARG_155	NH2	C_GLU_185	OE2	3.144
3BZ4	C_HIS_189	ND1	C_ASP_151	OD2	3.072
3BZ4	D_LYS_3	NZ	D_GLU_5	OE1	3.731
3BZ4	D_ARG_38	NH1	D_ASP_86	OD1	2.733
3BZ4	D_ARG_38	NH2	D_GLU_46	OE1	3.389
3BZ4	D_ARG_38	NH2	D_GLU_46	OE2	3.315
3BZ4	D_ARG_38	NH2	D_ASP_86	OD1	3.699
3BZ4	D_ARG_52	NH2	D_GLU_50	OE2	2.968

3BZ4	D_ARG_71	NH2	D_ASP_73	OD1	3.463
3BZ4	D_ARG_83	NH1	D_GLU_85	OE2	3.445
3BZ4	D_ARG_83	NH2	D_GLU_85	OE2	3.957
3BZ4	D_ARG_83	NH2	D_ASP_86	OD1	2.967
3BZ4	D_ARG_83	NH2	D_ASP_86	OD2	3.511
3BZ4	D_LYS_210	NZ	C_GLU_123	OE2	2.929
3BZ4	E_LYS_27	NZ	E_GLU_93	OE1	2.598
3BZ4	E_LYS_27	NZ	E_GLU_93	OE2	3.386
3BZ4	E_HIS_27D	ND1	E_ASP_28	OD1	3.329
3BZ4	E_HIS_27D	ND1	E_ASP_28	OD2	3.369
3BZ4	E_ARG_61	NH1	E_ASP_82	OD1	3.767
3BZ4	E_ARG_61	NH1	E_ASP_82	OD2	2.681
3BZ4	E_ARG_61	NH2	E_GLU_79	OE1	3.679
3BZ4	E_ARG_61	NH2	E_GLU_79	OE2	3.909
3BZ4	E_ARG_61	NH2	E_ASP_82	OD1	2.988
3BZ4	E_ARG_61	NH2	E_ASP_82	OD2	3.375
3BZ4	E_ARG_96	NH2	F_GLU_50	OE1	3.659
3BZ4	E_ARG_96	NH2	F_GLU_50	OE2	3.062
3BZ4	E_LYS_103	NZ	E_ASP_165	OD1	3.694
3BZ4	E_LYS_142	NZ	E_GLU_105	OE1	2.683
3BZ4	E_LYS_147	NZ	E_GLU_154	OE1	3.191
3BZ4	E_LYS_149	NZ	E_GLU_195	OE2	3.492
3BZ4	E_ARG_155	NH1	E_GLU_185	OE2	2.852
3BZ4	E_ARG_155	NH2	E_GLU_185	OE1	3.247
3BZ4	E_ARG_155	NH2	E_GLU_185	OE2	3.385
3BZ4	E_LYS_183	NZ	E_GLU_187	OE1	3.938
3BZ4	E_ARG_188	NH1	E_ASP_184	OD1	2.897
3BZ4	E_HIS_189	ND1	E_ASP_151	OD2	2.915
3BZ4	E_LYS_199	NZ	E_ASP_110	OD2	3.617
3BZ4	F_ARG_38	NH1	F_ASP_86	OD1	2.816
3BZ4	F_ARG_38	NH2	F_GLU_46	OE1	3.339
3BZ4	F_ARG_38	NH2	F_GLU_46	OE2	3.116
3BZ4	F_ARG_38	NH2	F_ASP_86	OD1	3.767
3BZ4	F_ARG_52	NH2	F_GLU_50	OE2	2.956
3BZ4	F_LYS_66	NZ	F_ASP_86	OD1	3.548
3BZ4	F_LYS_66	NZ	F_ASP_86	OD2	2.726
3BZ4	F_ARG_71	NH2	F_ASP_73	OD1	3.320
3BZ4	F_LYS_75	NZ	F_ASP_72	OD2	3.820
3BZ4	F_LYS_210	NZ	E_GLU_123	OE2	2.855
3BZ4	G_LYS_27	NZ	G_GLU_93	OE1	3.193
3BZ4	G_LYS_27	NZ	G_GLU_93	OE2	3.324
3BZ4	G_HIS_27D	ND1	G_ASP_28	OD1	3.438
3BZ4	G_HIS_27D	ND1	G_ASP_28	OD2	3.691
3BZ4	G_LYS_39	NZ	G_GLU_81	OE2	3.982
3BZ4	G_ARG_61	NH1	G_ASP_82	OD1	3.687
3BZ4	G_ARG_61	NH1	G_ASP_82	OD2	2.777
3BZ4	G_ARG_61	NH2	G_GLU_79	OE1	3.890
3BZ4	G_ARG_61	NH2	G_GLU_81	OE2	3.793
3BZ4	G_ARG_61	NH2	G_ASP_82	OD1	3.189
3BZ4	G_ARG_61	NH2	G_ASP_82	OD2	3.680
3BZ4	G_ARG_96	NH2	H_GLU_50	OE1	3.659
3BZ4	G_ARG_96	NH2	H_GLU_50	OE2	3.021
3BZ4	G_LYS_147	NZ	C_GLU_154	OE1	3.559
3BZ4	G_LYS_149	NZ	G_GLU_195	OE1	3.699
3BZ4	G_LYS_149	NZ	G_GLU_195	OE2	3.854
3BZ4	G_ARG_188	NH1	G_ASP_184	OD1	3.650
3BZ4	G_HIS_189	ND1	G_ASP_151	OD2	3.087
3BZ4	G_LYS_199	NZ	G_ASP_110	OD2	3.816

3BZ4	H_ARG_38	NH1	H_ASP_86	OD1	2.822
3BZ4	H_ARG_38	NH2	H_GLU_46	OE1	3.285
3BZ4	H_ARG_38	NH2	H_GLU_46	OE2	3.289
3BZ4	H_ARG_38	NH2	H_ASP_86	OD1	3.691
3BZ4	H_ARG_52	NH2	H_GLU_50	OE2	3.000
3BZ4	H_LYS_66	NZ	H_ASP_86	OD1	3.582
3BZ4	H_LYS_66	NZ	H_ASP_86	OD2	2.709
3BZ4	H_ARG_71	NH2	H_ASP_73	OD1	3.418

Table 378: 3BZ4-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3C09	L_ARG_60	NH2	L_ASP_81	OD1	3.198
3C09	L_ARG_60	NH2	L_ASP_81	OD2	3.773
3C09	L_HIS_93	NE2	D_ASP_434	OD1	2.739
3C09	L_HIS_93	NE2	D_ASP_434	OD2	3.466
3C09	L_HIS_188	ND1	L_ASP_150	OD1	3.925
3C09	H_HIS_32	NE2	H_ASP_100	OD2	3.604
3C09	H_HIS_32	NE2	H_ASP_102	OD1	3.701
3C09	H_ARG_38	NH2	H_GLU_46	OE1	2.766
3C09	H_ARG_38	NH2	H_GLU_46	OE2	3.957
3C09	H_ARG_57	NH2	D_GLU_431	OE1	3.682
3C09	H_LYS_151	NZ	H_ASP_152	OD2	3.689
3C09	A_HIS_346	NE2	A_ASP_344	OD2	3.992
3C09	A_HIS_394	NE2	A_ASP_369	OD1	3.580
3C09	A_ARG_403	NH1	A_GLU_376	OE1	2.815
3C09	A_ARG_403	NH1	A_GLU_376	OE2	3.396
3C09	A_LYS_407	NZ	A_ASP_434	OD2	3.026
3C09	A_ARG_427	NH1	A_GLU_397	OE1	3.943
3C09	A_ARG_427	NH2	A_ASP_392	OD2	3.700
3C09	A_ARG_427	NH2	A_ASP_498	OD1	3.376
3C09	A_LYS_454	NZ	C_ASP_100	OD1	2.467
3C09	A_LYS_463	NZ	B_ASP_49	OD2	2.856
3C09	B_ARG_60	NH2	B_ASP_81	OD1	2.668
3C09	B_ARG_60	NH2	B_ASP_81	OD2	3.698
3C09	B_HIS_93	NE2	A_ASP_434	OD1	2.346
3C09	C_LYS_12	NZ	C_GLU_10	OE1	3.298
3C09	C_HIS_32	NE2	C_ASP_102	OD1	3.417
3C09	C_HIS_35	ND1	C_GLU_50	OE2	3.377
3C09	C_HIS_35	NE2	C_GLU_50	OE2	3.892
3C09	C_ARG_38	NH1	C_ASP_90	OD1	3.955
3C09	C_ARG_38	NH2	C_GLU_46	OE1	2.986
3C09	C_ARG_38	NH2	C_GLU_46	OE2	3.298
3C09	D_HIS_394	ND1	D_ASP_369	OD1	3.451
3C09	D_ARG_403	NH2	D_GLU_376	OE1	3.699
3C09	D_ARG_403	NH2	D_GLU_376	OE2	3.471
3C09	D_LYS_407	NZ	D_ASP_434	OD1	3.698
3C09	D_LYS_407	NZ	D_ASP_434	OD2	2.480
3C09	D_LYS_454	NZ	H_ASP_100	OD2	3.482
3C09	D_LYS_463	NZ	L_ASP_49	OD2	3.418

Table 379: 3C09-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3C5S	A_ARG_61	NH1	A_ASP_82	OD2	3.030
3C5S	A_ARG_61	NH2	A_GLU_79	OE2	3.851
3C5S	A_ARG_61	NH2	A_ASP_82	OD1	3.184
3C5S	A_ARG_61	NH2	A_ASP_82	OD2	3.437
3C5S	A_ARG_96	NH2	B_GLU_50	OE1	3.517
3C5S	A_ARG_96	NH2	B_GLU_50	OE2	2.932
3C5S	A_LYS_103	NZ	A_ASP_165	OD1	3.305
3C5S	A_LYS_147	NZ	A_GLU_154	OE1	2.905
3C5S	A_LYS_149	NZ	A_GLU_195	OE1	2.670
3C5S	A_ARG_188	NH1	A_ASP_184	OD1	2.405
3C5S	A_LYS_199	NZ	A_ASP_110	OD1	3.889
3C5S	A_LYS_199	NZ	A_ASP_110	OD2	2.335
3C5S	B_LYS_3	NZ	B_GLU_5	OE1	3.341
3C5S	B_ARG_38	NH1	B_ASP_86	OD1	2.908
3C5S	B_ARG_38	NH2	B_GLU_46	OE1	3.058
3C5S	B_ARG_38	NH2	B_ASP_86	OD1	3.943
3C5S	B_LYS_43	NZ	B_GLU_46	OE2	2.800
3C5S	B_ARG_52	NH2	B_GLU_50	OE2	2.999
3C5S	B_LYS_64	NZ	B_GLU_61	OE1	2.552
3C5S	B_LYS_64	NZ	B_GLU_61	OE2	3.116
3C5S	B_ARG_71	NH2	B_ASP_73	OD1	3.320
3C5S	B_LYS_75	NZ	B_ASP_72	OD2	3.056
3C5S	B_ARG_83	NH2	B_ASP_86	OD1	3.087
3C5S	B_ARG_83	NH2	B_ASP_86	OD2	3.434
3C5S	B_LYS_210	NZ	A_GLU_123	OE2	3.553
3C5S	C_ARG_61	NH1	C_ASP_82	OD1	3.085
3C5S	C_ARG_61	NH2	C_GLU_79	OE1	3.892
3C5S	C_ARG_61	NH2	C_GLU_79	OE2	3.694
3C5S	C_ARG_61	NH2	C_GLU_81	OE2	2.868
3C5S	C_ARG_61	NH2	C_ASP_82	OD1	3.573
3C5S	C_ARG_61	NH2	C_ASP_82	OD2	3.274
3C5S	C_ARG_96	NH2	D_GLU_50	OE1	3.571
3C5S	C_ARG_96	NH2	D_GLU_50	OE2	2.973
3C5S	C_LYS_103	NZ	C_ASP_165	OD1	3.149
3C5S	C_LYS_142	NZ	C_GLU_105	OE2	3.286
3C5S	C_LYS_147	NZ	C_GLU_154	OE1	2.994
3C5S	C_LYS_149	NZ	C_GLU_195	OE1	2.716
3C5S	C_LYS_149	NZ	C_GLU_195	OE2	3.839
3C5S	C_ARG_155	NH1	C_GLU_185	OE1	3.904
3C5S	C_ARG_155	NH2	C_GLU_185	OE1	3.268
3C5S	C_ARG_188	NH2	C_ASP_184	OD2	3.258
3C5S	C_HIS_189	ND1	C_ASP_151	OD2	2.806
3C5S	C_LYS_199	NZ	C_ASP_110	OD2	2.615
3C5S	C_ARG_211	NH1	C_GLU_187	OE1	3.163
3C5S	D_LYS_3	NZ	D_GLU_5	OE2	3.300
3C5S	D_ARG_38	NH1	D_ASP_86	OD1	2.823
3C5S	D_ARG_38	NH2	D_GLU_46	OE1	3.094
3C5S	D_ARG_38	NH2	D_GLU_46	OE2	3.865
3C5S	D_ARG_38	NH2	D_ASP_86	OD1	3.695
3C5S	D_ARG_52	NH2	D_GLU_50	OE2	2.971
3C5S	D_LYS_66	NZ	D_ASP_86	OD1	3.839
3C5S	D_LYS_66	NZ	D_ASP_86	OD2	2.657
3C5S	D_ARG_71	NH2	D_ASP_73	OD1	3.461

Table 380: 3C5S-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3C6S	A_LYS_27	NZ	F_GLU_61	OE1	2.945
3C6S	A_HIS_27D	NE2	A_ASP_28	OD2	3.782
3C6S	A_ARG_61	NH1	A_ASP_82	OD1	3.871
3C6S	A_ARG_61	NH1	A_ASP_82	OD2	2.772
3C6S	A_ARG_61	NH2	A_GLU_79	OE1	3.467
3C6S	A_ARG_61	NH2	A_GLU_81	OE2	3.840
3C6S	A_ARG_61	NH2	A_ASP_82	OD1	3.008
3C6S	A_ARG_61	NH2	A_ASP_82	OD2	3.321
3C6S	A_ARG_96	NH2	B_GLU_50	OE1	3.551
3C6S	A_ARG_96	NH2	B_GLU_50	OE2	2.936
3C6S	A_LYS_103	NZ	A_ASP_165	OD1	3.865
3C6S	A_LYS_147	NZ	A_GLU_154	OE1	3.762
3C6S	A_LYS_149	NZ	A_GLU_195	OE1	3.629
3C6S	A_LYS_149	NZ	A_GLU_195	OE2	3.115
3C6S	A_ARG_155	NH1	A_GLU_185	OE1	2.818
3C6S	A_ARG_155	NH1	A_GLU_185	OE2	3.763
3C6S	A_ARG_155	NH2	A_GLU_185	OE1	3.570
3C6S	A_ARG_155	NH2	A_GLU_185	OE2	3.121
3C6S	A_HIS_189	ND1	A_ASP_151	OD2	3.710
3C6S	B_LYS_3	NZ	B_GLU_5	OE1	3.976
3C6S	B_ARG_38	NH1	B_ASP_86	OD1	2.860
3C6S	B_ARG_38	NH2	B_GLU_46	OE1	3.287
3C6S	B_ARG_38	NH2	B_GLU_46	OE2	3.192
3C6S	B_ARG_38	NH2	B_ASP_86	OD1	3.858
3C6S	B_ARG_52	NH2	B_GLU_50	OE2	3.018
3C6S	B_LYS_64	NZ	B_GLU_61	OE1	3.776
3C6S	B_LYS_66	NZ	B_ASP_86	OD1	3.351
3C6S	B_LYS_66	NZ	B_ASP_86	OD2	2.603
3C6S	B_ARG_71	NH2	B_ASP_73	OD1	3.493
3C6S	B_ARG_83	NH2	B_GLU_85	OE2	3.633
3C6S	B_LYS_207	NZ	B_ASP_209	OD2	3.344
3C6S	B_LYS_210	NZ	A_GLU_123	OE2	2.871
3C6S	C_HIS_27D	NE2	C_ASP_28	OD2	3.911
3C6S	C_LYS_39	NZ	C_GLU_81	OE2	2.611
3C6S	C_ARG_61	NH1	C_ASP_82	OD1	3.977
3C6S	C_ARG_61	NH1	C_ASP_82	OD2	2.797
3C6S	C_ARG_61	NH2	C_GLU_79	OE1	3.899
3C6S	C_ARG_61	NH2	C_ASP_82	OD1	3.285
3C6S	C_ARG_61	NH2	C_ASP_82	OD2	3.465
3C6S	C_ARG_96	NH2	D_GLU_50	OE1	3.699
3C6S	C_ARG_96	NH2	D_GLU_50	OE2	2.915
3C6S	C_LYS_149	NZ	C_GLU_195	OE2	3.377
3C6S	C_ARG_155	NH1	C_GLU_185	OE1	2.919
3C6S	C_ARG_155	NH2	C_GLU_185	OE1	3.617
3C6S	C_ARG_155	NH2	C_GLU_185	OE2	3.372
3C6S	C_LYS_183	NZ	C_GLU_187	OE1	3.948
3C6S	C_ARG_188	NH1	C_ASP_184	OD1	3.896
3C6S	C_ARG_188	NH1	C_ASP_184	OD2	3.104
3C6S	C_ARG_188	NH2	C_GLU_185	OE1	3.688
3C6S	C_HIS_189	ND1	C_ASP_151	OD2	2.779
3C6S	C_LYS_199	NZ	C_ASP_110	OD2	3.859
3C6S	D_LYS_3	NZ	D_GLU_5	OE1	2.880
3C6S	D_LYS_3	NZ	D_GLU_5	OE2	3.546
3C6S	D_ARG_38	NH1	D_ASP_86	OD1	2.816
3C6S	D_ARG_38	NH2	D_GLU_46	OE1	3.293
3C6S	D_ARG_38	NH2	D_GLU_46	OE2	3.209
3C6S	D_ARG_38	NH2	D_ASP_86	OD1	3.686

3C6S	D_ARG_52	NH2	D_GLU_50	OE2	2.953
3C6S	D_LYS_64	NZ	D_GLU_61	OE1	2.522
3C6S	D_LYS_66	NZ	D_ASP_86	OD1	3.557
3C6S	D_LYS_66	NZ	D_ASP_86	OD2	2.620
3C6S	D_ARG_71	NH2	D_ASP_73	OD1	3.499
3C6S	D_LYS_115	NZ	H_GLU_85	OE1	3.000
3C6S	D_LYS_115	NZ	H_GLU_85	OE2	3.884
3C6S	D_LYS_210	NZ	C_GLU_123	OE2	2.801
3C6S	E_LYS_27	NZ	A_ASP_1	OD1	3.387
3C6S	E_LYS_27	NZ	A_ASP_1	OD2	3.431
3C6S	E_HIS_27D	NE2	E_ASP_28	OD2	3.987
3C6S	E_ARG_61	NH1	E_ASP_82	OD1	3.693
3C6S	E_ARG_61	NH1	E_ASP_82	OD2	2.790
3C6S	E_ARG_61	NH2	E_GLU_79	OE1	3.369
3C6S	E_ARG_61	NH2	E_GLU_81	OE2	3.772
3C6S	E_ARG_61	NH2	E_ASP_82	OD1	2.890
3C6S	E_ARG_61	NH2	E_ASP_82	OD2	3.360
3C6S	E_ARG_96	NH2	F_GLU_50	OE1	3.703
3C6S	E_ARG_96	NH2	F_GLU_50	OE2	3.164
3C6S	E_LYS_149	NZ	E_GLU_195	OE1	3.276
3C6S	E_LYS_149	NZ	E_GLU_195	OE2	3.217
3C6S	E_ARG_155	NH1	E_GLU_185	OE2	3.054
3C6S	E_ARG_155	NH2	E_GLU_185	OE1	3.295
3C6S	E_ARG_155	NH2	E_GLU_185	OE2	3.558
3C6S	E_LYS_183	NZ	E_GLU_187	OE1	3.890
3C6S	E_ARG_188	NH1	E_ASP_184	OD1	3.999
3C6S	E_ARG_188	NH1	E_ASP_184	OD2	2.649
3C6S	E_ARG_188	NH2	E_GLU_185	OE2	3.771
3C6S	E_HIS_189	ND1	E_ASP_151	OD2	2.858
3C6S	E_LYS_199	NZ	E_ASP_110	OD2	3.786
3C6S	F_ARG_38	NH1	F_ASP_86	OD1	2.884
3C6S	F_ARG_38	NH2	F_GLU_46	OE1	3.272
3C6S	F_ARG_38	NH2	F_GLU_46	OE2	3.427
3C6S	F_ARG_38	NH2	F_ASP_86	OD1	3.691
3C6S	F_ARG_52	NH2	F_GLU_50	OE2	2.936
3C6S	F_LYS_64	NZ	F_GLU_61	OE1	3.674
3C6S	F_LYS_64	NZ	F_GLU_61	OE2	3.896
3C6S	F_LYS_66	NZ	F_ASP_86	OD1	3.774
3C6S	F_LYS_66	NZ	F_ASP_86	OD2	2.770
3C6S	F_ARG_71	NH2	F_ASP_73	OD1	3.453
3C6S	F_LYS_207	NZ	F_ASP_209	OD1	2.611
3C6S	F_LYS_207	NZ	F_ASP_209	OD2	3.473
3C6S	F_LYS_210	NZ	E_GLU_123	OE2	3.016
3C6S	G_LYS_27	NZ	G_GLU_93	OE1	2.636
3C6S	G_LYS_27	NZ	G_GLU_93	OE2	3.112
3C6S	G_HIS_27D	NE2	G_ASP_28	OD2	3.978
3C6S	G_ARG_61	NH1	G_ASP_82	OD2	2.808
3C6S	G_ARG_61	NH2	G_GLU_79	OE1	3.851
3C6S	G_ARG_61	NH2	G_ASP_82	OD1	3.155
3C6S	G_ARG_61	NH2	G_ASP_82	OD2	3.092
3C6S	G_ARG_96	NH2	H_GLU_50	OE1	3.733
3C6S	G_ARG_96	NH2	H_GLU_50	OE2	2.958
3C6S	G_LYS_147	NZ	G_GLU_154	OE2	3.966
3C6S	G_LYS_149	NZ	G_GLU_195	OE1	3.546
3C6S	G_LYS_149	NZ	G_GLU_195	OE2	3.011
3C6S	G_ARG_155	NH1	G_GLU_185	OE2	3.226
3C6S	G_LYS_169	NZ	G_GLU_81	OE1	2.347
3C6S	G_LYS_169	NZ	G_GLU_81	OE2	3.920

3C6S	G_ARG_188	NH2	G_GLU_185	OE1	2.920
3C6S	G_HIS_189	ND1	G_ASP_151	OD2	3.004
3C6S	G_HIS_189	NE2	G_GLU_185	OE1	3.998
3C6S	G_LYS_199	NZ	G_ASP_110	OD2	3.920
3C6S	H_LYS_3	NZ	H_GLU_5	OE1	2.755
3C6S	H_ARG_38	NH1	H_ASP_86	OD1	2.900
3C6S	H_ARG_38	NH2	H_GLU_46	OE1	3.369
3C6S	H_ARG_38	NH2	H_GLU_46	OE2	3.273
3C6S	H_ARG_38	NH2	H_ASP_86	OD1	3.683
3C6S	H_ARG_52	NH2	H_GLU_50	OE2	3.044
3C6S	H_ARG_71	NH2	H_ASP_73	OD1	3.344
3C6S	H_LYS_75	NZ	H_ASP_72	OD2	3.808
3C6S	H_ARG_83	NH1	H_GLU_85	OE2	3.502
3C6S	H_ARG_83	NH2	H_ASP_86	OD1	2.979
3C6S	H_ARG_83	NH2	H_ASP_86	OD2	3.571
3C6S	H_LYS_210	NZ	G_GLU_123	OE2	2.402

Table 381: 3C6S-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3CVH	A_HIS_3	ND1	A_ASP_29	OD1	3.340
3CVH	A_HIS_3	ND1	A_ASP_29	OD2	3.186
3CVH	A_ARG_6	NH2	A_ASP_30	OD1	3.294
3CVH	A_ARG_14	NH1	A_ASP_39	OD2	2.927
3CVH	A_ARG_14	NH2	A_ASP_39	OD1	3.777
3CVH	A_ARG_14	NH2	A_ASP_39	OD2	2.767
3CVH	A_ARG_21	NH2	A_ASP_37	OD1	3.377
3CVH	A_ARG_21	NH2	A_ASP_37	OD2	2.615
3CVH	A_ARG_35	NH1	A_GLU_32	OE1	2.677
3CVH	A_ARG_35	NH1	A_GLU_32	OE2	2.491
3CVH	A_ARG_44	NH2	A_GLU_61	OE1	2.791
3CVH	A_ARG_48	NH1	B_ASP_53	OD2	3.820
3CVH	A_ARG_48	NH2	A_GLU_32	OE2	3.651
3CVH	A_ARG_48	NH2	B_ASP_53	OD2	2.637
3CVH	A_ARG_62	NH1	L_GLU_26	OE1	3.514
3CVH	A_ARG_62	NH1	L_GLU_26	OE2	3.458
3CVH	A_ARG_62	NH2	L_GLU_26	OE1	3.664
3CVH	A_LYS_66	NZ	A_GLU_63	OE1	2.982
3CVH	A_LYS_66	NZ	A_GLU_63	OE2	3.930
3CVH	A_ARG_75	NH1	A_GLU_19	OE1	2.649
3CVH	A_ARG_75	NH1	A_GLU_71	OE1	3.442
3CVH	A_ARG_75	NH2	A_GLU_19	OE1	3.819
3CVH	A_ARG_75	NH2	A_GLU_71	OE1	3.726
3CVH	A_HIS_93	ND1	A_ASP_119	OD1	3.615
3CVH	A_HIS_93	ND1	A_ASP_119	OD2	2.743
3CVH	A_ARG_108	NH2	M_GLU_223	OE2	3.938
3CVH	A_ARG_155	NH2	A_GLU_152	OE1	3.097
3CVH	A_ARG_155	NH2	A_GLU_152	OE2	2.655
3CVH	A_ARG_157	NH2	A_GLU_161	OE2	3.326
3CVH	A_ARG_170	NH2	A_GLU_55	OE1	2.438
3CVH	A_ARG_170	NH2	A_GLU_55	OE2	3.042
3CVH	A_ARG_181	NH2	A_ASP_183	OD2	3.102
3CVH	A_HIS_192	ND1	B_ASP_98	OD2	3.410
3CVH	B_LYS_3	NZ	B_ASP_59	OD2	3.798
3CVH	B_LYS_19	NZ	B_GLU_16	OE1	3.984
3CVH	B_LYS_83	NZ	B_GLU_36	OE1	3.948
3CVH	C_LYS_7	NZ	H_ASP_49	OD1	3.577
3CVH	C_LYS_7	NZ	H_ASP_49	OD2	3.552
3CVH	H_LYS_37	NZ	H_ASP_89	OD1	4.000
3CVH	H_LYS_66	NZ	H_ASP_89	OD1	3.905
3CVH	H_LYS_66	NZ	H_ASP_89	OD2	2.944
3CVH	H_LYS_98	NZ	H_ASP_34	OD1	3.326
3CVH	H_LYS_98	NZ	H_ASP_34	OD2	3.016
3CVH	H_LYS_98	NZ	H_ASP_49	OD2	3.605
3CVH	H_LYS_215	NZ	L_GLU_122	OE2	2.643
3CVH	L_LYS_23	NZ	L_ASP_69	OD1	2.944
3CVH	L_LYS_23	NZ	L_ASP_69	OD2	3.859
3CVH	L_ARG_60	NH1	L_GLU_80	OE1	3.977
3CVH	L_ARG_60	NH2	L_GLU_80	OE1	3.053
3CVH	L_ARG_60	NH2	L_ASP_81	OD1	3.208
3CVH	L_ARG_60	NH2	L_ASP_81	OD2	2.613
3CVH	L_ARG_67	NH2	L_ASP_27	OD1	3.678
3CVH	L_ARG_67	NH2	L_ASP_27	OD2	2.811
3CVH	L_LYS_146	NZ	L_GLU_153	OE1	3.893
3CVH	L_LYS_146	NZ	L_GLU_153	OE2	3.978
3CVH	L_LYS_148	NZ	L_GLU_194	OE1	3.826
3CVH	L_ARG_154	NH1	L_GLU_184	OE1	3.751

3CVH	L_LYS_182	NZ	L_GLU_186	OE1	3.005
3CVH	L_LYS_182	NZ	L_GLU_186	OE2	3.813
3CVH	L_ARG_187	NH2	L_ASP_183	OD1	3.139
3CVH	L_ARG_187	NH2	L_ASP_183	OD2	2.810
3CVH	L_LYS_198	NZ	L_ASP_109	OD2	3.543
3CVH	M_HIS_3	ND1	M_ASP_29	OD1	2.963
3CVH	M_HIS_3	ND1	M_ASP_29	OD2	2.771
3CVH	M_ARG_14	NH1	M_ASP_39	OD1	3.573
3CVH	M_ARG_14	NH2	M_ASP_39	OD1	2.587
3CVH	M_ARG_21	NH1	M_ASP_39	OD2	3.455
3CVH	M_ARG_21	NH2	M_ASP_37	OD1	3.446
3CVH	M_ARG_21	NH2	M_ASP_37	OD2	2.717
3CVH	M_ARG_21	NH2	M_ASP_39	OD2	3.712
3CVH	M_ARG_35	NH2	M_GLU_32	OE1	3.151
3CVH	M_ARG_35	NH2	M_GLU_32	OE2	3.351
3CVH	M_ARG_48	NH1	M_GLU_46	OE1	3.444
3CVH	M_ARG_48	NH1	M_GLU_46	OE2	3.832
3CVH	M_ARG_48	NH1	N_ASP_53	OD2	3.601
3CVH	M_ARG_48	NH2	M_GLU_32	OE2	3.692
3CVH	M_ARG_48	NH2	N_ASP_53	OD2	2.621
3CVH	M_ARG_50	NH2	M_GLU_53	OE2	3.272
3CVH	M_ARG_62	NH1	R_GLU_26	OE1	3.418
3CVH	M_ARG_62	NH2	R_GLU_26	OE1	3.162
3CVH	M_ARG_62	NH2	R_GLU_26	OE2	2.706
3CVH	M_LYS_66	NZ	M_GLU_63	OE1	3.245
3CVH	M_ARG_75	NH1	M_GLU_19	OE1	3.628
3CVH	M_ARG_75	NH2	M_GLU_71	OE1	3.921
3CVH	M_ARG_75	NH2	M_GLU_71	OE2	2.545
3CVH	M_HIS_93	ND1	M_ASP_119	OD1	3.830
3CVH	M_HIS_93	ND1	M_ASP_119	OD2	2.828
3CVH	M_ARG_108	NH2	A_GLU_223	OE1	3.207
3CVH	M_ARG_108	NH2	A_GLU_223	OE2	3.250
3CVH	M_ARG_111	NH1	M_GLU_128	OE2	3.369
3CVH	M_ARG_111	NH2	M_GLU_128	OE2	2.639
3CVH	M_HIS_145	ND1	M_GLU_148	OE1	3.811
3CVH	M_ARG_155	NH2	M_GLU_152	OE1	3.335
3CVH	M_ARG_155	NH2	M_GLU_152	OE2	2.756
3CVH	M_ARG_157	NH2	M_GLU_161	OE1	2.814
3CVH	M_ARG_157	NH2	M_GLU_161	OE2	3.333
3CVH	M_ARG_169	NH1	A_GLU_268	OE2	3.364
3CVH	M_ARG_170	NH2	M_GLU_55	OE1	2.487
3CVH	M_ARG_170	NH2	M_GLU_55	OE2	3.462
3CVH	M_ARG_181	NH2	M_ASP_183	OD2	3.222
3CVH	N_LYS_83	NZ	N_GLU_36	OE1	2.685
3CVH	N_LYS_83	NZ	N_GLU_36	OE2	3.981
3CVH	O_LYS_7	NZ	Q_ASP_49	OD1	3.648
3CVH	O_LYS_7	NZ	Q_ASP_49	OD2	3.052
3CVH	Q_LYS_37	NZ	Q_ASP_89	OD1	3.997
3CVH	Q_LYS_98	NZ	Q_ASP_34	OD1	3.064
3CVH	Q_LYS_98	NZ	Q_ASP_34	OD2	2.433
3CVH	Q_LYS_98	NZ	Q_ASP_49	OD2	3.431
3CVH	Q_LYS_215	NZ	R_GLU_122	OE1	3.557
3CVH	R_ARG_60	NH1	R_ASP_81	OD1	3.125
3CVH	R_ARG_60	NH1	R_ASP_81	OD2	2.738
3CVH	R_ARG_60	NH2	R_GLU_80	OE1	3.793
3CVH	R_LYS_102	NZ	R_ASP_164	OD1	3.388
3CVH	R_LYS_141	NZ	R_GLU_104	OE1	3.136
3CVH	R_LYS_148	NZ	R_GLU_194	OE1	3.875

3CVH	R_ARG_154	NH2	R_GLU_184	OE1	3.709
3CVH	R_HIS_188	ND1	R_ASP_150	OD2	3.342
3CVH	R_HIS_188	NE2	R_GLU_184	OE2	3.904

Table 382: 3CVH-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3CXD	L_ARG_61	NH2	L_GLU_81	OE2	3.336
3CXD	L_ARG_61	NH2	L_ASP_82	OD1	3.305
3CXD	L_ARG_61	NH2	L_ASP_82	OD2	2.791
3CXD	L_LYS_147	NZ	L_GLU_154	OE2	3.401
3CXD	L_LYS_149	NZ	L_GLU_195	OE2	2.939
3CXD	L_ARG_155	NH1	L_GLU_185	OE1	3.386
3CXD	L_ARG_155	NH2	L_GLU_185	OE1	3.845
3CXD	L_ARG_155	NH2	L_GLU_185	OE2	3.314
3CXD	L_ARG_188	NH2	L_ASP_184	OD1	3.219
3CXD	L_HIS_189	ND1	L_ASP_151	OD2	2.794
3CXD	L_LYS_199	NZ	L_ASP_110	OD1	3.656
3CXD	L_LYS_199	NZ	L_ASP_110	OD2	3.337
3CXD	H_ARG_38	NH1	H_GLU_46	OE1	3.619
3CXD	H_ARG_38	NH1	H_GLU_46	OE2	2.600
3CXD	H_ARG_38	NH2	H_ASP_92	OD1	2.807
3CXD	H_ARG_52	NH1	P_ASP_47	OD1	3.830
3CXD	H_ARG_52	NH1	P_ASP_47	OD2	3.528
3CXD	H_LYS_67	NZ	H_ASP_64	OD1	2.806
3CXD	H_ARG_69	NH1	H_ASP_92	OD2	2.720
3CXD	H_ARG_69	NH2	H_ASP_92	OD1	3.121
3CXD	H_ARG_69	NH2	H_ASP_92	OD2	2.861
3CXD	H_ARG_74	NH2	H_ASP_76	OD1	3.600
3CXD	H_ARG_100	NH2	H_ASP_104	OD1	3.226
3CXD	H_ARG_100	NH2	H_ASP_104	OD2	2.671

Table 383: 3CXD-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3D0L	A_ARG_37	NH1	A_GLU_81	OE2	3.366
3D0L	A_ARG_37	NH1	A_ASP_82	OD1	2.929
3D0L	A_ARG_37	NH2	A_GLU_81	OE2	3.080
3D0L	A_ARG_61	NH2	A_GLU_81	OE1	3.374
3D0L	A_ARG_61	NH2	A_ASP_82	OD1	2.776
3D0L	A_ARG_61	NH2	A_ASP_82	OD2	3.420
3D0L	A_HIS_96	NE2	C_ASP_5	OD1	3.014
3D0L	A_LYS_149	NZ	A_GLU_195	OE1	3.487
3D0L	A_LYS_183	NZ	A_GLU_187	OE2	3.124
3D0L	A_LYS_190	NZ	A_GLU_213	OE2	3.283
3D0L	B_ARG_38	NH1	B_GLU_46	OE1	2.512
3D0L	B_ARG_38	NH1	B_GLU_46	OE2	3.477
3D0L	B_ARG_38	NH2	B_ASP_86	OD1	2.546
3D0L	B_LYS_57	NZ	B_ASP_55	OD2	3.516
3D0L	B_ARG_58	NH1	B_ASP_56	OD1	2.533
3D0L	B_ARG_58	NH1	B_ASP_56	OD2	3.774
3D0L	B_ARG_58	NH2	B_ASP_56	OD1	3.951
3D0L	B_ARG_58	NH2	C_GLU_3	OE1	3.473
3D0L	B_ARG_58	NH2	C_GLU_3	OE2	3.109
3D0L	B_ARG_66	NH1	B_ASP_86	OD1	3.615
3D0L	B_ARG_66	NH2	B_ASP_86	OD1	3.276
3D0L	B_ARG_66	NH2	B_ASP_86	OD2	2.898
3D0L	B_HIS_94	ND1	B_ASP_101	OD1	2.602
3D0L	B_HIS_94	ND1	B_ASP_101	OD2	3.437
3D0L	B_ARG_95	NH1	C_ASP_5	OD1	2.695
3D0L	B_ARG_95	NH1	C_ASP_5	OD2	3.449
3D0L	B_ARG_95	NH2	C_ASP_5	OD1	3.596
3D0L	B_ARG_95	NH2	C_ASP_5	OD2	3.078
3D0L	B_ARG_96	NH1	A_GLU_55	OE1	3.284
3D0L	B_ARG_96	NH1	A_GLU_55	OE2	3.522
3D0L	B_ARG_96	NH1	B_ASP_101	OD2	3.433
3D0L	B_ARG_96	NH2	A_GLU_55	OE1	3.455
3D0L	B_LYS_143	NZ	B_ASP_144	OD1	3.418
3D0L	B_LYS_143	NZ	B_ASP_144	OD2	3.784
3D0L	B_ARG_210	NH2	B_GLU_212	OE1	2.865
3D0L	C_LYS_6	NZ	B_ASP_54	OD1	2.251
3D0L	C_LYS_6	NZ	B_ASP_54	OD2	2.930
3D0L	C_LYS_6	NZ	B_ASP_56	OD2	3.751

Table 384: 3D0L-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3D0V	A_ARG_37	NH1	A_ASP_82	OD1	2.771
3D0V	A_ARG_61	NH2	A_GLU_81	OE2	3.952
3D0V	A_ARG_61	NH2	A_ASP_82	OD1	2.926
3D0V	A_ARG_61	NH2	A_ASP_82	OD2	3.288
3D0V	A_ARG_79	NH1	A_GLU_81	OE2	3.015
3D0V	A_ARG_79	NH2	A_GLU_81	OE2	2.700
3D0V	A_HIS_96	NE2	C_ASP_5	OD1	2.775
3D0V	A_LYS_149	NZ	A_GLU_195	OE1	3.493
3D0V	A_LYS_149	NZ	A_GLU_195	OE2	3.064
3D0V	A_LYS_183	NZ	A_GLU_187	OE2	3.032
3D0V	A_ARG_211	NH1	A_GLU_187	OE1	3.976
3D0V	B_ARG_38	NH1	B_GLU_46	OE1	2.804
3D0V	B_ARG_38	NH1	B_GLU_46	OE2	3.705
3D0V	B_ARG_38	NH2	B_ASP_86	OD1	2.434
3D0V	B_LYS_57	NZ	B_ASP_55	OD1	3.625
3D0V	B_LYS_57	NZ	B_ASP_55	OD2	3.392
3D0V	B_ARG_58	NH1	B_ASP_56	OD1	3.726
3D0V	B_ARG_58	NH1	B_ASP_56	OD2	2.549
3D0V	B_ARG_58	NH2	B_ASP_56	OD2	3.911
3D0V	B_ARG_58	NH2	C_GLU_3	OE1	2.733
3D0V	B_ARG_66	NH1	B_ASP_86	OD1	3.446
3D0V	B_ARG_66	NH1	B_ASP_86	OD2	3.728
3D0V	B_ARG_66	NH2	B_ASP_86	OD1	3.289
3D0V	B_ARG_66	NH2	B_ASP_86	OD2	2.373
3D0V	B_HIS_94	ND1	B_ASP_101	OD1	2.627
3D0V	B_HIS_94	ND1	B_ASP_101	OD2	3.607
3D0V	B_ARG_95	NH1	C_ASP_5	OD1	2.808
3D0V	B_ARG_95	NH1	C_ASP_5	OD2	3.484
3D0V	B_ARG_95	NH2	C_ASP_5	OD1	3.359
3D0V	B_ARG_95	NH2	C_ASP_5	OD2	2.831
3D0V	B_ARG_96	NH1	A_GLU_55	OE1	3.250
3D0V	B_ARG_96	NH1	A_GLU_55	OE2	3.216
3D0V	B_ARG_96	NH1	B_ASP_101	OD2	3.014
3D0V	B_ARG_96	NH2	A_GLU_55	OE1	3.184
3D0V	B_LYS_143	NZ	B_ASP_144	OD1	3.460
3D0V	B_LYS_143	NZ	B_ASP_144	OD2	3.988
3D0V	B_LYS_209	NZ	A_GLU_123	OE1	3.487
3D0V	B_ARG_210	NH1	B_GLU_212	OE1	2.267
3D0V	B_ARG_210	NH2	B_GLU_212	OE1	3.360
3D0V	C_LYS_6	NZ	B_ASP_54	OD1	3.609
3D0V	C_LYS_6	NZ	B_ASP_54	OD2	2.826
3D0V	C_LYS_6	NZ	B_ASP_56	OD1	3.006

Table 385: 3D0V-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3D9A	C_LYS_601	NZ	C_GLU_607	OE2	3.151
3D9A	C_LYS_697	NZ	H_ASP_332	OD2	2.741
3D9A	C_LYS_697	NZ	H_ASP_399	OD1	2.864
3D9A	C_LYS_697	NZ	H_ASP_399	OD2	3.300
3D9A	L_ARG_24	NH2	L_ASP_70	OD1	3.000
3D9A	L_ARG_24	NH2	L_ASP_70	OD2	3.752
3D9A	L_ARG_61	NH1	L_GLU_79	OE1	3.658
3D9A	L_ARG_61	NH1	L_GLU_79	OE2	3.448
3D9A	L_ARG_61	NH2	L_GLU_79	OE1	3.298
3D9A	L_ARG_61	NH2	L_ASP_82	OD1	2.829
3D9A	L_ARG_61	NH2	L_ASP_82	OD2	3.674
3D9A	L_LYS_147	NZ	L_GLU_154	OE1	3.943
3D9A	L_LYS_149	NZ	L_GLU_195	OE2	3.477
3D9A	L_LYS_169	NZ	L_ASP_167	OD2	3.989
3D9A	L_LYS_199	NZ	L_ASP_110	OD1	3.878
3D9A	L_LYS_199	NZ	L_ASP_110	OD2	3.357
3D9A	H_ARG_338	NH1	H_ASP_389	OD1	2.834
3D9A	H_ARG_338	NH2	H_GLU_346	OE1	2.922
3D9A	H_ARG_338	NH2	H_ASP_389	OD1	3.583
3D9A	H_ARG_366	NH1	H_ASP_389	OD1	2.956
3D9A	H_ARG_366	NH1	H_ASP_389	OD2	3.486
3D9A	H_ARG_366	NH2	H_ASP_389	OD1	3.662
3D9A	H_ARG_366	NH2	H_ASP_389	OD2	2.925
3D9A	H_LYS_508	NZ	L_GLU_123	OE1	3.029
3D9A	H_LYS_508	NZ	L_GLU_123	OE2	3.809

Table 386: 3D9A-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3DRO	A_ARG_37	NH1	A_ASP_82	OD1	2.782
3DRO	A_ARG_61	NH2	A_ASP_82	OD1	2.866
3DRO	A_ARG_61	NH2	A_ASP_82	OD2	3.498
3DRO	A_ARG_107	NH1	A_ASP_17	OD2	3.044
3DRO	A_ARG_107	NH2	A_ASP_17	OD2	3.360
3DRO	A_LYS_149	NZ	A_GLU_195	OE2	3.983
3DRO	A_LYS_183	NZ	A_GLU_187	OE1	3.983
3DRO	A_LYS_183	NZ	A_GLU_187	OE2	3.458
3DRO	A_LYS_188	NZ	A_ASP_185	OD1	3.977
3DRO	A_LYS_190	NZ	A_GLU_213	OE2	3.164
3DRO	B_ARG_1	NH1	B_ASP_101	OD2	3.834
3DRO	B_ARG_38	NH1	B_GLU_46	OE1	2.549
3DRO	B_ARG_38	NH1	B_GLU_46	OE2	3.279
3DRO	B_ARG_38	NH2	B_GLU_46	OE1	3.448
3DRO	B_ARG_38	NH2	B_ASP_86	OD1	3.555
3DRO	B_ARG_58	NH1	B_ASP_56	OD2	3.804
3DRO	B_ARG_66	NH1	B_ASP_86	OD1	3.732
3DRO	B_ARG_66	NH2	B_ASP_86	OD1	3.385
3DRO	B_ARG_66	NH2	B_ASP_86	OD2	2.816
3DRO	B_HIS_94	ND1	B_ASP_101	OD1	2.877
3DRO	B_HIS_94	ND1	B_ASP_101	OD2	3.841
3DRO	B_ARG_95	NH1	P_ASP_5	OD1	3.590
3DRO	B_ARG_95	NH1	P_ASP_5	OD2	3.370
3DRO	B_ARG_95	NH2	P_ASP_5	OD2	3.007
3DRO	B_ARG_96	NH1	B_ASP_101	OD2	2.827
3DRO	B_ARG_96	NH2	A_GLU_55	OE1	2.727
3DRO	B_ARG_96	NH2	A_GLU_55	OE2	3.426
3DRO	B_ARG_96	NH2	B_ASP_101	OD2	3.688
3DRO	B_LYS_143	NZ	B_ASP_144	OD1	3.378
3DRO	B_LYS_143	NZ	B_ASP_144	OD2	3.463
3DRO	B_LYS_209	NZ	A_GLU_123	OE1	3.782
3DRO	B_ARG_210	NH2	B_GLU_212	OE1	3.532
3DRO	P_LYS_6	NZ	B_ASP_54	OD1	2.913
3DRO	P_LYS_6	NZ	B_ASP_54	OD2	3.775
3DRO	P_LYS_6	NZ	B_ASP_56	OD1	3.330
3DRO	P_LYS_6	NZ	B_ASP_56	OD2	3.868

Table 387: 3DRO-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3DRQ	A_ARG_37	NH1	A_ASP_82	OD1	2.863
3DRQ	A_LYS_39	NZ	A_GLU_81	OE1	2.913
3DRQ	A_ARG_61	NH2	A_ASP_82	OD1	2.860
3DRQ	A_ARG_61	NH2	A_ASP_82	OD2	3.418
3DRQ	A_HIS_96	NE2	C_ASP_5	OD1	2.866
3DRQ	A_ARG_107	NH1	A_ASP_17	OD2	3.572
3DRQ	A_LYS_149	NZ	A_GLU_195	OE1	3.681
3DRQ	A_LYS_183	NZ	A_GLU_187	OE2	3.873
3DRQ	A_LYS_190	NZ	A_GLU_213	OE2	3.586
3DRQ	B_ARG_1	NH1	B_ASP_101	OD2	3.864
3DRQ	B_ARG_38	NH1	B_GLU_46	OE1	2.536
3DRQ	B_ARG_38	NH1	B_GLU_46	OE2	3.423
3DRQ	B_ARG_38	NH2	B_ASP_86	OD1	2.585
3DRQ	B_LYS_57	NZ	B_ASP_55	OD2	3.992
3DRQ	B_ARG_58	NH1	B_ASP_56	OD2	3.411
3DRQ	B_ARG_58	NH2	C_GLU_3	OE1	3.516
3DRQ	B_ARG_66	NH1	B_ASP_86	OD1	3.694
3DRQ	B_ARG_66	NH2	B_ASP_86	OD1	3.360
3DRQ	B_ARG_66	NH2	B_ASP_86	OD2	2.903
3DRQ	B_HIS_94	ND1	B_ASP_101	OD1	2.538
3DRQ	B_HIS_94	ND1	B_ASP_101	OD2	3.527
3DRQ	B_ARG_95	NH1	C_ASP_5	OD1	2.806
3DRQ	B_ARG_95	NH1	C_ASP_5	OD2	3.209
3DRQ	B_ARG_95	NH2	C_ASP_5	OD1	3.572
3DRQ	B_ARG_95	NH2	C_ASP_5	OD2	2.688
3DRQ	B_ARG_96	NH1	A_GLU_55	OE1	2.721
3DRQ	B_ARG_96	NH1	A_GLU_55	OE2	2.397
3DRQ	B_ARG_96	NH1	B_ASP_101	OD2	3.478
3DRQ	B_ARG_96	NH2	A_GLU_55	OE1	3.293
3DRQ	B_LYS_143	NZ	B_ASP_144	OD1	3.320
3DRQ	B_LYS_143	NZ	B_ASP_144	OD2	3.881
3DRQ	B_LYS_209	NZ	A_GLU_123	OE1	3.837
3DRQ	C_LYS_6	NZ	B_ASP_54	OD1	2.921
3DRQ	C_LYS_6	NZ	B_ASP_54	OD2	2.342
3DRQ	C_LYS_6	NZ	B_ASP_56	OD1	3.006

Table 388: 3DRQ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3DSF	L_ARG_61	NH1	L_GLU_81	OE2	3.610
3DSF	L_ARG_61	NH2	L_GLU_81	OE2	2.775
3DSF	L_ARG_61	NH2	L_ASP_82	OD1	3.453
3DSF	L_ARG_61	NH2	L_ASP_82	OD2	2.517
3DSF	L_LYS_147	NZ	L_GLU_154	OE2	3.411
3DSF	L_LYS_149	NZ	L_GLU_195	OE2	3.065
3DSF	L_ARG_155	NH1	L_GLU_185	OE1	3.133
3DSF	L_ARG_155	NH2	L_GLU_185	OE1	3.886
3DSF	L_ARG_155	NH2	L_GLU_185	OE2	3.560
3DSF	L_ARG_188	NH2	L_ASP_184	OD1	3.232
3DSF	L_HIS_189	ND1	L_ASP_151	OD2	2.709
3DSF	L_LYS_199	NZ	L_ASP_110	OD1	3.100
3DSF	L_LYS_199	NZ	L_ASP_110	OD2	2.808
3DSF	H_ARG_38	NH1	H_GLU_46	OE1	3.258
3DSF	H_ARG_38	NH1	H_GLU_46	OE2	2.451
3DSF	H_ARG_38	NH2	H_ASP_92	OD1	2.841
3DSF	H_ARG_52	NH1	P_ASP_47	OD2	3.172
3DSF	H_LYS_67	NZ	H_ASP_64	OD1	3.269
3DSF	H_ARG_69	NH1	H_ASP_92	OD2	2.681
3DSF	H_ARG_69	NH2	H_ASP_92	OD1	3.011
3DSF	H_ARG_69	NH2	H_ASP_92	OD2	3.022
3DSF	H_ARG_74	NH2	H_ASP_76	OD1	3.842
3DSF	H_ARG_100	NH2	H_ASP_104	OD1	3.055
3DSF	H_ARG_100	NH2	H_ASP_104	OD2	2.952

Table 389: 3DSF-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3EBA	A_ARG_49	NH1	A_ASP_52	OD1	3.900
3EBA	A_ARG_64	NH1	A_ASP_87	OD1	3.739
3EBA	A_ARG_64	NH1	A_ASP_87	OD2	2.820
3EBA	A_ARG_64	NH2	A_ASP_87	OD1	2.913
3EBA	A_ARG_64	NH2	A_ASP_87	OD2	3.515
3EBA	A_LYS_84	NZ	A_GLU_86	OE1	3.206
3EBA	B_LYS_69	NZ	B_ASP_67	OD2	3.295
3EBA	B_LYS_97	NZ	A_GLU_97	OE2	3.240
3EBA	B_ARG_101	NH1	A_ASP_109	OD1	3.083
3EBA	B_ARG_101	NH1	A_ASP_109	OD2	2.691
3EBA	B_ARG_101	NH2	A_ASP_109	OD1	3.308
3EBA	B_ARG_101	NH2	A_ASP_109	OD2	3.134

Table 390: 3EBA-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID** **residue name** **residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3EOA	L_ARG_24	NH2	L_ASP_70	OD1	3.574
3EOA	L_ARG_24	NH2	L_ASP_70	OD2	2.606
3EOA	L_ARG_61	NH1	L_GLU_81	OE2	3.484
3EOA	L_ARG_61	NH1	L_ASP_82	OD1	3.804
3EOA	L_LYS_149	NZ	L_GLU_195	OE1	2.415
3EOA	H_ARG_38	NH1	H_ASP_90	OD1	2.905
3EOA	H_ARG_38	NH2	H_GLU_46	OE2	3.821
3EOA	H_ARG_38	NH2	H_ASP_90	OD1	3.860
3EOA	H_ARG_67	NH1	H_ASP_90	OD2	2.949
3EOA	H_ARG_67	NH2	H_ASP_90	OD1	3.556
3EOA	H_ARG_67	NH2	H_ASP_90	OD2	3.648
3EOA	H_ARG_87	NH1	H_GLU_89	OE1	2.782
3EOA	H_ARG_98	NH1	H_ASP_109	OD2	2.755
3EOA	H_LYS_151	NZ	H_ASP_152	OD1	3.488
3EOA	H_LYS_151	NZ	H_ASP_152	OD2	3.869
3EOA	H_LYS_217	NZ	L_GLU_123	OE2	3.037
3EOA	L_LYS_149	NZ	L_ASP_145	OD1	2.783
3EOA	L_LYS_149	NZ	L_ASP_145	OD2	2.826
3EOA	L_LYS_155	NZ	L_ASP_152	OD1	3.581
3EOA	L_LYS_155	NZ	L_ASP_193	OD1	2.723
3EOA	L_LYS_159	NZ	L_ASP_156	OD1	3.990
3EOA	L_LYS_159	NZ	L_ASP_193	OD2	3.917
3EOA	L_LYS_178	NZ	L_GLU_180	OE1	3.466
3EOA	L_LYS_197	NZ	H_ASP_55	OD1	3.170
3EOA	L_LYS_197	NZ	H_GLU_57	OE1	2.719
3EOA	L_HIS_198	NE2	H_GLU_57	OE1	3.638
3EOA	L_HIS_198	NE2	H_GLU_57	OE2	3.098
3EOA	L_ARG_221	NH1	L_GLU_223	OE2	3.700
3EOA	L_ARG_227	NH2	L_ASP_131	OD2	2.628
3EOA	L_LYS_252	NZ	L_ASP_249	OD2	3.806
3EOA	A_ARG_61	NH1	A_GLU_81	OE2	3.839
3EOA	A_ARG_61	NH1	A_ASP_82	OD1	2.580
3EOA	A_ARG_61	NH1	A_ASP_82	OD2	3.564
3EOA	A_LYS_103	NZ	A_GLU_165	OE1	3.460
3EOA	A_LYS_103	NZ	A_GLU_165	OE2	3.931
3EOA	A_LYS_	NZ	A_GLU_	OE1	3.399
3EOA	A_LYS_	NZ	A_GLU_	OE2	3.445
3EOA	A_LYS_	NZ	A_GLU_	OE2	3.194
3EOA	A_ARG_	NH2	A_GLU_	OE2	3.408
3EOA	B_ARG_38	NH1	B_ASP_90	OD1	2.938
3EOA	B_ARG_38	NH2	B_GLU_46	OE2	3.688
3EOA	B_ARG_38	NH2	B_ASP_90	OD1	3.785
3EOA	B_ARG_67	NH1	B_ASP_90	OD1	3.358
3EOA	B_ARG_67	NH1	B_ASP_90	OD2	2.533
3EOA	B_ARG_67	NH2	B_ASP_90	OD1	3.191
3EOA	B_ARG_67	NH2	B_ASP_90	OD2	3.831
3EOA	B_ARG_98	NH1	B_ASP_109	OD1	3.621
3EOA	B_ARG_98	NH1	B_ASP_109	OD2	2.877
3EOA	B_LYS_	NZ	A_GLU_	OE2	3.673
3EOA	J_LYS_149	NZ	J_ASP_145	OD1	3.029
3EOA	J_LYS_149	NZ	J_GLU_293	OE2	2.826
3EOA	J_LYS_155	NZ	J_ASP_193	OD1	2.719
3EOA	J_LYS_159	NZ	J_ASP_193	OD2	3.556
3EOA	J_LYS_178	NZ	J_GLU_180	OE1	3.070
3EOA	J_LYS_178	NZ	J_GLU_180	OE2	3.956
3EOA	J_LYS_197	NZ	B_ASP_55	OD1	2.626
3EOA	J_LYS_197	NZ	B_ASP_55	OD2	2.997

3EOA	J_LYS_197	NZ	B_GLU_57	OE1	2.784
3EOA	J_HIS_198	NE2	B_GLU_57	OE1	3.322
3EOA	J_HIS_198	NE2	B_GLU_57	OE2	2.793
3EOA	J_ARG_221	NH1	J_GLU_223	OE1	3.385
3EOA	J_ARG_221	NH2	J_GLU_218	OE1	3.711
3EOA	J_ARG_227	NH2	J_ASP_131	OD2	3.169
3EOA	J_LYS_232	NZ	J_ASP_253	OD1	3.326

Table 391: 3EOA-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3EOB	L_ARG_24	NH2	L_ASP_70	OD2	3.407
3EOB	L_ARG_61	NH1	L_ASP_82	OD1	3.432
3EOB	L_ARG_108	NH2	L_ASP_170	OD1	2.979
3EOB	L_LYS_149	NZ	L_GLU_195	OE1	3.677
3EOB	H_ARG_38	NH1	H_ASP_90	OD1	3.001
3EOB	H_ARG_38	NH2	H_GLU_46	OE2	3.103
3EOB	H_ARG_38	NH2	H_ASP_90	OD1	3.672
3EOB	H_LYS_63	NZ	H_GLU_46	OE1	3.646
3EOB	H_ARG_67	NH1	H_ASP_90	OD1	3.982
3EOB	H_ARG_67	NH1	H_ASP_90	OD2	2.820
3EOB	H_ARG_67	NH2	H_ASP_90	OD1	3.369
3EOB	H_ARG_67	NH2	H_ASP_90	OD2	3.450
3EOB	H_ARG_87	NH1	H_GLU_89	OE1	3.348
3EOB	H_ARG_98	NH1	H_ASP_109	OD2	2.860
3EOB	H_LYS_217	NZ	L_GLU_123	OE2	3.176
3EOB	L_LYS_149	NZ	L_ASP_145	OD1	3.604
3EOB	L_LYS_149	NZ	L_ASP_145	OD2	2.585
3EOB	L_LYS_155	NZ	L_ASP_193	OD1	3.215
3EOB	L_LYS_159	NZ	L_ASP_193	OD2	3.529
3EOB	L_LYS_178	NZ	L_GLU_180	OE1	3.871
3EOB	L_LYS_197	NZ	H_GLU_57	OE1	2.792
3EOB	L_LYS_197	NZ	H_GLU_57	OE2	3.051
3EOB	L_HIS_198	ND1	H_GLU_57	OE2	3.691
3EOB	L_HIS_198	NE2	H_GLU_57	OE1	2.182
3EOB	L_HIS_198	NE2	H_GLU_57	OE2	2.522
3EOB	L_ARG_221	NH1	L_GLU_223	OE1	2.856
3EOB	L_ARG_227	NH2	L_ASP_131	OD2	2.963
3EOB	L_LYS_232	NZ	L_ASP_253	OD1	3.583
3EOB	L_HIS_264	NE2	J_GLU_241	OE1	2.369
3EOB	L_HIS_264	NE2	J_GLU_241	OE2	2.595
3EOB	L_HIS_275	ND1	L_GLU_272	OE2	3.714
3EOB	A_ARG_24	NH2	A_ASP_70	OD1	3.782
3EOB	A_ARG_24	NH2	A_ASP_70	OD2	3.414
3EOB	A_ARG_61	NH1	A_GLU_81	OE2	3.358
3EOB	A_ARG_61	NH1	A_ASP_82	OD1	2.901
3EOB	A_ARG_61	NH1	A_ASP_82	OD2	3.391
3EOB	A_ARG_108	NH2	A_ASP_170	OD1	3.529
3EOB	A_LYS_	NZ	A_GLU_	OE1	3.265
3EOB	B_ARG_38	NH1	B_ASP_90	OD1	3.354
3EOB	B_ARG_38	NH2	B_GLU_46	OE2	3.502
3EOB	B_ARG_38	NH2	B_ASP_90	OD1	3.996
3EOB	B_LYS_63	NZ	B_GLU_46	OE1	3.294
3EOB	B_ARG_67	NH1	B_ASP_90	OD2	2.904
3EOB	B_ARG_67	NH2	B_ASP_90	OD1	3.362
3EOB	B_ARG_67	NH2	B_ASP_90	OD2	3.179
3EOB	B_ARG_87	NH1	B_GLU_89	OE1	2.946
3EOB	B_ARG_98	NH1	B_ASP_109	OD2	3.051
3EOB	B_LYS_	NZ	A_GLU_	OE1	3.788
3EOB	B_LYS_	NZ	A_GLU_	OE2	3.219
3EOB	J_LYS_149	NZ	J_ASP_145	OD1	2.827
3EOB	J_LYS_149	NZ	J_ASP_145	OD2	3.169
3EOB	J_LYS_155	NZ	J_ASP_193	OD1	3.290
3EOB	J_LYS_159	NZ	J_ASP_193	OD1	3.983
3EOB	J_LYS_159	NZ	J_ASP_193	OD2	2.888
3EOB	J_LYS_197	NZ	B_ASP_55	OD1	3.833
3EOB	J_LYS_197	NZ	B_GLU_57	OE1	2.107
3EOB	J_LYS_197	NZ	B_GLU_57	OE2	3.802

3EOB	J_HIS_198	ND1	B_GLU_57	OE2	3.839
3EOB	J_HIS_198	NE2	B_GLU_57	OE1	2.356
3EOB	J_HIS_198	NE2	B_GLU_57	OE2	2.609
3EOB	J_ARG_221	NH1	J_GLU_223	OE1	3.220
3EOB	J_ARG_227	NH2	J_ASP_131	OD2	2.997
3EOB	J_LYS_232	NZ	J_ASP_253	OD1	3.217
3EOB	J_HIS_264	NE2	I_GLU_241	OE1	2.434
3EOB	J_HIS_264	NE2	I_GLU_241	OE2	2.722
3EOB	J_LYS_294	NZ	J_ASP_290	OD2	3.936

Table 392: 3EOB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3ESU	F_ARG_61	NH2	F_GLU_81	OE2	3.099
3ESU	F_ARG_61	NH2	F_ASP_82	OD1	2.818
3ESU	F_ARG_61	NH2	F_ASP_82	OD2	3.481
3ESU	F_LYS_103	NZ	F_GLU_105	OE2	3.657
3ESU	F_LYS_1038	NZ	F_ASP_1086	OD1	3.978
3ESU	F_LYS_1062	NZ	F_GLU_1046	OE1	2.626
3ESU	F_LYS_1062	NZ	F_GLU_1046	OE2	3.804
3ESU	F_LYS_1066	NZ	F_ASP_1086	OD1	3.810
3ESU	F_LYS_1066	NZ	F_ASP_1086	OD2	2.823
3ESU	F_ARG_1094	NH1	F_ASP_1024	OD2	2.978

Table 393: 3ESU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3ESV	F_LYS_0	NZ	G_ASP_1054	OD1	3.499
3ESV	F_LYS_0	NZ	G_ASP_1054	OD2	2.774
3ESV	F_LYS_0	NZ	G_ASP_1056	OD2	3.090
3ESV	F_ARG_61	NH1	F_GLU_79	OE1	3.359
3ESV	F_ARG_61	NH2	F_GLU_79	OE1	3.662
3ESV	F_ARG_61	NH2	F_GLU_81	OE2	3.198
3ESV	F_ARG_61	NH2	F_ASP_82	OD1	2.780
3ESV	F_ARG_61	NH2	F_ASP_82	OD2	3.438
3ESV	F_LYS_1066	NZ	F_ASP_1086	OD1	3.900
3ESV	F_LYS_1066	NZ	F_ASP_1086	OD2	2.918
3ESV	F_ARG_1094	NH1	F_ASP_1101	OD2	3.844
3ESV	F_ARG_1094	NH2	F_ASP_1101	OD2	3.978
3ESV	F_ARG_1099	NH2	F_ASP_1101	OD2	3.038
3ESV	G_ARG_53	NH1	F_ASP_1056	OD1	2.802
3ESV	G_ARG_53	NH2	F_ASP_1056	OD1	3.489
3ESV	G_ARG_61	NH1	G_GLU_79	OE1	2.958
3ESV	G_ARG_61	NH2	G_GLU_79	OE1	3.174
3ESV	G_ARG_61	NH2	G_GLU_81	OE1	2.849
3ESV	G_ARG_61	NH2	G_ASP_82	OD1	2.663
3ESV	G_ARG_61	NH2	G_ASP_82	OD2	3.554
3ESV	G_LYS_103	NZ	G_GLU_105	OE1	3.664
3ESV	G_LYS_1066	NZ	G_ASP_1086	OD1	3.520
3ESV	G_LYS_1066	NZ	G_ASP_1086	OD2	2.664
3ESV	G_ARG_1099	NH2	G_ASP_1101	OD2	3.345

Table 394: 3ESV-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3ET9	F_ARG_61	NH2	F_GLU_81	OE2	3.021
3ET9	F_ARG_61	NH2	F_ASP_82	OD1	2.714
3ET9	F_ARG_61	NH2	F_ASP_82	OD2	3.090
3ET9	F_LYS_103	NZ	F_GLU_105	OE1	3.734
3ET9	F_LYS_1038	NZ	F_ASP_1086	OD1	3.668
3ET9	F_LYS_1062	NZ	F_GLU_1046	OE1	3.916
3ET9	F_LYS_1066	NZ	F_ASP_1086	OD2	3.146
3ET9	F_ARG_1094	NH1	F_ASP_1024	OD1	3.640
3ET9	F_ARG_1094	NH1	F_ASP_1024	OD2	2.893

Table 395: 3ET9-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3ETB	F_ARG_24	NH1	G_ASP_70	OD1	3.579
3ETB	F_ARG_24	NH1	G_ASP_70	OD2	3.034
3ETB	F_ARG_24	NH2	G_ASP_70	OD1	3.608
3ETB	F_ARG_24	NH2	G_ASP_70	OD2	3.774
3ETB	F_ARG_30	NH1	J_ASP_658	OD2	3.129
3ETB	F_ARG_53	NH1	J_GLU_654	OE1	3.838
3ETB	F_ARG_53	NH2	J_GLU_654	OE1	3.771
3ETB	F_ARG_61	NH1	F_GLU_79	OE2	3.574
3ETB	F_ARG_61	NH2	F_GLU_79	OE1	3.945
3ETB	F_ARG_61	NH2	F_ASP_82	OD1	2.649
3ETB	F_ARG_61	NH2	F_ASP_82	OD2	2.469
3ETB	F_ARG_1050	NH2	J_ASP_683	OD2	3.114
3ETB	F_LYS_1062	NZ	F_GLU_1046	OE1	3.184
3ETB	F_LYS_1062	NZ	F_GLU_1046	OE2	3.847
3ETB	F_LYS_1066	NZ	F_ASP_1086	OD2	3.203
3ETB	F_ARG_1094	NH1	F_ASP_1101	OD1	2.832
3ETB	G_ARG_24	NH1	F_ASP_70	OD1	3.633
3ETB	G_ARG_24	NH1	F_ASP_70	OD2	3.127
3ETB	G_ARG_24	NH2	F_ASP_70	OD1	3.702
3ETB	G_ARG_24	NH2	F_ASP_70	OD2	3.878
3ETB	G_ARG_30	NH1	K_ASP_658	OD2	3.266
3ETB	G_ARG_53	NH2	K_ASP_648	OD2	3.972
3ETB	G_ARG_53	NH2	K_GLU_654	OE1	3.990
3ETB	G_ARG_61	NH1	G_GLU_79	OE2	3.534
3ETB	G_ARG_61	NH2	G_GLU_79	OE1	3.999
3ETB	G_ARG_61	NH2	G_ASP_82	OD1	2.660
3ETB	G_ARG_61	NH2	G_ASP_82	OD2	2.433
3ETB	G_ARG_1050	NH2	K_ASP_683	OD1	3.853
3ETB	G_ARG_1050	NH2	K_ASP_683	OD2	2.796
3ETB	G_LYS_1062	NZ	G_GLU_1046	OE1	3.161
3ETB	G_LYS_1062	NZ	G_GLU_1046	OE2	3.812
3ETB	G_LYS_1066	NZ	G_ASP_1086	OD2	3.138
3ETB	G_ARG_1094	NH1	G_ASP_1101	OD1	2.918
3ETB	H_ARG_24	NH1	L_ASP_70	OD1	3.544
3ETB	H_ARG_24	NH1	L_ASP_70	OD2	3.118
3ETB	H_ARG_24	NH2	L_ASP_70	OD1	3.662
3ETB	H_ARG_24	NH2	L_ASP_70	OD2	3.905
3ETB	H_ARG_30	NH1	L_ASP_658	OD1	3.824
3ETB	H_ARG_30	NH1	L_ASP_658	OD2	2.913
3ETB	H_ARG_53	NH1	L_GLU_654	OE1	3.771
3ETB	H_ARG_53	NH2	L_GLU_654	OE1	3.669
3ETB	H_ARG_61	NH1	H_GLU_79	OE2	3.579
3ETB	H_ARG_61	NH2	H_GLU_79	OE1	3.984
3ETB	H_ARG_61	NH2	H_ASP_82	OD1	2.635
3ETB	H_ARG_61	NH2	H_ASP_82	OD2	2.472
3ETB	H_ARG_1050	NH2	L_ASP_683	OD2	3.159
3ETB	H_LYS_1062	NZ	H_GLU_1046	OE1	3.123
3ETB	H_LYS_1062	NZ	H_GLU_1046	OE2	3.731
3ETB	H_LYS_1066	NZ	H_ASP_1086	OD1	3.989
3ETB	H_LYS_1066	NZ	H_ASP_1086	OD2	3.171
3ETB	H_ARG_1094	NH1	H_ASP_1101	OD1	2.766
3ETB	I_ARG_24	NH1	H_ASP_70	OD1	3.448
3ETB	I_ARG_24	NH1	H_ASP_70	OD2	2.998
3ETB	I_ARG_24	NH2	H_ASP_70	OD1	3.537
3ETB	I_ARG_24	NH2	H_ASP_70	OD2	3.789
3ETB	I_ARG_30	NH1	M_ASP_658	OD2	3.315
3ETB	I_ARG_53	NH1	M_GLU_654	OE1	3.885

3ETB	I_ARG_53	NH2	M_GLU_654	OE1	3.890
3ETB	I_ARG_61	NH1	I_GLU_79	OE2	3.590
3ETB	I_ARG_61	NH2	I_ASP_82	OD1	2.608
3ETB	I_ARG_61	NH2	I_ASP_82	OD2	2.422
3ETB	I_ARG_1050	NH2	M_ASP_683	OD2	3.093
3ETB	I_LYS_1062	NZ	I_GLU_1046	OE1	3.276
3ETB	I_LYS_1062	NZ	I_GLU_1046	OE2	3.841
3ETB	I_LYS_1066	NZ	I_ASP_1086	OD1	3.951
3ETB	I_LYS_1066	NZ	I_ASP_1086	OD2	3.038
3ETB	I_ARG_1094	NH1	I_ASP_1101	OD1	2.853
3ETB	J_HIS_597	ND1	J_GLU_704	OE2	3.548
3ETB	J_HIS_597	NE2	J_ASP_608	OD1	2.727
3ETB	J_LYS_613	NZ	J_GLU_609	OE1	3.973
3ETB	J_LYS_633	NZ	J_ASP_634	OD1	3.253
3ETB	J_LYS_653	NZ	G_ASP_17	OD1	2.972
3ETB	J_ARG_659	NH1	J_ASP_661	OD1	3.263
3ETB	J_ARG_659	NH1	J_ASP_661	OD2	3.124
3ETB	J_ARG_659	NH2	J_ASP_661	OD1	3.589
3ETB	J_ARG_669	NH2	J_ASP_671	OD1	3.245
3ETB	J_ARG_669	NH2	J_ASP_671	OD2	3.457
3ETB	J_LYS_679	NZ	J_GLU_625	OE1	3.523
3ETB	J_LYS_684	NZ	F_ASP_1054	OD1	3.728
3ETB	J_LYS_684	NZ	F_ASP_1054	OD2	3.401
3ETB	J_LYS_684	NZ	F_ASP_1056	OD1	3.220
3ETB	J_LYS_684	NZ	F_ASP_1056	OD2	3.481
3ETB	K_HIS_597	ND1	K_GLU_704	OE2	3.588
3ETB	K_HIS_597	NE2	K_ASP_608	OD1	2.693
3ETB	K_HIS_597	NE2	K_ASP_608	OD2	3.992
3ETB	K_LYS_613	NZ	K_GLU_609	OE1	3.913
3ETB	K_LYS_633	NZ	K_ASP_634	OD1	3.167
3ETB	K_LYS_653	NZ	F_ASP_17	OD1	3.083
3ETB	K_ARG_659	NH1	K_ASP_661	OD1	3.380
3ETB	K_ARG_659	NH1	K_ASP_661	OD2	3.241
3ETB	K_ARG_659	NH2	K_ASP_661	OD1	3.692
3ETB	K_ARG_669	NH2	K_ASP_671	OD1	3.263
3ETB	K_ARG_669	NH2	K_ASP_671	OD2	3.367
3ETB	K_LYS_679	NZ	K_GLU_625	OE1	3.601
3ETB	K_LYS_684	NZ	G_ASP_1054	OD1	3.379
3ETB	K_LYS_684	NZ	G_ASP_1054	OD2	3.075
3ETB	K_LYS_684	NZ	G_ASP_1056	OD1	3.162
3ETB	K_LYS_684	NZ	G_ASP_1056	OD2	3.578
3ETB	L_HIS_597	ND1	L_GLU_704	OE2	3.614
3ETB	L_HIS_597	NE2	L_ASP_608	OD1	2.704
3ETB	L_LYS_613	NZ	L_GLU_609	OE1	3.941
3ETB	L_LYS_633	NZ	L_ASP_634	OD1	3.041
3ETB	L_LYS_653	NZ	I_ASP_17	OD1	2.978
3ETB	L_ARG_659	NH1	L_ASP_661	OD1	3.373
3ETB	L_ARG_659	NH1	L_ASP_661	OD2	3.245
3ETB	L_ARG_659	NH2	L_ASP_661	OD1	3.600
3ETB	L_ARG_669	NH2	L_ASP_671	OD1	3.400
3ETB	L_ARG_669	NH2	L_ASP_671	OD2	3.495
3ETB	L_LYS_679	NZ	L_GLU_625	OE1	3.532
3ETB	L_LYS_684	NZ	H_ASP_1056	OD1	3.616
3ETB	L_LYS_684	NZ	H_ASP_1056	OD2	3.187
3ETB	M_HIS_597	ND1	M_GLU_704	OE2	3.644
3ETB	M_HIS_597	NE2	M_ASP_608	OD1	2.880
3ETB	M_LYS_613	NZ	M_GLU_609	OE1	3.907
3ETB	M_LYS_633	NZ	M_ASP_634	OD1	3.141

3ETB	M_LYS_653	NZ	H_ASP_17	OD1	3.060
3ETB	M_ARG_659	NH1	M_ASP_661	OD1	3.383
3ETB	M_ARG_659	NH1	M_ASP_661	OD2	3.234
3ETB	M_ARG_659	NH2	M_ASP_661	OD1	3.730
3ETB	M_ARG_669	NH2	M_ASP_671	OD1	3.256
3ETB	M_ARG_669	NH2	M_ASP_671	OD2	3.369
3ETB	M_LYS_679	NZ	M_GLU_625	OE1	3.500
3ETB	M_LYS_684	NZ	I_ASP_1054	OD1	3.625
3ETB	M_LYS_684	NZ	I_ASP_1054	OD2	3.167
3ETB	M_LYS_684	NZ	I_ASP_1056	OD1	3.241
3ETB	M_LYS_684	NZ	I_ASP_1056	OD2	3.478

Table 396: 3ETB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3EYV	L_LYS_55	NZ	H_ASP_102	OD2	3.565
3EYV	L_ARG_66	NH2	L_GLU_86	OE2	3.710
3EYV	L_ARG_66	NH2	L_ASP_87	OD1	2.915
3EYV	L_ARG_66	NH2	L_ASP_87	OD2	3.931
3EYV	L_LYS_108	NZ	L_GLU_170	OE1	3.179
3EYV	L_LYS_154	NZ	L_GLU_200	OE2	3.356
3EYV	L_LYS_188	NZ	L_GLU_192	OE1	3.296
3EYV	L_LYS_188	NZ	L_GLU_192	OE2	2.586
3EYV	L_HIS_194	ND1	L_ASP_156	OD2	2.824
3EYV	L_HIS_194	NE2	L_ASP_190	OD1	3.486
3EYV	H_ARG_38	NH1	H_ASP_90	OD1	2.819
3EYV	H_ARG_38	NH2	H_GLU_46	OE1	3.776
3EYV	H_ARG_38	NH2	H_GLU_46	OE2	3.233
3EYV	H_ARG_38	NH2	H_ASP_90	OD1	3.948
3EYV	H_LYS_65	NZ	H_ASP_59	OD1	2.876
3EYV	H_ARG_67	NH1	H_ASP_90	OD1	3.779
3EYV	H_ARG_67	NH1	H_ASP_90	OD2	2.779
3EYV	H_ARG_67	NH2	H_ASP_90	OD1	3.386
3EYV	H_ARG_67	NH2	H_ASP_90	OD2	3.752
3EYV	H_ARG_101	NH1	H_ASP_31	OD2	3.262
3EYV	H_ARG_101	NH2	H_ASP_31	OD2	3.521
3EYV	H_LYS_149	NZ	H_ASP_150	OD1	3.279
3EYV	H_LYS_149	NZ	H_ASP_150	OD2	3.718
3EYV	H_LYS_212	NZ	H_ASP_214	OD1	3.958
3EYV	H_LYS_212	NZ	H_ASP_214	OD2	2.546
3EYV	H_LYS_215	NZ	L_GLU_128	OE2	3.627
3EYV	H_LYS_216	NZ	H_GLU_218	OE2	3.932
3EYV	A_LYS_55	NZ	B_ASP_102	OD2	3.151
3EYV	A_ARG_66	NH2	A_GLU_86	OE2	3.631
3EYV	A_ARG_66	NH2	A_ASP_87	OD1	3.103
3EYV	A_ARG_66	NH2	A_ASP_87	OD2	3.416
3EYV	A_LYS_108	NZ	A_GLU_170	OE1	3.086
3EYV	A_LYS_108	NZ	A_GLU_170	OE2	3.645
3EYV	A_LYS_154	NZ	A_GLU_200	OE1	3.963
3EYV	A_LYS_154	NZ	A_GLU_200	OE2	2.945
3EYV	A_LYS_193	NZ	A_ASP_190	OD1	3.557
3EYV	A_HIS_194	ND1	A_ASP_156	OD1	2.892
3EYV	B_ARG_38	NH1	B_ASP_90	OD1	2.718
3EYV	B_ARG_38	NH2	B_GLU_46	OE1	3.428
3EYV	B_ARG_38	NH2	B_GLU_46	OE2	3.023
3EYV	B_ARG_38	NH2	B_ASP_90	OD1	3.972
3EYV	B_LYS_65	NZ	B_ASP_59	OD1	2.790
3EYV	B_ARG_67	NH1	B_ASP_90	OD1	3.866
3EYV	B_ARG_67	NH1	B_ASP_90	OD2	2.720
3EYV	B_ARG_67	NH2	B_ASP_90	OD1	3.285
3EYV	B_ARG_67	NH2	B_ASP_90	OD2	3.497
3EYV	B_ARG_87	NH1	B_GLU_89	OE1	3.883
3EYV	B_ARG_101	NH1	B_ASP_31	OD2	3.502
3EYV	B_LYS_220	NZ	A_ASP_127	OD2	3.402

Table 397: 3EYV-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3FMG	L_LYS_50	NZ	H_ASP_106	OD1	3.132
3FMG	L_ARG_61	NH1	L_ASP_82	OD1	3.084
3FMG	L_ARG_61	NH1	L_ASP_82	OD2	2.397
3FMG	L_ARG_61	NH2	L_GLU_81	OE2	3.990
3FMG	L_ARG_61	NH2	L_ASP_82	OD2	3.861
3FMG	L_LYS_103	NZ	L_GLU_105	OE2	2.781
3FMG	L_LYS_103	NZ	L_ASP_165	OD1	3.422
3FMG	L_LYS_103	NZ	L_ASP_165	OD2	3.673
3FMG	L_LYS_147	NZ	L_GLU_154	OE1	3.671
3FMG	L_LYS_149	NZ	L_GLU_195	OE1	2.879
3FMG	L_LYS_149	NZ	L_GLU_195	OE2	3.536
3FMG	L_ARG_155	NH1	L_GLU_185	OE2	3.733
3FMG	L_ARG_155	NH2	L_GLU_185	OE2	3.838
3FMG	L_LYS_169	NZ	L_ASP_167	OD1	3.814
3FMG	L_LYS_183	NZ	L_GLU_187	OE1	3.890
3FMG	L_LYS_183	NZ	L_GLU_187	OE2	3.515
3FMG	L_HIS_189	ND1	L_ASP_151	OD2	3.000
3FMG	L_HIS_189	NE2	L_GLU_185	OE1	3.777
3FMG	L_LYS_199	NZ	L_ASP_110	OD1	3.137
3FMG	L_LYS_199	NZ	L_ASP_110	OD2	3.503
3FMG	H_LYS_19	NZ	H_GLU_10	OE1	2.764
3FMG	H_LYS_19	NZ	H_GLU_10	OE2	2.857
3FMG	H_LYS_38	NZ	H_ASP_92	OD1	3.712
3FMG	H_LYS_64	NZ	L_ASP_1	OD2	3.241
3FMG	H_LYS_68	NZ	H_ASP_92	OD1	3.504
3FMG	H_LYS_68	NZ	H_ASP_92	OD2	2.490
3FMG	H_ARG_100	NH1	H_ASP_111	OD1	2.791
3FMG	H_ARG_100	NH1	H_ASP_111	OD2	3.868
3FMG	H_ARG_100	NH2	H_ASP_111	OD1	3.539
3FMG	H_ARG_100	NH2	H_ASP_111	OD2	3.163
3FMG	H_HIS_102	ND1	H_ASP_111	OD2	2.692
3FMG	H_HIS_108	ND1	H_GLU_35	OE1	3.839
3FMG	H_HIS_108	ND1	H_GLU_50	OE1	3.875
3FMG	H_HIS_108	ND1	H_GLU_50	OE2	3.683
3FMG	H_HIS_108	NE2	H_GLU_50	OE1	3.647
3FMG	H_LYS_125	NZ	H_ASP_193	OD2	3.410
3FMG	H_LYS_228	NZ	H_ASP_230	OD1	2.777
3FMG	A_LYS_143	NZ	A_GLU_88	OE1	3.153
3FMG	A_LYS_183	NZ	A_ASP_228	OD2	3.491
3FMG	A_LYS_194	NZ	A_GLU_217	OE2	2.678
3FMG	A_LYS_250	NZ	A_ASP_179	OD1	3.375
3FMG	A_LYS_251	NZ	A_ASP_157	OD1	2.865
3FMG	A_LYS_251	NZ	A_ASP_157	OD2	3.990
3FMG	A_ARG_255	NH1	A_GLU_162	OE1	3.900
3FMG	A_ARG_255	NH1	A_GLU_162	OE2	3.506
3FMG	A_ARG_255	NH2	A_GLU_162	OE1	3.265
3FMG	A_ARG_283	NH1	A_GLU_256	OE1	2.718
3FMG	A_ARG_283	NH1	A_GLU_256	OE2	3.791
3FMG	A_ARG_283	NH2	A_GLU_256	OE1	3.447
3FMG	A_ARG_283	NH2	A_GLU_256	OE2	2.994
3FMG	A_LYS_312	NZ	A_GLU_282	OE1	3.755
3FMG	A_LYS_312	NZ	A_GLU_282	OE2	3.300

Table 398: 3FMG-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3G39	A_ARG_57	NH2	A_ASP_59	OD1	3.706
3G39	A_ARG_57	NH2	A_ASP_59	OD2	2.784
3G39	A_ARG_125	NH2	A_GLU_159	OE1	3.701
3G39	A_ARG_125	NH2	A_GLU_159	OE2	2.699
3G39	A_ARG_155	NH2	A_ASP_143	OD1	3.190
3G39	A_ARG_155	NH2	A_ASP_143	OD2	3.105

Table 399: 3G39-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3G3A	A_ARG_57	NH2	A_ASP_59	OD2	3.133
3G3A	A_ARG_155	NH1	A_ASP_143	OD1	3.039
3G3A	A_ARG_155	NH1	A_ASP_143	OD2	3.682
3G3A	B_LYS_1	NZ	B_GLU_7	OE2	2.851
3G3A	B_ARG_61	NH2	A_ASP_59	OD2	3.447
3G3A	B_ARG_73	NH1	A_ASP_61	OD1	2.630
3G3A	B_ARG_73	NH1	A_ASP_61	OD2	3.494
3G3A	B_ARG_73	NH2	A_ASP_59	OD2	3.260
3G3A	B_ARG_73	NH2	A_ASP_61	OD1	3.287
3G3A	B_ARG_73	NH2	A_ASP_61	OD2	2.479
3G3A	B_LYS_97	NZ	B_ASP_101	OD1	3.864
3G3A	B_LYS_97	NZ	B_ASP_101	OD2	3.365
3G3A	B_ARG_112	NH1	A_ASP_141	OD1	3.611
3G3A	B_ARG_112	NH1	A_ASP_141	OD2	2.906
3G3A	B_ARG_112	NH2	A_ASP_141	OD1	2.901
3G3A	B_ARG_112	NH2	A_ASP_141	OD2	3.689
3G3A	B_ARG_112	NH2	A_ASP_143	OD2	3.389
3G3A	C_LYS_43	NZ	C_GLU_45	OE2	3.006
3G3A	C_ARG_57	NH2	C_ASP_59	OD1	3.619
3G3A	C_ARG_57	NH2	C_ASP_59	OD2	2.899
3G3A	C_ARG_94	NH2	C_ASP_119	OD1	3.786
3G3A	C_ARG_155	NH1	C_ASP_143	OD1	2.753
3G3A	C_ARG_155	NH1	C_ASP_143	OD2	3.605
3G3A	D_LYS_1	NZ	D_GLU_7	OE1	3.499
3G3A	D_LYS_1	NZ	D_GLU_7	OE2	2.566
3G3A	D_ARG_61	NH1	C_ASP_59	OD2	3.676
3G3A	D_ARG_61	NH2	C_ASP_59	OD1	3.900
3G3A	D_ARG_61	NH2	C_ASP_59	OD2	3.137
3G3A	D_ARG_73	NH1	C_ASP_61	OD1	3.720
3G3A	D_ARG_73	NH1	C_ASP_61	OD2	2.705
3G3A	D_ARG_73	NH2	C_ASP_59	OD2	2.913
3G3A	D_ARG_73	NH2	C_ASP_61	OD1	2.638
3G3A	D_ARG_73	NH2	C_ASP_61	OD2	3.209
3G3A	D_LYS_97	NZ	D_ASP_101	OD1	3.653
3G3A	D_LYS_97	NZ	D_ASP_101	OD2	2.889
3G3A	D_ARG_112	NH1	C_ASP_141	OD1	3.483
3G3A	D_ARG_112	NH1	C_ASP_141	OD2	2.837
3G3A	D_ARG_112	NH2	C_ASP_141	OD1	2.752
3G3A	D_ARG_112	NH2	C_ASP_141	OD2	3.622
3G3A	D_ARG_112	NH2	C_ASP_143	OD2	3.602
3G3A	E_ARG_57	NH2	E_ASP_59	OD1	3.565
3G3A	E_ARG_57	NH2	E_ASP_59	OD2	3.054
3G3A	E_ARG_155	NH1	E_ASP_143	OD1	2.889
3G3A	F_LYS_1	NZ	F_GLU_7	OE2	2.598
3G3A	F_ARG_61	NH1	E_ASP_59	OD2	3.922
3G3A	F_ARG_61	NH2	E_ASP_59	OD1	3.681
3G3A	F_ARG_61	NH2	E_ASP_59	OD2	2.804
3G3A	F_ARG_73	NH1	E_ASP_61	OD1	3.367
3G3A	F_ARG_73	NH1	E_ASP_61	OD2	2.915
3G3A	F_ARG_73	NH2	E_ASP_59	OD2	2.686
3G3A	F_ARG_73	NH2	E_ASP_61	OD1	2.874
3G3A	F_ARG_73	NH2	E_ASP_61	OD2	3.960
3G3A	F_LYS_97	NZ	F_ASP_101	OD1	3.077
3G3A	F_LYS_97	NZ	F_ASP_101	OD2	2.523
3G3A	F_ARG_112	NH1	E_ASP_141	OD1	3.733
3G3A	F_ARG_112	NH1	E_ASP_141	OD2	3.195
3G3A	F_ARG_112	NH2	E_ASP_141	OD1	3.001

3G3A	F_ARG_112	NH2	E_ASP_141	OD2	3.839
3G3A	F_ARG_112	NH2	E_ASP_143	OD2	3.491
3G3A	G_ARG_57	NH2	G_ASP_59	OD1	3.304
3G3A	G_ARG_57	NH2	G_ASP_59	OD2	2.668
3G3A	G_ARG_125	NH2	G_GLU_159	OE1	3.890
3G3A	G_ARG_125	NH2	G_GLU_159	OE2	3.239
3G3A	G_ARG_155	NH1	G_ASP_143	OD1	3.004
3G3A	G_ARG_155	NH1	G_ASP_143	OD2	3.791
3G3A	H_LYS_1	NZ	H_GLU_7	OE2	2.729
3G3A	H_LYS_13	NZ	H_ASP_18	OD2	3.987
3G3A	H_ARG_61	NH2	G_ASP_59	OD2	3.367
3G3A	H_ARG_73	NH1	G_ASP_59	OD2	3.259
3G3A	H_ARG_73	NH2	G_ASP_59	OD2	3.473
3G3A	H_ARG_73	NH2	G_ASP_61	OD1	2.486
3G3A	H_ARG_73	NH2	G_ASP_61	OD2	2.698
3G3A	H_ARG_112	NH1	G_ASP_141	OD1	3.280
3G3A	H_ARG_112	NH1	G_ASP_143	OD2	3.578
3G3A	H_ARG_112	NH2	G_ASP_141	OD1	3.102
3G3A	H_ARG_112	NH2	G_ASP_141	OD2	2.609

Table 400: 3G3A-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3G3B	A.LYS_43	NZ	A.GLU_45	OE1	2.858
3G3B	A.LYS_43	NZ	A.GLU_45	OE2	2.415
3G3B	A.ARG_57	NH2	A.ASP_59	OD1	3.729
3G3B	A.ARG_57	NH2	A.ASP_59	OD2	2.852
3G3B	A.HIS_142	ND1	A.ASP_143	OD1	3.605
3G3B	A.ARG_155	NH1	A.ASP_143	OD1	2.852
3G3B	B.LYS_1	NZ	B.GLU_7	OE1	3.921
3G3B	B.LYS_1	NZ	B.GLU_7	OE2	2.875
3G3B	B.ARG_61	NH2	A.ASP_59	OD1	3.551
3G3B	B.ARG_61	NH2	A.ASP_59	OD2	3.590
3G3B	B.ARG_73	NH1	A.ASP_61	OD1	2.527
3G3B	B.ARG_73	NH1	A.ASP_61	OD2	3.439
3G3B	B.ARG_73	NH2	A.ASP_59	OD2	2.967
3G3B	B.ARG_73	NH2	A.ASP_61	OD1	3.469
3G3B	B.ARG_73	NH2	A.ASP_61	OD2	2.765
3G3B	B.ARG_112	NH1	A.ASP_141	OD1	3.569
3G3B	B.ARG_112	NH1	A.ASP_141	OD2	2.625
3G3B	B.ARG_112	NH2	A.ASP_141	OD1	2.926
3G3B	B.ARG_112	NH2	A.ASP_141	OD2	3.538
3G3B	B.ARG_112	NH2	A.ASP_143	OD2	3.804
3G3B	B.ARG_125	NH1	B.ASP_119	OD1	3.478
3G3B	B.ARG_125	NH1	B.ASP_119	OD2	3.346
3G3B	C.LYS_43	NZ	C.GLU_45	OE1	3.803
3G3B	C.LYS_43	NZ	C.GLU_45	OE2	3.490
3G3B	C.ARG_57	NH2	C.ASP_59	OD1	3.660
3G3B	C.ARG_57	NH2	C.ASP_59	OD2	2.836
3G3B	C.HIS_142	NE2	C.ASP_143	OD1	3.850
3G3B	C.ARG_155	NH2	C.ASP_143	OD1	2.863
3G3B	C.ARG_155	NH2	C.ASP_143	OD2	3.947
3G3B	D.LYS_1	NZ	D.GLU_7	OE2	2.651
3G3B	D.LYS_13	NZ	D.ASP_18	OD2	3.185
3G3B	D.ARG_61	NH2	C.ASP_59	OD1	3.954
3G3B	D.ARG_73	NH1	C.ASP_61	OD1	2.753
3G3B	D.ARG_73	NH1	C.ASP_61	OD2	3.824
3G3B	D.ARG_73	NH2	C.ASP_59	OD2	3.136
3G3B	D.ARG_73	NH2	C.ASP_61	OD1	3.224
3G3B	D.ARG_73	NH2	C.ASP_61	OD2	2.702
3G3B	D.ARG_112	NH1	C.ASP_141	OD1	3.812
3G3B	D.ARG_112	NH1	C.ASP_141	OD2	2.690
3G3B	D.ARG_112	NH2	C.ASP_141	OD1	2.826
3G3B	D.ARG_112	NH2	C.ASP_141	OD2	3.301
3G3B	D.ARG_112	NH2	C.ASP_143	OD2	3.656
3G3B	D.ARG_125	NH2	D.ASP_119	OD1	2.448
3G3B	D.ARG_125	NH2	D.ASP_119	OD2	3.449
3G3B	E.ARG_57	NH2	E.ASP_59	OD1	3.602
3G3B	E.ARG_57	NH2	E.ASP_59	OD2	2.890
3G3B	E.HIS_142	ND1	E.ASP_143	OD1	3.479
3G3B	E.ARG_155	NH2	E.ASP_143	OD1	3.325
3G3B	F.LYS_1	NZ	F.GLU_7	OE1	3.789
3G3B	F.LYS_1	NZ	F.GLU_7	OE2	2.690
3G3B	F.ARG_61	NH2	E.ASP_59	OD2	3.820
3G3B	F.ARG_73	NH1	E.ASP_61	OD1	2.535
3G3B	F.ARG_73	NH1	E.ASP_61	OD2	3.949
3G3B	F.ARG_73	NH2	E.ASP_59	OD2	2.812
3G3B	F.ARG_73	NH2	E.ASP_61	OD1	3.056
3G3B	F.ARG_73	NH2	E.ASP_61	OD2	2.934
3G3B	F.ARG_112	NH1	E.ASP_141	OD2	2.714

3G3B	F_ARG_112	NH2	E_ASP_141	OD1	3.020
3G3B	F_ARG_112	NH2	E_ASP_141	OD2	3.176
3G3B	F_ARG_112	NH2	E_ASP_143	OD2	3.737
3G3B	G_ARG_57	NH2	G_ASP_59	OD1	3.515
3G3B	G_ARG_57	NH2	G_ASP_59	OD2	3.110
3G3B	G_HIS_142	NE2	G_ASP_143	OD1	3.761
3G3B	G_ARG_155	NH2	G_ASP_143	OD1	2.619
3G3B	G_ARG_155	NH2	G_ASP_143	OD2	3.786
3G3B	H_LYS_1	NZ	H_GLU_7	OE1	3.238
3G3B	H_LYS_1	NZ	H_GLU_7	OE2	2.526
3G3B	H_ARG_61	NH1	H_ASP_48	OD2	3.554
3G3B	H_ARG_73	NH1	G_ASP_61	OD1	2.839
3G3B	H_ARG_73	NH1	G_ASP_61	OD2	3.791
3G3B	H_ARG_73	NH2	G_ASP_59	OD2	2.431
3G3B	H_ARG_73	NH2	G_ASP_61	OD1	3.464
3G3B	H_ARG_73	NH2	G_ASP_61	OD2	2.896
3G3B	H_ARG_112	NH1	G_ASP_141	OD1	3.676
3G3B	H_ARG_112	NH1	G_ASP_141	OD2	2.564
3G3B	H_ARG_112	NH2	G_ASP_141	OD1	2.813
3G3B	H_ARG_112	NH2	G_ASP_141	OD2	3.280
3G3B	H_ARG_112	NH2	G_ASP_143	OD2	3.506

Table 401: 3G3B-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3GGW	A_LYS_27	NZ	A_GLU_93	OE1	3.004
3GGW	A_LYS_27	NZ	A_GLU_93	OE2	3.494
3GGW	A_HIS_27D	ND1	A_ASP_28	OD1	3.397
3GGW	A_HIS_27D	ND1	A_ASP_28	OD2	3.638
3GGW	A_ARG_61	NH1	A_ASP_82	OD1	3.619
3GGW	A_ARG_61	NH1	A_ASP_82	OD2	2.849
3GGW	A_ARG_61	NH2	A_GLU_79	OE1	3.759
3GGW	A_ARG_61	NH2	A_ASP_82	OD1	2.856
3GGW	A_ARG_61	NH2	A_ASP_82	OD2	3.530
3GGW	A_ARG_96	NH2	B_GLU_50	OE1	3.590
3GGW	A_ARG_96	NH2	B_GLU_50	OE2	2.762
3GGW	A_ARG_155	NH1	A_GLU_185	OE1	3.605
3GGW	A_ARG_188	NH2	A_GLU_185	OE2	2.743
3GGW	A_HIS_189	ND1	A_GLU_185	OE1	3.933
3GGW	A_LYS_199	NZ	A_ASP_110	OD2	3.552
3GGW	B_ARG_38	NH1	B_ASP_86	OD1	2.900
3GGW	B_ARG_38	NH2	B_GLU_46	OE1	3.283
3GGW	B_ARG_38	NH2	B_GLU_46	OE2	3.311
3GGW	B_ARG_38	NH2	B_ASP_86	OD1	3.834
3GGW	B_LYS_43	NZ	B_GLU_42	OE2	3.946
3GGW	B_ARG_52	NH1	E_ASP_4	OD2	3.092
3GGW	B_LYS_64	NZ	B_GLU_61	OE1	3.190
3GGW	B_LYS_66	NZ	B_ASP_86	OD1	3.381
3GGW	B_LYS_66	NZ	B_ASP_86	OD2	2.679
3GGW	B_ARG_71	NH2	B_ASP_73	OD1	3.573
3GGW	B_ARG_83	NH1	B_GLU_85	OE1	3.507
3GGW	B_LYS_207	NZ	B_ASP_209	OD1	3.783
3GGW	B_LYS_207	NZ	B_ASP_209	OD2	2.712
3GGW	B_LYS_210	NZ	A_GLU_123	OE2	3.208
3GGW	C_ARG_24	NH2	C_ASP_70	OD2	3.799
3GGW	C_LYS_27	NZ	C_GLU_93	OE1	2.551
3GGW	C_HIS_27D	ND1	C_ASP_28	OD1	3.282
3GGW	C_HIS_27D	ND1	C_ASP_28	OD2	3.541
3GGW	C_LYS_39	NZ	C_GLU_81	OE2	2.827
3GGW	C_ARG_61	NH1	C_ASP_82	OD1	3.646
3GGW	C_ARG_61	NH1	C_ASP_82	OD2	2.827
3GGW	C_ARG_61	NH2	C_GLU_79	OE1	3.494
3GGW	C_ARG_61	NH2	C_GLU_79	OE2	3.557
3GGW	C_ARG_61	NH2	C_ASP_82	OD1	2.827
3GGW	C_ARG_61	NH2	C_ASP_82	OD2	3.383
3GGW	C_ARG_96	NH2	D_GLU_50	OE1	3.555
3GGW	C_ARG_96	NH2	D_GLU_50	OE2	2.962
3GGW	C_LYS_142	NZ	C_GLU_105	OE1	3.612
3GGW	C_ARG_155	NH1	C_GLU_185	OE1	2.976
3GGW	C_ARG_155	NH1	C_GLU_185	OE2	3.624
3GGW	C_ARG_155	NH2	C_GLU_185	OE1	3.679
3GGW	C_ARG_155	NH2	C_GLU_185	OE2	2.798
3GGW	C_LYS_183	NZ	C_GLU_187	OE1	2.937
3GGW	C_LYS_183	NZ	C_GLU_187	OE2	3.524
3GGW	C_ARG_188	NH2	C_ASP_184	OD1	3.157
3GGW	C_ARG_188	NH2	C_ASP_184	OD2	3.938
3GGW	C_LYS_199	NZ	C_ASP_110	OD2	3.525
3GGW	D_ARG_38	NH1	D_ASP_86	OD1	2.856
3GGW	D_ARG_38	NH2	D_GLU_46	OE1	3.438
3GGW	D_ARG_38	NH2	D_GLU_46	OE2	3.122
3GGW	D_ARG_38	NH2	D_ASP_86	OD1	3.653
3GGW	D_ARG_52	NH1	F_ASP_4	OD2	3.127

3GGW	D_LYS_64	NZ	D_GLU_61	OE1	2.566
3GGW	D_LYS_64	NZ	D_GLU_61	OE2	3.883
3GGW	D_LYS_66	NZ	D_ASP_86	OD1	3.597
3GGW	D_LYS_66	NZ	D_ASP_86	OD2	2.711
3GGW	D_ARG_71	NH2	D_ASP_73	OD1	3.666
3GGW	D_LYS_210	NZ	C_GLU_123	OE2	2.871
3GGW	D_ARG_215	NH2	C_GLU_213	OE1	3.834
3GGW	D_ARG_215	NH2	C_GLU_213	OE2	2.618

Table 402: 3GGW-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3GHB	L_ARG_61	NH1	L_ASP_82	OD1	3.774
3GHB	L_ARG_61	NH1	L_ASP_82	OD2	2.845
3GHB	L_ARG_61	NH2	L_ASP_82	OD1	2.959
3GHB	L_ARG_61	NH2	L_ASP_82	OD2	3.458
3GHB	L_LYS_110	NZ	L_GLU_198	OE1	2.584
3GHB	L_HIS_188	NE2	L_ASP_151	OD2	3.966
3GHB	H_ARG_38	NH1	H_ASP_86	OD1	2.865
3GHB	H_ARG_38	NH2	H_GLU_46	OE1	2.815
3GHB	H_ARG_38	NH2	H_GLU_46	OE2	3.771
3GHB	H_ARG_50	NH1	H_ASP_58	OD2	3.042
3GHB	H_ARG_66	NH1	H_ASP_86	OD1	3.838
3GHB	H_ARG_66	NH1	H_ASP_86	OD2	2.797
3GHB	H_ARG_66	NH2	H_ASP_86	OD1	3.183
3GHB	H_ARG_66	NH2	H_ASP_86	OD2	3.533
3GHB	H_ARG_71	NH2	H_ASP_73	OD1	3.367
3GHB	H_LYS_83	NZ	H_GLU_85	OE2	3.603
3GHB	H_LYS_143	NZ	L_GLU_124	OE2	2.614
3GHB	H_LYS_209	NZ	L_GLU_123	OE1	2.751
3GHB	H_LYS_209	NZ	L_GLU_123	OE2	3.411
3GHB	P_LYS_305	NZ	H_GLU_100E	OE1	3.508
3GHB	P_LYS_305	NZ	H_ASP_100F	OD2	3.835
3GHB	M_ARG_61	NH1	M_ASP_82	OD1	3.907
3GHB	M_ARG_61	NH1	M_ASP_82	OD2	3.095
3GHB	M_ARG_61	NH2	M_ASP_82	OD1	2.973
3GHB	M_ARG_61	NH2	M_ASP_82	OD2	3.466
3GHB	M_LYS_110	NZ	M_GLU_198	OE1	2.627
3GHB	I_ARG_38	NH1	I_ASP_86	OD1	2.974
3GHB	I_ARG_38	NH2	I_GLU_46	OE1	2.852
3GHB	I_ARG_38	NH2	I_GLU_46	OE2	3.761
3GHB	I_ARG_38	NH2	I_ASP_86	OD1	3.952
3GHB	I_ARG_50	NH1	I_ASP_58	OD2	2.747
3GHB	I_ARG_66	NH1	I_ASP_86	OD1	3.695
3GHB	I_ARG_66	NH1	I_ASP_86	OD2	2.620
3GHB	I_ARG_66	NH2	I_ASP_86	OD1	3.166
3GHB	I_ARG_66	NH2	I_ASP_86	OD2	3.599
3GHB	I_ARG_71	NH2	I_ASP_73	OD1	3.399
3GHB	I_LYS_75	NZ	I_ASP_72	OD2	3.232
3GHB	I_LYS_143	NZ	M_GLU_124	OE2	2.607
3GHB	I_LYS_209	NZ	M_GLU_123	OE1	2.988
3GHB	I_LYS_209	NZ	M_GLU_123	OE2	3.773
3GHB	I_ARG_210	NH1	I_GLU_212	OE2	3.691
3GHB	Q_LYS_305	NZ	I_ASP_100F	OD1	3.174

Table 403: 3GHB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3GHE	L_LYS_53	NZ	L_ASP_50	OD2	3.235
3GHE	L_ARG_61	NH1	L_ASP_82	OD1	2.784
3GHE	L_ARG_61	NH1	L_ASP_82	OD2	3.800
3GHE	L_ARG_61	NH2	L_ASP_82	OD1	3.483
3GHE	L_ARG_61	NH2	L_ASP_82	OD2	3.001
3GHE	L_LYS_149	NZ	L_GLU_203	OE2	2.932
3GHE	H_ARG_38	NH1	H_ASP_86	OD1	3.169
3GHE	H_ARG_38	NH2	H_GLU_46	OE1	2.908
3GHE	H_LYS_64	NZ	H_ASP_61	OD2	2.560
3GHE	H_ARG_66	NH1	H_ASP_86	OD2	2.889
3GHE	H_ARG_66	NH2	H_ASP_86	OD1	2.967
3GHE	H_ARG_66	NH2	H_ASP_86	OD2	3.314
3GHE	H_ARG_94	NH2	H_ASP_101	OD1	2.641
3GHE	H_ARG_94	NH2	H_ASP_101	OD2	3.324
3GHE	H_LYS_143	NZ	L_GLU_124	OE2	2.684
3GHE	H_LYS_209	NZ	L_GLU_123	OE1	2.541
3GHE	H_LYS_209	NZ	L_GLU_123	OE2	3.149
3GHE	H_ARG_210	NH1	H_GLU_212	OE2	2.984
3GHE	H_ARG_210	NH2	H_GLU_212	OE2	3.330
3GHE	P_ARG_304	NH1	H_ASP_100A	OD1	3.397
3GHE	P_ARG_304	NH2	H_ASP_100A	OD1	3.243
3GHE	P_ARG_304	NH2	H_ASP_100A	OD2	3.833
3GHE	P_HIS_308	ND1	H_ASP_100H	OD2	3.415
3GHE	P_ARG_315	NH1	H_GLU_95	OE1	3.518
3GHE	P_ARG_315	NH1	H_GLU_95	OE2	2.720
3GHE	P_ARG_315	NH2	H_GLU_95	OE2	3.104

Table 404: 3GHE-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3GJF	A_HIS_3	NE2	A_ASP_29	OD2	3.680
3GJF	A_ARG_6	NH1	A_ASP_102	OD1	3.006
3GJF	A_ARG_14	NH1	A_ASP_39	OD1	3.408
3GJF	A_ARG_14	NH1	A_ASP_39	OD2	2.727
3GJF	A_ARG_14	NH2	A_ASP_39	OD1	2.801
3GJF	A_ARG_14	NH2	A_ASP_39	OD2	3.691
3GJF	A_ARG_17	NH1	A_ASP_39	OD2	3.993
3GJF	A_ARG_21	NH1	A_ASP_39	OD2	3.840
3GJF	A_ARG_21	NH2	A_ASP_37	OD1	3.518
3GJF	A_ARG_21	NH2	A_ASP_37	OD2	2.869
3GJF	A_ARG_35	NH1	A_GLU_46	OE2	3.379
3GJF	A_ARG_35	NH2	A_GLU_46	OE2	2.626
3GJF	A_ARG_44	NH1	A_ASP_61	OD1	3.185
3GJF	A_ARG_44	NH2	A_ASP_61	OD1	2.672
3GJF	A_ARG_48	NH2	B_ASP_53	OD2	3.786
3GJF	A_ARG_65	NH1	L_ASP_52	OD1	3.134
3GJF	A_ARG_65	NH1	L_ASP_52	OD2	3.382
3GJF	A_ARG_65	NH2	L_ASP_52	OD1	2.989
3GJF	A_ARG_65	NH2	L_ASP_52	OD2	3.338
3GJF	A_LYS_66	NZ	A_GLU_63	OE2	2.881
3GJF	A_ARG_75	NH1	A_GLU_19	OE1	2.951
3GJF	A_ARG_75	NH1	A_GLU_19	OE2	2.915
3GJF	A_HIS_93	ND1	A_ASP_119	OD1	3.615
3GJF	A_HIS_93	ND1	A_ASP_119	OD2	2.772
3GJF	A_ARG_97	NH2	A_ASP_77	OD2	3.819
3GJF	A_ARG_111	NH1	A_GLU_128	OE1	3.014
3GJF	A_ARG_111	NH1	A_GLU_128	OE2	3.991
3GJF	A_LYS_121	NZ	A_ASP_137	OD1	2.725
3GJF	A_LYS_144	NZ	A_GLU_148	OE2	2.717
3GJF	A_HIS_151	ND1	A_GLU_154	OE1	3.544
3GJF	A_ARG_170	NH2	A_GLU_55	OE1	2.781
3GJF	A_ARG_170	NH2	A_GLU_55	OE2	3.295
3GJF	A_LYS_176	NZ	A_GLU_177	OE2	2.868
3GJF	A_ARG_181	NH2	A_ASP_183	OD2	3.746
3GJF	A_HIS_191	ND1	A_GLU_254	OE2	3.677
3GJF	A_HIS_191	NE2	A_GLU_254	OE2	3.660
3GJF	A_ARG_219	NH1	A_GLU_222	OE2	3.609
3GJF	B_ARG_45	NH1	B_ASP_38	OD1	3.417
3GJF	B_ARG_81	NH1	B_ASP_38	OD2	3.146
3GJF	D_HIS_3	NE2	D_ASP_29	OD2	3.680
3GJF	D_ARG_6	NH1	D_ASP_102	OD1	2.883
3GJF	D_ARG_14	NH1	D_ASP_39	OD1	3.632
3GJF	D_ARG_14	NH1	D_ASP_39	OD2	2.832
3GJF	D_ARG_14	NH2	D_ASP_39	OD1	2.791
3GJF	D_ARG_14	NH2	D_ASP_39	OD2	3.560
3GJF	D_ARG_21	NH2	D_ASP_37	OD1	3.457
3GJF	D_ARG_21	NH2	D_ASP_37	OD2	2.717
3GJF	D_ARG_35	NH1	D_GLU_46	OE1	2.983
3GJF	D_ARG_35	NH2	E_ASP_53	OD1	3.050
3GJF	D_ARG_35	NH2	E_ASP_53	OD2	3.940
3GJF	D_ARG_44	NH1	D_ASP_61	OD1	3.254
3GJF	D_ARG_44	NH2	D_ASP_61	OD1	2.599
3GJF	D_ARG_48	NH2	E_ASP_53	OD1	3.764
3GJF	D_ARG_48	NH2	E_ASP_53	OD2	3.452
3GJF	D_ARG_65	NH1	K_ASP_52	OD1	3.173
3GJF	D_ARG_65	NH1	K_ASP_52	OD2	3.530
3GJF	D_ARG_65	NH2	K_ASP_52	OD1	3.166

3GJF	D_ARG_65	NH2	K_ASP_52	OD2	2.445
3GJF	D_LYS_66	NZ	D_GLU_63	OE1	3.919
3GJF	D_LYS_66	NZ	D_GLU_63	OE2	2.898
3GJF	D_ARG_82	NH1	D_GLU_89	OE1	3.854
3GJF	D_ARG_82	NH1	D_GLU_89	OE2	3.318
3GJF	D_ARG_82	NH2	D_GLU_89	OE2	3.224
3GJF	D_HIS_93	ND1	D_ASP_119	OD1	3.533
3GJF	D_HIS_93	ND1	D_ASP_119	OD2	2.640
3GJF	D_ARG_97	NH2	D_ASP_77	OD2	3.677
3GJF	D_LYS_144	NZ	D_GLU_148	OE1	3.748
3GJF	D_LYS_144	NZ	D_GLU_148	OE2	2.769
3GJF	D_ARG_170	NH2	D_GLU_55	OE1	2.756
3GJF	D_ARG_170	NH2	D_GLU_55	OE2	3.140
3GJF	D_LYS_176	NZ	D_GLU_177	OE1	2.829
3GJF	D_ARG_181	NH2	D_ASP_183	OD2	3.518
3GJF	D_HIS_191	NE2	D_GLU_254	OE2	3.719
3GJF	E_LYS_6	NZ	D_GLU_232	OE1	3.774
3GJF	E_LYS_6	NZ	D_GLU_232	OE2	2.502
3GJF	E_ARG_45	NH1	E_ASP_38	OD1	3.925
3GJF	E_ARG_81	NH1	E_ASP_38	OD2	3.008
3GJF	L_HIS_51	ND1	L_ASP_52	OD2	2.609
3GJF	L_ARG_56	NH1	L_ASP_62	OD1	3.571
3GJF	L_ARG_63	NH1	L_ASP_84	OD1	2.750
3GJF	L_ARG_63	NH1	L_ASP_84	OD2	3.305
3GJF	L_ARG_63	NH2	L_ASP_84	OD1	3.570
3GJF	L_ARG_63	NH2	L_ASP_84	OD2	2.571
3GJF	K_HIS_51	ND1	K_ASP_52	OD2	2.643
3GJF	K_ARG_56	NH1	K_ASP_62	OD1	3.501
3GJF	K_ARG_63	NH2	K_GLU_83	OE1	3.808
3GJF	K_ARG_63	NH2	K_ASP_84	OD1	2.545
3GJF	K_ARG_63	NH2	K_ASP_84	OD2	3.209
3GJF	K_LYS_169	NZ	K_GLU_85	OE1	2.843
3GJF	H_ARG_38	NH1	H_ASP_90	OD1	2.830
3GJF	H_ARG_38	NH2	H_GLU_46	OE1	3.081
3GJF	H_ARG_38	NH2	H_GLU_46	OE2	3.817
3GJF	H_ARG_38	NH2	H_ASP_90	OD1	3.756
3GJF	H_ARG_67	NH1	H_ASP_90	OD1	3.830
3GJF	H_ARG_67	NH1	H_ASP_90	OD2	2.795
3GJF	H_ARG_67	NH2	H_ASP_90	OD1	3.041
3GJF	H_ARG_67	NH2	H_ASP_90	OD2	3.477
3GJF	H_LYS_216	NZ	H_GLU_218	OE2	2.600
3GJF	M_ARG_38	NH1	M_ASP_90	OD1	2.821
3GJF	M_ARG_38	NH2	M_GLU_46	OE1	3.436
3GJF	M_ARG_38	NH2	M_GLU_46	OE2	2.897
3GJF	M_ARG_38	NH2	M_ASP_90	OD1	3.855
3GJF	M_LYS_65	NZ	M_ASP_62	OD1	3.858
3GJF	M_ARG_67	NH1	M_ASP_90	OD1	3.892
3GJF	M_ARG_67	NH1	M_ASP_90	OD2	2.801
3GJF	M_ARG_67	NH2	M_ASP_90	OD1	3.068
3GJF	M_ARG_67	NH2	M_ASP_90	OD2	3.441
3GJF	M_LYS_215	NZ	K_GLU_126	OE1	3.244
3GJF	M_LYS_215	NZ	K_GLU_126	OE2	2.553

Table 405: 3GJF-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3GNM	L_ARG_66	NH1	L_ASP_87	OD1	3.577
3GNM	L_ARG_66	NH1	L_ASP_87	OD2	2.682
3GNM	L_ARG_66	NH2	L_GLU_84	OE1	3.405
3GNM	L_ARG_66	NH2	L_ASP_87	OD1	2.573
3GNM	L_ARG_66	NH2	L_ASP_87	OD2	3.204
3GNM	L_LYS_152	NZ	L_GLU_159	OE1	3.752
3GNM	L_LYS_154	NZ	L_GLU_200	OE1	2.730
3GNM	L_ARG_160	NH1	L_GLU_190	OE2	3.689
3GNM	L_ARG_160	NH2	L_GLU_190	OE2	2.931
3GNM	L_LYS_188	NZ	L_GLU_192	OE1	3.327
3GNM	L_LYS_188	NZ	L_GLU_192	OE2	3.845
3GNM	L_LYS_204	NZ	L_ASP_115	OD2	2.734
3GNM	H_ARG_40	NH2	H_GLU_89	OE1	3.735
3GNM	H_ARG_65	NH2	H_ASP_66	OD1	3.349
3GNM	H_ARG_65	NH2	H_ASP_66	OD2	3.203
3GNM	H_LYS_67	NZ	H_ASP_90	OD1	3.628
3GNM	H_LYS_67	NZ	H_ASP_90	OD2	2.714
3GNM	H_ARG_98	NH2	H_ASP_106	OD1	3.662
3GNM	H_ARG_98	NH2	H_ASP_106	OD2	2.562
3GNM	H_ARG_169	NH1	L_ASP_172	OD1	3.348
3GNM	H_ARG_169	NH2	L_ASP_172	OD1	3.542
3GNM	H_ARG_169	NH2	L_ASP_175	OD1	3.297
3GNM	H_LYS_213	NZ	L_GLU_128	OE1	2.721
3GNM	H_LYS_213	NZ	L_GLU_128	OE2	3.840

Table 406: 3GNM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3GO1	L_ARG_61	NH1	L_ASP_82	OD1	3.138
3GO1	L_ARG_61	NH1	L_ASP_82	OD2	3.572
3GO1	L_ARG_61	NH2	L_ASP_82	OD1	3.465
3GO1	L_ARG_61	NH2	L_ASP_82	OD2	2.449
3GO1	L_LYS_166	NZ	L_GLU_83	OE2	2.723
3GO1	L_HIS_188	ND1	L_ASP_151	OD2	3.200
3GO1	H_ARG_38	NH1	H_ASP_86	OD1	2.757
3GO1	H_ARG_38	NH2	H_GLU_46	OE1	3.013
3GO1	H_ARG_38	NH2	H_ASP_86	OD1	3.570
3GO1	H_ARG_66	NH1	H_ASP_86	OD1	3.680
3GO1	H_ARG_66	NH1	H_ASP_86	OD2	3.112
3GO1	H_ARG_66	NH2	H_ASP_86	OD1	2.980
3GO1	H_ARG_66	NH2	H_ASP_86	OD2	3.607
3GO1	H_LYS_143	NZ	H_ASP_144	OD1	3.162
3GO1	H_LYS_143	NZ	H_ASP_144	OD2	3.468
3GO1	H_LYS_209	NZ	L_GLU_123	OE1	2.728
3GO1	H_LYS_209	NZ	L_GLU_123	OE2	3.471
3GO1	P_LYS_305	NZ	L_ASP_51	OD1	2.931
3GO1	P_ARG_315	NH1	H_GLU_95	OE2	3.127
3GO1	P_ARG_315	NH2	H_GLU_95	OE2	2.921
3GO1	P_ARG_315	NH2	H_ASP_100A	OD2	3.393

Table 407: 3GO1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3HAE	A_HIS_3	NE2	A_ASP_29	OD2	3.587
3HAE	A_ARG_6	NH1	A_ASP_102	OD1	2.847
3HAE	A_ARG_6	NH2	A_ASP_102	OD1	3.019
3HAE	A_ARG_6	NH2	A_ASP_102	OD2	3.923
3HAE	A_ARG_14	NH1	A_ASP_39	OD1	3.472
3HAE	A_ARG_14	NH1	A_ASP_39	OD2	3.188
3HAE	A_ARG_14	NH2	A_ASP_39	OD1	2.664
3HAE	A_ARG_14	NH2	A_ASP_39	OD2	3.862
3HAE	A_ARG_21	NH2	A_ASP_37	OD1	3.621
3HAE	A_ARG_21	NH2	A_ASP_37	OD2	2.935
3HAE	A_ARG_35	NH1	B_ASP_53	OD1	3.527
3HAE	A_ARG_35	NH1	B_ASP_53	OD2	2.844
3HAE	A_ARG_35	NH2	A_GLU_46	OE2	3.050
3HAE	A_ARG_44	NH1	A_ASP_61	OD1	3.254
3HAE	A_ARG_44	NH2	A_ASP_61	OD1	3.535
3HAE	A_ARG_48	NH2	B_ASP_53	OD2	3.583
3HAE	A_ARG_65	NH1	L_ASP_52	OD1	3.495
3HAE	A_ARG_65	NH1	L_ASP_52	OD2	2.908
3HAE	A_ARG_65	NH2	L_ASP_52	OD1	3.452
3HAE	A_ARG_65	NH2	L_ASP_52	OD2	3.099
3HAE	A_LYS_66	NZ	A_GLU_63	OE1	3.753
3HAE	A_LYS_66	NZ	A_GLU_63	OE2	2.237
3HAE	A_HIS_93	ND1	A_ASP_119	OD1	3.412
3HAE	A_HIS_93	ND1	A_ASP_119	OD2	2.765
3HAE	A_ARG_97	NH2	A_ASP_77	OD2	3.602
3HAE	A_ARG_111	NH1	A_GLU_128	OE1	2.647
3HAE	A_LYS_121	NZ	A_ASP_137	OD1	3.114
3HAE	A_LYS_144	NZ	A_GLU_148	OE1	3.429
3HAE	A_LYS_144	NZ	A_GLU_148	OE2	3.081
3HAE	A_HIS_151	ND1	A_GLU_154	OE1	3.731
3HAE	A_ARG_170	NH2	A_GLU_55	OE1	3.140
3HAE	A_ARG_170	NH2	A_GLU_55	OE2	3.964
3HAE	A_ARG_256	NH2	A_ASP_220	OD1	2.688
3HAE	B_LYS_6	NZ	A_GLU_232	OE2	2.622
3HAE	B_ARG_81	NH1	B_ASP_38	OD2	2.783
3HAE	D_ARG_6	NH2	D_ASP_102	OD1	2.556
3HAE	D_ARG_6	NH2	D_ASP_102	OD2	2.949
3HAE	D_ARG_14	NH1	D_ASP_39	OD2	3.857
3HAE	D_ARG_14	NH2	D_ASP_39	OD1	2.936
3HAE	D_ARG_14	NH2	D_ASP_39	OD2	3.916
3HAE	D_ARG_21	NH1	D_ASP_37	OD2	3.671
3HAE	D_ARG_21	NH2	D_ASP_37	OD2	3.722
3HAE	D_ARG_21	NH2	D_ASP_39	OD2	3.808
3HAE	D_ARG_35	NH1	D_GLU_46	OE2	3.262
3HAE	D_ARG_35	NH1	E_ASP_53	OD1	3.949
3HAE	D_ARG_35	NH1	E_ASP_53	OD2	3.963
3HAE	D_ARG_35	NH2	E_ASP_53	OD1	3.106
3HAE	D_ARG_44	NH1	D_ASP_61	OD1	3.859
3HAE	D_ARG_44	NH2	D_ASP_61	OD1	2.693
3HAE	D_ARG_48	NH2	E_ASP_53	OD2	3.593
3HAE	D_ARG_65	NH1	G_ASP_52	OD1	3.201
3HAE	D_ARG_65	NH2	G_ASP_52	OD1	2.885
3HAE	D_ARG_65	NH2	G_ASP_52	OD2	3.031
3HAE	D_LYS_66	NZ	D_GLU_63	OE2	2.605
3HAE	D_ARG_75	NH1	D_GLU_19	OE1	3.280
3HAE	D_ARG_75	NH1	D_GLU_19	OE2	3.330
3HAE	D_ARG_75	NH2	D_GLU_19	OE2	2.623

3HAE	D_ARG_82	NH1	D_GLU_89	OE2	3.821
3HAE	D_ARG_82	NH2	D_GLU_89	OE2	2.676
3HAE	D_HIS_93	ND1	D_ASP_119	OD1	3.379
3HAE	D_HIS_93	ND1	D_ASP_119	OD2	3.104
3HAE	D_ARG_97	NH2	D_ASP_77	OD2	3.161
3HAE	D_ARG_108	NH2	D_ASP_106	OD2	3.619
3HAE	D_ARG_111	NH1	D_GLU_128	OE1	3.567
3HAE	D_ARG_111	NH2	D_GLU_128	OE1	3.292
3HAE	D_LYS_144	NZ	D_GLU_148	OE2	3.433
3HAE	D_HIS_151	ND1	D_GLU_154	OE1	3.330
3HAE	D_ARG_170	NH2	D_GLU_55	OE1	2.334
3HAE	D_ARG_170	NH2	D_GLU_55	OE2	3.072
3HAE	D_LYS_176	NZ	D_GLU_177	OE2	3.306
3HAE	D_ARG_181	NH2	D_ASP_183	OD2	3.347
3HAE	D_ARG_256	NH2	D_ASP_220	OD1	2.715
3HAE	E_LYS_41	NZ	E_ASP_76	OD2	3.802
3HAE	E_ARG_81	NH1	E_ASP_38	OD2	3.706
3HAE	J_HIS_3	NE2	J_ASP_29	OD2	3.809
3HAE	J_ARG_6	NH1	J_ASP_102	OD1	2.906
3HAE	J_ARG_6	NH1	J_ASP_102	OD2	3.945
3HAE	J_ARG_6	NH2	J_ASP_102	OD1	2.506
3HAE	J_ARG_14	NH1	J_ASP_39	OD1	3.669
3HAE	J_ARG_14	NH1	J_ASP_39	OD2	2.840
3HAE	J_ARG_14	NH2	J_ASP_39	OD1	2.935
3HAE	J_ARG_14	NH2	J_ASP_39	OD2	3.651
3HAE	J_ARG_21	NH2	J_ASP_37	OD1	3.222
3HAE	J_ARG_21	NH2	J_ASP_37	OD2	2.441
3HAE	J_ARG_35	NH1	J_GLU_46	OE1	3.957
3HAE	J_ARG_35	NH1	J_GLU_46	OE2	2.953
3HAE	J_ARG_35	NH2	K_ASP_53	OD1	3.520
3HAE	J_ARG_44	NH1	J_ASP_61	OD1	3.422
3HAE	J_ARG_44	NH2	J_ASP_61	OD1	3.290
3HAE	J_ARG_48	NH2	K_ASP_53	OD1	3.945
3HAE	J_ARG_48	NH2	K_ASP_53	OD2	3.051
3HAE	J_ARG_65	NH1	N_ASP_52	OD1	3.749
3HAE	J_ARG_65	NH2	N_ASP_52	OD1	2.440
3HAE	J_ARG_65	NH2	N_ASP_52	OD2	2.989
3HAE	J_LYS_66	NZ	J_GLU_63	OE1	2.982
3HAE	J_LYS_66	NZ	J_GLU_63	OE2	2.809
3HAE	J_HIS_93	ND1	J_ASP_119	OD1	3.377
3HAE	J_HIS_93	ND1	J_ASP_119	OD2	2.805
3HAE	J_ARG_108	NH2	J_ASP_106	OD1	3.482
3HAE	J_ARG_108	NH2	J_ASP_106	OD2	3.608
3HAE	J_LYS_121	NZ	J_ASP_137	OD1	3.426
3HAE	J_HIS_151	ND1	J_GLU_154	OE1	3.986
3HAE	J_ARG_170	NH2	J_GLU_55	OE1	2.482
3HAE	J_ARG_170	NH2	J_GLU_55	OE2	3.313
3HAE	J_ARG_181	NH2	J_ASP_183	OD2	3.327
3HAE	J_HIS_191	ND1	J_GLU_254	OE2	3.434
3HAE	J_ARG_256	NH2	J_ASP_220	OD1	3.258
3HAE	K_ARG_81	NH1	K_ASP_38	OD2	2.492
3HAE	P_HIS_3	NE2	P_ASP_29	OD2	3.769
3HAE	P_ARG_6	NH1	P_ASP_102	OD1	2.755
3HAE	P_ARG_6	NH2	P_ASP_102	OD1	3.424
3HAE	P_ARG_14	NH1	P_ASP_39	OD1	3.423
3HAE	P_ARG_14	NH1	P_ASP_39	OD2	3.000
3HAE	P_ARG_14	NH2	P_ASP_39	OD1	2.960
3HAE	P_ARG_14	NH2	P_ASP_39	OD2	3.984

3HAE	P_ARG_21	NH2	P_ASP_37	OD1	3.733
3HAE	P_ARG_21	NH2	P_ASP_37	OD2	3.125
3HAE	P_ARG_35	NH1	P_GLU_46	OE2	3.659
3HAE	P_ARG_35	NH1	Q_ASP_53	OD2	3.921
3HAE	P_ARG_35	NH2	P_GLU_46	OE2	2.679
3HAE	P_ARG_44	NH1	P_ASP_61	OD1	3.128
3HAE	P_ARG_44	NH2	P_ASP_61	OD1	3.068
3HAE	P_ARG_48	NH2	Q_ASP_53	OD1	3.566
3HAE	P_ARG_48	NH2	Q_ASP_53	OD2	2.872
3HAE	P_ARG_65	NH1	S_ASP_52	OD1	3.579
3HAE	P_ARG_65	NH1	S_ASP_52	OD2	3.466
3HAE	P_ARG_65	NH2	S_ASP_52	OD1	3.120
3HAE	P_ARG_65	NH2	S_ASP_52	OD2	2.826
3HAE	P_LYS_66	NZ	P_GLU_63	OE1	3.514
3HAE	P_LYS_66	NZ	P_GLU_63	OE2	3.135
3HAE	P_HIS_93	ND1	P_ASP_119	OD1	3.199
3HAE	P_HIS_93	ND1	P_ASP_119	OD2	2.626
3HAE	P_ARG_97	NH2	P_ASP_77	OD2	3.656
3HAE	P_ARG_108	NH2	P_ASP_106	OD1	3.268
3HAE	P_ARG_108	NH2	P_ASP_106	OD2	2.709
3HAE	P_ARG_111	NH1	P_GLU_128	OE1	3.578
3HAE	P_LYS_144	NZ	P_GLU_148	OE1	3.286
3HAE	P_HIS_151	ND1	P_GLU_154	OE1	3.029
3HAE	P_ARG_157	NH2	P_GLU_161	OE1	3.353
3HAE	P_ARG_157	NH2	P_GLU_161	OE2	3.284
3HAE	P_ARG_170	NH1	P_GLU_55	OE1	3.443
3HAE	P_ARG_170	NH1	P_GLU_55	OE2	3.001
3HAE	P_ARG_170	NH2	P_GLU_55	OE1	3.201
3HAE	P_ARG_170	NH2	P_GLU_55	OE2	3.200
3HAE	P_ARG_181	NH2	P_ASP_183	OD2	3.944
3HAE	P_HIS_191	ND1	P_GLU_254	OE2	3.652
3HAE	P_HIS_191	NE2	P_GLU_254	OE2	3.983
3HAE	P_ARG_256	NH2	P_ASP_220	OD2	2.906
3HAE	Q_LYS_6	NZ	P_GLU_232	OE2	3.965
3HAE	Q_ARG_45	NH1	Q_ASP_38	OD1	3.784
3HAE	Q_ARG_45	NH2	Q_GLU_47	OE1	3.894
3HAE	Q_LYS_75	NZ	Q_GLU_74	OE2	3.176
3HAE	L_HIS_51	ND1	L_ASP_52	OD2	3.196
3HAE	L_ARG_63	NH1	L_GLU_83	OE1	3.861
3HAE	L_ARG_63	NH1	L_ASP_84	OD1	3.672
3HAE	L_ARG_63	NH1	L_ASP_84	OD2	3.946
3HAE	L_ARG_63	NH2	L_ASP_84	OD1	2.766
3HAE	L_ARG_63	NH2	L_ASP_84	OD2	2.158
3HAE	L_HIS_87	ND1	L_ASP_105	OD1	3.871
3HAE	L_HIS_87	NE2	L_ASP_105	OD1	3.639
3HAE	L_LYS_169	NZ	L_GLU_85	OE1	2.871
3HAE	G_HIS_51	ND1	G_ASP_52	OD2	2.400
3HAE	G_ARG_63	NH1	G_ASP_84	OD1	3.142
3HAE	G_ARG_63	NH1	G_ASP_84	OD2	3.199
3HAE	G_ARG_63	NH2	G_ASP_84	OD1	3.746
3HAE	G_ARG_63	NH2	G_ASP_84	OD2	2.857
3HAE	G_LYS_169	NZ	G_GLU_85	OE1	2.988
3HAE	N_HIS_51	ND1	N_ASP_52	OD2	2.806
3HAE	N_ARG_63	NH1	N_ASP_84	OD1	3.108
3HAE	N_ARG_63	NH1	N_ASP_84	OD2	3.603
3HAE	N_ARG_63	NH2	N_ASP_84	OD1	3.712
3HAE	N_ARG_63	NH2	N_ASP_84	OD2	2.760
3HAE	N_HIS_87	ND1	N_ASP_105	OD1	3.966

3HAE	N_HIS_87	NE2	N_ASP_105	OD1	3.798
3HAE	N_LYS_132	NZ	O_ASP_150	OD2	3.615
3HAE	N_LYS_169	NZ	N_GLU_85	OE1	3.035
3HAE	N_LYS_169	NZ	N_GLU_85	OE2	3.916
3HAE	S_HIS_51	ND1	S_ASP_52	OD2	2.614
3HAE	S_ARG_63	NH1	S_ASP_84	OD1	3.147
3HAE	S_ARG_63	NH1	S_ASP_84	OD2	3.129
3HAE	S_ARG_63	NH2	S_ASP_84	OD1	3.845
3HAE	S_ARG_63	NH2	S_ASP_84	OD2	2.474
3HAE	S_HIS_87	ND1	S_ASP_105	OD1	3.612
3HAE	S_HIS_87	NE2	S_ASP_105	OD1	3.221
3HAE	S_LYS_169	NZ	S_GLU_85	OE2	3.086
3HAE	S_LYS_174	NZ	S_ASP_141	OD2	3.360
3HAE	H_ARG_38	NH1	H_ASP_90	OD1	3.222
3HAE	H_ARG_38	NH2	H_GLU_46	OE1	3.510
3HAE	H_ARG_38	NH2	H_GLU_46	OE2	2.712
3HAE	H_ARG_38	NH2	H_ASP_90	OD1	4.000
3HAE	H_LYS_65	NZ	H_ASP_62	OD1	3.122
3HAE	H_ARG_67	NH1	H_ASP_90	OD1	3.984
3HAE	H_ARG_67	NH1	H_ASP_90	OD2	2.555
3HAE	H_ARG_67	NH2	H_ASP_90	OD1	2.773
3HAE	H_ARG_67	NH2	H_ASP_90	OD2	2.913
3HAE	H_LYS_76	NZ	H_ASP_73	OD1	3.678
3HAE	H_LYS_215	NZ	L_GLU_126	OE1	3.537
3HAE	H_LYS_215	NZ	L_GLU_126	OE2	3.674
3HAE	L_ARG_38	NH1	L_ASP_90	OD1	3.105
3HAE	L_ARG_38	NH2	L_GLU_46	OE1	3.780
3HAE	L_ARG_38	NH2	L_GLU_46	OE2	2.913
3HAE	L_ARG_38	NH2	L_ASP_90	OD1	3.959
3HAE	L_LYS_65	NZ	L_ASP_62	OD1	2.989
3HAE	L_ARG_67	NH1	L_ASP_90	OD2	2.847
3HAE	L_ARG_67	NH2	L_ASP_90	OD1	2.911
3HAE	L_ARG_67	NH2	L_ASP_90	OD2	3.060
3HAE	L_LYS_76	NZ	L_ASP_73	OD1	3.921
3HAE	L_LYS_149	NZ	L_ASP_150	OD1	3.830
3HAE	L_LYS_212	NZ	L_ASP_214	OD1	2.825
3HAE	L_LYS_212	NZ	L_ASP_214	OD2	3.108
3HAE	L_LYS_215	NZ	G_GLU_126	OE1	3.678
3HAE	L_LYS_216	NZ	L_GLU_218	OE2	3.121
3HAE	O_ARG_38	NH1	O_ASP_90	OD1	2.713
3HAE	O_ARG_38	NH2	O_GLU_46	OE1	3.369
3HAE	O_ARG_38	NH2	O_GLU_46	OE2	3.065
3HAE	O_ARG_38	NH2	O_ASP_90	OD1	3.703
3HAE	O_ARG_67	NH1	O_ASP_90	OD2	2.733
3HAE	O_ARG_67	NH2	O_ASP_90	OD1	3.178
3HAE	O_ARG_67	NH2	O_ASP_90	OD2	3.173
3HAE	O_LYS_215	NZ	N_GLU_126	OE2	3.736
3HAE	O_LYS_216	NZ	O_GLU_218	OE2	3.610
3HAE	T_ARG_38	NH1	T_ASP_90	OD1	3.080
3HAE	T_ARG_38	NH2	T_GLU_46	OE1	3.373
3HAE	T_ARG_38	NH2	T_GLU_46	OE2	2.779
3HAE	T_ARG_38	NH2	T_ASP_90	OD1	3.979
3HAE	T_ARG_67	NH1	T_ASP_90	OD2	2.923
3HAE	T_ARG_67	NH2	T_ASP_90	OD1	3.524
3HAE	T_ARG_67	NH2	T_ASP_90	OD2	3.612
3HAE	T_LYS_212	NZ	T_ASP_214	OD1	3.968
3HAE	T_LYS_215	NZ	S_GLU_126	OE1	2.660
3HAE	T_LYS_215	NZ	S_GLU_126	OE2	3.779

3HAE	T_LYS_216	NZ	T_GLU_218	OE2	3.675
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Table 408: 3HAE-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3HFM	L_HIS_34	ND1	H_ASP_99	OD1	3.756
3HFM	L_HIS_34	ND1	H_ASP_99	OD2	3.698
3HFM	L_LYS_49	NZ	H_ASP_99	OD1	3.423
3HFM	L_ARG_61	NH1	L_ASP_82	OD1	2.585
3HFM	L_ARG_61	NH1	L_ASP_82	OD2	2.332
3HFM	L_ARG_61	NH2	L_GLU_79	OE1	3.732
3HFM	L_ARG_108	NH1	L_ASP_170	OD1	3.833
3HFM	L_LYS_142	NZ	L_GLU_105	OE2	3.995
3HFM	L_LYS_147	NZ	L_GLU_154	OE2	3.463
3HFM	L_LYS_149	NZ	L_GLU_195	OE1	3.304
3HFM	L_LYS_149	NZ	L_GLU_195	OE2	3.873
3HFM	L_HIS_189	ND1	L_ASP_151	OD1	2.425
3HFM	L_LYS_199	NZ	L_ASP_110	OD2	3.937
3HFM	H_ARG_38	NH1	H_ASP_89	OD2	3.586
3HFM	H_ARG_38	NH2	H_GLU_46	OE1	3.434
3HFM	H_ARG_38	NH2	H_GLU_46	OE2	2.361
3HFM	H_ARG_66	NH1	H_ASP_89	OD1	2.908
3HFM	H_ARG_66	NH1	H_ASP_89	OD2	3.682
3HFM	H_ARG_66	NH2	H_ASP_89	OD1	3.356
3HFM	H_ARG_66	NH2	H_ASP_89	OD2	2.574
3HFM	H_LYS_209	NZ	L_GLU_123	OE1	2.622
3HFM	H_ARG_213	NH2	L_GLU_123	OE1	3.991
3HFM	Y_LYS_1	NZ	Y_GLU_7	OE1	2.881
3HFM	Y_LYS_1	NZ	Y_GLU_7	OE2	2.663
3HFM	Y_LYS_97	NZ	H_ASP_32	OD1	3.609
3HFM	Y_ARG_125	NH1	Y_ASP_119	OD2	3.874

Table 409: 3HFM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3HI6	A_LYS_155	NZ	A_ASP_193	OD1	2.768
3HI6	A_LYS_178	NZ	A_GLU_180	OE1	3.586
3HI6	A_ARG_221	NH1	A_GLU_218	OE1	3.057
3HI6	A_ARG_227	NH2	A_ASP_131	OD1	2.862
3HI6	A_LYS_252	NZ	A_ASP_249	OD2	3.996
3HI6	A_LYS_287	NZ	A_GLU_301	OE1	3.340
3HI6	A_LYS_287	NZ	A_GLU_301	OE2	2.773
3HI6	A_LYS_304	NZ	A_GLU_301	OE2	2.760
3HI6	B_LYS_155	NZ	B_ASP_193	OD1	3.786
3HI6	B_LYS_159	NZ	B_ASP_193	OD1	3.099
3HI6	B_LYS_159	NZ	B_ASP_193	OD2	3.154
3HI6	B_LYS_178	NZ	B_GLU_180	OE1	2.889
3HI6	B_ARG_221	NH1	B_GLU_223	OE2	2.829
3HI6	B_ARG_221	NH2	B_GLU_218	OE1	3.646
3HI6	B_ARG_227	NH2	B_ASP_131	OD1	2.921
3HI6	B_LYS_304	NZ	B_GLU_301	OE2	3.130
3HI6	H_ARG_38	NH1	H_ASP_90	OD1	3.103
3HI6	H_ARG_38	NH2	H_GLU_46	OE1	3.371
3HI6	H_ARG_38	NH2	H_GLU_46	OE2	3.628
3HI6	H_LYS_65	NZ	H_ASP_62	OD1	3.388
3HI6	H_ARG_67	NH1	H_ASP_90	OD1	3.897
3HI6	H_ARG_67	NH1	H_ASP_90	OD2	2.936
3HI6	H_ARG_67	NH2	H_ASP_90	OD1	3.035
3HI6	H_ARG_67	NH2	H_ASP_90	OD2	3.561
3HI6	H_LYS_150	NZ	H_ASP_151	OD1	3.237
3HI6	H_LYS_150	NZ	H_ASP_151	OD2	3.331
3HI6	H_LYS_216	NZ	L_GLU_122	OE1	2.896
3HI6	H_LYS_216	NZ	L_GLU_122	OE2	3.887
3HI6	H_ARG_217	NH2	H_GLU_219	OE1	3.060
3HI6	L_ARG_61	NH2	L_ASP_82	OD1	2.928
3HI6	L_ARG_61	NH2	L_ASP_82	OD2	3.639
3HI6	L_LYS_102	NZ	L_GLU_164	OE1	3.006
3HI6	L_LYS_102	NZ	L_GLU_164	OE2	3.181
3HI6	L_LYS_106	NZ	L_ASP_17	OD2	3.521
3HI6	L_ARG_141	NH1	L_GLU_164	OE2	3.935
3HI6	L_HIS_188	ND1	L_ASP_150	OD2	2.681
3HI6	X_ARG_38	NH1	X_ASP_90	OD1	2.944
3HI6	X_ARG_38	NH2	X_GLU_46	OE1	3.305
3HI6	X_ARG_38	NH2	X_GLU_46	OE2	3.929
3HI6	X_ARG_38	NH2	X_ASP_90	OD1	3.837
3HI6	X_ARG_67	NH1	X_ASP_90	OD2	3.146
3HI6	X_ARG_67	NH2	X_ASP_90	OD1	3.168
3HI6	X_ARG_67	NH2	X_ASP_90	OD2	3.554
3HI6	X_LYS_150	NZ	X_ASP_151	OD2	3.620
3HI6	X_LYS_216	NZ	Y_GLU_122	OE1	3.212
3HI6	Y_ARG_	NH1	Y_ASP_70	OD1	2.911
3HI6	Y_ARG_	NH1	Y_ASP_70	OD2	3.450
3HI6	Y_ARG_	NH2	Y_ASP_70	OD1	3.656
3HI6	Y_ARG_61	NH2	Y_GLU_81	OE1	3.524
3HI6	Y_ARG_61	NH2	Y_ASP_82	OD1	2.775
3HI6	Y_ARG_61	NH2	Y_ASP_82	OD2	3.667
3HI6	Y_HIS_188	ND1	Y_ASP_150	OD2	3.043

Table 410: 3HI6-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3HMG	A_LYS_27	NZ	A_ASP_32	OD2	2.671
3HMG	A_HIS_56	ND1	A_ASP_85	OD2	3.968
3HMG	A_ARG_57	NH1	A_GLU_82	OE1	2.607
3HMG	A_ARG_57	NH1	A_GLU_82	OE2	3.527
3HMG	A_HIS_75	ND1	A_ASP_73	OD1	3.517
3HMG	A_HIS_75	ND1	A_ASP_73	OD2	2.768
3HMG	A_HIS_75	NE2	A_ASP_63	OD1	3.581
3HMG	A_ARG_90	NH1	A_ASP_60	OD1	2.768
3HMG	A_ARG_90	NH1	A_ASP_60	OD2	3.650
3HMG	A_LYS_92	NZ	A_ASP_271	OD2	3.725
3HMG	A_ARG_109	NH1	B_GLU_67	OE1	3.372
3HMG	A_ARG_109	NH1	B_GLU_67	OE2	2.849
3HMG	A_ARG_109	NH2	A_GLU_89	OE1	3.268
3HMG	A_ARG_109	NH2	A_GLU_89	OE2	2.513
3HMG	A_ARG_141	NH1	A_ASP_77	OD1	2.813
3HMG	A_ARG_141	NH1	A_ASP_77	OD2	3.101
3HMG	A_LYS_176	NZ	A_GLU_123	OE1	2.594
3HMG	A_LYS_176	NZ	A_GLU_123	OE2	3.871
3HMG	A_HIS_183	NE2	A_GLU_190	OE1	3.525
3HMG	A_ARG_208	NH2	A_ASP_241	OD2	2.755
3HMG	A_LYS_238	NZ	A_ASP_175	OD1	2.646
3HMG	A_LYS_238	NZ	A_ASP_175	OD2	3.452
3HMG	A_LYS_238	NZ	F_GLU_72	OE2	2.747
3HMG	A_ARG_261	NH1	A_GLU_119	OE1	2.789
3HMG	A_ARG_261	NH1	A_GLU_119	OE2	2.604
3HMG	A_ARG_261	NH2	A_GLU_119	OE1	3.241
3HMG	A_LYS_264	NZ	A_ASP_85	OD1	3.861
3HMG	A_LYS_264	NZ	A_ASP_85	OD2	2.924
3HMG	A_ARG_269	NH2	B_GLU_67	OE1	2.883
3HMG	A_LYS_292	NZ	A_ASP_291	OD1	2.917
3HMG	A_LYS_299	NZ	B_GLU_69	OE1	3.233
3HMG	A_LYS_310	NZ	B_ASP_90	OD1	2.577
3HMG	A_LYS_315	NZ	A_GLU_41	OE2	3.626
3HMG	B_ARG_25	NH1	A_GLU_325	OE1	3.777
3HMG	B_LYS_51	NZ	B_GLU_103	OE2	2.839
3HMG	B_ARG_54	NH1	F_GLU_97	OE1	2.798
3HMG	B_ARG_54	NH2	B_GLU_57	OE1	2.910
3HMG	B_ARG_54	NH2	B_GLU_57	OE2	3.325
3HMG	B_ARG_54	NH2	F_GLU_97	OE1	3.127
3HMG	B_LYS_62	NZ	F_ASP_86	OD1	2.986
3HMG	B_LYS_62	NZ	F_ASP_86	OD2	2.761
3HMG	B_LYS_62	NZ	F_ASP_90	OD1	3.490
3HMG	B_LYS_62	NZ	F_ASP_90	OD2	2.774
3HMG	B_HIS_64	NE2	F_ASP_79	OD1	3.991
3HMG	B_HIS_64	NE2	F_ASP_79	OD2	3.618
3HMG	B_LYS_68	NZ	B_GLU_85	OE1	3.186
3HMG	B_LYS_68	NZ	B_GLU_85	OE2	2.686
3HMG	B_ARG_76	NH1	D_GLU_74	OE1	3.445
3HMG	B_ARG_76	NH1	D_GLU_74	OE2	2.823
3HMG	B_ARG_76	NH1	D_GLU_81	OE1	2.738
3HMG	B_ARG_76	NH1	D_GLU_81	OE2	3.615
3HMG	B_ARG_76	NH2	D_GLU_74	OE1	2.830
3HMG	B_ARG_76	NH2	D_GLU_74	OE2	3.630
3HMG	B_LYS_117	NZ	B_GLU_114	OE1	2.569
3HMG	B_LYS_117	NZ	B_GLU_114	OE2	3.024
3HMG	B_ARG_123	NH1	F_GLU_132	OE2	3.281
3HMG	B_ARG_123	NH2	B_GLU_120	OE1	2.630

3HMG	B_ARG_123	NH2	B_GLU_120	OE2	3.334
3HMG	B_ARG_124	NH1	F_GLU_132	OE1	3.422
3HMG	B_ARG_124	NH1	F_GLU_132	OE2	3.128
3HMG	B_ARG_124	NH2	B_GLU_120	OE1	3.713
3HMG	B_ARG_127	NH2	F_GLU_131	OE1	2.404
3HMG	B_ARG_153	NH2	B_GLU_150	OE2	2.579
3HMG	B_HIS_159	NE2	B_ASP_160	OD2	3.179
3HMG	B_ARG_163	NH1	F_GLU_131	OE1	2.713
3HMG	B_ARG_163	NH1	F_GLU_131	OE2	2.661
3HMG	B_ARG_170	NH1	B_GLU_128	OE1	2.573
3HMG	B_ARG_170	NH2	B_GLU_131	OE2	2.707
3HMG	B_ARG_170	NH2	D_GLU_128	OE1	3.667
3HMG	B_ARG_170	NH2	D_GLU_128	OE2	3.704
3HMG	C_LYS_27	NZ	C_ASP_32	OD2	2.666
3HMG	C_HIS_56	ND1	C_ASP_85	OD2	3.933
3HMG	C_ARG_57	NH1	C_GLU_82	OE1	2.582
3HMG	C_ARG_57	NH1	C_GLU_82	OE2	3.551
3HMG	C_HIS_75	ND1	C_ASP_73	OD1	3.511
3HMG	C_HIS_75	ND1	C_ASP_73	OD2	2.757
3HMG	C_HIS_75	NE2	C_ASP_63	OD1	3.577
3HMG	C_ARG_90	NH1	C_ASP_60	OD1	2.751
3HMG	C_ARG_90	NH1	C_ASP_60	OD2	3.640
3HMG	C_LYS_92	NZ	C_ASP_271	OD2	3.710
3HMG	C_ARG_109	NH1	D_GLU_67	OE1	3.376
3HMG	C_ARG_109	NH1	D_GLU_67	OE2	2.842
3HMG	C_ARG_109	NH2	C_GLU_89	OE1	3.278
3HMG	C_ARG_109	NH2	C_GLU_89	OE2	2.563
3HMG	C_ARG_141	NH1	C_ASP_77	OD1	2.813
3HMG	C_ARG_141	NH1	C_ASP_77	OD2	3.109
3HMG	C_LYS_176	NZ	C_GLU_123	OE1	2.579
3HMG	C_LYS_176	NZ	C_GLU_123	OE2	3.881
3HMG	C_HIS_183	NE2	C_GLU_190	OE1	3.534
3HMG	C_ARG_208	NH2	C_ASP_241	OD2	2.719
3HMG	C_LYS_238	NZ	B_GLU_72	OE2	2.625
3HMG	C_LYS_238	NZ	C_ASP_175	OD1	2.646
3HMG	C_LYS_238	NZ	C_ASP_175	OD2	3.428
3HMG	C_ARG_261	NH1	C_GLU_119	OE1	2.776
3HMG	C_ARG_261	NH1	C_GLU_119	OE2	2.620
3HMG	C_ARG_261	NH2	C_GLU_119	OE1	3.254
3HMG	C_LYS_264	NZ	C_ASP_85	OD1	3.851
3HMG	C_LYS_264	NZ	C_ASP_85	OD2	2.872
3HMG	C_ARG_269	NH2	D_GLU_67	OE1	2.813
3HMG	C_LYS_292	NZ	C_ASP_291	OD1	2.970
3HMG	C_LYS_299	NZ	D_GLU_69	OE1	3.251
3HMG	C_LYS_310	NZ	D_ASP_90	OD1	2.544
3HMG	C_LYS_315	NZ	C_GLU_41	OE2	3.625
3HMG	D_LYS_51	NZ	D_GLU_103	OE2	2.876
3HMG	D_ARG_54	NH1	B_GLU_97	OE1	2.804
3HMG	D_ARG_54	NH2	B_GLU_97	OE1	3.138
3HMG	D_ARG_54	NH2	D_GLU_57	OE1	2.911
3HMG	D_ARG_54	NH2	D_GLU_57	OE2	3.348
3HMG	D_LYS_62	NZ	B_ASP_86	OD1	2.985
3HMG	D_LYS_62	NZ	B_ASP_86	OD2	2.721
3HMG	D_LYS_62	NZ	B_ASP_90	OD1	3.453
3HMG	D_LYS_62	NZ	B_ASP_90	OD2	2.701
3HMG	D_HIS_64	NE2	B_ASP_79	OD1	3.960
3HMG	D_HIS_64	NE2	B_ASP_79	OD2	3.444
3HMG	D_LYS_68	NZ	D_GLU_85	OE1	3.145

3HMG	D_LYS_68	NZ	D_GLU_85	OE2	2.743
3HMG	D_ARG_76	NH1	F_GLU_74	OE1	3.513
3HMG	D_ARG_76	NH1	F_GLU_74	OE2	2.767
3HMG	D_ARG_76	NH1	F_GLU_81	OE1	2.643
3HMG	D_ARG_76	NH1	F_GLU_81	OE2	3.636
3HMG	D_ARG_76	NH2	F_GLU_74	OE1	2.766
3HMG	D_ARG_76	NH2	F_GLU_74	OE2	3.449
3HMG	D_LYS_117	NZ	D_GLU_114	OE1	2.579
3HMG	D_LYS_117	NZ	D_GLU_114	OE2	3.024
3HMG	D_ARG_123	NH1	B_GLU_132	OE2	3.299
3HMG	D_ARG_123	NH2	D_GLU_120	OE1	2.630
3HMG	D_ARG_123	NH2	D_GLU_120	OE2	3.353
3HMG	D_ARG_124	NH1	B_GLU_132	OE1	3.459
3HMG	D_ARG_124	NH1	B_GLU_132	OE2	3.169
3HMG	D_ARG_124	NH2	D_GLU_120	OE1	3.725
3HMG	D_ARG_127	NH2	B_GLU_131	OE1	2.449
3HMG	D_ARG_153	NH2	D_GLU_150	OE1	2.831
3HMG	D_HIS_159	NE2	D_ASP_160	OD2	3.206
3HMG	D_ARG_163	NH1	B_GLU_131	OE1	2.694
3HMG	D_ARG_163	NH1	B_GLU_131	OE2	2.707
3HMG	D_ARG_170	NH1	D_GLU_128	OE1	2.604
3HMG	D_ARG_170	NH2	D_GLU_131	OE2	2.731
3HMG	D_ARG_170	NH2	F_GLU_128	OE1	3.716
3HMG	D_ARG_170	NH2	F_GLU_128	OE2	3.859
3HMG	E_LYS_27	NZ	E_ASP_32	OD2	2.652
3HMG	E_HIS_56	ND1	E_ASP_85	OD2	3.934
3HMG	E_ARG_57	NH1	E_GLU_82	OE1	2.626
3HMG	E_ARG_57	NH1	E_GLU_82	OE2	3.570
3HMG	E_HIS_75	ND1	E_ASP_73	OD1	3.497
3HMG	E_HIS_75	ND1	E_ASP_73	OD2	2.783
3HMG	E_HIS_75	NE2	E_ASP_63	OD1	3.565
3HMG	E_ARG_90	NH1	E_ASP_60	OD1	2.760
3HMG	E_ARG_90	NH1	E_ASP_60	OD2	3.651
3HMG	E_LYS_92	NZ	E_ASP_271	OD2	3.691
3HMG	E_ARG_109	NH1	F_GLU_67	OE1	3.402
3HMG	E_ARG_109	NH1	F_GLU_67	OE2	2.841
3HMG	E_ARG_109	NH2	E_GLU_89	OE1	3.254
3HMG	E_ARG_109	NH2	E_GLU_89	OE2	2.493
3HMG	E_ARG_141	NH1	E_ASP_77	OD1	2.813
3HMG	E_ARG_141	NH1	E_ASP_77	OD2	3.105
3HMG	E_LYS_176	NZ	E_GLU_123	OE1	2.615
3HMG	E_LYS_176	NZ	E_GLU_123	OE2	3.893
3HMG	E_HIS_183	NE2	E_GLU_190	OE1	3.535
3HMG	E_ARG_208	NH2	E_ASP_241	OD2	2.774
3HMG	E_LYS_238	NZ	D_GLU_72	OE2	2.745
3HMG	E_LYS_238	NZ	E_ASP_175	OD1	2.643
3HMG	E_LYS_238	NZ	E_ASP_175	OD2	3.469
3HMG	E_ARG_261	NH1	E_GLU_119	OE1	2.788
3HMG	E_ARG_261	NH1	E_GLU_119	OE2	2.617
3HMG	E_ARG_261	NH2	E_GLU_119	OE1	3.257
3HMG	E_LYS_264	NZ	E_ASP_85	OD1	3.857
3HMG	E_LYS_264	NZ	E_ASP_85	OD2	2.875
3HMG	E_ARG_269	NH2	F_GLU_67	OE1	2.840
3HMG	E_LYS_292	NZ	E_ASP_291	OD1	2.926
3HMG	E_LYS_299	NZ	F_GLU_69	OE1	3.192
3HMG	E_LYS_310	NZ	F_ASP_90	OD1	2.563
3HMG	E_LYS_315	NZ	E_GLU_41	OE2	3.619
3HMG	F_ARG_25	NH1	E_GLU_325	OE2	3.879

3HMG	F_ARG_25	NH2	E_GLU_325	OE2	3.668
3HMG	F_LYS_51	NZ	F_GLU_103	OE2	2.823
3HMG	F_ARG_54	NH1	D_GLU_97	OE1	2.700
3HMG	F_ARG_54	NH2	D_GLU_97	OE1	3.155
3HMG	F_ARG_54	NH2	F_GLU_57	OE1	2.900
3HMG	F_ARG_54	NH2	F_GLU_57	OE2	3.295
3HMG	F_LYS_62	NZ	D_ASP_86	OD1	2.928
3HMG	F_LYS_62	NZ	D_ASP_86	OD2	2.697
3HMG	F_LYS_62	NZ	D_ASP_90	OD1	3.563
3HMG	F_LYS_62	NZ	D_ASP_90	OD2	2.800
3HMG	F_HIS_64	NE2	D_ASP_79	OD1	3.875
3HMG	F_HIS_64	NE2	D_ASP_79	OD2	3.441
3HMG	F_LYS_68	NZ	F_GLU_85	OE1	3.194
3HMG	F_LYS_68	NZ	F_GLU_85	OE2	2.724
3HMG	F_ARG_76	NH1	B_GLU_74	OE1	3.414
3HMG	F_ARG_76	NH1	B_GLU_74	OE2	2.793
3HMG	F_ARG_76	NH1	B_GLU_81	OE1	2.687
3HMG	F_ARG_76	NH1	B_GLU_81	OE2	3.711
3HMG	F_ARG_76	NH2	B_GLU_74	OE1	2.734
3HMG	F_ARG_76	NH2	B_GLU_74	OE2	3.548
3HMG	F_LYS_117	NZ	F_GLU_114	OE1	2.569
3HMG	F_LYS_117	NZ	F_GLU_114	OE2	3.073
3HMG	F_ARG_123	NH1	D_GLU_132	OE2	3.319
3HMG	F_ARG_123	NH2	F_GLU_120	OE1	2.637
3HMG	F_ARG_123	NH2	F_GLU_120	OE2	3.351
3HMG	F_ARG_124	NH1	D_GLU_132	OE1	3.517
3HMG	F_ARG_124	NH1	D_GLU_132	OE2	3.294
3HMG	F_ARG_124	NH1	F_GLU_120	OE1	3.989
3HMG	F_ARG_124	NH2	F_GLU_120	OE1	3.690
3HMG	F_ARG_127	NH2	D_GLU_131	OE1	2.559
3HMG	F_HIS_159	NE2	F_ASP_160	OD2	3.217
3HMG	F_ARG_163	NH1	D_GLU_131	OE1	2.673
3HMG	F_ARG_163	NH1	D_GLU_131	OE2	2.666
3HMG	F_ARG_170	NH1	F_GLU_128	OE1	2.616
3HMG	F_ARG_170	NH2	B_GLU_128	OE1	3.705
3HMG	F_ARG_170	NH2	B_GLU_128	OE2	3.753
3HMG	F_ARG_170	NH2	F_GLU_131	OE2	2.717

Table 411: 3HMG-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3HZK	A_LYS_24	NZ	A_ASP_70	OD1	3.032
3HZK	A_LYS_24	NZ	A_ASP_70	OD2	3.302
3HZK	A_ARG_61	NH1	A_ASP_82	OD1	2.826
3HZK	A_ARG_61	NH1	A_ASP_82	OD2	3.622
3HZK	A_ARG_95	NH2	B_ASP_95	OD1	3.611
3HZK	A_ARG_95	NH2	B_ASP_95	OD2	2.795
3HZK	A_LYS_102	NZ	A_GLU_104	OE1	3.918
3HZK	A_LYS_148	NZ	A_GLU_194	OE1	3.895
3HZK	A_LYS_148	NZ	A_GLU_194	OE2	3.185
3HZK	A_ARG_154	NH1	A_GLU_184	OE1	3.701
3HZK	A_ARG_154	NH2	A_GLU_184	OE1	3.490
3HZK	A_LYS_182	NZ	A_GLU_186	OE1	2.645
3HZK	A_LYS_182	NZ	A_GLU_186	OE2	3.525
3HZK	A_HIS_188	ND1	A_ASP_150	OD2	3.092
3HZK	A_LYS_198	NZ	A_ASP_109	OD2	3.722
3HZK	B_ARG_38	NH1	B_ASP_86	OD2	2.994
3HZK	B_ARG_38	NH2	B_GLU_46	OE1	3.036
3HZK	B_ARG_38	NH2	B_GLU_46	OE2	3.939
3HZK	B_ARG_38	NH2	B_ASP_86	OD2	3.973
3HZK	B_ARG_52	NH1	B_GLU_58	OE2	2.780
3HZK	B_ARG_52	NH2	B_GLU_58	OE2	3.087
3HZK	B_ARG_66	NH1	B_ASP_86	OD1	2.850
3HZK	B_ARG_66	NH1	B_ASP_86	OD2	3.686
3HZK	B_ARG_66	NH2	B_ASP_86	OD1	3.613
3HZK	B_ARG_66	NH2	B_ASP_86	OD2	2.940
3HZK	B_ARG_94	NH2	B_ASP_101	OD1	3.902
3HZK	B_ARG_94	NH2	B_ASP_101	OD2	2.967
3HZK	B_LYS_207	NZ	A_GLU_122	OE2	3.993

Table 412: 3HZK-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3HZM	A_LYS_24	NZ	A_ASP_70	OD1	2.853
3HZM	A_LYS_24	NZ	A_ASP_70	OD2	3.528
3HZM	A_LYS_39	NZ	A_GLU_81	OE2	3.193
3HZM	A_ARG_61	NH1	A_GLU_81	OE1	3.361
3HZM	A_ARG_61	NH1	A_ASP_82	OD1	2.891
3HZM	A_ARG_61	NH1	A_ASP_82	OD2	3.592
3HZM	A_ARG_95	NH2	B_ASP_95	OD1	3.493
3HZM	A_ARG_95	NH2	B_ASP_95	OD2	2.771
3HZM	A_ARG_95	NH2	B_ASP_100E	OD1	3.831
3HZM	A_LYS_146	NZ	A_GLU_153	OE2	3.706
3HZM	A_LYS_148	NZ	A_GLU_194	OE1	3.173
3HZM	A_LYS_148	NZ	A_GLU_194	OE2	2.785
3HZM	A_ARG_154	NH1	A_GLU_184	OE2	3.270
3HZM	A_LYS_182	NZ	A_GLU_186	OE1	3.833
3HZM	A_LYS_182	NZ	A_GLU_186	OE2	3.992
3HZM	A_ARG_187	NH2	A_GLU_184	OE1	3.077
3HZM	A_HIS_188	ND1	A_ASP_150	OD2	3.055
3HZM	A_HIS_188	NE2	A_GLU_184	OE1	3.680
3HZM	A_HIS_188	NE2	A_GLU_184	OE2	3.167
3HZM	A_LYS_198	NZ	A_ASP_109	OD2	3.763
3HZM	B_ARG_38	NH1	B_ASP_86	OD2	2.747
3HZM	B_ARG_38	NH2	B_GLU_46	OE1	2.957
3HZM	B_ARG_38	NH2	B_GLU_46	OE2	3.921
3HZM	B_ARG_38	NH2	B_ASP_86	OD2	3.860
3HZM	B_ARG_52	NH1	B_GLU_58	OE2	2.944
3HZM	B_ARG_52	NH2	B_GLU_58	OE2	2.835
3HZM	B_ARG_66	NH1	B_ASP_86	OD1	2.764
3HZM	B_ARG_66	NH1	B_ASP_86	OD2	3.758
3HZM	B_ARG_66	NH2	B_ASP_86	OD1	3.543
3HZM	B_ARG_66	NH2	B_ASP_86	OD2	3.021
3HZM	B_ARG_94	NH2	B_ASP_101	OD1	3.649
3HZM	B_ARG_94	NH2	B_ASP_101	OD2	2.613
3HZM	B_LYS_207	NZ	A_GLU_122	OE2	3.353

Table 413: 3HZM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3HZV	A_LYS_24	NZ	A_ASP_70	OD1	3.175
3HZV	A_LYS_24	NZ	A_ASP_70	OD2	3.513
3HZV	A_LYS_39	NZ	A_GLU_81	OE2	2.855
3HZV	A_ARG_61	NH1	A_GLU_81	OE1	3.565
3HZV	A_ARG_61	NH1	A_ASP_82	OD1	2.789
3HZV	A_ARG_61	NH1	A_ASP_82	OD2	3.461
3HZV	A_ARG_95	NH2	B_ASP_95	OD1	3.498
3HZV	A_ARG_95	NH2	B_ASP_95	OD2	2.821
3HZV	A_ARG_95	NH2	B_ASP_100E	OD1	3.905
3HZV	A_LYS_148	NZ	A_GLU_194	OE1	3.263
3HZV	A_LYS_148	NZ	A_GLU_194	OE2	3.225
3HZV	A_LYS_182	NZ	A_GLU_186	OE1	3.453
3HZV	A_ARG_187	NH2	A_GLU_184	OE1	2.816
3HZV	A_HIS_188	ND1	A_ASP_150	OD2	2.755
3HZV	A_HIS_188	NE2	A_GLU_184	OE1	3.971
3HZV	A_HIS_188	NE2	A_GLU_184	OE2	3.358
3HZV	A_LYS_198	NZ	A_ASP_109	OD2	3.800
3HZV	B_ARG_38	NH1	B_ASP_86	OD2	2.840
3HZV	B_ARG_38	NH2	B_GLU_46	OE1	3.130
3HZV	B_ARG_38	NH2	B_ASP_86	OD2	3.863
3HZV	B_ARG_52	NH1	B_GLU_58	OE2	2.906
3HZV	B_ARG_52	NH2	B_GLU_58	OE2	2.746
3HZV	B_ARG_66	NH1	B_ASP_86	OD1	2.687
3HZV	B_ARG_66	NH1	B_ASP_86	OD2	3.671
3HZV	B_ARG_66	NH2	B_ASP_86	OD1	3.381
3HZV	B_ARG_66	NH2	B_ASP_86	OD2	2.850
3HZV	B_ARG_94	NH2	B_ASP_101	OD1	3.676
3HZV	B_ARG_94	NH2	B_ASP_101	OD2	2.608
3HZV	B_LYS_207	NZ	A_GLU_122	OE2	3.521

Table 414: 3HZV-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3HZY	A_LYS_24	NZ	A_ASP_70	OD1	2.966
3HZY	A_LYS_24	NZ	A_ASP_70	OD2	3.808
3HZY	A_LYS_39	NZ	A_GLU_81	OE2	3.561
3HZY	A_ARG_54	NH2	A_ASP_60	OD2	3.979
3HZY	A_ARG_61	NH1	A_ASP_82	OD1	2.810
3HZY	A_ARG_61	NH1	A_ASP_82	OD2	3.525
3HZY	A_ARG_95	NH2	B_ASP_95	OD1	3.688
3HZY	A_ARG_95	NH2	B_ASP_95	OD2	3.045
3HZY	A_ARG_95	NH2	B_ASP_100E	OD1	3.820
3HZY	A_LYS_146	NZ	A_GLU_153	OE2	3.963
3HZY	A_LYS_148	NZ	A_GLU_194	OE1	2.878
3HZY	A_LYS_148	NZ	A_GLU_194	OE2	3.571
3HZY	A_ARG_154	NH1	A_GLU_184	OE2	3.171
3HZY	A_ARG_187	NH2	A_GLU_184	OE1	2.952
3HZY	A_HIS_188	ND1	A_ASP_150	OD2	3.206
3HZY	A_HIS_188	NE2	A_GLU_184	OE2	3.220
3HZY	A_LYS_198	NZ	A_ASP_109	OD2	3.836
3HZY	B_LYS_3	NZ	B_GLU_1	OE2	3.921
3HZY	B_ARG_38	NH1	B_ASP_86	OD2	2.721
3HZY	B_ARG_38	NH2	B_ASP_86	OD2	3.756
3HZY	B_ARG_52	NH1	B_GLU_58	OE2	2.797
3HZY	B_ARG_52	NH2	B_GLU_58	OE2	2.569
3HZY	B_ARG_66	NH1	B_ASP_86	OD1	2.833
3HZY	B_ARG_66	NH1	B_ASP_86	OD2	3.703
3HZY	B_ARG_66	NH2	B_ASP_86	OD1	3.472
3HZY	B_ARG_66	NH2	B_ASP_86	OD2	2.924
3HZY	B_ARG_94	NH2	B_ASP_101	OD1	3.400
3HZY	B_ARG_94	NH2	B_ASP_101	OD2	2.530
3HZY	B_LYS_207	NZ	A_GLU_122	OE2	3.902

Table 415: 3HZY-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3I02	A_ARG_61	NH1	A_ASP_82	OD1	3.000
3I02	A_ARG_61	NH1	A_ASP_82	OD2	3.958
3I02	A_ARG_95	NH2	B_ASP_95	OD2	3.028
3I02	A_LYS_102	NZ	A_GLU_104	OE2	2.902
3I02	A_LYS_146	NZ	A_GLU_194	OE2	2.628
3I02	A_LYS_148	NZ	A_GLU_194	OE2	3.134
3I02	A_ARG_154	NH1	A_GLU_184	OE2	3.155
3I02	A_LYS_182	NZ	A_ASP_183	OD1	3.921
3I02	A_LYS_182	NZ	A_GLU_186	OE2	2.799
3I02	A_ARG_187	NH2	A_GLU_184	OE1	2.793
3I02	A_HIS_188	ND1	A_ASP_150	OD2	3.259
3I02	A_LYS_198	NZ	A_ASP_109	OD1	3.541
3I02	A_LYS_198	NZ	A_ASP_109	OD2	3.982
3I02	B_ARG_38	NH1	B_ASP_86	OD2	2.730
3I02	B_ARG_38	NH2	B_GLU_46	OE1	3.082
3I02	B_ARG_38	NH2	B_GLU_46	OE2	3.832
3I02	B_ARG_38	NH2	B_ASP_86	OD2	3.854
3I02	B_ARG_52	NH1	B_ASP_58	OD2	3.947
3I02	B_ARG_52	NH2	B_ASP_58	OD2	3.567
3I02	B_ARG_66	NH1	B_ASP_86	OD1	2.819
3I02	B_ARG_66	NH1	B_ASP_86	OD2	3.716
3I02	B_ARG_66	NH2	B_ASP_86	OD1	3.582
3I02	B_ARG_66	NH2	B_ASP_86	OD2	3.033
3I02	B_ARG_94	NH2	B_ASP_101	OD2	2.982
3I02	B_ARG_98	NH1	B_ASP_100	OD2	3.749
3I02	B_ARG_98	NH2	B_ASP_100	OD2	3.470
3I02	B_ARG_98	NH2	B_ASP_100A	OD1	3.832
3I02	B_ARG_98	NH2	B_ASP_100A	OD2	3.991
3I02	C_LYS_24	NZ	C_ASP_70	OD2	3.426
3I02	C_ARG_61	NH1	C_ASP_82	OD1	2.423
3I02	C_ARG_61	NH1	C_ASP_82	OD2	3.328
3I02	C_ARG_95	NH2	D_ASP_95	OD1	3.601
3I02	C_ARG_95	NH2	D_ASP_95	OD2	2.826
3I02	C_LYS_102	NZ	C_GLU_104	OE2	3.372
3I02	C_ARG_187	NH2	C_GLU_184	OE1	2.763
3I02	C_HIS_188	NE2	C_GLU_184	OE2	3.413
3I02	C_LYS_198	NZ	C_ASP_109	OD1	3.870
3I02	C_LYS_198	NZ	C_ASP_109	OD2	2.949
3I02	D_ARG_38	NH1	D_ASP_86	OD2	2.646
3I02	D_ARG_38	NH2	D_GLU_46	OE1	2.952
3I02	D_ARG_38	NH2	D_GLU_46	OE2	3.936
3I02	D_ARG_38	NH2	D_ASP_86	OD2	3.805
3I02	D_ARG_52	NH1	D_ASP_58	OD2	3.197
3I02	D_ARG_52	NH2	D_ASP_58	OD2	2.792
3I02	D_ARG_66	NH1	D_ASP_86	OD1	2.833
3I02	D_ARG_66	NH1	D_ASP_86	OD2	3.584
3I02	D_ARG_66	NH2	D_ASP_86	OD1	3.662
3I02	D_ARG_66	NH2	D_ASP_86	OD2	2.930
3I02	D_ARG_94	NH2	D_ASP_101	OD2	2.660
3I02	D_ARG_97	NH2	D_ASP_100A	OD2	3.024
3I02	D_LYS_208	NZ	C_GLU_122	OE2	3.585

Table 416: 3I02-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3I9G	H_ARG_38	NH2	H_GLU_46	OE1	2.845
3I9G	H_ARG_38	NH2	H_GLU_46	OE2	3.261
3I9G	H_ARG_53	NH2	H_ASP_31	OD1	2.786
3I9G	H_ARG_94	NH1	H_ASP_101	OD1	3.167
3I9G	H_ARG_94	NH1	H_ASP_101	OD2	3.902
3I9G	H_LYS_143	NZ	H_ASP_144	OD1	3.018
3I9G	H_LYS_143	NZ	H_ASP_144	OD2	2.935
3I9G	H_ARG_210	NH2	H_GLU_212	OE2	2.989
3I9G	L_LYS_42	NZ	L_GLU_39	OE1	2.937
3I9G	L_ARG_61	NH2	L_GLU_81	OE1	3.841
3I9G	L_ARG_61	NH2	L_ASP_82	OD1	2.775
3I9G	L_ARG_61	NH2	L_ASP_82	OD2	3.368
3I9G	L_LYS_149	NZ	L_GLU_195	OE1	3.806
3I9G	L_LYS_149	NZ	L_GLU_195	OE2	3.005
3I9G	L_LYS_183	NZ	L_GLU_187	OE1	3.717
3I9G	L_LYS_183	NZ	L_GLU_187	OE2	3.176

Table 417: 3I9G-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3IET	A_LYS_50	NZ	X_GLU_8	OE1	3.701
3IET	A_LYS_50	NZ	X_GLU_8	OE2	3.403
3IET	A_ARG_61	NH1	A_GLU_79	OE1	3.211
3IET	A_ARG_61	NH1	A_GLU_79	OE2	3.820
3IET	A_ARG_61	NH2	A_ASP_82	OD1	3.553
3IET	A_ARG_61	NH2	A_ASP_82	OD2	2.781
3IET	A_LYS_149	NZ	A_GLU_195	OE1	2.884
3IET	A_LYS_149	NZ	A_GLU_195	OE2	3.548
3IET	A_ARG_155	NH1	A_GLU_185	OE2	3.262
3IET	A_LYS_183	NZ	A_GLU_187	OE1	3.582
3IET	A_LYS_183	NZ	A_GLU_187	OE2	3.667
3IET	A_ARG_188	NH1	A_GLU_185	OE1	3.150
3IET	A_HIS_189	ND1	A_ASP_151	OD1	2.682
3IET	A_HIS_189	NE2	A_GLU_185	OE1	3.596
3IET	A_HIS_189	NE2	A_GLU_185	OE2	3.220
3IET	A_LYS_199	NZ	A_ASP_110	OD1	3.761
3IET	A_LYS_199	NZ	A_ASP_110	OD2	3.765
3IET	B_ARG_38	NH1	B_GLU_46	OE1	3.404
3IET	B_ARG_38	NH1	B_GLU_46	OE2	3.350
3IET	B_ARG_38	NH2	B_ASP_86	OD1	2.967
3IET	B_LYS_43	NZ	B_GLU_46	OE1	3.606
3IET	B_LYS_43	NZ	B_GLU_46	OE2	2.694
3IET	B_ARG_52	NH1	B_GLU_50	OE1	3.452
3IET	B_HIS_55	NE2	B_ASP_73	OD1	2.597
3IET	B_HIS_55	NE2	B_ASP_73	OD2	3.551
3IET	B_LYS_64	NZ	B_GLU_61	OE1	2.971
3IET	B_ARG_66	NH1	B_ASP_86	OD1	2.974
3IET	B_ARG_66	NH1	B_ASP_86	OD2	3.464
3IET	B_ARG_66	NH2	B_ASP_86	OD1	3.752
3IET	B_ARG_66	NH2	B_ASP_86	OD2	2.865
3IET	B_ARG_71	NH1	B_ASP_73	OD2	3.338
3IET	B_ARG_83	NH2	B_GLU_85	OE2	3.927
3IET	B_LYS_96	NZ	B_ASP_31	OD2	3.537
3IET	B_ARG_98	NH1	B_ASP_35	OD1	2.639
3IET	B_ARG_98	NH1	B_ASP_35	OD2	3.020
3IET	B_ARG_98	NH1	B_GLU_50	OE2	3.794
3IET	B_LYS_208	NZ	A_GLU_123	OE1	3.818
3IET	C_ARG_54	NH2	C_ASP_60	OD2	3.637
3IET	C_ARG_61	NH1	C_GLU_79	OE1	3.085
3IET	C_ARG_61	NH2	C_GLU_79	OE1	3.940
3IET	C_ARG_61	NH2	C_ASP_82	OD1	2.938
3IET	C_ARG_61	NH2	C_ASP_82	OD2	3.003
3IET	C_LYS_147	NZ	C_GLU_154	OE1	3.272
3IET	C_LYS_149	NZ	C_GLU_195	OE2	3.728
3IET	C_ARG_188	NH1	C_GLU_185	OE1	3.678
3IET	C_HIS_189	ND1	C_ASP_151	OD1	2.372
3IET	C_HIS_189	NE2	C_GLU_185	OE1	3.376
3IET	C_HIS_189	NE2	C_GLU_185	OE2	2.388
3IET	C_LYS_199	NZ	C_ASP_110	OD1	3.614
3IET	D_ARG_38	NH1	D_GLU_46	OE1	3.769
3IET	D_ARG_38	NH1	D_GLU_46	OE2	3.554
3IET	D_ARG_38	NH2	D_ASP_86	OD1	3.017
3IET	D_ARG_52	NH1	D_GLU_50	OE1	3.520
3IET	D_HIS_55	ND1	A_ASP_143	OD1	3.412
3IET	D_HIS_55	ND1	A_ASP_143	OD2	3.385
3IET	D_HIS_55	NE2	D_ASP_73	OD1	2.773
3IET	D_HIS_55	NE2	D_ASP_73	OD2	3.630

3IET	D_LYS_64	NZ	D_GLU_61	OE1	2.801
3IET	D_LYS_64	NZ	D_GLU_61	OE2	3.652
3IET	D_ARG_66	NH1	D_ASP_86	OD1	2.949
3IET	D_ARG_66	NH1	D_ASP_86	OD2	3.534
3IET	D_ARG_66	NH2	D_ASP_86	OD1	3.686
3IET	D_ARG_66	NH2	D_ASP_86	OD2	2.898
3IET	D_ARG_71	NH1	D_ASP_73	OD2	3.179
3IET	D_LYS_75	NZ	D_ASP_72	OD1	3.887
3IET	D_LYS_75	NZ	D_ASP_72	OD2	3.840
3IET	D_LYS_96	NZ	D_ASP_31	OD2	3.952
3IET	D_ARG_98	NH1	D_ASP_35	OD1	2.733
3IET	D_ARG_98	NH1	D_ASP_35	OD2	2.840
3IET	D_LYS_114	NZ	D_ASP_173	OD2	3.662
3IET	D_LYS_208	NZ	C_GLU_123	OE2	3.321
3IET	D_LYS_209	NZ	D_GLU_211	OE1	3.547

Table 418: 3IET-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3IF1	A_ARG_24	NH1	A_ASP_70	OD2	3.644
3IF1	A_ARG_24	NH2	A_ASP_70	OD2	3.131
3IF1	A_ARG_61	NH1	A_GLU_79	OE1	3.948
3IF1	A_ARG_61	NH1	A_GLU_79	OE2	3.315
3IF1	A_ARG_61	NH2	A_ASP_82	OD1	2.825
3IF1	A_ARG_61	NH2	A_ASP_82	OD2	2.702
3IF1	A_LYS_142	NZ	A_GLU_105	OE2	3.983
3IF1	A_LYS_147	NZ	A_GLU_154	OE1	3.522
3IF1	A_LYS_149	NZ	A_GLU_195	OE1	2.902
3IF1	A_ARG_155	NH1	A_GLU_185	OE2	2.578
3IF1	A_ARG_188	NH1	A_GLU_185	OE1	3.024
3IF1	A_HIS_189	ND1	A_ASP_151	OD1	2.587
3IF1	A_HIS_189	NE2	A_GLU_185	OE1	3.887
3IF1	A_HIS_189	NE2	A_GLU_185	OE2	3.017
3IF1	A_LYS_199	NZ	A_ASP_110	OD1	2.811
3IF1	A_LYS_199	NZ	A_ASP_110	OD2	3.664
3IF1	B_ARG_38	NH1	B_GLU_46	OE1	3.546
3IF1	B_ARG_38	NH1	B_GLU_46	OE2	3.505
3IF1	B_ARG_38	NH1	B_ASP_86	OD1	3.939
3IF1	B_ARG_38	NH2	B_ASP_86	OD1	3.024
3IF1	B_LYS_43	NZ	B_GLU_46	OE1	3.786
3IF1	B_LYS_43	NZ	B_GLU_46	OE2	2.709
3IF1	B_ARG_52	NH1	B_GLU_50	OE1	3.600
3IF1	B_HIS_55	NE2	B_ASP_73	OD1	2.678
3IF1	B_HIS_55	NE2	B_ASP_73	OD2	3.590
3IF1	B_LYS_64	NZ	B_GLU_61	OE1	3.313
3IF1	B_ARG_66	NH1	B_ASP_86	OD1	3.142
3IF1	B_ARG_66	NH1	B_ASP_86	OD2	3.480
3IF1	B_ARG_66	NH2	B_ASP_86	OD1	3.813
3IF1	B_ARG_66	NH2	B_ASP_86	OD2	2.708
3IF1	B_ARG_71	NH1	B_ASP_73	OD2	3.261
3IF1	B_LYS_96	NZ	B_ASP_31	OD2	3.416
3IF1	B_ARG_98	NH1	B_ASP_35	OD1	2.801
3IF1	B_ARG_98	NH1	B_ASP_35	OD2	2.999
3IF1	B_ARG_98	NH1	B_GLU_50	OE1	3.809
3IF1	B_ARG_98	NH1	B_GLU_50	OE2	3.524
3IF1	B_ARG_98	NH2	B_GLU_50	OE1	3.792
3IF1	B_ARG_98	NH2	B_GLU_50	OE2	3.692
3IF1	C_ARG_24	NH1	C_ASP_70	OD2	3.431
3IF1	C_ARG_24	NH2	C_ASP_70	OD2	2.995
3IF1	C_ARG_61	NH1	C_GLU_79	OE2	3.277
3IF1	C_ARG_61	NH2	C_ASP_82	OD1	2.778
3IF1	C_ARG_61	NH2	C_ASP_82	OD2	2.710
3IF1	C_LYS_147	NZ	C_GLU_154	OE1	3.247
3IF1	C_LYS_149	NZ	C_GLU_195	OE1	3.400
3IF1	C_ARG_155	NH1	C_GLU_185	OE2	2.578
3IF1	C_ARG_188	NH1	C_GLU_185	OE1	2.910
3IF1	C_HIS_189	ND1	C_ASP_151	OD1	2.543
3IF1	C_HIS_189	NE2	C_GLU_185	OE2	2.831
3IF1	C_LYS_199	NZ	C_ASP_110	OD1	2.846
3IF1	C_LYS_199	NZ	C_ASP_110	OD2	3.766
3IF1	D_ARG_38	NH1	D_GLU_46	OE1	3.513
3IF1	D_ARG_38	NH1	D_GLU_46	OE2	3.484
3IF1	D_ARG_38	NH2	D_ASP_86	OD1	3.055
3IF1	D_LYS_43	NZ	D_GLU_46	OE1	3.762
3IF1	D_LYS_43	NZ	D_GLU_46	OE2	3.359
3IF1	D_ARG_52	NH1	D_GLU_50	OE1	3.903

3IF1	D_LYS_52B	NZ	A_ASP_143	OD2	3.658
3IF1	D_HIS_55	ND1	A_ASP_143	OD1	3.559
3IF1	D_HIS_55	ND1	A_ASP_143	OD2	3.251
3IF1	D_HIS_55	NE2	D_ASP_73	OD1	2.642
3IF1	D_HIS_55	NE2	D_ASP_73	OD2	3.393
3IF1	D_LYS_64	NZ	D_GLU_61	OE1	3.366
3IF1	D_ARG_66	NH1	D_ASP_86	OD1	2.982
3IF1	D_ARG_66	NH1	D_ASP_86	OD2	3.435
3IF1	D_ARG_66	NH2	D_ASP_86	OD1	3.897
3IF1	D_ARG_66	NH2	D_ASP_86	OD2	2.982
3IF1	D_ARG_71	NH1	D_ASP_73	OD2	3.435
3IF1	D_ARG_98	NH1	D_ASP_35	OD1	2.797
3IF1	D_ARG_98	NH1	D_ASP_35	OD2	2.984
3IF1	D_ARG_98	NH1	D_GLU_50	OE1	3.619
3IF1	D_ARG_98	NH1	D_GLU_50	OE2	3.743
3IF1	D_ARG_98	NH2	D_GLU_50	OE1	3.809
3IF1	D_ARG_98	NH2	D_GLU_50	OE2	3.688
3IF1	D_LYS_209	NZ	D_GLU_211	OE1	3.626
3IF1	D_LYS_209	NZ	D_GLU_211	OE2	3.891

Table 419: 3IF1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3IJH	A_ARG_54	NH1	A_ASP_60	OD1	3.984
3IJH	A_ARG_61	NH1	A_ASP_82	OD1	3.244
3IJH	A_ARG_61	NH1	A_ASP_82	OD2	2.314
3IJH	A_ARG_61	NH2	A_ASP_82	OD1	3.682
3IJH	A_ARG_95	NH2	B_ASP_95	OD1	3.392
3IJH	A_ARG_95	NH2	B_ASP_95	OD2	2.832
3IJH	A_ARG_95	NH2	B_GLU_100E	OE1	3.920
3IJH	A_LYS_148	NZ	A_GLU_194	OE1	3.527
3IJH	A_LYS_148	NZ	A_GLU_194	OE2	2.720
3IJH	A_ARG_154	NH2	A_GLU_184	OE2	3.756
3IJH	A_HIS_188	ND1	A_ASP_150	OD2	2.926
3IJH	A_LYS_198	NZ	A_ASP_109	OD2	3.088
3IJH	B_ARG_38	NH1	B_ASP_86	OD2	2.842
3IJH	B_ARG_38	NH2	B_GLU_46	OE1	3.209
3IJH	B_ARG_38	NH2	B_ASP_86	OD2	3.896
3IJH	B_ARG_52	NH1	B_GLU_58	OE2	2.824
3IJH	B_ARG_52	NH2	B_GLU_58	OE2	3.202
3IJH	B_ARG_66	NH1	B_ASP_86	OD1	2.813
3IJH	B_ARG_66	NH1	B_ASP_86	OD2	3.750
3IJH	B_ARG_66	NH2	B_ASP_86	OD1	3.334
3IJH	B_ARG_66	NH2	B_ASP_86	OD2	2.758
3IJH	B_ARG_83	NH1	B_ASP_86	OD2	3.914
3IJH	B_ARG_164	NH1	A_ASP_166	OD1	3.428
3IJH	B_ARG_164	NH2	A_ASP_166	OD1	3.938
3IJH	B_LYS_208	NZ	A_GLU_122	OE1	2.744
3IJH	C_LYS_24	NZ	C_ASP_70	OD2	3.835
3IJH	C_ARG_54	NH1	C_ASP_60	OD1	3.972
3IJH	C_ARG_61	NH1	C_ASP_82	OD1	2.606
3IJH	C_ARG_61	NH1	C_ASP_82	OD2	2.580
3IJH	C_ARG_95	NH2	D_ASP_95	OD1	3.394
3IJH	C_ARG_95	NH2	D_ASP_95	OD2	2.734
3IJH	C_LYS_102	NZ	C_GLU_104	OE2	3.655
3IJH	C_LYS_146	NZ	C_GLU_153	OE2	3.796
3IJH	C_LYS_148	NZ	C_GLU_194	OE1	3.503
3IJH	C_LYS_148	NZ	C_GLU_194	OE2	3.158
3IJH	C_LYS_198	NZ	C_ASP_109	OD2	3.332
3IJH	D_ARG_38	NH1	D_ASP_86	OD2	2.796
3IJH	D_ARG_38	NH2	D_GLU_46	OE1	3.273
3IJH	D_ARG_38	NH2	D_ASP_86	OD2	3.880
3IJH	D_ARG_52	NH1	D_GLU_58	OE2	2.836
3IJH	D_ARG_52	NH2	D_GLU_58	OE2	3.043
3IJH	D_ARG_66	NH1	D_ASP_86	OD1	2.773
3IJH	D_ARG_66	NH1	D_ASP_86	OD2	3.767
3IJH	D_ARG_66	NH2	D_ASP_86	OD1	3.326
3IJH	D_ARG_66	NH2	D_ASP_86	OD2	2.861
3IJH	D_ARG_83	NH1	D_GLU_85	OE2	2.756
3IJH	D_ARG_164	NH1	C_ASP_166	OD1	3.593
3IJH	D_ARG_164	NH2	C_ASP_166	OD1	3.440
3IJH	D_ARG_209	NH1	D_GLU_211	OE2	3.993
3IJH	D_ARG_209	NH2	D_GLU_211	OE1	3.933

Table 420: 3IJH-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3IJS	A_ARG_61	NH1	A_ASP_82	OD1	2.832
3IJS	A_ARG_61	NH1	A_ASP_82	OD2	2.527
3IJS	A_ARG_61	NH2	A_GLU_81	OE1	3.669
3IJS	A_ARG_61	NH2	A_ASP_82	OD1	3.818
3IJS	A_ARG_95	NH2	B_ASP_95	OD1	3.603
3IJS	A_ARG_95	NH2	B_ASP_95	OD2	3.018
3IJS	A_ARG_95	NH2	B_GLU_100E	OE1	3.734
3IJS	A_LYS_102	NZ	A_GLU_104	OE2	3.940
3IJS	A_LYS_146	NZ	A_GLU_153	OE2	3.777
3IJS	A_LYS_148	NZ	A_GLU_194	OE1	3.285
3IJS	A_LYS_148	NZ	A_GLU_194	OE2	2.974
3IJS	A_LYS_182	NZ	A_GLU_186	OE1	2.825
3IJS	A_LYS_182	NZ	A_GLU_186	OE2	2.949
3IJS	A_HIS_188	ND1	A_ASP_150	OD2	2.814
3IJS	A_LYS_198	NZ	A_ASP_109	OD2	3.057
3IJS	B_ARG_38	NH1	B_ASP_86	OD2	2.852
3IJS	B_ARG_38	NH2	B_GLU_46	OE1	3.406
3IJS	B_ARG_38	NH2	B_ASP_86	OD2	3.872
3IJS	B_ARG_52	NH1	B_GLU_58	OE2	2.821
3IJS	B_ARG_52	NH2	B_GLU_58	OE2	2.883
3IJS	B_ARG_66	NH1	B_ASP_86	OD1	2.838
3IJS	B_ARG_66	NH1	B_ASP_86	OD2	3.824
3IJS	B_ARG_66	NH2	B_ASP_86	OD1	3.278
3IJS	B_ARG_66	NH2	B_ASP_86	OD2	2.729
3IJS	B_ARG_83	NH1	B_GLU_85	OE2	3.989
3IJS	B_ARG_164	NH1	A_ASP_166	OD1	3.855
3IJS	B_LYS_208	NZ	A_GLU_122	OE1	2.963
3IJS	C_ARG_54	NH1	C_ASP_60	OD2	3.567
3IJS	C_ARG_61	NH1	C_ASP_82	OD1	2.893
3IJS	C_ARG_61	NH1	C_ASP_82	OD2	3.574
3IJS	C_ARG_95	NH2	D_ASP_95	OD1	3.466
3IJS	C_ARG_95	NH2	D_ASP_95	OD2	2.795
3IJS	C_ARG_95	NH2	D_GLU_100E	OE1	3.752
3IJS	C_LYS_102	NZ	C_GLU_104	OE2	3.639
3IJS	C_LYS_146	NZ	C_GLU_153	OE1	3.935
3IJS	C_LYS_148	NZ	C_GLU_194	OE2	3.029
3IJS	C_ARG_154	NH2	C_GLU_184	OE2	3.755
3IJS	C_HIS_188	ND1	C_ASP_150	OD2	3.093
3IJS	C_LYS_198	NZ	C_ASP_109	OD2	3.489
3IJS	D_ARG_38	NH1	D_ASP_86	OD2	2.884
3IJS	D_ARG_38	NH2	D_GLU_46	OE1	3.237
3IJS	D_ARG_38	NH2	D_GLU_46	OE2	3.977
3IJS	D_ARG_52	NH1	D_GLU_58	OE2	3.033
3IJS	D_ARG_52	NH2	D_GLU_58	OE2	3.006
3IJS	D_ARG_66	NH1	D_ASP_86	OD1	2.827
3IJS	D_ARG_66	NH1	D_ASP_86	OD2	3.633
3IJS	D_ARG_66	NH2	D_ASP_86	OD1	3.506
3IJS	D_ARG_66	NH2	D_ASP_86	OD2	2.897
3IJS	D_ARG_164	NH1	C_ASP_166	OD1	3.815
3IJS	D_ARG_164	NH2	C_ASP_166	OD1	3.576
3IJS	D_LYS_208	NZ	C_GLU_122	OE1	3.219
3IJS	D_LYS_208	NZ	C_GLU_122	OE2	2.679
3IJS	D_ARG_209	NH1	D_GLU_211	OE2	2.704

Table 421: 3IJS-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3IJY	A_LYS_24	NZ	A_ASP_70	OD2	3.532
3IJY	A_ARG_54	NH1	A_ASP_60	OD1	3.326
3IJY	A_ARG_54	NH2	A_ASP_60	OD1	3.494
3IJY	A_ARG_61	NH1	A_ASP_82	OD1	2.847
3IJY	A_ARG_61	NH1	A_ASP_82	OD2	2.458
3IJY	A_ARG_61	NH2	A_GLU_81	OE1	3.326
3IJY	A_ARG_61	NH2	A_ASP_82	OD1	3.959
3IJY	A_ARG_95	NH2	B_ASP_95	OD1	3.420
3IJY	A_ARG_95	NH2	B_ASP_95	OD2	2.800
3IJY	A_ARG_95	NH2	B_GLU_100E	OE1	3.751
3IJY	A_LYS_148	NZ	A_GLU_194	OE1	3.793
3IJY	A_LYS_148	NZ	A_GLU_194	OE2	3.098
3IJY	A_HIS_188	ND1	A_ASP_150	OD2	3.295
3IJY	A_LYS_198	NZ	A_ASP_109	OD1	3.840
3IJY	A_LYS_198	NZ	A_ASP_109	OD2	3.869
3IJY	B_ARG_38	NH1	B_ASP_86	OD2	2.847
3IJY	B_ARG_38	NH2	B_GLU_46	OE1	3.463
3IJY	B_ARG_38	NH2	B_ASP_86	OD2	3.755
3IJY	B_ARG_52	NH1	B_GLU_58	OE2	3.349
3IJY	B_ARG_52	NH2	B_GLU_58	OE2	3.866
3IJY	B_ARG_66	NH1	B_ASP_86	OD1	3.730
3IJY	B_ARG_66	NH2	B_ASP_86	OD1	2.942
3IJY	B_ARG_66	NH2	B_ASP_86	OD2	2.730
3IJY	B_ARG_83	NH1	B_GLU_85	OE2	3.920
3IJY	B_ARG_83	NH1	B_ASP_86	OD2	3.633
3IJY	B_ARG_164	NH2	A_ASP_166	OD1	3.730
3IJY	B_ARG_164	NH2	A_ASP_166	OD2	3.693
3IJY	B_LYS_208	NZ	A_GLU_122	OE1	2.748
3IJY	B_ARG_209	NH2	B_GLU_211	OE2	3.922
3IJY	C_ARG_54	NH1	C_ASP_60	OD1	3.685
3IJY	C_ARG_61	NH1	C_ASP_82	OD1	2.672
3IJY	C_ARG_61	NH1	C_ASP_82	OD2	2.698
3IJY	C_ARG_95	NH2	D_ASP_95	OD1	2.992
3IJY	C_ARG_95	NH2	D_ASP_95	OD2	2.767
3IJY	C_ARG_95	NH2	D_GLU_100E	OE1	3.905
3IJY	C_LYS_102	NZ	C_GLU_104	OE2	3.111
3IJY	C_LYS_148	NZ	C_GLU_194	OE1	3.624
3IJY	C_LYS_148	NZ	C_GLU_194	OE2	2.838
3IJY	C_ARG_154	NH1	C_GLU_184	OE2	3.667
3IJY	D_ARG_38	NH1	D_ASP_86	OD2	3.093
3IJY	D_ARG_38	NH2	D_GLU_46	OE1	3.401
3IJY	D_ARG_52	NH1	D_GLU_58	OE2	3.273
3IJY	D_ARG_52	NH2	D_GLU_58	OE2	3.154
3IJY	D_ARG_66	NH1	D_ASP_86	OD1	2.831
3IJY	D_ARG_66	NH1	D_ASP_86	OD2	3.858
3IJY	D_ARG_66	NH2	D_ASP_86	OD1	3.574
3IJY	D_ARG_66	NH2	D_ASP_86	OD2	3.130
3IJY	D_ARG_83	NH1	D_GLU_85	OE2	2.929
3IJY	D_ARG_164	NH2	C_ASP_166	OD1	3.199
3IJY	D_ARG_209	NH1	D_GLU_211	OE2	2.725

Table 422: 3IJY-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3IKC	A_ARG_54	NH1	A_ASP_60	OD1	3.615
3IKC	A_ARG_54	NH2	A_ASP_60	OD1	3.863
3IKC	A_ARG_61	NH1	A_ASP_82	OD1	2.899
3IKC	A_ARG_61	NH1	A_ASP_82	OD2	2.400
3IKC	A_ARG_61	NH2	A_GLU_81	OE1	3.912
3IKC	A_ARG_61	NH2	A_ASP_82	OD1	3.699
3IKC	A_ARG_95	NH2	B_ASP_95	OD1	3.326
3IKC	A_ARG_95	NH2	B_ASP_95	OD2	2.867
3IKC	A_ARG_95	NH2	B_GLU_100E	OE1	3.865
3IKC	A_LYS_148	NZ	A_GLU_194	OE1	3.579
3IKC	A_LYS_148	NZ	A_GLU_194	OE2	2.692
3IKC	A_ARG_154	NH2	A_GLU_184	OE2	3.624
3IKC	A_HIS_188	ND1	A_ASP_150	OD2	2.784
3IKC	A_LYS_198	NZ	A_ASP_109	OD2	3.594
3IKC	B_ARG_38	NH1	B_ASP_86	OD2	2.851
3IKC	B_ARG_38	NH2	B_GLU_46	OE1	3.629
3IKC	B_ARG_38	NH2	B_GLU_46	OE2	3.974
3IKC	B_ARG_38	NH2	B_ASP_86	OD2	3.641
3IKC	B_ARG_52	NH1	B_GLU_58	OE2	2.895
3IKC	B_ARG_52	NH2	B_GLU_58	OE2	3.215
3IKC	B_ARG_66	NH1	B_ASP_86	OD1	3.007
3IKC	B_ARG_66	NH2	B_ASP_86	OD1	3.019
3IKC	B_ARG_66	NH2	B_ASP_86	OD2	2.604
3IKC	B_ARG_83	NH1	B_ASP_86	OD2	3.982
3IKC	B_LYS_208	NZ	A_GLU_122	OE1	3.042
3IKC	C_LYS_24	NZ	C_ASP_70	OD2	3.866
3IKC	C_ARG_54	NH1	C_ASP_60	OD1	3.727
3IKC	C_ARG_61	NH1	C_ASP_82	OD1	2.574
3IKC	C_ARG_61	NH1	C_ASP_82	OD2	2.683
3IKC	C_ARG_95	NH2	D_ASP_95	OD1	3.250
3IKC	C_ARG_95	NH2	D_ASP_95	OD2	2.670
3IKC	C_LYS_102	NZ	C_GLU_104	OE2	3.309
3IKC	C_LYS_148	NZ	C_GLU_194	OE1	3.402
3IKC	C_LYS_148	NZ	C_GLU_194	OE2	2.783
3IKC	C_ARG_154	NH1	C_GLU_184	OE2	3.991
3IKC	C_LYS_198	NZ	C_ASP_109	OD2	3.716
3IKC	D_ARG_38	NH1	D_ASP_86	OD2	2.796
3IKC	D_ARG_38	NH2	D_GLU_46	OE1	3.035
3IKC	D_ARG_38	NH2	D_GLU_46	OE2	3.845
3IKC	D_ARG_52	NH1	D_GLU_58	OE2	2.859
3IKC	D_ARG_52	NH2	D_GLU_58	OE2	3.107
3IKC	D_ARG_66	NH1	D_ASP_86	OD1	2.890
3IKC	D_ARG_66	NH1	D_ASP_86	OD2	3.713
3IKC	D_ARG_66	NH2	D_ASP_86	OD1	3.634
3IKC	D_ARG_66	NH2	D_ASP_86	OD2	3.025
3IKC	D_ARG_83	NH1	D_GLU_85	OE2	2.787
3IKC	D_ARG_164	NH1	C_ASP_166	OD1	3.903
3IKC	D_ARG_164	NH2	C_ASP_166	OD1	3.107
3IKC	D_ARG_209	NH1	D_GLU_211	OE2	3.689
3IKC	D_ARG_209	NH2	D_GLU_211	OE1	3.739

Table 423: 3IKC-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3IU3	A_ARG_29	NH2	K_ASP_6	OD1	2.779
3IU3	A_HIS_33	ND1	A_ASP_97	OD1	3.722
3IU3	A_HIS_33	NE2	A_ASP_97	OD1	3.462
3IU3	A_LYS_36	NZ	A_ASP_88	OD1	3.600
3IU3	A_ARG_96	NH2	A_ASP_103	OD1	3.718
3IU3	A_ARG_96	NH2	A_ASP_103	OD2	2.602
3IU3	A_LYS_211	NZ	B_GLU_120	OE1	2.457
3IU3	B_LYS_52	NZ	B_ASP_49	OD2	3.235
3IU3	B_ARG_60	NH1	B_GLU_80	OE2	3.898
3IU3	B_ARG_60	NH1	B_ASP_81	OD1	2.333
3IU3	B_ARG_60	NH1	B_ASP_81	OD2	2.901
3IU3	B_ARG_60	NH2	B_GLU_78	OE1	3.558
3IU3	B_ARG_60	NH2	B_GLU_78	OE2	3.050
3IU3	B_ARG_90	NH1	B_ASP_49	OD1	2.801
3IU3	B_ARG_90	NH1	K_ASP_56	OD2	3.059
3IU3	B_ARG_90	NH2	B_ASP_49	OD1	2.779
3IU3	B_LYS_100	NZ	B_GLU_162	OE1	3.331
3IU3	B_LYS_100	NZ	B_GLU_162	OE2	3.171
3IU3	B_LYS_146	NZ	B_GLU_192	OE1	3.006
3IU3	B_LYS_146	NZ	B_GLU_192	OE2	3.977
3IU3	B_HIS_186	ND1	B_ASP_148	OD2	3.079
3IU3	C_ARG_29	NH1	J_ASP_6	OD1	3.038
3IU3	C_ARG_29	NH1	J_ASP_6	OD2	3.788
3IU3	C_ARG_29	NH2	J_ASP_6	OD1	3.464
3IU3	C_HIS_33	ND1	C_ASP_97	OD2	3.423
3IU3	C_HIS_33	NE2	C_ASP_97	OD2	3.493
3IU3	C_ARG_38	NH2	C_GLU_87	OE2	3.961
3IU3	C_LYS_61	NZ	C_GLU_44	OE2	2.894
3IU3	C_LYS_65	NZ	C_ASP_88	OD2	3.093
3IU3	C_LYS_67	NZ	C_GLU_80	OE2	3.813
3IU3	C_ARG_96	NH1	C_ASP_103	OD1	3.896
3IU3	C_ARG_96	NH1	C_ASP_103	OD2	2.604
3IU3	C_LYS_145	NZ	C_ASP_146	OD1	3.489
3IU3	C_LYS_145	NZ	C_ASP_146	OD2	3.988
3IU3	C_LYS_211	NZ	D_GLU_120	OE2	3.231
3IU3	C_ARG_212	NH1	C_GLU_214	OE1	3.436
3IU3	C_ARG_212	NH1	C_GLU_214	OE2	3.171
3IU3	D_LYS_52	NZ	D_ASP_49	OD2	2.969
3IU3	D_ARG_60	NH1	D_GLU_78	OE1	3.425
3IU3	D_ARG_60	NH1	D_GLU_78	OE2	3.777
3IU3	D_ARG_60	NH2	D_GLU_78	OE1	3.729
3IU3	D_ARG_60	NH2	D_ASP_81	OD1	2.613
3IU3	D_ARG_60	NH2	D_ASP_81	OD2	3.360
3IU3	D_ARG_90	NH1	D_ASP_49	OD1	2.486
3IU3	D_ARG_90	NH1	D_ASP_49	OD2	3.966
3IU3	D_ARG_90	NH2	D_ASP_49	OD1	2.791
3IU3	D_ARG_90	NH2	J_ASP_56	OD2	3.101
3IU3	D_LYS_100	NZ	D_GLU_162	OE1	3.352
3IU3	D_LYS_100	NZ	D_GLU_162	OE2	3.241
3IU3	D_ARG_139	NH2	D_GLU_102	OE1	3.961
3IU3	D_ARG_139	NH2	D_GLU_102	OE2	2.898
3IU3	D_LYS_146	NZ	D_GLU_192	OE1	3.339
3IU3	D_HIS_186	ND1	D_ASP_148	OD2	3.055
3IU3	H_ARG_29	NH1	I_ASP_6	OD1	3.964
3IU3	H_ARG_29	NH1	I_ASP_6	OD2	3.865
3IU3	H_ARG_29	NH2	I_ASP_6	OD1	2.749
3IU3	H_ARG_29	NH2	I_ASP_6	OD2	3.378

3IU3	H_HIS_33	ND1	H_ASP_97	OD2	3.649
3IU3	H_HIS_33	NE2	H_ASP_97	OD2	3.672
3IU3	H_ARG_38	NH2	H_GLU_87	OE2	3.294
3IU3	H_LYS_65	NZ	H_ASP_88	OD1	3.023
3IU3	H_LYS_65	NZ	H_ASP_88	OD2	2.754
3IU3	H_ARG_96	NH2	H_ASP_103	OD1	3.935
3IU3	H_ARG_96	NH2	H_ASP_103	OD2	2.794
3IU3	H_HIS_166	NE2	L_ASP_164	OD1	3.898
3IU3	H_LYS_211	NZ	L_GLU_120	OE2	3.694
3IU3	L_ARG_29	NH2	L_ASP_56	OD2	3.164
3IU3	L_LYS_52	NZ	L_ASP_49	OD2	2.964
3IU3	L_ARG_60	NH1	L_GLU_78	OE1	3.113
3IU3	L_ARG_60	NH1	L_GLU_78	OE2	3.592
3IU3	L_ARG_60	NH2	L_GLU_78	OE1	3.507
3IU3	L_ARG_60	NH2	L_GLU_80	OE1	3.605
3IU3	L_ARG_60	NH2	L_ASP_81	OD1	2.623
3IU3	L_ARG_60	NH2	L_ASP_81	OD2	3.232
3IU3	L_ARG_90	NH1	L_ASP_49	OD1	2.693
3IU3	L_ARG_90	NH2	L_ASP_49	OD1	2.879
3IU3	L_ARG_90	NH2	L_ASP_56	OD1	2.806
3IU3	L_LYS_100	NZ	L_GLU_102	OE2	3.519
3IU3	L_LYS_100	NZ	L_GLU_162	OE1	3.094
3IU3	L_LYS_100	NZ	L_GLU_162	OE2	3.091
3IU3	L_ARG_139	NH1	L_GLU_102	OE2	3.791
3IU3	L_ARG_139	NH2	L_GLU_102	OE1	3.338
3IU3	L_ARG_139	NH2	L_GLU_102	OE2	2.994
3IU3	L_LYS_185	NZ	L_ASP_182	OD1	3.411
3IU3	L_HIS_186	ND1	L_ASP_148	OD2	2.793
3IU3	L_ARG_36	NH1	H_ASP_55	OD1	3.819
3IU3	L_ARG_36	NH2	H_ASP_55	OD1	3.008
3IU3	L_ARG_36	NH2	H_ASP_55	OD2	2.747
3IU3	L_ARG_117	NH2	L_GLU_106	OE2	3.361
3IU3	I_HIS_120	NE2	L_ASP_4	OD2	3.993
3IU3	J_ARG_117	NH2	J_GLU_113	OE1	3.255
3IU3	J_ARG_117	NH2	J_GLU_113	OE2	3.394
3IU3	K_LYS_16	NZ	K_GLU_116	OE1	3.890
3IU3	K_ARG_117	NH2	K_GLU_113	OE1	3.765
3IU3	K_ARG_117	NH2	K_GLU_113	OE2	3.085
3IU3	K_HIS_120	NE2	K_ASP_4	OD1	3.824

Table 424: 3IU3-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3IU4	H_ARG_38	NH1	H_ASP_86	OD1	2.694
3IU4	H_ARG_38	NH2	H_GLU_46	OE1	2.936
3IU4	H_ARG_38	NH2	H_GLU_46	OE2	3.977
3IU4	H_ARG_38	NH2	H_ASP_86	OD1	3.682
3IU4	H_ARG_66	NH1	H_ASP_86	OD1	3.618
3IU4	H_ARG_66	NH1	H_ASP_86	OD2	2.904
3IU4	H_ARG_66	NH2	H_ASP_86	OD1	2.858
3IU4	H_ARG_66	NH2	H_ASP_86	OD2	3.468
3IU4	H_LYS_143	NZ	H_ASP_144	OD1	3.173
3IU4	H_LYS_143	NZ	H_ASP_144	OD2	3.097
3IU4	H_LYS_210	NZ	H_GLU_212	OE2	3.515
3IU4	L_ARG_54	NH2	L_ASP_60	OD1	3.494
3IU4	L_ARG_61	NH2	L_ASP_82	OD1	2.721
3IU4	L_ARG_61	NH2	L_ASP_82	OD2	3.542
3IU4	L_LYS_103	NZ	L_GLU_165	OE1	2.777
3IU4	L_LYS_103	NZ	L_GLU_165	OE2	3.441
3IU4	L_LYS_149	NZ	L_GLU_195	OE2	3.735
3IU4	L_LYS_190	NZ	L_GLU_213	OE2	2.585

Table 425: 3IU4-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3IVK	L_ARG_25	NH2	L_ASP_71	OD1	3.565
3IVK	L_ARG_25	NH2	L_ASP_71	OD2	3.118
3IVK	L_ARG_62	NH2	L_GLU_82	OE1	3.240
3IVK	L_ARG_62	NH2	L_ASP_83	OD1	3.041
3IVK	L_ARG_62	NH2	L_ASP_83	OD2	3.362
3IVK	L_LYS_104	NZ	L_GLU_106	OE2	2.881
3IVK	L_ARG_143	NH1	L_GLU_106	OE2	2.980
3IVK	L_LYS_150	NZ	L_GLU_196	OE2	2.646
3IVK	H_ARG_41	NH1	H_ASP_93	OD1	2.697
3IVK	H_ARG_41	NH2	H_GLU_49	OE1	3.359
3IVK	H_ARG_41	NH2	H_GLU_49	OE2	3.688
3IVK	H_ARG_41	NH2	H_ASP_93	OD1	3.849
3IVK	H_ARG_70	NH1	H_ASP_93	OD2	2.963
3IVK	H_ARG_70	NH2	H_ASP_93	OD1	2.795
3IVK	H_ARG_70	NH2	H_ASP_93	OD2	2.668
3IVK	H_LYS_79	NZ	H_ASP_76	OD2	3.978
3IVK	H_ARG_101	NH2	H_ASP_113	OD2	3.051
3IVK	H_ARG_107	NH1	H_ASP_113	OD2	3.782
3IVK	H_LYS_155	NZ	H_ASP_156	OD1	3.783
3IVK	H_LYS_155	NZ	H_ASP_156	OD2	3.283
3IVK	H_LYS_218	NZ	H_ASP_220	OD1	3.490
3IVK	H_LYS_218	NZ	H_ASP_220	OD2	3.548
3IVK	H_LYS_222	NZ	H_GLU_224	OE1	3.186
3IVK	H_LYS_222	NZ	H_GLU_224	OE2	3.235
3IVK	B_ARG_25	NH2	B_ASP_71	OD1	3.579
3IVK	B_ARG_25	NH2	B_ASP_71	OD2	3.085
3IVK	B_ARG_62	NH2	B_GLU_82	OE1	3.276
3IVK	B_ARG_62	NH2	B_ASP_83	OD1	3.056
3IVK	B_ARG_62	NH2	B_ASP_83	OD2	3.370
3IVK	B_LYS_104	NZ	B_GLU_106	OE2	2.879
3IVK	B_ARG_143	NH1	B_GLU_106	OE2	2.970
3IVK	B_LYS_150	NZ	B_GLU_196	OE2	2.638
3IVK	A_ARG_41	NH1	A_ASP_93	OD1	2.649
3IVK	A_ARG_41	NH2	A_GLU_49	OE1	3.405
3IVK	A_ARG_41	NH2	A_GLU_49	OE2	3.702
3IVK	A_ARG_41	NH2	A_ASP_93	OD1	3.815
3IVK	A_ARG_70	NH1	A_ASP_93	OD2	2.973
3IVK	A_ARG_70	NH2	A_ASP_93	OD1	2.836
3IVK	A_ARG_70	NH2	A_ASP_93	OD2	2.675
3IVK	A_LYS_79	NZ	A_ASP_76	OD2	3.988
3IVK	A_ARG_101	NH2	A_ASP_113	OD2	3.070
3IVK	A_ARG_107	NH1	A_ASP_113	OD2	3.837
3IVK	A_LYS_155	NZ	A_ASP_156	OD1	3.802
3IVK	A_LYS_155	NZ	A_ASP_156	OD2	3.283
3IVK	A_LYS_218	NZ	A_ASP_220	OD1	3.505
3IVK	A_LYS_218	NZ	A_ASP_220	OD2	3.577
3IVK	A_LYS_222	NZ	A_GLU_224	OE1	3.213
3IVK	A_LYS_222	NZ	A_GLU_224	OE2	3.240

Table 426: 3IVK-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3J5M	A_LYS_46	NZ	A_GLU_492	OE1	3.718
3J5M	A_LYS_46	NZ	A_GLU_492	OE2	2.915
3J5M	A_HIS_66	ND1	A_GLU_64	OE2	3.151
3J5M	A_ARG_143	NH2	A_GLU_145	OE1	2.805
3J5M	A_ARG_143	NH2	A_GLU_145	OE2	3.445
3J5M	A_LYS_229	NZ	A_GLU_83	OE1	2.907
3J5M	A_LYS_231	NZ	A_GLU_268	OE2	2.874
3J5M	A_HIS_249	NE2	A_GLU_482	OE1	3.482
3J5M	A_LYS_282	NZ	A_GLU_275	OE1	2.857
3J5M	A_LYS_282	NZ	A_GLU_275	OE2	3.935
3J5M	A_LYS_344	NZ	A_GLU_340	OE2	3.897
3J5M	A_LYS_421	NZ	A_GLU_145	OE2	3.812
3J5M	A_ARG_429	NH2	D_ASP_74	OD1	3.207
3J5M	A_ARG_429	NH2	D_ASP_74	OD2	3.203
3J5M	A_ARG_456	NH1	A_GLU_466	OE1	2.968
3J5M	A_ARG_476	NH2	A_ASP_474	OD1	3.858
3J5M	A_ARG_480	NH1	A_ASP_477	OD1	2.834
3J5M	A_LYS_487	NZ	A_GLU_91	OE2	2.895
3J5M	C_ARG_54	NH2	C_ASP_60	OD1	2.987
3J5M	C_ARG_61	NH1	C_GLU_79	OE2	3.926
3J5M	C_ARG_61	NH2	C_GLU_79	OE1	3.624
3J5M	C_ARG_61	NH2	C_ASP_82	OD1	3.040
3J5M	C_ARG_61	NH2	C_ASP_82	OD2	3.088
3J5M	C_ARG_103	NH2	C_GLU_165	OE1	2.814
3J5M	C_ARG_142	NH1	C_GLU_165	OE1	3.243
3J5M	C_ARG_142	NH2	C_GLU_105	OE2	3.198
3J5M	C_LYS_149	NZ	C_GLU_195	OE1	3.376
3J5M	C_LYS_149	NZ	C_GLU_195	OE2	2.944
3J5M	C_HIS_189	ND1	C_ASP_151	OD2	2.803
3J5M	D_ARG_19	NH1	D_ASP_81	OD2	3.870
3J5M	D_ARG_19	NH2	D_ASP_81	OD2	3.177
3J5M	D_ARG_31	NH2	D_ASP_27	OD2	3.998
3J5M	D_ARG_38	NH1	D_ASP_86	OD1	2.857
3J5M	D_ARG_38	NH2	D_GLU_46	OE2	2.922
3J5M	D_LYS_52	NZ	A_ASP_474	OD2	2.827
3J5M	D_LYS_52	NZ	D_GLU_33	OE2	3.615
3J5M	D_ARG_64	NH2	A_ASP_457	OD2	3.079
3J5M	D_ARG_73	NH2	D_GLU_30	OE1	2.847
3J5M	D_ARG_73	NH2	D_GLU_30	OE2	3.839
3J5M	D_LYS_209	NZ	C_GLU_123	OE1	3.480
3J5M	D_LYS_209	NZ	C_GLU_123	OE2	2.844
3J5M	D_LYS_214	NZ	C_ASP_122	OD2	2.841
3J5M	E_LYS_46	NZ	E_GLU_492	OE1	3.718
3J5M	E_LYS_46	NZ	E_GLU_492	OE2	2.915
3J5M	E_HIS_66	ND1	E_GLU_64	OE2	3.151
3J5M	E_ARG_143	NH2	E_GLU_145	OE1	2.804
3J5M	E_ARG_143	NH2	E_GLU_145	OE2	3.444
3J5M	E_LYS_229	NZ	E_GLU_83	OE1	2.907
3J5M	E_LYS_231	NZ	E_GLU_268	OE2	2.874
3J5M	E_HIS_249	NE2	E_GLU_482	OE1	3.482
3J5M	E_LYS_282	NZ	E_GLU_275	OE1	2.858
3J5M	E_LYS_282	NZ	E_GLU_275	OE2	3.935
3J5M	E_LYS_344	NZ	E_GLU_340	OE2	3.897
3J5M	E_LYS_421	NZ	E_GLU_145	OE2	3.812
3J5M	E_ARG_429	NH2	H_ASP_74	OD1	3.207
3J5M	E_ARG_429	NH2	H_ASP_74	OD2	3.202
3J5M	E_ARG_456	NH1	E_GLU_466	OE1	2.967

3J5M	E_ARG_476	NH2	E_ASP_474	OD1	3.859
3J5M	E_ARG_480	NH1	E_ASP_477	OD1	2.834
3J5M	E_LYS_487	NZ	E_GLU_91	OE2	2.894
3J5M	G_ARG_54	NH2	G_ASP_60	OD1	2.988
3J5M	G_ARG_61	NH1	G_GLU_79	OE2	3.925
3J5M	G_ARG_61	NH2	G_GLU_79	OE1	3.624
3J5M	G_ARG_61	NH2	G_ASP_82	OD1	3.040
3J5M	G_ARG_61	NH2	G_ASP_82	OD2	3.087
3J5M	G_ARG_103	NH2	G_GLU_165	OE1	2.814
3J5M	G_ARG_142	NH1	G_GLU_165	OE1	3.243
3J5M	G_ARG_142	NH2	G_GLU_105	OE2	3.199
3J5M	G_LYS_149	NZ	G_GLU_195	OE1	3.376
3J5M	G_LYS_149	NZ	G_GLU_195	OE2	2.944
3J5M	G_HIS_189	ND1	G_ASP_151	OD2	2.802
3J5M	H_ARG_19	NH1	H_ASP_81	OD2	3.869
3J5M	H_ARG_19	NH2	H_ASP_81	OD2	3.177
3J5M	H_ARG_31	NH2	H_ASP_27	OD2	3.998
3J5M	H_ARG_38	NH1	H_ASP_86	OD1	2.857
3J5M	H_ARG_38	NH2	H_GLU_46	OE2	2.922
3J5M	H_LYS_52	NZ	E_ASP_474	OD2	2.827
3J5M	H_LYS_52	NZ	H_GLU_33	OE2	3.614
3J5M	H_ARG_64	NH2	E_ASP_457	OD2	3.078
3J5M	H_ARG_73	NH2	H_GLU_30	OE1	2.847
3J5M	H_ARG_73	NH2	H_GLU_30	OE2	3.840
3J5M	H_LYS_209	NZ	G_GLU_123	OE1	3.479
3J5M	H_LYS_209	NZ	G_GLU_123	OE2	2.843
3J5M	H_LYS_214	NZ	G_ASP_122	OD2	2.842
3J5M	I_LYS_46	NZ	I_GLU_492	OE1	3.718
3J5M	I_LYS_46	NZ	I_GLU_492	OE2	2.915
3J5M	I_HIS_66	ND1	I_GLU_64	OE2	3.151
3J5M	I_ARG_143	NH2	I_GLU_145	OE1	2.805
3J5M	I_ARG_143	NH2	I_GLU_145	OE2	3.445
3J5M	I_LYS_229	NZ	I_GLU_83	OE1	2.907
3J5M	I_LYS_231	NZ	I_GLU_268	OE2	2.875
3J5M	I_HIS_249	NE2	I_GLU_482	OE1	3.482
3J5M	I_LYS_282	NZ	I_GLU_275	OE1	2.857
3J5M	I_LYS_282	NZ	I_GLU_275	OE2	3.934
3J5M	I_LYS_344	NZ	I_GLU_340	OE2	3.896
3J5M	I_LYS_421	NZ	I_GLU_145	OE2	3.811
3J5M	I_ARG_429	NH2	L_ASP_74	OD1	3.207
3J5M	I_ARG_429	NH2	L_ASP_74	OD2	3.202
3J5M	I_ARG_456	NH1	I_GLU_466	OE1	2.967
3J5M	I_ARG_476	NH2	L_ASP_474	OD1	3.859
3J5M	I_ARG_480	NH1	L_ASP_477	OD1	2.834
3J5M	I_LYS_487	NZ	I_GLU_91	OE2	2.895
3J5M	K_ARG_54	NH2	K_ASP_60	OD1	2.987
3J5M	K_ARG_61	NH1	K_GLU_79	OE2	3.926
3J5M	K_ARG_61	NH2	K_GLU_79	OE1	3.624
3J5M	K_ARG_61	NH2	K_ASP_82	OD1	3.041
3J5M	K_ARG_61	NH2	K_ASP_82	OD2	3.088
3J5M	K_ARG_103	NH2	K_GLU_165	OE1	2.814
3J5M	K_ARG_142	NH1	K_GLU_165	OE1	3.243
3J5M	K_ARG_142	NH2	K_GLU_105	OE2	3.198
3J5M	K_LYS_149	NZ	K_GLU_195	OE1	3.376
3J5M	K_LYS_149	NZ	K_GLU_195	OE2	2.944
3J5M	K_HIS_189	ND1	K_ASP_151	OD2	2.803
3J5M	L_ARG_19	NH1	L_ASP_81	OD2	3.870
3J5M	L_ARG_19	NH2	L_ASP_81	OD2	3.177

3J5M	L_ARG_31	NH2	L_ASP_27	OD2	3.998
3J5M	L_ARG_38	NH1	L_ASP_86	OD1	2.857
3J5M	L_ARG_38	NH2	L_GLU_46	OE2	2.922
3J5M	L_LYS_52	NZ	L_ASP_474	OD2	2.827
3J5M	L_LYS_52	NZ	L_GLU_33	OE2	3.615
3J5M	L_ARG_64	NH2	L_ASP_457	OD2	3.078
3J5M	L_ARG_73	NH2	L_GLU_30	OE1	2.847
3J5M	L_ARG_73	NH2	L_GLU_30	OE2	3.839
3J5M	L_LYS_209	NZ	K_GLU_123	OE1	3.480
3J5M	L_LYS_209	NZ	K_GLU_123	OE2	2.844
3J5M	L_LYS_214	NZ	K_ASP_122	OD2	2.841

Table 427: 3J5M-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3J70	A_ARG_38	NH1	A_ASP_86	OD1	3.866
3J70	A_ARG_38	NH2	A_GLU_46	OE1	2.795
3J70	A_ARG_38	NH2	A_ASP_86	OD1	2.823
3J70	A_LYS_62	NZ	A_GLU_46	OE2	2.813
3J70	A_ARG_64	NH2	B_ASP_1	OD1	2.676
3J70	A_ARG_66	NH2	A_ASP_86	OD2	2.896
3J70	A_ARG_83	NH2	A_GLU_85	OE2	3.748
3J70	A_LYS_209	NZ	B_GLU_123	OE1	3.744
3J70	A_LYS_209	NZ	B_GLU_123	OE2	2.604
3J70	A_LYS_210	NZ	A_GLU_212	OE1	3.567
3J70	A_LYS_214	NZ	A_GLU_212	OE1	3.762
3J70	A_LYS_214	NZ	A_GLU_212	OE2	3.583
3J70	B_ARG_61	NH2	B_ASP_82	OD1	2.797
3J70	B_ARG_61	NH2	B_ASP_82	OD2	2.800
3J70	B_LYS_103	NZ	B_GLU_165	OE1	2.848
3J70	B_LYS_103	NZ	B_GLU_165	OE2	3.750
3J70	B_ARG_108	NH1	B_ASP_170	OD2	3.189
3J70	B_LYS_149	NZ	B_GLU_195	OE1	3.334
3J70	B_LYS_149	NZ	B_GLU_195	OE2	2.862
3J70	C_LYS_8	NZ	C_GLU_119	OE1	2.764
3J70	C_HIS_27	ND1	C_GLU_85	OE1	3.187
3J70	C_LYS_29	NZ	C_GLU_85	OE1	3.965
3J70	C_LYS_29	NZ	D_ASP_279	OD2	2.704
3J70	C_LYS_46	NZ	C_ASP_56	OD1	2.811
3J70	C_LYS_50	NZ	C_GLU_77	OE1	2.765
3J70	C_LYS_50	NZ	C_GLU_77	OE2	3.345
3J70	C_ARG_54	NH1	C_ASP_78	OD2	2.875
3J70	C_ARG_54	NH2	C_ASP_78	OD1	2.822
3J70	C_ARG_54	NH2	C_ASP_78	OD2	2.827
3J70	C_ARG_59	NH1	D_ASP_368	OD1	3.842
3J70	C_ARG_59	NH1	D_ASP_368	OD2	2.986
3J70	C_ARG_59	NH2	D_ASP_368	OD1	2.621
3J70	C_ARG_59	NH2	D_ASP_368	OD2	3.173
3J70	C_LYS_72	NZ	C_ASP_56	OD2	2.565
3J70	C_LYS_90	NZ	C_GLU_85	OE2	2.709
3J70	C_HIS_107	ND1	C_ASP_105	OD2	3.850
3J70	C_ARG_134	NH2	C_ASP_153	OD1	3.650
3J70	C_ARG_134	NH2	C_ASP_153	OD2	3.960
3J70	D_LYS_46	NZ	D_GLU_492	OE1	2.843
3J70	D_LYS_46	NZ	D_GLU_492	OE2	2.835
3J70	D_LYS_130	NZ	D_GLU_150	OE2	2.774
3J70	D_ARG_146	NH1	C_GLU_169	OE1	2.841
3J70	D_ARG_146	NH1	C_GLU_169	OE2	2.796
3J70	D_ARG_146	NH2	C_GLU_169	OE1	3.599
3J70	D_LYS_171	NZ	C_GLU_13	OE1	3.949
3J70	D_LYS_192	NZ	D_ASP_137	OD2	2.718
3J70	D_LYS_207	NZ	D_GLU_381	OE2	2.776
3J70	D_HIS_249	NE2	D_GLU_482	OE1	2.775
3J70	D_LYS_282	NZ	D_ASP_279	OD1	2.794
3J70	D_LYS_322	NZ	A_ASP_95	OD2	2.908
3J70	D_ARG_327	NH2	A_ASP_52	OD2	3.286
3J70	D_LYS_337	NZ	D_GLU_293	OE2	2.865
3J70	D_LYS_348	NZ	D_GLU_269	OE1	2.779
3J70	D_LYS_348	NZ	D_GLU_269	OE2	3.998
3J70	D_ARG_419	NH1	A_ASP_54	OD1	3.985
3J70	D_ARG_456	NH1	D_GLU_466	OE1	2.870
3J70	D_ARG_456	NH1	D_GLU_466	OE2	2.877

3J70	D_ARG_469	NH1	D_ASP_457	OD1	2.823
3J70	D_ARG_469	NH1	D_ASP_457	OD2	3.449
3J70	D_ARG_469	NH2	D_ASP_457	OD2	3.357
3J70	D_ARG_476	NH1	D_ASP_474	OD1	2.860
3J70	D_ARG_480	NH1	D_ASP_474	OD2	2.862
3J70	D_ARG_480	NH1	D_ASP_477	OD1	2.641
3J70	D_ARG_480	NH1	D_ASP_477	OD2	3.954
3J70	D_ARG_480	NH2	D_ASP_474	OD2	3.415
3J70	D_LYS_487	NZ	D_GLU_47	OE2	3.606
3J70	D_LYS_487	NZ	D_GLU_91	OE2	2.796
3J70	M_ARG_38	NH1	M_ASP_86	OD1	3.866
3J70	M_ARG_38	NH2	M_GLU_46	OE1	2.795
3J70	M_ARG_38	NH2	M_ASP_86	OD1	2.824
3J70	M_LYS_62	NZ	M_GLU_46	OE2	2.814
3J70	M_ARG_64	NH2	N_ASP_1	OD1	2.677
3J70	M_ARG_66	NH2	M_ASP_86	OD2	2.896
3J70	M_ARG_83	NH2	M_GLU_85	OE2	3.748
3J70	M_LYS_209	NZ	N_GLU_123	OE1	3.744
3J70	M_LYS_209	NZ	N_GLU_123	OE2	2.604
3J70	M_LYS_210	NZ	M_GLU_212	OE1	3.567
3J70	M_LYS_214	NZ	M_GLU_212	OE1	3.762
3J70	M_LYS_214	NZ	M_GLU_212	OE2	3.583
3J70	N_ARG_61	NH2	N_ASP_82	OD1	2.798
3J70	N_ARG_61	NH2	N_ASP_82	OD2	2.800
3J70	N_LYS_103	NZ	N_GLU_165	OE1	2.848
3J70	N_LYS_103	NZ	N_GLU_165	OE2	3.750
3J70	N_ARG_108	NH1	N_ASP_170	OD2	3.190
3J70	N_LYS_149	NZ	N_GLU_195	OE1	3.334
3J70	N_LYS_149	NZ	N_GLU_195	OE2	2.861
3J70	O_LYS_8	NZ	O_GLU_119	OE1	2.765
3J70	O_HIS_27	ND1	O_GLU_85	OE1	3.187
3J70	O_LYS_29	NZ	O_GLU_85	OE1	3.964
3J70	O_LYS_29	NZ	P_ASP_279	OD2	2.704
3J70	O_LYS_46	NZ	O_ASP_56	OD1	2.811
3J70	O_LYS_50	NZ	O_GLU_77	OE1	2.765
3J70	O_LYS_50	NZ	O_GLU_77	OE2	3.346
3J70	O_ARG_54	NH1	O_ASP_78	OD2	2.875
3J70	O_ARG_54	NH2	O_ASP_78	OD1	2.822
3J70	O_ARG_54	NH2	O_ASP_78	OD2	2.827
3J70	O_ARG_59	NH1	P_ASP_368	OD1	3.842
3J70	O_ARG_59	NH1	P_ASP_368	OD2	2.986
3J70	O_ARG_59	NH2	P_ASP_368	OD1	2.620
3J70	O_ARG_59	NH2	P_ASP_368	OD2	3.173
3J70	O_LYS_72	NZ	O_ASP_56	OD2	2.565
3J70	O_LYS_90	NZ	O_GLU_85	OE2	2.709
3J70	O_HIS_107	ND1	O_ASP_105	OD2	3.851
3J70	O_ARG_134	NH2	O_ASP_153	OD1	3.650
3J70	O_ARG_134	NH2	O_ASP_153	OD2	3.960
3J70	P_LYS_46	NZ	P_GLU_492	OE1	2.843
3J70	P_LYS_46	NZ	P_GLU_492	OE2	2.835
3J70	P_LYS_130	NZ	P_GLU_150	OE2	2.774
3J70	P_ARG_146	NH1	O_GLU_169	OE1	2.841
3J70	P_ARG_146	NH1	O_GLU_169	OE2	2.796
3J70	P_ARG_146	NH2	O_GLU_169	OE1	3.599
3J70	P_LYS_171	NZ	O_GLU_13	OE1	3.948
3J70	P_LYS_192	NZ	P_ASP_137	OD2	2.718
3J70	P_LYS_207	NZ	P_GLU_381	OE2	2.776
3J70	P_HIS_249	NE2	P_GLU_482	OE1	2.775

3J70	P_LYS_282	NZ	P_ASP_279	OD1	2.794
3J70	P_LYS_322	NZ	M_ASP_95	OD2	2.909
3J70	P_ARG_327	NH2	M_ASP_52	OD2	3.286
3J70	P_LYS_337	NZ	P_GLU_293	OE2	2.865
3J70	P_LYS_348	NZ	P_GLU_269	OE1	2.779
3J70	P_LYS_348	NZ	P_GLU_269	OE2	3.999
3J70	P_ARG_419	NH1	M_ASP_54	OD1	3.985
3J70	P_ARG_456	NH1	P_GLU_466	OE1	2.870
3J70	P_ARG_456	NH1	P_GLU_466	OE2	2.877
3J70	P_ARG_469	NH1	P_ASP_457	OD1	2.823
3J70	P_ARG_469	NH1	P_ASP_457	OD2	3.450
3J70	P_ARG_469	NH2	P_ASP_457	OD2	3.357
3J70	P_ARG_476	NH1	P_ASP_474	OD1	2.859
3J70	P_ARG_480	NH1	P_ASP_474	OD2	2.862
3J70	P_ARG_480	NH1	P_ASP_477	OD1	2.642
3J70	P_ARG_480	NH1	P_ASP_477	OD2	3.954
3J70	P_ARG_480	NH2	P_ASP_474	OD2	3.415
3J70	P_LYS_487	NZ	P_GLU_47	OE2	3.605
3J70	P_LYS_487	NZ	P_GLU_91	OE2	2.797
3J70	R_ARG_38	NH1	R_ASP_86	OD1	3.866
3J70	R_ARG_38	NH2	R_GLU_46	OE1	2.795
3J70	R_ARG_38	NH2	R_ASP_86	OD1	2.824
3J70	R_LYS_62	NZ	R_GLU_46	OE2	2.814
3J70	R_ARG_64	NH2	S_ASP_1	OD1	2.677
3J70	R_ARG_66	NH2	R_ASP_86	OD2	2.896
3J70	R_ARG_83	NH2	R_GLU_85	OE2	3.748
3J70	R_LYS_209	NZ	S_GLU_123	OE1	3.743
3J70	R_LYS_209	NZ	S_GLU_123	OE2	2.603
3J70	R_LYS_210	NZ	R_GLU_212	OE1	3.567
3J70	R_LYS_214	NZ	R_GLU_212	OE1	3.762
3J70	R_LYS_214	NZ	R_GLU_212	OE2	3.584
3J70	S_ARG_61	NH2	S_ASP_82	OD1	2.798
3J70	S_ARG_61	NH2	S_ASP_82	OD2	2.800
3J70	S_LYS_103	NZ	S_GLU_165	OE1	2.848
3J70	S_LYS_103	NZ	S_GLU_165	OE2	3.750
3J70	S_ARG_108	NH1	S_ASP_170	OD2	3.190
3J70	S_LYS_149	NZ	S_GLU_195	OE1	3.334
3J70	S_LYS_149	NZ	S_GLU_195	OE2	2.862
3J70	T_LYS_8	NZ	T_GLU_119	OE1	2.764
3J70	T_HIS_27	ND1	T_GLU_85	OE1	3.187
3J70	T_LYS_29	NZ	T_GLU_85	OE1	3.965
3J70	T_LYS_29	NZ	U_ASP_279	OD2	2.704
3J70	T_LYS_46	NZ	T_ASP_56	OD1	2.811
3J70	T_LYS_50	NZ	T_GLU_77	OE1	2.766
3J70	T_LYS_50	NZ	T_GLU_77	OE2	3.346
3J70	T_ARG_54	NH1	T_ASP_78	OD2	2.876
3J70	T_ARG_54	NH2	T_ASP_78	OD1	2.822
3J70	T_ARG_54	NH2	T_ASP_78	OD2	2.826
3J70	T_ARG_59	NH1	U_ASP_368	OD1	3.842
3J70	T_ARG_59	NH1	U_ASP_368	OD2	2.986
3J70	T_ARG_59	NH2	U_ASP_368	OD1	2.621
3J70	T_ARG_59	NH2	U_ASP_368	OD2	3.174
3J70	T_LYS_72	NZ	T_ASP_56	OD2	2.565
3J70	T_LYS_90	NZ	T_GLU_85	OE2	2.710
3J70	T_HIS_107	ND1	T_ASP_105	OD2	3.850
3J70	T_ARG_134	NH2	T_ASP_153	OD1	3.650
3J70	T_ARG_134	NH2	T_ASP_153	OD2	3.960
3J70	U_LYS_46	NZ	U_GLU_492	OE1	2.842

3J70	U_LYS_46	NZ	U_GLU_492	OE2	2.835
3J70	U_LYS_130	NZ	U_GLU_150	OE2	2.774
3J70	U_ARG_146	NH1	T_GLU_169	OE1	2.840
3J70	U_ARG_146	NH1	T_GLU_169	OE2	2.796
3J70	U_ARG_146	NH2	T_GLU_169	OE1	3.599
3J70	U_LYS_171	NZ	T_GLU_13	OE1	3.949
3J70	U_LYS_192	NZ	U_ASP_137	OD2	2.718
3J70	U_LYS_207	NZ	U_GLU_381	OE2	2.777
3J70	U_HIS_249	NE2	U_GLU_482	OE1	2.776
3J70	U_LYS_282	NZ	U_ASP_279	OD1	2.794
3J70	U_LYS_322	NZ	R_ASP_95	OD2	2.909
3J70	U_ARG_327	NH2	R_ASP_52	OD2	3.287
3J70	U_LYS_337	NZ	U_GLU_293	OE2	2.865
3J70	U_LYS_348	NZ	U_GLU_269	OE1	2.778
3J70	U_LYS_348	NZ	U_GLU_269	OE2	3.998
3J70	U_ARG_419	NH1	R_ASP_54	OD1	3.985
3J70	U_ARG_456	NH1	U_GLU_466	OE1	2.869
3J70	U_ARG_456	NH1	U_GLU_466	OE2	2.877
3J70	U_ARG_469	NH1	U_ASP_457	OD1	2.823
3J70	U_ARG_469	NH1	U_ASP_457	OD2	3.449
3J70	U_ARG_469	NH2	U_ASP_457	OD2	3.356
3J70	U_ARG_476	NH1	U_ASP_474	OD1	2.860
3J70	U_ARG_480	NH1	U_ASP_474	OD2	2.861
3J70	U_ARG_480	NH1	U_ASP_477	OD1	2.641
3J70	U_ARG_480	NH1	U_ASP_477	OD2	3.954
3J70	U_ARG_480	NH2	U_ASP_474	OD2	3.415
3J70	U_LYS_487	NZ	U_GLU_47	OE2	3.606
3J70	U_LYS_487	NZ	U_GLU_91	OE2	2.796

Table 428: 3J70-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3JCC	A_LYS_46	NZ	A_GLU_492	OE1	3.517
3JCC	A_LYS_227	NZ	A_GLU_83	OE2	3.448
3JCC	A_ARG_429	NH2	D_ASP_63	OD2	3.854
3JCC	A_ARG_456	NH2	A_GLU_466	OE1	3.660
3JCC	A_ARG_456	NH2	A_GLU_466	OE2	3.547
3JCC	A_ARG_469	NH2	A_ASP_457	OD2	3.023
3JCC	A_ARG_476	NH1	A_ASP_474	OD1	3.399
3JCC	A_ARG_476	NH1	A_ASP_474	OD2	2.964
3JCC	A_ARG_480	NH2	A_ASP_477	OD1	2.803
3JCC	A_LYS_485	NZ	A_GLU_267	OE2	3.722
3JCC	A_LYS_487	NZ	A_ASP_47	OD2	3.970
3JCC	B_ARG_61	NH1	B_ASP_82	OD2	2.931
3JCC	B_ARG_61	NH2	B_ASP_82	OD1	3.215
3JCC	B_ARG_61	NH2	B_ASP_82	OD2	3.003
3JCC	B_HIS_189	ND1	B_ASP_152	OD2	2.901
3JCC	C_ARG_38	NH1	C_ASP_86	OD1	2.894
3JCC	C_ARG_38	NH2	C_GLU_46	OE1	2.884
3JCC	C_ARG_38	NH2	C_ASP_86	OD1	3.828
3JCC	C_ARG_66	NH1	C_ASP_86	OD1	3.699
3JCC	C_ARG_66	NH1	C_ASP_86	OD2	2.932
3JCC	C_ARG_66	NH2	C_ASP_86	OD1	3.002
3JCC	C_ARG_66	NH2	C_ASP_86	OD2	3.413
3JCC	C_LYS_73	NZ	C_ASP_53	OD1	3.190
3JCC	C_LYS_73	NZ	C_ASP_53	OD2	3.723
3JCC	C_LYS_207	NZ	B_GLU_124	OE1	3.629
3JCC	D_LYS_8	NZ	D_GLU_119	OE1	3.039
3JCC	D_LYS_8	NZ	D_GLU_119	OE2	3.886
3JCC	D_LYS_29	NZ	D_GLU_85	OE1	2.956
3JCC	D_LYS_29	NZ	D_GLU_85	OE2	3.072
3JCC	D_ARG_54	NH1	D_ASP_78	OD2	2.902
3JCC	D_ARG_54	NH2	D_ASP_78	OD1	3.053
3JCC	D_ARG_54	NH2	D_ASP_78	OD2	2.965
3JCC	D_ARG_58	NH1	D_GLU_13	OE1	3.576
3JCC	D_ARG_58	NH1	D_GLU_13	OE2	3.174
3JCC	D_ARG_58	NH2	D_GLU_13	OE1	2.940
3JCC	D_ARG_58	NH2	D_GLU_13	OE2	3.860
3JCC	D_ARG_59	NH2	A_ASP_368	OD1	2.961
3JCC	D_ARG_59	NH2	A_ASP_368	OD2	3.986
3JCC	E_LYS_46	NZ	E_GLU_492	OE1	3.569
3JCC	E_LYS_46	NZ	E_GLU_492	OE2	3.703
3JCC	E_LYS_97	NZ	E_GLU_275	OE2	3.827
3JCC	E_LYS_227	NZ	E_GLU_83	OE1	3.969
3JCC	E_LYS_227	NZ	E_GLU_83	OE2	3.697
3JCC	E_LYS_282	NZ	E_GLU_275	OE1	3.981
3JCC	E_ARG_298	NH2	E_GLU_381	OE1	3.660
3JCC	E_ARG_298	NH2	E_GLU_381	OE2	3.777
3JCC	E_LYS_305	NZ	E_ASP_321	OD2	3.131
3JCC	E_ARG_456	NH1	E_GLU_466	OE1	3.660
3JCC	E_ARG_456	NH1	E_GLU_466	OE2	3.969
3JCC	E_ARG_456	NH2	E_GLU_466	OE1	3.908
3JCC	E_ARG_456	NH2	E_GLU_466	OE2	3.604
3JCC	E_ARG_469	NH1	E_ASP_457	OD1	3.767
3JCC	E_ARG_480	NH1	E_ASP_477	OD1	3.074
3JCC	E_LYS_485	NZ	E_GLU_267	OE2	3.897
3JCC	E_LYS_487	NZ	E_ASP_47	OD2	3.681
3JCC	E_LYS_490	NZ	E_GLU_49	OE2	2.934
3JCC	I_LYS_46	NZ	I_GLU_492	OE1	3.919

3JCC	I_ARG_166	NH2	I_ASP_167	OD2	3.510
3JCC	I_LYS_227	NZ	I_GLU_83	OE2	3.974
3JCC	I_LYS_305	NZ	I_ASP_321	OD2	3.762
3JCC	I_ARG_456	NH2	I_GLU_466	OE1	3.385
3JCC	I_ARG_456	NH2	I_GLU_466	OE2	3.431
3JCC	I_ARG_476	NH1	I_ASP_474	OD2	3.645
3JCC	I_ARG_480	NH1	I_ASP_477	OD1	3.186
3JCC	I_LYS_490	NZ	I_GLU_49	OE2	3.753

Table 429: 3JCC-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3KS0	L_ARG_63	NH2	L_GLU_83	OE2	3.743
3KS0	L_ARG_63	NH2	L_ASP_84	OD1	3.432
3KS0	L_ARG_63	NH2	L_ASP_84	OD2	3.922
3KS0	L_LYS_113	NZ	L_GLU_201	OE1	3.009
3KS0	H_ARG_38	NH1	H_ASP_89	OD1	2.927
3KS0	H_ARG_38	NH2	H_GLU_46	OE1	2.737
3KS0	H_LYS_39	NZ	L_GLU_40	OE1	3.686
3KS0	H_LYS_39	NZ	L_GLU_40	OE2	2.843
3KS0	H_ARG_66	NH1	H_ASP_89	OD1	2.901
3KS0	H_ARG_66	NH1	H_ASP_89	OD2	3.003
3KS0	H_ARG_66	NH2	H_ASP_89	OD1	3.781
3KS0	H_ARG_97	NH2	H_ASP_105	OD1	3.237
3KS0	H_ARG_97	NH2	H_ASP_105	OD2	2.854
3KS0	H_LYS_147	NZ	L_GLU_127	OE2	3.112
3KS0	H_LYS_212	NZ	L_GLU_126	OE1	3.920
3KS0	H_LYS_212	NZ	L_GLU_126	OE2	3.042
3KS0	A_LYS_18	NZ	A_GLU_15	OE2	3.032
3KS0	A_HIS_19	ND1	A_GLU_15	OE1	3.858
3KS0	A_HIS_19	NE2	A_GLU_15	OE1	3.591
3KS0	A_HIS_19	NE2	A_ASP_24	OD1	3.901
3KS0	A_HIS_19	NE2	A_ASP_24	OD2	3.803
3KS0	A_LYS_79	NZ	A_ASP_35	OD2	3.088
3KS0	A_LYS_80	NZ	A_ASP_72	OD1	2.255
3KS0	A_LYS_80	NZ	A_ASP_72	OD2	3.580
3KS0	J_ARG_63	NH2	J_GLU_83	OE2	3.774
3KS0	J_ARG_63	NH2	J_ASP_84	OD1	2.968
3KS0	J_ARG_63	NH2	J_ASP_84	OD2	3.838
3KS0	J_LYS_113	NZ	J_GLU_201	OE1	3.035
3KS0	J_HIS_191	NE2	J_ASP_154	OD2	3.977
3KS0	K_ARG_38	NH1	K_ASP_89	OD1	2.723
3KS0	K_ARG_38	NH2	K_GLU_46	OE1	2.728
3KS0	K_ARG_38	NH2	K_GLU_46	OE2	3.919
3KS0	K_LYS_39	NZ	J_GLU_40	OE1	3.754
3KS0	K_LYS_39	NZ	J_GLU_40	OE2	2.934
3KS0	K_ARG_66	NH1	K_ASP_89	OD1	3.466
3KS0	K_ARG_66	NH1	K_ASP_89	OD2	2.993
3KS0	K_ARG_66	NH2	K_ASP_89	OD1	3.246
3KS0	K_ARG_97	NH1	K_ASP_27	OD2	3.899
3KS0	K_ARG_97	NH2	K_ASP_105	OD1	3.477
3KS0	K_ARG_97	NH2	K_ASP_105	OD2	3.126
3KS0	K_LYS_147	NZ	J_GLU_127	OE2	3.169
3KS0	K_LYS_212	NZ	J_GLU_126	OE1	3.344
3KS0	K_LYS_212	NZ	J_GLU_126	OE2	2.562
3KS0	B_LYS_18	NZ	B_GLU_15	OE2	3.407
3KS0	B_HIS_19	NE2	B_GLU_15	OE1	3.733
3KS0	B_HIS_19	NE2	B_ASP_24	OD1	3.929
3KS0	B_LYS_79	NZ	B_ASP_35	OD2	3.032
3KS0	B_LYS_80	NZ	B_ASP_72	OD1	2.482
3KS0	B_LYS_80	NZ	B_ASP_72	OD2	3.798

Table 430: 3KS0-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3L7E	L_ARG_61	NH1	L_ASP_82	OD1	3.610
3L7E	L_ARG_61	NH1	L_ASP_82	OD2	2.820
3L7E	L_ARG_61	NH2	L_GLU_79	OE1	3.380
3L7E	L_ARG_61	NH2	L_GLU_79	OE2	3.052
3L7E	L_ARG_61	NH2	L_ASP_82	OD1	3.146
3L7E	L_ARG_61	NH2	L_ASP_82	OD2	3.585
3L7E	L_LYS_103	NZ	L_GLU_165	OE1	2.700
3L7E	L_LYS_145	NZ	L_GLU_161	OE1	3.739
3L7E	L_LYS_145	NZ	L_GLU_161	OE2	2.941
3L7E	L_LYS_149	NZ	L_GLU_195	OE2	3.782
3L7E	H_ARG_40	NH1	H_ASP_91	OD1	2.619
3L7E	H_ARG_40	NH2	H_GLU_48	OE1	3.221
3L7E	H_ARG_40	NH2	H_ASP_91	OD1	3.670
3L7E	H_ARG_68	NH1	H_ASP_91	OD1	3.997
3L7E	H_ARG_68	NH1	H_ASP_91	OD2	3.070
3L7E	H_ARG_68	NH2	H_ASP_91	OD1	3.385
3L7E	H_ARG_68	NH2	H_ASP_91	OD2	3.481
3L7E	H_ARG_99	NH2	H_ASP_109	OD1	3.758
3L7E	H_ARG_99	NH2	H_ASP_109	OD2	2.966
3L7E	H_LYS_151	NZ	H_ASP_152	OD1	3.202
3L7E	H_LYS_151	NZ	H_ASP_152	OD2	3.603
3L7E	H_LYS_214	NZ	H_ASP_216	OD2	3.774
3L7E	H_LYS_217	NZ	L_GLU_123	OE1	3.175
3L7E	H_LYS_218	NZ	H_GLU_220	OE2	2.784
3L7E	A_ARG_61	NH1	A_ASP_82	OD1	3.894
3L7E	A_ARG_61	NH1	A_ASP_82	OD2	2.738
3L7E	A_ARG_61	NH2	A_GLU_79	OE1	3.630
3L7E	A_ARG_61	NH2	A_GLU_79	OE2	3.597
3L7E	A_ARG_61	NH2	A_ASP_82	OD1	2.858
3L7E	A_ARG_61	NH2	A_ASP_82	OD2	3.208
3L7E	A_LYS_103	NZ	A_GLU_165	OE1	2.858
3L7E	A_LYS_103	NZ	A_GLU_165	OE2	3.136
3L7E	A_LYS_149	NZ	A_GLU_195	OE1	2.753
3L7E	A_ARG_211	NH2	A_GLU_187	OE2	3.405
3L7E	B_ARG_40	NH1	B_ASP_91	OD1	2.997
3L7E	B_ARG_40	NH2	B_GLU_48	OE1	3.270
3L7E	B_ARG_40	NH2	B_GLU_48	OE2	3.888
3L7E	B_ARG_40	NH2	B_ASP_91	OD1	3.815
3L7E	B_LYS_59	NZ	B_ASP_57	OD1	3.071
3L7E	B_LYS_59	NZ	B_ASP_57	OD2	3.376
3L7E	B_ARG_68	NH1	B_ASP_91	OD2	3.159
3L7E	B_ARG_68	NH2	B_ASP_91	OD1	2.945
3L7E	B_ARG_68	NH2	B_ASP_91	OD2	2.970
3L7E	B_ARG_99	NH2	B_ASP_109	OD1	3.495
3L7E	B_ARG_99	NH2	B_ASP_109	OD2	2.485
3L7E	B_LYS_151	NZ	B_ASP_152	OD1	3.115
3L7E	B_LYS_151	NZ	B_ASP_152	OD2	3.672
3L7E	B_LYS_217	NZ	A_GLU_123	OE1	2.697
3L7E	B_LYS_217	NZ	A_GLU_123	OE2	3.970
3L7E	B_LYS_218	NZ	B_GLU_220	OE2	3.907

Table 431: 3L7E-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3LZF	A_LYS_53	NZ	A_ASP_276	OD1	3.007
3LZF	A_LYS_63	NZ	A_GLU_75	OE1	3.244
3LZF	A_ARG_109	NH1	A_GLU_89	OE1	2.815
3LZF	A_ARG_109	NH1	A_GLU_89	OE2	3.490
3LZF	A_ARG_109	NH2	A_GLU_89	OE1	3.694
3LZF	A_ARG_109	NH2	A_GLU_89	OE2	3.025
3LZF	A_ARG_109	NH2	B_GLU_69	OE1	3.970
3LZF	A_ARG_109	NH2	B_GLU_69	OE2	2.555
3LZF	A_LYS_133A	NZ	A_GLU_131	OE1	3.911
3LZF	A_ARG_149	NH2	A_ASP_77	OD1	3.274
3LZF	A_ARG_149	NH2	A_ASP_77	OD2	2.737
3LZF	A_LYS_157	NZ	H_ASP_52	OD1	3.712
3LZF	A_LYS_157	NZ	H_ASP_52	OD2	3.952
3LZF	A_LYS_157	NZ	H_ASP_54	OD2	2.960
3LZF	A_LYS_163	NZ	A_GLU_246	OE1	3.633
3LZF	A_LYS_166	NZ	L_ASP_93	OD1	2.890
3LZF	A_LYS_166	NZ	L_ASP_93	OD2	2.667
3LZF	A_LYS_174	NZ	A_GLU_119	OE1	2.507
3LZF	A_LYS_174	NZ	A_GLU_119	OE2	3.039
3LZF	A_HIS_184	ND1	A_GLU_216	OE1	3.917
3LZF	A_LYS_208	NZ	A_GLU_238	OE2	3.278
3LZF	A_ARG_262	NH2	A_GLU_175	OE1	3.039
3LZF	A_ARG_262	NH2	A_GLU_175	OE2	3.035
3LZF	A_ARG_310	NH1	B_ASP_90	OD1	2.412
3LZF	A_ARG_310	NH2	B_ASP_90	OD1	3.228
3LZF	A_ARG_315	NH1	A_ASP_24	OD2	3.770
3LZF	A_ARG_321	NH1	A_GLU_31	OE1	3.446
3LZF	A_ARG_321	NH1	A_GLU_31	OE2	3.361
3LZF	B_LYS_51	NZ	B_GLU_103	OE1	2.812
3LZF	B_LYS_68	NZ	A_GLU_110	OE1	3.290
3LZF	B_LYS_68	NZ	A_GLU_110	OE2	2.778
3LZF	B_LYS_82	NZ	B_ASP_86	OD2	3.052
3LZF	B_ARG_116	NH2	B_GLU_120	OE1	3.732
3LZF	B_ARG_116	NH2	B_GLU_120	OE2	3.831
3LZF	B_LYS_123	NZ	B_GLU_132	OE2	2.843
3LZF	B_LYS_143	NZ	B_GLU_29	OE1	3.843
3LZF	B_LYS_143	NZ	B_GLU_29	OE2	3.948
3LZF	B_ARG_153	NH2	B_GLU_150	OE2	3.778
3LZF	H_ARG_38	NH1	H_ASP_86	OD1	2.752
3LZF	H_ARG_38	NH2	H_GLU_46	OE1	2.805
3LZF	H_ARG_38	NH2	H_ASP_86	OD1	3.834
3LZF	H_ARG_66	NH1	H_ASP_86	OD2	3.179
3LZF	H_ARG_66	NH2	H_ASP_86	OD1	3.026
3LZF	H_ARG_66	NH2	H_ASP_86	OD2	3.038
3LZF	H_LYS_71	NZ	H_ASP_55	OD1	2.502
3LZF	H_ARG_94	NH2	H_ASP_101	OD2	2.420
3LZF	H_ARG_97	NH1	H_ASP_52	OD1	2.811
3LZF	H_ARG_97	NH1	H_ASP_52	OD2	3.899
3LZF	H_ARG_97	NH2	H_ASP_52	OD1	2.854
3LZF	H_ARG_97	NH2	H_ASP_52	OD2	2.731
3LZF	H_ARG_97	NH2	H_ASP_53	OD1	2.942
3LZF	H_ARG_100D	NH2	H_ASP_100A	OD2	2.691
3LZF	H_LYS_145	NZ	H_ASP_146	OD1	3.565
3LZF	H_LYS_221	NZ	L_GLU_123	OE2	3.483
3LZF	L_ARG_61	NH2	L_ASP_82	OD1	3.298
3LZF	L_ARG_61	NH2	L_ASP_82	OD2	3.277
3LZF	L_LYS_103	NZ	L_ASP_85	OD1	3.336

3LZF	L.LYS_166	NZ	L.GLU_83	OE1	2.813
3LZF	L.HIS_189	ND1	L.ASP_	OD2	3.741

Table 432: 3LZF-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3M18	A_ARG_55	NH1	A_ASP_80	OD1	3.709
3M18	A_ARG_136	NH2	A_GLU_134	OE2	2.915
3M18	A_LYS_232	NZ	A_ASP_230	OD1	3.832
3M18	A_LYS_232	NZ	A_ASP_230	OD2	2.770
3M18	A_ARG_235	NH2	A_ASP_224	OD1	3.588
3M18	A_ARG_235	NH2	A_ASP_224	OD2	3.213
3M18	B_LYS_1	NZ	B_GLU_7	OE2	2.569
3M18	B_LYS_13	NZ	B_ASP_18	OD2	3.673
3M18	B_ARG_61	NH1	B_ASP_48	OD2	3.299
3M18	B_ARG_125	NH1	B_ASP_119	OD2	3.044
3M18	B_ARG_125	NH2	B_ASP_119	OD1	3.195
3M18	B_ARG_125	NH2	B_ASP_119	OD2	3.443

Table 433: 3M18-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID residue name residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3M19	A_LYS_59	NZ	A_GLU_37	OE2	3.221
3M19	A_HIS_104	ND1	A_ASP_79	OD1	3.554
3M19	A_HIS_104	NE2	A_ASP_79	OD1	3.514
3M19	A_HIS_104	NE2	A_ASP_79	OD2	3.839
3M19	A_ARG_128	NH1	A_ASP_103	OD2	3.998
3M19	A_ARG_128	NH2	A_ASP_103	OD2	3.816
3M19	A_ARG_136	NH2	A_GLU_134	OE2	2.501
3M19	A_LYS_243	NZ	A_GLU_245	OE2	3.905
3M19	B_HIS_104	ND1	B_ASP_79	OD1	3.606
3M19	B_HIS_104	NE2	B_ASP_79	OD1	3.640
3M19	B_HIS_104	NE2	B_ASP_79	OD2	3.894
3M19	B_ARG_128	NH1	B_ASP_103	OD2	3.698
3M19	B_ARG_128	NH2	B_ASP_103	OD2	3.517
3M19	B_ARG_136	NH2	B_GLU_134	OE1	2.918
3M19	B_ARG_136	NH2	B_GLU_134	OE2	3.574
3M19	B_LYS_152	NZ	B_ASP_127	OD1	3.986
3M19	B_LYS_152	NZ	B_ASP_127	OD2	3.666
3M19	B_ARG_194	NH2	B_ASP_191	OD2	3.254

Table 434: 3M19-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3MLR	L_LYS_27	NZ	L_ASP_92	OD1	2.852
3MLR	L_LYS_31	NZ	L_ASP_30	OD1	3.628
3MLR	L_LYS_31	NZ	L_ASP_30	OD2	3.071
3MLR	L_ARG_61	NH1	L_ASP_82	OD1	3.647
3MLR	L_ARG_61	NH1	L_ASP_82	OD2	2.892
3MLR	L_ARG_61	NH2	L_ASP_82	OD1	2.845
3MLR	L_ARG_61	NH2	L_ASP_82	OD2	3.527
3MLR	L_LYS_66	NZ	L_ASP_51	OD1	3.042
3MLR	L_LYS_66	NZ	L_ASP_51	OD2	3.142
3MLR	L_ARG_106A	NH2	L_ASP_85	OD1	3.458
3MLR	L_ARG_106A	NH2	L_ASP_85	OD2	3.111
3MLR	L_LYS_153	NZ	L_GLU_207	OE2	3.546
3MLR	H_ARG_38	NH2	H_GLU_46	OE1	2.819
3MLR	H_ARG_94	NH2	H_ASP_101	OD1	3.334
3MLR	H_ARG_94	NH2	H_ASP_101	OD2	2.709
3MLR	H_LYS_129	NZ	L_ASP_142	OD2	3.806
3MLR	H_LYS_209	NZ	L_GLU_127	OE2	3.182
3MLR	P_LYS_304	NZ	H_ASP_31	OD1	3.470
3MLR	P_LYS_305	NZ	H_ASP_54	OD1	2.683
3MLR	P_LYS_305	NZ	H_ASP_54	OD2	3.624
3MLR	P_LYS_305	NZ	H_ASP_56	OD2	3.011

Table 435: 3MLR-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3MLS	L_LYS_27	NZ	L_ASP_92	OD1	3.433
3MLS	L_LYS_27	NZ	L_ASP_92	OD2	3.469
3MLS	L_LYS_31	NZ	L_ASP_30	OD1	3.032
3MLS	L_LYS_31	NZ	L_ASP_30	OD2	2.898
3MLS	L_ARG_61	NH1	L_ASP_82	OD1	3.401
3MLS	L_ARG_61	NH2	L_ASP_82	OD1	3.515
3MLS	L_ARG_61	NH2	L_ASP_82	OD2	3.451
3MLS	L_LYS_66	NZ	L_ASP_51	OD1	3.260
3MLS	L_LYS_66	NZ	L_ASP_51	OD2	3.251
3MLS	L_LYS_69	NZ	L_ASP_29	OD1	3.080
3MLS	L_ARG_106A	NH2	L_ASP_85	OD1	3.981
3MLS	L_ARG_106A	NH2	L_ASP_85	OD2	3.840
3MLS	H_ARG_38	NH1	H_ASP_86	OD1	3.821
3MLS	H_ARG_38	NH2	H_GLU_46	OE1	3.613
3MLS	H_ARG_38	NH2	H_GLU_46	OE2	3.084
3MLS	H_LYS_73	NZ	H_ASP_53	OD1	3.435
3MLS	H_LYS_73	NZ	L_ASP_31	OD1	3.962
3MLS	H_LYS_73	NZ	L_ASP_31	OD2	2.716
3MLS	H_LYS_73	NZ	L_ASP_53	OD1	3.242
3MLS	H_LYS_73	NZ	L_ASP_53	OD2	3.339
3MLS	H_ARG_94	NH2	H_ASP_101	OD1	2.712
3MLS	H_ARG_94	NH2	H_ASP_101	OD2	2.782
3MLS	H_LYS_117	NZ	J_GLU_10	OE1	3.515
3MLS	H_LYS_143	NZ	L_GLU_128	OE2	2.664
3MLS	H_LYS_209	NZ	L_GLU_127	OE1	2.677
3MLS	H_LYS_210	NZ	H_GLU_212	OE2	2.981
3MLS	P_ARG_11	NH1	H_GLU_99	OE1	3.690
3MLS	P_ARG_11	NH1	H_GLU_99	OE2	3.548
3MLS	P_ARG_11	NH2	H_GLU_99	OE1	3.097
3MLS	P_ARG_11	NH2	H_GLU_99	OE2	3.355
3MLS	P_LYS_12	NZ	H_ASP_54	OD1	3.420
3MLS	P_LYS_12	NZ	H_ASP_54	OD2	2.807
3MLS	P_LYS_12	NZ	H_ASP_56	OD1	3.833
3MLS	P_LYS_12	NZ	H_ASP_56	OD2	3.175
3MLS	M_LYS_27	NZ	M_ASP_92	OD1	2.791
3MLS	M_LYS_27	NZ	M_ASP_92	OD2	3.981
3MLS	M_LYS_31	NZ	M_ASP_30	OD1	2.980
3MLS	M_LYS_31	NZ	M_ASP_30	OD2	3.022
3MLS	M_ARG_61	NH1	M_ASP_82	OD2	2.881
3MLS	M_ARG_61	NH2	M_ASP_82	OD1	3.067
3MLS	M_ARG_61	NH2	M_ASP_82	OD2	3.143
3MLS	M_LYS_66	NZ	M_ASP_51	OD1	3.245
3MLS	M_LYS_66	NZ	M_ASP_51	OD2	3.348
3MLS	M_LYS_69	NZ	M_ASP_29	OD1	3.369
3MLS	M_ARG_106A	NH2	M_ASP_85	OD1	3.977
3MLS	M_ARG_106A	NH2	M_ASP_85	OD2	3.547
3MLS	M_LYS_170	NZ	M_GLU_83	OE1	3.910
3MLS	I_ARG_38	NH2	I_GLU_46	OE1	2.757
3MLS	I_ARG_38	NH2	I_GLU_46	OE2	3.394
3MLS	I_ARG_94	NH2	I_ASP_101	OD1	3.196
3MLS	I_ARG_94	NH2	I_ASP_101	OD2	2.556
3MLS	I_LYS_143	NZ	M_GLU_128	OE2	2.744
3MLS	I_LYS_210	NZ	I_GLU_212	OE2	3.234
3MLS	Q_LYS_12	NZ	I_ASP_54	OD1	2.683
3MLS	Q_LYS_12	NZ	I_ASP_54	OD2	3.484
3MLS	Q_LYS_12	NZ	I_ASP_56	OD1	3.650
3MLS	N_LYS_27	NZ	N_ASP_92	OD1	2.638

3MLS	N_LYS_27	NZ	N_ASP_92	OD2	3.279
3MLS	N_LYS_31	NZ	N_ASP_92	OD1	3.789
3MLS	N_ARG_61	NH1	N_ASP_82	OD1	3.670
3MLS	N_ARG_61	NH1	N_ASP_82	OD2	2.886
3MLS	N_ARG_61	NH2	N_ASP_82	OD1	2.936
3MLS	N_ARG_61	NH2	N_ASP_82	OD2	3.467
3MLS	N_LYS_66	NZ	N_ASP_51	OD1	2.940
3MLS	N_LYS_66	NZ	N_ASP_51	OD2	2.905
3MLS	N_LYS_69	NZ	N_ASP_26	OD2	3.361
3MLS	N_LYS_97	NZ	J_GLU_64	OE2	3.402
3MLS	N_ARG_106A	NH1	N_ASP_85	OD1	3.854
3MLS	N_ARG_106A	NH2	N_ASP_85	OD1	3.571
3MLS	N_ARG_106A	NH2	N_ASP_85	OD2	3.057
3MLS	N_LYS_153	NZ	N_GLU_207	OE2	2.702
3MLS	N_HIS_192	ND1	N_ASP_155	OD1	2.942
3MLS	N_LYS_193	NZ	N_ASP_155	OD1	3.885
3MLS	N_LYS_193	NZ	N_ASP_155	OD2	3.535
3MLS	J_ARG_38	NH2	J_GLU_46	OE1	3.096
3MLS	J_ARG_38	NH2	J_GLU_46	OE2	3.226
3MLS	J_ARG_94	NH2	J_ASP_101	OD1	3.116
3MLS	J_ARG_94	NH2	J_ASP_101	OD2	2.667
3MLS	J_LYS_117	NZ	H_GLU_10	OE1	3.984
3MLS	J_LYS_209	NZ	N_GLU_127	OE2	3.428
3MLS	J_LYS_210	NZ	J_GLU_212	OE1	2.956
3MLS	J_LYS_210	NZ	J_GLU_212	OE2	3.284
3MLS	R_LYS_12	NZ	J_ASP_54	OD1	2.569
3MLS	R_LYS_12	NZ	J_ASP_54	OD2	3.629
3MLS	R_LYS_12	NZ	J_ASP_56	OD2	2.975
3MLS	O_LYS_27	NZ	O_ASP_92	OD1	3.055
3MLS	O_LYS_27	NZ	O_ASP_92	OD2	3.636
3MLS	O_LYS_31	NZ	O_ASP_30	OD1	3.500
3MLS	O_LYS_31	NZ	O_ASP_30	OD2	3.178
3MLS	O_ARG_61	NH1	O_ASP_82	OD1	3.846
3MLS	O_ARG_61	NH1	O_ASP_82	OD2	3.018
3MLS	O_ARG_61	NH2	O_ASP_82	OD1	2.964
3MLS	O_ARG_61	NH2	O_ASP_82	OD2	3.525
3MLS	O_LYS_66	NZ	O_ASP_51	OD1	3.127
3MLS	O_LYS_66	NZ	O_ASP_51	OD2	3.042
3MLS	O_LYS_69	NZ	O_ASP_26	OD1	3.632
3MLS	O_LYS_69	NZ	O_ASP_29	OD2	3.396
3MLS	O_ARG_106A	NH2	O_ASP_85	OD1	3.674
3MLS	O_ARG_106A	NH2	O_ASP_85	OD2	3.358
3MLS	O_LYS_153	NZ	O_GLU_207	OE1	2.594
3MLS	O_HIS_192	NE2	O_ASP_155	OD2	3.869
3MLS	K_ARG_38	NH2	K_GLU_46	OE1	2.675
3MLS	K_ARG_38	NH2	K_GLU_46	OE2	3.386
3MLS	K_ARG_94	NH1	K_ASP_101	OD1	2.987
3MLS	K_ARG_94	NH1	K_ASP_101	OD2	2.783
3MLS	K_LYS_117	NZ	L_GLU_10	OE1	3.985
3MLS	K_LYS_210	NZ	K_GLU_212	OE1	3.047
3MLS	S_LYS_12	NZ	K_ASP_54	OD1	2.573
3MLS	S_LYS_12	NZ	K_ASP_54	OD2	3.736
3MLS	S_LYS_12	NZ	K_ASP_56	OD2	3.122

Table 436: 3MLS-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3MLT	L.LYS_27	NZ	L.ASP_26	OD1	2.656
3MLT	L.LYS_31	NZ	L.ASP_92	OD1	3.056
3MLT	L.ARG_61	NH1	L.ASP_82	OD1	3.939
3MLT	L.ARG_61	NH1	L.ASP_82	OD2	2.821
3MLT	L.ARG_61	NH2	L.ASP_82	OD1	2.818
3MLT	L.ARG_61	NH2	L.ASP_82	OD2	3.100
3MLT	L.LYS_66	NZ	L.ASP_51	OD1	2.985
3MLT	L.ARG_106A	NH2	L.ASP_85	OD1	3.829
3MLT	L.ARG_106A	NH2	L.ASP_85	OD2	3.125
3MLT	H.ARG_38	NH2	H.GLU_46	OE1	3.303
3MLT	H.ARG_38	NH2	H.GLU_46	OE2	2.941
3MLT	H.ARG_94	NH2	H.ASP_101	OD1	3.578
3MLT	H.ARG_94	NH2	H.ASP_101	OD2	2.428
3MLT	P.ARG_304	NH1	H.ASP_31	OD1	2.766
3MLT	P.LYS_305	NZ	H.ASP_54	OD1	2.503
3MLT	P.LYS_305	NZ	H.ASP_54	OD2	3.276
3MLT	P.LYS_305	NZ	H.ASP_56	OD2	2.482
3MLT	A.ARG_61	NH1	A.ASP_82	OD1	3.737
3MLT	A.ARG_61	NH1	A.ASP_82	OD2	2.967
3MLT	A.ARG_61	NH2	A.ASP_82	OD1	2.371
3MLT	A.ARG_61	NH2	A.ASP_82	OD2	3.018
3MLT	A.LYS_66	NZ	A.ASP_51	OD1	2.928
3MLT	A.LYS_66	NZ	A.ASP_51	OD2	3.040
3MLT	A.LYS_69	NZ	A.ASP_26	OD2	2.462
3MLT	A.ARG_106A	NH2	A.ASP_85	OD1	3.818
3MLT	A.ARG_106A	NH2	A.ASP_85	OD2	2.999
3MLT	A.LYS_114	NZ	A.GLU_202	OE2	3.077
3MLT	B.ARG_38	NH2	B.GLU_46	OE1	3.094
3MLT	B.ARG_38	NH2	B.GLU_46	OE2	3.367
3MLT	B.ARG_94	NH2	B.ASP_101	OD1	3.119
3MLT	B.ARG_94	NH2	B.ASP_101	OD2	2.679
3MLT	B.LYS_209	NZ	A.GLU_127	OE2	3.807
3MLT	C.LYS_305	NZ	B.ASP_54	OD1	3.099
3MLT	C.LYS_305	NZ	B.ASP_54	OD2	3.737
3MLT	C.LYS_305	NZ	B.ASP_56	OD2	3.095
3MLT	D.LYS_27	NZ	D.ASP_92	OD1	3.259
3MLT	D.LYS_27	NZ	D.ASP_92	OD2	3.970
3MLT	D.ARG_61	NH1	D.ASP_82	OD1	3.697
3MLT	D.ARG_61	NH1	D.ASP_82	OD2	3.252
3MLT	D.ARG_61	NH2	D.ASP_82	OD1	2.341
3MLT	D.ARG_61	NH2	D.ASP_82	OD2	3.303
3MLT	D.LYS_66	NZ	D.ASP_51	OD1	3.307
3MLT	D.ARG_106A	NH1	D.ASP_85	OD1	3.298
3MLT	D.ARG_106A	NH1	D.ASP_85	OD2	2.670
3MLT	E.ARG_38	NH2	E.GLU_46	OE1	2.985
3MLT	E.ARG_38	NH2	E.GLU_46	OE2	2.979
3MLT	E.LYS_73	NZ	E.ASP_53	OD1	3.727
3MLT	E.ARG_94	NH2	E.ASP_101	OD1	3.644
3MLT	E.ARG_94	NH2	E.ASP_101	OD2	2.588
3MLT	E.LYS_143	NZ	E.ASP_144	OD1	3.787
3MLT	E.LYS_209	NZ	D.GLU_127	OE2	3.591
3MLT	E.LYS_210	NZ	E.GLU_212	OE2	3.760
3MLT	G.LYS_27	NZ	G.ASP_92	OD2	2.642
3MLT	G.ARG_61	NH1	G.ASP_82	OD1	3.714
3MLT	G.ARG_61	NH1	G.ASP_82	OD2	2.758
3MLT	G.ARG_61	NH2	G.ASP_82	OD1	2.637
3MLT	G.ARG_61	NH2	G.ASP_82	OD2	2.852

3MLT	G_LYS_66	NZ	G_ASP_51	OD1	3.206
3MLT	G_LYS_66	NZ	G_ASP_51	OD2	2.686
3MLT	G_LYS_69	NZ	G_ASP_26	OD2	3.323
3MLT	G_ARG_106A	NH2	G_ASP_85	OD1	3.421
3MLT	G_ARG_106A	NH2	G_ASP_85	OD2	2.884
3MLT	G_LYS_153	NZ	G_GLU_207	OE2	2.787
3MLT	I_ARG_38	NH2	I_GLU_46	OE1	3.057
3MLT	I_ARG_38	NH2	I_GLU_46	OE2	3.429
3MLT	I_LYS_73	NZ	I_ASP_53	OD1	3.113
3MLT	I_ARG_94	NH2	I_ASP_101	OD1	3.494
3MLT	I_ARG_94	NH2	I_ASP_101	OD2	2.793
3MLT	I_LYS_209	NZ	G_GLU_127	OE2	3.669
3MLT	I_LYS_210	NZ	I_GLU_212	OE2	3.480

Table 437: 3MLT-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID** **residue name** **residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3MLU	L_LYS_27	NZ	L_ASP_92	OD1	2.977
3MLU	L_LYS_27	NZ	L_ASP_92	OD2	3.686
3MLU	L_LYS_31	NZ	L_ASP_30	OD1	2.935
3MLU	L_ARG_61	NH1	L_ASP_82	OD1	3.030
3MLU	L_ARG_61	NH1	L_ASP_82	OD2	2.397
3MLU	L_ARG_61	NH2	L_ASP_82	OD1	3.188
3MLU	L_ARG_61	NH2	L_ASP_82	OD2	3.941
3MLU	L_LYS_66	NZ	L_ASP_51	OD1	3.330
3MLU	L_LYS_66	NZ	L_ASP_51	OD2	3.601
3MLU	L_LYS_69	NZ	L_ASP_29	OD1	3.656
3MLU	L_ARG_106A	NH1	L_ASP_85	OD1	2.728
3MLU	L_ARG_106A	NH1	L_ASP_85	OD2	2.846
3MLU	L_ARG_106A	NH2	L_ASP_85	OD2	3.672
3MLU	L_LYS_133	NZ	H_ASP_144	OD2	3.641
3MLU	H_ARG_38	NH2	H_GLU_46	OE1	2.684
3MLU	H_ARG_38	NH2	H_GLU_46	OE2	3.582
3MLU	H_ARG_94	NH2	H_ASP_101	OD1	3.350
3MLU	H_ARG_94	NH2	H_ASP_101	OD2	2.802
3MLU	H_LYS_143	NZ	H_ASP_144	OD1	3.930
3MLU	P_LYS_305	NZ	H_ASP_54	OD1	2.586
3MLU	P_LYS_305	NZ	H_ASP_54	OD2	3.496
3MLU	P_LYS_305	NZ	H_ASP_56	OD2	3.684

Table 438: 3MLU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3MLV	L_LYS_27	NZ	L_ASP_92	OD1	2.732
3MLV	L_LYS_27	NZ	L_ASP_92	OD2	3.328
3MLV	L_LYS_31	NZ	L_ASP_30	OD1	3.535
3MLV	L_LYS_31	NZ	L_ASP_30	OD2	3.503
3MLV	L_ARG_61	NH1	L_ASP_82	OD1	3.622
3MLV	L_ARG_61	NH1	L_ASP_82	OD2	2.916
3MLV	L_ARG_61	NH2	L_ASP_82	OD1	2.553
3MLV	L_ARG_61	NH2	L_ASP_82	OD2	3.370
3MLV	L_LYS_66	NZ	L_ASP_51	OD1	3.119
3MLV	L_LYS_66	NZ	L_ASP_51	OD2	3.196
3MLV	L_LYS_69	NZ	L_ASP_26	OD1	3.247
3MLV	L_ARG_106A	NH2	L_ASP_85	OD2	3.095
3MLV	L_LYS_153	NZ	L_GLU_207	OE2	3.705
3MLV	H_ARG_38	NH2	H_GLU_46	OE1	2.542
3MLV	H_LYS_73	NZ	H_ASP_53	OD1	3.402
3MLV	H_ARG_94	NH2	H_ASP_101	OD1	2.930
3MLV	H_ARG_94	NH2	H_ASP_101	OD2	2.968
3MLV	P_ARG_304	NH1	H_ASP_31	OD1	3.750
3MLV	P_LYS_305	NZ	H_ASP_54	OD1	2.508
3MLV	P_LYS_305	NZ	H_ASP_54	OD2	3.477
3MLV	P_LYS_305	NZ	H_ASP_56	OD2	2.918
3MLV	M_LYS_27	NZ	M_ASP_92	OD1	3.721
3MLV	M_LYS_27	NZ	M_ASP_92	OD2	3.379
3MLV	M_LYS_31	NZ	M_ASP_30	OD1	3.507
3MLV	M_LYS_31	NZ	M_ASP_30	OD2	3.277
3MLV	M_ARG_54	NH1	M_GLU_60	OE1	3.723
3MLV	M_ARG_61	NH1	M_ASP_82	OD2	2.841
3MLV	M_ARG_61	NH2	M_ASP_82	OD1	2.635
3MLV	M_ARG_61	NH2	M_ASP_82	OD2	2.881
3MLV	M_LYS_66	NZ	M_ASP_51	OD1	2.909
3MLV	M_LYS_66	NZ	M_ASP_51	OD2	3.135
3MLV	M_LYS_97	NZ	N_GLU_64	OE1	2.901
3MLV	M_ARG_106A	NH1	M_ASP_85	OD1	3.025
3MLV	M_ARG_106A	NH1	M_ASP_85	OD2	3.882
3MLV	M_LYS_133	NZ	M_GLU_128	OE2	3.108
3MLV	M_LYS_153	NZ	M_GLU_207	OE1	3.506
3MLV	M_LYS_153	NZ	M_GLU_207	OE2	2.957
3MLV	N_ARG_38	NH2	N_GLU_46	OE1	3.294
3MLV	N_ARG_38	NH2	N_GLU_46	OE2	3.518
3MLV	N_HIS_58	NE2	N_ASP_56	OD1	3.956
3MLV	N_ARG_94	NH2	N_ASP_101	OD1	2.759
3MLV	N_ARG_94	NH2	N_ASP_101	OD2	2.721
3MLV	N_LYS_117	NZ	N_ASP_144	OD2	3.293
3MLV	N_LYS_210	NZ	N_GLU_212	OE1	3.364
3MLV	Q_ARG_304	NH1	N_GLU_99	OE2	3.900
3MLV	Q_ARG_304	NH2	N_GLU_99	OE2	3.849
3MLV	Q_LYS_305	NZ	N_ASP_54	OD1	3.154
3MLV	Q_LYS_305	NZ	N_ASP_54	OD2	3.686
3MLV	Q_LYS_305	NZ	N_ASP_56	OD2	2.702

Table 439: 3MLV-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3MLW	L_ARG_50	NH1	H_ASP_100G	OD1	2.178
3MLW	L_ARG_50	NH1	H_ASP_100G	OD2	3.432
3MLW	L_ARG_61	NH1	L_ASP_82	OD1	3.181
3MLW	L_ARG_61	NH1	L_ASP_82	OD2	2.655
3MLW	L_ARG_61	NH2	L_ASP_82	OD1	3.279
3MLW	L_ARG_61	NH2	L_ASP_82	OD2	3.991
3MLW	L_LYS_66	NZ	L_ASP_51	OD1	3.270
3MLW	L_LYS_66	NZ	L_ASP_51	OD2	3.246
3MLW	L_ARG_95	NH2	L_ASP_95D	OD1	3.851
3MLW	L_ARG_95	NH2	L_ASP_95D	OD2	3.710
3MLW	L_LYS_129	NZ	H_ASP_144	OD2	3.472
3MLW	L_HIS_188	ND1	L_ASP_151	OD1	3.480
3MLW	H_LYS_12	NZ	H_GLU_10	OE2	3.873
3MLW	H_ARG_38	NH2	H_GLU_46	OE2	2.598
3MLW	H_ARG_58	NH1	L_ASP_95D	OD1	3.535
3MLW	H_ARG_58	NH1	L_ASP_95D	OD2	2.585
3MLW	H_ARG_66	NH1	H_GLU_83	OE1	3.904
3MLW	H_ARG_66	NH1	H_ASP_86	OD1	3.710
3MLW	H_ARG_66	NH1	H_ASP_86	OD2	3.995
3MLW	H_ARG_66	NH2	H_GLU_83	OE1	3.901
3MLW	H_ARG_66	NH2	H_ASP_86	OD1	3.540
3MLW	H_ARG_66	NH2	H_ASP_86	OD2	2.479
3MLW	H_LYS_143	NZ	H_ASP_144	OD1	3.302
3MLW	H_LYS_210	NZ	H_GLU_212	OE2	3.365
3MLW	P_LYS_303	NZ	H_ASP_31	OD2	3.075
3MLW	P_ARG_304	NH1	H_ASP_31	OD1	3.646
3MLW	P_LYS_305	NZ	H_ASP_54	OD1	3.646
3MLW	P_LYS_305	NZ	H_ASP_54	OD2	2.863
3MLW	P_LYS_305	NZ	H_ASP_56	OD1	3.537
3MLW	P_ARG_315	NH1	L_ASP_93	OD1	2.718
3MLW	P_ARG_315	NH1	L_ASP_93	OD2	3.239
3MLW	M_ARG_50	NH2	L_ASP_100G	OD1	2.708
3MLW	M_ARG_50	NH2	L_ASP_100G	OD2	3.923
3MLW	M_ARG_54	NH2	M_ASP_60	OD2	3.038
3MLW	M_ARG_61	NH1	M_ASP_82	OD1	3.703
3MLW	M_ARG_61	NH1	M_ASP_82	OD2	2.485
3MLW	M_ARG_61	NH2	M_ASP_82	OD1	3.327
3MLW	M_ARG_61	NH2	M_ASP_82	OD2	3.484
3MLW	M_LYS_66	NZ	M_ASP_51	OD1	3.422
3MLW	M_LYS_66	NZ	M_ASP_51	OD2	3.571
3MLW	M_ARG_95	NH2	M_ASP_95D	OD1	3.135
3MLW	M_ARG_95	NH2	M_ASP_95D	OD2	3.399
3MLW	M_LYS_149	NZ	M_GLU_203	OE1	3.625
3MLW	I_LYS_12	NZ	I_GLU_10	OE2	3.682
3MLW	I_ARG_58	NH1	M_ASP_95D	OD1	2.653
3MLW	I_ARG_58	NH1	M_ASP_95D	OD2	3.643
3MLW	I_ARG_66	NH1	L_ASP_86	OD1	3.246
3MLW	I_ARG_66	NH1	L_ASP_86	OD2	3.692
3MLW	I_ARG_66	NH2	L_ASP_86	OD1	3.577
3MLW	I_ARG_66	NH2	L_ASP_86	OD2	2.544
3MLW	I_LYS_143	NZ	L_ASP_144	OD1	3.053
3MLW	I_LYS_209	NZ	M_GLU_123	OE1	2.581
3MLW	I_LYS_209	NZ	M_GLU_123	OE2	3.213
3MLW	I_LYS_210	NZ	I_GLU_212	OE1	3.364
3MLW	Q_LYS_305	NZ	L_ASP_54	OD2	3.005
3MLW	Q_LYS_305	NZ	L_ASP_56	OD1	2.747
3MLW	Q_ARG_315	NH1	M_ASP_93	OD1	3.021

Table 440: 3MLW-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3MLX	L_LYS_53	NZ	L_GLU_50	OE1	2.558
3MLX	L_ARG_61	NH1	L_ASP_82	OD1	3.582
3MLX	L_ARG_61	NH1	L_ASP_82	OD2	2.890
3MLX	L_ARG_61	NH2	L_ASP_82	OD1	2.629
3MLX	L_ARG_61	NH2	L_ASP_82	OD2	3.257
3MLX	L_LYS_110	NZ	L_GLU_198	OE1	3.541
3MLX	L_LYS_110	NZ	L_GLU_198	OE2	2.823
3MLX	L_ARG_189	NH1	L_ASP_151	OD2	3.869
3MLX	H_ARG_38	NH1	H_ASP_86	OD1	2.668
3MLX	H_ARG_38	NH2	H_GLU_46	OE1	2.979
3MLX	H_ARG_38	NH2	H_ASP_86	OD1	3.494
3MLX	H_ARG_66	NH1	H_ASP_86	OD1	3.775
3MLX	H_ARG_66	NH1	H_ASP_86	OD2	3.101
3MLX	H_ARG_66	NH2	H_ASP_86	OD1	3.040
3MLX	H_ARG_66	NH2	H_ASP_86	OD2	3.650
3MLX	H_ARG_94	NH2	H_ASP_101	OD1	3.962
3MLX	H_ARG_94	NH2	H_ASP_101	OD2	2.675
3MLX	H_HIS_100	NE2	H_GLU_98	OE1	3.039
3MLX	H_ARG_100D	NH1	H_ASP_100B	OD1	3.189
3MLX	H_ARG_100D	NH1	H_ASP_100B	OD2	2.525
3MLX	H_ARG_100D	NH2	H_ASP_100B	OD2	3.445
3MLX	H_LYS_143	NZ	L_GLU_124	OE2	3.021
3MLX	H_LYS_143	NZ	H_ASP_144	OD2	3.971
3MLX	H_LYS_210	NZ	H_GLU_212	OE1	3.310
3MLX	P_HIS_308	ND1	H_GLU_98	OE2	3.800
3MLX	P_HIS_308	NE2	H_GLU_98	OE2	3.892
3MLX	M_LYS_53	NZ	M_GLU_50	OE1	2.998
3MLX	M_ARG_61	NH1	M_ASP_82	OD1	3.548
3MLX	M_ARG_61	NH1	M_ASP_82	OD2	2.848
3MLX	M_ARG_61	NH2	M_ASP_82	OD1	2.885
3MLX	M_ARG_61	NH2	M_ASP_82	OD2	3.369
3MLX	M_LYS_110	NZ	M_GLU_198	OE1	3.722
3MLX	M_LYS_110	NZ	M_GLU_198	OE2	2.779
3MLX	I_ARG_38	NH1	I_ASP_86	OD1	2.800
3MLX	I_ARG_38	NH2	I_GLU_46	OE1	2.963
3MLX	I_ARG_38	NH2	I_ASP_86	OD1	3.764
3MLX	I_ARG_66	NH1	I_ASP_86	OD1	3.651
3MLX	I_ARG_66	NH1	I_ASP_86	OD2	3.063
3MLX	I_ARG_66	NH2	I_ASP_86	OD1	2.826
3MLX	I_ARG_66	NH2	I_ASP_86	OD2	3.585
3MLX	I_ARG_94	NH2	I_ASP_101	OD1	3.940
3MLX	I_ARG_94	NH2	I_ASP_101	OD2	2.619
3MLX	I_ARG_100D	NH2	I_ASP_100B	OD1	3.500
3MLX	I_LYS_143	NZ	M_GLU_124	OE2	2.608
3MLX	I_LYS_214	NZ	M_GLU_123	OE1	3.588
3MLX	Q_HIS_308	ND1	I_GLU_98	OE1	3.280

Table 441: 3MLX-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3MLY	L_LYS_53	NZ	L_GLU_50	OE1	2.642
3MLY	L_ARG_61	NH1	L_ASP_82	OD1	3.644
3MLY	L_ARG_61	NH1	L_ASP_82	OD2	2.899
3MLY	L_ARG_61	NH2	L_ASP_82	OD1	2.860
3MLY	L_ARG_61	NH2	L_ASP_82	OD2	3.465
3MLY	L_LYS_110	NZ	L_GLU_198	OE2	2.940
3MLY	L_ARG_189	NH1	L_ASP_151	OD2	3.794
3MLY	L_ARG_189	NH2	L_ASP_151	OD1	3.939
3MLY	L_ARG_189	NH2	L_ASP_151	OD2	3.922
3MLY	H_ARG_38	NH1	H_ASP_86	OD1	2.772
3MLY	H_ARG_38	NH2	H_GLU_46	OE1	3.019
3MLY	H_ARG_38	NH2	H_ASP_86	OD1	3.609
3MLY	H_ARG_66	NH1	H_ASP_86	OD1	3.669
3MLY	H_ARG_66	NH1	H_ASP_86	OD2	3.034
3MLY	H_ARG_66	NH2	H_ASP_86	OD1	2.918
3MLY	H_ARG_66	NH2	H_ASP_86	OD2	3.605
3MLY	H_ARG_94	NH2	H_ASP_101	OD1	3.843
3MLY	H_ARG_94	NH2	H_ASP_101	OD2	2.725
3MLY	H_ARG_100D	NH1	H_ASP_100B	OD1	3.662
3MLY	H_ARG_100D	NH1	H_ASP_100B	OD2	2.984
3MLY	H_ARG_100D	NH2	H_ASP_100B	OD2	3.444
3MLY	H_LYS_143	NZ	L_GLU_124	OE2	3.991
3MLY	H_LYS_143	NZ	H_ASP_144	OD1	3.690
3MLY	H_LYS_143	NZ	H_ASP_144	OD2	3.304
3MLY	H_LYS_210	NZ	H_GLU_212	OE1	3.480
3MLY	H_LYS_214	NZ	L_GLU_123	OE1	3.745
3MLY	P_LYS_308	NZ	L_GLU_50	OE1	3.397
3MLY	P_LYS_308	NZ	L_GLU_50	OE2	3.390
3MLY	M_LYS_53	NZ	M_GLU_50	OE1	3.091
3MLY	M_ARG_61	NH1	M_ASP_82	OD1	3.807
3MLY	M_ARG_61	NH1	M_ASP_82	OD2	2.828
3MLY	M_ARG_61	NH2	M_ASP_82	OD1	2.920
3MLY	M_ARG_61	NH2	M_ASP_82	OD2	3.357
3MLY	M_LYS_110	NZ	M_GLU_198	OE1	3.945
3MLY	M_LYS_110	NZ	M_GLU_198	OE2	2.680
3MLY	I_ARG_38	NH1	I_ASP_86	OD1	2.750
3MLY	I_ARG_38	NH2	I_GLU_46	OE1	3.018
3MLY	I_ARG_38	NH2	I_ASP_86	OD1	3.672
3MLY	I_ARG_66	NH1	I_ASP_86	OD1	3.657
3MLY	I_ARG_66	NH1	I_ASP_86	OD2	2.961
3MLY	I_ARG_66	NH2	I_ASP_86	OD1	2.888
3MLY	I_ARG_66	NH2	I_ASP_86	OD2	3.536
3MLY	I_ARG_94	NH2	I_ASP_101	OD1	3.875
3MLY	I_ARG_94	NH2	I_ASP_101	OD2	2.678
3MLY	I_ARG_100D	NH2	I_ASP_100B	OD1	3.986
3MLY	I_ARG_100D	NH2	I_ASP_100B	OD2	3.120
3MLY	I_LYS_143	NZ	M_GLU_124	OE2	2.661
3MLY	I_LYS_214	NZ	M_GLU_123	OE1	3.594

Table 442: 3MLY-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3MLZ	L_LYS_	NZ	L_GLU_	OE1	2.997
3MLZ	L_ARG_	NH1	L_ASP_	OD1	3.594
3MLZ	L_ARG_	NH1	L_ASP_	OD2	2.458
3MLZ	L_ARG_	NH2	L_ASP_	OD1	3.627
3MLZ	L_ARG_	NH2	L_ASP_	OD2	3.688
3MLZ	H_ARG_	NH1	H_ASP_	OD1	2.831
3MLZ	H_ARG_	NH2	H_GLU_	OE1	2.975
3MLZ	H_ARG_	NH2	H_GLU_	OE2	3.939
3MLZ	H_ARG_	NH2	H_ASP_	OD1	3.724
3MLZ	H_ARG_	NH1	H_ASP_	OD1	3.168
3MLZ	H_ARG_	NH1	H_ASP_	OD2	2.769
3MLZ	H_ARG_	NH2	H_ASP_	OD1	2.975
3MLZ	H_ARG_	NH2	H_ASP_	OD2	3.884
3MLZ	H_ARG_	NH2	H_ASP_	OD1	3.878
3MLZ	H_ARG_	NH2	H_ASP_	OD2	3.028
3MLZ	H_HIS_	ND1	H_ASP_	OD2	3.791
3MLZ	H_HIS_	NE2	H_GLU_	OE1	3.406
3MLZ	H_HIS_	NE2	H_GLU_	OE2	3.681
3MLZ	H_ARG_	NH2	H_ASP_	OD2	2.582
3MLZ	H_LYS_	NZ	L_GLU_	OE1	3.724
3MLZ	H_LYS_	NZ	L_GLU_	OE2	3.184
3MLZ	H_LYS_	NZ	L_GLU_	OE2	2.805
3MLZ	H_LYS_	NZ	L_GLU_	OE1	3.039
3MLZ	H_LYS_	NZ	L_GLU_	OE2	3.262

Table 443: 3MLZ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3NFP	A_ARG_33	NH1	K_ASP_4	OD1	3.227
3NFP	A_ARG_33	NH2	K_ASP_6	OD1	3.995
3NFP	A_ARG_33	NH2	K_ASP_6	OD2	2.804
3NFP	A_HIS_35	NE2	K_ASP_4	OD1	3.568
3NFP	A_HIS_35	NE2	K_ASP_4	OD2	3.384
3NFP	A_ARG_38	NH1	A_GLU_46	OE1	3.521
3NFP	A_ARG_38	NH1	A_GLU_46	OE2	2.606
3NFP	A_ARG_38	NH2	A_GLU_46	OE1	3.385
3NFP	A_ARG_38	NH2	A_GLU_46	OE2	3.747
3NFP	A_LYS_63	NZ	A_GLU_46	OE1	3.380
3NFP	A_LYS_67	NZ	A_ASP_90	OD2	3.506
3NFP	A_LYS_146	NZ	A_ASP_147	OD1	3.848
3NFP	A_LYS_146	NZ	A_ASP_147	OD2	3.462
3NFP	B_LYS_38	NZ	B_ASP_80	OD1	3.548
3NFP	B_LYS_38	NZ	B_ASP_80	OD2	3.365
3NFP	B_ARG_60	NH2	B_ASP_81	OD1	2.805
3NFP	B_ARG_60	NH2	B_ASP_81	OD2	3.684
3NFP	B_LYS_125	NZ	B_GLU_122	OE1	3.467
3NFP	B_LYS_148	NZ	B_GLU_194	OE1	2.803
3NFP	B_LYS_148	NZ	B_GLU_194	OE2	3.777
3NFP	B_HIS_188	ND1	B_ASP_150	OD2	2.700
3NFP	H_ARG_33	NH1	I_ASP_4	OD2	2.868
3NFP	H_ARG_33	NH2	I_ASP_6	OD2	3.531
3NFP	H_HIS_35	NE2	I_ASP_4	OD1	3.314
3NFP	H_HIS_35	NE2	I_ASP_4	OD2	3.660
3NFP	H_ARG_38	NH2	H_GLU_46	OE1	3.221
3NFP	H_ARG_38	NH2	H_GLU_46	OE2	2.659
3NFP	H_LYS_67	NZ	H_ASP_90	OD2	3.005
3NFP	H_LYS_212	NZ	L_GLU_122	OE1	3.767
3NFP	L_LYS_38	NZ	L_ASP_80	OD1	3.309
3NFP	L_ARG_60	NH2	L_ASP_81	OD1	2.888
3NFP	L_ARG_60	NH2	L_ASP_81	OD2	3.365
3NFP	L_LYS_148	NZ	L_GLU_194	OE1	3.812
3NFP	L_LYS_148	NZ	L_GLU_194	OE2	2.763
3NFP	L_LYS_182	NZ	L_GLU_186	OE2	3.310
3NFP	L_HIS_188	ND1	L_ASP_150	OD2	3.342
3NFP	I_ARG_117	NH2	I_GLU_113	OE1	3.200
3NFP	I_ARG_117	NH2	I_GLU_113	OE2	2.798
3NFP	I_HIS_120	NE2	H_GLU_59	OE1	3.799
3NFP	I_HIS_120	NE2	H_GLU_59	OE2	3.285
3NFP	K_ARG_117	NH1	K_GLU_106	OE2	2.607
3NFP	K_ARG_117	NH2	K_GLU_113	OE1	3.049
3NFP	K_ARG_117	NH2	K_GLU_113	OE2	2.896
3NFP	K_HIS_120	NE2	A_GLU_59	OE2	3.393

Table 444: 3NFP-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3NGB	G_LYS_46	NZ	G_GLU_492	OE1	3.975
3NGB	G_LYS_	NZ	G_GLU_	OE1	3.767
3NGB	G_HIS_	NE2	G_GLU_	OE1	3.641
3NGB	G_HIS_	ND1	G_GLU_	OE2	2.917
3NGB	G_LYS_97	NZ	G_GLU_275	OE2	3.810
3NGB	G_LYS_97	NZ	H_ASP_99	OD2	3.903
3NGB	G_LYS_	NZ	G_GLU_	OE1	3.983
3NGB	G_LYS_	NZ	G_GLU_	OE2	3.483
3NGB	G_HIS_	NE2	G_GLU_	OE1	3.355
3NGB	G_LYS_282	NZ	G_GLU_275	OE1	3.701
3NGB	G_ARG_456	NH1	G_GLU_466	OE2	3.510
3NGB	G_ARG_469	NH2	G_ASP_457	OD1	2.956
3NGB	G_LYS_476	NZ	G_GLU_102	OE1	2.614
3NGB	G_ARG_480	NH1	G_ASP_477	OD1	2.964
3NGB	G_ARG_480	NH2	G_GLU_102	OE2	3.814
3NGB	G_LYS_487	NZ	G_ASP_47	OD1	2.938
3NGB	G_LYS_487	NZ	G_ASP_47	OD2	3.396
3NGB	G_LYS_487	NZ	G_GLU_91	OE1	2.798
3NGB	H_LYS_12	NZ	H_GLU_16	OE2	3.621
3NGB	H_ARG_38	NH1	H_GLU_46	OE1	3.003
3NGB	H_ARG_38	NH2	H_ASP_86	OD1	2.813
3NGB	H_ARG_66	NH1	H_ASP_86	OD1	3.475
3NGB	H_ARG_66	NH2	H_ASP_86	OD1	2.969
3NGB	H_ARG_66	NH2	H_ASP_86	OD2	2.693
3NGB	H_ARG_71	NH1	G_ASP_368	OD1	3.623
3NGB	H_ARG_71	NH1	G_ASP_368	OD2	3.004
3NGB	H_ARG_71	NH2	G_ASP_368	OD1	2.815
3NGB	H_ARG_71	NH2	G_ASP_368	OD2	3.723
3NGB	H_ARG_82A	NH1	H_GLU_81	OE2	3.784
3NGB	H_LYS_209	NZ	L_GLU_125	OE1	3.421
3NGB	H_LYS_209	NZ	L_GLU_125	OE2	3.841
3NGB	H_LYS_210	NZ	H_GLU_212	OE2	3.426
3NGB	L_ARG_61	NH1	L_ASP_82	OD2	2.817
3NGB	L_ARG_61	NH2	L_ASP_82	OD1	3.422
3NGB	L_ARG_61	NH2	L_ASP_82	OD2	2.949
3NGB	L_LYS_109	NZ	L_GLU_17	OE1	3.534
3NGB	L_LYS_151	NZ	L_GLU_197	OE2	3.936
3NGB	L_HIS_191	ND1	L_ASP_153	OD2	2.883
3NGB	L_HIS_191	NE2	L_ASP_187	OD2	3.579
3NGB	L_ARG_213	NH2	L_GLU_189	OE1	2.766
3NGB	A_LYS_46	NZ	A_GLU_492	OE1	3.410
3NGB	A_HIS_66	ND1	A_GLU_64	OE2	2.775
3NGB	A_LYS_97	NZ	B_ASP_99	OD2	3.768
3NGB	A_LYS_207	NZ	A_GLU_381	OE1	3.837
3NGB	A_LYS_207	NZ	A_GLU_381	OE2	2.908
3NGB	A_LYS_231	NZ	A_GLU_267	OE2	3.487
3NGB	A_HIS_249	NE2	A_GLU_482	OE1	3.108
3NGB	A_LYS_282	NZ	A_GLU_275	OE1	3.363
3NGB	A_LYS_343	NZ	A_GLU_405	OE2	2.857
3NGB	A_LYS_348	NZ	A_GLU_269	OE1	3.929
3NGB	A_LYS_348	NZ	A_GLU_269	OE2	3.717
3NGB	A_ARG_456	NH1	A_GLU_466	OE1	3.489
3NGB	A_ARG_469	NH2	A_ASP_457	OD1	2.818
3NGB	A_LYS_476	NZ	A_GLU_102	OE1	2.746
3NGB	A_ARG_480	NH1	A_ASP_477	OD1	3.036
3NGB	A_ARG_480	NH2	A_GLU_102	OE2	3.823
3NGB	A_LYS_487	NZ	A_ASP_47	OD1	3.201

3NGB	A_LYS_487	NZ	A_ASP_47	OD2	3.287
3NGB	A_LYS_487	NZ	A_GLU_91	OE1	2.776
3NGB	B_LYS_12	NZ	B_GLU_16	OE2	3.669
3NGB	B_ARG_38	NH1	B_ASP_86	OD1	3.017
3NGB	B_ARG_38	NH2	B_GLU_46	OE1	3.330
3NGB	B_ARG_38	NH2	B_GLU_46	OE2	3.608
3NGB	B_ARG_38	NH2	B_ASP_86	OD1	3.928
3NGB	B_ARG_66	NH1	B_ASP_86	OD1	3.986
3NGB	B_ARG_66	NH2	B_ASP_86	OD1	3.009
3NGB	B_ARG_66	NH2	B_ASP_86	OD2	2.581
3NGB	B_ARG_71	NH1	A_ASP_368	OD1	3.647
3NGB	B_ARG_71	NH1	A_ASP_368	OD2	2.944
3NGB	B_ARG_71	NH2	A_ASP_368	OD1	2.895
3NGB	B_ARG_71	NH2	A_ASP_368	OD2	3.718
3NGB	B_ARG_82A	NH1	B_GLU_81	OE2	3.349
3NGB	B_HIS_102	NE2	B_GLU_101	OE1	3.498
3NGB	B_LYS_209	NZ	C_GLU_125	OE1	2.774
3NGB	B_LYS_209	NZ	C_GLU_125	OE2	2.799
3NGB	C_ARG_61	NH1	C_ASP_82	OD2	2.721
3NGB	C_ARG_61	NH2	C_GLU_79	OE1	3.703
3NGB	C_ARG_61	NH2	C_ASP_82	OD1	3.248
3NGB	C_ARG_61	NH2	C_ASP_82	OD2	2.976
3NGB	C_LYS_109	NZ	C_GLU_17	OE1	3.524
3NGB	C_LYS_151	NZ	C_GLU_197	OE2	3.960
3NGB	C_LYS_185	NZ	C_GLU_189	OE2	3.711
3NGB	C_HIS_191	ND1	C_ASP_153	OD2	2.841
3NGB	C_ARG_213	NH2	C_GLU_189	OE1	2.808
3NGB	D_LYS_46	NZ	D_GLU_492	OE1	2.932
3NGB	D_HIS_66	ND1	D_GLU_64	OE2	2.933
3NGB	D_LYS_97	NZ	D_GLU_275	OE2	3.702
3NGB	D_LYS_97	NZ	E_ASP_99	OD1	3.709
3NGB	D_LYS_207	NZ	D_GLU_381	OE1	3.872
3NGB	D_LYS_207	NZ	D_GLU_381	OE2	3.299
3NGB	D_LYS_231	NZ	D_GLU_267	OE2	3.490
3NGB	D_HIS_249	NE2	D_GLU_482	OE1	3.177
3NGB	D_LYS_282	NZ	D_GLU_275	OE1	2.984
3NGB	D_LYS_282	NZ	D_GLU_275	OE2	3.901
3NGB	D_ARG_327	NH1	D_ASP_325	OD1	3.823
3NGB	D_LYS_348	NZ	D_GLU_269	OE2	3.794
3NGB	D_LYS_348	NZ	D_GLU_351	OE1	3.701
3NGB	D_ARG_456	NH1	D_GLU_466	OE2	3.539
3NGB	D_ARG_469	NH2	D_ASP_457	OD1	2.868
3NGB	D_LYS_476	NZ	D_GLU_102	OE1	2.805
3NGB	D_LYS_476	NZ	D_GLU_102	OE2	3.737
3NGB	D_ARG_480	NH1	D_ASP_477	OD1	2.794
3NGB	D_LYS_487	NZ	D_ASP_47	OD1	3.083
3NGB	D_LYS_487	NZ	D_ASP_47	OD2	3.202
3NGB	D_LYS_487	NZ	D_GLU_91	OE1	2.774
3NGB	E_LYS_12	NZ	E_GLU_16	OE2	3.601
3NGB	E_ARG_38	NH1	E_GLU_46	OE1	2.881
3NGB	E_ARG_38	NH2	E_ASP_86	OD1	2.976
3NGB	E_ARG_53	NH2	E_ASP_31	OD1	3.658
3NGB	E_ARG_66	NH2	E_ASP_86	OD1	2.908
3NGB	E_ARG_66	NH2	E_ASP_86	OD2	2.859
3NGB	E_ARG_71	NH1	D_ASP_368	OD1	3.715
3NGB	E_ARG_71	NH1	D_ASP_368	OD2	3.074
3NGB	E_ARG_71	NH2	D_ASP_368	OD1	3.026
3NGB	E_ARG_71	NH2	D_ASP_368	OD2	3.848

3NGB	E_ARG_82A	NH1	E_GLU_81	OE2	3.296
3NGB	E_LYS_	NZ	E_ASP_	OD1	3.774
3NGB	E_HIS_164	ND1	F_ASP_169	OD1	3.984
3NGB	E_LYS_	NZ	F_GLU_	OE1	3.345
3NGB	E_LYS_	NZ	F_GLU_	OE2	2.927
3NGB	F_ARG_61	NH1	F_ASP_82	OD2	3.066
3NGB	F_ARG_61	NH2	F_ASP_82	OD1	3.415
3NGB	F_ARG_61	NH2	F_ASP_82	OD2	2.796
3NGB	F_LYS_109	NZ	F_GLU_17	OE1	3.447
3NGB	F_HIS_	ND1	F_ASP_	OD2	2.855
3NGB	F_ARG_	NH1	F_GLU_	OE1	3.426
3NGB	I_LYS_46	NZ	I_GLU_492	OE1	3.345
3NGB	I_LYS_97	NZ	J_ASP_99	OD1	3.443
3NGB	I_LYS_207	NZ	I_GLU_381	OE1	3.684
3NGB	I_LYS_207	NZ	I_GLU_381	OE2	3.363
3NGB	I_HIS_249	NE2	I_GLU_482	OE1	3.245
3NGB	I_LYS_282	NZ	I_GLU_275	OE1	3.040
3NGB	I_LYS_348	NZ	I_GLU_269	OE2	3.888
3NGB	I_LYS_348	NZ	I_GLU_351	OE1	3.585
3NGB	I_ARG_456	NH1	I_GLU_466	OE1	3.750
3NGB	I_ARG_456	NH1	I_GLU_466	OE2	3.932
3NGB	I_ARG_469	NH2	I_ASP_457	OD1	3.266
3NGB	I_LYS_476	NZ	I_GLU_102	OE1	2.886
3NGB	I_LYS_476	NZ	I_GLU_102	OE2	3.914
3NGB	I_ARG_480	NH1	I_ASP_477	OD1	2.955
3NGB	I_LYS_487	NZ	I_ASP_47	OD1	2.972
3NGB	I_LYS_487	NZ	I_ASP_47	OD2	3.331
3NGB	I_LYS_487	NZ	I_GLU_91	OE1	3.195
3NGB	J_LYS_12	NZ	J_GLU_16	OE2	3.692
3NGB	J_ARG_19	NH1	J_GLU_81	OE1	3.898
3NGB	J_ARG_38	NH1	J_GLU_46	OE1	3.036
3NGB	J_ARG_38	NH1	J_GLU_46	OE2	3.958
3NGB	J_ARG_38	NH2	J_ASP_86	OD1	3.148
3NGB	J_ARG_53	NH2	J_ASP_31	OD1	3.422
3NGB	J_ARG_66	NH2	J_ASP_86	OD1	2.966
3NGB	J_ARG_66	NH2	J_ASP_86	OD2	2.680
3NGB	J_ARG_71	NH1	I_ASP_368	OD1	3.645
3NGB	J_ARG_71	NH1	I_ASP_368	OD2	3.125
3NGB	J_ARG_71	NH2	I_ASP_368	OD1	3.120
3NGB	J_ARG_82A	NH1	J_GLU_81	OE2	3.471
3NGB	J_HIS_102	NE2	J_GLU_101	OE1	3.491
3NGB	J_LYS_143	NZ	J_ASP_144	OD1	3.698
3NGB	J_LYS_209	NZ	K_GLU_125	OE1	2.929
3NGB	J_LYS_209	NZ	K_GLU_125	OE2	3.060
3NGB	J_LYS_210	NZ	J_GLU_212	OE2	3.040
3NGB	J_LYS_214	NZ	K_ASP_124	OD1	3.305
3NGB	K_ARG_24	NH1	K_ASP_70	OD1	3.807
3NGB	K_ARG_24	NH2	K_ASP_70	OD1	3.052
3NGB	K_ARG_61	NH1	K_ASP_82	OD2	2.794
3NGB	K_ARG_61	NH2	K_GLU_79	OE2	3.644
3NGB	K_ARG_61	NH2	K_ASP_82	OD1	3.448
3NGB	K_ARG_61	NH2	K_ASP_82	OD2	3.147
3NGB	K_LYS_109	NZ	K_GLU_17	OE1	3.600
3NGB	K_LYS_151	NZ	K_GLU_197	OE2	2.833
3NGB	K_LYS_185	NZ	K_GLU_189	OE2	3.051

Table 445: 3NGB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3NH7	H_ARG_38	NH1	H_ASP_90	OD1	3.170
3NH7	H_ARG_38	NH2	H_GLU_46	OE1	2.648
3NH7	H_ARG_38	NH2	H_GLU_46	OE2	3.155
3NH7	H_LYS_65	NZ	H_ASP_62	OD1	3.429
3NH7	H_ARG_67	NH1	H_ASP_90	OD1	3.942
3NH7	H_ARG_67	NH1	H_ASP_90	OD2	3.259
3NH7	H_ARG_67	NH2	H_ASP_90	OD1	3.009
3NH7	H_ARG_67	NH2	H_ASP_90	OD2	3.648
3NH7	H_ARG_98	NH1	H_ASP_108	OD1	3.173
3NH7	H_ARG_98	NH1	H_ASP_108	OD2	2.691
3NH7	H_ARG_98	NH1	A_ASP_67	OD2	3.819
3NH7	H_ARG_98	NH2	A_ASP_67	OD1	2.850
3NH7	H_ARG_98	NH2	A_ASP_67	OD2	2.389
3NH7	H_ARG_100	NH2	A_GLU_64	OE2	3.004
3NH7	H_HIS_102	ND1	A_GLU_64	OE1	2.378
3NH7	H_ARG_104	NH2	A_GLU_81	OE1	3.515
3NH7	H_ARG_104	NH2	A_GLU_81	OE2	2.462
3NH7	H_HIS_109	ND1	H_ASP_108	OD1	3.252
3NH7	H_HIS_109	ND1	H_ASP_108	OD2	3.832
3NH7	H_LYS_216	NZ	L_GLU_125	OE2	3.557
3NH7	H_LYS_217	NZ	H_GLU_219	OE2	2.342
3NH7	L_ARG_60	NH1	L_ASP_81	OD1	2.484
3NH7	L_ARG_60	NH1	L_ASP_81	OD2	2.037
3NH7	L_ARG_60	NH2	L_GLU_80	OE2	3.016
3NH7	L_ARG_60	NH2	L_ASP_81	OD1	3.954
3NH7	L_LYS_112	NZ	L_GLU_200	OE1	3.379
3NH7	L_HIS_190	ND1	L_ASP_153	OD2	3.719
3NH7	A_LYS_79	NZ	L_ASP_50	OD1	3.333
3NH7	A_LYS_79	NZ	L_ASP_50	OD2	3.058
3NH7	A_LYS_92	NZ	H_GLU_99	OE1	3.975
3NH7	A_LYS_92	NZ	H_GLU_99	OE2	3.561
3NH7	A_ARG_96	NH1	A_GLU_65	OE1	3.606
3NH7	A_ARG_96	NH1	A_GLU_65	OE2	2.868
3NH7	I_ARG_38	NH1	I_ASP_90	OD1	2.985
3NH7	I_ARG_38	NH2	I_GLU_46	OE1	2.998
3NH7	I_ARG_38	NH2	I_GLU_46	OE2	3.375
3NH7	I_LYS_65	NZ	I_ASP_62	OD1	3.472
3NH7	I_ARG_67	NH1	I_ASP_90	OD1	3.848
3NH7	I_ARG_67	NH1	I_ASP_90	OD2	2.660
3NH7	I_ARG_67	NH2	I_ASP_90	OD1	2.985
3NH7	I_ARG_67	NH2	I_ASP_90	OD2	3.250
3NH7	I_ARG_98	NH1	I_ASP_108	OD1	3.301
3NH7	I_ARG_98	NH1	I_ASP_108	OD2	2.609
3NH7	I_ARG_98	NH1	B_ASP_67	OD2	3.924
3NH7	I_ARG_98	NH2	B_ASP_67	OD1	3.388
3NH7	I_ARG_98	NH2	B_ASP_67	OD2	2.296
3NH7	I_ARG_100	NH2	B_GLU_64	OE2	2.996
3NH7	I_HIS_102	ND1	B_GLU_64	OE1	2.707
3NH7	I_ARG_104	NH2	B_GLU_81	OE1	3.637
3NH7	I_ARG_104	NH2	B_GLU_81	OE2	2.502
3NH7	I_HIS_109	ND1	I_ASP_108	OD1	3.553
3NH7	I_HIS_109	ND1	I_ASP_108	OD2	3.821
3NH7	I_LYS_216	NZ	M_GLU_125	OE1	3.301
3NH7	I_LYS_216	NZ	M_GLU_125	OE2	3.320
3NH7	I_LYS_217	NZ	I_GLU_219	OE2	3.028
3NH7	M_ARG_60	NH1	M_ASP_81	OD1	2.461
3NH7	M_ARG_60	NH1	M_ASP_81	OD2	1.882

3NH7	M_ARG_60	NH2	M_GLU_80	OE2	3.159
3NH7	M_ARG_60	NH2	M_ASP_81	OD1	3.816
3NH7	M_LYS_112	NZ	M_GLU_200	OE1	3.202
3NH7	M_HIS_190	ND1	M_ASP_153	OD2	3.749
3NH7	B_LYS_79	NZ	M_ASP_50	OD1	3.625
3NH7	B_LYS_79	NZ	M_ASP_50	OD2	2.953
3NH7	B_LYS_92	NZ	I_GLU_99	OE1	3.831
3NH7	B_LYS_92	NZ	I_GLU_99	OE2	3.683
3NH7	B_ARG_96	NH1	B_GLU_65	OE1	3.695
3NH7	B_ARG_96	NH1	B_GLU_65	OE2	2.714
3NH7	J_ARG_38	NH1	J_ASP_90	OD1	2.984
3NH7	J_ARG_38	NH2	J_GLU_46	OE1	2.989
3NH7	J_ARG_38	NH2	J_GLU_46	OE2	3.443
3NH7	J_LYS_65	NZ	J_ASP_62	OD1	3.599
3NH7	J_ARG_67	NH1	J_ASP_90	OD1	3.748
3NH7	J_ARG_67	NH1	J_ASP_90	OD2	2.498
3NH7	J_ARG_67	NH2	J_ASP_90	OD1	3.051
3NH7	J_ARG_67	NH2	J_ASP_90	OD2	3.237
3NH7	J_ARG_98	NH1	J_ASP_108	OD1	3.197
3NH7	J_ARG_98	NH1	J_ASP_108	OD2	2.669
3NH7	J_ARG_98	NH1	C_ASP_67	OD2	3.893
3NH7	J_ARG_98	NH2	C_ASP_67	OD1	3.313
3NH7	J_ARG_98	NH2	C_ASP_67	OD2	2.401
3NH7	J_ARG_100	NH2	C_GLU_64	OE2	3.173
3NH7	J_HIS_102	ND1	C_GLU_64	OE1	2.668
3NH7	J_ARG_104	NH2	C_GLU_81	OE1	3.595
3NH7	J_ARG_104	NH2	C_GLU_81	OE2	2.634
3NH7	J_HIS_109	ND1	J_ASP_108	OD1	3.604
3NH7	J_HIS_109	ND1	J_ASP_108	OD2	3.993
3NH7	J_LYS_216	NZ	N_GLU_125	OE1	2.816
3NH7	J_LYS_216	NZ	N_GLU_125	OE2	3.044
3NH7	J_LYS_217	NZ	J_GLU_219	OE2	3.134
3NH7	N_ARG_60	NH1	N_ASP_81	OD1	2.494
3NH7	N_ARG_60	NH1	N_ASP_81	OD2	2.049
3NH7	N_ARG_60	NH2	N_GLU_80	OE2	3.067
3NH7	N_ARG_60	NH2	N_ASP_81	OD1	3.767
3NH7	N_LYS_112	NZ	N_GLU_200	OE1	3.295
3NH7	N_HIS_190	ND1	N_ASP_153	OD2	3.738
3NH7	C_LYS_79	NZ	N_ASP_50	OD1	3.064
3NH7	C_LYS_79	NZ	N_ASP_50	OD2	3.315
3NH7	C_LYS_92	NZ	J_GLU_99	OE1	3.721
3NH7	C_LYS_92	NZ	J_GLU_99	OE2	3.806
3NH7	C_ARG_96	NH1	C_GLU_65	OE1	3.714
3NH7	C_ARG_96	NH1	C_GLU_65	OE2	2.792
3NH7	K_ARG_38	NH1	K_ASP_90	OD1	2.979
3NH7	K_ARG_38	NH2	K_GLU_46	OE1	2.902
3NH7	K_ARG_38	NH2	K_GLU_46	OE2	3.544
3NH7	K_LYS_65	NZ	K_ASP_62	OD1	3.572
3NH7	K_ARG_67	NH1	K_ASP_90	OD1	3.729
3NH7	K_ARG_67	NH1	K_ASP_90	OD2	2.672
3NH7	K_ARG_67	NH2	K_ASP_90	OD1	2.973
3NH7	K_ARG_67	NH2	K_ASP_90	OD2	3.433
3NH7	K_ARG_98	NH1	K_ASP_108	OD1	3.399
3NH7	K_ARG_98	NH1	K_ASP_108	OD2	2.677
3NH7	K_ARG_98	NH1	D_ASP_67	OD2	3.348
3NH7	K_ARG_98	NH2	D_ASP_67	OD1	3.350
3NH7	K_ARG_98	NH2	D_ASP_67	OD2	2.647
3NH7	K_ARG_100	NH2	D_GLU_64	OE2	3.101

3NH7	K_HIS_102	ND1	D_GLU_64	OE1	2.313
3NH7	K_ARG_104	NH2	D_GLU_81	OE1	3.830
3NH7	K_ARG_104	NH2	D_GLU_81	OE2	2.800
3NH7	K_HIS_109	ND1	K_ASP_108	OD1	3.611
3NH7	K_HIS_109	ND1	K_ASP_108	OD2	3.969
3NH7	K_LYS_216	NZ	O_GLU_125	OE1	3.159
3NH7	K_LYS_216	NZ	O_GLU_125	OE2	3.376
3NH7	K_LYS_217	NZ	K_GLU_219	OE2	3.149
3NH7	O_ARG_60	NH1	O_ASP_81	OD1	2.503
3NH7	O_ARG_60	NH1	O_ASP_81	OD2	2.023
3NH7	O_ARG_60	NH2	O_GLU_80	OE2	3.060
3NH7	O_LYS_112	NZ	O_GLU_200	OE1	3.202
3NH7	O_HIS_190	ND1	O_ASP_153	OD2	3.736
3NH7	D_LYS_79	NZ	O_ASP_50	OD1	3.661
3NH7	D_LYS_79	NZ	O_ASP_50	OD2	3.355
3NH7	D_LYS_92	NZ	K_GLU_99	OE1	3.766
3NH7	D_LYS_92	NZ	K_GLU_99	OE2	3.832
3NH7	D_ARG_96	NH1	D_GLU_65	OE1	3.668
3NH7	D_ARG_96	NH1	D_GLU_65	OE2	2.730

Table 446: 3NH7-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3NZ8	A_LYS_62	NZ	A_GLU_46	OE2	3.140
3NZ8	A_LYS_64	NZ	A_GLU_61	OE2	2.792
3NZ8	A_ARG_94	NH2	A_ASP_101	OD1	3.538
3NZ8	A_ARG_94	NH2	A_ASP_101	OD2	2.636
3NZ8	A_HIS_164	NE2	B_ASP_167	OD1	3.115
3NZ8	A_LYS_208	NZ	B_GLU_123	OE2	3.283
3NZ8	B_ARG_24	NH2	B_ASP_70	OD1	3.560
3NZ8	B_LYS_39	NZ	B_GLU_81	OE1	3.652
3NZ8	B_ARG_61	NH1	B_ASP_82	OD1	3.498
3NZ8	B_ARG_61	NH1	B_ASP_82	OD2	3.472
3NZ8	B_ARG_61	NH2	B_GLU_79	OE1	3.670
3NZ8	B_ARG_61	NH2	B_ASP_82	OD1	3.552
3NZ8	B_ARG_61	NH2	B_ASP_82	OD2	2.363
3NZ8	B_HIS_189	ND1	B_ASP_151	OD2	2.708
3NZ8	B_LYS_199	NZ	B_ASP_110	OD2	2.820
3NZ8	H_LYS_62	NZ	H_GLU_46	OE1	3.871
3NZ8	H_LYS_62	NZ	H_GLU_46	OE2	3.041
3NZ8	H_LYS_64	NZ	H_GLU_61	OE1	2.981
3NZ8	H_ARG_94	NH2	H_ASP_101	OD1	2.752
3NZ8	H_ARG_94	NH2	H_ASP_101	OD2	3.572
3NZ8	H_LYS_208	NZ	L_GLU_123	OE2	3.808
3NZ8	L_ARG_61	NH1	L_GLU_79	OE1	3.401
3NZ8	L_ARG_61	NH2	L_GLU_79	OE1	3.938
3NZ8	L_ARG_61	NH2	L_ASP_82	OD1	2.739
3NZ8	L_ARG_61	NH2	L_ASP_82	OD2	2.929
3NZ8	L_LYS_103	NZ	L_ASP_165	OD1	2.546
3NZ8	L_LYS_147	NZ	L_GLU_154	OE2	3.916
3NZ8	L_LYS_149	NZ	L_GLU_195	OE2	3.208
3NZ8	L_ARG_155	NH1	L_GLU_185	OE1	3.404
3NZ8	L_ARG_155	NH2	L_GLU_185	OE1	2.909
3NZ8	L_ARG_155	NH2	L_GLU_185	OE2	2.942
3NZ8	L_LYS_183	NZ	L_GLU_187	OE1	3.631
3NZ8	L_LYS_183	NZ	L_GLU_187	OE2	3.993
3NZ8	L_HIS_189	ND1	L_ASP_151	OD2	2.961
3NZ8	L_HIS_189	NE2	L_GLU_185	OE2	3.576

Table 447: 3NZ8-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3O2D	L_ARG_61	NH1	L_GLU_81	OE2	3.060
3O2D	L_ARG_61	NH1	L_ASP_82	OD1	2.620
3O2D	L_ARG_61	NH1	L_ASP_82	OD2	3.291
3O2D	L_ARG_61	NH2	L_GLU_81	OE2	3.508
3O2D	L_ARG_95	NH1	H_GLU_95	OE2	2.847
3O2D	L_ARG_95	NH2	H_GLU_95	OE2	3.717
3O2D	L_LYS_102	NZ	L_GLU_164	OE1	3.911
3O2D	L_LYS_148	NZ	L_GLU_194	OE1	2.853
3O2D	L_HIS_188	ND1	L_ASP_150	OD2	3.198
3O2D	L_HIS_188	NE2	L_ASP_184	OD1	3.050
3O2D	L_ARG_210	NH2	L_GLU_186	OE1	3.119
3O2D	H_HIS_35	NE2	H_GLU_95	OE2	2.861
3O2D	H_ARG_38	NH2	H_ASP_46	OD2	3.124
3O2D	H_LYS_66	NZ	H_ASP_86	OD1	2.870
3O2D	H_LYS_66	NZ	H_ASP_86	OD2	2.859
3O2D	H_ARG_83	NH1	H_GLU_85	OE2	3.005
3O2D	H_ARG_83	NH2	H_ASP_86	OD1	3.533
3O2D	H_LYS_143	NZ	H_ASP_144	OD1	3.677
3O2D	H_LYS_209	NZ	L_GLU_122	OE1	2.503
3O2D	H_LYS_209	NZ	L_GLU_122	OE2	3.547
3O2D	H_ARG_210	NH1	H_GLU_212	OE2	3.400
3O2D	A_LYS_8	NZ	A_GLU_119	OE1	3.898
3O2D	A_LYS_8	NZ	A_GLU_119	OE2	2.918
3O2D	A_HIS_27	NE2	A_GLU_85	OE1	3.858
3O2D	A_LYS_29	NZ	A_GLU_85	OE1	3.824
3O2D	A_ARG_54	NH1	A_ASP_78	OD1	3.603
3O2D	A_ARG_54	NH1	A_ASP_78	OD2	2.872
3O2D	A_ARG_54	NH2	A_ASP_78	OD1	3.001
3O2D	A_ARG_54	NH2	A_ASP_78	OD2	3.706
3O2D	A_LYS_90	NZ	A_GLU_92	OE1	3.860
3O2D	A_ARG_134	NH1	A_GLU_150	OE1	3.461
3O2D	A_LYS_171	NZ	A_GLU_169	OE1	3.959

Table 448: 3O2D-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3O41	L_LYS_39	NZ	L_GLU_81	OE1	3.974
3O41	L_ARG_61	NH1	L_GLU_79	OE1	3.261
3O41	L_ARG_61	NH1	L_GLU_79	OE2	3.697
3O41	L_ARG_61	NH1	L_GLU_81	OE2	3.860
3O41	L_ARG_61	NH2	L_GLU_79	OE2	3.810
3O41	L_ARG_61	NH2	L_GLU_81	OE2	2.759
3O41	L_ARG_61	NH2	L_ASP_82	OD1	2.918
3O41	L_ARG_61	NH2	L_ASP_82	OD2	3.904
3O41	L_LYS_149	NZ	L_GLU_195	OE1	2.951
3O41	L_LYS_149	NZ	L_GLU_195	OE2	3.097
3O41	L_ARG_155	NH2	L_GLU_185	OE2	3.569
3O41	L_HIS_189	ND1	L_ASP_151	OD2	3.090
3O41	L_LYS_199	NZ	L_ASP_110	OD2	3.725
3O41	H_ARG_38	NH1	H_ASP_86	OD1	2.779
3O41	H_ARG_38	NH2	H_GLU_46	OE1	3.126
3O41	H_ARG_38	NH2	H_ASP_86	OD1	3.703
3O41	H_LYS_57	NZ	H_ASP_55	OD1	3.135
3O41	H_LYS_57	NZ	H_ASP_55	OD2	3.981
3O41	H_ARG_58	NH1	H_ASP_56	OD1	2.885
3O41	H_ARG_58	NH1	H_ASP_56	OD2	2.978
3O41	H_ARG_58	NH2	H_ASP_56	OD2	2.836
3O41	H_ARG_66	NH1	H_ASP_86	OD1	3.749
3O41	H_ARG_66	NH1	H_ASP_86	OD2	2.911
3O41	H_ARG_66	NH2	H_ASP_86	OD1	2.994
3O41	H_ARG_66	NH2	H_ASP_86	OD2	3.466
3O41	H_ARG_94	NH1	A_GLU_191	OE1	2.970
3O41	H_ARG_94	NH1	A_GLU_191	OE2	3.394
3O41	H_ARG_94	NH2	A_GLU_191	OE1	3.744
3O41	H_ARG_94	NH2	A_GLU_191	OE2	2.660
3O41	H_LYS_208	NZ	L_GLU_123	OE2	3.054
3O41	A_ARG_38	NH1	A_ASP_86	OD1	2.874
3O41	A_ARG_38	NH2	A_GLU_46	OE1	2.942
3O41	A_ARG_38	NH2	A_ASP_86	OD1	3.757
3O41	A_LYS_57	NZ	A_ASP_55	OD1	3.432
3O41	A_LYS_57	NZ	A_ASP_55	OD2	3.491
3O41	A_ARG_58	NH1	A_ASP_56	OD1	2.791
3O41	A_ARG_58	NH1	A_ASP_56	OD2	3.222
3O41	A_ARG_58	NH2	A_ASP_56	OD1	3.748
3O41	A_ARG_58	NH2	A_ASP_56	OD2	2.672
3O41	A_ARG_66	NH1	A_ASP_86	OD1	3.581
3O41	A_ARG_66	NH1	A_ASP_86	OD2	2.922
3O41	A_ARG_66	NH2	A_ASP_86	OD1	2.880
3O41	A_ARG_66	NH2	A_ASP_86	OD2	3.514
3O41	A_ARG_75	NH1	A_ASP_72	OD2	2.827
3O41	A_LYS_208	NZ	B_GLU_123	OE2	2.651
3O41	B_ARG_24	NH1	B_ASP_70	OD1	3.055
3O41	B_ARG_24	NH1	B_ASP_70	OD2	2.756
3O41	B_LYS_39	NZ	B_GLU_81	OE1	3.471
3O41	B_ARG_61	NH1	B_GLU_79	OE1	3.277
3O41	B_ARG_61	NH1	B_GLU_79	OE2	3.207
3O41	B_ARG_61	NH2	B_GLU_79	OE2	3.637
3O41	B_ARG_61	NH2	B_GLU_81	OE2	3.110
3O41	B_ARG_61	NH2	B_ASP_82	OD1	2.801
3O41	B_ARG_61	NH2	B_ASP_82	OD2	3.822
3O41	B_LYS_149	NZ	B_GLU_195	OE2	3.553
3O41	B_ARG_155	NH2	B_GLU_185	OE1	3.463
3O41	B_ARG_155	NH2	B_GLU_185	OE2	2.863

3O41	B_HIS_189	ND1	B_ASP_151	OD2	3.087
3O41	B_LYS_199	NZ	B_ASP_110	OD2	3.995
3O41	P_LYS_433	NZ	H_ASP_54	OD1	3.659
3O41	P_LYS_433	NZ	H_ASP_54	OD2	2.887
3O41	P_LYS_433	NZ	H_ASP_56	OD2	2.760
3O41	C_LYS_433	NZ	A_ASP_54	OD1	3.503
3O41	C_LYS_433	NZ	A_ASP_54	OD2	2.671
3O41	C_LYS_433	NZ	A_ASP_56	OD2	2.936

Table 449: 3O41-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3O45	L_LYS_39	NZ	L_GLU_81	OE1	3.955
3O45	L_ARG_61	NH1	L_GLU_79	OE1	3.563
3O45	L_ARG_61	NH1	L_GLU_79	OE2	3.651
3O45	L_ARG_61	NH2	L_GLU_79	OE2	3.980
3O45	L_ARG_61	NH2	L_GLU_81	OE2	2.981
3O45	L_ARG_61	NH2	L_ASP_82	OD1	2.891
3O45	L_LYS_149	NZ	L_GLU_195	OE1	3.064
3O45	L_LYS_149	NZ	L_GLU_195	OE2	2.826
3O45	L_ARG_155	NH2	L_GLU_185	OE2	2.881
3O45	L_HIS_189	ND1	L_ASP_151	OD2	3.388
3O45	L_LYS_199	NZ	L_ASP_110	OD2	3.915
3O45	H_ARG_38	NH1	H_ASP_86	OD1	2.834
3O45	H_ARG_38	NH2	H_GLU_46	OE1	3.512
3O45	H_ARG_38	NH2	H_ASP_86	OD1	3.614
3O45	H_LYS_57	NZ	H_ASP_55	OD1	2.960
3O45	H_LYS_57	NZ	H_ASP_55	OD2	3.684
3O45	H_ARG_58	NH1	H_ASP_56	OD1	2.872
3O45	H_ARG_58	NH1	H_ASP_56	OD2	2.820
3O45	H_ARG_58	NH2	H_ASP_56	OD2	3.333
3O45	H_ARG_66	NH1	H_ASP_86	OD2	2.963
3O45	H_ARG_66	NH2	H_ASP_86	OD1	3.158
3O45	H_ARG_66	NH2	H_ASP_86	OD2	3.218
3O45	H_LYS_71	NZ	H_ASP_55	OD1	3.837
3O45	H_ARG_94	NH1	A_GLU_191	OE1	3.085
3O45	H_ARG_94	NH1	A_GLU_191	OE2	3.621
3O45	H_ARG_94	NH2	A_GLU_191	OE1	3.709
3O45	H_ARG_94	NH2	A_GLU_191	OE2	2.802
3O45	H_LYS_208	NZ	L_GLU_123	OE2	3.033
3O45	A_ARG_38	NH1	A_ASP_86	OD1	2.784
3O45	A_ARG_38	NH2	A_GLU_46	OE1	3.151
3O45	A_ARG_38	NH2	A_ASP_86	OD1	3.920
3O45	A_LYS_57	NZ	A_ASP_55	OD1	3.779
3O45	A_LYS_57	NZ	A_ASP_55	OD2	3.231
3O45	A_ARG_58	NH1	A_ASP_56	OD1	2.824
3O45	A_ARG_58	NH1	A_ASP_56	OD2	3.062
3O45	A_ARG_58	NH2	A_ASP_56	OD2	2.817
3O45	A_ARG_66	NH1	A_ASP_86	OD2	2.985
3O45	A_ARG_66	NH2	A_ASP_86	OD1	2.861
3O45	A_ARG_66	NH2	A_ASP_86	OD2	3.279
3O45	A_LYS_71	NZ	A_ASP_55	OD1	3.913
3O45	A_ARG_75	NH1	A_ASP_72	OD2	3.016
3O45	A_LYS_208	NZ	B_GLU_123	OE2	2.878
3O45	B_ARG_24	NH1	B_ASP_70	OD1	2.848
3O45	B_ARG_24	NH1	B_ASP_70	OD2	2.930
3O45	B_LYS_39	NZ	B_GLU_81	OE1	3.627
3O45	B_ARG_61	NH1	B_GLU_79	OE1	3.550
3O45	B_ARG_61	NH1	B_GLU_79	OE2	3.481
3O45	B_ARG_61	NH2	B_GLU_79	OE2	3.674
3O45	B_ARG_61	NH2	B_GLU_81	OE2	3.283
3O45	B_ARG_61	NH2	B_ASP_82	OD1	2.929
3O45	B_ARG_61	NH2	B_ASP_82	OD2	3.946
3O45	B_LYS_149	NZ	B_GLU_195	OE2	3.399
3O45	B_ARG_155	NH2	B_GLU_185	OE1	3.860
3O45	B_ARG_155	NH2	B_GLU_185	OE2	2.997
3O45	B_HIS_189	ND1	B_ASP_151	OD2	3.113
3O45	B_LYS_199	NZ	B_ASP_110	OD2	3.896
3O45	P_LYS_433	NZ	H_ASP_54	OD1	3.518

3O45	P_LYS_433	NZ	H_ASP_54	OD2	2.818
3O45	P_LYS_433	NZ	H_ASP_56	OD2	2.927
3O45	C_LYS_433	NZ	A_ASP_54	OD1	3.297
3O45	C_LYS_433	NZ	A_ASP_54	OD2	2.723
3O45	C_LYS_433	NZ	A_ASP_56	OD2	2.899

Table 450: 3O45-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3OJD	A_ARG_61	NH2	A_GLU_81	OE1	3.519
3OJD	A_ARG_61	NH2	A_ASP_82	OD1	2.711
3OJD	A_ARG_61	NH2	A_ASP_82	OD2	3.501
3OJD	A_LYS_149	NZ	A_GLU_195	OE1	3.123
3OJD	A_LYS_149	NZ	A_GLU_195	OE2	3.726
3OJD	A_ARG_155	NH2	A_GLU_185	OE2	2.919
3OJD	A_LYS_183	NZ	A_GLU_187	OE2	3.320
3OJD	A_HIS_189	ND1	A_ASP_151	OD2	2.920
3OJD	A_HIS_189	NE2	A_GLU_185	OE1	3.630
3OJD	B_LYS_13	NZ	B_GLU_16	OE2	2.846
3OJD	B_LYS_64	NZ	B_ASP_61	OD1	3.166
3OJD	B_ARG_66	NH1	B_ASP_86	OD1	3.558
3OJD	B_ARG_66	NH1	B_ASP_86	OD2	2.686
3OJD	B_ARG_66	NH2	B_ASP_86	OD1	2.934
3OJD	B_ARG_66	NH2	B_ASP_86	OD2	3.558
3OJD	B_LYS_83	NZ	B_GLU_85	OE1	3.736
3OJD	B_LYS_83	NZ	B_GLU_85	OE2	2.635
3OJD	B_ARG_94	NH2	B_ASP_101	OD1	2.661
3OJD	B_ARG_94	NH2	B_ASP_101	OD2	3.562
3OJD	B_LYS_205	NZ	B_ASP_207	OD1	3.219
3OJD	B_LYS_205	NZ	B_ASP_207	OD2	3.147
3OJD	B_LYS_208	NZ	A_GLU_123	OE2	3.588
3OJD	B_ARG_213	NH1	A_GLU_213	OE2	3.118
3OJD	B_ARG_213	NH2	A_GLU_213	OE2	3.609

Table 451: 3OJD-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3P0V	L_ARG_61	NH2	L_GLU_81	OE2	3.980
3P0V	L_ARG_61	NH2	L_ASP_82	OD1	2.725
3P0V	L_ARG_61	NH2	L_ASP_82	OD2	3.097
3P0V	L_LYS_103	NZ	L_GLU_165	OE2	2.532
3P0V	L_LYS_149	NZ	L_GLU_195	OE1	3.890
3P0V	L_LYS_149	NZ	L_GLU_195	OE2	2.540
3P0V	L_LYS_188	NZ	L_ASP_185	OD1	3.371
3P0V	H_HIS_35	NE2	H_GLU_50	OE1	3.401
3P0V	H_HIS_35	NE2	H_GLU_95	OE2	3.628
3P0V	H_ARG_38	NH1	H_ASP_86	OD1	2.715
3P0V	H_ARG_38	NH2	H_GLU_46	OE1	3.599
3P0V	H_ARG_38	NH2	H_ASP_86	OD1	3.530
3P0V	H_LYS_64	NZ	H_ASP_58	OD1	3.681
3P0V	H_ARG_66	NH1	H_ASP_86	OD1	3.613
3P0V	H_ARG_66	NH1	H_ASP_86	OD2	3.306
3P0V	H_ARG_66	NH2	H_ASP_86	OD1	3.888
3P0V	H_ARG_83	NH1	H_GLU_85	OE2	3.227
3P0V	H_ARG_94	NH2	H_ASP_32	OD2	3.649
3P0V	H_ARG_97	NH1	H_ASP_32	OD1	3.877
3P0V	H_ARG_97	NH1	H_ASP_32	OD2	3.520
3P0V	H_LYS_143	NZ	H_ASP_144	OD2	3.455
3P0V	M_ARG_24	NH1	M_ASP_70	OD1	2.624
3P0V	M_ARG_61	NH2	M_GLU_81	OE2	3.977
3P0V	M_ARG_61	NH2	M_ASP_82	OD1	2.677
3P0V	M_ARG_61	NH2	M_ASP_82	OD2	3.250
3P0V	M_LYS_103	NZ	M_GLU_165	OE2	2.754
3P0V	M_LYS_149	NZ	M_GLU_195	OE2	2.947
3P0V	M_LYS_188	NZ	M_ASP_185	OD1	3.655
3P0V	I_HIS_35	NE2	I_GLU_50	OE1	3.344
3P0V	I_HIS_35	NE2	I_GLU_95	OE2	3.386
3P0V	I_ARG_38	NH1	I_ASP_86	OD1	2.831
3P0V	I_ARG_38	NH2	I_GLU_46	OE1	3.289
3P0V	I_ARG_38	NH2	I_GLU_46	OE2	3.805
3P0V	I_ARG_38	NH2	I_ASP_86	OD1	3.779
3P0V	I_LYS_64	NZ	I_ASP_58	OD1	3.535
3P0V	I_ARG_66	NH1	I_ASP_86	OD1	3.463
3P0V	I_ARG_66	NH1	I_ASP_86	OD2	3.181
3P0V	I_ARG_66	NH2	I_ASP_86	OD1	3.209
3P0V	I_ARG_66	NH2	I_ASP_86	OD2	3.655
3P0V	I_ARG_83	NH1	I_GLU_85	OE2	2.465
3P0V	I_ARG_94	NH2	I_ASP_32	OD1	3.895
3P0V	I_ARG_94	NH2	I_ASP_32	OD2	3.368
3P0V	I_LYS_143	NZ	I_ASP_144	OD2	3.595

Table 452: 3P0V-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3P0Y	A_LYS_322	NZ	A_ASP_323	OD1	3.929
3P0Y	A_LYS_372	NZ	A_ASP_369	OD1	3.817
3P0Y	A_LYS_372	NZ	A_GLU_397	OE2	3.911
3P0Y	A_HIS_394	NE2	A_ASP_369	OD1	3.176
3P0Y	A_ARG_403	NH2	A_GLU_376	OE2	3.071
3P0Y	A_LYS_407	NZ	A_ASP_434	OD2	2.888
3P0Y	A_ARG_427	NH1	A_ASP_392	OD2	3.627
3P0Y	A_ARG_427	NH1	A_ASP_498	OD1	3.045
3P0Y	A_ARG_427	NH2	A_GLU_397	OE1	3.220
3P0Y	A_LYS_455	NZ	A_GLU_489	OE1	3.791
3P0Y	A_LYS_455	NZ	A_GLU_489	OE2	3.520
3P0Y	A_LYS_463	NZ	H_GLU_95	OE2	2.859
3P0Y	A_LYS_465	NZ	H_GLU_50	OE1	2.656
3P0Y	A_LYS_465	NZ	H_GLU_50	OE2	3.845
3P0Y	A_LYS_465	NZ	H_GLU_95	OE1	2.777
3P0Y	A_LYS_465	NZ	H_GLU_95	OE2	3.671
3P0Y	H_HIS_35	NE2	H_GLU_50	OE1	3.331
3P0Y	H_HIS_35	NE2	H_GLU_95	OE1	3.467
3P0Y	H_ARG_38	NH1	H_ASP_86	OD1	2.814
3P0Y	H_ARG_38	NH2	H_GLU_46	OE1	3.115
3P0Y	H_ARG_38	NH2	H_GLU_46	OE2	3.997
3P0Y	H_ARG_38	NH2	H_ASP_86	OD1	3.796
3P0Y	H_LYS_64	NZ	H_ASP_61	OD1	3.749
3P0Y	H_ARG_66	NH1	H_ASP_86	OD1	3.756
3P0Y	H_ARG_66	NH1	H_ASP_86	OD2	2.816
3P0Y	H_ARG_66	NH2	H_ASP_86	OD1	3.074
3P0Y	H_ARG_66	NH2	H_ASP_86	OD2	3.530
3P0Y	H_LYS_75	NZ	H_ASP_72	OD2	3.063
3P0Y	H_ARG_94	NH2	H_ASP_101	OD1	3.544
3P0Y	H_ARG_94	NH2	H_ASP_101	OD2	2.757
3P0Y	H_ARG_97	NH1	A_ASP_436	OD1	2.876
3P0Y	H_ARG_97	NH1	A_ASP_436	OD2	3.533
3P0Y	H_ARG_97	NH2	A_ASP_436	OD1	3.647
3P0Y	H_ARG_97	NH2	A_ASP_436	OD2	2.823
3P0Y	H_LYS_143	NZ	H_ASP_144	OD1	3.090
3P0Y	H_LYS_143	NZ	H_ASP_144	OD2	3.144
3P0Y	H_LYS_209	NZ	L_GLU_123	OE1	2.674
3P0Y	H_LYS_209	NZ	L_GLU_123	OE2	3.317
3P0Y	H_LYS_210	NZ	H_GLU_212	OE1	3.756
3P0Y	L_ARG_61	NH2	L_GLU_81	OE2	3.697
3P0Y	L_ARG_61	NH2	L_ASP_82	OD1	2.833
3P0Y	L_ARG_61	NH2	L_ASP_82	OD2	3.670
3P0Y	L_LYS_149	NZ	L_GLU_195	OE1	2.821
3P0Y	L_HIS_189	ND1	L_ASP_151	OD2	3.174
3P0Y	L_LYS_190	NZ	L_GLU_213	OE2	3.914

Table 453: 3P0Y-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3P11	H_HIS_35	NE2	H_GLU_50	OE1	3.507
3P11	H_HIS_35	NE2	H_GLU_95	OE2	3.809
3P11	H_ARG_38	NH1	H_ASP_86	OD1	3.036
3P11	H_ARG_38	NH2	H_GLU_46	OE1	2.678
3P11	H_ARG_38	NH2	H_GLU_46	OE2	3.985
3P11	H_LYS_64	NZ	H_ASP_58	OD1	3.516
3P11	H_ARG_66	NH1	H_ASP_86	OD2	3.567
3P11	H_ARG_66	NH2	H_ASP_86	OD1	3.699
3P11	H_ARG_94	NH1	H_ASP_101	OD1	3.477
3P11	H_ARG_94	NH1	H_ASP_101	OD2	3.282
3P11	H_ARG_94	NH2	H_ASP_32	OD2	3.500
3P11	H_ARG_97	NH1	H_ASP_32	OD1	3.837
3P11	L_ARG_24	NH1	L_ASP_70	OD2	3.972
3P11	L_ARG_61	NH1	L_GLU_81	OE2	3.937
3P11	L_ARG_61	NH2	L_GLU_81	OE2	3.076
3P11	L_ARG_61	NH2	L_ASP_82	OD1	2.965
3P11	L_ARG_61	NH2	L_ASP_82	OD2	3.758
3P11	L_LYS_103	NZ	L_GLU_105	OE1	3.365
3P11	L_LYS_103	NZ	L_GLU_165	OE2	2.876
3P11	L_LYS_183	NZ	L_GLU_187	OE1	2.907
3P11	A_HIS_51	ND1	A_GLU_74	OE1	3.956
3P11	A_ARG_62	NH1	A_GLU_38	OE1	3.231
3P11	A_ARG_62	NH2	A_GLU_63	OE2	3.811
3P11	A_ARG_87	NH1	A_GLU_63	OE1	3.389
3P11	A_ARG_116	NH1	A_ASP_182	OD1	3.330
3P11	A_ARG_116	NH1	A_ASP_182	OD2	2.794
3P11	A_LYS_	NZ	A_GLU_131	OE1	3.633
3P11	A_ARG_	NH2	A_ASP_134	OD2	3.573
3P11	A_HIS_209	NE2	A_ASP_221	OD1	3.391
3P11	A_LYS_260	NZ	A_ASP_232	OD1	3.022
3P11	A_LYS_290	NZ	A_ASP_278	OD1	2.957
3P11	A_ARG_402	NH1	A_GLU_373	OE1	3.428
3P11	A_ARG_441	NH1	H_ASP_58	OD2	3.356
3P11	A_ARG_441	NH1	L_GLU_94	OE1	2.859
3P11	A_ARG_441	NH1	L_GLU_94	OE2	3.310
3P11	A_ARG_441	NH2	L_GLU_94	OE2	3.075
3P11	A_ARG_456	NH1	A_GLU_429	OE1	3.324
3P11	A_ARG_456	NH2	A_GLU_429	OE1	3.225
3P11	A_LYS_466	NZ	H_GLU_95	OE1	2.568
3P11	A_LYS_466	NZ	H_GLU_95	OE2	3.227
3P11	A_HIS_467	ND1	H_GLU_50	OE2	3.466
3P11	A_HIS_467	ND1	L_GLU_94	OE2	3.926
3P11	A_HIS_467	NE2	H_GLU_50	OE1	3.754
3P11	A_HIS_467	NE2	H_GLU_50	OE2	3.679
3P11	A_HIS_467	NE2	H_GLU_95	OE2	3.533
3P11	A_ARG_469	NH1	A_GLU_477	OE1	3.032
3P11	A_ARG_469	NH2	A_ASP_473	OD2	3.365
3P11	A_ARG_469	NH2	A_GLU_477	OE1	3.595
3P11	A_ARG_469	NH2	A_GLU_477	OE2	3.199

Table 454: 3P11-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3PGF	A_LYS_15	NZ	A_ASP_14	OD1	2.931
3PGF	A_LYS_15	NZ	A_GLU_111	OE2	3.982
3PGF	A_LYS_26	NZ	A_ASP_30	OD2	2.898
3PGF	A_LYS_83	NZ	A_ASP_87	OD1	3.179
3PGF	A_ARG_98	NH1	A_ASP_95	OD1	2.849
3PGF	A_LYS_140	NZ	A_ASP_136	OD1	3.415
3PGF	A_LYS_140	NZ	A_ASP_136	OD2	2.764
3PGF	A_HIS_203	ND1	A_ASP_136	OD2	2.718
3PGF	A_LYS_251	NZ	A_ASP_164	OD1	3.745
3PGF	A_LYS_251	NZ	A_ASP_164	OD2	2.761
3PGF	A_ARG_316	NH1	A_ASP_236	OD1	3.984
3PGF	A_ARG_316	NH1	A_ASP_236	OD2	3.954
3PGF	A_ARG_316	NH2	A_ASP_314	OD2	2.795
3PGF	A_LYS_326	NZ	A_GLU_322	OE2	2.961
3PGF	H_ARG_38	NH1	H_ASP_86	OD1	3.038
3PGF	H_ARG_38	NH2	H_GLU_46	OE1	2.948
3PGF	H_ARG_66	NH1	H_ASP_86	OD1	3.643
3PGF	H_ARG_66	NH1	H_ASP_86	OD2	2.938
3PGF	H_ARG_66	NH2	H_ASP_86	OD1	3.135
3PGF	H_ARG_66	NH2	H_ASP_86	OD2	3.904
3PGF	H_ARG_94	NH2	H_ASP_101	OD1	3.471
3PGF	H_ARG_94	NH2	H_ASP_101	OD2	2.638
3PGF	L_ARG_24	NH1	L_ASP_70	OD1	3.567
3PGF	L_ARG_24	NH1	L_ASP_70	OD2	3.066
3PGF	L_ARG_61	NH2	L_GLU_81	OE2	3.869
3PGF	L_ARG_61	NH2	L_ASP_82	OD1	2.691
3PGF	L_ARG_61	NH2	L_ASP_82	OD2	3.502
3PGF	L_ARG_66	NH1	A_GLU_309	OE2	3.045
3PGF	L_ARG_66	NH2	A_GLU_309	OE2	2.501
3PGF	L_LYS_149	NZ	L_GLU_195	OE2	3.143
3PGF	L_LYS_190	NZ	L_GLU_213	OE2	3.299

Table 455: 3PGF-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3PNW	A_ARG_62	NH2	A_GLU_82	OE2	2.760
3PNW	A_ARG_62	NH2	A_ASP_83	OD1	3.251
3PNW	A_LYS_106	NZ	A_GLU_168	OE1	3.588
3PNW	A_LYS_106	NZ	A_GLU_168	OE2	3.143
3PNW	A_LYS_152	NZ	A_GLU_198	OE1	3.462
3PNW	A_HIS_192	ND1	A_ASP_154	OD2	2.766
3PNW	B_ARG_41	NH1	B_GLU_49	OE1	3.120
3PNW	B_ARG_41	NH1	B_GLU_49	OE2	3.686
3PNW	B_ARG_41	NH1	B_ASP_93	OD1	3.860
3PNW	B_ARG_41	NH2	B_ASP_93	OD1	2.838
3PNW	B_ARG_70	NH1	B_ASP_93	OD1	3.254
3PNW	B_ARG_70	NH1	B_ASP_93	OD2	3.946
3PNW	B_ARG_70	NH2	B_ASP_93	OD1	3.639
3PNW	B_ARG_70	NH2	B_ASP_93	OD2	2.902
3PNW	B_LYS_79	NZ	B_ASP_76	OD2	2.841
3PNW	B_ARG_90	NH1	B_GLU_92	OE1	3.741
3PNW	B_ARG_101	NH2	B_ASP_117	OD2	3.317
3PNW	B_ARG_104	NH1	C_GLU_599	OE1	3.048
3PNW	B_LYS_159	NZ	B_ASP_160	OD1	3.439
3PNW	C_LYS_557	NZ	C_ASP_560	OD1	3.049
3PNW	C_LYS_557	NZ	C_ASP_560	OD2	3.693
3PNW	C_LYS_590	NZ	C_GLU_576	OE1	3.383
3PNW	D_ARG_25	NH1	J_GLU_82	OE1	2.858
3PNW	D_ARG_25	NH1	J_GLU_82	OE2	3.430
3PNW	D_ARG_25	NH2	J_GLU_82	OE1	3.626
3PNW	D_ARG_25	NH2	J_GLU_82	OE2	3.034
3PNW	D_ARG_62	NH2	D_GLU_82	OE2	3.353
3PNW	D_ARG_62	NH2	D_ASP_83	OD1	3.192
3PNW	D_ARG_62	NH2	D_ASP_83	OD2	3.678
3PNW	D_ARG_145	NH1	D_GLU_108	OE2	3.475
3PNW	D_ARG_145	NH2	D_GLU_108	OE1	3.526
3PNW	D_ARG_145	NH2	D_GLU_108	OE2	3.197
3PNW	D_LYS_152	NZ	D_GLU_198	OE1	3.454
3PNW	D_LYS_152	NZ	D_GLU_198	OE2	3.452
3PNW	D_LYS_186	NZ	D_GLU_190	OE1	3.419
3PNW	D_LYS_186	NZ	D_GLU_190	OE2	2.925
3PNW	D_HIS_192	ND1	D_ASP_154	OD2	2.749
3PNW	E_ARG_41	NH1	E_GLU_49	OE1	3.072
3PNW	E_ARG_41	NH1	E_GLU_49	OE2	3.615
3PNW	E_ARG_41	NH1	E_ASP_93	OD1	3.772
3PNW	E_ARG_41	NH2	E_ASP_93	OD1	2.776
3PNW	E_LYS_68	NZ	E_ASP_65	OD1	2.738
3PNW	E_ARG_70	NH1	E_ASP_93	OD1	3.047
3PNW	E_ARG_70	NH1	E_ASP_93	OD2	3.582
3PNW	E_ARG_70	NH2	E_ASP_93	OD1	3.597
3PNW	E_ARG_70	NH2	E_ASP_93	OD2	2.576
3PNW	E_LYS_79	NZ	E_ASP_76	OD2	2.902
3PNW	E_ARG_101	NH2	E_ASP_117	OD2	3.400
3PNW	E_ARG_104	NH1	F_GLU_599	OE2	2.653
3PNW	E_LYS_159	NZ	E_ASP_160	OD1	3.050
3PNW	E_LYS_159	NZ	E_ASP_160	OD2	2.633
3PNW	F_LYS_590	NZ	F_GLU_576	OE2	3.831
3PNW	G_ARG_25	NH1	G_ASP_71	OD1	3.445
3PNW	G_ARG_25	NH1	G_ASP_71	OD2	2.863
3PNW	G_ARG_62	NH2	G_GLU_82	OE2	3.208
3PNW	G_ARG_62	NH2	G_ASP_83	OD1	2.937
3PNW	G_ARG_62	NH2	G_ASP_83	OD2	3.584

3PNW	G_LYS_106	NZ	G_GLU_168	OE1	2.721
3PNW	G_LYS_106	NZ	G_GLU_168	OE2	3.243
3PNW	G_LYS_152	NZ	G_GLU_198	OE2	3.706
3PNW	G_LYS_186	NZ	G_GLU_190	OE2	3.219
3PNW	G_HIS_192	ND1	G_ASP_154	OD2	3.161
3PNW	G_HIS_192	NE2	G_ASP_188	OD1	3.976
3PNW	H_ARG_41	NH1	H_GLU_49	OE1	3.103
3PNW	H_ARG_41	NH1	H_GLU_49	OE2	3.667
3PNW	H_ARG_41	NH1	H_ASP_93	OD1	3.761
3PNW	H_ARG_41	NH2	H_ASP_93	OD1	2.861
3PNW	H_LYS_68	NZ	H_ASP_65	OD1	2.900
3PNW	H_ARG_70	NH1	H_ASP_93	OD1	3.098
3PNW	H_ARG_70	NH1	H_ASP_93	OD2	3.479
3PNW	H_ARG_70	NH2	H_ASP_93	OD1	3.791
3PNW	H_ARG_70	NH2	H_ASP_93	OD2	2.662
3PNW	H_LYS_79	NZ	H_ASP_76	OD2	3.008
3PNW	H_ARG_90	NH1	H_GLU_92	OE2	3.922
3PNW	H_ARG_101	NH2	H_ASP_117	OD2	3.291
3PNW	H_ARG_104	NH1	L_GLU_599	OE1	3.020
3PNW	H_LYS_159	NZ	H_ASP_160	OD1	3.348
3PNW	H_LYS_159	NZ	H_ASP_160	OD2	3.221
3PNW	L_LYS_590	NZ	L_GLU_576	OE1	3.342
3PNW	J_ARG_25	NH2	J_ASP_71	OD1	3.699
3PNW	J_ARG_62	NH2	J_GLU_82	OE2	3.268
3PNW	J_ARG_62	NH2	J_ASP_83	OD1	3.032
3PNW	J_ARG_62	NH2	J_ASP_83	OD2	3.641
3PNW	J_LYS_106	NZ	J_GLU_168	OE1	2.693
3PNW	J_LYS_106	NZ	J_GLU_168	OE2	3.468
3PNW	J_ARG_145	NH1	J_GLU_108	OE1	3.314
3PNW	J_ARG_145	NH1	J_GLU_108	OE2	2.910
3PNW	J_ARG_145	NH2	J_GLU_108	OE1	3.149
3PNW	J_LYS_152	NZ	J_GLU_198	OE2	2.718
3PNW	J_HIS_192	ND1	J_ASP_154	OD2	2.849
3PNW	J_ARG_214	NH2	J_GLU_190	OE1	3.561
3PNW	K_ARG_41	NH1	K_GLU_49	OE1	3.097
3PNW	K_ARG_41	NH1	K_GLU_49	OE2	3.636
3PNW	K_ARG_41	NH1	K_ASP_93	OD1	3.969
3PNW	K_ARG_41	NH2	K_ASP_93	OD1	2.946
3PNW	K_LYS_68	NZ	K_ASP_65	OD1	2.902
3PNW	K_ARG_70	NH1	K_ASP_93	OD1	3.172
3PNW	K_ARG_70	NH1	K_ASP_93	OD2	3.777
3PNW	K_ARG_70	NH2	K_ASP_93	OD1	3.650
3PNW	K_ARG_70	NH2	K_ASP_93	OD2	2.817
3PNW	K_LYS_79	NZ	K_ASP_76	OD2	3.145
3PNW	K_ARG_101	NH2	K_ASP_117	OD2	3.216
3PNW	K_ARG_104	NH1	L_GLU_599	OE1	2.888
3PNW	K_ARG_104	NH1	L_GLU_599	OE2	2.772
3PNW	K_ARG_104	NH2	L_GLU_599	OE2	3.083
3PNW	K_LYS_159	NZ	K_ASP_160	OD1	3.020
3PNW	K_LYS_159	NZ	K_ASP_160	OD2	2.839
3PNW	M_ARG_62	NH2	M_GLU_82	OE2	2.988
3PNW	M_ARG_62	NH2	M_ASP_83	OD1	2.932
3PNW	M_ARG_62	NH2	M_ASP_83	OD2	3.718
3PNW	M_LYS_106	NZ	M_GLU_168	OE1	3.752
3PNW	M_LYS_106	NZ	M_GLU_168	OE2	2.837
3PNW	M_LYS_152	NZ	M_GLU_198	OE1	3.636
3PNW	M_LYS_152	NZ	M_GLU_198	OE2	3.599
3PNW	M_LYS_191	NZ	M_ASP_188	OD1	2.912

3PNW	M_HIS_192	ND1	M_ASP_154	OD2	3.108
3PNW	N_ARG_41	NH1	N_GLU_49	OE1	3.141
3PNW	N_ARG_41	NH1	N_GLU_49	OE2	3.699
3PNW	N_ARG_41	NH1	N_ASP_93	OD1	3.824
3PNW	N_ARG_41	NH2	N_ASP_93	OD1	2.841
3PNW	N_ARG_70	NH1	N_ASP_93	OD1	3.199
3PNW	N_ARG_70	NH1	N_ASP_93	OD2	3.846
3PNW	N_ARG_70	NH2	N_ASP_93	OD1	3.653
3PNW	N_ARG_70	NH2	N_ASP_93	OD2	2.921
3PNW	N_LYS_79	NZ	N_ASP_76	OD2	2.793
3PNW	N_ARG_101	NH2	N_ASP_117	OD2	3.225
3PNW	N_LYS_159	NZ	N_ASP_160	OD1	3.030
3PNW	N_LYS_159	NZ	N_ASP_160	OD2	3.040
3PNW	O_LYS_557	NZ	O_ASP_560	OD1	3.174
3PNW	O_LYS_557	NZ	O_ASP_560	OD2	3.756
3PNW	P_ARG_25	NH2	P_ASP_71	OD1	3.282
3PNW	P_ARG_25	NH2	P_ASP_71	OD2	3.069
3PNW	P_ARG_62	NH2	P_GLU_82	OE2	3.510
3PNW	P_ARG_62	NH2	P_ASP_83	OD1	2.765
3PNW	P_ARG_62	NH2	P_ASP_83	OD2	3.484
3PNW	P_LYS_106	NZ	P_GLU_108	OE2	3.990
3PNW	P_LYS_106	NZ	P_GLU_168	OE1	2.957
3PNW	P_LYS_106	NZ	P_GLU_168	OE2	2.919
3PNW	P_LYS_152	NZ	P_GLU_198	OE1	3.282
3PNW	P_LYS_186	NZ	P_GLU_190	OE1	3.349
3PNW	P_LYS_186	NZ	P_GLU_190	OE2	3.801
3PNW	Q_ARG_41	NH1	Q_GLU_49	OE1	2.971
3PNW	Q_ARG_41	NH1	Q_GLU_49	OE2	3.698
3PNW	Q_ARG_41	NH1	Q_ASP_93	OD1	3.890
3PNW	Q_ARG_41	NH2	Q_ASP_93	OD1	2.813
3PNW	Q_LYS_68	NZ	Q_ASP_65	OD1	2.792
3PNW	Q_ARG_70	NH1	Q_ASP_93	OD1	3.070
3PNW	Q_ARG_70	NH1	Q_ASP_93	OD2	3.435
3PNW	Q_ARG_70	NH2	Q_ASP_93	OD1	3.828
3PNW	Q_ARG_70	NH2	Q_ASP_93	OD2	2.681
3PNW	Q_LYS_79	NZ	Q_ASP_76	OD2	3.067
3PNW	Q_ARG_101	NH2	Q_ASP_117	OD2	3.288
3PNW	Q_ARG_104	NH1	R_GLU_599	OE1	3.284
3PNW	Q_LYS_159	NZ	Q_ASP_160	OD1	2.929
3PNW	Q_LYS_159	NZ	Q_ASP_160	OD2	2.916
3PNW	R_LYS_590	NZ	R_GLU_576	OE1	3.429
3PNW	S_ARG_62	NH2	S_GLU_82	OE2	3.335
3PNW	S_ARG_62	NH2	S_ASP_83	OD1	3.032
3PNW	S_LYS_106	NZ	S_GLU_168	OE1	2.994
3PNW	S_LYS_106	NZ	S_GLU_168	OE2	3.350
3PNW	S_LYS_186	NZ	S_GLU_190	OE2	3.826
3PNW	S_HIS_192	ND1	S_ASP_154	OD2	2.873
3PNW	S_ARG_214	NH2	S_GLU_190	OE1	3.425
3PNW	T_ARG_41	NH1	T_GLU_49	OE1	3.208
3PNW	T_ARG_41	NH1	T_GLU_49	OE2	3.692
3PNW	T_ARG_41	NH1	T_ASP_93	OD1	3.888
3PNW	T_ARG_41	NH2	T_ASP_93	OD1	2.764
3PNW	T_ARG_70	NH1	T_ASP_93	OD1	2.873
3PNW	T_ARG_70	NH1	T_ASP_93	OD2	3.677
3PNW	T_ARG_70	NH2	T_ASP_93	OD1	3.433
3PNW	T_ARG_70	NH2	T_ASP_93	OD2	2.704
3PNW	T_LYS_79	NZ	T_ASP_76	OD2	2.965
3PNW	T_ARG_101	NH2	T_ASP_117	OD2	3.568

3PNW	T_ARG_104	NH1	U_GLU_599	OE2	2.955
3PNW	T_LYS_159	NZ	T_ASP_160	OD1	2.985
3PNW	T_LYS_159	NZ	T_ASP_160	OD2	2.572
3PNW	U_LYS_590	NZ	U_GLU_576	OE1	3.326
3PNW	V_ARG_62	NH2	V_GLU_82	OE2	3.071
3PNW	V_ARG_62	NH2	V_ASP_83	OD1	3.114
3PNW	V_ARG_62	NH2	V_ASP_83	OD2	3.749
3PNW	V_LYS_106	NZ	V_GLU_168	OE1	3.033
3PNW	V_LYS_106	NZ	V_GLU_168	OE2	2.809
3PNW	V_LYS_152	NZ	V_GLU_198	OE1	3.564
3PNW	V_LYS_152	NZ	V_GLU_198	OE2	3.540
3PNW	V_LYS_186	NZ	V_GLU_190	OE1	3.466
3PNW	V_HIS_192	ND1	V_ASP_154	OD2	2.830
3PNW	W_ARG_41	NH1	W_GLU_49	OE1	3.191
3PNW	W_ARG_41	NH1	W_GLU_49	OE2	3.754
3PNW	W_ARG_41	NH1	W_ASP_93	OD1	3.797
3PNW	W_ARG_41	NH2	W_ASP_93	OD1	2.759
3PNW	W_ARG_70	NH1	W_ASP_93	OD1	3.055
3PNW	W_ARG_70	NH1	W_ASP_93	OD2	3.508
3PNW	W_ARG_70	NH2	W_ASP_93	OD1	3.808
3PNW	W_ARG_70	NH2	W_ASP_93	OD2	2.825
3PNW	W_LYS_79	NZ	W_ASP_76	OD2	3.031
3PNW	W_ARG_101	NH2	W_ASP_117	OD2	3.265
3PNW	W_ARG_104	NH2	X_GLU_599	OE2	3.113
3PNW	W_LYS_159	NZ	W_ASP_160	OD1	3.077
3PNW	W_LYS_159	NZ	W_ASP_160	OD2	3.386
3PNW	X_LYS_590	NZ	X_GLU_576	OE1	3.570

Table 456: 3PNW-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3PP4	H_ARG_38	NH1	H_ASP_90	OD1	2.857
3PP4	H_ARG_38	NH2	H_ASP_90	OD1	3.876
3PP4	H_ARG_50	NH2	H_ASP_59	OD2	3.031
3PP4	H_LYS_63	NZ	H_GLU_46	OE1	3.948
3PP4	H_ARG_67	NH1	H_ASP_90	OD1	3.622
3PP4	H_ARG_67	NH1	H_ASP_90	OD2	2.862
3PP4	H_ARG_67	NH2	H_ASP_90	OD1	2.967
3PP4	H_ARG_67	NH2	H_ASP_90	OD2	3.587
3PP4	H_ARG_87	NH2	H_GLU_89	OE2	3.547
3PP4	H_LYS_149	NZ	H_ASP_150	OD1	3.507
3PP4	H_LYS_215	NZ	L_GLU_128	OE1	3.038
3PP4	H_LYS_215	NZ	L_GLU_128	OE2	2.948
3PP4	L_LYS_27	NZ	L_GLU_98	OE1	2.607
3PP4	L_LYS_27	NZ	L_GLU_98	OE2	3.934
3PP4	L_ARG_66	NH2	L_ASP_87	OD1	2.843
3PP4	L_ARG_66	NH2	L_ASP_87	OD2	3.715
3PP4	L_LYS_108	NZ	L_GLU_170	OE1	2.761
3PP4	L_LYS_108	NZ	L_GLU_170	OE2	3.634
3PP4	L_ARG_147	NH1	L_GLU_110	OE1	3.275
3PP4	L_ARG_147	NH1	L_GLU_110	OE2	3.845
3PP4	L_ARG_147	NH2	L_GLU_110	OE1	3.278
3PP4	L_ARG_147	NH2	L_GLU_110	OE2	2.614
3PP4	L_LYS_154	NZ	L_GLU_200	OE1	2.680
3PP4	L_LYS_188	NZ	L_GLU_192	OE2	3.037
3PP4	L_HIS_194	ND1	L_ASP_156	OD2	3.533
3PP4	P_LYS_175	NZ	H_ASP_57	OD2	3.518

Table 457: 3PP4-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3Q3G	C_ARG_67	NH1	C_GLU_87	OE2	3.777
3Q3G	C_ARG_67	NH1	C_ASP_88	OD1	2.749
3Q3G	C_ARG_67	NH1	C_ASP_88	OD2	3.177
3Q3G	C_ARG_67	NH2	C_GLU_87	OE2	3.999
3Q3G	C_LYS_109	NZ	D_GLU_44	OE1	3.620
3Q3G	C_LYS_113	NZ	C_GLU_17	OE1	3.434
3Q3G	C_LYS_113	NZ	C_GLU_17	OE2	3.287
3Q3G	C_LYS_153	NZ	C_GLU_160	OE2	3.996
3Q3G	C_LYS_153	NZ	C_GLU_201	OE1	3.776
3Q3G	C_LYS_155	NZ	C_GLU_201	OE2	3.559
3Q3G	C_ARG_161	NH2	C_GLU_191	OE2	3.538
3Q3G	C_LYS_205	NZ	C_ASP_116	OD1	3.501
3Q3G	C_LYS_205	NZ	C_ASP_116	OD2	3.005
3Q3G	D_LYS_21	NZ	H_GLU_202	OE2	2.633
3Q3G	D_ARG_42	NH1	D_GLU_48	OE1	3.596
3Q3G	D_ARG_52	NH1	G_GLU_179	OE2	3.405
3Q3G	D_ARG_52	NH2	G_GLU_178	OE1	2.845
3Q3G	D_ARG_52	NH2	G_GLU_179	OE2	2.628
3Q3G	D_LYS_69	NZ	D_ASP_92	OD1	3.860
3Q3G	D_LYS_69	NZ	D_ASP_92	OD2	2.915
3Q3G	D_LYS_219	NZ	C_GLU_129	OE2	3.237
3Q3G	G_ARG_152	NH1	G_ASP_149	OD1	2.824
3Q3G	G_LYS_166	NZ	G_GLU_320	OE1	3.506
3Q3G	G_ARG_196	NH1	G_GLU_155	OE1	2.640
3Q3G	G_ARG_196	NH1	G_GLU_155	OE2	3.732
3Q3G	G_ARG_196	NH2	G_GLU_155	OE1	3.730
3Q3G	G_ARG_196	NH2	G_GLU_155	OE2	3.858
3Q3G	G_ARG_196	NH2	G_GLU_162	OE1	2.809
3Q3G	G_ARG_208	NH1	D_GLU_101	OE1	3.693
3Q3G	G_ARG_208	NH1	D_GLU_101	OE2	2.792
3Q3G	G_ARG_208	NH1	G_GLU_178	OE2	2.763
3Q3G	G_ARG_208	NH2	D_GLU_101	OE1	2.994
3Q3G	G_ARG_208	NH2	D_GLU_101	OE2	3.045
3Q3G	G_LYS_217	NZ	G_GLU_221	OE2	3.531
3Q3G	G_ARG_220	NH2	G_GLU_258	OE1	3.606
3Q3G	G_ARG_220	NH2	G_GLU_258	OE2	3.754
3Q3G	G_ARG_230	NH1	G_ASP_132	OD1	3.893
3Q3G	G_ARG_230	NH1	G_ASP_134	OD1	2.660
3Q3G	G_ARG_230	NH2	G_ASP_132	OD1	3.914
3Q3G	G_LYS_235	NZ	G_GLU_262	OE1	3.889
3Q3G	G_ARG_266	NH1	G_ASP_260	OD1	2.915
3Q3G	G_ARG_266	NH2	G_ASP_260	OD1	3.197
3Q3G	G_LYS_279	NZ	G_GLU_244	OE2	3.345
3Q3G	G_LYS_306	NZ	G_GLU_303	OE2	2.592
3Q3G	G_ARG_313	NH2	G_GLU_314	OE2	2.833
3Q3G	A_ARG_67	NH1	A_GLU_87	OE2	3.721
3Q3G	A_ARG_67	NH1	A_ASP_88	OD1	2.647
3Q3G	A_ARG_67	NH1	A_ASP_88	OD2	3.126
3Q3G	A_ARG_67	NH2	A_GLU_87	OE2	3.644
3Q3G	A_LYS_113	NZ	A_GLU_17	OE1	3.382
3Q3G	A_LYS_113	NZ	A_GLU_17	OE2	3.288
3Q3G	A_LYS_153	NZ	A_GLU_201	OE1	3.786
3Q3G	A_ARG_161	NH1	A_GLU_191	OE2	3.907
3Q3G	A_ARG_161	NH2	A_GLU_191	OE2	2.992
3Q3G	A_LYS_205	NZ	A_ASP_116	OD1	3.527
3Q3G	A_LYS_205	NZ	A_ASP_116	OD2	2.946
3Q3G	B_LYS_21	NZ	K_GLU_202	OE2	2.668

3Q3G	B_ARG_42	NH2	B_GLU_91	OE2	2.813
3Q3G	B_ARG_52	NH1	E_GLU_179	OE2	3.409
3Q3G	B_ARG_52	NH2	E_GLU_178	OE1	2.858
3Q3G	B_ARG_52	NH2	E_GLU_179	OE2	2.617
3Q3G	B_LYS_69	NZ	B_ASP_92	OD1	3.850
3Q3G	B_LYS_69	NZ	B_ASP_92	OD2	2.909
3Q3G	B_LYS_219	NZ	A_GLU_129	OE2	3.294
3Q3G	E_ARG_152	NH1	E_ASP_149	OD1	2.849
3Q3G	E_ARG_196	NH1	E_GLU_155	OE2	3.730
3Q3G	E_ARG_196	NH2	E_GLU_162	OE1	2.828
3Q3G	E_ARG_208	NH1	B_GLU_101	OE1	3.701
3Q3G	E_ARG_208	NH1	B_GLU_101	OE2	2.888
3Q3G	E_ARG_208	NH1	E_GLU_178	OE2	2.758
3Q3G	E_ARG_208	NH2	B_GLU_101	OE1	3.046
3Q3G	E_ARG_208	NH2	B_GLU_101	OE2	3.227
3Q3G	E_LYS_217	NZ	E_GLU_221	OE2	3.514
3Q3G	E_ARG_220	NH2	E_GLU_258	OE1	3.606
3Q3G	E_ARG_220	NH2	E_GLU_258	OE2	3.748
3Q3G	E_ARG_230	NH1	E_ASP_132	OD1	3.896
3Q3G	E_ARG_230	NH1	E_ASP_134	OD1	2.958
3Q3G	E_ARG_230	NH2	E_ASP_132	OD1	3.948
3Q3G	E_LYS_235	NZ	E_GLU_262	OE1	3.891
3Q3G	E_ARG_266	NH1	E_ASP_260	OD1	2.728
3Q3G	E_ARG_266	NH2	E_ASP_260	OD1	3.401
3Q3G	E_ARG_276	NH1	E_ASP_273	OD1	3.848
3Q3G	E_LYS_306	NZ	E_GLU_303	OE1	3.875
3Q3G	E_LYS_306	NZ	E_GLU_303	OE2	2.953
3Q3G	E_ARG_313	NH2	E_GLU_314	OE2	2.838
3Q3G	F_ARG_67	NH1	F_GLU_87	OE2	3.457
3Q3G	F_ARG_67	NH1	F_ASP_88	OD1	2.936
3Q3G	F_ARG_67	NH1	F_ASP_88	OD2	3.406
3Q3G	F_ARG_67	NH2	F_GLU_87	OE2	3.930
3Q3G	F_LYS_113	NZ	F_GLU_17	OE1	3.384
3Q3G	F_LYS_113	NZ	F_GLU_17	OE2	3.304
3Q3G	F_LYS_153	NZ	F_GLU_201	OE1	3.790
3Q3G	F_LYS_155	NZ	F_GLU_160	OE2	3.570
3Q3G	F_ARG_161	NH1	F_GLU_191	OE2	3.911
3Q3G	F_ARG_161	NH2	F_GLU_191	OE2	3.286
3Q3G	F_LYS_205	NZ	F_ASP_116	OD1	3.529
3Q3G	F_LYS_205	NZ	F_ASP_116	OD2	2.950
3Q3G	H_LYS_40	NZ	H_ASP_92	OD1	3.981
3Q3G	H_ARG_42	NH2	H_GLU_91	OE2	3.153
3Q3G	H_ARG_52	NH1	L_GLU_179	OE2	3.532
3Q3G	H_ARG_52	NH2	L_GLU_178	OE1	2.972
3Q3G	H_ARG_52	NH2	L_GLU_179	OE2	2.629
3Q3G	H_LYS_61	NZ	L_GLU_179	OE2	3.923
3Q3G	H_LYS_69	NZ	H_ASP_92	OD1	3.838
3Q3G	H_LYS_69	NZ	H_ASP_92	OD2	2.905
3Q3G	H_LYS_219	NZ	F_GLU_129	OE2	3.319
3Q3G	I_ARG_152	NH1	I_ASP_149	OD1	2.842
3Q3G	I_ARG_196	NH1	L_GLU_155	OE1	2.643
3Q3G	I_ARG_196	NH1	L_GLU_155	OE2	3.755
3Q3G	I_ARG_196	NH2	L_GLU_155	OE1	3.725
3Q3G	I_ARG_196	NH2	L_GLU_155	OE2	3.863
3Q3G	I_ARG_196	NH2	L_GLU_162	OE1	2.829
3Q3G	I_ARG_208	NH1	H_GLU_101	OE1	3.704
3Q3G	I_ARG_208	NH1	H_GLU_101	OE2	2.809
3Q3G	I_ARG_208	NH1	L_GLU_178	OE2	2.759

3Q3G	I_ARG_208	NH2	H_GLU_101	OE1	3.098
3Q3G	I_ARG_208	NH2	H_GLU_101	OE2	3.125
3Q3G	I_LYS_217	NZ	I_GLU_221	OE2	3.508
3Q3G	I_ARG_220	NH2	I_GLU_258	OE1	3.602
3Q3G	I_ARG_220	NH2	I_GLU_258	OE2	3.748
3Q3G	I_ARG_230	NH1	I_ASP_132	OD1	3.884
3Q3G	I_ARG_230	NH1	I_ASP_134	OD1	2.627
3Q3G	I_ARG_230	NH2	I_ASP_132	OD1	3.901
3Q3G	I_LYS_235	NZ	I_GLU_262	OE1	3.888
3Q3G	I_ARG_266	NH1	I_ASP_260	OD1	2.847
3Q3G	I_ARG_266	NH2	I_ASP_260	OD1	3.632
3Q3G	I_ARG_276	NH1	I_ASP_273	OD1	3.306
3Q3G	I_ARG_293	NH1	I_ASP_294	OD1	2.569
3Q3G	I_ARG_293	NH1	I_ASP_294	OD2	3.199
3Q3G	I_ARG_293	NH2	I_ASP_294	OD2	3.674
3Q3G	I_LYS_306	NZ	I_GLU_303	OE2	2.953
3Q3G	I_ARG_313	NH2	I_GLU_314	OE2	2.841
3Q3G	J_ARG_67	NH1	J_GLU_87	OE2	3.904
3Q3G	J_ARG_67	NH1	J_ASP_88	OD1	2.685
3Q3G	J_ARG_67	NH1	J_ASP_88	OD2	2.963
3Q3G	J_ARG_67	NH2	J_GLU_87	OE2	3.860
3Q3G	J_LYS_109	NZ	K_GLU_44	OE1	3.972
3Q3G	J_LYS_113	NZ	J_GLU_17	OE1	3.413
3Q3G	J_LYS_113	NZ	J_GLU_17	OE2	3.281
3Q3G	J_LYS_153	NZ	J_GLU_201	OE1	3.780
3Q3G	J_LYS_155	NZ	J_GLU_201	OE2	2.804
3Q3G	J_ARG_161	NH1	J_GLU_191	OE2	3.912
3Q3G	J_ARG_161	NH2	J_GLU_191	OE2	3.262
3Q3G	J_LYS_205	NZ	J_ASP_116	OD1	3.511
3Q3G	J_LYS_205	NZ	J_ASP_116	OD2	2.982
3Q3G	K_LYS_40	NZ	K_ASP_92	OD1	3.980
3Q3G	K_ARG_52	NH1	L_GLU_179	OE2	3.394
3Q3G	K_ARG_52	NH2	L_GLU_178	OE1	2.871
3Q3G	K_ARG_52	NH2	L_GLU_179	OE2	2.626
3Q3G	K_LYS_69	NZ	K_ASP_92	OD1	3.854
3Q3G	K_LYS_69	NZ	K_ASP_92	OD2	2.911
3Q3G	K_LYS_219	NZ	J_GLU_129	OE2	3.216
3Q3G	L_ARG_152	NH1	L_ASP_149	OD1	2.835
3Q3G	L_ARG_196	NH1	L_GLU_155	OE1	2.611
3Q3G	L_ARG_196	NH1	L_GLU_155	OE2	3.736
3Q3G	L_ARG_196	NH2	L_GLU_155	OE1	3.784
3Q3G	L_ARG_196	NH2	L_GLU_162	OE1	2.844
3Q3G	L_ARG_208	NH1	K_GLU_101	OE1	3.706
3Q3G	L_ARG_208	NH1	K_GLU_101	OE2	2.777
3Q3G	L_ARG_208	NH1	L_GLU_178	OE2	2.802
3Q3G	L_ARG_208	NH2	K_GLU_101	OE1	3.099
3Q3G	L_ARG_208	NH2	K_GLU_101	OE2	3.162
3Q3G	L_LYS_217	NZ	L_GLU_221	OE2	3.517
3Q3G	L_ARG_220	NH2	L_GLU_258	OE1	3.603
3Q3G	L_ARG_220	NH2	L_GLU_258	OE2	3.763
3Q3G	L_ARG_230	NH1	L_ASP_132	OD1	3.881
3Q3G	L_ARG_230	NH1	L_ASP_134	OD1	2.707
3Q3G	L_ARG_230	NH1	L_ASP_134	OD2	3.460
3Q3G	L_ARG_230	NH2	L_ASP_132	OD1	3.905
3Q3G	L_LYS_235	NZ	L_GLU_262	OE1	3.906
3Q3G	L_ARG_266	NH1	L_ASP_260	OD1	2.751
3Q3G	L_ARG_266	NH2	L_ASP_260	OD1	2.771
3Q3G	L_ARG_266	NH2	L_ASP_260	OD2	3.493

3Q3G	L_ARG_276	NH2	L_ASP_273	OD1	3.904
3Q3G	L_ARG_276	NH2	L_ASP_273	OD2	3.992
3Q3G	L_ARG_281	NH1	L_GLU_278	OE2	3.655
3Q3G	L_LYS_306	NZ	L_GLU_303	OE2	3.422
3Q3G	L_ARG_313	NH2	L_GLU_314	OE2	2.844

Table 458: 3Q3G-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3QA3	C_LYS_24	NZ	C_ASP_76	OD2	3.522
3QA3	C_ARG_67	NH1	C_GLU_87	OE2	3.269
3QA3	C_ARG_67	NH1	C_ASP_88	OD1	2.660
3QA3	C_ARG_67	NH1	C_ASP_88	OD2	2.924
3QA3	C_ARG_67	NH2	C_GLU_87	OE2	3.168
3QA3	C_LYS_109	NZ	C_ASP_171	OD1	3.926
3QA3	C_LYS_109	NZ	D_GLU_44	OE1	3.919
3QA3	C_LYS_113	NZ	C_GLU_17	OE1	3.598
3QA3	C_LYS_113	NZ	C_GLU_17	OE2	3.105
3QA3	C_LYS_155	NZ	C_GLU_201	OE2	3.611
3QA3	C_ARG_161	NH2	C_GLU_191	OE2	3.603
3QA3	C_LYS_189	NZ	C_GLU_193	OE1	3.703
3QA3	C_LYS_205	NZ	C_ASP_116	OD1	3.367
3QA3	C_LYS_205	NZ	C_ASP_116	OD2	2.961
3QA3	C_ARG_217	NH1	C_GLU_193	OE2	3.785
3QA3	D_LYS_21	NZ	B_GLU_202	OE2	2.710
3QA3	D_LYS_40	NZ	D_ASP_92	OD1	3.621
3QA3	D_ARG_42	NH2	D_GLU_91	OE1	3.456
3QA3	D_ARG_52	NH1	G_GLU_179	OE2	3.492
3QA3	D_ARG_52	NH2	G_GLU_178	OE1	3.012
3QA3	D_ARG_52	NH2	G_GLU_179	OE2	2.776
3QA3	D_LYS_61	NZ	G_GLU_179	OE1	3.896
3QA3	D_LYS_61	NZ	G_GLU_179	OE2	3.867
3QA3	D_LYS_69	NZ	D_ASP_92	OD2	3.339
3QA3	D_LYS_219	NZ	C_GLU_129	OE2	3.586
3QA3	G_ARG_151	NH1	G_GLU_155	OE1	3.186
3QA3	G_ARG_151	NH1	G_GLU_155	OE2	3.465
3QA3	G_ARG_152	NH1	G_ASP_149	OD1	3.120
3QA3	G_ARG_196	NH2	G_GLU_162	OE1	3.407
3QA3	G_ARG_208	NH1	D_GLU_101	OE1	3.094
3QA3	G_ARG_208	NH1	D_GLU_101	OE2	3.755
3QA3	G_ARG_208	NH1	G_GLU_178	OE2	2.905
3QA3	G_ARG_208	NH2	D_GLU_101	OE1	2.802
3QA3	G_LYS_217	NZ	G_GLU_221	OE1	3.238
3QA3	G_LYS_217	NZ	G_GLU_221	OE2	3.591
3QA3	G_ARG_220	NH2	G_GLU_258	OE1	3.098
3QA3	G_ARG_220	NH2	G_GLU_258	OE2	3.589
3QA3	G_ARG_230	NH1	G_ASP_134	OD1	2.776
3QA3	G_LYS_235	NZ	G_GLU_262	OE1	3.322
3QA3	G_ARG_266	NH1	G_ASP_260	OD1	3.130
3QA3	G_ARG_266	NH2	G_ASP_260	OD1	3.273
3QA3	G_ARG_266	NH2	G_ASP_260	OD2	3.917
3QA3	G_ARG_281	NH1	G_GLU_278	OE2	3.336
3QA3	G_ARG_293	NH2	G_ASP_294	OD2	3.535
3QA3	G_LYS_306	NZ	F_GLU_61	OE1	2.676
3QA3	G_LYS_306	NZ	F_GLU_61	OE2	3.962
3QA3	G_ARG_313	NH2	G_GLU_314	OE2	3.236
3QA3	A_LYS_24	NZ	A_ASP_76	OD2	3.526
3QA3	A_ARG_67	NH1	A_GLU_87	OE2	3.266
3QA3	A_ARG_67	NH1	A_ASP_88	OD1	2.659
3QA3	A_ARG_67	NH1	A_ASP_88	OD2	2.926
3QA3	A_ARG_67	NH2	A_GLU_87	OE2	3.154
3QA3	A_LYS_109	NZ	A_ASP_171	OD1	3.971
3QA3	A_LYS_113	NZ	A_GLU_17	OE1	3.580
3QA3	A_LYS_113	NZ	A_GLU_17	OE2	3.100
3QA3	A_LYS_155	NZ	A_GLU_201	OE2	2.971
3QA3	A_LYS_205	NZ	A_ASP_116	OD1	3.377

3QA3	A_LYS_205	NZ	A_ASP_116	OD2	2.963
3QA3	B_LYS_40	NZ	B_ASP_92	OD1	3.602
3QA3	B_ARG_52	NH1	E_GLU_179	OE2	3.674
3QA3	B_ARG_52	NH2	E_GLU_178	OE1	3.139
3QA3	B_ARG_52	NH2	E_GLU_179	OE2	2.772
3QA3	B_LYS_61	NZ	E_GLU_179	OE1	3.626
3QA3	B_LYS_61	NZ	E_GLU_179	OE2	3.531
3QA3	B_LYS_69	NZ	B_ASP_92	OD2	3.326
3QA3	B_LYS_219	NZ	A_GLU_129	OE2	3.689
3QA3	E_ARG_152	NH1	E_ASP_149	OD1	3.421
3QA3	E_ARG_152	NH1	E_GLU_303	OE2	3.891
3QA3	E_ARG_196	NH1	E_GLU_155	OE2	2.779
3QA3	E_ARG_196	NH1	E_GLU_162	OE1	3.631
3QA3	E_ARG_196	NH2	E_GLU_155	OE1	3.951
3QA3	E_ARG_196	NH2	E_GLU_155	OE2	3.547
3QA3	E_ARG_196	NH2	E_GLU_162	OE1	3.609
3QA3	E_ARG_208	NH1	B_GLU_101	OE1	3.112
3QA3	E_ARG_208	NH1	B_GLU_101	OE2	3.639
3QA3	E_ARG_208	NH1	E_GLU_178	OE1	3.992
3QA3	E_ARG_208	NH1	E_GLU_178	OE2	2.905
3QA3	E_ARG_208	NH2	B_GLU_101	OE1	2.913
3QA3	E_ARG_208	NH2	B_GLU_101	OE2	3.978
3QA3	E_LYS_217	NZ	E_GLU_221	OE1	3.240
3QA3	E_LYS_217	NZ	E_GLU_221	OE2	3.588
3QA3	E_ARG_220	NH2	E_GLU_258	OE1	3.091
3QA3	E_ARG_220	NH2	E_GLU_258	OE2	3.588
3QA3	E_ARG_230	NH1	E_ASP_134	OD1	2.769
3QA3	E_LYS_235	NZ	E_GLU_262	OE1	3.320
3QA3	E_ARG_266	NH1	E_ASP_260	OD1	3.181
3QA3	E_ARG_266	NH2	E_ASP_260	OD1	3.305
3QA3	E_ARG_281	NH1	E_GLU_278	OE2	2.753
3QA3	F_LYS_24	NZ	F_ASP_76	OD2	3.520
3QA3	F_ARG_67	NH1	F_GLU_87	OE2	3.259
3QA3	F_ARG_67	NH1	F_ASP_88	OD1	2.663
3QA3	F_ARG_67	NH1	F_ASP_88	OD2	2.926
3QA3	F_ARG_67	NH2	F_GLU_87	OE2	3.150
3QA3	F_LYS_113	NZ	F_GLU_17	OE1	3.577
3QA3	F_LYS_113	NZ	F_GLU_17	OE2	3.091
3QA3	F_LYS_153	NZ	F_GLU_201	OE1	3.153
3QA3	F_LYS_155	NZ	F_GLU_201	OE1	3.670
3QA3	F_LYS_155	NZ	F_GLU_201	OE2	3.187
3QA3	F_HIS_195	ND1	F_ASP_157	OD2	2.743
3QA3	F_LYS_205	NZ	F_ASP_116	OD1	3.352
3QA3	F_LYS_205	NZ	F_ASP_116	OD2	2.987
3QA3	F_ARG_217	NH1	F_GLU_193	OE2	3.646
3QA3	H_LYS_21	NZ	K_GLU_202	OE1	2.630
3QA3	H_LYS_40	NZ	H_ASP_92	OD1	3.607
3QA3	H_ARG_52	NH1	L_GLU_179	OE2	3.536
3QA3	H_ARG_52	NH2	L_GLU_178	OE1	3.079
3QA3	H_ARG_52	NH2	L_GLU_179	OE2	2.753
3QA3	H_LYS_61	NZ	L_GLU_179	OE1	3.833
3QA3	H_LYS_61	NZ	L_GLU_179	OE2	3.714
3QA3	H_LYS_69	NZ	H_ASP_92	OD2	3.333
3QA3	H_LYS_219	NZ	F_GLU_129	OE2	3.683
3QA3	I_ARG_151	NH1	L_GLU_155	OE1	3.176
3QA3	I_ARG_151	NH1	L_GLU_155	OE2	3.423
3QA3	I_ARG_152	NH1	I_ASP_149	OD1	3.295
3QA3	I_ARG_208	NH1	H_GLU_101	OE1	2.952

3QA3	I_ARG_208	NH1	H_GLU_101	OE2	3.280
3QA3	I_ARG_208	NH1	L_GLU_178	OE2	2.910
3QA3	I_ARG_208	NH2	H_GLU_101	OE1	2.858
3QA3	I_ARG_208	NH2	H_GLU_101	OE2	3.749
3QA3	I_LYS_217	NZ	L_GLU_221	OE1	3.237
3QA3	I_LYS_217	NZ	L_GLU_221	OE2	3.599
3QA3	I_ARG_220	NH2	L_GLU_258	OE1	3.094
3QA3	I_ARG_220	NH2	L_GLU_258	OE2	3.593
3QA3	I_ARG_230	NH1	L_ASP_134	OD1	2.778
3QA3	I_LYS_235	NZ	L_GLU_262	OE1	3.330
3QA3	I_ARG_266	NH1	L_ASP_260	OD1	2.823
3QA3	I_ARG_266	NH2	L_ASP_260	OD1	2.813
3QA3	I_ARG_266	NH2	L_ASP_260	OD2	3.696
3QA3	I_ARG_293	NH2	L_ASP_294	OD2	3.520
3QA3	I_LYS_306	NZ	C_GLU_61	OE1	3.836
3QA3	J_LYS_24	NZ	J_ASP_76	OD2	3.532
3QA3	J_ARG_67	NH1	J_GLU_87	OE2	3.263
3QA3	J_ARG_67	NH1	J_ASP_88	OD1	2.670
3QA3	J_ARG_67	NH1	J_ASP_88	OD2	2.921
3QA3	J_ARG_67	NH2	J_GLU_87	OE2	3.148
3QA3	J_LYS_109	NZ	K_GLU_44	OE1	3.982
3QA3	J_LYS_113	NZ	J_GLU_17	OE1	3.620
3QA3	J_LYS_113	NZ	J_GLU_17	OE2	3.124
3QA3	J_LYS_205	NZ	J_ASP_116	OD1	3.342
3QA3	J_LYS_205	NZ	J_ASP_116	OD2	2.981
3QA3	K_LYS_40	NZ	K_ASP_92	OD1	3.624
3QA3	K_ARG_52	NH1	L_GLU_179	OE2	3.477
3QA3	K_ARG_52	NH2	L_GLU_178	OE1	3.052
3QA3	K_ARG_52	NH2	L_GLU_179	OE2	2.734
3QA3	K_LYS_61	NZ	L_GLU_179	OE1	3.839
3QA3	K_LYS_61	NZ	L_GLU_179	OE2	3.819
3QA3	K_LYS_69	NZ	K_ASP_92	OD2	3.339
3QA3	K_LYS_219	NZ	J_GLU_129	OE2	3.538
3QA3	L_ARG_152	NH1	L_ASP_149	OD1	3.084
3QA3	L_LYS_165	NZ	L_GLU_162	OE2	3.035
3QA3	L_ARG_196	NH2	L_GLU_162	OE1	3.491
3QA3	L_ARG_208	NH1	K_GLU_101	OE1	3.296
3QA3	L_ARG_208	NH1	K_GLU_101	OE2	3.152
3QA3	L_ARG_208	NH1	L_GLU_178	OE1	3.993
3QA3	L_ARG_208	NH1	L_GLU_178	OE2	2.907
3QA3	L_ARG_208	NH2	K_GLU_101	OE1	3.120
3QA3	L_ARG_208	NH2	K_GLU_101	OE2	3.548
3QA3	L_LYS_217	NZ	L_GLU_221	OE1	3.242
3QA3	L_LYS_217	NZ	L_GLU_221	OE2	3.595
3QA3	L_ARG_220	NH2	L_GLU_258	OE1	3.097
3QA3	L_ARG_220	NH2	L_GLU_258	OE2	3.600
3QA3	L_ARG_230	NH1	L_ASP_134	OD1	2.780
3QA3	L_LYS_235	NZ	L_GLU_262	OE1	3.332
3QA3	L_ARG_266	NH1	L_ASP_260	OD1	2.676
3QA3	L_ARG_266	NH2	L_ASP_260	OD1	3.599
3QA3	L_LYS_279	NZ	L_GLU_244	OE1	3.218
3QA3	L_LYS_279	NZ	L_GLU_244	OE2	3.599
3QA3	L_ARG_281	NH1	L_GLU_278	OE2	2.973
3QA3	L_ARG_293	NH2	L_ASP_294	OD2	3.523

Table 459: 3QA3-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3QG6	A_ARG.61	NH1	A_ASP.82	OD1	3.432
3QG6	A_ARG.61	NH1	A_ASP.82	OD2	2.717
3QG6	A_ARG.61	NH2	A_GLU.79	OE1	3.943
3QG6	A_ARG.61	NH2	A_ASP.82	OD1	3.288
3QG6	A_ARG.61	NH2	A_ASP.82	OD2	3.964
3QG6	A_LYS.142	NZ	A_GLU.105	OE1	3.461
3QG6	A_LYS.142	NZ	A_GLU.105	OE2	3.669
3QG6	A_LYS.147	NZ	A_GLU.154	OE1	3.545
3QG6	A_LYS.149	NZ	A_GLU.195	OE1	2.687
3QG6	A_LYS.149	NZ	A_GLU.195	OE2	3.955
3QG6	A_ARG.155	NH1	A_GLU.185	OE1	3.832
3QG6	A_ARG.155	NH1	A_GLU.185	OE2	3.376
3QG6	A_ARG.155	NH2	A_GLU.185	OE1	3.065
3QG6	A_ARG.155	NH2	A_GLU.185	OE2	3.907
3QG6	A_LYS.183	NZ	A_GLU.187	OE1	3.106
3QG6	A_LYS.183	NZ	A_GLU.187	OE2	3.334
3QG6	A_ARG.188	NH1	H_ASP.86	OD2	3.997
3QG6	A_ARG.188	NH2	H_ASP.86	OD1	3.422
3QG6	A_HIS.189	ND1	A_ASP.151	OD2	2.899
3QG6	A_HIS.189	NE2	A_GLU.185	OE2	3.272
3QG6	A_HIS.189	NE2	H_GLU.85	OE1	3.361
3QG6	A_HIS.189	NE2	H_GLU.85	OE2	3.215
3QG6	A_LYS.199	NZ	A_ASP.110	OD2	3.955
3QG6	B_ARG.38	NH1	B_ASP.86	OD1	2.928
3QG6	B_ARG.38	NH2	B_GLU.46	OE1	2.323
3QG6	B_LYS.44	NZ	B_GLU.46	OE2	3.659
3QG6	B_LYS.44	NZ	L_ASP.151	OD2	2.912
3QG6	B_LYS.64	NZ	L_GLU.187	OE1	3.778
3QG6	B_LYS.75	NZ	B_ASP.72	OD2	3.646
3QG6	B_ARG.94	NH2	B_ASP.101	OD2	2.932
3QG6	B_LYS.221	NZ	A_GLU.123	OE1	2.433
3QG6	H_ARG.38	NH1	H_ASP.86	OD1	2.717
3QG6	H_ARG.38	NH2	H_GLU.46	OE1	2.691
3QG6	H_ARG.38	NH2	H_ASP.86	OD1	3.824
3QG6	H_LYS.44	NZ	A_ASP.151	OD2	2.924
3QG6	H_LYS.44	NZ	H_GLU.46	OE2	3.702
3QG6	H_LYS.64	NZ	A_GLU.187	OE1	3.924
3QG6	H_LYS.75	NZ	H_ASP.72	OD2	3.688
3QG6	H_ARG.94	NH1	H_ASP.101	OD2	2.954
3QG6	H_LYS.221	NZ	L_GLU.123	OE1	2.733
3QG6	L_ARG.61	NH1	L_ASP.82	OD1	2.705
3QG6	L_ARG.61	NH1	L_ASP.82	OD2	2.689
3QG6	L_ARG.61	NH2	L_GLU.79	OE1	3.908
3QG6	L_ARG.61	NH2	L_GLU.79	OE2	3.936
3QG6	L_LYS.142	NZ	L_GLU.105	OE1	3.323
3QG6	L_LYS.142	NZ	L_GLU.105	OE2	3.219
3QG6	L_LYS.147	NZ	L_GLU.154	OE1	3.582
3QG6	L_LYS.149	NZ	L_GLU.195	OE1	2.845
3QG6	L_ARG.155	NH1	L_GLU.185	OE1	3.862
3QG6	L_ARG.155	NH1	L_GLU.185	OE2	3.392
3QG6	L_ARG.155	NH2	L_GLU.185	OE1	3.092
3QG6	L_ARG.155	NH2	L_GLU.185	OE2	3.899
3QG6	L_LYS.183	NZ	L_GLU.187	OE1	3.324
3QG6	L_LYS.183	NZ	L_GLU.187	OE2	3.444
3QG6	L_HIS.189	ND1	L_ASP.151	OD2	2.895
3QG6	L_HIS.189	NE2	B_GLU.85	OE1	3.320
3QG6	L_HIS.189	NE2	B_GLU.85	OE2	3.623

3QG6	L_HIS_189	NE2	L_GLU_185	OE2	3.346
3QG6	L_LYS_199	NZ	L_ASP_110	OD2	3.663

Table 460: 3QG6-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3QG7	H_ARG_38	NH1	H_ASP_86	OD1	2.959
3QG7	H_ARG_38	NH2	H_GLU_46	OE1	2.726
3QG7	H_ARG_94	NH2	H_ASP_101	OD2	3.399
3QG7	H_LYS_221	NZ	L_GLU_123	OE2	2.769
3QG7	H_LYS_222	NZ	H_GLU_226	OE2	3.925
3QG7	L_ARG_61	NH1	L_ASP_82	OD2	3.032
3QG7	L_ARG_61	NH2	L_GLU_79	OE1	3.794
3QG7	L_ARG_61	NH2	L_ASP_82	OD1	3.231
3QG7	L_ARG_61	NH2	L_ASP_82	OD2	3.013
3QG7	L_LYS_103	NZ	L_ASP_165	OD1	3.787
3QG7	L_LYS_147	NZ	L_GLU_195	OE1	3.261
3QG7	L_LYS_149	NZ	L_GLU_195	OE1	3.464
3QG7	L_LYS_149	NZ	L_GLU_195	OE2	2.727
3QG7	L_ARG_155	NH1	L_GLU_185	OE1	2.977
3QG7	L_LYS_183	NZ	L_GLU_187	OE1	2.941
3QG7	L_LYS_183	NZ	L_GLU_187	OE2	2.894
3QG7	L_LYS_199	NZ	L_ASP_110	OD2	3.998

Table 461: 3QG7-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3QO1	A_ARG_24	NH1	A_ASP_75	OD1	3.412
3QO1	A_ARG_24	NH2	A_ASP_75	OD1	2.963
3QO1	A_ARG_31	NH1	A_ASP_37	OD1	3.003
3QO1	A_ARG_31	NH2	A_ASP_33	OD1	3.693
3QO1	A_ARG_31	NH2	A_ASP_33	OD2	3.104
3QO1	A_HIS_35	ND1	A_ASP_33	OD1	3.949
3QO1	A_HIS_35	ND1	A_ASP_33	OD2	3.517
3QO1	A_LYS_44	NZ	A_GLU_86	OE1	3.342
3QO1	A_ARG_59	NH2	A_ASP_65	OD1	3.479
3QO1	A_ARG_66	NH2	A_ASP_87	OD1	2.560
3QO1	A_ARG_66	NH2	A_ASP_87	OD2	2.753
3QO1	B_ARG_38	NH1	B_GLU_46	OE1	3.400
3QO1	B_ARG_38	NH1	B_ASP_92	OD1	3.707
3QO1	B_ARG_38	NH2	B_ASP_92	OD1	2.890
3QO1	B_LYS_52	NZ	B_GLU_56	OE2	2.709
3QO1	B_ARG_53	NH1	B_GLU_56	OE1	3.115
3QO1	B_ARG_69	NH1	B_ASP_92	OD1	3.910
3QO1	B_ARG_69	NH1	B_ASP_92	OD2	2.658
3QO1	B_ARG_69	NH2	B_ASP_92	OD1	3.220
3QO1	B_ARG_69	NH2	B_ASP_92	OD2	3.334
3QO1	B_ARG_74	NH1	B_ASP_58	OD1	2.936
3QO1	B_ARG_74	NH2	B_ASP_58	OD1	3.003
3QO1	B_ARG_74	NH2	B_ASP_58	OD2	3.404
3QO1	B_ARG_74	NH2	B_ASP_76	OD1	3.459
3QO1	B_ARG_74	NH2	B_ASP_76	OD2	2.806
3QO1	B_ARG_101	NH1	A_GLU_39	OE1	3.830
3QO1	B_ARG_101	NH1	A_GLU_39	OE2	2.711
3QO1	B_ARG_101	NH2	A_GLU_39	OE1	2.782
3QO1	B_ARG_101	NH2	A_GLU_39	OE2	3.238
3QO1	B_LYS_149	NZ	B_ASP_150	OD1	3.291
3QO1	B_LYS_149	NZ	B_ASP_150	OD2	3.610
3QO1	B_LYS_215	NZ	A_GLU_128	OE1	3.939
3QO1	B_ARG_216	NH2	B_GLU_218	OE2	3.982

Table 462: 3QO1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3QUM	P_ARG_36	NH1	A_ASP_94	OD2	3.603
3QUM	P_ARG_36	NH1	B_GLU_58	OE1	3.234
3QUM	P_ARG_36	NH1	B_GLU_58	OE2	3.373
3QUM	P_ARG_36	NH2	B_GLU_58	OE1	3.423
3QUM	P_HIS_57	ND1	P_ASP_102	OD1	3.257
3QUM	P_HIS_57	ND1	P_ASP_102	OD2	2.714
3QUM	P_LYS_62	NZ	B_GLU_58	OE2	3.762
3QUM	P_LYS_119	NZ	H_ASP_54	OD1	2.788
3QUM	P_LYS_119	NZ	H_ASP_54	OD2	3.700
3QUM	P_LYS_119	NZ	H_ASP_56	OD2	3.000
3QUM	P_LYS_230	NZ	P_GLU_129	OE1	3.910
3QUM	P_LYS_236	NZ	P_ASP_240	OD1	3.355
3QUM	P_LYS_236	NZ	P_ASP_240	OD2	3.879
3QUM	L_ARG_24	NH2	L_ASP_70	OD2	3.454
3QUM	L_LYS_27	NZ	L_GLU_93	OE2	2.631
3QUM	L_ARG_50	NH2	P_GLU_23	OE1	2.715
3QUM	L_ARG_61	NH1	L_ASP_82	OD1	3.063
3QUM	L_ARG_61	NH1	L_ASP_82	OD2	2.700
3QUM	L_ARG_61	NH2	L_GLU_79	OE1	3.466
3QUM	L_LYS_149	NZ	L_GLU_195	OE1	3.180
3QUM	L_LYS_149	NZ	L_GLU_195	OE2	2.848
3QUM	L_HIS_189	ND1	L_ASP_151	OD1	3.513
3QUM	L_HIS_189	ND1	L_ASP_151	OD2	3.827
3QUM	H_ARG_50	NH1	H_ASP_95	OD2	2.461
3QUM	H_LYS_62	NZ	H_GLU_46	OE1	2.726
3QUM	H_LYS_66	NZ	H_ASP_86	OD1	3.700
3QUM	H_LYS_66	NZ	H_ASP_86	OD2	2.890
3QUM	H_ARG_94	NH2	H_ASP_101	OD1	3.980
3QUM	H_ARG_94	NH2	H_ASP_101	OD2	2.778
3QUM	H_ARG_98	NH2	P_ASP_159	OD1	3.868
3QUM	H_ARG_98	NH2	P_ASP_159	OD2	3.474
3QUM	H_HIS_164	NE2	L_ASP_167	OD1	3.746
3QUM	H_LYS_208	NZ	L_GLU_123	OE1	3.317
3QUM	A_ARG_61	NH1	A_ASP_82	OD2	2.784
3QUM	A_ARG_61	NH2	A_ASP_82	OD2	3.879
3QUM	A_ARG_68	NH2	A_ASP_27C	OD2	3.611
3QUM	A_ARG_188	NH1	A_GLU_185	OE1	3.541
3QUM	A_ARG_188	NH1	A_GLU_185	OE2	2.650
3QUM	A_HIS_189	ND1	A_ASP_151	OD2	3.524
3QUM	A_HIS_189	NE2	A_GLU_185	OE1	3.506
3QUM	A_LYS_207	NZ	M_ASP_70	OD2	3.646
3QUM	B_ARG_40	NH1	B_GLU_85	OE2	3.723
3QUM	B_LYS_62	NZ	A_ASP_1	OD1	3.967
3QUM	B_LYS_62	NZ	A_ASP_1	OD2	3.654
3QUM	B_LYS_64	NZ	B_ASP_65	OD1	3.709
3QUM	B_LYS_64	NZ	B_ASP_65	OD2	3.188
3QUM	B_ARG_94	NH2	B_ASP_102	OD1	3.002
3QUM	B_ARG_94	NH2	B_ASP_102	OD2	3.802
3QUM	B_LYS_209	NZ	A_GLU_123	OE1	3.994
3QUM	B_LYS_209	NZ	A_GLU_123	OE2	2.553
3QUM	Q_HIS_57	ND1	Q_ASP_102	OD2	3.489
3QUM	Q_ARG_69	NH1	Q_GLU_77	OE1	2.522
3QUM	Q_ARG_69	NH2	Q_GLU_77	OE1	2.832
3QUM	Q_LYS_119	NZ	K_ASP_54	OD1	3.579
3QUM	Q_LYS_119	NZ	K_ASP_54	OD2	2.557
3QUM	Q_LYS_119	NZ	K_ASP_56	OD2	3.138
3QUM	Q_LYS_230	NZ	Q_GLU_129	OE2	2.982

3QUM	M_ARG_24	NH2	B_ASP_131	OD1	2.867
3QUM	M_ARG_24	NH2	B_ASP_131	OD2	3.402
3QUM	M_ARG_50	NH1	Q_GLU_21	OE2	3.456
3QUM	M_ARG_50	NH2	Q_GLU_21	OE2	3.792
3QUM	M_ARG_61	NH1	M_GLU_79	OE1	2.865
3QUM	M_ARG_61	NH1	M_GLU_79	OE2	3.959
3QUM	M_ARG_61	NH2	M_GLU_79	OE1	3.169
3QUM	M_ARG_61	NH2	M_ASP_82	OD1	2.669
3QUM	M_ARG_61	NH2	M_ASP_82	OD2	2.826
3QUM	M_LYS_183	NZ	M_GLU_187	OE1	3.466
3QUM	K_ARG_50	NH1	K_ASP_95	OD2	2.549
3QUM	K_LYS_58	NZ	Q_ASP_116	OD2	3.811
3QUM	K_LYS_58	NZ	K_ASP_56	OD1	3.915
3QUM	K_LYS_58	NZ	K_ASP_56	OD2	3.991
3QUM	K_LYS_62	NZ	M_ASP_1	OD1	2.803
3QUM	K_LYS_66	NZ	K_ASP_86	OD1	3.473
3QUM	K_LYS_66	NZ	K_ASP_86	OD2	3.448
3QUM	K_ARG_94	NH2	K_ASP_101	OD1	2.367
3QUM	K_ARG_94	NH2	K_ASP_101	OD2	2.940
3QUM	K_ARG_98	NH2	Q_ASP_159	OD2	3.098
3QUM	K_LYS_208	NZ	M_GLU_123	OE1	3.358
3QUM	K_ARG_213	NH2	K_ASP_214	OD2	3.796
3QUM	C_ARG_24	NH1	C_ASP_70	OD1	3.778
3QUM	C_ARG_24	NH1	C_ASP_70	OD2	2.622
3QUM	C_ARG_24	NH2	C_ASP_70	OD1	2.926
3QUM	C_ARG_24	NH2	C_ASP_70	OD2	3.340
3QUM	C_LYS_39	NZ	C_ASP_81	OD1	2.883
3QUM	C_ARG_61	NH1	C_GLU_79	OE1	2.943
3QUM	C_ARG_61	NH1	C_ASP_82	OD2	3.848
3QUM	C_ARG_61	NH2	C_ASP_82	OD1	3.376
3QUM	C_ARG_61	NH2	C_ASP_82	OD2	3.578
3QUM	C_LYS_142	NZ	C_GLU_105	OE1	2.648
3QUM	C_LYS_142	NZ	C_GLU_105	OE2	3.163
3QUM	C_LYS_147	NZ	C_GLU_195	OE2	3.770
3QUM	C_LYS_149	NZ	C_GLU_195	OE1	2.711
3QUM	C_LYS_149	NZ	C_GLU_195	OE2	3.595
3QUM	C_ARG_188	NH1	C_GLU_185	OE1	3.368
3QUM	D_LYS_38	NZ	D_GLU_46	OE2	3.663
3QUM	D_ARG_40	NH1	D_GLU_85	OE1	2.968
3QUM	D_LYS_66	NZ	D_ASP_86	OD1	3.445
3QUM	D_ARG_94	NH2	D_ASP_102	OD2	2.430
3QUM	D_ARG_97	NH1	C_GLU_55	OE1	3.578
3QUM	D_ARG_97	NH1	C_GLU_55	OE2	3.784
3QUM	D_ARG_97	NH2	Q_GLU_110	OE2	3.547

Table 463: 3QUM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3R08	L_ARG_61	NH1	L_GLU_79	OE1	3.254
3R08	L_ARG_61	NH1	L_GLU_79	OE2	3.378
3R08	L_ARG_61	NH2	L_GLU_79	OE1	2.676
3R08	L_ARG_61	NH2	L_GLU_81	OE2	3.468
3R08	L_ARG_61	NH2	L_ASP_82	OD1	3.777
3R08	L_ARG_61	NH2	L_ASP_82	OD2	3.454
3R08	L_LYS_103	NZ	L_ASP_165	OD1	3.486
3R08	L_LYS_142	NZ	L_GLU_105	OE1	3.662
3R08	L_LYS_147	NZ	L_GLU_195	OE1	2.773
3R08	L_LYS_155	NZ	L_ASP_185	OD2	3.988
3R08	L_ARG_156	NH1	L_GLU_154	OE2	3.311
3R08	L_LYS_183	NZ	L_GLU_187	OE2	3.914
3R08	L_ARG_188	NH1	L_ASP_185	OD1	3.352
3R08	L_HIS_189	ND1	L_ASP_151	OD2	3.760
3R08	L_HIS_189	NE2	L_ASP_185	OD1	3.852
3R08	L_LYS_199	NZ	L_ASP_110	OD2	3.241
3R08	L_LYS_207	NZ	H_ASP_129	OD1	3.653
3R08	L_LYS_207	NZ	H_ASP_129	OD2	2.868
3R08	L_ARG_211	NH1	L_GLU_187	OE1	3.899
3R08	L_ARG_211	NH2	L_GLU_187	OE1	3.052
3R08	H_ARG_38	NH1	H_ASP_86	OD1	3.285
3R08	H_ARG_38	NH2	H_GLU_46	OE1	3.027
3R08	H_ARG_43	NH1	H_GLU_46	OE1	3.166
3R08	H_ARG_43	NH1	H_GLU_46	OE2	2.679
3R08	H_ARG_43	NH2	H_GLU_46	OE1	3.767
3R08	H_ARG_43	NH2	H_GLU_46	OE2	3.517
3R08	H_LYS_58	NZ	E_GLU_4	OE2	3.175
3R08	H_ARG_66	NH1	H_ASP_86	OD1	3.453
3R08	H_ARG_66	NH1	H_ASP_86	OD2	3.405
3R08	H_LYS_83	NZ	H_GLU_85	OE2	3.138
3R08	H_ARG_94	NH2	H_ASP_96	OD1	3.331
3R08	H_ARG_94	NH2	H_ASP_96	OD2	3.042
3R08	H_LYS_99	NZ	L_ASP_56	OD2	3.746
3R08	E_HIS_45	ND1	E_ASP_43	OD2	3.535
3R08	E_LYS_69	NZ	E_GLU_4	OE1	2.708
3R08	E_LYS_76	NZ	E_GLU_53	OE2	3.300

Table 464: 3R08-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3SE8	G.HIS.66	ND1	G.GLU.64	OE2	2.819
3SE8	G.LYS.207	NZ	G.GLU.381	OE1	3.451
3SE8	G.LYS.207	NZ	G.GLU.381	OE2	2.740
3SE8	G.LYS.231	NZ	G.GLU.267	OE1	3.718
3SE8	G.HIS.249	NE2	G.GLU.482	OE1	2.997
3SE8	G.LYS.282	NZ	G.GLU.275	OE1	2.928
3SE8	G.LYS.282	NZ	H.ASP.100C	OD2	3.668
3SE8	G.LYS.343	NZ	G.GLU.347	OE1	3.295
3SE8	G.LYS.348	NZ	G.GLU.269	OE2	2.902
3SE8	G.LYS.348	NZ	G.GLU.351	OE1	2.955
3SE8	G.LYS.348	NZ	G.GLU.351	OE2	3.971
3SE8	G.LYS.350	NZ	G.GLU.347	OE1	3.922
3SE8	G.LYS.357	NZ	G.GLU.466	OE2	3.935
3SE8	G.ARG.379	NH2	G.ASP.211	OD1	3.636
3SE8	G.ARG.379	NH2	G.ASP.211	OD2	3.899
3SE8	G.ARG.456	NH1	G.GLU.466	OE1	3.921
3SE8	G.ARG.469	NH2	G.ASP.457	OD1	2.926
3SE8	G.ARG.469	NH2	G.ASP.457	OD2	3.898
3SE8	G.LYS.476	NZ	G.GLU.102	OE1	2.540
3SE8	G.ARG.480	NH1	G.ASP.477	OD1	2.656
3SE8	G.LYS.487	NZ	G.ASP.47	OD1	2.902
3SE8	G.LYS.487	NZ	G.GLU.91	OE1	2.578
3SE8	H.LYS.19	NZ	H.GLU.81	OE1	3.800
3SE8	H.ARG.38	NH1	H.GLU.46	OE1	2.640
3SE8	H.ARG.38	NH1	H.ASP.86	OD1	3.748
3SE8	H.ARG.38	NH2	H.ASP.86	OD1	2.672
3SE8	H.ARG.66	NH1	H.ASP.86	OD1	3.543
3SE8	H.ARG.66	NH1	H.ASP.86	OD2	3.893
3SE8	H.ARG.66	NH2	H.ASP.86	OD1	3.365
3SE8	H.ARG.66	NH2	H.ASP.86	OD2	2.596
3SE8	H.ARG.71	NH1	G.ASP.368	OD1	3.115
3SE8	H.ARG.71	NH1	G.ASP.368	OD2	3.763
3SE8	H.ARG.71	NH2	G.ASP.368	OD1	3.733
3SE8	H.ARG.71	NH2	G.ASP.368	OD2	2.907
3SE8	H.LYS.143	NZ	H.ASP.144	OD1	3.313
3SE8	H.LYS.143	NZ	H.ASP.144	OD2	3.811
3SE8	H.LYS.209	NZ	L.GLU.123	OE1	3.768
3SE8	H.LYS.210	NZ	H.GLU.212	OE1	2.816
3SE8	H.LYS.210	NZ	H.GLU.212	OE2	3.024
3SE8	L.LYS.24	NZ	L.ASP.70	OD1	2.618
3SE8	L.LYS.24	NZ	L.ASP.70	OD2	3.708
3SE8	L.ARG.39	NH1	L.GLU.81	OE1	3.909
3SE8	L.ARG.53	NH1	L.ASP.50	OD2	3.743
3SE8	L.ARG.61	NH2	L.ASP.82	OD1	2.770
3SE8	L.ARG.61	NH2	L.ASP.82	OD2	3.437
3SE8	L.ARG.142	NH1	L.GLU.103	OE1	3.000
3SE8	L.ARG.142	NH1	L.GLU.103	OE2	3.759
3SE8	L.ARG.142	NH2	L.GLU.103	OE1	3.192
3SE8	L.ARG.142	NH2	L.GLU.103	OE2	2.840
3SE8	L.ARG.142	NH2	L.GLU.105	OE2	3.734
3SE8	L.LYS.188	NZ	L.ASP.185	OD2	3.776

Table 465: 3SE8-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3SE9	G_HIS_66	ND1	G_GLU_64	OE2	2.728
3SE9	G_LYS_207	NZ	G_GLU_381	OE1	3.396
3SE9	G_LYS_207	NZ	G_GLU_381	OE2	3.043
3SE9	G_HIS_249	NE2	G_GLU_482	OE1	3.086
3SE9	G_LYS_282	NZ	G_GLU_275	OE1	3.135
3SE9	G_LYS_343	NZ	G_GLU_347	OE2	2.995
3SE9	G_LYS_348	NZ	G_GLU_269	OE2	3.584
3SE9	G_LYS_348	NZ	G_GLU_351	OE1	3.691
3SE9	G_LYS_357	NZ	G_GLU_466	OE1	3.212
3SE9	G_ARG_456	NH1	G_GLU_466	OE2	2.713
3SE9	G_ARG_469	NH1	G_ASP_457	OD1	2.966
3SE9	G_ARG_469	NH1	G_ASP_457	OD2	3.436
3SE9	G_LYS_476	NZ	G_GLU_102	OE1	2.755
3SE9	G_LYS_476	NZ	G_GLU_102	OE2	3.946
3SE9	G_ARG_480	NH1	G_ASP_477	OD1	3.009
3SE9	G_ARG_480	NH2	G_GLU_102	OE2	3.763
3SE9	G_LYS_487	NZ	G_ASP_47	OD1	2.626
3SE9	G_LYS_487	NZ	G_ASP_47	OD2	3.721
3SE9	G_LYS_487	NZ	G_GLU_91	OE1	2.626
3SE9	H_ARG_19	NH2	H_ASP_81	OD1	3.575
3SE9	H_ARG_19	NH2	H_ASP_81	OD2	3.127
3SE9	H_ARG_31	NH2	H_GLU_30	OE2	3.962
3SE9	H_ARG_38	NH1	H_ASP_86	OD1	2.864
3SE9	H_ARG_38	NH2	H_GLU_46	OE1	3.505
3SE9	H_ARG_64	NH1	G_ASP_457	OD2	3.853
3SE9	H_ARG_64	NH2	G_ASP_457	OD1	3.358
3SE9	H_ARG_64	NH2	G_ASP_457	OD2	3.280
3SE9	H_ARG_66	NH1	H_ASP_62	OD1	3.472
3SE9	H_ARG_66	NH1	H_ASP_62	OD2	2.990
3SE9	H_ARG_66	NH1	H_ASP_86	OD1	3.657
3SE9	H_ARG_66	NH1	H_ASP_86	OD2	3.617
3SE9	H_ARG_66	NH2	H_ASP_86	OD1	3.675
3SE9	H_ARG_66	NH2	H_ASP_86	OD2	2.373
3SE9	H_ARG_71	NH1	G_ASP_368	OD1	3.515
3SE9	H_ARG_71	NH1	G_ASP_368	OD2	2.768
3SE9	H_ARG_71	NH2	G_ASP_368	OD1	3.012
3SE9	H_ARG_71	NH2	G_ASP_368	OD2	3.769
3SE9	H_ARG_94	NH2	H_ASP_101	OD1	2.737
3SE9	H_ARG_94	NH2	H_ASP_101	OD2	3.906
3SE9	H_LYS_143	NZ	H_ASP_144	OD1	3.511
3SE9	H_LYS_209	NZ	L_GLU_123	OE1	3.388
3SE9	H_LYS_214	NZ	L_ASP_122	OD1	3.332
3SE9	L_ARG_61	NH1	L_ASP_82	OD1	2.919
3SE9	L_ARG_61	NH1	L_ASP_82	OD2	3.116
3SE9	L_LYS_183	NZ	L_GLU_187	OE1	2.818
3SE9	L_HIS_189	ND1	L_ASP_151	OD2	2.887

Table 466: 3SE9-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3SGD	L_LYS_24	NZ	L_ASP_75	OD1	2.783
3SGD	L_ARG_51	NH2	L_ASP_60	OD1	3.495
3SGD	L_ARG_51	NH2	L_ASP_60	OD2	3.021
3SGD	L_ARG_66	NH1	L_ASP_87	OD1	3.680
3SGD	L_ARG_66	NH1	L_ASP_87	OD2	2.782
3SGD	L_ARG_66	NH2	L_GLU_84	OE1	3.767
3SGD	L_ARG_66	NH2	L_ASP_87	OD1	2.989
3SGD	L_ARG_66	NH2	L_ASP_87	OD2	3.564
3SGD	L_HIS_98	ND1	L_ASP_31	OD2	3.644
3SGD	L_LYS_152	NZ	L_GLU_159	OE1	3.644
3SGD	L_LYS_152	NZ	L_GLU_159	OE2	3.885
3SGD	L_LYS_154	NZ	L_GLU_200	OE1	3.346
3SGD	L_LYS_154	NZ	L_GLU_200	OE2	3.354
3SGD	L_ARG_160	NH2	L_GLU_190	OE1	2.808
3SGD	L_ARG_160	NH2	L_GLU_190	OE2	2.668
3SGD	L_ARG_193	NH1	L_ASP_189	OD2	2.692
3SGD	L_ARG_193	NH2	L_GLU_190	OE2	3.962
3SGD	L_HIS_194	ND1	L_ASP_156	OD2	2.735
3SGD	L_HIS_194	NE2	L_GLU_190	OE2	3.628
3SGD	L_LYS_204	NZ	L_ASP_115	OD2	3.348
3SGD	L_LYS_204	NZ	J_ASP_75	OD1	3.665
3SGD	L_LYS_204	NZ	J_ASP_75	OD2	3.246
3SGD	H_ARG_38	NH1	H_ASP_92	OD2	2.803
3SGD	H_ARG_38	NH2	H_GLU_46	OE2	3.026
3SGD	H_ARG_38	NH2	H_ASP_92	OD2	3.826
3SGD	H_LYS_43	NZ	J_ASP_68	OD1	3.910
3SGD	H_ARG_69	NH1	H_ASP_92	OD1	2.725
3SGD	H_ARG_69	NH1	H_ASP_92	OD2	3.812
3SGD	H_ARG_69	NH2	H_ASP_92	OD1	3.411
3SGD	H_ARG_69	NH2	H_ASP_92	OD2	3.054
3SGD	H_ARG_74	NH2	H_ASP_76	OD1	3.619
3SGD	H_LYS_210	NZ	L_GLU_128	OE1	3.898
3SGD	L_LYS_24	NZ	L_ASP_75	OD1	3.796
3SGD	L_LYS_24	NZ	L_ASP_75	OD2	2.962
3SGD	L_ARG_44	NH2	L_GLU_86	OE2	3.752
3SGD	L_ARG_51	NH2	L_ASP_60	OD1	2.717
3SGD	L_ARG_51	NH2	L_ASP_60	OD2	3.541
3SGD	L_ARG_66	NH1	L_ASP_87	OD1	3.518
3SGD	L_ARG_66	NH1	L_ASP_87	OD2	2.585
3SGD	L_ARG_66	NH2	L_GLU_84	OE1	3.635
3SGD	L_ARG_66	NH2	L_GLU_86	OE1	3.914
3SGD	L_ARG_66	NH2	L_GLU_86	OE2	3.879
3SGD	L_ARG_66	NH2	L_ASP_87	OD1	2.899
3SGD	L_ARG_66	NH2	L_ASP_87	OD2	3.479
3SGD	L_ARG_82	NH1	L_GLU_84	OE2	2.800
3SGD	L_ARG_82	NH2	L_GLU_84	OE2	3.178
3SGD	L_LYS_154	NZ	L_GLU_200	OE1	3.141
3SGD	L_LYS_154	NZ	L_GLU_200	OE2	2.988
3SGD	L_LYS_174	NZ	L_ASP_172	OD1	3.706
3SGD	L_LYS_174	NZ	L_ASP_172	OD2	3.091
3SGD	L_LYS_174	NZ	L_ASP_175	OD1	3.919
3SGD	L_ARG_193	NH2	L_ASP_189	OD2	2.737
3SGD	L_HIS_194	ND1	L_ASP_156	OD2	2.901
3SGD	L_LYS_204	NZ	L_ASP_115	OD2	3.676
3SGD	J_LYS_19	NZ	L_ASP_148	OD1	3.248
3SGD	J_LYS_19	NZ	L_ASP_148	OD2	2.952
3SGD	J_ARG_38	NH1	J_ASP_92	OD2	2.794

3SGD	J_ARG_38	NH2	J_GLU_46	OE1	3.737
3SGD	J_ARG_38	NH2	J_GLU_46	OE2	2.952
3SGD	J_ARG_38	NH2	J_ASP_92	OD2	3.905
3SGD	J_ARG_69	NH1	J_ASP_92	OD1	2.689
3SGD	J_ARG_69	NH1	J_ASP_92	OD2	3.808
3SGD	J_ARG_69	NH2	J_ASP_92	OD1	3.488
3SGD	J_ARG_69	NH2	J_ASP_92	OD2	3.217
3SGD	J_ARG_74	NH2	J_ASP_76	OD1	3.467

Table 467: 3SGD-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3SKJ	L_ARG_24	NH1	L_GLU_70	OE1	3.770
3SKJ	L_ARG_61	NH2	L_ASP_82	OD1	2.965
3SKJ	L_ARG_61	NH2	L_ASP_82	OD2	3.776
3SKJ	L_ARG_96	NH1	H_GLU_100I	OE1	2.505
3SKJ	L_ARG_96	NH1	H_GLU_100I	OE2	2.799
3SKJ	L_LYS_103	NZ	L_GLU_165	OE1	2.601
3SKJ	L_LYS_103	NZ	L_GLU_165	OE2	3.499
3SKJ	L_HIS_189	ND1	L_ASP_151	OD2	3.871
3SKJ	L_ARG_211	NH2	L_GLU_187	OE2	3.617
3SKJ	H_HIS_31	ND1	H_ASP_96	OD2	2.640
3SKJ	H_HIS_31	NE2	E_GLU_133	OE2	3.297
3SKJ	H_ARG_38	NH1	H_ASP_86	OD1	2.911
3SKJ	H_ARG_38	NH2	H_GLU_46	OE1	3.116
3SKJ	H_ARG_38	NH2	H_GLU_46	OE2	3.301
3SKJ	H_ARG_38	NH2	H_ASP_86	OD1	3.993
3SKJ	H_ARG_50	NH1	H_GLU_100I	OE1	3.128
3SKJ	H_LYS_64	NZ	H_ASP_61	OD2	3.941
3SKJ	H_ARG_66	NH1	H_ASP_86	OD1	3.677
3SKJ	H_ARG_66	NH2	H_ASP_86	OD1	3.495
3SKJ	H_ARG_66	NH2	H_ASP_86	OD2	2.568
3SKJ	H_HIS_161	NE2	L_ASP_167	OD2	3.763
3SKJ	H_LYS_206	NZ	L_GLU_123	OE1	2.501
3SKJ	H_LYS_206	NZ	L_GLU_123	OE2	3.323
3SKJ	H_ARG_207	NH1	H_GLU_209	OE2	3.580
3SKJ	M_ARG_24	NH1	M_GLU_70	OE1	3.068
3SKJ	M_ARG_24	NH1	M_GLU_70	OE2	3.024
3SKJ	M_ARG_24	NH2	M_GLU_70	OE1	3.407
3SKJ	M_LYS_39	NZ	M_ASP_81	OD1	2.568
3SKJ	M_ARG_61	NH2	M_ASP_82	OD1	2.991
3SKJ	M_ARG_61	NH2	M_ASP_82	OD2	2.909
3SKJ	M_ARG_96	NH2	I_GLU_100I	OE1	3.081
3SKJ	M_ARG_96	NH2	I_GLU_100I	OE2	3.831
3SKJ	M_LYS_103	NZ	M_GLU_165	OE2	3.149
3SKJ	M_LYS_149	NZ	M_GLU_195	OE2	3.240
3SKJ	M_LYS_188	NZ	M_ASP_185	OD2	3.381
3SKJ	I_ARG_38	NH1	I_ASP_86	OD1	2.866
3SKJ	I_ARG_38	NH2	I_GLU_46	OE1	3.262
3SKJ	I_ARG_38	NH2	I_GLU_46	OE2	3.203
3SKJ	I_LYS_43	NZ	L_ASP_1	OD1	3.862
3SKJ	I_ARG_50	NH1	I_GLU_100I	OE1	3.217
3SKJ	I_ARG_50	NH1	I_GLU_100I	OE2	3.198
3SKJ	I_ARG_66	NH1	I_ASP_86	OD1	3.975
3SKJ	I_ARG_66	NH1	I_ASP_86	OD2	2.891
3SKJ	I_ARG_66	NH2	I_ASP_86	OD1	3.263
3SKJ	I_ARG_66	NH2	I_ASP_86	OD2	3.539
3SKJ	I_ARG_83	NH1	I_GLU_85	OE1	3.307
3SKJ	I_ARG_83	NH1	I_GLU_85	OE2	3.711
3SKJ	I_LYS_140	NZ	I_ASP_141	OD1	2.912
3SKJ	I_LYS_140	NZ	I_ASP_141	OD2	3.281
3SKJ	I_LYS_211	NZ	M_ASP_122	OD2	3.816
3SKJ	I_LYS_211	NZ	M_GLU_123	OE1	3.612
3SKJ	E_LYS_112	NZ	E_ASP_54	OD1	3.156
3SKJ	E_ARG_144	NH1	E_GLU_142	OE1	3.346
3SKJ	E_ARG_144	NH2	E_ASP_119	OD1	3.475
3SKJ	E_ARG_144	NH2	E_GLU_142	OE1	3.494
3SKJ	E_ARG_171	NH1	E_GLU_73	OE1	3.665
3SKJ	E_ARG_171	NH1	E_GLU_73	OE2	3.183

3SKJ	E_ARG_171	NH2	E_GLU_4	OE1	2.631
3SKJ	E_LYS_176	NZ	E_GLU_66	OE2	2.522

Table 468: 3SKJ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3SY0	A_LYS_24	NZ	A_ASP_70	OD1	2.683
3SY0	A_LYS_24	NZ	A_ASP_70	OD2	3.488
3SY0	A_LYS_39	NZ	A_GLU_81	OE1	2.857
3SY0	A_ARG_61	NH1	A_GLU_81	OE2	3.627
3SY0	A_ARG_61	NH1	A_ASP_82	OD1	2.753
3SY0	A_ARG_61	NH1	A_ASP_82	OD2	3.623
3SY0	A_ARG_95	NH2	B_ASP_95	OD1	3.609
3SY0	A_ARG_95	NH2	B_ASP_95	OD2	2.821
3SY0	A_LYS_146	NZ	A_GLU_194	OE2	3.742
3SY0	A_LYS_148	NZ	A_GLU_194	OE1	2.676
3SY0	A_LYS_148	NZ	A_GLU_194	OE2	2.913
3SY0	A_LYS_182	NZ	A_GLU_186	OE1	2.287
3SY0	A_LYS_182	NZ	A_GLU_186	OE2	3.835
3SY0	A_ARG_187	NH2	A_GLU_184	OE1	2.876
3SY0	A_HIS_188	ND1	A_ASP_150	OD2	2.895
3SY0	A_HIS_188	NE2	A_GLU_184	OE2	2.965
3SY0	A_LYS_198	NZ	A_ASP_109	OD2	3.892
3SY0	B_ARG_38	NH1	B_ASP_86	OD2	2.779
3SY0	B_ARG_38	NH2	B_GLU_46	OE1	3.151
3SY0	B_ARG_38	NH2	B_GLU_46	OE2	4.000
3SY0	B_ARG_38	NH2	B_ASP_86	OD2	3.804
3SY0	B_ARG_52	NH1	B_GLU_56	OE2	2.894
3SY0	B_ARG_52	NH2	B_GLU_56	OE2	3.121
3SY0	B_ARG_64	NH1	B_ASP_86	OD1	2.875
3SY0	B_ARG_64	NH1	B_ASP_86	OD2	3.721
3SY0	B_ARG_64	NH2	B_ASP_86	OD1	3.464
3SY0	B_ARG_64	NH2	B_ASP_86	OD2	2.919
3SY0	B_HIS_96	ND1	B_GLU_100A	OE2	3.230
3SY0	B_HIS_96	NE2	B_GLU_100A	OE2	3.820
3SY0	B_ARG_100B	NH1	A_GLU_55	OE1	2.843
3SY0	B_ARG_100B	NH1	A_GLU_55	OE2	3.786
3SY0	B_LYS_206	NZ	A_GLU_122	OE1	3.980

Table 469: 3SY0-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3T4Y	A_LYS_24	NZ	A_ASP_70	OD1	2.903
3T4Y	A_LYS_24	NZ	A_ASP_70	OD2	3.502
3T4Y	A_LYS_39	NZ	A_GLU_81	OE2	3.124
3T4Y	A_ARG_61	NH1	A_GLU_81	OE1	3.284
3T4Y	A_ARG_61	NH1	A_ASP_82	OD1	2.653
3T4Y	A_ARG_61	NH1	A_ASP_82	OD2	3.419
3T4Y	A_ARG_95	NH2	B_ASP_95	OD1	3.796
3T4Y	A_ARG_95	NH2	B_ASP_95	OD2	2.951
3T4Y	A_LYS_148	NZ	A_GLU_194	OE1	2.908
3T4Y	A_LYS_148	NZ	A_GLU_194	OE2	3.013
3T4Y	A_ARG_187	NH2	A_GLU_184	OE1	2.855
3T4Y	A_HIS_188	ND1	A_ASP_150	OD2	2.865
3T4Y	A_HIS_188	NE2	A_GLU_184	OE2	2.755
3T4Y	B_ARG_38	NH1	B_ASP_86	OD2	2.806
3T4Y	B_ARG_38	NH2	B_GLU_46	OE1	3.203
3T4Y	B_ARG_38	NH2	B_GLU_85	OE2	3.852
3T4Y	B_ARG_38	NH2	B_ASP_86	OD2	3.884
3T4Y	B_ARG_52	NH1	B_GLU_56	OE2	2.817
3T4Y	B_ARG_52	NH2	B_GLU_56	OE2	2.987
3T4Y	B_ARG_64	NH1	B_ASP_86	OD1	2.822
3T4Y	B_ARG_64	NH1	B_ASP_86	OD2	3.726
3T4Y	B_ARG_64	NH2	B_ASP_86	OD1	3.460
3T4Y	B_ARG_64	NH2	B_ASP_86	OD2	2.866
3T4Y	B_HIS_96	ND1	B_GLU_100A	OE2	3.510
3T4Y	B_HIS_96	NE2	B_GLU_100A	OE2	3.981
3T4Y	B_ARG_100B	NH1	A_GLU_55	OE1	3.824
3T4Y	B_ARG_100B	NH1	A_GLU_55	OE2	2.840
3T4Y	B_LYS_206	NZ	A_GLU_122	OE2	2.652

Table 470: 3T4Y-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3T65	B_ARG_38	NH1	B_ASP_86	OD2	2.756
3T65	B_ARG_38	NH2	B_GLU_46	OE1	3.099
3T65	B_ARG_38	NH2	B_GLU_85	OE1	3.408
3T65	B_ARG_38	NH2	B_ASP_86	OD2	3.896
3T65	B_ARG_52	NH1	B_GLU_56	OE2	2.912
3T65	B_ARG_52	NH2	B_GLU_56	OE2	3.090
3T65	B_ARG_64	NH1	B_ASP_86	OD1	2.927
3T65	B_ARG_64	NH1	B_ASP_86	OD2	3.734
3T65	B_ARG_64	NH2	B_ASP_86	OD1	3.486
3T65	B_ARG_64	NH2	B_ASP_86	OD2	2.925
3T65	B_HIS_96	ND1	B_GLU_100A	OE2	3.351
3T65	B_HIS_96	NE2	B_GLU_100A	OE2	3.804
3T65	B_ARG_100B	NH1	A_GLU_55	OE1	3.841
3T65	B_ARG_100B	NH1	A_GLU_55	OE2	2.883
3T65	A_LYS_24	NZ	A_ASP_70	OD1	2.811
3T65	A_LYS_24	NZ	A_ASP_70	OD2	3.571
3T65	A_LYS_39	NZ	A_GLU_81	OE2	3.467
3T65	A_ARG_54	NH2	A_ASP_60	OD1	3.593
3T65	A_ARG_61	NH1	A_GLU_81	OE1	3.085
3T65	A_ARG_61	NH1	A_ASP_82	OD1	2.841
3T65	A_ARG_61	NH1	A_ASP_82	OD2	3.657
3T65	A_ARG_95	NH2	B_ASP_95	OD1	3.666
3T65	A_ARG_95	NH2	B_ASP_95	OD2	2.866
3T65	A_LYS_146	NZ	A_GLU_153	OE2	3.733
3T65	A_LYS_148	NZ	A_GLU_194	OE1	2.726
3T65	A_LYS_148	NZ	A_GLU_194	OE2	3.149
3T65	A_LYS_182	NZ	A_GLU_186	OE1	3.601
3T65	A_LYS_182	NZ	A_GLU_186	OE2	3.775
3T65	A_ARG_187	NH2	A_GLU_184	OE1	2.825
3T65	A_HIS_188	ND1	A_ASP_150	OD2	2.935
3T65	A_HIS_188	NE2	A_GLU_184	OE2	2.940
3T65	A_LYS_198	NZ	A_ASP_109	OD2	3.914

Table 471: 3T65-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3T77	A_LYS_24	NZ	A_ASP_70	OD1	2.759
3T77	A_LYS_24	NZ	A_ASP_70	OD2	3.590
3T77	A_LYS_39	NZ	A_GLU_81	OE1	3.726
3T77	A_ARG_61	NH2	A_GLU_81	OE2	3.966
3T77	A_ARG_61	NH2	A_ASP_82	OD1	2.868
3T77	A_ARG_61	NH2	A_ASP_82	OD2	3.521
3T77	A_ARG_95	NH2	B_ASP_95	OD1	3.723
3T77	A_ARG_95	NH2	B_ASP_95	OD2	2.997
3T77	A_LYS_102	NZ	A_GLU_104	OE1	3.775
3T77	A_LYS_102	NZ	A_GLU_104	OE2	3.007
3T77	A_LYS_148	NZ	A_GLU_194	OE1	3.783
3T77	A_LYS_148	NZ	A_GLU_194	OE2	2.306
3T77	A_LYS_182	NZ	A_GLU_186	OE1	3.731
3T77	A_ARG_187	NH2	A_GLU_184	OE1	2.585
3T77	A_HIS_188	ND1	A_ASP_150	OD2	3.031
3T77	A_HIS_188	NE2	A_GLU_184	OE2	2.771
3T77	A_LYS_198	NZ	A_ASP_109	OD1	3.952
3T77	B_ARG_38	NH1	B_ASP_86	OD2	2.829
3T77	B_ARG_38	NH2	B_GLU_46	OE1	3.138
3T77	B_ARG_38	NH2	B_ASP_86	OD2	3.744
3T77	B_ARG_52	NH1	B_GLU_56	OE2	2.717
3T77	B_ARG_52	NH2	B_GLU_56	OE2	3.056
3T77	B_ARG_64	NH1	B_ASP_86	OD1	2.807
3T77	B_ARG_64	NH1	B_ASP_86	OD2	3.626
3T77	B_ARG_64	NH2	B_ASP_86	OD1	3.476
3T77	B_ARG_64	NH2	B_ASP_86	OD2	2.870
3T77	B_HIS_96	ND1	B_GLU_100A	OE1	3.974
3T77	B_HIS_96	NE2	B_GLU_100A	OE1	2.416
3T77	B_ARG_100B	NH1	A_GLU_55	OE1	3.125
3T77	B_ARG_100B	NH1	A_GLU_55	OE2	2.687
3T77	B_LYS_206	NZ	A_GLU_122	OE2	3.917

Table 472: 3T77-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3THM	L_ARG_31	NH1	L_ASP_94	OD1	2.844
3THM	L_ARG_31	NH1	L_ASP_94	OD2	2.885
3THM	L_ARG_55	NH1	L_ASP_61	OD2	3.667
3THM	L_ARG_62	NH2	L_ASP_83	OD1	3.471
3THM	L_ARG_62	NH2	L_ASP_83	OD2	2.633
3THM	L_ARG_77	NH1	L_ASP_78	OD2	2.791
3THM	L_HIS_192	ND1	L_ASP_155	OD1	2.840
3THM	L_ARG_193	NH1	L_ASP_155	OD2	3.695
3THM	L_ARG_193	NH2	L_ASP_155	OD1	3.787
3THM	H_ARG_40	NH1	H_ASP_96	OD1	2.763
3THM	H_ARG_40	NH2	H_GLU_48	OE1	3.112
3THM	H_ARG_40	NH2	H_ASP_96	OD1	3.732
3THM	H_ARG_73	NH1	H_ASP_96	OD1	3.781
3THM	H_ARG_73	NH1	H_ASP_96	OD2	3.095
3THM	H_ARG_73	NH2	H_ASP_96	OD1	2.910
3THM	H_ARG_73	NH2	H_ASP_96	OD2	3.508
3THM	H_LYS_82	NZ	H_ASP_79	OD2	3.975
3THM	H_ARG_104	NH2	H_ASP_120	OD1	3.520
3THM	H_ARG_104	NH2	H_ASP_120	OD2	2.748
3THM	H_LYS_225	NZ	H_ASP_227	OD2	3.663
3THM	H_LYS_229	NZ	H_GLU_231	OE1	3.584
3THM	F_HIS_38	ND1	F_ASP_56	OD1	3.082
3THM	F_HIS_38	ND1	F_ASP_56	OD2	2.768
3THM	F_LYS_45	NZ	L_GLU_97	OE2	3.172
3THM	F_LYS_53	NZ	F_GLU_63	OE1	2.774
3THM	F_LYS_78	NZ	L_ASP_52	OD1	3.702
3THM	F_ARG_112	NH2	F_GLU_98	OE1	3.774

Table 473: 3THM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3TJE	L_ARG_31	NH1	L_ASP_94	OD1	2.809
3TJE	L_ARG_62	NH1	L_ASP_83	OD1	3.626
3TJE	L_ARG_62	NH1	L_ASP_83	OD2	2.774
3TJE	L_ARG_62	NH2	L_ASP_83	OD1	2.866
3TJE	L_ARG_62	NH2	L_ASP_83	OD2	3.498
3TJE	L_ARG_77	NH1	L_ASP_78	OD2	2.738
3TJE	L_ARG_77	NH2	L_ASP_61	OD2	3.491
3TJE	L_LYS_114	NZ	L_GLU_202	OE2	3.788
3TJE	H_ARG_40	NH1	H_ASP_96	OD1	2.839
3TJE	H_ARG_40	NH2	H_GLU_48	OE1	3.044
3TJE	H_ARG_40	NH2	H_ASP_96	OD1	3.722
3TJE	H_ARG_73	NH1	H_ASP_96	OD1	3.710
3TJE	H_ARG_73	NH1	H_ASP_96	OD2	2.838
3TJE	H_ARG_73	NH2	H_ASP_96	OD1	2.943
3TJE	H_ARG_73	NH2	H_ASP_96	OD2	3.439
3TJE	H_ARG_104	NH2	H_ASP_120	OD1	3.469
3TJE	H_ARG_104	NH2	H_ASP_120	OD2	2.676
3TJE	H_LYS_225	NZ	H_ASP_227	OD2	3.295
3TJE	H_LYS_229	NZ	H_GLU_231	OE1	3.568
3TJE	F_LYS_53	NZ	F_GLU_63	OE1	2.653
3TJE	F_HIS_95	ND1	F_ASP_92	OD2	3.202
3TJE	F_ARG_105	NH1	F_GLU_71	OE1	3.450
3TJE	F_ARG_105	NH1	F_GLU_71	OE2	3.955
3TJE	F_ARG_105	NH2	F_GLU_71	OE2	3.995
3TJE	F_LYS_110	NZ	F_GLU_100	OE1	2.868
3TJE	F_LYS_110	NZ	F_GLU_100	OE2	3.645
3TJE	F_ARG_112	NH2	F_GLU_98	OE2	3.462
3TJE	F_LYS_114	NZ	F_GLU_93	OE2	3.047
3TJE	F_HIS_126	NE2	F_ASP_128	OD1	3.055
3TJE	F_HIS_126	NE2	F_ASP_128	OD2	3.467

Table 474: 3TJE-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3U1S	L_LYS_24	NZ	L_ASP_70	OD2	3.165
3U1S	L_HIS_27D	NE2	H_ASP_100B	OD2	2.859
3U1S	L_ARG_61	NH1	L_ASP_82	OD1	3.331
3U1S	L_ARG_61	NH1	L_ASP_82	OD2	2.471
3U1S	L_ARG_61	NH2	L_GLU_79	OE1	3.597
3U1S	L_ARG_61	NH2	L_GLU_79	OE2	3.692
3U1S	L_ARG_61	NH2	L_ASP_82	OD1	2.705
3U1S	L_ARG_61	NH2	L_ASP_82	OD2	3.338
3U1S	L_LYS_149	NZ	L_GLU_195	OE2	2.775
3U1S	L_HIS_189	ND1	L_ASP_151	OD2	3.043
3U1S	H_LYS_12	NZ	H_GLU_10	OE2	3.798
3U1S	H_ARG_38	NH1	H_ASP_86	OD1	2.812
3U1S	H_ARG_38	NH2	H_GLU_46	OE1	3.161
3U1S	H_ARG_38	NH2	H_ASP_86	OD1	3.811
3U1S	H_HIS_52A	ND1	H_GLU_52B	OE1	3.637
3U1S	H_HIS_52A	NE2	H_ASP_33	OD1	3.943
3U1S	H_HIS_52A	NE2	H_GLU_52B	OE1	3.544
3U1S	H_HIS_52A	NE2	H_GLU_52B	OE2	3.663
3U1S	H_LYS_60	NZ	H_GLU_46	OE1	3.515
3U1S	H_LYS_60	NZ	H_GLU_46	OE2	2.683
3U1S	H_ARG_64	NH1	H_ASP_86	OD1	3.631
3U1S	H_ARG_64	NH1	H_ASP_86	OD2	3.169
3U1S	H_ARG_64	NH2	H_ASP_86	OD1	2.578
3U1S	H_ARG_64	NH2	H_ASP_86	OD2	3.420
3U1S	H_LYS_97	NZ	H_ASP_33	OD1	2.873
3U1S	H_LYS_97	NZ	H_ASP_33	OD2	3.430
3U1S	H_LYS_97	NZ	H_GLU_52B	OE1	2.747
3U1S	H_LYS_97	NZ	H_GLU_52B	OE2	3.729
3U1S	H_ARG_99	NH1	H_GLU_52B	OE1	3.885
3U1S	H_ARG_99	NH1	H_GLU_52B	OE2	3.932
3U1S	H_ARG_99	NH1	H_ASP_53	OD1	2.841
3U1S	H_ARG_99	NH1	H_ASP_53	OD2	3.415
3U1S	H_ARG_99	NH2	H_ASP_53	OD1	3.710
3U1S	H_ARG_99	NH2	H_ASP_53	OD2	2.972
3U1S	H_ARG_99	NH2	H_ASP_100R	OD1	3.526
3U1S	H_ARG_99	NH2	H_ASP_100R	OD2	2.851
3U1S	H_ARG_100A	NH1	H_GLU_100N	OE2	3.328
3U1S	H_LYS_211	NZ	H_ASP_213	OD1	2.712
3U1S	H_LYS_211	NZ	H_ASP_213	OD2	3.729
3U1S	H_LYS_214	NZ	L_GLU_123	OE1	3.475
3U1S	H_LYS_215	NZ	H_GLU_217	OE2	3.772

Table 475: 3U1S-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3U2S	H_ARG_31	NH1	H_ASP_100L	OD2	3.978
3U2S	H_ARG_31	NH2	H_ASP_100L	OD1	3.963
3U2S	H_ARG_31	NH2	H_ASP_100L	OD2	2.965
3U2S	H_HIS_35	NE2	H_GLU_95	OE1	2.640
3U2S	H_ARG_38	NH1	H_ASP_86	OD1	2.839
3U2S	H_ARG_38	NH2	H_GLU_46	OE1	3.925
3U2S	H_ARG_38	NH2	H_GLU_46	OE2	2.923
3U2S	H_ARG_38	NH2	H_ASP_86	OD1	3.911
3U2S	H_LYS_52	NZ	H_ASP_100I	OD2	3.366
3U2S	H_ARG_66	NH1	H_ASP_86	OD1	3.572
3U2S	H_ARG_66	NH1	H_ASP_86	OD2	2.527
3U2S	H_ARG_66	NH2	H_ASP_86	OD1	2.931
3U2S	H_ARG_66	NH2	H_ASP_86	OD2	3.433
3U2S	H_ARG_94	NH2	H_ASP_101	OD1	3.597
3U2S	H_ARG_94	NH2	H_ASP_101	OD2	2.850
3U2S	L_LYS_53	NZ	L_ASP_50	OD2	2.841
3U2S	L_ARG_54	NH2	C_ASP_167	OD1	3.525
3U2S	L_ARG_54	NH2	C_ASP_167	OD2	3.282
3U2S	L_ARG_61	NH1	L_ASP_82	OD1	3.649
3U2S	L_ARG_61	NH1	L_ASP_82	OD2	2.861
3U2S	L_ARG_61	NH2	L_ASP_82	OD1	2.965
3U2S	L_ARG_61	NH2	L_ASP_82	OD2	3.572
3U2S	L_LYS_66	NZ	L_GLU_31	OE2	2.988
3U2S	L_ARG_95A	NH1	H_ASP_61	OD1	2.794
3U2S	L_ARG_95A	NH1	H_ASP_61	OD2	3.373
3U2S	L_ARG_95A	NH2	H_ASP_61	OD1	2.338
3U2S	L_ARG_96	NH2	H_GLU_95	OE1	3.743
3U2S	L_ARG_96	NH2	H_GLU_95	OE2	2.869
3U2S	L_LYS_129	NZ	H_ASP_144	OD1	3.881
3U2S	L_HIS_188	ND1	L_ASP_151	OD2	3.681
3U2S	G_ARG_168	NH2	H_ASP_100L	OD1	3.358
3U2S	G_ARG_168	NH2	H_ASP_100L	OD2	3.104
3U2S	G_LYS_171	NZ	H_ASP_100I	OD1	3.178
3U2S	A_ARG_31	NH2	A_ASP_100L	OD1	3.437
3U2S	A_ARG_31	NH2	A_ASP_100L	OD2	3.464
3U2S	A_HIS_35	NE2	A_GLU_95	OE1	2.700
3U2S	A_ARG_38	NH1	A_ASP_86	OD1	2.886
3U2S	A_ARG_38	NH2	A_GLU_46	OE1	3.872
3U2S	A_ARG_38	NH2	A_GLU_46	OE2	2.898
3U2S	A_ARG_38	NH2	A_ASP_86	OD1	3.831
3U2S	A_LYS_52	NZ	A_ASP_100I	OD2	3.513
3U2S	A_ARG_66	NH1	A_ASP_86	OD1	3.554
3U2S	A_ARG_66	NH1	A_ASP_86	OD2	2.481
3U2S	A_ARG_66	NH2	A_ASP_86	OD1	3.013
3U2S	A_ARG_66	NH2	A_ASP_86	OD2	3.477
3U2S	A_ARG_83	NH1	A_GLU_85	OE1	2.914
3U2S	A_ARG_94	NH2	A_ASP_101	OD1	3.528
3U2S	A_ARG_94	NH2	A_ASP_101	OD2	2.897
3U2S	A_LYS_143	NZ	B_GLU_124	OE2	3.550
3U2S	B_LYS_53	NZ	B_ASP_50	OD2	2.754
3U2S	B_ARG_61	NH1	B_ASP_82	OD1	3.698
3U2S	B_ARG_61	NH1	B_ASP_82	OD2	2.775
3U2S	B_ARG_61	NH2	B_ASP_82	OD1	2.930
3U2S	B_ARG_61	NH2	B_ASP_82	OD2	3.413
3U2S	B_LYS_66	NZ	B_GLU_31	OE2	3.053
3U2S	B_ARG_95A	NH1	A_ASP_61	OD1	2.632
3U2S	B_ARG_95A	NH1	A_ASP_61	OD2	3.483

3U2S	B_ARG_95A	NH2	A_ASP_61	OD1	3.270
3U2S	B_ARG_96	NH2	A_GLU_95	OE1	3.738
3U2S	B_ARG_96	NH2	A_GLU_95	OE2	2.983
3U2S	C_ARG_168	NH2	A_ASP_100L	OD1	2.424
3U2S	C_ARG_168	NH2	A_ASP_100L	OD2	3.228
3U2S	C_LYS_169	NZ	C_ASP_223	OD1	3.001
3U2S	C_LYS_169	NZ	C_ASP_223	OD2	3.464
3U2S	C_LYS_169	NZ	C_GLU_239	OE2	2.484
3U2S	C_LYS_171	NZ	A_ASP_100I	OD1	3.279

Table 476: 3U2S-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3U36	H_HIS_35	NE2	H_GLU_95	OE1	2.791
3U36	H_ARG_38	NH1	H_ASP_86	OD1	3.091
3U36	H_ARG_38	NH2	H_GLU_46	OE2	3.256
3U36	H_ARG_66	NH1	H_ASP_86	OD1	3.636
3U36	H_ARG_66	NH1	H_ASP_86	OD2	2.875
3U36	H_ARG_66	NH2	H_ASP_86	OD1	3.304
3U36	H_ARG_66	NH2	H_ASP_86	OD2	3.804
3U36	H_ARG_83	NH1	H_GLU_85	OE2	3.153
3U36	H_ARG_94	NH2	H_ASP_101	OD1	3.359
3U36	H_ARG_94	NH2	H_ASP_101	OD2	2.948
3U36	H_LYS_210	NZ	H_GLU_212	OE1	3.728
3U36	L_LYS_53	NZ	L_ASP_50	OD2	3.306
3U36	L_ARG_61	NH1	L_ASP_82	OD1	3.774
3U36	L_ARG_61	NH1	L_ASP_82	OD2	2.558
3U36	L_ARG_61	NH2	L_ASP_82	OD1	2.956
3U36	L_ARG_61	NH2	L_ASP_82	OD2	3.131
3U36	L_LYS_66	NZ	L_GLU_31	OE1	3.601
3U36	L_LYS_66	NZ	L_GLU_31	OE2	3.328
3U36	L_LYS_89	NZ	H_GLU_95	OE1	3.857
3U36	L_ARG_95A	NH1	H_ASP_61	OD1	3.290
3U36	L_ARG_95A	NH1	H_ASP_61	OD2	1.959
3U36	L_ARG_95A	NH2	H_ASP_61	OD1	3.530
3U36	L_ARG_95A	NH2	H_ASP_61	OD2	3.624
3U36	L_ARG_96	NH2	H_GLU_95	OE2	3.606
3U36	L_HIS_188	ND1	L_ASP_151	OD2	3.797
3U36	A_HIS_35	NE2	A_GLU_95	OE1	2.797
3U36	A_ARG_38	NH1	A_ASP_86	OD1	3.094
3U36	A_ARG_38	NH2	A_GLU_46	OE1	3.989
3U36	A_ARG_38	NH2	A_GLU_46	OE2	3.229
3U36	A_ARG_66	NH1	A_ASP_86	OD1	3.636
3U36	A_ARG_66	NH1	A_ASP_86	OD2	2.878
3U36	A_ARG_66	NH2	A_ASP_86	OD1	3.312
3U36	A_ARG_66	NH2	A_ASP_86	OD2	3.805
3U36	A_ARG_83	NH1	A_GLU_85	OE2	3.159
3U36	A_ARG_94	NH2	A_ASP_101	OD1	3.386
3U36	A_ARG_94	NH2	A_ASP_101	OD2	2.941
3U36	A_LYS_210	NZ	A_GLU_212	OE1	3.743
3U36	B_LYS_53	NZ	B_ASP_50	OD2	3.349
3U36	B_ARG_61	NH1	B_ASP_82	OD1	3.756
3U36	B_ARG_61	NH1	B_ASP_82	OD2	2.547
3U36	B_ARG_61	NH2	B_ASP_82	OD1	2.945
3U36	B_ARG_61	NH2	B_ASP_82	OD2	3.139
3U36	B_LYS_66	NZ	B_GLU_31	OE1	3.580
3U36	B_LYS_66	NZ	B_GLU_31	OE2	3.318
3U36	B_LYS_89	NZ	A_GLU_95	OE1	3.772
3U36	B_ARG_95A	NH1	A_ASP_61	OD1	3.519
3U36	B_ARG_95A	NH1	A_ASP_61	OD2	2.198
3U36	B_ARG_95A	NH2	A_ASP_61	OD1	3.831
3U36	B_ARG_95A	NH2	A_ASP_61	OD2	3.817
3U36	B_ARG_96	NH2	A_GLU_95	OE2	3.395
3U36	B_LYS_129	NZ	A_ASP_144	OD1	3.769
3U36	B_HIS_188	ND1	B_ASP_151	OD2	3.839
3U36	C_HIS_35	NE2	C_GLU_95	OE1	2.789
3U36	C_ARG_38	NH1	C_ASP_86	OD1	3.079
3U36	C_ARG_38	NH2	C_GLU_46	OE2	3.262
3U36	C_ARG_38	NH2	C_ASP_86	OD1	3.997
3U36	C_ARG_66	NH1	C_ASP_86	OD1	3.625

3U36	C_ARG_66	NH1	C_ASP_86	OD2	2.865
3U36	C_ARG_66	NH2	C_ASP_86	OD1	3.335
3U36	C_ARG_66	NH2	C_ASP_86	OD2	3.835
3U36	C_ARG_83	NH1	C_GLU_85	OE2	3.161
3U36	C_ARG_94	NH2	C_ASP_101	OD1	3.358
3U36	C_ARG_94	NH2	C_ASP_101	OD2	2.963
3U36	C_LYS_210	NZ	C_GLU_212	OE1	3.726
3U36	D_LYS_53	NZ	D_ASP_50	OD2	3.331
3U36	D_ARG_61	NH1	D_ASP_82	OD1	3.763
3U36	D_ARG_61	NH1	D_ASP_82	OD2	2.558
3U36	D_ARG_61	NH2	D_ASP_82	OD1	2.940
3U36	D_ARG_61	NH2	D_ASP_82	OD2	3.134
3U36	D_LYS_66	NZ	D_GLU_31	OE1	3.617
3U36	D_LYS_66	NZ	D_GLU_31	OE2	3.349
3U36	D_LYS_89	NZ	C_GLU_95	OE1	3.877
3U36	D_ARG_95A	NH1	C_ASP_61	OD1	3.266
3U36	D_ARG_95A	NH1	C_ASP_61	OD2	2.045
3U36	D_ARG_95A	NH2	C_ASP_61	OD1	3.629
3U36	D_ARG_95A	NH2	C_ASP_61	OD2	3.782
3U36	D_ARG_96	NH2	C_GLU_95	OE2	3.569
3U36	D_HIS_188	ND1	D_ASP_151	OD2	3.779
3U36	E_HIS_35	NE2	E_GLU_95	OE1	2.788
3U36	E_ARG_38	NH1	E_ASP_86	OD1	3.110
3U36	E_ARG_38	NH2	E_GLU_46	OE2	3.229
3U36	E_ARG_66	NH1	E_ASP_86	OD1	3.638
3U36	E_ARG_66	NH1	E_ASP_86	OD2	2.884
3U36	E_ARG_66	NH2	E_ASP_86	OD1	3.328
3U36	E_ARG_66	NH2	E_ASP_86	OD2	3.837
3U36	E_ARG_83	NH1	E_GLU_85	OE2	3.161
3U36	E_ARG_94	NH2	E_ASP_101	OD1	3.373
3U36	E_ARG_94	NH2	E_ASP_101	OD2	2.982
3U36	E_LYS_210	NZ	E_GLU_212	OE1	3.712
3U36	F_LYS_53	NZ	F_ASP_50	OD2	3.348
3U36	F_ARG_61	NH1	F_ASP_82	OD1	3.756
3U36	F_ARG_61	NH1	F_ASP_82	OD2	2.549
3U36	F_ARG_61	NH2	F_ASP_82	OD1	2.945
3U36	F_ARG_61	NH2	F_ASP_82	OD2	3.125
3U36	F_LYS_66	NZ	F_GLU_31	OE1	3.599
3U36	F_LYS_66	NZ	F_GLU_31	OE2	3.326
3U36	F_ARG_95A	NH1	E_ASP_61	OD1	3.076
3U36	F_ARG_95A	NH1	E_ASP_61	OD2	1.876
3U36	F_ARG_95A	NH2	E_ASP_61	OD1	3.424
3U36	F_ARG_95A	NH2	E_ASP_61	OD2	3.670
3U36	F_ARG_96	NH2	E_GLU_95	OE2	3.739
3U36	F_HIS_188	ND1	F_ASP_151	OD2	3.814

Table 477: 3U36-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3UBX	A_ARG_21	NH2	A_GLU_92	OE1	3.225
3UBX	A_ARG_21	NH2	A_GLU_92	OE2	2.650
3UBX	A_ARG_25	NH2	A_ASP_27	OD1	3.138
3UBX	A_ARG_25	NH2	A_ASP_27	OD2	3.670
3UBX	A_ARG_25	NH2	A_ASP_43	OD2	3.995
3UBX	A_ARG_39	NH2	B_ASP_53	OD2	3.336
3UBX	A_LYS_51	NZ	A_GLU_243	OE1	2.918
3UBX	A_LYS_51	NZ	A_GLU_243	OE2	3.104
3UBX	A_HIS_203	ND1	A_ASP_252	OD1	3.478
3UBX	A_ARG_204	NH1	A_GLU_258	OE2	2.763
3UBX	A_ARG_204	NH2	A_GLU_258	OE2	2.916
3UBX	A_ARG_264	NH2	A_ASP_274	OD2	3.397
3UBX	A_LYS_266	NZ	A_ASP_274	OD2	2.636
3UBX	A_HIS_282	NE2	B_ASP_98	OD1	3.815
3UBX	A_HIS_282	NE2	B_ASP_98	OD2	3.128
3UBX	B_ARG_12	NH2	A_ASP_242	OD1	3.715
3UBX	B_ARG_12	NH2	A_ASP_242	OD2	3.324
3UBX	B_LYS_19	NZ	B_GLU_16	OE1	3.108
3UBX	B_LYS_19	NZ	B_GLU_16	OE2	3.855
3UBX	B_LYS_	NZ	B_ASP_76	OD2	3.469
3UBX	B_HIS_67	NE2	B_GLU_50	OE1	3.182
3UBX	D_ARG_21	NH2	D_GLU_92	OE1	3.198
3UBX	D_ARG_21	NH2	D_GLU_92	OE2	2.624
3UBX	D_ARG_	NH2	D_ASP_	OD1	3.097
3UBX	D_ARG_	NH2	D_ASP_	OD2	3.631
3UBX	D_ARG_	NH2	E_ASP_	OD2	3.464
3UBX	D_LYS_	NZ	D_GLU_	OE1	2.938
3UBX	D_LYS_	NZ	D_GLU_	OE2	3.121
3UBX	D_HIS_	ND1	D_ASP_	OD1	3.543
3UBX	D_ARG_	NH1	D_GLU_	OE2	2.718
3UBX	D_ARG_	NH2	D_GLU_	OE2	2.872
3UBX	D_ARG_	NH2	D_ASP_	OD2	3.382
3UBX	D_LYS_	NZ	D_ASP_	OD2	2.644
3UBX	D_HIS_	NE2	E_ASP_	OD1	3.963
3UBX	D_HIS_	NE2	E_ASP_	OD2	3.193
3UBX	E_ARG_	NH2	D_ASP_	OD1	3.594
3UBX	E_ARG_	NH2	D_ASP_	OD2	3.257
3UBX	E_LYS_	NZ	E_GLU_	OE1	3.157
3UBX	E_LYS_	NZ	E_GLU_	OE2	3.909
3UBX	E_HIS_	ND1	D_GLU_97	OE1	3.846
3UBX	E_LYS_	NZ	E_ASP_	OD2	3.547
3UBX	E_HIS_	NE2	E_GLU_	OE1	3.185
3UBX	L_ARG_32	NH2	A_ASP_80	OD1	3.479
3UBX	L_ARG_32	NH2	A_ASP_80	OD2	3.348
3UBX	L_ARG_32	NH2	A_ASP_153	OD2	3.795
3UBX	L_ARG_61	NH2	L_ASP_82	OD1	2.895
3UBX	L_ARG_61	NH2	L_ASP_82	OD2	3.241
3UBX	L_LYS_103	NZ	L_ASP_165	OD1	3.380
3UBX	L_LYS_142	NZ	L_GLU_105	OE1	2.881
3UBX	L_LYS_142	NZ	L_GLU_105	OE2	3.829
3UBX	L_LYS_	NZ	L_GLU_	OE1	3.629
3UBX	L_LYS_	NZ	L_GLU_	OE2	3.666
3UBX	L_ARG_	NH1	L_GLU_	OE2	3.855
3UBX	L_LYS_169	NZ	L_GLU_81	OE1	3.852
3UBX	L_LYS_169	NZ	L_GLU_81	OE2	3.096
3UBX	L_HIS_	NE2	L_GLU_	OE2	3.994
3UBX	L_LYS_	NZ	L_ASP_	OD2	3.189

3UBX	H_LYS_12	NZ	H_GLU_10	OE2	3.934
3UBX	H_LYS_65	NZ	H_ASP_62	OD1	3.945
3UBX	H_ARG_67	NH2	H_ASP_90	OD1	2.984
3UBX	H_ARG_67	NH2	H_ASP_90	OD2	2.362
3UBX	H_ARG_103	NH2	A_ASP_80	OD1	2.578
3UBX	H_LYS_215	NZ	L_GLU_123	OE1	3.082
3UBX	H_LYS_215	NZ	L_GLU_123	OE2	3.481
3UBX	I_ARG_32	NH2	D_ASP_80	OD1	3.383
3UBX	I_ARG_32	NH2	D_ASP_80	OD2	3.294
3UBX	I_ARG_32	NH2	D_ASP_153	OD2	3.950
3UBX	I_ARG_61	NH2	I_ASP_82	OD1	2.893
3UBX	I_ARG_61	NH2	I_ASP_82	OD2	3.343
3UBX	I_LYS_103	NZ	I_ASP_165	OD1	3.385
3UBX	I_LYS_142	NZ	I_GLU_105	OE1	2.848
3UBX	I_LYS_142	NZ	I_GLU_105	OE2	3.795
3UBX	I_LYS_149	NZ	I_GLU_195	OE1	3.611
3UBX	I_LYS_149	NZ	I_GLU_195	OE2	3.678
3UBX	I_ARG_155	NH1	I_GLU_185	OE2	3.804
3UBX	I_LYS_169	NZ	L_GLU_81	OE1	3.837
3UBX	I_LYS_169	NZ	L_GLU_81	OE2	3.130
3UBX	I_LYS_199	NZ	I_ASP_110	OD2	3.216
3UBX	G_LYS_12	NZ	G_GLU_10	OE2	3.983
3UBX	G_ARG_67	NH2	G_ASP_90	OD1	3.006
3UBX	G_ARG_67	NH2	G_ASP_90	OD2	2.366
3UBX	G_ARG_103	NH2	D_ASP_80	OD1	2.614
3UBX	G_LYS_215	NZ	I_GLU_123	OE1	3.204
3UBX	G_LYS_215	NZ	I_GLU_123	OE2	3.514

Table 478: 3UBX-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3UJI	L_LYS_53	NZ	L_GLU_50	OE1	2.671
3UJI	L_ARG_61	NH2	L_ASP_82	OD1	2.783
3UJI	L_ARG_61	NH2	L_ASP_82	OD2	3.833
3UJI	L_LYS_66	NZ	L_ASP_51	OD1	2.934
3UJI	L_LYS_66	NZ	L_ASP_51	OD2	3.132
3UJI	L_LYS_103	NZ	L_ASP_85	OD1	2.947
3UJI	L_LYS_103	NZ	L_ASP_85	OD2	3.475
3UJI	L_LYS_110	NZ	L_GLU_198	OE1	2.866
3UJI	L_LYS_110	NZ	L_GLU_198	OE2	3.915
3UJI	L_HIS_188	ND1	L_ASP_151	OD2	3.040
3UJI	L_LYS_189	NZ	L_ASP_151	OD1	3.884
3UJI	H_LYS_12	NZ	H_GLU_16	OE1	3.975
3UJI	H_LYS_73	NZ	H_ASP_53	OD2	3.330
3UJI	H_ARG_94	NH2	H_ASP_101	OD1	3.451
3UJI	H_ARG_94	NH2	H_ASP_101	OD2	2.842
3UJI	H_LYS_143	NZ	L_GLU_124	OE2	2.632
3UJI	H_LYS_206	NZ	H_ASP_208	OD1	3.500
3UJI	H_LYS_209	NZ	L_GLU_123	OE1	3.097
3UJI	H_LYS_209	NZ	L_GLU_123	OE2	2.701
3UJI	H_LYS_210	NZ	H_GLU_212	OE1	3.946
3UJI	H_LYS_210	NZ	H_GLU_212	OE2	3.699
3UJI	P_LYS_305	NZ	H_ASP_54	OD1	2.722
3UJI	P_LYS_305	NZ	H_ASP_54	OD2	3.687
3UJI	P_LYS_305	NZ	H_ASP_56	OD2	2.744
3UJI	P_HIS_308	ND1	H_GLU_98	OE1	2.731
3UJI	P_HIS_308	ND1	H_GLU_98	OE2	3.371

Table 479: 3UJI-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3UJJ	L_LYS_39	NZ	L_ASP_81	OD2	3.776
3UJJ	L_ARG_61	NH1	L_ASP_81	OD1	3.440
3UJJ	L_ARG_61	NH1	L_ASP_82	OD1	2.656
3UJJ	L_ARG_61	NH1	L_ASP_82	OD2	3.380
3UJJ	L_ARG_66	NH2	L_ASP_51	OD1	3.920
3UJJ	L_ARG_66	NH2	L_ASP_51	OD2	2.951
3UJJ	H_ARG_38	NH2	H_GLU_46	OE1	3.170
3UJJ	H_ARG_38	NH2	H_GLU_46	OE2	3.073
3UJJ	H_ARG_58	NH2	H_ASP_56	OD1	3.555
3UJJ	H_ARG_58	NH2	H_ASP_56	OD2	2.847
3UJJ	H_LYS_143	NZ	H_ASP_144	OD1	2.864
3UJJ	H_LYS_143	NZ	H_ASP_144	OD2	2.969
3UJJ	H_LYS_209	NZ	L_GLU_123	OE1	2.859
3UJJ	H_LYS_209	NZ	L_GLU_123	OE2	2.771
3UJJ	H_LYS_210	NZ	H_GLU_212	OE2	2.981
3UJJ	P_LYS_305	NZ	H_ASP_54	OD1	3.600
3UJJ	P_LYS_305	NZ	H_ASP_54	OD2	2.628
3UJJ	P_LYS_305	NZ	H_ASP_56	OD2	2.857
3UJJ	P_ARG_308	NH2	L_GLU_50	OE2	2.898

Table 480: 3UJJ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID** **residue name** **residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3UJT	H_LYS_19	NZ	H_ASP_78	OD1	2.829
3UJT	H_HIS_35	ND1	H_GLU_50	OE1	3.828
3UJT	H_HIS_35	NE2	H_GLU_50	OE1	3.223
3UJT	H_ARG_40	NH1	H_GLU_85	OE2	3.140
3UJT	H_LYS_64	NZ	H_GLU_61	OE1	2.811
3UJT	H_LYS_66	NZ	H_ASP_86	OD1	3.766
3UJT	H_LYS_66	NZ	H_ASP_86	OD2	2.865
3UJT	H_LYS_143	NZ	M_ASP_60	OD2	3.914
3UJT	H_LYS_208	NZ	L_GLU_123	OE2	2.966
3UJT	H_LYS_209	NZ	H_GLU_211	OE2	3.384
3UJT	L_ARG_61	NH2	L_ASP_82	OD1	2.769
3UJT	L_ARG_61	NH2	L_ASP_82	OD2	3.414
3UJT	L_LYS_103	NZ	L_ASP_85	OD1	3.942
3UJT	L_LYS_149	NZ	L_GLU_195	OE2	3.036
3UJT	L_ARG_155	NH1	L_GLU_185	OE1	2.986
3UJT	L_ARG_155	NH2	L_GLU_185	OE1	3.804
3UJT	L_LYS_183	NZ	L_GLU_187	OE1	3.131
3UJT	L_LYS_183	NZ	L_GLU_187	OE2	3.169
3UJT	L_HIS_189	ND1	L_ASP_151	OD2	3.929
3UJT	L_HIS_35	ND1	L_GLU_50	OE1	3.921
3UJT	L_HIS_35	NE2	L_GLU_50	OE1	3.458
3UJT	L_ARG_40	NH1	L_GLU_85	OE1	3.716
3UJT	L_LYS_66	NZ	L_ASP_86	OD1	3.625
3UJT	L_LYS_66	NZ	L_ASP_86	OD2	2.830
3UJT	L_HIS_164	NE2	M_ASP_167	OD1	3.917
3UJT	L_LYS_208	NZ	M_GLU_123	OE2	3.024
3UJT	L_LYS_209	NZ	L_GLU_211	OE2	3.830
3UJT	M_LYS_39	NZ	M_GLU_81	OE2	3.196
3UJT	M_ARG_61	NH2	M_GLU_81	OE1	3.337
3UJT	M_ARG_61	NH2	M_ASP_82	OD1	2.863
3UJT	M_ARG_61	NH2	M_ASP_82	OD2	3.614
3UJT	M_LYS_103	NZ	M_GLU_105	OE2	3.799
3UJT	M_LYS_147	NZ	M_GLU_154	OE1	3.066
3UJT	M_LYS_149	NZ	M_GLU_195	OE2	3.255
3UJT	M_LYS_183	NZ	M_GLU_187	OE1	3.301
3UJT	M_HIS_189	ND1	M_ASP_151	OD2	2.746
3UJT	M_LYS_199	NZ	M_ASP_110	OD2	3.794

Table 481: 3UJT-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3UO1	H_ARG_38	NH1	H_ASP_90	OD1	3.119
3UO1	H_ARG_38	NH2	H_GLU_46	OE1	3.165
3UO1	H_ARG_67	NH1	H_ASP_90	OD2	2.918
3UO1	H_ARG_67	NH2	H_ASP_90	OD1	3.039
3UO1	H_ARG_67	NH2	H_ASP_90	OD2	3.214
3UO1	H_ARG_87	NH1	H_GLU_89	OE2	3.676
3UO1	H_ARG_98	NH2	H_ASP_105	OD1	3.545
3UO1	H_ARG_98	NH2	H_ASP_105	OD2	2.915
3UO1	H_LYS_147	NZ	H_GLU_175	OE2	3.203
3UO1	H_LYS_212	NZ	L_GLU_127	OE2	2.634
3UO1	L_ARG_24	NH2	L_ASP_75	OD1	3.866
3UO1	L_ARG_66	NH1	L_ASP_87	OD1	3.885
3UO1	L_ARG_66	NH1	L_ASP_87	OD2	2.800
3UO1	L_ARG_66	NH2	L_GLU_84	OE1	3.875
3UO1	L_ARG_66	NH2	L_GLU_84	OE2	3.880
3UO1	L_ARG_66	NH2	L_ASP_87	OD1	3.014
3UO1	L_ARG_66	NH2	L_ASP_87	OD2	3.371
3UO1	L_LYS_153	NZ	L_GLU_199	OE1	3.850
3UO1	L_LYS_153	NZ	L_GLU_199	OE2	3.003
3UO1	L_ARG_159	NH1	L_GLU_189	OE1	3.609
3UO1	L_ARG_159	NH2	L_GLU_189	OE1	3.559
3UO1	L_ARG_192	NH2	L_ASP_188	OD1	3.033
3UO1	L_HIS_193	ND1	L_ASP_155	OD2	2.858
3UO1	L_LYS_203	NZ	L_ASP_114	OD2	3.912

Table 482: 3UO1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3UYR	H_ARG_38	NH1	H_ASP_90	OD1	3.056
3UYR	H_ARG_38	NH2	H_GLU_46	OE1	3.014
3UYR	H_ARG_67	NH1	H_ASP_90	OD2	3.083
3UYR	H_ARG_67	NH2	H_ASP_90	OD1	3.206
3UYR	H_ARG_67	NH2	H_ASP_90	OD2	3.238
3UYR	H_ARG_98	NH2	H_ASP_105	OD1	3.584
3UYR	H_ARG_98	NH2	H_ASP_105	OD2	2.920
3UYR	H_LYS_212	NZ	L_GLU_127	OE2	2.869
3UYR	H_LYS_213	NZ	H_GLU_215	OE2	3.848
3UYR	L_ARG_24	NH1	L_ASP_75	OD1	3.439
3UYR	L_ARG_59	NH1	L_ASP_65	OD1	3.730
3UYR	L_ARG_66	NH1	L_ASP_87	OD1	3.905
3UYR	L_ARG_66	NH1	L_ASP_87	OD2	2.920
3UYR	L_ARG_66	NH2	L_GLU_84	OE1	3.701
3UYR	L_ARG_66	NH2	L_GLU_84	OE2	3.783
3UYR	L_ARG_66	NH2	L_ASP_87	OD1	3.182
3UYR	L_ARG_66	NH2	L_ASP_87	OD2	3.579
3UYR	L_LYS_153	NZ	L_GLU_199	OE2	3.046
3UYR	L_ARG_192	NH2	L_ASP_188	OD1	3.145
3UYR	L_HIS_193	ND1	L_ASP_155	OD2	2.932
3UYR	L_LYS_203	NZ	L_ASP_114	OD2	3.650

Table 483: 3UYR-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3V4P	A_HIS_28	NE2	A_ASP_138	OD1	3.437
3V4P	A_ARG_57	NH2	A_GLU_69	OE1	3.613
3V4P	A_ARG_57	NH2	A_GLU_69	OE2	3.235
3V4P	A_LYS_126	NZ	A_GLU_88	OE1	3.906
3V4P	A_LYS_126	NZ	A_GLU_88	OE2	3.280
3V4P	A_LYS_157	NZ	A_GLU_160	OE1	3.915
3V4P	A_LYS_203	NZ	A_GLU_255	OE2	3.829
3V4P	A_ARG_228	NH1	A_GLU_234	OE2	3.256
3V4P	A_ARG_228	NH2	A_GLU_234	OE2	3.842
3V4P	A_HIS_242	NE2	A_GLU_243	OE1	3.925
3V4P	A_LYS_247	NZ	A_GLU_263	OE2	2.474
3V4P	A_LYS_265	NZ	A_GLU_243	OE2	3.624
3V4P	A_ARG_305	NH1	A_ASP_329	OD1	2.732
3V4P	A_ARG_305	NH2	A_ASP_329	OD1	2.778
3V4P	A_ARG_305	NH2	A_ASP_329	OD2	3.464
3V4P	A_LYS_330	NZ	A_GLU_360	OE1	3.537
3V4P	A_LYS_330	NZ	A_ASP_361	OD1	3.264
3V4P	A_LYS_330	NZ	A_ASP_361	OD2	3.668
3V4P	A_ARG_334	NH1	A_GLU_337	OE1	3.017
3V4P	A_ARG_334	NH1	A_GLU_337	OE2	2.987
3V4P	A_ARG_334	NH2	A_GLU_302	OE2	3.593
3V4P	A_ARG_384	NH1	A_GLU_386	OE1	3.396
3V4P	A_ARG_384	NH2	A_GLU_360	OE1	2.505
3V4P	A_ARG_384	NH2	A_ASP_361	OD2	3.166
3V4P	A_ARG_384	NH2	A_GLU_386	OE1	3.325
3V4P	A_ARG_429	NH2	A_ASP_408	OD2	3.082
3V4P	A_ARG_499	NH1	A_ASP_489	OD2	3.923
3V4P	A_ARG_499	NH1	A_ASP_537	OD2	3.979
3V4P	A_ARG_532	NH1	A_ASP_534	OD2	3.421
3V4P	A_LYS_533	NZ	A_GLU_455	OE1	3.724
3V4P	A_LYS_533	NZ	A_GLU_455	OE2	3.681
3V4P	A_ARG_536	NH2	A_ASP_534	OD1	3.784
3V4P	A_LYS_574	NZ	A_ASP_375	OD1	2.978
3V4P	B_ARG_108	NH2	B_GLU_450	OE1	2.652
3V4P	B_ARG_110	NH1	B_GLU_85	OE1	3.635
3V4P	B_ARG_110	NH2	B_GLU_450	OE2	3.758
3V4P	B_ARG_124	NH2	B_ASP_89	OD1	3.110
3V4P	B_ARG_124	NH2	B_ASP_89	OD2	3.634
3V4P	B_LYS_146	NZ	B_GLU_202	OE2	2.939
3V4P	B_LYS_180	NZ	B_ASP_244	OD1	3.554
3V4P	B_LYS_180	NZ	B_ASP_244	OD2	2.740
3V4P	B_ARG_194	NH1	H_ASP_102	OD1	2.860
3V4P	B_ARG_194	NH1	H_ASP_102	OD2	2.764
3V4P	B_ARG_200	NH2	H_ASP_102	OD1	3.172
3V4P	B_ARG_259	NH2	B_ASP_134	OD1	2.676
3V4P	B_HIS_274	ND1	B_ASP_278	OD2	2.831
3V4P	B_HIS_274	NE2	B_ASP_179	OD2	3.371
3V4P	B_HIS_274	NE2	B_ASP_237	OD2	2.863
3V4P	B_HIS_293	NE2	B_ASP_289	OD1	2.750
3V4P	B_HIS_293	NE2	B_ASP_289	OD2	2.939
3V4P	B_ARG_302	NH2	B_GLU_305	OE1	3.376
3V4P	B_ARG_399	NH1	B_GLU_390	OE1	3.166
3V4P	B_ARG_399	NH1	B_GLU_390	OE2	2.988
3V4P	B_ARG_399	NH2	B_GLU_390	OE2	3.915
3V4P	B_LYS_402	NZ	B_GLU_404	OE2	3.864
3V4P	B_HIS_434	NE2	B_GLU_432	OE1	3.790
3V4P	B_ARG_439	NH2	B_GLU_377	OE1	3.416

3V4P	B_HIS_452	ND1	B_GLU_450	OE2	3.943
3V4P	C_HIS_28	NE2	C_ASP_138	OD1	3.435
3V4P	C_ARG_57	NH2	C_GLU_69	OE1	3.610
3V4P	C_ARG_57	NH2	C_GLU_69	OE2	3.231
3V4P	C_LYS_126	NZ	C_GLU_88	OE1	3.915
3V4P	C_LYS_126	NZ	C_GLU_88	OE2	3.295
3V4P	C_LYS_157	NZ	C_GLU_160	OE1	3.917
3V4P	C_LYS_203	NZ	C_GLU_255	OE2	3.826
3V4P	C_ARG_228	NH1	C_GLU_234	OE2	3.252
3V4P	C_ARG_228	NH2	C_GLU_234	OE2	3.840
3V4P	C_HIS_242	NE2	C_GLU_243	OE1	3.935
3V4P	C_LYS_247	NZ	C_GLU_263	OE2	2.476
3V4P	C_LYS_265	NZ	C_GLU_243	OE2	3.624
3V4P	C_ARG_305	NH1	C_ASP_329	OD1	2.736
3V4P	C_ARG_305	NH2	C_ASP_329	OD1	2.777
3V4P	C_ARG_305	NH2	C_ASP_329	OD2	3.462
3V4P	C_LYS_330	NZ	C_GLU_360	OE1	3.551
3V4P	C_LYS_330	NZ	C_ASP_361	OD1	3.262
3V4P	C_LYS_330	NZ	C_ASP_361	OD2	3.668
3V4P	C_ARG_334	NH1	C_GLU_337	OE1	3.021
3V4P	C_ARG_334	NH1	C_GLU_337	OE2	2.997
3V4P	C_ARG_334	NH2	C_GLU_302	OE2	3.598
3V4P	C_ARG_384	NH1	C_GLU_386	OE1	3.393
3V4P	C_ARG_384	NH2	C_GLU_360	OE1	2.506
3V4P	C_ARG_384	NH2	C_ASP_361	OD2	3.170
3V4P	C_ARG_384	NH2	C_GLU_386	OE1	3.316
3V4P	C_ARG_429	NH2	C_ASP_408	OD2	3.082
3V4P	C_ARG_499	NH1	C_ASP_489	OD2	3.928
3V4P	C_ARG_499	NH1	C_ASP_537	OD2	3.667
3V4P	C_ARG_532	NH1	C_ASP_534	OD2	3.504
3V4P	C_LYS_533	NZ	C_GLU_455	OE1	3.658
3V4P	C_ARG_536	NH2	C_ASP_534	OD1	3.773
3V4P	C_LYS_574	NZ	C_ASP_375	OD1	3.893
3V4P	D_ARG_108	NH2	D_GLU_450	OE1	2.653
3V4P	D_ARG_110	NH1	D_GLU_85	OE1	3.633
3V4P	D_ARG_110	NH2	D_GLU_450	OE2	3.756
3V4P	D_ARG_124	NH2	D_ASP_89	OD1	3.117
3V4P	D_ARG_124	NH2	D_ASP_89	OD2	3.640
3V4P	D_LYS_146	NZ	D_GLU_202	OE2	2.944
3V4P	D_LYS_180	NZ	D_ASP_244	OD1	3.559
3V4P	D_LYS_180	NZ	D_ASP_244	OD2	2.747
3V4P	D_ARG_194	NH1	M_ASP_102	OD1	2.738
3V4P	D_ARG_194	NH1	M_ASP_102	OD2	2.760
3V4P	D_ARG_200	NH2	M_ASP_102	OD1	3.233
3V4P	D_ARG_259	NH2	D_ASP_134	OD1	2.676
3V4P	D_HIS_274	ND1	D_ASP_278	OD2	2.837
3V4P	D_HIS_274	NE2	D_ASP_179	OD2	3.371
3V4P	D_HIS_274	NE2	D_ASP_237	OD2	2.865
3V4P	D_HIS_293	NE2	D_ASP_289	OD1	2.751
3V4P	D_HIS_293	NE2	D_ASP_289	OD2	2.938
3V4P	D_ARG_302	NH2	D_GLU_305	OE1	3.367
3V4P	D_ARG_399	NH1	D_GLU_390	OE1	3.160
3V4P	D_ARG_399	NH1	D_GLU_390	OE2	2.983
3V4P	D_ARG_399	NH2	D_GLU_390	OE2	3.909
3V4P	D_LYS_402	NZ	D_GLU_404	OE2	3.866
3V4P	D_HIS_434	NE2	D_GLU_432	OE1	3.794
3V4P	D_ARG_439	NH2	D_GLU_377	OE1	3.413
3V4P	D_HIS_452	ND1	D_GLU_450	OE2	3.942

3V4P	H_HIS_35	ND1	H_GLU_50	OE1	3.827
3V4P	H_ARG_40	NH1	H_GLU_46	OE2	3.925
3V4P	H_ARG_40	NH2	H_GLU_46	OE2	3.891
3V4P	H_LYS_63	NZ	H_GLU_46	OE1	3.617
3V4P	H_LYS_67	NZ	H_ASP_90	OD1	3.016
3V4P	H_LYS_67	NZ	H_ASP_90	OD2	2.785
3V4P	H_ARG_98	NH2	H_ASP_109	OD1	3.538
3V4P	H_ARG_98	NH2	H_ASP_109	OD2	2.869
3V4P	H_LYS_151	NZ	H_GLU_179	OE1	3.924
3V4P	H_LYS_151	NZ	H_GLU_179	OE2	3.342
3V4P	H_HIS_172	ND1	L_ASP_172	OD2	3.780
3V4P	H_LYS_216	NZ	L_GLU_128	OE2	3.270
3V4P	L_ARG_24	NH2	L_ASP_75	OD2	3.872
3V4P	L_ARG_66	NH2	L_GLU_86	OE1	3.540
3V4P	L_ARG_66	NH2	L_ASP_87	OD1	2.923
3V4P	L_ARG_66	NH2	L_ASP_87	OD2	3.479
3V4P	L_HIS_194	ND1	L_ASP_156	OD1	3.668
3V4P	L_HIS_194	ND1	L_ASP_156	OD2	3.022
3V4P	M_HIS_35	ND1	M_GLU_50	OE1	3.826
3V4P	M_ARG_40	NH1	M_GLU_46	OE2	3.929
3V4P	M_ARG_40	NH2	M_GLU_46	OE2	3.895
3V4P	M_LYS_63	NZ	M_GLU_46	OE1	3.628
3V4P	M_LYS_67	NZ	M_ASP_90	OD1	3.021
3V4P	M_LYS_67	NZ	M_ASP_90	OD2	2.783
3V4P	M_ARG_98	NH2	M_ASP_109	OD1	3.527
3V4P	M_ARG_98	NH2	M_ASP_109	OD2	2.863
3V4P	M_LYS_151	NZ	M_GLU_179	OE1	3.922
3V4P	M_LYS_151	NZ	M_GLU_179	OE2	3.343
3V4P	M_HIS_172	ND1	N_ASP_172	OD2	3.600
3V4P	M_LYS_216	NZ	N_GLU_128	OE2	3.408
3V4P	N_ARG_24	NH2	N_ASP_75	OD2	3.878
3V4P	N_ARG_66	NH2	N_GLU_86	OE1	3.541
3V4P	N_ARG_66	NH2	N_ASP_87	OD1	2.925
3V4P	N_ARG_66	NH2	N_ASP_87	OD2	3.479
3V4P	N_HIS_194	ND1	N_ASP_156	OD1	3.669
3V4P	N_HIS_194	ND1	N_ASP_156	OD2	3.021

Table 484: 3V4P-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3V4U	H_ARG_38	NH1	H_ASP_90	OD1	3.026
3V4U	H_ARG_38	NH2	H_GLU_46	OE1	2.923
3V4U	H_ARG_38	NH2	H_ASP_90	OD1	3.942
3V4U	H_ARG_67	NH1	H_ASP_90	OD2	3.062
3V4U	H_ARG_67	NH2	H_ASP_90	OD1	3.515
3V4U	H_ARG_67	NH2	H_ASP_90	OD2	3.172
3V4U	H_ARG_98	NH2	H_ASP_105	OD1	3.657
3V4U	H_ARG_98	NH2	H_ASP_105	OD2	3.151
3V4U	H_LYS_147	NZ	H_GLU_175	OE2	2.827
3V4U	H_LYS_212	NZ	L_GLU_127	OE2	2.667
3V4U	L_ARG_24	NH2	L_ASP_75	OD1	3.756
3V4U	L_ARG_66	NH1	L_ASP_87	OD1	3.777
3V4U	L_ARG_66	NH1	L_ASP_87	OD2	2.819
3V4U	L_ARG_66	NH2	L_GLU_84	OE1	3.720
3V4U	L_ARG_66	NH2	L_GLU_84	OE2	3.860
3V4U	L_ARG_66	NH2	L_ASP_87	OD1	2.775
3V4U	L_ARG_66	NH2	L_ASP_87	OD2	3.243
3V4U	L_LYS_153	NZ	L_GLU_199	OE1	3.350
3V4U	L_LYS_153	NZ	L_GLU_199	OE2	2.923
3V4U	L_ARG_159	NH1	L_GLU_189	OE1	2.754
3V4U	L_ARG_159	NH2	L_GLU_189	OE1	3.366
3V4U	L_LYS_187	NZ	L_GLU_191	OE2	3.065
3V4U	L_ARG_192	NH2	L_ASP_188	OD1	3.394

Table 485: 3V4U-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3V4V	A_HIS_28	NE2	A_ASP_138	OD1	3.625
3V4V	A_ARG_57	NH2	A_GLU_69	OE2	3.446
3V4V	A_LYS_126	NZ	A_GLU_88	OE1	3.984
3V4V	A_LYS_126	NZ	A_GLU_88	OE2	3.844
3V4V	A_LYS_157	NZ	A_GLU_160	OE1	3.707
3V4V	A_LYS_203	NZ	A_GLU_255	OE2	4.000
3V4V	A_ARG_228	NH2	A_GLU_234	OE2	3.810
3V4V	A_HIS_242	NE2	A_GLU_243	OE1	3.962
3V4V	A_LYS_247	NZ	A_GLU_263	OE2	2.864
3V4V	A_ARG_301	NH2	A_GLU_302	OE1	3.852
3V4V	A_ARG_305	NH1	A_ASP_329	OD1	2.728
3V4V	A_ARG_305	NH2	A_ASP_329	OD1	2.929
3V4V	A_ARG_305	NH2	A_ASP_329	OD2	3.468
3V4V	A_LYS_330	NZ	A_GLU_360	OE1	3.937
3V4V	A_LYS_330	NZ	A_ASP_361	OD1	3.025
3V4V	A_LYS_330	NZ	A_ASP_361	OD2	3.585
3V4V	A_ARG_334	NH1	A_GLU_337	OE1	3.450
3V4V	A_ARG_334	NH1	A_GLU_337	OE2	3.152
3V4V	A_ARG_334	NH2	A_GLU_302	OE2	3.584
3V4V	A_ARG_384	NH1	A_GLU_386	OE1	3.340
3V4V	A_ARG_384	NH2	A_GLU_360	OE1	2.718
3V4V	A_ARG_384	NH2	A_ASP_361	OD2	3.178
3V4V	A_ARG_384	NH2	A_GLU_386	OE1	2.970
3V4V	A_ARG_429	NH2	A_ASP_408	OD2	2.821
3V4V	A_ARG_499	NH1	A_ASP_489	OD2	3.736
3V4V	A_ARG_499	NH1	A_ASP_537	OD2	3.000
3V4V	A_ARG_499	NH2	A_ASP_537	OD2	3.346
3V4V	A_ARG_532	NH1	A_ASP_534	OD2	3.643
3V4V	A_LYS_533	NZ	A_GLU_455	OE1	3.618
3V4V	A_ARG_536	NH2	A_ASP_534	OD1	3.812
3V4V	A_LYS_574	NZ	A_ASP_375	OD1	3.230
3V4V	A_LYS_574	NZ	A_ASP_375	OD2	3.530
3V4V	B_ARG_108	NH2	B_GLU_450	OE1	2.540
3V4V	B_ARG_110	NH1	B_GLU_85	OE1	3.653
3V4V	B_ARG_110	NH2	B_GLU_450	OE2	3.788
3V4V	B_ARG_124	NH2	B_ASP_89	OD1	3.503
3V4V	B_LYS_180	NZ	B_ASP_244	OD1	3.343
3V4V	B_LYS_180	NZ	B_ASP_244	OD2	2.615
3V4V	B_ARG_194	NH1	H_ASP_102	OD1	2.874
3V4V	B_ARG_194	NH1	H_ASP_102	OD2	3.211
3V4V	B_ARG_200	NH2	H_ASP_102	OD1	3.237
3V4V	B_ARG_259	NH2	B_ASP_134	OD1	2.874
3V4V	B_HIS_274	ND1	B_ASP_278	OD2	3.045
3V4V	B_HIS_274	NE2	B_ASP_179	OD2	3.250
3V4V	B_HIS_274	NE2	B_ASP_237	OD2	3.128
3V4V	B_HIS_293	NE2	B_ASP_289	OD1	2.625
3V4V	B_HIS_293	NE2	B_ASP_289	OD2	2.924
3V4V	B_ARG_302	NH2	B_GLU_305	OE1	3.474
3V4V	B_ARG_399	NH1	B_GLU_390	OE1	2.982
3V4V	B_ARG_399	NH1	B_GLU_390	OE2	2.814
3V4V	B_ARG_399	NH2	B_GLU_390	OE2	3.187
3V4V	B_LYS_402	NZ	B_GLU_404	OE2	3.543
3V4V	B_HIS_434	NE2	B_GLU_432	OE1	3.549
3V4V	B_ARG_439	NH2	B_GLU_377	OE1	3.529
3V4V	B_HIS_452	ND1	B_GLU_450	OE2	3.839
3V4V	H_HIS_35	ND1	H_GLU_50	OE1	3.868
3V4V	H_HIS_35	NE2	H_GLU_50	OE1	3.873

3V4V	H_ARG_40	NH2	H_GLU_89	OE1	3.118
3V4V	H_LYS_63	NZ	H_GLU_46	OE1	3.657
3V4V	H_LYS_67	NZ	H_ASP_90	OD1	2.996
3V4V	H_LYS_67	NZ	H_ASP_90	OD2	2.684
3V4V	H_ARG_98	NH2	H_ASP_109	OD1	3.554
3V4V	H_ARG_98	NH2	H_ASP_109	OD2	2.682
3V4V	H_LYS_151	NZ	H_GLU_179	OE2	3.864
3V4V	H_HIS_172	ND1	L_ASP_172	OD1	3.644
3V4V	H_LYS_216	NZ	L_GLU_128	OE2	3.607
3V4V	L_ARG_66	NH2	L_GLU_86	OE1	3.477
3V4V	L_ARG_66	NH2	L_ASP_87	OD1	3.326
3V4V	L_ARG_66	NH2	L_ASP_87	OD2	3.224
3V4V	L_LYS_152	NZ	L_GLU_200	OE2	3.741
3V4V	L_HIS_194	ND1	L_ASP_156	OD1	3.854
3V4V	L_HIS_194	ND1	L_ASP_156	OD2	2.969
3V4V	C_HIS_28	NE2	C_ASP_138	OD1	3.619
3V4V	C_ARG_57	NH2	C_GLU_69	OE2	3.454
3V4V	C_LYS_126	NZ	C_GLU_88	OE1	3.966
3V4V	C_LYS_126	NZ	C_GLU_88	OE2	3.832
3V4V	C_LYS_157	NZ	C_GLU_160	OE1	3.712
3V4V	C_ARG_228	NH2	C_GLU_234	OE2	3.809
3V4V	C_HIS_242	NE2	C_GLU_243	OE1	3.957
3V4V	C_LYS_247	NZ	C_GLU_263	OE2	2.858
3V4V	C_ARG_301	NH2	C_GLU_302	OE1	3.856
3V4V	C_ARG_305	NH1	C_ASP_329	OD1	2.717
3V4V	C_ARG_305	NH2	C_ASP_329	OD1	2.917
3V4V	C_ARG_305	NH2	C_ASP_329	OD2	3.457
3V4V	C_LYS_330	NZ	C_GLU_360	OE1	3.928
3V4V	C_LYS_330	NZ	C_ASP_361	OD1	3.024
3V4V	C_LYS_330	NZ	C_ASP_361	OD2	3.579
3V4V	C_ARG_334	NH1	C_GLU_337	OE1	3.446
3V4V	C_ARG_334	NH1	C_GLU_337	OE2	3.179
3V4V	C_ARG_334	NH2	C_GLU_302	OE2	3.589
3V4V	C_ARG_373	NH2	C_GLU_575	OE2	3.832
3V4V	C_ARG_384	NH1	C_GLU_386	OE1	3.331
3V4V	C_ARG_384	NH2	C_GLU_360	OE1	2.721
3V4V	C_ARG_384	NH2	C_ASP_361	OD2	3.178
3V4V	C_ARG_384	NH2	C_GLU_386	OE1	2.966
3V4V	C_ARG_429	NH2	C_ASP_408	OD2	2.836
3V4V	C_ARG_499	NH1	C_ASP_489	OD2	3.733
3V4V	C_ARG_499	NH1	C_ASP_537	OD2	3.002
3V4V	C_ARG_499	NH2	C_ASP_537	OD2	3.340
3V4V	C_ARG_532	NH1	C_ASP_534	OD2	3.655
3V4V	C_LYS_533	NZ	C_GLU_455	OE1	3.182
3V4V	C_LYS_533	NZ	C_GLU_455	OE2	3.301
3V4V	C_ARG_536	NH2	C_ASP_534	OD1	3.809
3V4V	C_LYS_573	NZ	C_ASP_577	OD1	3.849
3V4V	C_LYS_574	NZ	C_ASP_346	OD2	3.367
3V4V	C_LYS_574	NZ	C_ASP_348	OD2	3.730
3V4V	D_ARG_108	NH2	D_GLU_450	OE1	2.539
3V4V	D_ARG_110	NH1	D_GLU_85	OE1	3.659
3V4V	D_ARG_110	NH2	D_GLU_450	OE2	3.785
3V4V	D_ARG_124	NH2	D_ASP_89	OD1	3.506
3V4V	D_LYS_146	NZ	D_GLU_202	OE2	3.999
3V4V	D_LYS_180	NZ	D_ASP_244	OD1	3.344
3V4V	D_LYS_180	NZ	D_ASP_244	OD2	2.642
3V4V	D_ARG_194	NH1	M_ASP_102	OD1	2.657
3V4V	D_ARG_194	NH1	M_ASP_102	OD2	2.923

3V4V	D_ARG_200	NH2	M_ASP_102	OD1	3.070
3V4V	D_ARG_259	NH2	D_ASP_134	OD1	2.871
3V4V	D_HIS_274	ND1	D_ASP_278	OD2	3.033
3V4V	D_HIS_274	NE2	D_ASP_179	OD2	3.229
3V4V	D_HIS_274	NE2	D_ASP_237	OD2	3.108
3V4V	D_HIS_293	NE2	D_ASP_289	OD1	2.628
3V4V	D_HIS_293	NE2	D_ASP_289	OD2	2.920
3V4V	D_ARG_302	NH2	D_GLU_305	OE1	3.475
3V4V	D_ARG_399	NH1	D_GLU_390	OE1	2.981
3V4V	D_ARG_399	NH1	D_GLU_390	OE2	2.805
3V4V	D_ARG_399	NH2	D_GLU_390	OE2	3.180
3V4V	D_LYS_402	NZ	D_GLU_404	OE2	3.526
3V4V	D_HIS_434	NE2	D_GLU_432	OE1	3.565
3V4V	D_ARG_439	NH2	D_GLU_377	OE1	3.517
3V4V	D_HIS_452	ND1	D_GLU_450	OE2	3.844
3V4V	M_HIS_35	ND1	M_GLU_50	OE1	3.871
3V4V	M_HIS_35	NE2	M_GLU_50	OE1	3.860
3V4V	M_ARG_40	NH2	M_GLU_89	OE1	3.456
3V4V	M_LYS_63	NZ	M_GLU_46	OE1	3.661
3V4V	M_LYS_67	NZ	M_ASP_90	OD1	2.998
3V4V	M_LYS_67	NZ	M_ASP_90	OD2	2.683
3V4V	M_ARG_98	NH2	M_ASP_109	OD1	3.565
3V4V	M_ARG_98	NH2	M_ASP_109	OD2	2.672
3V4V	M_LYS_151	NZ	M_GLU_179	OE2	3.863
3V4V	M_HIS_172	ND1	N_ASP_172	OD1	3.594
3V4V	M_LYS_216	NZ	N_GLU_128	OE2	3.217
3V4V	N_ARG_66	NH2	N_GLU_86	OE1	3.488
3V4V	N_ARG_66	NH2	N_ASP_87	OD1	3.328
3V4V	N_ARG_66	NH2	N_ASP_87	OD2	3.226
3V4V	N_LYS_152	NZ	N_GLU_200	OE2	3.759
3V4V	N_HIS_194	ND1	N_ASP_156	OD1	3.862
3V4V	N_HIS_194	ND1	N_ASP_156	OD2	2.969

Table 486: 3V4V-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3V52	H_ARG_38	NH1	H_ASP_90	OD1	3.011
3V52	H_ARG_38	NH2	H_GLU_46	OE1	2.934
3V52	H_ARG_67	NH1	H_ASP_90	OD2	3.055
3V52	H_ARG_67	NH2	H_ASP_90	OD1	3.178
3V52	H_ARG_67	NH2	H_ASP_90	OD2	3.296
3V52	H_ARG_98	NH2	H_ASP_105	OD1	3.591
3V52	H_ARG_98	NH2	H_ASP_105	OD2	2.829
3V52	H_LYS_212	NZ	L_GLU_127	OE2	2.929
3V52	H_LYS_213	NZ	H_GLU_215	OE2	3.959
3V52	L_ARG_66	NH1	L_ASP_87	OD1	3.858
3V52	L_ARG_66	NH1	L_ASP_87	OD2	2.692
3V52	L_ARG_66	NH2	L_GLU_84	OE1	3.797
3V52	L_ARG_66	NH2	L_GLU_84	OE2	3.912
3V52	L_ARG_66	NH2	L_ASP_87	OD1	3.033
3V52	L_ARG_66	NH2	L_ASP_87	OD2	3.323
3V52	L_LYS_153	NZ	L_GLU_199	OE2	2.980
3V52	L_ARG_159	NH1	L_GLU_189	OE1	3.150
3V52	L_ARG_159	NH2	L_GLU_189	OE1	2.854
3V52	L_ARG_192	NH2	L_ASP_188	OD1	3.092
3V52	L_ARG_192	NH2	L_ASP_188	OD2	3.931
3V52	L_HIS_193	ND1	L_ASP_155	OD2	2.916
3V52	L_LYS_203	NZ	L_ASP_114	OD2	2.574

Table 487: 3V52-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3V6F	A_ARG_38	NH1	A_ASP_86	OD1	2.911
3V6F	A_ARG_38	NH2	A_GLU_46	OE1	3.291
3V6F	A_ARG_38	NH2	A_GLU_46	OE2	3.661
3V6F	A_ARG_38	NH2	A_ASP_86	OD1	3.667
3V6F	A_LYS_64	NZ	A_ASP_61	OD1	2.842
3V6F	A_ARG_66	NH1	A_ASP_86	OD1	3.978
3V6F	A_ARG_66	NH1	A_ASP_86	OD2	2.845
3V6F	A_ARG_66	NH2	A_ASP_86	OD1	3.048
3V6F	A_ARG_66	NH2	A_ASP_86	OD2	3.388
3V6F	A_LYS_75	NZ	A_ASP_72	OD2	3.618
3V6F	A_ARG_94	NH1	A_ASP_106	OD1	3.312
3V6F	A_ARG_94	NH1	A_ASP_106	OD2	3.358
3V6F	A_LYS_213	NZ	B_GLU_130	OE1	3.799
3V6F	B_ARG_60	NH1	B_ASP_66	OD1	3.189
3V6F	B_ARG_60	NH2	B_ASP_66	OD1	3.662
3V6F	B_ARG_67	NH2	B_ASP_88	OD1	2.925
3V6F	B_ARG_67	NH2	B_ASP_88	OD2	3.716
3V6F	B_ARG_162	NH1	B_GLU_192	OE2	3.473
3V6F	B_ARG_195	NH1	B_GLU_192	OE1	3.435
3V6F	B_ARG_195	NH1	B_GLU_192	OE2	2.954
3V6F	B_HIS_196	ND1	B_GLU_192	OE2	3.778
3V6F	C_ARG_38	NH1	C_ASP_86	OD1	2.982
3V6F	C_ARG_38	NH2	C_GLU_46	OE1	3.377
3V6F	C_ARG_38	NH2	C_GLU_46	OE2	3.714
3V6F	C_ARG_38	NH2	C_ASP_86	OD1	3.729
3V6F	C_LYS_64	NZ	C_ASP_61	OD1	2.824
3V6F	C_ARG_66	NH1	C_ASP_86	OD1	3.704
3V6F	C_ARG_66	NH1	C_ASP_86	OD2	2.748
3V6F	C_ARG_66	NH2	C_ASP_86	OD1	3.318
3V6F	C_ARG_66	NH2	C_ASP_86	OD2	3.791
3V6F	C_LYS_75	NZ	C_ASP_72	OD2	3.653
3V6F	C_ARG_94	NH1	C_ASP_106	OD1	3.027
3V6F	C_ARG_94	NH1	C_ASP_106	OD2	2.907
3V6F	C_LYS_213	NZ	D_GLU_130	OE1	3.956
3V6F	D_ARG_60	NH1	D_ASP_66	OD1	3.192
3V6F	D_ARG_60	NH2	D_ASP_66	OD1	3.669
3V6F	D_ARG_67	NH2	D_ASP_88	OD1	2.880
3V6F	D_ARG_67	NH2	D_ASP_88	OD2	3.702
3V6F	D_ARG_162	NH1	D_GLU_192	OE2	3.490
3V6F	D_ARG_195	NH1	D_GLU_192	OE1	3.464
3V6F	D_ARG_195	NH1	D_GLU_192	OE2	2.977
3V6F	D_HIS_196	ND1	D_GLU_192	OE2	3.829
3V6F	E_ARG_38	NH1	E_ASP_86	OD1	2.938
3V6F	E_ARG_38	NH2	E_GLU_46	OE1	3.288
3V6F	E_ARG_38	NH2	E_GLU_46	OE2	3.689
3V6F	E_ARG_38	NH2	E_ASP_86	OD1	3.691
3V6F	E_LYS_64	NZ	E_ASP_61	OD1	3.118
3V6F	E_ARG_66	NH1	E_ASP_86	OD1	3.831
3V6F	E_ARG_66	NH1	E_ASP_86	OD2	2.617
3V6F	E_ARG_66	NH2	E_ASP_86	OD1	2.929
3V6F	E_ARG_66	NH2	E_ASP_86	OD2	3.284
3V6F	E_LYS_75	NZ	E_ASP_72	OD2	3.617
3V6F	E_ARG_94	NH1	E_ASP_106	OD1	3.312
3V6F	E_ARG_94	NH1	E_ASP_106	OD2	3.177
3V6F	E_LYS_213	NZ	F_GLU_130	OE1	3.763
3V6F	F_ARG_60	NH1	F_ASP_66	OD1	3.236
3V6F	F_ARG_60	NH2	F_ASP_66	OD1	3.718

3V6F	F_ARG_67	NH2	F_ASP_88	OD1	2.889
3V6F	F_ARG_67	NH2	F_ASP_88	OD2	3.693
3V6F	F_LYS_114	NZ	F_GLU_17	OE1	3.958
3V6F	F_ARG_162	NH1	F_GLU_192	OE2	3.447
3V6F	F_ARG_195	NH1	F_GLU_192	OE1	3.438
3V6F	F_ARG_195	NH1	F_GLU_192	OE2	2.943
3V6F	F_HIS_196	ND1	F_GLU_192	OE2	3.828
3V6F	H_ARG_38	NH1	H_ASP_86	OD1	2.929
3V6F	H_ARG_38	NH2	H_GLU_46	OE1	3.278
3V6F	H_ARG_38	NH2	H_GLU_46	OE2	3.715
3V6F	H_ARG_38	NH2	H_ASP_86	OD1	3.746
3V6F	H_LYS_64	NZ	H_ASP_61	OD1	2.949
3V6F	H_ARG_66	NH1	H_ASP_86	OD1	3.602
3V6F	H_ARG_66	NH1	H_ASP_86	OD2	2.554
3V6F	H_ARG_66	NH2	H_ASP_86	OD1	2.925
3V6F	H_ARG_66	NH2	H_ASP_86	OD2	3.444
3V6F	H_LYS_75	NZ	H_ASP_72	OD2	3.633
3V6F	H_ARG_94	NH1	H_ASP_106	OD1	3.513
3V6F	H_ARG_94	NH1	H_ASP_106	OD2	2.779
3V6F	H_HIS_169	NE2	L_ASP_174	OD1	3.656
3V6F	L_ARG_60	NH1	L_ASP_66	OD1	3.201
3V6F	L_ARG_60	NH2	L_ASP_66	OD1	3.668
3V6F	L_ARG_67	NH2	L_ASP_88	OD1	2.904
3V6F	L_ARG_67	NH2	L_ASP_88	OD2	3.773
3V6F	L_ARG_162	NH1	L_GLU_192	OE2	3.508
3V6F	L_ARG_195	NH1	L_GLU_192	OE1	3.445
3V6F	L_ARG_195	NH1	L_GLU_192	OE2	2.967
3V6F	L_HIS_196	ND1	L_GLU_192	OE2	3.834

Table 488: 3V6F-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3WII	L_ARG_24	NH1	L_ASP_70	OD1	3.918
3WII	L_ARG_24	NH1	L_ASP_70	OD2	2.824
3WII	L_ARG_61	NH1	L_GLU_81	OE1	3.206
3WII	L_ARG_61	NH1	L_ASP_82	OD1	2.733
3WII	L_ARG_61	NH1	L_ASP_82	OD2	3.500
3WII	L_LYS_103	NZ	L_GLU_105	OE2	3.849
3WII	L_LYS_149	NZ	L_GLU_195	OE1	3.529
3WII	L_LYS_149	NZ	L_GLU_195	OE2	2.994
3WII	L_ARG_155	NH1	L_GLU_185	OE2	3.108
3WII	L_ARG_155	NH2	L_GLU_185	OE1	3.573
3WII	L_ARG_155	NH2	L_GLU_185	OE2	3.738
3WII	L_LYS_183	NZ	L_GLU_187	OE1	2.854
3WII	L_LYS_183	NZ	L_GLU_187	OE2	2.954
3WII	L_HIS_189	ND1	L_ASP_151	OD2	2.633
3WII	L_LYS_199	NZ	L_GLU_110	OE2	3.646
3WII	H_LYS_67	NZ	H_ASP_90	OD1	3.761
3WII	H_LYS_67	NZ	H_ASP_90	OD2	2.892
3WII	H_ARG_98	NH2	H_ASP_107	OD1	3.653
3WII	H_ARG_98	NH2	H_ASP_107	OD2	2.796
3WII	H_LYS_214	NZ	L_GLU_123	OE2	3.755
3WII	H_LYS_215	NZ	H_GLU_217	OE2	3.819
3WII	M_ARG_61	NH1	M_GLU_81	OE1	3.086
3WII	M_ARG_61	NH1	M_ASP_82	OD1	2.841
3WII	M_ARG_61	NH1	M_ASP_82	OD2	3.629
3WII	M_LYS_103	NZ	M_GLU_105	OE2	3.685
3WII	M_LYS_147	NZ	M_GLU_154	OE1	3.932
3WII	M_LYS_149	NZ	M_GLU_195	OE1	3.414
3WII	M_LYS_149	NZ	M_GLU_195	OE2	2.992
3WII	M_ARG_155	NH1	M_GLU_185	OE2	3.084
3WII	M_ARG_155	NH2	M_GLU_185	OE1	3.729
3WII	M_ARG_155	NH2	M_GLU_185	OE2	3.794
3WII	M_HIS_189	ND1	M_ASP_151	OD2	2.674
3WII	I_LYS_67	NZ	I_ASP_90	OD1	3.687
3WII	I_LYS_67	NZ	I_ASP_90	OD2	2.807
3WII	I_ARG_98	NH2	I_ASP_107	OD1	3.645
3WII	I_ARG_98	NH2	I_ASP_107	OD2	2.793
3WII	I_LYS_214	NZ	M_GLU_123	OE1	2.678
3WII	I_LYS_214	NZ	M_GLU_123	OE2	3.619
3WII	I_LYS_215	NZ	I_GLU_217	OE2	3.670

Table 489: 3WII-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3WN5	A_ARG_255	NH1	A_ASP_249	OD1	2.832
3WN5	A_HIS_285	NE2	A_GLU_283	OE2	3.642
3WN5	A_LYS_317	NZ	A_ASP_312	OD1	2.941
3WN5	A_LYS_320	NZ	A_GLU_333	OE1	3.207
3WN5	A_LYS_338	NZ	A_GLU_430	OE1	3.924
3WN5	A_LYS_338	NZ	A_GLU_430	OE2	3.222
3WN5	A_LYS_370	NZ	B_GLU_357	OE2	3.815
3WN5	A_LYS_409	NZ	B_ASP_399	OD2	3.327
3WN5	A_ARG_416	NH1	A_GLU_388	OE1	3.624
3WN5	A_ARG_416	NH1	A_GLU_388	OE2	3.234
3WN5	A_ARG_416	NH2	A_GLU_388	OE1	2.983
3WN5	A_ARG_416	NH2	A_GLU_388	OE2	3.949
3WN5	B_LYS_248	NZ	B_GLU_380	OE1	2.957
3WN5	B_LYS_248	NZ	B_GLU_380	OE2	3.881
3WN5	B_ARG_255	NH1	B_ASP_249	OD1	2.667
3WN5	B_HIS_285	NE2	B_GLU_283	OE2	2.816
3WN5	B_LYS_317	NZ	B_ASP_312	OD1	3.123
3WN5	B_LYS_320	NZ	B_GLU_333	OE1	3.014
3WN5	B_LYS_338	NZ	B_GLU_430	OE1	3.374
3WN5	B_LYS_370	NZ	A_GLU_357	OE1	3.801
3WN5	B_LYS_409	NZ	A_ASP_399	OD1	3.830
3WN5	B_LYS_409	NZ	A_ASP_399	OD2	3.511
3WN5	B_ARG_416	NH1	B_GLU_388	OE1	2.996
3WN5	B_ARG_416	NH1	B_GLU_388	OE2	3.505
3WN5	B_ARG_416	NH2	B_GLU_388	OE1	3.528
3WN5	B_ARG_416	NH2	B_GLU_388	OE2	2.698
3WN5	C_LYS_4	NZ	C_ASP_77	OD1	3.098
3WN5	C_LYS_4	NZ	C_ASP_77	OD2	2.841
3WN5	C_ARG_67	NH1	C_GLU_65	OE1	3.514
3WN5	C_HIS_84	ND1	C_GLU_163	OE1	3.890
3WN5	C_HIS_84	NE2	C_GLU_82	OE1	2.954
3WN5	C_HIS_104	NE2	C_ASP_135	OD2	2.827
3WN5	C_HIS_108	ND1	C_ASP_20	OD2	3.561
3WN5	C_HIS_108	NE2	C_ASP_20	OD1	3.787
3WN5	C_LYS_117	NZ	B_ASP_265	OD2	2.853
3WN5	C_ARG_127	NH1	C_ASP_145	OD1	3.210
3WN5	C_ARG_127	NH2	C_ASP_145	OD1	3.171
3WN5	C_HIS_131	NE2	B_ASP_270	OD1	3.342
3WN5	C_HIS_131	NE2	B_ASP_270	OD2	2.619
3WN5	D_LYS_248	NZ	D_GLU_380	OE1	2.793
3WN5	D_LYS_248	NZ	D_GLU_380	OE2	3.908
3WN5	D_HIS_268	NE2	D_GLU_294	OE2	3.025
3WN5	D_HIS_285	NE2	D_GLU_283	OE2	3.554
3WN5	D_LYS_317	NZ	D_ASP_312	OD1	2.899
3WN5	D_LYS_320	NZ	D_GLU_333	OE1	3.733
3WN5	D_LYS_338	NZ	D_GLU_430	OE1	3.660
3WN5	D_LYS_338	NZ	D_GLU_430	OE2	3.172
3WN5	D_ARG_344	NH1	D_ASP_401	OD2	3.301
3WN5	D_LYS_370	NZ	E_GLU_357	OE2	3.279
3WN5	D_LYS_409	NZ	E_ASP_399	OD2	3.246
3WN5	D_ARG_416	NH2	D_GLU_388	OE1	2.919
3WN5	D_ARG_416	NH2	D_GLU_388	OE2	3.802
3WN5	E_LYS_248	NZ	E_GLU_380	OE1	2.911
3WN5	E_ARG_255	NH1	E_ASP_249	OD1	3.513
3WN5	E_HIS_285	NE2	E_GLU_283	OE2	3.997
3WN5	E_LYS_320	NZ	E_GLU_333	OE1	3.266
3WN5	E_LYS_338	NZ	E_GLU_430	OE1	3.039

3WN5	E_LYS_338	NZ	E_GLU_430	OE2	3.495
3WN5	E_ARG_344	NH1	E_ASP_401	OD2	3.679
3WN5	E_LYS_370	NZ	D_GLU_357	OE1	3.843
3WN5	E_LYS_409	NZ	D_ASP_399	OD2	2.789
3WN5	E_ARG_416	NH1	E_GLU_388	OE1	2.774
3WN5	E_ARG_416	NH2	E_GLU_388	OE1	3.165
3WN5	E_ARG_416	NH2	E_GLU_388	OE2	3.510
3WN5	F_HIS_84	ND1	F_GLU_163	OE1	3.205
3WN5	F_HIS_84	NE2	F_GLU_82	OE1	3.100
3WN5	F_HIS_104	NE2	F_ASP_135	OD2	2.820
3WN5	F_HIS_108	ND1	F_ASP_20	OD2	3.674
3WN5	F_HIS_108	NE2	F_ASP_20	OD1	3.365
3WN5	F_HIS_108	NE2	F_ASP_20	OD2	3.881
3WN5	F_LYS_117	NZ	E_ASP_265	OD2	3.157
3WN5	F_ARG_127	NH1	F_ASP_145	OD1	3.151
3WN5	F_ARG_127	NH2	F_ASP_145	OD1	3.144
3WN5	F_HIS_131	NE2	E_ASP_270	OD2	2.923
3WN5	F_LYS_140	NZ	F_GLU_100	OE1	3.841

Table 490: 3WN5-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3X0E	A_LYS_124	NZ	A_ASP_195	OD1	3.186
3X0E	A_LYS_124	NZ	A_ASP_195	OD2	2.999
3X0E	A_LYS_187	NZ	A_ASP_155	OD1	2.836
3X0E	A_LYS_187	NZ	A_ASP_155	OD2	3.800
3X0E	A_HIS_191	NE2	A_ASP_128	OD1	2.835
3X0E	A_HIS_191	NE2	A_ASP_128	OD2	3.342
3X0E	B_LYS_124	NZ	B_ASP_195	OD1	2.748
3X0E	B_LYS_124	NZ	B_ASP_195	OD2	3.043
3X0E	B_LYS_144	NZ	B_ASP_138	OD2	3.823
3X0E	B_HIS_191	NE2	B_ASP_128	OD1	2.682
3X0E	B_HIS_191	NE2	B_ASP_128	OD2	3.448

Table 491: 3X0E-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3X0F	A_LYS_124	NZ	A_ASP_195	OD1	2.914
3X0F	A_LYS_124	NZ	A_ASP_195	OD2	3.712
3X0F	A_LYS_148	NZ	A_GLU_152	OE2	2.835
3X0F	A_ARG_171	NH2	A_ASP_138	OD1	3.978
3X0F	A_ARG_171	NH2	A_ASP_138	OD2	3.900
3X0F	A_HIS_191	NE2	A_ASP_128	OD1	2.650
3X0F	A_HIS_191	NE2	A_ASP_128	OD2	3.274
3X0F	B_LYS_124	NZ	B_ASP_195	OD2	3.594
3X0F	B_ARG_171	NH2	B_ASP_138	OD1	2.531
3X0F	B_HIS_191	NE2	B_ASP_128	OD1	2.685
3X0F	B_HIS_191	NE2	B_ASP_128	OD2	3.306

Table 492: 3X0F-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4A6Y	A_ARG_23	NH1	A_ASP_71	OD1	3.205
4A6Y	A_ARG_23	NH1	A_ASP_71	OD2	3.345
4A6Y	A_ARG_23	NH2	A_ASP_71	OD2	3.364
4A6Y	A_ARG_63	NH2	A_GLU_83	OE2	2.831
4A6Y	A_ARG_63	NH2	A_ASP_84	OD1	3.057
4A6Y	A_ARG_63	NH2	A_ASP_84	OD2	3.695
4A6Y	A_LYS_72	NZ	A_ASP_71	OD1	3.673
4A6Y	A_ARG_186	NH2	H_ASP_180	OD2	3.656
4A6Y	A_ARG_190	NH1	H_GLU_89	OE2	3.969
4A6Y	A_HIS_191	ND1	A_ASP_154	OD2	3.123
4A6Y	A_ARG_211	NH2	A_GLU_189	OE1	3.962
4A6Y	A_ARG_211	NH2	A_GLU_189	OE2	2.597
4A6Y	B_ARG_40	NH1	B_GLU_89	OE1	2.984
4A6Y	B_ARG_40	NH1	B_GLU_89	OE2	3.972
4A6Y	B_ARG_40	NH2	B_GLU_89	OE1	3.630
4A6Y	B_LYS_65	NZ	B_GLU_62	OE1	3.475
4A6Y	B_LYS_67	NZ	B_ASP_90	OD1	3.299
4A6Y	B_LYS_67	NZ	B_ASP_90	OD2	3.248
4A6Y	B_ARG_98	NH2	B_ASP_108	OD1	3.444
4A6Y	B_ARG_98	NH2	B_ASP_108	OD2	3.726
4A6Y	B_LYS_150	NZ	A_GLU_127	OE2	3.258
4A6Y	H_LYS_38	NZ	H_ASP_90	OD1	3.850
4A6Y	H_ARG_40	NH2	H_GLU_89	OE1	2.546
4A6Y	H_ARG_40	NH2	H_GLU_89	OE2	3.778
4A6Y	H_LYS_67	NZ	H_ASP_90	OD1	3.781
4A6Y	H_LYS_67	NZ	H_ASP_90	OD2	3.430
4A6Y	H_ARG_98	NH2	H_ASP_108	OD1	3.889
4A6Y	H_ARG_98	NH2	H_ASP_108	OD2	2.725
4A6Y	H_LYS_150	NZ	L_GLU_127	OE2	3.131
4A6Y	H_HIS_171	NE2	L_ASP_141	OD1	3.968
4A6Y	L_ARG_63	NH2	L_ASP_84	OD1	3.284
4A6Y	L_LYS_113	NZ	L_GLU_201	OE2	3.880
4A6Y	L_ARG_190	NH2	B_GLU_89	OE2	3.440
4A6Y	L_HIS_191	ND1	L_ASP_154	OD2	2.878

Table 493: 4A6Y-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4AG4	A_ARG_40	NH1	A_ASP_68	OD2	3.311
4AG4	A_ARG_40	NH2	A_ASP_68	OD1	3.723
4AG4	A_ARG_40	NH2	A_ASP_68	OD2	3.146
4AG4	A_ARG_60	NH1	A_ASP_55	OD1	3.893
4AG4	A_ARG_60	NH2	A_ASP_55	OD1	2.714
4AG4	A_ARG_60	NH2	A_ASP_55	OD2	2.648
4AG4	A_ARG_63	NH2	A_ASP_44	OD1	3.060
4AG4	A_ARG_105	NH2	A_GLU_113	OE1	2.869
4AG4	A_ARG_105	NH2	A_GLU_113	OE2	2.817
4AG4	A_ARG_119	NH1	A_GLU_83	OE1	3.220
4AG4	A_ARG_119	NH1	A_GLU_83	OE2	3.262
4AG4	A_ARG_119	NH2	A_GLU_83	OE1	3.601
4AG4	A_ARG_124	NH1	A_ASP_216	OD2	3.269
4AG4	A_ARG_124	NH2	A_ASP_216	OD1	3.026
4AG4	A_ARG_124	NH2	A_ASP_216	OD2	2.840
4AG4	A_ARG_162	NH1	A_ASP_90	OD1	2.607
4AG4	A_ARG_162	NH1	A_ASP_90	OD2	3.377
4AG4	A_ARG_162	NH2	A_ASP_90	OD1	3.110
4AG4	A_ARG_162	NH2	A_ASP_90	OD2	2.698
4AG4	A_ARG_242	NH2	A_ASP_240	OD1	3.701
4AG4	A_ARG_242	NH2	A_ASP_240	OD2	3.113
4AG4	A_ARG_278	NH2	A_ASP_275	OD1	3.438
4AG4	A_ARG_278	NH2	A_ASP_275	OD2	3.642
4AG4	A_ARG_304	NH2	A_GLU_302	OE1	3.291
4AG4	A_ARG_307	NH2	A_GLU_314	OE2	3.264
4AG4	A_ARG_330	NH2	A_ASP_328	OD2	3.952
4AG4	A_ARG_332	NH1	A_ASP_328	OD2	3.874
4AG4	A_ARG_349	NH1	A_GLU_269	OE2	2.534
4AG4	H_LYS_62	NZ	H_GLU_46	OE1	3.542
4AG4	H_LYS_62	NZ	H_GLU_46	OE2	3.611
4AG4	H_ARG_94	NH2	H_ASP_101	OD1	3.424
4AG4	H_ARG_94	NH2	H_ASP_101	OD2	2.703
4AG4	H_LYS_208	NZ	L_GLU_123	OE2	2.708
4AG4	L_ARG_61	NH1	L_GLU_81	OE2	3.821
4AG4	L_ARG_61	NH2	L_GLU_81	OE2	3.157
4AG4	L_ARG_61	NH2	L_ASP_82	OD1	2.518
4AG4	L_ARG_61	NH2	L_ASP_82	OD2	3.022
4AG4	L_LYS_103	NZ	L_GLU_105	OE2	3.708
4AG4	L_LYS_103	NZ	L_ASP_165	OD1	3.872
4AG4	L_LYS_103	NZ	L_ASP_165	OD2	3.264
4AG4	L_LYS_147	NZ	L_GLU_154	OE1	3.276
4AG4	L_ARG_155	NH2	L_GLU_185	OE1	3.301
4AG4	L_HIS_189	ND1	L_ASP_151	OD2	2.672
4AG4	L_LYS_199	NZ	L_ASP_110	OD2	3.556

Table 494: 4AG4-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4B50	A_ARG_38	NH1	A_ASP_86	OD1	2.836
4B50	A_ARG_38	NH2	A_GLU_46	OE1	3.561
4B50	A_ARG_38	NH2	A_ASP_86	OD1	3.779
4B50	A_ARG_66	NH1	A_ASP_86	OD1	3.976
4B50	A_ARG_66	NH1	A_ASP_86	OD2	2.773
4B50	A_ARG_66	NH2	A_ASP_86	OD1	3.265
4B50	A_ARG_66	NH2	A_ASP_86	OD2	3.358
4B50	A_ARG_93	NH1	A_GLU_95	OE2	3.608
4B50	A_ARG_93	NH2	A_GLU_95	OE2	3.523
4B50	A_ARG_93	NH2	A_ASP_101	OD1	3.368
4B50	A_ARG_93	NH2	A_ASP_101	OD2	2.912

Table 495: 4B50-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4BH7	A_ARG_24	NH1	A_ASP_70	OD1	3.258
4BH7	A_ARG_24	NH1	A_ASP_70	OD2	3.469
4BH7	A_ARG_24	NH2	A_ASP_70	OD2	3.985
4BH7	A_ARG_61	NH1	A_GLU_79	OE1	2.456
4BH7	A_ARG_61	NH1	A_GLU_79	OE2	3.328
4BH7	A_ARG_61	NH2	A_GLU_79	OE1	3.232
4BH7	A_ARG_61	NH2	A_GLU_81	OE1	3.871
4BH7	A_ARG_61	NH2	A_ASP_82	OD1	3.092
4BH7	A_ARG_61	NH2	A_ASP_82	OD2	3.325
4BH7	A_LYS_103	NZ	A_ASP_165	OD1	3.734
4BH7	A_LYS_147	NZ	A_GLU_154	OE2	3.502
4BH7	A_LYS_149	NZ	A_GLU_195	OE1	3.693
4BH7	A_LYS_149	NZ	A_GLU_195	OE2	2.842
4BH7	A_ARG_155	NH1	A_GLU_185	OE1	3.587
4BH7	A_ARG_155	NH1	A_GLU_185	OE2	2.731
4BH7	A_ARG_155	NH2	A_GLU_185	OE1	3.886
4BH7	A_LYS_183	NZ	A_GLU_187	OE2	3.868
4BH7	A_LYS_199	NZ	A_ASP_110	OD1	3.983
4BH7	A_LYS_199	NZ	A_ASP_110	OD2	3.698
4BH7	B_LYS_38	NZ	B_ASP_90	OD1	3.793
4BH7	B_ARG_40	NH2	B_GLU_89	OE1	3.542
4BH7	B_ARG_40	NH2	B_GLU_89	OE2	2.796
4BH7	B_LYS_63	NZ	B_GLU_46	OE1	3.614
4BH7	B_LYS_63	NZ	B_GLU_46	OE2	2.841
4BH7	B_ARG_98	NH2	B_ASP_109	OD1	3.844
4BH7	B_ARG_98	NH2	B_ASP_109	OD2	2.412

Table 496: 4BH7-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4BH8	A_ARG_24	NH2	A_ASP_70	OD2	3.331
4BH8	A_ARG_61	NH1	A_GLU_79	OE1	3.277
4BH8	A_ARG_61	NH2	A_GLU_79	OE1	3.420
4BH8	A_ARG_61	NH2	A_GLU_81	OE2	3.313
4BH8	A_ARG_61	NH2	A_ASP_82	OD1	2.737
4BH8	A_ARG_61	NH2	A_ASP_82	OD2	3.137
4BH8	A_LYS_103	NZ	A_ASP_165	OD1	3.847
4BH8	A_LYS_142	NZ	A_ASP_143	OD1	3.850
4BH8	A_LYS_147	NZ	A_GLU_154	OE1	3.754
4BH8	A_LYS_149	NZ	A_GLU_195	OE1	3.565
4BH8	A_LYS_149	NZ	A_GLU_195	OE2	2.762
4BH8	A_ARG_155	NH1	A_GLU_185	OE2	2.660
4BH8	A_ARG_155	NH2	A_GLU_185	OE1	3.812
4BH8	A_ARG_155	NH2	A_GLU_185	OE2	3.243
4BH8	A_LYS_183	NZ	A_GLU_187	OE1	2.950
4BH8	A_LYS_183	NZ	A_GLU_187	OE2	3.305
4BH8	A_LYS_199	NZ	A_ASP_110	OD1	3.983
4BH8	A_LYS_199	NZ	A_ASP_110	OD2	3.388
4BH8	B_ARG_40	NH1	B_GLU_89	OE1	3.007
4BH8	B_ARG_40	NH2	B_GLU_46	OE1	3.740
4BH8	B_LYS_63	NZ	B_GLU_46	OE1	3.869
4BH8	B_LYS_63	NZ	B_GLU_46	OE2	2.693
4BH8	B_ARG_98	NH2	B_ASP_109	OD1	3.876
4BH8	B_ARG_98	NH2	B_ASP_109	OD2	2.532

Table 497: 4BH8-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4C83	A_HIS_35	NE2	A_ASP_95	OD1	2.464
4C83	A_ARG_38	NH1	A_ASP_86	OD1	3.261
4C83	A_ARG_38	NH2	A_GLU_46	OE1	3.691
4C83	A_ARG_38	NH2	A_GLU_46	OE2	3.824
4C83	A_ARG_66	NH1	A_ASP_86	OD1	3.704
4C83	A_ARG_66	NH1	A_ASP_86	OD2	2.349
4C83	A_ARG_66	NH2	A_ASP_86	OD1	3.078
4C83	A_ARG_66	NH2	A_ASP_86	OD2	3.279
4C83	A_ARG_83	NH2	A_GLU_85	OE2	3.570
4C83	A_ARG_94	NH1	A_GLU_96	OE1	2.827
4C83	A_ARG_94	NH1	A_GLU_96	OE2	2.141
4C83	B_LYS_53	NZ	B_ASP_50	OD1	3.953
4C83	B_LYS_53	NZ	B_ASP_50	OD2	3.875
4C83	B_ARG_61	NH1	B_GLU_79	OE1	3.356
4C83	B_ARG_61	NH1	B_ASP_82	OD1	3.496
4C83	B_ARG_61	NH1	B_ASP_82	OD2	2.349
4C83	B_ARG_61	NH2	B_GLU_79	OE1	3.840
4C83	B_ARG_61	NH2	B_ASP_82	OD1	2.878
4C83	B_ARG_61	NH2	B_ASP_82	OD2	3.259
4C83	B_LYS_103	NZ	B_GLU_105	OE1	3.618
4C83	B_LYS_103	NZ	B_GLU_105	OE2	3.871
4C83	B_LYS_147	NZ	B_GLU_154	OE2	3.593
4C83	B_LYS_149	NZ	B_GLU_195	OE1	2.933
4C83	B_LYS_149	NZ	B_GLU_195	OE2	2.669
4C83	B_ARG_155	NH2	B_GLU_185	OE2	3.551
4C83	B_ARG_188	NH1	B_GLU_185	OE1	3.402
4C83	C_HIS_35	NE2	C_ASP_95	OD1	2.757
4C83	C_ARG_38	NH1	C_ASP_86	OD1	3.096
4C83	C_ARG_38	NH2	C_GLU_46	OE1	3.335
4C83	C_ARG_38	NH2	C_ASP_86	OD1	3.866
4C83	C_ARG_66	NH1	C_ASP_86	OD2	3.260
4C83	C_ARG_66	NH2	C_ASP_86	OD1	2.653
4C83	C_ARG_66	NH2	C_ASP_86	OD2	1.985
4C83	C_ARG_94	NH1	C_GLU_96	OE1	3.930
4C83	C_ARG_94	NH1	C_GLU_96	OE2	1.996
4C83	C_ARG_94	NH2	C_GLU_96	OE2	3.476
4C83	C_LYS_208	NZ	D_GLU_123	OE1	2.304
4C83	C_LYS_208	NZ	D_GLU_123	OE2	2.598
4C83	D_LYS_53	NZ	D_ASP_50	OD2	3.324
4C83	D_ARG_61	NH1	D_GLU_79	OE1	3.777
4C83	D_ARG_61	NH1	D_ASP_82	OD1	2.299
4C83	D_ARG_61	NH1	D_ASP_82	OD2	2.134
4C83	D_ARG_61	NH2	D_GLU_79	OE1	3.916
4C83	D_ARG_61	NH2	D_ASP_82	OD1	3.608
4C83	D_LYS_103	NZ	D_GLU_105	OE2	3.442
4C83	D_LYS_103	NZ	D_ASP_165	OD1	3.353
4C83	D_LYS_147	NZ	D_GLU_154	OE2	3.595
4C83	D_LYS_149	NZ	D_GLU_195	OE1	3.533
4C83	D_LYS_149	NZ	D_GLU_195	OE2	2.856
4C83	D_ARG_155	NH2	D_GLU_185	OE2	3.932
4C83	D_LYS_183	NZ	D_ASP_184	OD1	3.344
4C83	D_HIS_189	ND1	D_ASP_151	OD2	2.752
4C83	D_LYS_199	NZ	D_ASP_110	OD1	3.795

Table 498: 4C83-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4CJD	A_LYS_35	NZ	A_ASP_31	OD1	3.731
4CJD	A_LYS_35	NZ	A_ASP_31	OD2	2.727
4CJD	A_LYS_52	NZ	A_ASP_55	OD1	2.992
4CJD	A_ARG_68	NH1	A_ASP_74	OD1	3.693
4CJD	A_ARG_68	NH1	A_ASP_74	OD2	3.009
4CJD	A_ARG_68	NH2	A_ASP_74	OD1	2.966
4CJD	A_ARG_68	NH2	A_ASP_74	OD2	3.665
4CJD	A_LYS_76	NZ	A_GLU_72	OE2	3.775

Table 499: 4CJD-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4DAG	A_ARG_40	NH2	A_ASP_336	OD1	2.596
4DAG	A_ARG_40	NH2	A_ASP_336	OD2	3.693
4DAG	A_ARG_91	NH1	A_GLU_92	OE1	3.086
4DAG	A_ARG_248	NH1	A_ASP_224	OD2	2.986
4DAG	A_ARG_252	NH2	A_ASP_224	OD1	2.791
4DAG	A_ARG_304	NH2	A_ASP_306	OD2	3.086
4DAG	A_LYS_312	NZ	A_GLU_345	OE1	3.422
4DAG	A_HIS_332	NE2	A_ASP_280	OD1	3.787
4DAG	H_ARG_38	NH1	H_GLU_46	OE2	3.364
4DAG	H_ARG_38	NH2	H_ASP_89	OD1	3.055
4DAG	H_ARG_66	NH1	H_ASP_89	OD1	3.443
4DAG	H_ARG_66	NH1	H_ASP_89	OD2	3.823
4DAG	H_ARG_66	NH2	H_ASP_89	OD1	3.179
4DAG	H_ARG_66	NH2	H_ASP_89	OD2	2.772
4DAG	H_LYS_75	NZ	H_ASP_72	OD2	3.891
4DAG	H_ARG_97	NH2	H_ASP_110	OD2	2.600
4DAG	H_ARG_101	NH2	A_GLU_33	OE1	3.620
4DAG	H_ARG_101	NH2	A_GLU_33	OE2	2.107
4DAG	H_LYS_152	NZ	H_ASP_153	OD2	3.881
4DAG	L_LYS_46	NZ	A_ASP_414	OD1	3.558
4DAG	L_LYS_46	NZ	A_ASP_414	OD2	3.550
4DAG	L_LYS_50	NZ	L_ASP_111	OD1	3.845
4DAG	L_ARG_80	NH2	L_ASP_101	OD1	3.368
4DAG	L_ARG_80	NH2	L_ASP_101	OD2	3.445
4DAG	L_LYS_186	NZ	L_GLU_102	OE1	3.649
4DAG	L_LYS_186	NZ	L_GLU_102	OE2	2.377

Table 500: 4DAG-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4DGV	H_HIS_35	NE2	H_ASP_95	OD2	2.670
4DGV	H_ARG_38	NH1	H_ASP_86	OD1	2.801
4DGV	H_ARG_38	NH2	H_GLU_46	OE1	3.005
4DGV	H_ARG_38	NH2	H_GLU_46	OE2	3.829
4DGV	H_ARG_38	NH2	H_ASP_86	OD1	3.806
4DGV	H_ARG_64	NH1	H_ASP_61	OD1	2.727
4DGV	H_ARG_64	NH2	H_ASP_61	OD1	2.493
4DGV	H_ARG_66	NH1	H_ASP_86	OD1	3.757
4DGV	H_ARG_66	NH1	H_ASP_86	OD2	2.704
4DGV	H_ARG_66	NH2	H_ASP_86	OD1	3.075
4DGV	H_ARG_66	NH2	H_ASP_86	OD2	3.481
4DGV	H_ARG_94	NH2	H_ASP_101	OD1	3.600
4DGV	H_ARG_94	NH2	H_ASP_101	OD2	2.840
4DGV	H_LYS_143	NZ	H_ASP_144	OD1	3.303
4DGV	H_LYS_143	NZ	H_ASP_144	OD2	3.171
4DGV	H_LYS_209	NZ	L_GLU_123	OE1	2.915
4DGV	H_LYS_209	NZ	L_GLU_123	OE2	3.422
4DGV	H_LYS_210	NZ	H_GLU_212	OE2	3.411
4DGV	L_ARG_61	NH1	L_ASP_82	OD2	2.699
4DGV	L_ARG_61	NH2	L_GLU_79	OE1	3.439
4DGV	L_ARG_61	NH2	L_GLU_79	OE2	3.431
4DGV	L_ARG_61	NH2	L_ASP_82	OD1	3.032
4DGV	L_ARG_61	NH2	L_ASP_82	OD2	3.080
4DGV	L_LYS_149	NZ	L_GLU_195	OE1	3.591
4DGV	L_LYS_149	NZ	L_GLU_195	OE2	3.604
4DGV	L_HIS_189	ND1	L_ASP_151	OD2	3.493

Table 501: 4DGV-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4DGY	H_HIS_35	NE2	H_ASP_95	OD2	2.790
4DGY	H_ARG_38	NH1	H_ASP_86	OD1	2.922
4DGY	H_ARG_38	NH2	H_GLU_46	OE1	2.965
4DGY	H_ARG_38	NH2	H_GLU_46	OE2	3.707
4DGY	H_LYS_43	NZ	H_GLU_85	OE1	3.738
4DGY	H_ARG_64	NH1	H_ASP_61	OD1	2.545
4DGY	H_ARG_64	NH2	H_ASP_61	OD1	3.007
4DGY	H_ARG_66	NH1	H_ASP_86	OD1	3.675
4DGY	H_ARG_66	NH1	H_ASP_86	OD2	2.708
4DGY	H_ARG_66	NH2	H_ASP_86	OD1	3.089
4DGY	H_ARG_66	NH2	H_ASP_86	OD2	3.611
4DGY	H_LYS_83	NZ	H_GLU_85	OE2	2.758
4DGY	H_ARG_94	NH2	H_ASP_101	OD1	3.594
4DGY	H_ARG_94	NH2	H_ASP_101	OD2	2.861
4DGY	H_LYS_143	NZ	H_ASP_144	OD1	3.074
4DGY	H_LYS_143	NZ	H_ASP_144	OD2	3.615
4DGY	H_LYS_210	NZ	H_GLU_212	OE1	3.786
4DGY	H_LYS_214	NZ	L_ASP_122	OD1	3.699
4DGY	H_LYS_214	NZ	L_ASP_122	OD2	2.517
4DGY	L_ARG_61	NH2	L_ASP_82	OD1	2.957
4DGY	L_ARG_61	NH2	L_ASP_82	OD2	3.558
4DGY	L_LYS_149	NZ	L_GLU_195	OE1	2.631
4DGY	L_HIS_189	ND1	L_ASP_185	OD1	2.991
4DGY	L_ARG_211	NH1	L_GLU_187	OE1	3.660

Table 502: 4DGY-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4E9O	X_LYS_13	NZ	X_ASP_83	OD1	2.596
4E9O	X_LYS_13	NZ	X_ASP_83	OD2	3.399
4E9O	X_HIS_80	ND1	X_GLU_90	OE1	3.847
4E9O	X_HIS_80	ND1	X_GLU_90	OE2	3.037
4E9O	X_LYS_100	NZ	X_ASP_112	OD2	2.817
4E9O	X_HIS_110	NE2	X_GLU_106	OE2	2.743
4E9O	X_HIS_192	ND1	X_ASP_194	OD1	3.800
4E9O	X_HIS_192	ND1	X_ASP_194	OD2	3.793
4E9O	X_HIS_192	NE2	X_ASP_125	OD1	3.109
4E9O	X_ARG_200	NH1	X_ASP_74	OD1	3.919
4E9O	X_ARG_200	NH2	X_ASP_74	OD1	3.092

Table 503: 4E9O-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4EBQ	H_ARG_41	NH2	H_GLU_90	OE2	3.943
4EBQ	H_LYS_64	NZ	H_GLU_47	OE1	3.182
4EBQ	H_LYS_68	NZ	H_ASP_91	OD1	3.801
4EBQ	H_LYS_68	NZ	H_ASP_91	OD2	2.849
4EBQ	H_ARG_99	NH2	H_ASP_108	OD1	3.551
4EBQ	H_ARG_99	NH2	H_ASP_108	OD2	2.902
4EBQ	H_LYS_215	NZ	L_GLU_123	OE2	2.960
4EBQ	H_LYS_216	NZ	H_GLU_218	OE2	3.694
4EBQ	L_ARG_61	NH1	L_GLU_79	OE1	3.472
4EBQ	L_ARG_61	NH1	L_GLU_79	OE2	3.398
4EBQ	L_ARG_61	NH2	L_GLU_79	OE1	3.555
4EBQ	L_ARG_61	NH2	L_GLU_81	OE2	2.928
4EBQ	L_ARG_61	NH2	L_ASP_82	OD1	2.828
4EBQ	L_ARG_61	NH2	L_ASP_82	OD2	3.746
4EBQ	L_LYS_149	NZ	L_GLU_195	OE1	3.126
4EBQ	L_HIS_189	ND1	L_ASP_151	OD2	2.598
4EBQ	L_HIS_198	NE2	L_ASP_143	OD1	3.201
4EBQ	L_HIS_198	NE2	L_ASP_143	OD2	3.999
4EBQ	L_ARG_211	NH1	L_GLU_187	OE1	3.580

Table 504: 4EBQ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID residue name residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4EDW	V_LYS_25	NZ	V_GLU_55	OE2	2.812
4EDW	V_ARG_59	NH1	V_ASP_16	OD2	3.820
4EDW	V_ARG_69	NH1	V_ASP_16	OD2	3.587
4EDW	V_ARG_69	NH1	V_ASP_65	OD2	3.446
4EDW	V_ARG_69	NH2	V_ASP_16	OD1	2.627
4EDW	V_ARG_69	NH2	V_ASP_16	OD2	3.468
4EDW	V_HIS_75	ND1	V_ASP_72	OD2	3.959
4EDW	V_HIS_84	NE2	V_ASP_105	OD1	3.310
4EDW	V_ARG_100	NH2	V_ASP_93	OD2	3.018
4EDW	L_ARG_61	NH2	L_GLU_81	OE2	3.755
4EDW	L_ARG_61	NH2	L_ASP_82	OD1	3.001
4EDW	L_LYS_149	NZ	L_GLU_195	OE1	3.988
4EDW	L_LYS_149	NZ	L_GLU_195	OE2	3.571
4EDW	H_ARG_38	NH1	H_ASP_86	OD1	2.786
4EDW	H_ARG_38	NH2	H_GLU_46	OE1	3.202
4EDW	H_ARG_38	NH2	H_GLU_46	OE2	3.836
4EDW	H_ARG_38	NH2	H_ASP_86	OD1	3.735
4EDW	H_LYS_64	NZ	H_ASP_58	OD1	3.460
4EDW	H_ARG_66	NH1	H_ASP_86	OD1	3.705
4EDW	H_ARG_66	NH1	H_ASP_86	OD2	3.011
4EDW	H_ARG_66	NH2	H_ASP_86	OD1	3.297
4EDW	H_ARG_66	NH2	H_ASP_86	OD2	3.810
4EDW	H_ARG_94	NH1	H_ASP_101	OD1	3.531
4EDW	H_ARG_94	NH1	H_ASP_101	OD2	3.123
4EDW	H_LYS_143	NZ	H_ASP_144	OD1	3.362
4EDW	H_LYS_143	NZ	H_ASP_144	OD2	3.438
4EDW	H_LYS_206	NZ	H_ASP_199	OD1	3.486
4EDW	H_LYS_206	NZ	H_ASP_199	OD2	3.672
4EDW	H_LYS_209	NZ	L_GLU_123	OE2	2.707

Table 505: 4EDW-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4EDX	W.LYS_25	NZ	W.GLU_55	OE1	3.801
4EDX	W.LYS_25	NZ	W.GLU_55	OE2	2.552
4EDX	W.LYS_32	NZ	H.ASP_58	OD1	2.886
4EDX	W.LYS_32	NZ	H.ASP_58	OD2	2.677
4EDX	W.LYS_34	NZ	W.ASP_93	OD1	3.065
4EDX	W.LYS_34	NZ	W.ASP_93	OD2	3.190
4EDX	W.ARG_69	NH1	W.ASP_16	OD1	3.423
4EDX	W.ARG_69	NH1	W.ASP_16	OD2	3.292
4EDX	W.ARG_69	NH2	W.ASP_16	OD1	3.501
4EDX	W.ARG_69	NH2	W.ASP_16	OD2	3.076
4EDX	W.HIS_75	ND1	W.ASP_72	OD1	2.972
4EDX	W.HIS_75	ND1	W.ASP_72	OD2	2.422
4EDX	W.HIS_75	NE2	W.ASP_72	OD1	3.095
4EDX	W.HIS_75	NE2	W.ASP_72	OD2	3.906
4EDX	W.HIS_84	NE2	W.ASP_105	OD1	3.552
4EDX	A.ARG_24	NH1	A.ASP_70	OD1	2.849
4EDX	A.ARG_24	NH1	A.ASP_70	OD2	3.069
4EDX	A.ARG_53	NH1	W.GLU_11	OE1	2.795
4EDX	A.ARG_61	NH1	A.GLU_79	OE1	3.710
4EDX	A.ARG_61	NH1	A.GLU_79	OE2	3.737
4EDX	A.ARG_61	NH2	A.GLU_81	OE2	3.420
4EDX	A.ARG_61	NH2	A.ASP_82	OD1	2.960
4EDX	A.ARG_61	NH2	A.ASP_82	OD2	3.581
4EDX	A.LYS_142	NZ	A.ASP_143	OD2	3.962
4EDX	A.LYS_149	NZ	A.GLU_195	OE1	3.345
4EDX	A.ARG_155	NH1	A.GLU_185	OE2	3.186
4EDX	A.ARG_155	NH2	A.GLU_185	OE1	3.161
4EDX	A.ARG_155	NH2	A.GLU_185	OE2	3.235
4EDX	A.HIS_189	ND1	A.ASP_151	OD2	2.695
4EDX	A.LYS_199	NZ	A.ASP_110	OD2	3.513
4EDX	B.ARG_38	NH1	B.ASP_86	OD1	2.727
4EDX	B.ARG_38	NH2	B.GLU_46	OE1	3.309
4EDX	B.ARG_38	NH2	B.GLU_46	OE2	3.547
4EDX	B.ARG_38	NH2	B.ASP_86	OD1	3.872
4EDX	B.ARG_66	NH1	B.ASP_86	OD1	3.949
4EDX	B.ARG_66	NH2	B.ASP_86	OD1	3.356
4EDX	B.ARG_66	NH2	B.ASP_86	OD2	2.590
4EDX	B.ARG_83	NH1	B.ASP_85	OD2	3.918
4EDX	B.ARG_94	NH2	B.ASP_101	OD1	3.751
4EDX	B.ARG_94	NH2	B.ASP_101	OD2	2.789
4EDX	B.LYS_221	NZ	A.GLU_123	OE2	3.878
4EDX	V.LYS_25	NZ	V.GLU_55	OE2	2.718
4EDX	V.LYS_32	NZ	B.ASP_58	OD1	3.117
4EDX	V.LYS_32	NZ	B.ASP_58	OD2	2.681
4EDX	V.LYS_34	NZ	V.ASP_93	OD1	2.694
4EDX	V.LYS_34	NZ	V.ASP_93	OD2	3.572
4EDX	V.ARG_69	NH1	V.ASP_16	OD1	3.521
4EDX	V.HIS_75	ND1	V.ASP_72	OD2	2.859
4EDX	V.HIS_84	NE2	V.ASP_105	OD1	3.612
4EDX	V.LYS_88	NZ	B.ASP_54	OD2	3.805
4EDX	V.ARG_100	NH1	V.ASP_30	OD2	3.837
4EDX	L.ARG_24	NH1	L.ASP_70	OD1	2.767
4EDX	L.ARG_24	NH1	L.ASP_70	OD2	3.056
4EDX	L.ARG_53	NH1	V.GLU_11	OE1	3.269
4EDX	L.ARG_61	NH1	L.GLU_79	OE1	3.421
4EDX	L.ARG_61	NH1	L.GLU_79	OE2	3.637
4EDX	L.ARG_61	NH2	L.GLU_79	OE1	3.585

4EDX	L_ARG_61	NH2	L_GLU_81	OE1	3.985
4EDX	L_ARG_61	NH2	L_GLU_81	OE2	3.833
4EDX	L_ARG_61	NH2	L_ASP_82	OD1	3.225
4EDX	L_LYS_149	NZ	L_GLU_195	OE1	3.431
4EDX	L_LYS_149	NZ	L_GLU_195	OE2	2.686
4EDX	L_ARG_155	NH1	L_GLU_185	OE1	3.892
4EDX	L_ARG_155	NH1	L_GLU_185	OE2	3.334
4EDX	L_ARG_155	NH2	L_GLU_185	OE1	3.107
4EDX	L_ARG_155	NH2	L_GLU_185	OE2	3.593
4EDX	L_LYS_199	NZ	L_ASP_110	OD2	2.658
4EDX	L_ARG_211	NH1	L_GLU_187	OE1	3.902
4EDX	H_ARG_38	NH1	H_ASP_86	OD1	2.944
4EDX	H_ARG_38	NH2	H_GLU_46	OE1	3.536
4EDX	H_ARG_38	NH2	H_GLU_46	OE2	3.204
4EDX	H_ARG_66	NH2	H_ASP_86	OD1	3.277
4EDX	H_ARG_66	NH2	H_ASP_86	OD2	2.900
4EDX	H_ARG_94	NH2	H_ASP_101	OD1	3.827
4EDX	H_ARG_94	NH2	H_ASP_101	OD2	3.037
4EDX	H_LYS_221	NZ	L_GLU_123	OE2	3.893
4EDX	H_LYS_222	NZ	H_GLU_226	OE2	3.370

Table 506: 4EDX-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4ETQ	H_ARG_41	NH1	H_GLU_90	OE1	3.867
4ETQ	H_ARG_41	NH2	H_GLU_90	OE1	3.122
4ETQ	H_ARG_60	NH1	C_ASP_179	OD1	3.609
4ETQ	H_ARG_60	NH2	C_ASP_179	OD1	3.375
4ETQ	H_LYS_68	NZ	H_ASP_91	OD2	3.125
4ETQ	H_ARG_99	NH2	H_ASP_108	OD1	3.442
4ETQ	H_ARG_99	NH2	H_ASP_108	OD2	2.818
4ETQ	H_ARG_103	NH1	C_GLU_217	OE1	3.862
4ETQ	H_ARG_103	NH1	C_GLU_217	OE2	2.754
4ETQ	H_ARG_103	NH2	C_GLU_217	OE2	2.933
4ETQ	H_LYS_215	NZ	L_GLU_123	OE2	3.075
4ETQ	L_ARG_61	NH1	L_GLU_79	OE1	3.879
4ETQ	L_ARG_61	NH1	L_GLU_79	OE2	3.227
4ETQ	L_ARG_61	NH2	L_GLU_81	OE1	3.581
4ETQ	L_ARG_61	NH2	L_ASP_82	OD1	2.731
4ETQ	L_ARG_61	NH2	L_ASP_82	OD2	3.292
4ETQ	L_LYS_142	NZ	L_GLU_105	OE2	3.174
4ETQ	L_LYS_147	NZ	L_GLU_195	OE2	3.710
4ETQ	L_LYS_149	NZ	L_GLU_195	OE1	3.106
4ETQ	L_ARG_155	NH2	L_GLU_185	OE1	3.585
4ETQ	L_ARG_155	NH2	L_GLU_185	OE2	2.828
4ETQ	L_LYS_183	NZ	L_GLU_187	OE1	3.169
4ETQ	L_LYS_183	NZ	L_GLU_187	OE2	2.853
4ETQ	L_HIS_189	ND1	L_ASP_151	OD2	2.872
4ETQ	L_LYS_199	NZ	L_ASP_110	OD2	3.675
4ETQ	A_LYS_39	NZ	A_GLU_90	OE1	3.180
4ETQ	A_LYS_39	NZ	A_GLU_90	OE2	3.761
4ETQ	A_LYS_68	NZ	A_ASP_91	OD1	3.615
4ETQ	A_LYS_68	NZ	A_ASP_91	OD2	2.627
4ETQ	A_ARG_99	NH2	A_ASP_108	OD1	3.812
4ETQ	A_ARG_99	NH2	A_ASP_108	OD2	2.756
4ETQ	A_ARG_103	NH1	X_GLU_217	OE1	2.753
4ETQ	A_ARG_103	NH1	X_GLU_217	OE2	3.565
4ETQ	A_ARG_103	NH2	X_GLU_217	OE1	2.983
4ETQ	A_ARG_103	NH2	X_GLU_217	OE2	3.995
4ETQ	A_LYS_215	NZ	B_GLU_123	OE2	3.774
4ETQ	B_ARG_61	NH1	B_GLU_79	OE1	3.950
4ETQ	B_ARG_61	NH1	B_GLU_79	OE2	3.355
4ETQ	B_ARG_61	NH2	B_GLU_81	OE2	3.928
4ETQ	B_ARG_61	NH2	B_ASP_82	OD1	2.543
4ETQ	B_ARG_61	NH2	B_ASP_82	OD2	3.461
4ETQ	B_LYS_149	NZ	B_GLU_195	OE1	3.167
4ETQ	B_ARG_155	NH1	B_GLU_185	OE1	3.157
4ETQ	B_ARG_155	NH1	B_GLU_185	OE2	3.489
4ETQ	B_ARG_155	NH2	B_GLU_185	OE2	3.114
4ETQ	B_LYS_183	NZ	B_GLU_187	OE1	3.261
4ETQ	B_LYS_183	NZ	B_GLU_187	OE2	2.751
4ETQ	B_HIS_189	ND1	B_ASP_151	OD2	2.691
4ETQ	B_LYS_199	NZ	B_ASP_110	OD2	3.415
4ETQ	X_LYS_14	NZ	X_GLU_11	OE1	2.773
4ETQ	X_LYS_14	NZ	X_GLU_11	OE2	3.470
4ETQ	X_HIS_27	NE2	X_ASP_25	OD1	3.152
4ETQ	X_HIS_27	NE2	X_ASP_25	OD2	2.861
4ETQ	X_ARG_44	NH1	A_GLU_56	OE1	3.611
4ETQ	X_ARG_44	NH1	A_GLU_56	OE2	3.023
4ETQ	X_HIS_80	ND1	X_GLU_90	OE1	3.588
4ETQ	X_HIS_80	ND1	X_GLU_90	OE2	2.761

4ETQ	X_LYS_100	NZ	X_ASP_112	OD2	2.820
4ETQ	X_LYS_108	NZ	A_GLU_58	OE2	3.014
4ETQ	X_LYS_108	NZ	X_GLU_105	OE2	3.377
4ETQ	X_LYS_109	NZ	X_GLU_106	OE1	3.662
4ETQ	X_HIS_110	NE2	X_GLU_106	OE2	3.990
4ETQ	X_HIS_192	ND1	X_ASP_194	OD1	3.490
4ETQ	X_HIS_192	NE2	X_ASP_125	OD2	3.701
4ETQ	X_ARG_200	NH1	X_ASP_74	OD1	3.672
4ETQ	X_ARG_200	NH2	X_ASP_74	OD1	3.193
4ETQ	X_ARG_220	NH1	A_ASP_105	OD1	3.937
4ETQ	X_ARG_220	NH2	A_ASP_105	OD1	2.929
4ETQ	C_HIS_27	NE2	C_ASP_25	OD2	2.566
4ETQ	C_ARG_44	NH1	H_GLU_56	OE1	2.601
4ETQ	C_HIS_80	ND1	C_GLU_90	OE1	3.837
4ETQ	C_HIS_80	ND1	C_GLU_90	OE2	2.937
4ETQ	C_LYS_100	NZ	C_ASP_112	OD1	3.753
4ETQ	C_LYS_100	NZ	C_ASP_112	OD2	2.909
4ETQ	C_LYS_109	NZ	C_GLU_106	OE1	3.550
4ETQ	C_HIS_110	ND1	C_GLU_106	OE2	3.980
4ETQ	C_HIS_192	ND1	C_ASP_194	OD2	3.346
4ETQ	C_HIS_192	NE2	C_ASP_125	OD1	3.763
4ETQ	C_ARG_200	NH1	C_ASP_74	OD1	3.594
4ETQ	C_ARG_200	NH2	C_ASP_74	OD1	3.106
4ETQ	C_ARG_220	NH1	H_ASP_105	OD1	3.872
4ETQ	C_ARG_220	NH2	H_ASP_105	OD1	3.103

Table 507: 4ETQ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4F33	A_LYS_39	NZ	A_ASP_83	OD1	2.996
4F33	A_LYS_53	NZ	A_ASP_50	OD2	3.806
4F33	A_ARG_61	NH1	A_GLU_79	OE1	3.342
4F33	A_ARG_61	NH1	A_GLU_79	OE2	3.490
4F33	A_ARG_61	NH2	A_GLU_79	OE1	3.654
4F33	A_ARG_61	NH2	A_GLU_81	OE2	3.050
4F33	A_ARG_61	NH2	A_ASP_82	OD1	2.710
4F33	A_ARG_61	NH2	A_ASP_82	OD2	3.535
4F33	A_LYS_103	NZ	A_GLU_165	OE1	3.608
4F33	A_LYS_103	NZ	A_GLU_165	OE2	2.863
4F33	A_LYS_149	NZ	A_GLU_195	OE1	2.590
4F33	A_LYS_149	NZ	A_GLU_195	OE2	3.755
4F33	A_LYS_183	NZ	A_GLU_187	OE1	2.975
4F33	A_LYS_183	NZ	A_GLU_187	OE2	2.979
4F33	A_LYS_188	NZ	A_ASP_185	OD1	3.192
4F33	A_HIS_189	ND1	A_ASP_151	OD2	3.095
4F33	B_LYS_19	NZ	B_ASP_82	OD1	2.810
4F33	B_LYS_19	NZ	B_ASP_82	OD2	3.855
4F33	B_LYS_63	NZ	B_GLU_46	OE1	3.902
4F33	B_LYS_63	NZ	B_GLU_46	OE2	2.703
4F33	B_LYS_67	NZ	B_ASP_90	OD1	3.672
4F33	B_LYS_67	NZ	B_ASP_90	OD2	2.735
4F33	B_ARG_98	NH2	B_ASP_107	OD1	3.642
4F33	B_ARG_98	NH2	B_ASP_107	OD2	2.737
4F33	B_ARG_104	NH1	B_ASP_107	OD2	2.783
4F33	B_ARG_104	NH2	B_ASP_102	OD1	3.769
4F33	B_ARG_104	NH2	B_ASP_102	OD2	2.871
4F33	B_LYS_149	NZ	B_ASP_150	OD1	3.476
4F33	B_LYS_212	NZ	B_ASP_214	OD1	2.935
4F33	B_LYS_212	NZ	B_ASP_214	OD2	3.480
4F33	B_LYS_215	NZ	A_GLU_123	OE1	2.676
4F33	B_LYS_215	NZ	A_GLU_123	OE2	3.528
4F33	B_LYS_216	NZ	B_GLU_218	OE2	3.538
4F33	C_LYS_39	NZ	C_ASP_83	OD1	3.023
4F33	C_ARG_61	NH1	C_GLU_79	OE1	3.546
4F33	C_ARG_61	NH1	C_GLU_79	OE2	3.480
4F33	C_ARG_61	NH2	C_GLU_79	OE1	3.378
4F33	C_ARG_61	NH2	C_GLU_81	OE2	3.030
4F33	C_ARG_61	NH2	C_ASP_82	OD1	2.905
4F33	C_ARG_61	NH2	C_ASP_82	OD2	3.629
4F33	C_LYS_103	NZ	C_GLU_165	OE1	3.632
4F33	C_LYS_103	NZ	C_GLU_165	OE2	2.738
4F33	C_LYS_149	NZ	C_GLU_195	OE1	2.670
4F33	C_LYS_149	NZ	C_GLU_195	OE2	3.770
4F33	C_LYS_183	NZ	C_GLU_187	OE1	2.957
4F33	C_LYS_183	NZ	C_GLU_187	OE2	3.355
4F33	C_HIS_189	ND1	C_ASP_151	OD2	3.653
4F33	D_LYS_19	NZ	D_ASP_82	OD1	2.919
4F33	D_LYS_19	NZ	D_ASP_82	OD2	3.318
4F33	D_LYS_63	NZ	D_GLU_46	OE1	3.665
4F33	D_LYS_63	NZ	D_GLU_46	OE2	2.603
4F33	D_LYS_67	NZ	D_ASP_90	OD1	3.611
4F33	D_LYS_67	NZ	D_ASP_90	OD2	2.762
4F33	D_ARG_98	NH2	D_ASP_107	OD1	3.663
4F33	D_ARG_98	NH2	D_ASP_107	OD2	2.741
4F33	D_ARG_104	NH1	D_ASP_107	OD2	2.826
4F33	D_ARG_104	NH2	D_ASP_102	OD1	3.818

4F33	D_ARG_104	NH2	D_ASP_102	OD2	2.913
4F33	D_LYS_149	NZ	D_ASP_150	OD1	3.466
4F33	D_LYS_149	NZ	D_ASP_150	OD2	3.828
4F33	D_LYS_212	NZ	D_ASP_214	OD1	2.938
4F33	D_LYS_212	NZ	D_ASP_214	OD2	3.473
4F33	D_LYS_215	NZ	C_GLU_123	OE1	2.787
4F33	D_LYS_215	NZ	C_GLU_123	OE2	3.695
4F33	D_LYS_216	NZ	D_GLU_218	OE2	3.391
4F33	E_LYS_39	NZ	E_ASP_83	OD1	2.874
4F33	E_LYS_53	NZ	E_ASP_50	OD2	3.486
4F33	E_ARG_61	NH1	E_GLU_79	OE1	3.890
4F33	E_ARG_61	NH1	E_GLU_79	OE2	3.753
4F33	E_ARG_61	NH2	E_GLU_79	OE1	3.703
4F33	E_ARG_61	NH2	E_GLU_81	OE2	3.201
4F33	E_ARG_61	NH2	E_ASP_82	OD1	2.824
4F33	E_ARG_61	NH2	E_ASP_82	OD2	3.545
4F33	E_LYS_103	NZ	E_GLU_165	OE1	3.553
4F33	E_LYS_103	NZ	E_GLU_165	OE2	3.041
4F33	E_LYS_149	NZ	E_GLU_195	OE1	2.766
4F33	E_LYS_149	NZ	E_GLU_195	OE2	3.971
4F33	E_LYS_183	NZ	E_GLU_187	OE1	3.278
4F33	E_LYS_183	NZ	E_GLU_187	OE2	2.769
4F33	E_LYS_188	NZ	E_ASP_185	OD1	3.409
4F33	E_HIS_189	ND1	E_ASP_151	OD2	3.133
4F33	F_LYS_19	NZ	F_ASP_82	OD1	3.043
4F33	F_LYS_63	NZ	F_GLU_46	OE1	3.844
4F33	F_LYS_63	NZ	F_GLU_46	OE2	2.677
4F33	F_LYS_67	NZ	F_ASP_90	OD1	3.822
4F33	F_LYS_67	NZ	F_ASP_90	OD2	2.975
4F33	F_ARG_98	NH2	F_ASP_107	OD1	3.603
4F33	F_ARG_98	NH2	F_ASP_107	OD2	2.766
4F33	F_ARG_104	NH1	F_ASP_107	OD2	2.837
4F33	F_ARG_104	NH2	F_ASP_102	OD1	3.766
4F33	F_ARG_104	NH2	F_ASP_102	OD2	2.901
4F33	F_LYS_149	NZ	F_ASP_150	OD1	3.004
4F33	F_LYS_149	NZ	F_ASP_150	OD2	3.043
4F33	F_LYS_212	NZ	D_ASP_214	OD2	3.519
4F33	F_LYS_212	NZ	F_ASP_214	OD1	3.366
4F33	F_LYS_212	NZ	F_ASP_214	OD2	3.190
4F33	F_LYS_215	NZ	E_GLU_123	OE1	2.609
4F33	F_LYS_215	NZ	E_GLU_123	OE2	3.626
4F33	G_LYS_39	NZ	G_ASP_83	OD1	2.914
4F33	G_LYS_53	NZ	G_ASP_50	OD2	3.491
4F33	G_ARG_61	NH1	G_GLU_79	OE1	3.696
4F33	G_ARG_61	NH1	G_GLU_79	OE2	3.825
4F33	G_ARG_61	NH2	G_GLU_79	OE1	3.720
4F33	G_ARG_61	NH2	G_GLU_81	OE2	2.958
4F33	G_ARG_61	NH2	G_ASP_82	OD1	2.734
4F33	G_ARG_61	NH2	G_ASP_82	OD2	3.619
4F33	G_LYS_103	NZ	G_GLU_165	OE1	3.422
4F33	G_LYS_103	NZ	G_GLU_165	OE2	2.954
4F33	G_LYS_149	NZ	G_GLU_195	OE1	3.155
4F33	G_LYS_183	NZ	G_GLU_187	OE1	3.171
4F33	G_LYS_183	NZ	G_GLU_187	OE2	3.240
4F33	G_HIS_189	ND1	G_ASP_151	OD2	2.855
4F33	H_LYS_19	NZ	H_ASP_82	OD1	2.977
4F33	H_LYS_19	NZ	H_ASP_82	OD2	3.331
4F33	H_LYS_63	NZ	H_GLU_46	OE1	3.962

4F33	H_LYS_63	NZ	H_GLU_46	OE2	2.721
4F33	H_LYS_67	NZ	H_ASP_90	OD1	3.773
4F33	H_LYS_67	NZ	H_ASP_90	OD2	2.822
4F33	H_ARG_98	NH2	H_ASP_107	OD1	3.660
4F33	H_ARG_98	NH2	H_ASP_107	OD2	2.794
4F33	H_ARG_104	NH1	H_ASP_107	OD2	2.850
4F33	H_ARG_104	NH2	H_ASP_102	OD1	3.752
4F33	H_ARG_104	NH2	H_ASP_102	OD2	2.926
4F33	H_LYS_149	NZ	H_ASP_150	OD1	3.202
4F33	H_LYS_149	NZ	H_ASP_150	OD2	3.778
4F33	H_LYS_212	NZ	H_ASP_214	OD1	3.294
4F33	H_LYS_212	NZ	H_ASP_214	OD2	3.751
4F33	H_LYS_215	NZ	G_GLU_123	OE1	2.968
4F33	H_LYS_215	NZ	G_GLU_123	OE2	3.966

Table 508: 4F33-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4F3F	A_LYS_39	NZ	A_ASP_83	OD1	3.139
4F3F	A_LYS_53	NZ	A_ASP_50	OD2	3.180
4F3F	A_ARG_61	NH1	A_GLU_79	OE1	3.186
4F3F	A_ARG_61	NH2	A_GLU_79	OE1	3.636
4F3F	A_ARG_61	NH2	A_GLU_81	OE2	2.949
4F3F	A_ARG_61	NH2	A_ASP_82	OD1	2.598
4F3F	A_ARG_61	NH2	A_ASP_82	OD2	3.459
4F3F	A_HIS_94	NE2	C_GLU_18	OE1	3.664
4F3F	A_HIS_94	NE2	C_GLU_18	OE2	3.880
4F3F	A_LYS_103	NZ	A_GLU_165	OE1	2.677
4F3F	A_LYS_103	NZ	A_GLU_165	OE2	3.463
4F3F	A_LYS_126	NZ	A_ASP_122	OD2	3.488
4F3F	A_LYS_149	NZ	A_GLU_195	OE1	3.346
4F3F	A_LYS_149	NZ	A_GLU_195	OE2	3.599
4F3F	A_LYS_188	NZ	A_ASP_185	OD1	3.466
4F3F	A_HIS_189	ND1	A_ASP_151	OD2	2.913
4F3F	B_LYS_67	NZ	B_ASP_90	OD1	3.515
4F3F	B_LYS_67	NZ	B_ASP_90	OD2	2.923
4F3F	B_ARG_98	NH2	B_ASP_107	OD1	3.433
4F3F	B_ARG_98	NH2	B_ASP_107	OD2	2.792
4F3F	B_LYS_149	NZ	B_ASP_150	OD1	3.423
4F3F	B_LYS_149	NZ	B_ASP_150	OD2	3.482
4F3F	C_LYS_11	NZ	C_GLU_27	OE1	3.675
4F3F	C_LYS_11	NZ	C_GLU_27	OE2	2.987
4F3F	C_LYS_24	NZ	A_ASP_50	OD1	2.832
4F3F	C_LYS_24	NZ	A_ASP_50	OD2	3.865
4F3F	C_ARG_43	NH2	C_GLU_15	OE2	2.883
4F3F	C_LYS_60	NZ	C_GLU_29	OE1	3.765
4F3F	C_LYS_60	NZ	C_GLU_29	OE2	3.687

Table 509: 4F3F-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4FFV	A_ARG_39	NH1	A_ASP_45	OD1	3.963
4FFV	A_ARG_39	NH1	A_ASP_45	OD2	2.719
4FFV	A_ARG_39	NH2	A_ASP_45	OD1	3.080
4FFV	A_ARG_39	NH2	A_ASP_45	OD2	3.080
4FFV	A_ARG_59	NH2	A_ASP_102	OD1	3.051
4FFV	A_ARG_109	NH1	A_GLU_65	OE1	3.268
4FFV	A_ARG_109	NH1	A_GLU_65	OE2	3.741
4FFV	A_ARG_109	NH2	A_GLU_65	OE1	2.989
4FFV	A_LYS_120	NZ	A_ASP_740	OD2	3.330
4FFV	A_ARG_123	NH2	A_GLU_203	OE1	3.682
4FFV	A_ARG_123	NH2	A_GLU_203	OE2	2.712
4FFV	A_HIS_160	ND1	A_ASP_108	OD2	2.635
4FFV	A_HIS_160	NE2	A_GLU_175	OE1	3.358
4FFV	A_HIS_160	NE2	A_GLU_175	OE2	2.796
4FFV	A_LYS_161	NZ	A_ASP_272	OD1	2.746
4FFV	A_LYS_161	NZ	A_ASP_272	OD2	3.688
4FFV	A_ARG_182	NH1	A_ASP_169	OD1	3.856
4FFV	A_ARG_182	NH1	A_ASP_169	OD2	2.767
4FFV	A_ARG_182	NH2	A_ASP_169	OD2	3.302
4FFV	A_ARG_308	NH2	A_ASP_327	OD2	3.552
4FFV	A_ARG_316	NH1	A_ASP_295	OD2	3.083
4FFV	A_ARG_316	NH2	A_GLU_669	OE1	3.538
4FFV	A_ARG_316	NH2	A_GLU_669	OE2	2.880
4FFV	A_ARG_354	NH2	A_GLU_404	OE1	2.806
4FFV	A_HIS_361	NE2	A_GLU_359	OE2	3.865
4FFV	A_LYS_371	NZ	A_GLU_345	OE1	3.266
4FFV	A_LYS_380	NZ	A_ASP_589	OD1	3.110
4FFV	A_LYS_380	NZ	A_ASP_589	OD2	3.542
4FFV	A_HIS_381	NE2	A_ASP_375	OD2	3.813
4FFV	A_LYS_443	NZ	A_GLU_422	OE1	2.784
4FFV	A_LYS_443	NZ	A_GLU_422	OE2	3.590
4FFV	A_LYS_513	NZ	A_ASP_557	OD1	3.202
4FFV	A_LYS_514	NZ	A_ASP_516	OD2	3.647
4FFV	A_ARG_524	NH1	A_GLU_425	OE1	3.869
4FFV	A_LYS_555	NZ	A_ASP_546	OD1	3.412
4FFV	A_LYS_555	NZ	A_ASP_546	OD2	3.059
4FFV	A_ARG_561	NH1	A_ASP_557	OD1	2.919
4FFV	A_ARG_561	NH1	A_ASP_557	OD2	3.499
4FFV	A_ARG_561	NH2	A_ASP_557	OD1	3.437
4FFV	A_ARG_561	NH2	A_ASP_557	OD2	2.894
4FFV	A_ARG_582	NH2	A_GLU_605	OE2	3.235
4FFV	A_ARG_582	NH2	A_ASP_606	OD1	2.825
4FFV	A_ARG_582	NH2	A_ASP_606	OD2	3.726
4FFV	A_LYS_597	NZ	A_ASP_679	OD1	2.818
4FFV	A_LYS_597	NZ	A_ASP_679	OD2	3.476
4FFV	A_ARG_624	NH2	A_ASP_621	OD2	3.551
4FFV	A_LYS_649	NZ	A_GLU_700	OE2	3.425
4FFV	A_ARG_659	NH1	A_GLU_661	OE1	2.918
4FFV	A_ARG_659	NH1	A_GLU_661	OE2	3.900
4FFV	A_ARG_659	NH2	B_GLU_242	OE2	2.683
4FFV	A_LYS_697	NZ	A_GLU_694	OE1	2.696
4FFV	A_HIS_705	NE2	A_ASP_709	OD2	3.369
4FFV	A_HIS_741	ND1	A_ASP_709	OD1	3.395
4FFV	A_HIS_741	ND1	A_ASP_709	OD2	2.789
4FFV	A_HIS_755	ND1	B_ASP_730	OD1	2.996
4FFV	B_ARG_39	NH1	B_ASP_45	OD1	2.616
4FFV	B_ARG_39	NH1	B_ASP_45	OD2	3.948

4FFV	B_ARG_39	NH2	B_ASP_45	OD1	3.428
4FFV	B_ARG_39	NH2	B_ASP_45	OD2	3.350
4FFV	B_ARG_59	NH2	B_ASP_102	OD1	2.946
4FFV	B_ARG_109	NH2	B_GLU_65	OE1	2.873
4FFV	B_ARG_109	NH2	B_GLU_65	OE2	3.587
4FFV	B_ARG_123	NH2	B_GLU_203	OE1	3.775
4FFV	B_ARG_123	NH2	B_GLU_203	OE2	2.935
4FFV	B_HIS_160	ND1	B_ASP_108	OD2	2.803
4FFV	B_HIS_160	NE2	B_GLU_175	OE1	2.723
4FFV	B_HIS_160	NE2	B_GLU_175	OE2	3.449
4FFV	B_LYS_161	NZ	B_ASP_272	OD1	2.924
4FFV	B_ARG_182	NH2	B_ASP_169	OD1	2.817
4FFV	B_ARG_308	NH1	B_ASP_327	OD1	2.983
4FFV	B_ARG_308	NH1	B_ASP_327	OD2	2.869
4FFV	B_ARG_316	NH1	B_GLU_669	OE1	3.104
4FFV	B_ARG_316	NH1	B_GLU_669	OE2	3.019
4FFV	B_ARG_316	NH2	B_ASP_295	OD2	3.354
4FFV	B_ARG_354	NH2	B_GLU_404	OE1	2.935
4FFV	B_LYS_371	NZ	B_GLU_345	OE1	2.807
4FFV	B_LYS_467	NZ	B_GLU_80	OE2	3.637
4FFV	B_ARG_485	NH2	B_ASP_488	OD1	2.633
4FFV	B_LYS_513	NZ	B_ASP_557	OD1	3.220
4FFV	B_ARG_524	NH1	B_GLU_425	OE1	3.953
4FFV	B_ARG_524	NH2	B_GLU_425	OE1	3.954
4FFV	B_LYS_555	NZ	B_ASP_546	OD1	3.219
4FFV	B_LYS_555	NZ	B_ASP_546	OD2	3.109
4FFV	B_ARG_561	NH1	B_ASP_557	OD1	2.961
4FFV	B_ARG_561	NH1	B_ASP_557	OD2	3.596
4FFV	B_ARG_561	NH2	B_ASP_557	OD1	3.466
4FFV	B_ARG_561	NH2	B_ASP_557	OD2	2.798
4FFV	B_ARG_582	NH2	B_ASP_606	OD1	2.846
4FFV	B_ARG_582	NH2	B_ASP_606	OD2	3.802
4FFV	B_ARG_612	NH1	B_GLU_609	OE2	3.858
4FFV	B_LYS_623	NZ	B_ASP_621	OD1	3.779
4FFV	B_ARG_624	NH1	B_ASP_621	OD2	2.973
4FFV	B_ARG_659	NH1	B_GLU_661	OE1	3.697
4FFV	B_ARG_659	NH1	B_GLU_661	OE2	2.842
4FFV	B_ARG_659	NH2	A_GLU_242	OE2	2.592
4FFV	B_LYS_697	NZ	B_GLU_694	OE2	3.213
4FFV	B_HIS_705	NE2	B_ASP_709	OD2	3.391
4FFV	B_HIS_741	ND1	B_ASP_709	OD1	3.377
4FFV	B_HIS_741	ND1	B_ASP_709	OD2	2.794
4FFV	B_HIS_755	ND1	A_ASP_730	OD1	2.989
4FFV	B_HIS_755	ND1	A_ASP_730	OD2	3.942
4FFV	C_ARG_60	NH2	C_GLU_78	OE2	2.738
4FFV	C_LYS_146	NZ	C_GLU_153	OE2	3.897
4FFV	D_LYS_54	NZ	B_GLU_89	OE1	3.460
4FFV	D_LYS_54	NZ	B_GLU_89	OE2	3.556
4FFV	D_LYS_54	NZ	D_ASP_31	OD1	3.816
4FFV	D_LYS_63	NZ	D_GLU_46	OE2	3.471
4FFV	D_LYS_67	NZ	D_ASP_90	OD2	2.846
4FFV	D_ARG_98	NH2	D_ASP_105	OD1	3.968
4FFV	D_ARG_98	NH2	D_ASP_105	OD2	2.804
4FFV	D_LYS_209	NZ	D_ASP_211	OD1	3.459
4FFV	L_ARG_60	NH1	L_GLU_78	OE2	3.980
4FFV	L_ARG_60	NH2	L_GLU_80	OE2	2.908
4FFV	L_ARG_76	NH1	L_GLU_78	OE2	3.920
4FFV	L_ARG_76	NH2	L_GLU_78	OE2	3.454

4FFV	L_LYS_146	NZ	L_GLU_153	OE2	3.863
4FFV	L_LYS_148	NZ	L_GLU_194	OE1	3.895
4FFV	L_LYS_168	NZ	L_ASP_169	OD2	3.641
4FFV	H_LYS_54	NZ	A_GLU_89	OE1	3.584
4FFV	H_LYS_54	NZ	A_GLU_89	OE2	3.871
4FFV	H_LYS_63	NZ	H_GLU_46	OE2	3.768
4FFV	H_LYS_67	NZ	H_ASP_90	OD1	2.976
4FFV	H_LYS_67	NZ	H_ASP_90	OD2	3.578
4FFV	H_ARG_98	NH1	H_ASP_105	OD1	3.804
4FFV	H_ARG_98	NH1	H_ASP_105	OD2	3.268
4FFV	H_ARG_98	NH2	H_ASP_105	OD2	3.823
4FFV	H_HIS_168	NE2	L_ASP_166	OD1	3.178
4FFV	H_HIS_168	NE2	L_ASP_166	OD2	3.870
4FFV	H_LYS_209	NZ	H_ASP_211	OD1	3.064

Table 510: 4FFV-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4FFW	A_ARG_39	NH2	A_ASP_45	OD1	3.225
4FFW	A_ARG_39	NH2	A_ASP_45	OD2	2.703
4FFW	A_ARG_109	NH1	A_GLU_65	OE1	3.415
4FFW	A_ARG_109	NH1	A_GLU_65	OE2	3.525
4FFW	A_ARG_109	NH2	A_GLU_65	OE1	3.203
4FFW	A_LYS_120	NZ	A_ASP_740	OD2	3.434
4FFW	A_ARG_123	NH2	A_GLU_203	OE2	3.187
4FFW	A_HIS_160	NE2	A_ASP_108	OD2	3.962
4FFW	A_LYS_161	NZ	A_ASP_272	OD1	2.704
4FFW	A_ARG_182	NH1	A_ASP_169	OD2	2.886
4FFW	A_ARG_308	NH2	A_ASP_327	OD2	3.670
4FFW	A_ARG_316	NH1	A_ASP_295	OD2	3.273
4FFW	A_ARG_316	NH2	A_GLU_669	OE1	3.641
4FFW	A_ARG_316	NH2	A_GLU_669	OE2	2.963
4FFW	A_ARG_354	NH2	A_GLU_404	OE1	3.227
4FFW	A_HIS_361	NE2	A_GLU_359	OE2	3.514
4FFW	A_LYS_371	NZ	A_GLU_345	OE1	2.680
4FFW	A_LYS_380	NZ	A_ASP_589	OD1	3.098
4FFW	A_LYS_380	NZ	A_ASP_589	OD2	2.829
4FFW	A_LYS_443	NZ	A_GLU_422	OE1	2.937
4FFW	A_LYS_513	NZ	A_ASP_557	OD1	3.106
4FFW	A_ARG_524	NH1	A_GLU_425	OE1	2.739
4FFW	A_LYS_555	NZ	A_ASP_546	OD1	3.312
4FFW	A_ARG_561	NH1	A_ASP_557	OD1	2.928
4FFW	A_ARG_561	NH1	A_ASP_557	OD2	3.570
4FFW	A_ARG_561	NH2	A_ASP_557	OD1	3.591
4FFW	A_ARG_561	NH2	A_ASP_557	OD2	3.082
4FFW	A_ARG_582	NH2	A_GLU_605	OE2	3.554
4FFW	A_ARG_582	NH2	A_ASP_606	OD1	3.161
4FFW	A_ARG_582	NH2	A_ASP_606	OD2	3.803
4FFW	A_LYS_597	NZ	A_ASP_679	OD1	2.982
4FFW	A_ARG_624	NH2	A_ASP_621	OD2	3.236
4FFW	A_LYS_649	NZ	A_GLU_700	OE2	3.883
4FFW	A_ARG_659	NH1	A_GLU_661	OE1	3.045
4FFW	A_ARG_659	NH2	B_GLU_242	OE2	3.187
4FFW	A_LYS_697	NZ	A_GLU_694	OE1	3.166
4FFW	A_HIS_705	NE2	A_ASP_709	OD2	3.560
4FFW	A_HIS_741	ND1	A_ASP_709	OD1	3.680
4FFW	A_HIS_741	ND1	A_ASP_709	OD2	2.834
4FFW	A_HIS_755	ND1	B_ASP_730	OD1	3.111
4FFW	B_ARG_39	NH1	B_ASP_45	OD1	3.148
4FFW	B_ARG_39	NH2	B_ASP_45	OD1	3.305
4FFW	B_ARG_39	NH2	B_ASP_45	OD2	3.479
4FFW	B_ARG_59	NH2	B_ASP_102	OD1	3.000
4FFW	B_ARG_109	NH2	B_GLU_65	OE1	3.413
4FFW	B_ARG_109	NH2	B_GLU_65	OE2	3.745
4FFW	B_LYS_120	NZ	B_ASP_740	OD2	3.578
4FFW	B_ARG_123	NH2	B_GLU_203	OE2	2.505
4FFW	B_HIS_160	ND1	B_ASP_108	OD2	3.785
4FFW	B_HIS_160	NE2	B_GLU_175	OE1	2.698
4FFW	B_HIS_160	NE2	B_GLU_175	OE2	3.643
4FFW	B_LYS_161	NZ	B_ASP_272	OD1	3.156
4FFW	B_ARG_182	NH2	B_ASP_169	OD1	2.942
4FFW	B_ARG_308	NH1	B_ASP_327	OD1	3.218
4FFW	B_ARG_308	NH1	B_ASP_327	OD2	2.634
4FFW	B_ARG_316	NH1	B_GLU_669	OE1	2.973
4FFW	B_ARG_316	NH1	B_GLU_669	OE2	3.097

4FFW	B_ARG_316	NH2	B_ASP_295	OD2	3.399
4FFW	B_LYS_330	NZ	B_ASP_307	OD2	3.516
4FFW	B_ARG_354	NH2	B_GLU_404	OE1	2.920
4FFW	B_ARG_356	NH2	B_ASP_300	OD2	3.885
4FFW	B_LYS_371	NZ	B_GLU_345	OE1	2.782
4FFW	B_LYS_371	NZ	B_GLU_345	OE2	3.778
4FFW	B_LYS_380	NZ	B_ASP_589	OD2	3.568
4FFW	B_ARG_485	NH2	B_ASP_488	OD1	3.387
4FFW	B_LYS_513	NZ	B_ASP_557	OD1	3.212
4FFW	B_LYS_514	NZ	B_ASP_516	OD1	3.257
4FFW	B_ARG_524	NH1	B_GLU_425	OE1	3.639
4FFW	B_LYS_555	NZ	B_ASP_546	OD1	3.368
4FFW	B_ARG_561	NH1	B_ASP_557	OD1	3.049
4FFW	B_ARG_561	NH1	B_ASP_557	OD2	3.722
4FFW	B_ARG_561	NH2	B_ASP_557	OD1	3.485
4FFW	B_ARG_561	NH2	B_ASP_557	OD2	3.243
4FFW	B_ARG_582	NH2	B_ASP_606	OD1	3.041
4FFW	B_LYS_597	NZ	B_ASP_679	OD1	3.641
4FFW	B_LYS_623	NZ	B_ASP_621	OD1	3.750
4FFW	B_ARG_624	NH1	B_ASP_621	OD2	3.247
4FFW	B_ARG_659	NH1	B_GLU_661	OE2	2.930
4FFW	B_ARG_659	NH2	A_GLU_242	OE2	3.068
4FFW	B_ARG_670	NH2	B_GLU_204	OE1	3.913
4FFW	B_HIS_705	NE2	B_ASP_709	OD2	3.534
4FFW	B_HIS_741	ND1	B_ASP_709	OD1	3.671
4FFW	B_HIS_741	ND1	B_ASP_709	OD2	2.858
4FFW	C_ARG_60	NH2	C_GLU_80	OE2	3.345
4FFW	C_LYS_146	NZ	C_GLU_153	OE1	3.486
4FFW	C_LYS_146	NZ	C_GLU_153	OE2	3.680
4FFW	C_ARG_154	NH1	C_GLU_184	OE2	3.454
4FFW	C_ARG_154	NH2	C_GLU_184	OE2	3.842
4FFW	C_LYS_182	NZ	C_GLU_186	OE2	2.882
4FFW	D_LYS_54	NZ	B_GLU_89	OE1	3.085
4FFW	D_LYS_54	NZ	B_GLU_89	OE2	3.381
4FFW	D_LYS_63	NZ	D_GLU_46	OE2	3.795
4FFW	D_LYS_67	NZ	D_ASP_90	OD2	2.893
4FFW	D_ARG_98	NH2	D_ASP_105	OD1	3.888
4FFW	D_ARG_98	NH2	D_ASP_105	OD2	3.038
4FFW	H_LYS_54	NZ	A_GLU_89	OE1	3.517
4FFW	H_LYS_54	NZ	A_GLU_89	OE2	3.666
4FFW	H_LYS_63	NZ	H_GLU_46	OE2	3.928
4FFW	H_ARG_98	NH2	H_ASP_105	OD1	3.858
4FFW	H_ARG_98	NH2	H_ASP_105	OD2	3.152
4FFW	H_HIS_168	NE2	L_ASP_166	OD1	3.737
4FFW	L_ARG_60	NH1	L_GLU_78	OE2	3.910
4FFW	L_ARG_60	NH2	L_GLU_80	OE2	3.325
4FFW	L_ARG_60	NH2	L_ASP_81	OD1	2.865
4FFW	L_ARG_60	NH2	L_ASP_81	OD2	3.727
4FFW	L_LYS_	NZ	L_GLU_	OE2	3.349

Table 511: 4FFW-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4FQH	H_ARG_38	NH1	H_ASP_86	OD1	2.793
4FQH	H_ARG_38	NH2	H_ASP_86	OD1	3.878
4FQH	H_LYS_62	NZ	H_ASP_46	OD2	3.060
4FQH	H_ARG_66	NH1	H_ASP_86	OD1	3.673
4FQH	H_ARG_66	NH1	H_ASP_86	OD2	2.888
4FQH	H_ARG_66	NH2	H_ASP_86	OD1	2.891
4FQH	H_ARG_66	NH2	H_ASP_86	OD2	3.511
4FQH	H_ARG_94	NH1	H_ASP_101	OD1	3.949
4FQH	H_ARG_94	NH1	H_ASP_101	OD2	3.141
4FQH	H_ARG_94	NH2	H_ASP_101	OD1	3.729
4FQH	H_ARG_94	NH2	H_ASP_101	OD2	3.721
4FQH	H_LYS_143	NZ	L_GLU_124	OE2	2.906
4FQH	H_LYS_214	NZ	L_GLU_123	OE1	3.752
4FQH	H_LYS_214	NZ	L_GLU_123	OE2	2.217
4FQH	L_ARG_30	NH1	L_ASP_93	OD2	3.341
4FQH	L_ARG_31	NH1	L_ASP_93	OD1	2.902
4FQH	L_ARG_31	NH1	L_ASP_93	OD2	3.963
4FQH	L_ARG_61	NH2	L_ASP_82	OD1	2.708
4FQH	L_ARG_61	NH2	L_ASP_82	OD2	3.349
4FQH	L_HIS_188	ND1	L_ASP_151	OD1	2.726
4FQH	A_ARG_38	NH1	A_ASP_86	OD1	2.939
4FQH	A_LYS_62	NZ	A_ASP_46	OD1	3.347
4FQH	A_LYS_62	NZ	A_ASP_46	OD2	2.737
4FQH	A_ARG_66	NH1	A_ASP_86	OD1	3.497
4FQH	A_ARG_66	NH1	A_ASP_86	OD2	2.905
4FQH	A_ARG_66	NH2	A_ASP_86	OD1	2.643
4FQH	A_ARG_66	NH2	A_ASP_86	OD2	3.511
4FQH	A_LYS_143	NZ	A_ASP_144	OD2	3.998
4FQH	A_LYS_143	NZ	B_GLU_124	OE2	3.049
4FQH	A_LYS_214	NZ	B_GLU_123	OE1	3.132
4FQH	B_ARG_31	NH2	B_ASP_93	OD1	2.853
4FQH	B_ARG_61	NH2	B_ASP_82	OD1	2.666
4FQH	B_ARG_61	NH2	B_ASP_82	OD2	3.538

Table 512: 4FQH-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4FQI	A_LYS_45	NZ	A_ASP_41	OD1	3.116
4FQI	A_LYS_45	NZ	A_ASP_41	OD2	2.607
4FQI	A_LYS_46	NZ	A_GLU_44	OE1	2.647
4FQI	A_LYS_46	NZ	A_GLU_44	OE2	3.567
4FQI	A_ARG_62	NH1	A_GLU_78	OE1	3.913
4FQI	A_ARG_62	NH1	A_GLU_78	OE2	3.007
4FQI	A_LYS_90	NZ	A_GLU_273	OE1	2.798
4FQI	A_LYS_109	NZ	A_GLU_89	OE1	2.835
4FQI	A_LYS_109	NZ	A_GLU_89	OE2	3.759
4FQI	A_LYS_109	NZ	B_GLU_69	OE1	2.615
4FQI	A_LYS_109	NZ	B_GLU_69	OE2	3.205
4FQI	A_ARG_149	NH2	A_ASP_77	OD1	3.711
4FQI	A_ARG_149	NH2	A_ASP_77	OD2	2.863
4FQI	A_HIS_184	NE2	A_GLU_231	OE1	2.822
4FQI	A_ARG_216	NH1	A_GLU_231	OE1	3.982
4FQI	A_ARG_216	NH2	A_GLU_231	OE1	3.265
4FQI	A_LYS_259	NZ	A_GLU_119	OE1	3.578
4FQI	A_LYS_261	NZ	A_GLU_83A	OE1	3.943
4FQI	A_LYS_261	NZ	A_GLU_83A	OE2	2.598
4FQI	A_LYS_262	NZ	A_ASP_175	OD2	3.224
4FQI	A_LYS_269	NZ	A_GLU_89	OE1	2.759
4FQI	A_LYS_307	NZ	B_GLU_64	OE2	3.371
4FQI	A_LYS_310	NZ	B_ASP_90	OD1	2.687
4FQI	A_LYS_310	NZ	B_ASP_90	OD2	3.739
4FQI	B_LYS_51	NZ	B_GLU_103	OE1	2.743
4FQI	B_ARG_68	NH1	B_GLU_85	OE2	3.042
4FQI	B_LYS_82	NZ	B_ASP_86	OD2	2.769
4FQI	B_ARG_123	NH2	B_ASP_120	OD1	3.250
4FQI	B_ARG_153	NH2	B_GLU_150	OE2	2.775
4FQI	B_ARG_167	NH2	B_GLU_164	OE1	3.918
4FQI	B_ARG_167	NH2	B_GLU_164	OE2	2.444
4FQI	B_ARG_170	NH1	B_ASP_128	OD1	3.871
4FQI	B_ARG_170	NH1	B_ASP_128	OD2	3.616
4FQI	B_ARG_170	NH2	B_ASP_128	OD2	3.649
4FQI	H_ARG_38	NH1	H_ASP_86	OD1	2.837
4FQI	H_ARG_38	NH2	H_ASP_86	OD1	3.841
4FQI	H_LYS_62	NZ	H_ASP_46	OD1	3.985
4FQI	H_LYS_62	NZ	H_ASP_46	OD2	2.950
4FQI	H_ARG_66	NH1	H_ASP_86	OD1	3.456
4FQI	H_ARG_66	NH1	H_ASP_86	OD2	2.873
4FQI	H_ARG_66	NH2	H_ASP_86	OD1	2.889
4FQI	H_ARG_66	NH2	H_ASP_86	OD2	3.655
4FQI	H_LYS_143	NZ	L_GLU_124	OE2	2.947
4FQI	H_LYS_206	NZ	H_ASP_208	OD1	2.657
4FQI	H_LYS_206	NZ	H_ASP_208	OD2	3.897
4FQI	L_ARG_30	NH1	L_ASP_93	OD2	2.748
4FQI	L_ARG_30	NH2	L_ASP_93	OD2	3.772
4FQI	L_ARG_31	NH2	L_ASP_93	OD1	2.914
4FQI	L_ARG_31	NH2	L_ASP_93	OD2	3.671
4FQI	L_ARG_61	NH2	L_GLU_81	OE2	3.854
4FQI	L_ARG_61	NH2	L_ASP_82	OD1	2.818
4FQI	L_ARG_61	NH2	L_ASP_82	OD2	3.558

Table 513: 4FQI-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4G6A	C_ARG_38	NH1	C_ASP_86	OD1	2.901
4G6A	C_ARG_38	NH2	C_GLU_46	OE1	2.973
4G6A	C_ARG_38	NH2	C_ASP_86	OD1	3.508
4G6A	C_ARG_64	NH1	D_ASP_94	OD1	3.792
4G6A	C_ARG_64	NH1	D_ASP_94	OD2	3.701
4G6A	C_ARG_66	NH1	C_ASP_86	OD1	3.401
4G6A	C_ARG_66	NH1	C_ASP_86	OD2	2.759
4G6A	C_ARG_66	NH2	C_ASP_86	OD1	2.824
4G6A	C_ARG_66	NH2	C_ASP_86	OD2	3.567
4G6A	C_LYS_143	NZ	C_ASP_144	OD1	3.200
4G6A	C_LYS_143	NZ	C_ASP_144	OD2	3.786
4G6A	C_LYS_209	NZ	D_GLU_123	OE1	2.784
4G6A	C_LYS_209	NZ	D_GLU_123	OE2	3.529
4G6A	C_LYS_210	NZ	C_GLU_212	OE2	3.247
4G6A	D_ARG_18	NH2	D_ASP_76	OD2	2.934
4G6A	D_ARG_18	NH2	L_GLU_27	OE2	3.721
4G6A	D_LYS_39	NZ	D_ASP_81	OD1	2.823
4G6A	D_ARG_61	NH1	D_ASP_82	OD1	3.328
4G6A	D_ARG_61	NH1	D_ASP_82	OD2	2.369
4G6A	D_ARG_61	NH2	D_ASP_82	OD1	2.953
4G6A	D_ARG_61	NH2	D_ASP_82	OD2	3.506
4G6A	D_LYS_149	NZ	D_GLU_195	OE1	3.087
4G6A	D_LYS_183	NZ	D_GLU_187	OE1	3.747
4G6A	D_LYS_183	NZ	D_GLU_187	OE2	3.452
4G6A	D_LYS_188	NZ	D_ASP_185	OD1	3.129
4G6A	D_HIS_189	ND1	D_ASP_151	OD2	3.322
4G6A	D_LYS_190	NZ	D_GLU_213	OE2	2.978
4G6A	H_ARG_38	NH1	H_ASP_86	OD1	3.081
4G6A	H_ARG_38	NH2	H_GLU_46	OE1	3.078
4G6A	H_ARG_38	NH2	H_ASP_86	OD1	3.738
4G6A	H_ARG_64	NH2	L_ASP_94	OD1	3.443
4G6A	H_ARG_64	NH2	L_ASP_94	OD2	3.275
4G6A	H_ARG_66	NH1	H_ASP_86	OD1	3.684
4G6A	H_ARG_66	NH1	H_ASP_86	OD2	3.528
4G6A	H_ARG_66	NH2	H_ASP_86	OD1	2.640
4G6A	H_ARG_66	NH2	H_ASP_86	OD2	3.507
4G6A	H_LYS_143	NZ	H_ASP_144	OD1	3.327
4G6A	H_LYS_143	NZ	H_ASP_144	OD2	3.934
4G6A	H_LYS_206	NZ	H_ASP_208	OD1	2.915
4G6A	H_LYS_206	NZ	H_ASP_208	OD2	3.666
4G6A	H_LYS_209	NZ	L_GLU_123	OE1	2.940
4G6A	H_LYS_209	NZ	L_GLU_123	OE2	3.622
4G6A	H_LYS_210	NZ	H_GLU_212	OE2	3.489
4G6A	L_ARG_18	NH2	L_ASP_76	OD2	3.695
4G6A	L_LYS_39	NZ	L_ASP_81	OD1	2.869
4G6A	L_LYS_39	NZ	L_ASP_81	OD2	3.930
4G6A	L_ARG_61	NH1	L_ASP_82	OD1	3.564
4G6A	L_ARG_61	NH1	L_ASP_82	OD2	2.948
4G6A	L_ARG_61	NH2	L_ASP_82	OD1	3.384
4G6A	L_LYS_149	NZ	L_GLU_195	OE2	3.404
4G6A	L_LYS_183	NZ	L_GLU_187	OE1	3.001
4G6A	L_LYS_183	NZ	L_GLU_187	OE2	3.388
4G6A	L_LYS_190	NZ	L_GLU_213	OE2	3.611

Table 514: 4G6A-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4G6F	H_ARG_38	NH1	H_ASP_86	OD1	2.906
4G6F	H_ARG_38	NH2	H_GLU_46	OE1	3.116
4G6F	H_ARG_38	NH2	H_GLU_46	OE2	3.531
4G6F	H_ARG_38	NH2	H_ASP_86	OD1	3.904
4G6F	H_ARG_50	NH1	H_ASP_58	OD2	3.658
4G6F	H_ARG_50	NH1	H_GLU_100J	OE1	3.226
4G6F	H_ARG_50	NH1	H_GLU_100J	OE2	2.985
4G6F	H_ARG_50	NH2	H_ASP_58	OD2	2.110
4G6F	H_ARG_66	NH1	H_ASP_86	OD1	3.936
4G6F	H_ARG_66	NH1	H_ASP_86	OD2	2.633
4G6F	H_ARG_66	NH2	H_ASP_86	OD1	3.136
4G6F	H_ARG_66	NH2	H_ASP_86	OD2	3.299
4G6F	H_ARG_83	NH2	H_GLU_85	OE1	3.916
4G6F	H_ARG_94	NH2	H_ASP_102	OD2	3.304
4G6F	H_LYS_143	NZ	H_ASP_144	OD2	3.573
4G6F	H_LYS_143	NZ	L_GLU_125	OE2	3.341
4G6F	H_LYS_209	NZ	L_GLU_124	OE1	3.080
4G6F	H_LYS_209	NZ	L_GLU_124	OE2	2.558
4G6F	H_ARG_210	NH1	H_GLU_212	OE2	3.716
4G6F	B_ARG_38	NH1	B_ASP_86	OD1	3.151
4G6F	B_ARG_38	NH2	B_GLU_46	OE1	3.414
4G6F	B_ARG_38	NH2	B_GLU_46	OE2	3.922
4G6F	B_ARG_50	NH1	B_ASP_58	OD2	3.630
4G6F	B_ARG_50	NH1	B_GLU_100J	OE1	3.222
4G6F	B_ARG_50	NH1	B_GLU_100J	OE2	2.975
4G6F	B_ARG_50	NH2	B_ASP_58	OD2	2.343
4G6F	B_ARG_66	NH1	B_ASP_86	OD1	3.598
4G6F	B_ARG_66	NH1	B_ASP_86	OD2	2.769
4G6F	B_ARG_66	NH2	B_ASP_86	OD1	2.916
4G6F	B_ARG_66	NH2	B_ASP_86	OD2	3.570
4G6F	B_ARG_83	NH2	B_GLU_85	OE1	3.938
4G6F	B_ARG_94	NH2	B_ASP_102	OD2	3.253
4G6F	B_LYS_143	NZ	D_GLU_125	OE2	2.735
4G6F	B_LYS_209	NZ	D_GLU_124	OE1	3.470
4G6F	B_LYS_209	NZ	D_GLU_124	OE2	2.107
4G6F	L_ARG_29	NH1	L_ASP_26	OD1	3.314
4G6F	L_HIS_31	ND1	H_GLU_100I	OE2	2.912
4G6F	L_ARG_54	NH1	L_ASP_60	OD1	3.621
4G6F	L_ARG_61	NH2	L_GLU_81	OE1	3.555
4G6F	L_ARG_61	NH2	L_ASP_82	OD1	2.760
4G6F	L_ARG_61	NH2	L_ASP_82	OD2	3.527
4G6F	L_ARG_91	NH1	H_GLU_100J	OE2	2.715
4G6F	L_ARG_91	NH2	H_GLU_100J	OE2	2.951
4G6F	L_LYS_103	NZ	L_ASP_83	OD1	2.500
4G6F	L_LYS_111	NZ	L_GLU_199	OE1	3.003
4G6F	L_LYS_150	NZ	L_GLU_204	OE2	2.904
4G6F	D_HIS_31	ND1	B_GLU_100I	OE2	2.954
4G6F	D_ARG_54	NH1	D_ASP_60	OD1	3.426
4G6F	D_ARG_61	NH2	D_ASP_82	OD1	2.776
4G6F	D_ARG_61	NH2	D_ASP_82	OD2	3.304
4G6F	D_ARG_91	NH1	B_GLU_100J	OE2	2.854
4G6F	D_ARG_91	NH2	B_GLU_100J	OE2	2.880
4G6F	D_ARG_95B	NH2	B_ASP_58	OD1	3.343
4G6F	D_LYS_103	NZ	D_ASP_83	OD1	2.777
4G6F	D_LYS_111	NZ	D_GLU_199	OE1	3.031
4G6F	D_LYS_150	NZ	D_GLU_204	OE1	3.970
4G6F	D_LYS_150	NZ	D_GLU_204	OE2	2.492

4G6F	D_LYS_167	NZ	D_ASP_83	OD2	3.935
4G6F	D_LYS_172	NZ	D_ASP_139	OD2	3.592
4G6F	D_ARG_190	NH2	D_ASP_152	OD2	3.898
4G6F	P_LYS_665	NZ	P_GLU_662	OE2	3.965
4G6F	F_LYS_665	NZ	F_GLU_662	OE1	3.301
4G6F	F_LYS_665	NZ	F_GLU_662	OE2	2.956

Table 515: 4G6F-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4GMT	L_LYS_24	NZ	L_ASP_70	OD1	3.260
4GMT	L_LYS_24	NZ	L_ASP_70	OD2	3.149
4GMT	L_ARG_61	NH2	L_GLU_81	OE2	3.799
4GMT	L_ARG_61	NH2	L_ASP_82	OD1	3.260
4GMT	L_ARG_61	NH2	L_ASP_82	OD2	2.628
4GMT	L_ARG_108	NH1	L_ASP_170	OD1	3.942
4GMT	L_LYS_142	NZ	L_ASP_143	OD1	3.297
4GMT	L_LYS_142	NZ	L_ASP_143	OD2	2.972
4GMT	L_LYS_147	NZ	L_GLU_195	OE1	3.733
4GMT	L_LYS_149	NZ	L_GLU_195	OE2	3.437
4GMT	L_ARG_155	NH1	L_GLU_185	OE2	3.030
4GMT	L_ARG_155	NH2	L_GLU_185	OE1	3.075
4GMT	L_ARG_155	NH2	L_GLU_185	OE2	2.988
4GMT	L_HIS_189	ND1	L_ASP_151	OD2	3.653
4GMT	L_LYS_199	NZ	L_ASP_110	OD2	2.866
4GMT	L_ARG_211	NH1	L_GLU_187	OE2	3.717
4GMT	H_LYS_12	NZ	H_GLU_10	OE1	3.698
4GMT	H_ARG_40	NH1	H_GLU_85	OE1	3.459
4GMT	H_ARG_40	NH2	H_GLU_85	OE1	3.548
4GMT	H_LYS_64	NZ	H_GLU_61	OE1	3.355
4GMT	H_LYS_64	NZ	H_GLU_61	OE2	3.496
4GMT	H_LYS_66	NZ	H_ASP_86	OD2	3.279
4GMT	H_HIS_164	NE2	L_ASP_167	OD2	3.650
4GMT	H_LYS_205	NZ	H_ASP_207	OD1	2.972
4GMT	H_LYS_205	NZ	H_ASP_207	OD2	3.617
4GMT	M_ARG_61	NH1	M_GLU_81	OE2	3.800
4GMT	M_ARG_61	NH2	M_GLU_81	OE2	3.404
4GMT	M_ARG_61	NH2	M_ASP_82	OD1	3.417
4GMT	M_ARG_61	NH2	M_ASP_82	OD2	2.761
4GMT	M_LYS_103	NZ	M_GLU_85	OE1	3.664
4GMT	M_LYS_107	NZ	M_ASP_17	OD2	3.878
4GMT	M_LYS_142	NZ	M_ASP_143	OD1	2.867
4GMT	M_ARG_155	NH1	M_GLU_185	OE1	3.423
4GMT	M_ARG_188	NH2	M_GLU_185	OE2	2.544
4GMT	M_LYS_199	NZ	M_ASP_110	OD2	3.054
4GMT	I_LYS_38	NZ	I_GLU_46	OE1	3.821
4GMT	I_ARG_40	NH1	I_GLU_85	OE1	2.810
4GMT	I_ARG_40	NH2	I_GLU_85	OE1	3.101
4GMT	I_ARG_40	NH2	I_GLU_85	OE2	3.496
4GMT	I_LYS_64	NZ	I_GLU_61	OE1	2.992
4GMT	I_LYS_66	NZ	I_ASP_86	OD1	3.775
4GMT	I_LYS_66	NZ	I_ASP_86	OD2	3.105
4GMT	I_LYS_205	NZ	I_ASP_207	OD1	3.730

Table 516: 4GMT-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4GXU	A_LYS_	NZ	F_GLU_	OE1	3.529
4GXU	A_LYS_	NZ	F_GLU_	OE2	3.469
4GXU	A_LYS_53	NZ	A_ASP_276	OD1	3.005
4GXU	A_LYS_	NZ	A_GLU_75	OE1	2.922
4GXU	A_ARG_109	NH1	A_GLU_89	OE1	2.638
4GXU	A_ARG_109	NH1	A_GLU_89	OE2	3.793
4GXU	A_ARG_109	NH2	A_GLU_89	OE1	3.235
4GXU	A_ARG_109	NH2	A_GLU_89	OE2	3.010
4GXU	A_ARG_109	NH2	B_GLU_69	OE1	3.987
4GXU	A_ARG_109	NH2	B_GLU_69	OE2	3.286
4GXU	A_ARG_149	NH2	A_ASP_77	OD1	3.644
4GXU	A_ARG_149	NH2	A_ASP_77	OD2	2.613
4GXU	A_LYS_163	NZ	A_GLU_246	OE1	2.988
4GXU	A_LYS_163	NZ	A_GLU_246	OE2	3.949
4GXU	A_LYS_174	NZ	A_GLU_119	OE1	2.547
4GXU	A_LYS_174	NZ	A_GLU_119	OE2	3.226
4GXU	A_LYS_208	NZ	A_GLU_238	OE1	3.242
4GXU	A_LYS_208	NZ	A_GLU_238	OE2	3.214
4GXU	A_ARG_262	NH2	A_GLU_175	OE1	3.438
4GXU	A_ARG_262	NH2	A_GLU_175	OE2	2.905
4GXU	A_ARG_	NH1	B_ASP_	OD1	2.648
4GXU	A_ARG_	NH2	B_ASP_	OD1	2.545
4GXU	A_ARG_	NH1	A_GLU_	OE2	3.223
4GXU	A_ARG_	NH2	A_GLU_	OE2	3.931
4GXU	B_LYS_	NZ	B_GLU_	OE1	2.602
4GXU	B_LYS_58	NZ	B_GLU_57	OE1	3.935
4GXU	B_LYS_58	NZ	D_GLU_97	OE1	3.748
4GXU	B_LYS_68	NZ	A_GLU_110	OE2	3.492
4GXU	B_ARG_76	NH1	F_GLU_74	OE1	3.015
4GXU	B_ARG_76	NH1	F_GLU_74	OE2	2.935
4GXU	B_ARG_76	NH2	E_GLU_107	OE2	3.559
4GXU	B_ARG_76	NH2	F_GLU_74	OE2	2.547
4GXU	B_LYS_83	NZ	F_ASP_85	OD1	3.431
4GXU	B_LYS_83	NZ	F_ASP_85	OD2	3.614
4GXU	B_ARG_	NH2	D_ASP_	OD2	3.432
4GXU	B_ARG_	NH1	F_GLU_	OE1	3.168
4GXU	B_ARG_	NH2	F_GLU_	OE1	3.085
4GXU	B_ARG_	NH2	F_GLU_	OE2	3.110
4GXU	B_LYS_	NZ	B_GLU_	OE1	3.038
4GXU	B_LYS_	NZ	B_GLU_	OE2	3.952
4GXU	B_ARG_	NH1	B_GLU_	OE2	2.823
4GXU	B_LYS_	NZ	B_GLU_	OE1	3.999
4GXU	C_LYS_32	NZ	B_GLU_57	OE1	3.823
4GXU	C_LYS_32	NZ	B_GLU_57	OE2	3.681
4GXU	C_LYS_	NZ	C_ASP_276	OD1	3.258
4GXU	C_LYS_63	NZ	C_GLU_75	OE1	3.089
4GXU	C_ARG_109	NH1	C_GLU_89	OE1	2.661
4GXU	C_ARG_109	NH1	C_GLU_89	OE2	3.514
4GXU	C_ARG_109	NH2	C_GLU_89	OE1	3.287
4GXU	C_ARG_109	NH2	C_GLU_89	OE2	2.852
4GXU	C_ARG_109	NH2	D_GLU_69	OE1	3.507
4GXU	C_ARG_109	NH2	D_GLU_69	OE2	3.205
4GXU	C_ARG_149	NH2	C_ASP_77	OD1	3.970
4GXU	C_ARG_149	NH2	C_ASP_77	OD2	3.229
4GXU	C_LYS_163	NZ	C_GLU_246	OE1	3.356
4GXU	C_LYS_	NZ	C_GLU_119	OE1	2.755
4GXU	C_LYS_	NZ	C_GLU_119	OE2	2.730

4GXU	C_LYS_208	NZ	C_GLU_238	OE1	3.337
4GXU	C_LYS_208	NZ	C_GLU_238	OE2	3.528
4GXU	C_LYS_	NZ	C_GLU_	OE2	3.454
4GXU	C_ARG_310	NH1	D_ASP_90	OD1	3.385
4GXU	C_ARG_310	NH2	D_ASP_90	OD1	3.336
4GXU	C_ARG_321	NH1	C_GLU_31	OE2	3.152
4GXU	C_ARG_321	NH2	C_GLU_31	OE2	3.675
4GXU	D_HIS_	NE2	D_ASP_	OD1	3.647
4GXU	D_LYS_	NZ	D_GLU_	OE1	2.571
4GXU	D_LYS_	NZ	D_GLU_	OE1	3.860
4GXU	D_LYS_68	NZ	C_GLU_110	OE2	3.981
4GXU	D_ARG_76	NH1	B_GLU_74	OE1	2.948
4GXU	D_ARG_76	NH1	B_GLU_74	OE2	3.453
4GXU	D_ARG_76	NH2	A_GLU_107	OE2	3.465
4GXU	D_ARG_76	NH2	B_GLU_74	OE1	3.835
4GXU	D_ARG_76	NH2	B_GLU_74	OE2	2.916
4GXU	D_LYS_83	NZ	B_ASP_85	OD1	3.057
4GXU	D_LYS_83	NZ	B_ASP_85	OD2	3.527
4GXU	D_ARG_	NH2	F_ASP_	OD2	3.392
4GXU	D_ARG_	NH1	B_GLU_	OE1	2.743
4GXU	D_ARG_	NH1	B_GLU_	OE2	3.931
4GXU	D_ARG_	NH2	B_GLU_	OE1	2.897
4GXU	D_ARG_	NH2	B_GLU_	OE2	2.579
4GXU	D_ARG_	NH2	D_GLU_	OE2	3.558
4GXU	D_LYS_	NZ	D_GLU_	OE1	3.191
4GXU	D_LYS_	NZ	D_GLU_	OE2	3.786
4GXU	D_ARG_	NH1	D_GLU_	OE2	2.518
4GXU	D_LYS_	NZ	D_GLU_	OE1	3.949
4GXU	E_LYS_	NZ	D_GLU_	OE1	3.848
4GXU	E_LYS_	NZ	D_GLU_	OE2	3.549
4GXU	E_LYS_	NZ	E_ASP_	OD1	3.280
4GXU	E_LYS_	NZ	E_GLU_	OE1	3.829
4GXU	E_LYS_	NZ	E_GLU_	OE1	2.868
4GXU	E_ARG_109	NH1	E_GLU_89	OE1	2.836
4GXU	E_ARG_109	NH1	E_GLU_89	OE2	3.830
4GXU	E_ARG_109	NH2	E_GLU_89	OE1	3.271
4GXU	E_ARG_109	NH2	E_GLU_89	OE2	2.995
4GXU	E_ARG_109	NH2	F_GLU_69	OE1	3.819
4GXU	E_ARG_109	NH2	F_GLU_69	OE2	3.459
4GXU	E_ARG_149	NH2	E_ASP_77	OD2	3.169
4GXU	E_LYS_163	NZ	E_GLU_246	OE1	3.757
4GXU	E_LYS_	NZ	E_GLU_	OE1	2.406
4GXU	E_LYS_	NZ	E_GLU_	OE2	3.375
4GXU	E_LYS_208	NZ	E_GLU_	OE1	3.387
4GXU	E_LYS_208	NZ	E_GLU_238	OE2	3.285
4GXU	E_ARG_262	NH2	E_GLU_	OE1	3.936
4GXU	E_ARG_262	NH2	E_GLU_	OE2	3.458
4GXU	E_LYS_	NZ	E_GLU_	OE2	3.797
4GXU	E_ARG_310	NH1	F_ASP_90	OD1	2.704
4GXU	E_ARG_310	NH2	F_ASP_90	OD1	2.770
4GXU	E_ARG_	NH1	E_GLU_	OE1	3.512
4GXU	E_ARG_	NH1	E_GLU_	OE2	2.851
4GXU	E_ARG_	NH2	E_GLU_	OE2	3.048
4GXU	F_LYS_	NZ	F_GLU_	OE1	2.531
4GXU	F_LYS_	NZ	B_GLU_	OE1	3.893
4GXU	F_LYS_68	NZ	E_GLU_110	OE2	3.968
4GXU	F_ARG_76	NH1	D_GLU_74	OE1	2.787
4GXU	F_ARG_76	NH1	D_GLU_74	OE2	3.366

4GXU	F_ARG_76	NH2	C_GLU_107	OE2	3.548
4GXU	F_ARG_76	NH2	D_GLU_74	OE1	3.616
4GXU	F_ARG_76	NH2	D_GLU_74	OE2	2.732
4GXU	F_LYS_83	NZ	D_ASP_85	OD1	3.339
4GXU	F_LYS_83	NZ	D_ASP_85	OD2	3.717
4GXU	F_ARG_	NH2	B_ASP_	OD2	3.670
4GXU	F_ARG_	NH1	D_GLU_	OE1	3.077
4GXU	F_ARG_	NH2	D_GLU_	OE1	2.952
4GXU	F_ARG_	NH2	D_GLU_	OE2	3.074
4GXU	F_ARG_	NH2	F_GLU_	OE2	3.328
4GXU	F_LYS_	NZ	F_GLU_	OE1	3.535
4GXU	F_LYS_	NZ	F_GLU_	OE2	3.712
4GXU	F_ARG_	NH1	F_GLU_	OE2	2.854
4GXU	G_LYS_	NZ	J_GLU_	OE1	3.601
4GXU	G_LYS_	NZ	J_GLU_	OE2	3.403
4GXU	G_LYS_	NZ	G_ASP_	OD1	3.005
4GXU	G_LYS_	NZ	G_GLU_	OE1	2.980
4GXU	G_ARG_	NH1	G_GLU_	OE1	2.812
4GXU	G_ARG_	NH1	G_GLU_	OE2	3.396
4GXU	G_ARG_	NH2	G_GLU_	OE1	3.672
4GXU	G_ARG_	NH2	G_GLU_	OE2	2.896
4GXU	G_ARG_	NH2	H_GLU_	OE2	3.183
4GXU	G_ARG_	NH2	G_ASP_	OD1	3.470
4GXU	G_ARG_	NH2	G_ASP_	OD2	2.671
4GXU	G_LYS_	NZ	G_GLU_	OE1	3.089
4GXU	G_LYS_	NZ	G_GLU_	OE2	3.833
4GXU	G_LYS_	NZ	G_GLU_	OE1	2.593
4GXU	G_LYS_	NZ	G_GLU_	OE2	3.863
4GXU	G_LYS_	NZ	G_GLU_	OE1	3.478
4GXU	G_ARG_	NH2	G_GLU_	OE1	3.819
4GXU	G_ARG_	NH2	G_GLU_	OE2	3.300
4GXU	G_ARG_	NH1	H_ASP_	OD1	2.337
4GXU	G_ARG_	NH2	H_ASP_	OD1	2.900
4GXU	G_ARG_	NH1	G_ASP_	OD1	3.664
4GXU	G_ARG_	NH1	G_GLU_	OE1	3.532
4GXU	G_ARG_	NH1	G_GLU_	OE2	3.002
4GXU	G_ARG_	NH2	G_GLU_	OE2	3.072
4GXU	H_HIS_	NE2	H_ASP_	OD1	3.881
4GXU	H_LYS_	NZ	H_GLU_	OE1	2.920
4GXU	H_LYS_	NZ	L_GLU_	OE1	3.639
4GXU	H_LYS_	NZ	G_GLU_	OE2	3.438
4GXU	H_ARG_	NH1	J_GLU_	OE1	2.612
4GXU	H_ARG_	NH1	J_GLU_	OE2	3.374
4GXU	H_ARG_	NH2	L_GLU_	OE2	3.506
4GXU	H_ARG_	NH2	J_GLU_	OE1	3.326
4GXU	H_ARG_	NH2	J_GLU_	OE2	2.517
4GXU	H_LYS_	NZ	J_ASP_	OD1	2.938
4GXU	H_LYS_	NZ	J_ASP_	OD2	3.368
4GXU	H_ARG_	NH2	L_ASP_	OD2	3.212
4GXU	H_ARG_	NH1	J_GLU_	OE1	3.044
4GXU	H_ARG_	NH2	J_GLU_	OE1	2.714
4GXU	H_ARG_	NH2	J_GLU_	OE2	3.067
4GXU	H_LYS_	NZ	H_GLU_	OE1	3.090
4GXU	H_ARG_	NH1	H_GLU_	OE2	2.508
4GXU	H_LYS_	NZ	H_GLU_	OE1	3.808
4GXU	H_LYS_	NZ	H_GLU_	OE2	3.001
4GXU	I_LYS_	NZ	L_GLU_	OE1	3.747
4GXU	I_LYS_	NZ	L_GLU_	OE2	3.353

4GXU	I.LYS_	NZ	I.ASP_	OD1	3.170
4GXU	I.LYS_	NZ	I.GLU_	OE1	2.809
4GXU	I.ARG_	NH1	I.GLU_	OE1	2.622
4GXU	I.ARG_	NH1	I.GLU_	OE2	3.326
4GXU	I.ARG_	NH2	I.GLU_	OE1	3.446
4GXU	I.ARG_	NH2	I.GLU_	OE2	2.752
4GXU	I.ARG_	NH2	J.GLU_	OE1	3.762
4GXU	I.ARG_	NH2	J.GLU_	OE2	2.924
4GXU	I.ARG_	NH2	I.ASP_	OD1	3.969
4GXU	I.ARG_	NH2	I.ASP_	OD2	2.932
4GXU	I.LYS_	NZ	I.GLU_	OE1	3.315
4GXU	I.LYS_	NZ	I.GLU_	OE2	3.981
4GXU	I.LYS_	NZ	I.GLU_	OE1	2.410
4GXU	I.LYS_	NZ	I.GLU_	OE2	3.536
4GXU	I.LYS_	NZ	I.GLU_	OE1	3.215
4GXU	I.ARG_	NH2	I.GLU_	OE2	3.984
4GXU	I.LYS_	NZ	I.GLU_	OE1	3.949
4GXU	I.LYS_	NZ	I.GLU_	OE2	3.673
4GXU	I.ARG_	NH1	J.ASP_	OD1	2.388
4GXU	I.ARG_	NH2	J.ASP_	OD1	2.649
4GXU	I.ARG_	NH1	I.GLU_	OE1	3.395
4GXU	I.ARG_	NH1	I.GLU_	OE2	2.991
4GXU	I.ARG_	NH2	I.GLU_	OE2	3.022
4GXU	J.HIS_	NE2	J.ASP_	OD1	3.723
4GXU	J.LYS_	NZ	J.GLU_	OE1	2.696
4GXU	J.LYS_	NZ	H.GLU_	OE1	3.949
4GXU	J.LYS_	NZ	I.GLU_	OE2	3.674
4GXU	J.ARG_	NH1	L.GLU_	OE1	2.912
4GXU	J.ARG_	NH1	L.GLU_	OE2	3.322
4GXU	J.ARG_	NH2	K.GLU_	OE2	3.542
4GXU	J.ARG_	NH2	L.GLU_	OE1	3.621
4GXU	J.ARG_	NH2	L.GLU_	OE2	2.520
4GXU	J.LYS_	NZ	L.ASP_	OD1	3.139
4GXU	J.LYS_	NZ	L.ASP_	OD2	3.566
4GXU	J.ARG_	NH2	H.ASP_	OD2	3.270
4GXU	J.ARG_	NH1	L.GLU_	OE1	3.377
4GXU	J.ARG_	NH2	J.GLU_	OE2	3.805
4GXU	J.ARG_	NH2	L.GLU_	OE1	2.504
4GXU	J.ARG_	NH2	L.GLU_	OE2	3.208
4GXU	J.LYS_	NZ	J.GLU_	OE1	3.200
4GXU	J.LYS_	NZ	J.GLU_	OE2	3.922
4GXU	J.ARG_	NH1	J.GLU_	OE2	2.706
4GXU	J.LYS_	NZ	J.GLU_	OE1	3.514
4GXU	J.LYS_	NZ	J.GLU_	OE2	3.322
4GXU	K.LYS_	NZ	H.GLU_	OE2	3.068
4GXU	K.LYS_	NZ	K.ASP_	OD1	3.466
4GXU	K.LYS_	NZ	K.GLU_	OE1	2.616
4GXU	K.ARG_	NH1	K.GLU_	OE1	2.847
4GXU	K.ARG_	NH1	K.GLU_	OE2	3.789
4GXU	K.ARG_	NH2	K.GLU_	OE1	3.337
4GXU	K.ARG_	NH2	K.GLU_	OE2	2.934
4GXU	K.ARG_	NH2	L.GLU_	OE1	3.835
4GXU	K.ARG_	NH2	L.GLU_	OE2	3.159
4GXU	K.ARG_	NH2	K.ASP_	OD1	3.461
4GXU	K.ARG_	NH2	K.ASP_	OD2	2.584
4GXU	K.LYS_	NZ	K.GLU_	OE1	2.688
4GXU	K.LYS_	NZ	K.GLU_	OE2	3.997
4GXU	K.LYS_	NZ	K.GLU_	OE1	3.262

4GXU	K_LYS_	NZ	K_GLU_	OE2	2.919
4GXU	K_ARG_	NH2	K_GLU_	OE1	3.557
4GXU	K_ARG_	NH2	K_GLU_	OE2	3.243
4GXU	K_ARG_	NH1	L_ASP_	OD1	2.447
4GXU	K_ARG_	NH2	L_ASP_	OD1	2.754
4GXU	K_ARG_	NH1	K_GLU_	OE1	3.546
4GXU	K_ARG_	NH1	K_GLU_	OE2	2.807
4GXU	K_ARG_	NH2	K_GLU_	OE2	3.397
4GXU	L_LYS_	NZ	L_GLU_	OE1	2.769
4GXU	L_LYS_	NZ	J_GLU_	OE1	3.674
4GXU	L_LYS_	NZ	L_GLU_	OE1	3.962
4GXU	L_LYS_	NZ	K_GLU_	OE2	3.305
4GXU	L_ARG_	NH1	H_GLU_	OE1	2.958
4GXU	L_ARG_	NH1	H_GLU_	OE2	3.138
4GXU	L_ARG_	NH2	G_GLU_	OE2	3.886
4GXU	L_ARG_	NH2	H_GLU_	OE1	3.887
4GXU	L_ARG_	NH2	H_GLU_	OE2	2.595
4GXU	L_LYS_	NZ	H_ASP_	OD1	2.732
4GXU	L_LYS_	NZ	H_ASP_	OD2	3.190
4GXU	L_ARG_	NH2	J_ASP_	OD2	3.583
4GXU	L_ARG_	NH1	H_GLU_	OE1	3.044
4GXU	L_ARG_	NH2	H_GLU_	OE1	2.477
4GXU	L_ARG_	NH2	H_GLU_	OE2	3.036
4GXU	L_ARG_	NH2	L_GLU_	OE2	3.856
4GXU	L_LYS_	NZ	L_GLU_	OE1	2.914
4GXU	L_LYS_	NZ	L_GLU_	OE2	3.773
4GXU	L_LYS_	NZ	L_GLU_	OE2	3.996
4GXU	L_LYS_	NZ	L_GLU_	OE1	3.816
4GXU	L_ARG_	NH1	L_GLU_	OE1	3.472
4GXU	L_LYS_	NZ	L_GLU_	OE1	3.566
4GXU	M_ARG_	NH2	H_GLU_	OE2	3.356
4GXU	M_HIS_35	NE2	M_GLU_95	OE1	2.618
4GXU	M_ARG_	NH1	M_ASP_	OD1	2.787
4GXU	M_ARG_	NH2	M_GLU_46	OE1	3.155
4GXU	M_ARG_	NH2	M_GLU_46	OE2	3.384
4GXU	M_ARG_	NH2	M_ASP_	OD1	3.807
4GXU	M_ARG_	NH1	M_ASP_	OD1	2.866
4GXU	M_ARG_	NH1	M_ASP_	OD1	3.767
4GXU	M_ARG_	NH1	M_ASP_	OD2	2.685
4GXU	M_ARG_	NH2	M_ASP_	OD1	3.010
4GXU	M_ARG_	NH2	M_ASP_	OD2	3.446
4GXU	M_LYS_	NZ	N_GLU_	OE2	2.851
4GXU	M_LYS_	NZ	N_GLU_	OE1	3.371
4GXU	M_ARG_210	NH1	M_GLU_212	OE2	3.375
4GXU	N_ARG_61	NH1	N_ASP_82	OD1	3.079
4GXU	N_ARG_61	NH1	N_ASP_82	OD2	3.905
4GXU	N_ARG_61	NH2	N_ASP_82	OD1	3.806
4GXU	N_ARG_61	NH2	N_ASP_82	OD2	3.473
4GXU	N_HIS_95C	NE2	N_ASP_92	OD2	3.978
4GXU	N_LYS_149	NZ	N_GLU_203	OE1	3.458
4GXU	N_LYS_149	NZ	N_GLU_203	OE2	3.365
4GXU	N_LYS_	NZ	N_GLU_	OE2	3.800
4GXU	N_ARG_189	NH2	N_ASP_151	OD2	3.992
4GXU	O_HIS_35	NE2	O_GLU_95	OE1	2.632
4GXU	O_ARG_38	NH1	O_ASP_86	OD1	2.799
4GXU	O_ARG_38	NH2	O_GLU_46	OE1	3.065
4GXU	O_ARG_38	NH2	O_GLU_46	OE2	3.637
4GXU	O_ARG_38	NH2	O_ASP_86	OD1	3.453

4GXU	O_ARG_55	NH1	O_ASP_53	OD1	3.043
4GXU	O_ARG_66	NH1	O_ASP_86	OD2	2.898
4GXU	O_ARG_66	NH2	O_ASP_86	OD1	3.023
4GXU	O_ARG_66	NH2	O_ASP_86	OD2	2.955
4GXU	P_ARG_61	NH1	P_ASP_82	OD1	2.845
4GXU	P_ARG_61	NH2	P_ASP_82	OD1	3.213
4GXU	P_ARG_61	NH2	P_ASP_82	OD2	3.256
4GXU	P_HIS_95C	NE2	P_ASP_92	OD2	3.801
4GXU	Q_HIS_35	NE2	Q_GLU_95	OE1	2.629
4GXU	Q_ARG_38	NH1	Q_ASP_	OD1	2.771
4GXU	Q_ARG_38	NH2	Q_GLU_46	OE1	3.023
4GXU	Q_ARG_38	NH2	Q_GLU_46	OE2	3.310
4GXU	Q_ARG_38	NH2	Q_ASP_	OD1	3.767
4GXU	Q_ARG_	NH1	Q_ASP_53	OD1	2.937
4GXU	Q_ARG_	NH1	Q_ASP_	OD2	3.290
4GXU	Q_ARG_	NH2	Q_ASP_	OD1	3.283
4GXU	Q_ARG_	NH2	Q_ASP_	OD2	3.512
4GXU	Q_LYS_143	NZ	R_GLU_124	OE2	3.025
4GXU	Q_LYS_209	NZ	R_GLU_123	OE1	3.619
4GXU	Q_LYS_209	NZ	R_GLU_123	OE2	3.564
4GXU	Q_ARG_210	NH1	Q_GLU_212	OE2	3.790
4GXU	R_ARG_61	NH1	R_ASP_82	OD1	3.111
4GXU	R_ARG_61	NH2	R_ASP_82	OD1	3.457
4GXU	R_ARG_61	NH2	R_ASP_82	OD2	3.282
4GXU	R_HIS_95C	NE2	R_ASP_92	OD2	3.471
4GXU	R_LYS_103	NZ	R_GLU_83	OE1	3.281
4GXU	R_LYS_149	NZ	R_GLU_203	OE1	3.940
4GXU	R_LYS_149	NZ	R_GLU_203	OE2	3.587
4GXU	R_LYS_166	NZ	R_GLU_83	OE1	3.059
4GXU	R_ARG_189	NH2	R_ASP_151	OD2	3.874
4GXU	S_HIS_	NE2	S_GLU_	OE1	2.529
4GXU	S_ARG_	NH1	S_ASP_	OD1	2.740
4GXU	S_ARG_	NH2	S_GLU_	OE1	3.285
4GXU	S_ARG_	NH2	S_GLU_	OE2	3.746
4GXU	S_ARG_	NH2	S_ASP_	OD1	2.949
4GXU	S_ARG_	NH1	S_ASP_	OD1	3.061
4GXU	S_ARG_	NH1	S_ASP_	OD2	3.313
4GXU	S_ARG_	NH2	S_ASP_	OD1	3.673
4GXU	S_ARG_	NH2	S_ASP_	OD2	3.715
4GXU	T_ARG_	NH1	T_ASP_	OD1	3.011
4GXU	T_ARG_	NH1	T_ASP_	OD2	3.957
4GXU	T_ARG_	NH2	T_GLU_	OE2	3.945
4GXU	T_ARG_	NH2	T_ASP_	OD1	3.986
4GXU	T_ARG_	NH2	T_ASP_	OD2	3.749
4GXU	T_HIS_	NE2	T_ASP_	OD1	3.982
4GXU	T_HIS_	NE2	T_ASP_	OD2	3.480
4GXU	U_HIS_	NE2	U_GLU_	OE1	2.653
4GXU	U_ARG_	NH1	U_ASP_	OD1	2.802
4GXU	U_ARG_	NH2	U_GLU_	OE1	3.190
4GXU	U_ARG_	NH2	U_GLU_	OE2	3.845
4GXU	U_ARG_	NH2	U_ASP_	OD1	3.446
4GXU	U_ARG_	NH1	U_ASP_	OD1	2.649
4GXU	U_ARG_	NH1	U_ASP_	OD1	3.706
4GXU	U_ARG_	NH1	U_ASP_	OD2	2.832
4GXU	U_ARG_	NH2	U_ASP_	OD1	3.260
4GXU	U_ARG_	NH2	U_ASP_	OD2	3.829
4GXU	V_ARG_	NH1	V_ASP_	OD1	2.994
4GXU	V_ARG_	NH1	V_ASP_	OD2	3.811

4GXU	V_ARG_	NH2	V_GLU_	OE2	3.535
4GXU	V_ARG_	NH2	V_ASP_	OD1	3.986
4GXU	V_ARG_	NH2	V_ASP_	OD2	3.677
4GXU	V_HIS_	NE2	V_ASP_	OD2	3.617
4GXU	V_LYS_	NZ	V_GLU_	OE1	3.869
4GXU	W_HIS_	NE2	W_GLU_	OE1	2.707
4GXU	W_ARG_	NH1	W_ASP_	OD1	3.050
4GXU	W_ARG_	NH2	W_GLU_	OE1	2.832
4GXU	W_ARG_	NH2	W_GLU_	OE2	3.553
4GXU	W_ARG_	NH2	W_ASP_	OD1	3.987
4GXU	W_ARG_	NH1	W_ASP_	OD1	3.089
4GXU	W_ARG_	NH1	W_ASP_	OD2	3.168
4GXU	W_ARG_	NH2	W_ASP_	OD1	3.409
4GXU	W_ARG_	NH2	W_ASP_	OD2	3.720
4GXU	X_ARG_	NH1	X_ASP_	OD1	2.797
4GXU	X_ARG_	NH1	X_ASP_	OD2	3.814
4GXU	X_ARG_	NH2	X_GLU_	OE2	3.994
4GXU	X_ARG_	NH2	X_ASP_	OD1	3.445
4GXU	X_ARG_	NH2	X_ASP_	OD2	3.232
4GXU	X_HIS_	NE2	X_ASP_	OD2	3.599
4GXU	X_LYS_	NZ	X_GLU_	OE1	3.798

Table 517: 4GXU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4GXV	H_HIS_35	NE2	H_GLU_95	OE1	2.785
4GXV	H_ARG_38	NH1	H_ASP_86	OD1	3.019
4GXV	H_ARG_38	NH2	H_GLU_46	OE1	2.905
4GXV	H_LYS_64	NZ	H_ASP_61	OD2	3.173
4GXV	H_ARG_66	NH1	H_ASP_86	OD1	3.703
4GXV	H_ARG_66	NH1	H_ASP_86	OD2	2.746
4GXV	H_ARG_66	NH2	H_ASP_86	OD1	2.952
4GXV	H_ARG_66	NH2	H_ASP_86	OD2	3.509
4GXV	H_ARG_83	NH2	H_GLU_85	OE2	3.727
4GXV	H_HIS_100C	ND1	H_ASP_100B	OD1	3.205
4GXV	H_LYS_143	NZ	L_GLU_124	OE2	2.866
4GXV	H_LYS_209	NZ	L_GLU_123	OE1	3.472
4GXV	H_LYS_209	NZ	L_GLU_123	OE2	2.731
4GXV	L_ARG_61	NH2	L_GLU_81	OE2	3.689
4GXV	L_ARG_61	NH2	L_ASP_82	OD1	3.502
4GXV	L_ARG_61	NH2	L_ASP_82	OD2	2.802
4GXV	L_HIS_35	NE2	L_GLU_95	OE1	2.829
4GXV	L_ARG_38	NH1	L_ASP_86	OD1	2.848
4GXV	L_ARG_38	NH2	L_GLU_46	OE1	2.855
4GXV	L_ARG_38	NH2	L_GLU_46	OE2	3.582
4GXV	L_ARG_38	NH2	L_ASP_86	OD1	3.824
4GXV	L_ARG_55	NH1	L_ASP_53	OD1	3.307
4GXV	L_ARG_66	NH1	L_ASP_86	OD1	3.857
4GXV	L_ARG_66	NH1	L_ASP_86	OD2	2.776
4GXV	L_ARG_66	NH2	L_ASP_86	OD1	2.973
4GXV	L_ARG_66	NH2	L_ASP_86	OD2	3.413
4GXV	L_LYS_143	NZ	M_GLU_124	OE2	2.455
4GXV	L_LYS_209	NZ	M_GLU_123	OE1	2.930
4GXV	L_LYS_209	NZ	M_GLU_123	OE2	3.487
4GXV	L_ARG_210	NH1	L_GLU_212	OE2	3.879
4GXV	M_ARG_61	NH1	M_ASP_82	OD1	2.653
4GXV	M_ARG_61	NH1	M_ASP_82	OD2	3.622
4GXV	M_ARG_61	NH2	M_ASP_82	OD1	3.282
4GXV	M_ARG_61	NH2	M_ASP_82	OD2	2.922
4GXV	M_HIS_95C	NE2	M_ASP_92	OD2	3.598
4GXV	M_LYS_149	NZ	M_GLU_203	OE1	2.967
4GXV	M_LYS_149	NZ	M_GLU_203	OE2	3.317
4GXV	M_LYS_186	NZ	M_GLU_183	OE2	3.984

Table 518: 4GXV-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4GXX	A_LYS_32	NZ	D_GLU_57	OE1	3.386
4GXX	A_LYS_53	NZ	A_ASP_276	OD1	2.754
4GXX	A_LYS_63	NZ	A_GLU_75	OE1	2.652
4GXX	A_ARG_109	NH1	A_GLU_89	OE1	2.892
4GXX	A_ARG_109	NH1	A_GLU_89	OE2	3.475
4GXX	A_ARG_109	NH2	A_GLU_89	OE1	3.797
4GXX	A_ARG_109	NH2	A_GLU_89	OE2	3.059
4GXX	A_ARG_109	NH2	B_GLU_69	OE2	3.594
4GXX	A_ARG_149	NH2	A_ASP_77	OD1	3.790
4GXX	A_ARG_149	NH2	A_ASP_77	OD2	2.838
4GXX	A_LYS_163	NZ	A_GLU_246	OE1	3.535
4GXX	A_LYS_163	NZ	A_GLU_246	OE2	2.771
4GXX	A_LYS_174	NZ	A_GLU_119	OE1	2.872
4GXX	A_LYS_174	NZ	A_GLU_119	OE2	3.399
4GXX	A_HIS_183	NE2	A_GLU_190	OE2	3.881
4GXX	A_ARG_262	NH2	A_GLU_175	OE1	2.990
4GXX	A_ARG_262	NH2	A_GLU_175	OE2	3.463
4GXX	A_LYS_280	NZ	A_GLU_304	OE2	3.580
4GXX	A_ARG_310	NH1	B_ASP_90	OD1	2.488
4GXX	A_ARG_310	NH2	B_ASP_90	OD1	2.951
4GXX	A_ARG_315	NH1	A_ASP_24	OD1	3.593
4GXX	A_ARG_315	NH1	A_ASP_24	OD2	3.965
4GXX	A_ARG_321	NH1	A_GLU_31	OE1	3.882
4GXX	A_ARG_321	NH1	A_GLU_31	OE2	3.177
4GXX	A_ARG_321	NH2	A_GLU_31	OE2	3.764
4GXX	B_LYS_51	NZ	B_GLU_103	OE1	3.113
4GXX	B_LYS_58	NZ	B_GLU_57	OE1	3.239
4GXX	B_LYS_58	NZ	F_GLU_97	OE1	3.721
4GXX	B_LYS_68	NZ	A_GLU_110	OE2	2.734
4GXX	B_ARG_76	NH1	D_GLU_74	OE1	2.782
4GXX	B_ARG_76	NH1	D_GLU_74	OE2	3.511
4GXX	B_ARG_76	NH2	C_GLU_107	OE2	3.651
4GXX	B_ARG_76	NH2	D_GLU_74	OE1	3.625
4GXX	B_ARG_76	NH2	D_GLU_74	OE2	2.818
4GXX	B_LYS_82	NZ	B_ASP_86	OD1	3.639
4GXX	B_LYS_82	NZ	B_ASP_86	OD2	2.969
4GXX	B_LYS_83	NZ	D_ASP_85	OD1	2.661
4GXX	B_LYS_83	NZ	D_ASP_85	OD2	3.421
4GXX	B_ARG_106	NH2	F_ASP_109	OD2	3.780
4GXX	B_ARG_116	NH2	B_GLU_120	OE2	3.845
4GXX	B_ARG_116	NH2	D_GLU_120	OE1	2.669
4GXX	B_LYS_123	NZ	B_GLU_132	OE1	2.906
4GXX	B_LYS_123	NZ	B_GLU_132	OE2	3.252
4GXX	B_LYS_	NZ	B_GLU_	OE1	3.764
4GXX	B_LYS_	NZ	B_GLU_139	OE2	3.010
4GXX	B_LYS_	NZ	B_GLU_	OE1	3.439
4GXX	B_ARG_153	NH1	B_GLU_150	OE2	2.852
4GXX	C_LYS_32	NZ	F_GLU_57	OE2	3.165
4GXX	C_LYS_53	NZ	C_ASP_276	OD1	3.539
4GXX	C_LYS_63	NZ	C_GLU_75	OE2	3.863
4GXX	C_ARG_109	NH1	C_GLU_89	OE1	2.866
4GXX	C_ARG_109	NH1	C_GLU_89	OE2	3.437
4GXX	C_ARG_109	NH2	C_GLU_89	OE1	3.601
4GXX	C_ARG_109	NH2	C_GLU_89	OE2	2.826
4GXX	C_ARG_109	NH2	D_GLU_69	OE1	3.802
4GXX	C_ARG_109	NH2	D_GLU_69	OE2	3.427
4GXX	C_ARG_149	NH2	C_ASP_77	OD1	3.699

4GXX	C_ARG_149	NH2	C_ASP_77	OD2	2.803
4GXX	C_LYS_174	NZ	C_GLU_119	OE1	3.067
4GXX	C_LYS_174	NZ	C_GLU_119	OE2	3.650
4GXX	C_LYS_208	NZ	C_GLU_238	OE1	3.321
4GXX	C_LYS_208	NZ	C_GLU_238	OE2	3.002
4GXX	C_ARG_262	NH2	C_GLU_175	OE1	3.519
4GXX	C_ARG_262	NH2	C_GLU_175	OE2	2.926
4GXX	C_LYS_280	NZ	C_GLU_304	OE1	3.956
4GXX	C_ARG_310	NH1	D_ASP_90	OD1	2.336
4GXX	C_ARG_310	NH2	D_ASP_86	OD1	3.727
4GXX	C_ARG_310	NH2	D_ASP_90	OD1	3.012
4GXX	C_ARG_315	NH1	C_ASP_24	OD2	3.922
4GXX	D_LYS_51	NZ	D_GLU_103	OE1	2.595
4GXX	D_LYS_58	NZ	B_GLU_97	OE1	3.529
4GXX	D_LYS_68	NZ	C_GLU_110	OE2	2.872
4GXX	D_ARG_76	NH1	F_GLU_74	OE1	2.910
4GXX	D_ARG_76	NH1	F_GLU_74	OE2	3.571
4GXX	D_ARG_76	NH2	E_GLU_107	OE2	3.622
4GXX	D_ARG_76	NH2	F_GLU_74	OE1	3.615
4GXX	D_ARG_76	NH2	F_GLU_74	OE2	2.803
4GXX	D_LYS_83	NZ	F_ASP_85	OD1	2.774
4GXX	D_LYS_83	NZ	F_ASP_85	OD2	3.514
4GXX	D_ARG_106	NH2	B_ASP_109	OD2	3.920
4GXX	D_ARG_116	NH1	F_GLU_120	OE1	3.357
4GXX	D_ARG_116	NH2	D_GLU_120	OE1	3.858
4GXX	D_ARG_116	NH2	F_GLU_120	OE1	3.225
4GXX	D_ARG_116	NH2	F_GLU_120	OE2	3.007
4GXX	D_LYS_123	NZ	D_GLU_132	OE1	3.074
4GXX	D_LYS_123	NZ	D_GLU_132	OE2	3.639
4GXX	D_LYS_131	NZ	D_GLU_139	OE2	3.654
4GXX	D_ARG_153	NH1	D_GLU_150	OE2	2.580
4GXX	E_LYS_32	NZ	B_GLU_57	OE2	3.237
4GXX	E_LYS_53	NZ	E_ASP_276	OD1	3.134
4GXX	E_LYS_63	NZ	E_GLU_75	OE1	2.624
4GXX	E_ARG_109	NH1	E_GLU_89	OE1	2.778
4GXX	E_ARG_109	NH1	E_GLU_89	OE2	3.312
4GXX	E_ARG_109	NH2	E_GLU_89	OE1	3.734
4GXX	E_ARG_109	NH2	E_GLU_89	OE2	2.889
4GXX	E_ARG_109	NH2	F_GLU_69	OE1	3.858
4GXX	E_ARG_109	NH2	F_GLU_69	OE2	2.773
4GXX	E_ARG_149	NH2	E_ASP_77	OD1	3.759
4GXX	E_ARG_149	NH2	E_ASP_77	OD2	2.793
4GXX	E_LYS_163	NZ	E_GLU_246	OE1	3.415
4GXX	E_LYS_174	NZ	E_GLU_119	OE1	2.751
4GXX	E_LYS_174	NZ	E_GLU_119	OE2	3.791
4GXX	E_LYS_208	NZ	E_GLU_238	OE1	3.310
4GXX	E_LYS_208	NZ	E_GLU_238	OE2	3.144
4GXX	E_ARG_262	NH2	E_GLU_175	OE1	3.412
4GXX	E_ARG_262	NH2	E_GLU_175	OE2	3.052
4GXX	E_ARG_310	NH1	F_ASP_90	OD1	2.470
4GXX	E_ARG_310	NH2	F_ASP_90	OD1	2.925
4GXX	E_ARG_315	NH1	E_ASP_24	OD1	3.908
4GXX	E_ARG_321	NH1	E_GLU_31	OE1	3.912
4GXX	E_ARG_321	NH1	E_GLU_31	OE2	2.977
4GXX	E_ARG_321	NH2	E_GLU_31	OE2	3.461
4GXX	F_HIS_26	NE2	F_ASP_146	OD1	3.842
4GXX	F_LYS_51	NZ	F_GLU_103	OE1	2.680
4GXX	F_LYS_58	NZ	D_GLU_97	OE1	3.142

4GXX	F_LYS_68	NZ	E_GLU_110	OE2	2.982
4GXX	F_ARG_76	NH1	B_GLU_74	OE1	2.798
4GXX	F_ARG_76	NH1	B_GLU_74	OE2	3.572
4GXX	F_ARG_76	NH2	A_GLU_107	OE2	3.644
4GXX	F_ARG_76	NH2	B_GLU_74	OE1	3.566
4GXX	F_ARG_76	NH2	B_GLU_74	OE2	2.823
4GXX	F_LYS_83	NZ	B_ASP_85	OD1	2.859
4GXX	F_LYS_83	NZ	B_ASP_85	OD2	3.462
4GXX	F_ARG_106	NH2	D_ASP_109	OD2	3.576
4GXX	F_ARG_116	NH1	B_GLU_120	OE1	2.775
4GXX	F_ARG_116	NH1	B_GLU_120	OE2	3.643
4GXX	F_ARG_116	NH2	B_GLU_120	OE1	3.285
4GXX	F_ARG_116	NH2	B_GLU_120	OE2	2.552
4GXX	F_ARG_116	NH2	F_GLU_120	OE2	3.662
4GXX	F_LYS_123	NZ	F_GLU_132	OE1	2.969
4GXX	F_LYS_123	NZ	F_GLU_132	OE2	3.560
4GXX	F_LYS_	NZ	F_GLU_139	OE2	3.889
4GXX	F_ARG_153	NH1	F_GLU_150	OE2	2.818
4GXX	F_LYS_	NZ	F_GLU_	OE1	3.562
4GXX	F_LYS_	NZ	F_GLU_	OE2	3.737

Table 519: 4GXX-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4H0G	A_LYS_64	NZ	A_GLU_47	OE1	3.762
4H0G	A_LYS_64	NZ	A_GLU_47	OE2	3.209
4H0G	A_LYS_68	NZ	A_ASP_91	OD1	2.637
4H0G	A_LYS_68	NZ	A_ASP_91	OD2	2.768
4H0G	A_ARG_99	NH2	A_ASP_108	OD1	3.595
4H0G	A_ARG_99	NH2	A_ASP_108	OD2	3.122
4H0G	A_ARG_205	NH2	A_ASP_226	OD1	2.570
4H0G	A_ARG_205	NH2	A_ASP_226	OD2	3.224
4H0G	A_LYS_247	NZ	A_GLU_249	OE1	2.645

Table 520: 4H0G-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4H0H	B_LYS_64	NZ	B_GLU_47	OE2	2.501
4H0H	B_LYS_68	NZ	B_ASP_91	OD1	3.545
4H0H	B_LYS_68	NZ	B_ASP_91	OD2	2.692
4H0H	B_ARG_99	NH2	B_ASP_108	OD1	3.511
4H0H	B_ARG_99	NH2	B_ASP_108	OD2	2.749
4H0H	B_ARG_163	NH1	B_ASP_214	OD1	3.546
4H0H	B_ARG_163	NH2	B_ASP_214	OD1	3.756
4H0H	B_ARG_205	NH1	B_GLU_223	OE2	3.240
4H0H	B_ARG_205	NH2	B_GLU_223	OE1	3.635
4H0H	B_ARG_205	NH2	B_GLU_223	OE2	3.897
4H0H	B_ARG_205	NH2	B_GLU_225	OE1	2.872
4H0H	B_ARG_205	NH2	B_ASP_226	OD1	2.832
4H0H	B_ARG_205	NH2	B_ASP_226	OD2	3.613
4H0H	B_ARG_221	NH2	B_GLU_223	OE2	2.851

Table 521: 4H0H-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4H0I	A_LYS_68	NZ	A_ASP_91	OD1	3.664
4H0I	A_LYS_68	NZ	A_ASP_91	OD2	2.815
4H0I	A_ARG_99	NH2	A_ASP_108	OD1	3.509
4H0I	A_ARG_99	NH2	A_ASP_108	OD2	2.911
4H0I	A_ARG_163	NH2	A_ASP_214	OD1	2.763
4H0I	A_ARG_205	NH1	A_GLU_223	OE2	3.851
4H0I	A_ARG_205	NH2	A_GLU_225	OE2	2.757
4H0I	A_ARG_205	NH2	A_ASP_226	OD1	3.005
4H0I	A_ARG_205	NH2	A_ASP_226	OD2	3.508
4H0I	A_ARG_221	NH2	A_GLU_223	OE2	3.683
4H0I	A_LYS_247	NZ	A_GLU_249	OE1	3.405
4H0I	A_LYS_247	NZ	A_GLU_249	OE2	3.892

Table 522: 4H0I-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID** **residue name** **residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4H8W	G_HIS_66	ND1	G_GLU_64	OE2	2.743
4H8W	G_LYS_207	NZ	G_GLU_381	OE1	3.361
4H8W	G_LYS_207	NZ	G_GLU_381	OE2	2.825
4H8W	G_LYS_227	NZ	G_GLU_83	OE1	3.758
4H8W	G_LYS_231	NZ	G_GLU_267	OE1	2.924
4H8W	G_HIS_249	NE2	G_GLU_482	OE1	2.960
4H8W	G_LYS_282	NZ	G_GLU_275	OE1	2.895
4H8W	G_LYS_343	NZ	G_GLU_347	OE2	3.998
4H8W	G_LYS_348	NZ	G_GLU_269	OE1	3.647
4H8W	G_LYS_348	NZ	G_GLU_269	OE2	3.325
4H8W	G_LYS_348	NZ	G_GLU_351	OE2	2.761
4H8W	G_ARG_379	NH1	G_ASP_211	OD2	3.811
4H8W	G_ARG_456	NH1	G_GLU_466	OE1	2.922
4H8W	G_ARG_456	NH1	G_GLU_466	OE2	3.660
4H8W	G_ARG_469	NH2	G_ASP_457	OD1	3.748
4H8W	G_ARG_469	NH2	G_ASP_457	OD2	2.810
4H8W	G_LYS_476	NZ	G_GLU_102	OE1	3.752
4H8W	G_ARG_480	NH1	G_ASP_477	OD1	2.732
4H8W	G_LYS_485	NZ	G_GLU_267	OE2	3.866
4H8W	G_LYS_487	NZ	G_ASP_47	OD1	2.663
4H8W	G_LYS_487	NZ	G_ASP_47	OD2	3.551
4H8W	G_LYS_487	NZ	G_GLU_91	OE1	3.873
4H8W	G_LYS_487	NZ	G_GLU_91	OE2	3.127
4H8W	H_ARG_38	NH1	H_ASP_86	OD2	2.753
4H8W	H_ARG_38	NH2	H_GLU_46	OE1	2.942
4H8W	H_ARG_38	NH2	H_GLU_46	OE2	3.785
4H8W	H_ARG_38	NH2	H_ASP_86	OD2	3.820
4H8W	H_ARG_55	NH1	G_ASP_107	OD1	3.623
4H8W	H_ARG_55	NH1	G_ASP_107	OD2	3.025
4H8W	H_ARG_66	NH1	H_ASP_86	OD1	3.602
4H8W	H_ARG_66	NH1	H_ASP_86	OD2	3.242
4H8W	H_ARG_66	NH2	H_ASP_86	OD1	2.663
4H8W	H_ARG_66	NH2	H_ASP_86	OD2	3.744
4H8W	H_LYS_94	NZ	H_ASP_101	OD1	3.932
4H8W	H_LYS_94	NZ	H_ASP_101	OD2	3.783
4H8W	H_LYS_209	NZ	L_GLU_124	OE1	2.673
4H8W	H_LYS_209	NZ	L_GLU_124	OE2	2.808
4H8W	H_ARG_210	NH2	H_GLU_212	OE2	3.750
4H8W	L_ARG_61	NH1	L_ASP_82	OD1	3.642
4H8W	L_ARG_61	NH1	L_ASP_82	OD2	2.727
4H8W	L_ARG_61	NH2	L_ASP_82	OD1	2.875
4H8W	L_ARG_61	NH2	L_ASP_82	OD2	3.419
4H8W	L_LYS_167	NZ	L_GLU_83	OE1	3.479
4H8W	L_LYS_167	NZ	L_GLU_83	OE2	2.659
4H8W	L_ARG_190	NH1	L_ASP_152	OD1	3.209
4H8W	L_ARG_190	NH1	L_ASP_152	OD2	3.525
4H8W	C_LYS_8	NZ	C_GLU_119	OE1	2.938
4H8W	C_LYS_29	NZ	C_GLU_85	OE1	3.161
4H8W	C_LYS_29	NZ	C_GLU_85	OE2	3.156
4H8W	C_ARG_54	NH1	C_ASP_78	OD1	3.760
4H8W	C_ARG_54	NH1	C_ASP_78	OD2	2.826
4H8W	C_ARG_54	NH2	C_ASP_78	OD1	2.862
4H8W	C_ARG_54	NH2	C_ASP_78	OD2	3.438
4H8W	C_ARG_58	NH2	C_GLU_13	OE1	3.422
4H8W	C_ARG_58	NH2	C_GLU_13	OE2	2.940
4H8W	C_ARG_59	NH1	G_ASP_368	OD1	2.952
4H8W	C_ARG_59	NH1	G_ASP_368	OD2	3.318

4H8W	C_ARG_59	NH2	G_ASP_368	OD1	3.741
4H8W	C_ARG_59	NH2	G_ASP_368	OD2	2.611
4H8W	C_ARG_134	NH1	C_GLU_150	OE2	3.466
4H8W	C_ARG_134	NH2	C_GLU_150	OE2	2.720
4H8W	C_ARG_134	NH2	C_ASP_153	OD1	2.923
4H8W	C_ARG_134	NH2	C_ASP_153	OD2	3.632

Table 523: 4H8W-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4HF5	A_LYS_45	NZ	A_ASP_41	OD1	3.023
4HF5	A_LYS_45	NZ	A_ASP_41	OD2	2.738
4HF5	A_LYS_50	NZ	A_GLU_275	OE1	3.846
4HF5	A_LYS_109	NZ	A_GLU_89	OE1	3.835
4HF5	A_LYS_109	NZ	B_GLU_69	OE1	3.017
4HF5	A_LYS_119	NZ	A_GLU_255	OE2	3.751
4HF5	A_LYS_123	NZ	A_GLU_255	OE1	3.191
4HF5	A_ARG_137	NH1	H_ASP_97	OD2	2.969
4HF5	A_ARG_137	NH2	H_ASP_97	OD1	3.008
4HF5	A_ARG_137	NH2	H_ASP_97	OD2	2.797
4HF5	A_HIS_183	NE2	A_GLU_190	OE2	3.373
4HF5	A_HIS_184	NE2	A_GLU_231	OE1	3.723
4HF5	A_LYS_262	NZ	A_GLU_83	OE1	3.426
4HF5	A_LYS_262	NZ	A_GLU_83	OE2	2.633
4HF5	A_ARG_263	NH1	A_GLU_174	OE2	3.471
4HF5	A_ARG_263	NH2	A_GLU_174	OE2	2.803
4HF5	A_LYS_269	NZ	A_GLU_89	OE1	3.758
4HF5	A_LYS_269	NZ	B_GLU_69	OE1	2.931
4HF5	A_LYS_269	NZ	B_GLU_69	OE2	3.200
4HF5	A_LYS_280	NZ	A_GLU_278	OE2	2.927
4HF5	A_LYS_307	NZ	B_GLU_64	OE2	3.558
4HF5	A_LYS_310	NZ	B_ASP_90	OD1	2.877
4HF5	A_ARG_321	NH1	A_GLU_31	OE1	2.994
4HF5	A_ARG_321	NH1	A_GLU_31	OE2	2.844
4HF5	A_ARG_321	NH2	A_GLU_31	OE1	3.793
4HF5	B_LYS_51	NZ	B_GLU_103	OE1	3.501
4HF5	B_ARG_75	NH1	B_GLU_78	OE1	2.803
4HF5	B_ARG_75	NH1	B_GLU_78	OE2	3.443
4HF5	B_ARG_75	NH2	B_GLU_78	OE1	2.681
4HF5	B_LYS_82	NZ	B_ASP_86	OD1	3.014
4HF5	B_ARG_123	NH1	B_ASP_120	OD2	3.836
4HF5	B_LYS_143	NZ	A_ASP_11	OD2	3.934
4HF5	B_ARG_170	NH2	B_ASP_128	OD2	3.090
4HF5	H_ARG_38	NH1	H_ASP_86	OD1	3.397
4HF5	H_ARG_38	NH2	H_GLU_46	OE1	3.432
4HF5	H_ARG_38	NH2	H_GLU_46	OE2	3.377
4HF5	H_ARG_64	NH1	H_ASP_61	OD1	3.700
4HF5	H_ARG_64	NH2	H_ASP_61	OD1	3.901
4HF5	H_ARG_66	NH1	H_ASP_86	OD1	3.656
4HF5	H_ARG_66	NH2	H_ASP_86	OD1	2.847
4HF5	H_ARG_66	NH2	H_ASP_86	OD2	2.651
4HF5	H_LYS_75	NZ	H_ASP_72	OD1	3.287
4HF5	H_ARG_94	NH2	H_ASP_101	OD1	3.485
4HF5	H_ARG_94	NH2	H_ASP_101	OD2	2.891
4HF5	H_LYS_143	NZ	H_ASP_144	OD1	2.973
4HF5	H_LYS_143	NZ	H_ASP_144	OD2	2.934
4HF5	L_HIS_53	ND1	L_GLU_52	OE1	3.652
4HF5	L_HIS_53	NE2	L_GLU_52	OE1	3.847
4HF5	L_ARG_54	NH2	L_ASP_60	OD1	2.781
4HF5	L_ARG_61	NH2	L_ASP_82	OD1	3.562
4HF5	L_LYS_66	NZ	L_ASP_51	OD1	3.019
4HF5	L_LYS_66	NZ	L_ASP_51	OD2	3.023
4HF5	L_LYS_103	NZ	L_ASP_85	OD1	3.547
4HF5	L_LYS_103	NZ	L_ASP_85	OD2	2.955

Table 524: 4HF5-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4HGK	A_HIS_9	ND1	A_GLU_6	OE2	3.257
4HGK	A_HIS_9	ND1	A_ASP_13	OD2	3.915
4HGK	A_HIS_9	NE2	A_ASP_13	OD1	3.802
4HGK	A_HIS_9	NE2	A_ASP_13	OD2	2.774
4HGK	A_ARG_10	NH1	A_ASP_255	OD2	2.741
4HGK	A_ARG_10	NH2	A_GLU_6	OE2	3.561
4HGK	A_LYS_12	NZ	A_GLU_57	OE2	2.562
4HGK	A_LYS_51	NZ	A_GLU_16	OE1	2.813
4HGK	A_HIS_67	ND1	A_ASP_249	OD1	3.864
4HGK	A_HIS_67	NE2	A_ASP_249	OD1	2.767
4HGK	A_HIS_67	NE2	A_ASP_249	OD2	3.220
4HGK	A_LYS_73	NZ	A_GLU_45	OE1	3.064
4HGK	A_ARG_98	NH1	A_ASP_72	OD1	2.860
4HGK	A_ARG_98	NH2	A_ASP_72	OD1	3.120
4HGK	A_ARG_98	NH2	A_GLU_95	OE2	2.998
4HGK	A_HIS_105	NE2	A_GLU_86	OE1	3.472
4HGK	A_ARG_117	NH2	A_ASP_183	OD1	3.422
4HGK	A_ARG_117	NH2	A_ASP_183	OD2	3.534
4HGK	A_ARG_144	NH1	A_GLU_141	OE1	3.085
4HGK	A_ARG_145	NH2	A_GLU_141	OE1	2.935
4HGK	A_ARG_160	NH1	A_GLU_285	OE2	3.710
4HGK	A_LYS_162	NZ	A_GLU_131	OE2	3.380
4HGK	A_LYS_174	NZ	A_ASP_121	OD1	3.589
4HGK	A_LYS_181	NZ	A_GLU_167	OE1	2.954
4HGK	A_LYS_181	NZ	A_GLU_167	OE2	3.073
4HGK	A_ARG_186	NH1	A_ASP_187	OD1	3.404
4HGK	A_LYS_190	NZ	A_GLU_425	OE1	3.698
4HGK	A_LYS_190	NZ	A_GLU_425	OE2	3.906
4HGK	A_ARG_209	NH1	A_ASP_324	OD1	3.792
4HGK	A_ARG_209	NH2	A_ASP_324	OD1	3.124
4HGK	A_ARG_209	NH2	A_GLU_354	OE1	3.847
4HGK	A_ARG_209	NH2	A_GLU_354	OE2	3.387
4HGK	A_LYS_212	NZ	A_GLU_208	OE2	3.796
4HGK	A_LYS_225	NZ	A_ASP_296	OD1	3.782
4HGK	A_LYS_225	NZ	A_ASP_296	OD2	3.781
4HGK	A_LYS_233	NZ	A_ASP_237	OD1	3.352
4HGK	A_LYS_233	NZ	A_ASP_237	OD2	2.652
4HGK	A_LYS_240	NZ	A_ASP_256	OD2	3.517
4HGK	A_ARG_257	NH1	A_GLU_153	OE2	3.027
4HGK	A_ARG_257	NH2	A_GLU_153	OE2	2.860
4HGK	A_LYS_274	NZ	A_GLU_294	OE1	3.878
4HGK	A_LYS_274	NZ	A_GLU_294	OE2	3.129
4HGK	A_HIS_288	ND1	A_GLU_153	OE1	2.949
4HGK	A_HIS_288	ND1	A_GLU_153	OE2	3.659
4HGK	A_LYS_323	NZ	A_GLU_358	OE1	2.748
4HGK	A_LYS_323	NZ	A_GLU_358	OE2	3.753
4HGK	A_ARG_336	NH1	A_GLU_333	OE1	2.887
4HGK	A_ARG_336	NH1	A_GLU_333	OE2	3.968
4HGK	A_ARG_337	NH1	A_GLU_333	OE1	2.815
4HGK	A_ARG_337	NH2	A_GLU_333	OE1	3.771
4HGK	A_ARG_348	NH1	A_GLU_450	OE2	3.559
4HGK	A_ARG_348	NH2	A_GLU_450	OE2	2.854
4HGK	A_LYS_378	NZ	A_ASP_375	OD1	3.797
4HGK	A_ARG_428	NH2	A_GLU_425	OE2	3.049
4HGK	A_ARG_485	NH1	A_GLU_383	OE2	3.444
4HGK	A_ARG_485	NH2	A_GLU_383	OE1	2.699
4HGK	A_ARG_485	NH2	A_GLU_383	OE2	3.000

4HGK	A_ARG_485	NH2	A_GLU_450	OE2	3.657
4HGK	B_LYS_4	NZ	B_GLU_57	OE1	3.991
4HGK	B_HIS_9	ND1	B_GLU_6	OE2	3.774
4HGK	B_HIS_9	NE2	B_ASP_13	OD2	2.894
4HGK	B_ARG_10	NH1	B_ASP_255	OD2	2.787
4HGK	B_ARG_10	NH2	B_GLU_6	OE2	3.189
4HGK	B_LYS_12	NZ	B_GLU_57	OE1	3.527
4HGK	B_LYS_12	NZ	B_GLU_57	OE2	3.163
4HGK	B_LYS_51	NZ	B_GLU_16	OE1	2.848
4HGK	B_HIS_67	ND1	B_ASP_249	OD1	3.381
4HGK	B_HIS_67	NE2	B_ASP_249	OD1	2.384
4HGK	B_HIS_67	NE2	B_ASP_249	OD2	2.929
4HGK	B_LYS_73	NZ	B_GLU_45	OE1	3.090
4HGK	B_ARG_98	NH1	B_ASP_72	OD1	2.872
4HGK	B_ARG_98	NH2	B_ASP_72	OD1	3.149
4HGK	B_ARG_98	NH2	B_GLU_95	OE2	3.021
4HGK	B_HIS_105	NE2	B_GLU_86	OE1	3.473
4HGK	B_ARG_117	NH1	B_ASP_183	OD1	3.152
4HGK	B_ARG_117	NH2	B_ASP_183	OD1	2.607
4HGK	B_ARG_117	NH2	B_ASP_183	OD2	3.783
4HGK	B_ARG_144	NH1	B_GLU_141	OE1	3.094
4HGK	B_ARG_145	NH2	B_GLU_141	OE1	2.948
4HGK	B_ARG_160	NH1	B_GLU_285	OE2	3.974
4HGK	B_LYS_162	NZ	B_GLU_131	OE2	3.359
4HGK	B_LYS_181	NZ	B_GLU_167	OE1	2.749
4HGK	B_LYS_181	NZ	B_GLU_167	OE2	2.805
4HGK	B_LYS_205	NZ	B_GLU_465	OE2	3.218
4HGK	B_ARG_209	NH2	B_ASP_324	OD1	3.305
4HGK	B_ARG_209	NH2	B_GLU_354	OE2	3.723
4HGK	B_LYS_225	NZ	B_ASP_296	OD1	3.981
4HGK	B_LYS_233	NZ	B_ASP_237	OD1	3.425
4HGK	B_LYS_233	NZ	B_ASP_237	OD2	2.618
4HGK	B_LYS_240	NZ	B_ASP_256	OD2	3.510
4HGK	B_HIS_247	NE2	B_ASP_249	OD2	3.558
4HGK	B_ARG_257	NH1	B_GLU_153	OE1	3.383
4HGK	B_ARG_257	NH2	B_GLU_153	OE1	2.959
4HGK	B_LYS_262	NZ	B_GLU_266	OE1	3.407
4HGK	B_LYS_262	NZ	B_GLU_266	OE2	3.772
4HGK	B_LYS_274	NZ	B_GLU_294	OE1	3.883
4HGK	B_LYS_274	NZ	B_GLU_294	OE2	3.144
4HGK	B_HIS_288	ND1	B_GLU_153	OE1	3.601
4HGK	B_HIS_288	ND1	B_GLU_153	OE2	2.554
4HGK	B_LYS_317	NZ	B_ASP_314	OD2	3.790
4HGK	B_LYS_323	NZ	B_GLU_358	OE1	2.750
4HGK	B_LYS_323	NZ	B_GLU_358	OE2	3.753
4HGK	B_ARG_336	NH1	B_GLU_333	OE1	2.876
4HGK	B_ARG_336	NH1	B_GLU_333	OE2	3.980
4HGK	B_ARG_337	NH1	B_GLU_333	OE1	2.817
4HGK	B_ARG_337	NH2	B_GLU_333	OE1	3.764
4HGK	B_ARG_348	NH1	B_GLU_450	OE2	3.585
4HGK	B_ARG_348	NH2	B_GLU_450	OE2	2.871
4HGK	B_LYS_378	NZ	B_ASP_375	OD1	3.753
4HGK	B_LYS_389	NZ	B_GLU_393	OE1	3.466
4HGK	B_ARG_445	NH1	B_GLU_442	OE2	3.842
4HGK	B_ARG_445	NH2	B_GLU_442	OE2	3.028
4HGK	B_ARG_485	NH1	B_GLU_383	OE2	3.455
4HGK	B_ARG_485	NH2	B_GLU_383	OE1	2.708
4HGK	B_ARG_485	NH2	B_GLU_383	OE2	3.008

4HGK	B_ARG_485	NH2	B_GLU_450	OE2	3.644
4HGK	C_ARG_21	NH1	C_ASP_45	OD2	2.805
4HGK	C_ARG_21	NH2	C_ASP_23	OD2	3.642
4HGK	C_ARG_21	NH2	C_ASP_45	OD2	3.962
4HGK	C_LYS_65	NZ	B_GLU_230	OE1	3.917
4HGK	C_LYS_65	NZ	C_ASP_113	OD2	3.638
4HGK	C_ARG_73	NH2	C_ASP_96	OD1	2.911
4HGK	C_ARG_73	NH2	C_ASP_96	OD2	3.688
4HGK	C_ARG_103	NH1	B_GLU_230	OE1	3.099
4HGK	C_ARG_103	NH2	B_GLU_230	OE1	3.263
4HGK	C_ARG_103	NH2	B_GLU_230	OE2	3.968
4HGK	C_ARG_103	NH2	C_ASP_113	OD1	3.388
4HGK	C_ARG_103	NH2	C_ASP_113	OD2	2.979
4HGK	D_ARG_21	NH1	D_ASP_45	OD2	2.813
4HGK	D_ARG_21	NH2	D_ASP_45	OD2	3.945
4HGK	D_ARG_27	NH1	D_ASP_23	OD1	3.814
4HGK	D_ARG_57	NH2	D_ASP_96	OD1	3.778
4HGK	D_LYS_65	NZ	A_GLU_230	OE1	3.741
4HGK	D_LYS_65	NZ	D_ASP_113	OD2	3.664
4HGK	D_ARG_73	NH2	D_ASP_96	OD1	3.000
4HGK	D_ARG_73	NH2	D_ASP_96	OD2	3.124
4HGK	D_ARG_103	NH1	A_GLU_230	OE1	3.115
4HGK	D_ARG_103	NH2	A_GLU_230	OE1	3.112
4HGK	D_ARG_103	NH2	A_GLU_230	OE2	3.907
4HGK	D_ARG_103	NH2	D_ASP_113	OD1	3.384
4HGK	D_ARG_103	NH2	D_ASP_113	OD2	2.984

Table 525: 4HGK-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4HH9	A_ARG_54	NH1	C_ASP_50	OD2	3.238
4HH9	A_ARG_54	NH2	C_ASP_50	OD2	3.183
4HH9	A_ARG_61	NH1	A_GLU_79	OE1	3.519
4HH9	A_ARG_61	NH1	A_GLU_79	OE2	3.676
4HH9	A_ARG_61	NH2	A_GLU_79	OE1	3.286
4HH9	A_ARG_61	NH2	A_GLU_81	OE1	3.129
4HH9	A_ARG_61	NH2	A_ASP_82	OD1	3.001
4HH9	A_ARG_61	NH2	A_ASP_82	OD2	3.679
4HH9	A_ARG_91	NH2	A_ASP_50	OD1	2.827
4HH9	A_LYS_149	NZ	A_GLU_195	OE1	3.346
4HH9	A_LYS_183	NZ	A_GLU_187	OE2	3.477
4HH9	B_HIS_35	NE2	B_GLU_95	OE2	2.800
4HH9	B_ARG_38	NH1	B_ASP_86	OD1	2.849
4HH9	B_ARG_38	NH2	B_ASP_86	OD1	3.956
4HH9	B_LYS_64	NZ	B_ASP_61	OD1	2.675
4HH9	B_ARG_66	NH1	B_ASP_86	OD1	3.513
4HH9	B_ARG_66	NH1	B_ASP_86	OD2	3.921
4HH9	B_ARG_66	NH2	B_ASP_86	OD1	3.293
4HH9	B_ARG_66	NH2	B_ASP_86	OD2	2.337
4HH9	B_LYS_75	NZ	B_ASP_72	OD2	2.839
4HH9	B_ARG_94	NH2	B_ASP_101	OD1	3.522
4HH9	B_ARG_94	NH2	B_ASP_101	OD2	2.685
4HH9	B_LYS_143	NZ	B_ASP_144	OD1	3.830
4HH9	B_LYS_209	NZ	A_GLU_123	OE1	3.274
4HH9	B_LYS_209	NZ	A_GLU_123	OE2	3.488
4HH9	B_LYS_214	NZ	A_ASP_122	OD1	3.788
4HH9	C_ARG_24	NH2	C_ASP_70	OD2	3.842
4HH9	C_ARG_54	NH1	A_ASP_50	OD2	2.782
4HH9	C_ARG_54	NH2	A_ASP_50	OD2	3.752
4HH9	C_ARG_61	NH1	C_GLU_79	OE1	3.726
4HH9	C_ARG_61	NH1	C_GLU_79	OE2	3.687
4HH9	C_ARG_61	NH2	C_GLU_79	OE1	3.548
4HH9	C_ARG_61	NH2	C_GLU_81	OE1	3.056
4HH9	C_ARG_61	NH2	C_ASP_82	OD1	2.727
4HH9	C_ARG_61	NH2	C_ASP_82	OD2	3.346
4HH9	C_ARG_91	NH2	C_ASP_50	OD1	2.719
4HH9	C_LYS_149	NZ	C_GLU_195	OE1	3.641
4HH9	C_LYS_149	NZ	C_GLU_195	OE2	3.059
4HH9	C_HIS_189	NE2	C_ASP_151	OD2	3.983
4HH9	C_ARG_211	NH1	C_GLU_187	OE1	3.912
4HH9	D_HIS_35	NE2	D_GLU_95	OE2	2.710
4HH9	D_ARG_38	NH1	D_ASP_86	OD1	2.846
4HH9	D_ARG_38	NH2	D_ASP_86	OD1	3.935
4HH9	D_ARG_66	NH1	D_ASP_86	OD1	3.013
4HH9	D_ARG_66	NH1	D_ASP_86	OD2	3.359
4HH9	D_ARG_66	NH2	D_ASP_86	OD1	3.871
4HH9	D_ARG_66	NH2	D_ASP_86	OD2	2.760
4HH9	D_ARG_94	NH2	D_ASP_101	OD1	3.831
4HH9	D_ARG_94	NH2	D_ASP_101	OD2	2.965
4HH9	D_LYS_129	NZ	C_GLU_213	OE1	3.401
4HH9	D_LYS_129	NZ	C_GLU_213	OE2	3.163
4HH9	D_LYS_143	NZ	D_ASP_144	OD1	3.474
4HH9	D_LYS_143	NZ	D_ASP_144	OD2	3.679
4HH9	D_LYS_209	NZ	C_GLU_123	OE2	3.057
4HH9	D_LYS_210	NZ	D_GLU_212	OE1	3.242
4HH9	D_LYS_214	NZ	C_ASP_122	OD2	3.367

Table 526: 4HH9-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4HHA	A_ARG_61	NH1	A_GLU_79	OE1	3.133
4HHA	A_ARG_61	NH2	A_GLU_79	OE1	3.839
4HHA	A_ARG_61	NH2	A_ASP_82	OD1	2.950
4HHA	A_ARG_61	NH2	A_ASP_82	OD2	3.472
4HHA	A_ARG_91	NH2	A_ASP_50	OD1	2.826
4HHA	A_ARG_103	NH1	A_GLU_105	OE1	3.652
4HHA	A_ARG_103	NH2	A_GLU_105	OE1	3.992
4HHA	A_LYS_107	NZ	A_GLU_17	OE1	3.316
4HHA	A_LYS_107	NZ	A_GLU_17	OE2	3.376
4HHA	A_LYS_149	NZ	A_GLU_195	OE2	2.569
4HHA	A_ARG_211	NH1	A_GLU_187	OE1	2.769
4HHA	B_HIS_32	ND1	P_GLU_1	OE1	4.000
4HHA	B_HIS_32	NE2	P_GLU_1	OE1	3.076
4HHA	B_HIS_32	NE2	P_GLU_1	OE2	2.639
4HHA	B_HIS_35	NE2	B_GLU_95	OE2	2.765
4HHA	B_ARG_38	NH1	B_ASP_86	OD1	2.958
4HHA	B_ARG_66	NH1	B_ASP_86	OD1	3.061
4HHA	B_ARG_66	NH1	B_ASP_86	OD2	3.374
4HHA	B_ARG_66	NH2	B_ASP_86	OD1	3.930
4HHA	B_ARG_66	NH2	B_ASP_86	OD2	2.793
4HHA	B_ARG_87	NH2	B_GLU_148	OE1	3.817
4HHA	B_ARG_87	NH2	B_GLU_148	OE2	3.007
4HHA	B_ARG_94	NH1	P_GLU_1	OE2	3.723
4HHA	B_ARG_94	NH2	B_ASP_101	OD1	3.771
4HHA	B_ARG_94	NH2	B_ASP_101	OD2	2.779
4HHA	B_ARG_94	NH2	P_GLU_1	OE2	3.026
4HHA	B_LYS_143	NZ	B_ASP_144	OD1	3.788
4HHA	B_HIS_164	NE2	A_ASP_167	OD1	3.917
4HHA	B_LYS_209	NZ	A_GLU_123	OE2	2.754
4HHA	B_LYS_210	NZ	B_GLU_212	OE1	3.348

Table 527: 4HHA-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4HIE	A_ARG_24	NH1	A_ASP_70	OD2	2.822
4HIE	A_ARG_61	NH2	A_GLU_81	OE1	3.581
4HIE	A_ARG_61	NH2	A_ASP_82	OD1	2.932
4HIE	A_ARG_61	NH2	A_ASP_82	OD2	3.691
4HIE	A_ARG_91	NH2	B_GLU_95	OE1	3.457
4HIE	A_ARG_91	NH2	B_GLU_95	OE2	3.317
4HIE	A_LYS_188	NZ	A_ASP_185	OD1	3.766
4HIE	B_HIS_35	NE2	B_GLU_95	OE2	2.692
4HIE	B_ARG_38	NH2	B_GLU_46	OE1	3.053
4HIE	B_ARG_38	NH2	B_GLU_46	OE2	3.761
4HIE	B_ARG_66	NH1	B_ASP_86	OD1	2.947
4HIE	B_ARG_66	NH1	B_ASP_86	OD2	3.482
4HIE	B_ARG_66	NH2	B_ASP_86	OD1	3.793
4HIE	B_ARG_66	NH2	B_ASP_86	OD2	2.815
4HIE	B_LYS_94	NZ	B_ASP_101	OD1	3.259
4HIE	B_LYS_94	NZ	B_ASP_101	OD2	2.919
4HIE	B_LYS_143	NZ	B_ASP_144	OD1	3.226
4HIE	B_LYS_143	NZ	B_ASP_144	OD2	3.341
4HIE	B_LYS_201	NZ	B_ASP_199	OD2	3.632

Table 528: 4HIE-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID residue name residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4HIH	A_ARG_24	NH1	A_ASP_70	OD1	3.074
4HIH	A_ARG_24	NH1	A_ASP_70	OD2	2.888
4HIH	A_ARG_61	NH2	A_GLU_81	OE1	3.240
4HIH	A_ARG_61	NH2	A_ASP_82	OD1	2.810
4HIH	A_ARG_61	NH2	A_ASP_82	OD2	3.489
4HIH	A_ARG_91	NH2	B_GLU_95	OE1	3.470
4HIH	A_ARG_91	NH2	B_GLU_95	OE2	3.314
4HIH	A_LYS_107	NZ	A_GLU_17	OE1	3.699
4HIH	A_LYS_149	NZ	A_GLU_195	OE1	3.559
4HIH	A_LYS_169	NZ	A_ASP_170	OD2	3.069
4HIH	A_LYS_188	NZ	A_ASP_185	OD1	3.565
4HIH	A_ARG_211	NH1	A_GLU_187	OE1	3.810
4HIH	B_HIS_35	NE2	B_GLU_95	OE2	2.814
4HIH	B_ARG_38	NH2	B_GLU_46	OE1	3.181
4HIH	B_ARG_38	NH2	B_GLU_46	OE2	3.797
4HIH	B_ARG_55	NH1	B_ASP_53	OD1	3.769
4HIH	B_ARG_55	NH1	B_ASP_53	OD2	3.363
4HIH	B_ARG_66	NH1	B_ASP_86	OD1	3.461
4HIH	B_ARG_66	NH2	B_ASP_86	OD1	3.186
4HIH	B_ARG_66	NH2	B_ASP_86	OD2	2.400
4HIH	B_LYS_94	NZ	B_ASP_101	OD1	3.233
4HIH	B_LYS_94	NZ	B_ASP_101	OD2	2.906
4HIH	B_LYS_143	NZ	B_ASP_144	OD1	3.210
4HIH	B_LYS_143	NZ	B_ASP_144	OD2	3.587
4HIH	B_LYS_209	NZ	A_GLU_123	OE1	2.853
4HIH	B_LYS_209	NZ	A_GLU_123	OE2	3.685
4HIH	C_ARG_24	NH1	C_ASP_70	OD2	2.725
4HIH	C_ARG_24	NH2	C_ASP_70	OD2	2.940
4HIH	C_ARG_61	NH2	C_ASP_82	OD1	3.061
4HIH	C_ARG_61	NH2	C_ASP_82	OD2	3.666
4HIH	C_ARG_91	NH2	D_GLU_95	OE1	3.527
4HIH	C_ARG_91	NH2	D_GLU_95	OE2	3.339
4HIH	C_LYS_169	NZ	C_ASP_167	OD1	3.850
4HIH	C_LYS_169	NZ	C_ASP_170	OD2	3.306
4HIH	C_LYS_183	NZ	C_GLU_187	OE2	3.644
4HIH	C_LYS_188	NZ	C_ASP_185	OD1	3.956
4HIH	C_ARG_211	NH1	C_GLU_187	OE1	3.874
4HIH	D_HIS_35	NE2	D_GLU_95	OE2	2.717
4HIH	D_ARG_38	NH2	D_GLU_46	OE1	2.906
4HIH	D_ARG_38	NH2	D_GLU_46	OE2	3.704
4HIH	D_ARG_55	NH1	D_ASP_53	OD2	3.143
4HIH	D_LYS_64	NZ	D_ASP_61	OD1	3.074
4HIH	D_ARG_66	NH1	D_ASP_86	OD1	3.418
4HIH	D_ARG_66	NH1	D_ASP_86	OD2	3.903
4HIH	D_ARG_66	NH2	D_ASP_86	OD1	3.186
4HIH	D_ARG_66	NH2	D_ASP_86	OD2	2.280
4HIH	D_LYS_94	NZ	D_ASP_101	OD1	3.190
4HIH	D_LYS_94	NZ	D_ASP_101	OD2	2.845
4HIH	D_LYS_143	NZ	D_ASP_144	OD1	2.994
4HIH	D_LYS_143	NZ	D_ASP_144	OD2	3.430
4HIH	D_LYS_209	NZ	C_GLU_123	OE1	2.616
4HIH	D_LYS_209	NZ	C_GLU_123	OE2	2.820

Table 529: 4HHH-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4HII	A_ARG_24	NH1	A_ASP_70	OD1	2.503
4HII	A_ARG_24	NH1	A_ASP_70	OD2	2.815
4HII	A_ARG_61	NH2	A_GLU_81	OE1	2.820
4HII	A_ARG_61	NH2	A_ASP_82	OD1	3.181
4HII	A_ARG_61	NH2	A_ASP_82	OD2	3.709
4HII	A_ARG_91	NH2	B_GLU_95	OE1	3.439
4HII	A_ARG_91	NH2	B_GLU_95	OE2	3.542
4HII	A_LYS_107	NZ	A_GLU_17	OE1	3.144
4HII	A_LYS_107	NZ	A_GLU_17	OE2	3.461
4HII	A_LYS_183	NZ	A_GLU_187	OE2	3.590
4HII	B_HIS_35	NE2	B_GLU_95	OE2	2.635
4HII	B_ARG_38	NH2	B_GLU_46	OE1	3.115
4HII	B_ARG_38	NH2	B_GLU_46	OE2	3.676
4HII	B_ARG_55	NH1	B_ASP_53	OD2	2.693
4HII	B_LYS_64	NZ	B_ASP_61	OD1	3.295
4HII	B_ARG_66	NH1	B_ASP_86	OD1	3.781
4HII	B_ARG_66	NH2	B_ASP_86	OD1	3.392
4HII	B_ARG_66	NH2	B_ASP_86	OD2	2.480
4HII	B_LYS_94	NZ	B_ASP_101	OD1	3.440
4HII	B_LYS_94	NZ	B_ASP_101	OD2	3.082
4HII	B_LYS_143	NZ	B_ASP_144	OD1	3.286
4HII	B_LYS_143	NZ	B_ASP_144	OD2	3.429
4HII	B_LYS_201	NZ	B_ASP_199	OD2	3.171
4HII	B_LYS_209	NZ	A_GLU_123	OE1	2.845
4HII	B_LYS_209	NZ	A_GLU_123	OE2	2.723
4HII	C_ARG_24	NH1	C_ASP_70	OD2	2.819
4HII	C_ARG_24	NH2	C_ASP_70	OD2	3.355
4HII	C_ARG_61	NH2	C_ASP_82	OD1	3.075
4HII	C_ARG_61	NH2	C_ASP_82	OD2	3.678
4HII	C_ARG_91	NH1	D_GLU_95	OE2	3.915
4HII	C_ARG_91	NH2	D_GLU_95	OE1	3.687
4HII	C_ARG_91	NH2	D_GLU_95	OE2	3.380
4HII	C_ARG_211	NH1	C_GLU_187	OE1	3.789
4HII	D_HIS_35	NE2	D_GLU_95	OE2	2.645
4HII	D_ARG_38	NH2	D_GLU_46	OE1	2.570
4HII	D_ARG_38	NH2	D_GLU_46	OE2	3.392
4HII	D_ARG_55	NH1	D_ASP_53	OD2	3.825
4HII	D_LYS_64	NZ	D_ASP_61	OD1	2.713
4HII	D_ARG_66	NH1	D_ASP_86	OD1	3.823
4HII	D_ARG_66	NH2	D_ASP_86	OD1	2.954
4HII	D_ARG_66	NH2	D_ASP_86	OD2	2.357
4HII	D_LYS_94	NZ	D_ASP_101	OD1	3.250
4HII	D_LYS_94	NZ	D_ASP_101	OD2	2.971
4HII	D_LYS_143	NZ	D_ASP_144	OD1	3.120
4HII	D_LYS_143	NZ	D_ASP_144	OD2	3.351
4HII	D_LYS_201	NZ	D_ASP_199	OD2	3.563

Table 530: 4HII-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4HIJ	A_ARG_24	NH1	A_ASP_70	OD2	2.299
4HIJ	A_ARG_24	NH2	A_ASP_70	OD2	3.791
4HIJ	A_ARG_61	NH2	A_GLU_81	OE1	2.950
4HIJ	A_ARG_61	NH2	A_ASP_82	OD1	3.410
4HIJ	A_ARG_61	NH2	A_ASP_82	OD2	3.898
4HIJ	A_ARG_91	NH1	B_GLU_95	OE2	3.962
4HIJ	A_ARG_91	NH2	B_GLU_95	OE1	3.390
4HIJ	A_ARG_91	NH2	B_GLU_95	OE2	3.274
4HIJ	A_LYS_107	NZ	A_GLU_17	OE1	3.611
4HIJ	B_HIS_35	NE2	B_GLU_95	OE2	2.959
4HIJ	B_ARG_38	NH1	B_ASP_86	OD1	3.073
4HIJ	B_ARG_38	NH2	B_GLU_46	OE1	3.833
4HIJ	B_ARG_66	NH2	B_ASP_86	OD1	3.357
4HIJ	B_ARG_66	NH2	B_ASP_86	OD2	2.483
4HIJ	B_LYS_94	NZ	B_ASP_101	OD1	3.665
4HIJ	B_LYS_94	NZ	B_ASP_101	OD2	3.228
4HIJ	B_LYS_143	NZ	B_ASP_144	OD1	3.068
4HIJ	B_LYS_143	NZ	B_ASP_144	OD2	3.410
4HIJ	B_LYS_201	NZ	B_ASP_199	OD2	3.924
4HIJ	C_ARG_24	NH1	C_ASP_70	OD1	2.906
4HIJ	C_ARG_24	NH1	C_ASP_70	OD2	2.387
4HIJ	C_ARG_24	NH2	C_ASP_70	OD2	3.911
4HIJ	C_ARG_61	NH2	C_ASP_82	OD1	3.100
4HIJ	C_ARG_61	NH2	C_ASP_82	OD2	3.911
4HIJ	C_ARG_91	NH2	D_GLU_95	OE1	3.772
4HIJ	C_ARG_91	NH2	D_GLU_95	OE2	3.260
4HIJ	C_ARG_211	NH1	C_GLU_187	OE1	3.642
4HIJ	D_HIS_35	NE2	D_GLU_95	OE2	3.142
4HIJ	D_ARG_38	NH1	D_GLU_46	OE1	2.836
4HIJ	D_ARG_38	NH1	D_GLU_46	OE2	3.204
4HIJ	D_ARG_38	NH2	D_GLU_46	OE1	2.304
4HIJ	D_ARG_38	NH2	D_GLU_46	OE2	3.866
4HIJ	D_ARG_66	NH1	D_ASP_86	OD1	3.893
4HIJ	D_ARG_66	NH2	D_ASP_86	OD1	3.106
4HIJ	D_ARG_66	NH2	D_ASP_86	OD2	2.216
4HIJ	D_ARG_83	NH1	D_GLU_85	OE1	3.248
4HIJ	D_LYS_94	NZ	D_ASP_101	OD1	3.449
4HIJ	D_LYS_94	NZ	D_ASP_101	OD2	2.903
4HIJ	D_LYS_143	NZ	D_ASP_144	OD1	3.444
4HIJ	D_LYS_201	NZ	D_ASP_199	OD2	3.897
4HIJ	D_LYS_209	NZ	C_GLU_123	OE2	3.644

Table 531: 4HIJ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4HK0	A_ARG_38	NH1	A_ASP_90	OD1	3.774
4HK0	A_ARG_38	NH2	A_GLU_46	OE1	3.385
4HK0	A_LYS_63	NZ	A_GLU_46	OE1	3.620
4HK0	A_LYS_63	NZ	A_GLU_46	OE2	2.816
4HK0	A_ARG_98	NH1	A_ASP_114	OD1	2.925
4HK0	A_ARG_98	NH1	A_ASP_114	OD2	2.908
4HK0	A_LYS_156	NZ	A_ASP_157	OD2	3.983
4HK0	A_LYS_222	NZ	B_GLU_125	OE2	2.735
4HK0	B_HIS_33	ND1	B_ASP_49	OD1	3.937
4HK0	B_ARG_53	NH2	B_GLU_59	OE1	3.235
4HK0	B_ARG_60	NH1	B_ASP_81	OD1	3.686
4HK0	B_ARG_60	NH1	B_ASP_81	OD2	2.420
4HK0	B_ARG_60	NH2	B_GLU_78	OE1	3.881
4HK0	B_ARG_60	NH2	B_GLU_78	OE2	3.957
4HK0	B_ARG_60	NH2	B_ASP_81	OD1	2.791
4HK0	B_ARG_60	NH2	B_ASP_81	OD2	3.073
4HK0	B_LYS_168	NZ	B_GLU_82	OE1	2.997
4HK0	C_LYS_12	NZ	C_GLU_10	OE1	3.899
4HK0	C_ARG_38	NH1	C_ASP_90	OD1	3.244
4HK0	C_ARG_38	NH2	C_GLU_46	OE1	3.777
4HK0	C_LYS_63	NZ	C_GLU_46	OE1	3.276
4HK0	C_LYS_63	NZ	C_GLU_46	OE2	3.058
4HK0	C_ARG_98	NH1	C_ASP_114	OD1	3.138
4HK0	C_ARG_98	NH1	C_ASP_114	OD2	3.046
4HK0	C_ARG_104	NH2	D_ASP_95	OD2	3.573
4HK0	C_ARG_223	NH1	C_GLU_225	OE2	2.198
4HK0	D_HIS_33	ND1	D_ASP_49	OD1	3.742
4HK0	D_ARG_60	NH1	D_ASP_81	OD1	3.821
4HK0	D_ARG_60	NH1	D_ASP_81	OD2	2.677
4HK0	D_ARG_60	NH2	D_GLU_78	OE1	3.974
4HK0	D_ARG_60	NH2	D_GLU_78	OE2	3.744
4HK0	D_ARG_60	NH2	D_ASP_81	OD1	2.869
4HK0	D_ARG_60	NH2	D_ASP_81	OD2	3.194
4HK0	D_LYS_104	NZ	B_ASP_50	OD1	3.601
4HK0	D_LYS_104	NZ	B_ASP_50	OD2	2.755
4HK0	D_LYS_168	NZ	D_GLU_82	OE1	2.591
4HK0	D_LYS_168	NZ	D_GLU_82	OE2	3.531

Table 532: 4HK0-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4HK3	J_LYS_12	NZ	J_GLU_10	OE1	3.915
4HK3	J_ARG_38	NH2	J_GLU_46	OE1	2.769
4HK3	J_ARG_38	NH2	J_GLU_46	OE2	3.282
4HK3	J_LYS_63	NZ	J_GLU_46	OE2	2.332
4HK3	J_ARG_87	NH1	J_ASP_89	OD2	2.971
4HK3	J_ARG_87	NH2	J_ASP_89	OD2	3.577
4HK3	J_ARG_98	NH2	J_ASP_114	OD2	3.696
4HK3	J_LYS_222	NZ	N_GLU_125	OE2	3.801
4HK3	N_ARG_60	NH1	N_ASP_81	OD1	3.992
4HK3	N_ARG_60	NH1	N_ASP_81	OD2	2.782
4HK3	N_ARG_60	NH2	N_GLU_78	OE1	3.386
4HK3	N_ARG_60	NH2	N_ASP_81	OD1	3.085
4HK3	N_ARG_60	NH2	N_ASP_81	OD2	3.312
4HK3	N_LYS_168	NZ	N_GLU_82	OE1	3.394
4HK3	N_HIS_190	ND1	N_ASP_153	OD2	3.547
4HK3	N_ARG_191	NH2	N_ASP_153	OD1	3.900

Table 533: 4HK3-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4HKB	J_ARG_12	NH2	J_GLU_10	OE1	3.239
4HKB	J_ARG_12	NH2	J_GLU_10	OE2	3.220
4HKB	J_LYS_19	NZ	J_GLU_82	OE1	3.848
4HKB	J_LYS_23	NZ	C_ASP_73	OD1	3.505
4HKB	J_ARG_38	NH1	J_ASP_90	OD1	3.980
4HKB	J_ARG_38	NH2	J_GLU_46	OE1	3.646
4HKB	J_LYS_63	NZ	J_GLU_46	OE1	3.117
4HKB	J_LYS_63	NZ	J_GLU_46	OE2	3.110
4HKB	J_ARG_72	NH2	A_GLU_10	OE1	3.065
4HKB	J_ARG_72	NH2	A_GLU_10	OE2	2.664
4HKB	J_ARG_87	NH1	J_ASP_89	OD2	3.926
4HKB	J_ARG_87	NH2	J_ASP_89	OD2	2.996
4HKB	J_ARG_98	NH2	J_ASP_114	OD2	3.564
4HKB	J_LYS_222	NZ	N_GLU_125	OE1	3.188
4HKB	J_LYS_222	NZ	N_GLU_125	OE2	3.564
4HKB	A_ARG_12	NH2	A_GLU_10	OE1	3.493
4HKB	A_ARG_12	NH2	A_GLU_10	OE2	3.910
4HKB	A_LYS_19	NZ	A_GLU_82	OE2	2.857
4HKB	A_LYS_63	NZ	A_GLU_46	OE1	2.508
4HKB	A_LYS_63	NZ	A_GLU_46	OE2	3.155
4HKB	A_ARG_72	NH2	C_GLU_10	OE1	3.154
4HKB	A_ARG_72	NH2	C_GLU_10	OE2	2.755
4HKB	A_ARG_87	NH2	A_ASP_90	OD1	3.948
4HKB	A_ARG_98	NH1	A_ASP_114	OD2	3.306
4HKB	A_LYS_156	NZ	B_GLU_126	OE2	3.919
4HKB	A_LYS_222	NZ	B_GLU_125	OE1	3.019
4HKB	A_LYS_222	NZ	B_GLU_125	OE2	3.903
4HKB	C_LYS_63	NZ	E_ASP_89	OD1	3.939
4HKB	C_LYS_63	NZ	E_ASP_89	OD2	3.374
4HKB	C_ARG_87	NH2	E_ASP_90	OD1	3.045
4HKB	C_ARG_87	NH2	E_ASP_90	OD2	2.962
4HKB	C_ARG_98	NH2	C_ASP_114	OD2	3.961
4HKB	C_LYS_222	NZ	D_GLU_125	OE1	3.332
4HKB	C_LYS_222	NZ	D_GLU_125	OE2	3.836
4HKB	E_LYS_23	NZ	G_ASP_73	OD1	2.630
4HKB	E_ARG_38	NH2	E_GLU_46	OE1	2.965
4HKB	E_LYS_63	NZ	C_ASP_89	OD1	3.625
4HKB	E_LYS_63	NZ	C_ASP_89	OD2	3.095
4HKB	E_ARG_72	NH1	I_GLU_10	OE1	2.874
4HKB	E_ARG_72	NH1	I_GLU_10	OE2	2.849
4HKB	E_ARG_87	NH1	C_ASP_90	OD1	3.489
4HKB	E_ARG_87	NH1	C_ASP_90	OD2	3.954
4HKB	E_ARG_87	NH2	C_ASP_90	OD1	3.930
4HKB	E_ARG_87	NH2	C_ASP_90	OD2	3.219
4HKB	E_ARG_98	NH1	E_ASP_114	OD1	3.817
4HKB	E_ARG_98	NH2	E_ASP_114	OD1	3.776
4HKB	E_ARG_98	NH2	E_ASP_114	OD2	3.131
4HKB	E_LYS_222	NZ	F_GLU_125	OE2	3.327
4HKB	G_ARG_12	NH2	G_GLU_10	OE1	3.730
4HKB	G_LYS_63	NZ	G_GLU_46	OE1	3.337
4HKB	G_LYS_63	NZ	G_GLU_46	OE2	2.386
4HKB	G_ARG_87	NH1	J_ASP_90	OD1	3.108
4HKB	G_ARG_87	NH1	J_ASP_90	OD2	3.912
4HKB	G_ARG_87	NH2	J_ASP_90	OD2	3.607
4HKB	G_ARG_98	NH1	G_ASP_114	OD1	3.184
4HKB	G_ARG_98	NH1	G_ASP_114	OD2	2.840
4HKB	I_ARG_12	NH1	I_GLU_10	OE2	3.852

4HKB	I_ARG_12	NH2	I_GLU_10	OE1	2.937
4HKB	I_ARG_12	NH2	I_GLU_10	OE2	2.684
4HKB	I_LYS_63	NZ	I_GLU_46	OE1	3.642
4HKB	I_LYS_63	NZ	I_GLU_46	OE2	2.727
4HKB	I_ARG_72	NH2	G_GLU_10	OE1	3.560
4HKB	I_ARG_72	NH2	G_GLU_10	OE2	2.553
4HKB	I_ARG_87	NH2	I_ASP_90	OD1	3.524
4HKB	I_ARG_98	NH1	I_ASP_114	OD1	2.891
4HKB	I_ARG_98	NH1	I_ASP_114	OD2	2.660
4HKB	I_LYS_222	NZ	K_GLU_125	OE2	3.211
4HKB	N_ARG_29	NH1	J_ASP_107	OD1	3.664
4HKB	N_ARG_29	NH1	J_ASP_107	OD2	2.469
4HKB	N_ARG_31	NH1	N_ASP_33	OD2	3.836
4HKB	N_ARG_31	NH2	N_ASP_33	OD1	2.568
4HKB	N_ARG_31	NH2	N_ASP_33	OD2	3.159
4HKB	N_ARG_60	NH1	N_GLU_78	OE1	3.549
4HKB	N_ARG_60	NH2	N_GLU_78	OE1	3.300
4HKB	N_ARG_60	NH2	N_GLU_78	OE2	3.943
4HKB	N_ARG_60	NH2	N_ASP_81	OD1	3.653
4HKB	N_ARG_60	NH2	N_ASP_81	OD2	3.144
4HKB	N_ARG_76	NH2	N_GLU_59	OE1	3.931
4HKB	N_LYS_104	NZ	N_ASP_84	OD1	3.498
4HKB	N_LYS_131	NZ	J_ASP_157	OD2	3.951
4HKB	B_ARG_29	NH1	A_ASP_107	OD2	3.659
4HKB	B_LYS_30	NZ	B_ASP_91	OD1	3.949
4HKB	B_ARG_31	NH2	B_ASP_33	OD1	3.960
4HKB	B_ARG_31	NH2	B_ASP_33	OD2	3.759
4HKB	B_ARG_60	NH1	B_GLU_78	OE2	3.613
4HKB	B_ARG_60	NH2	B_ASP_81	OD1	3.250
4HKB	B_ARG_60	NH2	B_ASP_81	OD2	3.168
4HKB	D_ARG_29	NH1	C_ASP_107	OD2	3.254
4HKB	D_LYS_30	NZ	D_ASP_91	OD1	2.419
4HKB	D_ARG_60	NH1	D_ASP_81	OD2	3.419
4HKB	D_ARG_60	NH2	D_ASP_81	OD1	2.947
4HKB	D_ARG_60	NH2	D_ASP_81	OD2	2.756
4HKB	D_LYS_173	NZ	D_ASP_140	OD1	3.957
4HKB	F_ARG_60	NH1	F_GLU_78	OE2	3.243
4HKB	F_ARG_60	NH1	F_ASP_81	OD2	3.702
4HKB	F_ARG_60	NH2	F_GLU_78	OE2	3.760
4HKB	F_ARG_60	NH2	F_ASP_81	OD1	3.084
4HKB	F_ARG_60	NH2	F_ASP_81	OD2	2.449
4HKB	H_ARG_29	NH1	G_ASP_107	OD2	3.325
4HKB	H_ARG_29	NH2	G_ASP_107	OD2	3.189
4HKB	H_LYS_30	NZ	H_ASP_91	OD1	3.082
4HKB	H_ARG_31	NH1	H_ASP_33	OD1	3.793
4HKB	H_ARG_31	NH1	H_ASP_33	OD2	3.908
4HKB	H_ARG_31	NH2	H_ASP_33	OD1	2.388
4HKB	H_ARG_31	NH2	H_ASP_33	OD2	3.779
4HKB	H_ARG_60	NH1	H_GLU_78	OE1	3.666
4HKB	H_ARG_60	NH2	H_GLU_78	OE1	3.977
4HKB	H_ARG_60	NH2	H_ASP_81	OD1	2.952
4HKB	H_ARG_60	NH2	H_ASP_81	OD2	3.391
4HKB	K_ARG_31	NH1	I_ASP_107	OD2	3.242
4HKB	K_ARG_60	NH1	K_GLU_78	OE1	2.918
4HKB	K_ARG_60	NH1	K_ASP_81	OD2	3.967
4HKB	K_ARG_60	NH2	K_GLU_78	OE1	3.867
4HKB	K_ARG_60	NH2	K_ASP_81	OD1	3.109
4HKB	K_ARG_60	NH2	K_ASP_81	OD2	3.013

4HKB	K_LYS_168	NZ	K_GLU_82	OE1	3.989
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Table 534: 4HKB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4HKX	E_LYS_86	NZ	E_GLU_90	OE2	3.670
4HKX	E_ARG_106	NH1	E_GLU_85	OE1	2.849
4HKX	E_ARG_106	NH1	E_GLU_85	OE2	3.341
4HKX	E_ARG_117	NH2	E_GLU_72	OE1	2.670
4HKX	E_ARG_117	NH2	E_GLU_72	OE2	3.532
4HKX	E_ARG_192	NH1	B_ASP_95	OD2	3.293
4HKX	E_ARG_192	NH2	E_GLU_198	OE1	3.620
4HKX	E_ARG_192	NH2	E_GLU_198	OE2	3.387
4HKX	E_HIS_208	NE2	E_GLU_238	OE2	2.261
4HKX	E_LYS_219	NZ	E_GLU_227	OE1	3.854
4HKX	E_LYS_219	NZ	B_ASP_93	OD1	2.877
4HKX	E_LYS_219	NZ	B_ASP_93	OD2	3.792
4HKX	E_LYS_222	NZ	E_ASP_225	OD1	3.665
4HKX	E_ARG_255	NH2	E_GLU_119	OE2	3.522
4HKX	E_ARG_262	NH1	E_GLU_175	OE2	3.705
4HKX	E_ARG_262	NH2	E_GLU_175	OE1	3.350
4HKX	E_ARG_262	NH2	E_GLU_175	OE2	2.626
4HKX	A_ARG_12	NH1	A_GLU_10	OE1	2.383
4HKX	A_ARG_12	NH2	A_GLU_10	OE1	3.758
4HKX	A_ARG_38	NH1	A_ASP_90	OD1	3.193
4HKX	A_ARG_38	NH2	A_GLU_46	OE1	3.363
4HKX	A_LYS_63	NZ	A_GLU_46	OE1	3.731
4HKX	A_LYS_63	NZ	A_GLU_46	OE2	3.103
4HKX	A_ARG_87	NH2	A_ASP_89	OD2	3.799
4HKX	A_ARG_98	NH1	A_ASP_114	OD1	3.449
4HKX	A_ARG_98	NH1	A_ASP_114	OD2	2.980
4HKX	A_LYS_222	NZ	B_GLU_125	OE1	3.981
4HKX	B_ARG_29	NH2	A_ASP_107	OD2	3.853
4HKX	B_ARG_31	NH1	B_ASP_33	OD1	2.677
4HKX	B_ARG_31	NH1	B_ASP_33	OD2	2.578
4HKX	B_ARG_60	NH1	B_ASP_81	OD1	3.864
4HKX	B_ARG_60	NH1	B_ASP_81	OD2	2.652
4HKX	B_ARG_60	NH2	B_GLU_78	OE1	3.882
4HKX	B_ARG_60	NH2	B_GLU_78	OE2	3.841
4HKX	B_ARG_60	NH2	B_ASP_81	OD1	3.111
4HKX	B_ARG_60	NH2	B_ASP_81	OD2	3.335
4HKX	B_LYS_104	NZ	B_ASP_84	OD1	2.803
4HKX	B_LYS_104	NZ	B_ASP_84	OD2	3.287
4HKX	B_LYS_112	NZ	B_GLU_200	OE1	2.796
4HKX	B_LYS_131	NZ	A_ASP_157	OD2	3.310
4HKX	B_HIS_190	ND1	B_ASP_153	OD2	3.199

Table 535: 4HKX-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4HLZ	A_LYS_45	NZ	A_ASP_41	OD1	3.467
4HLZ	A_LYS_45	NZ	A_ASP_41	OD2	2.740
4HLZ	A_LYS_50	NZ	A_GLU_275	OE1	3.453
4HLZ	A_ARG_94	NH1	A_ASP_63	OD1	3.722
4HLZ	A_ARG_94	NH1	A_ASP_63	OD2	2.940
4HLZ	A_LYS_109	NZ	A_GLU_89	OE1	2.563
4HLZ	A_LYS_109	NZ	A_GLU_89	OE2	3.402
4HLZ	A_LYS_109	NZ	B_GLU_69	OE1	3.478
4HLZ	A_LYS_109	NZ	B_GLU_69	OE2	2.999
4HLZ	A_LYS_119	NZ	A_GLU_255	OE2	3.868
4HLZ	A_LYS_123	NZ	A_GLU_255	OE1	3.335
4HLZ	A_LYS_123	NZ	A_GLU_255	OE2	2.676
4HLZ	A_ARG_149	NH1	A_ASP_77	OD2	3.932
4HLZ	A_ARG_149	NH2	A_ASP_77	OD1	3.367
4HLZ	A_ARG_149	NH2	A_ASP_77	OD2	2.770
4HLZ	A_LYS_165	NZ	A_GLU_246	OE1	3.809
4HLZ	A_HIS_184	NE2	A_GLU_231	OE1	3.401
4HLZ	A_ARG_263	NH2	A_GLU_174	OE1	3.264
4HLZ	A_LYS_269	NZ	A_GLU_89	OE1	3.398
4HLZ	A_LYS_310	NZ	B_ASP_90	OD1	2.429
4HLZ	A_LYS_310	NZ	B_ASP_90	OD2	3.948
4HLZ	A_LYS_313	NZ	A_ASP_27	OD2	3.590
4HLZ	A_ARG_321	NH1	A_GLU_31	OE1	3.534
4HLZ	A_ARG_321	NH1	A_GLU_31	OE2	3.033
4HLZ	A_ARG_321	NH2	A_GLU_31	OE1	2.812
4HLZ	A_ARG_321	NH2	A_GLU_31	OE2	3.752
4HLZ	B_LYS_51	NZ	B_GLU_103	OE1	2.548
4HLZ	B_LYS_58	NZ	F_GLU_97	OE1	3.865
4HLZ	B_LYS_58	NZ	F_GLU_97	OE2	3.885
4HLZ	B_ARG_75	NH1	B_GLU_78	OE1	2.253
4HLZ	B_ARG_75	NH1	B_GLU_78	OE2	3.633
4HLZ	B_ARG_76	NH1	D_GLU_74	OE1	2.838
4HLZ	B_ARG_76	NH1	D_GLU_74	OE2	3.993
4HLZ	B_ARG_76	NH2	D_GLU_74	OE1	3.145
4HLZ	B_ARG_76	NH2	D_GLU_74	OE2	2.917
4HLZ	B_LYS_82	NZ	B_ASP_86	OD1	3.774
4HLZ	B_LYS_82	NZ	B_ASP_86	OD2	2.458
4HLZ	B_LYS_83	NZ	D_GLU_85	OE2	2.459
4HLZ	B_ARG_106	NH2	F_ASP_109	OD2	3.278
4HLZ	B_ARG_123	NH2	B_ASP_120	OD1	3.032
4HLZ	B_LYS_131	NZ	B_GLU_139	OE2	3.861
4HLZ	B_LYS_143	NZ	A_ASP_11	OD1	3.527
4HLZ	B_LYS_143	NZ	A_ASP_11	OD2	3.714
4HLZ	B_LYS_143	NZ	B_ASP_29	OD1	3.825
4HLZ	B_LYS_143	NZ	B_ASP_29	OD2	2.836
4HLZ	B_ARG_170	NH1	B_ASP_128	OD2	3.529
4HLZ	B_ARG_170	NH2	B_ASP_128	OD2	3.130
4HLZ	C_ARG_32	NH1	F_GLU_57	OE1	3.413
4HLZ	C_LYS_45	NZ	C_ASP_41	OD1	3.408
4HLZ	C_LYS_45	NZ	C_ASP_41	OD2	2.813
4HLZ	C_LYS_90	NZ	C_ASP_63	OD1	3.022
4HLZ	C_LYS_90	NZ	C_ASP_63	OD2	3.647
4HLZ	C_ARG_94	NH1	C_GLU_75	OE1	3.383
4HLZ	C_ARG_94	NH1	C_ASP_95	OD1	3.179
4HLZ	C_ARG_94	NH1	C_ASP_95	OD2	3.935
4HLZ	C_LYS_109	NZ	C_GLU_89	OE1	2.906
4HLZ	C_LYS_109	NZ	C_GLU_89	OE2	3.287

4HLZ	C_LYS_109	NZ	D_GLU_69	OE1	2.904
4HLZ	C_LYS_109	NZ	D_GLU_69	OE2	3.394
4HLZ	C_ARG_126	NH2	C_ASP_125	OD2	3.430
4HLZ	C_ARG_149	NH1	C_ASP_77	OD2	3.631
4HLZ	C_ARG_149	NH2	C_ASP_77	OD1	3.636
4HLZ	C_ARG_149	NH2	C_ASP_77	OD2	2.529
4HLZ	C_HIS_184	NE2	C_GLU_231	OE1	3.054
4HLZ	C_ARG_263	NH2	C_GLU_174	OE1	2.955
4HLZ	C_ARG_263	NH2	C_GLU_174	OE2	3.891
4HLZ	C_LYS_269	NZ	C_GLU_89	OE1	2.769
4HLZ	C_LYS_310	NZ	D_ASP_86	OD2	2.827
4HLZ	C_LYS_310	NZ	D_ASP_90	OD1	2.357
4HLZ	C_LYS_310	NZ	D_ASP_90	OD2	3.459
4HLZ	C_LYS_313	NZ	C_ASP_27	OD2	2.972
4HLZ	C_ARG_321	NH1	C_GLU_31	OE1	3.468
4HLZ	C_ARG_321	NH1	C_GLU_31	OE2	3.239
4HLZ	C_ARG_321	NH2	C_GLU_31	OE1	3.056
4HLZ	C_ARG_321	NH2	C_GLU_31	OE2	3.827
4HLZ	D_LYS_51	NZ	D_GLU_103	OE1	2.956
4HLZ	D_LYS_58	NZ	B_GLU_97	OE1	2.796
4HLZ	D_LYS_58	NZ	D_GLU_57	OE2	3.744
4HLZ	D_ARG_75	NH1	D_GLU_78	OE1	3.640
4HLZ	D_ARG_75	NH1	D_GLU_78	OE2	2.859
4HLZ	D_ARG_76	NH1	F_GLU_74	OE1	3.279
4HLZ	D_ARG_76	NH1	F_GLU_74	OE2	2.976
4HLZ	D_ARG_76	NH2	E_GLU_107	OE2	3.277
4HLZ	D_ARG_76	NH2	F_GLU_74	OE2	2.480
4HLZ	D_LYS_83	NZ	F_GLU_85	OE2	2.714
4HLZ	D_ARG_106	NH2	B_ASP_109	OD2	3.865
4HLZ	D_LYS_116	NZ	D_ASP_120	OD2	3.998
4HLZ	D_ARG_123	NH2	D_ASP_120	OD1	2.808
4HLZ	D_LYS_131	NZ	F_ASP_128	OD1	3.317
4HLZ	D_LYS_167	NZ	D_GLU_164	OE1	2.593
4HLZ	E_LYS_45	NZ	E_ASP_41	OD1	3.643
4HLZ	E_LYS_45	NZ	E_ASP_41	OD2	2.964
4HLZ	E_LYS_90	NZ	E_ASP_63	OD1	3.784
4HLZ	E_LYS_109	NZ	E_GLU_89	OE1	3.198
4HLZ	E_LYS_109	NZ	E_GLU_89	OE2	3.420
4HLZ	E_LYS_109	NZ	F_GLU_69	OE1	2.572
4HLZ	E_LYS_109	NZ	F_GLU_69	OE2	3.930
4HLZ	E_LYS_123	NZ	E_GLU_255	OE1	3.027
4HLZ	E_ARG_149	NH2	E_ASP_77	OD1	3.597
4HLZ	E_ARG_149	NH2	E_ASP_77	OD2	3.190
4HLZ	E_HIS_183	NE2	E_GLU_190	OE2	3.927
4HLZ	E_LYS_259	NZ	E_GLU_116C	OE1	3.783
4HLZ	E_LYS_259	NZ	E_GLU_116C	OE2	3.326
4HLZ	E_LYS_269	NZ	E_GLU_89	OE1	3.197
4HLZ	E_LYS_280	NZ	E_GLU_304	OE1	3.278
4HLZ	E_LYS_310	NZ	F_ASP_86	OD1	3.890
4HLZ	E_LYS_310	NZ	F_ASP_90	OD1	3.800
4HLZ	E_ARG_321	NH1	E_GLU_31	OE1	3.413
4HLZ	E_ARG_321	NH1	E_GLU_31	OE2	2.743
4HLZ	E_ARG_321	NH2	E_GLU_31	OE1	3.001
4HLZ	E_ARG_321	NH2	E_GLU_31	OE2	3.732
4HLZ	F_LYS_51	NZ	F_GLU_103	OE1	2.737
4HLZ	F_LYS_58	NZ	D_GLU_97	OE1	3.641
4HLZ	F_ARG_75	NH1	F_GLU_78	OE1	2.620
4HLZ	F_ARG_75	NH2	F_GLU_78	OE1	3.832

4HLZ	F_ARG_76	NH1	B_GLU_74	OE1	3.514
4HLZ	F_ARG_76	NH1	B_GLU_74	OE2	3.227
4HLZ	F_ARG_76	NH2	B_GLU_74	OE1	3.962
4HLZ	F_ARG_76	NH2	B_GLU_74	OE2	2.467
4HLZ	F_ARG_106	NH1	F_GLU_103	OE2	3.652
4HLZ	F_LYS_116	NZ	F_ASP_120	OD2	2.737
4HLZ	F_ARG_123	NH2	F_ASP_120	OD1	2.964
4HLZ	F_LYS_131	NZ	F_GLU_139	OE1	3.361
4HLZ	F_LYS_131	NZ	F_GLU_139	OE2	3.419
4HLZ	F_LYS_143	NZ	F_ASP_29	OD1	2.830
4HLZ	F_ARG_170	NH1	F_ASP_128	OD2	3.604
4HLZ	F_ARG_170	NH2	F_ASP_128	OD2	3.330
4HLZ	G_ARG_38	NH1	G_ASP_86	OD1	3.271
4HLZ	G_ARG_38	NH2	G_GLU_46	OE1	3.356
4HLZ	G_ARG_38	NH2	G_GLU_46	OE2	3.777
4HLZ	G_ARG_38	NH2	G_ASP_86	OD1	3.890
4HLZ	G_ARG_52	NH2	G_ASP_32	OD1	2.343
4HLZ	G_ARG_52	NH2	G_ASP_32	OD2	3.536
4HLZ	G_ARG_66	NH1	G_ASP_86	OD1	3.326
4HLZ	G_ARG_66	NH1	G_ASP_86	OD2	2.639
4HLZ	G_ARG_66	NH2	G_ASP_86	OD1	3.814
4HLZ	G_ARG_83	NH1	G_GLU_85	OE1	3.950
4HLZ	H_ARG_63	NH2	H_ASP_84	OD1	2.596
4HLZ	H_ARG_63	NH2	H_ASP_84	OD2	2.745
4HLZ	H_LYS_144	NZ	H_GLU_107	OE1	3.903
4HLZ	H_LYS_144	NZ	H_GLU_107	OE2	3.652
4HLZ	H_LYS_151	NZ	H_GLU_197	OE1	3.384
4HLZ	H_LYS_151	NZ	H_GLU_197	OE2	3.081
4HLZ	H_LYS_201	NZ	H_ASP_112	OD2	3.156
4HLZ	H_ARG_213	NH2	H_GLU_189	OE1	2.950
4HLZ	I_ARG_38	NH1	I_ASP_86	OD2	2.915
4HLZ	I_ARG_38	NH2	I_GLU_46	OE1	3.111
4HLZ	I_ARG_38	NH2	I_GLU_46	OE2	3.673
4HLZ	I_ARG_38	NH2	I_ASP_86	OD2	3.591
4HLZ	I_ARG_52	NH2	I_ASP_32	OD1	2.561
4HLZ	I_ARG_52	NH2	I_ASP_32	OD2	3.549
4HLZ	I_ARG_66	NH1	I_ASP_86	OD1	2.650
4HLZ	I_ARG_66	NH1	I_ASP_86	OD2	3.900
4HLZ	I_ARG_66	NH2	I_ASP_86	OD1	3.129
4HLZ	I_ARG_66	NH2	I_ASP_86	OD2	2.801
4HLZ	I_ARG_71	NH2	I_ASP_31	OD2	3.990
4HLZ	I_ARG_83	NH2	I_GLU_85	OE1	3.778
4HLZ	I_LYS_96	NZ	D_ASP_46	OD1	2.912
4HLZ	I_LYS_96	NZ	D_ASP_46	OD2	3.655
4HLZ	I_LYS_205	NZ	I_ASP_207	OD1	2.427
4HLZ	I_LYS_208	NZ	J_GLU_125	OE2	3.495
4HLZ	I_ARG_213	NH2	J_GLU_125	OE1	3.227
4HLZ	I_ARG_213	NH2	J_GLU_125	OE2	3.829
4HLZ	J_ARG_63	NH2	J_ASP_84	OD2	2.740
4HLZ	J_LYS_149	NZ	J_GLU_156	OE2	3.758
4HLZ	J_LYS_151	NZ	J_GLU_197	OE2	2.583
4HLZ	J_ARG_157	NH2	J_GLU_187	OE1	3.252
4HLZ	J_ARG_190	NH1	J_ASP_186	OD2	3.881
4HLZ	J_ARG_190	NH2	J_ASP_186	OD2	3.287
4HLZ	J_LYS_201	NZ	J_ASP_112	OD1	3.693
4HLZ	J_LYS_201	NZ	J_ASP_112	OD2	2.715
4HLZ	K_ARG_38	NH1	K_ASP_86	OD2	2.904
4HLZ	K_ARG_38	NH2	K_GLU_46	OE1	3.825

4HLZ	K_ARG_38	NH2	K_GLU_46	OE2	3.374
4HLZ	K_ARG_38	NH2	K_ASP_86	OD2	3.795
4HLZ	K_ARG_52	NH2	K_ASP_32	OD2	3.514
4HLZ	K_ARG_66	NH1	K_ASP_86	OD1	2.524
4HLZ	K_ARG_66	NH2	K_ASP_86	OD1	2.641
4HLZ	K_ARG_66	NH2	K_ASP_86	OD2	2.778
4HLZ	L_ARG_63	NH2	L_ASP_84	OD1	3.511
4HLZ	L_ARG_63	NH2	L_ASP_84	OD2	3.426
4HLZ	L_LYS_151	NZ	L_GLU_197	OE2	3.915

Table 536: 4HLZ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4HMG	A.LYS_27	NZ	B.GLU_97	OE1	2.795
4HMG	A.LYS_27	NZ	B.GLU_97	OE2	3.247
4HMG	A.LYS_50	NZ	A.ASP_275	OD1	2.738
4HMG	A.HIS_56	NE2	A.GLU_280	OE2	3.458
4HMG	A.ARG_57	NH1	A.GLU_82	OE1	2.930
4HMG	A.ARG_57	NH1	A.GLU_82	OE2	3.739
4HMG	A.ARG_57	NH2	A.GLU_82	OE1	3.316
4HMG	A.HIS_75	ND1	A.ASP_73	OD1	2.731
4HMG	A.HIS_75	ND1	A.ASP_73	OD2	3.421
4HMG	A.HIS_75	NE2	A.ASP_63	OD1	3.435
4HMG	A.ARG_90	NH1	A.ASP_60	OD1	2.846
4HMG	A.ARG_90	NH1	A.ASP_60	OD2	3.713
4HMG	A.ARG_109	NH1	B.GLU_67	OE1	3.584
4HMG	A.ARG_109	NH1	B.GLU_67	OE2	2.773
4HMG	A.ARG_109	NH2	A.GLU_89	OE1	3.290
4HMG	A.ARG_109	NH2	A.GLU_89	OE2	2.543
4HMG	A.ARG_141	NH1	A.ASP_77	OD1	2.714
4HMG	A.ARG_141	NH1	A.ASP_77	OD2	3.370
4HMG	A.ARG_141	NH2	A.ASP_77	OD1	2.707
4HMG	A.LYS_176	NZ	A.GLU_123	OE1	2.555
4HMG	A.LYS_176	NZ	A.GLU_123	OE2	3.715
4HMG	A.HIS_183	NE2	A.GLU_190	OE1	3.735
4HMG	A.ARG_207	NH2	A.ASP_241	OD1	3.612
4HMG	A.ARG_208	NH2	A.ASP_241	OD1	3.591
4HMG	A.ARG_208	NH2	A.ASP_241	OD2	2.706
4HMG	A.LYS_238	NZ	A.ASP_175	OD1	2.945
4HMG	A.LYS_238	NZ	A.ASP_175	OD2	2.559
4HMG	A.LYS_238	NZ	F.GLU_72	OE2	2.782
4HMG	A.ARG_261	NH1	A.GLU_119	OE1	3.272
4HMG	A.ARG_261	NH1	A.GLU_119	OE2	3.090
4HMG	A.ARG_261	NH2	A.GLU_119	OE1	2.807
4HMG	A.ARG_261	NH2	A.GLU_119	OE2	2.795
4HMG	A.LYS_264	NZ	A.ASP_85	OD1	3.254
4HMG	A.LYS_264	NZ	A.ASP_85	OD2	2.704
4HMG	A.ARG_269	NH2	B.GLU_67	OE1	2.783
4HMG	A.LYS_292	NZ	A.ASP_291	OD1	2.976
4HMG	A.LYS_292	NZ	A.ASP_291	OD2	2.795
4HMG	A.LYS_310	NZ	B.ASP_90	OD1	3.350
4HMG	A.LYS_310	NZ	B.ASP_90	OD2	2.711
4HMG	A.LYS_315	NZ	A.GLU_41	OE2	3.691
4HMG	B.LYS_51	NZ	B.GLU_103	OE2	2.574
4HMG	B.ARG_54	NH1	F.GLU_97	OE1	3.078
4HMG	B.ARG_54	NH2	B.GLU_57	OE1	2.870
4HMG	B.ARG_54	NH2	B.GLU_57	OE2	3.339
4HMG	B.ARG_54	NH2	E.ASP_32	OD2	3.863
4HMG	B.ARG_54	NH2	F.GLU_97	OE1	3.088
4HMG	B.LYS_62	NZ	F.ASP_86	OD1	2.890
4HMG	B.LYS_62	NZ	F.ASP_86	OD2	2.630
4HMG	B.LYS_62	NZ	F.ASP_90	OD1	3.620
4HMG	B.LYS_62	NZ	F.ASP_90	OD2	3.931
4HMG	B.HIS_64	NE2	F.ASP_79	OD2	3.785
4HMG	B.LYS_68	NZ	B.GLU_85	OE1	2.990
4HMG	B.LYS_68	NZ	B.GLU_85	OE2	2.568
4HMG	B.ARG_76	NH1	D.GLU_74	OE1	2.796
4HMG	B.ARG_76	NH1	D.GLU_74	OE2	3.711
4HMG	B.ARG_76	NH1	D.GLU_81	OE1	2.672
4HMG	B.ARG_76	NH1	D.GLU_81	OE2	3.308

4HMG	B_ARG_76	NH2	D_GLU_74	OE1	3.404
4HMG	B_ARG_76	NH2	D_GLU_74	OE2	2.827
4HMG	B_LYS_117	NZ	B_GLU_114	OE1	2.600
4HMG	B_LYS_117	NZ	B_GLU_114	OE2	3.394
4HMG	B_ARG_123	NH1	F_GLU_132	OE2	3.178
4HMG	B_ARG_123	NH2	B_GLU_120	OE1	2.819
4HMG	B_ARG_123	NH2	B_GLU_120	OE2	2.567
4HMG	B_ARG_124	NH1	F_GLU_132	OE1	3.359
4HMG	B_ARG_124	NH1	F_GLU_132	OE2	3.102
4HMG	B_ARG_124	NH2	B_GLU_120	OE2	3.559
4HMG	B_ARG_127	NH2	F_GLU_131	OE1	2.525
4HMG	B_LYS_143	NZ	B_ASP_145	OD2	3.353
4HMG	B_HIS_159	NE2	B_ASP_160	OD1	3.910
4HMG	B_HIS_159	NE2	B_ASP_160	OD2	3.133
4HMG	B_ARG_163	NH1	F_GLU_131	OE1	3.338
4HMG	B_ARG_163	NH1	F_GLU_131	OE2	2.796
4HMG	B_ARG_163	NH2	F_GLU_131	OE1	2.694
4HMG	B_ARG_163	NH2	F_GLU_131	OE2	3.492
4HMG	B_ARG_170	NH1	B_GLU_128	OE1	2.770
4HMG	B_ARG_170	NH2	B_GLU_131	OE2	2.764
4HMG	B_ARG_170	NH2	D_GLU_128	OE1	3.784
4HMG	B_ARG_170	NH2	D_GLU_128	OE2	3.698
4HMG	C_LYS_27	NZ	D_GLU_97	OE1	2.789
4HMG	C_LYS_27	NZ	D_GLU_97	OE2	3.246
4HMG	C_LYS_50	NZ	C_ASP_275	OD1	2.725
4HMG	C_HIS_56	NE2	C_GLU_280	OE2	3.428
4HMG	C_ARG_57	NH1	C_GLU_82	OE1	2.906
4HMG	C_ARG_57	NH1	C_GLU_82	OE2	3.723
4HMG	C_ARG_57	NH2	C_GLU_82	OE1	3.281
4HMG	C_HIS_75	ND1	C_ASP_73	OD1	2.703
4HMG	C_HIS_75	ND1	C_ASP_73	OD2	3.384
4HMG	C_HIS_75	NE2	C_ASP_63	OD1	3.436
4HMG	C_ARG_90	NH1	C_ASP_60	OD1	2.839
4HMG	C_ARG_90	NH1	C_ASP_60	OD2	3.741
4HMG	C_ARG_109	NH1	D_GLU_67	OE1	3.616
4HMG	C_ARG_109	NH1	D_GLU_67	OE2	2.791
4HMG	C_ARG_109	NH2	C_GLU_89	OE1	3.304
4HMG	C_ARG_109	NH2	C_GLU_89	OE2	2.531
4HMG	C_ARG_141	NH1	C_ASP_77	OD1	2.711
4HMG	C_ARG_141	NH1	C_ASP_77	OD2	3.370
4HMG	C_ARG_141	NH2	C_ASP_77	OD1	2.681
4HMG	C_LYS_176	NZ	C_GLU_123	OE1	2.557
4HMG	C_LYS_176	NZ	C_GLU_123	OE2	3.685
4HMG	C_HIS_183	NE2	C_GLU_190	OE1	3.742
4HMG	C_ARG_207	NH2	C_ASP_241	OD1	3.569
4HMG	C_ARG_208	NH2	C_ASP_241	OD1	3.571
4HMG	C_ARG_208	NH2	C_ASP_241	OD2	2.695
4HMG	C_LYS_238	NZ	B_GLU_72	OE2	2.606
4HMG	C_LYS_238	NZ	C_ASP_175	OD1	2.940
4HMG	C_LYS_238	NZ	C_ASP_175	OD2	2.570
4HMG	C_ARG_261	NH1	C_GLU_119	OE1	3.250
4HMG	C_ARG_261	NH1	C_GLU_119	OE2	3.087
4HMG	C_ARG_261	NH2	C_GLU_119	OE1	2.811
4HMG	C_ARG_261	NH2	C_GLU_119	OE2	2.823
4HMG	C_LYS_264	NZ	C_ASP_85	OD1	3.271
4HMG	C_LYS_264	NZ	C_ASP_85	OD2	2.729
4HMG	C_ARG_269	NH2	D_GLU_67	OE1	2.764
4HMG	C_LYS_292	NZ	C_ASP_291	OD1	2.981

4HMG	C_LYS_292	NZ	C_ASP_291	OD2	2.812
4HMG	C_LYS_310	NZ	D_ASP_90	OD1	3.321
4HMG	C_LYS_310	NZ	D_ASP_90	OD2	2.697
4HMG	C_LYS_315	NZ	C_GLU_41	OE2	3.694
4HMG	C_LYS_326	NZ	D_GLU_15	OE1	3.836
4HMG	C_LYS_326	NZ	D_GLU_15	OE2	2.684
4HMG	D_LYS_51	NZ	D_GLU_103	OE2	2.595
4HMG	D_ARG_54	NH1	B_GLU_97	OE1	3.076
4HMG	D_ARG_54	NH2	A_ASP_32	OD2	3.995
4HMG	D_ARG_54	NH2	B_GLU_97	OE1	3.112
4HMG	D_ARG_54	NH2	D_GLU_57	OE1	2.847
4HMG	D_ARG_54	NH2	D_GLU_57	OE2	3.364
4HMG	D_LYS_62	NZ	B_ASP_86	OD1	2.940
4HMG	D_LYS_62	NZ	B_ASP_86	OD2	2.591
4HMG	D_LYS_62	NZ	B_ASP_90	OD1	3.586
4HMG	D_LYS_62	NZ	B_ASP_90	OD2	3.891
4HMG	D_HIS_64	NE2	B_ASP_79	OD2	3.731
4HMG	D_LYS_68	NZ	D_GLU_85	OE1	2.969
4HMG	D_LYS_68	NZ	D_GLU_85	OE2	2.606
4HMG	D_ARG_76	NH1	F_GLU_74	OE1	2.745
4HMG	D_ARG_76	NH1	F_GLU_74	OE2	3.756
4HMG	D_ARG_76	NH1	F_GLU_81	OE1	2.644
4HMG	D_ARG_76	NH1	F_GLU_81	OE2	3.314
4HMG	D_ARG_76	NH2	F_GLU_74	OE1	3.255
4HMG	D_ARG_76	NH2	F_GLU_74	OE2	2.777
4HMG	D_LYS_117	NZ	D_GLU_114	OE1	2.606
4HMG	D_LYS_117	NZ	D_GLU_114	OE2	3.387
4HMG	D_ARG_123	NH1	B_GLU_132	OE2	3.157
4HMG	D_ARG_123	NH2	D_GLU_120	OE1	2.828
4HMG	D_ARG_123	NH2	D_GLU_120	OE2	2.538
4HMG	D_ARG_124	NH1	B_GLU_132	OE1	3.347
4HMG	D_ARG_124	NH1	B_GLU_132	OE2	3.074
4HMG	D_ARG_124	NH2	D_GLU_120	OE2	3.592
4HMG	D_ARG_127	NH2	B_GLU_131	OE1	2.541
4HMG	D_LYS_143	NZ	D_ASP_145	OD2	3.357
4HMG	D_HIS_159	NE2	D_ASP_160	OD1	3.925
4HMG	D_HIS_159	NE2	D_ASP_160	OD2	3.140
4HMG	D_ARG_163	NH1	B_GLU_131	OE1	3.321
4HMG	D_ARG_163	NH1	B_GLU_131	OE2	2.801
4HMG	D_ARG_163	NH2	B_GLU_131	OE1	2.729
4HMG	D_ARG_163	NH2	B_GLU_131	OE2	3.526
4HMG	D_ARG_170	NH1	D_GLU_128	OE1	2.798
4HMG	D_ARG_170	NH2	D_GLU_131	OE2	2.778
4HMG	D_ARG_170	NH2	F_GLU_128	OE1	3.859
4HMG	D_ARG_170	NH2	F_GLU_128	OE2	3.829
4HMG	E_LYS_27	NZ	F_GLU_97	OE1	2.764
4HMG	E_LYS_27	NZ	F_GLU_97	OE2	3.247
4HMG	E_LYS_50	NZ	E_ASP_275	OD1	2.749
4HMG	E_HIS_56	NE2	E_GLU_280	OE2	3.460
4HMG	E_ARG_57	NH1	E_GLU_82	OE1	2.908
4HMG	E_ARG_57	NH1	E_GLU_82	OE2	3.750
4HMG	E_ARG_57	NH2	E_GLU_82	OE1	3.320
4HMG	E_HIS_75	ND1	E_ASP_73	OD1	2.714
4HMG	E_HIS_75	ND1	E_ASP_73	OD2	3.391
4HMG	E_HIS_75	NE2	E_ASP_63	OD1	3.445
4HMG	E_ARG_90	NH1	E_ASP_60	OD1	2.880
4HMG	E_ARG_90	NH1	E_ASP_60	OD2	3.726
4HMG	E_ARG_109	NH1	F_GLU_67	OE1	3.614

4HMG	E_ARG_109	NH1	F_GLU_67	OE2	2.773
4HMG	E_ARG_109	NH2	E_GLU_89	OE1	3.299
4HMG	E_ARG_109	NH2	E_GLU_89	OE2	2.546
4HMG	E_ARG_141	NH1	E_ASP_77	OD1	2.709
4HMG	E_ARG_141	NH1	E_ASP_77	OD2	3.383
4HMG	E_ARG_141	NH2	E_ASP_77	OD1	2.687
4HMG	E_LYS_176	NZ	E_GLU_123	OE1	2.598
4HMG	E_LYS_176	NZ	E_GLU_123	OE2	3.726
4HMG	E_HIS_183	NE2	E_GLU_190	OE1	3.747
4HMG	E_ARG_207	NH2	E_ASP_241	OD1	3.575
4HMG	E_ARG_208	NH2	E_ASP_241	OD1	3.603
4HMG	E_ARG_208	NH2	E_ASP_241	OD2	2.770
4HMG	E_LYS_238	NZ	D_GLU_72	OE2	2.707
4HMG	E_LYS_238	NZ	E_ASP_175	OD1	2.946
4HMG	E_LYS_238	NZ	E_ASP_175	OD2	2.555
4HMG	E_ARG_261	NH1	E_GLU_119	OE1	3.244
4HMG	E_ARG_261	NH1	E_GLU_119	OE2	3.073
4HMG	E_ARG_261	NH2	E_GLU_119	OE1	2.813
4HMG	E_ARG_261	NH2	E_GLU_119	OE2	2.815
4HMG	E_LYS_264	NZ	E_ASP_85	OD1	3.266
4HMG	E_LYS_264	NZ	E_ASP_85	OD2	2.734
4HMG	E_ARG_269	NH2	F_GLU_67	OE1	2.739
4HMG	E_LYS_292	NZ	E_ASP_291	OD1	3.009
4HMG	E_LYS_292	NZ	E_ASP_291	OD2	2.847
4HMG	E_LYS_310	NZ	F_ASP_90	OD1	3.300
4HMG	E_LYS_310	NZ	F_ASP_90	OD2	2.685
4HMG	E_LYS_315	NZ	E_GLU_41	OE2	3.689
4HMG	F_ARG_25	NH1	E_GLU_325	OE1	3.853
4HMG	F_LYS_51	NZ	F_GLU_103	OE2	2.620
4HMG	F_ARG_54	NH1	D_GLU_97	OE1	3.052
4HMG	F_ARG_54	NH2	C_ASP_32	OD2	3.923
4HMG	F_ARG_54	NH2	D_GLU_97	OE1	3.130
4HMG	F_ARG_54	NH2	F_GLU_57	OE1	2.861
4HMG	F_ARG_54	NH2	F_GLU_57	OE2	3.350
4HMG	F_LYS_62	NZ	D_ASP_86	OD1	2.900
4HMG	F_LYS_62	NZ	D_ASP_86	OD2	2.597
4HMG	F_LYS_62	NZ	D_ASP_90	OD1	3.664
4HMG	F_LYS_62	NZ	D_ASP_90	OD2	3.951
4HMG	F_HIS_64	NE2	D_ASP_79	OD2	3.646
4HMG	F_LYS_68	NZ	F_GLU_85	OE1	3.007
4HMG	F_LYS_68	NZ	F_GLU_85	OE2	2.563
4HMG	F_ARG_76	NH1	B_GLU_74	OE1	2.714
4HMG	F_ARG_76	NH1	B_GLU_74	OE2	3.687
4HMG	F_ARG_76	NH1	B_GLU_81	OE1	2.651
4HMG	F_ARG_76	NH1	B_GLU_81	OE2	3.434
4HMG	F_ARG_76	NH2	B_GLU_74	OE1	3.281
4HMG	F_ARG_76	NH2	B_GLU_74	OE2	2.711
4HMG	F_LYS_117	NZ	F_GLU_114	OE1	2.613
4HMG	F_LYS_117	NZ	F_GLU_114	OE2	3.409
4HMG	F_ARG_123	NH1	D_GLU_132	OE2	3.178
4HMG	F_ARG_123	NH2	F_GLU_120	OE1	2.836
4HMG	F_ARG_123	NH2	F_GLU_120	OE2	2.539
4HMG	F_ARG_124	NH1	D_GLU_132	OE1	3.402
4HMG	F_ARG_124	NH1	D_GLU_132	OE2	3.132
4HMG	F_ARG_124	NH2	F_GLU_120	OE2	3.562
4HMG	F_ARG_127	NH2	D_GLU_131	OE1	2.579
4HMG	F_LYS_143	NZ	F_ASP_145	OD2	3.346
4HMG	F_ARG_153	NH2	F_GLU_150	OE1	2.613

4HMG	F_HIS_159	NE2	F_ASP_160	OD1	3.932
4HMG	F_HIS_159	NE2	F_ASP_160	OD2	3.131
4HMG	F_ARG_163	NH1	D_GLU_131	OE1	3.299
4HMG	F_ARG_163	NH1	D_GLU_131	OE2	2.816
4HMG	F_ARG_163	NH2	D_GLU_131	OE1	2.752
4HMG	F_ARG_163	NH2	D_GLU_131	OE2	3.575
4HMG	F_ARG_170	NH1	F_GLU_128	OE1	2.781
4HMG	F_ARG_170	NH2	B_GLU_128	OE1	3.815
4HMG	F_ARG_170	NH2	B_GLU_128	OE2	3.719
4HMG	F_ARG_170	NH2	F_GLU_131	OE2	2.764

Table 537: 4HMG-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4HWB	A_ARG_230	NH2	H_ASP_56	OD2	3.246
4HWB	A_ARG_285	NH2	A_GLU_237	OE1	2.762
4HWB	A_ARG_285	NH2	A_GLU_237	OE2	3.252
4HWB	A_ARG_287	NH2	A_GLU_235	OE1	2.730
4HWB	A_ARG_287	NH2	A_GLU_235	OE2	3.307
4HWB	H_ARG_39	NH2	H_GLU_47	OE2	3.027
4HWB	H_ARG_99	NH2	H_ASP_107	OD1	3.362
4HWB	H_ARG_99	NH2	H_ASP_107	OD2	2.612
4HWB	H_LYS_149	NZ	H_ASP_150	OD1	3.433
4HWB	H_LYS_149	NZ	H_ASP_150	OD2	3.050
4HWB	H_LYS_215	NZ	L_GLU_120	OE2	3.469
4HWB	L_ARG_24	NH1	L_ASP_71	OD2	3.912
4HWB	L_ARG_62	NH2	L_GLU_82	OE1	3.563
4HWB	L_ARG_62	NH2	L_ASP_83	OD1	3.123
4HWB	L_ARG_62	NH2	L_ASP_83	OD2	3.996
4HWB	L_LYS_146	NZ	L_GLU_192	OE2	2.824
4HWB	L_LYS_180	NZ	L_GLU_184	OE2	3.810
4HWB	L_HIS_186	ND1	L_ASP_148	OD2	3.236

Table 538: 4HWB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4HXA	L_HIS_34	ND1	L_ASP_50	OD2	3.892
4HXA	L_ARG_61	NH1	L_GLU_79	OE1	3.572
4HXA	L_ARG_61	NH1	L_GLU_79	OE2	3.959
4HXA	L_ARG_61	NH2	L_GLU_79	OE1	3.712
4HXA	L_ARG_61	NH2	L_GLU_81	OE2	2.919
4HXA	L_ARG_61	NH2	L_ASP_82	OD1	2.910
4HXA	L_ARG_61	NH2	L_ASP_82	OD2	3.687
4HXA	L_LYS_103	NZ	L_ASP_165	OD1	3.306
4HXA	L_LYS_142	NZ	L_GLU_105	OE1	2.359
4HXA	L_LYS_142	NZ	L_GLU_105	OE2	3.217
4HXA	L_LYS_147	NZ	L_GLU_154	OE2	3.699
4HXA	L_LYS_183	NZ	L_GLU_187	OE1	2.855
4HXA	L_LYS_183	NZ	L_GLU_187	OE2	3.206
4HXA	L_HIS_189	ND1	L_ASP_151	OD1	2.656
4HXA	L_LYS_199	NZ	L_ASP_110	OD1	2.782
4HXA	H_ARG_33	NH2	H_ASP_53	OD2	3.146
4HXA	H_ARG_38	NH1	H_ASP_86	OD1	2.911
4HXA	H_ARG_38	NH2	H_GLU_46	OE1	3.220
4HXA	H_ARG_38	NH2	H_GLU_46	OE2	3.961
4HXA	H_ARG_38	NH2	H_ASP_86	OD1	3.758
4HXA	H_ARG_66	NH1	H_ASP_86	OD1	3.213
4HXA	H_ARG_66	NH1	H_ASP_86	OD2	3.541
4HXA	H_ARG_66	NH2	H_ASP_86	OD1	3.547
4HXA	H_ARG_66	NH2	H_ASP_86	OD2	2.335
4HXA	H_ARG_71	NH2	H_ASP_73	OD2	3.421
4HXA	H_LYS_75	NZ	H_ASP_72	OD1	2.706
4HXA	H_ARG_94	NH2	H_ASP_101	OD1	2.566
4HXA	H_ARG_94	NH2	H_ASP_101	OD2	3.802
4HXA	H_ARG_98	NH1	L_ASP_50	OD1	2.959
4HXA	H_ARG_98	NH1	L_ASP_50	OD2	3.607
4HXA	H_HIS_164	NE2	L_ASP_167	OD1	3.601
4HXA	H_LYS_205	NZ	H_ASP_207	OD1	3.339
4HXA	H_LYS_205	NZ	H_ASP_207	OD2	2.614

Table 539: 4HXA-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4HXB	L_ARG_61	NH1	L_ASP_82	OD1	3.754
4HXB	L_ARG_61	NH1	L_ASP_82	OD2	2.851
4HXB	L_ARG_61	NH2	L_GLU_79	OE2	3.892
4HXB	L_ARG_61	NH2	L_GLU_81	OE2	3.579
4HXB	L_ARG_61	NH2	L_ASP_82	OD1	2.893
4HXB	L_ARG_61	NH2	L_ASP_82	OD2	3.275
4HXB	L_LYS_147	NZ	L_GLU_195	OE2	2.100
4HXB	L_LYS_149	NZ	L_GLU_195	OE1	2.509
4HXB	L_LYS_149	NZ	L_GLU_195	OE2	3.644
4HXB	L_ARG_155	NH1	L_GLU_185	OE2	3.650
4HXB	L_ARG_155	NH2	L_GLU_185	OE1	2.787
4HXB	L_ARG_155	NH2	L_GLU_185	OE2	2.877
4HXB	L_LYS_183	NZ	L_GLU_187	OE1	3.719
4HXB	L_HIS_189	ND1	L_ASP_151	OD2	2.591
4HXB	L_HIS_189	NE2	L_GLU_185	OE2	3.681
4HXB	L_LYS_199	NZ	L_ASP_110	OD2	3.163
4HXB	H_LYS_12	NZ	H_GLU_10	OE2	3.536
4HXB	H_LYS_46	NZ	H_ASP_62	OD2	2.395
4HXB	H_LYS_64	NZ	H_GLU_61	OE1	2.630
4HXB	H_LYS_64	NZ	H_GLU_61	OE2	2.953
4HXB	H_ARG_66	NH1	H_ASP_86	OD1	3.620
4HXB	H_ARG_66	NH1	H_ASP_86	OD2	2.850
4HXB	H_ARG_66	NH2	H_ASP_86	OD1	2.767
4HXB	H_ARG_66	NH2	H_ASP_86	OD2	3.484
4HXB	H_LYS_83	NZ	H_GLU_85	OE1	2.634
4HXB	H_ARG_94	NH1	H_ASP_101	OD1	3.226
4HXB	H_ARG_94	NH1	H_ASP_101	OD2	2.767
4HXB	H_ARG_96	NH1	L_ASP_94	OD1	3.212
4HXB	H_ARG_96	NH1	L_ASP_94	OD2	2.665
4HXB	H_ARG_96	NH2	L_ASP_94	OD1	2.669
4HXB	H_ARG_96	NH2	L_ASP_94	OD2	3.708

Table 540: 4HXB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4I2X	A_LYS_24	NZ	A_ASP_70	OD1	3.809
4I2X	A_ARG_61	NH2	A_ASP_82	OD1	2.612
4I2X	A_ARG_61	NH2	A_ASP_82	OD2	3.075
4I2X	A_LYS_147	NZ	A_GLU_154	OE2	3.876
4I2X	A_LYS_149	NZ	A_GLU_195	OE2	3.016
4I2X	A_ARG_155	NH2	A_GLU_185	OE1	2.492
4I2X	A_LYS_199	NZ	A_ASP_110	OD2	3.998
4I2X	A_ARG_211	NH1	A_GLU_187	OE1	2.914
4I2X	B_LYS_38	NZ	B_ASP_90	OD1	3.997
4I2X	B_LYS_59	NZ	E_GLU_10	OE2	3.418
4I2X	B_LYS_65	NZ	E_ASP_208	OD1	3.256
4I2X	B_LYS_67	NZ	B_ASP_90	OD1	3.836
4I2X	B_LYS_67	NZ	B_ASP_90	OD2	2.957
4I2X	B_LYS_214	NZ	A_GLU_123	OE2	3.742
4I2X	C_ARG_61	NH2	C_GLU_81	OE2	3.536
4I2X	C_ARG_61	NH2	C_ASP_82	OD1	2.611
4I2X	C_ARG_61	NH2	C_ASP_82	OD2	3.223
4I2X	C_LYS_147	NZ	C_GLU_154	OE2	3.881
4I2X	C_LYS_147	NZ	C_GLU_195	OE1	3.855
4I2X	C_LYS_149	NZ	C_GLU_195	OE2	3.745
4I2X	C_ARG_155	NH1	C_GLU_185	OE1	3.098
4I2X	C_ARG_155	NH2	C_GLU_185	OE1	2.928
4I2X	C_LYS_183	NZ	C_GLU_187	OE2	3.224
4I2X	C_LYS_199	NZ	C_ASP_110	OD1	3.402
4I2X	C_LYS_199	NZ	C_ASP_110	OD2	3.168
4I2X	C_ARG_211	NH1	C_GLU_187	OE1	3.303
4I2X	D_ARG_40	NH1	D_GLU_89	OE1	3.368
4I2X	D_ARG_40	NH2	D_GLU_89	OE1	3.617
4I2X	D_LYS_63	NZ	C_ASP_1	OD2	3.656
4I2X	D_LYS_65	NZ	F_ASP_208	OD1	3.848
4I2X	D_LYS_67	NZ	D_ASP_90	OD1	3.613
4I2X	D_LYS_67	NZ	D_ASP_90	OD2	3.084
4I2X	D_HIS_170	ND1	C_ASP_167	OD2	3.958
4I2X	D_LYS_211	NZ	D_ASP_213	OD1	3.197
4I2X	D_LYS_214	NZ	C_GLU_123	OE2	3.815
4I2X	E_HIS_24	ND1	E_GLU_10	OE1	3.035
4I2X	E_ARG_40	NH2	E_GLU_47	OE1	3.242
4I2X	E_ARG_40	NH2	E_GLU_47	OE2	3.478
4I2X	E_ARG_46	NH1	E_GLU_103	OE1	2.979
4I2X	E_ARG_46	NH2	E_GLU_103	OE1	3.021
4I2X	E_ARG_59	NH1	E_ASP_85	OD1	2.932
4I2X	E_ARG_59	NH1	E_ASP_85	OD2	3.555
4I2X	E_ARG_59	NH2	E_ASP_85	OD1	3.558
4I2X	E_ARG_59	NH2	E_ASP_85	OD2	2.755
4I2X	E_HIS_143	ND1	E_GLU_141	OE1	3.000
4I2X	E_HIS_143	ND1	E_GLU_141	OE2	3.158
4I2X	E_LYS_153	NZ	E_GLU_160	OE1	3.145
4I2X	E_LYS_153	NZ	E_GLU_160	OE2	3.307
4I2X	E_LYS_156	NZ	E_ASP_188	OD2	3.753
4I2X	E_LYS_156	NZ	E_ASP_191	OD1	3.430
4I2X	E_LYS_156	NZ	E_ASP_191	OD2	2.599
4I2X	E_ARG_180	NH2	E_ASP_169	OD2	3.719
4I2X	E_ARG_193	NH1	E_GLU_274	OE2	3.753
4I2X	E_ARG_193	NH2	E_GLU_274	OE2	2.935
4I2X	E_ARG_211	NH2	E_GLU_199	OE2	2.968
4I2X	E_ARG_221	NH1	E_ASP_306	OD2	2.386
4I2X	E_ARG_246	NH1	E_GLU_227	OE1	3.432

4I2X	E_ARG_266	NH1	E_GLU_259	OE2	2.959
4I2X	F_HIS_24	ND1	F_GLU_10	OE1	3.383
4I2X	F_ARG_40	NH2	F_GLU_47	OE1	2.707
4I2X	F_ARG_40	NH2	F_GLU_47	OE2	3.337
4I2X	F_ARG_46	NH1	F_GLU_103	OE1	3.160
4I2X	F_ARG_46	NH1	F_GLU_103	OE2	3.864
4I2X	F_ARG_46	NH2	F_GLU_103	OE1	3.013
4I2X	F_ARG_59	NH1	F_ASP_85	OD1	2.871
4I2X	F_ARG_59	NH1	F_ASP_85	OD2	2.922
4I2X	F_ARG_59	NH2	F_ASP_85	OD1	3.943
4I2X	F_ARG_59	NH2	F_ASP_85	OD2	2.928
4I2X	F_HIS_143	ND1	F_GLU_141	OE1	2.771
4I2X	F_HIS_143	ND1	F_GLU_141	OE2	3.495
4I2X	F_LYS_156	NZ	F_ASP_188	OD2	3.315
4I2X	F_LYS_156	NZ	F_ASP_191	OD2	3.515
4I2X	F_ARG_180	NH1	E_GLU_47	OE1	3.834
4I2X	F_ARG_211	NH2	F_GLU_199	OE2	2.770
4I2X	F_ARG_221	NH1	F_ASP_306	OD2	2.711
4I2X	F_ARG_246	NH1	F_GLU_227	OE1	2.969
4I2X	F_ARG_266	NH1	F_GLU_259	OE2	3.157

Table 541: 4I2X-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4I3R	G_LYS_282	NZ	H_GLU_33	OE1	3.996
4I3R	G_LYS_282	NZ	H_GLU_33	OE2	2.684
4I3R	G_LYS_351	NZ	G_GLU_269	OE1	3.563
4I3R	G_ARG_456	NH1	G_GLU_466	OE1	3.067
4I3R	G_ARG_469	NH2	G_ASP_457	OD1	3.936
4I3R	G_ARG_469	NH2	G_ASP_457	OD2	2.877
4I3R	H_ARG_19	NH1	H_ASP_81	OD1	3.627
4I3R	H_ARG_19	NH1	H_ASP_81	OD2	3.350
4I3R	H_ARG_38	NH1	H_ASP_86	OD1	3.177
4I3R	H_ARG_38	NH2	H_GLU_46	OE1	3.721
4I3R	H_ARG_38	NH2	H_ASP_86	OD1	3.995
4I3R	H_LYS_52	NZ	H_GLU_33	OE2	3.671
4I3R	H_ARG_64	NH2	G_ASP_457	OD1	3.551
4I3R	H_ARG_64	NH2	G_ASP_457	OD2	3.482
4I3R	H_ARG_66	NH1	H_ASP_62	OD1	3.277
4I3R	H_ARG_66	NH1	H_ASP_62	OD2	3.049
4I3R	H_ARG_66	NH1	H_ASP_86	OD1	3.545
4I3R	H_ARG_66	NH1	H_ASP_86	OD2	3.903
4I3R	H_ARG_66	NH2	H_ASP_86	OD1	3.310
4I3R	H_ARG_66	NH2	H_ASP_86	OD2	2.449
4I3R	H_ARG_71	NH1	G_ASP_368	OD1	3.996
4I3R	H_ARG_71	NH1	G_ASP_368	OD2	2.319
4I3R	H_ARG_71	NH2	G_ASP_368	OD1	3.997
4I3R	H_ARG_71	NH2	G_ASP_368	OD2	3.530
4I3R	H_ARG_94	NH1	H_ASP_101	OD1	2.785
4I3R	H_ARG_94	NH1	H_ASP_101	OD2	2.504
4I3R	H_LYS_96	NZ	H_ASP_101	OD2	3.693
4I3R	H_LYS_143	NZ	H_ASP_144	OD1	3.690
4I3R	H_LYS_143	NZ	H_ASP_144	OD2	3.274
4I3R	H_LYS_206	NZ	H_ASP_208	OD1	3.805
4I3R	H_LYS_209	NZ	L_GLU_123	OE2	2.484
4I3R	L_LYS_39	NZ	L_GLU_81	OE1	3.444
4I3R	L_ARG_54	NH2	L_ASP_60	OD1	2.979
4I3R	L_ARG_61	NH1	L_ASP_82	OD1	2.605
4I3R	L_ARG_61	NH1	L_ASP_82	OD2	2.581
4I3R	L_ARG_61	NH2	L_GLU_79	OE1	3.506
4I3R	L_ARG_61	NH2	L_GLU_79	OE2	3.423
4I3R	L_ARG_103	NH1	L_GLU_105	OE2	3.685
4I3R	L_ARG_107	NH2	L_GLU_17	OE1	3.953
4I3R	L_ARG_107	NH2	L_GLU_17	OE2	3.600
4I3R	L_LYS_149	NZ	L_GLU_195	OE2	3.690
4I3R	L_LYS_183	NZ	L_GLU_187	OE2	3.197

Table 542: 4I3R-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4I3S	G_LYS_282	NZ	G_GLU_275	OE1	3.977
4I3S	G_LYS_282	NZ	H_GLU_33	OE1	3.669
4I3S	G_LYS_282	NZ	H_GLU_33	OE2	3.690
4I3S	G_ARG_456	NH1	G_GLU_466	OE2	3.826
4I3S	G_ARG_469	NH2	G_ASP_457	OD2	3.288
4I3S	H_ARG_19	NH1	H_ASP_81	OD2	3.959
4I3S	H_ARG_31	NH1	H_ASP_27	OD2	3.996
4I3S	H_ARG_31	NH2	H_ASP_27	OD2	3.298
4I3S	H_ARG_38	NH1	H_ASP_86	OD1	2.791
4I3S	H_ARG_38	NH2	H_GLU_46	OE1	3.972
4I3S	H_ARG_38	NH2	H_ASP_86	OD1	3.641
4I3S	H_ARG_64	NH2	G_ASP_457	OD1	3.430
4I3S	H_ARG_64	NH2	G_ASP_457	OD2	3.082
4I3S	H_ARG_66	NH1	H_ASP_86	OD1	3.764
4I3S	H_ARG_66	NH1	H_ASP_86	OD2	3.474
4I3S	H_ARG_66	NH2	H_ASP_62	OD2	3.970
4I3S	H_ARG_66	NH2	H_ASP_86	OD1	2.906
4I3S	H_ARG_66	NH2	H_ASP_86	OD2	3.336
4I3S	H_ARG_71	NH1	G_ASP_368	OD1	3.370
4I3S	H_ARG_71	NH1	G_ASP_368	OD2	3.053
4I3S	H_ARG_71	NH2	G_ASP_368	OD1	3.484
4I3S	H_ARG_94	NH1	H_ASP_101	OD1	3.080
4I3S	H_ARG_94	NH1	H_ASP_101	OD2	2.812
4I3S	H_LYS_209	NZ	L_GLU_123	OE1	2.882
4I3S	L_ARG_54	NH1	L_ASP_60	OD1	3.742
4I3S	L_ARG_54	NH2	L_ASP_60	OD1	3.363
4I3S	L_ARG_61	NH1	L_GLU_79	OE2	2.892
4I3S	L_ARG_61	NH2	L_ASP_82	OD1	3.478
4I3S	L_ARG_103	NH1	L_GLU_105	OE1	3.837
4I3S	L_ARG_211	NH1	L_GLU_187	OE1	3.303
4I3S	L_ARG_211	NH2	L_GLU_187	OE1	3.109

Table 543: 4I3S-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4JAM	H_LYS_13	NZ	H_GLU_16	OE2	3.105
4JAM	H_ARG_38	NH1	H_ASP_86	OD1	2.909
4JAM	H_ARG_38	NH2	H_GLU_46	OE2	3.439
4JAM	H_ARG_38	NH2	H_ASP_86	OD1	3.603
4JAM	H_ARG_66	NH1	H_ASP_86	OD1	3.959
4JAM	H_ARG_66	NH1	H_ASP_86	OD2	3.260
4JAM	H_ARG_66	NH2	H_ASP_86	OD1	2.963
4JAM	H_ARG_66	NH2	H_ASP_86	OD2	3.519
4JAM	H_LYS_143	NZ	H_ASP_144	OD1	2.996
4JAM	H_LYS_143	NZ	H_ASP_144	OD2	3.461
4JAM	H_LYS_209	NZ	L_GLU_123	OE2	3.865
4JAM	H_LYS_210	NZ	H_GLU_212	OE2	3.818
4JAM	L_LYS_53	NZ	L_GLU_50	OE1	2.810
4JAM	L_ARG_54	NH1	L_ASP_60	OD1	3.496
4JAM	L_ARG_54	NH2	L_ASP_60	OD1	3.753
4JAM	L_ARG_61	NH2	L_ASP_82	OD1	2.928
4JAM	L_ARG_61	NH2	L_ASP_82	OD2	3.591
4JAM	L_LYS_110	NZ	L_GLU_198	OE1	2.600
4JAM	L_LYS_110	NZ	L_GLU_198	OE2	3.111
4JAM	L_LYS_149	NZ	L_GLU_203	OE1	2.760
4JAM	A_ARG_38	NH1	A_ASP_86	OD1	2.792
4JAM	A_ARG_38	NH2	A_GLU_46	OE1	3.309
4JAM	A_ARG_38	NH2	A_ASP_86	OD1	3.667
4JAM	A_ARG_66	NH1	A_ASP_86	OD1	3.551
4JAM	A_ARG_66	NH1	A_ASP_86	OD2	3.941
4JAM	A_ARG_66	NH2	A_ASP_86	OD1	3.154
4JAM	A_ARG_66	NH2	A_ASP_86	OD2	2.339
4JAM	A_LYS_143	NZ	A_ASP_144	OD1	3.127
4JAM	A_LYS_143	NZ	A_ASP_144	OD2	3.610
4JAM	A_LYS_206	NZ	A_ASP_208	OD1	2.503
4JAM	A_LYS_206	NZ	A_ASP_208	OD2	3.012
4JAM	A_LYS_209	NZ	B_GLU_123	OE2	3.814
4JAM	A_LYS_210	NZ	A_GLU_212	OE2	3.874
4JAM	B_LYS_53	NZ	B_GLU_50	OE1	2.752
4JAM	B_ARG_61	NH2	B_ASP_82	OD1	2.903
4JAM	B_ARG_61	NH2	B_ASP_82	OD2	3.571
4JAM	B_LYS_110	NZ	B_GLU_198	OE2	3.885
4JAM	B_LYS_149	NZ	B_GLU_203	OE1	3.006
4JAM	B_ARG_189	NH1	B_ASP_151	OD1	3.987
4JAM	B_ARG_189	NH1	B_ASP_151	OD2	3.937

Table 544: 4JAM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4JAN	G_LYS_282	NZ	G_GLU_275	OE1	3.474
4JAN	G_LYS_360	NZ	G_GLU_362	OE1	3.523
4JAN	G_ARG_456	NH1	G_GLU_466	OE1	3.351
4JAN	G_ARG_456	NH1	G_GLU_466	OE2	3.176
4JAN	G_ARG_469	NH2	G_GLU_362	OE2	3.387
4JAN	H_ARG_38	NH1	H_ASP_86	OD1	3.352
4JAN	H_ARG_38	NH2	H_GLU_46	OE1	3.075
4JAN	H_ARG_66	NH1	H_ASP_86	OD1	3.928
4JAN	H_ARG_66	NH1	H_ASP_86	OD2	3.649
4JAN	H_ARG_66	NH2	H_ASP_86	OD1	2.680
4JAN	H_ARG_66	NH2	H_ASP_86	OD2	3.194
4JAN	H_ARG_97	NH2	G_ASP_368	OD2	2.609
4JAN	H_ARG_97	NH2	G_GLU_370	OE1	2.554
4JAN	H_LYS_143	NZ	H_ASP_144	OD2	3.820
4JAN	H_LYS_143	NZ	L_GLU_124	OE2	3.811
4JAN	H_LYS_209	NZ	L_GLU_123	OE1	2.888
4JAN	L_LYS_53	NZ	L_GLU_50	OE1	2.884
4JAN	L_ARG_61	NH2	L_ASP_82	OD1	2.695
4JAN	L_ARG_61	NH2	L_ASP_82	OD2	3.778
4JAN	L_ARG_107	NH1	L_GLU_83	OE1	3.896
4JAN	L_LYS_110	NZ	L_GLU_198	OE1	2.837
4JAN	L_LYS_129	NZ	H_ASP_144	OD2	3.458
4JAN	L_LYS_344	NZ	L_GLU_290	OE1	3.334
4JAN	L_LYS_357	NZ	L_ASP_464	OD1	2.885
4JAN	L_LYS_360	NZ	L_GLU_362	OE1	3.054
4JAN	L_ARG_456	NH1	L_GLU_466	OE1	3.190
4JAN	L_ARG_456	NH1	L_GLU_466	OE2	3.591
4JAN	L_ARG_469	NH1	L_GLU_362	OE2	3.886
4JAN	L_ARG_469	NH2	L_GLU_362	OE2	3.292
4JAN	L_ARG_469	NH2	L_ASP_457	OD2	3.746
4JAN	A_ARG_38	NH1	A_ASP_86	OD1	3.100
4JAN	A_ARG_38	NH2	A_GLU_46	OE1	2.957
4JAN	A_ARG_38	NH2	A_ASP_86	OD1	3.991
4JAN	A_LYS_43	NZ	A_ASP_86	OD1	3.939
4JAN	A_ARG_66	NH1	A_ASP_86	OD2	3.380
4JAN	A_ARG_66	NH2	A_ASP_86	OD1	3.178
4JAN	A_ARG_66	NH2	A_ASP_86	OD2	3.385
4JAN	A_ARG_97	NH2	L_ASP_368	OD1	2.825
4JAN	A_ARG_97	NH2	L_ASP_368	OD2	3.792
4JAN	A_ARG_97	NH2	L_GLU_370	OE1	3.106
4JAN	A_LYS_143	NZ	A_ASP_144	OD1	3.191
4JAN	A_LYS_143	NZ	A_ASP_144	OD2	3.150
4JAN	A_LYS_209	NZ	B_GLU_123	OE1	3.788
4JAN	A_LYS_209	NZ	B_GLU_123	OE2	3.189
4JAN	A_LYS_210	NZ	A_GLU_212	OE2	3.659
4JAN	B_LYS_53	NZ	B_GLU_50	OE1	2.587
4JAN	B_ARG_61	NH2	B_ASP_82	OD1	2.736
4JAN	B_ARG_61	NH2	B_ASP_82	OD2	3.458
4JAN	B_HIS_188	NE2	B_ASP_151	OD2	3.951

Table 545: 4JAN-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4JHA	H_ARG_30	NH2	H_GLU_73	OE1	2.826
4JHA	H_ARG_30	NH2	H_GLU_73	OE2	3.416
4JHA	H_ARG_38	NH1	H_ASP_86	OD1	2.732
4JHA	H_ARG_38	NH2	H_GLU_85	OE1	3.002
4JHA	H_ARG_38	NH2	H_ASP_86	OD1	3.574
4JHA	H_LYS_62	NZ	H_GLU_46	OE1	3.088
4JHA	H_LYS_62	NZ	H_GLU_46	OE2	3.359
4JHA	H_LYS_62	NZ	H_GLU_85	OE1	3.798
4JHA	H_ARG_66	NH1	H_ASP_86	OD1	3.556
4JHA	H_ARG_66	NH1	H_ASP_86	OD2	2.912
4JHA	H_ARG_66	NH2	H_GLU_85	OE1	3.941
4JHA	H_ARG_66	NH2	H_GLU_85	OE2	3.694
4JHA	H_ARG_66	NH2	H_ASP_86	OD1	2.845
4JHA	H_ARG_66	NH2	H_ASP_86	OD2	3.591
4JHA	H_ARG_83	NH1	H_GLU_85	OE2	3.452
4JHA	H_HIS_100G	ND1	H_GLU_95	OE1	2.690
4JHA	H_HIS_100G	ND1	H_GLU_95	OE2	3.485
4JHA	H_LYS_143	NZ	H_ASP_144	OD1	3.717
4JHA	L_ARG_61	NH2	L_GLU_81	OE2	3.203
4JHA	L_ARG_61	NH2	L_ASP_82	OD1	2.990
4JHA	L_ARG_61	NH2	L_ASP_82	OD2	3.835
4JHA	L_LYS_103	NZ	L_GLU_165	OE1	3.560
4JHA	L_HIS_189	ND1	L_ASP_151	OD1	3.067
4JHA	L_HIS_189	ND1	L_ASP_151	OD2	2.332

Table 546: 4JHA-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4JHW	H_LYS_12	NZ	H_GLU_10	OE1	3.774
4JHW	H_LYS_12	NZ	H_GLU_10	OE2	3.410
4JHW	H_ARG_30	NH2	H_GLU_73	OE1	3.253
4JHW	H_ARG_30	NH2	H_GLU_73	OE2	3.595
4JHW	H_ARG_38	NH1	H_ASP_86	OD1	2.933
4JHW	H_ARG_38	NH2	H_GLU_85	OE1	3.397
4JHW	H_LYS_62	NZ	H_GLU_46	OE1	3.508
4JHW	H_LYS_62	NZ	H_GLU_46	OE2	3.235
4JHW	H_ARG_66	NH1	H_ASP_86	OD1	3.796
4JHW	H_ARG_66	NH1	H_ASP_86	OD2	3.522
4JHW	H_ARG_66	NH2	H_ASP_86	OD1	3.083
4JHW	H_ARG_83	NH1	H_GLU_85	OE2	3.470
4JHW	H_HIS_100G	ND1	H_GLU_95	OE1	2.582
4JHW	H_HIS_100G	ND1	H_GLU_95	OE2	3.471
4JHW	H_LYS_143	NZ	H_ASP_144	OD1	3.702
4JHW	L_ARG_61	NH2	L_GLU_81	OE2	2.896
4JHW	L_ARG_61	NH2	L_ASP_82	OD1	3.273
4JHW	L_ARG_61	NH2	L_ASP_82	OD2	3.811
4JHW	L_LYS_103	NZ	L_GLU_165	OE1	3.410
4JHW	L_LYS_103	NZ	L_GLU_165	OE2	3.764
4JHW	L_HIS_189	ND1	L_ASP_151	OD1	3.229
4JHW	L_HIS_189	ND1	L_ASP_151	OD2	2.338
4JHW	F_ARG_49	NH2	F_ASP_368	OD1	3.536
4JHW	F_LYS_85	NZ	F_GLU_82	OE1	3.836
4JHW	F_LYS_166	NZ	F_GLU_163	OE2	3.574
4JHW	F_LYS_168	NZ	F_GLU_294	OE1	3.244
4JHW	F_LYS_176	NZ	F_ASP_263	OD2	3.508
4JHW	F_LYS_191	NZ	F_GLU_60	OE2	3.607
4JHW	F_LYS_191	NZ	F_ASP_194	OD2	3.605
4JHW	F_LYS_196	NZ	F_GLU_60	OE1	2.692
4JHW	F_LYS_209	NZ	H_ASP_101	OD2	3.535
4JHW	F_LYS_209	NZ	L_GLU_55	OE1	2.845
4JHW	F_LYS_209	NZ	L_GLU_55	OE2	3.356
4JHW	F_ARG_229	NH1	F_GLU_256	OE1	3.739
4JHW	F_ARG_229	NH1	F_GLU_256	OE2	3.024
4JHW	F_ARG_229	NH2	F_GLU_256	OE1	2.796
4JHW	F_ARG_229	NH2	F_GLU_256	OE2	3.605
4JHW	F_ARG_235	NH2	F_GLU_236	OE2	3.517
4JHW	F_ARG_336	NH2	F_ASP_338	OD1	3.908
4JHW	F_ARG_336	NH2	F_ASP_338	OD2	3.114
4JHW	F_ARG_364	NH1	F_ASP_310	OD1	2.617
4JHW	F_ARG_364	NH2	F_ASP_310	OD1	2.621
4JHW	F_LYS_433	NZ	F_ASP_440	OD2	3.857
4JHW	F_LYS_461	NZ	F_ASP_448	OD1	2.628
4JHW	F_LYS_498	NZ	F_GLU_487	OE1	3.211
4JHW	F_LYS_498	NZ	F_GLU_487	OE2	3.707
4JHW	F_ARG_507	NH1	F_GLU_511	OE2	3.100

Table 547: 4JHW-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4JO1	L_LYS_39	NZ	L_ASP_81	OD2	2.927
4JO1	L_LYS_53	NZ	L_ASP_50	OD1	2.687
4JO1	L_ARG_61	NH1	L_ASP_82	OD1	2.727
4JO1	L_ARG_61	NH1	L_ASP_82	OD2	3.457
4JO1	L_ARG_61	NH2	L_ASP_82	OD1	3.476
4JO1	L_ARG_61	NH2	L_ASP_82	OD2	2.757
4JO1	L_LYS_138	NZ	L_ASP_169	OD1	2.582
4JO1	L_LYS_162	NZ	L_ASP_142	OD1	2.686
4JO1	L_LYS_162	NZ	L_ASP_142	OD2	3.695
4JO1	H_ARG_38	NH1	H_ASP_86	OD2	2.789
4JO1	H_ARG_38	NH2	H_GLU_46	OE1	3.151
4JO1	H_ARG_38	NH2	H_ASP_86	OD2	3.780
4JO1	H_ARG_66	NH1	H_ASP_86	OD1	2.959
4JO1	H_ARG_66	NH1	H_ASP_86	OD2	3.751
4JO1	H_ARG_66	NH2	H_ASP_86	OD1	3.523
4JO1	H_ARG_66	NH2	H_ASP_86	OD2	3.003
4JO1	P_ARG_304	NH1	H_ASP_34	OD1	3.045
4JO1	P_ARG_304	NH1	H_ASP_34	OD2	3.346
4JO1	P_ARG_304	NH2	H_ASP_34	OD2	2.892
4JO1	M_LYS_39	NZ	M_ASP_81	OD2	2.924
4JO1	M_LYS_53	NZ	M_ASP_50	OD1	2.678
4JO1	M_ARG_61	NH1	M_ASP_82	OD1	2.722
4JO1	M_ARG_61	NH1	M_ASP_82	OD2	3.406
4JO1	M_ARG_61	NH2	M_ASP_82	OD1	3.488
4JO1	M_ARG_61	NH2	M_ASP_82	OD2	2.707
4JO1	M_LYS_138	NZ	M_ASP_169	OD1	2.539
4JO1	M_LYS_162	NZ	M_ASP_142	OD1	2.679
4JO1	M_LYS_162	NZ	M_ASP_142	OD2	3.651
4JO1	I_ARG_38	NH1	I_ASP_86	OD2	2.786
4JO1	I_ARG_38	NH2	I_GLU_46	OE1	3.154
4JO1	I_ARG_38	NH2	I_ASP_86	OD2	3.771
4JO1	I_ARG_66	NH1	I_ASP_86	OD1	3.031
4JO1	I_ARG_66	NH1	I_ASP_86	OD2	3.805
4JO1	I_ARG_66	NH2	I_ASP_86	OD1	3.492
4JO1	I_ARG_66	NH2	I_ASP_86	OD2	2.959
4JO1	Q_ARG_304	NH1	I_ASP_34	OD1	2.949
4JO1	Q_ARG_304	NH1	I_ASP_34	OD2	3.344
4JO1	Q_ARG_304	NH2	I_ASP_34	OD1	3.946
4JO1	Q_ARG_304	NH2	I_ASP_34	OD2	2.878

Table 548: 4JO1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4JO2	L_LYS_39	NZ	L_ASP_81	OD2	2.922
4JO2	L_LYS_53	NZ	L_ASP_50	OD1	3.017
4JO2	L_ARG_61	NH1	L_ASP_82	OD1	3.605
4JO2	L_ARG_61	NH1	L_ASP_82	OD2	2.772
4JO2	L_ARG_61	NH2	L_ASP_82	OD1	3.007
4JO2	L_ARG_61	NH2	L_ASP_82	OD2	3.330
4JO2	L_LYS_138	NZ	L_ASP_169	OD2	3.573
4JO2	L_LYS_162	NZ	L_ASP_142	OD2	3.171
4JO2	H_ARG_38	NH1	H_ASP_86	OD2	2.606
4JO2	H_ARG_38	NH2	H_GLU_46	OE1	2.897
4JO2	H_ARG_38	NH2	H_ASP_86	OD2	3.987
4JO2	H_ARG_66	NH1	H_ASP_86	OD1	2.938
4JO2	H_ARG_66	NH1	H_ASP_86	OD2	3.840
4JO2	H_ARG_66	NH2	H_ASP_86	OD1	3.186
4JO2	H_ARG_66	NH2	H_ASP_86	OD2	2.917
4JO2	P_ARG_304	NH1	H_ASP_34	OD1	2.726
4JO2	P_ARG_304	NH1	H_ASP_34	OD2	3.333
4JO2	P_ARG_304	NH2	H_ASP_34	OD1	3.721
4JO2	P_ARG_304	NH2	H_ASP_34	OD2	2.854
4JO2	M_LYS_39	NZ	M_ASP_81	OD1	3.476
4JO2	M_LYS_39	NZ	M_ASP_81	OD2	3.290
4JO2	M_LYS_53	NZ	M_ASP_50	OD2	3.292
4JO2	M_ARG_61	NH1	M_ASP_82	OD1	3.140
4JO2	M_ARG_61	NH1	M_ASP_82	OD2	3.618
4JO2	M_ARG_61	NH2	M_ASP_82	OD1	3.726
4JO2	M_ARG_61	NH2	M_ASP_82	OD2	2.780
4JO2	M_LYS_138	NZ	M_ASP_169	OD2	2.742
4JO2	M_LYS_162	NZ	M_ASP_142	OD1	3.921
4JO2	M_LYS_162	NZ	M_ASP_142	OD2	3.385
4JO2	I_ARG_38	NH1	I_ASP_86	OD2	2.900
4JO2	I_ARG_38	NH2	I_GLU_46	OE1	3.086
4JO2	I_ARG_38	NH2	I_ASP_86	OD2	3.924
4JO2	I_ARG_66	NH1	I_ASP_86	OD1	2.929
4JO2	I_ARG_66	NH1	I_ASP_86	OD2	3.643
4JO2	I_ARG_66	NH2	I_ASP_86	OD1	3.202
4JO2	I_ARG_66	NH2	I_ASP_86	OD2	2.584
4JO2	I_LYS_199	NZ	I_ASP_201	OD1	3.625
4JO2	I_LYS_199	NZ	I_ASP_201	OD2	3.197
4JO2	Q_ARG_304	NH1	I_ASP_34	OD1	2.965
4JO2	Q_ARG_304	NH1	I_ASP_34	OD2	3.252
4JO2	Q_ARG_304	NH2	I_ASP_34	OD2	3.328

Table 549: 4JO2-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4JO3	L_LYS_39	NZ	L_ASP_81	OD1	3.210
4JO3	L_LYS_39	NZ	L_ASP_81	OD2	3.108
4JO3	L_ARG_61	NH1	L_ASP_82	OD1	3.683
4JO3	L_ARG_61	NH1	L_ASP_82	OD2	2.743
4JO3	L_ARG_61	NH2	L_ASP_82	OD1	2.826
4JO3	L_ARG_61	NH2	L_ASP_82	OD2	3.482
4JO3	L_LYS_162	NZ	L_ASP_142	OD1	2.811
4JO3	L_LYS_162	NZ	L_ASP_142	OD2	3.312
4JO3	H_ARG_38	NH1	H_ASP_86	OD2	2.684
4JO3	H_ARG_38	NH2	H_GLU_46	OE1	3.692
4JO3	H_ARG_38	NH2	H_ASP_86	OD2	3.553
4JO3	H_ARG_54	NH1	P_GLU_321	OE1	3.970
4JO3	H_ARG_66	NH1	H_ASP_86	OD1	2.860
4JO3	H_ARG_66	NH1	H_ASP_86	OD2	3.702
4JO3	H_ARG_66	NH2	H_ASP_86	OD1	3.555
4JO3	H_ARG_66	NH2	H_ASP_86	OD2	3.007
4JO3	H_ARG_94	NH1	H_ASP_101	OD1	2.669
4JO3	H_ARG_94	NH1	H_ASP_101	OD2	3.152
4JO3	P_ARG_327	NH1	L_ASP_1	OD1	2.994
4JO3	P_ARG_327	NH2	L_ASP_1	OD1	2.732
4JO3	P_ARG_327	NH2	L_GLU_27	OE1	3.272
4JO3	P_ARG_327	NH2	L_GLU_27	OE2	3.099
4JO3	M_LYS_39	NZ	M_ASP_81	OD1	3.363
4JO3	M_LYS_39	NZ	M_ASP_81	OD2	3.485
4JO3	M_ARG_61	NH1	M_ASP_82	OD1	3.977
4JO3	M_ARG_61	NH1	M_ASP_82	OD2	2.819
4JO3	M_ARG_61	NH2	M_ASP_82	OD1	2.923
4JO3	M_ARG_61	NH2	M_ASP_82	OD2	3.229
4JO3	M_LYS_162	NZ	M_ASP_142	OD1	3.056
4JO3	M_LYS_162	NZ	M_ASP_142	OD2	3.799
4JO3	I_ARG_38	NH1	I_ASP_86	OD2	2.673
4JO3	I_ARG_38	NH2	I_GLU_46	OE1	3.528
4JO3	I_ARG_38	NH2	I_GLU_46	OE2	3.898
4JO3	I_ARG_38	NH2	I_ASP_86	OD2	3.887
4JO3	I_ARG_66	NH1	I_ASP_86	OD1	3.159
4JO3	I_ARG_66	NH1	I_ASP_86	OD2	3.577
4JO3	I_ARG_66	NH2	I_ASP_86	OD1	3.570
4JO3	I_ARG_66	NH2	I_ASP_86	OD2	2.893
4JO3	I_ARG_94	NH1	I_ASP_101	OD1	2.954
4JO3	I_ARG_94	NH1	I_ASP_101	OD2	3.750
4JO3	Q_ARG_327	NH1	M_ASP_1	OD1	3.248
4JO3	Q_ARG_327	NH2	M_ASP_1	OD1	2.447
4JO3	Q_ARG_327	NH2	M_ASP_1	OD2	3.524
4JO3	Q_ARG_327	NH2	M_GLU_27	OE1	3.837
4JO3	Q_ARG_327	NH2	M_GLU_27	OE2	3.723

Table 550: 4JO3-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4JO4	L.LYS_39	NZ	L.ASP_81	OD1	3.937
4JO4	L.LYS_39	NZ	L.ASP_81	OD2	3.155
4JO4	L.ARG_61	NH1	L.ASP_82	OD1	3.796
4JO4	L.ARG_61	NH1	L.ASP_82	OD2	2.750
4JO4	L.ARG_61	NH2	L.ASP_82	OD1	3.079
4JO4	L.ARG_61	NH2	L.ASP_82	OD2	3.445
4JO4	L.LYS_162	NZ	L.ASP_142	OD1	2.940
4JO4	L.LYS_162	NZ	L.ASP_142	OD2	3.881
4JO4	H.ARG_38	NH1	H.ASP_86	OD2	2.736
4JO4	H.ARG_38	NH2	H.GLU_46	OE1	3.500
4JO4	H.ARG_38	NH2	H.GLU_46	OE2	3.857
4JO4	H.ARG_38	NH2	H.ASP_86	OD2	3.761
4JO4	H.ARG_66	NH1	H.ASP_86	OD1	2.970
4JO4	H.ARG_66	NH1	H.ASP_86	OD2	3.623
4JO4	H.ARG_66	NH2	H.ASP_86	OD1	3.534
4JO4	H.ARG_66	NH2	H.ASP_86	OD2	2.909
4JO4	H.ARG_94	NH1	H.ASP_101	OD1	2.897
4JO4	H.ARG_94	NH1	H.ASP_101	OD2	3.447
4JO4	M.LYS_39	NZ	M.ASP_81	OD1	2.860
4JO4	M.LYS_39	NZ	M.ASP_81	OD2	3.880
4JO4	M.ARG_61	NH1	M.ASP_82	OD1	3.524
4JO4	M.ARG_61	NH1	M.ASP_82	OD2	2.695
4JO4	M.ARG_61	NH2	M.ASP_82	OD1	2.799
4JO4	M.ARG_61	NH2	M.ASP_82	OD2	3.460
4JO4	M.LYS_162	NZ	M.ASP_142	OD1	2.860
4JO4	M.LYS_162	NZ	M.ASP_142	OD2	3.801
4JO4	I.ARG_38	NH1	I.ASP_86	OD2	2.762
4JO4	I.ARG_38	NH2	I.GLU_46	OE1	3.585
4JO4	I.ARG_38	NH2	I.GLU_46	OE2	3.974
4JO4	I.ARG_38	NH2	I.ASP_86	OD2	3.717
4JO4	I.ARG_66	NH1	I.ASP_86	OD1	2.993
4JO4	I.ARG_66	NH1	I.ASP_86	OD2	3.710
4JO4	I.ARG_66	NH2	I.ASP_86	OD1	3.487
4JO4	I.ARG_66	NH2	I.ASP_86	OD2	2.841
4JO4	I.ARG_94	NH1	I.ASP_101	OD1	3.375
4JO4	I.ARG_94	NH1	I.ASP_101	OD2	2.907

Table 551: 4JO4-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4K24	A_LYS_46	NZ	U_GLU_33	OE2	3.632
4K24	A_LYS_46	NZ	U_GLU_36	OE2	2.856
4K24	A_ARG_69	NH1	A_ASP_65	OD2	2.685
4K24	A_HIS_87	ND1	U_ASP_11	OD1	3.994
4K24	A_ARG_88	NH1	A_ASP_90	OD1	2.450
4K24	A_ARG_88	NH1	A_ASP_90	OD2	2.041
4K24	A_ARG_88	NH2	A_ASP_90	OD2	3.515
4K24	A_ARG_108	NH2	A_ASP_106	OD1	3.775
4K24	A_ARG_109	NH2	A_GLU_125	OE1	3.204
4K24	A_ARG_109	NH2	A_GLU_125	OE2	3.379
4K24	A_ARG_110	NH2	A_GLU_125	OE1	3.434
4K24	B_LYS_6	NZ	B_GLU_38	OE1	3.295
4K24	B_LYS_6	NZ	B_GLU_38	OE2	3.051
4K24	H_LYS_62	NZ	L_ASP_1	OD1	3.610
4K24	H_ARG_66	NH2	H_ASP_86	OD1	3.579
4K24	H_ARG_66	NH2	H_ASP_86	OD2	3.959
4K24	H_ARG_94	NH2	H_ASP_101	OD2	3.501
4K24	H_LYS_205	NZ	H_ASP_207	OD1	3.964
4K24	H_LYS_208	NZ	L_GLU_123	OE1	2.286
4K24	H_LYS_208	NZ	L_GLU_123	OE2	3.345
4K24	L_ARG_46	NH2	L_ASP_55	OD1	2.623
4K24	L_ARG_46	NH2	L_ASP_55	OD2	2.874
4K24	L_ARG_61	NH1	L_GLU_79	OE1	3.659
4K24	L_ARG_61	NH1	L_ASP_82	OD2	3.380
4K24	L_ARG_61	NH2	L_GLU_79	OE1	2.490
4K24	L_ARG_61	NH2	L_GLU_79	OE2	3.979
4K24	L_ARG_61	NH2	L_ASP_82	OD1	3.491
4K24	L_ARG_61	NH2	L_ASP_82	OD2	3.569
4K24	L_LYS_142	NZ	L_ASP_143	OD1	3.088
4K24	L_LYS_147	NZ	L_GLU_154	OE1	3.964
4K24	L_LYS_147	NZ	L_GLU_154	OE2	3.385
4K24	L_LYS_147	NZ	L_GLU_195	OE2	3.600
4K24	L_HIS_189	ND1	L_GLU_185	OE2	3.464
4K24	L_HIS_189	NE2	L_ASP_151	OD2	3.905
4K24	L_ARG_211	NH1	L_GLU_187	OE1	3.878
4K24	L_ARG_211	NH2	L_GLU_187	OE1	2.437
4K24	U_ARG_25	NH1	U_GLU_42	OE2	3.583
4K24	U_ARG_25	NH1	U_GLU_68	OE1	3.761
4K24	U_ARG_25	NH2	U_GLU_42	OE2	3.008
4K24	U_ARG_30	NH1	U_GLU_37	OE2	3.811
4K24	U_ARG_30	NH2	U_GLU_37	OE1	3.105
4K24	U_ARG_30	NH2	U_GLU_37	OE2	2.352
4K24	U_LYS_50	NZ	U_GLU_68	OE2	3.702
4K24	U_LYS_50	NZ	U_ASP_254	OD1	3.827
4K24	U_ARG_53	NH1	U_ASP_254	OD1	3.567
4K24	U_ARG_53	NH1	U_ASP_254	OD2	3.288
4K24	U_ARG_53	NH2	U_ASP_254	OD1	3.503
4K24	U_ARG_53	NH2	U_ASP_254	OD2	3.622
4K24	U_LYS_62	NZ	U_GLU_33	OE1	3.765
4K24	U_ARG_91	NH1	B_ASP_22	OD2	3.233
4K24	U_ARG_91	NH2	B_ASP_22	OD1	3.988
4K24	U_ARG_91	NH2	B_ASP_22	OD2	3.635
4K24	U_HIS_143	ND1	U_GLU_106	OE2	3.213
4K24	U_ARG_145	NH1	U_ASP_124	OD1	3.705
4K24	U_ARG_145	NH2	U_ASP_124	OD1	2.588
4K24	U_ARG_145	NH2	U_ASP_124	OD2	3.556
4K24	U_LYS_175	NZ	U_GLU_178	OE2	3.964

Table 552: 4K24-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4K2U	A_LYS_	NZ	A_GLU_	OE1	3.768
4K2U	A_LYS_	NZ	A_GLU_	OE2	2.609
4K2U	A_ARG_	NH1	A_ASP_	OD1	2.573
4K2U	A_ARG_	NH1	A_ASP_	OD2	3.255
4K2U	A_LYS_	NZ	A_ASP_	OD1	2.738
4K2U	A_LYS_	NZ	A_ASP_	OD1	3.468
4K2U	A_ARG_	NH1	A_ASP_	OD2	2.783
4K2U	A_ARG_	NH2	A_ASP_	OD2	2.667
4K2U	A_ARG_	NH2	A_GLU_	OE1	3.027
4K2U	A_ARG_	NH2	A_GLU_	OE2	3.639
4K2U	A_ARG_	NH1	A_ASP_	OD2	3.283
4K2U	A_ARG_	NH2	A_ASP_	OD1	3.700
4K2U	A_ARG_	NH2	A_ASP_	OD2	2.890
4K2U	A_ARG_	NH2	A_ASP_	OD2	3.924
4K2U	A_LYS_	NZ	A_GLU_	OE1	3.682
4K2U	A_LYS_	NZ	A_GLU_	OE2	3.521
4K2U	A_LYS_	NZ	A_ASP_	OD2	3.301
4K2U	A_LYS_	NZ	A_ASP_	OD2	3.690
4K2U	A_ARG_	NH1	A_GLU_	OE1	3.492
4K2U	A_ARG_	NH1	A_GLU_	OE2	3.531
4K2U	A_ARG_	NH2	A_GLU_	OE1	3.963
4K2U	A_ARG_	NH2	A_GLU_	OE2	2.886
4K2U	A_HIS_	NE2	A_GLU_	OE1	3.170
4K2U	A_LYS_	NZ	A_GLU_	OE1	3.297
4K2U	A_LYS_	NZ	A_GLU_	OE2	3.450
4K2U	A_ARG_	NH1	A_ASP_	OD1	3.497
4K2U	A_ARG_	NH2	A_ASP_	OD1	3.758
4K2U	B_LYS_	NZ	B_GLU_	OE1	3.571
4K2U	B_LYS_	NZ	B_GLU_	OE2	2.646
4K2U	B_ARG_	NH1	B_ASP_	OD1	2.642
4K2U	B_ARG_	NH1	B_ASP_	OD2	3.466
4K2U	B_LYS_	NZ	B_ASP_	OD1	2.561
4K2U	B_ARG_	NH1	B_ASP_	OD2	2.664
4K2U	B_ARG_	NH2	B_ASP_	OD2	2.621
4K2U	B_ARG_	NH2	B_GLU_	OE1	3.057
4K2U	B_ARG_	NH2	B_GLU_	OE2	3.570
4K2U	B_ARG_	NH1	B_ASP_	OD2	3.462
4K2U	B_ARG_	NH2	B_ASP_	OD1	3.706
4K2U	B_ARG_	NH2	B_ASP_	OD2	3.043
4K2U	B_ARG_	NH2	B_ASP_	OD2	3.804
4K2U	B_LYS_	NZ	B_GLU_	OE1	3.474
4K2U	B_LYS_	NZ	B_GLU_	OE2	3.437
4K2U	B_LYS_	NZ	B_GLU_	OE2	3.372
4K2U	B_LYS_	NZ	B_ASP_	OD2	3.125
4K2U	B_ARG_	NH1	B_GLU_	OE2	2.841
4K2U	B_ARG_	NH2	B_GLU_	OE1	3.192
4K2U	B_ARG_	NH2	B_GLU_	OE2	3.341
4K2U	B_LYS_	NZ	B_GLU_	OE1	3.826
4K2U	B_HIS_	NE2	B_GLU_	OE1	3.714
4K2U	B_LYS_	NZ	B_GLU_	OE1	3.312
4K2U	B_LYS_	NZ	B_GLU_	OE2	3.705
4K2U	B_ARG_	NH1	B_ASP_	OD1	3.090
4K2U	B_ARG_	NH2	B_ASP_	OD1	3.461
4K2U	B_LYS_	NZ	B_GLU_	OE2	3.384
4K2U	B_LYS_	NZ	B_ASP_	OD1	3.229
4K2U	B_LYS_	NZ	B_ASP_	OD2	2.796
4K2U	H_ARG_	NH1	H_GLU_	OE1	3.927

4K2U	H_LYS_	NZ	H_ASP_	OD1	3.481
4K2U	H_LYS_	NZ	H_ASP_	OD2	3.636
4K2U	H_LYS_	NZ	L_ASP_	OD2	2.646
4K2U	H_LYS_	NZ	H_ASP_	OD1	3.694
4K2U	H_LYS_	NZ	H_ASP_	OD2	2.669
4K2U	H_ARG_	NH2	H_ASP_	OD1	3.475
4K2U	H_ARG_	NH2	H_GLU_	OE1	2.820
4K2U	H_LYS_	NZ	L_GLU_	OE2	3.160
4K2U	L_ARG_	NH1	L_GLU_	OE1	3.521
4K2U	L_ARG_	NH2	L_GLU_	OE1	2.623
4K2U	L_LYS_	NZ	L_ASP_	OD1	3.612
4K2U	L_LYS_	NZ	L_ASP_	OD2	3.457
4K2U	L_LYS_	NZ	M_ASP_	OD2	2.895
4K2U	L_LYS_	NZ	L_ASP_	OD1	3.839
4K2U	L_LYS_	NZ	L_ASP_	OD2	2.840
4K2U	L_ARG_	NH2	L_ASP_	OD1	3.888
4K2U	L_ARG_	NH2	L_GLU_	OE1	2.738
4K2U	L_ARG_	NH1	L_ASP_	OD1	2.627
4K2U	L_ARG_	NH1	L_ASP_	OD2	2.684
4K2U	L_ARG_	NH1	A_GLU_	OE1	2.808
4K2U	L_ARG_	NH1	A_GLU_	OE2	3.439
4K2U	L_ARG_	NH2	A_GLU_	OE1	3.591
4K2U	L_ARG_	NH2	A_GLU_	OE2	2.619
4K2U	L_ARG_	NH1	L_GLU_	OE1	3.276
4K2U	L_ARG_	NH1	L_GLU_	OE2	3.602
4K2U	L_ARG_	NH2	L_GLU_	OE2	3.191
4K2U	L_ARG_	NH2	L_GLU_	OE1	3.486
4K2U	L_ARG_	NH2	L_ASP_	OD1	3.236
4K2U	L_ARG_	NH2	L_ASP_	OD2	3.657
4K2U	L_LYS_	NZ	L_GLU_	OE1	3.754
4K2U	L_LYS_	NZ	L_GLU_	OE2	2.528
4K2U	L_ARG_	NH1	L_GLU_	OE2	3.762
4K2U	L_ARG_	NH2	L_GLU_	OE1	3.990
4K2U	L_ARG_	NH2	L_GLU_	OE2	2.325
4K2U	L_HIS_	ND1	L_ASP_	OD2	2.555
4K2U	M_ARG_	NH1	M_ASP_	OD1	2.384
4K2U	M_ARG_	NH1	M_ASP_	OD2	3.237
4K2U	M_ARG_	NH1	B_GLU_	OE1	2.744
4K2U	M_ARG_	NH1	B_GLU_	OE2	3.321
4K2U	M_ARG_	NH2	B_GLU_	OE1	3.489
4K2U	M_ARG_	NH2	B_GLU_	OE2	2.673
4K2U	M_HIS_	ND1	L_GLU_	OE2	3.997
4K2U	M_ARG_	NH1	M_GLU_	OE2	3.472
4K2U	M_ARG_	NH2	M_GLU_	OE2	3.787
4K2U	M_ARG_	NH2	M_GLU_	OE1	3.410
4K2U	M_ARG_	NH2	M_ASP_	OD1	3.140
4K2U	M_ARG_	NH2	M_ASP_	OD1	3.175
4K2U	M_LYS_	NZ	M_GLU_	OE1	3.487
4K2U	M_LYS_	NZ	M_GLU_	OE2	2.899
4K2U	M_HIS_	ND1	M_ASP_	OD2	2.547

Table 553: 4K2U-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4KI5	C_HIS_35	NE2	C_GLU_99	OE1	2.952
4KI5	C_LYS_46	NZ	C_ASP_63	OD2	2.850
4KI5	C_LYS_65	NZ	C_ASP_62	OD1	3.382
4KI5	C_ARG_67	NH1	C_ASP_90	OD1	3.757
4KI5	C_ARG_67	NH1	C_ASP_90	OD2	2.867
4KI5	C_ARG_67	NH2	C_ASP_90	OD1	3.010
4KI5	C_ARG_67	NH2	C_ASP_90	OD2	3.538
4KI5	C_ARG_98	NH1	C_ASP_100	OD1	3.340
4KI5	C_LYS_211	NZ	D_GLU_122	OE2	2.907
4KI5	C_ARG_216	NH2	C_GLU_214	OE1	3.340
4KI5	D_ARG_60	NH2	D_GLU_80	OE2	3.447
4KI5	D_ARG_60	NH2	D_ASP_81	OD1	2.653
4KI5	D_ARG_60	NH2	D_ASP_81	OD2	3.443
4KI5	D_LYS_102	NZ	D_ASP_164	OD1	3.660
4KI5	D_LYS_102	NZ	D_ASP_164	OD2	3.125
4KI5	D_LYS_146	NZ	D_GLU_153	OE1	3.729
4KI5	D_LYS_148	NZ	D_GLU_194	OE1	2.836
4KI5	D_ARG_154	NH1	D_GLU_184	OE1	3.010
4KI5	D_ARG_154	NH2	D_GLU_184	OE1	3.600
4KI5	D_LYS_182	NZ	D_GLU_186	OE2	3.376
4KI5	D_HIS_188	ND1	D_ASP_150	OD2	2.808
4KI5	D_HIS_197	ND1	D_ASP_142	OD1	2.559
4KI5	D_HIS_197	ND1	D_ASP_142	OD2	3.147
4KI5	E_ARG_40	NH2	E_GLU_89	OE2	3.648
4KI5	E_ARG_63	NH1	E_GLU_46	OE2	2.566
4KI5	E_LYS_65	NZ	E_GLU_62	OE1	3.306
4KI5	E_LYS_65	NZ	E_GLU_62	OE2	3.510
4KI5	E_LYS_67	NZ	E_ASP_90	OD1	3.938
4KI5	E_LYS_67	NZ	E_ASP_90	OD2	2.897
4KI5	E_ARG_98	NH2	E_ASP_110	OD1	3.380
4KI5	E_ARG_98	NH2	E_ASP_110	OD2	2.498
4KI5	E_LYS_217	NZ	F_GLU_123	OE2	3.401
4KI5	E_LYS_218	NZ	E_GLU_220	OE2	3.129
4KI5	E_ARG_222	NH1	F_GLU_123	OE1	3.106
4KI5	E_ARG_222	NH1	F_GLU_123	OE2	3.925
4KI5	E_ARG_222	NH2	F_GLU_123	OE1	3.823
4KI5	E_ARG_222	NH2	F_GLU_123	OE2	3.234
4KI5	F_ARG_24	NH2	F_ASP_70	OD1	3.045
4KI5	F_ARG_24	NH2	F_ASP_70	OD2	2.870
4KI5	F_ARG_46	NH2	F_ASP_55	OD2	3.256
4KI5	F_ARG_61	NH1	F_ASP_79	OD2	3.671
4KI5	F_ARG_61	NH2	F_ASP_79	OD2	3.651
4KI5	F_ARG_61	NH2	F_ASP_82	OD1	2.633
4KI5	F_ARG_61	NH2	F_ASP_82	OD2	3.268
4KI5	F_ARG_66	NH1	F_GLU_28	OE2	3.847
4KI5	F_ARG_66	NH2	F_GLU_28	OE2	3.615
4KI5	F_LYS_103	NZ	F_ASP_165	OD1	3.937
4KI5	F_LYS_103	NZ	F_ASP_165	OD2	3.643
4KI5	F_LYS_149	NZ	F_GLU_195	OE1	2.911
4KI5	F_ARG_155	NH1	F_GLU_185	OE2	3.880
4KI5	F_ARG_155	NH2	F_GLU_185	OE2	2.938
4KI5	F_LYS_169	NZ	F_GLU_81	OE2	3.864
4KI5	F_LYS_183	NZ	F_ASP_184	OD1	2.750
4KI5	F_HIS_189	ND1	F_ASP_151	OD2	2.998
4KI5	F_ARG_211	NH2	F_GLU_187	OE1	3.825
4KI5	M_ARG_2209	NH2	M_ASP_2187	OD2	2.570
4KI5	M_ARG_2215	NH1	C_ASP_100	OD1	2.868

4KI5	M_ARG_2215	NH1	C_ASP_100	OD2	3.241
4KI5	M_ARG_2215	NH2	C_ASP_100	OD1	3.324
4KI5	M_ARG_2215	NH2	C_ASP_100	OD2	2.939
4KI5	M_ARG_2215	NH2	C_ASP_101	OD2	3.819
4KI5	M_LYS_2227	NZ	E_GLU_50	OE1	3.493
4KI5	M_ARG_2304	NH2	M_ASP_2233	OD1	3.696
4KI5	M_ARG_2304	NH2	M_ASP_2233	OD2	3.280

Table 554: 4KI5-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4KJY	A.LYS_39	NZ	B.ASP_100	OD1	2.809
4KJY	A.LYS_41	NZ	A.GLU_97	OE2	2.999
4KJY	A.LYS_41	NZ	A.GLU_106	OE1	2.835
4KJY	A.ARG_45	NH1	A.ASP_62	OD1	3.701
4KJY	A.ARG_45	NH1	A.ASP_62	OD2	2.667
4KJY	A.ARG_45	NH2	A.ASP_62	OD2	2.900
4KJY	A.HIS_90	NE2	A.ASP_62	OD2	3.464
4KJY	A.ARG_103	NH2	A.GLU_100	OE1	3.259
4KJY	A.ARG_103	NH2	A.GLU_100	OE2	3.050
4KJY	B.ARG_46	NH1	B.GLU_102	OE1	3.091
4KJY	B.ARG_46	NH2	B.GLU_102	OE1	3.045
4KJY	B.ARG_53	NH1	A.GLU_97	OE2	3.571
4KJY	B.ARG_53	NH1	A.GLU_106	OE1	3.135
4KJY	B.ARG_59	NH1	B.ASP_85	OD1	3.565
4KJY	B.ARG_59	NH2	B.ASP_85	OD1	3.099
4KJY	B.ARG_59	NH2	B.ASP_85	OD2	2.288
4KJY	B.ARG_68	NH1	B.GLU_65	OE1	3.402
4KJY	B.ARG_68	NH2	B.GLU_65	OE1	3.828
4KJY	B.ARG_69	NH1	A.GLU_35	OE1	2.737
4KJY	B.ARG_69	NH1	A.GLU_35	OE2	3.607
4KJY	B.ARG_69	NH1	A.GLU_100	OE2	2.961
4KJY	B.ARG_69	NH2	A.GLU_35	OE1	3.476
4KJY	B.ARG_69	NH2	A.GLU_35	OE2	2.813
4KJY	B.LYS_96	NZ	A.GLU_97	OE1	2.567
4KJY	B.LYS_96	NZ	B.ASP_100	OD1	3.158
4KJY	B.LYS_96	NZ	B.ASP_100	OD2	2.571
4KJY	B.LYS_104	NZ	B.GLU_3	OE1	3.935
4KJY	B.LYS_104	NZ	B.GLU_3	OE2	3.416
4KJY	C.LYS_41	NZ	C.GLU_97	OE2	2.660
4KJY	C.LYS_41	NZ	C.GLU_106	OE1	2.848
4KJY	C.ARG_45	NH1	C.ASP_62	OD2	3.404
4KJY	C.ARG_45	NH2	C.ASP_62	OD1	3.143
4KJY	C.ARG_45	NH2	C.ASP_62	OD2	3.381
4KJY	C.LYS_67	NZ	C.GLU_69	OE1	3.854
4KJY	C.LYS_67	NZ	C.GLU_69	OE2	2.799
4KJY	C.LYS_81	NZ	C.GLU_69	OE2	2.680
4KJY	C.HIS_90	NE2	C.ASP_62	OD2	3.141
4KJY	C.ARG_103	NH2	C.GLU_100	OE1	3.185
4KJY	C.ARG_103	NH2	C.GLU_100	OE2	3.021
4KJY	D.ARG_40	NH1	A.GLU_29	OE1	3.310
4KJY	D.ARG_40	NH2	A.GLU_29	OE1	3.253
4KJY	D.ARG_40	NH2	A.GLU_29	OE2	2.999
4KJY	D.ARG_40	NH2	B.GLU_70	OE1	3.440
4KJY	D.ARG_46	NH1	D.GLU_102	OE1	3.026
4KJY	D.ARG_46	NH2	D.GLU_102	OE1	2.981
4KJY	D.ARG_53	NH1	C.GLU_97	OE2	3.949
4KJY	D.ARG_53	NH2	C.GLU_104	OE1	3.112
4KJY	D.ARG_53	NH2	C.GLU_104	OE2	3.607
4KJY	D.ARG_59	NH1	D.ASP_85	OD1	3.248
4KJY	D.ARG_59	NH2	D.ASP_85	OD1	3.278
4KJY	D.ARG_59	NH2	D.ASP_85	OD2	2.654
4KJY	D.ARG_68	NH2	D.GLU_65	OE1	2.908
4KJY	D.ARG_69	NH1	C.GLU_35	OE1	2.786
4KJY	D.ARG_69	NH1	C.GLU_35	OE2	3.903
4KJY	D.ARG_69	NH1	C.GLU_100	OE2	3.005
4KJY	D.ARG_69	NH2	C.GLU_35	OE1	3.286
4KJY	D.ARG_69	NH2	C.GLU_35	OE2	2.868

4KJY	D_LYS_96	NZ	C_GLU_97	OE1	2.747
4KJY	D_LYS_96	NZ	D_ASP_100	OD1	3.105
4KJY	D_LYS_96	NZ	D_ASP_100	OD2	2.750
4KJY	D_LYS_104	NZ	D_GLU_3	OE1	2.954

Table 555: 4KJY-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4KPH	L_LYS_39	NZ	L_GLU_81	OE1	3.604
4KPH	L_ARG_61	NH1	L_ASP_82	OD1	3.220
4KPH	L_ARG_61	NH1	L_ASP_82	OD2	2.394
4KPH	L_ARG_61	NH2	L_GLU_79	OE1	3.711
4KPH	L_ARG_61	NH2	L_GLU_79	OE2	3.781
4KPH	L_ARG_61	NH2	L_ASP_82	OD1	2.574
4KPH	L_ARG_61	NH2	L_ASP_82	OD2	3.380
4KPH	L_ARG_61	NH2	L_GLU_85	OE2	3.345
4KPH	L_LYS_103	NZ	L_ASP_85	OD1	2.968
4KPH	L_LYS_103	NZ	L_ASP_85	OD2	3.649
4KPH	L_LYS_147	NZ	L_GLU_154	OE2	3.845
4KPH	L_LYS_149	NZ	L_GLU_195	OE1	3.580
4KPH	L_LYS_149	NZ	L_GLU_195	OE2	2.888
4KPH	L_ARG_155	NH1	L_GLU_185	OE2	3.834
4KPH	L_LYS_169	NZ	L_GLU_81	OE2	3.946
4KPH	L_ARG_188	NH1	L_GLU_185	OE1	2.941
4KPH	L_ARG_188	NH2	L_GLU_185	OE1	3.830
4KPH	L_HIS_189	ND1	L_ASP_151	OD2	3.425
4KPH	L_HIS_189	NE2	L_GLU_185	OE2	3.271
4KPH	L_LYS_199	NZ	L_ASP_110	OD2	3.817
4KPH	H_ARG_38	NH1	H_ASP_86	OD1	2.609
4KPH	H_ARG_38	NH2	H_GLU_46	OE2	2.879
4KPH	H_ARG_38	NH2	H_ASP_86	OD1	3.494
4KPH	H_ARG_66	NH1	H_ASP_86	OD1	3.691
4KPH	H_ARG_66	NH1	H_ASP_86	OD2	3.301
4KPH	H_ARG_66	NH2	H_ASP_86	OD1	2.689
4KPH	H_ARG_66	NH2	H_ASP_86	OD2	2.980
4KPH	H_LYS_75	NZ	H_ASP_72	OD2	2.680
4KPH	H_LYS_208	NZ	L_GLU_123	OE2	2.903
4KPH	M_LYS_39	NZ	M_GLU_81	OE1	3.784
4KPH	M_ARG_61	NH1	M_ASP_82	OD1	3.526
4KPH	M_ARG_61	NH1	M_ASP_82	OD2	2.643
4KPH	M_ARG_61	NH2	M_GLU_79	OE1	3.955
4KPH	M_ARG_61	NH2	M_GLU_79	OE2	3.623
4KPH	M_ARG_61	NH2	M_ASP_82	OD1	2.593
4KPH	M_ARG_61	NH2	M_ASP_82	OD2	3.290
4KPH	I_ARG_38	NH1	I_ASP_86	OD1	2.756
4KPH	I_ARG_38	NH2	I_GLU_46	OE1	2.881
4KPH	I_ARG_38	NH2	I_ASP_86	OD1	3.615
4KPH	I_ARG_66	NH1	I_ASP_86	OD1	3.166
4KPH	I_ARG_66	NH1	I_ASP_86	OD2	2.662
4KPH	I_ARG_66	NH2	I_ASP_86	OD1	3.175
4KPH	I_ARG_66	NH2	I_ASP_86	OD2	3.816
4KPH	I_LYS_75	NZ	I_ASP_72	OD2	2.592
4KPH	I_LYS_208	NZ	M_GLU_123	OE2	2.312

Table 556: 4KPH-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4KRL	B_ARG_19	NH2	B_ASP_80	OD2	3.165
4KRL	B_ARG_30	NH1	A_ASP_355	OD1	3.258
4KRL	B_ARG_30	NH1	A_ASP_355	OD2	2.275
4KRL	B_ARG_30	NH2	A_ASP_355	OD1	3.549
4KRL	B_ARG_30	NH2	A_ASP_355	OD2	3.938
4KRL	B_ARG_38	NH1	B_ASP_90	OD2	3.344
4KRL	B_ARG_38	NH2	B_GLU_46	OE1	2.859
4KRL	B_ARG_38	NH2	B_ASP_90	OD2	3.931
4KRL	B_ARG_67	NH1	B_ASP_90	OD1	2.738
4KRL	B_ARG_67	NH1	B_ASP_90	OD2	3.832
4KRL	B_ARG_67	NH2	B_ASP_90	OD1	3.067
4KRL	B_ARG_67	NH2	B_ASP_90	OD2	2.979
4KRL	A_ARG_353	NH1	B_GLU_110	OE1	2.654
4KRL	A_ARG_353	NH2	B_ASP_112	OD1	3.873
4KRL	A_ARG_353	NH2	B_ASP_112	OD2	2.978
4KRL	A_LYS_372	NZ	A_GLU_397	OE2	2.311
4KRL	A_HIS_394	NE2	A_ASP_369	OD1	3.965
4KRL	A_ARG_403	NH1	A_GLU_376	OE1	2.323
4KRL	A_ARG_403	NH1	A_GLU_376	OE2	3.739
4KRL	A_LYS_407	NZ	A_ASP_434	OD1	3.147
4KRL	A_LYS_407	NZ	A_ASP_434	OD2	3.510
4KRL	A_ARG_427	NH1	A_GLU_397	OE1	3.352
4KRL	A_ARG_427	NH2	A_GLU_495	OE1	3.797
4KRL	A_ARG_427	NH2	A_ASP_498	OD1	2.739
4KRL	A_ARG_427	NH2	A_ASP_498	OD2	3.969
4KRL	A_LYS_455	NZ	A_GLU_489	OE2	3.930
4KRL	A_LYS_463	NZ	A_ASP_436	OD2	3.876

Table 557: 4KRL-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4KRM	A_HIS_334	ND1	A_GLU_320	OE1	3.977
4KRM	A_HIS_334	ND1	A_GLU_320	OE2	2.370
4KRM	A_HIS_334	NE2	A_GLU_320	OE2	3.990
4KRM	A_ARG_353	NH1	B_GLU_110	OE1	2.811
4KRM	A_ARG_353	NH2	B_ASP_112	OD1	3.965
4KRM	A_ARG_353	NH2	B_ASP_112	OD2	2.932
4KRM	A_LYS_372	NZ	A_GLU_397	OE2	3.950
4KRM	A_ARG_390	NH1	A_ASP_369	OD1	3.291
4KRM	A_ARG_390	NH2	A_ASP_369	OD1	3.166
4KRM	A_ARG_390	NH2	A_ASP_369	OD2	3.036
4KRM	A_HIS_394	ND1	A_ASP_392	OD1	3.439
4KRM	A_HIS_394	ND1	A_ASP_392	OD2	3.192
4KRM	A_HIS_394	ND1	A_GLU_397	OE1	3.878
4KRM	A_HIS_394	NE2	A_ASP_392	OD2	2.923
4KRM	A_ARG_403	NH2	A_GLU_376	OE1	2.698
4KRM	A_LYS_407	NZ	A_ASP_434	OD1	2.923
4KRM	A_LYS_407	NZ	H_GLU_5	OE1	3.498
4KRM	A_LYS_407	NZ	H_GLU_5	OE2	3.022
4KRM	A_LYS_463	NZ	A_ASP_436	OD2	3.346
4KRM	B_ARG_19	NH2	B_ASP_80	OD1	2.971
4KRM	B_ARG_30	NH1	A_ASP_355	OD1	3.162
4KRM	B_ARG_30	NH1	A_ASP_355	OD2	2.423
4KRM	B_ARG_30	NH2	A_ASP_355	OD1	3.525
4KRM	B_ARG_38	NH1	B_ASP_90	OD2	2.849
4KRM	B_ARG_38	NH2	B_GLU_46	OE1	3.190
4KRM	B_ARG_38	NH2	B_ASP_90	OD2	3.870
4KRM	B_ARG_67	NH1	B_ASP_90	OD1	2.285
4KRM	B_ARG_67	NH1	B_ASP_90	OD2	3.184
4KRM	B_ARG_67	NH2	B_ASP_90	OD2	3.620
4KRM	C_LYS_310	NZ	C_GLU_308	OE2	3.505
4KRM	C_HIS_334	ND1	C_GLU_320	OE1	3.487
4KRM	C_ARG_353	NH1	D_GLU_110	OE1	2.866
4KRM	C_ARG_353	NH2	D_ASP_112	OD2	3.218
4KRM	C_LYS_372	NZ	C_GLU_397	OE2	3.670
4KRM	C_HIS_394	NE2	C_GLU_397	OE1	2.760
4KRM	C_HIS_394	NE2	C_GLU_397	OE2	3.646
4KRM	C_ARG_403	NH1	C_GLU_376	OE1	2.996
4KRM	C_ARG_403	NH2	C_GLU_431	OE2	3.962
4KRM	C_LYS_407	NZ	C_ASP_434	OD1	2.908
4KRM	C_ARG_427	NH1	C_GLU_397	OE1	3.430
4KRM	C_ARG_427	NH2	C_ASP_498	OD1	2.428
4KRM	C_ARG_427	NH2	C_ASP_498	OD2	3.809
4KRM	C_LYS_455	NZ	C_GLU_489	OE1	2.730
4KRM	C_LYS_455	NZ	C_GLU_489	OE2	3.273
4KRM	C_LYS_463	NZ	C_ASP_436	OD2	3.365
4KRM	D_ARG_19	NH2	D_ASP_80	OD1	3.355
4KRM	D_ARG_19	NH2	D_ASP_80	OD2	3.916
4KRM	D_ARG_30	NH1	C_ASP_355	OD1	3.295
4KRM	D_ARG_30	NH1	C_ASP_355	OD2	2.452
4KRM	D_ARG_30	NH2	C_ASP_355	OD1	3.096
4KRM	D_ARG_30	NH2	C_ASP_355	OD2	3.699
4KRM	D_ARG_38	NH1	D_ASP_90	OD2	3.036
4KRM	D_ARG_38	NH2	D_GLU_46	OE1	3.135
4KRM	D_ARG_67	NH2	D_ASP_90	OD1	2.355
4KRM	D_ARG_67	NH2	D_ASP_90	OD2	3.277
4KRM	E_HIS_334	ND1	E_GLU_320	OE2	2.610
4KRM	E_ARG_353	NH1	F_GLU_110	OE1	2.855

4KRM	E_ARG_353	NH2	F_ASP_112	OD2	2.965
4KRM	E_LYS_372	NZ	E_GLU_397	OE2	3.677
4KRM	E_LYS_375	NZ	E_GLU_308	OE2	3.450
4KRM	E_ARG_390	NH1	E_ASP_369	OD1	3.281
4KRM	E_HIS_394	ND1	E_GLU_397	OE1	3.143
4KRM	E_HIS_394	ND1	E_GLU_397	OE2	3.895
4KRM	E_HIS_394	NE2	E_GLU_397	OE1	3.783
4KRM	E_HIS_394	NE2	E_GLU_397	OE2	3.447
4KRM	E_ARG_403	NH1	E_GLU_376	OE1	2.574
4KRM	E_ARG_403	NH1	E_GLU_376	OE2	3.773
4KRM	E_LYS_407	NZ	E_ASP_434	OD1	2.654
4KRM	E_LYS_407	NZ	E_ASP_434	OD2	3.337
4KRM	E_LYS_407	NZ	L_GLU_5	OE1	3.054
4KRM	E_LYS_407	NZ	L_GLU_5	OE2	2.995
4KRM	E_ARG_427	NH1	E_GLU_495	OE1	3.905
4KRM	E_ARG_427	NH1	E_ASP_498	OD1	3.791
4KRM	E_ARG_427	NH2	E_ASP_498	OD1	2.763
4KRM	E_ARG_427	NH2	E_ASP_498	OD2	3.959
4KRM	F_ARG_19	NH2	F_ASP_80	OD1	2.815
4KRM	F_ARG_30	NH1	E_ASP_355	OD1	3.119
4KRM	F_ARG_30	NH1	E_ASP_355	OD2	2.396
4KRM	F_ARG_30	NH2	E_ASP_355	OD1	3.504
4KRM	F_ARG_38	NH1	F_ASP_90	OD2	2.948
4KRM	F_ARG_38	NH2	F_GLU_46	OE1	2.970
4KRM	F_ARG_38	NH2	F_ASP_90	OD2	3.609
4KRM	F_ARG_67	NH1	F_ASP_90	OD1	3.689
4KRM	F_ARG_67	NH1	F_ASP_90	OD2	3.954
4KRM	F_ARG_67	NH2	F_ASP_90	OD1	2.190
4KRM	F_ARG_67	NH2	F_ASP_90	OD2	3.534
4KRM	G_LYS_310	NZ	G_GLU_376	OE2	3.271
4KRM	G_ARG_353	NH1	H_GLU_110	OE1	3.021
4KRM	G_ARG_353	NH2	H_ASP_112	OD2	3.118
4KRM	G_LYS_372	NZ	G_GLU_397	OE1	3.892
4KRM	G_LYS_372	NZ	G_GLU_397	OE2	2.517
4KRM	G_LYS_375	NZ	G_GLU_308	OE2	2.881
4KRM	G_HIS_394	ND1	G_GLU_397	OE1	3.232
4KRM	G_ARG_403	NH1	G_GLU_376	OE1	2.469
4KRM	G_LYS_407	NZ	B_GLU_5	OE1	3.493
4KRM	G_LYS_407	NZ	B_GLU_5	OE2	2.984
4KRM	G_LYS_407	NZ	G_ASP_434	OD1	2.773
4KRM	G_ARG_427	NH1	G_GLU_397	OE1	2.912
4KRM	G_ARG_427	NH2	G_ASP_392	OD2	3.305
4KRM	G_ARG_427	NH2	G_ASP_498	OD1	3.141
4KRM	G_LYS_463	NZ	G_ASP_436	OD2	2.681
4KRM	G_ARG_497	NH2	G_GLU_495	OE1	3.599
4KRM	H_ARG_19	NH2	H_ASP_80	OD1	3.560
4KRM	H_ARG_19	NH2	H_ASP_80	OD2	3.970
4KRM	H_ARG_27	NH1	G_ASP_323	OD1	2.688
4KRM	H_ARG_27	NH2	G_ASP_323	OD1	3.952
4KRM	H_ARG_30	NH1	G_ASP_355	OD1	3.358
4KRM	H_ARG_30	NH1	G_ASP_355	OD2	2.448
4KRM	H_ARG_30	NH2	G_ASP_355	OD1	3.423
4KRM	H_ARG_30	NH2	G_ASP_355	OD2	3.935
4KRM	H_ARG_38	NH1	H_ASP_90	OD2	2.777
4KRM	H_ARG_38	NH2	H_GLU_46	OE1	3.420
4KRM	H_ARG_38	NH2	H_ASP_90	OD2	3.551
4KRM	H_ARG_67	NH1	H_ASP_90	OD2	3.818
4KRM	H_ARG_67	NH2	H_ASP_90	OD1	2.298

4KRM	H_ARG_67	NH2	H_ASP_90	OD2	3.171
4KRM	I_ARG_353	NH1	J_GLU_110	OE1	2.862
4KRM	I_ARG_353	NH2	J_ASP_112	OD2	2.998
4KRM	I_ARG_390	NH2	L_ASP_369	OD1	2.686
4KRM	I_ARG_390	NH2	L_ASP_369	OD2	3.689
4KRM	I_ARG_403	NH1	I_GLU_376	OE1	2.441
4KRM	I_LYS_407	NZ	L_ASP_434	OD2	3.279
4KRM	I_ARG_427	NH1	I_GLU_397	OE1	3.054
4KRM	I_ARG_427	NH2	L_ASP_498	OD1	3.187
4KRM	I_LYS_463	NZ	L_ASP_436	OD2	3.450
4KRM	J_ARG_19	NH2	J_ASP_80	OD1	3.277
4KRM	J_ARG_30	NH1	L_ASP_355	OD1	3.164
4KRM	J_ARG_30	NH1	L_ASP_355	OD2	2.382
4KRM	J_ARG_30	NH2	L_ASP_355	OD1	3.707
4KRM	J_ARG_38	NH1	J_ASP_90	OD2	2.970
4KRM	J_ARG_38	NH2	J_GLU_46	OE1	3.503
4KRM	J_ARG_38	NH2	J_ASP_90	OD2	3.921
4KRM	J_ARG_54	NH1	J_ASP_56	OD1	3.183
4KRM	J_ARG_54	NH1	J_ASP_56	OD2	2.886
4KRM	J_ARG_54	NH2	J_ASP_56	OD2	3.668
4KRM	J_ARG_67	NH1	J_ASP_90	OD1	3.429
4KRM	J_ARG_67	NH1	J_ASP_90	OD2	3.042
4KRM	J_ARG_67	NH2	J_ASP_90	OD1	2.611
4KRM	J_ARG_67	NH2	J_ASP_90	OD2	3.747
4KRM	K_HIS_334	ND1	K_GLU_320	OE2	3.444
4KRM	K_ARG_353	NH1	L_GLU_110	OE1	2.887
4KRM	K_ARG_353	NH1	L_ASP_112	OD2	3.973
4KRM	K_ARG_353	NH2	L_ASP_112	OD2	2.890
4KRM	K_LYS_375	NZ	K_GLU_400	OE2	3.857
4KRM	K_HIS_394	ND1	K_GLU_397	OE1	3.459
4KRM	K_HIS_394	NE2	K_GLU_397	OE1	3.631
4KRM	K_HIS_394	NE2	K_GLU_397	OE2	3.863
4KRM	K_ARG_403	NH1	K_GLU_376	OE1	3.745
4KRM	K_ARG_403	NH1	K_GLU_376	OE2	2.249
4KRM	K_LYS_407	NZ	K_ASP_434	OD1	3.042
4KRM	K_LYS_407	NZ	K_ASP_434	OD2	3.679
4KRM	K_ARG_427	NH2	K_ASP_498	OD1	3.193
4KRM	L_ARG_19	NH2	L_ASP_80	OD1	3.556
4KRM	L_ARG_30	NH1	K_ASP_355	OD1	3.487
4KRM	L_ARG_30	NH1	K_ASP_355	OD2	2.441
4KRM	L_ARG_30	NH2	K_ASP_355	OD1	3.452
4KRM	L_ARG_30	NH2	K_ASP_355	OD2	3.835
4KRM	L_ARG_38	NH1	L_ASP_90	OD2	3.094
4KRM	L_ARG_38	NH2	L_GLU_46	OE1	3.277
4KRM	L_ARG_67	NH1	L_ASP_90	OD1	3.933
4KRM	L_ARG_67	NH1	L_ASP_90	OD2	3.289
4KRM	L_ARG_67	NH2	L_ASP_90	OD1	2.604
4KRM	L_ARG_67	NH2	L_ASP_90	OD2	3.420

Table 558: 4KRM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4KRO	A_ARG_310	NH2	A_GLU_376	OE2	2.978
4KRO	A_HIS_394	NE2	A_ASP_369	OD1	3.673
4KRO	A_ARG_403	NH1	A_GLU_376	OE1	2.481
4KRO	A_ARG_403	NH1	A_GLU_376	OE2	3.999
4KRO	A_ARG_403	NH2	B_ASP_118	OD2	3.168
4KRO	A_ARG_405	NH2	B_ASP_118	OD1	3.123
4KRO	A_ARG_405	NH2	B_ASP_118	OD2	3.849
4KRO	A_LYS_407	NZ	A_ASP_434	OD1	3.794
4KRO	A_LYS_407	NZ	A_ASP_434	OD2	2.246
4KRO	A_ARG_427	NH1	A_GLU_397	OE1	3.467
4KRO	A_ARG_427	NH2	A_ASP_498	OD1	2.615
4KRO	A_LYS_443	NZ	D_ASP_58	OD1	2.597
4KRO	A_LYS_443	NZ	D_ASP_58	OD2	3.457
4KRO	A_LYS_465	NZ	D_ASP_103	OD2	2.400
4KRO	A_LYS_476	NZ	A_GLU_472	OE1	3.768
4KRO	A_ARG_503	NH1	A_ASP_513	OD1	3.566
4KRO	A_ARG_507	NH2	A_GLU_524	OE1	3.712
4KRO	A_HIS_594	NE2	A_ASP_588	OD1	2.943
4KRO	B_ARG_27	NH1	A_GLU_431	OE1	3.073
4KRO	B_ARG_27	NH2	A_GLU_431	OE1	3.933
4KRO	B_ARG_113	NH1	B_ASP_116	OD2	3.449
4KRO	B_ARG_113	NH2	B_ASP_116	OD1	2.666
4KRO	B_ARG_113	NH2	B_ASP_116	OD2	3.479
4KRO	C_LYS_49	NZ	D_GLU_105	OE2	3.247
4KRO	C_ARG_61	NH1	C_GLU_79	OE2	3.404
4KRO	C_ARG_61	NH2	C_GLU_81	OE2	3.298
4KRO	C_ARG_61	NH2	C_ASP_82	OD1	2.644
4KRO	C_ARG_61	NH2	C_ASP_82	OD2	3.807
4KRO	C_LYS_103	NZ	C_GLU_165	OE1	3.774
4KRO	C_LYS_103	NZ	C_GLU_165	OE2	3.693
4KRO	D_ARG_38	NH1	D_ASP_89	OD1	3.529
4KRO	D_ARG_38	NH2	D_GLU_46	OE1	2.983
4KRO	D_ARG_38	NH2	D_GLU_46	OE2	3.441
4KRO	D_ARG_66	NH1	D_ASP_89	OD2	3.598
4KRO	D_ARG_66	NH2	D_ASP_89	OD1	2.749
4KRO	D_ARG_66	NH2	D_ASP_89	OD2	3.332
4KRO	D_LYS_149	NZ	D_ASP_150	OD1	3.048
4KRO	D_LYS_149	NZ	D_ASP_150	OD2	2.797

Table 559: 4KRO-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4KRP	A_ARG_310	NH2	A_GLU_376	OE1	3.735
4KRP	A_ARG_310	NH2	A_GLU_376	OE2	2.935
4KRP	A_HIS_394	NE2	A_ASP_369	OD1	3.309
4KRP	A_ARG_403	NH1	A_GLU_376	OE1	2.285
4KRP	A_ARG_403	NH2	B_ASP_115	OD2	3.818
4KRP	A_ARG_405	NH1	B_GLU_113	OE1	2.923
4KRP	A_ARG_405	NH2	B_GLU_113	OE1	3.376
4KRP	A_ARG_405	NH2	B_ASP_115	OD1	2.626
4KRP	A_LYS_407	NZ	A_ASP_434	OD2	2.386
4KRP	A_ARG_427	NH2	A_ASP_392	OD2	3.997
4KRP	A_ARG_427	NH2	A_ASP_498	OD1	2.593
4KRP	A_ARG_427	NH2	A_ASP_498	OD2	3.626
4KRP	A_LYS_443	NZ	D_ASP_58	OD1	2.649
4KRP	A_LYS_443	NZ	D_ASP_58	OD2	3.951
4KRP	A_LYS_455	NZ	A_GLU_489	OE1	2.953
4KRP	A_LYS_455	NZ	A_GLU_489	OE2	2.814
4KRP	A_LYS_463	NZ	A_ASP_436	OD2	3.639
4KRP	A_LYS_465	NZ	D_ASP_103	OD2	2.931
4KRP	A_ARG_497	NH2	A_GLU_495	OE1	3.513
4KRP	A_ARG_507	NH2	A_GLU_524	OE1	3.179
4KRP	A_ARG_550	NH1	A_GLU_527	OE2	2.828
4KRP	A_ARG_550	NH2	A_GLU_527	OE1	3.298
4KRP	A_ARG_550	NH2	A_GLU_527	OE2	2.540
4KRP	A_HIS_560	NE2	A_GLU_537	OE1	3.908
4KRP	A_LYS_585	NZ	A_ASP_563	OD1	2.533
4KRP	C_LYS_49	NZ	C_GLU_53	OE1	2.808
4KRP	C_ARG_61	NH1	C_GLU_79	OE2	3.577
4KRP	C_ARG_61	NH2	C_GLU_79	OE1	3.975
4KRP	C_ARG_61	NH2	C_GLU_81	OE1	3.909
4KRP	C_ARG_61	NH2	C_GLU_81	OE2	3.782
4KRP	C_ARG_61	NH2	C_ASP_82	OD1	2.795
4KRP	C_ARG_61	NH2	C_ASP_82	OD2	3.835
4KRP	C_LYS_103	NZ	C_GLU_105	OE2	2.819
4KRP	C_LYS_149	NZ	C_GLU_195	OE1	2.866
4KRP	D_ARG_38	NH1	D_ASP_89	OD1	2.914
4KRP	D_ARG_38	NH2	D_GLU_46	OE1	3.258
4KRP	D_ARG_38	NH2	D_ASP_89	OD1	3.860
4KRP	D_ARG_66	NH1	D_ASP_89	OD1	3.718
4KRP	D_ARG_66	NH1	D_ASP_89	OD2	3.786
4KRP	D_ARG_66	NH2	D_ASP_89	OD1	2.586
4KRP	D_ARG_66	NH2	D_ASP_89	OD2	3.503
4KRP	D_LYS_149	NZ	D_ASP_150	OD1	3.078
4KRP	D_LYS_149	NZ	D_ASP_150	OD2	2.845
4KRP	B_ARG_27	NH1	A_GLU_431	OE1	3.144
4KRP	B_ARG_27	NH2	B_GLU_1	OE2	3.797

Table 560: 4KRP-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4KV5	C_LYS_26	NZ	C_ASP_23	OD2	3.341
4KV5	C_LYS_60	NZ	G_ASP_56	OD2	3.911
4KV5	C_LYS_60	NZ	G_GLU_74	OE2	3.252
4KV5	C_ARG_94	NH1	E_ASP_231	OD2	3.776
4KV5	C_ARG_107	NH1	C_GLU_84	OE1	2.912
4KV5	D_LYS_26	NZ	D_ASP_23	OD2	3.617
4KV5	D_LYS_60	NZ	E_GLU_74	OE2	3.237
4KV5	D_ARG_107	NH1	D_GLU_84	OE1	2.427
4KV5	D_ARG_107	NH1	D_GLU_84	OE2	3.699
4KV5	A_LYS_26	NZ	A_ASP_23	OD1	3.905
4KV5	A_LYS_26	NZ	A_ASP_23	OD2	3.181
4KV5	A_ARG_94	NH1	H_ASP_231	OD2	3.628
4KV5	A_ARG_107	NH1	A_GLU_84	OE1	2.439
4KV5	A_ARG_107	NH1	A_GLU_84	OE2	3.529
4KV5	B_LYS_26	NZ	B_ASP_23	OD2	3.176
4KV5	B_LYS_60	NZ	H_ASP_56	OD2	3.938
4KV5	B_LYS_60	NZ	H_GLU_74	OE2	3.524
4KV5	B_ARG_107	NH1	B_GLU_84	OE1	2.808
4KV5	B_ARG_107	NH1	B_GLU_84	OE2	3.463
4KV5	J_LYS_12	NZ	J_GLU_10	OE1	3.764
4KV5	J_ARG_38	NH1	J_ASP_90	OD1	3.233
4KV5	J_ARG_38	NH2	J_GLU_46	OE1	3.110
4KV5	J_ARG_38	NH2	J_ASP_90	OD1	3.659
4KV5	J_ARG_63	NH1	J_GLU_138	OE2	3.309
4KV5	J_ARG_63	NH2	J_GLU_46	OE1	3.549
4KV5	J_ARG_63	NH2	J_GLU_46	OE2	2.611
4KV5	J_ARG_67	NH1	J_ASP_90	OD2	3.363
4KV5	J_ARG_67	NH2	J_ASP_90	OD1	3.304
4KV5	J_ARG_67	NH2	J_ASP_90	OD2	3.334
4KV5	J_ARG_161	NH1	J_ASP_208	OD2	3.042
4KV5	J_ARG_199	NH1	J_GLU_217	OE2	3.577
4KV5	J_ARG_199	NH1	J_GLU_219	OE1	3.495
4KV5	J_ARG_199	NH1	J_ASP_220	OD1	2.798
4KV5	J_ARG_199	NH1	J_ASP_220	OD2	3.031
4KV5	J_ARG_199	NH2	J_GLU_217	OE1	3.655
4KV5	H_LYS_12	NZ	H_GLU_10	OE1	3.355
4KV5	H_ARG_38	NH1	H_ASP_90	OD1	3.401
4KV5	H_ARG_38	NH2	H_GLU_46	OE1	3.103
4KV5	H_ARG_38	NH2	H_ASP_90	OD1	3.880
4KV5	H_ARG_63	NH1	H_GLU_138	OE2	3.222
4KV5	H_ARG_63	NH2	H_GLU_46	OE1	3.904
4KV5	H_ARG_63	NH2	H_GLU_46	OE2	3.081
4KV5	H_ARG_67	NH1	H_ASP_90	OD2	3.586
4KV5	H_ARG_67	NH2	H_ASP_90	OD1	3.193
4KV5	H_ARG_67	NH2	H_ASP_90	OD2	3.057
4KV5	H_ARG_161	NH1	H_ASP_208	OD1	3.304
4KV5	H_ARG_161	NH1	H_ASP_208	OD2	2.542
4KV5	H_LYS_177	NZ	H_GLU_219	OE2	3.873
4KV5	H_ARG_199	NH1	H_GLU_219	OE1	3.591
4KV5	H_ARG_199	NH1	H_ASP_220	OD1	2.535
4KV5	H_ARG_199	NH1	H_ASP_220	OD2	2.810
4KV5	H_ARG_199	NH2	H_GLU_217	OE1	3.657
4KV5	E_LYS_12	NZ	E_GLU_10	OE1	3.582
4KV5	E_ARG_38	NH1	E_ASP_90	OD1	3.243
4KV5	E_ARG_38	NH2	E_GLU_46	OE1	3.194
4KV5	E_ARG_38	NH2	E_ASP_90	OD1	3.863
4KV5	E_ARG_63	NH1	E_GLU_138	OE2	3.426

4KV5	E_ARG_63	NH2	E_GLU_46	OE1	3.563
4KV5	E_ARG_63	NH2	E_GLU_46	OE2	3.213
4KV5	E_ARG_67	NH1	E_ASP_90	OD2	3.666
4KV5	E_ARG_67	NH2	E_ASP_90	OD1	2.990
4KV5	E_ARG_67	NH2	E_ASP_90	OD2	3.041
4KV5	E_ARG_161	NH1	E_ASP_208	OD1	3.920
4KV5	E_ARG_161	NH1	E_ASP_208	OD2	2.895
4KV5	E_LYS_177	NZ	E_GLU_219	OE2	3.890
4KV5	E_ARG_199	NH1	E_GLU_217	OE2	3.831
4KV5	E_ARG_199	NH1	E_GLU_219	OE1	3.226
4KV5	E_ARG_199	NH1	E_ASP_220	OD1	3.288
4KV5	E_ARG_199	NH1	E_ASP_220	OD2	3.702
4KV5	E_ARG_199	NH2	E_GLU_217	OE1	3.523
4KV5	G_LYS_12	NZ	G_GLU_10	OE1	3.677
4KV5	G_ARG_38	NH1	G_ASP_90	OD1	3.460
4KV5	G_ARG_38	NH2	G_GLU_46	OE1	2.859
4KV5	G_ARG_38	NH2	G_ASP_90	OD1	3.976
4KV5	G_ARG_63	NH1	G_GLU_138	OE2	3.087
4KV5	G_ARG_63	NH2	G_GLU_46	OE1	3.637
4KV5	G_ARG_63	NH2	G_GLU_46	OE2	2.834
4KV5	G_ARG_67	NH1	G_ASP_90	OD2	3.423
4KV5	G_ARG_67	NH2	G_ASP_90	OD1	3.401
4KV5	G_ARG_67	NH2	G_ASP_90	OD2	3.441
4KV5	G_ARG_161	NH1	G_ASP_208	OD1	3.631
4KV5	G_ARG_161	NH1	G_ASP_208	OD2	2.851
4KV5	G_ARG_199	NH1	G_GLU_217	OE2	3.903
4KV5	G_ARG_199	NH1	G_GLU_219	OE1	3.208
4KV5	G_ARG_199	NH1	G_GLU_219	OE2	3.799
4KV5	G_ARG_199	NH1	G_ASP_220	OD1	3.065
4KV5	G_ARG_199	NH1	G_ASP_220	OD2	3.673
4KV5	G_ARG_199	NH2	G_GLU_217	OE1	3.544

Table 561: 4KV5-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4KXZ	A_ARG_26	NH1	A_ASP_27	OD1	3.110
4KXZ	A_ARG_26	NH1	A_ASP_27	OD2	2.701
4KXZ	A_ARG_60	NH2	J_GLU_74	OE1	3.804
4KXZ	A_LYS_107	NZ	A_GLU_84	OE1	2.831
4KXZ	A_LYS_110	NZ	A_ASP_55	OD1	3.869
4KXZ	A_LYS_110	NZ	A_ASP_55	OD2	3.509
4KXZ	B_ARG_26	NH1	B_ASP_27	OD1	3.225
4KXZ	B_ARG_26	NH1	B_ASP_27	OD2	2.899
4KXZ	B_LYS_37	NZ	B_GLU_35	OE2	3.695
4KXZ	B_ARG_60	NH2	H_ASP_56	OD1	3.585
4KXZ	B_ARG_60	NH2	H_GLU_74	OE1	3.374
4KXZ	B_ARG_60	NH2	H_GLU_74	OE2	3.199
4KXZ	B_LYS_107	NZ	B_GLU_84	OE1	2.748
4KXZ	D_ARG_26	NH1	D_ASP_27	OD1	3.954
4KXZ	D_ARG_26	NH1	D_ASP_27	OD2	3.663
4KXZ	D_LYS_37	NZ	D_GLU_35	OE1	2.767
4KXZ	D_LYS_37	NZ	D_GLU_35	OE2	3.981
4KXZ	D_ARG_60	NH1	N_GLU_74	OE2	3.775
4KXZ	D_ARG_60	NH2	N_GLU_74	OE2	2.746
4KXZ	D_LYS_110	NZ	D_ASP_55	OD1	3.900
4KXZ	D_LYS_110	NZ	D_ASP_55	OD2	3.944
4KXZ	E_ARG_26	NH1	E_ASP_27	OD1	3.052
4KXZ	E_ARG_26	NH1	E_ASP_27	OD2	2.752
4KXZ	E_LYS_37	NZ	E_GLU_35	OE1	2.815
4KXZ	E_ARG_60	NH1	Q_GLU_74	OE1	3.619
4KXZ	E_LYS_107	NZ	E_GLU_84	OE1	2.833
4KXZ	E_LYS_110	NZ	E_ASP_55	OD1	3.262
4KXZ	E_LYS_110	NZ	E_ASP_55	OD2	3.430
4KXZ	H_LYS_12	NZ	H_GLU_10	OE1	3.843
4KXZ	H_ARG_38	NH1	H_ASP_90	OD1	2.815
4KXZ	H_ARG_38	NH2	H_GLU_46	OE2	3.360
4KXZ	H_ARG_38	NH2	H_ASP_90	OD1	3.535
4KXZ	H_ARG_63	NH1	H_GLU_46	OE2	2.772
4KXZ	H_ARG_67	NH1	H_ASP_90	OD1	3.629
4KXZ	H_ARG_67	NH1	H_ASP_90	OD2	2.716
4KXZ	H_ARG_67	NH2	H_ASP_90	OD1	3.064
4KXZ	H_ARG_67	NH2	H_ASP_90	OD2	3.651
4KXZ	H_LYS_150	NZ	H_ASP_151	OD1	3.357
4KXZ	H_LYS_150	NZ	H_ASP_151	OD2	3.542
4KXZ	H_LYS_208	NZ	H_ASP_206	OD2	3.838
4KXZ	H_HIS_219	NE2	Q_ASP_56	OD2	3.789
4KXZ	H_HIS_223	ND1	Q_GLU_82	OE1	3.688
4KXZ	H_HIS_223	ND1	Q_GLU_82	OE2	3.984
4KXZ	H_HIS_223	ND1	L_ASP_123	OD1	3.085
4KXZ	H_HIS_223	NE2	Q_GLU_82	OE2	3.368
4KXZ	H_HIS_223	NE2	L_ASP_123	OD1	3.457
4KXZ	J_LYS_12	NZ	J_GLU_10	OE1	3.778
4KXZ	J_ARG_38	NH1	J_ASP_90	OD1	3.085
4KXZ	J_ARG_38	NH2	J_GLU_46	OE1	3.558
4KXZ	J_ARG_38	NH2	J_ASP_90	OD1	3.950
4KXZ	J_ARG_63	NH1	J_GLU_46	OE2	2.664
4KXZ	J_ARG_67	NH1	J_ASP_90	OD1	3.719
4KXZ	J_ARG_67	NH1	J_ASP_90	OD2	2.552
4KXZ	J_ARG_67	NH2	J_ASP_90	OD1	2.776
4KXZ	J_ARG_67	NH2	J_ASP_90	OD2	3.166
4KXZ	J_LYS_150	NZ	J_ASP_151	OD1	3.358
4KXZ	J_LYS_150	NZ	J_ASP_151	OD2	3.511

4KXZ	J_LYS_208	NZ	J_ASP_206	OD2	3.900
4KXZ	J_LYS_216	NZ	I_GLU_124	OE1	2.736
4KXZ	J_LYS_216	NZ	I_GLU_124	OE2	3.105
4KXZ	N_LYS_12	NZ	N_GLU_10	OE1	3.790
4KXZ	N_ARG_38	NH1	N_ASP_90	OD1	3.020
4KXZ	N_ARG_38	NH2	N_GLU_46	OE1	3.356
4KXZ	N_ARG_38	NH2	N_ASP_90	OD1	3.762
4KXZ	N_ARG_63	NH1	N_GLU_46	OE2	2.704
4KXZ	N_ARG_67	NH1	N_ASP_90	OD1	3.612
4KXZ	N_ARG_67	NH1	N_ASP_90	OD2	2.733
4KXZ	N_ARG_67	NH2	N_ASP_90	OD1	3.034
4KXZ	N_ARG_67	NH2	N_ASP_90	OD2	3.633
4KXZ	N_ARG_87	NH2	N_GLU_89	OE1	3.697
4KXZ	N_LYS_150	NZ	N_ASP_151	OD1	3.348
4KXZ	N_LYS_150	NZ	N_ASP_151	OD2	3.490
4KXZ	N_LYS_208	NZ	N_ASP_206	OD2	3.916
4KXZ	N_HIS_219	NE2	J_ASP_56	OD2	3.889
4KXZ	N_HIS_223	ND1	J_GLU_82	OE1	3.240
4KXZ	N_HIS_223	ND1	M_ASP_123	OD1	3.197
4KXZ	N_HIS_223	NE2	J_GLU_82	OE1	3.650
4KXZ	N_HIS_223	NE2	J_GLU_82	OE2	3.394
4KXZ	N_HIS_223	NE2	M_ASP_123	OD1	3.310
4KXZ	Q_LYS_12	NZ	Q_GLU_10	OE1	3.907
4KXZ	Q_ARG_38	NH1	Q_ASP_90	OD1	3.058
4KXZ	Q_ARG_38	NH2	Q_GLU_46	OE1	3.407
4KXZ	Q_ARG_38	NH2	Q_ASP_90	OD1	3.856
4KXZ	Q_ARG_63	NH1	Q_GLU_46	OE2	2.707
4KXZ	Q_ARG_67	NH1	Q_ASP_90	OD1	3.587
4KXZ	Q_ARG_67	NH1	Q_ASP_90	OD2	2.735
4KXZ	Q_ARG_67	NH2	Q_ASP_90	OD1	3.009
4KXZ	Q_ARG_67	NH2	Q_ASP_90	OD2	3.660
4KXZ	Q_LYS_150	NZ	Q_ASP_151	OD1	3.335
4KXZ	Q_LYS_150	NZ	Q_ASP_151	OD2	3.512
4KXZ	Q_LYS_208	NZ	Q_ASP_206	OD2	3.889
4KXZ	I_ARG_24	NH1	I_ASP_71	OD1	3.813
4KXZ	I_ARG_24	NH2	I_ASP_71	OD1	3.864
4KXZ	I_ARG_24	NH2	I_ASP_71	OD2	3.073
4KXZ	I_ARG_55	NH1	I_ASP_61	OD1	3.473
4KXZ	I_ARG_62	NH1	I_GLU_82	OE1	3.700
4KXZ	I_ARG_62	NH1	I_ASP_83	OD1	3.621
4KXZ	I_ARG_62	NH1	I_ASP_83	OD2	2.958
4KXZ	I_LYS_108	NZ	I_GLU_17	OE2	3.073
4KXZ	I_LYS_150	NZ	I_GLU_196	OE1	2.905
4KXZ	I_HIS_190	ND1	I_ASP_152	OD1	2.847
4KXZ	I_HIS_190	NE2	I_ASP_186	OD1	3.845
4KXZ	L_ARG_24	NH1	L_ASP_71	OD1	3.783
4KXZ	L_ARG_24	NH2	L_ASP_71	OD1	3.857
4KXZ	L_ARG_24	NH2	L_ASP_71	OD2	3.080
4KXZ	L_ARG_62	NH1	L_GLU_82	OE1	3.794
4KXZ	L_ARG_62	NH1	L_ASP_83	OD1	3.459
4KXZ	L_ARG_62	NH1	L_ASP_83	OD2	2.664
4KXZ	L_ARG_78	NH2	L_ASP_61	OD1	3.145
4KXZ	L_ARG_104	NH1	L_GLU_166	OE1	3.969
4KXZ	L_LYS_127	NZ	L_GLU_124	OE1	3.662
4KXZ	L_LYS_127	NZ	L_GLU_124	OE2	3.133
4KXZ	L_LYS_150	NZ	L_GLU_196	OE1	2.895
4KXZ	L_HIS_190	ND1	L_ASP_152	OD1	3.069
4KXZ	L_HIS_190	NE2	L_ASP_186	OD1	3.912

4KXZ	M_ARG_24	NH1	M_ASP_71	OD1	3.817
4KXZ	M_ARG_24	NH2	M_ASP_71	OD1	3.870
4KXZ	M_ARG_24	NH2	M_ASP_71	OD2	3.074
4KXZ	M_ARG_62	NH1	M_GLU_82	OE1	3.945
4KXZ	M_ARG_62	NH1	M_ASP_83	OD1	2.966
4KXZ	M_ARG_62	NH1	M_ASP_83	OD2	2.505
4KXZ	M_ARG_104	NH1	M_GLU_166	OE1	3.774
4KXZ	M_LYS_127	NZ	M_GLU_124	OE1	3.654
4KXZ	M_LYS_127	NZ	M_GLU_124	OE2	3.133
4KXZ	M_LYS_150	NZ	M_GLU_196	OE1	2.934
4KXZ	M_HIS_190	ND1	M_ASP_152	OD1	2.804
4KXZ	M_HIS_190	NE2	M_ASP_186	OD1	3.796
4KXZ	P_ARG_24	NH1	P_ASP_71	OD1	3.864
4KXZ	P_ARG_24	NH2	P_ASP_71	OD1	3.911
4KXZ	P_ARG_24	NH2	P_ASP_71	OD2	3.105
4KXZ	P_ARG_62	NH1	P_GLU_82	OE1	3.797
4KXZ	P_ARG_62	NH1	P_ASP_83	OD1	3.211
4KXZ	P_ARG_62	NH1	P_ASP_83	OD2	2.770
4KXZ	P_ARG_104	NH1	P_GLU_166	OE1	3.937
4KXZ	P_LYS_127	NZ	P_GLU_124	OE1	3.704
4KXZ	P_LYS_127	NZ	P_GLU_124	OE2	3.171
4KXZ	P_LYS_150	NZ	P_GLU_196	OE1	2.899
4KXZ	P_HIS_190	ND1	P_ASP_186	OD1	3.702

Table 562: 4KXZ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4LQF	A_HIS_113	NE2	A_GLU_129	OE1	3.149
4LQF	A_HIS_113	NE2	A_GLU_129	OE2	3.669
4LQF	A_ARG_176	NH1	A_GLU_174	OE1	2.869
4LQF	A_ARG_176	NH2	A_GLU_174	OE1	2.927
4LQF	H_ARG_38	NH1	H_ASP_90	OD1	2.938
4LQF	H_ARG_38	NH2	H_GLU_46	OE1	3.480
4LQF	H_ARG_38	NH2	H_GLU_46	OE2	3.018
4LQF	H_ARG_38	NH2	H_ASP_90	OD1	3.987
4LQF	H_LYS_65	NZ	H_ASP_62	OD1	3.431
4LQF	H_ARG_67	NH1	H_ASP_90	OD1	3.786
4LQF	H_ARG_67	NH1	H_ASP_90	OD2	2.716
4LQF	H_ARG_67	NH2	H_ASP_90	OD1	2.856
4LQF	H_ARG_67	NH2	H_ASP_90	OD2	3.328
4LQF	H_ARG_98	NH2	H_ASP_105	OD1	3.789
4LQF	H_ARG_98	NH2	H_ASP_105	OD2	2.616
4LQF	H_LYS_212	NZ	L_GLU_129	OE1	2.714
4LQF	H_LYS_212	NZ	L_GLU_129	OE2	3.879
4LQF	H_LYS_213	NZ	H_GLU_215	OE2	3.811
4LQF	L_ARG_24	NH2	L_ASP_75	OD1	3.452
4LQF	L_LYS_55	NZ	A_ASP_170	OD2	2.731
4LQF	L_ARG_59	NH2	L_ASP_65	OD1	3.368
4LQF	L_ARG_66	NH1	L_GLU_84	OE1	3.227
4LQF	L_ARG_66	NH2	L_GLU_84	OE1	3.232
4LQF	L_ARG_66	NH2	L_GLU_86	OE1	3.495
4LQF	L_ARG_66	NH2	L_ASP_87	OD1	2.884
4LQF	L_ARG_66	NH2	L_ASP_87	OD2	3.750
4LQF	L_LYS_109	NZ	L_ASP_171	OD1	3.085
4LQF	L_LYS_153	NZ	L_GLU_201	OE2	3.416
4LQF	L_LYS_155	NZ	L_GLU_201	OE1	2.827
4LQF	L_LYS_155	NZ	L_GLU_201	OE2	3.989
4LQF	L_ARG_161	NH1	L_GLU_191	OE2	2.916
4LQF	L_ARG_161	NH2	L_GLU_191	OE2	3.407
4LQF	L_LYS_189	NZ	L_ASP_190	OD1	2.644
4LQF	L_HIS_195	ND1	L_ASP_157	OD2	2.742
4LQF	L_HIS_195	NE2	L_GLU_191	OE2	3.503
4LQF	L_LYS_205	NZ	L_ASP_116	OD1	3.781
4LQF	L_LYS_205	NZ	L_ASP_116	OD2	2.661

Table 563: 4LQF-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4LSS	G.LYS_46	NZ	G.GLU_492	OE2	3.983
4LSS	G.LYS_59	NZ	G.ASP_57	OD1	3.236
4LSS	G.LYS_59	NZ	G.ASP_57	OD2	3.806
4LSS	G.HIS_66	ND1	G.GLU_64	OE2	2.739
4LSS	G.LYS_97	NZ	G.GLU_275	OE2	2.397
4LSS	G.LYS_97	NZ	H.ASP_99	OD2	3.791
4LSS	G.LYS_207	NZ	G.GLU_381	OE1	3.905
4LSS	G.LYS_207	NZ	G.GLU_381	OE2	3.089
4LSS	G.LYS_229	NZ	G.GLU_83	OE2	3.491
4LSS	G.HIS_249	NE2	G.GLU_482	OE1	3.577
4LSS	G.LYS_282	NZ	G.GLU_275	OE1	3.241
4LSS	G.ARG_335	NH2	G.ASP_412	OD2	3.767
4LSS	G.LYS_351	NZ	G.GLU_269	OE2	3.712
4LSS	G.ARG_419	NH2	G.ASP_325	OD1	3.444
4LSS	G.ARG_419	NH2	G.ASP_325	OD2	2.969
4LSS	G.ARG_429	NH1	G.ASP_113	OD1	3.219
4LSS	G.ARG_429	NH1	G.ASP_113	OD2	3.237
4LSS	G.ARG_429	NH2	G.ASP_113	OD2	2.924
4LSS	G.ARG_456	NH1	G.GLU_466	OE1	3.330
4LSS	G.ARG_469	NH2	G.ASP_457	OD2	2.938
4LSS	G.ARG_476	NH1	G.GLU_102	OE1	3.477
4LSS	G.ARG_476	NH1	G.GLU_102	OE2	3.366
4LSS	G.ARG_476	NH2	G.ASP_474	OD2	3.933
4LSS	G.ARG_476	NH2	H.ASP_31	OD1	3.839
4LSS	G.ARG_480	NH1	G.ASP_477	OD1	2.752
4LSS	G.LYS_485	NZ	G.GLU_267	OE2	3.906
4LSS	G.LYS_487	NZ	G.GLU_91	OE1	2.643
4LSS	H.ARG_19	NH2	H.GLU_81	OE1	3.566
4LSS	H.ARG_38	NH1	H.ASP_86	OD1	3.014
4LSS	H.ARG_38	NH2	H.GLU_46	OE1	3.219
4LSS	H.ARG_38	NH2	H.ASP_86	OD1	3.812
4LSS	H.ARG_53	NH2	H.ASP_31	OD1	3.384
4LSS	H.ARG_61	NH2	G.GLU_466	OE1	3.951
4LSS	H.ARG_66	NH1	H.ASP_86	OD1	3.855
4LSS	H.ARG_66	NH2	H.ASP_86	OD1	2.799
4LSS	H.ARG_66	NH2	H.ASP_86	OD2	2.736
4LSS	H.ARG_71	NH1	G.ASP_368	OD1	3.719
4LSS	H.ARG_71	NH1	G.ASP_368	OD2	3.126
4LSS	H.ARG_71	NH2	G.ASP_368	OD1	3.278
4LSS	H.ARG_82A	NH1	H.GLU_81	OE2	3.430
4LSS	H.LYS_209	NZ	L.GLU_125	OE1	3.429
4LSS	H.LYS_209	NZ	L.GLU_125	OE2	3.562
4LSS	H.LYS_210	NZ	H.GLU_212	OE2	3.090
4LSS	L.ARG_24	NH2	L.ASP_70	OD1	3.687
4LSS	L.ARG_24	NH2	L.ASP_70	OD2	3.435
4LSS	L.ARG_54	NH1	L.ASP_60	OD2	3.825
4LSS	L.ARG_61	NH1	L.ASP_82	OD1	3.979
4LSS	L.ARG_61	NH1	L.ASP_82	OD2	2.997
4LSS	L.ARG_61	NH2	L.GLU_79	OE1	3.337
4LSS	L.ARG_61	NH2	L.ASP_82	OD1	3.196
4LSS	L.ARG_61	NH2	L.ASP_82	OD2	3.376
4LSS	L.LYS_109	NZ	L.GLU_17	OE1	3.541
4LSS	L.LYS_109	NZ	L.GLU_17	OE2	3.227
4LSS	L.LYS_109	NZ	L.ASP_107	OD1	3.475
4LSS	L.LYS_151	NZ	L.GLU_197	OE2	3.341

Table 564: 4LSS-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4LST	G_HIS_66	ND1	G_GLU_64	OE1	3.932
4LST	G_HIS_66	ND1	G_GLU_64	OE2	2.793
4LST	G_LYS_207	NZ	G_GLU_381	OE1	2.992
4LST	G_LYS_207	NZ	G_GLU_381	OE2	2.424
4LST	G_HIS_249	NE2	G_GLU_482	OE1	3.272
4LST	G_LYS_282	NZ	G_GLU_275	OE1	2.940
4LST	G_LYS_357	NZ	G_ASP_461	OD2	3.749
4LST	G_LYS_357	NZ	G_ASP_464	OD1	3.358
4LST	G_LYS_357	NZ	L_GLU_1	OE1	2.783
4LST	G_LYS_360	NZ	G_GLU_362	OE1	3.583
4LST	G_ARG_419	NH2	G_ASP_325	OD1	3.855
4LST	G_ARG_419	NH2	G_ASP_325	OD2	3.169
4LST	G_ARG_456	NH1	G_GLU_466	OE1	3.211
4LST	G_ARG_469	NH1	G_GLU_362	OE2	3.557
4LST	G_ARG_469	NH2	G_GLU_362	OE2	3.437
4LST	G_ARG_469	NH2	G_ASP_457	OD2	3.388
4LST	G_ARG_476	NH1	G_ASP_474	OD1	3.272
4LST	G_ARG_476	NH1	G_ASP_474	OD2	2.826
4LST	G_ARG_480	NH1	G_ASP_477	OD1	3.383
4LST	H_LYS_12	NZ	H_GLU_16	OE2	3.461
4LST	H_ARG_38	NH1	H_ASP_86	OD1	2.980
4LST	H_ARG_38	NH2	H_GLU_46	OE1	3.044
4LST	H_ARG_38	NH2	H_ASP_86	OD1	3.692
4LST	H_LYS_43	NZ	H_ASP_85	OD1	3.823
4LST	H_ARG_53	NH1	H_ASP_31	OD1	3.186
4LST	H_ARG_53	NH2	H_ASP_31	OD1	3.110
4LST	H_ARG_61	NH1	G_GLU_466	OE1	3.812
4LST	H_ARG_61	NH2	G_ASP_461	OD1	2.947
4LST	H_ARG_66	NH1	H_ASP_86	OD1	3.435
4LST	H_ARG_66	NH2	H_ASP_86	OD1	2.875
4LST	H_ARG_66	NH2	H_ASP_86	OD2	2.791
4LST	H_ARG_71	NH1	G_ASP_368	OD1	3.527
4LST	H_ARG_71	NH1	G_ASP_368	OD2	2.632
4LST	H_ARG_71	NH2	G_ASP_368	OD1	2.939
4LST	H_ARG_71	NH2	G_ASP_368	OD2	3.624
4LST	H_ARG_82A	NH1	H_GLU_81	OE2	3.069
4LST	H_HIS_102	NE2	H_GLU_101	OE1	3.589
4LST	H_LYS_143	NZ	H_ASP_144	OD2	3.387
4LST	H_LYS_209	NZ	L_GLU_125	OE2	3.921
4LST	H_LYS_214	NZ	L_ASP_124	OD1	3.010
4LST	H_LYS_214	NZ	L_ASP_124	OD2	3.020
4LST	L_ARG_24	NH1	L_ASP_70	OD1	3.104
4LST	L_ARG_24	NH1	L_ASP_70	OD2	3.678
4LST	L_ARG_61	NH1	L_ASP_82	OD1	3.975
4LST	L_ARG_61	NH1	L_ASP_82	OD2	2.621
4LST	L_ARG_61	NH2	L_GLU_79	OE1	3.426
4LST	L_ARG_61	NH2	L_ASP_82	OD1	3.303
4LST	L_ARG_61	NH2	L_ASP_82	OD2	3.231
4LST	L_LYS_109	NZ	L_GLU_17	OE1	2.684
4LST	L_LYS_185	NZ	L_GLU_189	OE2	3.865

Table 565: 4LST-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4LU5	A_HIS_113	NE2	A_GLU_129	OE2	3.983
4LU5	A_LYS_161	NZ	A_ASP_146	OD1	3.296
4LU5	A_LYS_161	NZ	A_GLU_149	OE1	3.749
4LU5	A_LYS_161	NZ	A_GLU_149	OE2	3.934
4LU5	A_ARG_176	NH1	A_ASP_150	OD1	2.940
4LU5	A_ARG_176	NH2	A_GLU_174	OE1	2.726
4LU5	B_HIS_113	ND1	B_ASP_115	OD1	3.948
4LU5	B_LYS_161	NZ	B_ASP_146	OD1	3.334
4LU5	B_LYS_161	NZ	B_GLU_149	OE2	3.499
4LU5	B_ARG_176	NH1	B_ASP_150	OD2	3.286
4LU5	B_ARG_176	NH2	B_GLU_174	OE1	3.070
4LU5	H_ARG_38	NH1	H_ASP_90	OD1	2.792
4LU5	H_ARG_38	NH2	H_GLU_46	OE1	3.705
4LU5	H_ARG_38	NH2	H_ASP_90	OD1	3.789
4LU5	H_ARG_44	NH1	H_GLU_42	OE2	3.479
4LU5	H_ARG_44	NH2	H_GLU_46	OE2	3.762
4LU5	H_LYS_65	NZ	H_ASP_62	OD1	3.768
4LU5	H_ARG_67	NH1	H_ASP_90	OD1	3.815
4LU5	H_ARG_67	NH1	H_ASP_90	OD2	2.768
4LU5	H_ARG_67	NH2	H_ASP_90	OD1	2.850
4LU5	H_ARG_67	NH2	H_ASP_90	OD2	3.112
4LU5	H_ARG_98	NH2	B_ASP_168	OD2	3.392
4LU5	H_LYS_208	NZ	L_GLU_128	OE1	3.058
4LU5	H_LYS_208	NZ	L_GLU_128	OE2	3.445
4LU5	H_LYS_209	NZ	H_GLU_211	OE1	2.959
4LU5	L_ARG_51	NH1	H_ASP_101	OD1	3.227
4LU5	L_ARG_51	NH2	H_ASP_101	OD1	2.925
4LU5	L_ARG_51	NH2	L_ASP_60	OD1	2.906
4LU5	L_ARG_51	NH2	L_ASP_60	OD2	3.008
4LU5	L_ARG_66	NH1	L_GLU_84	OE1	3.197
4LU5	L_ARG_66	NH1	L_GLU_84	OE2	3.353
4LU5	L_ARG_66	NH2	L_ASP_87	OD1	2.665
4LU5	L_ARG_66	NH2	L_ASP_87	OD2	2.880
4LU5	L_ARG_82	NH2	L_GLU_84	OE2	3.688
4LU5	L_LYS_108	NZ	L_GLU_110	OE2	3.434
4LU5	L_LYS_154	NZ	L_GLU_200	OE1	3.567
4LU5	L_ARG_160	NH2	L_GLU_190	OE1	3.714
4LU5	L_ARG_160	NH2	L_GLU_190	OE2	2.875
4LU5	L_LYS_174	NZ	L_GLU_86	OE2	3.749
4LU5	L_LYS_188	NZ	L_GLU_192	OE1	2.486
4LU5	L_HIS_194	ND1	L_ASP_156	OD2	2.594
4LU5	L_LYS_204	NZ	L_ASP_115	OD2	3.897
4LU5	I_ARG_38	NH1	I_ASP_90	OD1	2.773
4LU5	I_ARG_38	NH2	I_GLU_46	OE1	3.420
4LU5	I_ARG_38	NH2	I_ASP_90	OD1	3.756
4LU5	I_ARG_44	NH1	I_GLU_42	OE1	3.393
4LU5	I_ARG_44	NH1	I_GLU_42	OE2	2.926
4LU5	I_ARG_44	NH2	I_GLU_42	OE2	3.842
4LU5	I_ARG_44	NH2	I_GLU_46	OE2	3.631
4LU5	I_LYS_65	NZ	I_ASP_62	OD1	3.327
4LU5	I_ARG_67	NH1	I_ASP_90	OD1	3.710
4LU5	I_ARG_67	NH1	I_ASP_90	OD2	2.762
4LU5	I_ARG_67	NH2	I_ASP_90	OD1	2.979
4LU5	I_ARG_67	NH2	I_ASP_90	OD2	3.184
4LU5	I_ARG_98	NH2	A_ASP_168	OD2	3.317
4LU5	I_LYS_209	NZ	I_GLU_211	OE2	3.549
4LU5	M_LYS_24	NZ	M_ASP_75	OD1	3.847

4LU5	M_ARG_51	NH1	I_ASP_101	OD2	3.086
4LU5	M_ARG_51	NH2	I_ASP_101	OD1	3.927
4LU5	M_ARG_51	NH2	I_ASP_101	OD2	2.770
4LU5	M_ARG_51	NH2	M_ASP_60	OD1	3.599
4LU5	M_ARG_51	NH2	M_ASP_60	OD2	3.102
4LU5	M_ARG_66	NH1	M_GLU_84	OE1	3.699
4LU5	M_ARG_66	NH1	M_GLU_84	OE2	3.904
4LU5	M_ARG_66	NH2	M_ASP_87	OD1	2.686
4LU5	M_ARG_66	NH2	M_ASP_87	OD2	3.050
4LU5	M_ARG_82	NH1	M_GLU_84	OE2	2.836
4LU5	M_LYS_152	NZ	M_GLU_200	OE2	3.478
4LU5	M_LYS_154	NZ	M_GLU_200	OE1	3.458
4LU5	M_LYS_154	NZ	M_GLU_200	OE2	3.926
4LU5	M_ARG_160	NH1	M_GLU_190	OE2	3.887
4LU5	M_ARG_160	NH2	M_GLU_190	OE2	2.853
4LU5	M_LYS_188	NZ	M_GLU_192	OE1	3.556
4LU5	M_ARG_193	NH1	M_ASP_189	OD2	3.951
4LU5	M_HIS_194	ND1	M_ASP_156	OD2	2.781
4LU5	M_LYS_204	NZ	M_ASP_115	OD2	3.771

Table 566: 4LU5-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4M1D	L_ARG_61	NH1	L_ASP_82	OD1	3.859
4M1D	L_ARG_61	NH1	L_ASP_82	OD2	2.922
4M1D	L_ARG_61	NH2	L_ASP_82	OD1	2.932
4M1D	L_ARG_61	NH2	L_ASP_82	OD2	3.341
4M1D	L_LYS_103	NZ	L_GLU_83	OE2	3.169
4M1D	L_LYS_110	NZ	L_GLU_198	OE1	2.670
4M1D	L_LYS_129	NZ	H_ASP_144	OD2	3.436
4M1D	L_LYS_149	NZ	L_GLU_203	OE2	3.944
4M1D	H_ARG_38	NH1	H_ASP_86	OD1	2.929
4M1D	H_ARG_38	NH2	H_GLU_46	OE1	3.018
4M1D	H_ARG_38	NH2	H_GLU_46	OE2	3.822
4M1D	H_ARG_38	NH2	H_ASP_86	OD1	3.988
4M1D	H_ARG_50	NH1	H_ASP_58	OD2	2.819
4M1D	H_ARG_66	NH1	H_ASP_86	OD1	3.809
4M1D	H_ARG_66	NH1	H_ASP_86	OD2	2.702
4M1D	H_ARG_66	NH2	H_ASP_86	OD1	3.069
4M1D	H_ARG_66	NH2	H_ASP_86	OD2	3.476
4M1D	H_ARG_71	NH2	H_ASP_73	OD1	3.470
4M1D	H_LYS_143	NZ	L_GLU_124	OE2	2.547
4M1D	H_LYS_209	NZ	L_GLU_123	OE1	2.798
4M1D	H_LYS_209	NZ	L_GLU_123	OE2	2.782
4M1D	P_ARG_315	NH2	H_ASP_95	OD2	3.175
4M1D	M_ARG_61	NH1	M_ASP_82	OD1	3.820
4M1D	M_ARG_61	NH1	M_ASP_82	OD2	2.675
4M1D	M_ARG_61	NH2	M_ASP_82	OD1	2.789
4M1D	M_ARG_61	NH2	M_ASP_82	OD2	3.154
4M1D	M_LYS_149	NZ	M_GLU_203	OE2	3.156
4M1D	I_ARG_38	NH1	I_ASP_86	OD1	2.903
4M1D	I_ARG_38	NH2	I_GLU_46	OE1	3.115
4M1D	I_ARG_38	NH2	I_GLU_46	OE2	3.904
4M1D	I_ARG_38	NH2	I_ASP_86	OD1	3.856
4M1D	I_ARG_50	NH1	I_ASP_58	OD2	2.888
4M1D	I_ARG_66	NH1	I_ASP_86	OD1	3.904
4M1D	I_ARG_66	NH1	I_ASP_86	OD2	2.765
4M1D	I_ARG_66	NH2	I_ASP_86	OD1	3.096
4M1D	I_ARG_66	NH2	I_ASP_86	OD2	3.440
4M1D	I_ARG_71	NH2	I_ASP_73	OD1	3.398
4M1D	I_LYS_209	NZ	M_GLU_123	OE1	3.060
4M1D	I_LYS_209	NZ	M_GLU_123	OE2	2.485
4M1D	I_ARG_210	NH1	I_GLU_212	OE2	3.506
4M1D	Q_ARG_315	NH2	I_ASP_95	OD2	3.051

Table 567: 4M1D-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4M1G	L_ARG_62	NH2	L_GLU_82	OE2	3.764
4M1G	L_ARG_62	NH2	L_ASP_83	OD1	2.800
4M1G	L_ARG_62	NH2	L_ASP_83	OD2	3.468
4M1G	L_LYS_104	NZ	L_ASP_166	OD1	2.839
4M1G	L_LYS_143	NZ	L_GLU_106	OE1	2.794
4M1G	L_LYS_143	NZ	L_GLU_106	OE2	3.443
4M1G	L_LYS_150	NZ	L_GLU_196	OE1	3.090
4M1G	L_LYS_150	NZ	L_GLU_196	OE2	3.774
4M1G	L_ARG_156	NH1	L_GLU_186	OE2	2.941
4M1G	L_ARG_189	NH2	L_ASP_185	OD2	3.981
4M1G	L_HIS_190	ND1	L_ASP_152	OD2	2.973
4M1G	L_LYS_200	NZ	L_ASP_111	OD2	3.784
4M1G	H_ARG_38	NH1	H_GLU_46	OE1	3.046
4M1G	H_ARG_38	NH1	H_ASP_89	OD1	3.832
4M1G	H_ARG_38	NH2	H_ASP_89	OD1	2.835
4M1G	H_ARG_66	NH1	H_ASP_89	OD1	3.787
4M1G	H_ARG_66	NH1	H_ASP_89	OD2	2.752
4M1G	H_ARG_66	NH2	H_ASP_89	OD1	2.894
4M1G	H_ARG_66	NH2	H_ASP_89	OD2	3.336
4M1G	H_LYS_97	NZ	H_ASP_106	OD1	3.138
4M1G	H_LYS_97	NZ	H_ASP_106	OD2	2.944
4M1G	H_LYS_210	NZ	H_ASP_212	OD2	3.380
4M1G	H_LYS_213	NZ	L_GLU_124	OE2	2.837
4M1G	H_ARG_218	NH2	L_GLU_124	OE1	2.657
4M1G	H_ARG_218	NH2	L_GLU_124	OE2	3.648
4M1G	A_LYS_161	NZ	H_ASP_31	OD1	3.895
4M1G	A_LYS_161	NZ	A_ASP_146	OD1	2.636
4M1G	A_ARG_176	NH2	A_GLU_174	OE2	2.901
4M1G	B_LYS_161	NZ	B_ASP_146	OD1	3.297
4M1G	B_ARG_176	NH1	B_GLU_174	OE1	3.072
4M1G	B_ARG_176	NH2	B_ASP_150	OD1	3.937
4M1G	B_ARG_176	NH2	B_GLU_174	OE1	3.174

Table 568: 4M1G-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4M3J	A_ARG.66	NH1	A_ASP.89	OD1	2.995
4M3J	A_ARG.66	NH1	A_ASP.89	OD2	3.290
4M3J	A_ARG.66	NH2	A_ASP.89	OD1	3.827
4M3J	A_ARG.66	NH2	A_ASP.89	OD2	2.608
4M3J	B_ARG.19	NH2	B_GLU.81	OE2	4.000
4M3J	B_ARG.38	NH1	B_ASP.89	OD1	2.933
4M3J	B_ARG.38	NH2	B_GLU.46	OE2	3.526
4M3J	B_ARG.66	NH1	B_ASP.89	OD1	2.977
4M3J	B_ARG.66	NH1	B_ASP.89	OD2	3.346
4M3J	B_ARG.66	NH2	B_ASP.89	OD1	3.861
4M3J	B_ARG.66	NH2	B_ASP.89	OD2	2.734

Table 569: 4M3J-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4M3K	A_LYS_43	NZ	A_GLU_64	OE1	3.810
4M3K	A_LYS_43	NZ	A_GLU_64	OE2	3.952
4M3K	A_ARG_61	NH2	A_GLU_37	OE1	2.874
4M3K	A_ARG_61	NH2	A_GLU_37	OE2	2.937
4M3K	A_LYS_73	NZ	A_GLU_166	OE2	3.458
4M3K	A_ARG_128	NH2	A_ASP_124	OD1	2.865
4M3K	A_ARG_128	NH2	A_ASP_124	OD2	3.740
4M3K	A_LYS_149	NZ	A_GLU_163	OE2	2.784
4M3K	A_LYS_154	NZ	A_GLU_151	OE1	3.231
4M3K	A_ARG_164	NH2	A_ASP_179	OD2	2.865
4M3K	A_ARG_184	NH2	A_ASP_63	OD1	3.681
4M3K	A_ARG_184	NH2	A_ASP_63	OD2	2.944
4M3K	A_ARG_204	NH1	A_GLU_196	OE2	2.953
4M3K	A_ARG_204	NH2	A_GLU_196	OE2	3.454
4M3K	A_LYS_212	NZ	A_GLU_230	OE2	3.176
4M3K	A_ARG_213	NH2	A_ASP_124	OD2	3.388
4M3K	A_ARG_213	NH2	A_ASP_209	OD2	3.177
4M3K	A_ARG_244	NH2	A_ASP_276	OD1	3.324
4M3K	A_ARG_244	NH2	A_ASP_276	OD2	3.717
4M3K	A_ARG_267	NH2	A_ASP_41	OD2	2.755
4M3K	A_LYS_277	NZ	A_GLU_281	OE2	3.368
4M3K	A_LYS_284	NZ	A_GLU_281	OE2	3.066
4M3K	A_LYS_288	NZ	A_ASP_32	OD1	3.999
4M3K	B_ARG_38	NH1	B_ASP_89	OD1	2.927
4M3K	B_ARG_38	NH2	B_GLU_46	OE2	3.059
4M3K	B_ARG_66	NH1	B_ASP_89	OD1	3.228
4M3K	B_ARG_66	NH1	B_ASP_89	OD2	3.507
4M3K	B_ARG_66	NH2	B_ASP_89	OD1	3.903
4M3K	B_ARG_66	NH2	B_ASP_89	OD2	2.748

Table 570: 4M3K-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4M5Y	H_ARG_38	NH1	H_ASP_86	OD1	2.740
4M5Y	H_ARG_38	NH2	H_GLU_46	OE1	3.005
4M5Y	H_ARG_38	NH2	H_GLU_46	OE2	3.867
4M5Y	H_ARG_38	NH2	H_ASP_86	OD1	3.427
4M5Y	H_LYS_60	NZ	H_GLU_46	OE2	3.961
4M5Y	H_ARG_66	NH1	H_ASP_86	OD1	3.597
4M5Y	H_ARG_66	NH1	H_ASP_86	OD2	3.103
4M5Y	H_ARG_66	NH2	H_ASP_86	OD1	3.032
4M5Y	H_ARG_66	NH2	H_ASP_86	OD2	3.612
4M5Y	H_ARG_94	NH2	H_ASP_101	OD1	3.590
4M5Y	H_ARG_94	NH2	H_ASP_101	OD2	2.687
4M5Y	H_LYS_143	NZ	L_GLU_124	OE2	2.602
4M5Y	H_ARG_210	NH1	H_GLU_212	OE2	3.298
4M5Y	L_ARG_61	NH1	L_ASP_82	OD1	3.807
4M5Y	L_ARG_61	NH1	L_ASP_82	OD2	2.837
4M5Y	L_ARG_61	NH2	L_GLU_79	OE1	3.774
4M5Y	L_ARG_61	NH2	L_GLU_79	OE2	3.834
4M5Y	L_ARG_61	NH2	L_ASP_82	OD1	2.987
4M5Y	L_ARG_61	NH2	L_ASP_82	OD2	3.453
4M5Y	L_LYS_103	NZ	L_ASP_85	OD1	2.950
4M5Y	L_LYS_103	NZ	L_ASP_85	OD2	3.655
4M5Y	L_LYS_166	NZ	L_GLU_83	OE1	3.021
4M5Y	I_ARG_38	NH1	I_ASP_86	OD1	2.800
4M5Y	I_ARG_38	NH2	I_GLU_46	OE1	3.015
4M5Y	I_ARG_38	NH2	I_GLU_46	OE2	3.972
4M5Y	I_ARG_38	NH2	I_ASP_86	OD1	3.483
4M5Y	I_LYS_60	NZ	I_GLU_46	OE2	3.961
4M5Y	I_ARG_66	NH1	I_ASP_86	OD1	3.585
4M5Y	I_ARG_66	NH1	I_ASP_86	OD2	3.054
4M5Y	I_ARG_66	NH2	I_ASP_86	OD1	3.004
4M5Y	I_ARG_66	NH2	I_ASP_86	OD2	3.622
4M5Y	I_ARG_94	NH2	I_ASP_101	OD1	3.599
4M5Y	I_ARG_94	NH2	I_ASP_101	OD2	2.713
4M5Y	I_LYS_143	NZ	M_GLU_124	OE2	2.668
4M5Y	I_ARG_210	NH2	I_GLU_212	OE1	3.354
4M5Y	I_ARG_210	NH2	I_GLU_212	OE2	2.881
4M5Y	M_ARG_61	NH1	M_ASP_82	OD1	3.838
4M5Y	M_ARG_61	NH1	M_ASP_82	OD2	2.829
4M5Y	M_ARG_61	NH2	M_GLU_79	OE1	3.888
4M5Y	M_ARG_61	NH2	M_GLU_79	OE2	3.912
4M5Y	M_ARG_61	NH2	M_ASP_82	OD1	2.982
4M5Y	M_ARG_61	NH2	M_ASP_82	OD2	3.418
4M5Y	M_LYS_103	NZ	M_ASP_85	OD1	2.936
4M5Y	M_LYS_103	NZ	M_ASP_85	OD2	3.698
4M5Y	M_LYS_166	NZ	M_GLU_83	OE1	2.838

Table 571: 4M5Y-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4M7J	H_ARG_38	NH1	H_ASP_86	OD1	2.851
4M7J	H_ARG_38	NH2	H_GLU_46	OE1	2.998
4M7J	H_ARG_38	NH2	H_GLU_46	OE2	3.979
4M7J	H_ARG_38	NH2	H_ASP_86	OD1	3.844
4M7J	H_ARG_66	NH1	H_ASP_86	OD1	3.723
4M7J	H_ARG_66	NH1	H_ASP_86	OD2	2.912
4M7J	H_ARG_66	NH2	H_ASP_86	OD1	2.833
4M7J	H_ARG_66	NH2	H_ASP_86	OD2	3.435
4M7J	H_ARG_94	NH2	H_ASP_100	OD1	2.757
4M7J	H_ARG_94	NH2	H_ASP_100	OD2	3.594
4M7J	H_LYS_208	NZ	L_GLU_123	OE1	3.727
4M7J	H_LYS_208	NZ	L_GLU_123	OE2	3.593
4M7J	L_ARG_24	NH2	L_ASP_70	OD1	2.939
4M7J	L_ARG_24	NH2	L_ASP_70	OD2	3.255
4M7J	L_ARG_61	NH1	L_GLU_79	OE1	3.494
4M7J	L_ARG_61	NH1	L_GLU_79	OE2	3.711
4M7J	L_ARG_61	NH1	L_GLU_81	OE2	3.788
4M7J	L_ARG_61	NH2	L_GLU_79	OE1	3.751
4M7J	L_ARG_61	NH2	L_GLU_81	OE2	3.003
4M7J	L_ARG_61	NH2	L_ASP_82	OD1	2.487
4M7J	L_ARG_61	NH2	L_ASP_82	OD2	3.268
4M7J	L_LYS_103	NZ	L_GLU_105	OE1	3.663
4M7J	L_LYS_142	NZ	L_GLU_105	OE1	3.970
4M7J	L_LYS_149	NZ	L_GLU_195	OE2	3.349
4M7J	L_ARG_155	NH1	L_GLU_185	OE1	3.230
4M7J	L_ARG_155	NH1	L_GLU_185	OE2	3.937
4M7J	L_ARG_155	NH2	L_GLU_185	OE1	3.656
4M7J	L_ARG_155	NH2	L_GLU_185	OE2	2.916
4M7J	L_HIS_189	ND1	L_ASP_151	OD2	3.046
4M7J	L_LYS_199	NZ	L_ASP_110	OD1	3.848
4M7J	L_LYS_199	NZ	L_ASP_110	OD2	2.665

Table 572: 4M7J-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4M7Z	B_ARG_38	NH1	B_ASP_86	OD1	2.932
4M7Z	B_ARG_38	NH2	B_ASP_86	OD1	3.472
4M7Z	B_ARG_66	NH1	B_ASP_86	OD2	3.153
4M7Z	B_ARG_66	NH2	B_ASP_86	OD1	2.921
4M7Z	B_ARG_66	NH2	B_ASP_86	OD2	2.946
4M7Z	B_LYS_208	NZ	C_GLU_123	OE1	3.318
4M7Z	B_LYS_208	NZ	C_GLU_123	OE2	3.881
4M7Z	H_ARG_38	NH1	H_ASP_86	OD1	2.917
4M7Z	H_ARG_38	NH2	H_ASP_86	OD1	3.458
4M7Z	H_ARG_66	NH1	H_ASP_86	OD2	3.181
4M7Z	H_ARG_66	NH2	H_ASP_86	OD1	2.909
4M7Z	H_ARG_66	NH2	H_ASP_86	OD2	2.975
4M7Z	H_LYS_208	NZ	L_GLU_123	OE1	3.192
4M7Z	C_ARG_54	NH2	C_ASP_60	OD1	3.316
4M7Z	C_ARG_61	NH1	C_GLU_79	OE1	3.863
4M7Z	C_ARG_61	NH2	C_GLU_79	OE1	3.870
4M7Z	C_ARG_61	NH2	C_ASP_82	OD1	2.761
4M7Z	C_ARG_61	NH2	C_ASP_82	OD2	3.263
4M7Z	C_LYS_103	NZ	C_ASP_165	OD1	2.648
4M7Z	C_LYS_103	NZ	C_ASP_165	OD2	3.360
4M7Z	C_LYS_142	NZ	C_GLU_105	OE2	2.662
4M7Z	C_LYS_149	NZ	C_GLU_195	OE2	3.957
4M7Z	C_ARG_155	NH2	C_GLU_185	OE1	3.931
4M7Z	C_LYS_183	NZ	C_GLU_187	OE1	3.956
4M7Z	C_LYS_183	NZ	C_GLU_187	OE2	2.784
4M7Z	C_ARG_188	NH2	C_GLU_185	OE2	2.653
4M7Z	C_HIS_189	ND1	C_ASP_151	OD2	2.788
4M7Z	C_HIS_189	NE2	C_GLU_185	OE1	2.917
4M7Z	C_LYS_199	NZ	C_ASP_110	OD1	3.655
4M7Z	C_LYS_199	NZ	C_ASP_110	OD2	3.049
4M7Z	L_ARG_24	NH2	L_ASP_70	OD1	3.791
4M7Z	L_ARG_54	NH2	L_ASP_60	OD1	3.293
4M7Z	L_ARG_61	NH1	L_GLU_79	OE1	3.704
4M7Z	L_ARG_61	NH1	L_GLU_79	OE2	3.709
4M7Z	L_ARG_61	NH2	L_ASP_82	OD1	2.705
4M7Z	L_ARG_61	NH2	L_ASP_82	OD2	2.341
4M7Z	L_LYS_103	NZ	L_ASP_165	OD1	2.672
4M7Z	L_LYS_103	NZ	L_ASP_165	OD2	3.377
4M7Z	L_LYS_142	NZ	L_GLU_105	OE1	3.125
4M7Z	L_LYS_147	NZ	L_GLU_195	OE1	3.579
4M7Z	L_LYS_149	NZ	L_GLU_195	OE2	3.946
4M7Z	L_ARG_155	NH1	L_GLU_185	OE2	3.594
4M7Z	L_ARG_155	NH2	L_GLU_185	OE2	2.584
4M7Z	L_LYS_183	NZ	L_GLU_187	OE1	3.987
4M7Z	L_LYS_183	NZ	L_GLU_187	OE2	2.788
4M7Z	L_HIS_189	ND1	L_ASP_151	OD2	2.804
4M7Z	L_LYS_199	NZ	L_ASP_110	OD1	3.668
4M7Z	L_LYS_199	NZ	L_ASP_110	OD2	3.056

Table 573: 4M7Z-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4M93	L_ARG_24	NH1	L_ASP_70	OD1	3.616
4M93	L_ARG_24	NH2	L_ASP_70	OD1	3.168
4M93	L_ARG_24	NH2	L_ASP_70	OD2	3.984
4M93	L_ARG_61	NH1	L_GLU_79	OE1	2.878
4M93	L_ARG_61	NH1	L_GLU_79	OE2	3.335
4M93	L_ARG_61	NH2	L_GLU_79	OE1	2.843
4M93	L_ARG_61	NH2	L_GLU_81	OE1	3.821
4M93	L_ARG_61	NH2	L_ASP_82	OD1	2.762
4M93	L_ARG_61	NH2	L_ASP_82	OD2	3.319
4M93	L_LYS_103	NZ	L_GLU_105	OE1	3.651
4M93	L_LYS_142	NZ	L_GLU_105	OE2	3.741
4M93	L_LYS_147	NZ	L_GLU_154	OE2	3.291
4M93	L_LYS_149	NZ	L_GLU_195	OE1	3.825
4M93	L_LYS_149	NZ	L_GLU_195	OE2	2.937
4M93	L_ARG_155	NH1	L_GLU_185	OE1	3.047
4M93	L_ARG_155	NH2	L_GLU_185	OE1	3.711
4M93	L_ARG_155	NH2	L_GLU_185	OE2	3.785
4M93	L_HIS_189	ND1	L_ASP_151	OD2	3.324
4M93	H_ARG_38	NH1	H_ASP_86	OD1	2.784
4M93	H_ARG_38	NH2	H_GLU_46	OE1	2.935
4M93	H_ARG_38	NH2	H_GLU_46	OE2	3.934
4M93	H_ARG_38	NH2	H_ASP_86	OD1	3.972
4M93	H_ARG_66	NH1	H_ASP_86	OD1	3.479
4M93	H_ARG_66	NH1	H_ASP_86	OD2	2.918
4M93	H_ARG_66	NH2	H_ASP_86	OD1	2.693
4M93	H_ARG_66	NH2	H_ASP_86	OD2	3.421
4M93	H_LYS_208	NZ	L_GLU_123	OE1	3.795
4M93	C_ARG_24	NH1	C_ASP_70	OD1	3.167
4M93	C_ARG_61	NH1	C_GLU_79	OE1	3.833
4M93	C_ARG_61	NH1	C_GLU_79	OE2	3.475
4M93	C_ARG_61	NH2	C_GLU_79	OE1	3.979
4M93	C_ARG_61	NH2	C_GLU_81	OE1	3.225
4M93	C_ARG_61	NH2	C_ASP_82	OD1	2.620
4M93	C_ARG_61	NH2	C_ASP_82	OD2	3.543
4M93	C_LYS_149	NZ	C_GLU_195	OE2	3.911
4M93	C_ARG_155	NH1	C_GLU_185	OE1	2.917
4M93	C_LYS_169	NZ	C_ASP_170	OD1	2.606
4M93	C_LYS_183	NZ	C_GLU_187	OE2	3.968
4M93	C_HIS_189	ND1	C_ASP_151	OD2	2.956
4M93	C_LYS_199	NZ	C_ASP_110	OD2	3.011
4M93	B_ARG_38	NH1	B_ASP_86	OD1	2.720
4M93	B_ARG_38	NH2	B_GLU_46	OE1	3.263
4M93	B_ARG_38	NH2	B_ASP_86	OD1	3.854
4M93	B_ARG_66	NH1	B_ASP_86	OD1	3.675
4M93	B_ARG_66	NH1	B_ASP_86	OD2	3.114
4M93	B_ARG_66	NH2	B_ASP_86	OD1	2.983
4M93	B_ARG_66	NH2	B_ASP_86	OD2	3.452
4M93	B_LYS_208	NZ	C_GLU_123	OE1	3.203

Table 574: 4M93-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4MA1	B_LYS_5	NZ	F_GLU_187	OE1	3.315
4MA1	B_ARG_38	NH1	B_ASP_86	OD1	2.969
4MA1	B_ARG_38	NH2	B_GLU_46	OE1	3.713
4MA1	B_ARG_66	NH1	B_ASP_86	OD1	3.588
4MA1	B_ARG_66	NH1	B_ASP_86	OD2	2.940
4MA1	B_ARG_66	NH2	B_ASP_86	OD1	2.611
4MA1	B_ARG_66	NH2	B_ASP_86	OD2	3.400
4MA1	B_LYS_208	NZ	C_GLU_123	OE1	3.857
4MA1	E_ARG_38	NH1	E_ASP_86	OD1	3.045
4MA1	E_ARG_38	NH2	E_GLU_46	OE1	3.606
4MA1	E_ARG_38	NH2	E_ASP_86	OD1	3.907
4MA1	E_ARG_66	NH1	E_ASP_86	OD2	3.475
4MA1	E_ARG_66	NH2	E_ASP_86	OD1	2.678
4MA1	E_ARG_66	NH2	E_ASP_86	OD2	3.064
4MA1	H_ARG_38	NH1	H_ASP_86	OD1	2.748
4MA1	H_ARG_38	NH2	H_GLU_46	OE1	3.316
4MA1	H_ARG_38	NH2	H_GLU_46	OE2	3.996
4MA1	H_ARG_38	NH2	H_ASP_86	OD1	3.832
4MA1	H_ARG_66	NH1	H_ASP_86	OD1	3.691
4MA1	H_ARG_66	NH1	H_ASP_86	OD2	2.891
4MA1	H_ARG_66	NH2	H_ASP_86	OD1	2.643
4MA1	H_ARG_66	NH2	H_ASP_86	OD2	3.187
4MA1	H_LYS_208	NZ	L_GLU_123	OE1	3.752
4MA1	C_ARG_61	NH1	C_GLU_79	OE1	3.057
4MA1	C_ARG_61	NH2	C_GLU_79	OE1	3.843
4MA1	C_ARG_61	NH2	C_GLU_81	OE1	3.130
4MA1	C_ARG_61	NH2	C_ASP_82	OD1	2.795
4MA1	C_ARG_61	NH2	C_ASP_82	OD2	3.615
4MA1	C_LYS_103	NZ	C_GLU_105	OE1	2.684
4MA1	C_LYS_142	NZ	C_GLU_105	OE1	3.393
4MA1	C_LYS_142	NZ	C_GLU_105	OE2	3.621
4MA1	C_LYS_149	NZ	C_GLU_195	OE1	2.926
4MA1	C_ARG_155	NH1	C_GLU_185	OE1	3.289
4MA1	C_ARG_155	NH1	C_GLU_185	OE2	3.515
4MA1	C_ARG_155	NH2	C_GLU_185	OE2	3.110
4MA1	C_LYS_183	NZ	C_GLU_187	OE2	3.186
4MA1	C_HIS_189	ND1	C_ASP_151	OD2	3.088
4MA1	C_LYS_199	NZ	C_ASP_110	OD2	3.151
4MA1	F_ARG_24	NH2	F_ASP_70	OD2	2.964
4MA1	F_ARG_61	NH1	F_GLU_79	OE1	3.869
4MA1	F_ARG_61	NH1	F_GLU_79	OE2	3.320
4MA1	F_ARG_61	NH2	F_GLU_79	OE1	3.924
4MA1	F_ARG_61	NH2	F_GLU_81	OE2	3.033
4MA1	F_ARG_61	NH2	F_ASP_82	OD1	2.712
4MA1	F_ARG_61	NH2	F_ASP_82	OD2	3.811
4MA1	F_ARG_77	NH2	F_GLU_79	OE2	3.716
4MA1	F_LYS_103	NZ	F_GLU_105	OE2	2.828
4MA1	F_LYS_142	NZ	F_GLU_105	OE1	3.726
4MA1	F_LYS_142	NZ	F_GLU_105	OE2	3.145
4MA1	F_LYS_149	NZ	F_GLU_195	OE2	2.884
4MA1	F_ARG_155	NH1	F_GLU_185	OE1	3.214
4MA1	F_ARG_155	NH1	F_GLU_185	OE2	3.510
4MA1	F_ARG_155	NH2	F_GLU_185	OE2	2.964
4MA1	F_LYS_183	NZ	F_GLU_187	OE2	3.006
4MA1	F_HIS_189	ND1	F_ASP_151	OD2	2.997
4MA1	F_LYS_199	NZ	F_ASP_110	OD2	3.201
4MA1	L_ARG_61	NH1	L_GLU_79	OE2	3.784

4MA1	L_ARG_61	NH2	L_GLU_79	OE2	3.895
4MA1	L_ARG_61	NH2	L_GLU_81	OE1	3.533
4MA1	L_ARG_61	NH2	L_ASP_82	OD1	2.756
4MA1	L_ARG_61	NH2	L_ASP_82	OD2	3.629
4MA1	L_LYS_142	NZ	L_GLU_105	OE1	2.731
4MA1	L_LYS_142	NZ	L_GLU_105	OE2	3.970
4MA1	L_LYS_149	NZ	L_GLU_195	OE1	3.692
4MA1	L_LYS_149	NZ	L_GLU_195	OE2	2.968
4MA1	L_ARG_155	NH1	L_GLU_185	OE1	3.117
4MA1	L_ARG_155	NH1	L_GLU_185	OE2	3.471
4MA1	L_ARG_155	NH2	L_GLU_185	OE2	3.260
4MA1	L_LYS_183	NZ	L_GLU_187	OE2	3.272
4MA1	L_HIS_189	ND1	L_ASP_151	OD2	2.941
4MA1	L_LYS_199	NZ	L_ASP_110	OD2	3.106

Table 575: 4MA1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4N0Y	H_LYS_12	NZ	H_GLU_10	OE1	3.602
4N0Y	H_HIS_35	NE2	H_ASP_95	OD2	2.820
4N0Y	H_ARG_38	NH1	H_ASP_86	OD1	2.849
4N0Y	H_ARG_38	NH2	H_ASP_86	OD1	3.733
4N0Y	H_ARG_62	NH1	H_GLU_46	OE1	3.633
4N0Y	H_ARG_62	NH1	H_GLU_46	OE2	2.564
4N0Y	H_ARG_66	NH1	H_ASP_86	OD1	3.587
4N0Y	H_ARG_66	NH1	H_ASP_86	OD2	2.986
4N0Y	H_ARG_66	NH2	H_ASP_86	OD1	2.907
4N0Y	H_ARG_66	NH2	H_ASP_86	OD2	3.646
4N0Y	H_LYS_143	NZ	H_ASP_144	OD1	3.625
4N0Y	H_LYS_143	NZ	H_ASP_144	OD2	3.475
4N0Y	H_LYS_209	NZ	L_GLU_123	OE1	2.939
4N0Y	H_LYS_210	NZ	H_GLU_212	OE1	3.922
4N0Y	L_ARG_61	NH2	L_GLU_81	OE2	3.404
4N0Y	L_ARG_61	NH2	L_ASP_82	OD1	2.584
4N0Y	L_ARG_61	NH2	L_ASP_82	OD2	3.315
4N0Y	L_LYS_110	NZ	L_GLU_198	OE1	3.860

Table 576: 4N0Y-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4N1H	A_LYS_35	NZ	A_ASP_32	OD1	2.685
4N1H	A_ARG_61	NH2	A_GLU_37	OE1	3.246
4N1H	A_ARG_61	NH2	A_GLU_37	OE2	3.574
4N1H	A_LYS_73	NZ	A_GLU_166	OE1	3.851
4N1H	A_LYS_111	NZ	C_GLU_202	OE1	3.097
4N1H	A_LYS_111	NZ	C_GLU_202	OE2	2.712
4N1H	A_HIS_112	ND1	C_GLU_205	OE2	3.407
4N1H	A_HIS_112	NE2	C_GLU_202	OE1	2.950
4N1H	A_HIS_112	NE2	C_GLU_205	OE2	3.971
4N1H	A_ARG_128	NH1	C_GLU_89	OE1	3.101
4N1H	A_ARG_128	NH2	A_ASP_124	OD1	3.594
4N1H	A_ARG_128	NH2	A_ASP_124	OD2	3.398
4N1H	A_LYS_149	NZ	A_GLU_163	OE1	3.271
4N1H	A_LYS_150	NZ	B_ASP_115	OD2	2.748
4N1H	A_ARG_153	NH2	B_ASP_106	OD1	3.262
4N1H	A_ARG_153	NH2	B_ASP_106	OD2	3.262
4N1H	A_LYS_154	NZ	A_GLU_151	OE1	3.414
4N1H	A_LYS_154	NZ	A_GLU_151	OE2	2.635
4N1H	A_ARG_164	NH2	A_ASP_179	OD2	2.730
4N1H	A_ARG_184	NH2	A_ASP_63	OD1	3.800
4N1H	A_ARG_184	NH2	A_ASP_63	OD2	3.087
4N1H	A_ARG_204	NH2	A_GLU_196	OE2	3.365
4N1H	A_LYS_212	NZ	A_GLU_230	OE2	3.115
4N1H	A_ARG_213	NH2	A_ASP_209	OD1	2.990
4N1H	A_ARG_213	NH2	A_ASP_209	OD2	2.705
4N1H	A_ARG_222	NH2	A_ASP_233	OD1	3.305
4N1H	A_ARG_244	NH2	A_ASP_276	OD1	3.949
4N1H	A_ARG_244	NH2	A_ASP_276	OD2	3.570
4N1H	A_ARG_267	NH2	A_ASP_41	OD2	3.599
4N1H	A_LYS_284	NZ	A_GLU_281	OE1	3.697
4N1H	A_LYS_284	NZ	A_GLU_281	OE2	2.598
4N1H	B_ARG_38	NH1	B_ASP_90	OD1	3.247
4N1H	B_ARG_38	NH2	B_GLU_46	OE2	3.382
4N1H	B_ARG_38	NH2	B_ASP_90	OD1	3.865
4N1H	B_ARG_67	NH2	B_ASP_90	OD1	2.723
4N1H	B_ARG_67	NH2	B_ASP_90	OD2	2.861
4N1H	C_LYS_43	NZ	C_GLU_64	OE2	2.688
4N1H	C_ARG_61	NH2	C_GLU_37	OE1	2.807
4N1H	C_ARG_61	NH2	C_GLU_37	OE2	3.294
4N1H	C_LYS_73	NZ	C_GLU_166	OE2	3.581
4N1H	C_LYS_149	NZ	C_GLU_163	OE1	3.581
4N1H	C_LYS_149	NZ	C_GLU_163	OE2	3.310
4N1H	C_LYS_149	NZ	D_ASP_106	OD1	3.587
4N1H	C_LYS_149	NZ	D_ASP_106	OD2	3.735
4N1H	C_LYS_150	NZ	D_ASP_115	OD1	3.157
4N1H	C_ARG_153	NH2	D_ASP_106	OD1	2.772
4N1H	C_LYS_154	NZ	C_GLU_151	OE1	3.966
4N1H	C_LYS_154	NZ	C_GLU_151	OE2	3.090
4N1H	C_ARG_164	NH2	C_ASP_179	OD2	2.708
4N1H	C_ARG_204	NH2	A_GLU_121	OE2	3.425
4N1H	C_LYS_212	NZ	C_GLU_230	OE2	3.370
4N1H	C_ARG_213	NH2	C_ASP_209	OD2	2.965
4N1H	C_ARG_222	NH2	C_ASP_233	OD1	3.546
4N1H	C_ARG_244	NH2	C_ASP_276	OD1	3.134
4N1H	C_ARG_267	NH2	C_ASP_41	OD2	2.979
4N1H	C_LYS_277	NZ	C_GLU_281	OE2	3.711
4N1H	C_LYS_284	NZ	C_GLU_281	OE1	3.788

4N1H	C_LYS_284	NZ	C_GLU_281	OE2	2.689
4N1H	D_ARG_38	NH1	D_ASP_90	OD1	2.942
4N1H	D_ARG_38	NH2	D_ASP_90	OD1	3.612
4N1H	D_ARG_45	NH1	D_GLU_111	OE1	3.652
4N1H	D_ARG_45	NH1	D_GLU_111	OE2	3.043
4N1H	D_LYS_65	NZ	D_ASP_62	OD1	2.639
4N1H	D_LYS_65	NZ	D_ASP_62	OD2	3.577
4N1H	D_ARG_67	NH1	D_ASP_90	OD1	2.750
4N1H	D_ARG_67	NH1	D_ASP_90	OD2	3.293
4N1H	D_ARG_67	NH2	D_ASP_90	OD1	3.769
4N1H	D_ARG_67	NH2	D_ASP_90	OD2	2.732

Table 577: 4N1H-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4NBX	A.LYS_31	NZ	A.GLU_20	OE1	3.754
4NBX	A.LYS_31	NZ	A.GLU_20	OE2	2.760
4NBX	A.ARG_75	NH2	A.ASP_65	OD1	3.378
4NBX	B.ARG_34	NH1	B.ASP_39	OD2	2.728
4NBX	B.ARG_34	NH2	B.ASP_39	OD2	3.692
4NBX	B.ARG_45	NH1	B.ASP_97	OD1	3.021
4NBX	B.ARG_45	NH2	B.GLU_53	OE2	3.422
4NBX	B.ARG_52	NH2	B.ASP_115	OD1	3.103
4NBX	B.ARG_52	NH2	B.ASP_115	OD2	3.478
4NBX	B.ARG_74	NH1	B.ASP_97	OD1	3.854
4NBX	B.ARG_74	NH1	B.ASP_97	OD2	2.776
4NBX	B.ARG_74	NH2	B.ASP_97	OD1	2.873
4NBX	B.ARG_74	NH2	B.ASP_97	OD2	3.326
4NBX	B.LYS_83	NZ	B.ASP_80	OD2	3.208
4NBX	B.ARG_114	NH2	B.GLU_116	OE1	3.887

Table 578: 4NBX-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4NBY	A_LYS_42	NZ	A_GLU_97	OE1	2.799
4NBY	A_LYS_149	NZ	A_GLU_138	OE1	2.480
4NBY	A_LYS_149	NZ	A_GLU_138	OE2	3.061
4NBY	A_ARG_193	NH2	A_ASP_183	OD1	3.347
4NBY	B_ARG_34	NH1	B_ASP_39	OD1	2.677
4NBY	B_ARG_34	NH2	B_ASP_39	OD1	3.790
4NBY	B_ARG_45	NH1	B_ASP_97	OD1	2.996
4NBY	B_ARG_45	NH2	B_GLU_53	OE2	3.496
4NBY	B_ARG_52	NH2	B_ASP_115	OD2	3.092
4NBY	B_ARG_74	NH1	B_ASP_97	OD1	3.798
4NBY	B_ARG_74	NH1	B_ASP_97	OD2	2.779
4NBY	B_ARG_74	NH2	B_ASP_97	OD1	2.996
4NBY	B_ARG_74	NH2	B_ASP_97	OD2	3.496
4NBY	C_ARG_34	NH1	C_ASP_39	OD1	2.785
4NBY	C_ARG_34	NH2	C_ASP_39	OD1	3.629
4NBY	C_ARG_45	NH1	C_ASP_97	OD1	2.914
4NBY	C_ARG_45	NH2	C_GLU_53	OE2	3.403
4NBY	C_ARG_45	NH2	C_ASP_97	OD1	3.956
4NBY	C_LYS_72	NZ	C_ASP_69	OD1	3.359
4NBY	C_ARG_74	NH1	C_ASP_97	OD1	3.947
4NBY	C_ARG_74	NH1	C_ASP_97	OD2	2.935
4NBY	C_ARG_74	NH2	C_ASP_97	OD1	2.957
4NBY	C_ARG_74	NH2	C_ASP_97	OD2	3.430
4NBY	C_LYS_83	NZ	C_ASP_80	OD2	3.758

Table 579: 4NBY-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4NBZ	A_LYS_31	NZ	A_GLU_20	OE2	2.992
4NBZ	A_ARG_75	NH2	A_ASP_65	OD2	3.115
4NBZ	B_ARG_38	NH1	B_ASP_90	OD1	2.831
4NBZ	B_ARG_38	NH2	B_GLU_46	OE2	3.420
4NBZ	B_ARG_38	NH2	B_ASP_90	OD1	3.761
4NBZ	B_ARG_67	NH1	B_ASP_90	OD1	3.836
4NBZ	B_ARG_67	NH1	B_ASP_90	OD2	2.796
4NBZ	B_ARG_67	NH2	B_ASP_90	OD1	3.068
4NBZ	B_ARG_67	NH2	B_ASP_90	OD2	3.514
4NBZ	B_ARG_104	NH1	B_ASP_107	OD2	2.788
4NBZ	B_ARG_104	NH1	B_GLU_110	OE2	2.708
4NBZ	B_ARG_104	NH2	B_ASP_107	OD2	3.003
4NBZ	C_LYS_31	NZ	C_GLU_20	OE2	3.958
4NBZ	C_ARG_75	NH2	C_ASP_65	OD2	3.050
4NBZ	D_ARG_38	NH1	D_ASP_90	OD1	2.888
4NBZ	D_ARG_38	NH2	D_ASP_90	OD1	3.800
4NBZ	D_ARG_67	NH1	D_ASP_90	OD1	3.887
4NBZ	D_ARG_67	NH1	D_ASP_90	OD2	2.770
4NBZ	D_ARG_67	NH2	D_ASP_90	OD1	3.220
4NBZ	D_ARG_67	NH2	D_ASP_90	OD2	3.516
4NBZ	D_ARG_104	NH1	D_ASP_107	OD2	3.039
4NBZ	D_ARG_104	NH2	D_ASP_107	OD2	2.649
4NBZ	D_ARG_104	NH2	D_GLU_110	OE2	2.846

Table 580: 4NBZ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4NC0	A_LYS_20	NZ	A_ASP_18	OD2	3.612
4NC0	A_LYS_21	NZ	A_ASP_69	OD2	3.571
4NC0	A_ARG_102	NH2	A_ASP_92	OD1	3.131
4NC0	A_LYS_149	NZ	A_GLU_138	OE1	3.144
4NC0	A_LYS_149	NZ	A_GLU_138	OE2	3.032
4NC0	B_ARG_38	NH1	B_ASP_90	OD1	2.856
4NC0	B_ARG_38	NH2	B_GLU_46	OE2	3.008
4NC0	B_ARG_38	NH2	B_ASP_90	OD1	3.917
4NC0	B_ARG_67	NH1	B_ASP_90	OD1	3.847
4NC0	B_ARG_67	NH1	B_ASP_90	OD2	2.731
4NC0	B_ARG_67	NH2	B_ASP_90	OD1	3.092
4NC0	B_ARG_67	NH2	B_ASP_90	OD2	3.455
4NC0	B_ARG_104	NH2	B_GLU_110	OE2	3.883

Table 581: 4NC0-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4NC1	A_LYS_122	NZ	A_GLU_84	OE1	3.788
4NC1	A_ARG_133	NH1	D_ASP_115	OD2	3.145
4NC1	A_LYS_149	NZ	A_GLU_138	OE2	3.865
4NC1	C_ARG_34	NH1	C_ASP_39	OD1	2.542
4NC1	C_ARG_34	NH2	C_ASP_39	OD1	3.596
4NC1	C_ARG_45	NH1	C_ASP_97	OD1	3.313
4NC1	C_ARG_45	NH2	C_GLU_53	OE2	3.315
4NC1	C_ARG_52	NH2	C_ASP_115	OD2	3.087
4NC1	C_LYS_72	NZ	C_ASP_69	OD1	2.940
4NC1	C_ARG_74	NH1	C_ASP_97	OD2	3.393
4NC1	C_ARG_74	NH2	C_ASP_97	OD1	3.034
4NC1	C_ARG_74	NH2	C_ASP_97	OD2	3.018
4NC1	C_ARG_114	NH1	D_ASP_115	OD1	3.051
4NC1	C_ARG_114	NH1	D_ASP_115	OD2	3.046
4NC1	C_ARG_114	NH2	D_ASP_115	OD1	2.896
4NC1	E_ARG_38	NH1	E_ASP_90	OD1	3.159
4NC1	E_ARG_38	NH2	E_GLU_46	OE2	3.512
4NC1	E_ARG_38	NH2	E_ASP_90	OD1	3.704
4NC1	E_ARG_67	NH1	E_ASP_90	OD1	3.858
4NC1	E_ARG_67	NH1	E_ASP_90	OD2	2.770
4NC1	E_ARG_67	NH2	E_ASP_90	OD1	2.972
4NC1	E_ARG_67	NH2	E_ASP_90	OD2	3.415
4NC1	E_LYS_87	NZ	E_GLU_89	OE2	3.782
4NC1	E_ARG_104	NH1	E_ASP_107	OD1	2.648
4NC1	E_ARG_104	NH1	E_GLU_110	OE2	3.366
4NC1	E_ARG_104	NH2	E_ASP_107	OD1	3.918
4NC1	B_HIS_63	ND1	B_GLU_84	OE1	3.153
4NC1	B_HIS_63	ND1	B_GLU_84	OE2	3.732
4NC1	B_ARG_102	NH1	B_ASP_92	OD1	3.669
4NC1	B_ARG_102	NH1	B_ASP_92	OD2	3.606
4NC1	B_ARG_102	NH2	B_ASP_92	OD1	3.288
4NC1	B_ARG_133	NH2	C_ASP_115	OD2	3.404
4NC1	B_LYS_149	NZ	B_GLU_138	OE1	3.187
4NC1	B_LYS_149	NZ	B_GLU_138	OE2	3.383
4NC1	B_LYS_154	NZ	B_ASP_152	OD2	3.007
4NC1	D_ARG_34	NH1	D_ASP_39	OD1	2.692
4NC1	D_ARG_34	NH2	D_ASP_39	OD1	3.446
4NC1	D_ARG_45	NH1	D_ASP_97	OD1	3.007
4NC1	D_ARG_45	NH2	D_GLU_53	OE2	3.250
4NC1	D_ARG_52	NH2	D_ASP_115	OD2	2.993
4NC1	D_ARG_63	NH1	B_ASP_112	OD2	3.125
4NC1	D_LYS_72	NZ	D_ASP_69	OD1	2.783
4NC1	D_ARG_74	NH1	D_ASP_97	OD1	3.561
4NC1	D_ARG_74	NH1	D_ASP_97	OD2	2.537
4NC1	D_ARG_74	NH2	D_ASP_97	OD1	2.939
4NC1	D_ARG_74	NH2	D_ASP_97	OD2	3.487
4NC1	D_ARG_114	NH1	C_ASP_115	OD1	2.908
4NC1	D_ARG_114	NH2	C_ASP_115	OD1	2.942
4NC1	F_ARG_38	NH1	F_ASP_90	OD1	2.906
4NC1	F_ARG_38	NH2	F_GLU_46	OE2	3.353
4NC1	F_LYS_65	NZ	F_ASP_62	OD1	3.606
4NC1	F_ARG_67	NH1	F_ASP_90	OD1	3.956
4NC1	F_ARG_67	NH1	F_ASP_90	OD2	2.763
4NC1	F_ARG_67	NH2	F_ASP_90	OD1	2.876
4NC1	F_ARG_67	NH2	F_ASP_90	OD2	3.144
4NC1	F_ARG_104	NH2	F_ASP_107	OD1	2.987

Table 582: 4NC1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4NC2	A_LYS_41	NZ	A_GLU_78	OE1	2.781
4NC2	A_LYS_41	NZ	A_GLU_78	OE2	3.286
4NC2	A_HIS_67	ND1	A_GLU_76	OE1	3.371
4NC2	A_HIS_67	ND1	A_GLU_76	OE2	3.155
4NC2	A_ARG_92	NH2	A_ASP_87	OD1	3.549
4NC2	A_ARG_92	NH2	A_ASP_87	OD2	3.725
4NC2	B_ARG_38	NH1	B_ASP_89	OD1	2.682
4NC2	B_ARG_38	NH2	B_GLU_46	OE2	3.122
4NC2	B_ARG_38	NH2	B_ASP_89	OD1	3.705
4NC2	B_ARG_66	NH1	B_ASP_89	OD2	2.844
4NC2	B_ARG_66	NH2	B_ASP_89	OD1	3.155
4NC2	B_ARG_66	NH2	B_ASP_89	OD2	3.294
4NC2	B_LYS_86	NZ	B_GLU_88	OE1	3.812
4NC2	B_ARG_104	NH2	B_ASP_102	OD1	3.825
4NC2	B_ARG_104	NH2	B_ASP_102	OD2	2.662

Table 583: 4NC2-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4NGH	L_ARG_54	NH2	L_ASP_60	OD1	3.463
4NGH	L_ARG_61	NH1	L_GLU_79	OE1	3.684
4NGH	L_ARG_61	NH2	L_GLU_81	OE2	3.634
4NGH	L_ARG_61	NH2	L_ASP_82	OD1	2.877
4NGH	L_ARG_61	NH2	L_ASP_82	OD2	3.482
4NGH	L_LYS_188	NZ	L_ASP_185	OD2	3.961
4NGH	L_HIS_189	ND1	L_ASP_151	OD2	3.057
4NGH	H_ARG_38	NH1	H_ASP_86	OD1	3.532
4NGH	H_ARG_38	NH2	H_ASP_86	OD1	2.824
4NGH	H_ARG_62	NH2	H_GLU_46	OE1	2.983
4NGH	H_ARG_66	NH1	H_ASP_86	OD1	3.419
4NGH	H_ARG_66	NH1	H_ASP_86	OD2	2.324
4NGH	H_ARG_66	NH2	H_ASP_86	OD1	3.466
4NGH	H_ARG_66	NH2	H_ASP_86	OD2	3.699
4NGH	H_LYS_145	NZ	H_ASP_146	OD1	3.519
4NGH	H_LYS_145	NZ	H_ASP_146	OD2	3.560
4NGH	H_LYS_228	NZ	L_ASP_122	OD1	3.887

Table 584: 4NGH-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4NHC	L_ARG_24	NH1	L_ASP_70	OD2	3.488
4NHC	L_ARG_24	NH2	L_ASP_70	OD1	2.813
4NHC	L_ARG_24	NH2	L_ASP_70	OD2	3.633
4NHC	L_ARG_61	NH1	L_GLU_81	OE2	3.514
4NHC	L_ARG_61	NH2	L_GLU_81	OE2	3.347
4NHC	L_ARG_61	NH2	L_ASP_82	OD1	2.882
4NHC	L_ARG_61	NH2	L_ASP_82	OD2	3.443
4NHC	L_LYS_103	NZ	L_GLU_165	OE1	3.841
4NHC	L_HIS_189	ND1	L_ASP_151	OD2	3.138
4NHC	H_ARG_38	NH1	H_GLU_46	OE2	3.463
4NHC	H_ARG_38	NH1	H_ASP_86	OD1	3.758
4NHC	H_ARG_38	NH2	H_ASP_86	OD1	2.917
4NHC	H_ARG_62	NH1	H_GLU_46	OE1	2.931
4NHC	H_ARG_62	NH1	H_GLU_46	OE2	3.111
4NHC	H_ARG_66	NH1	H_ASP_86	OD1	2.881
4NHC	H_ARG_66	NH1	H_ASP_86	OD2	2.433
4NHC	H_LYS_145	NZ	H_ASP_146	OD1	3.579
4NHC	H_LYS_145	NZ	H_ASP_146	OD2	3.804
4NHC	H_LYS_222	NZ	H_GLU_226	OE1	3.793

Table 585: 4NHC-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID** **residue name** **residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4NIK	A_ARG_35	NH2	A_ASP_29	OD2	3.085
4NIK	A_ARG_41	NH2	A_ASP_70	OD2	3.597
4NIK	A_ARG_145	NH1	A_ASP_136	OD2	2.773
4NIK	A_LYS_153	NZ	B_ASP_104	OD1	3.730
4NIK	A_LYS_153	NZ	B_ASP_104	OD2	2.794
4NIK	A_LYS_153	NZ	B_GLU_186	OE2	2.639
4NIK	A_LYS_189	NZ	A_GLU_186	OE2	3.854
4NIK	A_LYS_206	NZ	A_GLU_204	OE1	3.160
4NIK	A_LYS_213	NZ	A_ASP_181	OD1	3.738
4NIK	A_LYS_221	NZ	A_GLU_225	OE1	3.992
4NIK	B_ARG_40	NH1	B_ASP_92	OD1	3.000
4NIK	B_ARG_40	NH2	B_GLU_48	OE1	3.129
4NIK	B_ARG_40	NH2	B_ASP_92	OD1	3.930
4NIK	B_ARG_69	NH1	B_ASP_92	OD2	3.600
4NIK	B_ARG_69	NH2	B_ASP_92	OD1	3.146
4NIK	B_ARG_69	NH2	B_ASP_92	OD2	2.929
4NIK	B_ARG_100	NH2	B_ASP_107	OD2	2.770
4NIK	B_ARG_197	NH1	B_ASP_218	OD1	2.833
4NIK	B_ARG_197	NH1	B_ASP_218	OD2	3.035
4NIK	B_LYS_202	NZ	B_ASP_187	OD1	2.979
4NIK	B_LYS_202	NZ	B_ASP_187	OD2	3.172

Table 586: 4NIK-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4NZR	H_ARG_38	NH1	H_ASP_86	OD1	2.731
4NZR	H_ARG_38	NH2	H_GLU_46	OE1	2.782
4NZR	H_ARG_38	NH2	H_ASP_86	OD1	3.585
4NZR	H_LYS_43	NZ	H_GLU_46	OE1	3.101
4NZR	H_HIS_52	NE2	H_ASP_31G	OD1	2.604
4NZR	H_LYS_60	NZ	H_GLU_46	OE2	3.047
4NZR	H_LYS_60	NZ	L_GLU_1	OE1	3.647
4NZR	H_ARG_66	NH1	H_ASP_86	OD1	3.620
4NZR	H_ARG_66	NH1	H_ASP_86	OD2	2.979
4NZR	H_ARG_66	NH2	H_ASP_86	OD1	3.027
4NZR	H_ARG_66	NH2	H_ASP_86	OD2	3.661
4NZR	H_ARG_94	NH2	H_ASP_101	OD1	3.578
4NZR	H_ARG_94	NH2	H_ASP_101	OD2	2.728
4NZR	H_ARG_96	NH2	H_ASP_101	OD2	2.950
4NZR	H_HIS_97	NE2	L_GLU_50	OE2	3.635
4NZR	H_HIS_98	NE2	L_GLU_50	OE1	2.875
4NZR	H_HIS_172	NE2	L_ASP_167	OD2	3.398
4NZR	H_LYS_221	NZ	L_GLU_123	OE2	2.989
4NZR	H_ARG_222	NH2	H_GLU_226	OE1	3.956
4NZR	H_ARG_222	NH2	H_GLU_226	OE2	3.389
4NZR	L_ARG_24	NH2	L_GLU_70	OE1	3.307
4NZR	L_ARG_61	NH1	L_ASP_82	OD1	3.803
4NZR	L_ARG_61	NH1	L_ASP_82	OD2	2.705
4NZR	L_ARG_61	NH2	L_ASP_82	OD1	2.855
4NZR	L_ARG_61	NH2	L_ASP_82	OD2	3.226
4NZR	L_LYS_103	NZ	L_GLU_165	OE1	3.228
4NZR	L_LYS_183	NZ	L_GLU_187	OE1	3.271
4NZR	L_LYS_183	NZ	L_GLU_187	OE2	3.181
4NZR	L_LYS_188	NZ	L_ASP_185	OD1	3.734
4NZR	L_HIS_189	ND1	L_ASP_151	OD2	2.848
4NZR	M_LYS_114	NZ	L_GLU_17	OE1	3.119
4NZR	M_LYS_130	NZ	M_ASP_87	OD2	3.899
4NZR	M_LYS_141	NZ	M_GLU_124	OE1	3.708
4NZR	M_LYS_141	NZ	M_GLU_124	OE2	2.958
4NZR	M_ARG_167	NH2	M_ASP_339	OD1	2.843
4NZR	M_LYS_218	NZ	M_GLU_261	OE1	3.674
4NZR	M_LYS_218	NZ	M_GLU_261	OE2	3.033
4NZR	M_LYS_242	NZ	M_GLU_261	OE1	2.962
4NZR	M_LYS_249	NZ	M_ASP_250	OD1	2.926
4NZR	M_LYS_249	NZ	M_ASP_250	OD2	3.476
4NZR	M_ARG_269	NH1	M_ASP_217	OD2	2.818
4NZR	M_ARG_269	NH2	M_ASP_217	OD2	3.169
4NZR	M_LYS_289	NZ	M_GLU_311	OE1	2.888
4NZR	M_LYS_289	NZ	M_GLU_313	OE1	3.192
4NZR	M_LYS_289	NZ	M_GLU_313	OE2	2.704
4NZR	M_LYS_370	NZ	M_GLU_420	OE1	2.609
4NZR	M_ARG_380	NH1	M_GLU_383	OE1	2.654
4NZR	M_ARG_380	NH1	M_GLU_383	OE2	3.072
4NZR	M_ARG_381	NH2	M_GLU_162	OE1	2.997
4NZR	M_ARG_384	NH2	L_GLU_81	OE1	3.444
4NZR	M_ARG_384	NH2	L_GLU_81	OE2	3.239
4NZR	M_LYS_397	NZ	M_ASP_396	OD1	2.896
4NZR	M_LYS_397	NZ	M_ASP_396	OD2	3.739
4NZR	M_ARG_416	NH1	M_GLU_464	OE1	3.487
4NZR	M_ARG_416	NH1	M_GLU_464	OE2	2.684
4NZR	M_ARG_416	NH2	M_ASP_412	OD1	3.736
4NZR	M_ARG_416	NH2	M_GLU_464	OE1	2.883

4NZR	M_ARG_416	NH2	M_GLU_464	OE2	3.634
4NZR	M_LYS_419	NZ	M_GLU_451	OE2	3.987
4NZR	M_ARG_430	NH1	M_ASP_411	OD1	2.838
4NZR	M_ARG_430	NH1	M_ASP_411	OD2	3.179
4NZR	M_ARG_430	NH2	M_ASP_408	OD1	3.554
4NZR	M_ARG_430	NH2	M_ASP_411	OD1	3.944
4NZR	M_ARG_430	NH2	M_ASP_411	OD2	2.828
4NZR	M_ARG_438	NH2	M_ASP_396	OD2	3.613
4NZR	M_ARG_454	NH1	M_ASP_412	OD1	2.790
4NZR	M_ARG_454	NH2	M_ASP_412	OD1	3.325
4NZR	M_ARG_457	NH1	H_ASP_31E	OD1	2.958
4NZR	M_ARG_457	NH1	H_ASP_31E	OD2	3.096
4NZR	M_ARG_457	NH2	H_ASP_31E	OD1	3.746
4NZR	M_ARG_457	NH2	H_ASP_31E	OD2	2.554

Table 587: 4NZR-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4NZZ	M_ARG_99	NH1	M_GLU_162	OE1	3.515
4NZZ	M_ARG_99	NH1	M_GLU_162	OE2	2.816
4NZZ	M_ARG_99	NH2	M_GLU_162	OE1	2.782
4NZZ	M_ARG_99	NH2	M_GLU_162	OE2	3.647
4NZZ	M_ARG_99	NH2	L ASP_60	OD1	3.096
4NZZ	M_LYS_130	NZ	M_GLU_85	OE2	3.790
4NZZ	M_LYS_141	NZ	M_GLU_124	OE1	3.986
4NZZ	M_LYS_141	NZ	M_GLU_124	OE2	3.262
4NZZ	M_ARG_167	NH2	M ASP_339	OD1	3.102
4NZZ	M_ARG_185	NH2	M_GLU_313	OE2	3.948
4NZZ	M_ARG_192	NH2	M ASP_189	OD1	3.955
4NZZ	M_LYS_218	NZ	M_GLU_261	OE1	3.101
4NZZ	M_LYS_218	NZ	M_GLU_261	OE2	2.614
4NZZ	M_LYS_242	NZ	M_GLU_261	OE1	2.807
4NZZ	M_LYS_249	NZ	M ASP_250	OD1	3.040
4NZZ	M_LYS_249	NZ	M ASP_250	OD2	3.872
4NZZ	M_LYS_255	NZ	M ASP_259	OD1	3.504
4NZZ	M_LYS_255	NZ	M ASP_259	OD2	2.413
4NZZ	M_LYS_289	NZ	M_GLU_311	OE1	2.933
4NZZ	M_LYS_289	NZ	M_GLU_313	OE1	3.576
4NZZ	M_LYS_289	NZ	M_GLU_313	OE2	2.891
4NZZ	M_LYS_370	NZ	M_GLU_420	OE1	2.990
4NZZ	M_ARG_380	NH1	M_GLU_383	OE1	2.676
4NZZ	M_ARG_380	NH1	M_GLU_383	OE2	2.970
4NZZ	M_ARG_381	NH2	M_GLU_162	OE1	3.002
4NZZ	M_ARG_384	NH2	L_GLU_81	OE1	3.193
4NZZ	M_ARG_384	NH2	L_GLU_81	OE2	3.684
4NZZ	M_LYS_397	NZ	M ASP_396	OD1	2.602
4NZZ	M_LYS_397	NZ	M ASP_396	OD2	3.737
4NZZ	M_ARG_416	NH2	M ASP_412	OD2	3.317
4NZZ	M_LYS_419	NZ	M_GLU_451	OE2	3.820
4NZZ	M_ARG_430	NH1	M ASP_408	OD1	3.883
4NZZ	M_ARG_430	NH2	M ASP_408	OD1	2.461
4NZZ	M_ARG_430	NH2	M ASP_411	OD2	3.064
4NZZ	M_ARG_438	NH1	M_GLU_426	OE1	2.584
4NZZ	M_ARG_438	NH2	M_GLU_426	OE1	3.586
4NZZ	M_ARG_438	NH2	M_GLU_427	OE1	3.398
4NZZ	M_ARG_454	NH2	M ASP_408	OD1	3.446
4NZZ	M_ARG_454	NH2	M ASP_411	OD2	3.646
4NZZ	H_LYS_19	NZ	H_GLU_81	OE1	3.595
4NZZ	H_ARG_38	NH1	H ASP_86	OD1	2.816
4NZZ	H_ARG_38	NH2	H ASP_86	OD1	3.377
4NZZ	H_LYS_62	NZ	H ASP_46	OD1	3.175
4NZZ	H_LYS_62	NZ	H ASP_46	OD2	3.992
4NZZ	H_ARG_66	NH1	H ASP_86	OD2	3.140
4NZZ	H_ARG_66	NH2	H ASP_86	OD1	2.815
4NZZ	H_ARG_66	NH2	H ASP_86	OD2	3.193
4NZZ	H_LYS_145	NZ	L_GLU_124	OE2	2.541
4NZZ	H_LYS_218	NZ	H ASP_220	OD2	3.664
4NZZ	L_ARG_31	NH1	L ASP_93	OD1	3.320
4NZZ	L_ARG_31	NH1	L ASP_93	OD2	2.823
4NZZ	L_ARG_61	NH1	L ASP_82	OD1	3.965
4NZZ	L_ARG_61	NH1	L ASP_82	OD2	2.961
4NZZ	L_ARG_61	NH2	L ASP_82	OD1	2.857
4NZZ	L_ARG_61	NH2	L ASP_82	OD2	3.259
4NZZ	L_LYS_149	NZ	L_GLU_206	OE1	3.814
4NZZ	L_LYS_166	NZ	L_GLU_83	OE2	3.236

Table 588: 4NZZ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4NZU	L_ARG_61	NH2	L_GLU_81	OE2	3.339
4NZU	L_ARG_61	NH2	L_ASP_82	OD1	2.846
4NZU	L_ARG_61	NH2	L_ASP_82	OD2	3.553
4NZU	L_HIS_90	NE2	L_ASP_93	OD1	3.539
4NZU	L_LYS_149	NZ	L_GLU_195	OE1	2.806
4NZU	L_LYS_169	NZ	L_ASP_170	OD2	3.815
4NZU	L_HIS_189	ND1	L_ASP_151	OD2	3.001
4NZU	L_HIS_189	NE2	L_ASP_185	OD1	3.093
4NZU	L_ARG_211	NH1	L_GLU_187	OE1	3.760
4NZU	H_ARG_38	NH1	H_ASP_86	OD1	2.872
4NZU	H_ARG_38	NH2	H_GLU_46	OE2	3.007
4NZU	H_ARG_38	NH2	H_ASP_86	OD1	3.843
4NZU	H_ARG_66	NH1	H_ASP_86	OD1	3.832
4NZU	H_ARG_66	NH1	H_ASP_86	OD2	2.798
4NZU	H_ARG_66	NH2	H_ASP_86	OD1	3.266
4NZU	H_ARG_66	NH2	H_ASP_86	OD2	3.679
4NZU	H_ARG_94	NH2	H_ASP_97	OD1	2.847
4NZU	H_LYS_100E	NZ	L_ASP_50	OD1	3.991
4NZU	H_LYS_100E	NZ	L_ASP_50	OD2	2.752
4NZU	H_LYS_145	NZ	H_ASP_146	OD1	3.213
4NZU	H_LYS_145	NZ	H_ASP_146	OD2	3.743
4NZU	H_LYS_218	NZ	H_ASP_220	OD1	3.972
4NZU	H_LYS_218	NZ	H_ASP_220	OD2	3.728
4NZU	H_LYS_221	NZ	L_GLU_123	OE2	2.899

Table 589: 4NZU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4O5L	L_ARG_61	NH1	L_ASP_82	OD1	3.592
4O5L	L_ARG_61	NH1	L_ASP_82	OD2	2.774
4O5L	L_ARG_61	NH2	L_ASP_82	OD1	2.915
4O5L	L_ARG_61	NH2	L_ASP_82	OD2	3.469
4O5L	H_LYS_12	NZ	H_GLU_10	OE2	3.928
4O5L	H_ARG_38	NH1	H_ASP_86	OD1	2.874
4O5L	H_ARG_38	NH2	H_GLU_46	OE1	3.001
4O5L	H_ARG_38	NH2	H_ASP_86	OD1	3.839
4O5L	H_LYS_62	NZ	H_GLU_46	OE1	3.697
4O5L	H_LYS_62	NZ	H_GLU_46	OE2	2.608
4O5L	H_ARG_66	NH1	H_ASP_86	OD1	3.710
4O5L	H_ARG_66	NH1	H_ASP_86	OD2	2.867
4O5L	H_ARG_66	NH2	H_ASP_86	OD1	2.964
4O5L	H_ARG_66	NH2	H_ASP_86	OD2	3.444
4O5L	H_LYS_100I	NZ	L_ASP_93	OD1	2.723
4O5L	H_LYS_100I	NZ	L_ASP_93	OD2	3.455
4O5L	H_LYS_210	NZ	H_GLU_212	OE2	3.158

Table 590: 4O5L-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4OLU	G.HIS.66	ND1	G.GLU.64	OE1	3.959
4OLU	G.HIS.66	ND1	G.GLU.64	OE2	2.779
4OLU	G.LYS.97	NZ	G.GLU.275	OE2	3.740
4OLU	G.LYS.97	NZ	H.ASP.100B	OD1	3.513
4OLU	G.LYS.97	NZ	H.ASP.100B	OD2	2.385
4OLU	G.LYS.207	NZ	G.GLU.381	OE1	3.549
4OLU	G.LYS.207	NZ	G.GLU.381	OE2	2.955
4OLU	G.HIS.249	NE2	G.GLU.482	OE1	2.876
4OLU	G.LYS.282	NZ	G.GLU.275	OE1	3.870
4OLU	G.LYS.343	NZ	G.GLU.347	OE2	2.649
4OLU	G.LYS.348	NZ	G.GLU.269	OE2	3.261
4OLU	G.LYS.350	NZ	G.GLU.347	OE2	3.965
4OLU	G.LYS.357	NZ	G.GLU.466	OE2	3.506
4OLU	G.ARG.379	NH2	G.ASP.211	OD1	3.811
4OLU	G.ARG.456	NH1	G.GLU.466	OE1	3.682
4OLU	G.ARG.469	NH2	G.ASP.457	OD1	3.894
4OLU	G.ARG.469	NH2	G.ASP.457	OD2	2.873
4OLU	G.LYS.476	NZ	G.GLU.102	OE1	2.812
4OLU	G.LYS.476	NZ	G.GLU.102	OE2	3.887
4OLU	G.ARG.480	NH1	G.ASP.477	OD1	2.835
4OLU	G.LYS.487	NZ	G.ASP.47	OD1	2.977
4OLU	G.LYS.487	NZ	G.ASP.47	OD2	3.556
4OLU	G.LYS.487	NZ	G.GLU.91	OE1	2.775
4OLU	H.ARG.19	NH2	H.GLU.81	OE1	3.190
4OLU	H.ARG.38	NH1	H.ASP.86	OD1	2.943
4OLU	H.ARG.38	NH2	H.GLU.46	OE1	2.821
4OLU	H.ARG.38	NH2	H.GLU.46	OE2	3.765
4OLU	H.ARG.38	NH2	H.ASP.86	OD1	3.966
4OLU	H.ARG.61	NH1	G.GLU.466	OE1	2.734
4OLU	H.ARG.66	NH2	H.ASP.86	OD1	3.375
4OLU	H.ARG.66	NH2	H.ASP.86	OD2	3.135
4OLU	H.ARG.71	NH1	G.ASP.368	OD1	3.753
4OLU	H.ARG.71	NH1	G.ASP.368	OD2	2.863
4OLU	H.ARG.71	NH2	G.ASP.368	OD1	3.092
4OLU	H.ARG.71	NH2	G.ASP.368	OD2	3.692
4OLU	H.ARG.82A	NH1	H.GLU.81	OE2	3.267
4OLU	H.HIS.102	NE2	H.GLU.101	OE1	3.618
4OLU	H.LYS.143	NZ	H.ASP.144	OD1	3.446
4OLU	H.LYS.209	NZ	L.GLU.125	OE1	3.927
4OLU	H.LYS.209	NZ	L.GLU.125	OE2	3.166
4OLU	H.LYS.210	NZ	H.GLU.212	OE1	3.680
4OLU	L.ARG.24	NH1	L.ASP.70	OD1	3.438
4OLU	L.ARG.24	NH1	L.ASP.70	OD2	3.910
4OLU	L.ARG.24	NH2	L.ASP.70	OD1	3.381
4OLU	L.ARG.24	NH2	L.ASP.70	OD2	3.367
4OLU	L.ARG.61	NH1	L.ASP.82	OD1	3.876
4OLU	L.ARG.61	NH1	L.ASP.82	OD2	2.552
4OLU	L.ARG.61	NH2	L.GLU.79	OE1	3.652
4OLU	L.ARG.61	NH2	L.GLU.79	OE2	3.968
4OLU	L.ARG.61	NH2	L.ASP.82	OD1	3.189
4OLU	L.ARG.61	NH2	L.ASP.82	OD2	3.276
4OLU	L.LYS.109	NZ	L.GLU.17	OE2	3.752
4OLU	L.LYS.151	NZ	L.GLU.197	OE1	3.524

Table 591: 4OLU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4OLV	G.HIS.66	ND1	G.GLU.64	OE1	3.978
4OLV	G.HIS.66	ND1	G.GLU.64	OE2	2.916
4OLV	G.LYS.97	NZ	G.GLU.275	OE1	3.722
4OLV	G.LYS.97	NZ	G.GLU.275	OE2	2.587
4OLV	G.LYS.97	NZ	H.ASP.100B	OD1	3.067
4OLV	G.LYS.97	NZ	H.ASP.100B	OD2	2.942
4OLV	G.LYS.207	NZ	G.GLU.381	OE1	3.681
4OLV	G.LYS.207	NZ	G.GLU.381	OE2	2.814
4OLV	G.HIS.249	NE2	G.GLU.482	OE1	2.670
4OLV	G.LYS.282	NZ	G.GLU.275	OE1	3.553
4OLV	G.LYS.343	NZ	G.GLU.347	OE2	2.439
4OLV	G.LYS.348	NZ	G.GLU.269	OE2	3.240
4OLV	G.LYS.357	NZ	G.GLU.466	OE2	3.394
4OLV	G.ARG.456	NH1	G.GLU.466	OE1	3.770
4OLV	G.ARG.469	NH2	G.ASP.457	OD2	3.028
4OLV	G.LYS.476	NZ	G.GLU.102	OE1	2.934
4OLV	G.LYS.476	NZ	G.GLU.102	OE2	3.534
4OLV	G.ARG.480	NH1	G.ASP.477	OD1	2.701
4OLV	G.ARG.480	NH2	G.GLU.102	OE2	3.998
4OLV	G.LYS.487	NZ	G.ASP.47	OD1	3.089
4OLV	G.LYS.487	NZ	G.ASP.47	OD2	3.641
4OLV	G.LYS.487	NZ	G.GLU.91	OE1	2.653
4OLV	H.ARG.19	NH2	H.GLU.81	OE1	3.551
4OLV	H.ARG.38	NH1	H.ASP.86	OD1	2.917
4OLV	H.ARG.38	NH2	H.GLU.46	OE1	2.756
4OLV	H.ARG.38	NH2	H.GLU.46	OE2	3.739
4OLV	H.ARG.38	NH2	H.ASP.86	OD1	3.920
4OLV	H.ARG.61	NH1	G.GLU.466	OE1	2.769
4OLV	H.ARG.66	NH1	H.ASP.86	OD1	3.961
4OLV	H.ARG.66	NH2	H.ASP.86	OD1	3.054
4OLV	H.ARG.66	NH2	H.ASP.86	OD2	2.735
4OLV	H.ARG.71	NH1	G.ASP.368	OD1	3.700
4OLV	H.ARG.71	NH1	G.ASP.368	OD2	2.815
4OLV	H.ARG.71	NH2	G.ASP.368	OD1	3.136
4OLV	H.ARG.71	NH2	G.ASP.368	OD2	3.717
4OLV	H.ARG.82A	NH1	H.GLU.81	OE1	3.993
4OLV	H.ARG.82A	NH1	H.GLU.81	OE2	3.151
4OLV	H.HIS.102	NE2	H.GLU.101	OE1	3.357
4OLV	H.LYS.209	NZ	L.GLU.125	OE1	3.978
4OLV	H.LYS.209	NZ	L.GLU.125	OE2	3.214
4OLV	H.LYS.210	NZ	H.GLU.212	OE1	2.484
4OLV	L.ARG.24	NH2	L.ASP.70	OD1	3.226
4OLV	L.ARG.24	NH2	L.ASP.70	OD2	2.875
4OLV	L.ARG.61	NH1	L.ASP.82	OD1	3.700
4OLV	L.ARG.61	NH1	L.ASP.82	OD2	2.636
4OLV	L.ARG.61	NH2	L.GLU.79	OE1	3.645
4OLV	L.ARG.61	NH2	L.GLU.79	OE2	3.982
4OLV	L.ARG.61	NH2	L.ASP.82	OD1	3.217
4OLV	L.ARG.61	NH2	L.ASP.82	OD2	3.476
4OLV	L.LYS.109	NZ	L.GLU.17	OE2	2.752
4OLV	L.LYS.151	NZ	L.GLU.197	OE1	3.476
4OLV	L.LYS.151	NZ	L.GLU.197	OE2	3.958

Table 592: 4OLV-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4OLW	G.HIS_66	ND1	G.GLU_64	OE2	2.882
4OLW	G.LYS_97	NZ	G.GLU_275	OE1	3.783
4OLW	G.LYS_97	NZ	G.GLU_275	OE2	2.873
4OLW	G.LYS_97	NZ	H.ASP_100B	OD1	3.637
4OLW	G.LYS_97	NZ	H.ASP_100B	OD2	3.575
4OLW	G.LYS_207	NZ	G.GLU_381	OE1	3.441
4OLW	G.LYS_207	NZ	G.GLU_381	OE2	3.248
4OLW	G.HIS_249	NE2	G.GLU_482	OE1	2.947
4OLW	G.LYS_343	NZ	G.GLU_347	OE2	2.661
4OLW	G.LYS_348	NZ	G.GLU_269	OE2	2.637
4OLW	G.LYS_348	NZ	G.GLU_351	OE1	2.952
4OLW	G.LYS_357	NZ	G.GLU_466	OE2	3.143
4OLW	G.ARG_379	NH2	G.ASP_211	OD2	3.654
4OLW	G.ARG_469	NH2	G.ASP_457	OD2	3.245
4OLW	G.LYS_476	NZ	G.GLU_102	OE1	2.987
4OLW	G.LYS_476	NZ	G.GLU_102	OE2	3.972
4OLW	G.ARG_480	NH1	G.ASP_477	OD1	2.768
4OLW	G.ARG_480	NH2	G.GLU_102	OE2	3.752
4OLW	G.LYS_487	NZ	G.ASP_47	OD1	3.005
4OLW	G.LYS_487	NZ	G.ASP_47	OD2	3.475
4OLW	G.LYS_487	NZ	G.GLU_91	OE1	2.972
4OLW	H.ARG_19	NH2	H.GLU_81	OE1	3.633
4OLW	H.ARG_38	NH1	H.ASP_86	OD1	2.849
4OLW	H.ARG_38	NH2	H.GLU_46	OE1	3.103
4OLW	H.ARG_38	NH2	H.GLU_46	OE2	3.816
4OLW	H.ARG_38	NH2	H.ASP_86	OD1	3.655
4OLW	H.ARG_61	NH1	G.GLU_466	OE1	2.598
4OLW	H.ARG_61	NH2	G.GLU_466	OE1	3.969
4OLW	H.ARG_66	NH2	H.ASP_86	OD1	2.804
4OLW	H.ARG_66	NH2	H.ASP_86	OD2	2.718
4OLW	H.ARG_71	NH1	G.ASP_368	OD1	3.570
4OLW	H.ARG_71	NH1	G.ASP_368	OD2	2.966
4OLW	H.ARG_71	NH2	G.ASP_368	OD1	3.028
4OLW	H.ARG_71	NH2	G.ASP_368	OD2	3.898
4OLW	H.ARG_82A	NH1	H.GLU_81	OE2	3.263
4OLW	H.ARG_100A	NH2	G.GLU_106	OE1	3.908
4OLW	H.HIS_102	NE2	H.GLU_101	OE1	3.698
4OLW	H.LYS_209	NZ	L.GLU_125	OE1	2.861
4OLW	H.LYS_209	NZ	L.GLU_125	OE2	2.764
4OLW	H.LYS_210	NZ	H.GLU_212	OE1	3.770
4OLW	H.LYS_214	NZ	L.ASP_124	OD1	3.031
4OLW	H.LYS_214	NZ	L.ASP_124	OD2	3.691
4OLW	L.ARG_24	NH1	L.ASP_70	OD1	3.761
4OLW	L.ARG_24	NH1	L.ASP_70	OD2	3.911
4OLW	L.ARG_24	NH2	L.ASP_70	OD1	3.614
4OLW	L.ARG_24	NH2	L.ASP_70	OD2	3.428
4OLW	L.ARG_61	NH1	L.ASP_82	OD2	2.747
4OLW	L.ARG_61	NH2	L.GLU_79	OE1	3.693
4OLW	L.ARG_61	NH2	L.GLU_79	OE2	3.864
4OLW	L.ARG_61	NH2	L.ASP_82	OD1	3.396
4OLW	L.ARG_61	NH2	L.ASP_82	OD2	2.990
4OLW	L.LYS_109	NZ	L.GLU_17	OE2	2.961

Table 593: 4OLW-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4OLX	G.HIS.66	ND1	G.GLU.64	OE1	3.879
4OLX	G.HIS.66	ND1	G.GLU.64	OE2	2.717
4OLX	G.LYS.97	NZ	G.GLU.275	OE2	3.052
4OLX	G.LYS.97	NZ	H.ASP.100B	OD1	3.339
4OLX	G.LYS.97	NZ	H.ASP.100B	OD2	2.904
4OLX	G.LYS.121	NZ	G.ASP.113	OD1	3.856
4OLX	G.LYS.207	NZ	G.GLU.381	OE1	3.451
4OLX	G.LYS.207	NZ	G.GLU.381	OE2	3.129
4OLX	G.HIS.249	NE2	G.GLU.482	OE1	3.186
4OLX	G.LYS.282	NZ	G.GLU.275	OE1	3.971
4OLX	G.LYS.343	NZ	G.GLU.347	OE2	2.614
4OLX	G.LYS.348	NZ	G.GLU.269	OE2	2.682
4OLX	G.LYS.348	NZ	G.GLU.351	OE1	3.091
4OLX	G.ARG.379	NH2	G.ASP.211	OD2	3.162
4OLX	G.ARG.456	NH1	G.GLU.466	OE1	3.738
4OLX	G.ARG.469	NH2	G.ASP.457	OD2	3.011
4OLX	G.LYS.476	NZ	G.GLU.102	OE1	2.845
4OLX	G.LYS.476	NZ	G.GLU.102	OE2	3.693
4OLX	G.ARG.480	NH1	G.ASP.477	OD1	2.869
4OLX	G.LYS.487	NZ	G.ASP.47	OD1	2.956
4OLX	G.LYS.487	NZ	G.ASP.47	OD2	3.569
4OLX	G.LYS.487	NZ	G.GLU.91	OE1	2.836
4OLX	H.ARG.19	NH2	H.GLU.81	OE1	3.130
4OLX	H.ARG.38	NH1	H.ASP.86	OD1	2.798
4OLX	H.ARG.38	NH2	H.GLU.46	OE1	2.957
4OLX	H.ARG.38	NH2	H.GLU.46	OE2	3.969
4OLX	H.ARG.38	NH2	H.ASP.86	OD1	3.641
4OLX	H.ARG.61	NH1	G.GLU.466	OE1	2.655
4OLX	H.ARG.66	NH1	H.ASP.86	OD1	3.694
4OLX	H.ARG.66	NH2	H.ASP.86	OD1	2.980
4OLX	H.ARG.66	NH2	H.ASP.86	OD2	2.792
4OLX	H.ARG.71	NH1	G.ASP.368	OD1	3.883
4OLX	H.ARG.71	NH1	G.ASP.368	OD2	2.896
4OLX	H.ARG.71	NH2	G.ASP.368	OD1	3.066
4OLX	H.ARG.71	NH2	G.ASP.368	OD2	3.572
4OLX	H.ARG.82A	NH1	H.GLU.81	OE2	3.153
4OLX	H.ARG.100A	NH2	G.GLU.106	OE1	3.646
4OLX	H.HIS.102	NE2	H.GLU.101	OE1	3.407
4OLX	H.LYS.209	NZ	L.GLU.125	OE2	3.132
4OLX	H.LYS.210	NZ	H.GLU.212	OE1	3.806
4OLX	L.ARG.24	NH1	L.ASP.70	OD1	3.727
4OLX	L.ARG.24	NH1	L.ASP.70	OD2	3.694
4OLX	L.ARG.24	NH2	L.ASP.70	OD1	3.311
4OLX	L.ARG.24	NH2	L.ASP.70	OD2	3.200
4OLX	L.ARG.61	NH1	L.ASP.82	OD1	3.778
4OLX	L.ARG.61	NH1	L.ASP.82	OD2	2.580
4OLX	L.ARG.61	NH2	L.GLU.79	OE1	3.684
4OLX	L.ARG.61	NH2	L.GLU.79	OE2	3.925
4OLX	L.ARG.61	NH2	L.ASP.82	OD1	3.428
4OLX	L.ARG.61	NH2	L.ASP.82	OD2	3.600
4OLX	L.LYS.109	NZ	L.GLU.17	OE2	3.701

Table 594: 4OLX-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4OLY	G.HIS.66	ND1	G.GLU.64	OE1	3.788
4OLY	G.HIS.66	ND1	G.GLU.64	OE2	2.753
4OLY	G.LYS.97	NZ	G.GLU.275	OE2	3.627
4OLY	G.LYS.97	NZ	H.ASP.100B	OD1	3.240
4OLY	G.LYS.97	NZ	H.ASP.100B	OD2	2.829
4OLY	G.LYS.207	NZ	G.GLU.381	OE1	3.205
4OLY	G.LYS.207	NZ	G.GLU.381	OE2	2.631
4OLY	G.HIS.249	NE2	G.GLU.482	OE1	3.173
4OLY	G.LYS.343	NZ	G.GLU.347	OE2	2.662
4OLY	G.LYS.348	NZ	G.GLU.269	OE2	3.719
4OLY	G.LYS.350	NZ	G.GLU.347	OE2	3.790
4OLY	G.LYS.357	NZ	G.GLU.466	OE2	3.515
4OLY	G.ARG.379	NH1	G.ASP.211	OD2	3.852
4OLY	G.ARG.379	NH2	G.ASP.211	OD2	2.543
4OLY	G.ARG.456	NH1	G.GLU.466	OE1	3.658
4OLY	G.ARG.469	NH2	G.ASP.457	OD1	3.982
4OLY	G.ARG.469	NH2	G.ASP.457	OD2	2.914
4OLY	G.LYS.476	NZ	G.GLU.102	OE1	2.927
4OLY	G.LYS.476	NZ	G.GLU.102	OE2	3.744
4OLY	G.ARG.480	NH1	G.ASP.477	OD1	2.751
4OLY	G.LYS.487	NZ	G.ASP.47	OD1	3.049
4OLY	G.LYS.487	NZ	G.ASP.47	OD2	3.763
4OLY	G.LYS.487	NZ	G.GLU.91	OE1	2.756
4OLY	H.ARG.19	NH2	H.GLU.81	OE1	3.423
4OLY	H.ARG.38	NH1	H.ASP.86	OD1	2.745
4OLY	H.ARG.38	NH2	H.GLU.46	OE1	2.979
4OLY	H.ARG.38	NH2	H.GLU.46	OE2	3.847
4OLY	H.ARG.38	NH2	H.ASP.86	OD1	3.687
4OLY	H.ARG.61	NH1	G.GLU.466	OE1	2.641
4OLY	H.ARG.66	NH1	H.ASP.86	OD1	3.641
4OLY	H.ARG.66	NH2	H.ASP.86	OD1	3.013
4OLY	H.ARG.66	NH2	H.ASP.86	OD2	2.555
4OLY	H.ARG.71	NH1	G.ASP.368	OD1	3.538
4OLY	H.ARG.71	NH1	G.ASP.368	OD2	2.816
4OLY	H.ARG.71	NH2	G.ASP.368	OD1	3.002
4OLY	H.ARG.71	NH2	G.ASP.368	OD2	3.765
4OLY	H.ARG.82A	NH1	H.GLU.81	OE2	3.546
4OLY	H.HIS.102	NE2	H.GLU.101	OE1	3.748
4OLY	H.LYS.209	NZ	L.GLU.125	OE1	3.888
4OLY	H.LYS.209	NZ	L.GLU.125	OE2	3.336
4OLY	H.LYS.210	NZ	H.GLU.212	OE1	3.837
4OLY	L.ARG.24	NH1	L.ASP.70	OD1	3.758
4OLY	L.ARG.24	NH1	L.ASP.70	OD2	3.814
4OLY	L.ARG.24	NH2	L.ASP.70	OD1	3.375
4OLY	L.ARG.24	NH2	L.ASP.70	OD2	3.161
4OLY	L.ARG.61	NH1	L.ASP.82	OD2	2.658
4OLY	L.ARG.61	NH2	L.GLU.79	OE1	3.938
4OLY	L.ARG.61	NH2	L.ASP.82	OD1	3.043
4OLY	L.ARG.61	NH2	L.ASP.82	OD2	2.970

Table 595: 4OLY-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4OLZ	G.HIS.66	ND1	G.GLU.64	OE1	3.923
4OLZ	G.HIS.66	ND1	G.GLU.64	OE2	2.689
4OLZ	G.LYS.97	NZ	G.GLU.275	OE1	3.801
4OLZ	G.LYS.97	NZ	G.GLU.275	OE2	2.401
4OLZ	G.LYS.97	NZ	H.ASP.100B	OD1	3.552
4OLZ	G.LYS.97	NZ	H.ASP.100B	OD2	3.545
4OLZ	G.LYS.207	NZ	G.GLU.381	OE1	3.397
4OLZ	G.LYS.207	NZ	G.GLU.381	OE2	3.037
4OLZ	G.HIS.249	NE2	G.GLU.482	OE1	2.924
4OLZ	G.LYS.282	NZ	G.GLU.275	OE1	3.959
4OLZ	G.LYS.343	NZ	G.GLU.347	OE2	2.767
4OLZ	G.LYS.348	NZ	G.GLU.269	OE2	2.968
4OLZ	G.LYS.348	NZ	G.GLU.351	OE1	3.207
4OLZ	G.ARG.379	NH2	G.ASP.211	OD2	3.935
4OLZ	G.ARG.469	NH2	G.ASP.457	OD1	3.787
4OLZ	G.ARG.469	NH2	G.ASP.457	OD2	2.835
4OLZ	G.LYS.476	NZ	G.GLU.102	OE1	2.783
4OLZ	G.LYS.476	NZ	G.GLU.102	OE2	3.635
4OLZ	G.ARG.480	NH1	G.ASP.477	OD1	2.745
4OLZ	G.LYS.487	NZ	G.ASP.47	OD1	2.885
4OLZ	G.LYS.487	NZ	G.ASP.47	OD2	3.377
4OLZ	G.LYS.487	NZ	G.GLU.91	OE1	2.760
4OLZ	H.ARG.19	NH2	H.GLU.81	OE1	3.284
4OLZ	H.ARG.38	NH1	H.ASP.86	OD1	2.920
4OLZ	H.ARG.38	NH2	H.GLU.46	OE1	3.145
4OLZ	H.ARG.38	NH2	H.ASP.86	OD1	3.640
4OLZ	H.ARG.61	NH1	G.GLU.466	OE1	2.620
4OLZ	H.ARG.66	NH2	H.ASP.86	OD1	2.412
4OLZ	H.ARG.66	NH2	H.ASP.86	OD2	3.005
4OLZ	H.ARG.71	NH1	G.ASP.368	OD1	3.472
4OLZ	H.ARG.71	NH1	G.ASP.368	OD2	2.715
4OLZ	H.ARG.71	NH2	G.ASP.368	OD1	2.877
4OLZ	H.ARG.71	NH2	G.ASP.368	OD2	3.685
4OLZ	H.ARG.82A	NH1	H.GLU.81	OE2	3.365
4OLZ	H.HIS.102	NE2	H.GLU.101	OE1	3.537
4OLZ	H.LYS.143	NZ	H.ASP.144	OD1	3.616
4OLZ	H.LYS.209	NZ	L.GLU.125	OE1	3.703
4OLZ	H.LYS.209	NZ	L.GLU.125	OE2	3.063
4OLZ	H.LYS.210	NZ	H.GLU.212	OE1	3.813
4OLZ	H.LYS.214	NZ	L.ASP.124	OD1	3.528
4OLZ	H.LYS.214	NZ	L.ASP.124	OD2	3.896
4OLZ	L.ARG.24	NH2	L.ASP.70	OD1	3.107
4OLZ	L.ARG.24	NH2	L.ASP.70	OD2	2.518
4OLZ	L.ARG.61	NH1	L.ASP.82	OD1	3.951
4OLZ	L.ARG.61	NH1	L.ASP.82	OD2	2.771
4OLZ	L.ARG.61	NH2	L.GLU.79	OE1	3.245
4OLZ	L.ARG.61	NH2	L.GLU.79	OE2	3.953
4OLZ	L.ARG.61	NH2	L.ASP.82	OD1	3.377
4OLZ	L.ARG.61	NH2	L.ASP.82	OD2	3.458
4OLZ	L.LYS.109	NZ	L.GLU.17	OE2	2.896

Table 596: 4OLZ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4OM0	G.HIS.66	ND1	G.GLU.64	OE1	3.833
4OM0	G.HIS.66	ND1	G.GLU.64	OE2	2.725
4OM0	G.LYS.97	NZ	G.GLU.275	OE1	3.804
4OM0	G.LYS.97	NZ	G.GLU.275	OE2	2.555
4OM0	G.LYS.97	NZ	H.ASP.100B	OD1	3.843
4OM0	G.LYS.97	NZ	H.ASP.100B	OD2	3.296
4OM0	G.LYS.207	NZ	G.GLU.381	OE1	3.664
4OM0	G.LYS.207	NZ	G.GLU.381	OE2	3.001
4OM0	G.HIS.249	NE2	G.GLU.482	OE1	3.206
4OM0	G.LYS.282	NZ	G.GLU.275	OE1	3.687
4OM0	G.LYS.343	NZ	G.GLU.347	OE2	2.544
4OM0	G.LYS.348	NZ	G.GLU.269	OE2	2.992
4OM0	G.LYS.348	NZ	G.GLU.351	OE1	3.079
4OM0	G.ARG.379	NH2	G.ASP.211	OD1	3.805
4OM0	G.ARG.469	NH2	G.ASP.457	OD1	3.868
4OM0	G.ARG.469	NH2	G.ASP.457	OD2	2.885
4OM0	G.LYS.476	NZ	G.GLU.102	OE1	2.824
4OM0	G.ARG.480	NH1	G.ASP.477	OD1	2.762
4OM0	G.ARG.480	NH2	G.GLU.102	OE2	3.978
4OM0	G.LYS.487	NZ	G.ASP.47	OD1	2.993
4OM0	G.LYS.487	NZ	G.ASP.47	OD2	3.296
4OM0	G.LYS.487	NZ	G.GLU.91	OE1	2.866
4OM0	H.ARG.19	NH2	H.GLU.81	OE1	3.635
4OM0	H.ARG.38	NH1	H.ASP.86	OD1	2.891
4OM0	H.ARG.38	NH2	H.GLU.46	OE1	3.152
4OM0	H.ARG.38	NH2	H.GLU.46	OE2	3.952
4OM0	H.ARG.38	NH2	H.ASP.86	OD1	3.799
4OM0	H.ARG.61	NH1	G.GLU.466	OE1	2.871
4OM0	H.ARG.66	NH1	H.ASP.86	OD1	3.542
4OM0	H.ARG.66	NH2	H.ASP.86	OD1	3.067
4OM0	H.ARG.66	NH2	H.ASP.86	OD2	2.679
4OM0	H.ARG.71	NH1	G.ASP.368	OD1	3.724
4OM0	H.ARG.71	NH1	G.ASP.368	OD2	2.771
4OM0	H.ARG.71	NH2	G.ASP.368	OD1	3.189
4OM0	H.ARG.71	NH2	G.ASP.368	OD2	3.713
4OM0	H.ARG.82A	NH1	H.GLU.81	OE2	3.957
4OM0	H.HIS.102	NE2	H.GLU.101	OE1	3.389
4OM0	H.LYS.143	NZ	H.ASP.144	OD1	3.715
4OM0	H.LYS.209	NZ	L.GLU.125	OE2	3.121
4OM0	H.LYS.210	NZ	H.GLU.212	OE1	3.995
4OM0	L.ARG.24	NH1	L.ASP.70	OD1	3.645
4OM0	L.ARG.24	NH1	L.ASP.70	OD2	3.913
4OM0	L.ARG.24	NH2	L.ASP.70	OD1	3.504
4OM0	L.ARG.24	NH2	L.ASP.70	OD2	3.395
4OM0	L.ARG.61	NH1	L.ASP.82	OD1	3.878
4OM0	L.ARG.61	NH1	L.ASP.82	OD2	2.597
4OM0	L.ARG.61	NH2	L.GLU.79	OE1	3.542
4OM0	L.ARG.61	NH2	L.GLU.79	OE2	3.993
4OM0	L.ARG.61	NH2	L.ASP.82	OD1	3.348
4OM0	L.ARG.61	NH2	L.ASP.82	OD2	3.442

Table 597: 4OM0-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4OM1	G.HIS.66	ND1	G.GLU.64	OE1	3.968
4OM1	G.HIS.66	ND1	G.GLU.64	OE2	2.708
4OM1	G.LYS.97	NZ	G.GLU.275	OE1	3.600
4OM1	G.LYS.97	NZ	G.GLU.275	OE2	2.568
4OM1	G.LYS.97	NZ	H.ASP.100B	OD1	3.927
4OM1	G.LYS.97	NZ	H.ASP.100B	OD2	3.635
4OM1	G.LYS.207	NZ	G.GLU.381	OE1	3.308
4OM1	G.LYS.207	NZ	G.GLU.381	OE2	2.686
4OM1	G.HIS.249	NE2	G.GLU.482	OE1	3.036
4OM1	G.LYS.282	NZ	G.GLU.275	OE1	3.818
4OM1	G.LYS.343	NZ	G.GLU.347	OE2	2.690
4OM1	G.LYS.348	NZ	G.GLU.351	OE1	3.702
4OM1	G.LYS.357	NZ	G.GLU.466	OE2	2.685
4OM1	G.LYS.357	NZ	L.GLU.1	OE2	3.763
4OM1	G.ARG.379	NH2	G.ASP.211	OD2	3.954
4OM1	G.ARG.456	NH1	G.GLU.466	OE1	3.023
4OM1	G.ARG.469	NH2	G.ASP.457	OD1	3.972
4OM1	G.ARG.469	NH2	G.ASP.457	OD2	2.755
4OM1	G.LYS.476	NZ	G.GLU.102	OE1	2.848
4OM1	G.LYS.476	NZ	G.GLU.102	OE2	3.744
4OM1	G.ARG.480	NH1	G.ASP.477	OD1	2.846
4OM1	G.LYS.487	NZ	G.ASP.47	OD1	2.990
4OM1	G.LYS.487	NZ	G.ASP.47	OD2	3.195
4OM1	G.LYS.487	NZ	G.GLU.91	OE1	2.549
4OM1	H.ARG.19	NH2	H.GLU.81	OE1	3.387
4OM1	H.ARG.38	NH1	H.ASP.86	OD1	2.946
4OM1	H.ARG.38	NH2	H.GLU.46	OE1	2.854
4OM1	H.ARG.38	NH2	H.GLU.46	OE2	3.922
4OM1	H.ARG.38	NH2	H.ASP.86	OD1	3.859
4OM1	H.ARG.66	NH1	H.ASP.86	OD1	3.431
4OM1	H.ARG.66	NH2	H.ASP.86	OD1	2.947
4OM1	H.ARG.66	NH2	H.ASP.86	OD2	2.686
4OM1	H.ARG.71	NH1	G.ASP.368	OD1	3.565
4OM1	H.ARG.71	NH1	G.ASP.368	OD2	2.752
4OM1	H.ARG.71	NH2	G.ASP.368	OD1	3.031
4OM1	H.ARG.71	NH2	G.ASP.368	OD2	3.734
4OM1	H.ARG.82A	NH1	H.GLU.81	OE2	3.380
4OM1	H.LYS.96	NZ	H.GLU.101	OE1	3.890
4OM1	H.LYS.96	NZ	H.GLU.101	OE2	3.816
4OM1	H.HIS.102	NE2	H.GLU.101	OE1	3.730
4OM1	H.LYS.209	NZ	L.GLU.125	OE1	3.639
4OM1	H.LYS.209	NZ	L.GLU.125	OE2	3.008
4OM1	H.LYS.210	NZ	H.GLU.212	OE1	3.752
4OM1	L.ARG.24	NH2	L.ASP.70	OD1	3.182
4OM1	L.ARG.24	NH2	L.ASP.70	OD2	2.699
4OM1	L.ARG.61	NH1	L.ASP.82	OD1	3.829
4OM1	L.ARG.61	NH1	L.ASP.82	OD2	2.671
4OM1	L.ARG.61	NH2	L.GLU.79	OE1	3.602
4OM1	L.ARG.61	NH2	L.GLU.79	OE2	3.954
4OM1	L.ARG.61	NH2	L.ASP.82	OD1	3.243
4OM1	L.ARG.61	NH2	L.ASP.82	OD2	3.379
4OM1	L.LYS.109	NZ	L.GLU.17	OE1	3.450
4OM1	L.LYS.109	NZ	L.GLU.17	OE2	2.771
4OM1	L.HIS.191	ND1	L.ASP.153	OD2	2.919

Table 598: 4OM1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4OT1	A_ARG_131	NH1	A_GLU_422	OE2	3.994
4OT1	A_ARG_357	NH2	A_ASP_122	OD2	2.900
4OT1	A_LYS_378	NZ	A_ASP_362	OD1	3.505
4OT1	A_LYS_378	NZ	A_ASP_362	OD2	3.358
4OT1	A_LYS_379	NZ	A_GLU_359	OE2	2.737
4OT1	A_ARG_393	NH1	A_ASP_390	OD1	2.905
4OT1	A_ARG_393	NH2	A_ASP_390	OD1	2.768
4OT1	A_LYS_435	NZ	A_GLU_413	OE2	2.567
4OT1	H_ARG_12	NH1	H_GLU_10	OE1	3.166
4OT1	H_ARG_12	NH2	H_GLU_10	OE1	3.283
4OT1	H_LYS_30	NZ	H_ASP_31	OD1	3.047
4OT1	H_ARG_38	NH1	H_ASP_90	OD1	2.615
4OT1	H_ARG_38	NH2	H_GLU_46	OE1	3.314
4OT1	H_ARG_38	NH2	H_ASP_90	OD1	3.679
4OT1	H_LYS_63	NZ	H_GLU_46	OE1	3.385
4OT1	H_LYS_63	NZ	H_GLU_46	OE2	2.667
4OT1	H_ARG_67	NH1	H_ASP_90	OD1	3.883
4OT1	H_ARG_67	NH1	H_ASP_90	OD2	3.033
4OT1	H_ARG_67	NH2	H_ASP_90	OD1	3.016
4OT1	H_ARG_67	NH2	H_ASP_90	OD2	3.552
4OT1	H_ARG_87	NH2	H_ASP_89	OD1	3.432
4OT1	H_ARG_87	NH2	H_ASP_89	OD2	2.704
4OT1	H_ARG_98	NH2	H_ASP_119	OD1	3.496
4OT1	H_ARG_98	NH2	H_ASP_119	OD2	2.884
4OT1	H_HIS_115	ND1	H_ASP_99	OD1	2.738
4OT1	H_HIS_115	ND1	H_ASP_99	OD2	3.714
4OT1	H_LYS_161	NZ	L_GLU_127	OE2	2.572
4OT1	H_LYS_227	NZ	L_GLU_126	OE1	2.521
4OT1	H_LYS_227	NZ	L_GLU_126	OE2	3.241
4OT1	L_LYS_54	NZ	L_ASP_51	OD2	3.014
4OT1	L_ARG_55	NH1	L_ASP_61	OD1	3.917
4OT1	L_ARG_62	NH1	L_ASP_83	OD1	2.721
4OT1	L_ARG_62	NH1	L_ASP_83	OD2	3.462
4OT1	L_ARG_62	NH2	L_ASP_83	OD1	3.562
4OT1	L_ARG_62	NH2	L_ASP_83	OD2	2.996
4OT1	L_LYS_67	NZ	A_GLU_361	OE2	3.026
4OT1	L_LYS_152	NZ	L_GLU_206	OE1	3.999
4OT1	L_LYS_152	NZ	L_GLU_206	OE2	2.900

Table 599: 4OT1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4OTX	L_ARG_54	NH1	L_ASP_60	OD1	3.335
4OTX	L_ARG_54	NH2	L_ASP_60	OD1	2.587
4OTX	L_ARG_61	NH2	L_GLU_81	OE1	3.052
4OTX	L_ARG_61	NH2	L_ASP_82	OD1	2.662
4OTX	L_ARG_61	NH2	L_ASP_82	OD2	3.622
4OTX	L_LYS_149	NZ	L_GLU_195	OE1	3.784
4OTX	L_HIS_189	ND1	L_ASP_151	OD2	2.906
4OTX	H_LYS_62	NZ	H_GLU_46	OE1	3.813
4OTX	H_LYS_62	NZ	H_GLU_46	OE2	2.843
4OTX	H_LYS_66	NZ	H_ASP_86	OD1	3.726
4OTX	H_LYS_66	NZ	H_ASP_86	OD2	2.772
4OTX	M_LYS_24	NZ	M_ASP_70	OD1	3.831
4OTX	M_ARG_54	NH2	M_ASP_60	OD1	3.076
4OTX	M_ARG_61	NH2	M_GLU_81	OE2	2.931
4OTX	M_ARG_61	NH2	M_ASP_82	OD1	2.705
4OTX	M_ARG_61	NH2	M_ASP_82	OD2	3.780
4OTX	M_ARG_155	NH1	M_GLU_185	OE2	2.645
4OTX	M_ARG_155	NH2	M_GLU_185	OE1	3.700
4OTX	M_ARG_155	NH2	M_GLU_185	OE2	3.518
4OTX	M_HIS_189	ND1	M_ASP_151	OD2	2.662
4OTX	M_ARG_211	NH1	M_GLU_187	OE2	3.522
4OTX	I_LYS_62	NZ	I_GLU_46	OE2	2.424
4OTX	I_LYS_66	NZ	I_ASP_86	OD2	2.972
4OTX	I_ARG_94	NH2	I_ASP_101	OD2	3.905
4OTX	I_LYS_209	NZ	I_GLU_211	OE1	3.618

Table 600: 4OTX-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4P49	A_LYS_33	NZ	A_GLU_76	OE2	3.764
4P49	A_ARG_56	NH2	A_GLU_76	OE1	3.151
4P49	A_ARG_56	NH2	A_ASP_77	OD1	2.851
4P49	A_ARG_56	NH2	A_ASP_77	OD2	3.564
4P49	A_ARG_158	NH1	A_ASP_211	OD1	2.929
4P49	A_ARG_158	NH2	A_GLU_166	OE1	3.049
4P49	A_ARG_158	NH2	A_ASP_211	OD1	3.847
4P49	A_ARG_188	NH1	A_ASP_211	OD1	3.709
4P49	A_ARG_188	NH1	A_ASP_211	OD2	2.796
4P49	A_ARG_188	NH2	A_ASP_211	OD1	2.980
4P49	A_ARG_188	NH2	A_ASP_211	OD2	3.547
4P49	A_ARG_219	NH2	A_ASP_232	OD1	3.462
4P49	A_ARG_219	NH2	A_ASP_232	OD2	2.815
4P49	A_HIS_221	ND1	A_ASP_232	OD2	2.753
4P49	A_HIS_236	ND1	A_GLU_126	OE1	3.338
4P49	A_HIS_236	NE2	A_ASP_125	OD1	2.678
4P49	A_HIS_236	NE2	A_GLU_126	OE1	3.576

Table 601: 4P49-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4P9H	C_LYS_7	NZ	C_ASP_10	OD2	3.690
4P9H	C_LYS_8	NZ	C_GLU_119	OE1	3.955
4P9H	C_LYS_8	NZ	C_GLU_119	OE2	2.953
4P9H	C_LYS_29	NZ	C_GLU_85	OE1	3.562
4P9H	C_LYS_29	NZ	C_GLU_85	OE2	3.697
4P9H	C_ARG_54	NH1	C_ASP_78	OD2	2.976
4P9H	C_ARG_54	NH2	C_ASP_78	OD1	3.086
4P9H	C_ARG_54	NH2	C_ASP_78	OD2	2.930
4P9H	C_ARG_58	NH1	C_GLU_13	OE1	2.881
4P9H	C_ARG_58	NH1	C_GLU_13	OE2	2.882
4P9H	C_ARG_58	NH2	C_GLU_13	OE2	3.671
4P9H	C_ARG_59	NH1	G_ASP_368	OD1	2.832
4P9H	C_ARG_59	NH1	G_ASP_368	OD2	3.395
4P9H	C_ARG_59	NH2	G_ASP_368	OD1	3.561
4P9H	C_ARG_59	NH2	G_ASP_368	OD2	2.514
4P9H	C_LYS_171	NZ	C_GLU_169	OE2	3.618
4P9H	G_HIS_66	ND1	G_GLU_64	OE1	3.936
4P9H	G_HIS_66	ND1	G_GLU_64	OE2	2.459
4P9H	G_LYS_227	NZ	G_GLU_83	OE2	3.669
4P9H	G_HIS_249	NE2	G_GLU_482	OE1	2.955
4P9H	G_LYS_282	NZ	G_GLU_275	OE1	3.022
4P9H	G_LYS_282	NZ	G_GLU_275	OE2	3.961
4P9H	G_LYS_348	NZ	G_GLU_269	OE1	2.726
4P9H	G_LYS_348	NZ	G_GLU_351	OE1	3.154
4P9H	G_LYS_348	NZ	G_GLU_351	OE2	3.034
4P9H	G_LYS_357	NZ	G_GLU_466	OE2	2.986
4P9H	G_ARG_456	NH1	G_GLU_466	OE1	3.795
4P9H	G_ARG_456	NH1	G_GLU_466	OE2	3.185
4P9H	G_ARG_469	NH2	G_ASP_457	OD2	3.218
4P9H	G_LYS_476	NZ	G_GLU_102	OE1	2.706
4P9H	G_ARG_480	NH1	G_ASP_477	OD1	3.014
4P9H	G_ARG_480	NH2	G_GLU_102	OE2	3.549
4P9H	G_LYS_487	NZ	G_ASP_47	OD1	3.793
4P9H	G_LYS_487	NZ	G_ASP_47	OD2	2.540
4P9H	G_LYS_487	NZ	G_GLU_91	OE2	2.794
4P9H	H_ARG_38	NH1	H_ASP_86	OD1	2.679
4P9H	H_ARG_38	NH2	H_GLU_46	OE1	3.970
4P9H	H_ARG_38	NH2	H_ASP_86	OD1	3.498
4P9H	H_HIS_61	NE2	L_ASP_1	OD2	3.817
4P9H	H_ARG_66	NH2	H_ASP_86	OD1	2.897
4P9H	H_ARG_66	NH2	H_ASP_86	OD2	2.412
4P9H	H_LYS_143	NZ	H_ASP_144	OD1	3.073
4P9H	H_LYS_143	NZ	H_ASP_144	OD2	2.969
4P9H	L_ARG_24	NH2	L_ASP_70	OD1	3.255
4P9H	L_ARG_61	NH1	L_GLU_81	OE2	3.724
4P9H	L_ARG_61	NH1	L_ASP_82	OD1	3.931
4P9H	L_ARG_61	NH1	L_ASP_82	OD2	2.983
4P9H	L_ARG_61	NH2	L_GLU_81	OE2	2.893
4P9H	L_ARG_61	NH2	L_ASP_82	OD1	3.839

Table 602: 4P9H-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4PTT	A_ARG_24	NH1	A_ASP_70	OD1	3.965
4PTT	A_ARG_24	NH1	A_ASP_70	OD2	3.009
4PTT	A_ARG_53	NH1	A_ASP_50	OD2	3.791
4PTT	A_ARG_53	NH2	A_ASP_50	OD2	2.752
4PTT	A_ARG_61	NH1	A_GLU_79	OE1	3.274
4PTT	A_ARG_61	NH2	A_GLU_79	OE1	3.194
4PTT	A_ARG_61	NH2	A_GLU_81	OE1	3.963
4PTT	A_ARG_61	NH2	A_ASP_82	OD1	2.721
4PTT	A_ARG_61	NH2	A_ASP_82	OD2	3.451
4PTT	A_ARG_91	NH2	B_GLU_95	OE1	3.477
4PTT	A_ARG_91	NH2	B_GLU_95	OE2	3.208
4PTT	A_LYS_107	NZ	A_GLU_17	OE1	3.991
4PTT	A_LYS_107	NZ	A_GLU_17	OE2	3.451
4PTT	A_LYS_149	NZ	A_GLU_195	OE1	2.707
4PTT	A_LYS_149	NZ	A_GLU_195	OE2	2.811
4PTT	A_LYS_188	NZ	A_ASP_185	OD1	3.692
4PTT	A_ARG_211	NH1	A_GLU_187	OE1	3.911
4PTT	B_HIS_32	ND1	B_ASP_97	OD1	3.351
4PTT	B_HIS_32	NE2	B_ASP_97	OD1	3.881
4PTT	B_HIS_35	NE2	B_GLU_95	OE2	2.791
4PTT	B_ARG_38	NH1	B_ASP_86	OD1	2.956
4PTT	B_ARG_38	NH2	B_GLU_46	OE1	3.058
4PTT	B_ARG_38	NH2	B_GLU_46	OE2	3.774
4PTT	B_ARG_66	NH1	B_ASP_86	OD1	3.031
4PTT	B_ARG_66	NH1	B_ASP_86	OD2	3.456
4PTT	B_ARG_66	NH2	B_ASP_86	OD1	3.848
4PTT	B_ARG_66	NH2	B_ASP_86	OD2	2.768
4PTT	B_LYS_94	NZ	B_ASP_97	OD1	2.735
4PTT	B_LYS_94	NZ	B_ASP_97	OD2	3.827
4PTT	B_LYS_94	NZ	B_ASP_101	OD1	3.084
4PTT	B_LYS_94	NZ	B_ASP_101	OD2	2.853
4PTT	B_LYS_143	NZ	B_ASP_144	OD1	3.257
4PTT	B_LYS_143	NZ	B_ASP_144	OD2	3.722
4PTT	B_LYS_209	NZ	A_GLU_123	OE2	3.476
4PTT	B_ARG_210	NH1	B_GLU_212	OE2	3.500
4PTT	B_ARG_210	NH2	B_GLU_212	OE2	2.861

Table 603: 4PTT-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4PTU	A_ARG_24	NH1	A_ASP_70	OD2	3.705
4PTU	A_ARG_53	NH1	A_ASP_50	OD2	3.480
4PTU	A_ARG_53	NH2	A_ASP_50	OD2	2.718
4PTU	A_ARG_61	NH1	A_GLU_79	OE1	3.172
4PTU	A_ARG_61	NH2	A_GLU_79	OE1	3.200
4PTU	A_ARG_61	NH2	A_ASP_82	OD1	2.746
4PTU	A_ARG_61	NH2	A_ASP_82	OD2	3.514
4PTU	A_ARG_91	NH2	B_GLU_95	OE1	3.438
4PTU	A_ARG_91	NH2	B_GLU_95	OE2	3.334
4PTU	A_LYS_107	NZ	A_GLU_17	OE1	3.740
4PTU	A_LYS_107	NZ	A_GLU_17	OE2	3.243
4PTU	A_LYS_149	NZ	A_GLU_195	OE1	3.016
4PTU	A_LYS_149	NZ	A_GLU_195	OE2	3.379
4PTU	A_LYS_183	NZ	A_GLU_187	OE1	2.720
4PTU	A_LYS_188	NZ	A_ASP_185	OD1	3.765
4PTU	A_HIS_189	ND1	A_ASP_151	OD2	3.327
4PTU	B_HIS_32	ND1	B_ASP_97	OD1	3.387
4PTU	B_HIS_32	NE2	B_ASP_97	OD1	3.899
4PTU	B_HIS_35	NE2	B_GLU_95	OE2	2.750
4PTU	B_ARG_38	NH1	B_ASP_86	OD1	2.924
4PTU	B_ARG_38	NH2	B_GLU_46	OE1	3.021
4PTU	B_ARG_38	NH2	B_GLU_46	OE2	3.729
4PTU	B_ARG_38	NH2	B_ASP_86	OD1	3.966
4PTU	B_ARG_66	NH1	B_ASP_86	OD1	3.085
4PTU	B_ARG_66	NH1	B_ASP_86	OD2	3.410
4PTU	B_ARG_66	NH2	B_ASP_86	OD1	3.877
4PTU	B_ARG_66	NH2	B_ASP_86	OD2	2.723
4PTU	B_LYS_94	NZ	B_ASP_97	OD1	2.781
4PTU	B_LYS_94	NZ	B_ASP_97	OD2	3.846
4PTU	B_LYS_94	NZ	B_ASP_101	OD1	3.172
4PTU	B_LYS_94	NZ	B_ASP_101	OD2	2.801
4PTU	B_LYS_143	NZ	B_ASP_144	OD1	3.236
4PTU	B_LYS_143	NZ	B_ASP_144	OD2	3.531
4PTU	B_LYS_209	NZ	A_GLU_123	OE1	3.628
4PTU	B_ARG_210	NH1	B_GLU_212	OE2	3.352

Table 604: 4PTU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4Q6I	A_ARG_24	NH2	A_ASP_70	OD1	3.547
4Q6I	A_LYS_49	NZ	A_GLU_55	OE1	3.733
4Q6I	A_LYS_49	NZ	B_ASP_100A	OD1	2.964
4Q6I	A_ARG_61	NH1	A_GLU_79	OE1	3.355
4Q6I	A_ARG_61	NH1	A_GLU_79	OE2	3.338
4Q6I	A_ARG_61	NH1	A_GLU_81	OE2	3.926
4Q6I	A_ARG_61	NH2	A_GLU_79	OE2	3.547
4Q6I	A_ARG_61	NH2	A_GLU_81	OE2	3.022
4Q6I	A_ARG_61	NH2	A_ASP_82	OD1	2.927
4Q6I	A_ARG_61	NH2	A_ASP_82	OD2	3.845
4Q6I	A_LYS_103	NZ	A_GLU_105	OE2	3.808
4Q6I	A_LYS_142	NZ	A_GLU_105	OE1	3.421
4Q6I	A_LYS_142	NZ	A_GLU_105	OE2	2.841
4Q6I	A_LYS_147	NZ	A_GLU_154	OE1	3.796
4Q6I	A_LYS_149	NZ	A_GLU_195	OE1	3.162
4Q6I	A_LYS_149	NZ	A_GLU_195	OE2	3.016
4Q6I	A_ARG_155	NH1	A_GLU_185	OE2	3.506
4Q6I	A_HIS_189	ND1	A_ASP_151	OD2	2.954
4Q6I	B_HIS_66	ND1	B_ASP_61	OD1	3.699
4Q6I	B_HIS_66	ND1	B_ASP_61	OD2	3.085
4Q6I	B_HIS_66	NE2	B_ASP_86	OD1	3.906
4Q6I	B_HIS_66	NE2	B_ASP_86	OD2	2.658
4Q6I	B_ARG_94	NH2	B_ASP_101	OD1	3.897
4Q6I	B_ARG_94	NH2	B_ASP_101	OD2	2.713
4Q6I	B_LYS_208	NZ	A_GLU_123	OE2	2.822
4Q6I	C_LYS_8	NZ	C_GLU_119	OE1	2.805
4Q6I	C_HIS_27	NE2	C_GLU_85	OE1	3.053
4Q6I	C_LYS_50	NZ	C_GLU_77	OE2	3.944
4Q6I	C_LYS_50	NZ	L_GLU_93	OE2	2.549
4Q6I	C_ARG_54	NH1	C_ASP_78	OD2	2.778
4Q6I	C_ARG_54	NH2	C_ASP_78	OD1	3.552
4Q6I	C_ARG_54	NH2	C_ASP_78	OD2	3.385
4Q6I	C_ARG_134	NH1	C_GLU_150	OE1	2.907
4Q6I	C_ARG_134	NH1	C_GLU_150	OE2	3.926
4Q6I	C_LYS_136	NZ	C_ASP_153	OD1	3.102
4Q6I	C_LYS_136	NZ	C_ASP_153	OD2	3.702
4Q6I	C_LYS_167	NZ	C_GLU_169	OE2	3.766
4Q6I	C_LYS_181	NZ	G_GLU_56	OE1	2.499
4Q6I	D_ARG_24	NH2	D_ASP_70	OD1	3.494
4Q6I	D_LYS_49	NZ	D_GLU_55	OE1	3.186
4Q6I	D_LYS_49	NZ	D_GLU_55	OE2	3.674
4Q6I	D_LYS_49	NZ	E_ASP_100A	OD1	3.008
4Q6I	D_ARG_61	NH1	D_GLU_79	OE1	3.297
4Q6I	D_ARG_61	NH1	D_GLU_79	OE2	3.483
4Q6I	D_ARG_61	NH2	D_GLU_79	OE2	3.497
4Q6I	D_ARG_61	NH2	D_GLU_81	OE2	3.188
4Q6I	D_ARG_61	NH2	D_ASP_82	OD1	3.128
4Q6I	D_ARG_61	NH2	D_ASP_82	OD2	3.997
4Q6I	D_LYS_142	NZ	D_GLU_105	OE1	3.699
4Q6I	D_LYS_142	NZ	D_GLU_105	OE2	2.690
4Q6I	D_LYS_147	NZ	D_GLU_154	OE1	3.636
4Q6I	D_LYS_149	NZ	D_GLU_195	OE1	3.195
4Q6I	D_LYS_149	NZ	D_GLU_195	OE2	2.990
4Q6I	D_ARG_155	NH1	D_GLU_185	OE2	3.476
4Q6I	D_ARG_155	NH2	D_GLU_185	OE2	3.858
4Q6I	D_HIS_189	ND1	D_ASP_151	OD2	2.792
4Q6I	E_HIS_66	ND1	E_ASP_61	OD1	3.611

4Q6I	E_HIS.66	ND1	E_ASP.61	OD2	3.049
4Q6I	E_HIS.66	NE2	E_ASP.86	OD1	3.914
4Q6I	E_HIS.66	NE2	E_ASP.86	OD2	2.560
4Q6I	E_ARG.94	NH2	E_ASP.101	OD1	3.957
4Q6I	E_ARG.94	NH2	E_ASP.101	OD2	2.680
4Q6I	E_LYS.208	NZ	D_GLU.123	OE2	3.047
4Q6I	F_ARG.24	NH2	F_ASP.70	OD1	3.340
4Q6I	F_ARG.24	NH2	F_ASP.70	OD2	3.665
4Q6I	F_LYS.49	NZ	F_GLU.55	OE1	3.518
4Q6I	F_LYS.49	NZ	G_ASP.100A	OD1	3.146
4Q6I	F_ARG.61	NH1	F_GLU.79	OE1	3.116
4Q6I	F_ARG.61	NH1	F_GLU.79	OE2	3.200
4Q6I	F_ARG.61	NH2	F_GLU.79	OE2	3.435
4Q6I	F_ARG.61	NH2	F_GLU.81	OE2	3.194
4Q6I	F_ARG.61	NH2	F_ASP.82	OD1	2.864
4Q6I	F_ARG.61	NH2	F_ASP.82	OD2	3.691
4Q6I	F_LYS.103	NZ	F_GLU.105	OE2	3.989
4Q6I	F_LYS.142	NZ	F_GLU.105	OE1	3.572
4Q6I	F_LYS.142	NZ	F_GLU.105	OE2	2.671
4Q6I	F_LYS.147	NZ	F_GLU.154	OE1	3.784
4Q6I	F_LYS.149	NZ	F_GLU.195	OE1	3.282
4Q6I	F_LYS.149	NZ	F_GLU.195	OE2	2.913
4Q6I	F_ARG.155	NH1	F_GLU.185	OE2	3.619
4Q6I	F_ARG.155	NH2	F_GLU.185	OE2	3.997
4Q6I	F_HIS.189	ND1	F_ASP.151	OD2	2.927
4Q6I	G_HIS.66	ND1	G_ASP.61	OD1	3.622
4Q6I	G_HIS.66	ND1	G_ASP.61	OD2	3.038
4Q6I	G_HIS.66	NE2	G_ASP.86	OD1	3.886
4Q6I	G_HIS.66	NE2	G_ASP.86	OD2	2.589
4Q6I	G_ARG.94	NH2	G_ASP.101	OD1	3.834
4Q6I	G_ARG.94	NH2	G_ASP.101	OD2	2.611
4Q6I	G_LYS.208	NZ	F_GLU.123	OE2	3.409
4Q6I	H_HIS.66	ND1	H_ASP.61	OD1	3.559
4Q6I	H_HIS.66	ND1	H_ASP.61	OD2	2.808
4Q6I	H_HIS.66	NE2	H_ASP.86	OD1	3.762
4Q6I	H_HIS.66	NE2	H_ASP.86	OD2	2.594
4Q6I	H_ARG.94	NH2	H_ASP.101	OD1	3.987
4Q6I	H_ARG.94	NH2	H_ASP.101	OD2	2.731
4Q6I	H_LYS.208	NZ	L_GLU.123	OE2	3.045
4Q6I	I_LYS.8	NZ	I_GLU.119	OE1	2.686
4Q6I	I_LYS.8	NZ	I_GLU.119	OE2	3.813
4Q6I	I_HIS.27	NE2	I_GLU.85	OE1	3.108
4Q6I	I_LYS.50	NZ	F_GLU.93	OE2	2.473
4Q6I	I_LYS.50	NZ	I_GLU.77	OE2	3.955
4Q6I	I_ARG.54	NH1	I_ASP.78	OD2	2.649
4Q6I	I_ARG.54	NH2	I_ASP.78	OD1	3.358
4Q6I	I_ARG.54	NH2	I_ASP.78	OD2	3.298
4Q6I	I_ARG.134	NH1	I_GLU.150	OE1	2.570
4Q6I	I_ARG.134	NH1	I_GLU.150	OE2	3.190
4Q6I	I_LYS.136	NZ	I_ASP.153	OD1	2.871
4Q6I	I_LYS.136	NZ	I_ASP.153	OD2	3.533
4Q6I	I_LYS.167	NZ	I_GLU.169	OE2	3.738
4Q6I	I_LYS.181	NZ	H_GLU.56	OE1	3.345
4Q6I	J_LYS.8	NZ	J_GLU.119	OE1	2.575
4Q6I	J_LYS.8	NZ	J_GLU.119	OE2	3.660
4Q6I	J_HIS.27	NE2	J_GLU.85	OE1	3.112
4Q6I	J_LYS.50	NZ	D_GLU.93	OE2	2.666
4Q6I	J_LYS.50	NZ	J_GLU.77	OE2	3.985

4Q6I	J_ARG_54	NH1	J_ASP_78	OD2	2.642
4Q6I	J_ARG_54	NH2	J_ASP_78	OD1	3.414
4Q6I	J_ARG_54	NH2	J_ASP_78	OD2	3.086
4Q6I	J_ARG_134	NH1	J_GLU_150	OE1	3.114
4Q6I	J_LYS_136	NZ	J_ASP_153	OD1	2.951
4Q6I	J_LYS_136	NZ	J_ASP_153	OD2	3.722
4Q6I	J_LYS_167	NZ	J_GLU_169	OE2	3.737
4Q6I	K_LYS_8	NZ	K_GLU_119	OE1	2.674
4Q6I	K_LYS_8	NZ	K_GLU_119	OE2	3.835
4Q6I	K_HIS_27	NE2	K_GLU_85	OE1	2.922
4Q6I	K_LYS_50	NZ	A_GLU_93	OE2	2.835
4Q6I	K_LYS_50	NZ	K_GLU_77	OE2	3.766
4Q6I	K_ARG_54	NH1	K_ASP_78	OD2	2.757
4Q6I	K_ARG_54	NH2	K_ASP_78	OD1	3.522
4Q6I	K_ARG_54	NH2	K_ASP_78	OD2	3.092
4Q6I	K_ARG_134	NH1	K_GLU_150	OE1	2.737
4Q6I	K_ARG_134	NH1	K_GLU_150	OE2	2.516
4Q6I	K_LYS_136	NZ	K_ASP_153	OD1	3.074
4Q6I	K_LYS_136	NZ	K_ASP_153	OD2	3.548
4Q6I	L_ARG_24	NH2	L_ASP_70	OD1	3.386
4Q6I	L_ARG_24	NH2	L_ASP_70	OD2	3.804
4Q6I	L_LYS_49	NZ	H_ASP_100A	OD1	3.063
4Q6I	L_LYS_49	NZ	L_GLU_55	OE1	3.608
4Q6I	L_ARG_61	NH1	L_GLU_79	OE1	3.293
4Q6I	L_ARG_61	NH1	L_GLU_79	OE2	3.453
4Q6I	L_ARG_61	NH2	L_GLU_79	OE2	3.533
4Q6I	L_ARG_61	NH2	L_GLU_81	OE2	3.058
4Q6I	L_ARG_61	NH2	L_ASP_82	OD1	3.103
4Q6I	L_LYS_142	NZ	L_GLU_105	OE1	3.663
4Q6I	L_LYS_142	NZ	L_GLU_105	OE2	2.645
4Q6I	L_LYS_147	NZ	L_GLU_154	OE1	3.681
4Q6I	L_LYS_149	NZ	L_GLU_195	OE1	3.252
4Q6I	L_LYS_149	NZ	L_GLU_195	OE2	2.874
4Q6I	L_ARG_155	NH1	L_GLU_185	OE2	3.717
4Q6I	L_ARG_155	NH2	L_GLU_185	OE2	3.978
4Q6I	L_HIS_189	ND1	L_ASP_151	OD2	2.862

Table 605: 4Q6I-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4Q97	A_LYS_181	NZ	A_GLU_215	OE1	3.508
4Q97	A_LYS_181	NZ	A_GLU_215	OE2	2.452
4Q97	A_ARG_218	NH2	A_GLU_215	OE1	3.903
4Q97	A_ARG_240	NH2	A_GLU_238	OE1	2.864
4Q97	A_ARG_240	NH2	A_GLU_238	OE2	3.199
4Q97	B_LYS_181	NZ	B_GLU_215	OE1	3.498
4Q97	B_LYS_181	NZ	B_GLU_215	OE2	2.431
4Q97	B_ARG_218	NH2	B_GLU_215	OE1	3.910
4Q97	B_ARG_240	NH2	B_GLU_238	OE1	2.853
4Q97	B_ARG_240	NH2	B_GLU_238	OE2	3.203

Table 606: 4Q97-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4Q9B	A_ARG_250	NH1	A_GLU_268	OE2	2.895
4Q9B	A_ARG_288	NH1	A_GLU_316	OE1	3.608
4Q9B	A_ARG_288	NH1	A_GLU_316	OE2	2.926
4Q9B	A_ARG_288	NH2	A_GLU_316	OE1	2.765
4Q9B	A_ARG_288	NH2	A_GLU_316	OE2	3.617
4Q9B	A_ARG_309	NH1	A_GLU_295	OE1	2.883
4Q9B	A_ARG_309	NH1	A_GLU_295	OE2	3.399
4Q9B	A_ARG_309	NH1	B_GLU_255	OE1	3.484
4Q9B	A_ARG_309	NH1	B_GLU_255	OE2	2.912
4Q9B	A_ARG_309	NH2	B_GLU_255	OE2	3.212
4Q9B	A_ARG_339	NH2	A_GLU_322	OE1	3.788
4Q9B	A_ARG_339	NH2	A_GLU_322	OE2	2.973
4Q9B	A_ARG_341	NH1	A_GLU_322	OE2	3.129
4Q9B	B_ARG_250	NH1	B_GLU_268	OE2	2.773
4Q9B	B_ARG_288	NH1	B_GLU_316	OE1	3.649
4Q9B	B_ARG_288	NH1	B_GLU_316	OE2	2.767
4Q9B	B_ARG_288	NH2	B_GLU_316	OE1	2.902
4Q9B	B_ARG_288	NH2	B_GLU_316	OE2	3.570
4Q9B	B_ARG_309	NH1	A_GLU_255	OE1	3.145
4Q9B	B_ARG_309	NH1	A_GLU_255	OE2	2.858
4Q9B	B_ARG_309	NH1	B_GLU_295	OE1	3.156
4Q9B	B_ARG_309	NH1	B_GLU_295	OE2	3.958
4Q9B	B_ARG_309	NH2	B_GLU_295	OE1	2.549
4Q9B	B_ARG_339	NH2	B_GLU_322	OE1	2.438
4Q9B	B_ARG_339	NH2	B_GLU_322	OE2	3.097
4Q9B	B_ARG_341	NH2	B_GLU_322	OE2	2.672

Table 607: 4Q9B-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4Q9C	A_LYS_388	NZ	A_GLU_422	OE1	3.305
4Q9C	A_LYS_428	NZ	A_ASP_390	OD2	3.566

Table 608: 4Q9C-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4QEX	A_LYS_17	NZ	A_GLU_71	OE1	3.725
4QEX	A_LYS_17	NZ	A_GLU_71	OE2	2.956
4QEX	A_ARG_18	NH1	A_ASP_39	OD1	2.342
4QEX	A_ARG_18	NH1	A_ASP_39	OD2	2.888
4QEX	A_ARG_18	NH2	A_ASP_39	OD1	3.858
4QEX	A_LYS_19	NZ	A_ASP_80	OD1	2.818
4QEX	A_LYS_19	NZ	A_ASP_80	OD2	3.469
4QEX	A_LYS_26	NZ	A_ASP_108	OD1	3.934
4QEX	A_ARG_40	NH1	A_ASP_97	OD2	2.989
4QEX	A_ARG_40	NH2	A_ASP_97	OD2	2.794
4QEX	A_ARG_40	NH2	A_GLU_182	OE1	3.072
4QEX	A_ARG_40	NH2	A_GLU_182	OE2	3.122
4QEX	A_ARG_41	NH1	A_ASP_108	OD2	2.767
4QEX	A_ARG_41	NH2	A_ASP_106	OD1	3.672
4QEX	A_ARG_41	NH2	A_ASP_106	OD2	2.658
4QEX	A_ARG_41	NH2	A_ASP_108	OD2	3.573
4QEX	A_LYS_61	NZ	A_GLU_146	OE2	3.762
4QEX	A_LYS_78	NZ	A_ASP_90	OD1	3.235
4QEX	A_ARG_140	NH1	A_GLU_117	OE2	3.439
4QEX	A_LYS_141	NZ	A_GLU_172	OE1	3.378
4QEX	A_HIS_159	NE2	A_GLU_158	OE2	3.794
4QEX	A_LYS_181	NZ	A_GLU_173	OE1	3.704
4QEX	A_LYS_181	NZ	A_GLU_173	OE2	3.359
4QEX	A_ARG_191	NH2	A_ASP_263	OD2	3.924
4QEX	A_ARG_194	NH2	A_GLU_190	OE2	3.371
4QEX	A_LYS_199	NZ	A_GLU_276	OE2	3.126
4QEX	A_LYS_230	NZ	A_ASP_274	OD1	3.711
4QEX	A_LYS_230	NZ	A_ASP_274	OD2	3.195
4QEX	A_LYS_284	NZ	A_ASP_309	OD2	3.762
4QEX	A_LYS_284	NZ	A_ASP_312	OD1	3.824
4QEX	A_LYS_284	NZ	A_ASP_312	OD2	2.849
4QEX	A_LYS_320	NZ	A_ASP_311	OD1	3.730
4QEX	A_LYS_333	NZ	A_GLU_331	OE1	2.647
4QEX	A_LYS_341	NZ	A_GLU_545	OE1	3.181
4QEX	A_LYS_341	NZ	A_GLU_545	OE2	2.966
4QEX	A_LYS_341	NZ	H_ASP_53	OD1	3.875
4QEX	A_ARG_348	NH1	A_ASP_405	OD2	3.055
4QEX	A_ARG_348	NH2	A_ASP_405	OD2	2.876
4QEX	A_ARG_348	NH2	A_GLU_488	OE1	3.045
4QEX	A_ARG_348	NH2	A_GLU_488	OE2	3.938
4QEX	A_ARG_349	NH2	A_ASP_414	OD1	3.531
4QEX	A_ARG_349	NH2	A_ASP_414	OD2	2.996
4QEX	A_LYS_384	NZ	A_GLU_306	OE1	3.997
4QEX	A_LYS_384	NZ	A_GLU_306	OE2	3.752
4QEX	A_ARG_385	NH2	A_ASP_324	OD1	3.155
4QEX	A_LYS_386	NZ	A_GLU_351	OE1	3.481
4QEX	A_LYS_386	NZ	A_GLU_351	OE2	3.992
4QEX	A_ARG_422	NH2	H_ASP_97	OD2	3.116
4QEX	A_LYS_423	NZ	A_ASP_358	OD1	3.415
4QEX	A_LYS_423	NZ	A_ASP_358	OD2	3.036
4QEX	A_LYS_427	NZ	A_ASP_362	OD1	2.843
4QEX	A_ARG_437	NH2	A_ASP_442	OD2	3.346
4QEX	A_LYS_443	NZ	A_ASP_447	OD1	3.941
4QEX	A_LYS_443	NZ	A_ASP_447	OD2	2.889
4QEX	A_ARG_484	NH1	A_ASP_408	OD2	3.149
4QEX	A_ARG_484	NH2	A_ASP_405	OD1	3.156
4QEX	A_ARG_484	NH2	A_ASP_405	OD2	3.109

4QEX	A_ARG_484	NH2	A_ASP_408	OD2	3.711
4QEX	A_LYS_497	NZ	A_GLU_582	OE1	2.757
4QEX	A_LYS_531	NZ	A_GLU_535	OE2	3.270
4QEX	A_LYS_532	NZ	A_GLU_535	OE1	3.348
4QEX	A_LYS_532	NZ	A_GLU_535	OE2	3.847
4QEX	A_LYS_573	NZ	A_GLU_394	OE2	3.110
4QEX	L_ARG_18	NH2	L_ASP_76	OD1	3.851
4QEX	L_ARG_24	NH2	L_ASP_70	OD2	3.377
4QEX	L_LYS_27	NZ	L_GLU_93	OE1	3.354
4QEX	L_ARG_39	NH1	L_ASP_81	OD1	3.904
4QEX	L_ARG_61	NH1	L_ASP_82	OD1	2.872
4QEX	L_ARG_61	NH1	L_ASP_82	OD2	2.775
4QEX	L_ARG_61	NH2	L_GLU_79	OE1	3.798
4QEX	L_ARG_61	NH2	L_ASP_82	OD1	2.840
4QEX	L_ARG_61	NH2	L_ASP_82	OD2	3.147
4QEX	L_LYS_149	NZ	L_GLU_154	OE1	3.545
4QEX	L_ARG_155	NH2	L_GLU_185	OE2	3.880
4QEX	L_HIS_189	ND1	L_ASP_151	OD2	3.464
4QEX	L_LYS_199	NZ	L_ASP_110	OD2	3.727
4QEX	H_LYS_38	NZ	H_ASP_86	OD1	3.545
4QEX	H_LYS_62	NZ	H_ASP_46	OD1	3.147
4QEX	H_LYS_62	NZ	H_ASP_46	OD2	3.315
4QEX	H_LYS_66	NZ	H_ASP_86	OD2	3.686
4QEX	H_ARG_82A	NH2	H_GLU_81	OE1	3.257
4QEX	B_LYS_17	NZ	B_GLU_71	OE1	3.723
4QEX	B_LYS_17	NZ	B_GLU_71	OE2	2.955
4QEX	B_ARG_18	NH1	B_ASP_39	OD1	2.348
4QEX	B_ARG_18	NH1	B_ASP_39	OD2	2.891
4QEX	B_ARG_18	NH2	B_ASP_39	OD1	3.859
4QEX	B_LYS_19	NZ	B_ASP_80	OD1	2.821
4QEX	B_LYS_19	NZ	B_ASP_80	OD2	3.471
4QEX	B_LYS_26	NZ	B_ASP_108	OD1	3.946
4QEX	B_ARG_40	NH1	B_ASP_97	OD2	2.987
4QEX	B_ARG_40	NH2	B_ASP_97	OD2	2.795
4QEX	B_ARG_40	NH2	B_GLU_182	OE1	3.067
4QEX	B_ARG_40	NH2	B_GLU_182	OE2	3.120
4QEX	B_ARG_41	NH1	B_ASP_108	OD2	2.740
4QEX	B_ARG_41	NH2	B_ASP_106	OD1	3.677
4QEX	B_ARG_41	NH2	B_ASP_106	OD2	2.651
4QEX	B_ARG_41	NH2	B_ASP_108	OD2	3.554
4QEX	B_LYS_61	NZ	B_GLU_146	OE2	3.752
4QEX	B_LYS_78	NZ	B_ASP_90	OD1	3.242
4QEX	B_LYS_125	NZ	B_GLU_130	OE1	3.909
4QEX	B_ARG_140	NH1	B_GLU_117	OE2	3.438
4QEX	B_LYS_141	NZ	B_GLU_172	OE1	3.375
4QEX	B_HIS_159	NE2	B_GLU_158	OE2	3.791
4QEX	B_LYS_181	NZ	B_GLU_173	OE1	3.691
4QEX	B_LYS_181	NZ	B_GLU_173	OE2	3.345
4QEX	B_ARG_191	NH2	B_ASP_263	OD2	3.920
4QEX	B_ARG_194	NH2	B_GLU_190	OE2	3.366
4QEX	B_LYS_199	NZ	B_GLU_276	OE2	3.126
4QEX	B_LYS_230	NZ	B_ASP_274	OD1	3.714
4QEX	B_LYS_230	NZ	B_ASP_274	OD2	3.188
4QEX	B_LYS_284	NZ	B_ASP_309	OD2	3.751
4QEX	B_LYS_284	NZ	B_ASP_312	OD1	3.816
4QEX	B_LYS_284	NZ	B_ASP_312	OD2	2.842
4QEX	B_LYS_320	NZ	B_ASP_311	OD1	3.720
4QEX	B_LYS_333	NZ	B_GLU_331	OE1	2.649

4QEX	B_LYS_341	NZ	B_GLU_545	OE1	3.179
4QEX	B_LYS_341	NZ	B_GLU_545	OE2	2.971
4QEX	B_ARG_348	NH1	B_ASP_405	OD2	3.038
4QEX	B_ARG_348	NH2	B_ASP_405	OD2	2.871
4QEX	B_ARG_348	NH2	B_GLU_488	OE1	3.051
4QEX	B_ARG_348	NH2	B_GLU_488	OE2	3.938
4QEX	B_ARG_349	NH2	B_ASP_414	OD1	3.521
4QEX	B_ARG_349	NH2	B_ASP_414	OD2	2.994
4QEX	B_LYS_384	NZ	B_GLU_306	OE2	3.763
4QEX	B_ARG_385	NH2	B_ASP_324	OD1	3.156
4QEX	B_LYS_386	NZ	B_GLU_351	OE1	3.485
4QEX	B_LYS_386	NZ	B_GLU_351	OE2	3.984
4QEX	B_LYS_423	NZ	B_ASP_358	OD1	3.425
4QEX	B_LYS_423	NZ	B_ASP_358	OD2	3.036
4QEX	B_LYS_427	NZ	B_ASP_362	OD1	2.827
4QEX	B_ARG_437	NH2	B_ASP_442	OD2	3.351
4QEX	B_LYS_443	NZ	B_ASP_447	OD1	3.938
4QEX	B_LYS_443	NZ	B_ASP_447	OD2	2.877
4QEX	B_ARG_484	NH1	B_ASP_408	OD2	3.150
4QEX	B_ARG_484	NH2	B_ASP_405	OD1	3.172
4QEX	B_ARG_484	NH2	B_ASP_405	OD2	3.124
4QEX	B_ARG_484	NH2	B_ASP_408	OD2	3.702
4QEX	B_LYS_497	NZ	B_GLU_582	OE1	2.759
4QEX	B_LYS_531	NZ	B_GLU_535	OE2	3.281
4QEX	B_LYS_532	NZ	B_GLU_535	OE1	3.369
4QEX	B_LYS_532	NZ	B_GLU_535	OE2	3.868
4QEX	B_LYS_573	NZ	B_GLU_394	OE2	3.119
4QEX	M_ARG_18	NH2	M_ASP_76	OD1	3.849
4QEX	M_ARG_24	NH2	M_ASP_70	OD2	3.380
4QEX	M_LYS_27	NZ	M_GLU_93	OE1	3.352
4QEX	M_ARG_39	NH1	M_ASP_81	OD1	3.900
4QEX	M_ARG_61	NH1	M_ASP_82	OD1	2.873
4QEX	M_ARG_61	NH1	M_ASP_82	OD2	2.791
4QEX	M_ARG_61	NH2	M_GLU_79	OE1	3.795
4QEX	M_ARG_61	NH2	M_ASP_82	OD1	2.843
4QEX	M_ARG_61	NH2	M_ASP_82	OD2	3.151
4QEX	M_LYS_149	NZ	M_GLU_154	OE1	3.545
4QEX	M_ARG_155	NH2	M_GLU_185	OE2	3.873
4QEX	M_HIS_189	ND1	M_ASP_151	OD2	3.467
4QEX	M_LYS_199	NZ	M_ASP_110	OD2	3.724
4QEX	I_LYS_38	NZ	I_ASP_86	OD1	3.550
4QEX	I_LYS_62	NZ	I_ASP_46	OD1	3.149
4QEX	I_LYS_62	NZ	I_ASP_46	OD2	3.316
4QEX	I_LYS_66	NZ	I_ASP_86	OD2	3.689
4QEX	I_ARG_82A	NH2	I_GLU_81	OE1	3.265

Table 609: 4QEX-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4QHU	L_LYS_30	NZ	L_ASP_29	OD1	3.579
4QHU	L_LYS_30	NZ	L_ASP_91	OD2	3.632
4QHU	L_ARG_60	NH2	L_GLU_80	OE2	3.111
4QHU	L_ARG_60	NH2	L_ASP_81	OD1	2.567
4QHU	L_ARG_60	NH2	L_ASP_81	OD2	3.488
4QHU	L_LYS_104	NZ	L_ASP_84	OD1	3.091
4QHU	L_LYS_104	NZ	L_ASP_84	OD2	3.639
4QHU	L_LYS_151	NZ	L_GLU_205	OE1	3.904
4QHU	L_LYS_151	NZ	L_GLU_205	OE2	3.118
4QHU	L_LYS_168	NZ	L_GLU_82	OE2	2.712
4QHU	L_ARG_191	NH2	L_ASP_153	OD1	3.474
4QHU	L_ARG_191	NH2	L_ASP_153	OD2	3.847
4QHU	H_ARG_38	NH1	H_ASP_90	OD1	2.949
4QHU	H_ARG_38	NH2	H_GLU_46	OE1	3.628
4QHU	H_ARG_38	NH2	H_GLU_46	OE2	3.083
4QHU	H_ARG_38	NH2	H_ASP_90	OD1	3.976
4QHU	H_LYS_65	NZ	H_ASP_62	OD1	2.679
4QHU	H_ARG_67	NH1	H_ASP_90	OD1	3.783
4QHU	H_ARG_67	NH1	H_ASP_90	OD2	2.761
4QHU	H_ARG_67	NH2	H_ASP_90	OD1	3.192
4QHU	H_ARG_67	NH2	H_ASP_90	OD2	3.606
4QHU	H_LYS_76	NZ	H_ASP_73	OD2	3.381
4QHU	H_ARG_98	NH1	H_ASP_103	OD1	3.756
4QHU	H_ARG_98	NH1	H_ASP_103	OD2	2.704
4QHU	H_LYS_208	NZ	H_ASP_210	OD1	3.995
4QHU	A_LYS_30	NZ	A_ASP_91	OD2	4.000
4QHU	A_ARG_60	NH1	A_GLU_80	OE2	3.278
4QHU	A_ARG_60	NH1	A_ASP_81	OD1	2.573
4QHU	A_ARG_60	NH1	A_ASP_81	OD2	3.449
4QHU	A_LYS_104	NZ	A_ASP_84	OD1	3.029
4QHU	A_LYS_104	NZ	A_ASP_84	OD2	3.813
4QHU	A_LYS_168	NZ	A_GLU_82	OE1	3.026
4QHU	A_HIS_190	ND1	A_ASP_153	OD2	2.727
4QHU	A_ARG_191	NH1	A_ASP_153	OD1	3.616
4QHU	A_ARG_191	NH2	A_ASP_153	OD1	3.771
4QHU	A_ARG_191	NH2	A_ASP_153	OD2	3.954
4QHU	B_ARG_38	NH1	B_ASP_90	OD1	2.780
4QHU	B_ARG_38	NH2	B_GLU_46	OE1	3.193
4QHU	B_ARG_38	NH2	B_GLU_46	OE2	3.721
4QHU	B_ARG_38	NH2	B_ASP_90	OD1	3.946
4QHU	B_LYS_65	NZ	B_ASP_62	OD1	3.086
4QHU	B_ARG_67	NH1	B_ASP_90	OD1	3.968
4QHU	B_ARG_67	NH1	B_ASP_90	OD2	2.779
4QHU	B_ARG_67	NH2	B_ASP_90	OD1	3.132
4QHU	B_ARG_67	NH2	B_ASP_90	OD2	3.380
4QHU	B_ARG_98	NH2	B_ASP_103	OD1	3.608
4QHU	B_ARG_98	NH2	B_ASP_103	OD2	2.836
4QHU	B_LYS_145	NZ	A_GLU_126	OE2	2.821
4QHU	B_LYS_212	NZ	B_GLU_214	OE2	3.019
4QHU	C_ARG_20	NH2	C_ASP_15	OD1	3.523
4QHU	C_HIS_29	ND1	D_GLU_113	OE1	3.672
4QHU	C_ARG_31	NH1	D_GLU_113	OE2	3.297
4QHU	C_ARG_31	NH2	D_GLU_113	OE1	3.241
4QHU	C_ARG_31	NH2	D_GLU_113	OE2	3.844
4QHU	C_ARG_39	NH1	L_ASP_52	OD1	3.835
4QHU	C_ARG_39	NH1	L_ASP_52	OD2	2.646
4QHU	C_ARG_46	NH1	C_ASP_42	OD1	3.319

4QHU	C_ARG_55	NH1	L_ASP_49	OD1	2.860
4QHU	C_ARG_55	NH1	L_ASP_49	OD2	3.543
4QHU	C_ARG_55	NH1	C_GLU_57	OE2	3.286
4QHU	C_ARG_55	NH2	C_GLU_57	OE2	2.950
4QHU	C_HIS_86	ND1	C_ASP_84	OD1	2.680
4QHU	C_ARG_100	NH1	C_ASP_58	OD2	2.953
4QHU	C_ARG_100	NH2	C_ASP_58	OD1	3.928
4QHU	C_ARG_100	NH2	C_ASP_58	OD2	3.080
4QHU	C_ARG_111	NH1	C_GLU_102	OE2	2.856
4QHU	D_ARG_46	NH1	D_ASP_42	OD1	3.904
4QHU	D_ARG_55	NH1	D_GLU_57	OE1	2.360
4QHU	D_ARG_55	NH2	D_GLU_57	OE1	3.394
4QHU	D_HIS_86	ND1	D_ASP_84	OD1	2.832
4QHU	D_ARG_100	NH1	D_ASP_58	OD1	3.905
4QHU	D_ARG_100	NH1	D_ASP_58	OD2	3.109
4QHU	D_ARG_100	NH2	D_ASP_58	OD2	3.081
4QHU	D_ARG_100	NH2	D_GLU_113	OE2	3.668
4QHU	D_LYS_114	NZ	D_GLU_95	OE2	2.739

Table 610: 4QHU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4QTI	H_ARG_38	NH2	H_GLU_46	OE1	3.681
4QTI	H_ARG_38	NH2	H_GLU_46	OE2	2.663
4QTI	H_LYS_67	NZ	H_ASP_90	OD1	3.556
4QTI	H_LYS_67	NZ	H_ASP_90	OD2	2.827
4QTI	H_ARG_98	NH2	H_ASP_110	OD2	3.023
4QTI	H_LYS_217	NZ	L_GLU_123	OE2	2.684
4QTI	L_ARG_24	NH1	L_ASP_70	OD1	3.175
4QTI	L_ARG_24	NH1	L_ASP_70	OD2	2.707
4QTI	L_ARG_24	NH2	L_ASP_70	OD1	3.394
4QTI	L_ARG_24	NH2	L_ASP_70	OD2	3.619
4QTI	L_ARG_46	NH2	L_ASP_55	OD1	2.886
4QTI	L_ARG_46	NH2	L_ASP_55	OD2	3.715
4QTI	L_ARG_61	NH2	L_ASP_82	OD1	2.723
4QTI	L_ARG_61	NH2	L_ASP_82	OD2	3.112
4QTI	L_ARG_66	NH1	L_ASP_28	OD2	3.786
4QTI	L_LYS_103	NZ	L_GLU_105	OE1	2.889
4QTI	L_LYS_103	NZ	L_GLU_105	OE2	3.497
4QTI	L_LYS_147	NZ	L_GLU_154	OE1	3.641
4QTI	L_LYS_149	NZ	L_GLU_195	OE1	2.748
4QTI	L_ARG_188	NH2	L_ASP_184	OD1	3.219
4QTI	L_HIS_189	ND1	L_ASP_151	OD2	3.900
4QTI	L_LYS_199	NZ	L_ASP_110	OD2	3.524
4QTI	L_ARG_211	NH2	L_GLU_187	OE2	2.655
4QTI	U_ARG_2	NH1	U_GLU_16	OE1	3.772
4QTI	U_ARG_2	NH1	U_GLU_16	OE2	3.501
4QTI	U_ARG_25	NH2	U_GLU_42	OE2	3.368
4QTI	U_LYS_50	NZ	U_GLU_230	OE2	3.973
4QTI	U_ARG_53	NH1	U_ASP_254	OD2	3.882
4QTI	U_ARG_53	NH2	U_ASP_254	OD1	3.258
4QTI	U_ARG_58	NH2	H_ASP_103	OD2	2.819
4QTI	U_ARG_89	NH1	H_ASP_99	OD2	3.048
4QTI	U_ARG_91	NH1	H_ASP_99	OD1	2.759
4QTI	U_ARG_91	NH1	H_ASP_99	OD2	2.751
4QTI	U_ARG_91	NH2	H_ASP_99	OD2	3.786
4QTI	U_ARG_116	NH1	H_ASP_103	OD2	3.777
4QTI	U_ARG_116	NH2	H_ASP_103	OD1	3.889
4QTI	U_HIS_143	NE2	U_GLU_183	OE2	3.484
4QTI	U_LYS_175	NZ	U_GLU_94	OE2	2.662
4QTI	U_LYS_198	NZ	U_ASP_163	OD1	2.860
4QTI	U_LYS_198	NZ	U_ASP_163	OD2	3.382
4QTI	U_ARG_239	NH1	U_ASP_277	OD1	2.952
4QTI	U_ARG_239	NH1	U_ASP_277	OD2	3.438
4QTI	U_ARG_239	NH2	U_ASP_277	OD1	3.749
4QTI	U_ARG_239	NH2	U_ASP_277	OD2	2.737
4QTI	U_HIS_273	ND1	U_ASP_275	OD1	3.694
4QTI	U_HIS_273	ND1	U_ASP_275	OD2	3.712

Table 611: 4QTI-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4QXG	H_ARG_38	NH1	H_GLU_46	OE1	3.582
4QXG	H_ARG_38	NH1	H_GLU_46	OE2	3.109
4QXG	H_ARG_38	NH2	H_ASP_90	OD1	3.835
4QXG	H_LYS_87	NZ	H_ASP_90	OD1	2.584
4QXG	H_LYS_87	NZ	H_ASP_90	OD2	3.997
4QXG	H_ARG_98	NH2	H_ASP_100	OD2	3.302
4QXG	H_ARG_98	NH2	H_ASP_105	OD1	3.741
4QXG	H_ARG_98	NH2	H_ASP_105	OD2	2.750
4QXG	H_LYS_147	NZ	H_ASP_148	OD1	3.049
4QXG	H_LYS_147	NZ	H_ASP_148	OD2	3.141
4QXG	H_LYS_213	NZ	L_GLU_124	OE2	3.477
4QXG	L_ARG_24	NH2	L_ASP_71	OD2	3.349
4QXG	L_ARG_55	NH1	L_ASP_61	OD1	3.811
4QXG	L_ARG_55	NH2	L_ASP_61	OD1	3.150
4QXG	L_ARG_62	NH2	L_GLU_82	OE2	3.622
4QXG	L_ARG_62	NH2	L_ASP_83	OD1	2.986
4QXG	L_ARG_62	NH2	L_ASP_83	OD2	3.699
4QXG	L_LYS_150	NZ	L_GLU_196	OE1	2.605
4QXG	L_HIS_190	ND1	L_ASP_152	OD2	2.741
4QXG	L_LYS_191	NZ	L_GLU_214	OE1	3.615
4QXG	L_LYS_191	NZ	L_GLU_214	OE2	3.288

Table 612: 4QXG-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4R2G	E_LYS_121	NZ	E_GLU_429	OE2	2.858
4R2G	E_LYS_236	NZ	E_ASP_275	OD1	2.708
4R2G	E_HIS_249	NE2	E_GLU_482	OE1	3.748
4R2G	E_LYS_269	NZ	E_GLU_347	OE1	3.075
4R2G	E_ARG_298	NH1	E_GLU_381	OE1	3.375
4R2G	E_ARG_298	NH1	E_GLU_381	OE2	2.613
4R2G	E_LYS_348	NZ	E_GLU_351	OE1	3.563
4R2G	E_LYS_357	NZ	E_GLU_466	OE1	3.854
4R2G	E_ARG_456	NH1	E_GLU_466	OE1	3.060
4R2G	E_ARG_456	NH1	E_GLU_466	OE2	3.336
4R2G	E_ARG_469	NH2	E_ASP_457	OD2	2.761
4R2G	E_ARG_476	NH1	E_GLU_102	OE1	3.512
4R2G	E_ARG_476	NH1	E_GLU_102	OE2	3.993
4R2G	E_ARG_476	NH2	E_ASP_474	OD1	3.762
4R2G	E_ARG_476	NH2	E_ASP_474	OD2	3.245
4R2G	E_ARG_480	NH1	E_ASP_477	OD1	2.966
4R2G	F_LYS_8	NZ	F_GLU_119	OE1	2.961
4R2G	F_LYS_8	NZ	F_GLU_119	OE2	3.833
4R2G	F_LYS_29	NZ	E_ASP_279	OD2	2.979
4R2G	F_LYS_29	NZ	F_GLU_85	OE1	3.831
4R2G	F_ARG_54	NH1	F_ASP_78	OD1	3.678
4R2G	F_ARG_54	NH1	F_ASP_78	OD2	2.955
4R2G	F_ARG_54	NH2	F_ASP_78	OD1	3.395
4R2G	F_ARG_54	NH2	F_ASP_78	OD2	3.824
4R2G	F_ARG_58	NH1	F_GLU_13	OE1	3.679
4R2G	F_ARG_58	NH1	F_GLU_13	OE2	2.912
4R2G	F_ARG_58	NH2	F_GLU_13	OE2	3.429
4R2G	F_ARG_59	NH1	E_ASP_368	OD1	2.950
4R2G	F_ARG_59	NH1	E_ASP_368	OD2	2.577
4R2G	F_ARG_59	NH2	E_ASP_368	OD2	3.352
4R2G	F_LYS_90	NZ	F_GLU_85	OE2	3.878
4R2G	P_ARG_31	NH2	P_ASP_66A	OD1	3.703
4R2G	P_ARG_61	NH1	P_GLU_79	OE1	3.610
4R2G	P_ARG_61	NH1	P_ASP_82	OD1	2.724
4R2G	P_ARG_61	NH1	P_ASP_82	OD2	2.827
4R2G	P_ARG_61	NH2	P_ASP_82	OD2	2.747
4R2G	P_ARG_103	NH2	P_ASP_85	OD1	3.554
4R2G	P_ARG_103	NH2	P_ASP_85	OD2	3.072
4R2G	P_LYS_167	NZ	P_GLU_83	OE2	2.375
4R2G	Q_ARG_38	NH1	Q_ASP_86	OD1	2.531
4R2G	Q_ARG_38	NH2	Q_GLU_46	OE2	3.197
4R2G	Q_ARG_38	NH2	Q_ASP_86	OD1	3.417
4R2G	Q_ARG_66	NH1	Q_ASP_86	OD2	3.138
4R2G	Q_ARG_66	NH2	Q_ASP_86	OD1	3.109
4R2G	Q_ARG_66	NH2	Q_ASP_86	OD2	3.353
4R2G	Q_ARG_71	NH2	Q_GLU_55	OE1	2.657
4R2G	Q_ARG_96	NH1	Q_ASP_101	OD2	2.840
4R2G	Q_ARG_96	NH2	Q_ASP_101	OD1	3.076
4R2G	Q_ARG_96	NH2	Q_ASP_101	OD2	2.587
4R2G	Q_ARG_100	NH2	P_ASP_66A	OD2	2.815
4R2G	Q_LYS_227	NZ	P_GLU_124	OE2	3.083
4R2G	B_LYS_29	NZ	O_ASP_279	OD2	3.448
4R2G	B_ARG_54	NH1	B_ASP_78	OD1	2.279
4R2G	B_ARG_54	NH1	B_ASP_78	OD2	2.720
4R2G	B_ARG_54	NH2	B_ASP_78	OD1	3.403
4R2G	B_ARG_54	NH2	B_ASP_78	OD2	1.961
4R2G	B_ARG_58	NH1	B_GLU_13	OE2	3.274

4R2G	B_ARG_58	NH2	B_GLU_13	OE2	3.415
4R2G	B_ARG_59	NH1	O_ASP_368	OD1	2.838
4R2G	B_ARG_59	NH1	O_ASP_368	OD2	3.428
4R2G	B_ARG_59	NH2	O_ASP_368	OD1	3.471
4R2G	B_ARG_59	NH2	O_ASP_368	OD2	2.776
4R2G	B_ARG_134	NH1	B_ASP_153	OD1	3.163
4R2G	B_ARG_134	NH2	B_ASP_153	OD1	3.693
4R2G	C_ARG_31	NH1	C_ASP_66A	OD1	3.082
4R2G	C_ARG_54	NH1	C_GLU_60	OE2	3.362
4R2G	C_ARG_61	NH1	C_GLU_79	OE1	3.445
4R2G	C_ARG_61	NH1	C_ASP_82	OD1	3.443
4R2G	C_ARG_61	NH1	C_ASP_82	OD2	2.957
4R2G	C_ARG_61	NH2	C_ASP_82	OD2	3.224
4R2G	C_ARG_103	NH1	C_ASP_85	OD1	3.613
4R2G	C_ARG_103	NH2	C_ASP_85	OD2	3.803
4R2G	C_LYS_167	NZ	C_GLU_83	OE2	3.124
4R2G	C_HIS_189	ND1	C_ASP_152	OD1	3.916
4R2G	C_HIS_189	ND1	C_ASP_152	OD2	2.449
4R2G	D_ARG_13	NH2	D_GLU_16	OE1	3.234
4R2G	D_ARG_13	NH2	D_GLU_16	OE2	2.237
4R2G	D_ARG_38	NH1	D_ASP_86	OD1	2.671
4R2G	D_ARG_38	NH2	D_GLU_46	OE1	3.784
4R2G	D_ARG_38	NH2	D_GLU_46	OE2	3.013
4R2G	D_ARG_38	NH2	D_ASP_86	OD1	3.766
4R2G	D_ARG_66	NH1	D_ASP_86	OD1	3.577
4R2G	D_ARG_66	NH1	D_ASP_86	OD2	3.981
4R2G	D_ARG_66	NH2	D_ASP_86	OD1	3.085
4R2G	D_ARG_66	NH2	D_ASP_86	OD2	3.712
4R2G	D_ARG_71	NH2	D_GLU_55	OE1	2.726
4R2G	D_ARG_71	NH2	D_GLU_55	OE2	3.442
4R2G	D_ARG_96	NH1	D_ASP_101	OD2	3.369
4R2G	D_ARG_100	NH2	C_ASP_66A	OD2	3.131
4R2G	D_LYS_227	NZ	C_GLU_124	OE1	3.473
4R2G	D_LYS_227	NZ	C_GLU_124	OE2	3.405
4R2G	H_LYS_8	NZ	H_GLU_119	OE1	2.920
4R2G	H_LYS_8	NZ	H_GLU_119	OE2	3.405
4R2G	H_LYS_29	NZ	H_GLU_85	OE1	3.621
4R2G	H_LYS_29	NZ	H_GLU_85	OE2	3.077
4R2G	H_LYS_29	NZ	K_ASP_279	OD1	2.934
4R2G	H_LYS_46	NZ	H_ASP_56	OD2	3.403
4R2G	H_ARG_54	NH1	H_ASP_78	OD1	3.987
4R2G	H_ARG_54	NH1	H_ASP_78	OD2	2.782
4R2G	H_ARG_54	NH2	H_ASP_78	OD1	2.816
4R2G	H_ARG_54	NH2	H_ASP_78	OD2	3.143
4R2G	H_ARG_59	NH1	K_ASP_368	OD1	2.502
4R2G	H_ARG_59	NH1	K_ASP_368	OD2	3.259
4R2G	H_LYS_90	NZ	H_GLU_85	OE2	3.434
4R2G	H_LYS_171	NZ	H_GLU_169	OE1	3.154
4R2G	I_ARG_31	NH1	I_ASP_66A	OD1	3.172
4R2G	I_ARG_61	NH1	I_ASP_82	OD1	2.991
4R2G	I_ARG_61	NH1	I_ASP_82	OD2	3.035
4R2G	I_ARG_61	NH2	I_ASP_82	OD2	2.782
4R2G	I_ARG_103	NH1	I_ASP_85	OD1	2.492
4R2G	I_ARG_103	NH1	I_ASP_85	OD2	3.056
4R2G	I_ARG_103	NH2	I_ASP_85	OD1	3.464
4R2G	I_ARG_103	NH2	I_ASP_85	OD2	3.445
4R2G	I_LYS_167	NZ	I_GLU_83	OE1	3.520
4R2G	I_LYS_167	NZ	I_GLU_83	OE2	3.546

4R2G	I_HIS_189	ND1	I_ASP_152	OD2	3.243
4R2G	J_ARG_38	NH1	J_ASP_86	OD1	2.814
4R2G	J_ARG_38	NH2	J_GLU_46	OE1	3.964
4R2G	J_ARG_38	NH2	J_GLU_46	OE2	3.167
4R2G	J_ARG_38	NH2	J_ASP_86	OD1	3.659
4R2G	J_ARG_66	NH1	J_ASP_86	OD1	3.625
4R2G	J_ARG_66	NH1	J_ASP_86	OD2	3.378
4R2G	J_ARG_66	NH2	J_ASP_86	OD1	2.765
4R2G	J_ARG_66	NH2	J_ASP_86	OD2	3.353
4R2G	J_ARG_71	NH1	J_GLU_55	OE1	3.851
4R2G	J_ARG_96	NH2	J_ASP_101	OD1	3.956
4R2G	J_ARG_96	NH2	J_ASP_101	OD2	3.793
4R2G	J_ARG_100	NH2	I_ASP_66A	OD2	3.189
4R2G	J_LYS_161	NZ	I_GLU_125	OE2	3.537
4R2G	L_LYS_8	NZ	L_GLU_119	OE1	3.207
4R2G	L_LYS_29	NZ	L_GLU_85	OE2	3.720
4R2G	L_LYS_29	NZ	A_ASP_279	OD1	3.450
4R2G	L_ARG_54	NH1	L_ASP_78	OD1	3.725
4R2G	L_ARG_54	NH1	L_ASP_78	OD2	2.856
4R2G	L_ARG_54	NH2	L_ASP_78	OD1	3.320
4R2G	L_ARG_54	NH2	L_ASP_78	OD2	3.657
4R2G	L_ARG_59	NH1	A_ASP_368	OD1	2.642
4R2G	L_ARG_59	NH1	A_ASP_368	OD2	2.825
4R2G	L_ARG_59	NH2	A_ASP_368	OD1	3.793
4R2G	L_ARG_59	NH2	A_ASP_368	OD2	2.422
4R2G	L_LYS_90	NZ	L_GLU_85	OE1	3.363
4R2G	M_ARG_31	NH1	M_ASP_66A	OD1	2.301
4R2G	M_ARG_31	NH2	M_ASP_66A	OD1	3.968
4R2G	M_ARG_61	NH1	M_GLU_79	OE1	3.516
4R2G	M_ARG_61	NH1	M_ASP_82	OD1	3.186
4R2G	M_ARG_61	NH1	M_ASP_82	OD2	3.220
4R2G	M_ARG_61	NH2	M_ASP_82	OD1	3.607
4R2G	M_ARG_61	NH2	M_ASP_82	OD2	2.287
4R2G	M_ARG_103	NH2	M_ASP_85	OD1	3.750
4R2G	M_ARG_103	NH2	M_ASP_85	OD2	2.638
4R2G	M_LYS_167	NZ	M_GLU_83	OE2	3.138
4R2G	M_HIS_189	ND1	M_ASP_152	OD2	3.175
4R2G	M_LYS_190	NZ	M_ASP_152	OD1	3.703
4R2G	M_LYS_190	NZ	M_ASP_152	OD2	3.996
4R2G	N_ARG_38	NH1	N_ASP_86	OD1	2.735
4R2G	N_ARG_38	NH2	N_GLU_46	OE2	2.998
4R2G	N_ARG_38	NH2	N_ASP_86	OD1	3.645
4R2G	N_ARG_66	NH1	N_ASP_86	OD1	3.424
4R2G	N_ARG_66	NH1	N_ASP_86	OD2	3.369
4R2G	N_ARG_66	NH2	N_ASP_86	OD1	3.057
4R2G	N_ARG_66	NH2	N_ASP_86	OD2	3.652
4R2G	N_ARG_71	NH2	N_GLU_55	OE1	3.590
4R2G	N_ARG_71	NH2	N_GLU_55	OE2	2.787
4R2G	N_ARG_96	NH2	N_ASP_101	OD2	3.284
4R2G	N_ARG_100	NH2	M_ASP_66A	OD2	3.592
4R2G	N_LYS_161	NZ	M_GLU_125	OE2	2.706
4R2G	N_LYS_228	NZ	N_GLU_230	OE2	3.127
4R2G	O_LYS_121	NZ	O_ASP_113	OD1	3.734
4R2G	O_LYS_121	NZ	O_GLU_429	OE2	2.953
4R2G	O_LYS_231	NZ	O_GLU_267	OE1	3.348
4R2G	O_LYS_236	NZ	O_ASP_275	OD1	3.482
4R2G	O_HIS_249	NE2	O_GLU_482	OE1	3.152
4R2G	O_LYS_282	NZ	O_ASP_275	OD2	3.470

4R2G	O_ARG_298	NH1	O_GLU_381	OE1	3.809
4R2G	O_ARG_327	NH1	D_GLU_100I	OE2	3.858
4R2G	O_LYS_348	NZ	O_GLU_351	OE1	3.344
4R2G	O_LYS_348	NZ	O_GLU_351	OE2	3.244
4R2G	O_LYS_357	NZ	O_GLU_466	OE1	3.349
4R2G	O_LYS_400	NZ	O_ASP_397	OD2	3.952
4R2G	O_ARG_456	NH2	O_GLU_466	OE2	3.589
4R2G	O_ARG_469	NH2	O_ASP_457	OD1	3.913
4R2G	O_ARG_469	NH2	O_ASP_457	OD2	2.731
4R2G	O_ARG_476	NH1	O_ASP_474	OD1	3.974
4R2G	O_ARG_476	NH2	O_ASP_474	OD1	3.817
4R2G	O_ARG_476	NH2	O_ASP_474	OD2	3.016
4R2G	O_ARG_480	NH1	O_ASP_477	OD1	3.400
4R2G	A_LYS_121	NZ	A_ASP_113	OD1	3.373
4R2G	A_LYS_236	NZ	A_ASP_275	OD1	3.935
4R2G	A_LYS_236	NZ	A_ASP_275	OD2	3.895
4R2G	A_ARG_298	NH2	A_GLU_381	OE2	3.354
4R2G	A_ARG_327	NH1	N_GLU_100I	OE1	3.235
4R2G	A_LYS_348	NZ	A_GLU_351	OE1	3.114
4R2G	A_LYS_348	NZ	A_GLU_351	OE2	3.018
4R2G	A_LYS_357	NZ	A_GLU_466	OE1	3.762
4R2G	A_ARG_456	NH2	A_GLU_466	OE1	3.604
4R2G	A_ARG_456	NH2	A_GLU_466	OE2	3.481
4R2G	A_ARG_469	NH2	A_ASP_457	OD2	3.008
4R2G	A_ARG_476	NH2	A_ASP_474	OD2	3.246
4R2G	A_ARG_480	NH1	A_ASP_477	OD1	3.318
4R2G	K_LYS_121	NZ	K_GLU_429	OE2	2.599
4R2G	K_LYS_236	NZ	K_ASP_275	OD1	3.419
4R2G	K_HIS_249	NE2	K_GLU_482	OE1	3.520
4R2G	K_ARG_298	NH1	K_GLU_381	OE2	3.970
4R2G	K_ARG_298	NH2	K_GLU_381	OE2	3.778
4R2G	K_LYS_348	NZ	K_GLU_351	OE1	3.371
4R2G	K_LYS_348	NZ	K_GLU_351	OE2	3.265
4R2G	K_ARG_350	NH2	K_ASP_397	OD1	3.693
4R2G	K_LYS_357	NZ	K_GLU_466	OE2	3.015
4R2G	K_ARG_469	NH2	K_ASP_457	OD2	3.592
4R2G	K_ARG_476	NH1	K_ASP_474	OD2	3.916
4R2G	K_ARG_476	NH2	K_ASP_474	OD2	3.188
4R2G	K_ARG_480	NH1	K_ASP_477	OD1	2.647
4R2G	K_LYS_487	NZ	K_ASP_92	OD1	3.177

Table 613: 4R2G-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4R4H	A_HIS_66	ND1	A_GLU_64	OE1	3.252
4R4H	A_LYS_207	NZ	A_GLU_380	OE1	3.742
4R4H	A_LYS_207	NZ	A_GLU_380	OE2	3.215
4R4H	A_HIS_249	NE2	A_GLU_482	OE1	2.873
4R4H	A_LYS_348	NZ	A_ASP_269	OD2	3.101
4R4H	A_LYS_348	NZ	A_GLU_351	OE1	3.859
4R4H	A_LYS_356	NZ	A_GLU_466	OE2	2.887
4R4H	A_ARG_455	NH1	A_GLU_466	OE1	3.185
4R4H	A_ARG_455	NH1	A_GLU_466	OE2	3.399
4R4H	A_ARG_469	NH2	A_ASP_456	OD2	3.413
4R4H	A_ARG_476	NH1	A_ASP_474	OD1	3.458
4R4H	A_ARG_480	NH1	A_ASP_477	OD1	2.787
4R4H	A_LYS_487	NZ	A_GLU_47	OE2	3.588
4R4H	A_LYS_487	NZ	A_GLU_91	OE2	2.837
4R4H	B_LYS_7	NZ	B_ASP_10	OD2	3.666
4R4H	B_LYS_29	NZ	A_ASP_279	OD1	2.795
4R4H	B_LYS_29	NZ	B_GLU_85	OE1	3.423
4R4H	B_LYS_29	NZ	B_GLU_85	OE2	3.572
4R4H	B_ARG_54	NH1	B_ASP_78	OD2	2.980
4R4H	B_ARG_54	NH2	B_ASP_78	OD1	3.209
4R4H	B_ARG_54	NH2	B_ASP_78	OD2	3.205
4R4H	B_ARG_58	NH1	B_GLU_13	OE1	3.001
4R4H	B_ARG_58	NH1	B_GLU_13	OE2	3.359
4R4H	B_ARG_58	NH2	B_GLU_13	OE2	3.123
4R4H	B_ARG_59	NH1	A_ASP_367	OD1	3.294
4R4H	B_ARG_59	NH1	A_ASP_367	OD2	3.409
4R4H	B_ARG_59	NH2	A_ASP_367	OD2	3.834
4R4H	B_LYS_171	NZ	B_GLU_169	OE1	3.963
4R4H	B_LYS_171	NZ	B_GLU_169	OE2	3.179
4R4H	L_ARG_61	NH2	L_GLU_81	OE2	2.783
4R4H	L_ARG_61	NH2	L_ASP_82	OD1	3.470
4R4H	L_LYS_	NZ	L_GLU_	OE1	2.933
4R4H	L_HIS_	ND1	L_ASP_	OD2	2.805
4R4H	L_HIS_	NE2	L_ASP_	OD1	3.352
4R4H	H_HIS_32	ND1	H_GLU_27	OE2	3.036
4R4H	H_HIS_32	NE2	H_GLU_27	OE2	3.485
4R4H	H_ARG_38	NH1	H_ASP_89	OD1	3.491
4R4H	H_ARG_38	NH2	H_GLU_46	OE1	3.502
4R4H	H_ARG_38	NH2	H_GLU_46	OE2	3.452
4R4H	H_LYS_52	NZ	A_ASP_78	OD1	3.615
4R4H	H_ARG_66	NH1	H_ASP_89	OD2	3.497
4R4H	H_ARG_66	NH2	H_ASP_89	OD1	3.408
4R4H	H_ARG_66	NH2	H_ASP_89	OD2	3.604
4R4H	H_LYS_75	NZ	H_ASP_72	OD2	3.924
4R4H	H_ARG_97	NH1	H_GLU_27	OE1	2.972
4R4H	H_ARG_97	NH1	H_GLU_27	OE2	2.769
4R4H	H_ARG_98	NH1	H_GLU_50	OE1	3.064
4R4H	H_ARG_98	NH1	H_GLU_50	OE2	3.007
4R4H	H_LYS_	NZ	H_ASP_	OD1	2.850
4R4H	H_LYS_	NZ	H_ASP_	OD2	3.439
4R4H	H_LYS_	NZ	H_GLU_	OE2	3.585
4R4H	H_LYS_	NZ	L_ASP_	OD2	3.470

Table 614: 4R4H-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4R7D	A_ARG_39	NH1	A_ASP_90	OD1	2.757
4R7D	A_ARG_39	NH2	A_GLU_47	OE1	3.609
4R7D	A_ARG_39	NH2	A_GLU_47	OE2	3.143
4R7D	A_ARG_39	NH2	A_ASP_90	OD1	3.533
4R7D	A_LYS_65	NZ	A_ASP_59	OD1	3.382
4R7D	A_ARG_67	NH1	A_ASP_90	OD2	3.363
4R7D	A_ARG_67	NH2	A_ASP_90	OD1	3.104
4R7D	A_ARG_67	NH2	A_ASP_90	OD2	3.445
4R7D	A_LYS_76	NZ	A_ASP_73	OD2	3.850
4R7D	A_LYS_148	NZ	A_ASP_149	OD1	3.326
4R7D	A_LYS_148	NZ	A_ASP_149	OD2	3.734
4R7D	A_LYS_214	NZ	B_GLU_123	OE1	3.736
4R7D	B_ARG_61	NH1	B_GLU_81	OE1	3.280
4R7D	B_ARG_61	NH1	B_ASP_82	OD1	2.669
4R7D	B_ARG_61	NH1	B_ASP_82	OD2	3.082
4R7D	B_ARG_61	NH2	B_GLU_81	OE1	3.146
4R7D	B_LYS_107	NZ	D_ASP_9	OD2	3.947
4R7D	B_LYS_126	NZ	B_ASP_122	OD1	2.338
4R7D	B_ARG_142	NH1	B_GLU_143	OE1	3.636
4R7D	B_ARG_142	NH2	B_GLU_105	OE1	3.989
4R7D	B_LYS_149	NZ	B_GLU_195	OE1	3.373
4R7D	B_LYS_149	NZ	B_GLU_195	OE2	3.135
4R7D	B_HIS_189	ND1	B_ASP_151	OD2	2.870
4R7D	C_ARG_39	NH1	C_ASP_90	OD1	2.627
4R7D	C_ARG_39	NH2	C_GLU_47	OE2	3.405
4R7D	C_ARG_39	NH2	C_ASP_90	OD1	3.918
4R7D	C_ARG_67	NH1	C_ASP_90	OD1	3.705
4R7D	C_ARG_67	NH1	C_ASP_90	OD2	3.301
4R7D	C_ARG_67	NH2	C_ASP_90	OD1	3.685
4R7D	C_LYS_99	NZ	C_ASP_103	OD2	3.216
4R7D	C_LYS_148	NZ	C_ASP_149	OD1	3.368
4R7D	C_LYS_211	NZ	C_ASP_213	OD1	2.945
4R7D	D_LYS_18	NZ	B_ASP_70	OD2	3.792
4R7D	D_HIS_32	NE2	D_ASP_31	OD1	3.817
4R7D	D_ARG_61	NH2	D_ASP_82	OD1	2.539
4R7D	D_ARG_61	NH2	D_ASP_82	OD2	3.670
4R7D	D_LYS_103	NZ	D_GLU_165	OE1	3.985
4R7D	D_LYS_107	NZ	B_ASP_9	OD2	3.503
4R7D	D_HIS_189	ND1	D_ASP_151	OD2	2.473
4R7D	E_ARG_39	NH1	E_ASP_90	OD1	2.896
4R7D	E_ARG_39	NH2	E_GLU_47	OE1	3.759
4R7D	E_ARG_39	NH2	E_GLU_47	OE2	3.092
4R7D	E_ARG_67	NH1	E_ASP_90	OD1	3.553
4R7D	E_ARG_67	NH1	E_ASP_90	OD2	3.603
4R7D	E_ARG_67	NH2	E_ASP_90	OD1	3.329
4R7D	E_ARG_67	NH2	E_ASP_90	OD2	3.799
4R7D	E_LYS_76	NZ	E_ASP_73	OD2	3.684
4R7D	E_LYS_148	NZ	E_ASP_149	OD2	2.850
4R7D	E_LYS_214	NZ	F_GLU_123	OE1	3.862
4R7D	E_LYS_214	NZ	F_GLU_123	OE2	3.571
4R7D	E_ARG_215	NH1	E_GLU_217	OE1	3.936
4R7D	E_ARG_215	NH1	E_GLU_217	OE2	3.249
4R7D	E_ARG_215	NH2	E_GLU_217	OE1	2.728
4R7D	E_ARG_215	NH2	E_GLU_217	OE2	3.501
4R7D	F_LYS_16	NZ	F_GLU_79	OE2	3.230
4R7D	F_HIS_32	NE2	F_ASP_31	OD1	3.921
4R7D	F_ARG_61	NH2	F_ASP_82	OD1	2.326

4R7D	F_ARG_61	NH2	F_ASP_82	OD2	2.732
4R7D	F_LYS_103	NZ	F_GLU_165	OE1	3.918
4R7D	F_LYS_103	NZ	F_GLU_165	OE2	3.931
4R7D	F_LYS_149	NZ	F_GLU_195	OE1	3.595
4R7D	F_LYS_149	NZ	F_GLU_195	OE2	3.164
4R7D	F_LYS_169	NZ	F_GLU_81	OE2	3.685
4R7D	G_ARG_39	NH1	G_ASP_90	OD1	2.853
4R7D	G_ARG_39	NH2	G_GLU_47	OE2	2.958
4R7D	G_ARG_39	NH2	G_ASP_90	OD1	3.467
4R7D	G_LYS_65	NZ	G_ASP_59	OD1	3.423
4R7D	G_ARG_67	NH1	G_ASP_90	OD1	3.986
4R7D	G_ARG_67	NH1	G_ASP_90	OD2	3.243
4R7D	G_ARG_67	NH2	G_ASP_90	OD1	2.698
4R7D	G_ARG_67	NH2	G_ASP_90	OD2	3.350
4R7D	G_LYS_99	NZ	G_ASP_103	OD2	3.638
4R7D	G_LYS_148	NZ	G_ASP_149	OD2	2.977
4R7D	H_HIS_32	NE2	H_ASP_31	OD1	3.837
4R7D	H_ARG_61	NH1	H_GLU_79	OE1	3.684
4R7D	H_ARG_61	NH2	H_GLU_81	OE1	3.325
4R7D	H_ARG_61	NH2	H_ASP_82	OD1	2.892
4R7D	H_ARG_61	NH2	H_ASP_82	OD2	3.435
4R7D	H_LYS_126	NZ	H_ASP_122	OD2	3.954
4R7D	H_ARG_142	NH1	H_GLU_143	OE1	3.953
4R7D	H_ARG_142	NH2	H_GLU_105	OE2	3.620
4R7D	H_LYS_149	NZ	H_GLU_195	OE2	2.396
4R7D	H_LYS_183	NZ	H_GLU_187	OE2	3.853
4R7D	H_LYS_188	NZ	H_ASP_185	OD1	3.959
4R7D	H_HIS_189	ND1	H_ASP_151	OD2	2.743
4R7D	I_ARG_39	NH1	I_ASP_90	OD1	2.779
4R7D	I_ARG_39	NH2	I_GLU_47	OE2	3.308
4R7D	I_ARG_39	NH2	I_ASP_90	OD1	3.305
4R7D	I_LYS_65	NZ	I_ASP_59	OD1	3.650
4R7D	I_ARG_67	NH1	I_ASP_90	OD2	3.228
4R7D	I_ARG_67	NH2	I_ASP_90	OD1	2.929
4R7D	I_ARG_67	NH2	I_ASP_90	OD2	3.207
4R7D	I_HIS_169	NE2	J_ASP_167	OD1	3.970
4R7D	I_LYS_211	NZ	I_ASP_213	OD1	3.549
4R7D	J_LYS_16	NZ	J_GLU_79	OE2	3.737
4R7D	J_LYS_18	NZ	N_ASP_70	OD1	3.913
4R7D	J_ARG_24	NH2	N_GLU_17	OE1	3.275
4R7D	J_ARG_24	NH2	N_GLU_17	OE2	2.135
4R7D	J_ARG_61	NH1	J_GLU_79	OE1	3.344
4R7D	J_ARG_61	NH1	J_GLU_79	OE2	3.871
4R7D	J_ARG_61	NH2	J_GLU_81	OE1	3.710
4R7D	J_ARG_61	NH2	J_ASP_82	OD1	3.792
4R7D	J_HIS_189	ND1	J_ASP_151	OD2	3.674
4R7D	K_ARG_39	NH1	K_ASP_90	OD1	3.019
4R7D	K_ARG_39	NH2	K_GLU_47	OE1	3.928
4R7D	K_ARG_39	NH2	K_GLU_47	OE2	3.206
4R7D	K_ARG_39	NH2	K_ASP_90	OD1	3.749
4R7D	K_ARG_67	NH1	K_ASP_90	OD1	3.223
4R7D	K_ARG_67	NH1	K_ASP_90	OD2	3.237
4R7D	K_ARG_67	NH2	K_ASP_90	OD1	3.233
4R7D	K_LYS_76	NZ	K_ASP_73	OD2	3.794
4R7D	K_LYS_99	NZ	K_ASP_103	OD1	2.821
4R7D	K_LYS_148	NZ	K_ASP_149	OD2	3.160
4R7D	K_HIS_169	NE2	L_ASP_167	OD2	3.666
4R7D	K_LYS_214	NZ	L_GLU_123	OE1	3.074

4R7D	L_HIS_32	NE2	L_ASP_31	OD1	3.658
4R7D	L_LYS_49	NZ	K_ASP_100	OD2	3.591
4R7D	L_ARG_61	NH2	L_GLU_79	OE1	3.885
4R7D	L_ARG_61	NH2	L_GLU_79	OE2	3.873
4R7D	L_LYS_149	NZ	L_GLU_195	OE1	3.728
4R7D	L_LYS_149	NZ	L_GLU_195	OE2	3.660
4R7D	L_LYS_188	NZ	L_ASP_185	OD1	3.757
4R7D	L_HIS_189	ND1	L_ASP_151	OD2	2.882
4R7D	M_ARG_39	NH1	M_ASP_90	OD1	2.741
4R7D	M_ARG_39	NH2	M_GLU_47	OE2	3.151
4R7D	M_ARG_39	NH2	M_ASP_90	OD1	3.559
4R7D	M_LYS_65	NZ	M_ASP_59	OD1	3.528
4R7D	M_ARG_67	NH1	M_ASP_90	OD2	3.446
4R7D	M_ARG_67	NH2	M_ASP_90	OD1	3.853
4R7D	M_LYS_76	NZ	M_ASP_73	OD2	3.604
4R7D	M_LYS_99	NZ	M_ASP_103	OD2	2.528
4R7D	M_LYS_148	NZ	M_ASP_149	OD1	3.371
4R7D	M_LYS_211	NZ	M_ASP_213	OD1	3.991
4R7D	M_LYS_214	NZ	N_GLU_123	OE1	3.058
4R7D	M_LYS_214	NZ	N_GLU_123	OE2	2.866
4R7D	M_ARG_215	NH2	M_GLU_217	OE1	3.754
4R7D	N_ARG_61	NH1	N_GLU_79	OE1	3.461
4R7D	N_LYS_103	NZ	N_GLU_165	OE1	3.691
4R7D	N_LYS_107	NZ	J_ASP_9	OD2	3.244
4R7D	N_LYS_149	NZ	N_GLU_195	OE1	3.733
4R7D	N_LYS_149	NZ	N_GLU_195	OE2	3.015
4R7D	N_HIS_189	ND1	N_ASP_151	OD2	2.626
4R7D	O_ARG_39	NH1	O_ASP_90	OD1	2.621
4R7D	O_ARG_39	NH2	O_GLU_47	OE2	2.902
4R7D	O_ARG_39	NH2	O_ASP_90	OD1	3.952
4R7D	O_ARG_67	NH1	O_ASP_90	OD2	3.648
4R7D	O_ARG_67	NH2	O_ASP_90	OD1	2.490
4R7D	O_ARG_67	NH2	O_ASP_90	OD2	2.748
4R7D	O_LYS_76	NZ	O_ASP_73	OD2	3.837
4R7D	O_LYS_214	NZ	P_GLU_123	OE1	2.454
4R7D	O_LYS_214	NZ	P_GLU_123	OE2	3.167
4R7D	O_ARG_215	NH1	O_GLU_217	OE1	2.819
4R7D	O_ARG_215	NH1	O_GLU_217	OE2	2.975
4R7D	O_ARG_215	NH2	O_GLU_217	OE1	3.432
4R7D	P_LYS_16	NZ	P_GLU_79	OE2	3.343
4R7D	P_ARG_61	NH2	P_ASP_82	OD1	2.934
4R7D	P_ARG_61	NH2	P_ASP_82	OD2	3.314
4R7D	P_ARG_142	NH1	P_GLU_143	OE1	3.551
4R7D	P_ARG_142	NH2	P_GLU_105	OE1	3.275
4R7D	P_ARG_142	NH2	P_GLU_105	OE2	3.523
4R7D	P_LYS_149	NZ	P_GLU_195	OE1	3.907
4R7D	P_LYS_149	NZ	P_GLU_195	OE2	2.589
4R7D	P_HIS_189	ND1	P_ASP_151	OD2	3.283

Table 615: 4R7D-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4R7N	A_ARG_39	NH1	A_ASP_90	OD1	2.825
4R7N	A_ARG_39	NH2	A_GLU_47	OE2	3.023
4R7N	A_ARG_39	NH2	A_ASP_90	OD1	3.603
4R7N	A_ARG_67	NH1	A_ASP_90	OD1	3.650
4R7N	A_ARG_67	NH1	A_ASP_90	OD2	2.898
4R7N	A_ARG_67	NH2	A_ASP_90	OD1	3.091
4R7N	A_ARG_67	NH2	A_ASP_90	OD2	3.794
4R7N	A_ARG_98	NH1	A_ASP_100	OD2	3.775
4R7N	A_ARG_98	NH2	A_ASP_100	OD2	2.512
4R7N	A_LYS_148	NZ	A_ASP_149	OD1	2.897
4R7N	A_LYS_148	NZ	A_ASP_149	OD2	2.755
4R7N	A_LYS_214	NZ	B_GLU_123	OE1	3.674
4R7N	A_LYS_214	NZ	B_GLU_123	OE2	3.683
4R7N	B_LYS_16	NZ	B_GLU_79	OE1	3.765
4R7N	B_LYS_16	NZ	B_GLU_79	OE2	3.236
4R7N	B_ARG_24	NH2	J_GLU_17	OE1	3.625
4R7N	B_ARG_24	NH2	J_GLU_17	OE2	2.355
4R7N	B_ARG_61	NH1	B_GLU_81	OE1	3.359
4R7N	B_ARG_61	NH2	B_GLU_81	OE1	3.738
4R7N	B_ARG_61	NH2	B_ASP_82	OD1	2.397
4R7N	B_ARG_61	NH2	B_ASP_82	OD2	3.170
4R7N	B_LYS_103	NZ	B_GLU_165	OE1	3.820
4R7N	B_LYS_107	NZ	J_ASP_9	OD2	3.605
4R7N	B_LYS_149	NZ	B_GLU_195	OE2	2.745
4R7N	C_ARG_39	NH1	C_ASP_90	OD1	2.845
4R7N	C_ARG_39	NH2	C_GLU_47	OE2	2.963
4R7N	C_ARG_39	NH2	C_ASP_90	OD1	3.701
4R7N	C_ARG_67	NH1	C_ASP_90	OD1	3.078
4R7N	C_ARG_67	NH1	C_ASP_90	OD2	2.222
4R7N	C_ARG_67	NH2	C_ASP_90	OD1	2.771
4R7N	C_ARG_67	NH2	C_ASP_90	OD2	3.580
4R7N	C_LYS_76	NZ	C_ASP_73	OD2	2.761
4R7N	C_ARG_98	NH2	C_ASP_100	OD2	3.773
4R7N	C_LYS_211	NZ	C_ASP_213	OD1	3.637
4R7N	C_LYS_214	NZ	D_GLU_123	OE1	2.537
4R7N	C_LYS_214	NZ	D_GLU_123	OE2	3.321
4R7N	C_ARG_215	NH1	C_GLU_217	OE2	3.613
4R7N	C_ARG_215	NH2	C_GLU_217	OE1	3.821
4R7N	C_ARG_215	NH2	C_GLU_217	OE2	3.518
4R7N	D_ARG_24	NH2	F_GLU_17	OE1	3.787
4R7N	D_ARG_24	NH2	F_GLU_17	OE2	2.414
4R7N	D_ARG_61	NH1	D_GLU_81	OE1	3.464
4R7N	D_ARG_61	NH1	D_ASP_82	OD1	2.853
4R7N	D_ARG_61	NH1	D_ASP_82	OD2	3.611
4R7N	D_ARG_61	NH2	D_GLU_81	OE1	3.128
4R7N	D_LYS_103	NZ	D_GLU_165	OE1	3.770
4R7N	D_LYS_107	NZ	F_ASP_9	OD2	3.633
4R7N	D_LYS_149	NZ	D_GLU_195	OE2	3.176
4R7N	D_HIS_189	ND1	D_ASP_151	OD2	3.153
4R7N	E_ARG_39	NH1	E_ASP_90	OD1	2.803
4R7N	E_ARG_39	NH2	E_GLU_47	OE1	3.978
4R7N	E_ARG_39	NH2	E_GLU_47	OE2	3.076
4R7N	E_ARG_39	NH2	E_ASP_90	OD1	3.735
4R7N	E_LYS_65	NZ	E_ASP_59	OD1	3.735
4R7N	E_ARG_67	NH1	E_ASP_90	OD1	3.124
4R7N	E_ARG_67	NH1	E_ASP_90	OD2	3.240
4R7N	E_ARG_98	NH1	E_ASP_100	OD2	3.090

4R7N	E_ARG_98	NH2	E_ASP_100	OD2	2.869
4R7N	E_HIS_169	NE2	F_ASP_167	OD1	3.616
4R7N	E_HIS_169	NE2	F_ASP_167	OD2	3.474
4R7N	E_LYS_214	NZ	F_GLU_123	OE2	3.072
4R7N	F_LYS_16	NZ	F_GLU_79	OE1	3.193
4R7N	F_LYS_16	NZ	F_GLU_79	OE2	2.766
4R7N	F_ARG_24	NH2	D_GLU_17	OE1	3.696
4R7N	F_ARG_24	NH2	D_GLU_17	OE2	2.325
4R7N	F_ARG_61	NH2	F_GLU_81	OE2	3.726
4R7N	F_ARG_61	NH2	F_ASP_82	OD1	2.275
4R7N	F_ARG_61	NH2	F_ASP_82	OD2	3.114
4R7N	F_LYS_103	NZ	F_GLU_165	OE1	3.429
4R7N	F_LYS_107	NZ	D_ASP_9	OD2	3.641
4R7N	F_ARG_142	NH1	F_GLU_143	OE1	3.991
4R7N	F_ARG_142	NH2	F_GLU_105	OE1	3.315
4R7N	F_LYS_149	NZ	F_GLU_195	OE1	3.479
4R7N	F_LYS_149	NZ	F_GLU_195	OE2	2.946
4R7N	G_ARG_39	NH1	G_ASP_90	OD1	2.781
4R7N	G_ARG_39	NH2	G_GLU_47	OE1	3.904
4R7N	G_ARG_39	NH2	G_GLU_47	OE2	2.981
4R7N	G_ARG_39	NH2	G_ASP_90	OD1	3.571
4R7N	G_LYS_65	NZ	G_ASP_59	OD1	3.786
4R7N	G_ARG_67	NH1	G_ASP_90	OD1	3.700
4R7N	G_ARG_67	NH1	G_ASP_90	OD2	2.751
4R7N	G_ARG_67	NH2	G_ASP_90	OD1	3.048
4R7N	G_ARG_67	NH2	G_ASP_90	OD2	3.620
4R7N	G_ARG_98	NH1	G_ASP_100	OD1	3.954
4R7N	G_ARG_98	NH1	G_ASP_100	OD2	2.296
4R7N	G_ARG_98	NH2	G_ASP_100	OD2	3.918
4R7N	G_LYS_214	NZ	H_GLU_123	OE1	2.389
4R7N	G_LYS_214	NZ	H_GLU_123	OE2	3.440
4R7N	G_ARG_215	NH2	G_GLU_217	OE2	3.692
4R7N	H_LYS_16	NZ	H_GLU_79	OE1	3.784
4R7N	H_LYS_16	NZ	H_GLU_79	OE2	3.778
4R7N	H_ARG_24	NH2	L_GLU_17	OE1	3.413
4R7N	H_ARG_24	NH2	L_GLU_17	OE2	2.312
4R7N	H_ARG_61	NH1	H_GLU_81	OE1	3.674
4R7N	H_ARG_61	NH1	H_ASP_82	OD1	2.998
4R7N	H_ARG_61	NH1	H_ASP_82	OD2	3.659
4R7N	H_ARG_61	NH2	H_GLU_81	OE1	3.398
4R7N	H_LYS_103	NZ	H_GLU_165	OE1	3.531
4R7N	H_LYS_149	NZ	H_GLU_195	OE2	2.677
4R7N	I_ARG_39	NH1	I_ASP_90	OD1	2.559
4R7N	I_ARG_39	NH2	I_GLU_47	OE2	3.220
4R7N	I_ARG_39	NH2	I_ASP_90	OD1	3.236
4R7N	I_ARG_67	NH1	I_ASP_90	OD1	3.787
4R7N	I_ARG_67	NH1	I_ASP_90	OD2	2.994
4R7N	I_ARG_67	NH2	I_ASP_90	OD1	2.852
4R7N	I_ARG_67	NH2	I_ASP_90	OD2	3.576
4R7N	I_ARG_98	NH1	I_ASP_100	OD2	3.172
4R7N	I_ARG_98	NH2	I_ASP_100	OD2	3.171
4R7N	I_LYS_214	NZ	J_GLU_123	OE1	3.635
4R7N	I_LYS_214	NZ	J_GLU_123	OE2	2.942
4R7N	J_ARG_24	NH2	B_GLU_17	OE1	3.555
4R7N	J_ARG_24	NH2	B_GLU_17	OE2	2.304
4R7N	J_ARG_61	NH1	J_ASP_82	OD1	2.881
4R7N	J_ARG_61	NH1	J_ASP_82	OD2	2.940
4R7N	J_ARG_142	NH2	J_GLU_105	OE1	3.516

4R7N	J_LYS_149	NZ	J_GLU_195	OE1	2.936
4R7N	K_ARG_39	NH1	K_ASP_90	OD1	2.585
4R7N	K_ARG_39	NH2	K_GLU_47	OE2	3.296
4R7N	K_ARG_39	NH2	K_ASP_90	OD1	3.354
4R7N	K_ARG_67	NH1	K_ASP_90	OD1	3.756
4R7N	K_ARG_67	NH1	K_ASP_90	OD2	2.865
4R7N	K_ARG_67	NH2	K_ASP_90	OD1	3.074
4R7N	K_ARG_67	NH2	K_ASP_90	OD2	3.668
4R7N	K_ARG_98	NH2	K_ASP_100	OD2	3.706
4R7N	K_LYS_148	NZ	K_ASP_149	OD1	2.955
4R7N	K_LYS_148	NZ	K_ASP_149	OD2	2.836
4R7N	K_LYS_214	NZ	L_GLU_123	OE2	3.794
4R7N	K_ARG_215	NH2	K_GLU_217	OE2	2.789
4R7N	L_LYS_16	NZ	L_GLU_79	OE1	3.348
4R7N	L_LYS_16	NZ	L_GLU_79	OE2	3.110
4R7N	L_ARG_24	NH2	H_GLU_17	OE1	3.531
4R7N	L_ARG_24	NH2	H_GLU_17	OE2	2.313
4R7N	L_ARG_61	NH1	L_ASP_82	OD1	3.398
4R7N	L_ARG_61	NH1	L_ASP_82	OD2	2.327
4R7N	L_ARG_61	NH2	L_ASP_82	OD1	2.642
4R7N	L_ARG_61	NH2	L_ASP_82	OD2	3.265
4R7N	L_LYS_103	NZ	L_GLU_165	OE1	3.773
4R7N	L_LYS_149	NZ	L_GLU_195	OE1	3.879
4R7N	L_LYS_149	NZ	L_GLU_195	OE2	3.013
4R7N	M_ARG_39	NH1	M_ASP_90	OD1	2.831
4R7N	M_ARG_39	NH2	M_GLU_47	OE2	3.008
4R7N	M_ARG_39	NH2	M_ASP_90	OD1	3.609
4R7N	M_ARG_67	NH1	M_ASP_90	OD2	3.507
4R7N	M_ARG_67	NH2	M_ASP_90	OD1	3.326
4R7N	M_ARG_67	NH2	M_ASP_90	OD2	3.775
4R7N	M_LYS_76	NZ	M_ASP_73	OD1	3.417
4R7N	M_LYS_76	NZ	M_ASP_73	OD2	3.788
4R7N	M_ARG_98	NH1	M_ASP_100	OD2	2.760
4R7N	M_ARG_98	NH2	M_ASP_100	OD2	2.685
4R7N	M_LYS_148	NZ	M_ASP_149	OD1	2.958
4R7N	M_LYS_148	NZ	M_ASP_149	OD2	2.802
4R7N	N_ARG_24	NH2	P_GLU_17	OE1	3.814
4R7N	N_ARG_24	NH2	P_GLU_17	OE2	2.289
4R7N	N_ARG_61	NH1	N_GLU_79	OE1	2.882
4R7N	N_ARG_61	NH1	N_ASP_82	OD1	2.547
4R7N	N_ARG_61	NH1	N_ASP_82	OD2	3.212
4R7N	N_ARG_61	NH2	N_GLU_79	OE1	3.252
4R7N	N_LYS_103	NZ	N_GLU_165	OE1	3.332
4R7N	N_LYS_107	NZ	P_ASP_9	OD2	3.591
4R7N	N_LYS_149	NZ	N_GLU_195	OE1	2.916
4R7N	N_HIS_189	ND1	N_ASP_151	OD2	2.809
4R7N	N_LYS_190	NZ	N_GLU_187	OE1	3.890
4R7N	O_ARG_39	NH1	O_ASP_90	OD1	2.710
4R7N	O_ARG_39	NH2	O_GLU_47	OE1	3.778
4R7N	O_ARG_39	NH2	O_GLU_47	OE2	2.955
4R7N	O_ARG_39	NH2	O_ASP_90	OD1	3.975
4R7N	O_ARG_67	NH1	O_ASP_90	OD1	3.623
4R7N	O_ARG_67	NH1	O_ASP_90	OD2	2.994
4R7N	O_ARG_67	NH2	O_ASP_90	OD1	3.294
4R7N	O_ARG_98	NH2	O_ASP_100	OD2	3.721
4R7N	O_HIS_169	NE2	P_ASP_167	OD2	3.725
4R7N	P_ARG_24	NH2	N_GLU_17	OE1	3.525
4R7N	P_ARG_24	NH2	N_GLU_17	OE2	2.277

4R7N	P_ARG_61	NH1	P_GLU_79	OE1	2.179
4R7N	P_ARG_61	NH1	P_GLU_79	OE2	3.956
4R7N	P_ARG_61	NH2	P_GLU_79	OE1	3.623
4R7N	P_LYS_103	NZ	P_GLU_165	OE1	3.040
4R7N	P_ARG_108	NH1	P_GLU_105	OE2	2.550
4R7N	P_ARG_108	NH2	P_GLU_105	OE2	3.860
4R7N	P_LYS_149	NZ	P_GLU_195	OE1	3.164
4R7N	P_LYS_149	NZ	P_GLU_195	OE2	3.343
4R7N	P_LYS_188	NZ	P_ASP_185	OD1	3.703
4R7N	P_HIS_189	ND1	P_ASP_151	OD2	2.247
4R7N	Q_ARG_39	NH1	Q_ASP_90	OD1	2.764
4R7N	Q_ARG_39	NH2	Q_GLU_47	OE1	3.665
4R7N	Q_ARG_39	NH2	Q_GLU_47	OE2	2.481
4R7N	Q_ARG_67	NH2	Q_ASP_90	OD1	3.614
4R7N	Q_ARG_67	NH2	Q_ASP_90	OD2	2.212
4R7N	Q_ARG_98	NH1	Q_ASP_100	OD2	2.913
4R7N	Q_ARG_98	NH2	Q_ASP_100	OD2	2.616
4R7N	Q_LYS_148	NZ	Q_ASP_149	OD1	3.127
4R7N	Q_LYS_148	NZ	Q_ASP_149	OD2	2.663
4R7N	Q_LYS_211	NZ	G_ASP_213	OD2	3.009
4R7N	Q_LYS_214	NZ	R_GLU_123	OE1	3.438
4R7N	Q_LYS_214	NZ	R_GLU_123	OE2	3.002
4R7N	Q_ARG_215	NH2	Q_GLU_217	OE2	3.165
4R7N	R_ARG_61	NH2	R_ASP_82	OD1	3.978
4R7N	R_LYS_103	NZ	R_GLU_165	OE1	2.945
4R7N	R_LYS_103	NZ	R_GLU_165	OE2	3.633
4R7N	R_LYS_145	NZ	F_ASP_93	OD2	3.627
4R7N	R_LYS_149	NZ	R_GLU_195	OE1	3.543
4R7N	R_LYS_149	NZ	R_GLU_195	OE2	2.531
4R7N	R_LYS_188	NZ	R_ASP_185	OD1	2.716
4R7N	R_LYS_188	NZ	R_ASP_185	OD2	3.719
4R7N	S_ARG_39	NH1	S_ASP_90	OD1	2.779
4R7N	S_ARG_39	NH2	S_GLU_47	OE2	3.044
4R7N	S_ARG_39	NH2	S_ASP_90	OD1	3.585
4R7N	S_ARG_67	NH1	S_ASP_90	OD1	3.352
4R7N	S_ARG_67	NH1	S_ASP_90	OD2	2.290
4R7N	S_ARG_67	NH2	S_ASP_90	OD1	2.345
4R7N	S_ARG_67	NH2	S_ASP_90	OD2	3.063
4R7N	S_ARG_98	NH1	S_ASP_100	OD2	2.688
4R7N	S_ARG_98	NH2	S_ASP_100	OD2	2.786
4R7N	S_LYS_148	NZ	S_ASP_149	OD1	3.013
4R7N	S_LYS_148	NZ	S_ASP_149	OD2	2.778
4R7N	S_LYS_214	NZ	T_GLU_123	OE1	3.934
4R7N	S_LYS_214	NZ	T_GLU_123	OE2	3.931
4R7N	T_LYS_16	NZ	T_GLU_79	OE1	3.838
4R7N	T_LYS_16	NZ	T_GLU_79	OE2	3.370
4R7N	T_ARG_61	NH1	T_GLU_81	OE1	3.260
4R7N	T_ARG_61	NH2	T_GLU_81	OE1	3.615
4R7N	T_ARG_61	NH2	T_ASP_82	OD1	2.440
4R7N	T_ARG_61	NH2	T_ASP_82	OD2	3.240
4R7N	T_LYS_103	NZ	T_GLU_165	OE1	3.688
4R7N	T_LYS_149	NZ	T_GLU_195	OE2	2.601

Table 616: 4R7N-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4R9Y	L_ARG_86	NH2	L_ASP_107	OD1	3.056
4R9Y	L_ARG_86	NH2	L_ASP_107	OD2	2.747
4R9Y	L_LYS_128	NZ	L_ASP_190	OD2	3.847
4R9Y	L_LYS_174	NZ	L_GLU_220	OE1	2.876
4R9Y	L_ARG_180	NH2	L_GLU_210	OE2	3.355
4R9Y	L_HIS_214	ND1	L_GLU_210	OE1	3.897
4R9Y	H_LYS_37	NZ	H_GLU_45	OE1	2.976
4R9Y	H_ARG_66	NH1	H_GLU_88	OE2	2.888
4R9Y	H_ARG_66	NH2	H_GLU_88	OE2	3.617
4R9Y	H_LYS_214	NZ	L_GLU_148	OE2	2.745
4R9Y	B_LYS_50	NZ	B_GLU_28	OE2	3.071
4R9Y	A_LYS_50	NZ	A_GLU_28	OE2	2.662
4R9Y	M_ARG_79	NH2	M_ASP_85	OD1	3.700
4R9Y	M_ARG_86	NH2	M_ASP_107	OD1	2.946
4R9Y	M_ARG_86	NH2	M_ASP_107	OD2	2.694
4R9Y	M_LYS_128	NZ	M_ASP_190	OD1	3.808
4R9Y	M_LYS_128	NZ	M_ASP_190	OD2	3.124
4R9Y	M_LYS_	NZ	M_GLU_	OE1	3.152
4R9Y	M_ARG_	NH2	M_GLU_	OE2	3.203
4R9Y	M_HIS_	ND1	M_GLU_	OE1	3.630
4R9Y	M_LYS_	NZ	M_ASP_	OD1	3.535
4R9Y	M_LYS_	NZ	M_ASP_	OD2	3.766
4R9Y	N_LYS_37	NZ	N_GLU_45	OE1	2.708
4R9Y	N_ARG_66	NH1	N_GLU_88	OE2	3.382
4R9Y	N_ARG_66	NH2	N_GLU_88	OE2	3.864
4R9Y	N_LYS_	NZ	M_GLU_	OE2	3.272

Table 617: 4R9Y-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4RAU	A_ARG_39	NH1	A_ASP_84	OD1	3.918
4RAU	A_ARG_63	NH1	A_ASP_84	OD1	3.252
4RAU	A_ARG_63	NH1	A_ASP_84	OD2	2.474
4RAU	A_ARG_63	NH2	A_GLU_81	OE1	3.641
4RAU	A_LYS_95	NZ	C_ASP_7	OD1	3.997
4RAU	A_LYS_95	NZ	C_ASP_7	OD2	3.077
4RAU	A_LYS_105	NZ	A_ASP_167	OD1	3.803
4RAU	A_LYS_144	NZ	A_GLU_107	OE1	3.648
4RAU	A_LYS_149	NZ	A_GLU_156	OE1	3.640
4RAU	A_LYS_149	NZ	A_GLU_156	OE2	3.515
4RAU	A_LYS_151	NZ	A_GLU_197	OE1	3.640
4RAU	A_LYS_151	NZ	A_GLU_197	OE2	2.823
4RAU	A_LYS_185	NZ	A_GLU_189	OE1	3.707
4RAU	A_LYS_185	NZ	A_GLU_189	OE2	3.597
4RAU	A_HIS_191	ND1	A_ASP_153	OD2	2.734
4RAU	A_LYS_201	NZ	A_ASP_112	OD2	3.033
4RAU	B_ARG_40	NH1	B_ASP_92	OD1	3.503
4RAU	B_ARG_40	NH2	B_GLU_48	OE1	3.720
4RAU	B_ARG_40	NH2	B_GLU_48	OE2	3.277
4RAU	B_ARG_46	NH1	B_GLU_44	OE1	3.716
4RAU	B_ARG_69	NH1	B_ASP_92	OD2	2.694
4RAU	B_ARG_69	NH2	B_ASP_92	OD1	3.312
4RAU	B_ARG_69	NH2	B_ASP_92	OD2	3.295
4RAU	B_ARG_89	NH1	B_GLU_91	OE1	3.989
4RAU	B_ARG_100	NH2	B_ASP_109	OD1	3.691
4RAU	B_ARG_100	NH2	B_ASP_109	OD2	2.652
4RAU	D_ARG_39	NH1	D_ASP_84	OD1	3.919
4RAU	D_ARG_63	NH1	D_ASP_84	OD1	3.251
4RAU	D_ARG_63	NH1	D_ASP_84	OD2	2.476
4RAU	D_ARG_63	NH2	D_GLU_81	OE1	3.630
4RAU	D_LYS_95	NZ	F_ASP_7	OD1	3.860
4RAU	D_LYS_105	NZ	D_ASP_167	OD1	3.863
4RAU	D_LYS_144	NZ	D_GLU_107	OE1	3.652
4RAU	D_LYS_149	NZ	D_GLU_156	OE1	3.639
4RAU	D_LYS_149	NZ	D_GLU_156	OE2	3.516
4RAU	D_LYS_151	NZ	D_GLU_197	OE1	3.630
4RAU	D_LYS_151	NZ	D_GLU_197	OE2	2.814
4RAU	D_LYS_185	NZ	D_GLU_189	OE1	3.707
4RAU	D_LYS_185	NZ	D_GLU_189	OE2	3.596
4RAU	D_HIS_191	ND1	D_ASP_153	OD2	2.728
4RAU	D_LYS_201	NZ	D_ASP_112	OD2	3.033
4RAU	E_ARG_40	NH1	E_ASP_92	OD1	3.503
4RAU	E_ARG_40	NH2	E_GLU_48	OE1	3.725
4RAU	E_ARG_40	NH2	E_GLU_48	OE2	3.283
4RAU	E_ARG_46	NH1	E_GLU_44	OE1	3.723
4RAU	E_ARG_69	NH1	E_ASP_92	OD2	2.692
4RAU	E_ARG_69	NH2	E_ASP_92	OD1	3.311
4RAU	E_ARG_69	NH2	E_ASP_92	OD2	3.296
4RAU	E_ARG_89	NH1	E_GLU_91	OE1	3.988
4RAU	E_ARG_100	NH2	E_ASP_109	OD1	3.682
4RAU	E_ARG_100	NH2	E_ASP_109	OD2	2.642
4RAU	G_ARG_39	NH1	G_ASP_84	OD1	3.926
4RAU	G_LYS_41	NZ	G_GLU_83	OE2	3.332
4RAU	G_ARG_63	NH1	G_ASP_84	OD1	3.251
4RAU	G_ARG_63	NH1	G_ASP_84	OD2	2.480
4RAU	G_ARG_63	NH2	G_GLU_81	OE1	3.649
4RAU	G_LYS_95	NZ	I_ASP_7	OD1	3.805

4RAU	G_LYS_95	NZ	I_ASP_7	OD2	2.755
4RAU	G_LYS_105	NZ	G_ASP_167	OD1	3.810
4RAU	G_LYS_144	NZ	G_GLU_107	OE1	3.652
4RAU	G_LYS_149	NZ	G_GLU_156	OE1	3.643
4RAU	G_LYS_149	NZ	G_GLU_156	OE2	3.517
4RAU	G_LYS_151	NZ	G_GLU_197	OE1	3.632
4RAU	G_LYS_151	NZ	G_GLU_197	OE2	2.815
4RAU	G_LYS_185	NZ	G_GLU_189	OE1	3.707
4RAU	G_LYS_185	NZ	G_GLU_189	OE2	3.598
4RAU	G_HIS_191	ND1	G_ASP_153	OD2	2.730
4RAU	G_LYS_201	NZ	G_ASP_112	OD2	3.033
4RAU	H_ARG_40	NH1	H_ASP_92	OD1	3.494
4RAU	H_ARG_40	NH2	H_GLU_48	OE1	3.724
4RAU	H_ARG_40	NH2	H_GLU_48	OE2	3.281
4RAU	H_ARG_46	NH1	H_GLU_44	OE1	3.700
4RAU	H_ARG_69	NH1	H_ASP_92	OD2	2.699
4RAU	H_ARG_69	NH2	H_ASP_92	OD1	3.317
4RAU	H_ARG_69	NH2	H_ASP_92	OD2	3.297
4RAU	H_ARG_89	NH1	H_GLU_91	OE1	3.985
4RAU	H_ARG_100	NH2	H_ASP_109	OD1	3.685
4RAU	H_ARG_100	NH2	H_ASP_109	OD2	2.644
4RAU	J_ARG_39	NH1	J_ASP_84	OD1	3.913
4RAU	J_ARG_63	NH1	J_ASP_84	OD1	3.253
4RAU	J_ARG_63	NH1	J_ASP_84	OD2	2.480
4RAU	J_ARG_63	NH2	J_GLU_81	OE1	3.649
4RAU	J_LYS_105	NZ	J_ASP_167	OD1	3.805
4RAU	J_LYS_144	NZ	J_GLU_107	OE1	3.646
4RAU	J_LYS_149	NZ	J_GLU_156	OE1	3.641
4RAU	J_LYS_149	NZ	J_GLU_156	OE2	3.516
4RAU	J_LYS_151	NZ	J_GLU_197	OE1	3.631
4RAU	J_LYS_151	NZ	J_GLU_197	OE2	2.814
4RAU	J_LYS_171	NZ	J_ASP_169	OD2	3.647
4RAU	J_LYS_185	NZ	J_GLU_189	OE1	3.708
4RAU	J_LYS_185	NZ	J_GLU_189	OE2	3.602
4RAU	J_HIS_191	ND1	J_ASP_153	OD2	2.728
4RAU	J_LYS_201	NZ	J_ASP_112	OD2	3.034
4RAU	K_ARG_40	NH1	K_ASP_92	OD1	3.498
4RAU	K_ARG_40	NH2	K_GLU_48	OE1	3.722
4RAU	K_ARG_40	NH2	K_GLU_48	OE2	3.276
4RAU	K_ARG_46	NH1	K_GLU_44	OE1	3.698
4RAU	K_ARG_69	NH1	K_ASP_92	OD2	2.699
4RAU	K_ARG_69	NH2	K_ASP_92	OD1	3.319
4RAU	K_ARG_69	NH2	K_ASP_92	OD2	3.299
4RAU	K_ARG_89	NH1	K_GLU_91	OE1	3.987
4RAU	K_ARG_100	NH2	K_ASP_109	OD1	3.690
4RAU	K_ARG_100	NH2	K_ASP_109	OD2	2.645
4RAU	K_LYS_216	NZ	J_GLU_125	OE2	3.935
4RAU	M_ARG_39	NH1	M_ASP_84	OD1	3.922
4RAU	M_ARG_63	NH1	M_ASP_84	OD1	3.250
4RAU	M_ARG_63	NH1	M_ASP_84	OD2	2.472
4RAU	M_ARG_63	NH2	M_GLU_81	OE1	3.646
4RAU	M_LYS_105	NZ	M_ASP_167	OD1	3.861
4RAU	M_LYS_149	NZ	M_GLU_156	OE1	3.646
4RAU	M_LYS_149	NZ	M_GLU_156	OE2	3.522
4RAU	M_LYS_151	NZ	M_GLU_197	OE1	3.627
4RAU	M_LYS_151	NZ	M_GLU_197	OE2	2.809
4RAU	M_LYS_185	NZ	M_GLU_189	OE1	3.710
4RAU	M_LYS_185	NZ	M_GLU_189	OE2	3.598

4RAU	M_HIS_191	ND1	M_ASP_153	OD2	2.731
4RAU	M_LYS_201	NZ	M_ASP_112	OD2	3.028
4RAU	N_ARG_40	NH1	N_ASP_92	OD1	3.508
4RAU	N_ARG_40	NH2	N_GLU_48	OE1	3.718
4RAU	N_ARG_40	NH2	N_GLU_48	OE2	3.273
4RAU	N_ARG_46	NH2	N_GLU_44	OE1	2.944
4RAU	N_ARG_69	NH1	N_ASP_92	OD2	2.695
4RAU	N_ARG_69	NH2	N_ASP_92	OD1	3.318
4RAU	N_ARG_69	NH2	N_ASP_92	OD2	3.302
4RAU	N_ARG_89	NH1	N_GLU_91	OE1	3.987
4RAU	N_ARG_100	NH2	N_ASP_109	OD1	3.684
4RAU	N_ARG_100	NH2	N_ASP_109	OD2	2.647
4RAU	O_ARG_49	NH2	X_ASP_7	OD1	2.993
4RAU	O_ARG_49	NH2	X_ASP_7	OD2	3.647
4RAU	P_ARG_39	NH1	P_ASP_84	OD1	3.913
4RAU	P_ARG_63	NH1	P_ASP_84	OD1	3.257
4RAU	P_ARG_63	NH1	P_ASP_84	OD2	2.479
4RAU	P_ARG_63	NH2	P_GLU_81	OE1	3.679
4RAU	P_LYS_	NZ	R_ASP_	OD1	3.104
4RAU	P_LYS_105	NZ	P_ASP_167	OD1	3.844
4RAU	P_LYS_144	NZ	P_GLU_107	OE1	3.654
4RAU	P_LYS_149	NZ	P_GLU_156	OE1	3.641
4RAU	P_LYS_149	NZ	P_GLU_156	OE2	3.516
4RAU	P_LYS_151	NZ	P_GLU_197	OE1	3.629
4RAU	P_LYS_151	NZ	P_GLU_197	OE2	2.811
4RAU	P_LYS_185	NZ	P_GLU_189	OE1	3.705
4RAU	P_LYS_185	NZ	P_GLU_189	OE2	3.595
4RAU	P_HIS_191	ND1	P_ASP_153	OD2	2.722
4RAU	P_LYS_201	NZ	P_ASP_112	OD2	3.034
4RAU	Q_ARG_40	NH1	Q_ASP_92	OD1	3.502
4RAU	Q_ARG_40	NH2	Q_GLU_48	OE1	3.727
4RAU	Q_ARG_40	NH2	Q_GLU_48	OE2	3.276
4RAU	Q_ARG_46	NH1	Q_GLU_44	OE1	3.700
4RAU	Q_ARG_69	NH1	Q_ASP_92	OD2	2.695
4RAU	Q_ARG_69	NH2	Q_ASP_92	OD1	3.314
4RAU	Q_ARG_69	NH2	Q_ASP_92	OD2	3.297
4RAU	Q_ARG_89	NH1	Q_GLU_91	OE1	3.990
4RAU	Q_ARG_100	NH2	Q_ASP_109	OD1	3.684
4RAU	Q_ARG_100	NH2	Q_ASP_109	OD2	2.645
4RAU	S_ARG_39	NH2	S_ASP_84	OD1	2.426
4RAU	S_ARG_63	NH1	S_ASP_84	OD1	3.257
4RAU	S_ARG_63	NH1	S_ASP_84	OD2	2.480
4RAU	S_ARG_63	NH2	S_GLU_81	OE1	3.645
4RAU	S_LYS_105	NZ	S_ASP_167	OD1	3.810
4RAU	S_LYS_144	NZ	S_GLU_107	OE1	3.627
4RAU	S_LYS_149	NZ	S_GLU_156	OE1	3.640
4RAU	S_LYS_149	NZ	S_GLU_156	OE2	3.514
4RAU	S_LYS_151	NZ	S_GLU_197	OE1	3.630
4RAU	S_LYS_151	NZ	S_GLU_197	OE2	2.813
4RAU	S_LYS_185	NZ	S_GLU_189	OE1	3.708
4RAU	S_LYS_185	NZ	S_GLU_189	OE2	3.598
4RAU	S_HIS_191	ND1	S_ASP_153	OD2	2.725
4RAU	S_LYS_201	NZ	S_ASP_112	OD2	3.035
4RAU	T_ARG_40	NH1	T_ASP_92	OD1	3.503
4RAU	T_ARG_40	NH2	T_GLU_48	OE1	3.728
4RAU	T_ARG_40	NH2	T_GLU_48	OE2	3.283
4RAU	T_ARG_46	NH1	T_GLU_44	OE1	3.699
4RAU	T_ARG_69	NH1	T_ASP_92	OD2	2.696

4RAU	T_ARG_69	NH2	T_ASP_92	OD1	3.316
4RAU	T_ARG_69	NH2	T_ASP_92	OD2	3.295
4RAU	T_ARG_89	NH1	T_GLU_91	OE1	3.989
4RAU	T_ARG_100	NH2	T_ASP_109	OD1	3.693
4RAU	T_ARG_100	NH2	T_ASP_109	OD2	2.653
4RAU	V_ARG_39	NH1	V_ASP_84	OD1	3.915
4RAU	V_ARG_63	NH1	V_ASP_84	OD1	3.255
4RAU	V_ARG_63	NH1	V_ASP_84	OD2	2.479
4RAU	V_ARG_63	NH2	V_GLU_81	OE1	3.648
4RAU	V_LYS_95	NZ	X_ASP_7	OD1	3.972
4RAU	V_LYS_95	NZ	X_ASP_7	OD2	3.050
4RAU	V_LYS_105	NZ	V_ASP_167	OD1	3.821
4RAU	V_LYS_144	NZ	V_GLU_107	OE1	3.639
4RAU	V_LYS_149	NZ	V_GLU_156	OE1	3.641
4RAU	V_LYS_149	NZ	V_GLU_156	OE2	3.514
4RAU	V_LYS_151	NZ	V_GLU_197	OE1	3.631
4RAU	V_LYS_151	NZ	V_GLU_197	OE2	2.814
4RAU	V_LYS_185	NZ	V_GLU_189	OE1	3.708
4RAU	V_LYS_185	NZ	V_GLU_189	OE2	3.599
4RAU	V_HIS_191	ND1	V_ASP_153	OD2	2.732
4RAU	V_LYS_201	NZ	V_ASP_112	OD2	3.032
4RAU	W_ARG_40	NH1	W_ASP_92	OD1	3.502
4RAU	W_ARG_40	NH2	W_GLU_48	OE1	3.718
4RAU	W_ARG_40	NH2	W_GLU_48	OE2	3.275
4RAU	W_ARG_46	NH1	W_GLU_44	OE1	3.702
4RAU	W_ARG_69	NH1	W_ASP_92	OD2	2.696
4RAU	W_ARG_69	NH2	W_ASP_92	OD1	3.317
4RAU	W_ARG_69	NH2	W_ASP_92	OD2	3.298
4RAU	W_ARG_89	NH1	W_GLU_91	OE1	3.988
4RAU	W_ARG_100	NH2	W_ASP_109	OD1	3.693
4RAU	W_ARG_100	NH2	W_ASP_109	OD2	2.652
4RAU	X_ARG_49	NH2	O_ASP_7	OD1	2.791
4RAU	X_ARG_49	NH2	O_ASP_7	OD2	3.699

Table 618: 4RAU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4RRP	A_ARG_24	NH2	A_ASP_70	OD1	3.536
4RRP	A_ARG_24	NH2	A_ASP_70	OD2	3.877
4RRP	A_ARG_61	NH2	A_GLU_81	OE2	3.090
4RRP	A_ARG_61	NH2	A_ASP_82	OD1	2.844
4RRP	A_ARG_61	NH2	A_ASP_82	OD2	3.386
4RRP	A_LYS_149	NZ	A_GLU_195	OE1	2.796
4RRP	A_LYS_149	NZ	A_GLU_195	OE2	3.574
4RRP	A_LYS_169	NZ	A_ASP_167	OD1	3.364
4RRP	A_LYS_169	NZ	A_ASP_167	OD2	3.265
4RRP	A_LYS_183	NZ	A_GLU_187	OE1	3.356
4RRP	A_LYS_183	NZ	A_GLU_187	OE2	2.482
4RRP	A_LYS_188	NZ	A_ASP_185	OD1	3.338
4RRP	G_ARG_38	NH1	G_ASP_86	OD1	3.090
4RRP	G_ARG_38	NH2	G_GLU_46	OE1	3.292
4RRP	G_ARG_38	NH2	G_GLU_46	OE2	3.713
4RRP	G_ARG_38	NH2	G_ASP_86	OD1	3.929
4RRP	G_LYS_64	NZ	G_ASP_61	OD1	3.718
4RRP	G_ARG_66	NH1	G_ASP_86	OD1	3.753
4RRP	G_ARG_66	NH1	G_ASP_86	OD2	2.642
4RRP	G_ARG_66	NH2	G_ASP_86	OD1	3.093
4RRP	G_ARG_66	NH2	G_ASP_86	OD2	3.474
4RRP	G_LYS_75	NZ	G_ASP_72	OD2	3.613
4RRP	G_ARG_94	NH1	G_ASP_101	OD2	2.572
4RRP	G_LYS_143	NZ	G_ASP_144	OD1	3.513
4RRP	G_LYS_143	NZ	G_ASP_144	OD2	3.377
4RRP	G_LYS_214	NZ	A_ASP_122	OD1	3.271
4RRP	G_LYS_214	NZ	A_ASP_122	OD2	3.253
4RRP	B_ARG_24	NH1	B_ASP_70	OD1	2.974
4RRP	B_ARG_24	NH2	B_ASP_70	OD1	3.509
4RRP	B_ARG_24	NH2	B_ASP_70	OD2	3.520
4RRP	B_ARG_61	NH1	Q_GLU_32	OE1	3.055
4RRP	B_ARG_61	NH1	Q_GLU_32	OE2	3.683
4RRP	B_ARG_61	NH2	B_GLU_81	OE2	3.319
4RRP	B_ARG_61	NH2	B_ASP_82	OD1	2.867
4RRP	B_ARG_61	NH2	B_ASP_82	OD2	3.594
4RRP	B_ARG_61	NH2	Q_GLU_32	OE2	3.637
4RRP	B_LYS_103	NZ	B_GLU_165	OE1	2.902
4RRP	B_LYS_103	NZ	B_GLU_165	OE2	2.974
4RRP	B_LYS_149	NZ	B_GLU_195	OE2	2.877
4RRP	B_LYS_188	NZ	B_ASP_185	OD1	3.756
4RRP	B_HIS_189	ND1	B_ASP_151	OD2	3.126
4RRP	H_ARG_38	NH1	H_ASP_86	OD1	2.743
4RRP	H_ARG_38	NH2	H_GLU_46	OE1	3.267
4RRP	H_ARG_38	NH2	H_GLU_46	OE2	3.655
4RRP	H_ARG_38	NH2	H_ASP_86	OD1	3.792
4RRP	H_ARG_66	NH1	H_ASP_86	OD2	2.961
4RRP	H_ARG_66	NH2	H_ASP_86	OD1	3.400
4RRP	H_ARG_66	NH2	H_ASP_86	OD2	3.201
4RRP	H_ARG_94	NH2	H_ASP_101	OD1	3.922
4RRP	H_ARG_94	NH2	H_ASP_101	OD2	2.800
4RRP	H_LYS_143	NZ	H_ASP_144	OD1	3.372
4RRP	H_LYS_143	NZ	H_ASP_144	OD2	3.115
4RRP	H_LYS_210	NZ	H_GLU_212	OE2	3.908
4RRP	C_ARG_24	NH1	C_ASP_70	OD1	3.210
4RRP	C_ARG_24	NH1	C_ASP_70	OD2	3.811
4RRP	C_ARG_24	NH2	C_ASP_70	OD1	3.266
4RRP	C_ARG_24	NH2	C_ASP_70	OD2	3.021

4RRP	C_ARG_61	NH2	C_GLU_81	OE2	3.872
4RRP	C_ARG_61	NH2	C_ASP_82	OD1	2.499
4RRP	C_ARG_61	NH2	C_ASP_82	OD2	3.003
4RRP	C_LYS_103	NZ	C_GLU_105	OE1	2.759
4RRP	C_LYS_103	NZ	C_GLU_165	OE1	3.916
4RRP	C_LYS_188	NZ	C_ASP_185	OD1	3.719
4RRP	I_ARG_38	NH1	I_ASP_86	OD1	3.037
4RRP	I_ARG_38	NH2	I_GLU_46	OE1	3.102
4RRP	I_ARG_38	NH2	I_GLU_46	OE2	3.753
4RRP	I_LYS_64	NZ	I_ASP_61	OD1	2.958
4RRP	I_ARG_66	NH1	I_ASP_86	OD1	3.306
4RRP	I_ARG_66	NH1	I_ASP_86	OD2	3.894
4RRP	I_ARG_66	NH2	I_ASP_86	OD1	3.160
4RRP	I_ARG_66	NH2	I_ASP_86	OD2	2.282
4RRP	I_ARG_94	NH1	I_ASP_101	OD2	2.705
4RRP	I_LYS_143	NZ	I_ASP_144	OD1	3.710
4RRP	D_ARG_24	NH2	D_ASP_70	OD1	3.941
4RRP	D_ARG_61	NH2	D_GLU_81	OE2	3.108
4RRP	D_ARG_61	NH2	D_ASP_82	OD1	2.819
4RRP	D_ARG_61	NH2	D_ASP_82	OD2	3.344
4RRP	D_LYS_103	NZ	D_GLU_165	OE1	3.545
4RRP	D_LYS_103	NZ	D_GLU_165	OE2	3.420
4RRP	D_LYS_149	NZ	D_GLU_195	OE2	2.585
4RRP	D_LYS_188	NZ	D_ASP_185	OD1	2.752
4RRP	D_HIS_189	ND1	D_ASP_151	OD2	3.191
4RRP	J_ARG_38	NH1	J_ASP_86	OD1	3.091
4RRP	J_ARG_38	NH2	J_GLU_46	OE1	3.176
4RRP	J_ARG_38	NH2	J_ASP_86	OD1	3.697
4RRP	J_ARG_66	NH1	J_ASP_86	OD1	3.907
4RRP	J_ARG_66	NH1	J_ASP_86	OD2	2.891
4RRP	J_ARG_66	NH2	J_ASP_86	OD1	2.922
4RRP	J_ARG_66	NH2	J_ASP_86	OD2	3.426
4RRP	J_ARG_83	NH1	J_GLU_85	OE2	3.812
4RRP	J_ARG_94	NH2	J_ASP_101	OD1	3.162
4RRP	J_LYS_143	NZ	J_ASP_144	OD1	3.206
4RRP	J_LYS_143	NZ	J_ASP_144	OD2	3.279
4RRP	J_LYS_210	NZ	J_GLU_212	OE2	3.248
4RRP	J_LYS_214	NZ	D_ASP_122	OD1	3.176
4RRP	J_LYS_214	NZ	D_ASP_122	OD2	2.924
4RRP	E_ARG_24	NH1	E_ASP_70	OD1	3.504
4RRP	E_ARG_24	NH1	E_ASP_70	OD2	2.757
4RRP	E_ARG_24	NH2	E_ASP_70	OD1	3.612
4RRP	E_ARG_24	NH2	E_ASP_70	OD2	3.877
4RRP	E_ARG_61	NH2	E_GLU_81	OE2	3.265
4RRP	E_ARG_61	NH2	E_ASP_82	OD1	2.971
4RRP	E_ARG_61	NH2	E_ASP_82	OD2	3.278
4RRP	E_LYS_103	NZ	E_GLU_165	OE1	3.997
4RRP	E_ARG_108	NH1	E_ASP_170	OD1	3.279
4RRP	E_LYS_188	NZ	E_ASP_185	OD1	3.369
4RRP	E_HIS_189	ND1	E_ASP_151	OD2	3.342
4RRP	K_ARG_38	NH1	K_ASP_86	OD1	3.316
4RRP	K_ARG_38	NH2	K_GLU_46	OE1	3.348
4RRP	K_ARG_38	NH2	K_GLU_46	OE2	3.150
4RRP	K_ARG_38	NH2	K_ASP_86	OD1	3.806
4RRP	K_ARG_66	NH1	K_ASP_86	OD1	3.794
4RRP	K_ARG_66	NH1	K_ASP_86	OD2	2.585
4RRP	K_ARG_94	NH2	K_ASP_101	OD2	3.065
4RRP	K_LYS_143	NZ	K_ASP_144	OD1	3.052

4RRP	K_LYS_143	NZ	K_ASP_144	OD2	3.747
4RRP	K_LYS_210	NZ	K_GLU_212	OE2	3.209
4RRP	F_ARG_24	NH1	F_ASP_70	OD1	3.513
4RRP	F_ARG_24	NH2	F_ASP_70	OD1	3.347
4RRP	F_ARG_24	NH2	F_ASP_70	OD2	3.453
4RRP	F_ARG_61	NH2	F_GLU_81	OE2	3.201
4RRP	F_ARG_61	NH2	F_ASP_82	OD1	3.111
4RRP	F_ARG_61	NH2	F_ASP_82	OD2	2.880
4RRP	F_LYS_183	NZ	F_GLU_187	OE2	3.854
4RRP	F_HIS_189	ND1	F_ASP_151	OD2	3.499
4RRP	L_ARG_38	NH1	L_ASP_86	OD1	2.782
4RRP	L_ARG_38	NH2	L_GLU_46	OE1	2.958
4RRP	L_ARG_38	NH2	L_GLU_46	OE2	3.099
4RRP	L_ARG_38	NH2	L_ASP_86	OD1	3.809
4RRP	L_ARG_66	NH1	L_ASP_86	OD2	3.387
4RRP	L_ARG_66	NH2	L_ASP_86	OD1	3.433
4RRP	L_ARG_66	NH2	L_ASP_86	OD2	3.328
4RRP	L_ARG_94	NH1	L_ASP_101	OD1	2.541
4RRP	L_ARG_94	NH2	L_ASP_101	OD1	3.963
4RRP	L_HIS_164	NE2	F_ASP_167	OD1	3.853
4RRP	L_LYS_214	NZ	F_ASP_122	OD2	3.247
4RRP	M_LYS_10	NZ	M_GLU_25	OE2	2.815
4RRP	M_LYS_10	NZ	N_GLU_29	OE1	3.876
4RRP	M_LYS_10	NZ	N_GLU_29	OE2	3.237
4RRP	M_LYS_41	NZ	M_GLU_39	OE1	3.872
4RRP	M_ARG_104	NH1	M_ASP_102	OD2	2.905
4RRP	M_ARG_104	NH2	M_ASP_102	OD2	3.495
4RRP	M_ARG_108	NH2	M_GLU_105	OE1	3.086
4RRP	M_ARG_108	NH2	M_GLU_105	OE2	3.305
4RRP	M_ARG_123	NH1	M_GLU_120	OE1	3.669
4RRP	M_ARG_123	NH1	M_GLU_120	OE2	3.750
4RRP	M_HIS_134	ND1	M_ASP_118	OD2	2.756
4RRP	M_HIS_134	ND1	M_GLU_119	OE1	3.923
4RRP	N_LYS_10	NZ	M_GLU_29	OE1	3.319
4RRP	N_LYS_10	NZ	M_GLU_29	OE2	2.389
4RRP	N_LYS_10	NZ	N_GLU_25	OE1	2.628
4RRP	N_HIS_36	ND1	N_ASP_102	OD1	3.589
4RRP	N_HIS_36	ND1	N_ASP_102	OD2	3.342
4RRP	N_ARG_104	NH1	N_ASP_102	OD2	2.932
4RRP	N_ARG_104	NH2	N_ASP_102	OD2	3.308
4RRP	N_ARG_108	NH2	N_GLU_105	OE1	3.337
4RRP	N_ARG_108	NH2	N_GLU_105	OE2	2.984
4RRP	O_LYS_10	NZ	O_GLU_25	OE2	3.092
4RRP	O_LYS_35	NZ	O_GLU_156	OE2	3.793
4RRP	O_LYS_41	NZ	O_GLU_56	OE1	3.628
4RRP	O_LYS_71	NZ	O_GLU_25	OE2	3.721
4RRP	O_ARG_104	NH1	O_ASP_102	OD2	3.187
4RRP	O_ARG_104	NH2	O_ASP_102	OD2	2.791
4RRP	O_ARG_108	NH2	O_GLU_105	OE2	3.068
4RRP	O_ARG_123	NH1	Q_ASP_54	OD1	3.356
4RRP	O_ARG_123	NH1	Q_ASP_54	OD2	3.533
4RRP	O_ARG_123	NH2	O_GLU_120	OE1	3.551
4RRP	O_ARG_123	NH2	Q_ASP_54	OD2	3.134
4RRP	O_HIS_134	ND1	O_ASP_118	OD1	3.804
4RRP	O_HIS_134	ND1	O_ASP_118	OD2	2.643
4RRP	O_HIS_134	NE2	N_GLU_121	OE1	3.780
4RRP	O_HIS_134	NE2	N_GLU_121	OE2	3.192
4RRP	O_ARG_145	NH2	Q_GLU_116	OE1	3.921

4RRP	O_ARG_145	NH2	Q_GLU_116	OE2	3.324
4RRP	P_LYS_10	NZ	P_GLU_25	OE2	2.613
4RRP	P_HIS_36	ND1	P_ASP_102	OD1	3.540
4RRP	P_HIS_36	NE2	P_ASP_102	OD2	3.863
4RRP	P_ARG_49	NH1	P_GLU_88	OE2	3.737
4RRP	P_HIS_53	ND1	P_ASP_54	OD1	3.310
4RRP	P_ARG_104	NH1	P_ASP_102	OD2	2.923
4RRP	P_ARG_104	NH2	P_ASP_102	OD2	3.980
4RRP	P_ARG_108	NH2	P_GLU_105	OE1	2.888
4RRP	P_ARG_108	NH2	P_GLU_105	OE2	3.217
4RRP	P_ARG_123	NH2	P_GLU_120	OE1	2.430
4RRP	P_HIS_134	ND1	P_ASP_118	OD1	3.512
4RRP	P_HIS_134	ND1	P_ASP_118	OD2	2.998
4RRP	P_HIS_134	ND1	P_GLU_119	OE2	3.490
4RRP	P_HIS_134	NE2	P_ASP_133	OD2	3.140
4RRP	Q_LYS_10	NZ	Q_GLU_25	OE2	2.946
4RRP	Q_HIS_36	NE2	Q_ASP_102	OD2	3.552
4RRP	Q_LYS_41	NZ	Q_GLU_56	OE1	3.618
4RRP	Q_HIS_53	ND1	Q_GLU_88	OE2	3.194
4RRP	Q_ARG_104	NH1	Q_ASP_102	OD1	3.295
4RRP	Q_ARG_108	NH2	Q_GLU_105	OE1	3.208
4RRP	Q_ARG_108	NH2	Q_GLU_105	OE2	3.290
4RRP	Q_ARG_123	NH1	Q_GLU_120	OE1	3.019
4RRP	Q_HIS_134	ND1	Q_ASP_118	OD1	3.096
4RRP	Q_HIS_134	ND1	Q_ASP_118	OD2	3.045
4RRP	Q_ARG_145	NH1	O_GLU_116	OE2	3.050
4RRP	Q_ARG_145	NH2	O_GLU_116	OE2	3.244
4RRP	R_LYS_10	NZ	R_GLU_25	OE2	2.771
4RRP	R_LYS_41	NZ	R_GLU_56	OE2	3.957
4RRP	R_LYS_71	NZ	R_GLU_25	OE1	3.947
4RRP	R_LYS_71	NZ	R_GLU_25	OE2	3.610
4RRP	R_ARG_104	NH1	R_ASP_102	OD2	3.150
4RRP	R_ARG_104	NH2	R_ASP_102	OD2	3.913
4RRP	R_ARG_108	NH2	R_GLU_105	OE1	3.360
4RRP	R_ARG_108	NH2	R_GLU_105	OE2	3.892
4RRP	R_HIS_134	NE2	R_GLU_119	OE2	3.581

Table 619: 4RRP-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4TRP	H_LYS_63	NZ	H_GLU_46	OE1	3.694
4TRP	H_LYS_63	NZ	H_GLU_46	OE2	2.776
4TRP	H_ARG_67	NH1	H_ASP_90	OD1	3.592
4TRP	H_ARG_67	NH1	H_ASP_90	OD2	2.874
4TRP	H_ARG_67	NH2	H_ASP_90	OD1	2.862
4TRP	H_ARG_67	NH2	H_ASP_90	OD2	3.539
4TRP	H_LYS_208	NZ	L_GLU_129	OE2	3.281
4TRP	H_LYS_209	NZ	H_GLU_211	OE1	3.661
4TRP	H_LYS_209	NZ	H_GLU_211	OE2	3.286
4TRP	L_ARG_66	NH2	L_GLU_86	OE1	3.076
4TRP	L_ARG_66	NH2	L_ASP_87	OD1	2.816
4TRP	L_ARG_66	NH2	L_ASP_87	OD2	3.551
4TRP	L_LYS_153	NZ	L_GLU_160	OE1	2.821
4TRP	L_LYS_153	NZ	L_GLU_160	OE2	3.459
4TRP	L_LYS_155	NZ	L_GLU_201	OE1	2.685
4TRP	L_LYS_155	NZ	L_GLU_201	OE2	3.225
4TRP	L_ARG_161	NH1	L_GLU_191	OE1	3.775
4TRP	L_ARG_161	NH1	L_GLU_191	OE2	2.926
4TRP	L_ARG_161	NH2	L_GLU_191	OE1	3.592
4TRP	L_ARG_161	NH2	L_GLU_191	OE2	3.079
4TRP	L_ARG_194	NH1	L_ASP_190	OD2	2.875
4TRP	L_HIS_195	ND1	L_ASP_157	OD2	2.604
4TRP	L_LYS_205	NZ	L_ASP_116	OD1	3.811
4TRP	L_LYS_205	NZ	L_ASP_116	OD2	3.031

Table 620: 4TRP-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4TUJ	A_ARG_38	NH1	A_ASP_90	OD1	2.738
4TUJ	A_ARG_38	NH2	A_GLU_46	OE1	3.121
4TUJ	A_ARG_38	NH2	A_ASP_90	OD1	3.886
4TUJ	A_ARG_67	NH1	A_ASP_90	OD1	3.524
4TUJ	A_ARG_67	NH1	A_ASP_90	OD2	2.860
4TUJ	A_ARG_67	NH2	A_ASP_90	OD1	3.074
4TUJ	A_ARG_67	NH2	A_ASP_90	OD2	3.761
4TUJ	B_ARG_59	NH1	B_ASP_65	OD1	3.932
4TUJ	B_ARG_66	NH1	B_GLU_84	OE1	3.650
4TUJ	B_ARG_66	NH1	B_GLU_84	OE2	3.183
4TUJ	B_ARG_66	NH2	B_GLU_84	OE1	3.557
4TUJ	B_ARG_66	NH2	B_GLU_86	OE1	2.800
4TUJ	B_ARG_66	NH2	B_ASP_87	OD1	2.741
4TUJ	B_ARG_66	NH2	B_ASP_87	OD2	3.500
4TUJ	B_LYS_153	NZ	B_GLU_160	OE1	2.671
4TUJ	B_LYS_153	NZ	B_GLU_160	OE2	2.941
4TUJ	B_LYS_155	NZ	B_GLU_201	OE1	2.816
4TUJ	B_LYS_155	NZ	B_GLU_201	OE2	3.174
4TUJ	B_HIS_195	ND1	B_ASP_157	OD2	3.098
4TUJ	B_LYS_205	NZ	B_ASP_116	OD1	3.715
4TUJ	B_LYS_205	NZ	B_ASP_116	OD2	2.602
4TUJ	C_ARG_38	NH1	C_ASP_90	OD1	2.708
4TUJ	C_ARG_38	NH2	C_GLU_46	OE1	3.153
4TUJ	C_ARG_38	NH2	C_ASP_90	OD1	3.791
4TUJ	C_ARG_67	NH1	C_ASP_90	OD1	3.571
4TUJ	C_ARG_67	NH1	C_ASP_90	OD2	2.878
4TUJ	C_ARG_67	NH2	C_ASP_90	OD1	2.853
4TUJ	C_ARG_67	NH2	C_ASP_90	OD2	3.465
4TUJ	D_ARG_66	NH1	D_GLU_84	OE1	3.649
4TUJ	D_ARG_66	NH1	D_GLU_84	OE2	3.433
4TUJ	D_ARG_66	NH2	D_GLU_84	OE1	3.528
4TUJ	D_ARG_66	NH2	D_ASP_87	OD1	2.665
4TUJ	D_ARG_66	NH2	D_ASP_87	OD2	3.342
4TUJ	D_LYS_148	NZ	D_GLU_111	OE1	2.802
4TUJ	D_LYS_148	NZ	D_GLU_111	OE2	3.509
4TUJ	D_LYS_155	NZ	D_GLU_201	OE1	2.443
4TUJ	D_LYS_155	NZ	D_GLU_201	OE2	3.654

Table 621: 4TUJ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4TUK	H_ARG_38	NH1	H_ASP_90	OD1	2.774
4TUK	H_ARG_38	NH2	H_GLU_46	OE1	2.957
4TUK	H_ARG_38	NH2	H_ASP_90	OD1	3.936
4TUK	H_LYS_63	NZ	H_GLU_46	OE1	3.702
4TUK	H_LYS_63	NZ	H_GLU_46	OE2	2.804
4TUK	H_ARG_67	NH1	H_ASP_90	OD1	3.628
4TUK	H_ARG_67	NH1	H_ASP_90	OD2	2.878
4TUK	H_ARG_67	NH2	H_ASP_90	OD1	2.889
4TUK	H_ARG_67	NH2	H_ASP_90	OD2	3.540
4TUK	H_LYS_208	NZ	L_GLU_129	OE2	3.061
4TUK	L_ARG_24	NH2	L_ASP_75	OD2	3.142
4TUK	L_ARG_66	NH2	L_GLU_86	OE1	3.710
4TUK	L_ARG_66	NH2	L_GLU_86	OE2	3.717
4TUK	L_ARG_66	NH2	L_ASP_87	OD1	2.787
4TUK	L_ARG_66	NH2	L_ASP_87	OD2	3.636
4TUK	L_LYS_148	NZ	L_GLU_111	OE1	3.533
4TUK	L_LYS_148	NZ	L_GLU_111	OE2	2.823
4TUK	L_LYS_153	NZ	L_GLU_160	OE1	2.835
4TUK	L_LYS_153	NZ	L_GLU_160	OE2	3.347
4TUK	L_LYS_155	NZ	L_GLU_201	OE1	2.857
4TUK	L_LYS_155	NZ	L_GLU_201	OE2	3.381
4TUK	L_HIS_195	ND1	L_ASP_157	OD2	2.878
4TUK	L_LYS_205	NZ	L_ASP_116	OD1	3.635
4TUK	L_LYS_205	NZ	L_ASP_116	OD2	3.012

Table 622: 4TUK-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4TUL	H_ARG_38	NH1	H_ASP_90	OD1	2.759
4TUL	H_ARG_38	NH2	H_GLU_46	OE1	2.795
4TUL	H_ARG_38	NH2	H_GLU_46	OE2	3.616
4TUL	H_LYS_63	NZ	H_GLU_46	OE1	3.726
4TUL	H_LYS_63	NZ	H_GLU_46	OE2	2.751
4TUL	H_ARG_67	NH1	H_ASP_90	OD1	3.442
4TUL	H_ARG_67	NH1	H_ASP_90	OD2	2.779
4TUL	H_ARG_67	NH2	H_ASP_90	OD1	2.973
4TUL	H_ARG_67	NH2	H_ASP_90	OD2	3.614
4TUL	H_LYS_205	NZ	H_ASP_207	OD2	3.859
4TUL	H_LYS_208	NZ	L_GLU_129	OE1	3.059
4TUL	H_LYS_208	NZ	L_GLU_129	OE2	2.741
4TUL	H_LYS_209	NZ	H_GLU_211	OE2	3.869
4TUL	L_ARG_66	NH1	L_GLU_84	OE1	3.630
4TUL	L_ARG_66	NH2	L_GLU_84	OE1	3.505
4TUL	L_ARG_66	NH2	L_GLU_84	OE2	3.947
4TUL	L_ARG_66	NH2	L_ASP_87	OD1	2.922
4TUL	L_ARG_66	NH2	L_ASP_87	OD2	3.565
4TUL	L_LYS_148	NZ	L_GLU_111	OE1	2.732
4TUL	L_LYS_148	NZ	L_GLU_111	OE2	3.835
4TUL	L_LYS_153	NZ	L_GLU_160	OE1	2.798
4TUL	L_LYS_153	NZ	L_GLU_160	OE2	3.593
4TUL	L_LYS_155	NZ	L_GLU_201	OE1	2.684
4TUL	L_LYS_155	NZ	L_GLU_201	OE2	3.268
4TUL	L_HIS_195	ND1	L_ASP_157	OD2	2.731
4TUL	L_LYS_205	NZ	L_ASP_116	OD1	3.657
4TUL	L_LYS_205	NZ	L_ASP_116	OD2	2.664

Table 623: 4TUL-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4TUO	A_ARG_38	NH1	A_ASP_90	OD1	2.863
4TUO	A_ARG_38	NH2	A_GLU_46	OE1	3.170
4TUO	A_ARG_38	NH2	A_ASP_90	OD1	3.978
4TUO	A_LYS_63	NZ	A_GLU_46	OE1	3.760
4TUO	A_LYS_63	NZ	A_GLU_46	OE2	2.759
4TUO	A_ARG_67	NH1	A_ASP_90	OD1	3.571
4TUO	A_ARG_67	NH1	A_ASP_90	OD2	2.889
4TUO	A_ARG_67	NH2	A_ASP_90	OD1	3.053
4TUO	A_ARG_67	NH2	A_ASP_90	OD2	3.693
4TUO	A_LYS_208	NZ	B_GLU_129	OE1	3.043
4TUO	B_ARG_66	NH1	B_GLU_84	OE2	3.371
4TUO	B_ARG_66	NH2	B_GLU_84	OE1	3.783
4TUO	B_ARG_66	NH2	B_GLU_86	OE1	2.770
4TUO	B_ARG_66	NH2	B_ASP_87	OD1	2.806
4TUO	B_ARG_66	NH2	B_ASP_87	OD2	3.596
4TUO	B_ARG_82	NH1	B_GLU_84	OE2	3.609
4TUO	B_LYS_153	NZ	B_GLU_160	OE1	3.151
4TUO	B_LYS_153	NZ	C_GLU_10	OE2	3.051
4TUO	B_LYS_155	NZ	B_GLU_201	OE1	2.809
4TUO	B_LYS_155	NZ	B_GLU_201	OE2	3.457
4TUO	B_ARG_161	NH1	B_GLU_191	OE1	3.847
4TUO	B_ARG_161	NH1	B_GLU_191	OE2	3.170
4TUO	B_ARG_161	NH2	B_GLU_191	OE1	3.069
4TUO	B_ARG_161	NH2	B_GLU_191	OE2	3.668
4TUO	B_HIS_195	ND1	B_ASP_157	OD2	3.859
4TUO	B_LYS_205	NZ	B_ASP_116	OD1	3.307
4TUO	B_LYS_205	NZ	B_ASP_116	OD2	3.070
4TUO	C_ARG_38	NH1	C_ASP_90	OD1	2.853
4TUO	C_ARG_38	NH2	C_GLU_46	OE1	3.152
4TUO	C_LYS_63	NZ	C_GLU_46	OE1	3.805
4TUO	C_LYS_63	NZ	C_GLU_46	OE2	2.709
4TUO	C_ARG_67	NH1	C_ASP_90	OD1	3.699
4TUO	C_ARG_67	NH1	C_ASP_90	OD2	2.901
4TUO	C_ARG_67	NH2	C_ASP_90	OD1	3.051
4TUO	C_ARG_67	NH2	C_ASP_90	OD2	3.598
4TUO	C_LYS_208	NZ	D_GLU_129	OE1	2.720
4TUO	C_LYS_208	NZ	D_GLU_129	OE2	3.136
4TUO	C_LYS_209	NZ	C_GLU_211	OE2	2.713
4TUO	D_ARG_66	NH1	D_GLU_84	OE1	3.352
4TUO	D_ARG_66	NH1	D_GLU_84	OE2	3.741
4TUO	D_ARG_66	NH2	D_GLU_84	OE2	3.775
4TUO	D_ARG_66	NH2	D_GLU_86	OE2	3.297
4TUO	D_ARG_66	NH2	D_ASP_87	OD1	2.690
4TUO	D_ARG_66	NH2	D_ASP_87	OD2	3.681
4TUO	D_LYS_148	NZ	D_GLU_111	OE1	3.722
4TUO	D_LYS_148	NZ	D_GLU_111	OE2	2.538
4TUO	D_LYS_153	NZ	D_GLU_160	OE1	3.774
4TUO	D_LYS_155	NZ	D_GLU_201	OE1	3.955
4TUO	D_ARG_161	NH1	D_GLU_191	OE1	3.866
4TUO	D_ARG_194	NH1	D_ASP_190	OD1	3.370
4TUO	D_ARG_194	NH1	D_ASP_190	OD2	2.866
4TUO	D_HIS_195	ND1	D_ASP_157	OD2	3.872
4TUO	D_HIS_195	NE2	D_GLU_191	OE1	2.622
4TUO	D_LYS_205	NZ	D_ASP_116	OD1	3.469
4TUO	D_LYS_205	NZ	D_ASP_116	OD2	2.762

Table 624: 4TUO-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4U0Q	A_HIS_187	NE2	A_ASP_183	OD1	2.822
4U0Q	A_HIS_187	NE2	A_ASP_183	OD2	3.914
4U0Q	A_LYS_211	NZ	A_GLU_215	OE2	3.825
4U0Q	A_LYS_221	NZ	A_ASP_172	OD1	3.037
4U0Q	A_HIS_240	NE2	A_GLU_168	OE1	2.387
4U0Q	A_HIS_240	NE2	A_GLU_168	OE2	3.627
4U0Q	A_LYS_302	NZ	A_ASP_305	OD1	3.987
4U0Q	A_LYS_302	NZ	A_ASP_305	OD2	2.715
4U0Q	A_LYS_310	NZ	A_ASP_230	OD2	2.731
4U0Q	A_LYS_366	NZ	A_GLU_362	OE1	3.983
4U0Q	A_HIS_414	NE2	A_GLU_391	OE1	2.780
4U0Q	A_HIS_414	NE2	A_GLU_391	OE2	3.302
4U0Q	A_ARG_423	NH2	A_ASP_162	OD2	3.272
4U0Q	A_HIS_427	NE2	A_ASP_162	OD1	3.792
4U0Q	A_LYS_434	NZ	A_GLU_465	OE2	2.539
4U0Q	A_LYS_436	NZ	A_ASP_440	OD1	3.388
4U0Q	A_LYS_436	NZ	A_ASP_440	OD2	3.258
4U0Q	A_LYS_441	NZ	A_ASP_461	OD1	2.915
4U0Q	A_LYS_441	NZ	A_ASP_461	OD2	3.189
4U0Q	A_LYS_441	NZ	A_GLU_465	OE1	3.453
4U0Q	A_ARG_458	NH2	A_GLU_454	OE1	3.364
4U0Q	A_ARG_476	NH1	A_ASP_473	OD1	3.385
4U0Q	A_LYS_486	NZ	A_GLU_239	OE1	3.379
4U0Q	A_LYS_486	NZ	A_GLU_239	OE2	2.794
4U0Q	A_HIS_489	NE2	A_GLU_168	OE1	2.333
4U0Q	A_HIS_489	NE2	A_GLU_239	OE1	3.275
4U0Q	A_HIS_495	NE2	D_GLU_31	OE1	3.802
4U0Q	A_HIS_495	NE2	D_GLU_31	OE2	2.620
4U0Q	A_HIS_496	ND1	D_GLU_31	OE1	3.680
4U0Q	B_HIS_53	ND1	B_GLU_64	OE1	2.648
4U0Q	B_HIS_53	ND1	B_GLU_64	OE2	3.336
4U0Q	B_ARG_54	NH2	B_GLU_92	OE1	2.778
4U0Q	B_ARG_54	NH2	B_GLU_92	OE2	3.437
4U0Q	B_LYS_148	NZ	B_GLU_155	OE2	3.304
4U0Q	B_ARG_157	NH1	B_ASP_179	OD2	3.570
4U0Q	B_ARG_157	NH2	B_ASP_179	OD1	2.730
4U0Q	B_ARG_157	NH2	B_ASP_179	OD2	2.748
4U0Q	B_HIS_170	ND1	D_GLU_172	OE1	2.788
4U0Q	B_HIS_170	NE2	B_GLU_168	OE1	3.394
4U0Q	B_ARG_184	NH2	B_ASP_147	OD2	3.560
4U0Q	C_HIS_187	NE2	C_ASP_183	OD1	2.825
4U0Q	C_HIS_187	NE2	C_ASP_183	OD2	3.905
4U0Q	C_LYS_211	NZ	C_GLU_215	OE2	3.781
4U0Q	C_LYS_221	NZ	C_ASP_172	OD1	3.043
4U0Q	C_HIS_240	NE2	C_GLU_168	OE1	2.360
4U0Q	C_HIS_240	NE2	C_GLU_168	OE2	3.605
4U0Q	C_LYS_310	NZ	C_ASP_230	OD2	2.754
4U0Q	C_LYS_327	NZ	C_ASP_331	OD1	3.020
4U0Q	C_LYS_327	NZ	C_ASP_331	OD2	3.351
4U0Q	C_LYS_411	NZ	C_ASP_408	OD1	3.493
4U0Q	C_HIS_414	NE2	C_GLU_391	OE2	3.600
4U0Q	C_ARG_423	NH2	C_ASP_162	OD2	3.190
4U0Q	C_HIS_427	NE2	C_ASP_162	OD1	3.751
4U0Q	C_LYS_434	NZ	C_GLU_465	OE2	2.762
4U0Q	C_LYS_436	NZ	C_ASP_440	OD1	3.394
4U0Q	C_LYS_436	NZ	C_ASP_440	OD2	3.260
4U0Q	C_LYS_441	NZ	C_ASP_461	OD1	3.208

4U0Q	C_LYS_441	NZ	C_ASP_461	OD2	2.815
4U0Q	C_LYS_441	NZ	C_GLU_465	OE1	3.460
4U0Q	C_ARG_476	NH2	C_ASP_473	OD1	2.770
4U0Q	C_LYS_486	NZ	C_GLU_239	OE1	3.354
4U0Q	C_LYS_486	NZ	C_GLU_239	OE2	2.814
4U0Q	C_HIS_489	NE2	C_GLU_168	OE1	2.335
4U0Q	C_HIS_489	NE2	C_GLU_239	OE1	3.280
4U0Q	C_HIS_495	ND1	B_ASP_32	OD2	3.411
4U0Q	D_HIS_53	ND1	D_GLU_64	OE1	2.807
4U0Q	D_HIS_53	ND1	D_GLU_64	OE2	3.881
4U0Q	D_ARG_54	NH2	D_GLU_92	OE1	2.781
4U0Q	D_ARG_54	NH2	D_GLU_92	OE2	3.453
4U0Q	D_LYS_63	NZ	D_ASP_65	OD1	3.005
4U0Q	D_LYS_63	NZ	D_ASP_65	OD2	3.008
4U0Q	D_ARG_106	NH1	D_GLU_129	OE1	2.747
4U0Q	D_ARG_106	NH1	D_GLU_129	OE2	3.871
4U0Q	D_LYS_148	NZ	D_GLU_155	OE2	3.319
4U0Q	D_ARG_157	NH1	D_ASP_179	OD1	3.344
4U0Q	D_ARG_157	NH1	D_ASP_179	OD2	2.708
4U0Q	D_ARG_157	NH2	D_GLU_155	OE1	3.810
4U0Q	D_ARG_157	NH2	D_ASP_179	OD1	2.790
4U0Q	D_ARG_157	NH2	D_ASP_179	OD2	3.368
4U0Q	D_HIS_170	ND1	B_GLU_172	OE1	2.879
4U0Q	D_HIS_170	ND1	B_GLU_172	OE2	2.959
4U0Q	D_HIS_170	NE2	D_GLU_168	OE1	3.465
4U0Q	D_ARG_184	NH2	D_ASP_147	OD2	3.553
4U0Q	D_LYS_191	NZ	C_GLU_362	OE2	3.108

Table 625: 4U0Q-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4U3X	A_ARG_38	NH1	A_ASP_90	OD1	2.898
4U3X	A_ARG_67	NH1	A_ASP_90	OD1	3.886
4U3X	A_ARG_67	NH1	A_ASP_90	OD2	2.695
4U3X	A_ARG_67	NH2	A_ASP_90	OD1	3.163
4U3X	A_ARG_67	NH2	A_ASP_90	OD2	3.392
4U3X	A_LYS_98	NZ	A_GLU_32	OE2	3.316
4U3X	A_HIS_106	NE2	B_GLU_35	OE1	2.597
4U3X	A_HIS_106	NE2	B_GLU_35	OE2	3.650
4U3X	B_LYS_1	NZ	B_GLU_7	OE1	2.763
4U3X	B_LYS_1	NZ	B_GLU_7	OE2	3.987
4U3X	B_ARG_61	NH1	A_ASP_33	OD2	2.723
4U3X	B_ARG_61	NH2	A_ASP_33	OD2	2.983
4U3X	B_ARG_112	NH2	A_ASP_109	OD1	3.763
4U3X	B_ARG_112	NH2	A_ASP_109	OD2	3.035
4U3X	B_ARG_125	NH1	B_ASP_119	OD2	3.378
4U3X	B_ARG_125	NH2	B_ASP_119	OD1	3.266
4U3X	B_ARG_125	NH2	B_ASP_119	OD2	3.781
4U3X	C_ARG_38	NH1	C_ASP_90	OD1	3.008
4U3X	C_ARG_38	NH2	C_ASP_90	OD1	3.918
4U3X	C_ARG_67	NH1	C_ASP_90	OD1	3.636
4U3X	C_ARG_67	NH1	C_ASP_90	OD2	3.951
4U3X	C_ARG_67	NH2	C_ASP_90	OD1	3.430
4U3X	C_ARG_67	NH2	C_ASP_90	OD2	2.349
4U3X	C_LYS_98	NZ	C_GLU_32	OE1	3.558
4U3X	C_LYS_98	NZ	C_GLU_32	OE2	2.950
4U3X	C_HIS_106	NE2	D_GLU_35	OE1	2.720
4U3X	C_HIS_106	NE2	D_GLU_35	OE2	3.669
4U3X	D_LYS_1	NZ	D_GLU_7	OE1	3.339
4U3X	D_LYS_1	NZ	D_GLU_7	OE2	2.952
4U3X	D_LYS_13	NZ	D_ASP_18	OD2	3.704
4U3X	D_ARG_61	NH1	C_ASP_33	OD2	3.116
4U3X	D_ARG_61	NH2	C_ASP_33	OD2	3.400
4U3X	D_ARG_112	NH2	C_ASP_109	OD2	3.567
4U3X	D_ARG_125	NH1	D_ASP_119	OD1	3.983
4U3X	D_ARG_125	NH1	D_ASP_119	OD2	3.205
4U3X	D_ARG_125	NH2	D_ASP_119	OD1	3.233
4U3X	D_ARG_125	NH2	D_ASP_119	OD2	3.715

Table 626: 4U3X-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4U6G	H_ARG_38	NH1	H_ASP_86	OD1	3.182
4U6G	H_ARG_38	NH2	H_GLU_46	OE1	3.518
4U6G	H_ARG_38	NH2	H_GLU_46	OE2	3.054
4U6G	H_ARG_50	NH1	H_ASP_58	OD2	3.942
4U6G	H_ARG_50	NH1	H_GLU_100J	OE1	3.369
4U6G	H_ARG_50	NH1	H_GLU_100J	OE2	2.951
4U6G	H_ARG_50	NH2	H_ASP_58	OD2	2.415
4U6G	H_ARG_66	NH1	H_ASP_86	OD2	3.486
4U6G	H_ARG_66	NH2	H_ASP_86	OD1	3.579
4U6G	H_ARG_66	NH2	H_ASP_86	OD2	3.807
4U6G	H_ARG_94	NH2	H_ASP_102	OD1	2.954
4U6G	H_LYS_143	NZ	L_GLU_125	OE2	3.603
4U6G	H_LYS_209	NZ	L_GLU_124	OE1	2.829
4U6G	H_LYS_209	NZ	L_GLU_124	OE2	2.866
4U6G	H_ARG_210	NH1	H_GLU_212	OE2	3.692
4U6G	H_ARG_210	NH2	H_GLU_212	OE2	3.652
4U6G	L_ARG_29	NH1	L_ASP_26	OD1	3.440
4U6G	L_HIS_31	ND1	H_GLU_100I	OE2	3.196
4U6G	L_ARG_54	NH1	L_ASP_60	OD1	3.819
4U6G	L_ARG_61	NH1	B_GLU_81	OE1	3.298
4U6G	L_ARG_61	NH2	L_ASP_82	OD1	3.284
4U6G	L_ARG_61	NH2	L_ASP_82	OD2	3.928
4U6G	L_ARG_91	NH1	H_GLU_100J	OE1	3.679
4U6G	L_ARG_91	NH1	H_GLU_100J	OE2	3.478
4U6G	L_ARG_91	NH2	H_GLU_100J	OE2	3.428
4U6G	L_LYS_93	NZ	L_GLU_3	OE2	3.425
4U6G	L_LYS_103	NZ	L_ASP_83	OD1	2.775
4U6G	L_LYS_150	NZ	L_GLU_204	OE2	3.294
4U6G	A_ARG_38	NH1	A_ASP_86	OD1	3.130
4U6G	A_ARG_38	NH2	A_GLU_46	OE2	3.390
4U6G	A_ARG_50	NH1	A_GLU_100J	OE1	2.748
4U6G	A_ARG_50	NH1	A_GLU_100J	OE2	2.961
4U6G	A_ARG_50	NH2	A_ASP_58	OD2	2.646
4U6G	A_ARG_50	NH2	A_GLU_100J	OE2	3.684
4U6G	A_ARG_66	NH1	A_ASP_86	OD2	3.552
4U6G	A_ARG_66	NH2	A_ASP_86	OD1	3.394
4U6G	A_ARG_66	NH2	A_ASP_86	OD2	3.979
4U6G	A_ARG_94	NH2	A_ASP_102	OD1	2.808
4U6G	A_LYS_143	NZ	B_GLU_125	OE2	3.217
4U6G	A_LYS_201	NZ	H_ASP_30	OD1	3.983
4U6G	A_LYS_209	NZ	B_GLU_124	OE1	2.769
4U6G	A_LYS_209	NZ	B_GLU_124	OE2	3.063
4U6G	B_ARG_29	NH1	B_ASP_26	OD1	3.536
4U6G	B_HIS_31	ND1	A_GLU_100I	OE2	3.102
4U6G	B_ARG_54	NH1	B_ASP_60	OD1	3.700
4U6G	B_ARG_61	NH2	B_GLU_81	OE1	3.869
4U6G	B_ARG_61	NH2	B_ASP_82	OD1	3.159
4U6G	B_ARG_61	NH2	B_ASP_82	OD2	3.682
4U6G	B_ARG_91	NH1	A_GLU_100J	OE1	3.587
4U6G	B_ARG_91	NH1	A_GLU_100J	OE2	3.310
4U6G	B_ARG_91	NH2	A_GLU_100J	OE2	3.407
4U6G	B_LYS_103	NZ	B_ASP_83	OD1	2.873
4U6G	B_LYS_111	NZ	B_GLU_199	OE1	3.272
4U6G	B_LYS_150	NZ	B_GLU_204	OE1	3.711
4U6G	B_LYS_150	NZ	B_GLU_204	OE2	3.254

Table 627: 4U6G-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4U6V	H_HIS_35	NE2	H_ASP_98	OD1	3.305
4U6V	H_HIS_35	NE2	H_ASP_98	OD2	2.654
4U6V	H_ARG_38	NH1	H_ASP_89	OD2	2.858
4U6V	H_ARG_38	NH2	H_GLU_46	OE1	3.188
4U6V	H_ARG_38	NH2	H_GLU_46	OE2	3.968
4U6V	H_ARG_38	NH2	H_ASP_89	OD2	3.604
4U6V	H_ARG_66	NH1	H_ASP_89	OD1	2.752
4U6V	H_ARG_66	NH1	H_ASP_89	OD2	3.786
4U6V	H_ARG_66	NH2	H_ASP_89	OD1	3.455
4U6V	H_ARG_66	NH2	H_ASP_89	OD2	2.979
4U6V	H_ARG_97	NH2	H_ASP_110	OD2	2.478
4U6V	H_ARG_99	NH2	H_ASP_110	OD1	3.312
4U6V	H_ARG_99	NH2	L_GLU_55	OE1	2.660
4U6V	H_ARG_99	NH2	L_GLU_55	OE2	2.823
4U6V	H_HIS_105	NE2	A_ASP_183	OD1	3.150
4U6V	H_HIS_105	NE2	A_ASP_183	OD2	3.236
4U6V	H_LYS_152	NZ	H_ASP_153	OD1	3.594
4U6V	H_LYS_152	NZ	H_ASP_153	OD2	3.480
4U6V	H_LYS_215	NZ	H_ASP_217	OD1	3.333
4U6V	H_LYS_215	NZ	H_ASP_217	OD2	3.285
4U6V	H_LYS_218	NZ	L_GLU_122	OE1	2.258
4U6V	H_LYS_218	NZ	L_GLU_122	OE2	3.923
4U6V	H_ARG_219	NH1	H_GLU_221	OE1	3.555
4U6V	L_ARG_24	NH2	L_GLU_70	OE1	3.373
4U6V	L_LYS_39	NZ	L_ASP_81	OD1	3.062
4U6V	L_LYS_39	NZ	L_ASP_81	OD2	3.255
4U6V	L_ARG_61	NH2	L_ASP_82	OD1	2.876
4U6V	L_ARG_61	NH2	L_ASP_82	OD2	3.235
4U6V	L_ARG_141	NH1	L_GLU_164	OE2	3.480
4U6V	L_ARG_141	NH2	L_GLU_104	OE1	3.162
4U6V	L_ARG_141	NH2	L_GLU_104	OE2	3.384
4U6V	L_ARG_141	NH2	L_GLU_164	OE1	3.915
4U6V	L_ARG_141	NH2	L_GLU_164	OE2	3.880
4U6V	L_LYS_148	NZ	L_GLU_194	OE2	3.817
4U6V	L_LYS_187	NZ	L_ASP_184	OD1	3.136
4U6V	A_LYS_36	NZ	A_GLU_280	OE1	3.134
4U6V	A_LYS_46	NZ	A_ASP_44	OD2	3.954
4U6V	A_LYS_51	NZ	A_ASP_44	OD2	3.960
4U6V	A_LYS_51	NZ	A_GLU_289	OE2	3.066
4U6V	A_ARG_56	NH2	A_ASP_227	OD1	3.348
4U6V	A_ARG_56	NH2	A_ASP_227	OD2	2.841
4U6V	A_LYS_85	NZ	A_GLU_250	OE2	3.967
4U6V	A_ARG_104	NH2	A_ASP_100	OD1	3.350
4U6V	A_ARG_104	NH2	A_ASP_100	OD2	2.842
4U6V	A_LYS_147	NZ	A_GLU_111	OE1	3.728
4U6V	A_LYS_163	NZ	A_ASP_162	OD2	3.943
4U6V	A_LYS_164	NZ	A_GLU_158	OE1	3.750
4U6V	A_ARG_184	NH2	A_ASP_254	OD1	2.848
4U6V	A_ARG_184	NH2	A_ASP_254	OD2	2.966
4U6V	A_ARG_184	NH2	A_ASP_272	OD1	2.573
4U6V	A_ARG_200	NH1	H_ASP_56	OD1	3.722
4U6V	A_ARG_200	NH1	H_ASP_56	OD2	3.481
4U6V	A_LYS_205	NZ	A_GLU_70	OE1	3.668
4U6V	A_LYS_205	NZ	A_GLU_70	OE2	3.472
4U6V	A_ARG_236	NH1	A_ASP_44	OD1	3.407
4U6V	A_ARG_236	NH2	A_ASP_44	OD1	3.125
4U6V	A_ARG_251	NH2	A_ASP_276	OD2	3.363

4U6V	A_ARG_253	NH2	A_ASP_276	OD1	2.926
4U6V	A_ARG_253	NH2	A_ASP_276	OD2	3.227
4U6V	A_LYS_266	NZ	L_ASP_93	OD1	2.981
4U6V	A_LYS_271	NZ	A_ASP_185	OD1	2.718
4U6V	A_LYS_273	NZ	A_ASP_255	OD2	3.278
4U6V	A_ARG_277	NH2	A_GLU_250	OE1	2.466
4U6V	A_ARG_281	NH2	A_ASP_246	OD1	2.738
4U6V	K_HIS_35	NE2	K_ASP_98	OD1	3.310
4U6V	K_HIS_35	NE2	K_ASP_98	OD2	2.683
4U6V	K_ARG_38	NH1	K_ASP_89	OD2	2.844
4U6V	K_ARG_38	NH2	K_GLU_46	OE1	3.203
4U6V	K_ARG_38	NH2	K_GLU_46	OE2	3.978
4U6V	K_ARG_38	NH2	K_ASP_89	OD2	3.616
4U6V	K_ARG_66	NH1	K_ASP_89	OD1	2.744
4U6V	K_ARG_66	NH1	K_ASP_89	OD2	3.770
4U6V	K_ARG_66	NH2	K_ASP_89	OD1	3.441
4U6V	K_ARG_66	NH2	K_ASP_89	OD2	2.968
4U6V	K_ARG_97	NH2	K_ASP_110	OD2	2.501
4U6V	K_ARG_99	NH2	K_ASP_110	OD1	3.302
4U6V	K_ARG_99	NH2	M_GLU_55	OE1	2.606
4U6V	K_ARG_99	NH2	M_GLU_55	OE2	2.857
4U6V	K_HIS_105	NE2	B_ASP_183	OD1	2.992
4U6V	K_HIS_105	NE2	B_ASP_183	OD2	3.142
4U6V	K_LYS_152	NZ	K_ASP_153	OD1	3.584
4U6V	K_LYS_152	NZ	K_ASP_153	OD2	3.467
4U6V	K_LYS_215	NZ	K_ASP_217	OD1	3.339
4U6V	K_LYS_215	NZ	K_ASP_217	OD2	3.278
4U6V	K_LYS_218	NZ	M_GLU_122	OE1	2.653
4U6V	K_ARG_219	NH1	K_GLU_221	OE1	3.551
4U6V	M_ARG_24	NH2	M_GLU_70	OE1	3.369
4U6V	M_LYS_39	NZ	M_ASP_81	OD1	3.066
4U6V	M_LYS_39	NZ	M_ASP_81	OD2	3.241
4U6V	M_ARG_61	NH2	M_ASP_82	OD1	2.871
4U6V	M_ARG_61	NH2	M_ASP_82	OD2	3.232
4U6V	M_ARG_141	NH1	M_GLU_164	OE2	3.486
4U6V	M_ARG_141	NH2	M_GLU_104	OE1	3.180
4U6V	M_ARG_141	NH2	M_GLU_104	OE2	3.454
4U6V	M_ARG_141	NH2	M_GLU_164	OE1	3.895
4U6V	M_ARG_141	NH2	M_GLU_164	OE2	3.876
4U6V	M_LYS_148	NZ	M_GLU_194	OE1	3.300
4U6V	M_LYS_168	NZ	M_ASP_166	OD1	3.534
4U6V	M_LYS_168	NZ	M_ASP_169	OD2	3.988
4U6V	M_LYS_187	NZ	M_ASP_184	OD1	3.129
4U6V	M_HIS_188	ND1	M_ASP_150	OD2	3.072
4U6V	B_LYS_36	NZ	B_GLU_280	OE1	3.143
4U6V	B_LYS_46	NZ	B_ASP_44	OD2	3.962
4U6V	B_LYS_51	NZ	B_ASP_44	OD2	3.959
4U6V	B_LYS_51	NZ	B_GLU_289	OE2	3.068
4U6V	B_ARG_56	NH2	B_ASP_227	OD1	3.358
4U6V	B_ARG_56	NH2	B_ASP_227	OD2	2.849
4U6V	B_LYS_85	NZ	B_GLU_250	OE2	3.970
4U6V	B_ARG_104	NH2	B_ASP_100	OD1	3.340
4U6V	B_ARG_104	NH2	B_ASP_100	OD2	2.845
4U6V	B_LYS_147	NZ	B_GLU_111	OE1	3.726
4U6V	B_LYS_163	NZ	B_ASP_162	OD2	3.942
4U6V	B_LYS_164	NZ	B_GLU_158	OE1	3.594
4U6V	B_ARG_184	NH2	B_ASP_254	OD1	2.852
4U6V	B_ARG_184	NH2	B_ASP_254	OD2	2.960

4U6V	B_ARG_184	NH2	B_ASP_272	OD1	2.585
4U6V	B_ARG_200	NH1	K_ASP_56	OD1	3.809
4U6V	B_ARG_200	NH1	K_ASP_56	OD2	3.557
4U6V	B_LYS_205	NZ	B_GLU_70	OE1	3.673
4U6V	B_LYS_205	NZ	B_GLU_70	OE2	3.473
4U6V	B_ARG_236	NH1	B_ASP_44	OD1	3.418
4U6V	B_ARG_236	NH2	B_ASP_44	OD1	3.133
4U6V	B_ARG_251	NH2	B_ASP_276	OD2	3.376
4U6V	B_ARG_253	NH2	B_ASP_276	OD1	2.931
4U6V	B_ARG_253	NH2	B_ASP_276	OD2	3.222
4U6V	B_LYS_266	NZ	M_ASP_93	OD1	3.145
4U6V	B_LYS_271	NZ	B_ASP_185	OD1	2.724
4U6V	B_LYS_273	NZ	B_ASP_255	OD2	3.277
4U6V	B_ARG_277	NH2	B_GLU_250	OE1	2.460
4U6V	B_ARG_281	NH2	B_ASP_246	OD1	2.737

Table 628: 4U6V-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4UAO	A_ARG_73	NH2	A_GLU_201	OE1	3.924
4UAO	A_ARG_73	NH2	A_GLU_201	OE2	3.498
4UAO	A_ARG_120	NH1	A_GLU_123	OE1	3.546
4UAO	A_ARG_120	NH1	A_ASP_216	OD2	3.693
4UAO	A_ARG_120	NH2	A_GLU_123	OE1	3.780
4UAO	A_LYS_122	NZ	A_ASP_216	OD2	2.797
4UAO	A_LYS_190	NZ	A_ASP_158	OD2	3.237
4UAO	A_LYS_190	NZ	A_GLU_187	OE2	3.980
4UAO	A_LYS_237	NZ	A_GLU_78	OE1	3.297
4UAO	A_ARG_249	NH1	A_GLU_187	OE1	3.415
4UAO	A_ARG_249	NH1	A_GLU_381	OE1	3.557
4UAO	A_ARG_249	NH1	A_GLU_381	OE2	3.345
4UAO	A_ARG_249	NH2	A_GLU_187	OE1	3.981
4UAO	A_LYS_250	NZ	A_GLU_381	OE2	3.404
4UAO	A_LYS_256	NZ	A_GLU_267	OE1	2.830
4UAO	A_LYS_256	NZ	A_GLU_267	OE2	3.541
4UAO	A_ARG_277	NH1	A_GLU_275	OE1	2.891
4UAO	A_ARG_280	NH1	A_ASP_230	OD1	2.845
4UAO	A_ARG_280	NH1	A_ASP_230	OD2	3.123
4UAO	A_ARG_280	NH2	A_ASP_230	OD2	3.328
4UAO	A_ARG_284	NH2	A_ASP_224	OD1	3.788
4UAO	A_ARG_284	NH2	A_ASP_224	OD2	3.066
4UAO	A_ARG_296	NH2	A_GLU_288	OE1	2.772
4UAO	A_ARG_317	NH1	C_GLU_100B	OE2	3.537
4UAO	A_ARG_317	NH2	C_GLU_100B	OE1	3.794
4UAO	A_ARG_317	NH2	C_GLU_100B	OE2	2.800
4UAO	A_LYS_336	NZ	A_ASP_79	OD1	2.775
4UAO	A_LYS_336	NZ	A_ASP_79	OD2	3.272
4UAO	A_LYS_353	NZ	A_GLU_273	OE1	3.628
4UAO	A_LYS_360	NZ	A_ASP_63	OD1	3.580
4UAO	A_LYS_360	NZ	A_ASP_63	OD2	3.421
4UAO	B_ARG_61	NH2	B_ASP_82	OD1	3.532
4UAO	B_ARG_66	NH2	B_ASP_28	OD1	3.432
4UAO	B_LYS_92	NZ	B_ASP_28	OD2	3.374
4UAO	B_ARG_103	NH2	B_ASP_165	OD1	2.738
4UAO	B_ARG_108	NH1	B_ASP_170	OD2	3.952
4UAO	B_LYS_149	NZ	B_GLU_195	OE2	3.010
4UAO	B_ARG_155	NH1	B_ASP_157	OD1	3.116
4UAO	B_ARG_155	NH1	B_ASP_185	OD2	3.521
4UAO	B_ARG_155	NH2	B_ASP_185	OD1	3.054
4UAO	B_ARG_155	NH2	B_ASP_185	OD2	3.232
4UAO	B_HIS_189	ND1	B_ASP_185	OD1	3.890
4UAO	B_LYS_199	NZ	B_ASP_110	OD1	3.495
4UAO	B_LYS_199	NZ	B_ASP_110	OD2	3.079
4UAO	C_ARG_38	NH1	C_ASP_86	OD1	3.163
4UAO	C_ARG_38	NH2	C_GLU_46	OE1	3.888
4UAO	C_ARG_38	NH2	C_GLU_46	OE2	3.064
4UAO	C_ARG_38	NH2	C_ASP_86	OD1	3.804
4UAO	C_ARG_56	NH1	A_GLU_81	OE2	2.819
4UAO	C_ARG_56	NH2	A_ASP_174	OD1	3.129
4UAO	C_ARG_56	NH2	A_ASP_174	OD2	2.857
4UAO	C_ARG_66	NH1	C_GLU_83	OE1	3.463
4UAO	C_ARG_66	NH1	C_ASP_86	OD1	2.970
4UAO	C_ARG_66	NH1	C_ASP_86	OD2	2.789
4UAO	C_ARG_66	NH2	C_GLU_83	OE1	3.731
4UAO	C_ARG_94	NH1	C_GLU_100B	OE1	2.986
4UAO	C_ARG_94	NH1	C_ASP_101	OD1	3.545

4UAO	C_ARG_94	NH1	C_ASP_101	OD2	3.032
4UAO	C_ARG_95	NH1	C_ASP_100C	OD2	2.956
4UAO	C_ARG_95	NH2	A_GLU_173	OE2	3.027

Table 629: 4UAO-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4UV6	A_ARG_73	NH1	A_GLU_201	OE1	2.994
4UV6	A_ARG_73	NH1	A_GLU_201	OE2	3.932
4UV6	A_ARG_73	NH2	A_GLU_201	OE1	3.217
4UV6	A_ARG_73	NH2	A_GLU_201	OE2	2.666
4UV6	A_ARG_73	NH2	A_GLU_288	OE2	3.591
4UV6	A_ARG_120	NH1	A_GLU_123	OE2	3.707
4UV6	A_ARG_120	NH2	A_ASP_216	OD1	3.645
4UV6	A_LYS_122	NZ	A_ASP_216	OD1	3.360
4UV6	A_ARG_146	NH2	A_ASP_133	OD2	3.248
4UV6	A_LYS_148	NZ	A_GLU_145	OE2	3.128
4UV6	A_LYS_190	NZ	A_ASP_158	OD2	3.666
4UV6	A_LYS_222	NZ	A_GLU_104	OE2	2.916
4UV6	A_LYS_237	NZ	A_GLU_78	OE1	2.996
4UV6	A_LYS_237	NZ	A_GLU_78	OE2	3.806
4UV6	A_LYS_246	NZ	A_ASP_242	OD2	3.993
4UV6	A_ARG_249	NH1	A_GLU_187	OE1	3.777
4UV6	A_ARG_249	NH1	A_GLU_187	OE2	2.741
4UV6	A_ARG_249	NH2	A_GLU_187	OE1	2.790
4UV6	A_ARG_249	NH2	A_GLU_187	OE2	3.285
4UV6	A_ARG_249	NH2	A_GLU_381	OE1	3.049
4UV6	A_ARG_249	NH2	A_GLU_381	OE2	2.841
4UV6	A_LYS_256	NZ	A_GLU_267	OE1	3.465
4UV6	A_LYS_256	NZ	A_GLU_267	OE2	3.209
4UV6	A_LYS_256	NZ	A_ASP_367	OD2	3.488
4UV6	A_ARG_277	NH2	A_GLU_275	OE2	3.331
4UV6	A_ARG_280	NH1	A_ASP_230	OD1	2.732
4UV6	A_ARG_280	NH1	A_ASP_230	OD2	3.546
4UV6	A_ARG_280	NH2	A_GLU_227	OE1	3.879
4UV6	A_ARG_280	NH2	A_ASP_230	OD1	3.530
4UV6	A_ARG_280	NH2	A_ASP_230	OD2	2.776
4UV6	A_ARG_284	NH2	A_ASP_224	OD1	3.612
4UV6	A_ARG_284	NH2	A_ASP_224	OD2	3.190
4UV6	A_ARG_296	NH2	A_GLU_288	OE2	3.629
4UV6	A_ARG_313	NH1	A_GLU_310	OE1	2.851
4UV6	A_ARG_313	NH1	A_GLU_310	OE2	3.172
4UV6	A_LYS_321	NZ	A_ASP_318	OD1	3.965
4UV6	A_LYS_336	NZ	A_ASP_79	OD1	3.453
4UV6	A_LYS_336	NZ	A_ASP_79	OD2	3.112
4UV6	A_LYS_336	NZ	A_ASP_333	OD1	3.782
4UV6	A_HIS_378	NE2	A_GLU_381	OE2	3.710
4UV6	B_ARG_73	NH1	B_GLU_201	OE1	3.228
4UV6	B_ARG_73	NH2	B_GLU_201	OE1	3.286
4UV6	B_ARG_73	NH2	B_GLU_201	OE2	2.695
4UV6	B_ARG_73	NH2	B_GLU_288	OE2	3.736
4UV6	B_LYS_148	NZ	B_GLU_145	OE2	3.156
4UV6	B_ARG_180	NH2	A_GLU_396	OE2	2.784
4UV6	B_LYS_190	NZ	B_ASP_158	OD2	3.677
4UV6	B_LYS_222	NZ	B_GLU_104	OE2	2.924
4UV6	B_LYS_237	NZ	B_GLU_78	OE1	2.994
4UV6	B_LYS_237	NZ	B_GLU_78	OE2	3.805
4UV6	B_LYS_246	NZ	B_ASP_242	OD2	3.993
4UV6	B_ARG_249	NH1	B_GLU_187	OE1	3.799
4UV6	B_ARG_249	NH1	B_GLU_187	OE2	2.742
4UV6	B_ARG_249	NH2	B_GLU_187	OE1	2.790
4UV6	B_ARG_249	NH2	B_GLU_187	OE2	3.296
4UV6	B_ARG_249	NH2	B_GLU_381	OE1	3.038
4UV6	B_ARG_249	NH2	B_GLU_381	OE2	2.812

4UV6	B_LYS_256	NZ	B_GLU_267	OE1	3.476
4UV6	B_LYS_256	NZ	B_GLU_267	OE2	3.242
4UV6	B_LYS_256	NZ	B_ASP_367	OD2	3.465
4UV6	B_ARG_277	NH2	B_GLU_275	OE2	3.309
4UV6	B_ARG_280	NH1	B_ASP_230	OD1	2.709
4UV6	B_ARG_280	NH1	B_ASP_230	OD2	3.518
4UV6	B_ARG_280	NH2	B_GLU_227	OE2	3.911
4UV6	B_ARG_280	NH2	B_ASP_230	OD1	3.525
4UV6	B_ARG_280	NH2	B_ASP_230	OD2	2.745
4UV6	B_ARG_284	NH2	B_ASP_224	OD1	3.584
4UV6	B_ARG_284	NH2	B_ASP_224	OD2	3.156
4UV6	B_ARG_313	NH1	B_GLU_310	OE1	2.951
4UV6	B_ARG_313	NH1	B_GLU_310	OE2	2.848
4UV6	B_ARG_313	NH2	A_GLU_60	OE1	2.768
4UV6	B_LYS_321	NZ	B_ASP_318	OD1	3.922
4UV6	B_LYS_336	NZ	B_ASP_79	OD2	3.702
4UV6	B_LYS_336	NZ	B_ASP_333	OD1	3.823
4UV6	B_HIS_378	NE2	B_GLU_381	OE2	3.739

Table 630: 4UV6-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4WEU	D_ARG_838	NH1	D_ASP_890	OD1	3.018
4WEU	D_ARG_838	NH2	D_GLU_846	OE1	2.933
4WEU	D_ARG_838	NH2	D_GLU_846	OE2	3.823
4WEU	D_ARG_867	NH1	D_ASP_890	OD1	3.567
4WEU	D_ARG_867	NH1	D_ASP_890	OD2	2.686
4WEU	D_ARG_867	NH2	D_ASP_890	OD1	2.946
4WEU	D_ARG_867	NH2	D_ASP_890	OD2	3.615
4WEU	D_LYS_887	NZ	A_GLU_145	OE1	3.143
4WEU	A_LYS_49	NZ	A_GLU_240	OE2	2.906
4WEU	A_ARG_64	NH1	A_GLU_26	OE2	3.571
4WEU	A_LYS_66	NZ	A_GLU_26	OE1	3.929
4WEU	A_ARG_96	NH1	A_GLU_94	OE2	3.701
4WEU	A_ARG_96	NH1	B_GLU_94	OE1	3.636
4WEU	A_ARG_96	NH1	B_GLU_94	OE2	3.058
4WEU	A_ARG_96	NH2	B_GLU_94	OE1	2.949
4WEU	A_ARG_96	NH2	B_GLU_94	OE2	3.852
4WEU	A_LYS_104	NZ	A_GLU_101	OE1	3.418
4WEU	A_LYS_120	NZ	A_GLU_89	OE1	2.914
4WEU	A_ARG_136	NH1	D_GLU_889	OE1	2.898
4WEU	A_ARG_136	NH2	A_GLU_145	OE1	3.553
4WEU	A_HIS_155	NE2	A_GLU_152	OE2	2.869
4WEU	A_LYS_172	NZ	A_GLU_170	OE2	3.445
4WEU	B_LYS_49	NZ	B_GLU_240	OE1	3.611
4WEU	B_LYS_49	NZ	B_GLU_240	OE2	3.160
4WEU	B_ARG_64	NH1	B_GLU_26	OE2	3.559
4WEU	B_LYS_66	NZ	B_GLU_26	OE1	3.923
4WEU	B_ARG_96	NH1	A_GLU_94	OE1	3.754
4WEU	B_ARG_96	NH1	A_GLU_94	OE2	2.795
4WEU	B_ARG_96	NH1	B_GLU_94	OE2	3.704
4WEU	B_ARG_96	NH2	A_GLU_94	OE1	2.707
4WEU	B_ARG_96	NH2	A_GLU_94	OE2	3.344
4WEU	B_LYS_120	NZ	B_GLU_89	OE1	2.742
4WEU	B_ARG_136	NH2	B_GLU_145	OE1	3.533
4WEU	B_HIS_155	NE2	B_GLU_152	OE1	3.472
4WEU	B_HIS_155	NE2	B_GLU_152	OE2	2.880
4WEU	B_LYS_172	NZ	B_GLU_170	OE2	3.468
4WEU	B_ARG_198	NH1	B_GLU_67	OE2	2.375
4WEU	B_ARG_198	NH2	B_GLU_67	OE2	3.911
4WEU	E_ARG_838	NH1	E_ASP_890	OD1	3.012
4WEU	E_ARG_838	NH2	E_GLU_846	OE1	2.950
4WEU	E_ARG_838	NH2	E_GLU_846	OE2	3.817
4WEU	E_ARG_867	NH1	E_ASP_890	OD1	3.574
4WEU	E_ARG_867	NH1	E_ASP_890	OD2	2.661
4WEU	E_ARG_867	NH2	E_ASP_890	OD1	2.927
4WEU	E_ARG_867	NH2	E_ASP_890	OD2	3.566

Table 631: 4WEU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4WHT	A_ARG_38	NH1	A_ASP_90	OD1	2.990
4WHT	A_ARG_38	NH2	A_GLU_46	OE1	2.993
4WHT	A_ARG_38	NH2	A_GLU_89	OE1	3.403
4WHT	A_ARG_61	NH2	A_GLU_46	OE2	3.778
4WHT	A_LYS_65	NZ	A_ASP_62	OD1	3.169
4WHT	A_ARG_67	NH1	A_ASP_90	OD1	3.859
4WHT	A_ARG_67	NH1	A_ASP_90	OD2	2.717
4WHT	A_ARG_67	NH2	A_GLU_89	OE1	3.463
4WHT	A_ARG_67	NH2	A_ASP_90	OD1	3.102
4WHT	A_ARG_67	NH2	A_ASP_90	OD2	3.428
4WHT	A_ARG_98	NH1	A_ASP_100	OD1	3.573
4WHT	A_ARG_98	NH1	A_ASP_100	OD2	2.704
4WHT	A_LYS_207	NZ	B_GLU_127	OE1	2.607
4WHT	A_LYS_207	NZ	B_GLU_127	OE2	3.670
4WHT	C_ARG_38	NH1	C_ASP_90	OD1	2.946
4WHT	C_ARG_38	NH2	C_GLU_46	OE1	2.996
4WHT	C_ARG_38	NH2	C_GLU_89	OE1	3.393
4WHT	C_ARG_61	NH2	C_GLU_46	OE2	3.777
4WHT	C_LYS_65	NZ	C_ASP_62	OD1	3.197
4WHT	C_ARG_67	NH1	C_ASP_90	OD1	3.881
4WHT	C_ARG_67	NH1	C_ASP_90	OD2	2.676
4WHT	C_ARG_67	NH2	C_GLU_89	OE1	3.528
4WHT	C_ARG_67	NH2	C_ASP_90	OD1	3.088
4WHT	C_ARG_67	NH2	C_ASP_90	OD2	3.360
4WHT	C_ARG_98	NH2	C_ASP_100	OD1	3.559
4WHT	C_ARG_98	NH2	C_ASP_100	OD2	2.716
4WHT	C_LYS_204	NZ	C_ASP_206	OD1	2.994
4WHT	C_LYS_204	NZ	C_ASP_206	OD2	3.710
4WHT	C_LYS_207	NZ	D_GLU_127	OE1	3.293
4WHT	E_ARG_38	NH1	E_ASP_90	OD1	2.955
4WHT	E_ARG_38	NH2	E_GLU_46	OE1	2.986
4WHT	E_ARG_38	NH2	E_GLU_89	OE1	3.434
4WHT	E_ARG_61	NH2	E_GLU_46	OE2	3.795
4WHT	E_LYS_65	NZ	E_ASP_62	OD1	3.160
4WHT	E_ARG_67	NH1	E_ASP_90	OD1	3.902
4WHT	E_ARG_67	NH1	E_ASP_90	OD2	2.757
4WHT	E_ARG_67	NH2	E_GLU_89	OE1	3.512
4WHT	E_ARG_67	NH2	E_ASP_90	OD1	3.132
4WHT	E_ARG_67	NH2	E_ASP_90	OD2	3.444
4WHT	E_ARG_98	NH2	E_ASP_100	OD1	3.535
4WHT	E_ARG_98	NH2	E_ASP_100	OD2	2.656
4WHT	E_LYS_204	NZ	E_ASP_206	OD1	2.987
4WHT	E_LYS_204	NZ	E_ASP_206	OD2	3.777
4WHT	E_LYS_207	NZ	F_GLU_127	OE1	3.118
4WHT	G_ARG_38	NH1	G_ASP_90	OD1	2.947
4WHT	G_ARG_38	NH2	G_GLU_46	OE1	2.995
4WHT	G_ARG_61	NH2	G_GLU_46	OE2	3.807
4WHT	G_LYS_65	NZ	G_ASP_62	OD1	3.270
4WHT	G_ARG_67	NH1	G_ASP_90	OD1	3.770
4WHT	G_ARG_67	NH1	G_ASP_90	OD2	2.706
4WHT	G_ARG_67	NH2	G_ASP_90	OD1	3.124
4WHT	G_ARG_67	NH2	G_ASP_90	OD2	3.413
4WHT	G_ARG_98	NH2	G_ASP_100	OD1	3.568
4WHT	G_ARG_98	NH2	G_ASP_100	OD2	2.686
4WHT	G_LYS_204	NZ	G_ASP_206	OD1	2.980
4WHT	G_LYS_204	NZ	G_ASP_206	OD2	3.681
4WHT	G_LYS_204	NZ	U_ASP_206	OD2	3.854

4WHT	I_ARG_38	NH1	I_ASP_90	OD1	2.871
4WHT	I_ARG_38	NH2	I_GLU_46	OE1	3.011
4WHT	I_ARG_38	NH2	I_ASP_90	OD1	3.937
4WHT	I_ARG_61	NH2	I_GLU_46	OE2	3.804
4WHT	I_LYS_65	NZ	I_ASP_62	OD1	3.703
4WHT	I_LYS_65	NZ	R_GLU_84	OE2	3.044
4WHT	I_ARG_67	NH1	I_ASP_90	OD1	3.990
4WHT	I_ARG_67	NH1	I_ASP_90	OD2	2.725
4WHT	I_ARG_67	NH2	I_ASP_90	OD1	3.173
4WHT	I_ARG_67	NH2	I_ASP_90	OD2	3.289
4WHT	I_ARG_98	NH2	I_ASP_100	OD1	3.524
4WHT	I_ARG_98	NH2	I_ASP_100	OD2	2.670
4WHT	I_LYS_207	NZ	J_GLU_127	OE1	2.774
4WHT	I_LYS_207	NZ	J_GLU_127	OE2	3.846
4WHT	J_ARG_24	NH1	J_ASP_75	OD1	2.778
4WHT	J_ARG_24	NH1	J_ASP_75	OD2	3.695
4WHT	J_ARG_66	NH2	J_ASP_87	OD1	2.769
4WHT	J_ARG_66	NH2	J_ASP_87	OD2	3.342
4WHT	J_LYS_153	NZ	J_GLU_199	OE1	3.137
4WHT	J_LYS_153	NZ	J_GLU_199	OE2	3.249
4WHT	J_ARG_159	NH1	J_ASP_189	OD1	3.763
4WHT	J_ARG_159	NH1	J_ASP_189	OD2	2.878
4WHT	J_ARG_159	NH2	J_ASP_189	OD1	2.936
4WHT	J_ARG_159	NH2	J_ASP_189	OD2	3.572
4WHT	J_LYS_187	NZ	J_GLU_191	OE1	2.768
4WHT	J_HIS_193	ND1	J_ASP_189	OD1	3.761
4WHT	J_LYS_203	NZ	J_ASP_114	OD2	2.967
4WHT	K_ARG_38	NH1	K_GLU_89	OE1	3.948
4WHT	K_ARG_38	NH1	K_ASP_90	OD1	2.761
4WHT	K_ARG_38	NH2	K_GLU_46	OE1	2.930
4WHT	K_ARG_38	NH2	K_GLU_89	OE1	3.349
4WHT	K_LYS_65	NZ	K_ASP_62	OD1	3.187
4WHT	K_ARG_67	NH1	K_ASP_90	OD1	3.739
4WHT	K_ARG_67	NH1	K_ASP_90	OD2	2.796
4WHT	K_ARG_67	NH2	K_GLU_89	OE1	3.552
4WHT	K_ARG_67	NH2	K_ASP_90	OD1	3.403
4WHT	K_ARG_67	NH2	K_ASP_90	OD2	3.608
4WHT	K_ARG_98	NH2	K_ASP_100	OD1	3.517
4WHT	K_ARG_98	NH2	K_ASP_100	OD2	2.664
4WHT	K_LYS_204	NZ	K_ASP_206	OD1	2.984
4WHT	K_LYS_204	NZ	K_ASP_206	OD2	3.680
4WHT	K_LYS_207	NZ	L_GLU_127	OE1	2.813
4WHT	M_ARG_38	NH1	M_ASP_90	OD1	2.959
4WHT	M_ARG_38	NH2	M_GLU_46	OE1	2.979
4WHT	M_ARG_38	NH2	M_GLU_89	OE1	3.377
4WHT	M_ARG_61	NH2	M_GLU_46	OE2	3.777
4WHT	M_LYS_65	NZ	M_ASP_62	OD1	3.185
4WHT	M_ARG_67	NH1	M_ASP_90	OD1	3.861
4WHT	M_ARG_67	NH1	M_ASP_90	OD2	2.742
4WHT	M_ARG_67	NH2	M_GLU_89	OE1	3.527
4WHT	M_ARG_67	NH2	M_ASP_90	OD1	3.102
4WHT	M_ARG_67	NH2	M_ASP_90	OD2	3.458
4WHT	M_ARG_98	NH2	M_ASP_100	OD1	3.946
4WHT	M_ARG_98	NH2	M_ASP_100	OD2	3.534
4WHT	M_LYS_204	NZ	K_ASP_206	OD2	2.701
4WHT	M_LYS_207	NZ	N_GLU_127	OE1	3.186
4WHT	O_ARG_38	NH1	O_ASP_90	OD1	2.964
4WHT	O_ARG_38	NH2	O_GLU_46	OE1	3.022

4WHT	O_ARG_38	NH2	O_GLU_89	OE1	3.336
4WHT	O_ARG_61	NH2	O_GLU_46	OE2	3.788
4WHT	O_LYS_65	NZ	O_ASP_62	OD1	3.252
4WHT	O_ARG_67	NH1	O_ASP_90	OD1	3.841
4WHT	O_ARG_67	NH1	O_ASP_90	OD2	2.724
4WHT	O_ARG_67	NH2	O_GLU_89	OE1	3.541
4WHT	O_ARG_67	NH2	O_ASP_90	OD1	3.068
4WHT	O_ARG_67	NH2	O_ASP_90	OD2	3.434
4WHT	O_ARG_98	NH2	O_ASP_100	OD1	3.531
4WHT	O_ARG_98	NH2	O_ASP_100	OD2	2.711
4WHT	O_LYS_204	NZ	O_ASP_206	OD1	2.964
4WHT	O_LYS_204	NZ	O_ASP_206	OD2	3.737
4WHT	O_LYS_207	NZ	P_GLU_127	OE1	3.812
4WHT	O_LYS_207	NZ	P_GLU_127	OE2	2.822
4WHT	Q_ARG_38	NH1	Q_ASP_90	OD1	2.935
4WHT	Q_ARG_38	NH2	Q_GLU_46	OE1	3.059
4WHT	Q_ARG_38	NH2	Q_ASP_90	OD1	3.866
4WHT	Q_ARG_61	NH2	Q_GLU_46	OE2	3.813
4WHT	Q_LYS_65	NZ	Q_ASP_62	OD1	3.159
4WHT	Q_ARG_67	NH1	Q_ASP_90	OD1	3.892
4WHT	Q_ARG_67	NH1	Q_ASP_90	OD2	2.790
4WHT	Q_ARG_67	NH2	Q_ASP_90	OD1	3.108
4WHT	Q_ARG_67	NH2	Q_ASP_90	OD2	3.473
4WHT	Q_ARG_98	NH2	Q_ASP_100	OD1	3.545
4WHT	Q_ARG_98	NH2	Q_ASP_100	OD2	2.754
4WHT	Q_LYS_207	NZ	R_GLU_127	OE1	2.572
4WHT	Q_LYS_207	NZ	R_GLU_127	OE2	3.627
4WHT	S_ARG_38	NH1	S_ASP_90	OD1	2.866
4WHT	S_ARG_38	NH2	S_GLU_46	OE1	2.984
4WHT	S_ARG_38	NH2	S_GLU_89	OE1	3.382
4WHT	S_ARG_38	NH2	S_ASP_90	OD1	3.993
4WHT	S_ARG_61	NH2	S_GLU_46	OE1	3.723
4WHT	S_ARG_61	NH2	S_GLU_46	OE2	3.200
4WHT	S_ARG_67	NH1	S_ASP_90	OD2	2.809
4WHT	S_ARG_67	NH2	S_GLU_89	OE1	3.479
4WHT	S_ARG_67	NH2	S_ASP_90	OD1	3.317
4WHT	S_ARG_67	NH2	S_ASP_90	OD2	3.452
4WHT	S_LYS_76	NZ	S_ASP_73	OD2	2.618
4WHT	S_ARG_98	NH2	S_ASP_100	OD1	3.534
4WHT	S_ARG_98	NH2	S_ASP_100	OD2	2.742
4WHT	S_LYS_204	NZ	S_ASP_206	OD1	3.164
4WHT	S_LYS_207	NZ	T_GLU_127	OE1	3.197
4WHT	U_ARG_38	NH1	U_ASP_90	OD1	2.992
4WHT	U_ARG_38	NH2	U_GLU_46	OE1	3.032
4WHT	U_ARG_38	NH2	U_GLU_89	OE1	3.377
4WHT	U_ARG_61	NH2	U_GLU_46	OE2	3.808
4WHT	U_LYS_65	NZ	U_ASP_62	OD1	3.172
4WHT	U_ARG_67	NH1	U_ASP_90	OD1	3.855
4WHT	U_ARG_67	NH1	U_ASP_90	OD2	2.721
4WHT	U_ARG_67	NH2	U_GLU_89	OE1	3.526
4WHT	U_ARG_67	NH2	U_ASP_90	OD1	3.080
4WHT	U_ARG_67	NH2	U_ASP_90	OD2	3.418
4WHT	U_ARG_98	NH2	U_ASP_100	OD1	3.455
4WHT	U_ARG_98	NH2	U_ASP_100	OD2	2.628
4WHT	U_LYS_204	NZ	G_ASP_206	OD2	3.954
4WHT	U_LYS_204	NZ	U_ASP_206	OD1	2.956
4WHT	U_LYS_204	NZ	U_ASP_206	OD2	3.682
4WHT	U_LYS_207	NZ	V_GLU_127	OE1	3.622

4WHT	X_ARG_38	NH1	X_ASP_90	OD1	2.631
4WHT	X_ARG_38	NH2	X_GLU_46	OE1	3.058
4WHT	X_ARG_38	NH2	X_GLU_46	OE2	3.652
4WHT	X_ARG_38	NH2	X_ASP_90	OD1	3.918
4WHT	X_ARG_61	NH2	X_GLU_46	OE2	3.153
4WHT	X_LYS_65	NZ	X_ASP_62	OD1	3.157
4WHT	X_ARG_67	NH1	X_ASP_90	OD1	3.978
4WHT	X_ARG_67	NH1	X_ASP_90	OD2	2.777
4WHT	X_ARG_67	NH2	X_ASP_90	OD1	3.272
4WHT	X_ARG_67	NH2	X_ASP_90	OD2	3.480
4WHT	X_ARG_98	NH2	X_ASP_100	OD1	3.516
4WHT	X_ARG_98	NH2	X_ASP_100	OD2	2.709
4WHT	X_LYS_207	NZ	Y_GLU_127	OE2	2.718
4WHT	B_ARG_24	NH1	B_ASP_75	OD1	2.804
4WHT	B_ARG_24	NH1	B_ASP_75	OD2	3.712
4WHT	B_ARG_66	NH2	B_ASP_87	OD1	2.784
4WHT	B_ARG_66	NH2	B_ASP_87	OD2	3.450
4WHT	B_LYS_111	NZ	J_GLU_73	OE2	3.842
4WHT	B_LYS_153	NZ	B_GLU_199	OE1	3.076
4WHT	B_LYS_153	NZ	B_GLU_199	OE2	3.271
4WHT	B_ARG_159	NH1	B_ASP_189	OD1	3.800
4WHT	B_ARG_159	NH1	B_ASP_189	OD2	2.909
4WHT	B_ARG_159	NH2	B_ASP_189	OD1	2.972
4WHT	B_ARG_159	NH2	B_ASP_189	OD2	3.584
4WHT	B_LYS_	NZ	B_GLU_	OE1	2.805
4WHT	B_HIS_193	ND1	B_ASP_155	OD2	3.362
4WHT	B_HIS_193	NE2	B_ASP_189	OD1	3.524
4WHT	B_LYS_203	NZ	B_ASP_114	OD2	2.836
4WHT	D_ARG_24	NH1	D_ASP_75	OD1	2.773
4WHT	D_ARG_24	NH1	D_ASP_75	OD2	3.816
4WHT	D_ARG_44	NH1	D_GLU_86	OE2	3.678
4WHT	D_ARG_44	NH2	D_GLU_86	OE2	2.752
4WHT	D_ARG_66	NH2	D_ASP_87	OD1	2.868
4WHT	D_ARG_66	NH2	D_ASP_87	OD2	3.621
4WHT	D_LYS_151	NZ	D_GLU_199	OE2	3.961
4WHT	D_LYS_151	NZ	L_GLU_191	OE2	3.259
4WHT	D_LYS_153	NZ	D_GLU_199	OE1	3.094
4WHT	D_LYS_153	NZ	D_GLU_199	OE2	3.252
4WHT	D_ARG_159	NH1	D_ASP_189	OD1	3.780
4WHT	D_ARG_159	NH1	D_ASP_189	OD2	2.927
4WHT	D_ARG_159	NH2	D_ASP_189	OD1	2.960
4WHT	D_ARG_159	NH2	D_ASP_189	OD2	3.602
4WHT	D_LYS_187	NZ	I_GLU_114	OE1	3.576
4WHT	D_LYS_187	NZ	I_GLU_114	OE2	3.498
4WHT	D_LYS_187	NZ	D_GLU_191	OE1	2.796
4WHT	D_HIS_193	ND1	D_ASP_189	OD1	3.687
4WHT	D_LYS_203	NZ	D_ASP_114	OD2	2.798
4WHT	F_ARG_24	NH1	F_ASP_75	OD1	2.809
4WHT	F_ARG_24	NH1	F_ASP_75	OD2	3.755
4WHT	F_ARG_66	NH2	F_GLU_86	OE1	3.638
4WHT	F_ARG_66	NH2	F_GLU_86	OE2	3.286
4WHT	F_ARG_66	NH2	F_ASP_87	OD1	2.757
4WHT	F_ARG_66	NH2	F_ASP_87	OD2	3.450
4WHT	F_LYS_151	NZ	F_GLU_199	OE2	3.084
4WHT	F_LYS_153	NZ	F_GLU_199	OE1	3.224
4WHT	F_LYS_153	NZ	F_GLU_199	OE2	3.396
4WHT	F_ARG_159	NH1	F_ASP_189	OD1	3.759
4WHT	F_ARG_159	NH1	F_ASP_189	OD2	2.800

4WHT	F_ARG_159	NH2	F_ASP_189	OD1	2.952
4WHT	F_ARG_159	NH2	F_ASP_189	OD2	3.529
4WHT	F_ARG_160	NH2	F_GLU_158	OE2	3.114
4WHT	F_LYS_187	NZ	F_GLU_191	OE1	2.776
4WHT	F_HIS_193	ND1	F_ASP_155	OD2	3.338
4WHT	F_HIS_193	NE2	F_ASP_189	OD1	3.541
4WHT	H_ARG_24	NH1	H_ASP_75	OD1	2.789
4WHT	H_ARG_24	NH1	H_ASP_75	OD2	3.775
4WHT	H_ARG_66	NH1	Q_ASP_62	OD2	3.949
4WHT	H_ARG_66	NH2	H_ASP_87	OD1	2.787
4WHT	H_ARG_66	NH2	H_ASP_87	OD2	3.453
4WHT	H_LYS_151	NZ	H_GLU_199	OE2	3.589
4WHT	H_LYS_153	NZ	H_GLU_199	OE1	3.108
4WHT	H_LYS_153	NZ	H_GLU_199	OE2	3.315
4WHT	H_ARG_159	NH1	H_ASP_189	OD1	3.818
4WHT	H_ARG_159	NH1	H_ASP_189	OD2	2.990
4WHT	H_ARG_159	NH2	H_ASP_189	OD1	2.984
4WHT	H_ARG_159	NH2	H_ASP_189	OD2	3.636
4WHT	H_LYS_187	NZ	H_GLU_191	OE1	2.806
4WHT	H_HIS_193	ND1	H_ASP_155	OD2	3.385
4WHT	H_HIS_193	NE2	H_ASP_189	OD1	3.584
4WHT	H_LYS_203	NZ	H_ASP_114	OD2	2.843
4WHT	L_ARG_24	NH1	L_ASP_75	OD1	2.813
4WHT	L_ARG_24	NH1	L_ASP_75	OD2	3.652
4WHT	L_ARG_66	NH2	L_ASP_87	OD1	2.659
4WHT	L_ARG_66	NH2	L_ASP_87	OD2	3.387
4WHT	L_LYS_151	NZ	L_GLU_158	OE1	3.149
4WHT	L_LYS_151	NZ	L_GLU_158	OE2	3.351
4WHT	L_LYS_153	NZ	L_GLU_199	OE1	3.106
4WHT	L_LYS_153	NZ	L_GLU_199	OE2	3.200
4WHT	L_ARG_159	NH1	L_ASP_189	OD1	3.780
4WHT	L_ARG_159	NH1	L_ASP_189	OD2	2.946
4WHT	L_ARG_159	NH2	L_ASP_189	OD1	2.925
4WHT	L_ARG_159	NH2	L_ASP_189	OD2	3.602
4WHT	L_LYS_187	NZ	L_GLU_191	OE1	2.795
4WHT	L_HIS_193	ND1	L_ASP_155	OD2	3.400
4WHT	L_HIS_193	NE2	L_ASP_189	OD1	3.590
4WHT	L_LYS_203	NZ	L_ASP_114	OD2	2.774
4WHT	N_ARG_24	NH1	N_ASP_75	OD1	3.802
4WHT	N_ARG_24	NH1	N_ASP_75	OD2	3.728
4WHT	N_ARG_66	NH2	N_ASP_87	OD1	2.772
4WHT	N_ARG_66	NH2	N_ASP_87	OD2	3.477
4WHT	N_LYS_151	NZ	N_GLU_199	OE2	3.991
4WHT	N_LYS_153	NZ	N_GLU_199	OE1	3.073
4WHT	N_LYS_153	NZ	N_GLU_199	OE2	3.236
4WHT	N_ARG_159	NH1	N_ASP_189	OD2	3.146
4WHT	N_ARG_159	NH2	N_ASP_189	OD1	2.954
4WHT	N_ARG_159	NH2	N_ASP_189	OD2	3.533
4WHT	N_ARG_160	NH2	N_GLU_158	OE1	2.762
4WHT	N_LYS_187	NZ	K_GLU_114	OE1	3.270
4WHT	N_LYS_187	NZ	K_GLU_114	OE2	3.221
4WHT	N_LYS_187	NZ	N_GLU_191	OE1	2.851
4WHT	N_HIS_193	ND1	N_ASP_189	OD1	3.702
4WHT	N_LYS_203	NZ	N_ASP_147	OD2	3.088
4WHT	P_ARG_24	NH1	P_ASP_75	OD1	2.762
4WHT	P_ARG_24	NH1	P_ASP_75	OD2	3.651
4WHT	P_ARG_66	NH2	P_ASP_87	OD1	2.759
4WHT	P_ARG_66	NH2	P_ASP_87	OD2	3.423

4WHT	P_LYS_151	NZ	P_GLU_199	OE1	3.866
4WHT	P_LYS_153	NZ	P_GLU_199	OE1	3.110
4WHT	P_LYS_153	NZ	P_GLU_199	OE2	3.243
4WHT	P_ARG_159	NH1	P_ASP_189	OD1	3.789
4WHT	P_ARG_159	NH1	P_ASP_189	OD2	2.890
4WHT	P_ARG_159	NH2	P_ASP_189	OD1	2.989
4WHT	P_ARG_159	NH2	P_ASP_189	OD2	3.601
4WHT	P_LYS_187	NZ	P_GLU_191	OE1	2.785
4WHT	P_HIS_193	ND1	P_ASP_155	OD2	3.395
4WHT	P_HIS_193	NE2	P_ASP_189	OD1	3.524
4WHT	R_ARG_24	NH1	R_ASP_75	OD1	2.839
4WHT	R_ARG_24	NH1	R_ASP_75	OD2	3.562
4WHT	R_ARG_66	NH2	R_ASP_87	OD1	2.765
4WHT	R_ARG_66	NH2	R_ASP_87	OD2	3.213
4WHT	R_LYS_153	NZ	R_GLU_199	OE1	3.156
4WHT	R_LYS_153	NZ	R_GLU_199	OE2	3.439
4WHT	R_ARG_159	NH1	R_ASP_189	OD1	3.788
4WHT	R_ARG_159	NH1	R_ASP_189	OD2	2.882
4WHT	R_ARG_159	NH2	R_ASP_189	OD1	2.978
4WHT	R_ARG_159	NH2	R_ASP_189	OD2	3.578
4WHT	R_LYS_187	NZ	R_GLU_191	OE1	2.817
4WHT	R_HIS_193	ND1	R_ASP_189	OD1	3.674
4WHT	R_LYS_203	NZ	R_ASP_114	OD2	2.819
4WHT	T_ARG_24	NH1	T_ASP_75	OD1	2.790
4WHT	T_ARG_24	NH1	T_ASP_75	OD2	3.795
4WHT	T_ARG_66	NH2	T_ASP_87	OD1	2.749
4WHT	T_ARG_66	NH2	T_ASP_87	OD2	3.461
4WHT	T_LYS_153	NZ	T_GLU_199	OE1	3.110
4WHT	T_LYS_153	NZ	T_GLU_199	OE2	3.186
4WHT	T_ARG_159	NH1	T_ASP_189	OD1	3.798
4WHT	T_ARG_159	NH1	T_ASP_189	OD2	2.872
4WHT	T_ARG_159	NH2	T_ASP_189	OD1	3.018
4WHT	T_ARG_159	NH2	T_ASP_189	OD2	3.596
4WHT	T_LYS_187	NZ	T_GLU_191	OE1	3.436
4WHT	T_LYS_187	NZ	T_GLU_191	OE2	3.114
4WHT	T_HIS_193	ND1	T_ASP_155	OD2	2.632
4WHT	T_HIS_193	NE2	T_ASP_189	OD1	3.485
4WHT	T_LYS_203	NZ	T_ASP_114	OD2	2.869
4WHT	V_ARG_66	NH2	V_ASP_87	OD1	2.798
4WHT	V_ARG_66	NH2	V_ASP_87	OD2	3.518
4WHT	V_LYS_151	NZ	V_GLU_199	OE2	2.908
4WHT	V_LYS_153	NZ	V_GLU_199	OE1	3.090
4WHT	V_LYS_153	NZ	V_GLU_199	OE2	3.267
4WHT	V_ARG_159	NH1	V_ASP_189	OD1	3.784
4WHT	V_ARG_159	NH1	V_ASP_189	OD2	2.899
4WHT	V_ARG_159	NH2	V_ASP_189	OD1	2.972
4WHT	V_ARG_159	NH2	V_ASP_189	OD2	3.593
4WHT	V_LYS_187	NZ	G_GLU_114	OE1	3.353
4WHT	V_LYS_187	NZ	G_GLU_114	OE2	3.189
4WHT	V_LYS_187	NZ	V_GLU_191	OE1	2.841
4WHT	V_HIS_193	NE2	V_ASP_189	OD1	3.541
4WHT	Y_ARG_24	NH1	Y_ASP_75	OD1	3.206
4WHT	Y_ARG_24	NH1	Y_ASP_75	OD2	2.692
4WHT	Y_ARG_66	NH2	Y_GLU_86	OE2	3.955
4WHT	Y_ARG_66	NH2	Y_ASP_87	OD1	2.832
4WHT	Y_ARG_66	NH2	Y_ASP_87	OD2	3.932
4WHT	Y_LYS_153	NZ	Y_GLU_199	OE1	3.170
4WHT	Y_LYS_153	NZ	Y_GLU_199	OE2	2.813

4WHT	Y_ARG_159	NH1	Y_GLU_158	OE1	3.340
4WHT	Y_ARG_160	NH1	Y_ASP_165	OD2	3.538
4WHT	Y_ARG_160	NH2	Y_ASP_165	OD2	3.332
4WHT	Y_HIS_193	ND1	Y_ASP_155	OD2	3.964
4WHT	Y_LYS_203	NZ	Y_ASP_114	OD2	2.871

Table 632: 4WHT-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4WHY	G_ARG_38	NH1	G_ASP_90	OD1	3.796
4WHY	G_ARG_38	NH2	G_GLU_46	OE1	3.426
4WHY	G_ARG_38	NH2	G_GLU_89	OE1	3.357
4WHY	G_ARG_61	NH2	G_GLU_46	OE2	3.723
4WHY	G_LYS_65	NZ	G_ASP_62	OD1	2.662
4WHY	G_ARG_67	NH1	G_ASP_90	OD1	3.682
4WHY	G_ARG_67	NH1	G_ASP_90	OD2	2.803
4WHY	G_ARG_67	NH2	G_GLU_89	OE1	3.560
4WHY	G_ARG_67	NH2	G_ASP_90	OD1	3.140
4WHY	G_ARG_67	NH2	G_ASP_90	OD2	3.738
4WHY	G_ARG_98	NH2	G_ASP_100	OD1	3.694
4WHY	G_ARG_98	NH2	G_ASP_100	OD2	2.760
4WHY	H_ARG_24	NH1	H_ASP_75	OD1	3.176
4WHY	H_ARG_24	NH1	H_ASP_75	OD2	3.772
4WHY	H_ARG_24	NH2	H_ASP_75	OD1	3.589
4WHY	H_ARG_66	NH2	H_GLU_86	OE2	3.670
4WHY	H_ARG_66	NH2	H_ASP_87	OD1	2.742
4WHY	H_ARG_66	NH2	H_ASP_87	OD2	3.368
4WHY	H_LYS_153	NZ	H_GLU_199	OE1	2.781
4WHY	H_ARG_159	NH1	H_ASP_161	OD2	3.986
4WHY	H_ARG_159	NH2	H_ASP_189	OD2	3.516
4WHY	H_LYS_187	NZ	H_GLU_191	OE1	3.190
4WHY	H_HIS_193	NE2	H_ASP_189	OD1	2.905
4WHY	H_LYS_203	NZ	H_ASP_114	OD2	2.769
4WHY	I_ARG_38	NH1	I_ASP_90	OD1	2.978
4WHY	I_ARG_38	NH2	I_GLU_46	OE1	3.414
4WHY	I_ARG_38	NH2	I_GLU_89	OE1	3.357
4WHY	I_ARG_38	NH2	I_ASP_90	OD1	3.749
4WHY	I_ARG_61	NH2	I_GLU_46	OE2	3.662
4WHY	I_LYS_65	NZ	I_ASP_62	OD1	2.662
4WHY	I_ARG_67	NH1	I_ASP_90	OD1	3.785
4WHY	I_ARG_67	NH1	I_ASP_90	OD2	2.958
4WHY	I_ARG_67	NH2	I_GLU_89	OE1	3.554
4WHY	I_ARG_67	NH2	I_ASP_90	OD1	3.099
4WHY	I_ARG_67	NH2	I_ASP_90	OD2	3.665
4WHY	I_ARG_98	NH2	I_ASP_100	OD1	3.706
4WHY	I_ARG_98	NH2	I_ASP_100	OD2	2.729
4WHY	I_LYS_204	NZ	I_ASP_206	OD1	3.011
4WHY	I_LYS_204	NZ	I_ASP_206	OD2	3.199
4WHY	J_ARG_24	NH1	J_ASP_75	OD1	3.069
4WHY	J_ARG_24	NH2	J_ASP_75	OD1	3.630
4WHY	J_ARG_66	NH1	J_GLU_84	OE1	3.874
4WHY	J_ARG_66	NH2	J_GLU_86	OE2	3.624
4WHY	J_ARG_66	NH2	J_ASP_87	OD1	2.726
4WHY	J_ARG_66	NH2	J_ASP_87	OD2	3.349
4WHY	J_LYS_153	NZ	J_GLU_199	OE1	3.490
4WHY	J_LYS_153	NZ	J_GLU_199	OE2	3.292
4WHY	J_ARG_159	NH1	J_ASP_189	OD2	3.515
4WHY	J_ARG_159	NH2	J_ASP_189	OD1	3.310
4WHY	J_ARG_159	NH2	J_ASP_189	OD2	3.228
4WHY	J_LYS_187	NZ	J_GLU_191	OE1	3.198
4WHY	J_HIS_193	NE2	J_ASP_189	OD1	2.893
4WHY	J_LYS_203	NZ	J_ASP_114	OD2	2.763
4WHY	K_ARG_38	NH1	K_ASP_90	OD1	2.916
4WHY	K_ARG_38	NH2	K_GLU_46	OE1	3.411
4WHY	K_ARG_38	NH2	K_GLU_89	OE1	3.357
4WHY	K_ARG_38	NH2	K_ASP_90	OD1	3.663

4WHY	K_LYS_43	NZ	K_GLU_46	OE2	3.479
4WHY	K_ARG_61	NH2	K_GLU_46	OE1	3.975
4WHY	K_ARG_61	NH2	K_GLU_46	OE2	3.699
4WHY	K_LYS_65	NZ	K_ASP_62	OD1	2.646
4WHY	K_ARG_67	NH1	K_ASP_90	OD2	3.001
4WHY	K_ARG_67	NH2	K_GLU_89	OE1	3.597
4WHY	K_ARG_67	NH2	K_ASP_90	OD1	3.410
4WHY	K_ARG_67	NH2	K_ASP_90	OD2	3.539
4WHY	K_ARG_98	NH2	K_ASP_100	OD1	3.492
4WHY	K_ARG_98	NH2	K_ASP_100	OD2	2.572
4WHY	K_LYS_204	NZ	G_ASP_206	OD2	3.182
4WHY	K_LYS_204	NZ	K_ASP_206	OD1	3.046
4WHY	K_LYS_204	NZ	K_ASP_206	OD2	3.729
4WHY	K_LYS_207	NZ	L_GLU_127	OE1	3.798
4WHY	L_ARG_66	NH1	L_GLU_84	OE2	3.906
4WHY	L_ARG_66	NH2	L_GLU_86	OE2	3.615
4WHY	L_ARG_66	NH2	L_ASP_87	OD1	2.731
4WHY	L_ARG_66	NH2	L_ASP_87	OD2	3.360
4WHY	L_LYS_153	NZ	L_GLU_199	OE1	3.524
4WHY	L_LYS_153	NZ	L_GLU_199	OE2	3.214
4WHY	L_ARG_159	NH1	L_ASP_189	OD1	3.322
4WHY	L_ARG_159	NH1	L_ASP_189	OD2	2.478
4WHY	L_ARG_159	NH2	L_ASP_189	OD1	3.410
4WHY	L_ARG_159	NH2	L_ASP_189	OD2	3.993
4WHY	L_LYS_187	NZ	G_GLU_114	OE1	3.275
4WHY	L_LYS_187	NZ	G_GLU_114	OE2	3.634
4WHY	L_LYS_187	NZ	L_GLU_191	OE1	3.202
4WHY	L_HIS_193	NE2	L_ASP_189	OD1	2.644
4WHY	M_ARG_38	NH1	M_ASP_90	OD1	3.063
4WHY	M_ARG_38	NH2	M_GLU_46	OE1	3.415
4WHY	M_ARG_38	NH2	M_GLU_89	OE1	3.380
4WHY	M_ARG_61	NH2	M_GLU_46	OE2	3.734
4WHY	M_LYS_65	NZ	M_ASP_62	OD1	2.631
4WHY	M_ARG_67	NH1	M_ASP_90	OD1	3.787
4WHY	M_ARG_67	NH1	M_ASP_90	OD2	2.862
4WHY	M_ARG_67	NH2	M_GLU_89	OE1	3.563
4WHY	M_ARG_67	NH2	M_ASP_90	OD1	3.288
4WHY	M_ARG_67	NH2	M_ASP_90	OD2	3.753
4WHY	M_ARG_87	NH1	M_GLU_89	OE1	3.642
4WHY	M_ARG_87	NH1	M_GLU_89	OE2	2.644
4WHY	M_ARG_98	NH2	M_ASP_100	OD1	3.669
4WHY	M_ARG_98	NH2	M_ASP_100	OD2	2.644
4WHY	M_LYS_207	NZ	N_GLU_127	OE1	3.795
4WHY	N_ARG_24	NH1	N_ASP_75	OD1	3.064
4WHY	N_ARG_24	NH2	N_ASP_75	OD1	3.627
4WHY	N_ARG_66	NH1	N_GLU_84	OE1	3.806
4WHY	N_ARG_66	NH2	N_GLU_86	OE2	3.626
4WHY	N_ARG_66	NH2	N_ASP_87	OD1	2.746
4WHY	N_ARG_66	NH2	N_ASP_87	OD2	3.352
4WHY	N_LYS_153	NZ	N_GLU_199	OE1	3.388
4WHY	N_LYS_153	NZ	N_GLU_199	OE2	3.311
4WHY	N_ARG_159	NH1	N_ASP_189	OD1	3.704
4WHY	N_ARG_159	NH1	N_ASP_189	OD2	2.785
4WHY	N_ARG_159	NH2	N_ASP_189	OD2	3.806
4WHY	N_LYS_187	NZ	L_GLU_114	OE1	2.397
4WHY	N_LYS_187	NZ	L_GLU_114	OE2	3.551
4WHY	N_LYS_187	NZ	N_GLU_191	OE1	3.175
4WHY	N_HIS_193	NE2	N_ASP_189	OD1	2.893

4WHY	N_LYS_203	NZ	N_ASP_114	OD2	2.778
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Table 633: 4WHY-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4WUU	A_HIS_3	ND1	A_ASP_29	OD1	3.341
4WUU	A_HIS_3	ND1	A_ASP_29	OD2	2.929
4WUU	A_ARG_6	NH2	A_ASP_102	OD1	3.941
4WUU	A_ARG_6	NH2	A_ASP_102	OD2	3.738
4WUU	A_ARG_14	NH2	A_ASP_39	OD1	3.219
4WUU	A_ARG_14	NH2	A_ASP_39	OD2	2.950
4WUU	A_ARG_21	NH1	A_ASP_39	OD2	2.675
4WUU	A_ARG_21	NH2	A_ASP_37	OD2	3.480
4WUU	A_ARG_35	NH1	B_ASP_53	OD1	3.025
4WUU	A_ARG_35	NH1	B_ASP_53	OD2	3.278
4WUU	A_ARG_35	NH2	A_GLU_46	OE1	3.105
4WUU	A_ARG_44	NH1	A_ASP_61	OD1	3.882
4WUU	A_ARG_44	NH2	A_ASP_61	OD1	3.159
4WUU	A_ARG_48	NH2	B_ASP_53	OD1	3.607
4WUU	A_ARG_48	NH2	B_ASP_53	OD2	3.368
4WUU	A_HIS_74	ND1	A_ASP_77	OD2	3.868
4WUU	A_ARG_75	NH1	A_GLU_19	OE2	3.917
4WUU	A_ARG_82	NH1	A_GLU_89	OE2	3.819
4WUU	A_ARG_82	NH2	A_GLU_89	OE2	3.766
4WUU	A_HIS_93	ND1	A_ASP_119	OD1	3.903
4WUU	A_HIS_93	ND1	A_ASP_119	OD2	3.323
4WUU	A_ARG_111	NH2	A_ASP_102	OD2	3.306
4WUU	A_ARG_157	NH1	A_GLU_161	OE1	3.446
4WUU	A_ARG_157	NH1	A_GLU_161	OE2	3.465
4WUU	A_ARG_157	NH2	A_GLU_161	OE1	3.936
4WUU	A_ARG_170	NH2	A_GLU_55	OE1	3.101
4WUU	A_ARG_170	NH2	A_GLU_55	OE2	3.506
4WUU	A_ARG_181	NH1	A_ASP_183	OD2	3.977
4WUU	A_HIS_191	NE2	A_GLU_254	OE2	3.880
4WUU	A_HIS_197	ND1	A_GLU_198	OE1	3.876
4WUU	B_ARG_3	NH2	B_ASP_59	OD1	3.704
4WUU	B_LYS_19	NZ	B_GLU_16	OE1	3.969
4WUU	B_LYS_19	NZ	B_GLU_16	OE2	3.703
4WUU	B_ARG_45	NH2	B_GLU_47	OE2	2.936
4WUU	B_LYS_94	NZ	B_GLU_77	OE2	3.352
4WUU	D_ARG_62	NH2	D_GLU_82	OE2	3.196
4WUU	D_ARG_62	NH2	D_ASP_83	OD1	2.858
4WUU	D_ARG_62	NH2	D_ASP_83	OD2	3.260
4WUU	D_LYS_114	NZ	D_GLU_202	OE1	2.842
4WUU	E_LYS_12	NZ	E_GLU_16	OE2	3.576
4WUU	E_ARG_38	NH2	E_GLU_46	OE1	2.721
4WUU	E_ARG_38	NH2	E_GLU_46	OE2	3.649
4WUU	E_ARG_50	NH1	A_GLU_166	OE2	3.181
4WUU	E_ARG_50	NH2	A_GLU_166	OE1	3.839
4WUU	E_ARG_50	NH2	A_GLU_166	OE2	2.671
4WUU	E_LYS_87	NZ	E_ASP_90	OD1	3.097
4WUU	E_ARG_98	NH2	E_ASP_109	OD2	3.982
4WUU	E_ARG_218	NH1	E_GLU_220	OE1	3.981
4WUU	E_ARG_218	NH2	E_GLU_220	OE1	3.055

Table 634: 4WUU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4XVJ	A_ARG_1	NH2	L_ASP_51	OD1	3.482
4XVJ	H_ARG_38	NH1	H_ASP_90	OD2	3.020
4XVJ	H_ARG_38	NH2	H_GLU_46	OE1	2.936
4XVJ	H_LYS_65	NZ	H_ASP_62	OD1	3.256
4XVJ	H_ARG_67	NH1	H_ASP_90	OD1	2.560
4XVJ	H_ARG_67	NH1	H_ASP_90	OD2	3.768
4XVJ	H_ARG_67	NH2	H_ASP_90	OD1	3.378
4XVJ	H_ARG_67	NH2	H_ASP_90	OD2	3.034
4XVJ	H_ARG_98	NH2	H_ASP_115	OD1	3.741
4XVJ	H_ARG_98	NH2	H_ASP_115	OD2	2.973
4XVJ	L_LYS_17	NZ	L_ASP_75	OD2	3.177
4XVJ	L_ARG_62	NH1	L_ASP_83	OD1	3.002
4XVJ	L_ARG_62	NH1	L_ASP_83	OD2	3.479
4XVJ	L_ARG_62	NH2	L_ASP_83	OD1	3.793
4XVJ	L_ARG_62	NH2	L_ASP_83	OD2	2.894

Table 635: 4XVJ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4YHP	P_LYS_4	NZ	H_ASP_62	OD1	3.318
4YHP	A_ARG_38	NH1	A_ASP_90	OD1	2.967
4YHP	A_ARG_38	NH2	A_GLU_46	OE1	2.987
4YHP	A_ARG_67	NH1	A_ASP_90	OD1	3.983
4YHP	A_ARG_67	NH1	A_ASP_90	OD2	2.902
4YHP	A_ARG_67	NH2	A_ASP_90	OD1	2.805
4YHP	A_ARG_67	NH2	A_ASP_90	OD2	3.034
4YHP	A_LYS_76	NZ	A_ASP_73	OD1	3.954
4YHP	A_LYS_76	NZ	A_ASP_73	OD2	3.046
4YHP	A_ARG_98	NH2	A_ASP_109	OD1	3.450
4YHP	A_ARG_98	NH2	A_ASP_109	OD2	2.693
4YHP	A_LYS_151	NZ	A_ASP_152	OD1	3.053
4YHP	A_LYS_151	NZ	A_ASP_152	OD2	3.629
4YHP	A_LYS_214	NZ	A_ASP_216	OD1	3.351
4YHP	A_LYS_218	NZ	A_GLU_220	OE2	2.671
4YHP	A_LYS_222	NZ	B_ASP_123	OD2	3.677
4YHP	B_ARG_53	NH2	B_GLU_59	OE1	3.593
4YHP	B_ARG_60	NH1	B_ASP_81	OD1	3.610
4YHP	B_ARG_60	NH1	B_ASP_81	OD2	2.819
4YHP	B_ARG_60	NH2	B_GLU_78	OE2	3.931
4YHP	B_ARG_60	NH2	B_ASP_81	OD1	3.172
4YHP	B_ARG_60	NH2	B_ASP_81	OD2	3.721
4YHP	B_LYS_104	NZ	B_ASP_84	OD1	3.453
4YHP	B_LYS_104	NZ	B_GLU_166	OE2	3.500
4YHP	B_LYS_150	NZ	B_GLU_196	OE1	3.634
4YHP	B_LYS_150	NZ	B_GLU_196	OE2	3.240
4YHP	B_LYS_184	NZ	B_GLU_188	OE1	3.665
4YHP	B_LYS_184	NZ	B_GLU_188	OE2	2.296
4YHP	Q_LYS_4	NZ	C_ASP_62	OD1	3.313
4YHP	C_ARG_38	NH1	C_ASP_90	OD1	2.918
4YHP	C_ARG_38	NH2	C_GLU_46	OE1	2.810
4YHP	C_ARG_38	NH2	C_ASP_90	OD1	3.983
4YHP	C_ARG_67	NH1	C_ASP_90	OD1	3.935
4YHP	C_ARG_67	NH1	C_ASP_90	OD2	2.912
4YHP	C_ARG_67	NH2	C_ASP_90	OD1	3.223
4YHP	C_ARG_67	NH2	C_ASP_90	OD2	3.530
4YHP	C_ARG_98	NH2	C_ASP_109	OD1	3.729
4YHP	C_ARG_98	NH2	C_ASP_109	OD2	2.531
4YHP	C_LYS_151	NZ	C_ASP_152	OD1	3.396
4YHP	C_LYS_151	NZ	C_ASP_152	OD2	3.552
4YHP	C_LYS_218	NZ	C_GLU_220	OE2	3.718
4YHP	C_LYS_222	NZ	D_ASP_123	OD1	3.776
4YHP	C_LYS_222	NZ	D_ASP_123	OD2	3.442
4YHP	D_ARG_60	NH1	D_ASP_81	OD1	3.548
4YHP	D_ARG_60	NH1	D_ASP_81	OD2	2.563
4YHP	D_ARG_60	NH2	D_GLU_78	OE1	3.956
4YHP	D_ARG_60	NH2	D_ASP_81	OD1	3.366
4YHP	D_ARG_60	NH2	D_ASP_81	OD2	3.671
4YHP	D_LYS_104	NZ	D_ASP_84	OD1	3.616
4YHP	D_LYS_104	NZ	D_ASP_84	OD2	3.921
4YHP	D_LYS_104	NZ	D_GLU_166	OE1	3.541
4YHP	D_LYS_104	NZ	D_GLU_166	OE2	2.873
4YHP	D_LYS_150	NZ	D_GLU_196	OE1	3.981
4YHP	D_LYS_150	NZ	D_GLU_196	OE2	2.313
4YHP	D_LYS_189	NZ	D_ASP_186	OD1	2.853
4YHP	D_HIS_190	ND1	D_ASP_152	OD2	2.771
4YHP	D_HIS_190	NE2	L_GLU_59	OE2	2.478

4YHP	E_ARG_38	NH1	E_ASP_90	OD1	3.131
4YHP	E_ARG_38	NH2	E_GLU_46	OE1	2.855
4YHP	E_ARG_67	NH1	E_ASP_90	OD1	3.715
4YHP	E_ARG_67	NH1	E_ASP_90	OD2	2.746
4YHP	E_ARG_67	NH2	E_ASP_90	OD1	3.053
4YHP	E_ARG_67	NH2	E_ASP_90	OD2	3.561
4YHP	E_ARG_98	NH2	E_ASP_109	OD1	3.385
4YHP	E_ARG_98	NH2	E_ASP_109	OD2	2.631
4YHP	E_LYS_151	NZ	E_ASP_152	OD1	3.289
4YHP	E_LYS_151	NZ	E_ASP_152	OD2	3.442
4YHP	E_LYS_222	NZ	F_ASP_123	OD1	3.304
4YHP	E_LYS_222	NZ	F_ASP_123	OD2	2.842
4YHP	H_ARG_38	NH1	H_ASP_90	OD1	2.947
4YHP	H_ARG_38	NH2	H_GLU_46	OE1	2.947
4YHP	H_ARG_38	NH2	H_ASP_90	OD1	3.968
4YHP	H_ARG_67	NH1	H_ASP_90	OD1	3.789
4YHP	H_ARG_67	NH1	H_ASP_90	OD2	2.848
4YHP	H_ARG_67	NH2	H_ASP_90	OD1	3.026
4YHP	H_ARG_67	NH2	H_ASP_90	OD2	3.449
4YHP	H_LYS_76	NZ	H_ASP_73	OD2	3.599
4YHP	H_ARG_98	NH2	H_ASP_109	OD1	3.571
4YHP	H_ARG_98	NH2	H_ASP_109	OD2	2.451
4YHP	H_LYS_151	NZ	H_ASP_152	OD1	3.964
4YHP	H_LYS_151	NZ	H_ASP_152	OD2	3.805
4YHP	H_LYS_218	NZ	H_GLU_220	OE1	3.935
4YHP	L_ARG_60	NH1	L_ASP_81	OD1	3.435
4YHP	L_ARG_60	NH1	L_ASP_81	OD2	2.451
4YHP	L_ARG_60	NH2	L_GLU_78	OE2	3.891
4YHP	L_ARG_60	NH2	L_ASP_81	OD1	3.204
4YHP	L_ARG_60	NH2	L_ASP_81	OD2	3.593
4YHP	L_LYS_104	NZ	L_ASP_84	OD1	2.935
4YHP	L_LYS_104	NZ	L_ASP_84	OD2	3.845
4YHP	L_LYS_104	NZ	L_GLU_166	OE2	3.174
4YHP	L_LYS_150	NZ	L_GLU_196	OE2	2.309
4YHP	L_LYS_189	NZ	L_ASP_186	OD1	2.837
4YHP	L_HIS_190	ND1	L_ASP_152	OD2	2.727
4YHP	F_HIS_33	ND1	F_ASP_49	OD1	3.954
4YHP	F_ARG_60	NH1	F_ASP_81	OD1	3.515
4YHP	F_ARG_60	NH1	F_ASP_81	OD2	2.794
4YHP	F_ARG_60	NH2	F_GLU_78	OE2	3.996
4YHP	F_ARG_60	NH2	F_ASP_81	OD1	3.303
4YHP	F_ARG_60	NH2	F_ASP_81	OD2	3.936
4YHP	F_LYS_104	NZ	F_ASP_84	OD1	3.436
4YHP	F_LYS_104	NZ	F_GLU_166	OE2	3.438
4YHP	F_HIS_190	ND1	F_ASP_152	OD2	3.922

Table 636: 4YHP-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4YHY	C_HIS_33	ND1	C_ASP_49	OD1	3.834
4YHY	C_ARG_60	NH1	C_ASP_81	OD1	3.547
4YHY	C_ARG_60	NH1	C_ASP_81	OD2	2.684
4YHY	C_ARG_60	NH2	C_GLU_78	OE1	3.841
4YHY	C_ARG_60	NH2	C_ASP_81	OD1	2.796
4YHY	C_ARG_60	NH2	C_ASP_81	OD2	3.359
4YHY	C_LYS_104	NZ	C_ASP_84	OD1	3.080
4YHY	C_LYS_104	NZ	C_ASP_84	OD2	3.747
4YHY	C_LYS_104	NZ	C_GLU_166	OE1	3.855
4YHY	C_LYS_104	NZ	C_GLU_166	OE2	3.371
4YHY	C_LYS_184	NZ	C_GLU_188	OE1	2.479
4YHY	C_LYS_184	NZ	C_GLU_188	OE2	3.850
4YHY	C_LYS_189	NZ	C_ASP_186	OD1	3.979
4YHY	C_HIS_190	ND1	C_ASP_152	OD2	3.638
4YHY	B_ARG_38	NH1	B_ASP_90	OD1	2.962
4YHY	B_ARG_38	NH2	B_GLU_46	OE1	3.075
4YHY	B_ARG_38	NH2	B_ASP_90	OD1	3.920
4YHY	B_ARG_67	NH1	B_ASP_90	OD1	3.667
4YHY	B_ARG_67	NH1	B_ASP_90	OD2	2.922
4YHY	B_ARG_67	NH2	B_ASP_90	OD1	2.906
4YHY	B_ARG_67	NH2	B_ASP_90	OD2	3.527
4YHY	B_ARG_98	NH2	B_ASP_109	OD1	3.412
4YHY	B_ARG_98	NH2	B_ASP_109	OD2	2.741
4YHY	B_LYS_151	NZ	B_ASP_152	OD1	3.708
4YHY	B_LYS_151	NZ	B_ASP_152	OD2	3.789
4YHY	B_LYS_218	NZ	B_GLU_220	OE2	3.937
4YHY	H_ARG_38	NH1	H_ASP_90	OD1	2.943
4YHY	H_ARG_38	NH2	H_GLU_46	OE1	3.065
4YHY	H_ARG_38	NH2	H_ASP_90	OD1	3.927
4YHY	H_ARG_67	NH1	H_ASP_90	OD1	3.683
4YHY	H_ARG_67	NH1	H_ASP_90	OD2	2.873
4YHY	H_ARG_67	NH2	H_ASP_90	OD1	2.953
4YHY	H_ARG_67	NH2	H_ASP_90	OD2	3.520
4YHY	H_ARG_98	NH2	H_ASP_109	OD1	3.446
4YHY	H_ARG_98	NH2	H_ASP_109	OD2	2.805
4YHY	H_LYS_151	NZ	H_ASP_152	OD1	3.926
4YHY	L_HIS_33	ND1	L_ASP_49	OD1	3.834
4YHY	L_ARG_60	NH1	L_ASP_81	OD1	3.514
4YHY	L_ARG_60	NH1	L_ASP_81	OD2	2.687
4YHY	L_ARG_60	NH2	L_GLU_78	OE1	3.800
4YHY	L_ARG_60	NH2	L_ASP_81	OD1	2.830
4YHY	L_ARG_60	NH2	L_ASP_81	OD2	3.411
4YHY	L_LYS_104	NZ	L_ASP_84	OD1	3.118
4YHY	L_LYS_104	NZ	L_ASP_84	OD2	3.782
4YHY	L_LYS_104	NZ	L_GLU_166	OE1	3.846
4YHY	L_LYS_104	NZ	L_GLU_166	OE2	3.435
4YHY	L_LYS_184	NZ	L_GLU_188	OE1	2.816
4YHY	L_LYS_189	NZ	L_ASP_186	OD1	3.965
4YHY	L_HIS_190	ND1	L_ASP_152	OD2	3.667

Table 637: 4YHY-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4YHZ	H_ARG_38	NH1	H_ASP_90	OD1	3.041
4YHZ	H_ARG_38	NH2	H_GLU_46	OE1	2.993
4YHZ	H_ARG_67	NH1	H_ASP_90	OD1	3.565
4YHZ	H_ARG_67	NH1	H_ASP_90	OD2	2.787
4YHZ	H_ARG_67	NH2	H_ASP_90	OD1	3.041
4YHZ	H_ARG_67	NH2	H_ASP_90	OD2	3.647
4YHZ	H_ARG_98	NH2	H_ASP_109	OD1	3.319
4YHZ	H_ARG_98	NH2	H_ASP_109	OD2	2.731
4YHZ	H_ARG_102	NH1	L_ASP_52	OD2	3.952
4YHZ	H_LYS_151	NZ	H_ASP_152	OD1	3.146
4YHZ	H_LYS_151	NZ	H_ASP_152	OD2	3.730
4YHZ	H_LYS_218	NZ	H_GLU_220	OE2	2.294
4YHZ	L_ARG_60	NH1	L_ASP_81	OD1	3.699
4YHZ	L_ARG_60	NH1	L_ASP_81	OD2	2.763
4YHZ	L_ARG_60	NH2	L_GLU_78	OE2	3.725
4YHZ	L_ARG_60	NH2	L_ASP_81	OD1	2.809
4YHZ	L_ARG_60	NH2	L_ASP_81	OD2	3.312
4YHZ	L_LYS_104	NZ	L_ASP_84	OD1	2.930
4YHZ	L_LYS_104	NZ	L_ASP_84	OD2	3.859
4YHZ	L_LYS_104	NZ	L_GLU_166	OE2	3.711
4YHZ	L_LYS_150	NZ	L_GLU_196	OE1	3.382
4YHZ	L_LYS_150	NZ	L_GLU_196	OE2	3.096
4YHZ	L_LYS_189	NZ	L_ASP_186	OD1	3.342

Table 638: 4YHZ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4YNY	A_ARG.57	NH1	A_ASP.109	OD1	2.933
4YNY	A_ARG.57	NH2	A_GLU.65	OE1	3.525
4YNY	A_ARG.57	NH2	A_GLU.65	OE2	3.243
4YNY	A_ARG.57	NH2	A_ASP.109	OD1	3.948
4YNY	A_ARG.86	NH1	A_ASP.109	OD1	3.716
4YNY	A_ARG.86	NH1	A_ASP.109	OD2	2.746
4YNY	A_ARG.86	NH2	A_ASP.109	OD1	3.047
4YNY	A_ARG.86	NH2	A_ASP.109	OD2	3.560
4YNY	A_ARG.106	NH2	A_GLU.108	OE1	3.999
4YNY	A_LYS.117	NZ	A_ASP.124	OD1	3.494
4YNY	A_LYS.117	NZ	A_ASP.124	OD2	2.864
4YNY	A_LYS.166	NZ	B_GLU.146	OE2	2.702
4YNY	B_LYS.73	NZ	B_ASP.72	OD2	3.025
4YNY	B_ARG.81	NH1	B_ASP.104	OD1	3.819
4YNY	B_ARG.81	NH1	B_ASP.104	OD2	2.603
4YNY	B_ARG.81	NH2	B_ASP.104	OD1	2.915
4YNY	B_ARG.81	NH2	B_ASP.104	OD2	3.187
4YNY	B_LYS.132	NZ	B_GLU.219	OE2	3.320
4YNY	B_LYS.188	NZ	B_GLU.105	OE1	3.576
4YNY	B_LYS.188	NZ	B_GLU.105	OE2	2.488
4YNY	B_LYS.192	NZ	B_ASP.160	OD1	3.032
4YNY	B_ARG.200	NH2	B_ASP.182	OD1	3.555
4YNY	B_ARG.200	NH2	B_ASP.182	OD2	2.866
4YNY	C_ARG.57	NH1	C_ASP.109	OD1	2.834
4YNY	C_ARG.57	NH2	C_GLU.65	OE1	3.680
4YNY	C_ARG.57	NH2	C_GLU.65	OE2	3.119
4YNY	C_ARG.57	NH2	C_ASP.109	OD1	3.921
4YNY	C_ARG.86	NH1	C_ASP.109	OD1	3.790
4YNY	C_ARG.86	NH1	C_ASP.109	OD2	2.710
4YNY	C_ARG.86	NH2	C_ASP.109	OD1	3.106
4YNY	C_ARG.86	NH2	C_ASP.109	OD2	3.542
4YNY	C_LYS.117	NZ	C_ASP.124	OD1	3.354
4YNY	C_LYS.117	NZ	C_ASP.124	OD2	2.744
4YNY	C_LYS.166	NZ	D_GLU.146	OE2	2.776
4YNY	D_LYS.73	NZ	D_ASP.72	OD1	3.416
4YNY	D_ARG.81	NH1	D_ASP.104	OD1	3.697
4YNY	D_ARG.81	NH1	D_ASP.104	OD2	2.693
4YNY	D_ARG.81	NH2	D_ASP.104	OD1	2.906
4YNY	D_ARG.81	NH2	D_ASP.104	OD2	3.380
4YNY	D_LYS.188	NZ	D_GLU.105	OE1	3.077
4YNY	D_LYS.192	NZ	D_ASP.160	OD2	3.867
4YNY	D_ARG.200	NH2	D_ASP.182	OD1	3.317
4YNY	D_ARG.200	NH2	D_ASP.182	OD2	3.323

Table 639: 4YNY-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4YO0	A_ARG_57	NH1	A_ASP_109	OD1	3.022
4YO0	A_ARG_57	NH2	A_GLU_65	OE1	3.398
4YO0	A_LYS_76	NZ	E_ASP_11	OD1	3.807
4YO0	A_LYS_76	NZ	E_ASP_11	OD2	3.094
4YO0	A_ARG_86	NH1	A_ASP_109	OD1	3.794
4YO0	A_ARG_86	NH1	A_ASP_109	OD2	2.742
4YO0	A_ARG_86	NH2	A_ASP_109	OD1	2.929
4YO0	A_ARG_86	NH2	A_ASP_109	OD2	3.356
4YO0	A_LYS_95	NZ	A_ASP_92	OD2	3.971
4YO0	A_LYS_117	NZ	A_ASP_124	OD1	3.329
4YO0	A_LYS_117	NZ	A_ASP_124	OD2	2.540
4YO0	A_LYS_166	NZ	B_GLU_146	OE2	2.816
4YO0	B_ARG_81	NH2	B_ASP_104	OD1	2.781
4YO0	B_ARG_81	NH2	B_ASP_104	OD2	3.330
4YO0	B_LYS_188	NZ	B_GLU_105	OE2	2.712
4YO0	B_LYS_192	NZ	B_ASP_160	OD1	3.003
4YO0	B_ARG_200	NH1	B_ASP_182	OD1	3.660
4YO0	B_ARG_200	NH1	B_ASP_182	OD2	2.289
4YO0	C_ARG_57	NH1	C_ASP_109	OD1	2.959
4YO0	C_ARG_57	NH2	C_GLU_65	OE1	3.257
4YO0	C_ARG_57	NH2	C_ASP_109	OD1	3.982
4YO0	C_LYS_76	NZ	F_GLU_10	OE2	3.111
4YO0	C_LYS_76	NZ	F_ASP_11	OD1	3.515
4YO0	C_LYS_76	NZ	F_ASP_11	OD2	2.782
4YO0	C_ARG_86	NH1	C_ASP_109	OD1	3.789
4YO0	C_ARG_86	NH1	C_ASP_109	OD2	2.778
4YO0	C_ARG_86	NH2	C_ASP_109	OD1	2.949
4YO0	C_ARG_86	NH2	C_ASP_109	OD2	3.459
4YO0	C_LYS_117	NZ	C_ASP_124	OD1	3.359
4YO0	C_LYS_117	NZ	C_ASP_124	OD2	2.756
4YO0	C_LYS_166	NZ	D_GLU_146	OE2	2.660
4YO0	C_LYS_231	NZ	D_GLU_145	OE1	3.828
4YO0	C_LYS_231	NZ	D_GLU_145	OE2	3.815
4YO0	D_LYS_188	NZ	D_GLU_105	OE1	2.881
4YO0	D_LYS_192	NZ	D_ASP_160	OD1	2.854
4YO0	D_ARG_200	NH1	D_ASP_182	OD2	2.726

Table 640: 4YO0-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4Z0X	A_LYS_30	NZ	A_ASP_91	OD1	2.897
4Z0X	A_ARG_60	NH1	A_ASP_81	OD1	3.753
4Z0X	A_ARG_60	NH1	A_ASP_81	OD2	2.721
4Z0X	A_ARG_60	NH2	A_ASP_81	OD1	3.000
4Z0X	A_ARG_60	NH2	A_ASP_81	OD2	3.078
4Z0X	B_LYS_37	NZ	B_GLU_35	OE1	3.057
4Z0X	B_ARG_63	NH1	B_ASP_115	OD1	2.995
4Z0X	B_ARG_63	NH2	B_GLU_71	OE2	3.549
4Z0X	B_ARG_63	NH2	B_ASP_115	OD1	3.828
4Z0X	B_ARG_92	NH1	B_ASP_115	OD1	3.502
4Z0X	B_ARG_92	NH1	B_ASP_115	OD2	2.905
4Z0X	B_ARG_92	NH2	B_ASP_115	OD1	2.679
4Z0X	B_ARG_92	NH2	B_ASP_115	OD2	3.355
4Z0X	B_ARG_123	NH1	B_ASP_132	OD1	3.837
4Z0X	C_LYS_446	NZ	A_ASP_50	OD1	3.873
4Z0X	C_LYS_446	NZ	A_ASP_50	OD2	2.440

Table 641: 4Z0X-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4ZD3	H_ARG_43	NH2	H_GLU_51	OE1	2.895
4ZD3	H_ARG_43	NH2	H_GLU_51	OE2	3.597
4ZD3	H_ARG_66	NH2	H_ASP_64	OD1	3.286
4ZD3	H_ARG_66	NH2	H_ASP_64	OD2	2.638
4ZD3	H_ARG_106	NH2	H_ASP_116	OD1	3.450
4ZD3	H_ARG_106	NH2	H_ASP_116	OD2	3.904
4ZD3	H_HIS_108	ND1	H_ASP_116	OD1	3.941
4ZD3	H_HIS_108	ND1	H_ASP_116	OD2	2.771
4ZD3	H_HIS_108	NE2	L_GLU_68	OE1	2.549
4ZD3	H_HIS_108	NE2	L_GLU_68	OE2	3.986
4ZD3	H_LYS_158	NZ	H_ASP_159	OD1	3.455
4ZD3	H_LYS_158	NZ	H_ASP_159	OD2	3.407
4ZD3	H_LYS_224	NZ	L_GLU_143	OE2	2.997
4ZD3	L_ARG_75	NH2	L_ASP_98	OD1	2.930
4ZD3	L_ARG_75	NH2	L_ASP_98	OD2	3.672
4ZD3	L_LYS_123	NZ	L_GLU_185	OE2	3.206
4ZD3	L_ARG_128	NH2	L_ASP_190	OD1	3.816
4ZD3	L_LYS_169	NZ	L_GLU_215	OE1	2.511

Table 642: 4ZD3-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4ZFF	A_ARG_38	NH1	A_ASP_86	OD1	2.818
4ZFF	A_ARG_38	NH2	A_GLU_46	OE2	2.795
4ZFF	A_ARG_66	NH1	A_ASP_86	OD1	3.744
4ZFF	A_ARG_66	NH1	A_ASP_86	OD2	2.802
4ZFF	A_ARG_66	NH2	A_ASP_86	OD1	2.833
4ZFF	A_ARG_66	NH2	A_ASP_86	OD2	3.432
4ZFF	A_LYS_75	NZ	A_ASP_72	OD2	3.517
4ZFF	A_ARG_94	NH2	A_ASP_101	OD1	2.782
4ZFF	A_ARG_94	NH2	A_ASP_101	OD2	3.644
4ZFF	A_LYS_143	NZ	A_ASP_144	OD2	3.566
4ZFF	A_LYS_209	NZ	B_GLU_123	OE1	3.193
4ZFF	B_ARG_61	NH1	B_GLU_81	OE2	3.817
4ZFF	B_ARG_61	NH1	B_ASP_82	OD1	2.656
4ZFF	B_ARG_61	NH1	B_ASP_82	OD2	3.672
4ZFF	B_LYS_149	NZ	B_GLU_195	OE2	2.800
4ZFF	B_HIS_189	ND1	B_ASP_151	OD1	3.097
4ZFF	B_HIS_189	ND1	B_ASP_151	OD2	3.583
4ZFF	C_ARG_23	NH1	D_GLU_30	OE1	3.414
4ZFF	C_ARG_56	NH1	C_GLU_38	OE2	3.486
4ZFF	C_ARG_56	NH2	C_GLU_38	OE1	2.778
4ZFF	C_ARG_56	NH2	C_GLU_38	OE2	3.528
4ZFF	C_ARG_82	NH2	C_GLU_42	OE1	3.647
4ZFF	C_ARG_82	NH2	C_GLU_42	OE2	2.877
4ZFF	C_HIS_99	NE2	C_GLU_73	OE2	3.973
4ZFF	C_ARG_105	NH2	C_GLU_103	OE1	3.895
4ZFF	C_ARG_105	NH2	C_GLU_103	OE2	2.902
4ZFF	C_LYS_107	NZ	C_GLU_64	OE1	3.791
4ZFF	C_LYS_107	NZ	C_GLU_64	OE2	3.768
4ZFF	D_ARG_23	NH2	D_ASP_19	OD2	3.386
4ZFF	D_ARG_56	NH1	D_GLU_38	OE2	3.530
4ZFF	D_ARG_56	NH2	D_GLU_38	OE1	2.807
4ZFF	D_ARG_56	NH2	D_GLU_38	OE2	3.533
4ZFF	D_ARG_82	NH1	D_GLU_42	OE1	2.977
4ZFF	D_ARG_82	NH1	D_GLU_42	OE2	3.475
4ZFF	D_LYS_84	NZ	D_GLU_44	OE1	2.813
4ZFF	D_LYS_84	NZ	D_GLU_44	OE2	3.787
4ZFF	D_HIS_99	NE2	D_GLU_73	OE2	3.971
4ZFF	D_ARG_105	NH2	D_GLU_103	OE1	3.892
4ZFF	D_ARG_105	NH2	D_GLU_103	OE2	2.901
4ZFF	D_LYS_107	NZ	D_GLU_64	OE1	3.795
4ZFF	D_LYS_107	NZ	D_GLU_64	OE2	3.756
4ZFF	H_ARG_38	NH1	H_ASP_86	OD1	3.173
4ZFF	H_ARG_38	NH2	H_GLU_46	OE2	3.109
4ZFF	H_ARG_66	NH1	H_ASP_86	OD1	3.724
4ZFF	H_ARG_66	NH1	H_ASP_86	OD2	2.802
4ZFF	H_ARG_66	NH2	H_ASP_86	OD1	2.829
4ZFF	H_ARG_66	NH2	H_ASP_86	OD2	3.437
4ZFF	H_LYS_75	NZ	H_ASP_72	OD2	3.526
4ZFF	H_ARG_94	NH2	H_ASP_101	OD1	2.747
4ZFF	H_ARG_94	NH2	H_ASP_101	OD2	3.634
4ZFF	H_LYS_143	NZ	H_ASP_144	OD2	3.565
4ZFF	H_LYS_209	NZ	L_GLU_123	OE1	3.731
4ZFF	L_ARG_61	NH1	L_GLU_81	OE2	3.489
4ZFF	L_ARG_61	NH1	L_ASP_82	OD1	2.794
4ZFF	L_ARG_61	NH1	L_ASP_82	OD2	3.847
4ZFF	L_LYS_	NZ	L_GLU_195	OE1	3.785
4ZFF	L_LYS_	NZ	L_GLU_195	OE2	2.790

4ZFF	L_LYS_	NZ	L_ASP_	OD1	3.960
4ZFF	L_HIS_	ND1	L_ASP_	OD1	3.345

Table 643: 4ZFF-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4ZFG	A_ARG_282	NH1	A_GLU_286	OE2	2.789
4ZFG	A_ARG_337	NH2	A_GLU_341	OE2	3.147
4ZFG	A_LYS_343	NZ	A_GLU_395	OE1	3.481
4ZFG	A_LYS_343	NZ	A_GLU_395	OE2	2.744
4ZFG	A_ARG_400	NH2	A_ASP_422	OD1	3.271
4ZFG	A_LYS_478	NZ	A_ASP_377	OD1	2.811
4ZFG	H_ARG_38	NH1	H_ASP_86	OD1	2.945
4ZFG	H_ARG_38	NH2	H_GLU_46	OE1	3.779
4ZFG	H_ARG_38	NH2	H_GLU_46	OE2	2.970
4ZFG	H_ARG_38	NH2	H_ASP_86	OD1	3.795
4ZFG	H_ARG_66	NH1	H_ASP_86	OD1	3.748
4ZFG	H_ARG_66	NH1	H_ASP_86	OD2	2.697
4ZFG	H_ARG_66	NH2	H_ASP_86	OD1	3.191
4ZFG	H_ARG_66	NH2	H_ASP_86	OD2	3.631
4ZFG	H_ARG_94	NH2	H_ASP_101	OD1	2.815
4ZFG	H_ARG_94	NH2	H_ASP_101	OD2	3.685
4ZFG	H_LYS_143	NZ	H_ASP_144	OD1	3.369
4ZFG	H_LYS_143	NZ	H_ASP_144	OD2	3.092
4ZFG	H_LYS_209	NZ	L_GLU_123	OE1	2.808
4ZFG	H_LYS_210	NZ	H_GLU_212	OE1	3.187
4ZFG	H_LYS_210	NZ	H_GLU_212	OE2	3.341
4ZFG	L_ARG_61	NH2	L_GLU_81	OE2	3.382
4ZFG	L_ARG_61	NH2	L_ASP_82	OD1	2.847
4ZFG	L_ARG_61	NH2	L_ASP_82	OD2	3.547
4ZFG	L_LYS_149	NZ	L_GLU_195	OE1	2.802
4ZFG	L_HIS_189	ND1	L_ASP_151	OD2	3.313

Table 644: 4ZFG-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4ZFO	F_HIS_19	NE2	A_GLU_50	OE1	2.994
4ZFO	F_HIS_19	NE2	A_GLU_50	OE2	3.320
4ZFO	L_LYS_24	NZ	L_ASP_70	OD1	2.843
4ZFO	L_LYS_24	NZ	L_ASP_70	OD2	3.681
4ZFO	L_ARG_41	NH1	L_GLU_165	OE1	2.854
4ZFO	L_ARG_41	NH1	L_GLU_165	OE2	3.771
4ZFO	L_ARG_41	NH2	L_GLU_165	OE1	3.602
4ZFO	L_ARG_41	NH2	L_GLU_165	OE2	3.007
4ZFO	L_ARG_61	NH1	L_GLU_81	OE2	3.554
4ZFO	L_ARG_61	NH1	L_ASP_82	OD1	2.833
4ZFO	L_ARG_61	NH1	L_ASP_82	OD2	3.587
4ZFO	L_LYS_149	NZ	L_GLU_195	OE2	3.249
4ZFO	L_HIS_189	ND1	L_ASP_151	OD2	2.754
4ZFO	H_ARG_38	NH1	H_ASP_90	OD1	2.859
4ZFO	H_ARG_38	NH2	H_GLU_46	OE2	3.054
4ZFO	H_ARG_38	NH2	H_ASP_90	OD1	3.757
4ZFO	H_ARG_39	NH1	L_GLU_85	OE2	3.425
4ZFO	H_ARG_39	NH2	L_GLU_85	OE1	3.703
4ZFO	H_ARG_39	NH2	L_GLU_85	OE2	2.644
4ZFO	H_LYS_67	NZ	H_ASP_90	OD1	3.687
4ZFO	H_LYS_67	NZ	H_ASP_90	OD2	2.794
4ZFO	H_LYS_150	NZ	H_ASP_151	OD1	3.394
4ZFO	H_LYS_216	NZ	L_GLU_123	OE2	3.666
4ZFO	H_ARG_217	NH2	H_GLU_219	OE1	3.524
4ZFO	B_LYS_24	NZ	B_ASP_70	OD1	2.732
4ZFO	B_LYS_24	NZ	B_ASP_70	OD2	3.699
4ZFO	B_ARG_61	NH1	B_GLU_81	OE1	3.604
4ZFO	B_ARG_61	NH1	B_ASP_82	OD1	2.928
4ZFO	B_ARG_61	NH1	B_ASP_82	OD2	3.562
4ZFO	B_LYS_103	NZ	B_GLU_165	OE1	3.091
4ZFO	B_LYS_103	NZ	B_GLU_165	OE2	2.652
4ZFO	B_LYS_149	NZ	B_GLU_195	OE1	2.655
4ZFO	B_LYS_149	NZ	B_GLU_195	OE2	3.647
4ZFO	B_LYS_183	NZ	B_GLU_187	OE2	3.657
4ZFO	B_LYS_188	NZ	B_ASP_185	OD1	2.524
4ZFO	B_HIS_189	ND1	B_ASP_151	OD2	2.980
4ZFO	A_ARG_31	NH1	A_ASP_102	OD1	3.536
4ZFO	A_ARG_31	NH1	A_ASP_102	OD2	2.769
4ZFO	A_ARG_38	NH1	A_ASP_90	OD1	2.884
4ZFO	A_ARG_38	NH2	A_GLU_46	OE1	3.650
4ZFO	A_ARG_38	NH2	A_GLU_46	OE2	2.886
4ZFO	A_ARG_38	NH2	A_ASP_90	OD1	3.988
4ZFO	A_ARG_39	NH1	B_GLU_85	OE1	3.845
4ZFO	A_ARG_39	NH2	B_GLU_85	OE1	2.855
4ZFO	A_ARG_39	NH2	B_GLU_85	OE2	3.746
4ZFO	A_LYS_67	NZ	A_ASP_90	OD1	3.473
4ZFO	A_LYS_67	NZ	A_ASP_90	OD2	2.764
4ZFO	A_LYS_150	NZ	A_ASP_151	OD1	3.442
4ZFO	K_HIS_19	NE2	H_GLU_50	OE1	2.755
4ZFO	K_HIS_19	NE2	H_GLU_50	OE2	3.392

Table 645: 4ZFO-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4ZH7	A_ARG_32	NH1	A_ASP_28	OD1	2.616
4ZH7	A_ARG_32	NH1	A_ASP_28	OD2	2.970
4ZH7	A_LYS_155	NZ	A_GLU_151	OE2	3.235
4ZH7	A_ARG_169	NH2	A_ASP_257	OD2	3.147
4ZH7	A_LYS_175	NZ	A_GLU_176	OE2	3.803
4ZH7	A_LYS_251	NZ	A_GLU_253	OE1	3.001
4ZH7	A_LYS_251	NZ	A_GLU_253	OE2	3.952
4ZH7	A_LYS_313	NZ	A_ASP_317	OD2	2.913
4ZH7	A_LYS_343	NZ	A_ASP_350	OD1	3.604
4ZH7	A_LYS_343	NZ	A_ASP_350	OD2	2.780
4ZH7	A_LYS_366	NZ	A_GLU_320	OE2	2.717
4ZH7	A_LYS_437	NZ	A_GLU_381	OE1	3.484
4ZH7	A_LYS_437	NZ	A_GLU_381	OE2	3.811
4ZH7	A_ARG_466	NH2	A_ASP_458	OD1	2.975
4ZH7	A_ARG_466	NH2	A_ASP_458	OD2	3.143

Table 646: 4ZH7-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5A2I	H_ARG_38	NH1	H_ASP_86	OD1	2.884
5A2I	H_ARG_38	NH2	H_GLU_46	OE1	3.128
5A2I	H_ARG_38	NH2	H_GLU_46	OE2	3.996
5A2I	H_ARG_38	NH2	H_ASP_86	OD1	3.809
5A2I	H_ARG_52	NH1	H_GLU_50	OE2	2.458
5A2I	H_HIS_58	ND1	H_GLU_50	OE2	2.942
5A2I	H_ARG_66	NH1	H_ASP_86	OD1	3.097
5A2I	H_ARG_66	NH1	H_ASP_86	OD2	3.703
5A2I	H_ARG_66	NH2	H_ASP_86	OD1	3.277
5A2I	H_ARG_66	NH2	H_ASP_86	OD2	2.349
5A2I	H_ARG_71	NH2	H_ASP_73	OD1	3.396
5A2I	H_ARG_1024	NH1	H_ASP_1069	OD2	3.870
5A2I	H_ARG_1024	NH2	H_ASP_1069	OD1	2.961
5A2I	H_ARG_1024	NH2	H_ASP_1069	OD2	3.137
5A2I	H_HIS_1042	ND1	H_GLU_1038	OE2	3.431
5A2I	H_HIS_1042	ND1	H_ASP_1041	OD1	3.140
5A2I	H_HIS_1042	NE2	H_ASP_1041	OD1	2.854
5A2I	H_ARG_1061	NH2	H_GLU_1081	OE2	3.967
5A2I	H_ARG_1061	NH2	H_ASP_1082	OD1	2.886
5A2I	H_ARG_1061	NH2	H_ASP_1082	OD2	3.803

Table 647: 5A2I-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5A2J	H_ARG_38	NH1	H_ASP_86	OD1	2.875
5A2J	H_ARG_38	NH2	H_GLU_46	OE1	3.145
5A2J	H_ARG_38	NH2	H_GLU_46	OE2	3.372
5A2J	H_ARG_38	NH2	H_ASP_86	OD1	3.987
5A2J	H_LYS_43	NZ	H_GLU_46	OE1	3.646
5A2J	H_LYS_43	NZ	H_GLU_85	OE1	2.765
5A2J	H_ARG_52	NH2	H_GLU_50	OE2	2.945
5A2J	H_ARG_66	NH1	H_ASP_86	OD1	3.341
5A2J	H_ARG_66	NH1	H_ASP_86	OD2	3.539
5A2J	H_ARG_66	NH2	H_ASP_86	OD1	3.626
5A2J	H_ARG_66	NH2	H_ASP_86	OD2	2.364
5A2J	H_ARG_71	NH2	H_ASP_73	OD1	3.334
5A2J	H_LYS_75	NZ	H_ASP_72	OD2	3.979
5A2J	H_ARG_83	NH1	H_GLU_85	OE2	3.360
5A2J	H_ARG_1024	NH1	H_ASP_1069	OD1	3.811
5A2J	H_ARG_1024	NH1	H_ASP_1069	OD2	2.838
5A2J	H_ARG_1024	NH2	H_ASP_1069	OD1	3.142
5A2J	H_ARG_1024	NH2	H_ASP_1069	OD2	3.430
5A2J	H_HIS_1042	ND1	H_GLU_1038	OE2	3.360
5A2J	H_ARG_1061	NH2	H_GLU_1081	OE2	3.894
5A2J	H_ARG_1061	NH2	H_ASP_1082	OD1	2.853
5A2J	H_ARG_1061	NH2	H_ASP_1082	OD2	3.674

Table 648: 5A2J-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5A2K	H_ARG_38	NH1	H_ASP_86	OD1	2.875
5A2K	H_ARG_38	NH2	H_GLU_46	OE1	2.994
5A2K	H_ARG_38	NH2	H_GLU_46	OE2	3.664
5A2K	H_ARG_38	NH2	H_ASP_86	OD1	3.944
5A2K	H_LYS_43	NZ	H_GLU_46	OE1	3.807
5A2K	H_LYS_43	NZ	H_GLU_85	OE1	3.399
5A2K	H_ARG_52	NH1	H_GLU_50	OE1	3.946
5A2K	H_ARG_52	NH1	H_GLU_50	OE2	2.653
5A2K	H_HIS_58	ND1	H_GLU_50	OE2	2.712
5A2K	H_ARG_66	NH1	H_ASP_86	OD1	3.221
5A2K	H_ARG_66	NH1	H_ASP_86	OD2	3.625
5A2K	H_ARG_66	NH2	H_ASP_86	OD1	3.474
5A2K	H_ARG_66	NH2	H_ASP_86	OD2	2.358
5A2K	H_ARG_71	NH2	H_ASP_73	OD1	3.340
5A2K	H_ARG_83	NH1	H_GLU_85	OE2	3.612
5A2K	H_HIS_1042	ND1	H_GLU_1038	OE2	3.466
5A2K	H_HIS_1042	NE2	H_ASP_1041	OD1	3.782
5A2K	H_ARG_1061	NH2	H_GLU_1081	OE2	3.980
5A2K	H_ARG_1061	NH2	H_ASP_1082	OD1	2.834
5A2K	H_ARG_1061	NH2	H_ASP_1082	OD2	3.700

Table 649: 5A2K-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5A2L	H_ARG_38	NH1	H_ASP_86	OD1	2.857
5A2L	H_ARG_38	NH2	H_GLU_46	OE1	3.272
5A2L	H_ARG_38	NH2	H_GLU_46	OE2	3.166
5A2L	H_ARG_38	NH2	H_ASP_86	OD1	3.882
5A2L	H_LYS_43	NZ	H_GLU_46	OE1	2.594
5A2L	H_LYS_43	NZ	H_GLU_46	OE2	3.749
5A2L	H_LYS_43	NZ	H_GLU_85	OE1	3.820
5A2L	H_ARG_52	NH1	H_GLU_50	OE2	2.656
5A2L	H_HIS_58	ND1	H_GLU_50	OE2	2.623
5A2L	H_ARG_66	NH1	H_ASP_86	OD1	3.373
5A2L	H_ARG_66	NH1	H_ASP_86	OD2	3.769
5A2L	H_ARG_66	NH2	H_ASP_86	OD1	3.135
5A2L	H_ARG_66	NH2	H_ASP_86	OD2	2.092
5A2L	H_ARG_71	NH2	H_ASP_73	OD1	3.516
5A2L	H_ARG_83	NH1	H_GLU_85	OE2	3.111
5A2L	H_ARG_1024	NH1	H_ASP_1069	OD2	3.824
5A2L	H_ARG_1024	NH2	H_ASP_1069	OD1	3.107
5A2L	H_ARG_1024	NH2	H_ASP_1069	OD2	2.735
5A2L	H_HIS_1042	ND1	H_GLU_1038	OE2	3.532
5A2L	H_ARG_1061	NH2	H_GLU_1081	OE2	3.627
5A2L	H_ARG_1061	NH2	H_ASP_1082	OD1	2.860
5A2L	H_ARG_1061	NH2	H_ASP_1082	OD2	3.701
5A2L	H_LYS_1103	NZ	H_GLU_1083	OE2	3.909

Table 650: 5A2L-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5A7X	A_LYS.121	NZ	A_GLU.429	OE1	3.568
5A7X	A_LYS.121	NZ	A_GLU.429	OE2	2.734
5A7X	A_LYS.207	NZ	A_GLU.381	OE1	3.945
5A7X	A_LYS.207	NZ	A_GLU.381	OE2	3.126
5A7X	A_LYS.232	NZ	A_GLU.351	OE1	3.994
5A7X	A_HIS.249	NE2	A_GLU.482	OE1	3.525
5A7X	A_LYS.282	NZ	A_GLU.275	OE1	3.953
5A7X	A_LYS.282	NZ	A_GLU.275	OE2	2.643
5A7X	A_LYS.348	NZ	A_GLU.269	OE1	3.207
5A7X	A_LYS.348	NZ	A_GLU.351	OE1	3.940
5A7X	A_LYS.348	NZ	A_GLU.351	OE2	3.259
5A7X	A_LYS.350	NZ	A_ASP.395	OD2	3.580
5A7X	A_LYS.357	NZ	A_GLU.466	OE2	3.719
5A7X	A_ARG.419	NH1	D_GLU.100B	OE1	3.000
5A7X	A_ARG.419	NH1	D_GLU.100B	OE2	3.675
5A7X	A_ARG.419	NH2	D_GLU.99	OE1	2.292
5A7X	A_ARG.419	NH2	D_GLU.100B	OE2	3.969
5A7X	A_ARG.456	NH2	A_GLU.466	OE1	3.535
5A7X	A_ARG.456	NH2	A_GLU.466	OE2	3.469
5A7X	A_ARG.469	NH2	A_ASP.457	OD2	3.234
5A7X	A_ARG.476	NH1	A_ASP.474	OD1	3.441
5A7X	A_ARG.476	NH2	A_GLU.102	OE1	3.296
5A7X	A_ARG.476	NH2	A_GLU.102	OE2	3.010
5A7X	A_LYS.487	NZ	A_GLU.91	OE1	3.525
5A7X	A_LYS.490	NZ	A_GLU.492	OE1	3.300
5A7X	B_LYS.29	NZ	B_GLU.85	OE1	2.833
5A7X	B_LYS.29	NZ	B_GLU.85	OE2	3.848
5A7X	B_LYS.35	NZ	A_ASP.457	OD1	3.741
5A7X	B_ARG.54	NH1	B_ASP.78	OD1	3.987
5A7X	B_ARG.54	NH1	B_ASP.78	OD2	2.755
5A7X	B_ARG.54	NH2	B_ASP.78	OD1	2.666
5A7X	B_ARG.54	NH2	B_ASP.78	OD2	2.988
5A7X	B_ARG.59	NH1	A_ASP.368	OD1	3.154
5A7X	B_ARG.59	NH1	A_ASP.368	OD2	3.344
5A7X	B_ARG.59	NH2	A_ASP.368	OD1	2.976
5A7X	B_ARG.59	NH2	A_ASP.368	OD2	2.433
5A7X	B_HIS.107	ND1	B_ASP.105	OD1	3.166
5A7X	B_HIS.107	ND1	B_ASP.105	OD2	2.892
5A7X	B_ARG.134	NH2	B_ASP.153	OD1	3.765
5A7X	B_LYS.136	NZ	B_GLU.150	OE2	3.886
5A7X	B_LYS.136	NZ	B_ASP.153	OD1	3.937
5A7X	B_LYS.136	NZ	B_ASP.153	OD2	2.987
5A7X	B_LYS.171	NZ	B_GLU.169	OE2	2.874
5A7X	C_ARG.61	NH2	C_GLU.81	OE2	3.127
5A7X	C_ARG.61	NH2	C_ASP.82	OD1	3.575
5A7X	C_ARG.95B	NH2	C_ASP.1	OD2	2.985
5A7X	C_HIS.189	ND1	C_ASP.151	OD2	2.584
5A7X	C_HIS.189	NE2	C_ASP.185	OD1	2.801
5A7X	C_HIS.189	NE2	C_ASP.185	OD2	3.600
5A7X	C_ARG.211	NH1	C_GLU.187	OE1	3.852
5A7X	D_ARG.31	NH2	D_ASP.100A	OD1	3.069
5A7X	D_ARG.31	NH2	D_ASP.100A	OD2	3.614
5A7X	D_ARG.38	NH1	D_GLU.46	OE1	2.778
5A7X	D_ARG.38	NH1	D_GLU.46	OE2	3.341
5A7X	D_ARG.38	NH2	D_ASP.86	OD1	2.685
5A7X	D_ARG.50	NH2	D_GLU.97	OE2	2.331
5A7X	D_ARG.66	NH1	D_ASP.86	OD2	3.597

5A7X	D_ARG_66	NH2	D_ASP_86	OD1	2.740
5A7X	D_ARG_66	NH2	D_ASP_86	OD2	2.415
5A7X	D_LYS_73	NZ	D_ASP_55	OD1	2.968
5A7X	D_ARG_82A	NH2	D_GLU_81	OE1	3.271
5A7X	D_LYS_143	NZ	D_ASP_144	OD1	2.614
5A7X	D_LYS_143	NZ	D_ASP_144	OD2	3.235
5A7X	D_HIS_164	NE2	C_ASP_167	OD1	3.880
5A7X	D_HIS_164	NE2	C_ASP_167	OD2	2.506
5A7X	D_LYS_206	NZ	D_ASP_208	OD1	3.965
5A7X	D_LYS_209	NZ	C_GLU_123	OE1	3.513
5A7X	D_LYS_209	NZ	C_GLU_123	OE2	3.583
5A7X	E_LYS_121	NZ	E_GLU_429	OE1	3.567
5A7X	E_LYS_121	NZ	E_GLU_429	OE2	2.734
5A7X	E_LYS_207	NZ	E_GLU_381	OE1	3.946
5A7X	E_LYS_207	NZ	E_GLU_381	OE2	3.125
5A7X	E_LYS_232	NZ	E_GLU_351	OE1	3.995
5A7X	E_HIS_249	NE2	E_GLU_482	OE1	3.525
5A7X	E_LYS_282	NZ	E_GLU_275	OE1	3.954
5A7X	E_LYS_282	NZ	E_GLU_275	OE2	2.642
5A7X	E_LYS_348	NZ	E_GLU_269	OE1	3.207
5A7X	E_LYS_348	NZ	E_GLU_351	OE1	3.941
5A7X	E_LYS_348	NZ	E_GLU_351	OE2	3.259
5A7X	E_LYS_350	NZ	E_ASP_395	OD2	3.580
5A7X	E_LYS_357	NZ	E_GLU_466	OE2	3.719
5A7X	E_ARG_419	NH1	H_GLU_100B	OE1	2.998
5A7X	E_ARG_419	NH1	H_GLU_100B	OE2	3.674
5A7X	E_ARG_419	NH2	H_GLU_99	OE1	2.293
5A7X	E_ARG_419	NH2	H_GLU_100B	OE2	3.968
5A7X	E_ARG_456	NH2	E_GLU_466	OE1	3.536
5A7X	E_ARG_456	NH2	E_GLU_466	OE2	3.468
5A7X	E_ARG_469	NH2	E_ASP_457	OD2	3.234
5A7X	E_ARG_476	NH1	E_ASP_474	OD1	3.440
5A7X	E_ARG_476	NH2	E_GLU_102	OE1	3.296
5A7X	E_ARG_476	NH2	E_GLU_102	OE2	3.010
5A7X	E_LYS_487	NZ	E_GLU_91	OE1	3.524
5A7X	E_LYS_490	NZ	E_GLU_492	OE1	3.301
5A7X	F_LYS_29	NZ	F_GLU_85	OE1	2.832
5A7X	F_LYS_29	NZ	F_GLU_85	OE2	3.847
5A7X	F_LYS_35	NZ	E_ASP_457	OD1	3.741
5A7X	F_ARG_54	NH1	F_ASP_78	OD1	3.987
5A7X	F_ARG_54	NH1	F_ASP_78	OD2	2.755
5A7X	F_ARG_54	NH2	F_ASP_78	OD1	2.666
5A7X	F_ARG_54	NH2	F_ASP_78	OD2	2.988
5A7X	F_ARG_59	NH1	E_ASP_368	OD1	3.154
5A7X	F_ARG_59	NH1	E_ASP_368	OD2	3.343
5A7X	F_ARG_59	NH2	E_ASP_368	OD1	2.977
5A7X	F_ARG_59	NH2	E_ASP_368	OD2	2.434
5A7X	F_HIS_107	ND1	F_ASP_105	OD1	3.166
5A7X	F_HIS_107	ND1	F_ASP_105	OD2	2.891
5A7X	F_ARG_134	NH2	F_ASP_153	OD1	3.765
5A7X	F_LYS_136	NZ	F_GLU_150	OE2	3.883
5A7X	F_LYS_136	NZ	F_ASP_153	OD1	3.936
5A7X	F_LYS_136	NZ	F_ASP_153	OD2	2.987
5A7X	F_LYS_171	NZ	F_GLU_169	OE2	2.875
5A7X	G_ARG_61	NH2	G_GLU_81	OE2	3.126
5A7X	G_ARG_61	NH2	G_ASP_82	OD1	3.576
5A7X	G_ARG_95B	NH2	G_ASP_1	OD2	2.984
5A7X	G_HIS_189	ND1	G_ASP_151	OD2	2.584

5A7X	G_HIS_189	NE2	G_ASP_185	OD1	2.802
5A7X	G_HIS_189	NE2	G_ASP_185	OD2	3.599
5A7X	G_ARG_211	NH1	G_GLU_187	OE1	3.852
5A7X	H_ARG_31	NH2	H_ASP_100A	OD1	3.070
5A7X	H_ARG_31	NH2	H_ASP_100A	OD2	3.615
5A7X	H_ARG_38	NH1	H_GLU_46	OE1	2.780
5A7X	H_ARG_38	NH1	H_GLU_46	OE2	3.343
5A7X	H_ARG_38	NH2	H_ASP_86	OD1	2.684
5A7X	H_ARG_50	NH2	H_GLU_97	OE2	2.333
5A7X	H_ARG_66	NH1	H_ASP_86	OD2	3.598
5A7X	H_ARG_66	NH2	H_ASP_86	OD1	2.739
5A7X	H_ARG_66	NH2	H_ASP_86	OD2	2.416
5A7X	H_LYS_73	NZ	H_ASP_55	OD1	2.968
5A7X	H_ARG_82A	NH2	H_GLU_81	OE1	3.271
5A7X	H_LYS_143	NZ	H_ASP_144	OD1	2.614
5A7X	H_LYS_143	NZ	H_ASP_144	OD2	3.234
5A7X	H_HIS_164	NE2	G_ASP_167	OD1	3.880
5A7X	H_HIS_164	NE2	G_ASP_167	OD2	2.505
5A7X	H_LYS_206	NZ	H_ASP_208	OD1	3.966
5A7X	H_LYS_209	NZ	G_GLU_123	OE1	3.512
5A7X	H_LYS_209	NZ	G_GLU_123	OE2	3.584
5A7X	I_LYS_121	NZ	I_GLU_429	OE1	3.568
5A7X	I_LYS_121	NZ	I_GLU_429	OE2	2.736
5A7X	I_LYS_207	NZ	I_GLU_381	OE1	3.945
5A7X	I_LYS_207	NZ	I_GLU_381	OE2	3.127
5A7X	I_LYS_232	NZ	I_GLU_351	OE1	3.995
5A7X	I_HIS_249	NE2	I_GLU_482	OE1	3.525
5A7X	I_LYS_282	NZ	I_GLU_275	OE1	3.953
5A7X	I_LYS_282	NZ	I_GLU_275	OE2	2.643
5A7X	I_LYS_348	NZ	I_GLU_269	OE1	3.206
5A7X	I_LYS_348	NZ	I_GLU_351	OE1	3.941
5A7X	I_LYS_348	NZ	I_GLU_351	OE2	3.259
5A7X	I_LYS_350	NZ	I_ASP_395	OD2	3.579
5A7X	I_LYS_357	NZ	I_GLU_466	OE2	3.720
5A7X	I_ARG_419	NH1	L_GLU_100B	OE1	2.999
5A7X	I_ARG_419	NH1	L_GLU_100B	OE2	3.675
5A7X	I_ARG_419	NH2	L_GLU_99	OE1	2.293
5A7X	I_ARG_419	NH2	L_GLU_100B	OE2	3.968
5A7X	I_ARG_456	NH2	I_GLU_466	OE1	3.536
5A7X	I_ARG_456	NH2	I_GLU_466	OE2	3.468
5A7X	I_ARG_469	NH2	I_ASP_457	OD2	3.234
5A7X	I_ARG_476	NH1	I_ASP_474	OD1	3.441
5A7X	I_ARG_476	NH2	I_GLU_102	OE1	3.297
5A7X	I_ARG_476	NH2	I_GLU_102	OE2	3.009
5A7X	I_LYS_487	NZ	I_GLU_91	OE1	3.523
5A7X	I_LYS_490	NZ	I_GLU_492	OE1	3.300
5A7X	J_LYS_29	NZ	J_GLU_85	OE1	2.833
5A7X	J_LYS_29	NZ	J_GLU_85	OE2	3.848
5A7X	J_LYS_35	NZ	I_ASP_457	OD1	3.740
5A7X	J_ARG_54	NH1	J_ASP_78	OD1	3.987
5A7X	J_ARG_54	NH1	J_ASP_78	OD2	2.755
5A7X	J_ARG_54	NH2	J_ASP_78	OD1	2.665
5A7X	J_ARG_54	NH2	J_ASP_78	OD2	2.989
5A7X	J_ARG_59	NH1	I_ASP_368	OD1	3.154
5A7X	J_ARG_59	NH1	I_ASP_368	OD2	3.344
5A7X	J_ARG_59	NH2	I_ASP_368	OD1	2.976
5A7X	J_ARG_59	NH2	I_ASP_368	OD2	2.433
5A7X	J_HIS_107	ND1	J_ASP_105	OD1	3.166

5A7X	J_HIS_107	ND1	J_ASP_105	OD2	2.892
5A7X	J_ARG_134	NH2	J_ASP_153	OD1	3.765
5A7X	J_LYS_136	NZ	J_GLU_150	OE2	3.885
5A7X	J_LYS_136	NZ	J_ASP_153	OD1	3.936
5A7X	J_LYS_136	NZ	J_ASP_153	OD2	2.987
5A7X	J_LYS_171	NZ	J_GLU_169	OE2	2.873
5A7X	K_ARG_61	NH2	K_GLU_81	OE2	3.128
5A7X	K_ARG_61	NH2	K_ASP_82	OD1	3.577
5A7X	K_ARG_95B	NH2	K_ASP_1	OD2	2.985
5A7X	K_HIS_189	ND1	K_ASP_151	OD2	2.584
5A7X	K_HIS_189	NE2	K_ASP_185	OD1	2.801
5A7X	K_HIS_189	NE2	K_ASP_185	OD2	3.597
5A7X	K_ARG_211	NH1	K_GLU_187	OE1	3.851
5A7X	L_ARG_31	NH2	L_ASP_100A	OD1	3.070
5A7X	L_ARG_31	NH2	L_ASP_100A	OD2	3.615
5A7X	L_ARG_38	NH1	L_GLU_46	OE1	2.779
5A7X	L_ARG_38	NH1	L_GLU_46	OE2	3.342
5A7X	L_ARG_38	NH2	L_ASP_86	OD1	2.685
5A7X	L_ARG_50	NH2	L_GLU_97	OE2	2.332
5A7X	L_ARG_66	NH1	L_ASP_86	OD2	3.598
5A7X	L_ARG_66	NH2	L_ASP_86	OD1	2.739
5A7X	L_ARG_66	NH2	L_ASP_86	OD2	2.415
5A7X	L_LYS_73	NZ	L_ASP_55	OD1	2.968
5A7X	L_ARG_82A	NH2	L_GLU_81	OE1	3.271
5A7X	L_LYS_143	NZ	L_ASP_144	OD1	2.615
5A7X	L_LYS_143	NZ	L_ASP_144	OD2	3.236
5A7X	L_HIS_164	NE2	K_ASP_167	OD1	3.880
5A7X	L_HIS_164	NE2	K_ASP_167	OD2	2.504
5A7X	L_LYS_206	NZ	L_ASP_208	OD1	3.966
5A7X	L_LYS_209	NZ	K_GLU_123	OE1	3.514
5A7X	L_LYS_209	NZ	K_GLU_123	OE2	3.585
5A7X	M_ARG_24	NH2	M_ASP_70	OD1	3.351
5A7X	M_ARG_24	NH2	M_ASP_70	OD2	2.877
5A7X	M_ARG_61	NH1	M_ASP_82	OD1	3.079
5A7X	M_ARG_61	NH1	M_ASP_82	OD2	3.077
5A7X	M_ARG_61	NH2	M_GLU_81	OE2	3.862
5A7X	M_LYS_103	NZ	M_GLU_165	OE1	3.804
5A7X	M_LYS_149	NZ	M_GLU_195	OE1	2.746
5A7X	M_LYS_149	NZ	M_GLU_195	OE2	3.963
5A7X	M_LYS_183	NZ	M_GLU_187	OE2	2.699
5A7X	M_HIS_189	ND1	M_ASP_151	OD1	3.975
5A7X	M_HIS_189	ND1	M_ASP_151	OD2	2.261
5A7X	N_ARG_38	NH1	N_ASP_86	OD1	3.024
5A7X	N_ARG_38	NH2	N_GLU_46	OE1	3.886
5A7X	N_ARG_66	NH1	N_ASP_86	OD1	3.550
5A7X	N_ARG_66	NH1	N_ASP_86	OD2	2.799
5A7X	N_ARG_66	NH2	N_ASP_86	OD1	2.933
5A7X	N_ARG_66	NH2	N_ASP_86	OD2	3.625
5A7X	N_LYS_82A	NZ	N_GLU_81	OE2	2.705
5A7X	N_HIS_100F	ND1	N_ASP_100G	OD2	3.940
5A7X	N_LYS_143	NZ	N_ASP_144	OD1	3.370
5A7X	N_LYS_143	NZ	N_ASP_144	OD2	3.506
5A7X	N_LYS_206	NZ	N_ASP_208	OD2	3.418
5A7X	O_ARG_24	NH2	O_ASP_70	OD1	3.351
5A7X	O_ARG_24	NH2	O_ASP_70	OD2	2.877
5A7X	O_ARG_61	NH1	O_ASP_82	OD1	3.079
5A7X	O_ARG_61	NH1	O_ASP_82	OD2	3.077
5A7X	O_ARG_61	NH2	O_GLU_81	OE2	3.862

5A7X	O_LYS_103	NZ	O_GLU_165	OE1	3.804
5A7X	O_LYS_149	NZ	O_GLU_195	OE1	2.747
5A7X	O_LYS_149	NZ	O_GLU_195	OE2	3.963
5A7X	O_LYS_183	NZ	O_GLU_187	OE2	2.699
5A7X	O_HIS_189	ND1	O_ASP_151	OD1	3.974
5A7X	O_HIS_189	ND1	O_ASP_151	OD2	2.260
5A7X	P_ARG_38	NH1	P_ASP_86	OD1	3.023
5A7X	P_ARG_38	NH2	P_GLU_46	OE1	3.886
5A7X	P_ARG_66	NH1	P_ASP_86	OD1	3.549
5A7X	P_ARG_66	NH1	P_ASP_86	OD2	2.799
5A7X	P_ARG_66	NH2	P_ASP_86	OD1	2.932
5A7X	P_ARG_66	NH2	P_ASP_86	OD2	3.625
5A7X	P_LYS_82A	NZ	P_GLU_81	OE2	2.706
5A7X	P_HIS_100F	ND1	P_ASP_100G	OD2	3.938
5A7X	P_LYS_143	NZ	P_ASP_144	OD1	3.371
5A7X	P_LYS_143	NZ	P_ASP_144	OD2	3.506
5A7X	P_LYS_206	NZ	P_ASP_208	OD2	3.418
5A7X	Q_ARG_24	NH2	Q_ASP_70	OD1	3.350
5A7X	Q_ARG_24	NH2	Q_ASP_70	OD2	2.876
5A7X	Q_ARG_61	NH1	Q_ASP_82	OD1	3.081
5A7X	Q_ARG_61	NH1	Q_ASP_82	OD2	3.078
5A7X	Q_ARG_61	NH2	Q_GLU_81	OE2	3.863
5A7X	Q_LYS_103	NZ	Q_GLU_165	OE1	3.804
5A7X	Q_LYS_149	NZ	Q_GLU_195	OE1	2.747
5A7X	Q_LYS_149	NZ	Q_GLU_195	OE2	3.963
5A7X	Q_LYS_183	NZ	Q_GLU_187	OE2	2.698
5A7X	Q_HIS_189	ND1	Q_ASP_151	OD1	3.974
5A7X	Q_HIS_189	ND1	Q_ASP_151	OD2	2.260
5A7X	R_ARG_38	NH1	R_ASP_86	OD1	3.024
5A7X	R_ARG_38	NH2	R_GLU_46	OE1	3.886
5A7X	R_ARG_66	NH1	R_ASP_86	OD1	3.548
5A7X	R_ARG_66	NH1	R_ASP_86	OD2	2.798
5A7X	R_ARG_66	NH2	R_ASP_86	OD1	2.932
5A7X	R_ARG_66	NH2	R_ASP_86	OD2	3.625
5A7X	R_LYS_82A	NZ	R_GLU_81	OE2	2.705
5A7X	R_HIS_100F	ND1	R_ASP_100G	OD2	3.938
5A7X	R_LYS_143	NZ	R_ASP_144	OD1	3.370
5A7X	R_LYS_143	NZ	R_ASP_144	OD2	3.506
5A7X	R_LYS_206	NZ	R_ASP_208	OD2	3.419

Table 651: 5A7X-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5A8H	A_LYS.121	NZ	A_GLU.429	OE1	3.567
5A8H	A_LYS.121	NZ	A_GLU.429	OE2	2.735
5A8H	A_LYS.207	NZ	A_GLU.381	OE1	3.945
5A8H	A_LYS.207	NZ	A_GLU.381	OE2	3.126
5A8H	A_LYS.232	NZ	A_GLU.351	OE1	3.995
5A8H	A_HIS.249	NE2	A_GLU.482	OE1	3.525
5A8H	A_LYS.282	NZ	A_GLU.275	OE1	3.954
5A8H	A_LYS.282	NZ	A_GLU.275	OE2	2.643
5A8H	A_LYS.348	NZ	A_GLU.269	OE1	3.206
5A8H	A_LYS.348	NZ	A_GLU.351	OE1	3.941
5A8H	A_LYS.348	NZ	A_GLU.351	OE2	3.259
5A8H	A_LYS.350	NZ	A_ASP.395	OD2	3.579
5A8H	A_LYS.357	NZ	A_GLU.466	OE2	3.720
5A8H	A_ARG.419	NH1	D_GLU.100B	OE1	2.999
5A8H	A_ARG.419	NH1	D_GLU.100B	OE2	3.674
5A8H	A_ARG.419	NH2	D_GLU.99	OE1	2.292
5A8H	A_ARG.419	NH2	D_GLU.100B	OE2	3.968
5A8H	A_ARG.456	NH2	A_GLU.466	OE1	3.537
5A8H	A_ARG.456	NH2	A_GLU.466	OE2	3.468
5A8H	A_ARG.469	NH2	A_ASP.457	OD2	3.234
5A8H	A_ARG.476	NH1	A_ASP.474	OD1	3.441
5A8H	A_ARG.476	NH2	A_GLU.102	OE1	3.296
5A8H	A_ARG.476	NH2	A_GLU.102	OE2	3.009
5A8H	A_LYS.487	NZ	A_GLU.91	OE1	3.523
5A8H	A_LYS.490	NZ	A_GLU.492	OE1	3.301
5A8H	B_LYS.29	NZ	B_GLU.85	OE1	2.833
5A8H	B_LYS.29	NZ	B_GLU.85	OE2	3.848
5A8H	B_LYS.35	NZ	A_ASP.457	OD1	3.740
5A8H	B_ARG.54	NH1	B_ASP.78	OD1	3.987
5A8H	B_ARG.54	NH1	B_ASP.78	OD2	2.755
5A8H	B_ARG.54	NH2	B_ASP.78	OD1	2.665
5A8H	B_ARG.54	NH2	B_ASP.78	OD2	2.988
5A8H	B_ARG.59	NH1	A_ASP.368	OD1	3.154
5A8H	B_ARG.59	NH1	A_ASP.368	OD2	3.342
5A8H	B_ARG.59	NH2	A_ASP.368	OD1	2.977
5A8H	B_ARG.59	NH2	A_ASP.368	OD2	2.433
5A8H	B_HIS.107	ND1	B_ASP.105	OD1	3.166
5A8H	B_HIS.107	ND1	B_ASP.105	OD2	2.891
5A8H	B_ARG.134	NH2	B_ASP.153	OD1	3.766
5A8H	B_LYS.136	NZ	B_GLU.150	OE2	3.884
5A8H	B_LYS.136	NZ	B_ASP.153	OD1	3.937
5A8H	B_LYS.136	NZ	B_ASP.153	OD2	2.986
5A8H	B_LYS.171	NZ	B_GLU.169	OE2	2.874
5A8H	C_ARG.61	NH2	C_GLU.81	OE2	3.127
5A8H	C_ARG.61	NH2	C_ASP.82	OD1	3.576
5A8H	C_ARG.95B	NH2	C_ASP.1	OD2	2.985
5A8H	C_HIS.189	ND1	C_ASP.151	OD2	2.585
5A8H	C_HIS.189	NE2	C_ASP.185	OD1	2.803
5A8H	C_HIS.189	NE2	C_ASP.185	OD2	3.599
5A8H	C_ARG.211	NH1	C_GLU.187	OE1	3.851
5A8H	D_ARG.31	NH2	D_ASP.100A	OD1	3.070
5A8H	D_ARG.31	NH2	D_ASP.100A	OD2	3.615
5A8H	D_ARG.38	NH1	D_GLU.46	OE1	2.779
5A8H	D_ARG.38	NH1	D_GLU.46	OE2	3.342
5A8H	D_ARG.38	NH2	D_ASP.86	OD1	2.684
5A8H	D_ARG.50	NH2	D_GLU.97	OE2	2.333
5A8H	D_ARG.66	NH1	D_ASP.86	OD2	3.597

5A8H	D_ARG_66	NH2	D_ASP_86	OD1	2.739
5A8H	D_ARG_66	NH2	D_ASP_86	OD2	2.414
5A8H	D_LYS_73	NZ	D_ASP_55	OD1	2.968
5A8H	D_ARG_82A	NH2	D_GLU_81	OE1	3.271
5A8H	D_LYS_143	NZ	D_ASP_144	OD1	2.615
5A8H	D_LYS_143	NZ	D_ASP_144	OD2	3.235
5A8H	D_HIS_164	NE2	C_ASP_167	OD1	3.880
5A8H	D_HIS_164	NE2	C_ASP_167	OD2	2.505
5A8H	D_LYS_206	NZ	D_ASP_208	OD1	3.966
5A8H	D_LYS_209	NZ	C_GLU_123	OE1	3.514
5A8H	D_LYS_209	NZ	C_GLU_123	OE2	3.584
5A8H	E_ARG_24	NH2	E_ASP_70	OD1	3.351
5A8H	E_ARG_24	NH2	E_ASP_70	OD2	2.876
5A8H	E_ARG_61	NH1	E_ASP_82	OD1	3.079
5A8H	E_ARG_61	NH1	E_ASP_82	OD2	3.077
5A8H	E_ARG_61	NH2	E_GLU_81	OE2	3.862
5A8H	E_LYS_103	NZ	E_GLU_165	OE1	3.805
5A8H	E_LYS_149	NZ	E_GLU_195	OE1	2.746
5A8H	E_LYS_149	NZ	E_GLU_195	OE2	3.963
5A8H	E_LYS_183	NZ	E_GLU_187	OE2	2.699
5A8H	E_HIS_189	ND1	E_ASP_151	OD1	3.975
5A8H	E_HIS_189	ND1	E_ASP_151	OD2	2.260
5A8H	F_ARG_38	NH1	F_ASP_86	OD1	3.024
5A8H	F_ARG_38	NH2	F_GLU_46	OE1	3.885
5A8H	F_ARG_66	NH1	F_ASP_86	OD1	3.548
5A8H	F_ARG_66	NH1	F_ASP_86	OD2	2.798
5A8H	F_ARG_66	NH2	F_ASP_86	OD1	2.933
5A8H	F_ARG_66	NH2	F_ASP_86	OD2	3.625
5A8H	F_LYS_82A	NZ	F_GLU_81	OE2	2.706
5A8H	F_LYS_100	NZ	A_GLU_91	OE1	3.015
5A8H	F_LYS_100	NZ	A_GLU_91	OE2	3.536
5A8H	F_HIS_100F	ND1	F_ASP_100G	OD2	3.939
5A8H	F_LYS_143	NZ	F_ASP_144	OD1	3.370
5A8H	F_LYS_143	NZ	F_ASP_144	OD2	3.507
5A8H	F_LYS_206	NZ	F_ASP_208	OD2	3.418
5A8H	G_LYS_121	NZ	G_GLU_429	OE1	3.567
5A8H	G_LYS_121	NZ	G_GLU_429	OE2	2.734
5A8H	G_LYS_207	NZ	G_GLU_381	OE1	3.945
5A8H	G_LYS_207	NZ	G_GLU_381	OE2	3.127
5A8H	G_LYS_232	NZ	G_GLU_351	OE1	3.995
5A8H	G_HIS_249	NE2	G_GLU_482	OE1	3.524
5A8H	G_LYS_282	NZ	G_GLU_275	OE1	3.953
5A8H	G_LYS_282	NZ	G_GLU_275	OE2	2.642
5A8H	G_LYS_348	NZ	G_GLU_269	OE1	3.206
5A8H	G_LYS_348	NZ	G_GLU_351	OE1	3.942
5A8H	G_LYS_348	NZ	G_GLU_351	OE2	3.260
5A8H	G_LYS_350	NZ	G_ASP_395	OD2	3.580
5A8H	G_LYS_357	NZ	G_GLU_466	OE2	3.719
5A8H	G_ARG_419	NH1	J_GLU_100B	OE1	2.998
5A8H	G_ARG_419	NH1	J_GLU_100B	OE2	3.675
5A8H	G_ARG_419	NH2	J_GLU_99	OE1	2.292
5A8H	G_ARG_419	NH2	J_GLU_100B	OE2	3.969
5A8H	G_ARG_456	NH2	G_GLU_466	OE1	3.536
5A8H	G_ARG_456	NH2	G_GLU_466	OE2	3.469
5A8H	G_ARG_469	NH2	G_ASP_457	OD2	3.234
5A8H	G_ARG_476	NH1	G_ASP_474	OD1	3.441
5A8H	G_ARG_476	NH2	G_GLU_102	OE1	3.297
5A8H	G_ARG_476	NH2	G_GLU_102	OE2	3.010

5A8H	G_LYS_487	NZ	G_GLU_91	OE1	3.524
5A8H	G_LYS_490	NZ	G_GLU_492	OE1	3.300
5A8H	H_LYS_29	NZ	H_GLU_85	OE1	2.833
5A8H	H_LYS_29	NZ	H_GLU_85	OE2	3.847
5A8H	H_LYS_35	NZ	G_ASP_457	OD1	3.741
5A8H	H_ARG_54	NH1	H_ASP_78	OD1	3.987
5A8H	H_ARG_54	NH1	H_ASP_78	OD2	2.755
5A8H	H_ARG_54	NH2	H_ASP_78	OD1	2.666
5A8H	H_ARG_54	NH2	H_ASP_78	OD2	2.989
5A8H	H_ARG_59	NH1	G_ASP_368	OD1	3.154
5A8H	H_ARG_59	NH1	G_ASP_368	OD2	3.343
5A8H	H_ARG_59	NH2	G_ASP_368	OD1	2.977
5A8H	H_ARG_59	NH2	G_ASP_368	OD2	2.433
5A8H	H_HIS_107	ND1	H_ASP_105	OD1	3.165
5A8H	H_HIS_107	ND1	H_ASP_105	OD2	2.890
5A8H	H_ARG_134	NH2	H_ASP_153	OD1	3.766
5A8H	H_LYS_136	NZ	H_GLU_150	OE2	3.885
5A8H	H_LYS_136	NZ	H_ASP_153	OD1	3.936
5A8H	H_LYS_136	NZ	H_ASP_153	OD2	2.987
5A8H	H_LYS_171	NZ	H_GLU_169	OE2	2.874
5A8H	I_ARG_61	NH2	I_GLU_81	OE2	3.127
5A8H	I_ARG_61	NH2	I_ASP_82	OD1	3.576
5A8H	I_ARG_95B	NH2	I_ASP_1	OD2	2.985
5A8H	I_HIS_189	ND1	I_ASP_151	OD2	2.585
5A8H	I_HIS_189	NE2	I_ASP_185	OD1	2.802
5A8H	I_HIS_189	NE2	I_ASP_185	OD2	3.598
5A8H	I_ARG_211	NH1	I_GLU_187	OE1	3.851
5A8H	J_ARG_31	NH2	J_ASP_100A	OD1	3.070
5A8H	J_ARG_31	NH2	J_ASP_100A	OD2	3.615
5A8H	J_ARG_38	NH1	J_GLU_46	OE1	2.778
5A8H	J_ARG_38	NH1	J_GLU_46	OE2	3.342
5A8H	J_ARG_38	NH2	J_ASP_86	OD1	2.685
5A8H	J_ARG_50	NH2	J_GLU_97	OE2	2.333
5A8H	J_ARG_66	NH1	J_ASP_86	OD2	3.597
5A8H	J_ARG_66	NH2	J_ASP_86	OD1	2.739
5A8H	J_ARG_66	NH2	J_ASP_86	OD2	2.414
5A8H	J_LYS_73	NZ	J_ASP_55	OD1	2.968
5A8H	J_ARG_82A	NH2	J_GLU_81	OE1	3.271
5A8H	J_LYS_143	NZ	J_ASP_144	OD1	2.615
5A8H	J_LYS_143	NZ	J_ASP_144	OD2	3.235
5A8H	J_HIS_164	NE2	I_ASP_167	OD1	3.881
5A8H	J_HIS_164	NE2	I_ASP_167	OD2	2.505
5A8H	J_LYS_206	NZ	J_ASP_208	OD1	3.966
5A8H	J_LYS_209	NZ	I_GLU_123	OE1	3.513
5A8H	J_LYS_209	NZ	I_GLU_123	OE2	3.584
5A8H	K_ARG_24	NH2	K_ASP_70	OD1	3.351
5A8H	K_ARG_24	NH2	K_ASP_70	OD2	2.876
5A8H	K_ARG_61	NH1	K_ASP_82	OD1	3.079
5A8H	K_ARG_61	NH1	K_ASP_82	OD2	3.077
5A8H	K_ARG_61	NH2	K_GLU_81	OE2	3.862
5A8H	K_LYS_103	NZ	K_GLU_165	OE1	3.804
5A8H	K_LYS_149	NZ	K_GLU_195	OE1	2.745
5A8H	K_LYS_149	NZ	K_GLU_195	OE2	3.962
5A8H	K_LYS_183	NZ	K_GLU_187	OE2	2.699
5A8H	K_HIS_189	ND1	K_ASP_151	OD1	3.974
5A8H	K_HIS_189	ND1	K_ASP_151	OD2	2.260
5A8H	L_ARG_38	NH1	L_ASP_86	OD1	3.025
5A8H	L_ARG_38	NH2	L_GLU_46	OE1	3.886

5A8H	L_ARG_66	NH1	L_ASP_86	OD1	3.549
5A8H	L_ARG_66	NH1	L_ASP_86	OD2	2.799
5A8H	L_ARG_66	NH2	L_ASP_86	OD1	2.933
5A8H	L_ARG_66	NH2	L_ASP_86	OD2	3.625
5A8H	L_LYS_82A	NZ	L_GLU_81	OE2	2.706
5A8H	L_LYS_100	NZ	G_GLU_87	OE1	2.922
5A8H	L_LYS_100	NZ	G_GLU_87	OE2	3.552
5A8H	L_HIS_100E	NE2	G_GLU_91	OE2	3.049
5A8H	L_HIS_100F	ND1	L_ASP_100G	OD2	3.939
5A8H	L_LYS_143	NZ	L_ASP_144	OD1	3.369
5A8H	L_LYS_143	NZ	L_ASP_144	OD2	3.505
5A8H	L_LYS_206	NZ	L_ASP_208	OD2	3.418
5A8H	M_LYS_121	NZ	M_GLU_429	OE1	3.568
5A8H	M_LYS_121	NZ	M_GLU_429	OE2	2.734
5A8H	M_LYS_207	NZ	M_GLU_381	OE1	3.945
5A8H	M_LYS_207	NZ	M_GLU_381	OE2	3.127
5A8H	M_LYS_232	NZ	M_GLU_351	OE1	3.995
5A8H	M_HIS_249	NE2	M_GLU_482	OE1	3.525
5A8H	M_LYS_282	NZ	M_GLU_275	OE1	3.953
5A8H	M_LYS_282	NZ	M_GLU_275	OE2	2.642
5A8H	M_LYS_348	NZ	M_GLU_269	OE1	3.206
5A8H	M_LYS_348	NZ	M_GLU_351	OE1	3.941
5A8H	M_LYS_348	NZ	M_GLU_351	OE2	3.259
5A8H	M_LYS_350	NZ	M_ASP_395	OD2	3.579
5A8H	M_LYS_357	NZ	M_GLU_466	OE2	3.719
5A8H	M_ARG_419	NH1	P_GLU_100B	OE1	2.999
5A8H	M_ARG_419	NH1	P_GLU_100B	OE2	3.675
5A8H	M_ARG_419	NH2	P_GLU_99	OE1	2.292
5A8H	M_ARG_419	NH2	P_GLU_100B	OE2	3.969
5A8H	M_ARG_456	NH2	M_GLU_466	OE1	3.537
5A8H	M_ARG_456	NH2	M_GLU_466	OE2	3.469
5A8H	M_ARG_469	NH2	M_ASP_457	OD2	3.235
5A8H	M_ARG_476	NH1	M_ASP_474	OD1	3.441
5A8H	M_ARG_476	NH2	M_GLU_102	OE1	3.296
5A8H	M_ARG_476	NH2	M_GLU_102	OE2	3.009
5A8H	M_LYS_487	NZ	M_GLU_91	OE1	3.525
5A8H	M_LYS_490	NZ	M_GLU_492	OE1	3.300
5A8H	N_LYS_29	NZ	N_GLU_85	OE1	2.833
5A8H	N_LYS_29	NZ	N_GLU_85	OE2	3.848
5A8H	N_LYS_35	NZ	M_ASP_457	OD1	3.741
5A8H	N_ARG_54	NH1	N_ASP_78	OD1	3.987
5A8H	N_ARG_54	NH1	N_ASP_78	OD2	2.755
5A8H	N_ARG_54	NH2	N_ASP_78	OD1	2.666
5A8H	N_ARG_54	NH2	N_ASP_78	OD2	2.989
5A8H	N_ARG_59	NH1	M_ASP_368	OD1	3.154
5A8H	N_ARG_59	NH1	M_ASP_368	OD2	3.343
5A8H	N_ARG_59	NH2	M_ASP_368	OD1	2.977
5A8H	N_ARG_59	NH2	M_ASP_368	OD2	2.433
5A8H	N_HIS_107	ND1	N_ASP_105	OD1	3.166
5A8H	N_HIS_107	ND1	N_ASP_105	OD2	2.891
5A8H	N_ARG_134	NH2	N_ASP_153	OD1	3.765
5A8H	N_LYS_136	NZ	N_GLU_150	OE2	3.885
5A8H	N_LYS_136	NZ	N_ASP_153	OD1	3.936
5A8H	N_LYS_136	NZ	N_ASP_153	OD2	2.986
5A8H	N_LYS_171	NZ	N_GLU_169	OE2	2.873
5A8H	O_ARG_61	NH2	O_GLU_81	OE2	3.127
5A8H	O_ARG_61	NH2	O_ASP_82	OD1	3.576
5A8H	O_ARG_95B	NH2	O_ASP_1	OD2	2.985

5A8H	O_LYS.145	NZ	C_GLU.17	OE1	3.474
5A8H	O_LYS.145	NZ	C_GLU.17	OE2	2.123
5A8H	O_HIS.189	ND1	O_ASP.151	OD2	2.585
5A8H	O_HIS.189	NE2	O_ASP.185	OD1	2.802
5A8H	O_HIS.189	NE2	O_ASP.185	OD2	3.598
5A8H	O_ARG.211	NH1	O_GLU.187	OE1	3.851
5A8H	P_ARG.31	NH2	P_ASP.100A	OD1	3.070
5A8H	P_ARG.31	NH2	P_ASP.100A	OD2	3.615
5A8H	P_ARG.38	NH1	P_GLU.46	OE1	2.780
5A8H	P_ARG.38	NH1	P_GLU.46	OE2	3.342
5A8H	P_ARG.38	NH2	P_ASP.86	OD1	2.685
5A8H	P_ARG.50	NH2	P_GLU.97	OE2	2.332
5A8H	P_ARG.66	NH1	P_ASP.86	OD2	3.598
5A8H	P_ARG.66	NH2	P_ASP.86	OD1	2.740
5A8H	P_ARG.66	NH2	P_ASP.86	OD2	2.415
5A8H	P_LYS.73	NZ	P_ASP.55	OD1	2.967
5A8H	P_ARG.82A	NH2	P_GLU.81	OE1	3.272
5A8H	P_LYS.143	NZ	P_ASP.144	OD1	2.615
5A8H	P_LYS.143	NZ	P_ASP.144	OD2	3.235
5A8H	P_HIS.164	NE2	O_ASP.167	OD1	3.881
5A8H	P_HIS.164	NE2	O_ASP.167	OD2	2.505
5A8H	P_LYS.206	NZ	P_ASP.208	OD1	3.966
5A8H	P_LYS.209	NZ	O_GLU.123	OE1	3.514
5A8H	P_LYS.209	NZ	O_GLU.123	OE2	3.584
5A8H	Q_ARG.24	NH2	Q_ASP.70	OD1	3.351
5A8H	Q_ARG.24	NH2	Q_ASP.70	OD2	2.877
5A8H	Q_ARG.61	NH1	Q_ASP.82	OD1	3.079
5A8H	Q_ARG.61	NH1	Q_ASP.82	OD2	3.077
5A8H	Q_ARG.61	NH2	Q_GLU.81	OE2	3.861
5A8H	Q_LYS.103	NZ	Q_GLU.165	OE1	3.805
5A8H	Q_LYS.149	NZ	Q_GLU.195	OE1	2.746
5A8H	Q_LYS.149	NZ	Q_GLU.195	OE2	3.963
5A8H	Q_LYS.183	NZ	Q_GLU.187	OE2	2.700
5A8H	Q_HIS.189	ND1	Q_ASP.151	OD1	3.975
5A8H	Q_HIS.189	ND1	Q_ASP.151	OD2	2.261
5A8H	R_ARG.38	NH1	R_ASP.86	OD1	3.024
5A8H	R_ARG.38	NH2	R_GLU.46	OE1	3.885
5A8H	R_ARG.66	NH1	R_ASP.86	OD1	3.548
5A8H	R_ARG.66	NH1	R_ASP.86	OD2	2.798
5A8H	R_ARG.66	NH2	R_ASP.86	OD1	2.932
5A8H	R_ARG.66	NH2	R_ASP.86	OD2	3.625
5A8H	R_LYS.82A	NZ	R_GLU.81	OE2	2.706
5A8H	R_HIS.100E	ND1	M_GLU.87	OE2	2.709
5A8H	R_HIS.100E	NE2	M_GLU.87	OE2	3.097
5A8H	R_HIS.100F	ND1	R_ASP.100G	OD2	3.938
5A8H	R_LYS.143	NZ	R_ASP.144	OD1	3.369
5A8H	R_LYS.143	NZ	R_ASP.144	OD2	3.506
5A8H	R_LYS.206	NZ	R_ASP.208	OD2	3.418

Table 652: 5A8H-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5AZE	L_HIS_36	NE2	H_GLU_105	OE2	2.756
5AZE	L_ARG_63	NH2	L_GLU_83	OE1	3.980
5AZE	L_ARG_63	NH2	L_GLU_83	OE2	3.863
5AZE	L_ARG_63	NH2	L_ASP_84	OD1	2.738
5AZE	L_ARG_63	NH2	L_ASP_84	OD2	3.659
5AZE	L_LYS_154	NZ	L_GLU_208	OE1	3.064
5AZE	L_LYS_154	NZ	L_GLU_208	OE2	3.679
5AZE	L_HIS_193	ND1	L_ASP_156	OD2	2.884
5AZE	H_LYS_12	NZ	H_GLU_10	OE1	3.838
5AZE	H_HIS_35	NE2	H_ASP_99	OD1	3.262
5AZE	H_ARG_38	NH1	H_GLU_46	OE1	2.776
5AZE	H_ARG_38	NH2	H_ASP_90	OD1	2.628
5AZE	H_ARG_67	NH1	H_ASP_90	OD1	3.423
5AZE	H_ARG_67	NH1	H_ASP_90	OD2	3.983
5AZE	H_ARG_67	NH2	H_ASP_90	OD1	3.299
5AZE	H_ARG_67	NH2	H_ASP_90	OD2	2.559
5AZE	H_ARG_98	NH2	H_ASP_109	OD1	3.795
5AZE	H_ARG_98	NH2	H_ASP_109	OD2	3.043
5AZE	H_LYS_137	NZ	L_ASP_143	OD2	2.939
5AZE	H_LYS_214	NZ	H_ASP_216	OD1	3.542
5AZE	H_LYS_214	NZ	H_ASP_216	OD2	3.113
5AZE	H_LYS_217	NZ	L_GLU_128	OE2	2.701

Table 653: 5AZE-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5BW7	A_LYS_248	NZ	A_GLU_380	OE1	3.595
5BW7	A_LYS_248	NZ	A_GLU_380	OE2	2.687
5BW7	A_ARG_255	NH2	A_ASP_249	OD2	3.416
5BW7	A_HIS_285	NE2	A_GLU_283	OE2	3.140
5BW7	A_ARG_292	NH2	A_GLU_272	OE1	3.982
5BW7	A_ARG_292	NH2	A_GLU_272	OE2	2.655
5BW7	A_LYS_317	NZ	A_ASP_312	OD1	3.705
5BW7	A_LYS_320	NZ	A_GLU_333	OE2	3.392
5BW7	A_LYS_338	NZ	A_GLU_430	OE1	3.180
5BW7	A_LYS_338	NZ	A_GLU_430	OE2	3.249
5BW7	A_LYS_370	NZ	B_GLU_357	OE2	3.993
5BW7	A_LYS_409	NZ	B_ASP_399	OD1	3.864
5BW7	A_LYS_409	NZ	B_ASP_399	OD2	2.990
5BW7	A_ARG_416	NH1	A_GLU_388	OE1	2.970
5BW7	A_ARG_416	NH1	A_GLU_388	OE2	3.913
5BW7	A_ARG_416	NH2	A_GLU_388	OE1	3.370
5BW7	A_ARG_416	NH2	A_GLU_388	OE2	2.800
5BW7	B_LYS_248	NZ	B_GLU_380	OE1	3.958
5BW7	B_LYS_248	NZ	B_GLU_380	OE2	2.755
5BW7	B_ARG_255	NH2	B_ASP_249	OD1	2.907
5BW7	B_HIS_268	NE2	B_GLU_294	OE1	3.100
5BW7	B_HIS_268	NE2	B_GLU_294	OE2	3.206
5BW7	B_ARG_301	NH1	B_GLU_293	OE1	3.024
5BW7	B_LYS_317	NZ	B_ASP_312	OD1	3.532
5BW7	B_LYS_320	NZ	B_GLU_333	OE1	2.787
5BW7	B_LYS_320	NZ	B_GLU_333	OE2	3.803
5BW7	B_LYS_338	NZ	B_GLU_430	OE1	3.215
5BW7	B_LYS_338	NZ	B_GLU_430	OE2	3.370
5BW7	B_ARG_344	NH1	B_ASP_401	OD2	3.270
5BW7	B_LYS_370	NZ	A_GLU_357	OE2	3.748
5BW7	B_LYS_409	NZ	A_ASP_399	OD1	3.328
5BW7	B_LYS_409	NZ	A_ASP_399	OD2	2.988
5BW7	B_ARG_416	NH1	B_GLU_388	OE1	3.138
5BW7	B_ARG_416	NH1	B_GLU_388	OE2	3.904
5BW7	B_ARG_416	NH2	B_GLU_388	OE1	3.540
5BW7	B_ARG_416	NH2	B_GLU_388	OE2	2.872
5BW7	C_ARG_18	NH1	C_GLU_85	OE1	3.505
5BW7	C_HIS_87	NE2	C_GLU_85	OE1	2.748
5BW7	C_ARG_97	NH2	C_ASP_104	OD2	2.992
5BW7	C_HIS_107	NE2	C_ASP_138	OD2	2.660
5BW7	C_HIS_111	NE2	C_ASP_23	OD1	2.716
5BW7	C_HIS_111	NE2	C_ASP_23	OD2	3.022
5BW7	C_LYS_120	NZ	A_ASP_265	OD2	2.730
5BW7	C_ARG_130	NH1	C_ASP_148	OD1	3.404
5BW7	C_ARG_130	NH2	C_ASP_148	OD1	3.221
5BW7	C_LYS_131	NZ	A_GLU_269	OE1	3.414
5BW7	C_LYS_131	NZ	A_GLU_269	OE2	2.642

Table 654: 5BW7-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5CMA	A_ARG_45	NH2	A_GLU_42	OE2	3.432
5CMA	A_ARG_61	NH1	A_ASP_82	OD1	3.594
5CMA	A_ARG_61	NH1	A_ASP_82	OD2	2.573
5CMA	A_LYS_149	NZ	A_GLU_195	OE1	3.918
5CMA	A_LYS_149	NZ	A_GLU_195	OE2	3.051
5CMA	A_LYS_183	NZ	A_GLU_187	OE1	2.559
5CMA	A_LYS_183	NZ	A_GLU_187	OE2	3.255
5CMA	A_HIS_189	ND1	A_ASP_151	OD2	2.867
5CMA	B_ARG_38	NH1	B_ASP_90	OD1	3.651
5CMA	B_ARG_38	NH2	B_GLU_46	OE2	3.149
5CMA	B_ARG_40	NH1	B_GLU_89	OE2	3.793
5CMA	B_LYS_67	NZ	B_ASP_90	OD1	3.746
5CMA	B_LYS_67	NZ	B_ASP_90	OD2	3.140
5CMA	B_LYS_148	NZ	B_ASP_149	OD1	2.890
5CMA	B_LYS_148	NZ	B_ASP_149	OD2	3.271
5CMA	B_LYS_214	NZ	A_GLU_123	OE1	2.706
5CMA	B_LYS_214	NZ	A_GLU_123	OE2	3.531
5CMA	B_ARG_215	NH2	B_GLU_217	OE2	3.910

Table 655: 5CMA-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5CP3	A_LYS_24	NZ	A_ASP_75	OD1	2.942
5CP3	A_ARG_51	NH2	A_ASP_60	OD2	3.029
5CP3	A_ARG_62	NH2	A_ASP_60	OD1	3.616
5CP3	A_ARG_62	NH2	A_ASP_60	OD2	2.822
5CP3	A_ARG_66	NH1	A_ASP_87	OD1	3.163
5CP3	A_ARG_66	NH1	A_ASP_87	OD2	2.516
5CP3	A_ARG_66	NH2	A_ASP_87	OD1	2.966
5CP3	A_ARG_66	NH2	A_ASP_87	OD2	3.742
5CP3	A_LYS_154	NZ	A_GLU_200	OE1	3.304
5CP3	A_LYS_154	NZ	A_GLU_200	OE2	3.326
5CP3	A_ARG_160	NH2	A_GLU_190	OE1	3.660
5CP3	A_HIS_194	ND1	A_ASP_156	OD2	3.197
5CP3	A_LYS_204	NZ	A_GLU_115	OE2	2.402
5CP3	H_ARG_39	NH1	H_ASP_90	OD1	2.626
5CP3	H_ARG_39	NH2	H_GLU_47	OE1	2.850
5CP3	H_ARG_39	NH2	H_ASP_90	OD1	3.448
5CP3	H_ARG_67	NH1	H_ASP_90	OD1	3.807
5CP3	H_ARG_67	NH1	H_ASP_90	OD2	2.888
5CP3	H_ARG_67	NH2	H_ASP_90	OD1	3.094
5CP3	H_ARG_67	NH2	H_ASP_90	OD2	3.526
5CP3	H_LYS_207	NZ	A_GLU_128	OE2	2.762

Table 656: 5CP3-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5CP7	A_LYS_24	NZ	A_ASP_75	OD1	3.319
5CP7	A_LYS_24	NZ	A_ASP_75	OD2	2.961
5CP7	A_ARG_51	NH2	A_ASP_60	OD1	2.851
5CP7	A_ARG_62	NH1	A_ASP_60	OD1	3.820
5CP7	A_ARG_62	NH1	A_ASP_60	OD2	3.151
5CP7	A_ARG_62	NH2	A_ASP_60	OD2	3.961
5CP7	A_ARG_66	NH1	A_ASP_87	OD1	3.341
5CP7	A_ARG_66	NH1	A_ASP_87	OD2	2.576
5CP7	A_ARG_66	NH2	A_ASP_87	OD1	2.858
5CP7	A_ARG_66	NH2	A_ASP_87	OD2	3.668
5CP7	A_LYS_154	NZ	A_GLU_200	OE1	3.247
5CP7	A_LYS_154	NZ	A_GLU_200	OE2	3.620
5CP7	A_ARG_160	NH2	A_GLU_190	OE1	3.902
5CP7	A_HIS_194	ND1	A_ASP_156	OD1	2.879
5CP7	A_LYS_204	NZ	A_ASP_115	OD2	3.110
5CP7	B_ARG_39	NH1	B_ASP_90	OD1	2.860
5CP7	B_ARG_39	NH2	B_GLU_47	OE1	2.798
5CP7	B_ARG_39	NH2	B_ASP_90	OD1	3.702
5CP7	B_ARG_67	NH1	B_ASP_90	OD1	3.401
5CP7	B_ARG_67	NH1	B_ASP_90	OD2	3.152
5CP7	B_ARG_67	NH2	B_ASP_90	OD1	2.884
5CP7	B_ARG_67	NH2	B_ASP_90	OD2	3.459
5CP7	B_LYS_76	NZ	B_ASP_73	OD1	3.357
5CP7	B_LYS_76	NZ	B_ASP_73	OD2	2.651
5CP7	B_LYS_204	NZ	B_ASP_206	OD1	2.613
5CP7	B_LYS_204	NZ	B_ASP_206	OD2	3.566
5CP7	B_LYS_207	NZ	C_GLU_128	OE2	3.335
5CP7	C_LYS_24	NZ	C_ASP_75	OD1	2.777
5CP7	C_ARG_51	NH2	C_ASP_60	OD1	2.666
5CP7	C_LYS_58	NZ	H_ASP_1	OD1	3.663
5CP7	C_LYS_58	NZ	H_ASP_1	OD2	3.316
5CP7	C_ARG_62	NH1	C_ASP_60	OD1	3.272
5CP7	C_ARG_62	NH1	C_ASP_60	OD2	2.754
5CP7	C_ARG_66	NH1	C_GLU_84	OE2	3.677
5CP7	C_ARG_66	NH2	C_GLU_86	OE1	3.796
5CP7	C_ARG_66	NH2	C_ASP_87	OD1	3.282
5CP7	C_ARG_66	NH2	C_ASP_87	OD2	3.388
5CP7	C_LYS_154	NZ	C_GLU_200	OE1	3.236
5CP7	C_LYS_154	NZ	C_GLU_200	OE2	3.406
5CP7	C_HIS_194	ND1	C_ASP_156	OD1	3.216
5CP7	D_ARG_39	NH1	D_ASP_90	OD1	3.144
5CP7	D_ARG_39	NH2	D_GLU_47	OE1	2.804
5CP7	D_ARG_39	NH2	D_ASP_90	OD1	3.507
5CP7	D_ARG_67	NH1	D_ASP_90	OD1	3.613
5CP7	D_ARG_67	NH1	D_ASP_90	OD2	2.972
5CP7	D_ARG_67	NH2	D_ASP_90	OD1	2.843
5CP7	D_ARG_67	NH2	D_ASP_90	OD2	3.447
5CP7	D_LYS_207	NZ	E_GLU_128	OE2	2.825
5CP7	E_LYS_24	NZ	E_ASP_75	OD1	2.820
5CP7	E_LYS_24	NZ	E_ASP_75	OD2	3.689
5CP7	E_ARG_44	NH1	E_ASP_87	OD1	3.971
5CP7	E_LYS_50	NZ	E_ASP_60	OD2	2.506
5CP7	E_ARG_51	NH2	E_ASP_60	OD1	2.623
5CP7	E_ARG_66	NH2	E_GLU_84	OE1	2.942
5CP7	E_ARG_66	NH2	E_ASP_87	OD1	3.262
5CP7	E_ARG_66	NH2	E_ASP_87	OD2	2.428
5CP7	E_ARG_193	NH2	E_GLU_190	OE1	3.878

5CP7	E_HIS_194	ND1	E_ASP_156	OD1	3.868
5CP7	E_LYS_204	NZ	E_ASP_115	OD2	2.617
5CP7	F_ARG_39	NH1	F_ASP_90	OD1	3.469
5CP7	F_ARG_39	NH2	F_GLU_47	OE1	2.925
5CP7	F_ARG_67	NH1	F_ASP_90	OD1	3.818
5CP7	F_ARG_67	NH1	F_ASP_90	OD2	2.761
5CP7	F_ARG_67	NH2	F_ASP_90	OD1	2.929
5CP7	F_ARG_67	NH2	F_ASP_90	OD2	3.414
5CP7	F_LYS_76	NZ	F_ASP_73	OD2	2.874
5CP7	F_HIS_163	ND1	G_ASP_172	OD2	3.652
5CP7	F_LYS_207	NZ	G_GLU_128	OE2	3.951
5CP7	G_ARG_44	NH1	G_GLU_86	OE2	3.392
5CP7	G_ARG_51	NH2	G_ASP_60	OD1	3.311
5CP7	G_ARG_66	NH1	G_GLU_84	OE1	3.858
5CP7	G_ARG_66	NH1	G_GLU_84	OE2	3.754
5CP7	G_ARG_66	NH2	G_GLU_84	OE2	3.523
5CP7	G_ARG_66	NH2	G_ASP_87	OD1	3.495
5CP7	G_ARG_66	NH2	G_ASP_87	OD2	3.175
5CP7	G_ARG_82	NH2	G_ASP_65	OD1	3.926
5CP7	G_LYS_152	NZ	G_GLU_159	OE1	3.709
5CP7	G_ARG_160	NH1	G_GLU_190	OE1	3.944
5CP7	G_LYS_204	NZ	G_ASP_115	OD2	3.779
5CP7	H_ARG_39	NH1	H_ASP_90	OD1	2.809
5CP7	H_ARG_39	NH2	H_GLU_47	OE1	3.145
5CP7	H_ARG_39	NH2	H_ASP_90	OD1	3.745
5CP7	H_ARG_67	NH1	H_ASP_90	OD1	3.710
5CP7	H_ARG_67	NH1	H_ASP_90	OD2	3.464
5CP7	H_ARG_67	NH2	H_ASP_90	OD1	2.784
5CP7	H_ARG_67	NH2	H_ASP_90	OD2	3.529
5CP7	H_LYS_207	NZ	A_GLU_128	OE2	3.290

Table 657: 5CP7-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5DFV	A.LYS.116	NZ	A.ASP.117	OD2	3.422
5DFV	A.LYS.124	NZ	A.ASP.195	OD1	3.196
5DFV	A.LYS.124	NZ	A.ASP.195	OD2	2.771
5DFV	A.LYS.171	NZ	C.ASP.288	OD1	3.582
5DFV	A.LYS.171	NZ	C.ASP.288	OD2	2.737
5DFV	A.LYS.171	NZ	C.ASP.290	OD2	2.874
5DFV	A.HIS.191	NE2	A.ASP.128	OD1	3.031
5DFV	A.HIS.191	NE2	A.ASP.128	OD2	2.615
5DFV	B.LYS.124	NZ	B.ASP.195	OD1	2.682
5DFV	B.LYS.124	NZ	B.ASP.195	OD2	3.204
5DFV	B.LYS.171	NZ	E.ASP.288	OD1	3.695
5DFV	B.LYS.171	NZ	E.ASP.288	OD2	3.653
5DFV	B.LYS.171	NZ	E.ASP.290	OD2	2.646
5DFV	B.HIS.191	NE2	B.ASP.128	OD1	2.625
5DFV	B.HIS.191	NE2	B.ASP.128	OD2	3.194
5DFV	C.LYS.203	NZ	C.ASP.324	OD1	3.802
5DFV	C.ARG.251	NH2	C.GLU.351	OE1	2.978
5DFV	C.ARG.251	NH2	C.GLU.351	OE2	3.038
5DFV	C.LYS.301	NZ	C.ASP.324	OD1	3.240
5DFV	C.LYS.301	NZ	C.ASP.324	OD2	2.740
5DFV	C.ARG.398	NH1	C.ASP.394	OD1	2.945
5DFV	C.ARG.398	NH1	C.ASP.394	OD2	3.790
5DFV	C.ARG.398	NH2	D.GLU.698	OE1	3.277
5DFV	C.LYS.1095	NZ	C.GLU.1097	OE1	3.280
5DFV	C.ARG.1099	NH1	C.GLU.1097	OE1	3.200
5DFV	C.ARG.1099	NH2	C.GLU.1097	OE1	3.340
5DFV	C.ARG.1099	NH2	C.GLU.1097	OE2	3.202
5DFV	D.ARG.551	NH1	D.ASP.716	OD1	3.170
5DFV	D.ARG.551	NH1	D.ASP.716	OD2	3.766
5DFV	D.ARG.551	NH2	D.ASP.716	OD1	3.082
5DFV	D.ARG.551	NH2	D.ASP.716	OD2	3.372
5DFV	D.LYS.556	NZ	D.GLU.755	OE1	3.326
5DFV	D.ARG.705	NH1	D.GLU.725	OE2	3.117
5DFV	D.ARG.705	NH1	D.GLU.727	OE2	3.146
5DFV	D.ARG.705	NH1	D.ASP.728	OD2	3.659
5DFV	D.ARG.705	NH2	D.GLU.725	OE1	3.510
5DFV	D.ARG.705	NH2	D.GLU.725	OE2	3.133
5DFV	D.LYS.2039	NZ	D.GLU.2087	OE1	3.958
5DFV	D.LYS.2041	NZ	D.GLU.2087	OE1	3.712
5DFV	D.LYS.2041	NZ	D.GLU.2087	OE2	2.836
5DFV	D.LYS.2091	NZ	D.ASP.2002	OD1	3.903
5DFV	D.ARG.2103	NH1	D.GLU.2079	OE1	3.925
5DFV	E.ARG.251	NH2	E.GLU.351	OE1	2.986
5DFV	E.ARG.251	NH2	E.GLU.351	OE2	2.952
5DFV	E.LYS.301	NZ	E.ASP.324	OD2	2.835
5DFV	E.ARG.398	NH1	F.GLU.698	OE2	3.319
5DFV	E.ARG.398	NH2	E.ASP.394	OD1	3.919
5DFV	E.ARG.398	NH2	E.ASP.394	OD2	2.696
5DFV	E.LYS.1094	NZ	F.GLU.2015	OE1	3.713
5DFV	E.LYS.1095	NZ	E.GLU.1097	OE1	2.895
5DFV	E.ARG.1099	NH1	F.GLU.2105	OE2	3.679
5DFV	F.ARG.551	NH1	F.ASP.716	OD2	3.150
5DFV	F.LYS.556	NZ	F.GLU.755	OE1	2.676
5DFV	F.LYS.556	NZ	F.GLU.755	OE2	3.758
5DFV	F.LYS.615	NZ	F.GLU.698	OE2	3.399
5DFV	F.ARG.705	NH1	F.GLU.727	OE2	3.693
5DFV	F.ARG.705	NH1	F.ASP.728	OD1	3.492

5DFV	F_ARG_705	NH1	F_ASP_728	OD2	3.045
5DFV	F_LYS_2041	NZ	F_GLU_2087	OE1	3.680
5DFV	F_LYS_2041	NZ	F_GLU_2087	OE2	2.777
5DFV	F_LYS_2091	NZ	F_ASP_2002	OD1	2.898
5DFV	F_LYS_2091	NZ	F_ASP_2002	OD2	2.887

Table 658: 5DFV-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5DFW	A_LYS_124	NZ	A_ASP_195	OD1	3.150
5DFW	A_LYS_124	NZ	A_ASP_195	OD2	3.337
5DFW	A_LYS_171	NZ	H_ASP_156	OD2	2.691
5DFW	A_LYS_171	NZ	H_ASP_253	OD1	2.751
5DFW	A_LYS_171	NZ	H_ASP_253	OD2	3.799
5DFW	A_LYS_187	NZ	A_ASP_155	OD2	3.976
5DFW	A_HIS_191	NE2	A_ASP_128	OD1	3.407
5DFW	A_HIS_191	NE2	A_ASP_128	OD2	2.578
5DFW	A_LYS_193	NZ	A_ASP_155	OD1	3.885
5DFW	H_LYS_203	NZ	H_ASP_324	OD1	3.276
5DFW	H_ARG_251	NH2	A_ASP_138	OD1	3.392
5DFW	H_ARG_251	NH2	A_ASP_138	OD2	2.698
5DFW	H_LYS_292	NZ	A_ASP_138	OD1	3.884
5DFW	H_LYS_292	NZ	A_ASP_138	OD2	2.950
5DFW	H_LYS_292	NZ	A_ASP_139	OD1	3.019
5DFW	H_LYS_296	NZ	H_ASP_294	OD1	3.151
5DFW	H_LYS_301	NZ	H_ASP_324	OD1	3.890
5DFW	H_LYS_301	NZ	H_ASP_324	OD2	3.833
5DFW	H_ARG_705	NH1	H_GLU_727	OE2	3.307
5DFW	H_ARG_705	NH2	H_ASP_728	OD2	2.557
5DFW	H_LYS_806	NZ	H_GLU_808	OE2	3.023

Table 659: 5DFW-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5DMI	A_LYS_46	NZ	L_ASP_31	OD1	2.761
5DMI	A_LYS_46	NZ	L_ASP_31	OD2	3.234
5DMI	A_HIS_76	ND1	H_ASP_100A	OD2	3.977
5DMI	A_HIS_78	ND1	A_GLU_74	OE1	3.991
5DMI	A_HIS_78	NE2	A_GLU_74	OE2	3.806
5DMI	H_ARG_66	NH1	H_ASP_86	OD1	3.834
5DMI	H_ARG_66	NH1	H_ASP_86	OD2	2.698
5DMI	H_ARG_66	NH2	H_ASP_86	OD1	3.014
5DMI	H_ARG_66	NH2	H_ASP_86	OD2	2.861
5DMI	H_LYS_221	NZ	L_GLU_123	OE2	3.105
5DMI	L_ARG_45	NH1	L_GLU_42	OE1	2.998
5DMI	L_ARG_45	NH1	L_GLU_42	OE2	3.354
5DMI	L_ARG_45	NH2	L_GLU_42	OE1	2.809
5DMI	L_ARG_61	NH1	L_GLU_81	OE1	3.011
5DMI	L_ARG_61	NH1	L_ASP_82	OD1	2.794
5DMI	L_ARG_61	NH1	L_ASP_82	OD2	3.657
5DMI	L_ARG_61	NH2	L_GLU_79	OE1	3.312
5DMI	L_ARG_61	NH2	L_GLU_79	OE2	3.348
5DMI	L_LYS_103	NZ	L_GLU_105	OE1	3.441
5DMI	L_LYS_103	NZ	L_GLU_165	OE2	3.954
5DMI	L_LYS_149	NZ	L_GLU_195	OE2	2.814
5DMI	L_LYS_183	NZ	L_GLU_187	OE1	2.795
5DMI	L_LYS_188	NZ	L_ASP_185	OD1	2.852
5DMI	L_ARG_211	NH1	L_GLU_187	OE2	3.522

Table 660: 5DMI-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5DMJ	A_HIS_78	NE2	A_GLU_74	OE2	3.682
5DMJ	A_HIS_162	NE2	A_GLU_159	OE1	3.307
5DMJ	B_ARG_38	NH1	B_GLU_46	OE1	3.733
5DMJ	B_ARG_38	NH1	B_GLU_46	OE2	3.183
5DMJ	B_ARG_38	NH1	B_ASP_86	OD1	3.833
5DMJ	B_ARG_38	NH2	B_ASP_86	OD1	2.916
5DMJ	B_ARG_66	NH1	B_ASP_86	OD1	3.274
5DMJ	B_ARG_66	NH1	B_ASP_86	OD2	2.599
5DMJ	B_ARG_66	NH2	B_ASP_86	OD1	3.293
5DMJ	B_ARG_83	NH2	G_ASP_72	OD1	3.449
5DMJ	B_LYS_94	NZ	B_ASP_102	OD1	3.363
5DMJ	D_HIS_78	NE2	D_GLU_74	OE2	3.689
5DMJ	D_ARG_123	NH1	D_ASP_140	OD2	3.071
5DMJ	D_HIS_162	NE2	D_GLU_159	OE1	3.282
5DMJ	D_LYS_181	NZ	D_ASP_180	OD2	3.498
5DMJ	E_ARG_38	NH1	E_GLU_46	OE1	3.747
5DMJ	E_ARG_38	NH1	E_GLU_46	OE2	3.182
5DMJ	E_ARG_38	NH1	E_ASP_86	OD1	3.846
5DMJ	E_ARG_38	NH2	E_ASP_86	OD1	2.939
5DMJ	E_ARG_66	NH1	E_ASP_86	OD1	3.321
5DMJ	E_ARG_66	NH1	E_ASP_86	OD2	2.623
5DMJ	E_ARG_66	NH2	E_ASP_86	OD1	3.325
5DMJ	E_LYS_75	NZ	E_ASP_72	OD2	3.917
5DMJ	E_LYS_94	NZ	E_ASP_102	OD1	3.533
5DMJ	F_HIS_78	NE2	F_GLU_74	OE2	3.703
5DMJ	F_HIS_162	NE2	F_GLU_159	OE1	3.306
5DMJ	G_ARG_38	NH1	G_GLU_46	OE1	3.769
5DMJ	G_ARG_38	NH1	G_GLU_46	OE2	3.178
5DMJ	G_ARG_38	NH1	G_ASP_86	OD1	3.862
5DMJ	G_ARG_38	NH2	G_ASP_86	OD1	2.937
5DMJ	G_ARG_66	NH1	G_ASP_86	OD1	3.324
5DMJ	G_ARG_66	NH1	G_ASP_86	OD2	2.634
5DMJ	G_ARG_66	NH2	G_ASP_86	OD1	3.327
5DMJ	G_LYS_75	NZ	B_GLU_85	OE1	3.187
5DMJ	G_LYS_94	NZ	G_ASP_102	OD1	3.775

Table 661: 5DMJ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5DWU	B_ARG_377	NH2	B_ASP_379	OD1	3.390
5DWU	B_ARG_407	NH1	B_ASP_435	OD1	2.835
5DWU	B_ARG_407	NH2	B_ASP_435	OD1	3.962
5DWU	H_ARG_38	NH1	H_ASP_90	OD1	2.590
5DWU	H_ARG_38	NH2	H_GLU_46	OE1	2.502
5DWU	H_ARG_52	NH1	A_ASP_107	OD1	3.435
5DWU	H_ARG_52	NH1	A_ASP_107	OD2	2.568
5DWU	H_ARG_52	NH2	A_ASP_107	OD1	2.685
5DWU	H_ARG_52	NH2	A_ASP_107	OD2	3.250
5DWU	H_ARG_98	NH2	H_ASP_105	OD2	3.961
5DWU	L_ARG_61	NH1	L_ASP_82	OD1	3.900
5DWU	L_ARG_61	NH2	L_ASP_82	OD1	2.608
5DWU	L_ARG_61	NH2	L_ASP_82	OD2	2.917
5DWU	L_HIS_189	ND1	L_ASP_151	OD2	3.598

Table 662: 5DWU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5ERW	A_LYS_12	NZ	A_GLU_10	OE1	2.949
5ERW	A_ARG_38	NH1	A_ASP_90	OD1	2.885
5ERW	A_ARG_38	NH2	A_GLU_46	OE1	3.486
5ERW	A_ARG_38	NH2	A_GLU_46	OE2	3.818
5ERW	A_ARG_38	NH2	A_ASP_90	OD1	3.778
5ERW	A_ARG_67	NH1	A_ASP_90	OD2	2.657
5ERW	A_ARG_67	NH2	A_ASP_90	OD1	3.007
5ERW	A_ARG_67	NH2	A_ASP_90	OD2	3.030
5ERW	A_ARG_87	NH1	A_GLU_89	OE2	3.913
5ERW	A_ARG_103	NH1	B_ASP_49	OD2	2.990
5ERW	A_LYS_214	NZ	B_GLU_122	OE1	2.490
5ERW	B_LYS_30	NZ	B_ASP_91	OD1	2.653
5ERW	B_HIS_33	ND1	B_ASP_49	OD1	3.753
5ERW	B_ARG_60	NH2	B_ASP_81	OD1	2.998
5ERW	B_ARG_60	NH2	B_ASP_81	OD2	2.524
5ERW	B_LYS_102	NZ	B_ASP_84	OD1	3.442
5ERW	B_LYS_102	NZ	B_ASP_84	OD2	3.632
5ERW	B_LYS_102	NZ	B_ASP_164	OD1	3.634
5ERW	B_LYS_146	NZ	B_GLU_153	OE1	2.547
5ERW	B_LYS_146	NZ	B_GLU_153	OE2	3.654
5ERW	B_LYS_148	NZ	B_GLU_194	OE1	3.651
5ERW	B_LYS_148	NZ	B_GLU_194	OE2	2.963
5ERW	B_ARG_154	NH1	B_GLU_184	OE1	3.549
5ERW	B_LYS_168	NZ	B_ASP_166	OD2	3.760
5ERW	B_LYS_182	NZ	B_GLU_186	OE1	3.952
5ERW	B_LYS_182	NZ	B_GLU_186	OE2	2.341
5ERW	B_HIS_188	ND1	B_ASP_150	OD2	2.455
5ERW	B_LYS_198	NZ	B_ASP_109	OD1	3.278
5ERW	B_LYS_198	NZ	B_ASP_109	OD2	2.412
5ERW	C_LYS_446	NZ	B_ASP_50	OD1	3.926
5ERW	C_LYS_446	NZ	B_ASP_50	OD2	2.398

Table 663: 5ERW-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5EZI	H_ARG_45	NH2	H_ASP_42	OD2	3.860
5EZI	H_ARG_52	NH1	H_GLU_60	OE1	3.045
5EZI	H_ARG_52	NH1	H_ASP_104	OD1	3.782
5EZI	H_ARG_52	NH2	H_ASP_104	OD1	2.793
5EZI	H_LYS_79	NZ	H_ASP_80	OD1	3.553
5EZI	H_LYS_79	NZ	H_ASP_80	OD2	3.228
5EZI	H_LYS_81	NZ	H_ASP_104	OD1	3.557
5EZI	H_LYS_81	NZ	H_ASP_104	OD2	2.766
5EZI	H_ARG_112	NH2	H_ASP_121	OD1	3.513
5EZI	H_ARG_112	NH2	H_ASP_121	OD2	2.756
5EZI	L_ARG_54	NH1	L_ASP_56	OD2	3.800
5EZI	L_ARG_54	NH2	L_ASP_56	OD1	3.697
5EZI	L_ARG_54	NH2	L_ASP_56	OD2	2.546
5EZI	L_ARG_78	NH2	L_ASP_84	OD1	3.854
5EZI	L_ARG_85	NH2	L_GLU_105	OE2	3.655
5EZI	L_ARG_85	NH2	L_ASP_106	OD1	2.746
5EZI	L_ARG_85	NH2	L_ASP_106	OD2	3.689
5EZI	L_ARG_120	NH1	H_GLU_64	OE1	3.561
5EZI	L_ARG_120	NH1	H_GLU_64	OE2	2.826
5EZI	L_LYS_166	NZ	L_GLU_129	OE2	3.752
5EZI	L_LYS_173	NZ	L_GLU_219	OE1	3.356
5EZI	L_LYS_173	NZ	L_GLU_219	OE2	2.974
5EZI	L_ARG_179	NH1	L_GLU_209	OE1	3.490
5EZI	L_ARG_179	NH1	L_GLU_209	OE2	3.054
5EZI	L_ARG_179	NH2	L_GLU_209	OE1	3.322
5EZI	L_HIS_213	ND1	L_ASP_175	OD2	3.083
5EZI	L_LYS_223	NZ	L_ASP_134	OD2	3.368

Table 664: 5EZI-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5EZJ	A_ARG_52	NH1	A_GLU_60	OE1	2.978
5EZJ	A_ARG_52	NH1	A_ASP_104	OD1	3.803
5EZJ	A_ARG_52	NH2	A_ASP_104	OD1	2.735
5EZJ	A_LYS_79	NZ	A_ASP_80	OD1	3.518
5EZJ	A_LYS_79	NZ	A_ASP_80	OD2	2.915
5EZJ	A_LYS_81	NZ	A_ASP_104	OD1	3.567
5EZJ	A_LYS_81	NZ	A_ASP_104	OD2	2.848
5EZJ	A_ARG_112	NH2	A_ASP_121	OD1	2.747
5EZJ	A_ARG_112	NH2	A_ASP_121	OD2	3.431
5EZJ	A_LYS_228	NZ	B_GLU_147	OE1	3.274
5EZJ	A_LYS_229	NZ	A_GLU_231	OE2	3.771
5EZJ	B_LYS_48	NZ	B_ASP_94	OD1	3.784
5EZJ	B_LYS_48	NZ	B_ASP_94	OD2	2.891
5EZJ	B_ARG_54	NH2	B_ASP_56	OD1	3.856
5EZJ	B_ARG_54	NH2	B_ASP_56	OD2	2.671
5EZJ	B_ARG_78	NH2	B_ASP_84	OD1	3.656
5EZJ	B_ARG_85	NH1	B_ASP_106	OD1	2.928
5EZJ	B_ARG_85	NH1	B_ASP_106	OD2	3.850
5EZJ	B_ARG_120	NH1	A_GLU_64	OE1	3.637
5EZJ	B_ARG_120	NH1	A_GLU_64	OE2	2.843
5EZJ	B_LYS_127	NZ	B_GLU_129	OE1	3.869
5EZJ	B_LYS_173	NZ	B_GLU_219	OE1	3.389
5EZJ	B_LYS_173	NZ	B_GLU_219	OE2	2.427
5EZJ	B_ARG_179	NH1	B_GLU_209	OE1	3.217
5EZJ	B_ARG_179	NH1	B_GLU_209	OE2	3.402
5EZJ	B_ARG_179	NH2	B_GLU_209	OE1	3.880
5EZJ	B_ARG_179	NH2	B_GLU_209	OE2	2.776
5EZJ	B_HIS_213	ND1	B_ASP_175	OD2	3.143

Table 665: 5EZJ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5EZL	A_ARG_45	NH2	A_ASP_42	OD2	3.885
5EZL	A_ARG_52	NH1	A_GLU_60	OE1	3.345
5EZL	A_ARG_52	NH1	A_ASP_104	OD1	3.820
5EZL	A_ARG_52	NH2	A_ASP_104	OD1	2.908
5EZL	A_LYS_81	NZ	A_ASP_104	OD1	3.524
5EZL	A_LYS_81	NZ	A_ASP_104	OD2	2.698
5EZL	A_ARG_112	NH1	A_ASP_121	OD2	2.196
5EZL	A_LYS_228	NZ	B_GLU_147	OE1	3.314
5EZL	A_LYS_229	NZ	A_GLU_231	OE2	2.784
5EZL	B_ARG_54	NH2	B_ASP_56	OD1	3.684
5EZL	B_ARG_54	NH2	B_ASP_56	OD2	2.960
5EZL	B_ARG_78	NH2	B_ASP_84	OD1	3.876
5EZL	B_ARG_85	NH1	B_ASP_106	OD1	2.623
5EZL	B_ARG_85	NH1	B_ASP_106	OD2	2.985
5EZL	B_ARG_120	NH1	A_GLU_64	OE1	3.901
5EZL	B_ARG_120	NH1	A_GLU_64	OE2	2.804
5EZL	B_LYS_127	NZ	B_GLU_129	OE2	3.626
5EZL	B_LYS_173	NZ	B_GLU_219	OE1	3.456
5EZL	B_LYS_173	NZ	B_GLU_219	OE2	2.709
5EZL	B_LYS_223	NZ	B_ASP_134	OD2	3.131
5EZL	H_ARG_52	NH1	H_GLU_60	OE1	3.219
5EZL	H_ARG_52	NH1	H_GLU_60	OE2	3.769
5EZL	H_ARG_52	NH1	H_ASP_104	OD1	3.785
5EZL	H_ARG_52	NH2	H_ASP_104	OD1	3.045
5EZL	H_LYS_81	NZ	H_ASP_104	OD1	3.442
5EZL	H_LYS_81	NZ	H_ASP_104	OD2	2.623
5EZL	H_ARG_112	NH1	H_ASP_121	OD1	3.400
5EZL	H_ARG_112	NH1	H_ASP_121	OD2	2.409
5EZL	H_LYS_228	NZ	L_GLU_147	OE2	3.445
5EZL	H_LYS_229	NZ	H_GLU_231	OE2	2.742
5EZL	L_ARG_54	NH2	L_ASP_56	OD1	3.764
5EZL	L_ARG_54	NH2	L_ASP_56	OD2	2.783
5EZL	L_LYS_63	NZ	L_GLU_105	OE1	3.769
5EZL	L_ARG_78	NH1	L_ASP_84	OD1	3.894
5EZL	L_ARG_78	NH2	L_ASP_84	OD1	3.679
5EZL	L_ARG_85	NH2	L_GLU_105	OE1	3.813
5EZL	L_ARG_85	NH2	L_GLU_105	OE2	3.287
5EZL	L_ARG_85	NH2	L_ASP_106	OD1	3.191
5EZL	L_ARG_85	NH2	L_ASP_106	OD2	3.915
5EZL	L_ARG_120	NH1	H_GLU_64	OE1	3.668
5EZL	L_ARG_120	NH1	H_GLU_64	OE2	2.626
5EZL	L_LYS_127	NZ	L_ASP_189	OD1	3.123
5EZL	L_LYS_173	NZ	L_GLU_219	OE2	2.984
5EZL	L_LYS_223	NZ	L_ASP_134	OD2	3.564

Table 666: 5EZL-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5EZN	A_ARG_58	NH1	E_ASP_336	OD2	3.940
5EZN	A_ARG_58	NH2	E_ASP_336	OD2	2.479
5EZN	A_HIS_76	ND1	A_ASP_92	OD2	3.010
5EZN	A_HIS_76	NE2	A_GLU_74	OE2	3.795
5EZN	A_LYS_81	NZ	A_GLU_59	OE1	3.642
5EZN	A_LYS_95	NZ	A_ASP_92	OD2	2.550
5EZN	A_ARG_102	NH2	A_ASP_67	OD2	3.108
5EZN	A_HIS_104	NE2	A_ASP_121	OD1	3.856
5EZN	A_HIS_134	NE2	A_ASP_98	OD2	3.544
5EZN	A_LYS_188	NZ	A_GLU_123	OE1	3.017
5EZN	E_LYS_204	NZ	A_GLU_113	OE1	2.243
5EZN	E_LYS_204	NZ	A_GLU_113	OE2	3.142
5EZN	E_LYS_215	NZ	E_GLU_265	OE2	3.398
5EZN	E_LYS_220	NZ	E_ASP_245	OD2	3.852
5EZN	E_ARG_229	NH2	E_ASP_282	OD1	2.680
5EZN	E_ARG_229	NH2	E_ASP_282	OD2	3.870
5EZN	E_HIS_240	NE2	E_ASP_282	OD1	3.980
5EZN	E_LYS_251	NZ	B_GLU_72	OE2	3.130
5EZN	E_ARG_271	NH1	E_GLU_257	OE2	3.148
5EZN	E_LYS_334	NZ	E_GLU_337	OE1	3.441
5EZN	E_LYS_334	NZ	E_GLU_337	OE2	3.486
5EZN	B_ARG_36	NH1	B_GLU_38	OE2	3.346
5EZN	B_LYS_69	NZ	B_GLU_72	OE1	2.194
5EZN	B_LYS_69	NZ	B_GLU_74	OE1	3.478
5EZN	B_HIS_76	ND1	B_ASP_92	OD2	3.694
5EZN	B_LYS_81	NZ	B_GLU_59	OE2	2.979
5EZN	B_ARG_102	NH2	B_ASP_67	OD2	3.883
5EZN	B_HIS_134	ND1	B_GLU_148	OE1	3.830
5EZN	B_HIS_134	NE2	B_GLU_148	OE1	3.515
5EZN	B_ARG_135	NH1	G_GLU_206	OE2	3.927
5EZN	B_ARG_135	NH2	G_GLU_206	OE2	3.596
5EZN	G_LYS_204	NZ	B_GLU_112	OE1	2.749
5EZN	G_LYS_204	NZ	B_GLU_112	OE2	3.972
5EZN	G_LYS_204	NZ	B_GLU_113	OE2	3.260
5EZN	G_LYS_215	NZ	G_ASP_194	OD1	3.377
5EZN	G_LYS_215	NZ	G_ASP_194	OD2	2.294
5EZN	G_ARG_229	NH1	G_ASP_282	OD1	3.051
5EZN	G_ARG_229	NH2	G_ASP_282	OD1	3.739
5EZN	G_HIS_240	NE2	G_ASP_282	OD1	3.769
5EZN	G_LYS_262	NZ	G_GLU_265	OE1	3.917
5EZN	G_LYS_316	NZ	G_GLU_302	OE2	2.834
5EZN	G_LYS_334	NZ	G_GLU_337	OE1	3.582
5EZN	G_LYS_334	NZ	G_GLU_337	OE2	2.552
5EZN	G_ARG_339	NH2	G_ASP_336	OD2	3.484

Table 667: 5EZN-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5EZO	H_ARG_56	NH1	H_GLU_64	OE1	3.259
5EZO	H_ARG_56	NH1	H_ASP_108	OD1	3.756
5EZO	H_ARG_56	NH2	H_ASP_108	OD1	2.964
5EZO	H_LYS_85	NZ	H_ASP_108	OD1	3.343
5EZO	H_LYS_85	NZ	H_ASP_108	OD2	3.101
5EZO	H_ARG_116	NH1	H_ASP_125	OD1	3.598
5EZO	H_ARG_116	NH1	H_ASP_125	OD2	2.331
5EZO	H_LYS_232	NZ	L_GLU_143	OE1	3.314
5EZO	H_LYS_232	NZ	L_GLU_143	OE2	2.456
5EZO	H_LYS_233	NZ	H_GLU_235	OE2	3.779
5EZO	L_ARG_50	NH1	A_ASP_66	OD1	3.943
5EZO	L_ARG_50	NH1	A_ASP_66	OD2	3.721
5EZO	L_LYS_59	NZ	L_GLU_101	OE1	3.526
5EZO	L_ARG_74	NH1	L_ASP_80	OD1	3.915
5EZO	L_ARG_81	NH1	L_GLU_101	OE2	3.291
5EZO	L_ARG_81	NH1	L_ASP_102	OD1	3.399
5EZO	L_ARG_81	NH1	L_ASP_102	OD2	3.360
5EZO	L_ARG_81	NH2	L_GLU_101	OE2	3.105
5EZO	L_ARG_116	NH1	H_GLU_68	OE1	3.718
5EZO	L_ARG_116	NH1	H_GLU_68	OE2	2.774
5EZO	L_LYS_123	NZ	L_ASP_185	OD1	3.241
5EZO	L_LYS_123	NZ	L_ASP_185	OD2	3.353
5EZO	L_LYS_219	NZ	L_ASP_130	OD2	3.420
5EZO	A_ARG_36	NH1	A_GLU_38	OE2	2.554
5EZO	A_LYS_43	NZ	A_ASP_85	OD2	3.209
5EZO	A_HIS_76	ND1	A_ASP_92	OD2	2.596
5EZO	A_LYS_81	NZ	A_GLU_59	OE2	2.928
5EZO	A_ARG_102	NH2	A_ASP_67	OD2	2.790
5EZO	A_LYS_129	NZ	A_GLU_122	OE2	3.798
5EZO	A_HIS_134	ND1	A_GLU_148	OE1	3.764
5EZO	A_ARG_135	NH1	A_GLU_206	OE2	3.876
5EZO	A_ARG_135	NH2	A_GLU_206	OE2	3.659
5EZO	A_LYS_186	NZ	A_ASP_195	OD1	2.722
5EZO	A_LYS_192	NZ	A_ASP_217	OD2	3.683
5EZO	A_LYS_204	NZ	A_GLU_112	OE1	3.269
5EZO	A_LYS_204	NZ	A_GLU_113	OE2	3.314
5EZO	A_ARG_229	NH2	A_ASP_282	OD1	2.774
5EZO	A_ARG_229	NH2	A_ASP_282	OD2	3.510
5EZO	A_HIS_240	NE2	A_ASP_282	OD1	3.983
5EZO	A_ARG_271	NH1	A_GLU_257	OE1	3.813
5EZO	A_LYS_316	NZ	A_GLU_302	OE2	3.408
5EZO	A_LYS_334	NZ	A_GLU_337	OE1	3.354
5EZO	A_LYS_334	NZ	A_GLU_337	OE2	2.671
5EZO	A_ARG_339	NH2	A_ASP_336	OD2	3.220

Table 668: 5EZO-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5GGV	L_ARG_24	NH1	L_ASP_70	OD1	2.800
5GGV	L_ARG_24	NH1	L_ASP_70	OD2	3.234
5GGV	L_ARG_24	NH2	L_ASP_70	OD1	3.597
5GGV	L_ARG_61	NH2	L_GLU_81	OE2	3.323
5GGV	L_ARG_61	NH2	L_ASP_82	OD1	2.670
5GGV	L_ARG_61	NH2	L_ASP_82	OD2	3.226
5GGV	L_LYS_149	NZ	L_GLU_195	OE1	3.933
5GGV	L_LYS_183	NZ	L_GLU_187	OE2	3.997
5GGV	L_HIS_189	ND1	L_ASP_151	OD2	2.820
5GGV	L_LYS_190	NZ	L_GLU_213	OE2	2.696
5GGV	H_HIS_35	NE2	H_ASP_99	OD2	2.983
5GGV	H_ARG_38	NH1	H_ASP_90	OD1	2.864
5GGV	H_ARG_38	NH2	H_GLU_46	OE1	3.166
5GGV	H_ARG_38	NH2	H_ASP_90	OD1	3.783
5GGV	H_ARG_67	NH1	H_ASP_90	OD1	3.548
5GGV	H_ARG_67	NH1	H_ASP_90	OD2	3.804
5GGV	H_ARG_67	NH2	H_ASP_90	OD1	3.503
5GGV	H_ARG_67	NH2	H_ASP_90	OD2	2.364
5GGV	H_LYS_76	NZ	H_ASP_73	OD2	3.976
5GGV	H_ARG_98	NH2	H_ASP_113	OD1	3.862
5GGV	H_ARG_98	NH2	H_ASP_113	OD2	2.927
5GGV	H_ARG_101	NH1	Y_GLU_97	OE2	3.572
5GGV	H_LYS_155	NZ	H_ASP_156	OD1	3.101
5GGV	H_LYS_155	NZ	H_ASP_156	OD2	3.435
5GGV	H_LYS_221	NZ	L_GLU_123	OE1	2.304
5GGV	H_LYS_221	NZ	L_GLU_123	OE2	3.975

Table 669: 5GGV-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5GKR	A_ARG_38	NH1	A_ASP_86	OD1	2.742
5GKR	A_ARG_38	NH2	A_GLU_46	OE1	2.810
5GKR	A_ARG_38	NH2	A_ASP_86	OD1	3.641
5GKR	A_ARG_66	NH1	A_ASP_86	OD1	3.332
5GKR	A_ARG_66	NH1	A_ASP_86	OD2	3.801
5GKR	A_ARG_66	NH2	A_ASP_86	OD1	3.354
5GKR	A_ARG_66	NH2	A_ASP_86	OD2	2.729
5GKR	A_ARG_94	NH1	A_ASP_101	OD1	3.700
5GKR	A_ARG_94	NH1	A_ASP_101	OD2	2.566
5GKR	A_LYS_143	NZ	B_GLU_125	OE2	2.806
5GKR	A_LYS_201	NZ	A_ASP_199	OD2	2.935
5GKR	A_LYS_206	NZ	A_ASP_199	OD1	3.198
5GKR	A_LYS_209	NZ	B_GLU_124	OE1	2.825
5GKR	A_LYS_209	NZ	B_GLU_124	OE2	3.325
5GKR	B_LYS_53	NZ	B_ASP_50	OD2	3.716
5GKR	B_ARG_61	NH2	B_GLU_81	OE2	3.803
5GKR	B_ARG_61	NH2	B_ASP_82	OD1	2.896
5GKR	B_ARG_61	NH2	B_ASP_82	OD2	3.817
5GKR	B_LYS_130	NZ	A_ASP_144	OD2	3.639
5GKR	B_LYS_164	NZ	B_ASP_85	OD2	2.873
5GKR	B_HIS_189	ND1	B_ASP_152	OD2	3.078
5GKR	C_ARG_38	NH1	C_ASP_86	OD1	2.720
5GKR	C_ARG_38	NH2	C_GLU_46	OE2	2.991
5GKR	C_ARG_38	NH2	C_ASP_86	OD1	3.638
5GKR	C_ARG_66	NH1	C_ASP_86	OD1	3.317
5GKR	C_ARG_66	NH1	C_ASP_86	OD2	3.769
5GKR	C_ARG_66	NH2	C_ASP_86	OD1	3.362
5GKR	C_ARG_66	NH2	C_ASP_86	OD2	2.717
5GKR	C_ARG_94	NH2	C_ASP_101	OD1	3.797
5GKR	C_ARG_94	NH2	C_ASP_101	OD2	2.747
5GKR	C_LYS_143	NZ	D_GLU_125	OE2	2.591
5GKR	C_LYS_206	NZ	C_ASP_199	OD1	3.203
5GKR	C_LYS_209	NZ	D_GLU_124	OE1	2.486
5GKR	C_LYS_209	NZ	D_GLU_124	OE2	2.893
5GKR	D_LYS_53	NZ	D_ASP_50	OD2	3.715
5GKR	D_ARG_61	NH1	D_ASP_82	OD1	3.020
5GKR	D_ARG_61	NH1	D_ASP_82	OD2	3.903
5GKR	D_LYS_130	NZ	C_ASP_144	OD2	3.574
5GKR	D_LYS_164	NZ	D_ASP_85	OD2	2.940
5GKR	D_ARG_190	NH2	D_ASP_152	OD1	3.635

Table 670: 5GKR-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5GKS	A_ARG_38	NH1	A_ASP_86	OD1	2.822
5GKS	A_ARG_38	NH2	A_GLU_46	OE1	2.937
5GKS	A_ARG_38	NH2	A_ASP_86	OD1	3.692
5GKS	A_ARG_66	NH1	A_ASP_86	OD1	3.105
5GKS	A_ARG_66	NH1	A_ASP_86	OD2	3.788
5GKS	A_ARG_66	NH2	A_ASP_86	OD1	3.456
5GKS	A_ARG_66	NH2	A_ASP_86	OD2	2.799
5GKS	A_ARG_94	NH1	A_ASP_101	OD1	3.889
5GKS	A_ARG_94	NH1	A_ASP_101	OD2	2.710
5GKS	A_ARG_96	NH2	A_ASP_101	OD2	3.709
5GKS	A_LYS_143	NZ	A_ASP_144	OD1	3.345
5GKS	A_LYS_143	NZ	A_ASP_144	OD2	3.710
5GKS	A_LYS_	NZ	A_ASP_	OD2	3.919
5GKS	A_LYS_	NZ	B_GLU_124	OE1	3.518
5GKS	A_LYS_	NZ	B_GLU_124	OE2	2.790
5GKS	B_LYS_53	NZ	B_ASP_50	OD2	3.623
5GKS	B_ARG_	NH1	B_ASP_	OD1	2.870
5GKS	B_ARG_	NH1	B_ASP_82	OD2	3.493
5GKS	B_LYS_111	NZ	B_GLU_199	OE1	3.161
5GKS	B_LYS_130	NZ	A_ASP_144	OD2	3.783
5GKS	B_LYS_150	NZ	B_GLU_204	OE2	3.960
5GKS	B_LYS_164	NZ	B_ASP_85	OD2	3.552
5GKS	B_HIS_189	ND1	B_ASP_152	OD2	3.043
5GKS	C_ARG_	NH1	C_ASP_	OD1	2.746
5GKS	C_ARG_	NH2	C_GLU_	OE1	3.164
5GKS	C_ARG_	NH2	C_ASP_	OD1	3.556
5GKS	C_ARG_66	NH1	C_ASP_	OD1	3.136
5GKS	C_ARG_66	NH1	C_ASP_	OD2	3.770
5GKS	C_ARG_66	NH2	C_ASP_	OD1	3.522
5GKS	C_ARG_66	NH2	C_ASP_	OD2	2.841
5GKS	C_ARG_	NH1	C_ASP_	OD1	3.682
5GKS	C_ARG_	NH1	C_ASP_	OD2	2.656
5GKS	C_ARG_	NH2	C_ASP_	OD2	3.498
5GKS	C_LYS_	NZ	C_ASP_	OD1	3.276
5GKS	C_LYS_	NZ	C_ASP_	OD2	3.251
5GKS	C_LYS_	NZ	C_ASP_	OD2	3.224
5GKS	C_LYS_	NZ	C_ASP_	OD1	3.903
5GKS	C_LYS_	NZ	C_ASP_	OD2	3.334
5GKS	C_LYS_	NZ	D_GLU_	OE1	3.455
5GKS	C_LYS_	NZ	D_GLU_	OE2	2.665
5GKS	D_LYS_	NZ	D_ASP_	OD2	3.974
5GKS	D_ARG_	NH1	D_ASP_	OD1	2.964
5GKS	D_ARG_	NH1	D_GLU_	OE2	3.512
5GKS	D_ARG_	NH1	D_ASP_	OD1	2.891
5GKS	D_ARG_	NH1	D_ASP_	OD2	3.896
5GKS	D_LYS_	NZ	D_GLU_	OE1	2.751
5GKS	D_LYS_	NZ	D_GLU_	OE2	3.899
5GKS	D_HIS_189	ND1	D_ASP_152	OD2	3.002

Table 671: 5GKS-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5HDQ	A_HIS_40	NE2	A_ASP_58	OD1	2.837
5HDQ	A_HIS_50	NE2	A_GLU_189	OE2	3.103
5HDQ	A_HIS_50	NE2	A_ASP_264	OD1	3.865
5HDQ	A_HIS_50	NE2	A_ASP_264	OD2	3.335
5HDQ	A_HIS_123	ND1	A_ASP_121	OD2	2.936
5HDQ	A_HIS_123	NE2	A_GLU_189	OE1	3.291
5HDQ	A_HIS_123	NE2	A_GLU_189	OE2	3.492
5HDQ	A_HIS_123	NE2	A_ASP_264	OD1	2.880
5HDQ	A_HIS_123	NE2	A_ASP_264	OD2	3.860
5HDQ	A_HIS_149	ND1	A_ASP_146	OD1	3.055
5HDQ	A_HIS_149	ND1	A_ASP_146	OD2	2.834
5HDQ	A_LYS_172	NZ	A_ASP_129	OD1	3.820
5HDQ	A_LYS_193	NZ	A_GLU_208	OE2	3.325
5HDQ	A_HIS_230	ND1	A_GLU_181	OE1	3.289
5HDQ	A_HIS_234	ND1	H_ASP_97	OD2	3.865
5HDQ	A_LYS_243	NZ	A_GLU_260	OE2	3.481
5HDQ	A_LYS_254	NZ	A_GLU_251	OE1	3.552
5HDQ	A_LYS_278	NZ	A_ASP_274	OD1	2.808
5HDQ	A_HIS_288	NE2	A_ASP_177	OD1	3.242
5HDQ	A_HIS_288	NE2	A_ASP_177	OD2	3.881
5HDQ	H_LYS_62	NZ	H_GLU_46	OE1	3.737
5HDQ	H_LYS_62	NZ	H_GLU_46	OE2	2.605
5HDQ	H_LYS_66	NZ	H_ASP_86	OD1	3.893
5HDQ	H_LYS_66	NZ	H_ASP_86	OD2	2.747
5HDQ	H_ARG_94	NH1	H_ASP_101	OD1	3.466
5HDQ	H_ARG_94	NH1	H_ASP_101	OD2	2.979
5HDQ	H_LYS_95	NZ	A_ASP_256	OD2	3.739
5HDQ	H_LYS_208	NZ	L_GLU_123	OE1	2.947
5HDQ	L_LYS_24	NZ	L_ASP_70	OD2	2.740
5HDQ	L_ARG_54	NH1	L_ASP_60	OD1	3.546
5HDQ	L_ARG_61	NH1	L_GLU_81	OE1	3.772
5HDQ	L_ARG_61	NH1	L_ASP_82	OD1	2.690
5HDQ	L_ARG_61	NH1	L_ASP_82	OD2	3.697
5HDQ	L_LYS_103	NZ	L_GLU_105	OE2	3.387
5HDQ	L_LYS_142	NZ	L_GLU_105	OE1	3.286
5HDQ	L_LYS_142	NZ	L_GLU_105	OE2	2.974
5HDQ	L_LYS_149	NZ	L_GLU_195	OE2	3.652
5HDQ	L_LYS_183	NZ	L_GLU_187	OE1	2.880
5HDQ	L_LYS_183	NZ	L_GLU_187	OE2	3.085
5HDQ	L_HIS_189	ND1	L_ASP_151	OD2	2.925
5HDQ	L_HIS_189	NE2	L_GLU_185	OE1	3.931
5HDQ	L_HIS_189	NE2	L_GLU_185	OE2	3.287

Table 672: 5HDQ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5HMG	A_LYS_27	NZ	B_GLU_97	OE1	2.931
5HMG	A_LYS_27	NZ	B_GLU_97	OE2	3.005
5HMG	A_HIS_56	ND1	A_ASP_85	OD2	3.602
5HMG	A_ARG_57	NH1	A_GLU_82	OE1	2.653
5HMG	A_ARG_57	NH1	A_GLU_82	OE2	3.746
5HMG	A_HIS_75	ND1	A_ASP_73	OD1	3.505
5HMG	A_HIS_75	ND1	A_ASP_73	OD2	2.667
5HMG	A_HIS_75	NE2	A_ASP_63	OD1	3.736
5HMG	A_ARG_90	NH1	A_ASP_60	OD1	2.782
5HMG	A_ARG_90	NH1	A_ASP_60	OD2	3.490
5HMG	A_ARG_109	NH1	B_GLU_67	OE1	2.841
5HMG	A_ARG_109	NH1	B_GLU_67	OE2	3.185
5HMG	A_ARG_109	NH2	A_GLU_89	OE1	2.955
5HMG	A_ARG_109	NH2	A_GLU_89	OE2	2.579
5HMG	A_ARG_141	NH1	A_ASP_77	OD1	3.382
5HMG	A_ARG_141	NH1	A_ASP_77	OD2	3.145
5HMG	A_ARG_141	NH2	A_ASP_77	OD1	2.618
5HMG	A_ARG_141	NH2	A_ASP_77	OD2	2.942
5HMG	A_LYS_176	NZ	A_GLU_123	OE1	2.608
5HMG	A_LYS_176	NZ	A_GLU_123	OE2	3.621
5HMG	A_HIS_183	NE2	A_GLU_190	OE1	3.761
5HMG	A_ARG_207	NH2	A_ASP_241	OD1	3.512
5HMG	A_ARG_261	NH1	A_GLU_119	OE1	3.028
5HMG	A_ARG_261	NH1	A_GLU_119	OE2	3.069
5HMG	A_ARG_261	NH2	A_GLU_119	OE1	2.801
5HMG	A_ARG_261	NH2	A_GLU_119	OE2	2.923
5HMG	A_LYS_264	NZ	A_ASP_85	OD1	3.963
5HMG	A_LYS_264	NZ	A_ASP_85	OD2	2.713
5HMG	A_ARG_269	NH1	B_GLU_67	OE1	3.577
5HMG	A_ARG_269	NH2	B_GLU_67	OE1	3.220
5HMG	A_LYS_292	NZ	A_ASP_291	OD1	2.545
5HMG	A_LYS_299	NZ	B_GLU_69	OE1	3.343
5HMG	A_LYS_310	NZ	B_ASP_86	OD1	3.434
5HMG	A_LYS_310	NZ	B_ASP_90	OD1	2.661
5HMG	A_LYS_315	NZ	A_GLU_41	OE2	2.757
5HMG	B_LYS_51	NZ	B_GLU_103	OE2	2.773
5HMG	B_ARG_54	NH1	F_GLU_97	OE1	2.843
5HMG	B_ARG_54	NH2	B_GLU_57	OE2	3.728
5HMG	B_ARG_54	NH2	F_GLU_97	OE1	2.937
5HMG	B_LYS_58	NZ	B_GLU_57	OE1	3.084
5HMG	B_LYS_58	NZ	B_GLU_57	OE2	3.561
5HMG	B_LYS_58	NZ	F_GLU_97	OE1	3.606
5HMG	B_LYS_58	NZ	F_GLU_97	OE2	3.524
5HMG	B_LYS_62	NZ	F_ASP_86	OD1	3.085
5HMG	B_LYS_62	NZ	F_ASP_86	OD2	2.792
5HMG	B_LYS_62	NZ	F_ASP_90	OD1	3.679
5HMG	B_LYS_62	NZ	F_ASP_90	OD2	2.748
5HMG	B_HIS_64	NE2	F_ASP_79	OD2	3.617
5HMG	B_LYS_68	NZ	B_GLU_85	OE1	3.409
5HMG	B_LYS_68	NZ	B_GLU_85	OE2	2.733
5HMG	B_ARG_76	NH1	D_GLU_74	OE1	3.275
5HMG	B_ARG_76	NH1	D_GLU_74	OE2	2.882
5HMG	B_ARG_76	NH1	D_GLU_81	OE1	2.781
5HMG	B_ARG_76	NH1	D_GLU_81	OE2	3.484
5HMG	B_ARG_76	NH2	D_GLU_74	OE1	2.814
5HMG	B_ARG_76	NH2	D_GLU_74	OE2	3.691
5HMG	B_LYS_117	NZ	B_GLU_114	OE1	2.674

5HMG	B_LYS_117	NZ	B_GLU_114	OE2	3.512
5HMG	B_ARG_123	NH1	B_GLU_120	OE1	3.893
5HMG	B_ARG_123	NH1	F_GLU_132	OE2	3.002
5HMG	B_ARG_123	NH2	B_GLU_120	OE1	2.612
5HMG	B_ARG_123	NH2	B_GLU_120	OE2	3.339
5HMG	B_ARG_124	NH1	B_GLU_120	OE1	3.640
5HMG	B_ARG_124	NH1	F_GLU_132	OE1	3.424
5HMG	B_ARG_124	NH1	F_GLU_132	OE2	3.265
5HMG	B_ARG_124	NH2	B_GLU_120	OE1	3.919
5HMG	B_ARG_127	NH2	F_GLU_131	OE1	2.537
5HMG	B_LYS_143	NZ	B_ASP_145	OD1	2.698
5HMG	B_ARG_153	NH2	B_GLU_150	OE1	3.021
5HMG	B_HIS_159	NE2	B_ASP_160	OD2	3.062
5HMG	B_ARG_163	NH1	F_GLU_131	OE1	2.770
5HMG	B_ARG_163	NH1	F_GLU_131	OE2	2.532
5HMG	B_ARG_170	NH1	B_GLU_128	OE1	3.922
5HMG	B_ARG_170	NH1	B_GLU_131	OE2	3.597
5HMG	B_ARG_170	NH1	D_GLU_128	OE1	3.169
5HMG	B_ARG_170	NH1	D_GLU_128	OE2	3.597
5HMG	B_ARG_170	NH2	B_GLU_128	OE1	3.011
5HMG	C_LYS_27	NZ	D_GLU_97	OE1	2.934
5HMG	C_LYS_27	NZ	D_GLU_97	OE2	2.988
5HMG	C_HIS_56	ND1	C_ASP_85	OD2	3.578
5HMG	C_ARG_57	NH1	C_GLU_82	OE1	2.634
5HMG	C_ARG_57	NH1	C_GLU_82	OE2	3.752
5HMG	C_HIS_75	ND1	C_ASP_73	OD1	3.515
5HMG	C_HIS_75	ND1	C_ASP_73	OD2	2.678
5HMG	C_HIS_75	NE2	C_ASP_63	OD1	3.699
5HMG	C_ARG_90	NH1	C_ASP_60	OD1	2.783
5HMG	C_ARG_90	NH1	C_ASP_60	OD2	3.521
5HMG	C_ARG_109	NH1	D_GLU_67	OE1	2.853
5HMG	C_ARG_109	NH1	D_GLU_67	OE2	3.184
5HMG	C_ARG_109	NH2	C_GLU_89	OE1	2.925
5HMG	C_ARG_109	NH2	C_GLU_89	OE2	2.571
5HMG	C_ARG_141	NH1	C_ASP_77	OD1	3.417
5HMG	C_ARG_141	NH1	C_ASP_77	OD2	3.195
5HMG	C_ARG_141	NH2	C_ASP_77	OD1	2.635
5HMG	C_ARG_141	NH2	C_ASP_77	OD2	2.953
5HMG	C_LYS_176	NZ	C_GLU_123	OE1	2.578
5HMG	C_LYS_176	NZ	C_GLU_123	OE2	3.604
5HMG	C_HIS_183	NE2	C_GLU_190	OE1	3.762
5HMG	C_ARG_207	NH2	C_ASP_241	OD1	3.485
5HMG	C_ARG_261	NH1	C_GLU_119	OE1	3.007
5HMG	C_ARG_261	NH1	C_GLU_119	OE2	3.058
5HMG	C_ARG_261	NH2	C_GLU_119	OE1	2.812
5HMG	C_ARG_261	NH2	C_GLU_119	OE2	2.915
5HMG	C_LYS_264	NZ	C_ASP_85	OD1	3.974
5HMG	C_LYS_264	NZ	C_ASP_85	OD2	2.709
5HMG	C_ARG_269	NH1	D_GLU_67	OE1	3.552
5HMG	C_ARG_269	NH2	D_GLU_67	OE1	3.173
5HMG	C_LYS_292	NZ	C_ASP_291	OD1	2.561
5HMG	C_LYS_299	NZ	D_GLU_69	OE1	3.348
5HMG	C_LYS_310	NZ	D_ASP_86	OD1	3.449
5HMG	C_LYS_310	NZ	D_ASP_90	OD1	2.638
5HMG	C_LYS_315	NZ	C_GLU_41	OE2	2.755
5HMG	D_LYS_51	NZ	D_GLU_103	OE2	2.776
5HMG	D_ARG_54	NH1	B_GLU_97	OE1	2.819
5HMG	D_ARG_54	NH2	B_GLU_97	OE1	2.943

5HMG	D_ARG_54	NH2	D_GLU_57	OE2	3.747
5HMG	D_LYS_58	NZ	B_GLU_97	OE1	3.646
5HMG	D_LYS_58	NZ	B_GLU_97	OE2	3.528
5HMG	D_LYS_58	NZ	D_GLU_57	OE1	3.109
5HMG	D_LYS_58	NZ	D_GLU_57	OE2	3.568
5HMG	D_LYS_62	NZ	B_ASP_86	OD1	3.110
5HMG	D_LYS_62	NZ	B_ASP_86	OD2	2.718
5HMG	D_LYS_62	NZ	B_ASP_90	OD1	3.686
5HMG	D_LYS_62	NZ	B_ASP_90	OD2	2.685
5HMG	D_HIS_64	NE2	B_ASP_79	OD2	3.446
5HMG	D_LYS_68	NZ	D_GLU_85	OE1	3.418
5HMG	D_LYS_68	NZ	D_GLU_85	OE2	2.785
5HMG	D_ARG_76	NH1	F_GLU_74	OE1	3.349
5HMG	D_ARG_76	NH1	F_GLU_74	OE2	2.805
5HMG	D_ARG_76	NH1	F_GLU_81	OE1	2.685
5HMG	D_ARG_76	NH1	F_GLU_81	OE2	3.513
5HMG	D_ARG_76	NH2	F_GLU_74	OE1	2.710
5HMG	D_ARG_76	NH2	F_GLU_74	OE2	3.478
5HMG	D_LYS_117	NZ	D_GLU_114	OE1	2.687
5HMG	D_LYS_117	NZ	D_GLU_114	OE2	3.495
5HMG	D_ARG_123	NH1	B_GLU_132	OE2	2.981
5HMG	D_ARG_123	NH1	D_GLU_120	OE1	3.874
5HMG	D_ARG_123	NH2	D_GLU_120	OE1	2.616
5HMG	D_ARG_123	NH2	D_GLU_120	OE2	3.345
5HMG	D_ARG_124	NH1	B_GLU_132	OE1	3.466
5HMG	D_ARG_124	NH1	B_GLU_132	OE2	3.303
5HMG	D_ARG_124	NH1	D_GLU_120	OE1	3.636
5HMG	D_ARG_124	NH2	D_GLU_120	OE1	3.931
5HMG	D_ARG_127	NH2	B_GLU_131	OE1	2.578
5HMG	D_LYS_143	NZ	D_ASP_145	OD1	2.713
5HMG	D_ARG_153	NH2	D_GLU_150	OE1	2.620
5HMG	D_HIS_159	NE2	D_ASP_160	OD2	3.088
5HMG	D_ARG_163	NH1	B_GLU_131	OE1	2.694
5HMG	D_ARG_163	NH1	B_GLU_131	OE2	2.571
5HMG	D_ARG_170	NH1	D_GLU_128	OE1	3.949
5HMG	D_ARG_170	NH1	D_GLU_131	OE2	3.612
5HMG	D_ARG_170	NH1	F_GLU_128	OE1	3.252
5HMG	D_ARG_170	NH1	F_GLU_128	OE2	3.705
5HMG	D_ARG_170	NH2	D_GLU_128	OE1	3.068
5HMG	E_LYS_27	NZ	F_GLU_97	OE1	2.935
5HMG	E_LYS_27	NZ	F_GLU_97	OE2	3.012
5HMG	E_HIS_56	ND1	E_ASP_85	OD2	3.574
5HMG	E_ARG_57	NH1	E_GLU_82	OE1	2.672
5HMG	E_ARG_57	NH1	E_GLU_82	OE2	3.760
5HMG	E_HIS_75	ND1	E_ASP_73	OD1	3.480
5HMG	E_HIS_75	ND1	E_ASP_73	OD2	2.665
5HMG	E_HIS_75	NE2	E_ASP_63	OD1	3.721
5HMG	E_ARG_90	NH1	E_ASP_60	OD1	2.808
5HMG	E_ARG_90	NH1	E_ASP_60	OD2	3.495
5HMG	E_ARG_109	NH1	F_GLU_67	OE1	2.825
5HMG	E_ARG_109	NH1	F_GLU_67	OE2	3.180
5HMG	E_ARG_109	NH2	E_GLU_89	OE1	2.931
5HMG	E_ARG_109	NH2	E_GLU_89	OE2	2.544
5HMG	E_ARG_141	NH1	E_ASP_77	OD1	3.401
5HMG	E_ARG_141	NH1	E_ASP_77	OD2	3.198
5HMG	E_ARG_141	NH2	E_ASP_77	OD1	2.626
5HMG	E_ARG_141	NH2	E_ASP_77	OD2	2.960
5HMG	E_LYS_176	NZ	E_GLU_123	OE1	2.587

5HMG	E_LYS_176	NZ	E_GLU_123	OE2	3.609
5HMG	E_HIS_183	NE2	E_GLU_190	OE1	3.758
5HMG	E_ARG_207	NH2	E_ASP_241	OD1	3.508
5HMG	E_ARG_261	NH1	E_GLU_119	OE1	2.998
5HMG	E_ARG_261	NH1	E_GLU_119	OE2	3.065
5HMG	E_ARG_261	NH2	E_GLU_119	OE1	2.789
5HMG	E_ARG_261	NH2	E_GLU_119	OE2	2.904
5HMG	E_LYS_264	NZ	E_ASP_85	OD1	3.978
5HMG	E_LYS_264	NZ	E_ASP_85	OD2	2.713
5HMG	E_ARG_269	NH1	F_GLU_67	OE1	3.584
5HMG	E_ARG_269	NH2	F_GLU_67	OE1	3.233
5HMG	E_LYS_292	NZ	E_ASP_291	OD1	2.537
5HMG	E_LYS_299	NZ	F_GLU_69	OE1	3.318
5HMG	E_LYS_310	NZ	F_ASP_86	OD1	3.440
5HMG	E_LYS_310	NZ	F_ASP_90	OD1	2.621
5HMG	E_LYS_315	NZ	E_GLU_41	OE2	2.747
5HMG	F_LYS_51	NZ	F_GLU_103	OE2	2.774
5HMG	F_ARG_54	NH1	D_GLU_97	OE1	2.726
5HMG	F_ARG_54	NH2	D_GLU_97	OE1	2.912
5HMG	F_ARG_54	NH2	F_GLU_57	OE2	3.744
5HMG	F_LYS_58	NZ	D_GLU_97	OE1	3.765
5HMG	F_LYS_58	NZ	D_GLU_97	OE2	3.593
5HMG	F_LYS_58	NZ	F_GLU_57	OE1	3.108
5HMG	F_LYS_58	NZ	F_GLU_57	OE2	3.569
5HMG	F_LYS_62	NZ	D_ASP_86	OD1	3.013
5HMG	F_LYS_62	NZ	D_ASP_86	OD2	2.694
5HMG	F_LYS_62	NZ	D_ASP_90	OD1	3.718
5HMG	F_LYS_62	NZ	D_ASP_90	OD2	2.750
5HMG	F_HIS_64	NE2	D_ASP_79	OD1	3.885
5HMG	F_HIS_64	NE2	D_ASP_79	OD2	3.364
5HMG	F_LYS_68	NZ	F_GLU_85	OE1	3.382
5HMG	F_LYS_68	NZ	F_GLU_85	OE2	2.722
5HMG	F_ARG_76	NH1	B_GLU_74	OE1	3.251
5HMG	F_ARG_76	NH1	B_GLU_74	OE2	2.826
5HMG	F_ARG_76	NH1	B_GLU_81	OE1	2.735
5HMG	F_ARG_76	NH1	B_GLU_81	OE2	3.601
5HMG	F_ARG_76	NH2	B_GLU_74	OE1	2.649
5HMG	F_ARG_76	NH2	B_GLU_74	OE2	3.569
5HMG	F_LYS_117	NZ	F_GLU_114	OE1	2.666
5HMG	F_LYS_117	NZ	F_GLU_114	OE2	3.516
5HMG	F_ARG_123	NH1	D_GLU_132	OE2	2.992
5HMG	F_ARG_123	NH1	F_GLU_120	OE1	3.906
5HMG	F_ARG_123	NH2	F_GLU_120	OE1	2.639
5HMG	F_ARG_123	NH2	F_GLU_120	OE2	3.377
5HMG	F_ARG_124	NH1	D_GLU_132	OE1	3.514
5HMG	F_ARG_124	NH1	D_GLU_132	OE2	3.395
5HMG	F_ARG_124	NH1	F_GLU_120	OE1	3.630
5HMG	F_ARG_124	NH2	F_GLU_120	OE1	3.883
5HMG	F_ARG_127	NH2	D_GLU_131	OE1	2.609
5HMG	F_LYS_143	NZ	F_ASP_145	OD1	2.695
5HMG	F_HIS_159	NE2	F_ASP_160	OD2	3.088
5HMG	F_ARG_163	NH1	D_GLU_131	OE1	2.712
5HMG	F_ARG_163	NH1	D_GLU_131	OE2	2.596
5HMG	F_ARG_170	NH1	B_GLU_128	OE1	3.210
5HMG	F_ARG_170	NH1	B_GLU_128	OE2	3.530
5HMG	F_ARG_170	NH1	F_GLU_128	OE1	3.950
5HMG	F_ARG_170	NH1	F_GLU_131	OE2	3.600
5HMG	F_ARG_170	NH2	F_GLU_128	OE1	3.064

Table 673: 5HMG-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5I4F	A_LYS_64	NZ	A_GLU_47	OE2	2.666
5I4F	A_LYS_68	NZ	A_ASP_91	OD1	3.548
5I4F	A_LYS_68	NZ	A_ASP_91	OD2	2.948
5I4F	A_ARG_99	NH2	A_ASP_108	OD1	3.501
5I4F	A_ARG_99	NH2	A_ASP_108	OD2	2.781
5I4F	A_ARG_198	NH2	A_ASP_204	OD1	3.850
5I4F	A_ARG_205	NH1	A_GLU_223	OE2	3.321
5I4F	A_ARG_205	NH2	A_GLU_223	OE1	3.768
5I4F	A_ARG_205	NH2	A_GLU_223	OE2	3.756
5I4F	A_ARG_205	NH2	A_GLU_225	OE2	2.829
5I4F	A_ARG_205	NH2	A_ASP_226	OD1	2.710
5I4F	A_ARG_205	NH2	A_ASP_226	OD2	3.577

Table 674: 5I4F-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID** **residue name** **residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5I76	A_ARG_24	NH1	A_ASP_70	OD2	3.774
5I76	A_LYS_49	NZ	A_GLU_53	OE1	2.941
5I76	A_LYS_49	NZ	B_GLU_105	OE1	3.995
5I76	A_ARG_61	NH1	A_GLU_79	OE2	3.393
5I76	A_ARG_61	NH1	A_GLU_81	OE2	3.803
5I76	A_ARG_61	NH2	A_GLU_79	OE2	3.760
5I76	A_ARG_61	NH2	A_GLU_81	OE2	2.766
5I76	A_ARG_61	NH2	A_ASP_82	OD1	2.773
5I76	A_ARG_61	NH2	A_ASP_82	OD2	3.589
5I76	A_LYS_103	NZ	A_GLU_165	OE1	3.841
5I76	A_LYS_145	NZ	A_GLU_143	OE1	3.548
5I76	A_LYS_145	NZ	A_GLU_143	OE2	2.870
5I76	A_LYS_149	NZ	A_GLU_195	OE1	2.637
5I76	A_HIS_189	ND1	A_ASP_151	OD2	3.111
5I76	A_HIS_189	NE2	A_ASP_185	OD1	3.124
5I76	B_ARG_38	NH1	B_ASP_89	OD1	2.810
5I76	B_ARG_38	NH2	B_GLU_46	OE1	3.124
5I76	B_ARG_38	NH2	B_ASP_89	OD1	3.773
5I76	B_ARG_66	NH1	B_ASP_89	OD1	3.709
5I76	B_ARG_66	NH1	B_ASP_89	OD2	2.960
5I76	B_ARG_66	NH2	B_ASP_89	OD1	2.836
5I76	B_ARG_66	NH2	B_ASP_89	OD2	3.415
5I76	B_LYS_149	NZ	B_ASP_150	OD1	3.571
5I76	B_LYS_215	NZ	A_GLU_123	OE1	2.731
5I76	B_LYS_215	NZ	A_GLU_123	OE2	2.888
5I76	B_ARG_216	NH2	B_GLU_218	OE1	2.687
5I76	B_LYS_220	NZ	A_ASP_122	OD2	3.474
5I76	C_ARG_24	NH1	A_ASP_70	OD1	3.725
5I76	C_ARG_24	NH1	A_ASP_70	OD2	2.949
5I76	C_ARG_24	NH1	C_ASP_70	OD1	3.422
5I76	C_ARG_24	NH2	A_ASP_70	OD1	3.138
5I76	C_ARG_24	NH2	A_ASP_70	OD2	3.394
5I76	C_LYS_49	NZ	C_GLU_53	OE1	2.642
5I76	C_ARG_61	NH1	C_GLU_79	OE2	3.544
5I76	C_ARG_61	NH1	C_GLU_81	OE2	3.961
5I76	C_ARG_61	NH2	C_GLU_79	OE2	3.781
5I76	C_ARG_61	NH2	C_GLU_81	OE2	2.825
5I76	C_ARG_61	NH2	C_ASP_82	OD1	2.761
5I76	C_ARG_61	NH2	C_ASP_82	OD2	3.560
5I76	C_LYS_103	NZ	C_ASP_85	OD1	3.711
5I76	C_LYS_103	NZ	C_ASP_85	OD2	3.969
5I76	C_LYS_103	NZ	C_GLU_165	OE1	3.241
5I76	C_LYS_103	NZ	C_GLU_165	OE2	3.658
5I76	C_LYS_149	NZ	C_GLU_195	OE1	2.493
5I76	C_LYS_183	NZ	C_GLU_187	OE1	3.091
5I76	C_LYS_183	NZ	C_GLU_187	OE2	3.350
5I76	C_HIS_189	ND1	C_ASP_151	OD2	2.352
5I76	D_ARG_38	NH1	D_ASP_89	OD1	2.883
5I76	D_ARG_38	NH2	D_GLU_46	OE1	3.400
5I76	D_ARG_38	NH2	D_ASP_89	OD1	3.880
5I76	D_ARG_66	NH1	D_ASP_89	OD1	3.587
5I76	D_ARG_66	NH1	D_ASP_89	OD2	2.851
5I76	D_ARG_66	NH2	D_ASP_89	OD1	2.736
5I76	D_ARG_66	NH2	D_ASP_89	OD2	3.459
5I76	D_LYS_149	NZ	D_ASP_150	OD1	2.862
5I76	D_LYS_149	NZ	D_ASP_150	OD2	2.853
5I76	D_LYS_215	NZ	C_GLU_123	OE1	2.596

5I76	D_LYS_215	NZ	C_GLU_123	OE2	3.738
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Table 675: 5I76-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5IHL	A_HIS_78	NE2	A_ASP_69	OD1	3.151
5IHL	A_HIS_78	NE2	A_GLU_74	OE1	3.112
5IHL	A_HIS_78	NE2	A_GLU_74	OE2	3.476
5IHL	A_LYS_81	NZ	A_ASP_100	OD2	3.844
5IHL	A_ARG_123	NH1	A_ASP_140	OD2	3.023
5IHL	A_ARG_123	NH2	A_ASP_140	OD2	3.466
5IHL	A_LYS_132	NZ	A_GLU_144	OE2	3.445
5IHL	B_ARG_38	NH1	B_GLU_46	OE2	3.444
5IHL	B_ARG_38	NH1	B_ASP_86	OD1	3.975
5IHL	B_ARG_38	NH2	B_ASP_86	OD1	3.323
5IHL	B_ARG_66	NH1	B_ASP_86	OD1	3.298
5IHL	B_ARG_66	NH1	B_ASP_86	OD2	2.656
5IHL	B_ARG_66	NH2	B_ASP_86	OD1	3.517
5IHL	D_HIS_78	NE2	D_ASP_69	OD1	3.189
5IHL	D_HIS_78	NE2	D_GLU_74	OE1	3.120
5IHL	D_HIS_78	NE2	D_GLU_74	OE2	3.496
5IHL	D_ARG_123	NH2	D_ASP_140	OD2	3.433
5IHL	D_HIS_162	NE2	D_GLU_159	OE1	3.297
5IHL	E_ARG_38	NH1	E_ASP_86	OD1	3.969
5IHL	E_ARG_38	NH2	E_ASP_86	OD1	3.308
5IHL	E_ARG_66	NH1	E_ASP_86	OD1	3.287
5IHL	E_ARG_66	NH1	E_ASP_86	OD2	2.657
5IHL	E_ARG_66	NH2	E_ASP_86	OD1	3.504
5IHL	F_HIS_78	ND1	F_ASP_69	OD1	3.127
5IHL	F_HIS_78	NE2	F_GLU_74	OE1	3.224
5IHL	F_HIS_110	ND1	F_ASP_140	OD1	3.789
5IHL	F_HIS_110	ND1	F_ASP_140	OD2	2.873
5IHL	F_ARG_123	NH1	F_ASP_140	OD2	3.408
5IHL	F_HIS_162	NE2	F_GLU_159	OE1	2.954
5IHL	G_ARG_38	NH1	G_GLU_46	OE1	3.917
5IHL	G_ARG_38	NH1	G_GLU_46	OE2	3.596
5IHL	G_ARG_38	NH1	G_ASP_86	OD1	3.962
5IHL	G_ARG_38	NH2	G_ASP_86	OD1	3.314
5IHL	G_ARG_66	NH1	G_ASP_86	OD1	3.297
5IHL	G_ARG_66	NH1	G_ASP_86	OD2	2.675
5IHL	G_ARG_66	NH2	G_ASP_86	OD1	3.505
5IHL	H_LYS_29	NZ	H_GLU_28	OE1	3.389
5IHL	H_HIS_78	NE2	H_ASP_69	OD1	3.188
5IHL	H_HIS_78	NE2	H_GLU_74	OE1	3.148
5IHL	H_HIS_78	NE2	H_GLU_74	OE2	3.496
5IHL	I_ARG_38	NH1	I_GLU_46	OE1	3.944
5IHL	I_ARG_38	NH1	I_GLU_46	OE2	3.555
5IHL	I_ARG_38	NH1	I_ASP_86	OD1	3.950
5IHL	I_ARG_38	NH2	I_ASP_86	OD1	3.321
5IHL	I_ARG_66	NH1	I_ASP_86	OD1	3.272
5IHL	I_ARG_66	NH1	I_ASP_86	OD2	2.644
5IHL	I_ARG_66	NH2	I_ASP_86	OD1	3.520

Table 676: 5IHL-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5ITB	H_ARG_43	NH1	H_ASP_98	OD1	2.808
5ITB	H_ARG_43	NH2	H_GLU_51	OE1	2.922
5ITB	H_ARG_43	NH2	H_GLU_51	OE2	3.615
5ITB	H_ARG_43	NH2	H_ASP_98	OD1	3.996
5ITB	H_ARG_75	NH1	H_ASP_98	OD1	3.710
5ITB	H_ARG_75	NH1	H_ASP_98	OD2	2.943
5ITB	H_ARG_75	NH2	H_ASP_98	OD1	3.077
5ITB	H_ARG_75	NH2	H_ASP_98	OD2	3.700
5ITB	H_ARG_107	NH1	H_ASP_114	OD1	3.122
5ITB	H_ARG_111	NH1	L_GLU_68	OE1	3.426
5ITB	H_ARG_111	NH2	H_ASP_114	OD2	2.687
5ITB	H_ARG_111	NH2	H_ASP_116	OD2	3.548
5ITB	H_ARG_111	NH2	L_GLU_68	OE1	2.856
5ITB	H_LYS_224	NZ	L_GLU_143	OE1	3.323
5ITB	H_LYS_224	NZ	L_GLU_143	OE2	2.099
5ITB	H_ARG_225	NH2	H_GLU_227	OE2	3.950
5ITB	L_LYS_45	NZ	L_ASP_97	OD1	3.221
5ITB	L_LYS_45	NZ	L_ASP_97	OD2	3.180
5ITB	L_ARG_75	NH2	L_ASP_98	OD1	2.991
5ITB	L_ARG_75	NH2	L_ASP_98	OD2	3.652
5ITB	L_LYS_203	NZ	L_GLU_207	OE1	3.111
5ITB	L_LYS_203	NZ	L_GLU_207	OE2	2.934
5ITB	L_HIS_209	ND1	L_ASP_171	OD2	3.207
5ITB	L_HIS_209	NE2	L_ASP_205	OD1	2.812
5ITB	L_HIS_209	NE2	L_ASP_205	OD2	3.009

Table 677: 5ITB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5J3D	A_ARG_43	NH1	A_ASP_98	OD1	2.896
5J3D	A_ARG_43	NH2	A_GLU_51	OE1	2.997
5J3D	A_ARG_43	NH2	A_GLU_51	OE2	2.988
5J3D	A_ARG_75	NH1	A_ASP_98	OD1	3.601
5J3D	A_ARG_75	NH1	A_ASP_98	OD2	3.013
5J3D	A_ARG_75	NH2	A_ASP_98	OD1	3.254
5J3D	A_ARG_95	NH2	A_GLU_97	OE2	3.552
5J3D	A_ARG_107	NH1	A_ASP_114	OD1	3.567
5J3D	A_ARG_111	NH2	A_ASP_114	OD2	3.401
5J3D	A_ARG_111	NH2	B_GLU_68	OE1	3.664
5J3D	A_LYS_158	NZ	A_ASP_159	OD1	3.439
5J3D	A_LYS_158	NZ	A_ASP_159	OD2	3.508
5J3D	A_LYS_224	NZ	B_GLU_143	OE1	3.390
5J3D	A_LYS_229	NZ	B_ASP_142	OD1	3.902
5J3D	A_LYS_229	NZ	B_ASP_142	OD2	3.196
5J3D	B_LYS_45	NZ	B_ASP_97	OD1	3.783
5J3D	B_ARG_75	NH2	B_ASP_97	OD2	3.805
5J3D	B_LYS_123	NZ	B_GLU_185	OE2	3.379
5J3D	B_LYS_169	NZ	B_GLU_215	OE2	3.640
5J3D	B_LYS_203	NZ	B_GLU_207	OE2	2.374
5J3D	B_HIS_209	ND1	B_ASP_171	OD1	3.892
5J3D	B_HIS_209	ND1	B_ASP_171	OD2	2.212
5J3D	C_ARG_	NH1	C_ASP_	OD1	3.000
5J3D	C_ARG_	NH2	C_GLU_	OE1	3.686
5J3D	C_ARG_	NH2	C_ASP_	OD1	3.849
5J3D	C_ARG_	NH1	C_ASP_	OD1	3.639
5J3D	C_ARG_	NH1	C_ASP_	OD2	3.007
5J3D	C_ARG_	NH2	C_ASP_	OD1	3.160
5J3D	C_ARG_	NH2	C_ASP_	OD2	3.889
5J3D	C_ARG_107	NH1	C_ASP_114	OD1	2.971
5J3D	C_ARG_107	NH1	C_ASP_114	OD2	3.218
5J3D	C_ARG_111	NH2	C_ASP_114	OD2	3.073
5J3D	C_ARG_111	NH2	D_GLU_68	OE1	3.489
5J3D	C_LYS_	NZ	C_ASP_	OD1	3.508
5J3D	C_LYS_	NZ	C_ASP_	OD2	3.782
5J3D	C_LYS_	NZ	D_GLU_	OE1	3.377
5J3D	C_LYS_	NZ	D_ASP_	OD1	2.847
5J3D	C_LYS_	NZ	D_ASP_	OD2	2.791
5J3D	D_ARG_75	NH2	D_ASP_97	OD1	3.325
5J3D	D_LYS_	NZ	D_GLU_	OE1	3.275
5J3D	D_LYS_	NZ	D_GLU_	OE2	2.521
5J3D	D_LYS_	NZ	D_GLU_	OE1	3.944
5J3D	D_LYS_	NZ	D_GLU_	OE2	3.225
5J3D	D_HIS_	ND1	D_ASP_	OD2	2.270
5J3D	E_ARG_49	NH2	F_ASP_368	OD1	2.801
5J3D	E_ARG_49	NH2	F_ASP_368	OD2	3.628
5J3D	E_LYS_80	NZ	E_ASP_84	OD2	2.975
5J3D	E_LYS_85	NZ	E_GLU_82	OE1	3.904
5J3D	E_LYS_85	NZ	E_GLU_82	OE2	3.954
5J3D	F_LYS_	NZ	I_GLU_	OE2	3.850
5J3D	F_HIS_	NE2	F_GLU_	OE1	3.357
5J3D	F_LYS_191	NZ	F_ASP_194	OD2	3.179
5J3D	F_LYS_196	NZ	I_ASP_489	OD1	2.634
5J3D	F_LYS_196	NZ	I_ASP_489	OD2	3.067
5J3D	F_LYS_201	NZ	F_ASP_200	OD2	3.113
5J3D	F_ARG_229	NH1	F_GLU_256	OE1	3.268
5J3D	F_ARG_229	NH1	F_GLU_256	OE2	2.433

5J3D	F_ARG_229	NH2	F_GLU_256	OE1	2.288
5J3D	F_ARG_229	NH2	F_GLU_256	OE2	3.196
5J3D	F_ARG_235	NH1	I_GLU_232	OE1	3.071
5J3D	F_ARG_235	NH1	I_GLU_232	OE2	2.514
5J3D	F_ARG_235	NH2	F_GLU_232	OE2	3.966
5J3D	F_LYS_272	NZ	B_ASP_56	OD2	3.606
5J3D	F_LYS_293	NZ	F_GLU_295	OE2	3.714
5J3D	F_ARG_336	NH2	F_ASP_338	OD1	2.882
5J3D	F_ARG_336	NH2	F_ASP_338	OD2	3.428
5J3D	F_ARG_364	NH1	F_ASP_310	OD1	3.194
5J3D	F_ARG_364	NH2	F_ASP_310	OD1	2.918
5J3D	F_LYS_399	NZ	K_ASP_392	OD1	3.567
5J3D	F_LYS_470	NZ	J_GLU_60	OE1	3.190
5J3D	F_LYS_470	NZ	J_GLU_60	OE2	3.891
5J3D	G_ARG_49	NH2	I_ASP_368	OD1	3.151
5J3D	G_LYS_80	NZ	G_ASP_84	OD2	2.927
5J3D	G_LYS_85	NZ	G_GLU_82	OE2	3.889
5J3D	H_ARG_43	NH1	H_ASP_98	OD1	2.849
5J3D	H_ARG_43	NH2	H_GLU_51	OE1	3.608
5J3D	H_ARG_43	NH2	H_GLU_51	OE2	3.183
5J3D	H_ARG_43	NH2	H_ASP_98	OD1	3.954
5J3D	H_ARG_75	NH1	H_ASP_98	OD2	3.150
5J3D	H_ARG_75	NH2	H_ASP_98	OD1	3.434
5J3D	H_ARG_75	NH2	H_ASP_98	OD2	3.495
5J3D	H_ARG_107	NH1	H_ASP_114	OD1	3.119
5J3D	H_ARG_107	NH1	H_ASP_114	OD2	3.930
5J3D	H_ARG_111	NH2	H_ASP_114	OD2	2.954
5J3D	H_ARG_111	NH2	L_GLU_68	OE1	3.466
5J3D	H_LYS_158	NZ	H_ASP_159	OD1	3.555
5J3D	H_LYS_158	NZ	H_ASP_159	OD2	3.908
5J3D	H_LYS_224	NZ	L_GLU_143	OE1	3.364
5J3D	H_LYS_	NZ	L_ASP_	OD1	3.352
5J3D	H_LYS_	NZ	L_ASP_	OD2	3.692
5J3D	I_LYS_	NZ	K_GLU_	OE1	3.226
5J3D	I_LYS_	NZ	K_GLU_	OE2	3.914
5J3D	I_LYS_	NZ	I_GLU_	OE1	3.318
5J3D	I_LYS_191	NZ	I_ASP_194	OD2	3.257
5J3D	I_LYS_196	NZ	K_ASP_489	OD1	2.833
5J3D	I_LYS_196	NZ	K_ASP_489	OD2	3.027
5J3D	I_LYS_201	NZ	I_ASP_200	OD2	3.213
5J3D	I_ARG_229	NH1	I_GLU_256	OE1	3.887
5J3D	I_ARG_229	NH1	I_GLU_256	OE2	2.592
5J3D	I_ARG_229	NH2	I_GLU_256	OE1	2.607
5J3D	I_ARG_229	NH2	I_GLU_256	OE2	2.843
5J3D	I_ARG_235	NH1	K_GLU_232	OE1	3.110
5J3D	I_ARG_235	NH1	K_GLU_232	OE2	2.664
5J3D	I_LYS_272	NZ	D_ASP_56	OD2	3.795
5J3D	I_LYS_293	NZ	I_GLU_295	OE2	3.743
5J3D	I_ARG_336	NH2	I_ASP_338	OD1	3.080
5J3D	I_ARG_336	NH2	I_ASP_338	OD2	3.543
5J3D	I_ARG_364	NH1	I_ASP_310	OD1	3.192
5J3D	I_ARG_364	NH2	I_ASP_310	OD1	2.780
5J3D	I_LYS_399	NZ	F_ASP_392	OD1	3.746
5J3D	I_LYS_470	NZ	E_GLU_60	OE1	3.634
5J3D	I_LYS_470	NZ	E_GLU_60	OE2	3.872
5J3D	J_ARG_49	NH2	K_ASP_368	OD1	3.049
5J3D	J_ARG_49	NH2	K_ASP_368	OD2	3.898
5J3D	J_LYS_80	NZ	J_ASP_84	OD2	3.423

5J3D	J_LYS_85	NZ	J_GLU_82	OE1	3.982
5J3D	J_LYS_85	NZ	J_GLU_82	OE2	3.902
5J3D	J_LYS_87	NZ	K_GLU_294	OE1	3.791
5J3D	K_LYS_	NZ	F_GLU_	OE1	2.905
5J3D	K_LYS_	NZ	K_GLU_	OE1	3.429
5J3D	K_LYS_191	NZ	K_ASP_194	OD2	3.194
5J3D	K_LYS_196	NZ	F_ASP_489	OD1	2.822
5J3D	K_LYS_196	NZ	F_ASP_489	OD2	3.022
5J3D	K_LYS_201	NZ	K_ASP_200	OD2	2.845
5J3D	K_ARG_229	NH1	K_GLU_256	OE1	3.743
5J3D	K_ARG_229	NH1	K_GLU_256	OE2	2.813
5J3D	K_ARG_229	NH2	K_GLU_256	OE1	2.714
5J3D	K_ARG_229	NH2	K_GLU_256	OE2	3.345
5J3D	K_ARG_235	NH1	F_GLU_232	OE1	2.445
5J3D	K_ARG_235	NH1	F_GLU_232	OE2	2.683
5J3D	K_ARG_235	NH2	F_GLU_232	OE2	3.814
5J3D	K_ARG_235	NH2	K_GLU_232	OE2	3.561
5J3D	K_LYS_293	NZ	K_GLU_295	OE2	3.880
5J3D	K_ARG_336	NH2	K_ASP_338	OD1	2.871
5J3D	K_ARG_336	NH2	K_ASP_338	OD2	3.213
5J3D	K_LYS_359	NZ	K_GLU_356	OE2	3.629
5J3D	K_ARG_364	NH1	K_ASP_310	OD1	3.298
5J3D	K_ARG_364	NH2	K_ASP_310	OD1	2.637
5J3D	K_ARG_364	NH2	K_ASP_310	OD2	3.766
5J3D	K_LYS_399	NZ	L_ASP_392	OD1	3.598
5J3D	K_LYS_470	NZ	G_GLU_60	OE1	3.953
5J3D	L_ARG_75	NH2	L_ASP_97	OD2	3.011
5J3D	L_LYS_123	NZ	L_GLU_185	OE2	3.382
5J3D	L_LYS_169	NZ	L_GLU_215	OE2	3.052
5J3D	L_LYS_203	NZ	L_GLU_207	OE1	3.556
5J3D	L_LYS_203	NZ	L_GLU_207	OE2	2.397
5J3D	L_HIS_209	ND1	L_ASP_171	OD2	2.293

Table 678: 5J3D-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5JO5	H_ARG_38	NH1	H_ASP_86	OD1	2.872
5JO5	H_ARG_38	NH2	H_GLU_46	OE1	3.137
5JO5	H_ARG_38	NH2	H_ASP_86	OD1	3.899
5JO5	H_ARG_50	NH1	H_ASP_58	OD2	3.272
5JO5	H_ARG_50	NH1	H_GLU_100J	OE1	3.655
5JO5	H_ARG_50	NH1	H_GLU_100J	OE2	3.015
5JO5	H_ARG_50	NH2	H_ASP_58	OD2	2.837
5JO5	H_ARG_66	NH1	H_ASP_86	OD1	3.782
5JO5	H_ARG_66	NH1	H_ASP_86	OD2	2.781
5JO5	H_ARG_66	NH2	H_ASP_86	OD1	3.036
5JO5	H_ARG_66	NH2	H_ASP_86	OD2	3.534
5JO5	H_ARG_71	NH2	H_ASP_73	OD1	3.590
5JO5	H_LYS_75	NZ	H_ASP_72	OD2	3.855
5JO5	H_ARG_94	NH1	H_ASP_102	OD2	2.698
5JO5	H_LYS_143	NZ	L_GLU_124	OE2	2.459
5JO5	H_LYS_206	NZ	H_ASP_208	OD1	3.914
5JO5	H_LYS_206	NZ	H_ASP_208	OD2	3.240
5JO5	H_LYS_209	NZ	L_GLU_	OE2	2.531
5JO5	L_ARG_61	NH2	L_GLU_81	OE2	2.979
5JO5	L_ARG_61	NH2	L_ASP_82	OD1	2.750
5JO5	L_ARG_61	NH2	L_ASP_82	OD2	3.466
5JO5	L_ARG_91	NH1	H_GLU_100J	OE2	3.301
5JO5	L_ARG_91	NH2	H_GLU_100J	OE2	2.691
5JO5	L_ARG_95B	NH2	H_ASP_58	OD1	3.439
5JO5	L_LYS_110	NZ	L_GLU_198	OE1	2.940
5JO5	L_LYS_149	NZ	L_GLU_203	OE2	3.049
5JO5	A_ARG_38	NH1	A_ASP_86	OD1	2.834
5JO5	A_ARG_38	NH2	A_GLU_46	OE1	3.010
5JO5	A_ARG_38	NH2	A_ASP_86	OD1	3.868
5JO5	A_ARG_50	NH1	A_ASP_58	OD2	3.242
5JO5	A_ARG_50	NH1	A_GLU_100J	OE1	3.684
5JO5	A_ARG_50	NH1	A_GLU_100J	OE2	2.906
5JO5	A_ARG_50	NH2	A_ASP_58	OD2	2.882
5JO5	A_ARG_66	NH1	A_ASP_86	OD1	3.892
5JO5	A_ARG_66	NH1	A_ASP_86	OD2	2.803
5JO5	A_ARG_66	NH2	A_ASP_86	OD1	3.001
5JO5	A_ARG_66	NH2	A_ASP_86	OD2	3.402
5JO5	A_ARG_71	NH2	A_ASP_73	OD1	3.562
5JO5	A_ARG_94	NH1	A_ASP_102	OD2	2.584
5JO5	A_LYS_143	NZ	B_GLU_124	OE2	2.618
5JO5	A_LYS_209	NZ	B_GLU_123	OE2	2.545
5JO5	A_ARG_210	NH1	A_GLU_212	OE2	3.723
5JO5	A_ARG_210	NH2	A_GLU_212	OE2	3.222
5JO5	B_ARG_61	NH2	B_GLU_81	OE2	3.302
5JO5	B_ARG_61	NH2	B_ASP_82	OD1	2.664
5JO5	B_ARG_61	NH2	B_ASP_82	OD2	3.454
5JO5	B_ARG_91	NH1	A_GLU_100J	OE2	3.353
5JO5	B_ARG_91	NH2	A_GLU_100J	OE2	3.038
5JO5	C_ARG_38	NH1	C_ASP_86	OD1	2.847
5JO5	C_ARG_38	NH2	C_GLU_46	OE1	3.028
5JO5	C_ARG_38	NH2	C_ASP_86	OD1	3.875
5JO5	C_ARG_50	NH1	C_ASP_58	OD2	2.775
5JO5	C_ARG_50	NH2	C_ASP_58	OD2	3.216
5JO5	C_ARG_50	NH2	C_GLU_100J	OE1	3.640
5JO5	C_ARG_50	NH2	C_GLU_100J	OE2	2.862
5JO5	C_ARG_66	NH1	C_ASP_86	OD1	3.889
5JO5	C_ARG_66	NH1	C_ASP_86	OD2	2.829

5JO5	C_ARG_66	NH2	C_ASP_86	OD1	3.094
5JO5	C_ARG_66	NH2	C_ASP_86	OD2	3.488
5JO5	C_ARG_71	NH2	C_ASP_73	OD1	3.622
5JO5	C_ARG_94	NH1	C_ASP_102	OD2	2.554
5JO5	C_LYS_143	NZ	D_GLU_124	OE2	2.788
5JO5	C_LYS_209	NZ	D_GLU_123	OE2	2.583
5JO5	C_ARG_	NH1	C_GLU_	OE2	2.988
5JO5	D_ARG_61	NH2	D_ASP_82	OD1	2.885
5JO5	D_ARG_61	NH2	D_ASP_82	OD2	3.652
5JO5	D_ARG_91	NH1	C_GLU_100J	OE2	3.302
5JO5	D_ARG_91	NH2	C_GLU_100J	OE2	3.077
5JO5	D_LYS_93	NZ	D_GLU_3	OE2	3.062
5JO5	D_ARG_95B	NH2	C_ASP_58	OD1	3.978
5JO5	D_LYS_149	NZ	D_GLU_203	OE2	2.721
5JO5	D_HIS_188	ND1	D_ASP_151	OD2	2.674
5JO5	E_ARG_38	NH1	E_ASP_86	OD1	2.821
5JO5	E_ARG_38	NH2	E_GLU_46	OE1	3.015
5JO5	E_ARG_38	NH2	E_GLU_46	OE2	3.976
5JO5	E_ARG_38	NH2	E_ASP_86	OD1	3.922
5JO5	E_ARG_50	NH1	E_ASP_58	OD2	2.782
5JO5	E_ARG_50	NH2	E_ASP_58	OD2	3.264
5JO5	E_ARG_50	NH2	E_GLU_100J	OE1	3.626
5JO5	E_ARG_50	NH2	E_GLU_100J	OE2	2.982
5JO5	E_ARG_66	NH1	E_ASP_86	OD1	3.801
5JO5	E_ARG_66	NH1	E_ASP_86	OD2	2.750
5JO5	E_ARG_66	NH2	E_ASP_86	OD1	3.037
5JO5	E_ARG_66	NH2	E_ASP_86	OD2	3.493
5JO5	E_ARG_71	NH2	E_ASP_73	OD1	3.535
5JO5	E_LYS_75	NZ	E_ASP_72	OD2	3.717
5JO5	E_ARG_94	NH2	E_ASP_102	OD2	2.730
5JO5	E_LYS_143	NZ	F_GLU_124	OE2	2.545
5JO5	E_LYS_209	NZ	F_GLU_123	OE2	2.567
5JO5	E_ARG_210	NH1	E_GLU_212	OE2	3.744
5JO5	E_ARG_210	NH2	E_GLU_212	OE2	3.125
5JO5	F_ARG_54	NH1	F_ASP_60	OD1	2.423
5JO5	F_ARG_61	NH2	F_GLU_81	OE2	3.010
5JO5	F_ARG_61	NH2	F_ASP_82	OD1	2.807
5JO5	F_ARG_61	NH2	F_ASP_82	OD2	3.560
5JO5	F_ARG_91	NH1	E_GLU_100J	OE2	3.369
5JO5	F_ARG_91	NH2	E_GLU_100J	OE2	2.722
5JO5	F_ARG_95B	NH2	E_ASP_58	OD1	3.518
5JO5	F_LYS_110	NZ	F_GLU_198	OE1	2.973

Table 679: 5JO5-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5JOF	H_LYS_12	NZ	H_GLU_10	OE1	3.976
5JOF	H_ARG_38	NH1	H_ASP_86	OD1	2.816
5JOF	H_ARG_38	NH2	H_GLU_46	OE1	2.389
5JOF	H_ARG_38	NH2	H_GLU_46	OE2	3.859
5JOF	H_LYS_62	NZ	H_GLU_46	OE2	2.776
5JOF	H_ARG_66	NH1	H_ASP_86	OD2	2.820
5JOF	H_ARG_66	NH2	H_ASP_86	OD1	3.127
5JOF	H_ARG_66	NH2	H_ASP_86	OD2	3.314
5JOF	H_LYS_212	NZ	L_GLU_123	OE2	3.883
5JOF	H_LYS_213	NZ	H_GLU_215	OE1	3.500
5JOF	H_LYS_217	NZ	L_ASP_122	OD2	3.165
5JOF	L_ARG_54	NH1	L_ASP_60	OD1	3.764
5JOF	L_ARG_61	NH2	L_GLU_81	OE2	3.643
5JOF	L_ARG_61	NH2	L_ASP_82	OD1	3.848
5JOF	L_ARG_61	NH2	L_ASP_82	OD2	3.642
5JOF	L_ARG_142	NH1	L_GLU_103	OE1	3.845
5JOF	L_ARG_142	NH1	L_GLU_105	OE2	3.937
5JOF	L_ARG_142	NH2	L_GLU_103	OE1	3.654
5JOF	L_ARG_142	NH2	L_GLU_103	OE2	2.697
5JOF	L_ARG_142	NH2	L_GLU_105	OE2	3.736
5JOF	L_LYS_149	NZ	L_GLU_195	OE1	3.071
5JOF	A_LYS_12	NZ	A_GLU_10	OE1	3.516
5JOF	A_HIS_35	NE2	A_ASP_100C	OD1	2.627
5JOF	A_ARG_38	NH1	A_GLU_46	OE1	3.912
5JOF	A_ARG_38	NH1	A_ASP_86	OD1	3.722
5JOF	A_ARG_38	NH2	A_ASP_86	OD1	2.667
5JOF	A_ARG_66	NH1	A_ASP_86	OD1	2.903
5JOF	A_ARG_66	NH1	A_ASP_86	OD2	2.899
5JOF	A_ARG_83	NH2	A_ASP_85	OD2	3.607
5JOF	A_LYS_143	NZ	A_ASP_144	OD1	3.485
5JOF	A_LYS_209	NZ	B_GLU_123	OE1	3.449
5JOF	A_LYS_209	NZ	B_GLU_123	OE2	3.809
5JOF	B_ARG_24	NH1	C_ASP_99	OD1	2.692
5JOF	B_ARG_24	NH1	C_ASP_99	OD2	3.960
5JOF	B_ARG_61	NH2	B_GLU_81	OE2	3.500
5JOF	B_ARG_61	NH2	B_ASP_82	OD1	3.535
5JOF	B_ARG_61	NH2	B_ASP_82	OD2	3.507
5JOF	B_ARG_77	NH1	B_GLU_79	OE1	3.191
5JOF	B_ARG_77	NH1	B_GLU_79	OE2	3.717
5JOF	B_HIS_189	ND1	B_ASP_151	OD2	2.926
5JOF	C_LYS_12	NZ	C_GLU_10	OE1	3.233
5JOF	C_HIS_35	NE2	C_ASP_100C	OD1	2.684
5JOF	C_ARG_38	NH1	C_ASP_86	OD1	3.621
5JOF	C_ARG_38	NH2	C_GLU_46	OE1	3.694
5JOF	C_ARG_38	NH2	C_ASP_86	OD1	3.344
5JOF	C_LYS_62	NZ	C_GLU_46	OE1	3.985
5JOF	C_LYS_62	NZ	C_GLU_46	OE2	3.097
5JOF	C_ARG_66	NH1	C_ASP_86	OD1	3.730
5JOF	C_ARG_66	NH1	C_ASP_86	OD2	2.579
5JOF	C_ARG_94	NH1	B_GLU_1	OE2	2.653
5JOF	C_ARG_94	NH2	B_GLU_1	OE2	3.195
5JOF	C_LYS_210	NZ	C_GLU_212	OE1	3.967
5JOF	C_LYS_214	NZ	D_ASP_122	OD2	3.772
5JOF	C_LYS_214	NZ	D_GLU_123	OE1	2.987
5JOF	C_LYS_214	NZ	D_GLU_123	OE2	3.631
5JOF	D_ARG_24	NH2	D_ASP_70	OD2	3.929
5JOF	D_LYS_39	NZ	D_GLU_81	OE2	3.210

5JOF	D_ARG_54	NH1	D_ASP_60	OD1	3.417
5JOF	D_ARG_54	NH2	D_ASP_60	OD1	2.714
5JOF	D_ARG_61	NH1	D_GLU_79	OE1	3.968
5JOF	D_ARG_61	NH2	D_GLU_79	OE1	3.623
5JOF	D_ARG_61	NH2	D_ASP_82	OD1	3.619
5JOF	D_LYS_149	NZ	D_GLU_195	OE1	3.879
5JOF	D_LYS_183	NZ	D_GLU_187	OE1	3.559
5JOF	D_ARG_211	NH2	D_GLU_187	OE2	3.871
5JOF	E_HIS_35	NE2	E_ASP_100C	OD1	3.045
5JOF	E_ARG_38	NH1	E_ASP_86	OD1	2.429
5JOF	E_ARG_38	NH2	E_GLU_46	OE1	3.439
5JOF	E_ARG_38	NH2	E_ASP_86	OD1	3.968
5JOF	E_LYS_62	NZ	E_GLU_46	OE1	3.849
5JOF	E_LYS_62	NZ	E_GLU_46	OE2	3.146
5JOF	E_ARG_66	NH1	E_ASP_86	OD1	3.702
5JOF	E_ARG_66	NH1	E_ASP_86	OD2	2.671
5JOF	E_LYS_209	NZ	F_GLU_123	OE1	2.331
5JOF	E_LYS_209	NZ	F_GLU_123	OE2	3.588
5JOF	E_LYS_214	NZ	F_ASP_122	OD2	3.802
5JOF	F_ARG_54	NH1	F_ASP_60	OD1	2.591
5JOF	F_ARG_61	NH1	F_ASP_82	OD1	2.348
5JOF	F_ARG_61	NH1	F_ASP_82	OD2	1.974
5JOF	F_ARG_61	NH2	F_ASP_82	OD1	3.989
5JOF	F_LYS_149	NZ	F_GLU_195	OE1	2.606
5JOF	F_LYS_183	NZ	F_GLU_187	OE1	3.917
5JOF	F_LYS_183	NZ	F_GLU_187	OE2	3.217

Table 680: 5JOF-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5JR1	H_ARG_38	NH1	H_ASP_86	OD1	2.944
5JR1	H_ARG_38	NH2	H_GLU_46	OE2	2.675
5JR1	H_ARG_38	NH2	H_ASP_86	OD1	3.952
5JR1	H_ARG_50	NH1	H_GLU_100J	OE1	3.342
5JR1	H_ARG_50	NH1	H_GLU_100J	OE2	3.375
5JR1	H_ARG_50	NH2	H_GLU_100J	OE1	3.986
5JR1	H_LYS_52	NZ	H_ASP_53	OD1	2.855
5JR1	H_ARG_66	NH1	H_ASP_86	OD1	3.760
5JR1	H_ARG_66	NH1	H_ASP_86	OD2	2.716
5JR1	H_ARG_66	NH2	H_ASP_86	OD1	3.157
5JR1	H_ARG_66	NH2	H_ASP_86	OD2	3.593
5JR1	H_ARG_71	NH2	H_ASP_73	OD1	3.546
5JR1	H_ARG_94	NH1	H_ASP_102	OD2	2.955
5JR1	H_LYS_143	NZ	H_ASP_144	OD1	3.485
5JR1	H_LYS_143	NZ	H_ASP_144	OD2	2.637
5JR1	H_HIS_164	NE2	L_ASP_139	OD1	3.232
5JR1	H_HIS_164	NE2	L_ASP_139	OD2	3.168
5JR1	H_LYS_206	NZ	H_ASP_208	OD1	2.690
5JR1	L_HIS_31	ND1	H_ASP_100	OD2	3.496
5JR1	L_HIS_31	ND1	H_GLU_100I	OE2	3.149
5JR1	L_ARG_61	NH2	L_GLU_81	OE2	3.044
5JR1	L_ARG_61	NH2	L_ASP_82	OD1	2.738
5JR1	L_ARG_61	NH2	L_ASP_82	OD2	3.536
5JR1	L_ARG_95B	NH1	H_ASP_58	OD1	3.367
5JR1	L_ARG_95B	NH1	H_ASP_58	OD2	3.787
5JR1	L_ARG_95B	NH2	H_ASP_58	OD1	3.502
5JR1	L_ARG_95B	NH2	H_ASP_58	OD2	2.474
5JR1	L_LYS_110	NZ	L_GLU_199	OE1	2.769
5JR1	L_HIS_189	ND1	L_ASP_152	OD2	3.281

Table 681: 5JR1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5JUE	L_ARG_61	NH1	L_ASP_82	OD1	2.841
5JUE	L_ARG_61	NH1	L_ASP_82	OD2	3.261
5JUE	L_ARG_61	NH2	L_ASP_82	OD1	3.675
5JUE	L_ARG_61	NH2	L_ASP_82	OD2	2.578
5JUE	L_LYS_103	NZ	L_ASP_165	OD1	3.155
5JUE	L_LYS_147	NZ	L_GLU_154	OE1	3.955
5JUE	L_LYS_149	NZ	L_GLU_195	OE1	3.435
5JUE	L_LYS_149	NZ	L_GLU_195	OE2	2.940
5JUE	L_ARG_155	NH1	L_GLU_185	OE1	2.977
5JUE	L_ARG_155	NH1	L_GLU_185	OE2	3.732
5JUE	L_ARG_155	NH2	L_GLU_185	OE1	3.822
5JUE	L_ARG_155	NH2	L_GLU_185	OE2	3.203
5JUE	L_ARG_188	NH2	L_ASP_184	OD1	3.007
5JUE	L_ARG_188	NH2	L_ASP_184	OD2	3.926
5JUE	L_HIS_189	ND1	L_ASP_151	OD2	2.628
5JUE	L_LYS_199	NZ	L_ASP_110	OD1	3.968
5JUE	L_LYS_199	NZ	L_ASP_110	OD2	3.647
5JUE	H_LYS_66	NZ	H_ASP_86	OD1	3.729
5JUE	H_LYS_66	NZ	H_ASP_86	OD2	2.761
5JUE	H_ARG_94	NH2	H_ASP_101	OD1	3.685
5JUE	H_ARG_94	NH2	H_ASP_101	OD2	2.851
5JUE	H_LYS_208	NZ	L_GLU_123	OE1	2.809
5JUE	H_LYS_208	NZ	L_GLU_123	OE2	2.812
5JUE	H_LYS_209	NZ	H_GLU_211	OE1	3.891

Table 682: 5JUE-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5JXA	H_ARG_38	NH1	H_ASP_86	OD1	2.740
5JXA	H_ARG_38	NH2	H_GLU_46	OE1	2.757
5JXA	H_ARG_38	NH2	H_ASP_86	OD1	3.580
5JXA	H_ARG_66	NH1	H_ASP_86	OD1	3.702
5JXA	H_ARG_66	NH1	H_ASP_86	OD2	3.100
5JXA	H_ARG_66	NH2	H_ASP_86	OD1	2.964
5JXA	H_ARG_66	NH2	H_ASP_86	OD2	3.681
5JXA	H_ARG_95	NH1	H_ASP_99	OD1	3.572
5JXA	H_ARG_95	NH2	H_ASP_99	OD1	2.948
5JXA	H_LYS_143	NZ	H_ASP_144	OD1	2.917
5JXA	H_LYS_143	NZ	H_ASP_144	OD2	3.163
5JXA	H_LYS_209	NZ	L_GLU_123	OE1	3.277
5JXA	H_LYS_210	NZ	H_GLU_212	OE1	2.675
5JXA	H_LYS_210	NZ	H_GLU_212	OE2	3.292
5JXA	H_LYS_214	NZ	L_ASP_122	OD1	2.755
5JXA	H_LYS_214	NZ	L_ASP_122	OD2	3.275
5JXA	L_LYS_24	NZ	L_ASP_70	OD1	2.561
5JXA	L_LYS_24	NZ	L_ASP_70	OD2	3.785
5JXA	L_ARG_39	NH2	L_GLU_81	OE1	3.801
5JXA	L_ARG_61	NH2	L_ASP_82	OD1	2.836
5JXA	L_ARG_61	NH2	L_ASP_82	OD2	3.523
5JXA	L_ARG_142	NH1	L_GLU_103	OE1	2.871
5JXA	L_ARG_142	NH1	L_GLU_103	OE2	3.755
5JXA	L_ARG_142	NH2	L_GLU_103	OE1	3.345
5JXA	L_ARG_142	NH2	L_GLU_103	OE2	2.786
5JXA	L_ARG_142	NH2	L_GLU_105	OE2	3.779
5JXA	L_LYS_149	NZ	L_GLU_195	OE2	3.064
5JXA	L_LYS_188	NZ	L_ASP_185	OD1	2.848
5JXA	L_HIS_189	ND1	L_ASP_151	OD2	3.368

Table 683: 5JXA-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5KZP	H_HIS_35	NE2	H_ASP_99	OD2	2.522
5KZP	H_ARG_38	NH1	H_ASP_90	OD1	2.873
5KZP	H_ARG_38	NH2	H_GLU_46	OE1	3.219
5KZP	H_ARG_38	NH2	H_GLU_46	OE2	3.666
5KZP	H_ARG_38	NH2	H_ASP_90	OD1	3.689
5KZP	H_ARG_65	NH1	H_ASP_62	OD1	2.911
5KZP	H_ARG_65	NH2	H_ASP_62	OD1	2.885
5KZP	H_ARG_67	NH1	H_ASP_90	OD1	3.700
5KZP	H_ARG_67	NH1	H_ASP_90	OD2	2.484
5KZP	H_ARG_67	NH2	H_ASP_90	OD1	2.918
5KZP	H_ARG_67	NH2	H_ASP_90	OD2	3.301
5KZP	H_ARG_98	NH2	H_ASP_111	OD1	3.703
5KZP	H_ARG_98	NH2	H_ASP_111	OD2	2.809
5KZP	H_LYS_153	NZ	H_ASP_154	OD1	3.314
5KZP	H_LYS_153	NZ	H_ASP_154	OD2	3.555
5KZP	H_LYS_224	NZ	L_ASP_122	OD2	3.852
5KZP	L_ARG_61	NH1	L_GLU_79	OE1	3.104
5KZP	L_ARG_61	NH1	L_GLU_79	OE2	3.279
5KZP	L_ARG_61	NH2	L_GLU_79	OE2	3.588
5KZP	L_ARG_61	NH2	L_GLU_81	OE1	3.551
5KZP	L_ARG_61	NH2	L_ASP_82	OD1	2.835
5KZP	L_ARG_61	NH2	L_ASP_82	OD2	3.395
5KZP	L_ARG_103	NH1	L_GLU_105	OE1	3.734
5KZP	L_ARG_103	NH2	L_GLU_105	OE1	3.962
5KZP	L_LYS_149	NZ	L_GLU_195	OE1	3.543
5KZP	L_LYS_183	NZ	L_GLU_187	OE2	3.769
5KZP	E_HIS_35	NE2	E_ASP_99	OD2	2.563
5KZP	E_ARG_38	NH1	E_ASP_90	OD1	3.683
5KZP	E_ARG_65	NH1	E_ASP_62	OD1	2.341
5KZP	E_ARG_65	NH2	E_ASP_62	OD1	2.619
5KZP	E_ARG_65	NH2	K_GLU_1	OE2	3.580
5KZP	E_ARG_98	NH2	E_ASP_111	OD1	3.416
5KZP	E_ARG_98	NH2	E_ASP_111	OD2	2.790
5KZP	E_LYS_153	NZ	E_ASP_154	OD1	2.756
5KZP	E_LYS_153	NZ	E_ASP_154	OD2	2.951
5KZP	E_LYS_219	NZ	L_GLU_123	OE1	2.944
5KZP	E_LYS_219	NZ	L_GLU_123	OE2	2.510
5KZP	L_ARG_24	NH1	L_ASP_70	OD1	3.891
5KZP	L_ARG_24	NH1	L_ASP_70	OD2	3.598
5KZP	L_ARG_61	NH2	L_GLU_81	OE1	3.907
5KZP	L_ARG_61	NH2	L_ASP_82	OD1	2.991
5KZP	L_ARG_61	NH2	L_ASP_82	OD2	3.614
5KZP	L_HIS_189	ND1	L_ASP_185	OD1	3.770
5KZP	F_HIS_35	NE2	F_ASP_99	OD2	2.631
5KZP	F_ARG_38	NH1	F_ASP_90	OD1	2.940
5KZP	F_ARG_38	NH2	F_GLU_46	OE1	2.834
5KZP	F_ARG_38	NH2	F_GLU_46	OE2	3.617
5KZP	F_ARG_65	NH1	F_ASP_62	OD1	2.904
5KZP	F_ARG_65	NH2	F_ASP_62	OD1	2.941
5KZP	F_ARG_67	NH1	F_ASP_90	OD1	3.792
5KZP	F_ARG_67	NH1	F_ASP_90	OD2	2.747
5KZP	F_ARG_67	NH2	F_ASP_90	OD1	3.178
5KZP	F_ARG_67	NH2	F_ASP_90	OD2	3.633
5KZP	F_ARG_98	NH2	F_ASP_111	OD1	3.568
5KZP	F_ARG_98	NH2	F_ASP_111	OD2	2.783
5KZP	F_LYS_139	NZ	J_GLU_213	OE2	2.615
5KZP	F_LYS_153	NZ	F_ASP_154	OD2	3.275

5KZP	J_ARG_61	NH2	J_GLU_81	OE1	3.789
5KZP	J_ARG_61	NH2	J_ASP_82	OD1	2.791
5KZP	J_ARG_61	NH2	J_ASP_82	OD2	3.369
5KZP	J_ARG_211	NH1	J_GLU_187	OE1	3.757
5KZP	J_ARG_211	NH2	J_GLU_187	OE1	3.382
5KZP	G_HIS_35	NE2	G_ASP_99	OD2	3.393
5KZP	G_ARG_38	NH1	G_ASP_90	OD1	3.839
5KZP	G_ARG_38	NH2	G_GLU_46	OE1	3.198
5KZP	G_ARG_38	NH2	G_GLU_46	OE2	3.193
5KZP	G_ARG_65	NH2	G_ASP_62	OD1	3.015
5KZP	G_ARG_67	NH1	G_ASP_90	OD2	3.513
5KZP	G_LYS_87	NZ	G_GLU_89	OE1	2.242
5KZP	G_LYS_87	NZ	G_GLU_89	OE2	3.284
5KZP	G_ARG_98	NH2	G_ASP_111	OD1	3.923
5KZP	G_ARG_98	NH2	G_ASP_111	OD2	3.052
5KZP	G_LYS_153	NZ	G_ASP_154	OD1	2.784
5KZP	G_LYS_153	NZ	G_ASP_154	OD2	3.265
5KZP	G_LYS_219	NZ	K_GLU_123	OE2	3.381
5KZP	G_LYS_220	NZ	G_GLU_222	OE1	3.746
5KZP	G_LYS_220	NZ	G_GLU_222	OE2	2.332
5KZP	K_ARG_24	NH2	K_ASP_70	OD1	2.089
5KZP	K_ARG_24	NH2	K_ASP_70	OD2	3.470
5KZP	K_ARG_61	NH2	K_GLU_81	OE1	3.540
5KZP	K_ARG_61	NH2	K_ASP_82	OD1	2.863
5KZP	K_ARG_61	NH2	K_ASP_82	OD2	3.407
5KZP	K_ARG_103	NH1	K_GLU_105	OE2	3.064
5KZP	K_HIS_189	ND1	K_ASP_185	OD1	3.899
5KZP	K_ARG_211	NH1	K_GLU_187	OE2	3.000
5KZP	K_ARG_211	NH2	K_GLU_187	OE2	3.195

Table 684: 5KZP-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5LDN	A_ARG.72	NH2	A_ASP.74	OD1	3.403
5LDN	A_ARG.72	NH2	A_ASP.74	OD2	3.634
5LDN	A_LYS.80	NZ	A_ASP.71	OD2	3.125
5LDN	A_LYS.80	NZ	A_GLU.73	OE1	3.933
5LDN	A_LYS.80	NZ	A_GLU.73	OE2	2.939
5LDN	A_LYS.80	NZ	A_GLU.581	OE1	2.882
5LDN	A_ARG.82	NH1	A_ASP.71	OD2	3.811
5LDN	A_ARG.82	NH1	A_GLU.581	OE1	2.442
5LDN	A_ARG.82	NH2	A_GLU.581	OE1	3.951
5LDN	A_LYS.193	NZ	A_GLU.188	OE2	3.913
5LDN	A_ARG.221	NH2	A_GLU.288	OE1	2.862
5LDN	A_ARG.221	NH2	A_GLU.288	OE2	3.399
5LDN	A_LYS.225	NZ	A_ASP.135	OD1	3.401
5LDN	A_LYS.225	NZ	A_ASP.135	OD2	3.221
5LDN	A_LYS.238	NZ	A_ASP.291	OD2	3.266
5LDN	A_LYS.238	NZ	A_GLU.293	OE2	3.311
5LDN	A_ARG.311	NH2	A_GLU.136	OE1	3.150
5LDN	A_ARG.311	NH2	A_GLU.136	OE2	3.587
5LDN	A_ARG.363	NH1	A_ASP.359	OD1	3.274
5LDN	A_ARG.363	NH2	A_ASP.923	OD1	2.881
5LDN	A_ARG.363	NH2	A_ASP.923	OD2	3.367
5LDN	A_ARG.379	NH1	A_ASP.330	OD1	3.918
5LDN	A_ARG.379	NH1	A_ASP.330	OD2	3.115
5LDN	A_ARG.379	NH2	A_ASP.330	OD1	2.861
5LDN	A_ARG.379	NH2	A_ASP.330	OD2	3.485
5LDN	A_ARG.398	NH2	A_ASP.866	OD1	2.806
5LDN	A_ARG.398	NH2	A_ASP.866	OD2	3.196
5LDN	A_HIS.403	NE2	A_GLU.401	OE1	3.143
5LDN	A_LYS.440	NZ	A_ASP.447	OD2	3.777
5LDN	A_LYS.483	NZ	A_ASP.910	OD2	3.275
5LDN	A_LYS.505	NZ	A_ASP.501	OD1	3.131
5LDN	A_LYS.505	NZ	A_ASP.501	OD2	3.450
5LDN	A_ARG.506	NH2	A_ASP.482	OD1	3.756
5LDN	A_ARG.506	NH2	A_ASP.482	OD2	3.168
5LDN	A_ARG.522	NH2	A_GLU.401	OE2	3.872
5LDN	A_ARG.538	NH1	A_ASP.394	OD2	3.250
5LDN	A_ARG.545	NH2	A_ASP.391	OD1	2.660
5LDN	A_ARG.545	NH2	A_ASP.391	OD2	3.895
5LDN	A_ARG.553	NH1	A_ASP.107	OD1	3.270
5LDN	A_ARG.553	NH1	A_ASP.107	OD2	3.176
5LDN	A_HIS.558	NE2	A_ASP.101	OD1	3.369
5LDN	A_HIS.558	NE2	A_ASP.101	OD2	2.749
5LDN	A_LYS.564	NZ	A_GLU.366	OE1	2.705
5LDN	A_LYS.586	NZ	A_ASP.74	OD2	3.049
5LDN	A_ARG.601	NH1	A_ASP.587	OD1	3.101
5LDN	A_ARG.601	NH1	A_ASP.587	OD2	2.666
5LDN	A_ARG.634	NH2	A_GLU.630	OE2	3.382
5LDN	A_ARG.675	NH1	A_GLU.920	OE2	3.980
5LDN	A_ARG.675	NH2	A_GLU.920	OE2	3.771
5LDN	A_LYS.683	NZ	A_GLU.911	OE1	2.897
5LDN	A_LYS.719	NZ	A_GLU.741	OE1	3.754
5LDN	A_LYS.719	NZ	A_GLU.741	OE2	3.492
5LDN	A_LYS.745	NZ	A_ASP.907	OD1	3.711
5LDN	A_LYS.745	NZ	A_ASP.907	OD2	2.722
5LDN	A_ARG.746	NH1	A_GLU.743	OE1	2.687
5LDN	A_ARG.746	NH1	A_GLU.743	OE2	2.969
5LDN	A_ARG.802	NH1	A_ASP.526	OD2	3.579

5LDN	A_LYS_862	NZ	A_ASP_526	OD1	2.598
5LDN	A_LYS_862	NZ	A_ASP_529	OD1	3.751
5LDN	A_LYS_862	NZ	A_ASP_529	OD2	2.683
5LDN	A_ARG_871	NH1	A_GLU_920	OE2	3.400
5LDN	A_HIS_898	ND1	A_ASP_725	OD1	3.639
5LDN	A_HIS_898	ND1	A_ASP_725	OD2	2.775
5LDN	A_ARG_926	NH2	A_ASP_639	OD2	3.350
5LDN	A_HIS_928	ND1	A_ASP_639	OD1	2.832
5LDN	A_HIS_928	ND1	A_ASP_639	OD2	3.728
5LDN	A_HIS_928	NE2	A_ASP_636	OD2	3.490
5LDN	A_ARG_932	NH1	A_ASP_89	OD2	3.407
5LDN	A_ARG_932	NH2	A_ASP_89	OD1	3.679
5LDN	A_ARG_932	NH2	A_ASP_89	OD2	2.766
5LDN	A_ARG_932	NH2	A_GLU_630	OE1	3.434
5LDN	A_ARG_932	NH2	A_GLU_630	OE2	3.081
5LDN	A_ARG_941	NH1	A_ASP_362	OD1	3.367
5LDN	A_ARG_941	NH1	A_ASP_362	OD2	3.176
5LDN	A_ARG_941	NH2	A_ASP_362	OD1	3.000
5LDN	A_ARG_941	NH2	A_ASP_362	OD2	3.971
5LDN	L_LYS_44	NZ	L_ASP_90	OD1	2.996
5LDN	L_ARG_81	NH1	L_ASP_102	OD1	3.268
5LDN	L_ARG_81	NH1	L_ASP_102	OD2	2.452
5LDN	L_ARG_81	NH2	L_ASP_102	OD1	3.517
5LDN	L_ARG_	NH1	L_GLU_	OE1	3.301
5LDN	L_ARG_	NH2	L_GLU_	OE1	3.915
5LDN	L_ARG_	NH1	L_GLU_	OE2	3.234
5LDN	L_HIS_	ND1	L_ASP_	OD1	3.989
5LDN	L_HIS_	ND1	L_ASP_	OD2	2.838
5LDN	H_ARG_37	NH1	H_ASP_88	OD1	2.969
5LDN	H_ARG_37	NH2	H_GLU_45	OE2	3.151
5LDN	H_ARG_65	NH1	H_ASP_88	OD1	3.733
5LDN	H_ARG_65	NH1	H_ASP_	OD2	3.243
5LDN	H_ARG_65	NH2	H_ASP_88	OD1	2.798
5LDN	H_ARG_65	NH2	H_ASP_	OD2	3.381
5LDN	H_LYS_70	NZ	H_ASP_72	OD2	3.198
5LDN	H_ARG_	NH1	H_ASP_	OD1	3.345
5LDN	H_ARG_	NH2	H_ASP_	OD1	3.435
5LDN	H_LYS_	NZ	L_GLU_	OE1	3.019

Table 685: 5LDN-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5M2C	A_LYS_124	NZ	A_ASP_195	OD1	2.994
5M2C	A_LYS_124	NZ	A_ASP_195	OD2	3.852
5M2C	A_LYS_144	NZ	A_ASP_138	OD1	2.840
5M2C	A_LYS_171	NZ	A_ASP_138	OD1	3.119
5M2C	A_LYS_187	NZ	A_ASP_155	OD1	3.762
5M2C	A_LYS_187	NZ	A_ASP_155	OD2	3.179
5M2C	A_HIS_191	NE2	A_ASP_128	OD1	3.269
5M2C	A_HIS_191	NE2	A_ASP_128	OD2	2.695
5M2C	B_LYS_124	NZ	B_ASP_195	OD1	3.117
5M2C	B_LYS_124	NZ	B_ASP_195	OD2	3.775
5M2C	B_LYS_144	NZ	B_ASP_138	OD1	2.798
5M2C	B_LYS_171	NZ	B_ASP_138	OD1	3.131
5M2C	B_LYS_187	NZ	B_ASP_155	OD1	3.683
5M2C	B_LYS_187	NZ	B_ASP_155	OD2	3.174
5M2C	B_HIS_191	NE2	B_ASP_128	OD1	3.220
5M2C	B_HIS_191	NE2	B_ASP_128	OD2	2.713

Table 686: 5M2C-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5M33	A_LYS_124	NZ	A_ASP_195	OD1	2.806
5M33	A_LYS_124	NZ	A_ASP_195	OD2	3.061
5M33	A_LYS_187	NZ	A_ASP_155	OD1	2.820
5M33	A_HIS_191	NE2	A_ASP_128	OD1	3.390
5M33	A_HIS_191	NE2	A_ASP_128	OD2	2.760
5M33	A_LYS_193	NZ	A_GLU_188	OE1	2.934
5M33	B_LYS_124	NZ	B_ASP_195	OD1	3.243
5M33	B_LYS_124	NZ	B_ASP_195	OD2	2.646
5M33	B_HIS_191	NE2	B_ASP_128	OD1	3.361
5M33	B_HIS_191	NE2	B_ASP_128	OD2	2.690

Table 687: 5M33-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5M3D	A_LYS_116	NZ	A_ASP_117	OD1	3.826
5M3D	A_LYS_124	NZ	A_ASP_195	OD1	3.095
5M3D	A_LYS_124	NZ	A_ASP_195	OD2	2.681
5M3D	A_LYS_144	NZ	A_ASP_138	OD1	3.722
5M3D	A_LYS_148	NZ	A_GLU_152	OE2	2.745
5M3D	A_LYS_187	NZ	A_ASP_155	OD2	2.929
5M3D	A_HIS_191	NE2	A_ASP_128	OD1	3.275
5M3D	A_HIS_191	NE2	A_ASP_128	OD2	2.681
5M3D	A_LYS_201	NZ	A_ASP_196	OD1	3.448
5M3D	B_LYS_116	NZ	B_ASP_117	OD1	3.148
5M3D	B_LYS_124	NZ	B_ASP_195	OD1	2.979
5M3D	B_LYS_124	NZ	B_ASP_195	OD2	2.591
5M3D	B_LYS_144	NZ	B_ASP_138	OD1	3.668
5M3D	B_LYS_148	NZ	B_GLU_152	OE2	2.496
5M3D	B_LYS_187	NZ	B_ASP_155	OD2	3.090
5M3D	B_HIS_191	NE2	B_ASP_128	OD1	3.349
5M3D	B_HIS_191	NE2	B_ASP_128	OD2	2.596
5M3D	C_LYS_124	NZ	C_ASP_195	OD1	2.934
5M3D	C_LYS_124	NZ	C_ASP_195	OD2	3.127
5M3D	C_LYS_148	NZ	C_GLU_152	OE2	2.588
5M3D	C_LYS_171	NZ	C_ASP_137	OD1	3.243
5M3D	C_LYS_171	NZ	C_ASP_137	OD2	3.458
5M3D	C_LYS_187	NZ	C_ASP_155	OD2	3.290
5M3D	C_HIS_191	NE2	C_ASP_128	OD1	3.231
5M3D	C_HIS_191	NE2	C_ASP_128	OD2	2.539
5M3D	D_LYS_124	NZ	D_ASP_195	OD1	3.141
5M3D	D_LYS_124	NZ	D_ASP_195	OD2	3.445
5M3D	D_LYS_148	NZ	D_GLU_152	OE1	3.259
5M3D	D_LYS_171	NZ	D_ASP_137	OD1	2.423
5M3D	D_LYS_171	NZ	D_ASP_137	OD2	3.425
5M3D	D_LYS_187	NZ	D_ASP_155	OD2	3.128
5M3D	D_HIS_191	NE2	D_ASP_128	OD1	3.228
5M3D	D_HIS_191	NE2	D_ASP_128	OD2	2.528

Table 688: 5M3D-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5M3T	A_LYS_124	NZ	A_ASP_195	OD1	3.045
5M3T	A_LYS_124	NZ	A_ASP_195	OD2	3.381
5M3T	A_LYS_144	NZ	A_ASP_137	OD1	3.126
5M3T	A_HIS_191	NE2	A_ASP_128	OD1	2.701
5M3T	A_HIS_191	NE2	A_ASP_128	OD2	3.351
5M3T	B_LYS_116	NZ	B_ASP_117	OD1	3.281
5M3T	B_LYS_124	NZ	B_ASP_195	OD1	2.763
5M3T	B_LYS_124	NZ	B_ASP_195	OD2	2.942
5M3T	B_LYS_144	NZ	B_ASP_138	OD1	2.688
5M3T	B_LYS_144	NZ	B_ASP_138	OD2	3.938
5M3T	B_LYS_148	NZ	B_GLU_152	OE2	3.571
5M3T	B_LYS_187	NZ	B_ASP_155	OD1	3.212
5M3T	B_HIS_191	NE2	B_ASP_128	OD1	2.761
5M3T	B_HIS_191	NE2	B_ASP_128	OD2	3.127

Table 689: 5M3T-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5M4R	A_LYS_124	NZ	A_ASP_195	OD1	3.169
5M4R	A_LYS_124	NZ	A_ASP_195	OD2	3.633
5M4R	A_LYS_171	NZ	A_ASP_138	OD1	2.609
5M4R	A_LYS_187	NZ	A_ASP_155	OD2	3.101
5M4R	A_HIS_191	NE2	A_ASP_128	OD1	3.374
5M4R	A_HIS_191	NE2	A_ASP_128	OD2	2.535
5M4R	B_LYS_124	NZ	B_ASP_195	OD1	3.161
5M4R	B_LYS_124	NZ	B_ASP_195	OD2	3.629
5M4R	B_LYS_144	NZ	B_ASP_138	OD1	2.408
5M4R	B_LYS_187	NZ	B_ASP_155	OD1	3.374
5M4R	B_HIS_191	NE2	B_ASP_128	OD1	3.385
5M4R	B_HIS_191	NE2	B_ASP_128	OD2	2.546
5M4R	C_LYS_124	NZ	C_ASP_195	OD1	3.153
5M4R	C_LYS_124	NZ	C_ASP_195	OD2	3.571
5M4R	C_LYS_171	NZ	C_ASP_138	OD1	3.210
5M4R	C_LYS_187	NZ	C_ASP_155	OD1	3.818
5M4R	C_HIS_191	NE2	C_ASP_128	OD1	3.374
5M4R	C_HIS_191	NE2	C_ASP_128	OD2	2.549
5M4R	D_LYS_124	NZ	D_ASP_195	OD1	3.169
5M4R	D_LYS_124	NZ	D_ASP_195	OD2	3.626
5M4R	D_LYS_187	NZ	D_ASP_155	OD1	3.733
5M4R	D_LYS_187	NZ	D_ASP_155	OD2	3.658
5M4R	D_HIS_191	NE2	D_ASP_128	OD1	3.367
5M4R	D_HIS_191	NE2	D_ASP_128	OD2	2.515
5M4R	E_LYS_124	NZ	E_ASP_195	OD1	3.158
5M4R	E_LYS_124	NZ	E_ASP_195	OD2	3.599
5M4R	E_LYS_144	NZ	E_ASP_137	OD2	3.235
5M4R	E_LYS_187	NZ	E_ASP_155	OD1	3.706
5M4R	E_HIS_191	NE2	E_ASP_128	OD1	3.375
5M4R	E_HIS_191	NE2	E_ASP_128	OD2	2.532
5M4R	E_LYS_201	NZ	E_ASP_196	OD1	3.587

Table 690: 5M4R-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5MO9	H_HIS_35	NE2	H_GLU_33	OE1	3.220
5MO9	H_HIS_43	NE2	H_GLU_89	OE1	3.753
5MO9	H_LYS_63	NZ	H_GLU_46	OE1	3.930
5MO9	H_LYS_63	NZ	H_GLU_46	OE2	3.238
5MO9	H_LYS_67	NZ	H_ASP_90	OD1	3.821
5MO9	H_LYS_67	NZ	H_ASP_90	OD2	2.804
5MO9	H_ARG_84	NH1	H_GLU_82	OE1	3.999
5MO9	H_ARG_84	NH1	H_GLU_82	OE2	3.132
5MO9	H_LYS_146	NZ	H_ASP_147	OD1	3.365
5MO9	H_LYS_146	NZ	H_ASP_147	OD2	3.626
5MO9	H_LYS_212	NZ	L_GLU_128	OE2	3.509
5MO9	H_LYS_213	NZ	H_GLU_215	OE2	3.368
5MO9	L_LYS_44	NZ	L_GLU_86	OE2	3.853
5MO9	L_LYS_55	NZ	X_GLU_371	OE2	2.811
5MO9	L_ARG_59	NH1	L_ASP_65	OD1	3.142
5MO9	L_ARG_66	NH1	L_ASP_87	OD1	3.324
5MO9	L_ARG_66	NH1	L_ASP_87	OD2	2.775
5MO9	L_ARG_66	NH2	L_ASP_87	OD1	2.980
5MO9	L_ARG_66	NH2	L_ASP_87	OD2	3.846
5MO9	L_LYS_108	NZ	L_GLU_170	OE2	3.379
5MO9	L_LYS_154	NZ	L_GLU_200	OE2	3.767
5MO9	X_HIS_343	NE2	X_GLU_341	OE2	3.960
5MO9	X_LYS_364	NZ	H_GLU_33	OE2	2.799
5MO9	X_LYS_364	NZ	H_ASP_52	OD1	3.966
5MO9	X_LYS_369	NZ	X_GLU_371	OE1	3.611
5MO9	X_LYS_372	NZ	X_ASP_370	OD1	3.437

Table 691: 5MO9-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5N2B	A_LYS_82	NZ	A_ASP_144	OD1	3.469

Table 692: 5N2B-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5N4J	L_ARG_38	NH1	H_ASP_100	OD1	2.794
5N4J	L_ARG_38	NH1	H_ASP_100	OD2	3.589
5N4J	L_ARG_60	NH2	L_ASP_66	OD1	3.938
5N4J	L_ARG_67	NH2	L_GLU_87	OE2	2.853
5N4J	L_ARG_67	NH2	L_ASP_88	OD1	2.770
5N4J	L_ARG_67	NH2	L_ASP_88	OD2	3.658
5N4J	L_LYS_174	NZ	L_GLU_89	OE2	2.818
5N4J	H_LYS_11	NZ	H_GLU_9	OE1	3.995
5N4J	H_ARG_37	NH1	H_ASP_89	OD1	2.887
5N4J	H_ARG_37	NH2	H_GLU_45	OE1	3.779
5N4J	H_ARG_37	NH2	H_GLU_45	OE2	3.178
5N4J	H_ARG_37	NH2	H_ASP_89	OD1	3.973
5N4J	H_LYS_62	NZ	H_GLU_45	OE1	2.843
5N4J	H_LYS_62	NZ	H_GLU_45	OE2	3.909
5N4J	H_ARG_66	NH1	H_ASP_89	OD1	3.808
5N4J	H_ARG_66	NH1	H_ASP_89	OD2	2.928
5N4J	H_ARG_66	NH2	H_ASP_89	OD1	2.878
5N4J	H_ARG_66	NH2	H_ASP_89	OD2	3.415
5N4J	H_ARG_83	NH1	H_GLU_81	OE1	2.921
5N4J	H_ARG_86	NH2	H_ASP_88	OD1	3.231
5N4J	H_ARG_86	NH2	H_ASP_88	OD2	2.601
5N4J	H_ARG_97	NH2	H_ASP_102	OD1	3.488
5N4J	H_ARG_97	NH2	H_ASP_102	OD2	2.852
5N4J	H_LYS_210	NZ	L_GLU_131	OE1	2.936
5N4J	H_LYS_210	NZ	L_GLU_131	OE2	3.282
5N4J	H_ARG_211	NH1	H_GLU_213	OE2	3.986

Table 693: 5N4J-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5N7B	H_ARG_38	NH1	H_ASP_92	OD1	2.899
5N7B	H_ARG_38	NH2	H_GLU_46	OE1	3.245
5N7B	H_ARG_38	NH2	H_GLU_46	OE2	3.600
5N7B	H_ARG_38	NH2	H_ASP_92	OD1	3.935
5N7B	H_LYS_43	NZ	H_GLU_46	OE1	3.841
5N7B	H_LYS_43	NZ	H_GLU_91	OE1	3.761
5N7B	H_ARG_52	NH1	H_GLU_50	OE2	2.676
5N7B	H_ARG_69	NH1	H_ASP_92	OD1	3.313
5N7B	H_ARG_69	NH1	H_ASP_92	OD2	3.638
5N7B	H_ARG_69	NH2	H_ASP_92	OD1	3.498
5N7B	H_ARG_69	NH2	H_ASP_92	OD2	2.337
5N7B	H_ARG_74	NH2	H_ASP_76	OD1	3.523
5N7B	H_ARG_89	NH1	H_GLU_91	OE2	3.715
5N7B	H_HIS_1051	ND1	H_GLU_1047	OE2	2.925
5N7B	H_HIS_1051	NE2	H_ASP_1050	OD1	3.871
5N7B	H_ARG_1070	NH2	H_GLU_1090	OE2	3.894
5N7B	H_ARG_1070	NH2	H_ASP_1091	OD1	2.787
5N7B	H_ARG_1070	NH2	H_ASP_1091	OD2	3.671

Table 694: 5N7B-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5N7W	A_LYS_12	NZ	A_GLU_10	OE1	3.956
5N7W	A_ARG_38	NH1	A_ASP_90	OD1	2.843
5N7W	A_ARG_38	NH2	A_GLU_46	OE1	3.305
5N7W	A_ARG_38	NH2	A_ASP_90	OD1	3.827
5N7W	A_LYS_63	NZ	A_GLU_46	OE1	3.619
5N7W	A_LYS_63	NZ	A_GLU_46	OE2	2.845
5N7W	A_ARG_67	NH1	A_ASP_90	OD1	3.584
5N7W	A_ARG_67	NH1	A_ASP_90	OD2	2.765
5N7W	A_ARG_67	NH2	A_ASP_90	OD1	2.880
5N7W	A_ARG_67	NH2	A_ASP_90	OD2	3.520
5N7W	A_ARG_98	NH2	A_ASP_107	OD1	3.757
5N7W	A_ARG_98	NH2	A_ASP_107	OD2	2.848
5N7W	A_LYS_149	NZ	B_GLU_126	OE2	2.961
5N7W	A_LYS_215	NZ	B_GLU_125	OE1	2.755
5N7W	A_LYS_215	NZ	B_GLU_125	OE2	3.335
5N7W	B_LYS_39	NZ	B_GLU_81	OE2	3.652
5N7W	B_ARG_61	NH2	B_ASP_82	OD1	2.909
5N7W	B_ARG_61	NH2	B_ASP_82	OD2	3.717
5N7W	B_HIS_190	ND1	B_ASP_153	OD2	2.856
5N7W	H_LYS_12	NZ	H_GLU_10	OE1	3.973
5N7W	H_ARG_38	NH1	H_ASP_90	OD1	2.822
5N7W	H_ARG_38	NH2	H_GLU_46	OE1	3.307
5N7W	H_ARG_38	NH2	H_ASP_90	OD1	3.828
5N7W	H_LYS_63	NZ	H_GLU_46	OE1	3.613
5N7W	H_LYS_63	NZ	H_GLU_46	OE2	2.860
5N7W	H_ARG_67	NH1	H_ASP_90	OD1	3.649
5N7W	H_ARG_67	NH1	H_ASP_90	OD2	2.788
5N7W	H_ARG_67	NH2	H_ASP_90	OD1	2.914
5N7W	H_ARG_67	NH2	H_ASP_90	OD2	3.510
5N7W	H_ARG_98	NH2	H_ASP_107	OD1	3.723
5N7W	H_ARG_98	NH2	H_ASP_107	OD2	2.808
5N7W	H_LYS_149	NZ	L_GLU_126	OE2	2.605
5N7W	H_ARG_216	NH2	H_GLU_218	OE2	2.838
5N7W	L_LYS_39	NZ	L_GLU_81	OE1	3.895
5N7W	L_ARG_61	NH1	L_GLU_81	OE2	3.879
5N7W	L_ARG_61	NH2	L_GLU_81	OE2	3.018
5N7W	L_ARG_61	NH2	L_ASP_82	OD1	2.869
5N7W	L_ARG_61	NH2	L_ASP_82	OD2	3.688
5N7W	X_HIS_54	NE2	X_GLU_68	OE1	3.783
5N7W	X_ARG_55	NH1	X_GLU_57	OE2	2.811
5N7W	X_ARG_55	NH2	X_GLU_57	OE2	2.683
5N7W	X_ARG_100	NH1	X_ASP_58	OD1	3.676
5N7W	X_ARG_100	NH1	X_ASP_58	OD2	3.093
5N7W	X_ARG_100	NH2	X_ASP_58	OD2	2.743
5N7W	X_ARG_100	NH2	X_GLU_113	OE2	3.977
5N7W	X_ARG_101	NH2	X_GLU_60	OE1	3.293
5N7W	X_ARG_101	NH2	X_GLU_60	OE2	3.261
5N7W	X_HIS_105	NE2	X_GLU_60	OE1	3.956
5N7W	X_HIS_105	NE2	X_GLU_60	OE2	4.000
5N7W	X_ARG_111	NH2	X_GLU_102	OE1	3.583
5N7W	Y_ARG_46	NH1	Y_ASP_42	OD2	2.678
5N7W	Y_ARG_55	NH2	Y_GLU_57	OE2	2.650
5N7W	Y_ARG_100	NH1	Y_ASP_58	OD1	3.688
5N7W	Y_ARG_100	NH1	Y_ASP_58	OD2	3.136
5N7W	Y_ARG_100	NH2	Y_ASP_58	OD2	2.751
5N7W	Y_ARG_100	NH2	Y_GLU_113	OE1	3.830
5N7W	Y_ARG_101	NH2	Y_GLU_60	OE1	3.497

5N7W	Y_ARG_101	NH2	Y_GLU_60	OE2	3.078
5N7W	Y_HIS_105	NE2	Y_GLU_60	OE1	3.784
5N7W	Y_HIS_105	NE2	Y_GLU_60	OE2	3.473
5N7W	Y_ARG_111	NH2	Y_GLU_102	OE1	3.366

Table 695: 5N7W-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5N88	H_ARG_38	NH1	H_ASP_90	OD1	2.861
5N88	H_ARG_38	NH2	H_GLU_46	OE1	2.966
5N88	H_ARG_38	NH2	H_GLU_46	OE2	3.874
5N88	H_ARG_38	NH2	H_ASP_90	OD1	3.775
5N88	H_ARG_53	NH2	H_ASP_105	OD1	3.754
5N88	H_ARG_53	NH2	H_ASP_105	OD2	2.841
5N88	H_LYS_65	NZ	H_ASP_62	OD1	2.674
5N88	H_ARG_67	NH1	H_ASP_90	OD1	3.790
5N88	H_ARG_67	NH1	H_ASP_90	OD2	2.789
5N88	H_ARG_67	NH2	H_ASP_90	OD1	3.111
5N88	H_ARG_67	NH2	H_ASP_90	OD2	3.597
5N88	H_ARG_98	NH2	H_ASP_115	OD1	3.514
5N88	H_ARG_98	NH2	H_ASP_115	OD2	2.816
5N88	D_ARG_351	NH2	D_GLU_379	OE1	2.947
5N88	D_ARG_354	NH1	D_GLU_379	OE1	3.813
5N88	D_ARG_354	NH2	D_GLU_358	OE1	3.788
5N88	D_ARG_354	NH2	D_GLU_358	OE2	3.296
5N88	D_ARG_354	NH2	D_GLU_379	OE1	3.408
5N88	D_ARG_354	NH2	D_GLU_379	OE2	2.654
5N88	D_ARG_372	NH1	D_ASP_369	OD2	3.104
5N88	D_LYS_392	NZ	D_ASP_349	OD1	3.585
5N88	D_LYS_392	NZ	D_ASP_349	OD2	3.429
5N88	D_HIS_393	NE2	D_ASP_349	OD1	2.893
5N88	D_LYS_415	NZ	D_ASP_378	OD1	2.913
5N88	A_ARG_38	NH1	A_ASP_90	OD1	2.946
5N88	A_ARG_38	NH2	A_GLU_46	OE1	2.784
5N88	A_ARG_38	NH2	A_ASP_90	OD1	3.960
5N88	A_LYS_65	NZ	A_ASP_62	OD1	2.935
5N88	A_ARG_67	NH1	A_ASP_90	OD1	3.771
5N88	A_ARG_67	NH1	A_ASP_90	OD2	2.724
5N88	A_ARG_67	NH2	A_ASP_90	OD1	3.229
5N88	A_ARG_67	NH2	A_ASP_90	OD2	3.677
5N88	A_LYS_76	NZ	A_ASP_73	OD2	3.426
5N88	A_ARG_87	NH1	A_GLU_89	OE1	3.467
5N88	A_ARG_87	NH2	A_GLU_89	OE1	3.356
5N88	A_ARG_98	NH2	A_ASP_115	OD1	3.457
5N88	A_ARG_98	NH2	A_ASP_115	OD2	3.121
5N88	E_ARG_372	NH2	E_GLU_358	OE1	2.751
5N88	E_ARG_372	NH2	E_GLU_358	OE2	3.550
5N88	E_LYS_392	NZ	E_ASP_349	OD1	2.862
5N88	E_LYS_392	NZ	E_ASP_349	OD2	3.023
5N88	E_HIS_393	NE2	E_ASP_349	OD1	3.833
5N88	E_LYS_415	NZ	E_ASP_378	OD1	2.913
5N88	E_LYS_415	NZ	E_ASP_378	OD2	3.971

Table 696: 5N88-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5NPH	H.LYS_63	NZ	H.GLU_46	OE1	2.774
5NPH	H.LYS_63	NZ	H.GLU_46	OE2	3.824
5NPH	H.LYS_67	NZ	H.ASP_90	OD1	3.768
5NPH	H.LYS_67	NZ	H.ASP_90	OD2	2.830
5NPH	H.ARG_84	NH2	H.GLU_82	OE2	2.962
5NPH	H.ARG_98	NH2	H.ASP_108	OD1	3.726
5NPH	H.ARG_98	NH2	H.ASP_108	OD2	2.829
5NPH	H.LYS_215	NZ	L.GLU_123	OE2	2.787
5NPH	L.ARG_61	NH2	L.GLU_81	OE1	2.810
5NPH	L.ARG_61	NH2	L.ASP_82	OD1	2.818
5NPH	L.ARG_61	NH2	L.ASP_82	OD2	3.582
5NPH	L.LYS_93	NZ	A.GLU_533	OE1	3.679
5NPH	L.LYS_149	NZ	L.GLU_195	OE1	3.660
5NPH	L.HIS_189	ND1	L.ASP_151	OD2	3.036
5NPH	L.LYS_199	NZ	L.ASP_110	OD2	2.799

Table 697: 5NPH-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5NPI	A_LYS_63	NZ	A_GLU_46	OE1	2.778
5NPI	A_LYS_63	NZ	A_GLU_46	OE2	3.947
5NPI	A_LYS_67	NZ	A_ASP_90	OD1	3.854
5NPI	A_LYS_67	NZ	A_ASP_90	OD2	2.867
5NPI	A_ARG_98	NH2	A_ASP_108	OD1	3.690
5NPI	A_ARG_98	NH2	A_ASP_108	OD2	2.811
5NPI	A_HIS_181	NE2	B_GLU_10	OE1	3.570
5NPI	A_HIS_181	NE2	B_GLU_10	OE2	3.750
5NPI	A_ARG_201	NH2	A_GLU_221	OE1	2.818
5NPI	A_ARG_201	NH2	A_ASP_222	OD1	2.795
5NPI	A_ARG_201	NH2	A_ASP_222	OD2	3.637
5NPI	A_LYS_243	NZ	A_GLU_245	OE1	3.089
5NPI	B_LYS_63	NZ	B_GLU_46	OE1	2.773
5NPI	B_LYS_63	NZ	B_GLU_46	OE2	3.955
5NPI	B_LYS_67	NZ	B_ASP_90	OD1	3.936
5NPI	B_LYS_67	NZ	B_ASP_90	OD2	2.892
5NPI	B_ARG_98	NH2	B_ASP_108	OD1	3.701
5NPI	B_ARG_98	NH2	B_ASP_108	OD2	2.749
5NPI	B_HIS_181	NE2	A_GLU_10	OE1	3.757
5NPI	B_HIS_181	NE2	A_GLU_10	OE2	3.882
5NPI	B_ARG_201	NH2	B_GLU_221	OE1	2.813
5NPI	B_ARG_201	NH2	B_ASP_222	OD1	2.796
5NPI	B_ARG_201	NH2	B_ASP_222	OD2	3.658
5NPI	B_LYS_233	NZ	E_GLU_533	OE1	3.924
5NPI	B_LYS_243	NZ	B_GLU_245	OE1	3.090

Table 698: 5NPI-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5NPJ	A_LYS_63	NZ	A_GLU_46	OE1	2.799
5NPJ	A_LYS_67	NZ	A_ASP_90	OD1	3.867
5NPJ	A_LYS_67	NZ	A_ASP_90	OD2	2.954
5NPJ	A_ARG_98	NH2	A_ASP_108	OD1	3.695
5NPJ	A_ARG_98	NH2	A_ASP_108	OD2	2.771
5NPJ	A_HIS_181	NE2	B_GLU_10	OE1	3.540
5NPJ	A_HIS_181	NE2	B_GLU_10	OE2	3.793
5NPJ	A_ARG_201	NH2	A_GLU_221	OE1	2.812
5NPJ	A_ARG_201	NH2	A_ASP_222	OD1	2.769
5NPJ	A_ARG_201	NH2	A_ASP_222	OD2	3.614
5NPJ	A_LYS_243	NZ	A_GLU_245	OE1	2.814
5NPJ	B_LYS_63	NZ	B_GLU_46	OE1	2.797
5NPJ	B_LYS_67	NZ	B_ASP_90	OD1	3.887
5NPJ	B_LYS_67	NZ	B_ASP_90	OD2	2.961
5NPJ	B_ARG_98	NH2	B_ASP_108	OD1	3.704
5NPJ	B_ARG_98	NH2	B_ASP_108	OD2	2.768
5NPJ	B_HIS_181	NE2	A_GLU_10	OE1	3.734
5NPJ	B_HIS_181	NE2	A_GLU_10	OE2	3.967
5NPJ	B_ARG_201	NH2	B_GLU_221	OE1	2.825
5NPJ	B_ARG_201	NH2	B_ASP_222	OD1	2.760
5NPJ	B_ARG_201	NH2	B_ASP_222	OD2	3.648
5NPJ	B_LYS_243	NZ	B_GLU_245	OE1	2.926

Table 699: 5NPJ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5NST	A_ARG_39	NH1	C_GLU_81	OE1	3.260
5NST	A_ARG_39	NH1	C_GLU_81	OE2	3.263
5NST	A_ARG_39	NH2	C_GLU_81	OE1	3.038
5NST	A_ARG_61	NH1	A_ASP_82	OD1	3.453
5NST	A_ARG_61	NH1	A_ASP_82	OD2	2.620
5NST	A_ARG_61	NH2	A_ASP_82	OD1	3.456
5NST	A_ARG_61	NH2	A_ASP_82	OD2	3.977
5NST	A_LYS_147	NZ	A_GLU_195	OE2	3.805
5NST	A_LYS_149	NZ	A_GLU_195	OE1	3.194
5NST	A_LYS_149	NZ	A_GLU_195	OE2	3.752
5NST	A_ARG_155	NH1	A_GLU_185	OE2	3.200
5NST	A_ARG_155	NH2	A_GLU_185	OE2	2.920
5NST	A_HIS_189	ND1	A_ASP_151	OD2	3.206
5NST	A_LYS_199	NZ	A_ASP_110	OD1	3.008
5NST	A_LYS_199	NZ	A_ASP_110	OD2	3.591
5NST	B_ARG_33	NH2	B_ASP_27	OD1	3.734
5NST	B_ARG_33	NH2	B_ASP_27	OD2	3.892
5NST	B_ARG_39	NH1	B_ASP_90	OD1	3.041
5NST	B_ARG_39	NH2	B_GLU_47	OE1	3.114
5NST	B_ARG_39	NH2	B_ASP_90	OD1	3.726
5NST	B_HIS_53	NE2	B_GLU_51	OE2	3.083
5NST	B_ARG_67	NH1	B_ASP_90	OD1	3.015
5NST	B_ARG_67	NH1	B_ASP_90	OD2	2.796
5NST	B_ARG_67	NH2	B_ASP_90	OD1	3.245
5NST	B_LYS_76	NZ	B_ASP_73	OD2	2.807
5NST	B_ARG_98	NH1	B_ASP_27	OD2	2.918
5NST	B_ARG_98	NH2	B_ASP_238	OD1	3.501
5NST	B_ARG_98	NH2	B_ASP_238	OD2	2.970
5NST	B_LYS_103	NZ	B_ASP_233	OD1	2.837
5NST	B_ARG_112	NH1	B_ASP_198	OD1	3.483
5NST	B_ARG_112	NH1	B_ASP_198	OD2	3.324
5NST	B_ARG_112	NH2	B_ASP_198	OD1	3.105
5NST	B_ARG_134	NH1	B_GLU_167	OE1	3.225
5NST	B_ARG_143	NH2	B_ASP_154	OD1	3.483
5NST	B_ARG_143	NH2	B_ASP_154	OD2	3.145
5NST	B_ARG_169	NH1	B_GLU_118	OE1	3.192
5NST	B_ARG_169	NH2	B_GLU_167	OE2	3.020
5NST	B_ARG_171	NH1	B_ASP_173	OD1	2.814
5NST	B_ARG_171	NH2	B_ASP_173	OD1	3.985
5NST	B_ARG_184	NH2	B_GLU_145	OE1	3.999
5NST	B_LYS_345	NZ	A_GLU_123	OE1	3.069
5NST	C_ARG_24	NH2	C_ASP_70	OD2	2.795
5NST	C_ARG_39	NH1	A_GLU_81	OE1	3.247
5NST	C_ARG_39	NH1	A_GLU_81	OE2	3.139
5NST	C_ARG_39	NH2	A_GLU_81	OE1	3.004
5NST	C_ARG_61	NH2	C_GLU_81	OE2	3.339
5NST	C_ARG_61	NH2	C_ASP_82	OD1	2.949
5NST	C_ARG_61	NH2	C_ASP_82	OD2	3.501
5NST	C_ARG_103	NH1	C_ASP_165	OD1	3.414
5NST	C_LYS_147	NZ	C_GLU_195	OE2	3.756
5NST	C_LYS_149	NZ	C_GLU_195	OE1	3.043
5NST	C_LYS_149	NZ	C_GLU_195	OE2	3.450
5NST	C_ARG_188	NH1	C_ASP_151	OD2	2.746
5NST	C_ARG_188	NH2	C_GLU_187	OE1	2.814
5NST	C_LYS_199	NZ	C_ASP_110	OD1	3.560
5NST	C_LYS_199	NZ	C_ASP_110	OD2	3.855
5NST	D_ARG_33	NH2	D_ASP_27	OD2	3.973

5NST	D_ARG_39	NH1	D_ASP_90	OD1	3.042
5NST	D_ARG_39	NH2	D_GLU_47	OE1	3.103
5NST	D_ARG_39	NH2	D_ASP_90	OD1	3.721
5NST	D_HIS_53	NE2	D_GLU_51	OE2	2.781
5NST	D_ARG_67	NH1	D_ASP_90	OD1	2.697
5NST	D_ARG_67	NH1	D_ASP_90	OD2	3.158
5NST	D_LYS_76	NZ	D_ASP_73	OD2	2.790
5NST	D_LYS_82	NZ	D_ASP_84	OD2	3.904
5NST	D_ARG_98	NH1	D_ASP_27	OD2	2.885
5NST	D_ARG_98	NH2	D_ASP_238	OD1	3.522
5NST	D_ARG_98	NH2	D_ASP_238	OD2	2.972
5NST	D_LYS_103	NZ	D_ASP_233	OD1	3.094
5NST	D_LYS_103	NZ	D_ASP_233	OD2	3.059
5NST	D_ARG_112	NH1	D_ASP_198	OD1	3.172
5NST	D_ARG_112	NH1	D_ASP_198	OD2	3.063
5NST	D_ARG_112	NH2	D_ASP_198	OD1	2.909
5NST	D_ARG_134	NH1	D_GLU_165	OE1	3.890
5NST	D_ARG_134	NH1	D_GLU_167	OE1	3.201
5NST	D_ARG_143	NH2	D_ASP_154	OD1	3.487
5NST	D_ARG_143	NH2	D_ASP_154	OD2	3.164
5NST	D_ARG_169	NH1	D_GLU_118	OE1	3.163
5NST	D_ARG_169	NH2	D_GLU_167	OE2	3.007
5NST	D_ARG_171	NH1	D_ASP_173	OD1	2.813
5NST	D_ARG_171	NH2	D_ASP_173	OD1	3.989
5NST	D_LYS_345	NZ	C_GLU_123	OE2	3.272

Table 700: 5NST-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5NUZ	A_LYS_66	NZ	A_ASP_86	OD1	3.693
5NUZ	A_LYS_66	NZ	A_ASP_86	OD2	2.849
5NUZ	A_ARG_94	NH2	A_ASP_101	OD1	3.574
5NUZ	A_ARG_94	NH2	A_ASP_101	OD2	2.713
5NUZ	A_ARG_95	NH1	C_ASP_114	OD1	3.502
5NUZ	A_ARG_95	NH1	C_ASP_114	OD2	2.701
5NUZ	A_ARG_95	NH2	A_ASP_100A	OD2	3.027
5NUZ	A_ARG_95	NH2	C_ASP_114	OD1	2.822
5NUZ	A_ARG_95	NH2	C_ASP_114	OD2	3.585
5NUZ	A_LYS_208	NZ	B_GLU_123	OE1	3.889
5NUZ	A_LYS_208	NZ	B_GLU_123	OE2	2.684
5NUZ	H_LYS_66	NZ	H_ASP_86	OD1	3.692
5NUZ	H_LYS_66	NZ	H_ASP_86	OD2	2.845
5NUZ	H_ARG_94	NH2	H_ASP_101	OD1	3.585
5NUZ	H_ARG_94	NH2	H_ASP_101	OD2	2.715
5NUZ	H_ARG_95	NH1	D_ASP_114	OD1	3.679
5NUZ	H_ARG_95	NH1	D_ASP_114	OD2	2.753
5NUZ	H_ARG_95	NH2	H_ASP_100A	OD2	3.002
5NUZ	H_ARG_95	NH2	D_ASP_114	OD1	2.850
5NUZ	H_ARG_95	NH2	D_ASP_114	OD2	3.470
5NUZ	H_LYS_208	NZ	L_GLU_123	OE2	2.982
5NUZ	B_ARG_24	NH1	B_ASP_70	OD1	3.493
5NUZ	B_ARG_24	NH1	B_ASP_70	OD2	3.358
5NUZ	B_ARG_61	NH1	B_ASP_81	OD1	3.247
5NUZ	B_ARG_61	NH1	B_ASP_82	OD1	2.766
5NUZ	B_ARG_61	NH1	B_ASP_82	OD2	3.636
5NUZ	B_ARG_61	NH2	L_GLU_79	OE1	3.072
5NUZ	B_ARG_61	NH2	L_GLU_79	OE2	3.676
5NUZ	B_LYS_92	NZ	B_GLU_93	OE2	2.758
5NUZ	B_LYS_103	NZ	B_GLU_105	OE2	3.588
5NUZ	B_LYS_142	NZ	B_GLU_105	OE1	3.907
5NUZ	B_LYS_142	NZ	B_GLU_105	OE2	2.608
5NUZ	B_LYS_147	NZ	B_GLU_195	OE1	3.572
5NUZ	B_LYS_149	NZ	B_GLU_195	OE2	3.615
5NUZ	B_ARG_155	NH1	B_GLU_185	OE1	3.558
5NUZ	B_ARG_155	NH1	B_GLU_185	OE2	3.557
5NUZ	B_ARG_155	NH2	B_GLU_185	OE2	2.757
5NUZ	B_ARG_188	NH1	B_GLU_185	OE1	3.922
5NUZ	B_HIS_189	ND1	B_ASP_151	OD2	3.016
5NUZ	B_LYS_199	NZ	B_ASP_110	OD2	3.082
5NUZ	C_LYS_181	NZ	C_GLU_186	OE1	3.275
5NUZ	C_LYS_191	NZ	C_ASP_159	OD1	3.275
5NUZ	C_LYS_191	NZ	C_ASP_159	OD2	2.624
5NUZ	C_LYS_193	NZ	C_ASP_205	OD2	3.554
5NUZ	C_LYS_211	NZ	A_ASP_54	OD1	3.758
5NUZ	C_LYS_211	NZ	A_ASP_54	OD2	3.058
5NUZ	C_LYS_211	NZ	A_ASP_56	OD2	2.861
5NUZ	C_LYS_216	NZ	C_ASP_113	OD1	2.638
5NUZ	L_ARG_61	NH1	L_ASP_82	OD1	2.773
5NUZ	L_ARG_61	NH1	L_ASP_82	OD2	3.655
5NUZ	L_ARG_61	NH2	B_GLU_79	OE1	3.765
5NUZ	L_ARG_61	NH2	B_GLU_79	OE2	2.966
5NUZ	L_LYS_92	NZ	L_GLU_93	OE2	2.743
5NUZ	L_LYS_103	NZ	L_GLU_105	OE2	3.583
5NUZ	L_LYS_142	NZ	L_GLU_105	OE1	3.968
5NUZ	L_LYS_142	NZ	L_GLU_105	OE2	2.583
5NUZ	L_LYS_149	NZ	L_GLU_195	OE2	3.652

5NUZ	L_ARG_155	NH1	L_GLU_185	OE1	3.502
5NUZ	L_ARG_155	NH1	L_GLU_185	OE2	3.552
5NUZ	L_ARG_155	NH2	L_GLU_185	OE2	2.742
5NUZ	L_LYS_183	NZ	L_GLU_187	OE2	3.902
5NUZ	L_HIS_189	ND1	L_ASP_151	OD2	3.012
5NUZ	L_LYS_199	NZ	L_ASP_110	OD2	3.059
5NUZ	D_LYS_169	NZ	D_GLU_171	OE1	3.996
5NUZ	D_LYS_181	NZ	D_ASP_205	OD2	3.184
5NUZ	D_LYS_190	NZ	D_GLU_186	OE2	3.856
5NUZ	D_LYS_191	NZ	D_ASP_159	OD1	3.278
5NUZ	D_LYS_191	NZ	D_ASP_159	OD2	2.625
5NUZ	D_LYS_193	NZ	D_ASP_205	OD2	3.551
5NUZ	D_LYS_211	NZ	H_ASP_54	OD1	3.910
5NUZ	D_LYS_211	NZ	H_ASP_54	OD2	3.105
5NUZ	D_LYS_211	NZ	H_ASP_56	OD2	2.803
5NUZ	D_LYS_216	NZ	D_ASP_113	OD1	2.650

Table 701: 5NUZ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5O14	A_LYS_67	NZ	A_ASP_28	OD1	3.407
5O14	A_LYS_67	NZ	A_ASP_28	OD2	3.007
5O14	A_ARG_75	NH2	A_GLU_95	OE2	3.608
5O14	A_ARG_80	NH1	A_GLU_44	OE1	2.660
5O14	A_ARG_80	NH1	A_GLU_44	OE2	2.889
5O14	A_ARG_80	NH2	A_GLU_92	OE2	3.706
5O14	A_HIS_103	ND1	A_GLU_137	OE1	2.640
5O14	A_HIS_103	ND1	A_GLU_137	OE2	3.720
5O14	A_ARG_127	NH1	A_GLU_112	OE1	2.708
5O14	A_ARG_127	NH1	A_GLU_112	OE2	3.026
5O14	A_ARG_127	NH1	A_ASP_160	OD1	3.772
5O14	A_ARG_127	NH2	A_ASP_160	OD1	2.801
5O14	A_ARG_127	NH2	A_ASP_160	OD2	2.429
5O14	A_ARG_130	NH1	A_GLU_92	OE1	2.377
5O14	A_ARG_130	NH1	A_GLU_92	OE2	3.180
5O14	A_ARG_130	NH2	A_GLU_92	OE2	3.816
5O14	A_ARG_149	NH1	A_ASP_171	OD2	3.921
5O14	A_LYS_180	NZ	A_GLU_182	OE1	3.683
5O14	A_LYS_180	NZ	A_GLU_182	OE2	3.327
5O14	A_LYS_185	NZ	H_ASP_55	OD1	3.249
5O14	A_LYS_185	NZ	H_ASP_55	OD2	2.764
5O14	A_LYS_185	NZ	H_ASP_57	OD2	2.802
5O14	A_ARG_204	NH1	A_ASP_142	OD1	3.025
5O14	A_ARG_204	NH1	A_ASP_142	OD2	3.586
5O14	A_ARG_204	NH1	B_GLU_218	OE1	3.625
5O14	A_LYS_254	NZ	A_ASP_71	OD1	3.427
5O14	A_LYS_254	NZ	A_ASP_71	OD2	2.831
5O14	B_LYS_67	NZ	B_ASP_28	OD1	3.290
5O14	B_LYS_67	NZ	B_ASP_28	OD2	3.377
5O14	B_ARG_75	NH2	B_GLU_95	OE2	3.639
5O14	B_ARG_80	NH1	B_GLU_92	OE1	2.081
5O14	B_ARG_80	NH1	B_GLU_92	OE2	3.936
5O14	B_HIS_103	ND1	B_GLU_137	OE1	2.779
5O14	B_ARG_127	NH1	B_GLU_112	OE1	3.567
5O14	B_ARG_127	NH1	B_GLU_112	OE2	3.007
5O14	B_ARG_127	NH1	B_ASP_160	OD1	3.642
5O14	B_ARG_127	NH1	B_ASP_160	OD2	3.977
5O14	B_ARG_127	NH2	B_ASP_160	OD1	3.089
5O14	B_ARG_127	NH2	B_ASP_160	OD2	2.271
5O14	B_ARG_130	NH1	B_GLU_92	OE1	3.575
5O14	B_ARG_130	NH2	B_GLU_92	OE1	3.187
5O14	B_ARG_130	NH2	B_GLU_92	OE2	2.572
5O14	B_LYS_180	NZ	B_GLU_182	OE1	3.557
5O14	B_LYS_180	NZ	B_GLU_182	OE2	3.069
5O14	B_LYS_185	NZ	C_ASP_55	OD1	3.234
5O14	B_LYS_185	NZ	C_ASP_55	OD2	2.720
5O14	B_LYS_185	NZ	C_ASP_57	OD2	2.736
5O14	B_ARG_204	NH2	B_ASP_142	OD1	2.625
5O14	B_ARG_204	NH2	B_ASP_142	OD2	3.290
5O14	B_HIS_248	ND1	B_GLU_239	OE2	3.868
5O14	B_LYS_254	NZ	B_ASP_71	OD1	3.441
5O14	B_LYS_254	NZ	B_ASP_71	OD2	2.876
5O14	C_ARG_38	NH2	C_GLU_46	OE1	3.250
5O14	C_ARG_38	NH2	C_GLU_46	OE2	3.275
5O14	C_ARG_54	NH2	B_ASP_161	OD1	2.870
5O14	C_ARG_54	NH2	B_ASP_161	OD2	3.505
5O14	C_ARG_59	NH2	C_ASP_57	OD1	3.868

5O14	C_ARG_59	NH2	C_ASP_57	OD2	2.946
5O14	C_ARG_67	NH1	C_ASP_90	OD1	3.547
5O14	C_ARG_67	NH1	C_ASP_90	OD2	2.749
5O14	C_ARG_67	NH2	C_ASP_90	OD1	2.849
5O14	C_ARG_67	NH2	C_ASP_90	OD2	3.598
5O14	C_LYS_152	NZ	C_ASP_153	OD1	3.378
5O14	C_LYS_152	NZ	C_ASP_153	OD2	3.892
5O14	C_LYS_218	NZ	D_GLU_124	OE1	3.107
5O14	C_LYS_219	NZ	C_GLU_221	OE2	3.134
5O14	D_ARG_18	NH1	A_GLU_218	OE1	3.301
5O14	D_ARG_61	NH2	D_GLU_81	OE1	3.945
5O14	D_ARG_61	NH2	D_ASP_82	OD1	2.914
5O14	D_ARG_61	NH2	D_ASP_82	OD2	3.547
5O14	D_LYS_104	NZ	D_GLU_166	OE1	3.330
5O14	D_HIS_190	ND1	D_ASP_152	OD2	2.554
5O14	L_ARG_61	NH2	L_GLU_81	OE2	3.920
5O14	L_ARG_61	NH2	L_ASP_82	OD1	2.835
5O14	L_ARG_61	NH2	L_ASP_82	OD2	3.469
5O14	L_HIS_190	ND1	L_ASP_152	OD2	2.475
5O14	H_ARG_38	NH2	H_GLU_46	OE1	3.594
5O14	H_ARG_38	NH2	H_GLU_46	OE2	3.310
5O14	H_ARG_54	NH1	A_ASP_161	OD1	2.861
5O14	H_ARG_54	NH1	A_ASP_161	OD2	3.283
5O14	H_ARG_59	NH1	L_ASP_94	OD1	3.733
5O14	H_ARG_59	NH1	L_ASP_94	OD2	3.698
5O14	H_ARG_59	NH2	H_ASP_57	OD2	3.228
5O14	H_ARG_67	NH1	H_ASP_90	OD1	2.800
5O14	H_ARG_67	NH1	H_ASP_90	OD2	3.115
5O14	H_ARG_67	NH2	H_ASP_90	OD1	3.984
5O14	H_ARG_67	NH2	H_ASP_90	OD2	2.770
5O14	H_LYS_152	NZ	H_ASP_153	OD1	3.488
5O14	H_LYS_152	NZ	H_ASP_153	OD2	3.902

Table 702: 5O14-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5O1R	A_HIS_325	NE2	A_ASP_359	OD2	3.546
5O1R	A_ARG_339	NH1	H_ASP_100	OD1	3.968
5O1R	A_ARG_339	NH1	H_ASP_100	OD2	3.203
5O1R	A_ARG_339	NH2	A_ASP_356	OD2	3.370
5O1R	A_HIS_362	ND1	A_ASP_359	OD1	3.211
5O1R	A_HIS_362	ND1	A_ASP_359	OD2	3.253
5O1R	B_HIS_325	NE2	B_ASP_359	OD2	3.534
5O1R	B_HIS_327	ND1	B_ASP_359	OD2	3.365
5O1R	B_HIS_327	NE2	B_GLU_329	OE1	3.540
5O1R	B_ARG_339	NH1	I_ASP_100	OD1	3.595
5O1R	B_ARG_339	NH1	I_ASP_100	OD2	2.991
5O1R	B_ARG_339	NH2	B_ASP_356	OD2	3.328
5O1R	B_HIS_362	ND1	B_ASP_359	OD1	3.462
5O1R	B_HIS_362	ND1	B_ASP_359	OD2	3.359
5O1R	B_LYS_369	NZ	B_ASP_352	OD1	3.251
5O1R	B_LYS_369	NZ	B_ASP_352	OD2	3.231
5O1R	B_LYS_414	NZ	B_GLU_329	OE1	2.817
5O1R	H_ARG_40	NH1	H_ASP_91	OD1	2.787
5O1R	H_ARG_40	NH2	H_GLU_48	OE1	3.205
5O1R	H_ARG_40	NH2	H_ASP_91	OD1	3.587
5O1R	H_ARG_68	NH1	H_ASP_91	OD1	3.869
5O1R	H_ARG_68	NH1	H_ASP_91	OD2	2.814
5O1R	H_ARG_68	NH2	H_ASP_91	OD1	2.730
5O1R	H_ARG_68	NH2	H_ASP_91	OD2	3.072
5O1R	H_LYS_77	NZ	H_ASP_74	OD2	3.598
5O1R	H_ARG_99	NH1	H_ASP_111	OD2	2.787
5O1R	H_ARG_99	NH2	H_ASP_111	OD2	3.771
5O1R	H_ARG_101	NH1	H_ASP_111	OD1	3.295
5O1R	H_LYS_153	NZ	H_ASP_154	OD1	3.367
5O1R	H_LYS_153	NZ	H_ASP_154	OD2	3.373
5O1R	H_LYS_216	NZ	H_ASP_218	OD1	2.810
5O1R	H_LYS_216	NZ	H_ASP_218	OD2	3.814
5O1R	I_ARG_40	NH1	I_ASP_91	OD1	2.950
5O1R	I_ARG_40	NH2	I_GLU_48	OE1	3.324
5O1R	I_ARG_40	NH2	I_ASP_91	OD1	3.459
5O1R	I_ARG_68	NH1	I_ASP_91	OD1	3.823
5O1R	I_ARG_68	NH1	I_ASP_91	OD2	2.796
5O1R	I_ARG_68	NH2	I_ASP_91	OD1	2.735
5O1R	I_ARG_68	NH2	I_ASP_91	OD2	3.137
5O1R	I_ARG_99	NH1	I_ASP_111	OD2	2.797
5O1R	I_ARG_99	NH2	I_ASP_111	OD2	3.787
5O1R	I_ARG_101	NH1	I_ASP_111	OD1	3.285
5O1R	I_LYS_153	NZ	I_ASP_154	OD1	3.364
5O1R	I_LYS_153	NZ	I_ASP_154	OD2	3.368
5O1R	L_ARG_61	NH2	L_ASP_82	OD1	2.771
5O1R	L_ARG_61	NH2	L_ASP_82	OD2	3.474
5O1R	L_ARG_106	NH2	L_ASP_17	OD2	3.826
5O1R	L_LYS_148	NZ	L_GLU_194	OE1	3.986
5O1R	L_LYS_148	NZ	L_GLU_194	OE2	3.121
5O1R	L_LYS_187	NZ	L_ASP_184	OD2	2.794
5O1R	L_ARG_210	NH1	L_GLU_186	OE1	3.088
5O1R	M_ARG_61	NH2	M_ASP_82	OD1	2.703
5O1R	M_ARG_61	NH2	M_ASP_82	OD2	3.538
5O1R	M_ARG_106	NH2	M_ASP_17	OD2	3.805
5O1R	M_LYS_148	NZ	M_GLU_194	OE1	3.979
5O1R	M_LYS_148	NZ	M_GLU_194	OE2	3.088
5O1R	M_LYS_168	NZ	M_ASP_166	OD2	3.194

5O1R	M_LYS_168	NZ	M_ASP_169	OD1	3.618
5O1R	M_LYS_187	NZ	M_ASP_184	OD2	2.800
5O1R	M_HIS_188	ND1	M_ASP_150	OD2	3.718

Table 703: 5O1R-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5OLM	A_HIS_0	NE2	B_GLU_97	OE1	2.769
5OLM	A_HIS_0	NE2	B_GLU_97	OE2	2.598
5OLM	A_ARG_6	NH2	B_GLU_82	OE1	3.071
5OLM	A_ARG_67	NH1	A_GLU_25	OE1	3.750
5OLM	A_ARG_67	NH1	A_GLU_25	OE2	3.549
5OLM	A_ARG_118	NH2	A_GLU_12	OE1	3.821
5OLM	A_ARG_118	NH2	A_GLU_12	OE2	2.560
5OLM	A_LYS_119	NZ	A_ASP_21	OD1	2.937
5OLM	A_LYS_119	NZ	A_ASP_21	OD2	3.505
5OLM	A_HIS_120	ND1	A_ASP_106	OD2	2.406
5OLM	A_HIS_120	NE2	A_ASP_106	OD2	3.755
5OLM	A_HIS_123	ND1	A_ASP_106	OD1	3.485
5OLM	A_HIS_123	ND1	A_ASP_106	OD2	3.274
5OLM	B_HIS_0	NE2	A_GLU_97	OE1	2.741
5OLM	B_HIS_0	NE2	A_GLU_97	OE2	3.001
5OLM	B_ARG_6	NH2	A_GLU_82	OE2	2.559
5OLM	B_ARG_67	NH1	B_GLU_25	OE1	3.574
5OLM	B_ARG_118	NH1	B_GLU_12	OE1	2.892
5OLM	B_ARG_118	NH1	B_GLU_12	OE2	3.281
5OLM	B_LYS_119	NZ	B_ASP_21	OD1	2.647
5OLM	B_LYS_119	NZ	B_ASP_21	OD2	3.211
5OLM	B_HIS_120	ND1	B_ASP_106	OD2	2.889
5OLM	B_HIS_123	ND1	B_ASP_106	OD2	2.910

Table 704: 5OLM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5OPY	H_ARG.38	NH1	H_ASP.90	OD1	3.516
5OPY	H_ARG.38	NH2	H_GLU.46	OE1	3.707
5OPY	H_ARG.38	NH2	H_GLU.46	OE2	3.605
5OPY	H_ARG.67	NH1	H_ASP.90	OD1	3.928
5OPY	H_ARG.67	NH1	H_ASP.90	OD2	2.808
5OPY	H_ARG.67	NH2	H_ASP.90	OD1	3.025
5OPY	H_ARG.67	NH2	H_ASP.90	OD2	3.394
5OPY	H_LYS.212	NZ	L_GLU.123	OE2	3.578
5OPY	L_ARG.61	NH1	L_ASP.82	OD1	3.825
5OPY	L_ARG.61	NH1	L_ASP.82	OD2	2.771
5OPY	L_ARG.61	NH2	L_GLU.79	OE1	3.579
5OPY	L_ARG.61	NH2	L_GLU.79	OE2	3.640
5OPY	L_ARG.61	NH2	L_ASP.82	OD1	3.036
5OPY	L_ARG.61	NH2	L_ASP.82	OD2	3.486
5OPY	L_LYS.147	NZ	L_GLU.154	OE2	3.483
5OPY	L_LYS.149	NZ	L_GLU.195	OE1	3.661
5OPY	L_LYS.149	NZ	L_GLU.195	OE2	3.217
5OPY	L_ARG.155	NH2	L_GLU.185	OE1	3.459
5OPY	L_LYS.183	NZ	L_GLU.187	OE1	3.576
5OPY	L_LYS.183	NZ	L_GLU.187	OE2	2.833
5OPY	L_HIS.189	ND1	L_ASP.151	OD2	3.278
5OPY	L_HIS.189	NE2	L_GLU.185	OE1	2.982
5OPY	L_HIS.189	NE2	L_GLU.185	OE2	3.936
5OPY	L_LYS.199	NZ	L_ASP.143	OD1	3.965

Table 705: 5OPY-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5OWP	H_ARG_38	NH1	H_ASP_92	OD1	2.637
5OWP	H_ARG_38	NH2	H_GLU_46	OE1	3.304
5OWP	H_ARG_38	NH2	H_GLU_46	OE2	3.626
5OWP	H_ARG_38	NH2	H_ASP_92	OD1	3.777
5OWP	H_ARG_52	NH1	H_GLU_50	OE1	3.856
5OWP	H_ARG_52	NH1	H_GLU_50	OE2	2.567
5OWP	H_HIS_61	ND1	H_GLU_50	OE2	2.863
5OWP	H_ARG_69	NH1	H_ASP_92	OD1	3.470
5OWP	H_ARG_69	NH1	H_ASP_92	OD2	3.501
5OWP	H_ARG_69	NH2	H_ASP_92	OD1	3.595
5OWP	H_ARG_69	NH2	H_ASP_92	OD2	2.233
5OWP	H_ARG_74	NH2	H_ASP_76	OD1	3.541
5OWP	H_ARG_89	NH1	H_GLU_91	OE1	3.703
5OWP	H_HIS_1051	ND1	H_GLU_1047	OE2	3.012
5OWP	H_HIS_1051	NE2	H_ASP_1050	OD1	3.919
5OWP	H_ARG_1070	NH2	H_GLU_1090	OE2	3.696
5OWP	H_ARG_1070	NH2	H_ASP_1091	OD1	2.948
5OWP	H_ARG_1070	NH2	H_ASP_1091	OD2	3.682

Table 706: 5OWP-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5SV3	A_ARG_38	NH1	A_ASP_90	OD1	2.898
5SV3	A_ARG_38	NH2	A_GLU_46	OE1	3.409
5SV3	A_ARG_38	NH2	A_GLU_46	OE2	3.843
5SV3	A_ARG_53	NH2	A_ASP_31	OD1	3.179
5SV3	A_ARG_67	NH1	A_ASP_90	OD1	3.708
5SV3	A_ARG_67	NH1	A_ASP_90	OD2	2.739
5SV3	A_ARG_67	NH2	A_ASP_90	OD1	3.001
5SV3	A_ARG_67	NH2	A_ASP_90	OD2	3.495
5SV3	A_ARG_108	NH2	A_ASP_59	OD1	2.902
5SV3	A_ARG_108	NH2	A_ASP_59	OD2	3.573
5SV3	B_ARG_56	NH2	B_GLU_99	OE2	2.640
5SV3	B_ARG_85	NH1	B_ASP_110	OD1	3.300
5SV3	B_ARG_85	NH2	B_ASP_110	OD1	3.843
5SV3	B_HIS_106	NE2	B_GLU_102	OE1	3.940
5SV3	B_HIS_106	NE2	B_GLU_102	OE2	3.110
5SV3	B_ARG_134	NH2	B_GLU_127	OE2	3.441
5SV3	C_ARG_38	NH1	C_ASP_90	OD1	2.882
5SV3	C_ARG_38	NH2	C_GLU_46	OE1	3.359
5SV3	C_ARG_53	NH2	C_ASP_31	OD1	3.440
5SV3	C_ARG_65	NH1	C_ASP_59	OD1	3.685
5SV3	C_ARG_67	NH1	C_ASP_90	OD1	3.690
5SV3	C_ARG_67	NH1	C_ASP_90	OD2	2.685
5SV3	C_ARG_67	NH2	C_ASP_90	OD1	3.040
5SV3	C_ARG_67	NH2	C_ASP_90	OD2	3.474
5SV3	C_ARG_108	NH2	C_ASP_59	OD1	2.968
5SV3	C_ARG_108	NH2	C_ASP_59	OD2	3.652
5SV3	D_ARG_56	NH1	D_ASP_75	OD1	2.619
5SV3	D_ARG_56	NH1	D_ASP_75	OD2	3.392
5SV3	D_ARG_56	NH2	D_ASP_75	OD1	3.670
5SV3	D_ARG_56	NH2	D_ASP_75	OD2	2.993
5SV3	D_ARG_56	NH2	D_ASP_100	OD1	3.462
5SV3	D_ARG_85	NH2	D_GLU_61	OE2	3.968
5SV3	D_HIS_106	NE2	D_GLU_102	OE2	2.939
5SV3	D_ARG_134	NH2	D_GLU_127	OE2	3.653

Table 707: 5SV3-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5SV4	A_ARG_38	NH1	A_ASP_90	OD1	2.712
5SV4	A_ARG_38	NH2	A_ASP_90	OD1	3.862
5SV4	A_ARG_53	NH2	A_ASP_31	OD1	3.931
5SV4	A_ARG_65	NH1	A_ASP_62	OD1	3.431
5SV4	A_ARG_65	NH2	A_ASP_59	OD1	3.543
5SV4	A_ARG_67	NH1	A_ASP_90	OD1	3.932
5SV4	A_ARG_67	NH1	A_ASP_90	OD2	2.726
5SV4	A_ARG_67	NH2	A_ASP_90	OD1	2.988
5SV4	A_ARG_67	NH2	A_ASP_90	OD2	3.261
5SV4	A_LYS_76	NZ	A_ASP_73	OD2	3.315
5SV4	A_ARG_108	NH2	A_ASP_59	OD1	3.667
5SV4	A_ARG_108	NH2	A_ASP_59	OD2	3.318
5SV4	A_HIS_115	ND1	A_GLU_1	OE1	3.848
5SV4	B_ARG_38	NH1	B_ASP_90	OD1	2.707
5SV4	B_ARG_38	NH2	B_GLU_46	OE2	3.766
5SV4	B_ARG_38	NH2	B_ASP_90	OD1	3.824
5SV4	B_ARG_65	NH2	B_ASP_59	OD1	2.826
5SV4	B_ARG_67	NH1	B_ASP_90	OD1	3.935
5SV4	B_ARG_67	NH1	B_ASP_90	OD2	2.734
5SV4	B_ARG_67	NH2	B_ASP_90	OD1	2.973
5SV4	B_ARG_67	NH2	B_ASP_90	OD2	3.240
5SV4	B_LYS_76	NZ	B_ASP_73	OD2	2.871
5SV4	B_ARG_108	NH2	B_ASP_59	OD2	3.154
5SV4	B_HIS_115	NE2	B_GLU_1	OE1	3.463

Table 708: 5SV4-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5T6P	A_ARG_24	NH2	A_ASP_75	OD1	3.082
5T6P	A_ARG_24	NH2	A_ASP_75	OD2	3.476
5T6P	A_LYS_58	NZ	F_ASP_3	OD2	1.997
5T6P	A_ARG_66	NH1	A_ASP_87	OD1	3.333
5T6P	A_ARG_66	NH1	A_ASP_87	OD2	2.414
5T6P	A_ARG_66	NH2	A_GLU_84	OE1	3.740
5T6P	A_ARG_66	NH2	A_ASP_87	OD1	2.866
5T6P	A_ARG_66	NH2	A_ASP_87	OD2	3.216
5T6P	A_LYS_152	NZ	A_GLU_200	OE2	3.883
5T6P	A_LYS_154	NZ	A_GLU_200	OE1	3.251
5T6P	A_LYS_154	NZ	A_GLU_200	OE2	3.726
5T6P	A_ARG_160	NH1	A_GLU_190	OE2	3.359
5T6P	A_ARG_160	NH2	A_GLU_190	OE1	3.571
5T6P	A_ARG_160	NH2	A_GLU_190	OE2	3.087
5T6P	A_LYS_174	NZ	C_GLU_128	OE2	3.605
5T6P	A_LYS_188	NZ	A_GLU_192	OE1	3.265
5T6P	A_LYS_188	NZ	A_GLU_192	OE2	2.843
5T6P	A_HIS_194	ND1	A_ASP_156	OD2	2.597
5T6P	A_LYS_204	NZ	A_ASP_115	OD2	3.286
5T6P	B_ARG_38	NH1	B_ASP_90	OD1	3.096
5T6P	B_ARG_38	NH2	B_GLU_46	OE1	3.132
5T6P	B_ARG_38	NH2	B_ASP_90	OD1	3.992
5T6P	B_ARG_44	NH1	B_GLU_42	OE1	3.832
5T6P	B_ARG_44	NH2	B_GLU_42	OE1	3.154
5T6P	B_LYS_65	NZ	B_ASP_62	OD1	3.614
5T6P	B_ARG_67	NH2	B_ASP_90	OD1	3.026
5T6P	B_ARG_67	NH2	B_ASP_90	OD2	2.391
5T6P	C_ARG_24	NH2	C_ASP_75	OD1	2.942
5T6P	C_ARG_24	NH2	C_ASP_75	OD2	3.165
5T6P	C_ARG_55	NH1	E_ASP_3	OD2	3.191
5T6P	C_LYS_58	NZ	E_ASP_3	OD2	2.925
5T6P	C_ARG_59	NH2	C_ASP_65	OD1	3.527
5T6P	C_ARG_66	NH1	C_ASP_87	OD1	3.426
5T6P	C_ARG_66	NH1	C_ASP_87	OD2	2.481
5T6P	C_ARG_66	NH2	C_GLU_84	OE1	3.835
5T6P	C_ARG_66	NH2	C_GLU_84	OE2	3.800
5T6P	C_ARG_66	NH2	C_ASP_87	OD1	3.132
5T6P	C_ARG_66	NH2	C_ASP_87	OD2	3.431
5T6P	C_LYS_154	NZ	C_GLU_200	OE1	3.347
5T6P	C_ARG_160	NH1	C_GLU_190	OE2	3.251
5T6P	C_ARG_160	NH2	C_GLU_190	OE1	3.781
5T6P	C_ARG_160	NH2	C_GLU_190	OE2	3.563
5T6P	C_LYS_188	NZ	C_GLU_192	OE1	3.328
5T6P	C_LYS_188	NZ	C_GLU_192	OE2	3.157
5T6P	C_HIS_194	ND1	C_ASP_156	OD2	2.748
5T6P	C_LYS_204	NZ	C_ASP_115	OD2	3.242
5T6P	D_ARG_38	NH1	D_ASP_90	OD1	2.948
5T6P	D_ARG_38	NH2	D_GLU_46	OE1	3.287
5T6P	D_ARG_44	NH2	D_GLU_42	OE1	3.539
5T6P	D_LYS_65	NZ	D_ASP_62	OD1	3.833
5T6P	D_ARG_67	NH2	D_ASP_90	OD1	2.581
5T6P	D_ARG_67	NH2	D_ASP_90	OD2	2.532
5T6P	E_ARG_5	NH2	C_GLU_39	OE1	3.351
5T6P	E_ARG_5	NH2	C_GLU_39	OE2	2.626
5T6P	F_ARG_5	NH2	A_GLU_39	OE1	3.661
5T6P	F_ARG_5	NH2	A_GLU_39	OE2	2.718

Table 709: 5T6P-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5T78	A_ARG_24	NH2	A_ASP_75	OD1	3.292
5T78	A_ARG_24	NH2	A_ASP_75	OD2	3.506
5T78	A_LYS_44	NZ	A_GLU_86	OE2	3.456
5T78	A_LYS_58	NZ	F_ASP_3	OD1	2.579
5T78	A_LYS_58	NZ	F_ASP_3	OD2	3.334
5T78	A_ARG_66	NH1	A_ASP_87	OD1	3.316
5T78	A_ARG_66	NH1	A_ASP_87	OD2	2.549
5T78	A_ARG_66	NH2	A_GLU_84	OE1	3.229
5T78	A_ARG_66	NH2	A_GLU_84	OE2	3.938
5T78	A_ARG_66	NH2	A_ASP_87	OD1	2.866
5T78	A_ARG_66	NH2	A_ASP_87	OD2	3.475
5T78	A_LYS_152	NZ	A_GLU_200	OE2	3.993
5T78	A_LYS_154	NZ	A_GLU_200	OE1	3.160
5T78	A_LYS_154	NZ	A_GLU_200	OE2	3.631
5T78	A_ARG_160	NH1	A_GLU_190	OE2	2.874
5T78	A_ARG_160	NH2	A_GLU_190	OE1	3.635
5T78	A_ARG_160	NH2	A_GLU_190	OE2	3.190
5T78	A_LYS_188	NZ	A_GLU_192	OE1	3.158
5T78	A_LYS_188	NZ	A_GLU_192	OE2	2.974
5T78	A_HIS_194	ND1	A_ASP_156	OD2	2.728
5T78	A_LYS_204	NZ	A_ASP_115	OD1	3.976
5T78	A_LYS_204	NZ	A_ASP_115	OD2	3.220
5T78	B_LYS_3	NZ	B_GLU_1	OE2	3.096
5T78	B_ARG_38	NH1	B_ASP_90	OD1	2.890
5T78	B_ARG_38	NH2	B_GLU_46	OE1	3.379
5T78	B_ARG_38	NH2	B_ASP_90	OD1	3.918
5T78	B_ARG_44	NH2	B_GLU_42	OE1	2.944
5T78	B_ARG_67	NH2	B_ASP_90	OD1	2.740
5T78	B_ARG_67	NH2	B_ASP_90	OD2	2.732
5T78	F_ARG_5	NH1	A_GLU_39	OE1	2.678
5T78	F_ARG_5	NH1	A_GLU_39	OE2	2.480
5T78	C_ARG_24	NH2	C_ASP_75	OD1	3.347
5T78	C_ARG_24	NH2	C_ASP_75	OD2	3.277
5T78	C_ARG_55	NH2	E_ASP_3	OD1	3.685
5T78	C_LYS_58	NZ	E_ASP_3	OD1	2.753
5T78	C_LYS_58	NZ	E_ASP_3	OD2	2.872
5T78	C_ARG_59	NH1	C_ASP_65	OD1	2.623
5T78	C_ARG_66	NH1	C_ASP_87	OD1	3.605
5T78	C_ARG_66	NH1	C_ASP_87	OD2	2.346
5T78	C_ARG_66	NH2	C_GLU_84	OE1	3.346
5T78	C_ARG_66	NH2	C_GLU_84	OE2	3.846
5T78	C_ARG_66	NH2	C_GLU_86	OE2	3.475
5T78	C_ARG_66	NH2	C_ASP_87	OD1	3.004
5T78	C_ARG_66	NH2	C_ASP_87	OD2	3.187
5T78	C_LYS_154	NZ	C_GLU_200	OE1	3.236
5T78	C_ARG_160	NH1	C_GLU_190	OE1	3.681
5T78	C_ARG_160	NH1	C_GLU_190	OE2	2.945
5T78	C_ARG_160	NH2	C_GLU_190	OE1	3.366
5T78	C_ARG_160	NH2	C_GLU_190	OE2	3.933
5T78	C_LYS_188	NZ	C_GLU_192	OE1	3.411
5T78	C_LYS_188	NZ	C_GLU_192	OE2	3.168
5T78	C_HIS_194	ND1	C_ASP_156	OD2	2.579
5T78	C_LYS_204	NZ	C_ASP_115	OD2	3.148
5T78	D_ARG_38	NH1	D_ASP_90	OD1	2.853
5T78	D_ARG_38	NH2	D_GLU_46	OE1	3.156
5T78	D_ARG_38	NH2	D_ASP_90	OD1	3.962
5T78	D_ARG_67	NH2	D_ASP_90	OD1	2.642

5T78	D_ARG_67	NH2	D_ASP_90	OD2	2.478
5T78	D_LYS_211	NZ	C_GLU_128	OE1	3.376
5T78	E_ARG_5	NH1	C_GLU_39	OE1	2.693
5T78	E_ARG_5	NH1	C_GLU_39	OE2	2.664

Table 710: 5T78-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5TCX	A_LYS_124	NZ	A_ASP_195	OD1	3.385
5TCX	A_LYS_124	NZ	A_ASP_195	OD2	2.891
5TCX	A_LYS_144	NZ	A_ASP_138	OD1	2.296
5TCX	A_LYS_171	NZ	A_ASP_138	OD1	3.371
5TCX	A_LYS_187	NZ	A_ASP_155	OD1	3.854
5TCX	A_LYS_187	NZ	A_ASP_155	OD2	3.942
5TCX	A_HIS_191	NE2	A_ASP_128	OD1	2.502
5TCX	A_HIS_191	NE2	A_ASP_128	OD2	3.422
5TCX	A_LYS_193	NZ	A_GLU_188	OE2	2.937
5TCX	A_LYS_201	NZ	A_ASP_196	OD2	3.323

Table 711: 5TCX-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5TIH	A_HIS_3	ND1	A_GLU_333	OE1	3.713
5TIH	A_LYS_28	NZ	A_GLU_83	OE1	3.102
5TIH	A_ARG_29	NH2	A_ASP_307	OD2	2.694
5TIH	A_LYS_40	NZ	A_ASP_38	OD1	3.409
5TIH	A_LYS_40	NZ	A_ASP_38	OD2	3.673
5TIH	A_HIS_47	ND1	A_ASP_63	OD2	2.822
5TIH	A_LYS_52	NZ	A_GLU_30	OE1	2.433
5TIH	A_LYS_52	NZ	A_GLU_30	OE2	3.751
5TIH	A_LYS_66	NZ	L_ASP_92	OD1	3.482
5TIH	A_ARG_73	NH2	A_ASP_38	OD2	3.662
5TIH	A_HIS_75	NE2	A_ASP_92	OD1	3.360
5TIH	A_LYS_100	NZ	A_ASP_124	OD1	3.619
5TIH	A_ARG_106	NH1	A_GLU_177	OE2	3.261
5TIH	A_LYS_130	NZ	A_ASP_165	OD1	3.418
5TIH	A_LYS_130	NZ	A_ASP_165	OD2	3.868
5TIH	A_LYS_157	NZ	A_ASP_160	OD1	3.149
5TIH	A_LYS_157	NZ	A_ASP_166	OD1	2.621
5TIH	A_LYS_164	NZ	A_GLU_236	OE1	3.487
5TIH	A_LYS_164	NZ	A_GLU_236	OE2	2.956
5TIH	A_LYS_175	NZ	A_GLU_84	OE1	2.559
5TIH	A_LYS_175	NZ	A_GLU_84	OE2	3.472
5TIH	A_LYS_186	NZ	A_ASP_188	OD2	3.836
5TIH	A_LYS_205	NZ	A_ASP_259	OD1	3.347
5TIH	A_LYS_205	NZ	A_GLU_308	OE1	3.703
5TIH	A_LYS_205	NZ	A_GLU_308	OE2	3.973
5TIH	A_HIS_211	NE2	A_ASP_253	OD1	3.623
5TIH	A_LYS_305	NZ	A_GLU_308	OE1	2.934
5TIH	A_LYS_305	NZ	A_GLU_308	OE2	3.911
5TIH	H_HIS_35	NE2	A_ASP_69	OD1	2.973
5TIH	H_HIS_35	NE2	A_ASP_69	OD2	3.535
5TIH	H_ARG_67	NH2	H_ASP_90	OD1	3.399
5TIH	H_ARG_67	NH2	H_ASP_90	OD2	3.193
5TIH	H_ARG_100	NH2	A_ASP_69	OD1	3.080
5TIH	H_ARG_101	NH2	A_GLU_119	OE1	3.357
5TIH	H_ARG_101	NH2	A_GLU_119	OE2	3.359
5TIH	L_ARG_24	NH1	L_ASP_70	OD1	2.418
5TIH	L_ARG_24	NH1	L_ASP_70	OD2	3.060
5TIH	L_ARG_24	NH2	L_ASP_70	OD2	3.324
5TIH	L_LYS_39	NZ	L_GLU_81	OE2	3.732
5TIH	L_LYS_45	NZ	L_GLU_81	OE2	3.780
5TIH	L_ARG_46	NH2	L_ASP_55	OD1	3.597
5TIH	L_ARG_46	NH2	L_ASP_55	OD2	2.892
5TIH	L_ARG_61	NH2	L_GLU_81	OE1	3.907
5TIH	L_ARG_61	NH2	L_ASP_82	OD1	3.126
5TIH	L_ARG_61	NH2	L_ASP_82	OD2	3.816
5TIH	L_ARG_66	NH2	L_GLU_28	OE1	2.831
5TIH	L_ARG_66	NH2	L_GLU_28	OE2	3.769
5TIH	L_LYS_103	NZ	L_ASP_85	OD2	3.969
5TIH	L_LYS_142	NZ	L_GLU_105	OE1	3.302
5TIH	L_LYS_142	NZ	L_GLU_105	OE2	3.271
5TIH	L_LYS_147	NZ	L_GLU_195	OE2	3.679
5TIH	L_LYS_149	NZ	L_GLU_195	OE1	3.506
5TIH	L_LYS_149	NZ	L_GLU_195	OE2	3.625
5TIH	L_ARG_155	NH1	L_GLU_185	OE1	3.848
5TIH	L_ARG_155	NH2	L_GLU_185	OE1	3.868
5TIH	L_HIS_189	ND1	L_ASP_151	OD2	3.122
5TIH	L_ARG_211	NH1	L_GLU_187	OE2	3.061

Table 712: 5TIH-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5TIK	A_HIS_3	ND1	D_GLU_9	OE2	3.832
5TIK	A_HIS_3	NE2	B_GLU_9	OE2	3.597
5TIK	A_LYS_28	NZ	A_GLU_83	OE1	3.971
5TIK	A_HIS_47	NE2	A_GLU_45	OE1	3.808
5TIK	A_HIS_47	NE2	A_GLU_45	OE2	2.915
5TIK	A_HIS_47	NE2	A_ASP_63	OD2	3.962
5TIK	A_LYS_52	NZ	A_GLU_30	OE1	3.759
5TIK	A_LYS_52	NZ	A_GLU_30	OE2	2.781
5TIK	A_HIS_75	NE2	A_ASP_92	OD1	3.609
5TIK	A_HIS_75	NE2	A_ASP_92	OD2	3.079
5TIK	A_ARG_145	NH1	A_ASP_234	OD2	3.502
5TIK	A_ARG_145	NH2	A_ASP_234	OD1	2.795
5TIK	A_ARG_145	NH2	A_ASP_234	OD2	3.031
5TIK	A_LYS_157	NZ	A_ASP_160	OD1	3.965
5TIK	A_LYS_157	NZ	A_ASP_161	OD1	3.943
5TIK	A_LYS_157	NZ	A_ASP_166	OD1	3.100
5TIK	A_LYS_164	NZ	A_ASP_160	OD1	3.523
5TIK	A_LYS_175	NZ	A_ASP_81	OD2	2.307
5TIK	A_LYS_175	NZ	A_GLU_84	OE2	2.899
5TIK	A_LYS_182	NZ	A_ASP_165	OD2	3.588
5TIK	A_LYS_205	NZ	A_GLU_308	OE1	3.830
5TIK	A_LYS_205	NZ	A_GLU_308	OE2	3.734
5TIK	A_HIS_211	NE2	A_ASP_253	OD1	3.988
5TIK	A_LYS_287	NZ	A_GLU_273	OE2	3.653
5TIK	A_LYS_305	NZ	A_GLU_308	OE1	3.281
5TIK	A_LYS_305	NZ	A_GLU_308	OE2	3.263
5TIK	B_HIS_3	NE2	A_GLU_9	OE1	3.627
5TIK	B_HIS_3	NE2	A_GLU_9	OE2	3.175
5TIK	B_HIS_3	NE2	C_GLU_9	OE1	3.296
5TIK	B_HIS_3	NE2	C_GLU_9	OE2	3.823
5TIK	B_LYS_28	NZ	B_GLU_83	OE1	3.175
5TIK	B_LYS_28	NZ	B_GLU_83	OE2	3.839
5TIK	B_HIS_47	ND1	B_ASP_63	OD2	3.018
5TIK	B_LYS_52	NZ	B_GLU_30	OE1	3.671
5TIK	B_HIS_75	NE2	B_ASP_92	OD2	2.903
5TIK	B_LYS_100	NZ	B_ASP_124	OD1	3.470
5TIK	B_LYS_100	NZ	B_ASP_124	OD2	2.292
5TIK	B_ARG_106	NH2	B_GLU_177	OE2	3.673
5TIK	B_LYS_157	NZ	B_ASP_161	OD1	3.470
5TIK	B_LYS_157	NZ	B_ASP_166	OD1	2.331
5TIK	B_LYS_157	NZ	B_ASP_166	OD2	3.739
5TIK	B_LYS_175	NZ	B_GLU_84	OE1	3.721
5TIK	B_LYS_175	NZ	B_GLU_84	OE2	3.186
5TIK	B_LYS_182	NZ	B_ASP_165	OD1	3.333
5TIK	B_LYS_186	NZ	B_GLU_236	OE1	2.882
5TIK	B_LYS_186	NZ	B_GLU_236	OE2	3.887
5TIK	B_LYS_205	NZ	B_ASP_259	OD2	3.092
5TIK	B_HIS_211	NE2	B_ASP_253	OD1	3.835
5TIK	B_ARG_242	NH2	B_GLU_228	OE2	3.300
5TIK	B_LYS_290	NZ	A_GLU_281	OE1	3.703
5TIK	B_LYS_305	NZ	B_GLU_308	OE1	2.748
5TIK	B_ARG_310	NH2	B_ASP_307	OD2	3.708
5TIK	C_HIS_3	NE2	B_GLU_9	OE1	2.908
5TIK	C_ARG_29	NH2	B_ASP_259	OD2	3.311
5TIK	C_HIS_47	ND1	C_ASP_63	OD2	3.231
5TIK	C_LYS_52	NZ	C_GLU_30	OE1	3.235
5TIK	C_LYS_52	NZ	C_GLU_30	OE2	3.319

5TIK	C_LYS_66	NZ	C_ASP_63	OD2	3.918
5TIK	C_LYS_99	NZ	C_GLU_93	OE2	2.385
5TIK	C_ARG_106	NH2	C_GLU_177	OE2	3.784
5TIK	C_LYS_157	NZ	C_ASP_161	OD1	3.341
5TIK	C_LYS_157	NZ	C_ASP_161	OD2	3.707
5TIK	C_LYS_157	NZ	C_ASP_166	OD1	2.361
5TIK	C_HIS_173	ND1	C_ASP_174	OD2	3.723
5TIK	C_LYS_175	NZ	C_GLU_84	OE1	3.431
5TIK	C_LYS_175	NZ	C_GLU_84	OE2	2.598
5TIK	C_LYS_182	NZ	C_ASP_165	OD2	3.481
5TIK	C_LYS_186	NZ	C_GLU_232	OE1	3.373
5TIK	C_LYS_205	NZ	C_ASP_259	OD1	2.434
5TIK	C_LYS_205	NZ	C_ASP_259	OD2	3.747
5TIK	C_LYS_205	NZ	C_GLU_308	OE1	3.839
5TIK	C_LYS_205	NZ	C_GLU_308	OE2	3.684
5TIK	C_LYS_287	NZ	C_GLU_273	OE1	3.786
5TIK	C_LYS_305	NZ	C_GLU_308	OE1	3.517
5TIK	C_LYS_305	NZ	C_GLU_308	OE2	3.437
5TIK	C_ARG_310	NH1	C_ASP_307	OD2	3.297
5TIK	D_HIS_3	NE2	A_GLU_9	OE1	2.950
5TIK	D_HIS_3	NE2	A_GLU_9	OE2	2.918
5TIK	D_ARG_7	NH1	D_GLU_9	OE1	3.447
5TIK	D_LYS_28	NZ	D_GLU_83	OE1	3.595
5TIK	D_LYS_28	NZ	D_GLU_83	OE2	2.506
5TIK	D_HIS_47	ND1	D_ASP_63	OD2	2.503
5TIK	D_LYS_52	NZ	D_GLU_30	OE1	2.944
5TIK	D_LYS_52	NZ	D_GLU_30	OE2	3.601
5TIK	D_HIS_75	NE2	D_ASP_92	OD1	3.926
5TIK	D_LYS_99	NZ	D_GLU_91	OE1	3.765
5TIK	D_ARG_106	NH1	D_GLU_177	OE1	3.872
5TIK	D_ARG_106	NH1	D_GLU_177	OE2	3.044
5TIK	D_ARG_106	NH2	D_GLU_177	OE2	3.983
5TIK	D_LYS_157	NZ	D_ASP_161	OD1	2.995
5TIK	D_LYS_157	NZ	D_ASP_166	OD1	2.612
5TIK	D_LYS_157	NZ	D_ASP_166	OD2	3.577
5TIK	D_LYS_175	NZ	D_GLU_146	OE1	3.788
5TIK	D_LYS_205	NZ	D_GLU_308	OE2	3.635
5TIK	D_LYS_287	NZ	D_GLU_273	OE1	3.724
5TIK	D_LYS_305	NZ	D_GLU_308	OE1	3.354
5TIK	D_LYS_305	NZ	D_GLU_308	OE2	2.963

Table 713: 5TIK-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5TL5	L.LYS_24	NZ	L.ASP_74	OD1	3.254
5TL5	L.LYS_24	NZ	L.ASP_74	OD2	3.141
5TL5	L.ARG_65	NH1	L.ASP_86	OD1	3.543
5TL5	L.ARG_65	NH1	L.ASP_86	OD2	2.755
5TL5	L.ARG_65	NH2	L.GLU_85	OE2	3.698
5TL5	L.ARG_65	NH2	L.ASP_86	OD1	2.948
5TL5	L.ARG_65	NH2	L.ASP_86	OD2	3.662
5TL5	L.LYS_153	NZ	L.GLU_199	OE1	2.824
5TL5	L.HIS_193	ND1	L.ASP_189	OD1	3.571
5TL5	L.ARG_215	NH1	L.GLU_191	OE1	3.322
5TL5	H.ARG_40	NH1	H.GLU_89	OE1	3.264
5TL5	H.ARG_40	NH2	H.GLU_89	OE1	3.195
5TL5	H.ARG_40	NH2	H.GLU_89	OE2	3.409
5TL5	H.ARG_50	NH1	L.ASP_98	OD1	2.887
5TL5	H.ARG_50	NH1	L.ASP_98	OD2	3.532
5TL5	H.ARG_50	NH2	L.ASP_98	OD1	3.785
5TL5	H.ARG_50	NH2	L.ASP_98	OD2	2.933
5TL5	H.LYS_67	NZ	H.ASP_90	OD1	3.648
5TL5	H.LYS_67	NZ	H.ASP_90	OD2	2.769
5TL5	H.ARG_98	NH2	H.ASP_100	OD1	3.835
5TL5	H.LYS_150	NZ	H.ASP_151	OD1	3.624
5TL5	H.LYS_150	NZ	H.ASP_151	OD2	3.145
5TL5	H.LYS_216	NZ	L.GLU_127	OE1	3.027
5TL5	H.LYS_216	NZ	L.GLU_127	OE2	3.571
5TL5	A.LYS_17	NZ	H.ASP_55	OD1	3.610
5TL5	A.LYS_17	NZ	H.ASP_55	OD2	2.637
5TL5	A.LYS_17	NZ	H.ASP_57	OD1	2.990
5TL5	A.HIS_36	NE2	H.ASP_104	OD1	3.017
5TL5	A.HIS_36	NE2	H.ASP_104	OD2	2.947
5TL5	A.ARG_37	NH2	H.ASP_104	OD2	2.895
5TL5	A.ARG_58	NH1	A.ASP_54	OD1	3.167
5TL5	A.ARG_58	NH1	A.ASP_54	OD2	3.803
5TL5	A.ARG_58	NH1	A.GLU_62	OE2	3.990
5TL5	A.ARG_58	NH2	A.ASP_54	OD1	2.943
5TL5	A.ARG_58	NH2	A.GLU_62	OE2	3.654
5TL5	A.ARG_65	NH1	A.GLU_96	OE2	3.447
5TL5	A.ARG_65	NH2	A.GLU_96	OE2	3.907
5TL5	A.ARG_74	NH1	A.GLU_83	OE1	3.799
5TL5	A.ARG_74	NH2	A.GLU_83	OE1	3.360

Table 714: 5TL5-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5TLJ	A_ARG_65	NH1	A_GLU_83	OE2	2.851
5TLJ	A_ARG_65	NH1	A_GLU_85	OE2	3.561
5TLJ	A_ARG_65	NH2	A_ASP_86	OD1	2.756
5TLJ	A_ARG_65	NH2	A_ASP_86	OD2	2.866
5TLJ	A_LYS_153	NZ	A_GLU_199	OE1	3.517
5TLJ	A_LYS_153	NZ	A_GLU_199	OE2	2.835
5TLJ	A_ARG_215	NH1	A_GLU_191	OE1	2.713
5TLJ	B_LYS_38	NZ	B_GLU_46	OE1	3.196
5TLJ	B_LYS_38	NZ	B_ASP_90	OD1	3.704
5TLJ	B_ARG_40	NH1	B_GLU_89	OE2	2.861
5TLJ	B_ARG_50	NH1	A_ASP_98	OD1	2.672
5TLJ	B_ARG_50	NH1	A_ASP_98	OD2	3.926
5TLJ	B_LYS_63	NZ	B_GLU_46	OE1	3.698
5TLJ	B_LYS_63	NZ	B_GLU_89	OE1	3.182
5TLJ	B_LYS_63	NZ	B_GLU_89	OE2	3.310
5TLJ	B_LYS_67	NZ	B_ASP_90	OD2	3.121
5TLJ	B_LYS_150	NZ	B_ASP_151	OD1	3.569
5TLJ	B_LYS_150	NZ	B_ASP_151	OD2	3.604
5TLJ	B_LYS_213	NZ	B_ASP_215	OD2	3.942
5TLJ	C_ARG_65	NH1	C_ASP_86	OD1	2.756
5TLJ	C_ARG_65	NH1	C_ASP_86	OD2	2.971
5TLJ	C_ARG_65	NH2	C_GLU_83	OE1	3.613
5TLJ	C_ARG_65	NH2	C_ASP_86	OD1	3.864
5TLJ	C_LYS_153	NZ	C_GLU_199	OE1	3.775
5TLJ	C_LYS_153	NZ	C_GLU_199	OE2	3.308
5TLJ	C_HIS_193	ND1	C_ASP_189	OD1	3.530
5TLJ	C_ARG_215	NH1	C_GLU_191	OE2	3.808
5TLJ	C_ARG_215	NH2	C_GLU_191	OE2	3.846
5TLJ	D_ARG_38	NH1	D_ASP_90	OD1	3.566
5TLJ	D_ARG_38	NH2	D_GLU_46	OE1	2.710
5TLJ	D_ARG_38	NH2	D_GLU_46	OE2	3.743
5TLJ	D_ARG_38	NH2	D_ASP_90	OD1	3.868
5TLJ	D_ARG_67	NH1	D_ASP_90	OD2	3.824
5TLJ	D_ARG_67	NH2	D_ASP_90	OD1	3.650
5TLJ	D_ARG_100	NH1	X_ASP_43	OD2	3.396
5TLJ	D_ARG_100	NH2	C_GLU_59	OE1	2.703
5TLJ	D_ARG_100	NH2	C_GLU_59	OE2	3.403
5TLJ	D_ARG_100	NH2	X_ASP_43	OD2	3.844
5TLJ	D_LYS_147	NZ	D_ASP_148	OD1	3.264
5TLJ	D_LYS_147	NZ	D_ASP_148	OD2	2.806
5TLJ	E_LYS_24	NZ	E_ASP_74	OD1	3.563
5TLJ	E_ARG_65	NH1	E_GLU_83	OE2	3.709
5TLJ	E_ARG_65	NH2	E_GLU_85	OE1	3.881
5TLJ	E_ARG_65	NH2	E_ASP_86	OD1	2.674
5TLJ	E_ARG_65	NH2	E_ASP_86	OD2	3.332
5TLJ	E_ARG_146	NH2	E_GLU_169	OE1	3.285
5TLJ	E_ARG_215	NH1	E_GLU_191	OE2	3.303
5TLJ	F_LYS_38	NZ	F_GLU_46	OE1	3.804
5TLJ	F_ARG_50	NH1	E_ASP_98	OD1	3.689
5TLJ	F_ARG_50	NH1	E_ASP_98	OD2	2.897
5TLJ	F_ARG_50	NH2	E_ASP_98	OD1	3.671
5TLJ	F_ARG_50	NH2	E_ASP_98	OD2	3.575
5TLJ	F_LYS_63	NZ	F_GLU_89	OE1	3.558
5TLJ	F_LYS_67	NZ	F_ASP_90	OD1	3.830
5TLJ	F_LYS_67	NZ	F_ASP_90	OD2	3.115
5TLJ	F_ARG_98	NH1	F_ASP_100	OD1	3.189
5TLJ	F_ARG_98	NH1	F_ASP_100	OD2	3.943

5TLJ	F_LYS_150	NZ	F_ASP_151	OD1	3.468
5TLJ	F_HIS_171	ND1	E_ASP_171	OD1	3.892
5TLJ	F_HIS_171	NE2	E_ASP_171	OD2	3.411
5TLJ	F_LYS_217	NZ	F_GLU_219	OE2	2.788
5TLJ	G_ARG_24	NH2	G_ASP_74	OD1	3.512
5TLJ	G_ARG_65	NH1	G_GLU_83	OE1	3.877
5TLJ	G_ARG_65	NH1	G_ASP_86	OD1	3.552
5TLJ	G_ARG_65	NH1	G_ASP_86	OD2	2.689
5TLJ	G_ARG_65	NH2	G_GLU_83	OE1	3.030
5TLJ	G_LYS_187	NZ	G_GLU_191	OE2	3.996
5TLJ	H_ARG_38	NH1	H_GLU_46	OE1	3.968
5TLJ	H_ARG_38	NH1	H_ASP_90	OD1	3.590
5TLJ	H_ARG_38	NH2	H_GLU_46	OE1	2.850
5TLJ	H_ARG_38	NH2	H_GLU_46	OE2	3.149
5TLJ	H_ARG_38	NH2	H_ASP_90	OD1	3.501
5TLJ	H_ARG_67	NH1	H_ASP_90	OD1	3.809
5TLJ	H_ARG_67	NH1	H_ASP_90	OD2	2.805
5TLJ	H_ARG_67	NH2	H_ASP_90	OD1	3.038
5TLJ	H_ARG_67	NH2	H_ASP_90	OD2	3.316
5TLJ	H_ARG_76	NH2	H_ASP_73	OD2	3.334
5TLJ	H_ARG_98	NH2	H_ASP_105	OD2	3.277
5TLJ	H_ARG_100	NH2	G_GLU_59	OE1	2.761
5TLJ	H_LYS_147	NZ	H_ASP_148	OD1	3.556
5TLJ	H_LYS_147	NZ	H_ASP_148	OD2	2.892
5TLJ	X_LYS_17	NZ	B_ASP_57	OD2	3.053
5TLJ	X_HIS_36	NE2	B_ASP_104	OD1	3.121
5TLJ	X_HIS_36	NE2	B_ASP_104	OD2	2.886
5TLJ	X_ARG_58	NH1	X_GLU_62	OE2	2.792
5TLJ	X_ARG_58	NH2	X_ASP_54	OD1	3.157
5TLJ	X_ARG_58	NH2	X_GLU_62	OE2	3.987
5TLJ	X_ARG_65	NH2	X_GLU_83	OE2	3.778

Table 715: 5TLJ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5TLK	A_LYS_24	NZ	A_ASP_74	OD1	3.675
5TLK	A_ARG_65	NH1	A_ASP_86	OD1	3.826
5TLK	A_ARG_65	NH1	A_ASP_86	OD2	2.689
5TLK	A_ARG_65	NH2	A_GLU_83	OE2	3.993
5TLK	A_ARG_65	NH2	A_ASP_86	OD1	3.142
5TLK	A_ARG_65	NH2	A_ASP_86	OD2	3.459
5TLK	A_LYS_107	NZ	A_GLU_169	OE2	3.867
5TLK	A_LYS_153	NZ	A_GLU_199	OE1	2.764
5TLK	B_ARG_50	NH1	A_ASP_98	OD1	3.277
5TLK	B_ARG_50	NH1	A_ASP_98	OD2	2.898
5TLK	B_ARG_50	NH2	A_ASP_98	OD1	2.923
5TLK	B_LYS_63	NZ	B_GLU_46	OE1	3.471
5TLK	B_LYS_63	NZ	B_GLU_46	OE2	3.192
5TLK	B_LYS_67	NZ	B_ASP_90	OD1	3.881
5TLK	B_LYS_67	NZ	B_ASP_90	OD2	2.993
5TLK	B_LYS_150	NZ	B_ASP_151	OD1	3.046
5TLK	B_LYS_150	NZ	B_ASP_151	OD2	2.798
5TLK	B_LYS_216	NZ	A_GLU_127	OE1	3.067
5TLK	B_LYS_216	NZ	A_GLU_127	OE2	3.588
5TLK	C_ARG_24	NH1	C_ASP_74	OD1	3.109
5TLK	C_ARG_24	NH1	C_ASP_74	OD2	2.746
5TLK	C_LYS_27	NZ	C_GLU_97	OE1	3.042
5TLK	C_ARG_57	NH2	X_ASP_43	OD1	3.384
5TLK	C_ARG_65	NH1	C_ASP_86	OD1	3.594
5TLK	C_ARG_65	NH1	C_ASP_86	OD2	2.481
5TLK	C_ARG_65	NH2	C_ASP_86	OD1	2.770
5TLK	C_ARG_65	NH2	C_ASP_86	OD2	3.157
5TLK	C_LYS_107	NZ	C_GLU_169	OE2	2.732
5TLK	C_LYS_153	NZ	C_GLU_199	OE1	2.786
5TLK	C_LYS_153	NZ	C_GLU_199	OE2	3.954
5TLK	C_LYS_187	NZ	C_GLU_191	OE2	3.768
5TLK	C_ARG_215	NH1	C_GLU_191	OE1	3.277
5TLK	D_ARG_38	NH1	D_ASP_90	OD1	2.987
5TLK	D_ARG_38	NH2	D_GLU_46	OE1	2.875
5TLK	D_ARG_38	NH2	D_GLU_46	OE2	3.558
5TLK	D_ARG_38	NH2	D_ASP_90	OD1	3.987
5TLK	D_LYS_65	NZ	D_ASP_62	OD1	2.814
5TLK	D_ARG_67	NH1	D_ASP_90	OD2	2.614
5TLK	D_ARG_67	NH2	D_ASP_90	OD1	3.114
5TLK	D_ARG_67	NH2	D_ASP_90	OD2	3.161
5TLK	D_ARG_98	NH2	D_ASP_105	OD1	3.927
5TLK	D_ARG_98	NH2	D_ASP_105	OD2	2.700
5TLK	D_ARG_100	NH1	X_ASP_43	OD2	2.904
5TLK	D_ARG_100	NH2	C_GLU_59	OE1	2.708
5TLK	D_ARG_100	NH2	C_GLU_59	OE2	3.299
5TLK	D_ARG_100	NH2	X_ASP_43	OD2	3.882
5TLK	D_LYS_147	NZ	D_ASP_148	OD1	3.173
5TLK	D_LYS_147	NZ	D_ASP_148	OD2	3.344
5TLK	E_ARG_65	NH1	E_ASP_86	OD1	3.727
5TLK	E_ARG_65	NH1	E_ASP_86	OD2	2.581
5TLK	E_ARG_65	NH2	E_GLU_83	OE1	3.517
5TLK	E_ARG_65	NH2	E_ASP_86	OD1	2.787
5TLK	E_ARG_65	NH2	E_ASP_86	OD2	3.198
5TLK	E_LYS_153	NZ	E_GLU_199	OE1	2.662
5TLK	E_LYS_187	NZ	E_GLU_191	OE1	3.794
5TLK	F_LYS_38	NZ	F_ASP_90	OD1	3.722
5TLK	F_ARG_40	NH1	F_GLU_89	OE1	3.871

5TLK	F_ARG_40	NH2	F_GLU_89	OE1	3.823
5TLK	F_ARG_40	NH2	F_GLU_89	OE2	2.772
5TLK	F_ARG_50	NH1	E_ASP_98	OD1	3.086
5TLK	F_ARG_50	NH1	E_ASP_98	OD2	3.224
5TLK	F_ARG_50	NH2	E_ASP_98	OD1	2.767
5TLK	F_ARG_50	NH2	E_ASP_98	OD2	3.943
5TLK	F_LYS_67	NZ	F_ASP_90	OD2	3.364
5TLK	F_ARG_98	NH1	F_ASP_100	OD1	3.582
5TLK	F_LYS_150	NZ	F_ASP_151	OD1	3.689
5TLK	G_ARG_24	NH1	G_ASP_74	OD2	2.978
5TLK	G_ARG_24	NH2	G_ASP_74	OD1	3.856
5TLK	G_ARG_24	NH2	G_ASP_74	OD2	3.656
5TLK	G_LYS_27	NZ	G_GLU_97	OE1	3.620
5TLK	G_ARG_33	NH1	Y_GLU_24	OE2	3.993
5TLK	G_ARG_33	NH2	Y_GLU_24	OE2	3.475
5TLK	G_ARG_65	NH1	G_ASP_86	OD1	3.101
5TLK	G_ARG_65	NH1	G_ASP_86	OD2	2.770
5TLK	G_ARG_65	NH2	G_GLU_85	OE2	3.596
5TLK	G_LYS_107	NZ	G_GLU_169	OE2	3.886
5TLK	G_LYS_153	NZ	G_GLU_199	OE1	2.760
5TLK	G_LYS_187	NZ	G_GLU_191	OE2	2.938
5TLK	G_HIS_193	ND1	G_ASP_189	OD1	3.813
5TLK	G_ARG_215	NH1	G_GLU_191	OE1	3.873
5TLK	H_ARG_38	NH1	H_ASP_90	OD1	2.755
5TLK	H_ARG_38	NH2	H_GLU_46	OE1	3.268
5TLK	H_ARG_38	NH2	H_GLU_46	OE2	3.476
5TLK	H_ARG_38	NH2	H_ASP_90	OD1	3.679
5TLK	H_LYS_65	NZ	H_ASP_62	OD1	3.982
5TLK	H_ARG_67	NH1	H_ASP_90	OD2	2.783
5TLK	H_ARG_67	NH2	H_ASP_90	OD1	2.925
5TLK	H_ARG_67	NH2	H_ASP_90	OD2	2.986
5TLK	H_ARG_98	NH2	H_ASP_105	OD1	3.818
5TLK	H_ARG_98	NH2	H_ASP_105	OD2	2.712
5TLK	H_ARG_100	NH1	G_GLU_59	OE1	3.531
5TLK	H_ARG_100	NH1	Y_ASP_43	OD2	3.423
5TLK	H_ARG_100	NH2	G_GLU_59	OE1	2.787
5TLK	H_ARG_100	NH2	G_GLU_59	OE2	3.306
5TLK	H_LYS_147	NZ	H_ASP_148	OD1	3.296
5TLK	H_LYS_147	NZ	H_ASP_148	OD2	3.127
5TLK	H_LYS_213	NZ	G_GLU_127	OE1	3.569
5TLK	X_LYS_17	NZ	B_ASP_55	OD1	3.914
5TLK	X_LYS_17	NZ	B_ASP_55	OD2	3.018
5TLK	X_LYS_17	NZ	B_ASP_57	OD2	3.114
5TLK	X_HIS_36	NE2	B_ASP_104	OD1	3.010
5TLK	X_HIS_36	NE2	B_ASP_104	OD2	2.891
5TLK	X_ARG_37	NH2	B_ASP_104	OD1	2.703
5TLK	X_HIS_56	ND1	X_ASP_54	OD1	3.625
5TLK	X_ARG_58	NH2	X_ASP_54	OD1	2.720
5TLK	X_ARG_58	NH2	X_ASP_54	OD2	3.583
5TLK	X_ARG_74	NH1	X_GLU_83	OE2	3.772
5TLK	X_ARG_74	NH2	X_GLU_83	OE2	3.777
5TLK	Y_LYS_17	NZ	F_ASP_55	OD1	3.581
5TLK	Y_LYS_17	NZ	F_ASP_55	OD2	3.170
5TLK	Y_LYS_17	NZ	F_ASP_57	OD2	3.380
5TLK	Y_HIS_36	NE2	F_ASP_104	OD1	3.198
5TLK	Y_HIS_36	NE2	F_ASP_104	OD2	2.793
5TLK	Y_ARG_37	NH2	F_ASP_104	OD1	3.616
5TLK	Y_ARG_58	NH2	Y_ASP_54	OD1	3.024

5TLK	Y_ARG_74	NH1	Y_GLU_83	OE2	3.804
5TLK	Y_ARG_74	NH2	Y_GLU_83	OE2	3.441

Table 716: 5TLK-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5TRU	L_ARG_24	NH1	L_ASP_71	OD2	3.954
5TRU	L_ARG_55	NH2	L_ASP_61	OD1	3.408
5TRU	L_ARG_62	NH2	L_ASP_83	OD1	2.775
5TRU	L_ARG_62	NH2	L_ASP_83	OD2	3.715
5TRU	L_LYS_150	NZ	L_GLU_196	OE1	3.945
5TRU	L_HIS_190	ND1	L_ASP_152	OD2	3.931
5TRU	H_ARG_38	NH1	H_ASP_90	OD1	2.859
5TRU	H_ARG_38	NH2	H_GLU_46	OE1	3.419
5TRU	H_ARG_38	NH2	H_ASP_90	OD1	3.391
5TRU	H_ARG_67	NH1	H_ASP_90	OD1	3.755
5TRU	H_ARG_67	NH1	H_ASP_90	OD2	2.634
5TRU	H_ARG_67	NH2	H_ASP_90	OD1	2.978
5TRU	H_ARG_67	NH2	H_ASP_90	OD2	3.388
5TRU	H_ARG_98	NH2	H_ASP_106	OD1	3.783
5TRU	H_ARG_98	NH2	H_ASP_106	OD2	2.740
5TRU	H_LYS_148	NZ	H_ASP_149	OD1	3.967
5TRU	H_LYS_148	NZ	H_ASP_149	OD2	3.741
5TRU	L_ARG_55	NH2	L_ASP_61	OD1	2.796
5TRU	L_ARG_62	NH2	L_ASP_83	OD1	2.608
5TRU	L_ARG_62	NH2	L_ASP_83	OD2	3.126
5TRU	L_ARG_78	NH1	L_GLU_80	OE2	2.858
5TRU	L_LYS_104	NZ	L_GLU_166	OE2	3.131
5TRU	L_LYS_127	NZ	L_ASP_123	OD2	3.360
5TRU	h_ARG_38	NH1	h_ASP_90	OD1	2.730
5TRU	h_ARG_38	NH2	h_GLU_46	OE1	3.334
5TRU	h_ARG_38	NH2	h_ASP_90	OD1	3.607
5TRU	h_ARG_67	NH1	h_ASP_90	OD1	3.906
5TRU	h_ARG_67	NH1	h_ASP_90	OD2	2.771
5TRU	h_ARG_67	NH2	h_ASP_90	OD1	3.264
5TRU	h_ARG_67	NH2	h_ASP_90	OD2	3.554
5TRU	h_ARG_98	NH2	h_ASP_106	OD2	3.484
5TRU	h_HIS_169	NE2	L_ASP_168	OD2	3.995

Table 717: 5TRU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5TZ2	H_LYS_12	NZ	H_GLU_16	OE1	3.837
5TZ2	H_ARG_38	NH2	H_GLU_46	OE1	3.145
5TZ2	H_ARG_38	NH2	H_GLU_46	OE2	3.092
5TZ2	H_ARG_59	NH2	H_ASP_57	OD1	3.404
5TZ2	H_ARG_59	NH2	H_ASP_57	OD2	2.670
5TZ2	H_ARG_98	NH2	H_ASP_108	OD1	3.872
5TZ2	H_ARG_98	NH2	H_ASP_108	OD2	2.930
5TZ2	H_ARG_101	NH1	C_ASP_46	OD2	3.182
5TZ2	H_HIS_105	NE2	C_ASP_51	OD1	2.798
5TZ2	H_HIS_105	NE2	C_ASP_51	OD2	2.654
5TZ2	H_LYS_150	NZ	H_ASP_151	OD1	3.764
5TZ2	L_ARG_61	NH2	L_ASP_82	OD1	3.176
5TZ2	L_ARG_61	NH2	L_ASP_82	OD2	3.586
5TZ2	C_LYS_41	NZ	C_ASP_46	OD1	2.641
5TZ2	C_ARG_45	NH1	C_ASP_62	OD2	3.329
5TZ2	C_ARG_45	NH2	C_ASP_62	OD1	3.717
5TZ2	C_ARG_45	NH2	C_ASP_62	OD2	3.722
5TZ2	C_LYS_56	NZ	H_ASP_55	OD1	3.222
5TZ2	C_LYS_56	NZ	H_ASP_55	OD2	2.489
5TZ2	C_LYS_56	NZ	H_ASP_57	OD2	3.354
5TZ2	C_HIS_90	NE2	C_ASP_62	OD2	3.559
5TZ2	C_ARG_103	NH2	C_GLU_29	OE2	3.947
5TZ2	C_ARG_103	NH2	C_GLU_100	OE1	2.920
5TZ2	C_ARG_103	NH2	C_GLU_100	OE2	3.895

Table 718: 5TZ2-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5TZT	B_ARG_82	NH2	H_ASP_31	OD1	2.783
5TZT	B_ARG_82	NH2	H_ASP_31	OD2	3.806
5TZT	B_LYS_108	NZ	B_GLU_110	OE2	3.764
5TZT	B_HIS_194	ND1	B_ASP_156	OD2	2.786
5TZT	A_LYS_19	NZ	A_GLU_82	OE1	3.806
5TZT	A_ARG_38	NH1	A_ASP_90	OD2	3.536
5TZT	A_ARG_38	NH2	A_GLU_46	OE1	3.836
5TZT	A_ARG_38	NH2	A_GLU_46	OE2	2.074
5TZT	A_LYS_63	NZ	A_GLU_46	OE1	3.429
5TZT	A_LYS_63	NZ	A_GLU_46	OE2	3.935
5TZT	A_ARG_67	NH1	A_ASP_90	OD1	3.187
5TZT	A_ARG_67	NH1	A_ASP_90	OD2	3.312
5TZT	A_ARG_67	NH2	A_ASP_90	OD1	2.897
5TZT	A_ARG_87	NH1	A_GLU_89	OE1	3.756
5TZT	A_ARG_98	NH1	A_ASP_105	OD1	3.423
5TZT	A_ARG_98	NH1	A_ASP_105	OD2	2.447
5TZT	A_HIS_102	ND1	D_GLU_104	OE2	3.803
5TZT	L_LYS_55	NZ	C_GLU_104	OE1	3.704
5TZT	L_LYS_55	NZ	C_GLU_104	OE2	2.899
5TZT	L_ARG_66	NH1	L_ASP_87	OD1	3.313
5TZT	L_ARG_66	NH1	L_ASP_87	OD2	2.679
5TZT	L_ARG_66	NH2	L_GLU_84	OE1	2.654
5TZT	L_ARG_66	NH2	L_GLU_84	OE2	3.502
5TZT	L_HIS_194	ND1	L_ASP_156	OD2	3.224
5TZT	H_ARG_38	NH2	H_GLU_46	OE1	3.226
5TZT	H_LYS_63	NZ	H_GLU_46	OE2	3.670
5TZT	H_ARG_67	NH2	H_ASP_90	OD2	3.363
5TZT	H_ARG_98	NH1	H_ASP_105	OD1	3.531
5TZT	H_ARG_98	NH1	H_ASP_105	OD2	2.846
5TZT	H_ARG_98	NH2	H_ASP_105	OD1	3.738
5TZT	H_HIS_102	ND1	C_GLU_104	OE1	2.856
5TZT	C_ARG_45	NH1	C_ASP_62	OD1	2.637
5TZT	C_ARG_45	NH1	C_ASP_62	OD2	2.581
5TZT	C_ARG_45	NH2	C_ASP_62	OD1	3.454
5TZT	C_HIS_90	NE2	C_ASP_62	OD1	3.571
5TZT	D_HIS_90	NE2	D_ASP_62	OD1	3.274
5TZT	D_ARG_103	NH2	D_GLU_100	OE1	2.563
5TZT	D_ARG_114	NH1	D_GLU_11	OE1	3.807
5TZT	D_ARG_114	NH1	D_GLU_11	OE2	3.964

Table 719: 5TZT-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5TZU	L.LYS_49	NZ	C.ASP_51	OD1	3.523
5TZU	L.LYS_49	NZ	C.ASP_51	OD2	2.772
5TZU	L.ARG_61	NH1	L.GLU_79	OE1	3.734
5TZU	L.ARG_61	NH1	L.GLU_81	OE2	3.054
5TZU	L.ARG_61	NH1	L.ASP_82	OD1	2.764
5TZU	L.ARG_61	NH1	L.ASP_82	OD2	3.551
5TZU	L.ARG_61	NH2	L.GLU_79	OE1	3.680
5TZU	L.ARG_96	NH1	C.GLU_104	OE1	3.230
5TZU	L.ARG_96	NH1	C.GLU_104	OE2	3.808
5TZU	L.ARG_96	NH2	C.GLU_104	OE1	2.901
5TZU	L.LYS_103	NZ	L.GLU_165	OE1	3.822
5TZU	L.LYS_103	NZ	L.GLU_165	OE2	3.206
5TZU	L.ARG_211	NH1	L.GLU_187	OE1	3.562
5TZU	H.ARG_38	NH1	H.ASP_90	OD2	2.785
5TZU	H.ARG_38	NH2	H.GLU_46	OE1	2.862
5TZU	H.ARG_38	NH2	H.GLU_46	OE2	3.976
5TZU	H.ARG_38	NH2	H.ASP_90	OD2	3.917
5TZU	H.ARG_67	NH1	H.ASP_90	OD1	2.777
5TZU	H.ARG_67	NH1	H.ASP_90	OD2	3.488
5TZU	H.ARG_67	NH2	H.ASP_90	OD1	3.415
5TZU	H.ARG_67	NH2	H.ASP_90	OD2	3.088
5TZU	H.ARG_98	NH2	H.ASP_106	OD1	3.900
5TZU	H.ARG_98	NH2	H.ASP_106	OD2	2.795
5TZU	H.LYS_214	NZ	L.GLU_123	OE1	2.584
5TZU	H.LYS_214	NZ	L.GLU_123	OE2	3.416
5TZU	C.LYS_39	NZ	L.ASP_31	OD1	3.076
5TZU	C.LYS_39	NZ	L.ASP_31	OD2	2.978
5TZU	C.LYS_39	NZ	C.ASP_46	OD1	3.593
5TZU	C.LYS_39	NZ	C.GLU_97	OE2	3.431
5TZU	C.LYS_41	NZ	C.ASP_46	OD2	2.556
5TZU	C.ARG_45	NH1	C.ASP_62	OD2	3.407
5TZU	C.ARG_45	NH2	C.ASP_62	OD1	3.389
5TZU	C.ARG_45	NH2	C.ASP_62	OD2	3.679
5TZU	C.HIS_90	NE2	C.ASP_62	OD2	3.453
5TZU	C.ARG_103	NH1	C.GLU_29	OE2	3.912
5TZU	C.ARG_103	NH2	C.GLU_29	OE1	3.883
5TZU	C.ARG_103	NH2	C.GLU_100	OE1	3.920
5TZU	C.ARG_103	NH2	C.GLU_100	OE2	3.101

Table 720: 5TZU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5U3J	H_ARG_38	NH1	H_ASP_86	OD1	2.854
5U3J	H_ARG_38	NH2	H_GLU_46	OE1	3.279
5U3J	H_ARG_38	NH2	H_GLU_46	OE2	3.381
5U3J	H_ARG_50	NH2	H_GLU_58	OE1	2.789
5U3J	H_ARG_52A	NH1	H_ASP_53	OD1	3.274
5U3J	H_ARG_52A	NH1	H_ASP_53	OD2	3.547
5U3J	H_ARG_52A	NH1	A_ASP_674	OD1	3.805
5U3J	H_ARG_52A	NH1	A_ASP_674	OD2	3.646
5U3J	H_ARG_52A	NH2	A_ASP_674	OD2	3.216
5U3J	H_LYS_52C	NZ	A_ASP_674	OD1	3.151
5U3J	H_LYS_52C	NZ	A_ASP_674	OD2	3.836
5U3J	H_ARG_66	NH1	H_ASP_86	OD1	3.711
5U3J	H_ARG_66	NH1	H_ASP_86	OD2	2.572
5U3J	H_ARG_66	NH2	H_ASP_86	OD1	2.894
5U3J	H_ARG_66	NH2	H_ASP_86	OD2	3.336
5U3J	H_ARG_71	NH2	H_ASP_73	OD1	3.654
5U3J	H_LYS_143	NZ	H_ASP_144	OD1	3.689
5U3J	H_LYS_209	NZ	L_GLU_123	OE1	3.171
5U3J	H_LYS_209	NZ	L_GLU_123	OE2	2.412
5U3J	L_ARG_24	NH1	L_ASP_70	OD1	3.454
5U3J	L_ARG_24	NH1	L_ASP_70	OD2	3.616
5U3J	L_LYS_39	NZ	L_GLU_81	OE1	2.718
5U3J	L_ARG_61	NH2	L_ASP_82	OD2	3.220
5U3J	L_LYS_149	NZ	L_GLU_195	OE1	2.981
5U3J	L_LYS_188	NZ	L_ASP_185	OD1	3.489
5U3J	L_ARG_211	NH1	L_GLU_187	OE2	3.588

Table 721: 5U3J-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5U3N	H_ARG_38	NH1	H_ASP_86	OD1	3.106
5U3N	H_ARG_38	NH2	H_GLU_46	OE1	3.388
5U3N	H_ARG_38	NH2	H_GLU_46	OE2	3.678
5U3N	H_ARG_50	NH2	H_ASP_58	OD2	3.019
5U3N	H_ARG_52A	NH1	A_ASP_674	OD2	2.997
5U3N	H_ARG_52A	NH2	H_ASP_53	OD1	2.927
5U3N	H_ARG_52A	NH2	H_ASP_53	OD2	3.679
5U3N	H_ARG_52A	NH2	A_ASP_674	OD1	3.173
5U3N	H_ARG_52A	NH2	A_ASP_674	OD2	3.047
5U3N	H_ARG_66	NH1	H_ASP_86	OD1	3.888
5U3N	H_ARG_66	NH1	H_ASP_86	OD2	2.734
5U3N	H_ARG_66	NH2	H_ASP_86	OD1	3.118
5U3N	H_ARG_66	NH2	H_ASP_86	OD2	3.431
5U3N	H_ARG_71	NH2	H_ASP_73	OD1	3.283
5U3N	H_ARG_100B	NH1	L_ASP_31	OD1	3.593
5U3N	H_ARG_100B	NH1	L_ASP_31	OD2	2.967
5U3N	H_ARG_100B	NH2	H_GLU_100E	OE1	3.425
5U3N	H_ARG_100B	NH2	H_GLU_100E	OE2	2.907
5U3N	H_ARG_100B	NH2	L_ASP_31	OD1	2.974
5U3N	H_ARG_100B	NH2	L_ASP_31	OD2	3.816
5U3N	H_LYS_143	NZ	H_ASP_144	OD1	3.337
5U3N	H_LYS_209	NZ	L_GLU_123	OE1	3.254
5U3N	H_ARG_210	NH1	H_GLU_212	OE2	3.469
5U3N	H_ARG_210	NH2	H_GLU_212	OE2	3.206
5U3N	L_LYS_30	NZ	H_GLU_100E	OE1	3.899
5U3N	L_ARG_55	NH2	H_ASP_101	OD1	3.682
5U3N	L_ARG_55	NH2	H_ASP_101	OD2	2.901
5U3N	L_ARG_61	NH1	L_ASP_82	OD1	3.771
5U3N	L_ARG_61	NH1	L_ASP_82	OD2	2.649
5U3N	L_ARG_61	NH2	L_ASP_82	OD1	3.486
5U3N	L_ARG_61	NH2	L_ASP_82	OD2	3.672
5U3N	L_LYS_149	NZ	L_GLU_195	OE1	2.891
5U3N	L_LYS_190	NZ	L_GLU_213	OE1	3.468
5U3N	L_ARG_211	NH1	L_GLU_187	OE2	3.281

Table 722: 5U3N-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5UCB	H_ARG_38	NH1	H_ASP_86	OD1	2.881
5UCB	H_ARG_38	NH2	H_GLU_46	OE1	3.076
5UCB	H_ARG_38	NH2	H_GLU_46	OE2	3.531
5UCB	H_ARG_38	NH2	H_ASP_86	OD1	3.930
5UCB	H_ARG_66	NH1	H_ASP_86	OD1	3.749
5UCB	H_ARG_66	NH1	H_ASP_86	OD2	2.753
5UCB	H_ARG_66	NH2	H_ASP_86	OD1	3.062
5UCB	H_ARG_66	NH2	H_ASP_86	OD2	3.559
5UCB	H_ARG_94	NH2	H_ASP_101	OD2	3.041
5UCB	H_LYS_143	NZ	H_ASP_144	OD1	3.312
5UCB	H_LYS_143	NZ	H_ASP_144	OD2	3.791
5UCB	L_ARG_24	NH1	L_ASP_70	OD1	3.024
5UCB	L_ARG_24	NH1	L_ASP_70	OD2	3.164
5UCB	L_ARG_61	NH2	L_GLU_81	OE2	3.626
5UCB	L_ARG_61	NH2	L_ASP_82	OD1	2.851
5UCB	L_ARG_61	NH2	L_ASP_82	OD2	3.578
5UCB	L_ARG_66	NH2	B_ASP_51	OD1	2.894
5UCB	L_LYS_103	NZ	L_GLU_165	OE1	2.767
5UCB	L_LYS_103	NZ	L_GLU_165	OE2	3.262
5UCB	L_LYS_149	NZ	L_GLU_195	OE1	3.236
5UCB	L_LYS_149	NZ	L_GLU_195	OE2	2.876
5UCB	L_LYS_188	NZ	L_ASP_185	OD1	3.509
5UCB	B_LYS_16	NZ	B_ASP_132	OD1	2.899
5UCB	B_LYS_40	NZ	B_GLU_55	OE1	3.387
5UCB	B_HIS_52	NE2	B_GLU_87	OE1	3.757
5UCB	B_ARG_103	NH1	B_ASP_101	OD2	2.895
5UCB	B_ARG_103	NH2	B_ASP_101	OD2	3.593
5UCB	B_ARG_107	NH2	B_GLU_104	OE1	3.008
5UCB	B_ARG_107	NH2	B_GLU_104	OE2	3.594
5UCB	B_ARG_122	NH2	B_GLU_119	OE1	3.126
5UCB	B_HIS_133	ND1	B_ASP_117	OD1	2.951
5UCB	B_HIS_133	ND1	B_ASP_117	OD2	3.612
5UCB	B_HIS_133	ND1	B_GLU_118	OE2	3.928
5UCB	B_ARG_144	NH2	L_ASP_91	OD1	2.844
5UCB	B_ARG_144	NH2	L_ASP_91	OD2	3.495

Table 723: 5UCB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5UEA	A_ARG_38	NH1	A_ASP_86	OD1	2.925
5UEA	A_ARG_38	NH2	A_GLU_46	OE1	3.053
5UEA	A_ARG_38	NH2	A_GLU_46	OE2	3.718
5UEA	A_ARG_38	NH2	A_ASP_86	OD1	3.982
5UEA	A_LYS_64	NZ	A_ASP_61	OD1	3.564
5UEA	A_ARG_66	NH1	A_ASP_86	OD1	3.801
5UEA	A_ARG_66	NH1	A_ASP_86	OD2	2.753
5UEA	A_ARG_66	NH2	A_ASP_86	OD1	3.014
5UEA	A_ARG_66	NH2	A_ASP_86	OD2	3.470
5UEA	A_LYS_75	NZ	A_ASP_72	OD2	2.831
5UEA	A_ARG_83	NH1	A_GLU_85	OE2	3.478
5UEA	A_ARG_94	NH1	A_ASP_101	OD2	3.648
5UEA	A_LYS_143	NZ	A_ASP_144	OD1	3.213
5UEA	A_LYS_143	NZ	A_ASP_144	OD2	3.068
5UEA	A_LYS_210	NZ	A_GLU_212	OE2	3.717
5UEA	X_LYS_10	NZ	X_GLU_25	OE1	2.830
5UEA	X_LYS_10	NZ	X_GLU_25	OE2	3.963
5UEA	X_LYS_10	NZ	D_GLU_29	OE1	3.740
5UEA	X_LYS_10	NZ	D_GLU_29	OE2	2.855
5UEA	X_HIS_36	ND1	X_ASP_102	OD1	3.747
5UEA	X_HIS_53	ND1	X_ASP_54	OD1	3.697
5UEA	X_HIS_53	NE2	X_ASP_54	OD1	3.655
5UEA	X_LYS_71	NZ	D_GLU_29	OE2	3.320
5UEA	X_ARG_104	NH1	X_ASP_102	OD2	3.117
5UEA	X_ARG_104	NH2	X_ASP_102	OD2	3.925
5UEA	X_ARG_108	NH2	X_GLU_105	OE1	2.916
5UEA	X_ARG_108	NH2	X_GLU_105	OE2	3.333
5UEA	X_ARG_123	NH2	X_GLU_120	OE1	3.394
5UEA	X_HIS_134	ND1	X_ASP_118	OD2	2.696
5UEA	X_HIS_134	ND1	X_GLU_119	OE1	3.900
5UEA	X_HIS_134	NE2	X_ASP_133	OD2	3.951
5UEA	H_ARG_38	NH1	H_ASP_86	OD1	2.893
5UEA	H_ARG_38	NH2	H_GLU_46	OE1	3.038
5UEA	H_ARG_38	NH2	H_GLU_46	OE2	3.945
5UEA	H_ARG_38	NH2	H_ASP_86	OD1	3.946
5UEA	H_ARG_66	NH1	H_ASP_86	OD1	3.977
5UEA	H_ARG_66	NH1	H_ASP_86	OD2	2.837
5UEA	H_ARG_66	NH2	H_ASP_86	OD1	3.030
5UEA	H_ARG_66	NH2	H_ASP_86	OD2	3.367
5UEA	H_LYS_75	NZ	H_ASP_72	OD2	3.470
5UEA	H_ARG_94	NH1	H_ASP_101	OD2	3.608
5UEA	H_LYS_143	NZ	H_ASP_144	OD1	3.356
5UEA	H_LYS_143	NZ	H_ASP_144	OD2	3.506
5UEA	D_LYS_10	NZ	X_GLU_29	OE1	3.485
5UEA	D_LYS_10	NZ	X_GLU_29	OE2	2.490
5UEA	D_LYS_10	NZ	D_GLU_25	OE1	2.206
5UEA	D_LYS_10	NZ	D_GLU_25	OE2	3.753
5UEA	D_HIS_36	NE2	D_ASP_102	OD2	3.900
5UEA	D_LYS_70	NZ	X_GLU_29	OE2	3.861
5UEA	D_ARG_104	NH1	D_ASP_102	OD2	3.466
5UEA	D_ARG_108	NH2	D_GLU_105	OE1	2.929
5UEA	D_ARG_108	NH2	D_GLU_105	OE2	3.455
5UEA	D_HIS_134	ND1	D_ASP_118	OD2	2.708
5UEA	L_ARG_24	NH2	L_ASP_70	OD1	3.498
5UEA	L_ARG_24	NH2	L_ASP_70	OD2	2.931
5UEA	L_ARG_61	NH2	L_GLU_81	OE2	3.429
5UEA	L_ARG_61	NH2	L_ASP_82	OD1	2.822

5UEA	L_ARG_61	NH2	L_ASP_82	OD2	3.535
5UEA	L_LYS_103	NZ	L_GLU_165	OE1	2.845
5UEA	L_LYS_103	NZ	L_GLU_165	OE2	3.041
5UEA	L_LYS_149	NZ	L_GLU_195	OE1	3.248
5UEA	L_LYS_183	NZ	L_GLU_187	OE1	3.535
5UEA	L_LYS_183	NZ	L_GLU_187	OE2	2.491
5UEA	B_ARG_24	NH1	B_ASP_70	OD1	2.938
5UEA	B_ARG_24	NH1	B_ASP_70	OD2	3.769
5UEA	B_ARG_61	NH2	B_GLU_81	OE2	3.252
5UEA	B_ARG_61	NH2	B_ASP_82	OD1	2.947
5UEA	B_ARG_61	NH2	B_ASP_82	OD2	3.541
5UEA	B_LYS_103	NZ	B_GLU_165	OE1	3.082
5UEA	B_LYS_103	NZ	B_GLU_165	OE2	2.513
5UEA	B_LYS_107	NZ	B_ASP_17	OD2	3.363
5UEA	B_ARG_142	NH1	B_GLU_105	OE1	2.937
5UEA	B_ARG_142	NH1	B_GLU_105	OE2	2.716
5UEA	B_ARG_142	NH2	B_GLU_105	OE1	2.783
5UEA	B_LYS_149	NZ	B_GLU_195	OE1	3.063
5UEA	B_LYS_183	NZ	B_GLU_187	OE2	3.815
5UEA	B_ARG_211	NH1	B_GLU_187	OE1	3.735

Table 724: 5UEA-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5UEK	A_LYS_10	NZ	A_GLU_25	OE1	3.987
5UEK	A_HIS_36	ND1	A_ASP_154	OD1	3.867
5UEK	A_HIS_36	NE2	A_ASP_102	OD1	3.958
5UEK	A_LYS_41	NZ	A_GLU_39	OE1	3.964
5UEK	A_LYS_41	NZ	A_GLU_56	OE1	2.739
5UEK	A_ARG_49	NH1	A_GLU_88	OE1	3.431
5UEK	A_ARG_104	NH1	A_ASP_102	OD2	2.895
5UEK	A_ARG_104	NH2	A_ASP_102	OD2	3.461
5UEK	A_ARG_108	NH2	A_GLU_105	OE1	2.914
5UEK	A_ARG_108	NH2	A_GLU_105	OE2	3.466
5UEK	A_ARG_123	NH1	A_GLU_116	OE1	3.682
5UEK	A_HIS_134	ND1	A_ASP_133	OD1	2.831
5UEK	A_HIS_134	NE2	A_GLU_119	OE1	3.693
5UEK	A_ARG_145	NH2	L_ASP_91	OD1	2.787
5UEK	A_ARG_145	NH2	L_ASP_91	OD2	3.426
5UEK	H_ARG_38	NH1	H_ASP_86	OD2	2.930
5UEK	H_ARG_38	NH2	H_GLU_46	OE1	3.662
5UEK	H_ARG_38	NH2	H_GLU_46	OE2	3.239
5UEK	H_ARG_38	NH2	H_GLU_85	OE1	2.889
5UEK	H_ARG_38	NH2	H_ASP_86	OD2	3.876
5UEK	H_ARG_66	NH1	H_ASP_86	OD1	2.840
5UEK	H_ARG_66	NH1	H_ASP_86	OD2	3.752
5UEK	H_ARG_66	NH2	H_GLU_85	OE1	3.536
5UEK	H_ARG_66	NH2	H_ASP_86	OD1	3.599
5UEK	H_ARG_66	NH2	H_ASP_86	OD2	3.048
5UEK	H_ARG_83	NH1	H_GLU_85	OE2	3.252
5UEK	H_ARG_94	NH2	H_ASP_101	OD1	3.975
5UEK	H_ARG_94	NH2	H_ASP_101	OD2	2.845
5UEK	H_LYS_143	NZ	H_ASP_144	OD1	3.123
5UEK	H_LYS_143	NZ	H_ASP_144	OD2	3.057
5UEK	H_LYS_210	NZ	H_GLU_212	OE1	3.851
5UEK	H_LYS_210	NZ	H_GLU_212	OE2	2.516
5UEK	L_ARG_24	NH1	L_ASP_70	OD1	3.080
5UEK	L_ARG_24	NH1	L_ASP_70	OD2	2.941
5UEK	L_ARG_61	NH2	L_GLU_81	OE1	3.355
5UEK	L_ARG_61	NH2	L_ASP_82	OD1	2.825
5UEK	L_ARG_61	NH2	L_ASP_82	OD2	3.599
5UEK	L_ARG_66	NH2	A_ASP_52	OD1	2.873
5UEK	L_LYS_103	NZ	L_GLU_105	OE2	2.640
5UEK	L_LYS_103	NZ	L_GLU_165	OE1	3.290
5UEK	L_LYS_149	NZ	L_GLU_195	OE2	3.692
5UEK	L_LYS_183	NZ	L_GLU_187	OE1	2.986

Table 725: 5UEK-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5UG0	A_LYS_44	NZ	A_ASP_276	OD1	3.145
5UG0	A_ARG_106	NH1	A_GLU_85	OE1	3.304
5UG0	A_ARG_106	NH1	B_GLU_69	OE1	3.096
5UG0	A_ARG_106	NH1	B_GLU_69	OE2	3.964
5UG0	A_ARG_106	NH2	A_GLU_85	OE1	2.806
5UG0	A_ARG_106	NH2	A_GLU_85	OE2	3.674
5UG0	A_ARG_106	NH2	B_GLU_69	OE1	3.415
5UG0	A_ARG_106	NH2	B_GLU_69	OE2	3.059
5UG0	A_HIS_141	ND1	A_GLU_70	OE2	2.794
5UG0	A_LYS_149	NZ	A_GLU_72	OE1	3.216
5UG0	A_LYS_149	NZ	A_GLU_72	OE2	2.794
5UG0	A_LYS_172	NZ	A_GLU_116	OE2	3.654
5UG0	A_ARG_192	NH1	A_GLU_198	OE1	3.844
5UG0	A_ARG_192	NH1	A_GLU_198	OE2	3.866
5UG0	A_LYS_222	NZ	A_ASP_225	OD1	3.696
5UG0	A_LYS_222	NZ	A_GLU_227	OE2	3.476
5UG0	A_LYS_222	NZ	D_ASP_107	OD2	3.472
5UG0	A_ARG_255	NH2	A_GLU_119	OE2	3.754
5UG0	A_ARG_255	NH2	A_GLU_124	OE2	3.685
5UG0	A_ARG_262	NH1	A_GLU_175	OE1	3.614
5UG0	A_ARG_262	NH1	A_GLU_175	OE2	2.850
5UG0	A_ARG_311	NH1	B_ASP_90	OD1	2.840
5UG0	A_ARG_311	NH2	B_ASP_86	OD1	2.770
5UG0	A_ARG_311	NH2	B_ASP_90	OD1	3.313
5UG0	A_ARG_322	NH2	A_GLU_25	OE2	3.810
5UG0	B_LYS_68	NZ	A_GLU_107	OE2	3.009
5UG0	B_ARG_75	NH1	B_GLU_78	OE2	3.343
5UG0	B_LYS_116	NZ	B_GLU_120	OE2	3.389
5UG0	B_LYS_123	NZ	B_GLU_120	OE1	3.342
5UG0	B_LYS_123	NZ	B_GLU_120	OE2	3.653
5UG0	B_LYS_131	NZ	B_GLU_139	OE1	3.933
5UG0	B_LYS_153	NZ	B_GLU_150	OE1	3.568
5UG0	B_LYS_153	NZ	B_GLU_150	OE2	2.976
5UG0	B_LYS_161	NZ	B_GLU_165	OE1	3.465
5UG0	C_ARG_55	NH1	C_ASP_61	OD1	3.504
5UG0	C_ARG_62	NH2	C_GLU_82	OE1	3.126
5UG0	C_ARG_62	NH2	C_GLU_82	OE2	3.930
5UG0	C_ARG_62	NH2	C_ASP_83	OD1	2.816
5UG0	C_ARG_62	NH2	C_ASP_83	OD2	3.378
5UG0	C_LYS_109	NZ	C_GLU_107	OE1	3.664
5UG0	C_ARG_144	NH1	C_GLU_107	OE1	3.309
5UG0	C_ARG_144	NH1	C_GLU_107	OE2	3.710
5UG0	C_ARG_144	NH1	C_GLU_167	OE1	3.879
5UG0	C_ARG_144	NH2	C_GLU_167	OE1	3.902
5UG0	C_ARG_144	NH2	C_GLU_167	OE2	3.194
5UG0	C_LYS_147	NZ	C_GLU_145	OE2	2.927
5UG0	C_LYS_151	NZ	C_GLU_197	OE1	3.587
5UG0	C_LYS_151	NZ	C_GLU_197	OE2	3.166
5UG0	C_HIS_191	ND1	C_ASP_153	OD2	3.193
5UG0	D_ARG_38	NH1	D_ASP_89	OD1	3.285
5UG0	D_ARG_38	NH2	D_GLU_46	OE1	3.648
5UG0	D_ARG_38	NH2	D_ASP_89	OD1	3.488
5UG0	D_ARG_86	NH2	D_ASP_89	OD1	3.223
5UG0	D_ARG_100	NH1	A_ASP_190	OD1	3.522
5UG0	D_ARG_100	NH1	A_ASP_190	OD2	3.877
5UG0	D_HIS_178	NE2	C_ASP_169	OD2	3.490
5UG0	D_LYS_223	NZ	C_GLU_125	OE2	3.392

Table 726: 5UG0-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5UJZ	A_LYS_86	NZ	A_GLU_90	OE2	3.056
5UJZ	A_ARG_106	NH1	A_GLU_85	OE1	3.777
5UJZ	A_ARG_106	NH1	A_GLU_85	OE2	2.785
5UJZ	A_ARG_106	NH1	B_GLU_569	OE2	3.797
5UJZ	A_ARG_106	NH2	A_GLU_85	OE1	3.157
5UJZ	A_ARG_106	NH2	A_GLU_85	OE2	3.125
5UJZ	A_ARG_106	NH2	B_GLU_569	OE1	3.958
5UJZ	A_ARG_106	NH2	B_GLU_569	OE2	3.070
5UJZ	A_HIS_141	ND1	A_GLU_70	OE2	3.820
5UJZ	A_LYS_174	NZ	A_GLU_116	OE2	3.728
5UJZ	A_ARG_192	NH2	A_GLU_198	OE2	2.656
5UJZ	A_HIS_208	ND1	A_GLU_238	OE2	3.816
5UJZ	A_LYS_219	NZ	A_GLU_227	OE2	3.960
5UJZ	A_ARG_262	NH1	A_GLU_175	OE1	2.805
5UJZ	A_ARG_262	NH1	A_GLU_175	OE2	3.687
5UJZ	A_ARG_311	NH1	B_ASP_586	OD1	3.689
5UJZ	A_ARG_311	NH1	B_ASP_590	OD1	3.217
5UJZ	A_ARG_311	NH1	B_ASP_590	OD2	3.955
5UJZ	A_ARG_311	NH2	B_ASP_586	OD1	2.782
5UJZ	B_LYS_551	NZ	B_GLU_603	OE1	3.842
5UJZ	B_LYS_558	NZ	F_GLU_597	OE1	3.688
5UJZ	B_LYS_558	NZ	F_GLU_597	OE2	3.874
5UJZ	B_ARG_576	NH1	D_GLU_574	OE1	3.986
5UJZ	B_ARG_576	NH1	D_GLU_574	OE2	3.042
5UJZ	B_ARG_576	NH2	C_GLU_104	OE2	3.168
5UJZ	B_LYS_582	NZ	B_ASP_586	OD2	3.643
5UJZ	B_LYS_583	NZ	D_ASP_585	OD1	3.717
5UJZ	B_ARG_606	NH2	F_ASP_609	OD2	2.744
5UJZ	B_LYS_623	NZ	B_GLU_632	OE2	3.820
5UJZ	B_LYS_631	NZ	B_GLU_639	OE1	3.976
5UJZ	B_LYS_643	NZ	A_GLU_4	OE1	2.954
5UJZ	B_LYS_643	NZ	A_ASP_5	OD1	2.763
5UJZ	B_LYS_643	NZ	A_ASP_5	OD2	3.863
5UJZ	B_LYS_643	NZ	B_GLU_529	OE2	3.375
5UJZ	B_LYS_653	NZ	B_GLU_650	OE1	3.647
5UJZ	B_LYS_661	NZ	B_GLU_647	OE1	3.374
5UJZ	B_ARG_670	NH2	B_GLU_671	OE2	2.839
5UJZ	C_LYS_86	NZ	C_GLU_90	OE2	3.056
5UJZ	C_ARG_106	NH1	C_GLU_85	OE1	3.777
5UJZ	C_ARG_106	NH1	C_GLU_85	OE2	2.784
5UJZ	C_ARG_106	NH1	D_GLU_569	OE2	3.872
5UJZ	C_ARG_106	NH2	C_GLU_85	OE1	3.158
5UJZ	C_ARG_106	NH2	C_GLU_85	OE2	3.125
5UJZ	C_ARG_106	NH2	D_GLU_569	OE2	3.260
5UJZ	C_HIS_141	ND1	C_GLU_70	OE2	3.819
5UJZ	C_LYS_174	NZ	C_GLU_116	OE2	3.728
5UJZ	C_ARG_192	NH2	C_GLU_198	OE2	2.657
5UJZ	C_HIS_208	ND1	C_GLU_238	OE2	3.817
5UJZ	C_LYS_219	NZ	C_GLU_227	OE2	3.960
5UJZ	C_ARG_262	NH1	C_GLU_175	OE1	2.805
5UJZ	C_ARG_262	NH1	C_GLU_175	OE2	3.686
5UJZ	C_ARG_311	NH1	D_ASP_586	OD1	3.865
5UJZ	C_ARG_311	NH1	D_ASP_590	OD1	3.148
5UJZ	C_ARG_311	NH1	D_ASP_590	OD2	3.998
5UJZ	C_ARG_311	NH2	D_ASP_586	OD1	2.921
5UJZ	D_LYS_551	NZ	D_GLU_603	OE1	3.842
5UJZ	D_LYS_558	NZ	B_GLU_597	OE1	3.772

5UJZ	D_LYS_572	NZ	E_GLU_238	OE1	3.910
5UJZ	D_ARG_576	NH1	F_GLU_574	OE1	3.863
5UJZ	D_ARG_576	NH1	F_GLU_574	OE2	2.716
5UJZ	D_ARG_576	NH2	E_GLU_104	OE2	3.170
5UJZ	D_LYS_582	NZ	D_ASP_586	OD2	3.642
5UJZ	D_LYS_583	NZ	F_ASP_585	OD1	3.807
5UJZ	D_ARG_606	NH2	B_ASP_609	OD2	2.766
5UJZ	D_LYS_623	NZ	D_GLU_632	OE2	3.820
5UJZ	D_LYS_631	NZ	D_GLU_639	OE1	3.976
5UJZ	D_LYS_643	NZ	C_GLU_4	OE1	3.185
5UJZ	D_LYS_643	NZ	C_ASP_5	OD1	2.519
5UJZ	D_LYS_643	NZ	C_ASP_5	OD2	3.642
5UJZ	D_LYS_643	NZ	D_GLU_529	OE2	3.375
5UJZ	D_LYS_653	NZ	D_GLU_650	OE1	3.648
5UJZ	D_LYS_661	NZ	D_GLU_647	OE1	3.376
5UJZ	D_ARG_670	NH2	D_GLU_671	OE2	2.839
5UJZ	E_LYS_86	NZ	E_GLU_90	OE2	3.056
5UJZ	E_ARG_106	NH1	E_GLU_85	OE1	3.777
5UJZ	E_ARG_106	NH1	E_GLU_85	OE2	2.784
5UJZ	E_ARG_106	NH2	E_GLU_85	OE1	3.158
5UJZ	E_ARG_106	NH2	E_GLU_85	OE2	3.126
5UJZ	E_ARG_106	NH2	F_GLU_569	OE2	3.361
5UJZ	E_HIS_141	ND1	E_GLU_70	OE2	3.819
5UJZ	E_LYS_174	NZ	E_GLU_116	OE2	3.728
5UJZ	E_ARG_192	NH2	E_GLU_198	OE2	2.656
5UJZ	E_HIS_208	ND1	E_GLU_238	OE2	3.816
5UJZ	E_LYS_219	NZ	E_GLU_227	OE2	3.960
5UJZ	E_ARG_262	NH1	E_GLU_175	OE1	2.805
5UJZ	E_ARG_262	NH1	E_GLU_175	OE2	3.687
5UJZ	E_ARG_311	NH1	F_ASP_586	OD1	3.477
5UJZ	E_ARG_311	NH1	F_ASP_590	OD1	3.629
5UJZ	E_ARG_311	NH2	F_ASP_586	OD1	2.793
5UJZ	F_LYS_551	NZ	F_GLU_603	OE1	3.843
5UJZ	F_ARG_576	NH1	B_GLU_574	OE1	3.655
5UJZ	F_ARG_576	NH1	B_GLU_574	OE2	2.847
5UJZ	F_ARG_576	NH2	A_GLU_104	OE2	3.211
5UJZ	F_LYS_582	NZ	F_ASP_586	OD2	3.643
5UJZ	F_LYS_583	NZ	B_ASP_585	OD1	3.548
5UJZ	F_ARG_606	NH2	D_ASP_609	OD2	2.609
5UJZ	F_LYS_623	NZ	F_GLU_632	OE2	3.821
5UJZ	F_LYS_631	NZ	F_GLU_639	OE1	3.976
5UJZ	F_LYS_643	NZ	E_GLU_4	OE1	3.009
5UJZ	F_LYS_643	NZ	E_ASP_5	OD1	2.882
5UJZ	F_LYS_643	NZ	E_ASP_5	OD2	3.935
5UJZ	F_LYS_643	NZ	F_GLU_529	OE2	3.375
5UJZ	F_LYS_653	NZ	F_GLU_650	OE1	3.646
5UJZ	F_LYS_661	NZ	F_GLU_647	OE1	3.375
5UJZ	F_ARG_670	NH2	F_GLU_671	OE2	2.839
5UJZ	G_HIS_160	NE2	G_ASP_158	OD1	3.708
5UJZ	G_ARG_163	NH1	G_ASP_214	OD1	3.087
5UJZ	G_ARG_163	NH2	G_GLU_171	OE1	2.822
5UJZ	G_ARG_163	NH2	G_GLU_171	OE2	3.867
5UJZ	G_ARG_191	NH1	G_ASP_214	OD2	3.584
5UJZ	G_ARG_225	NH1	A_ASP_190	OD1	3.090
5UJZ	G_ARG_225	NH1	A_ASP_190	OD2	3.996
5UJZ	G_ARG_225	NH2	A_ASP_190	OD1	3.715
5UJZ	G_ARG_225	NH2	A_ASP_190	OD2	3.410
5UJZ	H_HIS_160	NE2	H_ASP_158	OD1	3.708

5UJZ	H_ARG_163	NH1	H_ASP_214	OD1	3.088
5UJZ	H_ARG_163	NH2	H_GLU_171	OE1	2.821
5UJZ	H_ARG_163	NH2	H_GLU_171	OE2	3.867
5UJZ	H_ARG_191	NH1	H_ASP_214	OD2	3.583
5UJZ	H_ARG_225	NH1	C_ASP_190	OD1	3.041
5UJZ	H_ARG_225	NH2	C_ASP_190	OD1	3.552
5UJZ	H_ARG_225	NH2	C_ASP_190	OD2	3.366
5UJZ	I_HIS_160	NE2	I_ASP_158	OD1	3.708
5UJZ	I_ARG_163	NH1	I_ASP_214	OD1	3.088
5UJZ	I_ARG_163	NH2	I_GLU_171	OE1	2.823
5UJZ	I_ARG_163	NH2	I_GLU_171	OE2	3.868
5UJZ	I_ARG_191	NH1	I_ASP_214	OD2	3.584
5UJZ	I_ARG_225	NH1	E_ASP_190	OD1	3.119
5UJZ	I_ARG_225	NH1	E_ASP_190	OD2	3.970
5UJZ	I_ARG_225	NH2	E_ASP_190	OD1	3.713
5UJZ	I_ARG_225	NH2	E_ASP_190	OD2	3.347

Table 727: 5UJZ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5UK0	A_LYS_86	NZ	A_GLU_90	OE2	3.309
5UK0	A_ARG_106	NH1	A_GLU_85	OE1	3.645
5UK0	A_ARG_106	NH1	A_GLU_85	OE2	3.045
5UK0	A_ARG_106	NH1	B_GLU_569	OE2	3.967
5UK0	A_ARG_106	NH2	A_GLU_85	OE1	3.291
5UK0	A_ARG_106	NH2	A_GLU_85	OE2	3.562
5UK0	A_ARG_106	NH2	B_GLU_569	OE2	3.244
5UK0	A_LYS_174	NZ	A_GLU_116	OE2	3.452
5UK0	A_ARG_192	NH2	A_GLU_198	OE2	2.543
5UK0	A_HIS_208	ND1	A_GLU_238	OE2	3.818
5UK0	A_HIS_208	NE2	A_GLU_238	OE2	3.885
5UK0	A_ARG_220	NH2	C_ASP_241	OD1	3.711
5UK0	A_ARG_220	NH2	C_ASP_241	OD2	3.819
5UK0	A_ARG_262	NH1	A_GLU_175	OE1	3.069
5UK0	A_ARG_311	NH1	B_ASP_590	OD1	3.139
5UK0	A_ARG_311	NH1	B_ASP_590	OD2	3.961
5UK0	A_ARG_311	NH2	B_ASP_586	OD1	3.197
5UK0	B_LYS_551	NZ	B_GLU_603	OE1	3.035
5UK0	B_LYS_558	NZ	F_GLU_597	OE1	3.717
5UK0	B_LYS_568	NZ	A_GLU_107	OE2	3.962
5UK0	B_ARG_576	NH1	D_GLU_574	OE1	2.500
5UK0	B_ARG_576	NH1	D_GLU_574	OE2	3.431
5UK0	B_ARG_576	NH2	C_GLU_104	OE2	3.446
5UK0	B_ARG_576	NH2	D_GLU_574	OE1	3.430
5UK0	B_ARG_576	NH2	D_GLU_574	OE2	3.016
5UK0	B_LYS_582	NZ	B_ASP_586	OD2	3.693
5UK0	B_ARG_606	NH2	F_ASP_609	OD2	2.765
5UK0	B_LYS_623	NZ	B_GLU_632	OE2	3.579
5UK0	B_LYS_643	NZ	A_GLU_4	OE1	2.724
5UK0	B_LYS_643	NZ	A_ASP_5	OD1	2.705
5UK0	B_LYS_643	NZ	A_ASP_5	OD2	3.831
5UK0	B_LYS_643	NZ	B_GLU_529	OE2	3.437
5UK0	B_LYS_661	NZ	B_GLU_647	OE1	3.387
5UK0	B_ARG_670	NH2	B_GLU_671	OE2	2.699
5UK0	C_LYS_86	NZ	C_GLU_90	OE2	3.309
5UK0	C_ARG_106	NH1	C_GLU_85	OE1	3.646
5UK0	C_ARG_106	NH1	C_GLU_85	OE2	3.045
5UK0	C_ARG_106	NH1	D_GLU_569	OE2	3.998
5UK0	C_ARG_106	NH2	C_GLU_85	OE1	3.291
5UK0	C_ARG_106	NH2	C_GLU_85	OE2	3.562
5UK0	C_ARG_106	NH2	D_GLU_569	OE2	3.213
5UK0	C_LYS_174	NZ	C_GLU_116	OE2	3.452
5UK0	C_ARG_192	NH2	C_GLU_198	OE2	2.542
5UK0	C_HIS_208	ND1	C_GLU_238	OE2	3.819
5UK0	C_HIS_208	NE2	C_GLU_238	OE2	3.885
5UK0	C_ARG_220	NH2	E_ASP_241	OD1	3.755
5UK0	C_ARG_220	NH2	E_ASP_241	OD2	3.891
5UK0	C_ARG_262	NH1	C_GLU_175	OE1	3.069
5UK0	C_ARG_311	NH1	D_ASP_586	OD1	3.901
5UK0	C_ARG_311	NH1	D_ASP_590	OD1	3.110
5UK0	C_ARG_311	NH1	D_ASP_590	OD2	3.851
5UK0	C_ARG_311	NH2	D_ASP_586	OD1	2.981
5UK0	D_LYS_551	NZ	D_GLU_603	OE1	3.035
5UK0	D_LYS_558	NZ	B_GLU_597	OE1	3.800
5UK0	D_LYS_572	NZ	E_GLU_238	OE1	3.723
5UK0	D_ARG_576	NH1	F_GLU_574	OE1	2.823
5UK0	D_ARG_576	NH1	F_GLU_574	OE2	3.743

5UK0	D_ARG_576	NH2	E_GLU_104	OE2	3.003
5UK0	D_ARG_576	NH2	F_GLU_574	OE1	3.596
5UK0	D_ARG_576	NH2	F_GLU_574	OE2	3.278
5UK0	D_LYS_582	NZ	D_ASP_586	OD2	3.695
5UK0	D_ARG_606	NH2	B_ASP_609	OD2	2.683
5UK0	D_LYS_623	NZ	D_GLU_632	OE2	3.578
5UK0	D_LYS_643	NZ	C_GLU_4	OE1	2.844
5UK0	D_LYS_643	NZ	C_ASP_5	OD1	2.693
5UK0	D_LYS_643	NZ	C_ASP_5	OD2	3.673
5UK0	D_LYS_643	NZ	D_GLU_529	OE2	3.436
5UK0	D_LYS_661	NZ	D_GLU_647	OE1	3.387
5UK0	D_ARG_670	NH2	D_GLU_671	OE2	2.700
5UK0	E_LYS_86	NZ	E_GLU_90	OE2	3.309
5UK0	E_ARG_106	NH1	E_GLU_85	OE1	3.645
5UK0	E_ARG_106	NH1	E_GLU_85	OE2	3.045
5UK0	E_ARG_106	NH1	F_GLU_569	OE2	3.924
5UK0	E_ARG_106	NH2	E_GLU_85	OE1	3.291
5UK0	E_ARG_106	NH2	E_GLU_85	OE2	3.563
5UK0	E_ARG_106	NH2	F_GLU_569	OE2	3.130
5UK0	E_LYS_174	NZ	E_GLU_116	OE2	3.453
5UK0	E_ARG_192	NH2	E_GLU_198	OE2	2.543
5UK0	E_HIS_208	ND1	E_GLU_238	OE2	3.818
5UK0	E_HIS_208	NE2	E_GLU_238	OE2	3.885
5UK0	E_ARG_220	NH2	A_ASP_241	OD1	3.703
5UK0	E_ARG_220	NH2	A_ASP_241	OD2	3.860
5UK0	E_ARG_262	NH1	E_GLU_175	OE1	3.069
5UK0	E_ARG_311	NH1	F_ASP_586	OD1	3.927
5UK0	E_ARG_311	NH1	F_ASP_590	OD1	3.174
5UK0	E_ARG_311	NH1	F_ASP_590	OD2	3.882
5UK0	E_ARG_311	NH2	F_ASP_586	OD1	3.095
5UK0	F_LYS_551	NZ	F_GLU_603	OE1	3.034
5UK0	F_LYS_558	NZ	D_GLU_597	OE1	3.758
5UK0	F_LYS_568	NZ	E_GLU_107	OE2	3.989
5UK0	F_LYS_572	NZ	A_GLU_238	OE1	3.995
5UK0	F_ARG_576	NH1	B_GLU_574	OE1	2.515
5UK0	F_ARG_576	NH1	B_GLU_574	OE2	3.607
5UK0	F_ARG_576	NH2	A_GLU_104	OE2	3.281
5UK0	F_ARG_576	NH2	B_GLU_574	OE1	3.248
5UK0	F_ARG_576	NH2	B_GLU_574	OE2	3.003
5UK0	F_LYS_582	NZ	F_ASP_586	OD2	3.694
5UK0	F_ARG_606	NH2	D_ASP_609	OD2	2.740
5UK0	F_LYS_623	NZ	F_GLU_632	OE2	3.578
5UK0	F_LYS_643	NZ	E_GLU_4	OE1	2.987
5UK0	F_LYS_643	NZ	E_ASP_5	OD1	2.694
5UK0	F_LYS_643	NZ	E_ASP_5	OD2	3.721
5UK0	F_LYS_643	NZ	F_GLU_529	OE2	3.437
5UK0	F_LYS_661	NZ	F_GLU_647	OE1	3.387
5UK0	F_ARG_670	NH2	F_GLU_671	OE2	2.698
5UK0	G_ARG_163	NH1	G_ASP_214	OD1	2.891
5UK0	G_ARG_163	NH2	G_GLU_171	OE1	2.986
5UK0	G_ARG_163	NH2	G_GLU_171	OE2	3.691
5UK0	G_ARG_191	NH1	G_ASP_214	OD2	3.874
5UK0	G_ARG_225	NH1	A_ASP_190	OD1	3.056
5UK0	G_ARG_225	NH1	A_ASP_190	OD2	3.844
5UK0	G_ARG_225	NH1	G_ASP_233	OD1	3.964
5UK0	G_ARG_225	NH2	A_ASP_190	OD1	3.909
5UK0	G_ARG_225	NH2	A_ASP_190	OD2	3.442
5UK0	H_ARG_163	NH1	H_ASP_214	OD1	2.890

5UK0	H_ARG_163	NH2	H_GLU_171	OE1	2.986
5UK0	H_ARG_163	NH2	H_GLU_171	OE2	3.690
5UK0	H_ARG_191	NH1	H_ASP_214	OD2	3.874
5UK0	H_ARG_225	NH1	C_ASP_190	OD1	3.008
5UK0	H_ARG_225	NH1	C_ASP_190	OD2	3.873
5UK0	H_ARG_225	NH1	H_ASP_233	OD1	3.965
5UK0	H_ARG_225	NH2	C_ASP_190	OD1	3.782
5UK0	H_ARG_225	NH2	C_ASP_190	OD2	3.377
5UK0	I_ARG_163	NH1	I_ASP_214	OD1	2.890
5UK0	I_ARG_163	NH2	I_GLU_171	OE1	2.985
5UK0	I_ARG_163	NH2	I_GLU_171	OE2	3.690
5UK0	I_ARG_191	NH1	I_ASP_214	OD2	3.873
5UK0	I_ARG_225	NH1	E_ASP_190	OD1	3.078
5UK0	I_ARG_225	NH1	E_ASP_190	OD2	3.875
5UK0	I_ARG_225	NH1	I_ASP_233	OD1	3.965
5UK0	I_ARG_225	NH2	E_ASP_190	OD1	3.886
5UK0	I_ARG_225	NH2	E_ASP_190	OD2	3.433

Table 728: 5UK0-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5UK1	A_LYS_44	NZ	A_ASP_276	OD2	3.906
5UK1	A_LYS_86	NZ	A_GLU_90	OE2	3.504
5UK1	A_ARG_106	NH1	A_GLU_85	OE1	3.701
5UK1	A_ARG_106	NH1	A_GLU_85	OE2	3.090
5UK1	A_ARG_106	NH1	B_GLU_569	OE2	3.892
5UK1	A_ARG_106	NH2	A_GLU_85	OE1	3.008
5UK1	A_ARG_106	NH2	A_GLU_85	OE2	3.228
5UK1	A_ARG_106	NH2	B_GLU_569	OE2	2.755
5UK1	A_LYS_174	NZ	A_GLU_116	OE2	3.687
5UK1	A_ARG_192	NH2	A_GLU_198	OE2	2.985
5UK1	A_ARG_262	NH1	A_GLU_175	OE1	3.086
5UK1	A_ARG_311	NH1	B_ASP_590	OD1	2.545
5UK1	A_ARG_311	NH1	B_ASP_590	OD2	3.367
5UK1	A_ARG_311	NH2	B_ASP_586	OD1	3.117
5UK1	A_ARG_322	NH2	A_GLU_25	OE1	3.980
5UK1	B_LYS_558	NZ	F_GLU_597	OE1	3.470
5UK1	B_ARG_576	NH1	D_GLU_574	OE1	3.845
5UK1	B_ARG_576	NH1	D_GLU_574	OE2	3.273
5UK1	B_ARG_576	NH2	C_GLU_104	OE2	2.839
5UK1	B_LYS_582	NZ	B_ASP_586	OD2	3.755
5UK1	B_ARG_606	NH2	F_ASP_609	OD2	3.320
5UK1	B_LYS_623	NZ	B_GLU_632	OE2	3.460
5UK1	B_LYS_631	NZ	B_GLU_639	OE1	3.968
5UK1	B_LYS_643	NZ	A_GLU_4	OE1	2.898
5UK1	B_LYS_643	NZ	A_ASP_5	OD1	2.632
5UK1	B_LYS_643	NZ	A_ASP_5	OD2	3.703
5UK1	B_LYS_643	NZ	B_GLU_529	OE2	3.727
5UK1	B_LYS_653	NZ	B_GLU_650	OE1	3.697
5UK1	B_LYS_661	NZ	B_GLU_647	OE1	3.063
5UK1	B_ARG_670	NH2	B_GLU_671	OE2	2.925
5UK1	C_LYS_44	NZ	C_ASP_276	OD2	3.906
5UK1	C_LYS_86	NZ	C_GLU_90	OE2	3.504
5UK1	C_ARG_106	NH1	C_GLU_85	OE1	3.701
5UK1	C_ARG_106	NH1	C_GLU_85	OE2	3.090
5UK1	C_ARG_106	NH2	C_GLU_85	OE1	3.009
5UK1	C_ARG_106	NH2	C_GLU_85	OE2	3.227
5UK1	C_ARG_106	NH2	D_GLU_569	OE2	3.108
5UK1	C_LYS_174	NZ	C_GLU_116	OE2	3.686
5UK1	C_ARG_192	NH2	C_GLU_198	OE2	2.984
5UK1	C_ARG_262	NH1	C_GLU_175	OE1	3.087
5UK1	C_ARG_311	NH1	D_ASP_590	OD1	2.901
5UK1	C_ARG_311	NH1	D_ASP_590	OD2	3.798
5UK1	C_ARG_311	NH2	D_ASP_586	OD1	3.261
5UK1	C_ARG_322	NH2	C_GLU_25	OE1	3.979
5UK1	D_LYS_558	NZ	B_GLU_597	OE1	3.543
5UK1	D_ARG_576	NH1	F_GLU_574	OE1	3.490
5UK1	D_ARG_576	NH1	F_GLU_574	OE2	3.058
5UK1	D_ARG_576	NH2	E_GLU_104	OE2	3.186
5UK1	D_LYS_582	NZ	D_ASP_586	OD2	3.755
5UK1	D_ARG_606	NH2	B_ASP_609	OD2	3.177
5UK1	D_LYS_623	NZ	D_GLU_632	OE2	3.460
5UK1	D_LYS_631	NZ	D_GLU_639	OE1	3.968
5UK1	D_LYS_643	NZ	C_GLU_4	OE1	3.015
5UK1	D_LYS_643	NZ	C_ASP_5	OD1	2.615
5UK1	D_LYS_643	NZ	C_ASP_5	OD2	3.806
5UK1	D_LYS_643	NZ	D_GLU_529	OE2	3.727
5UK1	D_LYS_653	NZ	D_GLU_650	OE1	3.695

5UK1	D_LYS_661	NZ	D_GLU_647	OE1	3.063
5UK1	D_ARG_670	NH2	D_GLU_671	OE2	2.927
5UK1	E_LYS_44	NZ	E_ASP_276	OD2	3.905
5UK1	E_LYS_86	NZ	E_GLU_90	OE2	3.505
5UK1	E_ARG_106	NH1	E_GLU_85	OE1	3.700
5UK1	E_ARG_106	NH1	E_GLU_85	OE2	3.089
5UK1	E_ARG_106	NH2	E_GLU_85	OE1	3.009
5UK1	E_ARG_106	NH2	E_GLU_85	OE2	3.227
5UK1	E_ARG_106	NH2	F_GLU_569	OE2	2.991
5UK1	E_LYS_174	NZ	E_GLU_116	OE2	3.687
5UK1	E_ARG_192	NH2	E_GLU_198	OE2	2.984
5UK1	E_ARG_262	NH1	E_GLU_175	OE1	3.086
5UK1	E_ARG_311	NH1	F_ASP_590	OD1	2.696
5UK1	E_ARG_311	NH1	F_ASP_590	OD2	3.637
5UK1	E_ARG_311	NH2	F_ASP_586	OD1	3.291
5UK1	E_ARG_322	NH2	E_GLU_25	OE1	3.980
5UK1	F_LYS_558	NZ	D_GLU_597	OE1	3.566
5UK1	F_ARG_576	NH1	B_GLU_574	OE1	3.570
5UK1	F_ARG_576	NH1	B_GLU_574	OE2	3.065
5UK1	F_ARG_576	NH2	A_GLU_104	OE2	3.295
5UK1	F_LYS_582	NZ	F_ASP_586	OD2	3.755
5UK1	F_ARG_606	NH2	D_ASP_609	OD2	3.182
5UK1	F_LYS_623	NZ	F_GLU_632	OE2	3.459
5UK1	F_LYS_631	NZ	F_GLU_639	OE1	3.967
5UK1	F_LYS_643	NZ	E_GLU_4	OE1	3.024
5UK1	F_LYS_643	NZ	E_ASP_5	OD1	2.503
5UK1	F_LYS_643	NZ	E_ASP_5	OD2	3.650
5UK1	F_LYS_643	NZ	F_GLU_529	OE2	3.727
5UK1	F_LYS_653	NZ	F_GLU_650	OE1	3.696
5UK1	F_LYS_661	NZ	F_GLU_647	OE1	3.063
5UK1	F_ARG_670	NH2	F_GLU_671	OE2	2.926
5UK1	G_HIS_160	NE2	G_ASP_158	OD1	3.432
5UK1	G_ARG_163	NH1	G_ASP_214	OD1	2.991
5UK1	G_ARG_163	NH2	G_GLU_171	OE1	2.756
5UK1	G_ARG_163	NH2	G_GLU_171	OE2	3.832
5UK1	G_ARG_225	NH1	A_ASP_190	OD1	2.887
5UK1	G_ARG_225	NH1	A_ASP_190	OD2	3.709
5UK1	G_ARG_225	NH2	A_ASP_190	OD1	3.956
5UK1	G_ARG_225	NH2	A_ASP_190	OD2	3.555
5UK1	H_HIS_160	NE2	H_ASP_158	OD1	3.431
5UK1	H_ARG_163	NH1	H_ASP_214	OD1	2.991
5UK1	H_ARG_163	NH2	H_GLU_171	OE1	2.756
5UK1	H_ARG_163	NH2	H_GLU_171	OE2	3.832
5UK1	H_ARG_225	NH1	C_ASP_190	OD1	2.683
5UK1	H_ARG_225	NH1	C_ASP_190	OD2	3.511
5UK1	H_ARG_225	NH2	C_ASP_190	OD1	3.809
5UK1	H_ARG_225	NH2	C_ASP_190	OD2	3.346
5UK1	I_HIS_160	NE2	I_ASP_158	OD1	3.432
5UK1	I_ARG_163	NH1	I_ASP_214	OD1	2.991
5UK1	I_ARG_163	NH2	I_GLU_171	OE1	2.756
5UK1	I_ARG_163	NH2	I_GLU_171	OE2	3.832
5UK1	I_ARG_225	NH1	E_ASP_190	OD1	2.885
5UK1	I_ARG_225	NH1	E_ASP_190	OD2	3.789
5UK1	I_ARG_225	NH2	E_ASP_190	OD1	3.888
5UK1	I_ARG_225	NH2	E_ASP_190	OD2	3.567

Table 729: 5UK1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5UK2	A_LYS_86	NZ	A_GLU_90	OE2	3.657
5UK2	A_ARG_106	NH1	A_GLU_85	OE2	2.898
5UK2	A_ARG_106	NH1	B_GLU_569	OE2	3.935
5UK2	A_ARG_106	NH2	A_GLU_85	OE1	3.401
5UK2	A_ARG_106	NH2	A_GLU_85	OE2	3.141
5UK2	A_ARG_106	NH2	B_GLU_569	OE2	2.216
5UK2	A_HIS_141	ND1	A_GLU_70	OE2	3.497
5UK2	A_LYS_174	NZ	A_GLU_116	OE2	3.324
5UK2	A_ARG_192	NH2	A_GLU_198	OE2	3.178
5UK2	A_HIS_208	ND1	A_GLU_238	OE2	3.989
5UK2	A_LYS_219	NZ	A_GLU_227	OE2	3.929
5UK2	A_ARG_262	NH1	A_GLU_175	OE1	3.101
5UK2	A_ARG_311	NH1	B_ASP_586	OD1	3.877
5UK2	A_ARG_311	NH1	B_ASP_590	OD1	2.946
5UK2	A_ARG_311	NH1	B_ASP_590	OD2	3.729
5UK2	A_ARG_311	NH2	B_ASP_586	OD1	3.044
5UK2	B_LYS_551	NZ	B_GLU_603	OE1	3.663
5UK2	B_LYS_558	NZ	F_GLU_597	OE1	3.672
5UK2	B_LYS_568	NZ	A_GLU_107	OE1	3.896
5UK2	B_ARG_576	NH1	D_GLU_574	OE1	3.949
5UK2	B_ARG_576	NH1	D_GLU_574	OE2	2.806
5UK2	B_ARG_576	NH2	C_GLU_104	OE2	3.501
5UK2	B_LYS_582	NZ	B_ASP_586	OD2	3.917
5UK2	B_LYS_583	NZ	D_ASP_585	OD1	3.241
5UK2	B_LYS_583	NZ	D_ASP_585	OD2	3.954
5UK2	B_ARG_606	NH2	F_ASP_609	OD2	2.779
5UK2	B_LYS_623	NZ	B_GLU_632	OE2	3.089
5UK2	B_LYS_643	NZ	A_GLU_4	OE1	3.076
5UK2	B_LYS_643	NZ	A_ASP_5	OD1	2.565
5UK2	B_LYS_643	NZ	A_ASP_5	OD2	3.717
5UK2	B_LYS_643	NZ	B_GLU_529	OE2	3.623
5UK2	B_LYS_661	NZ	B_GLU_647	OE1	3.251
5UK2	B_ARG_670	NH2	B_GLU_671	OE2	2.809
5UK2	C_LYS_86	NZ	C_GLU_90	OE2	3.657
5UK2	C_ARG_106	NH1	C_GLU_85	OE2	2.898
5UK2	C_ARG_106	NH1	D_GLU_569	OE2	3.977
5UK2	C_ARG_106	NH2	C_GLU_85	OE1	3.401
5UK2	C_ARG_106	NH2	C_GLU_85	OE2	3.141
5UK2	C_ARG_106	NH2	D_GLU_569	OE2	2.287
5UK2	C_HIS_141	ND1	C_GLU_70	OE2	3.498
5UK2	C_LYS_174	NZ	C_GLU_116	OE2	3.326
5UK2	C_ARG_192	NH2	C_GLU_198	OE2	3.177
5UK2	C_HIS_208	ND1	C_GLU_238	OE2	3.990
5UK2	C_LYS_219	NZ	C_GLU_227	OE2	3.929
5UK2	C_ARG_262	NH1	C_GLU_175	OE1	3.100
5UK2	C_ARG_311	NH1	D_ASP_586	OD1	3.894
5UK2	C_ARG_311	NH1	D_ASP_590	OD1	2.932
5UK2	C_ARG_311	NH1	D_ASP_590	OD2	3.727
5UK2	C_ARG_311	NH2	D_ASP_586	OD1	3.043
5UK2	D_LYS_551	NZ	D_GLU_603	OE1	3.662
5UK2	D_LYS_558	NZ	B_GLU_597	OE1	3.518
5UK2	D_LYS_558	NZ	B_GLU_597	OE2	3.929
5UK2	D_LYS_568	NZ	C_GLU_107	OE1	3.830
5UK2	D_ARG_576	NH1	F_GLU_574	OE1	3.823
5UK2	D_ARG_576	NH1	F_GLU_574	OE2	2.724
5UK2	D_ARG_576	NH2	E_GLU_104	OE2	3.539
5UK2	D_LYS_582	NZ	D_ASP_586	OD2	3.917

5UK2	D_LYS_583	NZ	F_ASP_585	OD1	3.067
5UK2	D_LYS_583	NZ	F_ASP_585	OD2	3.783
5UK2	D_ARG_606	NH2	B_ASP_609	OD2	2.604
5UK2	D_LYS_623	NZ	D_GLU_632	OE2	3.089
5UK2	D_LYS_643	NZ	C_GLU_4	OE1	3.112
5UK2	D_LYS_643	NZ	C_ASP_5	OD1	2.525
5UK2	D_LYS_643	NZ	C_ASP_5	OD2	3.631
5UK2	D_LYS_643	NZ	D_GLU_529	OE2	3.624
5UK2	D_LYS_661	NZ	D_GLU_647	OE1	3.251
5UK2	D_ARG_670	NH2	D_GLU_671	OE2	2.809
5UK2	E_LYS_86	NZ	E_GLU_90	OE2	3.657
5UK2	E_ARG_106	NH1	E_GLU_85	OE2	2.898
5UK2	E_ARG_106	NH1	F_GLU_569	OE2	3.948
5UK2	E_ARG_106	NH2	E_GLU_85	OE1	3.401
5UK2	E_ARG_106	NH2	E_GLU_85	OE2	3.140
5UK2	E_ARG_106	NH2	F_GLU_569	OE2	2.300
5UK2	E_HIS_141	ND1	E_GLU_70	OE2	3.497
5UK2	E_LYS_174	NZ	E_GLU_116	OE2	3.326
5UK2	E_ARG_192	NH2	E_GLU_198	OE2	3.179
5UK2	E_HIS_208	ND1	E_GLU_238	OE2	3.988
5UK2	E_LYS_219	NZ	E_GLU_227	OE2	3.928
5UK2	E_ARG_262	NH1	E_GLU_175	OE1	3.100
5UK2	E_ARG_311	NH1	F_ASP_586	OD1	3.963
5UK2	E_ARG_311	NH1	F_ASP_590	OD1	2.962
5UK2	E_ARG_311	NH1	F_ASP_590	OD2	3.800
5UK2	E_ARG_311	NH2	F_ASP_586	OD1	3.154
5UK2	F_LYS_551	NZ	F_GLU_603	OE1	3.663
5UK2	F_LYS_558	NZ	D_GLU_597	OE1	3.583
5UK2	F_LYS_558	NZ	D_GLU_597	OE2	3.900
5UK2	F_LYS_568	NZ	E_GLU_107	OE1	3.789
5UK2	F_ARG_576	NH1	B_GLU_574	OE1	3.881
5UK2	F_ARG_576	NH1	B_GLU_574	OE2	2.699
5UK2	F_ARG_576	NH2	A_GLU_104	OE2	3.688
5UK2	F_LYS_582	NZ	F_ASP_586	OD2	3.917
5UK2	F_LYS_583	NZ	B_ASP_585	OD1	3.058
5UK2	F_LYS_583	NZ	B_ASP_585	OD2	3.745
5UK2	F_ARG_606	NH2	D_ASP_609	OD2	2.605
5UK2	F_LYS_623	NZ	F_GLU_632	OE2	3.089
5UK2	F_LYS_643	NZ	E_GLU_4	OE1	3.293
5UK2	F_LYS_643	NZ	E_ASP_5	OD1	2.450
5UK2	F_LYS_643	NZ	E_ASP_5	OD2	3.677
5UK2	F_LYS_643	NZ	F_GLU_529	OE2	3.624
5UK2	F_LYS_661	NZ	F_GLU_647	OE1	3.251
5UK2	F_ARG_670	NH2	F_GLU_671	OE2	2.809
5UK2	G_HIS_160	NE2	G_ASP_158	OD1	3.898
5UK2	G_ARG_163	NH1	G_ASP_214	OD1	2.808
5UK2	G_ARG_163	NH2	G_GLU_171	OE1	3.032
5UK2	G_ARG_163	NH2	G_GLU_171	OE2	3.708
5UK2	G_ARG_225	NH1	A_ASP_190	OD1	2.979
5UK2	G_ARG_225	NH1	A_ASP_190	OD2	3.894
5UK2	G_ARG_225	NH2	A_ASP_190	OD1	3.206
5UK2	G_ARG_225	NH2	A_ASP_190	OD2	2.785
5UK2	H_HIS_160	NE2	H_ASP_158	OD1	3.898
5UK2	H_ARG_163	NH1	H_ASP_214	OD1	2.808
5UK2	H_ARG_163	NH2	H_GLU_171	OE1	3.032
5UK2	H_ARG_163	NH2	H_GLU_171	OE2	3.708
5UK2	H_ARG_225	NH1	C_ASP_190	OD1	3.085
5UK2	H_ARG_225	NH2	C_ASP_190	OD1	3.195

5UK2	H_ARG_225	NH2	C_ASP_190	OD2	2.865
5UK2	I_HIS_160	NE2	I_ASP_158	OD1	3.898
5UK2	I_ARG_163	NH1	I_ASP_214	OD1	2.807
5UK2	I_ARG_163	NH2	I_GLU_171	OE1	3.032
5UK2	I_ARG_163	NH2	I_GLU_171	OE2	3.708
5UK2	I_ARG_225	NH1	E_ASP_190	OD1	2.888
5UK2	I_ARG_225	NH1	E_ASP_190	OD2	3.869
5UK2	I_ARG_225	NH2	E_ASP_190	OD1	3.014
5UK2	I_ARG_225	NH2	E_ASP_190	OD2	2.625

Table 730: 5UK2-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5UR8	A_ARG_38	NH2	A_GLU_46	OE1	3.406
5UR8	A_ARG_38	NH2	A_GLU_46	OE2	2.842
5UR8	A_ARG_59	NH1	B_ASP_95	OD1	3.084
5UR8	A_ARG_59	NH1	B_ASP_95	OD2	3.357
5UR8	A_ARG_59	NH2	A_ASP_57	OD1	2.972
5UR8	A_ARG_59	NH2	A_ASP_57	OD2	3.995
5UR8	A_ARG_67	NH1	A_ASP_90	OD1	2.756
5UR8	A_ARG_67	NH1	A_ASP_90	OD2	3.331
5UR8	A_ARG_67	NH2	A_ASP_90	OD1	3.669
5UR8	A_ARG_67	NH2	A_ASP_90	OD2	2.616
5UR8	A_LYS_138	NZ	B_GLU_215	OE2	2.961
5UR8	A_LYS_152	NZ	A_ASP_153	OD1	3.501
5UR8	A_LYS_152	NZ	A_ASP_153	OD2	3.066
5UR8	B_ARG_62	NH2	B_GLU_82	OE2	3.548
5UR8	B_ARG_62	NH2	B_ASP_83	OD1	2.828
5UR8	B_ARG_62	NH2	B_ASP_83	OD2	3.632
5UR8	B_LYS_105	NZ	B_GLU_167	OE1	2.973
5UR8	B_LYS_105	NZ	B_GLU_167	OE2	3.906
5UR8	B_LYS_151	NZ	B_GLU_197	OE1	2.809
5UR8	B_LYS_151	NZ	B_GLU_197	OE2	3.414
5UR8	B_LYS_190	NZ	B_ASP_187	OD1	3.286
5UR8	B_HIS_191	ND1	B_ASP_153	OD1	3.243

Table 731: 5UR8-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5VF2	A.LYS_64	NZ	A.GLU_47	OE2	2.716
5VF2	A.LYS_68	NZ	A.ASP_91	OD1	3.611
5VF2	A.LYS_68	NZ	A.ASP_91	OD2	2.737
5VF2	A.ARG_99	NH2	A.ASP_108	OD1	3.519
5VF2	A.ARG_99	NH2	A.ASP_108	OD2	2.783

Table 732: 5VF2-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5VL3	Q_HIS_28	NE2	Q_GLU_130	OE2	3.358
5VL3	Q_ARG_75	NH1	Q_GLU_78	OE2	3.350
5VL3	Q_ARG_91	NH1	Q_ASP_113	OD1	3.515
5VL3	Q_ARG_91	NH1	Q_ASP_113	OD2	2.674
5VL3	Q_ARG_91	NH2	Q_ASP_113	OD1	3.050
5VL3	Q_ARG_91	NH2	Q_ASP_113	OD2	3.746
5VL3	Q_HIS_110	ND1	Q_GLU_36	OE1	3.316
5VL3	Q_HIS_110	ND1	Q_GLU_36	OE2	2.335
5VL3	Q_HIS_213	NE2	H_GLU_58	OE2	3.352
5VL3	Q_LYS_239	NZ	Q_GLU_150	OE1	3.878
5VL3	Q_LYS_239	NZ	Q_GLU_150	OE2	3.128
5VL3	Q_LYS_243	NZ	Q_GLU_153	OE1	2.660
5VL3	Q_LYS_243	NZ	Q_GLU_153	OE2	2.886
5VL3	Q_LYS_281	NZ	Q_ASP_282	OD2	3.077
5VL3	Q_LYS_306	NZ	Q_GLU_322	OE1	3.813
5VL3	R_HIS_28	NE2	R_GLU_130	OE2	3.389
5VL3	R_LYS_70	NZ	R_ASP_72	OD1	3.096
5VL3	R_ARG_91	NH1	R_ASP_113	OD1	3.738
5VL3	R_ARG_91	NH1	R_ASP_113	OD2	2.609
5VL3	R_ARG_91	NH2	R_ASP_113	OD1	2.934
5VL3	R_ARG_91	NH2	R_ASP_113	OD2	3.371
5VL3	R_HIS_110	ND1	R_GLU_36	OE1	3.943
5VL3	R_HIS_110	ND1	R_GLU_36	OE2	2.329
5VL3	R_ARG_120	NH2	T_GLU_54	OE2	3.782
5VL3	R_LYS_127	NZ	R_GLU_122	OE2	3.799
5VL3	R_LYS_127	NZ	T_GLU_54	OE1	2.927
5VL3	R_LYS_127	NZ	T_GLU_122	OE1	2.999
5VL3	R_HIS_213	NE2	A_GLU_58	OE2	3.157
5VL3	R_LYS_239	NZ	R_GLU_150	OE1	3.277
5VL3	R_LYS_247	NZ	R_GLU_266	OE2	3.438
5VL3	R_LYS_281	NZ	R_ASP_282	OD2	3.188
5VL3	R_LYS_306	NZ	R_GLU_322	OE1	3.817
5VL3	R_ARG_319	NH2	R_GLU_322	OE2	3.267
5VL3	S_LYS_23	NZ	S_ASP_50	OD2	3.917
5VL3	S_HIS_28	NE2	S_GLU_130	OE2	3.287
5VL3	S_ARG_75	NH1	S_GLU_78	OE2	2.970
5VL3	S_LYS_100	NZ	S_ASP_97	OD2	2.933
5VL3	S_LYS_205	NZ	S_GLU_156	OE2	3.382
5VL3	S_HIS_213	NE2	C_GLU_58	OE2	3.140
5VL3	S_LYS_227	NZ	S_ASP_225	OD1	3.967
5VL3	S_LYS_239	NZ	S_GLU_150	OE2	3.417
5VL3	S_LYS_243	NZ	S_GLU_153	OE1	2.988
5VL3	S_LYS_243	NZ	S_GLU_153	OE2	2.544
5VL3	S_LYS_281	NZ	S_ASP_282	OD2	3.330
5VL3	S_LYS_306	NZ	S_GLU_322	OE1	3.934
5VL3	T_HIS_28	NE2	T_GLU_130	OE2	3.482
5VL3	T_ARG_75	NH1	T_GLU_78	OE2	2.965
5VL3	T_ARG_91	NH2	T_ASP_113	OD1	2.973
5VL3	T_ARG_91	NH2	T_ASP_113	OD2	2.700
5VL3	T_LYS_98	NZ	T_ASP_52	OD2	3.823
5VL3	T_HIS_110	ND1	T_GLU_36	OE1	3.602
5VL3	T_HIS_110	ND1	T_GLU_36	OE2	2.613
5VL3	T_LYS_127	NZ	R_GLU_54	OE1	3.658
5VL3	T_LYS_127	NZ	R_GLU_122	OE1	3.863
5VL3	T_LYS_205	NZ	T_GLU_156	OE1	3.981
5VL3	T_HIS_213	NE2	E_GLU_58	OE2	3.636
5VL3	T_LYS_239	NZ	T_GLU_150	OE2	3.518

5VL3	T_LYS_243	NZ	T_GLU_153	OE1	3.300
5VL3	T_LYS_243	NZ	T_GLU_153	OE2	2.403
5VL3	T_LYS_247	NZ	T_GLU_266	OE2	3.696
5VL3	T_LYS_281	NZ	T_ASP_282	OD2	3.114
5VL3	T_ARG_319	NH2	T_GLU_322	OE2	3.136
5VL3	A_ARG_38	NH1	A_GLU_46	OE2	3.328
5VL3	A_ARG_53	NH2	R_ASP_232	OD1	3.883
5VL3	A_ARG_53	NH2	R_ASP_232	OD2	3.340
5VL3	A_LYS_66	NZ	A_ASP_86	OD1	3.151
5VL3	A_LYS_66	NZ	A_ASP_86	OD2	3.194
5VL3	A_ARG_83	NH2	A_GLU_85	OE1	2.855
5VL3	A_ARG_83	NH2	A_GLU_85	OE2	3.048
5VL3	A_ARG_95	NH1	R_GLU_179	OE1	3.121
5VL3	A_ARG_95	NH1	R_GLU_179	OE2	3.607
5VL3	A_ARG_95	NH2	R_GLU_179	OE2	3.046
5VL3	A_LYS_210	NZ	B_GLU_124	OE2	3.976
5VL3	A_LYS_215	NZ	A_GLU_213	OE1	2.311
5VL3	C_ARG_38	NH1	C_GLU_46	OE2	3.106
5VL3	C_ARG_53	NH2	S_ASP_232	OD2	3.370
5VL3	C_ARG_94	NH1	C_ASP_96	OD1	3.364
5VL3	C_ARG_94	NH2	C_ASP_96	OD1	3.938
5VL3	C_ARG_95	NH1	S_GLU_179	OE1	3.505
5VL3	C_ARG_95	NH1	S_GLU_179	OE2	3.184
5VL3	C_ARG_95	NH2	S_GLU_179	OE2	3.815
5VL3	C_LYS_144	NZ	C_ASP_145	OD1	3.207
5VL3	C_LYS_144	NZ	C_ASP_145	OD2	2.725
5VL3	E_ARG_38	NH1	E_GLU_46	OE2	3.258
5VL3	E_ARG_53	NH2	T_ASP_232	OD1	3.852
5VL3	E_ARG_53	NH2	T_ASP_232	OD2	3.470
5VL3	E_ARG_83	NH1	E_ASP_86	OD1	3.861
5VL3	E_ARG_94	NH1	E_ASP_96	OD1	2.513
5VL3	E_ARG_95	NH1	T_GLU_179	OE1	2.688
5VL3	E_ARG_95	NH1	T_GLU_179	OE2	2.993
5VL3	E_ARG_95	NH2	T_GLU_179	OE2	3.079
5VL3	E_LYS_144	NZ	E_ASP_145	OD1	2.943
5VL3	E_LYS_144	NZ	E_ASP_145	OD2	2.901
5VL3	E_LYS_210	NZ	F_GLU_	OE2	3.778
5VL3	E_LYS_	NZ	F_ASP_	OD2	3.984
5VL3	H_ARG_38	NH1	H_GLU_46	OE2	2.851
5VL3	H_ARG_53	NH2	Q_ASP_232	OD1	3.950
5VL3	H_ARG_53	NH2	Q_ASP_232	OD2	3.411
5VL3	H_LYS_66	NZ	H_ASP_86	OD1	3.327
5VL3	H_LYS_66	NZ	H_ASP_86	OD2	2.190
5VL3	H_ARG_83	NH2	H_GLU_85	OE1	3.339
5VL3	H_ARG_83	NH2	H_GLU_85	OE2	3.382
5VL3	H_ARG_94	NH1	H_ASP_96	OD1	3.684
5VL3	H_ARG_95	NH1	Q_GLU_179	OE1	3.431
5VL3	H_ARG_95	NH1	Q_GLU_179	OE2	3.819
5VL3	H_ARG_95	NH2	Q_GLU_179	OE2	3.149
5VL3	H_LYS_144	NZ	H_ASP_145	OD1	2.853
5VL3	H_LYS_144	NZ	H_ASP_145	OD2	2.951
5VL3	B_ARG_61	NH2	B_GLU_81	OE1	3.497
5VL3	B_ARG_61	NH2	B_ASP_82	OD1	2.798
5VL3	B_ARG_61	NH2	B_ASP_82	OD2	3.720
5VL3	D_ARG_61	NH2	D_GLU_81	OE1	3.609
5VL3	D_ARG_61	NH2	D_ASP_82	OD1	3.084
5VL3	D_ARG_61	NH2	D_ASP_82	OD2	3.921
5VL3	D_LYS_150	NZ	D_GLU_196	OE1	3.872

5VL3	D_LYS_150	NZ	D_GLU_196	OE2	3.186
5VL3	D_LYS_189	NZ	D_ASP_186	OD1	3.734
5VL3	F_ARG_61	NH1	F_GLU_81	OE2	3.708
5VL3	F_ARG_61	NH2	F_GLU_81	OE2	2.960
5VL3	F_ARG_61	NH2	F_ASP_82	OD1	2.834
5VL3	F_ARG_61	NH2	F_ASP_82	OD2	3.453
5VL3	F_LYS_150	NZ	F_GLU_196	OE1	3.617
5VL3	F_LYS_150	NZ	F_GLU_196	OE2	3.530
5VL3	L_ARG_18	NH2	R_GLU_36	OE2	3.892
5VL3	L_ARG_61	NH2	L_GLU_81	OE1	3.403
5VL3	L_ARG_61	NH2	L_ASP_82	OD1	2.637
5VL3	L_ARG_61	NH2	L_ASP_82	OD2	3.407
5VL3	L_LYS_150	NZ	L_GLU_196	OE1	3.651
5VL3	L_LYS_150	NZ	L_GLU_196	OE2	3.240

Table 733: 5VL3-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5VN8	G_LYS_34	NZ	A_ASP_612	OD1	3.263
5VN8	G_LYS_46	NZ	A_GLU_632	OE1	3.416
5VN8	G_LYS_46	NZ	A_GLU_632	OE2	2.866
5VN8	G_LYS_282	NZ	G_GLU_275	OE1	3.041
5VN8	G_ARG_337	NH1	G_GLU_290	OE1	3.439
5VN8	G_ARG_337	NH1	G_GLU_290	OE2	3.645
5VN8	G_ARG_337	NH1	G_GLU_340	OE1	3.059
5VN8	G_LYS_348	NZ	G_GLU_269	OE2	2.496
5VN8	G_LYS_348	NZ	G_GLU_351	OE1	3.775
5VN8	G_LYS_356	NZ	G_GLU_466	OE2	2.685
5VN8	G_ARG_456	NH1	G_GLU_466	OE2	3.971
5VN8	G_ARG_469	NH2	G_ASP_457	OD2	3.488
5VN8	G_ARG_476	NH2	G_GLU_102	OE1	2.991
5VN8	G_ARG_476	NH2	G_GLU_102	OE2	3.449
5VN8	G_LYS_487	NZ	G_GLU_47	OE1	3.496
5VN8	G_LYS_487	NZ	G_GLU_91	OE2	3.186
5VN8	A_ARG_542	NH2	C_GLU_647	OE2	2.749
5VN8	A_ARG_579	NH1	C_GLU_584	OE1	3.931
5VN8	H_LYS_12	NZ	H_GLU_10	OE2	2.532
5VN8	H_ARG_28	NH1	G_ASP_457	OD1	2.893
5VN8	H_ARG_38	NH1	H_ASP_86	OD1	2.826
5VN8	H_ARG_38	NH2	H_GLU_46	OE1	3.729
5VN8	H_ARG_38	NH2	H_GLU_46	OE2	2.857
5VN8	H_LYS_62	NZ	H_GLU_46	OE1	3.455
5VN8	H_ARG_66	NH2	H_ASP_86	OD1	3.206
5VN8	H_ARG_66	NH2	H_ASP_86	OD2	2.433
5VN8	H_ARG_82A	NH1	H_ASP_65	OD1	3.493
5VN8	H_ARG_94	NH2	H_ASP_101	OD2	3.929
5VN8	L_HIS_27	NE2	L_GLU_1	OE2	2.752
5VN8	L_HIS_49	ND1	H_ASP_101	OD1	3.097
5VN8	L_ARG_61	NH1	L_ASP_82	OD2	2.660
5VN8	L_ARG_61	NH2	L_GLU_81	OE2	3.818
5VN8	L_ARG_61	NH2	L_ASP_82	OD1	3.890
5VN8	L_ARG_61	NH2	L_ASP_82	OD2	2.783
5VN8	L_LYS_103	NZ	L_GLU_105	OE1	3.506
5VN8	D_LYS_34	NZ	B_ASP_612	OD1	3.397
5VN8	D_LYS_46	NZ	B_GLU_632	OE1	3.407
5VN8	D_LYS_46	NZ	B_GLU_632	OE2	2.853
5VN8	D_LYS_282	NZ	D_GLU_275	OE1	3.041
5VN8	D_ARG_337	NH1	D_GLU_290	OE1	3.439
5VN8	D_ARG_337	NH1	D_GLU_290	OE2	3.644
5VN8	D_ARG_337	NH1	D_GLU_340	OE1	3.058
5VN8	D_LYS_348	NZ	D_GLU_269	OE2	2.495
5VN8	D_LYS_348	NZ	D_GLU_351	OE1	3.775
5VN8	D_LYS_356	NZ	D_GLU_466	OE2	2.685
5VN8	D_ARG_456	NH1	D_GLU_466	OE2	3.971
5VN8	D_ARG_469	NH2	D_ASP_457	OD2	3.488
5VN8	D_ARG_476	NH2	D_GLU_102	OE1	2.992
5VN8	D_ARG_476	NH2	D_GLU_102	OE2	3.449
5VN8	D_LYS_487	NZ	D_GLU_47	OE1	3.496
5VN8	D_LYS_487	NZ	D_GLU_91	OE2	3.186
5VN8	B_ARG_542	NH2	A_GLU_647	OE1	3.985
5VN8	B_ARG_542	NH2	A_GLU_647	OE2	2.712
5VN8	B_ARG_579	NH1	A_GLU_584	OE1	3.986
5VN8	F_LYS_12	NZ	F_GLU_10	OE2	2.532
5VN8	F_ARG_28	NH1	D_ASP_457	OD1	2.808
5VN8	F_ARG_38	NH1	F_ASP_86	OD1	2.826

5VN8	F_ARG_38	NH2	F_GLU_46	OE1	3.728
5VN8	F_ARG_38	NH2	F_GLU_46	OE2	2.856
5VN8	F_LYS_62	NZ	F_GLU_46	OE1	3.454
5VN8	F_ARG_66	NH2	F_ASP_86	OD1	3.206
5VN8	F_ARG_66	NH2	F_ASP_86	OD2	2.433
5VN8	F_ARG_82A	NH1	F_ASP_65	OD1	3.494
5VN8	F_ARG_94	NH2	F_ASP_101	OD2	3.929
5VN8	J_HIS_27	NE2	J_GLU_1	OE2	2.753
5VN8	J_HIS_49	ND1	F_ASP_101	OD1	3.213
5VN8	J_ARG_61	NH1	J_ASP_82	OD2	2.661
5VN8	J_ARG_61	NH2	J_GLU_81	OE2	3.818
5VN8	J_ARG_61	NH2	J_ASP_82	OD1	3.889
5VN8	J_ARG_61	NH2	J_ASP_82	OD2	2.783
5VN8	J_LYS_103	NZ	J_GLU_105	OE1	3.505
5VN8	E_LYS_34	NZ	C_ASP_612	OD1	3.266
5VN8	E_LYS_46	NZ	C_GLU_632	OE1	3.380
5VN8	E_LYS_46	NZ	C_GLU_632	OE2	2.776
5VN8	E_LYS_282	NZ	E_GLU_275	OE1	3.041
5VN8	E_ARG_337	NH1	E_GLU_290	OE1	3.439
5VN8	E_ARG_337	NH1	E_GLU_290	OE2	3.643
5VN8	E_ARG_337	NH1	E_GLU_340	OE1	3.057
5VN8	E_LYS_348	NZ	E_GLU_269	OE2	2.495
5VN8	E_LYS_348	NZ	E_GLU_351	OE1	3.775
5VN8	E_LYS_356	NZ	E_GLU_466	OE2	2.685
5VN8	E_ARG_456	NH1	E_GLU_466	OE2	3.971
5VN8	E_ARG_469	NH2	E_ASP_457	OD2	3.488
5VN8	E_ARG_476	NH2	E_GLU_102	OE1	2.991
5VN8	E_ARG_476	NH2	E_GLU_102	OE2	3.449
5VN8	E_LYS_487	NZ	E_GLU_47	OE1	3.496
5VN8	E_LYS_487	NZ	E_GLU_91	OE2	3.186
5VN8	C_ARG_542	NH2	B_GLU_647	OE2	2.738
5VN8	C_ARG_579	NH1	B_GLU_584	OE1	3.772
5VN8	I_LYS_12	NZ	I_GLU_10	OE2	2.532
5VN8	I_ARG_28	NH1	E_ASP_457	OD1	3.234
5VN8	I_ARG_38	NH1	I_ASP_86	OD1	2.826
5VN8	I_ARG_38	NH2	I_GLU_46	OE1	3.728
5VN8	I_ARG_38	NH2	I_GLU_46	OE2	2.857
5VN8	I_LYS_62	NZ	I_GLU_46	OE1	3.455
5VN8	I_ARG_66	NH2	I_ASP_86	OD1	3.206
5VN8	I_ARG_66	NH2	I_ASP_86	OD2	2.435
5VN8	I_ARG_82A	NH1	I_ASP_65	OD1	3.494
5VN8	I_ARG_94	NH2	I_ASP_101	OD2	3.929
5VN8	K_HIS_27	NE2	K_GLU_1	OE2	2.754
5VN8	K_HIS_49	ND1	I_ASP_101	OD1	3.072
5VN8	K_HIS_49	NE2	I_ASP_101	OD1	3.981
5VN8	K_ARG_61	NH1	K_ASP_82	OD2	2.660
5VN8	K_ARG_61	NH2	K_GLU_81	OE2	3.818
5VN8	K_ARG_61	NH2	K_ASP_82	OD1	3.890
5VN8	K_ARG_61	NH2	K_ASP_82	OD2	2.783
5VN8	K_LYS_103	NZ	K_GLU_105	OE1	3.505

Table 734: 5VN8-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5VXJ	A_ARG_55	NH2	A_ASP_309	OD2	2.897
5VXJ	A_LYS_63	NZ	A_GLU_64	OE1	2.911
5VXJ	A_ARG_101	NH2	A_ASP_97	OD2	3.249
5VXJ	A_LYS_151	NZ	A_GLU_147	OE1	3.093
5VXJ	A_LYS_151	NZ	A_GLU_147	OE2	3.176
5VXJ	A_LYS_196	NZ	A_ASP_261	OD1	2.840
5VXJ	A_LYS_197	NZ	A_GLU_201	OE1	3.559
5VXJ	A_LYS_197	NZ	A_GLU_201	OE2	2.683
5VXJ	A_LYS_203	NZ	A_ASP_254	OD1	2.485
5VXJ	A_LYS_203	NZ	A_ASP_254	OD2	3.995
5VXJ	A_LYS_205	NZ	A_ASP_166	OD2	2.597
5VXJ	A_LYS_207	NZ	A_GLU_204	OE2	3.657
5VXJ	A_LYS_207	NZ	A_ASP_208	OD2	3.848
5VXJ	A_LYS_291	NZ	A_ASP_287	OD2	2.858
5VXJ	A_LYS_300	NZ	A_GLU_229	OE2	3.809
5VXJ	B_ARG_19	NH2	A_ASP_97	OD1	2.652
5VXJ	B_ARG_38	NH1	B_ASP_90	OD1	2.762
5VXJ	B_ARG_38	NH2	B_GLU_46	OE2	3.072
5VXJ	B_ARG_38	NH2	B_ASP_90	OD1	3.724
5VXJ	B_ARG_50	NH1	L_GLU_200	OE1	2.921
5VXJ	B_ARG_50	NH2	L_GLU_200	OE1	3.757
5VXJ	B_ARG_67	NH1	B_ASP_90	OD2	2.822
5VXJ	B_ARG_67	NH2	B_ASP_90	OD1	2.956
5VXJ	B_ARG_67	NH2	B_ASP_90	OD2	3.171
5VXJ	B_LYS_76	NZ	A_GLU_122	OE1	2.874
5VXJ	B_HIS_80	NE2	A_ASP_144	OD1	3.165
5VXJ	B_HIS_80	NE2	A_ASP_144	OD2	3.364
5VXJ	C_ARG_55	NH2	C_ASP_309	OD1	3.860
5VXJ	C_ARG_55	NH2	C_ASP_309	OD2	2.973
5VXJ	C_LYS_72	NZ	C_GLU_76	OE2	3.986
5VXJ	C_HIS_81	NE2	C_GLU_77	OE1	3.864
5VXJ	C_ARG_101	NH2	C_ASP_97	OD2	3.028
5VXJ	C_ARG_111	NH1	C_ASP_126	OD1	3.446
5VXJ	C_LYS_137	NZ	C_ASP_124	OD1	3.580
5VXJ	C_LYS_137	NZ	C_ASP_124	OD2	3.859
5VXJ	C_LYS_151	NZ	C_GLU_147	OE1	3.347
5VXJ	C_LYS_151	NZ	C_GLU_147	OE2	3.417
5VXJ	C_LYS_189	NZ	C_GLU_268	OE1	3.664
5VXJ	C_LYS_196	NZ	C_ASP_261	OD1	2.639
5VXJ	C_LYS_196	NZ	C_ASP_261	OD2	3.513
5VXJ	C_LYS_197	NZ	C_GLU_201	OE1	2.594
5VXJ	C_LYS_197	NZ	C_GLU_201	OE2	3.519
5VXJ	C_LYS_203	NZ	C_ASP_254	OD1	2.687
5VXJ	C_LYS_205	NZ	C_ASP_166	OD2	2.854
5VXJ	C_LYS_207	NZ	C_GLU_204	OE1	3.423
5VXJ	C_LYS_207	NZ	C_GLU_204	OE2	2.767
5VXJ	C_LYS_275	NZ	C_ASP_272	OD2	3.447
5VXJ	D_ARG_19	NH1	C_ASP_97	OD1	3.252
5VXJ	D_ARG_31	NH1	D_ASP_102	OD1	3.380
5VXJ	D_ARG_38	NH1	D_ASP_90	OD1	2.860
5VXJ	D_ARG_38	NH2	D_GLU_46	OE2	2.886
5VXJ	D_ARG_50	NH1	E_GLU_200	OE1	3.721
5VXJ	D_ARG_50	NH2	E_GLU_200	OE1	3.781
5VXJ	D_ARG_67	NH1	D_ASP_90	OD1	3.893
5VXJ	D_ARG_67	NH1	D_ASP_90	OD2	2.756
5VXJ	D_ARG_67	NH2	D_ASP_90	OD1	2.919
5VXJ	D_ARG_67	NH2	D_ASP_90	OD2	3.254

5VXJ	D_LYS_76	NZ	C_GLU_122	OE1	3.854
5VXJ	D_HIS_80	NE2	C_ASP_144	OD1	3.067
5VXJ	D_HIS_80	NE2	C_ASP_144	OD2	3.196
5VXJ	E_ARG_55	NH2	E_ASP_309	OD1	3.935
5VXJ	E_ARG_55	NH2	E_ASP_309	OD2	2.817
5VXJ	E_ARG_101	NH1	E_ASP_97	OD2	2.865
5VXJ	E_LYS_119	NZ	E_GLU_120	OE2	3.261
5VXJ	E_LYS_137	NZ	F_ASP_73	OD1	3.543
5VXJ	E_LYS_137	NZ	F_ASP_73	OD2	2.771
5VXJ	E_LYS_151	NZ	E_GLU_154	OE1	3.893
5VXJ	E_LYS_196	NZ	E_ASP_261	OD1	3.147
5VXJ	E_LYS_196	NZ	E_ASP_261	OD2	3.896
5VXJ	E_LYS_197	NZ	E_GLU_201	OE1	3.410
5VXJ	E_LYS_197	NZ	E_GLU_201	OE2	2.471
5VXJ	E_LYS_203	NZ	E_ASP_254	OD1	2.551
5VXJ	E_LYS_203	NZ	E_ASP_254	OD2	3.950
5VXJ	E_LYS_205	NZ	E_ASP_166	OD2	2.795
5VXJ	E_LYS_207	NZ	E_GLU_204	OE2	3.844
5VXJ	E_LYS_207	NZ	E_ASP_208	OD1	3.647
5VXJ	E_LYS_207	NZ	E_ASP_208	OD2	3.353
5VXJ	E_LYS_275	NZ	E_ASP_272	OD1	3.514
5VXJ	E_LYS_275	NZ	E_ASP_272	OD2	3.831
5VXJ	E_LYS_291	NZ	E_ASP_287	OD2	3.845
5VXJ	E_LYS_291	NZ	E_GLU_288	OE2	3.598
5VXJ	F_ARG_19	NH2	E_ASP_97	OD1	2.921
5VXJ	F_ARG_38	NH1	F_ASP_90	OD1	2.919
5VXJ	F_ARG_38	NH2	F_GLU_46	OE2	2.728
5VXJ	F_ARG_50	NH1	G_GLU_200	OE1	3.576
5VXJ	F_ARG_50	NH2	G_GLU_200	OE1	2.702
5VXJ	F_ARG_67	NH1	F_ASP_90	OD1	3.836
5VXJ	F_ARG_67	NH1	F_ASP_90	OD2	2.827
5VXJ	F_ARG_67	NH2	F_ASP_90	OD1	3.120
5VXJ	F_ARG_67	NH2	F_ASP_90	OD2	3.574
5VXJ	F_LYS_76	NZ	E_GLU_122	OE1	3.693
5VXJ	F_HIS_80	NE2	E_ASP_144	OD1	3.009
5VXJ	F_HIS_80	NE2	E_ASP_144	OD2	3.134
5VXJ	F_ARG_106	NH2	F_ASP_102	OD1	3.541
5VXJ	G_ARG_55	NH2	G_ASP_309	OD1	3.852
5VXJ	G_ARG_55	NH2	G_ASP_309	OD2	3.242
5VXJ	G_ARG_101	NH2	G_ASP_97	OD2	3.466
5VXJ	G_HIS_115	ND1	G_GLU_112	OE1	3.174
5VXJ	G_LYS_119	NZ	G_GLU_120	OE2	3.684
5VXJ	G_LYS_137	NZ	G_ASP_124	OD2	3.625
5VXJ	G_LYS_137	NZ	H_ASP_73	OD1	3.131
5VXJ	G_LYS_137	NZ	H_ASP_73	OD2	2.336
5VXJ	G_LYS_151	NZ	G_GLU_147	OE1	3.540
5VXJ	G_LYS_151	NZ	G_GLU_147	OE2	3.043
5VXJ	G_LYS_196	NZ	G_ASP_261	OD1	2.809
5VXJ	G_LYS_197	NZ	G_GLU_201	OE1	3.460
5VXJ	G_LYS_197	NZ	G_GLU_201	OE2	2.587
5VXJ	G_LYS_203	NZ	G_ASP_254	OD1	2.489
5VXJ	G_LYS_203	NZ	G_ASP_254	OD2	3.948
5VXJ	G_LYS_205	NZ	G_ASP_166	OD2	2.817
5VXJ	G_LYS_207	NZ	G_GLU_204	OE2	3.639
5VXJ	G_LYS_207	NZ	G_ASP_208	OD1	3.592
5VXJ	G_LYS_207	NZ	G_ASP_208	OD2	3.456
5VXJ	G_LYS_291	NZ	G_GLU_288	OE1	3.119
5VXJ	H_ARG_19	NH2	G_ASP_97	OD1	2.467

5VXJ	H_ARG_31	NH1	H_ASP_102	OD1	3.947
5VXJ	H_ARG_31	NH2	H_ASP_102	OD1	3.898
5VXJ	H_ARG_38	NH1	H_ASP_90	OD1	2.996
5VXJ	H_ARG_38	NH2	H_GLU_46	OE1	3.400
5VXJ	H_LYS_65	NZ	H_ASP_62	OD1	3.343
5VXJ	H_ARG_67	NH1	H_ASP_90	OD1	3.939
5VXJ	H_ARG_67	NH1	H_ASP_90	OD2	2.890
5VXJ	H_ARG_67	NH2	H_ASP_90	OD1	3.245
5VXJ	H_ARG_67	NH2	H_ASP_90	OD2	3.633
5VXJ	H_LYS_76	NZ	G_ASP_124	OD2	3.951
5VXJ	H_HIS_80	NE2	G_ASP_144	OD1	3.186
5VXJ	H_HIS_80	NE2	G_ASP_144	OD2	3.321
5VXJ	H_ARG_106	NH2	H_ASP_102	OD2	2.976
5VXJ	I_ARG_55	NH2	I_ASP_309	OD2	3.083
5VXJ	I_HIS_81	NE2	I_GLU_77	OE1	3.831
5VXJ	I_ARG_101	NH2	I_ASP_97	OD2	3.365
5VXJ	I_LYS_137	NZ	J_ASP_73	OD1	3.804
5VXJ	I_LYS_137	NZ	J_ASP_73	OD2	2.902
5VXJ	I_LYS_151	NZ	I_GLU_147	OE1	3.728
5VXJ	I_LYS_151	NZ	I_GLU_147	OE2	3.585
5VXJ	I_LYS_196	NZ	I_ASP_261	OD1	2.688
5VXJ	I_LYS_196	NZ	I_ASP_261	OD2	3.785
5VXJ	I_LYS_197	NZ	I_GLU_201	OE1	3.642
5VXJ	I_LYS_197	NZ	I_GLU_201	OE2	2.731
5VXJ	I_LYS_203	NZ	I_ASP_254	OD1	2.602
5VXJ	I_LYS_205	NZ	I_ASP_166	OD2	2.773
5VXJ	I_LYS_207	NZ	I_GLU_204	OE1	3.025
5VXJ	I_LYS_207	NZ	I_GLU_204	OE2	3.929
5VXJ	I_LYS_275	NZ	I_ASP_272	OD1	3.295
5VXJ	I_LYS_275	NZ	I_ASP_272	OD2	2.777
5VXJ	I_LYS_300	NZ	I_GLU_229	OE1	3.150
5VXJ	J_ARG_19	NH2	I_ASP_97	OD1	2.772
5VXJ	J_ARG_31	NH1	J_ASP_102	OD1	3.834
5VXJ	J_ARG_38	NH1	J_ASP_90	OD1	2.886
5VXJ	J_ARG_38	NH2	J_GLU_46	OE2	2.770
5VXJ	J_LYS_65	NZ	J_ASP_62	OD1	2.928
5VXJ	J_ARG_67	NH1	J_ASP_90	OD1	3.756
5VXJ	J_ARG_67	NH1	J_ASP_90	OD2	2.548
5VXJ	J_ARG_67	NH2	J_ASP_90	OD1	2.840
5VXJ	J_ARG_67	NH2	J_ASP_90	OD2	3.177
5VXJ	J_LYS_76	NZ	I_GLU_122	OE2	2.338
5VXJ	J_HIS_80	NE2	I_ASP_144	OD1	3.036
5VXJ	J_HIS_80	NE2	I_ASP_144	OD2	3.151

Table 735: 5VXJ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5VXK	B_ARG_38	NH1	B_ASP_90	OD1	3.007
5VXK	B_ARG_38	NH2	B_GLU_46	OE1	3.833
5VXK	B_ARG_38	NH2	B_GLU_89	OE2	3.179
5VXK	B_ARG_67	NH1	B_ASP_90	OD1	3.692
5VXK	B_ARG_67	NH1	B_ASP_90	OD2	3.910
5VXK	B_ARG_67	NH2	B_ASP_90	OD1	3.395
5VXK	B_ARG_67	NH2	B_ASP_90	OD2	2.274
5VXK	B_HIS_80	NE2	B_ASP_73	OD2	3.665
5VXK	B_ARG_100	NH2	B_ASP_31	OD2	3.630
5VXK	A_LYS_151	NZ	A_GLU_147	OE1	2.685
5VXK	A_LYS_151	NZ	A_GLU_147	OE2	3.996
5VXK	A_LYS_196	NZ	A_ASP_261	OD2	2.739
5VXK	A_LYS_203	NZ	A_ASP_254	OD1	2.600
5VXK	A_LYS_203	NZ	A_ASP_254	OD2	3.429
5VXK	A_LYS_205	NZ	A_ASP_166	OD1	3.632
5VXK	A_LYS_225	NZ	A_GLU_229	OE1	3.736
5VXK	A_LYS_291	NZ	A_ASP_287	OD1	3.331
5VXK	A_LYS_291	NZ	A_GLU_288	OE1	3.331
5VXK	A_LYS_291	NZ	A_GLU_288	OE2	2.840
5VXK	A_LYS_313	NZ	A_ASP_309	OD2	3.376

Table 736: 5VXK-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5VXL	A_ARG_55	NH1	A_ASP_309	OD1	3.335
5VXL	A_ARG_55	NH1	A_ASP_309	OD2	2.392
5VXL	A_ARG_101	NH1	A_ASP_97	OD1	3.775
5VXL	A_ARG_101	NH1	A_ASP_97	OD2	3.730
5VXL	A_ARG_101	NH2	A_ASP_97	OD1	3.151
5VXL	A_ARG_101	NH2	A_ASP_97	OD2	2.610
5VXL	A_LYS_151	NZ	A_GLU_147	OE1	2.946
5VXL	A_LYS_151	NZ	A_GLU_147	OE2	3.503
5VXL	A_LYS_189	NZ	A_GLU_268	OE1	3.767
5VXL	A_LYS_196	NZ	A_ASP_261	OD1	2.987
5VXL	A_LYS_197	NZ	A_GLU_201	OE2	2.961
5VXL	A_LYS_203	NZ	A_ASP_254	OD1	2.551
5VXL	A_LYS_203	NZ	A_ASP_254	OD2	3.633
5VXL	A_LYS_205	NZ	A_ASP_166	OD1	3.841
5VXL	A_LYS_205	NZ	A_ASP_166	OD2	2.867
5VXL	A_LYS_205	NZ	B_ASP_52	OD2	2.998
5VXL	A_LYS_291	NZ	A_ASP_287	OD2	3.686
5VXL	B_ARG_19	NH2	B_GLU_83	OE1	3.609
5VXL	B_ARG_38	NH1	B_ASP_91	OD1	2.974
5VXL	B_ARG_38	NH2	B_GLU_46	OE1	3.298
5VXL	B_ARG_38	NH2	B_GLU_46	OE2	3.686
5VXL	B_LYS_66	NZ	B_ASP_63	OD1	2.473
5VXL	B_ARG_68	NH1	B_ASP_91	OD2	2.829
5VXL	B_ARG_68	NH2	B_ASP_91	OD1	3.190
5VXL	B_ARG_68	NH2	B_ASP_91	OD2	3.203
5VXL	B_ARG_79	NH1	B_GLU_77	OE1	3.438
5VXL	B_ARG_102	NH1	A_GLU_201	OE1	3.097
5VXL	B_ARG_102	NH2	A_GLU_201	OE1	3.202
5VXL	B_ARG_102	NH2	A_GLU_201	OE2	2.871

Table 737: 5VXL-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5VXM	A_ARG_55	NH2	A_ASP_309	OD2	2.709
5VXM	A_HIS_81	ND1	A_GLU_64	OE1	2.699
5VXM	A_HIS_81	ND1	A_GLU_64	OE2	3.443
5VXM	A_LYS_203	NZ	A_ASP_254	OD1	3.048
5VXM	A_LYS_205	NZ	A_ASP_166	OD2	2.794
5VXM	A_LYS_205	NZ	B_ASP_53	OD1	3.221
5VXM	A_LYS_205	NZ	B_ASP_53	OD2	3.090
5VXM	A_LYS_240	NZ	A_ASP_208	OD2	3.009
5VXM	A_LYS_291	NZ	A_ASP_287	OD1	3.603
5VXM	A_LYS_291	NZ	A_ASP_287	OD2	3.020
5VXM	A_LYS_291	NZ	A_GLU_288	OE2	2.698
5VXM	B_ARG_38	NH1	B_ASP_90	OD1	2.771
5VXM	B_ARG_38	NH2	B_GLU_46	OE1	3.784
5VXM	B_ARG_38	NH2	B_GLU_46	OE2	3.779
5VXM	B_ARG_38	NH2	B_ASP_90	OD1	3.793
5VXM	B_ARG_59	NH2	A_GLU_201	OE1	3.364
5VXM	B_LYS_65	NZ	B_ASP_62	OD1	2.888
5VXM	B_ARG_67	NH1	B_ASP_90	OD1	3.808
5VXM	B_ARG_67	NH1	B_ASP_90	OD2	2.755
5VXM	B_ARG_67	NH2	B_ASP_90	OD1	3.073
5VXM	B_ARG_67	NH2	B_ASP_90	OD2	3.515

Table 738: 5VXM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5VXR	H_ARG_38	NH1	H_ASP_89	OD1	2.812
5VXR	H_ARG_38	NH2	H_GLU_46	OE1	2.830
5VXR	H_ARG_38	NH2	H_ASP_89	OD1	3.607
5VXR	H_ARG_66	NH1	H_ASP_89	OD1	3.628
5VXR	H_ARG_66	NH1	H_ASP_89	OD2	3.027
5VXR	H_ARG_66	NH2	H_ASP_89	OD1	2.986
5VXR	H_ARG_66	NH2	H_ASP_89	OD2	3.606
5VXR	H_ARG_97	NH2	H_ASP_27	OD2	3.982
5VXR	H_LYS_214	NZ	L_GLU_123	OE2	2.932
5VXR	H_LYS_215	NZ	H_GLU_217	OE1	3.858
5VXR	L_ARG_24	NH1	L_ASP_70	OD1	3.927
5VXR	L_LYS_39	NZ	L_ASP_81	OD1	2.793
5VXR	L_LYS_39	NZ	L_ASP_81	OD2	3.461
5VXR	L_ARG_61	NH1	L_ASP_82	OD1	3.414
5VXR	L_ARG_61	NH1	L_ASP_82	OD2	2.748
5VXR	L_ARG_61	NH2	L_GLU_79	OE1	3.909
5VXR	L_ARG_61	NH2	L_ASP_82	OD1	2.825
5VXR	L_ARG_61	NH2	L_ASP_82	OD2	3.695
5VXR	L_LYS_147	NZ	L_GLU_154	OE2	3.969
5VXR	L_LYS_149	NZ	L_GLU_195	OE1	3.427
5VXR	L_LYS_149	NZ	L_GLU_195	OE2	3.261
5VXR	L_ARG_155	NH2	L_GLU_185	OE1	3.900
5VXR	L_HIS_189	ND1	L_ASP_151	OD2	2.731
5VXR	L_LYS_199	NZ	L_ASP_110	OD2	3.874

Table 739: 5VXR-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5VZR	H_HIS_35	NE2	H_ASP_100C	OD1	2.839
5VZR	H_HIS_35	NE2	H_ASP_100C	OD2	3.345
5VZR	H_ARG_66	NH1	H_ASP_86	OD1	3.315
5VZR	H_ARG_66	NH1	H_ASP_86	OD2	2.889
5VZR	H_ARG_66	NH2	H_ASP_86	OD1	2.686
5VZR	H_ARG_66	NH2	H_ASP_86	OD2	3.653
5VZR	H_ARG_94	NH2	H_ASP_101	OD1	3.645
5VZR	H_ARG_94	NH2	H_ASP_101	OD2	2.665
5VZR	H_LYS_219	NZ	L_GLU_123	OE2	3.208
5VZR	L_LYS_39	NZ	L_ASP_81	OD1	3.338
5VZR	L_LYS_39	NZ	L_ASP_81	OD2	2.831
5VZR	L_ARG_61	NH1	L_ASP_82	OD1	3.560
5VZR	L_ARG_61	NH1	L_ASP_82	OD2	2.794
5VZR	L_ARG_61	NH2	L_GLU_79	OE2	3.432
5VZR	L_ARG_61	NH2	L_ASP_82	OD1	2.758
5VZR	L_ARG_61	NH2	L_ASP_82	OD2	3.575
5VZR	L_ARG_96	NH2	H_ASP_100C	OD2	3.042
5VZR	L_LYS_147	NZ	L_GLU_195	OE2	3.957
5VZR	L_LYS_149	NZ	L_GLU_195	OE1	3.473
5VZR	L_LYS_149	NZ	L_GLU_195	OE2	3.623
5VZR	L_ARG_155	NH1	L_GLU_185	OE1	3.298
5VZR	L_ARG_155	NH2	L_GLU_185	OE1	3.461
5VZR	L_LYS_183	NZ	L_GLU_187	OE1	3.869
5VZR	L_HIS_189	ND1	L_ASP_151	OD2	2.938
5VZR	L_LYS_199	NZ	L_ASP_110	OD1	3.115
5VZR	L_LYS_199	NZ	L_ASP_110	OD2	3.180
5VZR	A_HIS_35	NE2	A_ASP_100C	OD1	2.841
5VZR	A_HIS_35	NE2	A_ASP_100C	OD2	3.362
5VZR	A_ARG_66	NH1	A_ASP_86	OD1	3.497
5VZR	A_ARG_66	NH1	A_ASP_86	OD2	2.943
5VZR	A_ARG_66	NH2	A_ASP_86	OD1	2.855
5VZR	A_ARG_66	NH2	A_ASP_86	OD2	3.669
5VZR	A_ARG_94	NH2	A_ASP_101	OD1	3.759
5VZR	A_ARG_94	NH2	A_ASP_101	OD2	2.688
5VZR	A_LYS_219	NZ	B_GLU_123	OE1	3.381
5VZR	B_ARG_24	NH1	B_ASP_70	OD1	3.001
5VZR	B_ARG_24	NH1	B_ASP_70	OD2	3.957
5VZR	B_LYS_39	NZ	B_ASP_81	OD1	3.456
5VZR	B_LYS_39	NZ	B_ASP_81	OD2	2.971
5VZR	B_ARG_61	NH1	B_ASP_82	OD1	3.543
5VZR	B_ARG_61	NH1	B_ASP_82	OD2	2.682
5VZR	B_ARG_61	NH2	B_GLU_79	OE2	3.666
5VZR	B_ARG_61	NH2	B_ASP_82	OD1	2.894
5VZR	B_ARG_61	NH2	B_ASP_82	OD2	3.609
5VZR	B_ARG_96	NH2	A_ASP_100C	OD2	2.983
5VZR	B_LYS_147	NZ	B_GLU_154	OE1	3.313
5VZR	B_LYS_147	NZ	B_GLU_154	OE2	3.668
5VZR	B_LYS_149	NZ	B_GLU_195	OE1	2.858
5VZR	B_LYS_149	NZ	B_GLU_195	OE2	3.431
5VZR	B_ARG_155	NH2	B_GLU_185	OE2	3.691
5VZR	B_LYS_183	NZ	B_GLU_187	OE1	3.084
5VZR	B_LYS_183	NZ	B_GLU_187	OE2	3.264
5VZR	B_ARG_188	NH2	B_GLU_185	OE1	2.762
5VZR	B_HIS_189	ND1	B_ASP_151	OD2	3.256
5VZR	B_HIS_189	NE2	B_GLU_185	OE2	2.898

Table 740: 5VZR-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5W2B	H_ARG_41	NH1	H_ASP_93	OD1	2.811
5W2B	H_ARG_41	NH2	H_GLU_49	OE1	3.026
5W2B	H_ARG_41	NH2	H_GLU_49	OE2	3.821
5W2B	H_ARG_41	NH2	H_ASP_93	OD1	3.696
5W2B	H_LYS_68	NZ	H_ASP_65	OD1	3.641
5W2B	H_ARG_70	NH1	H_ASP_93	OD2	3.880
5W2B	H_ARG_70	NH2	H_ASP_93	OD1	3.178
5W2B	H_ARG_70	NH2	H_ASP_93	OD2	3.275
5W2B	H_ARG_90	NH1	H_GLU_92	OE2	3.439
5W2B	H_ARG_101	NH2	H_ASP_116	OD1	3.885
5W2B	H_ARG_101	NH2	H_ASP_116	OD2	2.522
5W2B	H_LYS_158	NZ	H_ASP_159	OD1	3.610
5W2B	H_LYS_158	NZ	H_ASP_159	OD2	3.126
5W2B	H_LYS_225	NZ	H_GLU_227	OE2	3.518
5W2B	L_ARG_25	NH1	L_ASP_71	OD2	3.833
5W2B	L_ARG_25	NH2	L_ASP_71	OD2	3.096
5W2B	L_ARG_62	NH1	L_GLU_82	OE2	3.995
5W2B	L_ARG_62	NH2	L_GLU_82	OE2	2.777
5W2B	L_ARG_62	NH2	L_ASP_83	OD1	2.811
5W2B	L_ARG_62	NH2	L_ASP_83	OD2	3.485
5W2B	L_LYS_104	NZ	L_GLU_166	OE1	2.996
5W2B	L_LYS_104	NZ	L_GLU_166	OE2	3.194
5W2B	L_LYS_127	NZ	L_ASP_123	OD1	2.992
5W2B	L_LYS_127	NZ	L_ASP_123	OD2	3.947
5W2B	L_ARG_143	NH1	L_GLU_106	OE1	3.368
5W2B	L_ARG_143	NH1	L_GLU_106	OE2	3.850
5W2B	L_ARG_143	NH2	L_GLU_106	OE1	3.513
5W2B	L_ARG_143	NH2	L_GLU_106	OE2	2.678
5W2B	L_LYS_150	NZ	L_GLU_196	OE1	3.463
5W2B	L_HIS_190	ND1	L_ASP_152	OD2	3.239
5W2B	A_HIS_653	NE2	A_GLU_649	OE1	3.647
5W2B	A_LYS_672	NZ	A_GLU_674	OE2	3.333
5W2B	A_ARG_728	NH1	A_ASP_729	OD1	3.255
5W2B	A_HIS_738	ND1	A_ASP_682	OD1	3.266
5W2B	A_HIS_738	ND1	A_ASP_682	OD2	2.866

Table 741: 5W2B-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5W9H	A_ARG.758	NH1	p_ASP.740	OD1	3.106
5W9H	A_LYS.779	NZ	A_GLU.1148	OE1	2.900
5W9H	A_LYS.801	NZ	A_ASP.843	OD1	2.837
5W9H	A_LYS.801	NZ	A_ASP.843	OD2	3.404
5W9H	A_LYS.807	NZ	A_GLU.818	OE2	3.090
5W9H	A_ARG.841	NH2	A_ASP.844	OD2	2.768
5W9H	A_ARG.847	NH2	A_ASP.844	OD1	2.690
5W9H	A_ARG.887	NH2	A_ASP.892	OD1	2.869
5W9H	A_ARG.887	NH2	A_ASP.892	OD2	3.887
5W9H	A_HIS.1020	NE2	A_ASP.1024	OD2	2.968
5W9H	A_ARG.1057	NH1	A_ASP.1053	OD2	3.477
5W9H	A_ARG.1057	NH2	A_ASP.1053	OD1	3.268
5W9H	A_ARG.1057	NH2	A_ASP.1053	OD2	3.305
5W9H	A_LYS.1102	NZ	A_GLU.793	OE1	2.898
5W9H	A_LYS.1102	NZ	A_GLU.793	OE2	3.271
5W9H	A_ARG.1113	NH1	A_GLU.1105	OE1	3.282
5W9H	A_ARG.1113	NH1	A_GLU.1105	OE2	3.829
5W9H	A_ARG.1113	NH2	D_GLU.1105	OE1	3.583
5W9H	A_HIS.1138	NE2	A_GLU.793	OE1	3.148
5W9H	A_LYS.1174	NZ	A_GLU.1183	OE1	2.609
5W9H	A_ARG.1179	NH2	B_ASP.31	OD1	2.752
5W9H	B_LYS.19	NZ	B_GLU.81	OE1	3.976
5W9H	B_LYS.38	NZ	B_ASP.86	OD1	3.271
5W9H	B_LYS.62	NZ	B_GLU.46	OE1	2.834
5W9H	B_LYS.62	NZ	B_GLU.46	OE2	3.973
5W9H	B_ARG.66	NH2	B_ASP.86	OD1	2.870
5W9H	B_ARG.66	NH2	B_ASP.86	OD2	3.022
5W9H	B_ARG.94	NH2	B_ASP.101	OD2	2.758
5W9H	B_LYS.95	NZ	B_ASP.100C	OD2	3.768
5W9H	C_ARG.24	NH1	C_ASP.70	OD1	2.971
5W9H	C_ARG.24	NH1	C_ASP.70	OD2	3.712
5W9H	C_ARG.61	NH1	C_ASP.82	OD1	3.151
5W9H	C_ARG.61	NH1	C_ASP.82	OD2	3.358
5W9H	C_LYS.92	NZ	C_GLU.93	OE1	3.334
5W9H	C_ARG.96	NH1	B_ASP.100C	OD2	2.859
5W9H	C_ARG.96	NH2	A_GLU.1183	OE1	3.871
5W9H	C_ARG.96	NH2	A_GLU.1183	OE2	2.827
5W9H	C_ARG.96	NH2	B_ASP.100C	OD2	2.885
5W9H	C_LYS.103	NZ	C_GLU.105	OE1	3.465
5W9H	D_LYS.779	NZ	D_ASP.771	OD2	3.242
5W9H	D_LYS.779	NZ	D_GLU.1148	OE1	3.666
5W9H	D_LYS.801	NZ	D_ASP.843	OD1	2.844
5W9H	D_LYS.801	NZ	D_ASP.843	OD2	3.387
5W9H	D_LYS.816	NZ	D_ASP.1064	OD1	3.505
5W9H	D_LYS.816	NZ	D_ASP.1064	OD2	2.929
5W9H	D_ARG.841	NH1	D_GLU.1090	OE1	2.843
5W9H	D_ARG.841	NH2	D_GLU.1090	OE1	2.754
5W9H	D_ARG.847	NH2	D_ASP.844	OD1	2.671
5W9H	D_ARG.887	NH2	D_ASP.892	OD1	2.891
5W9H	D_ARG.887	NH2	D_ASP.892	OD2	3.987
5W9H	D_HIS.1020	NE2	D_ASP.1024	OD1	3.700
5W9H	D_HIS.1020	NE2	D_ASP.1024	OD2	3.194
5W9H	D_ARG.1057	NH1	D_ASP.1053	OD1	3.487
5W9H	D_LYS.1102	NZ	D_GLU.793	OE1	2.907
5W9H	D_LYS.1102	NZ	D_GLU.793	OE2	3.062
5W9H	D_ARG.1113	NH1	G_GLU.1105	OE1	3.247
5W9H	D_ARG.1113	NH2	D_GLU.1105	OE1	3.897

5W9H	D_ARG.1113	NH2	D_GLU.1105	OE2	3.876
5W9H	D_HIS.1138	NE2	D_GLU.793	OE1	2.876
5W9H	D_LYS.1174	NZ	D_GLU.1183	OE2	2.738
5W9H	E_LYS.38	NZ	E_ASP.86	OD1	3.906
5W9H	E_LYS.62	NZ	E_GLU.46	OE1	2.861
5W9H	E_LYS.62	NZ	E_GLU.46	OE2	3.757
5W9H	E_ARG.66	NH1	E_ASP.86	OD1	2.947
5W9H	E_ARG.66	NH1	E_ASP.86	OD2	3.381
5W9H	E_ARG.94	NH2	E_ASP.101	OD2	3.822
5W9H	E_LYS.95	NZ	E_ASP.100C	OD1	3.733
5W9H	F_ARG.61	NH1	F_ASP.82	OD1	3.217
5W9H	F_ARG.61	NH1	F_ASP.82	OD2	3.689
5W9H	F_ARG.61	NH2	F_ASP.82	OD1	3.660
5W9H	F_ARG.61	NH2	F_ASP.82	OD2	2.716
5W9H	F_ARG.96	NH1	E_ASP.100C	OD2	2.830
5W9H	F_ARG.96	NH2	E_ASP.100C	OD2	2.948
5W9H	G_ARG.758	NH1	r_ASP.740	OD1	2.922
5W9H	G_LYS.779	NZ	G_ASP.771	OD2	2.887
5W9H	G_LYS.779	NZ	G_GLU.1148	OE1	3.575
5W9H	G_LYS.801	NZ	G_ASP.843	OD1	2.852
5W9H	G_LYS.801	NZ	G_ASP.843	OD2	3.379
5W9H	G_LYS.807	NZ	G_GLU.818	OE1	2.858
5W9H	G_LYS.807	NZ	G_GLU.818	OE2	3.782
5W9H	G_LYS.816	NZ	G_ASP.1064	OD1	3.397
5W9H	G_LYS.816	NZ	G_ASP.1064	OD2	2.986
5W9H	G_ARG.841	NH2	G_ASP.844	OD2	2.751
5W9H	G_ARG.847	NH2	G_ASP.844	OD1	2.677
5W9H	G_ARG.887	NH2	G_ASP.892	OD1	2.871
5W9H	G_ARG.887	NH2	G_ASP.892	OD2	3.986
5W9H	G_HIS.1020	NE2	G_ASP.1024	OD2	2.969
5W9H	G_LYS.1102	NZ	G_GLU.793	OE1	3.868
5W9H	G_LYS.1102	NZ	G_GLU.793	OE2	3.570
5W9H	G_ARG.1113	NH2	A_GLU.1105	OE1	3.110
5W9H	G_HIS.1138	NE2	G_GLU.793	OE2	2.825
5W9H	G_LYS.1174	NZ	G_GLU.1183	OE1	2.701
5W9H	G_ARG.1179	NH2	H_ASP.31	OD1	2.809
5W9H	H_LYS.38	NZ	H_ASP.86	OD1	3.793
5W9H	H_LYS.62	NZ	H_GLU.46	OE1	3.235
5W9H	H_LYS.62	NZ	H_GLU.46	OE2	2.887
5W9H	H_ARG.66	NH1	H_ASP.86	OD1	3.910
5W9H	H_ARG.66	NH1	H_ASP.86	OD2	3.798
5W9H	H_ARG.66	NH2	H_ASP.86	OD1	3.900
5W9H	H_ARG.66	NH2	H_ASP.86	OD2	2.887
5W9H	H_ARG.94	NH2	H_ASP.101	OD2	2.744
5W9H	H_LYS.95	NZ	H_ASP.100C	OD1	3.649
5W9H	I_ARG.24	NH1	I_ASP.70	OD1	2.956
5W9H	I_ARG.24	NH1	I_ASP.70	OD2	3.606
5W9H	I_ARG.24	NH2	I_ASP.70	OD1	3.918
5W9H	I_ARG.61	NH1	I_GLU.79	OE2	2.865
5W9H	I_ARG.61	NH1	I_ASP.82	OD1	3.820
5W9H	I_ARG.61	NH1	I_ASP.82	OD2	3.014
5W9H	I_ARG.61	NH2	I_GLU.79	OE2	2.954
5W9H	I_ARG.96	NH1	H_ASP.100C	OD2	2.791
5W9H	I_ARG.96	NH2	G_GLU.1183	OE2	2.911
5W9H	I_ARG.96	NH2	H_ASP.100C	OD2	2.950
5W9H	p_HIS.81	ND1	p_ASP.80	OD1	3.485
5W9H	p_LYS.99	NZ	p_GLU.32	OE1	2.779
5W9H	p_LYS.110	NZ	p_ASP.83	OD2	2.727

5W9H	p_ARG_119	NH2	p_ASP_54	OD2	3.407
5W9H	p_LYS_142	NZ	p_GLU_252	OE1	3.739
5W9H	p_LYS_142	NZ	p_GLU_252	OE2	3.528
5W9H	p_ARG_190	NH1	p_ASP_24	OD2	3.182
5W9H	p_ARG_190	NH2	p_ASP_24	OD2	3.492
5W9H	p_HIS_194	NE2	p_GLU_32	OE1	3.741
5W9H	p_ARG_235	NH2	p_GLU_188	OE1	2.810
5W9H	p_ARG_235	NH2	p_GLU_188	OE2	3.752
5W9H	p_ARG_269	NH1	p_GLU_252	OE1	3.003
5W9H	p_ARG_334	NH2	p_ASP_330	OD1	3.952
5W9H	p_ARG_334	NH2	p_ASP_330	OD2	3.020
5W9H	p_ARG_335	NH2	p_ASP_326	OD2	2.866
5W9H	p_ARG_401	NH2	p_ASP_444	OD1	3.583
5W9H	p_ARG_401	NH2	p_ASP_444	OD2	2.889
5W9H	p_LYS_496	NZ	p_GLU_536	OE1	3.232
5W9H	p_LYS_496	NZ	p_GLU_536	OE2	3.655
5W9H	p_LYS_502	NZ	p_GLU_513	OE2	2.865
5W9H	p_ARG_614	NH2	p_GLU_605	OE2	2.933
5W9H	p_ARG_629	NH1	p_GLU_376	OE1	3.493
5W9H	p_ARG_629	NH1	p_ASP_644	OD1	2.871
5W9H	p_ARG_629	NH1	p_ASP_644	OD2	3.990
5W9H	p_ARG_629	NH2	p_ASP_644	OD1	2.880
5W9H	p_ARG_629	NH2	p_ASP_644	OD2	3.886
5W9H	p_LYS_665	NZ	p_ASP_355	OD2	3.928
5W9H	p_HIS_681	NE2	D_ASP_910	OD1	2.819
5W9H	p_HIS_681	NE2	D_ASP_910	OD2	3.760
5W9H	p_ARG_694	NH1	p_ASP_343	OD1	3.986
5W9H	p_ARG_694	NH1	p_ASP_343	OD2	2.926
5W9H	p_ARG_694	NH2	p_ASP_343	OD1	3.403
5W9H	p_ARG_694	NH2	p_ASP_343	OD2	3.427
5W9H	p_LYS_728	NZ	p_ASP_726	OD2	2.881
5W9H	q_LYS_99	NZ	q_GLU_32	OE1	2.764
5W9H	q_LYS_110	NZ	q_ASP_83	OD2	2.762
5W9H	q_LYS_110	NZ	q_ASP_108	OD2	3.795
5W9H	q_ARG_119	NH2	q_ASP_54	OD2	3.096
5W9H	q_LYS_142	NZ	q_GLU_252	OE1	2.907
5W9H	q_LYS_142	NZ	q_GLU_252	OE2	3.991
5W9H	q_ARG_181	NH1	q_ASP_174	OD2	3.114
5W9H	q_HIS_194	NE2	q_GLU_32	OE1	3.504
5W9H	q_HIS_208	ND1	q_ASP_213	OD2	3.767
5W9H	q_ARG_235	NH1	q_ASP_24	OD1	3.943
5W9H	q_ARG_235	NH1	q_ASP_24	OD2	3.081
5W9H	q_ARG_235	NH2	q_ASP_24	OD2	2.878
5W9H	q_ARG_235	NH2	q_GLU_188	OE1	2.783
5W9H	q_ARG_235	NH2	q_GLU_188	OE2	3.707
5W9H	q_ARG_269	NH1	q_GLU_252	OE2	3.153
5W9H	q_ARG_335	NH2	q_ASP_326	OD2	2.856
5W9H	q_ARG_401	NH2	q_ASP_444	OD1	3.945
5W9H	q_ARG_401	NH2	q_ASP_444	OD2	3.807
5W9H	q_LYS_502	NZ	q_GLU_513	OE2	2.769
5W9H	q_LYS_543	NZ	q_GLU_549	OE1	3.143
5W9H	q_LYS_543	NZ	q_GLU_549	OE2	2.917
5W9H	q_LYS_587	NZ	q_GLU_382	OE2	2.893
5W9H	q_ARG_614	NH1	q_GLU_605	OE2	3.381
5W9H	q_ARG_629	NH1	q_ASP_644	OD1	3.524
5W9H	q_ARG_629	NH1	q_ASP_644	OD2	3.882
5W9H	q_LYS_668	NZ	q_ASP_355	OD1	3.851
5W9H	q_HIS_681	ND1	q_GLU_680	OE2	3.860

5W9H	q_LYS_728	NZ	q_ASP_726	OD2	2.831
5W9H	r_LYS_27	NZ	r_GLU_230	OE2	2.686
5W9H	r_LYS_52	NZ	r_ASP_49	OD2	3.239
5W9H	r_LYS_99	NZ	r_GLU_32	OE1	2.778
5W9H	r_LYS_110	NZ	r_ASP_83	OD2	3.861
5W9H	r_LYS_110	NZ	r_ASP_108	OD1	3.126
5W9H	r_LYS_110	NZ	r_ASP_108	OD2	3.630
5W9H	r_ARG_119	NH2	r_ASP_54	OD2	3.338
5W9H	r_LYS_142	NZ	r_GLU_252	OE2	3.806
5W9H	r_ARG_181	NH1	r_ASP_174	OD2	3.239
5W9H	r_ARG_190	NH1	r_ASP_24	OD1	3.106
5W9H	r_ARG_190	NH1	r_ASP_24	OD2	3.916
5W9H	r_ARG_190	NH2	r_ASP_24	OD1	2.743
5W9H	r_HIS_194	NE2	r_GLU_32	OE1	3.751
5W9H	r_ARG_235	NH2	r_GLU_188	OE1	3.176
5W9H	r_ARG_269	NH1	r_GLU_252	OE1	3.002
5W9H	r_ARG_335	NH2	r_ASP_326	OD2	2.830
5W9H	r_ARG_401	NH2	r_ASP_444	OD1	3.679
5W9H	r_ARG_401	NH2	r_ASP_444	OD2	3.146
5W9H	r_LYS_413	NZ	r_GLU_382	OE1	3.858
5W9H	r_LYS_413	NZ	r_GLU_382	OE2	2.731
5W9H	r_LYS_502	NZ	r_GLU_513	OE1	3.965
5W9H	r_LYS_502	NZ	r_GLU_513	OE2	2.807
5W9H	r_ARG_511	NH2	r_ASP_509	OD2	3.938
5W9H	r_ARG_614	NH1	r_GLU_605	OE2	3.430
5W9H	r_ARG_629	NH2	r_ASP_644	OD1	3.737
5W9H	r_LYS_665	NZ	r_GLU_666	OE2	2.722
5W9H	r_HIS_681	NE2	A_ASP_910	OD1	2.850
5W9H	r_HIS_681	NE2	A_ASP_910	OD2	3.840
5W9H	r_LYS_728	NZ	r_ASP_726	OD2	2.800

Table 742: 5W9H-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5W9I	A_ARG.758	NH1	B_ASP.740	OD1	2.830
5W9I	A_LYS.779	NZ	A_ASP.771	OD2	2.920
5W9I	A_LYS.779	NZ	A_GLU.1148	OE1	3.679
5W9I	A_LYS.801	NZ	A_ASP.843	OD1	2.853
5W9I	A_LYS.801	NZ	A_ASP.843	OD2	3.508
5W9I	A_LYS.807	NZ	A_GLU.818	OE1	3.679
5W9I	A_LYS.807	NZ	A_GLU.818	OE2	2.901
5W9I	A_LYS.816	NZ	A_ASP.1064	OD1	3.819
5W9I	A_LYS.816	NZ	A_ASP.1064	OD2	3.674
5W9I	A_ARG.841	NH1	A_GLU.1090	OE1	2.870
5W9I	A_ARG.841	NH2	A_GLU.1090	OE1	2.843
5W9I	A_ARG.847	NH1	F_ASP.726	OD1	3.733
5W9I	A_ARG.847	NH1	F_ASP.726	OD2	2.884
5W9I	A_ARG.847	NH2	A_ASP.844	OD1	2.784
5W9I	A_ARG.887	NH2	A_ASP.892	OD1	2.922
5W9I	A_HIS.1020	NE2	A_ASP.1024	OD2	3.009
5W9I	A_LYS.1021	NZ	A_GLU.1017	OE2	3.419
5W9I	A_LYS.1102	NZ	A_GLU.793	OE1	2.923
5W9I	A_LYS.1102	NZ	A_GLU.793	OE2	2.903
5W9I	A_ARG.1113	NH1	A_GLU.1105	OE1	2.902
5W9I	A_ARG.1113	NH1	A_GLU.1105	OE2	3.646
5W9I	A_ARG.1113	NH2	L_GLU.1105	OE2	2.773
5W9I	A_HIS.1138	NE2	A_GLU.793	OE2	2.945
5W9I	A_LYS.1174	NZ	A_GLU.1183	OE1	2.820
5W9I	A_ARG.1179	NH2	C_ASP.31	OD1	2.834
5W9I	B_LYS.99	NZ	B_GLU.32	OE1	2.800
5W9I	B_LYS.110	NZ	B_ASP.83	OD2	2.763
5W9I	B_ARG.119	NH2	B_ASP.54	OD2	3.186
5W9I	B_LYS.142	NZ	B_GLU.252	OE1	2.883
5W9I	B_HIS.194	NE2	B_GLU.32	OE1	3.646
5W9I	B_ARG.235	NH1	B_ASP.24	OD1	3.781
5W9I	B_ARG.235	NH1	B_ASP.24	OD2	3.330
5W9I	B_ARG.235	NH2	B_ASP.24	OD2	2.925
5W9I	B_ARG.235	NH2	B_GLU.188	OE1	2.886
5W9I	B_ARG.235	NH2	B_GLU.188	OE2	3.821
5W9I	B_ARG.335	NH2	B_ASP.326	OD2	2.866
5W9I	B_ARG.614	NH1	B_GLU.367	OE2	2.904
5W9I	B_ARG.614	NH2	B_GLU.367	OE2	2.914
5W9I	B_ARG.629	NH1	B_GLU.376	OE1	3.454
5W9I	B_ARG.629	NH1	B_ASP.644	OD1	2.966
5W9I	B_ARG.629	NH1	B_ASP.644	OD2	3.812
5W9I	B_ARG.629	NH2	B_ASP.644	OD1	2.995
5W9I	B_LYS.665	NZ	B_GLU.357	OE1	2.866
5W9I	B_LYS.665	NZ	B_GLU.357	OE2	3.798
5W9I	B_LYS.668	NZ	B_ASP.355	OD1	2.986
5W9I	B_HIS.681	NE2	L_ASP.910	OD1	2.801
5W9I	B_HIS.681	NE2	L_ASP.910	OD2	3.893
5W9I	B_LYS.728	NZ	B_ASP.726	OD2	2.881
5W9I	C_LYS.38	NZ	C_ASP.86	OD1	3.889
5W9I	C_LYS.62	NZ	C_GLU.46	OE1	3.450
5W9I	C_LYS.62	NZ	C_GLU.46	OE2	2.930
5W9I	C_ARG.66	NH1	C_ASP.86	OD1	3.145
5W9I	C_ARG.66	NH1	C_ASP.86	OD2	3.495
5W9I	C_ARG.66	NH2	C_ASP.86	OD1	3.789
5W9I	C_ARG.66	NH2	C_ASP.86	OD2	2.783
5W9I	C_ARG.94	NH2	C_ASP.101	OD1	2.867
5W9I	C_ARG.94	NH2	C_ASP.101	OD2	3.643

5W9I	C_LYS_95	NZ	C_ASP_100C	OD1	3.543
5W9I	C_LYS_95	NZ	C_ASP_100C	OD2	3.727
5W9I	D_ARG_24	NH2	D_ASP_70	OD1	2.945
5W9I	D_ARG_24	NH2	D_ASP_70	OD2	3.831
5W9I	D_ARG_61	NH1	D_ASP_82	OD1	3.202
5W9I	D_ARG_61	NH1	D_ASP_82	OD2	3.681
5W9I	D_ARG_61	NH2	D_ASP_82	OD1	3.712
5W9I	D_ARG_61	NH2	D_ASP_82	OD2	2.777
5W9I	D_ARG_96	NH1	C_ASP_100C	OD2	2.837
5W9I	D_ARG_96	NH2	A_GLU_1183	OE2	2.862
5W9I	D_ARG_96	NH2	C_ASP_100C	OD2	2.920
5W9I	D_LYS_103	NZ	D_GLU_105	OE2	3.345
5W9I	E_ARG_758	NH1	F_ASP_740	OD1	2.820
5W9I	E_LYS_779	NZ	E_ASP_771	OD2	2.924
5W9I	E_LYS_779	NZ	E_GLU_1148	OE1	3.718
5W9I	E_LYS_801	NZ	E_ASP_843	OD1	2.850
5W9I	E_LYS_801	NZ	E_ASP_843	OD2	3.507
5W9I	E_LYS_807	NZ	E_GLU_818	OE1	3.745
5W9I	E_LYS_807	NZ	E_GLU_818	OE2	3.005
5W9I	E_LYS_816	NZ	E_ASP_1064	OD1	3.825
5W9I	E_LYS_816	NZ	E_ASP_1064	OD2	3.707
5W9I	E_ARG_841	NH1	E_GLU_1090	OE1	2.868
5W9I	E_ARG_841	NH2	E_GLU_1090	OE1	2.843
5W9I	E_ARG_847	NH1	J_ASP_726	OD1	3.709
5W9I	E_ARG_847	NH1	J_ASP_726	OD2	2.881
5W9I	E_ARG_847	NH2	E_ASP_844	OD1	2.801
5W9I	E_ARG_887	NH2	E_ASP_892	OD1	2.928
5W9I	E_HIS_1020	NE2	E_ASP_1024	OD2	2.999
5W9I	E_LYS_1021	NZ	E_GLU_1017	OE2	3.409
5W9I	E_LYS_1102	NZ	E_GLU_793	OE1	2.968
5W9I	E_LYS_1102	NZ	E_GLU_793	OE2	2.898
5W9I	E_ARG_1113	NH1	E_GLU_1105	OE1	2.970
5W9I	E_ARG_1113	NH2	E_GLU_1105	OE1	3.046
5W9I	E_ARG_1113	NH2	E_GLU_1105	OE2	3.856
5W9I	E_HIS_1138	NE2	E_GLU_793	OE2	2.952
5W9I	E_LYS_1174	NZ	E_GLU_1183	OE1	2.800
5W9I	E_ARG_1179	NH2	G_ASP_31	OD1	2.831
5W9I	F_LYS_99	NZ	F_GLU_32	OE1	2.800
5W9I	F_LYS_110	NZ	F_ASP_83	OD2	2.755
5W9I	F_ARG_119	NH2	F_ASP_54	OD2	3.152
5W9I	F_LYS_142	NZ	F_GLU_252	OE1	2.880
5W9I	F_HIS_194	NE2	F_GLU_32	OE1	3.655
5W9I	F_ARG_235	NH1	F_ASP_24	OD1	3.849
5W9I	F_ARG_235	NH1	F_ASP_24	OD2	3.358
5W9I	F_ARG_235	NH2	F_ASP_24	OD2	2.934
5W9I	F_ARG_235	NH2	F_GLU_188	OE1	2.870
5W9I	F_ARG_235	NH2	F_GLU_188	OE2	3.760
5W9I	F_ARG_335	NH2	F_ASP_326	OD2	2.868
5W9I	F_ARG_614	NH1	F_GLU_367	OE2	3.306
5W9I	F_ARG_614	NH2	F_GLU_367	OE2	3.411
5W9I	F_ARG_629	NH1	F_GLU_376	OE1	3.445
5W9I	F_ARG_629	NH1	F_ASP_644	OD1	2.966
5W9I	F_ARG_629	NH1	F_ASP_644	OD2	3.809
5W9I	F_ARG_629	NH2	F_ASP_644	OD1	2.990
5W9I	F_LYS_665	NZ	F_GLU_357	OE1	2.866
5W9I	F_LYS_665	NZ	F_GLU_357	OE2	3.810
5W9I	F_HIS_681	NE2	A_ASP_910	OD1	2.878
5W9I	F_HIS_681	NE2	A_ASP_910	OD2	3.982

5W9I	F_HIS.681	NE2	F_GLU.680	OE2	3.229
5W9I	F_LYS.728	NZ	F_ASP.726	OD2	2.885
5W9I	G_LYS.38	NZ	G_ASP.86	OD1	3.902
5W9I	G_LYS.62	NZ	G_GLU.46	OE1	3.433
5W9I	G_LYS.62	NZ	G_GLU.46	OE2	2.934
5W9I	G_ARG.66	NH1	G_ASP.86	OD1	3.147
5W9I	G_ARG.66	NH1	G_ASP.86	OD2	3.501
5W9I	G_ARG.66	NH2	G_ASP.86	OD1	3.792
5W9I	G_ARG.66	NH2	G_ASP.86	OD2	2.779
5W9I	G_ARG.94	NH2	G_ASP.101	OD1	3.649
5W9I	G_ARG.94	NH2	G_ASP.101	OD2	2.843
5W9I	G_LYS.95	NZ	G_ASP.100C	OD1	3.513
5W9I	G_LYS.95	NZ	G_ASP.100C	OD2	3.725
5W9I	H_ARG.24	NH2	H_ASP.70	OD1	2.942
5W9I	H_ARG.24	NH2	H_ASP.70	OD2	3.817
5W9I	H_ARG.61	NH1	H_ASP.82	OD1	3.183
5W9I	H_ARG.61	NH1	H_ASP.82	OD2	3.671
5W9I	H_ARG.61	NH2	H_ASP.82	OD1	3.703
5W9I	H_ARG.61	NH2	H_ASP.82	OD2	2.773
5W9I	H_LYS.92	NZ	H_GLU.93	OE1	3.454
5W9I	H_ARG.96	NH1	G_ASP.100C	OD2	2.856
5W9I	H_ARG.96	NH2	E_GLU.1183	OE2	2.871
5W9I	H_ARG.96	NH2	G_ASP.100C	OD2	2.925
5W9I	H_LYS.103	NZ	H_GLU.105	OE2	3.616
5W9I	I_ARG.758	NH1	J_ASP.740	OD1	2.804
5W9I	I_LYS.779	NZ	I_ASP.771	OD2	2.925
5W9I	I_LYS.779	NZ	I_GLU.1148	OE1	3.696
5W9I	I_LYS.801	NZ	I_ASP.843	OD1	2.847
5W9I	I_LYS.801	NZ	I_ASP.843	OD2	3.503
5W9I	I_LYS.807	NZ	I_GLU.818	OE1	3.621
5W9I	I_LYS.807	NZ	I_GLU.818	OE2	2.894
5W9I	I_LYS.816	NZ	I_ASP.1064	OD1	3.871
5W9I	I_LYS.816	NZ	I_ASP.1064	OD2	3.720
5W9I	I_ARG.841	NH1	I_GLU.1090	OE1	2.860
5W9I	I_ARG.841	NH2	I_GLU.1090	OE1	2.839
5W9I	I_ARG.847	NH1	B_ASP.726	OD1	3.716
5W9I	I_ARG.847	NH1	B_ASP.726	OD2	2.881
5W9I	I_ARG.847	NH2	I_ASP.844	OD1	2.793
5W9I	I_ARG.887	NH2	I_ASP.892	OD1	2.930
5W9I	I_HIS.1020	NE2	I_ASP.1024	OD2	3.008
5W9I	I_LYS.1021	NZ	I_GLU.1017	OE2	3.414
5W9I	I_LYS.1102	NZ	I_GLU.793	OE1	2.931
5W9I	I_LYS.1102	NZ	I_GLU.793	OE2	2.910
5W9I	I_ARG.1113	NH1	I_GLU.1105	OE1	2.967
5W9I	I_ARG.1113	NH1	I_GLU.1105	OE2	3.647
5W9I	I_ARG.1113	NH2	E_GLU.1105	OE2	2.821
5W9I	I_HIS.1138	NE2	I_GLU.793	OE2	2.948
5W9I	I_LYS.1174	NZ	I_GLU.1183	OE1	2.809
5W9I	I_ARG.1179	NH2	K_ASP.31	OD1	2.785
5W9I	J_LYS.99	NZ	J_GLU.32	OE1	2.800
5W9I	J_LYS.110	NZ	J_ASP.83	OD2	2.766
5W9I	J_ARG.119	NH2	J_ASP.54	OD2	3.206
5W9I	J_LYS.142	NZ	J_GLU.252	OE1	2.986
5W9I	J_HIS.194	NE2	J_GLU.32	OE1	3.656
5W9I	J_ARG.235	NH1	J_ASP.24	OD1	3.840
5W9I	J_ARG.235	NH1	J_ASP.24	OD2	3.366
5W9I	J_ARG.235	NH2	J_ASP.24	OD2	2.931
5W9I	J_ARG.235	NH2	J_GLU.188	OE1	2.868

5W9I	J_ARG_235	NH2	J_GLU_188	OE2	3.758
5W9I	J_ARG_335	NH2	J_ASP_326	OD2	2.865
5W9I	J_ARG_614	NH1	J_GLU_367	OE2	3.042
5W9I	J_ARG_614	NH2	J_GLU_367	OE2	3.261
5W9I	J_ARG_629	NH1	J_ASP_644	OD1	2.970
5W9I	J_ARG_629	NH1	J_ASP_644	OD2	3.960
5W9I	J_ARG_629	NH2	J_ASP_644	OD1	3.193
5W9I	J_LYS_665	NZ	J_GLU_357	OE1	2.867
5W9I	J_LYS_665	NZ	J_GLU_357	OE2	3.780
5W9I	J_LYS_668	NZ	J_ASP_355	OD1	3.043
5W9I	J_HIS_681	NE2	E_ASP_910	OD1	2.832
5W9I	J_HIS_681	NE2	J_GLU_680	OE2	3.209
5W9I	J_LYS_728	NZ	J_ASP_726	OD2	2.883
5W9I	K_LYS_38	NZ	K_ASP_86	OD1	3.899
5W9I	K_LYS_62	NZ	K_GLU_46	OE1	3.395
5W9I	K_LYS_62	NZ	K_GLU_46	OE2	2.930
5W9I	K_ARG_66	NH1	K_ASP_86	OD1	3.149
5W9I	K_ARG_66	NH1	K_ASP_86	OD2	3.507
5W9I	K_ARG_66	NH2	K_ASP_86	OD1	3.795
5W9I	K_ARG_66	NH2	K_ASP_86	OD2	2.786
5W9I	K_ARG_94	NH2	K_ASP_101	OD1	2.859
5W9I	K_ARG_94	NH2	K_ASP_101	OD2	3.615
5W9I	K_LYS_95	NZ	K_ASP_100C	OD1	3.504
5W9I	K_LYS_95	NZ	K_ASP_100C	OD2	3.759
5W9I	L_ARG_24	NH1	L_ASP_70	OD1	2.947
5W9I	L_ARG_24	NH1	L_ASP_70	OD2	3.851
5W9I	L_ARG_61	NH1	L_ASP_82	OD1	3.190
5W9I	L_ARG_61	NH1	L_ASP_82	OD2	3.680
5W9I	L_ARG_61	NH2	L_ASP_82	OD1	3.703
5W9I	L_ARG_61	NH2	L_ASP_82	OD2	2.775
5W9I	L_LYS_92	NZ	L_GLU_93	OE1	3.397
5W9I	L_ARG_96	NH1	K_ASP_100C	OD2	2.856
5W9I	L_ARG_96	NH2	L_GLU_1183	OE2	2.872
5W9I	L_ARG_96	NH2	K_ASP_100C	OD2	2.922
5W9I	L_LYS_103	NZ	L_GLU_105	OE2	3.808

Table 743: 5W9I-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5W9J	D_LYS_779	NZ	D_GLU_1148	OE1	2.939
5W9J	D_LYS_801	NZ	D_ASP_843	OD1	3.375
5W9J	D_LYS_807	NZ	D_GLU_818	OE1	2.817
5W9J	D_LYS_807	NZ	D_GLU_818	OE2	3.422
5W9J	D_LYS_816	NZ	D_ASP_1064	OD1	3.520
5W9J	D_LYS_816	NZ	D_ASP_1064	OD2	3.973
5W9J	D_ARG_841	NH2	D_ASP_844	OD2	2.773
5W9J	D_ARG_847	NH2	D_ASP_844	OD1	2.691
5W9J	D_ARG_887	NH1	D_ASP_892	OD1	2.879
5W9J	D_HIS_1020	NE2	D_ASP_1024	OD1	3.785
5W9J	D_HIS_1020	NE2	D_ASP_1024	OD2	2.892
5W9J	D_ARG_1057	NH2	D_ASP_1053	OD1	3.921
5W9J	D_LYS_1102	NZ	D_GLU_793	OE1	2.814
5W9J	D_LYS_1102	NZ	D_GLU_793	OE2	3.963
5W9J	D_ARG_1113	NH1	D_GLU_1105	OE1	3.016
5W9J	D_ARG_1113	NH2	G_GLU_1105	OE1	3.627
5W9J	D_ARG_1113	NH2	G_GLU_1105	OE2	2.779
5W9J	D_HIS_1138	NE2	D_GLU_793	OE2	2.844
5W9J	E_HIS_35	NE2	E_ASP_100C	OD2	3.981
5W9J	E_LYS_38	NZ	E_GLU_46	OE1	3.833
5W9J	E_LYS_38	NZ	E_ASP_86	OD1	2.905
5W9J	E_LYS_62	NZ	E_GLU_46	OE2	2.796
5W9J	E_ARG_94	NH1	E_ASP_101	OD2	3.268
5W9J	E_LYS_95	NZ	E_ASP_100C	OD2	2.845
5W9J	F_ARG_61	NH1	F_ASP_82	OD1	3.198
5W9J	F_ARG_61	NH1	F_ASP_82	OD2	3.745
5W9J	F_ARG_61	NH2	F_GLU_79	OE1	3.635
5W9J	F_ARG_61	NH2	F_ASP_82	OD1	3.645
5W9J	F_ARG_61	NH2	F_ASP_82	OD2	2.778
5W9J	F_ARG_96	NH1	E_ASP_100C	OD1	3.873
5W9J	F_ARG_96	NH1	E_ASP_100C	OD2	3.469
5W9J	A_LYS_779	NZ	A_GLU_1148	OE1	2.940
5W9J	A_LYS_801	NZ	A_ASP_843	OD1	3.375
5W9J	A_LYS_807	NZ	A_GLU_818	OE1	2.817
5W9J	A_LYS_807	NZ	A_GLU_818	OE2	3.422
5W9J	A_LYS_816	NZ	A_ASP_1064	OD1	3.520
5W9J	A_LYS_816	NZ	A_ASP_1064	OD2	3.973
5W9J	A_ARG_841	NH2	A_ASP_844	OD2	2.773
5W9J	A_ARG_847	NH2	A_ASP_844	OD1	2.691
5W9J	A_ARG_887	NH1	A_ASP_892	OD1	2.879
5W9J	A_HIS_1020	NE2	A_ASP_1024	OD1	3.785
5W9J	A_HIS_1020	NE2	A_ASP_1024	OD2	2.892
5W9J	A_ARG_1057	NH2	A_ASP_1053	OD1	3.921
5W9J	A_LYS_1102	NZ	A_GLU_793	OE1	2.814
5W9J	A_LYS_1102	NZ	A_GLU_793	OE2	3.964
5W9J	A_ARG_1113	NH1	A_GLU_1105	OE1	3.016
5W9J	A_ARG_1113	NH2	D_GLU_1105	OE1	3.626
5W9J	A_ARG_1113	NH2	D_GLU_1105	OE2	2.778
5W9J	A_HIS_1138	NE2	A_GLU_793	OE2	2.844
5W9J	B_HIS_35	NE2	B_ASP_100C	OD2	3.981
5W9J	B_LYS_38	NZ	B_GLU_46	OE1	3.833
5W9J	B_LYS_38	NZ	B_ASP_86	OD1	2.905
5W9J	B_LYS_62	NZ	B_GLU_46	OE2	2.796
5W9J	B_ARG_94	NH1	B_ASP_101	OD2	3.270
5W9J	B_LYS_95	NZ	B_ASP_100C	OD2	2.844
5W9J	C_ARG_61	NH1	C_ASP_82	OD1	3.196
5W9J	C_ARG_61	NH1	C_ASP_82	OD2	3.745

5W9J	C_ARG_61	NH2	C_GLU_79	OE1	3.636
5W9J	C_ARG_61	NH2	C_ASP_82	OD1	3.644
5W9J	C_ARG_61	NH2	C_ASP_82	OD2	2.779
5W9J	C_ARG_96	NH1	B_ASP_100C	OD1	3.873
5W9J	C_ARG_96	NH1	B_ASP_100C	OD2	3.470
5W9J	G_LYS_779	NZ	G_GLU_1148	OE1	2.940
5W9J	G_LYS_801	NZ	G_ASP_843	OD1	3.374
5W9J	G_LYS_807	NZ	G_GLU_818	OE1	2.817
5W9J	G_LYS_807	NZ	G_GLU_818	OE2	3.421
5W9J	G_LYS_816	NZ	G_ASP_1064	OD1	3.521
5W9J	G_LYS_816	NZ	G_ASP_1064	OD2	3.973
5W9J	G_ARG_841	NH2	G_ASP_844	OD2	2.773
5W9J	G_ARG_847	NH2	G_ASP_844	OD1	2.691
5W9J	G_ARG_887	NH1	G_ASP_892	OD1	2.880
5W9J	G_HIS_1020	NE2	G_ASP_1024	OD1	3.785
5W9J	G_HIS_1020	NE2	G_ASP_1024	OD2	2.892
5W9J	G_ARG_1057	NH2	G_ASP_1053	OD1	3.921
5W9J	G_LYS_1102	NZ	G_GLU_793	OE1	2.813
5W9J	G_LYS_1102	NZ	G_GLU_793	OE2	3.963
5W9J	G_ARG_1113	NH1	G_GLU_1105	OE1	3.016
5W9J	G_ARG_1113	NH2	A_GLU_1105	OE1	3.626
5W9J	G_ARG_1113	NH2	A_GLU_1105	OE2	2.777
5W9J	G_HIS_1138	NE2	G_GLU_793	OE2	2.844
5W9J	H_HIS_35	NE2	H_ASP_100C	OD2	3.981
5W9J	H_LYS_38	NZ	H_GLU_46	OE1	3.832
5W9J	H_LYS_38	NZ	H_ASP_86	OD1	2.905
5W9J	H_LYS_62	NZ	H_GLU_46	OE2	2.795
5W9J	H_ARG_94	NH1	H_ASP_101	OD2	3.269
5W9J	H_LYS_95	NZ	H_ASP_100C	OD2	2.844
5W9J	I_ARG_61	NH1	I_ASP_82	OD1	3.197
5W9J	I_ARG_61	NH1	I_ASP_82	OD2	3.745
5W9J	I_ARG_61	NH2	I_GLU_79	OE1	3.636
5W9J	I_ARG_61	NH2	I_ASP_82	OD1	3.644
5W9J	I_ARG_61	NH2	I_ASP_82	OD2	2.779
5W9J	I_ARG_96	NH1	H_ASP_100C	OD1	3.873
5W9J	I_ARG_96	NH1	H_ASP_100C	OD2	3.470
5W9J	J_LYS_52	NZ	J_ASP_49	OD2	2.757
5W9J	J_HIS_81	ND1	J_ASP_80	OD1	3.851
5W9J	J_LYS_99	NZ	J_ASP_34	OD2	2.722
5W9J	J_LYS_110	NZ	J_ASP_108	OD1	3.409
5W9J	J_LYS_110	NZ	J_ASP_108	OD2	3.230
5W9J	J_ARG_119	NH1	J_ASP_54	OD2	3.696
5W9J	J_ARG_119	NH2	J_ASP_54	OD2	3.009
5W9J	J_ARG_181	NH1	J_ASP_174	OD2	3.331
5W9J	J_ARG_190	NH1	J_ASP_24	OD1	3.612
5W9J	J_ARG_190	NH1	J_ASP_24	OD2	3.889
5W9J	J_ARG_190	NH2	J_ASP_24	OD1	2.692
5W9J	J_ARG_235	NH2	J_GLU_188	OE1	2.796
5W9J	J_ARG_334	NH2	J_ASP_330	OD2	3.710
5W9J	J_ARG_335	NH2	J_ASP_326	OD2	3.031
5W9J	J_ARG_401	NH2	J_ASP_444	OD1	3.639
5W9J	J_ARG_401	NH2	J_ASP_444	OD2	3.140
5W9J	J_LYS_502	NZ	J_GLU_513	OE2	2.796
5W9J	J_LYS_543	NZ	J_GLU_549	OE2	3.291
5W9J	J_LYS_587	NZ	J_GLU_382	OE2	2.820
5W9J	J_ARG_614	NH2	J_GLU_605	OE2	2.932
5W9J	J_LYS_665	NZ	J_GLU_666	OE2	2.774
5W9J	J_LYS_728	NZ	J_ASP_726	OD2	2.840

5W9J	K_LYS_52	NZ	K_ASP_49	OD2	2.756
5W9J	K_HIS_81	ND1	K_ASP_80	OD1	3.851
5W9J	K_LYS_99	NZ	K_ASP_34	OD2	2.723
5W9J	K_LYS_110	NZ	K_ASP_108	OD1	3.410
5W9J	K_LYS_110	NZ	K_ASP_108	OD2	3.231
5W9J	K_ARG_119	NH1	K_ASP_54	OD2	3.694
5W9J	K_ARG_119	NH2	K_ASP_54	OD2	3.008
5W9J	K_ARG_181	NH1	K_ASP_174	OD2	3.331
5W9J	K_ARG_190	NH1	K_ASP_24	OD1	3.611
5W9J	K_ARG_190	NH1	K_ASP_24	OD2	3.890
5W9J	K_ARG_190	NH2	K_ASP_24	OD1	2.691
5W9J	K_ARG_235	NH2	K_GLU_188	OE1	2.796
5W9J	K_ARG_334	NH2	K_ASP_330	OD2	3.710
5W9J	K_ARG_335	NH2	K_ASP_326	OD2	3.030
5W9J	K_ARG_401	NH2	K_ASP_444	OD1	3.638
5W9J	K_ARG_401	NH2	K_ASP_444	OD2	3.140
5W9J	K_LYS_502	NZ	K_GLU_513	OE2	2.796
5W9J	K_LYS_543	NZ	K_GLU_549	OE2	3.291
5W9J	K_LYS_587	NZ	K_GLU_382	OE2	2.819
5W9J	K_ARG_614	NH2	K_GLU_605	OE2	2.931
5W9J	K_LYS_665	NZ	K_GLU_666	OE2	2.774
5W9J	K_LYS_728	NZ	K_ASP_726	OD2	2.839
5W9J	L_LYS_52	NZ	L_ASP_49	OD2	2.756
5W9J	L_HIS_81	ND1	L_ASP_80	OD1	3.851
5W9J	L_LYS_99	NZ	L_ASP_34	OD2	2.724
5W9J	L_LYS_110	NZ	L_ASP_108	OD1	3.409
5W9J	L_LYS_110	NZ	L_ASP_108	OD2	3.231
5W9J	L_ARG_119	NH1	L_ASP_54	OD2	3.695
5W9J	L_ARG_119	NH2	L_ASP_54	OD2	3.009
5W9J	L_ARG_181	NH1	L_ASP_174	OD2	3.331
5W9J	L_ARG_190	NH1	L_ASP_24	OD1	3.612
5W9J	L_ARG_190	NH1	L_ASP_24	OD2	3.889
5W9J	L_ARG_190	NH2	L_ASP_24	OD1	2.692
5W9J	L_ARG_235	NH2	L_GLU_188	OE1	2.796
5W9J	L_ARG_334	NH2	L_ASP_330	OD2	3.710
5W9J	L_ARG_335	NH2	L_ASP_326	OD2	3.031
5W9J	L_ARG_401	NH2	L_ASP_444	OD1	3.638
5W9J	L_ARG_401	NH2	L_ASP_444	OD2	3.140
5W9J	L_LYS_502	NZ	L_GLU_513	OE2	2.796
5W9J	L_LYS_543	NZ	L_GLU_549	OE2	3.291
5W9J	L_LYS_587	NZ	L_GLU_382	OE2	2.820
5W9J	L_ARG_614	NH2	L_GLU_605	OE2	2.931
5W9J	L_LYS_665	NZ	L_GLU_666	OE2	2.773
5W9J	L_LYS_728	NZ	L_ASP_726	OD2	2.839

Table 744: 5W9J-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5W9K	A_ARG.758	NH1	J_ASP.740	OD1	3.054
5W9K	A_LYS.801	NZ	A_ASP.843	OD1	2.794
5W9K	A_LYS.801	NZ	A_ASP.843	OD2	3.729
5W9K	A_LYS.807	NZ	A_GLU.818	OE2	3.490
5W9K	A_ARG.841	NH2	A_ASP.844	OD2	2.781
5W9K	A_ARG.847	NH2	A_ASP.844	OD1	2.722
5W9K	A_ARG.887	NH2	A_ASP.892	OD1	2.945
5W9K	A_LYS.995	NZ	A_ASP.868	OD1	3.265
5W9K	A_LYS.995	NZ	A_ASP.868	OD2	1.942
5W9K	A_HIS.1020	NE2	A_ASP.1024	OD2	2.878
5W9K	A_LYS.1102	NZ	A_GLU.793	OE1	2.948
5W9K	A_LYS.1102	NZ	A_GLU.793	OE2	3.271
5W9K	A_ARG.1113	NH1	A_GLU.1105	OE1	3.481
5W9K	A_ARG.1113	NH1	A_GLU.1105	OE2	2.966
5W9K	A_ARG.1113	NH2	D_GLU.1105	OE1	3.698
5W9K	A_HIS.1138	NE2	A_GLU.793	OE1	2.957
5W9K	A_LYS.1174	NZ	A_GLU.1183	OE2	3.009
5W9K	B_LYS.62	NZ	B_GLU.46	OE1	2.956
5W9K	B_LYS.62	NZ	B_GLU.46	OE2	3.368
5W9K	B_ARG.66	NH2	B_ASP.86	OD2	3.716
5W9K	B_ARG.94	NH2	B_ASP.101	OD2	2.759
5W9K	B_LYS.95	NZ	B_ASP.100C	OD2	3.608
5W9K	C_ARG.61	NH1	C_GLU.79	OE1	3.492
5W9K	C_LYS.92	NZ	C_GLU.93	OE1	2.823
5W9K	C_ARG.96	NH1	B_ASP.100C	OD2	2.822
5W9K	C_ARG.96	NH2	A_GLU.1183	OE1	3.683
5W9K	C_ARG.96	NH2	B_ASP.100C	OD2	3.420
5W9K	C_LYS.103	NZ	C_GLU.105	OE1	3.546
5W9K	D_LYS.779	NZ	D_ASP.771	OD2	2.911
5W9K	D_LYS.779	NZ	D_GLU.1148	OE1	3.847
5W9K	D_LYS.801	NZ	D_ASP.843	OD1	3.006
5W9K	D_LYS.807	NZ	D_GLU.818	OE1	2.844
5W9K	D_LYS.807	NZ	D_GLU.818	OE2	3.659
5W9K	D_ARG.841	NH2	D_GLU.1090	OE1	3.013
5W9K	D_ARG.841	NH2	D_GLU.1090	OE2	3.315
5W9K	D_ARG.847	NH1	D_ASP.844	OD1	2.982
5W9K	D_ARG.847	NH2	A_GLU.1017	OE2	3.108
5W9K	D_ARG.847	NH2	D_ASP.844	OD1	2.962
5W9K	D_ARG.887	NH2	D_ASP.892	OD1	2.947
5W9K	D_HIS.1020	NE2	D_ASP.1024	OD1	3.582
5W9K	D_HIS.1020	NE2	D_ASP.1024	OD2	3.188
5W9K	D_ARG.1057	NH1	D_ASP.1053	OD1	3.444
5W9K	D_LYS.1102	NZ	D_GLU.793	OE1	2.980
5W9K	D_LYS.1102	NZ	D_GLU.793	OE2	3.212
5W9K	D_ARG.1113	NH1	G_GLU.1105	OE2	3.336
5W9K	D_ARG.1113	NH2	D_GLU.1105	OE1	3.680
5W9K	D_ARG.1113	NH2	D_GLU.1105	OE2	3.676
5W9K	D_HIS.1138	NE2	D_GLU.793	OE1	3.055
5W9K	E_LYS.62	NZ	E_GLU.46	OE1	2.864
5W9K	E_LYS.62	NZ	E_GLU.46	OE2	3.729
5W9K	E_ARG.66	NH1	E_ASP.86	OD1	2.957
5W9K	E_ARG.66	NH1	E_ASP.86	OD2	3.366
5W9K	E_ARG.94	NH1	E_ASP.101	OD2	3.378
5W9K	E_ARG.94	NH2	E_ASP.101	OD2	2.893
5W9K	E_LYS.95	NZ	E_ASP.100C	OD1	3.994
5W9K	F_ARG.24	NH1	F_ASP.70	OD1	2.969
5W9K	F_ARG.24	NH1	F_ASP.70	OD2	3.751

5W9K	F_ARG_61	NH1	F_GLU_79	OE1	3.263
5W9K	F_ARG_61	NH1	F_GLU_79	OE2	3.365
5W9K	F_ARG_61	NH2	F_GLU_79	OE2	3.136
5W9K	F_ARG_96	NH1	E_ASP_100C	OD2	2.856
5W9K	F_ARG_96	NH2	D_GLU_1183	OE2	3.059
5W9K	F_ARG_96	NH2	E_ASP_100C	OD2	3.317
5W9K	G_ARG_758	NH1	L_ASP_740	OD1	3.028
5W9K	G_ARG_758	NH2	L_ASP_740	OD1	3.483
5W9K	G_LYS_801	NZ	G_ASP_843	OD1	2.854
5W9K	G_LYS_801	NZ	G_ASP_843	OD2	3.469
5W9K	G_LYS_816	NZ	G_ASP_1064	OD2	3.838
5W9K	G_ARG_847	NH1	K_ASP_726	OD2	3.336
5W9K	G_ARG_847	NH2	G_ASP_844	OD1	2.739
5W9K	G_ARG_887	NH2	G_ASP_892	OD1	2.989
5W9K	G_ARG_887	NH2	G_ASP_892	OD2	3.967
5W9K	G_HIS_1020	NE2	G_ASP_1024	OD2	2.997
5W9K	G_LYS_1035	NZ	G_GLU_1039	OE2	2.927
5W9K	G_ARG_1057	NH1	G_ASP_1053	OD2	3.710
5W9K	G_ARG_1057	NH2	G_ASP_1053	OD1	3.602
5W9K	G_ARG_1057	NH2	G_ASP_1053	OD2	3.839
5W9K	G_LYS_1102	NZ	G_GLU_793	OE1	2.948
5W9K	G_LYS_1102	NZ	G_GLU_793	OE2	3.330
5W9K	G_ARG_1113	NH1	G_GLU_1105	OE1	3.508
5W9K	G_ARG_1113	NH1	G_GLU_1105	OE2	2.905
5W9K	G_ARG_1113	NH2	A_GLU_1105	OE2	3.565
5W9K	G_HIS_1138	NE2	G_GLU_793	OE1	3.027
5W9K	G_LYS_1174	NZ	G_GLU_1183	OE1	3.901
5W9K	H_LYS_62	NZ	H_GLU_46	OE1	3.402
5W9K	H_LYS_62	NZ	H_GLU_46	OE2	2.946
5W9K	H_ARG_66	NH2	H_ASP_86	OD2	2.876
5W9K	H_ARG_94	NH2	H_ASP_101	OD2	2.768
5W9K	H_LYS_95	NZ	H_ASP_100C	OD2	3.668
5W9K	I_ARG_24	NH1	I_ASP_70	OD1	3.017
5W9K	I_ARG_24	NH2	I_ASP_70	OD1	3.829
5W9K	I_LYS_92	NZ	I_GLU_93	OE1	2.854
5W9K	I_ARG_96	NH1	H_ASP_100C	OD2	2.828
5W9K	I_ARG_96	NH2	G_GLU_1183	OE2	3.651
5W9K	I_ARG_96	NH2	H_ASP_100C	OD2	3.553
5W9K	I_LYS_103	NZ	I_GLU_105	OE1	3.522
5W9K	J_HIS_81	ND1	J_ASP_80	OD1	3.968
5W9K	J_LYS_99	NZ	J_GLU_32	OE1	2.810
5W9K	J_LYS_110	NZ	J_ASP_83	OD2	2.940
5W9K	J_LYS_142	NZ	J_GLU_247	OE1	3.288
5W9K	J_LYS_142	NZ	J_GLU_249	OE2	2.849
5W9K	J_ARG_190	NH1	J_ASP_24	OD1	3.560
5W9K	J_ARG_190	NH1	J_ASP_24	OD2	3.246
5W9K	J_ARG_190	NH2	J_ASP_24	OD1	2.727
5W9K	J_ARG_190	NH2	J_ASP_24	OD2	3.757
5W9K	J_HIS_194	NE2	J_GLU_32	OE1	3.514
5W9K	J_ARG_235	NH1	J_GLU_188	OE1	2.902
5W9K	J_ARG_235	NH1	J_GLU_188	OE2	3.519
5W9K	J_ARG_334	NH2	J_ASP_330	OD1	3.961
5W9K	J_ARG_334	NH2	J_ASP_330	OD2	3.087
5W9K	J_ARG_335	NH2	J_ASP_326	OD2	2.876
5W9K	J_ARG_401	NH2	J_ASP_444	OD1	3.806
5W9K	J_ARG_401	NH2	J_ASP_444	OD2	3.280
5W9K	J_LYS_502	NZ	J_GLU_513	OE2	3.504
5W9K	J_ARG_505	NH1	J_GLU_549	OE1	3.692

5W9K	J_ARG.629	NH1	J_GLU.376	OE2	3.955
5W9K	J_LYS.665	NZ	J_ASP.355	OD2	3.949
5W9K	J_HIS.681	NE2	D_ASP.910	OD1	2.963
5W9K	J_ARG.694	NH1	J_ASP.343	OD2	3.085
5W9K	J_ARG.694	NH2	J_ASP.343	OD2	2.916
5W9K	J_ARG.700	NH2	A_GLU.756	OE2	2.841
5W9K	J_LYS.728	NZ	J_GLU.666	OE1	3.931
5W9K	J_LYS.728	NZ	J_GLU.666	OE2	3.368
5W9K	K_HIS.81	ND1	K_ASP.80	OD1	3.713
5W9K	K_LYS.99	NZ	K_GLU.32	OE1	2.842
5W9K	K_LYS.142	NZ	K_GLU.252	OE2	3.341
5W9K	K_ARG.190	NH1	K_GLU.188	OE1	2.901
5W9K	K_HIS.194	NE2	K_GLU.32	OE1	3.703
5W9K	K_ARG.235	NH1	K_GLU.188	OE2	3.498
5W9K	K_ARG.335	NH2	K_ASP.326	OD2	2.914
5W9K	K_ARG.401	NH2	K_ASP.444	OD1	3.980
5W9K	K_ARG.401	NH2	K_ASP.444	OD2	3.862
5W9K	K_LYS.502	NZ	K_GLU.513	OE1	2.884
5W9K	K_LYS.502	NZ	K_GLU.513	OE2	3.989
5W9K	K_LYS.543	NZ	K_GLU.549	OE1	3.288
5W9K	K_LYS.543	NZ	K_GLU.549	OE2	3.352
5W9K	K_LYS.587	NZ	K_GLU.382	OE2	2.948
5W9K	K_LYS.665	NZ	K_GLU.666	OE2	2.821
5W9K	K_LYS.668	NZ	K_ASP.355	OD1	3.287
5W9K	K_LYS.668	NZ	K_ASP.355	OD2	3.232
5W9K	K_LYS.728	NZ	K_ASP.726	OD2	2.912
5W9K	L_LYS.27	NZ	L_GLU.230	OE2	3.262
5W9K	L_HIS.81	ND1	L_ASP.80	OD1	3.835
5W9K	L_LYS.99	NZ	L_GLU.32	OE2	3.537
5W9K	L_LYS.99	NZ	L_ASP.34	OD2	3.570
5W9K	L_LYS.110	NZ	L_ASP.83	OD2	2.905
5W9K	L_ARG.119	NH1	L_ASP.54	OD2	3.602
5W9K	L_LYS.142	NZ	L_GLU.252	OE2	3.115
5W9K	L_ARG.190	NH1	L_ASP.24	OD2	3.340
5W9K	L_ARG.190	NH2	L_GLU.188	OE2	3.335
5W9K	L_HIS.194	NE2	L_GLU.32	OE1	3.901
5W9K	L_ARG.235	NH1	L_GLU.188	OE1	2.872
5W9K	L_ARG.269	NH1	L_GLU.252	OE1	2.853
5W9K	L_ARG.334	NH2	L_ASP.330	OD1	3.920
5W9K	L_ARG.334	NH2	L_ASP.330	OD2	3.026
5W9K	L_ARG.335	NH2	L_ASP.326	OD2	2.940
5W9K	L_ARG.401	NH2	L_ASP.444	OD1	3.708
5W9K	L_ARG.401	NH2	L_ASP.444	OD2	3.216
5W9K	L_LYS.496	NZ	L_GLU.536	OE1	2.998
5W9K	L_LYS.496	NZ	L_GLU.536	OE2	3.594
5W9K	L_LYS.502	NZ	L_GLU.513	OE2	3.474
5W9K	L_ARG.505	NH1	L_GLU.549	OE1	2.874
5W9K	L_ARG.629	NH1	L_GLU.376	OE2	3.648
5W9K	L_ARG.629	NH1	L_ASP.644	OD1	2.887
5W9K	L_ARG.629	NH1	L_ASP.644	OD2	3.878
5W9K	L_ARG.629	NH2	L_ASP.644	OD1	2.829
5W9K	L_ARG.629	NH2	L_ASP.644	OD2	3.918
5W9K	L_HIS.681	NE2	A_ASP.910	OD1	3.027
5W9K	L_HIS.681	NE2	A_ASP.910	OD2	3.875
5W9K	L_ARG.691	NH2	L_ASP.343	OD1	3.689
5W9K	L_ARG.694	NH1	L_ASP.343	OD2	3.049
5W9K	L_ARG.694	NH2	L_ASP.343	OD2	2.912
5W9K	L_ARG.700	NH2	G_GLU.756	OE2	2.893

5W9K	L.LYS.728	NZ	L.ASP.726	OD2	2.874
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Table 745: 5W9K-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5W9L	A_ARG.758	NH1	B_ASP.740	OD1	2.964
5W9L	A_ARG.758	NH2	B_ASP.740	OD1	3.858
5W9L	A_LYS.801	NZ	A_ASP.843	OD1	2.802
5W9L	A_LYS.801	NZ	A_ASP.843	OD2	3.510
5W9L	A_LYS.807	NZ	A_GLU.818	OE1	2.932
5W9L	A_LYS.807	NZ	A_GLU.818	OE2	3.202
5W9L	A_ARG.841	NH1	A_ASP.844	OD2	3.517
5W9L	A_ARG.847	NH2	A_ASP.844	OD1	2.713
5W9L	A_ARG.887	NH2	A_ASP.892	OD1	2.862
5W9L	A_ARG.887	NH2	A_ASP.892	OD2	3.937
5W9L	A_HIS.1020	NE2	A_ASP.1024	OD2	2.890
5W9L	A_LYS.1021	NZ	A_GLU.793	OE1	3.715
5W9L	A_LYS.1021	NZ	A_GLU.793	OE2	2.898
5W9L	A_ARG.1057	NH2	A_ASP.1053	OD1	3.565
5W9L	A_ARG.1057	NH2	A_ASP.1053	OD2	2.794
5W9L	A_ARG.1113	NH1	A_GLU.1105	OE1	3.356
5W9L	A_ARG.1113	NH1	A_GLU.1105	OE2	2.777
5W9L	A_ARG.1113	NH2	D_GLU.1105	OE1	3.448
5W9L	A_ARG.1113	NH2	D_GLU.1105	OE2	2.879
5W9L	D_LYS.779	NZ	D_ASP.771	OD2	2.899
5W9L	D_LYS.801	NZ	D_ASP.843	OD1	2.808
5W9L	D_LYS.801	NZ	D_ASP.843	OD2	3.150
5W9L	D_LYS.807	NZ	D_GLU.818	OE1	3.544
5W9L	D_LYS.807	NZ	D_GLU.818	OE2	2.846
5W9L	D_ARG.841	NH1	D_GLU.1090	OE1	2.693
5W9L	D_ARG.841	NH1	D_GLU.1090	OE2	3.687
5W9L	D_ARG.841	NH2	D_GLU.1090	OE1	3.508
5W9L	D_ARG.841	NH2	D_GLU.1090	OE2	3.018
5W9L	D_ARG.847	NH1	D_ASP.844	OD1	3.540
5W9L	D_ARG.847	NH2	D_ASP.844	OD1	2.650
5W9L	D_ARG.887	NH2	D_ASP.892	OD1	2.968
5W9L	D_HIS.1020	NE2	D_ASP.1024	OD1	3.581
5W9L	D_HIS.1020	NE2	D_ASP.1024	OD2	2.693
5W9L	D_LYS.1102	NZ	D_GLU.793	OE1	2.889
5W9L	D_LYS.1102	NZ	D_GLU.793	OE2	3.224
5W9L	D_LYS.1174	NZ	D_GLU.1183	OE1	2.743
5W9L	E_LYS.62	NZ	E_GLU.46	OE2	2.839
5W9L	E_ARG.66	NH1	E_ASP.86	OD1	2.896
5W9L	E_ARG.66	NH1	E_ASP.86	OD2	3.239
5W9L	E_ARG.66	NH2	E_ASP.86	OD1	3.963
5W9L	E_ARG.94	NH1	E_ASP.101	OD2	2.725
5W9L	E_LYS.95	NZ	E_ASP.100C	OD1	3.912
5W9L	F_ARG.61	NH1	F_ASP.82	OD1	3.203
5W9L	F_ARG.61	NH1	F_ASP.82	OD2	3.638
5W9L	F_ARG.61	NH2	F_GLU.79	OE2	3.934
5W9L	F_ARG.61	NH2	F_ASP.82	OD1	3.694
5W9L	F_ARG.61	NH2	F_ASP.82	OD2	2.714
5W9L	F_LYS.92	NZ	F_GLU.93	OE1	2.893
5W9L	F_ARG.96	NH1	E_ASP.100C	OD2	3.246
5W9L	F_ARG.96	NH2	D_GLU.1183	OE2	2.643
5W9L	F_ARG.96	NH2	E_ASP.100C	OD2	3.370
5W9L	G_ARG.758	NH1	J_ASP.740	OD1	2.859
5W9L	G_ARG.758	NH2	J_ASP.740	OD1	3.792
5W9L	G_LYS.801	NZ	G_ASP.843	OD1	2.779
5W9L	G_LYS.801	NZ	G_ASP.843	OD2	2.846
5W9L	G_LYS.807	NZ	G_GLU.818	OE1	2.853
5W9L	G_LYS.807	NZ	G_GLU.818	OE2	3.467

5W9L	G_ARG.841	NH1	G_GLU.1090	OE1	3.667
5W9L	G_ARG.841	NH1	G_GLU.1090	OE2	2.809
5W9L	G_ARG.841	NH2	G_GLU.1090	OE1	2.982
5W9L	G_ARG.841	NH2	G_GLU.1090	OE2	3.598
5W9L	G_ARG.847	NH1	G_ASP.844	OD1	3.281
5W9L	G_ARG.847	NH2	G_ASP.844	OD1	2.692
5W9L	G_ARG.887	NH2	G_ASP.892	OD1	2.920
5W9L	G_HIS.1020	NE2	G_ASP.1024	OD1	3.996
5W9L	G_HIS.1020	NE2	G_ASP.1024	OD2	2.966
5W9L	G_LYS.1021	NZ	G_GLU.793	OE1	3.707
5W9L	G_LYS.1021	NZ	G_GLU.793	OE2	2.887
5W9L	G_LYS.1035	NZ	G_GLU.1039	OE2	2.763
5W9L	G_LYS.1174	NZ	G_GLU.1183	OE2	2.797
5W9L	G_ARG.1179	NH2	H_ASP.31	OD1	2.753
5W9L	H_LYS.19	NZ	H_GLU.81	OE1	3.889
5W9L	H_LYS.38	NZ	H_GLU.46	OE1	2.832
5W9L	H_LYS.62	NZ	H_GLU.46	OE2	3.395
5W9L	H_ARG.66	NH1	H_ASP.86	OD1	3.754
5W9L	H_ARG.66	NH1	H_ASP.86	OD2	3.742
5W9L	H_ARG.66	NH2	H_ASP.86	OD1	3.914
5W9L	H_ARG.66	NH2	H_ASP.86	OD2	2.831
5W9L	H_ARG.94	NH2	H_ASP.101	OD2	2.725
5W9L	H_LYS.95	NZ	H_ASP.100C	OD1	3.863
5W9L	I_ARG.24	NH1	I_ASP.70	OD1	2.847
5W9L	I_ARG.24	NH1	I_ASP.70	OD2	3.591
5W9L	I_ARG.61	NH1	I_GLU.79	OE2	2.866
5W9L	I_ARG.61	NH1	I_ASP.82	OD1	3.906
5W9L	I_ARG.61	NH1	I_ASP.82	OD2	2.956
5W9L	I_ARG.61	NH2	I_GLU.79	OE2	2.901
5W9L	I_LYS.92	NZ	I_GLU.93	OE1	2.785
5W9L	I_ARG.96	NH1	H_ASP.100C	OD2	2.945
5W9L	I_ARG.96	NH2	H_ASP.100C	OD2	2.982
5W9L	B_LYS.27	NZ	B_GLU.230	OE2	3.782
5W9L	B_LYS.99	NZ	B_GLU.32	OE1	2.878
5W9L	B_LYS.110	NZ	B_ASP.83	OD2	2.826
5W9L	B_ARG.119	NH2	B_ASP.54	OD2	3.988
5W9L	B_LYS.142	NZ	B_GLU.252	OE1	2.955
5W9L	B_HIS.194	NE2	B_GLU.32	OE1	3.596
5W9L	B_ARG.235	NH1	B_ASP.24	OD1	3.631
5W9L	B_ARG.235	NH1	B_ASP.24	OD2	2.911
5W9L	B_ARG.235	NH2	B_ASP.24	OD2	3.191
5W9L	B_ARG.235	NH2	B_GLU.188	OE1	3.770
5W9L	B_ARG.235	NH2	B_GLU.188	OE2	2.915
5W9L	B_ARG.335	NH2	B_ASP.326	OD2	2.950
5W9L	B_ARG.401	NH2	B_ASP.444	OD1	3.583
5W9L	B_ARG.401	NH2	B_ASP.444	OD2	2.888
5W9L	B_LYS.496	NZ	B_GLU.536	OE1	3.232
5W9L	B_LYS.496	NZ	B_GLU.536	OE2	3.655
5W9L	B_LYS.502	NZ	B_GLU.513	OE2	2.865
5W9L	B_ARG.614	NH2	B_GLU.605	OE2	2.923
5W9L	B_ARG.629	NH1	B_GLU.376	OE1	3.464
5W9L	B_ARG.629	NH1	B_ASP.644	OD1	2.816
5W9L	B_ARG.629	NH2	B_ASP.644	OD1	2.786
5W9L	B_HIS.681	NE2	D_ASP.910	OD1	2.803
5W9L	B_HIS.681	NE2	D_ASP.910	OD2	3.795
5W9L	B_ARG.691	NH1	B_ASP.343	OD2	3.571
5W9L	B_ARG.700	NH1	A_GLU.756	OE2	2.893
5W9L	B_LYS.728	NZ	B_ASP.726	OD2	2.978

5W9L	C_HIS_81	ND1	C_ASP_80	OD1	3.849
5W9L	C_LYS_99	NZ	C_GLU_32	OE1	2.902
5W9L	C_LYS_99	NZ	C_GLU_32	OE2	3.891
5W9L	C_LYS_110	NZ	C_ASP_83	OD2	2.851
5W9L	C_LYS_142	NZ	C_GLU_252	OE1	2.960
5W9L	C_ARG_181	NH1	C_ASP_174	OD2	3.375
5W9L	C_HIS_208	ND1	C_ASP_213	OD2	3.867
5W9L	C_ARG_235	NH1	C_ASP_24	OD1	3.815
5W9L	C_ARG_235	NH1	C_ASP_24	OD2	3.367
5W9L	C_ARG_235	NH2	C_ASP_24	OD2	2.948
5W9L	C_ARG_235	NH2	C_GLU_188	OE1	3.081
5W9L	C_ARG_235	NH2	C_GLU_188	OE2	3.858
5W9L	C_ARG_269	NH1	C_GLU_252	OE2	3.121
5W9L	C_ARG_334	NH2	C_ASP_330	OD2	3.055
5W9L	C_ARG_335	NH2	C_ASP_326	OD2	2.939
5W9L	C_ARG_401	NH2	C_ASP_444	OD1	3.945
5W9L	C_ARG_401	NH2	C_ASP_444	OD2	3.806
5W9L	C_LYS_502	NZ	C_GLU_513	OE2	2.769
5W9L	C_LYS_543	NZ	C_GLU_549	OE1	3.142
5W9L	C_LYS_543	NZ	C_GLU_549	OE2	2.917
5W9L	C_LYS_587	NZ	C_GLU_382	OE2	2.765
5W9L	C_ARG_614	NH2	C_GLU_605	OE2	2.923
5W9L	C_ARG_691	NH2	C_ASP_343	OD1	3.440
5W9L	C_LYS_728	NZ	C_ASP_726	OD2	2.825
5W9L	J_LYS_99	NZ	J_GLU_32	OE1	2.885
5W9L	J_LYS_110	NZ	J_ASP_83	OD2	2.834
5W9L	J_LYS_110	NZ	J_ASP_108	OD2	3.969
5W9L	J_ARG_119	NH2	J_ASP_54	OD2	3.754
5W9L	J_LYS_142	NZ	J_GLU_252	OE1	3.881
5W9L	J_ARG_181	NH1	J_ASP_174	OD2	3.154
5W9L	J_ARG_190	NH1	J_ASP_24	OD1	3.142
5W9L	J_ARG_190	NH2	J_ASP_24	OD1	2.772
5W9L	J_HIS_194	NE2	J_GLU_32	OE1	3.916
5W9L	J_ARG_235	NH2	J_GLU_188	OE1	3.860
5W9L	J_ARG_235	NH2	J_GLU_188	OE2	2.919
5W9L	J_ARG_334	NH2	J_ASP_330	OD2	3.039
5W9L	J_ARG_335	NH2	J_ASP_326	OD2	2.959
5W9L	J_ARG_401	NH2	J_ASP_444	OD1	3.680
5W9L	J_ARG_401	NH2	J_ASP_444	OD2	3.147
5W9L	J_LYS_413	NZ	J_GLU_382	OE1	3.990
5W9L	J_LYS_413	NZ	J_GLU_382	OE2	2.824
5W9L	J_LYS_502	NZ	J_GLU_513	OE1	3.965
5W9L	J_LYS_502	NZ	J_GLU_513	OE2	2.807
5W9L	J_ARG_511	NH2	J_ASP_509	OD2	3.938
5W9L	J_ARG_614	NH2	J_GLU_605	OE1	2.958
5W9L	J_ARG_614	NH2	J_GLU_605	OE2	3.605
5W9L	J_ARG_629	NH1	J_GLU_376	OE1	3.967
5W9L	J_ARG_629	NH1	J_ASP_644	OD1	2.719
5W9L	J_ARG_629	NH2	J_ASP_644	OD1	2.638
5W9L	J_ARG_629	NH2	J_ASP_644	OD2	3.881
5W9L	J_LYS_665	NZ	J_GLU_666	OE2	2.675
5W9L	J_HIS_681	NE2	A_ASP_910	OD1	2.810
5W9L	J_HIS_681	NE2	A_ASP_910	OD2	3.815
5W9L	J_LYS_728	NZ	J_ASP_726	OD2	2.753

Table 746: 5W9L-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5W9M	A_ARG.758	NH1	E_ASP.740	OD1	2.862
5W9M	A_ARG.758	NH2	E_ASP.740	OD1	2.970
5W9M	A_LYS.801	NZ	A_ASP.843	OD1	2.883
5W9M	A_LYS.801	NZ	A_ASP.843	OD2	3.678
5W9M	A_ARG.841	NH1	A_GLU.1090	OE1	3.685
5W9M	A_ARG.841	NH1	A_GLU.1090	OE2	2.836
5W9M	A_ARG.841	NH2	A_GLU.1090	OE1	2.984
5W9M	A_ARG.841	NH2	A_GLU.1090	OE2	3.616
5W9M	A_ARG.847	NH1	J_ASP.726	OD2	3.850
5W9M	A_ARG.847	NH2	A_ASP.844	OD1	2.786
5W9M	A_ARG.887	NH2	A_ASP.892	OD1	2.933
5W9M	A_HIS.1020	NE2	A_ASP.1024	OD2	3.018
5W9M	A_LYS.1035	NZ	A_GLU.1039	OE2	2.904
5W9M	A_ARG.1057	NH2	A_ASP.1053	OD1	2.900
5W9M	A_ARG.1057	NH2	A_ASP.1053	OD2	3.314
5W9M	A_LYS.1102	NZ	A_GLU.793	OE1	2.817
5W9M	A_LYS.1102	NZ	A_GLU.793	OE2	3.330
5W9M	A_ARG.1113	NH1	A_GLU.1105	OE1	2.883
5W9M	A_ARG.1113	NH1	A_GLU.1105	OE2	3.760
5W9M	A_ARG.1113	NH2	A_GLU.1105	OE1	2.893
5W9M	A_HIS.1138	NE2	A_GLU.793	OE2	2.874
5W9M	A_LYS.1174	NZ	A_GLU.1183	OE1	2.780
5W9M	B_LYS.38	NZ	B_GLU.46	OE2	3.812
5W9M	B_LYS.62	NZ	B_GLU.46	OE1	2.808
5W9M	B_LYS.62	NZ	B_GLU.46	OE2	3.864
5W9M	B_ARG.66	NH2	B_ASP.86	OD1	2.831
5W9M	B_ARG.66	NH2	B_ASP.86	OD2	3.198
5W9M	C_ARG.61	NH1	C_GLU.79	OE1	2.869
5W9M	C_ARG.96	NH1	B_ASP.100C	OD2	2.894
5W9M	C_ARG.96	NH2	A_GLU.1183	OE2	2.938
5W9M	C_ARG.96	NH2	B_ASP.100C	OD2	2.940
5W9M	C_LYS.103	NZ	C_GLU.105	OE1	3.072
5W9M	D_LYS.779	NZ	D_GLU.1148	OE1	2.693
5W9M	D_LYS.801	NZ	D_ASP.843	OD1	2.885
5W9M	D_LYS.801	NZ	D_ASP.843	OD2	3.585
5W9M	D_LYS.816	NZ	D_ASP.1064	OD1	3.628
5W9M	D_LYS.816	NZ	D_ASP.1064	OD2	3.861
5W9M	D_ARG.841	NH2	D_GLU.1090	OE1	3.446
5W9M	D_ARG.841	NH2	D_GLU.1090	OE2	2.981
5W9M	D_ARG.847	NH1	A_GLU.1017	OE2	3.300
5W9M	D_ARG.847	NH2	A_GLU.1017	OE2	3.532
5W9M	D_ARG.847	NH2	D_ASP.844	OD1	2.832
5W9M	D_ARG.887	NH2	D_ASP.892	OD1	2.922
5W9M	D_LYS.995	NZ	D_ASP.868	OD1	3.932
5W9M	D_LYS.995	NZ	D_ASP.868	OD2	2.628
5W9M	D_HIS.1020	NE2	D_ASP.1024	OD1	3.644
5W9M	D_HIS.1020	NE2	D_ASP.1024	OD2	3.049
5W9M	D_LYS.1102	NZ	D_GLU.793	OE1	3.825
5W9M	D_ARG.1113	NH1	D_GLU.1105	OE1	2.819
5W9M	D_ARG.1113	NH1	D_GLU.1105	OE2	3.747
5W9M	D_ARG.1113	NH2	D_GLU.1105	OE1	3.533
5W9M	D_ARG.1113	NH2	D_GLU.1105	OE2	2.987
5W9M	D_HIS.1138	NE2	D_GLU.793	OE2	2.837
5W9M	D_LYS.1174	NZ	D_GLU.1183	OE2	2.795
5W9M	G_ARG.758	NH1	J_ASP.740	OD1	2.816
5W9M	G_ARG.758	NH2	J_ASP.740	OD1	3.407
5W9M	G_LYS.779	NZ	G_ASP.771	OD2	2.927

5W9M	G_LYS_779	NZ	G_GLU_1148	OE1	3.707
5W9M	G_LYS_801	NZ	G_ASP_843	OD1	2.888
5W9M	G_LYS_801	NZ	G_ASP_843	OD2	3.840
5W9M	G_LYS_807	NZ	G_GLU_818	OE2	3.982
5W9M	G_ARG_841	NH1	G_GLU_1090	OE1	3.659
5W9M	G_ARG_841	NH1	G_GLU_1090	OE2	2.832
5W9M	G_ARG_841	NH2	G_GLU_1090	OE1	2.944
5W9M	G_ARG_841	NH2	G_GLU_1090	OE2	3.615
5W9M	G_ARG_847	NH2	G_ASP_844	OD1	2.704
5W9M	G_ARG_887	NH2	G_ASP_892	OD1	2.967
5W9M	G_HIS_1020	NE2	G_ASP_1024	OD1	3.635
5W9M	G_HIS_1020	NE2	G_ASP_1024	OD2	3.025
5W9M	G_LYS_1100	NZ	G_ASP_1101	OD1	2.964
5W9M	G_LYS_1102	NZ	G_GLU_793	OE2	3.845
5W9M	G_ARG_1113	NH1	G_GLU_1105	OE1	2.863
5W9M	G_ARG_1113	NH1	G_GLU_1105	OE2	3.297
5W9M	G_ARG_1113	NH2	A_GLU_1105	OE1	3.823
5W9M	G_ARG_1113	NH2	A_GLU_1105	OE2	2.800
5W9M	G_HIS_1138	NE2	G_GLU_793	OE2	2.857
5W9M	G_LYS_1174	NZ	G_GLU_1183	OE1	2.907
5W9M	G_ARG_1179	NH1	H_ASP_31	OD1	3.713
5W9M	H_LYS_62	NZ	H_GLU_46	OE1	3.377
5W9M	H_LYS_62	NZ	H_GLU_46	OE2	2.872
5W9M	H_ARG_66	NH1	H_ASP_86	OD1	3.768
5W9M	H_ARG_66	NH1	H_ASP_86	OD2	3.866
5W9M	H_ARG_66	NH2	H_ASP_86	OD1	3.905
5W9M	H_ARG_66	NH2	H_ASP_86	OD2	2.981
5W9M	H_ARG_94	NH1	H_ASP_101	OD2	3.814
5W9M	H_ARG_94	NH2	H_ASP_101	OD2	2.908
5W9M	H_LYS_95	NZ	H_ASP_100C	OD1	3.555
5W9M	H_LYS_95	NZ	H_ASP_100C	OD2	2.929
5W9M	I_ARG_61	NH1	I_GLU_79	OE1	2.897
5W9M	I_ARG_61	NH1	I_ASP_82	OD1	3.868
5W9M	I_ARG_61	NH1	I_ASP_82	OD2	2.952
5W9M	I_ARG_61	NH2	I_GLU_79	OE1	2.900
5W9M	I_ARG_96	NH1	H_ASP_100C	OD2	2.840
5W9M	I_ARG_96	NH2	G_GLU_1183	OE2	2.957
5W9M	I_ARG_96	NH2	H_ASP_100C	OD2	3.363
5W9M	I_LYS_103	NZ	I_GLU_105	OE2	3.254
5W9M	E_LYS_27	NZ	E_GLU_230	OE2	3.877
5W9M	E_LYS_52	NZ	E_ASP_49	OD2	3.990
5W9M	E_HIS_81	ND1	E_ASP_80	OD1	3.823
5W9M	E_LYS_99	NZ	E_GLU_32	OE1	2.847
5W9M	E_LYS_110	NZ	E_ASP_83	OD2	2.742
5W9M	E_LYS_142	NZ	E_GLU_252	OE1	3.416
5W9M	E_LYS_142	NZ	E_GLU_252	OE2	3.425
5W9M	E_ARG_181	NH1	E_ASP_174	OD2	3.814
5W9M	E_HIS_194	NE2	E_GLU_32	OE1	3.141
5W9M	E_ARG_235	NH1	E_GLU_188	OE1	3.017
5W9M	E_ARG_335	NH2	E_ASP_326	OD2	2.919
5W9M	E_ARG_401	NH2	E_ASP_444	OD1	3.595
5W9M	E_ARG_401	NH2	E_ASP_444	OD2	2.975
5W9M	E_LYS_496	NZ	E_GLU_536	OE1	2.925
5W9M	E_LYS_496	NZ	E_GLU_536	OE2	3.563
5W9M	E_LYS_502	NZ	E_GLU_513	OE2	2.857
5W9M	E_ARG_505	NH1	E_GLU_549	OE1	2.887
5W9M	E_ARG_505	NH2	E_GLU_549	OE1	3.647
5W9M	E_ARG_629	NH1	E_GLU_376	OE2	3.561

5W9M	E_ARG.629	NH1	E_ASP.644	OD1	2.850
5W9M	E_ARG.629	NH2	E_ASP.644	OD1	2.751
5W9M	E_ARG.629	NH2	E_ASP.644	OD2	3.949
5W9M	E_LYS.665	NZ	E_GLU.666	OE2	2.766
5W9M	E_HIS.681	NE2	D_ASP.910	OD1	2.869
5W9M	E_HIS.681	NE2	D_ASP.910	OD2	3.974
5W9M	E_ARG.691	NH2	E_ASP.343	OD1	3.021
5W9M	E_ARG.700	NH2	A_GLU.756	OE1	3.024
5W9M	E_ARG.700	NH2	A_GLU.756	OE2	3.469
5W9M	E_LYS.728	NZ	E_ASP.726	OD2	2.871
5W9M	F_HIS.81	ND1	F_ASP.80	OD1	3.780
5W9M	F_LYS.99	NZ	F_GLU.32	OE1	3.190
5W9M	F_LYS.99	NZ	F_GLU.32	OE2	3.555
5W9M	F_LYS.110	NZ	F_ASP.83	OD2	3.405
5W9M	F_LYS.110	NZ	F_ASP.108	OD1	3.183
5W9M	F_LYS.110	NZ	F_ASP.108	OD2	3.399
5W9M	F_ARG.119	NH1	F_ASP.54	OD2	3.785
5W9M	F_ARG.119	NH2	F_ASP.54	OD2	3.047
5W9M	F_LYS.142	NZ	F_GLU.252	OE1	2.921
5W9M	F_HIS.194	NE2	F_GLU.32	OE1	3.759
5W9M	F_ARG.235	NH1	F_GLU.188	OE2	3.596
5W9M	F_ARG.334	NH2	F_ASP.330	OD1	3.977
5W9M	F_ARG.334	NH2	F_ASP.330	OD2	3.003
5W9M	F_ARG.335	NH2	F_ASP.326	OD2	2.919
5W9M	F_ARG.401	NH2	F_ASP.444	OD1	3.837
5W9M	F_ARG.401	NH2	F_ASP.444	OD2	3.316
5W9M	F_LYS.502	NZ	F_GLU.513	OE1	2.889
5W9M	F_LYS.543	NZ	F_GLU.549	OE2	3.751
5W9M	F_LYS.587	NZ	F_GLU.382	OE2	2.825
5W9M	F_ARG.614	NH2	F_GLU.605	OE1	2.961
5W9M	F_HIS.681	NE2	G_ASP.910	OD1	2.934
5W9M	F_HIS.681	NE2	G_ASP.910	OD2	3.892
5W9M	F_ARG.691	NH2	F_ASP.343	OD1	2.990
5W9M	F_LYS.728	NZ	F_ASP.726	OD1	3.991
5W9M	F_LYS.728	NZ	F_ASP.726	OD2	2.816
5W9M	J_HIS.81	ND1	J_ASP.80	OD1	3.900
5W9M	J_LYS.99	NZ	J_ASP.34	OD2	2.828
5W9M	J_ARG.119	NH2	J_ASP.54	OD2	3.814
5W9M	J_LYS.142	NZ	J_GLU.252	OE1	3.757
5W9M	J_LYS.142	NZ	J_GLU.252	OE2	3.691
5W9M	J_HIS.194	NE2	J_GLU.32	OE1	3.474
5W9M	J_ARG.235	NH2	J_GLU.188	OE1	3.932
5W9M	J_ARG.235	NH2	J_GLU.188	OE2	2.863
5W9M	J_ARG.334	NH2	J_ASP.330	OD1	3.986
5W9M	J_ARG.334	NH2	J_ASP.330	OD2	2.914
5W9M	J_ARG.335	NH2	J_ASP.326	OD2	2.924
5W9M	J_ARG.401	NH2	J_ASP.444	OD1	3.669
5W9M	J_ARG.401	NH2	J_ASP.444	OD2	3.110
5W9M	J_LYS.413	NZ	J_GLU.382	OE1	3.999
5W9M	J_LYS.413	NZ	J_GLU.382	OE2	2.963
5W9M	J_HIS.486	NE2	J_GLU.565	OE2	3.789
5W9M	J_LYS.496	NZ	J_GLU.536	OE2	3.687
5W9M	J_LYS.502	NZ	J_GLU.513	OE1	2.953
5W9M	J_LYS.502	NZ	J_GLU.513	OE2	3.624
5W9M	J_ARG.511	NH2	J_ASP.509	OD2	3.887
5W9M	J_ARG.629	NH1	J_ASP.644	OD1	2.859
5W9M	J_ARG.629	NH2	J_ASP.644	OD1	2.744
5W9M	J_ARG.629	NH2	J_ASP.644	OD2	3.852

5W9M	J_HIS_681	NE2	A_ASP_910	OD1	3.021
5W9M	J_LYS_728	NZ	J_ASP_726	OD2	2.879

Table 747: 5W9M-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5W9N	A_ARG.758	NH1	H_ASP.740	OD1	3.061
5W9N	A_ARG.758	NH2	H_ASP.740	OD1	3.534
5W9N	A_LYS.801	NZ	A_ASP.843	OD1	2.885
5W9N	A_LYS.801	NZ	A_ASP.843	OD2	3.553
5W9N	A_LYS.816	NZ	A_ASP.1064	OD2	3.955
5W9N	A_ARG.841	NH2	A_ASP.844	OD2	2.840
5W9N	A_ARG.847	NH2	A_ASP.844	OD1	2.793
5W9N	A_ARG.887	NH2	A_ASP.892	OD1	2.922
5W9N	A_ARG.887	NH2	A_ASP.892	OD2	3.858
5W9N	A_HIS.1020	NE2	A_ASP.1024	OD2	2.929
5W9N	A_ARG.1057	NH1	A_ASP.1053	OD1	3.524
5W9N	A_LYS.1102	NZ	A_GLU.793	OE1	2.942
5W9N	A_LYS.1102	NZ	A_GLU.793	OE2	3.253
5W9N	A_HIS.1138	NE2	A_GLU.793	OE1	2.975
5W9N	B_LYS.62	NZ	B_GLU.46	OE1	3.336
5W9N	B_LYS.62	NZ	B_GLU.46	OE2	2.950
5W9N	B_ARG.66	NH2	B_ASP.86	OD1	2.875
5W9N	B_ARG.66	NH2	B_ASP.86	OD2	3.096
5W9N	B_ARG.94	NH2	B_ASP.101	OD2	2.805
5W9N	B_LYS.95	NZ	B_ASP.100C	OD2	3.671
5W9N	C_ARG.24	NH1	C_ASP.70	OD1	2.929
5W9N	C_ARG.24	NH1	C_ASP.70	OD2	3.584
5W9N	C_ARG.24	NH2	C_ASP.70	OD1	3.992
5W9N	C_LYS.92	NZ	C_GLU.93	OE1	2.776
5W9N	C_ARG.96	NH1	B_ASP.100C	OD2	2.860
5W9N	C_ARG.96	NH2	A_GLU.1183	OE2	2.942
5W9N	C_ARG.96	NH2	B_ASP.100C	OD2	3.629
5W9N	C_LYS.103	NZ	C_GLU.105	OE1	3.535
5W9N	D_LYS.779	NZ	D_ASP.771	OD2	2.906
5W9N	D_LYS.779	NZ	D_GLU.1148	OE1	3.841
5W9N	D_LYS.801	NZ	D_ASP.843	OD1	2.866
5W9N	D_LYS.801	NZ	D_ASP.843	OD2	3.784
5W9N	D_LYS.807	NZ	D_GLU.818	OE1	2.846
5W9N	D_LYS.807	NZ	D_GLU.818	OE2	3.746
5W9N	D_LYS.816	NZ	D_ASP.1064	OD1	3.551
5W9N	D_LYS.816	NZ	D_ASP.1064	OD2	2.989
5W9N	D_ARG.841	NH2	D_ASP.844	OD2	2.860
5W9N	D_ARG.847	NH2	D_ASP.844	OD1	2.752
5W9N	D_ARG.887	NH2	D_ASP.892	OD1	2.921
5W9N	D_HIS.1020	NE2	D_ASP.1024	OD1	3.511
5W9N	D_HIS.1020	NE2	D_ASP.1024	OD2	3.177
5W9N	D_LYS.1102	NZ	D_GLU.793	OE1	2.862
5W9N	D_LYS.1102	NZ	D_GLU.793	OE2	3.547
5W9N	D_ARG.1113	NH1	D_GLU.1105	OE1	2.833
5W9N	D_ARG.1113	NH1	D_GLU.1105	OE2	3.606
5W9N	D_ARG.1113	NH2	D_GLU.1105	OE1	3.657
5W9N	D_ARG.1113	NH2	D_GLU.1105	OE2	2.979
5W9N	D_HIS.1138	NE2	D_GLU.793	OE1	3.682
5W9N	E_LYS.62	NZ	E_GLU.46	OE1	2.853
5W9N	E_LYS.62	NZ	E_GLU.46	OE2	3.766
5W9N	E_ARG.94	NH1	E_ASP.101	OD2	3.322
5W9N	E_ARG.94	NH2	E_ASP.101	OD2	2.876
5W9N	F_ARG.61	NH1	F_GLU.79	OE1	3.387
5W9N	F_ARG.61	NH1	F_GLU.79	OE2	3.250
5W9N	F_ARG.61	NH2	F_GLU.79	OE2	3.109
5W9N	F_ARG.96	NH1	E_ASP.100C	OD2	2.898
5W9N	F_ARG.96	NH2	D_GLU.1183	OE2	3.465

5W9N	F_ARG_96	NH2	E_ASP_100C	OD2	3.359
5W9N	F_LYS_103	NZ	F_GLU_105	OE2	3.523
5W9N	G_ARG_758	NH1	J_ASP_740	OD1	2.883
5W9N	G_ARG_758	NH2	J_ASP_740	OD1	3.992
5W9N	G_LYS_779	NZ	G_GLU_1148	OE1	3.821
5W9N	G_LYS_801	NZ	G_ASP_843	OD1	3.095
5W9N	G_LYS_807	NZ	G_GLU_818	OE1	2.848
5W9N	G_LYS_807	NZ	G_GLU_818	OE2	3.640
5W9N	G_ARG_841	NH2	G_ASP_844	OD2	2.821
5W9N	G_ARG_847	NH2	G_ASP_844	OD1	2.784
5W9N	G_ARG_887	NH2	G_ASP_892	OD1	2.977
5W9N	G_ARG_887	NH2	G_ASP_892	OD2	3.996
5W9N	G_HIS_1020	NE2	G_ASP_1024	OD1	3.933
5W9N	G_HIS_1020	NE2	G_ASP_1024	OD2	2.877
5W9N	G_ARG_1057	NH2	G_ASP_1053	OD1	2.973
5W9N	G_ARG_1057	NH2	G_ASP_1053	OD2	3.603
5W9N	G_LYS_1102	NZ	G_GLU_793	OE1	3.542
5W9N	G_LYS_1102	NZ	G_GLU_793	OE2	3.374
5W9N	G_ARG_1113	NH1	G_GLU_1105	OE1	3.319
5W9N	G_ARG_1113	NH2	A_GLU_1105	OE1	3.089
5W9N	G_HIS_1138	NE2	G_GLU_793	OE2	2.888
5W9N	H_LYS_99	NZ	H_GLU_32	OE1	2.795
5W9N	H_LYS_110	NZ	H_ASP_83	OD2	2.820
5W9N	H_ARG_119	NH2	H_ASP_54	OD2	3.318
5W9N	H_LYS_142	NZ	H_GLU_252	OE1	3.837
5W9N	H_LYS_142	NZ	H_GLU_252	OE2	3.110
5W9N	H_ARG_181	NH1	H_ASP_174	OD2	2.922
5W9N	H_HIS_194	NE2	H_GLU_32	OE1	3.891
5W9N	H_ARG_334	NH2	H_ASP_330	OD1	3.972
5W9N	H_ARG_334	NH2	H_ASP_330	OD2	3.030
5W9N	H_ARG_335	NH2	H_ASP_326	OD2	2.979
5W9N	H_ARG_401	NH2	H_ASP_444	OD1	3.754
5W9N	H_ARG_401	NH2	H_ASP_444	OD2	3.247
5W9N	H_LYS_496	NZ	H_GLU_536	OE1	3.049
5W9N	H_LYS_496	NZ	H_GLU_536	OE2	3.699
5W9N	H_LYS_502	NZ	H_GLU_513	OE2	3.408
5W9N	H_ARG_505	NH1	H_GLU_549	OE1	2.896
5W9N	H_ARG_505	NH2	H_GLU_549	OE1	3.946
5W9N	H_ARG_629	NH1	H_GLU_376	OE2	3.417
5W9N	H_ARG_629	NH1	H_ASP_644	OD1	2.873
5W9N	H_ARG_629	NH1	H_ASP_644	OD2	3.992
5W9N	H_ARG_629	NH2	H_ASP_644	OD1	2.928
5W9N	H_ARG_629	NH2	H_ASP_644	OD2	3.862
5W9N	H_HIS_681	NE2	D_ASP_910	OD1	2.909
5W9N	H_HIS_681	NE2	D_ASP_910	OD2	3.885
5W9N	H_ARG_691	NH2	H_ASP_343	OD1	3.539
5W9N	H_ARG_694	NH1	H_ASP_343	OD2	3.042
5W9N	H_ARG_694	NH2	H_ASP_343	OD2	2.913
5W9N	H_LYS_728	NZ	H_ASP_726	OD2	2.885
5W9N	I_LYS_99	NZ	I_GLU_32	OE1	2.834
5W9N	I_LYS_110	NZ	I_ASP_108	OD1	3.843
5W9N	I_LYS_110	NZ	I_ASP_108	OD2	3.078
5W9N	I_ARG_119	NH1	I_ASP_54	OD2	3.752
5W9N	I_ARG_119	NH2	I_ASP_54	OD2	3.062
5W9N	I_LYS_142	NZ	I_GLU_247	OE1	2.823
5W9N	I_LYS_142	NZ	I_GLU_249	OE2	2.931
5W9N	I_ARG_181	NH1	I_ASP_174	OD2	3.305
5W9N	I_ARG_190	NH1	I_GLU_188	OE2	2.866

5W9N	I_ARG_334	NH2	I_ASP_330	OD1	3.946
5W9N	I_ARG_334	NH2	I_ASP_330	OD2	3.014
5W9N	I_ARG_335	NH2	I_ASP_326	OD2	2.875
5W9N	I_ARG_401	NH2	I_ASP_444	OD1	3.778
5W9N	I_ARG_401	NH2	I_ASP_444	OD2	3.214
5W9N	I_LYS_502	NZ	I_GLU_513	OE2	2.781
5W9N	I_LYS_587	NZ	I_GLU_382	OE2	2.936
5W9N	I_ARG_614	NH1	I_GLU_605	OE2	3.987
5W9N	I_LYS_668	NZ	I_ASP_355	OD1	3.243
5W9N	I_LYS_668	NZ	I_ASP_355	OD2	3.427
5W9N	I_HIS_681	ND1	I_GLU_680	OE2	3.948
5W9N	I_LYS_728	NZ	I_ASP_726	OD2	2.845
5W9N	J_LYS_52	NZ	J_ASP_49	OD2	3.577
5W9N	J_HIS_81	ND1	J_ASP_80	OD1	3.829
5W9N	J_LYS_99	NZ	J_GLU_32	OE1	2.844
5W9N	J_ARG_119	NH1	J_ASP_54	OD2	3.500
5W9N	J_LYS_142	NZ	J_GLU_252	OE1	3.608
5W9N	J_LYS_142	NZ	J_GLU_252	OE2	3.253
5W9N	J_ARG_190	NH1	J_ASP_24	OD1	3.620
5W9N	J_ARG_190	NH1	J_ASP_24	OD2	3.407
5W9N	J_ARG_190	NH2	J_ASP_24	OD1	2.694
5W9N	J_ARG_190	NH2	J_ASP_24	OD2	3.854
5W9N	J_ARG_235	NH2	J_GLU_188	OE1	2.960
5W9N	J_ARG_235	NH2	J_GLU_188	OE2	3.595
5W9N	J_ARG_334	NH2	J_ASP_330	OD1	3.929
5W9N	J_ARG_334	NH2	J_ASP_330	OD2	2.885
5W9N	J_ARG_335	NH2	J_ASP_326	OD2	2.940
5W9N	J_ARG_401	NH2	J_ASP_444	OD1	3.745
5W9N	J_ARG_401	NH2	J_ASP_444	OD2	3.113
5W9N	J_LYS_413	NZ	J_GLU_382	OE1	3.770
5W9N	J_LYS_413	NZ	J_GLU_382	OE2	2.885
5W9N	J_LYS_502	NZ	J_GLU_513	OE1	3.403
5W9N	J_LYS_502	NZ	J_GLU_513	OE2	3.488
5W9N	J_ARG_511	NH2	J_ASP_509	OD2	3.316
5W9N	J_ARG_614	NH1	J_GLU_605	OE2	3.946
5W9N	J_ARG_629	NH1	J_ASP_644	OD1	2.925
5W9N	J_ARG_629	NH2	J_ASP_644	OD1	2.748
5W9N	J_ARG_629	NH2	J_ASP_644	OD2	3.827
5W9N	J_LYS_665	NZ	J_GLU_666	OE2	2.737
5W9N	J_HIS_681	NE2	A_ASP_910	OD1	2.923
5W9N	J_HIS_681	NE2	A_ASP_910	OD2	3.770
5W9N	J_LYS_728	NZ	J_ASP_726	OD1	3.992
5W9N	J_LYS_728	NZ	J_ASP_726	OD2	2.808

Table 748: 5W9N-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5W9O	A_ARG.758	NH1	J_ASP.740	OD1	2.989
5W9O	A_LYS.779	NZ	A_ASP.771	OD2	3.308
5W9O	A_LYS.779	NZ	A_GLU.1148	OE1	3.756
5W9O	A_LYS.801	NZ	A_ASP.843	OD1	2.906
5W9O	A_LYS.801	NZ	A_ASP.843	OD2	3.361
5W9O	A_LYS.807	NZ	A_GLU.818	OE1	3.592
5W9O	A_LYS.807	NZ	A_GLU.818	OE2	2.924
5W9O	A_ARG.841	NH2	A_ASP.844	OD2	2.838
5W9O	A_ARG.847	NH1	A_ASP.844	OD1	3.667
5W9O	A_ARG.847	NH2	A_ASP.844	OD1	2.759
5W9O	A_ARG.887	NH2	A_ASP.892	OD1	3.046
5W9O	A_ARG.887	NH2	A_ASP.892	OD2	3.709
5W9O	A_HIS.1020	NE2	A_ASP.1024	OD2	2.966
5W9O	A_LYS.1021	NZ	A_GLU.793	OE1	3.937
5W9O	A_LYS.1021	NZ	A_GLU.793	OE2	2.905
5W9O	A_ARG.1057	NH1	A_ASP.1053	OD1	2.779
5W9O	A_ARG.1113	NH1	A_GLU.1105	OE1	3.499
5W9O	A_ARG.1113	NH1	A_GLU.1105	OE2	2.983
5W9O	A_ARG.1113	NH2	D_GLU.1105	OE1	3.178
5W9O	A_ARG.1179	NH2	B_ASP.31	OD1	2.796
5W9O	B_LYS.38	NZ	B_GLU.46	OE1	2.988
5W9O	B_LYS.62	NZ	B_GLU.46	OE1	3.057
5W9O	B_LYS.62	NZ	B_GLU.46	OE2	3.242
5W9O	B_ARG.94	NH2	B_ASP.101	OD2	2.810
5W9O	B_LYS.95	NZ	B_ASP.100C	OD1	3.658
5W9O	C_ARG.24	NH2	C_ASP.70	OD1	3.533
5W9O	C_ARG.24	NH2	C_ASP.70	OD2	2.999
5W9O	C_ARG.61	NH1	C_GLU.79	OE2	2.984
5W9O	C_ARG.61	NH2	C_GLU.79	OE2	3.885
5W9O	C_LYS.92	NZ	C_GLU.93	OE1	2.863
5W9O	C_ARG.96	NH1	B_ASP.100C	OD2	3.180
5W9O	C_ARG.96	NH2	B_ASP.100C	OD2	2.879
5W9O	C_LYS.103	NZ	C_GLU.105	OE1	3.349
5W9O	D_LYS.779	NZ	D_ASP.771	OD2	2.942
5W9O	D_LYS.779	NZ	D_GLU.1148	OE1	3.819
5W9O	D_LYS.801	NZ	D_ASP.843	OD1	2.899
5W9O	D_LYS.801	NZ	D_ASP.843	OD2	3.628
5W9O	D_LYS.807	NZ	D_GLU.818	OE1	2.864
5W9O	D_LYS.807	NZ	D_GLU.818	OE2	3.460
5W9O	D_LYS.816	NZ	D_ASP.1064	OD1	3.778
5W9O	D_LYS.816	NZ	D_ASP.1064	OD2	2.905
5W9O	D_ARG.841	NH2	D_ASP.844	OD2	2.807
5W9O	D_ARG.847	NH1	J_ASP.726	OD2	2.979
5W9O	D_ARG.847	NH2	D_ASP.844	OD1	2.817
5W9O	D_ARG.887	NH2	D_ASP.892	OD1	3.050
5W9O	D_ARG.887	NH2	D_ASP.892	OD2	3.816
5W9O	D_HIS.1020	NE2	D_ASP.1024	OD1	3.793
5W9O	D_HIS.1020	NE2	D_ASP.1024	OD2	3.047
5W9O	D_ARG.1057	NH1	D_ASP.1053	OD1	3.689
5W9O	D_LYS.1102	NZ	D_GLU.793	OE1	2.930
5W9O	D_LYS.1102	NZ	D_GLU.793	OE2	3.237
5W9O	D_ARG.1113	NH1	G_GLU.1105	OE1	3.664
5W9O	D_ARG.1113	NH2	D_GLU.1105	OE1	3.068
5W9O	D_ARG.1113	NH2	D_GLU.1105	OE2	3.628
5W9O	D_HIS.1138	NE2	D_GLU.793	OE1	2.926
5W9O	E_LYS.38	NZ	E_ASP.86	OD1	3.864
5W9O	E_LYS.62	NZ	E_GLU.46	OE1	2.853

5W9O	E_LYS_62	NZ	E_GLU_46	OE2	3.614
5W9O	E_LYS_95	NZ	E_ASP_100C	OD1	3.641
5W9O	E_LYS_95	NZ	E_ASP_100C	OD2	3.940
5W9O	F_ARG_61	NH1	F_GLU_79	OE1	3.425
5W9O	F_ARG_61	NH1	F_GLU_79	OE2	3.162
5W9O	F_ARG_61	NH2	F_GLU_79	OE2	3.303
5W9O	F_ARG_96	NH1	E_ASP_100C	OD2	2.799
5W9O	F_ARG_96	NH2	D_GLU_1183	OE2	3.799
5W9O	F_ARG_96	NH2	E_ASP_100C	OD2	3.255
5W9O	G_ARG_758	NH1	L_ASP_740	OD1	2.934
5W9O	G_LYS_779	NZ	G_ASP_771	OD2	2.924
5W9O	G_LYS_779	NZ	G_GLU_1148	OE1	3.649
5W9O	G_LYS_801	NZ	G_ASP_843	OD1	2.865
5W9O	G_LYS_801	NZ	G_ASP_843	OD2	3.439
5W9O	G_LYS_807	NZ	G_GLU_818	OE1	2.891
5W9O	G_LYS_807	NZ	G_GLU_818	OE2	3.530
5W9O	G_LYS_816	NZ	G_ASP_1064	OD1	3.715
5W9O	G_LYS_816	NZ	G_ASP_1064	OD2	3.538
5W9O	G_ARG_841	NH1	G_GLU_1090	OE2	3.058
5W9O	G_ARG_847	NH1	K_ASP_726	OD2	3.097
5W9O	G_ARG_847	NH2	G_ASP_844	OD1	2.809
5W9O	G_ARG_887	NH2	G_ASP_892	OD1	2.982
5W9O	G_HIS_1020	NE2	G_ASP_1024	OD2	3.021
5W9O	G_LYS_1102	NZ	G_GLU_793	OE1	3.370
5W9O	G_LYS_1102	NZ	G_GLU_793	OE2	2.830
5W9O	G_ARG_1113	NH1	G_GLU_1105	OE1	3.501
5W9O	G_ARG_1113	NH1	G_GLU_1105	OE2	2.926
5W9O	G_HIS_1138	NE2	G_GLU_793	OE1	3.125
5W9O	G_LYS_1174	NZ	G_GLU_1183	OE1	2.745
5W9O	G_ARG_1179	NH2	H_ASP_31	OD1	2.843
5W9O	H_HIS_35	NE2	H_ASP_100C	OD1	3.649
5W9O	H_HIS_35	NE2	H_ASP_100C	OD2	3.605
5W9O	H_LYS_38	NZ	H_ASP_86	OD1	3.619
5W9O	H_LYS_62	NZ	H_GLU_46	OE1	2.840
5W9O	H_LYS_62	NZ	H_GLU_46	OE2	3.755
5W9O	H_ARG_66	NH2	H_ASP_86	OD2	3.025
5W9O	H_ARG_94	NH2	H_ASP_101	OD1	3.987
5W9O	H_ARG_94	NH2	H_ASP_101	OD2	2.829
5W9O	I_ARG_61	NH1	I_GLU_79	OE2	2.913
5W9O	I_ARG_61	NH1	I_ASP_82	OD1	3.774
5W9O	I_ARG_61	NH1	I_ASP_82	OD2	2.961
5W9O	I_ARG_61	NH2	I_GLU_79	OE2	3.003
5W9O	I_LYS_92	NZ	I_GLU_93	OE1	3.065
5W9O	I_ARG_96	NH1	H_ASP_100C	OD2	3.979
5W9O	I_ARG_96	NH2	G_GLU_1183	OE2	2.715
5W9O	I_ARG_96	NH2	H_ASP_100C	OD2	3.993
5W9O	J_LYS_27	NZ	J_GLU_230	OE2	3.475
5W9O	J_LYS_52	NZ	J_ASP_49	OD2	3.987
5W9O	J_LYS_99	NZ	J_GLU_32	OE1	3.930
5W9O	J_LYS_99	NZ	J_GLU_32	OE2	3.469
5W9O	J_LYS_99	NZ	J_ASP_34	OD2	3.652
5W9O	J_LYS_110	NZ	J_ASP_83	OD2	3.502
5W9O	J_LYS_110	NZ	J_ASP_108	OD1	3.336
5W9O	J_LYS_110	NZ	J_ASP_108	OD2	3.601
5W9O	J_ARG_119	NH2	J_ASP_54	OD2	3.505
5W9O	J_LYS_142	NZ	J_GLU_252	OE2	3.340
5W9O	J_HIS_194	NE2	J_GLU_32	OE1	2.883
5W9O	J_HIS_208	ND1	J_ASP_213	OD2	3.923

5W9O	J_HIS_208	NE2	J_ASP_213	OD2	3.787
5W9O	J_ARG_335	NH2	J_ASP_326	OD2	2.668
5W9O	J_ARG_401	NH2	J_ASP_444	OD2	3.561
5W9O	J_LYS_496	NZ	J_GLU_536	OE1	3.601
5W9O	J_LYS_502	NZ	J_GLU_513	OE2	2.998
5W9O	J_ARG_505	NH1	J_GLU_549	OE1	3.551
5W9O	J_ARG_614	NH2	J_GLU_605	OE2	3.078
5W9O	J_LYS_665	NZ	J_GLU_357	OE1	3.881
5W9O	J_LYS_665	NZ	J_GLU_357	OE2	2.936
5W9O	J_LYS_665	NZ	J_GLU_666	OE2	3.739
5W9O	J_HIS_681	NE2	D_ASP_910	OD1	2.932
5W9O	J_ARG_694	NH1	J_ASP_343	OD2	3.143
5W9O	J_ARG_694	NH2	J_ASP_343	OD2	2.962
5W9O	J_ARG_700	NH2	A_GLU_756	OE1	3.931
5W9O	J_ARG_700	NH2	A_GLU_756	OE2	2.914
5W9O	K_LYS_52	NZ	K_ASP_49	OD2	2.630
5W9O	K_LYS_99	NZ	K_GLU_32	OE1	2.833
5W9O	K_LYS_99	NZ	K_GLU_32	OE2	3.941
5W9O	K_LYS_110	NZ	K_ASP_83	OD2	3.249
5W9O	K_LYS_110	NZ	K_ASP_108	OD1	3.411
5W9O	K_LYS_110	NZ	K_ASP_108	OD2	3.722
5W9O	K_ARG_119	NH1	K_ASP_54	OD1	3.012
5W9O	K_ARG_119	NH1	K_ASP_54	OD2	3.524
5W9O	K_LYS_142	NZ	K_GLU_247	OE1	3.485
5W9O	K_LYS_142	NZ	K_GLU_249	OE2	2.994
5W9O	K_ARG_190	NH1	K_GLU_188	OE1	3.568
5W9O	K_HIS_194	NE2	K_GLU_32	OE1	3.387
5W9O	K_HIS_194	NE2	K_GLU_32	OE2	3.889
5W9O	K_HIS_208	NE2	K_ASP_213	OD2	3.790
5W9O	K_ARG_335	NH2	K_ASP_326	OD2	2.949
5W9O	K_ARG_401	NH2	K_ASP_444	OD1	3.796
5W9O	K_ARG_401	NH2	K_ASP_444	OD2	3.928
5W9O	K_LYS_502	NZ	K_GLU_513	OE2	2.673
5W9O	K_LYS_587	NZ	K_GLU_382	OE2	2.796
5W9O	K_ARG_629	NH1	K_ASP_644	OD1	2.889
5W9O	K_ARG_629	NH1	K_ASP_644	OD2	3.817
5W9O	K_LYS_665	NZ	K_ASP_355	OD1	3.037
5W9O	K_LYS_665	NZ	K_ASP_355	OD2	3.492
5W9O	K_ARG_694	NH1	K_ASP_343	OD2	3.613
5W9O	K_ARG_694	NH2	K_ASP_343	OD2	3.571
5W9O	L_LYS_27	NZ	L_GLU_230	OE2	3.874
5W9O	L_LYS_99	NZ	L_ASP_34	OD2	3.209
5W9O	L_ARG_119	NH2	L_ASP_54	OD2	3.705
5W9O	L_LYS_142	NZ	L_GLU_252	OE2	2.676
5W9O	L_HIS_194	NE2	L_GLU_32	OE1	3.367
5W9O	L_HIS_194	NE2	L_GLU_32	OE2	3.603
5W9O	L_HIS_208	NE2	L_ASP_213	OD2	3.918
5W9O	L_ARG_235	NH2	L_GLU_188	OE1	2.895
5W9O	L_ARG_235	NH2	L_GLU_188	OE2	3.955
5W9O	L_ARG_335	NH2	L_ASP_326	OD2	2.658
5W9O	L_ARG_401	NH2	L_ASP_444	OD1	3.946
5W9O	L_LYS_413	NZ	L_GLU_382	OE2	2.929
5W9O	L_LYS_502	NZ	L_GLU_513	OE1	3.607
5W9O	L_LYS_502	NZ	L_GLU_513	OE2	3.762
5W9O	L_ARG_614	NH2	L_GLU_605	OE1	3.049
5W9O	L_ARG_614	NH2	L_GLU_605	OE2	3.623
5W9O	L_ARG_629	NH1	L_ASP_644	OD1	2.908
5W9O	L_ARG_629	NH2	L_ASP_644	OD1	2.789

5W9O	L_ARG_629	NH2	L_ASP_644	OD2	3.634
5W9O	L_LYS_665	NZ	L_GLU_666	OE2	2.768
5W9O	L_HIS_681	NE2	A_ASP_910	OD1	3.028
5W9O	L_HIS_681	NE2	A_ASP_910	OD2	3.886
5W9O	L_HIS_681	NE2	L_GLU_680	OE2	3.236
5W9O	L_ARG_694	NH1	L_ASP_343	OD2	2.925
5W9O	L_ARG_694	NH2	L_ASP_343	OD2	3.698

Table 749: 5W9O-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5W9P	J_ARG_758	NH2	A_ASP_740	OD1	2.970
5W9P	J_LYS_779	NZ	J_ASP_771	OD2	2.978
5W9P	J_LYS_779	NZ	J_GLU_1148	OE1	2.979
5W9P	J_LYS_779	NZ	J_GLU_1148	OE2	3.840
5W9P	J_LYS_801	NZ	J_ASP_843	OD1	2.959
5W9P	J_LYS_801	NZ	J_ASP_843	OD2	3.857
5W9P	J_LYS_807	NZ	J_GLU_818	OE1	3.681
5W9P	J_LYS_807	NZ	J_GLU_818	OE2	2.920
5W9P	J_LYS_816	NZ	J_ASP_1064	OD1	3.615
5W9P	J_LYS_816	NZ	J_ASP_1064	OD2	2.986
5W9P	J_ARG_841	NH2	J_GLU_1090	OE1	2.927
5W9P	J_ARG_841	NH2	J_GLU_1090	OE2	3.745
5W9P	J_ARG_847	NH1	C_ASP_726	OD1	3.573
5W9P	J_ARG_847	NH1	C_ASP_726	OD2	2.973
5W9P	J_ARG_847	NH2	J_ASP_844	OD1	2.813
5W9P	J_ARG_887	NH2	J_ASP_892	OD1	2.929
5W9P	J_HIS_1020	NE2	J_ASP_1024	OD2	3.009
5W9P	J_LYS_1021	NZ	J_GLU_793	OE1	2.955
5W9P	J_LYS_1021	NZ	J_GLU_793	OE2	3.659
5W9P	J_ARG_1113	NH1	J_GLU_1105	OE1	3.033
5W9P	J_ARG_1113	NH2	H_GLU_1105	OE1	3.990
5W9P	J_ARG_1113	NH2	H_GLU_1105	OE2	2.796
5W9P	J_LYS_1174	NZ	J_GLU_1183	OE1	2.861
5W9P	J_ARG_1179	NH2	F_ASP_31	OD1	2.888
5W9P	A_LYS_52	NZ	A_ASP_49	OD2	2.805
5W9P	A_LYS_99	NZ	A_GLU_32	OE1	2.801
5W9P	A_LYS_110	NZ	A_ASP_83	OD2	2.816
5W9P	A_ARG_119	NH2	A_ASP_54	OD1	3.835
5W9P	A_ARG_119	NH2	A_ASP_54	OD2	3.031
5W9P	A_LYS_142	NZ	A_GLU_252	OE1	2.862
5W9P	A_HIS_194	NE2	A_GLU_32	OE1	3.536
5W9P	A_ARG_235	NH1	A_GLU_188	OE1	2.967
5W9P	A_ARG_235	NH1	A_GLU_188	OE2	3.856
5W9P	A_ARG_269	NH1	A_GLU_252	OE1	3.898
5W9P	A_ARG_269	NH1	A_GLU_252	OE2	2.880
5W9P	A_ARG_335	NH2	A_ASP_326	OD2	2.878
5W9P	A_ARG_614	NH1	A_GLU_367	OE2	2.943
5W9P	A_ARG_614	NH2	A_GLU_367	OE2	2.985
5W9P	A_ARG_629	NH1	A_GLU_376	OE1	3.647
5W9P	A_ARG_629	NH1	A_ASP_644	OD1	2.978
5W9P	A_ARG_629	NH2	A_ASP_644	OD1	2.931
5W9P	A_LYS_665	NZ	A_GLU_357	OE1	3.670
5W9P	A_LYS_665	NZ	A_GLU_357	OE2	2.942
5W9P	A_HIS_681	NE2	H_ASP_910	OD1	3.149
5W9P	A_HIS_681	NE2	H_ASP_910	OD2	3.352
5W9P	A_ARG_691	NH2	H_GLU_818	OE2	2.969
5W9P	A_ARG_694	NH2	A_ASP_343	OD1	2.962
5W9P	A_ARG_694	NH2	A_ASP_343	OD2	3.657
5W9P	A_ARG_700	NH2	J_GLU_756	OE2	2.978
5W9P	A_LYS_728	NZ	A_ASP_726	OD2	2.889
5W9P	F_LYS_62	NZ	F_GLU_46	OE1	2.994
5W9P	F_LYS_62	NZ	F_GLU_46	OE2	3.429
5W9P	F_ARG_66	NH1	F_ASP_86	OD1	3.067
5W9P	F_ARG_66	NH1	F_ASP_86	OD2	3.588
5W9P	F_ARG_66	NH2	F_ASP_86	OD1	3.743
5W9P	F_ARG_66	NH2	F_ASP_86	OD2	2.861
5W9P	F_ARG_94	NH2	F_ASP_101	OD1	3.927

5W9P	F_ARG_94	NH2	F_ASP_101	OD2	2.913
5W9P	F_LYS_95	NZ	F_ASP_100C	OD1	2.870
5W9P	F_LYS_95	NZ	F_ASP_100C	OD2	3.708
5W9P	G_ARG_1177	NH1	G_ASP_1198	OD1	3.165
5W9P	G_ARG_1177	NH1	G_ASP_1198	OD2	3.744
5W9P	G_ARG_1177	NH2	G_ASP_1198	OD1	3.713
5W9P	G_ARG_1177	NH2	G_ASP_1198	OD2	2.872
5W9P	G_ARG_1212	NH1	J_GLU_1183	OE2	3.421
5W9P	G_ARG_1212	NH2	J_GLU_1183	OE2	2.921
5W9P	G_ARG_1212	NH2	F_ASP_100C	OD2	2.848
5W9P	G_LYS_1219	NZ	G_GLU_1221	OE2	2.894
5W9P	B_ARG_758	NH2	C_ASP_740	OD1	2.971
5W9P	B_LYS_779	NZ	B_ASP_771	OD2	2.978
5W9P	B_LYS_779	NZ	B_GLU_1148	OE1	2.979
5W9P	B_LYS_779	NZ	B_GLU_1148	OE2	3.841
5W9P	B_LYS_801	NZ	B_ASP_843	OD1	2.958
5W9P	B_LYS_801	NZ	B_ASP_843	OD2	3.857
5W9P	B_LYS_807	NZ	B_GLU_818	OE1	3.681
5W9P	B_LYS_807	NZ	B_GLU_818	OE2	2.920
5W9P	B_LYS_816	NZ	B_ASP_1064	OD1	3.616
5W9P	B_LYS_816	NZ	B_ASP_1064	OD2	2.986
5W9P	B_ARG_841	NH2	B_GLU_1090	OE1	2.927
5W9P	B_ARG_841	NH2	B_GLU_1090	OE2	3.745
5W9P	B_ARG_847	NH1	I_ASP_726	OD1	3.572
5W9P	B_ARG_847	NH1	I_ASP_726	OD2	2.973
5W9P	B_ARG_847	NH2	B_ASP_844	OD1	2.813
5W9P	B_ARG_887	NH2	B_ASP_892	OD1	2.929
5W9P	B_HIS_1020	NE2	B_ASP_1024	OD2	3.009
5W9P	B_LYS_1021	NZ	B_GLU_793	OE1	2.955
5W9P	B_LYS_1021	NZ	B_GLU_793	OE2	3.659
5W9P	B_ARG_1113	NH1	B_GLU_1105	OE1	3.033
5W9P	B_ARG_1113	NH2	J_GLU_1105	OE1	3.989
5W9P	B_ARG_1113	NH2	J_GLU_1105	OE2	2.795
5W9P	B_LYS_1174	NZ	B_GLU_1183	OE1	2.862
5W9P	B_ARG_1179	NH2	D_ASP_31	OD1	2.887
5W9P	C_LYS_52	NZ	C_ASP_49	OD2	2.805
5W9P	C_LYS_99	NZ	C_GLU_32	OE1	2.802
5W9P	C_LYS_110	NZ	C_ASP_83	OD2	2.816
5W9P	C_ARG_119	NH2	C_ASP_54	OD1	3.834
5W9P	C_ARG_119	NH2	C_ASP_54	OD2	3.030
5W9P	C_LYS_142	NZ	C_GLU_252	OE1	2.862
5W9P	C_HIS_194	NE2	C_GLU_32	OE1	3.534
5W9P	C_ARG_235	NH1	C_GLU_188	OE1	2.966
5W9P	C_ARG_235	NH1	C_GLU_188	OE2	3.856
5W9P	C_ARG_269	NH1	C_GLU_252	OE1	3.899
5W9P	C_ARG_269	NH1	C_GLU_252	OE2	2.881
5W9P	C_ARG_335	NH2	C_ASP_326	OD2	2.876
5W9P	C_ARG_614	NH1	C_GLU_367	OE2	2.943
5W9P	C_ARG_614	NH2	C_GLU_367	OE2	2.984
5W9P	C_ARG_629	NH1	C_GLU_376	OE1	3.647
5W9P	C_ARG_629	NH1	C_ASP_644	OD1	2.978
5W9P	C_ARG_629	NH1	C_ASP_644	OD2	4.000
5W9P	C_ARG_629	NH2	C_ASP_644	OD1	2.931
5W9P	C_LYS_665	NZ	C_GLU_357	OE1	3.671
5W9P	C_LYS_665	NZ	C_GLU_357	OE2	2.942
5W9P	C_HIS_681	NE2	J_ASP_910	OD1	3.149
5W9P	C_HIS_681	NE2	J_ASP_910	OD2	3.352
5W9P	C_ARG_691	NH2	J_GLU_818	OE2	2.970

5W9P	C_ARG.694	NH2	C_ASP.343	OD1	2.962
5W9P	C_ARG.694	NH2	C_ASP.343	OD2	3.658
5W9P	C_ARG.700	NH2	B_GLU.756	OE2	2.978
5W9P	C_LYS.728	NZ	C_ASP.726	OD2	2.889
5W9P	D_LYS.62	NZ	D_GLU.46	OE1	2.993
5W9P	D_LYS.62	NZ	D_GLU.46	OE2	3.428
5W9P	D_ARG.66	NH1	D_ASP.86	OD1	3.067
5W9P	D_ARG.66	NH1	D_ASP.86	OD2	3.588
5W9P	D_ARG.66	NH2	D_ASP.86	OD1	3.743
5W9P	D_ARG.66	NH2	D_ASP.86	OD2	2.862
5W9P	D_ARG.94	NH2	D_ASP.101	OD1	3.928
5W9P	D_ARG.94	NH2	D_ASP.101	OD2	2.914
5W9P	D_LYS.95	NZ	D_ASP.100C	OD1	2.871
5W9P	D_LYS.95	NZ	D_ASP.100C	OD2	3.708
5W9P	E_ARG.1177	NH1	E_ASP.1198	OD1	3.165
5W9P	E_ARG.1177	NH1	E_ASP.1198	OD2	3.743
5W9P	E_ARG.1177	NH2	E_ASP.1198	OD1	3.713
5W9P	E_ARG.1177	NH2	E_ASP.1198	OD2	2.872
5W9P	E_ARG.1212	NH1	B_GLU.1183	OE2	3.420
5W9P	E_ARG.1212	NH2	B_GLU.1183	OE2	2.920
5W9P	E_ARG.1212	NH2	D_ASP.100C	OD2	2.848
5W9P	E_LYS.1219	NZ	E_GLU.1221	OE2	2.894
5W9P	H_ARG.758	NH2	I_ASP.740	OD1	2.969
5W9P	H_LYS.779	NZ	H_ASP.771	OD2	2.978
5W9P	H_LYS.779	NZ	H_GLU.1148	OE1	2.978
5W9P	H_LYS.779	NZ	H_GLU.1148	OE2	3.840
5W9P	H_LYS.801	NZ	H_ASP.843	OD1	2.959
5W9P	H_LYS.801	NZ	H_ASP.843	OD2	3.857
5W9P	H_LYS.807	NZ	H_GLU.818	OE1	3.681
5W9P	H_LYS.807	NZ	H_GLU.818	OE2	2.919
5W9P	H_LYS.816	NZ	H_ASP.1064	OD1	3.616
5W9P	H_LYS.816	NZ	H_ASP.1064	OD2	2.986
5W9P	H_ARG.841	NH2	H_GLU.1090	OE1	2.927
5W9P	H_ARG.841	NH2	H_GLU.1090	OE2	3.745
5W9P	H_ARG.847	NH1	A_ASP.726	OD1	3.572
5W9P	H_ARG.847	NH1	A_ASP.726	OD2	2.973
5W9P	H_ARG.847	NH2	H_ASP.844	OD1	2.813
5W9P	H_ARG.887	NH2	H_ASP.892	OD1	2.929
5W9P	H_HIS.1020	NE2	H_ASP.1024	OD2	3.010
5W9P	H_LYS.1021	NZ	H_GLU.793	OE1	2.954
5W9P	H_LYS.1021	NZ	H_GLU.793	OE2	3.659
5W9P	H_ARG.1113	NH1	H_GLU.1105	OE1	3.032
5W9P	H_ARG.1113	NH2	B_GLU.1105	OE1	3.989
5W9P	H_ARG.1113	NH2	B_GLU.1105	OE2	2.795
5W9P	H_LYS.1174	NZ	H_GLU.1183	OE1	2.861
5W9P	H_ARG.1179	NH2	K_ASP.31	OD1	2.888
5W9P	I_LYS.52	NZ	I_ASP.49	OD2	2.805
5W9P	I_LYS.99	NZ	I_GLU.32	OE1	2.802
5W9P	I_LYS.110	NZ	I_ASP.83	OD2	2.816
5W9P	I_ARG.119	NH2	I_ASP.54	OD1	3.835
5W9P	I_ARG.119	NH2	I_ASP.54	OD2	3.031
5W9P	I_LYS.142	NZ	I_GLU.252	OE1	2.862
5W9P	I_HIS.194	NE2	I_GLU.32	OE1	3.534
5W9P	I_ARG.235	NH1	I_GLU.188	OE1	2.967
5W9P	I_ARG.235	NH1	I_GLU.188	OE2	3.856
5W9P	I_ARG.269	NH1	I_GLU.252	OE1	3.899
5W9P	I_ARG.269	NH1	I_GLU.252	OE2	2.881
5W9P	I_ARG.335	NH2	I_ASP.326	OD2	2.877

5W9P	L_ARG.614	NH1	L_GLU_367	OE2	2.944
5W9P	L_ARG.614	NH2	L_GLU_367	OE2	2.985
5W9P	L_ARG.629	NH1	L_GLU_376	OE1	3.647
5W9P	L_ARG.629	NH1	L_ASP_644	OD1	2.978
5W9P	L_ARG.629	NH1	L_ASP_644	OD2	4.000
5W9P	L_ARG.629	NH2	L_ASP_644	OD1	2.931
5W9P	L_LYS.665	NZ	L_GLU_357	OE1	3.671
5W9P	L_LYS.665	NZ	L_GLU_357	OE2	2.942
5W9P	L_HIS.681	NE2	B_ASP_910	OD1	3.149
5W9P	L_HIS.681	NE2	B_ASP_910	OD2	3.352
5W9P	L_ARG.691	NH2	B_GLU_818	OE2	2.970
5W9P	L_ARG.694	NH2	L_ASP_343	OD1	2.962
5W9P	L_ARG.694	NH2	L_ASP_343	OD2	3.657
5W9P	L_ARG.700	NH2	H_GLU_756	OE2	2.977
5W9P	L_LYS.728	NZ	L_ASP_726	OD2	2.890
5W9P	K_LYS.62	NZ	K_GLU_46	OE1	2.994
5W9P	K_LYS.62	NZ	K_GLU_46	OE2	3.429
5W9P	K_ARG.66	NH1	K_ASP_86	OD1	3.067
5W9P	K_ARG.66	NH1	K_ASP_86	OD2	3.588
5W9P	K_ARG.66	NH2	K_ASP_86	OD1	3.743
5W9P	K_ARG.66	NH2	K_ASP_86	OD2	2.862
5W9P	K_ARG.94	NH2	K_ASP_101	OD1	3.928
5W9P	K_ARG.94	NH2	K_ASP_101	OD2	2.914
5W9P	K_LYS.95	NZ	K_ASP_100C	OD1	2.870
5W9P	K_LYS.95	NZ	K_ASP_100C	OD2	3.709
5W9P	L_ARG.1177	NH1	L_ASP_1198	OD1	3.165
5W9P	L_ARG.1177	NH1	L_ASP_1198	OD2	3.743
5W9P	L_ARG.1177	NH2	L_ASP_1198	OD1	3.713
5W9P	L_ARG.1177	NH2	L_ASP_1198	OD2	2.871
5W9P	L_ARG.1212	NH1	H_GLU_1183	OE2	3.420
5W9P	L_ARG.1212	NH2	H_GLU_1183	OE2	2.921
5W9P	L_ARG.1212	NH2	K_ASP_100C	OD2	2.848
5W9P	L_LYS.1219	NZ	L_GLU_1221	OE2	2.893

Table 750: 5W9P-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5WK4	D_ARG_29	NH2	E_ASP_36	OD1	3.168
5WK4	D_ARG_29	NH2	E_ASP_36	OD2	3.056
5WK4	D_ARG_38	NH1	D_ASP_36	OD1	3.446
5WK4	D_ARG_51	NH1	D_ASP_50	OD1	3.642
5WK4	D_ARG_51	NH1	D_ASP_50	OD2	3.657
5WK4	D_ARG_101	NH2	E_ASP_50	OD2	3.021
5WK4	D_ARG_199	NH1	D_ASP_187	OD1	3.481
5WK4	A_ARG_38	NH1	A_ASP_36	OD1	3.370
5WK4	A_ARG_51	NH2	A_ASP_50	OD1	3.057
5WK4	A_ARG_51	NH2	A_ASP_50	OD2	3.306
5WK4	A_HIS_174	NE2	D_GLU_65	OE2	2.738
5WK4	A_ARG_199	NH1	A_ASP_187	OD1	3.560
5WK4	B_ARG_29	NH2	C_ASP_36	OD1	3.257
5WK4	B_ARG_29	NH2	C_ASP_36	OD2	2.944
5WK4	B_ARG_38	NH1	B_ASP_36	OD1	3.452
5WK4	B_ARG_101	NH1	C_ASP_50	OD2	3.997
5WK4	B_ARG_101	NH2	C_ASP_50	OD2	2.811
5WK4	B_ARG_199	NH1	B_ASP_187	OD1	3.746
5WK4	B_ARG_199	NH1	B_ASP_187	OD2	3.724
5WK4	C_ARG_29	NH2	B_ASP_36	OD1	3.196
5WK4	C_ARG_29	NH2	B_ASP_36	OD2	3.146
5WK4	C_ARG_38	NH1	C_ASP_36	OD1	3.439
5WK4	C_ARG_51	NH2	C_ASP_50	OD1	3.405
5WK4	C_ARG_51	NH2	C_ASP_50	OD2	3.912
5WK4	C_ARG_101	NH1	B_ASP_50	OD2	3.840
5WK4	C_ARG_101	NH2	B_ASP_50	OD2	2.874
5WK4	C_ARG_199	NH1	C_ASP_187	OD1	3.232
5WK4	C_ARG_199	NH1	C_ASP_187	OD2	3.963
5WK4	C_LYS_210	NZ	C_GLU_160	OE1	3.001
5WK4	E_ARG_29	NH2	D_ASP_36	OD1	3.889
5WK4	E_ARG_38	NH1	E_ASP_36	OD1	3.587
5WK4	E_ARG_101	NH2	D_ASP_50	OD2	2.922
5WK4	E_ARG_199	NH1	E_ASP_187	OD1	3.573
5WK4	E_ARG_199	NH1	E_ASP_187	OD2	3.380
5WK4	E_LYS_210	NZ	E_GLU_160	OE1	3.540
5WK4	F_ARG_38	NH1	F_ASP_36	OD1	3.514
5WK4	F_ARG_51	NH1	F_ASP_50	OD1	3.360
5WK4	F_ARG_51	NH1	F_ASP_50	OD2	3.476

Table 751: 5WK4-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5WKQ	A_LYS_122	NZ	A_GLU_220	OE1	3.888
5WKQ	A_ARG_135	NH1	B_ASP_212	OD1	3.924
5WKQ	A_ARG_135	NH2	B_ASP_212	OD1	3.057
5WKQ	A_LYS_157	NZ	A_ASP_153	OD1	3.684
5WKQ	A_LYS_157	NZ	A_ASP_153	OD2	2.658
5WKQ	A_ARG_164	NH2	A_GLU_174	OE2	3.301
5WKQ	A_LYS_189	NZ	A_ASP_190	OD1	3.185
5WKQ	B_LYS_115	NZ	B_GLU_220	OE2	3.947
5WKQ	B_LYS_157	NZ	B_ASP_153	OD1	3.490
5WKQ	B_LYS_157	NZ	B_ASP_153	OD2	3.167
5WKQ	B_LYS_189	NZ	B_GLU_155	OE2	3.558
5WKQ	B_ARG_196	NH1	B_ASP_148	OD1	2.868
5WKQ	B_HIS_207	ND1	A_GLU_131	OE1	3.383
5WKQ	B_HIS_207	ND1	A_GLU_131	OE2	2.652
5WKQ	B_LYS_213	NZ	B_GLU_129	OE1	3.323

Table 752: 5WKQ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5WN9	H_ARG_38	NH1	H_GLU_46	OE1	3.227
5WN9	H_ARG_38	NH1	H_GLU_46	OE2	3.503
5WN9	H_ARG_38	NH1	H_ASP_90	OD1	3.902
5WN9	H_ARG_38	NH2	H_ASP_90	OD1	2.913
5WN9	H_LYS_63	NZ	H_GLU_46	OE1	3.637
5WN9	H_LYS_63	NZ	H_GLU_46	OE2	3.106
5WN9	H_ARG_67	NH1	H_ASP_90	OD1	3.282
5WN9	H_ARG_67	NH1	H_ASP_90	OD2	2.270
5WN9	H_ARG_67	NH2	H_ASP_90	OD1	3.376
5WN9	H_ARG_67	NH2	H_ASP_90	OD2	3.700
5WN9	H_ARG_84	NH1	H_GLU_82	OE1	3.057
5WN9	H_ARG_98	NH1	H_ASP_112	OD1	3.399
5WN9	H_ARG_98	NH1	H_ASP_112	OD2	2.841
5WN9	H_ARG_168	NH2	H_ASP_214	OD1	2.927
5WN9	H_ARG_168	NH2	H_ASP_214	OD2	3.594
5WN9	H_ARG_205	NH1	H_GLU_225	OE2	3.482
5WN9	H_ARG_205	NH1	H_ASP_226	OD1	2.888
5WN9	H_ARG_205	NH1	H_ASP_226	OD2	3.550

Table 753: 5WN9-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5WNA	H_ARG_28	NH2	H_GLU_31	OE2	3.703
5WNA	H_ARG_38	NH1	H_ASP_90	OD2	2.959
5WNA	H_ARG_38	NH2	H_GLU_46	OE1	3.180
5WNA	H_LYS_65	NZ	H_ASP_62	OD1	2.520
5WNA	H_ARG_67	NH1	H_ASP_90	OD1	3.443
5WNA	H_ARG_67	NH1	H_ASP_90	OD2	3.943
5WNA	H_ARG_67	NH2	H_ASP_90	OD1	3.917
5WNA	H_ARG_67	NH2	H_ASP_90	OD2	3.253
5WNA	H_LYS_111	NZ	H_GLU_2	OE1	2.349
5WNA	H_LYS_111	NZ	H_GLU_2	OE2	2.999
5WNA	H_LYS_154	NZ	H_ASP_155	OD2	3.921
5WNA	H_LYS_220	NZ	L_GLU_122	OE2	3.667
5WNA	H_LYS_221	NZ	H_GLU_223	OE2	2.498
5WNA	H_LYS_225	NZ	L_ASP_121	OD1	3.706
5WNA	L_HIS_32	ND1	L_GLU_50	OE1	2.885
5WNA	L_HIS_32	ND1	L_GLU_50	OE2	3.439
5WNA	L_LYS_39	NZ	D_GLU_81	OE1	2.898
5WNA	L_LYS_39	NZ	D_GLU_81	OE2	2.887
5WNA	L_ARG_61	NH2	L_GLU_81	OE2	2.586
5WNA	L_ARG_61	NH2	L_ASP_82	OD1	3.471
5WNA	L_ARG_61	NH2	L_ASP_82	OD2	2.813
5WNA	L_LYS_148	NZ	L_GLU_194	OE1	2.468
5WNA	L_LYS_148	NZ	L_GLU_194	OE2	3.864
5WNA	L_LYS_182	NZ	L_GLU_186	OE1	3.903
5WNA	L_LYS_182	NZ	L_GLU_186	OE2	3.646
5WNA	C_ARG_28	NH2	C_GLU_31	OE1	3.185
5WNA	C_ARG_38	NH1	C_ASP_90	OD1	2.822
5WNA	C_ARG_38	NH2	C_GLU_46	OE1	3.169
5WNA	C_ARG_38	NH2	C_GLU_46	OE2	3.973
5WNA	C_ARG_38	NH2	C_ASP_90	OD1	3.613
5WNA	C_LYS_65	NZ	C_ASP_62	OD2	2.607
5WNA	C_ARG_67	NH1	C_ASP_90	OD1	3.948
5WNA	C_ARG_67	NH1	C_ASP_90	OD2	3.192
5WNA	C_ARG_67	NH2	C_ASP_90	OD1	3.187
5WNA	C_ARG_67	NH2	C_ASP_90	OD2	3.777
5WNA	C_LYS_76	NZ	C_ASP_73	OD2	3.522
5WNA	C_LYS_111	NZ	C_GLU_2	OE1	3.732
5WNA	C_LYS_111	NZ	C_GLU_2	OE2	2.480
5WNA	C_LYS_154	NZ	C_ASP_155	OD1	3.662
5WNA	C_LYS_220	NZ	D_GLU_122	OE2	3.567
5WNA	C_LYS_221	NZ	C_GLU_223	OE1	3.081
5WNA	D_ARG_24	NH1	D_ASP_70	OD1	2.370
5WNA	D_ARG_24	NH1	D_ASP_70	OD2	2.529
5WNA	D_ARG_24	NH2	D_ASP_70	OD1	3.649
5WNA	D_HIS_32	ND1	D_GLU_50	OE1	3.272
5WNA	D_HIS_32	ND1	D_GLU_50	OE2	2.966
5WNA	D_LYS_39	NZ	L_GLU_81	OE1	3.744
5WNA	D_ARG_61	NH2	D_GLU_81	OE1	3.776
5WNA	D_ARG_61	NH2	D_ASP_82	OD1	3.311
5WNA	D_ARG_61	NH2	D_ASP_82	OD2	2.738
5WNA	D_LYS_148	NZ	D_GLU_194	OE2	3.083
5WNA	D_LYS_182	NZ	D_GLU_186	OE1	3.810
5WNA	D_LYS_182	NZ	D_GLU_186	OE2	3.086
5WNA	D_LYS_187	NZ	D_ASP_184	OD1	3.142

Table 754: 5WNA-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5WNB	H_ARG_19	NH1	H_GLU_82	OE1	2.506
5WNB	H_ARG_38	NH1	H_ASP_90	OD1	3.116
5WNB	H_ARG_38	NH2	H_GLU_46	OE1	3.477
5WNB	H_ARG_38	NH2	H_GLU_46	OE2	2.945
5WNB	H_ARG_38	NH2	H_ASP_90	OD1	3.843
5WNB	H_LYS_65	NZ	H_ASP_62	OD1	3.127
5WNB	H_ARG_67	NH1	H_ASP_90	OD2	3.008
5WNB	H_ARG_67	NH2	H_ASP_90	OD1	3.462
5WNB	H_ARG_67	NH2	H_ASP_90	OD2	3.519
5WNB	H_ARG_72	NH2	H_ASP_77	OD2	3.365
5WNB	H_LYS_76	NZ	H_ASP_73	OD2	3.433
5WNB	H_HIS_108	ND1	H_ASP_106	OD2	3.787
5WNB	H_HIS_108	NE2	H_ASP_106	OD2	2.649
5WNB	H_LYS_140	NZ	L_GLU_212	OE1	3.467
5WNB	H_LYS_140	NZ	L_GLU_212	OE2	3.708
5WNB	H_LYS_154	NZ	H_ASP_155	OD1	3.075
5WNB	H_LYS_154	NZ	H_ASP_155	OD2	2.337
5WNB	L_HIS_32	ND1	L_GLU_50	OE1	3.927
5WNB	L_HIS_32	ND1	L_GLU_50	OE2	3.082
5WNB	L_ARG_61	NH1	M_GLU_79	OE2	3.612
5WNB	L_ARG_61	NH2	L_GLU_81	OE1	3.333
5WNB	L_ARG_61	NH2	L_ASP_82	OD1	3.537
5WNB	L_ARG_61	NH2	L_ASP_82	OD2	2.770
5WNB	L_LYS_148	NZ	L_GLU_194	OE1	2.500
5WNB	L_LYS_187	NZ	L_ASP_184	OD2	3.098
5WNB	L_HIS_188	ND1	L_ASP_150	OD1	3.403
5WNB	L_ARG_38	NH1	L_ASP_90	OD2	3.224
5WNB	L_ARG_38	NH2	L_GLU_46	OE1	2.966
5WNB	L_ARG_38	NH2	L_GLU_46	OE2	3.754
5WNB	L_ARG_67	NH2	L_ASP_90	OD1	2.682
5WNB	L_ARG_67	NH2	L_ASP_90	OD2	3.569
5WNB	L_HIS_108	NE2	L_ASP_106	OD2	3.548
5WNB	L_LYS_154	NZ	L_ASP_155	OD1	2.470
5WNB	L_LYS_154	NZ	L_ASP_155	OD2	2.919
5WNB	M_HIS_32	ND1	M_GLU_50	OE1	2.976
5WNB	M_HIS_32	ND1	M_GLU_50	OE2	3.054
5WNB	M_ARG_61	NH2	M_GLU_81	OE1	3.769
5WNB	M_ARG_61	NH2	M_ASP_82	OD1	2.298
5WNB	M_ARG_61	NH2	M_ASP_82	OD2	3.245
5WNB	M_LYS_168	NZ	M_ASP_166	OD1	3.331
5WNB	M_LYS_168	NZ	M_ASP_166	OD2	3.217
5WNB	A_HIS_164	ND1	A_GLU_166	OE1	3.440
5WNB	A_HIS_164	NE2	A_ASP_162	OD1	3.262
5WNB	A_HIS_164	NE2	A_ASP_162	OD2	3.502
5WNB	B_HIS_164	ND1	B_GLU_166	OE1	3.999
5WNB	B_HIS_164	ND1	B_GLU_166	OE2	3.280
5WNB	B_HIS_164	NE2	B_ASP_162	OD1	3.381

Table 755: 5WNB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5XBM	A_ARG_59	NH2	A_GLU_79	OE1	3.378
5XBM	A_ARG_59	NH2	A_ASP_80	OD2	3.511
5XBM	A_LYS_140	NZ	A_GLU_103	OE2	3.814
5XBM	A_LYS_145	NZ	A_GLU_193	OE1	3.556
5XBM	A_LYS_145	NZ	A_GLU_193	OE2	2.956
5XBM	A_ARG_153	NH1	A_GLU_183	OE1	2.925
5XBM	A_ARG_153	NH2	A_GLU_183	OE1	3.437
5XBM	A_LYS_181	NZ	A_GLU_185	OE2	3.524
5XBM	A_LYS_205	NZ	B_ASP_139	OD1	3.654
5XBM	B_LYS_67	NZ	B_ASP_90	OD1	3.066
5XBM	B_LYS_67	NZ	B_ASP_90	OD2	2.464
5XBM	B_ARG_98	NH2	B_ASP_110	OD2	3.054
5XBM	B_LYS_217	NZ	A_GLU_121	OE1	2.614
5XBM	B_LYS_217	NZ	A_GLU_121	OE2	3.625
5XBM	C_ARG_77	NH1	C_GLU_79	OE1	3.381
5XBM	C_ARG_77	NH2	C_GLU_79	OE1	2.852
5XBM	C_ARG_95	NH1	C_ASP_254	OD2	2.603
5XBM	C_ARG_95	NH2	C_GLU_93	OE2	3.851
5XBM	C_ARG_95	NH2	C_GLU_413	OE1	3.677
5XBM	C_ARG_95	NH2	C_GLU_413	OE2	3.452
5XBM	C_LYS_97	NZ	C_ASP_252	OD2	3.959
5XBM	C_HIS_171	ND1	C_GLU_175	OE2	3.888
5XBM	C_ARG_192	NH2	C_ASP_194	OD2	3.106
5XBM	C_HIS_257	NE2	C_GLU_264	OE2	3.860
5XBM	C_ARG_294	NH1	C_GLU_361	OE2	3.640
5XBM	C_ARG_294	NH2	C_ASP_368	OD2	3.362
5XBM	C_LYS_296	NZ	C_GLU_364	OE1	3.065
5XBM	C_LYS_296	NZ	C_GLU_364	OE2	3.891
5XBM	C_HIS_341	NE2	C_GLU_85	OE2	2.443
5XBM	C_LYS_381	NZ	C_ASP_254	OD1	2.330
5XBM	C_LYS_391	NZ	C_ASP_393	OD2	3.425
5XBM	C_LYS_419	NZ	C_GLU_420	OE2	2.764
5XBM	D_ARG_59	NH1	D_ASP_80	OD2	3.136
5XBM	D_LYS_145	NZ	D_GLU_152	OE2	2.597
5XBM	D_ARG_153	NH2	D_GLU_183	OE2	3.712
5XBM	D_LYS_181	NZ	D_GLU_185	OE2	2.414
5XBM	D_ARG_209	NH1	D_GLU_185	OE1	3.438
5XBM	E_LYS_67	NZ	E_ASP_90	OD2	3.658
5XBM	E_ARG_98	NH1	E_ASP_110	OD1	3.749
5XBM	E_ARG_98	NH2	E_ASP_110	OD1	3.811
5XBM	E_LYS_217	NZ	D_GLU_121	OE2	3.463
5XBM	F_ARG_77	NH1	D_ASP_31	OD1	3.188
5XBM	F_ARG_77	NH1	F_GLU_79	OE1	3.586
5XBM	F_ARG_77	NH1	F_GLU_79	OE2	3.933
5XBM	F_ARG_77	NH2	D_ASP_31	OD1	3.156
5XBM	F_ARG_77	NH2	D_ASP_31	OD2	3.938
5XBM	F_ARG_77	NH2	F_GLU_73	OE1	3.951
5XBM	F_ARG_82	NH1	F_GLU_354	OE2	3.586
5XBM	F_ARG_95	NH2	F_GLU_93	OE1	3.848
5XBM	F_ARG_95	NH2	F_GLU_413	OE2	2.568
5XBM	F_LYS_129	NZ	F_ASP_127	OD1	3.700
5XBM	F_LYS_161	NZ	C_GLU_154	OE2	3.149
5XBM	F_HIS_171	ND1	F_GLU_175	OE1	3.652
5XBM	F_HIS_257	NE2	F_GLU_264	OE1	3.279
5XBM	F_HIS_257	NE2	F_GLU_264	OE2	3.085
5XBM	F_ARG_294	NH1	F_GLU_285	OE1	3.934
5XBM	F_ARG_294	NH2	F_GLU_285	OE1	2.990

5XBM	F_ARG_294	NH2	F_GLU_285	OE2	3.166
5XBM	F_ARG_294	NH2	F_ASP_368	OD1	3.670
5XBM	F_LYS_296	NZ	F_GLU_364	OE1	3.766
5XBM	F_LYS_296	NZ	F_GLU_364	OE2	3.585
5XBM	F_HIS_341	NE2	F_GLU_85	OE2	2.413
5XBM	F_LYS_391	NZ	F_ASP_393	OD2	3.195

Table 756: 5XBM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5XCQ	A_LYS_13	NZ	B_ASP_154	OD1	3.910
5XCQ	A_ARG_66	NH1	A_ASP_86	OD1	3.789
5XCQ	A_ARG_66	NH1	A_ASP_86	OD2	2.772
5XCQ	A_ARG_66	NH2	A_ASP_86	OD1	2.957
5XCQ	A_ARG_66	NH2	A_ASP_86	OD2	3.362
5XCQ	A_LYS_121	NZ	A_GLU_118	OE2	2.790
5XCQ	B_HIS_42	NE2	B_ASP_41	OD1	3.768
5XCQ	B_HIS_42	NE2	B_ASP_41	OD2	3.647
5XCQ	B_HIS_42	NE2	B_GLU_140	OE1	3.727
5XCQ	B_HIS_42	NE2	B_GLU_140	OE2	2.593
5XCQ	B_ARG_61	NH2	B_ASP_82	OD1	2.863
5XCQ	B_ARG_61	NH2	B_ASP_82	OD2	3.535
5XCQ	B_LYS_116	NZ	B_GLU_113	OE1	3.934
5XCQ	B_LYS_116	NZ	B_GLU_113	OE2	2.845
5XCQ	B_LYS_144	NZ	A_GLU_142	OE1	3.005
5XCQ	B_LYS_144	NZ	A_GLU_142	OE2	2.931

Table 757: 5XCQ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5XCR	A_LYS_13	NZ	B_ASP_154	OD1	3.316
5XCR	A_LYS_13	NZ	B_ASP_154	OD2	2.938
5XCR	A_ARG_66	NH1	A_ASP_86	OD1	3.686
5XCR	A_ARG_66	NH1	A_ASP_86	OD2	2.734
5XCR	A_ARG_66	NH2	A_ASP_86	OD1	2.875
5XCR	A_ARG_66	NH2	A_ASP_86	OD2	3.410
5XCR	A_LYS_121	NZ	A_GLU_118	OE2	2.719
5XCR	A_ARG_147	NH2	B_GLU_135	OE2	3.104
5XCR	A_LYS_149	NZ	B_ASP_41	OD1	2.692
5XCR	A_LYS_149	NZ	B_ASP_41	OD2	3.682
5XCR	A_LYS_153	NZ	B_ASP_41	OD1	3.567
5XCR	A_LYS_153	NZ	B_ASP_41	OD2	3.385
5XCR	B_ARG_61	NH2	B_GLU_81	OE2	3.905
5XCR	B_ARG_61	NH2	B_ASP_82	OD1	2.794
5XCR	B_ARG_61	NH2	B_ASP_82	OD2	3.586
5XCR	B_ARG_142	NH1	B_GLU_139	OE1	3.167
5XCR	B_LYS_144	NZ	A_GLU_142	OE1	2.665
5XCR	B_LYS_144	NZ	A_GLU_142	OE2	3.686
5XCR	D_LYS_13	NZ	D_GLU_16	OE2	3.937
5XCR	D_LYS_64	NZ	D_GLU_61	OE2	3.102
5XCR	D_ARG_66	NH1	D_ASP_86	OD1	3.572
5XCR	D_ARG_66	NH1	D_ASP_86	OD2	2.754
5XCR	D_ARG_66	NH2	D_ASP_86	OD1	2.764
5XCR	D_ARG_66	NH2	D_ASP_86	OD2	3.427
5XCR	D_LYS_149	NZ	E_ASP_41	OD1	2.596
5XCR	D_LYS_149	NZ	E_ASP_41	OD2	3.537
5XCR	D_LYS_149	NZ	E_GLU_137	OE1	2.552
5XCR	D_LYS_149	NZ	E_GLU_137	OE2	3.483
5XCR	D_ARG_154	NH2	E_ASP_131	OD1	2.972
5XCR	E_LYS_39	NZ	E_GLU_81	OE2	3.722
5XCR	E_ARG_61	NH2	E_GLU_81	OE1	3.056
5XCR	E_ARG_61	NH2	E_ASP_82	OD1	2.787
5XCR	E_ARG_61	NH2	E_ASP_82	OD2	3.509
5XCR	E_LYS_116	NZ	E_GLU_113	OE1	3.303
5XCR	E_LYS_116	NZ	E_GLU_113	OE2	3.987
5XCR	E_ARG_126	NH1	E_GLU_81	OE2	3.465
5XCR	E_LYS_144	NZ	D_GLU_142	OE1	2.644
5XCR	E_LYS_144	NZ	D_GLU_142	OE2	3.385

Table 758: 5XCR-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5XCS	A_ARG_38	NH1	A_ASP_86	OD1	2.824
5XCS	A_ARG_38	NH2	A_GLU_46	OE1	3.945
5XCS	A_ARG_38	NH2	A_GLU_46	OE2	3.011
5XCS	A_ARG_38	NH2	A_ASP_86	OD1	3.632
5XCS	A_LYS_43	NZ	B_GLU_140	OE2	2.517
5XCS	A_ARG_66	NH1	A_ASP_86	OD1	3.282
5XCS	A_ARG_66	NH1	A_ASP_86	OD2	2.652
5XCS	A_ARG_66	NH2	A_ASP_86	OD1	3.265
5XCS	A_ARG_66	NH2	A_ASP_86	OD2	3.877
5XCS	A_LYS_75	NZ	A_ASP_72	OD2	3.471
5XCS	A_ARG_94	NH2	A_GLU_96	OE1	2.939
5XCS	A_ARG_94	NH2	A_GLU_96	OE2	3.439
5XCS	A_ARG_95	NH1	B_ASP_91	OD1	2.738
5XCS	A_ARG_95	NH1	B_ASP_91	OD2	3.741
5XCS	A_ARG_95	NH2	B_ASP_91	OD1	3.421
5XCS	A_ARG_95	NH2	C_ASP_7	OD1	3.700
5XCS	A_ARG_95	NH2	C_ASP_7	OD2	2.872
5XCS	A_LYS_100A	NZ	B_GLU_55	OE1	2.609
5XCS	A_LYS_100A	NZ	B_GLU_55	OE2	3.239
5XCS	A_ARG_147	NH1	A_GLU_144	OE1	3.227
5XCS	A_LYS_149	NZ	B_GLU_137	OE1	3.069
5XCS	A_LYS_149	NZ	B_GLU_137	OE2	3.874
5XCS	B_ARG_61	NH2	B_GLU_81	OE2	3.146
5XCS	B_ARG_61	NH2	B_ASP_82	OD1	2.765
5XCS	B_ARG_61	NH2	B_ASP_82	OD2	3.342
5XCS	B_HIS_94	NE2	C_ASP_7	OD2	3.772
5XCS	B_LYS_103	NZ	B_GLU_105	OE2	3.336
5XCS	B_LYS_125	NZ	B_GLU_121	OE2	3.175
5XCS	B_ARG_142	NH2	B_GLU_139	OE1	3.838
5XCS	B_LYS_144	NZ	A_GLU_142	OE1	3.111
5XCS	B_LYS_144	NZ	A_GLU_142	OE2	3.511
5XCS	B_ARG_149	NH1	A_ASP_136	OD1	2.816

Table 759: 5XCS-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5XCT	A_ARG.66	NH1	A_ASP.86	OD1	3.743
5XCT	A_ARG.66	NH1	A_ASP.86	OD2	2.753
5XCT	A_ARG.66	NH2	A_ASP.86	OD1	2.868
5XCT	A_ARG.66	NH2	A_ASP.86	OD2	3.322
5XCT	A_ARG.131	NH2	A_ASP.116	OD2	3.928
5XCT	B_HIS.42	NE2	B_ASP.41	OD2	3.182
5XCT	B_HIS.42	NE2	B_GLU.140	OE1	3.857
5XCT	B_HIS.42	NE2	B_GLU.140	OE2	3.342
5XCT	B_ARG.61	NH2	B_ASP.82	OD1	2.811
5XCT	B_ARG.61	NH2	B_ASP.82	OD2	3.636
5XCT	B_LYS.144	NZ	A_GLU.142	OE1	2.822
5XCT	B_LYS.144	NZ	A_GLU.142	OE2	3.117

Table 760: 5XCT-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID** **residue name** **residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5XCU	A_LYS_13	NZ	B_ASP_154	OD2	3.098
5XCU	A_ARG_38	NH1	A_GLU_46	OE1	2.812
5XCU	A_ARG_38	NH1	A_GLU_46	OE2	3.498
5XCU	A_ARG_38	NH1	A_ASP_86	OD1	3.796
5XCU	A_ARG_38	NH2	A_ASP_86	OD1	2.904
5XCU	A_ARG_66	NH1	A_ASP_86	OD1	2.877
5XCU	A_ARG_66	NH1	A_ASP_86	OD2	3.351
5XCU	A_ARG_66	NH2	A_ASP_86	OD1	3.756
5XCU	A_ARG_66	NH2	A_ASP_86	OD2	2.690
5XCU	A_ARG_94	NH2	A_GLU_96	OE1	3.021
5XCU	A_ARG_94	NH2	A_GLU_96	OE2	3.420
5XCU	A_ARG_95	NH1	B_ASP_91	OD1	2.822
5XCU	A_ARG_95	NH1	B_ASP_91	OD2	3.880
5XCU	A_ARG_95	NH2	B_ASP_91	OD1	3.668
5XCU	A_ARG_95	NH2	C_ASP_7	OD1	3.592
5XCU	A_ARG_95	NH2	C_ASP_7	OD2	2.664
5XCU	A_LYS_100A	NZ	A_ASP_99	OD2	3.553
5XCU	A_LYS_100A	NZ	B_GLU_55	OE1	3.292
5XCU	A_LYS_100A	NZ	B_GLU_55	OE2	3.457
5XCU	A_LYS_121	NZ	A_GLU_118	OE1	2.230
5XCU	A_LYS_149	NZ	B_GLU_137	OE1	3.142
5XCU	A_LYS_149	NZ	B_GLU_137	OE2	3.674
5XCU	B_LYS_24	NZ	B_ASP_70	OD1	2.759
5XCU	B_LYS_24	NZ	B_ASP_70	OD2	2.992
5XCU	B_ARG_61	NH2	B_GLU_81	OE2	3.746
5XCU	B_ARG_61	NH2	B_ASP_82	OD1	2.826
5XCU	B_ARG_61	NH2	B_ASP_82	OD2	3.416
5XCU	B_HIS_94	NE2	C_ASP_7	OD2	3.530
5XCU	B_LYS_103	NZ	B_GLU_105	OE1	2.119
5XCU	B_LYS_116	NZ	B_GLU_113	OE2	2.757
5XCU	B_ARG_142	NH1	B_GLU_139	OE1	3.141
5XCU	B_ARG_142	NH2	D_GLU_100	OE1	3.626
5XCU	B_ARG_142	NH2	D_GLU_100	OE2	3.496
5XCU	B_LYS_144	NZ	A_GLU_142	OE1	2.843
5XCU	B_LYS_144	NZ	A_GLU_142	OE2	2.719
5XCU	B_ARG_149	NH2	A_ASP_136	OD1	3.520
5XCU	D_LYS_13	NZ	E_ASP_154	OD2	2.965
5XCU	D_ARG_38	NH1	D_ASP_86	OD1	2.931
5XCU	D_ARG_38	NH2	D_GLU_46	OE1	2.982
5XCU	D_ARG_52A	NH1	A_GLU_144	OE1	3.014
5XCU	D_ARG_52A	NH1	A_GLU_144	OE2	3.323
5XCU	D_ARG_52A	NH2	A_GLU_144	OE2	3.086
5XCU	D_ARG_66	NH1	D_ASP_86	OD1	3.903
5XCU	D_ARG_66	NH1	D_ASP_86	OD2	2.901
5XCU	D_ARG_66	NH2	D_ASP_86	OD1	3.158
5XCU	D_ARG_66	NH2	D_ASP_86	OD2	3.501
5XCU	D_ARG_94	NH2	D_GLU_96	OE1	3.413
5XCU	D_ARG_94	NH2	D_GLU_96	OE2	3.168
5XCU	D_ARG_95	NH1	E_ASP_91	OD1	2.736
5XCU	D_ARG_95	NH1	E_ASP_91	OD2	3.660
5XCU	D_ARG_95	NH2	E_ASP_91	OD1	3.272
5XCU	D_ARG_95	NH2	F_ASP_7	OD1	3.878
5XCU	D_ARG_95	NH2	F_ASP_7	OD2	3.169
5XCU	D_LYS_100A	NZ	D_ASP_99	OD2	3.711
5XCU	D_LYS_100A	NZ	E_GLU_55	OE1	3.852
5XCU	D_LYS_100A	NZ	E_GLU_55	OE2	2.994
5XCU	D_ARG_147	NH2	D_GLU_144	OE1	3.695

5XCU	D_LYS_149	NZ	E_GLU_137	OE1	2.785
5XCU	D_LYS_149	NZ	E_GLU_137	OE2	3.293
5XCU	E_LYS_24	NZ	E_ASP_70	OD1	3.892
5XCU	E_LYS_30F	NZ	B_GLU_139	OE1	2.662
5XCU	E_LYS_30F	NZ	B_GLU_139	OE2	3.287
5XCU	E_ARG_61	NH1	E_GLU_81	OE1	3.712
5XCU	E_ARG_61	NH1	E_ASP_82	OD1	3.146
5XCU	E_ARG_61	NH1	E_ASP_82	OD2	3.543
5XCU	E_HIS_94	NE2	F_ASP_7	OD2	3.551
5XCU	E_LYS_103	NZ	E_GLU_105	OE2	3.303
5XCU	E_ARG_142	NH1	E_GLU_139	OE2	3.171
5XCU	E_ARG_142	NH2	D_GLU_140	OE2	3.967
5XCU	E_LYS_144	NZ	D_GLU_142	OE1	3.438
5XCU	E_LYS_144	NZ	D_GLU_142	OE2	2.648

Table 761: 5XCU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5XCV	A_ARG_38	NH1	A_GLU_46	OE1	3.020
5XCV	A_ARG_38	NH1	A_ASP_86	OD1	3.966
5XCV	A_ARG_38	NH2	A_ASP_86	OD1	2.867
5XCV	A_LYS_56	NZ	C_GLU_10	OE2	3.165
5XCV	A_LYS_56	NZ	C_ASP_11	OD1	3.842
5XCV	A_LYS_56	NZ	C_ASP_11	OD2	2.877
5XCV	A_ARG_66	NH1	A_ASP_86	OD1	3.207
5XCV	A_ARG_66	NH1	A_ASP_86	OD2	3.568
5XCV	A_ARG_66	NH2	A_ASP_86	OD1	3.873
5XCV	A_ARG_66	NH2	A_ASP_86	OD2	2.785
5XCV	A_LYS_75	NZ	A_ASP_72	OD2	3.989
5XCV	A_ARG_83	NH2	A_GLU_85	OE2	3.625
5XCV	A_LYS_94	NZ	A_ASP_101	OD2	3.427
5XCV	A_LYS_121	NZ	A_GLU_118	OE1	2.490
5XCV	A_LYS_121	NZ	A_GLU_118	OE2	3.921
5XCV	A_ARG_131	NH1	D_GLU_142	OE2	2.857
5XCV	A_ARG_131	NH2	D_GLU_142	OE2	3.651
5XCV	A_LYS_149	NZ	B_GLU_137	OE1	3.135
5XCV	A_LYS_149	NZ	B_GLU_137	OE2	2.706
5XCV	A_ARG_154	NH2	B_ASP_131	OD1	2.532
5XCV	B_LYS_53	NZ	B_ASP_52	OD1	2.531
5XCV	B_LYS_53	NZ	B_ASP_52	OD2	3.942
5XCV	B_ARG_61	NH1	B_GLU_81	OE2	2.626
5XCV	B_ARG_61	NH1	B_ASP_82	OD1	3.375
5XCV	B_ARG_61	NH1	B_ASP_82	OD2	3.966
5XCV	B_ARG_61	NH2	B_ASP_82	OD1	2.920
5XCV	B_ARG_61	NH2	B_ASP_82	OD2	2.592
5XCV	B_ARG_142	NH1	B_GLU_135	OE2	3.241
5XCV	B_ARG_142	NH1	B_GLU_139	OE1	2.828
5XCV	B_ARG_142	NH2	B_GLU_135	OE1	3.178
5XCV	B_ARG_142	NH2	B_GLU_135	OE2	3.502
5XCV	B_LYS_144	NZ	A_GLU_142	OE1	2.798
5XCV	B_LYS_144	NZ	A_GLU_142	OE2	3.295
5XCV	B_ARG_149	NH2	A_ASP_136	OD1	3.863
5XCV	B_ARG_149	NH2	A_ASP_136	OD2	3.941
5XCV	D_ARG_38	NH1	D_GLU_46	OE1	3.023
5XCV	D_ARG_38	NH1	D_ASP_86	OD1	3.942
5XCV	D_ARG_38	NH2	D_ASP_86	OD1	2.784
5XCV	D_ARG_66	NH1	D_ASP_86	OD1	3.694
5XCV	D_ARG_66	NH1	D_ASP_86	OD2	2.840
5XCV	D_ARG_66	NH2	D_ASP_86	OD1	3.151
5XCV	D_ARG_66	NH2	D_ASP_86	OD2	3.768
5XCV	D_LYS_94	NZ	D_ASP_101	OD2	3.401
5XCV	D_LYS_121	NZ	D_GLU_118	OE1	3.518
5XCV	D_LYS_121	NZ	D_GLU_118	OE2	3.547
5XCV	D_ARG_131	NH1	A_GLU_142	OE2	2.791
5XCV	D_ARG_131	NH2	A_GLU_142	OE2	3.693
5XCV	D_LYS_149	NZ	E_GLU_137	OE1	2.622
5XCV	D_LYS_149	NZ	E_GLU_137	OE2	3.565
5XCV	D_LYS_153	NZ	E_GLU_40	OE2	3.944
5XCV	E_LYS_53	NZ	E_ASP_52	OD1	2.875
5XCV	E_ARG_61	NH2	E_ASP_82	OD1	3.461
5XCV	E_ARG_61	NH2	E_ASP_82	OD2	3.413
5XCV	E_LYS_116	NZ	E_GLU_113	OE2	3.173
5XCV	E_LYS_144	NZ	D_GLU_142	OE1	2.798
5XCV	E_LYS_144	NZ	D_GLU_142	OE2	3.738

Table 762: 5XCV-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5XJ3	A_ARG_38	NH1	A_ASP_90	OD1	3.056
5XJ3	A_ARG_38	NH2	A_GLU_46	OE1	3.585
5XJ3	A_ARG_38	NH2	A_GLU_46	OE2	3.163
5XJ3	A_ARG_38	NH2	A_GLU_89	OE1	3.576
5XJ3	A_ARG_67	NH1	A_GLU_89	OE2	3.733
5XJ3	A_ARG_67	NH2	A_ASP_90	OD1	2.978
5XJ3	A_ARG_67	NH2	A_ASP_90	OD2	2.554
5XJ3	A_ARG_87	NH1	A_GLU_89	OE2	3.859
5XJ3	A_ARG_98	NH1	A_ASP_106	OD2	3.164
5XJ3	B_ARG_55	NH1	B_ASP_61	OD1	2.406
5XJ3	B_ARG_62	NH2	B_GLU_82	OE2	2.865
5XJ3	B_ARG_62	NH2	B_ASP_83	OD1	3.259
5XJ3	B_LYS_104	NZ	B_GLU_106	OE1	3.023
5XJ3	C_ARG_75	NH1	C_ASP_123	OD1	3.835
5XJ3	C_LYS_130	NZ	C_GLU_132	OE1	3.977
5XJ3	D_ARG_38	NH1	D_ASP_90	OD1	3.121
5XJ3	D_ARG_38	NH2	D_GLU_46	OE2	3.650
5XJ3	D_ARG_38	NH2	D_GLU_89	OE1	3.831
5XJ3	D_ARG_38	NH2	D_ASP_90	OD1	4.000
5XJ3	D_ARG_67	NH1	D_GLU_89	OE2	3.568
5XJ3	D_ARG_67	NH2	D_ASP_90	OD1	2.936
5XJ3	D_ARG_67	NH2	D_ASP_90	OD2	2.379
5XJ3	D_ARG_87	NH1	D_GLU_89	OE2	3.625
5XJ3	D_ARG_98	NH1	D_ASP_106	OD2	3.382
5XJ3	E_ARG_55	NH1	E_ASP_61	OD1	2.462
5XJ3	E_ARG_62	NH2	E_GLU_82	OE2	2.848
5XJ3	E_ARG_62	NH2	E_ASP_83	OD1	3.444
5XJ3	E_LYS_104	NZ	E_GLU_106	OE1	2.817
5XJ3	G_ARG_38	NH1	G_ASP_90	OD1	3.040
5XJ3	G_ARG_38	NH2	G_GLU_46	OE1	3.607
5XJ3	G_ARG_38	NH2	G_GLU_46	OE2	3.241
5XJ3	G_ARG_38	NH2	G_GLU_89	OE1	3.847
5XJ3	G_ARG_67	NH1	G_GLU_89	OE2	3.528
5XJ3	G_ARG_67	NH2	G_ASP_90	OD1	2.953
5XJ3	G_ARG_67	NH2	G_ASP_90	OD2	2.607
5XJ3	G_ARG_87	NH1	G_GLU_89	OE2	3.758
5XJ3	G_ARG_98	NH1	G_ASP_106	OD2	3.240
5XJ3	H_ARG_55	NH1	H_ASP_61	OD1	2.456
5XJ3	H_ARG_62	NH2	H_GLU_82	OE2	3.013
5XJ3	H_ARG_62	NH2	H_ASP_83	OD1	3.165
5XJ3	H_LYS_104	NZ	H_GLU_106	OE1	3.016
5XJ3	I_LYS_130	NZ	I_GLU_132	OE1	3.959
5XJ3	J_ARG_38	NH1	J_ASP_90	OD1	3.001
5XJ3	J_ARG_38	NH2	J_GLU_46	OE1	3.663
5XJ3	J_ARG_38	NH2	J_GLU_46	OE2	3.259
5XJ3	J_ARG_38	NH2	J_GLU_89	OE1	3.925
5XJ3	J_ARG_67	NH1	J_GLU_89	OE2	3.761
5XJ3	J_ARG_67	NH2	J_ASP_90	OD1	3.129
5XJ3	J_ARG_67	NH2	J_ASP_90	OD2	2.474
5XJ3	J_ARG_87	NH1	J_GLU_89	OE2	3.928
5XJ3	J_ARG_98	NH1	J_ASP_106	OD2	3.259
5XJ3	K_ARG_55	NH1	K_ASP_61	OD1	2.399
5XJ3	K_ARG_55	NH2	K_ASP_61	OD1	3.996
5XJ3	K_ARG_62	NH2	K_GLU_82	OE2	2.984
5XJ3	K_ARG_62	NH2	K_ASP_83	OD1	3.334
5XJ3	K_LYS_104	NZ	K_GLU_106	OE1	2.971
5XJ3	L_LYS_130	NZ	L_GLU_132	OE1	3.881

Table 763: 5XJ3-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5XRT	A_LYS_27	NZ	B_GLU_97	OE2	3.178
5XRT	A_ARG_50	NH1	A_ASP_275	OD1	3.489
5XRT	A_HIS_75	ND1	A_ASP_73	OD1	2.934
5XRT	A_HIS_75	ND1	A_ASP_73	OD2	3.817
5XRT	A_ARG_90	NH2	A_ASP_60	OD1	3.541
5XRT	A_ARG_90	NH2	A_ASP_60	OD2	3.101
5XRT	A_ARG_109	NH1	B_GLU_67	OE2	3.059
5XRT	A_ARG_109	NH2	A_GLU_89	OE1	3.449
5XRT	A_ARG_109	NH2	B_GLU_67	OE2	3.511
5XRT	A_ARG_141	NH1	A_ASP_77	OD1	3.404
5XRT	A_ARG_141	NH1	A_ASP_77	OD2	2.369
5XRT	A_LYS_176	NZ	A_GLU_123	OE1	3.717
5XRT	A_LYS_176	NZ	A_GLU_123	OE2	2.851
5XRT	A_LYS_238	NZ	F_GLU_72	OE1	3.452
5XRT	A_LYS_238	NZ	F_GLU_72	OE2	2.683
5XRT	A_ARG_255	NH1	A_ASP_133	OD2	3.443
5XRT	A_ARG_255	NH2	A_ASP_133	OD2	3.614
5XRT	A_ARG_269	NH1	B_GLU_67	OE1	3.465
5XRT	A_LYS_292	NZ	A_ASP_291	OD2	3.086
5XRT	A_ARG_307	NH1	F_ASP_90	OD2	3.867
5XRT	A_ARG_307	NH2	F_ASP_90	OD2	3.590
5XRT	A_LYS_310	NZ	B_ASP_90	OD1	2.844
5XRT	A_LYS_315	NZ	A_GLU_41	OE1	3.734
5XRT	A_LYS_326	NZ	B_GLU_11	OE1	2.808
5XRT	A_LYS_326	NZ	B_GLU_11	OE2	2.925
5XRT	B_LYS_51	NZ	B_GLU_103	OE1	3.416
5XRT	B_ARG_54	NH1	F_GLU_97	OE2	3.836
5XRT	B_ARG_54	NH2	F_GLU_97	OE2	2.767
5XRT	B_LYS_62	NZ	F_ASP_86	OD1	3.336
5XRT	B_LYS_62	NZ	F_ASP_86	OD2	2.617
5XRT	B_LYS_62	NZ	F_ASP_90	OD1	3.654
5XRT	B_LYS_62	NZ	F_ASP_90	OD2	2.589
5XRT	B_HIS_64	NE2	F_ASP_79	OD2	3.582
5XRT	B_LYS_68	NZ	B_GLU_85	OE1	3.082
5XRT	B_LYS_68	NZ	B_GLU_85	OE2	2.799
5XRT	B_ARG_76	NH1	D_GLU_74	OE1	3.704
5XRT	B_ARG_76	NH1	D_GLU_74	OE2	3.032
5XRT	B_ARG_76	NH2	D_GLU_74	OE1	2.984
5XRT	B_ARG_76	NH2	D_GLU_74	OE2	3.801
5XRT	B_ARG_76	NH2	D_GLU_81	OE1	2.864
5XRT	B_ARG_76	NH2	D_GLU_81	OE2	3.722
5XRT	B_LYS_117	NZ	B_GLU_114	OE2	3.280
5XRT	B_ARG_121	NH2	B_ASP_37	OD2	3.079
5XRT	B_ARG_123	NH1	B_GLU_120	OE1	2.622
5XRT	B_ARG_123	NH1	B_GLU_120	OE2	3.886
5XRT	B_ARG_123	NH2	B_GLU_120	OE1	3.456
5XRT	B_ARG_123	NH2	F_ASP_132	OD2	3.663
5XRT	B_ARG_124	NH1	F_ASP_132	OD2	2.812
5XRT	B_ARG_127	NH2	F_GLU_131	OE1	3.103
5XRT	B_ARG_163	NH1	F_GLU_131	OE1	3.194
5XRT	B_ARG_163	NH1	F_GLU_131	OE2	3.563
5XRT	B_ARG_163	NH2	F_GLU_131	OE1	3.596
5XRT	B_ARG_163	NH2	F_GLU_131	OE2	2.598
5XRT	B_ARG_170	NH1	B_GLU_128	OE2	3.435
5XRT	B_ARG_170	NH2	B_GLU_131	OE2	3.245
5XRT	B_ARG_170	NH2	D_GLU_128	OE1	3.449
5XRT	B_ARG_170	NH2	D_GLU_128	OE2	3.578

5XRT	C_LYS_27	NZ	D_GLU_97	OE1	3.926
5XRT	C_LYS_27	NZ	D_GLU_97	OE2	3.340
5XRT	C_HIS_56	NE2	C_GLU_280	OE1	3.939
5XRT	C_HIS_75	ND1	C_ASP_73	OD1	2.939
5XRT	C_HIS_75	ND1	C_ASP_73	OD2	3.672
5XRT	C_ARG_90	NH2	C_ASP_60	OD1	3.078
5XRT	C_ARG_90	NH2	C_ASP_60	OD2	2.971
5XRT	C_ARG_109	NH1	D_GLU_67	OE2	2.932
5XRT	C_ARG_109	NH2	C_GLU_89	OE1	3.101
5XRT	C_ARG_141	NH2	C_ASP_77	OD1	3.277
5XRT	C_ARG_141	NH2	C_ASP_77	OD2	3.129
5XRT	C_LYS_176	NZ	C_GLU_123	OE2	3.009
5XRT	C_LYS_238	NZ	B_GLU_72	OE2	3.031
5XRT	C_ARG_255	NH1	C_ASP_133	OD1	3.530
5XRT	C_ARG_255	NH2	C_ASP_133	OD1	3.274
5XRT	C_ARG_269	NH1	D_GLU_67	OE1	3.251
5XRT	C_LYS_292	NZ	C_ASP_291	OD1	3.150
5XRT	C_ARG_307	NH2	B_ASP_90	OD2	3.134
5XRT	C_LYS_310	NZ	D_ASP_90	OD1	3.206
5XRT	C_LYS_310	NZ	D_ASP_90	OD2	3.892
5XRT	D_LYS_51	NZ	D_GLU_103	OE1	3.086
5XRT	D_ARG_54	NH2	B_GLU_97	OE2	3.066
5XRT	D_LYS_62	NZ	B_ASP_86	OD1	3.579
5XRT	D_LYS_62	NZ	B_ASP_86	OD2	3.058
5XRT	D_LYS_62	NZ	B_ASP_90	OD1	3.574
5XRT	D_LYS_62	NZ	B_ASP_90	OD2	2.797
5XRT	D_HIS_64	NE2	B_ASP_79	OD2	3.856
5XRT	D_LYS_68	NZ	D_GLU_85	OE1	3.229
5XRT	D_LYS_68	NZ	D_GLU_85	OE2	3.297
5XRT	D_ARG_76	NH1	F_GLU_74	OE1	3.338
5XRT	D_ARG_76	NH1	F_GLU_74	OE2	2.885
5XRT	D_ARG_76	NH2	F_GLU_74	OE1	2.652
5XRT	D_ARG_76	NH2	F_GLU_74	OE2	3.749
5XRT	D_ARG_76	NH2	F_GLU_81	OE1	2.506
5XRT	D_ARG_76	NH2	F_GLU_81	OE2	3.677
5XRT	D_LYS_117	NZ	D_GLU_114	OE2	2.877
5XRT	D_ARG_121	NH1	D_ASP_37	OD2	3.944
5XRT	D_ARG_121	NH2	D_ASP_37	OD1	3.995
5XRT	D_ARG_121	NH2	D_ASP_37	OD2	3.020
5XRT	D_ARG_123	NH1	D_GLU_120	OE1	2.708
5XRT	D_ARG_123	NH1	D_GLU_120	OE2	3.830
5XRT	D_ARG_123	NH2	B_ASP_132	OD2	3.975
5XRT	D_ARG_123	NH2	D_GLU_120	OE1	3.166
5XRT	D_ARG_124	NH1	B_ASP_132	OD1	3.986
5XRT	D_ARG_124	NH1	B_ASP_132	OD2	2.717
5XRT	D_ARG_127	NH2	B_GLU_131	OE1	2.649
5XRT	D_HIS_159	NE2	D_ASP_160	OD1	3.798
5XRT	D_HIS_159	NE2	D_ASP_160	OD2	3.813
5XRT	D_ARG_163	NH1	B_GLU_131	OE1	3.152
5XRT	D_ARG_163	NH1	B_GLU_131	OE2	3.070
5XRT	D_ARG_163	NH2	B_GLU_131	OE1	3.267
5XRT	D_ARG_163	NH2	B_GLU_131	OE2	2.951
5XRT	D_ARG_170	NH1	D_GLU_128	OE2	3.582
5XRT	D_ARG_170	NH2	D_GLU_131	OE2	3.591
5XRT	D_ARG_170	NH2	F_GLU_128	OE1	2.950
5XRT	D_ARG_170	NH2	F_GLU_128	OE2	3.791
5XRT	E_LYS_27	NZ	F_GLU_97	OE1	3.896
5XRT	E_LYS_27	NZ	F_GLU_97	OE2	3.675

5XRT	E_ARG_50	NH1	E_ASP_275	OD1	3.578
5XRT	E_HIS_56	NE2	E_GLU_280	OE1	3.346
5XRT	E_HIS_75	ND1	E_ASP_73	OD1	2.764
5XRT	E_ARG_90	NH2	E_ASP_60	OD1	3.458
5XRT	E_ARG_90	NH2	E_ASP_60	OD2	2.922
5XRT	E_ARG_109	NH1	F_GLU_67	OE2	2.719
5XRT	E_ARG_109	NH2	E_GLU_89	OE1	3.357
5XRT	E_ARG_109	NH2	F_GLU_67	OE2	3.732
5XRT	E_ARG_141	NH2	E_ASP_77	OD1	3.300
5XRT	E_ARG_141	NH2	E_ASP_77	OD2	3.765
5XRT	E_LYS_176	NZ	E_GLU_123	OE2	3.077
5XRT	E_LYS_238	NZ	D_GLU_72	OE2	3.742
5XRT	E_LYS_238	NZ	E_ASP_175	OD2	3.711
5XRT	E_ARG_255	NH1	E_ASP_133	OD1	2.710
5XRT	E_ARG_269	NH1	F_GLU_67	OE1	2.954
5XRT	E_ARG_269	NH1	F_GLU_67	OE2	3.996
5XRT	E_LYS_292	NZ	E_ASP_291	OD1	3.378
5XRT	E_ARG_307	NH1	D_ASP_90	OD2	3.580
5XRT	E_ARG_307	NH2	D_ASP_90	OD2	3.837
5XRT	E_LYS_310	NZ	F_ASP_90	OD1	3.115
5XRT	E_LYS_326	NZ	F_GLU_11	OE1	3.300
5XRT	F_LYS_51	NZ	F_GLU_103	OE1	3.279
5XRT	F_ARG_54	NH2	D_GLU_97	OE2	3.005
5XRT	F_LYS_62	NZ	D_ASP_86	OD1	3.549
5XRT	F_LYS_62	NZ	D_ASP_86	OD2	2.499
5XRT	F_LYS_62	NZ	D_ASP_90	OD1	3.666
5XRT	F_LYS_62	NZ	D_ASP_90	OD2	2.972
5XRT	F_HIS_64	NE2	D_ASP_79	OD2	3.194
5XRT	F_LYS_68	NZ	F_GLU_85	OE1	3.860
5XRT	F_LYS_68	NZ	F_GLU_85	OE2	3.605
5XRT	F_ARG_76	NH1	B_GLU_74	OE1	3.311
5XRT	F_ARG_76	NH1	B_GLU_74	OE2	3.105
5XRT	F_ARG_76	NH2	B_GLU_74	OE1	2.768
5XRT	F_ARG_76	NH2	B_GLU_74	OE2	3.989
5XRT	F_ARG_76	NH2	B_GLU_81	OE1	2.869
5XRT	F_ARG_76	NH2	B_GLU_81	OE2	3.812
5XRT	F_LYS_117	NZ	F_GLU_114	OE2	3.321
5XRT	F_ARG_121	NH2	F_ASP_37	OD2	3.444
5XRT	F_ARG_123	NH1	F_GLU_120	OE1	2.902
5XRT	F_ARG_123	NH1	F_GLU_120	OE2	2.669
5XRT	F_ARG_123	NH2	F_GLU_120	OE1	2.949
5XRT	F_ARG_124	NH1	D_ASP_132	OD2	3.024
5XRT	F_ARG_127	NH2	D_GLU_131	OE1	2.415
5XRT	F_HIS_159	ND1	F_ASP_160	OD1	3.993
5XRT	F_HIS_159	NE2	F_ASP_160	OD1	2.911
5XRT	F_ARG_163	NH1	D_GLU_131	OE1	3.516
5XRT	F_ARG_163	NH2	D_GLU_131	OE1	3.296
5XRT	F_ARG_163	NH2	D_GLU_131	OE2	2.611
5XRT	F_ARG_170	NH1	F_GLU_128	OE2	3.390
5XRT	F_ARG_170	NH2	B_GLU_128	OE1	3.475
5XRT	F_ARG_170	NH2	B_GLU_128	OE2	3.657
5XRT	F_ARG_170	NH2	F_GLU_128	OE2	3.860
5XRT	F_ARG_170	NH2	F_GLU_131	OE2	3.345
5XRT	F_LYS_174	NZ	B_ASP_160	OD1	3.902
5XRT	G_LYS_27	NZ	H_GLU_97	OE2	3.228
5XRT	G_ARG_50	NH1	G_ASP_275	OD1	3.487
5XRT	G_HIS_56	NE2	G_GLU_280	OE1	3.893
5XRT	G_HIS_75	ND1	G_ASP_73	OD1	2.567

5XRT	G_HIS_75	ND1	G_ASP_73	OD2	3.814
5XRT	G_LYS_82	NZ	E_GLU_119	OE1	3.805
5XRT	G_ARG_90	NH2	G_ASP_60	OD1	3.337
5XRT	G_ARG_90	NH2	G_ASP_60	OD2	3.035
5XRT	G_ARG_109	NH1	H_GLU_67	OE1	3.826
5XRT	G_ARG_109	NH1	H_GLU_67	OE2	2.804
5XRT	G_ARG_109	NH2	G_GLU_89	OE1	2.924
5XRT	G_ARG_141	NH2	G_ASP_77	OD1	3.443
5XRT	G_ARG_141	NH2	G_ASP_77	OD2	3.249
5XRT	G_LYS_176	NZ	G_GLU_123	OE2	3.413
5XRT	G_LYS_176	NZ	G_ASP_172	OD2	3.797
5XRT	G_LYS_238	NZ	G_ASP_175	OD1	3.036
5XRT	G_LYS_238	NZ	G_ASP_175	OD2	3.186
5XRT	G_ARG_255	NH1	G_ASP_133	OD2	3.599
5XRT	G_ARG_255	NH2	G_ASP_133	OD2	3.335
5XRT	G_ARG_269	NH1	H_GLU_67	OE1	3.306
5XRT	G_LYS_292	NZ	G_ASP_291	OD1	3.807
5XRT	G_LYS_292	NZ	G_ASP_291	OD2	3.964
5XRT	G_LYS_299	NZ	H_GLU_69	OE2	3.918
5XRT	G_LYS_310	NZ	H_ASP_90	OD1	2.955
5XRT	H_LYS_51	NZ	H_GLU_103	OE1	3.120
5XRT	H_LYS_68	NZ	H_GLU_85	OE1	3.706
5XRT	H_LYS_68	NZ	H_GLU_85	OE2	3.564
5XRT	H_LYS_117	NZ	H_GLU_114	OE2	3.149
5XRT	H_ARG_121	NH2	H_ASP_37	OD2	3.626
5XRT	H_ARG_123	NH1	H_GLU_120	OE1	3.412
5XRT	H_ARG_170	NH2	H_GLU_131	OE2	3.622

Table 764: 5XRT-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5XWD	A_ARG_48	NH1	A_GLU_73	OE2	3.630
5XWD	A_ARG_74	NH1	A_GLU_110	OE1	2.554
5XWD	A_ARG_74	NH1	A_GLU_110	OE2	3.566
5XWD	A_ARG_74	NH2	A_GLU_78	OE2	2.523
5XWD	A_ARG_84	NH2	A_GLU_60	OE1	3.684
5XWD	A_ARG_84	NH2	A_GLU_60	OE2	3.617
5XWD	A_ARG_114	NH1	A_GLU_78	OE1	3.452
5XWD	A_ARG_114	NH2	A_GLU_78	OE1	2.694
5XWD	A_ARG_198	NH1	A_ASP_142	OD2	3.491
5XWD	A_ARG_198	NH2	A_GLU_118	OE2	3.197
5XWD	A_ARG_220	NH1	A_GLU_221	OE1	3.463
5XWD	A_ARG_220	NH1	A_GLU_221	OE2	2.447
5XWD	A_ARG_220	NH2	A_GLU_221	OE2	3.674
5XWD	A_ARG_228	NH1	A_GLU_118	OE2	3.743
5XWD	A_ARG_228	NH2	A_GLU_118	OE2	3.666
5XWD	A_LYS_237	NZ	A_ASP_232	OD2	2.616
5XWD	A_LYS_260	NZ	A_ASP_232	OD1	2.521
5XWD	A_LYS_260	NZ	A_ASP_232	OD2	3.550
5XWD	A_LYS_260	NZ	A_GLU_233	OE2	3.396
5XWD	A_LYS_301	NZ	A_GLU_296	OE1	3.844
5XWD	A_LYS_303	NZ	A_GLU_296	OE2	3.546
5XWD	A_LYS_333	NZ	A_GLU_367	OE2	3.373
5XWD	A_ARG_353	NH2	D_ASP_96	OD2	3.335
5XWD	A_LYS_372	NZ	A_GLU_397	OE2	3.502
5XWD	A_ARG_390	NH1	A_ASP_369	OD1	3.207
5XWD	A_HIS_394	ND1	A_ASP_369	OD1	3.398
5XWD	A_HIS_394	NE2	A_GLU_397	OE2	3.209
5XWD	A_ARG_403	NH2	A_GLU_376	OE2	3.449
5XWD	A_LYS_407	NZ	A_ASP_434	OD2	3.832
5XWD	A_HIS_409	NE2	H_ASP_108	OD2	2.707
5XWD	A_ARG_427	NH1	A_ASP_498	OD1	2.268
5XWD	A_ARG_427	NH1	A_ASP_498	OD2	3.446
5XWD	A_ARG_427	NH2	A_ASP_392	OD2	3.547
5XWD	A_LYS_443	NZ	D_ASP_51	OD2	2.907
5XWD	A_LYS_455	NZ	A_GLU_489	OE1	2.906
5XWD	A_LYS_463	NZ	A_ASP_436	OD2	2.868
5XWD	A_LYS_465	NZ	D_ASP_53	OD2	3.314
5XWD	A_ARG_497	NH2	A_GLU_510	OE1	3.595
5XWD	A_ARG_507	NH1	A_GLU_524	OE1	3.565
5XWD	A_ARG_507	NH1	A_GLU_524	OE2	2.365
5XWD	A_ARG_550	NH2	A_GLU_527	OE2	2.299
5XWD	A_HIS_560	ND1	A_GLU_537	OE1	2.920
5XWD	A_HIS_560	ND1	A_GLU_537	OE2	3.490
5XWD	A_HIS_566	NE2	A_ASP_553	OD1	3.274
5XWD	A_HIS_566	NE2	A_ASP_553	OD2	3.788
5XWD	A_LYS_585	NZ	A_ASP_563	OD1	2.730
5XWD	A_LYS_585	NZ	A_ASP_563	OD2	3.880
5XWD	H_ARG_40	NH1	H_ASP_91	OD1	2.811
5XWD	H_ARG_40	NH2	H_GLU_48	OE1	3.427
5XWD	H_ARG_40	NH2	H_GLU_48	OE2	3.173
5XWD	H_ARG_40	NH2	H_ASP_91	OD1	3.631
5XWD	H_ARG_68	NH1	H_ASP_91	OD1	3.454
5XWD	H_ARG_68	NH1	H_ASP_91	OD2	3.334
5XWD	H_ARG_68	NH2	H_ASP_91	OD2	3.355
5XWD	H_ARG_99	NH1	H_ASP_108	OD2	3.765
5XWD	D_ARG_54	NH2	D_GLU_60	OE2	3.951
5XWD	D_ARG_61	NH1	D_GLU_79	OE2	3.685

5XWD	D_ARG_61	NH2	D_ASP_82	OD1	3.092
5XWD	D_ARG_61	NH2	D_ASP_82	OD2	2.961

Table 765: 5XWD-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5YC5	A_LYS_248	NZ	A_GLU_380	OE1	3.797
5YC5	A_LYS_248	NZ	A_GLU_380	OE2	2.893
5YC5	A_ARG_255	NH2	A_ASP_249	OD2	2.780
5YC5	A_HIS_268	NE2	A_GLU_294	OE1	3.378
5YC5	A_LYS_317	NZ	A_ASP_312	OD1	3.804
5YC5	A_LYS_320	NZ	A_GLU_333	OE1	3.131
5YC5	A_LYS_320	NZ	A_GLU_333	OE2	3.746
5YC5	A_LYS_322	NZ	A_GLU_333	OE2	3.405
5YC5	A_LYS_338	NZ	A_GLU_430	OE1	3.617
5YC5	A_LYS_338	NZ	A_GLU_430	OE2	3.041
5YC5	A_LYS_340	NZ	A_GLU_318	OE2	3.537
5YC5	A_ARG_344	NH2	A_ASP_401	OD1	3.750
5YC5	A_ARG_344	NH2	A_ASP_401	OD2	3.122
5YC5	A_LYS_409	NZ	B_ASP_399	OD1	3.635
5YC5	A_LYS_409	NZ	B_ASP_399	OD2	2.875
5YC5	A_ARG_416	NH1	A_GLU_388	OE1	3.188
5YC5	A_ARG_416	NH1	A_GLU_388	OE2	3.570
5YC5	A_ARG_416	NH2	A_GLU_388	OE2	2.991
5YC5	A_LYS_439	NZ	B_ASP_356	OD1	3.309
5YC5	B_LYS_248	NZ	B_GLU_380	OE1	3.889
5YC5	B_LYS_248	NZ	B_GLU_380	OE2	2.644
5YC5	B_ARG_255	NH2	B_ASP_249	OD1	3.838
5YC5	B_HIS_268	NE2	B_GLU_294	OE1	2.811
5YC5	B_HIS_268	NE2	B_GLU_294	OE2	3.075
5YC5	B_HIS_285	ND1	B_GLU_283	OE2	3.786
5YC5	B_LYS_317	NZ	B_ASP_312	OD1	3.231
5YC5	B_LYS_320	NZ	B_GLU_333	OE1	3.707
5YC5	B_LYS_338	NZ	B_GLU_430	OE1	3.390
5YC5	B_LYS_338	NZ	B_GLU_430	OE2	3.171
5YC5	B_LYS_340	NZ	B_GLU_318	OE2	3.467
5YC5	B_ARG_344	NH2	B_ASP_401	OD1	3.756
5YC5	B_ARG_344	NH2	B_ASP_401	OD2	2.965
5YC5	B_LYS_409	NZ	A_ASP_399	OD1	3.731
5YC5	B_LYS_409	NZ	A_ASP_399	OD2	2.920
5YC5	B_ARG_416	NH1	B_GLU_388	OE1	2.764
5YC5	B_ARG_416	NH1	B_GLU_388	OE2	3.921
5YC5	B_ARG_416	NH2	B_GLU_388	OE1	3.687
5YC5	C_LYS_7	NZ	C_ASP_80	OD1	3.624
5YC5	C_LYS_7	NZ	C_ASP_80	OD2	3.128
5YC5	C_ARG_18	NH1	C_GLU_85	OE1	3.674
5YC5	C_HIS_87	ND1	C_GLU_166	OE1	3.687
5YC5	C_HIS_87	ND1	C_GLU_166	OE2	2.703
5YC5	C_HIS_87	NE2	C_GLU_85	OE1	3.071
5YC5	C_ARG_97	NH2	C_ASP_104	OD2	3.100
5YC5	C_HIS_107	NE2	C_ASP_138	OD2	2.605
5YC5	C_HIS_111	NE2	C_ASP_23	OD1	2.779
5YC5	C_HIS_111	NE2	C_ASP_23	OD2	2.823
5YC5	C_LYS_120	NZ	A_ASP_265	OD2	2.563
5YC5	C_ARG_130	NH1	C_ASP_148	OD1	3.773
5YC5	C_ARG_130	NH2	C_ASP_148	OD1	3.062
5YC5	C_LYS_131	NZ	A_GLU_269	OE1	3.549
5YC5	C_LYS_131	NZ	A_GLU_269	OE2	2.940

Table 766: 5YC5-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5ZV3	A.LYS_67	NZ	H.ASP_54	OD1	3.656
5ZV3	A.LYS_67	NZ	H.ASP_54	OD2	2.636
5ZV3	A.LYS_67	NZ	H.ASP_56	OD2	3.213
5ZV3	H.LYS_12	NZ	H.GLU_16	OE1	3.523
5ZV3	H.ARG_38	NH2	H.GLU_46	OE1	3.368
5ZV3	H.ARG_38	NH2	H.GLU_46	OE2	2.729
5ZV3	H.ARG_58	NH1	H.ASP_56	OD1	3.153
5ZV3	H.ARG_58	NH1	H.ASP_56	OD2	2.840
5ZV3	H.ARG_58	NH2	A.ASP_65	OD1	3.187
5ZV3	H.ARG_58	NH2	H.ASP_56	OD2	3.078
5ZV3	H.ARG_97	NH1	A.GLU_62	OE2	3.412
5ZV3	H.ARG_97	NH2	A.GLU_62	OE1	3.676
5ZV3	H.ARG_97	NH2	A.GLU_62	OE2	3.134
5ZV3	H.LYS_100	NZ	A.GLU_62	OE1	2.715
5ZV3	H.LYS_143	NZ	H.ASP_144	OD1	3.086
5ZV3	H.LYS_143	NZ	H.ASP_144	OD2	2.913
5ZV3	H.LYS_206	NZ	H.ASP_208	OD1	2.838
5ZV3	H.LYS_206	NZ	H.ASP_208	OD2	3.804
5ZV3	H.LYS_209	NZ	L.GLU_123	OE1	3.860
5ZV3	L.ARG_61	NH2	L.GLU_81	OE1	3.640
5ZV3	L.ARG_61	NH2	L.GLU_81	OE2	2.887
5ZV3	L.ARG_61	NH2	L.ASP_82	OD1	2.840
5ZV3	L.ARG_61	NH2	L.ASP_82	OD2	3.594
5ZV3	L.LYS_149	NZ	L.GLU_195	OE1	3.451
5ZV3	L.LYS_149	NZ	L.GLU_195	OE2	3.726
5ZV3	L.LYS_169	NZ	L.ASP_167	OD1	3.271
5ZV3	L.LYS_169	NZ	L.ASP_167	OD2	2.906
5ZV3	L.LYS_169	NZ	L.ASP_170	OD2	3.903
5ZV3	L.LYS_183	NZ	L.GLU_187	OE1	3.966
5ZV3	L.LYS_183	NZ	L.GLU_187	OE2	3.971
5ZV3	L.LYS_188	NZ	L.ASP_185	OD1	3.915

Table 767: 5ZV3-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6A3V	A_ARG_211	NH1	A_GLU_132	OE1	3.731
6A3V	A_HIS_217	ND1	A_ASP_104	OD2	2.707
6A3V	A_HIS_217	NE2	A_GLU_219	OE2	3.407
6A3V	A_ARG_223	NH1	A_ASP_104	OD1	3.394
6A3V	B_ARG_41	NH2	B_ASP_38	OD2	2.943
6A3V	B_ARG_75	NH2	B_ASP_87	OD2	2.598
6A3V	B_HIS_93	ND1	B_ASP_105	OD1	3.013
6A3V	B_HIS_93	NE2	B_GLU_103	OE1	3.252
6A3V	B_ARG_130	NH1	B_ASP_105	OD2	2.750
6A3V	B_ARG_130	NH2	B_ASP_105	OD2	3.837
6A3V	C_ARG_223	NH1	C_ASP_104	OD2	3.845
6A3V	C_ARG_223	NH2	C_ASP_104	OD2	3.259
6A3V	C_HIS_224	NE2	C_GLU_156	OE1	3.858
6A3V	D_ARG_41	NH2	D_ASP_38	OD2	3.204
6A3V	D_ARG_73	NH1	D_ASP_87	OD1	3.159
6A3V	D_ARG_73	NH2	D_ASP_87	OD1	3.076
6A3V	D_LYS_76	NZ	D_GLU_85	OE2	3.594
6A3V	D_HIS_93	NE2	D_GLU_103	OE1	3.727
6A3V	D_LYS_129	NZ	D_ASP_105	OD2	3.162
6A3V	D_ARG_130	NH1	D_ASP_105	OD2	3.228
6A3V	D_LYS_152	NZ	D_ASP_119	OD2	3.272
6A3V	E_ARG_193	NH1	C_ASP_184	OD1	3.333
6A3V	E_ARG_211	NH1	E_GLU_132	OE1	3.556
6A3V	E_HIS_217	ND1	E_ASP_104	OD2	3.184
6A3V	E_HIS_217	NE2	E_GLU_219	OE2	3.906
6A3V	E_HIS_224	NE2	E_GLU_156	OE1	3.569
6A3V	F_ARG_75	NH2	F_ASP_87	OD2	2.816
6A3V	F_HIS_93	NE2	F_GLU_103	OE1	3.902
6A3V	F_LYS_118	NZ	F_GLU_111	OE2	3.173
6A3V	F_ARG_130	NH1	F_ASP_105	OD2	3.184
6A3V	F_ARG_130	NH2	F_ASP_105	OD2	3.490
6A3V	F_LYS_152	NZ	F_ASP_119	OD2	3.307
6A3V	G_ARG_211	NH1	G_GLU_132	OE1	3.434
6A3V	G_HIS_217	ND1	G_ASP_104	OD2	2.526
6A3V	G_ARG_223	NH1	G_ASP_104	OD1	3.210
6A3V	G_ARG_223	NH2	G_ASP_104	OD1	3.429
6A3V	G_ARG_239	NH2	G_GLU_243	OE1	3.944
6A3V	H_ARG_75	NH2	H_ASP_87	OD1	3.886
6A3V	H_ARG_75	NH2	H_ASP_87	OD2	3.340
6A3V	H_HIS_93	NE2	H_ASP_105	OD1	4.000
6A3V	I_ARG_193	NH1	K_ASP_184	OD1	3.791
6A3V	I_ARG_211	NH1	I_GLU_132	OE1	3.418
6A3V	I_ARG_211	NH2	I_GLU_132	OE1	3.588
6A3V	I_HIS_217	ND1	I_ASP_104	OD2	3.427
6A3V	I_ARG_223	NH1	I_ASP_104	OD1	3.086
6A3V	I_ARG_223	NH2	I_ASP_104	OD1	3.348
6A3V	I_ARG_223	NH2	I_ASP_104	OD2	3.799
6A3V	I_HIS_224	ND1	I_GLU_156	OE1	3.995
6A3V	J_ARG_73	NH1	J_ASP_87	OD2	3.305
6A3V	J_ARG_75	NH1	J_GLU_85	OE1	2.939
6A3V	J_ARG_75	NH1	J_GLU_85	OE2	3.776
6A3V	J_HIS_93	NE2	J_GLU_103	OE1	3.602
6A3V	J_LYS_129	NZ	J_ASP_105	OD2	3.649
6A3V	J_LYS_152	NZ	J_ASP_119	OD2	3.759
6A3V	K_ARG_211	NH1	K_GLU_132	OE1	3.841
6A3V	K_ARG_211	NH2	K_GLU_132	OE1	3.828
6A3V	K_HIS_217	ND1	K_ASP_104	OD2	3.054

6A3V	K_HIS_217	NE2	K_GLU_219	OE2	3.795
6A3V	K_ARG_223	NH1	K_ASP_104	OD1	3.294
6A3V	K_ARG_223	NH2	K_ASP_104	OD1	2.971
6A3V	K_ARG_223	NH2	K_ASP_104	OD2	3.952
6A3V	K_HIS_224	NE2	K_GLU_156	OE1	2.347
6A3V	K_ARG_239	NH1	K_GLU_243	OE1	3.687
6A3V	K_ARG_239	NH2	K_GLU_243	OE1	3.100
6A3V	L_ARG_41	NH2	L_ASP_38	OD2	2.939
6A3V	L_ARG_75	NH2	L_ASP_87	OD1	3.204
6A3V	L_ARG_75	NH2	L_ASP_87	OD2	2.988
6A3V	L_HIS_93	ND1	L_ASP_105	OD1	3.521
6A3V	L_LYS_118	NZ	L_GLU_111	OE1	3.470
6A3V	L_ARG_130	NH1	L_ASP_105	OD2	2.982
6A3V	M_ARG_211	NH1	M_GLU_132	OE1	3.246
6A3V	M_ARG_211	NH2	M_GLU_132	OE1	3.377
6A3V	M_HIS_217	ND1	M_ASP_104	OD2	3.857
6A3V	M_HIS_217	NE2	M_GLU_219	OE2	3.798
6A3V	M_ARG_223	NH2	M_ASP_104	OD1	3.607
6A3V	M_HIS_224	NE2	M_GLU_156	OE1	2.966
6A3V	N_ARG_41	NH1	N_ASP_38	OD2	3.719
6A3V	N_ARG_41	NH2	N_ASP_38	OD2	3.742
6A3V	N_ARG_73	NH1	N_ASP_87	OD2	3.095
6A3V	N_ARG_73	NH2	N_ASP_87	OD2	3.858
6A3V	N_HIS_93	NE2	N_GLU_103	OE1	3.849
6A3V	N_ARG_130	NH1	N_ASP_105	OD2	3.648
6A3V	N_LYS_144	NZ	N_ASP_142	OD2	3.634
6A3V	O_ARG_211	NH1	O_GLU_132	OE1	3.603
6A3V	O_HIS_217	NE2	O_ASP_104	OD2	3.976
6A3V	O_ARG_223	NH2	O_ASP_104	OD1	3.679
6A3V	P_ARG_41	NH1	P_ASP_38	OD2	3.282
6A3V	P_ARG_75	NH2	P_ASP_87	OD2	3.792
6A3V	P_LYS_118	NZ	P_GLU_111	OE1	3.659
6A3V	Q_ARG_211	NH1	Q_GLU_132	OE1	3.475
6A3V	Q_HIS_217	ND1	Q_ASP_104	OD2	2.963
6A3V	Q_ARG_223	NH1	Q_ASP_104	OD1	2.976
6A3V	Q_HIS_224	NE2	Q_GLU_156	OE1	3.942
6A3V	R_HIS_93	NE2	R_GLU_103	OE1	3.672
6A3V	R_LYS_118	NZ	R_GLU_111	OE1	3.192
6A3V	R_ARG_130	NH1	R_ASP_105	OD2	3.502
6A3V	S_ARG_211	NH2	S_GLU_132	OE1	3.631
6A3V	S_HIS_217	ND1	S_ASP_104	OD2	2.703
6A3V	S_HIS_217	NE2	S_GLU_219	OE2	3.257
6A3V	S_ARG_223	NH1	S_ASP_104	OD1	3.253
6A3V	S_HIS_224	NE2	S_GLU_156	OE1	3.213
6A3V	T_ARG_73	NH1	T_ASP_87	OD2	2.770
6A3V	T_ARG_73	NH2	T_ASP_87	OD2	3.434
6A3V	T_ARG_75	NH2	T_ASP_87	OD2	3.502
6A3V	T_ARG_130	NH1	T_ASP_105	OD2	3.621
6A3V	T_LYS_152	NZ	T_ASP_119	OD2	3.864
6A3V	U_ARG_193	NH1	W_ASP_184	OD1	2.218
6A3V	U_ARG_193	NH1	W_ASP_184	OD2	3.282
6A3V	U_ARG_193	NH2	W_ASP_184	OD1	3.966
6A3V	U_ARG_193	NH2	W_ASP_184	OD2	3.892
6A3V	U_HIS_217	ND1	U_ASP_104	OD2	2.618
6A3V	U_HIS_217	NE2	U_GLU_219	OE2	3.783
6A3V	U_ARG_223	NH1	U_ASP_104	OD1	2.826
6A3V	U_ARG_223	NH2	U_ASP_104	OD1	3.610
6A3V	U_ARG_223	NH2	U_ASP_104	OD2	3.971

6A3V	U_ARG_239	NH2	U_GLU_243	OE1	3.949
6A3V	V_ARG_41	NH1	V_ASP_38	OD2	3.081
6A3V	V_ARG_41	NH2	V_ASP_38	OD2	3.046
6A3V	V_ARG_73	NH2	V_ASP_87	OD2	3.990
6A3V	V_ARG_75	NH1	V_GLU_85	OE1	3.013
6A3V	V_LYS_152	NZ	V_ASP_119	OD2	3.972
6A3V	W_ARG_211	NH1	W_GLU_132	OE1	3.268
6A3V	W_ARG_211	NH2	W_GLU_132	OE1	3.360
6A3V	W_HIS_217	ND1	W_ASP_104	OD2	3.170
6A3V	W_ARG_223	NH1	W_ASP_104	OD1	2.419
6A3V	W_ARG_223	NH2	W_ASP_104	OD1	3.222
6A3V	W_ARG_223	NH2	W_ASP_104	OD2	3.772
6A3V	W_HIS_224	NE2	W_GLU_156	OE1	3.235
6A3V	W_ARG_239	NH1	W_GLU_243	OE1	3.294
6A3V	W_ARG_239	NH2	W_GLU_243	OE1	3.255
6A3V	X_ARG_41	NH1	X_ASP_38	OD2	3.260
6A3V	X_ARG_75	NH2	X_ASP_87	OD1	3.736
6A3V	X_ARG_75	NH2	X_ASP_87	OD2	2.379
6A3V	X_HIS_93	NE2	X_GLU_103	OE2	3.466
6A3V	X_LYS_152	NZ	X_ASP_119	OD2	3.649

Table 768: 6A3V-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6A3W	A_LYS_12	NZ	A_GLU_16	OE1	3.967
6A3W	A_ARG_38	NH2	A_GLU_46	OE1	3.186
6A3W	A_ARG_38	NH2	A_GLU_46	OE2	3.290
6A3W	A_ARG_98	NH1	A_ASP_104	OD1	3.876
6A3W	A_ARG_98	NH1	A_ASP_104	OD2	2.660
6A3W	B_ARG_61	NH1	B_ASP_82	OD1	2.815
6A3W	B_ARG_61	NH1	B_ASP_82	OD2	3.460
6A3W	C_ARG_73	NH1	C_ASP_87	OD1	3.716
6A3W	C_ARG_73	NH1	C_ASP_87	OD2	2.737
6A3W	C_ARG_75	NH1	C_ASP_87	OD2	3.237
6A3W	C_LYS_76	NZ	C_GLU_85	OE2	3.299
6A3W	C_HIS_93	ND1	C_ASP_105	OD1	2.579
6A3W	C_HIS_93	NE2	C_GLU_103	OE1	2.951
6A3W	C_LYS_107	NZ	E_ASP_30	OD2	3.465
6A3W	C_LYS_114	NZ	B_ASP_51	OD2	2.835
6A3W	C_ARG_134	NH1	C_ASP_127	OD1	3.596
6A3W	C_ARG_134	NH2	A_ASP_55	OD2	3.122
6A3W	C_ARG_134	NH2	C_ASP_127	OD2	3.828
6A3W	C_LYS_152	NZ	C_ASP_119	OD2	3.915
6A3W	D_ARG_38	NH2	D_GLU_46	OE1	3.287
6A3W	D_ARG_38	NH2	D_GLU_46	OE2	3.072
6A3W	D_LYS_43	NZ	K_ASP_26	OD1	2.407
6A3W	D_LYS_43	NZ	K_ASP_26	OD2	3.696
6A3W	D_ARG_98	NH1	D_ASP_104	OD1	3.875
6A3W	D_ARG_98	NH1	D_ASP_104	OD2	2.630
6A3W	E_ARG_61	NH1	E_ASP_82	OD1	2.951
6A3W	E_ARG_61	NH1	E_ASP_82	OD2	3.557
6A3W	F_ARG_73	NH1	F_ASP_87	OD1	3.885
6A3W	F_ARG_75	NH1	F_GLU_85	OE2	2.970
6A3W	F_ARG_75	NH2	F_GLU_85	OE1	3.905
6A3W	F_ARG_75	NH2	F_GLU_85	OE2	2.751
6A3W	F_LYS_76	NZ	F_GLU_85	OE2	3.766
6A3W	F_HIS_93	ND1	F_ASP_105	OD1	2.524
6A3W	F_HIS_93	NE2	F_GLU_103	OE1	2.635
6A3W	F_LYS_114	NZ	E_ASP_51	OD2	2.834
6A3W	F_ARG_134	NH1	F_ASP_127	OD1	3.399
6A3W	F_ARG_134	NH1	F_ASP_127	OD2	3.721
6A3W	F_ARG_134	NH2	D_ASP_55	OD1	3.962
6A3W	F_ARG_134	NH2	D_ASP_55	OD2	2.895
6A3W	F_LYS_152	NZ	F_ASP_119	OD2	3.783
6A3W	G_ARG_38	NH2	G_GLU_46	OE1	3.389
6A3W	G_ARG_38	NH2	G_GLU_46	OE2	3.208
6A3W	G_ARG_98	NH1	G_ASP_104	OD1	3.869
6A3W	G_ARG_98	NH1	G_ASP_104	OD2	2.668
6A3W	H_ARG_61	NH1	H_ASP_82	OD1	2.906
6A3W	H_ARG_61	NH1	H_ASP_82	OD2	3.552
6A3W	I_ARG_73	NH1	I_ASP_87	OD1	2.942
6A3W	I_ARG_73	NH1	I_ASP_87	OD2	3.979
6A3W	I_ARG_75	NH1	I_GLU_85	OE1	2.824
6A3W	I_ARG_75	NH2	I_GLU_85	OE1	2.900
6A3W	I_HIS_93	ND1	I_ASP_105	OD1	2.434
6A3W	I_HIS_93	NE2	I_GLU_103	OE1	3.040
6A3W	I_LYS_114	NZ	H_ASP_51	OD2	2.757
6A3W	I_LYS_115	NZ	L_ASP_119	OD1	3.708
6A3W	I_LYS_115	NZ	L_ASP_119	OD2	3.946
6A3W	I_ARG_134	NH1	I_ASP_127	OD1	2.960
6A3W	I_ARG_134	NH1	I_ASP_127	OD2	3.787

6A3W	I_ARG_134	NH2	G_ASP_55	OD1	3.740
6A3W	I_ARG_134	NH2	G_ASP_55	OD2	2.630
6A3W	I_ARG_154	NH1	E_ASP_26	OD1	2.965
6A3W	I_ARG_154	NH2	E_ASP_26	OD1	3.042
6A3W	J_ARG_38	NH2	J_GLU_46	OE1	3.258
6A3W	J_ARG_38	NH2	J_GLU_46	OE2	2.995
6A3W	J_ARG_98	NH1	J_ASP_104	OD1	3.897
6A3W	J_ARG_98	NH1	J_ASP_104	OD2	2.584
6A3W	K_ARG_61	NH1	K_ASP_82	OD1	2.841
6A3W	K_ARG_61	NH1	K_ASP_82	OD2	3.357
6A3W	K_LYS_105	NZ	K_GLU_83	OE2	3.649
6A3W	L_ARG_73	NH1	L_ASP_87	OD1	2.207
6A3W	L_ARG_73	NH1	L_ASP_87	OD2	3.450
6A3W	L_ARG_75	NH1	L_GLU_85	OE1	2.429
6A3W	L_ARG_75	NH2	L_GLU_85	OE1	3.919
6A3W	L_HIS_93	ND1	L_ASP_105	OD1	2.405
6A3W	L_HIS_93	NE2	L_GLU_103	OE1	2.765
6A3W	L_LYS_107	NZ	H_ASP_30	OD1	3.282
6A3W	L_LYS_107	NZ	H_ASP_30	OD2	2.525
6A3W	L_LYS_114	NZ	K_ASP_51	OD2	2.893
6A3W	L_ARG_134	NH1	L_ASP_127	OD1	3.199
6A3W	L_ARG_134	NH1	L_ASP_127	OD2	3.994
6A3W	L_ARG_134	NH2	J_ASP_55	OD1	3.749
6A3W	L_ARG_134	NH2	J_ASP_55	OD2	2.496
6A3W	L_LYS_152	NZ	L_GLU_153	OE1	2.608

Table 769: 6A3W-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6A76	L_ARG_61	NH1	L_ASP_82	OD1	3.683
6A76	L_ARG_61	NH1	L_ASP_82	OD2	2.680
6A76	L_ARG_61	NH2	L_ASP_82	OD1	3.015
6A76	L_ARG_61	NH2	L_ASP_82	OD2	3.572
6A76	L_LYS_103	NZ	L_ASP_165	OD1	3.109
6A76	L_LYS_142	NZ	L_GLU_105	OE2	3.334
6A76	L_LYS_149	NZ	L_GLU_195	OE1	3.105
6A76	L_LYS_149	NZ	L_GLU_195	OE2	3.126
6A76	L_ARG_155	NH1	L_GLU_185	OE1	3.296
6A76	L_ARG_155	NH1	L_GLU_185	OE2	3.384
6A76	L_LYS_183	NZ	L_GLU_187	OE1	3.631
6A76	L_LYS_183	NZ	L_GLU_187	OE2	3.456
6A76	L_ARG_188	NH1	L_ASP_184	OD1	3.485
6A76	L_HIS_189	ND1	L_ASP_151	OD2	3.115
6A76	L_HIS_189	NE2	L_GLU_185	OE2	3.849
6A76	L_LYS_199	NZ	L_ASP_110	OD1	3.384
6A76	H_ARG_36	NH1	H_GLU_44	OE1	2.863
6A76	H_ARG_36	NH1	H_ASP_88	OD2	3.886
6A76	H_ARG_36	NH2	H_ASP_88	OD2	2.856
6A76	H_ARG_42	NH1	H_ASP_40	OD1	3.023
6A76	H_ARG_65	NH1	H_ASP_88	OD1	2.744
6A76	H_ARG_65	NH1	H_ASP_88	OD2	3.775
6A76	H_ARG_65	NH2	H_ASP_88	OD1	3.457
6A76	H_ARG_65	NH2	H_ASP_88	OD2	2.986
6A76	H_LYS_74	NZ	H_ASP_71	OD2	3.113
6A76	H_ARG_96	NH1	H_ASP_108	OD1	3.592
6A76	H_ARG_96	NH1	H_ASP_108	OD2	2.860
6A76	H_LYS_213	NZ	L_GLU_123	OE1	3.460

Table 770: 6A76-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6A77	A_LYS_44	NZ	A_ASP_45	OD2	3.622
6A77	A_ARG_55	NH1	A_ASP_73	OD1	3.618
6A77	A_ARG_55	NH1	A_ASP_73	OD2	2.774
6A77	A_ARG_55	NH2	A_ASP_53	OD2	3.164
6A77	A_ARG_55	NH2	A_ASP_73	OD1	2.879
6A77	A_ARG_55	NH2	A_ASP_73	OD2	3.609
6A77	A_ARG_67	NH1	H_GLU_97	OE1	2.680
6A77	A_ARG_67	NH2	H_GLU_97	OE1	3.115
6A77	A_ARG_67	NH2	H_GLU_97	OE2	3.032
6A77	L_LYS_39	NZ	L_ASP_81	OD1	2.939
6A77	L_LYS_39	NZ	L_ASP_81	OD2	3.685
6A77	L_LYS_58	NZ	L_ASP_57	OD2	3.665
6A77	L_ARG_61	NH1	L_ASP_82	OD1	3.988
6A77	L_ARG_61	NH1	L_ASP_82	OD2	2.871
6A77	L_ARG_61	NH2	L_ASP_82	OD1	3.242
6A77	L_ARG_61	NH2	L_ASP_82	OD2	3.518
6A77	L_LYS_103	NZ	L_ASP_165	OD1	2.895
6A77	L_LYS_149	NZ	L_GLU_195	OE2	3.578
6A77	L_ARG_155	NH1	L_GLU_185	OE1	3.397
6A77	L_ARG_155	NH1	L_GLU_185	OE2	3.437
6A77	L_HIS_189	ND1	L_ASP_151	OD2	2.718
6A77	L_LYS_199	NZ	L_ASP_110	OD1	3.833
6A77	H_ARG_36	NH1	H_GLU_44	OE1	2.723
6A77	H_ARG_36	NH1	H_ASP_88	OD2	3.780
6A77	H_ARG_36	NH2	H_ASP_88	OD2	2.740
6A77	H_ARG_42	NH1	H_ASP_40	OD1	3.854
6A77	H_ARG_65	NH1	H_ASP_88	OD1	2.999
6A77	H_ARG_65	NH1	H_ASP_88	OD2	3.898
6A77	H_ARG_65	NH2	H_ASP_88	OD1	3.615
6A77	H_ARG_65	NH2	H_ASP_88	OD2	3.124
6A77	H_LYS_74	NZ	H_ASP_71	OD2	3.837
6A77	H_ARG_96	NH1	H_ASP_108	OD1	3.281
6A77	H_ARG_96	NH1	H_ASP_108	OD2	2.697

Table 771: 6A77-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6A78	A_LYS_44	NZ	A_ASP_45	OD2	2.854
6A78	A_ARG_55	NH1	A_ASP_73	OD1	3.832
6A78	A_ARG_55	NH1	A_ASP_73	OD2	2.833
6A78	A_ARG_55	NH2	A_ASP_73	OD1	2.906
6A78	A_ARG_55	NH2	A_ASP_73	OD2	3.320
6A78	A_LYS_57	NZ	H_GLU_97	OE1	3.795
6A78	L_ARG_61	NH1	L_ASP_82	OD1	3.686
6A78	L_ARG_61	NH1	L_ASP_82	OD2	2.718
6A78	L_ARG_61	NH2	L_ASP_82	OD1	2.728
6A78	L_ARG_61	NH2	L_ASP_82	OD2	3.282
6A78	L_HIS_79	NE2	L_ASP_81	OD1	3.422
6A78	L_HIS_79	NE2	L_ASP_81	OD2	3.962
6A78	L_LYS_103	NZ	L_GLU_105	OE1	3.231
6A78	H_ARG_36	NH1	H_GLU_44	OE1	2.888
6A78	H_ARG_36	NH1	H_ASP_88	OD2	3.771
6A78	H_ARG_36	NH2	H_ASP_88	OD2	2.790
6A78	H_ARG_42	NH1	H_ASP_40	OD1	2.849
6A78	H_ARG_42	NH2	H_ASP_40	OD1	3.906
6A78	H_ARG_65	NH1	H_ASP_88	OD1	2.758
6A78	H_ARG_65	NH1	H_ASP_88	OD2	3.837
6A78	H_ARG_65	NH2	H_ASP_88	OD1	3.387
6A78	H_ARG_65	NH2	H_ASP_88	OD2	2.998
6A78	H_LYS_85	NZ	H_GLU_87	OE1	2.690
6A78	H_LYS_85	NZ	H_GLU_87	OE2	2.968
6A78	H_ARG_96	NH1	H_ASP_108	OD1	3.531
6A78	H_ARG_96	NH1	H_ASP_108	OD2	2.835
6A78	B_LYS_44	NZ	B_ASP_45	OD2	2.857
6A78	B_ARG_55	NH1	B_ASP_73	OD1	3.872
6A78	B_ARG_55	NH1	B_ASP_73	OD2	2.818
6A78	B_ARG_55	NH2	B_ASP_73	OD1	2.889
6A78	B_ARG_55	NH2	B_ASP_73	OD2	3.230
6A78	M_ARG_61	NH1	M_ASP_82	OD1	3.726
6A78	M_ARG_61	NH1	M_ASP_82	OD2	2.765
6A78	M_ARG_61	NH2	M_ASP_82	OD1	2.709
6A78	M_ARG_61	NH2	M_ASP_82	OD2	3.204
6A78	M_HIS_79	NE2	M_ASP_81	OD1	3.457
6A78	M_LYS_103	NZ	M_GLU_105	OE1	2.516
6A78	I_ARG_36	NH1	I_GLU_44	OE1	2.879
6A78	I_ARG_36	NH1	I_ASP_88	OD2	3.824
6A78	I_ARG_36	NH2	I_ASP_88	OD2	2.775
6A78	I_ARG_42	NH1	I_ASP_40	OD1	3.724
6A78	I_LYS_63	NZ	B_ASP_23	OD1	3.699
6A78	I_ARG_65	NH1	I_ASP_88	OD1	2.785
6A78	I_ARG_65	NH1	I_ASP_88	OD2	3.893
6A78	I_ARG_65	NH2	I_ASP_88	OD1	3.383
6A78	I_ARG_65	NH2	I_ASP_88	OD2	3.054
6A78	I_LYS_85	NZ	I_GLU_87	OE1	3.246
6A78	I_LYS_85	NZ	I_GLU_87	OE2	3.483
6A78	I_ARG_96	NH1	I_ASP_108	OD1	3.557
6A78	I_ARG_96	NH1	I_ASP_108	OD2	2.895

Table 772: 6A78-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6A79	A_LYS_44	NZ	A_ASP_45	OD2	2.831
6A79	A_ARG_55	NH1	A_ASP_73	OD1	3.891
6A79	A_ARG_55	NH1	A_ASP_73	OD2	2.680
6A79	A_ARG_55	NH2	A_ASP_73	OD1	3.082
6A79	A_ARG_55	NH2	A_ASP_73	OD2	3.256
6A79	L_ARG_61	NH1	L_ASP_82	OD1	3.024
6A79	L_ARG_61	NH1	L_ASP_82	OD2	2.736
6A79	L_ARG_61	NH2	L_ASP_82	OD1	2.726
6A79	L_ARG_61	NH2	L_ASP_82	OD2	3.768
6A79	L_HIS_79	NE2	L_ASP_81	OD1	3.224
6A79	L_HIS_79	NE2	L_ASP_81	OD2	3.424
6A79	L_LYS_103	NZ	L_GLU_105	OE1	2.597
6A79	H_ARG_36	NH1	H_GLU_44	OE1	3.267
6A79	H_ARG_36	NH1	H_GLU_44	OE2	3.458
6A79	H_ARG_36	NH1	H_ASP_88	OD1	3.347
6A79	H_ARG_36	NH2	H_ASP_88	OD1	2.770
6A79	H_ARG_42	NH1	H_ASP_40	OD2	3.039
6A79	H_ARG_42	NH2	H_ASP_40	OD2	3.868
6A79	H_ARG_65	NH1	H_ASP_88	OD2	3.054
6A79	H_ARG_65	NH2	H_ASP_88	OD1	3.293
6A79	H_ARG_65	NH2	H_ASP_88	OD2	3.419
6A79	H_LYS_85	NZ	H_GLU_87	OE1	3.696
6A79	H_LYS_85	NZ	H_GLU_87	OE2	2.564
6A79	H_ARG_96	NH1	H_ASP_108	OD1	3.338
6A79	H_ARG_96	NH1	H_ASP_108	OD2	2.871
6A79	B_LYS_44	NZ	B_ASP_45	OD2	2.762
6A79	B_ARG_55	NH1	B_ASP_73	OD1	3.944
6A79	B_ARG_55	NH1	B_ASP_73	OD2	2.685
6A79	B_ARG_55	NH2	B_ASP_73	OD1	3.213
6A79	B_ARG_55	NH2	B_ASP_73	OD2	3.130
6A79	B_ARG_67	NH1	L_GLU_97	OE2	3.582
6A79	M_ARG_61	NH1	M_ASP_82	OD1	3.110
6A79	M_ARG_61	NH1	M_ASP_82	OD2	2.870
6A79	M_ARG_61	NH2	M_ASP_82	OD1	2.772
6A79	M_ARG_61	NH2	M_ASP_82	OD2	3.856
6A79	M_HIS_79	NE2	M_ASP_81	OD1	3.808
6A79	M_HIS_79	NE2	M_ASP_81	OD2	3.655
6A79	M_LYS_103	NZ	M_GLU_105	OE1	2.465
6A79	I_ARG_36	NH1	I_GLU_44	OE1	3.040
6A79	I_ARG_36	NH1	I_GLU_44	OE2	3.647
6A79	I_ARG_36	NH1	I_ASP_88	OD1	3.777
6A79	I_ARG_36	NH2	I_ASP_88	OD1	2.864
6A79	I_ARG_42	NH1	I_ASP_40	OD2	3.303
6A79	I_ARG_42	NH2	I_ASP_40	OD2	3.939
6A79	I_ARG_65	NH1	I_ASP_88	OD2	2.883
6A79	I_ARG_65	NH2	I_ASP_88	OD1	3.193
6A79	I_ARG_65	NH2	I_ASP_88	OD2	3.477
6A79	I_LYS_85	NZ	I_GLU_87	OE1	3.709
6A79	I_LYS_85	NZ	I_GLU_87	OE2	2.725
6A79	I_ARG_96	NH1	I_ASP_108	OD1	3.351
6A79	I_ARG_96	NH1	I_ASP_108	OD2	2.910

Table 773: 6A79-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6AL5	A_LYS_155	NZ	H_GLU_74	OE1	3.542
6AL5	A_ARG_163	NH1	A_ASP_162	OD1	3.779
6AL5	A_ARG_163	NH1	A_ASP_162	OD2	2.756
6AL5	A_ARG_163	NH2	A_ASP_162	OD2	3.912
6AL5	A_HIS_218	NE2	A_GLU_120	OE1	3.847
6AL5	A_HIS_218	NE2	A_GLU_120	OE2	3.910
6AL5	A_LYS_220	NZ	H_ASP_55	OD1	3.389
6AL5	A_LYS_220	NZ	H_ASP_55	OD2	2.832
6AL5	A_LYS_220	NZ	H_ASP_57	OD2	3.301
6AL5	A_ARG_237	NH1	A_ASP_255	OD1	3.153
6AL5	A_ARG_237	NH1	A_ASP_255	OD2	2.798
6AL5	A_ARG_277	NH2	A_ASP_32	OD1	2.744
6AL5	L_ARG_65	NH2	L_ASP_86	OD1	3.023
6AL5	L_ARG_65	NH2	L_ASP_86	OD2	3.003
6AL5	L_LYS_107	NZ	L_GLU_109	OE1	3.519
6AL5	L_LYS_107	NZ	L_GLU_169	OE1	3.283
6AL5	L_LYS_107	NZ	L_GLU_169	OE2	3.574
6AL5	L_ARG_146	NH1	L_GLU_109	OE1	2.818
6AL5	L_LYS_153	NZ	L_GLU_199	OE2	3.184
6AL5	L_LYS_187	NZ	L_GLU_191	OE2	3.556
6AL5	L_HIS_193	ND1	L_ASP_189	OD1	3.737
6AL5	H_ARG_38	NH1	H_ASP_90	OD1	3.791
6AL5	H_ARG_38	NH2	H_GLU_46	OE1	3.814
6AL5	H_ARG_67	NH1	H_ASP_90	OD1	3.408
6AL5	H_ARG_67	NH1	H_ASP_90	OD2	3.019
6AL5	H_ARG_67	NH2	H_ASP_90	OD1	3.382
6AL5	H_ARG_98	NH2	H_ASP_112	OD1	3.627
6AL5	H_ARG_98	NH2	H_ASP_112	OD2	2.814
6AL5	H_ARG_106	NH1	H_GLU_100	OE1	3.206
6AL5	H_ARG_106	NH1	H_GLU_100	OE2	2.772
6AL5	H_ARG_106	NH2	L_ASP_54	OD1	3.142
6AL5	H_ARG_106	NH2	L_ASP_54	OD2	3.298
6AL5	H_ARG_106	NH2	H_GLU_100	OE2	3.102
6AL5	H_LYS_154	NZ	H_ASP_155	OD1	3.510
6AL5	H_LYS_154	NZ	H_ASP_155	OD2	3.733
6AL5	H_LYS_220	NZ	L_GLU_127	OE1	3.220
6AL5	H_LYS_221	NZ	H_GLU_223	OE2	3.651

Table 774: 6AL5-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6ANA	H_LYS_64	NZ	H_ASP_65	OD1	3.910
6ANA	H_LYS_64	NZ	H_ASP_65	OD2	2.779
6ANA	H_LYS_66	NZ	H_ASP_86	OD1	3.581
6ANA	H_LYS_66	NZ	H_ASP_86	OD2	2.714
6ANA	H_ARG_94	NH2	H_ASP_96	OD1	3.718
6ANA	H_ARG_94	NH2	H_ASP_96	OD2	3.967
6ANA	H_LYS_142	NZ	H_ASP_143	OD1	3.131
6ANA	H_LYS_142	NZ	H_ASP_143	OD2	2.790
6ANA	H_ARG_209	NH1	H_GLU_211	OE1	3.669
6ANA	L_ARG_61	NH2	L_ASP_82	OD1	2.820
6ANA	L_ARG_61	NH2	L_ASP_82	OD2	3.661
6ANA	L_LYS_102	NZ	L_GLU_104	OE2	2.841
6ANA	L_LYS_148	NZ	L_GLU_194	OE2	2.623
6ANA	L_LYS_182	NZ	L_GLU_186	OE1	2.943
6ANA	L_LYS_182	NZ	L_GLU_186	OE2	3.303
6ANA	L_LYS_187	NZ	L_ASP_184	OD1	2.815
6ANA	L_LYS_189	NZ	L_GLU_212	OE2	2.496

Table 775: 6ANA-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6AND	H_ARG_38	NH1	H_GLU_46	OE2	2.978
6AND	H_ARG_38	NH1	H_ASP_86	OD1	3.864
6AND	H_ARG_38	NH2	H_ASP_86	OD1	2.906
6AND	H_ARG_50	NH2	H_ASP_95	OD1	3.873
6AND	H_ARG_50	NH2	H_ASP_95	OD2	3.421
6AND	H_LYS_62	NZ	H_GLU_46	OE1	2.841
6AND	H_LYS_62	NZ	H_GLU_46	OE2	3.776
6AND	H_ARG_66	NH1	H_ASP_86	OD1	3.755
6AND	H_ARG_66	NH1	H_ASP_86	OD2	2.814
6AND	H_ARG_66	NH2	H_ASP_86	OD1	2.852
6AND	H_ARG_66	NH2	H_ASP_86	OD2	3.248
6AND	H_ARG_94	NH2	H_ASP_101	OD1	3.615
6AND	H_ARG_94	NH2	H_ASP_101	OD2	2.990
6AND	H_LYS_143	NZ	H_ASP_144	OD1	3.840
6AND	H_LYS_209	NZ	L_GLU_123	OE1	2.684
6AND	H_LYS_209	NZ	L_GLU_123	OE2	3.876
6AND	L_LYS_50	NZ	H_ASP_100	OD1	3.188
6AND	L_ARG_61	NH2	L_GLU_81	OE2	3.449
6AND	L_ARG_61	NH2	L_ASP_82	OD1	2.730
6AND	L_ARG_61	NH2	L_ASP_82	OD2	3.513
6AND	L_LYS_103	NZ	L_GLU_165	OE1	3.616
6AND	L_LYS_103	NZ	L_GLU_165	OE2	3.146
6AND	L_LYS_149	NZ	L_GLU_195	OE2	2.858
6AND	L_LYS_188	NZ	L_ASP_185	OD1	3.465
6AND	L_HIS_189	ND1	L_ASP_151	OD2	3.034

Table 776: 6AND-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6ANI	H.HIS_35	ND1	H.GLU_50	OE1	3.692
6ANI	H.HIS_35	NE2	H.GLU_50	OE1	3.990
6ANI	H.LYS_66	NZ	H.ASP_86	OD1	3.842
6ANI	H.LYS_66	NZ	H.ASP_86	OD2	3.014
6ANI	H.ARG_83	NH2	H.ASP_85	OD2	3.086
6ANI	H.ARG_94	NH2	H.ASP_101	OD1	3.640
6ANI	H.ARG_94	NH2	H.ASP_101	OD2	2.660
6ANI	H.LYS_143	NZ	H.ASP_144	OD1	3.153
6ANI	H.LYS_143	NZ	H.ASP_144	OD2	2.622
6ANI	H.LYS_209	NZ	L.GLU_123	OE1	2.397
6ANI	H.LYS_210	NZ	H.GLU_212	OE1	2.867
6ANI	L.LYS_53	NZ	L.ASP_50	OD2	2.769
6ANI	L.ARG_61	NH1	L.GLU_81	OE2	3.915
6ANI	L.ARG_61	NH2	L.GLU_81	OE2	3.089
6ANI	L.ARG_61	NH2	L.ASP_82	OD1	2.623
6ANI	L.ARG_61	NH2	L.ASP_82	OD2	3.423
6ANI	L.LYS_149	NZ	L.GLU_195	OE1	3.748
6ANI	L.LYS_188	NZ	L.ASP_185	OD1	3.446
6ANI	I.HIS_35	ND1	I.GLU_50	OE1	3.825
6ANI	I.HIS_35	NE2	I.GLU_50	OE1	3.743
6ANI	I.LYS_66	NZ	I.ASP_86	OD1	3.950
6ANI	I.LYS_66	NZ	I.ASP_86	OD2	2.953
6ANI	I.ARG_83	NH2	I.ASP_85	OD2	2.907
6ANI	I.ARG_94	NH2	I.ASP_101	OD1	3.760
6ANI	I.ARG_94	NH2	I.ASP_101	OD2	2.654
6ANI	I.LYS_143	NZ	I.ASP_144	OD1	3.006
6ANI	I.LYS_143	NZ	I.ASP_144	OD2	2.878
6ANI	I.LYS_209	NZ	M.GLU_123	OE2	3.950
6ANI	I.LYS_210	NZ	I.GLU_212	OE2	3.076
6ANI	M.LYS_53	NZ	M.ASP_50	OD2	2.878
6ANI	M.ARG_61	NH2	M.ASP_82	OD1	2.930
6ANI	M.ARG_61	NH2	M.ASP_82	OD2	3.730
6ANI	M.HIS_189	ND1	M.ASP_151	OD2	3.008

Table 777: 6ANI-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6AQ7	A_ARG_155	NH1	A_GLU_195	OE1	2.727
6AQ7	A_ARG_155	NH1	A_GLU_195	OE2	3.462
6AQ7	A_ARG_155	NH2	A_ASP_201	OD1	3.324
6AQ7	A_ARG_155	NH2	A_ASP_201	OD2	3.430
6AQ7	A_ARG_163	NH2	A_ASP_177	OD2	2.708
6AQ7	A_LYS_203	NZ	A_GLU_206	OE1	2.779
6AQ7	A_LYS_203	NZ	A_GLU_206	OE2	3.528
6AQ7	H_HIS_34	NE2	A_GLU_199	OE1	3.934
6AQ7	H_HIS_34	NE2	A_GLU_199	OE2	2.717
6AQ7	H_ARG_37	NH1	H_ASP_89	OD1	2.941
6AQ7	H_ARG_37	NH2	H_GLU_45	OE1	2.823
6AQ7	H_ARG_37	NH2	H_ASP_89	OD1	3.962
6AQ7	H_ARG_49	NH1	A_GLU_199	OE2	2.744
6AQ7	H_LYS_66	NZ	H_ASP_89	OD1	3.144
6AQ7	H_LYS_66	NZ	H_ASP_89	OD2	2.568
6AQ7	H_ARG_97	NH2	H_ASP_103	OD1	3.527
6AQ7	H_ARG_97	NH2	H_ASP_103	OD2	2.817
6AQ7	H_LYS_209	NZ	L_GLU_127	OE2	2.651
6AQ7	L_LYS_24	NZ	L_ASP_74	OD1	3.475
6AQ7	L_LYS_24	NZ	L_ASP_74	OD2	3.224
6AQ7	L_LYS_53	NZ	L_GLU_59	OE1	3.832
6AQ7	L_ARG_65	NH2	L_GLU_85	OE2	3.459
6AQ7	L_ARG_65	NH2	L_ASP_86	OD1	2.720
6AQ7	L_ARG_65	NH2	L_ASP_86	OD2	3.600
6AQ7	L_LYS_146	NZ	L_GLU_109	OE1	3.899
6AQ7	L_LYS_151	NZ	L_GLU_158	OE2	3.172
6AQ7	L_LYS_153	NZ	L_GLU_199	OE1	3.387
6AQ7	L_LYS_153	NZ	L_GLU_199	OE2	2.997
6AQ7	L_ARG_159	NH1	L_GLU_189	OE2	3.035
6AQ7	L_ARG_159	NH2	L_GLU_189	OE2	3.333
6AQ7	L_HIS_193	ND1	L_ASP_155	OD2	2.747
6AQ7	L_LYS_203	NZ	L_ASP_114	OD1	3.000
6AQ7	L_LYS_203	NZ	L_ASP_114	OD2	2.913

Table 778: 6AQ7-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6ATT	A_ARG_25	NH2	A_ASP_22	OD1	3.000
6ATT	A_HIS_26	NE2	A_ASP_22	OD1	3.343
6ATT	A_ARG_76	NH1	A_ASP_54	OD1	2.778
6ATT	A_ARG_81	NH2	A_GLU_57	OE1	3.490
6ATT	A_ARG_81	NH2	A_GLU_57	OE2	3.603
6ATT	A_ARG_121	NH1	A_GLU_188	OE1	3.331
6ATT	A_ARG_121	NH1	A_ASP_189	OD1	3.785
6ATT	A_ARG_121	NH2	A_ASP_189	OD1	3.820
6ATT	A_ARG_135	NH1	A_ASP_96	OD1	3.753
6ATT	A_ARG_135	NH1	A_ASP_96	OD2	3.334
6ATT	A_ARG_135	NH2	A_ASP_96	OD2	3.651
6ATT	A_HIS_152	ND1	A_GLU_125	OE2	3.074
6ATT	A_ARG_166	NH1	A_ASP_143	OD2	3.858
6ATT	A_HIS_171	ND1	A_GLU_185	OE1	3.239
6ATT	A_ARG_204	NH1	A_GLU_125	OE1	3.451
6ATT	A_ARG_204	NH2	A_GLU_125	OE1	3.326
6ATT	A_ARG_204	NH2	A_GLU_125	OE2	3.886
6ATT	A_HIS_238	ND1	A_GLU_243	OE1	3.002
6ATT	A_HIS_238	ND1	A_GLU_243	OE2	3.743
6ATT	A_ARG_266	NH2	A_GLU_264	OE1	3.983
6ATT	A_ARG_308	NH1	A_ASP_304	OD2	3.570
6ATT	A_ARG_308	NH2	A_ASP_304	OD2	2.743
6ATT	A_HIS_	NE2	A_GLU_	OE1	2.757
6ATT	A_HIS_	NE2	A_GLU_	OE2	3.385
6ATT	A_ARG_329	NH1	A_GLU_330	OE1	3.614
6ATT	A_ARG_329	NH2	A_GLU_330	OE2	3.989
6ATT	A_ARG_	NH1	A_GLU_	OE1	2.988
6ATT	A_ARG_	NH1	A_GLU_357	OE2	3.696
6ATT	A_ARG_332	NH2	A_GLU_357	OE2	3.986
6ATT	A_LYS_	NZ	A_GLU_	OE1	3.919
6ATT	A_LYS_347	NZ	A_GLU_299	OE2	3.462
6ATT	A_LYS_347	NZ	A_GLU_383	OE2	3.837
6ATT	A_ARG_410	NH1	A_GLU_438	OE2	3.785
6ATT	A_ARG_410	NH2	A_GLU_383	OE1	3.874
6ATT	A_ARG_410	NH2	A_GLU_383	OE2	3.055
6ATT	A_ARG_412	NH1	A_GLU_299	OE1	3.365
6ATT	A_ARG_412	NH1	A_GLU_299	OE2	3.033
6ATT	A_ARG_412	NH2	A_GLU_299	OE2	3.491
6ATT	A_ARG_465	NH1	A_GLU_438	OE1	3.352
6ATT	A_ARG_477	NH1	A_GLU_485	OE1	3.071
6ATT	A_ARG_477	NH2	A_GLU_481	OE2	3.926
6ATT	A_ARG_477	NH2	A_GLU_485	OE1	3.540
6ATT	A_ARG_	NH1	A_GLU_	OE1	2.803
6ATT	A_ARG_	NH1	A_GLU_	OE2	3.745
6ATT	A_ARG_	NH1	A_GLU_	OE1	3.574
6ATT	A_ARG_	NH1	A_GLU_	OE2	2.811
6ATT	A_HIS_	ND1	A_GLU_	OE1	3.143
6ATT	A_HIS_	ND1	A_GLU_	OE2	3.018
6ATT	H_ARG_38	NH1	H_ASP_90	OD1	2.909
6ATT	H_ARG_38	NH2	H_GLU_46	OE1	3.113
6ATT	H_ARG_38	NH2	H_ASP_90	OD1	3.490
6ATT	H_ARG_67	NH1	H_ASP_90	OD1	3.630
6ATT	H_ARG_67	NH1	H_ASP_90	OD2	2.692
6ATT	H_ARG_67	NH2	H_ASP_90	OD1	3.064
6ATT	H_ARG_67	NH2	H_ASP_90	OD2	3.552
6ATT	H_ARG_98	NH2	H_ASP_109	OD2	3.700
6ATT	H_LYS_151	NZ	H_ASP_152	OD1	3.592

6ATT	H_LYS_151	NZ	H_ASP_152	OD2	3.811
6ATT	H_LYS_217	NZ	L_GLU_129	OE1	3.069
6ATT	H_ARG_218	NH1	H_GLU_220	OE2	2.838
6ATT	H_LYS_222	NZ	L_ASP_128	OD1	2.688
6ATT	L_ARG_32	NH1	A_GLU_216	OE1	2.742
6ATT	L_LYS_45	NZ	L_GLU_87	OE1	2.487
6ATT	L_ARG_67	NH1	L_GLU_85	OE1	3.360
6ATT	L_ARG_67	NH1	L_GLU_85	OE2	3.299
6ATT	L_ARG_67	NH2	L_ASP_88	OD1	2.767
6ATT	L_LYS_155	NZ	L_GLU_201	OE1	3.534
6ATT	L_LYS_155	NZ	L_GLU_201	OE2	3.250
6ATT	L_LYS_189	NZ	L_GLU_193	OE1	3.627
6ATT	L_LYS_189	NZ	L_GLU_193	OE2	3.286
6ATT	L_HIS_195	ND1	L_ASP_157	OD2	2.711

Table 779: 6ATT-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6AZZ	F_HIS_35	NE2	F_ASP_95	OD1	2.684
6AZZ	F_HIS_35	NE2	F_ASP_95	OD2	3.272
6AZZ	F_LYS_62	NZ	F_GLU_46	OE1	3.990
6AZZ	F_LYS_62	NZ	F_GLU_46	OE2	2.597
6AZZ	F_ARG_94	NH2	F_ASP_101	OD1	3.814
6AZZ	F_ARG_94	NH2	F_ASP_101	OD2	2.728
6AZZ	F_LYS_209	NZ	E_GLU_124	OE2	3.461
6AZZ	F_LYS_210	NZ	F_GLU_212	OE1	2.660
6AZZ	E_ARG_61	NH1	E_ASP_82	OD1	3.472
6AZZ	E_ARG_61	NH1	E_ASP_82	OD2	2.388
6AZZ	E_ARG_61	NH2	E_GLU_79	OE1	3.246
6AZZ	E_ARG_61	NH2	E_GLU_79	OE2	3.544
6AZZ	E_ARG_61	NH2	E_ASP_82	OD1	2.711
6AZZ	E_ARG_61	NH2	E_ASP_82	OD2	2.961
6AZZ	E_ARG_77	NH1	B_GLU_79	OE2	3.685
6AZZ	E_ARG_77	NH2	B_GLU_79	OE1	3.407
6AZZ	E_ARG_77	NH2	B_GLU_79	OE2	3.489
6AZZ	E_LYS_111	NZ	E_GLU_199	OE1	3.404
6AZZ	E_LYS_130	NZ	F_ASP_144	OD2	3.330
6AZZ	C_HIS_35	NE2	C_ASP_95	OD1	2.700
6AZZ	C_HIS_35	NE2	C_ASP_95	OD2	3.324
6AZZ	C_LYS_62	NZ	C_GLU_46	OE1	3.744
6AZZ	C_LYS_62	NZ	C_GLU_46	OE2	2.907
6AZZ	C_ARG_94	NH2	C_ASP_101	OD1	3.926
6AZZ	C_ARG_94	NH2	C_ASP_101	OD2	2.919
6AZZ	C_LYS_209	NZ	B_GLU_124	OE1	3.784
6AZZ	C_LYS_209	NZ	B_GLU_124	OE2	2.655
6AZZ	C_LYS_210	NZ	C_GLU_212	OE1	2.801
6AZZ	B_LYS_31	NZ	B_ASP_92	OD1	3.992
6AZZ	B_ARG_61	NH1	B_GLU_79	OE2	3.665
6AZZ	B_ARG_61	NH2	B_GLU_79	OE1	3.459
6AZZ	B_ARG_61	NH2	B_GLU_79	OE2	3.381
6AZZ	B_ARG_61	NH2	B_ASP_82	OD1	2.944
6AZZ	B_ARG_61	NH2	B_ASP_82	OD2	3.568
6AZZ	B_LYS_111	NZ	B_GLU_199	OE1	3.484
6AZZ	B_LYS_130	NZ	C_ASP_144	OD2	3.121
6AZZ	A_HIS_20	NE2	A_GLU_22	OE1	2.799
6AZZ	A_LYS_90	NZ	B_ASP_51	OD1	3.552
6AZZ	A_LYS_90	NZ	B_ASP_51	OD2	2.501
6AZZ	A_LYS_98	NZ	A_GLU_22	OE1	2.677
6AZZ	A_LYS_98	NZ	A_GLU_22	OE2	3.134
6AZZ	A_LYS_108	NZ	B_ASP_53	OD2	3.868
6AZZ	A_LYS_108	NZ	A_GLU_88	OE2	3.991
6AZZ	A_LYS_118	NZ	A_ASP_131	OD1	2.501
6AZZ	A_LYS_139	NZ	A_ASP_6	OD1	2.975
6AZZ	D_LYS_10	NZ	D_GLU_35	OE2	3.455
6AZZ	D_ARG_11	NH1	D_GLU_26	OE1	3.991
6AZZ	D_HIS_20	NE2	D_GLU_22	OE1	2.833
6AZZ	D_LYS_90	NZ	E_ASP_51	OD1	3.639
6AZZ	D_LYS_90	NZ	E_ASP_51	OD2	2.901
6AZZ	D_LYS_98	NZ	D_GLU_22	OE1	2.924
6AZZ	D_LYS_98	NZ	D_GLU_22	OE2	3.312
6AZZ	D_LYS_118	NZ	D_ASP_131	OD1	2.526
6AZZ	D_LYS_139	NZ	D_ASP_6	OD1	3.014
6AZZ	D_LYS_139	NZ	D_ASP_6	OD2	3.993

Table 780: 6AZZ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6B08	C_HIS_35	NE2	C_ASP_95	OD1	2.543
6B08	C_HIS_35	NE2	C_ASP_95	OD2	3.235
6B08	C_ARG_38	NH2	C_GLU_46	OE1	3.451
6B08	C_ARG_94	NH2	C_ASP_101	OD1	3.885
6B08	C_ARG_94	NH2	C_ASP_101	OD2	2.821
6B08	C_LYS_143	NZ	B_GLU_125	OE2	2.599
6B08	B_LYS_31	NZ	B_ASP_92	OD2	3.730
6B08	B_ARG_61	NH1	B_GLU_79	OE2	3.112
6B08	B_ARG_61	NH2	B_ASP_82	OD1	2.963
6B08	B_ARG_61	NH2	B_ASP_82	OD2	2.912
6B08	B_LYS_167	NZ	B_GLU_83	OE2	3.572
6B08	A_LYS_10	NZ	A_GLU_35	OE2	3.550
6B08	A_HIS_20	NE2	A_GLU_22	OE2	2.721
6B08	A_LYS_90	NZ	B_ASP_51	OD1	2.529
6B08	A_LYS_90	NZ	B_ASP_51	OD2	3.708
6B08	A_LYS_98	NZ	A_GLU_22	OE1	3.424
6B08	A_LYS_98	NZ	A_GLU_22	OE2	2.846
6B08	A_LYS_118	NZ	A_ASP_131	OD1	3.348
6B08	A_LYS_142	NZ	A_GLU_145	OE1	2.917
6B08	A_LYS_142	NZ	A_GLU_145	OE2	3.424

Table 781: 6B08-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6B0A	H_ARG_38	NH1	H_ASP_90	OD1	3.014
6B0A	H_ARG_38	NH2	H_GLU_46	OE2	3.036
6B0A	H_ARG_38	NH2	H_ASP_90	OD1	3.967
6B0A	H_LYS_65	NZ	H_ASP_62	OD1	3.558
6B0A	H_ARG_67	NH1	H_ASP_90	OD1	3.030
6B0A	H_ARG_67	NH1	H_ASP_90	OD2	2.551
6B0A	H_ARG_67	NH2	H_ASP_90	OD1	3.040
6B0A	H_ARG_67	NH2	H_ASP_90	OD2	3.966
6B0A	H_LYS_98	NZ	H_ASP_100	OD1	3.067
6B0A	H_LYS_98	NZ	H_ASP_113	OD1	3.416
6B0A	H_LYS_98	NZ	H_ASP_113	OD2	3.062
6B0A	H_LYS_218	NZ	H_ASP_220	OD1	3.753
6B0A	L_ARG_62	NH1	L_GLU_80	OE1	3.743
6B0A	L_ARG_62	NH1	L_GLU_80	OE2	3.406
6B0A	L_ARG_62	NH2	L_GLU_80	OE2	3.228
6B0A	L_ARG_62	NH2	L_GLU_82	OE1	3.824
6B0A	L_ARG_62	NH2	L_ASP_83	OD1	2.621
6B0A	L_ARG_62	NH2	L_ASP_83	OD2	3.165
6B0A	L_ARG_101	NH1	L_GLU_103	OE1	3.058
6B0A	L_HIS_187	ND1	L_ASP_149	OD2	2.488
6B0A	A_HIS_20	NE2	A_GLU_22	OE1	3.003
6B0A	A_LYS_90	NZ	A_ASP_78	OD2	3.536
6B0A	A_LYS_98	NZ	A_GLU_22	OE1	3.288
6B0A	A_LYS_98	NZ	A_GLU_22	OE2	2.898
6B0A	A_LYS_118	NZ	A_ASP_131	OD1	2.522

Table 782: 6B0A-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6B0E	A_ARG_46	NH2	A_ASP_55	OD1	3.681
6B0E	A_ARG_46	NH2	A_ASP_55	OD2	2.616
6B0E	A_ARG_54	NH2	A_ASP_60	OD1	3.407
6B0E	A_ARG_61	NH1	A_GLU_81	OE2	2.864
6B0E	A_ARG_61	NH1	A_ASP_82	OD1	2.718
6B0E	A_ARG_61	NH1	A_ASP_82	OD2	3.652
6B0E	A_ARG_61	NH2	A_GLU_79	OE1	3.681
6B0E	A_ARG_61	NH2	A_GLU_79	OE2	3.517
6B0E	A_ARG_61	NH2	A_GLU_81	OE2	3.930
6B0E	A_HIS_189	ND1	A_ASP_151	OD2	2.935
6B0E	B_ARG_38	NH1	B_ASP_86	OD1	3.019
6B0E	B_ARG_38	NH2	B_GLU_46	OE2	3.029
6B0E	B_ARG_38	NH2	B_ASP_86	OD1	3.941
6B0E	B_ARG_94	NH2	B_ASP_101	OD1	3.699
6B0E	B_ARG_94	NH2	B_ASP_101	OD2	2.508
6B0E	B_LYS_143	NZ	B_ASP_144	OD1	2.734
6B0E	B_LYS_143	NZ	B_ASP_144	OD2	3.061
6B0E	B_HIS_164	ND1	A_ASP_167	OD2	3.677
6B0E	E_HIS_20	NE2	E_GLU_22	OE1	2.862
6B0E	E_LYS_118	NZ	E_ASP_131	OD1	2.359
6B0E	E_LYS_142	NZ	E_GLU_145	OE1	3.928
6B0E	E_LYS_155	NZ	B_ASP_98	OD2	3.864

Table 783: 6B0E-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6B0G	C_ARG_24	NH1	C_ASP_70	OD1	3.644
6B0G	C_ARG_24	NH2	C_ASP_70	OD1	3.217
6B0G	C_ARG_46	NH2	C_ASP_55	OD1	3.667
6B0G	C_ARG_46	NH2	C_ASP_55	OD2	2.584
6B0G	C_ARG_54	NH2	C_ASP_60	OD1	2.717
6B0G	C_ARG_61	NH1	C_GLU_79	OE1	3.756
6B0G	C_ARG_61	NH1	C_GLU_79	OE2	3.832
6B0G	C_ARG_61	NH2	C_GLU_79	OE1	3.846
6B0G	C_ARG_61	NH2	C_ASP_82	OD1	2.542
6B0G	C_ARG_61	NH2	C_ASP_82	OD2	3.446
6B0G	C_LYS_103	NZ	C_GLU_165	OE1	3.504
6B0G	C_LYS_103	NZ	C_GLU_165	OE2	3.698
6B0G	C_LYS_149	NZ	C_GLU_195	OE1	3.121
6B0G	C_LYS_188	NZ	C_ASP_185	OD1	2.887
6B0G	C_HIS_189	ND1	C_ASP_151	OD2	3.287
6B0G	C_ARG_211	NH1	C_GLU_187	OE1	3.151
6B0G	D_ARG_38	NH1	D_ASP_86	OD1	2.889
6B0G	D_ARG_38	NH2	D_ASP_86	OD1	3.880
6B0G	D_LYS_62	NZ	D_GLU_46	OE1	3.387
6B0G	D_LYS_62	NZ	D_GLU_46	OE2	3.344
6B0G	D_ARG_66	NH1	D_ASP_86	OD1	3.686
6B0G	D_ARG_66	NH1	D_ASP_86	OD2	2.815
6B0G	D_ARG_66	NH2	D_ASP_86	OD1	2.895
6B0G	D_ARG_66	NH2	D_ASP_86	OD2	3.345
6B0G	D_ARG_82A	NH2	D_GLU_81	OE1	3.967
6B0G	D_LYS_94	NZ	D_ASP_101	OD1	3.857
6B0G	D_LYS_94	NZ	D_ASP_101	OD2	2.849
6B0G	D_ARG_100B	NH1	C_ASP_91	OD2	3.003
6B0G	D_ARG_100B	NH2	C_ASP_91	OD2	3.130
6B0G	D_LYS_148	NZ	D_ASP_149	OD1	3.128
6B0G	D_LYS_148	NZ	D_ASP_149	OD2	3.390
6B0G	D_LYS_214	NZ	C_GLU_123	OE2	3.176
6B0G	D_LYS_215	NZ	D_GLU_217	OE2	3.125
6B0G	E_ARG_11	NH1	E_GLU_39	OE2	3.696
6B0G	E_HIS_20	NE2	E_GLU_22	OE1	2.725
6B0G	E_LYS_90	NZ	E_ASP_78	OD2	3.931
6B0G	E_LYS_98	NZ	E_GLU_22	OE1	2.876
6B0G	E_LYS_98	NZ	E_GLU_22	OE2	3.660
6B0G	E_LYS_118	NZ	E_ASP_131	OD1	2.414
6B0G	E_LYS_139	NZ	E_ASP_6	OD1	2.804
6B0G	E_LYS_139	NZ	E_ASP_6	OD2	3.888
6B0G	E_LYS_155	NZ	D_ASP_98	OD2	2.837
6B0G	E_LYS_155	NZ	E_ASP_157	OD2	3.894

Table 784: 6B0G-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6B0H	I_ARG_11	NH1	I_GLU_39	OE1	2.905
6B0H	I_ARG_11	NH1	I_GLU_39	OE2	3.603
6B0H	I_ARG_11	NH2	I_GLU_39	OE1	3.421
6B0H	I_ARG_11	NH2	I_GLU_39	OE2	2.810
6B0H	I_HIS_20	NE2	I_GLU_22	OE1	2.759
6B0H	I_LYS_24	NZ	I_GLU_22	OE2	3.743
6B0H	I_LYS_90	NZ	I_ASP_78	OD2	2.698
6B0H	I_LYS_118	NZ	I_ASP_131	OD1	2.468
6B0H	I_LYS_127	NZ	I_ASP_124	OD2	3.708
6B0H	I_LYS_139	NZ	I_ASP_6	OD1	2.845
6B0H	I_LYS_139	NZ	I_ASP_6	OD2	3.883
6B0H	I_LYS_142	NZ	I_GLU_145	OE2	3.701
6B0H	I_LYS_155	NZ	I_ASP_157	OD2	3.811
6B0H	J_ARG_11	NH1	J_GLU_39	OE1	3.153
6B0H	J_ARG_11	NH1	J_GLU_39	OE2	3.697
6B0H	J_ARG_11	NH2	J_GLU_39	OE1	3.428
6B0H	J_ARG_11	NH2	J_GLU_39	OE2	2.670
6B0H	J_HIS_20	NE2	J_GLU_22	OE1	2.670
6B0H	J_LYS_24	NZ	J_GLU_22	OE2	3.866
6B0H	J_LYS_90	NZ	J_ASP_78	OD2	3.917
6B0H	J_LYS_98	NZ	J_GLU_22	OE2	3.958
6B0H	J_LYS_118	NZ	J_ASP_131	OD1	2.439
6B0H	J_LYS_127	NZ	J_ASP_124	OD1	3.354
6B0H	J_LYS_127	NZ	J_ASP_124	OD2	3.839
6B0H	J_LYS_139	NZ	J_ASP_6	OD1	3.036
6B0H	B_ARG_38	NH1	B_ASP_86	OD1	2.831
6B0H	B_ARG_38	NH2	B_GLU_46	OE1	3.367
6B0H	B_ARG_38	NH2	B_ASP_86	OD1	3.809
6B0H	B_LYS_43	NZ	B_GLU_46	OE2	3.945
6B0H	B_HIS_58	ND1	B_GLU_50	OE2	3.817
6B0H	B_ARG_66	NH1	B_ASP_86	OD1	3.737
6B0H	B_ARG_66	NH2	B_ASP_86	OD1	3.093
6B0H	B_ARG_66	NH2	B_ASP_86	OD2	2.466
6B0H	B_ARG_94	NH2	B_ASP_101	OD1	3.827
6B0H	B_ARG_94	NH2	B_ASP_101	OD2	2.750
6B0H	B_ARG_97	NH2	B_GLU_50	OE1	2.771
6B0H	B_ARG_97	NH2	B_GLU_50	OE2	3.459
6B0H	B_ARG_97	NH2	B_GLU_95	OE2	2.917
6B0H	B_LYS_144	NZ	B_ASP_145	OD1	3.326
6B0H	B_LYS_144	NZ	B_ASP_145	OD2	3.603
6B0H	D_ARG_38	NH1	D_ASP_86	OD1	2.588
6B0H	D_ARG_38	NH2	D_GLU_46	OE1	3.399
6B0H	D_ARG_38	NH2	D_ASP_86	OD1	3.688
6B0H	D_LYS_43	NZ	D_GLU_46	OE2	3.764
6B0H	D_HIS_58	ND1	D_GLU_50	OE1	3.722
6B0H	D_ARG_66	NH1	D_ASP_86	OD1	3.850
6B0H	D_ARG_66	NH1	D_ASP_86	OD2	3.946
6B0H	D_ARG_66	NH2	D_ASP_86	OD1	3.173
6B0H	D_ARG_66	NH2	D_ASP_86	OD2	2.383
6B0H	D_ARG_94	NH2	D_ASP_101	OD1	3.853
6B0H	D_ARG_94	NH2	D_ASP_101	OD2	2.885
6B0H	D_ARG_97	NH2	D_GLU_50	OE1	3.508
6B0H	D_ARG_97	NH2	D_GLU_50	OE2	2.823
6B0H	D_ARG_97	NH2	D_GLU_95	OE2	2.857
6B0H	D_LYS_144	NZ	D_ASP_145	OD1	3.294
6B0H	D_LYS_144	NZ	D_ASP_145	OD2	3.795
6B0H	D_LYS_207	NZ	D_ASP_209	OD1	3.527

6B0H	D_LYS_207	NZ	D_ASP_209	OD2	2.851
6B0H	A_ARG_61	NH1	A_GLU_81	OE2	3.989
6B0H	A_ARG_61	NH2	A_GLU_81	OE2	2.801
6B0H	A_ARG_61	NH2	A_ASP_82	OD1	2.591
6B0H	A_ARG_61	NH2	A_ASP_82	OD2	3.548
6B0H	A_LYS_149	NZ	A_GLU_195	OE1	2.772
6B0H	A_LYS_183	NZ	A_GLU_187	OE1	2.500
6B0H	A_LYS_183	NZ	A_GLU_187	OE2	3.165
6B0H	C_ARG_61	NH2	C_GLU_81	OE2	3.031
6B0H	C_ARG_61	NH2	C_ASP_82	OD1	2.583
6B0H	C_ARG_61	NH2	C_ASP_82	OD2	3.415
6B0H	C_LYS_149	NZ	C_GLU_195	OE1	2.730

Table 785: 6B0H-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6BE2	H_ARG_38	NH1	H_ASP_89	OD1	2.773
6BE2	H_ARG_38	NH2	H_GLU_46	OE1	3.073
6BE2	H_ARG_38	NH2	H_ASP_89	OD1	3.711
6BE2	H_ARG_66	NH1	H_ASP_89	OD1	3.581
6BE2	H_ARG_66	NH1	H_ASP_89	OD2	2.936
6BE2	H_ARG_66	NH2	H_ASP_89	OD1	2.937
6BE2	H_ARG_66	NH2	H_ASP_89	OD2	3.585
6BE2	H_ARG_97	NH2	H_ASP_112	OD1	3.701
6BE2	H_ARG_97	NH2	H_ASP_112	OD2	2.907
6BE2	H_LYS_154	NZ	L_GLU_129	OE2	2.747
6BE2	L_LYS_49	NZ	H_GLU_108	OE2	2.828
6BE2	L_ARG_65	NH1	L_ASP_86	OD1	3.600
6BE2	L_ARG_65	NH1	L_ASP_86	OD2	2.741
6BE2	L_ARG_65	NH2	L_ASP_86	OD1	2.925
6BE2	L_ARG_65	NH2	L_ASP_86	OD2	3.429
6BE2	L_ARG_100	NH2	H_ASP_98	OD1	2.914
6BE2	L_LYS_107	NZ	L_ASP_89	OD1	2.799
6BE2	L_LYS_107	NZ	L_ASP_89	OD2	3.237
6BE2	L_LYS_171	NZ	L_GLU_87	OE1	2.671

Table 786: 6BE2-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID** **residue name** **residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6BE3	H_ARG_38	NH1	H_ASP_89	OD1	2.759
6BE3	H_ARG_38	NH2	H_GLU_46	OE1	3.050
6BE3	H_ARG_38	NH2	H_ASP_89	OD1	3.706
6BE3	H_ARG_66	NH1	H_ASP_89	OD1	3.702
6BE3	H_ARG_66	NH1	H_ASP_89	OD2	3.027
6BE3	H_ARG_66	NH2	H_ASP_89	OD1	2.994
6BE3	H_ARG_66	NH2	H_ASP_89	OD2	3.609
6BE3	H_ARG_97	NH2	H_ASP_112	OD1	3.602
6BE3	H_ARG_97	NH2	H_ASP_112	OD2	2.963
6BE3	H_LYS_154	NZ	L_GLU_129	OE2	2.742
6BE3	H_LYS_220	NZ	L_GLU_128	OE1	3.265
6BE3	H_LYS_220	NZ	L_GLU_128	OE2	2.896
6BE3	L_LYS_49	NZ	H_GLU_108	OE2	2.860
6BE3	L_ARG_65	NH1	L_ASP_86	OD1	3.594
6BE3	L_ARG_65	NH1	L_ASP_86	OD2	2.669
6BE3	L_ARG_65	NH2	L_ASP_86	OD1	2.920
6BE3	L_ARG_65	NH2	L_ASP_86	OD2	3.411
6BE3	L_ARG_100	NH2	H_ASP_98	OD1	3.147
6BE3	L_ARG_100	NH2	H_ASP_109	OD1	3.865
6BE3	L_LYS_171	NZ	L_GLU_87	OE2	2.868

Table 787: 6BE3-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6BE4	H_ARG_38	NH1	H_ASP_89	OD2	2.649
6BE4	H_ARG_38	NH2	H_GLU_46	OE1	3.034
6BE4	H_ARG_38	NH2	H_ASP_89	OD2	3.562
6BE4	H_ARG_66	NH1	H_ASP_89	OD1	2.856
6BE4	H_ARG_66	NH1	H_ASP_89	OD2	3.787
6BE4	H_ARG_66	NH2	H_ASP_89	OD1	3.571
6BE4	H_ARG_66	NH2	H_ASP_89	OD2	3.108
6BE4	H_ARG_97	NH2	H_ASP_112	OD1	3.623
6BE4	H_ARG_97	NH2	H_ASP_112	OD2	3.151
6BE4	H_LYS_154	NZ	L_GLU_129	OE1	2.824
6BE4	H_LYS_221	NZ	H_GLU_223	OE2	2.728
6BE4	L_ARG_65	NH1	L_ASP_86	OD1	3.135
6BE4	L_ARG_65	NH2	L_ASP_86	OD1	3.000
6BE4	L_ARG_65	NH2	L_ASP_86	OD2	2.628
6BE4	L_ARG_100	NH2	H_ASP_98	OD1	3.253
6BE4	L_ARG_100	NH2	H_ASP_109	OD1	3.926
6BE4	L_LYS_171	NZ	L_GLU_87	OE1	3.243
6BE4	L_ARG_194	NH1	L_ASP_156	OD2	3.672
6BE4	L_ARG_194	NH2	L_ASP_156	OD1	3.622
6BE4	L_ARG_194	NH2	L_ASP_156	OD2	3.634

Table 788: 6BE4-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6BIT	I.HIS_35	NE2	H.GLU_54	OE1	3.340
6BIT	I.ARG_40	NH2	I.GLU_46	OE1	2.891
6BIT	I.ARG_50	NH1	I.GLU_57	OE1	3.032
6BIT	I.ARG_50	NH2	I.GLU_57	OE1	3.316
6BIT	I.ARG_50	NH2	H.ASP_100	OD1	3.331
6BIT	I.ARG_50	NH2	H.ASP_101	OD1	3.135
6BIT	I.ARG_50	NH2	H.ASP_101	OD2	3.871
6BIT	I.LYS_59	NZ	I.GLU_57	OE2	3.249
6BIT	I.LYS_59	NZ	H.ASP_100	OD1	3.680
6BIT	I.LYS_63	NZ	I.GLU_46	OE1	3.651
6BIT	I.LYS_63	NZ	I.GLU_46	OE2	2.777
6BIT	I.LYS_67	NZ	I.ASP_90	OD1	3.668
6BIT	I.LYS_67	NZ	I.ASP_90	OD2	3.222
6BIT	I.LYS_208	NZ	K.GLU_123	OE2	3.567
6BIT	I.ARG_213	NH1	L.ASP_143	OD1	3.423
6BIT	K.ARG_61	NH1	K.GLU_81	OE2	3.581
6BIT	K.ARG_61	NH1	K.ASP_82	OD1	2.603
6BIT	K.ARG_61	NH1	K.ASP_82	OD2	3.046
6BIT	K.ARG_61	NH2	K.GLU_81	OE2	3.311
6BIT	K.ARG_96	NH1	H.GLU_54	OE1	3.223
6BIT	K.ARG_96	NH2	H.GLU_54	OE1	2.904
6BIT	K.ARG_96	NH2	H.GLU_54	OE2	3.687
6BIT	K.LYS_103	NZ	K.ASP_165	OD1	3.785
6BIT	K.LYS_149	NZ	K.GLU_195	OE1	3.128
6BIT	K.LYS_149	NZ	K.GLU_195	OE2	3.026
6BIT	K.LYS_183	NZ	K.GLU_187	OE2	3.925
6BIT	K.LYS_199	NZ	K.ASP_110	OD1	3.991
6BIT	K.LYS_199	NZ	K.ASP_110	OD2	3.333
6BIT	H.ARG_24	NH1	H.ASP_10	OD1	2.961
6BIT	H.ARG_24	NH1	H.ASP_10	OD2	3.571
6BIT	H.ARG_40	NH2	H.GLU_47	OE1	2.715
6BIT	H.ARG_40	NH2	H.GLU_47	OE2	3.722
6BIT	H.ARG_46	NH1	H.GLU_103	OE1	2.965
6BIT	H.ARG_46	NH2	H.GLU_103	OE1	2.785
6BIT	H.LYS_53	NZ	I.ASP_52	OD1	3.518
6BIT	H.LYS_53	NZ	I.GLU_54	OE1	2.817
6BIT	H.ARG_59	NH1	H.ASP_85	OD1	2.707
6BIT	H.ARG_59	NH1	H.ASP_85	OD2	3.494
6BIT	H.ARG_59	NH2	H.ASP_85	OD1	3.485
6BIT	H.ARG_59	NH2	H.ASP_85	OD2	2.872
6BIT	H.LYS_96	NZ	I.ASP_52	OD2	2.786
6BIT	H.LYS_96	NZ	I.ASP_55	OD1	3.426
6BIT	H.LYS_96	NZ	I.ASP_55	OD2	2.655
6BIT	H.LYS_96	NZ	I.GLU_57	OE1	2.771
6BIT	H.LYS_105	NZ	H.GLU_3	OE2	2.864
6BIT	J.HIS_35	NE2	G.GLU_54	OE1	3.221
6BIT	J.ARG_40	NH1	J.GLU_89	OE1	3.452
6BIT	J.ARG_50	NH1	J.GLU_57	OE2	2.730
6BIT	J.ARG_50	NH2	J.GLU_57	OE2	3.003
6BIT	J.ARG_50	NH2	G.ASP_100	OD1	3.724
6BIT	J.ARG_50	NH2	G.ASP_101	OD1	3.330
6BIT	J.LYS_59	NZ	J.GLU_57	OE1	3.468
6BIT	J.LYS_67	NZ	J.ASP_90	OD1	3.323
6BIT	J.LYS_208	NZ	L.GLU_123	OE2	3.539
6BIT	L.ARG_61	NH1	L.GLU_81	OE2	3.351
6BIT	L.ARG_61	NH1	L.ASP_82	OD1	2.686
6BIT	L.ARG_61	NH1	L.ASP_82	OD2	3.128

6BIT	L_ARG_61	NH2	L_GLU_81	OE2	3.264
6BIT	L_ARG_96	NH1	G_GLU_54	OE1	3.007
6BIT	L_ARG_96	NH2	G_GLU_54	OE1	2.768
6BIT	L_ARG_96	NH2	G_GLU_54	OE2	3.419
6BIT	L_LYS_103	NZ	L_ASP_165	OD1	3.780
6BIT	L_LYS_169	NZ	L_ASP_167	OD1	3.582
6BIT	L_LYS_169	NZ	L_ASP_167	OD2	3.848
6BIT	L_LYS_183	NZ	L_GLU_187	OE2	3.386
6BIT	L_HIS_189	ND1	L_ASP_151	OD2	2.866
6BIT	G_ARG_24	NH2	G_ASP_10	OD1	2.805
6BIT	G_ARG_24	NH2	G_ASP_10	OD2	3.462
6BIT	G_ARG_40	NH2	G_GLU_47	OE1	2.503
6BIT	G_ARG_40	NH2	G_GLU_47	OE2	3.922
6BIT	G_ARG_46	NH1	G_GLU_103	OE1	3.088
6BIT	G_ARG_46	NH1	G_GLU_103	OE2	3.993
6BIT	G_ARG_46	NH2	G_GLU_103	OE1	2.832
6BIT	G_LYS_53	NZ	J_ASP_52	OD1	2.843
6BIT	G_LYS_53	NZ	J_ASP_52	OD2	3.656
6BIT	G_LYS_53	NZ	J_GLU_54	OE1	2.681
6BIT	G_ARG_59	NH1	G_ASP_85	OD1	3.056
6BIT	G_ARG_59	NH1	G_ASP_85	OD2	3.619
6BIT	G_ARG_59	NH2	G_ASP_85	OD1	3.597
6BIT	G_ARG_59	NH2	G_ASP_85	OD2	2.677
6BIT	G_LYS_96	NZ	J_ASP_52	OD2	2.719
6BIT	G_LYS_96	NZ	J_ASP_55	OD1	3.165
6BIT	G_LYS_96	NZ	J_ASP_55	OD2	2.701
6BIT	G_LYS_96	NZ	J_GLU_57	OE2	2.943
6BIT	G_LYS_105	NZ	G_GLU_3	OE1	3.650

Table 789: 6BIT-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6BRB	D_LYS_5	NZ	D_GLU_3	OE1	2.959
6BRB	D_LYS_5	NZ	D_GLU_3	OE2	3.636
6BRB	D_LYS_33	NZ	D_GLU_63	OE1	3.743
6BRB	D_ARG_69	NH2	D_GLU_27	OE1	3.803
6BRB	D_ARG_69	NH2	D_GLU_27	OE2	3.492

Table 790: 6BRB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6BXA	A_ARG_37	NH1	C_GLU_101	OE1	3.957
6BXA	A_ARG_37	NH1	C_GLU_101	OE2	3.920
6BXA	A_ARG_37	NH2	C_GLU_101	OE1	3.689
6BXA	A_ARG_37	NH2	C_GLU_101	OE2	2.525
6BXA	A_LYS_77	NZ	A_ASP_53	OD2	3.745
6BXA	A_LYS_77	NZ	A_GLU_79	OE2	3.822
6BXA	A_LYS_77	NZ	C_ASP_34	OD2	2.860
6BXA	A_ARG_88	NH1	A_GLU_112	OE2	2.776
6BXA	A_ARG_88	NH2	A_GLU_61	OE1	3.314
6BXA	A_LYS_102	NZ	C_ASP_34	OD1	2.955
6BXA	A_ARG_154	NH1	A_ASP_177	OD1	3.604
6BXA	A_ARG_154	NH1	A_ASP_177	OD2	2.924
6BXA	A_ARG_172	NH2	A_GLU_149	OE2	3.243
6BXA	A_LYS_184	NZ	A_ASP_211	OD2	2.992
6BXA	A_LYS_184	NZ	B_ASP_133	OD2	2.709
6BXA	A_ARG_203	NH1	A_ASP_177	OD2	3.223
6BXA	A_LYS_221	NZ	A_GLU_189	OE1	2.737
6BXA	A_LYS_221	NZ	A_GLU_189	OE2	3.962
6BXA	A_LYS_227	NZ	A_GLU_188	OE2	3.721
6BXA	A_LYS_242	NZ	A_GLU_214	OE1	2.824
6BXA	A_LYS_247	NZ	A_ASP_251	OD2	3.024
6BXA	A_LYS_287	NZ	A_GLU_290	OE1	3.206
6BXA	A_LYS_287	NZ	A_GLU_290	OE2	3.365
6BXA	A_LYS_365	NZ	A_ASP_364	OD2	2.586
6BXA	A_ARG_430	NH1	A_ASP_425	OD2	2.739
6BXA	A_ARG_436	NH1	A_ASP_432	OD1	3.991
6BXA	A_ARG_436	NH1	A_ASP_432	OD2	3.281
6BXA	A_ARG_436	NH2	A_ASP_432	OD1	3.255
6BXA	A_ARG_436	NH2	A_ASP_432	OD2	3.091
6BXA	A_ARG_459	NH2	A_GLU_445	OE1	3.182
6BXA	B_ARG_37	NH2	D_GLU_101	OE1	3.840
6BXA	B_ARG_37	NH2	D_GLU_101	OE2	2.839
6BXA	B_LYS_77	NZ	B_ASP_53	OD2	3.863
6BXA	B_LYS_77	NZ	B_GLU_79	OE1	3.945
6BXA	B_LYS_77	NZ	B_GLU_79	OE2	3.546
6BXA	B_LYS_77	NZ	D_ASP_34	OD1	2.907
6BXA	B_ARG_88	NH1	B_GLU_112	OE2	2.748
6BXA	B_ARG_88	NH2	B_GLU_61	OE1	3.185
6BXA	B_ARG_93	NH2	B_GLU_64	OE1	2.917
6BXA	B_ARG_93	NH2	B_GLU_64	OE2	2.657
6BXA	B_LYS_102	NZ	D_ASP_34	OD2	3.845
6BXA	B_ARG_154	NH2	B_ASP_177	OD2	4.000
6BXA	B_LYS_184	NZ	A_ASP_133	OD2	2.771
6BXA	B_LYS_184	NZ	B_ASP_211	OD2	2.792
6BXA	B_ARG_203	NH1	B_ASP_177	OD2	3.054
6BXA	B_LYS_242	NZ	B_GLU_214	OE2	3.352
6BXA	B_LYS_247	NZ	B_ASP_251	OD2	2.934
6BXA	C_ARG_125	NH1	C_GLU_127	OE1	2.840
6BXA	C_ARG_199	NH2	C_ASP_187	OD1	3.576
6BXA	C_ARG_199	NH2	C_ASP_187	OD2	3.048
6BXA	C_LYS_210	NZ	C_GLU_160	OE1	3.673
6BXA	D_ARG_125	NH1	D_GLU_127	OE1	2.909
6BXA	D_ARG_199	NH2	D_ASP_187	OD1	2.818
6BXA	D_ARG_199	NH2	D_ASP_187	OD2	3.045

Table 791: 6BXA-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6BXC	A_ARG_88	NH1	A_GLU_112	OE2	3.484
6BXC	A_LYS_102	NZ	A_GLU_79	OE2	2.891
6BXC	A_LYS_102	NZ	A_ASP_104	OD2	2.667
6BXC	A_ARG_154	NH1	A_ASP_177	OD1	3.409
6BXC	A_ARG_154	NH1	A_ASP_177	OD2	2.660
6BXC	A_ARG_172	NH2	A_GLU_149	OE2	2.307
6BXC	A_LYS_184	NZ	C_ASP_34	OD2	3.851
6BXC	A_HIS_198	NE2	D_GLU_65	OE2	3.317
6BXC	A_ARG_203	NH2	A_ASP_235	OD2	3.882
6BXC	A_LYS_247	NZ	A_ASP_251	OD2	3.104
6BXC	A_HIS_314	ND1	A_GLU_290	OE2	3.791
6BXC	A_ARG_358	NH2	A_ASP_333	OD1	3.683
6BXC	A_ARG_358	NH2	A_ASP_333	OD2	2.263
6BXC	B_LYS_77	NZ	B_ASP_53	OD2	3.559
6BXC	B_LYS_77	NZ	B_GLU_79	OE1	3.681
6BXC	B_LYS_77	NZ	B_GLU_79	OE2	3.867
6BXC	B_ARG_88	NH1	B_GLU_112	OE2	2.734
6BXC	B_ARG_88	NH2	B_GLU_61	OE1	3.021
6BXC	B_ARG_154	NH1	B_ASP_177	OD1	3.602
6BXC	B_ARG_154	NH1	B_ASP_177	OD2	2.827
6BXC	B_LYS_159	NZ	D_ASP_34	OD2	3.891
6BXC	B_ARG_172	NH1	B_GLU_123	OE2	3.880
6BXC	B_ARG_172	NH2	B_GLU_123	OE1	3.923
6BXC	B_ARG_172	NH2	B_GLU_123	OE2	3.236
6BXC	B_ARG_172	NH2	B_GLU_149	OE2	2.392
6BXC	B_LYS_182	NZ	D_GLU_81	OE2	3.361
6BXC	B_LYS_184	NZ	D_ASP_34	OD2	3.547
6BXC	B_ARG_203	NH1	B_ASP_177	OD2	3.785
6BXC	B_LYS_221	NZ	B_GLU_189	OE1	2.699
6BXC	B_LYS_227	NZ	B_GLU_188	OE1	3.703
6BXC	B_LYS_227	NZ	B_GLU_188	OE2	2.986
6BXC	B_LYS_247	NZ	B_ASP_251	OD2	2.562
6BXC	B_LYS_287	NZ	B_GLU_290	OE1	3.663
6BXC	B_HIS_314	ND1	B_GLU_290	OE2	3.748
6BXC	B_ARG_358	NH1	B_ASP_333	OD2	2.973
6BXC	B_ARG_358	NH2	B_ASP_333	OD2	3.373
6BXC	B_HIS_420	NE2	B_ASP_396	OD2	3.947

Table 792: 6BXC-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6BXD	A_ARG_125	NH1	A_GLU_101	OE2	3.973
6BXD	A_ARG_199	NH2	A_ASP_187	OD1	3.406
6BXD	A_LYS_210	NZ	A_GLU_160	OE1	3.837

Table 793: 6BXD-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6BXE	A_LYS_63	NZ	A_GLU_65	OE2	3.493
6BXE	A_HIS_125	NE2	B_GLU_81	OE2	2.552
6BXE	B_LYS_63	NZ	B_GLU_65	OE2	3.400
6BXE	B_HIS_125	NE2	A_GLU_81	OE2	3.833
6BXE	B_ARG_168	NH1	B_GLU_154	OE1	2.963

Table 794: 6BXE-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6BZU	A_ARG_38	NH1	A_ASP_86	OD1	2.830
6BZU	A_ARG_38	NH2	A_GLU_46	OE1	2.706
6BZU	A_ARG_38	NH2	A_GLU_46	OE2	3.949
6BZU	A_ARG_38	NH2	A_ASP_86	OD1	3.655
6BZU	A_ARG_64	NH2	B_ASP_94	OD1	3.703
6BZU	A_ARG_66	NH1	A_ASP_86	OD1	3.455
6BZU	A_ARG_66	NH1	A_ASP_86	OD2	2.992
6BZU	A_ARG_66	NH2	A_ASP_86	OD1	2.772
6BZU	A_ARG_66	NH2	A_ASP_86	OD2	3.274
6BZU	A_ARG_94	NH1	A_ASP_27	OD1	3.748
6BZU	A_ARG_94	NH1	A_ASP_27	OD2	3.345
6BZU	A_ARG_94	NH2	A_ASP_101	OD1	3.362
6BZU	A_ARG_94	NH2	A_ASP_101	OD2	2.575
6BZU	A_LYS_143	NZ	A_ASP_144	OD1	3.544
6BZU	A_LYS_206	NZ	A_ASP_208	OD1	3.589
6BZU	A_LYS_206	NZ	A_ASP_208	OD2	3.931
6BZU	A_LYS_209	NZ	B_GLU_123	OE2	3.980
6BZU	B_ARG_18	NH1	B_ASP_76	OD2	3.621
6BZU	B_ARG_18	NH2	B_ASP_76	OD2	3.174
6BZU	B_ARG_18	NH2	F_ASP_70	OD2	2.642
6BZU	B_ARG_24	NH1	B_ASP_70	OD1	3.347
6BZU	B_ARG_24	NH1	F_ASP_76	OD1	3.597
6BZU	B_ARG_24	NH1	F_ASP_76	OD2	2.861
6BZU	B_LYS_39	NZ	B_ASP_81	OD1	2.891
6BZU	B_LYS_39	NZ	B_ASP_81	OD2	2.853
6BZU	B_ARG_61	NH1	B_ASP_82	OD1	3.370
6BZU	B_ARG_61	NH1	B_ASP_82	OD2	2.618
6BZU	B_ARG_61	NH2	B_ASP_82	OD1	3.228
6BZU	B_ARG_61	NH2	B_ASP_82	OD2	3.877
6BZU	B_LYS_149	NZ	B_GLU_195	OE2	3.153
6BZU	B_LYS_183	NZ	B_GLU_187	OE1	3.079
6BZU	B_LYS_183	NZ	B_GLU_187	OE2	2.953
6BZU	B_HIS_189	ND1	B_ASP_151	OD1	3.911
6BZU	B_HIS_189	ND1	B_ASP_151	OD2	2.360
6BZU	C_ARG_38	NH1	C_ASP_86	OD1	2.726
6BZU	C_ARG_38	NH2	C_GLU_46	OE1	2.726
6BZU	C_ARG_38	NH2	C_GLU_46	OE2	3.930
6BZU	C_ARG_38	NH2	C_ASP_86	OD1	3.517
6BZU	C_ARG_64	NH2	D_ASP_94	OD1	3.618
6BZU	C_ARG_66	NH1	C_ASP_86	OD1	3.539
6BZU	C_ARG_66	NH1	C_ASP_86	OD2	2.951
6BZU	C_ARG_66	NH2	C_ASP_86	OD1	2.783
6BZU	C_ARG_66	NH2	C_ASP_86	OD2	3.152
6BZU	C_ARG_94	NH1	C_ASP_27	OD2	3.167
6BZU	C_ARG_94	NH2	C_ASP_101	OD1	3.308
6BZU	C_ARG_94	NH2	C_ASP_101	OD2	2.595
6BZU	C_LYS_143	NZ	C_ASP_144	OD1	3.728
6BZU	C_LYS_206	NZ	C_ASP_208	OD1	3.579
6BZU	C_LYS_206	NZ	C_ASP_208	OD2	3.842
6BZU	C_LYS_210	NZ	C_GLU_212	OE2	3.412
6BZU	D_ARG_18	NH1	D_ASP_76	OD2	3.756
6BZU	D_ARG_18	NH2	D_ASP_76	OD2	3.639
6BZU	D_ARG_24	NH2	D_ASP_70	OD1	2.824
6BZU	D_ARG_24	NH2	D_ASP_70	OD2	3.740
6BZU	D_LYS_39	NZ	D_ASP_81	OD1	2.752
6BZU	D_LYS_39	NZ	D_ASP_81	OD2	2.990
6BZU	D_ARG_61	NH1	D_ASP_82	OD1	3.166

6BZU	D_ARG_61	NH1	D_ASP_82	OD2	2.739
6BZU	D_ARG_61	NH2	D_ASP_82	OD1	3.480
6BZU	D_LYS_183	NZ	D_GLU_187	OE1	2.974
6BZU	D_LYS_183	NZ	D_GLU_187	OE2	3.283
6BZU	D_HIS_189	ND1	D_ASP_151	OD2	3.151
6BZU	E_ARG_38	NH1	E_ASP_86	OD1	2.631
6BZU	E_ARG_38	NH2	E_GLU_46	OE1	2.648
6BZU	E_ARG_38	NH2	E_GLU_46	OE2	3.839
6BZU	E_ARG_38	NH2	E_ASP_86	OD1	3.682
6BZU	E_ARG_64	NH2	F_ASP_94	OD1	3.701
6BZU	E_ARG_66	NH1	E_ASP_86	OD1	3.600
6BZU	E_ARG_66	NH1	E_ASP_86	OD2	3.079
6BZU	E_ARG_66	NH2	E_ASP_86	OD1	3.151
6BZU	E_ARG_66	NH2	E_ASP_86	OD2	3.506
6BZU	E_ARG_94	NH1	E_ASP_27	OD1	3.760
6BZU	E_ARG_94	NH1	E_ASP_27	OD2	3.069
6BZU	E_ARG_94	NH2	E_ASP_101	OD1	3.575
6BZU	E_ARG_94	NH2	E_ASP_101	OD2	3.123
6BZU	E_LYS_143	NZ	E_ASP_144	OD1	3.596
6BZU	E_LYS_206	NZ	E_ASP_208	OD1	3.535
6BZU	E_LYS_206	NZ	E_ASP_208	OD2	3.797
6BZU	F_ARG_18	NH1	F_ASP_76	OD2	3.679
6BZU	F_ARG_18	NH2	F_ASP_76	OD2	3.069
6BZU	F_ARG_24	NH1	B_ASP_76	OD1	3.333
6BZU	F_ARG_24	NH1	B_ASP_76	OD2	3.080
6BZU	F_LYS_39	NZ	F_ASP_81	OD1	2.757
6BZU	F_LYS_39	NZ	F_ASP_81	OD2	3.575
6BZU	F_ARG_61	NH1	F_ASP_82	OD1	3.022
6BZU	F_ARG_61	NH1	F_ASP_82	OD2	2.655
6BZU	F_ARG_61	NH2	F_ASP_82	OD1	3.315
6BZU	F_LYS_149	NZ	F_GLU_195	OE2	3.477
6BZU	F_LYS_183	NZ	F_GLU_187	OE1	3.247
6BZU	F_LYS_183	NZ	F_GLU_187	OE2	3.817
6BZU	F_HIS_189	ND1	F_ASP_151	OD2	2.440
6BZU	G_ARG_38	NH1	G_ASP_86	OD1	2.471
6BZU	G_ARG_38	NH2	G_GLU_46	OE1	2.713
6BZU	G_ARG_38	NH2	G_GLU_46	OE2	3.875
6BZU	G_ARG_38	NH2	G_ASP_86	OD1	3.468
6BZU	G_ARG_64	NH2	H_ASP_94	OD1	3.197
6BZU	G_ARG_64	NH2	H_ASP_94	OD2	3.837
6BZU	G_ARG_66	NH1	G_ASP_86	OD1	3.947
6BZU	G_ARG_66	NH1	G_ASP_86	OD2	3.042
6BZU	G_ARG_66	NH2	G_ASP_86	OD1	2.869
6BZU	G_ARG_66	NH2	G_ASP_86	OD2	2.950
6BZU	G_ARG_94	NH1	G_ASP_27	OD2	3.484
6BZU	G_ARG_94	NH2	G_ASP_101	OD1	3.468
6BZU	G_ARG_94	NH2	G_ASP_101	OD2	2.612
6BZU	G_LYS_143	NZ	G_ASP_144	OD1	3.677
6BZU	G_LYS_206	NZ	G_ASP_208	OD1	3.523
6BZU	G_LYS_206	NZ	G_ASP_208	OD2	3.779
6BZU	G_LYS_209	NZ	H_GLU_123	OE1	2.734
6BZU	G_LYS_209	NZ	H_GLU_123	OE2	3.547
6BZU	G_LYS_210	NZ	G_GLU_212	OE2	3.397
6BZU	H_ARG_18	NH1	H_ASP_76	OD2	3.879
6BZU	H_ARG_18	NH2	H_ASP_76	OD2	3.299
6BZU	H_LYS_39	NZ	H_ASP_81	OD1	2.621
6BZU	H_LYS_39	NZ	H_ASP_81	OD2	3.478
6BZU	H_ARG_61	NH1	H_ASP_82	OD1	3.357

6BZU	H_ARG_61	NH1	H_ASP_82	OD2	2.854
6BZU	H_ARG_61	NH2	H_ASP_82	OD1	3.381
6BZU	H_LYS_149	NZ	H_GLU_195	OE2	3.735
6BZU	H_LYS_183	NZ	H_GLU_187	OE1	3.364
6BZU	H_LYS_183	NZ	H_GLU_187	OE2	3.961
6BZU	H_LYS_188	NZ	H_ASP_185	OD1	3.876

Table 795: 6BZU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6BZV	E_ARG_38	NH1	E_ASP_86	OD1	2.844
6BZV	E_ARG_38	NH2	E_GLU_46	OE1	2.762
6BZV	E_ARG_38	NH2	E_ASP_86	OD1	3.884
6BZV	E_ARG_66	NH1	E_ASP_86	OD2	3.252
6BZV	E_ARG_66	NH1	C_GLU_85	OE2	3.540
6BZV	E_ARG_66	NH2	E_ASP_86	OD1	3.097
6BZV	E_ARG_66	NH2	E_ASP_86	OD2	3.221
6BZV	E_ARG_66	NH2	C_GLU_85	OE2	3.482
6BZV	E_ARG_94	NH1	E_ASP_27	OD2	2.862
6BZV	E_ARG_94	NH2	E_ASP_101	OD1	3.797
6BZV	E_ARG_94	NH2	E_ASP_101	OD2	2.904
6BZV	E_LYS_143	NZ	E_ASP_144	OD1	3.856
6BZV	E_LYS_206	NZ	G_ASP_208	OD2	3.271
6BZV	E_LYS_209	NZ	F_GLU_123	OE1	3.953
6BZV	E_LYS_209	NZ	F_GLU_123	OE2	2.713
6BZV	E_LYS_210	NZ	E_GLU_212	OE2	2.831
6BZV	F_ARG_18	NH2	F_ASP_76	OD2	3.890
6BZV	F_LYS_39	NZ	F_ASP_81	OD1	3.137
6BZV	F_LYS_39	NZ	F_ASP_81	OD2	3.795
6BZV	F_ARG_61	NH1	F_ASP_82	OD1	3.530
6BZV	F_ARG_61	NH1	F_ASP_82	OD2	2.932
6BZV	F_ARG_61	NH2	F_ASP_82	OD1	3.252
6BZV	F_LYS_188	NZ	F_ASP_185	OD1	3.910
6BZV	A_ARG_38	NH1	A_ASP_86	OD1	2.647
6BZV	A_ARG_38	NH2	A_GLU_46	OE1	3.008
6BZV	A_ARG_38	NH2	A_ASP_86	OD1	3.189
6BZV	A_ARG_66	NH1	A_ASP_86	OD2	3.345
6BZV	A_ARG_66	NH2	A_ASP_86	OD1	3.206
6BZV	A_ARG_66	NH2	A_ASP_86	OD2	3.333
6BZV	A_ARG_94	NH1	A_ASP_27	OD2	2.749
6BZV	A_ARG_94	NH2	A_ASP_101	OD1	3.799
6BZV	A_ARG_94	NH2	A_ASP_101	OD2	2.974
6BZV	A_LYS_143	NZ	A_ASP_144	OD1	3.960
6BZV	A_LYS_206	NZ	A_ASP_208	OD1	3.297
6BZV	A_LYS_206	NZ	A_ASP_208	OD2	3.789
6BZV	A_LYS_209	NZ	B_GLU_123	OE1	2.709
6BZV	A_LYS_209	NZ	B_GLU_123	OE2	3.439
6BZV	A_LYS_210	NZ	A_GLU_212	OE2	2.656
6BZV	B_ARG_18	NH2	B_ASP_76	OD2	3.495
6BZV	B_ARG_24	NH2	B_ASP_70	OD1	3.551
6BZV	B_ARG_24	NH2	B_ASP_70	OD2	3.558
6BZV	B_LYS_39	NZ	B_ASP_81	OD1	2.943
6BZV	B_LYS_39	NZ	B_ASP_81	OD2	3.840
6BZV	B_ARG_61	NH1	B_ASP_82	OD1	2.943
6BZV	B_ARG_61	NH1	B_ASP_82	OD2	2.669
6BZV	B_ARG_61	NH2	B_ASP_82	OD1	3.350
6BZV	B_LYS_149	NZ	B_GLU_195	OE2	3.685
6BZV	B_LYS_183	NZ	B_GLU_187	OE1	3.842
6BZV	C_ARG_38	NH1	C_ASP_86	OD1	2.657
6BZV	C_ARG_38	NH2	C_GLU_46	OE1	3.551
6BZV	C_ARG_38	NH2	C_ASP_86	OD1	3.055
6BZV	C_ARG_66	NH1	C_ASP_86	OD2	3.524
6BZV	C_ARG_66	NH2	C_ASP_86	OD1	3.405
6BZV	C_ARG_66	NH2	C_ASP_86	OD2	3.206
6BZV	C_ARG_94	NH1	C_ASP_27	OD2	2.994
6BZV	C_ARG_94	NH2	C_ASP_101	OD1	3.607
6BZV	C_ARG_94	NH2	C_ASP_101	OD2	3.021

6BZV	C_LYS_143	NZ	C_ASP_144	OD1	3.671
6BZV	C_LYS_206	NZ	C_ASP_208	OD1	2.715
6BZV	C_LYS_206	NZ	C_ASP_208	OD2	3.362
6BZV	C_LYS_209	NZ	D_GLU_123	OE1	2.619
6BZV	C_LYS_209	NZ	D_GLU_123	OE2	2.945
6BZV	C_LYS_210	NZ	C_GLU_212	OE2	2.891
6BZV	D_ARG_18	NH2	D_ASP_76	OD2	3.172
6BZV	D_ARG_24	NH2	D_ASP_70	OD1	2.988
6BZV	D_ARG_24	NH2	D_ASP_70	OD2	3.384
6BZV	D_LYS_39	NZ	D_ASP_81	OD1	2.720
6BZV	D_LYS_39	NZ	D_ASP_81	OD2	3.480
6BZV	D_ARG_61	NH1	D_ASP_82	OD1	2.908
6BZV	D_ARG_61	NH1	D_ASP_82	OD2	2.744
6BZV	D_ARG_61	NH2	D_GLU_79	OE1	3.805
6BZV	D_ARG_61	NH2	D_ASP_82	OD1	3.651
6BZV	D_LYS_183	NZ	D_GLU_187	OE1	3.827
6BZV	D_LYS_183	NZ	D_GLU_187	OE2	3.971
6BZV	G_ARG_38	NH1	G_ASP_86	OD1	2.748
6BZV	G_ARG_38	NH2	G_GLU_46	OE1	3.230
6BZV	G_ARG_38	NH2	G_ASP_86	OD1	3.248
6BZV	G_ARG_66	NH1	G_ASP_86	OD2	3.499
6BZV	G_ARG_66	NH2	G_ASP_86	OD1	3.475
6BZV	G_ARG_66	NH2	G_ASP_86	OD2	3.645
6BZV	G_ARG_94	NH1	G_ASP_27	OD1	2.468
6BZV	G_ARG_94	NH2	G_ASP_101	OD1	3.530
6BZV	G_ARG_94	NH2	G_ASP_101	OD2	3.139
6BZV	G_LYS_143	NZ	G_ASP_144	OD1	3.706
6BZV	G_HIS_164	NE2	H_ASP_167	OD1	3.817
6BZV	G_LYS_209	NZ	H_GLU_123	OE1	3.054
6BZV	G_LYS_209	NZ	H_GLU_123	OE2	3.192
6BZV	G_LYS_210	NZ	G_GLU_212	OE2	2.995
6BZV	H_ARG_18	NH2	H_ASP_76	OD2	3.078
6BZV	H_LYS_39	NZ	H_ASP_81	OD1	2.837
6BZV	H_LYS_39	NZ	H_ASP_81	OD2	3.626
6BZV	H_ARG_61	NH1	H_ASP_82	OD1	3.084
6BZV	H_ARG_61	NH1	H_ASP_82	OD2	2.483
6BZV	H_ARG_61	NH2	H_ASP_82	OD1	2.797
6BZV	H_ARG_61	NH2	H_ASP_82	OD2	3.746
6BZV	H_LYS_103	NZ	H_GLU_165	OE1	3.239
6BZV	H_LYS_103	NZ	H_GLU_165	OE2	2.963
6BZV	H_LYS_149	NZ	H_GLU_195	OE2	3.595
6BZV	H_LYS_183	NZ	H_GLU_187	OE1	3.837
6BZV	H_LYS_183	NZ	H_GLU_187	OE2	3.903

Table 796: 6BZV-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6BZW	C_ARG_38	NH1	C_ASP_86	OD1	2.855
6BZW	C_ARG_38	NH2	C_GLU_46	OE1	2.761
6BZW	C_ARG_38	NH2	C_GLU_46	OE2	3.900
6BZW	C_ARG_38	NH2	C_ASP_86	OD1	3.525
6BZW	C_ARG_66	NH1	C_ASP_86	OD1	3.684
6BZW	C_ARG_66	NH1	C_ASP_86	OD2	2.944
6BZW	C_ARG_66	NH2	C_ASP_86	OD1	2.982
6BZW	C_ARG_66	NH2	C_ASP_86	OD2	3.451
6BZW	C_ARG_94	NH1	C_ASP_27	OD2	3.411
6BZW	C_ARG_94	NH2	C_ASP_101	OD1	3.817
6BZW	C_ARG_94	NH2	C_ASP_101	OD2	2.574
6BZW	C_LYS_143	NZ	C_ASP_144	OD1	3.327
6BZW	C_LYS_143	NZ	C_ASP_144	OD2	2.941
6BZW	C_LYS_209	NZ	D_GLU_123	OE1	2.857
6BZW	C_LYS_209	NZ	D_GLU_123	OE2	3.990
6BZW	C_LYS_210	NZ	C_GLU_212	OE2	3.580
6BZW	D_ARG_18	NH2	H_GLU_93	OE1	3.070
6BZW	D_LYS_39	NZ	D_ASP_81	OD1	2.338
6BZW	D_LYS_39	NZ	D_ASP_81	OD2	3.833
6BZW	D_ARG_61	NH1	D_ASP_82	OD1	3.630
6BZW	D_ARG_61	NH1	D_ASP_82	OD2	2.695
6BZW	D_ARG_61	NH2	D_ASP_82	OD1	3.497
6BZW	D_ARG_61	NH2	D_ASP_82	OD2	3.898
6BZW	D_LYS_149	NZ	D_GLU_195	OE1	3.578
6BZW	D_LYS_188	NZ	D_ASP_185	OD1	3.347
6BZW	D_HIS_189	ND1	D_ASP_151	OD2	2.863
6BZW	D_ARG_211	NH2	D_GLU_187	OE1	2.961
6BZW	A_ARG_38	NH1	A_ASP_86	OD1	2.806
6BZW	A_ARG_38	NH2	A_GLU_46	OE1	2.810
6BZW	A_ARG_38	NH2	A_ASP_86	OD1	3.534
6BZW	A_ARG_66	NH1	A_ASP_86	OD1	3.766
6BZW	A_ARG_66	NH1	A_ASP_86	OD2	3.088
6BZW	A_ARG_66	NH2	A_ASP_86	OD1	2.975
6BZW	A_ARG_66	NH2	A_ASP_86	OD2	3.224
6BZW	A_ARG_94	NH1	A_ASP_27	OD2	3.062
6BZW	A_ARG_94	NH2	A_ASP_101	OD1	3.805
6BZW	A_ARG_94	NH2	A_ASP_101	OD2	2.322
6BZW	A_LYS_143	NZ	A_ASP_144	OD1	3.396
6BZW	A_LYS_143	NZ	A_ASP_144	OD2	2.710
6BZW	A_LYS_209	NZ	B_GLU_123	OE1	2.988
6BZW	A_LYS_210	NZ	A_GLU_212	OE2	3.336
6BZW	B_ARG_18	NH2	B_ASP_76	OD2	3.990
6BZW	B_LYS_39	NZ	B_ASP_81	OD1	2.457
6BZW	B_LYS_39	NZ	B_ASP_81	OD2	3.775
6BZW	B_ARG_61	NH1	B_ASP_82	OD1	3.435
6BZW	B_ARG_61	NH1	B_ASP_82	OD2	2.481
6BZW	B_ARG_61	NH2	B_ASP_82	OD1	2.977
6BZW	B_ARG_61	NH2	B_ASP_82	OD2	3.551
6BZW	B_ARG_68	NH1	B_ASP_27C	OD2	3.000
6BZW	B_LYS_149	NZ	B_GLU_195	OE1	3.533
6BZW	B_LYS_188	NZ	B_ASP_185	OD1	3.312
6BZW	B_HIS_189	ND1	B_ASP_151	OD2	2.735
6BZW	B_LYS_190	NZ	B_GLU_213	OE2	3.979
6BZW	B_ARG_211	NH2	B_GLU_187	OE1	3.195
6BZW	E_ARG_38	NH1	E_ASP_86	OD1	2.836
6BZW	E_ARG_38	NH2	E_GLU_46	OE1	2.758
6BZW	E_ARG_38	NH2	E_GLU_46	OE2	3.957

6BZW	E_ARG_38	NH2	E_ASP_86	OD1	3.594
6BZW	E_ARG_66	NH1	E_ASP_86	OD1	3.616
6BZW	E_ARG_66	NH1	E_ASP_86	OD2	2.872
6BZW	E_ARG_66	NH2	E_ASP_86	OD1	2.980
6BZW	E_ARG_66	NH2	E_ASP_86	OD2	3.348
6BZW	E_ARG_94	NH1	E_ASP_27	OD2	3.258
6BZW	E_ARG_94	NH2	E_ASP_101	OD1	3.737
6BZW	E_ARG_94	NH2	E_ASP_101	OD2	2.526
6BZW	E_LYS_143	NZ	E_ASP_144	OD1	2.783
6BZW	E_LYS_143	NZ	E_ASP_144	OD2	3.427
6BZW	E_LYS_209	NZ	F_GLU_123	OE1	2.583
6BZW	E_LYS_209	NZ	F_GLU_123	OE2	3.254
6BZW	E_LYS_210	NZ	E_GLU_212	OE2	3.361
6BZW	F_ARG_18	NH2	F_ASP_76	OD2	3.915
6BZW	F_LYS_39	NZ	F_ASP_81	OD1	2.665
6BZW	F_ARG_61	NH2	F_ASP_82	OD1	2.596
6BZW	F_ARG_61	NH2	F_ASP_82	OD2	3.915
6BZW	F_LYS_149	NZ	F_GLU_195	OE1	3.703
6BZW	F_LYS_188	NZ	F_ASP_185	OD1	3.561
6BZW	F_ARG_211	NH2	F_GLU_187	OE1	3.709
6BZW	G_ARG_38	NH1	G_ASP_86	OD1	2.636
6BZW	G_ARG_38	NH2	G_GLU_46	OE1	3.016
6BZW	G_ARG_38	NH2	G_ASP_86	OD1	3.345
6BZW	G_ARG_66	NH1	G_ASP_86	OD1	3.851
6BZW	G_ARG_66	NH1	G_ASP_86	OD2	3.048
6BZW	G_ARG_66	NH2	G_ASP_86	OD1	2.949
6BZW	G_ARG_66	NH2	G_ASP_86	OD2	3.330
6BZW	G_ARG_94	NH1	G_ASP_27	OD2	3.098
6BZW	G_ARG_94	NH2	G_ASP_101	OD1	3.595
6BZW	G_ARG_94	NH2	G_ASP_101	OD2	2.509
6BZW	G_LYS_143	NZ	G_ASP_144	OD1	2.922
6BZW	G_LYS_143	NZ	G_ASP_144	OD2	2.656
6BZW	G_LYS_209	NZ	H_GLU_123	OE1	2.709
6BZW	G_LYS_209	NZ	H_GLU_123	OE2	2.569
6BZW	H_LYS_39	NZ	H_ASP_81	OD1	2.836
6BZW	H_ARG_61	NH1	H_GLU_79	OE1	3.176
6BZW	H_ARG_61	NH2	H_GLU_79	OE1	3.932
6BZW	H_ARG_61	NH2	H_ASP_82	OD1	2.618
6BZW	H_ARG_61	NH2	H_ASP_82	OD2	3.730
6BZW	H_LYS_149	NZ	H_GLU_195	OE1	3.312
6BZW	H_LYS_188	NZ	H_ASP_185	OD1	3.591
6BZW	H_LYS_190	NZ	H_GLU_213	OE2	3.965
6BZW	H_ARG_211	NH2	H_GLU_187	OE1	2.787

Table 797: 6BZW-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6BZY	H_ARG_38	NH1	H_ASP_86	OD1	2.808
6BZY	H_ARG_38	NH2	H_GLU_46	OE1	3.237
6BZY	H_ARG_38	NH2	H_ASP_86	OD1	3.627
6BZY	H_ARG_66	NH1	H_ASP_86	OD1	3.726
6BZY	H_ARG_66	NH1	H_ASP_86	OD2	3.046
6BZY	H_ARG_66	NH2	H_ASP_86	OD1	3.005
6BZY	H_ARG_66	NH2	H_ASP_86	OD2	3.522
6BZY	L_LYS_39	NZ	L_ASP_81	OD1	3.422
6BZY	L_LYS_39	NZ	L_ASP_81	OD2	3.246
6BZY	L_ARG_61	NH1	L_GLU_79	OE1	3.883
6BZY	L_ARG_61	NH1	L_GLU_79	OE2	3.484
6BZY	L_ARG_61	NH2	L_GLU_79	OE2	3.709
6BZY	L_ARG_61	NH2	L_ASP_82	OD1	2.811
6BZY	L_ARG_61	NH2	L_ASP_82	OD2	3.630
6BZY	L_LYS_92	NZ	L_GLU_93	OE1	2.944
6BZY	L_LYS_149	NZ	L_GLU_195	OE1	3.863
6BZY	L_LYS_149	NZ	L_GLU_195	OE2	3.027
6BZY	L_ARG_155	NH1	L_GLU_185	OE2	3.136
6BZY	L_ARG_155	NH2	L_GLU_185	OE1	2.999
6BZY	L_ARG_155	NH2	L_GLU_185	OE2	3.270
6BZY	L_LYS_183	NZ	L_GLU_187	OE1	3.043
6BZY	L_LYS_183	NZ	L_GLU_187	OE2	3.003
6BZY	L_HIS_189	ND1	L_ASP_151	OD2	2.978
6BZY	L_LYS_199	NZ	L_ASP_110	OD1	3.404
6BZY	L_LYS_199	NZ	L_ASP_110	OD2	3.217

Table 798: 6BZY-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6C5H	H_ARG_38	NH1	H_ASP_86	OD1	2.721
6C5H	H_ARG_38	NH2	H_GLU_46	OE1	2.994
6C5H	H_ARG_38	NH2	H_ASP_86	OD1	3.747
6C5H	H_ARG_66	NH1	H_ASP_86	OD1	3.644
6C5H	H_ARG_66	NH1	H_ASP_86	OD2	2.991
6C5H	H_ARG_66	NH2	H_ASP_86	OD1	2.973
6C5H	H_ARG_66	NH2	H_ASP_86	OD2	3.516
6C5H	H_LYS_75	NZ	H_ASP_72	OD2	3.835
6C5H	H_ARG_94	NH2	H_ASP_100	OD1	2.833
6C5H	H_ARG_94	NH2	H_ASP_100	OD2	3.662
6C5H	H_LYS_208	NZ	L_GLU_123	OE1	3.569
6C5H	L_ARG_61	NH1	L_GLU_79	OE1	3.434
6C5H	L_ARG_61	NH1	L_GLU_79	OE2	3.291
6C5H	L_ARG_61	NH2	L_GLU_79	OE1	3.399
6C5H	L_ARG_61	NH2	L_GLU_81	OE1	2.979
6C5H	L_ARG_61	NH2	L_GLU_81	OE2	3.883
6C5H	L_ARG_61	NH2	L_ASP_82	OD1	2.822
6C5H	L_ARG_61	NH2	L_ASP_82	OD2	3.827
6C5H	L_LYS_142	NZ	L_GLU_105	OE1	3.070
6C5H	L_ARG_155	NH1	L_GLU_185	OE1	2.690
6C5H	L_ARG_155	NH1	L_GLU_185	OE2	3.698
6C5H	L_ARG_155	NH2	L_GLU_185	OE1	3.395
6C5H	L_ARG_155	NH2	L_GLU_185	OE2	2.806
6C5H	L_HIS_189	ND1	L_ASP_151	OD2	2.883
6C5H	L_LYS_199	NZ	L_ASP_110	OD1	3.394
6C5H	L_LYS_199	NZ	L_ASP_110	OD2	3.049
6C5H	L_ARG_211	NH1	L_GLU_187	OE2	3.775

Table 799: 6C5H-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6C5I	H_ARG_38	NH1	H_ASP_86	OD1	2.831
6C5I	H_ARG_38	NH2	H_ASP_86	OD1	3.788
6C5I	H_ARG_66	NH1	H_ASP_86	OD1	3.709
6C5I	H_ARG_66	NH1	H_ASP_86	OD2	3.027
6C5I	H_ARG_66	NH2	H_ASP_86	OD1	2.746
6C5I	H_ARG_66	NH2	H_ASP_86	OD2	3.384
6C5I	H_ARG_94	NH2	H_ASP_100	OD1	3.126
6C5I	H_ARG_94	NH2	H_ASP_100	OD2	3.618
6C5I	H_HIS_164	NE2	L_ASP_167	OD2	3.802
6C5I	H_LYS_208	NZ	L_GLU_123	OE1	3.192
6C5I	L_ARG_24	NH2	L_ASP_70	OD2	3.159
6C5I	L_ARG_61	NH1	L_GLU_79	OE2	3.233
6C5I	L_ARG_61	NH2	L_GLU_79	OE1	3.749
6C5I	L_ARG_61	NH2	L_GLU_79	OE2	3.995
6C5I	L_ARG_61	NH2	L_GLU_81	OE1	2.811
6C5I	L_ARG_61	NH2	L_ASP_82	OD1	2.855
6C5I	L_ARG_61	NH2	L_ASP_82	OD2	3.717
6C5I	L_LYS_147	NZ	L_GLU_154	OE1	2.837
6C5I	L_LYS_147	NZ	L_GLU_154	OE2	3.916
6C5I	L_LYS_149	NZ	L_GLU_195	OE2	3.136
6C5I	L_LYS_199	NZ	L_ASP_110	OD1	3.935
6C5I	L_LYS_199	NZ	L_ASP_110	OD2	3.250

Table 800: 6C5I-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6C5J	H_ARG_38	NH1	H_ASP_86	OD1	2.836
6C5J	H_ARG_38	NH2	H_GLU_46	OE1	3.113
6C5J	H_ARG_38	NH2	H_ASP_86	OD1	3.867
6C5J	H_ARG_66	NH1	H_ASP_86	OD1	3.634
6C5J	H_ARG_66	NH1	H_ASP_86	OD2	2.729
6C5J	H_ARG_66	NH2	H_ASP_86	OD1	2.996
6C5J	H_ARG_66	NH2	H_ASP_86	OD2	3.388
6C5J	H_ARG_94	NH2	H_ASP_100	OD1	2.849
6C5J	H_ARG_94	NH2	H_ASP_100	OD2	3.422
6C5J	H_HIS_164	ND1	L_ASP_167	OD1	3.598
6C5J	L_ARG_24	NH1	L_ASP_70	OD1	3.086
6C5J	L_ARG_24	NH2	L_ASP_70	OD1	3.332
6C5J	L_ARG_54	NH1	L_ASP_60	OD1	3.010
6C5J	L_ARG_54	NH2	L_ASP_60	OD1	3.261
6C5J	L_ARG_61	NH1	L_GLU_79	OE2	3.828
6C5J	L_ARG_61	NH1	L_ASP_82	OD1	3.025
6C5J	L_ARG_61	NH1	L_ASP_82	OD2	3.858
6C5J	L_ARG_61	NH2	L_ASP_82	OD1	3.240
6C5J	L_ARG_61	NH2	L_ASP_82	OD2	2.681
6C5J	L_LYS_103	NZ	L_ASP_165	OD1	2.761
6C5J	L_LYS_103	NZ	L_ASP_165	OD2	3.775
6C5J	L_LYS_147	NZ	L_GLU_195	OE1	4.000
6C5J	L_LYS_149	NZ	L_GLU_195	OE1	3.633
6C5J	L_LYS_149	NZ	L_GLU_195	OE2	3.074
6C5J	L_ARG_155	NH1	L_GLU_185	OE1	3.663
6C5J	L_ARG_155	NH2	L_GLU_185	OE1	3.950
6C5J	L_HIS_189	ND1	L_ASP_151	OD2	3.348
6C5J	L_HIS_189	NE2	L_GLU_185	OE2	3.487

Table 801: 6C5J-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6C5K	H_ARG_38	NH1	H_ASP_86	OD1	2.795
6C5K	H_ARG_38	NH2	H_GLU_46	OE1	3.031
6C5K	H_ARG_38	NH2	H_ASP_86	OD1	3.813
6C5K	H_ARG_66	NH1	H_ASP_86	OD1	3.655
6C5K	H_ARG_66	NH1	H_ASP_86	OD2	2.836
6C5K	H_ARG_66	NH2	H_ASP_86	OD1	2.955
6C5K	H_ARG_66	NH2	H_ASP_86	OD2	3.481
6C5K	H_LYS_75	NZ	H_ASP_72	OD2	2.938
6C5K	H_ARG_94	NH2	H_ASP_100	OD1	2.779
6C5K	H_ARG_94	NH2	H_ASP_100	OD2	3.677
6C5K	A_ARG_38	NH1	A_ASP_86	OD1	2.763
6C5K	A_ARG_38	NH2	A_GLU_46	OE1	3.011
6C5K	A_ARG_38	NH2	A_ASP_86	OD1	3.834
6C5K	A_LYS_43	NZ	A_GLU_46	OE2	3.601
6C5K	A_ARG_66	NH1	A_ASP_86	OD1	3.702
6C5K	A_ARG_66	NH1	A_ASP_86	OD2	2.833
6C5K	A_ARG_66	NH2	A_ASP_86	OD1	2.960
6C5K	A_ARG_66	NH2	A_ASP_86	OD2	3.480
6C5K	A_LYS_75	NZ	A_ASP_72	OD2	3.839
6C5K	A_ARG_94	NH2	A_ASP_100	OD1	2.772
6C5K	A_ARG_94	NH2	A_ASP_100	OD2	3.672
6C5K	L_ARG_61	NH1	L_GLU_79	OE2	3.364
6C5K	L_ARG_61	NH2	L_GLU_79	OE1	3.895
6C5K	L_ARG_61	NH2	L_ASP_82	OD1	2.830
6C5K	L_ARG_61	NH2	L_ASP_82	OD2	3.538
6C5K	L_LYS_142	NZ	L_GLU_105	OE1	3.073
6C5K	L_LYS_142	NZ	L_GLU_105	OE2	3.102
6C5K	L_ARG_155	NH1	L_GLU_185	OE2	3.793
6C5K	L_ARG_155	NH2	L_GLU_185	OE2	3.452
6C5K	L_HIS_189	ND1	L_ASP_151	OD2	3.191
6C5K	L_LYS_199	NZ	L_ASP_110	OD2	3.559
6C5K	B_ARG_61	NH1	B_ASP_82	OD1	3.628
6C5K	B_ARG_61	NH1	B_ASP_82	OD2	2.598
6C5K	B_ARG_61	NH2	B_GLU_79	OE1	3.919
6C5K	B_ARG_61	NH2	B_ASP_82	OD1	2.914
6C5K	B_ARG_61	NH2	B_ASP_82	OD2	3.428
6C5K	B_ARG_77	NH1	B_ASP_60	OD1	3.873
6C5K	B_ARG_77	NH2	B_ASP_60	OD1	3.181
6C5K	B_ARG_77	NH2	B_ASP_60	OD2	3.837
6C5K	B_LYS_142	NZ	B_GLU_105	OE1	2.957
6C5K	B_LYS_142	NZ	B_GLU_105	OE2	3.105
6C5K	B_LYS_147	NZ	B_GLU_154	OE1	3.468
6C5K	B_LYS_149	NZ	B_GLU_195	OE1	3.461
6C5K	B_LYS_149	NZ	B_GLU_195	OE2	3.022
6C5K	B_LYS_183	NZ	B_GLU_187	OE1	3.352
6C5K	B_LYS_183	NZ	B_GLU_187	OE2	3.700
6C5K	B_HIS_189	ND1	B_ASP_151	OD2	3.184
6C5K	B_LYS_199	NZ	B_ASP_110	OD2	3.547

Table 802: 6C5K-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6C6X	A_ARG_38	NH1	A_ASP_86	OD1	2.916
6C6X	A_ARG_38	NH2	A_GLU_46	OE1	3.235
6C6X	A_ARG_38	NH2	A_ASP_86	OD1	3.654
6C6X	A_ARG_66	NH1	A_ASP_86	OD1	3.723
6C6X	A_ARG_66	NH1	A_ASP_86	OD2	3.099
6C6X	A_ARG_66	NH2	A_ASP_86	OD1	2.823
6C6X	A_ARG_66	NH2	A_ASP_86	OD2	3.594
6C6X	A_LYS_75	NZ	A_ASP_72	OD2	3.085
6C6X	A_LYS_94	NZ	A_ASP_27	OD1	3.369
6C6X	A_LYS_94	NZ	A_ASP_27	OD2	3.236
6C6X	A_LYS_143	NZ	A_ASP_144	OD1	3.316
6C6X	A_LYS_143	NZ	A_ASP_144	OD2	3.281
6C6X	B_ARG_24	NH2	B_ASP_70	OD2	3.520
6C6X	B_ARG_61	NH1	B_GLU_81	OE2	3.777
6C6X	B_ARG_61	NH2	B_GLU_81	OE2	2.736
6C6X	B_ARG_61	NH2	B_ASP_82	OD1	2.804
6C6X	B_ARG_61	NH2	B_ASP_82	OD2	3.688
6C6X	B_ARG_66	NH1	B_ASP_28	OD1	3.798
6C6X	B_LYS_103	NZ	B_GLU_105	OE1	3.590
6C6X	B_LYS_103	NZ	B_GLU_165	OE2	3.918
6C6X	B_LYS_147	NZ	B_GLU_195	OE2	3.987
6C6X	B_LYS_155	NZ	B_GLU_185	OE2	2.799
6C6X	B_HIS_189	ND1	B_ASP_151	OD2	3.308
6C6X	B_LYS_207	NZ	A_GLU_133	OE1	3.861
6C6X	C_ARG_38	NH1	C_ASP_86	OD1	2.686
6C6X	C_ARG_38	NH2	C_GLU_46	OE1	3.038
6C6X	C_ARG_38	NH2	C_ASP_86	OD1	3.600
6C6X	C_ARG_66	NH1	C_ASP_86	OD1	3.306
6C6X	C_ARG_66	NH1	C_ASP_86	OD2	3.758
6C6X	C_ARG_66	NH2	C_ASP_86	OD1	3.273
6C6X	C_ARG_66	NH2	C_ASP_86	OD2	2.552
6C6X	C_LYS_75	NZ	C_ASP_72	OD2	3.346
6C6X	C_LYS_94	NZ	C_ASP_27	OD1	3.722
6C6X	C_LYS_94	NZ	C_ASP_27	OD2	2.313
6C6X	C_LYS_143	NZ	C_ASP_144	OD1	3.560
6C6X	C_LYS_143	NZ	C_ASP_144	OD2	3.637
6C6X	D_ARG_61	NH2	D_GLU_81	OE2	3.760
6C6X	D_ARG_61	NH2	D_ASP_82	OD1	2.628
6C6X	D_ARG_61	NH2	D_ASP_82	OD2	3.448
6C6X	D_ARG_66	NH1	D_ASP_28	OD1	3.243
6C6X	D_ARG_66	NH1	D_ASP_28	OD2	3.729
6C6X	D_LYS_149	NZ	D_GLU_195	OE1	2.932
6C6X	D_LYS_155	NZ	D_GLU_185	OE2	3.201
6C6X	D_HIS_189	ND1	D_GLU_185	OE1	3.992
6C6X	E_ARG_38	NH1	E_ASP_86	OD1	2.787
6C6X	E_ARG_38	NH2	E_GLU_46	OE2	3.116
6C6X	E_ARG_38	NH2	E_ASP_86	OD1	3.697
6C6X	E_ARG_66	NH1	E_ASP_86	OD1	3.910
6C6X	E_ARG_66	NH1	E_ASP_86	OD2	3.139
6C6X	E_ARG_66	NH2	E_ASP_86	OD1	2.977
6C6X	E_ARG_66	NH2	E_ASP_86	OD2	3.550
6C6X	E_LYS_75	NZ	E_ASP_72	OD2	3.750
6C6X	E_LYS_94	NZ	E_ASP_27	OD1	3.779
6C6X	E_LYS_94	NZ	E_ASP_27	OD2	2.090
6C6X	E_LYS_143	NZ	E_ASP_144	OD1	3.540
6C6X	E_LYS_143	NZ	E_ASP_144	OD2	3.461
6C6X	F_ARG_24	NH1	F_ASP_70	OD1	3.452

6C6X	F_ARG_24	NH1	F_ASP_70	OD2	3.656
6C6X	F_ARG_24	NH2	F_ASP_70	OD2	3.468
6C6X	F_ARG_61	NH2	F_GLU_81	OE1	3.978
6C6X	F_ARG_61	NH2	F_ASP_82	OD1	2.486
6C6X	F_ARG_61	NH2	F_ASP_82	OD2	3.255
6C6X	F_ARG_66	NH1	F_ASP_28	OD1	3.527
6C6X	F_LYS_149	NZ	F_GLU_195	OE2	3.170
6C6X	F_LYS_169	NZ	F_ASP_167	OD1	3.680
6C6X	F_LYS_169	NZ	F_ASP_167	OD2	3.672
6C6X	F_LYS_169	NZ	F_ASP_170	OD2	2.920
6C6X	F_HIS_189	ND1	F_ASP_151	OD2	3.007
6C6X	H_ARG_38	NH1	H_ASP_86	OD1	2.791
6C6X	H_ARG_38	NH2	H_GLU_46	OE1	3.334
6C6X	H_ARG_38	NH2	H_ASP_86	OD1	3.541
6C6X	H_ARG_50	NH2	H_ASP_58	OD2	3.546
6C6X	H_LYS_64	NZ	H_ASP_58	OD1	3.715
6C6X	H_ARG_66	NH1	H_ASP_86	OD1	3.732
6C6X	H_ARG_66	NH1	H_ASP_86	OD2	3.107
6C6X	H_ARG_66	NH2	H_ASP_86	OD1	2.991
6C6X	H_ARG_66	NH2	H_ASP_86	OD2	3.632
6C6X	H_LYS_75	NZ	H_ASP_72	OD2	2.419
6C6X	H_LYS_143	NZ	H_ASP_144	OD1	3.420
6C6X	H_LYS_143	NZ	H_ASP_144	OD2	3.402
6C6X	H_ARG_210	NH1	H_GLU_212	OE2	2.704
6C6X	H_ARG_210	NH2	H_GLU_212	OE2	3.451
6C6X	L_ARG_24	NH2	L_ASP_70	OD1	3.667
6C6X	L_ARG_24	NH2	L_ASP_70	OD2	3.530
6C6X	L_ARG_61	NH2	L_GLU_81	OE1	3.682
6C6X	L_ARG_61	NH2	L_ASP_82	OD1	2.742
6C6X	L_ARG_61	NH2	L_ASP_82	OD2	3.507
6C6X	L_ARG_66	NH2	L_ASP_28	OD1	3.147
6C6X	L_ARG_66	NH2	L_ASP_28	OD2	3.848
6C6X	L_LYS_103	NZ	L_GLU_165	OE1	2.822
6C6X	L_LYS_103	NZ	L_GLU_165	OE2	3.323
6C6X	L_ARG_142	NH1	L_GLU_105	OE1	3.994
6C6X	L_LYS_149	NZ	L_GLU_195	OE1	3.966
6C6X	L_LYS_149	NZ	L_GLU_195	OE2	2.484
6C6X	L_HIS_189	ND1	L_ASP_151	OD2	3.012

Table 803: 6C6X-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6C6Y	A_ARG_38	NH1	A_ASP_86	OD1	3.064
6C6Y	A_ARG_38	NH2	A_GLU_46	OE2	3.198
6C6Y	A_ARG_66	NH1	A_ASP_86	OD2	3.498
6C6Y	A_ARG_66	NH2	A_ASP_86	OD1	3.146
6C6Y	A_ARG_66	NH2	A_ASP_86	OD2	3.520
6C6Y	A_LYS_94	NZ	A_ASP_27	OD2	3.819
6C6Y	A_LYS_143	NZ	A_ASP_144	OD1	3.805
6C6Y	B_ARG_24	NH1	B_ASP_70	OD1	3.301
6C6Y	B_ARG_24	NH2	B_ASP_70	OD1	3.031
6C6Y	B_ARG_24	NH2	B_ASP_70	OD2	3.357
6C6Y	B_ARG_61	NH1	B_GLU_81	OE1	3.827
6C6Y	B_ARG_61	NH2	B_GLU_81	OE1	3.995
6C6Y	B_ARG_61	NH2	B_ASP_82	OD1	2.452
6C6Y	B_ARG_61	NH2	B_ASP_82	OD2	3.063
6C6Y	B_ARG_66	NH1	B_ASP_28	OD1	2.856
6C6Y	B_LYS_103	NZ	B_GLU_165	OE1	2.786
6C6Y	B_LYS_103	NZ	B_GLU_165	OE2	3.365
6C6Y	B_ARG_142	NH1	B_GLU_165	OE2	3.444
6C6Y	B_LYS_149	NZ	B_GLU_195	OE1	3.173
6C6Y	B_LYS_149	NZ	B_GLU_195	OE2	3.288
6C6Y	B_LYS_155	NZ	B_GLU_185	OE1	3.980
6C6Y	B_LYS_155	NZ	B_GLU_185	OE2	2.781
6C6Y	H_ARG_38	NH1	H_ASP_86	OD1	3.029
6C6Y	H_ARG_38	NH2	H_GLU_46	OE2	2.521
6C6Y	H_ARG_38	NH2	H_ASP_86	OD1	3.913
6C6Y	H_ARG_50	NH2	H_ASP_58	OD2	3.613
6C6Y	H_ARG_66	NH1	H_ASP_86	OD1	3.184
6C6Y	H_ARG_66	NH1	H_ASP_86	OD2	2.116
6C6Y	H_ARG_66	NH2	H_ASP_86	OD1	3.133
6C6Y	H_ARG_66	NH2	H_ASP_86	OD2	3.619
6C6Y	L_ARG_24	NH1	L_ASP_70	OD1	3.969
6C6Y	L_ARG_24	NH1	L_ASP_70	OD2	3.418
6C6Y	L_ARG_24	NH2	L_ASP_70	OD1	3.004
6C6Y	L_ARG_24	NH2	L_ASP_70	OD2	2.849
6C6Y	L_ARG_61	NH2	L_ASP_82	OD1	2.482
6C6Y	L_ARG_61	NH2	L_ASP_82	OD2	3.036
6C6Y	L_ARG_66	NH1	L_ASP_28	OD1	3.067
6C6Y	L_LYS_103	NZ	L_GLU_165	OE1	2.476
6C6Y	L_ARG_142	NH2	L_GLU_165	OE2	3.885
6C6Y	L_LYS_147	NZ	L_GLU_195	OE1	3.059
6C6Y	L_LYS_147	NZ	L_GLU_195	OE2	3.820
6C6Y	L_LYS_155	NZ	L_GLU_185	OE2	3.070
6C6Y	R_LYS_400	NZ	L_ASP_28	OD2	3.363
6C6Y	R_ARG_401	NH2	R_ASP_444	OD2	3.769
6C6Y	R_LYS_413	NZ	R_GLU_382	OE2	3.002
6C6Y	R_LYS_453	NZ	R_ASP_422	OD2	3.217
6C6Y	R_LYS_502	NZ	R_GLU_513	OE1	3.001
6C6Y	R_LYS_543	NZ	L_GLU_55	OE2	2.973
6C6Y	R_LYS_587	NZ	R_GLU_382	OE1	3.401
6C6Y	R_LYS_587	NZ	R_GLU_382	OE2	2.619
6C6Y	S_LYS_400	NZ	B_ASP_28	OD1	3.764
6C6Y	S_LYS_400	NZ	B_ASP_28	OD2	2.712
6C6Y	S_ARG_401	NH2	S_ASP_444	OD2	2.856
6C6Y	S_LYS_413	NZ	S_GLU_382	OE2	3.998
6C6Y	S_LYS_453	NZ	S_ASP_422	OD2	2.144
6C6Y	S_LYS_502	NZ	S_GLU_513	OE1	3.472
6C6Y	S_LYS_543	NZ	B_GLU_55	OE2	3.134

6C6Y	S_LYS_587	NZ	S_GLU_382	OE1	3.941
6C6Y	S_LYS_587	NZ	S_GLU_382	OE2	2.874

Table 804: 6C6Y-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6C6Z	A_ARG_401	NH2	A_ASP_444	OD1	3.459
6C6Z	A_ARG_401	NH2	A_ASP_444	OD2	2.937
6C6Z	A_LYS_453	NZ	A_ASP_422	OD1	3.282
6C6Z	A_LYS_453	NZ	A_ASP_422	OD2	3.866
6C6Z	A_ARG_542	NH1	C_GLU_95	OE1	3.387
6C6Z	A_ARG_542	NH1	C_GLU_95	OE2	2.704
6C6Z	A_ARG_542	NH2	C_GLU_95	OE1	2.635
6C6Z	A_ARG_542	NH2	C_GLU_95	OE2	3.577
6C6Z	B_ARG_401	NH2	B_ASP_444	OD1	3.464
6C6Z	B_ARG_401	NH2	B_ASP_444	OD2	3.103
6C6Z	B_LYS_453	NZ	B_ASP_422	OD2	2.962
6C6Z	B_LYS_502	NZ	B_GLU_513	OE2	2.909
6C6Z	B_ARG_542	NH1	H_GLU_95	OE1	3.238
6C6Z	B_ARG_542	NH1	H_GLU_95	OE2	2.770
6C6Z	B_ARG_542	NH2	H_GLU_95	OE1	2.578
6C6Z	B_ARG_542	NH2	H_GLU_95	OE2	3.689
6C6Z	B_LYS_543	NZ	B_GLU_549	OE2	3.799
6C6Z	C_LYS_12	NZ	C_GLU_10	OE1	3.923
6C6Z	C_ARG_38	NH1	C_ASP_86	OD1	2.775
6C6Z	C_ARG_38	NH2	C_GLU_46	OE1	3.971
6C6Z	C_ARG_38	NH2	C_ASP_86	OD1	3.678
6C6Z	C_LYS_62	NZ	C_GLU_46	OE1	3.517
6C6Z	C_LYS_62	NZ	C_GLU_46	OE2	2.404
6C6Z	C_ARG_66	NH1	C_ASP_86	OD1	3.649
6C6Z	C_ARG_66	NH1	C_ASP_86	OD2	2.887
6C6Z	C_ARG_66	NH2	C_ASP_86	OD1	2.965
6C6Z	C_ARG_66	NH2	C_ASP_86	OD2	3.656
6C6Z	C_LYS_143	NZ	C_ASP_144	OD1	3.698
6C6Z	C_LYS_209	NZ	D_GLU_123	OE1	2.970
6C6Z	C_LYS_209	NZ	D_GLU_123	OE2	3.150
6C6Z	C_LYS_214	NZ	D_ASP_122	OD2	2.844
6C6Z	D_ARG_24	NH2	D_ASP_70	OD1	3.771
6C6Z	D_ARG_24	NH2	D_ASP_70	OD2	3.462
6C6Z	D_HIS_27D	NE2	A_GLU_536	OE1	2.616
6C6Z	D_LYS_39	NZ	D_GLU_81	OE1	3.045
6C6Z	D_ARG_61	NH1	D_ASP_82	OD1	3.547
6C6Z	D_ARG_61	NH1	D_ASP_82	OD2	2.767
6C6Z	D_ARG_61	NH2	D_GLU_79	OE2	3.892
6C6Z	D_ARG_61	NH2	D_ASP_82	OD1	2.888
6C6Z	D_ARG_61	NH2	D_ASP_82	OD2	3.519
6C6Z	D_LYS_103	NZ	D_GLU_105	OE1	3.035
6C6Z	D_LYS_149	NZ	D_GLU_195	OE2	3.680
6C6Z	D_LYS_183	NZ	D_GLU_187	OE1	3.446
6C6Z	D_LYS_183	NZ	D_GLU_187	OE2	2.362
6C6Z	H_LYS_12	NZ	H_GLU_10	OE1	3.627
6C6Z	H_ARG_38	NH1	H_ASP_86	OD1	2.800
6C6Z	H_ARG_38	NH2	H_GLU_46	OE1	3.855
6C6Z	H_ARG_38	NH2	H_ASP_86	OD1	3.819
6C6Z	H_LYS_62	NZ	H_GLU_46	OE1	3.413
6C6Z	H_LYS_62	NZ	H_GLU_46	OE2	2.893
6C6Z	H_ARG_66	NH1	H_ASP_86	OD1	3.573
6C6Z	H_ARG_66	NH1	H_ASP_86	OD2	2.784
6C6Z	H_ARG_66	NH2	H_ASP_86	OD1	2.918
6C6Z	H_ARG_66	NH2	H_ASP_86	OD2	3.610
6C6Z	H_LYS_143	NZ	H_ASP_144	OD1	3.196
6C6Z	H_LYS_143	NZ	H_ASP_144	OD2	3.107
6C6Z	H_LYS_206	NZ	H_ASP_208	OD1	2.733

6C6Z	H_LYS_209	NZ	L_GLU_123	OE1	3.044
6C6Z	H_LYS_209	NZ	L_GLU_123	OE2	3.156
6C6Z	L_HIS_27D	NE2	B_GLU_536	OE1	2.931
6C6Z	L_LYS_39	NZ	L_GLU_81	OE1	3.674
6C6Z	L_ARG_61	NH1	L_ASP_82	OD1	3.616
6C6Z	L_ARG_61	NH1	L_ASP_82	OD2	2.658
6C6Z	L_ARG_61	NH2	L_ASP_82	OD1	2.969
6C6Z	L_ARG_61	NH2	L_ASP_82	OD2	3.526
6C6Z	L_LYS_169	NZ	L_ASP_170	OD2	3.960
6C6Z	L_LYS_183	NZ	L_GLU_187	OE1	2.903
6C6Z	L_LYS_183	NZ	L_GLU_187	OE2	3.197
6C6Z	L_LYS_188	NZ	L_ASP_185	OD1	3.953

Table 805: 6C6Z-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6CUJ	A_HIS_325	NE2	A_ASP_359	OD2	3.301
6CUJ	A_ARG_337	NH1	A_GLU_322	OE1	3.884
6CUJ	A_LYS_378	NZ	A_ASP_388	OD2	3.300
6CUJ	B_HIS_327	ND1	B_ASP_359	OD2	3.102
6CUJ	B_HIS_327	NE2	B_GLU_329	OE2	2.543
6CUJ	B_HIS_327	NE2	B_ASP_359	OD2	3.671
6CUJ	B_ARG_337	NH1	B_GLU_322	OE1	3.772
6CUJ	B_HIS_362	ND1	B_ASP_359	OD1	3.012
6CUJ	B_HIS_362	ND1	B_ASP_359	OD2	2.820
6CUJ	B_LYS_404	NZ	A_GLU_292	OE1	3.957

Table 806: 6CUJ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6DC3	H_ARG_38	NH1	H_ASP_86	OD1	2.959
6DC3	H_ARG_38	NH2	H_GLU_46	OE1	3.231
6DC3	H_ARG_38	NH2	H_GLU_46	OE2	3.389
6DC3	H_ARG_66	NH2	H_ASP_86	OD1	3.488
6DC3	H_ARG_66	NH2	H_ASP_86	OD2	2.922
6DC3	H_ARG_94	NH2	H_ASP_101	OD1	3.653
6DC3	H_ARG_94	NH2	H_ASP_101	OD2	2.581
6DC3	H_LYS_143	NZ	L_GLU_125	OE2	3.101
6DC3	H_LYS_209	NZ	L_GLU_124	OE1	3.719
6DC3	H_ARG_210	NH1	H_GLU_212	OE2	3.787
6DC3	H_ARG_210	NH2	H_GLU_212	OE2	3.635
6DC3	L_ARG_61	NH1	L_ASP_82	OD2	2.982
6DC3	L_ARG_61	NH2	L_ASP_82	OD1	2.867
6DC3	L_ARG_61	NH2	L_ASP_82	OD2	2.906
6DC3	F_ARG_49	NH1	F_ASP_368	OD1	2.816
6DC3	F_ARG_49	NH1	F_ASP_368	OD2	3.848
6DC3	F_LYS_166	NZ	F_GLU_163	OE1	2.612
6DC3	F_LYS_168	NZ	H_ASP_53	OD2	2.485
6DC3	F_LYS_176	NZ	F_ASP_263	OD1	3.442
6DC3	F_LYS_176	NZ	F_ASP_263	OD2	3.080
6DC3	F_LYS_191	NZ	F_GLU_60	OE1	2.907
6DC3	F_LYS_191	NZ	F_GLU_60	OE2	3.428
6DC3	F_LYS_196	NZ	F_GLU_295	OE1	2.816
6DC3	F_ARG_229	NH1	F_GLU_256	OE1	3.821
6DC3	F_ARG_229	NH1	F_GLU_256	OE2	2.936
6DC3	F_ARG_229	NH2	F_GLU_256	OE1	2.824
6DC3	F_ARG_229	NH2	F_GLU_256	OE2	3.412
6DC3	F_ARG_235	NH2	F_GLU_232	OE1	3.589
6DC3	F_ARG_235	NH2	F_GLU_232	OE2	3.188
6DC3	F_ARG_336	NH2	F_ASP_338	OD1	3.536
6DC3	F_ARG_336	NH2	F_ASP_338	OD2	3.006
6DC3	F_ARG_364	NH1	F_ASP_310	OD1	3.283
6DC3	F_ARG_364	NH2	F_ASP_310	OD1	2.353
6DC3	F_LYS_394	NZ	F_ASP_489	OD1	2.937
6DC3	F_LYS_433	NZ	F_ASP_440	OD1	3.790
6DC3	F_LYS_433	NZ	F_ASP_440	OD2	2.911
6DC3	F_LYS_461	NZ	F_ASP_448	OD1	3.211
6DC3	F_LYS_498	NZ	F_GLU_487	OE2	3.896

Table 807: 6DC3-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6DC4	H_HIS_35	NE2	H_GLU_52	OE2	2.774
6DC4	H_ARG_38	NH1	H_ASP_86	OD1	2.825
6DC4	H_ARG_38	NH2	H_GLU_46	OE1	3.316
6DC4	H_ARG_38	NH2	H_ASP_86	OD1	3.824
6DC4	H_LYS_62	NZ	H_GLU_46	OE1	3.857
6DC4	H_LYS_62	NZ	H_GLU_46	OE2	2.772
6DC4	H_ARG_66	NH1	H_ASP_86	OD1	3.550
6DC4	H_ARG_66	NH1	H_ASP_86	OD2	2.921
6DC4	H_ARG_66	NH2	H_ASP_86	OD1	2.875
6DC4	H_ARG_66	NH2	H_ASP_86	OD2	3.553
6DC4	H_LYS_143	NZ	H_ASP_144	OD1	2.940
6DC4	H_LYS_143	NZ	H_ASP_144	OD2	2.949
6DC4	H_LYS_209	NZ	L_GLU_123	OE1	3.056
6DC4	H_LYS_210	NZ	H_GLU_212	OE2	2.245
6DC4	L_ARG_24	NH2	L_ASP_70	OD1	2.900
6DC4	L_ARG_24	NH2	L_ASP_70	OD2	3.578
6DC4	L_ARG_61	NH2	L_GLU_81	OE2	3.633
6DC4	L_ARG_61	NH2	L_ASP_82	OD1	2.855
6DC4	L_ARG_61	NH2	L_ASP_82	OD2	3.416

Table 808: 6DC4-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID** **residue name** **residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6DC5	A_ARG_49	NH2	A_ASP_368	OD1	3.110
6DC5	A_LYS_85	NZ	A_GLU_82	OE1	3.470
6DC5	A_LYS_87	NZ	A_ASP_84	OD1	3.601
6DC5	A_LYS_156	NZ	D_GLU_463	OE1	3.876
6DC5	A_LYS_166	NZ	A_GLU_163	OE1	3.173
6DC5	A_LYS_166	NZ	A_GLU_163	OE2	3.169
6DC5	A_LYS_168	NZ	A_GLU_294	OE1	3.265
6DC5	A_LYS_176	NZ	A_ASP_263	OD2	2.052
6DC5	A_LYS_191	NZ	A_GLU_60	OE1	3.950
6DC5	A_LYS_196	NZ	A_ASP_200	OD2	2.872
6DC5	A_LYS_196	NZ	A_GLU_295	OE1	2.434
6DC5	A_LYS_196	NZ	A_GLU_295	OE2	3.186
6DC5	A_LYS_226	NZ	A_GLU_222	OE2	3.817
6DC5	A_ARG_229	NH1	A_GLU_256	OE1	3.604
6DC5	A_ARG_229	NH1	A_GLU_256	OE2	2.958
6DC5	A_ARG_229	NH2	A_GLU_256	OE1	2.962
6DC5	A_ARG_229	NH2	A_GLU_256	OE2	3.782
6DC5	A_ARG_235	NH1	A_GLU_232	OE1	2.605
6DC5	A_ARG_235	NH1	A_GLU_232	OE2	2.938
6DC5	A_ARG_336	NH2	A_ASP_338	OD1	3.564
6DC5	A_ARG_336	NH2	A_ASP_338	OD2	2.679
6DC5	A_ARG_364	NH1	A_ASP_310	OD1	2.528
6DC5	A_ARG_364	NH2	A_ASP_310	OD1	3.947
6DC5	A_LYS_394	NZ	A_ASP_489	OD1	2.355
6DC5	A_LYS_394	NZ	A_ASP_489	OD2	3.843
6DC5	A_LYS_399	NZ	G_GLU_497	OE2	2.871
6DC5	A_LYS_427	NZ	A_ASP_448	OD1	3.250
6DC5	A_LYS_427	NZ	A_ASP_448	OD2	2.579
6DC5	A_LYS_461	NZ	A_ASP_448	OD1	2.319
6DC5	A_LYS_498	NZ	A_GLU_487	OE1	3.625
6DC5	A_LYS_498	NZ	A_GLU_487	OE2	2.810
6DC5	D_LYS_42	NZ	D_GLU_31	OE2	3.526
6DC5	D_ARG_49	NH2	D_ASP_368	OD1	2.868
6DC5	D_LYS_75	NZ	G_GLU_218	OE2	2.912
6DC5	D_LYS_85	NZ	D_GLU_82	OE1	3.435
6DC5	D_LYS_166	NZ	D_GLU_163	OE1	3.454
6DC5	D_LYS_166	NZ	D_GLU_163	OE2	3.601
6DC5	D_LYS_168	NZ	D_GLU_294	OE1	3.339
6DC5	D_LYS_168	NZ	D_GLU_294	OE2	3.380
6DC5	D_LYS_176	NZ	D_ASP_263	OD1	3.729
6DC5	D_LYS_176	NZ	D_ASP_263	OD2	2.442
6DC5	D_LYS_196	NZ	D_ASP_200	OD2	2.508
6DC5	D_LYS_196	NZ	D_GLU_295	OE1	2.680
6DC5	D_LYS_196	NZ	D_GLU_295	OE2	3.385
6DC5	D_LYS_209	NZ	E_GLU_53	OE2	3.142
6DC5	D_LYS_209	NZ	E_ASP_100G	OD2	3.755
6DC5	D_LYS_226	NZ	D_GLU_222	OE2	3.264
6DC5	D_ARG_229	NH1	D_GLU_256	OE1	3.363
6DC5	D_ARG_229	NH1	D_GLU_256	OE2	3.131
6DC5	D_ARG_229	NH2	D_GLU_256	OE1	3.395
6DC5	D_ARG_235	NH1	D_GLU_232	OE1	3.378
6DC5	D_ARG_235	NH1	D_GLU_232	OE2	2.564
6DC5	D_ARG_336	NH2	D_ASP_338	OD1	3.496
6DC5	D_ARG_336	NH2	D_ASP_338	OD2	2.373
6DC5	D_ARG_364	NH1	D_ASP_310	OD1	2.428
6DC5	D_ARG_364	NH2	D_ASP_310	OD1	3.463
6DC5	D_LYS_394	NZ	D_ASP_489	OD1	2.520

6DC5	D_LYS_427	NZ	D_ASP_448	OD1	3.113
6DC5	D_LYS_427	NZ	D_ASP_448	OD2	2.130
6DC5	D_LYS_433	NZ	D_ASP_440	OD2	3.766
6DC5	G_ARG_49	NH2	G_ASP_368	OD1	3.771
6DC5	G_LYS_68	NZ	G_GLU_66	OE2	3.905
6DC5	G_LYS_77	NZ	A_GLU_222	OE2	3.675
6DC5	G_LYS_85	NZ	G_GLU_82	OE1	2.899
6DC5	G_LYS_87	NZ	G_ASP_84	OD1	3.393
6DC5	G_LYS_166	NZ	G_GLU_163	OE1	3.829
6DC5	G_LYS_166	NZ	G_GLU_163	OE2	3.728
6DC5	G_LYS_168	NZ	G_GLU_294	OE1	3.141
6DC5	G_LYS_176	NZ	G_ASP_263	OD1	3.769
6DC5	G_LYS_176	NZ	G_ASP_263	OD2	2.528
6DC5	G_LYS_191	NZ	G_GLU_60	OE1	3.637
6DC5	G_LYS_191	NZ	G_GLU_60	OE2	2.059
6DC5	G_LYS_196	NZ	G_GLU_295	OE1	3.725
6DC5	G_LYS_196	NZ	G_GLU_295	OE2	2.152
6DC5	G_LYS_209	NZ	H_GLU_53	OE2	3.533
6DC5	G_LYS_209	NZ	H_ASP_100G	OD2	3.715
6DC5	G_ARG_229	NH1	G_GLU_256	OE1	3.620
6DC5	G_ARG_229	NH1	G_GLU_256	OE2	2.755
6DC5	G_ARG_229	NH2	G_GLU_256	OE1	2.678
6DC5	G_ARG_229	NH2	G_GLU_256	OE2	3.180
6DC5	G_ARG_235	NH1	G_GLU_232	OE1	3.701
6DC5	G_ARG_235	NH1	G_GLU_232	OE2	2.639
6DC5	G_ARG_336	NH2	G_ASP_338	OD1	3.302
6DC5	G_ARG_364	NH1	G_ASP_310	OD1	2.671
6DC5	G_ARG_364	NH2	G_ASP_310	OD1	2.918
6DC5	G_LYS_399	NZ	D_GLU_497	OE1	3.390
6DC5	G_LYS_399	NZ	D_GLU_497	OE2	2.804
6DC5	G_LYS_461	NZ	G_ASP_448	OD1	3.243
6DC5	B_LYS_12	NZ	B_GLU_10	OE1	3.494
6DC5	B_HIS_35	NE2	B_GLU_52	OE2	2.642
6DC5	B_ARG_38	NH1	B_ASP_86	OD1	3.077
6DC5	B_ARG_38	NH2	B_GLU_46	OE1	3.245
6DC5	B_LYS_62	NZ	B_GLU_46	OE2	3.113
6DC5	B_ARG_66	NH1	B_ASP_86	OD1	3.647
6DC5	B_ARG_66	NH1	B_ASP_86	OD2	3.361
6DC5	B_ARG_66	NH2	B_ASP_86	OD1	2.784
6DC5	B_ARG_66	NH2	B_ASP_86	OD2	3.528
6DC5	B_LYS_143	NZ	B_ASP_144	OD1	3.448
6DC5	B_LYS_143	NZ	B_ASP_144	OD2	3.641
6DC5	B_LYS_209	NZ	C_GLU_123	OE1	2.374
6DC5	B_LYS_209	NZ	C_GLU_123	OE2	3.312
6DC5	B_LYS_210	NZ	B_GLU_212	OE2	2.833
6DC5	C_ARG_61	NH2	C_GLU_81	OE2	3.401
6DC5	C_ARG_61	NH2	C_ASP_82	OD1	3.387
6DC5	C_ARG_61	NH2	C_ASP_82	OD2	3.483
6DC5	E_LYS_12	NZ	E_GLU_10	OE1	3.386
6DC5	E_HIS_35	NE2	E_GLU_52	OE2	3.002
6DC5	E_ARG_38	NH1	E_ASP_86	OD1	3.042
6DC5	E_ARG_38	NH2	E_GLU_46	OE1	3.298
6DC5	E_LYS_62	NZ	E_GLU_46	OE1	3.343
6DC5	E_LYS_62	NZ	E_GLU_46	OE2	2.685
6DC5	E_ARG_66	NH1	E_ASP_86	OD1	3.530
6DC5	E_ARG_66	NH1	E_ASP_86	OD2	3.256
6DC5	E_ARG_66	NH2	E_ASP_86	OD1	2.815
6DC5	E_ARG_66	NH2	E_ASP_86	OD2	3.601

6DC5	E.LYS_143	NZ	E.ASP_144	OD1	3.756
6DC5	E.LYS_143	NZ	E.ASP_144	OD2	3.843
6DC5	E.LYS_209	NZ	F.GLU_123	OE1	3.793
6DC5	E.LYS_210	NZ	E.GLU_212	OE2	3.622
6DC5	F_ARG_24	NH1	F.ASP_70	OD1	3.764
6DC5	F_ARG_24	NH2	F.ASP_70	OD1	2.904
6DC5	F_ARG_24	NH2	F.ASP_70	OD2	2.994
6DC5	F_ARG_61	NH2	F.GLU_81	OE2	3.917
6DC5	F_ARG_61	NH2	F.ASP_82	OD1	2.920
6DC5	F_ARG_61	NH2	F.ASP_82	OD2	3.281
6DC5	F.LYS_103	NZ	F.ASP_105	OD1	3.853
6DC5	F.LYS_107	NZ	F.GLU_17	OE1	3.389
6DC5	F.LYS_107	NZ	F.GLU_17	OE2	3.533
6DC5	H.HIS_35	NE2	H.GLU_52	OE2	2.720
6DC5	H_ARG_38	NH1	H.ASP_86	OD1	3.016
6DC5	H_ARG_38	NH2	H.GLU_46	OE1	3.352
6DC5	H_ARG_38	NH2	H.ASP_86	OD1	3.965
6DC5	H.LYS_62	NZ	H.GLU_46	OE1	3.843
6DC5	H.LYS_62	NZ	H.GLU_46	OE2	2.697
6DC5	H_ARG_66	NH1	H.ASP_86	OD1	3.199
6DC5	H_ARG_66	NH1	H.ASP_86	OD2	2.905
6DC5	H_ARG_66	NH2	H.ASP_86	OD1	3.432
6DC5	H.LYS_143	NZ	H.ASP_144	OD1	3.438
6DC5	H.LYS_143	NZ	H.ASP_	OD2	3.755
6DC5	H.LYS_	NZ	I.GLU_	OE1	2.846
6DC5	H.LYS_	NZ	I.ASP_	OD1	3.400
6DC5	H.LYS_	NZ	I.ASP_	OD2	3.825
6DC5	I_ARG_24	NH1	I.ASP_70	OD2	3.681
6DC5	I_ARG_61	NH2	I.ASP_82	OD1	2.828
6DC5	I_ARG_61	NH2	I.ASP_82	OD2	3.083
6DC5	I.LYS_107	NZ	I.GLU_17	OE1	3.661
6DC5	I.LYS_107	NZ	I.GLU_17	OE2	3.133
6DC5	I.LYS_149	NZ	I.GLU_195	OE1	3.809

Table 809: 6DC5-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6DCV	L_ARG_18	NH2	L_ASP_76	OD1	3.175
6DCV	L_ARG_61	NH1	L_ASP_82	OD1	3.860
6DCV	L_ARG_61	NH1	L_ASP_82	OD2	2.769
6DCV	L_ARG_61	NH2	L_ASP_82	OD1	2.985
6DCV	L_ARG_61	NH2	L_ASP_82	OD2	3.307
6DCV	L_LYS_149	NZ	L_GLU_195	OE1	2.823
6DCV	L_LYS_149	NZ	L_GLU_195	OE2	3.954
6DCV	L_LYS_183	NZ	L_GLU_187	OE2	2.410
6DCV	L_LYS_188	NZ	L_ASP_185	OD1	3.076
6DCV	L_HIS_189	ND1	L_ASP_151	OD2	3.050
6DCV	H_ARG_12	NH1	H_GLU_10	OE1	3.321
6DCV	H_ARG_12	NH2	H_GLU_10	OE1	3.424
6DCV	H_LYS_43	NZ	L_ASP_9	OD1	3.193
6DCV	H_ARG_58	NH1	H_ASP_56	OD1	3.128
6DCV	H_ARG_58	NH1	H_ASP_56	OD2	3.930
6DCV	H_HIS_66	ND1	H_ASP_86	OD1	3.802
6DCV	H_HIS_66	NE2	H_ASP_86	OD2	3.695
6DCV	H_ARG_94	NH2	H_ASP_101	OD1	3.792
6DCV	H_ARG_94	NH2	H_ASP_101	OD2	3.895
6DCV	H_ARG_98	NH1	H_ASP_96	OD2	3.931
6DCV	H_ARG_98	NH2	H_ASP_31	OD2	3.613
6DCV	H_LYS_145	NZ	H_ASP_146	OD1	3.176
6DCV	H_LYS_145	NZ	H_ASP_146	OD2	2.821
6DCV	H_LYS_221	NZ	L_GLU_123	OE1	3.166
6DCV	H_ARG_222	NH1	H_GLU_226	OE2	3.915
6DCV	A_ARG_18	NH2	A_ASP_76	OD1	2.925
6DCV	A_ARG_61	NH1	A_ASP_82	OD1	3.927
6DCV	A_ARG_61	NH1	A_ASP_82	OD2	2.798
6DCV	A_ARG_61	NH2	A_ASP_82	OD1	2.940
6DCV	A_ARG_61	NH2	A_ASP_82	OD2	3.262
6DCV	A_LYS_149	NZ	A_GLU_195	OE1	2.726
6DCV	A_HIS_189	ND1	A_ASP_151	OD2	3.062
6DCV	B_ARG_12	NH1	B_GLU_10	OE1	3.306
6DCV	B_ARG_12	NH2	B_GLU_10	OE1	3.831
6DCV	B_LYS_13	NZ	B_GLU_16	OE2	3.930
6DCV	B_LYS_43	NZ	A_ASP_9	OD1	3.127
6DCV	B_ARG_58	NH1	B_ASP_56	OD1	3.719
6DCV	B_ARG_58	NH1	B_ASP_56	OD2	3.964
6DCV	B_ARG_58	NH2	B_ASP_56	OD2	3.300
6DCV	B_HIS_66	NE2	B_ASP_86	OD1	2.995
6DCV	B_HIS_66	NE2	B_ASP_86	OD2	3.037
6DCV	B_ARG_94	NH2	B_ASP_101	OD1	3.995
6DCV	B_ARG_94	NH2	B_ASP_101	OD2	3.590
6DCV	B_ARG_98	NH2	B_ASP_31	OD2	3.052
6DCV	B_LYS_145	NZ	B_ASP_146	OD1	3.023
6DCV	B_LYS_145	NZ	B_ASP_146	OD2	2.799
6DCV	B_LYS_221	NZ	A_GLU_123	OE1	3.096

Table 810: 6DCV-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6DCW	L_ARG_18	NH1	L_ASP_76	OD1	3.895
6DCW	L_ARG_54	NH2	L_ASP_60	OD1	3.555
6DCW	L_ARG_61	NH1	L_ASP_82	OD1	3.666
6DCW	L_ARG_61	NH1	L_ASP_82	OD2	2.742
6DCW	L_ARG_61	NH2	L_ASP_82	OD1	2.952
6DCW	L_ARG_61	NH2	L_ASP_82	OD2	3.481
6DCW	L_LYS_188	NZ	L_ASP_185	OD1	2.731
6DCW	L_HIS_189	ND1	L_ASP_151	OD2	3.503
6DCW	H_ARG_12	NH1	H_GLU_10	OE1	3.120
6DCW	H_ARG_12	NH2	H_GLU_10	OE1	3.789
6DCW	H_LYS_43	NZ	L_ASP_9	OD1	3.018
6DCW	H_ARG_58	NH2	H_ASP_56	OD1	3.918
6DCW	H_ARG_58	NH2	H_ASP_56	OD2	2.896
6DCW	H_HIS_66	NE2	H_ASP_86	OD1	3.111
6DCW	H_HIS_66	NE2	H_ASP_86	OD2	2.753
6DCW	H_ARG_94	NH2	H_ASP_101	OD1	3.488
6DCW	H_ARG_98	NH1	H_ASP_31	OD2	3.894
6DCW	H_ARG_98	NH2	H_ASP_96	OD1	3.809
6DCW	H_ARG_98	NH2	H_ASP_96	OD2	3.209
6DCW	H_LYS_145	NZ	H_ASP_146	OD1	3.440
6DCW	H_LYS_145	NZ	H_ASP_146	OD2	3.529
6DCW	T_LYS_317	NZ	H_ASP_54	OD1	3.849
6DCW	T_LYS_317	NZ	H_ASP_54	OD2	2.833
6DCW	T_LYS_317	NZ	H_ASP_56	OD2	2.597

Table 811: 6DCW-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6DDM	A_ARG_61	NH2	A_GLU_81	OE2	2.977
6DDM	A_ARG_61	NH2	A_ASP_82	OD1	2.747
6DDM	A_ARG_61	NH2	A_ASP_82	OD2	3.496
6DDM	A_LYS_103	NZ	A_GLU_165	OE1	2.802
6DDM	A_LYS_103	NZ	A_GLU_165	OE2	3.912
6DDM	A_LYS_149	NZ	A_GLU_195	OE1	2.933
6DDM	A_ARG_211	NH1	A_GLU_187	OE1	3.736
6DDM	C_ARG_213	NH2	C_GLU_277	OE2	3.529
6DDM	C_ARG_279	NH1	C_GLU_276	OE1	2.719
6DDM	C_ARG_279	NH2	C_ASP_242	OD2	2.805
6DDM	B_LYS_62	NZ	A_GLU_1	OE1	3.434
6DDM	B_LYS_62	NZ	A_GLU_1	OE2	2.992
6DDM	B_LYS_66	NZ	B_ASP_86	OD1	3.688
6DDM	B_LYS_66	NZ	B_ASP_86	OD2	2.870
6DDM	B_LYS_143	NZ	B_ASP_144	OD1	3.301
6DDM	B_LYS_143	NZ	B_ASP_144	OD2	3.964
6DDM	B_LYS_210	NZ	B_GLU_212	OE2	3.002

Table 812: 6DDM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6DDR	A_ARG_61	NH2	A_GLU_81	OE2	3.323
6DDR	A_ARG_61	NH2	A_ASP_82	OD1	2.814
6DDR	A_ARG_61	NH2	A_ASP_82	OD2	3.435
6DDR	A_LYS_103	NZ	A_GLU_165	OE1	2.937
6DDR	A_LYS_103	NZ	A_GLU_165	OE2	3.642
6DDR	A_LYS_149	NZ	A_GLU_195	OE1	3.062
6DDR	A_LYS_149	NZ	A_GLU_195	OE2	3.956
6DDR	A_HIS_189	ND1	A_ASP_151	OD2	2.733
6DDR	A_HIS_189	NE2	A_ASP_185	OD1	3.597
6DDR	B_LYS_38	NZ	B_ASP_85	OD2	3.921
6DDR	B_ARG_40	NH1	B_ASP_85	OD1	2.696
6DDR	B_ARG_40	NH2	B_GLU_46	OE1	2.989
6DDR	B_ARG_40	NH2	B_ASP_85	OD1	3.981
6DDR	B_LYS_66	NZ	B_ASP_86	OD1	3.678
6DDR	B_LYS_66	NZ	B_ASP_86	OD2	2.732
6DDR	B_LYS_143	NZ	B_ASP_144	OD1	3.277
6DDR	B_LYS_143	NZ	B_ASP_144	OD2	2.811
6DDR	B_LYS_209	NZ	A_GLU_123	OE1	3.270
6DDR	B_LYS_210	NZ	B_GLU_212	OE1	3.192
6DDR	C_ARG_213	NH1	C_GLU_277	OE2	3.507
6DDR	C_ARG_213	NH2	C_GLU_277	OE2	2.893
6DDR	C_HIS_248	NE2	C_ASP_249	OD1	3.810
6DDR	C_ARG_279	NH2	C_ASP_242	OD1	3.644
6DDR	C_ARG_279	NH2	C_ASP_242	OD2	2.939

Table 813: 6DDR-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6DDV	B.LYS_40	NZ	B.GLU_85	OE1	3.350
6DDV	B.LYS_62	NZ	B.GLU_46	OE1	2.630
6DDV	B.LYS_62	NZ	B.GLU_46	OE2	3.425
6DDV	B.ARG_64	NH1	B.ASP_65	OD2	3.653
6DDV	B.LYS_66	NZ	B.ASP_86	OD1	3.869
6DDV	B.LYS_66	NZ	B.ASP_86	OD2	2.750
6DDV	B.LYS_143	NZ	B.ASP_144	OD1	3.440
6DDV	B.LYS_143	NZ	B.ASP_144	OD2	3.403
6DDV	B.LYS_209	NZ	A.GLU_123	OE1	3.050
6DDV	B.LYS_209	NZ	A.GLU_123	OE2	3.197
6DDV	B.LYS_210	NZ	B.GLU_212	OE1	3.943
6DDV	B.LYS_210	NZ	B.GLU_212	OE2	3.102
6DDV	C.ARG_226	NH1	B.ASP_31	OD1	3.652
6DDV	C.ARG_226	NH1	B.ASP_31	OD2	2.831
6DDV	C.ARG_226	NH2	B.ASP_31	OD1	3.123
6DDV	C.ARG_226	NH2	B.ASP_31	OD2	3.778
6DDV	C.ARG_279	NH1	C.GLU_276	OE1	3.430
6DDV	C.ARG_279	NH1	C.GLU_276	OE2	2.920
6DDV	C.ARG_279	NH2	C.ASP_242	OD2	3.431
6DDV	A.LYS_50	NZ	C.ASP_255	OD1	3.063
6DDV	A.LYS_50	NZ	C.ASP_255	OD2	3.312
6DDV	A.ARG_61	NH2	A.ASP_82	OD1	2.731
6DDV	A.ARG_61	NH2	A.ASP_82	OD2	3.820
6DDV	A.LYS_103	NZ	A.GLU_165	OE1	2.682
6DDV	A.LYS_149	NZ	A.GLU_195	OE1	2.706

Table 814: 6DDV-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6DFG	A_LYS_168	NZ	A_ASP_167	OD1	3.182
6DFG	A_LYS_168	NZ	A_ASP_167	OD2	2.721
6DFG	A_LYS_229	NZ	A_GLU_83	OE1	3.608
6DFG	A_LYS_232	NZ	A_GLU_267	OE1	3.152
6DFG	A_LYS_232	NZ	A_GLU_268	OE1	3.241
6DFG	A_LYS_232	NZ	A_GLU_268	OE2	3.886
6DFG	A_LYS_282	NZ	A_GLU_275	OE1	2.361
6DFG	A_ARG_298	NH1	A_GLU_381	OE1	3.634
6DFG	A_ARG_298	NH1	A_GLU_381	OE2	3.774
6DFG	A_ARG_327	NH2	A_ASP_325	OD2	3.456
6DFG	A_ARG_476	NH1	A_ASP_474	OD1	3.432
6DFG	A_ARG_476	NH1	A_ASP_474	OD2	3.733
6DFG	A_ARG_480	NH1	A_ASP_477	OD1	2.382
6DFG	A_LYS_487	NZ	A_GLU_91	OE2	2.524
6DFG	A_LYS_490	NZ	A_GLU_492	OE2	2.373
6DFG	B_HIS_585	ND1	B_GLU_584	OE1	3.794
6DFG	B_HIS_585	NE2	A_GLU_492	OE2	3.210
6DFG	B_ARG_588	NH2	A_GLU_492	OE1	2.981
6DFG	B_ARG_588	NH2	A_GLU_492	OE2	3.149
6DFG	B_ARG_617	NH1	B_GLU_634	OE1	3.067
6DFG	B_ARG_617	NH1	B_GLU_634	OE2	2.965
6DFG	H_HIS_33	NE2	H_ASP_27	OD1	3.974
6DFG	H_ARG_38	NH1	H_ASP_86	OD1	3.005
6DFG	H_ARG_38	NH1	H_ASP_86	OD2	3.826
6DFG	H_ARG_38	NH2	H_GLU_46	OE1	3.689
6DFG	H_ARG_38	NH2	H_GLU_46	OE2	3.014
6DFG	H_ARG_38	NH2	H_ASP_86	OD1	2.880
6DFG	H_ARG_66	NH1	H_ASP_86	OD2	3.544
6DFG	H_ARG_94	NH1	H_ASP_27	OD1	3.807
6DFG	H_ARG_94	NH1	H_ASP_27	OD2	3.737
6DFG	H_ARG_94	NH2	H_ASP_101	OD1	3.688
6DFG	H_ARG_94	NH2	H_ASP_101	OD2	2.491
6DFG	L_ARG_31	NH1	A_ASP_140	OD2	3.569
6DFG	L_ARG_31	NH2	L_ASP_95	OD1	3.542
6DFG	L_ARG_37	NH1	L_ASP_82	OD1	3.979
6DFG	L_ARG_54	NH2	A_ASP_322	OD2	3.922
6DFG	L_ARG_61	NH1	L_ASP_82	OD2	3.243
6DFG	L_ARG_61	NH2	L_ASP_82	OD2	3.425
6DFG	L_LYS_96	NZ	H_ASP_50	OD2	3.294
6DFG	C_LYS_168	NZ	C_ASP_167	OD1	3.183
6DFG	C_LYS_168	NZ	C_ASP_167	OD2	2.721
6DFG	C_LYS_229	NZ	C_GLU_83	OE1	3.608
6DFG	C_LYS_232	NZ	C_GLU_267	OE1	3.151
6DFG	C_LYS_232	NZ	C_GLU_268	OE1	3.240
6DFG	C_LYS_232	NZ	C_GLU_268	OE2	3.886
6DFG	C_LYS_282	NZ	C_GLU_275	OE1	2.361
6DFG	C_ARG_298	NH1	C_GLU_381	OE1	3.635
6DFG	C_ARG_298	NH1	C_GLU_381	OE2	3.774
6DFG	C_ARG_327	NH2	C_ASP_325	OD2	3.457
6DFG	C_ARG_476	NH1	C_ASP_474	OD1	3.431
6DFG	C_ARG_476	NH1	C_ASP_474	OD2	3.733
6DFG	C_ARG_480	NH1	C_ASP_477	OD1	2.383
6DFG	C_LYS_487	NZ	C_GLU_91	OE2	2.525
6DFG	C_LYS_490	NZ	C_GLU_492	OE2	2.372
6DFG	E_HIS_585	ND1	E_GLU_584	OE1	3.793
6DFG	E_HIS_585	NE2	C_GLU_492	OE2	3.225
6DFG	E_ARG_588	NH2	C_GLU_492	OE1	2.984

6DFG	E_ARG_588	NH2	C_GLU_492	OE2	3.072
6DFG	E_ARG_617	NH1	E_GLU_634	OE1	3.067
6DFG	E_ARG_617	NH1	E_GLU_634	OE2	2.965
6DFG	G_HIS_33	NE2	G_ASP_27	OD1	3.974
6DFG	G_ARG_38	NH1	G_ASP_86	OD1	3.004
6DFG	G_ARG_38	NH1	G_ASP_86	OD2	3.826
6DFG	G_ARG_38	NH2	G_GLU_46	OE1	3.689
6DFG	G_ARG_38	NH2	G_GLU_46	OE2	3.013
6DFG	G_ARG_38	NH2	G_ASP_86	OD1	2.880
6DFG	G_ARG_66	NH1	G_ASP_86	OD2	3.543
6DFG	G_ARG_94	NH1	G_ASP_27	OD1	3.807
6DFG	G_ARG_94	NH1	G_ASP_27	OD2	3.738
6DFG	G_ARG_94	NH2	G_ASP_101	OD1	3.688
6DFG	G_ARG_94	NH2	G_ASP_101	OD2	2.492
6DFG	J_ARG_31	NH1	C_ASP_140	OD2	3.924
6DFG	J_ARG_31	NH2	J_ASP_95	OD1	3.542
6DFG	J_ARG_37	NH1	J_ASP_82	OD1	3.978
6DFG	J_ARG_61	NH1	J_ASP_82	OD2	3.243
6DFG	J_ARG_61	NH2	J_ASP_82	OD2	3.425
6DFG	J_LYS_96	NZ	G_ASP_50	OD2	3.096
6DFG	D_LYS_168	NZ	D_ASP_167	OD1	3.183
6DFG	D_LYS_168	NZ	D_ASP_167	OD2	2.721
6DFG	D_LYS_229	NZ	D_GLU_83	OE1	3.608
6DFG	D_LYS_232	NZ	D_GLU_267	OE1	3.152
6DFG	D_LYS_232	NZ	D_GLU_268	OE1	3.241
6DFG	D_LYS_232	NZ	D_GLU_268	OE2	3.886
6DFG	D_LYS_282	NZ	D_GLU_275	OE1	2.361
6DFG	D_ARG_298	NH1	D_GLU_381	OE1	3.634
6DFG	D_ARG_298	NH1	D_GLU_381	OE2	3.773
6DFG	D_ARG_327	NH2	D_ASP_325	OD2	3.457
6DFG	D_ARG_476	NH1	D_ASP_474	OD1	3.432
6DFG	D_ARG_476	NH1	D_ASP_474	OD2	3.733
6DFG	D_ARG_480	NH1	D_ASP_477	OD1	2.383
6DFG	D_LYS_487	NZ	D_GLU_91	OE2	2.524
6DFG	D_LYS_490	NZ	D_GLU_492	OE2	2.374
6DFG	F_HIS_585	ND1	F_GLU_584	OE1	3.793
6DFG	F_HIS_585	NE2	D_GLU_492	OE2	3.337
6DFG	F_ARG_588	NH2	D_GLU_492	OE1	2.974
6DFG	F_ARG_588	NH2	D_GLU_492	OE2	3.036
6DFG	F_ARG_617	NH1	F_GLU_634	OE1	3.067
6DFG	F_ARG_617	NH1	F_GLU_634	OE2	2.965
6DFG	I_HIS_33	NE2	I_ASP_27	OD1	3.975
6DFG	I_ARG_38	NH1	I_ASP_86	OD1	3.005
6DFG	I_ARG_38	NH1	I_ASP_86	OD2	3.826
6DFG	I_ARG_38	NH2	I_GLU_46	OE1	3.689
6DFG	I_ARG_38	NH2	I_GLU_46	OE2	3.014
6DFG	I_ARG_38	NH2	I_ASP_86	OD1	2.879
6DFG	I_ARG_66	NH1	I_ASP_86	OD2	3.544
6DFG	I_ARG_94	NH1	I_ASP_27	OD1	3.807
6DFG	I_ARG_94	NH1	I_ASP_27	OD2	3.738
6DFG	I_ARG_94	NH2	I_ASP_101	OD1	3.687
6DFG	I_ARG_94	NH2	I_ASP_101	OD2	2.491
6DFG	K_ARG_31	NH1	D_ASP_140	OD2	3.732
6DFG	K_ARG_31	NH2	K_ASP_95	OD1	3.542
6DFG	K_ARG_37	NH1	K_ASP_82	OD1	3.979
6DFG	K_ARG_61	NH1	K_ASP_82	OD2	3.243
6DFG	K_ARG_61	NH2	K_ASP_82	OD2	3.426
6DFG	K_LYS_96	NZ	I_ASP_50	OD2	3.268

Table 815: 6DFG-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6DFH	A_LYS_46	NZ	A_GLU_492	OE1	3.414
6DFH	A_HIS_85	NE2	A_GLU_87	OE2	3.841
6DFH	A_LYS_137	NZ	L_ASP_51	OD2	2.491
6DFH	A_ARG_192	NH1	D_GLU_164	OE2	3.939
6DFH	A_HIS_216	NE2	A_ASP_57	OD1	3.108
6DFH	A_HIS_216	NE2	A_ASP_57	OD2	2.891
6DFH	A_LYS_227	NZ	A_GLU_83	OE1	3.845
6DFH	A_LYS_227	NZ	A_GLU_83	OE2	2.457
6DFH	A_LYS_232	NZ	A_GLU_268	OE2	3.725
6DFH	A_HIS_249	NE2	A_GLU_482	OE1	3.926
6DFH	A_LYS_282	NZ	A_GLU_275	OE1	3.019
6DFH	A_LYS_282	NZ	A_GLU_275	OE2	3.829
6DFH	A_LYS_351	NZ	A_GLU_269	OE1	3.844
6DFH	A_LYS_351	NZ	A_GLU_269	OE2	3.223
6DFH	A_ARG_419	NH1	A_GLU_153	OE1	2.923
6DFH	A_ARG_419	NH1	A_GLU_153	OE2	3.091
6DFH	A_ARG_429	NH2	A_ASP_113	OD2	3.911
6DFH	A_ARG_476	NH1	A_GLU_102	OE1	3.544
6DFH	A_ARG_476	NH1	A_GLU_102	OE2	2.438
6DFH	A_ARG_476	NH2	A_ASP_474	OD2	3.340
6DFH	A_ARG_480	NH1	A_ASP_477	OD1	2.443
6DFH	A_LYS_487	NZ	A_ASP_47	OD1	3.477
6DFH	A_LYS_487	NZ	A_ASP_47	OD2	2.691
6DFH	A_LYS_487	NZ	A_GLU_91	OE2	3.894
6DFH	B_ARG_542	NH1	E_GLU_647	OE2	2.777
6DFH	B_LYS_574	NZ	A_ASP_107	OD1	3.419
6DFH	B_LYS_574	NZ	A_ASP_107	OD2	3.383
6DFH	B_ARG_588	NH2	A_GLU_492	OE1	3.118
6DFH	B_ARG_588	NH2	A_GLU_492	OE2	3.874
6DFH	H_ARG_38	NH1	H_ASP_86	OD1	3.690
6DFH	H_ARG_38	NH1	H_ASP_86	OD2	3.393
6DFH	H_ARG_38	NH2	H_GLU_46	OE1	3.255
6DFH	H_ARG_38	NH2	H_ASP_86	OD1	3.023
6DFH	H_ARG_38	NH2	H_ASP_86	OD2	3.384
6DFH	H_ARG_66	NH2	H_ASP_86	OD2	3.900
6DFH	H_ARG_94	NH1	H_ASP_101	OD2	3.387
6DFH	L_LYS_103	NZ	L_ASP_85	OD1	3.975
6DFH	C_LYS_46	NZ	C_GLU_492	OE1	3.413
6DFH	C_HIS_85	NE2	C_GLU_87	OE2	3.840
6DFH	C_LYS_137	NZ	J_ASP_51	OD2	2.536
6DFH	C_ARG_192	NH1	A_GLU_164	OE2	3.905
6DFH	C_HIS_216	NE2	C_ASP_57	OD1	3.108
6DFH	C_HIS_216	NE2	C_ASP_57	OD2	2.892
6DFH	C_LYS_227	NZ	C_GLU_83	OE1	3.845
6DFH	C_LYS_227	NZ	C_GLU_83	OE2	2.456
6DFH	C_LYS_232	NZ	C_GLU_268	OE2	3.726
6DFH	C_HIS_249	NE2	C_GLU_482	OE1	3.927
6DFH	C_LYS_282	NZ	C_GLU_275	OE1	3.018
6DFH	C_LYS_282	NZ	C_GLU_275	OE2	3.829
6DFH	C_LYS_351	NZ	C_GLU_269	OE1	3.844
6DFH	C_LYS_351	NZ	C_GLU_269	OE2	3.223
6DFH	C_ARG_419	NH1	C_GLU_153	OE1	2.923
6DFH	C_ARG_419	NH1	C_GLU_153	OE2	3.092
6DFH	C_ARG_429	NH2	C_ASP_113	OD2	3.910
6DFH	C_ARG_476	NH1	C_GLU_102	OE1	3.543
6DFH	C_ARG_476	NH1	C_GLU_102	OE2	2.438
6DFH	C_ARG_476	NH2	C_ASP_474	OD2	3.339

6DFH	C_ARG_480	NH1	C_ASP_477	OD1	2.443
6DFH	C_LYS_487	NZ	C_ASP_47	OD1	3.476
6DFH	C_LYS_487	NZ	C_ASP_47	OD2	2.691
6DFH	C_LYS_487	NZ	C_GLU_91	OE2	3.893
6DFH	E_ARG_542	NH1	F_GLU_647	OE2	2.777
6DFH	E_LYS_574	NZ	C_ASP_107	OD1	3.423
6DFH	E_LYS_574	NZ	C_ASP_107	OD2	3.381
6DFH	E_ARG_588	NH2	C_GLU_492	OE1	3.158
6DFH	E_ARG_588	NH2	C_GLU_492	OE2	3.904
6DFH	G_ARG_38	NH1	G_ASP_86	OD1	3.690
6DFH	G_ARG_38	NH1	G_ASP_86	OD2	3.393
6DFH	G_ARG_38	NH2	G_GLU_46	OE1	3.255
6DFH	G_ARG_38	NH2	G_ASP_86	OD1	3.022
6DFH	G_ARG_38	NH2	G_ASP_86	OD2	3.383
6DFH	G_ARG_66	NH2	G_ASP_86	OD2	3.900
6DFH	G_ARG_94	NH1	G_ASP_101	OD2	3.387
6DFH	J_LYS_103	NZ	J_ASP_85	OD1	3.976
6DFH	D_LYS_46	NZ	D_GLU_492	OE1	3.413
6DFH	D_HIS_85	NE2	D_GLU_87	OE2	3.840
6DFH	D_LYS_137	NZ	K_ASP_51	OD2	2.448
6DFH	D_ARG_192	NH1	C_GLU_164	OE2	3.902
6DFH	D_HIS_216	NE2	D_ASP_57	OD1	3.108
6DFH	D_HIS_216	NE2	D_ASP_57	OD2	2.891
6DFH	D_LYS_227	NZ	D_GLU_83	OE1	3.845
6DFH	D_LYS_227	NZ	D_GLU_83	OE2	2.456
6DFH	D_LYS_232	NZ	D_GLU_268	OE2	3.726
6DFH	D_HIS_249	NE2	D_GLU_482	OE1	3.926
6DFH	D_LYS_282	NZ	D_GLU_275	OE1	3.019
6DFH	D_LYS_282	NZ	D_GLU_275	OE2	3.830
6DFH	D_LYS_351	NZ	D_GLU_269	OE1	3.845
6DFH	D_LYS_351	NZ	D_GLU_269	OE2	3.223
6DFH	D_ARG_419	NH1	D_GLU_153	OE1	2.923
6DFH	D_ARG_419	NH1	D_GLU_153	OE2	3.092
6DFH	D_ARG_429	NH2	D_ASP_113	OD2	3.910
6DFH	D_ARG_476	NH1	D_GLU_102	OE1	3.543
6DFH	D_ARG_476	NH1	D_GLU_102	OE2	2.438
6DFH	D_ARG_476	NH2	D_ASP_474	OD2	3.339
6DFH	D_ARG_480	NH1	D_ASP_477	OD1	2.443
6DFH	D_LYS_487	NZ	D_ASP_47	OD1	3.476
6DFH	D_LYS_487	NZ	D_ASP_47	OD2	2.691
6DFH	D_LYS_487	NZ	D_GLU_91	OE2	3.894
6DFH	F_ARG_542	NH1	B_GLU_647	OE2	2.778
6DFH	F_LYS_574	NZ	D_ASP_107	OD1	3.408
6DFH	F_LYS_574	NZ	D_ASP_107	OD2	3.378
6DFH	F_ARG_588	NH2	D_GLU_492	OE1	3.059
6DFH	F_ARG_588	NH2	D_GLU_492	OE2	3.839
6DFH	I_ARG_38	NH1	I_ASP_86	OD1	3.691
6DFH	I_ARG_38	NH1	I_ASP_86	OD2	3.393
6DFH	I_ARG_38	NH2	I_GLU_46	OE1	3.255
6DFH	I_ARG_38	NH2	I_ASP_86	OD1	3.023
6DFH	I_ARG_38	NH2	I_ASP_86	OD2	3.383
6DFH	I_ARG_66	NH2	I_ASP_86	OD2	3.901
6DFH	I_ARG_94	NH1	I_ASP_101	OD2	3.386
6DFH	K_LYS_103	NZ	K_ASP_85	OD1	3.976

Table 816: 6DFH-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6DG2	A_HIS_35	NE2	A_GLU_50	OE1	2.810
6DG2	A_ARG_40	NH1	A_GLU_89	OE2	3.382
6DG2	A_ARG_40	NH2	A_GLU_89	OE2	3.578
6DG2	A_ARG_57	NH1	C_GLU_50	OE1	2.686
6DG2	A_ARG_57	NH1	C_GLU_50	OE2	3.712
6DG2	A_ARG_57	NH1	C_ASP_59	OD1	3.923
6DG2	A_ARG_57	NH2	C_GLU_50	OE1	3.412
6DG2	A_ARG_57	NH2	C_GLU_50	OE2	2.876
6DG2	A_LYS_65	NZ	A_GLU_62	OE1	2.446
6DG2	A_LYS_65	NZ	A_GLU_62	OE2	3.885
6DG2	A_LYS_67	NZ	A_ASP_90	OD1	3.375
6DG2	A_LYS_67	NZ	A_ASP_90	OD2	3.355
6DG2	A_ARG_98	NH2	A_ASP_106	OD1	3.809
6DG2	A_ARG_98	NH2	A_ASP_106	OD2	2.951
6DG2	A_LYS_148	NZ	A_ASP_149	OD1	3.488
6DG2	A_LYS_148	NZ	A_ASP_149	OD2	3.887
6DG2	A_LYS_211	NZ	A_ASP_213	OD1	2.323
6DG2	A_LYS_211	NZ	A_ASP_213	OD2	3.618
6DG2	A_LYS_215	NZ	A_GLU_217	OE2	3.590
6DG2	A_LYS_219	NZ	B_ASP_123	OD1	3.620
6DG2	A_LYS_219	NZ	B_ASP_123	OD2	3.832
6DG2	B_ARG_61	NH1	B_ASP_82	OD1	3.334
6DG2	B_ARG_61	NH1	B_ASP_82	OD2	3.815
6DG2	B_ARG_61	NH2	B_GLU_81	OE1	3.510
6DG2	B_ARG_61	NH2	B_ASP_82	OD1	3.338
6DG2	B_ARG_61	NH2	B_ASP_82	OD2	3.953
6DG2	B_LYS_104	NZ	B_GLU_166	OE1	3.797
6DG2	B_LYS_150	NZ	B_GLU_196	OE1	3.711
6DG2	B_LYS_150	NZ	B_GLU_196	OE2	2.891
6DG2	B_LYS_184	NZ	B_GLU_188	OE1	3.697
6DG2	B_LYS_184	NZ	B_GLU_188	OE2	2.997
6DG2	B_LYS_189	NZ	B_ASP_186	OD1	2.377
6DG2	C_HIS_35	NE2	C_GLU_50	OE2	2.691
6DG2	C_LYS_38	NZ	C_ASP_90	OD2	3.933
6DG2	C_ARG_40	NH1	C_GLU_89	OE1	3.263
6DG2	C_ARG_57	NH1	A_GLU_50	OE1	3.739
6DG2	C_ARG_57	NH1	A_GLU_50	OE2	2.758
6DG2	C_ARG_57	NH1	A_ASP_59	OD1	3.719
6DG2	C_ARG_57	NH2	A_GLU_50	OE1	2.935
6DG2	C_ARG_57	NH2	A_GLU_50	OE2	3.488
6DG2	C_LYS_63	NZ	C_GLU_46	OE2	3.257
6DG2	C_LYS_65	NZ	C_GLU_62	OE1	3.990
6DG2	C_LYS_67	NZ	C_ASP_90	OD1	2.743
6DG2	C_LYS_67	NZ	C_ASP_90	OD2	3.331
6DG2	C_ARG_98	NH2	C_ASP_106	OD1	3.590
6DG2	C_ARG_98	NH2	C_ASP_106	OD2	2.787
6DG2	C_LYS_148	NZ	C_ASP_149	OD1	3.517
6DG2	C_LYS_148	NZ	C_ASP_149	OD2	3.956
6DG2	C_LYS_215	NZ	C_GLU_217	OE1	3.786
6DG2	D_LYS_24	NZ	D_ASP_70	OD1	3.383
6DG2	D_LYS_39	NZ	D_GLU_81	OE2	2.693
6DG2	D_ARG_54	NH1	D_ASP_60	OD1	3.820
6DG2	D_ARG_54	NH2	D_ASP_60	OD1	3.271
6DG2	D_ARG_61	NH2	D_GLU_81	OE1	3.822
6DG2	D_ARG_61	NH2	D_ASP_82	OD1	3.113
6DG2	D_LYS_104	NZ	D_GLU_166	OE1	2.780
6DG2	D_LYS_150	NZ	D_GLU_196	OE1	3.724

6DG2	D_LYS_150	NZ	D_GLU_196	OE2	2.441
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Table 817: 6DG2-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6E62	P_LYS_307	NZ	P_ASP_386	OD2	3.669
6E62	P_HIS_308	NE2	P_ASP_386	OD2	2.759
6E62	P_HIS_324	NE2	P_GLU_362	OE1	3.607
6E62	P_HIS_324	NE2	P_GLU_362	OE2	3.765
6E62	P_HIS_330	NE2	P_ASP_426	OD1	2.903
6E62	P_HIS_330	NE2	P_ASP_426	OD2	3.266
6E62	P_LYS_394	NZ	P_GLU_385	OE2	3.213
6E62	P_LYS_413	NZ	H_ASP_100	OD1	3.190
6E62	P_LYS_413	NZ	H_ASP_100	OD2	2.736
6E62	P_LYS_416	NZ	L_ASP_51	OD2	2.614
6E62	P_LYS_417	NZ	P_ASP_321	OD1	2.847
6E62	H_ARG_38	NH1	H_GLU_46	OE1	2.901
6E62	H_ARG_38	NH1	H_GLU_46	OE2	3.315
6E62	H_ARG_38	NH2	H_ASP_86	OD2	3.041
6E62	H_LYS_64	NZ	H_ASP_61	OD1	3.685
6E62	H_ARG_66	NH1	H_ASP_86	OD1	3.196
6E62	H_ARG_66	NH2	H_ASP_86	OD1	2.873
6E62	H_ARG_66	NH2	H_ASP_86	OD2	2.687
6E62	H_ARG_94	NH2	H_ASP_101	OD2	2.512
6E62	H_ARG_97	NH1	P_ASP_347	OD2	3.575
6E62	H_ARG_97	NH1	H_ASP_100	OD1	2.302
6E62	H_ARG_97	NH2	H_ASP_100	OD1	3.098
6E62	H_LYS_143	NZ	L_GLU_124	OE2	2.458
6E62	H_LYS_209	NZ	L_GLU_123	OE1	3.996
6E62	H_LYS_209	NZ	L_GLU_123	OE2	3.607
6E62	H_LYS_210	NZ	H_GLU_212	OE1	3.306
6E62	H_LYS_210	NZ	H_GLU_212	OE2	3.355
6E62	L_ARG_61	NH1	L_ASP_82	OD1	2.647
6E62	L_ARG_61	NH1	L_ASP_82	OD2	2.836
6E62	L_ARG_61	NH2	L_ASP_82	OD1	3.964
6E62	L_LYS_110	NZ	L_GLU_198	OE1	3.168
6E62	L_LYS_110	NZ	L_GLU_198	OE2	3.580
6E62	L_HIS_188	NE2	L_ASP_151	OD2	3.831
6E62	A_HIS_308	NE2	A_ASP_386	OD2	3.782
6E62	A_HIS_324	NE2	A_GLU_362	OE2	3.283
6E62	A_HIS_330	NE2	A_ASP_426	OD1	2.479
6E62	A_HIS_330	NE2	A_ASP_426	OD2	3.398
6E62	A_HIS_338	NE2	A_GLU_333	OE2	3.680
6E62	A_LYS_394	NZ	A_GLU_385	OE2	2.787
6E62	A_LYS_413	NZ	B_ASP_100	OD1	3.041
6E62	A_LYS_413	NZ	B_ASP_100	OD2	2.916
6E62	A_LYS_416	NZ	C_ASP_51	OD2	2.944
6E62	A_LYS_417	NZ	A_ASP_321	OD1	2.603
6E62	B_ARG_38	NH1	B_GLU_46	OE1	3.293
6E62	B_ARG_38	NH1	B_GLU_46	OE2	3.910
6E62	B_ARG_38	NH1	B_ASP_86	OD2	3.877
6E62	B_ARG_38	NH2	B_ASP_86	OD2	2.880
6E62	B_ARG_66	NH1	B_ASP_86	OD1	2.876
6E62	B_ARG_66	NH1	B_ASP_86	OD2	3.625
6E62	B_ARG_66	NH2	B_ASP_86	OD1	3.290
6E62	B_ARG_66	NH2	B_ASP_86	OD2	2.657
6E62	B_ARG_83	NH1	H_GLU_1	OE1	3.696
6E62	B_ARG_83	NH1	H_GLU_1	OE2	3.867
6E62	B_ARG_83	NH2	H_GLU_1	OE1	3.783
6E62	B_ARG_83	NH2	H_GLU_1	OE2	3.983
6E62	B_ARG_94	NH2	B_ASP_101	OD2	2.599
6E62	B_ARG_97	NH1	B_ASP_100	OD1	2.912

6E62	B_LYS_143	NZ	C_GLU_124	OE2	2.797
6E62	B_LYS_210	NZ	B_GLU_212	OE1	3.652
6E62	B_LYS_210	NZ	B_GLU_212	OE2	2.960
6E62	C_ARG_54	NH1	C_ASP_60	OD2	3.657
6E62	C_ARG_61	NH1	C_ASP_82	OD2	3.397
6E62	C_ARG_61	NH2	C_ASP_82	OD1	3.278
6E62	C_ARG_61	NH2	C_ASP_82	OD2	2.476
6E62	C_LYS_103	NZ	C_GLU_83	OE2	3.303
6E62	C_LYS_110	NZ	C_GLU_198	OE1	2.849
6E62	C_LYS_110	NZ	C_GLU_198	OE2	3.942
6E62	C_LYS_149	NZ	C_GLU_203	OE1	2.875
6E62	C_LYS_149	NZ	C_GLU_203	OE2	3.215
6E62	C_LYS_156	NZ	L_GLU_81	OE2	3.985
6E62	C_HIS_188	NE2	C_ASP_151	OD2	3.860

Table 818: 6E62-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6E63	P_LYS_307	NZ	P_ASP_386	OD1	3.127
6E63	P_LYS_307	NZ	P_ASP_386	OD2	2.866
6E63	P_HIS_308	NE2	P_ASP_386	OD2	2.480
6E63	P_HIS_330	NE2	P_ASP_426	OD1	2.711
6E63	P_LYS_394	NZ	P_GLU_385	OE2	3.080
6E63	P_LYS_413	NZ	H_ASP_100	OD1	3.187
6E63	P_LYS_413	NZ	H_ASP_100	OD2	2.904
6E63	P_LYS_416	NZ	L_ASP_51	OD1	3.564
6E63	P_LYS_416	NZ	L_ASP_51	OD2	2.955
6E63	H_ARG_38	NH1	H_GLU_46	OE1	3.318
6E63	H_ARG_38	NH1	H_GLU_46	OE2	3.594
6E63	H_ARG_38	NH2	H_ASP_86	OD1	2.939
6E63	H_LYS_64	NZ	H_ASP_61	OD1	2.864
6E63	H_ARG_66	NH1	H_ASP_86	OD1	3.558
6E63	H_ARG_66	NH1	H_ASP_86	OD2	2.622
6E63	H_ARG_66	NH2	H_ASP_86	OD1	3.266
6E63	H_ARG_66	NH2	H_ASP_86	OD2	3.816
6E63	H_ARG_94	NH2	H_ASP_101	OD2	2.922
6E63	H_ARG_97	NH1	P_ASP_347	OD2	3.407
6E63	H_ARG_97	NH2	H_ASP_100	OD1	2.600
6E63	H_LYS_143	NZ	L_GLU_124	OE2	2.665
6E63	H_LYS_209	NZ	L_GLU_123	OE1	2.498
6E63	L_LYS_17	NZ	B_GLU_85	OE1	3.318
6E63	L_LYS_17	NZ	B_GLU_85	OE2	3.250
6E63	L_ARG_61	NH1	L_ASP_82	OD1	3.684
6E63	L_ARG_61	NH1	L_ASP_82	OD2	2.729
6E63	L_ARG_61	NH2	L_ASP_82	OD1	2.979
6E63	L_ARG_61	NH2	L_ASP_82	OD2	3.405
6E63	A_LYS_307	NZ	A_ASP_386	OD2	3.648
6E63	A_HIS_308	NE2	A_ASP_386	OD2	2.820
6E63	A_HIS_330	NE2	A_ASP_426	OD1	2.686
6E63	A_HIS_330	NE2	A_ASP_426	OD2	3.540
6E63	A_LYS_394	NZ	A_GLU_385	OE2	2.976
6E63	A_LYS_413	NZ	B_ASP_100	OD1	2.369
6E63	A_LYS_413	NZ	B_ASP_100	OD2	3.029
6E63	A_LYS_416	NZ	C_ASP_51	OD2	3.236
6E63	A_LYS_417	NZ	A_ASP_415	OD2	3.741
6E63	B_ARG_38	NH1	B_GLU_46	OE1	3.240
6E63	B_ARG_38	NH1	B_GLU_46	OE2	3.499
6E63	B_ARG_38	NH1	B_ASP_86	OD1	3.761
6E63	B_ARG_38	NH2	B_ASP_86	OD1	2.835
6E63	B_ARG_66	NH1	B_ASP_86	OD1	3.865
6E63	B_ARG_66	NH1	B_ASP_86	OD2	2.829
6E63	B_ARG_66	NH2	B_ASP_86	OD1	3.527
6E63	B_ARG_66	NH2	B_ASP_86	OD2	3.871
6E63	B_LYS_75	NZ	B_ASP_72	OD2	3.854
6E63	B_ARG_83	NH1	L_GLU_13	OE1	3.486
6E63	B_ARG_83	NH1	L_GLU_13	OE2	2.814
6E63	B_ARG_94	NH2	B_ASP_101	OD2	2.586
6E63	B_ARG_97	NH1	A_ASP_347	OD1	3.859
6E63	B_ARG_97	NH2	B_ASP_100	OD2	2.691
6E63	B_LYS_143	NZ	B_ASP_144	OD2	2.985
6E63	C_ARG_61	NH1	C_ASP_82	OD1	3.450
6E63	C_ARG_61	NH1	C_ASP_82	OD2	2.361
6E63	C_ARG_61	NH2	C_ASP_82	OD1	3.192
6E63	C_ARG_61	NH2	C_ASP_82	OD2	3.567
6E63	C_LYS_103	NZ	C_ASP_85	OD1	3.606

6E63	C_LYS_110	NZ	C_GLU_198	OE2	2.744
6E63	C_HIS_188	ND1	C_ASP_151	OD1	2.608

Table 819: 6E63-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6E64	H_ARG_38	NH1	H_GLU_46	OE1	3.189
6E64	H_ARG_38	NH1	H_GLU_46	OE2	3.661
6E64	H_ARG_38	NH1	H_ASP_86	OD2	3.741
6E64	H_ARG_38	NH2	H_ASP_86	OD2	2.909
6E64	H_ARG_66	NH1	H_ASP_86	OD1	2.379
6E64	H_ARG_66	NH1	H_ASP_86	OD2	3.616
6E64	H_ARG_66	NH2	H_ASP_86	OD1	3.004
6E64	H_ARG_66	NH2	H_ASP_86	OD2	2.769
6E64	H_ARG_83	NH2	H_GLU_85	OE1	3.958
6E64	H_ARG_94	NH2	H_ASP_101	OD2	2.952
6E64	H_ARG_97	NH1	H_ASP_100	OD1	3.380
6E64	H_ARG_97	NH2	H_ASP_100	OD1	3.101
6E64	H_LYS_143	NZ	L_GLU_124	OE2	2.942
6E64	H_LYS_209	NZ	L_GLU_123	OE2	2.774
6E64	H_LYS_210	NZ	H_GLU_212	OE1	3.202
6E64	H_LYS_210	NZ	H_GLU_212	OE2	3.230
6E64	L_ARG_54	NH1	L_ASP_60	OD2	3.879
6E64	L_ARG_61	NH1	L_ASP_82	OD1	3.199
6E64	L_ARG_61	NH1	L_ASP_82	OD2	2.244
6E64	L_ARG_61	NH2	L_GLU_81	OE2	2.926
6E64	L_ARG_61	NH2	L_ASP_82	OD1	3.741
6E64	L_LYS_110	NZ	L_GLU_198	OE1	3.205
6E64	L_LYS_110	NZ	L_GLU_198	OE2	3.935
6E64	L_LYS_149	NZ	L_GLU_203	OE2	3.889
6E64	A_ARG_38	NH1	A_GLU_46	OE1	3.590
6E64	A_ARG_38	NH1	A_GLU_46	OE2	3.959
6E64	A_ARG_38	NH1	A_ASP_86	OD2	3.714
6E64	A_ARG_38	NH2	A_ASP_86	OD2	2.885
6E64	A_ARG_66	NH1	A_ASP_86	OD1	2.673
6E64	A_ARG_66	NH1	A_ASP_86	OD2	3.501
6E64	A_ARG_66	NH2	A_ASP_86	OD2	3.885
6E64	A_ARG_94	NH2	A_ASP_101	OD2	2.800
6E64	A_ARG_97	NH1	A_ASP_100	OD1	2.610
6E64	A_LYS_209	NZ	B_GLU_123	OE1	3.569
6E64	A_LYS_209	NZ	B_GLU_123	OE2	2.777
6E64	A_LYS_210	NZ	A_GLU_212	OE1	2.858
6E64	B_ARG_54	NH1	B_ASP_60	OD2	3.850
6E64	B_ARG_61	NH1	B_ASP_82	OD1	3.141
6E64	B_ARG_61	NH1	B_ASP_82	OD2	2.224
6E64	B_ARG_61	NH2	B_GLU_81	OE2	3.154
6E64	B_LYS_110	NZ	B_GLU_198	OE1	3.325

Table 820: 6E64-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6E65	L_ARG_61	NH1	L_ASP_82	OD1	3.558
6E65	L_ARG_61	NH1	L_ASP_82	OD2	2.687
6E65	L_ARG_61	NH2	L_ASP_82	OD1	2.921
6E65	L_ARG_61	NH2	L_ASP_82	OD2	3.517
6E65	L_LYS_110	NZ	L_GLU_198	OE1	3.254
6E65	L_LYS_149	NZ	L_GLU_203	OE2	3.192
6E65	H_ARG_38	NH1	H_GLU_46	OE1	3.010
6E65	H_ARG_38	NH1	H_GLU_46	OE2	3.789
6E65	H_ARG_38	NH1	H_ASP_86	OD2	3.921
6E65	H_ARG_38	NH2	H_ASP_86	OD2	2.906
6E65	H_LYS_64	NZ	H_ASP_61	OD1	2.812
6E65	H_ARG_66	NH1	H_ASP_86	OD1	2.716
6E65	H_ARG_66	NH1	H_ASP_86	OD2	3.744
6E65	H_ARG_66	NH2	H_ASP_86	OD1	3.520
6E65	H_ARG_66	NH2	H_ASP_86	OD2	3.030
6E65	H_ARG_94	NH2	H_ASP_101	OD1	3.830
6E65	H_ARG_94	NH2	H_ASP_101	OD2	2.624
6E65	H_ARG_97	NH1	H_ASP_100	OD1	3.182
6E65	H_ARG_97	NH2	H_ASP_100	OD1	2.837
6E65	H_LYS_209	NZ	L_GLU_123	OE1	2.900
6E65	H_LYS_209	NZ	L_GLU_123	OE2	3.402
6E65	H_LYS_210	NZ	H_GLU_212	OE2	3.313

Table 821: 6E65-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6E8V	A_LYS_58	NZ	A_ASP_183	OD2	3.383
6E8V	A_ARG_64	NH1	A_ASP_115	OD1	3.736
6E8V	A_ARG_64	NH1	A_ASP_115	OD2	3.862
6E8V	A_ARG_64	NH2	A_GLU_72	OE1	2.461
6E8V	A_LYS_69	NZ	H_GLU_114	OE1	3.919
6E8V	A_LYS_69	NZ	H_GLU_114	OE2	3.267
6E8V	A_ARG_92	NH1	A_ASP_115	OD1	3.628
6E8V	A_ARG_92	NH1	A_ASP_115	OD2	2.200
6E8V	A_ARG_92	NH2	A_ASP_115	OD2	3.895
6E8V	A_HIS_129	NE2	A_GLU_179	OE1	3.896
6E8V	A_LYS_290	NZ	B_GLU_128	OE1	3.297
6E8V	A_LYS_290	NZ	B_GLU_128	OE2	3.454
6E8V	B_ARG_62	NH2	B_ASP_83	OD1	3.866
6E8V	B_ARG_62	NH2	B_ASP_83	OD2	3.065
6E8V	B_LYS_154	NZ	E_ASP_98	OD2	3.855
6E8V	B_LYS_212	NZ	B_GLU_215	OE2	3.054
6E8V	E_LYS_58	NZ	E_ASP_183	OD2	3.769
6E8V	E_ARG_64	NH1	E_ASP_115	OD1	3.111
6E8V	E_ARG_64	NH2	E_GLU_72	OE1	2.694
6E8V	E_ARG_64	NH2	E_GLU_72	OE2	3.880
6E8V	E_ARG_64	NH2	E_ASP_115	OD1	3.985
6E8V	E_ARG_92	NH1	E_ASP_115	OD1	2.769
6E8V	E_ARG_92	NH1	E_ASP_115	OD2	3.085
6E8V	E_HIS_129	NE2	E_GLU_179	OE2	3.144
6E8V	E_LYS_290	NZ	F_GLU_128	OE1	2.548
6E8V	E_LYS_290	NZ	F_GLU_128	OE2	3.232
6E8V	F_ARG_63	NH1	F_GLU_83	OE2	3.510
6E8V	F_ARG_63	NH1	F_ASP_84	OD1	3.568
6E8V	F_ARG_63	NH2	F_ASP_84	OD1	3.073
6E8V	F_ARG_63	NH2	F_ASP_84	OD2	2.536
6E8V	F_ARG_68	NH2	F_ASP_53	OD2	3.856
6E8V	H_LYS_58	NZ	H_ASP_183	OD2	3.692
6E8V	H_ARG_64	NH1	H_ASP_115	OD2	3.761
6E8V	H_ARG_64	NH2	H_GLU_72	OE1	3.369
6E8V	H_ARG_64	NH2	H_GLU_72	OE2	2.811
6E8V	H_LYS_69	NZ	H_GLU_72	OE2	3.846
6E8V	H_LYS_69	NZ	H_GLU_114	OE2	2.887
6E8V	H_ARG_92	NH1	H_ASP_115	OD1	3.257
6E8V	H_ARG_92	NH1	H_ASP_115	OD2	2.227
6E8V	H_ARG_92	NH2	H_ASP_115	OD2	3.949
6E8V	H_HIS_125	NE2	H_ASP_183	OD2	3.568
6E8V	H_HIS_129	NE2	H_GLU_179	OE2	2.966
6E8V	H_LYS_290	NZ	L_GLU_127	OE1	2.706
6E8V	H_LYS_290	NZ	L_GLU_127	OE2	2.554
6E8V	J_LYS_58	NZ	J_ASP_183	OD2	3.273
6E8V	J_ARG_64	NH1	J_ASP_115	OD2	3.190
6E8V	J_ARG_64	NH2	J_GLU_72	OE1	3.098
6E8V	J_ARG_92	NH1	J_ASP_115	OD1	2.752
6E8V	J_ARG_92	NH1	J_ASP_115	OD2	2.685
6E8V	J_HIS_129	NE2	J_GLU_179	OE2	3.681
6E8V	J_LYS_290	NZ	K_GLU_128	OE1	3.173
6E8V	J_LYS_290	NZ	K_GLU_128	OE2	2.611
6E8V	K_ARG_63	NH1	K_ASP_84	OD2	3.865
6E8V	K_ARG_63	NH2	K_ASP_84	OD1	2.385
6E8V	K_ARG_63	NH2	K_ASP_84	OD2	3.106
6E8V	K_LYS_212	NZ	H_GLU_101	OE1	3.767
6E8V	K_LYS_212	NZ	H_GLU_101	OE2	3.490

6E8V	K_LYS_212	NZ	K_GLU_215	OE1	3.501
6E8V	L_LYS_211	NZ	L_GLU_214	OE1	3.855
6E8V	L_LYS_211	NZ	L_GLU_214	OE2	3.483
6E8V	O_LYS_58	NZ	O_ASP_183	OD2	2.755
6E8V	O_ARG_64	NH1	O_ASP_115	OD1	2.759
6E8V	O_ARG_64	NH2	O_GLU_72	OE1	3.262
6E8V	O_ARG_64	NH2	O_GLU_72	OE2	2.920
6E8V	O_ARG_64	NH2	O_ASP_115	OD1	3.656
6E8V	O_ARG_92	NH1	O_ASP_115	OD1	3.104
6E8V	O_ARG_92	NH1	O_ASP_115	OD2	2.418
6E8V	O_ARG_92	NH2	O_ASP_115	OD1	3.944
6E8V	O_HIS_129	NE2	L_ASP_61	OD1	3.511
6E8V	O_HIS_129	NE2	O_GLU_179	OE1	3.633
6E8V	O_LYS_290	NZ	P_GLU_128	OE1	3.591
6E8V	P_ARG_56	NH2	P_ASP_62	OD1	3.947
6E8V	P_ARG_63	NH2	P_ASP_84	OD1	2.443
6E8V	P_ARG_63	NH2	P_ASP_84	OD2	3.024
6E8V	P_ARG_68	NH2	P_ASP_53	OD2	3.638
6E8V	P_LYS_171	NZ	P_GLU_85	OE1	3.474
6E8V	P_LYS_212	NZ	P_GLU_215	OE2	3.770
6E8V	U_ARG_64	NH1	U_ASP_115	OD1	2.978
6E8V	U_ARG_64	NH2	U_GLU_72	OE1	3.075
6E8V	U_ARG_64	NH2	U_GLU_72	OE2	3.322
6E8V	U_LYS_69	NZ	U_GLU_72	OE1	2.536
6E8V	U_ARG_92	NH1	U_ASP_115	OD1	3.227
6E8V	U_ARG_92	NH1	U_ASP_115	OD2	2.688
6E8V	U_LYS_290	NZ	V_GLU_128	OE1	2.346
6E8V	U_LYS_290	NZ	V_GLU_128	OE2	3.693
6E8V	V_ARG_63	NH1	V_GLU_83	OE2	3.928
6E8V	V_ARG_63	NH2	V_ASP_84	OD1	2.920
6E8V	V_ARG_63	NH2	V_ASP_84	OD2	2.400
6E8V	V_LYS_154	NZ	V_GLU_199	OE2	3.787
6E8V	V_LYS_212	NZ	V_GLU_215	OE1	3.212
6E8V	Y_ARG_64	NH1	Y_ASP_115	OD1	3.849
6E8V	Y_ARG_64	NH1	Y_ASP_115	OD2	3.924
6E8V	Y_ARG_64	NH2	Y_GLU_72	OE1	3.305
6E8V	Y_ARG_64	NH2	Y_GLU_72	OE2	3.450
6E8V	Y_ARG_64	NH2	Y_ASP_115	OD1	3.987
6E8V	Y_ARG_92	NH1	Y_ASP_115	OD1	3.320
6E8V	Y_ARG_92	NH1	Y_ASP_115	OD2	2.179
6E8V	Y_HIS_129	NE2	Y_GLU_179	OE1	2.918
6E8V	Y_LYS_290	NZ	Z_GLU_128	OE1	3.390
6E8V	Z_ARG_63	NH1	Z_ASP_84	OD1	3.893
6E8V	Z_ARG_63	NH2	Z_ASP_84	OD1	3.228
6E8V	Z_ARG_63	NH2	Z_ASP_84	OD2	2.268
6E8V	Z_LYS_171	NZ	Z_GLU_85	OE1	2.482
6E8V	Z_HIS_202	NE2	Z_GLU_203	OE1	3.581
6E8V	Z_LYS_212	NZ	Z_GLU_215	OE2	3.769
6E8V	c_LYS_58	NZ	c_ASP_183	OD2	3.320
6E8V	c_ARG_64	NH1	c_ASP_115	OD1	3.153
6E8V	c_ARG_64	NH2	c_GLU_72	OE1	2.815
6E8V	c_ARG_64	NH2	c_GLU_72	OE2	3.967
6E8V	c_ARG_92	NH1	c_ASP_115	OD1	2.545
6E8V	c_ARG_92	NH1	c_ASP_115	OD2	2.955
6E8V	c_HIS_125	ND1	K_ASP_62	OD1	3.174
6E8V	c_HIS_125	ND1	K_ASP_62	OD2	3.139
6E8V	c_HIS_125	NE2	c_ASP_183	OD2	2.451
6E8V	c_HIS_129	NE2	c_GLU_179	OE1	3.728

6E8V	c_LYS_290	NZ	d_GLU_128	OE1	2.357
6E8V	c_LYS_290	NZ	d_GLU_128	OE2	3.486
6E8V	d_ARG_63	NH2	d_ASP_84	OD1	3.212
6E8V	d_ARG_63	NH2	d_ASP_84	OD2	2.255
6E8V	d_LYS_154	NZ	d_GLU_199	OE1	2.319
6E8V	d_LYS_154	NZ	d_GLU_199	OE2	3.282

Table 822: 6E8V-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6E9G	A_ARG_38	NH1	A_GLU_46	OE1	3.009
6E9G	A_ARG_38	NH1	A_GLU_46	OE2	3.865
6E9G	A_ARG_38	NH1	A_ASP_89	OD1	3.731
6E9G	A_ARG_38	NH2	A_ASP_89	OD1	2.942
6E9G	A_ARG_124	NH1	A_ASP_126	OD1	3.428
6E9G	A_ARG_124	NH1	A_ASP_126	OD2	3.623
6E9G	A_LYS_259	NZ	A_ASP_261	OD1	3.382
6E9G	A_LYS_262	NZ	B_GLU_127	OE1	3.021
6E9G	A_LYS_262	NZ	B_GLU_127	OE2	3.870
6E9G	B_ARG_55	NH1	B_ASP_61	OD2	3.166
6E9G	B_ARG_55	NH2	B_ASP_61	OD1	3.953
6E9G	B_ARG_55	NH2	B_ASP_61	OD2	3.935
6E9G	B_ARG_62	NH1	B_ASP_83	OD1	3.754
6E9G	B_ARG_62	NH2	B_ASP_83	OD1	2.216
6E9G	B_ARG_62	NH2	B_ASP_83	OD2	3.767
6E9G	B_LYS_114	NZ	B_GLU_202	OE1	3.419

Table 823: 6E9G-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6E9H	A_LYS_58	NZ	A_ASP_57	OD2	3.854
6E9H	A_ARG_64	NH1	A_ASP_115	OD1	2.780
6E9H	A_ARG_64	NH2	A_GLU_72	OE1	3.005
6E9H	A_ARG_64	NH2	A_ASP_115	OD1	3.589
6E9H	A_ARG_92	NH1	A_ASP_115	OD1	3.583
6E9H	A_ARG_92	NH1	A_ASP_115	OD2	2.997
6E9H	A_ARG_92	NH2	A_ASP_115	OD1	3.156
6E9H	A_ARG_92	NH2	A_ASP_115	OD2	3.683
6E9H	A_HIS_125	NE2	A_GLU_181	OE2	3.054
6E9H	A_ARG_147	NH2	A_ASP_160	OD1	3.058
6E9H	A_ARG_147	NH2	A_ASP_160	OD2	3.404
6E9H	A_LYS_292	NZ	B_GLU_128	OE1	2.895
6E9H	A_LYS_292	NZ	B_GLU_128	OE2	3.744
6E9H	B_ARG_56	NH1	B_ASP_62	OD2	3.861
6E9H	B_ARG_56	NH2	B_ASP_62	OD2	3.548
6E9H	B_ARG_63	NH1	B_ASP_84	OD1	2.804
6E9H	B_ARG_63	NH1	B_ASP_84	OD2	3.553
6E9H	B_ARG_63	NH2	B_ASP_84	OD1	3.448
6E9H	B_ARG_63	NH2	B_ASP_84	OD2	2.780
6E9H	B_ARG_68	NH2	B_ASP_53	OD2	3.674
6E9H	B_LYS_154	NZ	B_GLU_199	OE1	3.479
6E9H	B_LYS_154	NZ	B_GLU_199	OE2	3.530
6E9H	B_LYS_171	NZ	B_GLU_85	OE1	2.299
6E9H	B_LYS_171	NZ	B_GLU_85	OE2	3.752

Table 824: 6E9H-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6E9I	A_LYS_58	NZ	A_ASP_182	OD2	3.602
6E9I	A_ARG_64	NH1	A_ASP_115	OD2	2.633
6E9I	A_ARG_64	NH2	A_GLU_72	OE2	3.049
6E9I	A_ARG_64	NH2	A_ASP_115	OD2	3.483
6E9I	A_ARG_92	NH1	A_ASP_115	OD1	3.516
6E9I	A_ARG_92	NH1	A_ASP_115	OD2	2.842
6E9I	A_ARG_92	NH2	A_ASP_115	OD1	3.099
6E9I	A_ARG_92	NH2	A_ASP_115	OD2	3.725
6E9I	A_ARG_109	NH2	D_ASP_95	OD1	3.782
6E9I	A_ARG_109	NH2	D_ASP_95	OD2	3.931
6E9I	A_HIS_125	NE2	A_GLU_178	OE2	3.001
6E9I	A_LYS_289	NZ	B_GLU_128	OE1	3.746
6E9I	A_LYS_289	NZ	B_GLU_128	OE2	2.925
6E9I	B_ARG_63	NH1	B_ASP_84	OD1	2.801
6E9I	B_ARG_63	NH1	B_ASP_84	OD2	2.588
6E9I	B_ARG_68	NH1	B_ASP_53	OD2	3.498
6E9I	B_LYS_171	NZ	B_GLU_85	OE1	2.942
6E9I	C_ARG_64	NH1	C_ASP_115	OD2	2.558
6E9I	C_ARG_64	NH2	C_GLU_72	OE2	2.949
6E9I	C_ARG_64	NH2	C_ASP_115	OD2	3.425
6E9I	C_ARG_92	NH1	C_ASP_115	OD1	3.394
6E9I	C_ARG_92	NH1	C_ASP_115	OD2	2.831
6E9I	C_ARG_92	NH2	C_ASP_115	OD1	3.153
6E9I	C_ARG_92	NH2	C_ASP_115	OD2	3.762
6E9I	C_HIS_125	NE2	C_GLU_178	OE1	3.090
6E9I	C_LYS_289	NZ	D_GLU_128	OE1	2.528
6E9I	C_LYS_289	NZ	D_GLU_128	OE2	3.968
6E9I	D_ARG_63	NH2	D_ASP_84	OD1	2.787
6E9I	D_ARG_63	NH2	D_ASP_84	OD2	2.635
6E9I	D_ARG_68	NH2	D_ASP_53	OD2	3.085
6E9I	D_LYS_115	NZ	D_GLU_203	OE2	3.399
6E9I	D_LYS_171	NZ	D_GLU_85	OE2	3.210
6E9I	H_LYS_58	NZ	H_ASP_57	OD1	3.428
6E9I	H_ARG_64	NH1	H_ASP_115	OD1	2.649
6E9I	H_ARG_64	NH2	H_GLU_72	OE1	2.999
6E9I	H_ARG_64	NH2	H_ASP_115	OD1	3.536
6E9I	H_LYS_69	NZ	H_GLU_114	OE2	3.957
6E9I	H_ARG_92	NH1	H_ASP_115	OD1	2.822
6E9I	H_ARG_92	NH1	H_ASP_115	OD2	3.288
6E9I	H_ARG_92	NH2	H_ASP_115	OD1	3.754
6E9I	H_ARG_92	NH2	H_ASP_115	OD2	3.182
6E9I	H_HIS_125	NE2	H_GLU_178	OE1	3.044
6E9I	H_LYS_289	NZ	L_GLU_128	OE1	3.811
6E9I	H_LYS_289	NZ	L_GLU_128	OE2	2.547
6E9I	L_ARG_56	NH1	L_ASP_62	OD2	3.686
6E9I	L_ARG_56	NH2	L_ASP_62	OD2	3.053
6E9I	L_ARG_63	NH1	L_ASP_84	OD1	3.024
6E9I	L_ARG_63	NH1	L_ASP_84	OD2	2.419
6E9I	L_ARG_63	NH2	L_GLU_83	OE1	3.490
6E9I	L_ARG_63	NH2	L_ASP_84	OD1	3.404
6E9I	L_ARG_68	NH1	L_ASP_53	OD2	3.356
6E9I	L_LYS_171	NZ	L_GLU_85	OE1	2.446

Table 825: 6E9I-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6E9K	A_LYS_32	NZ	A_ASP_31	OD1	2.993
6E9K	A_LYS_32	NZ	A_ASP_31	OD2	3.547
6E9K	A_ARG_38	NH1	A_ASP_89	OD1	2.700
6E9K	A_ARG_38	NH2	A_GLU_46	OE1	3.033
6E9K	A_ARG_38	NH2	A_ASP_89	OD1	3.664
6E9K	A_ARG_66	NH1	A_ASP_89	OD1	3.360
6E9K	A_ARG_66	NH1	A_ASP_89	OD2	2.516
6E9K	A_ARG_66	NH2	A_ASP_89	OD1	3.299
6E9K	A_ARG_66	NH2	A_ASP_89	OD2	3.549
6E9K	A_HIS_99	NE2	A_GLU_146	OE2	3.060
6E9K	A_ARG_103	NH1	A_GLU_146	OE1	3.769
6E9K	A_LYS_104	NZ	A_ASP_143	OD1	2.823
6E9K	A_LYS_104	NZ	A_ASP_143	OD2	3.004
6E9K	A_LYS_257	NZ	B_GLU_128	OE1	3.997
6E9K	A_LYS_257	NZ	B_GLU_128	OE2	3.056
6E9K	B_ARG_63	NH1	B_ASP_84	OD1	3.165
6E9K	B_ARG_63	NH1	B_ASP_84	OD2	2.396
6E9K	B_ARG_63	NH2	B_ASP_84	OD1	2.989
6E9K	B_ARG_63	NH2	B_ASP_84	OD2	3.593
6E9K	B_LYS_115	NZ	B_GLU_203	OE1	3.094
6E9K	B_LYS_154	NZ	B_GLU_199	OE2	3.249
6E9K	B_LYS_171	NZ	B_GLU_85	OE1	2.917

Table 826: 6E9K-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6E9Q	A_ARG_38	NH1	A_ASP_89	OD2	3.963
6E9Q	A_ARG_66	NH1	A_ASP_89	OD1	2.868
6E9Q	A_ARG_66	NH1	A_ASP_89	OD2	2.514
6E9Q	A_HIS_99	NE2	A_GLU_142	OE1	3.452
6E9Q	A_LYS_101	NZ	A_GLU_142	OE2	3.652
6E9Q	A_LYS_253	NZ	B_GLU_128	OE1	3.048
6E9Q	A_LYS_253	NZ	B_GLU_128	OE2	2.978
6E9Q	B_ARG_63	NH2	B_ASP_84	OD1	2.631
6E9Q	B_ARG_63	NH2	B_ASP_84	OD2	2.815
6E9Q	B_ARG_68	NH2	B_ASP_53	OD2	3.543
6E9Q	B_LYS_154	NZ	B_GLU_199	OE1	2.492
6E9Q	B_LYS_171	NZ	B_GLU_85	OE1	2.682
6E9Q	B_LYS_171	NZ	B_GLU_85	OE2	3.666
6E9Q	C_ARG_38	NH1	C_ASP_89	OD1	2.493
6E9Q	C_ARG_38	NH2	C_GLU_46	OE1	2.768
6E9Q	C_ARG_38	NH2	C_GLU_46	OE2	3.894
6E9Q	C_ARG_38	NH2	C_ASP_89	OD1	3.476
6E9Q	C_ARG_66	NH1	C_ASP_89	OD1	3.542
6E9Q	C_ARG_66	NH1	C_ASP_89	OD2	2.437
6E9Q	C_ARG_66	NH2	C_ASP_89	OD1	3.979
6E9Q	C_ARG_66	NH2	C_ASP_89	OD2	3.919
6E9Q	C_HIS_99	NE2	C_GLU_142	OE1	3.707
6E9Q	C_LYS_101	NZ	C_GLU_142	OE1	3.900
6E9Q	D_ARG_56	NH1	D_ASP_62	OD2	3.862
6E9Q	D_ARG_63	NH2	D_ASP_84	OD1	3.419
6E9Q	D_ARG_63	NH2	D_ASP_84	OD2	3.605
6E9Q	D_LYS_154	NZ	D_GLU_199	OE1	3.115
6E9Q	D_LYS_176	NZ	D_ASP_143	OD1	3.925
6E9Q	D_LYS_193	NZ	D_ASP_189	OD1	3.400
6E9Q	E_ARG_38	NH1	E_ASP_89	OD1	3.733
6E9Q	E_ARG_38	NH2	E_GLU_46	OE1	3.706
6E9Q	E_ARG_38	NH2	E_ASP_89	OD1	2.896
6E9Q	E_ARG_66	NH1	E_ASP_89	OD1	3.922
6E9Q	E_ARG_66	NH1	E_ASP_89	OD2	2.529
6E9Q	E_ARG_66	NH2	E_ASP_89	OD2	3.750
6E9Q	E_HIS_99	NE2	E_GLU_142	OE2	3.775
6E9Q	E_LYS_253	NZ	F_GLU_128	OE1	2.966
6E9Q	E_LYS_253	NZ	F_GLU_128	OE2	2.802
6E9Q	F_ARG_63	NH2	F_ASP_84	OD1	2.560
6E9Q	F_ARG_63	NH2	F_ASP_84	OD2	3.515
6E9Q	F_ARG_68	NH2	F_ASP_53	OD2	3.049
6E9Q	F_LYS_171	NZ	F_GLU_85	OE1	3.068
6E9Q	G_ARG_38	NH1	G_ASP_89	OD1	3.204
6E9Q	G_ARG_38	NH2	G_GLU_46	OE1	2.728
6E9Q	G_ARG_38	NH2	G_GLU_46	OE2	3.967
6E9Q	G_ARG_66	NH1	G_ASP_89	OD1	3.146
6E9Q	G_ARG_66	NH1	G_ASP_89	OD2	2.916
6E9Q	G_ARG_66	NH2	G_ASP_89	OD1	3.930
6E9Q	G_HIS_99	NE2	G_GLU_142	OE2	3.698

Table 827: 6E9Q-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6E9U	A_LYS_32	NZ	A_ASP_159	OD2	3.058
6E9U	A_ARG_38	NH1	A_ASP_89	OD1	2.696
6E9U	A_ARG_38	NH2	A_GLU_46	OE1	3.019
6E9U	A_ARG_38	NH2	A_ASP_89	OD1	3.469
6E9U	A_ARG_66	NH1	A_ASP_89	OD1	3.553
6E9U	A_ARG_66	NH1	A_ASP_89	OD2	2.571
6E9U	A_ARG_66	NH2	A_ASP_89	OD1	3.370
6E9U	A_ARG_66	NH2	A_ASP_89	OD2	3.619
6E9U	A_HIS_99	NE2	A_GLU_155	OE2	3.178
6E9U	A_LYS_104	NZ	A_ASP_133	OD2	2.359
6E9U	A_ARG_117	NH2	A_ASP_116	OD1	3.439
6E9U	A_ARG_117	NH2	A_ASP_116	OD2	3.943
6E9U	A_LYS_266	NZ	B_GLU_128	OE1	2.942
6E9U	A_LYS_266	NZ	B_GLU_128	OE2	2.747
6E9U	B_ARG_56	NH2	B_ASP_62	OD2	3.549
6E9U	B_ARG_63	NH2	B_ASP_84	OD1	2.519
6E9U	B_ARG_63	NH2	B_ASP_84	OD2	3.472
6E9U	B_ARG_168	NH2	B_ASP_87	OD1	3.330
6E9U	B_ARG_168	NH2	B_ASP_87	OD2	3.181

Table 828: 6E9U-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID residue name residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6EDU	D_LYS_348	NZ	D_GLU_269	OE1	2.947
6EDU	D_LYS_348	NZ	D_GLU_269	OE2	3.576
6EDU	D_LYS_421	NZ	L_GLU_54	OE2	2.920
6EDU	D_LYS_432	NZ	L_GLU_55	OE1	3.655
6EDU	D_LYS_432	NZ	L_GLU_55	OE2	3.439
6EDU	D_ARG_476	NH1	D_GLU_102	OE1	3.942
6EDU	D_ARG_476	NH1	D_GLU_102	OE2	2.435
6EDU	D_ARG_480	NH1	D_ASP_477	OD1	2.572
6EDU	D_LYS_487	NZ	D_GLU_47	OE2	2.857
6EDU	D_LYS_487	NZ	D_GLU_91	OE2	3.215
6EDU	E_LYS_348	NZ	E_GLU_269	OE1	2.948
6EDU	E_LYS_348	NZ	E_GLU_269	OE2	3.576
6EDU	E_LYS_421	NZ	N_GLU_54	OE2	3.004
6EDU	E_LYS_432	NZ	N_GLU_55	OE1	3.579
6EDU	E_LYS_432	NZ	N_GLU_55	OE2	3.398
6EDU	E_ARG_476	NH1	E_GLU_102	OE1	3.943
6EDU	E_ARG_476	NH1	E_GLU_102	OE2	2.436
6EDU	E_ARG_480	NH1	E_ASP_477	OD1	2.573
6EDU	E_LYS_487	NZ	E_GLU_47	OE2	2.857
6EDU	E_LYS_487	NZ	E_GLU_91	OE2	3.215
6EDU	F_LYS_348	NZ	F_GLU_269	OE1	2.947
6EDU	F_LYS_348	NZ	F_GLU_269	OE2	3.576
6EDU	F_LYS_421	NZ	J_GLU_54	OE2	3.064
6EDU	F_LYS_432	NZ	J_GLU_55	OE1	3.805
6EDU	F_LYS_432	NZ	J_GLU_55	OE2	3.577
6EDU	F_ARG_476	NH1	F_GLU_102	OE1	3.943
6EDU	F_ARG_476	NH1	F_GLU_102	OE2	2.437
6EDU	F_ARG_480	NH1	F_ASP_477	OD1	2.573
6EDU	F_LYS_487	NZ	F_GLU_47	OE2	2.856
6EDU	F_LYS_487	NZ	F_GLU_91	OE2	3.215
6EDU	G_LYS_22	NZ	F_GLU_102	OE1	3.040
6EDU	G_ARG_59	NH2	F_ASP_368	OD1	3.059
6EDU	G_LYS_72	NZ	G_ASP_56	OD2	3.829
6EDU	H_LYS_22	NZ	E_GLU_102	OE1	3.174
6EDU	H_ARG_59	NH2	E_ASP_368	OD1	3.166
6EDU	H_LYS_72	NZ	H_ASP_56	OD2	3.828
6EDU	I_LYS_22	NZ	D_GLU_102	OE1	3.053
6EDU	I_ARG_59	NH2	D_ASP_368	OD1	3.238
6EDU	I_LYS_72	NZ	I_ASP_56	OD2	3.828
6EDU	J_ARG_12	NH2	J_GLU_10	OE2	2.569
6EDU	J_LYS_19	NZ	J_GLU_82	OE2	3.419
6EDU	J_ARG_38	NH2	J_GLU_46	OE1	2.774
6EDU	J_ARG_38	NH2	J_GLU_46	OE2	3.579
6EDU	J_LYS_63	NZ	J_GLU_46	OE1	3.894
6EDU	J_LYS_63	NZ	J_GLU_46	OE2	3.217
6EDU	J_ARG_67	NH1	J_ASP_90	OD2	3.399
6EDU	J_ARG_67	NH2	J_ASP_90	OD1	3.817
6EDU	K_ARG_63	NH1	K_ASP_84	OD1	3.667
6EDU	K_ARG_63	NH1	K_ASP_84	OD2	3.012
6EDU	K_ARG_63	NH2	K_ASP_84	OD2	3.643
6EDU	L_ARG_12	NH2	L_GLU_10	OE2	2.570
6EDU	L_LYS_19	NZ	L_GLU_82	OE2	3.420
6EDU	L_ARG_38	NH2	L_GLU_46	OE1	2.773
6EDU	L_ARG_38	NH2	L_GLU_46	OE2	3.579
6EDU	L_LYS_63	NZ	L_GLU_46	OE1	3.894
6EDU	L_LYS_63	NZ	L_GLU_46	OE2	3.217
6EDU	L_ARG_67	NH1	L_ASP_90	OD2	3.399

6EDU	L_ARG_67	NH2	L_ASP_90	OD1	3.816
6EDU	M_ARG_63	NH1	M_ASP_84	OD1	3.667
6EDU	M_ARG_63	NH1	M_ASP_84	OD2	3.013
6EDU	M_ARG_63	NH2	M_ASP_84	OD2	3.645
6EDU	N_ARG_12	NH2	N_GLU_10	OE2	2.569
6EDU	N_LYS_19	NZ	N_GLU_82	OE2	3.419
6EDU	N_ARG_38	NH2	N_GLU_46	OE1	2.773
6EDU	N_ARG_38	NH2	N_GLU_46	OE2	3.579
6EDU	N_LYS_63	NZ	N_GLU_46	OE1	3.894
6EDU	N_LYS_63	NZ	N_GLU_46	OE2	3.217
6EDU	N_ARG_67	NH1	N_ASP_90	OD2	3.398
6EDU	N_ARG_67	NH2	N_ASP_90	OD1	3.817
6EDU	O_ARG_63	NH1	O_ASP_84	OD1	3.667
6EDU	O_ARG_63	NH1	O_ASP_84	OD2	3.013
6EDU	O_ARG_63	NH2	O_ASP_84	OD2	3.644
6EDU	P_ARG_39	NH1	P_ASP_93	OD1	3.407
6EDU	P_ARG_39	NH2	P_GLU_47	OE1	3.894
6EDU	P_ARG_39	NH2	P_GLU_47	OE2	3.043
6EDU	P_ARG_66	NH1	P_ASP_93	OD2	3.616
6EDU	P_ARG_66	NH2	P_ASP_93	OD2	2.801
6EDU	P_LYS_87	NZ	P_GLU_85	OE2	3.427
6EDU	P_LYS_107	NZ	F_GLU_91	OE1	3.324
6EDU	Q_ARG_24	NH1	Q_ASP_71	OD1	3.743
6EDU	Q_ARG_62	NH2	Q_GLU_82	OE2	3.021
6EDU	Q_ARG_62	NH2	Q_ASP_83	OD2	3.975
6EDU	R_ARG_39	NH1	R_ASP_93	OD1	3.408
6EDU	R_ARG_39	NH2	R_GLU_47	OE1	3.894
6EDU	R_ARG_39	NH2	R_GLU_47	OE2	3.044
6EDU	R_ARG_66	NH1	R_ASP_93	OD2	3.616
6EDU	R_ARG_66	NH2	R_ASP_93	OD2	2.800
6EDU	R_LYS_87	NZ	R_GLU_85	OE2	3.427
6EDU	R_LYS_107	NZ	D_GLU_91	OE1	3.704
6EDU	S_ARG_24	NH1	S_ASP_71	OD1	3.743
6EDU	S_ARG_62	NH2	S_GLU_82	OE2	3.020
6EDU	S_ARG_62	NH2	S_ASP_83	OD2	3.975
6EDU	T_ARG_39	NH1	T_ASP_93	OD1	3.408
6EDU	T_ARG_39	NH2	T_GLU_47	OE1	3.894
6EDU	T_ARG_39	NH2	T_GLU_47	OE2	3.043
6EDU	T_ARG_66	NH1	T_ASP_93	OD2	3.616
6EDU	T_ARG_66	NH2	T_ASP_93	OD2	2.801
6EDU	T_LYS_87	NZ	T_GLU_85	OE2	3.426
6EDU	T_LYS_107	NZ	E_GLU_91	OE1	3.475
6EDU	U_ARG_24	NH1	U_ASP_71	OD1	3.744
6EDU	U_ARG_62	NH2	U_GLU_82	OE2	3.020
6EDU	U_ARG_62	NH2	U_ASP_83	OD2	3.976

Table 829: 6EDU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6EJG	A_LYS_116	NZ	A_ASP_117	OD2	3.986
6EJG	A_LYS_124	NZ	A_ASP_195	OD1	3.544
6EJG	A_LYS_124	NZ	A_ASP_195	OD2	2.697
6EJG	A_LYS_171	NZ	C_ASP_224	OD2	3.396
6EJG	A_LYS_171	NZ	C_ASP_226	OD2	2.901
6EJG	A_HIS_191	NE2	A_ASP_128	OD1	3.062
6EJG	A_HIS_191	NE2	A_ASP_128	OD2	2.636
6EJG	A_LYS_193	NZ	A_ASP_155	OD1	3.682
6EJG	B_LYS_124	NZ	B_ASP_195	OD1	2.725
6EJG	B_LYS_124	NZ	B_ASP_195	OD2	3.034
6EJG	B_LYS_	NZ	B_ASP_	OD2	3.458
6EJG	B_LYS_	NZ	D_ASP_	OD1	3.521
6EJG	B_LYS_	NZ	D_ASP_	OD2	2.547
6EJG	B_LYS_	NZ	D_ASP_	OD2	2.932
6EJG	B_HIS_191	NE2	B_ASP_	OD1	2.701
6EJG	B_HIS_191	NE2	B_ASP_	OD2	3.241
6EJG	C_ARG_62	NH1	C_ASP_112	OD1	3.837
6EJG	C_ARG_62	NH2	C_ASP_112	OD1	3.201
6EJG	C_ARG_62	NH2	C_ASP_112	OD2	3.690
6EJG	C_LYS_65	NZ	C_GLU_135	OE1	3.179
6EJG	C_LYS_91	NZ	C_GLU_97	OE1	3.567
6EJG	C_ARG_103	NH1	C_GLU_123	OE2	3.023
6EJG	C_ARG_103	NH1	C_ASP_124	OD2	3.428
6EJG	C_ARG_103	NH2	C_GLU_121	OE2	3.520
6EJG	C_ARG_209	NH1	C_GLU_258	OE1	3.385
6EJG	C_ARG_209	NH1	C_GLU_258	OE2	3.605
6EJG	C_ARG_219	NH2	C_GLU_268	OE1	2.753
6EJG	C_ARG_219	NH2	C_GLU_268	OE2	3.078
6EJG	C_LYS_236	NZ	C_ASP_259	OD1	3.275
6EJG	C_LYS_236	NZ	C_ASP_259	OD2	2.696
6EJG	C_ARG_277	NH1	C_ASP_273	OD1	3.404
6EJG	C_ARG_277	NH1	C_ASP_273	OD2	3.492
6EJG	C_ARG_277	NH2	C_GLU_97	OE1	3.001
6EJG	D_ARG_	NH1	D_ASP_	OD1	2.944
6EJG	D_ARG_	NH1	D_ASP_	OD2	3.871
6EJG	D_ARG_	NH2	D_ASP_	OD1	3.096
6EJG	D_ARG_	NH2	D_ASP_	OD2	3.874
6EJG	D_LYS_	NZ	D_GLU_	OE1	2.983
6EJG	D_LYS_	NZ	D_GLU_	OE2	3.137
6EJG	D_ARG_	NH1	D_GLU_	OE2	3.108
6EJG	D_ARG_	NH1	D_ASP_	OD2	3.449
6EJG	D_ARG_	NH2	D_ASP_	OD1	2.957
6EJG	D_ARG_	NH2	D_ASP_	OD2	3.232
6EJG	D_LYS_	NZ	D_ASP_	OD1	3.981
6EJG	D_ARG_	NH2	D_GLU_	OE1	2.937
6EJG	D_ARG_	NH2	D_GLU_	OE2	3.024
6EJG	D_LYS_	NZ	D_ASP_	OD1	3.260
6EJG	D_LYS_	NZ	D_ASP_	OD2	2.656
6EJG	D_ARG_	NH1	D_ASP_	OD1	3.140
6EJG	D_ARG_	NH1	D_ASP_	OD2	3.900
6EJG	D_ARG_	NH2	D_GLU_	OE1	3.261
6EJG	D_ARG_	NH2	D_GLU_	OE2	3.642

Table 830: 6EJG-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6EJM	A_LYS_124	NZ	A_ASP_195	OD1	3.195
6EJM	A_LYS_124	NZ	A_ASP_195	OD2	2.580
6EJM	A_HIS_191	NE2	A_ASP_128	OD1	3.203
6EJM	A_HIS_191	NE2	A_ASP_128	OD2	2.407
6EJM	A_HIS_204	ND1	B_GLU_152	OE2	3.786
6EJM	B_LYS_124	NZ	B_ASP_195	OD1	2.563
6EJM	B_LYS_124	NZ	B_ASP_195	OD2	3.251
6EJM	B_HIS_191	NE2	B_ASP_128	OD1	2.629
6EJM	B_HIS_191	NE2	B_ASP_128	OD2	3.201
6EJM	B_LYS_193	NZ	B_GLU_188	OE2	3.576
6EJM	H_ARG_76	NH1	H_GLU_84	OE1	2.904
6EJM	H_ARG_76	NH1	H_ASP_128	OD1	3.983
6EJM	H_ARG_76	NH2	H_ASP_128	OD1	2.619
6EJM	H_ARG_105	NH1	H_ASP_128	OD1	3.929
6EJM	H_ARG_105	NH1	H_ASP_128	OD2	2.801
6EJM	H_ARG_105	NH2	H_ASP_128	OD1	3.282
6EJM	H_ARG_105	NH2	H_ASP_128	OD2	3.596
6EJM	H_LYS_114	NZ	H_ASP_111	OD1	3.878
6EJM	H_LYS_198	NZ	H_ASP_249	OD2	3.812
6EJM	H_ARG_225	NH2	H_ASP_142	OD2	3.513
6EJM	H_ARG_240	NH1	H_GLU_258	OE1	3.177
6EJM	H_ARG_240	NH1	H_GLU_258	OE2	3.066
6EJM	H_ARG_240	NH1	H_GLU_260	OE2	3.276
6EJM	H_ARG_240	NH1	H_ASP_261	OD2	3.562
6EJM	H_ARG_240	NH2	H_ASP_261	OD1	2.537
6EJM	H_ARG_240	NH2	H_ASP_261	OD2	2.801
6EJM	I_ARG_76	NH1	I_GLU_84	OE1	2.878
6EJM	I_ARG_76	NH2	I_ASP_128	OD1	2.699
6EJM	I_ARG_82	NH2	I_GLU_84	OE2	3.006
6EJM	I_ARG_105	NH1	I_ASP_128	OD1	3.783
6EJM	I_ARG_105	NH1	I_ASP_128	OD2	2.828
6EJM	I_ARG_105	NH2	I_ASP_128	OD1	3.082
6EJM	I_ARG_105	NH2	I_ASP_128	OD2	3.617
6EJM	I_ARG_225	NH2	I_ASP_142	OD2	3.785
6EJM	I_ARG_240	NH2	I_ASP_261	OD1	3.449
6EJM	I_ARG_240	NH2	I_ASP_261	OD2	2.659

Table 831: 6EJM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6EK2	A_LYS_124	NZ	A_ASP_195	OD1	3.535
6EK2	A_LYS_124	NZ	A_ASP_195	OD2	2.854
6EK2	A_LYS_187	NZ	A_ASP_189	OD1	3.611
6EK2	A_HIS_191	NE2	A_ASP_128	OD1	3.936
6EK2	A_HIS_191	NE2	A_ASP_128	OD2	2.649
6EK2	B_LYS_124	NZ	B_ASP_195	OD1	2.644
6EK2	B_LYS_124	NZ	B_ASP_195	OD2	3.630
6EK2	B_LYS_144	NZ	B_ASP_137	OD1	3.085
6EK2	B_HIS_191	NE2	B_ASP_128	OD1	2.602
6EK2	B_HIS_191	NE2	B_ASP_128	OD2	3.758
6EK2	B_LYS_193	NZ	B_ASP_189	OD1	3.150
6EK2	H_LYS_188	NZ	H_ASP_249	OD1	2.862
6EK2	H_HIS_204	NE2	H_ASP_268	OD1	2.734
6EK2	H_ARG_207	NH1	H_GLU_215	OE1	3.268
6EK2	H_ARG_207	NH1	H_GLU_215	OE2	3.622
6EK2	H_ARG_207	NH1	H_GLU_258	OE2	3.557
6EK2	H_ARG_207	NH2	H_ASP_259	OD1	2.945
6EK2	H_ARG_213	NH1	H_GLU_215	OE1	3.256
6EK2	H_ARG_213	NH1	H_GLU_215	OE2	3.614
6EK2	H_ARG_236	NH1	H_ASP_259	OD1	3.179
6EK2	H_ARG_236	NH1	H_ASP_259	OD2	2.190
6EK2	H_ARG_236	NH2	H_GLU_258	OE2	3.829
6EK2	H_ARG_236	NH2	H_ASP_259	OD1	3.282
6EK2	H_ARG_236	NH2	H_ASP_259	OD2	3.781
6EK2	H_LYS_247	NZ	H_ASP_249	OD1	3.816
6EK2	H_LYS_271	NZ	H_ASP_222	OD2	3.418
6EK2	H_LYS_362	NZ	H_ASP_408	OD2	3.909
6EK2	H_ARG_370	NH1	A_GLU_188	OE2	3.014
6EK2	H_ARG_370	NH2	A_GLU_188	OE1	3.920
6EK2	H_ARG_370	NH2	A_GLU_188	OE2	3.261
6EK2	H_ARG_399	NH1	H_ASP_420	OD1	3.412
6EK2	H_ARG_399	NH1	H_ASP_420	OD2	2.682
6EK2	H_LYS_441	NZ	H_GLU_443	OE2	3.288
6EK2	I_LYS_188	NZ	I_ASP_249	OD1	2.854
6EK2	I_HIS_204	NE2	I_ASP_268	OD2	2.800
6EK2	I_ARG_207	NH1	I_GLU_215	OE1	3.248
6EK2	I_ARG_207	NH1	I_GLU_215	OE2	3.625
6EK2	I_ARG_207	NH1	I_GLU_258	OE2	3.570
6EK2	I_ARG_207	NH2	I_ASP_259	OD1	2.867
6EK2	I_ARG_236	NH1	I_ASP_259	OD1	2.843
6EK2	I_ARG_236	NH1	I_ASP_259	OD2	2.628
6EK2	I_LYS_247	NZ	I_ASP_249	OD1	3.833
6EK2	I_LYS_271	NZ	I_ASP_222	OD2	3.427
6EK2	I_LYS_362	NZ	I_ASP_408	OD2	3.921
6EK2	I_ARG_370	NH1	B_GLU_188	OE1	2.817
6EK2	I_ARG_370	NH1	B_GLU_188	OE2	3.286
6EK2	I_ARG_370	NH2	B_GLU_188	OE1	3.837
6EK2	I_ARG_370	NH2	B_GLU_188	OE2	3.095
6EK2	I_ARG_399	NH1	I_ASP_420	OD1	3.393
6EK2	I_ARG_399	NH1	I_ASP_420	OD2	2.676
6EK2	I_LYS_441	NZ	I_GLU_443	OE2	3.785

Table 832: 6EK2-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6EUN	A_LYS_82	NZ	A_GLU_77	OE2	2.937
6EUN	A_LYS_87	NZ	B_GLU_47	OE1	3.058
6EUN	A_LYS_101	NZ	A_ASP_105	OD2	3.752
6EUN	A_LYS_107	NZ	C_ASP_105	OD1	3.488
6EUN	A_LYS_145	NZ	A_GLU_148	OE2	3.702
6EUN	A_LYS_167	NZ	C_ASP_165	OD1	3.883
6EUN	B_LYS_69	NZ	B_ASP_59	OD2	2.842
6EUN	B_LYS_82	NZ	B_GLU_77	OE2	2.936
6EUN	B_LYS_87	NZ	C_GLU_47	OE1	3.021
6EUN	B_LYS_101	NZ	B_ASP_105	OD2	3.762
6EUN	B_LYS_107	NZ	A_ASP_105	OD1	3.579
6EUN	B_LYS_145	NZ	B_GLU_148	OE2	3.617
6EUN	C_LYS_69	NZ	C_ASP_59	OD2	2.843
6EUN	C_LYS_82	NZ	C_GLU_77	OE2	2.928
6EUN	C_LYS_87	NZ	A_GLU_47	OE1	3.007
6EUN	C_LYS_101	NZ	C_ASP_105	OD2	3.754
6EUN	C_LYS_107	NZ	B_ASP_105	OD1	3.525
6EUN	C_LYS_145	NZ	C_GLU_148	OE2	3.782

Table 833: 6EUN-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6EUP	A.LYS_69	NZ	A.ASP_59	OD2	3.593
6EUP	A.LYS_87	NZ	B.GLU_47	OE1	2.842
6EUP	A.LYS_87	NZ	B.ASP_79	OD1	3.786
6EUP	A.LYS_107	NZ	C.ASP_105	OD1	3.538
6EUP	A.LYS_145	NZ	A.GLU_148	OE2	3.961
6EUP	B.LYS_69	NZ	B.ASP_75	OD1	3.179
6EUP	B.LYS_69	NZ	B.ASP_75	OD2	2.780
6EUP	B.LYS_87	NZ	C.GLU_47	OE1	2.811
6EUP	B.LYS_87	NZ	C.ASP_79	OD1	3.799
6EUP	B.LYS_107	NZ	A.ASP_105	OD1	3.723
6EUP	C.LYS_69	NZ	C.ASP_59	OD2	3.592
6EUP	C.LYS_87	NZ	A.GLU_47	OE1	2.814
6EUP	C.LYS_87	NZ	A.ASP_79	OD1	3.752
6EUP	C.LYS_107	NZ	B.ASP_105	OD1	3.560
6EUP	C.LYS_145	NZ	C.GLU_148	OE2	3.928

Table 834: 6EUP-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6EV1	A_ARG_40	NH1	A_GLU_46	OE1	3.790
6EV1	A_ARG_40	NH1	A_GLU_46	OE2	2.696
6EV1	A_ARG_40	NH2	A_GLU_46	OE2	2.910
6EV1	A_LYS_63	NZ	A_GLU_46	OE1	3.383
6EV1	A_LYS_67	NZ	A_ASP_90	OD1	3.842
6EV1	A_LYS_67	NZ	A_ASP_90	OD2	2.754
6EV1	A_LYS_147	NZ	A_ASP_148	OD1	3.932
6EV1	A_LYS_213	NZ	B_GLU_122	OE1	3.565
6EV1	B_HIS_33	NE2	B_ASP_49	OD1	3.832
6EV1	B_ARG_45	NH1	A_ASP_105	OD1	3.400
6EV1	B_LYS_52	NZ	B_ASP_49	OD2	3.765
6EV1	B_ARG_60	NH1	B_GLU_78	OE1	3.819
6EV1	B_ARG_60	NH1	B_GLU_78	OE2	3.655
6EV1	B_ARG_60	NH2	B_GLU_78	OE2	3.561
6EV1	B_ARG_60	NH2	B_GLU_80	OE2	2.733
6EV1	B_ARG_60	NH2	B_ASP_81	OD1	3.048
6EV1	B_ARG_60	NH2	B_ASP_81	OD2	3.747
6EV1	B_LYS_102	NZ	B_GLU_104	OE2	3.444
6EV1	B_LYS_102	NZ	B_GLU_164	OE2	3.563
6EV1	B_ARG_141	NH1	B_GLU_104	OE1	3.542
6EV1	B_ARG_141	NH1	B_GLU_104	OE2	2.887
6EV1	B_ARG_141	NH2	B_GLU_104	OE1	3.560
6EV1	B_ARG_141	NH2	B_GLU_104	OE2	2.857
6EV1	B_LYS_144	NZ	B_GLU_194	OE2	3.954
6EV1	B_LYS_148	NZ	B_GLU_194	OE1	2.745
6EV1	B_LYS_187	NZ	B_ASP_184	OD1	3.196
6EV1	C_LYS_38	NZ	C_GLU_89	OE2	2.747
6EV1	C_LYS_63	NZ	C_GLU_46	OE1	3.586
6EV1	C_LYS_63	NZ	C_GLU_46	OE2	3.868
6EV1	C_LYS_63	NZ	C_GLU_89	OE2	3.610
6EV1	C_LYS_67	NZ	C_ASP_90	OD1	3.419
6EV1	C_LYS_67	NZ	C_ASP_90	OD2	2.576
6EV1	C_LYS_147	NZ	C_ASP_148	OD1	3.591
6EV1	D_LYS_52	NZ	D_ASP_49	OD2	3.936
6EV1	D_ARG_60	NH1	D_GLU_78	OE1	3.982
6EV1	D_ARG_60	NH1	D_ASP_81	OD1	2.686
6EV1	D_ARG_60	NH1	D_ASP_81	OD2	2.341
6EV1	D_ARG_60	NH2	D_GLU_78	OE2	3.908
6EV1	D_ARG_60	NH2	D_GLU_80	OE2	2.672
6EV1	D_ARG_60	NH2	D_ASP_81	OD1	3.533
6EV1	D_LYS_102	NZ	D_GLU_104	OE2	2.957
6EV1	D_LYS_102	NZ	D_GLU_164	OE1	3.066
6EV1	D_ARG_141	NH1	D_GLU_104	OE1	3.100
6EV1	D_ARG_141	NH1	D_GLU_104	OE2	2.729
6EV1	D_ARG_141	NH2	D_GLU_104	OE1	3.502
6EV1	D_LYS_148	NZ	D_GLU_194	OE2	2.419
6EV1	D_LYS_187	NZ	D_ASP_184	OD1	2.568
6EV1	D_LYS_187	NZ	D_ASP_184	OD2	3.848
6EV1	E_ARG_40	NH1	E_GLU_46	OE1	3.238
6EV1	E_LYS_67	NZ	E_ASP_90	OD1	3.136
6EV1	E_LYS_67	NZ	E_ASP_90	OD2	3.150
6EV1	E_LYS_147	NZ	E_ASP_148	OD1	3.641
6EV1	E_LYS_147	NZ	E_ASP_148	OD2	3.538
6EV1	E_LYS_213	NZ	F_GLU_122	OE2	3.696
6EV1	E_LYS_214	NZ	E_GLU_216	OE2	3.745
6EV1	F_ARG_45	NH1	E_ASP_105	OD1	3.598
6EV1	F_LYS_52	NZ	F_ASP_49	OD2	3.409

6EV1	F_ARG_60	NH1	F_GLU_78	OE1	3.963
6EV1	F_ARG_60	NH2	F_GLU_80	OE2	2.462
6EV1	F_ARG_60	NH2	F_ASP_81	OD1	2.838
6EV1	F_ARG_60	NH2	F_ASP_81	OD2	3.378
6EV1	F_LYS_102	NZ	F_GLU_104	OE2	3.200
6EV1	F_LYS_102	NZ	F_GLU_164	OE1	3.253
6EV1	F_LYS_102	NZ	F_GLU_164	OE2	3.819
6EV1	F_ARG_141	NH1	F_GLU_142	OE2	3.956
6EV1	F_ARG_141	NH2	F_GLU_104	OE1	2.879
6EV1	F_ARG_141	NH2	F_GLU_104	OE2	2.315
6EV1	F_LYS_148	NZ	F_GLU_194	OE1	2.676
6EV1	F_LYS_187	NZ	F_ASP_184	OD1	3.320
6EV1	F_LYS_189	NZ	F_GLU_212	OE1	3.396
6EV1	G_ARG_40	NH1	G_GLU_46	OE1	3.181
6EV1	G_LYS_63	NZ	G_GLU_46	OE1	3.941
6EV1	G_LYS_63	NZ	G_GLU_46	OE2	3.486
6EV1	G_LYS_67	NZ	G_ASP_90	OD1	3.844
6EV1	G_LYS_67	NZ	G_ASP_90	OD2	3.076
6EV1	G_LYS_213	NZ	H_GLU_122	OE2	3.127
6EV1	H_HIS_33	NE2	H_ASP_49	OD1	3.831
6EV1	H_ARG_60	NH2	H_GLU_80	OE2	2.685
6EV1	H_ARG_60	NH2	H_ASP_81	OD1	3.172
6EV1	H_ARG_60	NH2	H_ASP_81	OD2	3.902
6EV1	H_LYS_102	NZ	H_GLU_104	OE2	2.463
6EV1	H_LYS_102	NZ	H_GLU_164	OE1	3.887
6EV1	H_LYS_102	NZ	H_GLU_164	OE2	3.148
6EV1	H_ARG_141	NH1	H_GLU_104	OE1	3.993
6EV1	H_ARG_141	NH2	H_GLU_104	OE1	2.709
6EV1	H_ARG_141	NH2	H_GLU_104	OE2	3.012
6EV1	H_HIS_188	ND1	H_ASP_150	OD2	3.547
6EV1	I_ARG_40	NH1	I_GLU_46	OE1	3.727
6EV1	I_ARG_40	NH1	I_GLU_46	OE2	2.502
6EV1	I_ARG_40	NH2	I_GLU_46	OE2	3.081
6EV1	I_LYS_67	NZ	I_ASP_90	OD1	3.185
6EV1	I_LYS_67	NZ	I_ASP_90	OD2	2.453
6EV1	I_LYS_147	NZ	I_ASP_148	OD1	3.802
6EV1	I_LYS_213	NZ	J_GLU_122	OE1	2.884
6EV1	I_LYS_213	NZ	J_GLU_122	OE2	3.812
6EV1	J_ARG_45	NH2	I_ASP_105	OD1	3.213
6EV1	J_ARG_45	NH2	I_ASP_105	OD2	3.457
6EV1	J_ARG_60	NH1	J_GLU_78	OE1	2.996
6EV1	J_ARG_60	NH2	J_GLU_78	OE1	2.740
6EV1	J_ARG_60	NH2	J_GLU_78	OE2	3.438
6EV1	J_ARG_60	NH2	J_GLU_80	OE1	3.708
6EV1	J_ARG_60	NH2	J_ASP_81	OD1	3.548
6EV1	J_LYS_102	NZ	J_GLU_164	OE1	3.206
6EV1	J_LYS_102	NZ	J_GLU_164	OE2	3.357
6EV1	J_ARG_141	NH1	J_GLU_104	OE1	3.574
6EV1	J_ARG_141	NH1	J_GLU_104	OE2	3.837
6EV1	J_ARG_141	NH2	J_GLU_104	OE1	3.635
6EV1	J_ARG_141	NH2	J_GLU_104	OE2	3.025
6EV1	J_LYS_148	NZ	J_GLU_194	OE1	2.568
6EV1	J_LYS_187	NZ	J_ASP_184	OD1	2.786
6EV1	J_HIS_188	ND1	J_ASP_150	OD2	3.581
6EV1	K_LYS_67	NZ	K_ASP_90	OD1	3.821
6EV1	K_LYS_67	NZ	K_ASP_90	OD2	3.131
6EV1	K_LYS_147	NZ	K_ASP_148	OD1	3.891
6EV1	K_LYS_147	NZ	K_ASP_148	OD2	3.991

6EV1	K_HIS_168	NE2	L_ASP_166	OD2	3.740
6EV1	K_LYS_213	NZ	L_GLU_122	OE1	3.450
6EV1	L_ARG_45	NH2	K_ASP_105	OD1	3.857
6EV1	L_LYS_52	NZ	L_ASP_49	OD2	3.305
6EV1	L_ARG_60	NH1	L_GLU_78	OE2	3.656
6EV1	L_ARG_60	NH2	L_GLU_80	OE2	2.289
6EV1	L_ARG_60	NH2	L_ASP_81	OD1	3.740
6EV1	L_LYS_102	NZ	L_GLU_104	OE1	3.803
6EV1	L_LYS_102	NZ	L_GLU_104	OE2	3.397
6EV1	L_LYS_102	NZ	L_GLU_164	OE1	3.211
6EV1	L_ARG_141	NH1	L_GLU_104	OE1	3.719
6EV1	L_LYS_148	NZ	L_GLU_194	OE1	2.763
6EV1	L_LYS_187	NZ	L_ASP_184	OD1	2.439
6EV1	L_LYS_187	NZ	L_ASP_184	OD2	3.983

Table 835: 6EV1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6EV2	A.LYS_63	NZ	A.GLU_46	OE2	3.111
6EV2	A.LYS_65	NZ	A.ASP_66	OD1	3.842
6EV2	A.LYS_65	NZ	A.ASP_66	OD2	2.879
6EV2	A.LYS_67	NZ	A.ASP_90	OD1	3.783
6EV2	A.LYS_67	NZ	A.ASP_90	OD2	2.679
6EV2	A.LYS_147	NZ	A.ASP_148	OD1	3.638
6EV2	A.LYS_213	NZ	B.GLU_122	OE1	3.442
6EV2	B.ARG_45	NH1	A.ASP_105	OD1	3.088
6EV2	B.LYS_52	NZ	B.ASP_49	OD2	3.559
6EV2	B.ARG_60	NH1	B.GLU_78	OE1	3.644
6EV2	B.ARG_60	NH1	B.GLU_78	OE2	3.977
6EV2	B.ARG_60	NH2	B.GLU_80	OE2	3.107
6EV2	B.ARG_60	NH2	B.ASP_81	OD1	2.872
6EV2	B.ARG_60	NH2	B.ASP_81	OD2	3.612
6EV2	B.LYS_102	NZ	B.GLU_104	OE1	3.573
6EV2	B.LYS_102	NZ	B.GLU_164	OE1	3.299
6EV2	B.LYS_102	NZ	B.GLU_164	OE2	3.878
6EV2	B.ARG_141	NH2	B.GLU_104	OE1	3.798
6EV2	B.ARG_141	NH2	B.GLU_104	OE2	3.715
6EV2	B.LYS_168	NZ	F.GLU_78	OE2	2.948
6EV2	B.LYS_182	NZ	B.GLU_186	OE2	3.804
6EV2	B.HIS_188	ND1	B.ASP_150	OD2	3.294
6EV2	B.HIS_217	NE2	B.GLU_186	OE2	3.191
6EV2	C.LYS_38	NZ	C.GLU_46	OE1	3.925
6EV2	C.ARG_40	NH1	C.GLU_89	OE1	2.530
6EV2	C.ARG_40	NH1	C.GLU_89	OE2	3.940
6EV2	C.ARG_40	NH2	C.GLU_89	OE1	2.841
6EV2	C.LYS_63	NZ	C.GLU_46	OE2	2.910
6EV2	C.LYS_67	NZ	C.ASP_90	OD1	3.799
6EV2	C.LYS_67	NZ	C.ASP_90	OD2	2.689
6EV2	C.LYS_147	NZ	C.ASP_148	OD1	3.909
6EV2	C.LYS_214	NZ	C.GLU_216	OE1	3.019
6EV2	C.LYS_214	NZ	C.GLU_216	OE2	3.275
6EV2	D.LYS_44	NZ	C.ASP_105	OD2	3.822
6EV2	D.ARG_45	NH1	C.ASP_105	OD1	3.142
6EV2	D.LYS_52	NZ	D.ASP_49	OD2	3.541
6EV2	D.ARG_60	NH1	D.GLU_78	OE1	3.997
6EV2	D.ARG_60	NH1	D.GLU_78	OE2	3.666
6EV2	D.ARG_60	NH2	D.GLU_80	OE2	2.969
6EV2	D.ARG_60	NH2	D.ASP_81	OD1	2.871
6EV2	D.ARG_60	NH2	D.ASP_81	OD2	3.679
6EV2	D.LYS_102	NZ	D.GLU_164	OE1	3.482
6EV2	D.ARG_141	NH2	D.GLU_104	OE1	3.236
6EV2	D.ARG_141	NH2	D.GLU_104	OE2	3.266
6EV2	D.LYS_148	NZ	D.GLU_194	OE1	3.886
6EV2	D.LYS_148	NZ	D.GLU_194	OE2	2.872
6EV2	D.LYS_168	NZ	H.GLU_78	OE2	3.198
6EV2	D.HIS_188	ND1	D.ASP_150	OD2	3.510
6EV2	E.ARG_40	NH1	E.GLU_89	OE1	3.472
6EV2	E.ARG_40	NH1	E.GLU_89	OE2	2.763
6EV2	E.ARG_40	NH2	E.GLU_89	OE2	2.889
6EV2	E.LYS_63	NZ	E.GLU_46	OE1	3.154
6EV2	E.LYS_63	NZ	E.GLU_46	OE2	2.770
6EV2	E.LYS_67	NZ	E.ASP_90	OD1	3.680
6EV2	E.LYS_67	NZ	E.ASP_90	OD2	2.852
6EV2	E.LYS_147	NZ	E.ASP_148	OD1	2.804
6EV2	E.LYS_147	NZ	E.ASP_148	OD2	3.429

6EV2	E_LYS_210	NZ	E_ASP_212	OD1	3.724
6EV2	E_LYS_210	NZ	E_ASP_212	OD2	3.578
6EV2	E_LYS_213	NZ	F_GLU_122	OE1	3.493
6EV2	E_LYS_214	NZ	E_GLU_216	OE2	2.823
6EV2	E_LYS_218	NZ	F_ASP_121	OD2	3.835
6EV2	F_ARG_45	NH1	E_ASP_105	OD1	2.818
6EV2	F_LYS_52	NZ	F_ASP_49	OD2	3.921
6EV2	F_ARG_60	NH1	F_GLU_78	OE2	3.617
6EV2	F_ARG_60	NH2	F_GLU_80	OE2	3.106
6EV2	F_ARG_60	NH2	F_ASP_81	OD1	2.910
6EV2	F_ARG_60	NH2	F_ASP_81	OD2	3.493
6EV2	F_LYS_102	NZ	F_GLU_104	OE2	3.866
6EV2	F_LYS_102	NZ	F_GLU_164	OE1	2.823
6EV2	F_LYS_102	NZ	F_GLU_164	OE2	3.600
6EV2	F_LYS_148	NZ	F_GLU_194	OE1	2.349
6EV2	F_LYS_168	NZ	B_GLU_78	OE1	3.747
6EV2	F_LYS_189	NZ	F_GLU_212	OE1	2.964
6EV2	F_LYS_189	NZ	F_GLU_212	OE2	3.194
6EV2	G_LYS_63	NZ	G_GLU_46	OE2	2.652
6EV2	G_LYS_67	NZ	G_ASP_90	OD1	3.758
6EV2	G_LYS_67	NZ	G_ASP_90	OD2	2.774
6EV2	G_LYS_147	NZ	G_ASP_148	OD1	3.806
6EV2	G_LYS_210	NZ	A_ASP_73	OD1	3.883
6EV2	G_LYS_210	NZ	A_ASP_73	OD2	2.404
6EV2	G_LYS_213	NZ	H_GLU_122	OE1	3.330
6EV2	G_LYS_213	NZ	H_GLU_122	OE2	3.779
6EV2	G_LYS_214	NZ	G_GLU_216	OE2	2.730
6EV2	H_ARG_45	NH1	G_ASP_105	OD1	3.108
6EV2	H_ARG_60	NH1	H_GLU_78	OE2	3.921
6EV2	H_ARG_60	NH2	H_GLU_80	OE2	2.991
6EV2	H_ARG_60	NH2	H_ASP_81	OD1	3.423
6EV2	H_ARG_60	NH2	H_ASP_81	OD2	2.856
6EV2	H_LYS_102	NZ	H_GLU_164	OE1	3.383
6EV2	H_ARG_141	NH2	H_GLU_104	OE1	3.404
6EV2	H_ARG_141	NH2	H_GLU_104	OE2	2.455
6EV2	H_LYS_148	NZ	H_GLU_194	OE1	2.710
6EV2	H_LYS_148	NZ	H_GLU_194	OE2	3.785
6EV2	H_LYS_168	NZ	D_GLU_78	OE2	3.686

Table 836: 6EV2-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6EWB	A_ARG_241	NH2	A_ASP_325	OD1	2.936
6EWB	A_ARG_241	NH2	A_ASP_325	OD2	3.696
6EWB	A_LYS_248	NZ	A_GLU_247	OE1	3.886
6EWB	A_ARG_345	NH1	A_GLU_376	OE2	3.889
6EWB	A_HIS_347	NE2	A_ASP_374	OD2	2.911
6EWB	A_HIS_396	ND1	A_ASP_391	OD2	3.943
6EWB	A_ARG_435	NH1	A_ASP_448	OD2	3.551
6EWB	A_ARG_435	NH2	A_ASP_450	OD1	3.333
6EWB	A_ARG_435	NH2	A_ASP_450	OD2	2.720
6EWB	A_ARG_476	NH1	A_ASP_518	OD2	2.712
6EWB	A_ARG_476	NH2	A_GLU_488	OE1	3.271
6EWB	A_LYS_490	NZ	A_GLU_429	OE2	3.221
6EWB	A_ARG_516	NH2	A_ASP_518	OD1	3.815
6EWB	A_ARG_516	NH2	A_ASP_518	OD2	3.445
6EWB	B_ARG_241	NH2	B_ASP_325	OD1	3.075
6EWB	B_ARG_241	NH2	B_ASP_325	OD2	3.936
6EWB	B_LYS_248	NZ	B_GLU_247	OE1	3.679
6EWB	B_ARG_345	NH1	B_GLU_376	OE2	3.796
6EWB	B_ARG_345	NH2	B_GLU_376	OE2	3.815
6EWB	B_HIS_347	ND1	B_ASP_370	OD1	3.328
6EWB	B_HIS_347	NE2	B_ASP_374	OD2	2.654
6EWB	B_ARG_373	NH1	B_ASP_372	OD2	3.813
6EWB	B_ARG_373	NH2	B_ASP_372	OD2	3.329
6EWB	B_ARG_435	NH1	B_ASP_448	OD2	3.850
6EWB	B_ARG_435	NH1	B_ASP_506	OD1	3.944
6EWB	B_ARG_435	NH2	B_ASP_450	OD1	3.359
6EWB	B_ARG_435	NH2	B_ASP_450	OD2	2.788
6EWB	B_ARG_476	NH1	B_ASP_518	OD2	2.823
6EWB	B_ARG_476	NH2	B_GLU_488	OE1	3.165
6EWB	B_LYS_490	NZ	B_GLU_429	OE2	3.030
6EWB	B_ARG_516	NH2	B_ASP_518	OD1	3.365
6EWB	B_ARG_516	NH2	B_ASP_518	OD2	2.936
6EWB	C_ARG_241	NH2	C_ASP_325	OD1	2.915
6EWB	C_ARG_241	NH2	C_ASP_325	OD2	3.721
6EWB	C_LYS_248	NZ	C_GLU_247	OE1	3.894
6EWB	C_ARG_345	NH1	C_GLU_376	OE2	3.422
6EWB	C_ARG_345	NH2	C_GLU_376	OE2	3.471
6EWB	C_HIS_347	ND1	C_ASP_370	OD1	3.346
6EWB	C_HIS_347	NE2	C_ASP_374	OD2	2.797
6EWB	C_HIS_396	ND1	C_ASP_391	OD2	3.992
6EWB	C_ARG_435	NH1	C_ASP_448	OD2	3.511
6EWB	C_ARG_435	NH2	C_ASP_450	OD1	3.163
6EWB	C_ARG_435	NH2	C_ASP_450	OD2	2.800
6EWB	C_ARG_476	NH1	C_GLU_488	OE1	2.525
6EWB	C_ARG_476	NH2	C_ASP_518	OD2	3.985
6EWB	C_LYS_490	NZ	C_GLU_429	OE1	3.972
6EWB	C_LYS_490	NZ	C_GLU_429	OE2	3.084
6EWB	C_ARG_516	NH2	C_ASP_518	OD1	3.755
6EWB	C_ARG_516	NH2	C_ASP_518	OD2	3.482
6EWB	D_ARG_241	NH2	D_ASP_325	OD1	3.023
6EWB	D_ARG_241	NH2	D_ASP_325	OD2	3.955
6EWB	D_LYS_248	NZ	D_GLU_247	OE1	3.969
6EWB	D_ARG_345	NH1	D_GLU_376	OE2	3.830
6EWB	D_HIS_347	ND1	D_ASP_370	OD1	3.312
6EWB	D_HIS_347	NE2	D_ASP_374	OD2	2.724
6EWB	D_HIS_417	NE2	L_GLU_80	OE2	3.932
6EWB	D_ARG_435	NH1	D_ASP_448	OD2	3.638

6EWB	D_ARG_435	NH2	D_ASP_450	OD1	3.210
6EWB	D_ARG_435	NH2	D_ASP_450	OD2	2.891
6EWB	D_ARG_476	NH1	D_ASP_518	OD2	2.514
6EWB	D_ARG_476	NH2	D_GLU_488	OE1	3.217
6EWB	D_LYS_490	NZ	D_GLU_429	OE2	2.925
6EWB	D_ARG_516	NH2	D_ASP_518	OD1	3.559
6EWB	D_ARG_516	NH2	D_ASP_518	OD2	3.083
6EWB	E_LYS_	NZ	E_ASP_	OD1	3.980
6EWB	E_ARG_98	NH1	B_ASP_341	OD1	3.977
6EWB	E_ARG_98	NH2	B_ASP_341	OD1	3.813
6EWB	E_ARG_101	NH1	F_ASP_49	OD1	2.895
6EWB	E_ARG_101	NH1	F_ASP_49	OD2	3.620
6EWB	F_ARG_	NH1	E_ASP_	OD1	3.803
6EWB	F_ARG_	NH1	E_ASP_	OD2	3.536
6EWB	F_LYS_52	NZ	A_ASP_448	OD1	3.722
6EWB	F_LYS_52	NZ	A_ASP_448	OD2	2.304
6EWB	F_LYS_52	NZ	F_ASP_49	OD2	3.153
6EWB	F_ARG_	NH1	F_GLU_	OE2	3.882
6EWB	F_ARG_	NH2	F_GLU_	OE2	2.849
6EWB	F_ARG_	NH2	F_ASP_	OD1	2.744
6EWB	F_ARG_	NH2	F_ASP_	OD2	3.294
6EWB	G_ARG_40	NH1	G_GLU_89	OE1	3.993
6EWB	G_ARG_40	NH2	G_GLU_89	OE2	3.112
6EWB	G_LYS_63	NZ	G_GLU_46	OE1	3.095
6EWB	G_LYS_63	NZ	G_GLU_46	OE2	3.462
6EWB	G_LYS_67	NZ	G_ASP_90	OD2	3.352
6EWB	G_ARG_98	NH1	D_ASP_341	OD1	3.850
6EWB	G_ARG_98	NH2	D_ASP_341	OD1	3.731
6EWB	G_ARG_101	NH1	I_ASP_49	OD1	2.830
6EWB	G_ARG_101	NH1	I_ASP_49	OD2	3.797
6EWB	H_ARG_40	NH1	H_GLU_89	OE1	3.969
6EWB	H_LYS_67	NZ	H_ASP_90	OD2	3.353
6EWB	H_ARG_98	NH1	A_ASP_341	OD2	3.948
6EWB	H_ARG_98	NH2	A_ASP_341	OD2	3.896
6EWB	H_ARG_101	NH1	L_ASP_49	OD1	2.509
6EWB	H_ARG_101	NH1	L_ASP_49	OD2	3.441
6EWB	H_LYS_208	NZ	H_ASP_210	OD1	3.387
6EWB	H_LYS_208	NZ	H_ASP_210	OD2	3.606
6EWB	I_ARG_45	NH1	G_ASP_104	OD1	3.731
6EWB	I_ARG_45	NH1	G_ASP_104	OD2	3.636
6EWB	I_LYS_52	NZ	C_ASP_448	OD1	3.564
6EWB	I_LYS_52	NZ	C_ASP_448	OD2	2.694
6EWB	I_LYS_52	NZ	I_ASP_49	OD2	3.594
6EWB	I_ARG_60	NH1	I_GLU_80	OE2	3.662
6EWB	I_ARG_60	NH2	I_GLU_80	OE2	2.362
6EWB	I_ARG_60	NH2	I_ASP_81	OD1	3.161
6EWB	I_ARG_60	NH2	I_ASP_81	OD2	3.779
6EWB	I_LYS_148	NZ	I_GLU_194	OE1	2.906
6EWB	I_LYS_148	NZ	I_GLU_194	OE2	3.891
6EWB	I_HIS_188	ND1	I_ASP_150	OD2	2.838
6EWB	J_LYS_38	NZ	J_ASP_90	OD1	3.994
6EWB	J_ARG_98	NH1	C_ASP_341	OD2	3.957
6EWB	J_ARG_98	NH2	C_ASP_341	OD2	3.467
6EWB	J_ARG_101	NH1	K_ASP_49	OD1	2.726
6EWB	J_ARG_101	NH1	K_ASP_49	OD2	3.581
6EWB	J_LYS_211	NZ	K_GLU_122	OE2	2.945
6EWB	K_ARG_45	NH1	J_ASP_104	OD2	3.826
6EWB	K_LYS_52	NZ	D_ASP_448	OD1	3.845

6EWB	K_LYS_52	NZ	D_ASP_448	OD2	2.608
6EWB	K_LYS_52	NZ	K_ASP_49	OD2	3.118
6EWB	K_ARG_60	NH2	K_GLU_80	OE1	3.852
6EWB	K_ARG_60	NH2	K_ASP_81	OD1	2.735
6EWB	K_ARG_60	NH2	K_ASP_81	OD2	3.577
6EWB	K_LYS_141	NZ	K_GLU_104	OE1	3.738
6EWB	K_LYS_141	NZ	K_GLU_104	OE2	2.397
6EWB	K_LYS_198	NZ	K_ASP_109	OD2	3.688
6EWB	L_ARG_45	NH1	H_ASP_104	OD1	3.721
6EWB	L_ARG_45	NH1	H_ASP_104	OD2	3.560
6EWB	L_LYS_52	NZ	B_ASP_448	OD1	3.690
6EWB	L_LYS_52	NZ	B_ASP_448	OD2	2.585
6EWB	L_LYS_52	NZ	L_ASP_49	OD2	3.133
6EWB	L_ARG_60	NH1	D_GLU_316	OE1	3.251
6EWB	L_ARG_60	NH1	D_GLU_316	OE2	3.266
6EWB	L_ARG_60	NH2	L_GLU_80	OE1	3.300
6EWB	L_ARG_60	NH2	L_ASP_81	OD1	2.716
6EWB	L_ARG_60	NH2	L_ASP_81	OD2	3.315
6EWB	L_LYS_102	NZ	L_ASP_164	OD2	3.771
6EWB	L_LYS_141	NZ	L_GLU_104	OE2	3.049
6EWB	L_HIS_188	ND1	L_ASP_150	OD1	3.713

Table 837: 6EWB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6FAB	L_ARG_24	NH1	L_ASP_70	OD1	2.789
6FAB	L_ARG_61	NH1	L_GLU_81	OE2	3.576
6FAB	L_ARG_61	NH2	L_GLU_81	OE1	2.864
6FAB	L_ARG_61	NH2	L_GLU_81	OE2	2.823
6FAB	L_ARG_61	NH2	L_ASP_82	OD1	2.715
6FAB	L_ARG_61	NH2	L_ASP_82	OD2	3.543
6FAB	L_LYS_107	NZ	L_ASP_110	OD1	3.024
6FAB	L_LYS_147	NZ	L_GLU_195	OE2	3.857
6FAB	L_LYS_149	NZ	L_GLU_195	OE1	2.545
6FAB	L_LYS_149	NZ	L_GLU_195	OE2	2.801
6FAB	L_LYS_169	NZ	L_ASP_167	OD1	2.717
6FAB	L_LYS_169	NZ	L_ASP_167	OD2	2.572
6FAB	L_LYS_183	NZ	L_GLU_187	OE1	2.518
6FAB	L_LYS_183	NZ	L_GLU_187	OE2	2.757
6FAB	L_ARG_188	NH1	L_ASP_184	OD1	2.649
6FAB	L_ARG_188	NH1	L_ASP_184	OD2	3.158
6FAB	L_ARG_188	NH2	L_ASP_184	OD1	3.720
6FAB	L_ARG_188	NH2	L_ASP_184	OD2	2.655
6FAB	L_ARG_188	NH2	L_GLU_185	OE1	2.879
6FAB	L_LYS_199	NZ	L_ASP_143	OD1	2.609
6FAB	L_LYS_199	NZ	L_ASP_143	OD2	2.563
6FAB	H_LYS_63	NZ	H_GLU_46	OE1	2.502
6FAB	H_LYS_63	NZ	H_GLU_46	OE2	3.193
6FAB	H_LYS_65	NZ	H_GLU_62	OE1	2.682
6FAB	H_LYS_65	NZ	H_GLU_62	OE2	2.720
6FAB	H_LYS_67	NZ	H_ASP_90	OD1	3.504
6FAB	H_LYS_67	NZ	H_ASP_90	OD2	2.658
6FAB	H_ARG_98	NH2	H_ASP_109	OD1	3.478
6FAB	H_ARG_98	NH2	H_ASP_109	OD2	2.734
6FAB	H_LYS_107	NZ	H_GLU_100	OE2	3.655
6FAB	H_LYS_107	NZ	H_ASP_109	OD2	2.865
6FAB	H_LYS_213	NZ	H_ASP_215	OD1	3.756
6FAB	H_LYS_213	NZ	H_ASP_215	OD2	2.836
6FAB	H_LYS_216	NZ	L_GLU_123	OE1	2.624
6FAB	H_LYS_216	NZ	L_GLU_123	OE2	2.770
6FAB	H_ARG_221	NH2	H_ASP_222	OD1	2.832
6FAB	H_ARG_221	NH2	H_ASP_222	OD2	3.565

Table 838: 6FAB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6FAX	L_ARG_61	NH2	L_ASP_82	OD1	2.582
6FAX	L_ARG_61	NH2	L_ASP_82	OD2	3.227
6FAX	L_LYS_103	NZ	L_GLU_165	OE1	3.961
6FAX	L_LYS_149	NZ	L_GLU_195	OE1	3.174
6FAX	L_LYS_149	NZ	L_GLU_195	OE2	3.580
6FAX	L_HIS_189	ND1	L_ASP_151	OD2	3.031
6FAX	H_LYS_19	NZ	H_GLU_82	OE1	3.254
6FAX	H_LYS_38	NZ	H_ASP_90	OD1	3.375
6FAX	H_LYS_63	NZ	H_GLU_46	OE1	3.943
6FAX	H_LYS_63	NZ	H_GLU_46	OE2	3.507
6FAX	H_LYS_67	NZ	H_ASP_90	OD2	3.573
6FAX	H_ARG_98	NH2	H_ASP_110	OD1	3.912
6FAX	H_ARG_98	NH2	H_ASP_110	OD2	3.034
6FAX	H_ARG_104	NH1	H_GLU_100	OE2	2.851
6FAX	H_ARG_104	NH2	R_GLU_21	OE1	3.986
6FAX	H_LYS_152	NZ	H_ASP_153	OD1	3.279
6FAX	H_LYS_152	NZ	H_ASP_153	OD2	3.260
6FAX	H_HIS_173	NE2	L_ASP_167	OD1	3.928
6FAX	H_LYS_218	NZ	L_GLU_123	OE1	3.125
6FAX	H_LYS_218	NZ	L_GLU_123	OE2	3.415
6FAX	R_HIS_78	NE2	R_GLU_74	OE1	3.706
6FAX	R_HIS_78	NE2	R_GLU_74	OE2	3.685

Table 839: 6FAX-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6FN1	A_ARG_40	NH1	A_ASP_369	OD1	2.632
6FN1	A_ARG_40	NH1	A_ASP_369	OD2	3.669
6FN1	A_ARG_40	NH2	A_ASP_369	OD1	3.084
6FN1	A_HIS_152	NE2	A_GLU_916	OE2	3.957
6FN1	A_ARG_173	NH2	A_GLU_169	OE1	2.871
6FN1	A_LYS_180	NZ	A_ASP_176	OD1	3.377
6FN1	A_LYS_180	NZ	A_ASP_176	OD2	3.959
6FN1	A_LYS_212	NZ	A_GLU_324	OE1	3.963
6FN1	A_LYS_212	NZ	A_GLU_324	OE2	2.762
6FN1	A_ARG_261	NH2	A_ASP_804	OD1	2.402
6FN1	A_ARG_261	NH2	A_ASP_804	OD2	3.659
6FN1	A_ARG_275	NH1	A_GLU_255	OE2	3.657
6FN1	A_ARG_275	NH1	A_GLU_272	OE1	3.157
6FN1	A_ARG_275	NH2	A_GLU_255	OE2	3.869
6FN1	A_ARG_285	NH2	A_GLU_282	OE2	2.865
6FN1	A_HIS_517	ND1	A_ASP_520	OD1	3.421
6FN1	A_HIS_517	ND1	A_ASP_520	OD2	3.421
6FN1	A_ARG_526	NH1	A_GLU_525	OE1	3.961
6FN1	A_ARG_526	NH1	A_GLU_525	OE2	2.166
6FN1	A_ARG_546	NH2	A_GLU_467	OE2	3.847
6FN1	A_ARG_576	NH2	A_ASP_573	OD1	2.465
6FN1	A_HIS_586	ND1	A_GLU_555	OE1	3.845
6FN1	A_HIS_586	NE2	A_GLU_555	OE2	3.514
6FN1	A_ARG_587	NH1	A_GLU_565	OE1	3.907
6FN1	A_ARG_587	NH2	A_GLU_565	OE1	3.568
6FN1	A_ARG_587	NH2	A_GLU_565	OE2	3.656
6FN1	A_HIS_611	ND1	A_ASP_612	OD1	3.740
6FN1	A_ARG_740	NH1	A_ASP_742	OD1	3.566
6FN1	A_ARG_740	NH1	A_ASP_742	OD2	2.936
6FN1	A_ARG_786	NH2	A_GLU_706	OE2	3.988
6FN1	A_ARG_797	NH1	A_ASP_1018	OD1	3.806
6FN1	A_ARG_797	NH1	A_ASP_1018	OD2	3.974
6FN1	A_LYS_807	NZ	A_ASP_805	OD1	3.714
6FN1	A_ARG_816	NH1	A_ASP_820	OD2	3.588
6FN1	A_LYS_825	NZ	A_GLU_781	OE2	3.696
6FN1	A_ARG_911	NH1	A_GLU_492	OE1	3.944
6FN1	A_LYS_914	NZ	A_GLU_485	OE2	3.976
6FN1	A_LYS_966	NZ	A_GLU_85	OE1	3.505
6FN1	A_LYS_966	NZ	A_GLU_85	OE2	2.563
6FN1	A_ARG_1084	NH2	A_ASP_1087	OD2	3.806
6FN1	A_ARG_1137	NH2	A_GLU_1143	OE1	3.300
6FN1	A_ARG_1137	NH2	A_GLU_1143	OE2	2.684
6FN1	A_ARG_1146	NH1	A_GLU_1142	OE2	3.522
6FN1	A_ARG_1146	NH2	A_GLU_1142	OE2	3.079
6FN1	A_HIS_1154	NE2	A_ASP_1158	OD1	3.475
6FN1	A_HIS_1154	NE2	A_ASP_1158	OD2	3.129
6FN1	A_ARG_1167	NH2	A_ASP_1123	OD1	2.431
6FN1	A_ARG_1167	NH2	A_ASP_1123	OD2	3.170
6FN1	A_ARG_1221	NH1	A_ASP_1218	OD1	3.994
6FN1	A_ARG_1221	NH2	A_ASP_1218	OD1	2.327
6FN1	B_ARG_24	NH1	B_ASP_75	OD1	3.067
6FN1	B_ARG_24	NH2	B_ASP_75	OD1	3.279
6FN1	B_ARG_59	NH1	B_ASP_65	OD1	2.228
6FN1	B_ARG_59	NH2	B_ASP_65	OD1	3.826
6FN1	B_ARG_66	NH1	B_GLU_84	OE1	3.321
6FN1	B_ARG_66	NH1	B_GLU_84	OE2	3.915
6FN1	B_ARG_66	NH1	B_ASP_87	OD2	2.881

6FN1	B_ARG_66	NH2	B_ASP_87	OD2	3.217
6FN1	B_LYS_153	NZ	B_GLU_160	OE1	2.476
6FN1	B_LYS_153	NZ	B_GLU_160	OE2	3.139
6FN1	B_LYS_189	NZ	B_GLU_193	OE1	3.697
6FN1	B_LYS_189	NZ	B_GLU_193	OE2	2.359
6FN1	B_ARG_194	NH1	B_GLU_191	OE1	3.707
6FN1	B_HIS_195	ND1	B_ASP_157	OD2	2.402
6FN1	B_HIS_195	NE2	B_GLU_191	OE2	2.859
6FN1	C_LYS_38	NZ	C_ASP_90	OD1	3.638
6FN1	C_ARG_98	NH1	C_ASP_110	OD1	3.210
6FN1	C_ARG_98	NH1	C_ASP_110	OD2	2.556
6FN1	C_ARG_98	NH2	C_ASP_110	OD2	3.769
6FN1	C_LYS_217	NZ	B_GLU_129	OE1	3.462
6FN1	C_LYS_217	NZ	B_GLU_129	OE2	2.375

Table 840: 6FN1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6FN4	A_ARG_40	NH1	A_ASP_369	OD1	3.044
6FN4	A_ARG_40	NH1	A_ASP_369	OD2	2.673
6FN4	A_ARG_40	NH2	A_ASP_369	OD1	2.550
6FN4	A_ARG_40	NH2	A_ASP_369	OD2	3.247
6FN4	A_HIS_152	NE2	A_GLU_916	OE2	3.942
6FN4	A_ARG_173	NH1	A_GLU_363	OE1	3.817
6FN4	A_ARG_209	NH1	A_GLU_73	OE2	3.499
6FN4	A_ARG_209	NH2	A_GLU_73	OE2	2.413
6FN4	A_LYS_212	NZ	A_GLU_324	OE2	3.760
6FN4	A_ARG_261	NH2	A_ASP_804	OD1	3.439
6FN4	A_ARG_275	NH1	A_GLU_272	OE2	3.706
6FN4	A_ARG_275	NH2	A_GLU_255	OE2	3.146
6FN4	A_ARG_275	NH2	A_GLU_272	OE1	2.485
6FN4	A_ARG_275	NH2	A_GLU_272	OE2	3.067
6FN4	A_LYS_394	NZ	A_GLU_392	OE2	3.872
6FN4	A_ARG_441	NH2	A_ASP_444	OD1	3.730
6FN4	A_ARG_441	NH2	A_ASP_444	OD2	3.767
6FN4	A_ARG_458	NH1	A_ASP_456	OD2	3.726
6FN4	A_ARG_458	NH2	A_ASP_456	OD2	3.316
6FN4	A_ARG_488	NH1	A_GLU_485	OE2	3.913
6FN4	A_ARG_491	NH2	A_GLU_498	OE1	3.157
6FN4	A_ARG_576	NH2	A_ASP_573	OD1	2.521
6FN4	A_HIS_586	NE2	A_GLU_555	OE2	3.330
6FN4	A_HIS_611	ND1	A_ASP_612	OD1	3.332
6FN4	A_LYS_747	NZ	A_ASP_742	OD1	2.172
6FN4	A_LYS_747	NZ	A_ASP_742	OD2	3.656
6FN4	A_LYS_807	NZ	A_ASP_805	OD1	2.940
6FN4	A_LYS_807	NZ	A_ASP_805	OD2	3.024
6FN4	A_ARG_904	NH2	A_ASP_163	OD2	3.996
6FN4	A_ARG_911	NH1	A_GLU_492	OE2	3.311
6FN4	A_LYS_914	NZ	A_GLU_485	OE1	2.840
6FN4	A_ARG_957	NH2	A_GLU_107	OE2	3.364
6FN4	A_LYS_966	NZ	A_GLU_85	OE2	2.855
6FN4	A_HIS_1006	ND1	A_ASP_820	OD2	3.743
6FN4	A_ARG_1084	NH2	A_ASP_1087	OD2	3.893
6FN4	A_ARG_1137	NH2	A_GLU_1143	OE1	3.629
6FN4	A_ARG_1137	NH2	A_GLU_1143	OE2	3.357
6FN4	A_HIS_1154	ND1	A_ASP_1158	OD2	3.508
6FN4	A_HIS_1154	NE2	A_ASP_1158	OD2	2.806
6FN4	A_LYS_1163	NZ	A_ASP_1158	OD1	3.925
6FN4	A_ARG_1221	NH1	A_ASP_1218	OD1	3.565
6FN4	A_ARG_1221	NH2	A_ASP_1218	OD1	2.235
6FN4	A_ARG_1232	NH1	A_GLU_1210	OE2	2.338
6FN4	B_LYS_55	NZ	A_ASP_743	OD1	2.728
6FN4	B_LYS_55	NZ	A_ASP_743	OD2	3.540
6FN4	B_ARG_59	NH1	B_ASP_65	OD1	2.795
6FN4	B_ARG_59	NH2	B_ASP_65	OD1	2.360
6FN4	B_ARG_66	NH1	B_GLU_84	OE1	3.279
6FN4	B_ARG_66	NH1	B_GLU_84	OE2	3.707
6FN4	B_ARG_66	NH1	B_ASP_87	OD1	3.527
6FN4	B_ARG_66	NH1	B_ASP_87	OD2	2.589
6FN4	B_ARG_66	NH2	B_ASP_87	OD2	2.765
6FN4	B_LYS_155	NZ	B_GLU_201	OE2	2.874
6FN4	B_HIS_195	ND1	B_ASP_157	OD2	2.468
6FN4	B_LYS_205	NZ	B_ASP_149	OD2	3.164
6FN4	C_LYS_38	NZ	C_ASP_90	OD1	3.032
6FN4	C_ARG_98	NH2	C_ASP_110	OD2	2.746

6FN4	C.LYS_217	NZ	B.GLU_129	OE2	3.828
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Table 841: 6FN4-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6FRJ	H_ARG_38	NH1	H_ASP_92	OD1	2.898
6FRJ	H_ARG_38	NH2	H_GLU_46	OE1	3.142
6FRJ	H_ARG_38	NH2	H_GLU_46	OE2	3.614
6FRJ	H_ARG_38	NH2	H_ASP_92	OD1	3.948
6FRJ	H_ARG_52	NH1	H_GLU_50	OE2	2.771
6FRJ	H_HIS_61	ND1	H_GLU_50	OE2	2.713
6FRJ	H_ARG_69	NH1	H_ASP_92	OD1	3.677
6FRJ	H_ARG_69	NH1	H_ASP_92	OD2	3.927
6FRJ	H_ARG_69	NH2	H_ASP_92	OD1	3.557
6FRJ	H_ARG_69	NH2	H_ASP_92	OD2	2.452
6FRJ	H_ARG_74	NH2	H_ASP_76	OD1	3.295
6FRJ	H_ARG_89	NH1	H_GLU_91	OE2	3.985
6FRJ	H_HIS_1051	ND1	H_GLU_1047	OE2	3.559
6FRJ	H_ARG_1070	NH2	H_GLU_1090	OE2	3.987
6FRJ	H_ARG_1070	NH2	H_ASP_1091	OD1	2.809
6FRJ	H_ARG_1070	NH2	H_ASP_1091	OD2	3.687

Table 842: 6FRJ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6GK7	L_ARG_67	NH1	L_ASP_88	OD1	3.869
6GK7	L_ARG_67	NH1	L_ASP_88	OD2	2.730
6GK7	L_ARG_67	NH2	L_ASP_88	OD1	3.654
6GK7	L_ARG_67	NH2	L_ASP_88	OD2	3.733
6GK7	L_LYS_155	NZ	L_GLU_201	OE1	2.758
6GK7	L_LYS_194	NZ	L_ASP_191	OD1	3.901
6GK7	L_HIS_195	ND1	L_ASP_157	OD2	3.421
6GK7	H_ARG_12	NH1	H_GLU_10	OE1	3.806
6GK7	H_LYS_43	NZ	L_ASP_9	OD1	3.203
6GK7	H_ARG_59	NH2	H_ASP_57	OD2	3.671
6GK7	H_HIS_67	NE2	H_ASP_90	OD1	2.917
6GK7	H_HIS_67	NE2	H_ASP_90	OD2	3.437
6GK7	H_ARG_98	NH2	H_ASP_110	OD1	3.856
6GK7	H_ARG_98	NH2	H_ASP_110	OD2	2.851
6GK7	H_ARG_102	NH2	H_ASP_100	OD1	3.141
6GK7	H_LYS_152	NZ	H_ASP_153	OD1	3.227
6GK7	H_LYS_152	NZ	H_ASP_153	OD2	3.445
6GK7	H_LYS_218	NZ	L_GLU_129	OE1	3.512
6GK7	H_LYS_218	NZ	L_GLU_129	OE2	3.016
6GK7	H_LYS_223	NZ	L_ASP_128	OD2	3.231
6GK7	A_LYS_317	NZ	H_ASP_55	OD2	2.761
6GK7	A_LYS_317	NZ	H_ASP_57	OD2	2.983

Table 843: 6GK7-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6GK8	H_ARG_38	NH1	H_ASP_90	OD1	3.902
6GK8	H_ARG_38	NH2	H_GLU_46	OE1	3.059
6GK8	H_ARG_38	NH2	H_GLU_46	OE2	3.561
6GK8	H_ARG_59	NH1	H_ASP_57	OD1	3.512
6GK8	H_ARG_59	NH1	H_ASP_57	OD2	2.923
6GK8	H_ARG_59	NH2	H_ASP_57	OD2	3.871
6GK8	H_ARG_59	NH2	L_ASP_65	OD1	3.295
6GK8	H_ARG_101	NH1	L_GLU_62	OE2	2.742
6GK8	H_ARG_101	NH2	L_GLU_62	OE2	3.142
6GK8	H_LYS_104	NZ	L_GLU_62	OE1	2.762
6GK8	H_LYS_104	NZ	L_GLU_62	OE2	3.928
6GK8	H_LYS_151	NZ	H_ASP_152	OD1	3.401
6GK8	H_LYS_151	NZ	H_ASP_152	OD2	3.307
6GK8	H_LYS_222	NZ	L_ASP_128	OD2	2.761
6GK8	L_ARG_32	NH1	L_GLU_57	OE2	3.709
6GK8	L_ARG_67	NH2	L_GLU_87	OE1	3.972
6GK8	L_ARG_67	NH2	L_GLU_87	OE2	2.995
6GK8	L_ARG_67	NH2	L_ASP_88	OD1	3.077
6GK8	L_ARG_67	NH2	L_ASP_88	OD2	3.854
6GK8	L_ARG_109	NH2	L_GLU_111	OE1	3.804
6GK8	L_ARG_148	NH2	L_GLU_171	OE2	3.424
6GK8	L_LYS_155	NZ	L_GLU_201	OE1	3.754
6GK8	L_LYS_194	NZ	L_ASP_191	OD1	3.678
6GK8	L_HIS_195	ND1	L_ASP_157	OD2	2.898
6GK8	L_LYS_67	NZ	H_ASP_55	OD1	3.586
6GK8	L_LYS_67	NZ	H_ASP_55	OD2	3.183
6GK8	L_LYS_67	NZ	H_ASP_57	OD2	3.085

Table 844: 6GK8-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6H2Y	D_HIS_30	ND1	D_ASP_29	OD2	2.968
6H2Y	D_LYS_74	NZ	D_ASP_32	OD1	3.080
6H2Y	D_LYS_74	NZ	D_ASP_32	OD2	3.146
6H2Y	D_LYS_79	NZ	L_ASP_52	OD1	3.126
6H2Y	D_ARG_82	NH1	D_GLU_102	OE1	3.225
6H2Y	D_HIS_110	ND1	D_GLU_144	OE1	3.692
6H2Y	D_LYS_120	NZ	L_ASP_95	OD2	2.910
6H2Y	D_HIS_173	ND1	D_GLU_188	OE2	3.534
6H2Y	D_HIS_173	NE2	D_GLU_188	OE2	3.951
6H2Y	D_ARG_186	NH1	D_GLU_188	OE2	2.556
6H2Y	D_ARG_186	NH2	D_GLU_194	OE1	3.470
6H2Y	D_HIS_189	NE2	D_GLU_188	OE1	3.353
6H2Y	D_LYS_191	NZ	L_ASP_50	OD2	2.715
6H2Y	D_ARG_236	NH1	D_ASP_235	OD2	3.896
6H2Y	D_LYS_260	NZ	D_ASP_78	OD1	3.223
6H2Y	D_LYS_260	NZ	D_ASP_78	OD2	3.636
6H2Y	D_LYS_260	NZ	D_GLU_239	OE2	3.969
6H2Y	H_ARG_38	NH1	H_ASP_90	OD2	2.735
6H2Y	H_ARG_38	NH2	H_GLU_46	OE1	3.600
6H2Y	H_ARG_38	NH2	H_ASP_90	OD2	3.880
6H2Y	H_ARG_56	NH2	D_GLU_58	OE1	3.564
6H2Y	H_ARG_56	NH2	D_GLU_58	OE2	3.905
6H2Y	H_LYS_63	NZ	H_GLU_46	OE1	3.969
6H2Y	H_LYS_63	NZ	H_GLU_46	OE2	2.764
6H2Y	H_ARG_67	NH1	H_ASP_90	OD1	2.793
6H2Y	H_ARG_67	NH1	H_ASP_90	OD2	3.306
6H2Y	H_ARG_67	NH2	H_ASP_90	OD1	3.797
6H2Y	H_ARG_67	NH2	H_ASP_90	OD2	3.132
6H2Y	H_LYS_215	NZ	L_GLU_125	OE1	3.261
6H2Y	H_LYS_215	NZ	L_GLU_125	OE2	2.865
6H2Y	L_ARG_60	NH1	L_ASP_81	OD1	3.946
6H2Y	L_ARG_60	NH1	L_ASP_81	OD2	2.714
6H2Y	L_ARG_60	NH2	L_ASP_81	OD1	2.835
6H2Y	L_ARG_60	NH2	L_ASP_81	OD2	3.155
6H2Y	L_ARG_92	NH1	D_ASP_166	OD2	3.217
6H2Y	L_ARG_92	NH2	D_GLU_119	OE1	3.274
6H2Y	L_ARG_92	NH2	D_GLU_119	OE2	3.244
6H2Y	L_ARG_92	NH2	D_ASP_166	OD1	3.891
6H2Y	L_ARG_92	NH2	D_ASP_166	OD2	2.328
6H2Y	L_LYS_104	NZ	L_ASP_84	OD1	2.864
6H2Y	L_LYS_104	NZ	L_ASP_84	OD2	2.840
6H2Y	L_LYS_168	NZ	L_GLU_82	OE1	2.735
6H2Y	L_LYS_168	NZ	L_GLU_82	OE2	3.700
6H2Y	L_HIS_190	ND1	L_ASP_153	OD2	3.040

Table 845: 6H2Y-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6I3Z	A_HIS_73	ND1	A_ASP_74	OD1	3.992
6I3Z	A_LYS_201	NZ	L_ASP_92	OD1	3.556
6I3Z	A_LYS_217	NZ	A_ASP_207	OD1	2.912
6I3Z	A_LYS_222	NZ	A_GLU_204	OE1	2.374
6I3Z	A_LYS_222	NZ	A_GLU_206	OE2	3.231
6I3Z	A_LYS_290	NZ	A_GLU_342	OE1	3.811
6I3Z	A_LYS_290	NZ	H_ASP_33	OD1	3.699
6I3Z	H_ARG_38	NH1	H_GLU_46	OE2	3.015
6I3Z	H_ARG_38	NH2	H_ASP_86	OD1	2.939
6I3Z	H_ARG_66	NH1	H_ASP_86	OD1	3.907
6I3Z	H_ARG_66	NH1	H_ASP_86	OD2	3.045
6I3Z	H_ARG_66	NH2	H_ASP_86	OD1	3.844
6I3Z	L_ARG_53	NH1	A_GLU_204	OE1	2.383
6I3Z	L_ARG_53	NH1	A_GLU_204	OE2	3.516
6I3Z	L_ARG_61	NH1	L_GLU_81	OE2	3.392
6I3Z	L_ARG_61	NH1	L_ASP_82	OD1	3.108
6I3Z	L_ARG_61	NH1	L_ASP_82	OD2	3.395
6I3Z	L_ARG_61	NH2	L_GLU_81	OE2	3.127
6I3Z	L_ARG_61	NH2	L_ASP_82	OD1	3.903
6I3Z	L_ARG_61	NH2	L_ASP_82	OD2	3.066

Table 846: 6I3Z-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6I9J	A_ARG_328	NH1	A_ASP_325	OD2	3.806
6I9J	A_ARG_328	NH2	A_ASP_329	OD1	3.559
6I9J	A_ARG_328	NH2	A_ASP_329	OD2	3.170

Table 847: 6I9J-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6IAP	A_LYS_4	NZ	A_GLU_84	OE1	3.796
6IAP	A_ARG_47	NH1	A_GLU_33	OE1	3.554
6IAP	A_ARG_47	NH1	A_GLU_33	OE2	2.707
6IAP	A_ARG_77	NH1	A_GLU_33	OE1	3.589
6IAP	A_ARG_77	NH1	A_GLU_33	OE2	2.806
6IAP	A_ARG_77	NH2	A_GLU_33	OE2	3.449
6IAP	A_ARG_165	NH1	A_GLU_134	OE1	2.832
6IAP	A_ARG_165	NH1	A_GLU_134	OE2	2.932
6IAP	D_ARG_61	NH2	D_ASP_82	OD1	2.957
6IAP	D_ARG_61	NH2	D_ASP_82	OD2	3.990
6IAP	D_ARG_96	NH2	A_GLU_80	OE1	3.466
6IAP	D_LYS_103	NZ	D_GLU_105	OE1	2.801
6IAP	D_LYS_103	NZ	D_GLU_165	OE1	3.070
6IAP	D_ARG_142	NH1	D_GLU_105	OE1	3.560
6IAP	D_LYS_149	NZ	D_GLU_195	OE2	3.829
6IAP	D_LYS_183	NZ	D_GLU_187	OE1	3.913
6IAP	D_HIS_189	ND1	D_ASP_151	OD2	3.610
6IAP	E_HIS_35	NE2	A_GLU_80	OE1	3.445
6IAP	E_ARG_38	NH1	E_GLU_46	OE1	3.245
6IAP	E_ARG_38	NH1	E_ASP_90	OD1	3.826
6IAP	E_ARG_38	NH2	E_ASP_90	OD1	2.938
6IAP	E_LYS_63	NZ	E_GLU_46	OE2	2.856
6IAP	E_ARG_67	NH1	E_ASP_90	OD1	3.217
6IAP	E_ARG_67	NH1	E_ASP_90	OD2	2.832
6IAP	E_ARG_98	NH1	E_ASP_105	OD2	2.742
6IAP	E_LYS_147	NZ	E_ASP_148	OD1	3.224
6IAP	E_LYS_147	NZ	E_ASP_148	OD2	2.946
6IAP	H_ARG_38	NH2	H_GLU_46	OE1	3.468
6IAP	H_LYS_65	NZ	H_GLU_62	OE1	2.882
6IAP	H_LYS_65	NZ	H_GLU_62	OE2	3.834
6IAP	H_ARG_87	NH1	H_GLU_89	OE1	2.796
6IAP	H_ARG_98	NH1	H_ASP_108	OD2	3.622
6IAP	H_ARG_99	NH1	H_GLU_50	OE1	2.819
6IAP	H_ARG_99	NH1	H_GLU_50	OE2	2.819
6IAP	H_ARG_99	NH2	A_ASP_98	OD1	2.689
6IAP	H_LYS_150	NZ	H_ASP_151	OD1	3.562
6IAP	H_LYS_150	NZ	H_ASP_151	OD2	3.534
6IAP	H_ARG_217	NH1	H_GLU_219	OE2	3.357
6IAP	L_ARG_24	NH1	L_ASP_70	OD1	3.449
6IAP	L_ARG_94	NH1	H_GLU_50	OE2	2.973
6IAP	L_ARG_94	NH2	A_ASP_123	OD2	3.888
6IAP	L_LYS_103	NZ	L_GLU_105	OE1	2.667
6IAP	L_LYS_126	NZ	L_GLU_123	OE1	3.630
6IAP	L_ARG_142	NH2	L_GLU_143	OE2	2.909
6IAP	L_LYS_149	NZ	L_GLU_195	OE2	3.247
6IAP	L_LYS_183	NZ	L_GLU_187	OE1	3.970
6IAP	L_HIS_189	ND1	L_ASP_151	OD2	3.405

Table 848: 6IAP-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6JMQ	A_LYS_112	NZ	A_GLU_265	OE2	3.737
6JMQ	A_ARG_419	NH1	A_GLU_426	OE1	3.417
6JMQ	A_ARG_419	NH1	A_GLU_426	OE2	2.358
6JMQ	A_ARG_419	NH2	A_GLU_426	OE1	2.551
6JMQ	A_ARG_419	NH2	A_GLU_426	OE2	3.223
6JMQ	B_ARG_211	NH2	B_ASP_540	OD1	3.901
6JMQ	B_ARG_211	NH2	B_ASP_540	OD2	3.653
6JMQ	B_LYS_298	NZ	B_ASP_343	OD1	3.798
6JMQ	B_LYS_298	NZ	B_ASP_343	OD2	2.773
6JMQ	B_LYS_300	NZ	B_ASP_249	OD1	2.988
6JMQ	B_LYS_300	NZ	B_ASP_249	OD2	3.168
6JMQ	B_ARG_313	NH2	B_ASP_281	OD2	2.986
6JMQ	B_ARG_348	NH1	B_ASP_349	OD2	3.884
6JMQ	B_LYS_354	NZ	B_ASP_355	OD1	3.767
6JMQ	B_LYS_354	NZ	B_ASP_355	OD2	3.182
6JMQ	B_ARG_374	NH1	B_ASP_343	OD1	3.786
6JMQ	B_HIS_414	ND1	B_GLU_413	OE1	3.881
6JMQ	B_HIS_414	NE2	B_GLU_413	OE1	3.761
6JMQ	B_HIS_414	NE2	B_GLU_413	OE2	3.827
6JMQ	B_LYS_510	NZ	B_GLU_493	OE2	3.727
6JMQ	B_ARG_525	NH1	B_GLU_605	OE1	3.564
6JMQ	B_ARG_525	NH1	B_GLU_605	OE2	3.265
6JMQ	B_ARG_525	NH2	B_GLU_605	OE1	2.626
6JMQ	B_ARG_525	NH2	B_GLU_605	OE2	3.608
6JMQ	B_HIS_556	NE2	B_ASP_540	OD2	3.806
6JMQ	B_LYS_592	NZ	B_GLU_610	OE1	3.993
6JMQ	B_ARG_603	NH1	B_GLU_620	OE1	2.595
6JMQ	B_ARG_603	NH1	B_GLU_620	OE2	3.221
6JMQ	B_ARG_613	NH1	B_GLU_610	OE2	3.252
6JMQ	B_HIS_619	ND1	B_ASP_571	OD1	3.990
6JMQ	B_ARG_625	NH2	B_GLU_533	OE2	3.458
6JMQ	B_ARG_625	NH2	B_GLU_561	OE1	3.849
6JMQ	C_ARG_38	NH1	C_ASP_89	OD1	3.785
6JMQ	C_ARG_38	NH2	C_GLU_46	OE1	2.796
6JMQ	C_ARG_38	NH2	C_GLU_46	OE2	3.808
6JMQ	C_ARG_66	NH1	C_ASP_89	OD1	3.398
6JMQ	C_ARG_66	NH1	C_ASP_89	OD2	2.424
6JMQ	C_ARG_66	NH2	C_ASP_89	OD1	3.049
6JMQ	C_ARG_66	NH2	C_ASP_89	OD2	3.597
6JMQ	C_HIS_169	NE2	D_ASP_173	OD2	3.860
6JMQ	C_LYS_213	NZ	D_GLU_129	OE1	3.825
6JMQ	D_ARG_67	NH2	D_ASP_88	OD1	2.846
6JMQ	D_ARG_67	NH2	D_ASP_88	OD2	3.134
6JMQ	D_LYS_109	NZ	D_GLU_111	OE2	3.564
6JMQ	D_LYS_155	NZ	D_GLU_160	OE1	3.318
6JMQ	D_LYS_155	NZ	D_GLU_201	OE1	2.847
6JMQ	D_LYS_155	NZ	D_GLU_201	OE2	3.538
6JMQ	D_ARG_194	NH2	D_GLU_191	OE1	2.521
6JMQ	D_ARG_194	NH2	D_GLU_191	OE2	3.913
6JMQ	D_HIS_195	ND1	D_ASP_157	OD1	3.523
6JMQ	D_HIS_195	ND1	D_ASP_157	OD2	3.075

Table 849: 6JMQ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6JMR	E_ARG_38	NH2	E_GLU_46	OE1	2.993
6JMR	E_ARG_66	NH1	E_ASP_89	OD2	3.421
6JMR	E_ARG_66	NH2	E_ASP_89	OD2	3.938
6JMR	F_LYS_152	NZ	F_GLU_159	OE2	3.268
6JMR	F_LYS_154	NZ	F_GLU_200	OE1	3.337
6JMR	F_LYS_154	NZ	F_GLU_200	OE2	3.361
6JMR	F_ARG_193	NH1	F_ASP_189	OD1	3.350
6JMR	F_ARG_193	NH2	F_GLU_190	OE1	2.696
6JMR	F_HIS_194	ND1	F_ASP_156	OD1	3.981
6JMR	F_HIS_194	ND1	F_ASP_156	OD2	2.412
6JMR	F_HIS_194	NE2	F_GLU_190	OE2	2.764
6JMR	B_ARG_211	NH1	B_ASP_558	OD1	3.360
6JMR	B_ARG_211	NH1	B_ASP_558	OD2	3.537
6JMR	B_ARG_211	NH2	B_ASP_558	OD1	3.693
6JMR	B_ARG_211	NH2	B_ASP_558	OD2	3.265
6JMR	B_LYS_255	NZ	B_ASP_528	OD1	2.933
6JMR	B_LYS_287	NZ	B_ASP_291	OD1	3.700
6JMR	B_LYS_287	NZ	B_ASP_291	OD2	2.415
6JMR	B_LYS_298	NZ	B_ASP_343	OD2	3.993
6JMR	B_LYS_300	NZ	B_ASP_249	OD1	3.273
6JMR	B_LYS_300	NZ	B_ASP_249	OD2	3.592
6JMR	B_ARG_303	NH2	B_ASP_373	OD2	3.818
6JMR	B_ARG_313	NH1	B_ASP_281	OD2	3.856
6JMR	B_ARG_313	NH2	B_ASP_281	OD2	2.988
6JMR	B_ARG_348	NH2	B_ASP_307	OD2	2.462
6JMR	B_LYS_354	NZ	B_ASP_355	OD2	2.401
6JMR	B_ARG_525	NH2	B_GLU_605	OE1	2.922
6JMR	B_ARG_603	NH1	B_GLU_620	OE1	3.059
6JMR	B_ARG_603	NH2	B_GLU_620	OE1	3.650
6JMR	B_HIS_619	ND1	B_ASP_571	OD1	3.672
6JMR	C_ARG_38	NH1	C_ASP_89	OD1	3.534
6JMR	C_ARG_38	NH2	C_ASP_89	OD1	3.797
6JMR	C_HIS_169	NE2	D_ASP_173	OD1	3.922
6JMR	D_ARG_67	NH2	D_ASP_88	OD1	2.789
6JMR	D_ARG_67	NH2	D_ASP_88	OD2	2.868
6JMR	D_LYS_113	NZ	D_GLU_17	OE1	3.374
6JMR	D_LYS_113	NZ	D_GLU_17	OE2	3.100
6JMR	D_LYS_155	NZ	D_GLU_201	OE1	3.651
6JMR	D_LYS_155	NZ	D_GLU_201	OE2	2.757
6JMR	D_LYS_175	NZ	D_GLU_87	OE1	3.592
6JMR	D_ARG_194	NH1	D_GLU_191	OE1	3.814
6JMR	D_ARG_194	NH2	D_GLU_191	OE1	2.418
6JMR	D_ARG_194	NH2	D_GLU_191	OE2	3.613
6JMR	D_HIS_195	ND1	D_ASP_157	OD2	3.249
6JMR	D_HIS_195	NE2	D_GLU_191	OE2	3.086

Table 850: 6JMR-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6K4Z	A_HIS_42	ND1	A_GLU_38	OE2	3.995
6K4Z	A_ARG_61	NH2	A_GLU_81	OE2	3.887
6K4Z	A_ARG_61	NH2	A_ASP_82	OD1	2.751
6K4Z	A_ARG_61	NH2	A_ASP_82	OD2	3.412
6K4Z	A_LYS_1064	NZ	A_GLU_1061	OE2	2.583
6K4Z	A_LYS_1066	NZ	A_ASP_1086	OD1	3.628
6K4Z	A_LYS_1066	NZ	A_ASP_1086	OD2	2.944
6K4Z	A_ARG_1094	NH1	A_ASP_1101	OD1	3.902
6K4Z	A_ARG_1094	NH1	A_ASP_1101	OD2	2.777
6K4Z	B_HIS_42	ND1	B_GLU_38	OE2	3.400
6K4Z	B_ARG_61	NH2	B_GLU_81	OE1	3.807
6K4Z	B_ARG_61	NH2	B_ASP_82	OD1	2.835
6K4Z	B_ARG_61	NH2	B_ASP_82	OD2	3.444
6K4Z	B_LYS_1064	NZ	B_GLU_1061	OE1	3.293
6K4Z	B_LYS_1064	NZ	B_GLU_1061	OE2	3.306
6K4Z	B_LYS_1066	NZ	B_ASP_1086	OD1	2.977
6K4Z	B_LYS_1066	NZ	B_ASP_1086	OD2	3.306
6K4Z	B_ARG_1094	NH2	B_ASP_1101	OD1	3.758
6K4Z	B_ARG_1094	NH2	B_ASP_1101	OD2	2.738

Table 851: 6K4Z-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID residue name residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6K7O	A_LYS_5	NZ	A_ASP_88	OD1	2.318
6K7O	A_LYS_5	NZ	A_ASP_88	OD2	3.371
6K7O	A_ARG_36	NH2	A_ASP_38	OD2	3.575
6K7O	A_LYS_55	NZ	A_GLU_53	OE2	3.732
6K7O	A_LYS_55	NZ	H_ASP_106	OD1	3.027
6K7O	A_ARG_72	NH1	A_GLU_40	OE1	3.011
6K7O	A_ARG_72	NH1	A_GLU_40	OE2	2.176
6K7O	A_ARG_74	NH2	A_GLU_40	OE2	2.314
6K7O	A_ARG_78	NH1	L_ASP_94	OD1	3.792
6K7O	A_ARG_78	NH2	L_ASP_94	OD1	2.709
6K7O	B_ARG_39	NH1	B_ASP_92	OD1	2.639
6K7O	B_ARG_39	NH2	B_GLU_47	OE1	3.803
6K7O	B_ARG_39	NH2	B_ASP_92	OD1	3.143
6K7O	B_LYS_67	NZ	B_ASP_64	OD1	3.307
6K7O	B_ARG_69	NH1	B_ASP_92	OD1	3.750
6K7O	B_ARG_69	NH1	B_ASP_92	OD2	2.232
6K7O	B_ARG_69	NH2	B_ASP_92	OD1	2.738
6K7O	B_ARG_69	NH2	B_ASP_92	OD2	2.835
6K7O	B_ARG_100	NH2	B_ASP_110	OD1	3.271
6K7O	B_ARG_100	NH2	B_ASP_110	OD2	3.077
6K7O	B_LYS_152	NZ	B_ASP_153	OD1	2.261
6K7O	B_LYS_152	NZ	B_ASP_153	OD2	3.089
6K7O	B_LYS_218	NZ	C_GLU_127	OE1	3.816
6K7O	B_LYS_218	NZ	C_GLU_127	OE2	2.813
6K7O	B_LYS_219	NZ	B_GLU_221	OE2	3.997
6K7O	B_LYS_223	NZ	C_ASP_126	OD1	2.273
6K7O	B_LYS_223	NZ	C_ASP_126	OD2	2.907
6K7O	C_ARG_62	NH1	C_GLU_82	OE1	3.128
6K7O	C_ARG_62	NH2	C_ASP_83	OD1	2.283
6K7O	C_ARG_62	NH2	C_ASP_83	OD2	3.026
6K7O	C_LYS_107	NZ	C_GLU_169	OE1	3.884
6K7O	C_LYS_153	NZ	C_GLU_199	OE1	2.343
6K7O	C_LYS_153	NZ	C_GLU_199	OE2	3.740
6K7O	C_ARG_215	NH1	C_GLU_191	OE1	3.258
6K7O	D_ARG_39	NH1	D_ASP_92	OD1	3.691
6K7O	D_ARG_39	NH2	D_GLU_47	OE1	3.378
6K7O	D_ARG_69	NH1	D_ASP_92	OD1	3.540
6K7O	D_ARG_69	NH1	D_ASP_92	OD2	3.004
6K7O	D_ARG_100	NH1	D_ASP_28	OD1	3.508
6K7O	D_ARG_100	NH2	D_ASP_110	OD1	3.621
6K7O	D_ARG_100	NH2	D_ASP_110	OD2	2.219
6K7O	D_LYS_152	NZ	D_ASP_153	OD1	2.709
6K7O	D_LYS_152	NZ	D_ASP_153	OD2	2.488
6K7O	D_LYS_215	NZ	G_ASP_189	OD2	2.832
6K7O	D_LYS_218	NZ	E_GLU_127	OE1	2.290
6K7O	D_LYS_218	NZ	E_GLU_127	OE2	3.074
6K7O	D_LYS_219	NZ	D_GLU_221	OE2	3.309
6K7O	D_LYS_223	NZ	E_ASP_126	OD1	3.765
6K7O	D_LYS_223	NZ	E_ASP_126	OD2	3.552
6K7O	E_ARG_62	NH1	E_GLU_82	OE1	3.785
6K7O	E_ARG_62	NH2	E_ASP_83	OD1	2.379
6K7O	E_ARG_62	NH2	E_ASP_83	OD2	2.884
6K7O	E_LYS_107	NZ	E_GLU_169	OE1	3.682
6K7O	E_LYS_107	NZ	E_GLU_169	OE2	3.861
6K7O	E_LYS_153	NZ	E_GLU_199	OE1	3.571
6K7O	E_LYS_187	NZ	E_GLU_191	OE1	3.589
6K7O	E_HIS_193	ND1	E_ASP_155	OD2	2.222

6K7O	E_ARG_215	NH1	E_GLU_191	OE1	3.183
6K7O	E_ARG_215	NH1	E_GLU_191	OE2	3.052
6K7O	F_ARG_39	NH1	F_ASP_92	OD1	3.160
6K7O	F_ARG_39	NH2	F_GLU_47	OE1	3.541
6K7O	F_ARG_39	NH2	F_ASP_92	OD1	3.852
6K7O	F_ARG_69	NH2	F_ASP_92	OD1	3.334
6K7O	F_ARG_69	NH2	F_ASP_92	OD2	2.262
6K7O	F_ARG_100	NH2	F_ASP_110	OD1	3.367
6K7O	F_ARG_100	NH2	F_ASP_110	OD2	2.302
6K7O	F_LYS_152	NZ	F_ASP_153	OD1	2.970
6K7O	F_LYS_152	NZ	F_ASP_153	OD2	3.514
6K7O	F_HIS_173	NE2	G_ASP_171	OD2	3.941
6K7O	G_ARG_51	NH2	F_ASP_106	OD2	3.980
6K7O	G_ARG_62	NH2	G_ASP_83	OD1	2.886
6K7O	G_ARG_62	NH2	G_ASP_83	OD2	2.569
6K7O	G_LYS_107	NZ	G_GLU_169	OE1	3.132
6K7O	G_LYS_107	NZ	G_GLU_169	OE2	2.495
6K7O	G_LYS_153	NZ	G_GLU_199	OE1	3.412
6K7O	G_ARG_215	NH1	G_GLU_191	OE1	2.817
6K7O	H_ARG_39	NH1	H_ASP_92	OD1	3.037
6K7O	H_ARG_39	NH2	H_GLU_47	OE2	3.357
6K7O	H_ARG_39	NH2	H_ASP_92	OD1	3.458
6K7O	H_ARG_69	NH1	H_ASP_92	OD1	3.457
6K7O	H_ARG_69	NH1	H_ASP_92	OD2	2.161
6K7O	H_ARG_69	NH2	H_ASP_92	OD1	3.051
6K7O	H_ARG_69	NH2	H_ASP_92	OD2	3.302
6K7O	H_ARG_100	NH1	H_ASP_28	OD1	3.046
6K7O	H_ARG_100	NH1	H_ASP_28	OD2	3.800
6K7O	H_ARG_100	NH2	H_ASP_110	OD1	3.159
6K7O	H_ARG_100	NH2	H_ASP_110	OD2	2.559
6K7O	H_LYS_152	NZ	H_ASP_153	OD1	3.285
6K7O	H_LYS_152	NZ	H_ASP_153	OD2	3.072
6K7O	H_HIS_173	NE2	L_ASP_171	OD2	3.862
6K7O	H_LYS_218	NZ	L_GLU_127	OE1	3.981
6K7O	H_LYS_219	NZ	H_GLU_221	OE1	3.644
6K7O	H_LYS_223	NZ	L_ASP_126	OD1	3.964
6K7O	L_ARG_62	NH1	L_GLU_82	OE1	3.867
6K7O	L_ARG_62	NH2	L_ASP_83	OD1	2.401
6K7O	L_ARG_62	NH2	L_ASP_83	OD2	2.682
6K7O	L_ARG_215	NH1	L_GLU_191	OE1	2.693
6K7O	P_LYS_5	NZ	P_ASP_88	OD1	3.227
6K7O	P_ARG_36	NH2	P_ASP_38	OD2	3.978
6K7O	P_LYS_55	NZ	B_ASP_106	OD1	3.340
6K7O	P_LYS_55	NZ	P_GLU_53	OE2	3.383
6K7O	P_ARG_72	NH1	P_GLU_40	OE2	3.046
6K7O	P_ARG_74	NH2	P_GLU_40	OE2	2.240
6K7O	P_ARG_78	NH1	C_ASP_94	OD1	2.583
6K7O	P_ARG_78	NH2	C_ASP_94	OD1	2.609
6K7O	R_LYS_5	NZ	R_ASP_88	OD1	2.725
6K7O	R_LYS_5	NZ	R_ASP_88	OD2	3.900
6K7O	R_LYS_55	NZ	F_ASP_106	OD1	2.834
6K7O	R_LYS_55	NZ	R_GLU_53	OE2	3.817
6K7O	R_ARG_72	NH1	R_GLU_40	OE1	3.051
6K7O	R_ARG_72	NH1	R_GLU_40	OE2	2.785
6K7O	R_ARG_74	NH2	R_GLU_40	OE2	2.444
6K7O	Q_LYS_5	NZ	Q_ASP_88	OD1	3.267
6K7O	Q_ARG_36	NH2	Q_ASP_38	OD2	3.639
6K7O	Q_LYS_55	NZ	D_ASP_106	OD1	3.172

6K7O	Q_ARG_59	NH1	H_GLU_221	OE1	3.018
6K7O	Q_ARG_59	NH1	H_GLU_221	OE2	3.413
6K7O	Q_ARG_59	NH2	H_GLU_221	OE1	3.299
6K7O	Q_ARG_59	NH2	H_GLU_221	OE2	2.855
6K7O	Q_ARG_72	NH1	Q_GLU_40	OE1	2.910
6K7O	Q_ARG_72	NH1	Q_GLU_40	OE2	2.362
6K7O	Q_ARG_74	NH2	Q_GLU_40	OE2	3.223
6K7O	Q_ARG_78	NH1	E_ASP_94	OD1	3.546
6K7O	Q_ARG_78	NH2	E_ASP_94	OD1	2.499

Table 852: 6K7O-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6KN9	A_HIS_112	ND1	A_GLU_41	OE1	3.585
6KN9	A_ARG_235	NH2	A_ASP_222	OD1	3.857
6KN9	A_ARG_235	NH2	A_ASP_222	OD2	2.742
6KN9	A_ARG_241	NH2	A_ASP_164	OD1	3.542
6KN9	A_ARG_241	NH2	A_ASP_164	OD2	3.212
6KN9	A_LYS_267	NZ	A_GLU_264	OE1	2.822
6KN9	A_LYS_267	NZ	A_GLU_264	OE2	3.577
6KN9	A_LYS_274	NZ	A_ASP_255	OD2	3.178
6KN9	A_LYS_274	NZ	A_GLU_318	OE2	3.699
6KN9	A_ARG_276	NH2	A_ASP_314	OD1	1.972
6KN9	A_ARG_281	NH1	D_ASP_111	OD1	2.228
6KN9	A_ARG_281	NH1	D_ASP_111	OD2	3.976
6KN9	A_LYS_288	NZ	A_GLU_299	OE1	3.349
6KN9	A_LYS_292	NZ	A_GLU_297	OE1	3.199
6KN9	A_LYS_292	NZ	A_GLU_297	OE2	3.595
6KN9	A_LYS_306	NZ	A_GLU_318	OE1	3.465
6KN9	A_LYS_309	NZ	A_ASP_314	OD2	2.944
6KN9	A_ARG_319	NH2	A_GLU_299	OE2	3.969
6KN9	A_ARG_333	NH1	A_ASP_330	OD1	3.681
6KN9	A_ARG_333	NH2	A_ASP_293	OD2	3.015
6KN9	B_ARG_241	NH2	B_ASP_164	OD2	3.877
6KN9	B_LYS_267	NZ	B_GLU_264	OE1	3.093
6KN9	B_LYS_267	NZ	B_GLU_264	OE2	3.256
6KN9	B_LYS_274	NZ	B_ASP_255	OD2	2.896
6KN9	B_LYS_274	NZ	B_GLU_318	OE1	3.770
6KN9	B_ARG_276	NH2	B_ASP_314	OD1	3.835
6KN9	B_ARG_281	NH2	E_ASP_111	OD1	2.487
6KN9	B_ARG_281	NH2	E_ASP_111	OD2	3.660
6KN9	B_LYS_288	NZ	B_GLU_299	OE1	3.279
6KN9	B_LYS_306	NZ	B_GLU_318	OE2	3.342
6KN9	B_LYS_309	NZ	B_ASP_314	OD2	2.507
6KN9	B_LYS_313	NZ	B_ASP_314	OD2	3.641
6KN9	B_ARG_319	NH1	B_GLU_304	OE1	3.890
6KN9	B_ARG_319	NH2	B_GLU_304	OE1	3.759
6KN9	B_ARG_319	NH2	B_GLU_304	OE2	3.666
6KN9	B_ARG_333	NH2	B_ASP_293	OD2	3.063
6KN9	C_HIS_112	ND1	C_GLU_41	OE1	2.327
6KN9	C_HIS_112	NE2	C_ASP_107	OD2	3.295
6KN9	C_ARG_235	NH2	C_ASP_222	OD1	3.959
6KN9	C_ARG_235	NH2	C_ASP_222	OD2	2.800
6KN9	C_ARG_241	NH2	C_ASP_164	OD1	3.385
6KN9	C_ARG_241	NH2	C_ASP_164	OD2	2.874
6KN9	C_LYS_274	NZ	C_ASP_255	OD2	3.106
6KN9	C_LYS_274	NZ	C_GLU_318	OE1	3.930
6KN9	C_ARG_276	NH2	C_ASP_314	OD1	3.434
6KN9	C_ARG_281	NH2	F_ASP_111	OD2	3.907
6KN9	C_LYS_288	NZ	C_GLU_299	OE1	3.086
6KN9	C_LYS_288	NZ	C_GLU_299	OE2	3.808
6KN9	C_LYS_306	NZ	C_GLU_318	OE2	3.670
6KN9	C_LYS_309	NZ	C_ASP_314	OD2	2.610
6KN9	C_ARG_319	NH1	C_GLU_299	OE2	3.995
6KN9	C_ARG_333	NH1	C_ASP_330	OD1	3.656
6KN9	C_ARG_333	NH2	C_ASP_293	OD2	2.842
6KN9	D_ARG_38	NH1	D_ASP_90	OD1	3.545
6KN9	D_ARG_38	NH2	D_GLU_46	OE1	2.628
6KN9	D_ARG_38	NH2	D_GLU_46	OE2	3.501
6KN9	D_LYS_43	NZ	D_GLU_89	OE1	3.952

6KN9	D_LYS_43	NZ	D_GLU_89	OE2	3.337
6KN9	D_ARG_67	NH1	D_ASP_90	OD1	3.041
6KN9	D_ARG_67	NH1	D_ASP_90	OD2	3.151
6KN9	D_ARG_67	NH2	D_ASP_90	OD1	3.897
6KN9	D_ARG_98	NH1	D_ASP_111	OD2	2.640
6KN9	D_ARG_201	NH2	D_ASP_222	OD1	2.871
6KN9	D_ARG_201	NH2	D_ASP_222	OD2	3.172
6KN9	F_ARG_38	NH1	F_ASP_90	OD1	3.168
6KN9	F_ARG_38	NH2	F_GLU_46	OE1	2.799
6KN9	F_ARG_38	NH2	F_GLU_46	OE2	3.293
6KN9	F_ARG_98	NH1	F_ASP_111	OD1	3.108
6KN9	F_ARG_98	NH1	F_ASP_111	OD2	2.892
6KN9	F_ARG_201	NH2	F_ASP_222	OD1	2.968
6KN9	F_ARG_201	NH2	F_ASP_222	OD2	3.406

Table 853: 6KN9-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6MH2	A_LYS_149	NZ	A_GLU_195	OE1	3.787
6MH2	A_LYS_149	NZ	A_GLU_195	OE2	3.621
6MH2	B_ARG_38	NH1	B_ASP_90	OD1	2.761
6MH2	B_ARG_38	NH2	B_GLU_46	OE1	3.270
6MH2	B_ARG_38	NH2	B_GLU_46	OE2	3.852
6MH2	B_ARG_38	NH2	B_ASP_90	OD1	3.946
6MH2	B_ARG_67	NH1	B_ASP_90	OD1	3.761
6MH2	B_ARG_67	NH1	B_ASP_90	OD2	2.763
6MH2	B_ARG_67	NH2	B_ASP_90	OD1	3.235
6MH2	B_ARG_67	NH2	B_ASP_90	OD2	3.604
6MH2	B_LYS_76	NZ	B_ASP_73	OD2	3.341
6MH2	B_ARG_98	NH2	B_ASP_108	OD1	3.946
6MH2	B_ARG_98	NH2	B_ASP_108	OD2	3.214
6MH2	B_LYS_150	NZ	B_ASP_151	OD1	3.564
6MH2	B_LYS_150	NZ	B_ASP_151	OD2	3.741
6MH2	C_ARG_61	NH2	C_ASP_82	OD1	3.009
6MH2	C_ARG_61	NH2	C_ASP_82	OD2	3.516
6MH2	C_ARG_66	NH1	C_ASP_28	OD1	3.766
6MH2	D_ARG_38	NH1	D_ASP_90	OD1	2.776
6MH2	D_ARG_38	NH2	D_GLU_46	OE1	2.980
6MH2	D_ARG_38	NH2	D_GLU_46	OE2	3.596
6MH2	D_ARG_38	NH2	D_ASP_90	OD1	3.851
6MH2	D_ARG_67	NH1	D_ASP_90	OD1	3.812
6MH2	D_ARG_67	NH1	D_ASP_90	OD2	2.537
6MH2	D_ARG_67	NH2	D_ASP_90	OD1	3.255
6MH2	D_ARG_67	NH2	D_ASP_90	OD2	3.479
6MH2	D_LYS_76	NZ	D_ASP_73	OD2	3.284
6MH2	D_ARG_98	NH2	D_ASP_108	OD2	2.820

Table 854: 6MH2-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6MHR	D_ARG_38	NH1	D_ASP_89	OD1	2.826
6MHR	D_ARG_38	NH2	D_GLU_46	OE1	3.169
6MHR	D_ARG_38	NH2	D_GLU_46	OE2	3.753
6MHR	D_ARG_38	NH2	D_ASP_89	OD1	3.916
6MHR	D_ARG_66	NH1	D_ASP_89	OD1	3.572
6MHR	D_ARG_66	NH1	D_ASP_89	OD2	2.987
6MHR	D_ARG_66	NH2	D_ASP_89	OD1	2.810
6MHR	D_ARG_66	NH2	D_ASP_89	OD2	3.631
6MHR	D_ARG_97	NH2	D_ASP_109	OD1	2.845
6MHR	D_ARG_97	NH2	D_ASP_109	OD2	3.931
6MHR	D_LYS_151	NZ	D_ASP_152	OD1	3.753
6MHR	D_LYS_151	NZ	D_ASP_152	OD2	3.790
6MHR	E_ARG_61	NH2	E_ASP_82	OD1	3.057
6MHR	E_ARG_61	NH2	E_ASP_82	OD2	3.583
6MHR	E_ARG_91	NH1	D_GLU_50	OE1	3.108
6MHR	E_ARG_91	NH1	D_ASP_98	OD2	3.892
6MHR	E_ARG_91	NH2	D_GLU_50	OE1	3.238
6MHR	E_ARG_91	NH2	D_GLU_50	OE2	3.082
6MHR	E_LYS_151	NZ	E_GLU_197	OE1	3.306
6MHR	E_LYS_151	NZ	E_GLU_197	OE2	2.656
6MHR	A_ARG_38	NH1	A_ASP_89	OD1	2.922
6MHR	A_ARG_38	NH2	A_GLU_46	OE1	3.494
6MHR	A_ARG_38	NH2	A_ASP_89	OD1	3.894
6MHR	A_ARG_66	NH1	A_ASP_89	OD1	3.791
6MHR	A_ARG_66	NH2	A_ASP_89	OD1	2.938
6MHR	A_ARG_66	NH2	A_ASP_89	OD2	2.504
6MHR	A_ARG_97	NH2	A_ASP_109	OD1	3.855
6MHR	A_ARG_97	NH2	A_ASP_109	OD2	2.834
6MHR	A_LYS_151	NZ	A_ASP_152	OD2	3.659
6MHR	A_LYS_217	NZ	B_GLU_125	OE2	2.775
6MHR	B_ARG_61	NH1	B_ASP_82	OD1	2.499
6MHR	B_ARG_61	NH1	B_ASP_82	OD2	2.707
6MHR	B_ARG_61	NH2	B_GLU_81	OE2	3.693
6MHR	B_ARG_91	NH1	A_GLU_50	OE1	3.086
6MHR	B_ARG_91	NH1	A_GLU_50	OE2	3.775
6MHR	B_ARG_91	NH1	A_ASP_98	OD2	3.351
6MHR	B_ARG_91	NH2	A_GLU_50	OE1	3.608
6MHR	B_ARG_91	NH2	A_GLU_50	OE2	2.934
6MHR	F_ARG_73	NH2	F_ASP_87	OD2	3.617
6MHR	F_ARG_75	NH1	F_ASP_87	OD1	3.232
6MHR	F_HIS_93	ND1	F_ASP_105	OD1	2.539
6MHR	F_HIS_93	NE2	F_GLU_103	OE1	2.711
6MHR	C_ARG_75	NH2	C_GLU_85	OE2	2.934
6MHR	C_HIS_	ND1	C_ASP_	OD1	2.729
6MHR	C_HIS_93	NE2	C_GLU_103	OE1	2.688
6MHR	C_ARG_	NH1	C_ASP_	OD1	3.364
6MHR	C_ARG_	NH2	C_ASP_	OD1	3.177

Table 855: 6MHR-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6MI2	A_LYS_12	NZ	A_GLU_16	OE2	3.989
6MI2	A_ARG_38	NH2	A_GLU_46	OE1	2.859
6MI2	A_ARG_38	NH2	A_GLU_46	OE2	3.408
6MI2	A_ARG_98	NH2	A_ASP_104	OD2	3.122
6MI2	B_ARG_60	NH2	B_ASP_81	OD1	3.443
6MI2	D_ARG_38	NH2	D_GLU_46	OE1	2.927
6MI2	D_ARG_38	NH2	D_GLU_46	OE2	2.802
6MI2	D_ARG_98	NH2	D_ASP_104	OD1	3.789
6MI2	D_ARG_98	NH2	D_ASP_104	OD2	2.702
6MI2	E_ARG_60	NH2	E_ASP_81	OD1	2.603
6MI2	E_ARG_60	NH2	E_ASP_81	OD2	2.973
6MI2	F_ARG_73	NH2	F_ASP_87	OD2	3.773
6MI2	F_HIS_93	ND1	F_ASP_105	OD1	2.788
6MI2	F_HIS_93	ND1	F_ASP_105	OD2	3.836
6MI2	F_HIS_93	NE2	F_GLU_103	OE2	3.226
6MI2	F_LYS_114	NZ	E_ASP_50	OD1	2.776
6MI2	F_LYS_114	NZ	E_ASP_50	OD2	3.977
6MI2	F_ARG_134	NH2	D_ASP_55	OD2	3.507
6MI2	F_ARG_134	NH2	F_ASP_127	OD1	3.458
6MI2	F_ARG_134	NH2	F_ASP_127	OD2	3.809
6MI2	C_ARG_73	NH2	C_ASP_87	OD1	3.648
6MI2	C_ARG_73	NH2	C_ASP_87	OD2	2.300
6MI2	C_HIS_93	ND1	C_ASP_105	OD1	2.396
6MI2	C_HIS_93	NE2	C_GLU_103	OE2	2.977
6MI2	C_LYS_114	NZ	B_ASP_50	OD1	3.683
6MI2	C_LYS_114	NZ	B_ASP_50	OD2	2.434
6MI2	C_ARG_134	NH1	C_ASP_127	OD2	3.259
6MI2	C_ARG_134	NH2	C_ASP_127	OD1	3.569
6MI2	C_ARG_134	NH2	C_ASP_127	OD2	3.076

Table 856: 6MI2-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6MN7	A_LYS_46	NZ	A_GLU_492	OE1	3.387
6MN7	A_LYS_46	NZ	A_GLU_492	OE2	2.895
6MN7	A_LYS_229	NZ	A_GLU_83	OE1	2.957
6MN7	A_LYS_232	NZ	A_GLU_268	OE1	3.584
6MN7	A_LYS_232	NZ	A_GLU_268	OE2	2.841
6MN7	A_LYS_282	NZ	A_GLU_275	OE1	2.868
6MN7	A_LYS_282	NZ	A_GLU_275	OE2	3.561
6MN7	A_ARG_308	NH2	A_GLU_164	OE1	3.817
6MN7	A_ARG_308	NH2	A_GLU_164	OE2	3.051
6MN7	A_LYS_351	NZ	A_GLU_269	OE1	2.814
6MN7	A_LYS_351	NZ	A_GLU_269	OE2	3.423
6MN7	A_ARG_429	NH1	A_ASP_113	OD1	3.456
6MN7	A_ARG_429	NH1	A_ASP_113	OD2	2.823
6MN7	A_ARG_429	NH2	A_ASP_113	OD2	3.973
6MN7	A_ARG_456	NH2	A_GLU_466	OE1	3.736
6MN7	A_ARG_456	NH2	A_GLU_466	OE2	2.975
6MN7	A_ARG_469	NH1	A_ASP_457	OD1	2.938
6MN7	A_ARG_469	NH2	A_ASP_457	OD1	3.933
6MN7	A_ARG_476	NH1	A_GLU_102	OE1	3.017
6MN7	A_ARG_476	NH1	A_GLU_102	OE2	3.686
6MN7	A_ARG_476	NH2	A_ASP_474	OD2	2.794
6MN7	A_ARG_480	NH1	A_ASP_477	OD1	3.065
6MN7	A_ARG_480	NH2	A_ASP_477	OD1	2.733
6MN7	A_LYS_487	NZ	A_ASP_47	OD1	3.272
6MN7	A_LYS_487	NZ	A_ASP_47	OD2	2.968
6MN7	A_LYS_487	NZ	A_GLU_91	OE2	2.917
6MN7	B_ARG_542	NH1	F_GLU_647	OE2	3.229
6MN7	B_LYS_574	NZ	A_ASP_107	OD1	3.285
6MN7	B_LYS_574	NZ	A_ASP_107	OD2	3.696
6MN7	B_ARG_579	NH2	F_GLU_584	OE1	2.844
6MN7	B_ARG_579	NH2	F_GLU_584	OE2	3.533
6MN7	B_ARG_585	NH1	B_ASP_589	OD1	3.926
6MN7	B_ARG_585	NH1	B_ASP_589	OD2	2.732
6MN7	B_ARG_585	NH2	B_ASP_589	OD2	3.591
6MN7	B_ARG_588	NH2	B_GLU_584	OE2	2.813
6MN7	B_ARG_617	NH1	B_GLU_621	OE2	2.445
6MN7	B_ARG_617	NH2	B_GLU_634	OE1	3.873
6MN7	B_ARG_617	NH2	B_GLU_634	OE2	2.744
6MN7	C_LYS_46	NZ	C_GLU_492	OE1	3.386
6MN7	C_LYS_46	NZ	C_GLU_492	OE2	2.894
6MN7	C_LYS_229	NZ	C_GLU_83	OE1	2.956
6MN7	C_LYS_232	NZ	C_GLU_268	OE1	3.583
6MN7	C_LYS_232	NZ	C_GLU_268	OE2	2.842
6MN7	C_LYS_282	NZ	C_GLU_275	OE1	2.869
6MN7	C_LYS_282	NZ	C_GLU_275	OE2	3.561
6MN7	C_ARG_308	NH2	C_GLU_164	OE1	3.817
6MN7	C_ARG_308	NH2	C_GLU_164	OE2	3.051
6MN7	C_LYS_351	NZ	C_GLU_269	OE1	2.813
6MN7	C_LYS_351	NZ	C_GLU_269	OE2	3.422
6MN7	C_ARG_429	NH1	C_ASP_113	OD1	3.457
6MN7	C_ARG_429	NH1	C_ASP_113	OD2	2.824
6MN7	C_ARG_429	NH2	C_ASP_113	OD2	3.973
6MN7	C_ARG_456	NH2	C_GLU_466	OE1	3.737
6MN7	C_ARG_456	NH2	C_GLU_466	OE2	2.976
6MN7	C_ARG_469	NH1	C_ASP_457	OD1	2.939
6MN7	C_ARG_469	NH2	C_ASP_457	OD1	3.933
6MN7	C_ARG_476	NH1	C_GLU_102	OE1	3.016

6MN7	C_ARG_476	NH1	C_GLU_102	OE2	3.686
6MN7	C_ARG_476	NH2	C_ASP_474	OD2	2.793
6MN7	C_ARG_480	NH1	C_ASP_477	OD1	3.066
6MN7	C_ARG_480	NH2	C_ASP_477	OD1	2.733
6MN7	C_LYS_487	NZ	C_ASP_47	OD1	3.273
6MN7	C_LYS_487	NZ	C_ASP_47	OD2	2.968
6MN7	C_LYS_487	NZ	C_GLU_91	OE2	2.918
6MN7	D_LYS_46	NZ	D_GLU_492	OE1	3.385
6MN7	D_LYS_46	NZ	D_GLU_492	OE2	2.893
6MN7	D_LYS_229	NZ	D_GLU_83	OE1	2.958
6MN7	D_LYS_232	NZ	D_GLU_268	OE1	3.583
6MN7	D_LYS_232	NZ	D_GLU_268	OE2	2.840
6MN7	D_LYS_282	NZ	D_GLU_275	OE1	2.869
6MN7	D_LYS_282	NZ	D_GLU_275	OE2	3.560
6MN7	D_ARG_308	NH2	D_GLU_164	OE1	3.817
6MN7	D_ARG_308	NH2	D_GLU_164	OE2	3.051
6MN7	D_LYS_351	NZ	D_GLU_269	OE1	2.813
6MN7	D_LYS_351	NZ	D_GLU_269	OE2	3.422
6MN7	D_ARG_429	NH1	D_ASP_113	OD1	3.456
6MN7	D_ARG_429	NH1	D_ASP_113	OD2	2.823
6MN7	D_ARG_429	NH2	D_ASP_113	OD2	3.972
6MN7	D_ARG_456	NH2	D_GLU_466	OE1	3.737
6MN7	D_ARG_456	NH2	D_GLU_466	OE2	2.975
6MN7	D_ARG_469	NH1	D_ASP_457	OD1	2.938
6MN7	D_ARG_469	NH2	D_ASP_457	OD1	3.933
6MN7	D_ARG_476	NH1	D_GLU_102	OE1	3.018
6MN7	D_ARG_476	NH1	D_GLU_102	OE2	3.687
6MN7	D_ARG_476	NH2	D_ASP_474	OD2	2.795
6MN7	D_ARG_480	NH1	D_ASP_477	OD1	3.065
6MN7	D_ARG_480	NH2	D_ASP_477	OD1	2.732
6MN7	D_LYS_487	NZ	D_ASP_47	OD1	3.273
6MN7	D_LYS_487	NZ	D_ASP_47	OD2	2.968
6MN7	D_LYS_487	NZ	D_GLU_91	OE2	2.917
6MN7	E_ARG_542	NH1	B_GLU_647	OE2	3.076
6MN7	E_LYS_574	NZ	C_ASP_107	OD1	3.286
6MN7	E_LYS_574	NZ	C_ASP_107	OD2	3.697
6MN7	E_ARG_579	NH2	B_GLU_584	OE1	2.796
6MN7	E_ARG_579	NH2	B_GLU_584	OE2	3.568
6MN7	E_ARG_585	NH1	E_ASP_589	OD1	3.925
6MN7	E_ARG_585	NH1	E_ASP_589	OD2	2.731
6MN7	E_ARG_585	NH2	E_ASP_589	OD2	3.591
6MN7	E_ARG_588	NH2	E_GLU_584	OE2	2.814
6MN7	E_ARG_617	NH1	E_GLU_621	OE2	2.446
6MN7	E_ARG_617	NH2	E_GLU_634	OE1	3.873
6MN7	E_ARG_617	NH2	E_GLU_634	OE2	2.744
6MN7	F_ARG_542	NH1	E_GLU_647	OE2	3.126
6MN7	F_LYS_574	NZ	D_ASP_107	OD1	3.285
6MN7	F_LYS_574	NZ	D_ASP_107	OD2	3.696
6MN7	F_ARG_579	NH2	E_GLU_584	OE1	2.859
6MN7	F_ARG_579	NH2	E_GLU_584	OE2	3.579
6MN7	F_ARG_585	NH1	F_ASP_589	OD1	3.927
6MN7	F_ARG_585	NH1	F_ASP_589	OD2	2.734
6MN7	F_ARG_585	NH2	F_ASP_589	OD2	3.592
6MN7	F_ARG_588	NH2	F_GLU_584	OE2	2.813
6MN7	F_ARG_617	NH1	F_GLU_621	OE2	2.447
6MN7	F_ARG_617	NH2	F_GLU_634	OE1	3.873
6MN7	F_ARG_617	NH2	F_GLU_634	OE2	2.744
6MN7	G_LYS_12	NZ	G_GLU_10	OE1	3.426

6MN7	G_ARG_38	NH1	G_GLU_46	OE1	3.285
6MN7	G_ARG_38	NH1	G_GLU_46	OE2	3.559
6MN7	G_ARG_38	NH1	G_ASP_89	OD1	3.445
6MN7	G_ARG_38	NH1	G_ASP_89	OD2	3.578
6MN7	G_ARG_38	NH2	G_ASP_90	OD1	2.915
6MN7	G_ARG_63	NH1	G_GLU_46	OE2	3.497
6MN7	G_ARG_67	NH1	G_ASP_90	OD1	2.860
6MN7	G_ARG_67	NH1	G_ASP_90	OD2	2.650
6MN7	G_ARG_67	NH2	G_ASP_90	OD1	2.942
6MN7	G_ARG_98	NH1	G_ASP_115	OD2	3.898
6MN7	G_ARG_188	NH1	G_GLU_208	OE2	3.991
6MN7	G_ARG_188	NH1	G_ASP_209	OD1	2.679
6MN7	G_ARG_188	NH1	G_ASP_209	OD2	2.661
6MN7	G_ARG_188	NH2	G_GLU_208	OE2	3.728
6MN7	G_ARG_188	NH2	G_ASP_209	OD1	3.908
6MN7	H_LYS_12	NZ	H_GLU_10	OE1	3.427
6MN7	H_ARG_38	NH1	H_GLU_46	OE1	3.285
6MN7	H_ARG_38	NH1	H_GLU_46	OE2	3.557
6MN7	H_ARG_38	NH1	H_ASP_89	OD1	3.443
6MN7	H_ARG_38	NH1	H_ASP_89	OD2	3.578
6MN7	H_ARG_38	NH2	H_ASP_90	OD1	2.915
6MN7	H_ARG_63	NH1	H_GLU_46	OE2	3.498
6MN7	H_ARG_67	NH1	H_ASP_90	OD1	2.859
6MN7	H_ARG_67	NH1	H_ASP_90	OD2	2.650
6MN7	H_ARG_67	NH2	H_ASP_90	OD1	2.942
6MN7	H_ARG_98	NH1	H_ASP_115	OD2	3.897
6MN7	H_ARG_188	NH1	H_GLU_208	OE2	3.991
6MN7	H_ARG_188	NH1	H_ASP_209	OD1	2.679
6MN7	H_ARG_188	NH1	H_ASP_209	OD2	2.663
6MN7	H_ARG_188	NH2	H_GLU_208	OE2	3.729
6MN7	H_ARG_188	NH2	H_ASP_209	OD1	3.908
6MN7	I_LYS_12	NZ	I_GLU_10	OE1	3.427
6MN7	I_ARG_38	NH1	I_GLU_46	OE1	3.285
6MN7	I_ARG_38	NH1	I_GLU_46	OE2	3.556
6MN7	I_ARG_38	NH1	I_ASP_89	OD1	3.444
6MN7	I_ARG_38	NH1	I_ASP_89	OD2	3.578
6MN7	I_ARG_38	NH2	I_ASP_90	OD1	2.915
6MN7	I_ARG_63	NH1	I_GLU_46	OE2	3.498
6MN7	I_ARG_67	NH1	I_ASP_90	OD1	2.860
6MN7	I_ARG_67	NH1	I_ASP_90	OD2	2.649
6MN7	I_ARG_67	NH2	I_ASP_90	OD1	2.942
6MN7	I_ARG_98	NH1	I_ASP_115	OD2	3.897
6MN7	I_ARG_188	NH1	I_GLU_208	OE2	3.991
6MN7	I_ARG_188	NH1	I_ASP_209	OD1	2.681
6MN7	I_ARG_188	NH1	I_ASP_209	OD2	2.663
6MN7	I_ARG_188	NH2	I_GLU_208	OE2	3.728
6MN7	I_ARG_188	NH2	I_ASP_209	OD1	3.910

Table 857: 6MN7-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6MPG	B_ARG_67	NH1	B_GLU_87	OE2	2.287
6MPG	B_ARG_67	NH1	B_ASP_88	OD1	3.091
6MPG	B_ARG_67	NH1	B_ASP_88	OD2	3.303
6MPG	B_ARG_67	NH2	B_GLU_87	OE2	3.585
6MPG	U_ARG_542	NH2	D_GLU_647	OE1	3.141
6MPG	U_ARG_542	NH2	D_GLU_647	OE2	2.524
6MPG	U_ARG_579	NH2	D_GLU_584	OE1	2.488
6MPG	U_ARG_588	NH2	U_GLU_584	OE2	2.498
6MPG	U_ARG_617	NH1	U_GLU_634	OE1	3.224
6MPG	U_ARG_617	NH1	U_GLU_634	OE2	3.055
6MPG	V_LYS_46	NZ	V_GLU_492	OE2	3.793
6MPG	V_LYS_65	NZ	V_GLU_64	OE2	2.921
6MPG	V_HIS_85	NE2	V_GLU_87	OE1	3.725
6MPG	V_HIS_105	NE2	V_ASP_474	OD1	3.796
6MPG	V_HIS_216	NE2	V_ASP_57	OD1	2.756
6MPG	V_HIS_216	NE2	V_ASP_57	OD2	3.780
6MPG	V_LYS_227	NZ	V_GLU_83	OE1	2.744
6MPG	V_LYS_227	NZ	V_GLU_83	OE2	3.617
6MPG	V_LYS_229	NZ	B_ASP_1	OD1	2.776
6MPG	V_LYS_231	NZ	V_GLU_268	OE1	2.210
6MPG	V_LYS_231	NZ	V_GLU_268	OE2	3.773
6MPG	V_LYS_231	NZ	V_GLU_269	OE1	3.900
6MPG	V_LYS_282	NZ	V_GLU_275	OE1	2.926
6MPG	V_ARG_298	NH1	V_GLU_381	OE1	3.522
6MPG	V_ARG_298	NH1	V_GLU_381	OE2	2.978
6MPG	V_ARG_298	NH2	V_GLU_381	OE1	3.713
6MPG	V_ARG_308	NH1	V_GLU_164	OE1	3.822
6MPG	V_LYS_421	NZ	V_ASP_180	OD1	3.836
6MPG	V_ARG_429	NH1	V_ASP_113	OD2	3.831
6MPG	V_ARG_429	NH2	V_ASP_113	OD1	3.803
6MPG	V_ARG_429	NH2	V_ASP_113	OD2	2.191
6MPG	V_ARG_469	NH2	V_ASP_457	OD2	3.540
6MPG	V_ARG_476	NH1	V_GLU_102	OE1	2.983
6MPG	V_ARG_476	NH1	V_GLU_102	OE2	2.663
6MPG	V_ARG_476	NH2	V_GLU_102	OE1	3.160
6MPG	V_ARG_480	NH1	V_ASP_477	OD1	2.648
6MPG	V_LYS_487	NZ	V_ASP_47	OD1	2.603
6MPG	V_LYS_487	NZ	V_ASP_47	OD2	3.288
6MPG	W_ARG_38	NH1	W_GLU_46	OE2	3.453
6MPG	W_ARG_38	NH1	W_ASP_89	OD1	3.905
6MPG	W_ARG_38	NH2	W_ASP_89	OD1	2.942
6MPG	W_ARG_66	NH2	W_ASP_89	OD2	3.660
6MPG	W_HIS_105	NE2	B_GLU_61	OE2	3.652
6MPG	m_ARG_38	NH1	m_ASP_86	OD1	2.924
6MPG	m_ARG_38	NH2	m_GLU_46	OE1	3.523
6MPG	m_ARG_38	NH2	m_GLU_46	OE2	3.688
6MPG	m_ARG_38	NH2	m_ASP_86	OD1	3.975
6MPG	m_LYS_73	NZ	m_ASP_53	OD1	3.849
6MPG	m_LYS_73	NZ	m_ASP_53	OD2	2.556
6MPG	n_ARG_61	NH1	n_ASP_60	OD1	3.630
6MPG	n_ARG_61	NH1	n_ASP_60	OD2	3.902
6MPG	n_ARG_94	NH1	V_ASP_321A	OD1	3.878
6MPG	n_ARG_95	NH2	n_GLU_25	OE2	3.812
6MPG	q_ARG_38	NH1	q_ASP_86	OD1	3.717
6MPG	q_ARG_38	NH2	q_ASP_86	OD1	3.650
6MPG	q_ARG_66	NH1	q_ASP_86	OD2	3.786
6MPG	q_ARG_66	NH2	q_ASP_86	OD1	3.709

6MPG	q_ARG_66	NH2	q_ASP_86	OD2	2.196
6MPG	r_ARG_60	NH1	r_ASP_81	OD2	3.768
6MPG	r_ARG_60	NH2	r_ASP_81	OD1	3.488
6MPG	r_ARG_60	NH2	r_ASP_81	OD2	2.219
6MPG	2_LYS_46	NZ	2_GLU_492	OE2	3.792
6MPG	2_LYS_65	NZ	2_GLU_64	OE2	2.922
6MPG	2_HIS_85	NE2	2_GLU_87	OE1	3.726
6MPG	2_HIS_105	NE2	2_ASP_474	OD1	3.795
6MPG	2_HIS_216	NE2	2_ASP_57	OD1	2.756
6MPG	2_HIS_216	NE2	2_ASP_57	OD2	3.779
6MPG	2_LYS_227	NZ	2_GLU_83	OE1	2.745
6MPG	2_LYS_227	NZ	2_GLU_83	OE2	3.617
6MPG	2_LYS_229	NZ	4_ASP_1	OD1	2.776
6MPG	2_LYS_231	NZ	2_GLU_268	OE1	2.210
6MPG	2_LYS_231	NZ	2_GLU_268	OE2	3.772
6MPG	2_LYS_231	NZ	2_GLU_269	OE1	3.900
6MPG	2_LYS_282	NZ	2_GLU_275	OE1	2.926
6MPG	2_ARG_298	NH1	2_GLU_381	OE1	3.521
6MPG	2_ARG_298	NH1	2_GLU_381	OE2	2.977
6MPG	2_ARG_298	NH2	2_GLU_381	OE1	3.713
6MPG	2_ARG_308	NH1	2_GLU_164	OE1	3.822
6MPG	2_LYS_421	NZ	2_ASP_180	OD1	3.837
6MPG	2_ARG_429	NH1	2_ASP_113	OD2	3.831
6MPG	2_ARG_429	NH2	2_ASP_113	OD1	3.804
6MPG	2_ARG_429	NH2	2_ASP_113	OD2	2.191
6MPG	2_ARG_469	NH2	2_ASP_457	OD2	3.540
6MPG	2_ARG_476	NH1	2_GLU_102	OE1	2.983
6MPG	2_ARG_476	NH1	2_GLU_102	OE2	2.663
6MPG	2_ARG_476	NH2	2_GLU_102	OE1	3.160
6MPG	2_ARG_480	NH1	2_ASP_477	OD1	2.648
6MPG	2_LYS_487	NZ	2_ASP_47	OD1	2.604
6MPG	2_LYS_487	NZ	2_ASP_47	OD2	3.288
6MPG	3_ARG_38	NH1	3_GLU_46	OE2	3.453
6MPG	3_ARG_38	NH1	3_ASP_89	OD1	3.905
6MPG	3_ARG_38	NH2	3_ASP_89	OD1	2.943
6MPG	3_ARG_66	NH2	3_ASP_89	OD2	3.660
6MPG	3_HIS_105	NE2	4_GLU_61	OE2	3.651
6MPG	4_ARG_67	NH1	4_GLU_87	OE2	2.288
6MPG	4_ARG_67	NH1	4_ASP_88	OD1	3.090
6MPG	4_ARG_67	NH1	4_ASP_88	OD2	3.302
6MPG	4_ARG_67	NH2	4_GLU_87	OE2	3.586
6MPG	5_ARG_38	NH1	5_ASP_86	OD1	2.924
6MPG	5_ARG_38	NH2	5_GLU_46	OE1	3.523
6MPG	5_ARG_38	NH2	5_GLU_46	OE2	3.688
6MPG	5_ARG_38	NH2	5_ASP_86	OD1	3.975
6MPG	5_LYS_73	NZ	5_ASP_53	OD1	3.850
6MPG	5_LYS_73	NZ	5_ASP_53	OD2	2.557
6MPG	6_ARG_61	NH1	6_ASP_60	OD1	3.630
6MPG	6_ARG_61	NH1	6_ASP_60	OD2	3.902
6MPG	6_ARG_94	NH1	2_ASP_321A	OD1	3.878
6MPG	6_ARG_95	NH2	6_GLU_25	OE2	3.812
6MPG	7_ARG_60	NH1	7_ASP_81	OD2	3.768
6MPG	7_ARG_60	NH2	7_ASP_81	OD1	3.488
6MPG	7_ARG_60	NH2	7_ASP_81	OD2	2.218
6MPG	8_ARG_38	NH1	8_ASP_86	OD1	3.717
6MPG	8_ARG_38	NH2	8_ASP_86	OD1	3.651
6MPG	8_ARG_66	NH1	8_ASP_86	OD2	3.787
6MPG	8_ARG_66	NH2	8_ASP_86	OD1	3.708

6MPG	8_ARG_66	NH2	8_ASP_86	OD2	2.195
6MPG	A_ARG_542	NH2	U_GLU_647	OE1	3.132
6MPG	A_ARG_542	NH2	U_GLU_647	OE2	2.525
6MPG	A_ARG_579	NH2	U_GLU_584	OE1	2.474
6MPG	A_ARG_588	NH2	A_GLU_584	OE2	2.498
6MPG	A_ARG_617	NH1	A_GLU_634	OE1	3.224
6MPG	A_ARG_617	NH1	A_GLU_634	OE2	3.054
6MPG	C_LYS_46	NZ	C_GLU_492	OE2	3.793
6MPG	C_LYS_65	NZ	C_GLU_64	OE2	2.921
6MPG	C_HIS_85	NE2	C_GLU_87	OE1	3.726
6MPG	C_HIS_105	NE2	C_ASP_474	OD1	3.796
6MPG	C_HIS_216	NE2	C_ASP_57	OD1	2.756
6MPG	C_HIS_216	NE2	C_ASP_57	OD2	3.780
6MPG	C_LYS_227	NZ	C_GLU_83	OE1	2.745
6MPG	C_LYS_227	NZ	C_GLU_83	OE2	3.617
6MPG	C_LYS_229	NZ	Y_ASP_1	OD1	2.776
6MPG	C_LYS_231	NZ	C_GLU_268	OE1	2.210
6MPG	C_LYS_231	NZ	C_GLU_268	OE2	3.773
6MPG	C_LYS_231	NZ	C_GLU_269	OE1	3.900
6MPG	C_LYS_282	NZ	C_GLU_275	OE1	2.926
6MPG	C_ARG_298	NH1	C_GLU_381	OE1	3.521
6MPG	C_ARG_298	NH1	C_GLU_381	OE2	2.977
6MPG	C_ARG_298	NH2	C_GLU_381	OE1	3.713
6MPG	C_ARG_308	NH1	C_GLU_164	OE1	3.822
6MPG	C_LYS_421	NZ	C_ASP_180	OD1	3.836
6MPG	C_ARG_429	NH1	C_ASP_113	OD2	3.831
6MPG	C_ARG_429	NH2	C_ASP_113	OD1	3.803
6MPG	C_ARG_429	NH2	C_ASP_113	OD2	2.191
6MPG	C_ARG_469	NH2	C_ASP_457	OD2	3.540
6MPG	C_ARG_476	NH1	C_GLU_102	OE1	2.983
6MPG	C_ARG_476	NH1	C_GLU_102	OE2	2.663
6MPG	C_ARG_476	NH2	C_GLU_102	OE1	3.160
6MPG	C_ARG_480	NH1	C_ASP_477	OD1	2.648
6MPG	C_LYS_487	NZ	C_ASP_47	OD1	2.604
6MPG	C_LYS_487	NZ	C_ASP_47	OD2	3.288
6MPG	D_ARG_542	NH2	A_GLU_647	OE1	3.137
6MPG	D_ARG_542	NH2	A_GLU_647	OE2	2.533
6MPG	D_ARG_579	NH2	A_GLU_584	OE1	2.479
6MPG	D_ARG_588	NH2	D_GLU_584	OE2	2.498
6MPG	D_ARG_617	NH1	D_GLU_634	OE1	3.224
6MPG	D_ARG_617	NH1	D_GLU_634	OE2	3.054
6MPG	M_ARG_38	NH1	M_ASP_86	OD1	2.924
6MPG	M_ARG_38	NH2	M_GLU_46	OE1	3.523
6MPG	M_ARG_38	NH2	M_GLU_46	OE2	3.688
6MPG	M_ARG_38	NH2	M_ASP_86	OD1	3.975
6MPG	M_LYS_73	NZ	M_ASP_53	OD1	3.849
6MPG	M_LYS_73	NZ	M_ASP_53	OD2	2.557
6MPG	N_ARG_61	NH1	N_ASP_60	OD1	3.630
6MPG	N_ARG_61	NH1	N_ASP_60	OD2	3.902
6MPG	N_ARG_94	NH1	C_ASP_321A	OD1	3.878
6MPG	N_ARG_95	NH2	N_GLU_25	OE2	3.813
6MPG	Q_ARG_38	NH1	Q_ASP_86	OD1	3.717
6MPG	Q_ARG_38	NH2	Q_ASP_86	OD1	3.651
6MPG	Q_ARG_66	NH1	Q_ASP_86	OD2	3.787
6MPG	Q_ARG_66	NH2	Q_ASP_86	OD1	3.708
6MPG	Q_ARG_66	NH2	Q_ASP_86	OD2	2.196
6MPG	R_ARG_60	NH1	R_ASP_81	OD2	3.768
6MPG	R_ARG_60	NH2	R_ASP_81	OD1	3.488

6MPG	R_ARG_60	NH2	R_ASP_81	OD2	2.219
6MPG	X_ARG_38	NH1	X_GLU_46	OE2	3.453
6MPG	X_ARG_38	NH1	X_ASP_89	OD1	3.905
6MPG	X_ARG_38	NH2	X_ASP_89	OD1	2.942
6MPG	X_ARG_66	NH2	X_ASP_89	OD2	3.661
6MPG	X_HIS_105	NE2	Y_GLU_61	OE2	3.651
6MPG	Y_ARG_67	NH1	Y_GLU_87	OE2	2.288
6MPG	Y_ARG_67	NH1	Y_ASP_88	OD1	3.090
6MPG	Y_ARG_67	NH1	Y_ASP_88	OD2	3.302
6MPG	Y_ARG_67	NH2	Y_GLU_87	OE2	3.586

Table 858: 6MPG-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6MPH	1.LYS_31A	NZ	A_GLU_87	OE1	2.457
6MPH	1.LYS_31A	NZ	A_GLU_87	OE2	3.919
6MPH	1.ARG_38	NH1	1.GLU_46	OE1	3.740
6MPH	1.ARG_38	NH1	1.GLU_46	OE2	2.866
6MPH	2.ARG_61	NH1	2.ASP_82	OD1	3.657
6MPH	2.ARG_96	NH1	1.GLU_95	OE1	3.340
6MPH	2.ARG_96	NH1	1.GLU_95	OE2	2.522
6MPH	3.LYS_31A	NZ	B_GLU_87	OE1	2.448
6MPH	3.LYS_31A	NZ	B_GLU_87	OE2	3.973
6MPH	3.ARG_38	NH1	3.GLU_46	OE1	3.744
6MPH	3.ARG_38	NH1	3.GLU_46	OE2	2.935
6MPH	4.ARG_61	NH1	4.ASP_82	OD1	3.637
6MPH	4.ARG_96	NH1	3.GLU_95	OE1	3.339
6MPH	4.ARG_96	NH1	3.GLU_95	OE2	2.507
6MPH	6.ARG_542	NH1	E_GLU_647	OE2	3.863
6MPH	6.ARG_542	NH2	E_GLU_647	OE1	3.449
6MPH	6.ARG_542	NH2	E_GLU_647	OE2	2.484
6MPH	6.ARG_579	NH2	E_GLU_584	OE1	2.833
6MPH	6.ARG_588	NH2	6_GLU_584	OE2	2.677
6MPH	6.ARG_617	NH1	6_GLU_634	OE2	2.791
6MPH	6.ARG_617	NH2	6_GLU_621	OE2	3.365
6MPH	A_LYS_46	NZ	A_GLU_492	OE2	3.500
6MPH	A_HIS_216	NE2	A_ASP_57	OD1	2.758
6MPH	A_HIS_216	NE2	A_ASP_57	OD2	3.293
6MPH	A_LYS_231	NZ	A_GLU_268	OE1	2.566
6MPH	A_LYS_231	NZ	A_GLU_268	OE2	3.911
6MPH	A_LYS_282	NZ	A_GLU_275	OE1	3.999
6MPH	A_LYS_282	NZ	f_ASP_114	OD1	3.470
6MPH	A_LYS_282	NZ	f_ASP_114	OD2	3.288
6MPH	A_ARG_298	NH1	A_GLU_381	OE1	2.662
6MPH	A_ARG_298	NH1	A_GLU_381	OE2	3.145
6MPH	A_ARG_298	NH2	A_GLU_381	OE1	3.543
6MPH	A_ARG_308	NH1	A_GLU_164	OE2	3.005
6MPH	A_ARG_327	NH2	X_GLU_100I	OE1	3.876
6MPH	A_LYS_351	NZ	A_GLU_269	OE1	3.880
6MPH	A_LYS_421	NZ	A_ASP_180	OD1	3.919
6MPH	A_ARG_429	NH1	A_ASP_113	OD1	3.710
6MPH	A_ARG_429	NH1	A_ASP_113	OD2	3.111
6MPH	A_ARG_429	NH2	A_ASP_113	OD1	3.007
6MPH	A_ARG_429	NH2	A_ASP_113	OD2	2.937
6MPH	A_ARG_469	NH2	A_ASP_457	OD2	3.457
6MPH	A_ARG_476	NH1	A_GLU_102	OE1	3.188
6MPH	A_ARG_476	NH1	A_GLU_102	OE2	2.587
6MPH	A_ARG_476	NH2	A_GLU_102	OE1	3.380
6MPH	A_ARG_480	NH1	A_ASP_477	OD1	2.475
6MPH	A_LYS_487	NZ	A_ASP_47	OD1	2.599
6MPH	A_LYS_487	NZ	A_ASP_47	OD2	3.570
6MPH	A_LYS_487	NZ	A_GLU_91	OE1	3.931
6MPH	B_LYS_46	NZ	B_GLU_492	OE2	3.523
6MPH	B_HIS_216	NE2	B_ASP_57	OD1	2.681
6MPH	B_HIS_216	NE2	B_ASP_57	OD2	3.250
6MPH	B_LYS_231	NZ	B_GLU_268	OE1	2.562
6MPH	B_LYS_231	NZ	B_GLU_268	OE2	3.926
6MPH	B_LYS_282	NZ	B_GLU_275	OE1	3.947
6MPH	B_LYS_282	NZ	g_ASP_114	OD1	3.432
6MPH	B_LYS_282	NZ	g_ASP_114	OD2	3.289
6MPH	B_ARG_298	NH1	B_GLU_381	OE1	2.635

6MPH	B_ARG_298	NH1	B_GLU_381	OE2	3.103
6MPH	B_ARG_298	NH2	B_GLU_381	OE1	3.494
6MPH	B_ARG_308	NH1	B_GLU_164	OE2	3.028
6MPH	B_ARG_327	NH2	Y_GLU_100I	OE1	3.899
6MPH	B_LYS_351	NZ	B_GLU_269	OE1	3.859
6MPH	B_LYS_421	NZ	B_ASP_180	OD1	3.823
6MPH	B_ARG_429	NH1	B_ASP_113	OD1	3.775
6MPH	B_ARG_429	NH1	B_ASP_113	OD2	3.138
6MPH	B_ARG_429	NH2	B_ASP_113	OD1	3.034
6MPH	B_ARG_429	NH2	B_ASP_113	OD2	2.894
6MPH	B_ARG_469	NH2	B_ASP_457	OD2	3.505
6MPH	B_ARG_476	NH1	B_GLU_102	OE1	3.172
6MPH	B_ARG_476	NH1	B_GLU_102	OE2	2.620
6MPH	B_ARG_476	NH2	B_GLU_102	OE1	3.414
6MPH	B_ARG_480	NH1	B_ASP_477	OD1	2.510
6MPH	B_LYS_487	NZ	B_ASP_47	OD1	2.597
6MPH	B_LYS_487	NZ	B_ASP_47	OD2	3.582
6MPH	B_LYS_487	NZ	B_GLU_91	OE1	3.935
6MPH	C_LYS_46	NZ	C_GLU_492	OE2	3.581
6MPH	C_HIS_216	NE2	C_ASP_57	OD1	2.733
6MPH	C_HIS_216	NE2	C_ASP_57	OD2	3.258
6MPH	C_LYS_231	NZ	C_GLU_268	OE1	2.574
6MPH	C_LYS_231	NZ	C_GLU_268	OE2	3.908
6MPH	C_LYS_282	NZ	C_GLU_275	OE1	3.963
6MPH	C_LYS_282	NZ	Q_ASP_114	OD1	3.383
6MPH	C_LYS_282	NZ	Q_ASP_114	OD2	3.272
6MPH	C_ARG_298	NH1	C_GLU_381	OE1	2.658
6MPH	C_ARG_298	NH1	C_GLU_381	OE2	3.166
6MPH	C_ARG_298	NH2	C_GLU_381	OE1	3.611
6MPH	C_ARG_308	NH1	C_GLU_164	OE2	2.979
6MPH	C_ARG_327	NH2	M_GLU_100I	OE1	3.872
6MPH	C_LYS_351	NZ	C_GLU_269	OE1	3.861
6MPH	C_LYS_421	NZ	C_ASP_180	OD1	3.916
6MPH	C_ARG_429	NH1	C_ASP_113	OD1	3.764
6MPH	C_ARG_429	NH1	C_ASP_113	OD2	3.172
6MPH	C_ARG_429	NH2	C_ASP_113	OD1	2.996
6MPH	C_ARG_429	NH2	C_ASP_113	OD2	2.906
6MPH	C_ARG_469	NH2	C_ASP_457	OD2	3.484
6MPH	C_ARG_476	NH1	C_GLU_102	OE1	3.185
6MPH	C_ARG_476	NH1	C_GLU_102	OE2	2.606
6MPH	C_ARG_476	NH2	C_GLU_102	OE1	3.401
6MPH	C_ARG_480	NH1	C_ASP_477	OD1	2.485
6MPH	C_LYS_487	NZ	C_ASP_47	OD1	2.672
6MPH	C_LYS_487	NZ	C_ASP_47	OD2	3.601
6MPH	C_LYS_487	NZ	C_GLU_91	OE1	3.831
6MPH	D_ARG_542	NH1	6_GLU_647	OE2	3.853
6MPH	D_ARG_542	NH2	6_GLU_647	OE1	3.460
6MPH	D_ARG_542	NH2	6_GLU_647	OE2	2.476
6MPH	D_ARG_579	NH2	6_GLU_584	OE1	2.760
6MPH	D_ARG_588	NH2	D_GLU_584	OE2	2.573
6MPH	D_ARG_617	NH1	D_GLU_634	OE2	2.801
6MPH	D_ARG_617	NH2	D_GLU_621	OE2	3.420
6MPH	E_ARG_542	NH1	D_GLU_647	OE2	3.888
6MPH	E_ARG_542	NH2	D_GLU_647	OE1	3.465
6MPH	E_ARG_542	NH2	D_GLU_647	OE2	2.463
6MPH	E_ARG_579	NH2	D_GLU_584	OE1	2.789
6MPH	E_ARG_588	NH2	E_GLU_584	OE2	2.573
6MPH	E_ARG_617	NH1	E_GLU_634	OE2	2.776

6MPH	E_ARG_617	NH2	E_GLU_621	OE2	3.431
6MPH	H_LYS_31A	NZ	C_GLU_87	OE1	2.458
6MPH	H_LYS_31A	NZ	C_GLU_87	OE2	3.969
6MPH	H_ARG_38	NH1	H_GLU_46	OE1	3.668
6MPH	H_ARG_38	NH1	H_GLU_46	OE2	2.976
6MPH	L_ARG_61	NH1	L ASP_82	OD1	3.612
6MPH	L_ARG_96	NH1	H_GLU_95	OE1	3.309
6MPH	L_ARG_96	NH1	H_GLU_95	OE2	2.530
6MPH	M_ARG_38	NH1	M ASP_86	OD1	3.017
6MPH	M_ARG_38	NH2	M_GLU_46	OE1	3.135
6MPH	M_ARG_38	NH2	M_GLU_46	OE2	3.398
6MPH	M_ARG_66	NH2	M ASP_86	OD1	3.623
6MPH	M_LYS_73	NZ	M ASP_53	OD1	3.608
6MPH	M_LYS_73	NZ	M ASP_53	OD2	2.901
6MPH	M_LYS_96	NZ	M ASP_100Q	OD2	3.995
6MPH	N_ARG_61	NH1	N ASP_60	OD1	3.566
6MPH	N_ARG_94	NH1	C ASP_321A	OD1	3.859
6MPH	Q_ARG_38	NH1	Q_GLU_46	OE1	3.730
6MPH	Q_ARG_38	NH2	Q ASP_97	OD1	3.305
6MPH	Q_ARG_67	NH2	Q ASP_97	OD1	3.545
6MPH	Q_ARG_67	NH2	Q ASP_97	OD2	3.021
6MPH	Q_ARG_72	NH2	C ASP_368	OD2	3.534
6MPH	R_ARG_40	NH2	R_GLU_103	OE2	3.768
6MPH	R_ARG_61	NH2	R ASP_82	OD1	3.293
6MPH	R_ARG_61	NH2	R ASP_82	OD2	2.978
6MPH	X_ARG_38	NH1	X ASP_86	OD1	3.079
6MPH	X_ARG_38	NH2	X_GLU_46	OE1	3.140
6MPH	X_ARG_38	NH2	X_GLU_46	OE2	3.408
6MPH	X_ARG_66	NH2	X ASP_86	OD1	3.580
6MPH	X_LYS_73	NZ	X ASP_53	OD1	3.586
6MPH	X_LYS_73	NZ	X ASP_53	OD2	2.898
6MPH	Y_ARG_38	NH1	Y ASP_86	OD1	3.102
6MPH	Y_ARG_38	NH2	Y_GLU_46	OE1	3.155
6MPH	Y_ARG_38	NH2	Y_GLU_46	OE2	3.384
6MPH	Y_ARG_66	NH2	Y ASP_86	OD1	3.575
6MPH	Y_LYS_73	NZ	Y ASP_53	OD1	3.614
6MPH	Y_LYS_73	NZ	Y ASP_53	OD2	2.911
6MPH	Z_ARG_61	NH1	Z ASP_60	OD1	3.627
6MPH	Z_ARG_94	NH1	A ASP_321A	OD1	3.890
6MPH	a_ARG_61	NH1	a ASP_60	OD1	3.574
6MPH	a_ARG_94	NH1	B ASP_321A	OD1	3.861
6MPH	f_ARG_38	NH1	f_GLU_46	OE1	3.663
6MPH	f_ARG_38	NH2	f ASP_97	OD1	3.333
6MPH	f_ARG_67	NH2	f ASP_97	OD1	3.553
6MPH	f_ARG_67	NH2	f ASP_97	OD2	3.049
6MPH	f_ARG_72	NH2	A ASP_368	OD2	3.577
6MPH	g_ARG_38	NH1	g_GLU_46	OE1	3.701
6MPH	g_ARG_38	NH2	g ASP_97	OD1	3.335
6MPH	g_ARG_67	NH2	g ASP_97	OD1	3.559
6MPH	g_ARG_67	NH2	g ASP_97	OD2	3.040
6MPH	g_ARG_72	NH2	B ASP_368	OD2	3.570
6MPH	h_ARG_40	NH2	h_GLU_103	OE2	3.735
6MPH	h_ARG_61	NH2	h ASP_82	OD1	3.222
6MPH	h_ARG_61	NH2	h ASP_82	OD2	2.932
6MPH	i_ARG_40	NH2	i_GLU_103	OE2	3.762
6MPH	i_ARG_61	NH2	i ASP_82	OD1	3.332
6MPH	i_ARG_61	NH2	i ASP_82	OD2	3.017

Table 859: 6MPH-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6MQC	A_ARG_	NH1	A_GLU_	OE1	3.064
6MQC	A_ARG_	NH1	A_ASP_	OD1	3.838
6MQC	A_ARG_	NH2	A_ASP_	OD1	3.330
6MQC	A_ARG_	NH2	A_ASP_	OD2	3.244
6MQC	A_ARG_	NH1	A_ASP_	OD1	3.212
6MQC	A_ARG_	NH1	A_ASP_	OD2	2.946
6MQC	A_ARG_	NH1	A_ASP_	OD1	2.770
6MQC	A_ARG_	NH1	B_ASP_	OD1	2.994
6MQC	A_ARG_	NH2	B_ASP_	OD1	2.820
6MQC	A_ARG_	NH2	A_ASP_	OD1	3.694
6MQC	A_ARG_	NH2	A_ASP_	OD2	2.674
6MQC	A_ARG_	NH1	B_ASP_	OD1	3.399
6MQC	A_ARG_	NH1	B_ASP_	OD2	3.078
6MQC	A_ARG_	NH1	B_ASP_	OD1	2.829
6MQC	A_ARG_	NH2	B_ASP_	OD1	2.822
6MQC	A_ARG_	NH2	B_ASP_	OD2	3.673
6MQC	A_ARG_	NH2	A_GLU_	OE2	3.410
6MQC	B_ARG_	NH1	B_ASP_	OD2	3.586
6MQC	B_LYS_	NZ	B_GLU_	OE1	3.361
6MQC	B_ARG_	NH1	B_ASP_	OD1	2.810
6MQC	B_ARG_	NH1	B_ASP_	OD2	3.319
6MQC	B_ARG_	NH2	B_ASP_	OD1	3.618
6MQC	B_ARG_	NH2	B_ASP_	OD2	2.613
6MQC	B_LYS_	NZ	B_GLU_	OE1	3.307
6MQC	B_HIS_	ND1	B_ASP_	OD1	2.832
6MQC	H_ARG_	NH1	H_GLU_	OE1	3.098
6MQC	H_ARG_	NH1	H_ASP_	OD1	3.684
6MQC	H_ARG_	NH2	H_ASP_	OD1	2.690
6MQC	H_ARG_	NH1	H_ASP_	OD1	3.063
6MQC	H_ARG_	NH1	H_ASP_	OD2	3.805
6MQC	H_ARG_	NH2	H_ASP_	OD1	3.624
6MQC	H_ARG_	NH2	H_ASP_	OD2	3.006
6MQC	H_ARG_	NH1	H_ASP_	OD1	2.952
6MQC	H_ARG_	NH1	L_ASP_	OD1	2.906
6MQC	H_ARG_	NH2	L_ASP_	OD1	2.999
6MQC	H_ARG_	NH2	H_ASP_	OD1	3.031
6MQC	H_ARG_	NH2	H_ASP_	OD2	3.958
6MQC	H_ARG_	NH1	L_ASP_	OD1	2.856
6MQC	H_ARG_	NH1	L_ASP_	OD2	3.748
6MQC	H_ARG_	NH2	L_ASP_	OD1	3.439
6MQC	H_ARG_	NH2	L_ASP_	OD2	3.140
6MQC	H_ARG_	NH2	L_ASP_	OD1	2.780
6MQC	H_ARG_	NH2	L_ASP_	OD2	3.923
6MQC	H_LYS_	NZ	H_ASP_	OD1	3.326
6MQC	L_ARG_	NH1	L_ASP_	OD2	3.327
6MQC	L_ARG_	NH1	L_ASP_	OD1	2.916
6MQC	L_ARG_	NH1	L_ASP_	OD2	3.414
6MQC	L_ARG_	NH2	L_ASP_	OD1	3.578
6MQC	L_ARG_	NH2	L_ASP_	OD2	2.554
6MQC	L_LYS_	NZ	L_GLU_	OE2	3.839
6MQC	L_LYS_	NZ	L_GLU_	OE1	3.867
6MQC	L_LYS_	NZ	L_GLU_	OE2	3.648
6MQC	L_HIS_	ND1	L_ASP_	OD1	2.866
6MQC	L_HIS_	NE2	L_GLU_	OE2	3.758

Table 860: 6MQC-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6MQE	B_ARG.61	NH1	B_GLU.81	OE2	2.972
6MQE	B_ARG.61	NH1	B_ASP.82	OD1	3.540
6MQE	B_ARG.61	NH1	B_ASP.82	OD2	3.139
6MQE	B_ARG.61	NH2	B_ASP.82	OD1	2.652
6MQE	B_ARG.61	NH2	B_ASP.82	OD2	3.672
6MQE	B_LYS.103	NZ	B_GLU.165	OE1	3.601
6MQE	B_LYS.126	NZ	B_GLU.122	OE1	2.295
6MQE	B_LYS.147	NZ	B_GLU.195	OE1	2.709
6MQE	B_LYS.149	NZ	B_GLU.195	OE2	3.823
6MQE	B_LYS.155	NZ	B_GLU.185	OE1	3.813
6MQE	B_LYS.155	NZ	B_GLU.185	OE2	2.543
6MQE	B_HIS.189	ND1	B_ASP.151	OD1	3.273
6MQE	B_HIS.189	NE2	B_GLU.185	OE1	2.265
6MQE	B_HIS.189	NE2	B_GLU.185	OE2	2.201
6MQE	A_ARG.38	NH1	A_GLU.46	OE2	3.135
6MQE	A_ARG.38	NH1	A_ASP.86	OD1	3.589
6MQE	A_ARG.38	NH2	A_ASP.86	OD1	2.950
6MQE	A_ARG.66	NH1	A_ASP.86	OD1	3.044
6MQE	A_ARG.66	NH1	A_ASP.86	OD2	2.613
6MQE	A_ARG.66	NH2	A_ASP.86	OD1	3.697
6MQE	A_LYS.75	NZ	A_ASP.72	OD2	2.759
6MQE	A_LYS.75	NZ	A_GLU.77	OE1	3.673
6MQE	A_ARG.95	NH1	A_ASP.101	OD1	3.112
6MQE	A_ARG.95	NH2	B_ASP.91	OD2	3.864
6MQE	A_ARG.100H	NH2	B_ASP.91	OD2	3.610
6MQE	H_ARG.38	NH1	H_GLU.46	OE1	2.700
6MQE	H_ARG.38	NH1	H_GLU.46	OE2	3.912
6MQE	H_ARG.38	NH1	H_ASP.86	OD2	3.737
6MQE	H_ARG.38	NH2	H_ASP.86	OD2	2.834
6MQE	H_ARG.66	NH1	H_ASP.86	OD1	2.676
6MQE	H_ARG.66	NH1	H_ASP.86	OD2	3.146
6MQE	H_ARG.66	NH2	H_ASP.86	OD2	3.716
6MQE	H_LYS.71	NZ	H_GLU.55	OE1	3.815
6MQE	H_LYS.71	NZ	H_GLU.55	OE2	3.654
6MQE	H_ARG.95	NH1	H_ASP.101	OD1	3.185
6MQE	H_ARG.95	NH1	L_ASP.91	OD1	3.360
6MQE	H_ARG.95	NH2	L_ASP.91	OD1	2.956
6MQE	H_ARG.100H	NH1	L_ASP.91	OD1	2.604
6MQE	H_ARG.100H	NH1	L_ASP.91	OD2	3.888
6MQE	H_ARG.210	NH1	H_GLU.212	OE1	2.890
6MQE	H_ARG.210	NH2	H_GLU.212	OE1	3.265
6MQE	L_ARG.61	NH1	L_ASP.82	OD1	2.728
6MQE	L_ARG.61	NH1	L_ASP.82	OD2	3.171
6MQE	L_ARG.61	NH2	L_ASP.82	OD1	3.670
6MQE	L_ARG.61	NH2	L_ASP.82	OD2	2.544
6MQE	L_LYS.103	NZ	L_GLU.165	OE1	2.963
6MQE	L_LYS.103	NZ	L_GLU.165	OE2	3.584
6MQE	L_LYS.126	NZ	L_ASP.123	OD1	3.637
6MQE	L_LYS.155	NZ	A_GLU.56	OE1	2.786
6MQE	L_LYS.155	NZ	L_GLU.185	OE2	3.322
6MQE	L_HIS.189	ND1	L_GLU.185	OE2	3.793
6MQE	L_HIS.189	NE2	A_GLU.56	OE1	3.428
6MQE	L_HIS.189	NE2	A_GLU.56	OE2	2.569
6MQE	L_HIS.189	NE2	L_GLU.185	OE2	3.601

Table 861: 6MQE-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6MQM	A_ARG_38	NH1	A_GLU_46	OE1	3.765
6MQM	A_ARG_38	NH1	A_GLU_46	OE2	2.771
6MQM	A_ARG_38	NH1	A_ASP_86	OD1	3.479
6MQM	A_ARG_38	NH2	A_ASP_86	OD1	2.674
6MQM	A_ARG_66	NH1	A_ASP_86	OD1	3.175
6MQM	A_ARG_66	NH1	A_ASP_86	OD2	3.748
6MQM	A_ARG_66	NH2	A_ASP_86	OD1	3.755
6MQM	A_ARG_66	NH2	A_ASP_86	OD2	2.918
6MQM	A_ARG_94	NH1	A_ASP_101	OD1	3.858
6MQM	A_ARG_94	NH1	A_ASP_101	OD2	3.426
6MQM	A_ARG_94	NH2	A_ASP_101	OD2	3.302
6MQM	A_LYS_206	NZ	A_ASP_208	OD1	3.694
6MQM	A_LYS_206	NZ	A_ASP_208	OD2	3.645
6MQM	A_LYS_210	NZ	A_GLU_212	OE1	3.835
6MQM	A_LYS_210	NZ	A_GLU_212	OE2	2.455
6MQM	B_ARG_61	NH1	B_ASP_82	OD1	3.379
6MQM	B_ARG_61	NH1	B_ASP_82	OD2	3.603
6MQM	B_ARG_96	NH1	A_GLU_95	OE1	3.968
6MQM	B_ARG_96	NH1	A_GLU_95	OE2	2.460
6MQM	B_LYS_103	NZ	B_GLU_165	OE1	3.460
6MQM	B_LYS_103	NZ	B_GLU_165	OE2	2.483
6MQM	B_LYS_126	NZ	B_GLU_122	OE2	3.847
6MQM	B_LYS_149	NZ	B_GLU_195	OE1	3.490
6MQM	D_ARG_38	NH1	D_GLU_46	OE2	3.038
6MQM	D_ARG_38	NH1	D_ASP_86	OD1	3.431
6MQM	D_ARG_38	NH2	D_ASP_86	OD1	2.590
6MQM	D_ARG_66	NH1	D_ASP_86	OD1	2.939
6MQM	D_ARG_66	NH1	D_ASP_86	OD2	2.983
6MQM	D_ARG_66	NH2	D_ASP_86	OD2	3.281
6MQM	D_LYS_206	NZ	D_ASP_208	OD1	3.752
6MQM	D_LYS_210	NZ	D_GLU_212	OE2	3.469
6MQM	E_ARG_61	NH1	E_ASP_82	OD1	3.174
6MQM	E_ARG_61	NH1	E_ASP_82	OD2	3.771
6MQM	E_ARG_96	NH1	D_GLU_95	OE2	2.376
6MQM	E_LYS_103	NZ	E_GLU_165	OE1	3.185
6MQM	E_LYS_103	NZ	E_GLU_165	OE2	2.355
6MQM	E_LYS_149	NZ	E_GLU_195	OE1	2.638
6MQM	E_HIS_189	NE2	E_ASP_185	OD1	3.808
6MQM	G_ARG_38	NH1	G_GLU_46	OE2	3.081
6MQM	G_ARG_38	NH1	G_ASP_86	OD1	3.241
6MQM	G_ARG_38	NH2	G_ASP_86	OD1	2.432
6MQM	G_ARG_66	NH1	G_ASP_86	OD1	3.284
6MQM	G_ARG_66	NH1	G_ASP_86	OD2	3.321
6MQM	G_ARG_66	NH2	G_ASP_86	OD2	2.999
6MQM	G_ARG_94	NH2	G_ASP_101	OD1	3.791
6MQM	G_ARG_94	NH2	G_ASP_101	OD2	2.962
6MQM	G_LYS_206	NZ	G_ASP_208	OD1	3.377
6MQM	G_LYS_206	NZ	G_ASP_208	OD2	3.969
6MQM	G_LYS_210	NZ	G_GLU_212	OE2	3.739
6MQM	H_ARG_61	NH1	H_ASP_82	OD1	3.357
6MQM	H_ARG_61	NH1	H_ASP_82	OD2	3.698
6MQM	H_ARG_61	NH2	H_GLU_79	OE2	3.084
6MQM	H_ARG_96	NH1	G_GLU_95	OE2	2.480
6MQM	H_LYS_103	NZ	H_GLU_165	OE1	2.991
6MQM	H_LYS_103	NZ	H_GLU_165	OE2	2.468
6MQM	H_LYS_126	NZ	H_GLU_122	OE2	3.719
6MQM	H_LYS_149	NZ	H_GLU_195	OE1	2.676

6MQM	H_HIS_189	ND1	H_ASP_151	OD1	3.088
6MQM	H_HIS_189	NE2	H_ASP_185	OD1	3.777
6MQM	J_ARG_38	NH1	J_GLU_46	OE2	3.367
6MQM	J_ARG_38	NH1	J_ASP_86	OD1	3.218
6MQM	J_ARG_38	NH2	J_ASP_86	OD1	2.641
6MQM	J_ARG_66	NH1	J_ASP_86	OD1	2.986
6MQM	J_ARG_66	NH1	J_ASP_86	OD2	3.538
6MQM	J_ARG_66	NH2	J_ASP_86	OD1	3.738
6MQM	J_ARG_66	NH2	J_ASP_86	OD2	2.783
6MQM	J_ARG_94	NH1	J_ASP_101	OD2	3.348
6MQM	J_ARG_94	NH2	J_ASP_101	OD2	2.919
6MQM	J_LYS_206	NZ	J_ASP_208	OD1	3.651
6MQM	J_LYS_206	NZ	J_ASP_208	OD2	3.476
6MQM	J_LYS_	NZ	J_GLU_	OE2	3.487
6MQM	K_ARG_61	NH1	K_ASP_82	OD1	2.973
6MQM	K_ARG_61	NH1	K_ASP_82	OD2	3.285
6MQM	K_ARG_96	NH1	J_GLU_95	OE1	3.782
6MQM	K_ARG_96	NH1	J_GLU_95	OE2	2.262
6MQM	K_LYS_103	NZ	K_GLU_165	OE2	2.763
6MQM	K_LYS_	NZ	K_GLU_	OE1	2.452
6MQM	K_HIS_	ND1	K_ASP_	OD1	3.413
6MQM	K_HIS_	NE2	K_ASP_	OD1	3.837

Table 862: 6MQM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6MQR	H_ARG_38	NH1	H_GLU_46	OE1	3.085
6MQR	H_ARG_38	NH1	H_ASP_86	OD1	3.945
6MQR	H_ARG_38	NH2	H_ASP_86	OD1	2.835
6MQR	H_ARG_41	NH2	H_GLU_148	OE1	3.805
6MQR	H_ARG_66	NH1	H_ASP_86	OD1	3.097
6MQR	H_ARG_66	NH1	H_ASP_86	OD2	3.599
6MQR	H_ARG_66	NH2	H_ASP_86	OD1	3.722
6MQR	H_ARG_66	NH2	H_ASP_86	OD2	3.135
6MQR	H_ARG_94	NH2	H_ASP_27	OD2	3.095
6MQR	H_ARG_96	NH1	H_ASP_101	OD2	3.599
6MQR	H_ARG_96	NH1	L_GLU_55	OE1	2.553
6MQR	H_LYS_143	NZ	H_ASP_144	OD1	3.883
6MQR	H_LYS_143	NZ	H_ASP_144	OD2	3.358
6MQR	L_LYS_30	NZ	L_ASP_28	OD2	3.556
6MQR	L_ARG_46	NH1	H_ASP_101	OD2	2.970
6MQR	L_ARG_46	NH1	L_GLU_55	OE1	3.253
6MQR	L_ARG_46	NH1	L_GLU_55	OE2	3.148
6MQR	L_ARG_46	NH2	H_GLU_95	OE2	3.587
6MQR	L_ARG_46	NH2	H_ASP_101	OD2	3.723
6MQR	L_HIS_49	ND1	L_GLU_55	OE1	3.996
6MQR	L_HIS_49	ND1	L_GLU_55	OE2	2.804
6MQR	L_ARG_61	NH1	L_GLU_81	OE1	3.715
6MQR	L_ARG_61	NH1	L_ASP_82	OD1	3.745
6MQR	L_ARG_61	NH1	L_ASP_82	OD2	2.987
6MQR	L_LYS_126	NZ	L_GLU_122	OE1	3.993
6MQR	L_ARG_142	NH2	L_GLU_161	OE2	3.937
6MQR	L_LYS_149	NZ	L_GLU_195	OE1	3.817
6MQR	L_LYS_149	NZ	L_GLU_195	OE2	2.808
6MQR	L_LYS_155	NZ	L_GLU_185	OE1	3.064
6MQR	L_LYS_169	NZ	L_ASP_167	OD2	3.796
6MQR	L_HIS_189	ND1	L_ASP_151	OD1	2.846
6MQR	L_HIS_189	NE2	L_GLU_185	OE1	2.682
6MQR	L_HIS_189	NE2	L_GLU_185	OE2	3.307

Table 863: 6MQR-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6MQS	A_ARG_39	NH1	A_ASP_91	OD1	3.081
6MQS	A_ARG_39	NH2	A_GLU_47	OE1	3.112
6MQS	A_ARG_39	NH2	A_ASP_91	OD1	3.076
6MQS	A_LYS_44	NZ	B_ASP_86	OD1	3.511
6MQS	A_ARG_45	NH1	A_GLU_47	OE2	3.645
6MQS	A_ARG_45	NH2	A_GLU_47	OE1	3.366
6MQS	A_ARG_68	NH2	A_ASP_91	OD1	3.145
6MQS	A_ARG_68	NH2	A_ASP_91	OD2	3.136
6MQS	A_ARG_138	NH1	B_GLU_214	OE1	3.046
6MQS	A_ARG_138	NH1	B_GLU_214	OE2	2.728
6MQS	A_LYS_152	NZ	A_ASP_153	OD1	3.592
6MQS	A_LYS_218	NZ	B_GLU_127	OE1	2.743
6MQS	A_LYS_218	NZ	B_GLU_127	OE2	3.002
6MQS	B_LYS_54	NZ	B_GLU_51	OE2	3.430
6MQS	B_ARG_62	NH1	B_ASP_83	OD1	2.524
6MQS	B_ARG_62	NH1	B_ASP_83	OD2	2.782
6MQS	B_LYS_114	NZ	B_GLU_202	OE1	3.365
6MQS	B_LYS_114	NZ	B_GLU_202	OE2	2.522
6MQS	B_LYS_153	NZ	B_GLU_207	OE1	2.539
6MQS	B_LYS_153	NZ	B_GLU_207	OE2	3.433
6MQS	B_LYS_170	NZ	B_GLU_106	OE1	3.760
6MQS	B_LYS_175	NZ	B_ASP_142	OD2	2.550
6MQS	B_HIS_192	ND1	B_ASP_155	OD1	3.151
6MQS	C_ARG_39	NH1	C_ASP_91	OD2	3.128
6MQS	C_ARG_39	NH2	C_GLU_47	OE2	3.179
6MQS	C_ARG_39	NH2	C_ASP_91	OD2	3.775
6MQS	C_LYS_44	NZ	D_ASP_86	OD1	2.946
6MQS	C_ARG_68	NH1	C_ASP_91	OD1	3.157
6MQS	C_ARG_68	NH1	C_ASP_91	OD2	3.255
6MQS	C_ARG_138	NH2	D_GLU_214	OE1	2.736
6MQS	C_ARG_138	NH2	D_GLU_214	OE2	3.220
6MQS	C_LYS_152	NZ	D_GLU_128	OE1	3.230
6MQS	C_LYS_215	NZ	C_ASP_217	OD1	3.836
6MQS	C_LYS_215	NZ	C_ASP_217	OD2	3.808
6MQS	C_LYS_218	NZ	D_GLU_127	OE1	2.641
6MQS	C_LYS_218	NZ	D_GLU_127	OE2	3.160
6MQS	D_LYS_54	NZ	D_GLU_51	OE2	2.149
6MQS	D_ARG_55	NH1	D_ASP_61	OD1	2.947
6MQS	D_ARG_55	NH2	D_ASP_61	OD1	3.758
6MQS	D_ARG_62	NH1	D_ASP_83	OD1	2.603
6MQS	D_ARG_62	NH1	D_ASP_83	OD2	3.278
6MQS	D_ARG_62	NH2	D_ASP_83	OD1	3.570
6MQS	D_ARG_62	NH2	D_ASP_83	OD2	2.546
6MQS	D_LYS_153	NZ	D_GLU_207	OE1	2.843
6MQS	D_LYS_153	NZ	D_GLU_207	OE2	3.321
6MQS	D_LYS_170	NZ	D_GLU_106	OE1	3.583
6MQS	D_HIS_192	ND1	D_ASP_155	OD1	2.450

Table 864: 6MQS-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6N16	A_ARG_38	NH1	A_GLU_46	OE1	3.309
6N16	A_ARG_38	NH1	A_ASP_86	OD1	3.572
6N16	A_ARG_38	NH2	A_ASP_86	OD1	2.610
6N16	A_ARG_66	NH1	A_ASP_86	OD1	3.129
6N16	A_ARG_66	NH1	A_ASP_86	OD2	3.512
6N16	A_ARG_66	NH2	A_ASP_86	OD1	3.997
6N16	A_ARG_66	NH2	A_ASP_86	OD2	3.156
6N16	A_LYS_71	NZ	A_GLU_55	OE2	3.830
6N16	A_ARG_105	NH1	C_GLU_64	OE1	3.566
6N16	A_ARG_105	NH2	C_GLU_64	OE1	3.522
6N16	A_ARG_105	NH2	C_GLU_64	OE2	3.717
6N16	A_HIS_164	NE2	B_ASP_167	OD2	3.486
6N16	A_ARG_210	NH2	A_GLU_212	OE2	3.118
6N16	B_ARG_24	NH1	B_ASP_70	OD1	3.099
6N16	B_ARG_24	NH2	B_ASP_70	OD1	2.017
6N16	B_ARG_24	NH2	B_ASP_70	OD2	3.393
6N16	B_HIS_30E	ND1	B_GLU_50	OE2	3.843
6N16	B_ARG_54	NH1	B_ASP_60	OD1	2.491
6N16	B_ARG_61	NH1	B_GLU_81	OE1	2.899
6N16	B_ARG_61	NH1	B_GLU_81	OE2	3.698
6N16	B_ARG_61	NH1	B_ASP_82	OD2	3.838
6N16	B_ARG_61	NH2	B_GLU_79	OE1	3.749
6N16	B_ARG_61	NH2	B_GLU_79	OE2	2.925
6N16	B_ARG_61	NH2	B_ASP_82	OD1	2.769
6N16	B_ARG_61	NH2	B_ASP_82	OD2	3.263
6N16	B_ARG_77	NH1	B_GLU_79	OE1	3.315
6N16	B_LYS_169	NZ	B_ASP_167	OD2	3.870
6N16	B_HIS_189	ND1	B_ASP_151	OD1	3.412
6N16	H_ARG_38	NH1	H_GLU_46	OE2	3.288
6N16	H_ARG_38	NH1	H_ASP_86	OD1	3.675
6N16	H_ARG_38	NH2	H_ASP_86	OD1	2.691
6N16	H_ARG_66	NH1	H_ASP_86	OD1	3.216
6N16	H_ARG_66	NH1	H_ASP_86	OD2	3.793
6N16	H_ARG_66	NH2	H_ASP_86	OD1	3.587
6N16	H_ARG_66	NH2	H_ASP_86	OD2	3.090
6N16	H_LYS_143	NZ	H_ASP_144	OD1	3.308
6N16	H_LYS_143	NZ	H_ASP_144	OD2	3.890
6N16	H_HIS_164	NE2	L_ASP_167	OD1	3.075
6N16	H_ARG_210	NH1	H_GLU_212	OE1	3.730
6N16	H_ARG_210	NH1	H_GLU_212	OE2	3.198
6N16	H_ARG_210	NH2	H_GLU_212	OE1	3.203
6N16	J_ARG_24	NH1	J_ASP_70	OD1	2.082
6N16	J_ARG_24	NH1	J_ASP_70	OD2	2.995
6N16	J_ARG_24	NH2	J_ASP_70	OD1	2.960
6N16	J_ARG_24	NH2	J_ASP_70	OD2	3.355
6N16	J_ARG_54	NH1	J_ASP_60	OD1	2.428
6N16	J_ARG_54	NH2	J_ASP_60	OD1	2.646
6N16	J_ARG_61	NH1	J_GLU_81	OE2	3.475
6N16	J_ARG_61	NH1	J_ASP_82	OD1	3.146
6N16	J_ARG_61	NH1	J_ASP_82	OD2	3.392
6N16	J_ARG_61	NH2	J_GLU_79	OE1	3.524
6N16	J_ARG_77	NH1	J_GLU_79	OE1	2.977
6N16	J_ARG_77	NH1	J_GLU_79	OE2	2.495
6N16	J_HIS_189	ND1	J_ASP_151	OD1	2.409
6N16	J_LYS_190	NZ	J_ASP_151	OD1	3.722
6N16	J_LYS_190	NZ	J_ASP_151	OD2	3.788
6N16	K_ARG_38	NH1	K_GLU_46	OE1	3.313

6N16	K_ARG_38	NH1	K_ASP_86	OD1	3.587
6N16	K_ARG_38	NH2	K_ASP_86	OD1	2.713
6N16	K_ARG_66	NH1	K_ASP_86	OD1	2.932
6N16	K_ARG_66	NH1	K_ASP_86	OD2	3.658
6N16	K_ARG_66	NH2	K_ASP_86	OD1	3.552
6N16	K_ARG_66	NH2	K_ASP_86	OD2	2.933
6N16	K_LYS_71	NZ	K_GLU_55	OE1	3.671
6N16	K_LYS_71	NZ	K_GLU_55	OE2	3.555
6N16	K_ARG_105	NH2	H_GLU_64	OE1	2.463
6N16	K_ARG_105	NH2	H_GLU_64	OE2	3.174
6N16	K_ARG_210	NH1	K_GLU_212	OE1	2.599
6N16	K_ARG_210	NH1	K_GLU_212	OE2	3.558
6N16	L_ARG_54	NH1	L_ASP_60	OD2	3.141
6N16	L_ARG_61	NH1	L_ASP_82	OD1	2.699
6N16	L_ARG_61	NH1	L_ASP_82	OD2	3.825
6N16	L_ARG_61	NH2	L_GLU_79	OE1	2.631
6N16	L_ARG_61	NH2	L_GLU_79	OE2	3.838
6N16	L_ARG_61	NH2	L_GLU_81	OE2	3.819
6N16	L_ARG_61	NH2	L_ASP_82	OD1	3.883
6N16	L_ARG_61	NH2	L_ASP_82	OD2	3.728
6N16	L_ARG_77	NH1	L_GLU_79	OE2	2.621
6N16	L_ARG_77	NH2	L_GLU_79	OE2	3.210
6N16	L_LYS_103	NZ	L_GLU_165	OE2	3.676
6N16	L_LYS_149	NZ	L_GLU_195	OE2	2.385
6N16	L_LYS_155	NZ	L_GLU_185	OE2	3.497
6N16	L_HIS_189	ND1	L_ASP_151	OD2	2.964
6N16	C_ARG_38	NH1	C_ASP_86	OD1	2.762
6N16	C_ARG_38	NH2	C_GLU_46	OE2	2.909
6N16	C_ARG_38	NH2	C_ASP_86	OD1	3.930
6N16	C_ARG_66	NH1	C_ASP_86	OD1	2.966
6N16	C_ARG_66	NH1	C_ASP_86	OD2	3.602
6N16	C_ARG_66	NH2	C_ASP_86	OD1	3.584
6N16	C_ARG_66	NH2	C_ASP_86	OD2	2.985
6N16	C_LYS_209	NZ	D_ASP_123	OD2	3.251
6N16	C_ARG_210	NH1	C_GLU_212	OE1	2.646
6N16	C_ARG_210	NH2	C_GLU_212	OE1	2.972
6N16	D_ARG_24	NH2	D_ASP_70	OD1	3.142
6N16	D_ARG_24	NH2	D_ASP_70	OD2	3.869
6N16	D_ARG_54	NH1	D_ASP_60	OD1	3.199
6N16	D_ARG_54	NH1	D_ASP_60	OD2	3.672
6N16	D_ARG_54	NH2	D_ASP_60	OD1	3.573
6N16	D_ARG_54	NH2	D_ASP_60	OD2	3.601
6N16	D_ARG_61	NH1	D_GLU_79	OE2	2.680
6N16	D_ARG_61	NH2	D_GLU_79	OE2	3.457
6N16	D_ARG_77	NH2	D_GLU_79	OE1	2.307
6N16	D_ARG_77	NH2	D_GLU_79	OE2	3.456
6N16	D_LYS_103	NZ	D_GLU_165	OE1	3.221
6N16	D_LYS_103	NZ	D_GLU_165	OE2	3.677
6N16	D_LYS_126	NZ	D_GLU_122	OE1	3.518
6N16	D_LYS_149	NZ	D_GLU_195	OE1	3.379

Table 865: 6N16-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6N1V	3_ARG_39	NH1	3_ASP_91	OD1	3.220
6N1V	3_ARG_39	NH2	3_GLU_47	OE1	2.848
6N1V	3_ARG_39	NH2	3_GLU_47	OE2	2.999
6N1V	3_LYS_44	NZ	4_ASP_86	OD1	3.675
6N1V	3_LYS_44	NZ	4_ASP_86	OD2	2.472
6N1V	3_LYS_44	NZ	4_GLU_106	OE1	3.723
6N1V	3_ARG_45	NH2	3_GLU_47	OE1	3.739
6N1V	3_ARG_138	NH1	4_GLU_214	OE1	2.573
6N1V	3_ARG_138	NH1	4_GLU_214	OE2	3.070
6N1V	3_ARG_138	NH2	4_GLU_214	OE2	3.291
6N1V	3_LYS_152	NZ	3_ASP_153	OD2	3.384
6N1V	3_LYS_218	NZ	4_GLU_127	OE1	3.611
6N1V	3_ARG_219	NH1	3_GLU_221	OE1	3.404
6N1V	4_LYS_54	NZ	4_GLU_51	OE1	3.248
6N1V	4_ARG_62	NH1	4_ASP_83	OD1	3.753
6N1V	4_ARG_62	NH1	4_ASP_83	OD2	3.947
6N1V	4_LYS_114	NZ	4_GLU_202	OE1	3.543
6N1V	4_LYS_114	NZ	4_GLU_202	OE2	2.746
6N1V	4_LYS_153	NZ	4_GLU_207	OE1	3.065
6N1V	4_LYS_153	NZ	4_GLU_207	OE2	3.086
6N1V	4_LYS_170	NZ	4_GLU_84	OE1	2.379
6N1V	4_LYS_175	NZ	4_ASP_142	OD1	3.116
6N1V	4_LYS_175	NZ	4_ASP_142	OD2	2.712
6N1V	4_HIS_192	ND1	4_ASP_155	OD1	3.682
6N1V	4_HIS_192	ND1	4_ASP_155	OD2	2.769
6N1V	B_LYS_46	NZ	B_GLU_492	OE2	2.855
6N1V	B_LYS_231	NZ	B_GLU_268	OE1	3.616
6N1V	B_LYS_231	NZ	B_GLU_268	OE2	2.737
6N1V	B_LYS_282	NZ	g_ASP_114	OD2	3.730
6N1V	B_ARG_298	NH1	B_GLU_381	OE1	3.416
6N1V	B_ARG_298	NH1	B_GLU_381	OE2	3.774
6N1V	B_ARG_298	NH2	B_GLU_381	OE1	3.507
6N1V	B_ARG_308	NH1	B_GLU_164	OE1	3.519
6N1V	B_ARG_308	NH1	B_GLU_164	OE2	2.477
6N1V	B_ARG_429	NH1	B_ASP_113	OD2	3.774
6N1V	B_ARG_429	NH2	B_ASP_113	OD1	3.650
6N1V	B_ARG_429	NH2	B_ASP_113	OD2	2.335
6N1V	B_ARG_469	NH1	B_ASP_457	OD1	3.545
6N1V	B_ARG_469	NH1	B_ASP_457	OD2	2.329
6N1V	B_ARG_476	NH1	B_GLU_102	OE2	3.982
6N1V	B_ARG_476	NH1	B_ASP_474	OD2	3.112
6N1V	B_ARG_476	NH2	B_GLU_102	OE1	3.903
6N1V	B_ARG_476	NH2	B_GLU_102	OE2	3.744
6N1V	B_ARG_480	NH1	B_ASP_477	OD1	2.992
6N1V	B_LYS_487	NZ	B_ASP_47	OD2	2.431
6N1V	B_ARG_504	NH2	D_GLU_657	OE2	3.905
6N1V	F_ARG_542	NH2	D_GLU_647	OE1	3.326
6N1V	F_ARG_542	NH2	D_GLU_647	OE2	2.831
6N1V	F_ARG_579	NH2	D_GLU_584	OE1	3.581
6N1V	F_ARG_588	NH2	F_GLU_584	OE2	2.394
6N1V	F_ARG_617	NH1	F_GLU_634	OE1	2.879
6N1V	F_ARG_617	NH1	F_GLU_634	OE2	2.871
6N1V	F_ARG_617	NH2	F_GLU_621	OE1	3.225
6N1V	Y_ARG_38	NH1	Y_ASP_86	OD1	2.536
6N1V	Y_ARG_38	NH2	Y_GLU_46	OE1	3.284
6N1V	Y_ARG_66	NH1	Y_ASP_86	OD2	3.359
6N1V	Y_ARG_66	NH2	Y_ASP_86	OD1	3.775

6N1V	Y_ARG_66	NH2	Y_ASP_86	OD2	3.105
6N1V	Y_LYS_73	NZ	Y_ASP_53	OD1	3.985
6N1V	Y_LYS_73	NZ	Y_ASP_53	OD2	2.420
6N1V	a_ARG_61	NH1	a_ASP_60	OD1	2.807
6N1V	g_LYS_19	NZ	g_GLU_89	OE1	3.749
6N1V	g_ARG_38	NH1	g_GLU_46	OE1	3.909
6N1V	g_ARG_38	NH1	g_GLU_46	OE2	3.659
6N1V	g_ARG_38	NH2	g_ASP_97	OD1	3.891
6N1V	g_ARG_72	NH1	B_ASP_368	OD2	3.927
6N1V	g_ARG_72	NH2	B_ASP_368	OD2	3.974
6N1V	i_ARG_61	NH2	i_ASP_82	OD1	3.042
6N1V	i_ARG_61	NH2	i_ASP_82	OD2	3.088
6N1V	l_ARG_39	NH1	l_ASP_91	OD1	3.219
6N1V	l_ARG_39	NH2	l_GLU_47	OE1	2.847
6N1V	l_ARG_39	NH2	l_GLU_47	OE2	3.000
6N1V	l_LYS_44	NZ	2_ASP_86	OD1	3.676
6N1V	l_LYS_44	NZ	2_ASP_86	OD2	2.473
6N1V	l_LYS_44	NZ	2_GLU_106	OE1	3.723
6N1V	l_ARG_45	NH2	l_GLU_47	OE1	3.739
6N1V	l_ARG_138	NH1	2_GLU_214	OE1	2.573
6N1V	l_ARG_138	NH1	2_GLU_214	OE2	3.069
6N1V	l_ARG_138	NH2	2_GLU_214	OE2	3.291
6N1V	l_LYS_152	NZ	l_ASP_153	OD2	3.384
6N1V	l_LYS_218	NZ	2_GLU_127	OE1	3.611
6N1V	l_ARG_219	NH1	l_GLU_221	OE1	3.404
6N1V	2_LYS_54	NZ	2_GLU_51	OE1	3.247
6N1V	2_ARG_62	NH1	2_ASP_83	OD1	3.752
6N1V	2_ARG_62	NH1	2_ASP_83	OD2	3.947
6N1V	2_LYS_114	NZ	2_GLU_202	OE1	3.543
6N1V	2_LYS_114	NZ	2_GLU_202	OE2	2.746
6N1V	2_LYS_153	NZ	2_GLU_207	OE1	3.064
6N1V	2_LYS_153	NZ	2_GLU_207	OE2	3.086
6N1V	2_LYS_170	NZ	2_GLU_84	OE1	2.379
6N1V	2_LYS_175	NZ	2_ASP_142	OD1	3.116
6N1V	2_LYS_175	NZ	2_ASP_142	OD2	2.712
6N1V	2_HIS_192	ND1	2_ASP_155	OD1	3.682
6N1V	2_HIS_192	ND1	2_ASP_155	OD2	2.769
6N1V	A_LYS_46	NZ	A_GLU_492	OE2	2.855
6N1V	A_LYS_231	NZ	A_GLU_268	OE1	3.617
6N1V	A_LYS_231	NZ	A_GLU_268	OE2	2.737
6N1V	A_LYS_282	NZ	f_ASP_114	OD2	3.729
6N1V	A_ARG_298	NH1	A_GLU_381	OE1	3.416
6N1V	A_ARG_298	NH1	A_GLU_381	OE2	3.774
6N1V	A_ARG_298	NH2	A_GLU_381	OE1	3.507
6N1V	A_ARG_308	NH1	A_GLU_164	OE1	3.518
6N1V	A_ARG_308	NH1	A_GLU_164	OE2	2.477
6N1V	A_ARG_429	NH1	A_ASP_113	OD2	3.775
6N1V	A_ARG_429	NH2	A_ASP_113	OD1	3.650
6N1V	A_ARG_429	NH2	A_ASP_113	OD2	2.336
6N1V	A_ARG_469	NH1	A_ASP_457	OD1	3.546
6N1V	A_ARG_469	NH1	A_ASP_457	OD2	2.329
6N1V	A_ARG_476	NH1	A_GLU_102	OE2	3.981
6N1V	A_ARG_476	NH1	A_ASP_474	OD2	3.112
6N1V	A_ARG_476	NH2	A_GLU_102	OE1	3.904
6N1V	A_ARG_476	NH2	A_GLU_102	OE2	3.744
6N1V	A_ARG_480	NH1	A_ASP_477	OD1	2.992
6N1V	A_LYS_487	NZ	A_ASP_47	OD2	2.431
6N1V	A_ARG_504	NH2	F_GLU_657	OE2	3.909

6N1V	E_ARG_542	NH2	F_GLU_647	OE1	3.328
6N1V	E_ARG_542	NH2	F_GLU_647	OE2	2.831
6N1V	E_ARG_579	NH2	F_GLU_584	OE1	3.583
6N1V	E_ARG_588	NH2	E_GLU_584	OE2	2.393
6N1V	E_ARG_617	NH1	E_GLU_634	OE1	2.879
6N1V	E_ARG_617	NH1	E_GLU_634	OE2	2.871
6N1V	E_ARG_617	NH2	E_GLU_621	OE1	3.225
6N1V	X_ARG_38	NH1	X_ASP_86	OD1	2.536
6N1V	X_ARG_38	NH2	X_GLU_46	OE1	3.284
6N1V	X_ARG_66	NH1	X_ASP_86	OD2	3.359
6N1V	X_ARG_66	NH2	X_ASP_86	OD1	3.775
6N1V	X_ARG_66	NH2	X_ASP_86	OD2	3.105
6N1V	X_LYS_73	NZ	X_ASP_53	OD1	3.985
6N1V	X_LYS_73	NZ	X_ASP_53	OD2	2.420
6N1V	Z_ARG_61	NH1	Z_ASP_60	OD1	2.807
6N1V	f_LYS_19	NZ	f_GLU_89	OE1	3.748
6N1V	f_ARG_38	NH1	f_GLU_46	OE1	3.909
6N1V	f_ARG_38	NH1	f_GLU_46	OE2	3.659
6N1V	f_ARG_38	NH2	f_ASP_97	OD1	3.891
6N1V	f_ARG_72	NH1	A_ASP_368	OD2	3.927
6N1V	f_ARG_72	NH2	A_ASP_368	OD2	3.974
6N1V	h_ARG_61	NH2	h_ASP_82	OD1	3.042
6N1V	h_ARG_61	NH2	h_ASP_82	OD2	3.088
6N1V	C_LYS_46	NZ	C_GLU_492	OE2	2.855
6N1V	C_LYS_231	NZ	C_GLU_268	OE1	3.617
6N1V	C_LYS_231	NZ	C_GLU_268	OE2	2.737
6N1V	C_LYS_282	NZ	Q_ASP_114	OD2	3.730
6N1V	C_ARG_298	NH1	C_GLU_381	OE1	3.416
6N1V	C_ARG_298	NH1	C_GLU_381	OE2	3.775
6N1V	C_ARG_298	NH2	C_GLU_381	OE1	3.507
6N1V	C_ARG_308	NH1	C_GLU_164	OE1	3.518
6N1V	C_ARG_308	NH1	C_GLU_164	OE2	2.477
6N1V	C_ARG_429	NH1	C_ASP_113	OD2	3.775
6N1V	C_ARG_429	NH2	C_ASP_113	OD1	3.651
6N1V	C_ARG_429	NH2	C_ASP_113	OD2	2.336
6N1V	C_ARG_469	NH1	C_ASP_457	OD1	3.545
6N1V	C_ARG_469	NH1	C_ASP_457	OD2	2.329
6N1V	C_ARG_476	NH1	C_GLU_102	OE2	3.982
6N1V	C_ARG_476	NH1	C_ASP_474	OD2	3.112
6N1V	C_ARG_476	NH2	C_GLU_102	OE1	3.904
6N1V	C_ARG_476	NH2	C_GLU_102	OE2	3.744
6N1V	C_ARG_480	NH1	C_ASP_477	OD1	2.992
6N1V	C_LYS_487	NZ	C_ASP_47	OD2	2.431
6N1V	C_ARG_504	NH2	E_GLU_657	OE2	3.907
6N1V	D_ARG_542	NH2	E_GLU_647	OE1	3.330
6N1V	D_ARG_542	NH2	E_GLU_647	OE2	2.832
6N1V	D_ARG_579	NH2	E_GLU_584	OE1	3.585
6N1V	D_ARG_588	NH2	D_GLU_584	OE2	2.394
6N1V	D_ARG_617	NH1	D_GLU_634	OE1	2.880
6N1V	D_ARG_617	NH1	D_GLU_634	OE2	2.871
6N1V	D_ARG_617	NH2	D_GLU_621	OE1	3.225
6N1V	H_ARG_39	NH1	H_ASP_91	OD1	3.220
6N1V	H_ARG_39	NH2	H_GLU_47	OE1	2.848
6N1V	H_ARG_39	NH2	H_GLU_47	OE2	3.000
6N1V	H_LYS_44	NZ	L_ASP_86	OD1	3.676
6N1V	H_LYS_44	NZ	L_ASP_86	OD2	2.472
6N1V	H_LYS_44	NZ	L_GLU_106	OE1	3.722
6N1V	H_ARG_45	NH2	H_GLU_47	OE1	3.739

6N1V	H_ARG_138	NH1	L_GLU_214	OE1	2.573
6N1V	H_ARG_138	NH1	L_GLU_214	OE2	3.069
6N1V	H_ARG_138	NH2	L_GLU_214	OE2	3.291
6N1V	H_LYS_152	NZ	H_ASP_153	OD2	3.384
6N1V	H_LYS_218	NZ	L_GLU_127	OE1	3.611
6N1V	H_ARG_219	NH1	H_GLU_221	OE1	3.404
6N1V	L_LYS_54	NZ	L_GLU_51	OE1	3.248
6N1V	L_ARG_62	NH1	L_ASP_83	OD1	3.753
6N1V	L_ARG_62	NH1	L_ASP_83	OD2	3.947
6N1V	L_LYS_114	NZ	L_GLU_202	OE1	3.542
6N1V	L_LYS_114	NZ	L_GLU_202	OE2	2.746
6N1V	L_LYS_153	NZ	L_GLU_207	OE1	3.065
6N1V	L_LYS_153	NZ	L_GLU_207	OE2	3.087
6N1V	L_LYS_170	NZ	L_GLU_84	OE1	2.379
6N1V	L_LYS_175	NZ	L_ASP_142	OD1	3.116
6N1V	L_LYS_175	NZ	L_ASP_142	OD2	2.712
6N1V	L_HIS_192	ND1	L_ASP_155	OD1	3.682
6N1V	L_HIS_192	ND1	L_ASP_155	OD2	2.769
6N1V	M_ARG_38	NH1	M_ASP_86	OD1	2.536
6N1V	M_ARG_38	NH2	M_GLU_46	OE1	3.284
6N1V	M_ARG_66	NH1	M_ASP_86	OD2	3.359
6N1V	M_ARG_66	NH2	M_ASP_86	OD1	3.775
6N1V	M_ARG_66	NH2	M_ASP_86	OD2	3.105
6N1V	M_LYS_73	NZ	M_ASP_53	OD1	3.985
6N1V	M_LYS_73	NZ	M_ASP_53	OD2	2.420
6N1V	N_ARG_61	NH1	N_ASP_60	OD1	2.808
6N1V	Q_LYS_19	NZ	Q_GLU_89	OE1	3.749
6N1V	Q_ARG_38	NH1	Q_GLU_46	OE1	3.909
6N1V	Q_ARG_38	NH1	Q_GLU_46	OE2	3.659
6N1V	Q_ARG_38	NH2	Q_ASP_97	OD1	3.891
6N1V	Q_ARG_72	NH1	C_ASP_368	OD2	3.927
6N1V	Q_ARG_72	NH2	C_ASP_368	OD2	3.975
6N1V	R_ARG_61	NH2	R_ASP_82	OD1	3.042
6N1V	R_ARG_61	NH2	R_ASP_82	OD2	3.088

Table 866: 6N1V-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6N1W	2_LYS_46	NZ	2_GLU_492	OE2	3.928
6N1W	2_LYS_227	NZ	2_GLU_83	OE1	2.543
6N1W	2_LYS_231	NZ	2_GLU_268	OE1	2.454
6N1W	2_LYS_231	NZ	2_GLU_268	OE2	3.957
6N1W	2_LYS_231	NZ	2_GLU_269	OE1	3.998
6N1W	2_HIS_249	NE2	2_GLU_83	OE1	3.939
6N1W	2_LYS_282	NZ	2_GLU_275	OE1	3.006
6N1W	2_ARG_298	NH1	2_GLU_381	OE1	3.635
6N1W	2_ARG_298	NH1	2_GLU_381	OE2	2.558
6N1W	2_ARG_298	NH2	2_GLU_381	OE1	3.709
6N1W	2_ARG_298	NH2	2_GLU_381	OE2	3.969
6N1W	2_ARG_308	NH1	2_GLU_164	OE1	3.421
6N1W	2_ARG_308	NH1	2_GLU_164	OE2	3.903
6N1W	2_ARG_327	NH2	m_GLU_100I	OE1	3.996
6N1W	2_LYS_421	NZ	2_ASP_180	OD1	3.450
6N1W	2_ARG_429	NH1	2_ASP_113	OD2	3.966
6N1W	2_ARG_429	NH2	2_ASP_113	OD1	3.893
6N1W	2_ARG_429	NH2	2_ASP_113	OD2	2.506
6N1W	2_ARG_469	NH2	2_ASP_457	OD2	2.809
6N1W	2_ARG_476	NH1	2_GLU_102	OE1	2.957
6N1W	2_ARG_476	NH1	2_GLU_102	OE2	3.101
6N1W	2_ARG_476	NH2	2_GLU_102	OE1	3.474
6N1W	2_ARG_480	NH1	2_ASP_477	OD1	2.941
6N1W	2_LYS_487	NZ	2_ASP_47	OD1	2.806
6N1W	2_LYS_487	NZ	2_ASP_47	OD2	3.509
6N1W	2_ARG_504	NH2	d_GLU_657	OE2	3.118
6N1W	3_ARG_38	NH1	3_GLU_46	OE1	2.665
6N1W	3_ARG_38	NH1	3_GLU_46	OE2	3.250
6N1W	3_ARG_38	NH2	3_ASP_86	OD1	2.625
6N1W	3_ARG_66	NH1	3_ASP_86	OD2	3.781
6N1W	3_LYS_71	NZ	3_GLU_55	OE2	3.265
6N1W	3_ARG_100H	NH1	3_ASP_101	OD2	3.227
6N1W	3_ARG_100H	NH2	4_ASP_91	OD2	3.241
6N1W	4_ARG_61	NH1	4_GLU_81	OE2	3.361
6N1W	4_ARG_61	NH1	4_ASP_82	OD1	3.254
6N1W	4_ARG_61	NH2	4_ASP_82	OD1	3.059
6N1W	4_ARG_61	NH2	4_ASP_82	OD2	2.679
6N1W	5_ARG_38	NH1	5_ASP_86	OD1	2.691
6N1W	5_ARG_38	NH2	5_GLU_46	OE1	3.484
6N1W	5_ARG_38	NH2	5_GLU_46	OE2	3.816
6N1W	5_ARG_38	NH2	5_ASP_86	OD1	3.929
6N1W	5_ARG_66	NH1	5_ASP_86	OD2	3.620
6N1W	5_ARG_66	NH2	5_ASP_86	OD1	3.504
6N1W	5_LYS_73	NZ	5_ASP_53	OD1	3.480
6N1W	5_LYS_73	NZ	5_ASP_53	OD2	2.933
6N1W	7_ARG_60	NH2	7_ASP_81	OD1	2.923
6N1W	7_ARG_60	NH2	7_ASP_81	OD2	2.939
6N1W	8_ARG_38	NH1	8_GLU_46	OE1	3.713
6N1W	8_ARG_38	NH1	8_ASP_86	OD1	3.761
6N1W	8_ARG_38	NH2	8_ASP_86	OD1	3.294
6N1W	8_ARG_66	NH1	8_ASP_86	OD2	3.879
6N1W	8_ARG_66	NH2	8_ASP_86	OD2	2.655
6N1W	A_ARG_542	NH1	d_GLU_647	OE1	3.516
6N1W	A_ARG_542	NH1	d_GLU_647	OE2	3.474
6N1W	A_ARG_542	NH2	d_GLU_647	OE1	2.848
6N1W	A_ARG_579	NH2	d_GLU_584	OE2	3.464
6N1W	A_LYS_601	NZ	d_GLU_654	OE1	3.802

6N1W	A_LYS_601	NZ	d_GLU_654	OE2	3.060
6N1W	A_ARG_617	NH1	A_GLU_634	OE2	3.959
6N1W	A_ARG_617	NH2	A_GLU_621	OE1	3.529
6N1W	C_LYS_46	NZ	C_GLU_492	OE2	3.859
6N1W	C_LYS_97	NZ	C_GLU_275	OE2	3.973
6N1W	C_LYS_227	NZ	C_GLU_83	OE1	2.695
6N1W	C_LYS_231	NZ	C_GLU_268	OE1	2.473
6N1W	C_LYS_231	NZ	C_GLU_268	OE2	3.970
6N1W	C_LYS_231	NZ	C_GLU_269	OE1	3.984
6N1W	C_HIS_249	NE2	C_GLU_83	OE1	3.866
6N1W	C_LYS_282	NZ	C_GLU_275	OE1	3.039
6N1W	C_ARG_298	NH1	C_GLU_381	OE1	3.780
6N1W	C_ARG_298	NH1	C_GLU_381	OE2	2.649
6N1W	C_ARG_298	NH2	C_GLU_381	OE1	3.748
6N1W	C_ARG_298	NH2	C_GLU_381	OE2	3.927
6N1W	C_ARG_308	NH1	C_GLU_164	OE1	3.469
6N1W	C_ARG_308	NH1	C_GLU_164	OE2	3.901
6N1W	C_LYS_421	NZ	C_ASP_180	OD1	3.498
6N1W	C_ARG_429	NH1	C_ASP_113	OD2	3.958
6N1W	C_ARG_429	NH2	C_ASP_113	OD1	3.756
6N1W	C_ARG_429	NH2	C_ASP_113	OD2	2.445
6N1W	C_ARG_469	NH2	C_ASP_457	OD2	2.859
6N1W	C_ARG_476	NH1	C_GLU_102	OE1	3.094
6N1W	C_ARG_476	NH1	C_GLU_102	OE2	3.309
6N1W	C_ARG_476	NH2	C_GLU_102	OE1	3.512
6N1W	C_ARG_480	NH1	C_ASP_477	OD1	2.924
6N1W	C_LYS_487	NZ	C_ASP_47	OD1	2.763
6N1W	C_LYS_487	NZ	C_ASP_47	OD2	3.509
6N1W	C_ARG_504	NH2	A_GLU_657	OE2	3.221
6N1W	D_ARG_542	NH1	A_GLU_647	OE1	3.273
6N1W	D_ARG_542	NH1	A_GLU_647	OE2	3.289
6N1W	D_ARG_542	NH2	A_GLU_647	OE1	2.942
6N1W	D_ARG_579	NH1	A_GLU_584	OE1	3.854
6N1W	D_ARG_579	NH2	A_GLU_584	OE2	3.567
6N1W	D_LYS_601	NZ	A_GLU_654	OE1	3.837
6N1W	D_LYS_601	NZ	A_GLU_654	OE2	3.044
6N1W	D_ARG_617	NH1	D_GLU_634	OE2	3.956
6N1W	D_ARG_617	NH2	D_GLU_621	OE1	3.541
6N1W	H_ARG_38	NH1	H_GLU_46	OE1	2.685
6N1W	H_ARG_38	NH1	H_GLU_46	OE2	3.187
6N1W	H_ARG_38	NH2	H_ASP_86	OD1	2.618
6N1W	H_ARG_66	NH1	H_ASP_86	OD2	3.806
6N1W	H_LYS_71	NZ	H_GLU_55	OE2	3.251
6N1W	H_ARG_100H	NH1	H_ASP_101	OD2	3.211
6N1W	H_ARG_100H	NH2	L_ASP_91	OD2	3.150
6N1W	L_ARG_61	NH1	L_GLU_81	OE2	3.442
6N1W	L_ARG_61	NH1	L_ASP_82	OD1	3.265
6N1W	L_ARG_61	NH2	L_ASP_82	OD1	3.076
6N1W	L_ARG_61	NH2	L_ASP_82	OD2	2.697
6N1W	M_ARG_38	NH1	M_ASP_86	OD1	2.569
6N1W	M_ARG_38	NH2	M_GLU_46	OE1	3.511
6N1W	M_ARG_38	NH2	M_GLU_46	OE2	3.792
6N1W	M_ARG_38	NH2	M_ASP_86	OD1	3.908
6N1W	M_ARG_66	NH1	M_ASP_86	OD2	3.739
6N1W	M_ARG_66	NH2	M_ASP_86	OD1	3.607
6N1W	M_LYS_73	NZ	M_ASP_53	OD1	3.504
6N1W	M_LYS_73	NZ	M_ASP_53	OD2	2.877
6N1W	Q_ARG_38	NH1	Q_GLU_46	OE1	3.699

6N1W	Q_ARG_38	NH1	Q_ASP_86	OD1	3.715
6N1W	Q_ARG_38	NH2	Q_ASP_86	OD1	3.040
6N1W	Q_ARG_66	NH1	Q_ASP_86	OD2	3.762
6N1W	Q_ARG_66	NH2	Q_ASP_86	OD2	2.524
6N1W	R_ARG_60	NH2	R_ASP_81	OD1	2.849
6N1W	R_ARG_60	NH2	R_ASP_81	OD2	2.945
6N1W	c_LYS_46	NZ	c_GLU_492	OE2	3.862
6N1W	c_LYS_227	NZ	c_GLU_83	OE1	2.652
6N1W	c_LYS_231	NZ	c_GLU_268	OE1	2.434
6N1W	c_LYS_231	NZ	c_GLU_268	OE2	3.951
6N1W	c_LYS_231	NZ	c_GLU_269	OE1	3.890
6N1W	c_HIS_249	NE2	c_GLU_83	OE1	3.931
6N1W	c_LYS_282	NZ	c_GLU_275	OE1	3.038
6N1W	c_ARG_298	NH1	c_GLU_381	OE1	3.531
6N1W	c_ARG_298	NH1	c_GLU_381	OE2	2.444
6N1W	c_ARG_298	NH2	c_GLU_381	OE1	3.806
6N1W	c_ARG_308	NH1	c_GLU_164	OE1	3.441
6N1W	c_ARG_308	NH1	c_GLU_164	OE2	3.830
6N1W	c_LYS_421	NZ	c_ASP_180	OD1	3.813
6N1W	c_ARG_429	NH1	c_ASP_113	OD2	3.970
6N1W	c_ARG_429	NH2	c_ASP_113	OD1	3.958
6N1W	c_ARG_429	NH2	c_ASP_113	OD2	2.540
6N1W	c_ARG_469	NH2	c_ASP_457	OD2	2.886
6N1W	c_ARG_476	NH1	c_GLU_102	OE1	2.901
6N1W	c_ARG_476	NH1	c_GLU_102	OE2	3.038
6N1W	c_ARG_476	NH2	c_GLU_102	OE1	3.473
6N1W	c_ARG_480	NH1	c_ASP_477	OD1	2.867
6N1W	c_LYS_487	NZ	c_ASP_47	OD1	2.950
6N1W	c_LYS_487	NZ	c_ASP_47	OD2	3.392
6N1W	c_LYS_487	NZ	c_GLU_91	OE1	3.967
6N1W	c_ARG_504	NH2	D_GLU_657	OE2	3.061
6N1W	d_ARG_542	NH1	D_GLU_647	OE1	3.482
6N1W	d_ARG_542	NH1	D_GLU_647	OE2	3.280
6N1W	d_ARG_542	NH2	D_GLU_647	OE1	2.854
6N1W	d_ARG_579	NH1	D_GLU_584	OE1	3.913
6N1W	d_ARG_579	NH2	D_GLU_584	OE2	3.653
6N1W	d_LYS_601	NZ	D_GLU_654	OE1	3.862
6N1W	d_LYS_601	NZ	D_GLU_654	OE2	3.082
6N1W	d_ARG_617	NH1	d_GLU_634	OE2	3.896
6N1W	d_ARG_617	NH2	d_GLU_621	OE1	3.678
6N1W	h_ARG_38	NH1	h_GLU_46	OE1	2.684
6N1W	h_ARG_38	NH1	h_GLU_46	OE2	3.228
6N1W	h_ARG_38	NH2	h_ASP_86	OD1	2.566
6N1W	h_ARG_66	NH1	h_ASP_86	OD2	3.765
6N1W	h_LYS_71	NZ	h_GLU_55	OE2	3.379
6N1W	h_ARG_100H	NH1	h_ASP_101	OD2	3.191
6N1W	h_ARG_100H	NH2	l_ASP_91	OD2	3.226
6N1W	l_ARG_61	NH1	l_GLU_81	OE2	3.471
6N1W	l_ARG_61	NH1	l_ASP_82	OD1	3.278
6N1W	l_ARG_61	NH2	l_ASP_82	OD1	3.046
6N1W	l_ARG_61	NH2	l_ASP_82	OD2	2.734
6N1W	m_ARG_38	NH1	m_ASP_86	OD1	2.662
6N1W	m_ARG_38	NH2	m_GLU_46	OE1	3.392
6N1W	m_ARG_38	NH2	m_GLU_46	OE2	3.730
6N1W	m_ARG_38	NH2	m_ASP_86	OD1	3.976
6N1W	m_ARG_66	NH1	m_ASP_86	OD2	3.631
6N1W	m_ARG_66	NH2	m_ASP_86	OD1	3.510
6N1W	m_LYS_73	NZ	m_ASP_53	OD1	3.489

6N1W	m_LYS_73	NZ	m_ASP_53	OD2	2.916
6N1W	q_ARG_38	NH1	q_GLU_46	OE1	3.649
6N1W	q_ARG_38	NH1	q_ASP_86	OD1	3.800
6N1W	q_ARG_38	NH2	q_ASP_86	OD1	3.194
6N1W	q_ARG_66	NH1	q_ASP_86	OD2	3.833
6N1W	q_ARG_66	NH2	q_ASP_86	OD2	2.511
6N1W	r_ARG_60	NH2	r_ASP_81	OD1	2.963
6N1W	r_ARG_60	NH2	r_ASP_81	OD2	3.033

Table 867: 6N1W-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6N5B	H_ARG_38	NH1	H_GLU_46	OE1	3.194
6N5B	H_ARG_38	NH1	H_GLU_46	OE2	3.841
6N5B	H_ARG_38	NH2	H_ASP_86	OD1	3.183
6N5B	H_LYS_64	NZ	H_ASP_61	OD1	3.760
6N5B	H_ARG_66	NH1	H_ASP_86	OD1	3.517
6N5B	H_ARG_66	NH1	H_ASP_86	OD2	3.589
6N5B	H_ARG_66	NH2	H_ASP_86	OD2	3.024
6N5B	H_LYS_149	NZ	L_GLU_128	OE2	3.031
6N5B	H_LYS_214	NZ	L_GLU_127	OE2	3.139
6N5B	L_ARG_63	NH2	L_ASP_84	OD1	2.528
6N5B	L_ARG_63	NH2	L_ASP_84	OD2	3.785
6N5B	L_LYS_170	NZ	L_GLU_85	OE2	2.862
6N5B	L_HIS_192	ND1	L_ASP_155	OD2	3.335
6N5B	B_ARG_53	NH1	B_GLU_79	OE1	3.394
6N5B	B_ARG_53	NH2	B_ASP_81	OD1	3.952
6N5B	B_ARG_86	NH2	B_ASP_56	OD1	3.915
6N5B	B_ARG_86	NH2	B_ASP_56	OD2	2.646
6N5B	B_ARG_105	NH2	B_GLU_85	OE1	3.089
6N5B	B_LYS_113	NZ	B_GLU_115	OE1	3.775
6N5B	B_ARG_137	NH1	B_ASP_73	OD1	2.745
6N5B	B_ARG_137	NH1	B_ASP_73	OD2	3.436
6N5B	B_ARG_137	NH2	B_ASP_142	OD2	3.308
6N5B	B_ARG_172	NH1	B_GLU_119	OE2	3.863
6N5B	B_HIS_253	ND1	B_GLU_119	OE1	2.944
6N5B	B_LYS_255	NZ	B_GLU_115	OE2	3.788

Table 868: 6N5B-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6N5D	A_HIS_56	ND1	A_ASP_85	OD2	3.953
6N5D	A_ARG_57	NH2	A_GLU_82	OE1	2.603
6N5D	A_HIS_75	ND1	A_ASP_73	OD1	2.834
6N5D	A_HIS_75	ND1	A_ASP_73	OD2	3.931
6N5D	A_ARG_90	NH2	A_ASP_60	OD1	3.337
6N5D	A_ARG_90	NH2	A_ASP_60	OD2	2.505
6N5D	A_LYS_92	NZ	A_ASP_271	OD2	3.373
6N5D	A_ARG_109	NH1	A_GLU_89	OE1	2.808
6N5D	A_ARG_109	NH1	A_GLU_89	OE2	3.783
6N5D	A_LYS_176	NZ	A_GLU_123	OE2	3.918
6N5D	A_LYS_238	NZ	A_ASP_175	OD1	3.849
6N5D	A_LYS_238	NZ	A_ASP_175	OD2	3.598
6N5D	A_LYS_259	NZ	A_GLU_119	OE2	3.730
6N5D	C_ARG_38	NH2	C_ASP_90	OD1	3.385
6N5D	C_ARG_67	NH1	C_ASP_90	OD1	3.989
6N5D	C_ARG_67	NH1	C_ASP_90	OD2	3.731
6N5D	C_ARG_67	NH2	C_ASP_90	OD1	3.488
6N5D	C_ARG_67	NH2	C_ASP_90	OD2	2.158
6N5D	C_LYS_149	NZ	D_GLU_127	OE2	2.211
6N5D	C_LYS_212	NZ	C_ASP_214	OD1	3.695
6N5D	C_LYS_215	NZ	D_GLU_126	OE1	3.361
6N5D	C_LYS_215	NZ	D_GLU_126	OE2	3.815
6N5D	C_ARG_216	NH1	C_GLU_218	OE1	2.311
6N5D	C_ARG_216	NH1	C_GLU_218	OE2	3.798
6N5D	C_ARG_216	NH2	C_GLU_218	OE1	3.283
6N5D	C_ARG_216	NH2	C_GLU_218	OE2	3.709
6N5D	B_ARG_57	NH2	B_GLU_82	OE1	2.558
6N5D	B_ARG_57	NH2	B_GLU_82	OE2	3.860
6N5D	B_HIS_75	ND1	B_ASP_73	OD1	2.685
6N5D	B_HIS_75	ND1	B_ASP_73	OD2	3.543
6N5D	B_ARG_90	NH2	B_ASP_60	OD1	3.667
6N5D	B_ARG_90	NH2	B_ASP_60	OD2	2.318
6N5D	B_LYS_92	NZ	B_ASP_271	OD2	2.554
6N5D	B_ARG_109	NH1	B_GLU_89	OE1	3.519
6N5D	B_ARG_141	NH1	B_ASP_77	OD2	2.444
6N5D	B_LYS_176	NZ	B_GLU_123	OE1	3.115
6N5D	B_ARG_261	NH2	B_GLU_119	OE1	3.598
6N5D	B_ARG_269	NH2	B_GLU_89	OE1	3.840
6N5D	B_LYS_315	NZ	B_GLU_41	OE1	3.513
6N5D	E_ARG_38	NH1	E_ASP_90	OD1	3.664
6N5D	E_ARG_38	NH2	E_GLU_46	OE1	3.505
6N5D	E_ARG_38	NH2	E_ASP_90	OD1	3.051
6N5D	E_LYS_65	NZ	E_ASP_62	OD1	3.737
6N5D	E_ARG_67	NH1	E_ASP_90	OD2	3.314
6N5D	E_ARG_67	NH2	E_ASP_90	OD1	3.968
6N5D	E_ARG_67	NH2	E_ASP_90	OD2	2.162
6N5D	E_LYS_149	NZ	F_GLU_127	OE2	3.376
6N5D	E_LYS_212	NZ	E_ASP_214	OD1	3.161
6N5D	E_ARG_216	NH2	E_GLU_218	OE2	2.928
6N5D	K_HIS_56	ND1	K_ASP_85	OD2	3.271
6N5D	K_ARG_57	NH2	K_GLU_82	OE1	2.301
6N5D	K_HIS_75	ND1	K_ASP_73	OD1	2.835
6N5D	K_HIS_75	ND1	K_ASP_73	OD2	3.740
6N5D	K_ARG_90	NH2	K_ASP_60	OD1	3.759
6N5D	K_ARG_90	NH2	K_ASP_60	OD2	3.274
6N5D	K_ARG_109	NH1	K_GLU_89	OE1	3.561
6N5D	K_ARG_141	NH1	K_ASP_77	OD2	3.970

6N5D	K_LYS_176	NZ	K_GLU_123	OE2	2.488
6N5D	K_LYS_238	NZ	K_ASP_175	OD1	2.613
6N5D	K_LYS_238	NZ	K_ASP_175	OD2	3.291
6N5D	K_LYS_315	NZ	K_GLU_41	OE1	2.260
6N5D	L_ARG_38	NH1	L_ASP_90	OD1	3.927
6N5D	L_ARG_38	NH2	L_ASP_90	OD1	3.768
6N5D	L_LYS_65	NZ	L_ASP_62	OD2	3.222
6N5D	L_ARG_67	NH1	L_ASP_90	OD1	3.866
6N5D	L_ARG_67	NH1	L_ASP_90	OD2	3.353
6N5D	L_ARG_67	NH2	L_ASP_90	OD1	3.826
6N5D	L_ARG_67	NH2	L_ASP_90	OD2	2.288
6N5D	L_LYS_149	NZ	N_GLU_127	OE2	2.091
6N5D	L_HIS_170	NE2	N_ASP_141	OD2	3.244
6N5D	L_LYS_212	NZ	L_ASP_214	OD1	2.499
6N5D	L_LYS_212	NZ	L_ASP_214	OD2	3.450
6N5D	F_ARG_63	NH2	F_ASP_84	OD1	3.578
6N5D	D_ARG_63	NH2	D_ASP_84	OD1	3.736
6N5D	D_HIS_191	ND1	D_ASP_154	OD1	3.992
6N5D	D_HIS_191	ND1	D_ASP_154	OD2	3.059

Table 869: 6N5D-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6N5E	A_HIS_56	NE2	A_GLU_280	OE2	3.185
6N5E	A_ARG_57	NH2	A_GLU_82	OE1	2.937
6N5E	A_HIS_75	ND1	A_ASP_73	OD1	2.982
6N5E	A_ARG_90	NH2	A_ASP_60	OD2	2.862
6N5E	A_LYS_92	NZ	A_ASP_63	OD1	3.254
6N5E	A_ARG_109	NH2	A_GLU_89	OE1	3.038
6N5E	A_ARG_109	NH2	A_GLU_89	OE2	3.184
6N5E	A_ARG_141	NH1	A_ASP_77	OD2	2.455
6N5E	A_ARG_141	NH2	A_ASP_77	OD2	3.946
6N5E	A_LYS_176	NZ	A_GLU_123	OE1	3.715
6N5E	A_LYS_176	NZ	A_GLU_123	OE2	2.160
6N5E	A_LYS_259	NZ	A_GLU_119	OE2	3.507
6N5E	A_ARG_261	NH2	A_GLU_119	OE1	3.324
6N5E	A_LYS_292	NZ	A_GLU_41	OE1	3.523
6N5E	B_LYS_50	NZ	B_ASP_275	OD2	3.461
6N5E	B_HIS_56	NE2	B_GLU_280	OE1	3.340
6N5E	B_ARG_57	NH2	B_GLU_82	OE1	3.063
6N5E	B_HIS_75	ND1	B_ASP_73	OD1	2.687
6N5E	B_HIS_75	ND1	B_ASP_73	OD2	3.481
6N5E	B_ARG_90	NH2	B_ASP_60	OD1	3.444
6N5E	B_ARG_90	NH2	B_ASP_60	OD2	2.891
6N5E	B_ARG_141	NH1	B_ASP_77	OD2	2.583
6N5E	B_ARG_141	NH2	B_ASP_77	OD2	3.726
6N5E	B_LYS_176	NZ	B_GLU_123	OE1	3.977
6N5E	B_LYS_176	NZ	B_GLU_123	OE2	2.397
6N5E	B_LYS_176	NZ	B_ASP_172	OD1	2.910
6N5E	B_ARG_261	NH2	B_GLU_119	OE1	3.905
6N5E	C_HIS_56	NE2	C_GLU_280	OE1	3.055
6N5E	C_ARG_57	NH2	C_GLU_82	OE1	3.487
6N5E	C_HIS_75	ND1	C_ASP_73	OD1	2.463
6N5E	C_HIS_75	ND1	C_ASP_73	OD2	3.598
6N5E	C_ARG_90	NH2	C_ASP_60	OD1	3.875
6N5E	C_ARG_90	NH2	C_ASP_60	OD2	3.604
6N5E	C_ARG_141	NH1	C_ASP_77	OD1	3.061
6N5E	C_ARG_141	NH1	C_ASP_77	OD2	2.463
6N5E	C_ARG_141	NH2	C_ASP_77	OD1	3.964
6N5E	C_LYS_176	NZ	C_GLU_123	OE2	2.465
6N5E	C_LYS_176	NZ	C_ASP_172	OD2	3.772
6N5E	C_ARG_207	NH1	C_ASP_241	OD1	3.296
6N5E	C_ARG_207	NH2	C_ASP_241	OD1	3.641
6N5E	C_LYS_259	NZ	C_GLU_119	OE1	3.550
6N5E	C_LYS_259	NZ	C_GLU_119	OE2	3.071
6N5E	C_ARG_261	NH2	C_GLU_119	OE1	3.746
6N5E	H_ARG_38	NH2	H_ASP_89	OD1	2.940
6N5E	H_ARG_44	NH2	H_GLU_42	OE1	3.999
6N5E	H_LYS_64	NZ	H_ASP_61	OD1	3.701
6N5E	H_ARG_66	NH1	H_ASP_89	OD2	3.385
6N5E	H_ARG_66	NH2	H_ASP_89	OD2	2.231
6N5E	H_LYS_214	NZ	H_ASP_216	OD1	2.519
6N5E	H_LYS_214	NZ	H_ASP_216	OD2	3.480
6N5E	H_LYS_217	NZ	I_GLU_126	OE2	2.748
6N5E	H_ARG_218	NH1	H_GLU_220	OE2	3.887
6N5E	H_ARG_218	NH2	H_GLU_220	OE2	2.803
6N5E	E_ARG_38	NH1	E_ASP_89	OD1	2.478
6N5E	E_ARG_38	NH2	E_GLU_46	OE1	3.997
6N5E	E_ARG_38	NH2	E_ASP_89	OD1	2.988
6N5E	E_LYS_64	NZ	E_ASP_61	OD1	2.968

6N5E	E_ARG_66	NH1	E_ASP_89	OD1	3.712
6N5E	E_ARG_66	NH1	E_ASP_89	OD2	2.993
6N5E	E_ARG_66	NH2	E_ASP_89	OD2	2.243
6N5E	E_ARG_75	NH1	E_ASP_72	OD2	3.012
6N5E	E_LYS_214	NZ	E_ASP_216	OD1	2.448
6N5E	E_LYS_214	NZ	E_ASP_216	OD2	3.601
6N5E	E_LYS_217	NZ	D_GLU_126	OE1	2.995
6N5E	E_LYS_217	NZ	D_GLU_126	OE2	2.272
6N5E	E_ARG_218	NH1	E_GLU_220	OE1	3.911
6N5E	E_ARG_218	NH1	E_GLU_220	OE2	2.563
6N5E	E_ARG_218	NH2	E_GLU_220	OE2	2.863
6N5E	E_LYS_222	NZ	D_GLU_126	OE1	3.688
6N5E	G_ARG_38	NH1	G_GLU_46	OE2	2.572
6N5E	G_ARG_38	NH2	G_ASP_89	OD1	3.217
6N5E	G_LYS_64	NZ	G_ASP_61	OD1	3.314
6N5E	G_LYS_64	NZ	G_ASP_61	OD2	3.572
6N5E	G_ARG_66	NH2	G_ASP_89	OD1	3.438
6N5E	G_ARG_66	NH2	G_ASP_89	OD2	3.428
6N5E	G_LYS_214	NZ	G_ASP_216	OD1	2.167
6N5E	G_LYS_217	NZ	F_GLU_126	OE2	3.351
6N5E	I_ARG_63	NH2	I_GLU_83	OE1	3.435
6N5E	I_ARG_63	NH2	I_ASP_84	OD1	2.372
6N5E	I_ARG_63	NH2	I_ASP_84	OD2	3.580
6N5E	I_LYS_189	NZ	I_GLU_186	OE1	2.386
6N5E	F_ARG_63	NH2	F_GLU_83	OE2	3.657
6N5E	F_ARG_63	NH2	F_ASP_84	OD1	2.359
6N5E	F_ARG_63	NH2	F_ASP_84	OD2	3.434
6N5E	D_ARG_63	NH2	D_ASP_84	OD1	2.410
6N5E	D_ARG_63	NH2	D_ASP_84	OD2	3.669

Table 870: 6N5E-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6N6B	A_ARG_118	NH1	A_GLU_119	OE2	3.576
6N6B	A_ARG_118	NH2	A_GLU_119	OE2	3.958
6N6B	A_ARG_118	NH2	A_GLU_425	OE1	2.971
6N6B	A_ARG_118	NH2	A_GLU_425	OE2	3.457
6N6B	A_LYS_128	NZ	A_GLU_162	OE1	3.900
6N6B	A_LYS_128	NZ	A_GLU_162	OE2	2.839
6N6B	A_ARG_152	NH2	A_ASP_198	OD1	3.511
6N6B	A_ARG_152	NH2	A_ASP_198	OD2	3.079
6N6B	A_ARG_156	NH1	A_GLU_119	OE1	3.104
6N6B	A_ARG_156	NH1	A_GLU_119	OE2	3.984
6N6B	A_ARG_156	NH2	A_GLU_119	OE1	2.722
6N6B	A_ARG_224	NH2	A_GLU_276	OE2	2.776
6N6B	A_ARG_283	NH2	A_ASP_355	OD2	3.221
6N6B	A_ARG_288	NH1	A_ASP_355	OD1	3.223
6N6B	A_ARG_288	NH1	A_ASP_355	OD2	3.540
6N6B	A_ARG_288	NH2	A_ASP_304	OD1	3.429
6N6B	A_ARG_288	NH2	A_ASP_304	OD2	3.339
6N6B	A_ARG_292	NH1	A_GLU_277	OE1	2.791
6N6B	A_ARG_292	NH1	A_GLU_277	OE2	3.678
6N6B	A_LYS_296	NZ	L_ASP_28	OD1	3.122
6N6B	A_LYS_296	NZ	L_ASP_28	OD2	3.000
6N6B	A_LYS_296	NZ	L_GLU_68	OE2	2.842
6N6B	A_ARG_300	NH1	A_ASP_324	OD1	3.902
6N6B	A_ARG_300	NH2	A_ASP_324	OD1	3.653
6N6B	A_LYS_344	NZ	A_GLU_369	OE1	2.725
6N6B	A_LYS_344	NZ	A_GLU_369	OE2	3.576
6N6B	A_ARG_364	NH1	A_ASP_330	OD1	3.580
6N6B	A_ARG_364	NH2	A_ASP_330	OD1	3.008
6N6B	A_ARG_364	NH2	A_ASP_330	OD2	3.328
6N6B	A_ARG_364	NH2	A_GLU_375	OE2	3.344
6N6B	A_ARG_394	NH2	A_GLU_375	OE1	2.841
6N6B	A_ARG_403	NH1	A_GLU_433	OE1	3.202
6N6B	A_ARG_403	NH2	A_GLU_432	OE1	3.164
6N6B	A_ARG_428	NH1	A_ASP_460	OD2	3.015
6N6B	A_ARG_428	NH2	A_GLU_433	OE1	3.667
6N6B	A_ARG_428	NH2	A_GLU_433	OE2	2.721
6N6B	A_LYS_431	NZ	K_ASP_101	OD1	3.959
6N6B	A_LYS_431	NZ	K_ASP_101	OD2	3.832
6N6B	K_ARG_39	NH1	K_ASP_90	OD1	2.897
6N6B	K_ARG_39	NH2	K_GLU_47	OE2	2.900
6N6B	K_ARG_39	NH2	K_ASP_90	OD1	3.537
6N6B	K_ARG_67	NH1	K_ASP_90	OD1	3.734
6N6B	K_ARG_67	NH1	K_ASP_90	OD2	2.854
6N6B	K_ARG_67	NH2	K_ASP_90	OD1	3.053
6N6B	K_ARG_67	NH2	K_ASP_90	OD2	3.660
6N6B	K_LYS_76	NZ	K_ASP_73	OD2	3.758
6N6B	K_ARG_98	NH2	K_ASP_106	OD1	3.697
6N6B	K_ARG_98	NH2	K_ASP_106	OD2	3.098
6N6B	K_HIS_169	NE2	L_ASP_167	OD1	3.738
6N6B	K_LYS_213	NZ	L_GLU_123	OE1	2.814
6N6B	K_LYS_213	NZ	L_GLU_123	OE2	3.044
6N6B	L_ARG_24	NH2	L_ASP_70	OD1	3.008
6N6B	L_ARG_24	NH2	L_ASP_70	OD2	3.990
6N6B	L_ARG_61	NH1	L_ASP_82	OD1	3.460
6N6B	L_ARG_61	NH1	L_ASP_82	OD2	2.694
6N6B	L_ARG_61	NH2	L_GLU_81	OE1	3.382
6N6B	L_ARG_61	NH2	L_ASP_82	OD1	3.002

6N6B	L_ARG_61	NH2	L_ASP_82	OD2	3.567
6N6B	L_LYS_103	NZ	L_ASP_165	OD2	3.902
6N6B	L_LYS_149	NZ	L_GLU_195	OE2	2.717
6N6B	L_ARG_155	NH1	L_GLU_185	OE2	3.590
6N6B	L_ARG_155	NH2	L_GLU_185	OE1	3.631
6N6B	L_ARG_155	NH2	L_GLU_185	OE2	2.832
6N6B	L_HIS_189	ND1	L_ASP_151	OD2	3.291
6N6B	L_ARG_211	NH1	L_GLU_187	OE1	3.717

Table 871: 6N6B-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6NB5	H_ARG_38	NH1	H_ASP_92	OD2	3.491
6NB5	H_ARG_38	NH2	H_GLU_46	OE1	2.486
6NB5	H_ARG_50	NH2	H_ASP_61	OD2	3.474
6NB5	H_LYS_52	NZ	H_GLU_56	OE2	3.363
6NB5	H_LYS_54	NZ	H_ASP_76	OD2	3.985
6NB5	H_ARG_69	NH1	H_ASP_92	OD1	2.701
6NB5	H_ARG_69	NH1	H_ASP_92	OD2	3.806
6NB5	H_ARG_69	NH2	H_ASP_92	OD1	3.650
6NB5	H_ARG_69	NH2	H_ASP_92	OD2	3.432
6NB5	H_LYS_78	NZ	H_ASP_75	OD2	3.471
6NB5	H_LYS_157	NZ	H_ASP_158	OD1	2.929
6NB5	H_LYS_157	NZ	H_ASP_158	OD2	3.584
6NB5	H_LYS_220	NZ	H_ASP_222	OD1	3.861
6NB5	H_LYS_223	NZ	L_GLU_126	OE1	3.229
6NB5	H_LYS_223	NZ	L_GLU_126	OE2	2.760
6NB5	H_ARG_224	NH2	H_GLU_226	OE2	3.546
6NB5	L_ARG_63	NH2	L_ASP_84	OD1	3.374
6NB5	L_ARG_63	NH2	L_ASP_84	OD2	3.503
6NB5	L_LYS_68	NZ	L_ASP_33	OD2	2.578
6NB5	L_LYS_113	NZ	L_GLU_201	OE1	2.506
6NB5	L_ARG_38	NH1	L_ASP_92	OD1	3.159
6NB5	L_ARG_38	NH2	L_GLU_46	OE1	2.869
6NB5	L_ARG_38	NH2	L_ASP_92	OD1	3.985
6NB5	L_ARG_50	NH1	L_ASP_61	OD2	3.493
6NB5	L_ARG_50	NH2	L_ASP_61	OD1	3.774
6NB5	L_ARG_69	NH1	L_ASP_92	OD1	2.838
6NB5	L_ARG_69	NH1	L_ASP_92	OD2	2.846
6NB5	L_ARG_69	NH2	L_ASP_92	OD1	3.249
6NB5	L_LYS_157	NZ	L_ASP_158	OD1	3.106
6NB5	L_LYS_157	NZ	M_GLU_127	OE2	3.828
6NB5	L_LYS_223	NZ	M_GLU_126	OE2	3.316
6NB5	M_ARG_63	NH1	M_ASP_84	OD1	2.715
6NB5	M_ARG_63	NH1	M_ASP_84	OD2	3.713
6NB5	M_ARG_63	NH2	M_ASP_84	OD1	3.329
6NB5	M_ARG_63	NH2	M_ASP_84	OD2	2.729
6NB5	M_LYS_107	NZ	M_GLU_85	OE1	3.669
6NB5	M_LYS_152	NZ	M_GLU_206	OE1	3.241
6NB5	M_LYS_152	NZ	M_GLU_206	OE2	3.589
6NB5	M_ARG_192	NH1	M_ASP_154	OD2	3.102

Table 872: 6NB5-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6NB8	H_ARG_38	NH1	H_ASP_90	OD1	2.818
6NB8	H_ARG_38	NH2	H_ASP_90	OD1	3.793
6NB8	H_ARG_67	NH1	H_ASP_90	OD1	3.807
6NB8	H_ARG_67	NH1	H_ASP_90	OD2	2.824
6NB8	H_ARG_67	NH2	H_ASP_90	OD1	3.012
6NB8	H_ARG_67	NH2	H_ASP_90	OD2	3.450
6NB8	H_ARG_72	NH2	H_ASP_74	OD1	3.534
6NB8	H_LYS_157	NZ	H_ASP_158	OD1	3.474
6NB8	H_LYS_223	NZ	L_GLU_128	OE1	2.783
6NB8	H_LYS_223	NZ	L_GLU_128	OE2	3.341
6NB8	L_ARG_51	NH1	H_ASP_113	OD1	2.821
6NB8	L_ARG_51	NH2	H_ASP_113	OD1	3.921
6NB8	L_ARG_51	NH2	H_ASP_115	OD1	3.423
6NB8	L_ARG_51	NH2	L_ASP_60	OD1	2.805
6NB8	L_ARG_51	NH2	L_ASP_60	OD2	3.641
6NB8	L_ARG_66	NH2	L_ASP_87	OD1	2.740
6NB8	L_ARG_66	NH2	L_ASP_87	OD2	3.561
6NB8	L_LYS_108	NZ	L_GLU_170	OE1	2.684
6NB8	L_LYS_108	NZ	L_GLU_170	OE2	3.357
6NB8	L_LYS_154	NZ	L_GLU_200	OE1	3.899
6NB8	L_LYS_154	NZ	L_GLU_200	OE2	2.642
6NB8	L_LYS_188	NZ	L_GLU_192	OE1	3.516
6NB8	L_LYS_188	NZ	L_GLU_192	OE2	2.963
6NB8	L_LYS_193	NZ	L_ASP_190	OD1	3.067
6NB8	L_HIS_194	ND1	L_ASP_156	OD2	3.106

Table 873: 6NB8-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6NC2	A_LYS_46	NZ	B_ASP_636	OD1	3.909
6NC2	A_ARG_59	NH1	A_ASP_57	OD1	2.814
6NC2	A_ARG_59	NH1	A_ASP_57	OD2	3.348
6NC2	A_ARG_59	NH2	A_ASP_57	OD1	3.635
6NC2	A_ARG_59	NH2	A_ASP_57	OD2	2.766
6NC2	A_LYS_155	NZ	A_ASP_133	OD1	2.379
6NC2	A_LYS_231	NZ	A_GLU_268	OE2	2.886
6NC2	A_LYS_232	NZ	A_GLU_269	OE1	3.666
6NC2	A_LYS_232	NZ	A_GLU_269	OE2	2.418
6NC2	A_LYS_282	NZ	A_ASP_279	OD2	2.788
6NC2	A_ARG_298	NH1	A_GLU_381	OE1	2.865
6NC2	A_ARG_298	NH1	A_GLU_381	OE2	2.959
6NC2	A_LYS_305	NZ	A_GLU_172	OE1	2.574
6NC2	A_LYS_305	NZ	A_GLU_172	OE2	3.869
6NC2	A_ARG_327	NH2	A_ASP_325	OD2	3.126
6NC2	A_LYS_337	NZ	A_GLU_293	OE1	2.932
6NC2	A_LYS_343	NZ	A_ASP_340	OD1	3.486
6NC2	A_LYS_348	NZ	A_GLU_269	OE1	2.894
6NC2	A_LYS_348	NZ	A_GLU_269	OE2	3.758
6NC2	A_LYS_348	NZ	A_GLU_351	OE2	3.738
6NC2	A_ARG_419	NH2	A_GLU_153	OE2	3.652
6NC2	A_LYS_421	NZ	A_GLU_370	OE2	2.787
6NC2	A_ARG_456	NH2	A_GLU_466	OE1	2.887
6NC2	A_ARG_456	NH2	A_GLU_466	OE2	3.857
6NC2	A_LYS_460	NZ	A_GLU_466	OE1	3.544
6NC2	A_ARG_476	NH1	A_GLU_102	OE1	3.959
6NC2	A_ARG_476	NH1	A_GLU_102	OE2	2.882
6NC2	A_ARG_476	NH2	A_ASP_474	OD1	3.950
6NC2	A_ARG_476	NH2	A_ASP_474	OD2	2.809
6NC2	A_ARG_480	NH2	A_ASP_477	OD1	3.009
6NC2	A_ARG_480	NH2	A_ASP_477	OD2	3.559
6NC2	A_LYS_487	NZ	A_GLU_47	OE1	3.379
6NC2	A_LYS_487	NZ	A_GLU_91	OE1	3.334
6NC2	A_LYS_490	NZ	A_GLU_492	OE1	3.377
6NC2	A_LYS_490	NZ	A_GLU_492	OE2	2.629
6NC2	A_LYS_500	NZ	I_ASP_664	OD1	2.780
6NC2	A_LYS_500	NZ	I_ASP_664	OD2	3.992
6NC2	A_ARG_503	NH1	B_GLU_654	OE1	3.759
6NC2	A_ARG_503	NH1	B_GLU_654	OE2	3.172
6NC2	B_ARG_542	NH1	I_GLU_647	OE1	2.800
6NC2	B_ARG_542	NH1	I_ASP_648	OD1	3.191
6NC2	B_ARG_542	NH2	I_ASP_648	OD1	3.498
6NC2	B_LYS_574	NZ	A_ASP_107	OD1	2.510
6NC2	B_LYS_574	NZ	A_ASP_107	OD2	3.688
6NC2	B_LYS_588	NZ	B_ASP_589	OD1	2.875
6NC2	B_LYS_617	NZ	B_GLU_634	OE2	2.908
6NC2	H_LYS_30	NZ	H_ASP_31	OD1	3.266
6NC2	H_LYS_30	NZ	H_ASP_31	OD2	2.768
6NC2	H_HIS_35	NE2	H_ASP_95	OD1	2.705
6NC2	H_ARG_38	NH1	H_ASP_86	OD1	2.970
6NC2	H_ARG_38	NH2	H_GLU_46	OE1	3.107
6NC2	H_ARG_38	NH2	H_GLU_46	OE2	3.826
6NC2	H_ARG_66	NH2	H_ASP_86	OD1	3.009
6NC2	H_ARG_66	NH2	H_ASP_86	OD2	3.729
6NC2	H_LYS_75	NZ	H_ASP_72	OD2	3.903
6NC2	H_ARG_82B	NH1	H_ASP_82A	OD2	2.740
6NC2	H_ARG_83	NH2	H_GLU_85	OE1	3.718

6NC2	H_ARG_83	NH2	H_GLU_85	OE2	3.237
6NC2	H_LYS_94	NZ	H_ASP_101	OD1	3.921
6NC2	H_ARG_96	NH1	L_ASP_50	OD1	3.082
6NC2	H_ARG_96	NH1	L_ASP_50	OD2	3.706
6NC2	H_ARG_96	NH2	L_ASP_50	OD1	3.892
6NC2	H_ARG_96	NH2	L_ASP_50	OD2	3.158
6NC2	H_ARG_99	NH2	H_ASP_31	OD1	3.800
6NC2	L_LYS_30	NZ	L_ASP_28	OD2	2.906
6NC2	L_ARG_37	NH1	L_ASP_82	OD1	3.215
6NC2	L_ARG_37	NH2	L_GLU_45	OE1	2.891
6NC2	L_ARG_37	NH2	L_GLU_45	OE2	3.981
6NC2	L_LYS_42	NZ	L_GLU_45	OE1	3.768
6NC2	L_LYS_103	NZ	L_GLU_105	OE1	3.671
6NC2	C_LYS_46	NZ	L_ASP_636	OD1	3.909
6NC2	C_ARG_59	NH1	C_ASP_57	OD1	2.814
6NC2	C_ARG_59	NH1	C_ASP_57	OD2	3.348
6NC2	C_ARG_59	NH2	C_ASP_57	OD1	3.635
6NC2	C_ARG_59	NH2	C_ASP_57	OD2	2.765
6NC2	C_LYS_155	NZ	C_ASP_133	OD1	2.379
6NC2	C_LYS_231	NZ	C_GLU_268	OE2	2.886
6NC2	C_LYS_232	NZ	C_GLU_269	OE1	3.666
6NC2	C_LYS_232	NZ	C_GLU_269	OE2	2.418
6NC2	C_LYS_282	NZ	C_ASP_279	OD2	2.788
6NC2	C_ARG_298	NH1	C_GLU_381	OE1	2.865
6NC2	C_ARG_298	NH1	C_GLU_381	OE2	2.960
6NC2	C_LYS_305	NZ	C_GLU_172	OE1	2.574
6NC2	C_LYS_305	NZ	C_GLU_172	OE2	3.869
6NC2	C_ARG_327	NH2	C_ASP_325	OD2	3.126
6NC2	C_LYS_337	NZ	C_GLU_293	OE1	2.932
6NC2	C_LYS_343	NZ	C_ASP_340	OD1	3.486
6NC2	C_LYS_348	NZ	C_GLU_269	OE1	2.894
6NC2	C_LYS_348	NZ	C_GLU_269	OE2	3.757
6NC2	C_LYS_348	NZ	C_GLU_351	OE2	3.738
6NC2	C_ARG_419	NH2	C_GLU_153	OE2	3.652
6NC2	C_LYS_421	NZ	C_GLU_370	OE2	2.787
6NC2	C_ARG_456	NH2	C_GLU_466	OE1	2.887
6NC2	C_ARG_456	NH2	C_GLU_466	OE2	3.857
6NC2	C_LYS_460	NZ	C_GLU_466	OE1	3.544
6NC2	C_ARG_476	NH1	C_GLU_102	OE1	3.959
6NC2	C_ARG_476	NH1	C_GLU_102	OE2	2.882
6NC2	C_ARG_476	NH2	C_ASP_474	OD1	3.950
6NC2	C_ARG_476	NH2	C_ASP_474	OD2	2.809
6NC2	C_ARG_480	NH2	C_ASP_477	OD1	3.009
6NC2	C_ARG_480	NH2	C_ASP_477	OD2	3.559
6NC2	C_LYS_487	NZ	C_GLU_47	OE1	3.379
6NC2	C_LYS_487	NZ	C_GLU_91	OE1	3.334
6NC2	C_LYS_490	NZ	C_GLU_492	OE1	3.377
6NC2	C_LYS_490	NZ	C_GLU_492	OE2	2.629
6NC2	C_LYS_500	NZ	J_ASP_664	OD1	2.780
6NC2	C_LYS_500	NZ	J_ASP_664	OD2	3.991
6NC2	C_ARG_503	NH1	L_GLU_654	OE1	3.760
6NC2	C_ARG_503	NH1	L_GLU_654	OE2	3.173
6NC2	L_ARG_542	NH1	J_GLU_647	OE1	2.801
6NC2	L_ARG_542	NH1	J_ASP_648	OD1	3.190
6NC2	L_ARG_542	NH2	J_ASP_648	OD1	3.498
6NC2	L_LYS_574	NZ	C_ASP_107	OD1	2.510
6NC2	L_LYS_574	NZ	C_ASP_107	OD2	3.688
6NC2	L_LYS_588	NZ	L_ASP_589	OD1	2.875

6NC2	I_LYS_617	NZ	I_GLU_634	OE2	2.908
6NC2	O_LYS_30	NZ	O_ASP_31	OD1	3.267
6NC2	O_LYS_30	NZ	O_ASP_31	OD2	2.768
6NC2	O_HIS_35	NE2	O_ASP_95	OD1	2.705
6NC2	O_ARG_38	NH1	O_ASP_86	OD1	2.971
6NC2	O_ARG_38	NH2	O_GLU_46	OE1	3.107
6NC2	O_ARG_38	NH2	O_GLU_46	OE2	3.826
6NC2	O_ARG_66	NH2	O_ASP_86	OD1	3.008
6NC2	O_ARG_66	NH2	O_ASP_86	OD2	3.729
6NC2	O_LYS_75	NZ	O_ASP_72	OD2	3.903
6NC2	O_ARG_82B	NH1	O_ASP_82A	OD2	2.740
6NC2	O_ARG_83	NH2	O_GLU_85	OE1	3.718
6NC2	O_ARG_83	NH2	O_GLU_85	OE2	3.238
6NC2	O_LYS_94	NZ	O_ASP_101	OD1	3.921
6NC2	O_ARG_96	NH1	T_ASP_50	OD1	3.082
6NC2	O_ARG_96	NH1	T_ASP_50	OD2	3.706
6NC2	O_ARG_96	NH2	T_ASP_50	OD1	3.892
6NC2	O_ARG_96	NH2	T_ASP_50	OD2	3.158
6NC2	O_ARG_99	NH2	O_ASP_31	OD1	3.799
6NC2	T_LYS_30	NZ	T_ASP_28	OD2	2.905
6NC2	T_ARG_37	NH1	T_ASP_82	OD1	3.216
6NC2	T_ARG_37	NH2	T_GLU_45	OE1	2.891
6NC2	T_ARG_37	NH2	T_GLU_45	OE2	3.981
6NC2	T_LYS_42	NZ	T_GLU_45	OE1	3.769
6NC2	T_LYS_103	NZ	T_GLU_105	OE1	3.670
6NC2	D_LYS_46	NZ	J_ASP_636	OD1	3.909
6NC2	D_ARG_59	NH1	D_ASP_57	OD1	2.814
6NC2	D_ARG_59	NH1	D_ASP_57	OD2	3.348
6NC2	D_ARG_59	NH2	D_ASP_57	OD1	3.635
6NC2	D_ARG_59	NH2	D_ASP_57	OD2	2.766
6NC2	D_LYS_155	NZ	D_ASP_133	OD1	2.379
6NC2	D_LYS_231	NZ	D_GLU_268	OE2	2.885
6NC2	D_LYS_232	NZ	D_GLU_269	OE1	3.666
6NC2	D_LYS_232	NZ	D_GLU_269	OE2	2.418
6NC2	D_LYS_282	NZ	D_ASP_279	OD2	2.787
6NC2	D_ARG_298	NH1	D_GLU_381	OE1	2.864
6NC2	D_ARG_298	NH1	D_GLU_381	OE2	2.959
6NC2	D_LYS_305	NZ	D_GLU_172	OE1	2.575
6NC2	D_LYS_305	NZ	D_GLU_172	OE2	3.868
6NC2	D_ARG_327	NH2	D_ASP_325	OD2	3.127
6NC2	D_LYS_337	NZ	D_GLU_293	OE1	2.931
6NC2	D_LYS_343	NZ	D_ASP_340	OD1	3.486
6NC2	D_LYS_348	NZ	D_GLU_269	OE1	2.894
6NC2	D_LYS_348	NZ	D_GLU_269	OE2	3.758
6NC2	D_LYS_348	NZ	D_GLU_351	OE2	3.738
6NC2	D_ARG_419	NH2	D_GLU_153	OE2	3.652
6NC2	D_LYS_421	NZ	D_GLU_370	OE2	2.786
6NC2	D_ARG_456	NH2	D_GLU_466	OE1	2.886
6NC2	D_ARG_456	NH2	D_GLU_466	OE2	3.857
6NC2	D_LYS_460	NZ	D_GLU_466	OE1	3.544
6NC2	D_ARG_476	NH1	D_GLU_102	OE1	3.959
6NC2	D_ARG_476	NH1	D_GLU_102	OE2	2.881
6NC2	D_ARG_476	NH2	D_ASP_474	OD1	3.950
6NC2	D_ARG_476	NH2	D_ASP_474	OD2	2.809
6NC2	D_ARG_480	NH2	D_ASP_477	OD1	3.009
6NC2	D_ARG_480	NH2	D_ASP_477	OD2	3.559
6NC2	D_LYS_487	NZ	D_GLU_47	OE1	3.379
6NC2	D_LYS_487	NZ	D_GLU_91	OE1	3.334

6NC2	D_LYS_490	NZ	D_GLU_492	OE1	3.377
6NC2	D_LYS_490	NZ	D_GLU_492	OE2	2.630
6NC2	D_LYS_500	NZ	B_ASP_664	OD1	2.780
6NC2	D_LYS_500	NZ	B_ASP_664	OD2	3.992
6NC2	D_ARG_503	NH1	J_GLU_654	OE1	3.759
6NC2	D_ARG_503	NH1	J_GLU_654	OE2	3.173
6NC2	J_ARG_542	NH1	B_GLU_647	OE1	2.800
6NC2	J_ARG_542	NH1	B_ASP_648	OD1	3.191
6NC2	J_ARG_542	NH2	B_ASP_648	OD1	3.498
6NC2	J_LYS_574	NZ	D_ASP_107	OD1	2.510
6NC2	J_LYS_574	NZ	D_ASP_107	OD2	3.688
6NC2	J_LYS_588	NZ	J_ASP_589	OD1	2.875
6NC2	J_LYS_617	NZ	J_GLU_634	OE2	2.908
6NC2	P_LYS_30	NZ	P_ASP_31	OD1	3.267
6NC2	P_LYS_30	NZ	P_ASP_31	OD2	2.768
6NC2	P_HIS_35	NE2	P_ASP_95	OD1	2.704
6NC2	P_ARG_38	NH1	P_ASP_86	OD1	2.970
6NC2	P_ARG_38	NH2	P_GLU_46	OE1	3.107
6NC2	P_ARG_38	NH2	P_GLU_46	OE2	3.826
6NC2	P_ARG_66	NH2	P_ASP_86	OD1	3.009
6NC2	P_ARG_66	NH2	P_ASP_86	OD2	3.730
6NC2	P_LYS_75	NZ	P_ASP_72	OD2	3.903
6NC2	P_ARG_82B	NH1	P_ASP_82A	OD2	2.740
6NC2	P_ARG_83	NH2	P_GLU_85	OE1	3.718
6NC2	P_ARG_83	NH2	P_GLU_85	OE2	3.237
6NC2	P_LYS_94	NZ	P_ASP_101	OD1	3.921
6NC2	P_ARG_96	NH1	U_ASP_50	OD1	3.083
6NC2	P_ARG_96	NH1	U_ASP_50	OD2	3.706
6NC2	P_ARG_96	NH2	U_ASP_50	OD1	3.893
6NC2	P_ARG_96	NH2	U_ASP_50	OD2	3.158
6NC2	P_ARG_99	NH2	P_ASP_31	OD1	3.800
6NC2	U_LYS_30	NZ	U_ASP_28	OD2	2.905
6NC2	U_ARG_37	NH1	U_ASP_82	OD1	3.215
6NC2	U_ARG_37	NH2	U_GLU_45	OE1	2.891
6NC2	U_ARG_37	NH2	U_GLU_45	OE2	3.981
6NC2	U_LYS_42	NZ	U_GLU_45	OE1	3.768
6NC2	U_LYS_103	NZ	U_GLU_105	OE1	3.671
6NC2	E_LYS_46	NZ	K_ASP_636	OD1	3.909
6NC2	E_ARG_59	NH1	E_ASP_57	OD1	2.814
6NC2	E_ARG_59	NH1	E_ASP_57	OD2	3.348
6NC2	E_ARG_59	NH2	E_ASP_57	OD1	3.635
6NC2	E_ARG_59	NH2	E_ASP_57	OD2	2.766
6NC2	E_LYS_155	NZ	E_ASP_133	OD1	2.379
6NC2	E_LYS_231	NZ	E_GLU_268	OE2	2.886
6NC2	E_LYS_232	NZ	E_GLU_269	OE1	3.666
6NC2	E_LYS_232	NZ	E_GLU_269	OE2	2.418
6NC2	E_LYS_282	NZ	E_ASP_279	OD2	2.788
6NC2	E_ARG_298	NH1	E_GLU_381	OE1	2.865
6NC2	E_ARG_298	NH1	E_GLU_381	OE2	2.959
6NC2	E_LYS_305	NZ	E_GLU_172	OE1	2.574
6NC2	E_LYS_305	NZ	E_GLU_172	OE2	3.869
6NC2	E_ARG_327	NH2	E_ASP_325	OD2	3.126
6NC2	E_LYS_337	NZ	E_GLU_293	OE1	2.932
6NC2	E_LYS_343	NZ	E_ASP_340	OD1	3.486
6NC2	E_LYS_348	NZ	E_GLU_269	OE1	2.894
6NC2	E_LYS_348	NZ	E_GLU_269	OE2	3.758
6NC2	E_LYS_348	NZ	E_GLU_351	OE2	3.738
6NC2	E_ARG_419	NH2	E_GLU_153	OE2	3.652

6NC2	E_LYS_421	NZ	E_GLU_370	OE2	2.787
6NC2	E_ARG_456	NH2	E_GLU_466	OE1	2.887
6NC2	E_ARG_456	NH2	E_GLU_466	OE2	3.857
6NC2	E_LYS_460	NZ	E_GLU_466	OE1	3.544
6NC2	E_ARG_476	NH1	E_GLU_102	OE1	3.959
6NC2	E_ARG_476	NH1	E_GLU_102	OE2	2.882
6NC2	E_ARG_476	NH2	E_ASP_474	OD1	3.950
6NC2	E_ARG_476	NH2	E_ASP_474	OD2	2.809
6NC2	E_ARG_480	NH2	E_ASP_477	OD1	3.009
6NC2	E_ARG_480	NH2	E_ASP_477	OD2	3.559
6NC2	E_LYS_487	NZ	E_GLU_47	OE1	3.379
6NC2	E_LYS_487	NZ	E_GLU_91	OE1	3.334
6NC2	E_LYS_490	NZ	E_GLU_492	OE1	3.377
6NC2	E_LYS_490	NZ	E_GLU_492	OE2	2.629
6NC2	E_LYS_500	NZ	M_ASP_664	OD1	2.780
6NC2	E_LYS_500	NZ	M_ASP_664	OD2	3.992
6NC2	E_ARG_503	NH1	K_GLU_654	OE1	3.759
6NC2	E_ARG_503	NH1	K_GLU_654	OE2	3.172
6NC2	K_ARG_542	NH1	M_GLU_647	OE1	2.800
6NC2	K_ARG_542	NH1	M_ASP_648	OD1	3.191
6NC2	K_ARG_542	NH2	M_ASP_648	OD1	3.498
6NC2	K_LYS_574	NZ	E_ASP_107	OD1	2.510
6NC2	K_LYS_574	NZ	E_ASP_107	OD2	3.688
6NC2	K_LYS_588	NZ	K_ASP_589	OD1	2.875
6NC2	K_LYS_617	NZ	K_GLU_634	OE2	2.908
6NC2	Q_LYS_30	NZ	Q_ASP_31	OD1	3.266
6NC2	Q_LYS_30	NZ	Q_ASP_31	OD2	2.768
6NC2	Q_HIS_35	NE2	Q_ASP_95	OD1	2.705
6NC2	Q_ARG_38	NH1	Q_ASP_86	OD1	2.970
6NC2	Q_ARG_38	NH2	Q_GLU_46	OE1	3.107
6NC2	Q_ARG_38	NH2	Q_GLU_46	OE2	3.826
6NC2	Q_ARG_66	NH2	Q_ASP_86	OD1	3.009
6NC2	Q_ARG_66	NH2	Q_ASP_86	OD2	3.729
6NC2	Q_LYS_75	NZ	Q_ASP_72	OD2	3.903
6NC2	Q_ARG_82B	NH1	Q_ASP_82A	OD2	2.740
6NC2	Q_ARG_83	NH2	Q_GLU_85	OE1	3.718
6NC2	Q_ARG_83	NH2	Q_GLU_85	OE2	3.237
6NC2	Q_LYS_94	NZ	Q_ASP_101	OD1	3.921
6NC2	Q_ARG_96	NH1	V_ASP_50	OD1	3.082
6NC2	Q_ARG_96	NH1	V_ASP_50	OD2	3.706
6NC2	Q_ARG_96	NH2	V_ASP_50	OD1	3.892
6NC2	Q_ARG_96	NH2	V_ASP_50	OD2	3.158
6NC2	Q_ARG_99	NH2	Q_ASP_31	OD1	3.800
6NC2	V_LYS_30	NZ	V_ASP_28	OD2	2.906
6NC2	V_ARG_37	NH1	V_ASP_82	OD1	3.215
6NC2	V_ARG_37	NH2	V_GLU_45	OE1	2.891
6NC2	V_ARG_37	NH2	V_GLU_45	OE2	3.981
6NC2	V_LYS_42	NZ	V_GLU_45	OE1	3.768
6NC2	V_LYS_103	NZ	V_GLU_105	OE1	3.671
6NC2	F_LYS_46	NZ	M_ASP_636	OD1	3.909
6NC2	F_ARG_59	NH1	F_ASP_57	OD1	2.814
6NC2	F_ARG_59	NH1	F_ASP_57	OD2	3.348
6NC2	F_ARG_59	NH2	F_ASP_57	OD1	3.635
6NC2	F_ARG_59	NH2	F_ASP_57	OD2	2.765
6NC2	F_LYS_155	NZ	F_ASP_133	OD1	2.379
6NC2	F_LYS_231	NZ	F_GLU_268	OE2	2.886
6NC2	F_LYS_232	NZ	F_GLU_269	OE1	3.666
6NC2	F_LYS_232	NZ	F_GLU_269	OE2	2.418

6NC2	F_LYS_282	NZ	F_ASP_279	OD2	2.788
6NC2	F_ARG_298	NH1	F_GLU_381	OE1	2.865
6NC2	F_ARG_298	NH1	F_GLU_381	OE2	2.960
6NC2	F_LYS_305	NZ	F_GLU_172	OE1	2.574
6NC2	F_LYS_305	NZ	F_GLU_172	OE2	3.869
6NC2	F_ARG_327	NH2	F_ASP_325	OD2	3.127
6NC2	F_LYS_337	NZ	F_GLU_293	OE1	2.932
6NC2	F_LYS_343	NZ	F_ASP_340	OD1	3.486
6NC2	F_LYS_348	NZ	F_GLU_269	OE1	2.894
6NC2	F_LYS_348	NZ	F_GLU_269	OE2	3.757
6NC2	F_LYS_348	NZ	F_GLU_351	OE2	3.738
6NC2	F_ARG_419	NH2	F_GLU_153	OE2	3.653
6NC2	F_LYS_421	NZ	F_GLU_370	OE2	2.787
6NC2	F_ARG_456	NH2	F_GLU_466	OE1	2.887
6NC2	F_ARG_456	NH2	F_GLU_466	OE2	3.857
6NC2	F_LYS_460	NZ	F_GLU_466	OE1	3.544
6NC2	F_ARG_476	NH1	F_GLU_102	OE1	3.959
6NC2	F_ARG_476	NH1	F_GLU_102	OE2	2.882
6NC2	F_ARG_476	NH2	F_ASP_474	OD1	3.950
6NC2	F_ARG_476	NH2	F_ASP_474	OD2	2.809
6NC2	F_ARG_480	NH2	F_ASP_477	OD1	3.009
6NC2	F_ARG_480	NH2	F_ASP_477	OD2	3.559
6NC2	F_LYS_487	NZ	F_GLU_47	OE1	3.379
6NC2	F_LYS_487	NZ	F_GLU_91	OE1	3.334
6NC2	F_LYS_490	NZ	F_GLU_492	OE1	3.377
6NC2	F_LYS_490	NZ	F_GLU_492	OE2	2.629
6NC2	F_LYS_500	NZ	N_ASP_664	OD1	2.780
6NC2	F_LYS_500	NZ	N_ASP_664	OD2	3.991
6NC2	F_ARG_503	NH1	M_GLU_654	OE1	3.759
6NC2	F_ARG_503	NH1	M_GLU_654	OE2	3.173
6NC2	M_ARG_542	NH1	N_GLU_647	OE1	2.801
6NC2	M_ARG_542	NH1	N_ASP_648	OD1	3.191
6NC2	M_ARG_542	NH2	N_ASP_648	OD1	3.498
6NC2	M_LYS_574	NZ	F_ASP_107	OD1	2.510
6NC2	M_LYS_574	NZ	F_ASP_107	OD2	3.688
6NC2	M_LYS_588	NZ	M_ASP_589	OD1	2.875
6NC2	M_LYS_617	NZ	M_GLU_634	OE2	2.907
6NC2	R_LYS_30	NZ	R_ASP_31	OD1	3.267
6NC2	R_LYS_30	NZ	R_ASP_31	OD2	2.768
6NC2	R_HIS_35	NE2	R_ASP_95	OD1	2.705
6NC2	R_ARG_38	NH1	R_ASP_86	OD1	2.970
6NC2	R_ARG_38	NH2	R_GLU_46	OE1	3.107
6NC2	R_ARG_38	NH2	R_GLU_46	OE2	3.826
6NC2	R_ARG_66	NH2	R_ASP_86	OD1	3.009
6NC2	R_ARG_66	NH2	R_ASP_86	OD2	3.729
6NC2	R_LYS_75	NZ	R_ASP_72	OD2	3.903
6NC2	R_ARG_82B	NH1	R_ASP_82A	OD2	2.739
6NC2	R_ARG_83	NH2	R_GLU_85	OE1	3.718
6NC2	R_ARG_83	NH2	R_GLU_85	OE2	3.238
6NC2	R_LYS_94	NZ	R_ASP_101	OD1	3.921
6NC2	R_ARG_96	NH1	W_ASP_50	OD1	3.082
6NC2	R_ARG_96	NH1	W_ASP_50	OD2	3.706
6NC2	R_ARG_96	NH2	W_ASP_50	OD1	3.892
6NC2	R_ARG_96	NH2	W_ASP_50	OD2	3.157
6NC2	R_ARG_99	NH2	R_ASP_31	OD1	3.799
6NC2	W_LYS_30	NZ	W_ASP_28	OD2	2.905
6NC2	W_ARG_37	NH1	W_ASP_82	OD1	3.215
6NC2	W_ARG_37	NH2	W_GLU_45	OE1	2.891

6NC2	W_ARG_37	NH2	W_GLU_45	OE2	3.981
6NC2	W_LYS_42	NZ	W_GLU_45	OE1	3.769
6NC2	W_LYS_103	NZ	W_GLU_105	OE1	3.671
6NC2	G_LYS_46	NZ	N_ASP_636	OD1	3.909
6NC2	G_ARG_59	NH1	G_ASP_57	OD1	2.814
6NC2	G_ARG_59	NH1	G_ASP_57	OD2	3.348
6NC2	G_ARG_59	NH2	G_ASP_57	OD1	3.635
6NC2	G_ARG_59	NH2	G_ASP_57	OD2	2.766
6NC2	G_LYS_155	NZ	G_ASP_133	OD1	2.379
6NC2	G_LYS_231	NZ	G_GLU_268	OE2	2.886
6NC2	G_LYS_232	NZ	G_GLU_269	OE1	3.666
6NC2	G_LYS_232	NZ	G_GLU_269	OE2	2.418
6NC2	G_LYS_282	NZ	G_ASP_279	OD2	2.787
6NC2	G_ARG_298	NH1	G_GLU_381	OE1	2.864
6NC2	G_ARG_298	NH1	G_GLU_381	OE2	2.959
6NC2	G_LYS_305	NZ	G_GLU_172	OE1	2.575
6NC2	G_LYS_305	NZ	G_GLU_172	OE2	3.868
6NC2	G_ARG_327	NH2	G_ASP_325	OD2	3.127
6NC2	G_LYS_337	NZ	G_GLU_293	OE1	2.931
6NC2	G_LYS_343	NZ	G_ASP_340	OD1	3.486
6NC2	G_LYS_348	NZ	G_GLU_269	OE1	2.894
6NC2	G_LYS_348	NZ	G_GLU_269	OE2	3.758
6NC2	G_LYS_348	NZ	G_GLU_351	OE2	3.738
6NC2	G_ARG_419	NH2	G_GLU_153	OE2	3.652
6NC2	G_LYS_421	NZ	G_GLU_370	OE2	2.786
6NC2	G_ARG_456	NH2	G_GLU_466	OE1	2.887
6NC2	G_ARG_456	NH2	G_GLU_466	OE2	3.857
6NC2	G_LYS_460	NZ	G_GLU_466	OE1	3.544
6NC2	G_ARG_476	NH1	G_GLU_102	OE1	3.959
6NC2	G_ARG_476	NH1	G_GLU_102	OE2	2.881
6NC2	G_ARG_476	NH2	G_ASP_474	OD1	3.950
6NC2	G_ARG_476	NH2	G_ASP_474	OD2	2.809
6NC2	G_ARG_480	NH2	G_ASP_477	OD1	3.009
6NC2	G_ARG_480	NH2	G_ASP_477	OD2	3.559
6NC2	G_LYS_487	NZ	G_GLU_47	OE1	3.379
6NC2	G_LYS_487	NZ	G_GLU_91	OE1	3.334
6NC2	G_LYS_490	NZ	G_GLU_492	OE1	3.377
6NC2	G_LYS_490	NZ	G_GLU_492	OE2	2.630
6NC2	G_LYS_500	NZ	K_ASP_664	OD1	2.780
6NC2	G_LYS_500	NZ	K_ASP_664	OD2	3.992
6NC2	G_ARG_503	NH1	N_GLU_654	OE1	3.759
6NC2	G_ARG_503	NH1	N_GLU_654	OE2	3.173
6NC2	N_ARG_542	NH1	K_GLU_647	OE1	2.800
6NC2	N_ARG_542	NH1	K_ASP_648	OD1	3.191
6NC2	N_ARG_542	NH2	K_ASP_648	OD1	3.498
6NC2	N_LYS_574	NZ	G_ASP_107	OD1	2.510
6NC2	N_LYS_574	NZ	G_ASP_107	OD2	3.688
6NC2	N_LYS_588	NZ	N_ASP_589	OD1	2.875
6NC2	N_LYS_617	NZ	N_GLU_634	OE2	2.908
6NC2	S_LYS_30	NZ	S_ASP_31	OD1	3.267
6NC2	S_LYS_30	NZ	S_ASP_31	OD2	2.768
6NC2	S_HIS_35	NE2	S_ASP_95	OD1	2.704
6NC2	S_ARG_38	NH1	S_ASP_86	OD1	2.970
6NC2	S_ARG_38	NH2	S_GLU_46	OE1	3.107
6NC2	S_ARG_38	NH2	S_GLU_46	OE2	3.826
6NC2	S_ARG_66	NH2	S_ASP_86	OD1	3.009
6NC2	S_ARG_66	NH2	S_ASP_86	OD2	3.730
6NC2	S_LYS_75	NZ	S_ASP_72	OD2	3.903

6NC2	S_ARG_82B	NH1	S_ASP_82A	OD2	2.740
6NC2	S_ARG_83	NH2	S_GLU_85	OE1	3.718
6NC2	S_ARG_83	NH2	S_GLU_85	OE2	3.237
6NC2	S_LYS_94	NZ	S_ASP_101	OD1	3.921
6NC2	S_ARG_96	NH1	X_ASP_50	OD1	3.082
6NC2	S_ARG_96	NH1	X_ASP_50	OD2	3.706
6NC2	S_ARG_96	NH2	X_ASP_50	OD1	3.892
6NC2	S_ARG_96	NH2	X_ASP_50	OD2	3.158
6NC2	S_ARG_99	NH2	S_ASP_31	OD1	3.800
6NC2	X_LYS_30	NZ	X_ASP_28	OD2	2.906
6NC2	X_ARG_37	NH1	X_ASP_82	OD1	3.215
6NC2	X_ARG_37	NH2	X_GLU_45	OE1	2.891
6NC2	X_ARG_37	NH2	X_GLU_45	OE2	3.981
6NC2	X_LYS_42	NZ	X_GLU_45	OE1	3.768
6NC2	X_LYS_103	NZ	X_GLU_105	OE1	3.671

Table 874: 6NC2-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6NC3	A_LYS_46	NZ	B_ASP_636	OD1	2.912
6NC3	A_LYS_46	NZ	B_ASP_636	OD2	3.719
6NC3	A_HIS_72	ND1	A_GLU_64	OE1	3.735
6NC3	A_LYS_117	NZ	A_ASP_113	OD1	3.847
6NC3	A_LYS_117	NZ	A_ASP_113	OD2	2.492
6NC3	A_LYS_155	NZ	A_ASP_133	OD1	2.486
6NC3	A_LYS_168	NZ	A_ASP_167	OD1	2.679
6NC3	A_LYS_168	NZ	A_ASP_167	OD2	3.249
6NC3	A_ARG_192	NH2	C_ASP_167	OD1	3.709
6NC3	A_ARG_192	NH2	C_ASP_167	OD2	3.548
6NC3	A_LYS_231	NZ	A_GLU_267	OE1	2.789
6NC3	A_LYS_231	NZ	A_GLU_267	OE2	3.511
6NC3	A_LYS_232	NZ	A_GLU_269	OE1	3.765
6NC3	A_LYS_232	NZ	A_GLU_269	OE2	2.544
6NC3	A_HIS_249	NE2	A_GLU_482	OE2	2.721
6NC3	A_LYS_290	NZ	A_GLU_268	OE1	3.516
6NC3	A_ARG_298	NH1	A_GLU_381	OE2	2.878
6NC3	A_LYS_305	NZ	A_GLU_172	OE1	2.502
6NC3	A_LYS_305	NZ	A_GLU_172	OE2	3.928
6NC3	A_LYS_337	NZ	A_GLU_293	OE2	2.661
6NC3	A_LYS_348	NZ	A_GLU_351	OE1	2.941
6NC3	A_LYS_348	NZ	A_GLU_351	OE2	3.643
6NC3	A_LYS_421	NZ	A_GLU_370	OE2	2.811
6NC3	A_LYS_432	NZ	A_ASP_113	OD1	2.553
6NC3	A_LYS_432	NZ	A_ASP_113	OD2	3.774
6NC3	A_LYS_432	NZ	A_GLU_429	OE1	3.926
6NC3	A_ARG_456	NH2	A_GLU_466	OE1	3.636
6NC3	A_ARG_456	NH2	A_GLU_466	OE2	2.864
6NC3	A_ARG_476	NH1	A_GLU_102	OE1	3.922
6NC3	A_ARG_476	NH1	A_GLU_102	OE2	3.112
6NC3	A_ARG_476	NH2	A_ASP_474	OD1	3.856
6NC3	A_ARG_476	NH2	A_ASP_474	OD2	3.033
6NC3	A_ARG_480	NH1	A_ASP_477	OD1	2.738
6NC3	A_ARG_480	NH2	A_ASP_477	OD1	3.897
6NC3	A_LYS_487	NZ	A_GLU_47	OE1	2.894
6NC3	A_LYS_487	NZ	A_GLU_47	OE2	3.821
6NC3	A_LYS_487	NZ	A_GLU_91	OE1	3.879
6NC3	A_ARG_503	NH2	B_GLU_654	OE1	3.773
6NC3	A_ARG_503	NH2	B_GLU_654	OE2	3.161
6NC3	B_ARG_542	NH2	J_GLU_647	OE1	2.826
6NC3	B_ARG_542	NH2	J_ASP_648	OD1	2.949
6NC3	B_ARG_542	NH2	J_ASP_648	OD2	3.670
6NC3	B_LYS_574	NZ	A_ASP_107	OD1	2.582
6NC3	B_LYS_574	NZ	A_ASP_107	OD2	2.711
6NC3	B_ARG_579	NH1	J_GLU_584	OE2	3.194
6NC3	B_ARG_585	NH2	A_GLU_492	OE1	2.939
6NC3	B_ARG_585	NH2	A_GLU_492	OE2	3.498
6NC3	B_LYS_617	NZ	B_GLU_634	OE1	2.815
6NC3	B_LYS_617	NZ	B_GLU_634	OE2	3.445
6NC3	H_LYS_12	NZ	H_GLU_10	OE1	3.786
6NC3	H_HIS_35	NE2	H_ASP_95	OD2	3.813
6NC3	H_ARG_38	NH1	H_ASP_86	OD1	2.638
6NC3	H_ARG_38	NH2	H_GLU_46	OE1	2.857
6NC3	H_ARG_38	NH2	H_GLU_46	OE2	3.919
6NC3	H_ARG_38	NH2	H_ASP_86	OD1	3.489
6NC3	H_LYS_62	NZ	H_GLU_46	OE2	2.819
6NC3	H_ARG_66	NH2	H_ASP_86	OD1	3.294

6NC3	H_ARG_66	NH2	H_ASP_86	OD2	3.014
6NC3	H_ARG_94	NH1	H_GLU_2	OE1	2.960
6NC3	H_ARG_94	NH2	H_GLU_2	OE1	3.018
6NC3	H_LYS_96	NZ	H_ASP_101	OD1	3.648
6NC3	H_LYS_96	NZ	H_ASP_101	OD2	2.449
6NC3	L_ARG_30	NH2	L_GLU_32	OE2	3.023
6NC3	L_ARG_61	NH1	L_GLU_81	OE2	3.991
6NC3	L_ARG_61	NH2	L_GLU_81	OE2	3.260
6NC3	L_ARG_61	NH2	L_ASP_82	OD1	2.918
6NC3	L_ARG_61	NH2	L_ASP_82	OD2	3.280
6NC3	L_LYS_103	NZ	L_GLU_105	OE2	3.920
6NC3	L_LYS_107	NZ	L_ASP_17	OD2	2.904
6NC3	C_LYS_46	NZ	L_ASP_636	OD1	2.913
6NC3	C_LYS_46	NZ	L_ASP_636	OD2	3.719
6NC3	C_HIS_72	ND1	C_GLU_64	OE1	3.735
6NC3	C_LYS_117	NZ	C_ASP_113	OD1	3.848
6NC3	C_LYS_117	NZ	C_ASP_113	OD2	2.492
6NC3	C_LYS_155	NZ	C_ASP_133	OD1	2.487
6NC3	C_LYS_168	NZ	C_ASP_167	OD1	2.679
6NC3	C_LYS_168	NZ	C_ASP_167	OD2	3.249
6NC3	C_ARG_192	NH2	D_ASP_167	OD1	3.709
6NC3	C_ARG_192	NH2	D_ASP_167	OD2	3.548
6NC3	C_LYS_231	NZ	C_GLU_267	OE1	2.789
6NC3	C_LYS_231	NZ	C_GLU_267	OE2	3.511
6NC3	C_LYS_232	NZ	C_GLU_269	OE1	3.765
6NC3	C_LYS_232	NZ	C_GLU_269	OE2	2.544
6NC3	C_HIS_249	NE2	C_GLU_482	OE2	2.721
6NC3	C_LYS_290	NZ	C_GLU_268	OE1	3.516
6NC3	C_ARG_298	NH1	C_GLU_381	OE2	2.878
6NC3	C_LYS_305	NZ	C_GLU_172	OE1	2.502
6NC3	C_LYS_305	NZ	C_GLU_172	OE2	3.929
6NC3	C_LYS_337	NZ	C_GLU_293	OE2	2.662
6NC3	C_LYS_348	NZ	C_GLU_351	OE1	2.941
6NC3	C_LYS_348	NZ	C_GLU_351	OE2	3.643
6NC3	C_LYS_421	NZ	C_GLU_370	OE2	2.811
6NC3	C_LYS_432	NZ	C_ASP_113	OD1	2.553
6NC3	C_LYS_432	NZ	C_ASP_113	OD2	3.774
6NC3	C_LYS_432	NZ	C_GLU_429	OE1	3.927
6NC3	C_ARG_456	NH2	C_GLU_466	OE1	3.636
6NC3	C_ARG_456	NH2	C_GLU_466	OE2	2.864
6NC3	C_ARG_476	NH1	C_GLU_102	OE1	3.922
6NC3	C_ARG_476	NH1	C_GLU_102	OE2	3.112
6NC3	C_ARG_476	NH2	C_ASP_474	OD1	3.856
6NC3	C_ARG_476	NH2	C_ASP_474	OD2	3.032
6NC3	C_ARG_480	NH1	C_ASP_477	OD1	2.738
6NC3	C_ARG_480	NH2	C_ASP_477	OD1	3.897
6NC3	C_LYS_487	NZ	C_GLU_47	OE1	2.894
6NC3	C_LYS_487	NZ	C_GLU_47	OE2	3.821
6NC3	C_LYS_487	NZ	C_GLU_91	OE1	3.878
6NC3	C_ARG_503	NH2	L_GLU_654	OE1	3.773
6NC3	C_ARG_503	NH2	L_GLU_654	OE2	3.161
6NC3	L_ARG_542	NH2	B_GLU_647	OE1	2.826
6NC3	L_ARG_542	NH2	B_ASP_648	OD1	2.949
6NC3	L_ARG_542	NH2	B_ASP_648	OD2	3.670
6NC3	L_LYS_574	NZ	C_ASP_107	OD1	2.581
6NC3	L_LYS_574	NZ	C_ASP_107	OD2	2.711
6NC3	L_ARG_579	NH1	B_GLU_584	OE2	3.194
6NC3	L_ARG_585	NH2	C_GLU_492	OE1	2.939

6NC3	I_ARG_585	NH2	C_GLU_492	OE2	3.498
6NC3	I_LYS_617	NZ	I_GLU_634	OE1	2.815
6NC3	I_LYS_617	NZ	I_GLU_634	OE2	3.445
6NC3	O_LYS_12	NZ	O_GLU_10	OE1	3.786
6NC3	O_HIS_35	NE2	O_ASP_95	OD2	3.813
6NC3	O_ARG_38	NH1	O_ASP_86	OD1	2.638
6NC3	O_ARG_38	NH2	O_GLU_46	OE1	2.857
6NC3	O_ARG_38	NH2	O_GLU_46	OE2	3.919
6NC3	O_ARG_38	NH2	O_ASP_86	OD1	3.489
6NC3	O_LYS_62	NZ	O_GLU_46	OE2	2.819
6NC3	O_ARG_66	NH2	O_ASP_86	OD1	3.294
6NC3	O_ARG_66	NH2	O_ASP_86	OD2	3.013
6NC3	O_ARG_94	NH1	O_GLU_2	OE1	2.959
6NC3	O_ARG_94	NH2	O_GLU_2	OE1	3.018
6NC3	O_LYS_96	NZ	O_ASP_101	OD1	3.647
6NC3	O_LYS_96	NZ	O_ASP_101	OD2	2.449
6NC3	T_ARG_30	NH2	T_GLU_32	OE2	3.022
6NC3	T_ARG_61	NH1	T_GLU_81	OE2	3.990
6NC3	T_ARG_61	NH2	T_GLU_81	OE2	3.260
6NC3	T_ARG_61	NH2	T_ASP_82	OD1	2.918
6NC3	T_ARG_61	NH2	T_ASP_82	OD2	3.280
6NC3	T_LYS_103	NZ	T_GLU_105	OE2	3.920
6NC3	T_LYS_107	NZ	T_ASP_17	OD2	2.904
6NC3	D_LYS_46	NZ	J_ASP_636	OD1	2.913
6NC3	D_LYS_46	NZ	J_ASP_636	OD2	3.719
6NC3	D_HIS_72	ND1	D_GLU_64	OE1	3.734
6NC3	D_LYS_117	NZ	D_ASP_113	OD1	3.848
6NC3	D_LYS_117	NZ	D_ASP_113	OD2	2.492
6NC3	D_LYS_155	NZ	D_ASP_133	OD1	2.487
6NC3	D_LYS_168	NZ	D_ASP_167	OD1	2.679
6NC3	D_LYS_168	NZ	D_ASP_167	OD2	3.249
6NC3	D_ARG_192	NH2	A_ASP_167	OD1	3.708
6NC3	D_ARG_192	NH2	A_ASP_167	OD2	3.548
6NC3	D_LYS_231	NZ	D_GLU_267	OE1	2.789
6NC3	D_LYS_231	NZ	D_GLU_267	OE2	3.510
6NC3	D_LYS_232	NZ	D_GLU_269	OE1	3.765
6NC3	D_LYS_232	NZ	D_GLU_269	OE2	2.544
6NC3	D_HIS_249	NE2	D_GLU_482	OE2	2.721
6NC3	D_LYS_290	NZ	D_GLU_268	OE1	3.516
6NC3	D_ARG_298	NH1	D_GLU_381	OE2	2.878
6NC3	D_LYS_305	NZ	D_GLU_172	OE1	2.502
6NC3	D_LYS_305	NZ	D_GLU_172	OE2	3.929
6NC3	D_LYS_337	NZ	D_GLU_293	OE2	2.661
6NC3	D_LYS_348	NZ	D_GLU_351	OE1	2.941
6NC3	D_LYS_348	NZ	D_GLU_351	OE2	3.643
6NC3	D_LYS_421	NZ	D_GLU_370	OE2	2.811
6NC3	D_LYS_432	NZ	D_ASP_113	OD1	2.553
6NC3	D_LYS_432	NZ	D_ASP_113	OD2	3.775
6NC3	D_LYS_432	NZ	D_GLU_429	OE1	3.926
6NC3	D_ARG_456	NH2	D_GLU_466	OE1	3.636
6NC3	D_ARG_456	NH2	D_GLU_466	OE2	2.864
6NC3	D_ARG_476	NH1	D_GLU_102	OE1	3.922
6NC3	D_ARG_476	NH1	D_GLU_102	OE2	3.112
6NC3	D_ARG_476	NH2	D_ASP_474	OD1	3.856
6NC3	D_ARG_476	NH2	D_ASP_474	OD2	3.032
6NC3	D_ARG_480	NH1	D_ASP_477	OD1	2.738
6NC3	D_ARG_480	NH2	D_ASP_477	OD1	3.897
6NC3	D_LYS_487	NZ	D_GLU_47	OE1	2.894

6NC3	D_LYS_487	NZ	D_GLU_47	OE2	3.821
6NC3	D_LYS_487	NZ	D_GLU_91	OE1	3.878
6NC3	D_ARG_503	NH2	J_GLU_654	OE1	3.773
6NC3	D_ARG_503	NH2	J_GLU_654	OE2	3.160
6NC3	J_ARG_542	NH2	I_GLU_647	OE1	2.825
6NC3	J_ARG_542	NH2	I_ASP_648	OD1	2.949
6NC3	J_ARG_542	NH2	I_ASP_648	OD2	3.670
6NC3	J_LYS_574	NZ	D_ASP_107	OD1	2.581
6NC3	J_LYS_574	NZ	D_ASP_107	OD2	2.710
6NC3	J_ARG_579	NH1	I_GLU_584	OE2	3.194
6NC3	J_ARG_585	NH2	D_GLU_492	OE1	2.939
6NC3	J_ARG_585	NH2	D_GLU_492	OE2	3.498
6NC3	J_LYS_617	NZ	J_GLU_634	OE1	2.815
6NC3	J_LYS_617	NZ	J_GLU_634	OE2	3.445
6NC3	P_LYS_12	NZ	P_GLU_10	OE1	3.785
6NC3	P_HIS_35	NE2	P_ASP_95	OD2	3.813
6NC3	P_ARG_38	NH1	P_ASP_86	OD1	2.638
6NC3	P_ARG_38	NH2	P_GLU_46	OE1	2.856
6NC3	P_ARG_38	NH2	P_GLU_46	OE2	3.919
6NC3	P_ARG_38	NH2	P_ASP_86	OD1	3.489
6NC3	P_LYS_62	NZ	P_GLU_46	OE2	2.819
6NC3	P_ARG_66	NH2	P_ASP_86	OD1	3.294
6NC3	P_ARG_66	NH2	P_ASP_86	OD2	3.014
6NC3	P_ARG_94	NH1	P_GLU_2	OE1	2.959
6NC3	P_ARG_94	NH2	P_GLU_2	OE1	3.018
6NC3	P_LYS_96	NZ	P_ASP_101	OD1	3.648
6NC3	P_LYS_96	NZ	P_ASP_101	OD2	2.449
6NC3	U_ARG_30	NH2	U_GLU_32	OE2	3.022
6NC3	U_ARG_61	NH1	U_GLU_81	OE2	3.991
6NC3	U_ARG_61	NH2	U_GLU_81	OE2	3.260
6NC3	U_ARG_61	NH2	U_ASP_82	OD1	2.918
6NC3	U_ARG_61	NH2	U_ASP_82	OD2	3.280
6NC3	U_LYS_103	NZ	U_GLU_105	OE2	3.920
6NC3	U_LYS_107	NZ	U_ASP_17	OD2	2.904
6NC3	E_LYS_46	NZ	K_ASP_636	OD1	2.912
6NC3	E_LYS_46	NZ	K_ASP_636	OD2	3.719
6NC3	E_HIS_72	ND1	E_GLU_64	OE1	3.735
6NC3	E_LYS_117	NZ	E_ASP_113	OD1	3.847
6NC3	E_LYS_117	NZ	E_ASP_113	OD2	2.492
6NC3	E_LYS_155	NZ	E_ASP_133	OD1	2.486
6NC3	E_LYS_168	NZ	E_ASP_167	OD1	2.679
6NC3	E_LYS_168	NZ	E_ASP_167	OD2	3.249
6NC3	E_ARG_192	NH2	F_ASP_167	OD1	3.709
6NC3	E_ARG_192	NH2	F_ASP_167	OD2	3.548
6NC3	E_LYS_231	NZ	E_GLU_267	OE1	2.789
6NC3	E_LYS_231	NZ	E_GLU_267	OE2	3.511
6NC3	E_LYS_232	NZ	E_GLU_269	OE1	3.765
6NC3	E_LYS_232	NZ	E_GLU_269	OE2	2.544
6NC3	E_HIS_249	NE2	E_GLU_482	OE2	2.721
6NC3	E_LYS_290	NZ	E_GLU_268	OE1	3.516
6NC3	E_ARG_298	NH1	E_GLU_381	OE2	2.878
6NC3	E_LYS_305	NZ	E_GLU_172	OE1	2.502
6NC3	E_LYS_305	NZ	E_GLU_172	OE2	3.928
6NC3	E_LYS_337	NZ	E_GLU_293	OE2	2.661
6NC3	E_LYS_348	NZ	E_GLU_351	OE1	2.941
6NC3	E_LYS_348	NZ	E_GLU_351	OE2	3.643
6NC3	E_LYS_421	NZ	E_GLU_370	OE2	2.811
6NC3	E_LYS_432	NZ	E_ASP_113	OD1	2.553

6NC3	E_LYS_432	NZ	E_ASP_113	OD2	3.774
6NC3	E_LYS_432	NZ	E_GLU_429	OE1	3.926
6NC3	E_ARG_456	NH2	E_GLU_466	OE1	3.636
6NC3	E_ARG_456	NH2	E_GLU_466	OE2	2.864
6NC3	E_ARG_476	NH1	E_GLU_102	OE1	3.922
6NC3	E_ARG_476	NH1	E_GLU_102	OE2	3.112
6NC3	E_ARG_476	NH2	E_ASP_474	OD1	3.856
6NC3	E_ARG_476	NH2	E_ASP_474	OD2	3.033
6NC3	E_ARG_480	NH1	E_ASP_477	OD1	2.738
6NC3	E_ARG_480	NH2	E_ASP_477	OD1	3.897
6NC3	E_LYS_487	NZ	E_GLU_47	OE1	2.894
6NC3	E_LYS_487	NZ	E_GLU_47	OE2	3.821
6NC3	E_LYS_487	NZ	E_GLU_91	OE1	3.879
6NC3	E_ARG_503	NH2	K_GLU_654	OE1	3.773
6NC3	E_ARG_503	NH2	K_GLU_654	OE2	3.161
6NC3	K_ARG_542	NH2	N_GLU_647	OE1	2.826
6NC3	K_ARG_542	NH2	N_ASP_648	OD1	2.949
6NC3	K_ARG_542	NH2	N_ASP_648	OD2	3.670
6NC3	K_LYS_574	NZ	E_ASP_107	OD1	2.582
6NC3	K_LYS_574	NZ	E_ASP_107	OD2	2.711
6NC3	K_ARG_579	NH1	N_GLU_584	OE2	3.194
6NC3	K_ARG_585	NH2	E_GLU_492	OE1	2.939
6NC3	K_ARG_585	NH2	E_GLU_492	OE2	3.498
6NC3	K_LYS_617	NZ	K_GLU_634	OE1	2.815
6NC3	K_LYS_617	NZ	K_GLU_634	OE2	3.445
6NC3	Q_LYS_12	NZ	Q_GLU_10	OE1	3.786
6NC3	Q_HIS_35	NE2	Q_ASP_95	OD2	3.813
6NC3	Q_ARG_38	NH1	Q_ASP_86	OD1	2.638
6NC3	Q_ARG_38	NH2	Q_GLU_46	OE1	2.857
6NC3	Q_ARG_38	NH2	Q_GLU_46	OE2	3.919
6NC3	Q_ARG_38	NH2	Q_ASP_86	OD1	3.489
6NC3	Q_LYS_62	NZ	Q_GLU_46	OE2	2.819
6NC3	Q_ARG_66	NH2	Q_ASP_86	OD1	3.294
6NC3	Q_ARG_66	NH2	Q_ASP_86	OD2	3.014
6NC3	Q_ARG_94	NH1	Q_GLU_2	OE1	2.960
6NC3	Q_ARG_94	NH2	Q_GLU_2	OE1	3.018
6NC3	Q_LYS_96	NZ	Q_ASP_101	OD1	3.648
6NC3	Q_LYS_96	NZ	Q_ASP_101	OD2	2.449
6NC3	V_ARG_30	NH2	V_GLU_32	OE2	3.023
6NC3	V_ARG_61	NH1	V_GLU_81	OE2	3.991
6NC3	V_ARG_61	NH2	V_GLU_81	OE2	3.260
6NC3	V_ARG_61	NH2	V_ASP_82	OD1	2.918
6NC3	V_ARG_61	NH2	V_ASP_82	OD2	3.280
6NC3	V_LYS_103	NZ	V_GLU_105	OE2	3.920
6NC3	V_LYS_107	NZ	V_ASP_17	OD2	2.904
6NC3	F_LYS_46	NZ	M_ASP_636	OD1	2.913
6NC3	F_LYS_46	NZ	M_ASP_636	OD2	3.719
6NC3	F_HIS_72	ND1	F_GLU_64	OE1	3.734
6NC3	F_LYS_117	NZ	F_ASP_113	OD1	3.848
6NC3	F_LYS_117	NZ	F_ASP_113	OD2	2.492
6NC3	F_LYS_155	NZ	F_ASP_133	OD1	2.487
6NC3	F_LYS_168	NZ	F_ASP_167	OD1	2.679
6NC3	F_LYS_168	NZ	F_ASP_167	OD2	3.249
6NC3	F_ARG_192	NH2	G_ASP_167	OD1	3.709
6NC3	F_ARG_192	NH2	G_ASP_167	OD2	3.548
6NC3	F_LYS_231	NZ	F_GLU_267	OE1	2.789
6NC3	F_LYS_231	NZ	F_GLU_267	OE2	3.511
6NC3	F_LYS_232	NZ	F_GLU_269	OE1	3.765

6NC3	F_LYS_232	NZ	F_GLU_269	OE2	2.544
6NC3	F_HIS_249	NE2	F_GLU_482	OE2	2.721
6NC3	F_LYS_290	NZ	F_GLU_268	OE1	3.516
6NC3	F_ARG_298	NH1	F_GLU_381	OE2	2.878
6NC3	F_LYS_305	NZ	F_GLU_172	OE1	2.502
6NC3	F_LYS_305	NZ	F_GLU_172	OE2	3.929
6NC3	F_LYS_337	NZ	F_GLU_293	OE2	2.662
6NC3	F_LYS_348	NZ	F_GLU_351	OE1	2.941
6NC3	F_LYS_348	NZ	F_GLU_351	OE2	3.643
6NC3	F_LYS_421	NZ	F_GLU_370	OE2	2.811
6NC3	F_LYS_432	NZ	F_ASP_113	OD1	2.553
6NC3	F_LYS_432	NZ	F_ASP_113	OD2	3.774
6NC3	F_LYS_432	NZ	F_GLU_429	OE1	3.927
6NC3	F_ARG_456	NH2	F_GLU_466	OE1	3.636
6NC3	F_ARG_456	NH2	F_GLU_466	OE2	2.864
6NC3	F_ARG_476	NH1	F_GLU_102	OE1	3.922
6NC3	F_ARG_476	NH1	F_GLU_102	OE2	3.112
6NC3	F_ARG_476	NH2	F_ASP_474	OD1	3.856
6NC3	F_ARG_476	NH2	F_ASP_474	OD2	3.032
6NC3	F_ARG_480	NH1	F_ASP_477	OD1	2.738
6NC3	F_ARG_480	NH2	F_ASP_477	OD1	3.897
6NC3	F_LYS_487	NZ	F_GLU_47	OE1	2.894
6NC3	F_LYS_487	NZ	F_GLU_47	OE2	3.821
6NC3	F_LYS_487	NZ	F_GLU_91	OE1	3.878
6NC3	F_ARG_503	NH2	M_GLU_654	OE1	3.773
6NC3	F_ARG_503	NH2	M_GLU_654	OE2	3.161
6NC3	M_ARG_542	NH2	K_GLU_647	OE1	2.826
6NC3	M_ARG_542	NH2	K_ASP_648	OD1	2.949
6NC3	M_ARG_542	NH2	K_ASP_648	OD2	3.670
6NC3	M_LYS_574	NZ	F_ASP_107	OD1	2.581
6NC3	M_LYS_574	NZ	F_ASP_107	OD2	2.711
6NC3	M_ARG_579	NH1	K_GLU_584	OE2	3.194
6NC3	M_ARG_585	NH2	F_GLU_492	OE1	2.939
6NC3	M_ARG_585	NH2	F_GLU_492	OE2	3.498
6NC3	M_LYS_617	NZ	M_GLU_634	OE1	2.815
6NC3	M_LYS_617	NZ	M_GLU_634	OE2	3.445
6NC3	R_LYS_12	NZ	R_GLU_10	OE1	3.786
6NC3	R_HIS_35	NE2	R_ASP_95	OD2	3.813
6NC3	R_ARG_38	NH1	R_ASP_86	OD1	2.638
6NC3	R_ARG_38	NH2	R_GLU_46	OE1	2.857
6NC3	R_ARG_38	NH2	R_GLU_46	OE2	3.919
6NC3	R_ARG_38	NH2	R_ASP_86	OD1	3.489
6NC3	R_LYS_62	NZ	R_GLU_46	OE2	2.819
6NC3	R_ARG_66	NH2	R_ASP_86	OD1	3.294
6NC3	R_ARG_66	NH2	R_ASP_86	OD2	3.013
6NC3	R_ARG_94	NH1	R_GLU_2	OE1	2.959
6NC3	R_ARG_94	NH2	R_GLU_2	OE1	3.018
6NC3	R_LYS_96	NZ	R_ASP_101	OD1	3.647
6NC3	R_LYS_96	NZ	R_ASP_101	OD2	2.449
6NC3	W_ARG_30	NH2	W_GLU_32	OE2	3.022
6NC3	W_ARG_61	NH1	W_GLU_81	OE2	3.990
6NC3	W_ARG_61	NH2	W_GLU_81	OE2	3.260
6NC3	W_ARG_61	NH2	W_ASP_82	OD1	2.918
6NC3	W_ARG_61	NH2	W_ASP_82	OD2	3.280
6NC3	W_LYS_103	NZ	W_GLU_105	OE2	3.920
6NC3	W_LYS_107	NZ	W_ASP_17	OD2	2.904
6NC3	G_LYS_46	NZ	N_ASP_636	OD1	2.913
6NC3	G_LYS_46	NZ	N_ASP_636	OD2	3.719

6NC3	G_HIS_72	ND1	G_GLU_64	OE1	3.735
6NC3	G_LYS_117	NZ	G_ASP_113	OD1	3.847
6NC3	G_LYS_117	NZ	G_ASP_113	OD2	2.492
6NC3	G_LYS_155	NZ	G_ASP_133	OD1	2.487
6NC3	G_LYS_168	NZ	G_ASP_167	OD1	2.679
6NC3	G_LYS_168	NZ	G_ASP_167	OD2	3.249
6NC3	G_ARG_192	NH2	E_ASP_167	OD1	3.708
6NC3	G_ARG_192	NH2	E_ASP_167	OD2	3.548
6NC3	G_LYS_231	NZ	G_GLU_267	OE1	2.789
6NC3	G_LYS_231	NZ	G_GLU_267	OE2	3.510
6NC3	G_LYS_232	NZ	G_GLU_269	OE1	3.765
6NC3	G_LYS_232	NZ	G_GLU_269	OE2	2.544
6NC3	G_HIS_249	NE2	G_GLU_482	OE2	2.721
6NC3	G_LYS_290	NZ	G_GLU_268	OE1	3.516
6NC3	G_ARG_298	NH1	G_GLU_381	OE2	2.878
6NC3	G_LYS_305	NZ	G_GLU_172	OE1	2.502
6NC3	G_LYS_305	NZ	G_GLU_172	OE2	3.929
6NC3	G_LYS_337	NZ	G_GLU_293	OE2	2.661
6NC3	G_LYS_348	NZ	G_GLU_351	OE1	2.941
6NC3	G_LYS_348	NZ	G_GLU_351	OE2	3.643
6NC3	G_LYS_421	NZ	G_GLU_370	OE2	2.811
6NC3	G_LYS_432	NZ	G_ASP_113	OD1	2.553
6NC3	G_LYS_432	NZ	G_ASP_113	OD2	3.775
6NC3	G_LYS_432	NZ	G_GLU_429	OE1	3.926
6NC3	G_ARG_456	NH2	G_GLU_466	OE1	3.636
6NC3	G_ARG_456	NH2	G_GLU_466	OE2	2.864
6NC3	G_ARG_476	NH1	G_GLU_102	OE1	3.922
6NC3	G_ARG_476	NH1	G_GLU_102	OE2	3.112
6NC3	G_ARG_476	NH2	G_ASP_474	OD1	3.856
6NC3	G_ARG_476	NH2	G_ASP_474	OD2	3.032
6NC3	G_ARG_480	NH1	G_ASP_477	OD1	2.738
6NC3	G_ARG_480	NH2	G_ASP_477	OD1	3.897
6NC3	G_LYS_487	NZ	G_GLU_47	OE1	2.894
6NC3	G_LYS_487	NZ	G_GLU_47	OE2	3.821
6NC3	G_LYS_487	NZ	G_GLU_91	OE1	3.878
6NC3	G_ARG_503	NH2	N_GLU_654	OE1	3.773
6NC3	G_ARG_503	NH2	N_GLU_654	OE2	3.160
6NC3	N_ARG_542	NH2	M_GLU_647	OE1	2.825
6NC3	N_ARG_542	NH2	M_ASP_648	OD1	2.949
6NC3	N_ARG_542	NH2	M_ASP_648	OD2	3.670
6NC3	N_LYS_574	NZ	G_ASP_107	OD1	2.581
6NC3	N_LYS_574	NZ	G_ASP_107	OD2	2.710
6NC3	N_ARG_579	NH1	M_GLU_584	OE2	3.194
6NC3	N_ARG_585	NH2	G_GLU_492	OE1	2.939
6NC3	N_ARG_585	NH2	G_GLU_492	OE2	3.498
6NC3	N_LYS_617	NZ	N_GLU_634	OE1	2.815
6NC3	N_LYS_617	NZ	N_GLU_634	OE2	3.445
6NC3	S_LYS_12	NZ	S_GLU_10	OE1	3.785
6NC3	S_HIS_35	NE2	S_ASP_95	OD2	3.813
6NC3	S_ARG_38	NH1	S_ASP_86	OD1	2.638
6NC3	S_ARG_38	NH2	S_GLU_46	OE1	2.856
6NC3	S_ARG_38	NH2	S_GLU_46	OE2	3.919
6NC3	S_ARG_38	NH2	S_ASP_86	OD1	3.489
6NC3	S_LYS_62	NZ	S_GLU_46	OE2	2.819
6NC3	S_ARG_66	NH2	S_ASP_86	OD1	3.294
6NC3	S_ARG_66	NH2	S_ASP_86	OD2	3.014
6NC3	S_ARG_94	NH1	S_GLU_2	OE1	2.959
6NC3	S_ARG_94	NH2	S_GLU_2	OE1	3.018

6NC3	S_LYS_96	NZ	S_ASP_101	OD1	3.648
6NC3	S_LYS_96	NZ	S_ASP_101	OD2	2.449
6NC3	X_ARG_30	NH2	X_GLU_32	OE2	3.022
6NC3	X_ARG_61	NH1	X_GLU_81	OE2	3.991
6NC3	X_ARG_61	NH2	X_GLU_81	OE2	3.260
6NC3	X_ARG_61	NH2	X_ASP_82	OD1	2.918
6NC3	X_ARG_61	NH2	X_ASP_82	OD2	3.280
6NC3	X_LYS_103	NZ	X_GLU_105	OE2	3.920
6NC3	X_LYS_107	NZ	X_ASP_17	OD2	2.904

Table 875: 6NC3-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6NEX	L_ARG_	NH2	L_GLU_	OE2	2.737
6NEX	L_ARG_	NH2	L_ASP_	OD1	2.840
6NEX	L_ARG_	NH2	L_ASP_	OD2	3.473
6NEX	L_LYS_	NZ	L_GLU_	OE2	3.642
6NEX	H_ARG_	NH1	H_ASP_	OD1	2.811
6NEX	H_ARG_	NH2	H_GLU_	OE1	2.941
6NEX	H_ARG_	NH2	H_GLU_	OE2	3.733
6NEX	H_ARG_	NH1	H_ASP_	OD1	3.160
6NEX	H_ARG_	NH1	H_ASP_	OD2	3.548
6NEX	H_ARG_	NH2	H_ASP_	OD1	3.762
6NEX	H_ARG_	NH2	H_ASP_	OD2	2.737
6NEX	H_LYS_	NZ	H_ASP_	OD1	3.770
6NEX	H_ARG_210	NH1	H_GLU_212	OE2	3.708
6NEX	H_ARG_210	NH2	H_GLU_212	OE1	3.957
6NEX	H_ARG_210	NH2	H_GLU_212	OE2	2.338
6NEX	A_ARG_	NH2	A_GLU_	OE2	2.672
6NEX	A_ARG_	NH2	A_ASP_	OD1	2.826
6NEX	A_ARG_	NH2	A_ASP_	OD2	3.589
6NEX	A_LYS_	NZ	A_GLU_	OE1	3.636
6NEX	A_LYS_	NZ	A_GLU_	OE2	3.384
6NEX	B_ARG_	NH1	B_ASP_	OD1	2.934
6NEX	B_ARG_	NH2	B_GLU_	OE2	2.957
6NEX	B_ARG_	NH2	B_ASP_	OD1	3.823
6NEX	B_LYS_	NZ	B_ASP_	OD1	3.270
6NEX	B_ARG_	NH1	B_ASP_	OD1	3.264
6NEX	B_ARG_	NH1	B_ASP_	OD2	3.612
6NEX	B_ARG_	NH2	B_ASP_	OD2	3.065
6NEX	B_ARG_	NH1	B_GLU_	OE2	2.598
6NEX	B_LYS_	NZ	B_ASP_	OD1	3.942
6NEX	B_LYS_209	NZ	A_GLU_126	OE2	3.298

Table 876: 6NEX-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6NF2	A.LYS_46	NZ	A.GLU_492	OE2	2.493
6NF2	A.LYS_46	NZ	I.ASP_632	OD2	2.876
6NF2	A.HIS_216	NE2	A.ASP_57	OD1	2.861
6NF2	A.HIS_216	NE2	A.ASP_57	OD2	2.990
6NF2	A.LYS_227	NZ	A.GLU_83	OE1	2.516
6NF2	A.LYS_227	NZ	A.GLU_83	OE2	3.523
6NF2	A.LYS_282	NZ	A.GLU_275	OE1	3.484
6NF2	A.LYS_282	NZ	A.GLU_275	OE2	3.921
6NF2	A.ARG_419	NH1	A.GLU_153	OE1	3.359
6NF2	A.ARG_419	NH2	A.GLU_153	OE1	3.820
6NF2	A.LYS_421	NZ	A.GLU_370	OE2	3.954
6NF2	A.ARG_429	NH1	A.ASP_113	OD1	2.605
6NF2	A.ARG_429	NH1	A.ASP_113	OD2	3.059
6NF2	A.ARG_429	NH2	A.ASP_113	OD1	3.615
6NF2	A.ARG_456	NH1	A.GLU_466	OE1	3.082
6NF2	A.ARG_456	NH1	A.GLU_466	OE2	3.859
6NF2	A.ARG_476	NH2	A.ASP_474	OD1	3.180
6NF2	A.LYS_487	NZ	A.ASP_47	OD1	2.705
6NF2	A.LYS_487	NZ	A.ASP_47	OD2	3.456
6NF2	A.LYS_487	NZ	A.GLU_91	OE1	3.205
6NF2	A.LYS_490	NZ	A.GLU_492	OE1	3.081
6NF2	A.ARG_504	NH2	R.GLU_657	OE2	3.927
6NF2	B.ARG_579	NH1	I.GLU_584	OE2	3.681
6NF2	B.LYS_601	NZ	I.GLU_654	OE1	2.983
6NF2	B.LYS_601	NZ	I.GLU_654	OE2	3.256
6NF2	B.ARG_617	NH1	B.GLU_634	OE1	3.898
6NF2	B.ARG_617	NH1	B.GLU_634	OE2	3.558
6NF2	B.ARG_617	NH2	B.GLU_634	OE1	2.451
6NF2	B.ARG_617	NH2	B.GLU_634	OE2	3.092
6NF2	C.LYS_19	NZ	C.GLU_81	OE2	3.460
6NF2	C.ARG_38	NH1	C.GLU_46	OE1	2.376
6NF2	C.ARG_38	NH2	C.ASP_86	OD1	2.835
6NF2	C.ARG_38	NH2	C.ASP_86	OD2	3.913
6NF2	C.ARG_61	NH1	G.GLU_466	OE1	3.610
6NF2	C.ARG_61	NH2	G.GLU_466	OE2	3.748
6NF2	C.ARG_66	NH2	C.ASP_86	OD2	2.541
6NF2	C.ARG_71	NH2	G.ASP_368	OD1	3.504
6NF2	D.ARG_38	NH1	D.ASP_81	OD2	3.918
6NF2	D.ARG_52	NH1	D.ASP_49	OD2	2.507
6NF2	D.ARG_60	NH1	D.ASP_78	OD1	3.451
6NF2	D.ARG_60	NH1	D.ASP_78	OD2	2.551
6NF2	D.ARG_60	NH1	D.ASP_81	OD1	3.827
6NF2	D.ARG_60	NH2	D.ASP_78	OD2	3.741
6NF2	D.ARG_60	NH2	D.ASP_81	OD1	2.673
6NF2	E.ARG_30	NH1	E.ASP_53	OD1	3.557
6NF2	E.ARG_30	NH1	E.ASP_53	OD2	3.208
6NF2	E.ARG_30	NH2	E.ASP_53	OD2	3.963
6NF2	E.ARG_38	NH2	E.GLU_46	OE1	2.920
6NF2	F.ARG_31	NH2	F.ASP_92	OD2	3.578
6NF2	F.ARG_61	NH2	F.GLU_79	OE1	2.683
6NF2	F.ARG_61	NH2	F.GLU_79	OE2	3.530
6NF2	F.ARG_61	NH2	F.ASP_82	OD1	3.710
6NF2	F.ARG_95	NH1	F.GLU_25	OE1	2.962
6NF2	F.ARG_95	NH1	F.ASP_92	OD2	3.472
6NF2	G.LYS_46	NZ	B.ASP_632	OD2	2.943
6NF2	G.LYS_46	NZ	G.GLU_492	OE2	2.493
6NF2	G.HIS_216	NE2	G.ASP_57	OD1	2.861

6NF2	G_HIS_216	NE2	G_ASP_57	OD2	2.990
6NF2	G_LYS_227	NZ	G_GLU_83	OE1	2.516
6NF2	G_LYS_227	NZ	G_GLU_83	OE2	3.523
6NF2	G_LYS_282	NZ	G_GLU_275	OE1	3.483
6NF2	G_LYS_282	NZ	G_GLU_275	OE2	3.920
6NF2	G_ARG_419	NH1	G_GLU_153	OE1	3.359
6NF2	G_ARG_419	NH2	G_GLU_153	OE1	3.821
6NF2	G_LYS_421	NZ	G_GLU_370	OE2	3.954
6NF2	G_ARG_429	NH1	G_ASP_113	OD1	2.606
6NF2	G_ARG_429	NH1	G_ASP_113	OD2	3.059
6NF2	G_ARG_429	NH2	G_ASP_113	OD1	3.615
6NF2	G_ARG_456	NH1	G_GLU_466	OE1	3.082
6NF2	G_ARG_456	NH1	G_GLU_466	OE2	3.857
6NF2	G_ARG_476	NH2	G_ASP_474	OD1	3.180
6NF2	G_LYS_487	NZ	G_ASP_47	OD1	2.706
6NF2	G_LYS_487	NZ	G_ASP_47	OD2	3.456
6NF2	G_LYS_487	NZ	G_GLU_91	OE1	3.206
6NF2	G_LYS_490	NZ	G_GLU_492	OE1	3.082
6NF2	G_ARG_504	NH2	L_GLU_657	OE2	3.805
6NF2	H_LYS_13	NZ	H_GLU_16	OE1	3.322
6NF2	H_ARG_66	NH1	H_ASP_86	OD1	2.849
6NF2	H_ARG_66	NH1	H_ASP_86	OD2	2.841
6NF2	H_ARG_100F	NH1	L_ASP_50	OD2	2.403
6NF2	H_ARG_100F	NH2	L_ASP_50	OD2	3.926
6NF2	I_ARG_579	NH1	R_GLU_584	OE2	3.624
6NF2	I_LYS_601	NZ	R_GLU_654	OE1	3.068
6NF2	I_LYS_601	NZ	R_GLU_654	OE2	3.333
6NF2	I_ARG_617	NH1	L_GLU_634	OE1	3.897
6NF2	I_ARG_617	NH1	L_GLU_634	OE2	3.558
6NF2	I_ARG_617	NH2	L_GLU_634	OE1	2.451
6NF2	I_ARG_617	NH2	L_GLU_634	OE2	3.093
6NF2	J_ARG_30	NH1	J_ASP_53	OD1	3.558
6NF2	J_ARG_30	NH1	J_ASP_53	OD2	3.207
6NF2	J_ARG_30	NH2	J_ASP_53	OD2	3.963
6NF2	J_ARG_38	NH2	J_GLU_46	OE1	2.921
6NF2	K_ARG_31	NH2	K_ASP_92	OD2	3.577
6NF2	K_ARG_61	NH2	K_GLU_79	OE1	2.684
6NF2	K_ARG_61	NH2	K_GLU_79	OE2	3.531
6NF2	K_ARG_61	NH2	K_ASP_82	OD1	3.710
6NF2	K_ARG_95	NH1	K_GLU_25	OE1	2.961
6NF2	K_ARG_95	NH1	K_ASP_92	OD2	3.471
6NF2	L_ARG_24	NH1	L_ASP_70	OD2	2.515
6NF2	L_ARG_54	NH1	L_ASP_60	OD1	3.948
6NF2	L_ARG_54	NH2	L_ASP_60	OD1	2.933
6NF2	L_ARG_61	NH1	L_GLU_79	OE1	3.691
6NF2	L_ARG_61	NH1	L_GLU_79	OE2	3.057
6NF2	L_ARG_61	NH2	L_GLU_79	OE1	3.745
6NF2	M_ARG_38	NH1	M_ASP_81	OD2	3.919
6NF2	M_ARG_52	NH1	M_ASP_49	OD2	2.507
6NF2	M_ARG_60	NH1	M_ASP_78	OD1	3.451
6NF2	M_ARG_60	NH1	M_ASP_78	OD2	2.551
6NF2	M_ARG_60	NH1	M_ASP_81	OD1	3.826
6NF2	M_ARG_60	NH2	M_ASP_78	OD2	3.741
6NF2	M_ARG_60	NH2	M_ASP_81	OD1	2.674
6NF2	N_LYS_19	NZ	N_GLU_81	OE2	3.461
6NF2	N_ARG_38	NH1	N_GLU_46	OE1	2.376
6NF2	N_ARG_38	NH2	N_ASP_86	OD1	2.835
6NF2	N_ARG_38	NH2	N_ASP_86	OD2	3.913

6NF2	N_ARG.61	NH1	A_GLU_466	OE1	3.592
6NF2	N_ARG.61	NH2	A_GLU_466	OE2	3.737
6NF2	N_ARG.66	NH2	N_ASP_86	OD2	2.541
6NF2	N_ARG.71	NH2	A_ASP_368	OD1	3.532
6NF2	O_LYS_13	NZ	O_GLU_16	OE1	3.322
6NF2	O_ARG.66	NH1	O_ASP_86	OD1	2.849
6NF2	O_ARG.66	NH1	O_ASP_86	OD2	2.841
6NF2	O_ARG.100F	NH1	P_ASP_50	OD2	2.825
6NF2	P_ARG.24	NH1	P_ASP_70	OD2	2.514
6NF2	P_ARG.54	NH1	P_ASP_60	OD1	3.948
6NF2	P_ARG.54	NH2	P_ASP_60	OD1	2.932
6NF2	P_ARG.61	NH1	P_GLU_79	OE1	3.692
6NF2	P_ARG.61	NH1	P_GLU_79	OE2	3.058
6NF2	P_ARG.61	NH2	P_GLU_79	OE1	3.745
6NF2	Q_LYS_46	NZ	Q_GLU_492	OE2	2.491
6NF2	Q_LYS_46	NZ	R_ASP_632	OD2	2.912
6NF2	Q_HIS_216	NE2	Q_ASP_57	OD1	2.861
6NF2	Q_HIS_216	NE2	Q_ASP_57	OD2	2.990
6NF2	Q_LYS_227	NZ	Q_GLU_83	OE1	2.514
6NF2	Q_LYS_227	NZ	Q_GLU_83	OE2	3.524
6NF2	Q_LYS_282	NZ	Q_GLU_275	OE1	3.483
6NF2	Q_LYS_282	NZ	Q_GLU_275	OE2	3.921
6NF2	Q_ARG.419	NH1	Q_GLU_153	OE1	3.360
6NF2	Q_ARG.419	NH2	Q_GLU_153	OE1	3.820
6NF2	Q_LYS_421	NZ	Q_GLU_370	OE2	3.955
6NF2	Q_ARG.429	NH1	Q_ASP_113	OD1	2.604
6NF2	Q_ARG.429	NH1	Q_ASP_113	OD2	3.059
6NF2	Q_ARG.429	NH2	Q_ASP_113	OD1	3.616
6NF2	Q_ARG.456	NH1	Q_GLU_466	OE1	3.084
6NF2	Q_ARG.456	NH1	Q_GLU_466	OE2	3.860
6NF2	Q_ARG.476	NH2	Q_ASP_474	OD1	3.179
6NF2	Q_LYS_487	NZ	Q_ASP_47	OD1	2.706
6NF2	Q_LYS_487	NZ	Q_ASP_47	OD2	3.457
6NF2	Q_LYS_487	NZ	Q_GLU_91	OE1	3.205
6NF2	Q_LYS_490	NZ	Q_GLU_492	OE1	3.080
6NF2	Q_ARG.504	NH2	B_GLU_657	OE2	3.920
6NF2	R_ARG.579	NH1	B_GLU_584	OE2	3.657
6NF2	R_LYS_601	NZ	B_GLU_654	OE1	3.130
6NF2	R_LYS_601	NZ	B_GLU_654	OE2	3.363
6NF2	R_ARG.617	NH1	R_GLU_634	OE1	3.896
6NF2	R_ARG.617	NH1	R_GLU_634	OE2	3.558
6NF2	R_ARG.617	NH2	R_GLU_634	OE1	2.450
6NF2	R_ARG.617	NH2	R_GLU_634	OE2	3.092
6NF2	S_ARG.30	NH1	S_ASP_53	OD1	3.557
6NF2	S_ARG.30	NH1	S_ASP_53	OD2	3.207
6NF2	S_ARG.30	NH2	S_ASP_53	OD2	3.964
6NF2	S_ARG.38	NH2	S_GLU_46	OE1	2.919
6NF2	T_ARG.31	NH2	T_ASP_92	OD2	3.577
6NF2	T_ARG.61	NH2	T_GLU_79	OE1	2.683
6NF2	T_ARG.61	NH2	T_GLU_79	OE2	3.530
6NF2	T_ARG.61	NH2	T_ASP_82	OD1	3.710
6NF2	T_ARG.95	NH1	T_GLU_25	OE1	2.962
6NF2	T_ARG.95	NH1	T_ASP_92	OD2	3.472
6NF2	U_ARG.38	NH1	U_ASP_81	OD2	3.919
6NF2	U_ARG.52	NH1	U_ASP_49	OD2	2.509
6NF2	U_ARG.60	NH1	U_ASP_78	OD1	3.451
6NF2	U_ARG.60	NH1	U_ASP_78	OD2	2.550
6NF2	U_ARG.60	NH1	U_ASP_81	OD1	3.827

6NF2	U_ARG_60	NH2	U_ASP_78	OD2	3.741
6NF2	U_ARG_60	NH2	U_ASP_81	OD1	2.673
6NF2	V_LYS_19	NZ	V_GLU_81	OE2	3.461
6NF2	V_ARG_38	NH1	V_GLU_46	OE1	2.376
6NF2	V_ARG_38	NH2	V_ASP_86	OD1	2.836
6NF2	V_ARG_38	NH2	V_ASP_86	OD2	3.912
6NF2	V_ARG_61	NH1	Q_GLU_466	OE1	3.626
6NF2	V_ARG_61	NH2	Q_GLU_466	OE2	3.762
6NF2	V_ARG_66	NH2	V_ASP_86	OD2	2.542
6NF2	V_ARG_71	NH2	Q_ASP_368	OD1	3.511
6NF2	W_LYS_13	NZ	W_GLU_16	OE1	3.322
6NF2	W_ARG_66	NH1	W_ASP_86	OD1	2.849
6NF2	W_ARG_66	NH1	W_ASP_86	OD2	2.842
6NF2	W_ARG_100F	NH1	X_ASP_50	OD2	2.242
6NF2	W_ARG_100F	NH2	X_ASP_50	OD2	3.856
6NF2	X_ARG_24	NH1	X_ASP_70	OD2	2.514
6NF2	X_ARG_54	NH1	X_ASP_60	OD1	3.949
6NF2	X_ARG_54	NH2	X_ASP_60	OD1	2.932
6NF2	X_ARG_61	NH1	X_GLU_79	OE1	3.693
6NF2	X_ARG_61	NH1	X_GLU_79	OE2	3.059
6NF2	X_ARG_61	NH2	X_GLU_79	OE1	3.746

Table 877: 6NF2-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6NF5	A_LYS_46	NZ	B_ASP_632	OD2	2.410
6NF5	A_LYS_97	NZ	A_GLU_275	OE2	3.695
6NF5	A_LYS_137	NZ	L_ASP_51	OD2	2.736
6NF5	A_LYS_168	NZ	A_ASP_167	OD2	2.451
6NF5	A_ARG_178	NH2	A_GLU_153	OE1	3.939
6NF5	A_ARG_192	NH1	J_GLU_164	OE2	3.009
6NF5	A_ARG_192	NH2	J_GLU_164	OE2	3.825
6NF5	A_LYS_229	NZ	A_GLU_83	OE2	2.843
6NF5	A_LYS_232	NZ	A_GLU_268	OE1	2.483
6NF5	A_HIS_249	NE2	A_GLU_482	OE1	3.152
6NF5	A_LYS_282	NZ	A_GLU_275	OE1	3.676
6NF5	A_LYS_421	NZ	A_GLU_370	OE2	2.968
6NF5	A_ARG_456	NH1	A_GLU_466	OE1	2.887
6NF5	A_ARG_469	NH1	A_ASP_457	OD1	2.731
6NF5	A_ARG_469	NH1	A_ASP_457	OD2	2.912
6NF5	A_ARG_476	NH1	A_GLU_102	OE1	3.769
6NF5	A_ARG_476	NH1	A_GLU_102	OE2	2.949
6NF5	A_ARG_476	NH2	A_ASP_474	OD1	3.812
6NF5	A_ARG_476	NH2	A_ASP_474	OD2	2.863
6NF5	A_ARG_480	NH1	A_ASP_477	OD1	2.619
6NF5	A_LYS_485	NZ	A_GLU_267	OE2	3.474
6NF5	A_LYS_487	NZ	A_ASP_47	OD1	2.966
6NF5	A_LYS_487	NZ	A_ASP_47	OD2	2.855
6NF5	A_LYS_487	NZ	A_GLU_91	OE1	3.852
6NF5	A_LYS_490	NZ	A_GLU_492	OE2	3.881
6NF5	B_ARG_542	NH1	D_GLU_647	OE1	3.182
6NF5	B_ARG_542	NH1	D_GLU_647	OE2	3.535
6NF5	B_ARG_542	NH2	D_GLU_647	OE1	3.979
6NF5	B_LYS_574	NZ	A_ASP_107	OD1	2.887
6NF5	B_HIS_585	NE2	A_GLU_492	OE1	3.726
6NF5	B_HIS_585	NE2	B_ASP_589	OD1	3.861
6NF5	B_HIS_585	NE2	B_ASP_589	OD2	3.640
6NF5	B_LYS_601	NZ	D_GLU_657	OE1	3.026
6NF5	B_ARG_617	NH1	B_GLU_634	OE1	2.939
6NF5	B_ARG_617	NH1	B_GLU_634	OE2	3.518
6NF5	B_ARG_617	NH2	B_GLU_621	OE2	3.903
6NF5	H_ARG_38	NH1	H_ASP_86	OD1	2.711
6NF5	H_ARG_38	NH2	H_GLU_46	OE1	2.805
6NF5	H_ARG_38	NH2	H_GLU_46	OE2	3.660
6NF5	H_ARG_38	NH2	H_ASP_86	OD1	3.921
6NF5	H_ARG_50	NH1	H_GLU_95	OE1	3.017
6NF5	H_ARG_66	NH1	H_ASP_86	OD1	3.025
6NF5	H_ARG_66	NH1	H_ASP_86	OD2	3.679
6NF5	H_ARG_66	NH2	H_ASP_86	OD1	3.529
6NF5	H_ARG_66	NH2	H_ASP_86	OD2	2.747
6NF5	L_ARG_61	NH2	L_ASP_82	OD1	3.053
6NF5	L_ARG_61	NH2	L_ASP_82	OD2	3.487
6NF5	L_LYS_103	NZ	L_ASP_85	OD1	2.813
6NF5	L_LYS_103	NZ	L_ASP_85	OD2	3.823
6NF5	K_ARG_38	NH1	K_ASP_86	OD1	3.164
6NF5	K_ARG_38	NH2	K_ASP_86	OD1	2.934
6NF5	K_ARG_53	NH1	B_ASP_659	OD1	3.261
6NF5	K_ARG_53	NH1	B_ASP_659	OD2	3.240
6NF5	K_ARG_53	NH2	B_ASP_659	OD1	3.591
6NF5	K_ARG_53	NH2	B_ASP_659	OD2	2.651
6NF5	K_ARG_66	NH1	K_ASP_86	OD1	3.713
6NF5	K_ARG_66	NH1	K_ASP_86	OD2	2.791

6NF5	K_ARG_66	NH2	K_ASP_86	OD1	3.225
6NF5	K_ARG_66	NH2	K_ASP_86	OD2	3.737
6NF5	K_LYS_75	NZ	K_ASP_72	OD2	3.956
6NF5	K_LYS_100E	NZ	K_ASP_101	OD1	3.994
6NF5	K_LYS_100E	NZ	K_ASP_101	OD2	2.688
6NF5	N_ARG_54	NH2	N_ASP_60	OD1	2.562
6NF5	N_ARG_61	NH2	N_ASP_82	OD1	3.061
6NF5	N_ARG_61	NH2	N_ASP_82	OD2	3.668
6NF5	N_ARG_103	NH1	N_ASP_85	OD1	3.116
6NF5	C_LYS_46	NZ	D_ASP_632	OD2	2.410
6NF5	C_LYS_97	NZ	C_GLU_275	OE2	3.696
6NF5	C_LYS_137	NZ	F_ASP_51	OD2	2.736
6NF5	C_LYS_168	NZ	C_ASP_167	OD2	2.451
6NF5	C_ARG_178	NH2	C_GLU_153	OE1	3.938
6NF5	C_ARG_192	NH1	A_GLU_164	OE2	3.009
6NF5	C_ARG_192	NH2	A_GLU_164	OE2	3.825
6NF5	C_LYS_229	NZ	C_GLU_83	OE2	2.843
6NF5	C_LYS_232	NZ	C_GLU_268	OE1	2.483
6NF5	C_HIS_249	NE2	C_GLU_482	OE1	3.152
6NF5	C_LYS_282	NZ	C_GLU_275	OE1	3.676
6NF5	C_LYS_421	NZ	C_GLU_370	OE2	2.968
6NF5	C_ARG_456	NH1	C_GLU_466	OE1	2.887
6NF5	C_ARG_469	NH1	C_ASP_457	OD1	2.731
6NF5	C_ARG_469	NH1	C_ASP_457	OD2	2.913
6NF5	C_ARG_476	NH1	C_GLU_102	OE1	3.769
6NF5	C_ARG_476	NH1	C_GLU_102	OE2	2.949
6NF5	C_ARG_476	NH2	C_ASP_474	OD1	3.813
6NF5	C_ARG_476	NH2	C_ASP_474	OD2	2.863
6NF5	C_ARG_480	NH1	C_ASP_477	OD1	2.619
6NF5	C_LYS_485	NZ	C_GLU_267	OE2	3.473
6NF5	C_LYS_487	NZ	C_ASP_47	OD1	2.966
6NF5	C_LYS_487	NZ	C_ASP_47	OD2	2.856
6NF5	C_LYS_487	NZ	C_GLU_91	OE1	3.852
6NF5	C_LYS_490	NZ	C_GLU_492	OE2	3.881
6NF5	D_ARG_542	NH1	M_GLU_647	OE1	3.182
6NF5	D_ARG_542	NH1	M_GLU_647	OE2	3.535
6NF5	D_ARG_542	NH2	M_GLU_647	OE1	3.978
6NF5	D_LYS_574	NZ	C_ASP_107	OD1	2.887
6NF5	D_HIS_585	NE2	C_GLU_492	OE1	3.725
6NF5	D_HIS_585	NE2	D_ASP_589	OD1	3.861
6NF5	D_HIS_585	NE2	D_ASP_589	OD2	3.640
6NF5	D_LYS_601	NZ	M_GLU_657	OE1	3.026
6NF5	D_ARG_617	NH1	D_GLU_634	OE1	2.940
6NF5	D_ARG_617	NH1	D_GLU_634	OE2	3.518
6NF5	D_ARG_617	NH2	D_GLU_621	OE2	3.903
6NF5	E_ARG_38	NH1	E_ASP_86	OD1	2.712
6NF5	E_ARG_38	NH2	E_GLU_46	OE1	2.805
6NF5	E_ARG_38	NH2	E_GLU_46	OE2	3.659
6NF5	E_ARG_38	NH2	E_ASP_86	OD1	3.922
6NF5	E_ARG_50	NH1	E_GLU_95	OE1	3.018
6NF5	E_ARG_66	NH1	E_ASP_86	OD1	3.025
6NF5	E_ARG_66	NH1	E_ASP_86	OD2	3.680
6NF5	E_ARG_66	NH2	E_ASP_86	OD1	3.528
6NF5	E_ARG_66	NH2	E_ASP_86	OD2	2.747
6NF5	F_ARG_61	NH2	F_ASP_82	OD1	3.053
6NF5	F_ARG_61	NH2	F_ASP_82	OD2	3.487
6NF5	F_LYS_103	NZ	F_ASP_85	OD1	2.813
6NF5	F_LYS_103	NZ	F_ASP_85	OD2	3.823

6NF5	G_ARG_38	NH1	G_ASP_86	OD1	3.165
6NF5	G_ARG_38	NH2	G_ASP_86	OD1	2.935
6NF5	G_ARG_53	NH1	D_ASP_659	OD1	3.261
6NF5	G_ARG_53	NH1	D_ASP_659	OD2	3.240
6NF5	G_ARG_53	NH2	D_ASP_659	OD1	3.591
6NF5	G_ARG_53	NH2	D_ASP_659	OD2	2.651
6NF5	G_ARG_66	NH1	G_ASP_86	OD1	3.712
6NF5	G_ARG_66	NH1	G_ASP_86	OD2	2.791
6NF5	G_ARG_66	NH2	G_ASP_86	OD1	3.225
6NF5	G_ARG_66	NH2	G_ASP_86	OD2	3.738
6NF5	G_LYS_75	NZ	G_ASP_72	OD2	3.956
6NF5	G_LYS_100E	NZ	G_ASP_101	OD1	3.994
6NF5	G_LYS_100E	NZ	G_ASP_101	OD2	2.688
6NF5	I_ARG_54	NH2	I_ASP_60	OD1	2.564
6NF5	I_ARG_61	NH2	I_ASP_82	OD1	3.061
6NF5	I_ARG_61	NH2	I_ASP_82	OD2	3.668
6NF5	I_ARG_103	NH1	I_ASP_85	OD1	3.116
6NF5	J_LYS_46	NZ	M_ASP_632	OD2	2.410
6NF5	J_LYS_97	NZ	J_GLU_275	OE2	3.696
6NF5	J_LYS_137	NZ	P_ASP_51	OD2	2.735
6NF5	J_LYS_168	NZ	J_ASP_167	OD2	2.451
6NF5	J_ARG_178	NH2	J_GLU_153	OE1	3.938
6NF5	J_ARG_192	NH1	C_GLU_164	OE2	3.010
6NF5	J_ARG_192	NH2	C_GLU_164	OE2	3.825
6NF5	J_LYS_229	NZ	J_GLU_83	OE2	2.843
6NF5	J_LYS_232	NZ	J_GLU_268	OE1	2.482
6NF5	J_HIS_249	NE2	J_GLU_482	OE1	3.151
6NF5	J_LYS_282	NZ	J_GLU_275	OE1	3.676
6NF5	J_LYS_421	NZ	J_GLU_370	OE2	2.968
6NF5	J_ARG_456	NH1	J_GLU_466	OE1	2.887
6NF5	J_ARG_469	NH1	J_ASP_457	OD1	2.730
6NF5	J_ARG_469	NH1	J_ASP_457	OD2	2.913
6NF5	J_ARG_476	NH1	J_GLU_102	OE1	3.770
6NF5	J_ARG_476	NH1	J_GLU_102	OE2	2.949
6NF5	J_ARG_476	NH2	J_ASP_474	OD1	3.812
6NF5	J_ARG_476	NH2	J_ASP_474	OD2	2.862
6NF5	J_ARG_480	NH1	J_ASP_477	OD1	2.619
6NF5	J_LYS_485	NZ	J_GLU_267	OE2	3.474
6NF5	J_LYS_487	NZ	J_ASP_47	OD1	2.966
6NF5	J_LYS_487	NZ	J_ASP_47	OD2	2.856
6NF5	J_LYS_487	NZ	J_GLU_91	OE1	3.851
6NF5	J_LYS_490	NZ	J_GLU_492	OE2	3.881
6NF5	M_ARG_542	NH1	B_GLU_647	OE1	3.182
6NF5	M_ARG_542	NH1	B_GLU_647	OE2	3.534
6NF5	M_ARG_542	NH2	B_GLU_647	OE1	3.979
6NF5	M_LYS_574	NZ	J_ASP_107	OD1	2.887
6NF5	M_HIS_585	NE2	J_GLU_492	OE1	3.726
6NF5	M_HIS_585	NE2	M_ASP_589	OD1	3.860
6NF5	M_HIS_585	NE2	M_ASP_589	OD2	3.640
6NF5	M_LYS_601	NZ	B_GLU_657	OE1	3.027
6NF5	M_ARG_617	NH1	M_GLU_634	OE1	2.940
6NF5	M_ARG_617	NH1	M_GLU_634	OE2	3.518
6NF5	M_ARG_617	NH2	M_GLU_621	OE2	3.902
6NF5	O_ARG_38	NH1	O_ASP_86	OD1	2.712
6NF5	O_ARG_38	NH2	O_GLU_46	OE1	2.805
6NF5	O_ARG_38	NH2	O_GLU_46	OE2	3.659
6NF5	O_ARG_38	NH2	O_ASP_86	OD1	3.922
6NF5	O_ARG_50	NH1	O_GLU_95	OE1	3.017

6NF5	O_ARG_66	NH1	O_ASP_86	OD1	3.025
6NF5	O_ARG_66	NH1	O_ASP_86	OD2	3.680
6NF5	O_ARG_66	NH2	O_ASP_86	OD1	3.529
6NF5	O_ARG_66	NH2	O_ASP_86	OD2	2.748
6NF5	P_ARG_61	NH2	P_ASP_82	OD1	3.053
6NF5	P_ARG_61	NH2	P_ASP_82	OD2	3.487
6NF5	P_LYS_103	NZ	P_ASP_85	OD1	2.813
6NF5	P_LYS_103	NZ	P_ASP_85	OD2	3.823
6NF5	Q_ARG_38	NH1	Q_ASP_86	OD1	3.164
6NF5	Q_ARG_38	NH2	Q_ASP_86	OD1	2.933
6NF5	Q_ARG_53	NH1	M_ASP_659	OD1	3.262
6NF5	Q_ARG_53	NH1	M_ASP_659	OD2	3.240
6NF5	Q_ARG_53	NH2	M_ASP_659	OD1	3.591
6NF5	Q_ARG_53	NH2	M_ASP_659	OD2	2.650
6NF5	Q_ARG_66	NH1	Q_ASP_86	OD1	3.713
6NF5	Q_ARG_66	NH1	Q_ASP_86	OD2	2.791
6NF5	Q_ARG_66	NH2	Q_ASP_86	OD1	3.225
6NF5	Q_ARG_66	NH2	Q_ASP_86	OD2	3.737
6NF5	Q_LYS_75	NZ	Q_ASP_72	OD2	3.956
6NF5	Q_LYS_100E	NZ	Q_ASP_101	OD1	3.994
6NF5	Q_LYS_100E	NZ	Q_ASP_101	OD2	2.688
6NF5	R_ARG_54	NH2	R_ASP_60	OD1	2.562
6NF5	R_ARG_61	NH2	R_ASP_82	OD1	3.061
6NF5	R_ARG_61	NH2	R_ASP_82	OD2	3.667
6NF5	R_ARG_103	NH1	R_ASP_85	OD1	3.116

Table 878: 6NF5-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6NFC	C_ARG_38	NH1	C_ASP_86	OD1	3.197
6NFC	C_ARG_38	NH2	C_ASP_86	OD1	2.953
6NFC	C_LYS_43	NZ	C_GLU_46	OE1	2.792
6NFC	C_LYS_43	NZ	C_GLU_46	OE2	3.534
6NFC	C_ARG_53	NH1	L_ASP_659	OD1	3.890
6NFC	C_ARG_53	NH1	L_ASP_659	OD2	2.842
6NFC	C_ARG_53	NH2	L_ASP_659	OD2	2.675
6NFC	C_LYS_64	NZ	C_ASP_61	OD1	2.498
6NFC	C_ARG_66	NH1	C_ASP_86	OD1	3.737
6NFC	C_ARG_66	NH1	C_ASP_86	OD2	2.795
6NFC	C_ARG_66	NH2	C_ASP_86	OD1	3.194
6NFC	C_ARG_66	NH2	C_ASP_86	OD2	3.686
6NFC	C_LYS_100E	NZ	C_ASP_101	OD2	2.741
6NFC	D_ARG_54	NH1	D_ASP_60	OD1	3.484
6NFC	D_ARG_61	NH1	D_ASP_82	OD1	3.021
6NFC	D_ARG_61	NH1	D_ASP_82	OD2	3.736
6NFC	D_ARG_103	NH2	D_ASP_85	OD1	3.716
6NFC	D_ARG_103	NH2	D_ASP_85	OD2	3.091
6NFC	A_LYS_46	NZ	B_ASP_632	OD1	3.913
6NFC	A_LYS_46	NZ	B_ASP_632	OD2	2.455
6NFC	A_LYS_97	NZ	A_GLU_275	OE2	3.627
6NFC	A_LYS_137	NZ	L_ASP_51	OD2	2.690
6NFC	A_ARG_178	NH2	A_GLU_153	OE1	3.848
6NFC	A_ARG_178	NH2	A_GLU_153	OE2	3.063
6NFC	A_LYS_227	NZ	A_GLU_83	OE1	2.893
6NFC	A_LYS_229	NZ	A_GLU_83	OE2	2.829
6NFC	A_LYS_231	NZ	A_GLU_268	OE2	3.327
6NFC	A_LYS_232	NZ	A_GLU_268	OE1	3.542
6NFC	A_LYS_232	NZ	A_GLU_269	OE2	3.983
6NFC	A_LYS_282	NZ	A_GLU_275	OE1	3.354
6NFC	A_ARG_298	NH2	A_GLU_381	OE1	3.053
6NFC	A_ARG_308	NH1	A_GLU_164	OE2	2.885
6NFC	A_LYS_335	NZ	A_ASP_412	OD2	2.571
6NFC	A_LYS_351	NZ	A_GLU_269	OE1	3.918
6NFC	A_LYS_351	NZ	A_GLU_269	OE2	3.924
6NFC	A_ARG_429	NH2	A_ASP_113	OD2	3.338
6NFC	A_ARG_456	NH2	A_GLU_466	OE1	2.989
6NFC	A_ARG_456	NH2	A_GLU_466	OE2	3.574
6NFC	A_ARG_469	NH2	A_ASP_457	OD1	3.689
6NFC	A_ARG_469	NH2	A_ASP_457	OD2	3.083
6NFC	A_ARG_476	NH1	A_ASP_474	OD1	3.258
6NFC	A_ARG_476	NH1	A_ASP_474	OD2	3.799
6NFC	A_ARG_476	NH2	A_GLU_102	OE1	3.757
6NFC	A_ARG_476	NH2	A_GLU_102	OE2	3.100
6NFC	A_ARG_480	NH1	A_ASP_477	OD1	2.962
6NFC	A_LYS_487	NZ	A_ASP_47	OD1	2.724
6NFC	A_LYS_487	NZ	A_ASP_47	OD2	3.863
6NFC	A_LYS_487	NZ	A_GLU_91	OE1	3.844
6NFC	B_ARG_542	NH1	G_GLU_647	OE1	3.297
6NFC	B_ARG_542	NH1	G_GLU_647	OE2	3.640
6NFC	B_LYS_574	NZ	A_GLU_106	OE1	3.608
6NFC	B_LYS_574	NZ	A_GLU_106	OE2	2.473
6NFC	B_ARG_579	NH2	G_GLU_584	OE1	3.071
6NFC	B_ARG_579	NH2	G_GLU_584	OE2	3.850
6NFC	B_HIS_585	NE2	B_ASP_589	OD2	3.555
6NFC	B_ARG_617	NH1	B_GLU_634	OE1	2.878
6NFC	B_ARG_617	NH1	B_GLU_634	OE2	3.440

6NFC	B_ARG_617	NH2	B_GLU_621	OE2	2.967
6NFC	H_LYS_19	NZ	H_GLU_81	OE1	3.943
6NFC	H_HIS_35	NE2	H_ASP_95	OD2	2.826
6NFC	H_ARG_38	NH1	H_ASP_86	OD1	2.925
6NFC	H_ARG_38	NH2	H_GLU_46	OE1	2.914
6NFC	H_ARG_38	NH2	H_GLU_46	OE2	3.729
6NFC	H_LYS_62	NZ	H_GLU_46	OE2	3.377
6NFC	H_ARG_66	NH2	H_ASP_86	OD1	2.882
6NFC	H_ARG_66	NH2	H_ASP_86	OD2	3.067
6NFC	H_ARG_98	NH2	H_ASP_95	OD1	3.740
6NFC	L_LYS_50	NZ	H_GLU_99	OE1	3.024
6NFC	L_ARG_61	NH1	L_GLU_81	OE2	3.132
6NFC	L_ARG_61	NH1	L_ASP_82	OD1	3.859
6NFC	L_ARG_61	NH1	L_ASP_82	OD2	2.905
6NFC	L_LYS_103	NZ	L_ASP_85	OD1	2.838
6NFC	L_LYS_103	NZ	L_ASP_85	OD2	3.467
6NFC	J_ARG_38	NH1	J_ASP_86	OD1	3.229
6NFC	J_ARG_38	NH2	J_ASP_86	OD1	2.989
6NFC	J_LYS_43	NZ	J_GLU_46	OE1	2.802
6NFC	J_LYS_43	NZ	J_GLU_46	OE2	3.573
6NFC	J_ARG_53	NH1	J_ASP_52A	OD1	3.966
6NFC	J_ARG_53	NH1	G_ASP_659	OD1	3.783
6NFC	J_ARG_53	NH1	G_ASP_659	OD2	2.774
6NFC	J_ARG_53	NH2	G_ASP_659	OD2	2.735
6NFC	J_LYS_64	NZ	J_ASP_61	OD1	2.518
6NFC	J_ARG_66	NH1	J_ASP_86	OD1	3.718
6NFC	J_ARG_66	NH1	J_ASP_86	OD2	2.782
6NFC	J_ARG_66	NH2	J_ASP_86	OD1	3.192
6NFC	J_ARG_66	NH2	J_ASP_86	OD2	3.698
6NFC	J_LYS_75	NZ	J_ASP_72	OD2	2.500
6NFC	J_LYS_100E	NZ	J_ASP_101	OD2	2.686
6NFC	M_ARG_103	NH2	M_ASP_85	OD1	3.649
6NFC	M_ARG_103	NH2	M_ASP_85	OD2	3.061
6NFC	E_LYS_46	NZ	E_GLU_492	OE1	2.958
6NFC	E_LYS_46	NZ	G_ASP_632	OD1	3.927
6NFC	E_LYS_46	NZ	G_ASP_632	OD2	2.442
6NFC	E_HIS_85	NE2	E_GLU_87	OE1	3.993
6NFC	E_ARG_178	NH2	E_GLU_153	OE1	3.884
6NFC	E_ARG_178	NH2	E_GLU_153	OE2	3.098
6NFC	E_LYS_227	NZ	E_GLU_83	OE1	2.898
6NFC	E_LYS_229	NZ	E_GLU_83	OE2	2.894
6NFC	E_LYS_232	NZ	E_GLU_269	OE2	3.820
6NFC	E_HIS_249	NE2	E_GLU_482	OE1	3.961
6NFC	E_LYS_282	NZ	E_GLU_275	OE1	2.898
6NFC	E_LYS_282	NZ	E_GLU_275	OE2	3.574
6NFC	E_ARG_298	NH1	E_GLU_381	OE2	3.008
6NFC	E_ARG_308	NH1	E_GLU_164	OE2	2.931
6NFC	E_LYS_335	NZ	E_ASP_412	OD1	3.769
6NFC	E_LYS_335	NZ	E_ASP_412	OD2	2.805
6NFC	E_LYS_351	NZ	E_GLU_269	OE2	3.378
6NFC	E_ARG_429	NH2	E_ASP_113	OD2	3.262
6NFC	E_ARG_456	NH2	E_GLU_466	OE1	2.769
6NFC	E_ARG_456	NH2	E_GLU_466	OE2	3.322
6NFC	E_ARG_469	NH2	E_ASP_457	OD1	3.712
6NFC	E_ARG_469	NH2	E_ASP_457	OD2	3.034
6NFC	E_ARG_476	NH1	E_ASP_474	OD1	3.318
6NFC	E_ARG_476	NH1	E_ASP_474	OD2	3.890
6NFC	E_ARG_476	NH2	E_GLU_102	OE1	3.764

6NFC	E_ARG_476	NH2	E_GLU_102	OE2	3.083
6NFC	E_ARG_480	NH1	E_ASP_477	OD1	2.952
6NFC	E_LYS_487	NZ	E_ASP_47	OD1	2.725
6NFC	E_LYS_487	NZ	E_ASP_47	OD2	3.874
6NFC	E_LYS_487	NZ	E_GLU_91	OE1	3.818
6NFC	E_ARG_500	NH2	I_ASP_664	OD1	2.950
6NFC	E_ARG_500	NH2	I_ASP_664	OD2	3.747
6NFC	G_ARG_542	NH1	I_GLU_647	OE1	3.321
6NFC	G_ARG_542	NH1	I_GLU_647	OE2	3.884
6NFC	G_LYS_574	NZ	E_GLU_106	OE1	3.312
6NFC	G_LYS_574	NZ	E_GLU_106	OE2	2.741
6NFC	G_ARG_579	NH2	I_GLU_584	OE1	3.032
6NFC	G_ARG_579	NH2	I_GLU_584	OE2	3.885
6NFC	G_HIS_585	NE2	G_ASP_589	OD2	3.475
6NFC	G_LYS_601	NZ	I_GLU_657	OE1	2.933
6NFC	G_LYS_601	NZ	I_GLU_657	OE2	3.730
6NFC	G_ARG_617	NH1	G_GLU_634	OE1	3.252
6NFC	G_ARG_617	NH1	G_GLU_634	OE2	3.637
6NFC	G_ARG_617	NH2	G_GLU_621	OE2	3.149
6NFC	F_LYS_46	NZ	F_GLU_492	OE1	3.791
6NFC	F_LYS_46	NZ	I_ASP_632	OD1	3.960
6NFC	F_LYS_46	NZ	I_ASP_632	OD2	2.474
6NFC	F_LYS_117	NZ	F_ASP_113	OD1	3.918
6NFC	F_LYS_117	NZ	F_ASP_113	OD2	2.461
6NFC	F_ARG_178	NH2	F_GLU_153	OE1	3.758
6NFC	F_LYS_227	NZ	F_GLU_83	OE1	2.903
6NFC	F_LYS_229	NZ	F_GLU_83	OE2	2.947
6NFC	F_LYS_232	NZ	F_GLU_268	OE1	3.618
6NFC	F_LYS_232	NZ	F_GLU_269	OE2	3.891
6NFC	F_HIS_249	NE2	F_GLU_482	OE1	3.968
6NFC	F_LYS_282	NZ	F_GLU_275	OE1	2.886
6NFC	F_LYS_282	NZ	F_GLU_275	OE2	3.568
6NFC	F_ARG_298	NH2	F_GLU_381	OE1	3.051
6NFC	F_ARG_308	NH1	F_GLU_164	OE2	2.946
6NFC	F_LYS_335	NZ	F_ASP_412	OD2	2.846
6NFC	F_LYS_351	NZ	F_GLU_269	OE1	3.913
6NFC	F_LYS_351	NZ	F_GLU_269	OE2	3.773
6NFC	F_ARG_429	NH1	F_ASP_113	OD1	3.014
6NFC	F_ARG_429	NH2	F_ASP_113	OD1	2.930
6NFC	F_ARG_456	NH2	F_GLU_466	OE1	2.974
6NFC	F_ARG_456	NH2	F_GLU_466	OE2	3.635
6NFC	F_ARG_469	NH2	F_ASP_457	OD1	3.660
6NFC	F_ARG_469	NH2	F_ASP_457	OD2	3.070
6NFC	F_ARG_476	NH1	F_ASP_474	OD1	3.311
6NFC	F_ARG_476	NH1	F_ASP_474	OD2	3.824
6NFC	F_ARG_476	NH2	F_GLU_102	OE1	3.903
6NFC	F_ARG_480	NH1	F_ASP_477	OD1	2.871
6NFC	F_LYS_487	NZ	F_ASP_47	OD1	2.719
6NFC	F_LYS_487	NZ	F_ASP_47	OD2	3.910
6NFC	F_LYS_502	NZ	B_ASP_664	OD1	3.023
6NFC	I_ARG_542	NH1	B_GLU_647	OE1	3.339
6NFC	I_ARG_542	NH1	B_GLU_647	OE2	3.856
6NFC	I_LYS_574	NZ	F_ASP_107	OD1	2.742
6NFC	I_ARG_579	NH2	B_GLU_584	OE1	3.222
6NFC	I_ARG_579	NH2	B_GLU_584	OE2	3.762
6NFC	I_HIS_585	NE2	I_ASP_589	OD2	3.720
6NFC	I_LYS_601	NZ	B_GLU_657	OE1	3.945
6NFC	I_ARG_617	NH1	I_GLU_634	OE1	3.726

6NFC	K_ARG_38	NH1	K_ASP_86	OD1	3.022
6NFC	K_ARG_38	NH2	K_GLU_46	OE1	2.916
6NFC	K_ARG_38	NH2	K_GLU_46	OE2	3.525
6NFC	K_ARG_53	NH1	B_ASP_659	OD1	3.915
6NFC	K_ARG_53	NH1	B_ASP_659	OD2	2.784
6NFC	K_ARG_53	NH2	B_ASP_659	OD2	2.738
6NFC	K_LYS_64	NZ	K_ASP_61	OD1	3.796
6NFC	K_ARG_66	NH1	K_ASP_86	OD1	3.739
6NFC	K_ARG_66	NH1	K_ASP_86	OD2	2.801
6NFC	K_ARG_66	NH2	K_ASP_86	OD1	3.263
6NFC	K_ARG_66	NH2	K_ASP_86	OD2	3.749
6NFC	K_LYS_75	NZ	K_ASP_72	OD2	3.979
6NFC	K_LYS_100E	NZ	K_ASP_101	OD2	2.756
6NFC	N_ARG_54	NH1	N_ASP_60	OD1	3.576
6NFC	N_ARG_61	NH1	N_ASP_82	OD1	2.937
6NFC	N_ARG_61	NH1	N_ASP_82	OD2	3.695
6NFC	N_ARG_103	NH2	N_ASP_85	OD1	3.716
6NFC	N_ARG_103	NH2	N_ASP_85	OD2	3.096

Table 879: 6NFC-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6NMR	L_ARG_24	NH1	L_GLU_70	OE2	3.158
6NMR	L_ARG_39	NH2	L_GLU_81	OE1	3.616
6NMR	L_ARG_61	NH1	L_GLU_81	OE2	3.707
6NMR	L_ARG_61	NH1	L_ASP_82	OD1	2.354
6NMR	L_ARG_61	NH1	L_ASP_82	OD2	2.889
6NMR	L_ARG_61	NH2	L_GLU_81	OE2	2.699
6NMR	L_ARG_61	NH2	L_ASP_82	OD1	3.976
6NMR	L_LYS_150	NZ	L_GLU_196	OE1	3.160
6NMR	L_HIS_190	ND1	L_ASP_152	OD2	3.477
6NMR	L_ARG_212	NH1	L_GLU_188	OE1	3.201
6NMR	H_ARG_38	NH1	H_GLU_46	OE2	3.009
6NMR	H_ARG_38	NH1	H_ASP_88	OD1	3.678
6NMR	H_ARG_38	NH2	H_ASP_88	OD1	2.935
6NMR	H_ARG_65	NH1	H_ASP_88	OD1	3.496
6NMR	H_ARG_65	NH1	H_ASP_88	OD2	2.506
6NMR	H_ARG_65	NH2	H_ASP_88	OD1	3.005
6NMR	H_ARG_65	NH2	H_ASP_88	OD2	3.455
6NMR	H_LYS_96	NZ	H_ASP_108	OD1	3.882
6NMR	H_LYS_96	NZ	H_ASP_108	OD2	2.332
6NMR	H_LYS_150	NZ	H_ASP_151	OD1	3.197
6NMR	H_LYS_150	NZ	H_ASP_151	OD2	3.273
6NMR	H_LYS_216	NZ	L_GLU_124	OE1	3.273
6NMR	H_LYS_216	NZ	L_GLU_124	OE2	3.010
6NMR	H_LYS_217	NZ	H_GLU_219	OE1	3.365
6NMR	H_LYS_217	NZ	H_GLU_219	OE2	3.978
6NMR	S_ARG_24	NH1	S_ASP_10	OD2	3.980
6NMR	S_ARG_24	NH2	S_ASP_10	OD1	3.502
6NMR	S_ARG_40	NH2	S_GLU_47	OE2	2.570
6NMR	S_ARG_46	NH1	S_GLU_103	OE1	3.842
6NMR	S_ARG_46	NH1	S_GLU_103	OE2	3.579
6NMR	S_ARG_46	NH2	S_GLU_103	OE2	2.903
6NMR	S_ARG_59	NH1	S_ASP_85	OD1	3.806
6NMR	S_ARG_59	NH1	S_ASP_85	OD2	3.028
6NMR	S_ARG_59	NH2	S_ASP_85	OD2	2.222
6NMR	S_ARG_69	NH1	L_GLU_55	OE1	3.247
6NMR	S_ARG_69	NH1	L_GLU_55	OE2	3.038
6NMR	S_ARG_69	NH2	L_GLU_55	OE2	3.173
6NMR	B_ARG_39	NH2	B_GLU_81	OE2	3.427
6NMR	B_ARG_61	NH1	B_ASP_82	OD1	2.926
6NMR	B_ARG_61	NH1	B_ASP_82	OD2	2.375
6NMR	B_ARG_61	NH2	B_GLU_81	OE2	3.579
6NMR	B_ARG_61	NH2	B_ASP_82	OD1	3.952
6NMR	B_LYS_189	NZ	B_ASP_186	OD1	3.729
6NMR	B_ARG_212	NH1	B_GLU_188	OE1	3.038
6NMR	A_ARG_38	NH1	A_GLU_46	OE1	2.680
6NMR	A_ARG_38	NH1	A_GLU_87	OE2	3.236
6NMR	A_ARG_38	NH2	A_GLU_87	OE2	3.845
6NMR	A_ARG_65	NH1	A_ASP_88	OD1	3.503
6NMR	A_ARG_65	NH1	A_ASP_88	OD2	2.589
6NMR	A_ARG_65	NH2	A_ASP_88	OD1	2.928
6NMR	A_ARG_65	NH2	A_ASP_88	OD2	3.469
6NMR	A_LYS_74	NZ	A_ASP_71	OD2	3.116
6NMR	A_LYS_150	NZ	A_ASP_151	OD1	3.635
6NMR	A_LYS_150	NZ	A_ASP_151	OD2	3.589
6NMR	E_ARG_40	NH1	E_GLU_47	OE1	3.843
6NMR	E_ARG_40	NH1	E_GLU_47	OE2	3.651
6NMR	E_ARG_59	NH1	E_ASP_85	OD2	3.106

6NMR	E_ARG_69	NH1	B_GLU_55	OE1	2.733
6NMR	E_ARG_69	NH1	B_GLU_55	OE2	2.469
6NMR	E_ARG_69	NH2	B_GLU_55	OE1	2.510
6NMR	E_ARG_69	NH2	B_GLU_55	OE2	3.637
6NMR	G_ARG_24	NH1	G_GLU_70	OE2	3.551
6NMR	G_ARG_61	NH1	G_GLU_81	OE1	3.642
6NMR	G_ARG_61	NH2	G_GLU_81	OE1	3.695
6NMR	G_ARG_61	NH2	G_ASP_82	OD1	3.089
6NMR	G_ARG_61	NH2	G_ASP_82	OD2	3.380
6NMR	G_LYS_150	NZ	G_GLU_196	OE1	2.752
6NMR	G_HIS_190	ND1	G_ASP_152	OD2	3.424
6NMR	G_HIS_190	NE2	G_ASP_186	OD1	3.299
6NMR	G_ARG_212	NH1	G_GLU_188	OE1	3.625
6NMR	F_ARG_38	NH1	F_GLU_46	OE1	2.763
6NMR	F_ARG_38	NH2	F_ASP_88	OD1	3.207
6NMR	F_LYS_63	NZ	F_ASP_60	OD1	3.920
6NMR	F_ARG_65	NH1	F_ASP_88	OD2	3.068
6NMR	F_ARG_65	NH2	F_ASP_88	OD1	3.379
6NMR	F_ARG_65	NH2	F_ASP_88	OD2	3.500
6NMR	F_LYS_96	NZ	F_ASP_108	OD1	3.703
6NMR	F_LYS_96	NZ	F_ASP_108	OD2	2.983
6NMR	F_LYS_150	NZ	F_ASP_151	OD2	3.277
6NMR	F_LYS_217	NZ	F_GLU_219	OE1	3.922
6NMR	I_ARG_46	NH1	I_GLU_103	OE2	3.225
6NMR	I_ARG_46	NH2	I_GLU_103	OE2	3.674
6NMR	I_ARG_69	NH1	G_GLU_55	OE1	3.183
6NMR	I_ARG_69	NH1	G_GLU_55	OE2	2.119
6NMR	I_ARG_69	NH1	F_ASP_108	OD2	3.629
6NMR	I_ARG_69	NH2	G_GLU_55	OE1	2.639
6NMR	I_ARG_69	NH2	G_GLU_55	OE2	3.327
6NMR	K_ARG_54	NH2	K_GLU_60	OE2	3.656
6NMR	K_ARG_61	NH1	K_GLU_81	OE1	3.042
6NMR	K_ARG_61	NH2	K_GLU_81	OE1	3.659
6NMR	K_ARG_61	NH2	K_ASP_82	OD1	2.679
6NMR	K_ARG_61	NH2	K_ASP_82	OD2	3.306
6NMR	K_LYS_104	NZ	K_GLU_106	OE2	3.287
6NMR	K_LYS_150	NZ	K_GLU_196	OE1	3.084
6NMR	K_HIS_190	ND1	K_ASP_186	OD1	3.859
6NMR	K_ARG_212	NH1	K_GLU_188	OE2	3.131
6NMR	J_ARG_38	NH1	J_GLU_46	OE1	3.889
6NMR	J_ARG_38	NH1	J_GLU_46	OE2	3.293
6NMR	J_ARG_38	NH1	J_ASP_88	OD1	3.807
6NMR	J_ARG_38	NH2	J_ASP_88	OD1	2.826
6NMR	J_ARG_65	NH1	J_ASP_88	OD1	3.631
6NMR	J_ARG_65	NH1	J_ASP_88	OD2	2.729
6NMR	J_ARG_65	NH2	J_ASP_88	OD1	3.014
6NMR	J_ARG_65	NH2	J_ASP_88	OD2	3.359
6NMR	M_ARG_24	NH1	M_ASP_10	OD1	3.002
6NMR	M_ARG_24	NH1	M_ASP_10	OD2	3.370
6NMR	M_ARG_59	NH1	M_ASP_85	OD1	3.222
6NMR	M_ARG_59	NH1	M_ASP_85	OD2	2.493
6NMR	M_ARG_59	NH2	M_ASP_85	OD1	2.536
6NMR	M_ARG_59	NH2	M_ASP_85	OD2	3.074
6NMR	M_ARG_69	NH1	J_ASP_108	OD1	3.945
6NMR	M_ARG_69	NH1	J_ASP_108	OD2	3.140
6NMR	M_ARG_69	NH2	K_GLU_55	OE1	3.608
6NMR	M_ARG_69	NH2	J_ASP_108	OD1	1.901
6NMR	M_ARG_69	NH2	J_ASP_108	OD2	2.331

Table 880: 6NMR-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6NMS	L_ARG_24	NH2	L_GLU_70	OE2	3.738
6NMS	L_ARG_54	NH1	L_ASP_60	OD1	3.255
6NMS	L_ARG_61	NH2	L_ASP_82	OD1	2.892
6NMS	L_ARG_61	NH2	L_ASP_82	OD2	3.481
6NMS	L_ARG_94	NH2	S_GLU_111	OE1	3.728
6NMS	L_LYS_104	NZ	L_GLU_166	OE1	2.765
6NMS	L_LYS_104	NZ	L_GLU_166	OE2	3.798
6NMS	L_LYS_184	NZ	L_GLU_188	OE2	3.523
6NMS	L_LYS_189	NZ	L_ASP_186	OD1	3.714
6NMS	L_HIS_190	ND1	L_ASP_152	OD2	3.478
6NMS	L_ARG_212	NH1	L_GLU_188	OE1	3.865
6NMS	H_ARG_38	NH1	H_ASP_90	OD1	2.876
6NMS	H_ARG_38	NH2	H_GLU_46	OE1	3.437
6NMS	H_ARG_38	NH2	H_GLU_46	OE2	3.436
6NMS	H_ARG_67	NH1	H_ASP_90	OD2	2.785
6NMS	H_ARG_67	NH2	H_ASP_90	OD1	3.162
6NMS	H_ARG_67	NH2	H_ASP_90	OD2	3.281
6NMS	H_LYS_98	NZ	H_ASP_107	OD2	3.621
6NMS	H_ARG_104	NH1	H_ASP_33	OD2	3.391
6NMS	H_ARG_104	NH1	H_GLU_99	OE1	2.855
6NMS	H_ARG_104	NH1	H_GLU_99	OE2	3.265
6NMS	H_ARG_104	NH2	S_GLU_111	OE1	3.455
6NMS	H_ARG_104	NH2	S_GLU_111	OE2	2.500
6NMS	H_LYS_149	NZ	H_ASP_150	OD1	3.443
6NMS	H_LYS_149	NZ	H_ASP_150	OD2	3.773
6NMS	H_LYS_215	NZ	L_GLU_124	OE1	3.565
6NMS	H_LYS_215	NZ	L_GLU_124	OE2	3.270
6NMS	H_LYS_220	NZ	L_GLU_214	OE1	3.397
6NMS	S_LYS_11	NZ	H_ASP_33	OD1	3.001
6NMS	S_LYS_11	NZ	H_GLU_99	OE1	2.549
6NMS	S_ARG_40	NH2	S_GLU_47	OE1	2.801
6NMS	S_ARG_46	NH1	S_GLU_103	OE2	2.751
6NMS	S_ARG_46	NH2	S_GLU_103	OE2	3.693
6NMS	S_LYS_53	NZ	S_ASP_101	OD2	3.950
6NMS	S_HIS_56	ND1	A_ASP_60	OD2	2.658
6NMS	S_ARG_59	NH1	S_ASP_85	OD1	2.788
6NMS	S_ARG_59	NH1	S_ASP_85	OD2	3.425
6NMS	S_ARG_59	NH2	S_ASP_85	OD1	3.472
6NMS	S_ARG_59	NH2	S_ASP_85	OD2	2.622
6NMS	A_ARG_54	NH1	A_ASP_60	OD1	3.517
6NMS	A_ARG_61	NH2	A_GLU_81	OE2	3.125
6NMS	A_ARG_61	NH2	A_ASP_82	OD1	2.833
6NMS	A_ARG_61	NH2	A_ASP_82	OD2	3.517
6NMS	A_ARG_94	NH2	C_GLU_111	OE2	3.453
6NMS	A_LYS_104	NZ	A_GLU_166	OE1	3.888
6NMS	A_LYS_104	NZ	A_GLU_166	OE2	3.097
6NMS	A_LYS_189	NZ	A_ASP_186	OD1	3.508
6NMS	A_HIS_190	ND1	A_ASP_152	OD2	3.250
6NMS	A_ARG_212	NH1	A_GLU_188	OE2	2.785
6NMS	B_ARG_38	NH1	B_ASP_90	OD1	2.896
6NMS	B_ARG_38	NH2	B_GLU_46	OE1	3.127
6NMS	B_ARG_38	NH2	B_GLU_46	OE2	3.624
6NMS	B_ARG_67	NH1	B_ASP_90	OD2	3.000
6NMS	B_ARG_67	NH2	B_ASP_90	OD1	3.281
6NMS	B_ARG_67	NH2	B_ASP_90	OD2	3.615
6NMS	B_LYS_98	NZ	B_ASP_108	OD2	3.767
6NMS	B_ARG_104	NH1	B_ASP_33	OD2	2.846

6NMS	B_ARG_104	NH1	B_GLU_99	OE1	2.968
6NMS	B_ARG_104	NH1	B_GLU_99	OE2	3.409
6NMS	B_ARG_104	NH2	C_GLU_111	OE1	2.703
6NMS	B_ARG_104	NH2	C_GLU_111	OE2	3.000
6NMS	B_LYS_149	NZ	B_ASP_150	OD1	3.211
6NMS	B_LYS_149	NZ	B_ASP_150	OD2	3.461
6NMS	C_LYS_11	NZ	B_ASP_33	OD2	3.490
6NMS	C_LYS_11	NZ	B_GLU_99	OE1	2.892
6NMS	C_ARG_24	NH1	C_ASP_10	OD1	2.731
6NMS	C_ARG_24	NH1	C_ASP_10	OD2	2.859
6NMS	C_ARG_40	NH2	C_GLU_47	OE1	2.382
6NMS	C_ARG_46	NH1	C_GLU_103	OE2	2.805
6NMS	C_ARG_46	NH2	C_GLU_103	OE2	3.029
6NMS	C_ARG_59	NH1	C_ASP_85	OD1	3.855
6NMS	C_ARG_59	NH1	C_ASP_85	OD2	3.301
6NMS	C_ARG_59	NH2	C_ASP_85	OD1	2.480
6NMS	C_ARG_59	NH2	C_ASP_85	OD2	3.376
6NMS	C_ARG_115	NH1	B_GLU_56	OE2	3.579
6NMS	C_ARG_115	NH2	B_GLU_56	OE2	2.699

Table 881: 6NMS-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6NMT	A_ARG_26	NH1	A_ASP_46	OD2	3.596
6NMT	A_ARG_26	NH2	C_ASP_10	OD1	3.433
6NMT	A_ARG_26	NH2	C_ASP_10	OD2	3.182
6NMT	A_ARG_56	NH2	A_ASP_76	OD1	3.261
6NMT	A_ARG_56	NH2	A_ASP_77	OD1	2.770
6NMT	A_ARG_56	NH2	A_ASP_77	OD2	3.625
6NMT	A_LYS_144	NZ	A_GLU_190	OE1	2.725
6NMT	A_HIS_184	ND1	A_ASP_146	OD2	2.798
6NMT	A_LYS_185	NZ	A_GLU_208	OE2	2.842
6NMT	A_ARG_206	NH1	A_GLU_182	OE1	3.022
6NMT	B_ARG_38	NH1	B_ASP_89	OD1	2.805
6NMT	B_ARG_38	NH2	B_GLU_46	OE1	2.846
6NMT	B_ARG_38	NH2	B_ASP_89	OD1	3.887
6NMT	B_ARG_56	NH2	C_GLU_111	OE2	3.542
6NMT	B_ARG_66	NH1	B_ASP_89	OD1	3.742
6NMT	B_ARG_66	NH1	B_ASP_89	OD2	2.824
6NMT	B_ARG_66	NH2	B_ASP_89	OD1	2.986
6NMT	B_ARG_66	NH2	B_ASP_89	OD2	3.478
6NMT	B_ARG_97	NH2	B_ASP_107	OD1	3.422
6NMT	B_ARG_97	NH2	B_ASP_107	OD2	2.766
6NMT	B_LYS_149	NZ	B_ASP_150	OD1	3.170
6NMT	B_LYS_149	NZ	B_ASP_150	OD2	2.917
6NMT	B_LYS_215	NZ	A_GLU_118	OE2	3.496
6NMT	C_LYS_11	NZ	A_ASP_91	OD1	2.678
6NMT	C_LYS_11	NZ	A_ASP_91	OD2	3.319
6NMT	C_ARG_40	NH2	C_GLU_47	OE2	2.784
6NMT	C_ARG_46	NH1	C_GLU_103	OE1	3.083
6NMT	C_ARG_46	NH2	C_GLU_103	OE1	3.045
6NMT	C_ARG_59	NH1	C_ASP_85	OD1	3.125
6NMT	C_ARG_59	NH1	C_ASP_85	OD2	3.925
6NMT	C_ARG_59	NH2	C_ASP_85	OD1	3.454
6NMT	C_ARG_59	NH2	C_ASP_85	OD2	2.809
6NMT	C_LYS_105	NZ	C_GLU_3	OE1	2.957

Table 882: 6NMT-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6NMU	L_ARG_24	NH1	L_ASP_70	OD1	3.847
6NMU	L_ARG_24	NH1	L_ASP_70	OD2	3.464
6NMU	L_LYS_32	NZ	S_ASP_85	OD1	3.326
6NMU	L_ARG_61	NH1	L_ASP_82	OD2	2.822
6NMU	L_ARG_61	NH2	L_ASP_82	OD1	2.930
6NMU	L_LYS_150	NH2	L_ASP_82	OD2	3.243
6NMU	L_LYS_150	NZ	L_GLU_196	OE1	3.282
6NMU	L_HIS_190	ND1	L_ASP_152	OD2	3.169
6NMU	H_ARG_13	NH1	H_GLU_16	OE2	3.522
6NMU	H_ARG_13	NH2	H_GLU_16	OE2	3.940
6NMU	H_ARG_38	NH1	H_ASP_90	OD2	3.008
6NMU	H_ARG_38	NH2	H_GLU_46	OE1	3.672
6NMU	H_ARG_38	NH2	H_GLU_46	OE2	3.384
6NMU	H_ARG_50	NH1	S_GLU_47	OE1	3.597
6NMU	H_ARG_50	NH1	S_GLU_47	OE2	3.084
6NMU	H_ARG_50	NH2	S_GLU_47	OE1	2.989
6NMU	H_ARG_50	NH2	S_GLU_47	OE2	3.577
6NMU	H_ARG_67	NH1	H_ASP_90	OD1	2.716
6NMU	H_ARG_67	NH1	H_ASP_90	OD2	3.953
6NMU	H_ARG_67	NH2	H_ASP_90	OD1	3.430
6NMU	H_ARG_67	NH2	H_ASP_90	OD2	3.165
6NMU	H_LYS_98	NZ	H_ASP_107	OD2	2.857
6NMU	H_LYS_149	NZ	H_ASP_150	OD1	3.438
6NMU	S_ARG_24	NH2	S_ASP_10	OD1	3.643
6NMU	S_ARG_24	NH2	S_ASP_10	OD2	2.829
6NMU	S_ARG_46	NH1	S_GLU_103	OE1	3.107
6NMU	S_ARG_46	NH2	S_GLU_103	OE1	3.375
6NMU	S_LYS_53	NZ	S_ASP_101	OD1	3.593
6NMU	S_LYS_53	NZ	S_ASP_101	OD2	3.819
6NMU	S_ARG_59	NH1	S_ASP_85	OD1	2.826
6NMU	S_ARG_59	NH1	S_ASP_85	OD2	3.250
6NMU	S_ARG_59	NH2	H_ASP_101	OD2	3.444
6NMU	S_ARG_59	NH2	S_ASP_85	OD1	3.666
6NMU	S_ARG_59	NH2	S_ASP_85	OD2	2.554
6NMU	A_LYS_32	NZ	C_ASP_85	OD1	3.635
6NMU	A_ARG_61	NH1	A_ASP_82	OD2	2.912
6NMU	A_ARG_61	NH2	A_ASP_82	OD1	3.034
6NMU	A_ARG_61	NH2	A_ASP_82	OD2	3.051
6NMU	A_ARG_98	NH2	A_GLU_1	OE2	3.553
6NMU	B_ARG_38	NH1	B_ASP_90	OD1	3.513
6NMU	B_ARG_38	NH2	B_GLU_46	OE1	3.545
6NMU	B_ARG_38	NH2	B_GLU_46	OE2	3.227
6NMU	B_ARG_50	NH1	C_GLU_47	OE1	3.989
6NMU	B_ARG_50	NH1	C_GLU_47	OE2	3.035
6NMU	B_ARG_50	NH2	C_GLU_47	OE1	2.804
6NMU	B_ARG_50	NH2	C_GLU_47	OE2	3.091
6NMU	B_ARG_67	NH1	B_ASP_90	OD1	3.761
6NMU	B_ARG_67	NH1	B_ASP_90	OD2	2.940
6NMU	B_ARG_67	NH2	B_ASP_90	OD1	2.900
6NMU	B_ARG_67	NH2	B_ASP_90	OD2	3.596
6NMU	B_LYS_98	NZ	B_ASP_107	OD1	2.896
6NMU	B_LYS_149	NZ	B_ASP_150	OD1	3.427
6NMU	B_LYS_149	NZ	B_ASP_150	OD2	3.506
6NMU	B_LYS_215	NZ	A_GLU_124	OE1	3.494
6NMU	B_LYS_215	NZ	A_GLU_124	OE2	3.379
6NMU	B_LYS_216	NZ	B_GLU_218	OE1	3.942
6NMU	C_ARG_24	NH1	C_ASP_10	OD1	3.661

6NMU	C_ARG_24	NH1	C_ASP_10	OD2	3.733
6NMU	C_ARG_24	NH2	C_ASP_10	OD1	3.751
6NMU	C_ARG_46	NH1	C_GLU_103	OE1	2.724
6NMU	C_ARG_46	NH2	C_GLU_103	OE1	3.025
6NMU	C_ARG_59	NH1	B_ASP_101	OD1	3.720
6NMU	C_ARG_59	NH1	B_ASP_101	OD2	2.808
6NMU	C_ARG_59	NH1	C_ASP_85	OD2	3.825
6NMU	C_ARG_59	NH2	C_ASP_85	OD1	2.746
6NMU	C_ARG_59	NH2	C_ASP_85	OD2	3.128

Table 883: 6NMU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6NMV	S_ARG_40	NH2	S_GLU_47	OE2	2.928
6NMV	S_ARG_46	NH1	S_GLU_103	OE1	2.838
6NMV	S_ARG_46	NH1	S_GLU_103	OE2	3.875
6NMV	S_ARG_46	NH2	S_GLU_103	OE1	3.070
6NMV	S_ARG_59	NH1	S_ASP_85	OD1	2.912
6NMV	S_ARG_59	NH1	S_ASP_85	OD2	3.273
6NMV	S_ARG_59	NH2	S_ASP_85	OD1	3.839
6NMV	S_ARG_59	NH2	S_ASP_85	OD2	2.616
6NMV	S_LYS_96	NZ	S_ASP_101	OD1	2.456
6NMV	S_LYS_96	NZ	S_ASP_101	OD2	3.521
6NMV	H_ARG_38	NH1	H_ASP_90	OD2	2.817
6NMV	H_ARG_38	NH2	H_ASP_90	OD2	3.510
6NMV	H_ARG_67	NH1	H_ASP_90	OD1	2.934
6NMV	H_ARG_67	NH1	H_ASP_90	OD2	3.250
6NMV	H_ARG_67	NH2	H_ASP_90	OD1	3.025
6NMV	H_ARG_67	NH2	H_ASP_90	OD2	2.954
6NMV	H_LYS_76	NZ	H_ASP_73	OD1	2.991
6NMV	H_LYS_76	NZ	H_ASP_73	OD2	2.854
6NMV	H_HIS_103	ND1	H_ASP_102	OD1	3.753
6NMV	H_HIS_103	ND1	H_ASP_102	OD2	3.398
6NMV	H_LYS_211	NZ	H_GLU_213	OE2	3.838
6NMV	L_ARG_56	NH2	L_GLU_76	OE1	3.634
6NMV	L_ARG_56	NH2	L_GLU_76	OE2	3.096
6NMV	L_ARG_56	NH2	L_ASP_77	OD1	2.690
6NMV	L_ARG_56	NH2	L_ASP_77	OD2	3.240
6NMV	L_LYS_162	NZ	L_GLU_78	OE2	3.175
6NMV	L_ARG_185	NH1	L_ASP_147	OD2	3.022

Table 884: 6NMV-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6O9B	A_HIS_3	ND1	A_ASP_29	OD1	3.484
6O9B	A_HIS_3	ND1	A_ASP_29	OD2	2.647
6O9B	A_ARG_6	NH2	A_ASP_102	OD1	3.670
6O9B	A_ARG_14	NH1	A_ASP_39	OD1	2.811
6O9B	A_ARG_14	NH1	A_ASP_39	OD2	3.600
6O9B	A_ARG_14	NH2	A_ASP_39	OD1	3.638
6O9B	A_ARG_14	NH2	A_ASP_39	OD2	2.902
6O9B	A_ARG_21	NH2	A_ASP_37	OD1	3.576
6O9B	A_ARG_21	NH2	A_ASP_37	OD2	2.758
6O9B	A_ARG_35	NH1	B_ASP_73	OD1	2.773
6O9B	A_ARG_35	NH1	B_ASP_73	OD2	3.974
6O9B	A_ARG_35	NH2	A_GLU_46	OE1	3.894
6O9B	A_ARG_35	NH2	A_GLU_46	OE2	3.171
6O9B	A_ARG_44	NH1	A_ASP_61	OD1	3.041
6O9B	A_ARG_44	NH2	A_ASP_61	OD1	3.227
6O9B	A_ARG_48	NH2	B_ASP_73	OD2	3.479
6O9B	A_ARG_75	NH1	A_GLU_19	OE2	3.730
6O9B	A_HIS_93	ND1	A_ASP_119	OD1	3.532
6O9B	A_HIS_93	ND1	A_ASP_119	OD2	2.838
6O9B	A_ARG_111	NH1	A_GLU_128	OE1	3.371
6O9B	A_ARG_111	NH2	A_ASP_102	OD2	3.967
6O9B	A_ARG_114	NH1	A_ASP_116	OD1	3.450
6O9B	A_ARG_114	NH1	A_ASP_116	OD2	2.611
6O9B	A_HIS_151	ND1	A_GLU_154	OE1	3.521
6O9B	A_HIS_151	ND1	A_GLU_154	OE2	3.425
6O9B	A_ARG_169	NH1	A_GLU_166	OE2	3.051
6O9B	A_ARG_170	NH1	A_GLU_166	OE1	3.610
6O9B	A_LYS_176	NZ	A_GLU_173	OE2	2.914
6O9B	A_ARG_181	NH1	A_ASP_183	OD2	2.854
6O9B	A_HIS_191	NE2	A_GLU_254	OE2	2.884
6O9B	A_HIS_192	ND1	B_ASP_118	OD2	3.864
6O9B	A_ARG_256	NH1	A_GLU_253	OE2	3.337
6O9B	A_ARG_256	NH2	A_ASP_220	OD1	3.231
6O9B	A_ARG_256	NH2	A_ASP_220	OD2	3.184
6O9B	B_ARG_65	NH2	B_ASP_58	OD1	3.970
6O9B	B_LYS_95	NZ	B_GLU_94	OE2	3.964
6O9B	B_ARG_101	NH1	B_ASP_58	OD2	3.244
6O9B	C_LYS_9	NZ	A_ASP_116	OD2	2.706

Table 885: 6O9B-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6O9C	A_HIS_3	ND1	A_ASP_29	OD1	3.533
6O9C	A_HIS_3	ND1	A_ASP_29	OD2	2.591
6O9C	A_ARG_14	NH2	A_ASP_39	OD1	3.395
6O9C	A_ARG_14	NH2	A_ASP_39	OD2	3.458
6O9C	A_ARG_21	NH1	A_ASP_39	OD2	3.725
6O9C	A_ARG_21	NH2	A_ASP_37	OD1	3.787
6O9C	A_ARG_21	NH2	A_ASP_37	OD2	3.069
6O9C	A_ARG_35	NH1	A_ASP_37	OD2	3.939
6O9C	A_ARG_35	NH1	B_ASP_73	OD1	3.395
6O9C	A_ARG_35	NH2	A_GLU_46	OE1	3.628
6O9C	A_ARG_35	NH2	A_GLU_46	OE2	2.787
6O9C	A_ARG_44	NH1	A_ASP_61	OD1	3.116
6O9C	A_ARG_44	NH2	A_ASP_61	OD1	2.964
6O9C	A_ARG_48	NH1	A_GLU_46	OE1	3.653
6O9C	A_ARG_48	NH2	A_GLU_46	OE1	3.457
6O9C	A_HIS_93	ND1	A_ASP_119	OD1	3.563
6O9C	A_HIS_93	ND1	A_ASP_119	OD2	2.884
6O9C	A_ARG_108	NH2	A_ASP_106	OD1	3.075
6O9C	A_ARG_111	NH1	A_ASP_102	OD2	3.448
6O9C	A_ARG_114	NH1	A_ASP_116	OD1	3.523
6O9C	A_ARG_114	NH1	A_ASP_116	OD2	2.739
6O9C	A_ARG_169	NH2	A_GLU_166	OE2	3.041
6O9C	A_ARG_170	NH1	A_GLU_166	OE1	3.871
6O9C	A_LYS_176	NZ	A_GLU_173	OE2	3.474
6O9C	A_HIS_191	NE2	A_GLU_254	OE2	2.693
6O9C	A_HIS_192	NE2	B_ASP_118	OD2	3.199
6O9C	A_ARG_202	NH1	B_ASP_118	OD2	3.014
6O9C	A_ARG_256	NH1	A_ASP_220	OD2	3.945
6O9C	A_ARG_256	NH1	A_GLU_253	OE2	3.454
6O9C	A_ARG_256	NH2	A_ASP_220	OD1	3.827
6O9C	A_ARG_256	NH2	A_ASP_220	OD2	2.698
6O9C	B_ARG_23	NH1	B_ASP_79	OD2	3.597
6O9C	B_LYS_26	NZ	A_GLU_232	OE2	3.913
6O9C	B_LYS_39	NZ	B_GLU_36	OE1	3.574
6O9C	B_ARG_65	NH1	B_ASP_58	OD1	3.907
6O9C	B_ARG_65	NH1	B_GLU_67	OE2	3.387
6O9C	B_ARG_101	NH2	B_ASP_58	OD2	3.040
6O9C	C_LYS_9	NZ	A_ASP_77	OD2	3.855
6O9C	C_LYS_9	NZ	A_ASP_116	OD2	2.984

Table 886: 6O9C-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6OGX	C_LYS_12	NZ	C_GLU_10	OE2	3.904
6OGX	C_ARG_38	NH1	C_ASP_90	OD1	2.937
6OGX	C_ARG_38	NH2	C_GLU_46	OE2	3.462
6OGX	C_ARG_67	NH1	C_ASP_90	OD1	3.674
6OGX	C_ARG_67	NH1	C_ASP_90	OD2	2.808
6OGX	C_ARG_67	NH2	C_ASP_90	OD1	2.780
6OGX	C_ARG_67	NH2	C_ASP_90	OD2	3.408
6OGX	C_ARG_101	NH2	C_ASP_50	OD1	2.908
6OGX	C_ARG_101	NH2	C_ASP_50	OD2	3.364
6OGX	C_LYS_147	NZ	C_ASP_148	OD1	3.403
6OGX	C_LYS_147	NZ	C_ASP_148	OD2	3.834
6OGX	C_LYS_213	NZ	D_GLU_123	OE1	2.791
6OGX	C_LYS_213	NZ	D_GLU_123	OE2	3.773
6OGX	C_LYS_218	NZ	D_ASP_122	OD2	3.785
6OGX	D_ARG_24	NH1	D_ASP_70	OD1	2.881
6OGX	D_ARG_24	NH2	D_ASP_70	OD1	3.409
6OGX	D_ARG_24	NH2	D_ASP_70	OD2	3.280
6OGX	D_ARG_55	NH2	G_ASP_117	OD1	2.990
6OGX	D_ARG_61	NH2	D_GLU_81	OE1	3.619
6OGX	D_ARG_61	NH2	D_ASP_82	OD1	2.844
6OGX	D_ARG_61	NH2	D_ASP_82	OD2	3.707
6OGX	D_HIS_189	ND1	D_ASP_151	OD2	3.260
6OGX	D_LYS_190	NZ	D_GLU_213	OE1	3.539
6OGX	G_ARG_95	NH1	H_ASP_99	OD1	3.462
6OGX	G_ARG_95	NH1	H_ASP_99	OD2	2.833
6OGX	G_ARG_95	NH2	H_ASP_99	OD1	2.923
6OGX	G_ARG_95	NH2	H_ASP_99	OD2	3.646
6OGX	G_LYS_96	NZ	G_GLU_94	OE2	3.997
6OGX	G_ARG_110	NH2	G_GLU_94	OE1	3.529
6OGX	G_LYS_120	NZ	G_ASP_117	OD1	3.499
6OGX	G_LYS_120	NZ	G_ASP_117	OD2	3.674
6OGX	H_LYS_12	NZ	H_GLU_10	OE1	3.316
6OGX	H_ARG_38	NH1	H_ASP_90	OD2	2.947
6OGX	H_ARG_38	NH2	H_GLU_46	OE1	3.229
6OGX	H_ARG_38	NH2	H_ASP_90	OD2	3.994
6OGX	H_LYS_63	NZ	H_GLU_46	OE1	3.798
6OGX	H_LYS_63	NZ	H_GLU_46	OE2	2.760
6OGX	H_ARG_67	NH1	H_ASP_90	OD1	3.110
6OGX	H_ARG_67	NH1	H_ASP_90	OD2	3.101
6OGX	H_ARG_67	NH2	H_ASP_90	OD1	3.614
6OGX	H_ARG_67	NH2	H_ASP_90	OD2	2.757
6OGX	H_ARG_87	NH2	H_GLU_89	OE2	3.153
6OGX	H_ARG_98	NH1	H_ASP_102	OD1	3.528
6OGX	H_ARG_98	NH1	H_ASP_102	OD2	2.722
6OGX	H_ARG_100	NH1	L_GLU_55	OE1	3.516
6OGX	H_ARG_100	NH1	L_GLU_55	OE2	2.787
6OGX	H_LYS_144	NZ	H_ASP_145	OD1	3.450
6OGX	H_LYS_144	NZ	H_ASP_145	OD2	2.902
6OGX	H_LYS_211	NZ	H_GLU_213	OE1	2.815
6OGX	L_ARG_61	NH2	L_ASP_82	OD1	2.857
6OGX	L_ARG_61	NH2	L_ASP_82	OD2	3.713
6OGX	L_LYS_103	NZ	L_GLU_165	OE1	2.789
6OGX	L_LYS_103	NZ	L_GLU_165	OE2	3.599

Table 887: 6OGX-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6OKM	H_LYS_12	NZ	H_GLU_10	OE1	3.648
6OKM	H_LYS_19	NZ	H_GLU_82	OE2	3.437
6OKM	H_ARG_38	NH1	H_ASP_90	OD1	2.918
6OKM	H_ARG_38	NH2	H_GLU_46	OE1	3.013
6OKM	H_ARG_38	NH2	H_ASP_90	OD1	3.782
6OKM	H_LYS_63	NZ	H_GLU_46	OE1	3.808
6OKM	H_LYS_63	NZ	H_GLU_46	OE2	2.757
6OKM	H_LYS_65	NZ	H_GLU_62	OE2	2.941
6OKM	H_ARG_67	NH1	H_ASP_90	OD1	3.731
6OKM	H_ARG_67	NH1	H_ASP_90	OD2	2.994
6OKM	H_ARG_67	NH2	H_ASP_90	OD1	2.792
6OKM	H_ARG_67	NH2	H_ASP_90	OD2	3.476
6OKM	H_ARG_98	NH1	H_ASP_102	OD1	3.580
6OKM	H_ARG_98	NH1	H_ASP_102	OD2	3.014
6OKM	H_ARG_100	NH1	L_GLU_55	OE1	2.851
6OKM	H_LYS_144	NZ	H_ASP_145	OD1	3.343
6OKM	H_LYS_144	NZ	H_ASP_145	OD2	2.800
6OKM	H_HIS_165	NE2	L_ASP_167	OD1	3.460
6OKM	H_LYS_210	NZ	L_GLU_123	OE2	3.540
6OKM	H_LYS_211	NZ	H_GLU_213	OE1	3.622
6OKM	H_LYS_215	NZ	L_ASP_122	OD1	3.237
6OKM	H_LYS_215	NZ	L_ASP_122	OD2	3.538
6OKM	L_HIS_24	ND1	L_ASP_70	OD1	2.785
6OKM	L_HIS_24	ND1	L_ASP_70	OD2	3.925
6OKM	L_ARG_61	NH2	L_GLU_81	OE2	3.773
6OKM	L_ARG_61	NH2	L_ASP_82	OD1	2.807
6OKM	L_ARG_61	NH2	L_ASP_82	OD2	3.536
6OKM	L_ARG_142	NH1	L_GLU_105	OE2	2.944
6OKM	L_ARG_142	NH1	L_GLU_165	OE1	3.753
6OKM	L_ARG_142	NH2	L_GLU_165	OE1	3.529
6OKM	L_ARG_142	NH2	L_GLU_165	OE2	2.617
6OKM	L_LYS_145	NZ	L_GLU_195	OE2	2.987
6OKM	L_LYS_183	NZ	L_GLU_187	OE1	3.533
6OKM	R_HIS_44	NE2	R_ASP_34	OD1	3.867
6OKM	R_ARG_47	NH1	R_ASP_34	OD1	3.651
6OKM	R_LYS_82	NZ	R_ASP_74	OD1	3.045
6OKM	R_ARG_95	NH1	H_ASP_99	OD1	3.347
6OKM	R_ARG_95	NH1	H_ASP_99	OD2	3.783
6OKM	R_ARG_95	NH2	H_ASP_99	OD1	3.371
6OKM	R_ARG_95	NH2	H_ASP_99	OD2	2.555

Table 888: 6OKM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6OKN	A_LYS_12	NZ	A_GLU_10	OE2	3.091
6OKN	A_ARG_38	NH1	A_ASP_90	OD1	2.825
6OKN	A_ARG_38	NH2	A_GLU_46	OE2	3.132
6OKN	A_LYS_63	NZ	A_GLU_46	OE1	3.198
6OKN	A_ARG_67	NH1	A_ASP_90	OD1	3.100
6OKN	A_ARG_67	NH1	A_ASP_90	OD2	3.478
6OKN	A_ARG_67	NH2	A_ASP_90	OD1	3.897
6OKN	A_ARG_67	NH2	A_ASP_90	OD2	2.783
6OKN	A_ARG_87	NH1	A_GLU_89	OE2	3.350
6OKN	A_ARG_101	NH2	A_ASP_50	OD1	2.814
6OKN	A_ARG_101	NH2	A_ASP_50	OD2	3.671
6OKN	A_LYS_210	NZ	A_ASP_212	OD1	3.571
6OKN	A_LYS_210	NZ	A_ASP_212	OD2	2.910
6OKN	A_LYS_213	NZ	B_GLU_123	OE1	3.312
6OKN	A_LYS_213	NZ	B_GLU_123	OE2	2.829
6OKN	A_LYS_214	NZ	A_GLU_216	OE1	2.957
6OKN	B_ARG_24	NH2	B_ASP_70	OD2	2.962
6OKN	B_ARG_61	NH2	B_ASP_82	OD1	2.800
6OKN	B_ARG_61	NH2	B_ASP_82	OD2	3.520
6OKN	B_LYS_103	NZ	B_GLU_165	OE1	3.396
6OKN	B_ARG_142	NH2	B_GLU_165	OE2	3.573
6OKN	B_LYS_149	NZ	B_GLU_195	OE1	3.927
6OKN	B_LYS_149	NZ	B_GLU_195	OE2	3.761
6OKN	B_LYS_183	NZ	B_GLU_187	OE2	3.169
6OKN	B_LYS_188	NZ	B_ASP_185	OD2	3.891
6OKN	B_HIS_189	ND1	B_ASP_151	OD2	2.830
6OKN	C_LYS_12	NZ	C_GLU_10	OE2	3.089
6OKN	C_LYS_19	NZ	C_GLU_82	OE1	3.422
6OKN	C_ARG_38	NH1	C_ASP_90	OD1	2.800
6OKN	C_ARG_38	NH2	C_GLU_46	OE2	3.128
6OKN	C_ARG_67	NH2	C_ASP_90	OD1	3.311
6OKN	C_ARG_67	NH2	C_ASP_90	OD2	2.765
6OKN	C_ARG_87	NH1	C_GLU_89	OE2	3.419
6OKN	C_LYS_147	NZ	C_ASP_148	OD1	3.408
6OKN	C_LYS_147	NZ	C_ASP_148	OD2	3.266
6OKN	C_LYS_210	NZ	C_ASP_212	OD1	3.569
6OKN	C_LYS_210	NZ	C_ASP_212	OD2	2.918
6OKN	C_LYS_213	NZ	D_GLU_123	OE1	3.356
6OKN	C_LYS_213	NZ	D_GLU_123	OE2	2.896
6OKN	C_LYS_214	NZ	C_GLU_216	OE1	2.949
6OKN	C_LYS_218	NZ	D_ASP_122	OD2	3.923
6OKN	D_ARG_24	NH2	D_ASP_70	OD2	2.953
6OKN	D_ARG_61	NH2	D_ASP_82	OD1	2.797
6OKN	D_ARG_61	NH2	D_ASP_82	OD2	3.516
6OKN	D_LYS_103	NZ	D_GLU_165	OE1	3.551
6OKN	D_ARG_142	NH1	D_GLU_143	OE2	3.897
6OKN	D_LYS_149	NZ	D_GLU_195	OE1	2.973
6OKN	D_LYS_149	NZ	D_GLU_195	OE2	3.725
6OKN	D_LYS_183	NZ	D_GLU_187	OE2	3.166
6OKN	D_LYS_188	NZ	D_ASP_185	OD1	3.552
6OKN	D_LYS_188	NZ	D_ASP_185	OD2	2.987
6OKN	D_HIS_189	ND1	D_ASP_151	OD2	2.861
6OKN	E_ARG_108	NH1	E_ASP_137	OD1	3.561
6OKN	E_ARG_110	NH1	E_GLU_94	OE2	3.361
6OKN	E_ARG_110	NH2	E_GLU_94	OE2	3.771
6OKN	R_ARG_108	NH2	R_ASP_137	OD1	3.846
6OKN	R_ARG_110	NH2	R_GLU_94	OE2	3.184

Table 889: 6OKN-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6OOR	A_ARG_25	NH1	A_ASP_43	OD1	3.325
6OOR	A_ARG_25	NH1	A_ASP_43	OD2	3.379
6OOR	A_ARG_25	NH2	A_ASP_43	OD2	3.436
6OOR	A_LYS_51	NZ	A_GLU_243	OE1	2.738
6OOR	A_LYS_51	NZ	A_GLU_243	OE2	3.127
6OOR	A_LYS_148	NZ	H_ASP_55	OD2	3.250
6OOR	A_HIS_203	ND1	A_ASP_252	OD1	2.639
6OOR	A_HIS_203	ND1	A_ASP_252	OD2	3.969
6OOR	A_ARG_264	NH2	A_ASP_274	OD2	3.670
6OOR	A_LYS_266	NZ	A_ASP_274	OD2	2.771
6OOR	B_ARG_12	NH2	A_ASP_242	OD1	3.946
6OOR	B_ARG_12	NH2	A_ASP_242	OD2	2.705
6OOR	B_HIS_34	NE2	A_GLU_97	OE1	2.803
6OOR	B_HIS_34	NE2	A_GLU_97	OE2	3.580
6OOR	B_LYS_48	NZ	B_GLU_50	OE2	3.789
6OOR	B_LYS_48	NZ	B_GLU_69	OE2	3.855
6OOR	L_ARG_66	NH2	L_GLU_86	OE2	3.235
6OOR	L_ARG_66	NH2	L_ASP_87	OD1	2.858
6OOR	L_ARG_66	NH2	L_ASP_87	OD2	3.400
6OOR	L_LYS_152	NZ	L_GLU_159	OE2	3.764
6OOR	L_LYS_154	NZ	L_GLU_200	OE1	2.808
6OOR	L_LYS_154	NZ	L_GLU_200	OE2	3.333
6OOR	L_ARG_160	NH2	L_ASP_190	OD1	3.044
6OOR	L_ARG_160	NH2	L_ASP_190	OD2	3.065
6OOR	L_ARG_161	NH2	L_GLU_159	OE1	3.906
6OOR	L_ARG_161	NH2	L_GLU_159	OE2	3.222
6OOR	L_HIS_194	ND1	L_ASP_190	OD1	3.947
6OOR	L_LYS_204	NZ	L_ASP_115	OD1	3.329
6OOR	L_LYS_204	NZ	L_ASP_115	OD2	2.404
6OOR	H_ARG_38	NH1	H_ASP_90	OD1	3.007
6OOR	H_ARG_38	NH2	H_GLU_46	OE2	2.874
6OOR	H_ARG_52	NH1	H_ASP_33	OD2	2.683
6OOR	H_ARG_61	NH1	H_GLU_46	OE1	3.910
6OOR	H_ARG_61	NH2	H_GLU_46	OE1	3.595
6OOR	H_ARG_67	NH1	H_ASP_90	OD1	3.879
6OOR	H_ARG_67	NH2	H_ASP_90	OD1	3.229
6OOR	H_ARG_67	NH2	H_ASP_90	OD2	2.355
6OOR	H_ARG_98	NH2	H_ASP_115	OD2	3.198
6OOR	H_ARG_109	NH2	A_ASP_80	OD1	2.917
6OOR	H_ARG_109	NH2	A_ASP_80	OD2	3.352
6OOR	H_LYS_220	NZ	L_GLU_128	OE1	2.677
6OOR	H_LYS_220	NZ	L_GLU_128	OE2	2.872

Table 890: 6OOR-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6OSY	2_HIS_216	NE2	2_ASP_57	OD1	3.190
6OSY	2_LYS_229	NZ	2_GLU_83	OE1	3.622
6OSY	2_LYS_229	NZ	2_GLU_83	OE2	2.450
6OSY	2_LYS_231	NZ	2_GLU_269	OE1	3.698
6OSY	2_LYS_231	NZ	2_GLU_269	OE2	3.406
6OSY	2_LYS_282	NZ	8_ASP_100C	OD2	3.941
6OSY	2_ARG_298	NH1	2_GLU_381	OE1	3.961
6OSY	2_ARG_469	NH1	2_ASP_457	OD1	3.797
6OSY	2_ARG_469	NH1	2_ASP_457	OD2	2.471
6OSY	2_ARG_469	NH2	2_ASP_457	OD2	3.905
6OSY	2_ARG_480	NH1	2_ASP_477	OD1	2.969
6OSY	2_LYS_487	NZ	2_ASP_47	OD1	2.484
6OSY	2_LYS_487	NZ	2_GLU_91	OE1	3.279
6OSY	5_ARG_38	NH1	5_ASP_86	OD1	2.426
6OSY	5_ARG_38	NH2	5_ASP_86	OD1	3.798
6OSY	5_HIS_52	ND1	5_ASP_53	OD1	3.541
6OSY	5_HIS_52	NE2	5_ASP_53	OD1	2.927
6OSY	5_ARG_66	NH2	5_ASP_86	OD1	2.765
6OSY	5_ARG_66	NH2	5_ASP_86	OD2	3.200
6OSY	6_ARG_54	NH1	6_ASP_60	OD2	3.135
6OSY	6_ARG_54	NH2	6_ASP_60	OD1	3.545
6OSY	6_ARG_54	NH2	6_ASP_60	OD2	3.739
6OSY	6_ARG_61	NH2	6_GLU_79	OE1	3.562
6OSY	6_ARG_61	NH2	6_GLU_79	OE2	2.945
6OSY	7_ARG_60	NH2	7_ASP_78	OD1	3.680
6OSY	7_LYS_76	NZ	7_ASP_78	OD1	3.618
6OSY	8_ARG_38	NH2	8_ASP_86	OD1	2.575
6OSY	8_ARG_61	NH1	2_GLU_466	OE2	3.827
6OSY	8_ARG_71	NH1	2_ASP_368	OD2	3.948
6OSY	8_ARG_71	NH2	2_ASP_368	OD2	3.279
6OSY	A_ARG_542	NH1	Q_GLU_647	OE2	3.907
6OSY	A_ARG_542	NH2	Q_GLU_647	OE1	3.187
6OSY	A_ARG_542	NH2	Q_GLU_647	OE2	2.660
6OSY	A_ARG_579	NH2	Q_GLU_584	OE1	3.706
6OSY	A_ARG_588	NH2	A_GLU_584	OE2	3.896
6OSY	A_ARG_617	NH1	A_GLU_634	OE1	3.782
6OSY	A_ARG_617	NH1	A_GLU_634	OE2	2.878
6OSY	B_HIS_85	NE2	B_GLU_87	OE2	3.796
6OSY	B_HIS_216	NE2	B_ASP_57	OD1	3.161
6OSY	B_LYS_229	NZ	B_GLU_83	OE1	3.600
6OSY	B_LYS_229	NZ	B_GLU_83	OE2	2.450
6OSY	B_LYS_231	NZ	B_GLU_269	OE1	3.715
6OSY	B_LYS_231	NZ	B_GLU_269	OE2	3.368
6OSY	B_LYS_282	NZ	F_ASP_100C	OD1	3.567
6OSY	B_LYS_282	NZ	F_ASP_100C	OD2	3.346
6OSY	B_LYS_421	NZ	B_ASP_180	OD1	3.951
6OSY	B_ARG_469	NH1	B_ASP_457	OD1	3.948
6OSY	B_ARG_469	NH1	B_ASP_457	OD2	2.695
6OSY	B_ARG_469	NH2	B_ASP_457	OD2	3.861
6OSY	B_ARG_480	NH1	B_ASP_477	OD1	3.023
6OSY	B_LYS_487	NZ	B_ASP_47	OD1	2.451
6OSY	B_LYS_487	NZ	B_GLU_91	OE1	3.497
6OSY	C_ARG_38	NH1	C_ASP_86	OD1	2.431
6OSY	C_ARG_38	NH2	C_ASP_86	OD1	3.856
6OSY	C_HIS_52	ND1	C_ASP_53	OD1	3.516
6OSY	C_HIS_52	NE2	C_ASP_53	OD1	2.951
6OSY	C_ARG_66	NH2	C_ASP_86	OD1	2.899

6OSY	C_ARG_66	NH2	C_ASP_86	OD2	3.310
6OSY	D_ARG_54	NH1	D_ASP_60	OD1	3.203
6OSY	D_ARG_54	NH2	D_ASP_60	OD1	3.673
6OSY	D_ARG_54	NH2	D_ASP_60	OD2	3.335
6OSY	D_ARG_61	NH2	D_GLU_79	OE1	3.529
6OSY	D_ARG_61	NH2	D_GLU_79	OE2	2.917
6OSY	E_ARG_60	NH2	E_ASP_78	OD1	3.663
6OSY	E_LYS_76	NZ	E_ASP_78	OD1	3.632
6OSY	F_ARG_38	NH1	F_ASP_86	OD1	3.966
6OSY	F_ARG_38	NH2	F_ASP_86	OD1	2.680
6OSY	F_ARG_66	NH1	F_ASP_86	OD2	3.886
6OSY	F_ARG_71	NH2	B_ASP_368	OD2	3.635
6OSY	G_ARG_542	NH1	A_GLU_647	OE2	3.983
6OSY	G_ARG_542	NH2	A_GLU_647	OE1	3.165
6OSY	G_ARG_542	NH2	A_GLU_647	OE2	2.705
6OSY	G_ARG_579	NH2	A_GLU_584	OE1	3.899
6OSY	G_ARG_588	NH2	G_GLU_584	OE2	3.357
6OSY	G_ARG_617	NH1	G_GLU_634	OE1	3.355
6OSY	G_ARG_617	NH1	G_GLU_634	OE2	2.448
6OSY	H_ARG_38	NH1	H_GLU_46	OE1	2.885
6OSY	H_ARG_38	NH1	H_GLU_46	OE2	3.190
6OSY	H_ARG_38	NH1	H_ASP_86	OD2	3.298
6OSY	H_ARG_38	NH2	H_ASP_86	OD2	2.451
6OSY	H_ARG_66	NH1	H_ASP_86	OD1	3.016
6OSY	H_ARG_66	NH1	H_ASP_86	OD2	2.795
6OSY	H_ARG_66	NH2	H_ASP_86	OD1	2.574
6OSY	H_ARG_66	NH2	H_ASP_86	OD2	3.909
6OSY	H_ARG_96	NH1	L_GLU_55	OE1	3.662
6OSY	H_HIS_100	ND1	2_GLU_87	OE2	3.031
6OSY	H_HIS_100	NE2	2_GLU_87	OE2	3.785
6OSY	I_ARG_38	NH1	I_GLU_46	OE1	2.963
6OSY	I_ARG_38	NH1	I_GLU_46	OE2	3.677
6OSY	I_ARG_38	NH1	I_ASP_86	OD1	3.365
6OSY	I_ARG_38	NH2	I_ASP_86	OD1	2.431
6OSY	I_ARG_66	NH1	I_ASP_86	OD1	2.805
6OSY	I_ARG_66	NH1	I_ASP_86	OD2	3.496
6OSY	I_ARG_66	NH2	I_ASP_86	OD1	3.389
6OSY	I_ARG_66	NH2	I_ASP_86	OD2	2.439
6OSY	I_ARG_96	NH1	J_GLU_55	OE2	3.419
6OSY	I_HIS_100	ND1	B_GLU_87	OE2	3.029
6OSY	I_HIS_100	NE2	B_GLU_87	OE2	3.781
6OSY	J_ARG_24	NH1	J_GLU_70	OE2	3.291
6OSY	J_LYS_30	NZ	J_ASP_28	OD2	3.933
6OSY	J_ARG_46	NH1	I_ASP_101	OD1	3.411
6OSY	J_ARG_46	NH1	I_ASP_101	OD2	2.599
6OSY	J_ARG_46	NH1	J_GLU_55	OE2	3.676
6OSY	J_ARG_61	NH1	J_GLU_81	OE1	2.792
6OSY	J_ARG_61	NH1	J_ASP_82	OD1	2.601
6OSY	J_ARG_61	NH1	J_ASP_82	OD2	3.417
6OSY	J_ARG_61	NH2	J_GLU_81	OE1	2.918
6OSY	K_HIS_85	NE2	K_GLU_87	OE2	3.406
6OSY	K_HIS_216	NE2	K_ASP_57	OD1	3.206
6OSY	K_LYS_229	NZ	K_GLU_83	OE1	3.712
6OSY	K_LYS_229	NZ	K_GLU_83	OE2	2.837
6OSY	K_LYS_231	NZ	K_GLU_269	OE1	3.711
6OSY	K_LYS_231	NZ	K_GLU_269	OE2	3.385
6OSY	K_LYS_282	NZ	P_ASP_100C	OD2	3.859
6OSY	K_LYS_421	NZ	K_ASP_180	OD1	3.938

6OSY	K_ARG_469	NH1	K_ASP_457	OD1	3.854
6OSY	K_ARG_469	NH1	K_ASP_457	OD2	2.579
6OSY	K_ARG_469	NH2	K_ASP_457	OD2	3.974
6OSY	K_ARG_480	NH1	K_ASP_477	OD1	3.037
6OSY	K_LYS_487	NZ	K_ASP_47	OD1	2.530
6OSY	K_LYS_487	NZ	K_ASP_47	OD2	3.781
6OSY	K_LYS_487	NZ	K_GLU_91	OE1	2.961
6OSY	L_ARG_24	NH1	L_GLU_70	OE2	3.285
6OSY	L_LYS_30	NZ	L_ASP_28	OD2	3.882
6OSY	L_ARG_46	NH1	H_ASP_101	OD1	3.509
6OSY	L_ARG_46	NH1	H_ASP_101	OD2	2.485
6OSY	L_ARG_46	NH1	L_GLU_55	OE1	3.489
6OSY	L_ARG_61	NH1	L_GLU_81	OE1	2.728
6OSY	L_ARG_61	NH1	L_ASP_82	OD1	2.575
6OSY	L_ARG_61	NH1	L_ASP_82	OD2	3.365
6OSY	L_ARG_61	NH2	L_GLU_81	OE1	2.971
6OSY	M_ARG_38	NH1	M_ASP_86	OD1	2.434
6OSY	M_ARG_38	NH2	M_ASP_86	OD1	3.790
6OSY	M_HIS_52	ND1	M_ASP_53	OD1	3.529
6OSY	M_HIS_52	NE2	M_ASP_53	OD1	2.931
6OSY	M_ARG_66	NH2	M_ASP_86	OD1	2.638
6OSY	M_ARG_66	NH2	M_ASP_86	OD2	3.176
6OSY	N_ARG_54	NH1	N_ASP_60	OD2	3.198
6OSY	N_ARG_54	NH2	N_ASP_60	OD1	3.491
6OSY	N_ARG_54	NH2	N_ASP_60	OD2	3.714
6OSY	N_ARG_61	NH2	N_GLU_79	OE1	3.680
6OSY	N_ARG_61	NH2	N_GLU_79	OE2	2.924
6OSY	O_ARG_60	NH2	O_ASP_78	OD1	3.714
6OSY	O_LYS_76	NZ	O_ASP_78	OD1	3.603
6OSY	P_ARG_38	NH1	P_ASP_86	OD1	3.657
6OSY	P_ARG_38	NH2	P_ASP_86	OD1	2.467
6OSY	P_ARG_66	NH1	P_ASP_86	OD2	3.897
6OSY	P_ARG_71	NH1	K_ASP_368	OD2	3.949
6OSY	P_ARG_71	NH2	K_ASP_368	OD2	3.325
6OSY	Q_ARG_542	NH1	G_GLU_647	OE2	3.913
6OSY	Q_ARG_542	NH2	G_GLU_647	OE1	3.228
6OSY	Q_ARG_542	NH2	G_GLU_647	OE2	2.706
6OSY	Q_ARG_617	NH1	Q_GLU_634	OE1	3.307
6OSY	Q_ARG_617	NH1	Q_GLU_634	OE2	2.450
6OSY	R_ARG_38	NH1	R_GLU_46	OE1	2.894
6OSY	R_ARG_38	NH1	R_ASP_86	OD1	3.489
6OSY	R_ARG_38	NH2	R_ASP_86	OD1	2.425
6OSY	R_ARG_66	NH1	R_ASP_86	OD1	3.291
6OSY	R_ARG_66	NH1	R_ASP_86	OD2	2.545
6OSY	R_ARG_66	NH2	R_ASP_86	OD1	3.724
6OSY	R_ARG_96	NH1	S_GLU_55	OE2	3.423
6OSY	R_HIS_100	ND1	K_GLU_87	OE1	3.719
6OSY	R_HIS_100	ND1	K_GLU_87	OE2	2.905
6OSY	R_HIS_100	NE2	K_GLU_87	OE1	3.960
6OSY	S_ARG_24	NH1	S_GLU_70	OE2	3.276
6OSY	S_LYS_30	NZ	S_ASP_28	OD1	3.818
6OSY	S_ARG_46	NH1	R_ASP_101	OD1	3.488
6OSY	S_ARG_46	NH1	R_ASP_101	OD2	2.503
6OSY	S_ARG_46	NH1	S_GLU_55	OE2	3.494
6OSY	S_ARG_61	NH1	S_GLU_81	OE1	2.746
6OSY	S_ARG_61	NH1	S_ASP_82	OD1	3.377
6OSY	S_ARG_61	NH1	S_ASP_82	OD2	2.556
6OSY	S_ARG_61	NH2	S_GLU_81	OE1	2.966

Table 891: 6OSY-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6OT1	B_ARG_542	NH2	D_GLU_647	OE1	2.021
6OT1	B_ARG_542	NH2	D_GLU_647	OE2	3.827
6OT1	B_ARG_588	NH2	B_GLU_584	OE2	2.977
6OT1	B_LYS_601	NZ	D_GLU_657	OE1	3.960
6OT1	B_LYS_601	NZ	D_GLU_657	OE2	3.832
6OT1	B_ARG_617	NH1	B_GLU_634	OE1	3.167
6OT1	B_ARG_617	NH1	B_GLU_634	OE2	2.669
6OT1	B_ARG_617	NH2	B_GLU_621	OE1	3.234
6OT1	B_ARG_617	NH2	B_GLU_621	OE2	3.259
6OT1	G_HIS_85	NE2	G_GLU_87	OE2	3.938
6OT1	G_HIS_216	NE2	G_ASP_57	OD1	2.810
6OT1	G_HIS_216	NE2	G_ASP_57	OD2	3.156
6OT1	G_LYS_229	NZ	G_GLU_83	OE2	3.683
6OT1	G_LYS_231	NZ	G_GLU_268	OE1	3.079
6OT1	G_LYS_231	NZ	G_GLU_268	OE2	3.577
6OT1	G_HIS_249	NE2	G_GLU_482	OE1	3.787
6OT1	G_LYS_282	NZ	G_GLU_275	OE2	3.607
6OT1	G_LYS_282	NZ	q_ASP_100C	OD2	3.404
6OT1	G_ARG_298	NH1	G_GLU_381	OE1	2.421
6OT1	G_ARG_298	NH1	G_GLU_381	OE2	3.196
6OT1	G_ARG_327	NH2	m_GLU_100I	OE1	3.817
6OT1	G_LYS_351	NZ	G_GLU_269	OE1	3.548
6OT1	G_ARG_429	NH1	G_ASP_113	OD1	3.405
6OT1	G_ARG_429	NH1	G_ASP_113	OD2	2.495
6OT1	G_ARG_469	NH1	G_ASP_457	OD1	2.847
6OT1	G_ARG_476	NH1	G_GLU_102	OE1	3.389
6OT1	G_ARG_476	NH1	G_ASP_474	OD2	3.647
6OT1	G_ARG_476	NH2	G_GLU_102	OE1	3.349
6OT1	G_ARG_476	NH2	G_GLU_102	OE2	3.433
6OT1	G_ARG_480	NH1	G_ASP_477	OD1	3.354
6OT1	G_LYS_487	NZ	G_ASP_47	OD1	2.584
6OT1	G_LYS_487	NZ	G_ASP_47	OD2	3.393
6OT1	G_LYS_487	NZ	G_GLU_91	OE2	2.597
6OT1	H_ARG_38	NH2	H_ASP_86	OD1	3.494
6OT1	H_LYS_71	NZ	H_GLU_55	OE2	3.697
6OT1	L_ARG_54	NH2	L_ASP_60	OD2	3.975
6OT1	L_ARG_61	NH1	L_GLU_81	OE2	3.772
6OT1	L_ARG_61	NH2	L_GLU_81	OE2	2.479
6OT1	m_ARG_38	NH1	m_ASP_86	OD1	3.011
6OT1	m_ARG_38	NH2	m_GLU_46	OE1	2.859
6OT1	m_ARG_38	NH2	m_GLU_46	OE2	3.063
6OT1	m_ARG_38	NH2	m_ASP_86	OD1	3.767
6OT1	m_HIS_52	ND1	m_ASP_53	OD1	3.328
6OT1	m_HIS_52	NE2	m_ASP_53	OD1	3.028
6OT1	m_ARG_66	NH1	m_ASP_86	OD2	2.461
6OT1	m_ARG_66	NH2	m_ASP_86	OD1	3.460
6OT1	m_ARG_66	NH2	m_ASP_86	OD2	3.125
6OT1	m_LYS_73	NZ	m_ASP_53	OD2	3.345
6OT1	m_LYS_96	NZ	m_ASP_100Q	OD1	3.813
6OT1	m_LYS_96	NZ	m_ASP_100Q	OD2	2.475
6OT1	n_ARG_31	NH1	n_ASP_92	OD2	2.719
6OT1	n_ARG_54	NH2	n_ASP_60	OD1	3.737
6OT1	n_ARG_54	NH2	n_ASP_60	OD2	2.630
6OT1	n_ARG_61	NH1	n_ASP_82	OD2	3.959
6OT1	n_ARG_61	NH2	n_GLU_79	OE2	3.140
6OT1	n_ARG_61	NH2	n_ASP_82	OD1	3.334
6OT1	n_ARG_61	NH2	n_ASP_82	OD2	3.994

6OT1	n_ARG_95	NH2	n_GLU_25	OE1	3.478
6OT1	q_ARG_38	NH1	q_ASP_86	OD1	2.452
6OT1	q_ARG_38	NH1	q_ASP_86	OD2	3.996
6OT1	q_ARG_38	NH2	q_GLU_46	OE1	2.492
6OT1	q_ARG_38	NH2	q_GLU_46	OE2	3.367
6OT1	q_ARG_66	NH2	q_ASP_86	OD2	2.599
6OT1	q_ARG_71	NH2	G_ASP_368	OD2	3.596
6OT1	r_LYS_24	NZ	r_ASP_69	OD1	3.076
6OT1	r_ARG_52	NH2	r_ASP_49	OD2	3.108
6OT1	r_ARG_53	NH1	r_ASP_59	OD1	3.647
6OT1	r_ARG_60	NH2	r_ASP_81	OD1	3.037
6OT1	r_ARG_60	NH2	r_ASP_81	OD2	2.674
6OT1	O_ARG_542	NH2	B_GLU_647	OE1	2.048
6OT1	O_ARG_542	NH2	B_GLU_647	OE2	3.874
6OT1	O_ARG_588	NH2	O_GLU_584	OE2	2.978
6OT1	O_LYS_601	NZ	B_GLU_657	OE1	3.934
6OT1	O_LYS_601	NZ	B_GLU_657	OE2	3.759
6OT1	O_ARG_617	NH1	O_GLU_634	OE1	3.167
6OT1	O_ARG_617	NH1	O_GLU_634	OE2	2.669
6OT1	O_ARG_617	NH2	O_GLU_621	OE1	3.234
6OT1	O_ARG_617	NH2	O_GLU_621	OE2	3.261
6OT1	E_HIS_85	NE2	E_GLU_87	OE2	3.938
6OT1	E_HIS_216	NE2	E_ASP_57	OD1	2.811
6OT1	E_HIS_216	NE2	E_ASP_57	OD2	3.156
6OT1	E_LYS_229	NZ	E_GLU_83	OE2	3.683
6OT1	E_LYS_231	NZ	E_GLU_268	OE1	3.077
6OT1	E_LYS_231	NZ	E_GLU_268	OE2	3.575
6OT1	E_HIS_249	NE2	E_GLU_482	OE1	3.787
6OT1	E_LYS_282	NZ	E_GLU_275	OE2	3.608
6OT1	E_LYS_282	NZ	J_ASP_100C	OD2	3.404
6OT1	E_ARG_298	NH1	E_GLU_381	OE1	2.420
6OT1	E_ARG_298	NH1	E_GLU_381	OE2	3.196
6OT1	E_ARG_327	NH2	F_GLU_100I	OE1	3.817
6OT1	E_LYS_351	NZ	E_GLU_269	OE1	3.548
6OT1	E_ARG_429	NH1	E_ASP_113	OD1	3.405
6OT1	E_ARG_429	NH1	E_ASP_113	OD2	2.495
6OT1	E_ARG_469	NH1	E_ASP_457	OD1	2.847
6OT1	E_ARG_476	NH1	E_GLU_102	OE1	3.389
6OT1	E_ARG_476	NH1	E_ASP_474	OD2	3.648
6OT1	E_ARG_476	NH2	E_GLU_102	OE1	3.349
6OT1	E_ARG_476	NH2	E_GLU_102	OE2	3.433
6OT1	E_ARG_480	NH1	E_ASP_477	OD1	3.353
6OT1	E_LYS_487	NZ	E_ASP_47	OD1	2.586
6OT1	E_LYS_487	NZ	E_ASP_47	OD2	3.398
6OT1	E_LYS_487	NZ	E_GLU_91	OE2	2.596
6OT1	A_ARG_38	NH2	A_ASP_86	OD1	3.495
6OT1	A_LYS_71	NZ	A_GLU_55	OE2	3.697
6OT1	C_ARG_54	NH2	C_ASP_60	OD2	3.977
6OT1	C_ARG_61	NH1	C_GLU_81	OE2	3.768
6OT1	C_ARG_61	NH2	C_GLU_81	OE2	2.478
6OT1	F_ARG_38	NH1	F_ASP_86	OD1	3.011
6OT1	F_ARG_38	NH2	F_GLU_46	OE1	2.859
6OT1	F_ARG_38	NH2	F_GLU_46	OE2	3.063
6OT1	F_ARG_38	NH2	F_ASP_86	OD1	3.766
6OT1	F_HIS_52	ND1	F_ASP_53	OD1	3.327
6OT1	F_HIS_52	NE2	F_ASP_53	OD1	3.026
6OT1	F_ARG_66	NH1	F_ASP_86	OD2	2.462
6OT1	F_ARG_66	NH2	F_ASP_86	OD1	3.460

6OT1	F_ARG_66	NH2	F_ASP_86	OD2	3.125
6OT1	F_LYS_73	NZ	F_ASP_53	OD2	3.344
6OT1	F_LYS_96	NZ	F_ASP_100Q	OD1	3.814
6OT1	F_LYS_96	NZ	F_ASP_100Q	OD2	2.475
6OT1	I_ARG_31	NH1	I_ASP_92	OD2	2.719
6OT1	I_ARG_54	NH2	I_ASP_60	OD1	3.738
6OT1	I_ARG_54	NH2	I_ASP_60	OD2	2.630
6OT1	I_ARG_61	NH1	I_ASP_82	OD2	3.959
6OT1	I_ARG_61	NH2	I_GLU_79	OE2	3.139
6OT1	I_ARG_61	NH2	I_ASP_82	OD1	3.334
6OT1	I_ARG_61	NH2	I_ASP_82	OD2	3.993
6OT1	I_ARG_95	NH2	I_GLU_25	OE1	3.478
6OT1	J_ARG_38	NH1	J_ASP_86	OD1	2.453
6OT1	J_ARG_38	NH1	J_ASP_86	OD2	3.995
6OT1	J_ARG_38	NH2	J_GLU_46	OE1	2.492
6OT1	J_ARG_38	NH2	J_GLU_46	OE2	3.368
6OT1	J_ARG_66	NH2	J_ASP_86	OD2	2.596
6OT1	J_ARG_71	NH2	E_ASP_368	OD2	3.599
6OT1	K_LYS_24	NZ	K_ASP_69	OD1	3.078
6OT1	K_ARG_52	NH2	K_ASP_49	OD2	3.106
6OT1	K_ARG_53	NH1	K_ASP_59	OD1	3.648
6OT1	K_ARG_60	NH2	K_ASP_81	OD1	3.037
6OT1	K_ARG_60	NH2	K_ASP_81	OD2	2.675
6OT1	D_ARG_542	NH2	O_GLU_647	OE1	2.015
6OT1	D_ARG_542	NH2	O_GLU_647	OE2	3.816
6OT1	D_ARG_588	NH2	D_GLU_584	OE2	2.978
6OT1	D_LYS_601	NZ	O_GLU_657	OE2	3.900
6OT1	D_ARG_617	NH1	D_GLU_634	OE1	3.168
6OT1	D_ARG_617	NH1	D_GLU_634	OE2	2.668
6OT1	D_ARG_617	NH2	D_GLU_621	OE1	3.233
6OT1	D_ARG_617	NH2	D_GLU_621	OE2	3.260
6OT1	P_HIS_85	NE2	P_GLU_87	OE2	3.938
6OT1	P_HIS_216	NE2	P_ASP_57	OD1	2.811
6OT1	P_HIS_216	NE2	P_ASP_57	OD2	3.156
6OT1	P_LYS_229	NZ	P_GLU_83	OE2	3.683
6OT1	P_LYS_231	NZ	P_GLU_268	OE1	3.078
6OT1	P_LYS_231	NZ	P_GLU_268	OE2	3.576
6OT1	P_HIS_249	NE2	P_GLU_482	OE1	3.788
6OT1	P_LYS_282	NZ	P_GLU_275	OE2	3.608
6OT1	P_LYS_282	NZ	S_ASP_100C	OD2	3.405
6OT1	P_ARG_298	NH1	P_GLU_381	OE1	2.420
6OT1	P_ARG_298	NH1	P_GLU_381	OE2	3.195
6OT1	P_ARG_327	NH2	Q_GLU_100I	OE1	3.817
6OT1	P_LYS_351	NZ	P_GLU_269	OE1	3.548
6OT1	P_ARG_429	NH1	P_ASP_113	OD1	3.405
6OT1	P_ARG_429	NH1	P_ASP_113	OD2	2.495
6OT1	P_ARG_469	NH1	P_ASP_457	OD1	2.848
6OT1	P_ARG_476	NH1	P_GLU_102	OE1	3.390
6OT1	P_ARG_476	NH1	P_ASP_474	OD2	3.647
6OT1	P_ARG_476	NH2	P_GLU_102	OE1	3.349
6OT1	P_ARG_476	NH2	P_GLU_102	OE2	3.433
6OT1	P_ARG_480	NH1	P_ASP_477	OD1	3.353
6OT1	P_LYS_487	NZ	P_ASP_47	OD1	2.584
6OT1	P_LYS_487	NZ	P_ASP_47	OD2	3.393
6OT1	P_LYS_487	NZ	P_GLU_91	OE2	2.596
6OT1	M_ARG_38	NH2	M_ASP_86	OD1	3.493
6OT1	M_LYS_71	NZ	M_GLU_55	OE2	3.697
6OT1	N_ARG_54	NH2	N_ASP_60	OD2	3.974

6OT1	N_ARG_61	NH1	N_GLU_81	OE2	3.770
6OT1	N_ARG_61	NH2	N_GLU_81	OE2	2.479
6OT1	Q_ARG_38	NH1	Q_ASP_86	OD1	3.012
6OT1	Q_ARG_38	NH2	Q_GLU_46	OE1	2.859
6OT1	Q_ARG_38	NH2	Q_GLU_46	OE2	3.063
6OT1	Q_ARG_38	NH2	Q_ASP_86	OD1	3.766
6OT1	Q_HIS_52	ND1	Q_ASP_53	OD1	3.327
6OT1	Q_HIS_52	NE2	Q_ASP_53	OD1	3.026
6OT1	Q_ARG_66	NH1	Q_ASP_86	OD2	2.462
6OT1	Q_ARG_66	NH2	Q_ASP_86	OD1	3.460
6OT1	Q_ARG_66	NH2	Q_ASP_86	OD2	3.125
6OT1	Q_LYS_73	NZ	Q_ASP_53	OD2	3.344
6OT1	Q_LYS_96	NZ	Q_ASP_100Q	OD1	3.814
6OT1	Q_LYS_96	NZ	Q_ASP_100Q	OD2	2.476
6OT1	R_ARG_31	NH1	R_ASP_92	OD2	2.718
6OT1	R_ARG_54	NH2	R_ASP_60	OD1	3.737
6OT1	R_ARG_54	NH2	R_ASP_60	OD2	2.630
6OT1	R_ARG_61	NH1	R_ASP_82	OD2	3.960
6OT1	R_ARG_61	NH2	R_GLU_79	OE2	3.139
6OT1	R_ARG_61	NH2	R_ASP_82	OD1	3.334
6OT1	R_ARG_61	NH2	R_ASP_82	OD2	3.995
6OT1	R_ARG_95	NH2	R_GLU_25	OE1	3.477
6OT1	S_ARG_38	NH1	S_ASP_86	OD1	2.452
6OT1	S_ARG_38	NH1	S_ASP_86	OD2	3.995
6OT1	S_ARG_38	NH2	S_GLU_46	OE1	2.492
6OT1	S_ARG_38	NH2	S_GLU_46	OE2	3.367
6OT1	S_ARG_66	NH2	S_ASP_86	OD2	2.599
6OT1	S_ARG_71	NH2	P_ASP_368	OD2	3.597
6OT1	T_LYS_24	NZ	T_ASP_69	OD1	3.076
6OT1	T_ARG_52	NH2	T_ASP_49	OD2	3.107
6OT1	T_ARG_53	NH1	T_ASP_59	OD1	3.647
6OT1	T_ARG_60	NH2	T_ASP_81	OD1	3.038
6OT1	T_ARG_60	NH2	T_ASP_81	OD2	2.673

Table 892: 6OT1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6P62	A_LYS_46	NZ	A_ASP_632	OD2	2.721
6P62	A_LYS_97	NZ	A_GLU_275	OE2	3.366
6P62	A_ARG_151	NH2	A_ASP_140	OD1	3.754
6P62	A_LYS_168	NZ	B_GLU_190	OE2	3.547
6P62	A_LYS_229	NZ	A_GLU_83	OE1	3.953
6P62	A_LYS_229	NZ	A_GLU_83	OE2	2.773
6P62	A_LYS_231	NZ	A_GLU_267	OE1	3.655
6P62	A_LYS_232	NZ	A_GLU_268	OE2	3.138
6P62	A_LYS_232	NZ	A_GLU_269	OE2	2.749
6P62	A_HIS_249	NE2	A_GLU_482	OE1	3.132
6P62	A_LYS_282	NZ	A_GLU_275	OE1	3.423
6P62	A_ARG_298	NH1	A_GLU_381	OE2	2.910
6P62	A_ARG_298	NH2	A_GLU_381	OE2	3.307
6P62	A_LYS_335	NZ	A_ASP_412	OD2	2.410
6P62	A_LYS_351	NZ	A_GLU_269	OE1	3.133
6P62	A_LYS_421	NZ	A_GLU_370	OE2	2.730
6P62	A_ARG_429	NH1	A_ASP_113	OD1	3.526
6P62	A_ARG_429	NH1	A_ASP_113	OD2	2.935
6P62	A_ARG_429	NH2	A_ASP_113	OD1	2.818
6P62	A_ARG_429	NH2	A_ASP_113	OD2	3.695
6P62	A_ARG_476	NH1	A_ASP_474	OD1	3.290
6P62	A_ARG_476	NH1	A_ASP_474	OD2	3.909
6P62	A_ARG_476	NH2	A_GLU_102	OE1	3.634
6P62	A_ARG_476	NH2	A_GLU_102	OE2	3.089
6P62	A_LYS_487	NZ	A_ASP_47	OD1	3.073
6P62	A_LYS_487	NZ	A_ASP_47	OD2	2.842
6P62	A_LYS_490	NZ	A_GLU_492	OE2	3.504
6P62	A_ARG_520	NH2	A_GLU_87	OE1	3.537
6P62	A_ARG_542	NH1	B_GLU_647	OE1	2.629
6P62	A_ARG_542	NH1	B_GLU_647	OE2	3.985
6P62	A_ARG_542	NH2	B_GLU_648	OE2	3.131
6P62	A_LYS_574	NZ	A_ASP_107	OD1	2.481
6P62	A_LYS_574	NZ	A_ASP_107	OD2	3.953
6P62	A_ARG_579	NH1	B_GLU_584	OE1	3.453
6P62	A_ARG_579	NH1	B_GLU_584	OE2	2.953
6P62	A_ARG_585	NH2	A_GLU_492	OE1	3.953
6P62	A_ARG_585	NH2	A_GLU_492	OE2	2.999
6P62	A_ARG_588	NH1	A_GLU_584	OE1	3.660
6P62	A_ARG_588	NH2	A_GLU_584	OE1	3.069
6P62	A_ARG_617	NH1	A_GLU_634	OE1	3.708
6P62	A_ARG_617	NH1	A_GLU_634	OE2	3.595
6P62	H_ARG_38	NH1	H_ASP_86	OD1	3.041
6P62	H_ARG_38	NH2	H_GLU_46	OE1	2.920
6P62	H_ARG_94	NH2	H_ASP_101	OD1	3.646
6P62	H_ARG_94	NH2	H_ASP_101	OD2	2.930
6P62	L_LYS_22	NZ	L_GLU_70	OE2	3.542
6P62	L_ARG_61	NH1	L_GLU_79	OE2	3.423
6P62	L_ARG_61	NH1	L_ASP_82	OD2	3.764
6P62	L_ARG_61	NH2	L_ASP_77	OD2	2.844
6P62	L_ARG_61	NH2	L_GLU_79	OE2	2.955
6P62	B_LYS_46	NZ	B_ASP_632	OD2	2.722
6P62	B_LYS_97	NZ	B_GLU_275	OE2	3.366
6P62	B_ARG_151	NH2	B_ASP_140	OD1	3.754
6P62	B_LYS_168	NZ	E_GLU_190	OE2	3.547
6P62	B_LYS_229	NZ	B_GLU_83	OE1	3.953
6P62	B_LYS_229	NZ	B_GLU_83	OE2	2.774
6P62	B_LYS_231	NZ	B_GLU_267	OE1	3.655

6P62	B_LYS_232	NZ	B_GLU_268	OE2	3.139
6P62	B_LYS_232	NZ	B_GLU_269	OE2	2.750
6P62	B_HIS_249	NE2	B_GLU_482	OE1	3.131
6P62	B_LYS_282	NZ	B_GLU_275	OE1	3.424
6P62	B_ARG_298	NH1	B_GLU_381	OE2	2.910
6P62	B_ARG_298	NH2	B_GLU_381	OE2	3.308
6P62	B_LYS_335	NZ	B_ASP_412	OD2	2.410
6P62	B_LYS_351	NZ	B_GLU_269	OE1	3.133
6P62	B_LYS_421	NZ	B_GLU_370	OE2	2.731
6P62	B_ARG_429	NH1	B_ASP_113	OD1	3.526
6P62	B_ARG_429	NH1	B_ASP_113	OD2	2.934
6P62	B_ARG_429	NH2	B_ASP_113	OD1	2.819
6P62	B_ARG_429	NH2	B_ASP_113	OD2	3.695
6P62	B_ARG_476	NH1	B_ASP_474	OD1	3.291
6P62	B_ARG_476	NH1	B_ASP_474	OD2	3.909
6P62	B_ARG_476	NH2	B_GLU_102	OE1	3.634
6P62	B_ARG_476	NH2	B_GLU_102	OE2	3.089
6P62	B_LYS_487	NZ	B_ASP_47	OD1	3.072
6P62	B_LYS_487	NZ	B_ASP_47	OD2	2.841
6P62	B_LYS_490	NZ	B_GLU_492	OE2	3.504
6P62	B_ARG_520	NH2	B_GLU_87	OE1	3.537
6P62	B_ARG_542	NH1	E_GLU_647	OE1	2.630
6P62	B_ARG_542	NH1	E_GLU_647	OE2	3.986
6P62	B_ARG_542	NH2	E_GLU_648	OE2	3.130
6P62	B_LYS_574	NZ	B_ASP_107	OD1	2.481
6P62	B_LYS_574	NZ	B_ASP_107	OD2	3.954
6P62	B_ARG_579	NH1	E_GLU_584	OE1	3.454
6P62	B_ARG_579	NH1	E_GLU_584	OE2	2.952
6P62	B_ARG_585	NH2	B_GLU_492	OE1	3.952
6P62	B_ARG_585	NH2	B_GLU_492	OE2	2.998
6P62	B_ARG_588	NH1	B_GLU_584	OE1	3.660
6P62	B_ARG_588	NH2	B_GLU_584	OE1	3.069
6P62	B_ARG_617	NH1	B_GLU_634	OE1	3.708
6P62	B_ARG_617	NH1	B_GLU_634	OE2	3.595
6P62	C_ARG_38	NH1	C_ASP_86	OD1	3.041
6P62	C_ARG_38	NH2	C_GLU_46	OE1	2.920
6P62	C_ARG_94	NH2	C_ASP_101	OD1	3.646
6P62	C_ARG_94	NH2	C_ASP_101	OD2	2.930
6P62	D_LYS_22	NZ	D_GLU_70	OE2	3.542
6P62	D_ARG_61	NH1	D_GLU_79	OE2	3.423
6P62	D_ARG_61	NH1	D_ASP_82	OD2	3.764
6P62	D_ARG_61	NH2	D_ASP_77	OD2	2.845
6P62	D_ARG_61	NH2	D_GLU_79	OE2	2.955
6P62	E_LYS_46	NZ	E_ASP_632	OD2	2.721
6P62	E_LYS_97	NZ	E_GLU_275	OE2	3.366
6P62	E_ARG_151	NH2	E_ASP_140	OD1	3.754
6P62	E_LYS_168	NZ	A_GLU_190	OE2	3.547
6P62	E_LYS_229	NZ	E_GLU_83	OE1	3.953
6P62	E_LYS_229	NZ	E_GLU_83	OE2	2.773
6P62	E_LYS_231	NZ	E_GLU_267	OE1	3.656
6P62	E_LYS_232	NZ	E_GLU_268	OE2	3.139
6P62	E_LYS_232	NZ	E_GLU_269	OE2	2.749
6P62	E_HIS_249	NE2	E_GLU_482	OE1	3.131
6P62	E_LYS_282	NZ	E_GLU_275	OE1	3.424
6P62	E_ARG_298	NH1	E_GLU_381	OE2	2.909
6P62	E_ARG_298	NH2	E_GLU_381	OE2	3.307
6P62	E_LYS_335	NZ	E_ASP_412	OD2	2.409
6P62	E_LYS_351	NZ	E_GLU_269	OE1	3.133

6P62	E_LYS_421	NZ	E_GLU_370	OE2	2.731
6P62	E_ARG_429	NH1	E_ASP_113	OD1	3.526
6P62	E_ARG_429	NH1	E_ASP_113	OD2	2.935
6P62	E_ARG_429	NH2	E_ASP_113	OD1	2.819
6P62	E_ARG_429	NH2	E_ASP_113	OD2	3.695
6P62	E_ARG_476	NH1	E_ASP_474	OD1	3.291
6P62	E_ARG_476	NH1	E_ASP_474	OD2	3.910
6P62	E_ARG_476	NH2	E_GLU_102	OE1	3.634
6P62	E_ARG_476	NH2	E_GLU_102	OE2	3.089
6P62	E_LYS_487	NZ	E_ASP_47	OD1	3.071
6P62	E_LYS_487	NZ	E_ASP_47	OD2	2.841
6P62	E_LYS_490	NZ	E_GLU_492	OE2	3.504
6P62	E_ARG_520	NH2	E_GLU_87	OE1	3.537
6P62	E_ARG_542	NH1	A_GLU_647	OE1	2.629
6P62	E_ARG_542	NH1	A_GLU_647	OE2	3.985
6P62	E_ARG_542	NH2	A_GLU_648	OE2	3.130
6P62	E_LYS_574	NZ	E_ASP_107	OD1	2.480
6P62	E_LYS_574	NZ	E_ASP_107	OD2	3.952
6P62	E_ARG_579	NH1	A_GLU_584	OE1	3.453
6P62	E_ARG_579	NH1	A_GLU_584	OE2	2.952
6P62	E_ARG_585	NH2	E_GLU_492	OE1	3.953
6P62	E_ARG_585	NH2	E_GLU_492	OE2	2.998
6P62	E_ARG_588	NH1	E_GLU_584	OE1	3.660
6P62	E_ARG_588	NH2	E_GLU_584	OE1	3.069
6P62	E_ARG_617	NH1	E_GLU_634	OE1	3.708
6P62	E_ARG_617	NH1	E_GLU_634	OE2	3.595
6P62	F_ARG_38	NH1	F_ASP_86	OD1	3.041
6P62	F_ARG_38	NH2	F_GLU_46	OE1	2.921
6P62	F_ARG_94	NH2	F_ASP_101	OD1	3.646
6P62	F_ARG_94	NH2	F_ASP_101	OD2	2.930
6P62	G_LYS_22	NZ	G_GLU_70	OE2	3.542
6P62	G_ARG_61	NH1	G_GLU_79	OE2	3.423
6P62	G_ARG_61	NH1	G_ASP_82	OD2	3.763
6P62	G_ARG_61	NH2	G_ASP_77	OD2	2.844
6P62	G_ARG_61	NH2	G_GLU_79	OE2	2.955

Table 893: 6P62-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6P65	A_LYS_46	NZ	A_ASP_632	OD2	2.391
6P65	A_LYS_185D	NZ	A_GLU_185A	OE1	3.592
6P65	A_LYS_185D	NZ	A_GLU_185A	OE2	3.302
6P65	A_LYS_227	NZ	A_GLU_83	OE1	2.949
6P65	A_LYS_227	NZ	A_GLU_83	OE2	3.484
6P65	A_HIS_249	NE2	A_GLU_482	OE1	3.021
6P65	A_LYS_282	NZ	A_GLU_275	OE1	2.833
6P65	A_LYS_282	NZ	A_GLU_275	OE2	3.523
6P65	A_ARG_298	NH2	A_GLU_381	OE1	3.069
6P65	A_LYS_305	NZ	A_ASP_322	OD1	2.972
6P65	A_LYS_305	NZ	A_ASP_322	OD2	2.511
6P65	A_ARG_340	NH2	A_ASP_337	OD1	2.733
6P65	A_ARG_340	NH2	A_ASP_337	OD2	3.882
6P65	A_ARG_344	NH1	A_GLU_290	OE1	3.426
6P65	A_ARG_344	NH1	A_GLU_290	OE2	3.021
6P65	A_LYS_348	NZ	A_GLU_351	OE1	2.894
6P65	A_LYS_348	NZ	A_GLU_351	OE2	3.938
6P65	A_ARG_419	NH2	A_GLU_153	OE1	2.875
6P65	A_LYS_421	NZ	A_GLU_370	OE2	2.921
6P65	A_ARG_429	NH1	A_ASP_113	OD1	3.603
6P65	A_ARG_429	NH1	A_ASP_113	OD2	2.908
6P65	A_ARG_429	NH2	A_ASP_113	OD1	2.815
6P65	A_ARG_429	NH2	A_ASP_113	OD2	3.611
6P65	A_LYS_446	NZ	A_GLU_293	OE2	3.260
6P65	A_ARG_456	NH1	A_GLU_466	OE1	3.094
6P65	A_ARG_456	NH1	A_GLU_466	OE2	3.849
6P65	A_ARG_469	NH1	A_ASP_457	OD2	2.839
6P65	A_ARG_469	NH2	A_ASP_457	OD2	3.804
6P65	A_ARG_476	NH1	A_ASP_474	OD1	3.178
6P65	A_ARG_476	NH1	A_ASP_474	OD2	3.851
6P65	A_ARG_476	NH2	A_GLU_102	OE1	3.708
6P65	A_ARG_476	NH2	A_GLU_102	OE2	3.051
6P65	A_LYS_485	NZ	A_GLU_267	OE2	2.827
6P65	A_LYS_487	NZ	A_ASP_47	OD1	2.922
6P65	A_LYS_487	NZ	A_ASP_47	OD2	2.883
6P65	A_LYS_492	NZ	A_GLU_490	OE1	3.434
6P65	A_LYS_492	NZ	A_GLU_490	OE2	2.781
6P65	A_ARG_500	NH1	L_GLU_30	OE1	3.144
6P65	A_ARG_500	NH1	L_GLU_30	OE2	3.804
6P65	A_ARG_500	NH2	L_GLU_30	OE1	3.741
6P65	A_ARG_500	NH2	L_GLU_30	OE2	2.979
6P65	A_ARG_542	NH2	B_ASP_648	OD1	3.154
6P65	A_LYS_574	NZ	A_ASP_107	OD1	2.461
6P65	A_LYS_574	NZ	A_ASP_107	OD2	3.497
6P65	A_LYS_588	NZ	A_GLU_584	OE2	2.713
6P65	A_LYS_617	NZ	A_GLU_634	OE1	3.411
6P65	A_LYS_658	NZ	A_GLU_654	OE1	2.575
6P65	H_ARG_38	NH2	H_GLU_46	OE1	3.002
6P65	H_LYS_71	NZ	A_GLU_87	OE1	2.936
6P65	H_LYS_71	NZ	A_GLU_87	OE2	2.864
6P65	H_ARG_94	NH2	H_ASP_33	OD1	3.585
6P65	H_ARG_94	NH2	H_ASP_33	OD2	3.145
6P65	H_LYS_100H	NZ	L_ASP_50	OD1	2.708
6P65	H_LYS_100H	NZ	L_ASP_50	OD2	2.597
6P65	L_ARG_95B	NH2	L_ASP_95D	OD2	3.668
6P65	B_LYS_46	NZ	B_ASP_632	OD2	2.391
6P65	B_LYS_185D	NZ	B_GLU_185A	OE1	3.593

6P65	B_LYS_185D	NZ	B_GLU_185A	OE2	3.302
6P65	B_LYS_227	NZ	B_GLU_83	OE1	2.949
6P65	B_LYS_227	NZ	B_GLU_83	OE2	3.484
6P65	B_HIS_249	NE2	B_GLU_482	OE1	3.021
6P65	B_LYS_282	NZ	B_GLU_275	OE1	2.833
6P65	B_LYS_282	NZ	B_GLU_275	OE2	3.523
6P65	B_ARG_298	NH2	B_GLU_381	OE1	3.068
6P65	B_LYS_305	NZ	B_ASP_322	OD1	2.972
6P65	B_LYS_305	NZ	B_ASP_322	OD2	2.511
6P65	B_ARG_340	NH2	B_ASP_337	OD1	2.733
6P65	B_ARG_340	NH2	B_ASP_337	OD2	3.883
6P65	B_ARG_344	NH1	B_GLU_290	OE1	3.427
6P65	B_ARG_344	NH1	B_GLU_290	OE2	3.022
6P65	B_LYS_348	NZ	B_GLU_351	OE1	2.895
6P65	B_LYS_348	NZ	B_GLU_351	OE2	3.939
6P65	B_ARG_419	NH2	B_GLU_153	OE1	2.875
6P65	B_LYS_421	NZ	B_GLU_370	OE2	2.921
6P65	B_ARG_429	NH1	B_ASP_113	OD1	3.603
6P65	B_ARG_429	NH1	B_ASP_113	OD2	2.908
6P65	B_ARG_429	NH2	B_ASP_113	OD1	2.816
6P65	B_ARG_429	NH2	B_ASP_113	OD2	3.612
6P65	B_LYS_446	NZ	B_GLU_293	OE2	3.260
6P65	B_ARG_456	NH1	B_GLU_466	OE1	3.095
6P65	B_ARG_456	NH1	B_GLU_466	OE2	3.849
6P65	B_ARG_469	NH1	B_ASP_457	OD2	2.839
6P65	B_ARG_469	NH2	B_ASP_457	OD2	3.803
6P65	B_ARG_476	NH1	B_ASP_474	OD1	3.178
6P65	B_ARG_476	NH1	B_ASP_474	OD2	3.851
6P65	B_ARG_476	NH2	B_GLU_102	OE1	3.708
6P65	B_ARG_476	NH2	B_GLU_102	OE2	3.050
6P65	B_LYS_485	NZ	B_GLU_267	OE2	2.826
6P65	B_LYS_487	NZ	B_ASP_47	OD1	2.922
6P65	B_LYS_487	NZ	B_ASP_47	OD2	2.883
6P65	B_LYS_492	NZ	B_GLU_490	OE1	3.434
6P65	B_LYS_492	NZ	B_GLU_490	OE2	2.782
6P65	B_ARG_500	NH1	D_GLU_30	OE1	3.143
6P65	B_ARG_500	NH1	D_GLU_30	OE2	3.804
6P65	B_ARG_500	NH2	D_GLU_30	OE1	3.741
6P65	B_ARG_500	NH2	D_GLU_30	OE2	2.979
6P65	B_ARG_542	NH2	E_ASP_648	OD1	3.155
6P65	B_LYS_574	NZ	B_ASP_107	OD1	2.460
6P65	B_LYS_574	NZ	B_ASP_107	OD2	3.496
6P65	B_LYS_588	NZ	B_GLU_584	OE2	2.714
6P65	B_LYS_617	NZ	B_GLU_634	OE1	3.411
6P65	B_LYS_658	NZ	B_GLU_654	OE1	2.576
6P65	C_ARG_38	NH2	C_GLU_46	OE1	3.002
6P65	C_LYS_71	NZ	B_GLU_87	OE1	2.936
6P65	C_LYS_71	NZ	B_GLU_87	OE2	2.864
6P65	C_ARG_94	NH2	C_ASP_33	OD1	3.585
6P65	C_ARG_94	NH2	C_ASP_33	OD2	3.145
6P65	C_LYS_100H	NZ	D_ASP_50	OD1	2.708
6P65	C_LYS_100H	NZ	D_ASP_50	OD2	2.597
6P65	D_ARG_95B	NH2	D_ASP_95D	OD2	3.668
6P65	E_LYS_46	NZ	E_ASP_632	OD2	2.391
6P65	E_LYS_185D	NZ	E_GLU_185A	OE1	3.592
6P65	E_LYS_185D	NZ	E_GLU_185A	OE2	3.302
6P65	E_LYS_227	NZ	E_GLU_83	OE1	2.949
6P65	E_LYS_227	NZ	E_GLU_83	OE2	3.484

6P65	E_HIS_249	NE2	E_GLU_482	OE1	3.021
6P65	E_LYS_282	NZ	E_GLU_275	OE1	2.834
6P65	E_LYS_282	NZ	E_GLU_275	OE2	3.523
6P65	E_ARG_298	NH2	E_GLU_381	OE1	3.068
6P65	E_LYS_305	NZ	E_ASP_322	OD1	2.973
6P65	E_LYS_305	NZ	E_ASP_322	OD2	2.510
6P65	E_ARG_340	NH2	E_ASP_337	OD1	2.733
6P65	E_ARG_340	NH2	E_ASP_337	OD2	3.883
6P65	E_ARG_344	NH1	E_GLU_290	OE1	3.426
6P65	E_ARG_344	NH1	E_GLU_290	OE2	3.021
6P65	E_LYS_348	NZ	E_GLU_351	OE1	2.895
6P65	E_LYS_348	NZ	E_GLU_351	OE2	3.939
6P65	E_ARG_419	NH2	E_GLU_153	OE1	2.874
6P65	E_LYS_421	NZ	E_GLU_370	OE2	2.921
6P65	E_ARG_429	NH1	E_ASP_113	OD1	3.603
6P65	E_ARG_429	NH1	E_ASP_113	OD2	2.907
6P65	E_ARG_429	NH2	E_ASP_113	OD1	2.816
6P65	E_ARG_429	NH2	E_ASP_113	OD2	3.611
6P65	E_LYS_446	NZ	E_GLU_293	OE2	3.260
6P65	E_ARG_456	NH1	E_GLU_466	OE1	3.094
6P65	E_ARG_456	NH1	E_GLU_466	OE2	3.849
6P65	E_ARG_469	NH1	E_ASP_457	OD2	2.839
6P65	E_ARG_469	NH2	E_ASP_457	OD2	3.804
6P65	E_ARG_476	NH1	E_ASP_474	OD1	3.178
6P65	E_ARG_476	NH1	E_ASP_474	OD2	3.850
6P65	E_ARG_476	NH2	E_GLU_102	OE1	3.708
6P65	E_ARG_476	NH2	E_GLU_102	OE2	3.050
6P65	E_LYS_485	NZ	E_GLU_267	OE2	2.828
6P65	E_LYS_487	NZ	E_ASP_47	OD1	2.921
6P65	E_LYS_487	NZ	E_ASP_47	OD2	2.883
6P65	E_LYS_492	NZ	E_GLU_490	OE1	3.434
6P65	E_LYS_492	NZ	E_GLU_490	OE2	2.782
6P65	E_ARG_500	NH1	G_GLU_30	OE1	3.143
6P65	E_ARG_500	NH1	G_GLU_30	OE2	3.804
6P65	E_ARG_500	NH2	G_GLU_30	OE1	3.741
6P65	E_ARG_500	NH2	G_GLU_30	OE2	2.979
6P65	E_ARG_542	NH2	A_ASP_648	OD1	3.154
6P65	E_LYS_574	NZ	E_ASP_107	OD1	2.460
6P65	E_LYS_574	NZ	E_ASP_107	OD2	3.496
6P65	E_LYS_588	NZ	E_GLU_584	OE2	2.714
6P65	E_LYS_617	NZ	E_GLU_634	OE1	3.411
6P65	E_LYS_658	NZ	E_GLU_654	OE1	2.576
6P65	F_ARG_38	NH2	F_GLU_46	OE1	3.002
6P65	F_LYS_71	NZ	E_GLU_87	OE1	2.935
6P65	F_LYS_71	NZ	E_GLU_87	OE2	2.865
6P65	F_ARG_94	NH2	F_ASP_33	OD1	3.585
6P65	F_ARG_94	NH2	F_ASP_33	OD2	3.145
6P65	F_LYS_100H	NZ	G_ASP_50	OD1	2.708
6P65	F_LYS_100H	NZ	G_ASP_50	OD2	2.596
6P65	G_ARG_95B	NH2	G_ASP_95D	OD2	3.668

Table 894: 6P65-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6PE8	A_ARG_38	NH1	A_ASP_90	OD1	3.071
6PE8	A_ARG_38	NH2	A_GLU_46	OE1	3.098
6PE8	A_ARG_38	NH2	A_ASP_90	OD1	3.704
6PE8	A_LYS_65	NZ	A_ASP_62	OD1	3.575
6PE8	A_ARG_67	NH1	A_ASP_90	OD1	3.779
6PE8	A_ARG_67	NH1	A_ASP_90	OD2	2.688
6PE8	A_ARG_67	NH2	A_ASP_90	OD1	3.147
6PE8	A_ARG_67	NH2	A_ASP_90	OD2	3.558
6PE8	A_ARG_98	NH2	A_ASP_104	OD2	2.902
6PE8	A_LYS_212	NZ	B_GLU_129	OE1	3.617
6PE8	A_LYS_212	NZ	B_GLU_129	OE2	2.921
6PE8	A_LYS_213	NZ	A_GLU_215	OE2	2.893
6PE8	A_LYS_217	NZ	B_ASP_128	OD2	3.408
6PE8	B_LYS_24	NZ	B_ASP_76	OD1	3.379
6PE8	B_LYS_36	NZ	U_GLU_98	OE2	3.943
6PE8	B_ARG_67	NH2	B_ASP_88	OD1	2.504
6PE8	B_ARG_67	NH2	B_ASP_88	OD2	3.136
6PE8	B_LYS_109	NZ	B_GLU_111	OE2	3.226
6PE8	B_LYS_155	NZ	B_GLU_201	OE2	3.818
6PE8	B_HIS_195	ND1	B_ASP_157	OD2	3.341
6PE8	H_ARG_38	NH1	H_ASP_90	OD1	3.238
6PE8	H_ARG_38	NH2	H_GLU_46	OE2	3.230
6PE8	H_ARG_38	NH2	H_ASP_90	OD1	3.857
6PE8	H_LYS_65	NZ	H_ASP_62	OD1	3.030
6PE8	H_ARG_67	NH1	H_ASP_90	OD1	3.620
6PE8	H_ARG_67	NH1	H_ASP_90	OD2	2.656
6PE8	H_ARG_67	NH2	H_ASP_90	OD1	3.125
6PE8	H_ARG_67	NH2	H_ASP_90	OD2	3.678
6PE8	H_ARG_98	NH2	H_ASP_104	OD1	3.497
6PE8	H_ARG_98	NH2	H_ASP_104	OD2	2.823
6PE8	H_LYS_146	NZ	H_ASP_147	OD1	3.006
6PE8	H_LYS_146	NZ	H_ASP_147	OD2	3.312
6PE8	H_LYS_212	NZ	L_GLU_129	OE1	2.763
6PE8	H_LYS_212	NZ	L_GLU_129	OE2	3.237
6PE8	L_LYS_36	NZ	T_GLU_98	OE1	3.975
6PE8	L_LYS_36	NZ	T_GLU_98	OE2	3.494
6PE8	L_ARG_67	NH1	L_ASP_88	OD1	2.489
6PE8	L_ARG_67	NH1	L_ASP_88	OD2	2.664
6PE8	L_ARG_67	NH2	L_GLU_87	OE2	3.818
6PE8	L_LYS_109	NZ	L_GLU_171	OE1	2.957
6PE8	L_LYS_109	NZ	L_GLU_171	OE2	3.577
6PE8	L_HIS_195	ND1	L_ASP_191	OD1	3.228
6PE8	L_ARG_217	NH1	L_GLU_193	OE2	3.407
6PE8	T_LYS_46	NZ	T_GLU_66	OE1	3.537
6PE8	T_HIS_78	NE2	T_GLU_74	OE2	3.145
6PE8	T_LYS_81	NZ	T_GLU_117	OE2	3.858
6PE8	T_ARG_90	NH1	T_GLU_106	OE2	3.299
6PE8	T_ARG_90	NH2	H_ASP_62	OD1	3.932
6PE8	T_LYS_94	NZ	L_ASP_97	OD1	2.502
6PE8	T_LYS_94	NZ	L_ASP_97	OD2	3.872
6PE8	T_ARG_123	NH1	T_ASP_140	OD2	3.487
6PE8	T_ARG_123	NH2	T_ASP_140	OD2	3.475
6PE8	U_HIS_78	NE2	U_GLU_74	OE2	3.728
6PE8	U_HIS_162	NE2	U_GLU_159	OE1	3.858
6PE8	U_HIS_162	NE2	U_GLU_159	OE2	3.289

Table 895: 6PE8-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6PE9	A_ARG_38	NH1	A_ASP_90	OD1	2.798
6PE9	A_ARG_38	NH2	A_GLU_46	OE1	3.159
6PE9	A_ARG_38	NH2	A_GLU_46	OE2	3.251
6PE9	A_ARG_38	NH2	A_ASP_90	OD1	3.887
6PE9	A_ARG_67	NH1	A_ASP_90	OD1	3.800
6PE9	A_ARG_67	NH1	A_ASP_90	OD2	2.750
6PE9	A_ARG_67	NH2	A_ASP_90	OD1	2.777
6PE9	A_ARG_67	NH2	A_ASP_90	OD2	3.300
6PE9	A_ARG_87	NH1	A_ASP_90	OD1	3.204
6PE9	A_ARG_98	NH2	A_ASP_104	OD1	3.991
6PE9	A_ARG_98	NH2	A_ASP_104	OD2	3.023
6PE9	A_LYS_146	NZ	A_ASP_147	OD1	3.217
6PE9	A_LYS_146	NZ	A_ASP_147	OD2	3.463
6PE9	A_LYS_212	NZ	B_GLU_129	OE1	3.227
6PE9	A_LYS_212	NZ	B_GLU_129	OE2	3.311
6PE9	A_LYS_213	NZ	A_GLU_215	OE2	2.756
6PE9	A_LYS_217	NZ	B_ASP_128	OD1	3.061
6PE9	A_LYS_217	NZ	B_ASP_128	OD2	3.113
6PE9	B_ARG_60	NH2	B_ASP_66	OD2	3.733
6PE9	B_ARG_67	NH2	B_GLU_87	OE2	3.721
6PE9	B_ARG_67	NH2	B_ASP_88	OD1	2.626
6PE9	B_ARG_67	NH2	B_ASP_88	OD2	3.531
6PE9	B_LYS_109	NZ	B_GLU_171	OE1	3.224
6PE9	B_LYS_109	NZ	B_GLU_171	OE2	3.604
6PE9	B_LYS_155	NZ	B_GLU_201	OE1	2.857
6PE9	B_LYS_155	NZ	B_GLU_201	OE2	3.583
6PE9	B_LYS_189	NZ	B_GLU_193	OE1	2.706
6PE9	B_HIS_195	ND1	B_ASP_157	OD2	3.250
6PE9	B_HIS_195	NE2	B_ASP_191	OD1	3.630
6PE9	C_LYS_13	NZ	U_GLU_107	OE2	3.461
6PE9	C_ARG_38	NH1	C_ASP_90	OD1	2.834
6PE9	C_ARG_38	NH2	C_GLU_46	OE1	3.774
6PE9	C_ARG_38	NH2	C_ASP_90	OD1	3.862
6PE9	C_ARG_67	NH1	C_ASP_90	OD1	3.690
6PE9	C_ARG_67	NH1	C_ASP_90	OD2	2.701
6PE9	C_ARG_67	NH2	C_ASP_90	OD1	3.027
6PE9	C_ARG_67	NH2	C_ASP_90	OD2	3.482
6PE9	C_ARG_87	NH1	C_GLU_89	OE1	2.999
6PE9	C_ARG_87	NH2	C_GLU_89	OE1	3.050
6PE9	C_ARG_98	NH2	C_ASP_104	OD1	3.544
6PE9	C_ARG_98	NH2	C_ASP_104	OD2	2.696
6PE9	C_LYS_212	NZ	D_GLU_129	OE1	2.716
6PE9	D_LYS_24	NZ	D_ASP_76	OD2	3.066
6PE9	D_LYS_36	NZ	G_GLU_98	OE2	3.800
6PE9	D_ARG_67	NH2	D_GLU_87	OE2	3.276
6PE9	D_ARG_67	NH2	D_ASP_88	OD1	2.629
6PE9	D_ARG_67	NH2	D_ASP_88	OD2	2.960
6PE9	D_LYS_109	NZ	D_GLU_111	OE2	3.968
6PE9	D_ARG_148	NH1	D_GLU_111	OE1	3.574
6PE9	D_ARG_148	NH1	D_GLU_111	OE2	3.676
6PE9	D_LYS_155	NZ	D_GLU_201	OE1	3.155
6PE9	D_LYS_189	NZ	D_GLU_193	OE2	3.713
6PE9	D_HIS_195	ND1	D_ASP_157	OD2	3.268
6PE9	D_HIS_195	NE2	D_ASP_191	OD1	3.868
6PE9	D_LYS_196	NZ	D_GLU_219	OE1	3.644
6PE9	D_LYS_196	NZ	D_GLU_219	OE2	3.664
6PE9	E_LYS_13	NZ	G_GLU_107	OE2	3.510

6PE9	E_ARG_38	NH1	E_ASP_90	OD1	3.156
6PE9	E_ARG_38	NH2	E_GLU_46	OE1	3.279
6PE9	E_ARG_38	NH2	E_ASP_90	OD1	3.604
6PE9	E_LYS_65	NZ	E_ASP_62	OD1	3.311
6PE9	E_ARG_67	NH1	E_ASP_90	OD1	3.553
6PE9	E_ARG_67	NH1	E_ASP_90	OD2	2.749
6PE9	E_ARG_67	NH2	E_ASP_90	OD1	2.879
6PE9	E_ARG_67	NH2	E_ASP_90	OD2	3.602
6PE9	E_ARG_87	NH1	E_GLU_89	OE1	2.875
6PE9	E_ARG_98	NH2	E_ASP_104	OD1	3.656
6PE9	E_ARG_98	NH2	E_ASP_104	OD2	2.618
6PE9	E_LYS_212	NZ	F_GLU_129	OE1	3.511
6PE9	E_LYS_212	NZ	F_GLU_129	OE2	3.915
6PE9	F_LYS_36	NZ	U_GLU_98	OE2	3.769
6PE9	F_ARG_67	NH2	F_GLU_87	OE2	3.406
6PE9	F_ARG_67	NH2	F_ASP_88	OD1	3.433
6PE9	F_ARG_67	NH2	F_ASP_88	OD2	3.747
6PE9	F_ARG_148	NH1	F_GLU_149	OE1	2.587
6PE9	F_LYS_155	NZ	F_GLU_201	OE1	2.986
6PE9	F_LYS_189	NZ	F_GLU_193	OE1	3.673
6PE9	F_HIS_195	ND1	F_ASP_157	OD2	2.583
6PE9	F_ARG_217	NH1	F_GLU_193	OE2	2.594
6PE9	F_ARG_217	NH2	F_GLU_193	OE2	3.577
6PE9	G_ARG_73	NH1	J_GLU_74	OE1	3.140
6PE9	G_ARG_73	NH2	J_GLU_74	OE1	2.423
6PE9	G_ARG_73	NH2	J_GLU_74	OE2	3.851
6PE9	G_LYS_94	NZ	D_ASP_97	OD1	2.957
6PE9	G_HIS_110	ND1	G_ASP_140	OD1	3.723
6PE9	G_HIS_110	ND1	G_ASP_140	OD2	3.419
6PE9	G_HIS_110	NE2	G_ASP_140	OD2	3.595
6PE9	H_ARG_38	NH1	H_ASP_90	OD1	2.812
6PE9	H_ARG_38	NH2	H_GLU_46	OE1	3.356
6PE9	H_ARG_38	NH2	H_ASP_90	OD1	3.422
6PE9	H_ARG_67	NH1	H_ASP_90	OD1	3.929
6PE9	H_ARG_67	NH1	H_ASP_90	OD2	2.687
6PE9	H_ARG_67	NH2	H_ASP_90	OD1	3.445
6PE9	H_ARG_67	NH2	H_ASP_90	OD2	3.625
6PE9	H_ARG_98	NH2	H_ASP_104	OD1	3.718
6PE9	H_ARG_98	NH2	H_ASP_104	OD2	3.048
6PE9	I_LYS_29	NZ	U_ASP_69	OD2	3.034
6PE9	I_ARG_73	NH1	U_GLU_74	OE1	3.681
6PE9	I_ARG_73	NH1	U_GLU_74	OE2	2.345
6PE9	I_ARG_73	NH2	U_GLU_74	OE2	3.507
6PE9	I_LYS_	NZ	I_GLU_	OE2	3.108
6PE9	J_ARG_73	NH1	G_GLU_74	OE1	3.931
6PE9	J_ARG_73	NH1	G_GLU_74	OE2	3.429
6PE9	K_ARG_38	NH1	K_ASP_90	OD1	3.525
6PE9	K_ARG_38	NH2	K_GLU_46	OE1	3.767
6PE9	K_ARG_38	NH2	K_GLU_46	OE2	3.741
6PE9	K_LYS_65	NZ	K_ASP_62	OD1	3.669
6PE9	K_ARG_67	NH1	K_ASP_90	OD2	2.819
6PE9	K_ARG_67	NH2	K_ASP_90	OD1	3.281
6PE9	K_ARG_67	NH2	K_ASP_90	OD2	2.919
6PE9	K_ARG_98	NH2	K_ASP_104	OD2	3.783
6PE9	L_LYS_24	NZ	L_ASP_76	OD1	3.672
6PE9	L_LYS_24	NZ	L_ASP_76	OD2	3.497
6PE9	L_ARG_67	NH2	L_ASP_88	OD1	2.613
6PE9	L_ARG_67	NH2	L_ASP_88	OD2	3.007

6PE9	L_LYS_109	NZ	L_GLU_111	OE2	2.907
6PE9	L_LYS_155	NZ	L_GLU_201	OE1	3.099
6PE9	L_LYS_155	NZ	L_GLU_201	OE2	3.866
6PE9	L_LYS_194	NZ	L_ASP_191	OD1	2.988
6PE9	L_LYS_196	NZ	L_GLU_219	OE1	3.947
6PE9	L_LYS_196	NZ	L_GLU_219	OE2	3.563
6PE9	M_LYS_24	NZ	M_ASP_76	OD2	2.801
6PE9	M_LYS_36	NZ	J_GLU_98	OE1	2.716
6PE9	M_ARG_67	NH2	M_GLU_87	OE2	3.490
6PE9	M_ARG_67	NH2	M_ASP_88	OD1	2.820
6PE9	M_ARG_67	NH2	M_ASP_88	OD2	3.597
6PE9	U_LYS_	NZ	L_ASP_	OD2	3.835
6PE9	U_LYS_	NZ	U_GLU_	OE1	3.844
6PE9	U_ARG_	NH2	L_GLU_	OE1	3.379
6PE9	U_ARG_	NH2	L_GLU_	OE2	2.907
6PE9	U_ARG_90	NH2	U_GLU_107	OE1	3.607
6PE9	U_LYS_94	NZ	F_ASP_97	OD1	2.940
6PE9	U_HIS_110	ND1	U_ASP_140	OD1	3.870
6PE9	U_HIS_110	NE2	U_ASP_140	OD2	3.135
6PE9	V_LYS_46	NZ	V_GLU_66	OE1	3.793
6PE9	V_LYS_81	NZ	V_ASP_100	OD2	3.343
6PE9	V_ARG_90	NH1	L_ASP_1	OD1	3.701
6PE9	V_ARG_90	NH1	V_GLU_106	OE1	3.470
6PE9	V_ARG_90	NH1	V_GLU_106	OE2	3.555
6PE9	V_ARG_90	NH2	L_ASP_1	OD1	3.047
6PE9	V_LYS_94	NZ	L_ASP_97	OD1	3.203

Table 896: 6PE9-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6PHB	I.HIS_20	NE2	I.GLU_22	OE2	2.552
6PHB	I.LYS_43	NZ	D.ASP_27	OD2	2.797
6PHB	I.LYS_47	NZ	C.GLU_55	OE1	3.460
6PHB	I.LYS_47	NZ	C.GLU_55	OE2	3.396
6PHB	I.LYS_47	NZ	D.ASP_105	OD2	2.626
6PHB	I.LYS_98	NZ	I.GLU_22	OE1	3.315
6PHB	I.LYS_98	NZ	I.GLU_22	OE2	2.997
6PHB	I.LYS_118	NZ	I.ASP_131	OD1	2.829
6PHB	C.ARG_61	NH2	C.GLU_81	OE2	3.398
6PHB	C.ARG_61	NH2	C.ASP_82	OD1	2.798
6PHB	C.ARG_61	NH2	C.ASP_82	OD2	3.548
6PHB	C.ARG_95	NH1	I.ASP_28	OD2	3.551
6PHB	C.ARG_95	NH1	I.GLU_39	OE2	3.728
6PHB	C.LYS_104	NZ	C.GLU_166	OE2	2.738
6PHB	C.LYS_150	NZ	C.GLU_196	OE1	2.587
6PHB	C.LYS_150	NZ	C.GLU_196	OE2	3.892
6PHB	C.LYS_189	NZ	C.ASP_186	OD1	3.064
6PHB	C.ARG_212	NH1	C.GLU_188	OE1	3.096
6PHB	D.ARG_38	NH1	D.ASP_89	OD1	2.792
6PHB	D.ARG_38	NH2	D.GLU_46	OE1	3.039
6PHB	D.ARG_38	NH2	D.GLU_46	OE2	3.983
6PHB	D.ARG_38	NH2	D.ASP_89	OD1	3.789
6PHB	D.ARG_50	NH1	I.GLU_39	OE2	3.791
6PHB	D.ARG_50	NH2	I.GLU_39	OE2	2.945
6PHB	D.ARG_66	NH1	D.ASP_89	OD1	3.229
6PHB	D.ARG_66	NH1	D.ASP_89	OD2	3.729
6PHB	D.ARG_66	NH2	D.ASP_89	OD1	3.250
6PHB	D.ARG_66	NH2	D.ASP_89	OD2	2.491
6PHB	D.LYS_147	NZ	D.ASP_148	OD1	3.275
6PHB	D.LYS_147	NZ	D.ASP_148	OD2	3.674
6PHB	D.LYS_213	NZ	C.GLU_124	OE1	2.534
6PHB	D.LYS_213	NZ	C.GLU_124	OE2	3.508
6PHB	E.HIS_20	NE2	E.GLU_22	OE1	2.558
6PHB	E.LYS_43	NZ	B.ASP_27	OD2	3.033
6PHB	E.LYS_47	NZ	A.GLU_55	OE1	3.560
6PHB	E.LYS_47	NZ	A.GLU_55	OE2	3.516
6PHB	E.LYS_47	NZ	B.ASP_105	OD1	2.522
6PHB	E.LYS_98	NZ	E.GLU_22	OE1	3.054
6PHB	E.LYS_98	NZ	E.GLU_22	OE2	3.330
6PHB	E.LYS_118	NZ	E.ASP_131	OD1	2.740
6PHB	E.LYS_142	NZ	E.GLU_145	OE2	3.699
6PHB	A.ARG_61	NH2	A.GLU_81	OE2	3.390
6PHB	A.ARG_61	NH2	A.ASP_82	OD1	2.898
6PHB	A.ARG_61	NH2	A.ASP_82	OD2	3.663
6PHB	A.ARG_95	NH1	E.ASP_28	OD1	3.463
6PHB	A.ARG_95	NH1	E.GLU_39	OE2	3.694
6PHB	A.LYS_104	NZ	A.GLU_166	OE1	2.724
6PHB	A.LYS_150	NZ	A.GLU_196	OE1	2.544
6PHB	A.LYS_150	NZ	A.GLU_196	OE2	3.867
6PHB	A.LYS_189	NZ	A.ASP_186	OD1	3.061
6PHB	A.ARG_212	NH2	A.GLU_188	OE2	2.964
6PHB	B.ARG_38	NH1	B.ASP_89	OD1	2.781
6PHB	B.ARG_38	NH2	B.GLU_46	OE1	3.033
6PHB	B.ARG_38	NH2	B.GLU_46	OE2	3.957
6PHB	B.ARG_38	NH2	B.ASP_89	OD1	3.799
6PHB	B.ARG_50	NH1	E.GLU_39	OE2	3.771
6PHB	B.ARG_50	NH2	E.GLU_39	OE2	2.963

6PHB	B_ARG_66	NH1	B_ASP_89	OD1	3.245
6PHB	B_ARG_66	NH1	B_ASP_89	OD2	3.725
6PHB	B_ARG_66	NH2	B_ASP_89	OD1	3.258
6PHB	B_ARG_66	NH2	B_ASP_89	OD2	2.482
6PHB	B_LYS_147	NZ	B_ASP_148	OD1	3.294
6PHB	B_LYS_147	NZ	B_ASP_148	OD2	3.635
6PHB	B_LYS_213	NZ	A_GLU_124	OE1	3.629
6PHB	B_LYS_213	NZ	A_GLU_124	OE2	2.552

Table 897: 6PHB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6PHC	I.LYS_2	NZ	A.GLU_96	OE1	3.433
6PHC	I.HIS_20	NE2	I.GLU_22	OE2	2.559
6PHC	I.LYS_40	NZ	I.ASP_28	OD1	2.981
6PHC	I.LYS_40	NZ	I.ASP_28	OD2	3.595
6PHC	I.LYS_98	NZ	I.GLU_22	OE2	3.581
6PHC	I.LYS_139	NZ	I.ASP_6	OD1	2.833
6PHC	A.ARG_38	NH1	A.ASP_86	OD1	2.881
6PHC	A.ARG_38	NH2	A.GLU_46	OE1	3.768
6PHC	A.ARG_38	NH2	A.GLU_46	OE2	2.978
6PHC	A.ARG_38	NH2	A.ASP_86	OD1	3.793
6PHC	A.LYS_64	NZ	A.ASP_61	OD2	2.874
6PHC	A.ARG_66	NH1	A.ASP_86	OD1	3.869
6PHC	A.ARG_66	NH2	A.ASP_86	OD1	3.269
6PHC	A.ARG_66	NH2	A.ASP_86	OD2	2.372
6PHC	A.ARG_94	NH2	A.ASP_101	OD1	3.528
6PHC	A.ARG_94	NH2	A.ASP_101	OD2	2.665
6PHC	A.LYS_143	NZ	A.ASP_144	OD1	3.692
6PHC	A.LYS_206	NZ	A.ASP_208	OD1	2.966
6PHC	A.LYS_206	NZ	A.ASP_208	OD2	3.137
6PHC	A.LYS_209	NZ	B.GLU_122	OE2	3.367
6PHC	A.LYS_210	NZ	A.GLU_212	OE2	2.900
6PHC	B.ARG_24	NH1	B.ASP_70	OD1	3.336
6PHC	B.ARG_61	NH1	B.ASP_82	OD1	3.307
6PHC	B.ARG_61	NH1	B.ASP_82	OD2	2.292
6PHC	B.ARG_61	NH2	B.GLU_81	OE2	3.528
6PHC	B.ARG_61	NH2	B.ASP_82	OD1	3.098
6PHC	B.ARG_61	NH2	B.ASP_82	OD2	3.416
6PHC	B.ARG_102	NH1	B.GLU_164	OE1	2.853
6PHC	B.LYS_106	NZ	B.GLU_17	OE2	3.611
6PHC	B.ARG_141	NH1	B.GLU_104	OE1	3.956
6PHC	B.ARG_141	NH2	B.GLU_104	OE1	2.662
6PHC	B.ARG_141	NH2	B.GLU_104	OE2	2.894
6PHC	B.LYS_148	NZ	B.GLU_194	OE1	2.588
6PHC	B.LYS_187	NZ	B.ASP_184	OD1	3.568
6PHC	E.LYS_2	NZ	C.GLU_96	OE2	3.166
6PHC	E.HIS_20	NE2	E.GLU_22	OE2	2.761
6PHC	E.LYS_118	NZ	E.ASP_131	OD1	3.884
6PHC	E.LYS_118	NZ	E.ASP_131	OD2	3.881
6PHC	E.LYS_139	NZ	E.ASP_6	OD1	2.752
6PHC	E.LYS_139	NZ	E.ASP_6	OD2	3.907
6PHC	E.LYS_155	NZ	E.ASP_157	OD2	3.939
6PHC	C.ARG_38	NH1	C.ASP_86	OD1	2.792
6PHC	C.ARG_38	NH2	C.GLU_46	OE1	3.747
6PHC	C.ARG_38	NH2	C.GLU_46	OE2	2.839
6PHC	C.ARG_38	NH2	C.ASP_86	OD1	3.865
6PHC	C.LYS_64	NZ	C.ASP_61	OD1	3.164
6PHC	C.ARG_66	NH2	C.ASP_86	OD1	3.190
6PHC	C.ARG_66	NH2	C.ASP_86	OD2	2.357
6PHC	C.LYS_75	NZ	A.GLU_1	OE1	3.102
6PHC	C.ARG_94	NH2	C.ASP_101	OD1	3.594
6PHC	C.ARG_94	NH2	C.ASP_101	OD2	2.564
6PHC	C.LYS_143	NZ	C.ASP_144	OD1	3.602
6PHC	C.LYS_143	NZ	C.ASP_144	OD2	3.997
6PHC	C.LYS_209	NZ	D.GLU_122	OE2	3.075
6PHC	D.ARG_24	NH1	D.ASP_70	OD1	2.338
6PHC	D.ARG_24	NH1	D.ASP_70	OD2	2.957
6PHC	D.ARG_24	NH2	D.ASP_70	OD1	3.768

6PHC	D_ARG_61	NH2	D_GLU_81	OE2	3.370
6PHC	D_ARG_61	NH2	D_ASP_82	OD1	3.166
6PHC	D_ARG_61	NH2	D_ASP_82	OD2	3.703
6PHC	D_LYS_106	NZ	D_GLU_17	OE2	3.862
6PHC	D_ARG_141	NH1	D_GLU_104	OE1	3.512
6PHC	D_ARG_141	NH1	D_GLU_104	OE2	3.995
6PHC	D_ARG_141	NH2	D_GLU_104	OE1	3.237
6PHC	D_ARG_141	NH2	D_GLU_104	OE2	2.397
6PHC	D_LYS_187	NZ	D_ASP_184	OD1	3.752

Table 898: 6PHC-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6PHD	H_HIS_3	NE2	H_GLU_1	OE1	3.723
6PHD	H_HIS_3	NE2	H_GLU_1	OE2	3.479
6PHD	H_ARG_38	NH1	H_ASP_92	OD1	3.022
6PHD	H_ARG_38	NH2	H_GLU_46	OE1	3.293
6PHD	H_ARG_38	NH2	H_GLU_46	OE2	3.635
6PHD	H_ARG_38	NH2	H_ASP_92	OD1	3.809
6PHD	H_ARG_50	NH1	H_ASP_35	OD1	3.977
6PHD	H_ARG_50	NH1	H_ASP_35	OD2	3.398
6PHD	H_ARG_52	NH1	H_ASP_61	OD2	3.597
6PHD	H_ARG_52	NH2	H_ASP_61	OD2	3.257
6PHD	H_ARG_52	NH2	C_ASP_131	OD2	3.559
6PHD	H_ARG_69	NH1	H_ASP_92	OD1	3.736
6PHD	H_ARG_69	NH1	H_ASP_92	OD2	2.629
6PHD	H_ARG_69	NH2	H_ASP_92	OD1	3.118
6PHD	H_ARG_69	NH2	H_ASP_92	OD2	3.528
6PHD	H_ARG_74	NH2	H_ASP_76	OD1	3.389
6PHD	H_ARG_100	NH2	H_ASP_116	OD1	3.601
6PHD	H_ARG_100	NH2	H_ASP_116	OD2	2.413
6PHD	H_ARG_107	NH1	H_GLU_106	OE2	3.946
6PHD	H_LYS_158	NZ	L_GLU_128	OE2	2.649
6PHD	H_LYS_224	NZ	L_GLU_127	OE1	2.532
6PHD	H_LYS_224	NZ	L_GLU_127	OE2	2.992
6PHD	H_LYS_225	NZ	H_GLU_227	OE2	3.183
6PHD	L_ARG_61	NH2	L_GLU_81	OE1	3.579
6PHD	L_ARG_61	NH2	L_ASP_82	OD1	3.221
6PHD	L_ARG_61	NH2	L_ASP_82	OD2	3.791
6PHD	L_LYS_106	NZ	L_ASP_85	OD1	3.546
6PHD	L_LYS_114	NZ	L_GLU_202	OE1	3.497
6PHD	L_HIS_192	ND1	L_ASP_155	OD2	4.000
6PHD	C_ARG_11	NH1	C_GLU_39	OE2	3.811
6PHD	C_ARG_11	NH2	C_GLU_39	OE1	3.053
6PHD	C_ARG_11	NH2	C_GLU_39	OE2	3.487
6PHD	C_HIS_20	NE2	C_GLU_22	OE1	3.024
6PHD	C_LYS_90	NZ	C_ASP_78	OD2	3.307
6PHD	C_LYS_98	NZ	C_GLU_22	OE1	2.852
6PHD	C_LYS_98	NZ	C_GLU_22	OE2	3.209
6PHD	C_LYS_118	NZ	H_ASP_109	OD1	3.874
6PHD	C_LYS_118	NZ	C_ASP_131	OD1	3.023
6PHD	C_LYS_127	NZ	C_ASP_124	OD1	3.895
6PHD	C_LYS_135	NZ	L_ASP_51	OD2	3.166
6PHD	C_LYS_139	NZ	C_ASP_6	OD1	3.503
6PHD	C_LYS_148	NZ	C_ASP_157	OD2	3.726
6PHD	C_LYS_148	NZ	C_ASP_160	OD1	3.495

Table 899: 6PHD-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6PHF	A_ARG_12	NH2	A_GLU_10	OE1	2.765
6PHF	A_ARG_38	NH1	A_ASP_90	OD1	3.178
6PHF	A_ARG_38	NH2	A_GLU_46	OE1	3.769
6PHF	A_ARG_38	NH2	A_GLU_89	OE1	3.880
6PHF	A_ARG_38	NH2	A_GLU_89	OE2	3.467
6PHF	A_LYS_63	NZ	A_GLU_46	OE2	2.996
6PHF	A_LYS_63	NZ	C_GLU_89	OE2	2.941
6PHF	A_ARG_67	NH1	A_ASP_90	OD1	3.640
6PHF	A_ARG_67	NH2	A_ASP_90	OD1	3.213
6PHF	A_ARG_67	NH2	A_ASP_90	OD2	2.825
6PHF	A_ARG_87	NH2	A_GLU_89	OE1	3.635
6PHF	A_ARG_98	NH1	A_ASP_108	OD1	3.223
6PHF	A_ARG_98	NH1	A_ASP_108	OD2	2.645
6PHF	A_ARG_98	NH2	A_ASP_108	OD2	3.048
6PHF	A_LYS_150	NZ	B_GLU_123	OE1	3.782
6PHF	A_LYS_216	NZ	B_GLU_122	OE1	2.642
6PHF	A_LYS_216	NZ	B_GLU_122	OE2	2.832
6PHF	G_HIS_20	NE2	G_GLU_22	OE2	2.627
6PHF	G_LYS_72	NZ	G_ASP_78	OD1	3.015
6PHF	G_LYS_98	NZ	G_GLU_22	OE1	3.385
6PHF	G_LYS_98	NZ	G_GLU_22	OE2	2.989
6PHF	G_LYS_118	NZ	G_ASP_131	OD1	2.874
6PHF	G_LYS_130	NZ	A_GLU_59	OE2	2.793
6PHF	G_LYS_135	NZ	B_ASP_48	OD1	3.917
6PHF	G_LYS_135	NZ	B_ASP_48	OD2	2.691
6PHF	G_LYS_148	NZ	G_ASP_160	OD1	2.301
6PHF	G_LYS_148	NZ	G_ASP_160	OD2	3.905
6PHF	B_LYS_28	NZ	B_ASP_89	OD2	3.634
6PHF	B_LYS_50	NZ	G_ASP_160	OD1	3.948
6PHF	B_LYS_50	NZ	G_ASP_160	OD2	3.455
6PHF	B_ARG_58	NH1	B_ASP_79	OD2	3.097
6PHF	B_ARG_58	NH2	B_ASP_79	OD1	3.588
6PHF	B_ARG_58	NH2	B_ASP_79	OD2	3.661
6PHF	B_LYS_165	NZ	B_GLU_80	OE1	2.830
6PHF	C_ARG_12	NH2	C_GLU_10	OE1	2.671
6PHF	C_ARG_38	NH1	C_ASP_90	OD1	3.218
6PHF	C_LYS_63	NZ	A_GLU_89	OE2	3.050
6PHF	C_LYS_63	NZ	C_GLU_46	OE2	3.084
6PHF	C_ARG_67	NH2	C_ASP_90	OD1	3.179
6PHF	C_ARG_87	NH1	C_GLU_89	OE1	3.091
6PHF	C_ARG_87	NH2	C_GLU_89	OE1	2.353
6PHF	C_ARG_87	NH2	C_ASP_90	OD1	3.900
6PHF	C_ARG_98	NH2	C_ASP_108	OD2	3.438
6PHF	C_LYS_150	NZ	D_GLU_123	OE2	2.663
6PHF	C_LYS_216	NZ	D_GLU_122	OE1	2.759
6PHF	C_LYS_216	NZ	D_GLU_122	OE2	3.120
6PHF	E_HIS_20	NE2	E_GLU_22	OE1	3.442
6PHF	E_LYS_72	NZ	E_ASP_78	OD1	3.439
6PHF	E_LYS_98	NZ	E_GLU_22	OE1	2.929
6PHF	E_LYS_98	NZ	E_GLU_22	OE2	3.612
6PHF	E_LYS_118	NZ	E_ASP_131	OD1	2.864
6PHF	E_LYS_130	NZ	C_GLU_59	OE2	2.474
6PHF	E_LYS_135	NZ	D_ASP_48	OD1	3.909
6PHF	E_LYS_135	NZ	D_ASP_48	OD2	2.579
6PHF	E_LYS_139	NZ	E_ASP_6	OD1	2.802
6PHF	D_LYS_24	NZ	D_ASP_23	OD1	3.810
6PHF	D_LYS_28	NZ	D_ASP_89	OD1	3.365

6PHF	D_ARG_58	NH2	D_ASP_79	OD1	2.632
6PHF	D_ARG_58	NH2	D_ASP_79	OD2	2.899

Table 900: 6PHF-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6PHG	A_ARG_38	NH1	A_ASP_90	OD1	2.955
6PHG	A_ARG_38	NH2	A_GLU_46	OE1	3.239
6PHG	A_ARG_38	NH2	A_ASP_90	OD1	3.782
6PHG	A_LYS_65	NZ	A_ASP_62	OD1	3.774
6PHG	A_ARG_67	NH1	A_ASP_90	OD1	3.754
6PHG	A_ARG_67	NH1	A_ASP_90	OD2	2.801
6PHG	A_ARG_67	NH2	A_ASP_90	OD1	2.872
6PHG	A_ARG_67	NH2	A_ASP_90	OD2	3.428
6PHG	A_LYS_76	NZ	A_ASP_73	OD2	3.739
6PHG	A_ARG_98	NH2	A_ASP_113	OD1	3.705
6PHG	A_ARG_98	NH2	A_ASP_113	OD2	2.616
6PHG	A_LYS_155	NZ	A_ASP_156	OD1	3.341
6PHG	A_LYS_155	NZ	A_ASP_156	OD2	2.879
6PHG	A_LYS_221	NZ	B_GLU_126	OE2	3.079
6PHG	A_LYS_222	NZ	A_GLU_224	OE1	3.525
6PHG	B_ARG_65	NH1	B_GLU_83	OE1	3.253
6PHG	B_ARG_65	NH1	B_GLU_83	OE2	3.558
6PHG	B_ARG_65	NH2	B_GLU_83	OE1	3.939
6PHG	B_ARG_65	NH2	B_ASP_86	OD1	2.611
6PHG	B_ARG_65	NH2	B_ASP_86	OD2	2.992
6PHG	B_ARG_81	NH2	B_GLU_83	OE2	2.886
6PHG	B_ARG_106	NH1	B_GLU_168	OE2	3.259
6PHG	B_LYS_152	NZ	B_GLU_198	OE1	3.024
6PHG	B_LYS_191	NZ	B_ASP_188	OD1	3.125
6PHG	B_ARG_214	NH1	B_GLU_190	OE1	3.537

Table 901: 6PHG-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6PHH	C_ARG_38	NH1	C_ASP_90	OD1	2.886
6PHH	C_ARG_38	NH2	C_GLU_46	OE1	3.069
6PHH	C_ARG_38	NH2	C_GLU_46	OE2	3.921
6PHH	C_ARG_38	NH2	C_ASP_90	OD1	3.682
6PHH	C_ARG_67	NH1	C_ASP_90	OD1	3.146
6PHH	C_ARG_67	NH1	C_ASP_90	OD2	3.531
6PHH	C_ARG_67	NH2	C_ASP_90	OD1	3.933
6PHH	C_ARG_67	NH2	C_ASP_90	OD2	2.855
6PHH	C_LYS_76	NZ	A_GLU_1	OE1	3.897
6PHH	C_ARG_98	NH2	C_ASP_113	OD1	3.626
6PHH	C_ARG_98	NH2	C_ASP_113	OD2	2.534
6PHH	C_LYS_155	NZ	C_ASP_156	OD1	3.705
6PHH	D_ARG_58	NH2	D_ASP_64	OD1	3.542
6PHH	D_ARG_65	NH2	D_ASP_86	OD1	2.596
6PHH	D_ARG_65	NH2	D_ASP_86	OD2	2.751
6PHH	D_ARG_106	NH1	D_GLU_168	OE1	3.672
6PHH	D_ARG_106	NH1	D_GLU_168	OE2	2.329
6PHH	A_ARG_38	NH1	A_ASP_90	OD1	2.820
6PHH	A_ARG_38	NH2	A_GLU_46	OE1	2.997
6PHH	A_ARG_38	NH2	A_GLU_46	OE2	3.785
6PHH	A_ARG_38	NH2	A_ASP_90	OD1	3.734
6PHH	A_LYS_65	NZ	A_ASP_62	OD1	2.552
6PHH	A_ARG_67	NH1	A_ASP_90	OD1	3.908
6PHH	A_ARG_67	NH1	A_ASP_90	OD2	2.904
6PHH	A_ARG_67	NH2	A_ASP_90	OD1	3.309
6PHH	A_ARG_67	NH2	A_ASP_90	OD2	3.733
6PHH	A_LYS_76	NZ	C_GLU_1	OE1	3.451
6PHH	A_ARG_98	NH2	A_GLU_100	OE1	3.744
6PHH	A_ARG_98	NH2	A_ASP_113	OD1	3.536
6PHH	A_ARG_98	NH2	A_ASP_113	OD2	2.500
6PHH	A_LYS_218	NZ	A_ASP_220	OD1	2.774
6PHH	A_LYS_218	NZ	A_ASP_220	OD2	3.847
6PHH	A_LYS_221	NZ	B_GLU_126	OE2	3.327
6PHH	B_ARG_24	NH1	B_ASP_74	OD1	3.370
6PHH	B_ARG_24	NH1	B_ASP_74	OD2	3.208
6PHH	B_ARG_24	NH2	B_ASP_74	OD1	3.944
6PHH	B_ARG_58	NH2	B_ASP_64	OD1	3.009
6PHH	B_ARG_65	NH2	B_ASP_86	OD1	2.841
6PHH	B_ARG_65	NH2	B_ASP_86	OD2	2.510
6PHH	B_ARG_106	NH1	B_GLU_168	OE2	2.682
6PHH	B_ARG_214	NH1	B_GLU_190	OE1	3.673

Table 902: 6PHH-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6PI7	A_HIS_317	NE2	A_GLU_316	OE1	3.899
6PI7	A_HIS_320	ND1	A_GLU_316	OE2	2.374
6PI7	A_HIS_320	NE2	A_GLU_418	OE2	2.831
6PI7	A_HIS_355	ND1	A_ASP_358	OD1	3.681
6PI7	A_HIS_355	ND1	A_ASP_358	OD2	2.824
6PI7	A_ARG_372	NH2	A_ASP_390	OD1	2.751
6PI7	A_ARG_372	NH2	A_ASP_390	OD2	3.246
6PI7	A_ARG_406	NH2	A_ASP_408	OD1	3.871
6PI7	A_ARG_406	NH2	A_ASP_408	OD2	2.514
6PI7	A_ARG_423	NH1	A_GLU_494	OE1	3.880
6PI7	A_HIS_444	NE2	A_ASP_473	OD2	2.887
6PI7	A_LYS_449	NZ	A_ASP_447	OD2	3.499
6PI7	A_LYS_489	NZ	A_GLU_485	OE1	2.489
6PI7	B_ARG_62	NH2	B_ASP_83	OD1	2.896
6PI7	B_ARG_62	NH2	B_ASP_83	OD2	3.659
6PI7	B_ARG_67	NH2	A_GLU_345	OE2	3.601
6PI7	C_ARG_41	NH1	C_GLU_49	OE1	3.463
6PI7	C_ARG_41	NH1	C_GLU_49	OE2	3.574
6PI7	C_ARG_41	NH1	C_ASP_93	OD1	3.486
6PI7	C_ARG_41	NH2	C_ASP_93	OD1	3.043
6PI7	C_ARG_70	NH1	C_ASP_93	OD1	3.039
6PI7	C_ARG_70	NH1	C_ASP_93	OD2	3.416
6PI7	C_ARG_70	NH2	C_ASP_93	OD1	3.898
6PI7	C_ARG_70	NH2	C_ASP_93	OD2	3.164
6PI7	C_ARG_101	NH2	C_ASP_115	OD1	3.986
6PI7	C_ARG_101	NH2	C_ASP_115	OD2	2.837
6PI7	C_HIS_103	NE2	C_ASP_115	OD2	3.124
6PI7	C_ARG_105	NH1	A_ASP_334	OD1	2.888
6PI7	D_HIS_317	NE2	D_GLU_316	OE1	3.914
6PI7	D_HIS_320	ND1	D_GLU_316	OE2	2.372
6PI7	D_HIS_320	NE2	D_GLU_418	OE2	2.836
6PI7	D_HIS_355	ND1	D_ASP_358	OD2	3.434
6PI7	D_ARG_372	NH2	D_ASP_390	OD1	2.758
6PI7	D_ARG_372	NH2	D_ASP_390	OD2	3.271
6PI7	D_ARG_406	NH2	D_ASP_408	OD1	3.860
6PI7	D_ARG_406	NH2	D_ASP_408	OD2	2.528
6PI7	D_ARG_423	NH1	D_GLU_494	OE1	3.849
6PI7	D_HIS_444	NE2	D_ASP_473	OD2	2.883
6PI7	D_LYS_449	NZ	D_ASP_447	OD2	3.509
6PI7	E_ARG_62	NH2	E_ASP_83	OD1	2.890
6PI7	E_ARG_62	NH2	E_ASP_83	OD2	3.662
6PI7	E_LYS_104	NZ	E_GLU_106	OE2	3.467
6PI7	E_LYS_150	NZ	E_GLU_196	OE1	3.393
6PI7	E_LYS_150	NZ	E_GLU_196	OE2	3.111
6PI7	F_ARG_41	NH1	F_GLU_49	OE1	3.460
6PI7	F_ARG_41	NH1	F_GLU_49	OE2	3.581
6PI7	F_ARG_41	NH1	F_ASP_93	OD1	3.467
6PI7	F_ARG_41	NH2	F_ASP_93	OD1	3.047
6PI7	F_ARG_70	NH1	F_ASP_93	OD1	3.056
6PI7	F_ARG_70	NH1	F_ASP_93	OD2	3.386
6PI7	F_ARG_70	NH2	F_ASP_93	OD1	3.902
6PI7	F_ARG_70	NH2	F_ASP_93	OD2	3.180
6PI7	F_ARG_101	NH2	F_ASP_115	OD1	3.992
6PI7	F_ARG_101	NH2	F_ASP_115	OD2	2.859
6PI7	F_HIS_103	NE2	F_ASP_115	OD2	3.117
6PI7	F_ARG_105	NH1	D_ASP_334	OD1	3.009
6PI7	G_ARG_4	NH1	A_ASP_385	OD1	3.497

6PI7	G_ARG_4	NH1	A_ASP_385	OD2	3.823
6PI7	G_ARG_4	NH2	A_ASP_385	OD1	3.602
6PI7	G_ARG_4	NH2	A_ASP_385	OD2	3.033
6PI7	G_ARG_6	NH1	A_GLU_433	OE2	2.847
6PI7	G_ARG_6	NH1	A_ASP_437	OD1	3.619
6PI7	G_ARG_6	NH2	A_ASP_437	OD1	2.997
6PI7	G_ARG_6	NH2	A_ASP_440	OD2	2.762

Table 903: 6PI7-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6PYC	H_ARG.67	NH2	H_GLU.87	OE2	3.339
6PYC	H_ARG.67	NH2	H_ASP.88	OD1	3.284
6PYC	H_ARG.67	NH2	H_ASP.88	OD2	3.903
6PYC	H_LYS.109	NZ	H_GLU.147	OE1	3.975
6PYC	H_LYS.142	NZ	H_ASP.143	OD1	3.360
6PYC	H_LYS.208	NZ	L_GLU.124	OE1	2.557
6PYC	H_LYS.208	NZ	L_GLU.124	OE2	3.571
6PYC	L_ARG.62	NH2	L_GLU.82	OE1	3.870
6PYC	L_ARG.62	NH2	L_ASP.83	OD1	2.885
6PYC	L_ARG.62	NH2	L_ASP.83	OD2	3.362
6PYC	L_LYS.108	NZ	B_ASP.32	OD1	2.949
6PYC	L_LYS.150	NZ	L_GLU.196	OE1	3.695
6PYC	L_LYS.184	NZ	L_GLU.188	OE1	2.615
6PYC	L_LYS.189	NZ	L_ASP.186	OD1	3.942
6PYC	A_ARG.38	NH1	A_ASP.90	OD1	2.858
6PYC	A_ARG.38	NH2	A_GLU.46	OE1	3.193
6PYC	A_ARG.38	NH2	A_GLU.46	OE2	3.336
6PYC	A_LYS.67	NZ	A_ASP.90	OD1	3.714
6PYC	A_LYS.67	NZ	A_ASP.90	OD2	3.477
6PYC	A_ARG.99	NH1	B_ASP.91	OD1	3.714
6PYC	B_LYS.53	NZ	L_GLU.17	OE1	3.141
6PYC	B_LYS.53	NZ	L_GLU.17	OE2	3.254
6PYC	B_ARG.61	NH1	B_GLU.81	OE2	3.676
6PYC	B_ARG.61	NH1	B_ASP.82	OD1	2.683
6PYC	B_ARG.61	NH1	B_ASP.82	OD2	3.599
6PYC	B_LYS.149	NZ	B_GLU.195	OE1	3.962
6PYC	B_LYS.149	NZ	B_GLU.195	OE2	3.345
6PYC	B_ARG.155	NH1	B_GLU.185	OE1	3.962
6PYC	B_ARG.155	NH1	B_GLU.185	OE2	3.253
6PYC	B_ARG.155	NH2	B_GLU.185	OE1	2.747
6PYC	B_ARG.155	NH2	B_GLU.185	OE2	3.418
6PYC	B_ARG.188	NH2	B_GLU.185	OE2	3.932
6PYC	B_LYS.199	NZ	B_ASP.110	OD2	3.197

Table 904: 6PYC-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6PYD	H_ARG_38	NH1	H_ASP_89	OD1	2.746
6PYD	H_ARG_38	NH2	H_GLU_46	OE1	2.703
6PYD	H_ARG_38	NH2	H_ASP_89	OD1	3.577
6PYD	H_ARG_66	NH1	H_ASP_89	OD1	3.629
6PYD	H_ARG_66	NH2	H_ASP_89	OD1	3.377
6PYD	H_ARG_66	NH2	H_ASP_89	OD2	2.647
6PYD	H_ARG_97	NH1	H_ASP_27	OD2	2.986
6PYD	H_ARG_97	NH2	H_ASP_105	OD1	3.627
6PYD	H_ARG_97	NH2	H_ASP_105	OD2	2.550
6PYD	H_LYS_147	NZ	H_ASP_148	OD1	3.103
6PYD	H_LYS_147	NZ	H_ASP_148	OD2	3.216
6PYD	H_LYS_213	NZ	L_GLU_127	OE1	3.352
6PYD	L_ARG_24	NH2	L_ASP_74	OD2	3.949
6PYD	L_ARG_65	NH1	L_GLU_83	OE2	3.750
6PYD	L_ARG_65	NH2	L_GLU_83	OE1	3.672
6PYD	L_ARG_65	NH2	L_GLU_85	OE1	3.120
6PYD	L_ARG_65	NH2	L_ASP_86	OD1	2.800
6PYD	L_ARG_65	NH2	L_ASP_86	OD2	3.601
6PYD	L_LYS_107	NZ	L_GLU_169	OE1	2.362
6PYD	L_HIS_193	ND1	L_ASP_155	OD2	3.270
6PYD	A_ARG_38	NH1	A_ASP_89	OD1	2.732
6PYD	A_ARG_38	NH2	A_GLU_46	OE1	2.704
6PYD	A_ARG_38	NH2	A_ASP_89	OD1	3.554
6PYD	A_ARG_66	NH1	A_ASP_89	OD1	3.626
6PYD	A_ARG_66	NH2	A_ASP_89	OD1	3.375
6PYD	A_ARG_66	NH2	A_ASP_89	OD2	2.645
6PYD	A_ARG_97	NH1	A_ASP_27	OD2	2.978
6PYD	A_ARG_97	NH2	A_ASP_105	OD1	3.618
6PYD	A_ARG_97	NH2	A_ASP_105	OD2	2.545
6PYD	A_LYS_147	NZ	A_ASP_148	OD1	3.105
6PYD	A_LYS_147	NZ	A_ASP_148	OD2	3.217
6PYD	A_LYS_213	NZ	B_GLU_127	OE1	3.596
6PYD	B_ARG_24	NH2	B_ASP_74	OD2	3.946
6PYD	B_ARG_65	NH1	B_GLU_83	OE2	3.749
6PYD	B_ARG_65	NH2	B_GLU_83	OE1	3.670
6PYD	B_ARG_65	NH2	B_GLU_85	OE1	3.121
6PYD	B_ARG_65	NH2	B_ASP_86	OD1	2.790
6PYD	B_ARG_65	NH2	B_ASP_86	OD2	3.597
6PYD	B_LYS_107	NZ	B_GLU_169	OE1	2.353
6PYD	B_LYS_192	NZ	B_ASP_189	OD1	3.073

Table 905: 6PYD-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6PZW	A_HIS_98	NE2	B_GLU_214	OE2	3.848
6PZW	A_ARG_118	NH2	A_GLU_425	OE1	3.722
6PZW	A_ARG_118	NH2	A_GLU_425	OE2	3.231
6PZW	A_ARG_130	NH1	A_GLU_128	OE2	2.902
6PZW	A_ARG_141	NH1	A_GLU_110	OE2	3.585
6PZW	A_ARG_156	NH2	A_GLU_119	OE2	2.799
6PZW	A_ARG_172	NH2	A_GLU_174	OE1	3.990
6PZW	A_ARG_172	NH2	A_GLU_174	OE2	3.068
6PZW	A_ARG_189	NH2	A_ASP_125	OD1	2.667
6PZW	A_ARG_224	NH2	A_GLU_276	OE2	3.019
6PZW	A_ARG_253	NH1	K_ASP_53	OD2	2.854
6PZW	A_ARG_253	NH2	A_ASP_251	OD1	3.916
6PZW	A_ARG_253	NH2	A_ASP_251	OD2	3.037
6PZW	A_ARG_253	NH2	K_ASP_53	OD2	2.999
6PZW	A_LYS_264	NZ	A_GLU_266	OE2	3.655
6PZW	A_LYS_273	NZ	A_ASP_339	OD1	2.481
6PZW	A_HIS_274	NE2	A_GLU_276	OE2	2.952
6PZW	A_ARG_292	NH2	A_GLU_276	OE1	2.826
6PZW	A_ARG_292	NH2	A_GLU_277	OE1	3.803
6PZW	A_ARG_292	NH2	A_GLU_277	OE2	3.606
6PZW	A_ARG_300	NH2	A_ASP_324	OD1	3.849
6PZW	A_HIS_312	ND1	A_GLU_266	OE1	2.834
6PZW	A_ARG_364	NH1	A_ASP_330	OD1	3.531
6PZW	A_ARG_364	NH1	A_ASP_330	OD2	3.075
6PZW	A_ARG_364	NH2	A_ASP_330	OD2	3.882
6PZW	A_ARG_364	NH2	A_GLU_375	OE2	3.232
6PZW	A_ARG_387	NH1	A_ASP_386	OD1	3.540
6PZW	A_ARG_387	NH1	A_ASP_386	OD2	2.586
6PZW	A_ARG_419	NH1	B_GLU_214	OE2	3.897
6PZW	A_ARG_428	NH1	A_ASP_460	OD2	2.906
6PZW	A_ARG_428	NH2	A_GLU_433	OE1	3.580
6PZW	A_ARG_428	NH2	A_GLU_433	OE2	3.020
6PZW	A_LYS_435	NZ	A_GLU_465	OE2	3.897
6PZW	I_ARG_61	NH1	I_ASP_82	OD1	3.701
6PZW	I_ARG_61	NH1	I_ASP_82	OD2	2.929
6PZW	I_ARG_61	NH2	I_ASP_82	OD1	2.966
6PZW	I_ARG_61	NH2	I_ASP_82	OD2	3.633
6PZW	I_LYS_103	NZ	I_ASP_85	OD1	2.829
6PZW	I_LYS_103	NZ	I_ASP_85	OD2	3.336
6PZW	K_HIS_35	NE2	K_ASP_95	OD2	2.981
6PZW	K_ARG_38	NH1	K_ASP_86	OD1	2.818
6PZW	K_ARG_38	NH2	K_GLU_46	OE1	3.500
6PZW	K_ARG_38	NH2	K_GLU_46	OE2	3.095
6PZW	K_ARG_38	NH2	K_ASP_86	OD1	3.867
6PZW	K_ARG_66	NH1	K_ASP_86	OD1	3.642
6PZW	K_ARG_66	NH1	K_ASP_86	OD2	2.868
6PZW	K_ARG_66	NH2	K_ASP_86	OD1	3.050
6PZW	K_ARG_66	NH2	K_ASP_86	OD2	3.680
6PZW	K_LYS_75	NZ	K_ASP_72	OD2	2.805
6PZW	K_LYS_94	NZ	K_ASP_101	OD2	2.905
6PZW	K_LYS_96	NZ	K_ASP_101	OD1	2.573
6PZW	K_LYS_96	NZ	K_ASP_101	OD2	3.869
6PZW	K_ARG_97	NH2	I_ASP_50	OD1	2.825
6PZW	K_ARG_97	NH2	I_ASP_50	OD2	3.390
6PZW	D_HIS_98	NE2	A_GLU_214	OE2	3.848
6PZW	D_ARG_118	NH2	D_GLU_425	OE1	3.722
6PZW	D_ARG_118	NH2	D_GLU_425	OE2	3.231

6PZW	D_ARG_130	NH1	D_GLU_128	OE2	2.902
6PZW	D_ARG_141	NH1	D_GLU_110	OE2	3.585
6PZW	D_ARG_156	NH2	D_GLU_119	OE2	2.799
6PZW	D_ARG_172	NH2	D_GLU_174	OE1	3.990
6PZW	D_ARG_172	NH2	D_GLU_174	OE2	3.068
6PZW	D_ARG_189	NH2	D_ASP_125	OD1	2.667
6PZW	D_ARG_224	NH2	D_GLU_276	OE2	3.019
6PZW	D_ARG_253	NH1	F_ASP_53	OD2	2.854
6PZW	D_ARG_253	NH2	D_ASP_251	OD1	3.916
6PZW	D_ARG_253	NH2	D_ASP_251	OD2	3.037
6PZW	D_ARG_253	NH2	F_ASP_53	OD2	2.999
6PZW	D_LYS_264	NZ	D_GLU_266	OE2	3.655
6PZW	D_LYS_273	NZ	D_ASP_339	OD1	2.481
6PZW	D_HIS_274	NE2	D_GLU_276	OE2	2.952
6PZW	D_ARG_292	NH2	D_GLU_276	OE1	2.826
6PZW	D_ARG_292	NH2	D_GLU_277	OE1	3.803
6PZW	D_ARG_292	NH2	D_GLU_277	OE2	3.606
6PZW	D_ARG_300	NH2	D_ASP_324	OD1	3.849
6PZW	D_HIS_312	ND1	D_GLU_266	OE1	2.834
6PZW	D_ARG_364	NH1	D_ASP_330	OD1	3.531
6PZW	D_ARG_364	NH1	D_ASP_330	OD2	3.075
6PZW	D_ARG_364	NH2	D_ASP_330	OD2	3.882
6PZW	D_ARG_364	NH2	D_GLU_375	OE2	3.232
6PZW	D_ARG_387	NH1	D_ASP_386	OD1	3.540
6PZW	D_ARG_387	NH1	D_ASP_386	OD2	2.586
6PZW	D_ARG_419	NH1	A_GLU_214	OE2	3.897
6PZW	D_ARG_428	NH1	D_ASP_460	OD2	2.906
6PZW	D_ARG_428	NH2	D_GLU_433	OE1	3.580
6PZW	D_ARG_428	NH2	D_GLU_433	OE2	3.020
6PZW	D_LYS_435	NZ	D_GLU_465	OE2	3.897
6PZW	E_ARG_61	NH1	E_ASP_82	OD1	3.701
6PZW	E_ARG_61	NH1	E_ASP_82	OD2	2.929
6PZW	E_ARG_61	NH2	E_ASP_82	OD1	2.966
6PZW	E_ARG_61	NH2	E_ASP_82	OD2	3.633
6PZW	E_LYS_103	NZ	E_ASP_85	OD1	2.829
6PZW	E_LYS_103	NZ	E_ASP_85	OD2	3.336
6PZW	F_HIS_35	NE2	F_ASP_95	OD2	2.981
6PZW	F_ARG_38	NH1	F_ASP_86	OD1	2.818
6PZW	F_ARG_38	NH2	F_GLU_46	OE1	3.500
6PZW	F_ARG_38	NH2	F_GLU_46	OE2	3.095
6PZW	F_ARG_38	NH2	F_ASP_86	OD1	3.867
6PZW	F_ARG_66	NH1	F_ASP_86	OD1	3.642
6PZW	F_ARG_66	NH1	F_ASP_86	OD2	2.868
6PZW	F_ARG_66	NH2	F_ASP_86	OD1	3.050
6PZW	F_ARG_66	NH2	F_ASP_86	OD2	3.680
6PZW	F_LYS_75	NZ	F_ASP_72	OD2	2.805
6PZW	F_LYS_94	NZ	F_ASP_101	OD2	2.905
6PZW	F_LYS_96	NZ	F_ASP_101	OD1	2.573
6PZW	F_LYS_96	NZ	F_ASP_101	OD2	3.869
6PZW	F_ARG_97	NH2	E_ASP_50	OD1	2.825
6PZW	F_ARG_97	NH2	E_ASP_50	OD2	3.390
6PZW	G_ARG_61	NH1	G_ASP_82	OD1	3.701
6PZW	G_ARG_61	NH1	G_ASP_82	OD2	2.929
6PZW	G_ARG_61	NH2	G_ASP_82	OD1	2.966
6PZW	G_ARG_61	NH2	G_ASP_82	OD2	3.633
6PZW	G_LYS_103	NZ	G_ASP_85	OD1	2.829
6PZW	G_LYS_103	NZ	G_ASP_85	OD2	3.336
6PZW	J_HIS_35	NE2	J_ASP_95	OD2	2.981

6PZW	J_ARG_38	NH1	J_ASP_86	OD1	2.818
6PZW	J_ARG_38	NH2	J_GLU_46	OE1	3.500
6PZW	J_ARG_38	NH2	J_GLU_46	OE2	3.095
6PZW	J_ARG_38	NH2	J_ASP_86	OD1	3.867
6PZW	J_ARG_66	NH1	J_ASP_86	OD1	3.642
6PZW	J_ARG_66	NH1	J_ASP_86	OD2	2.868
6PZW	J_ARG_66	NH2	J_ASP_86	OD1	3.050
6PZW	J_ARG_66	NH2	J_ASP_86	OD2	3.680
6PZW	J_LYS_75	NZ	J_ASP_72	OD2	2.805
6PZW	J_LYS_94	NZ	J_ASP_101	OD2	2.905
6PZW	J_LYS_96	NZ	J_ASP_101	OD1	2.573
6PZW	J_LYS_96	NZ	J_ASP_101	OD2	3.869
6PZW	J_ARG_97	NH2	G_ASP_50	OD1	2.825
6PZW	J_ARG_97	NH2	G_ASP_50	OD2	3.390
6PZW	C_HIS_98	NE2	D_GLU_214	OE2	3.848
6PZW	C_ARG_118	NH2	C_GLU_425	OE1	3.722
6PZW	C_ARG_118	NH2	C_GLU_425	OE2	3.231
6PZW	C_ARG_130	NH1	C_GLU_128	OE2	2.902
6PZW	C_ARG_141	NH1	C_GLU_110	OE2	3.585
6PZW	C_ARG_156	NH2	C_GLU_119	OE2	2.799
6PZW	C_ARG_172	NH2	C_GLU_174	OE1	3.990
6PZW	C_ARG_172	NH2	C_GLU_174	OE2	3.068
6PZW	C_ARG_189	NH2	C_ASP_125	OD1	2.667
6PZW	C_ARG_224	NH2	C_GLU_276	OE2	3.019
6PZW	C_ARG_253	NH1	J_ASP_53	OD2	2.854
6PZW	C_ARG_253	NH2	J_ASP_53	OD2	2.999
6PZW	C_ARG_253	NH2	C_ASP_251	OD1	3.916
6PZW	C_ARG_253	NH2	C_ASP_251	OD2	3.037
6PZW	C_LYS_264	NZ	C_GLU_266	OE2	3.655
6PZW	C_LYS_273	NZ	C_ASP_339	OD1	2.481
6PZW	C_HIS_274	NE2	C_GLU_276	OE2	2.952
6PZW	C_ARG_292	NH2	C_GLU_276	OE1	2.826
6PZW	C_ARG_292	NH2	C_GLU_277	OE1	3.803
6PZW	C_ARG_292	NH2	C_GLU_277	OE2	3.606
6PZW	C_ARG_300	NH2	C_ASP_324	OD1	3.849
6PZW	C_HIS_312	ND1	C_GLU_266	OE1	2.834
6PZW	C_ARG_364	NH1	C_ASP_330	OD1	3.531
6PZW	C_ARG_364	NH1	C_ASP_330	OD2	3.075
6PZW	C_ARG_364	NH2	C_ASP_330	OD2	3.882
6PZW	C_ARG_364	NH2	C_GLU_375	OE2	3.232
6PZW	C_ARG_387	NH1	C_ASP_386	OD1	3.540
6PZW	C_ARG_387	NH1	C_ASP_386	OD2	2.586
6PZW	C_ARG_419	NH1	D_GLU_214	OE2	3.897
6PZW	C_ARG_428	NH1	C_ASP_460	OD2	2.906
6PZW	C_ARG_428	NH2	C_GLU_433	OE1	3.580
6PZW	C_ARG_428	NH2	C_GLU_433	OE2	3.020
6PZW	C_LYS_435	NZ	C_GLU_465	OE2	3.897
6PZW	B_HIS_98	NE2	C_GLU_214	OE2	3.848
6PZW	B_ARG_118	NH2	B_GLU_425	OE1	3.722
6PZW	B_ARG_118	NH2	B_GLU_425	OE2	3.231
6PZW	B_ARG_130	NH1	B_GLU_128	OE2	2.902
6PZW	B_ARG_141	NH1	B_GLU_110	OE2	3.585
6PZW	B_ARG_156	NH2	B_GLU_119	OE2	2.799
6PZW	B_ARG_172	NH2	B_GLU_174	OE1	3.990
6PZW	B_ARG_172	NH2	B_GLU_174	OE2	3.068
6PZW	B_ARG_189	NH2	B_ASP_125	OD1	2.667
6PZW	B_ARG_224	NH2	B_GLU_276	OE2	3.019
6PZW	B_ARG_253	NH1	H_ASP_53	OD2	2.854

6PZW	B_ARG_253	NH2	B_ASP_251	OD1	3.916
6PZW	B_ARG_253	NH2	B_ASP_251	OD2	3.037
6PZW	B_ARG_253	NH2	H_ASP_53	OD2	2.999
6PZW	B_LYS_264	NZ	B_GLU_266	OE2	3.655
6PZW	B_LYS_273	NZ	B_ASP_339	OD1	2.481
6PZW	B_HIS_274	NE2	B_GLU_276	OE2	2.952
6PZW	B_ARG_292	NH2	B_GLU_276	OE1	2.826
6PZW	B_ARG_292	NH2	B_GLU_277	OE1	3.803
6PZW	B_ARG_292	NH2	B_GLU_277	OE2	3.606
6PZW	B_ARG_300	NH2	B_ASP_324	OD1	3.849
6PZW	B_HIS_312	ND1	B_GLU_266	OE1	2.834
6PZW	B_ARG_364	NH1	B_ASP_330	OD1	3.531
6PZW	B_ARG_364	NH1	B_ASP_330	OD2	3.075
6PZW	B_ARG_364	NH2	B_ASP_330	OD2	3.882
6PZW	B_ARG_364	NH2	B_GLU_375	OE2	3.232
6PZW	B_ARG_387	NH1	B_ASP_386	OD1	3.540
6PZW	B_ARG_387	NH1	B_ASP_386	OD2	2.586
6PZW	B_ARG_419	NH1	C_GLU_214	OE2	3.897
6PZW	B_ARG_428	NH1	B_ASP_460	OD2	2.906
6PZW	B_ARG_428	NH2	B_GLU_433	OE1	3.580
6PZW	B_ARG_428	NH2	B_GLU_433	OE2	3.020
6PZW	B_LYS_435	NZ	B_GLU_465	OE2	3.897
6PZW	L_ARG_61	NH1	L_ASP_82	OD1	3.701
6PZW	L_ARG_61	NH1	L_ASP_82	OD2	2.929
6PZW	L_ARG_61	NH2	L_ASP_82	OD1	2.966
6PZW	L_ARG_61	NH2	L_ASP_82	OD2	3.633
6PZW	L_LYS_103	NZ	L_ASP_85	OD1	2.829
6PZW	L_LYS_103	NZ	L_ASP_85	OD2	3.336
6PZW	H_HIS_35	NE2	H_ASP_95	OD2	2.981
6PZW	H_ARG_38	NH1	H_ASP_86	OD1	2.818
6PZW	H_ARG_38	NH2	H_GLU_46	OE1	3.500
6PZW	H_ARG_38	NH2	H_GLU_46	OE2	3.095
6PZW	H_ARG_38	NH2	H_ASP_86	OD1	3.867
6PZW	H_ARG_66	NH1	H_ASP_86	OD1	3.642
6PZW	H_ARG_66	NH1	H_ASP_86	OD2	2.868
6PZW	H_ARG_66	NH2	H_ASP_86	OD1	3.050
6PZW	H_ARG_66	NH2	H_ASP_86	OD2	3.680
6PZW	H_LYS_75	NZ	H_ASP_72	OD2	2.805
6PZW	H_LYS_94	NZ	H_ASP_101	OD2	2.905
6PZW	H_LYS_96	NZ	H_ASP_101	OD1	2.573
6PZW	H_LYS_96	NZ	H_ASP_101	OD2	3.869
6PZW	H_ARG_97	NH2	L_ASP_50	OD1	2.825
6PZW	H_ARG_97	NH2	L_ASP_50	OD2	3.390

Table 906: 6PZW-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6RPS	A_HIS_34	ND1	A_ASP_32	OD2	2.928
6RPS	A_HIS_34	NE2	A_ASP_36	OD1	3.392
6RPS	A_HIS_34	NE2	B_ASP_102	OD2	3.097
6RPS	A_HIS_64	NE2	H_ASP_54	OD2	2.837
6RPS	A_HIS_96	ND1	A_GLU_106	OE1	3.812
6RPS	A_HIS_96	ND1	A_GLU_106	OE2	3.696
6RPS	A_HIS_96	NE2	A_GLU_106	OE1	3.203
6RPS	A_HIS_103	ND1	A_ASP_102	OD1	3.719
6RPS	A_HIS_107	ND1	A_GLU_117	OE1	3.830
6RPS	A_HIS_107	ND1	A_GLU_117	OE2	2.892
6RPS	A_HIS_119	ND1	A_GLU_106	OE1	3.943
6RPS	A_HIS_119	NE2	A_GLU_117	OE2	2.681
6RPS	A_LYS_170	NZ	H_ASP_54	OD1	3.636
6RPS	A_LYS_170	NZ	H_ASP_54	OD2	2.590
6RPS	A_LYS_170	NZ	H_ASP_56	OD2	2.821
6RPS	A_ARG_213	NH1	A_GLU_190	OE1	3.317
6RPS	A_ARG_213	NH1	A_GLU_190	OE2	3.527
6RPS	A_HIS_234	ND1	H_ASP_56	OD2	3.904
6RPS	A_LYS_250	NZ	B_GLU_13	OE2	2.734
6RPS	B_HIS_34	ND1	B_ASP_32	OD2	2.934
6RPS	B_HIS_34	NE2	B_ASP_36	OD1	3.758
6RPS	B_HIS_34	NE2	B_ASP_36	OD2	3.233
6RPS	B_HIS_64	NE2	N_ASP_54	OD2	2.859
6RPS	B_HIS_96	ND1	B_GLU_106	OE1	3.814
6RPS	B_HIS_96	ND1	B_GLU_106	OE2	3.680
6RPS	B_HIS_96	NE2	B_GLU_106	OE1	3.214
6RPS	B_HIS_103	ND1	A_ASP_36	OD1	3.129
6RPS	B_HIS_103	ND1	A_ASP_36	OD2	3.954
6RPS	B_HIS_103	ND1	B_ASP_102	OD1	3.019
6RPS	B_HIS_107	ND1	B_GLU_117	OE1	3.839
6RPS	B_HIS_107	ND1	B_GLU_117	OE2	2.888
6RPS	B_HIS_119	ND1	B_GLU_106	OE1	3.928
6RPS	B_HIS_119	NE2	B_GLU_117	OE2	2.683
6RPS	B_LYS_170	NZ	N_ASP_54	OD1	3.719
6RPS	B_LYS_170	NZ	N_ASP_54	OD2	2.644
6RPS	B_LYS_170	NZ	N_ASP_56	OD2	2.839
6RPS	B_ARG_213	NH1	B_GLU_190	OE1	3.106
6RPS	B_ARG_213	NH1	B_GLU_190	OE2	3.685
6RPS	B_HIS_234	ND1	N_ASP_56	OD2	3.922
6RPS	B_LYS_250	NZ	A_GLU_13	OE2	2.991
6RPS	M_ARG_24	NH1	M_ASP_70	OD2	3.891
6RPS	M_ARG_61	NH1	M_GLU_79	OE1	3.422
6RPS	M_ARG_61	NH1	M_GLU_79	OE2	3.489
6RPS	M_ARG_61	NH2	M_GLU_79	OE1	3.623
6RPS	M_ARG_61	NH2	M_GLU_81	OE1	3.600
6RPS	M_ARG_61	NH2	M_ASP_82	OD1	2.623
6RPS	M_ARG_61	NH2	M_ASP_82	OD2	3.076
6RPS	M_LYS_149	NZ	M_GLU_195	OE1	3.183
6RPS	M_LYS_149	NZ	M_GLU_195	OE2	3.364
6RPS	N_ARG_38	NH1	N_GLU_86	OE2	2.950
6RPS	N_ARG_38	NH2	N_GLU_46	OE1	3.142
6RPS	N_ARG_38	NH2	N_GLU_46	OE2	3.953
6RPS	N_ARG_38	NH2	N_GLU_86	OE2	3.241
6RPS	N_ARG_50	NH2	N_ASP_95	OD2	3.876
6RPS	N_ARG_66	NH1	N_GLU_86	OE2	3.240
6RPS	N_ARG_66	NH2	N_GLU_86	OE1	2.816
6RPS	N_ARG_66	NH2	N_GLU_86	OE2	2.704

6RPS	N_ARG_94	NH2	N_ASP_101	OD2	3.208
6RPS	N_LYS_143	NZ	N_ASP_144	OD1	3.314
6RPS	N_LYS_143	NZ	N_ASP_144	OD2	3.375
6RPS	N_LYS_210	NZ	N_GLU_212	OE1	3.241
6RPS	N_LYS_214	NZ	M_ASP_122	OD1	3.095
6RPS	N_LYS_214	NZ	M_ASP_122	OD2	3.107
6RPS	L_ARG_24	NH1	L_ASP_70	OD2	3.896
6RPS	L_LYS_39	NZ	L_GLU_81	OE2	3.206
6RPS	L_ARG_45	NH2	L_GLU_81	OE2	3.948
6RPS	L_ARG_61	NH1	L_GLU_79	OE1	3.428
6RPS	L_ARG_61	NH1	L_GLU_79	OE2	3.496
6RPS	L_ARG_61	NH2	L_GLU_79	OE1	3.620
6RPS	L_ARG_61	NH2	L_ASP_82	OD1	2.624
6RPS	L_ARG_61	NH2	L_ASP_82	OD2	3.082
6RPS	L_LYS_149	NZ	L_GLU_195	OE1	3.146
6RPS	L_LYS_149	NZ	L_GLU_195	OE2	3.433
6RPS	H_ARG_38	NH1	H_GLU_86	OE2	2.972
6RPS	H_ARG_38	NH2	H_GLU_46	OE1	3.141
6RPS	H_ARG_38	NH2	H_GLU_46	OE2	3.931
6RPS	H_ARG_38	NH2	H_GLU_86	OE2	3.242
6RPS	H_ARG_50	NH2	H_ASP_95	OD2	3.877
6RPS	H_ARG_66	NH1	H_GLU_86	OE2	3.250
6RPS	H_ARG_66	NH2	H_GLU_86	OE1	2.806
6RPS	H_ARG_66	NH2	H_GLU_86	OE2	2.709
6RPS	H_ARG_94	NH2	H_ASP_101	OD2	3.183
6RPS	H_LYS_143	NZ	H_ASP_144	OD1	3.311
6RPS	H_LYS_143	NZ	H_ASP_144	OD2	3.365
6RPS	H_LYS_209	NZ	L_GLU_123	OE1	2.780
6RPS	H_LYS_209	NZ	L_GLU_123	OE2	3.710
6RPS	H_LYS_210	NZ	H_GLU_212	OE1	3.232

Table 907: 6RPS-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6S3T	A_HIS_48	ND1	A_ASP_79	OD1	3.030
6S3T	A_LYS_49	NZ	C_GLU_158	OE1	3.663
6S3T	A_ARG_66	NH1	A_ASP_140	OD2	3.290
6S3T	A_ARG_66	NH2	A_ASP_140	OD1	3.561
6S3T	A_ARG_66	NH2	A_ASP_343	OD1	2.921
6S3T	A_ARG_66	NH2	A_ASP_343	OD2	3.772
6S3T	A_LYS_90	NZ	A_ASP_63	OD1	3.963
6S3T	A_LYS_90	NZ	A_ASP_63	OD2	2.710
6S3T	A_LYS_110	NZ	A_GLU_82	OE1	3.367
6S3T	A_LYS_110	NZ	A_GLU_82	OE2	3.373
6S3T	A_ARG_141	NH1	A_ASP_210	OD1	3.859
6S3T	A_ARG_141	NH1	A_ASP_210	OD2	3.679
6S3T	A_ARG_141	NH2	A_ASP_61	OD1	2.655
6S3T	A_ARG_141	NH2	A_ASP_61	OD2	3.839
6S3T	A_LYS_148	NZ	A_ASP_131	OD1	3.035
6S3T	A_LYS_222	NZ	A_GLU_158	OE2	3.425
6S3T	A_LYS_222	NZ	A_GLU_162	OE2	3.965
6S3T	A_LYS_268	NZ	A_GLU_308	OE1	3.868
6S3T	A_LYS_306	NZ	A_ASP_334	OD1	3.070
6S3T	A_LYS_306	NZ	A_ASP_334	OD2	3.336
6S3T	A_LYS_327	NZ	A_ASP_324	OD1	3.861
6S3T	A_LYS_341	NZ	A_ASP_140	OD1	3.192
6S3T	A_ARG_355	NH1	A_GLU_82	OE1	3.960
6S3T	A_ARG_355	NH1	A_GLU_82	OE2	3.091
6S3T	A_ARG_366	NH1	A_ASP_150	OD2	3.723
6S3T	A_ARG_366	NH2	A_ASP_150	OD2	3.506
6S3T	A_LYS_383	NZ	A_ASP_156	OD2	3.389
6S3T	B_HIS_48	ND1	B_ASP_79	OD1	3.029
6S3T	B_LYS_49	NZ	L_GLU_158	OE1	3.761
6S3T	B_ARG_66	NH1	B_ASP_140	OD2	3.289
6S3T	B_ARG_66	NH2	B_ASP_140	OD1	3.563
6S3T	B_ARG_66	NH2	B_ASP_343	OD1	2.924
6S3T	B_ARG_66	NH2	B_ASP_343	OD2	3.774
6S3T	B_LYS_90	NZ	B_ASP_63	OD1	3.964
6S3T	B_LYS_90	NZ	B_ASP_63	OD2	2.710
6S3T	B_LYS_110	NZ	B_GLU_82	OE1	3.367
6S3T	B_LYS_110	NZ	B_GLU_82	OE2	3.374
6S3T	B_ARG_141	NH1	B_ASP_210	OD1	3.858
6S3T	B_ARG_141	NH1	B_ASP_210	OD2	3.682
6S3T	B_ARG_141	NH2	B_ASP_61	OD1	2.654
6S3T	B_ARG_141	NH2	B_ASP_61	OD2	3.837
6S3T	B_LYS_148	NZ	B_ASP_131	OD1	3.032
6S3T	B_LYS_175	NZ	B_ASP_177	OD2	3.891
6S3T	B_LYS_222	NZ	B_GLU_158	OE2	3.419
6S3T	B_LYS_222	NZ	B_GLU_162	OE2	3.964
6S3T	B_LYS_282	NZ	B_GLU_241	OE2	3.757
6S3T	B_LYS_306	NZ	B_ASP_334	OD1	3.070
6S3T	B_LYS_306	NZ	B_ASP_334	OD2	3.338
6S3T	B_LYS_327	NZ	B_ASP_324	OD1	3.858
6S3T	B_LYS_341	NZ	B_ASP_140	OD1	3.192
6S3T	B_ARG_355	NH1	B_GLU_352	OE1	2.881
6S3T	B_ARG_366	NH2	B_ASP_150	OD2	3.496
6S3T	B_LYS_383	NZ	B_ASP_156	OD2	3.383
6S3T	C_ARG_24	NH2	C_ASP_74	OD1	3.093
6S3T	C_ARG_24	NH2	C_ASP_74	OD2	3.742
6S3T	C_ARG_65	NH1	C_ASP_86	OD1	3.788
6S3T	C_ARG_65	NH1	C_ASP_86	OD2	2.683

6S3T	C_ARG_65	NH2	C_GLU_83	OE1	3.619
6S3T	C_ARG_65	NH2	C_ASP_86	OD1	3.107
6S3T	C_ARG_65	NH2	C_ASP_86	OD2	3.458
6S3T	C_LYS_151	NZ	C_GLU_158	OE2	3.956
6S3T	C_LYS_153	NZ	C_GLU_199	OE2	2.738
6S3T	D_ARG_35	NH1	S_ASP_332	OD1	3.467
6S3T	D_ARG_35	NH1	S_ASP_332	OD2	2.946
6S3T	D_ARG_35	NH2	S_ASP_332	OD2	3.071
6S3T	D_ARG_35	NH2	S_ASP_334	OD1	3.408
6S3T	D_ARG_40	NH1	D_GLU_48	OE1	3.019
6S3T	D_ARG_40	NH2	D_ASP_91	OD2	3.639
6S3T	D_ARG_68	NH1	D_ASP_91	OD1	3.381
6S3T	D_ARG_68	NH1	D_ASP_91	OD2	3.003
6S3T	D_ARG_68	NH2	D_ASP_91	OD1	3.560
6S3T	D_ARG_73	NH2	D_ASP_57	OD2	3.930
6S3T	D_HIS_171	NE2	C_ASP_171	OD2	3.832
6S3T	D_LYS_215	NZ	C_GLU_127	OE1	2.814
6S3T	D_LYS_215	NZ	C_GLU_127	OE2	3.990
6S3T	D_LYS_216	NZ	D_GLU_218	OE2	3.949
6S3T	I_ARG_24	NH2	I_ASP_74	OD1	3.090
6S3T	I_ARG_24	NH2	I_ASP_74	OD2	3.744
6S3T	I_ARG_65	NH1	I_GLU_83	OE1	3.576
6S3T	I_ARG_65	NH1	I_ASP_86	OD1	3.791
6S3T	I_ARG_65	NH1	I_ASP_86	OD2	2.684
6S3T	I_ARG_65	NH2	I_ASP_86	OD1	3.110
6S3T	I_ARG_65	NH2	I_ASP_86	OD2	3.459
6S3T	I_LYS_107	NZ	I_GLU_109	OE2	3.962
6S3T	I_LYS_151	NZ	I_GLU_158	OE1	3.422
6S3T	I_LYS_153	NZ	I_GLU_199	OE2	2.741
6S3T	E_ARG_35	NH1	T_ASP_332	OD1	3.561
6S3T	E_ARG_35	NH1	T_ASP_332	OD2	3.035
6S3T	E_ARG_35	NH2	T_ASP_332	OD2	3.163
6S3T	E_ARG_35	NH2	T_ASP_334	OD1	3.432
6S3T	E_ARG_40	NH1	E_ASP_91	OD1	3.668
6S3T	E_ARG_40	NH1	E_ASP_91	OD2	3.638
6S3T	E_ARG_40	NH2	E_GLU_48	OE1	2.851
6S3T	E_ARG_68	NH1	E_ASP_91	OD1	3.381
6S3T	E_ARG_68	NH1	E_ASP_91	OD2	3.005
6S3T	E_ARG_68	NH2	E_ASP_91	OD1	3.559
6S3T	E_ARG_73	NH2	E_ASP_57	OD2	3.938
6S3T	E_HIS_171	NE2	I_ASP_171	OD2	3.931
6S3T	E_LYS_215	NZ	I_GLU_127	OE1	3.013
6S3T	E_LYS_216	NZ	E_GLU_218	OE2	3.946
6S3T	M_ARG_24	NH2	M_ASP_74	OD1	3.084
6S3T	M_ARG_24	NH2	M_ASP_74	OD2	3.751
6S3T	M_ARG_65	NH1	M_GLU_83	OE1	3.576
6S3T	M_ARG_65	NH1	M_ASP_86	OD1	3.781
6S3T	M_ARG_65	NH1	M_ASP_86	OD2	2.680
6S3T	M_ARG_65	NH2	M_ASP_86	OD1	3.107
6S3T	M_ARG_65	NH2	M_ASP_86	OD2	3.455
6S3T	M_LYS_151	NZ	M_GLU_158	OE2	3.920
6S3T	M_LYS_153	NZ	M_GLU_199	OE1	3.748
6S3T	M_LYS_153	NZ	M_GLU_199	OE2	2.775
6S3T	N_ARG_35	NH1	A_ASP_332	OD1	3.796
6S3T	N_ARG_35	NH1	A_ASP_332	OD2	3.195
6S3T	N_ARG_35	NH2	A_ASP_332	OD1	3.883
6S3T	N_ARG_35	NH2	A_ASP_332	OD2	2.517
6S3T	N_ARG_35	NH2	A_ASP_334	OD2	3.989

6S3T	N_ARG_40	NH1	N_GLU_48	OE1	3.017
6S3T	N_ARG_40	NH2	N_ASP_91	OD2	3.633
6S3T	N_ARG_68	NH1	N_ASP_91	OD1	3.379
6S3T	N_ARG_68	NH1	N_ASP_91	OD2	3.002
6S3T	N_ARG_68	NH2	N_ASP_91	OD1	3.568
6S3T	N_ARG_73	NH2	S_GLU_44	OE2	2.482
6S3T	N_HIS_171	NE2	M_ASP_171	OD2	3.181
6S3T	N_LYS_215	NZ	M_GLU_127	OE1	2.964
6S3T	N_LYS_215	NZ	M_GLU_127	OE2	3.944
6S3T	N_LYS_216	NZ	N_GLU_218	OE2	3.948
6S3T	Q_ARG_24	NH2	Q_ASP_74	OD1	3.083
6S3T	Q_ARG_24	NH2	Q_ASP_74	OD2	3.750
6S3T	Q_ARG_65	NH1	Q_GLU_83	OE1	3.574
6S3T	Q_ARG_65	NH1	Q_ASP_86	OD1	3.785
6S3T	Q_ARG_65	NH1	Q_ASP_86	OD2	2.681
6S3T	Q_ARG_65	NH2	Q_ASP_86	OD1	3.108
6S3T	Q_ARG_65	NH2	Q_ASP_86	OD2	3.458
6S3T	Q_LYS_151	NZ	Q_GLU_199	OE1	2.666
6S3T	Q_LYS_151	NZ	Q_GLU_199	OE2	3.849
6S3T	Q_LYS_153	NZ	Q_GLU_199	OE2	2.742
6S3T	R_ARG_35	NH1	B_ASP_332	OD1	3.511
6S3T	R_ARG_35	NH1	B_ASP_332	OD2	2.943
6S3T	R_ARG_35	NH2	B_ASP_332	OD2	2.873
6S3T	R_ARG_35	NH2	B_ASP_334	OD1	3.424
6S3T	R_ARG_40	NH1	R_GLU_48	OE1	3.017
6S3T	R_ARG_40	NH2	R_ASP_91	OD2	3.634
6S3T	R_ARG_68	NH1	R_ASP_91	OD1	3.379
6S3T	R_ARG_68	NH1	R_ASP_91	OD2	3.002
6S3T	R_ARG_68	NH2	R_ASP_91	OD1	3.566
6S3T	R_ARG_73	NH2	T_GLU_44	OE2	2.709
6S3T	R_HIS_171	NE2	Q_ASP_171	OD2	3.265
6S3T	R_LYS_215	NZ	Q_GLU_127	OE1	2.948
6S3T	R_LYS_215	NZ	Q_GLU_127	OE2	3.831
6S3T	R_LYS_216	NZ	R_GLU_218	OE2	3.945
6S3T	S_HIS_48	ND1	S_ASP_79	OD1	3.027
6S3T	S_ARG_66	NH1	S_ASP_140	OD2	3.289
6S3T	S_ARG_66	NH2	S_ASP_140	OD1	3.557
6S3T	S_ARG_66	NH2	S_ASP_343	OD1	2.918
6S3T	S_ARG_66	NH2	S_ASP_343	OD2	3.764
6S3T	S_LYS_90	NZ	S_ASP_63	OD1	3.967
6S3T	S_LYS_90	NZ	S_ASP_63	OD2	2.710
6S3T	S_LYS_110	NZ	S_GLU_82	OE2	3.372
6S3T	S_ARG_141	NH1	S_ASP_210	OD1	3.860
6S3T	S_ARG_141	NH1	S_ASP_210	OD2	3.676
6S3T	S_ARG_141	NH2	S_ASP_61	OD1	2.655
6S3T	S_ARG_141	NH2	S_ASP_61	OD2	3.848
6S3T	S_LYS_148	NZ	S_ASP_131	OD1	3.009
6S3T	S_LYS_175	NZ	S_ASP_177	OD2	3.891
6S3T	S_LYS_306	NZ	S_ASP_334	OD1	3.069
6S3T	S_LYS_306	NZ	S_ASP_334	OD2	3.337
6S3T	S_LYS_327	NZ	S_ASP_324	OD1	3.856
6S3T	S_LYS_341	NZ	S_ASP_140	OD1	3.205
6S3T	S_LYS_383	NZ	S_ASP_156	OD2	3.396
6S3T	T_HIS_48	ND1	T_ASP_79	OD1	3.029
6S3T	T_ARG_66	NH1	T_ASP_140	OD2	3.288
6S3T	T_ARG_66	NH2	T_ASP_140	OD1	3.559
6S3T	T_ARG_66	NH2	T_ASP_343	OD1	2.920
6S3T	T_ARG_66	NH2	T_ASP_343	OD2	3.765

6S3T	T_LYS_90	NZ	T_ASP_63	OD1	3.971
6S3T	T_LYS_90	NZ	T_ASP_63	OD2	2.711
6S3T	T_LYS_110	NZ	T_GLU_82	OE1	3.369
6S3T	T_LYS_110	NZ	T_GLU_82	OE2	3.374
6S3T	T_ARG_141	NH1	T_ASP_210	OD1	3.860
6S3T	T_ARG_141	NH1	T_ASP_210	OD2	3.680
6S3T	T_ARG_141	NH2	T_ASP_61	OD1	2.654
6S3T	T_ARG_141	NH2	T_ASP_61	OD2	3.845
6S3T	T_LYS_148	NZ	T_ASP_131	OD1	3.022
6S3T	T_LYS_175	NZ	T_ASP_177	OD1	2.862
6S3T	T_LYS_306	NZ	T_ASP_334	OD1	3.070
6S3T	T_LYS_306	NZ	T_ASP_334	OD2	3.338
6S3T	T_LYS_327	NZ	T_ASP_324	OD1	3.858
6S3T	T_LYS_341	NZ	T_ASP_140	OD1	3.202
6S3T	T_ARG_355	NH1	T_GLU_82	OE1	3.957
6S3T	T_ARG_355	NH1	T_GLU_82	OE2	3.099
6S3T	T_ARG_366	NH1	T_GLU_370	OE2	3.935
6S3T	T_LYS_383	NZ	T_ASP_156	OD2	3.383

Table 908: 6S3T-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6U02	A_HIS_98	NE2	B_GLU_214	OE2	3.838
6U02	A_ARG_118	NH2	A_GLU_425	OE1	3.303
6U02	A_ARG_118	NH2	A_GLU_425	OE2	3.788
6U02	A_ARG_130	NH1	A_GLU_128	OE1	3.104
6U02	A_ARG_156	NH2	A_GLU_119	OE1	3.056
6U02	A_ARG_172	NH2	A_GLU_174	OE2	3.004
6U02	A_ARG_189	NH2	A_ASP_125	OD1	2.704
6U02	A_ARG_209	NH1	J_GLU_128	OE2	3.226
6U02	A_ARG_210	NH2	J_ASP_412	OD1	3.355
6U02	A_ARG_210	NH2	J_ASP_412	OD2	3.535
6U02	A_ARG_224	NH2	A_GLU_276	OE2	2.857
6U02	A_ARG_253	NH2	A_ASP_251	OD1	3.915
6U02	A_ARG_253	NH2	A_ASP_251	OD2	3.078
6U02	A_LYS_264	NZ	A_GLU_266	OE2	3.592
6U02	A_ARG_292	NH1	A_GLU_276	OE1	3.981
6U02	A_ARG_292	NH2	A_GLU_276	OE1	3.522
6U02	A_ARG_292	NH2	A_GLU_277	OE1	3.270
6U02	A_ARG_292	NH2	A_GLU_277	OE2	3.103
6U02	A_ARG_300	NH2	A_ASP_324	OD1	3.840
6U02	A_HIS_312	ND1	A_GLU_266	OE1	2.873
6U02	A_ARG_364	NH1	A_ASP_330	OD1	3.366
6U02	A_ARG_364	NH1	A_ASP_330	OD2	3.020
6U02	A_ARG_364	NH2	A_ASP_330	OD2	3.213
6U02	A_ARG_364	NH2	A_GLU_375	OE2	3.763
6U02	A_ARG_419	NH1	B_GLU_214	OE2	3.906
6U02	A_ARG_428	NH1	A_ASP_460	OD2	2.812
6U02	A_ARG_428	NH2	A_GLU_433	OE1	3.662
6U02	A_ARG_428	NH2	A_GLU_433	OE2	3.046
6U02	L_ARG_24	NH2	L_ASP_70	OD1	2.974
6U02	L_ARG_61	NH2	L_GLU_81	OE1	3.909
6U02	L_ARG_61	NH2	L_ASP_82	OD1	2.859
6U02	L_ARG_61	NH2	L_ASP_82	OD2	3.591
6U02	L_LYS_103	NZ	L_GLU_105	OE2	3.418
6U02	H_ARG_38	NH1	H_ASP_86	OD1	2.942
6U02	H_ARG_38	NH2	H_ASP_86	OD1	3.941
6U02	H_LYS_52	NZ	H_GLU_56	OE2	2.823
6U02	H_LYS_64	NZ	H_ASP_61	OD1	2.817
6U02	H_ARG_66	NH1	H_ASP_86	OD1	3.307
6U02	H_ARG_66	NH1	H_ASP_86	OD2	3.771
6U02	H_ARG_66	NH2	H_ASP_86	OD1	3.561
6U02	H_ARG_66	NH2	H_ASP_86	OD2	2.624
6U02	B_HIS_98	NE2	E_GLU_214	OE2	3.839
6U02	B_ARG_118	NH2	B_GLU_425	OE1	3.304
6U02	B_ARG_118	NH2	B_GLU_425	OE2	3.788
6U02	B_ARG_130	NH1	B_GLU_128	OE1	3.105
6U02	B_ARG_156	NH2	B_GLU_119	OE1	3.056
6U02	B_ARG_172	NH2	B_GLU_174	OE2	3.004
6U02	B_ARG_189	NH2	B_ASP_125	OD1	2.703
6U02	B_ARG_209	NH1	A_GLU_128	OE2	3.226
6U02	B_ARG_210	NH2	A_ASP_412	OD1	3.355
6U02	B_ARG_210	NH2	A_ASP_412	OD2	3.535
6U02	B_ARG_224	NH2	B_GLU_276	OE2	2.857
6U02	B_ARG_253	NH2	B_ASP_251	OD1	3.915
6U02	B_ARG_253	NH2	B_ASP_251	OD2	3.077
6U02	B_LYS_264	NZ	B_GLU_266	OE2	3.593
6U02	B_ARG_292	NH1	B_GLU_276	OE1	3.982
6U02	B_ARG_292	NH2	B_GLU_276	OE1	3.522

6U02	B_ARG_292	NH2	B_GLU_277	OE1	3.270
6U02	B_ARG_292	NH2	B_GLU_277	OE2	3.103
6U02	B_ARG_300	NH2	B_ASP_324	OD1	3.839
6U02	B_HIS_312	ND1	B_GLU_266	OE1	2.872
6U02	B_ARG_364	NH1	B_ASP_330	OD1	3.367
6U02	B_ARG_364	NH1	B_ASP_330	OD2	3.022
6U02	B_ARG_364	NH2	B_ASP_330	OD2	3.214
6U02	B_ARG_364	NH2	B_GLU_375	OE2	3.764
6U02	B_ARG_419	NH1	E_GLU_214	OE2	3.906
6U02	B_ARG_428	NH1	B_ASP_460	OD2	2.812
6U02	B_ARG_428	NH2	B_GLU_433	OE1	3.662
6U02	B_ARG_428	NH2	B_GLU_433	OE2	3.045
6U02	C_ARG_24	NH2	C_ASP_70	OD1	2.974
6U02	C_ARG_61	NH2	C_GLU_81	OE1	3.909
6U02	C_ARG_61	NH2	C_ASP_82	OD1	2.859
6U02	C_ARG_61	NH2	C_ASP_82	OD2	3.591
6U02	C_LYS_103	NZ	C_GLU_105	OE2	3.418
6U02	D_ARG_38	NH1	D_ASP_86	OD1	2.941
6U02	D_ARG_38	NH2	D_ASP_86	OD1	3.942
6U02	D_LYS_52	NZ	D_GLU_56	OE2	2.822
6U02	D_LYS_64	NZ	D_ASP_61	OD1	2.818
6U02	D_ARG_66	NH1	D_ASP_86	OD1	3.308
6U02	D_ARG_66	NH1	D_ASP_86	OD2	3.771
6U02	D_ARG_66	NH2	D_ASP_86	OD1	3.562
6U02	D_ARG_66	NH2	D_ASP_86	OD2	2.624
6U02	E_HIS_98	NE2	J_GLU_214	OE2	3.838
6U02	E_ARG_118	NH2	E_GLU_425	OE1	3.304
6U02	E_ARG_118	NH2	E_GLU_425	OE2	3.789
6U02	E_ARG_130	NH1	E_GLU_128	OE1	3.104
6U02	E_ARG_156	NH2	E_GLU_119	OE1	3.056
6U02	E_ARG_172	NH2	E_GLU_174	OE2	3.004
6U02	E_ARG_189	NH2	E_ASP_125	OD1	2.704
6U02	E_ARG_209	NH1	B_GLU_128	OE2	3.226
6U02	E_ARG_210	NH2	B_ASP_412	OD1	3.355
6U02	E_ARG_210	NH2	B_ASP_412	OD2	3.536
6U02	E_ARG_224	NH2	E_GLU_276	OE2	2.858
6U02	E_ARG_253	NH2	E_ASP_251	OD1	3.916
6U02	E_ARG_253	NH2	E_ASP_251	OD2	3.078
6U02	E_LYS_264	NZ	E_GLU_266	OE2	3.592
6U02	E_ARG_292	NH1	E_GLU_276	OE1	3.982
6U02	E_ARG_292	NH2	E_GLU_276	OE1	3.522
6U02	E_ARG_292	NH2	E_GLU_277	OE1	3.270
6U02	E_ARG_292	NH2	E_GLU_277	OE2	3.103
6U02	E_ARG_300	NH2	E_ASP_324	OD1	3.839
6U02	E_HIS_312	ND1	E_GLU_266	OE1	2.873
6U02	E_ARG_364	NH1	E_ASP_330	OD1	3.366
6U02	E_ARG_364	NH1	E_ASP_330	OD2	3.021
6U02	E_ARG_364	NH2	E_ASP_330	OD2	3.214
6U02	E_ARG_364	NH2	E_GLU_375	OE2	3.764
6U02	E_ARG_419	NH1	J_GLU_214	OE2	3.906
6U02	E_ARG_428	NH1	E_ASP_460	OD2	2.812
6U02	E_ARG_428	NH2	E_GLU_433	OE1	3.663
6U02	E_ARG_428	NH2	E_GLU_433	OE2	3.046
6U02	F_ARG_24	NH2	F_ASP_70	OD1	2.973
6U02	F_ARG_61	NH2	F_GLU_81	OE1	3.909
6U02	F_ARG_61	NH2	F_ASP_82	OD1	2.860
6U02	F_ARG_61	NH2	F_ASP_82	OD2	3.591
6U02	F_LYS_103	NZ	F_GLU_105	OE2	3.417

6U02	G_ARG_38	NH1	G_ASP_86	OD1	2.942
6U02	G_ARG_38	NH2	G_ASP_86	OD1	3.942
6U02	G_LYS_52	NZ	G_GLU_56	OE2	2.823
6U02	G_LYS_64	NZ	G_ASP_61	OD1	2.819
6U02	G_ARG_66	NH1	G_ASP_86	OD1	3.308
6U02	G_ARG_66	NH1	G_ASP_86	OD2	3.771
6U02	G_ARG_66	NH2	G_ASP_86	OD1	3.561
6U02	G_ARG_66	NH2	G_ASP_86	OD2	2.624
6U02	J_HIS_98	NE2	A_GLU_214	OE2	3.838
6U02	J_ARG_118	NH2	J_GLU_425	OE1	3.304
6U02	J_ARG_118	NH2	J_GLU_425	OE2	3.788
6U02	J_ARG_130	NH1	J_GLU_128	OE1	3.104
6U02	J_ARG_156	NH2	J_GLU_119	OE1	3.055
6U02	J_ARG_172	NH2	J_GLU_174	OE2	3.005
6U02	J_ARG_189	NH2	J_ASP_125	OD1	2.704
6U02	J_ARG_209	NH1	E_GLU_128	OE2	3.226
6U02	J_ARG_210	NH2	E_ASP_412	OD1	3.356
6U02	J_ARG_210	NH2	E_ASP_412	OD2	3.535
6U02	J_ARG_224	NH2	J_GLU_276	OE2	2.857
6U02	J_ARG_253	NH2	J_ASP_251	OD1	3.916
6U02	J_ARG_253	NH2	J_ASP_251	OD2	3.078
6U02	J_LYS_264	NZ	J_GLU_266	OE2	3.593
6U02	J_ARG_292	NH1	J_GLU_276	OE1	3.982
6U02	J_ARG_292	NH2	J_GLU_276	OE1	3.522
6U02	J_ARG_292	NH2	J_GLU_277	OE1	3.270
6U02	J_ARG_292	NH2	J_GLU_277	OE2	3.103
6U02	J_ARG_300	NH2	J_ASP_324	OD1	3.839
6U02	J_HIS_312	ND1	J_GLU_266	OE1	2.872
6U02	J_ARG_364	NH1	J_ASP_330	OD1	3.366
6U02	J_ARG_364	NH1	J_ASP_330	OD2	3.021
6U02	J_ARG_364	NH2	J_ASP_330	OD2	3.215
6U02	J_ARG_364	NH2	J_GLU_375	OE2	3.763
6U02	J_ARG_419	NH1	A_GLU_214	OE2	3.906
6U02	J_ARG_428	NH1	J_ASP_460	OD2	2.812
6U02	J_ARG_428	NH2	J_GLU_433	OE1	3.663
6U02	J_ARG_428	NH2	J_GLU_433	OE2	3.047
6U02	I_ARG_24	NH2	I_ASP_70	OD1	2.974
6U02	I_ARG_61	NH2	I_GLU_81	OE1	3.910
6U02	I_ARG_61	NH2	I_ASP_82	OD1	2.860
6U02	I_ARG_61	NH2	I_ASP_82	OD2	3.591
6U02	I_LYS_103	NZ	I_GLU_105	OE2	3.418
6U02	K_ARG_38	NH1	K_ASP_86	OD1	2.942
6U02	K_ARG_38	NH2	K_ASP_86	OD1	3.942
6U02	K_LYS_52	NZ	K_GLU_56	OE2	2.823
6U02	K_LYS_64	NZ	K_ASP_61	OD1	2.819
6U02	K_ARG_66	NH1	K_ASP_86	OD1	3.307
6U02	K_ARG_66	NH1	K_ASP_86	OD2	3.771
6U02	K_ARG_66	NH2	K_ASP_86	OD1	3.561
6U02	K_ARG_66	NH2	K_ASP_86	OD2	2.624

Table 909: 6U02-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6U1T	H_ARG_38	NH1	H_ASP_90	OD1	2.918
6U1T	H_ARG_38	NH2	H_GLU_46	OE1	3.164
6U1T	H_ARG_38	NH2	H_ASP_90	OD1	3.940
6U1T	H_ARG_67	NH1	H_ASP_90	OD1	3.821
6U1T	H_ARG_67	NH1	H_ASP_90	OD2	2.731
6U1T	H_ARG_67	NH2	H_ASP_90	OD1	3.017
6U1T	H_ARG_67	NH2	H_ASP_90	OD2	3.451
6U1T	L_ARG_61	NH2	L_ASP_82	OD1	2.857
6U1T	L_ARG_61	NH2	L_ASP_82	OD2	3.548
6U1T	L_LYS_142	NZ	L_GLU_105	OE1	3.135
6U1T	L_LYS_149	NZ	L_GLU_195	OE1	3.622
6U1T	L_LYS_149	NZ	L_GLU_195	OE2	2.931
6U1T	L_ARG_155	NH1	L_GLU_185	OE1	3.214
6U1T	L_ARG_155	NH1	L_GLU_185	OE2	3.203
6U1T	L_ARG_155	NH2	L_GLU_185	OE1	3.040
6U1T	L_HIS_189	ND1	L_ASP_151	OD2	3.058
6U1T	L_LYS_199	NZ	L_ASP_110	OD2	3.885

Table 910: 6U1T-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6U59	A_LYS_34	NZ	B_ASP_612	OD1	2.489
6U59	A_LYS_46	NZ	A_GLU_492	OE1	2.715
6U59	A_LYS_170	NZ	A_GLU_172	OE2	3.768
6U59	A_LYS_227	NZ	A_GLU_83	OE1	3.011
6U59	A_LYS_227	NZ	A_GLU_83	OE2	3.430
6U59	A_LYS_231	NZ	A_GLU_268	OE2	2.869
6U59	A_HIS_249	NE2	A_GLU_482	OE2	2.821
6U59	A_LYS_282	NZ	A_ASP_279	OD2	2.817
6U59	A_ARG_298	NH1	A_GLU_381	OE2	3.452
6U59	A_ARG_298	NH2	A_GLU_381	OE1	3.785
6U59	A_ARG_298	NH2	A_GLU_381	OE2	3.680
6U59	A_ARG_327	NH1	A_ASP_148A	OD1	3.884
6U59	A_ARG_327	NH1	A_ASP_148A	OD2	3.044
6U59	A_LYS_335	NZ	A_GLU_408	OE1	3.651
6U59	A_ARG_337	NH1	A_GLU_290	OE1	2.993
6U59	A_ARG_337	NH2	A_GLU_290	OE1	2.941
6U59	A_LYS_356	NZ	A_GLU_466	OE2	2.969
6U59	A_ARG_399	NH1	A_ASP_401	OD2	3.230
6U59	A_ARG_419	NH2	A_GLU_153	OE2	3.607
6U59	A_LYS_421	NZ	A_GLU_370	OE2	3.544
6U59	A_LYS_432	NZ	A_ASP_113	OD1	2.692
6U59	A_LYS_432	NZ	A_ASP_113	OD2	2.690
6U59	A_ARG_456	NH2	A_GLU_466	OE1	2.731
6U59	A_ARG_456	NH2	A_GLU_466	OE2	3.143
6U59	A_ARG_469	NH2	A_ASP_457	OD2	2.912
6U59	A_ARG_476	NH2	A_GLU_102	OE1	3.714
6U59	A_ARG_476	NH2	A_GLU_102	OE2	3.058
6U59	A_ARG_480	NH1	A_ASP_477	OD1	2.833
6U59	A_LYS_487	NZ	A_GLU_47	OE1	3.413
6U59	A_LYS_487	NZ	A_GLU_91	OE2	2.867
6U59	A_LYS_490	NZ	A_GLU_492	OE2	3.991
6U59	A_ARG_504	NH1	I_GLU_662	OE1	3.209
6U59	A_ARG_504	NH1	I_GLU_662	OE2	2.833
6U59	A_ARG_504	NH2	I_GLU_662	OE2	3.911
6U59	B_LYS_574	NZ	A_ASP_107	OD1	2.403
6U59	B_ARG_579	NH2	I_GLU_584	OE1	3.024
6U59	B_ARG_588	NH2	B_GLU_584	OE2	3.079
6U59	B_LYS_617	NZ	B_GLU_634	OE1	2.908
6U59	B_LYS_617	NZ	B_GLU_634	OE2	3.808
6U59	L_ARG_28	NH2	L_ASP_95D	OD2	3.021
6U59	L_ARG_50	NH1	A_GLU_269	OE2	3.175
6U59	L_ARG_50	NH2	A_GLU_268	OE1	2.965
6U59	L_ARG_50	NH2	A_GLU_269	OE2	3.221
6U59	L_ARG_61	NH1	L_GLU_79	OE1	3.076
6U59	L_ARG_61	NH1	L_ASP_82	OD2	2.866
6U59	L_ARG_61	NH2	L_ASP_77	OD2	3.575
6U59	L_ARG_61	NH2	L_GLU_79	OE1	3.931
6U59	L_ARG_95A	NH1	A_GLU_350	OE2	3.796
6U59	L_ARG_95A	NH2	A_GLU_350	OE1	3.217
6U59	L_ARG_95A	NH2	A_GLU_350	OE2	3.041
6U59	L_ARG_95A	NH2	A_GLU_351	OE1	3.921
6U59	H_ARG_38	NH1	H_ASP_86	OD1	2.876
6U59	H_ARG_38	NH2	H_GLU_46	OE1	2.785
6U59	H_ARG_38	NH2	H_GLU_46	OE2	3.942
6U59	H_ARG_66	NH1	H_ASP_86	OD1	2.903
6U59	H_ARG_66	NH1	H_ASP_86	OD2	3.436
6U59	C_LYS_34	NZ	D_ASP_612	OD1	2.489

6U59	C_LYS_46	NZ	C_GLU_492	OE1	2.715
6U59	C_LYS_170	NZ	C_GLU_172	OE2	3.768
6U59	C_LYS_227	NZ	C_GLU_83	OE1	3.011
6U59	C_LYS_227	NZ	C_GLU_83	OE2	3.430
6U59	C_LYS_231	NZ	C_GLU_268	OE2	2.869
6U59	C_HIS_249	NE2	C_GLU_482	OE2	2.820
6U59	C_LYS_282	NZ	C_ASP_279	OD2	2.817
6U59	C_ARG_298	NH1	C_GLU_381	OE2	3.453
6U59	C_ARG_298	NH2	C_GLU_381	OE1	3.785
6U59	C_ARG_298	NH2	C_GLU_381	OE2	3.680
6U59	C_ARG_327	NH1	C_ASP_148A	OD1	3.883
6U59	C_ARG_327	NH1	C_ASP_148A	OD2	3.044
6U59	C_LYS_335	NZ	C_GLU_408	OE1	3.651
6U59	C_ARG_337	NH1	C_GLU_290	OE1	2.993
6U59	C_ARG_337	NH2	C_GLU_290	OE1	2.942
6U59	C_LYS_356	NZ	C_GLU_466	OE2	2.969
6U59	C_ARG_399	NH1	C_ASP_401	OD2	3.229
6U59	C_ARG_419	NH2	C_GLU_153	OE2	3.607
6U59	C_LYS_421	NZ	C_GLU_370	OE2	3.543
6U59	C_LYS_432	NZ	C_ASP_113	OD1	2.692
6U59	C_LYS_432	NZ	C_ASP_113	OD2	2.691
6U59	C_ARG_456	NH2	C_GLU_466	OE1	2.732
6U59	C_ARG_456	NH2	C_GLU_466	OE2	3.144
6U59	C_ARG_469	NH2	C_ASP_457	OD2	2.911
6U59	C_ARG_476	NH2	C_GLU_102	OE1	3.714
6U59	C_ARG_476	NH2	C_GLU_102	OE2	3.058
6U59	C_ARG_480	NH1	C_ASP_477	OD1	2.832
6U59	C_LYS_487	NZ	C_GLU_47	OE1	3.414
6U59	C_LYS_487	NZ	C_GLU_91	OE2	2.866
6U59	C_LYS_490	NZ	C_GLU_492	OE2	3.991
6U59	C_ARG_504	NH1	B_GLU_662	OE1	3.208
6U59	C_ARG_504	NH1	B_GLU_662	OE2	2.832
6U59	C_ARG_504	NH2	B_GLU_662	OE2	3.910
6U59	D_LYS_574	NZ	C_ASP_107	OD1	2.403
6U59	D_ARG_579	NH2	B_GLU_584	OE1	3.024
6U59	D_ARG_588	NH2	D_GLU_584	OE2	3.079
6U59	D_LYS_617	NZ	D_GLU_634	OE1	2.908
6U59	D_LYS_617	NZ	D_GLU_634	OE2	3.808
6U59	E_ARG_28	NH2	E_ASP_95D	OD2	3.022
6U59	E_ARG_50	NH1	C_GLU_269	OE2	3.175
6U59	E_ARG_50	NH2	C_GLU_268	OE1	2.965
6U59	E_ARG_50	NH2	C_GLU_269	OE2	3.221
6U59	E_ARG_61	NH1	E_GLU_79	OE1	3.076
6U59	E_ARG_61	NH1	E_ASP_82	OD2	2.865
6U59	E_ARG_61	NH2	E_ASP_77	OD2	3.574
6U59	E_ARG_61	NH2	E_GLU_79	OE1	3.931
6U59	E_ARG_95A	NH1	C_GLU_350	OE2	3.795
6U59	E_ARG_95A	NH2	C_GLU_350	OE1	3.216
6U59	E_ARG_95A	NH2	C_GLU_350	OE2	3.040
6U59	E_ARG_95A	NH2	C_GLU_351	OE1	3.921
6U59	F_ARG_38	NH1	F_ASP_86	OD1	2.877
6U59	F_ARG_38	NH2	F_GLU_46	OE1	2.786
6U59	F_ARG_38	NH2	F_GLU_46	OE2	3.943
6U59	F_ARG_66	NH1	F_ASP_86	OD1	2.903
6U59	F_ARG_66	NH1	F_ASP_86	OD2	3.437
6U59	G_LYS_34	NZ	I_ASP_612	OD1	2.489
6U59	G_LYS_46	NZ	G_GLU_492	OE1	2.715
6U59	G_LYS_170	NZ	G_GLU_172	OE2	3.768

6U59	G_LYS_227	NZ	G_GLU_83	OE1	3.011
6U59	G_LYS_227	NZ	G_GLU_83	OE2	3.430
6U59	G_LYS_231	NZ	G_GLU_268	OE2	2.869
6U59	G_HIS_249	NE2	G_GLU_482	OE2	2.821
6U59	G_LYS_282	NZ	G_ASP_279	OD2	2.816
6U59	G_ARG_298	NH1	G_GLU_381	OE2	3.452
6U59	G_ARG_298	NH2	G_GLU_381	OE1	3.785
6U59	G_ARG_298	NH2	G_GLU_381	OE2	3.679
6U59	G_ARG_327	NH1	G_ASP_148A	OD1	3.883
6U59	G_ARG_327	NH1	G_ASP_148A	OD2	3.044
6U59	G_LYS_335	NZ	G_GLU_408	OE1	3.651
6U59	G_ARG_337	NH1	G_GLU_290	OE1	2.994
6U59	G_ARG_337	NH2	G_GLU_290	OE1	2.942
6U59	G_LYS_356	NZ	G_GLU_466	OE2	2.969
6U59	G_ARG_399	NH1	G_ASP_401	OD2	3.230
6U59	G_ARG_419	NH2	G_GLU_153	OE2	3.607
6U59	G_LYS_421	NZ	G_GLU_370	OE2	3.543
6U59	G_LYS_432	NZ	G_ASP_113	OD1	2.692
6U59	G_LYS_432	NZ	G_ASP_113	OD2	2.691
6U59	G_ARG_456	NH2	G_GLU_466	OE1	2.731
6U59	G_ARG_456	NH2	G_GLU_466	OE2	3.144
6U59	G_ARG_469	NH2	G_ASP_457	OD2	2.912
6U59	G_ARG_476	NH2	G_GLU_102	OE1	3.714
6U59	G_ARG_476	NH2	G_GLU_102	OE2	3.058
6U59	G_ARG_480	NH1	G_ASP_477	OD1	2.833
6U59	G_LYS_487	NZ	G_GLU_47	OE1	3.414
6U59	G_LYS_487	NZ	G_GLU_91	OE2	2.866
6U59	G_LYS_490	NZ	G_GLU_492	OE2	3.990
6U59	G_ARG_504	NH1	D_GLU_662	OE1	3.209
6U59	G_ARG_504	NH1	D_GLU_662	OE2	2.833
6U59	G_ARG_504	NH2	D_GLU_662	OE2	3.910
6U59	I_LYS_574	NZ	G_ASP_107	OD1	2.403
6U59	I_ARG_579	NH2	D_GLU_584	OE1	3.025
6U59	I_ARG_588	NH2	I_GLU_584	OE2	3.079
6U59	I_LYS_617	NZ	I_GLU_634	OE1	2.907
6U59	I_LYS_617	NZ	I_GLU_634	OE2	3.808
6U59	J_ARG_28	NH2	J_ASP_95D	OD2	3.022
6U59	J_ARG_50	NH1	G_GLU_269	OE2	3.175
6U59	J_ARG_50	NH2	G_GLU_268	OE1	2.965
6U59	J_ARG_50	NH2	G_GLU_269	OE2	3.220
6U59	J_ARG_61	NH1	J_GLU_79	OE1	3.077
6U59	J_ARG_61	NH1	J_ASP_82	OD2	2.866
6U59	J_ARG_61	NH2	J_ASP_77	OD2	3.574
6U59	J_ARG_61	NH2	J_GLU_79	OE1	3.931
6U59	J_ARG_95A	NH1	G_GLU_350	OE2	3.796
6U59	J_ARG_95A	NH2	G_GLU_350	OE1	3.217
6U59	J_ARG_95A	NH2	G_GLU_350	OE2	3.041
6U59	J_ARG_95A	NH2	G_GLU_351	OE1	3.921
6U59	K_ARG_38	NH1	K_ASP_86	OD1	2.876
6U59	K_ARG_38	NH2	K_GLU_46	OE1	2.786
6U59	K_ARG_38	NH2	K_GLU_46	OE2	3.943
6U59	K_ARG_66	NH1	K_ASP_86	OD1	2.904
6U59	K_ARG_66	NH1	K_ASP_86	OD2	3.437

Table 911: 6U59-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6UG7	L_ARG_60	NH1	L_GLU_78	OE1	3.385
6UG7	L_ARG_60	NH1	L_GLU_78	OE2	3.452
6UG7	L_ARG_60	NH2	L_GLU_78	OE1	3.649
6UG7	L_ARG_60	NH2	L_GLU_80	OE2	2.876
6UG7	L_ARG_60	NH2	L_ASP_81	OD1	2.780
6UG7	L_ARG_60	NH2	L_ASP_81	OD2	3.537
6UG7	L_LYS_148	NZ	L_GLU_194	OE2	2.618
6UG7	L_LYS_168	NZ	L_ASP_166	OD1	3.206
6UG7	L_LYS_168	NZ	L_ASP_166	OD2	3.551
6UG7	L_HIS_188	ND1	L_ASP_150	OD2	3.280
6UG7	H_ARG_38	NH1	H_ASP_89	OD1	2.846
6UG7	H_ARG_38	NH2	H_ASP_89	OD1	3.706
6UG7	H_HIS_60	NE2	L_GLU_1	OE1	2.854
6UG7	H_HIS_60	NE2	L_GLU_1	OE2	3.808
6UG7	H_ARG_66	NH1	H_ASP_89	OD1	3.754
6UG7	H_ARG_66	NH1	H_ASP_89	OD2	2.880
6UG7	H_ARG_66	NH2	H_ASP_89	OD1	3.067
6UG7	H_ARG_66	NH2	H_ASP_89	OD2	3.547
6UG7	H_LYS_147	NZ	H_ASP_148	OD1	3.523
6UG7	H_LYS_213	NZ	L_GLU_122	OE1	2.927
6UG7	H_LYS_213	NZ	L_GLU_122	OE2	3.960
6UG7	H_LYS_214	NZ	H_GLU_216	OE1	3.060

Table 912: 6UG7-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6UG8	L_ARG_60	NH1	L_GLU_78	OE1	3.498
6UG8	L_ARG_60	NH2	L_GLU_78	OE1	3.557
6UG8	L_ARG_60	NH2	L_GLU_80	OE2	2.819
6UG8	L_ARG_60	NH2	L_ASP_81	OD1	2.739
6UG8	L_ARG_60	NH2	L_ASP_81	OD2	3.504
6UG8	L_LYS_148	NZ	L_GLU_194	OE1	2.956
6UG8	L_LYS_148	NZ	L_GLU_194	OE2	3.899
6UG8	L_HIS_188	ND1	L_ASP_184	OD1	3.549
6UG8	H_ARG_38	NH1	H_ASP_89	OD1	2.810
6UG8	H_ARG_38	NH2	H_GLU_46	OE1	3.785
6UG8	H_ARG_38	NH2	H_GLU_46	OE2	2.904
6UG8	H_ARG_38	NH2	H_ASP_89	OD1	3.679
6UG8	H_HIS_60	NE2	L_GLU_1	OE1	3.688
6UG8	H_ARG_66	NH1	H_ASP_89	OD1	3.627
6UG8	H_ARG_66	NH1	H_ASP_89	OD2	2.995
6UG8	H_ARG_66	NH2	H_ASP_89	OD1	2.888
6UG8	H_ARG_66	NH2	H_ASP_89	OD2	3.572
6UG8	H_LYS_75	NZ	H_ASP_72	OD2	3.818
6UG8	H_LYS_147	NZ	H_ASP_148	OD1	3.749
6UG8	H_LYS_147	NZ	H_ASP_148	OD2	3.867
6UG8	H_LYS_213	NZ	L_GLU_122	OE1	2.779
6UG8	H_LYS_213	NZ	L_GLU_122	OE2	3.811
6UG8	H_LYS_214	NZ	H_GLU_216	OE1	3.891

Table 913: 6UG8-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6UG9	L_ARG_60	NH1	L_GLU_78	OE1	3.657
6UG9	L_ARG_60	NH2	L_GLU_80	OE2	2.753
6UG9	L_ARG_60	NH2	L_ASP_81	OD1	2.737
6UG9	L_ARG_60	NH2	L_ASP_81	OD2	3.762
6UG9	L_LYS_102	NZ	L_GLU_164	OE1	3.252
6UG9	L_LYS_102	NZ	L_GLU_164	OE2	2.915
6UG9	L_LYS_106	NZ	L_GLU_17	OE2	3.780
6UG9	L_ARG_141	NH1	L_GLU_164	OE2	3.279
6UG9	L_ARG_141	NH2	L_GLU_104	OE1	3.321
6UG9	L_ARG_141	NH2	L_GLU_104	OE2	3.680
6UG9	L_ARG_210	NH1	L_GLU_186	OE2	3.814
6UG9	H_ARG_38	NH1	H_ASP_89	OD1	2.732
6UG9	H_ARG_38	NH2	H_GLU_46	OE2	3.364
6UG9	H_ARG_38	NH2	H_ASP_89	OD1	3.514
6UG9	H_HIS_60	NE2	L_GLU_1	OE2	3.673
6UG9	H_HIS_60	NE2	H_GLU_46	OE1	3.948
6UG9	H_ARG_66	NH1	H_ASP_89	OD1	3.412
6UG9	H_ARG_66	NH1	H_ASP_89	OD2	3.392
6UG9	H_ARG_66	NH2	H_ASP_89	OD1	3.881
6UG9	H_ARG_66	NH2	H_ASP_89	OD2	2.589
6UG9	H_LYS_147	NZ	H_ASP_148	OD1	3.376
6UG9	H_LYS_147	NZ	H_ASP_148	OD2	3.331
6UG9	H_LYS_213	NZ	L_GLU_122	OE1	3.853
6UG9	H_LYS_214	NZ	H_GLU_216	OE2	3.824
6UG9	B_LYS_52	NZ	B_ASP_49	OD2	3.304
6UG9	B_ARG_60	NH2	B_GLU_80	OE2	3.597
6UG9	B_ARG_60	NH2	B_ASP_81	OD1	2.874
6UG9	B_ARG_60	NH2	B_ASP_81	OD2	3.455
6UG9	B_LYS_102	NZ	B_GLU_164	OE1	3.160
6UG9	B_LYS_102	NZ	B_GLU_164	OE2	3.546
6UG9	B_ARG_141	NH1	B_GLU_104	OE1	3.634
6UG9	B_ARG_141	NH1	B_GLU_104	OE2	3.870
6UG9	B_LYS_148	NZ	B_GLU_194	OE1	3.810
6UG9	B_LYS_148	NZ	B_GLU_194	OE2	3.615
6UG9	B_HIS_188	ND1	B_ASP_150	OD2	3.288
6UG9	B_ARG_210	NH1	B_GLU_186	OE1	3.776
6UG9	A_ARG_38	NH1	A_ASP_89	OD1	2.722
6UG9	A_ARG_38	NH2	A_GLU_46	OE2	3.287
6UG9	A_ARG_38	NH2	A_ASP_89	OD1	3.758
6UG9	A_HIS_60	NE2	B_GLU_1	OE1	3.507
6UG9	A_ARG_66	NH1	A_ASP_89	OD1	3.675
6UG9	A_ARG_66	NH1	A_ASP_89	OD2	2.753
6UG9	A_ARG_66	NH2	A_ASP_89	OD1	3.070
6UG9	A_ARG_66	NH2	A_ASP_89	OD2	3.506
6UG9	A_LYS_147	NZ	A_ASP_148	OD1	3.442
6UG9	A_LYS_147	NZ	A_ASP_148	OD2	3.550
6UG9	A_LYS_213	NZ	B_GLU_122	OE1	2.877
6UG9	A_LYS_214	NZ	A_GLU_216	OE1	2.984
6UG9	K_ARG_60	NH1	K_GLU_78	OE1	3.075
6UG9	K_ARG_60	NH1	K_GLU_78	OE2	3.972
6UG9	K_ARG_60	NH1	K_GLU_80	OE2	3.745
6UG9	K_ARG_60	NH1	K_ASP_81	OD1	2.816
6UG9	K_ARG_60	NH1	K_ASP_81	OD2	2.993
6UG9	K_ARG_60	NH2	K_GLU_78	OE1	3.769
6UG9	K_ARG_60	NH2	K_GLU_80	OE2	2.923
6UG9	K_LYS_102	NZ	K_GLU_104	OE1	3.987
6UG9	K_LYS_102	NZ	K_GLU_164	OE1	3.455

6UG9	K_LYS_102	NZ	K_GLU_164	OE2	3.139
6UG9	K_ARG_141	NH1	K_GLU_104	OE1	3.193
6UG9	K_ARG_141	NH1	K_GLU_104	OE2	2.932
6UG9	K_ARG_141	NH2	K_GLU_104	OE1	2.602
6UG9	K_ARG_141	NH2	K_GLU_104	OE2	3.840
6UG9	K_LYS_148	NZ	K_GLU_194	OE1	3.594
6UG9	K_LYS_148	NZ	K_GLU_194	OE2	2.938
6UG9	K_HIS_188	ND1	K_ASP_150	OD2	3.205
6UG9	K_HIS_188	NE2	K_ASP_184	OD1	3.818
6UG9	K_ARG_210	NH1	K_GLU_186	OE2	3.933
6UG9	J_ARG_38	NH1	J_ASP_89	OD1	2.782
6UG9	J_ARG_38	NH2	J_GLU_46	OE2	3.597
6UG9	J_ARG_38	NH2	J_ASP_89	OD1	3.861
6UG9	J_HIS_60	NE2	K_GLU_1	OE1	3.585
6UG9	J_ARG_66	NH2	J_ASP_89	OD1	2.909
6UG9	J_ARG_66	NH2	J_ASP_89	OD2	2.772
6UG9	J_LYS_75	NZ	J_ASP_72	OD2	3.024
6UG9	J_LYS_147	NZ	J_ASP_148	OD1	3.646
6UG9	J_LYS_213	NZ	K_GLU_122	OE1	2.648
6UG9	J_LYS_213	NZ	K_GLU_122	OE2	3.296
6UG9	J_LYS_214	NZ	J_GLU_216	OE1	3.149

Table 914: 6UG9-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6UGA	L_HIS_33	ND1	L_ASP_49	OD1	3.961
6UGA	L_LYS_52	NZ	L_ASP_49	OD2	3.704
6UGA	L_ARG_60	NH2	L_GLU_80	OE2	3.278
6UGA	L_ARG_60	NH2	L_ASP_81	OD1	2.749
6UGA	L_ARG_60	NH2	L_ASP_81	OD2	3.568
6UGA	L_LYS_102	NZ	L_GLU_104	OE2	3.070
6UGA	L_LYS_148	NZ	L_GLU_194	OE2	2.966
6UGA	L_LYS_182	NZ	L_GLU_186	OE2	3.117
6UGA	L_HIS_188	ND1	L_ASP_150	OD2	2.852
6UGA	H_ARG_38	NH1	H_ASP_89	OD1	2.990
6UGA	H_ARG_38	NH2	H_GLU_46	OE1	3.017
6UGA	H_ARG_38	NH2	H_ASP_89	OD1	3.417
6UGA	H_HIS_60	NE2	L_GLU_1	OE1	3.306
6UGA	H_ARG_66	NH1	H_ASP_89	OD1	3.849
6UGA	H_ARG_66	NH1	H_ASP_89	OD2	2.855
6UGA	H_ARG_66	NH2	H_ASP_89	OD1	2.858
6UGA	H_ARG_66	NH2	H_ASP_89	OD2	3.277
6UGA	H_LYS_147	NZ	H_ASP_148	OD1	3.129
6UGA	A_LYS_52	NZ	A_ASP_49	OD2	3.881
6UGA	A_ARG_60	NH1	A_GLU_80	OE1	3.935
6UGA	A_ARG_60	NH2	A_GLU_80	OE1	2.878
6UGA	A_ARG_60	NH2	A_ASP_81	OD1	2.757
6UGA	A_ARG_60	NH2	A_ASP_81	OD2	3.485
6UGA	A_LYS_144	NZ	A_GLU_194	OE1	3.405
6UGA	A_LYS_144	NZ	A_GLU_194	OE2	2.645
6UGA	A_LYS_182	NZ	A_GLU_186	OE2	3.697
6UGA	A_LYS_187	NZ	A_ASP_184	OD1	3.052
6UGA	A_ARG_210	NH2	A_GLU_186	OE1	3.370
6UGA	B_ARG_38	NH1	B_ASP_89	OD1	2.951
6UGA	B_ARG_38	NH2	B_ASP_89	OD1	3.625
6UGA	B_HIS_60	NE2	A_GLU_1	OE2	3.932
6UGA	B_ARG_66	NH1	B_ASP_89	OD1	3.747
6UGA	B_ARG_66	NH1	B_ASP_89	OD2	3.050
6UGA	B_ARG_66	NH2	B_ASP_89	OD1	3.323
6UGA	B_ARG_66	NH2	B_ASP_89	OD2	3.833
6UGA	B_LYS_147	NZ	B_ASP_148	OD1	3.437
6UGA	B_LYS_147	NZ	B_ASP_148	OD2	3.600
6UGA	B_HIS_168	NE2	A_ASP_166	OD1	3.218
6UGA	B_LYS_213	NZ	A_GLU_122	OE1	3.352

Table 915: 6UGA-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1A14	N_LYS_432	NZ	H_ASP_56	OD1	3.071

Table 916: Interfacial 1A14-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1A2Y	A_ARG_96	NH1	B_GLU_98	OE1	2.846
1A2Y	A_ARG_96	NH1	B_GLU_98	OE2	3.664
1A2Y	A_ARG_96	NH2	B_GLU_98	OE1	3.545
1A2Y	A_ARG_96	NH2	B_GLU_98	OE2	2.882

Table 917: Interfacial 1A2Y-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1A7L	A_LYS_219	NZ	B_GLU_131	OE1	3.835

Table 918: Interfacial 1A7L-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1A7N	L_ARG_96	NH1	H_GLU_298	OE1	2.957
1A7N	L_ARG_96	NH1	H_GLU_298	OE2	3.249
1A7N	L_ARG_96	NH2	H_GLU_298	OE2	3.297

Table 919: Interfacial 1A7N-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1A7P	L_ARG_96	NH2	H_GLU_298	OE1	3.845
1A7P	L_ARG_96	NH2	H_GLU_298	OE2	2.867

Table 920: Interfacial 1A7P-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1A7Q	L_ARG_96	NH1	H_GLU_298	OE1	2.615
1A7Q	L_ARG_96	NH1	H_GLU_298	OE2	3.239
1A7Q	L_ARG_96	NH2	H_GLU_298	OE1	3.431
1A7Q	L_ARG_96	NH2	H_GLU_298	OE2	2.621

Table 921: Interfacial 1A7Q-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1A7R	L_ARG_96	NH1	H_GLU_298	OE1	2.658
1A7R	L_ARG_96	NH1	H_GLU_298	OE2	3.535
1A7R	L_ARG_96	NH2	H_GLU_298	OE1	3.614
1A7R	L_ARG_96	NH2	H_GLU_298	OE2	2.905

Table 922: Interfacial 1A7R-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1ADQ	A_ARG_255	NH2	H_ASP_31	OD2	2.929
1ADQ	A_HIS_433	NE2	L_ASP_50	OD1	3.394
1ADQ	A_HIS_433	NE2	L_ASP_50	OD2	3.883
1ADQ	L_HIS_95B	NE2	H_ASP_61	OD2	3.425

Table 923: Interfacial 1ADQ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1BJ1	H_LYS_219	NZ	L_GLU_123	OE1	2.948
1BJ1	H_LYS_224	NZ	L ASP_122	OD2	2.691
1BJ1	V_ARG_23	NH1	W_GLU_30	OE1	3.305
1BJ1	W_ARG_23	NH1	V_GLU_30	OE1	3.351

Table 924: Interfacial 1BJ1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1BLN	B_LYS_221	NZ	A_GLU_123	OE2	2.688
1BLN	D_LYS_221	NZ	C_GLU_123	OE2	2.694

Table 925: Interfacial 1BLN-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1BQL	L_LYS_44	NZ	H_ASP_104	OD1	3.995
1BQL	L_ARG_45	NH2	H_ASP_104	OD2	3.212
1BQL	H_LYS_211	NZ	L_GLU_121	OE1	2.714
1BQL	H_LYS_211	NZ	L_GLU_121	OE2	2.963
1BQL	Y_ARG_45	NH1	H_GLU_50	OE1	3.800
1BQL	Y_ARG_45	NH1	H_GLU_50	OE2	2.920
1BQL	Y_LYS_68	NZ	H_GLU_50	OE1	3.561

Table 926: Interfacial 1BQL-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1BVK	A_ARG_96	NH2	B_GLU_98	OE1	2.978
1BVK	A_ARG_96	NH2	B_GLU_98	OE2	2.932
1BVK	D_ARG_96	NH2	E_GLU_98	OE1	2.525
1BVK	D_ARG_96	NH2	E_GLU_98	OE2	2.753

Table 927: Interfacial 1BVK-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1C08	C.LYS_97	NZ	B.ASP_32	OD1	2.620
1C08	C.LYS_97	NZ	B.ASP_32	OD2	3.999
1C08	C.LYS_97	NZ	B.ASP_99	OD2	2.365

Table 928: Interfacial 1C08-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1C12	B_LYS_508	NZ	A_GLU_123	OE2	3.314

Table 929: Interfacial 1C12-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1CE1	L_ARG_94	NH2	H_GLU_61	OE2	3.979
1CE1	L_ARG_96	NH1	H_GLU_101	OE1	2.707
1CE1	L_ARG_96	NH1	H_GLU_101	OE2	3.562
1CE1	L_ARG_96	NH2	H_GLU_101	OE1	3.509
1CE1	L_ARG_96	NH2	H_GLU_101	OE2	2.787
1CE1	H_ARG_52	NH2	P_ASP_7	OD1	3.481
1CE1	H_LYS_56	NZ	P_ASP_7	OD2	2.951

Table 930: Interfacial 1CE1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1CFS	B_LYS_207	NZ	A_GLU_123	OE1	3.526

Table 931: Interfacial 1CFS-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1CFT	B_LYS_207	NZ	A_GLU_123	OE1	2.550
1CFT	C_LYS_2	NZ	A_ASP_92	OD1	2.682

Table 932: Interfacial 1CFT-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1CG9	A_ARG_17	NH1	B_ASP_35	OD2	3.201
1CG9	A_ARG_17	NH2	B_ASP_35	OD1	3.038
1CG9	A_ARG_17	NH2	B_ASP_35	OD2	3.401
1CG9	A_ARG_48	NH2	B_ASP_54	OD1	3.456
1CG9	A_ARG_48	NH2	B_ASP_54	OD2	3.762
1CG9	A_HIS_192	ND1	B_ASP_99	OD2	3.812
1CG9	B_LYS_7	NZ	A_GLU_232	OE1	3.887

Table 933: Interfacial 1CG9-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1CLZ	L_LYS_207	NZ	H_ASP_130	OD1	3.119
1CLZ	L_LYS_207	NZ	H_ASP_130	OD2	3.445
1CLZ	H_ARG_172	NH1	L_ASP_170	OD2	3.885
1CLZ	H_ARG_172	NH2	L_ASP_170	OD2	3.384
1CLZ	H_LYS_221	NZ	L_GLU_123	OE1	3.750
1CLZ	H_LYS_221	NZ	L_GLU_123	OE2	2.509

Table 934: Interfacial 1CLZ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1CZ8	V_ARG_23	NH1	W_GLU_30	OE1	3.162
1CZ8	V_ARG_23	NH1	W_GLU_30	OE2	3.558
1CZ8	W_ARG_23	NH1	V_GLU_30	OE1	3.011
1CZ8	W_ARG_23	NH1	V_GLU_30	OE2	3.663
1CZ8	H_LYS_219	NZ	L_GLU_123	OE1	3.027
1CZ8	H_LYS_224	NZ	L_ASP_122	OD1	2.846
1CZ8	H_LYS_224	NZ	L_ASP_122	OD2	3.185
1CZ8	Y_LYS_219	NZ	X_GLU_123	OE2	3.832

Table 935: Interfacial 1CZ8-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1DBJ	H_LYS_221	NZ	L_GLU_123	OE1	3.386
1DBJ	H_LYS_221	NZ	L_GLU_123	OE2	2.770

Table 936: Interfacial 1DBJ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1DBK	H_HIS_172	ND1	L_ASP_167	OD2	3.619
1DBK	H_LYS_221	NZ	L_GLU_123	OE2	3.030

Table 937: Interfacial 1DBK-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1DBM	H_LYS_221	NZ	L_GLU_123	OE2	3.277

Table 938: Interfacial 1DBM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1DEE	A_ARG_24	NH1	D_GLU_1555	OE1	3.510
1DEE	B_ARG_674	NH1	A_ASP_167	OD2	3.579
1DEE	B_LYS_719	NZ	A_GLU_123	OE1	2.730
1DEE	B_LYS_719	NZ	A_GLU_123	OE2	3.113
1DEE	D_ARG_1519	NH1	G_ASP_1834	OD1	3.122
1DEE	D_ARG_1519	NH1	G_ASP_1834	OD2	3.064
1DEE	D_ARG_1519	NH2	G_ASP_1834	OD1	3.684
1DEE	D_ARG_1519	NH2	G_ASP_1834	OD2	2.875
1DEE	D_ARG_1674	NH1	C_ASP_1167	OD2	3.619
1DEE	D_LYS_1719	NZ	C_GLU_1123	OE1	3.687
1DEE	D_LYS_1719	NZ	C_GLU_1123	OE2	2.890
1DEE	F_ARG_2519	NH1	H_ASP_2834	OD1	3.463
1DEE	F_ARG_2519	NH1	H_ASP_2834	OD2	2.731
1DEE	F_ARG_2519	NH2	H_ASP_2834	OD1	3.523
1DEE	F_ARG_2519	NH2	H_ASP_2834	OD2	3.444
1DEE	F_ARG_2674	NH1	E_ASP_2167	OD2	3.989
1DEE	F_LYS_2719	NZ	E_GLU_2123	OE1	2.882
1DEE	F_LYS_2719	NZ	E_GLU_2123	OE2	3.779

Table 939: Interfacial 1DEE-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1DQD	H_LYS_217	NZ	L_GLU_122	OE2	3.953

Table 940: Interfacial 1DQD-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1DQJ	B_LYS_219	NZ	A_GLU_123	OE2	2.598
1DQJ	C_LYS_97	NZ	B_ASP_32	OD2	2.665

Table 941: Interfacial 1DQJ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1DQM	L_LYS_207	NZ	H_ASP_130	OD1	3.491
1DQM	L_LYS_207	NZ	H_ASP_130	OD2	3.782

Table 942: Interfacial 1DQM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1DQQ	A_LYS_49	NZ	B_ASP_101	OD1	2.957
1DQQ	B_LYS_216	NZ	D_ASP_218	OD1	2.965
1DQQ	B_LYS_219	NZ	A_GLU_123	OE2	2.763
1DQQ	C_LYS_49	NZ	D_ASP_101	OD1	3.456
1DQQ	C_LYS_49	NZ	D_ASP_101	OD2	3.943
1DQQ	D_LYS_219	NZ	C_GLU_123	OE1	3.088

Table 943: Interfacial 1DQQ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1DVF	A_ARG_96	NH1	B_GLU_98	OE1	2.616
1DVF	A_ARG_96	NH1	B_GLU_98	OE2	3.746
1DVF	A_ARG_96	NH2	B_GLU_98	OE1	3.400
1DVF	A_ARG_96	NH2	B_GLU_98	OE2	2.958
1DVF	D_HIS_33	NE2	B_ASP_100	OD1	3.569
1DVF	D_HIS_33	NE2	B_ASP_100	OD2	3.052

Table 944: Interfacial 1DVF-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1DZB	A.LYS_63	NZ	B.GLU_89	OE1	3.983
1DZB	A.LYS_67	NZ	B.ASP_90	OD2	3.792
1DZB	X.ARG_61	NH2	A.ASP_256	OD2	3.887
1DZB	X.LYS_73	NZ	A.ASP_256	OD1	3.412
1DZB	X.LYS_73	NZ	A.ASP_256	OD2	3.290
1DZB	X.ARG_112	NH2	A.ASP_31	OD2	3.878
1DZB	Y.LYS_73	NZ	B.ASP_256	OD1	3.559

Table 945: Interfacial 1DZB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1E4W	H_LYS_205	NZ	L_GLU_123	OE1	3.384
1E4W	H_LYS_205	NZ	L_GLU_123	OE2	3.066

Table 946: Interfacial 1E4W-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1E4X	I.LYS_205	NZ	M.GLU_123	OE1	2.874
1E4X	I.LYS_205	NZ	M.GLU_123	OE2	3.751
1E4X	Q.HIS_4	NE2	I.ASP_98	OD2	3.960

Table 947: Interfacial 1E4X-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1E6J	H_LYS_215	NZ	L_GLU_121	OE1	3.273
1E6J	H_LYS_215	NZ	L_GLU_121	OE2	3.199

Table 948: Interfacial 1E6J-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1E6O	H_LYS_215	NZ	L_GLU_121	OE1	2.731
1E6O	H_LYS_215	NZ	L_GLU_121	OE2	3.094

Table 949: Interfacial 1E6O-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1EJO	L_HIS_2038	NE2	H_ASP_2603	OD1	3.217
1EJO	H_ARG_2598	NH2	P_ASP_3143	OD1	3.795
1EJO	H_ARG_2598	NH2	P_ASP_3143	OD2	2.982
1EJO	H_LYS_2714	NZ	L_GLU_2127	OE1	2.933
1EJO	H_LYS_2714	NZ	L_GLU_2127	OE2	3.046
1EJO	P_ARG_3141	NH1	L_GLU_2027	OE2	3.696
1EJO	P_ARG_3141	NH1	L_GLU_2097	OE1	2.675
1EJO	P_ARG_3141	NH2	L_GLU_2027	OE2	3.441

Table 950: Interfacial 1EJO-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1EMT	H_LYS_63	NZ	L_ASP_1	OD1	3.310
1EMT	H_LYS_211	NZ	L_GLU_123	OE1	2.945
1EMT	H_LYS_211	NZ	L_GLU_123	OE2	2.554

Table 951: Interfacial 1EMT-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1ETZ	L_ARG_186	NH1	B_GLU_48	OE1	2.771
1ETZ	L_ARG_186	NH1	B_GLU_48	OE2	3.248
1ETZ	L_ARG_190	NH2	B_GLU_48	OE2	3.331
1ETZ	H_LYS_156	NZ	L_GLU_127	OE2	3.377
1ETZ	H_LYS_221	NZ	L_GLU_126	OE1	3.184
1ETZ	A_ARG_186	NH1	H_GLU_45	OE2	3.236
1ETZ	A_ARG_186	NH2	H_GLU_48	OE1	3.518
1ETZ	B_LYS_156	NZ	A_GLU_127	OE2	2.979
1ETZ	B_LYS_221	NZ	A_GLU_126	OE1	3.572

Table 952: Interfacial 1ETZ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1F11	B_LYS_221	NZ	A_GLU_123	OE2	3.880
1F11	D_LYS_221	NZ	C_GLU_123	OE2	3.786

Table 953: Interfacial 1F11-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1F4W	H_LYS_147	NZ	L_GLU_127	OE2	2.611
1F4W	H_LYS_212	NZ	L_GLU_126	OE1	2.614
1F4W	H_LYS_212	NZ	L_GLU_126	OE2	2.379

Table 954: Interfacial 1F4W-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1F4X	H_LYS_147	NZ	L_GLU_127	OE2	2.699
1F4X	H_LYS_212	NZ	L_GLU_126	OE1	2.421
1F4X	H_LYS_212	NZ	L_GLU_126	OE2	2.990

Table 955: Interfacial 1F4X-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1F4Y	H_LYS_212	NZ	L_GLU_126	OE2	3.609

Table 956: Interfacial 1F4Y-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1F8T	L_ARG_96	NH1	H_ASP_97	OD1	3.105
1F8T	L_ARG_96	NH1	H_ASP_97	OD2	3.586
1F8T	L_ARG_96	NH2	H_ASP_97	OD1	3.395
1F8T	L_ARG_96	NH2	H_ASP_97	OD2	2.424
1F8T	H_LYS_221	NZ	L_GLU_123	OE1	3.087

Table 957: Interfacial 1F8T-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1F90	L_LYS_30	NZ	E_GLU_4	OE1	2.620
1F90	L_LYS_30	NZ	E_GLU_4	OE2	2.679
1F90	L_ARG_96	NH2	H_ASP_97	OD1	2.720
1F90	L_ARG_96	NH2	H_ASP_97	OD2	2.722
1F90	H_LYS_221	NZ	L_GLU_123	OE2	3.675

Table 958: Interfacial 1F90-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1FBI	H.LYS_63	NZ	L.ASP_1	OD1	2.933
1FBI	H.LYS_63	NZ	L.ASP_1	OD2	2.804
1FBI	H.LYS_217	NZ	L.GLU_123	OE1	3.667
1FBI	X.HIS_15	ND1	H.ASP_55	OD1	3.190
1FBI	X.HIS_15	ND1	H.ASP_55	OD2	3.649
1FBI	X.LYS_96	NZ	H.ASP_52	OD2	2.922
1FBI	X.LYS_97	NZ	H.GLU_50	OE1	3.586
1FBI	X.LYS_97	NZ	H.GLU_50	OE2	2.898
1FBI	Q.LYS_63	NZ	P.ASP_1	OD1	3.020
1FBI	Q.LYS_63	NZ	P.ASP_1	OD2	3.850
1FBI	Y.HIS_15	ND1	Q.ASP_55	OD1	3.335
1FBI	Y.HIS_15	ND1	Q.ASP_55	OD2	3.838
1FBI	Y.LYS_96	NZ	Q.ASP_52	OD2	2.727
1FBI	Y.LYS_97	NZ	Q.GLU_50	OE1	2.828
1FBI	Y.LYS_97	NZ	Q.GLU_50	OE2	3.159

Table 959: Interfacial 1FBI-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1FCC	A_LYS_370	NZ	B_GLU_357	OE2	2.948
1FCC	A_LYS_409	NZ	B_ASP_399	OD2	2.859
1FCC	A_LYS_439	NZ	B_GLU_356	OE1	3.550
1FCC	A_LYS_439	NZ	B_GLU_356	OE2	3.522
1FCC	C_LYS_28	NZ	A_GLU_380	OE1	2.730
1FCC	C_LYS_28	NZ	A_GLU_380	OE2	3.982
1FCC	C_LYS_28	NZ	A_GLU_382	OE1	3.879
1FCC	C_LYS_28	NZ	A_GLU_382	OE2	2.866
1FCC	B_LYS_370	NZ	A_GLU_357	OE2	2.633
1FCC	B_LYS_409	NZ	A_ASP_399	OD2	3.360
1FCC	B_LYS_439	NZ	A_GLU_356	OE1	3.166
1FCC	B_LYS_439	NZ	A_GLU_356	OE2	3.295
1FCC	D_LYS_28	NZ	B_GLU_380	OE1	2.730
1FCC	D_LYS_28	NZ	B_GLU_380	OE2	3.982
1FCC	D_LYS_28	NZ	B_GLU_382	OE1	3.879
1FCC	D_LYS_28	NZ	B_GLU_382	OE2	2.865

Table 960: Interfacial 1FCC-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1FDL	L_ARG_96	NH1	H_GLU_98	OE1	3.307
1FDL	L_ARG_96	NH1	H_GLU_98	OE2	2.802
1FDL	L_ARG_96	NH2	H_GLU_98	OE1	2.754
1FDL	L_ARG_96	NH2	H_GLU_98	OE2	3.656
1FDL	H_LYS_211	NZ	L_GLU_123	OE1	2.896
1FDL	H_LYS_211	NZ	L_GLU_123	OE2	3.291

Table 961: Interfacial 1FDL-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1FJ1	A_ARG_188	NH2	E_GLU_196	OE2	3.475
1FJ1	A_HIS_189	ND1	E_GLU_196	OE1	3.723
1FJ1	A_HIS_189	NE2	E_GLU_196	OE1	3.502
1FJ1	B_ARG_47	NH1	A_ASP_1	OD1	3.251
1FJ1	B_ARG_47	NH2	A_ASP_1	OD1	2.492
1FJ1	C_HIS_189	NE2	F_GLU_196	OE1	3.808
1FJ1	D_ARG_47	NH1	C_ASP_1	OD1	3.296
1FJ1	D_ARG_47	NH2	C_ASP_1	OD1	2.800

Table 962: Interfacial 1FJ1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1FRG	L_LYS_213	NZ	H_ASP_354	OD1	3.324
1FRG	H_ARG_316	NH1	L_ASP_97	OD1	2.879
1FRG	H_ARG_316	NH2	L_ASP_97	OD1	3.078
1FRG	H_ARG_316	NH2	P_ASP_5	OD2	2.959
1FRG	H_LYS_322	NZ	L_GLU_61	OE1	2.861
1FRG	H_LYS_322	NZ	L_GLU_61	OE2	3.997
1FRG	H_LYS_432	NZ	L_GLU_129	OE1	3.086
1FRG	H_LYS_432	NZ	L_GLU_129	OE2	3.769

Table 963: Interfacial 1FRG-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1FUJ	A_LYS_187	NZ	B_GLU_97	OE1	3.506
1FUJ	B_ARG_143	NH1	A_ASP_61	OD2	3.455
1FUJ	B_LYS_187	NZ	A_GLU_97	OE1	3.870
1FUJ	C_ARG_143	NH2	D_ASP_61	OD1	3.394
1FUJ	C_ARG_143	NH2	D_ASP_61	OD2	3.428
1FUJ	C_LYS_187	NZ	D_GLU_97	OE2	2.917
1FUJ	D_HIS_147	ND1	C_GLU_97	OE1	3.734
1FUJ	D_LYS_187	NZ	C_GLU_97	OE1	3.930

Table 964: Interfacial 1FUJ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1FVD	A_ARG_18	NH1	C_ASP_70	OD2	3.361
1FVD	B_LYS_216	NZ	A_GLU_123	OE2	3.426
1FVD	C_ARG_18	NH1	A_ASP_70	OD2	3.065
1FVD	D_LYS_216	NZ	C_GLU_123	OE1	2.737

Table 965: Interfacial 1FVD-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1FVE	A_ARG_18	NH1	C_ASP_70	OD1	3.613
1FVE	A_ARG_18	NH1	C_ASP_70	OD2	3.316
1FVE	B_LYS_216	NZ	A_GLU_123	OE2	3.328

Table 966: Interfacial 1FVE-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1G6V	K_ARG_907	NH1	A_GLU_187	OE2	2.962
1G6V	K_ARG_909	NH1	A_GLU_187	OE1	3.909
1G6V	K_ARG_909	NH2	A_GLU_187	OE1	3.477

Table 967: Interfacial 1G6V-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1G7H	A_ARG_96	NH1	B_GLU_98	OE1	2.788
1G7H	A_ARG_96	NH1	B_GLU_98	OE2	3.317
1G7H	A_ARG_96	NH2	B_GLU_98	OE1	3.736
1G7H	A_ARG_96	NH2	B_GLU_98	OE2	2.819

Table 968: Interfacial 1G7H-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1G7I	A_ARG_96	NH1	B_GLU_98	OE1	2.881
1G7I	A_ARG_96	NH1	B_GLU_98	OE2	3.589
1G7I	A_ARG_96	NH2	B_GLU_98	OE1	3.599
1G7I	A_ARG_96	NH2	B_GLU_98	OE2	2.841

Table 969: Interfacial 1G7I-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1G7J	A_ARG_96	NH1	B_GLU_98	OE1	2.834
1G7J	A_ARG_96	NH1	B_GLU_98	OE2	3.535
1G7J	A_ARG_96	NH2	B_GLU_98	OE1	3.524
1G7J	A_ARG_96	NH2	B_GLU_98	OE2	2.694

Table 970: Interfacial 1G7J-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1G7L	A_ARG_96	NH1	B_GLU_98	OE1	2.744
1G7L	A_ARG_96	NH1	B_GLU_98	OE2	3.483
1G7L	A_ARG_96	NH2	B_GLU_98	OE1	3.535
1G7L	A_ARG_96	NH2	B_GLU_98	OE2	2.761

Table 971: Interfacial 1G7L-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1G7M	A_ARG_96	NH1	B_GLU_98	OE1	2.792
1G7M	A_ARG_96	NH1	B_GLU_98	OE2	3.493
1G7M	A_ARG_96	NH2	B_GLU_98	OE1	3.544
1G7M	A_ARG_96	NH2	B_GLU_98	OE2	2.732

Table 972: Interfacial 1G7M-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1G9M	G_ARG_419	NH1	H_GLU_103	OE2	3.773
1G9M	G_ARG_419	NH2	H_GLU_103	OE2	2.762
1G9M	G_ARG_419	NH2	H_GLU_108	OE2	3.794
1G9M	C_LYS_29	NZ	G_ASP_279	OD2	3.077
1G9M	C_ARG_59	NH1	G_ASP_368	OD1	3.576
1G9M	C_ARG_59	NH1	G_ASP_368	OD2	3.197
1G9M	C_ARG_59	NH2	G_ASP_368	OD1	2.550
1G9M	C_ARG_59	NH2	G_ASP_368	OD2	3.360

Table 973: Interfacial 1G9M-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1G9N	G_ARG_419	NH1	H_GLU_106	OE1	2.930
1G9N	G_ARG_419	NH1	H_GLU_106	OE2	3.665
1G9N	G_ARG_419	NH2	H_GLU_103	OE1	2.300
1G9N	G_ARG_419	NH2	H_GLU_106	OE2	3.990
1G9N	C_LYS_35	NZ	G_ASP_457	OD2	3.608
1G9N	C_ARG_59	NH1	G_ASP_368	OD1	3.032
1G9N	C_ARG_59	NH1	G_ASP_368	OD2	3.045
1G9N	C_ARG_59	NH2	G_ASP_368	OD1	2.609
1G9N	C_ARG_59	NH2	G_ASP_368	OD2	3.355
1G9N	H_LYS_224	NZ	L_GLU_125	OE1	3.507
1G9N	H_LYS_224	NZ	L_GLU_125	OE2	3.538
1G9N	H_LYS_229	NZ	L_ASP_124	OD2	3.557

Table 974: Interfacial 1G9N-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID residue name residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1GC1	G_ARG_419	NH1	H_GLU_106	OE1	2.761
1GC1	G_ARG_419	NH2	H_GLU_106	OE1	2.942
1GC1	G_ARG_419	NH2	H_GLU_108	OE1	3.887
1GC1	G_ARG_419	NH2	H_GLU_108	OE2	3.401
1GC1	C_LYS_29	NZ	G_ASP_279	OD1	2.748
1GC1	C_ARG_59	NH1	G_ASP_368	OD1	2.780
1GC1	C_ARG_59	NH1	G_ASP_368	OD2	3.645
1GC1	C_ARG_59	NH2	G_ASP_368	OD1	3.062
1GC1	C_ARG_59	NH2	G_ASP_368	OD2	2.481
1GC1	H_LYS_224	NZ	L_GLU_125	OE1	2.581
1GC1	H_LYS_224	NZ	L_GLU_125	OE2	3.963

Table 975: Interfacial 1GC1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1GGB	H_ARG_58	NH1	L_ASP_94	OD1	3.623
1GGB	H_ARG_58	NH2	L_ASP_94	OD1	2.873
1GGB	H_LYS_221	NZ	L_GLU_123	OE1	2.690
1GGB	H_LYS_221	NZ	L_GLU_123	OE2	3.205

Table 976: Interfacial 1GGB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1GGC	H_ARG_58	NH2	L_ASP_94	OD1	3.221
1GGC	H_LYS_221	NZ	L_GLU_123	OE1	2.942

Table 977: Interfacial 1GGC-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1GGI	H_ARG_58	NH2	L_ASP_94	OD2	3.749
1GGI	H_LYS_221	NZ	L_GLU_123	OE2	3.900
1GGI	P_LYS_312	NZ	H_ASP_54	OD1	2.914
1GGI	P_LYS_312	NZ	H_ASP_54	OD2	3.188
1GGI	P_LYS_312	NZ	H_ASP_56	OD1	2.830
1GGI	P_LYS_312	NZ	H_ASP_56	OD2	3.728
1GGI	J_ARG_58	NH2	M_ASP_94	OD2	3.966
1GGI	J_HIS_172	NE2	M_ASP_167	OD2	3.287
1GGI	J_LYS_221	NZ	M_GLU_123	OE1	3.528
1GGI	J_LYS_221	NZ	M_GLU_123	OE2	3.781
1GGI	Q_LYS_312	NZ	J_ASP_54	OD1	3.299
1GGI	Q_LYS_312	NZ	J_ASP_54	OD2	2.967
1GGI	Q_LYS_312	NZ	J_ASP_56	OD1	3.964
1GGI	Q_LYS_312	NZ	J_ASP_56	OD2	3.120

Table 978: Interfacial 1GGI-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1GPO	L_LYS_54	NZ	H_ASP_101	OD1	2.768
1GPO	L_LYS_54	NZ	H_ASP_101	OD2	3.525
1GPO	H_LYS_208	NZ	L_GLU_128	OE2	3.848
1GPO	M_LYS_54	NZ	L_ASP_101	OD1	3.704
1GPO	I_LYS_208	NZ	M_GLU_128	OE2	3.367

Table 979: Interfacial 1GPO-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1HEZ	A_ARG_24	NH1	C_ASP_70	OD1	3.567
1HEZ	A_ARG_24	NH1	C_ASP_70	OD2	3.209
1HEZ	B_LYS_219	NZ	A_GLU_123	OE1	2.923
1HEZ	B_LYS_219	NZ	A_GLU_123	OE2	2.722
1HEZ	C_ARG_24	NH1	E_ASP_855	OD1	2.717
1HEZ	C_LYS_107	NZ	E_ASP_867	OD1	2.620

Table 980: Interfacial 1HEZ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1HGD	A_LYS_27	NZ	B_GLU_97	OE1	2.787
1HGD	A_LYS_27	NZ	B_GLU_97	OE2	2.801
1HGD	A_ARG_109	NH2	B_GLU_67	OE1	3.474
1HGD	A_ARG_109	NH2	B_GLU_67	OE2	2.826
1HGD	A_LYS_238	NZ	F_GLU_72	OE1	2.925
1HGD	A_LYS_238	NZ	F_GLU_72	OE2	2.815
1HGD	A_ARG_269	NH1	B_GLU_67	OE1	2.758
1HGD	A_ARG_269	NH2	B_GLU_67	OE1	3.754
1HGD	A_LYS_299	NZ	B_GLU_69	OE2	2.769
1HGD	A_LYS_310	NZ	B_ASP_86	OD1	2.861
1HGD	A_LYS_310	NZ	B_ASP_90	OD1	2.569
1HGD	A_LYS_326	NZ	B_GLU_15	OE1	3.037
1HGD	A_LYS_326	NZ	B_GLU_15	OE2	2.743
1HGD	B_ARG_25	NH1	A_GLU_325	OE2	3.743
1HGD	B_ARG_25	NH2	A_GLU_325	OE2	3.016
1HGD	B_ARG_54	NH1	F_GLU_97	OE2	3.275
1HGD	B_ARG_54	NH2	F_GLU_97	OE2	2.774
1HGD	B_LYS_62	NZ	F_ASP_86	OD1	2.852
1HGD	B_LYS_62	NZ	F_ASP_86	OD2	2.612
1HGD	B_LYS_62	NZ	F_ASP_90	OD1	3.620
1HGD	B_LYS_62	NZ	F_ASP_90	OD2	2.727
1HGD	B_ARG_76	NH1	D_GLU_74	OE1	3.558
1HGD	B_ARG_76	NH1	D_GLU_74	OE2	2.838
1HGD	B_ARG_76	NH2	D_GLU_74	OE1	2.751
1HGD	B_ARG_76	NH2	D_GLU_74	OE2	3.529
1HGD	B_ARG_76	NH2	D_GLU_81	OE1	2.707
1HGD	B_ARG_76	NH2	D_GLU_81	OE2	3.498
1HGD	B_ARG_123	NH2	F_GLU_132	OE1	3.169
1HGD	B_ARG_124	NH2	F_GLU_132	OE1	3.011
1HGD	B_ARG_124	NH2	F_GLU_132	OE2	3.294
1HGD	B_ARG_127	NH1	F_GLU_131	OE1	2.471
1HGD	B_ARG_163	NH2	F_GLU_131	OE1	2.583
1HGD	B_ARG_163	NH2	F_GLU_131	OE2	2.596
1HGD	B_ARG_170	NH1	D_GLU_128	OE1	3.354
1HGD	B_ARG_170	NH1	D_GLU_128	OE2	3.628
1HGD	B_LYS_174	NZ	D_ASP_164	OD1	2.787
1HGD	B_LYS_174	NZ	D_ASP_164	OD2	2.517
1HGD	C_LYS_27	NZ	D_GLU_97	OE1	2.760
1HGD	C_LYS_27	NZ	D_GLU_97	OE2	2.799
1HGD	C_ARG_109	NH2	D_GLU_67	OE1	3.480
1HGD	C_ARG_109	NH2	D_GLU_67	OE2	2.867
1HGD	C_LYS_238	NZ	B_GLU_72	OE1	2.801
1HGD	C_LYS_238	NZ	B_GLU_72	OE2	2.746
1HGD	C_ARG_269	NH1	D_GLU_67	OE1	2.720
1HGD	C_ARG_269	NH2	D_GLU_67	OE1	3.733
1HGD	C_LYS_299	NZ	D_GLU_69	OE2	2.796
1HGD	C_LYS_310	NZ	D_ASP_86	OD1	2.878
1HGD	C_LYS_310	NZ	D_ASP_90	OD1	2.526
1HGD	C_LYS_326	NZ	D_GLU_15	OE1	2.784
1HGD	C_LYS_326	NZ	D_GLU_15	OE2	3.881
1HGD	D_ARG_54	NH1	B_GLU_97	OE2	3.293
1HGD	D_ARG_54	NH2	B_GLU_97	OE2	2.793
1HGD	D_LYS_62	NZ	B_ASP_86	OD1	2.884
1HGD	D_LYS_62	NZ	B_ASP_86	OD2	2.567
1HGD	D_LYS_62	NZ	B_ASP_90	OD1	3.576
1HGD	D_LYS_62	NZ	B_ASP_90	OD2	2.617
1HGD	D_ARG_76	NH1	F_GLU_74	OE1	3.379

1HGD	D_ARG_76	NH1	F_GLU_74	OE2	2.785
1HGD	D_ARG_76	NH2	F_GLU_74	OE1	2.687
1HGD	D_ARG_76	NH2	F_GLU_74	OE2	3.593
1HGD	D_ARG_76	NH2	F_GLU_81	OE1	2.649
1HGD	D_ARG_76	NH2	F_GLU_81	OE2	3.537
1HGD	D_ARG_123	NH2	B_GLU_132	OE1	3.120
1HGD	D_ARG_124	NH2	B_GLU_132	OE1	2.998
1HGD	D_ARG_124	NH2	B_GLU_132	OE2	3.261
1HGD	D_ARG_127	NH1	B_GLU_131	OE1	2.513
1HGD	D_ARG_163	NH2	B_GLU_131	OE1	2.583
1HGD	D_ARG_163	NH2	B_GLU_131	OE2	2.616
1HGD	D_ARG_170	NH1	F_GLU_128	OE1	3.487
1HGD	D_ARG_170	NH1	F_GLU_128	OE2	3.741
1HGD	D_LYS_174	NZ	F_ASP_164	OD1	2.806
1HGD	D_LYS_174	NZ	F_ASP_164	OD2	2.686
1HGD	E_LYS_27	NZ	F_GLU_97	OE1	2.794
1HGD	E_LYS_27	NZ	F_GLU_97	OE2	2.792
1HGD	E_ARG_109	NH2	F_GLU_67	OE1	3.474
1HGD	E_ARG_109	NH2	F_GLU_67	OE2	2.818
1HGD	E_LYS_238	NZ	D_GLU_72	OE1	2.872
1HGD	E_LYS_238	NZ	D_GLU_72	OE2	2.843
1HGD	E_ARG_269	NH1	F_GLU_67	OE1	2.732
1HGD	E_ARG_269	NH2	F_GLU_67	OE1	3.760
1HGD	E_LYS_299	NZ	F_GLU_69	OE2	2.767
1HGD	E_LYS_310	NZ	F_ASP_86	OD1	2.884
1HGD	E_LYS_310	NZ	F_ASP_90	OD1	2.533
1HGD	E_LYS_326	NZ	F_GLU_15	OE1	2.967
1HGD	E_LYS_326	NZ	F_GLU_15	OE2	3.203
1HGD	F_ARG_54	NH1	D_GLU_97	OE2	3.306
1HGD	F_ARG_54	NH2	D_GLU_97	OE2	2.719
1HGD	F_LYS_62	NZ	D_ASP_86	OD1	2.854
1HGD	F_LYS_62	NZ	D_ASP_86	OD2	2.590
1HGD	F_LYS_62	NZ	D_ASP_90	OD1	3.656
1HGD	F_LYS_62	NZ	D_ASP_90	OD2	2.713
1HGD	F_HIS_64	NE2	D_ASP_79	OD2	3.996
1HGD	F_ARG_76	NH1	B_GLU_74	OE1	3.419
1HGD	F_ARG_76	NH1	B_GLU_74	OE2	2.766
1HGD	F_ARG_76	NH2	B_GLU_74	OE1	2.711
1HGD	F_ARG_76	NH2	B_GLU_74	OE2	3.568
1HGD	F_ARG_76	NH2	B_GLU_81	OE1	2.637
1HGD	F_ARG_76	NH2	B_GLU_81	OE2	3.557
1HGD	F_ARG_123	NH2	D_GLU_132	OE1	3.156
1HGD	F_ARG_124	NH2	D_GLU_132	OE1	3.098
1HGD	F_ARG_124	NH2	D_GLU_132	OE2	3.292
1HGD	F_ARG_127	NH1	D_GLU_131	OE1	2.558
1HGD	F_ARG_163	NH2	D_GLU_131	OE1	2.583
1HGD	F_ARG_163	NH2	D_GLU_131	OE2	2.699
1HGD	F_ARG_170	NH1	B_GLU_128	OE1	3.398
1HGD	F_ARG_170	NH1	B_GLU_128	OE2	3.736
1HGD	F_LYS_174	NZ	B_ASP_164	OD1	2.545
1HGD	F_LYS_174	NZ	B_ASP_164	OD2	2.838

Table 981: Interfacial 1HGD-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1HGE	A_LYS_27	NZ	B_GLU_97	OE1	2.881
1HGE	A_LYS_27	NZ	B_GLU_97	OE2	2.803
1HGE	A_ARG_109	NH2	B_GLU_67	OE1	3.666
1HGE	A_ARG_109	NH2	B_GLU_67	OE2	2.737
1HGE	A_LYS_238	NZ	F_GLU_72	OE1	2.915
1HGE	A_LYS_238	NZ	F_GLU_72	OE2	2.732
1HGE	A_ARG_269	NH1	B_GLU_67	OE1	2.727
1HGE	A_ARG_269	NH2	B_GLU_67	OE1	3.813
1HGE	A_LYS_299	NZ	B_GLU_69	OE2	2.765
1HGE	A_LYS_310	NZ	B_ASP_86	OD1	2.860
1HGE	A_LYS_310	NZ	B_ASP_90	OD1	2.586
1HGE	A_LYS_310	NZ	B_ASP_90	OD2	3.982
1HGE	A_LYS_326	NZ	B_GLU_15	OE1	3.112
1HGE	A_LYS_326	NZ	B_GLU_15	OE2	2.788
1HGE	B_ARG_25	NH1	A_GLU_325	OE2	3.901
1HGE	B_ARG_25	NH2	A_GLU_325	OE2	3.058
1HGE	B_ARG_54	NH1	F_GLU_97	OE2	3.352
1HGE	B_ARG_54	NH2	F_GLU_97	OE2	2.840
1HGE	B_LYS_62	NZ	F_ASP_86	OD1	2.965
1HGE	B_LYS_62	NZ	F_ASP_86	OD2	2.602
1HGE	B_LYS_62	NZ	F_ASP_90	OD1	3.562
1HGE	B_LYS_62	NZ	F_ASP_90	OD2	2.691
1HGE	B_ARG_76	NH1	D_GLU_74	OE1	3.487
1HGE	B_ARG_76	NH1	D_GLU_74	OE2	2.838
1HGE	B_ARG_76	NH2	D_GLU_74	OE1	2.788
1HGE	B_ARG_76	NH2	D_GLU_74	OE2	3.585
1HGE	B_ARG_76	NH2	D_GLU_81	OE1	2.698
1HGE	B_ARG_76	NH2	D_GLU_81	OE2	3.486
1HGE	B_ARG_123	NH2	F_GLU_132	OE1	3.159
1HGE	B_ARG_124	NH2	F_GLU_132	OE1	3.028
1HGE	B_ARG_124	NH2	F_GLU_132	OE2	3.444
1HGE	B_ARG_127	NH1	F_GLU_131	OE1	2.492
1HGE	B_ARG_163	NH2	F_GLU_131	OE1	2.609
1HGE	B_ARG_163	NH2	F_GLU_131	OE2	2.622
1HGE	B_ARG_170	NH1	D_GLU_128	OE1	3.351
1HGE	B_ARG_170	NH1	D_GLU_128	OE2	3.595
1HGE	B_LYS_174	NZ	D_ASP_164	OD1	2.542
1HGE	B_LYS_174	NZ	D_ASP_164	OD2	2.784
1HGE	C_LYS_27	NZ	D_GLU_97	OE1	2.850
1HGE	C_LYS_27	NZ	D_GLU_97	OE2	2.792
1HGE	C_ARG_109	NH2	D_GLU_67	OE1	3.673
1HGE	C_ARG_109	NH2	D_GLU_67	OE2	2.784
1HGE	C_LYS_238	NZ	B_GLU_72	OE1	2.779
1HGE	C_LYS_238	NZ	B_GLU_72	OE2	2.668
1HGE	C_ARG_269	NH1	D_GLU_67	OE1	2.720
1HGE	C_ARG_269	NH2	D_GLU_67	OE1	3.811
1HGE	C_LYS_299	NZ	D_GLU_69	OE2	2.808
1HGE	C_LYS_310	NZ	D_ASP_86	OD1	2.890
1HGE	C_LYS_310	NZ	D_ASP_90	OD1	2.566
1HGE	C_LYS_310	NZ	D_ASP_90	OD2	3.955
1HGE	C_LYS_326	NZ	D_GLU_15	OE1	2.739
1HGE	C_LYS_326	NZ	D_GLU_15	OE2	3.731
1HGE	D_ARG_54	NH1	B_GLU_97	OE2	3.383
1HGE	D_ARG_54	NH2	B_GLU_97	OE2	2.866
1HGE	D_LYS_62	NZ	B_ASP_86	OD1	3.023
1HGE	D_LYS_62	NZ	B_ASP_86	OD2	2.550
1HGE	D_LYS_62	NZ	B_ASP_90	OD1	3.565

1HGE	D_LYS_62	NZ	B_ASP_90	OD2	2.627
1HGE	D_ARG_76	NH1	F_GLU_74	OE1	3.355
1HGE	D_ARG_76	NH1	F_GLU_74	OE2	2.783
1HGE	D_ARG_76	NH2	F_GLU_74	OE1	2.745
1HGE	D_ARG_76	NH2	F_GLU_74	OE2	3.636
1HGE	D_ARG_76	NH2	F_GLU_81	OE1	2.634
1HGE	D_ARG_76	NH2	F_GLU_81	OE2	3.497
1HGE	D_ARG_123	NH2	B_GLU_132	OE1	3.118
1HGE	D_ARG_124	NH2	B_GLU_132	OE1	3.002
1HGE	D_ARG_124	NH2	B_GLU_132	OE2	3.417
1HGE	D_ARG_127	NH1	B_GLU_131	OE1	2.524
1HGE	D_ARG_163	NH2	B_GLU_131	OE1	2.587
1HGE	D_ARG_163	NH2	B_GLU_131	OE2	2.600
1HGE	D_ARG_170	NH1	F_GLU_128	OE1	3.477
1HGE	D_ARG_170	NH1	F_GLU_128	OE2	3.701
1HGE	D_LYS_174	NZ	F_ASP_164	OD1	2.678
1HGE	D_LYS_174	NZ	F_ASP_164	OD2	2.785
1HGE	E_LYS_27	NZ	F_GLU_97	OE1	2.844
1HGE	E_LYS_27	NZ	F_GLU_97	OE2	2.791
1HGE	E_ARG_109	NH2	F_GLU_67	OE1	3.658
1HGE	E_ARG_109	NH2	F_GLU_67	OE2	2.776
1HGE	E_LYS_238	NZ	D_GLU_72	OE1	2.851
1HGE	E_LYS_238	NZ	D_GLU_72	OE2	2.740
1HGE	E_ARG_269	NH1	F_GLU_67	OE1	2.696
1HGE	E_ARG_269	NH2	F_GLU_67	OE1	3.784
1HGE	E_LYS_299	NZ	F_GLU_69	OE2	2.768
1HGE	E_LYS_310	NZ	F_ASP_86	OD1	2.863
1HGE	E_LYS_310	NZ	F_ASP_90	OD1	2.577
1HGE	E_LYS_310	NZ	F_ASP_90	OD2	3.952
1HGE	E_LYS_326	NZ	F_GLU_15	OE1	2.987
1HGE	E_LYS_326	NZ	F_GLU_15	OE2	3.095
1HGE	F_ARG_54	NH1	D_GLU_97	OE2	3.384
1HGE	F_ARG_54	NH2	D_GLU_97	OE2	2.800
1HGE	F_LYS_62	NZ	D_ASP_86	OD1	2.945
1HGE	F_LYS_62	NZ	D_ASP_86	OD2	2.535
1HGE	F_LYS_62	NZ	D_ASP_90	OD1	3.592
1HGE	F_LYS_62	NZ	D_ASP_90	OD2	2.671
1HGE	F_ARG_76	NH1	B_GLU_74	OE1	3.326
1HGE	F_ARG_76	NH1	B_GLU_74	OE2	2.732
1HGE	F_ARG_76	NH2	B_GLU_74	OE1	2.705
1HGE	F_ARG_76	NH2	B_GLU_74	OE2	3.590
1HGE	F_ARG_76	NH2	B_GLU_81	OE1	2.650
1HGE	F_ARG_76	NH2	B_GLU_81	OE2	3.592
1HGE	F_ARG_123	NH2	D_GLU_132	OE1	3.161
1HGE	F_ARG_124	NH2	D_GLU_132	OE1	3.085
1HGE	F_ARG_124	NH2	D_GLU_132	OE2	3.468
1HGE	F_ARG_127	NH1	D_GLU_131	OE1	2.578
1HGE	F_ARG_163	NH2	D_GLU_131	OE1	2.628
1HGE	F_ARG_163	NH2	D_GLU_131	OE2	2.698
1HGE	F_ARG_170	NH1	B_GLU_128	OE1	3.389
1HGE	F_ARG_170	NH1	B_GLU_128	OE2	3.679
1HGE	F_LYS_174	NZ	B_ASP_164	OD1	2.537
1HGE	F_LYS_174	NZ	B_ASP_164	OD2	2.796

Table 982: Interfacial 1HGE-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1HGF	A_LYS_27	NZ	B_GLU_97	OE1	2.809
1HGF	A_LYS_27	NZ	B_GLU_97	OE2	2.791
1HGF	A_ARG_109	NH2	B_GLU_67	OE1	3.699
1HGF	A_ARG_109	NH2	B_GLU_67	OE2	2.917
1HGF	A_LYS_238	NZ	F_GLU_72	OE1	2.852
1HGF	A_LYS_238	NZ	F_GLU_72	OE2	2.778
1HGF	A_ARG_269	NH1	B_GLU_67	OE1	2.939
1HGF	A_LYS_299	NZ	B_GLU_69	OE2	3.681
1HGF	A_LYS_310	NZ	B_ASP_86	OD1	2.820
1HGF	A_LYS_310	NZ	B_ASP_90	OD1	2.555
1HGF	A_LYS_310	NZ	B_ASP_90	OD2	3.978
1HGF	A_LYS_326	NZ	B_GLU_15	OE1	3.851
1HGF	A_LYS_326	NZ	B_GLU_15	OE2	3.863
1HGF	B_ARG_25	NH1	A_GLU_325	OE2	3.563
1HGF	B_ARG_25	NH2	A_GLU_325	OE2	2.989
1HGF	B_ARG_54	NH1	F_GLU_97	OE2	3.282
1HGF	B_ARG_54	NH2	F_GLU_97	OE2	2.831
1HGF	B_LYS_62	NZ	F_ASP_86	OD1	3.116
1HGF	B_LYS_62	NZ	F_ASP_86	OD2	2.708
1HGF	B_LYS_62	NZ	F_ASP_90	OD1	3.733
1HGF	B_LYS_62	NZ	F_ASP_90	OD2	2.767
1HGF	B_ARG_76	NH1	D_GLU_74	OE1	2.859
1HGF	B_ARG_76	NH1	D_GLU_74	OE2	3.561
1HGF	B_ARG_76	NH2	D_GLU_74	OE1	3.524
1HGF	B_ARG_76	NH2	D_GLU_74	OE2	2.746
1HGF	B_ARG_76	NH2	D_GLU_81	OE1	2.726
1HGF	B_ARG_76	NH2	D_GLU_81	OE2	3.662
1HGF	B_ARG_123	NH2	F_GLU_132	OE1	3.495
1HGF	B_ARG_124	NH2	F_GLU_132	OE1	3.111
1HGF	B_ARG_124	NH2	F_GLU_132	OE2	3.495
1HGF	B_ARG_127	NH1	F_GLU_131	OE1	2.468
1HGF	B_ARG_163	NH2	F_GLU_131	OE1	2.740
1HGF	B_ARG_163	NH2	F_GLU_131	OE2	2.533
1HGF	B_ARG_170	NH1	D_GLU_128	OE1	3.455
1HGF	B_ARG_170	NH1	D_GLU_128	OE2	3.294
1HGF	B_LYS_174	NZ	D_ASP_164	OD2	3.813
1HGF	C_LYS_27	NZ	D_GLU_97	OE1	2.824
1HGF	C_LYS_27	NZ	D_GLU_97	OE2	2.808
1HGF	C_ARG_109	NH2	D_GLU_67	OE1	3.698
1HGF	C_ARG_109	NH2	D_GLU_67	OE2	2.914
1HGF	C_LYS_238	NZ	B_GLU_72	OE1	2.746
1HGF	C_LYS_238	NZ	B_GLU_72	OE2	2.727
1HGF	C_ARG_269	NH1	D_GLU_67	OE1	2.900
1HGF	C_LYS_299	NZ	D_GLU_69	OE2	3.732
1HGF	C_LYS_310	NZ	D_ASP_86	OD1	2.839
1HGF	C_LYS_310	NZ	D_ASP_90	OD1	2.507
1HGF	C_LYS_310	NZ	D_ASP_90	OD2	3.941
1HGF	C_LYS_326	NZ	D_GLU_15	OE1	3.713
1HGF	D_ARG_54	NH1	B_GLU_97	OE2	3.314
1HGF	D_ARG_54	NH2	B_GLU_97	OE2	2.840
1HGF	D_LYS_62	NZ	B_ASP_86	OD1	3.122
1HGF	D_LYS_62	NZ	B_ASP_86	OD2	2.686
1HGF	D_LYS_62	NZ	B_ASP_90	OD1	3.703
1HGF	D_LYS_62	NZ	B_ASP_90	OD2	2.682
1HGF	D_ARG_76	NH1	F_GLU_74	OE1	2.790
1HGF	D_ARG_76	NH1	F_GLU_74	OE2	3.379
1HGF	D_ARG_76	NH2	F_GLU_74	OE1	3.594

1HGF	D_ARG_76	NH2	F_GLU_74	OE2	2.697
1HGF	D_ARG_76	NH2	F_GLU_81	OE1	2.644
1HGF	D_ARG_76	NH2	F_GLU_81	OE2	3.691
1HGF	D_ARG_123	NH2	B_GLU_132	OE1	3.407
1HGF	D_ARG_124	NH2	B_GLU_132	OE1	3.100
1HGF	D_ARG_124	NH2	B_GLU_132	OE2	3.442
1HGF	D_ARG_127	NH1	B_GLU_131	OE1	2.516
1HGF	D_ARG_163	NH2	B_GLU_131	OE1	2.704
1HGF	D_ARG_163	NH2	B_GLU_131	OE2	2.556
1HGF	D_ARG_170	NH1	F_GLU_128	OE1	3.604
1HGF	D_ARG_170	NH1	F_GLU_128	OE2	3.428
1HGF	E_LYS_27	NZ	F_GLU_97	OE1	2.793
1HGF	E_LYS_27	NZ	F_GLU_97	OE2	2.754
1HGF	E_ARG_109	NH2	F_GLU_67	OE1	3.694
1HGF	E_ARG_109	NH2	F_GLU_67	OE2	2.878
1HGF	E_LYS_238	NZ	D_GLU_72	OE1	2.831
1HGF	E_LYS_238	NZ	D_GLU_72	OE2	2.834
1HGF	E_ARG_269	NH1	F_GLU_67	OE1	2.906
1HGF	E_LYS_299	NZ	F_GLU_69	OE2	3.655
1HGF	E_LYS_310	NZ	F_ASP_86	OD1	2.832
1HGF	E_LYS_310	NZ	F_ASP_90	OD1	2.514
1HGF	E_LYS_310	NZ	F_ASP_90	OD2	3.973
1HGF	E_LYS_326	NZ	F_GLU_15	OE1	3.652
1HGF	E_LYS_326	NZ	F_GLU_15	OE2	3.771
1HGF	F_ARG_54	NH1	D_GLU_97	OE2	3.368
1HGF	F_ARG_54	NH2	D_GLU_97	OE2	2.791
1HGF	F_LYS_62	NZ	D_ASP_86	OD1	3.076
1HGF	F_LYS_62	NZ	D_ASP_86	OD2	2.672
1HGF	F_LYS_62	NZ	D_ASP_90	OD1	3.773
1HGF	F_LYS_62	NZ	D_ASP_90	OD2	2.752
1HGF	F_ARG_76	NH1	B_GLU_74	OE1	2.779
1HGF	F_ARG_76	NH1	B_GLU_74	OE2	3.420
1HGF	F_ARG_76	NH2	B_GLU_74	OE1	3.542
1HGF	F_ARG_76	NH2	B_GLU_74	OE2	2.707
1HGF	F_ARG_76	NH2	B_GLU_81	OE1	2.689
1HGF	F_ARG_76	NH2	B_GLU_81	OE2	3.716
1HGF	F_ARG_123	NH2	D_GLU_132	OE1	3.469
1HGF	F_ARG_124	NH2	D_GLU_132	OE1	3.198
1HGF	F_ARG_124	NH2	D_GLU_132	OE2	3.522
1HGF	F_ARG_127	NH1	D_GLU_131	OE1	2.568
1HGF	F_ARG_163	NH2	D_GLU_131	OE1	2.689
1HGF	F_ARG_163	NH2	D_GLU_131	OE2	2.644
1HGF	F_ARG_170	NH1	B_GLU_128	OE1	3.432
1HGF	F_ARG_170	NH1	B_GLU_128	OE2	3.366
1HGF	F_LYS_174	NZ	B_ASP_164	OD2	3.837

Table 983: Interfacial 1HGF-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1HGG	A_LYS_27	NZ	B_GLU_97	OE1	2.679
1HGG	A_LYS_27	NZ	B_GLU_97	OE2	2.904
1HGG	A_ARG_109	NH2	B_GLU_67	OE1	3.854
1HGG	A_ARG_109	NH2	B_GLU_67	OE2	2.838
1HGG	A_LYS_238	NZ	F_GLU_72	OE1	2.931
1HGG	A_LYS_238	NZ	F_GLU_72	OE2	2.744
1HGG	A_ARG_269	NH1	B_GLU_67	OE1	2.694
1HGG	A_ARG_269	NH2	B_GLU_67	OE1	3.814
1HGG	A_LYS_299	NZ	B_GLU_69	OE2	2.915
1HGG	A_LYS_310	NZ	B_ASP_86	OD1	2.852
1HGG	A_LYS_310	NZ	B_ASP_90	OD1	2.700
1HGG	A_LYS_310	NZ	B_ASP_90	OD2	3.923
1HGG	A_LYS_326	NZ	B_GLU_15	OE1	3.039
1HGG	A_LYS_326	NZ	B_GLU_15	OE2	2.830
1HGG	B_ARG_25	NH1	A_GLU_325	OE2	3.770
1HGG	B_ARG_25	NH2	A_GLU_325	OE2	2.944
1HGG	B_ARG_54	NH1	F_GLU_97	OE2	3.410
1HGG	B_ARG_54	NH2	F_GLU_97	OE2	2.750
1HGG	B_LYS_62	NZ	F_ASP_86	OD1	2.889
1HGG	B_LYS_62	NZ	F_ASP_86	OD2	2.639
1HGG	B_LYS_62	NZ	F_ASP_90	OD1	3.716
1HGG	B_LYS_62	NZ	F_ASP_90	OD2	2.650
1HGG	B_ARG_76	NH1	D_GLU_74	OE1	2.882
1HGG	B_ARG_76	NH1	D_GLU_74	OE2	3.580
1HGG	B_ARG_76	NH2	D_GLU_74	OE1	3.459
1HGG	B_ARG_76	NH2	D_GLU_74	OE2	2.820
1HGG	B_ARG_76	NH2	D_GLU_81	OE1	2.731
1HGG	B_ARG_76	NH2	D_GLU_81	OE2	3.473
1HGG	B_ARG_123	NH2	F_GLU_132	OE1	2.827
1HGG	B_ARG_124	NH2	F_GLU_132	OE1	3.221
1HGG	B_ARG_124	NH2	F_GLU_132	OE2	3.297
1HGG	B_ARG_127	NH1	F_GLU_131	OE1	2.465
1HGG	B_ARG_163	NH2	F_GLU_131	OE1	2.594
1HGG	B_ARG_163	NH2	F_GLU_131	OE2	2.562
1HGG	B_ARG_170	NH1	D_GLU_128	OE1	3.236
1HGG	B_ARG_170	NH1	D_GLU_128	OE2	3.289
1HGG	B_LYS_174	NZ	D_ASP_164	OD1	2.736
1HGG	B_LYS_174	NZ	D_ASP_164	OD2	2.575
1HGG	C_LYS_27	NZ	D_GLU_97	OE1	2.683
1HGG	C_LYS_27	NZ	D_GLU_97	OE2	2.941
1HGG	C_ARG_109	NH2	D_GLU_67	OE1	3.869
1HGG	C_ARG_109	NH2	D_GLU_67	OE2	2.853
1HGG	C_LYS_238	NZ	B_GLU_72	OE1	2.830
1HGG	C_LYS_238	NZ	B_GLU_72	OE2	2.699
1HGG	C_ARG_269	NH1	D_GLU_67	OE1	2.688
1HGG	C_ARG_269	NH2	D_GLU_67	OE1	3.820
1HGG	C_LYS_299	NZ	D_GLU_69	OE2	2.932
1HGG	C_LYS_310	NZ	D_ASP_86	OD1	2.859
1HGG	C_LYS_310	NZ	D_ASP_90	OD1	2.651
1HGG	C_LYS_310	NZ	D_ASP_90	OD2	3.858
1HGG	C_LYS_326	NZ	D_GLU_15	OE1	2.591
1HGG	C_LYS_326	NZ	D_GLU_15	OE2	3.450
1HGG	D_ARG_54	NH1	B_GLU_97	OE2	3.442
1HGG	D_ARG_54	NH2	B_GLU_97	OE2	2.764
1HGG	D_LYS_62	NZ	B_ASP_86	OD1	2.924
1HGG	D_LYS_62	NZ	B_ASP_86	OD2	2.567
1HGG	D_LYS_62	NZ	B_ASP_90	OD1	3.695

1HGG	D_LYS_62	NZ	B_ASP_90	OD2	2.575
1HGG	D_ARG_76	NH1	F_GLU_74	OE1	2.783
1HGG	D_ARG_76	NH1	F_GLU_74	OE2	3.379
1HGG	D_ARG_76	NH2	F_GLU_74	OE1	3.480
1HGG	D_ARG_76	NH2	F_GLU_74	OE2	2.737
1HGG	D_ARG_76	NH2	F_GLU_81	OE1	2.674
1HGG	D_ARG_76	NH2	F_GLU_81	OE2	3.521
1HGG	D_ARG_123	NH2	B_GLU_132	OE1	2.793
1HGG	D_ARG_124	NH2	B_GLU_132	OE1	3.241
1HGG	D_ARG_124	NH2	B_GLU_132	OE2	3.297
1HGG	D_ARG_127	NH1	B_GLU_131	OE1	2.475
1HGG	D_ARG_163	NH2	B_GLU_131	OE1	2.580
1HGG	D_ARG_163	NH2	B_GLU_131	OE2	2.598
1HGG	D_ARG_170	NH1	F_GLU_128	OE1	3.365
1HGG	D_ARG_170	NH1	F_GLU_128	OE2	3.390
1HGG	D_LYS_174	NZ	F_ASP_164	OD1	2.763
1HGG	D_LYS_174	NZ	F_ASP_164	OD2	2.711
1HGG	E_LYS_27	NZ	F_GLU_97	OE1	2.689
1HGG	E_LYS_27	NZ	F_GLU_97	OE2	2.909
1HGG	E_ARG_109	NH2	F_GLU_67	OE1	3.891
1HGG	E_ARG_109	NH2	F_GLU_67	OE2	2.876
1HGG	E_LYS_238	NZ	D_GLU_72	OE1	2.893
1HGG	E_LYS_238	NZ	D_GLU_72	OE2	2.782
1HGG	E_ARG_269	NH1	F_GLU_67	OE1	2.691
1HGG	E_ARG_269	NH2	F_GLU_67	OE1	3.830
1HGG	E_LYS_299	NZ	F_GLU_69	OE2	2.920
1HGG	E_LYS_310	NZ	F_ASP_86	OD1	2.871
1HGG	E_LYS_310	NZ	F_ASP_90	OD1	2.639
1HGG	E_LYS_310	NZ	F_ASP_90	OD2	3.900
1HGG	E_LYS_326	NZ	F_GLU_15	OE1	2.975
1HGG	E_LYS_326	NZ	F_GLU_15	OE2	3.000
1HGG	F_ARG_54	NH1	D_GLU_97	OE2	3.483
1HGG	F_ARG_54	NH2	D_GLU_97	OE2	2.727
1HGG	F_LYS_62	NZ	D_ASP_86	OD1	2.904
1HGG	F_LYS_62	NZ	D_ASP_86	OD2	2.582
1HGG	F_LYS_62	NZ	D_ASP_90	OD1	3.752
1HGG	F_LYS_62	NZ	D_ASP_90	OD2	2.595
1HGG	F_ARG_76	NH1	B_GLU_74	OE1	2.750
1HGG	F_ARG_76	NH1	B_GLU_74	OE2	3.432
1HGG	F_ARG_76	NH2	B_GLU_74	OE1	3.456
1HGG	F_ARG_76	NH2	B_GLU_74	OE2	2.786
1HGG	F_ARG_76	NH2	B_GLU_81	OE1	2.674
1HGG	F_ARG_76	NH2	B_GLU_81	OE2	3.545
1HGG	F_ARG_123	NH2	D_GLU_132	OE1	2.843
1HGG	F_ARG_124	NH2	D_GLU_132	OE1	3.317
1HGG	F_ARG_124	NH2	D_GLU_132	OE2	3.342
1HGG	F_ARG_127	NH1	D_GLU_131	OE1	2.523
1HGG	F_ARG_163	NH2	D_GLU_131	OE1	2.589
1HGG	F_ARG_163	NH2	D_GLU_131	OE2	2.640
1HGG	F_ARG_170	NH1	B_GLU_128	OE1	3.237
1HGG	F_ARG_170	NH1	B_GLU_128	OE2	3.354
1HGG	F_LYS_174	NZ	B_ASP_164	OD1	2.757
1HGG	F_LYS_174	NZ	B_ASP_164	OD2	2.547

Table 984: Interfacial 1HGG-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1HGH	A_LYS_27	NZ	B_GLU_97	OE1	2.856
1HGH	A_LYS_27	NZ	B_GLU_97	OE2	2.781
1HGH	A_ARG_109	NH2	B_GLU_67	OE1	3.697
1HGH	A_ARG_109	NH2	B_GLU_67	OE2	2.864
1HGH	A_LYS_238	NZ	F_GLU_72	OE1	2.921
1HGH	A_LYS_238	NZ	F_GLU_72	OE2	2.736
1HGH	A_ARG_269	NH1	B_GLU_67	OE1	2.720
1HGH	A_ARG_269	NH2	B_GLU_67	OE1	3.718
1HGH	A_LYS_299	NZ	B_GLU_69	OE2	2.918
1HGH	A_LYS_310	NZ	B_ASP_86	OD1	2.712
1HGH	A_LYS_310	NZ	B_ASP_90	OD1	2.578
1HGH	A_LYS_310	NZ	B_ASP_90	OD2	3.975
1HGH	A_LYS_326	NZ	B_GLU_15	OE1	3.092
1HGH	A_LYS_326	NZ	B_GLU_15	OE2	2.707
1HGH	B_ARG_25	NH1	A_GLU_325	OE2	3.971
1HGH	B_ARG_25	NH2	A_GLU_325	OE2	3.017
1HGH	B_ARG_54	NH1	F_GLU_97	OE2	3.285
1HGH	B_ARG_54	NH2	F_GLU_97	OE2	2.823
1HGH	B_LYS_62	NZ	F_ASP_86	OD1	3.064
1HGH	B_LYS_62	NZ	F_ASP_86	OD2	2.661
1HGH	B_LYS_62	NZ	F_ASP_90	OD1	3.547
1HGH	B_LYS_62	NZ	F_ASP_90	OD2	2.683
1HGH	B_ARG_76	NH1	D_GLU_74	OE1	3.707
1HGH	B_ARG_76	NH1	D_GLU_74	OE2	2.912
1HGH	B_ARG_76	NH2	D_GLU_74	OE1	2.889
1HGH	B_ARG_76	NH2	D_GLU_74	OE2	3.526
1HGH	B_ARG_76	NH2	D_GLU_81	OE1	2.765
1HGH	B_ARG_76	NH2	D_GLU_81	OE2	3.411
1HGH	B_ARG_123	NH2	F_GLU_132	OE1	3.134
1HGH	B_ARG_124	NH2	F_GLU_132	OE1	3.005
1HGH	B_ARG_124	NH2	F_GLU_132	OE2	3.302
1HGH	B_ARG_127	NH1	F_GLU_131	OE1	2.524
1HGH	B_ARG_163	NH2	F_GLU_131	OE1	2.607
1HGH	B_ARG_163	NH2	F_GLU_131	OE2	2.538
1HGH	B_ARG_170	NH1	D_GLU_128	OE1	3.253
1HGH	B_ARG_170	NH1	D_GLU_128	OE2	3.577
1HGH	B_LYS_174	NZ	D_ASP_164	OD1	2.767
1HGH	B_LYS_174	NZ	D_ASP_164	OD2	2.573
1HGH	C_LYS_27	NZ	D_GLU_97	OE1	2.897
1HGH	C_LYS_27	NZ	D_GLU_97	OE2	2.815
1HGH	C_ARG_109	NH2	D_GLU_67	OE1	3.686
1HGH	C_ARG_109	NH2	D_GLU_67	OE2	2.856
1HGH	C_LYS_238	NZ	B_GLU_72	OE1	2.713
1HGH	C_LYS_238	NZ	B_GLU_72	OE2	2.597
1HGH	C_ARG_269	NH1	D_GLU_67	OE1	2.732
1HGH	C_ARG_269	NH2	D_GLU_67	OE1	3.725
1HGH	C_LYS_299	NZ	D_GLU_69	OE2	2.939
1HGH	C_LYS_310	NZ	D_ASP_86	OD1	2.734
1HGH	C_LYS_310	NZ	D_ASP_90	OD1	2.551
1HGH	C_LYS_310	NZ	D_ASP_90	OD2	3.913
1HGH	C_LYS_326	NZ	D_GLU_15	OE1	2.774
1HGH	C_LYS_326	NZ	D_GLU_15	OE2	3.676
1HGH	D_ARG_54	NH1	B_GLU_97	OE2	3.277
1HGH	D_ARG_54	NH2	B_GLU_97	OE2	2.797
1HGH	D_LYS_62	NZ	B_ASP_86	OD1	3.011
1HGH	D_LYS_62	NZ	B_ASP_86	OD2	2.510
1HGH	D_LYS_62	NZ	B_ASP_90	OD1	3.543

1HGH	D_LYS_62	NZ	B_ASP_90	OD2	2.589
1HGH	D_ARG_76	NH1	F_GLU_74	OE1	3.430
1HGH	D_ARG_76	NH1	F_GLU_74	OE2	2.765
1HGH	D_ARG_76	NH2	F_GLU_74	OE1	2.747
1HGH	D_ARG_76	NH2	F_GLU_74	OE2	3.553
1HGH	D_ARG_76	NH2	F_GLU_81	OE1	2.698
1HGH	D_ARG_76	NH2	F_GLU_81	OE2	3.487
1HGH	D_ARG_123	NH2	B_GLU_132	OE1	3.141
1HGH	D_ARG_124	NH2	B_GLU_132	OE1	3.050
1HGH	D_ARG_124	NH2	B_GLU_132	OE2	3.354
1HGH	D_ARG_127	NH1	B_GLU_131	OE1	2.536
1HGH	D_ARG_163	NH2	B_GLU_131	OE1	2.609
1HGH	D_ARG_163	NH2	B_GLU_131	OE2	2.570
1HGH	D_ARG_170	NH1	F_GLU_128	OE1	3.352
1HGH	D_ARG_170	NH1	F_GLU_128	OE2	3.641
1HGH	D_LYS_174	NZ	F_ASP_164	OD1	2.863
1HGH	D_LYS_174	NZ	F_ASP_164	OD2	2.724
1HGH	E_LYS_27	NZ	F_GLU_97	OE1	2.917
1HGH	E_LYS_27	NZ	F_GLU_97	OE2	2.767
1HGH	E_ARG_109	NH2	F_GLU_67	OE1	3.698
1HGH	E_ARG_109	NH2	F_GLU_67	OE2	2.878
1HGH	E_LYS_238	NZ	D_GLU_72	OE1	2.870
1HGH	E_LYS_238	NZ	D_GLU_72	OE2	2.766
1HGH	E_ARG_269	NH1	F_GLU_67	OE1	2.705
1HGH	E_ARG_269	NH2	F_GLU_67	OE1	3.715
1HGH	E_LYS_299	NZ	F_GLU_69	OE2	2.896
1HGH	E_LYS_310	NZ	F_ASP_86	OD1	2.740
1HGH	E_LYS_310	NZ	F_ASP_90	OD1	2.571
1HGH	E_LYS_310	NZ	F_ASP_90	OD2	3.948
1HGH	E_LYS_326	NZ	F_GLU_15	OE1	2.900
1HGH	E_LYS_326	NZ	F_GLU_15	OE2	3.072
1HGH	F_ARG_54	NH1	D_GLU_97	OE2	3.293
1HGH	F_ARG_54	NH2	D_GLU_97	OE2	2.723
1HGH	F_LYS_62	NZ	D_ASP_86	OD1	3.012
1HGH	F_LYS_62	NZ	D_ASP_86	OD2	2.546
1HGH	F_LYS_62	NZ	D_ASP_90	OD1	3.612
1HGH	F_LYS_62	NZ	D_ASP_90	OD2	2.682
1HGH	F_ARG_76	NH1	B_GLU_74	OE1	3.509
1HGH	F_ARG_76	NH1	B_GLU_74	OE2	2.732
1HGH	F_ARG_76	NH2	B_GLU_74	OE1	2.780
1HGH	F_ARG_76	NH2	B_GLU_74	OE2	3.488
1HGH	F_ARG_76	NH2	B_GLU_81	OE1	2.709
1HGH	F_ARG_76	NH2	B_GLU_81	OE2	3.513
1HGH	F_ARG_123	NH2	D_GLU_132	OE1	3.148
1HGH	F_ARG_124	NH2	D_GLU_132	OE1	3.099
1HGH	F_ARG_124	NH2	D_GLU_132	OE2	3.356
1HGH	F_ARG_127	NH1	D_GLU_131	OE1	2.577
1HGH	F_ARG_163	NH2	D_GLU_131	OE1	2.600
1HGH	F_ARG_163	NH2	D_GLU_131	OE2	2.611
1HGH	F_ARG_170	NH1	B_GLU_128	OE1	3.225
1HGH	F_ARG_170	NH1	B_GLU_128	OE2	3.576
1HGH	F_LYS_174	NZ	B_ASP_164	OD1	2.776
1HGH	F_LYS_174	NZ	B_ASP_164	OD2	2.495

Table 985: Interfacial 1HGH-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1HGI	A_LYS_27	NZ	B_GLU_97	OE1	2.940
1HGI	A_LYS_27	NZ	B_GLU_97	OE2	2.900
1HGI	A_ARG_109	NH2	B_GLU_67	OE1	3.638
1HGI	A_ARG_109	NH2	B_GLU_67	OE2	2.797
1HGI	A_LYS_238	NZ	F_GLU_72	OE1	2.849
1HGI	A_LYS_238	NZ	F_GLU_72	OE2	2.839
1HGI	A_ARG_269	NH1	B_GLU_67	OE1	2.748
1HGI	A_ARG_269	NH2	B_GLU_67	OE1	3.823
1HGI	A_LYS_299	NZ	B_GLU_69	OE2	2.728
1HGI	A_LYS_310	NZ	B_ASP_86	OD1	2.759
1HGI	A_LYS_310	NZ	B_ASP_90	OD1	2.527
1HGI	A_LYS_326	NZ	B_GLU_15	OE1	3.374
1HGI	A_LYS_326	NZ	B_GLU_15	OE2	2.794
1HGI	B_ARG_25	NH1	A_GLU_325	OE2	3.734
1HGI	B_ARG_25	NH2	A_GLU_325	OE2	2.929
1HGI	B_ARG_54	NH1	F_GLU_97	OE2	3.222
1HGI	B_ARG_54	NH2	F_GLU_97	OE2	2.806
1HGI	B_LYS_62	NZ	F_ASP_86	OD1	2.942
1HGI	B_LYS_62	NZ	F_ASP_86	OD2	2.668
1HGI	B_LYS_62	NZ	F_ASP_90	OD1	3.332
1HGI	B_LYS_62	NZ	F_ASP_90	OD2	2.667
1HGI	B_ARG_76	NH1	D_GLU_74	OE1	3.625
1HGI	B_ARG_76	NH1	D_GLU_74	OE2	2.918
1HGI	B_ARG_76	NH2	D_GLU_74	OE1	2.861
1HGI	B_ARG_76	NH2	D_GLU_74	OE2	3.621
1HGI	B_ARG_76	NH2	D_GLU_81	OE1	2.708
1HGI	B_ARG_76	NH2	D_GLU_81	OE2	3.474
1HGI	B_ARG_123	NH2	F_GLU_132	OE1	3.105
1HGI	B_ARG_124	NH2	F_GLU_132	OE1	3.081
1HGI	B_ARG_124	NH2	F_GLU_132	OE2	3.356
1HGI	B_ARG_127	NH1	F_GLU_131	OE1	2.493
1HGI	B_ARG_163	NH2	F_GLU_131	OE1	2.586
1HGI	B_ARG_163	NH2	F_GLU_131	OE2	2.598
1HGI	B_ARG_170	NH1	D_GLU_128	OE1	3.640
1HGI	B_ARG_170	NH1	D_GLU_128	OE2	3.301
1HGI	B_LYS_174	NZ	D_ASP_164	OD1	2.745
1HGI	B_LYS_174	NZ	D_ASP_164	OD2	2.560
1HGI	C_LYS_27	NZ	D_GLU_97	OE1	2.951
1HGI	C_LYS_27	NZ	D_GLU_97	OE2	2.876
1HGI	C_ARG_109	NH2	D_GLU_67	OE1	3.637
1HGI	C_ARG_109	NH2	D_GLU_67	OE2	2.819
1HGI	C_LYS_238	NZ	B_GLU_72	OE1	2.671
1HGI	C_LYS_238	NZ	B_GLU_72	OE2	2.721
1HGI	C_ARG_269	NH1	D_GLU_67	OE1	2.753
1HGI	C_ARG_269	NH2	D_GLU_67	OE1	3.850
1HGI	C_LYS_299	NZ	D_GLU_69	OE2	2.739
1HGI	C_LYS_310	NZ	D_ASP_86	OD1	2.772
1HGI	C_LYS_310	NZ	D_ASP_90	OD1	2.525
1HGI	C_LYS_326	NZ	D_GLU_15	OE1	2.825
1HGI	C_LYS_326	NZ	D_GLU_15	OE2	3.570
1HGI	D_ARG_54	NH1	B_GLU_97	OE2	3.254
1HGI	D_ARG_54	NH2	B_GLU_97	OE2	2.808
1HGI	D_LYS_62	NZ	B_ASP_86	OD1	2.962
1HGI	D_LYS_62	NZ	B_ASP_86	OD2	2.570
1HGI	D_LYS_62	NZ	B_ASP_90	OD1	3.335
1HGI	D_LYS_62	NZ	B_ASP_90	OD2	2.541
1HGI	D_ARG_76	NH1	F_GLU_74	OE1	3.375

1HGI	D_ARG_76	NH1	F_GLU_74	OE2	2.776
1HGI	D_ARG_76	NH2	F_GLU_74	OE1	2.760
1HGI	D_ARG_76	NH2	F_GLU_74	OE2	3.657
1HGI	D_ARG_76	NH2	F_GLU_81	OE1	2.608
1HGI	D_ARG_76	NH2	F_GLU_81	OE2	3.506
1HGI	D_ARG_123	NH2	B_GLU_132	OE1	3.093
1HGI	D_ARG_124	NH2	B_GLU_132	OE1	3.096
1HGI	D_ARG_124	NH2	B_GLU_132	OE2	3.377
1HGI	D_ARG_127	NH1	B_GLU_131	OE1	2.513
1HGI	D_ARG_163	NH2	B_GLU_131	OE1	2.590
1HGI	D_ARG_163	NH2	B_GLU_131	OE2	2.616
1HGI	D_ARG_170	NH1	F_GLU_128	OE1	3.797
1HGI	D_ARG_170	NH1	F_GLU_128	OE2	3.417
1HGI	D_LYS_174	NZ	F_ASP_164	OD1	2.814
1HGI	D_LYS_174	NZ	F_ASP_164	OD2	2.727
1HGI	E_LYS_27	NZ	F_GLU_97	OE1	2.961
1HGI	E_LYS_27	NZ	F_GLU_97	OE2	2.862
1HGI	E_ARG_109	NH2	F_GLU_67	OE1	3.649
1HGI	E_ARG_109	NH2	F_GLU_67	OE2	2.781
1HGI	E_LYS_238	NZ	D_GLU_72	OE1	2.803
1HGI	E_LYS_238	NZ	D_GLU_72	OE2	2.859
1HGI	E_ARG_269	NH1	F_GLU_67	OE1	2.720
1HGI	E_ARG_269	NH2	F_GLU_67	OE1	3.815
1HGI	E_LYS_299	NZ	F_GLU_69	OE2	2.715
1HGI	E_LYS_310	NZ	F_ASP_86	OD1	2.757
1HGI	E_LYS_310	NZ	F_ASP_90	OD1	2.523
1HGI	E_LYS_326	NZ	F_GLU_15	OE1	2.882
1HGI	E_LYS_326	NZ	F_GLU_15	OE2	3.090
1HGI	F_ARG_54	NH1	D_GLU_97	OE2	3.254
1HGI	F_ARG_54	NH2	D_GLU_97	OE2	2.750
1HGI	F_LYS_62	NZ	D_ASP_86	OD1	2.884
1HGI	F_LYS_62	NZ	D_ASP_86	OD2	2.563
1HGI	F_LYS_62	NZ	D_ASP_90	OD1	3.358
1HGI	F_LYS_62	NZ	D_ASP_90	OD2	2.609
1HGI	F_ARG_76	NH1	B_GLU_74	OE1	3.420
1HGI	F_ARG_76	NH1	B_GLU_74	OE2	2.771
1HGI	F_ARG_76	NH2	B_GLU_74	OE1	2.763
1HGI	F_ARG_76	NH2	B_GLU_74	OE2	3.604
1HGI	F_ARG_76	NH2	B_GLU_81	OE1	2.645
1HGI	F_ARG_76	NH2	B_GLU_81	OE2	3.592
1HGI	F_ARG_123	NH2	D_GLU_132	OE1	3.144
1HGI	F_ARG_124	NH2	D_GLU_132	OE1	3.185
1HGI	F_ARG_124	NH2	D_GLU_132	OE2	3.386
1HGI	F_ARG_127	NH1	D_GLU_131	OE1	2.561
1HGI	F_ARG_163	NH2	D_GLU_131	OE1	2.567
1HGI	F_ARG_163	NH2	D_GLU_131	OE2	2.692
1HGI	F_ARG_170	NH1	B_GLU_128	OE1	3.621
1HGI	F_ARG_170	NH1	B_GLU_128	OE2	3.345
1HGI	F_LYS_174	NZ	B_ASP_164	OD1	2.789
1HGI	F_LYS_174	NZ	B_ASP_164	OD2	2.521

Table 986: Interfacial 1HGI-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1HGJ	A_LYS_27	NZ	B_GLU_97	OE1	2.775
1HGJ	A_LYS_27	NZ	B_GLU_97	OE2	2.807
1HGJ	A_ARG_109	NH2	B_GLU_67	OE1	3.648
1HGJ	A_ARG_109	NH2	B_GLU_67	OE2	2.748
1HGJ	A_LYS_238	NZ	F_GLU_72	OE1	2.903
1HGJ	A_LYS_238	NZ	F_GLU_72	OE2	2.788
1HGJ	A_ARG_269	NH1	B_GLU_67	OE1	2.736
1HGJ	A_ARG_269	NH2	B_GLU_67	OE1	3.791
1HGJ	A_LYS_299	NZ	B_GLU_69	OE2	2.821
1HGJ	A_LYS_310	NZ	B_ASP_86	OD1	2.922
1HGJ	A_LYS_310	NZ	B_ASP_90	OD1	2.569
1HGJ	A_LYS_326	NZ	B_GLU_15	OE1	3.187
1HGJ	A_LYS_326	NZ	B_GLU_15	OE2	2.826
1HGJ	B_ARG_25	NH1	A_GLU_325	OE2	3.775
1HGJ	B_ARG_25	NH2	A_GLU_325	OE2	2.974
1HGJ	B_ARG_54	NH1	F_GLU_97	OE2	3.272
1HGJ	B_ARG_54	NH2	F_GLU_97	OE2	2.774
1HGJ	B_LYS_62	NZ	F_ASP_86	OD1	2.863
1HGJ	B_LYS_62	NZ	F_ASP_86	OD2	2.651
1HGJ	B_LYS_62	NZ	F_ASP_90	OD1	3.453
1HGJ	B_LYS_62	NZ	F_ASP_90	OD2	2.738
1HGJ	B_ARG_76	NH1	D_GLU_74	OE1	3.648
1HGJ	B_ARG_76	NH1	D_GLU_74	OE2	2.885
1HGJ	B_ARG_76	NH2	D_GLU_74	OE1	2.846
1HGJ	B_ARG_76	NH2	D_GLU_74	OE2	3.547
1HGJ	B_ARG_76	NH2	D_GLU_81	OE1	2.721
1HGJ	B_ARG_76	NH2	D_GLU_81	OE2	3.500
1HGJ	B_ARG_123	NH2	F_GLU_132	OE1	3.120
1HGJ	B_ARG_124	NH2	F_GLU_132	OE1	3.095
1HGJ	B_ARG_124	NH2	F_GLU_132	OE2	3.375
1HGJ	B_ARG_127	NH1	F_GLU_131	OE1	2.484
1HGJ	B_ARG_163	NH2	F_GLU_131	OE1	2.591
1HGJ	B_ARG_163	NH2	F_GLU_131	OE2	2.571
1HGJ	B_ARG_170	NH1	D_GLU_128	OE1	3.291
1HGJ	B_ARG_170	NH1	D_GLU_128	OE2	3.706
1HGJ	B_LYS_174	NZ	D_ASP_164	OD1	2.810
1HGJ	B_LYS_174	NZ	D_ASP_164	OD2	2.550
1HGJ	C_LYS_27	NZ	D_GLU_97	OE1	2.755
1HGJ	C_LYS_27	NZ	D_GLU_97	OE2	2.824
1HGJ	C_ARG_109	NH2	D_GLU_67	OE1	3.638
1HGJ	C_ARG_109	NH2	D_GLU_67	OE2	2.758
1HGJ	C_LYS_238	NZ	B_GLU_72	OE1	2.749
1HGJ	C_LYS_238	NZ	B_GLU_72	OE2	2.713
1HGJ	C_ARG_269	NH1	D_GLU_67	OE1	2.708
1HGJ	C_ARG_269	NH2	D_GLU_67	OE1	3.781
1HGJ	C_LYS_299	NZ	D_GLU_69	OE2	2.827
1HGJ	C_LYS_310	NZ	D_ASP_86	OD1	2.943
1HGJ	C_LYS_310	NZ	D_ASP_90	OD1	2.532
1HGJ	C_LYS_326	NZ	D_GLU_15	OE1	2.911
1HGJ	C_LYS_326	NZ	D_GLU_15	OE2	3.904
1HGJ	D_ARG_54	NH1	B_GLU_97	OE2	3.338
1HGJ	D_ARG_54	NH2	B_GLU_97	OE2	2.835
1HGJ	D_LYS_62	NZ	B_ASP_86	OD1	2.910
1HGJ	D_LYS_62	NZ	B_ASP_86	OD2	2.574
1HGJ	D_LYS_62	NZ	B_ASP_90	OD1	3.419
1HGJ	D_LYS_62	NZ	B_ASP_90	OD2	2.622
1HGJ	D_ARG_76	NH1	F_GLU_74	OE1	3.424

1HGJ	D_ARG_76	NH1	F_GLU_74	OE2	2.763
1HGJ	D_ARG_76	NH2	F_GLU_74	OE1	2.714
1HGJ	D_ARG_76	NH2	F_GLU_74	OE2	3.550
1HGJ	D_ARG_76	NH2	F_GLU_81	OE1	2.684
1HGJ	D_ARG_76	NH2	F_GLU_81	OE2	3.574
1HGJ	D_ARG_123	NH2	B_GLU_132	OE1	3.075
1HGJ	D_ARG_124	NH2	B_GLU_132	OE1	3.055
1HGJ	D_ARG_124	NH2	B_GLU_132	OE2	3.342
1HGJ	D_ARG_127	NH1	B_GLU_131	OE1	2.514
1HGJ	D_ARG_163	NH2	B_GLU_131	OE1	2.599
1HGJ	D_ARG_163	NH2	B_GLU_131	OE2	2.594
1HGJ	D_ARG_170	NH1	F_GLU_128	OE1	3.405
1HGJ	D_ARG_170	NH1	F_GLU_128	OE2	3.769
1HGJ	D_LYS_174	NZ	F_ASP_164	OD1	2.824
1HGJ	D_LYS_174	NZ	F_ASP_164	OD2	2.673
1HGJ	E_LYS_27	NZ	F_GLU_97	OE1	2.779
1HGJ	E_LYS_27	NZ	F_GLU_97	OE2	2.813
1HGJ	E_ARG_109	NH2	F_GLU_67	OE1	3.635
1HGJ	E_ARG_109	NH2	F_GLU_67	OE2	2.759
1HGJ	E_LYS_238	NZ	D_GLU_72	OE1	2.865
1HGJ	E_LYS_238	NZ	D_GLU_72	OE2	2.804
1HGJ	E_ARG_269	NH1	F_GLU_67	OE1	2.691
1HGJ	E_ARG_269	NH2	F_GLU_67	OE1	3.759
1HGJ	E_LYS_299	NZ	F_GLU_69	OE2	2.806
1HGJ	E_LYS_310	NZ	F_ASP_86	OD1	2.930
1HGJ	E_LYS_310	NZ	F_ASP_90	OD1	2.553
1HGJ	E_LYS_326	NZ	F_GLU_15	OE1	2.874
1HGJ	E_LYS_326	NZ	F_GLU_15	OE2	3.254
1HGJ	F_ARG_54	NH1	D_GLU_97	OE2	3.349
1HGJ	F_ARG_54	NH2	D_GLU_97	OE2	2.771
1HGJ	F_LYS_62	NZ	D_ASP_86	OD1	2.846
1HGJ	F_LYS_62	NZ	D_ASP_86	OD2	2.568
1HGJ	F_LYS_62	NZ	D_ASP_90	OD1	3.467
1HGJ	F_LYS_62	NZ	D_ASP_90	OD2	2.658
1HGJ	F_ARG_76	NH1	B_GLU_74	OE1	3.383
1HGJ	F_ARG_76	NH1	B_GLU_74	OE2	2.704
1HGJ	F_ARG_76	NH2	B_GLU_74	OE1	2.715
1HGJ	F_ARG_76	NH2	B_GLU_74	OE2	3.551
1HGJ	F_ARG_76	NH2	B_GLU_81	OE1	2.654
1HGJ	F_ARG_76	NH2	B_GLU_81	OE2	3.611
1HGJ	F_ARG_123	NH2	D_GLU_132	OE1	3.110
1HGJ	F_ARG_124	NH2	D_GLU_132	OE1	3.125
1HGJ	F_ARG_124	NH2	D_GLU_132	OE2	3.360
1HGJ	F_ARG_127	NH1	D_GLU_131	OE1	2.554
1HGJ	F_ARG_163	NH2	D_GLU_131	OE1	2.636
1HGJ	F_ARG_163	NH2	D_GLU_131	OE2	2.696
1HGJ	F_ARG_170	NH1	B_GLU_128	OE1	3.311
1HGJ	F_ARG_170	NH1	B_GLU_128	OE2	3.766
1HGJ	F_LYS_174	NZ	B_ASP_164	OD1	2.859
1HGJ	F_LYS_174	NZ	B_ASP_164	OD2	2.554

Table 987: Interfacial 1HGJ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1HIL	A.LYS_28	NZ	B.ASP_99	OD1	3.388
1HIL	A.LYS_28	NZ	B.ASP_99	OD2	3.371
1HIL	A.LYS_30	NZ	B.ASP_99	OD2	3.991
1HIL	B.ARG_95	NH1	A.ASP_91	OD1	2.828
1HIL	B.ARG_95	NH1	A.ASP_91	OD2	3.804
1HIL	B.ARG_95	NH2	A.ASP_91	OD1	3.160
1HIL	B.ARG_95	NH2	A.ASP_91	OD2	3.904
1HIL	B.HIS_172	NE2	A.ASP_167	OD2	3.701
1HIL	B.LYS_221	NZ	A.GLU_123	OE1	2.980
1HIL	C.LYS_28	NZ	D.ASP_99	OD1	3.565
1HIL	C.LYS_28	NZ	D.ASP_99	OD2	3.509
1HIL	D.ARG_95	NH1	C.ASP_91	OD1	2.906
1HIL	D.ARG_95	NH1	C.ASP_91	OD2	3.993
1HIL	D.ARG_95	NH2	C.ASP_91	OD1	3.045
1HIL	D.ARG_95	NH2	C.ASP_91	OD2	3.822
1HIL	D.LYS_221	NZ	C.GLU_123	OE1	2.896
1HIL	D.LYS_221	NZ	C.GLU_123	OE2	3.091

Table 988: Interfacial 1HIL-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1HIM	L_ARG_95	NH1	H_ASP_91	OD1	3.100
1HIM	L_ARG_95	NH2	H_ASP_91	OD1	3.427
1HIM	L_ARG_95	NH2	P_ASP_104	OD1	3.909
1HIM	L_ARG_95	NH2	P_ASP_104	OD2	3.079
1HIM	L_LYS_221	NZ	H_GLU_123	OE1	3.486
1HIM	L_LYS_221	NZ	H_GLU_123	OE2	2.924
1HIM	J_LYS_28	NZ	M_GLU_100	OE1	3.991
1HIM	J_LYS_28	NZ	M_GLU_100	OE2	3.433
1HIM	M_ARG_95	NH1	J_ASP_91	OD1	2.854
1HIM	M_ARG_95	NH2	J_ASP_91	OD1	3.712
1HIM	M_ARG_95	NH2	R_ASP_104	OD1	2.834
1HIM	M_ARG_95	NH2	R_ASP_104	OD2	3.540

Table 989: Interfacial 1HIM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID residue name residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1HIN	L_LYS_28	NZ	H_GLU_100	OE2	2.975
1HIN	H_ARG_95	NH1	L_ASP_91	OD1	3.169
1HIN	H_ARG_95	NH1	P_ASP_104	OD1	3.889
1HIN	H_ARG_95	NH2	L_ASP_91	OD1	2.746

Table 990: Interfacial 1HIN-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1I8I	B_LYS_343	NZ	A_ASP_85	OD1	3.777
1I8I	C_LYS_502	NZ	A_GLU_50	OE1	3.673
1I8I	C_LYS_502	NZ	A_GLU_50	OE2	3.232

Table 991: Interfacial 1I8I-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1I8K	B_LYS_343	NZ	A_ASP_85	OD1	3.688
1I8K	B_LYS_343	NZ	A_ASP_85	OD2	2.833
1I8K	C_LYS_502	NZ	A_GLU_50	OE1	3.381
1I8K	C_LYS_502	NZ	A_GLU_50	OE2	3.653

Table 992: Interfacial 1I8K-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1I8M	H_LYS_208	NZ	L_GLU_123	OE1	2.918
1I8M	B_LYS_208	NZ	A_GLU_123	OE2	2.887

Table 993: Interfacial 1I8M-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1IC4	Y_LYS_97	NZ	H_ASP_99	OD1	2.657
1IC4	Y_LYS_97	NZ	H_ASP_99	OD2	3.938

Table 994: Interfacial 1IC4-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1IC5	Y_LYS_97	NZ	H_ASP_32	OD1	2.694

Table 995: Interfacial 1IC5-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1IFH	H_ARG_95	NH1	L_ASP_91	OD1	2.782
1IFH	H_ARG_95	NH2	P_ASP_104	OD1	2.974
1IFH	H_ARG_95	NH2	P_ASP_104	OD2	2.813
1IFH	H_LYS_221	NZ	L_GLU_123	OE1	3.267
1IFH	H_LYS_221	NZ	L_GLU_123	OE2	2.926

Table 996: Interfacial 1IFH-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1IGF	L_LYS_50	NZ	H_ASP_98	OD2	3.036
1IGF	H_LYS_221	NZ	L_GLU_123	OE1	3.549
1IGF	J_LYS_221	NZ	M_GLU_123	OE1	3.800
1IGF	J_LYS_221	NZ	M_GLU_123	OE2	3.750

Table 997: Interfacial 1IGF-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1IND	H_LYS_143	NZ	L_GLU_127	OE2	2.765
1IND	H_HIS_164	NE2	L_ASP_141	OD1	3.891

Table 998: Interfacial 1IND-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1INE	H_LYS_143	NZ	L_GLU_127	OE2	2.920
1INE	H_HIS_164	NE2	L_ASP_141	OD2	3.817

Table 999: Interfacial 1INE-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1IQW	L_ARG_100	NH2	H_GLU_50	OE1	2.572
1IQW	L_ARG_100	NH2	H_GLU_50	OE2	2.799
1IQW	H_HIS_172	NE2	L_ASP_171	OD1	3.594

Table 1000: Interfacial 1IQW-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1IT9	L_ARG_100	NH2	H_GLU_50	OE2	3.105
1IT9	H_LYS_217	NZ	L_GLU_127	OE1	3.545
1IT9	H_LYS_217	NZ	L_GLU_127	OE2	3.302

Table 1001: Interfacial 1IT9-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1J05	H.LYS_58	NZ	L.ASP_94	OD2	2.663
1J05	B.LYS_58	NZ	A.ASP_94	OD2	2.870

Table 1002: Interfacial 1J05-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1J1O	Y_LYS_97	NZ	H_ASP_32	OD1	2.636
1J1O	Y_LYS_97	NZ	H_ASP_32	OD2	3.985
1J1O	Y_LYS_97	NZ	H_ASP_99	OD1	3.590
1J1O	Y_LYS_97	NZ	H_ASP_99	OD2	2.896

Table 1003: Interfacial 1J1O-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1J1P	Y_LYS_97	NZ	H_ASP_32	OD1	2.700
1J1P	Y_LYS_97	NZ	H_ASP_99	OD1	3.721
1J1P	Y_LYS_97	NZ	H_ASP_99	OD2	2.595

Table 1004: Interfacial 1J1P-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1J1X	Y.LYS_97	NZ	H.ASP_32	OD1	2.655
1J1X	Y.LYS_97	NZ	H.ASP_32	OD2	3.935
1J1X	Y.LYS_97	NZ	H.ASP_99	OD1	3.479
1J1X	Y.LYS_97	NZ	H.ASP_99	OD2	2.956

Table 1005: Interfacial 1J1X-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1JFQ	H_LYS_516	NZ	L_GLU_123	OE1	3.003
1JFQ	H_LYS_516	NZ	L_GLU_123	OE2	3.095

Table 1006: Interfacial 1JFQ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1JHL	A_ARG_112	NH1	H_ASP_55	OD1	3.828
1JHL	A_ARG_112	NH1	H_ASP_55	OD2	3.112
1JHL	A_LYS_116	NZ	H_ASP_99	OD1	3.763
1JHL	A_LYS_116	NZ	H_ASP_99	OD2	3.232

Table 1007: Interfacial 1JHL-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1JPS	T_LYS_201	NZ	H_ASP_52	OD1	2.781

Table 1008: Interfacial 1JPS-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1JPT	H_LYS_213	NZ	L_GLU_123	OE1	3.226
1JPT	H_LYS_213	NZ	L_GLU_123	OE2	3.740

Table 1009: Interfacial 1JPT-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1JRH	LLYS_52	NZ	H_ASP_54	OD1	3.471
1JRH	LLYS_52	NZ	H_ASP_54	OD2	2.819
1JRH	LLYS_52	NZ	H_ASP_56	OD2	2.824
1JRH	L_ARG_84	NH2	L_GLU_27	OE1	3.652
1JRH	L_ARG_84	NH2	L_GLU_27	OE2	3.984

Table 1010: Interfacial 1JRH-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1K6Q	H_HIS_168	NE2	L_ASP_167	OD1	3.896

Table 1011: Interfacial 1K6Q-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1KB5	A_ARG_93	NH1	B_GLU_105	OE1	2.975
1KB5	A_ARG_93	NH1	B_GLU_105	OE2	3.412
1KB5	A_ARG_101	NH2	H_ASP_98	OD1	2.690
1KB5	L_LYS_27	NZ	B_ASP_54	OD1	3.460
1KB5	H_ARG_96	NH1	A_ASP_26	OD1	2.599
1KB5	H_ARG_96	NH1	A_ASP_26	OD2	2.834
1KB5	H_ARG_96	NH2	L_GLU_56	OE2	2.981

Table 1012: Interfacial 1KB5-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1KC5	H_LYS_211	NZ	L_GLU_123	OE2	2.759

Table 1013: Interfacial 1KC5-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1KCS	H_LYS_211	NZ	L_GLU_123	OE1	3.340
1KCS	H_LYS_211	NZ	L_GLU_123	OE2	2.904

Table 1014: Interfacial 1KCS-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1KIP	A_ARG_96	NH1	B_GLU_98	OE1	2.773
1KIP	A_ARG_96	NH1	B_GLU_98	OE2	3.817
1KIP	A_ARG_96	NH2	B_GLU_98	OE1	3.280
1KIP	A_ARG_96	NH2	B_GLU_98	OE2	2.802

Table 1015: Interfacial 1KIP-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1KIQ	A_ARG_96	NH1	B_GLU_98	OE1	2.812
1KIQ	A_ARG_96	NH1	B_GLU_98	OE2	3.589
1KIQ	A_ARG_96	NH2	B_GLU_98	OE1	3.677
1KIQ	A_ARG_96	NH2	B_GLU_98	OE2	2.919

Table 1016: Interfacial 1KIQ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1KIR	A_ARG_96	NH1	B_GLU_98	OE1	2.757
1KIR	A_ARG_96	NH1	B_GLU_98	OE2	3.582
1KIR	A_ARG_96	NH2	B_GLU_98	OE1	3.625
1KIR	A_ARG_96	NH2	B_GLU_98	OE2	2.980

Table 1017: Interfacial 1KIR-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1KTR	P_HIS_4	NE2	L_ASP_183	OD1	3.445
1KTR	P_HIS_4	NE2	L_ASP_183	OD2	2.673
1KTR	P_HIS_6	ND1	L_GLU_39	OE1	3.223
1KTR	P_HIS_6	ND1	L_GLU_39	OE2	2.811
1KTR	P_HIS_6	NE2	L_GLU_230	OE1	3.040
1KTR	P_HIS_6	NE2	L_GLU_230	OE2	3.199

Table 1018: Interfacial 1KTR-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1L7I	H_LYS_209	NZ	L_GLU_123	OE1	2.718

Table 1019: Interfacial 1L7I-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1LK3	A_LYS_130	NZ	L_ASP_1	OD1	2.906
1LK3	L_ARG_31	NH1	A_GLU_133	OE1	2.703
1LK3	H_LYS_23	NZ	L_GLU_121	OE2	2.800
1LK3	H_LYS_214	NZ	L_GLU_122	OE1	2.517
1LK3	B_LYS_130	NZ	M_ASP_1	OD1	2.851
1LK3	M_ARG_31	NH1	B_GLU_133	OE1	2.693
1LK3	I_LYS_63	NZ	M_ASP_1	OD2	3.881
1LK3	I_LYS_214	NZ	M_GLU_122	OE2	2.753

Table 1020: Interfacial 1LK3-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1M71	B_ARG_164	NH1	A_ASP_167	OD2	3.246
1M71	B_ARG_164	NH1	A_ASP_170	OD1	3.912
1M71	B_ARG_164	NH2	A_ASP_167	OD2	2.886
1M71	B_LYS_208	NZ	A_GLU_123	OE1	2.546
1M71	B_LYS_208	NZ	A_GLU_123	OE2	3.594

Table 1021: Interfacial 1M71-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1M7D	B_ARG_164	NH1	A_ASP_167	OD2	3.313
1M7D	B_ARG_164	NH1	A_ASP_170	OD1	3.795
1M7D	B_ARG_164	NH2	A_ASP_167	OD2	3.482
1M7D	B_LYS_208	NZ	A_GLU_123	OE1	2.586
1M7D	B_LYS_208	NZ	A_GLU_123	OE2	3.420

Table 1022: Interfacial 1M7D-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1M7I	B_ARG_164	NH1	A_ASP_167	OD2	3.340
1M7I	B_ARG_164	NH1	A_ASP_170	OD1	3.884
1M7I	B_ARG_164	NH2	A_ASP_167	OD2	3.473
1M7I	B_LYS_208	NZ	A_GLU_123	OE1	3.031
1M7I	B_LYS_208	NZ	A_GLU_123	OE2	3.016

Table 1023: Interfacial 1M7I-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1MFB	H_LYS_398	NZ	L_GLU_127	OE2	2.924
1MFB	H_LYS_463	NZ	L_GLU_126	OE1	3.780

Table 1024: Interfacial 1MFB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1MFC	H_LYS_398	NZ	L_GLU_127	OE2	2.815
1MFC	H_LYS_463	NZ	L_GLU_126	OE1	3.807

Table 1025: Interfacial 1MFC-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1MHH	B_LYS_208	NZ	A_GLU_123	OE2	3.019
1MHH	C_ARG_188	NH1	E_ASP_831	OD2	3.196
1MHH	C_ARG_188	NH2	E_ASP_831	OD2	3.360
1MHH	E_LYS_833	NZ	C_GLU_185	OE2	2.489
1MHH	F_LYS_1833	NZ	C_GLU_17	OE1	3.798

Table 1026: Interfacial 1MHH-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1MLB	B_LYS_211	NZ	A_GLU_123	OE1	3.556

Table 1027: Interfacial 1MLB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1MLC	E_ARG_45	NH2	B_GLU_50	OE2	3.032
1MLC	E_ARG_68	NH1	B_GLU_50	OE2	3.781
1MLC	E_ARG_68	NH2	B_GLU_35	OE2	2.927
1MLC	E_ARG_68	NH2	B_GLU_50	OE1	2.510
1MLC	E_ARG_68	NH2	B_GLU_50	OE2	3.189
1MLC	F_ARG_45	NH2	D_GLU_50	OE2	2.431
1MLC	F_ARG_68	NH2	D_GLU_35	OE2	3.266
1MLC	F_ARG_68	NH2	D_GLU_50	OE1	2.710
1MLC	F_ARG_68	NH2	D_GLU_50	OE2	3.606

Table 1028: Interfacial 1MLC-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1N64	H_LYS_208	NZ	L_GLU_123	OE1	3.752

Table 1029: Interfacial 1N64-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1NBY	B_LYS_508	NZ	A_GLU_123	OE1	2.458
1NBY	B_LYS_508	NZ	A_GLU_123	OE2	3.274
1NBY	C_LYS_697	NZ	B_ASP_332	OD1	3.949
1NBY	C_LYS_697	NZ	B_ASP_332	OD2	2.515

Table 1030: Interfacial 1NBY-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1NDG	B_HIS_360	NE2	A_ASP_1	OD2	3.716
1NDG	B_LYS_519	NZ	A_GLU_123	OE2	2.645
1NDG	C_LYS_697	NZ	B_ASP_332	OD1	3.996
1NDG	C_LYS_697	NZ	B_ASP_332	OD2	2.706
1NDG	C_LYS_697	NZ	B_ASP_399	OD1	2.922
1NDG	C_LYS_697	NZ	B_ASP_399	OD2	3.579

Table 1031: Interfacial 1NDG-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1NDM	B_LYS_519	NZ	A_GLU_123	OE1	3.184
1NDM	C_LYS_697	NZ	B_ASP_332	OD1	3.954
1NDM	C_LYS_697	NZ	B_ASP_332	OD2	2.468
1NDM	C_LYS_697	NZ	B_GLU_399	OE1	2.743

Table 1032: Interfacial 1NDM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1NGW	H_HIS_165	NE2	L_ASP_167	OD1	3.771
1NGW	H_LYS_210	NZ	L_GLU_123	OE1	3.544
1NGW	H_LYS_210	NZ	L_GLU_123	OE2	3.092
1NGW	B_HIS_165	NE2	A_ASP_167	OD1	3.804
1NGW	B_LYS_210	NZ	A_GLU_123	OE1	3.662
1NGW	B_LYS_210	NZ	A_GLU_123	OE2	3.240

Table 1033: Interfacial 1NGW-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1NGX	B_LYS_210	NZ	A_GLU_123	OE1	3.994
1NGX	L_LYS_45	NZ	H_ASP_102	OD2	3.800
1NGX	H_LYS_210	NZ	L_GLU_123	OE1	3.804

Table 1034: Interfacial 1NGX-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1NGY	B_LYS_215	NZ	A_ASP_122	OD1	3.713
1NGY	B_LYS_215	NZ	A_ASP_122	OD2	3.325

Table 1035: Interfacial 1NGY-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1NGZ	B_LYS_	NZ	A_GLU_	OE2	3.517

Table 1036: Interfacial 1NGZ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1NLB	H_LYS_208	NZ	L_GLU_123	OE1	3.572

Table 1037: Interfacial 1NLB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1NMC	N_LYS_432	NZ	H_ASP_56	OD1	2.750
1NMC	A_LYS_432	NZ	B_ASP_56	OD1	2.750

Table 1038: Interfacial 1NMC-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1OB1	A_ARG_61	NH2	F_ASP_59	OD1	3.421
1OB1	A_ARG_61	NH2	F_ASP_59	OD2	2.223
1OB1	B_HIS_164	NE2	A_ASP_166	OD2	3.671
1OB1	C_LYS_10	NZ	B_ASP_100	OD1	2.437
1OB1	C_LYS_80	NZ	D_GLU_79	OE1	3.373
1OB1	C_LYS_80	NZ	D_GLU_81	OE1	3.553
1OB1	C_LYS_80	NZ	D_GLU_81	OE2	2.714
1OB1	D_ARG_61	NH2	C_ASP_59	OD1	3.599
1OB1	D_ARG_61	NH2	C_ASP_59	OD2	2.460
1OB1	E_ARG_98	NH1	F_ASP_39	OD1	2.706
1OB1	E_HIS_164	NE2	D_ASP_166	OD2	3.790
1OB1	F_LYS_10	NZ	E_ASP_100	OD1	2.524
1OB1	F_LYS_80	NZ	A_GLU_79	OE1	3.743
1OB1	F_LYS_80	NZ	A_GLU_81	OE1	3.454
1OB1	F_LYS_80	NZ	A_GLU_81	OE2	2.796
1OB1	F_HIS_96	NE2	A_GLU_79	OE1	3.773

Table 1039: Interfacial 1OB1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1OP9	B_LYS_97	NZ	A_GLU_97	OE1	2.570
1OP9	B_ARG_101	NH1	A_ASP_109	OD1	3.213
1OP9	B_ARG_101	NH1	A_ASP_109	OD2	2.829
1OP9	B_ARG_101	NH2	A_ASP_109	OD1	2.793
1OP9	B_ARG_101	NH2	A_ASP_109	OD2	3.765

Table 1040: Interfacial 1OP9-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1OSP	H_ARG_99	NH1	L_GLU_55	OE1	3.970
1OSP	H_ARG_99	NH1	L_GLU_55	OE2	2.686
1OSP	H_ARG_99	NH2	O_ASP_92	OD1	3.355
1OSP	H_ARG_99	NH2	O_ASP_92	OD2	2.514
1OSP	H_LYS_215	NZ	L_GLU_123	OE1	2.783
1OSP	H_LYS_215	NZ	L_GLU_123	OE2	3.079
1OSP	O_LYS_46	NZ	L_ASP_66	OD2	3.087

Table 1041: Interfacial 1OSP-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1P2C	A_ARG_188	NH2	F_ASP_1518	OD1	2.778
1P2C	B_LYS_511	NZ	A_GLU_123	OE1	3.498
1P2C	C_ARG_645	NH2	B_GLU_350	OE1	2.980
1P2C	C_ARG_668	NH1	B_GLU_350	OE1	3.355
1P2C	C_ARG_668	NH1	B_GLU_350	OE2	3.681
1P2C	C_ARG_668	NH2	B_GLU_335	OE2	3.090
1P2C	C_ARG_668	NH2	B_GLU_350	OE1	3.316
1P2C	C_ARG_668	NH2	B_GLU_350	OE2	2.404
1P2C	E_LYS_1411	NZ	D_GLU_1023	OE1	3.897
1P2C	F_ARG_1545	NH2	E_GLU_1250	OE1	2.861
1P2C	F_ARG_1568	NH1	E_GLU_1250	OE1	3.580
1P2C	F_ARG_1568	NH1	E_GLU_1250	OE2	3.708
1P2C	F_ARG_1568	NH2	E_GLU_1235	OE2	2.833
1P2C	F_ARG_1568	NH2	E_GLU_1250	OE1	3.551
1P2C	F_ARG_1568	NH2	E_GLU_1250	OE2	2.418

Table 1042: Interfacial 1P2C-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1P4B	P_HIS_2	NE2	H_ASP_65	OD1	3.248
1P4B	P_HIS_2	NE2	H_ASP_65	OD2	3.747
1P4B	P_ARG_9	NH1	H_ASP_137	OD1	2.804
1P4B	P_ARG_9	NH1	H_ASP_137	OD2	3.838
1P4B	P_ARG_9	NH2	H_ASP_137	OD1	3.399
1P4B	P_ARG_9	NH2	H_ASP_137	OD2	3.080

Table 1043: Interfacial 1P4B-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1P7K	H.LYS_62	NZ	L.GLU_1	OE2	3.723
1P7K	H.LYS_208	NZ	L.GLU_123	OE1	3.517
1P7K	H.LYS_208	NZ	L.GLU_123	OE2	2.802
1P7K	B.LYS_62	NZ	A.GLU_1	OE2	2.848

Table 1044: Interfacial 1P7K-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1PG7	H_LYS_209	NZ	L_GLU_123	OE1	2.828
1PG7	H_LYS_209	NZ	L_GLU_123	OE2	3.697
1PG7	I_LYS_209	NZ	M_GLU_123	OE1	2.829
1PG7	I_LYS_209	NZ	M_GLU_123	OE2	3.963
1PG7	L_LYS_30	NZ	X_GLU_95	OE1	3.476
1PG7	L_LYS_30	NZ	X_GLU_95	OE2	2.795
1PG7	M_LYS_30	NZ	Z_GLU_95	OE2	3.166
1PG7	X_ARG_94	NH1	H_GLU_53	OE1	3.386
1PG7	X_ARG_94	NH1	H_GLU_53	OE2	3.321
1PG7	X_ARG_94	NH2	H_GLU_53	OE1	3.937
1PG7	X_ARG_94	NH2	H_GLU_53	OE2	2.866
1PG7	X_ARG_98	NH2	H_ASP_95	OD1	2.990
1PG7	X_ARG_98	NH2	H_ASP_95	OD2	3.561
1PG7	X_LYS_143	NZ	W_GLU_125	OE2	2.675
1PG7	X_HIS_164	NE2	W_GLU_139	OE2	3.801
1PG7	X_LYS_208	NZ	W_GLU_124	OE2	2.927
1PG7	Z_ARG_94	NH1	I_GLU_53	OE1	3.259
1PG7	Z_ARG_94	NH1	I_GLU_53	OE2	3.931
1PG7	Z_ARG_94	NH2	I_GLU_53	OE1	2.918
1PG7	Z_ARG_94	NH2	I_GLU_53	OE2	2.525
1PG7	Z_ARG_98	NH2	I_ASP_95	OD1	3.168
1PG7	Z_ARG_98	NH2	I_ASP_95	OD2	3.781
1PG7	Z_LYS_143	NZ	Y_GLU_125	OE2	2.901
1PG7	Z_LYS_208	NZ	Y_GLU_124	OE2	3.302

Table 1045: Interfacial 1PG7-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1PZ5	A_HIS_27D	NE2	C_ASP_2	OD1	2.720
1PZ5	B_ARG_164	NH1	A_ASP_167	OD2	3.218
1PZ5	B_ARG_164	NH2	A_ASP_167	OD2	3.712
1PZ5	B_LYS_208	NZ	A_GLU_123	OE1	2.648
1PZ5	B_LYS_208	NZ	A_GLU_123	OE2	3.713

Table 1046: Interfacial 1PZ5-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1Q9K	A_ARG_95	NH2	B_ASP_95	OD1	3.932
1Q9K	A_ARG_95	NH2	B_ASP_95	OD2	3.226
1Q9K	B_HIS_162	NE2	A_ASP_166	OD1	3.847

Table 1047: Interfacial 1Q9K-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1Q9L	B_LYS_206	NZ	A_GLU_122	OE2	3.242
1Q9L	D_ARG_100B	NH1	B_GLU_85	OE1	3.618
1Q9L	D_ARG_100B	NH1	B_GLU_85	OE2	3.115
1Q9L	D_HIS_162	NE2	C_ASP_166	OD1	3.172
1Q9L	A_ARG_95	NH2	B_ASP_95	OD2	3.284
1Q9L	C_ARG_95	NH2	D_ASP_95	OD2	3.309

Table 1048: Interfacial 1Q9L-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1Q9O	B_ARG_100	NH1	A_GLU_55	OE1	3.447
1Q9O	B_ARG_100	NH1	A_GLU_55	OE2	3.466
1Q9O	B_ARG_100	NH2	A_GLU_55	OE1	3.378
1Q9O	B_ARG_100	NH2	A_GLU_55	OE2	2.999
1Q9O	B_LYS_206	NZ	A_GLU_122	OE2	3.964
1Q9O	D_ARG_100	NH1	C_GLU_55	OE1	3.493
1Q9O	D_ARG_100	NH1	C_GLU_55	OE2	3.040
1Q9O	D_ARG_100	NH2	C_GLU_55	OE1	3.391
1Q9O	D_ARG_100	NH2	C_GLU_55	OE2	3.047
1Q9O	A_ARG_95	NH2	B_ASP_95	OD1	2.958
1Q9O	A_ARG_95	NH2	B_ASP_95	OD2	3.717
1Q9O	C_ARG_95	NH2	D_ASP_95	OD1	3.672
1Q9O	C_ARG_95	NH2	D_ASP_95	OD2	2.974

Table 1049: Interfacial 1Q9O-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1Q9W	A_ARG_95	NH2	B_ASP_95	OD1	2.949
1Q9W	A_ARG_95	NH2	B_ASP_95	OD2	3.845
1Q9W	B_ARG_100	NH1	A_GLU_55	OE1	2.615
1Q9W	B_ARG_100	NH1	A_GLU_55	OE2	3.657
1Q9W	B_ARG_100	NH2	A_GLU_55	OE1	2.891
1Q9W	B_ARG_100	NH2	A_GLU_55	OE2	3.820
1Q9W	C_ARG_95	NH2	D_ASP_95	OD1	2.929
1Q9W	C_ARG_95	NH2	D_ASP_95	OD2	3.831
1Q9W	D_ARG_100	NH1	C_GLU_55	OE1	3.356
1Q9W	D_ARG_100	NH1	C_GLU_55	OE2	3.002
1Q9W	D_ARG_100	NH2	C_GLU_55	OE1	3.373
1Q9W	D_ARG_100	NH2	C_GLU_55	OE2	3.045

Table 1050: Interfacial 1Q9W-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID residue name residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1QBL	H_LYS_212	NZ	L_GLU_123	OE1	3.581

Table 1051: Interfacial 1QBL-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1QBM	H_LYS_212	NZ	L_GLU_123	OE1	2.762
1QBM	H_LYS_212	NZ	L_GLU_123	OE2	3.773

Table 1052: Interfacial 1QBM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1QGC	1_ARG_124	NH1	2_ASP_41	OD1	3.642
1QGC	1_ARG_124	NH1	2_ASP_41	OD2	2.877
1QGC	1_ARG_124	NH2	2_ASP_41	OD1	3.740
1QGC	2_ARG_167	NH2	3_ASP_166	OD1	2.757
1QGC	2_ARG_167	NH2	3_ASP_166	OD2	2.777
1QGC	A_ARG_99	NH2	5_ASP_143	OD1	3.483
1QGC	A_LYS_215	NZ	4_GLU_127	OE2	3.716

Table 1053: Interfacial 1QGC-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1QKZ	H_LYS_208	NZ	L_GLU_123	OE2	2.582

Table 1054: Interfacial 1QKZ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1RZJ	G_ARG_419	NH2	H_GLU_99	OE2	2.591
1RZJ	C_LYS_29	NZ	G_ASP_279	OD2	3.209
1RZJ	C_LYS_35	NZ	G_ASP_457	OD2	3.838
1RZJ	C_ARG_59	NH1	G_ASP_368	OD1	3.788
1RZJ	C_ARG_59	NH1	G_ASP_368	OD2	3.342
1RZJ	C_ARG_59	NH2	G_ASP_368	OD1	2.531
1RZJ	C_ARG_59	NH2	G_ASP_368	OD2	3.174
1RZJ	H_LYS_209	NZ	L_GLU_123	OE1	3.812

Table 1055: Interfacial 1RZJ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1RZK	G_ARG_419	NH1	H_GLU_100B	OE1	2.999
1RZK	G_ARG_419	NH1	H_GLU_100B	OE2	3.674
1RZK	G_ARG_419	NH2	H_GLU_99	OE1	2.292
1RZK	G_ARG_419	NH2	H_GLU_100B	OE2	3.969
1RZK	C_LYS_35	NZ	G_ASP_457	OD2	3.741
1RZK	C_ARG_59	NH1	G_ASP_368	OD1	3.343
1RZK	C_ARG_59	NH1	G_ASP_368	OD2	3.154
1RZK	C_ARG_59	NH2	G_ASP_368	OD1	2.433
1RZK	C_ARG_59	NH2	G_ASP_368	OD2	2.977
1RZK	H_HIS_164	NE2	L_ASP_167	OD1	3.880
1RZK	H_HIS_164	NE2	L_ASP_167	OD2	2.505
1RZK	H_LYS_209	NZ	L_GLU_123	OE1	3.513
1RZK	H_LYS_209	NZ	L_GLU_123	OE2	3.584

Table 1056: Interfacial 1RZK-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1S5I	L_ARG_96	NH1	H_ASP_97	OD1	3.601
1S5I	L_ARG_96	NH2	H_ASP_97	OD1	2.496
1S5I	L_ARG_96	NH2	H_ASP_97	OD2	2.511
1S5I	H_HIS_172	NE2	L_ASP_167	OD2	3.741
1S5I	H_LYS_221	NZ	L_GLU_123	OE2	3.213

Table 1057: Interfacial 1S5I-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1S78	D_HIS_164	NE2	C_ASP_167	OD1	3.839
1S78	D_LYS_209	NZ	C_GLU_123	OE1	3.290
1S78	D_LYS_214	NZ	C_ASP_122	OD1	3.484

Table 1058: Interfacial 1S78-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1SM3	H_LYS_143	NZ	L_GLU_124	OE2	2.757

Table 1059: Interfacial 1SM3-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1SQ2	L_ARG_73	NH2	N_ASP_93	OD1	3.549
1SQ2	L_ARG_73	NH2	N_ASP_93	OD2	3.002
1SQ2	N_ARG_100	NH1	L_ASP_52	OD1	3.032
1SQ2	N_ARG_100	NH1	L_ASP_52	OD2	3.454
1SQ2	N_ARG_100	NH2	L_ASP_52	OD1	3.561
1SQ2	N_ARG_100	NH2	L_ASP_52	OD2	3.218

Table 1060: Interfacial 1SQ2-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1T6V	L_ARG_73	NH1	N_ASP_93	OD2	3.564
1T6V	L_ARG_73	NH2	N_ASP_93	OD1	3.874
1T6V	L_ARG_73	NH2	N_ASP_93	OD2	2.603
1T6V	N_ARG_100	NH1	L_ASP_52	OD1	2.973
1T6V	N_ARG_100	NH1	L_ASP_52	OD2	3.510
1T6V	N_ARG_100	NH2	L_ASP_52	OD1	3.501
1T6V	N_ARG_100	NH2	L_ASP_52	OD2	3.094
1T6V	M_ARG_73	NH2	O_ASP_93	OD1	3.734
1T6V	M_ARG_73	NH2	O_ASP_93	OD2	2.904
1T6V	M_LYS_97	NZ	N_ASP_106	OD1	3.749
1T6V	M_LYS_97	NZ	N_ASP_106	OD2	2.853
1T6V	O_ARG_100	NH1	M_ASP_52	OD1	3.232
1T6V	O_ARG_100	NH1	M_ASP_52	OD2	2.872
1T6V	O_ARG_100	NH2	M_ASP_52	OD1	3.920
1T6V	O_ARG_100	NH2	M_ASP_52	OD2	2.990

Table 1061: Interfacial 1T6V-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1TYE	A_HIS_30	ND1	E_ASP_429	OD2	3.896
1TYE	A_ARG_32	NH1	E_ASP_429	OD1	3.657
1TYE	A_ARG_32	NH1	E_ASP_429	OD2	2.825
1TYE	A_ARG_73	NH1	C_ASP_71	OD1	3.528
1TYE	A_ARG_73	NH1	C_ASP_71	OD2	3.396
1TYE	A_ARG_73	NH2	C_ASP_71	OD2	2.714
1TYE	A_ARG_73	NH2	C_GLU_75	OE1	3.907
1TYE	B_ARG_216	NH1	A_GLU_123	OE1	2.702
1TYE	B_LYS_253	NZ	A_ASP_232	OD2	3.290
1TYE	C_ARG_73	NH1	A_ASP_71	OD1	3.491
1TYE	C_ARG_73	NH2	A_ASP_71	OD1	3.688
1TYE	C_ARG_73	NH2	A_ASP_71	OD2	3.197
1TYE	D_ARG_216	NH1	C_GLU_123	OE1	2.914
1TYE	D_ARG_216	NH1	C_GLU_123	OE2	3.969
1TYE	D_LYS_253	NZ	C_ASP_232	OD2	3.400
1TYE	E_ARG_368	NH2	A_ASP_429	OD2	3.921
1TYE	F_ARG_216	NH1	E_GLU_123	OE1	2.938
1TYE	F_ARG_216	NH1	E_GLU_123	OE2	3.244
1TYE	F_LYS_253	NZ	E_ASP_232	OD2	3.394

Table 1062: Interfacial 1TYE-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID residue name residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1TZH	V_ARG_23	NH1	W_GLU_30	OE2	3.100
1TZH	V_HIS_90	NE2	H_ASP_33	OD1	2.826
1TZH	V_HIS_90	NE2	H_ASP_33	OD2	2.524
1TZH	W_ARG_23	NH1	V_GLU_30	OE1	3.346
1TZH	W_HIS_90	NE2	B_ASP_33	OD1	3.121
1TZH	W_HIS_90	NE2	B_ASP_33	OD2	2.585
1TZH	B_LYS_209	NZ	A_GLU_123	OE2	3.903
1TZH	H_HIS_164	NE2	L_ASP_167	OD1	3.495
1TZH	H_LYS_209	NZ	L_GLU_123	OE1	2.754
1TZH	H_LYS_209	NZ	L_GLU_123	OE2	3.404

Table 1063: Interfacial 1TZH-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1TZI	B_LYS_209	NZ	A_GLU_123	OE2	3.786

Table 1064: Interfacial 1TZI-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1U6A	H_HIS_164	NE2	L_ASP_167	OD1	3.994

Table 1065: Interfacial 1U6A-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1UA6	Y_LYS_97	NZ	H_ASP_32	OD1	2.722
1UA6	Y_LYS_97	NZ	H_ASP_99	OD2	2.674

Table 1066: Interfacial 1UA6-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1UAC	Y.LYS_97	NZ	H.ASP_32	OD1	2.750
1UAC	Y.LYS_97	NZ	H.ASP_32	OD2	3.845
1UAC	Y.LYS_97	NZ	H.ASP_99	OD2	2.749

Table 1067: Interfacial 1UAC-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1UCB	L_LYS_50	NZ	H_ASP_98	OD1	3.160
1UCB	H_LYS_221	NZ	L_GLU_123	OE1	3.128

Table 1068: Interfacial 1UCB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1UJ3	A_HIS_91	NE2	B_ASP_399	OD1	3.708
1UJ3	A_HIS_91	NE2	B_ASP_399	OD2	2.884
1UJ3	B_LYS_513	NZ	A_GLU_123	OE1	3.554
1UJ3	B_LYS_513	NZ	A_GLU_123	OE2	3.075
1UJ3	C_LYS_766	NZ	A_ASP_1	OD1	3.997
1UJ3	C_LYS_769	NZ	B_ASP_399	OD1	2.791
1UJ3	C_LYS_769	NZ	B_ASP_399	OD2	3.372
1UJ3	C_LYS_801	NZ	B_ASP_352	OD1	2.774
1UJ3	C_LYS_801	NZ	B_ASP_352	OD2	3.632

Table 1069: Interfacial 1UJ3-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1UWX	H_HIS_164	NE2	L_ASP_168	OD2	3.899
1UWX	H_LYS_208	NZ	L_GLU_124	OE2	2.744
1UWX	M_LYS_208	NZ	K_GLU_124	OE2	2.705

Table 1070: Interfacial 1UWX-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1UZ6	F_ARG_164	NH1	E_ASP_166	OD1	3.662
1UZ6	F_ARG_164	NH2	E_ASP_166	OD1	3.708
1UZ6	F_ARG_164	NH2	E_ASP_169	OD2	3.554
1UZ6	F_LYS_208	NZ	E_GLU_122	OE1	3.883
1UZ6	F_ARG_209	NH1	E_GLU_122	OE2	3.531
1UZ6	H_ARG_164	NH1	L_ASP_166	OD1	3.603
1UZ6	H_ARG_164	NH2	L_ASP_166	OD1	3.557
1UZ6	H_ARG_164	NH2	L_ASP_169	OD2	3.746
1UZ6	H_LYS_208	NZ	L_GLU_122	OE1	3.795
1UZ6	H_ARG_209	NH1	L_GLU_122	OE2	3.180
1UZ6	P_ARG_164	NH1	M_ASP_166	OD1	3.636
1UZ6	P_ARG_164	NH2	M_ASP_166	OD1	3.666
1UZ6	P_ARG_164	NH2	M_ASP_166	OD2	3.901
1UZ6	P_ARG_164	NH2	M_ASP_169	OD2	3.942
1UZ6	P_LYS_208	NZ	M_GLU_122	OE1	3.361
1UZ6	W_ARG_164	NH2	V_ASP_166	OD1	3.892
1UZ6	W_LYS_208	NZ	V_GLU_122	OE1	3.069

Table 1071: Interfacial 1UZ6-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1UZ8	B_ARG_164	NH1	A_ASP_166	OD1	3.299
1UZ8	B_ARG_164	NH2	A_ASP_166	OD1	3.745
1UZ8	B_ARG_164	NH2	A_ASP_169	OD2	3.660
1UZ8	H_ARG_164	NH1	L_ASP_166	OD1	3.385
1UZ8	H_ARG_164	NH2	L_ASP_166	OD1	3.573
1UZ8	H_ARG_164	NH2	L_ASP_169	OD2	3.234

Table 1072: Interfacial 1UZ8-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1V7M	L_ARG_95	NH1	H_GLU_50	OE1	3.532
1V7M	V_ARG_98	NH2	H_ASP_31	OD1	3.697
1V7M	M_ARG_95	NH1	I_GLU_50	OE1	3.801
1V7M	X_ARG_98	NH2	I_ASP_31	OD1	3.214

Table 1073: Interfacial 1V7M-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1V7N	L_ARG_95	NH1	H_GLU_50	OE1	3.194
1V7N	L_ARG_107	NH1	O_GLU_78	OE2	3.587
1V7N	L_ARG_107	NH2	O_GLU_78	OE1	3.844
1V7N	L_ARG_107	NH2	O_GLU_78	OE2	2.214
1V7N	H_ARG_216	NH2	Z_ASP_123	OD2	3.997
1V7N	M_ARG_95	NH1	I_GLU_50	OE1	2.984
1V7N	M_ARG_107	NH1	N_GLU_78	OE2	3.960
1V7N	M_ARG_107	NH2	N_GLU_78	OE1	3.607
1V7N	M_ARG_107	NH2	N_GLU_78	OE2	2.132
1V7N	N_ARG_95	NH1	J_GLU_50	OE1	3.631
1V7N	N_ARG_107	NH2	M_GLU_78	OE1	2.980
1V7N	N_ARG_107	NH2	M_GLU_78	OE2	2.369
1V7N	J_ARG_216	NH2	X_ASP_123	OD2	3.982
1V7N	O_ARG_95	NH1	K_GLU_50	OE1	2.735
1V7N	O_ARG_107	NH1	L_GLU_78	OE1	3.650
1V7N	O_ARG_107	NH1	L_GLU_78	OE2	3.114
1V7N	O_ARG_107	NH2	L_GLU_78	OE2	2.402
1V7N	V_ARG_98	NH2	H_ASP_31	OD1	3.580
1V7N	X_ARG_98	NH2	I_ASP_31	OD1	3.389
1V7N	X_HIS_121	ND1	J_ASP_217	OD1	2.619
1V7N	X_HIS_121	NE2	J_ASP_217	OD1	3.422
1V7N	Y_HIS_20	ND1	H_ASP_217	OD1	3.368
1V7N	Y_HIS_20	ND1	H_ASP_217	OD2	3.116
1V7N	Y_HIS_20	NE2	H_ASP_217	OD1	3.862
1V7N	Y_HIS_121	ND1	I_ASP_217	OD1	3.108
1V7N	Z_ARG_98	NH2	K_ASP_31	OD1	3.622
1V7N	Z_ARG_140	NH2	M_GLU_212	OE1	3.768

Table 1074: Interfacial 1V7N-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1VES	A_ARG_25	NH1	B_ASP_4	OD1	3.636
1VES	A_ARG_25	NH1	B_ASP_4	OD2	2.836
1VES	A_ARG_25	NH2	B_ASP_4	OD1	2.879
1VES	A_ARG_25	NH2	B_ASP_4	OD2	3.552
1VES	B_ARG_25	NH1	A_ASP_4	OD1	3.762
1VES	B_ARG_25	NH1	A_ASP_4	OD2	2.782
1VES	B_ARG_25	NH2	A_ASP_4	OD1	3.070
1VES	B_ARG_25	NH2	A_ASP_4	OD2	3.548

Table 1075: Interfacial 1VES-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1VFA	A_ARG_96	NH1	B_GLU_98	OE1	2.794
1VFA	A_ARG_96	NH1	B_GLU_98	OE2	3.600
1VFA	A_ARG_96	NH2	B_GLU_98	OE1	3.537
1VFA	A_ARG_96	NH2	B_GLU_98	OE2	2.928

Table 1076: Interfacial 1VFA-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1VFB	A_ARG_96	NH1	B_GLU_98	OE1	2.821
1VFB	A_ARG_96	NH1	B_GLU_98	OE2	3.695
1VFB	A_ARG_96	NH2	B_GLU_98	OE1	3.393
1VFB	A_ARG_96	NH2	B_GLU_98	OE2	2.813

Table 1077: Interfacial 1VFB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1W72	A_ARG_35	NH1	B_ASP_53	OD1	2.945
1W72	A_ARG_48	NH1	B_ASP_53	OD2	3.978
1W72	A_ARG_48	NH2	B_ASP_53	OD1	3.455
1W72	A_ARG_48	NH2	B_ASP_53	OD2	2.916
1W72	A_ARG_65	NH1	H_ASP_30	OD1	3.409
1W72	A_ARG_65	NH1	H_ASP_31	OD1	2.977
1W72	A_ARG_114	NH1	C_ASP_3	OD2	3.999
1W72	A_LYS_146	NZ	L_ASP_95A	OD1	3.112
1W72	A_LYS_146	NZ	L_ASP_95A	OD2	3.996
1W72	A_ARG_156	NH1	C_ASP_3	OD1	3.704
1W72	A_ARG_156	NH1	C_ASP_3	OD2	2.953
1W72	A_ARG_163	NH1	C_GLU_1	OE1	3.400
1W72	A_ARG_163	NH2	C_GLU_1	OE1	3.293
1W72	A_ARG_163	NH2	C_GLU_1	OE2	3.482
1W72	A_ARG_170	NH1	C_GLU_1	OE2	3.205
1W72	A_ARG_170	NH2	C_GLU_1	OE2	2.677
1W72	A_HIS_192	NE2	B_ASP_98	OD1	3.224
1W72	A_HIS_192	NE2	B_ASP_98	OD2	2.823
1W72	B_LYS_6	NZ	A_GLU_232	OE1	3.881
1W72	D_ARG_35	NH2	E_ASP_53	OD1	3.761
1W72	D_ARG_65	NH1	L_ASP_30	OD1	2.970
1W72	D_ARG_65	NH1	L_ASP_31	OD1	3.035
1W72	D_LYS_146	NZ	M_ASP_95A	OD2	3.397
1W72	D_ARG_156	NH1	F_ASP_3	OD1	3.644
1W72	D_ARG_156	NH1	F_ASP_3	OD2	3.082
1W72	D_ARG_163	NH1	F_GLU_1	OE1	3.609
1W72	D_ARG_163	NH1	F_GLU_1	OE2	3.022
1W72	D_HIS_192	NE2	E_ASP_98	OD2	3.123
1W72	E_LYS_6	NZ	D_GLU_232	OE2	2.863
1W72	H_LYS_145	NZ	L_GLU_124	OE2	2.720
1W72	H_LYS_221	NZ	L_GLU_123	OE1	2.737
1W72	H_LYS_221	NZ	L_GLU_123	OE2	3.946
1W72	I_LYS_145	NZ	M_GLU_124	OE2	2.470
1W72	I_LYS_228	NZ	M_GLU_123	OE2	3.514
1W72	M_HIS_95B	NE2	L_ASP_61	OD2	3.924

Table 1078: Interfacial 1W72-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1WEJ	L_HIS_30	ND1	F_GLU_104	OE1	2.984
1WEJ	L_HIS_30	ND1	F_GLU_104	OE2	2.758
1WEJ	H_ARG_50	NH1	F_GLU_62	OE2	3.319
1WEJ	H_ARG_50	NH2	F_GLU_62	OE2	2.823
1WEJ	H_LYS_212	NZ	L_GLU_123	OE2	3.963
1WEJ	F_LYS_60	NZ	H_ASP_100	OD2	3.322

Table 1079: Interfacial 1WEJ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1XF2	H.LYS.208	NZ	L.GLU.123	OE1	3.369
1XF2	H.LYS.208	NZ	L.GLU.123	OE2	2.577
1XF2	B.LYS.208	NZ	A.GLU.123	OE2	2.913

Table 1080: Interfacial 1XF2-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1XGY	L_ARG_50	NH2	P_GLU_6	OE1	2.621
1XGY	H_LYS_208	NZ	L_GLU_123	OE2	3.768
1XGY	M_ARG_50	NH2	Q_GLU_6	OE1	3.022
1XGY	I_LYS_208	NZ	M_GLU_123	OE2	3.551

Table 1081: Interfacial 1XGY-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1XIW	A_ARG_80	NH1	D_ASP_106	OD2	2.879
1XIW	A_ARG_94	NH2	B_GLU_7	OE1	3.648
1XIW	A_ARG_94	NH2	B_GLU_7	OE2	2.974
1XIW	B_LYS_2	NZ	A_ASP_42	OD1	3.017
1XIW	B_LYS_2	NZ	A_ASP_42	OD2	2.678
1XIW	C_ARG_31	NH1	A_ASP_86	OD1	2.919
1XIW	C_ARG_31	NH1	A_ASP_86	OD2	3.491
1XIW	C_ARG_31	NH2	A_ASP_86	OD1	3.709
1XIW	C_ARG_31	NH2	A_ASP_86	OD2	2.755
1XIW	C_ARG_54	NH1	F_GLU_6	OE1	2.951
1XIW	C_ARG_54	NH2	F_GLU_6	OE1	3.193
1XIW	C_ARG_54	NH2	F_GLU_6	OE2	3.073
1XIW	C_HIS_56	ND1	F_GLU_9	OE1	3.139
1XIW	C_HIS_56	ND1	F_GLU_9	OE2	2.963
1XIW	D_LYS_55	NZ	A_ASP_57	OD1	3.690
1XIW	E_ARG_80	NH1	H_ASP_106	OD2	2.741
1XIW	E_ARG_94	NH2	F_GLU_7	OE2	3.577
1XIW	F_LYS_2	NZ	E_ASP_42	OD1	3.079
1XIW	F_LYS_2	NZ	E_ASP_42	OD2	3.491
1XIW	G_ARG_31	NH1	E_ASP_86	OD1	3.076
1XIW	G_ARG_31	NH1	E_ASP_86	OD2	3.219
1XIW	G_ARG_31	NH2	E_ASP_86	OD2	2.817
1XIW	G_ARG_54	NH1	B_GLU_6	OE1	2.839
1XIW	G_ARG_54	NH2	B_GLU_6	OE1	3.146
1XIW	G_ARG_54	NH2	B_GLU_6	OE2	3.222
1XIW	G_HIS_56	ND1	B_GLU_9	OE1	2.509
1XIW	G_HIS_56	ND1	B_GLU_9	OE2	3.961

Table 1082: Interfacial 1XIW-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1YEI	L_LYS_30	NZ	H_GLU_100B	OE1	2.979
1YEI	L_LYS_45	NZ	H_ASP_101	OD1	2.746
1YEI	L_LYS_45	NZ	H_ASP_101	OD2	3.891
1YEI	L_ARG_46	NH2	H_ASP_101	OD1	3.707
1YEI	L_HIS_49	NE2	H_ASP_100C	OD1	3.542

Table 1083: Interfacial 1YEI-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1YEJ	L_LYS_45	NZ	H_ASP_101	OD1	2.790
1YEJ	L_LYS_45	NZ	H_ASP_101	OD2	3.988
1YEJ	L_ARG_46	NH2	H_ASP_101	OD1	3.745
1YEJ	L_HIS_49	NE2	H_ASP_100C	OD1	3.536
1YEJ	L_LYS_53	NZ	H_ASP_100C	OD1	3.377
1YEJ	L_LYS_53	NZ	H_ASP_100C	OD2	3.298

Table 1084: Interfacial 1YEJ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1YEK	L-LYS_30	NZ	H-GLU_100B	OE1	2.464
1YEK	L-LYS_45	NZ	H-ASP_101	OD1	2.830
1YEK	L-ARG_46	NH2	H-ASP_101	OD1	3.853
1YEK	L-HIS_49	NE2	H-ASP_100C	OD1	3.610

Table 1085: Interfacial 1YEK-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1YNT	A_ARG_24	NH1	C_ASP_1070	OD2	3.114
1YNT	A_ARG_24	NH2	C_ASP_1070	OD2	3.728
1YNT	B_LYS_563	NZ	A_ASP_1	OD1	2.935
1YNT	B_LYS_563	NZ	A_ASP_1	OD2	3.384
1YNT	B_LYS_713	NZ	A_GLU_123	OE1	3.645
1YNT	C_ARG_1024	NH1	A_ASP_70	OD2	3.173
1YNT	C_ARG_1024	NH2	A_ASP_70	OD2	3.802
1YNT	C_LYS_1107	NZ	E_GLU_869	OE1	3.719
1YNT	D_LYS_1563	NZ	C_ASP_1001	OD1	2.913
1YNT	D_LYS_1563	NZ	C_ASP_1001	OD2	3.385
1YNT	D_LYS_1713	NZ	C_GLU_1123	OE1	3.557
1YNT	E_LYS_824	NZ	A_ASP_143	OD1	3.012
1YNT	E_LYS_824	NZ	A_ASP_143	OD2	3.238
1YNT	E_LYS_833	NZ	A_ASP_17	OD2	3.941

Table 1086: Interfacial 1YNT-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1YQV	L_ARG_46	NH2	H_ASP_101	OD2	3.072
1YQV	H_LYS_221	NZ	L_GLU_123	OE1	3.123
1YQV	H_LYS_221	NZ	L_GLU_123	OE2	2.724
1YQV	Y_ARG_45	NH1	H_GLU_50	OE1	3.514
1YQV	Y_ARG_45	NH1	H_GLU_50	OE2	2.957
1YQV	Y_ARG_68	NH1	H_GLU_50	OE1	2.746
1YQV	Y_ARG_68	NH1	H_GLU_50	OE2	3.759
1YQV	Y_ARG_68	NH2	H_GLU_50	OE1	3.492
1YQV	Y_ARG_68	NH2	H_GLU_50	OE2	2.963

Table 1087: Interfacial 1YQV-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1YYL	G_ARG_419	NH1	H_GLU_100D	OE2	3.749
1YYL	G_ARG_419	NH2	H_GLU_99	OE2	2.852
1YYL	G_ARG_419	NH2	H_GLU_100D	OE1	3.510
1YYL	G_ARG_419	NH2	H_GLU_100D	OE2	2.773
1YYL	H_LYS_209	NZ	L_GLU_123	OE1	2.745
1YYL	H_LYS_209	NZ	L_GLU_123	OE2	3.202
1YYL	P_ARG_1419	NH1	R_GLU_1100B	OE1	3.247
1YYL	P_ARG_1419	NH2	R_GLU_1099	OE1	2.456
1YYL	P_ARG_1419	NH2	R_GLU_1100D	OE1	3.853
1YYL	R_LYS_1201	NZ	H_GLU_10	OE1	3.633
1YYL	R_LYS_1209	NZ	Q_GLU_1123	OE2	3.934
1YYL	S_ARG_1009	NH1	P_ASP_1368	OD2	3.204
1YYL	S_ARG_1009	NH2	P_ASP_1368	OD2	2.930

Table 1088: Interfacial 1YYL-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1YYM	G_ARG_419	NH2	H_GLU_99	OE2	2.868
1YYM	G_ARG_419	NH2	H_GLU_100D	OE1	3.511
1YYM	H_LYS_209	NZ	L_GLU_123	OE1	2.715
1YYM	H_LYS_209	NZ	L_GLU_123	OE2	2.976
1YYM	P_ARG_1419	NH1	R_GLU_1100B	OE1	2.635
1YYM	P_ARG_1419	NH2	R_GLU_1099	OE1	3.192
1YYM	S_ARG_1009	NH1	P_ASP_1368	OD2	3.572
1YYM	S_ARG_1009	NH2	P_ASP_1368	OD2	2.725

Table 1089: Interfacial 1YYM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
1ZEA	H_ARG_95	NH1	L_GLU_34	OE1	2.842
1ZEA	H_ARG_95	NH1	L_GLU_34	OE2	3.642
1ZEA	H_ARG_95	NH2	L_GLU_34	OE1	3.613
1ZEA	H_ARG_95	NH2	L_GLU_34	OE2	2.859
1ZEA	H_LYS_208	NZ	L_GLU_123	OE2	2.817

Table 1090: Interfacial 1ZEA-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2AAB	H_LYS_208	NZ	L_GLU_123	OE1	3.545

Table 1091: Interfacial 2AAB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2B2X	A_HIS_261	NE2	H_ASP_101	OD2	3.121
2B2X	H_HIS_169	NE2	L_ASP_171	OD2	3.832
2B2X	H_LYS_213	NZ	L_GLU_127	OE1	2.709
2B2X	H_LYS_213	NZ	L_GLU_127	OE2	3.416
2B2X	L_HIS_31	NE2	A_GLU_259	OE2	3.821
2B2X	B_HIS_261	NE2	I_ASP_101	OD2	3.107
2B2X	I_HIS_169	NE2	M_ASP_171	OD2	3.874
2B2X	I_LYS_213	NZ	M_GLU_127	OE2	3.245
2B2X	M_HIS_31	NE2	B_GLU_259	OE2	3.848

Table 1092: Interfacial 2B2X-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2B4C	G_ARG_	NH1	H_ASP_	OD2	3.237
2B4C	G_ARG_	NH2	H_ASP_	OD2	2.859
2B4C	G_LYS_	NZ	H_ASP_	OD2	2.598
2B4C	C_ARG_	NH1	H_GLU_	OE2	3.957
2B4C	C_ARG_	NH2	H_GLU_	OE2	3.405
2B4C	C_ARG_	NH1	G_ASP_	OD1	2.937
2B4C	C_ARG_	NH1	G_ASP_	OD2	3.245
2B4C	H_LYS_	NZ	L_GLU_	OE1	3.365
2B4C	H_LYS_209	NZ	L_GLU_123	OE2	3.837

Table 1093: Interfacial 2B4C-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2BDN	A_LYS_56	NZ	H_ASP_52	OD1	2.539
2BDN	A_LYS_56	NZ	H_ASP_52	OD2	3.792
2BDN	L_ARG_32	NH1	A_ASP_65	OD1	3.196
2BDN	L_ARG_32	NH1	A_ASP_68	OD1	2.578
2BDN	L_ARG_32	NH2	A_ASP_65	OD1	2.774
2BDN	H_ARG_98	NH1	A_GLU_39	OE2	3.155
2BDN	H_LYS_212	NZ	L_GLU_123	OE2	3.177

Table 1094: Interfacial 2BDN-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2BRR	H_ARG_213	NH1	L_GLU_123	OE1	2.600
2BRR	H_ARG_213	NH1	L_GLU_123	OE2	3.932
2BRR	H_ARG_213	NH2	L_GLU_123	OE1	3.110
2BRR	H_ARG_213	NH2	L_GLU_123	OE2	3.029
2BRR	P_LYS_7	NZ	H_ASP_95	OD1	3.067
2BRR	P_LYS_7	NZ	H_ASP_95	OD2	2.549
2BRR	P_HIS_11	ND1	Y_ASP_95	OD2	2.841
2BRR	Y_LYS_208	NZ	X_GLU_123	OE2	3.359
2BRR	Y_ARG_213	NH1	X_GLU_123	OE1	2.523
2BRR	Y_ARG_213	NH1	X_GLU_123	OE2	3.327
2BRR	Y_ARG_213	NH2	X_GLU_123	OE1	3.468
2BRR	Y_ARG_213	NH2	X_GLU_123	OE2	2.546

Table 1095: Interfacial 2BRR-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID residue name residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2DBL	H_LYS_221	NZ	L_GLU_123	OE2	3.660

Table 1096: Interfacial 2DBL-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2DQC	Y.LYS_97	NZ	H.ASP_32	OD1	2.612
2DQC	Y.LYS_97	NZ	H.ASP_32	OD2	3.998
2DQC	Y.LYS_97	NZ	H.ASP_99	OD1	3.500
2DQC	Y.LYS_97	NZ	H.ASP_99	OD2	2.637

Table 1097: Interfacial 2DQC-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2DQD	Y.LYS_97	NZ	H.ASP_32	OD1	2.767
2DQD	Y.LYS_97	NZ	H.ASP_32	OD2	3.965
2DQD	Y.LYS_97	NZ	H.ASP_99	OD1	3.334
2DQD	Y.LYS_97	NZ	H.ASP_99	OD2	3.048

Table 1098: Interfacial 2DQD-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2DQE	Y_LYS_97	NZ	H_ASP_32	OD1	2.650
2DQE	Y_LYS_97	NZ	H_ASP_99	OD1	3.314
2DQE	Y_LYS_97	NZ	H_ASP_99	OD2	2.899

Table 1099: Interfacial 2DQE-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2DQF	A_ARG_45	NH1	E_ASP_1	OD2	3.511
2DQF	A_LYS_49	NZ	B_ASP_99	OD1	3.470
2DQF	A_ARG_61	NH1	E_ASP_27	OD1	3.814
2DQF	C_LYS_97	NZ	B_ASP_99	OD1	3.543
2DQF	C_LYS_97	NZ	B_ASP_99	OD2	2.851
2DQF	D_LYS_39	NZ	B_ASP_1	OD1	3.005
2DQF	D_ARG_61	NH1	B_ASP_27	OD1	3.581
2DQF	F_LYS_97	NZ	E_ASP_99	OD2	3.165

Table 1100: Interfacial 2DQF-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2DQG	Y_LYS_97	NZ	H_ASP_32	OD1	3.992
2DQG	Y_LYS_97	NZ	H_ASP_32	OD2	2.695
2DQG	Y_LYS_97	NZ	H_ASP_99	OD1	3.156
2DQG	Y_LYS_97	NZ	H_ASP_99	OD2	3.019

Table 1101: Interfacial 2DQG-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2DQH	Y_LYS_97	NZ	H_ASP_32	OD1	2.777
2DQH	Y_LYS_97	NZ	H_ASP_99	OD1	3.694
2DQH	Y_LYS_97	NZ	H_ASP_99	OD2	2.635

Table 1102: Interfacial 2DQH-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2DQI	L.LYS_49	NZ	H.ASP_99	OD1	2.843
2DQI	L.LYS_49	NZ	H.ASP_101	OD1	3.541
2DQI	L.LYS_49	NZ	H.ASP_101	OD2	3.285
2DQI	Y.LYS_97	NZ	H.ASP_32	OD1	2.729

Table 1103: Interfacial 2DQI-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2DQJ	Y_LYS_97	NZ	H_ASP_32	OD1	2.638
2DQJ	Y_LYS_97	NZ	H_ASP_32	OD2	3.939
2DQJ	Y_LYS_97	NZ	H_ASP_99	OD1	3.482
2DQJ	Y_LYS_97	NZ	H_ASP_99	OD2	2.865

Table 1104: Interfacial 2DQJ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2DQT	L_LYS_50	NZ	H_ASP_100C	OD1	3.056
2DQT	H_ARG_100B	NH2	L_ASP_30	OD1	3.486
2DQT	H_ARG_100B	NH2	L_ASP_30	OD2	3.745

Table 1105: Interfacial 2DQT-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2DQU	L.LYS.50	NZ	H.ASP.100C	OD1	2.628
2DQU	L.LYS.50	NZ	H.ASP.100C	OD2	3.616
2DQU	H.ARG.100B	NH2	L.ASP.30	OD2	2.721
2DQU	H.LYS.208	NZ	L.GLU.123	OE2	2.915
2DQU	H.ARG.213	NH1	L.GLU.123	OE1	3.471

Table 1106: Interfacial 2DQU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2FB4	H_LYS_148	NZ	L_GLU_126	OE2	2.805
2FB4	H_LYS_214	NZ	L_GLU_125	OE1	3.053
2FB4	H_LYS_214	NZ	L_GLU_125	OE2	2.759

Table 1107: Interfacial 2FB4-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2FD6	A_HIS_87	ND1	U_ASP_11	OD2	3.705
2FD6	H_HIS_98	ND1	L_GLU_50	OE1	3.050
2FD6	H_HIS_98	ND1	L_GLU_50	OE2	3.997
2FD6	H_LYS_203	NZ	L_GLU_122	OE2	2.585
2FD6	U_ARG_192	NH1	H_GLU_58	OE2	2.359
2FD6	U_ARG_192	NH2	H_GLU_58	OE2	3.898

Table 1108: Interfacial 2FD6-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2FR4	H_LYS_208	NZ	L_GLU_123	OE2	3.199
2FR4	B_LYS_208	NZ	A_GLU_123	OE1	2.539

Table 1109: Interfacial 2FR4-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2H32	H_ARG_59	NH1	A_GLU_106	OE1	3.937
2H32	H_ARG_59	NH1	A_GLU_106	OE2	3.372
2H32	H_ARG_59	NH2	A_GLU_106	OE2	3.412

Table 1110: Interfacial 2H32-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2H9G	B_HIS_53	ND1	R_GLU_36	OE2	3.471
2H9G	B_LYS_209	NZ	A_GLU_123	OE1	2.713
2H9G	H_LYS_209	NZ	L_GLU_123	OE1	2.570

Table 1111: Interfacial 2H9G-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2HFG	H_ARG_95	NH2	R_ASP_26	OD1	2.783
2HFG	H_ARG_95	NH2	R_ASP_26	OD2	3.667
2HFG	H_LYS_209	NZ	L_GLU_122	OE1	3.336
2HFG	H_LYS_209	NZ	L_GLU_122	OE2	2.886

Table 1112: Interfacial 2HFG-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2HKF	L_LYS_55	NZ	P_ASP_6	OD1	2.651
2HKF	H_ARG_50	NH2	P_GLU_5	OE1	3.869
2HKF	H_ARG_50	NH2	P_GLU_5	OE2	2.886
2HKF	H_ARG_52	NH2	P_GLU_5	OE1	3.116
2HKF	H_LYS_214	NZ	L_GLU_128	OE2	2.891

Table 1113: Interfacial 2HKF-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2HMG	A.LYS_27	NZ	B.GLU_97	OE1	2.762
2HMG	A.LYS_27	NZ	B.GLU_97	OE2	3.001
2HMG	A.ARG_109	NH1	B.GLU_67	OE1	3.634
2HMG	A.ARG_109	NH1	B.GLU_67	OE2	2.959
2HMG	A.ARG_269	NH2	B.GLU_67	OE1	2.999
2HMG	A.LYS_299	NZ	B.GLU_69	OE1	3.169
2HMG	B.ARG_54	NH1	F.GLU_97	OE1	2.721
2HMG	B.ARG_54	NH2	F.GLU_97	OE1	3.280
2HMG	B.LYS_62	NZ	F.ASP_86	OD1	3.023
2HMG	B.LYS_62	NZ	F.ASP_86	OD2	2.718
2HMG	B.LYS_62	NZ	F.ASP_90	OD1	3.256
2HMG	B.LYS_62	NZ	F.ASP_90	OD2	2.780
2HMG	B.HIS_64	NE2	F.ASP_79	OD2	3.863
2HMG	B.ARG_76	NH1	D.GLU_74	OE1	3.508
2HMG	B.ARG_76	NH1	D.GLU_74	OE2	2.816
2HMG	B.ARG_76	NH1	D.GLU_81	OE1	2.774
2HMG	B.ARG_76	NH1	D.GLU_81	OE2	3.655
2HMG	B.ARG_76	NH2	D.GLU_74	OE1	2.915
2HMG	B.ARG_76	NH2	D.GLU_74	OE2	3.598
2HMG	B.ARG_123	NH1	F.GLU_132	OE2	3.122
2HMG	B.ARG_124	NH1	F.GLU_132	OE1	3.544
2HMG	B.ARG_124	NH1	F.GLU_132	OE2	3.040
2HMG	B.ARG_127	NH2	F.GLU_131	OE1	2.502
2HMG	B.ARG_163	NH1	F.GLU_131	OE1	2.668
2HMG	B.ARG_163	NH1	F.GLU_131	OE2	2.605
2HMG	B.ARG_170	NH1	D.GLU_128	OE1	3.860
2HMG	B.ARG_170	NH2	D.GLU_128	OE1	2.750
2HMG	B.ARG_170	NH2	D.GLU_128	OE2	3.837
2HMG	C.LYS_27	NZ	D.GLU_97	OE1	2.819
2HMG	C.LYS_27	NZ	D.GLU_97	OE2	3.060
2HMG	C.ARG_109	NH1	D.GLU_67	OE1	3.653
2HMG	C.ARG_109	NH1	D.GLU_67	OE2	2.947
2HMG	C.ARG_269	NH2	D.GLU_67	OE1	2.972
2HMG	C.LYS_299	NZ	D.GLU_69	OE1	3.147
2HMG	D.ARG_54	NH1	B.GLU_97	OE1	2.735
2HMG	D.ARG_54	NH2	B.GLU_97	OE1	3.312
2HMG	D.LYS_62	NZ	B.ASP_86	OD1	3.037
2HMG	D.LYS_62	NZ	B.ASP_86	OD2	2.683
2HMG	D.LYS_62	NZ	B.ASP_90	OD1	3.222
2HMG	D.LYS_62	NZ	B.ASP_90	OD2	2.673
2HMG	D.HIS_64	NE2	B.ASP_79	OD2	3.737
2HMG	D.ARG_76	NH1	F.GLU_74	OE1	3.549
2HMG	D.ARG_76	NH1	F.GLU_74	OE2	2.731
2HMG	D.ARG_76	NH1	F.GLU_81	OE1	2.698
2HMG	D.ARG_76	NH1	F.GLU_81	OE2	3.690
2HMG	D.ARG_76	NH2	F.GLU_74	OE1	2.828
2HMG	D.ARG_76	NH2	F.GLU_74	OE2	3.390
2HMG	D.ARG_123	NH1	B.GLU_132	OE2	3.058
2HMG	D.ARG_124	NH1	B.GLU_132	OE1	3.508
2HMG	D.ARG_124	NH1	B.GLU_132	OE2	3.040
2HMG	D.ARG_127	NH2	B.GLU_131	OE1	2.517
2HMG	D.ARG_163	NH1	B.GLU_131	OE1	2.667
2HMG	D.ARG_163	NH1	B.GLU_131	OE2	2.648
2HMG	D.ARG_170	NH1	F.GLU_128	OE1	3.974
2HMG	D.ARG_170	NH2	F.GLU_128	OE1	2.843
2HMG	E.LYS_27	NZ	F.GLU_97	OE1	2.743
2HMG	E.LYS_27	NZ	F.GLU_97	OE2	3.029

2HMG	E_ARG_109	NH1	F_GLU_67	OE1	3.629
2HMG	E_ARG_109	NH1	F_GLU_67	OE2	2.891
2HMG	E_ARG_269	NH2	F_GLU_67	OE1	2.967
2HMG	E_LYS_299	NZ	F_GLU_69	OE1	3.127
2HMG	F_ARG_54	NH1	D_GLU_97	OE1	2.701
2HMG	F_ARG_54	NH2	D_GLU_97	OE1	3.310
2HMG	F_LYS_62	NZ	D_ASP_86	OD1	2.945
2HMG	F_LYS_62	NZ	D_ASP_86	OD2	2.624
2HMG	F_LYS_62	NZ	D_ASP_90	OD1	3.290
2HMG	F_LYS_62	NZ	D_ASP_90	OD2	2.741
2HMG	F_HIS_64	NE2	D_ASP_79	OD2	3.679
2HMG	F_ARG_76	NH1	B_GLU_74	OE1	3.499
2HMG	F_ARG_76	NH1	B_GLU_74	OE2	2.732
2HMG	F_ARG_76	NH1	B_GLU_81	OE1	2.710
2HMG	F_ARG_76	NH1	B_GLU_81	OE2	3.754
2HMG	F_ARG_76	NH2	B_GLU_74	OE1	2.743
2HMG	F_ARG_76	NH2	B_GLU_74	OE2	3.373
2HMG	F_ARG_123	NH1	D_GLU_132	OE2	3.112
2HMG	F_ARG_124	NH1	D_GLU_132	OE1	3.531
2HMG	F_ARG_124	NH1	D_GLU_132	OE2	3.090
2HMG	F_ARG_127	NH2	D_GLU_131	OE1	2.569
2HMG	F_ARG_163	NH1	D_GLU_131	OE1	2.672
2HMG	F_ARG_163	NH1	D_GLU_131	OE2	2.717
2HMG	F_ARG_170	NH1	B_GLU_128	OE1	3.849
2HMG	F_ARG_170	NH2	B_GLU_128	OE1	2.798
2HMG	F_ARG_170	NH2	B_GLU_128	OE2	3.855

Table 1114: Interfacial 2HMG-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2HRP	L_LYS_30	NZ	H_ASP_100B	OD2	3.323
2HRP	L_ARG_61	NH1	M_GLU_79	OE1	2.692
2HRP	L_ARG_61	NH1	M_GLU_79	OE2	2.607
2HRP	L_ARG_108	NH1	N_ASP_1	OD1	3.613
2HRP	L_ARG_108	NH1	N_ASP_1	OD2	2.869
2HRP	L_ARG_108	NH2	N_ASP_1	OD1	3.306
2HRP	L_ARG_108	NH2	N_ASP_1	OD2	3.988
2HRP	H_LYS_205	NZ	N_ASP_207	OD2	3.339
2HRP	H_LYS_208	NZ	L_GLU_123	OE1	2.834
2HRP	M_LYS_30	NZ	N_ASP_100B	OD2	3.922
2HRP	M_ARG_61	NH1	L_GLU_79	OE1	2.827
2HRP	M_ARG_61	NH1	L_GLU_79	OE2	2.489
2HRP	M_ARG_61	NH2	L_GLU_79	OE1	3.658
2HRP	M_ARG_108	NH1	H_ASP_1	OD2	3.449
2HRP	N_LYS_208	NZ	M_GLU_123	OE1	2.875
2HRP	N_LYS_208	NZ	M_GLU_123	OE2	3.117

Table 1115: Interfacial 2HRP-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2I25	N_ARG_25	NH1	O_ASP_101	OD1	3.459
2I25	N_ARG_25	NH1	O_ASP_101	OD2	3.204
2I25	N_ARG_25	NH2	O_ASP_101	OD1	2.762
2I25	N_ARG_25	NH2	O_ASP_101	OD2	3.967
2I25	N_ARG_88	NH2	L_ASP_101	OD1	2.875
2I25	N_ARG_88	NH2	L_ASP_101	OD2	3.303
2I25	L_ARG_61	NH2	N_ASP_101	OD2	3.227
2I25	L_ARG_73	NH1	N_GLU_86	OE1	3.764
2I25	L_ARG_73	NH1	N_GLU_86	OE2	2.771
2I25	L_ARG_112	NH2	N_ASP_93	OD1	2.693
2I25	O_ARG_44	NH2	N_GLU_57	OE1	3.011
2I25	O_ARG_88	NH2	M_ASP_101	OD1	2.850
2I25	O_ARG_88	NH2	M_ASP_101	OD2	3.440
2I25	M_ARG_61	NH2	O_ASP_101	OD2	2.975
2I25	M_ARG_73	NH1	O_GLU_86	OE1	3.850
2I25	M_ARG_73	NH1	O_GLU_86	OE2	2.851
2I25	M_ARG_112	NH1	O_ASP_93	OD1	3.660
2I25	M_ARG_112	NH2	O_ASP_93	OD1	3.176

Table 1116: Interfacial 2I25-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2I26	N_ARG.88	NH2	L_ASP.101	OD1	3.268
2I26	N_ARG.88	NH2	L_ASP.101	OD2	3.652
2I26	L_ARG.73	NH1	N_GLU.86	OE2	3.511
2I26	L_ARG.73	NH2	N_GLU.86	OE1	3.590
2I26	L_ARG.73	NH2	N_GLU.86	OE2	3.542
2I26	L_ARG.112	NH1	N_ASP.93	OD2	3.838
2I26	L_ARG.112	NH2	N_ASP.93	OD2	3.391
2I26	O_ARG.88	NH1	M_ASP.101	OD1	2.648
2I26	O_ARG.88	NH1	M_ASP.101	OD2	2.840
2I26	M_ARG.73	NH1	O_GLU.86	OE1	2.832
2I26	M_ARG.73	NH1	O_GLU.86	OE2	3.677
2I26	M_ARG.112	NH1	O_ASP.93	OD2	3.127
2I26	M_ARG.112	NH2	O_ASP.93	OD2	3.198
2I26	P_ARG.88	NH1	Q_ASP.101	OD1	3.139
2I26	P_ARG.88	NH1	Q_ASP.101	OD2	3.016
2I26	Q_ARG.61	NH2	P_ASP.101	OD2	3.115
2I26	Q_ARG.73	NH1	P_GLU.86	OE2	2.623
2I26	Q_ARG.112	NH1	P_ASP.93	OD2	3.805
2I26	Q_ARG.112	NH2	P_ASP.93	OD2	3.685

Table 1117: Interfacial 2I26-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID** **residue name** **residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2I27	N_ARG_25	NH2	O_GLU_46	OE2	3.350

Table 1118: Interfacial 2I27-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2I5Y	G_ARG_419	NH1	H_GLU_100B	OE1	3.248
2I5Y	G_ARG_419	NH2	H_GLU_99	OE2	3.146
2I5Y	G_ARG_419	NH2	H_GLU_100D	OE2	2.601
2I5Y	H_LYS_201	NZ	R_GLU_10	OE2	3.615
2I5Y	H_LYS_209	NZ	L_GLU_123	OE1	2.531
2I5Y	H_LYS_209	NZ	L_GLU_123	OE2	3.403
2I5Y	P_ARG_419	NH1	R_GLU_99	OE2	3.800
2I5Y	P_ARG_419	NH1	R_GLU_100D	OE1	2.563
2I5Y	P_ARG_419	NH1	R_GLU_100D	OE2	3.898
2I5Y	R_LYS_209	NZ	Q_GLU_123	OE2	3.373
2I5Y	S_ARG_9	NH1	P_ASP_368	OD2	2.853
2I5Y	S_ARG_9	NH2	P_ASP_368	OD2	3.453

Table 1119: Interfacial 2I5Y-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID residue name residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2I60	G_ARG_419	NH2	H_GLU_99	OE1	3.736
2I60	G_ARG_419	NH2	H_GLU_99	OE2	2.767
2I60	G_ARG_419	NH2	H_GLU_100D	OE2	3.611
2I60	H_LYS_209	NZ	L_GLU_123	OE1	3.997
2I60	P_ARG_419	NH1	R_GLU_100B	OE1	3.610
2I60	P_ARG_419	NH2	R_GLU_99	OE1	3.892
2I60	R_LYS_209	NZ	Q_GLU_123	OE2	3.485
2I60	S_ARG_9	NH1	P_ASP_368	OD2	3.268
2I60	S_ARG_9	NH2	P_ASP_368	OD1	3.938
2I60	S_ARG_9	NH2	P_ASP_368	OD2	2.664

Table 1120: Interfacial 2I60-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2IFF	L_LYS_44	NZ	H_ASP_104	OD1	2.935
2IFF	L_ARG_45	NH2	H_ASP_104	OD2	3.348
2IFF	H_LYS_211	NZ	L_GLU_121	OE1	3.040
2IFF	H_LYS_211	NZ	L_GLU_121	OE2	2.921
2IFF	Y_ARG_45	NH1	H_GLU_50	OE1	3.425
2IFF	Y_ARG_45	NH1	H_GLU_50	OE2	2.959

Table 1121: Interfacial 2IFF-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2IG2	H_LYS_148	NZ	L_GLU_126	OE2	2.854
2IG2	H_LYS_214	NZ	L_GLU_125	OE1	3.816
2IG2	H_LYS_214	NZ	L_GLU_125	OE2	2.866

Table 1122: Interfacial 2IG2-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2IGF	H_LYS_221	NZ	L_GLU_123	OE1	3.203
2IGF	P_LYS_75	NZ	L_ASP_28	OD1	3.253
2IGF	P_LYS_75	NZ	L_ASP_28	OD2	2.849
2IGF	P_LYS_75	NZ	L_ASP_30	OD2	3.458

Table 1123: Interfacial 2IGF-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2J4W	D_LYS_427	NZ	H_ASP_52A	OD1	3.478
2J4W	D_LYS_427	NZ	H_ASP_52A	OD2	2.864
2J4W	H_LYS_221	NZ	L_GLU_123	OE1	3.280
2J4W	H_LYS_221	NZ	L_GLU_123	OE2	3.313

Table 1124: Interfacial 2J4W-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2J5L	A_LYS_485	NZ	C_ASP_52A	OD1	3.476
2J5L	A_LYS_485	NZ	C_ASP_52A	OD2	3.193

Table 1125: Interfacial 2J5L-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2JB6	B_LYS_216	NZ	A_GLU_128	OE2	3.078

Table 1126: Interfacial 2JB6-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2JEL	L_LYS_50	NZ	H_GLU_98	OE1	2.874
2JEL	L_LYS_50	NZ	P_GLU_66	OE1	3.050
2JEL	L_LYS_50	NZ	P_GLU_66	OE2	3.051

Table 1127: Interfacial 2JEL-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2NXY	A_ARG_419	NH1	D_GLU_3103	OE2	3.305
2NXY	A_ARG_419	NH2	D_GLU_3103	OE2	2.288
2NXY	B_LYS_1029	NZ	A_ASP_279	OD2	2.892
2NXY	B_ARG_1059	NH1	A_ASP_368	OD1	3.350
2NXY	B_ARG_1059	NH1	A_ASP_368	OD2	2.835
2NXY	B_ARG_1059	NH2	A_ASP_368	OD1	2.856
2NXY	B_ARG_1059	NH2	A_ASP_368	OD2	3.647
2NXY	D_LYS_3224	NZ	C_GLU_2125	OE2	3.113

Table 1128: Interfacial 2NXY-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2NXZ	A_ARG_419	NH1	D_GLU_3103	OE2	3.647
2NXZ	A_ARG_419	NH2	D_GLU_3103	OE2	2.536
2NXZ	B_LYS_1029	NZ	A_ASP_279	OD2	3.046
2NXZ	B_ARG_1059	NH1	A_ASP_368	OD1	3.623
2NXZ	B_ARG_1059	NH1	A_ASP_368	OD2	3.029
2NXZ	B_ARG_1059	NH2	A_ASP_368	OD1	2.916
2NXZ	B_ARG_1059	NH2	A_ASP_368	OD2	3.612
2NXZ	D_HIS_3179	NE2	C_ASP_2169	OD2	3.986
2NXZ	D_LYS_3224	NZ	C_GLU_2125	OE1	3.503
2NXZ	D_LYS_3224	NZ	C_GLU_2125	OE2	2.801

Table 1129: Interfacial 2NXZ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2NY0	A_ARG_419	NH1	D_GLU_3103	OE2	3.320
2NY0	A_ARG_419	NH2	D_GLU_3103	OE2	2.328
2NY0	B_LYS_1029	NZ	A_ASP_279	OD2	2.858
2NY0	B_ARG_1059	NH1	A_ASP_368	OD1	3.389
2NY0	B_ARG_1059	NH1	A_ASP_368	OD2	2.874
2NY0	B_ARG_1059	NH2	A_ASP_368	OD1	2.859
2NY0	B_ARG_1059	NH2	A_ASP_368	OD2	3.661
2NY0	D_LYS_3224	NZ	C_GLU_2125	OE2	3.518

Table 1130: Interfacial 2NY0-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2NY1	A_ARG_419	NH1	D_GLU_3103	OE2	3.396
2NY1	A_ARG_419	NH2	D_GLU_3103	OE1	3.789
2NY1	A_ARG_419	NH2	D_GLU_3103	OE2	2.363
2NY1	B_LYS_1029	NZ	A_ASP_279	OD2	3.031
2NY1	B_ARG_1059	NH1	A_ASP_368	OD1	3.481
2NY1	B_ARG_1059	NH1	A_ASP_368	OD2	3.131
2NY1	B_ARG_1059	NH2	A_ASP_368	OD1	2.526
2NY1	B_ARG_1059	NH2	A_ASP_368	OD2	3.458
2NY1	D_LYS_3224	NZ	C_GLU_2125	OE1	3.100
2NY1	D_LYS_3224	NZ	C_GLU_2125	OE2	3.945

Table 1131: Interfacial 2NY1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2NY2	A_ARG_419	NH1	D_GLU_3103	OE2	2.325
2NY2	A_ARG_419	NH2	D_GLU_3103	OE2	3.124
2NY2	B_LYS_1029	NZ	A_ASP_279	OD2	2.981
2NY2	B_ARG_1059	NH1	A_ASP_368	OD1	3.464
2NY2	B_ARG_1059	NH1	A_ASP_368	OD2	2.895
2NY2	B_ARG_1059	NH2	A_ASP_368	OD1	2.934
2NY2	B_ARG_1059	NH2	A_ASP_368	OD2	3.638
2NY2	D_LYS_3224	NZ	C_GLU_2125	OE2	2.721

Table 1132: Interfacial 2NY2-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2NY3	A_ARG_419	NH1	D_GLU_3103	OE2	3.671
2NY3	A_ARG_419	NH2	D_GLU_3103	OE1	3.681
2NY3	A_ARG_419	NH2	D_GLU_3103	OE2	2.058
2NY3	B_LYS_1029	NZ	A_ASP_279	OD2	3.124
2NY3	B_ARG_1059	NH1	A_ASP_368	OD1	2.775
2NY3	B_ARG_1059	NH1	A_ASP_368	OD2	3.550
2NY3	B_ARG_1059	NH2	A_ASP_368	OD1	3.449
2NY3	B_ARG_1059	NH2	A_ASP_368	OD2	2.862
2NY3	D_LYS_3224	NZ	C_GLU_2125	OE1	3.624
2NY3	D_LYS_3224	NZ	C_GLU_2125	OE2	2.832

Table 1133: Interfacial 2NY3-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2NY4	A_ARG_419	NH1	D_GLU_3103	OE2	3.167
2NY4	A_ARG_419	NH2	D_GLU_3103	OE2	2.562
2NY4	B_LYS_1029	NZ	A_ASP_279	OD2	3.126
2NY4	B_ARG_1059	NH1	A_ASP_368	OD1	3.376
2NY4	B_ARG_1059	NH1	A_ASP_368	OD2	2.816
2NY4	B_ARG_1059	NH2	A_ASP_368	OD1	2.784
2NY4	B_ARG_1059	NH2	A_ASP_368	OD2	3.537
2NY4	D_LYS_3224	NZ	C_GLU_2125	OE1	3.625
2NY4	D_LYS_3224	NZ	C_GLU_2125	OE2	3.179

Table 1134: Interfacial 2NY4-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2NY5	G_ARG_419	NH2	H_GLU_3103	OE2	3.818
2NY5	C_LYS_1029	NZ	G_ASP_279	OD2	3.358
2NY5	C_ARG_1059	NH1	G_ASP_368	OD1	3.253
2NY5	C_ARG_1059	NH1	G_ASP_368	OD2	2.656
2NY5	C_ARG_1059	NH2	G_ASP_368	OD1	2.825
2NY5	C_ARG_1059	NH2	G_ASP_368	OD2	3.554
2NY5	H_LYS_3224	NZ	L_GLU_2125	OE1	3.285
2NY5	H_LYS_3224	NZ	L_GLU_2125	OE2	3.364

Table 1135: Interfacial 2NY5-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2NY6	A_ARG_419	NH2	D_GLU_3103	OE1	3.563
2NY6	A_ARG_419	NH2	D_GLU_3103	OE2	2.589
2NY6	B_LYS_1029	NZ	A_ASP_279	OD2	3.061
2NY6	B_ARG_1059	NH1	A_ASP_368	OD1	2.945
2NY6	B_ARG_1059	NH1	A_ASP_368	OD2	2.767
2NY6	B_ARG_1059	NH2	A_ASP_368	OD1	3.097
2NY6	D_LYS_3224	NZ	C_GLU_2125	OE1	3.158
2NY6	D_LYS_3224	NZ	C_GLU_2125	OE2	2.701

Table 1136: Interfacial 2NY6-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2NY7	H.LYS_221	NZ	L.GLU_123	OE1	3.153
2NY7	L.ARG_32	NH1	H.ASP_100F	OD2	2.962

Table 1137: Interfacial 2NY7-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2OR9	H_ARG_53	NH2	P_GLU_8	OE2	3.967
2OR9	I_LYS_208	NZ	M_GLU_123	OE2	3.803

Table 1138: Interfacial 2OR9-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2OSL	L_HIS_33	NE2	H_ASP_105	OD1	3.260
2OSL	L_HIS_33	NE2	H_ASP_105	OD2	2.885
2OSL	L_ARG_107	NH2	B_GLU_194	OE2	3.976
2OSL	B_HIS_33	ND1	A_ASP_105	OD2	3.615
2OSL	B_HIS_33	NE2	A_ASP_105	OD2	3.957
2OSL	A_LYS_217	NZ	B_GLU_122	OE1	2.793

Table 1139: Interfacial 2OSL-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2OTU	B.LYS_87	NZ	F.ASP_31	OD1	3.793
2OTU	B.LYS_87	NZ	F.ASP_31	OD2	2.711
2OTU	F.ARG_100	NH1	E.ASP_60	OD1	3.255
2OTU	F.ARG_100	NH1	E.ASP_60	OD2	3.915
2OTU	H.ARG_44	NH1	C.ASP_60	OD1	3.017
2OTU	H.ARG_44	NH1	C.ASP_60	OD2	3.518
2OTU	H.ARG_44	NH2	C.ASP_60	OD1	3.945
2OTU	H.ARG_44	NH2	C.ASP_60	OD2	3.013
2OTU	H.LYS_87	NZ	D.ASP_31	OD1	3.910
2OTU	H.LYS_87	NZ	D.ASP_31	OD2	2.759

Table 1140: Interfacial 2OTU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2OTW	B_LYS_87	NZ	D_ASP_31	OD1	3.659
2OTW	B_LYS_87	NZ	D_ASP_31	OD2	2.671
2OTW	B_ARG_100	NH1	A_ASP_60	OD1	3.223
2OTW	B_ARG_100	NH1	A_ASP_60	OD2	3.943
2OTW	D_ARG_100	NH1	C_ASP_60	OD1	3.882
2OTW	D_ARG_100	NH1	C_ASP_60	OD2	3.653

Table 1141: Interfacial 2OTW-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2P8L	A_HIS_96	NE2	C_ASP_5	OD1	2.766
2P8L	B_ARG_58	NH1	C_GLU_3	OE1	1.911
2P8L	B_ARG_58	NH1	C_GLU_3	OE2	3.223
2P8L	B_ARG_58	NH2	C_GLU_3	OE1	3.943
2P8L	B_ARG_95	NH1	C_ASP_5	OD1	2.951
2P8L	B_ARG_95	NH1	C_ASP_5	OD2	3.619
2P8L	B_ARG_95	NH2	C_ASP_5	OD1	3.420
2P8L	B_ARG_95	NH2	C_ASP_5	OD2	2.971
2P8L	B_ARG_96	NH1	A_GLU_55	OE1	3.236
2P8L	B_ARG_96	NH1	A_GLU_55	OE2	3.320
2P8L	B_ARG_96	NH2	A_GLU_55	OE1	3.018
2P8L	B_LYS_209	NZ	A_GLU_123	OE1	3.743
2P8L	C_LYS_6	NZ	B_ASP_54	OD1	3.641
2P8L	C_LYS_6	NZ	B_ASP_54	OD2	3.025
2P8L	C_LYS_6	NZ	B_ASP_56	OD1	2.878

Table 1142: Interfacial 2P8L-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2P8M	A_HIS_96	NE2	C_ASP_3	OD2	2.613
2P8M	B_ARG_1	NH2	A_GLU_55	OE2	3.915
2P8M	B_ARG_58	NH2	C_GLU_1	OE1	2.510
2P8M	B_ARG_95	NH1	C_ASP_3	OD1	2.973
2P8M	B_ARG_95	NH1	C_ASP_3	OD2	3.042
2P8M	B_ARG_95	NH2	C_ASP_3	OD1	3.169
2P8M	B_ARG_96	NH1	A_GLU_55	OE1	3.351
2P8M	B_ARG_96	NH1	A_GLU_55	OE2	3.448
2P8M	B_ARG_96	NH2	A_GLU_55	OE1	3.393
2P8M	B_LYS_209	NZ	A_GLU_123	OE1	3.649
2P8M	C_LYS_4	NZ	B_ASP_54	OD1	2.903
2P8M	C_LYS_4	NZ	B_ASP_54	OD2	2.371
2P8M	C_LYS_4	NZ	B_ASP_56	OD2	3.183

Table 1143: Interfacial 2P8M-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2P8P	A_HIS_96	NE2	C_ASP_3	OD1	3.214
2P8P	B_ARG_58	NH2	C_GLU_1	OE2	3.147
2P8P	B_ARG_95	NH1	C_ASP_3	OD1	2.805
2P8P	B_ARG_95	NH1	C_ASP_3	OD2	3.510
2P8P	B_ARG_95	NH2	C_ASP_3	OD1	3.459
2P8P	B_ARG_95	NH2	C_ASP_3	OD2	2.629
2P8P	B_ARG_96	NH1	A_GLU_55	OE1	3.239
2P8P	B_ARG_96	NH1	A_GLU_55	OE2	3.518
2P8P	B_ARG_96	NH2	A_GLU_55	OE1	3.128
2P8P	B_LYS_210	NZ	A_GLU_123	OE1	3.349
2P8P	B_LYS_210	NZ	A_GLU_123	OE2	3.192
2P8P	C_LYS_4	NZ	B_ASP_54	OD1	3.623
2P8P	C_LYS_4	NZ	B_ASP_54	OD2	3.010
2P8P	C_LYS_4	NZ	B_ASP_56	OD2	2.836

Table 1144: Interfacial 2P8P-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2PR4	H_ARG_101	NH1	L_GLU_55	OE1	3.296
2PR4	H_ARG_101	NH1	L_GLU_55	OE2	3.376
2PR4	H_ARG_101	NH2	L_GLU_55	OE1	3.286
2PR4	H_LYS_228	NZ	L_GLU_123	OE1	3.151

Table 1145: Interfacial 2PR4-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2Q8A	A_LYS_203	NZ	L_ASP_32	OD1	3.044
2Q8A	A_LYS_203	NZ	L_ASP_32	OD2	2.513
2Q8A	L_ARG_96	NH1	A_ASP_204	OD1	2.971
2Q8A	L_ARG_96	NH1	A_ASP_204	OD2	2.580
2Q8A	L_ARG_96	NH2	A_ASP_204	OD1	2.882
2Q8A	L_ARG_96	NH2	A_ASP_204	OD2	3.927
2Q8A	L_ARG_96	NH2	H_GLU_59	OE2	3.755
2Q8A	H_HIS_35	NE2	A_ASP_204	OD2	3.930

Table 1146: Interfacial 2Q8A-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2Q8B	A_LYS_203	NZ	L_ASP_32	OD1	3.779
2Q8B	A_LYS_203	NZ	L_ASP_32	OD2	2.847
2Q8B	L_ARG_96	NH1	A_ASP_204	OD1	3.458
2Q8B	L_ARG_96	NH1	A_ASP_204	OD2	2.952
2Q8B	L_ARG_96	NH2	A_ASP_204	OD1	2.667
2Q8B	L_ARG_96	NH2	A_ASP_204	OD2	3.462

Table 1147: Interfacial 2Q8B-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2QAD	B_ARG_59	NH1	A_ASP_368	OD1	3.394
2QAD	B_ARG_59	NH1	A_ASP_368	OD2	2.749
2QAD	B_ARG_59	NH2	A_ASP_368	OD1	3.764
2QAD	C_LYS_50	NZ	D_GLU_100F	OE2	2.989
2QAD	C_LYS_55	NZ	D_ASP_101	OD1	3.312
2QAD	C_LYS_55	NZ	D_ASP_101	OD2	3.736
2QAD	F_ARG_59	NH1	E_ASP_368	OD1	2.855
2QAD	F_ARG_59	NH1	E_ASP_368	OD2	2.624
2QAD	F_ARG_59	NH2	E_ASP_368	OD1	3.681
2QAD	G_LYS_50	NZ	H_GLU_100F	OE2	3.151
2QAD	G_LYS_55	NZ	H_ASP_101	OD1	3.191
2QAD	G_LYS_55	NZ	H_ASP_101	OD2	3.496

Table 1148: Interfacial 2QAD-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID residue name residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2QQN	H_LYS_209	NZ	L_GLU_123	OE1	2.782
2QQN	H_LYS_209	NZ	L_GLU_123	OE2	3.506
2QQN	H_LYS_214	NZ	L_ASP_122	OD1	3.854

Table 1149: Interfacial 2QQN-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2R29	A_LYS_307	NZ	H_ASP_99	OD1	2.956
2R29	A_LYS_307	NZ	L_GLU_59	OE1	3.335
2R29	A_LYS_310	NZ	H_ASP_52	OD1	3.449
2R29	A_LYS_310	NZ	H_ASP_52	OD2	2.764
2R29	H_LYS_59	NZ	L_ASP_98	OD2	3.485
2R29	L_ARG_54	NH2	H_GLU_101	OE1	3.814
2R29	L_ARG_54	NH2	H_GLU_101	OE2	3.270
2R29	L_LYS_107	NZ	H_GLU_42	OE1	3.937

Table 1150: Interfacial 2R29-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2R69	A_LYS_307	NZ	H_ASP_99	OD2	3.631
2R69	H_LYS_59	NZ	L_ASP_98	OD2	3.723
2R69	H_LYS_211	NZ	L_GLU_127	OE1	3.695
2R69	H_LYS_211	NZ	L_GLU_127	OE2	3.159
2R69	L_ARG_31	NH2	A_GLU_311	OE2	3.151
2R69	L_ARG_54	NH2	H_GLU_101	OE1	2.992
2R69	L_ARG_54	NH2	H_GLU_101	OE2	2.911

Table 1151: Interfacial 2R69-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2UYL	A_ARG_101	NH1	B_GLU_99	OE1	3.183
2UYL	A_ARG_101	NH1	B_GLU_99	OE2	3.530
2UYL	A_ARG_101	NH2	B_GLU_99	OE2	3.803
2UYL	M_ARG_101	NH1	N_GLU_99	OE1	3.058
2UYL	M_ARG_101	NH1	N_GLU_99	OE2	3.775
2UYL	M_ARG_101	NH2	N_GLU_99	OE2	3.923
2UYL	N_HIS_170	NE2	M_ASP_172	OD1	3.811
2UYL	V_ARG_101	NH1	W_GLU_99	OE1	2.958
2UYL	V_ARG_101	NH1	W_GLU_99	OE2	3.417
2UYL	V_ARG_101	NH2	W_GLU_99	OE2	3.369
2UYL	X_ARG_101	NH1	Y_GLU_99	OE1	2.789
2UYL	X_ARG_101	NH1	Y_GLU_99	OE2	3.483
2UYL	X_ARG_101	NH2	Y_GLU_99	OE2	3.405

Table 1152: Interfacial 2UYL-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2VC2	A_ARG_77	NH1	H_ASP_102	OD1	3.536
2VC2	A_ARG_77	NH1	H_ASP_102	OD2	3.007
2VC2	A_ARG_77	NH2	H_ASP_102	OD1	2.794
2VC2	A_ARG_77	NH2	H_ASP_102	OD2	3.630
2VC2	B_ARG_216	NH2	A_GLU_123	OE2	3.081
2VC2	B_LYS_253	NZ	A_ASP_232	OD2	2.805
2VC2	H_LYS_214	NZ	L_GLU_123	OE2	3.240

Table 1153: Interfacial 2VC2-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2VDK	A_ARG_77	NH1	H_ASP_102	OD1	3.535
2VDK	A_ARG_77	NH1	H_ASP_102	OD2	3.168
2VDK	A_ARG_77	NH2	H_ASP_102	OD1	2.738
2VDK	A_ARG_77	NH2	H_ASP_102	OD2	3.673
2VDK	B_ARG_216	NH2	A_GLU_123	OE2	3.072
2VDK	B_LYS_253	NZ	A_ASP_232	OD2	2.921
2VDK	H_LYS_214	NZ	L_GLU_123	OE2	3.461

Table 1154: Interfacial 2VDK-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2VDL	A_ARG_77	NH1	H_ASP_102	OD1	3.566
2VDL	A_ARG_77	NH1	H_ASP_102	OD2	3.106
2VDL	A_ARG_77	NH2	H_ASP_102	OD1	2.722
2VDL	A_ARG_77	NH2	H_ASP_102	OD2	3.538
2VDL	B_ARG_216	NH2	A_GLU_123	OE2	3.160
2VDL	B_LYS_253	NZ	A_ASP_232	OD2	2.886
2VDL	H_LYS_59	NZ	A_GLU_117	OE2	3.964
2VDL	H_LYS_214	NZ	L_GLU_123	OE2	3.400

Table 1155: Interfacial 2VDL-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2VDM	A_ARG_77	NH1	H_ASP_102	OD1	3.512
2VDM	A_ARG_77	NH1	H_ASP_102	OD2	3.196
2VDM	A_ARG_77	NH2	H_ASP_102	OD1	2.762
2VDM	A_ARG_77	NH2	H_ASP_102	OD2	3.757
2VDM	B_ARG_216	NH2	A_GLU_123	OE2	2.982
2VDM	B_LYS_253	NZ	A_ASP_232	OD2	3.306
2VDM	H_LYS_214	NZ	L_GLU_123	OE2	3.334

Table 1156: Interfacial 2VDM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2VDN	A_ARG_77	NH1	H_ASP_102	OD1	3.491
2VDN	A_ARG_77	NH1	H_ASP_102	OD2	3.169
2VDN	A_ARG_77	NH2	H_ASP_102	OD1	2.808
2VDN	A_ARG_77	NH2	H_ASP_102	OD2	3.762
2VDN	B_ARG_216	NH2	A_GLU_123	OE2	2.995
2VDN	H_LYS_214	NZ	L_GLU_123	OE2	3.685

Table 1157: Interfacial 2VDN-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2VDO	A_ARG_77	NH1	H_ASP_102	OD1	3.703
2VDO	A_ARG_77	NH1	H_ASP_102	OD2	3.042
2VDO	A_ARG_77	NH2	H_ASP_102	OD1	2.789
2VDO	A_ARG_77	NH2	H_ASP_102	OD2	3.375
2VDO	B_ARG_216	NH2	A_GLU_123	OE2	3.092
2VDO	B_LYS_253	NZ	A_ASP_232	OD2	2.836
2VDO	C_LYS_406	NZ	A_ASP_224	OD1	2.673
2VDO	C_LYS_406	NZ	A_ASP_224	OD2	3.263

Table 1158: Interfacial 2VDO-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2VDP	A_ARG_77	NH1	H_ASP_102	OD1	3.519
2VDP	A_ARG_77	NH1	H_ASP_102	OD2	3.089
2VDP	A_ARG_77	NH2	H_ASP_102	OD1	2.733
2VDP	A_ARG_77	NH2	H_ASP_102	OD2	3.585
2VDP	B_ARG_216	NH2	A_GLU_123	OE2	3.038
2VDP	B_LYS_253	NZ	A_ASP_232	OD2	2.914
2VDP	C_LYS_406	NZ	A_ASP_224	OD1	2.604
2VDP	C_LYS_406	NZ	A_ASP_224	OD2	3.297
2VDP	H_LYS_214	NZ	L_GLU_123	OE2	3.425

Table 1159: Interfacial 2VDP-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2VDQ	A_ARG_77	NH1	H_ASP_102	OD1	3.603
2VDQ	A_ARG_77	NH1	H_ASP_102	OD2	3.057
2VDQ	A_ARG_77	NH2	H_ASP_102	OD1	2.765
2VDQ	A_ARG_77	NH2	H_ASP_102	OD2	3.398
2VDQ	B_ARG_216	NH2	A_GLU_123	OE2	2.900
2VDQ	B_LYS_253	NZ	A_ASP_232	OD2	3.522
2VDQ	C_ARG_408	NH1	A_ASP_224	OD1	3.059
2VDQ	C_ARG_408	NH1	A_ASP_224	OD2	3.490
2VDQ	C_ARG_408	NH2	A_ASP_224	OD1	3.054
2VDQ	C_ARG_408	NH2	A_ASP_224	OD2	3.761
2VDQ	H_LYS_59	NZ	A_GLU_117	OE2	3.921
2VDQ	H_LYS_214	NZ	L_GLU_123	OE2	3.223

Table 1160: Interfacial 2VDQ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID residue name residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2VDR	A_ARG_77	NH1	H_ASP_102	OD1	3.703
2VDR	A_ARG_77	NH1	H_ASP_102	OD2	3.091
2VDR	A_ARG_77	NH2	H_ASP_102	OD1	2.791
2VDR	A_ARG_77	NH2	H_ASP_102	OD2	3.414
2VDR	B_ARG_216	NH2	A_GLU_123	OE2	2.956
2VDR	B_LYS_253	NZ	A_ASP_232	OD2	3.191
2VDR	C_ARG_408	NH1	A_ASP_224	OD1	3.062
2VDR	C_ARG_408	NH1	A_ASP_224	OD2	3.850
2VDR	C_ARG_408	NH2	A_ASP_224	OD1	3.028
2VDR	C_ARG_408	NH2	A_ASP_224	OD2	3.839
2VDR	H_LYS_214	NZ	L_GLU_123	OE2	3.860

Table 1161: Interfacial 2VDR-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2VIR	B_LYS_	NZ	A_GLU_127	OE2	3.017
2VIR	B_HIS_173	NE2	A_ASP_141	OD1	3.726
2VIR	B_HIS_173	NE2	A_ASP_141	OD2	3.076
2VIR	B_LYS_217	NZ	A_GLU_126	OE2	3.903

Table 1162: Interfacial 2VIR-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2VIS	B_LYS_	NZ	A_GLU_127	OE2	2.999
2VIS	B_HIS_173	NE2	A_ASP_141	OD1	3.763
2VIS	B_HIS_173	NE2	A_ASP_141	OD2	3.158
2VIS	B_LYS_217	NZ	A_GLU_126	OE2	3.709

Table 1163: Interfacial 2VIS-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2VIT	B_LYS_	NZ	A_GLU_127	OE2	2.939
2VIT	B_HIS_173	NE2	A_ASP_141	OD1	3.614
2VIT	B_HIS_173	NE2	A_ASP_141	OD2	3.333
2VIT	B_LYS_217	NZ	A_GLU_126	OE2	3.872

Table 1164: Interfacial 2VIT-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2VIU	A_LYS_27	NZ	B_GLU_97	OE1	3.686
2VIU	A_LYS_27	NZ	B_GLU_97	OE2	2.721
2VIU	A_ARG_109	NH1	B_GLU_67	OE1	3.978
2VIU	A_ARG_109	NH1	B_GLU_67	OE2	3.053
2VIU	A_ARG_269	NH1	B_GLU_67	OE1	2.986
2VIU	A_LYS_310	NZ	B_ASP_90	OD1	2.868

Table 1165: Interfacial 2VIU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2VXS	H_LYS_143	NZ	L_GLU_125	OE2	2.772
2VXS	I_LYS_214	NZ	M_GLU_124	OE1	3.186
2VXS	J_LYS_	NZ	N_GLU_	OE1	2.922
2VXS	K_LYS_214	NZ	O_GLU_124	OE1	3.391
2VXS	N_LYS_	NZ	J_ASP_	OD2	3.949

Table 1166: Interfacial 2VXS-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2VXT	H_ARG_94	NH2	L_GLU_179	OE1	2.816
2VXT	H_ARG_94	NH2	L_GLU_179	OE2	3.466
2VXT	H_ARG_101	NH1	L_GLU_179	OE1	2.914
2VXT	H_LYS_208	NZ	L_GLU_123	OE2	2.940
2VXT	L_HIS_145	NE2	H_ASP_50	OD1	2.753
2VXT	L_LYS_148	NZ	H_ASP_56	OD2	2.664

Table 1167: Interfacial 2VXT-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2VXU	H.LYS_43	NZ	L.ASP_85	OD1	3.097
2VXU	I.LYS_208	NZ	M.GLU_123	OE1	2.734
2VXU	I.LYS_208	NZ	M.GLU_123	OE2	2.893

Table 1168: Interfacial 2VXU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2VXV	H_LYS_214	NZ	L_ASP_122	OD1	3.721
2VXV	H_LYS_214	NZ	L_ASP_122	OD2	2.868

Table 1169: Interfacial 2VXV-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2XZQ	H_LYS_150	NZ	L_GLU_127	OE2	3.822
2XZQ	H_LYS_215	NZ	L_GLU_126	OE2	2.689

Table 1170: Interfacial 2XZQ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2Y06	H_LYS_215	NZ	L_GLU_126	OE2	2.373

Table 1171: Interfacial 2Y06-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2Y07	H_LYS_215	NZ	L_GLU_126	OE2	2.390

Table 1172: Interfacial 2Y07-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2Y36	H_LYS_150	NZ	L_GLU_127	OE2	3.849
2Y36	H_LYS_215	NZ	L_GLU_126	OE2	2.707

Table 1173: Interfacial 2Y36-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2Y7S	A_ARG_127	NH1	B_GLU_118	OE1	3.457
2Y7S	A_LYS_218	NZ	B_ASP_85	OD1	3.014
2Y7S	B_ARG_41	NH2	A_GLU_238	OE2	2.757

Table 1174: Interfacial 2Y7S-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2YPV	A_ARG_130	NH2	L_ASP_92	OD1	2.916
2YPV	A_LYS_219	NZ	H_ASP_52	OD2	3.469
2YPV	A_LYS_241	NZ	H_ASP_99	OD2	2.741
2YPV	H_LYS_214	NZ	L_GLU_123	OE1	2.788
2YPV	H_LYS_214	NZ	L_GLU_123	OE2	2.975
2YPV	L_ARG_50	NH2	A_GLU_239	OE1	3.110
2YPV	L_ARG_50	NH2	A_GLU_239	OE2	3.975

Table 1175: Interfacial 2YPV-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2YWY	A.LYS_48	NZ	B.GLU_32	OE1	3.306
2YWY	A.LYS_48	NZ	B.GLU_32	OE2	2.998
2YWY	A.LYS_61	NZ	B.GLU_57	OE1	2.550
2YWY	A.LYS_61	NZ	B.GLU_57	OE2	3.211
2YWY	A.LYS_82	NZ	C.ASP_89	OD1	3.260
2YWY	B.ARG_33	NH2	A.GLU_32	OE1	3.506
2YWY	B.LYS_48	NZ	A.GLU_32	OE1	3.520
2YWY	B.LYS_48	NZ	A.GLU_32	OE2	2.757
2YWY	B.LYS_61	NZ	A.GLU_57	OE1	3.086
2YWY	C.LYS_48	NZ	D.GLU_32	OE1	2.723
2YWY	C.LYS_48	NZ	D.GLU_32	OE2	3.404
2YWY	C.LYS_61	NZ	D.GLU_57	OE1	2.801
2YWY	C.LYS_61	NZ	D.GLU_57	OE2	3.948
2YWY	D.LYS_48	NZ	C.GLU_32	OE1	3.239
2YWY	D.LYS_48	NZ	C.GLU_32	OE2	2.447
2YWY	D.LYS_61	NZ	C.GLU_57	OE1	2.837
2YWY	D.LYS_61	NZ	C.GLU_57	OE2	3.637

Table 1176: Interfacial 2YWY-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2ZCH	P_LYS_178	NZ	H_ASP_96	OD1	3.502
2ZCH	P_LYS_178	NZ	H_ASP_96	OD2	3.400
2ZCH	P_ARG_235	NH1	L_ASP_28	OD2	2.443
2ZCH	P_ARG_235	NH2	L_ASP_28	OD2	3.166
2ZCH	P_LYS_236	NZ	H_GLU_100C	OE2	3.089
2ZCH	H_ARG_50	NH2	L_ASP_94	OD1	2.658
2ZCH	H_ARG_50	NH2	L_ASP_94	OD2	2.887
2ZCH	H_LYS_208	NZ	L_GLU_123	OE1	3.921
2ZCH	H_LYS_208	NZ	L_GLU_123	OE2	3.396

Table 1177: Interfacial 2ZCH-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2ZCK	P_LYS_178	NZ	H_ASP_96	OD1	3.892
2ZCK	P_LYS_178	NZ	H_ASP_96	OD2	3.060
2ZCK	P_ARG_236	NH2	L_ASP_28	OD1	3.496
2ZCK	H_ARG_50	NH2	L_ASP_94	OD1	3.095
2ZCK	H_ARG_50	NH2	L_ASP_94	OD2	2.679
2ZCK	H_LYS_208	NZ	L_GLU_123	OE2	2.731

Table 1178: Interfacial 2ZCK-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2ZCL	P_LYS_178	NZ	H_ASP_96	OD1	3.272
2ZCL	P_LYS_178	NZ	H_ASP_96	OD2	2.771
2ZCL	P_ARG_235	NH2	L_ASP_28	OD1	3.392
2ZCL	H_ARG_50	NH2	L_ASP_94	OD1	3.155
2ZCL	H_ARG_50	NH2	L_ASP_94	OD2	2.864

Table 1179: Interfacial 2ZCL-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2ZNW	Y_LYS_97	NZ	A_ASP_154	OD1	2.612
2ZNW	Y_LYS_97	NZ	A_ASP_154	OD2	3.786
2ZNW	Y_LYS_97	NZ	A_ASP_221	OD1	3.143
2ZNW	Y_LYS_97	NZ	A_ASP_221	OD2	3.719
2ZNW	Y_LYS_116	NZ	B_ASP_203	OD1	2.664
2ZNW	Z_LYS_97	NZ	B_ASP_154	OD1	3.042
2ZNW	Z_LYS_97	NZ	B_ASP_221	OD1	2.782
2ZNW	Z_LYS_97	NZ	B_ASP_221	OD2	3.319
2ZNW	Z_LYS_116	NZ	A_ASP_203	OD1	2.989

Table 1180: Interfacial 2ZNW-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2ZNX	Y_LYS_97	NZ	A_ASP_154	OD1	2.701
2ZNX	Y_LYS_97	NZ	A_ASP_221	OD1	2.716
2ZNX	Y_LYS_97	NZ	A_ASP_221	OD2	3.355
2ZNX	Y_LYS_116	NZ	B_ASP_203	OD1	3.871
2ZNX	Y_LYS_116	NZ	B_ASP_203	OD2	2.956
2ZNX	B_LYS_135	NZ	Y_ASP_119	OD2	3.744
2ZNX	Z_LYS_97	NZ	B_ASP_154	OD1	2.804
2ZNX	Z_LYS_97	NZ	B_ASP_221	OD1	3.005
2ZNX	Z_LYS_97	NZ	B_ASP_221	OD2	3.520
2ZNX	Z_LYS_116	NZ	A_ASP_203	OD1	3.699
2ZNX	Z_LYS_116	NZ	A_ASP_203	OD2	3.427

Table 1181: Interfacial 2ZNX-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
2ZPK	L.HIS_95	NE2	H.ASP_62	OD1	3.977
2ZPK	H.LYS_143	NZ	L.GLU_125	OE2	2.882
2ZPK	H.LYS_208	NZ	L.GLU_124	OE2	3.548
2ZPK	I.LYS_143	NZ	M.GLU_125	OE2	2.672
2ZPK	I.LYS_208	NZ	M.GLU_124	OE2	3.137

Table 1182: Interfacial 2ZPK-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
32C2	B_LYS_214	NZ	A_GLU_126	OE1	3.056
32C2	B_LYS_214	NZ	A_GLU_126	OE2	3.702

Table 1183: Interfacial 32C2-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3A67	Y_LYS_96	NZ	L_ASP_31	OD1	2.774
3A67	Y_LYS_96	NZ	L_ASP_31	OD2	3.727
3A67	Y_LYS_97	NZ	H_ASP_32	OD1	2.657
3A67	Y_LYS_97	NZ	H_ASP_99	OD1	3.291
3A67	Y_LYS_97	NZ	H_ASP_99	OD2	2.885

Table 1184: Interfacial 3A67-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3A6B	Y_LYS_96	NZ	L_ASP_32	OD1	2.734
3A6B	Y_LYS_97	NZ	H_ASP_32	OD1	2.700
3A6B	Y_LYS_97	NZ	H_ASP_32	OD2	3.941
3A6B	Y_LYS_97	NZ	H_ASP_99	OD1	2.956
3A6B	Y_LYS_97	NZ	H_ASP_99	OD2	3.259

Table 1185: Interfacial 3A6B-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3A6C	Y_LYS_97	NZ	H_ASP_32	OD1	2.672
3A6C	Y_LYS_97	NZ	H_ASP_32	OD2	3.916
3A6C	Y_LYS_97	NZ	H_ASP_99	OD1	2.965
3A6C	Y_LYS_97	NZ	H_ASP_99	OD2	3.291

Table 1186: Interfacial 3A6C-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3B9K	H_LYS_221	NZ	L_GLU_123	OE1	2.886
3B9K	A_LYS_13	NZ	B_ASP_42	OD2	3.894
3B9K	B_LYS_27	NZ	H_ASP_32	OD1	2.409
3B9K	B_ARG_77	NH2	L_ASP_92	OD1	3.184
3B9K	B_ARG_78	NH2	L_ASP_92	OD1	2.834
3B9K	B_LYS_103	NZ	A_ASP_66	OD1	3.058
3B9K	D_LYS_221	NZ	C_GLU_123	OE1	3.178
3B9K	F_LYS_27	NZ	D_ASP_32	OD1	2.318
3B9K	F_ARG_77	NH2	C_ASP_92	OD1	2.984
3B9K	F_ARG_78	NH2	C_ASP_92	OD1	3.141
3B9K	F_ARG_78	NH2	C_ASP_92	OD2	3.951
3B9K	F_LYS_103	NZ	E_ASP_	OD1	3.044

Table 1187: Interfacial 3B9K-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID residue name residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3BDY	H_LYS_211	NZ	L_GLU_123	OE2	2.706

Table 1188: Interfacial 3BDY-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3BE1	H_ARG_50	NH1	A_ASP_560	OD2	3.215
3BE1	H_ARG_50	NH2	A_GLU_558	OE1	3.092
3BE1	H_ARG_50	NH2	A_GLU_558	OE2	3.263
3BE1	H_ARG_50	NH2	A_ASP_560	OD1	3.492
3BE1	H_ARG_50	NH2	A_ASP_560	OD2	3.175

Table 1189: Interfacial 3BE1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3BGF	S_ARG_426	NH1	H_ASP_56	OD1	3.504
3BGF	S_ARG_426	NH1	H_ASP_56	OD2	2.403
3BGF	S_LYS_439	NZ	A_ASP_480	OD2	3.161
3BGF	A_LYS_439	NZ	S_ASP_480	OD2	2.520
3BGF	H_LYS_210	NZ	L_GLU_123	OE1	3.997

Table 1190: Interfacial 3BGF-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3BIK	A_ARG_113	NH2	B_GLU_136	OE2	3.149
3BIK	A_ARG_125	NH2	B_GLU_136	OE1	3.033
3BIK	A_ARG_125	NH2	B_GLU_136	OE2	3.001

Table 1191: Interfacial 3BIK-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3BKY	H_LYS_138	NZ	L_GLU_212	OE2	2.743

Table 1192: Interfacial 3BKY-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3BO8	A_ARG_35	NH1	B_ASP_53	OD1	3.541
3BO8	A_ARG_48	NH1	B_ASP_53	OD1	3.101
3BO8	A_ARG_48	NH1	B_ASP_53	OD2	3.041
3BO8	A_ARG_48	NH2	B_ASP_53	OD1	3.771
3BO8	A_ARG_48	NH2	B_ASP_53	OD2	3.368
3BO8	A_ARG_156	NH1	C_ASP_3	OD1	3.842
3BO8	A_ARG_156	NH1	C_ASP_3	OD2	2.711
3BO8	A_ARG_163	NH2	C_GLU_1	OE1	3.484
3BO8	A_ARG_163	NH2	C_GLU_1	OE2	2.848
3BO8	A_ARG_170	NH1	C_GLU_1	OE2	2.801
3BO8	A_ARG_170	NH2	C_GLU_1	OE2	3.023
3BO8	A_HIS_192	NE2	B_ASP_98	OD1	3.566
3BO8	A_HIS_192	NE2	B_ASP_98	OD2	3.950

Table 1193: Interfacial 3BO8-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3BT2	A_HIS_87	ND1	U_ASP_11	OD2	3.629
3BT2	H_HIS_98	ND1	L_GLU_50	OE1	2.845
3BT2	H_HIS_98	ND1	L_GLU_50	OE2	2.191
3BT2	H_HIS_98	NE2	L_GLU_50	OE1	3.301
3BT2	H_HIS_98	NE2	L_GLU_50	OE2	3.904
3BT2	H_LYS_203	NZ	L_GLU_122	OE2	3.715
3BT2	U_ARG_91	NH1	B_ASP_22	OD1	3.502
3BT2	U_ARG_91	NH1	B_ASP_22	OD2	3.574
3BT2	U_ARG_91	NH2	B_ASP_22	OD1	3.066
3BT2	U_ARG_192	NH1	H_GLU_58	OE2	2.836

Table 1194: Interfacial 3BT2-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3BZ4	A_LYS_27	NZ	E_ASP_1	OD1	3.348
3BZ4	A_LYS_27	NZ	E_ASP_1	OD2	3.551
3BZ4	A_ARG_96	NH2	B_GLU_50	OE1	3.591
3BZ4	A_ARG_96	NH2	B_GLU_50	OE2	2.914
3BZ4	B_LYS_210	NZ	A_GLU_123	OE2	2.839
3BZ4	C_ARG_96	NH2	D_GLU_50	OE1	3.615
3BZ4	C_ARG_96	NH2	D_GLU_50	OE2	2.938
3BZ4	D_LYS_210	NZ	C_GLU_123	OE2	2.929
3BZ4	E_ARG_96	NH2	F_GLU_50	OE1	3.659
3BZ4	E_ARG_96	NH2	F_GLU_50	OE2	3.062
3BZ4	F_LYS_210	NZ	E_GLU_123	OE2	2.855
3BZ4	G_ARG_96	NH2	H_GLU_50	OE1	3.659
3BZ4	G_ARG_96	NH2	H_GLU_50	OE2	3.021
3BZ4	G_LYS_147	NZ	C_GLU_154	OE1	3.559

Table 1195: Interfacial 3BZ4-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3C09	L_HIS_93	NE2	D_ASP_434	OD1	2.739
3C09	L_HIS_93	NE2	D_ASP_434	OD2	3.466
3C09	H_ARG_57	NH2	D_GLU_431	OE1	3.682
3C09	A_LYS_454	NZ	C_ASP_100	OD1	2.467
3C09	A_LYS_463	NZ	B_ASP_49	OD2	2.856
3C09	B_HIS_93	NE2	A_ASP_434	OD1	2.346
3C09	D_LYS_454	NZ	H_ASP_100	OD2	3.482
3C09	D_LYS_463	NZ	L_ASP_49	OD2	3.418

Table 1196: Interfacial 3C09-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3C5S	A_ARG_96	NH2	B_GLU_50	OE1	3.517
3C5S	A_ARG_96	NH2	B_GLU_50	OE2	2.932
3C5S	B_LYS_210	NZ	A_GLU_123	OE2	3.553
3C5S	C_ARG_96	NH2	D_GLU_50	OE1	3.571
3C5S	C_ARG_96	NH2	D_GLU_50	OE2	2.973

Table 1197: Interfacial 3C5S-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3C6S	A_LYS_27	NZ	F_GLU_61	OE1	2.945
3C6S	A_ARG_96	NH2	B_GLU_50	OE1	3.551
3C6S	A_ARG_96	NH2	B_GLU_50	OE2	2.936
3C6S	B_LYS_210	NZ	A_GLU_123	OE2	2.871
3C6S	C_ARG_96	NH2	D_GLU_50	OE1	3.699
3C6S	C_ARG_96	NH2	D_GLU_50	OE2	2.915
3C6S	D_LYS_115	NZ	H_GLU_85	OE1	3.000
3C6S	D_LYS_115	NZ	H_GLU_85	OE2	3.884
3C6S	D_LYS_210	NZ	C_GLU_123	OE2	2.801
3C6S	E_LYS_27	NZ	A_ASP_1	OD1	3.387
3C6S	E_LYS_27	NZ	A_ASP_1	OD2	3.431
3C6S	E_ARG_96	NH2	F_GLU_50	OE1	3.703
3C6S	E_ARG_96	NH2	F_GLU_50	OE2	3.164
3C6S	F_LYS_210	NZ	E_GLU_123	OE2	3.016
3C6S	G_ARG_96	NH2	H_GLU_50	OE1	3.733
3C6S	G_ARG_96	NH2	H_GLU_50	OE2	2.958
3C6S	H_LYS_210	NZ	G_GLU_123	OE2	2.402

Table 1198: Interfacial 3C6S-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3CVH	A_ARG_48	NH1	B_ASP_53	OD2	3.820
3CVH	A_ARG_48	NH2	B_ASP_53	OD2	2.637
3CVH	A_ARG_62	NH1	L_GLU_26	OE1	3.514
3CVH	A_ARG_62	NH1	L_GLU_26	OE2	3.458
3CVH	A_ARG_62	NH2	L_GLU_26	OE1	3.664
3CVH	A_ARG_108	NH2	M_GLU_223	OE2	3.938
3CVH	A_HIS_192	ND1	B_ASP_98	OD2	3.410
3CVH	C_LYS_7	NZ	H_ASP_49	OD1	3.577
3CVH	C_LYS_7	NZ	H_ASP_49	OD2	3.552
3CVH	H_LYS_215	NZ	L_GLU_122	OE2	2.643
3CVH	M_ARG_48	NH1	N_ASP_53	OD2	3.601
3CVH	M_ARG_48	NH2	N_ASP_53	OD2	2.621
3CVH	M_ARG_62	NH1	R_GLU_26	OE1	3.418
3CVH	M_ARG_62	NH2	R_GLU_26	OE1	3.162
3CVH	M_ARG_62	NH2	R_GLU_26	OE2	2.706
3CVH	M_ARG_108	NH2	A_GLU_223	OE1	3.207
3CVH	M_ARG_108	NH2	A_GLU_223	OE2	3.250
3CVH	M_ARG_169	NH1	A_GLU_268	OE2	3.364
3CVH	O_LYS_7	NZ	Q_ASP_49	OD1	3.648
3CVH	O_LYS_7	NZ	Q_ASP_49	OD2	3.052
3CVH	Q_LYS_215	NZ	R_GLU_122	OE1	3.557

Table 1199: Interfacial 3CVH-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3CXD	H_ARG_52	NH1	P_ASP_47	OD1	3.830
3CXD	H_ARG_52	NH1	P_ASP_47	OD2	3.528

Table 1200: Interfacial 3CXD-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3D0L	A_HIS_96	NE2	C_ASP_5	OD1	3.014
3D0L	B_ARG_58	NH2	C_GLU_3	OE1	3.473
3D0L	B_ARG_58	NH2	C_GLU_3	OE2	3.109
3D0L	B_ARG_95	NH1	C_ASP_5	OD1	2.695
3D0L	B_ARG_95	NH1	C_ASP_5	OD2	3.449
3D0L	B_ARG_95	NH2	C_ASP_5	OD1	3.596
3D0L	B_ARG_95	NH2	C_ASP_5	OD2	3.078
3D0L	B_ARG_96	NH1	A_GLU_55	OE1	3.284
3D0L	B_ARG_96	NH1	A_GLU_55	OE2	3.522
3D0L	B_ARG_96	NH2	A_GLU_55	OE1	3.455
3D0L	C_LYS_6	NZ	B_ASP_54	OD1	2.251
3D0L	C_LYS_6	NZ	B_ASP_54	OD2	2.930
3D0L	C_LYS_6	NZ	B_ASP_56	OD2	3.751

Table 1201: Interfacial 3D0L-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3D0V	A_HIS_96	NE2	C_ASP_5	OD1	2.775
3D0V	B_ARG_58	NH2	C_GLU_3	OE1	2.733
3D0V	B_ARG_95	NH1	C_ASP_5	OD1	2.808
3D0V	B_ARG_95	NH1	C_ASP_5	OD2	3.484
3D0V	B_ARG_95	NH2	C_ASP_5	OD1	3.359
3D0V	B_ARG_95	NH2	C_ASP_5	OD2	2.831
3D0V	B_ARG_96	NH1	A_GLU_55	OE1	3.250
3D0V	B_ARG_96	NH1	A_GLU_55	OE2	3.216
3D0V	B_ARG_96	NH2	A_GLU_55	OE1	3.184
3D0V	B_LYS_209	NZ	A_GLU_123	OE1	3.487
3D0V	C_LYS_6	NZ	B_ASP_54	OD1	3.609
3D0V	C_LYS_6	NZ	B_ASP_54	OD2	2.826
3D0V	C_LYS_6	NZ	B_ASP_56	OD1	3.006

Table 1202: Interfacial 3D0V-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3D9A	C_LYS_697	NZ	H_ASP_332	OD2	2.741
3D9A	C_LYS_697	NZ	H_ASP_399	OD1	2.864
3D9A	C_LYS_697	NZ	H_ASP_399	OD2	3.300
3D9A	H_LYS_508	NZ	L_GLU_123	OE1	3.029
3D9A	H_LYS_508	NZ	L_GLU_123	OE2	3.809

Table 1203: Interfacial 3D9A-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3DRO	B_ARG_95	NH1	P_ASP_5	OD1	3.590
3DRO	B_ARG_95	NH1	P_ASP_5	OD2	3.370
3DRO	B_ARG_95	NH2	P_ASP_5	OD2	3.007
3DRO	B_ARG_96	NH2	A_GLU_55	OE1	2.727
3DRO	B_ARG_96	NH2	A_GLU_55	OE2	3.426
3DRO	B_LYS_209	NZ	A_GLU_123	OE1	3.782
3DRO	P_LYS_6	NZ	B_ASP_54	OD1	2.913
3DRO	P_LYS_6	NZ	B_ASP_54	OD2	3.775
3DRO	P_LYS_6	NZ	B_ASP_56	OD1	3.330
3DRO	P_LYS_6	NZ	B_ASP_56	OD2	3.868

Table 1204: Interfacial 3DRO-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3DRQ	A_HIS_96	NE2	C_ASP_5	OD1	2.866
3DRQ	B_ARG_58	NH2	C_GLU_3	OE1	3.516
3DRQ	B_ARG_95	NH1	C_ASP_5	OD1	2.806
3DRQ	B_ARG_95	NH1	C_ASP_5	OD2	3.209
3DRQ	B_ARG_95	NH2	C_ASP_5	OD1	3.572
3DRQ	B_ARG_95	NH2	C_ASP_5	OD2	2.688
3DRQ	B_ARG_96	NH1	A_GLU_55	OE1	2.721
3DRQ	B_ARG_96	NH1	A_GLU_55	OE2	2.397
3DRQ	B_ARG_96	NH2	A_GLU_55	OE1	3.293
3DRQ	B_LYS_209	NZ	A_GLU_123	OE1	3.837
3DRQ	C_LYS_6	NZ	B_ASP_54	OD1	2.921
3DRQ	C_LYS_6	NZ	B_ASP_54	OD2	2.342
3DRQ	C_LYS_6	NZ	B_ASP_56	OD1	3.006

Table 1205: Interfacial 3DRQ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3DSF	H_ARG_52	NH1	P_ASP_47	OD2	3.172

Table 1206: Interfacial 3DSF-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3EBA	B_LYS_97	NZ	A_GLU_97	OE2	3.240
3EBA	B_ARG_101	NH1	A_ASP_109	OD1	3.083
3EBA	B_ARG_101	NH1	A_ASP_109	OD2	2.691
3EBA	B_ARG_101	NH2	A_ASP_109	OD1	3.308
3EBA	B_ARG_101	NH2	A_ASP_109	OD2	3.134

Table 1207: Interfacial 3EBA-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3EOA	H_LYS_217	NZ	L_GLU_123	OE2	3.037
3EOA	I_LYS_197	NZ	H_ASP_55	OD1	3.170
3EOA	I_LYS_197	NZ	H_GLU_57	OE1	2.719
3EOA	I_HIS_198	NE2	H_GLU_57	OE1	3.638
3EOA	I_HIS_198	NE2	H_GLU_57	OE2	3.098
3EOA	B_LYS_	NZ	A_GLU_	OE2	3.673
3EOA	J_LYS_197	NZ	B_ASP_55	OD1	2.626
3EOA	J_LYS_197	NZ	B_ASP_55	OD2	2.997
3EOA	J_LYS_197	NZ	B_GLU_57	OE1	2.784
3EOA	J_HIS_198	NE2	B_GLU_57	OE1	3.322
3EOA	J_HIS_198	NE2	B_GLU_57	OE2	2.793

Table 1208: Interfacial 3EOA-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3EOB	H_LYS_217	NZ	L_GLU_123	OE2	3.176
3EOB	I_LYS_197	NZ	H_GLU_57	OE1	2.792
3EOB	I_LYS_197	NZ	H_GLU_57	OE2	3.051
3EOB	I_HIS_198	ND1	H_GLU_57	OE2	3.691
3EOB	I_HIS_198	NE2	H_GLU_57	OE1	2.182
3EOB	I_HIS_198	NE2	H_GLU_57	OE2	2.522
3EOB	I_HIS_264	NE2	J_GLU_241	OE1	2.369
3EOB	I_HIS_264	NE2	J_GLU_241	OE2	2.595
3EOB	B_LYS_	NZ	A_GLU_	OE1	3.788
3EOB	B_LYS_	NZ	A_GLU_	OE2	3.219
3EOB	J_LYS_197	NZ	B_ASP_55	OD1	3.833
3EOB	J_LYS_197	NZ	B_GLU_57	OE1	2.107
3EOB	J_LYS_197	NZ	B_GLU_57	OE2	3.802
3EOB	J_HIS_198	ND1	B_GLU_57	OE2	3.839
3EOB	J_HIS_198	NE2	B_GLU_57	OE1	2.356
3EOB	J_HIS_198	NE2	B_GLU_57	OE2	2.609
3EOB	J_HIS_264	NE2	I_GLU_241	OE1	2.434
3EOB	J_HIS_264	NE2	I_GLU_241	OE2	2.722

Table 1209: Interfacial 3EOB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3ESV	F_LYS_0	NZ	G_ASP_1054	OD1	3.499
3ESV	F_LYS_0	NZ	G_ASP_1054	OD2	2.774
3ESV	F_LYS_0	NZ	G_ASP_1056	OD2	3.090
3ESV	G_ARG_53	NH1	F_ASP_1056	OD1	2.802
3ESV	G_ARG_53	NH2	F_ASP_1056	OD1	3.489

Table 1210: Interfacial 3ESV-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3ETB	F_ARG_24	NH1	G_ASP_70	OD1	3.579
3ETB	F_ARG_24	NH1	G_ASP_70	OD2	3.034
3ETB	F_ARG_24	NH2	G_ASP_70	OD1	3.608
3ETB	F_ARG_24	NH2	G_ASP_70	OD2	3.774
3ETB	F_ARG_30	NH1	J_ASP_658	OD2	3.129
3ETB	F_ARG_53	NH1	J_GLU_654	OE1	3.838
3ETB	F_ARG_53	NH2	J_GLU_654	OE1	3.771
3ETB	F_ARG_1050	NH2	J_ASP_683	OD2	3.114
3ETB	G_ARG_24	NH1	F_ASP_70	OD1	3.633
3ETB	G_ARG_24	NH1	F_ASP_70	OD2	3.127
3ETB	G_ARG_24	NH2	F_ASP_70	OD1	3.702
3ETB	G_ARG_24	NH2	F_ASP_70	OD2	3.878
3ETB	G_ARG_30	NH1	K_ASP_658	OD2	3.266
3ETB	G_ARG_53	NH2	K_ASP_648	OD2	3.972
3ETB	G_ARG_53	NH2	K_GLU_654	OE1	3.990
3ETB	G_ARG_1050	NH2	K_ASP_683	OD1	3.853
3ETB	G_ARG_1050	NH2	K_ASP_683	OD2	2.796
3ETB	H_ARG_24	NH1	I_ASP_70	OD1	3.544
3ETB	H_ARG_24	NH1	I_ASP_70	OD2	3.118
3ETB	H_ARG_24	NH2	I_ASP_70	OD1	3.662
3ETB	H_ARG_24	NH2	I_ASP_70	OD2	3.905
3ETB	H_ARG_30	NH1	L_ASP_658	OD1	3.824
3ETB	H_ARG_30	NH1	L_ASP_658	OD2	2.913
3ETB	H_ARG_53	NH1	L_GLU_654	OE1	3.771
3ETB	H_ARG_53	NH2	L_GLU_654	OE1	3.669
3ETB	H_ARG_1050	NH2	L_ASP_683	OD2	3.159
3ETB	I_ARG_24	NH1	H_ASP_70	OD1	3.448
3ETB	I_ARG_24	NH1	H_ASP_70	OD2	2.998
3ETB	I_ARG_24	NH2	H_ASP_70	OD1	3.537
3ETB	I_ARG_24	NH2	H_ASP_70	OD2	3.789
3ETB	I_ARG_30	NH1	M_ASP_658	OD2	3.315
3ETB	I_ARG_53	NH1	M_GLU_654	OE1	3.885
3ETB	I_ARG_53	NH2	M_GLU_654	OE1	3.890
3ETB	I_ARG_1050	NH2	M_ASP_683	OD2	3.093
3ETB	J_LYS_653	NZ	G_ASP_17	OD1	2.972
3ETB	J_LYS_684	NZ	F_ASP_1054	OD1	3.728
3ETB	J_LYS_684	NZ	F_ASP_1054	OD2	3.401
3ETB	J_LYS_684	NZ	F_ASP_1056	OD1	3.220
3ETB	J_LYS_684	NZ	F_ASP_1056	OD2	3.481
3ETB	K_LYS_653	NZ	F_ASP_17	OD1	3.083
3ETB	K_LYS_684	NZ	G_ASP_1054	OD1	3.379
3ETB	K_LYS_684	NZ	G_ASP_1054	OD2	3.075
3ETB	K_LYS_684	NZ	G_ASP_1056	OD1	3.162
3ETB	K_LYS_684	NZ	G_ASP_1056	OD2	3.578
3ETB	L_LYS_653	NZ	I_ASP_17	OD1	2.978
3ETB	L_LYS_684	NZ	H_ASP_1056	OD1	3.616
3ETB	L_LYS_684	NZ	H_ASP_1056	OD2	3.187
3ETB	M_LYS_653	NZ	H_ASP_17	OD1	3.060
3ETB	M_LYS_684	NZ	I_ASP_1054	OD1	3.625
3ETB	M_LYS_684	NZ	I_ASP_1054	OD2	3.167
3ETB	M_LYS_684	NZ	I_ASP_1056	OD1	3.241
3ETB	M_LYS_684	NZ	I_ASP_1056	OD2	3.478

Table 1211: Interfacial 3ETB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3EYV	L_LYS_55	NZ	H_ASP_102	OD2	3.565
3EYV	H_LYS_215	NZ	L_GLU_128	OE2	3.627
3EYV	A_LYS_55	NZ	B_ASP_102	OD2	3.151
3EYV	B_LYS_220	NZ	A_ASP_127	OD2	3.402

Table 1212: Interfacial 3EYV-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3FMG	L_LYS_50	NZ	H_ASP_106	OD1	3.132
3FMG	H_LYS_64	NZ	L_ASP_1	OD2	3.241

Table 1213: Interfacial 3FMG-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3G3A	B_ARG_61	NH2	A_ASP_59	OD2	3.447
3G3A	B_ARG_73	NH1	A_ASP_61	OD1	2.630
3G3A	B_ARG_73	NH1	A_ASP_61	OD2	3.494
3G3A	B_ARG_73	NH2	A_ASP_59	OD2	3.260
3G3A	B_ARG_73	NH2	A_ASP_61	OD1	3.287
3G3A	B_ARG_73	NH2	A_ASP_61	OD2	2.479
3G3A	B_ARG_112	NH1	A_ASP_141	OD1	3.611
3G3A	B_ARG_112	NH1	A_ASP_141	OD2	2.906
3G3A	B_ARG_112	NH2	A_ASP_141	OD1	2.901
3G3A	B_ARG_112	NH2	A_ASP_141	OD2	3.689
3G3A	B_ARG_112	NH2	A_ASP_143	OD2	3.389
3G3A	D_ARG_61	NH1	C_ASP_59	OD2	3.676
3G3A	D_ARG_61	NH2	C_ASP_59	OD1	3.900
3G3A	D_ARG_61	NH2	C_ASP_59	OD2	3.137
3G3A	D_ARG_73	NH1	C_ASP_61	OD1	3.720
3G3A	D_ARG_73	NH1	C_ASP_61	OD2	2.705
3G3A	D_ARG_73	NH2	C_ASP_59	OD2	2.913
3G3A	D_ARG_73	NH2	C_ASP_61	OD1	2.638
3G3A	D_ARG_73	NH2	C_ASP_61	OD2	3.209
3G3A	D_ARG_112	NH1	C_ASP_141	OD1	3.483
3G3A	D_ARG_112	NH1	C_ASP_141	OD2	2.837
3G3A	D_ARG_112	NH2	C_ASP_141	OD1	2.752
3G3A	D_ARG_112	NH2	C_ASP_141	OD2	3.622
3G3A	D_ARG_112	NH2	C_ASP_143	OD2	3.602
3G3A	F_ARG_61	NH1	E_ASP_59	OD2	3.922
3G3A	F_ARG_61	NH2	E_ASP_59	OD1	3.681
3G3A	F_ARG_61	NH2	E_ASP_59	OD2	2.804
3G3A	F_ARG_73	NH1	E_ASP_61	OD1	3.367
3G3A	F_ARG_73	NH1	E_ASP_61	OD2	2.915
3G3A	F_ARG_73	NH2	E_ASP_59	OD2	2.686
3G3A	F_ARG_73	NH2	E_ASP_61	OD1	2.874
3G3A	F_ARG_73	NH2	E_ASP_61	OD2	3.960
3G3A	F_ARG_112	NH1	E_ASP_141	OD1	3.733
3G3A	F_ARG_112	NH1	E_ASP_141	OD2	3.195
3G3A	F_ARG_112	NH2	E_ASP_141	OD1	3.001
3G3A	F_ARG_112	NH2	E_ASP_141	OD2	3.839
3G3A	F_ARG_112	NH2	E_ASP_143	OD2	3.491
3G3A	H_ARG_61	NH2	G_ASP_59	OD2	3.367
3G3A	H_ARG_73	NH1	G_ASP_59	OD2	3.259
3G3A	H_ARG_73	NH2	G_ASP_59	OD2	3.473
3G3A	H_ARG_73	NH2	G_ASP_61	OD1	2.486
3G3A	H_ARG_73	NH2	G_ASP_61	OD2	2.698
3G3A	H_ARG_112	NH1	G_ASP_141	OD1	3.280
3G3A	H_ARG_112	NH1	G_ASP_143	OD2	3.578
3G3A	H_ARG_112	NH2	G_ASP_141	OD1	3.102
3G3A	H_ARG_112	NH2	G_ASP_141	OD2	2.609

Table 1214: Interfacial 3G3A-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3G3B	B_ARG_61	NH2	A_ASP_59	OD1	3.551
3G3B	B_ARG_61	NH2	A_ASP_59	OD2	3.590
3G3B	B_ARG_73	NH1	A_ASP_61	OD1	2.527
3G3B	B_ARG_73	NH1	A_ASP_61	OD2	3.439
3G3B	B_ARG_73	NH2	A_ASP_59	OD2	2.967
3G3B	B_ARG_73	NH2	A_ASP_61	OD1	3.469
3G3B	B_ARG_73	NH2	A_ASP_61	OD2	2.765
3G3B	B_ARG_112	NH1	A_ASP_141	OD1	3.569
3G3B	B_ARG_112	NH1	A_ASP_141	OD2	2.625
3G3B	B_ARG_112	NH2	A_ASP_141	OD1	2.926
3G3B	B_ARG_112	NH2	A_ASP_141	OD2	3.538
3G3B	B_ARG_112	NH2	A_ASP_143	OD2	3.804
3G3B	D_ARG_61	NH2	C_ASP_59	OD1	3.954
3G3B	D_ARG_73	NH1	C_ASP_61	OD1	2.753
3G3B	D_ARG_73	NH1	C_ASP_61	OD2	3.824
3G3B	D_ARG_73	NH2	C_ASP_59	OD2	3.136
3G3B	D_ARG_73	NH2	C_ASP_61	OD1	3.224
3G3B	D_ARG_73	NH2	C_ASP_61	OD2	2.702
3G3B	D_ARG_112	NH1	C_ASP_141	OD1	3.812
3G3B	D_ARG_112	NH1	C_ASP_141	OD2	2.690
3G3B	D_ARG_112	NH2	C_ASP_141	OD1	2.826
3G3B	D_ARG_112	NH2	C_ASP_141	OD2	3.301
3G3B	D_ARG_112	NH2	C_ASP_143	OD2	3.656
3G3B	F_ARG_61	NH2	E_ASP_59	OD2	3.820
3G3B	F_ARG_73	NH1	E_ASP_61	OD1	2.535
3G3B	F_ARG_73	NH1	E_ASP_61	OD2	3.949
3G3B	F_ARG_73	NH2	E_ASP_59	OD2	2.812
3G3B	F_ARG_73	NH2	E_ASP_61	OD1	3.056
3G3B	F_ARG_73	NH2	E_ASP_61	OD2	2.934
3G3B	F_ARG_112	NH1	E_ASP_141	OD2	2.714
3G3B	F_ARG_112	NH2	E_ASP_141	OD1	3.020
3G3B	F_ARG_112	NH2	E_ASP_141	OD2	3.176
3G3B	F_ARG_112	NH2	E_ASP_143	OD2	3.737
3G3B	H_ARG_73	NH1	G_ASP_61	OD1	2.839
3G3B	H_ARG_73	NH1	G_ASP_61	OD2	3.791
3G3B	H_ARG_73	NH2	G_ASP_59	OD2	2.431
3G3B	H_ARG_73	NH2	G_ASP_61	OD1	3.464
3G3B	H_ARG_73	NH2	G_ASP_61	OD2	2.896
3G3B	H_ARG_112	NH1	G_ASP_141	OD1	3.676
3G3B	H_ARG_112	NH1	G_ASP_141	OD2	2.564
3G3B	H_ARG_112	NH2	G_ASP_141	OD1	2.813
3G3B	H_ARG_112	NH2	G_ASP_141	OD2	3.280
3G3B	H_ARG_112	NH2	G_ASP_143	OD2	3.506

Table 1215: Interfacial 3G3B-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3GGW	A_ARG_96	NH2	B_GLU_50	OE1	3.590
3GGW	A_ARG_96	NH2	B_GLU_50	OE2	2.762
3GGW	B_ARG_52	NH1	E_ASP_4	OD2	3.092
3GGW	B_LYS_210	NZ	A_GLU_123	OE2	3.208
3GGW	C_ARG_96	NH2	D_GLU_50	OE1	3.555
3GGW	C_ARG_96	NH2	D_GLU_50	OE2	2.962
3GGW	D_ARG_52	NH1	F_ASP_4	OD2	3.127
3GGW	D_LYS_210	NZ	C_GLU_123	OE2	2.871
3GGW	D_ARG_215	NH2	C_GLU_213	OE1	3.834
3GGW	D_ARG_215	NH2	C_GLU_213	OE2	2.618

Table 1216: Interfacial 3GGW-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3GHB	H.LYS_143	NZ	L.GLU_124	OE2	2.614
3GHB	H.LYS_209	NZ	L.GLU_123	OE1	2.751
3GHB	H.LYS_209	NZ	L.GLU_123	OE2	3.411
3GHB	P.LYS_305	NZ	H.GLU_100E	OE1	3.508
3GHB	P.LYS_305	NZ	H.ASP_100F	OD2	3.835
3GHB	I.LYS_143	NZ	M.GLU_124	OE2	2.607
3GHB	I.LYS_209	NZ	M.GLU_123	OE1	2.988
3GHB	I.LYS_209	NZ	M.GLU_123	OE2	3.773
3GHB	Q.LYS_305	NZ	I.ASP_100F	OD1	3.174

Table 1217: Interfacial 3GHB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3GHE	H.LYS.143	NZ	L.GLU.124	OE2	2.684
3GHE	H.LYS.209	NZ	L.GLU.123	OE1	2.541
3GHE	H.LYS.209	NZ	L.GLU.123	OE2	3.149
3GHE	P.ARG.304	NH1	H.ASP.100A	OD1	3.397
3GHE	P.ARG.304	NH2	H.ASP.100A	OD1	3.243
3GHE	P.ARG.304	NH2	H.ASP.100A	OD2	3.833
3GHE	P.HIS.308	ND1	H.ASP.100H	OD2	3.415
3GHE	P.ARG.315	NH1	H.GLU.95	OE1	3.518
3GHE	P.ARG.315	NH1	H.GLU.95	OE2	2.720
3GHE	P.ARG.315	NH2	H.GLU.95	OE2	3.104

Table 1218: Interfacial 3GHE-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3GJF	A_ARG_48	NH2	B_ASP_53	OD2	3.786
3GJF	A_ARG_65	NH1	L_ASP_52	OD1	3.134
3GJF	A_ARG_65	NH1	L_ASP_52	OD2	3.382
3GJF	A_ARG_65	NH2	L_ASP_52	OD1	2.989
3GJF	A_ARG_65	NH2	L_ASP_52	OD2	3.338
3GJF	D_ARG_35	NH2	E_ASP_53	OD1	3.050
3GJF	D_ARG_35	NH2	E_ASP_53	OD2	3.940
3GJF	D_ARG_48	NH2	E_ASP_53	OD1	3.764
3GJF	D_ARG_48	NH2	E_ASP_53	OD2	3.452
3GJF	D_ARG_65	NH1	K_ASP_52	OD1	3.173
3GJF	D_ARG_65	NH1	K_ASP_52	OD2	3.530
3GJF	D_ARG_65	NH2	K_ASP_52	OD1	3.166
3GJF	D_ARG_65	NH2	K_ASP_52	OD2	2.445
3GJF	E_LYS_6	NZ	D_GLU_232	OE1	3.774
3GJF	E_LYS_6	NZ	D_GLU_232	OE2	2.502
3GJF	M_LYS_215	NZ	K_GLU_126	OE1	3.244
3GJF	M_LYS_215	NZ	K_GLU_126	OE2	2.553

Table 1219: Interfacial 3GJF-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3GNM	H_ARG_169	NH1	L_ASP_172	OD1	3.348
3GNM	H_ARG_169	NH2	L_ASP_172	OD1	3.542
3GNM	H_ARG_169	NH2	L_ASP_175	OD1	3.297
3GNM	H_LYS_213	NZ	L_GLU_128	OE1	2.721
3GNM	H_LYS_213	NZ	L_GLU_128	OE2	3.840

Table 1220: Interfacial 3GNM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3GO1	H.LYS.209	NZ	L.GLU.123	OE1	2.728
3GO1	H.LYS.209	NZ	L.GLU.123	OE2	3.471
3GO1	P.LYS.305	NZ	L.ASP.51	OD1	2.931
3GO1	P.ARG.315	NH1	H.GLU.95	OE2	3.127
3GO1	P.ARG.315	NH2	H.GLU.95	OE2	2.921
3GO1	P.ARG.315	NH2	H.ASP.100A	OD2	3.393

Table 1221: Interfacial 3GO1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3HAE	A_ARG_35	NH1	B_ASP_53	OD1	3.527
3HAE	A_ARG_35	NH1	B_ASP_53	OD2	2.844
3HAE	A_ARG_48	NH2	B_ASP_53	OD2	3.583
3HAE	A_ARG_65	NH1	L_ASP_52	OD1	3.495
3HAE	A_ARG_65	NH1	L_ASP_52	OD2	2.908
3HAE	A_ARG_65	NH2	L_ASP_52	OD1	3.452
3HAE	A_ARG_65	NH2	L_ASP_52	OD2	3.099
3HAE	B_LYS_6	NZ	A_GLU_232	OE2	2.622
3HAE	D_ARG_35	NH1	E_ASP_53	OD1	3.949
3HAE	D_ARG_35	NH1	E_ASP_53	OD2	3.963
3HAE	D_ARG_35	NH2	E_ASP_53	OD1	3.106
3HAE	D_ARG_48	NH2	E_ASP_53	OD2	3.593
3HAE	D_ARG_65	NH1	G_ASP_52	OD1	3.201
3HAE	D_ARG_65	NH2	G_ASP_52	OD1	2.885
3HAE	D_ARG_65	NH2	G_ASP_52	OD2	3.031
3HAE	J_ARG_35	NH2	K_ASP_53	OD1	3.520
3HAE	J_ARG_48	NH2	K_ASP_53	OD1	3.945
3HAE	J_ARG_48	NH2	K_ASP_53	OD2	3.051
3HAE	J_ARG_65	NH1	N_ASP_52	OD1	3.749
3HAE	J_ARG_65	NH2	N_ASP_52	OD1	2.440
3HAE	J_ARG_65	NH2	N_ASP_52	OD2	2.989
3HAE	P_ARG_35	NH1	Q_ASP_53	OD2	3.921
3HAE	P_ARG_48	NH2	Q_ASP_53	OD1	3.566
3HAE	P_ARG_48	NH2	Q_ASP_53	OD2	2.872
3HAE	P_ARG_65	NH1	S_ASP_52	OD1	3.579
3HAE	P_ARG_65	NH1	S_ASP_52	OD2	3.466
3HAE	P_ARG_65	NH2	S_ASP_52	OD1	3.120
3HAE	P_ARG_65	NH2	S_ASP_52	OD2	2.826
3HAE	Q_LYS_6	NZ	P_GLU_232	OE2	3.965
3HAE	N_LYS_132	NZ	O_ASP_150	OD2	3.615
3HAE	H_LYS_215	NZ	L_GLU_126	OE1	3.537
3HAE	H_LYS_215	NZ	L_GLU_126	OE2	3.674
3HAE	I_LYS_215	NZ	G_GLU_126	OE1	3.678
3HAE	O_LYS_215	NZ	N_GLU_126	OE2	3.736
3HAE	T_LYS_215	NZ	S_GLU_126	OE1	2.660
3HAE	T_LYS_215	NZ	S_GLU_126	OE2	3.779

Table 1222: Interfacial 3HAE-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3HFM	L_HIS_34	ND1	H_ASP_99	OD1	3.756
3HFM	L_HIS_34	ND1	H_ASP_99	OD2	3.698
3HFM	L_LYS_49	NZ	H_ASP_99	OD1	3.423
3HFM	H_LYS_209	NZ	L_GLU_123	OE1	2.622
3HFM	H_ARG_213	NH2	L_GLU_123	OE1	3.991
3HFM	Y_LYS_97	NZ	H_ASP_32	OD1	3.609

Table 1223: Interfacial 3HFM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3HI6	H_LYS_216	NZ	L_GLU_122	OE1	2.896
3HI6	H_LYS_216	NZ	L_GLU_122	OE2	3.887
3HI6	X_LYS_216	NZ	Y_GLU_122	OE1	3.212

Table 1224: Interfacial 3HI6-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3HMG	A_ARG_109	NH1	B_GLU_67	OE1	3.372
3HMG	A_ARG_109	NH1	B_GLU_67	OE2	2.849
3HMG	A_LYS_238	NZ	F_GLU_72	OE2	2.747
3HMG	A_ARG_269	NH2	B_GLU_67	OE1	2.883
3HMG	A_LYS_299	NZ	B_GLU_69	OE1	3.233
3HMG	A_LYS_310	NZ	B_ASP_90	OD1	2.577
3HMG	B_ARG_25	NH1	A_GLU_325	OE1	3.777
3HMG	B_ARG_54	NH1	F_GLU_97	OE1	2.798
3HMG	B_ARG_54	NH2	F_GLU_97	OE1	3.127
3HMG	B_LYS_62	NZ	F_ASP_86	OD1	2.986
3HMG	B_LYS_62	NZ	F_ASP_86	OD2	2.761
3HMG	B_LYS_62	NZ	F_ASP_90	OD1	3.490
3HMG	B_LYS_62	NZ	F_ASP_90	OD2	2.774
3HMG	B_HIS_64	NE2	F_ASP_79	OD1	3.991
3HMG	B_HIS_64	NE2	F_ASP_79	OD2	3.618
3HMG	B_ARG_76	NH1	D_GLU_74	OE1	3.445
3HMG	B_ARG_76	NH1	D_GLU_74	OE2	2.823
3HMG	B_ARG_76	NH1	D_GLU_81	OE1	2.738
3HMG	B_ARG_76	NH1	D_GLU_81	OE2	3.615
3HMG	B_ARG_76	NH2	D_GLU_74	OE1	2.830
3HMG	B_ARG_76	NH2	D_GLU_74	OE2	3.630
3HMG	B_ARG_123	NH1	F_GLU_132	OE2	3.281
3HMG	B_ARG_124	NH1	F_GLU_132	OE1	3.422
3HMG	B_ARG_124	NH1	F_GLU_132	OE2	3.128
3HMG	B_ARG_127	NH2	F_GLU_131	OE1	2.404
3HMG	B_ARG_163	NH1	F_GLU_131	OE1	2.713
3HMG	B_ARG_163	NH1	F_GLU_131	OE2	2.661
3HMG	B_ARG_170	NH2	D_GLU_128	OE1	3.667
3HMG	B_ARG_170	NH2	D_GLU_128	OE2	3.704
3HMG	C_ARG_109	NH1	D_GLU_67	OE1	3.376
3HMG	C_ARG_109	NH1	D_GLU_67	OE2	2.842
3HMG	C_LYS_238	NZ	B_GLU_72	OE2	2.625
3HMG	C_ARG_269	NH2	D_GLU_67	OE1	2.813
3HMG	C_LYS_299	NZ	D_GLU_69	OE1	3.251
3HMG	C_LYS_310	NZ	D_ASP_90	OD1	2.544
3HMG	D_ARG_54	NH1	B_GLU_97	OE1	2.804
3HMG	D_ARG_54	NH2	B_GLU_97	OE1	3.138
3HMG	D_LYS_62	NZ	B_ASP_86	OD1	2.985
3HMG	D_LYS_62	NZ	B_ASP_86	OD2	2.721
3HMG	D_LYS_62	NZ	B_ASP_90	OD1	3.453
3HMG	D_LYS_62	NZ	B_ASP_90	OD2	2.701
3HMG	D_HIS_64	NE2	B_ASP_79	OD1	3.960
3HMG	D_HIS_64	NE2	B_ASP_79	OD2	3.444
3HMG	D_ARG_76	NH1	F_GLU_74	OE1	3.513
3HMG	D_ARG_76	NH1	F_GLU_74	OE2	2.767
3HMG	D_ARG_76	NH1	F_GLU_81	OE1	2.643
3HMG	D_ARG_76	NH1	F_GLU_81	OE2	3.636
3HMG	D_ARG_76	NH2	F_GLU_74	OE1	2.766
3HMG	D_ARG_76	NH2	F_GLU_74	OE2	3.449
3HMG	D_ARG_123	NH1	B_GLU_132	OE2	3.299
3HMG	D_ARG_124	NH1	B_GLU_132	OE1	3.459
3HMG	D_ARG_124	NH1	B_GLU_132	OE2	3.169
3HMG	D_ARG_127	NH2	B_GLU_131	OE1	2.449
3HMG	D_ARG_163	NH1	B_GLU_131	OE1	2.694
3HMG	D_ARG_163	NH1	B_GLU_131	OE2	2.707
3HMG	D_ARG_170	NH2	F_GLU_128	OE1	3.716
3HMG	D_ARG_170	NH2	F_GLU_128	OE2	3.859

3HMG	E_ARG_109	NH1	F_GLU_67	OE1	3.402
3HMG	E_ARG_109	NH1	F_GLU_67	OE2	2.841
3HMG	E_LYS_238	NZ	D_GLU_72	OE2	2.745
3HMG	E_ARG_269	NH2	F_GLU_67	OE1	2.840
3HMG	E_LYS_299	NZ	F_GLU_69	OE1	3.192
3HMG	E_LYS_310	NZ	F_ASP_90	OD1	2.563
3HMG	F_ARG_25	NH1	E_GLU_325	OE2	3.879
3HMG	F_ARG_25	NH2	E_GLU_325	OE2	3.668
3HMG	F_ARG_54	NH1	D_GLU_97	OE1	2.700
3HMG	F_ARG_54	NH2	D_GLU_97	OE1	3.155
3HMG	F_LYS_62	NZ	D_ASP_86	OD1	2.928
3HMG	F_LYS_62	NZ	D_ASP_86	OD2	2.697
3HMG	F_LYS_62	NZ	D_ASP_90	OD1	3.563
3HMG	F_LYS_62	NZ	D_ASP_90	OD2	2.800
3HMG	F_HIS_64	NE2	D_ASP_79	OD1	3.875
3HMG	F_HIS_64	NE2	D_ASP_79	OD2	3.441
3HMG	F_ARG_76	NH1	B_GLU_74	OE1	3.414
3HMG	F_ARG_76	NH1	B_GLU_74	OE2	2.793
3HMG	F_ARG_76	NH1	B_GLU_81	OE1	2.687
3HMG	F_ARG_76	NH1	B_GLU_81	OE2	3.711
3HMG	F_ARG_76	NH2	B_GLU_74	OE1	2.734
3HMG	F_ARG_76	NH2	B_GLU_74	OE2	3.548
3HMG	F_ARG_123	NH1	D_GLU_132	OE2	3.319
3HMG	F_ARG_124	NH1	D_GLU_132	OE1	3.517
3HMG	F_ARG_124	NH1	D_GLU_132	OE2	3.294
3HMG	F_ARG_127	NH2	D_GLU_131	OE1	2.559
3HMG	F_ARG_163	NH1	D_GLU_131	OE1	2.673
3HMG	F_ARG_163	NH1	D_GLU_131	OE2	2.666
3HMG	F_ARG_170	NH2	B_GLU_128	OE1	3.705
3HMG	F_ARG_170	NH2	B_GLU_128	OE2	3.753

Table 1225: Interfacial 3HMG-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3HZK	A_ARG_95	NH2	B_ASP_95	OD1	3.611
3HZK	A_ARG_95	NH2	B_ASP_95	OD2	2.795
3HZK	B_LYS_207	NZ	A_GLU_122	OE2	3.993

Table 1226: Interfacial 3HZK-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3HZM	A_ARG_95	NH2	B_ASP_95	OD1	3.493
3HZM	A_ARG_95	NH2	B_ASP_95	OD2	2.771
3HZM	A_ARG_95	NH2	B_ASP_100E	OD1	3.831
3HZM	B_LYS_207	NZ	A_GLU_122	OE2	3.353

Table 1227: Interfacial 3HZM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3HZV	A_ARG_95	NH2	B_ASP_95	OD1	3.498
3HZV	A_ARG_95	NH2	B_ASP_95	OD2	2.821
3HZV	A_ARG_95	NH2	B_ASP_100E	OD1	3.905
3HZV	B_LYS_207	NZ	A_GLU_122	OE2	3.521

Table 1228: Interfacial 3HZV-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3HZY	A_ARG_95	NH2	B_ASP_95	OD1	3.688
3HZY	A_ARG_95	NH2	B_ASP_95	OD2	3.045
3HZY	A_ARG_95	NH2	B_ASP_100E	OD1	3.820
3HZY	B_LYS_207	NZ	A_GLU_122	OE2	3.902

Table 1229: Interfacial 3HZY-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3I02	A_ARG_95	NH2	B_ASP_95	OD2	3.028
3I02	C_ARG_95	NH2	D_ASP_95	OD1	3.601
3I02	C_ARG_95	NH2	D_ASP_95	OD2	2.826
3I02	D_LYS_208	NZ	C_GLU_122	OE2	3.585

Table 1230: Interfacial 3I02-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3IET	A_LYS_50	NZ	X_GLU_8	OE1	3.701
3IET	A_LYS_50	NZ	X_GLU_8	OE2	3.403
3IET	B_LYS_208	NZ	A_GLU_123	OE1	3.818
3IET	D_HIS_55	ND1	A_ASP_143	OD1	3.412
3IET	D_HIS_55	ND1	A_ASP_143	OD2	3.385
3IET	D_LYS_208	NZ	C_GLU_123	OE2	3.321

Table 1231: Interfacial 3IET-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3IF1	D_LYS_52B	NZ	A_ASP_143	OD2	3.658
3IF1	D_HIS_55	ND1	A_ASP_143	OD1	3.559
3IF1	D_HIS_55	ND1	A_ASP_143	OD2	3.251

Table 1232: Interfacial 3IF1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3IJH	A_ARG_95	NH2	B_ASP_95	OD1	3.392
3IJH	A_ARG_95	NH2	B_ASP_95	OD2	2.832
3IJH	A_ARG_95	NH2	B_GLU_100E	OE1	3.920
3IJH	B_ARG_164	NH1	A_ASP_166	OD1	3.428
3IJH	B_ARG_164	NH2	A_ASP_166	OD1	3.938
3IJH	B_LYS_208	NZ	A_GLU_122	OE1	2.744
3IJH	C_ARG_95	NH2	D_ASP_95	OD1	3.394
3IJH	C_ARG_95	NH2	D_ASP_95	OD2	2.734
3IJH	D_ARG_164	NH1	C_ASP_166	OD1	3.593
3IJH	D_ARG_164	NH2	C_ASP_166	OD1	3.440

Table 1233: Interfacial 3IJH-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3IJS	A_ARG_95	NH2	B_ASP_95	OD1	3.603
3IJS	A_ARG_95	NH2	B_ASP_95	OD2	3.018
3IJS	A_ARG_95	NH2	B_GLU_100E	OE1	3.734
3IJS	B_ARG_164	NH1	A_ASP_166	OD1	3.855
3IJS	B_LYS_208	NZ	A_GLU_122	OE1	2.963
3IJS	C_ARG_95	NH2	D_ASP_95	OD1	3.466
3IJS	C_ARG_95	NH2	D_ASP_95	OD2	2.795
3IJS	C_ARG_95	NH2	D_GLU_100E	OE1	3.752
3IJS	D_ARG_164	NH1	C_ASP_166	OD1	3.815
3IJS	D_ARG_164	NH2	C_ASP_166	OD1	3.576
3IJS	D_LYS_208	NZ	C_GLU_122	OE1	3.219
3IJS	D_LYS_208	NZ	C_GLU_122	OE2	2.679

Table 1234: Interfacial 3IJS-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID residue name residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3IJY	A_ARG_95	NH2	B_ASP_95	OD1	3.420
3IJY	A_ARG_95	NH2	B_ASP_95	OD2	2.800
3IJY	A_ARG_95	NH2	B_GLU_100E	OE1	3.751
3IJY	B_ARG_164	NH2	A_ASP_166	OD1	3.730
3IJY	B_ARG_164	NH2	A_ASP_166	OD2	3.693
3IJY	B_LYS_208	NZ	A_GLU_122	OE1	2.748
3IJY	C_ARG_95	NH2	D_ASP_95	OD1	2.992
3IJY	C_ARG_95	NH2	D_ASP_95	OD2	2.767
3IJY	C_ARG_95	NH2	D_GLU_100E	OE1	3.905
3IJY	D_ARG_164	NH2	C_ASP_166	OD1	3.199

Table 1235: Interfacial 3IJY-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3IKC	A_ARG_95	NH2	B_ASP_95	OD1	3.326
3IKC	A_ARG_95	NH2	B_ASP_95	OD2	2.867
3IKC	A_ARG_95	NH2	B_GLU_100E	OE1	3.865
3IKC	B_LYS_208	NZ	A_GLU_122	OE1	3.042
3IKC	C_ARG_95	NH2	D_ASP_95	OD1	3.250
3IKC	C_ARG_95	NH2	D_ASP_95	OD2	2.670
3IKC	D_ARG_164	NH1	C_ASP_166	OD1	3.903
3IKC	D_ARG_164	NH2	C_ASP_166	OD1	3.107

Table 1236: Interfacial 3IKC-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3IU3	A_ARG_29	NH2	K_ASP_6	OD1	2.779
3IU3	A_LYS_211	NZ	B_GLU_120	OE1	2.457
3IU3	B_ARG_90	NH1	K_ASP_56	OD2	3.059
3IU3	C_ARG_29	NH1	J_ASP_6	OD1	3.038
3IU3	C_ARG_29	NH1	J_ASP_6	OD2	3.788
3IU3	C_ARG_29	NH2	J_ASP_6	OD1	3.464
3IU3	C_LYS_211	NZ	D_GLU_120	OE2	3.231
3IU3	D_ARG_90	NH2	J_ASP_56	OD2	3.101
3IU3	H_ARG_29	NH1	I_ASP_6	OD1	3.964
3IU3	H_ARG_29	NH1	I_ASP_6	OD2	3.865
3IU3	H_ARG_29	NH2	I_ASP_6	OD1	2.749
3IU3	H_ARG_29	NH2	I_ASP_6	OD2	3.378
3IU3	H_HIS_166	NE2	L_ASP_164	OD1	3.898
3IU3	H_LYS_211	NZ	L_GLU_120	OE2	3.694
3IU3	L_ARG_29	NH2	I_ASP_56	OD2	3.164
3IU3	L_ARG_90	NH2	I_ASP_56	OD1	2.806
3IU3	L_ARG_36	NH1	H_ASP_55	OD1	3.819
3IU3	L_ARG_36	NH2	H_ASP_55	OD1	3.008
3IU3	L_ARG_36	NH2	H_ASP_55	OD2	2.747

Table 1237: Interfacial 3IU3-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID residue name residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3J5M	A_ARG_429	NH2	D_ASP_74	OD1	3.207
3J5M	A_ARG_429	NH2	D_ASP_74	OD2	3.203
3J5M	D_LYS_52	NZ	A_ASP_474	OD2	2.827
3J5M	D_ARG_64	NH2	A_ASP_457	OD2	3.079
3J5M	D_LYS_209	NZ	C_GLU_123	OE1	3.480
3J5M	D_LYS_209	NZ	C_GLU_123	OE2	2.844
3J5M	D_LYS_214	NZ	C_ASP_122	OD2	2.841
3J5M	E_ARG_429	NH2	H_ASP_74	OD1	3.207
3J5M	E_ARG_429	NH2	H_ASP_74	OD2	3.202
3J5M	H_LYS_52	NZ	E_ASP_474	OD2	2.827
3J5M	H_ARG_64	NH2	E_ASP_457	OD2	3.078
3J5M	H_LYS_209	NZ	G_GLU_123	OE1	3.479
3J5M	H_LYS_209	NZ	G_GLU_123	OE2	2.843
3J5M	H_LYS_214	NZ	G_ASP_122	OD2	2.842
3J5M	I_ARG_429	NH2	L_ASP_74	OD1	3.207
3J5M	I_ARG_429	NH2	L_ASP_74	OD2	3.202
3J5M	L_LYS_52	NZ	I_ASP_474	OD2	2.827
3J5M	L_ARG_64	NH2	I_ASP_457	OD2	3.078
3J5M	L_LYS_209	NZ	K_GLU_123	OE1	3.480
3J5M	L_LYS_209	NZ	K_GLU_123	OE2	2.844
3J5M	L_LYS_214	NZ	K_ASP_122	OD2	2.841

Table 1238: Interfacial 3J5M-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3J70	A_ARG_64	NH2	B_ASP_1	OD1	2.676
3J70	A_LYS_209	NZ	B_GLU_123	OE1	3.744
3J70	A_LYS_209	NZ	B_GLU_123	OE2	2.604
3J70	C_LYS_29	NZ	D_ASP_279	OD2	2.704
3J70	C_ARG_59	NH1	D_ASP_368	OD1	3.842
3J70	C_ARG_59	NH1	D_ASP_368	OD2	2.986
3J70	C_ARG_59	NH2	D_ASP_368	OD1	2.621
3J70	C_ARG_59	NH2	D_ASP_368	OD2	3.173
3J70	D_ARG_146	NH1	C_GLU_169	OE1	2.841
3J70	D_ARG_146	NH1	C_GLU_169	OE2	2.796
3J70	D_ARG_146	NH2	C_GLU_169	OE1	3.599
3J70	D_LYS_171	NZ	C_GLU_13	OE1	3.949
3J70	D_LYS_322	NZ	A_ASP_95	OD2	2.908
3J70	D_ARG_327	NH2	A_ASP_52	OD2	3.286
3J70	D_ARG_419	NH1	A_ASP_54	OD1	3.985
3J70	M_ARG_64	NH2	N_ASP_1	OD1	2.677
3J70	M_LYS_209	NZ	N_GLU_123	OE1	3.744
3J70	M_LYS_209	NZ	N_GLU_123	OE2	2.604
3J70	O_LYS_29	NZ	P_ASP_279	OD2	2.704
3J70	O_ARG_59	NH1	P_ASP_368	OD1	3.842
3J70	O_ARG_59	NH1	P_ASP_368	OD2	2.986
3J70	O_ARG_59	NH2	P_ASP_368	OD1	2.620
3J70	O_ARG_59	NH2	P_ASP_368	OD2	3.173
3J70	P_ARG_146	NH1	O_GLU_169	OE1	2.841
3J70	P_ARG_146	NH1	O_GLU_169	OE2	2.796
3J70	P_ARG_146	NH2	O_GLU_169	OE1	3.599
3J70	P_LYS_171	NZ	O_GLU_13	OE1	3.948
3J70	P_LYS_322	NZ	M_ASP_95	OD2	2.909
3J70	P_ARG_327	NH2	M_ASP_52	OD2	3.286
3J70	P_ARG_419	NH1	M_ASP_54	OD1	3.985
3J70	R_ARG_64	NH2	S_ASP_1	OD1	2.677
3J70	R_LYS_209	NZ	S_GLU_123	OE1	3.743
3J70	R_LYS_209	NZ	S_GLU_123	OE2	2.603
3J70	T_LYS_29	NZ	U_ASP_279	OD2	2.704
3J70	T_ARG_59	NH1	U_ASP_368	OD1	3.842
3J70	T_ARG_59	NH1	U_ASP_368	OD2	2.986
3J70	T_ARG_59	NH2	U_ASP_368	OD1	2.621
3J70	T_ARG_59	NH2	U_ASP_368	OD2	3.174
3J70	U_ARG_146	NH1	T_GLU_169	OE1	2.840
3J70	U_ARG_146	NH1	T_GLU_169	OE2	2.796
3J70	U_ARG_146	NH2	T_GLU_169	OE1	3.599
3J70	U_LYS_171	NZ	T_GLU_13	OE1	3.949
3J70	U_LYS_322	NZ	R_ASP_95	OD2	2.909
3J70	U_ARG_327	NH2	R_ASP_52	OD2	3.287
3J70	U_ARG_419	NH1	R_ASP_54	OD1	3.985

Table 1239: Interfacial 3J70-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3JCC	A_ARG_429	NH2	D_ASP_63	OD2	3.854
3JCC	C_LYS_207	NZ	B_GLU_124	OE1	3.629
3JCC	D_ARG_59	NH2	A_ASP_368	OD1	2.961
3JCC	D_ARG_59	NH2	A_ASP_368	OD2	3.986

Table 1240: Interfacial 3JCC-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3KS0	H_LYS_39	NZ	L_GLU_40	OE1	3.686
3KS0	H_LYS_39	NZ	L_GLU_40	OE2	2.843
3KS0	H_LYS_147	NZ	L_GLU_127	OE2	3.112
3KS0	H_LYS_212	NZ	L_GLU_126	OE1	3.920
3KS0	H_LYS_212	NZ	L_GLU_126	OE2	3.042
3KS0	K_LYS_39	NZ	J_GLU_40	OE1	3.754
3KS0	K_LYS_39	NZ	J_GLU_40	OE2	2.934
3KS0	K_LYS_147	NZ	J_GLU_127	OE2	3.169
3KS0	K_LYS_212	NZ	J_GLU_126	OE1	3.344
3KS0	K_LYS_212	NZ	J_GLU_126	OE2	2.562

Table 1241: Interfacial 3KS0-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3L7E	H.LYS.217	NZ	L.GLU.123	OE1	3.175
3L7E	B.LYS.217	NZ	A.GLU.123	OE1	2.697
3L7E	B.LYS.217	NZ	A.GLU.123	OE2	3.970

Table 1242: Interfacial 3L7E-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3LZF	A_ARG_109	NH2	B_GLU_69	OE1	3.970
3LZF	A_ARG_109	NH2	B_GLU_69	OE2	2.555
3LZF	A_LYS_157	NZ	H_ASP_52	OD1	3.712
3LZF	A_LYS_157	NZ	H_ASP_52	OD2	3.952
3LZF	A_LYS_157	NZ	H_ASP_54	OD2	2.960
3LZF	A_LYS_166	NZ	L_ASP_93	OD1	2.890
3LZF	A_LYS_166	NZ	L_ASP_93	OD2	2.667
3LZF	A_ARG_310	NH1	B_ASP_90	OD1	2.412
3LZF	A_ARG_310	NH2	B_ASP_90	OD1	3.228
3LZF	B_LYS_68	NZ	A_GLU_110	OE1	3.290
3LZF	B_LYS_68	NZ	A_GLU_110	OE2	2.778
3LZF	H_LYS_221	NZ	L_GLU_123	OE2	3.483

Table 1243: Interfacial 3LZF-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID residue name residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3MLR	H_LYS_129	NZ	L_ASP_142	OD2	3.806
3MLR	H_LYS_209	NZ	L_GLU_127	OE2	3.182
3MLR	P_LYS_304	NZ	H_ASP_31	OD1	3.470
3MLR	P_LYS_305	NZ	H_ASP_54	OD1	2.683
3MLR	P_LYS_305	NZ	H_ASP_54	OD2	3.624
3MLR	P_LYS_305	NZ	H_ASP_56	OD2	3.011

Table 1244: Interfacial 3MLR-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3MLS	H.LYS_73	NZ	I.ASP_31	OD1	3.962
3MLS	H.LYS_73	NZ	I.ASP_31	OD2	2.716
3MLS	H.LYS_73	NZ	I.ASP_53	OD1	3.242
3MLS	H.LYS_73	NZ	I.ASP_53	OD2	3.339
3MLS	H.LYS_117	NZ	J.GLU_10	OE1	3.515
3MLS	H.LYS_143	NZ	L.GLU_128	OE2	2.664
3MLS	H.LYS_209	NZ	L.GLU_127	OE1	2.677
3MLS	P.ARG_11	NH1	H.GLU_99	OE1	3.690
3MLS	P.ARG_11	NH1	H.GLU_99	OE2	3.548
3MLS	P.ARG_11	NH2	H.GLU_99	OE1	3.097
3MLS	P.ARG_11	NH2	H.GLU_99	OE2	3.355
3MLS	P.LYS_12	NZ	H.ASP_54	OD1	3.420
3MLS	P.LYS_12	NZ	H.ASP_54	OD2	2.807
3MLS	P.LYS_12	NZ	H.ASP_56	OD1	3.833
3MLS	P.LYS_12	NZ	H.ASP_56	OD2	3.175
3MLS	I.LYS_143	NZ	M.GLU_128	OE2	2.744
3MLS	Q.LYS_12	NZ	I.ASP_54	OD1	2.683
3MLS	Q.LYS_12	NZ	I.ASP_54	OD2	3.484
3MLS	Q.LYS_12	NZ	I.ASP_56	OD1	3.650
3MLS	N.LYS_97	NZ	J.GLU_64	OE2	3.402
3MLS	J.LYS_117	NZ	H.GLU_10	OE1	3.984
3MLS	J.LYS_209	NZ	N.GLU_127	OE2	3.428
3MLS	R.LYS_12	NZ	J.ASP_54	OD1	2.569
3MLS	R.LYS_12	NZ	J.ASP_54	OD2	3.629
3MLS	R.LYS_12	NZ	J.ASP_56	OD2	2.975
3MLS	K.LYS_117	NZ	L.GLU_10	OE1	3.985
3MLS	S.LYS_12	NZ	K.ASP_54	OD1	2.573
3MLS	S.LYS_12	NZ	K.ASP_54	OD2	3.736
3MLS	S.LYS_12	NZ	K.ASP_56	OD2	3.122

Table 1245: Interfacial 3MLS-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3MLT	P_ARG_304	NH1	H_ASP_31	OD1	2.766
3MLT	P_LYS_305	NZ	H_ASP_54	OD1	2.503
3MLT	P_LYS_305	NZ	H_ASP_54	OD2	3.276
3MLT	P_LYS_305	NZ	H_ASP_56	OD2	2.482
3MLT	B_LYS_209	NZ	A_GLU_127	OE2	3.807
3MLT	C_LYS_305	NZ	B_ASP_54	OD1	3.099
3MLT	C_LYS_305	NZ	B_ASP_54	OD2	3.737
3MLT	C_LYS_305	NZ	B_ASP_56	OD2	3.095
3MLT	E_LYS_209	NZ	D_GLU_127	OE2	3.591
3MLT	I_LYS_209	NZ	G_GLU_127	OE2	3.669

Table 1246: Interfacial 3MLT-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3MLU	L_LYS_133	NZ	H_ASP_144	OD2	3.641
3MLU	P_LYS_305	NZ	H_ASP_54	OD1	2.586
3MLU	P_LYS_305	NZ	H_ASP_54	OD2	3.496
3MLU	P_LYS_305	NZ	H_ASP_56	OD2	3.684

Table 1247: Interfacial 3MLU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3MLV	P_ARG_304	NH1	H_ASP_31	OD1	3.750
3MLV	P_LYS_305	NZ	H_ASP_54	OD1	2.508
3MLV	P_LYS_305	NZ	H_ASP_54	OD2	3.477
3MLV	P_LYS_305	NZ	H_ASP_56	OD2	2.918
3MLV	M_LYS_97	NZ	N_GLU_64	OE1	2.901
3MLV	Q_ARG_304	NH1	N_GLU_99	OE2	3.900
3MLV	Q_ARG_304	NH2	N_GLU_99	OE2	3.849
3MLV	Q_LYS_305	NZ	N_ASP_54	OD1	3.154
3MLV	Q_LYS_305	NZ	N_ASP_54	OD2	3.686
3MLV	Q_LYS_305	NZ	N_ASP_56	OD2	2.702

Table 1248: Interfacial 3MLV-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3MLW	L_ARG_50	NH1	H_ASP_100G	OD1	2.178
3MLW	L_ARG_50	NH1	H_ASP_100G	OD2	3.432
3MLW	L_LYS_129	NZ	H_ASP_144	OD2	3.472
3MLW	H_ARG_58	NH1	L_ASP_95D	OD1	3.535
3MLW	H_ARG_58	NH1	L_ASP_95D	OD2	2.585
3MLW	P_LYS_303	NZ	H_ASP_31	OD2	3.075
3MLW	P_ARG_304	NH1	H_ASP_31	OD1	3.646
3MLW	P_LYS_305	NZ	H_ASP_54	OD1	3.646
3MLW	P_LYS_305	NZ	H_ASP_54	OD2	2.863
3MLW	P_LYS_305	NZ	H_ASP_56	OD1	3.537
3MLW	P_ARG_315	NH1	L_ASP_93	OD1	2.718
3MLW	P_ARG_315	NH1	L_ASP_93	OD2	3.239
3MLW	M_ARG_50	NH2	L_ASP_100G	OD1	2.708
3MLW	M_ARG_50	NH2	L_ASP_100G	OD2	3.923
3MLW	L_ARG_58	NH1	M_ASP_95D	OD1	2.653
3MLW	L_ARG_58	NH1	M_ASP_95D	OD2	3.643
3MLW	L_LYS_209	NZ	M_GLU_123	OE1	2.581
3MLW	L_LYS_209	NZ	M_GLU_123	OE2	3.213
3MLW	Q_LYS_305	NZ	L_ASP_54	OD2	3.005
3MLW	Q_LYS_305	NZ	L_ASP_56	OD1	2.747
3MLW	Q_ARG_315	NH1	M_ASP_93	OD1	3.021

Table 1249: Interfacial 3MLW-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3MLX	H_LYS_143	NZ	L_GLU_124	OE2	3.021
3MLX	P_HIS_308	ND1	H_GLU_98	OE2	3.800
3MLX	P_HIS_308	NE2	H_GLU_98	OE2	3.892
3MLX	I_LYS_143	NZ	M_GLU_124	OE2	2.608
3MLX	I_LYS_214	NZ	M_GLU_123	OE1	3.588
3MLX	Q_HIS_308	ND1	L_GLU_98	OE1	3.280

Table 1250: Interfacial 3MLX-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3MLY	H_LYS_143	NZ	L_GLU_124	OE2	3.991
3MLY	H_LYS_214	NZ	L_GLU_123	OE1	3.745
3MLY	P_LYS_308	NZ	L_GLU_50	OE1	3.397
3MLY	P_LYS_308	NZ	L_GLU_50	OE2	3.390
3MLY	I_LYS_143	NZ	M_GLU_124	OE2	2.661
3MLY	I_LYS_214	NZ	M_GLU_123	OE1	3.594

Table 1251: Interfacial 3MLY-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3MLZ	H_LYS_	NZ	L_GLU_	OE1	3.724
3MLZ	H_LYS_	NZ	L_GLU_	OE2	3.184
3MLZ	H_LYS_	NZ	L_GLU_	OE2	2.805
3MLZ	H_LYS_	NZ	L_GLU_	OE1	3.039
3MLZ	H_LYS_	NZ	L_GLU_	OE2	3.262

Table 1252: Interfacial 3MLZ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3NFP	A_ARG_33	NH1	K_ASP_4	OD1	3.227
3NFP	A_ARG_33	NH2	K_ASP_6	OD1	3.995
3NFP	A_ARG_33	NH2	K_ASP_6	OD2	2.804
3NFP	A_HIS_35	NE2	K_ASP_4	OD1	3.568
3NFP	A_HIS_35	NE2	K_ASP_4	OD2	3.384
3NFP	H_ARG_33	NH1	I_ASP_4	OD2	2.868
3NFP	H_ARG_33	NH2	I_ASP_6	OD2	3.531
3NFP	H_HIS_35	NE2	I_ASP_4	OD1	3.314
3NFP	H_HIS_35	NE2	I_ASP_4	OD2	3.660
3NFP	H_LYS_212	NZ	L_GLU_122	OE1	3.767
3NFP	I_HIS_120	NE2	H_GLU_59	OE1	3.799
3NFP	I_HIS_120	NE2	H_GLU_59	OE2	3.285
3NFP	K_HIS_120	NE2	A_GLU_59	OE2	3.393

Table 1253: Interfacial 3NFP-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3NGB	G_LYS_97	NZ	H_ASP_99	OD2	3.903
3NGB	H_ARG_71	NH1	G_ASP_368	OD1	3.623
3NGB	H_ARG_71	NH1	G_ASP_368	OD2	3.004
3NGB	H_ARG_71	NH2	G_ASP_368	OD1	2.815
3NGB	H_ARG_71	NH2	G_ASP_368	OD2	3.723
3NGB	H_LYS_209	NZ	L_GLU_125	OE1	3.421
3NGB	H_LYS_209	NZ	L_GLU_125	OE2	3.841
3NGB	A_LYS_97	NZ	B_ASP_99	OD2	3.768
3NGB	B_ARG_71	NH1	A_ASP_368	OD1	3.647
3NGB	B_ARG_71	NH1	A_ASP_368	OD2	2.944
3NGB	B_ARG_71	NH2	A_ASP_368	OD1	2.895
3NGB	B_ARG_71	NH2	A_ASP_368	OD2	3.718
3NGB	B_LYS_209	NZ	C_GLU_125	OE1	2.774
3NGB	B_LYS_209	NZ	C_GLU_125	OE2	2.799
3NGB	D_LYS_97	NZ	E_ASP_99	OD1	3.709
3NGB	E_ARG_71	NH1	D_ASP_368	OD1	3.715
3NGB	E_ARG_71	NH1	D_ASP_368	OD2	3.074
3NGB	E_ARG_71	NH2	D_ASP_368	OD1	3.026
3NGB	E_ARG_71	NH2	D_ASP_368	OD2	3.848
3NGB	E_HIS_164	ND1	F_ASP_169	OD1	3.984
3NGB	E_LYS_	NZ	F_GLU_	OE1	3.345
3NGB	E_LYS_	NZ	F_GLU_	OE2	2.927
3NGB	L_LYS_97	NZ	J_ASP_99	OD1	3.443
3NGB	J_ARG_71	NH1	I_ASP_368	OD1	3.645
3NGB	J_ARG_71	NH1	I_ASP_368	OD2	3.125
3NGB	J_ARG_71	NH2	I_ASP_368	OD1	3.120
3NGB	J_LYS_209	NZ	K_GLU_125	OE1	2.929
3NGB	J_LYS_209	NZ	K_GLU_125	OE2	3.060
3NGB	J_LYS_214	NZ	K_ASP_124	OD1	3.305

Table 1254: Interfacial 3NGB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3NH7	H_ARG_98	NH1	A_ASP_67	OD2	3.819
3NH7	H_ARG_98	NH2	A_ASP_67	OD1	2.850
3NH7	H_ARG_98	NH2	A_ASP_67	OD2	2.389
3NH7	H_ARG_100	NH2	A_GLU_64	OE2	3.004
3NH7	H_HIS_102	ND1	A_GLU_64	OE1	2.378
3NH7	H_ARG_104	NH2	A_GLU_81	OE1	3.515
3NH7	H_ARG_104	NH2	A_GLU_81	OE2	2.462
3NH7	H_LYS_216	NZ	L_GLU_125	OE2	3.557
3NH7	A_LYS_79	NZ	L_ASP_50	OD1	3.333
3NH7	A_LYS_79	NZ	L_ASP_50	OD2	3.058
3NH7	A_LYS_92	NZ	H_GLU_99	OE1	3.975
3NH7	A_LYS_92	NZ	H_GLU_99	OE2	3.561
3NH7	I_ARG_98	NH1	B_ASP_67	OD2	3.924
3NH7	I_ARG_98	NH2	B_ASP_67	OD1	3.388
3NH7	I_ARG_98	NH2	B_ASP_67	OD2	2.296
3NH7	I_ARG_100	NH2	B_GLU_64	OE2	2.996
3NH7	I_HIS_102	ND1	B_GLU_64	OE1	2.707
3NH7	I_ARG_104	NH2	B_GLU_81	OE1	3.637
3NH7	I_ARG_104	NH2	B_GLU_81	OE2	2.502
3NH7	I_LYS_216	NZ	M_GLU_125	OE1	3.301
3NH7	I_LYS_216	NZ	M_GLU_125	OE2	3.320
3NH7	B_LYS_79	NZ	M_ASP_50	OD1	3.625
3NH7	B_LYS_79	NZ	M_ASP_50	OD2	2.953
3NH7	B_LYS_92	NZ	L_GLU_99	OE1	3.831
3NH7	B_LYS_92	NZ	L_GLU_99	OE2	3.683
3NH7	J_ARG_98	NH1	C_ASP_67	OD2	3.893
3NH7	J_ARG_98	NH2	C_ASP_67	OD1	3.313
3NH7	J_ARG_98	NH2	C_ASP_67	OD2	2.401
3NH7	J_ARG_100	NH2	C_GLU_64	OE2	3.173
3NH7	J_HIS_102	ND1	C_GLU_64	OE1	2.668
3NH7	J_ARG_104	NH2	C_GLU_81	OE1	3.595
3NH7	J_ARG_104	NH2	C_GLU_81	OE2	2.634
3NH7	J_LYS_216	NZ	N_GLU_125	OE1	2.816
3NH7	J_LYS_216	NZ	N_GLU_125	OE2	3.044
3NH7	C_LYS_79	NZ	N_ASP_50	OD1	3.064
3NH7	C_LYS_79	NZ	N_ASP_50	OD2	3.315
3NH7	C_LYS_92	NZ	J_GLU_99	OE1	3.721
3NH7	C_LYS_92	NZ	J_GLU_99	OE2	3.806
3NH7	K_ARG_98	NH1	D_ASP_67	OD2	3.348
3NH7	K_ARG_98	NH2	D_ASP_67	OD1	3.350
3NH7	K_ARG_98	NH2	D_ASP_67	OD2	2.647
3NH7	K_ARG_100	NH2	D_GLU_64	OE2	3.101
3NH7	K_HIS_102	ND1	D_GLU_64	OE1	2.313
3NH7	K_ARG_104	NH2	D_GLU_81	OE1	3.830
3NH7	K_ARG_104	NH2	D_GLU_81	OE2	2.800
3NH7	K_LYS_216	NZ	O_GLU_125	OE1	3.159
3NH7	K_LYS_216	NZ	O_GLU_125	OE2	3.376
3NH7	D_LYS_79	NZ	O_ASP_50	OD1	3.661
3NH7	D_LYS_79	NZ	O_ASP_50	OD2	3.355
3NH7	D_LYS_92	NZ	K_GLU_99	OE1	3.766
3NH7	D_LYS_92	NZ	K_GLU_99	OE2	3.832

Table 1255: Interfacial 3NH7-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3NZ8	A_HIS_164	NE2	B_ASP_167	OD1	3.115
3NZ8	A_LYS_208	NZ	B_GLU_123	OE2	3.283
3NZ8	H_LYS_208	NZ	L_GLU_123	OE2	3.808

Table 1256: Interfacial 3NZ8-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3O2D	L_ARG_95	NH1	H_GLU_95	OE2	2.847
3O2D	L_ARG_95	NH2	H_GLU_95	OE2	3.717
3O2D	H_LYS_209	NZ	L_GLU_122	OE1	2.503
3O2D	H_LYS_209	NZ	L_GLU_122	OE2	3.547

Table 1257: Interfacial 3O2D-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3O41	H_ARG_94	NH1	A_GLU_191	OE1	2.970
3O41	H_ARG_94	NH1	A_GLU_191	OE2	3.394
3O41	H_ARG_94	NH2	A_GLU_191	OE1	3.744
3O41	H_ARG_94	NH2	A_GLU_191	OE2	2.660
3O41	H_LYS_208	NZ	L_GLU_123	OE2	3.054
3O41	A_LYS_208	NZ	B_GLU_123	OE2	2.651
3O41	P_LYS_433	NZ	H_ASP_54	OD1	3.659
3O41	P_LYS_433	NZ	H_ASP_54	OD2	2.887
3O41	P_LYS_433	NZ	H_ASP_56	OD2	2.760
3O41	C_LYS_433	NZ	A_ASP_54	OD1	3.503
3O41	C_LYS_433	NZ	A_ASP_54	OD2	2.671
3O41	C_LYS_433	NZ	A_ASP_56	OD2	2.936

Table 1258: Interfacial 3O41-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID** **residue name** **residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3O45	H_ARG_94	NH1	A_GLU_191	OE1	3.085
3O45	H_ARG_94	NH1	A_GLU_191	OE2	3.621
3O45	H_ARG_94	NH2	A_GLU_191	OE1	3.709
3O45	H_ARG_94	NH2	A_GLU_191	OE2	2.802
3O45	H_LYS_208	NZ	L_GLU_123	OE2	3.033
3O45	A_LYS_208	NZ	B_GLU_123	OE2	2.878
3O45	P_LYS_433	NZ	H_ASP_54	OD1	3.518
3O45	P_LYS_433	NZ	H_ASP_54	OD2	2.818
3O45	P_LYS_433	NZ	H_ASP_56	OD2	2.927
3O45	C_LYS_433	NZ	A_ASP_54	OD1	3.297
3O45	C_LYS_433	NZ	A_ASP_54	OD2	2.723
3O45	C_LYS_433	NZ	A_ASP_56	OD2	2.899

Table 1259: Interfacial 3O45-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID** **residue name** **residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3OJD	B_LYS_208	NZ	A_GLU_123	OE2	3.588
3OJD	B_ARG_213	NH1	A_GLU_213	OE2	3.118
3OJD	B_ARG_213	NH2	A_GLU_213	OE2	3.609

Table 1260: Interfacial 3OJD-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3P0Y	A_LYS_463	NZ	H_GLU_95	OE2	2.859
3P0Y	A_LYS_465	NZ	H_GLU_50	OE1	2.656
3P0Y	A_LYS_465	NZ	H_GLU_50	OE2	3.845
3P0Y	A_LYS_465	NZ	H_GLU_95	OE1	2.777
3P0Y	A_LYS_465	NZ	H_GLU_95	OE2	3.671
3P0Y	H_ARG_97	NH1	A_ASP_436	OD1	2.876
3P0Y	H_ARG_97	NH1	A_ASP_436	OD2	3.533
3P0Y	H_ARG_97	NH2	A_ASP_436	OD1	3.647
3P0Y	H_ARG_97	NH2	A_ASP_436	OD2	2.823
3P0Y	H_LYS_209	NZ	L_GLU_123	OE1	2.674
3P0Y	H_LYS_209	NZ	L_GLU_123	OE2	3.317

Table 1261: Interfacial 3P0Y-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3P11	A_ARG_441	NH1	H_ASP_58	OD2	3.356
3P11	A_ARG_441	NH1	L_GLU_94	OE1	2.859
3P11	A_ARG_441	NH1	L_GLU_94	OE2	3.310
3P11	A_ARG_441	NH2	L_GLU_94	OE2	3.075
3P11	A_LYS_466	NZ	H_GLU_95	OE1	2.568
3P11	A_LYS_466	NZ	H_GLU_95	OE2	3.227
3P11	A_HIS_467	ND1	H_GLU_50	OE2	3.466
3P11	A_HIS_467	ND1	L_GLU_94	OE2	3.926
3P11	A_HIS_467	NE2	H_GLU_50	OE1	3.754
3P11	A_HIS_467	NE2	H_GLU_50	OE2	3.679
3P11	A_HIS_467	NE2	H_GLU_95	OE2	3.533

Table 1262: Interfacial 3P11-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3PGF	L_ARG_66	NH1	A_GLU_309	OE2	3.045
3PGF	L_ARG_66	NH2	A_GLU_309	OE2	2.501

Table 1263: Interfacial 3PGF-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3PNW	B_ARG_104	NH1	C_GLU_599	OE1	3.048
3PNW	D_ARG_25	NH1	J_GLU_82	OE1	2.858
3PNW	D_ARG_25	NH1	J_GLU_82	OE2	3.430
3PNW	D_ARG_25	NH2	J_GLU_82	OE1	3.626
3PNW	D_ARG_25	NH2	J_GLU_82	OE2	3.034
3PNW	E_ARG_104	NH1	F_GLU_599	OE2	2.653
3PNW	H_ARG_104	NH1	I_GLU_599	OE1	3.020
3PNW	K_ARG_104	NH1	L_GLU_599	OE1	2.888
3PNW	K_ARG_104	NH1	L_GLU_599	OE2	2.772
3PNW	K_ARG_104	NH2	L_GLU_599	OE2	3.083
3PNW	Q_ARG_104	NH1	R_GLU_599	OE1	3.284
3PNW	T_ARG_104	NH1	U_GLU_599	OE2	2.955
3PNW	W_ARG_104	NH2	X_GLU_599	OE2	3.113

Table 1264: Interfacial 3PNW-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3PP4	H_LYS_215	NZ	L_GLU_128	OE1	3.038
3PP4	H_LYS_215	NZ	L_GLU_128	OE2	2.948
3PP4	P_LYS_175	NZ	H_ASP_57	OD2	3.518

Table 1265: Interfacial 3PP4-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3Q3G	C_LYS_109	NZ	D_GLU_44	OE1	3.620
3Q3G	D_LYS_21	NZ	H_GLU_202	OE2	2.633
3Q3G	D_ARG_52	NH1	G_GLU_179	OE2	3.405
3Q3G	D_ARG_52	NH2	G_GLU_178	OE1	2.845
3Q3G	D_ARG_52	NH2	G_GLU_179	OE2	2.628
3Q3G	D_LYS_219	NZ	C_GLU_129	OE2	3.237
3Q3G	G_ARG_208	NH1	D_GLU_101	OE1	3.693
3Q3G	G_ARG_208	NH1	D_GLU_101	OE2	2.792
3Q3G	G_ARG_208	NH2	D_GLU_101	OE1	2.994
3Q3G	G_ARG_208	NH2	D_GLU_101	OE2	3.045
3Q3G	B_LYS_21	NZ	K_GLU_202	OE2	2.668
3Q3G	B_ARG_52	NH1	E_GLU_179	OE2	3.409
3Q3G	B_ARG_52	NH2	E_GLU_178	OE1	2.858
3Q3G	B_ARG_52	NH2	E_GLU_179	OE2	2.617
3Q3G	B_LYS_219	NZ	A_GLU_129	OE2	3.294
3Q3G	E_ARG_208	NH1	B_GLU_101	OE1	3.701
3Q3G	E_ARG_208	NH1	B_GLU_101	OE2	2.888
3Q3G	E_ARG_208	NH2	B_GLU_101	OE1	3.046
3Q3G	E_ARG_208	NH2	B_GLU_101	OE2	3.227
3Q3G	H_ARG_52	NH1	I_GLU_179	OE2	3.532
3Q3G	H_ARG_52	NH2	I_GLU_178	OE1	2.972
3Q3G	H_ARG_52	NH2	I_GLU_179	OE2	2.629
3Q3G	H_LYS_61	NZ	I_GLU_179	OE2	3.923
3Q3G	H_LYS_219	NZ	F_GLU_129	OE2	3.319
3Q3G	I_ARG_208	NH1	H_GLU_101	OE1	3.704
3Q3G	I_ARG_208	NH1	H_GLU_101	OE2	2.809
3Q3G	I_ARG_208	NH2	H_GLU_101	OE1	3.098
3Q3G	I_ARG_208	NH2	H_GLU_101	OE2	3.125
3Q3G	J_LYS_109	NZ	K_GLU_44	OE1	3.972
3Q3G	K_ARG_52	NH1	L_GLU_179	OE2	3.394
3Q3G	K_ARG_52	NH2	L_GLU_178	OE1	2.871
3Q3G	K_ARG_52	NH2	L_GLU_179	OE2	2.626
3Q3G	K_LYS_219	NZ	J_GLU_129	OE2	3.216
3Q3G	L_ARG_208	NH1	K_GLU_101	OE1	3.706
3Q3G	L_ARG_208	NH1	K_GLU_101	OE2	2.777
3Q3G	L_ARG_208	NH2	K_GLU_101	OE1	3.099
3Q3G	L_ARG_208	NH2	K_GLU_101	OE2	3.162

Table 1266: Interfacial 3Q3G-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3QA3	C_LYS_109	NZ	D_GLU_44	OE1	3.919
3QA3	D_LYS_21	NZ	B_GLU_202	OE2	2.710
3QA3	D_ARG_52	NH1	G_GLU_179	OE2	3.492
3QA3	D_ARG_52	NH2	G_GLU_178	OE1	3.012
3QA3	D_ARG_52	NH2	G_GLU_179	OE2	2.776
3QA3	D_LYS_61	NZ	G_GLU_179	OE1	3.896
3QA3	D_LYS_61	NZ	G_GLU_179	OE2	3.867
3QA3	D_LYS_219	NZ	C_GLU_129	OE2	3.586
3QA3	G_ARG_208	NH1	D_GLU_101	OE1	3.094
3QA3	G_ARG_208	NH1	D_GLU_101	OE2	3.755
3QA3	G_ARG_208	NH2	D_GLU_101	OE1	2.802
3QA3	G_LYS_306	NZ	F_GLU_61	OE1	2.676
3QA3	G_LYS_306	NZ	F_GLU_61	OE2	3.962
3QA3	B_ARG_52	NH1	E_GLU_179	OE2	3.674
3QA3	B_ARG_52	NH2	E_GLU_178	OE1	3.139
3QA3	B_ARG_52	NH2	E_GLU_179	OE2	2.772
3QA3	B_LYS_61	NZ	E_GLU_179	OE1	3.626
3QA3	B_LYS_61	NZ	E_GLU_179	OE2	3.531
3QA3	B_LYS_219	NZ	A_GLU_129	OE2	3.689
3QA3	E_ARG_208	NH1	B_GLU_101	OE1	3.112
3QA3	E_ARG_208	NH1	B_GLU_101	OE2	3.639
3QA3	E_ARG_208	NH2	B_GLU_101	OE1	2.913
3QA3	E_ARG_208	NH2	B_GLU_101	OE2	3.978
3QA3	H_LYS_21	NZ	K_GLU_202	OE1	2.630
3QA3	H_ARG_52	NH1	I_GLU_179	OE2	3.536
3QA3	H_ARG_52	NH2	I_GLU_178	OE1	3.079
3QA3	H_ARG_52	NH2	I_GLU_179	OE2	2.753
3QA3	H_LYS_61	NZ	I_GLU_179	OE1	3.833
3QA3	H_LYS_61	NZ	I_GLU_179	OE2	3.714
3QA3	H_LYS_219	NZ	F_GLU_129	OE2	3.683
3QA3	I_ARG_208	NH1	H_GLU_101	OE1	2.952
3QA3	I_ARG_208	NH1	H_GLU_101	OE2	3.280
3QA3	I_ARG_208	NH2	H_GLU_101	OE1	2.858
3QA3	I_ARG_208	NH2	H_GLU_101	OE2	3.749
3QA3	I_LYS_306	NZ	C_GLU_61	OE1	3.836
3QA3	J_LYS_109	NZ	K_GLU_44	OE1	3.982
3QA3	K_ARG_52	NH1	L_GLU_179	OE2	3.477
3QA3	K_ARG_52	NH2	L_GLU_178	OE1	3.052
3QA3	K_ARG_52	NH2	L_GLU_179	OE2	2.734
3QA3	K_LYS_61	NZ	L_GLU_179	OE1	3.839
3QA3	K_LYS_61	NZ	L_GLU_179	OE2	3.819
3QA3	K_LYS_219	NZ	J_GLU_129	OE2	3.538
3QA3	L_ARG_208	NH1	K_GLU_101	OE1	3.296
3QA3	L_ARG_208	NH1	K_GLU_101	OE2	3.152
3QA3	L_ARG_208	NH2	K_GLU_101	OE1	3.120
3QA3	L_ARG_208	NH2	K_GLU_101	OE2	3.548

Table 1267: Interfacial 3QA3-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3QG6	A_ARG_188	NH1	H_ASP_86	OD2	3.997
3QG6	A_ARG_188	NH2	H_ASP_86	OD1	3.422
3QG6	A_HIS_189	NE2	H_GLU_85	OE1	3.361
3QG6	A_HIS_189	NE2	H_GLU_85	OE2	3.215
3QG6	B_LYS_44	NZ	L_ASP_151	OD2	2.912
3QG6	B_LYS_64	NZ	L_GLU_187	OE1	3.778
3QG6	B_LYS_221	NZ	A_GLU_123	OE1	2.433
3QG6	H_LYS_44	NZ	A_ASP_151	OD2	2.924
3QG6	H_LYS_64	NZ	A_GLU_187	OE1	3.924
3QG6	H_LYS_221	NZ	L_GLU_123	OE1	2.733
3QG6	L_HIS_189	NE2	B_GLU_85	OE1	3.320
3QG6	L_HIS_189	NE2	B_GLU_85	OE2	3.623

Table 1268: Interfacial 3QG6-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID residue name residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3QG7	H_LYS_221	NZ	L_GLU_123	OE2	2.769

Table 1269: Interfacial 3QG7-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3QO1	B_ARG_101	NH1	A_GLU_39	OE1	3.830
3QO1	B_ARG_101	NH1	A_GLU_39	OE2	2.711
3QO1	B_ARG_101	NH2	A_GLU_39	OE1	2.782
3QO1	B_ARG_101	NH2	A_GLU_39	OE2	3.238
3QO1	B_LYS_215	NZ	A_GLU_128	OE1	3.939

Table 1270: Interfacial 3QO1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3QUM	P_ARG_36	NH1	A_ASP_94	OD2	3.603
3QUM	P_ARG_36	NH1	B_GLU_58	OE1	3.234
3QUM	P_ARG_36	NH1	B_GLU_58	OE2	3.373
3QUM	P_ARG_36	NH2	B_GLU_58	OE1	3.423
3QUM	P_LYS_62	NZ	B_GLU_58	OE2	3.762
3QUM	P_LYS_119	NZ	H_ASP_54	OD1	2.788
3QUM	P_LYS_119	NZ	H_ASP_54	OD2	3.700
3QUM	P_LYS_119	NZ	H_ASP_56	OD2	3.000
3QUM	L_ARG_50	NH2	P_GLU_23	OE1	2.715
3QUM	H_ARG_98	NH2	P_ASP_159	OD1	3.868
3QUM	H_ARG_98	NH2	P_ASP_159	OD2	3.474
3QUM	H_HIS_164	NE2	L_ASP_167	OD1	3.746
3QUM	H_LYS_208	NZ	L_GLU_123	OE1	3.317
3QUM	A_LYS_207	NZ	M_ASP_70	OD2	3.646
3QUM	B_LYS_62	NZ	A_ASP_1	OD1	3.967
3QUM	B_LYS_62	NZ	A_ASP_1	OD2	3.654
3QUM	B_LYS_209	NZ	A_GLU_123	OE1	3.994
3QUM	B_LYS_209	NZ	A_GLU_123	OE2	2.553
3QUM	Q_LYS_119	NZ	K_ASP_54	OD1	3.579
3QUM	Q_LYS_119	NZ	K_ASP_54	OD2	2.557
3QUM	Q_LYS_119	NZ	K_ASP_56	OD2	3.138
3QUM	M_ARG_24	NH2	B_ASP_131	OD1	2.867
3QUM	M_ARG_24	NH2	B_ASP_131	OD2	3.402
3QUM	M_ARG_50	NH1	Q_GLU_21	OE2	3.456
3QUM	M_ARG_50	NH2	Q_GLU_21	OE2	3.792
3QUM	K_LYS_58	NZ	Q_ASP_116	OD2	3.811
3QUM	K_LYS_62	NZ	M_ASP_1	OD1	2.803
3QUM	K_ARG_98	NH2	Q_ASP_159	OD2	3.098
3QUM	K_LYS_208	NZ	M_GLU_123	OE1	3.358
3QUM	D_ARG_97	NH1	C_GLU_55	OE1	3.578
3QUM	D_ARG_97	NH1	C_GLU_55	OE2	3.784
3QUM	D_ARG_97	NH2	Q_GLU_110	OE2	3.547

Table 1271: Interfacial 3QUM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3R08	L_LYS_207	NZ	H_ASP_129	OD1	3.653
3R08	L_LYS_207	NZ	H_ASP_129	OD2	2.868
3R08	H_LYS_58	NZ	E_GLU_4	OE2	3.175
3R08	H_LYS_99	NZ	L_ASP_56	OD2	3.746

Table 1272: Interfacial 3R08-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3SE8	G_LYS_282	NZ	H_ASP_100C	OD2	3.668
3SE8	H_ARG_71	NH1	G_ASP_368	OD1	3.115
3SE8	H_ARG_71	NH1	G_ASP_368	OD2	3.763
3SE8	H_ARG_71	NH2	G_ASP_368	OD1	3.733
3SE8	H_ARG_71	NH2	G_ASP_368	OD2	2.907
3SE8	H_LYS_209	NZ	L_GLU_123	OE1	3.768

Table 1273: Interfacial 3SE8-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3SE9	H_ARG_64	NH1	G_ASP_457	OD2	3.853
3SE9	H_ARG_64	NH2	G_ASP_457	OD1	3.358
3SE9	H_ARG_64	NH2	G_ASP_457	OD2	3.280
3SE9	H_ARG_71	NH1	G_ASP_368	OD1	3.515
3SE9	H_ARG_71	NH1	G_ASP_368	OD2	2.768
3SE9	H_ARG_71	NH2	G_ASP_368	OD1	3.012
3SE9	H_ARG_71	NH2	G_ASP_368	OD2	3.769
3SE9	H_LYS_209	NZ	L_GLU_123	OE1	3.388
3SE9	H_LYS_214	NZ	L_ASP_122	OD1	3.332

Table 1274: Interfacial 3SE9-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3SGD	L_LYS_204	NZ	J_ASP_75	OD1	3.665
3SGD	L_LYS_204	NZ	J_ASP_75	OD2	3.246
3SGD	H_LYS_43	NZ	J_ASP_68	OD1	3.910
3SGD	H_LYS_210	NZ	L_GLU_128	OE1	3.898
3SGD	J_LYS_19	NZ	L_ASP_148	OD1	3.248
3SGD	J_LYS_19	NZ	L_ASP_148	OD2	2.952

Table 1275: Interfacial 3SGD-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3SKJ	L_ARG_96	NH1	H_GLU_100I	OE1	2.505
3SKJ	L_ARG_96	NH1	H_GLU_100I	OE2	2.799
3SKJ	H_HIS_31	NE2	E_GLU_133	OE2	3.297
3SKJ	H_HIS_161	NE2	L ASP_167	OD2	3.763
3SKJ	H_LYS_206	NZ	L_GLU_123	OE1	2.501
3SKJ	H_LYS_206	NZ	L_GLU_123	OE2	3.323
3SKJ	M_ARG_96	NH2	I_GLU_100I	OE1	3.081
3SKJ	M_ARG_96	NH2	I_GLU_100I	OE2	3.831
3SKJ	I_LYS_43	NZ	L ASP_1	OD1	3.862
3SKJ	I_LYS_211	NZ	M ASP_122	OD2	3.816
3SKJ	I_LYS_211	NZ	M_GLU_123	OE1	3.612

Table 1276: Interfacial 3SKJ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3SY0	A_ARG_95	NH2	B_ASP_95	OD1	3.609
3SY0	A_ARG_95	NH2	B_ASP_95	OD2	2.821
3SY0	B_ARG_100B	NH1	A_GLU_55	OE1	2.843
3SY0	B_ARG_100B	NH1	A_GLU_55	OE2	3.786
3SY0	B_LYS_206	NZ	A_GLU_122	OE1	3.980

Table 1277: Interfacial 3SY0-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3T4Y	A_ARG_95	NH2	B_ASP_95	OD1	3.796
3T4Y	A_ARG_95	NH2	B_ASP_95	OD2	2.951
3T4Y	B_ARG_100B	NH1	A_GLU_55	OE1	3.824
3T4Y	B_ARG_100B	NH1	A_GLU_55	OE2	2.840
3T4Y	B_LYS_206	NZ	A_GLU_122	OE2	2.652

Table 1278: Interfacial 3T4Y-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3T65	B_ARG_100B	NH1	A_GLU_55	OE1	3.841
3T65	B_ARG_100B	NH1	A_GLU_55	OE2	2.883
3T65	A_ARG_95	NH2	B_ASP_95	OD1	3.666
3T65	A_ARG_95	NH2	B_ASP_95	OD2	2.866

Table 1279: Interfacial 3T65-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3T77	A_ARG_95	NH2	B_ASP_95	OD1	3.723
3T77	A_ARG_95	NH2	B_ASP_95	OD2	2.997
3T77	B_ARG_100B	NH1	A_GLU_55	OE1	3.125
3T77	B_ARG_100B	NH1	A_GLU_55	OE2	2.687
3T77	B_LYS_206	NZ	A_GLU_122	OE2	3.917

Table 1280: Interfacial 3T77-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3THM	F_LYS_45	NZ	L_GLU_97	OE2	3.172
3THM	F_LYS_78	NZ	L_ASP_52	OD1	3.702

Table 1281: Interfacial 3THM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3U1S	L.HIS_27D	NE2	H.ASP_100B	OD2	2.859
3U1S	H.LYS_214	NZ	L.GLU_123	OE1	3.475

Table 1282: Interfacial 3U1S-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3U2S	L_ARG_54	NH2	C_ASP_167	OD1	3.525
3U2S	L_ARG_54	NH2	C_ASP_167	OD2	3.282
3U2S	L_ARG_95A	NH1	H_ASP_61	OD1	2.794
3U2S	L_ARG_95A	NH1	H_ASP_61	OD2	3.373
3U2S	L_ARG_95A	NH2	H_ASP_61	OD1	2.338
3U2S	L_ARG_96	NH2	H_GLU_95	OE1	3.743
3U2S	L_ARG_96	NH2	H_GLU_95	OE2	2.869
3U2S	L_LYS_129	NZ	H_ASP_144	OD1	3.881
3U2S	G_ARG_168	NH2	H_ASP_100L	OD1	3.358
3U2S	G_ARG_168	NH2	H_ASP_100L	OD2	3.104
3U2S	G_LYS_171	NZ	H_ASP_100I	OD1	3.178
3U2S	A_LYS_143	NZ	B_GLU_124	OE2	3.550
3U2S	B_ARG_95A	NH1	A_ASP_61	OD1	2.632
3U2S	B_ARG_95A	NH1	A_ASP_61	OD2	3.483
3U2S	B_ARG_95A	NH2	A_ASP_61	OD1	3.270
3U2S	B_ARG_96	NH2	A_GLU_95	OE1	3.738
3U2S	B_ARG_96	NH2	A_GLU_95	OE2	2.983
3U2S	C_ARG_168	NH2	A_ASP_100L	OD1	2.424
3U2S	C_ARG_168	NH2	A_ASP_100L	OD2	3.228
3U2S	C_LYS_171	NZ	A_ASP_100I	OD1	3.279

Table 1283: Interfacial 3U2S-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3U36	L_LYS_89	NZ	H_GLU_95	OE1	3.857
3U36	L_ARG_95A	NH1	H_ASP_61	OD1	3.290
3U36	L_ARG_95A	NH1	H_ASP_61	OD2	1.959
3U36	L_ARG_95A	NH2	H_ASP_61	OD1	3.530
3U36	L_ARG_95A	NH2	H_ASP_61	OD2	3.624
3U36	L_ARG_96	NH2	H_GLU_95	OE2	3.606
3U36	B_LYS_89	NZ	A_GLU_95	OE1	3.772
3U36	B_ARG_95A	NH1	A_ASP_61	OD1	3.519
3U36	B_ARG_95A	NH1	A_ASP_61	OD2	2.198
3U36	B_ARG_95A	NH2	A_ASP_61	OD1	3.831
3U36	B_ARG_95A	NH2	A_ASP_61	OD2	3.817
3U36	B_ARG_96	NH2	A_GLU_95	OE2	3.395
3U36	B_LYS_129	NZ	A_ASP_144	OD1	3.769
3U36	D_LYS_89	NZ	C_GLU_95	OE1	3.877
3U36	D_ARG_95A	NH1	C_ASP_61	OD1	3.266
3U36	D_ARG_95A	NH1	C_ASP_61	OD2	2.045
3U36	D_ARG_95A	NH2	C_ASP_61	OD1	3.629
3U36	D_ARG_95A	NH2	C_ASP_61	OD2	3.782
3U36	D_ARG_96	NH2	C_GLU_95	OE2	3.569
3U36	F_ARG_95A	NH1	E_ASP_61	OD1	3.076
3U36	F_ARG_95A	NH1	E_ASP_61	OD2	1.876
3U36	F_ARG_95A	NH2	E_ASP_61	OD1	3.424
3U36	F_ARG_95A	NH2	E_ASP_61	OD2	3.670
3U36	F_ARG_96	NH2	E_GLU_95	OE2	3.739

Table 1284: Interfacial 3U36-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3UBX	A_ARG_39	NH2	B_ASP_53	OD2	3.336
3UBX	A_HIS_282	NE2	B_ASP_98	OD1	3.815
3UBX	A_HIS_282	NE2	B_ASP_98	OD2	3.128
3UBX	B_ARG_12	NH2	A_ASP_242	OD1	3.715
3UBX	B_ARG_12	NH2	A_ASP_242	OD2	3.324
3UBX	D_ARG_	NH2	E_ASP_	OD2	3.464
3UBX	D_HIS_	NE2	E_ASP_	OD1	3.963
3UBX	D_HIS_	NE2	E_ASP_	OD2	3.193
3UBX	E_ARG_	NH2	D_ASP_	OD1	3.594
3UBX	E_ARG_	NH2	D_ASP_	OD2	3.257
3UBX	E_HIS_	ND1	D_GLU_97	OE1	3.846
3UBX	L_ARG_32	NH2	A_ASP_80	OD1	3.479
3UBX	L_ARG_32	NH2	A_ASP_80	OD2	3.348
3UBX	L_ARG_32	NH2	A_ASP_153	OD2	3.795
3UBX	L_LYS_169	NZ	L_GLU_81	OE1	3.852
3UBX	L_LYS_169	NZ	L_GLU_81	OE2	3.096
3UBX	H_ARG_103	NH2	A_ASP_80	OD1	2.578
3UBX	H_LYS_215	NZ	L_GLU_123	OE1	3.082
3UBX	H_LYS_215	NZ	L_GLU_123	OE2	3.481
3UBX	I_ARG_32	NH2	D_ASP_80	OD1	3.383
3UBX	I_ARG_32	NH2	D_ASP_80	OD2	3.294
3UBX	I_ARG_32	NH2	D_ASP_153	OD2	3.950
3UBX	I_LYS_169	NZ	L_GLU_81	OE1	3.837
3UBX	I_LYS_169	NZ	L_GLU_81	OE2	3.130
3UBX	G_ARG_103	NH2	D_ASP_80	OD1	2.614
3UBX	G_LYS_215	NZ	L_GLU_123	OE1	3.204
3UBX	G_LYS_215	NZ	L_GLU_123	OE2	3.514

Table 1285: Interfacial 3UBX-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3UJI	H_LYS_143	NZ	L_GLU_124	OE2	2.632
3UJI	H_LYS_209	NZ	L_GLU_123	OE1	3.097
3UJI	H_LYS_209	NZ	L_GLU_123	OE2	2.701
3UJI	P_LYS_305	NZ	H_ASP_54	OD1	2.722
3UJI	P_LYS_305	NZ	H_ASP_54	OD2	3.687
3UJI	P_LYS_305	NZ	H_ASP_56	OD2	2.744
3UJI	P_HIS_308	ND1	H_GLU_98	OE1	2.731
3UJI	P_HIS_308	ND1	H_GLU_98	OE2	3.371

Table 1286: Interfacial 3UJI-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3UJJ	H_LYS_209	NZ	L_GLU_123	OE1	2.859
3UJJ	H_LYS_209	NZ	L_GLU_123	OE2	2.771
3UJJ	P_LYS_305	NZ	H_ASP_54	OD1	3.600
3UJJ	P_LYS_305	NZ	H_ASP_54	OD2	2.628
3UJJ	P_LYS_305	NZ	H_ASP_56	OD2	2.857
3UJJ	P_ARG_308	NH2	L_GLU_50	OE2	2.898

Table 1287: Interfacial 3UJJ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3UJT	H.LYS.143	NZ	M.ASP.60	OD2	3.914
3UJT	H.LYS.208	NZ	L.GLU.123	OE2	2.966
3UJT	L.HIS.164	NE2	M.ASP.167	OD1	3.917
3UJT	L.LYS.208	NZ	M.GLU.123	OE2	3.024

Table 1288: Interfacial 3UJT-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3UO1	H_LYS_212	NZ	L_GLU_127	OE2	2.634

Table 1289: Interfacial 3UO1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3UYR	H_LYS_212	NZ	L_GLU_127	OE2	2.869

Table 1290: Interfacial 3UYR-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3V4P	B_ARG_194	NH1	H_ASP_102	OD1	2.860
3V4P	B_ARG_194	NH1	H_ASP_102	OD2	2.764
3V4P	B_ARG_200	NH2	H_ASP_102	OD1	3.172
3V4P	D_ARG_194	NH1	M_ASP_102	OD1	2.738
3V4P	D_ARG_194	NH1	M_ASP_102	OD2	2.760
3V4P	D_ARG_200	NH2	M_ASP_102	OD1	3.233
3V4P	H_HIS_172	ND1	L_ASP_172	OD2	3.780
3V4P	H_LYS_216	NZ	L_GLU_128	OE2	3.270
3V4P	M_HIS_172	ND1	N_ASP_172	OD2	3.600
3V4P	M_LYS_216	NZ	N_GLU_128	OE2	3.408

Table 1291: Interfacial 3V4P-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3V4U	H_LYS_212	NZ	L_GLU_127	OE2	2.667

Table 1292: Interfacial 3V4U-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3V4V	B_ARG_194	NH1	H_ASP_102	OD1	2.874
3V4V	B_ARG_194	NH1	H_ASP_102	OD2	3.211
3V4V	B_ARG_200	NH2	H_ASP_102	OD1	3.237
3V4V	H_HIS_172	ND1	L_ASP_172	OD1	3.644
3V4V	H_LYS_216	NZ	L_GLU_128	OE2	3.607
3V4V	D_ARG_194	NH1	M_ASP_102	OD1	2.657
3V4V	D_ARG_194	NH1	M_ASP_102	OD2	2.923
3V4V	D_ARG_200	NH2	M_ASP_102	OD1	3.070
3V4V	M_HIS_172	ND1	N_ASP_172	OD1	3.594
3V4V	M_LYS_216	NZ	N_GLU_128	OE2	3.217

Table 1293: Interfacial 3V4V-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3V52	H_LYS_212	NZ	L_GLU_127	OE2	2.929

Table 1294: Interfacial 3V52-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3V6F	A_LYS.213	NZ	B_GLU_130	OE1	3.799
3V6F	C_LYS.213	NZ	D_GLU_130	OE1	3.956
3V6F	E_LYS.213	NZ	F_GLU_130	OE1	3.763
3V6F	H_HIS.169	NE2	L_ASP_174	OD1	3.656

Table 1295: Interfacial 3V6F-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3WIIH	H.LYS_214	NZ	L.GLU_123	OE2	3.755
3WIIH	I.LYS_214	NZ	M.GLU_123	OE1	2.678
3WIIH	I.LYS_214	NZ	M.GLU_123	OE2	3.619

Table 1296: Interfacial 3WIIH-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
3WN5	A_LYS_370	NZ	B_GLU_357	OE2	3.815
3WN5	A_LYS_409	NZ	B_ASP_399	OD2	3.327
3WN5	B_LYS_370	NZ	A_GLU_357	OE1	3.801
3WN5	B_LYS_409	NZ	A_ASP_399	OD1	3.830
3WN5	B_LYS_409	NZ	A_ASP_399	OD2	3.511
3WN5	C_LYS_117	NZ	B_ASP_265	OD2	2.853
3WN5	C_HIS_131	NE2	B_ASP_270	OD1	3.342
3WN5	C_HIS_131	NE2	B_ASP_270	OD2	2.619
3WN5	D_LYS_370	NZ	E_GLU_357	OE2	3.279
3WN5	D_LYS_409	NZ	E_ASP_399	OD2	3.246
3WN5	E_LYS_370	NZ	D_GLU_357	OE1	3.843
3WN5	E_LYS_409	NZ	D_ASP_399	OD2	2.789
3WN5	F_LYS_117	NZ	E_ASP_265	OD2	3.157
3WN5	F_HIS_131	NE2	E_ASP_270	OD2	2.923

Table 1297: Interfacial 3WN5-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4A6Y	A_ARG_186	NH2	H_ASP_180	OD2	3.656
4A6Y	A_ARG_190	NH1	H_GLU_89	OE2	3.969
4A6Y	B_LYS_150	NZ	A_GLU_127	OE2	3.258
4A6Y	H_LYS_150	NZ	L_GLU_127	OE2	3.131
4A6Y	H_HIS_171	NE2	L_ASP_141	OD1	3.968
4A6Y	L_ARG_190	NH2	B_GLU_89	OE2	3.440

Table 1298: Interfacial 4A6Y-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4AG4	H_LYS_208	NZ	L_GLU_123	OE2	2.708

Table 1299: Interfacial 4AG4-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4C83	C_LYS_208	NZ	D_GLU_123	OE1	2.304
4C83	C_LYS_208	NZ	D_GLU_123	OE2	2.598

Table 1300: Interfacial 4C83-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4DAG	H_ARG_101	NH2	A_GLU_33	OE1	3.620
4DAG	H_ARG_101	NH2	A_GLU_33	OE2	2.107
4DAG	L_LYS_46	NZ	A_ASP_414	OD1	3.558
4DAG	L_LYS_46	NZ	A_ASP_414	OD2	3.550

Table 1301: Interfacial 4DAG-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4DGV	H_LYS_209	NZ	L_GLU_123	OE1	2.915
4DGV	H_LYS_209	NZ	L_GLU_123	OE2	3.422

Table 1302: Interfacial 4DGV-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4DGY	H_LYS_214	NZ	L_ASP_122	OD1	3.699
4DGY	H_LYS_214	NZ	L_ASP_122	OD2	2.517

Table 1303: Interfacial 4DGY-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4EBQ	H_LYS_215	NZ	L_GLU_123	OE2	2.960

Table 1304: Interfacial 4EBQ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4EDW	H_LYS_209	NZ	L_GLU_123	OE2	2.707

Table 1305: Interfacial 4EDW-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4EDX	W.LYS_32	NZ	H.ASP_58	OD1	2.886
4EDX	W.LYS_32	NZ	H.ASP_58	OD2	2.677
4EDX	A.ARG_53	NH1	W.GLU_11	OE1	2.795
4EDX	B.LYS_221	NZ	A.GLU_123	OE2	3.878
4EDX	V.LYS_32	NZ	B.ASP_58	OD1	3.117
4EDX	V.LYS_32	NZ	B.ASP_58	OD2	2.681
4EDX	V.LYS_88	NZ	B.ASP_54	OD2	3.805
4EDX	L.ARG_53	NH1	V.GLU_11	OE1	3.269
4EDX	H.LYS_221	NZ	L.GLU_123	OE2	3.893

Table 1306: Interfacial 4EDX-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4ETQ	H_ARG_60	NH1	C_ASP_179	OD1	3.609
4ETQ	H_ARG_60	NH2	C_ASP_179	OD1	3.375
4ETQ	H_ARG_103	NH1	C_GLU_217	OE1	3.862
4ETQ	H_ARG_103	NH1	C_GLU_217	OE2	2.754
4ETQ	H_ARG_103	NH2	C_GLU_217	OE2	2.933
4ETQ	H_LYS_215	NZ	L_GLU_123	OE2	3.075
4ETQ	A_ARG_103	NH1	X_GLU_217	OE1	2.753
4ETQ	A_ARG_103	NH1	X_GLU_217	OE2	3.565
4ETQ	A_ARG_103	NH2	X_GLU_217	OE1	2.983
4ETQ	A_ARG_103	NH2	X_GLU_217	OE2	3.995
4ETQ	A_LYS_215	NZ	B_GLU_123	OE2	3.774
4ETQ	X_ARG_44	NH1	A_GLU_56	OE1	3.611
4ETQ	X_ARG_44	NH1	A_GLU_56	OE2	3.023
4ETQ	X_LYS_108	NZ	A_GLU_58	OE2	3.014
4ETQ	X_ARG_220	NH1	A_ASP_105	OD1	3.937
4ETQ	X_ARG_220	NH2	A_ASP_105	OD1	2.929
4ETQ	C_ARG_44	NH1	H_GLU_56	OE1	2.601
4ETQ	C_ARG_220	NH1	H_ASP_105	OD1	3.872
4ETQ	C_ARG_220	NH2	H_ASP_105	OD1	3.103

Table 1307: Interfacial 4ETQ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID residue name residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4F33	B_LYS_215	NZ	A_GLU_123	OE1	2.676
4F33	B_LYS_215	NZ	A_GLU_123	OE2	3.528
4F33	D_LYS_215	NZ	C_GLU_123	OE1	2.787
4F33	D_LYS_215	NZ	C_GLU_123	OE2	3.695
4F33	F_LYS_212	NZ	D_ASP_214	OD2	3.519
4F33	F_LYS_215	NZ	E_GLU_123	OE1	2.609
4F33	F_LYS_215	NZ	E_GLU_123	OE2	3.626
4F33	H_LYS_215	NZ	G_GLU_123	OE1	2.968
4F33	H_LYS_215	NZ	G_GLU_123	OE2	3.966

Table 1308: Interfacial 4F33-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4F3F	A_HIS_94	NE2	C_GLU_18	OE1	3.664
4F3F	A_HIS_94	NE2	C_GLU_18	OE2	3.880
4F3F	C_LYS_24	NZ	A_ASP_50	OD1	2.832
4F3F	C_LYS_24	NZ	A_ASP_50	OD2	3.865

Table 1309: Interfacial 4F3F-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4FFV	A_ARG_659	NH2	B_GLU_242	OE2	2.683
4FFV	A_HIS_755	ND1	B_ASP_730	OD1	2.996
4FFV	B_ARG_659	NH2	A_GLU_242	OE2	2.592
4FFV	B_HIS_755	ND1	A_ASP_730	OD1	2.989
4FFV	B_HIS_755	ND1	A_ASP_730	OD2	3.942
4FFV	D_LYS_54	NZ	B_GLU_89	OE1	3.460
4FFV	D_LYS_54	NZ	B_GLU_89	OE2	3.556
4FFV	H_LYS_54	NZ	A_GLU_89	OE1	3.584
4FFV	H_LYS_54	NZ	A_GLU_89	OE2	3.871
4FFV	H_HIS_168	NE2	L_ASP_166	OD1	3.178
4FFV	H_HIS_168	NE2	L_ASP_166	OD2	3.870

Table 1310: Interfacial 4FFV-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4FFW	A_ARG_659	NH2	B_GLU_242	OE2	3.187
4FFW	A_HIS_755	ND1	B_ASP_730	OD1	3.111
4FFW	B_ARG_659	NH2	A_GLU_242	OE2	3.068
4FFW	D_LYS_54	NZ	B_GLU_89	OE1	3.085
4FFW	D_LYS_54	NZ	B_GLU_89	OE2	3.381
4FFW	H_LYS_54	NZ	A_GLU_89	OE1	3.517
4FFW	H_LYS_54	NZ	A_GLU_89	OE2	3.666
4FFW	H_HIS_168	NE2	L_ASP_166	OD1	3.737

Table 1311: Interfacial 4FFW-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4FQH	H_LYS_143	NZ	L_GLU_124	OE2	2.906
4FQH	H_LYS_214	NZ	L_GLU_123	OE1	3.752
4FQH	H_LYS_214	NZ	L_GLU_123	OE2	2.217
4FQH	A_LYS_143	NZ	B_GLU_124	OE2	3.049
4FQH	A_LYS_214	NZ	B_GLU_123	OE1	3.132

Table 1312: Interfacial 4FQH-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4FQI	A_LYS_109	NZ	B_GLU_69	OE1	2.615
4FQI	A_LYS_109	NZ	B_GLU_69	OE2	3.205
4FQI	A_LYS_307	NZ	B_GLU_64	OE2	3.371
4FQI	A_LYS_310	NZ	B_ASP_90	OD1	2.687
4FQI	A_LYS_310	NZ	B_ASP_90	OD2	3.739
4FQI	H_LYS_143	NZ	L_GLU_124	OE2	2.947

Table 1313: Interfacial 4FQI-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4G6A	C_ARG_64	NH1	D_ASP_94	OD1	3.792
4G6A	C_ARG_64	NH1	D_ASP_94	OD2	3.701
4G6A	C_LYS_209	NZ	D_GLU_123	OE1	2.784
4G6A	C_LYS_209	NZ	D_GLU_123	OE2	3.529
4G6A	D_ARG_18	NH2	L_GLU_27	OE2	3.721
4G6A	H_ARG_64	NH2	L_ASP_94	OD1	3.443
4G6A	H_ARG_64	NH2	L_ASP_94	OD2	3.275
4G6A	H_LYS_209	NZ	L_GLU_123	OE1	2.940
4G6A	H_LYS_209	NZ	L_GLU_123	OE2	3.622

Table 1314: Interfacial 4G6A-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4G6F	H.LYS_143	NZ	L.GLU_125	OE2	3.341
4G6F	H.LYS_209	NZ	L.GLU_124	OE1	3.080
4G6F	H.LYS_209	NZ	L.GLU_124	OE2	2.558
4G6F	B.LYS_143	NZ	D.GLU_125	OE2	2.735
4G6F	B.LYS_209	NZ	D.GLU_124	OE1	3.470
4G6F	B.LYS_209	NZ	D.GLU_124	OE2	2.107
4G6F	L.HIS_31	ND1	H.GLU_100I	OE2	2.912
4G6F	L.ARG_91	NH1	H.GLU_100J	OE2	2.715
4G6F	L.ARG_91	NH2	H.GLU_100J	OE2	2.951
4G6F	D.HIS_31	ND1	B.GLU_100I	OE2	2.954
4G6F	D.ARG_91	NH1	B.GLU_100J	OE2	2.854
4G6F	D.ARG_91	NH2	B.GLU_100J	OE2	2.880
4G6F	D.ARG_95B	NH2	B.ASP_58	OD1	3.343

Table 1315: Interfacial 4G6F-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4GMT	H_HIS_164	NE2	L_ASP_167	OD2	3.650

Table 1316: Interfacial 4GMT-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4GXU	A_LYS_	NZ	F_GLU_	OE1	3.529
4GXU	A_LYS_	NZ	F_GLU_	OE2	3.469
4GXU	A_ARG_109	NH2	B_GLU_69	OE1	3.987
4GXU	A_ARG_109	NH2	B_GLU_69	OE2	3.286
4GXU	A_ARG_	NH1	B_ASP_	OD1	2.648
4GXU	A_ARG_	NH2	B_ASP_	OD1	2.545
4GXU	B_LYS_58	NZ	D_GLU_97	OE1	3.748
4GXU	B_LYS_68	NZ	A_GLU_110	OE2	3.492
4GXU	B_ARG_76	NH1	F_GLU_74	OE1	3.015
4GXU	B_ARG_76	NH1	F_GLU_74	OE2	2.935
4GXU	B_ARG_76	NH2	E_GLU_107	OE2	3.559
4GXU	B_ARG_76	NH2	F_GLU_74	OE2	2.547
4GXU	B_LYS_83	NZ	F_ASP_85	OD1	3.431
4GXU	B_LYS_83	NZ	F_ASP_85	OD2	3.614
4GXU	B_ARG_	NH2	D_ASP_	OD2	3.432
4GXU	B_ARG_	NH1	F_GLU_	OE1	3.168
4GXU	B_ARG_	NH2	F_GLU_	OE1	3.085
4GXU	B_ARG_	NH2	F_GLU_	OE2	3.110
4GXU	C_LYS_32	NZ	B_GLU_57	OE1	3.823
4GXU	C_LYS_32	NZ	B_GLU_57	OE2	3.681
4GXU	C_ARG_109	NH2	D_GLU_69	OE1	3.507
4GXU	C_ARG_109	NH2	D_GLU_69	OE2	3.205
4GXU	C_ARG_310	NH1	D_ASP_90	OD1	3.385
4GXU	C_ARG_310	NH2	D_ASP_90	OD1	3.336
4GXU	D_LYS_68	NZ	C_GLU_110	OE2	3.981
4GXU	D_ARG_76	NH1	B_GLU_74	OE1	2.948
4GXU	D_ARG_76	NH1	B_GLU_74	OE2	3.453
4GXU	D_ARG_76	NH2	A_GLU_107	OE2	3.465
4GXU	D_ARG_76	NH2	B_GLU_74	OE1	3.835
4GXU	D_ARG_76	NH2	B_GLU_74	OE2	2.916
4GXU	D_LYS_83	NZ	B_ASP_85	OD1	3.057
4GXU	D_LYS_83	NZ	B_ASP_85	OD2	3.527
4GXU	D_ARG_	NH2	F_ASP_	OD2	3.392
4GXU	D_ARG_	NH1	B_GLU_	OE1	2.743
4GXU	D_ARG_	NH1	B_GLU_	OE2	3.931
4GXU	D_ARG_	NH2	B_GLU_	OE1	2.897
4GXU	D_ARG_	NH2	B_GLU_	OE2	2.579
4GXU	E_LYS_	NZ	D_GLU_	OE1	3.848
4GXU	E_LYS_	NZ	D_GLU_	OE2	3.549
4GXU	E_ARG_109	NH2	F_GLU_69	OE1	3.819
4GXU	E_ARG_109	NH2	F_GLU_69	OE2	3.459
4GXU	E_ARG_310	NH1	F_ASP_90	OD1	2.704
4GXU	E_ARG_310	NH2	F_ASP_90	OD1	2.770
4GXU	F_LYS_	NZ	B_GLU_	OE1	3.893
4GXU	F_LYS_68	NZ	E_GLU_110	OE2	3.968
4GXU	F_ARG_76	NH1	D_GLU_74	OE1	2.787
4GXU	F_ARG_76	NH1	D_GLU_74	OE2	3.366
4GXU	F_ARG_76	NH2	C_GLU_107	OE2	3.548
4GXU	F_ARG_76	NH2	D_GLU_74	OE1	3.616
4GXU	F_ARG_76	NH2	D_GLU_74	OE2	2.732
4GXU	F_LYS_83	NZ	D_ASP_85	OD1	3.339
4GXU	F_LYS_83	NZ	D_ASP_85	OD2	3.717
4GXU	F_ARG_	NH2	B_ASP_	OD2	3.670
4GXU	F_ARG_	NH1	D_GLU_	OE1	3.077
4GXU	F_ARG_	NH2	D_GLU_	OE1	2.952
4GXU	F_ARG_	NH2	D_GLU_	OE2	3.074
4GXU	G_LYS_	NZ	J_GLU_	OE1	3.601

4GXU	G_LYS_	NZ	J_GLU_	OE2	3.403
4GXU	G_ARG_	NH2	H_GLU_	OE2	3.183
4GXU	G_ARG_	NH1	H_ASP_	OD1	2.337
4GXU	G_ARG_	NH2	H_ASP_	OD1	2.900
4GXU	H_LYS_	NZ	L_GLU_	OE1	3.639
4GXU	H_LYS_	NZ	G_GLU_	OE2	3.438
4GXU	H_ARG_	NH1	J_GLU_	OE1	2.612
4GXU	H_ARG_	NH1	J_GLU_	OE2	3.374
4GXU	H_ARG_	NH2	I_GLU_	OE2	3.506
4GXU	H_ARG_	NH2	J_GLU_	OE1	3.326
4GXU	H_ARG_	NH2	J_GLU_	OE2	2.517
4GXU	H_LYS_	NZ	J_ASP_	OD1	2.938
4GXU	H_LYS_	NZ	J_ASP_	OD2	3.368
4GXU	H_ARG_	NH2	L_ASP_	OD2	3.212
4GXU	H_ARG_	NH1	J_GLU_	OE1	3.044
4GXU	H_ARG_	NH2	J_GLU_	OE1	2.714
4GXU	H_ARG_	NH2	J_GLU_	OE2	3.067
4GXU	L_LYS_	NZ	L_GLU_	OE1	3.747
4GXU	L_LYS_	NZ	L_GLU_	OE2	3.353
4GXU	L_ARG_	NH2	J_GLU_	OE1	3.762
4GXU	L_ARG_	NH2	J_GLU_	OE2	2.924
4GXU	L_ARG_	NH1	J_ASP_	OD1	2.388
4GXU	L_ARG_	NH2	J_ASP_	OD1	2.649
4GXU	J_LYS_	NZ	H_GLU_	OE1	3.949
4GXU	J_LYS_	NZ	I_GLU_	OE2	3.674
4GXU	J_ARG_	NH1	L_GLU_	OE1	2.912
4GXU	J_ARG_	NH1	L_GLU_	OE2	3.322
4GXU	J_ARG_	NH2	K_GLU_	OE2	3.542
4GXU	J_ARG_	NH2	L_GLU_	OE1	3.621
4GXU	J_ARG_	NH2	L_GLU_	OE2	2.520
4GXU	J_LYS_	NZ	L_ASP_	OD1	3.139
4GXU	J_LYS_	NZ	L_ASP_	OD2	3.566
4GXU	J_ARG_	NH2	H_ASP_	OD2	3.270
4GXU	J_ARG_	NH1	L_GLU_	OE1	3.377
4GXU	J_ARG_	NH2	L_GLU_	OE1	2.504
4GXU	J_ARG_	NH2	L_GLU_	OE2	3.208
4GXU	K_LYS_	NZ	H_GLU_	OE2	3.068
4GXU	K_ARG_	NH2	L_GLU_	OE1	3.835
4GXU	K_ARG_	NH2	L_GLU_	OE2	3.159
4GXU	K_ARG_	NH1	L_ASP_	OD1	2.447
4GXU	K_ARG_	NH2	L_ASP_	OD1	2.754
4GXU	L_LYS_	NZ	J_GLU_	OE1	3.674
4GXU	L_LYS_	NZ	K_GLU_	OE2	3.305
4GXU	L_ARG_	NH1	H_GLU_	OE1	2.958
4GXU	L_ARG_	NH1	H_GLU_	OE2	3.138
4GXU	L_ARG_	NH2	G_GLU_	OE2	3.886
4GXU	L_ARG_	NH2	H_GLU_	OE1	3.887
4GXU	L_ARG_	NH2	H_GLU_	OE2	2.595
4GXU	L_LYS_	NZ	H_ASP_	OD1	2.732
4GXU	L_LYS_	NZ	H_ASP_	OD2	3.190
4GXU	L_ARG_	NH2	J_ASP_	OD2	3.583
4GXU	L_ARG_	NH1	H_GLU_	OE1	3.044
4GXU	L_ARG_	NH2	H_GLU_	OE1	2.477
4GXU	L_ARG_	NH2	H_GLU_	OE2	3.036
4GXU	M_ARG_	NH2	H_GLU_	OE2	3.356
4GXU	M_LYS_	NZ	N_GLU_	OE2	2.851
4GXU	M_LYS_	NZ	N_GLU_	OE1	3.371
4GXU	Q_LYS_143	NZ	R_GLU_124	OE2	3.025

4GXU	Q-LYS_209	NZ	R-GLU_123	OE1	3.619
4GXU	Q-LYS_209	NZ	R-GLU_123	OE2	3.564

Table 1317: Interfacial 4GXU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4GXV	H_LYS_143	NZ	L_GLU_124	OE2	2.866
4GXV	H_LYS_209	NZ	L_GLU_123	OE1	3.472
4GXV	H_LYS_209	NZ	L_GLU_123	OE2	2.731
4GXV	I_LYS_143	NZ	M_GLU_124	OE2	2.455
4GXV	I_LYS_209	NZ	M_GLU_123	OE1	2.930
4GXV	I_LYS_209	NZ	M_GLU_123	OE2	3.487

Table 1318: Interfacial 4GXV-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4GXX	A_LYS_32	NZ	D_GLU_57	OE1	3.386
4GXX	A_ARG_109	NH2	B_GLU_69	OE2	3.594
4GXX	A_ARG_310	NH1	B_ASP_90	OD1	2.488
4GXX	A_ARG_310	NH2	B_ASP_90	OD1	2.951
4GXX	B_LYS_58	NZ	F_GLU_97	OE1	3.721
4GXX	B_LYS_68	NZ	A_GLU_110	OE2	2.734
4GXX	B_ARG_76	NH1	D_GLU_74	OE1	2.782
4GXX	B_ARG_76	NH1	D_GLU_74	OE2	3.511
4GXX	B_ARG_76	NH2	C_GLU_107	OE2	3.651
4GXX	B_ARG_76	NH2	D_GLU_74	OE1	3.625
4GXX	B_ARG_76	NH2	D_GLU_74	OE2	2.818
4GXX	B_LYS_83	NZ	D_ASP_85	OD1	2.661
4GXX	B_LYS_83	NZ	D_ASP_85	OD2	3.421
4GXX	B_ARG_106	NH2	F_ASP_109	OD2	3.780
4GXX	B_ARG_116	NH2	D_GLU_120	OE1	2.669
4GXX	C_LYS_32	NZ	F_GLU_57	OE2	3.165
4GXX	C_ARG_109	NH2	D_GLU_69	OE1	3.802
4GXX	C_ARG_109	NH2	D_GLU_69	OE2	3.427
4GXX	C_ARG_310	NH1	D_ASP_90	OD1	2.336
4GXX	C_ARG_310	NH2	D_ASP_86	OD1	3.727
4GXX	C_ARG_310	NH2	D_ASP_90	OD1	3.012
4GXX	D_LYS_58	NZ	B_GLU_97	OE1	3.529
4GXX	D_LYS_68	NZ	C_GLU_110	OE2	2.872
4GXX	D_ARG_76	NH1	F_GLU_74	OE1	2.910
4GXX	D_ARG_76	NH1	F_GLU_74	OE2	3.571
4GXX	D_ARG_76	NH2	E_GLU_107	OE2	3.622
4GXX	D_ARG_76	NH2	F_GLU_74	OE1	3.615
4GXX	D_ARG_76	NH2	F_GLU_74	OE2	2.803
4GXX	D_LYS_83	NZ	F_ASP_85	OD1	2.774
4GXX	D_LYS_83	NZ	F_ASP_85	OD2	3.514
4GXX	D_ARG_106	NH2	B_ASP_109	OD2	3.920
4GXX	D_ARG_116	NH1	F_GLU_120	OE1	3.357
4GXX	D_ARG_116	NH2	F_GLU_120	OE1	3.225
4GXX	D_ARG_116	NH2	F_GLU_120	OE2	3.007
4GXX	E_LYS_32	NZ	B_GLU_57	OE2	3.237
4GXX	E_ARG_109	NH2	F_GLU_69	OE1	3.858
4GXX	E_ARG_109	NH2	F_GLU_69	OE2	2.773
4GXX	E_ARG_310	NH1	F_ASP_90	OD1	2.470
4GXX	E_ARG_310	NH2	F_ASP_90	OD1	2.925
4GXX	F_LYS_58	NZ	D_GLU_97	OE1	3.142
4GXX	F_LYS_68	NZ	E_GLU_110	OE2	2.982
4GXX	F_ARG_76	NH1	B_GLU_74	OE1	2.798
4GXX	F_ARG_76	NH1	B_GLU_74	OE2	3.572
4GXX	F_ARG_76	NH2	A_GLU_107	OE2	3.644
4GXX	F_ARG_76	NH2	B_GLU_74	OE1	3.566
4GXX	F_ARG_76	NH2	B_GLU_74	OE2	2.823
4GXX	F_LYS_83	NZ	B_ASP_85	OD1	2.859
4GXX	F_LYS_83	NZ	B_ASP_85	OD2	3.462
4GXX	F_ARG_106	NH2	D_ASP_109	OD2	3.576
4GXX	F_ARG_116	NH1	B_GLU_120	OE1	2.775
4GXX	F_ARG_116	NH1	B_GLU_120	OE2	3.643
4GXX	F_ARG_116	NH2	B_GLU_120	OE1	3.285
4GXX	F_ARG_116	NH2	B_GLU_120	OE2	2.552

Table 1319: Interfacial 4GXX-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4H8W	H_ARG_55	NH1	G_ASP_107	OD1	3.623
4H8W	H_ARG_55	NH1	G_ASP_107	OD2	3.025
4H8W	H_LYS_209	NZ	L_GLU_124	OE1	2.673
4H8W	H_LYS_209	NZ	L_GLU_124	OE2	2.808
4H8W	C_ARG_59	NH1	G_ASP_368	OD1	2.952
4H8W	C_ARG_59	NH1	G_ASP_368	OD2	3.318
4H8W	C_ARG_59	NH2	G_ASP_368	OD1	3.741
4H8W	C_ARG_59	NH2	G_ASP_368	OD2	2.611

Table 1320: Interfacial 4H8W-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4HF5	A_LYS_109	NZ	B_GLU_69	OE1	3.017
4HF5	A_ARG_137	NH1	H_ASP_97	OD2	2.969
4HF5	A_ARG_137	NH2	H_ASP_97	OD1	3.008
4HF5	A_ARG_137	NH2	H_ASP_97	OD2	2.797
4HF5	A_LYS_269	NZ	B_GLU_69	OE1	2.931
4HF5	A_LYS_269	NZ	B_GLU_69	OE2	3.200
4HF5	A_LYS_307	NZ	B_GLU_64	OE2	3.558
4HF5	A_LYS_310	NZ	B_ASP_90	OD1	2.877
4HF5	B_LYS_143	NZ	A_ASP_11	OD2	3.934

Table 1321: Interfacial 4HF5-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4HGK	C_LYS_65	NZ	B_GLU_230	OE1	3.917
4HGK	C_ARG_103	NH1	B_GLU_230	OE1	3.099
4HGK	C_ARG_103	NH2	B_GLU_230	OE1	3.263
4HGK	C_ARG_103	NH2	B_GLU_230	OE2	3.968
4HGK	D_LYS_65	NZ	A_GLU_230	OE1	3.741
4HGK	D_ARG_103	NH1	A_GLU_230	OE1	3.115
4HGK	D_ARG_103	NH2	A_GLU_230	OE1	3.112
4HGK	D_ARG_103	NH2	A_GLU_230	OE2	3.907

Table 1322: Interfacial 4HGK-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4HH9	A_ARG_54	NH1	C_ASP_50	OD2	3.238
4HH9	A_ARG_54	NH2	C_ASP_50	OD2	3.183
4HH9	B_LYS_209	NZ	A_GLU_123	OE1	3.274
4HH9	B_LYS_209	NZ	A_GLU_123	OE2	3.488
4HH9	B_LYS_214	NZ	A_ASP_122	OD1	3.788
4HH9	C_ARG_54	NH1	A_ASP_50	OD2	2.782
4HH9	C_ARG_54	NH2	A_ASP_50	OD2	3.752
4HH9	D_LYS_129	NZ	C_GLU_213	OE1	3.401
4HH9	D_LYS_129	NZ	C_GLU_213	OE2	3.163
4HH9	D_LYS_209	NZ	C_GLU_123	OE2	3.057
4HH9	D_LYS_214	NZ	C_ASP_122	OD2	3.367

Table 1323: Interfacial 4HH9-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4HHA	B_HIS_32	ND1	P_GLU_1	OE1	4.000
4HHA	B_HIS_32	NE2	P_GLU_1	OE1	3.076
4HHA	B_HIS_32	NE2	P_GLU_1	OE2	2.639
4HHA	B_ARG_94	NH1	P_GLU_1	OE2	3.723
4HHA	B_ARG_94	NH2	P_GLU_1	OE2	3.026
4HHA	B_HIS_164	NE2	A_ASP_167	OD1	3.917
4HHA	B_LYS_209	NZ	A_GLU_123	OE2	2.754

Table 1324: Interfacial 4HHA-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4HIE	A_ARG_91	NH2	B_GLU_95	OE1	3.457
4HIE	A_ARG_91	NH2	B_GLU_95	OE2	3.317

Table 1325: Interfacial 4HIE-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4HIH	A_ARG_91	NH2	B_GLU_95	OE1	3.470
4HIH	A_ARG_91	NH2	B_GLU_95	OE2	3.314
4HIH	B_LYS_209	NZ	A_GLU_123	OE1	2.853
4HIH	B_LYS_209	NZ	A_GLU_123	OE2	3.685
4HIH	C_ARG_91	NH2	D_GLU_95	OE1	3.527
4HIH	C_ARG_91	NH2	D_GLU_95	OE2	3.339
4HIH	D_LYS_209	NZ	C_GLU_123	OE1	2.616
4HIH	D_LYS_209	NZ	C_GLU_123	OE2	2.820

Table 1326: Interfacial 4HIH-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4HII	A_ARG_91	NH2	B_GLU_95	OE1	3.439
4HII	A_ARG_91	NH2	B_GLU_95	OE2	3.542
4HII	B_LYS_209	NZ	A_GLU_123	OE1	2.845
4HII	B_LYS_209	NZ	A_GLU_123	OE2	2.723
4HII	C_ARG_91	NH1	D_GLU_95	OE2	3.915
4HII	C_ARG_91	NH2	D_GLU_95	OE1	3.687
4HII	C_ARG_91	NH2	D_GLU_95	OE2	3.380

Table 1327: Interfacial 4HII-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4HIJ	A_ARG_91	NH1	B_GLU_95	OE2	3.962
4HIJ	A_ARG_91	NH2	B_GLU_95	OE1	3.390
4HIJ	A_ARG_91	NH2	B_GLU_95	OE2	3.274
4HIJ	C_ARG_91	NH2	D_GLU_95	OE1	3.772
4HIJ	C_ARG_91	NH2	D_GLU_95	OE2	3.260
4HIJ	D_LYS_209	NZ	C_GLU_123	OE2	3.644

Table 1328: Interfacial 4HIJ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4HK0	A_LYS_222	NZ	B_GLU_125	OE2	2.735
4HK0	C_ARG_104	NH2	D_ASP_95	OD2	3.573
4HK0	D_LYS_104	NZ	B_ASP_50	OD1	3.601
4HK0	D_LYS_104	NZ	B_ASP_50	OD2	2.755

Table 1329: Interfacial 4HK0-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4HK3	J_LYS_222	NZ	N_GLU_125	OE2	3.801

Table 1330: Interfacial 4HK3-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4HKB	J_LYS_23	NZ	C_ASP_73	OD1	3.505
4HKB	J_ARG_72	NH2	A_GLU_10	OE1	3.065
4HKB	J_ARG_72	NH2	A_GLU_10	OE2	2.664
4HKB	J_LYS_222	NZ	N_GLU_125	OE1	3.188
4HKB	J_LYS_222	NZ	N_GLU_125	OE2	3.564
4HKB	A_ARG_72	NH2	C_GLU_10	OE1	3.154
4HKB	A_ARG_72	NH2	C_GLU_10	OE2	2.755
4HKB	A_LYS_156	NZ	B_GLU_126	OE2	3.919
4HKB	A_LYS_222	NZ	B_GLU_125	OE1	3.019
4HKB	A_LYS_222	NZ	B_GLU_125	OE2	3.903
4HKB	C_LYS_63	NZ	E_ASP_89	OD1	3.939
4HKB	C_LYS_63	NZ	E_ASP_89	OD2	3.374
4HKB	C_ARG_87	NH2	E_ASP_90	OD1	3.045
4HKB	C_ARG_87	NH2	E_ASP_90	OD2	2.962
4HKB	C_LYS_222	NZ	D_GLU_125	OE1	3.332
4HKB	C_LYS_222	NZ	D_GLU_125	OE2	3.836
4HKB	E_LYS_23	NZ	G_ASP_73	OD1	2.630
4HKB	E_LYS_63	NZ	C_ASP_89	OD1	3.625
4HKB	E_LYS_63	NZ	C_ASP_89	OD2	3.095
4HKB	E_ARG_72	NH1	I_GLU_10	OE1	2.874
4HKB	E_ARG_72	NH1	I_GLU_10	OE2	2.849
4HKB	E_ARG_87	NH1	C_ASP_90	OD1	3.489
4HKB	E_ARG_87	NH1	C_ASP_90	OD2	3.954
4HKB	E_ARG_87	NH2	C_ASP_90	OD1	3.930
4HKB	E_ARG_87	NH2	C_ASP_90	OD2	3.219
4HKB	E_LYS_222	NZ	F_GLU_125	OE2	3.327
4HKB	G_ARG_87	NH1	J_ASP_90	OD1	3.108
4HKB	G_ARG_87	NH1	J_ASP_90	OD2	3.912
4HKB	G_ARG_87	NH2	J_ASP_90	OD2	3.607
4HKB	I_ARG_72	NH2	G_GLU_10	OE1	3.560
4HKB	I_ARG_72	NH2	G_GLU_10	OE2	2.553
4HKB	I_LYS_222	NZ	K_GLU_125	OE2	3.211
4HKB	N_ARG_29	NH1	J_ASP_107	OD1	3.664
4HKB	N_ARG_29	NH1	J_ASP_107	OD2	2.469
4HKB	N_LYS_131	NZ	J_ASP_157	OD2	3.951
4HKB	B_ARG_29	NH1	A_ASP_107	OD2	3.659
4HKB	D_ARG_29	NH1	C_ASP_107	OD2	3.254
4HKB	H_ARG_29	NH1	G_ASP_107	OD2	3.325
4HKB	H_ARG_29	NH2	G_ASP_107	OD2	3.189
4HKB	K_ARG_31	NH1	I_ASP_107	OD2	3.242

Table 1331: Interfacial 4HKB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4HKX	E_ARG_192	NH1	B_ASP_95	OD2	3.293
4HKX	E_LYS_219	NZ	B_ASP_93	OD1	2.877
4HKX	E_LYS_219	NZ	B_ASP_93	OD2	3.792
4HKX	A_LYS_222	NZ	B_GLU_125	OE1	3.981
4HKX	B_ARG_29	NH2	A_ASP_107	OD2	3.853
4HKX	B_LYS_131	NZ	A_ASP_157	OD2	3.310

Table 1332: Interfacial 4HKX-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4HLZ	A_LYS_109	NZ	B_GLU_69	OE1	3.478
4HLZ	A_LYS_109	NZ	B_GLU_69	OE2	2.999
4HLZ	A_LYS_310	NZ	B_ASP_90	OD1	2.429
4HLZ	A_LYS_310	NZ	B_ASP_90	OD2	3.948
4HLZ	B_LYS_58	NZ	F_GLU_97	OE1	3.865
4HLZ	B_LYS_58	NZ	F_GLU_97	OE2	3.885
4HLZ	B_ARG_76	NH1	D_GLU_74	OE1	2.838
4HLZ	B_ARG_76	NH1	D_GLU_74	OE2	3.993
4HLZ	B_ARG_76	NH2	D_GLU_74	OE1	3.145
4HLZ	B_ARG_76	NH2	D_GLU_74	OE2	2.917
4HLZ	B_LYS_83	NZ	D_GLU_85	OE2	2.459
4HLZ	B_ARG_106	NH2	F_ASP_109	OD2	3.278
4HLZ	B_LYS_143	NZ	A_ASP_11	OD1	3.527
4HLZ	B_LYS_143	NZ	A_ASP_11	OD2	3.714
4HLZ	C_ARG_32	NH1	F_GLU_57	OE1	3.413
4HLZ	C_LYS_109	NZ	D_GLU_69	OE1	2.904
4HLZ	C_LYS_109	NZ	D_GLU_69	OE2	3.394
4HLZ	C_LYS_310	NZ	D_ASP_86	OD2	2.827
4HLZ	C_LYS_310	NZ	D_ASP_90	OD1	2.357
4HLZ	C_LYS_310	NZ	D_ASP_90	OD2	3.459
4HLZ	D_LYS_58	NZ	B_GLU_97	OE1	2.796
4HLZ	D_ARG_76	NH1	F_GLU_74	OE1	3.279
4HLZ	D_ARG_76	NH1	F_GLU_74	OE2	2.976
4HLZ	D_ARG_76	NH2	E_GLU_107	OE2	3.277
4HLZ	D_ARG_76	NH2	F_GLU_74	OE2	2.480
4HLZ	D_LYS_83	NZ	F_GLU_85	OE2	2.714
4HLZ	D_ARG_106	NH2	B_ASP_109	OD2	3.865
4HLZ	D_LYS_131	NZ	F_ASP_128	OD1	3.317
4HLZ	E_LYS_109	NZ	F_GLU_69	OE1	2.572
4HLZ	E_LYS_109	NZ	F_GLU_69	OE2	3.930
4HLZ	E_LYS_310	NZ	F_ASP_86	OD1	3.890
4HLZ	E_LYS_310	NZ	F_ASP_90	OD1	3.800
4HLZ	F_LYS_58	NZ	D_GLU_97	OE1	3.641
4HLZ	F_ARG_76	NH1	B_GLU_74	OE1	3.514
4HLZ	F_ARG_76	NH1	B_GLU_74	OE2	3.227
4HLZ	F_ARG_76	NH2	B_GLU_74	OE1	3.962
4HLZ	F_ARG_76	NH2	B_GLU_74	OE2	2.467
4HLZ	I_LYS_96	NZ	D_ASP_46	OD1	2.912
4HLZ	I_LYS_96	NZ	D_ASP_46	OD2	3.655
4HLZ	I_LYS_208	NZ	J_GLU_125	OE2	3.495
4HLZ	I_ARG_213	NH2	J_GLU_125	OE1	3.227
4HLZ	I_ARG_213	NH2	J_GLU_125	OE2	3.829

Table 1333: Interfacial 4HLZ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4HMG	A.LYS_27	NZ	B.GLU_97	OE1	2.795
4HMG	A.LYS_27	NZ	B.GLU_97	OE2	3.247
4HMG	A.ARG_109	NH1	B.GLU_67	OE1	3.584
4HMG	A.ARG_109	NH1	B.GLU_67	OE2	2.773
4HMG	A.LYS_238	NZ	F.GLU_72	OE2	2.782
4HMG	A.ARG_269	NH2	B.GLU_67	OE1	2.783
4HMG	A.LYS_310	NZ	B.ASP_90	OD1	3.350
4HMG	A.LYS_310	NZ	B.ASP_90	OD2	2.711
4HMG	B.ARG_54	NH1	F.GLU_97	OE1	3.078
4HMG	B.ARG_54	NH2	E.ASP_32	OD2	3.863
4HMG	B.ARG_54	NH2	F.GLU_97	OE1	3.088
4HMG	B.LYS_62	NZ	F.ASP_86	OD1	2.890
4HMG	B.LYS_62	NZ	F.ASP_86	OD2	2.630
4HMG	B.LYS_62	NZ	F.ASP_90	OD1	3.620
4HMG	B.LYS_62	NZ	F.ASP_90	OD2	3.931
4HMG	B.HIS_64	NE2	F.ASP_79	OD2	3.785
4HMG	B.ARG_76	NH1	D.GLU_74	OE1	2.796
4HMG	B.ARG_76	NH1	D.GLU_74	OE2	3.711
4HMG	B.ARG_76	NH1	D.GLU_81	OE1	2.672
4HMG	B.ARG_76	NH1	D.GLU_81	OE2	3.308
4HMG	B.ARG_76	NH2	D.GLU_74	OE1	3.404
4HMG	B.ARG_76	NH2	D.GLU_74	OE2	2.827
4HMG	B.ARG_123	NH1	F.GLU_132	OE2	3.178
4HMG	B.ARG_124	NH1	F.GLU_132	OE1	3.359
4HMG	B.ARG_124	NH1	F.GLU_132	OE2	3.102
4HMG	B.ARG_127	NH2	F.GLU_131	OE1	2.525
4HMG	B.ARG_163	NH1	F.GLU_131	OE1	3.338
4HMG	B.ARG_163	NH1	F.GLU_131	OE2	2.796
4HMG	B.ARG_163	NH2	F.GLU_131	OE1	2.694
4HMG	B.ARG_163	NH2	F.GLU_131	OE2	3.492
4HMG	B.ARG_170	NH2	D.GLU_128	OE1	3.784
4HMG	B.ARG_170	NH2	D.GLU_128	OE2	3.698
4HMG	C.LYS_27	NZ	D.GLU_97	OE1	2.789
4HMG	C.LYS_27	NZ	D.GLU_97	OE2	3.246
4HMG	C.ARG_109	NH1	D.GLU_67	OE1	3.616
4HMG	C.ARG_109	NH1	D.GLU_67	OE2	2.791
4HMG	C.LYS_238	NZ	B.GLU_72	OE2	2.606
4HMG	C.ARG_269	NH2	D.GLU_67	OE1	2.764
4HMG	C.LYS_310	NZ	D.ASP_90	OD1	3.321
4HMG	C.LYS_310	NZ	D.ASP_90	OD2	2.697
4HMG	C.LYS_326	NZ	D.GLU_15	OE1	3.836
4HMG	C.LYS_326	NZ	D.GLU_15	OE2	2.684
4HMG	D.ARG_54	NH1	B.GLU_97	OE1	3.076
4HMG	D.ARG_54	NH2	A.ASP_32	OD2	3.995
4HMG	D.ARG_54	NH2	B.GLU_97	OE1	3.112
4HMG	D.LYS_62	NZ	B.ASP_86	OD1	2.940
4HMG	D.LYS_62	NZ	B.ASP_86	OD2	2.591
4HMG	D.LYS_62	NZ	B.ASP_90	OD1	3.586
4HMG	D.LYS_62	NZ	B.ASP_90	OD2	3.891
4HMG	D.HIS_64	NE2	B.ASP_79	OD2	3.731
4HMG	D.ARG_76	NH1	F.GLU_74	OE1	2.745
4HMG	D.ARG_76	NH1	F.GLU_74	OE2	3.756
4HMG	D.ARG_76	NH1	F.GLU_81	OE1	2.644
4HMG	D.ARG_76	NH1	F.GLU_81	OE2	3.314
4HMG	D.ARG_76	NH2	F.GLU_74	OE1	3.255
4HMG	D.ARG_76	NH2	F.GLU_74	OE2	2.777
4HMG	D.ARG_123	NH1	B.GLU_132	OE2	3.157

4HMG	D_ARG_124	NH1	B_GLU_132	OE1	3.347
4HMG	D_ARG_124	NH1	B_GLU_132	OE2	3.074
4HMG	D_ARG_127	NH2	B_GLU_131	OE1	2.541
4HMG	D_ARG_163	NH1	B_GLU_131	OE1	3.321
4HMG	D_ARG_163	NH1	B_GLU_131	OE2	2.801
4HMG	D_ARG_163	NH2	B_GLU_131	OE1	2.729
4HMG	D_ARG_163	NH2	B_GLU_131	OE2	3.526
4HMG	D_ARG_170	NH2	F_GLU_128	OE1	3.859
4HMG	D_ARG_170	NH2	F_GLU_128	OE2	3.829
4HMG	E_LYS_27	NZ	F_GLU_97	OE1	2.764
4HMG	E_LYS_27	NZ	F_GLU_97	OE2	3.247
4HMG	E_ARG_109	NH1	F_GLU_67	OE1	3.614
4HMG	E_ARG_109	NH1	F_GLU_67	OE2	2.773
4HMG	E_LYS_238	NZ	D_GLU_72	OE2	2.707
4HMG	E_ARG_269	NH2	F_GLU_67	OE1	2.739
4HMG	E_LYS_310	NZ	F_ASP_90	OD1	3.300
4HMG	E_LYS_310	NZ	F_ASP_90	OD2	2.685
4HMG	F_ARG_25	NH1	E_GLU_325	OE1	3.853
4HMG	F_ARG_54	NH1	D_GLU_97	OE1	3.052
4HMG	F_ARG_54	NH2	C_ASP_32	OD2	3.923
4HMG	F_ARG_54	NH2	D_GLU_97	OE1	3.130
4HMG	F_LYS_62	NZ	D_ASP_86	OD1	2.900
4HMG	F_LYS_62	NZ	D_ASP_86	OD2	2.597
4HMG	F_LYS_62	NZ	D_ASP_90	OD1	3.664
4HMG	F_LYS_62	NZ	D_ASP_90	OD2	3.951
4HMG	F_HIS_64	NE2	D_ASP_79	OD2	3.646
4HMG	F_ARG_76	NH1	B_GLU_74	OE1	2.714
4HMG	F_ARG_76	NH1	B_GLU_74	OE2	3.687
4HMG	F_ARG_76	NH1	B_GLU_81	OE1	2.651
4HMG	F_ARG_76	NH1	B_GLU_81	OE2	3.434
4HMG	F_ARG_76	NH2	B_GLU_74	OE1	3.281
4HMG	F_ARG_76	NH2	B_GLU_74	OE2	2.711
4HMG	F_ARG_123	NH1	D_GLU_132	OE2	3.178
4HMG	F_ARG_124	NH1	D_GLU_132	OE1	3.402
4HMG	F_ARG_124	NH1	D_GLU_132	OE2	3.132
4HMG	F_ARG_127	NH2	D_GLU_131	OE1	2.579
4HMG	F_ARG_163	NH1	D_GLU_131	OE1	3.299
4HMG	F_ARG_163	NH1	D_GLU_131	OE2	2.816
4HMG	F_ARG_163	NH2	D_GLU_131	OE1	2.752
4HMG	F_ARG_163	NH2	D_GLU_131	OE2	3.575
4HMG	F_ARG_170	NH2	B_GLU_128	OE1	3.815
4HMG	F_ARG_170	NH2	B_GLU_128	OE2	3.719

Table 1334: Interfacial 4HMG-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4HWB	A_ARG_230	NH2	H_ASP_56	OD2	3.246
4HWB	H_LYS_215	NZ	L_GLU_120	OE2	3.469

Table 1335: Interfacial 4HWB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4HXA	H_ARG_98	NH1	L_ASP_50	OD1	2.959
4HXA	H_ARG_98	NH1	L_ASP_50	OD2	3.607
4HXA	H_HIS_164	NE2	L_ASP_167	OD1	3.601

Table 1336: Interfacial 4HXA-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4HXB	H_ARG_96	NH1	L_ASP_94	OD1	3.212
4HXB	H_ARG_96	NH1	L_ASP_94	OD2	2.665
4HXB	H_ARG_96	NH2	L_ASP_94	OD1	2.669
4HXB	H_ARG_96	NH2	L_ASP_94	OD2	3.708

Table 1337: Interfacial 4HXB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4I2X	B.LYS_59	NZ	E.GLU_10	OE2	3.418
4I2X	B.LYS_65	NZ	E.ASP_208	OD1	3.256
4I2X	B.LYS_214	NZ	A.GLU_123	OE2	3.742
4I2X	D.LYS_63	NZ	C.ASP_1	OD2	3.656
4I2X	D.LYS_65	NZ	F.ASP_208	OD1	3.848
4I2X	D.HIS_170	ND1	C.ASP_167	OD2	3.958
4I2X	D.LYS_214	NZ	C.GLU_123	OE2	3.815
4I2X	F.ARG_180	NH1	E.GLU_47	OE1	3.834

Table 1338: Interfacial 4I2X-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4I3R	G_LYS_282	NZ	H_GLU_33	OE1	3.996
4I3R	G_LYS_282	NZ	H_GLU_33	OE2	2.684
4I3R	H_ARG_64	NH2	G_ASP_457	OD1	3.551
4I3R	H_ARG_64	NH2	G_ASP_457	OD2	3.482
4I3R	H_ARG_71	NH1	G_ASP_368	OD1	3.996
4I3R	H_ARG_71	NH1	G_ASP_368	OD2	2.319
4I3R	H_ARG_71	NH2	G_ASP_368	OD1	3.997
4I3R	H_ARG_71	NH2	G_ASP_368	OD2	3.530
4I3R	H_LYS_209	NZ	L_GLU_123	OE2	2.484

Table 1339: Interfacial 4I3R-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4I3S	G_LYS_282	NZ	H_GLU_33	OE1	3.669
4I3S	G_LYS_282	NZ	H_GLU_33	OE2	3.690
4I3S	H_ARG_64	NH2	G_ASP_457	OD1	3.430
4I3S	H_ARG_64	NH2	G_ASP_457	OD2	3.082
4I3S	H_ARG_71	NH1	G_ASP_368	OD1	3.370
4I3S	H_ARG_71	NH1	G_ASP_368	OD2	3.053
4I3S	H_ARG_71	NH2	G_ASP_368	OD1	3.484
4I3S	H_LYS_209	NZ	L_GLU_123	OE1	2.882

Table 1340: Interfacial 4I3S-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4JAM	H_LYS_209	NZ	L_GLU_123	OE2	3.865
4JAM	A_LYS_209	NZ	B_GLU_123	OE2	3.814

Table 1341: Interfacial 4JAM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4JAN	H_ARG_97	NH2	G_ASP_368	OD2	2.609
4JAN	H_ARG_97	NH2	G_GLU_370	OE1	2.554
4JAN	H_LYS_143	NZ	L_GLU_124	OE2	3.811
4JAN	H_LYS_209	NZ	L_GLU_123	OE1	2.888
4JAN	L_LYS_129	NZ	H_ASP_144	OD2	3.458
4JAN	A_ARG_97	NH2	I_ASP_368	OD1	2.825
4JAN	A_ARG_97	NH2	I_ASP_368	OD2	3.792
4JAN	A_ARG_97	NH2	I_GLU_370	OE1	3.106
4JAN	A_LYS_209	NZ	B_GLU_123	OE1	3.788
4JAN	A_LYS_209	NZ	B_GLU_123	OE2	3.189

Table 1342: Interfacial 4JAN-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4JHW	F_LYS_209	NZ	H_ASP_101	OD2	3.535
4JHW	F_LYS_209	NZ	L_GLU_55	OE1	2.845
4JHW	F_LYS_209	NZ	L_GLU_55	OE2	3.356

Table 1343: Interfacial 4JHW-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4JO1	P_ARG_304	NH1	H_ASP_34	OD1	3.045
4JO1	P_ARG_304	NH1	H_ASP_34	OD2	3.346
4JO1	P_ARG_304	NH2	H_ASP_34	OD2	2.892
4JO1	Q_ARG_304	NH1	L_ASP_34	OD1	2.949
4JO1	Q_ARG_304	NH1	L_ASP_34	OD2	3.344
4JO1	Q_ARG_304	NH2	L_ASP_34	OD1	3.946
4JO1	Q_ARG_304	NH2	L_ASP_34	OD2	2.878

Table 1344: Interfacial 4JO1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4JO2	P_ARG_304	NH1	H_ASP_34	OD1	2.726
4JO2	P_ARG_304	NH1	H_ASP_34	OD2	3.333
4JO2	P_ARG_304	NH2	H_ASP_34	OD1	3.721
4JO2	P_ARG_304	NH2	H_ASP_34	OD2	2.854
4JO2	Q_ARG_304	NH1	I_ASP_34	OD1	2.965
4JO2	Q_ARG_304	NH1	I_ASP_34	OD2	3.252
4JO2	Q_ARG_304	NH2	I_ASP_34	OD2	3.328

Table 1345: Interfacial 4JO2-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4JO3	H_ARG_54	NH1	P_GLU_321	OE1	3.970
4JO3	P_ARG_327	NH1	L_ASP_1	OD1	2.994
4JO3	P_ARG_327	NH2	L_ASP_1	OD1	2.732
4JO3	P_ARG_327	NH2	L_GLU_27	OE1	3.272
4JO3	P_ARG_327	NH2	L_GLU_27	OE2	3.099
4JO3	Q_ARG_327	NH1	M_ASP_1	OD1	3.248
4JO3	Q_ARG_327	NH2	M_ASP_1	OD1	2.447
4JO3	Q_ARG_327	NH2	M_ASP_1	OD2	3.524
4JO3	Q_ARG_327	NH2	M_GLU_27	OE1	3.837
4JO3	Q_ARG_327	NH2	M_GLU_27	OE2	3.723

Table 1346: Interfacial 4JO3-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4K24	A.LYS_46	NZ	U.GLU_33	OE2	3.632
4K24	A.LYS_46	NZ	U.GLU_36	OE2	2.856
4K24	A.HIS_87	ND1	U.ASP_11	OD1	3.994
4K24	H.LYS_62	NZ	L.ASP_1	OD1	3.610
4K24	H.LYS_208	NZ	L.GLU_123	OE1	2.286
4K24	H.LYS_208	NZ	L.GLU_123	OE2	3.345
4K24	U.ARG_91	NH1	B.ASP_22	OD2	3.233
4K24	U.ARG_91	NH2	B.ASP_22	OD1	3.988
4K24	U.ARG_91	NH2	B.ASP_22	OD2	3.635

Table 1347: Interfacial 4K24-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4K2U	H_LYS_	NZ	L_ASP_	OD2	2.646
4K2U	H_LYS_	NZ	L_GLU_	OE2	3.160
4K2U	L_LYS_	NZ	M_ASP_	OD2	2.895
4K2U	L_ARG_	NH1	A_GLU_	OE1	2.808
4K2U	L_ARG_	NH1	A_GLU_	OE2	3.439
4K2U	L_ARG_	NH2	A_GLU_	OE1	3.591
4K2U	L_ARG_	NH2	A_GLU_	OE2	2.619
4K2U	M_ARG_	NH1	B_GLU_	OE1	2.744
4K2U	M_ARG_	NH1	B_GLU_	OE2	3.321
4K2U	M_ARG_	NH2	B_GLU_	OE1	3.489
4K2U	M_ARG_	NH2	B_GLU_	OE2	2.673
4K2U	M_HIS_	ND1	L_GLU_	OE2	3.997

Table 1348: Interfacial 4K2U-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID** **residue name** **residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4KI5	C_LYS_211	NZ	D_GLU_122	OE2	2.907
4KI5	E_LYS_217	NZ	F_GLU_123	OE2	3.401
4KI5	E_ARG_222	NH1	F_GLU_123	OE1	3.106
4KI5	E_ARG_222	NH1	F_GLU_123	OE2	3.925
4KI5	E_ARG_222	NH2	F_GLU_123	OE1	3.823
4KI5	E_ARG_222	NH2	F_GLU_123	OE2	3.234
4KI5	M_ARG_2215	NH1	C_ASP_100	OD1	2.868
4KI5	M_ARG_2215	NH1	C_ASP_100	OD2	3.241
4KI5	M_ARG_2215	NH2	C_ASP_100	OD1	3.324
4KI5	M_ARG_2215	NH2	C_ASP_100	OD2	2.939
4KI5	M_ARG_2215	NH2	C_ASP_101	OD2	3.819
4KI5	M_LYS_2227	NZ	E_GLU_50	OE1	3.493

Table 1349: Interfacial 4KI5-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID residue name residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4KJY	A.LYS_39	NZ	B.ASP_100	OD1	2.809
4KJY	B.ARG_53	NH1	A.GLU_97	OE2	3.571
4KJY	B.ARG_53	NH1	A.GLU_106	OE1	3.135
4KJY	B.ARG_69	NH1	A.GLU_35	OE1	2.737
4KJY	B.ARG_69	NH1	A.GLU_35	OE2	3.607
4KJY	B.ARG_69	NH1	A.GLU_100	OE2	2.961
4KJY	B.ARG_69	NH2	A.GLU_35	OE1	3.476
4KJY	B.ARG_69	NH2	A.GLU_35	OE2	2.813
4KJY	B.LYS_96	NZ	A.GLU_97	OE1	2.567
4KJY	D.ARG_40	NH1	A.GLU_29	OE1	3.310
4KJY	D.ARG_40	NH2	A.GLU_29	OE1	3.253
4KJY	D.ARG_40	NH2	A.GLU_29	OE2	2.999
4KJY	D.ARG_40	NH2	B.GLU_70	OE1	3.440
4KJY	D.ARG_53	NH1	C.GLU_97	OE2	3.949
4KJY	D.ARG_53	NH2	C.GLU_104	OE1	3.112
4KJY	D.ARG_53	NH2	C.GLU_104	OE2	3.607
4KJY	D.ARG_69	NH1	C.GLU_35	OE1	2.786
4KJY	D.ARG_69	NH1	C.GLU_35	OE2	3.903
4KJY	D.ARG_69	NH1	C.GLU_100	OE2	3.005
4KJY	D.ARG_69	NH2	C.GLU_35	OE1	3.286
4KJY	D.ARG_69	NH2	C.GLU_35	OE2	2.868
4KJY	D.LYS_96	NZ	C.GLU_97	OE1	2.747

Table 1350: Interfacial 4KJY-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4KPH	L_ARG_61	NH2	L_GLU_85	OE2	3.345
4KPH	H_LYS_208	NZ	L_GLU_123	OE2	2.903
4KPH	L_LYS_208	NZ	M_GLU_123	OE2	2.312

Table 1351: Interfacial 4KPH-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4KRL	B_ARG_30	NH1	A_ASP_355	OD1	3.258
4KRL	B_ARG_30	NH1	A_ASP_355	OD2	2.275
4KRL	B_ARG_30	NH2	A_ASP_355	OD1	3.549
4KRL	B_ARG_30	NH2	A_ASP_355	OD2	3.938
4KRL	A_ARG_353	NH1	B_GLU_110	OE1	2.654
4KRL	A_ARG_353	NH2	B_ASP_112	OD1	3.873
4KRL	A_ARG_353	NH2	B_ASP_112	OD2	2.978

Table 1352: Interfacial 4KRL-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4KRM	A_ARG_353	NH1	B_GLU_110	OE1	2.811
4KRM	A_ARG_353	NH2	B_ASP_112	OD1	3.965
4KRM	A_ARG_353	NH2	B_ASP_112	OD2	2.932
4KRM	A_LYS_407	NZ	H_GLU_5	OE1	3.498
4KRM	A_LYS_407	NZ	H_GLU_5	OE2	3.022
4KRM	B_ARG_30	NH1	A_ASP_355	OD1	3.162
4KRM	B_ARG_30	NH1	A_ASP_355	OD2	2.423
4KRM	B_ARG_30	NH2	A_ASP_355	OD1	3.525
4KRM	C_ARG_353	NH1	D_GLU_110	OE1	2.866
4KRM	C_ARG_353	NH2	D_ASP_112	OD2	3.218
4KRM	D_ARG_30	NH1	C_ASP_355	OD1	3.295
4KRM	D_ARG_30	NH1	C_ASP_355	OD2	2.452
4KRM	D_ARG_30	NH2	C_ASP_355	OD1	3.096
4KRM	D_ARG_30	NH2	C_ASP_355	OD2	3.699
4KRM	E_ARG_353	NH1	F_GLU_110	OE1	2.855
4KRM	E_ARG_353	NH2	F_ASP_112	OD2	2.965
4KRM	E_LYS_407	NZ	L_GLU_5	OE1	3.054
4KRM	E_LYS_407	NZ	L_GLU_5	OE2	2.995
4KRM	F_ARG_30	NH1	E_ASP_355	OD1	3.119
4KRM	F_ARG_30	NH1	E_ASP_355	OD2	2.396
4KRM	F_ARG_30	NH2	E_ASP_355	OD1	3.504
4KRM	G_ARG_353	NH1	H_GLU_110	OE1	3.021
4KRM	G_ARG_353	NH2	H_ASP_112	OD2	3.118
4KRM	G_LYS_407	NZ	B_GLU_5	OE1	3.493
4KRM	G_LYS_407	NZ	B_GLU_5	OE2	2.984
4KRM	H_ARG_27	NH1	G_ASP_323	OD1	2.688
4KRM	H_ARG_27	NH2	G_ASP_323	OD1	3.952
4KRM	H_ARG_30	NH1	G_ASP_355	OD1	3.358
4KRM	H_ARG_30	NH1	G_ASP_355	OD2	2.448
4KRM	H_ARG_30	NH2	G_ASP_355	OD1	3.423
4KRM	H_ARG_30	NH2	G_ASP_355	OD2	3.935
4KRM	I_ARG_353	NH1	J_GLU_110	OE1	2.862
4KRM	I_ARG_353	NH2	J_ASP_112	OD2	2.998
4KRM	J_ARG_30	NH1	I_ASP_355	OD1	3.164
4KRM	J_ARG_30	NH1	I_ASP_355	OD2	2.382
4KRM	J_ARG_30	NH2	I_ASP_355	OD1	3.707
4KRM	K_ARG_353	NH1	L_GLU_110	OE1	2.887
4KRM	K_ARG_353	NH1	L_ASP_112	OD2	3.973
4KRM	K_ARG_353	NH2	L_ASP_112	OD2	2.890
4KRM	L_ARG_30	NH1	K_ASP_355	OD1	3.487
4KRM	L_ARG_30	NH1	K_ASP_355	OD2	2.441
4KRM	L_ARG_30	NH2	K_ASP_355	OD1	3.452
4KRM	L_ARG_30	NH2	K_ASP_355	OD2	3.835

Table 1353: Interfacial 4KRM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4KRO	A_ARG_403	NH2	B_ASP_118	OD2	3.168
4KRO	A_ARG_405	NH2	B_ASP_118	OD1	3.123
4KRO	A_ARG_405	NH2	B_ASP_118	OD2	3.849
4KRO	A_LYS_443	NZ	D_ASP_58	OD1	2.597
4KRO	A_LYS_443	NZ	D_ASP_58	OD2	3.457
4KRO	A_LYS_465	NZ	D_ASP_103	OD2	2.400
4KRO	B_ARG_27	NH1	A_GLU_431	OE1	3.073
4KRO	B_ARG_27	NH2	A_GLU_431	OE1	3.933
4KRO	C_LYS_49	NZ	D_GLU_105	OE2	3.247

Table 1354: Interfacial 4KRO-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4KRP	A_ARG_403	NH2	B_ASP_115	OD2	3.818
4KRP	A_ARG_405	NH1	B_GLU_113	OE1	2.923
4KRP	A_ARG_405	NH2	B_GLU_113	OE1	3.376
4KRP	A_ARG_405	NH2	B_ASP_115	OD1	2.626
4KRP	A_LYS_443	NZ	D_ASP_58	OD1	2.649
4KRP	A_LYS_443	NZ	D_ASP_58	OD2	3.951
4KRP	A_LYS_465	NZ	D_ASP_103	OD2	2.931
4KRP	B_ARG_27	NH1	A_GLU_431	OE1	3.144

Table 1355: Interfacial 4KRP-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4KV5	C.LYS_60	NZ	G.ASP_56	OD2	3.911
4KV5	C.LYS_60	NZ	G.GLU_74	OE2	3.252
4KV5	C.ARG_94	NH1	E.ASP_231	OD2	3.776
4KV5	D.LYS_60	NZ	E.GLU_74	OE2	3.237
4KV5	A.ARG_94	NH1	H.ASP_231	OD2	3.628
4KV5	B.LYS_60	NZ	H.ASP_56	OD2	3.938
4KV5	B.LYS_60	NZ	H.GLU_74	OE2	3.524

Table 1356: Interfacial 4KV5-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4KXZ	A_ARG_60	NH2	J_GLU_74	OE1	3.804
4KXZ	B_ARG_60	NH2	H_ASP_56	OD1	3.585
4KXZ	B_ARG_60	NH2	H_GLU_74	OE1	3.374
4KXZ	B_ARG_60	NH2	H_GLU_74	OE2	3.199
4KXZ	D_ARG_60	NH1	N_GLU_74	OE2	3.775
4KXZ	D_ARG_60	NH2	N_GLU_74	OE2	2.746
4KXZ	E_ARG_60	NH1	Q_GLU_74	OE1	3.619
4KXZ	H_HIS_219	NE2	Q_ASP_56	OD2	3.789
4KXZ	H_HIS_223	ND1	Q_GLU_82	OE1	3.688
4KXZ	H_HIS_223	ND1	Q_GLU_82	OE2	3.984
4KXZ	H_HIS_223	ND1	L_ASP_123	OD1	3.085
4KXZ	H_HIS_223	NE2	Q_GLU_82	OE2	3.368
4KXZ	H_HIS_223	NE2	L_ASP_123	OD1	3.457
4KXZ	J_LYS_216	NZ	I_GLU_124	OE1	2.736
4KXZ	J_LYS_216	NZ	I_GLU_124	OE2	3.105
4KXZ	N_HIS_219	NE2	J_ASP_56	OD2	3.889
4KXZ	N_HIS_223	ND1	J_GLU_82	OE1	3.240
4KXZ	N_HIS_223	ND1	M_ASP_123	OD1	3.197
4KXZ	N_HIS_223	NE2	J_GLU_82	OE1	3.650
4KXZ	N_HIS_223	NE2	J_GLU_82	OE2	3.394
4KXZ	N_HIS_223	NE2	M_ASP_123	OD1	3.310

Table 1357: Interfacial 4KXZ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4LQF	H_LYS_212	NZ	L_GLU_129	OE1	2.714
4LQF	H_LYS_212	NZ	L_GLU_129	OE2	3.879
4LQF	L_LYS_55	NZ	A_ASP_170	OD2	2.731

Table 1358: Interfacial 4LQF-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4LSS	G_LYS_97	NZ	H_ASP_99	OD2	3.791
4LSS	G_ARG_476	NH2	H_ASP_31	OD1	3.839
4LSS	H_ARG_61	NH2	G_GLU_466	OE1	3.951
4LSS	H_ARG_71	NH1	G_ASP_368	OD1	3.719
4LSS	H_ARG_71	NH1	G_ASP_368	OD2	3.126
4LSS	H_ARG_71	NH2	G_ASP_368	OD1	3.278
4LSS	H_LYS_209	NZ	L_GLU_125	OE1	3.429
4LSS	H_LYS_209	NZ	L_GLU_125	OE2	3.562

Table 1359: Interfacial 4LSS-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4LST	G_LYS_357	NZ	L_GLU_1	OE1	2.783
4LST	H_ARG_61	NH1	G_GLU_466	OE1	3.812
4LST	H_ARG_61	NH2	G_ASP_461	OD1	2.947
4LST	H_ARG_71	NH1	G_ASP_368	OD1	3.527
4LST	H_ARG_71	NH1	G_ASP_368	OD2	2.632
4LST	H_ARG_71	NH2	G_ASP_368	OD1	2.939
4LST	H_ARG_71	NH2	G_ASP_368	OD2	3.624
4LST	H_LYS_209	NZ	L_GLU_125	OE2	3.921
4LST	H_LYS_214	NZ	L_ASP_124	OD1	3.010
4LST	H_LYS_214	NZ	L_ASP_124	OD2	3.020

Table 1360: Interfacial 4LST-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4LU5	H_ARG_98	NH2	B_ASP_168	OD2	3.392
4LU5	H_LYS_208	NZ	L_GLU_128	OE1	3.058
4LU5	H_LYS_208	NZ	L_GLU_128	OE2	3.445
4LU5	L_ARG_51	NH1	H_ASP_101	OD1	3.227
4LU5	L_ARG_51	NH2	H_ASP_101	OD1	2.925
4LU5	L_ARG_98	NH2	A_ASP_168	OD2	3.317
4LU5	M_ARG_51	NH1	I_ASP_101	OD2	3.086
4LU5	M_ARG_51	NH2	I_ASP_101	OD1	3.927
4LU5	M_ARG_51	NH2	I_ASP_101	OD2	2.770

Table 1361: Interfacial 4LU5-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4M1D	L_LYS_129	NZ	H_ASP_144	OD2	3.436
4M1D	H_LYS_143	NZ	L_GLU_124	OE2	2.547
4M1D	H_LYS_209	NZ	L_GLU_123	OE1	2.798
4M1D	H_LYS_209	NZ	L_GLU_123	OE2	2.782
4M1D	P_ARG_315	NH2	H_ASP_95	OD2	3.175
4M1D	I_LYS_209	NZ	M_GLU_123	OE1	3.060
4M1D	I_LYS_209	NZ	M_GLU_123	OE2	2.485
4M1D	Q_ARG_315	NH2	I_ASP_95	OD2	3.051

Table 1362: Interfacial 4M1D-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4M1G	H_LYS_213	NZ	L_GLU_124	OE2	2.837
4M1G	H_ARG_218	NH2	L_GLU_124	OE1	2.657
4M1G	H_ARG_218	NH2	L_GLU_124	OE2	3.648
4M1G	A_LYS_161	NZ	H_ASP_31	OD1	3.895

Table 1363: Interfacial 4M1G-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4M5Y	H.LYS_143	NZ	L.GLU_124	OE2	2.602
4M5Y	I.LYS_143	NZ	M.GLU_124	OE2	2.668

Table 1364: Interfacial 4M5Y-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4M7J	H_LYS_208	NZ	L_GLU_123	OE1	3.727
4M7J	H_LYS_208	NZ	L_GLU_123	OE2	3.593

Table 1365: Interfacial 4M7J-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4M7Z	B_LYS_208	NZ	C_GLU_123	OE1	3.318
4M7Z	B_LYS_208	NZ	C_GLU_123	OE2	3.881
4M7Z	H_LYS_208	NZ	L_GLU_123	OE1	3.192

Table 1366: Interfacial 4M7Z-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4M93	H_LYS_208	NZ	L_GLU_123	OE1	3.795
4M93	B_LYS_208	NZ	C_GLU_123	OE1	3.203

Table 1367: Interfacial 4M93-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4MA1	B.LYS_5	NZ	F_GLU_187	OE1	3.315
4MA1	B.LYS_208	NZ	C_GLU_123	OE1	3.857
4MA1	H.LYS_208	NZ	L_GLU_123	OE1	3.752

Table 1368: Interfacial 4MA1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4N0Y	H_LYS_209	NZ	L_GLU_123	OE1	2.939

Table 1369: Interfacial 4N0Y-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4N1H	A_LYS_111	NZ	C_GLU_202	OE1	3.097
4N1H	A_LYS_111	NZ	C_GLU_202	OE2	2.712
4N1H	A_HIS_112	ND1	C_GLU_205	OE2	3.407
4N1H	A_HIS_112	NE2	C_GLU_202	OE1	2.950
4N1H	A_HIS_112	NE2	C_GLU_205	OE2	3.971
4N1H	A_ARG_128	NH1	C_GLU_89	OE1	3.101
4N1H	A_LYS_150	NZ	B_ASP_115	OD2	2.748
4N1H	A_ARG_153	NH2	B_ASP_106	OD1	3.262
4N1H	A_ARG_153	NH2	B_ASP_106	OD2	3.262
4N1H	C_LYS_149	NZ	D_ASP_106	OD1	3.587
4N1H	C_LYS_149	NZ	D_ASP_106	OD2	3.735
4N1H	C_LYS_150	NZ	D_ASP_115	OD1	3.157
4N1H	C_ARG_153	NH2	D_ASP_106	OD1	2.772
4N1H	C_ARG_204	NH2	A_GLU_121	OE2	3.425

Table 1370: Interfacial 4N1H-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4NC1	A_ARG_133	NH1	D_ASP_115	OD2	3.145
4NC1	C_ARG_114	NH1	D_ASP_115	OD1	3.051
4NC1	C_ARG_114	NH1	D_ASP_115	OD2	3.046
4NC1	C_ARG_114	NH2	D_ASP_115	OD1	2.896
4NC1	B_ARG_133	NH2	C_ASP_115	OD2	3.404
4NC1	D_ARG_63	NH1	B_ASP_112	OD2	3.125
4NC1	D_ARG_114	NH1	C_ASP_115	OD1	2.908
4NC1	D_ARG_114	NH2	C_ASP_115	OD1	2.942

Table 1371: Interfacial 4NC1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4NGH	HLYS_228	NZ	LASP_122	OD1	3.887

Table 1372: Interfacial 4NGH-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4NIK	A_LYS_153	NZ	B_ASP_104	OD1	3.730
4NIK	A_LYS_153	NZ	B_ASP_104	OD2	2.794
4NIK	A_LYS_153	NZ	B_GLU_186	OE2	2.639

Table 1373: Interfacial 4NIK-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4NZR	H_LYS_60	NZ	L_GLU_1	OE1	3.647
4NZR	H_HIS_97	NE2	L_GLU_50	OE2	3.635
4NZR	H_HIS_98	NE2	L_GLU_50	OE1	2.875
4NZR	H_HIS_172	NE2	L ASP_167	OD2	3.398
4NZR	H_LYS_221	NZ	L_GLU_123	OE2	2.989
4NZR	M_LYS_114	NZ	L_GLU_17	OE1	3.119
4NZR	M_ARG_384	NH2	L_GLU_81	OE1	3.444
4NZR	M_ARG_384	NH2	L_GLU_81	OE2	3.239
4NZR	M_ARG_457	NH1	H ASP_31E	OD1	2.958
4NZR	M_ARG_457	NH1	H ASP_31E	OD2	3.096
4NZR	M_ARG_457	NH2	H ASP_31E	OD1	3.746
4NZR	M_ARG_457	NH2	H ASP_31E	OD2	2.554

Table 1374: Interfacial 4NZR-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID residue name residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4NZT	M_ARG_99	NH2	L_ASP_60	OD1	3.096
4NZT	M_ARG_384	NH2	L_GLU_81	OE1	3.193
4NZT	M_ARG_384	NH2	L_GLU_81	OE2	3.684
4NZT	H_LYS_145	NZ	L_GLU_124	OE2	2.541

Table 1375: Interfacial 4NZT-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4NZU	H.LYS_100E	NZ	L.ASP_50	OD1	3.991
4NZU	H.LYS_100E	NZ	L.ASP_50	OD2	2.752
4NZU	H.LYS_221	NZ	L.GLU_123	OE2	2.899

Table 1376: Interfacial 4NZU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4O5L	H.LYS_100I	NZ	L.ASP_93	OD1	2.723
4O5L	H.LYS_100I	NZ	L.ASP_93	OD2	3.455

Table 1377: Interfacial 4O5L-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4OLU	G_LYS_97	NZ	H_ASP_100B	OD1	3.513
4OLU	G_LYS_97	NZ	H_ASP_100B	OD2	2.385
4OLU	H_ARG_61	NH1	G_GLU_466	OE1	2.734
4OLU	H_ARG_71	NH1	G_ASP_368	OD1	3.753
4OLU	H_ARG_71	NH1	G_ASP_368	OD2	2.863
4OLU	H_ARG_71	NH2	G_ASP_368	OD1	3.092
4OLU	H_ARG_71	NH2	G_ASP_368	OD2	3.692
4OLU	H_LYS_209	NZ	L_GLU_125	OE1	3.927
4OLU	H_LYS_209	NZ	L_GLU_125	OE2	3.166

Table 1378: Interfacial 4OLU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4OLV	G_LYS_97	NZ	H_ASP_100B	OD1	3.067
4OLV	G_LYS_97	NZ	H_ASP_100B	OD2	2.942
4OLV	H_ARG_61	NH1	G_GLU_466	OE1	2.769
4OLV	H_ARG_71	NH1	G_ASP_368	OD1	3.700
4OLV	H_ARG_71	NH1	G_ASP_368	OD2	2.815
4OLV	H_ARG_71	NH2	G_ASP_368	OD1	3.136
4OLV	H_ARG_71	NH2	G_ASP_368	OD2	3.717
4OLV	H_LYS_209	NZ	L_GLU_125	OE1	3.978
4OLV	H_LYS_209	NZ	L_GLU_125	OE2	3.214

Table 1379: Interfacial 4OLV-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4OLW	G_LYS_97	NZ	H_ASP_100B	OD1	3.637
4OLW	G_LYS_97	NZ	H_ASP_100B	OD2	3.575
4OLW	H_ARG_61	NH1	G_GLU_466	OE1	2.598
4OLW	H_ARG_61	NH2	G_GLU_466	OE1	3.969
4OLW	H_ARG_71	NH1	G_ASP_368	OD1	3.570
4OLW	H_ARG_71	NH1	G_ASP_368	OD2	2.966
4OLW	H_ARG_71	NH2	G_ASP_368	OD1	3.028
4OLW	H_ARG_71	NH2	G_ASP_368	OD2	3.898
4OLW	H_ARG_100A	NH2	G_GLU_106	OE1	3.908
4OLW	H_LYS_209	NZ	L_GLU_125	OE1	2.861
4OLW	H_LYS_209	NZ	L_GLU_125	OE2	2.764
4OLW	H_LYS_214	NZ	L_ASP_124	OD1	3.031
4OLW	H_LYS_214	NZ	L_ASP_124	OD2	3.691

Table 1380: Interfacial 4OLW-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4OLX	G_LYS_97	NZ	H_ASP_100B	OD1	3.339
4OLX	G_LYS_97	NZ	H_ASP_100B	OD2	2.904
4OLX	H_ARG_61	NH1	G_GLU_466	OE1	2.655
4OLX	H_ARG_71	NH1	G_ASP_368	OD1	3.883
4OLX	H_ARG_71	NH1	G_ASP_368	OD2	2.896
4OLX	H_ARG_71	NH2	G_ASP_368	OD1	3.066
4OLX	H_ARG_71	NH2	G_ASP_368	OD2	3.572
4OLX	H_ARG_100A	NH2	G_GLU_106	OE1	3.646
4OLX	H_LYS_209	NZ	L_GLU_125	OE2	3.132

Table 1381: Interfacial 4OLX-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4OLY	G_LYS_97	NZ	H_ASP_100B	OD1	3.240
4OLY	G_LYS_97	NZ	H_ASP_100B	OD2	2.829
4OLY	H_ARG_61	NH1	G_GLU_466	OE1	2.641
4OLY	H_ARG_71	NH1	G_ASP_368	OD1	3.538
4OLY	H_ARG_71	NH1	G_ASP_368	OD2	2.816
4OLY	H_ARG_71	NH2	G_ASP_368	OD1	3.002
4OLY	H_ARG_71	NH2	G_ASP_368	OD2	3.765
4OLY	H_LYS_209	NZ	L_GLU_125	OE1	3.888
4OLY	H_LYS_209	NZ	L_GLU_125	OE2	3.336

Table 1382: Interfacial 4OLY-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4OLZ	G_LYS_97	NZ	H_ASP_100B	OD1	3.552
4OLZ	G_LYS_97	NZ	H_ASP_100B	OD2	3.545
4OLZ	H_ARG_61	NH1	G_GLU_466	OE1	2.620
4OLZ	H_ARG_71	NH1	G_ASP_368	OD1	3.472
4OLZ	H_ARG_71	NH1	G_ASP_368	OD2	2.715
4OLZ	H_ARG_71	NH2	G_ASP_368	OD1	2.877
4OLZ	H_ARG_71	NH2	G_ASP_368	OD2	3.685
4OLZ	H_LYS_209	NZ	L_GLU_125	OE1	3.703
4OLZ	H_LYS_209	NZ	L_GLU_125	OE2	3.063
4OLZ	H_LYS_214	NZ	L_ASP_124	OD1	3.528
4OLZ	H_LYS_214	NZ	L_ASP_124	OD2	3.896

Table 1383: Interfacial 4OLZ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4OM0	G_LYS_97	NZ	H_ASP_100B	OD1	3.843
4OM0	G_LYS_97	NZ	H_ASP_100B	OD2	3.296
4OM0	H_ARG_61	NH1	G_GLU_466	OE1	2.871
4OM0	H_ARG_71	NH1	G_ASP_368	OD1	3.724
4OM0	H_ARG_71	NH1	G_ASP_368	OD2	2.771
4OM0	H_ARG_71	NH2	G_ASP_368	OD1	3.189
4OM0	H_ARG_71	NH2	G_ASP_368	OD2	3.713
4OM0	H_LYS_209	NZ	L_GLU_125	OE2	3.121

Table 1384: Interfacial 4OM0-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4OM1	G_LYS_97	NZ	H_ASP_100B	OD1	3.927
4OM1	G_LYS_97	NZ	H_ASP_100B	OD2	3.635
4OM1	G_LYS_357	NZ	L_GLU_1	OE2	3.763
4OM1	H_ARG_71	NH1	G_ASP_368	OD1	3.565
4OM1	H_ARG_71	NH1	G_ASP_368	OD2	2.752
4OM1	H_ARG_71	NH2	G_ASP_368	OD1	3.031
4OM1	H_ARG_71	NH2	G_ASP_368	OD2	3.734
4OM1	H_LYS_209	NZ	L_GLU_125	OE1	3.639
4OM1	H_LYS_209	NZ	L_GLU_125	OE2	3.008

Table 1385: Interfacial 4OM1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4OT1	H_LYS_161	NZ	L_GLU_127	OE2	2.572
4OT1	H_LYS_227	NZ	L_GLU_126	OE1	2.521
4OT1	H_LYS_227	NZ	L_GLU_126	OE2	3.241
4OT1	L_LYS_67	NZ	A_GLU_361	OE2	3.026

Table 1386: Interfacial 4OT1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4P9H	C_ARG_59	NH1	G_ASP_368	OD1	2.832
4P9H	C_ARG_59	NH1	G_ASP_368	OD2	3.395
4P9H	C_ARG_59	NH2	G_ASP_368	OD1	3.561
4P9H	C_ARG_59	NH2	G_ASP_368	OD2	2.514
4P9H	H_HIS_61	NE2	L_ASP_1	OD2	3.817

Table 1387: Interfacial 4P9H-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4PTT	A_ARG_91	NH2	B_GLU_95	OE1	3.477
4PTT	A_ARG_91	NH2	B_GLU_95	OE2	3.208
4PTT	B_LYS_209	NZ	A_GLU_123	OE2	3.476

Table 1388: Interfacial 4PTT-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4PTU	A_ARG_91	NH2	B_GLU_95	OE1	3.438
4PTU	A_ARG_91	NH2	B_GLU_95	OE2	3.334
4PTU	B_LYS_209	NZ	A_GLU_123	OE1	3.628

Table 1389: Interfacial 4PTU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4Q6I	A_LYS_49	NZ	B_ASP_100A	OD1	2.964
4Q6I	B_LYS_208	NZ	A_GLU_123	OE2	2.822
4Q6I	C_LYS_50	NZ	L_GLU_93	OE2	2.549
4Q6I	C_LYS_181	NZ	G_GLU_56	OE1	2.499
4Q6I	D_LYS_49	NZ	E_ASP_100A	OD1	3.008
4Q6I	E_LYS_208	NZ	D_GLU_123	OE2	3.047
4Q6I	F_LYS_49	NZ	G_ASP_100A	OD1	3.146
4Q6I	G_LYS_208	NZ	F_GLU_123	OE2	3.409
4Q6I	H_LYS_208	NZ	L_GLU_123	OE2	3.045
4Q6I	I_LYS_50	NZ	F_GLU_93	OE2	2.473
4Q6I	I_LYS_181	NZ	H_GLU_56	OE1	3.345
4Q6I	J_LYS_50	NZ	D_GLU_93	OE2	2.666
4Q6I	K_LYS_50	NZ	A_GLU_93	OE2	2.835
4Q6I	L_LYS_49	NZ	H_ASP_100A	OD1	3.063

Table 1390: Interfacial 4Q6I-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4Q9B	A_ARG_309	NH1	B_GLU_255	OE1	3.484
4Q9B	A_ARG_309	NH1	B_GLU_255	OE2	2.912
4Q9B	A_ARG_309	NH2	B_GLU_255	OE2	3.212
4Q9B	B_ARG_309	NH1	A_GLU_255	OE1	3.145
4Q9B	B_ARG_309	NH1	A_GLU_255	OE2	2.858

Table 1391: Interfacial 4Q9B-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4QEX	A_LYS_341	NZ	H_ASP_53	OD1	3.875
4QEX	A_ARG_422	NH2	H_ASP_97	OD2	3.116

Table 1392: Interfacial 4QEX-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4QHU	B_LYS_145	NZ	A_GLU_126	OE2	2.821
4QHU	C_HIS_29	ND1	D_GLU_113	OE1	3.672
4QHU	C_ARG_31	NH1	D_GLU_113	OE2	3.297
4QHU	C_ARG_31	NH2	D_GLU_113	OE1	3.241
4QHU	C_ARG_31	NH2	D_GLU_113	OE2	3.844
4QHU	C_ARG_39	NH1	L_ASP_52	OD1	3.835
4QHU	C_ARG_39	NH1	L_ASP_52	OD2	2.646
4QHU	C_ARG_55	NH1	L_ASP_49	OD1	2.860
4QHU	C_ARG_55	NH1	L_ASP_49	OD2	3.543

Table 1393: Interfacial 4QHU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4QTI	H_LYS_217	NZ	L_GLU_123	OE2	2.684
4QTI	U_ARG_58	NH2	H_ASP_103	OD2	2.819
4QTI	U_ARG_89	NH1	H_ASP_99	OD2	3.048
4QTI	U_ARG_91	NH1	H_ASP_99	OD1	2.759
4QTI	U_ARG_91	NH1	H_ASP_99	OD2	2.751
4QTI	U_ARG_91	NH2	H_ASP_99	OD2	3.786
4QTI	U_ARG_116	NH1	H_ASP_103	OD2	3.777
4QTI	U_ARG_116	NH2	H_ASP_103	OD1	3.889

Table 1394: Interfacial 4QTI-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4QXG	H_LYS_213	NZ	L_GLU_124	OE2	3.477

Table 1395: Interfacial 4QXG-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4R2G	F_LYS_29	NZ	E_ASP_279	OD2	2.979
4R2G	F_ARG_59	NH1	E_ASP_368	OD1	2.950
4R2G	F_ARG_59	NH1	E_ASP_368	OD2	2.577
4R2G	F_ARG_59	NH2	E_ASP_368	OD2	3.352
4R2G	Q_ARG_100	NH2	P_ASP_66A	OD2	2.815
4R2G	Q_LYS_227	NZ	P_GLU_124	OE2	3.083
4R2G	B_LYS_29	NZ	O_ASP_279	OD2	3.448
4R2G	B_ARG_59	NH1	O_ASP_368	OD1	2.838
4R2G	B_ARG_59	NH1	O_ASP_368	OD2	3.428
4R2G	B_ARG_59	NH2	O_ASP_368	OD1	3.471
4R2G	B_ARG_59	NH2	O_ASP_368	OD2	2.776
4R2G	D_ARG_100	NH2	C_ASP_66A	OD2	3.131
4R2G	D_LYS_227	NZ	C_GLU_124	OE1	3.473
4R2G	D_LYS_227	NZ	C_GLU_124	OE2	3.405
4R2G	H_LYS_29	NZ	K_ASP_279	OD1	2.934
4R2G	H_ARG_59	NH1	K_ASP_368	OD1	2.502
4R2G	H_ARG_59	NH1	K_ASP_368	OD2	3.259
4R2G	J_ARG_100	NH2	L_ASP_66A	OD2	3.189
4R2G	J_LYS_161	NZ	L_GLU_125	OE2	3.537
4R2G	L_LYS_29	NZ	A_ASP_279	OD1	3.450
4R2G	L_ARG_59	NH1	A_ASP_368	OD1	2.642
4R2G	L_ARG_59	NH1	A_ASP_368	OD2	2.825
4R2G	L_ARG_59	NH2	A_ASP_368	OD1	3.793
4R2G	L_ARG_59	NH2	A_ASP_368	OD2	2.422
4R2G	N_ARG_100	NH2	M_ASP_66A	OD2	3.592
4R2G	N_LYS_161	NZ	M_GLU_125	OE2	2.706
4R2G	O_ARG_327	NH1	D_GLU_100I	OE2	3.858
4R2G	A_ARG_327	NH1	N_GLU_100I	OE1	3.235

Table 1396: Interfacial 4R2G-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4R4H	B_LYS_29	NZ	A_ASP_279	OD1	2.795
4R4H	B_ARG_59	NH1	A_ASP_367	OD1	3.294
4R4H	B_ARG_59	NH1	A_ASP_367	OD2	3.409
4R4H	B_ARG_59	NH2	A_ASP_367	OD2	3.834
4R4H	H_LYS_52	NZ	A_ASP_78	OD1	3.615
4R4H	H_LYS_	NZ	L_ASP_	OD2	3.470

Table 1397: Interfacial 4R4H-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4R7D	A_LYS_214	NZ	B_GLU_123	OE1	3.736
4R7D	B_LYS_107	NZ	D_ASP_9	OD2	3.947
4R7D	D_LYS_18	NZ	B_ASP_70	OD2	3.792
4R7D	D_LYS_107	NZ	B_ASP_9	OD2	3.503
4R7D	E_LYS_214	NZ	F_GLU_123	OE1	3.862
4R7D	E_LYS_214	NZ	F_GLU_123	OE2	3.571
4R7D	I_HIS_169	NE2	J_ASP_167	OD1	3.970
4R7D	J_LYS_18	NZ	N_ASP_70	OD1	3.913
4R7D	J_ARG_24	NH2	N_GLU_17	OE1	3.275
4R7D	J_ARG_24	NH2	N_GLU_17	OE2	2.135
4R7D	K_HIS_169	NE2	L_ASP_167	OD2	3.666
4R7D	K_LYS_214	NZ	L_GLU_123	OE1	3.074
4R7D	L_LYS_49	NZ	K_ASP_100	OD2	3.591
4R7D	M_LYS_214	NZ	N_GLU_123	OE1	3.058
4R7D	M_LYS_214	NZ	N_GLU_123	OE2	2.866
4R7D	N_LYS_107	NZ	J_ASP_9	OD2	3.244
4R7D	O_LYS_214	NZ	P_GLU_123	OE1	2.454
4R7D	O_LYS_214	NZ	P_GLU_123	OE2	3.167

Table 1398: Interfacial 4R7D-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4R7N	A_LYS_214	NZ	B_GLU_123	OE1	3.674
4R7N	A_LYS_214	NZ	B_GLU_123	OE2	3.683
4R7N	B_ARG_24	NH2	J_GLU_17	OE1	3.625
4R7N	B_ARG_24	NH2	J_GLU_17	OE2	2.355
4R7N	B_LYS_107	NZ	J ASP_9	OD2	3.605
4R7N	C_LYS_214	NZ	D_GLU_123	OE1	2.537
4R7N	C_LYS_214	NZ	D_GLU_123	OE2	3.321
4R7N	D_ARG_24	NH2	F_GLU_17	OE1	3.787
4R7N	D_ARG_24	NH2	F_GLU_17	OE2	2.414
4R7N	D_LYS_107	NZ	F ASP_9	OD2	3.633
4R7N	E_HIS_169	NE2	F ASP_167	OD1	3.616
4R7N	E_HIS_169	NE2	F ASP_167	OD2	3.474
4R7N	E_LYS_214	NZ	F_GLU_123	OE2	3.072
4R7N	F_ARG_24	NH2	D_GLU_17	OE1	3.696
4R7N	F_ARG_24	NH2	D_GLU_17	OE2	2.325
4R7N	F_LYS_107	NZ	D ASP_9	OD2	3.641
4R7N	G_LYS_214	NZ	H_GLU_123	OE1	2.389
4R7N	G_LYS_214	NZ	H_GLU_123	OE2	3.440
4R7N	H_ARG_24	NH2	L_GLU_17	OE1	3.413
4R7N	H_ARG_24	NH2	L_GLU_17	OE2	2.312
4R7N	I_LYS_214	NZ	J_GLU_123	OE1	3.635
4R7N	I_LYS_214	NZ	J_GLU_123	OE2	2.942
4R7N	J_ARG_24	NH2	B_GLU_17	OE1	3.555
4R7N	J_ARG_24	NH2	B_GLU_17	OE2	2.304
4R7N	K_LYS_214	NZ	L_GLU_123	OE2	3.794
4R7N	L_ARG_24	NH2	H_GLU_17	OE1	3.531
4R7N	L_ARG_24	NH2	H_GLU_17	OE2	2.313
4R7N	N_ARG_24	NH2	P_GLU_17	OE1	3.814
4R7N	N_ARG_24	NH2	P_GLU_17	OE2	2.289
4R7N	N_LYS_107	NZ	P ASP_9	OD2	3.591
4R7N	O_HIS_169	NE2	P ASP_167	OD2	3.725
4R7N	P_ARG_24	NH2	N_GLU_17	OE1	3.525
4R7N	P_ARG_24	NH2	N_GLU_17	OE2	2.277
4R7N	Q_LYS_211	NZ	G ASP_213	OD2	3.009
4R7N	Q_LYS_214	NZ	R_GLU_123	OE1	3.438
4R7N	Q_LYS_214	NZ	R_GLU_123	OE2	3.002
4R7N	R_LYS_145	NZ	F ASP_93	OD2	3.627
4R7N	S_LYS_214	NZ	T_GLU_123	OE1	3.934
4R7N	S_LYS_214	NZ	T_GLU_123	OE2	3.931

Table 1399: Interfacial 4R7N-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4R9Y	H_LYS_214	NZ	L_GLU_148	OE2	2.745
4R9Y	N_LYS_	NZ	M_GLU_	OE2	3.272

Table 1400: Interfacial 4R9Y-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4RAU	A.LYS_95	NZ	C.ASP_7	OD1	3.997
4RAU	A.LYS_95	NZ	C.ASP_7	OD2	3.077
4RAU	D.LYS_95	NZ	F.ASP_7	OD1	3.860
4RAU	G.LYS_95	NZ	I.ASP_7	OD1	3.805
4RAU	G.LYS_95	NZ	I.ASP_7	OD2	2.755
4RAU	K.LYS_216	NZ	J.GLU_125	OE2	3.935
4RAU	O.ARG_49	NH2	X.ASP_7	OD1	2.993
4RAU	O.ARG_49	NH2	X.ASP_7	OD2	3.647
4RAU	P.LYS_	NZ	R.ASP_	OD1	3.104
4RAU	V.LYS_95	NZ	X.ASP_7	OD1	3.972
4RAU	V.LYS_95	NZ	X.ASP_7	OD2	3.050
4RAU	X.ARG_49	NH2	O.ASP_7	OD1	2.791
4RAU	X.ARG_49	NH2	O.ASP_7	OD2	3.699

Table 1401: Interfacial 4RAU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4RRP	G_LYS_214	NZ	A_ASP_122	OD1	3.271
4RRP	G_LYS_214	NZ	A_ASP_122	OD2	3.253
4RRP	B_ARG_61	NH1	Q_GLU_32	OE1	3.055
4RRP	B_ARG_61	NH1	Q_GLU_32	OE2	3.683
4RRP	B_ARG_61	NH2	Q_GLU_32	OE2	3.637
4RRP	J_LYS_214	NZ	D_ASP_122	OD1	3.176
4RRP	J_LYS_214	NZ	D_ASP_122	OD2	2.924
4RRP	L_HIS_164	NE2	F_ASP_167	OD1	3.853
4RRP	L_LYS_214	NZ	F_ASP_122	OD2	3.247
4RRP	M_LYS_10	NZ	N_GLU_29	OE1	3.876
4RRP	M_LYS_10	NZ	N_GLU_29	OE2	3.237
4RRP	N_LYS_10	NZ	M_GLU_29	OE1	3.319
4RRP	N_LYS_10	NZ	M_GLU_29	OE2	2.389
4RRP	O_ARG_123	NH1	Q_ASP_54	OD1	3.356
4RRP	O_ARG_123	NH1	Q_ASP_54	OD2	3.533
4RRP	O_ARG_123	NH2	Q_ASP_54	OD2	3.134
4RRP	O_HIS_134	NE2	N_GLU_121	OE1	3.780
4RRP	O_HIS_134	NE2	N_GLU_121	OE2	3.192
4RRP	O_ARG_145	NH2	Q_GLU_116	OE1	3.921
4RRP	O_ARG_145	NH2	Q_GLU_116	OE2	3.324
4RRP	Q_ARG_145	NH1	O_GLU_116	OE2	3.050
4RRP	Q_ARG_145	NH2	O_GLU_116	OE2	3.244

Table 1402: Interfacial 4RRP-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4TRP	H_LYS_208	NZ	L_GLU_129	OE2	3.281

Table 1403: Interfacial 4TRP-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4TUK	H_LYS_208	NZ	L_GLU_129	OE2	3.061

Table 1404: Interfacial 4TUK-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4TUL	H_LYS_208	NZ	L_GLU_129	OE1	3.059
4TUL	H_LYS_208	NZ	L_GLU_129	OE2	2.741

Table 1405: Interfacial 4TUL-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4TUO	A_LYS_208	NZ	B_GLU_129	OE1	3.043
4TUO	B_LYS_153	NZ	C_GLU_10	OE2	3.051
4TUO	C_LYS_208	NZ	D_GLU_129	OE1	2.720
4TUO	C_LYS_208	NZ	D_GLU_129	OE2	3.136

Table 1406: Interfacial 4TUO-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4U0Q	A_HIS_495	NE2	D_GLU_31	OE1	3.802
4U0Q	A_HIS_495	NE2	D_GLU_31	OE2	2.620
4U0Q	A_HIS_496	ND1	D_GLU_31	OE1	3.680
4U0Q	B_HIS_170	ND1	D_GLU_172	OE1	2.788
4U0Q	C_HIS_495	ND1	B_ASP_32	OD2	3.411
4U0Q	D_HIS_170	ND1	B_GLU_172	OE1	2.879
4U0Q	D_HIS_170	ND1	B_GLU_172	OE2	2.959
4U0Q	D_LYS_191	NZ	C_GLU_362	OE2	3.108

Table 1407: Interfacial 4U0Q-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4U3X	A_HIS_106	NE2	B_GLU_35	OE1	2.597
4U3X	A_HIS_106	NE2	B_GLU_35	OE2	3.650
4U3X	B_ARG_61	NH1	A_ASP_33	OD2	2.723
4U3X	B_ARG_61	NH2	A_ASP_33	OD2	2.983
4U3X	B_ARG_112	NH2	A_ASP_109	OD1	3.763
4U3X	B_ARG_112	NH2	A_ASP_109	OD2	3.035
4U3X	C_HIS_106	NE2	D_GLU_35	OE1	2.720
4U3X	C_HIS_106	NE2	D_GLU_35	OE2	3.669
4U3X	D_ARG_61	NH1	C_ASP_33	OD2	3.116
4U3X	D_ARG_61	NH2	C_ASP_33	OD2	3.400
4U3X	D_ARG_112	NH2	C_ASP_109	OD2	3.567

Table 1408: Interfacial 4U3X-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4U6G	H.LYS_143	NZ	L.GLU_125	OE2	3.603
4U6G	H.LYS_209	NZ	L.GLU_124	OE1	2.829
4U6G	H.LYS_209	NZ	L.GLU_124	OE2	2.866
4U6G	L.HIS_31	ND1	H.GLU_100I	OE2	3.196
4U6G	L.ARG_91	NH1	B.GLU_81	OE1	3.298
4U6G	L.ARG_91	NH1	H.GLU_100J	OE1	3.679
4U6G	L.ARG_91	NH1	H.GLU_100J	OE2	3.478
4U6G	L.ARG_91	NH2	H.GLU_100J	OE2	3.428
4U6G	A.LYS_143	NZ	B.GLU_125	OE2	3.217
4U6G	A.LYS_201	NZ	H.ASP_30	OD1	3.983
4U6G	A.LYS_209	NZ	B.GLU_124	OE1	2.769
4U6G	A.LYS_209	NZ	B.GLU_124	OE2	3.063
4U6G	B.HIS_31	ND1	A.GLU_100I	OE2	3.102
4U6G	B.ARG_91	NH1	A.GLU_100J	OE1	3.587
4U6G	B.ARG_91	NH1	A.GLU_100J	OE2	3.310
4U6G	B.ARG_91	NH2	A.GLU_100J	OE2	3.407

Table 1409: Interfacial 4U6G-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4U6V	H_ARG_99	NH2	L_GLU_55	OE1	2.660
4U6V	H_ARG_99	NH2	L_GLU_55	OE2	2.823
4U6V	H_HIS_105	NE2	A_ASP_183	OD1	3.150
4U6V	H_HIS_105	NE2	A_ASP_183	OD2	3.236
4U6V	H_LYS_218	NZ	L_GLU_122	OE1	2.258
4U6V	H_LYS_218	NZ	L_GLU_122	OE2	3.923
4U6V	A_ARG_200	NH1	H_ASP_56	OD1	3.722
4U6V	A_ARG_200	NH1	H_ASP_56	OD2	3.481
4U6V	A_LYS_266	NZ	L_ASP_93	OD1	2.981
4U6V	K_ARG_99	NH2	M_GLU_55	OE1	2.606
4U6V	K_ARG_99	NH2	M_GLU_55	OE2	2.857
4U6V	K_HIS_105	NE2	B_ASP_183	OD1	2.992
4U6V	K_HIS_105	NE2	B_ASP_183	OD2	3.142
4U6V	K_LYS_218	NZ	M_GLU_122	OE1	2.653
4U6V	B_ARG_200	NH1	K_ASP_56	OD1	3.809
4U6V	B_ARG_200	NH1	K_ASP_56	OD2	3.557
4U6V	B_LYS_266	NZ	M_ASP_93	OD1	3.145

Table 1410: Interfacial 4U6V-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4UAO	A_ARG_317	NH1	C_GLU_100B	OE2	3.537
4UAO	A_ARG_317	NH2	C_GLU_100B	OE1	3.794
4UAO	A_ARG_317	NH2	C_GLU_100B	OE2	2.800
4UAO	C_ARG_56	NH1	A_GLU_81	OE2	2.819
4UAO	C_ARG_56	NH2	A_ASP_174	OD1	3.129
4UAO	C_ARG_56	NH2	A_ASP_174	OD2	2.857
4UAO	C_ARG_95	NH2	A_GLU_173	OE2	3.027

Table 1411: Interfacial 4UAO-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4UV6	B_ARG_180	NH2	A_GLU_396	OE2	2.784
4UV6	B_ARG_313	NH2	A_GLU_60	OE1	2.768

Table 1412: Interfacial 4UV6-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4WEU	D_LYS_887	NZ	A_GLU_145	OE1	3.143
4WEU	A_ARG_96	NH1	B_GLU_94	OE1	3.636
4WEU	A_ARG_96	NH1	B_GLU_94	OE2	3.058
4WEU	A_ARG_96	NH2	B_GLU_94	OE1	2.949
4WEU	A_ARG_96	NH2	B_GLU_94	OE2	3.852
4WEU	A_ARG_136	NH1	D_GLU_889	OE1	2.898
4WEU	B_ARG_96	NH1	A_GLU_94	OE1	3.754
4WEU	B_ARG_96	NH1	A_GLU_94	OE2	2.795
4WEU	B_ARG_96	NH2	A_GLU_94	OE1	2.707
4WEU	B_ARG_96	NH2	A_GLU_94	OE2	3.344

Table 1413: Interfacial 4WEU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4WHT	A_LYS_207	NZ	B_GLU_127	OE1	2.607
4WHT	A_LYS_207	NZ	B_GLU_127	OE2	3.670
4WHT	C_LYS_207	NZ	D_GLU_127	OE1	3.293
4WHT	E_LYS_207	NZ	F_GLU_127	OE1	3.118
4WHT	G_LYS_204	NZ	U_ASP_206	OD2	3.854
4WHT	I_LYS_65	NZ	R_GLU_84	OE2	3.044
4WHT	I_LYS_207	NZ	J_GLU_127	OE1	2.774
4WHT	I_LYS_207	NZ	J_GLU_127	OE2	3.846
4WHT	K_LYS_207	NZ	L_GLU_127	OE1	2.813
4WHT	M_LYS_204	NZ	K_ASP_206	OD2	2.701
4WHT	M_LYS_207	NZ	N_GLU_127	OE1	3.186
4WHT	O_LYS_207	NZ	P_GLU_127	OE1	3.812
4WHT	O_LYS_207	NZ	P_GLU_127	OE2	2.822
4WHT	Q_LYS_207	NZ	R_GLU_127	OE1	2.572
4WHT	Q_LYS_207	NZ	R_GLU_127	OE2	3.627
4WHT	S_LYS_207	NZ	T_GLU_127	OE1	3.197
4WHT	U_LYS_204	NZ	G_ASP_206	OD2	3.954
4WHT	U_LYS_207	NZ	V_GLU_127	OE1	3.622
4WHT	X_LYS_207	NZ	Y_GLU_127	OE2	2.718
4WHT	B_LYS_111	NZ	J_GLU_73	OE2	3.842
4WHT	D_LYS_151	NZ	L_GLU_191	OE2	3.259
4WHT	D_LYS_187	NZ	I_GLU_114	OE1	3.576
4WHT	D_LYS_187	NZ	I_GLU_114	OE2	3.498
4WHT	H_ARG_66	NH1	Q_ASP_62	OD2	3.949
4WHT	N_LYS_187	NZ	K_GLU_114	OE1	3.270
4WHT	N_LYS_187	NZ	K_GLU_114	OE2	3.221
4WHT	V_LYS_187	NZ	G_GLU_114	OE1	3.353
4WHT	V_LYS_187	NZ	G_GLU_114	OE2	3.189

Table 1414: Interfacial 4WHT-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4WHY	K_LYS_204	NZ	G_ASP_206	OD2	3.182
4WHY	K_LYS_207	NZ	L_GLU_127	OE1	3.798
4WHY	L_LYS_187	NZ	G_GLU_114	OE1	3.275
4WHY	L_LYS_187	NZ	G_GLU_114	OE2	3.634
4WHY	M_LYS_207	NZ	N_GLU_127	OE1	3.795
4WHY	N_LYS_187	NZ	L_GLU_114	OE1	2.397
4WHY	N_LYS_187	NZ	L_GLU_114	OE2	3.551

Table 1415: Interfacial 4WHY-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4WUU	A_ARG_35	NH1	B_ASP_53	OD1	3.025
4WUU	A_ARG_35	NH1	B_ASP_53	OD2	3.278
4WUU	A_ARG_48	NH2	B_ASP_53	OD1	3.607
4WUU	A_ARG_48	NH2	B_ASP_53	OD2	3.368
4WUU	E_ARG_50	NH1	A_GLU_166	OE2	3.181
4WUU	E_ARG_50	NH2	A_GLU_166	OE1	3.839
4WUU	E_ARG_50	NH2	A_GLU_166	OE2	2.671

Table 1416: Interfacial 4WUU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4XVJ	A_ARG_1	NH2	L_ASP_51	OD1	3.482

Table 1417: Interfacial 4XVJ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4YHP	P_LYS_4	NZ	H_ASP_62	OD1	3.318
4YHP	A_LYS_222	NZ	B_ASP_123	OD2	3.677
4YHP	Q_LYS_4	NZ	C_ASP_62	OD1	3.313
4YHP	C_LYS_222	NZ	D_ASP_123	OD1	3.776
4YHP	C_LYS_222	NZ	D_ASP_123	OD2	3.442
4YHP	D_HIS_190	NE2	L_GLU_59	OE2	2.478
4YHP	E_LYS_222	NZ	F_ASP_123	OD1	3.304
4YHP	E_LYS_222	NZ	F_ASP_123	OD2	2.842

Table 1418: Interfacial 4YHP-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4YHZ	H_ARG_102	NH1	L_ASP_52	OD2	3.952

Table 1419: Interfacial 4YHZ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4YNY	A_LYS_166	NZ	B_GLU_146	OE2	2.702
4YNY	C_LYS_166	NZ	D_GLU_146	OE2	2.776

Table 1420: Interfacial 4YNY-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4YO0	A.LYS_76	NZ	E.ASP_11	OD1	3.807
4YO0	A.LYS_76	NZ	E.ASP_11	OD2	3.094
4YO0	A.LYS_166	NZ	B.GLU_146	OE2	2.816
4YO0	C.LYS_76	NZ	F.GLU_10	OE2	3.111
4YO0	C.LYS_76	NZ	F.ASP_11	OD1	3.515
4YO0	C.LYS_76	NZ	F.ASP_11	OD2	2.782
4YO0	C.LYS_166	NZ	D.GLU_146	OE2	2.660
4YO0	C.LYS_231	NZ	D.GLU_145	OE1	3.828
4YO0	C.LYS_231	NZ	D.GLU_145	OE2	3.815

Table 1421: Interfacial 4YO0-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4Z0X	C_LYS_446	NZ	A_ASP_50	OD1	3.873
4Z0X	C_LYS_446	NZ	A_ASP_50	OD2	2.440

Table 1422: Interfacial 4Z0X-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4ZD3	H_HIS_108	NE2	L_GLU_68	OE1	2.549
4ZD3	H_HIS_108	NE2	L_GLU_68	OE2	3.986
4ZD3	H_LYS_224	NZ	L_GLU_143	OE2	2.997

Table 1423: Interfacial 4ZD3-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4ZFF	A_LYS_209	NZ	B_GLU_123	OE1	3.193
4ZFF	C_ARG_23	NH1	D_GLU_30	OE1	3.414
4ZFF	H_LYS_209	NZ	L_GLU_123	OE1	3.731

Table 1424: Interfacial 4ZFF-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4ZFG	H_LYS_209	NZ	L_GLU_123	OE1	2.808

Table 1425: Interfacial 4ZFG-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
4ZFO	F_HIS_19	NE2	A_GLU_50	OE1	2.994
4ZFO	F_HIS_19	NE2	A_GLU_50	OE2	3.320
4ZFO	H_ARG_39	NH1	L_GLU_85	OE2	3.425
4ZFO	H_ARG_39	NH2	L_GLU_85	OE1	3.703
4ZFO	H_ARG_39	NH2	L_GLU_85	OE2	2.644
4ZFO	H_LYS_216	NZ	L_GLU_123	OE2	3.666
4ZFO	A_ARG_39	NH1	B_GLU_85	OE1	3.845
4ZFO	A_ARG_39	NH2	B_GLU_85	OE1	2.855
4ZFO	A_ARG_39	NH2	B_GLU_85	OE2	3.746
4ZFO	K_HIS_19	NE2	H_GLU_50	OE1	2.755
4ZFO	K_HIS_19	NE2	H_GLU_50	OE2	3.392

Table 1426: Interfacial 4ZFO-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5A7X	A_ARG_419	NH1	D_GLU_100B	OE1	3.000
5A7X	A_ARG_419	NH1	D_GLU_100B	OE2	3.675
5A7X	A_ARG_419	NH2	D_GLU_99	OE1	2.292
5A7X	A_ARG_419	NH2	D_GLU_100B	OE2	3.969
5A7X	B_LYS_35	NZ	A_ASP_457	OD1	3.741
5A7X	B_ARG_59	NH1	A_ASP_368	OD1	3.154
5A7X	B_ARG_59	NH1	A_ASP_368	OD2	3.344
5A7X	B_ARG_59	NH2	A_ASP_368	OD1	2.976
5A7X	B_ARG_59	NH2	A_ASP_368	OD2	2.433
5A7X	D_HIS_164	NE2	C_ASP_167	OD1	3.880
5A7X	D_HIS_164	NE2	C_ASP_167	OD2	2.506
5A7X	D_LYS_209	NZ	C_GLU_123	OE1	3.513
5A7X	D_LYS_209	NZ	C_GLU_123	OE2	3.583
5A7X	E_ARG_419	NH1	H_GLU_100B	OE1	2.998
5A7X	E_ARG_419	NH1	H_GLU_100B	OE2	3.674
5A7X	E_ARG_419	NH2	H_GLU_99	OE1	2.293
5A7X	E_ARG_419	NH2	H_GLU_100B	OE2	3.968
5A7X	F_LYS_35	NZ	E_ASP_457	OD1	3.741
5A7X	F_ARG_59	NH1	E_ASP_368	OD1	3.154
5A7X	F_ARG_59	NH1	E_ASP_368	OD2	3.343
5A7X	F_ARG_59	NH2	E_ASP_368	OD1	2.977
5A7X	F_ARG_59	NH2	E_ASP_368	OD2	2.434
5A7X	H_HIS_164	NE2	G_ASP_167	OD1	3.880
5A7X	H_HIS_164	NE2	G_ASP_167	OD2	2.505
5A7X	H_LYS_209	NZ	G_GLU_123	OE1	3.512
5A7X	H_LYS_209	NZ	G_GLU_123	OE2	3.584
5A7X	I_ARG_419	NH1	L_GLU_100B	OE1	2.999
5A7X	I_ARG_419	NH1	L_GLU_100B	OE2	3.675
5A7X	I_ARG_419	NH2	L_GLU_99	OE1	2.293
5A7X	I_ARG_419	NH2	L_GLU_100B	OE2	3.968
5A7X	J_LYS_35	NZ	I_ASP_457	OD1	3.740
5A7X	J_ARG_59	NH1	I_ASP_368	OD1	3.154
5A7X	J_ARG_59	NH1	I_ASP_368	OD2	3.344
5A7X	J_ARG_59	NH2	I_ASP_368	OD1	2.976
5A7X	J_ARG_59	NH2	I_ASP_368	OD2	2.433
5A7X	L_HIS_164	NE2	K_ASP_167	OD1	3.880
5A7X	L_HIS_164	NE2	K_ASP_167	OD2	2.504
5A7X	L_LYS_209	NZ	K_GLU_123	OE1	3.514
5A7X	L_LYS_209	NZ	K_GLU_123	OE2	3.585

Table 1427: Interfacial 5A7X-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5A8H	A_ARG_419	NH1	D_GLU_100B	OE1	2.999
5A8H	A_ARG_419	NH1	D_GLU_100B	OE2	3.674
5A8H	A_ARG_419	NH2	D_GLU_99	OE1	2.292
5A8H	A_ARG_419	NH2	D_GLU_100B	OE2	3.968
5A8H	B_LYS_35	NZ	A_ASP_457	OD1	3.740
5A8H	B_ARG_59	NH1	A_ASP_368	OD1	3.154
5A8H	B_ARG_59	NH1	A_ASP_368	OD2	3.342
5A8H	B_ARG_59	NH2	A_ASP_368	OD1	2.977
5A8H	B_ARG_59	NH2	A_ASP_368	OD2	2.433
5A8H	D_HIS_164	NE2	C_ASP_167	OD1	3.880
5A8H	D_HIS_164	NE2	C_ASP_167	OD2	2.505
5A8H	D_LYS_209	NZ	C_GLU_123	OE1	3.514
5A8H	D_LYS_209	NZ	C_GLU_123	OE2	3.584
5A8H	F_LYS_100	NZ	A_GLU_91	OE1	3.015
5A8H	F_LYS_100	NZ	A_GLU_91	OE2	3.536
5A8H	G_ARG_419	NH1	J_GLU_100B	OE1	2.998
5A8H	G_ARG_419	NH1	J_GLU_100B	OE2	3.675
5A8H	G_ARG_419	NH2	J_GLU_99	OE1	2.292
5A8H	G_ARG_419	NH2	J_GLU_100B	OE2	3.969
5A8H	H_LYS_35	NZ	G_ASP_457	OD1	3.741
5A8H	H_ARG_59	NH1	G_ASP_368	OD1	3.154
5A8H	H_ARG_59	NH1	G_ASP_368	OD2	3.343
5A8H	H_ARG_59	NH2	G_ASP_368	OD1	2.977
5A8H	H_ARG_59	NH2	G_ASP_368	OD2	2.433
5A8H	J_HIS_164	NE2	I_ASP_167	OD1	3.881
5A8H	J_HIS_164	NE2	I_ASP_167	OD2	2.505
5A8H	J_LYS_209	NZ	I_GLU_123	OE1	3.513
5A8H	J_LYS_209	NZ	I_GLU_123	OE2	3.584
5A8H	L_LYS_100	NZ	G_GLU_87	OE1	2.922
5A8H	L_LYS_100	NZ	G_GLU_87	OE2	3.552
5A8H	L_HIS_100E	NE2	G_GLU_91	OE2	3.049
5A8H	M_ARG_419	NH1	P_GLU_100B	OE1	2.999
5A8H	M_ARG_419	NH1	P_GLU_100B	OE2	3.675
5A8H	M_ARG_419	NH2	P_GLU_99	OE1	2.292
5A8H	M_ARG_419	NH2	P_GLU_100B	OE2	3.969
5A8H	N_LYS_35	NZ	M_ASP_457	OD1	3.741
5A8H	N_ARG_59	NH1	M_ASP_368	OD1	3.154
5A8H	N_ARG_59	NH1	M_ASP_368	OD2	3.343
5A8H	N_ARG_59	NH2	M_ASP_368	OD1	2.977
5A8H	N_ARG_59	NH2	M_ASP_368	OD2	2.433
5A8H	O_LYS_145	NZ	C_GLU_17	OE1	3.474
5A8H	O_LYS_145	NZ	C_GLU_17	OE2	2.123
5A8H	P_HIS_164	NE2	O_ASP_167	OD1	3.881
5A8H	P_HIS_164	NE2	O_ASP_167	OD2	2.505
5A8H	P_LYS_209	NZ	O_GLU_123	OE1	3.514
5A8H	P_LYS_209	NZ	O_GLU_123	OE2	3.584
5A8H	R_HIS_100E	ND1	M_GLU_87	OE2	2.709
5A8H	R_HIS_100E	NE2	M_GLU_87	OE2	3.097

Table 1428: Interfacial 5A8H-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5AZE	L_HIS_36	NE2	H_GLU_105	OE2	2.756
5AZE	H_LYS_137	NZ	L_ASP_143	OD2	2.939
5AZE	H_LYS_217	NZ	L_GLU_128	OE2	2.701

Table 1429: Interfacial 5AZE-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5BW7	A_LYS_370	NZ	B_GLU_357	OE2	3.993
5BW7	A_LYS_409	NZ	B_ASP_399	OD1	3.864
5BW7	A_LYS_409	NZ	B_ASP_399	OD2	2.990
5BW7	B_LYS_370	NZ	A_GLU_357	OE2	3.748
5BW7	B_LYS_409	NZ	A_ASP_399	OD1	3.328
5BW7	B_LYS_409	NZ	A_ASP_399	OD2	2.988
5BW7	C_LYS_120	NZ	A_ASP_265	OD2	2.730
5BW7	C_LYS_131	NZ	A_GLU_269	OE1	3.414
5BW7	C_LYS_131	NZ	A_GLU_269	OE2	2.642

Table 1430: Interfacial 5BW7-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5CMA	B_LYS_214	NZ	A_GLU_123	OE1	2.706
5CMA	B_LYS_214	NZ	A_GLU_123	OE2	3.531

Table 1431: Interfacial 5CMA-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5CP3	H_LYS_207	NZ	A_GLU_128	OE2	2.762

Table 1432: Interfacial 5CP3-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5CP7	B_LYS_207	NZ	C_GLU_128	OE2	3.335
5CP7	C_LYS_58	NZ	H_ASP_1	OD1	3.663
5CP7	C_LYS_58	NZ	H_ASP_1	OD2	3.316
5CP7	D_LYS_207	NZ	E_GLU_128	OE2	2.825
5CP7	F_HIS_163	ND1	G_ASP_172	OD2	3.652
5CP7	F_LYS_207	NZ	G_GLU_128	OE2	3.951
5CP7	H_LYS_207	NZ	A_GLU_128	OE2	3.290

Table 1433: Interfacial 5CP7-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5DFV	A_LYS_171	NZ	C_ASP_288	OD1	3.582
5DFV	A_LYS_171	NZ	C_ASP_288	OD2	2.737
5DFV	A_LYS_171	NZ	C_ASP_290	OD2	2.874
5DFV	B_LYS_171	NZ	E_ASP_288	OD1	3.695
5DFV	B_LYS_171	NZ	E_ASP_288	OD2	3.653
5DFV	B_LYS_171	NZ	E_ASP_290	OD2	2.646
5DFV	C_ARG_398	NH2	D_GLU_698	OE1	3.277
5DFV	E_ARG_398	NH1	F_GLU_698	OE2	3.319
5DFV	E_LYS_1094	NZ	F_GLU_2015	OE1	3.713
5DFV	E_ARG_1099	NH1	F_GLU_2105	OE2	3.679

Table 1434: Interfacial 5DFV-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5DFW	A_LYS_171	NZ	H_ASP_156	OD2	2.691
5DFW	A_LYS_171	NZ	H_ASP_253	OD1	2.751
5DFW	A_LYS_171	NZ	H_ASP_253	OD2	3.799
5DFW	H_ARG_251	NH2	A_ASP_138	OD1	3.392
5DFW	H_ARG_251	NH2	A_ASP_138	OD2	2.698
5DFW	H_LYS_292	NZ	A_ASP_138	OD1	3.884
5DFW	H_LYS_292	NZ	A_ASP_138	OD2	2.950
5DFW	H_LYS_292	NZ	A_ASP_139	OD1	3.019

Table 1435: Interfacial 5DFW-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5DMI	A_LYS_46	NZ	L_ASP_31	OD1	2.761
5DMI	A_LYS_46	NZ	L_ASP_31	OD2	3.234
5DMI	A_HIS_76	ND1	H_ASP_100A	OD2	3.977
5DMI	H_LYS_221	NZ	L_GLU_123	OE2	3.105

Table 1436: Interfacial 5DMI-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5DMJ	B_ARG_83	NH2	G_ASP_72	OD1	3.449
5DMJ	G_LYS_75	NZ	B_GLU_85	OE1	3.187

Table 1437: Interfacial 5DMJ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5DWU	H_ARG_52	NH1	A_ASP_107	OD1	3.435
5DWU	H_ARG_52	NH1	A_ASP_107	OD2	2.568
5DWU	H_ARG_52	NH2	A_ASP_107	OD1	2.685
5DWU	H_ARG_52	NH2	A_ASP_107	OD2	3.250

Table 1438: Interfacial 5DWU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5ERW	A_ARG_103	NH1	B_ASP_49	OD2	2.990
5ERW	A_LYS_214	NZ	B_GLU_122	OE1	2.490
5ERW	C_LYS_446	NZ	B_ASP_50	OD1	3.926
5ERW	C_LYS_446	NZ	B_ASP_50	OD2	2.398

Table 1439: Interfacial 5ERW-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5EZI	L_ARG_120	NH1	H_GLU_64	OE1	3.561
5EZI	L_ARG_120	NH1	H_GLU_64	OE2	2.826

Table 1440: Interfacial 5EZI-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5EZJ	A_LYS_228	NZ	B_GLU_147	OE1	3.274
5EZJ	B_ARG_120	NH1	A_GLU_64	OE1	3.637
5EZJ	B_ARG_120	NH1	A_GLU_64	OE2	2.843

Table 1441: Interfacial 5EZJ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5EZL	A_LYS_228	NZ	B_GLU_147	OE1	3.314
5EZL	B_ARG_120	NH1	A_GLU_64	OE1	3.901
5EZL	B_ARG_120	NH1	A_GLU_64	OE2	2.804
5EZL	H_LYS_228	NZ	L_GLU_147	OE2	3.445
5EZL	L_ARG_120	NH1	H_GLU_64	OE1	3.668
5EZL	L_ARG_120	NH1	H_GLU_64	OE2	2.626

Table 1442: Interfacial 5EZL-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5EZN	A_ARG_58	NH1	E_ASP_336	OD2	3.940
5EZN	A_ARG_58	NH2	E_ASP_336	OD2	2.479
5EZN	E_LYS_204	NZ	A_GLU_113	OE1	2.243
5EZN	E_LYS_204	NZ	A_GLU_113	OE2	3.142
5EZN	E_LYS_251	NZ	B_GLU_72	OE2	3.130
5EZN	B_ARG_135	NH1	G_GLU_206	OE2	3.927
5EZN	B_ARG_135	NH2	G_GLU_206	OE2	3.596
5EZN	G_LYS_204	NZ	B_GLU_112	OE1	2.749
5EZN	G_LYS_204	NZ	B_GLU_112	OE2	3.972
5EZN	G_LYS_204	NZ	B_GLU_113	OE2	3.260

Table 1443: Interfacial 5EZN-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5EZO	H_LYS_232	NZ	L_GLU_143	OE1	3.314
5EZO	H_LYS_232	NZ	L_GLU_143	OE2	2.456
5EZO	L_ARG_50	NH1	A_ASP_66	OD1	3.943
5EZO	L_ARG_50	NH1	A_ASP_66	OD2	3.721
5EZO	L_ARG_116	NH1	H_GLU_68	OE1	3.718
5EZO	L_ARG_116	NH1	H_GLU_68	OE2	2.774

Table 1444: Interfacial 5EZO-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5GGV	H_ARG_101	NH1	Y_GLU_97	OE2	3.572
5GGV	H_LYS_221	NZ	L_GLU_123	OE1	2.304
5GGV	H_LYS_221	NZ	L_GLU_123	OE2	3.975

Table 1445: Interfacial 5GGV-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5GKR	A_LYS_143	NZ	B_GLU_125	OE2	2.806
5GKR	A_LYS_209	NZ	B_GLU_124	OE1	2.825
5GKR	A_LYS_209	NZ	B_GLU_124	OE2	3.325
5GKR	B_LYS_130	NZ	A_ASP_144	OD2	3.639
5GKR	C_LYS_143	NZ	D_GLU_125	OE2	2.591
5GKR	C_LYS_209	NZ	D_GLU_124	OE1	2.486
5GKR	C_LYS_209	NZ	D_GLU_124	OE2	2.893
5GKR	D_LYS_130	NZ	C_ASP_144	OD2	3.574

Table 1446: Interfacial 5GKR-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5GKS	A_LYS_	NZ	B_GLU_124	OE1	3.518
5GKS	A_LYS_	NZ	B_GLU_124	OE2	2.790
5GKS	B_LYS_130	NZ	A_ASP_144	OD2	3.783
5GKS	C_LYS_	NZ	D_GLU_	OE1	3.455
5GKS	C_LYS_	NZ	D_GLU_	OE2	2.665

Table 1447: Interfacial 5GKS-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5HDQ	A_HIS_234	ND1	H_ASP_97	OD2	3.865
5HDQ	H_LYS_95	NZ	A_ASP_256	OD2	3.739
5HDQ	H_LYS_208	NZ	L_GLU_123	OE1	2.947

Table 1448: Interfacial 5HDQ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5HMG	A_LYS_27	NZ	B_GLU_97	OE1	2.931
5HMG	A_LYS_27	NZ	B_GLU_97	OE2	3.005
5HMG	A_ARG_109	NH1	B_GLU_67	OE1	2.841
5HMG	A_ARG_109	NH1	B_GLU_67	OE2	3.185
5HMG	A_ARG_269	NH1	B_GLU_67	OE1	3.577
5HMG	A_ARG_269	NH2	B_GLU_67	OE1	3.220
5HMG	A_LYS_299	NZ	B_GLU_69	OE1	3.343
5HMG	A_LYS_310	NZ	B_ASP_86	OD1	3.434
5HMG	A_LYS_310	NZ	B_ASP_90	OD1	2.661
5HMG	B_ARG_54	NH1	F_GLU_97	OE1	2.843
5HMG	B_ARG_54	NH2	F_GLU_97	OE1	2.937
5HMG	B_LYS_58	NZ	F_GLU_97	OE1	3.606
5HMG	B_LYS_58	NZ	F_GLU_97	OE2	3.524
5HMG	B_LYS_62	NZ	F_ASP_86	OD1	3.085
5HMG	B_LYS_62	NZ	F_ASP_86	OD2	2.792
5HMG	B_LYS_62	NZ	F_ASP_90	OD1	3.679
5HMG	B_LYS_62	NZ	F_ASP_90	OD2	2.748
5HMG	B_HIS_64	NE2	F_ASP_79	OD2	3.617
5HMG	B_ARG_76	NH1	D_GLU_74	OE1	3.275
5HMG	B_ARG_76	NH1	D_GLU_74	OE2	2.882
5HMG	B_ARG_76	NH1	D_GLU_81	OE1	2.781
5HMG	B_ARG_76	NH1	D_GLU_81	OE2	3.484
5HMG	B_ARG_76	NH2	D_GLU_74	OE1	2.814
5HMG	B_ARG_76	NH2	D_GLU_74	OE2	3.691
5HMG	B_ARG_123	NH1	F_GLU_132	OE2	3.002
5HMG	B_ARG_124	NH1	F_GLU_132	OE1	3.424
5HMG	B_ARG_124	NH1	F_GLU_132	OE2	3.265
5HMG	B_ARG_127	NH2	F_GLU_131	OE1	2.537
5HMG	B_ARG_163	NH1	F_GLU_131	OE1	2.770
5HMG	B_ARG_163	NH1	F_GLU_131	OE2	2.532
5HMG	B_ARG_170	NH1	D_GLU_128	OE1	3.169
5HMG	B_ARG_170	NH1	D_GLU_128	OE2	3.597
5HMG	C_LYS_27	NZ	D_GLU_97	OE1	2.934
5HMG	C_LYS_27	NZ	D_GLU_97	OE2	2.988
5HMG	C_ARG_109	NH1	D_GLU_67	OE1	2.853
5HMG	C_ARG_109	NH1	D_GLU_67	OE2	3.184
5HMG	C_ARG_269	NH1	D_GLU_67	OE1	3.552
5HMG	C_ARG_269	NH2	D_GLU_67	OE1	3.173
5HMG	C_LYS_299	NZ	D_GLU_69	OE1	3.348
5HMG	C_LYS_310	NZ	D_ASP_86	OD1	3.449
5HMG	C_LYS_310	NZ	D_ASP_90	OD1	2.638
5HMG	D_ARG_54	NH1	B_GLU_97	OE1	2.819
5HMG	D_ARG_54	NH2	B_GLU_97	OE1	2.943
5HMG	D_LYS_58	NZ	B_GLU_97	OE1	3.646
5HMG	D_LYS_58	NZ	B_GLU_97	OE2	3.528
5HMG	D_LYS_62	NZ	B_ASP_86	OD1	3.110
5HMG	D_LYS_62	NZ	B_ASP_86	OD2	2.718
5HMG	D_LYS_62	NZ	B_ASP_90	OD1	3.686
5HMG	D_LYS_62	NZ	B_ASP_90	OD2	2.685
5HMG	D_HIS_64	NE2	B_ASP_79	OD2	3.446
5HMG	D_ARG_76	NH1	F_GLU_74	OE1	3.349
5HMG	D_ARG_76	NH1	F_GLU_74	OE2	2.805
5HMG	D_ARG_76	NH1	F_GLU_81	OE1	2.685
5HMG	D_ARG_76	NH1	F_GLU_81	OE2	3.513
5HMG	D_ARG_76	NH2	F_GLU_74	OE1	2.710
5HMG	D_ARG_76	NH2	F_GLU_74	OE2	3.478
5HMG	D_ARG_123	NH1	B_GLU_132	OE2	2.981

5HMG	D_ARG_124	NH1	B_GLU_132	OE1	3.466
5HMG	D_ARG_124	NH1	B_GLU_132	OE2	3.303
5HMG	D_ARG_127	NH2	B_GLU_131	OE1	2.578
5HMG	D_ARG_163	NH1	B_GLU_131	OE1	2.694
5HMG	D_ARG_163	NH1	B_GLU_131	OE2	2.571
5HMG	D_ARG_170	NH1	F_GLU_128	OE1	3.252
5HMG	D_ARG_170	NH1	F_GLU_128	OE2	3.705
5HMG	E_LYS_27	NZ	F_GLU_97	OE1	2.935
5HMG	E_LYS_27	NZ	F_GLU_97	OE2	3.012
5HMG	E_ARG_109	NH1	F_GLU_67	OE1	2.825
5HMG	E_ARG_109	NH1	F_GLU_67	OE2	3.180
5HMG	E_ARG_269	NH1	F_GLU_67	OE1	3.584
5HMG	E_ARG_269	NH2	F_GLU_67	OE1	3.233
5HMG	E_LYS_299	NZ	F_GLU_69	OE1	3.318
5HMG	E_LYS_310	NZ	F_ASP_86	OD1	3.440
5HMG	E_LYS_310	NZ	F_ASP_90	OD1	2.621
5HMG	F_ARG_54	NH1	D_GLU_97	OE1	2.726
5HMG	F_ARG_54	NH2	D_GLU_97	OE1	2.912
5HMG	F_LYS_58	NZ	D_GLU_97	OE1	3.765
5HMG	F_LYS_58	NZ	D_GLU_97	OE2	3.593
5HMG	F_LYS_62	NZ	D_ASP_86	OD1	3.013
5HMG	F_LYS_62	NZ	D_ASP_86	OD2	2.694
5HMG	F_LYS_62	NZ	D_ASP_90	OD1	3.718
5HMG	F_LYS_62	NZ	D_ASP_90	OD2	2.750
5HMG	F_HIS_64	NE2	D_ASP_79	OD1	3.885
5HMG	F_HIS_64	NE2	D_ASP_79	OD2	3.364
5HMG	F_ARG_76	NH1	B_GLU_74	OE1	3.251
5HMG	F_ARG_76	NH1	B_GLU_74	OE2	2.826
5HMG	F_ARG_76	NH1	B_GLU_81	OE1	2.735
5HMG	F_ARG_76	NH1	B_GLU_81	OE2	3.601
5HMG	F_ARG_76	NH2	B_GLU_74	OE1	2.649
5HMG	F_ARG_76	NH2	B_GLU_74	OE2	3.569
5HMG	F_ARG_123	NH1	D_GLU_132	OE2	2.992
5HMG	F_ARG_124	NH1	D_GLU_132	OE1	3.514
5HMG	F_ARG_124	NH1	D_GLU_132	OE2	3.395
5HMG	F_ARG_127	NH2	D_GLU_131	OE1	2.609
5HMG	F_ARG_163	NH1	D_GLU_131	OE1	2.712
5HMG	F_ARG_163	NH1	D_GLU_131	OE2	2.596
5HMG	F_ARG_170	NH1	B_GLU_128	OE1	3.210
5HMG	F_ARG_170	NH1	B_GLU_128	OE2	3.530

Table 1449: Interfacial 5HMG-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5I76	A_LYS_49	NZ	B_GLU_105	OE1	3.995
5I76	B_LYS_215	NZ	A_GLU_123	OE1	2.731
5I76	B_LYS_215	NZ	A_GLU_123	OE2	2.888
5I76	B_LYS_220	NZ	A_ASP_122	OD2	3.474
5I76	C_ARG_24	NH1	A_ASP_70	OD1	3.725
5I76	C_ARG_24	NH1	A_ASP_70	OD2	2.949
5I76	C_ARG_24	NH2	A_ASP_70	OD1	3.138
5I76	C_ARG_24	NH2	A_ASP_70	OD2	3.394
5I76	D_LYS_215	NZ	C_GLU_123	OE1	2.596
5I76	D_LYS_215	NZ	C_GLU_123	OE2	3.738

Table 1450: Interfacial 5I76-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5ITB	H_ARG_111	NH1	L_GLU_68	OE1	3.426
5ITB	H_ARG_111	NH2	L_GLU_68	OE1	2.856
5ITB	H_LYS_224	NZ	L_GLU_143	OE1	3.323
5ITB	H_LYS_224	NZ	L_GLU_143	OE2	2.099

Table 1451: Interfacial 5ITB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5J3D	A_ARG_111	NH2	B_GLU_68	OE1	3.664
5J3D	A_LYS_224	NZ	B_GLU_143	OE1	3.390
5J3D	A_LYS_229	NZ	B_ASP_142	OD1	3.902
5J3D	A_LYS_229	NZ	B_ASP_142	OD2	3.196
5J3D	C_ARG_111	NH2	D_GLU_68	OE1	3.489
5J3D	C_LYS_	NZ	D_GLU_	OE1	3.377
5J3D	C_LYS_	NZ	D_ASP_	OD1	2.847
5J3D	C_LYS_	NZ	D_ASP_	OD2	2.791
5J3D	E_ARG_49	NH2	F_ASP_368	OD1	2.801
5J3D	E_ARG_49	NH2	F_ASP_368	OD2	3.628
5J3D	F_LYS_	NZ	I_GLU_	OE2	3.850
5J3D	F_LYS_196	NZ	I_ASP_489	OD1	2.634
5J3D	F_LYS_196	NZ	I_ASP_489	OD2	3.067
5J3D	F_ARG_235	NH1	I_GLU_232	OE1	3.071
5J3D	F_ARG_235	NH1	I_GLU_232	OE2	2.514
5J3D	F_LYS_272	NZ	B_ASP_56	OD2	3.606
5J3D	F_LYS_399	NZ	K_ASP_392	OD1	3.567
5J3D	F_LYS_470	NZ	J_GLU_60	OE1	3.190
5J3D	F_LYS_470	NZ	J_GLU_60	OE2	3.891
5J3D	G_ARG_49	NH2	I_ASP_368	OD1	3.151
5J3D	H_ARG_111	NH2	L_GLU_68	OE1	3.466
5J3D	H_LYS_224	NZ	L_GLU_143	OE1	3.364
5J3D	H_LYS_	NZ	L_ASP_	OD1	3.352
5J3D	H_LYS_	NZ	L_ASP_	OD2	3.692
5J3D	I_LYS_	NZ	K_GLU_	OE1	3.226
5J3D	I_LYS_	NZ	K_GLU_	OE2	3.914
5J3D	I_LYS_196	NZ	K_ASP_489	OD1	2.833
5J3D	I_LYS_196	NZ	K_ASP_489	OD2	3.027
5J3D	I_ARG_235	NH1	K_GLU_232	OE1	3.110
5J3D	I_ARG_235	NH1	K_GLU_232	OE2	2.664
5J3D	I_LYS_272	NZ	D_ASP_56	OD2	3.795
5J3D	I_LYS_399	NZ	F_ASP_392	OD1	3.746
5J3D	I_LYS_470	NZ	E_GLU_60	OE1	3.634
5J3D	I_LYS_470	NZ	E_GLU_60	OE2	3.872
5J3D	J_ARG_49	NH2	K_ASP_368	OD1	3.049
5J3D	J_ARG_49	NH2	K_ASP_368	OD2	3.898
5J3D	J_LYS_87	NZ	K_GLU_294	OE1	3.791
5J3D	K_LYS_	NZ	F_GLU_	OE1	2.905
5J3D	K_LYS_196	NZ	F_ASP_489	OD1	2.822
5J3D	K_LYS_196	NZ	F_ASP_489	OD2	3.022
5J3D	K_ARG_235	NH1	F_GLU_232	OE1	2.445
5J3D	K_ARG_235	NH1	F_GLU_232	OE2	2.683
5J3D	K_ARG_235	NH2	F_GLU_232	OE2	3.814
5J3D	K_LYS_399	NZ	I_ASP_392	OD1	3.598
5J3D	K_LYS_470	NZ	G_GLU_60	OE1	3.953

Table 1452: Interfacial 5J3D-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5JO5	H.LYS_143	NZ	L.GLU_124	OE2	2.459
5JO5	H.LYS_209	NZ	L.GLU_	OE2	2.531
5JO5	L.ARG_91	NH1	H.GLU_100J	OE2	3.301
5JO5	L.ARG_91	NH2	H.GLU_100J	OE2	2.691
5JO5	L.ARG_95B	NH2	H.ASP_58	OD1	3.439
5JO5	A.LYS_143	NZ	B.GLU_124	OE2	2.618
5JO5	A.LYS_209	NZ	B.GLU_123	OE2	2.545
5JO5	B.ARG_91	NH1	A.GLU_100J	OE2	3.353
5JO5	B.ARG_91	NH2	A.GLU_100J	OE2	3.038
5JO5	C.LYS_143	NZ	D.GLU_124	OE2	2.788
5JO5	C.LYS_209	NZ	D.GLU_123	OE2	2.583
5JO5	D.ARG_91	NH1	C.GLU_100J	OE2	3.302
5JO5	D.ARG_91	NH2	C.GLU_100J	OE2	3.077
5JO5	D.ARG_95B	NH2	C.ASP_58	OD1	3.978
5JO5	E.LYS_143	NZ	F.GLU_124	OE2	2.545
5JO5	E.LYS_209	NZ	F.GLU_123	OE2	2.567
5JO5	F.ARG_91	NH1	E.GLU_100J	OE2	3.369
5JO5	F.ARG_91	NH2	E.GLU_100J	OE2	2.722
5JO5	F.ARG_95B	NH2	E.ASP_58	OD1	3.518

Table 1453: Interfacial 5JO5-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID residue name residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5JOF	H_LYS_212	NZ	L_GLU_123	OE2	3.883
5JOF	H_LYS_217	NZ	L_ASP_122	OD2	3.165
5JOF	A_LYS_209	NZ	B_GLU_123	OE1	3.449
5JOF	A_LYS_209	NZ	B_GLU_123	OE2	3.809
5JOF	B_ARG_24	NH1	C_ASP_99	OD1	2.692
5JOF	B_ARG_24	NH1	C_ASP_99	OD2	3.960
5JOF	C_ARG_94	NH1	B_GLU_1	OE2	2.653
5JOF	C_ARG_94	NH2	B_GLU_1	OE2	3.195
5JOF	C_LYS_214	NZ	D_ASP_122	OD2	3.772
5JOF	C_LYS_214	NZ	D_GLU_123	OE1	2.987
5JOF	C_LYS_214	NZ	D_GLU_123	OE2	3.631
5JOF	E_LYS_209	NZ	F_GLU_123	OE1	2.331
5JOF	E_LYS_209	NZ	F_GLU_123	OE2	3.588
5JOF	E_LYS_214	NZ	F_ASP_122	OD2	3.802

Table 1454: Interfacial 5JOF-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5JR1	H_HIS_164	NE2	L_ASP_139	OD1	3.232
5JR1	H_HIS_164	NE2	L_ASP_139	OD2	3.168
5JR1	L_HIS_31	ND1	H_ASP_100	OD2	3.496
5JR1	L_HIS_31	ND1	H_GLU_100I	OE2	3.149
5JR1	L_ARG_95B	NH1	H_ASP_58	OD1	3.367
5JR1	L_ARG_95B	NH1	H_ASP_58	OD2	3.787
5JR1	L_ARG_95B	NH2	H_ASP_58	OD1	3.502
5JR1	L_ARG_95B	NH2	H_ASP_58	OD2	2.474

Table 1455: Interfacial 5JR1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5JUE	H_LYS_208	NZ	L_GLU_123	OE1	2.809
5JUE	H_LYS_208	NZ	L_GLU_123	OE2	2.812

Table 1456: Interfacial 5JUE-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5JXA	H_LYS_209	NZ	L_GLU_123	OE1	3.277
5JXA	H_LYS_214	NZ	L_ASP_122	OD1	2.755
5JXA	H_LYS_214	NZ	L_ASP_122	OD2	3.275

Table 1457: Interfacial 5JXA-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5KZP	H_LYS_224	NZ	L_ASP_122	OD2	3.852
5KZP	E_ARG_65	NH2	K_GLU_1	OE2	3.580
5KZP	E_LYS_219	NZ	I_GLU_123	OE1	2.944
5KZP	E_LYS_219	NZ	I_GLU_123	OE2	2.510
5KZP	F_LYS_139	NZ	J_GLU_213	OE2	2.615
5KZP	G_LYS_219	NZ	K_GLU_123	OE2	3.381

Table 1458: Interfacial 5KZP-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5LDN	H_LYS_	NZ	L_GLU_	OE1	3.019

Table 1459: Interfacial 5LDN-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5MO9	H_LYS_212	NZ	L_GLU_128	OE2	3.509
5MO9	L_LYS_55	NZ	X_GLU_371	OE2	2.811
5MO9	X_LYS_364	NZ	H_GLU_33	OE2	2.799
5MO9	X_LYS_364	NZ	H_ASP_52	OD1	3.966

Table 1460: Interfacial 5MO9-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5N4J	L_ARG_38	NH1	H_ASP_100	OD1	2.794
5N4J	L_ARG_38	NH1	H_ASP_100	OD2	3.589
5N4J	H_LYS_210	NZ	L_GLU_131	OE1	2.936
5N4J	H_LYS_210	NZ	L_GLU_131	OE2	3.282

Table 1461: Interfacial 5N4J-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5N7W	A_LYS.149	NZ	B_GLU.126	OE2	2.961
5N7W	A_LYS.215	NZ	B_GLU.125	OE1	2.755
5N7W	A_LYS.215	NZ	B_GLU.125	OE2	3.335
5N7W	H_LYS.149	NZ	L_GLU.126	OE2	2.605

Table 1462: Interfacial 5N7W-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5NPH	H_LYS_215	NZ	L_GLU_123	OE2	2.787
5NPH	L_LYS_93	NZ	A_GLU_533	OE1	3.679

Table 1463: Interfacial 5NPH-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5NPI	A_HIS_181	NE2	B_GLU_10	OE1	3.570
5NPI	A_HIS_181	NE2	B_GLU_10	OE2	3.750
5NPI	B_HIS_181	NE2	A_GLU_10	OE1	3.757
5NPI	B_HIS_181	NE2	A_GLU_10	OE2	3.882
5NPI	B_LYS_233	NZ	E_GLU_533	OE1	3.924

Table 1464: Interfacial 5NPI-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5NPJ	A.HIS.181	NE2	B.GLU.10	OE1	3.540
5NPJ	A.HIS.181	NE2	B.GLU.10	OE2	3.793
5NPJ	B.HIS.181	NE2	A.GLU.10	OE1	3.734
5NPJ	B.HIS.181	NE2	A.GLU.10	OE2	3.967

Table 1465: Interfacial 5NPJ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5NST	A_ARG_39	NH1	C_GLU_81	OE1	3.260
5NST	A_ARG_39	NH1	C_GLU_81	OE2	3.263
5NST	A_ARG_39	NH2	C_GLU_81	OE1	3.038
5NST	B_LYS_345	NZ	A_GLU_123	OE1	3.069
5NST	C_ARG_39	NH1	A_GLU_81	OE1	3.247
5NST	C_ARG_39	NH1	A_GLU_81	OE2	3.139
5NST	C_ARG_39	NH2	A_GLU_81	OE1	3.004
5NST	D_LYS_345	NZ	C_GLU_123	OE2	3.272

Table 1466: Interfacial 5NST-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5NUZ	A_ARG_95	NH1	C_ASP_114	OD1	3.502
5NUZ	A_ARG_95	NH1	C_ASP_114	OD2	2.701
5NUZ	A_ARG_95	NH2	C_ASP_114	OD1	2.822
5NUZ	A_ARG_95	NH2	C_ASP_114	OD2	3.585
5NUZ	A_LYS_208	NZ	B_GLU_123	OE1	3.889
5NUZ	A_LYS_208	NZ	B_GLU_123	OE2	2.684
5NUZ	H_ARG_95	NH1	D_ASP_114	OD1	3.679
5NUZ	H_ARG_95	NH1	D_ASP_114	OD2	2.753
5NUZ	H_ARG_95	NH2	D_ASP_114	OD1	2.850
5NUZ	H_ARG_95	NH2	D_ASP_114	OD2	3.470
5NUZ	H_LYS_208	NZ	L_GLU_123	OE2	2.982
5NUZ	B_ARG_61	NH2	L_GLU_79	OE1	3.072
5NUZ	B_ARG_61	NH2	L_GLU_79	OE2	3.676
5NUZ	C_LYS_211	NZ	A_ASP_54	OD1	3.758
5NUZ	C_LYS_211	NZ	A_ASP_54	OD2	3.058
5NUZ	C_LYS_211	NZ	A_ASP_56	OD2	2.861
5NUZ	L_ARG_61	NH2	B_GLU_79	OE1	3.765
5NUZ	L_ARG_61	NH2	B_GLU_79	OE2	2.966
5NUZ	D_LYS_211	NZ	H_ASP_54	OD1	3.910
5NUZ	D_LYS_211	NZ	H_ASP_54	OD2	3.105
5NUZ	D_LYS_211	NZ	H_ASP_56	OD2	2.803

Table 1467: Interfacial 5NUZ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5O14	A_LYS_185	NZ	H_ASP_55	OD1	3.249
5O14	A_LYS_185	NZ	H_ASP_55	OD2	2.764
5O14	A_LYS_185	NZ	H_ASP_57	OD2	2.802
5O14	A_ARG_204	NH1	B_GLU_218	OE1	3.625
5O14	B_LYS_185	NZ	C_ASP_55	OD1	3.234
5O14	B_LYS_185	NZ	C_ASP_55	OD2	2.720
5O14	B_LYS_185	NZ	C_ASP_57	OD2	2.736
5O14	C_ARG_54	NH2	B_ASP_161	OD1	2.870
5O14	C_ARG_54	NH2	B_ASP_161	OD2	3.505
5O14	C_LYS_218	NZ	D_GLU_124	OE1	3.107
5O14	D_ARG_18	NH1	A_GLU_218	OE1	3.301
5O14	H_ARG_54	NH1	A_ASP_161	OD1	2.861
5O14	H_ARG_54	NH1	A_ASP_161	OD2	3.283
5O14	H_ARG_59	NH1	L_ASP_94	OD1	3.733
5O14	H_ARG_59	NH1	L_ASP_94	OD2	3.698

Table 1468: Interfacial 5O14-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5O1R	A_ARG_339	NH1	H_ASP_100	OD1	3.968
5O1R	A_ARG_339	NH1	H_ASP_100	OD2	3.203
5O1R	B_ARG_339	NH1	L_ASP_100	OD1	3.595
5O1R	B_ARG_339	NH1	L_ASP_100	OD2	2.991

Table 1469: Interfacial 5O1R-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5OLM	A_HIS_0	NE2	B_GLU_97	OE1	2.769
5OLM	A_HIS_0	NE2	B_GLU_97	OE2	2.598
5OLM	A_ARG_6	NH2	B_GLU_82	OE1	3.071
5OLM	B_HIS_0	NE2	A_GLU_97	OE1	2.741
5OLM	B_HIS_0	NE2	A_GLU_97	OE2	3.001
5OLM	B_ARG_6	NH2	A_GLU_82	OE2	2.559

Table 1470: Interfacial 5OLM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5OPY	H_LYS_212	NZ	L_GLU_123	OE2	3.578

Table 1471: Interfacial 5OPY-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5T6P	A_LYS_58	NZ	F_ASP_3	OD2	1.997
5T6P	A_LYS_174	NZ	C_GLU_128	OE2	3.605
5T6P	C_ARG_55	NH1	E_ASP_3	OD2	3.191
5T6P	C_LYS_58	NZ	E_ASP_3	OD2	2.925
5T6P	E_ARG_5	NH2	C_GLU_39	OE1	3.351
5T6P	E_ARG_5	NH2	C_GLU_39	OE2	2.626
5T6P	F_ARG_5	NH2	A_GLU_39	OE1	3.661
5T6P	F_ARG_5	NH2	A_GLU_39	OE2	2.718

Table 1472: Interfacial 5T6P-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5T78	A.LYS_58	NZ	F.ASP_3	OD1	2.579
5T78	A.LYS_58	NZ	F.ASP_3	OD2	3.334
5T78	F.ARG_5	NH1	A.GLU_39	OE1	2.678
5T78	F.ARG_5	NH1	A.GLU_39	OE2	2.480
5T78	C.ARG_55	NH2	E.ASP_3	OD1	3.685
5T78	C.LYS_58	NZ	E.ASP_3	OD1	2.753
5T78	C.LYS_58	NZ	E.ASP_3	OD2	2.872
5T78	D.LYS_211	NZ	C.GLU_128	OE1	3.376
5T78	E.ARG_5	NH1	C.GLU_39	OE1	2.693
5T78	E.ARG_5	NH1	C.GLU_39	OE2	2.664

Table 1473: Interfacial 5T78-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5TIH	A_LYS_66	NZ	L_ASP_92	OD1	3.482
5TIH	H_HIS_35	NE2	A_ASP_69	OD1	2.973
5TIH	H_HIS_35	NE2	A_ASP_69	OD2	3.535
5TIH	H_ARG_100	NH2	A_ASP_69	OD1	3.080
5TIH	H_ARG_101	NH2	A_GLU_119	OE1	3.357
5TIH	H_ARG_101	NH2	A_GLU_119	OE2	3.359

Table 1474: Interfacial 5TIH-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5TIK	A_HIS_3	ND1	D_GLU_9	OE2	3.832
5TIK	A_HIS_3	NE2	B_GLU_9	OE2	3.597
5TIK	B_HIS_3	NE2	A_GLU_9	OE1	3.627
5TIK	B_HIS_3	NE2	A_GLU_9	OE2	3.175
5TIK	B_HIS_3	NE2	C_GLU_9	OE1	3.296
5TIK	B_HIS_3	NE2	C_GLU_9	OE2	3.823
5TIK	B_LYS_290	NZ	A_GLU_281	OE1	3.703
5TIK	C_HIS_3	NE2	B_GLU_9	OE1	2.908
5TIK	C_ARG_29	NH2	B_ASP_259	OD2	3.311
5TIK	D_HIS_3	NE2	A_GLU_9	OE1	2.950
5TIK	D_HIS_3	NE2	A_GLU_9	OE2	2.918

Table 1475: Interfacial 5TIK-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5TL5	H_ARG_50	NH1	L_ASP_98	OD1	2.887
5TL5	H_ARG_50	NH1	L_ASP_98	OD2	3.532
5TL5	H_ARG_50	NH2	L_ASP_98	OD1	3.785
5TL5	H_ARG_50	NH2	L_ASP_98	OD2	2.933
5TL5	H_LYS_216	NZ	L_GLU_127	OE1	3.027
5TL5	H_LYS_216	NZ	L_GLU_127	OE2	3.571
5TL5	A_LYS_17	NZ	H_ASP_55	OD1	3.610
5TL5	A_LYS_17	NZ	H_ASP_55	OD2	2.637
5TL5	A_LYS_17	NZ	H_ASP_57	OD1	2.990
5TL5	A_HIS_36	NE2	H_ASP_104	OD1	3.017
5TL5	A_HIS_36	NE2	H_ASP_104	OD2	2.947
5TL5	A_ARG_37	NH2	H_ASP_104	OD2	2.895

Table 1476: Interfacial 5TL5-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID residue name residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5TLJ	B_ARG_50	NH1	A_ASP_98	OD1	2.672
5TLJ	B_ARG_50	NH1	A_ASP_98	OD2	3.926
5TLJ	D_ARG_100	NH1	X_ASP_43	OD2	3.396
5TLJ	D_ARG_100	NH2	C_GLU_59	OE1	2.703
5TLJ	D_ARG_100	NH2	C_GLU_59	OE2	3.403
5TLJ	D_ARG_100	NH2	X_ASP_43	OD2	3.844
5TLJ	F_ARG_50	NH1	E_ASP_98	OD1	3.689
5TLJ	F_ARG_50	NH1	E_ASP_98	OD2	2.897
5TLJ	F_ARG_50	NH2	E_ASP_98	OD1	3.671
5TLJ	F_ARG_50	NH2	E_ASP_98	OD2	3.575
5TLJ	F_HIS_171	ND1	E_ASP_171	OD1	3.892
5TLJ	F_HIS_171	NE2	E_ASP_171	OD2	3.411
5TLJ	H_ARG_100	NH2	G_GLU_59	OE1	2.761
5TLJ	X_LYS_17	NZ	B_ASP_57	OD2	3.053
5TLJ	X_HIS_36	NE2	B_ASP_104	OD1	3.121
5TLJ	X_HIS_36	NE2	B_ASP_104	OD2	2.886

Table 1477: Interfacial 5TLJ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5TLK	B_ARG_50	NH1	A_ASP_98	OD1	3.277
5TLK	B_ARG_50	NH1	A_ASP_98	OD2	2.898
5TLK	B_ARG_50	NH2	A_ASP_98	OD1	2.923
5TLK	B_LYS_216	NZ	A_GLU_127	OE1	3.067
5TLK	B_LYS_216	NZ	A_GLU_127	OE2	3.588
5TLK	C_ARG_57	NH2	X_ASP_43	OD1	3.384
5TLK	D_ARG_100	NH1	X_ASP_43	OD2	2.904
5TLK	D_ARG_100	NH2	C_GLU_59	OE1	2.708
5TLK	D_ARG_100	NH2	C_GLU_59	OE2	3.299
5TLK	D_ARG_100	NH2	X_ASP_43	OD2	3.882
5TLK	F_ARG_50	NH1	E_ASP_98	OD1	3.086
5TLK	F_ARG_50	NH1	E_ASP_98	OD2	3.224
5TLK	F_ARG_50	NH2	E_ASP_98	OD1	2.767
5TLK	F_ARG_50	NH2	E_ASP_98	OD2	3.943
5TLK	G_ARG_33	NH1	Y_GLU_24	OE2	3.993
5TLK	G_ARG_33	NH2	Y_GLU_24	OE2	3.475
5TLK	H_ARG_100	NH1	G_GLU_59	OE1	3.531
5TLK	H_ARG_100	NH1	Y_ASP_43	OD2	3.423
5TLK	H_ARG_100	NH2	G_GLU_59	OE1	2.787
5TLK	H_ARG_100	NH2	G_GLU_59	OE2	3.306
5TLK	H_LYS_213	NZ	G_GLU_127	OE1	3.569
5TLK	X_LYS_17	NZ	B_ASP_55	OD1	3.914
5TLK	X_LYS_17	NZ	B_ASP_55	OD2	3.018
5TLK	X_LYS_17	NZ	B_ASP_57	OD2	3.114
5TLK	X_HIS_36	NE2	B_ASP_104	OD1	3.010
5TLK	X_HIS_36	NE2	B_ASP_104	OD2	2.891
5TLK	X_ARG_37	NH2	B_ASP_104	OD1	2.703
5TLK	Y_LYS_17	NZ	F_ASP_55	OD1	3.581
5TLK	Y_LYS_17	NZ	F_ASP_55	OD2	3.170
5TLK	Y_LYS_17	NZ	F_ASP_57	OD2	3.380
5TLK	Y_HIS_36	NE2	F_ASP_104	OD1	3.198
5TLK	Y_HIS_36	NE2	F_ASP_104	OD2	2.793
5TLK	Y_ARG_37	NH2	F_ASP_104	OD1	3.616

Table 1478: Interfacial 5TLK-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5TRU	h_HIS_169	NE2	l_ASP_168	OD2	3.995

Table 1479: Interfacial 5TRU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5TZ2	H_ARG_101	NH1	C_ASP_46	OD2	3.182
5TZ2	H_HIS_105	NE2	C_ASP_51	OD1	2.798
5TZ2	H_HIS_105	NE2	C_ASP_51	OD2	2.654
5TZ2	C_LYS_56	NZ	H_ASP_55	OD1	3.222
5TZ2	C_LYS_56	NZ	H_ASP_55	OD2	2.489
5TZ2	C_LYS_56	NZ	H_ASP_57	OD2	3.354

Table 1480: Interfacial 5TZ2-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5TZT	B_ARG_82	NH2	H_ASP_31	OD1	2.783
5TZT	B_ARG_82	NH2	H_ASP_31	OD2	3.806
5TZT	A_HIS_102	ND1	D_GLU_104	OE2	3.803
5TZT	L_LYS_55	NZ	C_GLU_104	OE1	3.704
5TZT	L_LYS_55	NZ	C_GLU_104	OE2	2.899
5TZT	H_HIS_102	ND1	C_GLU_104	OE1	2.856

Table 1481: Interfacial 5TZT-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5TZU	L_LYS_49	NZ	C_ASP_51	OD1	3.523
5TZU	L_LYS_49	NZ	C_ASP_51	OD2	2.772
5TZU	L_ARG_96	NH1	C_GLU_104	OE1	3.230
5TZU	L_ARG_96	NH1	C_GLU_104	OE2	3.808
5TZU	L_ARG_96	NH2	C_GLU_104	OE1	2.901
5TZU	H_LYS_214	NZ	L_GLU_123	OE1	2.584
5TZU	H_LYS_214	NZ	L_GLU_123	OE2	3.416
5TZU	C_LYS_39	NZ	L_ASP_31	OD1	3.076
5TZU	C_LYS_39	NZ	L_ASP_31	OD2	2.978

Table 1482: Interfacial 5TZU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5U3J	H_ARG_52A	NH1	A_ASP_674	OD1	3.805
5U3J	H_ARG_52A	NH1	A_ASP_674	OD2	3.646
5U3J	H_ARG_52A	NH2	A_ASP_674	OD2	3.216
5U3J	H_LYS_52C	NZ	A_ASP_674	OD1	3.151
5U3J	H_LYS_52C	NZ	A_ASP_674	OD2	3.836
5U3J	H_LYS_209	NZ	L_GLU_123	OE1	3.171
5U3J	H_LYS_209	NZ	L_GLU_123	OE2	2.412

Table 1483: Interfacial 5U3J-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5U3N	H_ARG_52A	NH1	A_ASP_674	OD2	2.997
5U3N	H_ARG_52A	NH2	A_ASP_674	OD1	3.173
5U3N	H_ARG_52A	NH2	A_ASP_674	OD2	3.047
5U3N	H_ARG_100B	NH1	L_ASP_31	OD1	3.593
5U3N	H_ARG_100B	NH1	L_ASP_31	OD2	2.967
5U3N	H_ARG_100B	NH2	L_ASP_31	OD1	2.974
5U3N	H_ARG_100B	NH2	L_ASP_31	OD2	3.816
5U3N	H_LYS_209	NZ	L_GLU_123	OE1	3.254
5U3N	L_LYS_30	NZ	H_GLU_100E	OE1	3.899
5U3N	L_ARG_55	NH2	H_ASP_101	OD1	3.682
5U3N	L_ARG_55	NH2	H_ASP_101	OD2	2.901

Table 1484: Interfacial 5U3N-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5UCB	L_ARG_66	NH2	B_ASP_51	OD1	2.894
5UCB	B_ARG_144	NH2	L_ASP_91	OD1	2.844
5UCB	B_ARG_144	NH2	L_ASP_91	OD2	3.495

Table 1485: Interfacial 5UCB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5UEA	X.LYS_10	NZ	D.GLU_29	OE1	3.740
5UEA	X.LYS_10	NZ	D.GLU_29	OE2	2.855
5UEA	X.LYS_71	NZ	D.GLU_29	OE2	3.320
5UEA	D.LYS_10	NZ	X.GLU_29	OE1	3.485
5UEA	D.LYS_10	NZ	X.GLU_29	OE2	2.490
5UEA	D.LYS_70	NZ	X.GLU_29	OE2	3.861

Table 1486: Interfacial 5UEA-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5UEK	A_ARG_145	NH2	L_ASP_91	OD1	2.787
5UEK	A_ARG_145	NH2	L_ASP_91	OD2	3.426
5UEK	L_ARG_66	NH2	A_ASP_52	OD1	2.873

Table 1487: Interfacial 5UEK-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5UG0	A_ARG_106	NH1	B_GLU_69	OE1	3.096
5UG0	A_ARG_106	NH1	B_GLU_69	OE2	3.964
5UG0	A_ARG_106	NH2	B_GLU_69	OE1	3.415
5UG0	A_ARG_106	NH2	B_GLU_69	OE2	3.059
5UG0	A_LYS_222	NZ	D_ASP_107	OD2	3.472
5UG0	A_ARG_311	NH1	B_ASP_90	OD1	2.840
5UG0	A_ARG_311	NH2	B_ASP_86	OD1	2.770
5UG0	A_ARG_311	NH2	B_ASP_90	OD1	3.313
5UG0	B_LYS_68	NZ	A_GLU_107	OE2	3.009
5UG0	D_ARG_100	NH1	A_ASP_190	OD1	3.522
5UG0	D_ARG_100	NH1	A_ASP_190	OD2	3.877
5UG0	D_HIS_178	NE2	C_ASP_169	OD2	3.490
5UG0	D_LYS_223	NZ	C_GLU_125	OE2	3.392

Table 1488: Interfacial 5UG0-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5UJZ	A_ARG_106	NH1	B_GLU_569	OE2	3.797
5UJZ	A_ARG_106	NH2	B_GLU_569	OE1	3.958
5UJZ	A_ARG_106	NH2	B_GLU_569	OE2	3.070
5UJZ	A_ARG_311	NH1	B_ASP_586	OD1	3.689
5UJZ	A_ARG_311	NH1	B_ASP_590	OD1	3.217
5UJZ	A_ARG_311	NH1	B_ASP_590	OD2	3.955
5UJZ	A_ARG_311	NH2	B_ASP_586	OD1	2.782
5UJZ	B_LYS_558	NZ	F_GLU_597	OE1	3.688
5UJZ	B_LYS_558	NZ	F_GLU_597	OE2	3.874
5UJZ	B_ARG_576	NH1	D_GLU_574	OE1	3.986
5UJZ	B_ARG_576	NH1	D_GLU_574	OE2	3.042
5UJZ	B_ARG_576	NH2	C_GLU_104	OE2	3.168
5UJZ	B_LYS_583	NZ	D_ASP_585	OD1	3.717
5UJZ	B_ARG_606	NH2	F_ASP_609	OD2	2.744
5UJZ	B_LYS_643	NZ	A_GLU_4	OE1	2.954
5UJZ	B_LYS_643	NZ	A_ASP_5	OD1	2.763
5UJZ	B_LYS_643	NZ	A_ASP_5	OD2	3.863
5UJZ	C_ARG_106	NH1	D_GLU_569	OE2	3.872
5UJZ	C_ARG_106	NH2	D_GLU_569	OE2	3.260
5UJZ	C_ARG_311	NH1	D_ASP_586	OD1	3.865
5UJZ	C_ARG_311	NH1	D_ASP_590	OD1	3.148
5UJZ	C_ARG_311	NH1	D_ASP_590	OD2	3.998
5UJZ	C_ARG_311	NH2	D_ASP_586	OD1	2.921
5UJZ	D_LYS_558	NZ	B_GLU_597	OE1	3.772
5UJZ	D_LYS_572	NZ	E_GLU_238	OE1	3.910
5UJZ	D_ARG_576	NH1	F_GLU_574	OE1	3.863
5UJZ	D_ARG_576	NH1	F_GLU_574	OE2	2.716
5UJZ	D_ARG_576	NH2	E_GLU_104	OE2	3.170
5UJZ	D_LYS_583	NZ	F_ASP_585	OD1	3.807
5UJZ	D_ARG_606	NH2	B_ASP_609	OD2	2.766
5UJZ	D_LYS_643	NZ	C_GLU_4	OE1	3.185
5UJZ	D_LYS_643	NZ	C_ASP_5	OD1	2.519
5UJZ	D_LYS_643	NZ	C_ASP_5	OD2	3.642
5UJZ	E_ARG_106	NH2	F_GLU_569	OE2	3.361
5UJZ	E_ARG_311	NH1	F_ASP_586	OD1	3.477
5UJZ	E_ARG_311	NH1	F_ASP_590	OD1	3.629
5UJZ	E_ARG_311	NH2	F_ASP_586	OD1	2.793
5UJZ	F_ARG_576	NH1	B_GLU_574	OE1	3.655
5UJZ	F_ARG_576	NH1	B_GLU_574	OE2	2.847
5UJZ	F_ARG_576	NH2	A_GLU_104	OE2	3.211
5UJZ	F_LYS_583	NZ	B_ASP_585	OD1	3.548
5UJZ	F_ARG_606	NH2	D_ASP_609	OD2	2.609
5UJZ	F_LYS_643	NZ	E_GLU_4	OE1	3.009
5UJZ	F_LYS_643	NZ	E_ASP_5	OD1	2.882
5UJZ	F_LYS_643	NZ	E_ASP_5	OD2	3.935
5UJZ	G_ARG_225	NH1	A_ASP_190	OD1	3.090
5UJZ	G_ARG_225	NH1	A_ASP_190	OD2	3.996
5UJZ	G_ARG_225	NH2	A_ASP_190	OD1	3.715
5UJZ	G_ARG_225	NH2	A_ASP_190	OD2	3.410
5UJZ	H_ARG_225	NH1	C_ASP_190	OD1	3.041
5UJZ	H_ARG_225	NH2	C_ASP_190	OD1	3.552
5UJZ	H_ARG_225	NH2	C_ASP_190	OD2	3.366
5UJZ	I_ARG_225	NH1	E_ASP_190	OD1	3.119
5UJZ	I_ARG_225	NH1	E_ASP_190	OD2	3.970
5UJZ	I_ARG_225	NH2	E_ASP_190	OD1	3.713
5UJZ	I_ARG_225	NH2	E_ASP_190	OD2	3.347

Table 1489: Interfacial 5UJZ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5UK0	A_ARG_106	NH1	B_GLU_569	OE2	3.967
5UK0	A_ARG_106	NH2	B_GLU_569	OE2	3.244
5UK0	A_ARG_220	NH2	C_ASP_241	OD1	3.711
5UK0	A_ARG_220	NH2	C_ASP_241	OD2	3.819
5UK0	A_ARG_311	NH1	B_ASP_590	OD1	3.139
5UK0	A_ARG_311	NH1	B_ASP_590	OD2	3.961
5UK0	A_ARG_311	NH2	B_ASP_586	OD1	3.197
5UK0	B_LYS_558	NZ	F_GLU_597	OE1	3.717
5UK0	B_LYS_568	NZ	A_GLU_107	OE2	3.962
5UK0	B_ARG_576	NH1	D_GLU_574	OE1	2.500
5UK0	B_ARG_576	NH1	D_GLU_574	OE2	3.431
5UK0	B_ARG_576	NH2	C_GLU_104	OE2	3.446
5UK0	B_ARG_576	NH2	D_GLU_574	OE1	3.430
5UK0	B_ARG_576	NH2	D_GLU_574	OE2	3.016
5UK0	B_ARG_606	NH2	F_ASP_609	OD2	2.765
5UK0	B_LYS_643	NZ	A_GLU_4	OE1	2.724
5UK0	B_LYS_643	NZ	A_ASP_5	OD1	2.705
5UK0	B_LYS_643	NZ	A_ASP_5	OD2	3.831
5UK0	C_ARG_106	NH1	D_GLU_569	OE2	3.998
5UK0	C_ARG_106	NH2	D_GLU_569	OE2	3.213
5UK0	C_ARG_220	NH2	E_ASP_241	OD1	3.755
5UK0	C_ARG_220	NH2	E_ASP_241	OD2	3.891
5UK0	C_ARG_311	NH1	D_ASP_586	OD1	3.901
5UK0	C_ARG_311	NH1	D_ASP_590	OD1	3.110
5UK0	C_ARG_311	NH1	D_ASP_590	OD2	3.851
5UK0	C_ARG_311	NH2	D_ASP_586	OD1	2.981
5UK0	D_LYS_558	NZ	B_GLU_597	OE1	3.800
5UK0	D_LYS_572	NZ	E_GLU_238	OE1	3.723
5UK0	D_ARG_576	NH1	F_GLU_574	OE1	2.823
5UK0	D_ARG_576	NH1	F_GLU_574	OE2	3.743
5UK0	D_ARG_576	NH2	E_GLU_104	OE2	3.003
5UK0	D_ARG_576	NH2	F_GLU_574	OE1	3.596
5UK0	D_ARG_576	NH2	F_GLU_574	OE2	3.278
5UK0	D_ARG_606	NH2	B_ASP_609	OD2	2.683
5UK0	D_LYS_643	NZ	C_GLU_4	OE1	2.844
5UK0	D_LYS_643	NZ	C_ASP_5	OD1	2.693
5UK0	D_LYS_643	NZ	C_ASP_5	OD2	3.673
5UK0	E_ARG_106	NH1	F_GLU_569	OE2	3.924
5UK0	E_ARG_106	NH2	F_GLU_569	OE2	3.130
5UK0	E_ARG_220	NH2	A_ASP_241	OD1	3.703
5UK0	E_ARG_220	NH2	A_ASP_241	OD2	3.860
5UK0	E_ARG_311	NH1	F_ASP_586	OD1	3.927
5UK0	E_ARG_311	NH1	F_ASP_590	OD1	3.174
5UK0	E_ARG_311	NH1	F_ASP_590	OD2	3.882
5UK0	E_ARG_311	NH2	F_ASP_586	OD1	3.095
5UK0	F_LYS_558	NZ	D_GLU_597	OE1	3.758
5UK0	F_LYS_568	NZ	E_GLU_107	OE2	3.989
5UK0	F_LYS_572	NZ	A_GLU_238	OE1	3.995
5UK0	F_ARG_576	NH1	B_GLU_574	OE1	2.515
5UK0	F_ARG_576	NH1	B_GLU_574	OE2	3.607
5UK0	F_ARG_576	NH2	A_GLU_104	OE2	3.281
5UK0	F_ARG_576	NH2	B_GLU_574	OE1	3.248
5UK0	F_ARG_576	NH2	B_GLU_574	OE2	3.003
5UK0	F_ARG_606	NH2	D_ASP_609	OD2	2.740
5UK0	F_LYS_643	NZ	E_GLU_4	OE1	2.987
5UK0	F_LYS_643	NZ	E_ASP_5	OD1	2.694
5UK0	F_LYS_643	NZ	E_ASP_5	OD2	3.721

5UK0	G_ARG_225	NH1	A_ASP_190	OD1	3.056
5UK0	G_ARG_225	NH1	A_ASP_190	OD2	3.844
5UK0	G_ARG_225	NH2	A_ASP_190	OD1	3.909
5UK0	G_ARG_225	NH2	A_ASP_190	OD2	3.442
5UK0	H_ARG_225	NH1	C_ASP_190	OD1	3.008
5UK0	H_ARG_225	NH1	C_ASP_190	OD2	3.873
5UK0	H_ARG_225	NH2	C_ASP_190	OD1	3.782
5UK0	H_ARG_225	NH2	C_ASP_190	OD2	3.377
5UK0	I_ARG_225	NH1	E_ASP_190	OD1	3.078
5UK0	I_ARG_225	NH1	E_ASP_190	OD2	3.875
5UK0	I_ARG_225	NH2	E_ASP_190	OD1	3.886
5UK0	I_ARG_225	NH2	E_ASP_190	OD2	3.433

Table 1490: Interfacial 5UK0-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5UK1	A_ARG_106	NH1	B_GLU_569	OE2	3.892
5UK1	A_ARG_106	NH2	B_GLU_569	OE2	2.755
5UK1	A_ARG_311	NH1	B_ASP_590	OD1	2.545
5UK1	A_ARG_311	NH1	B_ASP_590	OD2	3.367
5UK1	A_ARG_311	NH2	B_ASP_586	OD1	3.117
5UK1	B_LYS_558	NZ	F_GLU_597	OE1	3.470
5UK1	B_ARG_576	NH1	D_GLU_574	OE1	3.845
5UK1	B_ARG_576	NH1	D_GLU_574	OE2	3.273
5UK1	B_ARG_576	NH2	C_GLU_104	OE2	2.839
5UK1	B_ARG_606	NH2	F_ASP_609	OD2	3.320
5UK1	B_LYS_643	NZ	A_GLU_4	OE1	2.898
5UK1	B_LYS_643	NZ	A_ASP_5	OD1	2.632
5UK1	B_LYS_643	NZ	A_ASP_5	OD2	3.703
5UK1	C_ARG_106	NH2	D_GLU_569	OE2	3.108
5UK1	C_ARG_311	NH1	D_ASP_590	OD1	2.901
5UK1	C_ARG_311	NH1	D_ASP_590	OD2	3.798
5UK1	C_ARG_311	NH2	D_ASP_586	OD1	3.261
5UK1	D_LYS_558	NZ	B_GLU_597	OE1	3.543
5UK1	D_ARG_576	NH1	F_GLU_574	OE1	3.490
5UK1	D_ARG_576	NH1	F_GLU_574	OE2	3.058
5UK1	D_ARG_576	NH2	E_GLU_104	OE2	3.186
5UK1	D_ARG_606	NH2	B_ASP_609	OD2	3.177
5UK1	D_LYS_643	NZ	C_GLU_4	OE1	3.015
5UK1	D_LYS_643	NZ	C_ASP_5	OD1	2.615
5UK1	D_LYS_643	NZ	C_ASP_5	OD2	3.806
5UK1	E_ARG_106	NH2	F_GLU_569	OE2	2.991
5UK1	E_ARG_311	NH1	F_ASP_590	OD1	2.696
5UK1	E_ARG_311	NH1	F_ASP_590	OD2	3.637
5UK1	E_ARG_311	NH2	F_ASP_586	OD1	3.291
5UK1	F_LYS_558	NZ	D_GLU_597	OE1	3.566
5UK1	F_ARG_576	NH1	B_GLU_574	OE1	3.570
5UK1	F_ARG_576	NH1	B_GLU_574	OE2	3.065
5UK1	F_ARG_576	NH2	A_GLU_104	OE2	3.295
5UK1	F_ARG_606	NH2	D_ASP_609	OD2	3.182
5UK1	F_LYS_643	NZ	E_GLU_4	OE1	3.024
5UK1	F_LYS_643	NZ	E_ASP_5	OD1	2.503
5UK1	F_LYS_643	NZ	E_ASP_5	OD2	3.650
5UK1	G_ARG_225	NH1	A_ASP_190	OD1	2.887
5UK1	G_ARG_225	NH1	A_ASP_190	OD2	3.709
5UK1	G_ARG_225	NH2	A_ASP_190	OD1	3.956
5UK1	G_ARG_225	NH2	A_ASP_190	OD2	3.555
5UK1	H_ARG_225	NH1	C_ASP_190	OD1	2.683
5UK1	H_ARG_225	NH1	C_ASP_190	OD2	3.511
5UK1	H_ARG_225	NH2	C_ASP_190	OD1	3.809
5UK1	H_ARG_225	NH2	C_ASP_190	OD2	3.346
5UK1	I_ARG_225	NH1	E_ASP_190	OD1	2.885
5UK1	I_ARG_225	NH1	E_ASP_190	OD2	3.789
5UK1	I_ARG_225	NH2	E_ASP_190	OD1	3.888
5UK1	I_ARG_225	NH2	E_ASP_190	OD2	3.567

Table 1491: Interfacial 5UK1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5UK2	A_ARG_106	NH1	B_GLU_569	OE2	3.935
5UK2	A_ARG_106	NH2	B_GLU_569	OE2	2.216
5UK2	A_ARG_311	NH1	B_ASP_586	OD1	3.877
5UK2	A_ARG_311	NH1	B_ASP_590	OD1	2.946
5UK2	A_ARG_311	NH1	B_ASP_590	OD2	3.729
5UK2	A_ARG_311	NH2	B_ASP_586	OD1	3.044
5UK2	B_LYS_558	NZ	F_GLU_597	OE1	3.672
5UK2	B_LYS_568	NZ	A_GLU_107	OE1	3.896
5UK2	B_ARG_576	NH1	D_GLU_574	OE1	3.949
5UK2	B_ARG_576	NH1	D_GLU_574	OE2	2.806
5UK2	B_ARG_576	NH2	C_GLU_104	OE2	3.501
5UK2	B_LYS_583	NZ	D_ASP_585	OD1	3.241
5UK2	B_LYS_583	NZ	D_ASP_585	OD2	3.954
5UK2	B_ARG_606	NH2	F_ASP_609	OD2	2.779
5UK2	B_LYS_643	NZ	A_GLU_4	OE1	3.076
5UK2	B_LYS_643	NZ	A_ASP_5	OD1	2.565
5UK2	B_LYS_643	NZ	A_ASP_5	OD2	3.717
5UK2	C_ARG_106	NH1	D_GLU_569	OE2	3.977
5UK2	C_ARG_106	NH2	D_GLU_569	OE2	2.287
5UK2	C_ARG_311	NH1	D_ASP_586	OD1	3.894
5UK2	C_ARG_311	NH1	D_ASP_590	OD1	2.932
5UK2	C_ARG_311	NH1	D_ASP_590	OD2	3.727
5UK2	C_ARG_311	NH2	D_ASP_586	OD1	3.043
5UK2	D_LYS_558	NZ	B_GLU_597	OE1	3.518
5UK2	D_LYS_558	NZ	B_GLU_597	OE2	3.929
5UK2	D_LYS_568	NZ	C_GLU_107	OE1	3.830
5UK2	D_ARG_576	NH1	F_GLU_574	OE1	3.823
5UK2	D_ARG_576	NH1	F_GLU_574	OE2	2.724
5UK2	D_ARG_576	NH2	E_GLU_104	OE2	3.539
5UK2	D_LYS_583	NZ	F_ASP_585	OD1	3.067
5UK2	D_LYS_583	NZ	F_ASP_585	OD2	3.783
5UK2	D_ARG_606	NH2	B_ASP_609	OD2	2.604
5UK2	D_LYS_643	NZ	C_GLU_4	OE1	3.112
5UK2	D_LYS_643	NZ	C_ASP_5	OD1	2.525
5UK2	D_LYS_643	NZ	C_ASP_5	OD2	3.631
5UK2	E_ARG_106	NH1	F_GLU_569	OE2	3.948
5UK2	E_ARG_106	NH2	F_GLU_569	OE2	2.300
5UK2	E_ARG_311	NH1	F_ASP_586	OD1	3.963
5UK2	E_ARG_311	NH1	F_ASP_590	OD1	2.962
5UK2	E_ARG_311	NH1	F_ASP_590	OD2	3.800
5UK2	E_ARG_311	NH2	F_ASP_586	OD1	3.154
5UK2	F_LYS_558	NZ	D_GLU_597	OE1	3.583
5UK2	F_LYS_558	NZ	D_GLU_597	OE2	3.900
5UK2	F_LYS_568	NZ	E_GLU_107	OE1	3.789
5UK2	F_ARG_576	NH1	B_GLU_574	OE1	3.881
5UK2	F_ARG_576	NH1	B_GLU_574	OE2	2.699
5UK2	F_ARG_576	NH2	A_GLU_104	OE2	3.688
5UK2	F_LYS_583	NZ	B_ASP_585	OD1	3.058
5UK2	F_LYS_583	NZ	B_ASP_585	OD2	3.745
5UK2	F_ARG_606	NH2	D_ASP_609	OD2	2.605
5UK2	F_LYS_643	NZ	E_GLU_4	OE1	3.293
5UK2	F_LYS_643	NZ	E_ASP_5	OD1	2.450
5UK2	F_LYS_643	NZ	E_ASP_5	OD2	3.677
5UK2	G_ARG_225	NH1	A_ASP_190	OD1	2.979
5UK2	G_ARG_225	NH1	A_ASP_190	OD2	3.894
5UK2	G_ARG_225	NH2	A_ASP_190	OD1	3.206
5UK2	G_ARG_225	NH2	A_ASP_190	OD2	2.785

5UK2	H_ARG_225	NH1	C_ASP_190	OD1	3.085
5UK2	H_ARG_225	NH2	C_ASP_190	OD1	3.195
5UK2	H_ARG_225	NH2	C_ASP_190	OD2	2.865
5UK2	I_ARG_225	NH1	E_ASP_190	OD1	2.888
5UK2	I_ARG_225	NH1	E_ASP_190	OD2	3.869
5UK2	I_ARG_225	NH2	E_ASP_190	OD1	3.014
5UK2	I_ARG_225	NH2	E_ASP_190	OD2	2.625

Table 1492: Interfacial 5UK2-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5UR8	A_ARG_59	NH1	B_ASP_95	OD1	3.084
5UR8	A_ARG_59	NH1	B_ASP_95	OD2	3.357
5UR8	A_LYS_138	NZ	B_GLU_215	OE2	2.961

Table 1493: Interfacial 5UR8-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5VL3	Q_HIS_213	NE2	H_GLU_58	OE2	3.352
5VL3	R_ARG_120	NH2	T_GLU_54	OE2	3.782
5VL3	R_LYS_127	NZ	T_GLU_54	OE1	2.927
5VL3	R_LYS_127	NZ	T_GLU_122	OE1	2.999
5VL3	R_HIS_213	NE2	A_GLU_58	OE2	3.157
5VL3	S_HIS_213	NE2	C_GLU_58	OE2	3.140
5VL3	T_LYS_127	NZ	R_GLU_54	OE1	3.658
5VL3	T_LYS_127	NZ	R_GLU_122	OE1	3.863
5VL3	T_HIS_213	NE2	E_GLU_58	OE2	3.636
5VL3	A_ARG_53	NH2	R_ASP_232	OD1	3.883
5VL3	A_ARG_53	NH2	R_ASP_232	OD2	3.340
5VL3	A_ARG_95	NH1	R_GLU_179	OE1	3.121
5VL3	A_ARG_95	NH1	R_GLU_179	OE2	3.607
5VL3	A_ARG_95	NH2	R_GLU_179	OE2	3.046
5VL3	A_LYS_210	NZ	B_GLU_124	OE2	3.976
5VL3	C_ARG_53	NH2	S_ASP_232	OD2	3.370
5VL3	C_ARG_95	NH1	S_GLU_179	OE1	3.505
5VL3	C_ARG_95	NH1	S_GLU_179	OE2	3.184
5VL3	C_ARG_95	NH2	S_GLU_179	OE2	3.815
5VL3	E_ARG_53	NH2	T_ASP_232	OD1	3.852
5VL3	E_ARG_53	NH2	T_ASP_232	OD2	3.470
5VL3	E_ARG_95	NH1	T_GLU_179	OE1	2.688
5VL3	E_ARG_95	NH1	T_GLU_179	OE2	2.993
5VL3	E_ARG_95	NH2	T_GLU_179	OE2	3.079
5VL3	E_LYS_210	NZ	F_GLU_	OE2	3.778
5VL3	E_LYS_	NZ	F_ASP_	OD2	3.984
5VL3	H_ARG_53	NH2	Q_ASP_232	OD1	3.950
5VL3	H_ARG_53	NH2	Q_ASP_232	OD2	3.411
5VL3	H_ARG_95	NH1	Q_GLU_179	OE1	3.431
5VL3	H_ARG_95	NH1	Q_GLU_179	OE2	3.819
5VL3	H_ARG_95	NH2	Q_GLU_179	OE2	3.149
5VL3	L_ARG_18	NH2	R_GLU_36	OE2	3.892

Table 1494: Interfacial 5VL3-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5VN8	G_LYS_34	NZ	A_ASP_612	OD1	3.263
5VN8	G_LYS_46	NZ	A_GLU_632	OE1	3.416
5VN8	G_LYS_46	NZ	A_GLU_632	OE2	2.866
5VN8	A_ARG_542	NH2	C_GLU_647	OE2	2.749
5VN8	A_ARG_579	NH1	C_GLU_584	OE1	3.931
5VN8	H_ARG_28	NH1	G_ASP_457	OD1	2.893
5VN8	L_HIS_49	ND1	H_ASP_101	OD1	3.097
5VN8	D_LYS_34	NZ	B_ASP_612	OD1	3.397
5VN8	D_LYS_46	NZ	B_GLU_632	OE1	3.407
5VN8	D_LYS_46	NZ	B_GLU_632	OE2	2.853
5VN8	B_ARG_542	NH2	A_GLU_647	OE1	3.985
5VN8	B_ARG_542	NH2	A_GLU_647	OE2	2.712
5VN8	B_ARG_579	NH1	A_GLU_584	OE1	3.986
5VN8	F_ARG_28	NH1	D_ASP_457	OD1	2.808
5VN8	J_HIS_49	ND1	F_ASP_101	OD1	3.213
5VN8	E_LYS_34	NZ	C_ASP_612	OD1	3.266
5VN8	E_LYS_46	NZ	C_GLU_632	OE1	3.380
5VN8	E_LYS_46	NZ	C_GLU_632	OE2	2.776
5VN8	C_ARG_542	NH2	B_GLU_647	OE2	2.738
5VN8	C_ARG_579	NH1	B_GLU_584	OE1	3.772
5VN8	I_ARG_28	NH1	E_ASP_457	OD1	3.234
5VN8	K_HIS_49	ND1	I_ASP_101	OD1	3.072
5VN8	K_HIS_49	NE2	I_ASP_101	OD1	3.981

Table 1495: Interfacial 5VN8-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5VXJ	B_ARG_19	NH2	A_ASP_97	OD1	2.652
5VXJ	B_ARG_50	NH1	I_GLU_200	OE1	2.921
5VXJ	B_ARG_50	NH2	I_GLU_200	OE1	3.757
5VXJ	B_LYS_76	NZ	A_GLU_122	OE1	2.874
5VXJ	B_HIS_80	NE2	A_ASP_144	OD1	3.165
5VXJ	B_HIS_80	NE2	A_ASP_144	OD2	3.364
5VXJ	D_ARG_19	NH1	C_ASP_97	OD1	3.252
5VXJ	D_ARG_50	NH1	E_GLU_200	OE1	3.721
5VXJ	D_ARG_50	NH2	E_GLU_200	OE1	3.781
5VXJ	D_LYS_76	NZ	C_GLU_122	OE1	3.854
5VXJ	D_HIS_80	NE2	C_ASP_144	OD1	3.067
5VXJ	D_HIS_80	NE2	C_ASP_144	OD2	3.196
5VXJ	E_LYS_137	NZ	F_ASP_73	OD1	3.543
5VXJ	E_LYS_137	NZ	F_ASP_73	OD2	2.771
5VXJ	F_ARG_19	NH2	E_ASP_97	OD1	2.921
5VXJ	F_ARG_50	NH1	G_GLU_200	OE1	3.576
5VXJ	F_ARG_50	NH2	G_GLU_200	OE1	2.702
5VXJ	F_LYS_76	NZ	E_GLU_122	OE1	3.693
5VXJ	F_HIS_80	NE2	E_ASP_144	OD1	3.009
5VXJ	F_HIS_80	NE2	E_ASP_144	OD2	3.134
5VXJ	G_LYS_137	NZ	H_ASP_73	OD1	3.131
5VXJ	G_LYS_137	NZ	H_ASP_73	OD2	2.336
5VXJ	H_ARG_19	NH2	G_ASP_97	OD1	2.467
5VXJ	H_LYS_76	NZ	G_ASP_124	OD2	3.951
5VXJ	H_HIS_80	NE2	G_ASP_144	OD1	3.186
5VXJ	H_HIS_80	NE2	G_ASP_144	OD2	3.321
5VXJ	I_LYS_137	NZ	J_ASP_73	OD1	3.804
5VXJ	I_LYS_137	NZ	J_ASP_73	OD2	2.902
5VXJ	J_ARG_19	NH2	I_ASP_97	OD1	2.772
5VXJ	J_LYS_76	NZ	I_GLU_122	OE2	2.338
5VXJ	J_HIS_80	NE2	I_ASP_144	OD1	3.036
5VXJ	J_HIS_80	NE2	I_ASP_144	OD2	3.151

Table 1496: Interfacial 5VXJ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5VXL	A_LYS_205	NZ	B_ASP_52	OD2	2.998
5VXL	B_ARG_102	NH1	A_GLU_201	OE1	3.097
5VXL	B_ARG_102	NH2	A_GLU_201	OE1	3.202
5VXL	B_ARG_102	NH2	A_GLU_201	OE2	2.871

Table 1497: Interfacial 5VXL-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5VXM	A_LYS_205	NZ	B_ASP_53	OD1	3.221
5VXM	A_LYS_205	NZ	B_ASP_53	OD2	3.090
5VXM	B_ARG_59	NH2	A_GLU_201	OE1	3.364

Table 1498: Interfacial 5VXM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5VXR	H_LYS_214	NZ	L_GLU_123	OE2	2.932

Table 1499: Interfacial 5VXR-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5VZR	H.LYS_219	NZ	L.GLU_123	OE2	3.208
5VZR	L.ARG_96	NH2	H.ASP_100C	OD2	3.042
5VZR	A.LYS_219	NZ	B.GLU_123	OE1	3.381
5VZR	B.ARG_96	NH2	A.ASP_100C	OD2	2.983

Table 1500: Interfacial 5VZR-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5W9H	A_ARG_758	NH1	p_ASP_740	OD1	3.106
5W9H	A_ARG_1113	NH2	D_GLU_1105	OE1	3.583
5W9H	A_ARG_1179	NH2	B_ASP_31	OD1	2.752
5W9H	C_ARG_96	NH1	B_ASP_100C	OD2	2.859
5W9H	C_ARG_96	NH2	A_GLU_1183	OE1	3.871
5W9H	C_ARG_96	NH2	A_GLU_1183	OE2	2.827
5W9H	C_ARG_96	NH2	B_ASP_100C	OD2	2.885
5W9H	D_ARG_1113	NH1	G_GLU_1105	OE1	3.247
5W9H	F_ARG_96	NH1	E_ASP_100C	OD2	2.830
5W9H	F_ARG_96	NH2	E_ASP_100C	OD2	2.948
5W9H	G_ARG_758	NH1	r_ASP_740	OD1	2.922
5W9H	G_ARG_1113	NH2	A_GLU_1105	OE1	3.110
5W9H	G_ARG_1179	NH2	H_ASP_31	OD1	2.809
5W9H	I_ARG_96	NH1	H_ASP_100C	OD2	2.791
5W9H	I_ARG_96	NH2	G_GLU_1183	OE2	2.911
5W9H	I_ARG_96	NH2	H_ASP_100C	OD2	2.950
5W9H	p_HIS_681	NE2	D_ASP_910	OD1	2.819
5W9H	p_HIS_681	NE2	D_ASP_910	OD2	3.760
5W9H	r_HIS_681	NE2	A_ASP_910	OD1	2.850
5W9H	r_HIS_681	NE2	A_ASP_910	OD2	3.840

Table 1501: Interfacial 5W9H-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5W9I	A_ARG.758	NH1	B_ASP.740	OD1	2.830
5W9I	A_ARG.847	NH1	F_ASP.726	OD1	3.733
5W9I	A_ARG.847	NH1	F_ASP.726	OD2	2.884
5W9I	A_ARG.1113	NH2	I_GLU.1105	OE2	2.773
5W9I	A_ARG.1179	NH2	C_ASP.31	OD1	2.834
5W9I	B_HIS.681	NE2	I_ASP.910	OD1	2.801
5W9I	B_HIS.681	NE2	I_ASP.910	OD2	3.893
5W9I	D_ARG.96	NH1	C_ASP.100C	OD2	2.837
5W9I	D_ARG.96	NH2	A_GLU.1183	OE2	2.862
5W9I	D_ARG.96	NH2	C_ASP.100C	OD2	2.920
5W9I	E_ARG.758	NH1	F_ASP.740	OD1	2.820
5W9I	E_ARG.847	NH1	J_ASP.726	OD1	3.709
5W9I	E_ARG.847	NH1	J_ASP.726	OD2	2.881
5W9I	E_ARG.1179	NH2	G_ASP.31	OD1	2.831
5W9I	F_HIS.681	NE2	A_ASP.910	OD1	2.878
5W9I	F_HIS.681	NE2	A_ASP.910	OD2	3.982
5W9I	H_ARG.96	NH1	G_ASP.100C	OD2	2.856
5W9I	H_ARG.96	NH2	E_GLU.1183	OE2	2.871
5W9I	H_ARG.96	NH2	G_ASP.100C	OD2	2.925
5W9I	I_ARG.758	NH1	J_ASP.740	OD1	2.804
5W9I	I_ARG.847	NH1	B_ASP.726	OD1	3.716
5W9I	I_ARG.847	NH1	B_ASP.726	OD2	2.881
5W9I	I_ARG.1113	NH2	E_GLU.1105	OE2	2.821
5W9I	I_ARG.1179	NH2	K_ASP.31	OD1	2.785
5W9I	J_HIS.681	NE2	E_ASP.910	OD1	2.832
5W9I	L_ARG.96	NH1	K_ASP.100C	OD2	2.856
5W9I	L_ARG.96	NH2	I_GLU.1183	OE2	2.872
5W9I	L_ARG.96	NH2	K_ASP.100C	OD2	2.922

Table 1502: Interfacial 5W9I-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5W9J	D_ARG_1113	NH2	G_GLU_1105	OE1	3.627
5W9J	D_ARG_1113	NH2	G_GLU_1105	OE2	2.779
5W9J	F_ARG_96	NH1	E_ASP_100C	OD1	3.873
5W9J	F_ARG_96	NH1	E_ASP_100C	OD2	3.469
5W9J	A_ARG_1113	NH2	D_GLU_1105	OE1	3.626
5W9J	A_ARG_1113	NH2	D_GLU_1105	OE2	2.778
5W9J	C_ARG_96	NH1	B_ASP_100C	OD1	3.873
5W9J	C_ARG_96	NH1	B_ASP_100C	OD2	3.470
5W9J	G_ARG_1113	NH2	A_GLU_1105	OE1	3.626
5W9J	G_ARG_1113	NH2	A_GLU_1105	OE2	2.777
5W9J	I_ARG_96	NH1	H_ASP_100C	OD1	3.873
5W9J	I_ARG_96	NH1	H_ASP_100C	OD2	3.470

Table 1503: Interfacial 5W9J-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID** **residue name** **residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5W9K	A_ARG_758	NH1	J_ASP_740	OD1	3.054
5W9K	A_ARG_1113	NH2	D_GLU_1105	OE1	3.698
5W9K	C_ARG_96	NH1	B_ASP_100C	OD2	2.822
5W9K	C_ARG_96	NH2	A_GLU_1183	OE1	3.683
5W9K	C_ARG_96	NH2	B_ASP_100C	OD2	3.420
5W9K	D_ARG_847	NH2	A_GLU_1017	OE2	3.108
5W9K	D_ARG_1113	NH1	G_GLU_1105	OE2	3.336
5W9K	F_ARG_96	NH1	E_ASP_100C	OD2	2.856
5W9K	F_ARG_96	NH2	D_GLU_1183	OE2	3.059
5W9K	F_ARG_96	NH2	E_ASP_100C	OD2	3.317
5W9K	G_ARG_758	NH1	L_ASP_740	OD1	3.028
5W9K	G_ARG_758	NH2	L_ASP_740	OD1	3.483
5W9K	G_ARG_847	NH1	K_ASP_726	OD2	3.336
5W9K	G_ARG_1113	NH2	A_GLU_1105	OE2	3.565
5W9K	I_ARG_96	NH1	H_ASP_100C	OD2	2.828
5W9K	I_ARG_96	NH2	G_GLU_1183	OE2	3.651
5W9K	I_ARG_96	NH2	H_ASP_100C	OD2	3.553
5W9K	J_HIS_681	NE2	D_ASP_910	OD1	2.963
5W9K	J_ARG_700	NH2	A_GLU_756	OE2	2.841
5W9K	L_HIS_681	NE2	A_ASP_910	OD1	3.027
5W9K	L_HIS_681	NE2	A_ASP_910	OD2	3.875
5W9K	L_ARG_700	NH2	G_GLU_756	OE2	2.893

Table 1504: Interfacial 5W9K-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5W9L	A_ARG.758	NH1	B_ASP.740	OD1	2.964
5W9L	A_ARG.758	NH2	B_ASP.740	OD1	3.858
5W9L	A_ARG.1113	NH2	D_GLU.1105	OE1	3.448
5W9L	A_ARG.1113	NH2	D_GLU.1105	OE2	2.879
5W9L	F_ARG.96	NH1	E_ASP.100C	OD2	3.246
5W9L	F_ARG.96	NH2	D_GLU.1183	OE2	2.643
5W9L	F_ARG.96	NH2	E_ASP.100C	OD2	3.370
5W9L	G_ARG.758	NH1	J_ASP.740	OD1	2.859
5W9L	G_ARG.758	NH2	J_ASP.740	OD1	3.792
5W9L	G_ARG.1179	NH2	H_ASP.31	OD1	2.753
5W9L	I_ARG.96	NH1	H_ASP.100C	OD2	2.945
5W9L	I_ARG.96	NH2	H_ASP.100C	OD2	2.982
5W9L	B_HIS.681	NE2	D_ASP.910	OD1	2.803
5W9L	B_HIS.681	NE2	D_ASP.910	OD2	3.795
5W9L	B_ARG.700	NH1	A_GLU.756	OE2	2.893
5W9L	J_HIS.681	NE2	A_ASP.910	OD1	2.810
5W9L	J_HIS.681	NE2	A_ASP.910	OD2	3.815

Table 1505: Interfacial 5W9L-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5W9M	A_ARG.758	NH1	E_ASP.740	OD1	2.862
5W9M	A_ARG.758	NH2	E_ASP.740	OD1	2.970
5W9M	A_ARG.847	NH1	J_ASP.726	OD2	3.850
5W9M	C_ARG.96	NH1	B_ASP.100C	OD2	2.894
5W9M	C_ARG.96	NH2	A_GLU.1183	OE2	2.938
5W9M	C_ARG.96	NH2	B_ASP.100C	OD2	2.940
5W9M	D_ARG.847	NH1	A_GLU.1017	OE2	3.300
5W9M	D_ARG.847	NH2	A_GLU.1017	OE2	3.532
5W9M	G_ARG.758	NH1	J_ASP.740	OD1	2.816
5W9M	G_ARG.758	NH2	J_ASP.740	OD1	3.407
5W9M	G_ARG.1113	NH2	A_GLU.1105	OE1	3.823
5W9M	G_ARG.1113	NH2	A_GLU.1105	OE2	2.800
5W9M	G_ARG.1179	NH1	H_ASP.31	OD1	3.713
5W9M	I_ARG.96	NH1	H_ASP.100C	OD2	2.840
5W9M	I_ARG.96	NH2	G_GLU.1183	OE2	2.957
5W9M	I_ARG.96	NH2	H_ASP.100C	OD2	3.363
5W9M	E_HIS.681	NE2	D_ASP.910	OD1	2.869
5W9M	E_HIS.681	NE2	D_ASP.910	OD2	3.974
5W9M	E_ARG.700	NH2	A_GLU.756	OE1	3.024
5W9M	E_ARG.700	NH2	A_GLU.756	OE2	3.469
5W9M	F_HIS.681	NE2	G_ASP.910	OD1	2.934
5W9M	F_HIS.681	NE2	G_ASP.910	OD2	3.892
5W9M	J_HIS.681	NE2	A_ASP.910	OD1	3.021

Table 1506: Interfacial 5W9M-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5W9N	A_ARG_758	NH1	H_ASP_740	OD1	3.061
5W9N	A_ARG_758	NH2	H_ASP_740	OD1	3.534
5W9N	C_ARG_96	NH1	B_ASP_100C	OD2	2.860
5W9N	C_ARG_96	NH2	A_GLU_1183	OE2	2.942
5W9N	C_ARG_96	NH2	B_ASP_100C	OD2	3.629
5W9N	F_ARG_96	NH1	E_ASP_100C	OD2	2.898
5W9N	F_ARG_96	NH2	D_GLU_1183	OE2	3.465
5W9N	F_ARG_96	NH2	E_ASP_100C	OD2	3.359
5W9N	G_ARG_758	NH1	J_ASP_740	OD1	2.883
5W9N	G_ARG_758	NH2	J_ASP_740	OD1	3.992
5W9N	G_ARG_1113	NH2	A_GLU_1105	OE1	3.089
5W9N	H_HIS_681	NE2	D_ASP_910	OD1	2.909
5W9N	H_HIS_681	NE2	D_ASP_910	OD2	3.885
5W9N	J_HIS_681	NE2	A_ASP_910	OD1	2.923
5W9N	J_HIS_681	NE2	A_ASP_910	OD2	3.770

Table 1507: Interfacial 5W9N-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5W9O	A_ARG.758	NH1	J_ASP.740	OD1	2.989
5W9O	A_ARG.1113	NH2	D_GLU.1105	OE1	3.178
5W9O	A_ARG.1179	NH2	B_ASP.31	OD1	2.796
5W9O	C_ARG.96	NH1	B_ASP.100C	OD2	3.180
5W9O	C_ARG.96	NH2	B_ASP.100C	OD2	2.879
5W9O	D_ARG.847	NH1	J_ASP.726	OD2	2.979
5W9O	D_ARG.1113	NH1	G_GLU.1105	OE1	3.664
5W9O	F_ARG.96	NH1	E_ASP.100C	OD2	2.799
5W9O	F_ARG.96	NH2	D_GLU.1183	OE2	3.799
5W9O	F_ARG.96	NH2	E_ASP.100C	OD2	3.255
5W9O	G_ARG.758	NH1	L_ASP.740	OD1	2.934
5W9O	G_ARG.847	NH1	K_ASP.726	OD2	3.097
5W9O	G_ARG.1179	NH2	H_ASP.31	OD1	2.843
5W9O	I_ARG.96	NH1	H_ASP.100C	OD2	3.979
5W9O	I_ARG.96	NH2	G_GLU.1183	OE2	2.715
5W9O	I_ARG.96	NH2	H_ASP.100C	OD2	3.993
5W9O	J_HIS.681	NE2	D_ASP.910	OD1	2.932
5W9O	J_ARG.700	NH2	A_GLU.756	OE1	3.931
5W9O	J_ARG.700	NH2	A_GLU.756	OE2	2.914
5W9O	L_HIS.681	NE2	A_ASP.910	OD1	3.028
5W9O	L_HIS.681	NE2	A_ASP.910	OD2	3.886

Table 1508: Interfacial 5W9O-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5W9P	J_ARG.758	NH2	A_ASP.740	OD1	2.970
5W9P	J_ARG.847	NH1	C_ASP.726	OD1	3.573
5W9P	J_ARG.847	NH1	C_ASP.726	OD2	2.973
5W9P	J_ARG.1113	NH2	H_GLU.1105	OE1	3.990
5W9P	J_ARG.1113	NH2	H_GLU.1105	OE2	2.796
5W9P	J_ARG.1179	NH2	F_ASP.31	OD1	2.888
5W9P	A_HIS.681	NE2	H_ASP.910	OD1	3.149
5W9P	A_HIS.681	NE2	H_ASP.910	OD2	3.352
5W9P	A_ARG.691	NH2	H_GLU.818	OE2	2.969
5W9P	A_ARG.700	NH2	J_GLU.756	OE2	2.978
5W9P	G_ARG.1212	NH1	J_GLU.1183	OE2	3.421
5W9P	G_ARG.1212	NH2	J_GLU.1183	OE2	2.921
5W9P	G_ARG.1212	NH2	F_ASP.100C	OD2	2.848
5W9P	B_ARG.758	NH2	C_ASP.740	OD1	2.971
5W9P	B_ARG.847	NH1	I_ASP.726	OD1	3.572
5W9P	B_ARG.847	NH1	I_ASP.726	OD2	2.973
5W9P	B_ARG.1113	NH2	J_GLU.1105	OE1	3.989
5W9P	B_ARG.1113	NH2	J_GLU.1105	OE2	2.795
5W9P	B_ARG.1179	NH2	D_ASP.31	OD1	2.887
5W9P	C_HIS.681	NE2	J_ASP.910	OD1	3.149
5W9P	C_HIS.681	NE2	J_ASP.910	OD2	3.352
5W9P	C_ARG.691	NH2	J_GLU.818	OE2	2.970
5W9P	C_ARG.700	NH2	B_GLU.756	OE2	2.978
5W9P	E_ARG.1212	NH1	B_GLU.1183	OE2	3.420
5W9P	E_ARG.1212	NH2	B_GLU.1183	OE2	2.920
5W9P	E_ARG.1212	NH2	D_ASP.100C	OD2	2.848
5W9P	H_ARG.758	NH2	I_ASP.740	OD1	2.969
5W9P	H_ARG.847	NH1	A_ASP.726	OD1	3.572
5W9P	H_ARG.847	NH1	A_ASP.726	OD2	2.973
5W9P	H_ARG.1113	NH2	B_GLU.1105	OE1	3.989
5W9P	H_ARG.1113	NH2	B_GLU.1105	OE2	2.795
5W9P	H_ARG.1179	NH2	K_ASP.31	OD1	2.888
5W9P	I_HIS.681	NE2	B_ASP.910	OD1	3.149
5W9P	I_HIS.681	NE2	B_ASP.910	OD2	3.352
5W9P	I_ARG.691	NH2	B_GLU.818	OE2	2.970
5W9P	I_ARG.700	NH2	H_GLU.756	OE2	2.977
5W9P	L_ARG.1212	NH1	H_GLU.1183	OE2	3.420
5W9P	L_ARG.1212	NH2	H_GLU.1183	OE2	2.921
5W9P	L_ARG.1212	NH2	K_ASP.100C	OD2	2.848

Table 1509: Interfacial 5W9P-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5WK4	D_ARG_29	NH2	E_ASP_36	OD1	3.168
5WK4	D_ARG_29	NH2	E_ASP_36	OD2	3.056
5WK4	D_ARG_101	NH2	E_ASP_50	OD2	3.021
5WK4	A_HIS_174	NE2	D_GLU_65	OE2	2.738
5WK4	B_ARG_29	NH2	C_ASP_36	OD1	3.257
5WK4	B_ARG_29	NH2	C_ASP_36	OD2	2.944
5WK4	B_ARG_101	NH1	C_ASP_50	OD2	3.997
5WK4	B_ARG_101	NH2	C_ASP_50	OD2	2.811
5WK4	C_ARG_29	NH2	B_ASP_36	OD1	3.196
5WK4	C_ARG_29	NH2	B_ASP_36	OD2	3.146
5WK4	C_ARG_101	NH1	B_ASP_50	OD2	3.840
5WK4	C_ARG_101	NH2	B_ASP_50	OD2	2.874
5WK4	E_ARG_29	NH2	D_ASP_36	OD1	3.889
5WK4	E_ARG_101	NH2	D_ASP_50	OD2	2.922

Table 1510: Interfacial 5WK4-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5WKQ	A_ARG_135	NH1	B_ASP_212	OD1	3.924
5WKQ	A_ARG_135	NH2	B_ASP_212	OD1	3.057
5WKQ	B_HIS_207	ND1	A_GLU_131	OE1	3.383
5WKQ	B_HIS_207	ND1	A_GLU_131	OE2	2.652

Table 1511: Interfacial 5WKQ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5WNA	H_LYS_220	NZ	L_GLU_122	OE2	3.667
5WNA	H_LYS_225	NZ	L_ASP_121	OD1	3.706
5WNA	L_LYS_39	NZ	D_GLU_81	OE1	2.898
5WNA	L_LYS_39	NZ	D_GLU_81	OE2	2.887
5WNA	C_LYS_220	NZ	D_GLU_122	OE2	3.567
5WNA	D_LYS_39	NZ	L_GLU_81	OE1	3.744

Table 1512: Interfacial 5WNA-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5WNB	H_LYS_140	NZ	L_GLU_212	OE1	3.467
5WNB	H_LYS_140	NZ	L_GLU_212	OE2	3.708
5WNB	L_ARG_61	NH1	M_GLU_79	OE2	3.612

Table 1513: Interfacial 5WNB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5XBM	A_LYS_205	NZ	B_ASP_139	OD1	3.654
5XBM	B_LYS_217	NZ	A_GLU_121	OE1	2.614
5XBM	B_LYS_217	NZ	A_GLU_121	OE2	3.625
5XBM	E_LYS_217	NZ	D_GLU_121	OE2	3.463
5XBM	F_ARG_77	NH1	D_ASP_31	OD1	3.188
5XBM	F_ARG_77	NH2	D_ASP_31	OD1	3.156
5XBM	F_ARG_77	NH2	D_ASP_31	OD2	3.938
5XBM	F_LYS_161	NZ	C_GLU_154	OE2	3.149

Table 1514: Interfacial 5XBM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5XCQ	A_LYS_13	NZ	B_ASP_154	OD1	3.910
5XCQ	B_LYS_144	NZ	A_GLU_142	OE1	3.005
5XCQ	B_LYS_144	NZ	A_GLU_142	OE2	2.931

Table 1515: Interfacial 5XCQ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5XCR	A_LYS_13	NZ	B_ASP_154	OD1	3.316
5XCR	A_LYS_13	NZ	B_ASP_154	OD2	2.938
5XCR	A_ARG_147	NH2	B_GLU_135	OE2	3.104
5XCR	A_LYS_149	NZ	B_ASP_41	OD1	2.692
5XCR	A_LYS_149	NZ	B_ASP_41	OD2	3.682
5XCR	A_LYS_153	NZ	B_ASP_41	OD1	3.567
5XCR	A_LYS_153	NZ	B_ASP_41	OD2	3.385
5XCR	B_LYS_144	NZ	A_GLU_142	OE1	2.665
5XCR	B_LYS_144	NZ	A_GLU_142	OE2	3.686
5XCR	D_LYS_149	NZ	E_ASP_41	OD1	2.596
5XCR	D_LYS_149	NZ	E_ASP_41	OD2	3.537
5XCR	D_LYS_149	NZ	E_GLU_137	OE1	2.552
5XCR	D_LYS_149	NZ	E_GLU_137	OE2	3.483
5XCR	D_ARG_154	NH2	E_ASP_131	OD1	2.972
5XCR	E_LYS_144	NZ	D_GLU_142	OE1	2.644
5XCR	E_LYS_144	NZ	D_GLU_142	OE2	3.385

Table 1516: Interfacial 5XCR-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5XCS	A_LYS_43	NZ	B_GLU_140	OE2	2.517
5XCS	A_ARG_95	NH1	B_ASP_91	OD1	2.738
5XCS	A_ARG_95	NH1	B_ASP_91	OD2	3.741
5XCS	A_ARG_95	NH2	B_ASP_91	OD1	3.421
5XCS	A_ARG_95	NH2	C_ASP_7	OD1	3.700
5XCS	A_ARG_95	NH2	C_ASP_7	OD2	2.872
5XCS	A_LYS_100A	NZ	B_GLU_55	OE1	2.609
5XCS	A_LYS_100A	NZ	B_GLU_55	OE2	3.239
5XCS	A_LYS_149	NZ	B_GLU_137	OE1	3.069
5XCS	A_LYS_149	NZ	B_GLU_137	OE2	3.874
5XCS	B_HIS_94	NE2	C_ASP_7	OD2	3.772
5XCS	B_LYS_144	NZ	A_GLU_142	OE1	3.111
5XCS	B_LYS_144	NZ	A_GLU_142	OE2	3.511
5XCS	B_ARG_149	NH1	A_ASP_136	OD1	2.816

Table 1517: Interfacial 5XCS-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5XCT	B_LYS_144	NZ	A_GLU_142	OE1	2.822
5XCT	B_LYS_144	NZ	A_GLU_142	OE2	3.117

Table 1518: Interfacial 5XCT-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5XCU	A_LYS_13	NZ	B_ASP_154	OD2	3.098
5XCU	A_ARG_95	NH1	B_ASP_91	OD1	2.822
5XCU	A_ARG_95	NH1	B_ASP_91	OD2	3.880
5XCU	A_ARG_95	NH2	B_ASP_91	OD1	3.668
5XCU	A_ARG_95	NH2	C_ASP_7	OD1	3.592
5XCU	A_ARG_95	NH2	C_ASP_7	OD2	2.664
5XCU	A_LYS_100A	NZ	B_GLU_55	OE1	3.292
5XCU	A_LYS_100A	NZ	B_GLU_55	OE2	3.457
5XCU	A_LYS_149	NZ	B_GLU_137	OE1	3.142
5XCU	A_LYS_149	NZ	B_GLU_137	OE2	3.674
5XCU	B_HIS_94	NE2	C_ASP_7	OD2	3.530
5XCU	B_ARG_142	NH2	D_GLU_100	OE1	3.626
5XCU	B_ARG_142	NH2	D_GLU_100	OE2	3.496
5XCU	B_LYS_144	NZ	A_GLU_142	OE1	2.843
5XCU	B_LYS_144	NZ	A_GLU_142	OE2	2.719
5XCU	B_ARG_149	NH2	A_ASP_136	OD1	3.520
5XCU	D_LYS_13	NZ	E_ASP_154	OD2	2.965
5XCU	D_ARG_52A	NH1	A_GLU_144	OE1	3.014
5XCU	D_ARG_52A	NH1	A_GLU_144	OE2	3.323
5XCU	D_ARG_52A	NH2	A_GLU_144	OE2	3.086
5XCU	D_ARG_95	NH1	E_ASP_91	OD1	2.736
5XCU	D_ARG_95	NH1	E_ASP_91	OD2	3.660
5XCU	D_ARG_95	NH2	E_ASP_91	OD1	3.272
5XCU	D_ARG_95	NH2	F_ASP_7	OD1	3.878
5XCU	D_ARG_95	NH2	F_ASP_7	OD2	3.169
5XCU	D_LYS_100A	NZ	E_GLU_55	OE1	3.852
5XCU	D_LYS_100A	NZ	E_GLU_55	OE2	2.994
5XCU	D_LYS_149	NZ	E_GLU_137	OE1	2.785
5XCU	D_LYS_149	NZ	E_GLU_137	OE2	3.293
5XCU	E_LYS_30F	NZ	B_GLU_139	OE1	2.662
5XCU	E_LYS_30F	NZ	B_GLU_139	OE2	3.287
5XCU	E_HIS_94	NE2	F_ASP_7	OD2	3.551
5XCU	E_ARG_142	NH2	D_GLU_140	OE2	3.967
5XCU	E_LYS_144	NZ	D_GLU_142	OE1	3.438
5XCU	E_LYS_144	NZ	D_GLU_142	OE2	2.648

Table 1519: Interfacial 5XCU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5XCV	A_LYS_56	NZ	C_GLU_10	OE2	3.165
5XCV	A_LYS_56	NZ	C_ASP_11	OD1	3.842
5XCV	A_LYS_56	NZ	C_ASP_11	OD2	2.877
5XCV	A_ARG_131	NH1	D_GLU_142	OE2	2.857
5XCV	A_ARG_131	NH2	D_GLU_142	OE2	3.651
5XCV	A_LYS_149	NZ	B_GLU_137	OE1	3.135
5XCV	A_LYS_149	NZ	B_GLU_137	OE2	2.706
5XCV	A_ARG_154	NH2	B_ASP_131	OD1	2.532
5XCV	B_LYS_144	NZ	A_GLU_142	OE1	2.798
5XCV	B_LYS_144	NZ	A_GLU_142	OE2	3.295
5XCV	B_ARG_149	NH2	A_ASP_136	OD1	3.863
5XCV	B_ARG_149	NH2	A_ASP_136	OD2	3.941
5XCV	D_ARG_131	NH1	A_GLU_142	OE2	2.791
5XCV	D_ARG_131	NH2	A_GLU_142	OE2	3.693
5XCV	D_LYS_149	NZ	E_GLU_137	OE1	2.622
5XCV	D_LYS_149	NZ	E_GLU_137	OE2	3.565
5XCV	D_LYS_153	NZ	E_GLU_40	OE2	3.944
5XCV	E_LYS_144	NZ	D_GLU_142	OE1	2.798
5XCV	E_LYS_144	NZ	D_GLU_142	OE2	3.738

Table 1520: Interfacial 5XCV-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID residue name residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5XRT	A_LYS_27	NZ	B_GLU_97	OE2	3.178
5XRT	A_ARG_109	NH1	B_GLU_67	OE2	3.059
5XRT	A_ARG_109	NH2	B_GLU_67	OE2	3.511
5XRT	A_LYS_238	NZ	F_GLU_72	OE1	3.452
5XRT	A_LYS_238	NZ	F_GLU_72	OE2	2.683
5XRT	A_ARG_269	NH1	B_GLU_67	OE1	3.465
5XRT	A_ARG_307	NH1	F_ASP_90	OD2	3.867
5XRT	A_ARG_307	NH2	F_ASP_90	OD2	3.590
5XRT	A_LYS_310	NZ	B_ASP_90	OD1	2.844
5XRT	A_LYS_326	NZ	B_GLU_11	OE1	2.808
5XRT	A_LYS_326	NZ	B_GLU_11	OE2	2.925
5XRT	B_ARG_54	NH1	F_GLU_97	OE2	3.836
5XRT	B_ARG_54	NH2	F_GLU_97	OE2	2.767
5XRT	B_LYS_62	NZ	F_ASP_86	OD1	3.336
5XRT	B_LYS_62	NZ	F_ASP_86	OD2	2.617
5XRT	B_LYS_62	NZ	F_ASP_90	OD1	3.654
5XRT	B_LYS_62	NZ	F_ASP_90	OD2	2.589
5XRT	B_HIS_64	NE2	F_ASP_79	OD2	3.582
5XRT	B_ARG_76	NH1	D_GLU_74	OE1	3.704
5XRT	B_ARG_76	NH1	D_GLU_74	OE2	3.032
5XRT	B_ARG_76	NH2	D_GLU_74	OE1	2.984
5XRT	B_ARG_76	NH2	D_GLU_74	OE2	3.801
5XRT	B_ARG_76	NH2	D_GLU_81	OE1	2.864
5XRT	B_ARG_76	NH2	D_GLU_81	OE2	3.722
5XRT	B_ARG_123	NH2	F_ASP_132	OD2	3.663
5XRT	B_ARG_124	NH1	F_ASP_132	OD2	2.812
5XRT	B_ARG_127	NH2	F_GLU_131	OE1	3.103
5XRT	B_ARG_163	NH1	F_GLU_131	OE1	3.194
5XRT	B_ARG_163	NH1	F_GLU_131	OE2	3.563
5XRT	B_ARG_163	NH2	F_GLU_131	OE1	3.596
5XRT	B_ARG_163	NH2	F_GLU_131	OE2	2.598
5XRT	B_ARG_170	NH2	D_GLU_128	OE1	3.449
5XRT	B_ARG_170	NH2	D_GLU_128	OE2	3.578
5XRT	C_LYS_27	NZ	D_GLU_97	OE1	3.926
5XRT	C_LYS_27	NZ	D_GLU_97	OE2	3.340
5XRT	C_ARG_109	NH1	D_GLU_67	OE2	2.932
5XRT	C_LYS_238	NZ	B_GLU_72	OE2	3.031
5XRT	C_ARG_269	NH1	D_GLU_67	OE1	3.251
5XRT	C_ARG_307	NH2	B_ASP_90	OD2	3.134
5XRT	C_LYS_310	NZ	D_ASP_90	OD1	3.206
5XRT	C_LYS_310	NZ	D_ASP_90	OD2	3.892
5XRT	D_ARG_54	NH2	B_GLU_97	OE2	3.066
5XRT	D_LYS_62	NZ	B_ASP_86	OD1	3.579
5XRT	D_LYS_62	NZ	B_ASP_86	OD2	3.058
5XRT	D_LYS_62	NZ	B_ASP_90	OD1	3.574
5XRT	D_LYS_62	NZ	B_ASP_90	OD2	2.797
5XRT	D_HIS_64	NE2	B_ASP_79	OD2	3.856
5XRT	D_ARG_76	NH1	F_GLU_74	OE1	3.338
5XRT	D_ARG_76	NH1	F_GLU_74	OE2	2.885
5XRT	D_ARG_76	NH2	F_GLU_74	OE1	2.652
5XRT	D_ARG_76	NH2	F_GLU_74	OE2	3.749
5XRT	D_ARG_76	NH2	F_GLU_81	OE1	2.506
5XRT	D_ARG_76	NH2	F_GLU_81	OE2	3.677
5XRT	D_ARG_123	NH2	B_ASP_132	OD2	3.975
5XRT	D_ARG_124	NH1	B_ASP_132	OD1	3.986
5XRT	D_ARG_124	NH1	B_ASP_132	OD2	2.717
5XRT	D_ARG_127	NH2	B_GLU_131	OE1	2.649

5XRT	D_ARG_163	NH1	B_GLU_131	OE1	3.152
5XRT	D_ARG_163	NH1	B_GLU_131	OE2	3.070
5XRT	D_ARG_163	NH2	B_GLU_131	OE1	3.267
5XRT	D_ARG_163	NH2	B_GLU_131	OE2	2.951
5XRT	D_ARG_170	NH2	F_GLU_128	OE1	2.950
5XRT	D_ARG_170	NH2	F_GLU_128	OE2	3.791
5XRT	E_LYS_27	NZ	F_GLU_97	OE1	3.896
5XRT	E_LYS_27	NZ	F_GLU_97	OE2	3.675
5XRT	E_ARG_109	NH1	F_GLU_67	OE2	2.719
5XRT	E_ARG_109	NH2	F_GLU_67	OE2	3.732
5XRT	E_LYS_238	NZ	D_GLU_72	OE2	3.742
5XRT	E_ARG_269	NH1	F_GLU_67	OE1	2.954
5XRT	E_ARG_269	NH1	F_GLU_67	OE2	3.996
5XRT	E_ARG_307	NH1	D_ASP_90	OD2	3.580
5XRT	E_ARG_307	NH2	D_ASP_90	OD2	3.837
5XRT	E_LYS_310	NZ	F_ASP_90	OD1	3.115
5XRT	E_LYS_326	NZ	F_GLU_11	OE1	3.300
5XRT	F_ARG_54	NH2	D_GLU_97	OE2	3.005
5XRT	F_LYS_62	NZ	D_ASP_86	OD1	3.549
5XRT	F_LYS_62	NZ	D_ASP_86	OD2	2.499
5XRT	F_LYS_62	NZ	D_ASP_90	OD1	3.666
5XRT	F_LYS_62	NZ	D_ASP_90	OD2	2.972
5XRT	F_HIS_64	NE2	D_ASP_79	OD2	3.194
5XRT	F_ARG_76	NH1	B_GLU_74	OE1	3.311
5XRT	F_ARG_76	NH1	B_GLU_74	OE2	3.105
5XRT	F_ARG_76	NH2	B_GLU_74	OE1	2.768
5XRT	F_ARG_76	NH2	B_GLU_74	OE2	3.989
5XRT	F_ARG_76	NH2	B_GLU_81	OE1	2.869
5XRT	F_ARG_76	NH2	B_GLU_81	OE2	3.812
5XRT	F_ARG_124	NH1	D_ASP_132	OD2	3.024
5XRT	F_ARG_127	NH2	D_GLU_131	OE1	2.415
5XRT	F_ARG_163	NH1	D_GLU_131	OE1	3.516
5XRT	F_ARG_163	NH2	D_GLU_131	OE1	3.296
5XRT	F_ARG_163	NH2	D_GLU_131	OE2	2.611
5XRT	F_ARG_170	NH2	B_GLU_128	OE1	3.475
5XRT	F_ARG_170	NH2	B_GLU_128	OE2	3.657
5XRT	F_LYS_174	NZ	B_ASP_160	OD1	3.902
5XRT	G_LYS_27	NZ	H_GLU_97	OE2	3.228
5XRT	G_LYS_82	NZ	E_GLU_119	OE1	3.805
5XRT	G_ARG_109	NH1	H_GLU_67	OE1	3.826
5XRT	G_ARG_109	NH1	H_GLU_67	OE2	2.804
5XRT	G_ARG_269	NH1	H_GLU_67	OE1	3.306
5XRT	G_LYS_299	NZ	H_GLU_69	OE2	3.918
5XRT	G_LYS_310	NZ	H_ASP_90	OD1	2.955

Table 1521: Interfacial 5XRT-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5XWD	A_ARG_353	NH2	D_ASP_96	OD2	3.335
5XWD	A_HIS_409	NE2	H_ASP_108	OD2	2.707
5XWD	A_LYS_443	NZ	D_ASP_51	OD2	2.907
5XWD	A_LYS_465	NZ	D_ASP_53	OD2	3.314

Table 1522: Interfacial 5XWD-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5YC5	A_LYS_409	NZ	B_ASP_399	OD1	3.635
5YC5	A_LYS_409	NZ	B_ASP_399	OD2	2.875
5YC5	A_LYS_439	NZ	B_ASP_356	OD1	3.309
5YC5	B_LYS_409	NZ	A_ASP_399	OD1	3.731
5YC5	B_LYS_409	NZ	A_ASP_399	OD2	2.920
5YC5	C_LYS_120	NZ	A_ASP_265	OD2	2.563
5YC5	C_LYS_131	NZ	A_GLU_269	OE1	3.549
5YC5	C_LYS_131	NZ	A_GLU_269	OE2	2.940

Table 1523: Interfacial 5YC5-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
5ZV3	A.LYS_67	NZ	H.ASP_54	OD1	3.656
5ZV3	A.LYS_67	NZ	H.ASP_54	OD2	2.636
5ZV3	A.LYS_67	NZ	H.ASP_56	OD2	3.213
5ZV3	H.ARG_58	NH2	A.ASP_65	OD1	3.187
5ZV3	H.ARG_97	NH1	A.GLU_62	OE2	3.412
5ZV3	H.ARG_97	NH2	A.GLU_62	OE1	3.676
5ZV3	H.ARG_97	NH2	A.GLU_62	OE2	3.134
5ZV3	H.LYS_100	NZ	A.GLU_62	OE1	2.715
5ZV3	H.LYS_209	NZ	L.GLU_123	OE1	3.860

Table 1524: Interfacial 5ZV3-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6A3V	E_ARG_193	NH1	C_ASP_184	OD1	3.333
6A3V	I_ARG_193	NH1	K_ASP_184	OD1	3.791
6A3V	U_ARG_193	NH1	W_ASP_184	OD1	2.218
6A3V	U_ARG_193	NH1	W_ASP_184	OD2	3.282
6A3V	U_ARG_193	NH2	W_ASP_184	OD1	3.966
6A3V	U_ARG_193	NH2	W_ASP_184	OD2	3.892

Table 1525: Interfacial 6A3V-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6A3W	C_LYS_107	NZ	E_ASP_30	OD2	3.465
6A3W	C_LYS_114	NZ	B_ASP_51	OD2	2.835
6A3W	C_ARG_134	NH2	A_ASP_55	OD2	3.122
6A3W	D_LYS_43	NZ	K_ASP_26	OD1	2.407
6A3W	D_LYS_43	NZ	K_ASP_26	OD2	3.696
6A3W	F_LYS_114	NZ	E_ASP_51	OD2	2.834
6A3W	F_ARG_134	NH2	D_ASP_55	OD1	3.962
6A3W	F_ARG_134	NH2	D_ASP_55	OD2	2.895
6A3W	I_LYS_114	NZ	H_ASP_51	OD2	2.757
6A3W	I_LYS_115	NZ	L_ASP_119	OD1	3.708
6A3W	I_LYS_115	NZ	L_ASP_119	OD2	3.946
6A3W	I_ARG_134	NH2	G_ASP_55	OD1	3.740
6A3W	I_ARG_134	NH2	G_ASP_55	OD2	2.630
6A3W	I_ARG_154	NH1	E_ASP_26	OD1	2.965
6A3W	I_ARG_154	NH2	E_ASP_26	OD1	3.042
6A3W	L_LYS_107	NZ	H_ASP_30	OD1	3.282
6A3W	L_LYS_107	NZ	H_ASP_30	OD2	2.525
6A3W	L_LYS_114	NZ	K_ASP_51	OD2	2.893
6A3W	L_ARG_134	NH2	J_ASP_55	OD1	3.749
6A3W	L_ARG_134	NH2	J_ASP_55	OD2	2.496

Table 1526: Interfacial 6A3W-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6A76	H_LYS_213	NZ	L_GLU_123	OE1	3.460

Table 1527: Interfacial 6A76-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6A77	A_ARG_67	NH1	H_GLU_97	OE1	2.680
6A77	A_ARG_67	NH2	H_GLU_97	OE1	3.115
6A77	A_ARG_67	NH2	H_GLU_97	OE2	3.032

Table 1528: Interfacial 6A77-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6A78	A_LYS_57	NZ	H_GLU_97	OE1	3.795
6A78	L_LYS_63	NZ	B_ASP_23	OD1	3.699

Table 1529: Interfacial 6A78-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6A79	B_ARG_67	NH1	L_GLU_97	OE2	3.582

Table 1530: Interfacial 6A79-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6AL5	A_LYS_155	NZ	H_GLU_74	OE1	3.542
6AL5	A_LYS_220	NZ	H_ASP_55	OD1	3.389
6AL5	A_LYS_220	NZ	H_ASP_55	OD2	2.832
6AL5	A_LYS_220	NZ	H_ASP_57	OD2	3.301
6AL5	H_ARG_106	NH2	L_ASP_54	OD1	3.142
6AL5	H_ARG_106	NH2	L_ASP_54	OD2	3.298
6AL5	H_LYS_220	NZ	L_GLU_127	OE1	3.220

Table 1531: Interfacial 6AL5-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6AND	H_LYS_209	NZ	L_GLU_123	OE1	2.684
6AND	H_LYS_209	NZ	L_GLU_123	OE2	3.876
6AND	L_LYS_50	NZ	H_ASP_100	OD1	3.188

Table 1532: Interfacial 6AND-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6ANI	H_LYS_209	NZ	L_GLU_123	OE1	2.397
6ANI	I_LYS_209	NZ	M_GLU_123	OE2	3.950

Table 1533: Interfacial 6ANI-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6AQ7	H_HIS_34	NE2	A_GLU_199	OE1	3.934
6AQ7	H_HIS_34	NE2	A_GLU_199	OE2	2.717
6AQ7	H_ARG_49	NH1	A_GLU_199	OE2	2.744
6AQ7	H_LYS_209	NZ	L_GLU_127	OE2	2.651

Table 1534: Interfacial 6AQ7-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6ATT	H_LYS_217	NZ	L_GLU_129	OE1	3.069
6ATT	H_LYS_222	NZ	L_ASP_128	OD1	2.688
6ATT	L_ARG_32	NH1	A_GLU_216	OE1	2.742

Table 1535: Interfacial 6ATT-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6AZZ	F_LYS_209	NZ	E_GLU_124	OE2	3.461
6AZZ	E_ARG_77	NH1	B_GLU_79	OE2	3.685
6AZZ	E_ARG_77	NH2	B_GLU_79	OE1	3.407
6AZZ	E_ARG_77	NH2	B_GLU_79	OE2	3.489
6AZZ	E_LYS_130	NZ	F_ASP_144	OD2	3.330
6AZZ	C_LYS_209	NZ	B_GLU_124	OE1	3.784
6AZZ	C_LYS_209	NZ	B_GLU_124	OE2	2.655
6AZZ	B_LYS_130	NZ	C_ASP_144	OD2	3.121
6AZZ	A_LYS_90	NZ	B_ASP_51	OD1	3.552
6AZZ	A_LYS_90	NZ	B_ASP_51	OD2	2.501
6AZZ	A_LYS_108	NZ	B_ASP_53	OD2	3.868
6AZZ	D_LYS_90	NZ	E_ASP_51	OD1	3.639
6AZZ	D_LYS_90	NZ	E_ASP_51	OD2	2.901

Table 1536: Interfacial 6AZZ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6B08	C_LYS_143	NZ	B_GLU_125	OE2	2.599
6B08	A_LYS_90	NZ	B_ASP_51	OD1	2.529
6B08	A_LYS_90	NZ	B_ASP_51	OD2	3.708

Table 1537: Interfacial 6B08-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6B0E	B_HIS_164	ND1	A_ASP_167	OD2	3.677
6B0E	E_LYS_155	NZ	B_ASP_98	OD2	3.864

Table 1538: Interfacial 6B0E-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6B0G	D_ARG_100B	NH1	C_ASP_91	OD2	3.003
6B0G	D_ARG_100B	NH2	C_ASP_91	OD2	3.130
6B0G	D_LYS_214	NZ	C_GLU_123	OE2	3.176
6B0G	E_LYS_155	NZ	D_ASP_98	OD2	2.837

Table 1539: Interfacial 6B0G-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6BE2	H_LYS_154	NZ	L_GLU_129	OE2	2.747
6BE2	L_LYS_49	NZ	H_GLU_108	OE2	2.828
6BE2	L_ARG_100	NH2	H_ASP_98	OD1	2.914

Table 1540: Interfacial 6BE2-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6BE3	H_LYS_154	NZ	L_GLU_129	OE2	2.742
6BE3	H_LYS_220	NZ	L_GLU_128	OE1	3.265
6BE3	H_LYS_220	NZ	L_GLU_128	OE2	2.896
6BE3	L_LYS_49	NZ	H_GLU_108	OE2	2.860
6BE3	L_ARG_100	NH2	H_ASP_98	OD1	3.147
6BE3	L_ARG_100	NH2	H_ASP_109	OD1	3.865

Table 1541: Interfacial 6BE3-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6BE4	H_LYS_154	NZ	L_GLU_129	OE1	2.824
6BE4	L_ARG_100	NH2	H_ASP_98	OD1	3.253
6BE4	L_ARG_100	NH2	H_ASP_109	OD1	3.926

Table 1542: Interfacial 6BE4-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6BIT	I.HIS_35	NE2	H.GLU_54	OE1	3.340
6BIT	I.ARG_50	NH2	H.ASP_100	OD1	3.331
6BIT	I.ARG_50	NH2	H.ASP_101	OD1	3.135
6BIT	I.ARG_50	NH2	H.ASP_101	OD2	3.871
6BIT	I.LYS_59	NZ	H.ASP_100	OD1	3.680
6BIT	I.LYS_208	NZ	K.GLU_123	OE2	3.567
6BIT	I.ARG_213	NH1	L.ASP_143	OD1	3.423
6BIT	K.ARG_96	NH1	H.GLU_54	OE1	3.223
6BIT	K.ARG_96	NH2	H.GLU_54	OE1	2.904
6BIT	K.ARG_96	NH2	H.GLU_54	OE2	3.687
6BIT	H.LYS_53	NZ	L.ASP_52	OD1	3.518
6BIT	H.LYS_53	NZ	L.GLU_54	OE1	2.817
6BIT	H.LYS_96	NZ	L.ASP_52	OD2	2.786
6BIT	H.LYS_96	NZ	L.ASP_55	OD1	3.426
6BIT	H.LYS_96	NZ	L.ASP_55	OD2	2.655
6BIT	H.LYS_96	NZ	L.GLU_57	OE1	2.771
6BIT	J.HIS_35	NE2	G.GLU_54	OE1	3.221
6BIT	J.ARG_50	NH2	G.ASP_100	OD1	3.724
6BIT	J.ARG_50	NH2	G.ASP_101	OD1	3.330
6BIT	J.LYS_208	NZ	L.GLU_123	OE2	3.539
6BIT	L.ARG_96	NH1	G.GLU_54	OE1	3.007
6BIT	L.ARG_96	NH2	G.GLU_54	OE1	2.768
6BIT	L.ARG_96	NH2	G.GLU_54	OE2	3.419
6BIT	G.LYS_53	NZ	J.ASP_52	OD1	2.843
6BIT	G.LYS_53	NZ	J.ASP_52	OD2	3.656
6BIT	G.LYS_53	NZ	J.GLU_54	OE1	2.681
6BIT	G.LYS_96	NZ	J.ASP_52	OD2	2.719
6BIT	G.LYS_96	NZ	J.ASP_55	OD1	3.165
6BIT	G.LYS_96	NZ	J.ASP_55	OD2	2.701
6BIT	G.LYS_96	NZ	J.GLU_57	OE2	2.943

Table 1543: Interfacial 6BIT-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6BXA	A_ARG_37	NH1	C_GLU_101	OE1	3.957
6BXA	A_ARG_37	NH1	C_GLU_101	OE2	3.920
6BXA	A_ARG_37	NH2	C_GLU_101	OE1	3.689
6BXA	A_ARG_37	NH2	C_GLU_101	OE2	2.525
6BXA	A_LYS_77	NZ	C_ASP_34	OD2	2.860
6BXA	A_LYS_102	NZ	C_ASP_34	OD1	2.955
6BXA	A_LYS_184	NZ	B_ASP_133	OD2	2.709
6BXA	B_ARG_37	NH2	D_GLU_101	OE1	3.840
6BXA	B_ARG_37	NH2	D_GLU_101	OE2	2.839
6BXA	B_LYS_77	NZ	D_ASP_34	OD1	2.907
6BXA	B_LYS_102	NZ	D_ASP_34	OD2	3.845
6BXA	B_LYS_184	NZ	A_ASP_133	OD2	2.771

Table 1544: Interfacial 6BXA-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID residue name residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6BXC	A_LYS_184	NZ	C_ASP_34	OD2	3.851
6BXC	A_HIS_198	NE2	D_GLU_65	OE2	3.317
6BXC	B_LYS_159	NZ	D_ASP_34	OD2	3.891
6BXC	B_LYS_182	NZ	D_GLU_81	OE2	3.361
6BXC	B_LYS_184	NZ	D_ASP_34	OD2	3.547

Table 1545: Interfacial 6BXC-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6BXE	A_HIS_125	NE2	B_GLU_81	OE2	2.552
6BXE	B_HIS_125	NE2	A_GLU_81	OE2	3.833

Table 1546: Interfacial 6BXE-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6BZU	A_ARG_64	NH2	B_ASP_94	OD1	3.703
6BZU	A_LYS_209	NZ	B_GLU_123	OE2	3.980
6BZU	B_ARG_18	NH2	F_ASP_70	OD2	2.642
6BZU	B_ARG_24	NH1	F_ASP_76	OD1	3.597
6BZU	B_ARG_24	NH1	F_ASP_76	OD2	2.861
6BZU	C_ARG_64	NH2	D_ASP_94	OD1	3.618
6BZU	E_ARG_64	NH2	F_ASP_94	OD1	3.701
6BZU	F_ARG_24	NH1	B_ASP_76	OD1	3.333
6BZU	F_ARG_24	NH1	B_ASP_76	OD2	3.080
6BZU	G_ARG_64	NH2	H_ASP_94	OD1	3.197
6BZU	G_ARG_64	NH2	H_ASP_94	OD2	3.837
6BZU	G_LYS_209	NZ	H_GLU_123	OE1	2.734
6BZU	G_LYS_209	NZ	H_GLU_123	OE2	3.547

Table 1547: Interfacial 6BZU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6BZV	E_ARG_66	NH1	C_GLU_85	OE2	3.540
6BZV	E_ARG_66	NH2	C_GLU_85	OE2	3.482
6BZV	E_LYS_206	NZ	G_ASP_208	OD2	3.271
6BZV	E_LYS_209	NZ	F_GLU_123	OE1	3.953
6BZV	E_LYS_209	NZ	F_GLU_123	OE2	2.713
6BZV	A_LYS_209	NZ	B_GLU_123	OE1	2.709
6BZV	A_LYS_209	NZ	B_GLU_123	OE2	3.439
6BZV	C_LYS_209	NZ	D_GLU_123	OE1	2.619
6BZV	C_LYS_209	NZ	D_GLU_123	OE2	2.945
6BZV	G_HIS_164	NE2	H_ASP_167	OD1	3.817
6BZV	G_LYS_209	NZ	H_GLU_123	OE1	3.054
6BZV	G_LYS_209	NZ	H_GLU_123	OE2	3.192

Table 1548: Interfacial 6BZV-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID residue name residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6BZW	C_LYS_209	NZ	D_GLU_123	OE1	2.857
6BZW	C_LYS_209	NZ	D_GLU_123	OE2	3.990
6BZW	D_ARG_18	NH2	H_GLU_93	OE1	3.070
6BZW	A_LYS_209	NZ	B_GLU_123	OE1	2.988
6BZW	E_LYS_209	NZ	F_GLU_123	OE1	2.583
6BZW	E_LYS_209	NZ	F_GLU_123	OE2	3.254
6BZW	G_LYS_209	NZ	H_GLU_123	OE1	2.709
6BZW	G_LYS_209	NZ	H_GLU_123	OE2	2.569

Table 1549: Interfacial 6BZW-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6C5H	H_LYS_208	NZ	L_GLU_123	OE1	3.569

Table 1550: Interfacial 6C5H-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6C5I	H_HIS_164	NE2	L_ASP_167	OD2	3.802
6C5I	H_LYS_208	NZ	L_GLU_123	OE1	3.192

Table 1551: Interfacial 6C5I-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6C5J	H_HIS_164	ND1	L_ASP_167	OD1	3.598

Table 1552: Interfacial 6C5J-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6C6X	B_LYS_207	NZ	A_GLU_133	OE1	3.861

Table 1553: Interfacial 6C6X-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6C6Y	R_LYS_400	NZ	L_ASP_28	OD2	3.363
6C6Y	R_LYS_543	NZ	L_GLU_55	OE2	2.973
6C6Y	S_LYS_400	NZ	B_ASP_28	OD1	3.764
6C6Y	S_LYS_400	NZ	B_ASP_28	OD2	2.712
6C6Y	S_LYS_543	NZ	B_GLU_55	OE2	3.134

Table 1554: Interfacial 6C6Y-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6C6Z	A_ARG_542	NH1	C_GLU_95	OE1	3.387
6C6Z	A_ARG_542	NH1	C_GLU_95	OE2	2.704
6C6Z	A_ARG_542	NH2	C_GLU_95	OE1	2.635
6C6Z	A_ARG_542	NH2	C_GLU_95	OE2	3.577
6C6Z	B_ARG_542	NH1	H_GLU_95	OE1	3.238
6C6Z	B_ARG_542	NH1	H_GLU_95	OE2	2.770
6C6Z	B_ARG_542	NH2	H_GLU_95	OE1	2.578
6C6Z	B_ARG_542	NH2	H_GLU_95	OE2	3.689
6C6Z	C_LYS_209	NZ	D_GLU_123	OE1	2.970
6C6Z	C_LYS_209	NZ	D_GLU_123	OE2	3.150
6C6Z	C_LYS_214	NZ	D_ASP_122	OD2	2.844
6C6Z	D_HIS_27D	NE2	A_GLU_536	OE1	2.616
6C6Z	H_LYS_209	NZ	L_GLU_123	OE1	3.044
6C6Z	H_LYS_209	NZ	L_GLU_123	OE2	3.156
6C6Z	L_HIS_27D	NE2	B_GLU_536	OE1	2.931

Table 1555: Interfacial 6C6Z-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6CUJ	B_LYS_404	NZ	A_GLU_292	OE1	3.957

Table 1556: Interfacial 6CUJ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6DC3	H_LYS_143	NZ	L_GLU_125	OE2	3.101
6DC3	H_LYS_209	NZ	L_GLU_124	OE1	3.719
6DC3	F_LYS_168	NZ	H_ASP_53	OD2	2.485

Table 1557: Interfacial 6DC3-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6DC4	H_LYS_209	NZ	L_GLU_123	OE1	3.056

Table 1558: Interfacial 6DC4-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6DC5	A.LYS.156	NZ	D.GLU.463	OE1	3.876
6DC5	A.LYS.399	NZ	G.GLU.497	OE2	2.871
6DC5	D.LYS.75	NZ	G.GLU.218	OE2	2.912
6DC5	D.LYS.209	NZ	E.GLU.53	OE2	3.142
6DC5	D.LYS.209	NZ	E.ASP.100G	OD2	3.755
6DC5	G.LYS.77	NZ	A.GLU.222	OE2	3.675
6DC5	G.LYS.209	NZ	H.GLU.53	OE2	3.533
6DC5	G.LYS.209	NZ	H.ASP.100G	OD2	3.715
6DC5	G.LYS.399	NZ	D.GLU.497	OE1	3.390
6DC5	G.LYS.399	NZ	D.GLU.497	OE2	2.804
6DC5	B.LYS.209	NZ	C.GLU.123	OE1	2.374
6DC5	B.LYS.209	NZ	C.GLU.123	OE2	3.312
6DC5	E.LYS.209	NZ	F.GLU.123	OE1	3.793
6DC5	H.LYS.	NZ	I.GLU.	OE1	2.846
6DC5	H.LYS.	NZ	I.ASP.	OD1	3.400
6DC5	H.LYS.	NZ	I.ASP.	OD2	3.825

Table 1559: Interfacial 6DC5-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6DCV	H.LYS_43	NZ	L.ASP_9	OD1	3.193
6DCV	H.LYS_221	NZ	L.GLU_123	OE1	3.166
6DCV	B.LYS_43	NZ	A.ASP_9	OD1	3.127
6DCV	B.LYS_221	NZ	A.GLU_123	OE1	3.096

Table 1560: Interfacial 6DCV-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6DCW	H_LYS_43	NZ	L_ASP_9	OD1	3.018
6DCW	T_LYS_317	NZ	H_ASP_54	OD1	3.849
6DCW	T_LYS_317	NZ	H_ASP_54	OD2	2.833
6DCW	T_LYS_317	NZ	H_ASP_56	OD2	2.597

Table 1561: Interfacial 6DCW-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6DDM	B_LYS_62	NZ	A_GLU_1	OE1	3.434
6DDM	B_LYS_62	NZ	A_GLU_1	OE2	2.992

Table 1562: Interfacial 6DDM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6DDR	B_LYS_209	NZ	A_GLU_123	OE1	3.270

Table 1563: Interfacial 6DDR-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6DDV	B_LYS_209	NZ	A_GLU_123	OE1	3.050
6DDV	B_LYS_209	NZ	A_GLU_123	OE2	3.197
6DDV	C_ARG_226	NH1	B_ASP_31	OD1	3.652
6DDV	C_ARG_226	NH1	B_ASP_31	OD2	2.831
6DDV	C_ARG_226	NH2	B_ASP_31	OD1	3.123
6DDV	C_ARG_226	NH2	B_ASP_31	OD2	3.778
6DDV	A_LYS_50	NZ	C_ASP_255	OD1	3.063
6DDV	A_LYS_50	NZ	C_ASP_255	OD2	3.312

Table 1564: Interfacial 6DDV-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6DFG	B_HIS_585	NE2	A_GLU_492	OE2	3.210
6DFG	B_ARG_588	NH2	A_GLU_492	OE1	2.981
6DFG	B_ARG_588	NH2	A_GLU_492	OE2	3.149
6DFG	L_ARG_31	NH1	A_ASP_140	OD2	3.569
6DFG	L_ARG_54	NH2	A_ASP_322	OD2	3.922
6DFG	L_LYS_96	NZ	H_ASP_50	OD2	3.294
6DFG	E_HIS_585	NE2	C_GLU_492	OE2	3.225
6DFG	E_ARG_588	NH2	C_GLU_492	OE1	2.984
6DFG	E_ARG_588	NH2	C_GLU_492	OE2	3.072
6DFG	J_ARG_31	NH1	C_ASP_140	OD2	3.924
6DFG	J_LYS_96	NZ	G_ASP_50	OD2	3.096
6DFG	F_HIS_585	NE2	D_GLU_492	OE2	3.337
6DFG	F_ARG_588	NH2	D_GLU_492	OE1	2.974
6DFG	F_ARG_588	NH2	D_GLU_492	OE2	3.036
6DFG	K_ARG_31	NH1	D_ASP_140	OD2	3.732
6DFG	K_LYS_96	NZ	I_ASP_50	OD2	3.268

Table 1565: Interfacial 6DFG-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6DFH	A_LYS_137	NZ	L_ASP_51	OD2	2.491
6DFH	A_ARG_192	NH1	D_GLU_164	OE2	3.939
6DFH	B_ARG_542	NH1	E_GLU_647	OE2	2.777
6DFH	B_LYS_574	NZ	A_ASP_107	OD1	3.419
6DFH	B_LYS_574	NZ	A_ASP_107	OD2	3.383
6DFH	B_ARG_588	NH2	A_GLU_492	OE1	3.118
6DFH	B_ARG_588	NH2	A_GLU_492	OE2	3.874
6DFH	C_LYS_137	NZ	J_ASP_51	OD2	2.536
6DFH	C_ARG_192	NH1	A_GLU_164	OE2	3.905
6DFH	E_ARG_542	NH1	F_GLU_647	OE2	2.777
6DFH	E_LYS_574	NZ	C_ASP_107	OD1	3.423
6DFH	E_LYS_574	NZ	C_ASP_107	OD2	3.381
6DFH	E_ARG_588	NH2	C_GLU_492	OE1	3.158
6DFH	E_ARG_588	NH2	C_GLU_492	OE2	3.904
6DFH	D_LYS_137	NZ	K_ASP_51	OD2	2.448
6DFH	D_ARG_192	NH1	C_GLU_164	OE2	3.902
6DFH	F_ARG_542	NH1	B_GLU_647	OE2	2.778
6DFH	F_LYS_574	NZ	D_ASP_107	OD1	3.408
6DFH	F_LYS_574	NZ	D_ASP_107	OD2	3.378
6DFH	F_ARG_588	NH2	D_GLU_492	OE1	3.059
6DFH	F_ARG_588	NH2	D_GLU_492	OE2	3.839

Table 1566: Interfacial 6DFH-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6DG2	A_ARG_57	NH1	C_GLU_50	OE1	2.686
6DG2	A_ARG_57	NH1	C_GLU_50	OE2	3.712
6DG2	A_ARG_57	NH1	C_ASP_59	OD1	3.923
6DG2	A_ARG_57	NH2	C_GLU_50	OE1	3.412
6DG2	A_ARG_57	NH2	C_GLU_50	OE2	2.876
6DG2	A_LYS_219	NZ	B_ASP_123	OD1	3.620
6DG2	A_LYS_219	NZ	B_ASP_123	OD2	3.832
6DG2	C_ARG_57	NH1	A_GLU_50	OE1	3.739
6DG2	C_ARG_57	NH1	A_GLU_50	OE2	2.758
6DG2	C_ARG_57	NH1	A_ASP_59	OD1	3.719
6DG2	C_ARG_57	NH2	A_GLU_50	OE1	2.935
6DG2	C_ARG_57	NH2	A_GLU_50	OE2	3.488

Table 1567: Interfacial 6DG2-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID residue name residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6E62	P_LYS_413	NZ	H_ASP_100	OD1	3.190
6E62	P_LYS_413	NZ	H_ASP_100	OD2	2.736
6E62	P_LYS_416	NZ	L_ASP_51	OD2	2.614
6E62	H_ARG_97	NH1	P_ASP_347	OD2	3.575
6E62	H_LYS_143	NZ	L_GLU_124	OE2	2.458
6E62	H_LYS_209	NZ	L_GLU_123	OE1	3.996
6E62	H_LYS_209	NZ	L_GLU_123	OE2	3.607
6E62	A_LYS_413	NZ	B_ASP_100	OD1	3.041
6E62	A_LYS_413	NZ	B_ASP_100	OD2	2.916
6E62	A_LYS_416	NZ	C_ASP_51	OD2	2.944
6E62	B_ARG_83	NH1	H_GLU_1	OE1	3.696
6E62	B_ARG_83	NH1	H_GLU_1	OE2	3.867
6E62	B_ARG_83	NH2	H_GLU_1	OE1	3.783
6E62	B_ARG_83	NH2	H_GLU_1	OE2	3.983
6E62	B_LYS_143	NZ	C_GLU_124	OE2	2.797
6E62	C_LYS_156	NZ	L_GLU_81	OE2	3.985

Table 1568: Interfacial 6E62-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6E63	P_LYS_413	NZ	H_ASP_100	OD1	3.187
6E63	P_LYS_413	NZ	H_ASP_100	OD2	2.904
6E63	P_LYS_416	NZ	L_ASP_51	OD1	3.564
6E63	P_LYS_416	NZ	L_ASP_51	OD2	2.955
6E63	H_ARG_97	NH1	P_ASP_347	OD2	3.407
6E63	H_LYS_143	NZ	L_GLU_124	OE2	2.665
6E63	H_LYS_209	NZ	L_GLU_123	OE1	2.498
6E63	L_LYS_17	NZ	B_GLU_85	OE1	3.318
6E63	L_LYS_17	NZ	B_GLU_85	OE2	3.250
6E63	A_LYS_413	NZ	B_ASP_100	OD1	2.369
6E63	A_LYS_413	NZ	B_ASP_100	OD2	3.029
6E63	A_LYS_416	NZ	C_ASP_51	OD2	3.236
6E63	B_ARG_83	NH1	L_GLU_13	OE1	3.486
6E63	B_ARG_83	NH1	L_GLU_13	OE2	2.814
6E63	B_ARG_97	NH1	A_ASP_347	OD1	3.859

Table 1569: Interfacial 6E63-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6E64	H.LYS.143	NZ	L.GLU.124	OE2	2.942
6E64	H.LYS.209	NZ	L.GLU.123	OE2	2.774
6E64	A.LYS.209	NZ	B.GLU.123	OE1	3.569
6E64	A.LYS.209	NZ	B.GLU.123	OE2	2.777

Table 1570: Interfacial 6E64-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6E65	H_LYS_209	NZ	L_GLU_123	OE1	2.900
6E65	H_LYS_209	NZ	L_GLU_123	OE2	3.402

Table 1571: Interfacial 6E65-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6E8V	A_LYS_69	NZ	H_GLU_114	OE1	3.919
6E8V	A_LYS_69	NZ	H_GLU_114	OE2	3.267
6E8V	A_LYS_290	NZ	B_GLU_128	OE1	3.297
6E8V	A_LYS_290	NZ	B_GLU_128	OE2	3.454
6E8V	B_LYS_154	NZ	E_ASP_98	OD2	3.855
6E8V	E_LYS_290	NZ	F_GLU_128	OE1	2.548
6E8V	E_LYS_290	NZ	F_GLU_128	OE2	3.232
6E8V	H_LYS_290	NZ	L_GLU_127	OE1	2.706
6E8V	H_LYS_290	NZ	L_GLU_127	OE2	2.554
6E8V	J_LYS_290	NZ	K_GLU_128	OE1	3.173
6E8V	J_LYS_290	NZ	K_GLU_128	OE2	2.611
6E8V	K_LYS_212	NZ	H_GLU_101	OE1	3.767
6E8V	K_LYS_212	NZ	H_GLU_101	OE2	3.490
6E8V	O_HIS_129	NE2	L_ASP_61	OD1	3.511
6E8V	O_LYS_290	NZ	P_GLU_128	OE1	3.591
6E8V	U_LYS_290	NZ	V_GLU_128	OE1	2.346
6E8V	U_LYS_290	NZ	V_GLU_128	OE2	3.693
6E8V	Y_LYS_290	NZ	Z_GLU_128	OE1	3.390
6E8V	c_HIS_125	ND1	K_ASP_62	OD1	3.174
6E8V	c_HIS_125	ND1	K_ASP_62	OD2	3.139
6E8V	c_LYS_290	NZ	d_GLU_128	OE1	2.357
6E8V	c_LYS_290	NZ	d_GLU_128	OE2	3.486

Table 1572: Interfacial 6E8V-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6E9G	A_LYS_262	NZ	B_GLU_127	OE1	3.021
6E9G	A_LYS_262	NZ	B_GLU_127	OE2	3.870

Table 1573: Interfacial 6E9G-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6E9H	A_LYS_292	NZ	B_GLU_128	OE1	2.895
6E9H	A_LYS_292	NZ	B_GLU_128	OE2	3.744

Table 1574: Interfacial 6E9H-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6E9I	A_ARG_109	NH2	D_ASP_95	OD1	3.782
6E9I	A_ARG_109	NH2	D_ASP_95	OD2	3.931
6E9I	A_LYS_289	NZ	B_GLU_128	OE1	3.746
6E9I	A_LYS_289	NZ	B_GLU_128	OE2	2.925
6E9I	C_LYS_289	NZ	D_GLU_128	OE1	2.528
6E9I	C_LYS_289	NZ	D_GLU_128	OE2	3.968
6E9I	H_LYS_289	NZ	L_GLU_128	OE1	3.811
6E9I	H_LYS_289	NZ	L_GLU_128	OE2	2.547

Table 1575: Interfacial 6E9I-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6E9K	A_LYS_257	NZ	B_GLU_128	OE1	3.997
6E9K	A_LYS_257	NZ	B_GLU_128	OE2	3.056

Table 1576: Interfacial 6E9K-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6E9Q	A_LYS.253	NZ	B_GLU.128	OE1	3.048
6E9Q	A_LYS.253	NZ	B_GLU.128	OE2	2.978
6E9Q	E_LYS.253	NZ	F_GLU.128	OE1	2.966
6E9Q	E_LYS.253	NZ	F_GLU.128	OE2	2.802

Table 1577: Interfacial 6E9Q-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6E9U	A_LYS_266	NZ	B_GLU_128	OE1	2.942
6E9U	A_LYS_266	NZ	B_GLU_128	OE2	2.747

Table 1578: Interfacial 6E9U-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6EDU	D_LYS_421	NZ	L_GLU_54	OE2	2.920
6EDU	D_LYS_432	NZ	L_GLU_55	OE1	3.655
6EDU	D_LYS_432	NZ	L_GLU_55	OE2	3.439
6EDU	E_LYS_421	NZ	N_GLU_54	OE2	3.004
6EDU	E_LYS_432	NZ	N_GLU_55	OE1	3.579
6EDU	E_LYS_432	NZ	N_GLU_55	OE2	3.398
6EDU	F_LYS_421	NZ	J_GLU_54	OE2	3.064
6EDU	F_LYS_432	NZ	J_GLU_55	OE1	3.805
6EDU	F_LYS_432	NZ	J_GLU_55	OE2	3.577
6EDU	G_LYS_22	NZ	F_GLU_102	OE1	3.040
6EDU	G_ARG_59	NH2	F ASP_368	OD1	3.059
6EDU	H_LYS_22	NZ	E_GLU_102	OE1	3.174
6EDU	H_ARG_59	NH2	E ASP_368	OD1	3.166
6EDU	I_LYS_22	NZ	D_GLU_102	OE1	3.053
6EDU	I_ARG_59	NH2	D ASP_368	OD1	3.238
6EDU	P_LYS_107	NZ	F_GLU_91	OE1	3.324
6EDU	R_LYS_107	NZ	D_GLU_91	OE1	3.704
6EDU	T_LYS_107	NZ	E_GLU_91	OE1	3.475

Table 1579: Interfacial 6EDU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6EJG	A_LYS_171	NZ	C_ASP_224	OD2	3.396
6EJG	A_LYS_171	NZ	C_ASP_226	OD2	2.901
6EJG	B_LYS_	NZ	D_ASP_	OD1	3.521
6EJG	B_LYS_	NZ	D_ASP_	OD2	2.547
6EJG	B_LYS_	NZ	D_ASP_	OD2	2.932

Table 1580: Interfacial 6EJG-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6EJM	A_HIS_204	ND1	B_GLU_152	OE2	3.786

Table 1581: Interfacial 6EJM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6EK2	H_ARG_370	NH1	A_GLU_188	OE2	3.014
6EK2	H_ARG_370	NH2	A_GLU_188	OE1	3.920
6EK2	H_ARG_370	NH2	A_GLU_188	OE2	3.261
6EK2	I_ARG_370	NH1	B_GLU_188	OE1	2.817
6EK2	I_ARG_370	NH1	B_GLU_188	OE2	3.286
6EK2	I_ARG_370	NH2	B_GLU_188	OE1	3.837
6EK2	I_ARG_370	NH2	B_GLU_188	OE2	3.095

Table 1582: Interfacial 6EK2-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6EUN	A_LYS_87	NZ	B_GLU_47	OE1	3.058
6EUN	A_LYS_107	NZ	C_ASP_105	OD1	3.488
6EUN	A_LYS_167	NZ	C_ASP_165	OD1	3.883
6EUN	B_LYS_87	NZ	C_GLU_47	OE1	3.021
6EUN	B_LYS_107	NZ	A_ASP_105	OD1	3.579
6EUN	C_LYS_87	NZ	A_GLU_47	OE1	3.007
6EUN	C_LYS_107	NZ	B_ASP_105	OD1	3.525

Table 1583: Interfacial 6EUN-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6EUP	A.LYS_87	NZ	B.GLU_47	OE1	2.842
6EUP	A.LYS_87	NZ	B.ASP_79	OD1	3.786
6EUP	A.LYS_107	NZ	C.ASP_105	OD1	3.538
6EUP	B.LYS_87	NZ	C.GLU_47	OE1	2.811
6EUP	B.LYS_87	NZ	C.ASP_79	OD1	3.799
6EUP	B.LYS_107	NZ	A.ASP_105	OD1	3.723
6EUP	C.LYS_87	NZ	A.GLU_47	OE1	2.814
6EUP	C.LYS_87	NZ	A.ASP_79	OD1	3.752
6EUP	C.LYS_107	NZ	B.ASP_105	OD1	3.560

Table 1584: Interfacial 6EUP-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6EV1	A_LYS_213	NZ	B_GLU_122	OE1	3.565
6EV1	B_ARG_45	NH1	A_ASP_105	OD1	3.400
6EV1	E_LYS_213	NZ	F_GLU_122	OE2	3.696
6EV1	F_ARG_45	NH1	E_ASP_105	OD1	3.598
6EV1	G_LYS_213	NZ	H_GLU_122	OE2	3.127
6EV1	I_LYS_213	NZ	J_GLU_122	OE1	2.884
6EV1	I_LYS_213	NZ	J_GLU_122	OE2	3.812
6EV1	J_ARG_45	NH2	I_ASP_105	OD1	3.213
6EV1	J_ARG_45	NH2	I_ASP_105	OD2	3.457
6EV1	K_HIS_168	NE2	L_ASP_166	OD2	3.740
6EV1	K_LYS_213	NZ	L_GLU_122	OE1	3.450
6EV1	L_ARG_45	NH2	K_ASP_105	OD1	3.857

Table 1585: Interfacial 6EV1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID** **residue name** **residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6EV2	A_LYS_213	NZ	B_GLU_122	OE1	3.442
6EV2	B_ARG_45	NH1	A_ASP_105	OD1	3.088
6EV2	B_LYS_168	NZ	F_GLU_78	OE2	2.948
6EV2	D_LYS_44	NZ	C_ASP_105	OD2	3.822
6EV2	D_ARG_45	NH1	C_ASP_105	OD1	3.142
6EV2	D_LYS_168	NZ	H_GLU_78	OE2	3.198
6EV2	E_LYS_213	NZ	F_GLU_122	OE1	3.493
6EV2	E_LYS_218	NZ	F_ASP_121	OD2	3.835
6EV2	F_ARG_45	NH1	E_ASP_105	OD1	2.818
6EV2	F_LYS_168	NZ	B_GLU_78	OE1	3.747
6EV2	G_LYS_210	NZ	A_ASP_73	OD1	3.883
6EV2	G_LYS_210	NZ	A_ASP_73	OD2	2.404
6EV2	G_LYS_213	NZ	H_GLU_122	OE1	3.330
6EV2	G_LYS_213	NZ	H_GLU_122	OE2	3.779
6EV2	H_ARG_45	NH1	G_ASP_105	OD1	3.108
6EV2	H_LYS_168	NZ	D_GLU_78	OE2	3.686

Table 1586: Interfacial 6EV2-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6EWB	D_HIS_417	NE2	L_GLU_80	OE2	3.932
6EWB	E_ARG_98	NH1	B_ASP_341	OD1	3.977
6EWB	E_ARG_98	NH2	B_ASP_341	OD1	3.813
6EWB	E_ARG_101	NH1	F_ASP_49	OD1	2.895
6EWB	E_ARG_101	NH1	F_ASP_49	OD2	3.620
6EWB	F_ARG_	NH1	E_ASP_	OD1	3.803
6EWB	F_ARG_	NH1	E_ASP_	OD2	3.536
6EWB	F_LYS_52	NZ	A_ASP_448	OD1	3.722
6EWB	F_LYS_52	NZ	A_ASP_448	OD2	2.304
6EWB	G_ARG_98	NH1	D_ASP_341	OD1	3.850
6EWB	G_ARG_98	NH2	D_ASP_341	OD1	3.731
6EWB	G_ARG_101	NH1	I_ASP_49	OD1	2.830
6EWB	G_ARG_101	NH1	I_ASP_49	OD2	3.797
6EWB	H_ARG_98	NH1	A_ASP_341	OD2	3.948
6EWB	H_ARG_98	NH2	A_ASP_341	OD2	3.896
6EWB	H_ARG_101	NH1	L_ASP_49	OD1	2.509
6EWB	H_ARG_101	NH1	L_ASP_49	OD2	3.441
6EWB	I_ARG_45	NH1	G_ASP_104	OD1	3.731
6EWB	I_ARG_45	NH1	G_ASP_104	OD2	3.636
6EWB	I_LYS_52	NZ	C_ASP_448	OD1	3.564
6EWB	I_LYS_52	NZ	C_ASP_448	OD2	2.694
6EWB	J_ARG_98	NH1	C_ASP_341	OD2	3.957
6EWB	J_ARG_98	NH2	C_ASP_341	OD2	3.467
6EWB	J_ARG_101	NH1	K_ASP_49	OD1	2.726
6EWB	J_ARG_101	NH1	K_ASP_49	OD2	3.581
6EWB	J_LYS_211	NZ	K_GLU_122	OE2	2.945
6EWB	K_ARG_45	NH1	J_ASP_104	OD2	3.826
6EWB	K_LYS_52	NZ	D_ASP_448	OD1	3.845
6EWB	K_LYS_52	NZ	D_ASP_448	OD2	2.608
6EWB	L_ARG_45	NH1	H_ASP_104	OD1	3.721
6EWB	L_ARG_45	NH1	H_ASP_104	OD2	3.560
6EWB	L_LYS_52	NZ	B_ASP_448	OD1	3.690
6EWB	L_LYS_52	NZ	B_ASP_448	OD2	2.585
6EWB	L_ARG_60	NH1	D_GLU_316	OE1	3.251
6EWB	L_ARG_60	NH1	D_GLU_316	OE2	3.266

Table 1587: Interfacial 6EWB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6FAB	H_LYS_216	NZ	L_GLU_123	OE1	2.624
6FAB	H_LYS_216	NZ	L_GLU_123	OE2	2.770

Table 1588: Interfacial 6FAB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6FAX	H_ARG_104	NH2	R_GLU_21	OE1	3.986
6FAX	H_HIS_173	NE2	L_ASP_167	OD1	3.928
6FAX	H_LYS_218	NZ	L_GLU_123	OE1	3.125
6FAX	H_LYS_218	NZ	L_GLU_123	OE2	3.415

Table 1589: Interfacial 6FAX-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6FN1	C_LYS_217	NZ	B_GLU_129	OE1	3.462
6FN1	C_LYS_217	NZ	B_GLU_129	OE2	2.375

Table 1590: Interfacial 6FN1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6FN4	B.LYS_55	NZ	A.ASP_743	OD1	2.728
6FN4	B.LYS_55	NZ	A.ASP_743	OD2	3.540
6FN4	C.LYS_217	NZ	B.GLU_129	OE2	3.828

Table 1591: Interfacial 6FN4-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6GK7	H_LYS_43	NZ	L_ASP_9	OD1	3.203
6GK7	H_LYS_218	NZ	L_GLU_129	OE1	3.512
6GK7	H_LYS_218	NZ	L_GLU_129	OE2	3.016
6GK7	H_LYS_223	NZ	L_ASP_128	OD2	3.231
6GK7	A_LYS_317	NZ	H_ASP_55	OD2	2.761
6GK7	A_LYS_317	NZ	H_ASP_57	OD2	2.983

Table 1592: Interfacial 6GK7-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6GK8	H_ARG_59	NH2	L ASP_65	OD1	3.295
6GK8	H_ARG_101	NH1	L GLU_62	OE2	2.742
6GK8	H_ARG_101	NH2	L GLU_62	OE2	3.142
6GK8	H_LYS_104	NZ	L GLU_62	OE1	2.762
6GK8	H_LYS_104	NZ	L GLU_62	OE2	3.928
6GK8	H_LYS_222	NZ	L ASP_128	OD2	2.761
6GK8	L_ARG_32	NH1	L GLU_57	OE2	3.709
6GK8	L_LYS_67	NZ	H ASP_55	OD1	3.586
6GK8	L_LYS_67	NZ	H ASP_55	OD2	3.183
6GK8	L_LYS_67	NZ	H ASP_57	OD2	3.085

Table 1593: Interfacial 6GK8-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6H2Y	D_LYS_79	NZ	L_ASP_52	OD1	3.126
6H2Y	D_LYS_120	NZ	L_ASP_95	OD2	2.910
6H2Y	D_LYS_191	NZ	L_ASP_50	OD2	2.715
6H2Y	H_ARG_56	NH2	D_GLU_58	OE1	3.564
6H2Y	H_ARG_56	NH2	D_GLU_58	OE2	3.905
6H2Y	H_LYS_215	NZ	L_GLU_125	OE1	3.261
6H2Y	H_LYS_215	NZ	L_GLU_125	OE2	2.865
6H2Y	L_ARG_92	NH1	D_ASP_166	OD2	3.217
6H2Y	L_ARG_92	NH2	D_GLU_119	OE1	3.274
6H2Y	L_ARG_92	NH2	D_GLU_119	OE2	3.244
6H2Y	L_ARG_92	NH2	D_ASP_166	OD1	3.891
6H2Y	L_ARG_92	NH2	D_ASP_166	OD2	2.328

Table 1594: Interfacial 6H2Y-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID residue name residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6I3Z	A_LYS_201	NZ	L_ASP_92	OD1	3.556
6I3Z	A_LYS_290	NZ	H_ASP_33	OD1	3.699
6I3Z	L_ARG_53	NH1	A_GLU_204	OE1	2.383
6I3Z	L_ARG_53	NH1	A_GLU_204	OE2	3.516

Table 1595: Interfacial 6I3Z-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6IAP	D_ARG_96	NH2	A_GLU_80	OE1	3.466
6IAP	E_HIS_35	NE2	A_GLU_80	OE1	3.445
6IAP	H_ARG_99	NH2	A_ASP_98	OD1	2.689
6IAP	L_ARG_94	NH1	H_GLU_50	OE2	2.973
6IAP	L_ARG_94	NH2	A_ASP_123	OD2	3.888

Table 1596: Interfacial 6IAP-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6JMQ	C_HIS_169	NE2	D_ASP_173	OD2	3.860
6JMQ	C_LYS_213	NZ	D_GLU_129	OE1	3.825

Table 1597: Interfacial 6JMQ-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6JMR	C_HIS_169	NE2	D_ASP_173	OD1	3.922

Table 1598: Interfacial 6JMR-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6K7O	A_LYS_55	NZ	H_ASP_106	OD1	3.027
6K7O	A_ARG_78	NH1	L_ASP_94	OD1	3.792
6K7O	A_ARG_78	NH2	L_ASP_94	OD1	2.709
6K7O	B_LYS_218	NZ	C_GLU_127	OE1	3.816
6K7O	B_LYS_218	NZ	C_GLU_127	OE2	2.813
6K7O	B_LYS_223	NZ	C_ASP_126	OD1	2.273
6K7O	B_LYS_223	NZ	C_ASP_126	OD2	2.907
6K7O	D_LYS_215	NZ	G_ASP_189	OD2	2.832
6K7O	D_LYS_218	NZ	E_GLU_127	OE1	2.290
6K7O	D_LYS_218	NZ	E_GLU_127	OE2	3.074
6K7O	D_LYS_223	NZ	E_ASP_126	OD1	3.765
6K7O	D_LYS_223	NZ	E_ASP_126	OD2	3.552
6K7O	F_HIS_173	NE2	G_ASP_171	OD2	3.941
6K7O	G_ARG_51	NH2	F_ASP_106	OD2	3.980
6K7O	H_HIS_173	NE2	L_ASP_171	OD2	3.862
6K7O	H_LYS_218	NZ	L_GLU_127	OE1	3.981
6K7O	H_LYS_223	NZ	L_ASP_126	OD1	3.964
6K7O	P_LYS_55	NZ	B_ASP_106	OD1	3.340
6K7O	P_ARG_78	NH1	C_ASP_94	OD1	2.583
6K7O	P_ARG_78	NH2	C_ASP_94	OD1	2.609
6K7O	R_LYS_55	NZ	F_ASP_106	OD1	2.834
6K7O	Q_LYS_55	NZ	D_ASP_106	OD1	3.172
6K7O	Q_ARG_59	NH1	H_GLU_221	OE1	3.018
6K7O	Q_ARG_59	NH1	H_GLU_221	OE2	3.413
6K7O	Q_ARG_59	NH2	H_GLU_221	OE1	3.299
6K7O	Q_ARG_59	NH2	H_GLU_221	OE2	2.855
6K7O	Q_ARG_78	NH1	E_ASP_94	OD1	3.546
6K7O	Q_ARG_78	NH2	E_ASP_94	OD1	2.499

Table 1599: Interfacial 6K7O-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6KN9	A_ARG_281	NH1	D_ASP_111	OD1	2.228
6KN9	A_ARG_281	NH1	D_ASP_111	OD2	3.976
6KN9	B_ARG_281	NH2	E_ASP_111	OD1	2.487
6KN9	B_ARG_281	NH2	E_ASP_111	OD2	3.660
6KN9	C_ARG_281	NH2	F_ASP_111	OD2	3.907

Table 1600: Interfacial 6KN9-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6MHR	E_ARG_91	NH1	D_GLU_50	OE1	3.108
6MHR	E_ARG_91	NH1	D_ASP_98	OD2	3.892
6MHR	E_ARG_91	NH2	D_GLU_50	OE1	3.238
6MHR	E_ARG_91	NH2	D_GLU_50	OE2	3.082
6MHR	A_LYS_217	NZ	B_GLU_125	OE2	2.775
6MHR	B_ARG_91	NH1	A_GLU_50	OE1	3.086
6MHR	B_ARG_91	NH1	A_GLU_50	OE2	3.775
6MHR	B_ARG_91	NH1	A_ASP_98	OD2	3.351
6MHR	B_ARG_91	NH2	A_GLU_50	OE1	3.608
6MHR	B_ARG_91	NH2	A_GLU_50	OE2	2.934

Table 1601: Interfacial 6MHR-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6MI2	F_LYS_114	NZ	E_ASP_50	OD1	2.776
6MI2	F_LYS_114	NZ	E_ASP_50	OD2	3.977
6MI2	F_ARG_134	NH2	D_ASP_55	OD2	3.507
6MI2	C_LYS_114	NZ	B_ASP_50	OD1	3.683
6MI2	C_LYS_114	NZ	B_ASP_50	OD2	2.434

Table 1602: Interfacial 6MI2-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6MN7	B_ARG_542	NH1	F_GLU_647	OE2	3.229
6MN7	B_LYS_574	NZ	A_ASP_107	OD1	3.285
6MN7	B_LYS_574	NZ	A_ASP_107	OD2	3.696
6MN7	B_ARG_579	NH2	F_GLU_584	OE1	2.844
6MN7	B_ARG_579	NH2	F_GLU_584	OE2	3.533
6MN7	E_ARG_542	NH1	B_GLU_647	OE2	3.076
6MN7	E_LYS_574	NZ	C_ASP_107	OD1	3.286
6MN7	E_LYS_574	NZ	C_ASP_107	OD2	3.697
6MN7	E_ARG_579	NH2	B_GLU_584	OE1	2.796
6MN7	E_ARG_579	NH2	B_GLU_584	OE2	3.568
6MN7	F_ARG_542	NH1	E_GLU_647	OE2	3.126
6MN7	F_LYS_574	NZ	D_ASP_107	OD1	3.285
6MN7	F_LYS_574	NZ	D_ASP_107	OD2	3.696
6MN7	F_ARG_579	NH2	E_GLU_584	OE1	2.859
6MN7	F_ARG_579	NH2	E_GLU_584	OE2	3.579

Table 1603: Interfacial 6MN7-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6MPG	U_ARG_542	NH2	D_GLU_647	OE1	3.141
6MPG	U_ARG_542	NH2	D_GLU_647	OE2	2.524
6MPG	U_ARG_579	NH2	D_GLU_584	OE1	2.488
6MPG	V_LYS_229	NZ	B_ASP_1	OD1	2.776
6MPG	W_HIS_105	NE2	B_GLU_61	OE2	3.652
6MPG	n_ARG_94	NH1	V_ASP_321A	OD1	3.878
6MPG	2_LYS_229	NZ	4_ASP_1	OD1	2.776
6MPG	3_HIS_105	NE2	4_GLU_61	OE2	3.651
6MPG	6_ARG_94	NH1	2_ASP_321A	OD1	3.878
6MPG	A_ARG_542	NH2	U_GLU_647	OE1	3.132
6MPG	A_ARG_542	NH2	U_GLU_647	OE2	2.525
6MPG	A_ARG_579	NH2	U_GLU_584	OE1	2.474
6MPG	C_LYS_229	NZ	Y_ASP_1	OD1	2.776
6MPG	D_ARG_542	NH2	A_GLU_647	OE1	3.137
6MPG	D_ARG_542	NH2	A_GLU_647	OE2	2.533
6MPG	D_ARG_579	NH2	A_GLU_584	OE1	2.479
6MPG	N_ARG_94	NH1	C_ASP_321A	OD1	3.878
6MPG	X_HIS_105	NE2	Y_GLU_61	OE2	3.651

Table 1604: Interfacial 6MPG-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6MPH	1_LYS_31A	NZ	A_GLU_87	OE1	2.457
6MPH	1_LYS_31A	NZ	A_GLU_87	OE2	3.919
6MPH	2_ARG_96	NH1	1_GLU_95	OE1	3.340
6MPH	2_ARG_96	NH1	1_GLU_95	OE2	2.522
6MPH	3_LYS_31A	NZ	B_GLU_87	OE1	2.448
6MPH	3_LYS_31A	NZ	B_GLU_87	OE2	3.973
6MPH	4_ARG_96	NH1	3_GLU_95	OE1	3.339
6MPH	4_ARG_96	NH1	3_GLU_95	OE2	2.507
6MPH	6_ARG_542	NH1	E_GLU_647	OE2	3.863
6MPH	6_ARG_542	NH2	E_GLU_647	OE1	3.449
6MPH	6_ARG_542	NH2	E_GLU_647	OE2	2.484
6MPH	6_ARG_579	NH2	E_GLU_584	OE1	2.833
6MPH	A_LYS_282	NZ	f_ASP_114	OD1	3.470
6MPH	A_LYS_282	NZ	f_ASP_114	OD2	3.288
6MPH	A_ARG_327	NH2	X_GLU_100I	OE1	3.876
6MPH	B_LYS_282	NZ	g_ASP_114	OD1	3.432
6MPH	B_LYS_282	NZ	g_ASP_114	OD2	3.289
6MPH	B_ARG_327	NH2	Y_GLU_100I	OE1	3.899
6MPH	C_LYS_282	NZ	Q_ASP_114	OD1	3.383
6MPH	C_LYS_282	NZ	Q_ASP_114	OD2	3.272
6MPH	C_ARG_327	NH2	M_GLU_100I	OE1	3.872
6MPH	D_ARG_542	NH1	6_GLU_647	OE2	3.853
6MPH	D_ARG_542	NH2	6_GLU_647	OE1	3.460
6MPH	D_ARG_542	NH2	6_GLU_647	OE2	2.476
6MPH	D_ARG_579	NH2	6_GLU_584	OE1	2.760
6MPH	E_ARG_542	NH1	D_GLU_647	OE2	3.888
6MPH	E_ARG_542	NH2	D_GLU_647	OE1	3.465
6MPH	E_ARG_542	NH2	D_GLU_647	OE2	2.463
6MPH	E_ARG_579	NH2	D_GLU_584	OE1	2.789
6MPH	H_LYS_31A	NZ	C_GLU_87	OE1	2.458
6MPH	H_LYS_31A	NZ	C_GLU_87	OE2	3.969
6MPH	L_ARG_96	NH1	H_GLU_95	OE1	3.309
6MPH	L_ARG_96	NH1	H_GLU_95	OE2	2.530
6MPH	N_ARG_94	NH1	C_ASP_321A	OD1	3.859
6MPH	Q_ARG_72	NH2	C_ASP_368	OD2	3.534
6MPH	Z_ARG_94	NH1	A_ASP_321A	OD1	3.890
6MPH	a_ARG_94	NH1	B_ASP_321A	OD1	3.861
6MPH	f_ARG_72	NH2	A_ASP_368	OD2	3.577
6MPH	g_ARG_72	NH2	B_ASP_368	OD2	3.570

Table 1605: Interfacial 6MPH-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6MQC	A_ARG_	NH1	B_ASP_	OD1	2.994
6MQC	A_ARG_	NH2	B_ASP_	OD1	2.820
6MQC	A_ARG_	NH1	B_ASP_	OD1	3.399
6MQC	A_ARG_	NH1	B_ASP_	OD2	3.078
6MQC	A_ARG_	NH1	B_ASP_	OD1	2.829
6MQC	A_ARG_	NH2	B_ASP_	OD1	2.822
6MQC	A_ARG_	NH2	B_ASP_	OD2	3.673
6MQC	H_ARG_	NH1	L_ASP_	OD1	2.906
6MQC	H_ARG_	NH2	L_ASP_	OD1	2.999
6MQC	H_ARG_	NH1	L_ASP_	OD1	2.856
6MQC	H_ARG_	NH1	L_ASP_	OD2	3.748
6MQC	H_ARG_	NH2	L_ASP_	OD1	3.439
6MQC	H_ARG_	NH2	L_ASP_	OD2	3.140
6MQC	H_ARG_	NH2	L_ASP_	OD1	2.780
6MQC	H_ARG_	NH2	L_ASP_	OD2	3.923

Table 1606: Interfacial 6MQC-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6MQE	A_ARG_95	NH2	B_ASP_91	OD2	3.864
6MQE	A_ARG_100H	NH2	B_ASP_91	OD2	3.610
6MQE	H_ARG_95	NH1	L_ASP_91	OD1	3.360
6MQE	H_ARG_95	NH2	L_ASP_91	OD1	2.956
6MQE	H_ARG_100H	NH1	L_ASP_91	OD1	2.604
6MQE	H_ARG_100H	NH1	L_ASP_91	OD2	3.888
6MQE	L_LYS_155	NZ	A_GLU_56	OE1	2.786
6MQE	L_HIS_189	NE2	A_GLU_56	OE1	3.428
6MQE	L_HIS_189	NE2	A_GLU_56	OE2	2.569

Table 1607: Interfacial 6MQE-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6MQM	B_ARG_96	NH1	A_GLU_95	OE1	3.968
6MQM	B_ARG_96	NH1	A_GLU_95	OE2	2.460
6MQM	E_ARG_96	NH1	D_GLU_95	OE2	2.376
6MQM	H_ARG_96	NH1	G_GLU_95	OE2	2.480
6MQM	K_ARG_96	NH1	J_GLU_95	OE1	3.782
6MQM	K_ARG_96	NH1	J_GLU_95	OE2	2.262

Table 1608: Interfacial 6MQM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6MQR	H_ARG_96	NH1	L_GLU_55	OE1	2.553
6MQR	L_ARG_46	NH1	H_ASP_101	OD2	2.970
6MQR	L_ARG_46	NH2	H_GLU_95	OE2	3.587
6MQR	L_ARG_46	NH2	H_ASP_101	OD2	3.723

Table 1609: Interfacial 6MQR-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6MQS	A_LYS_44	NZ	B_ASP_86	OD1	3.511
6MQS	A_ARG_138	NH1	B_GLU_214	OE1	3.046
6MQS	A_ARG_138	NH1	B_GLU_214	OE2	2.728
6MQS	A_LYS_218	NZ	B_GLU_127	OE1	2.743
6MQS	A_LYS_218	NZ	B_GLU_127	OE2	3.002
6MQS	C_LYS_44	NZ	D_ASP_86	OD1	2.946
6MQS	C_ARG_138	NH2	D_GLU_214	OE1	2.736
6MQS	C_ARG_138	NH2	D_GLU_214	OE2	3.220
6MQS	C_LYS_152	NZ	D_GLU_128	OE1	3.230
6MQS	C_LYS_218	NZ	D_GLU_127	OE1	2.641
6MQS	C_LYS_218	NZ	D_GLU_127	OE2	3.160

Table 1610: Interfacial 6MQS-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6N16	A_ARG_105	NH1	C_GLU_64	OE1	3.566
6N16	A_ARG_105	NH2	C_GLU_64	OE1	3.522
6N16	A_ARG_105	NH2	C_GLU_64	OE2	3.717
6N16	A_HIS_164	NE2	B_ASP_167	OD2	3.486
6N16	H_HIS_164	NE2	L_ASP_167	OD1	3.075
6N16	K_ARG_105	NH2	H_GLU_64	OE1	2.463
6N16	K_ARG_105	NH2	H_GLU_64	OE2	3.174
6N16	C_LYS_209	NZ	D_ASP_123	OD2	3.251

Table 1611: Interfacial 6N16-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6N1V	3_LYS_44	NZ	4_ASP_86	OD1	3.675
6N1V	3_LYS_44	NZ	4_ASP_86	OD2	2.472
6N1V	3_LYS_44	NZ	4_GLU_106	OE1	3.723
6N1V	3_ARG_138	NH1	4_GLU_214	OE1	2.573
6N1V	3_ARG_138	NH1	4_GLU_214	OE2	3.070
6N1V	3_ARG_138	NH2	4_GLU_214	OE2	3.291
6N1V	3_LYS_218	NZ	4_GLU_127	OE1	3.611
6N1V	B_LYS_282	NZ	g_ASP_114	OD2	3.730
6N1V	B_ARG_504	NH2	D_GLU_657	OE2	3.905
6N1V	F_ARG_542	NH2	D_GLU_647	OE1	3.326
6N1V	F_ARG_542	NH2	D_GLU_647	OE2	2.831
6N1V	F_ARG_579	NH2	D_GLU_584	OE1	3.581
6N1V	g_ARG_72	NH1	B_ASP_368	OD2	3.927
6N1V	g_ARG_72	NH2	B_ASP_368	OD2	3.974
6N1V	1_LYS_44	NZ	2_ASP_86	OD1	3.676
6N1V	1_LYS_44	NZ	2_ASP_86	OD2	2.473
6N1V	1_LYS_44	NZ	2_GLU_106	OE1	3.723
6N1V	1_ARG_138	NH1	2_GLU_214	OE1	2.573
6N1V	1_ARG_138	NH1	2_GLU_214	OE2	3.069
6N1V	1_ARG_138	NH2	2_GLU_214	OE2	3.291
6N1V	1_LYS_218	NZ	2_GLU_127	OE1	3.611
6N1V	A_LYS_282	NZ	f_ASP_114	OD2	3.729
6N1V	A_ARG_504	NH2	F_GLU_657	OE2	3.909
6N1V	E_ARG_542	NH2	F_GLU_647	OE1	3.328
6N1V	E_ARG_542	NH2	F_GLU_647	OE2	2.831
6N1V	E_ARG_579	NH2	F_GLU_584	OE1	3.583
6N1V	f_ARG_72	NH1	A_ASP_368	OD2	3.927
6N1V	f_ARG_72	NH2	A_ASP_368	OD2	3.974
6N1V	C_LYS_282	NZ	Q_ASP_114	OD2	3.730
6N1V	C_ARG_504	NH2	E_GLU_657	OE2	3.907
6N1V	D_ARG_542	NH2	E_GLU_647	OE1	3.330
6N1V	D_ARG_542	NH2	E_GLU_647	OE2	2.832
6N1V	D_ARG_579	NH2	E_GLU_584	OE1	3.585
6N1V	H_LYS_44	NZ	L_ASP_86	OD1	3.676
6N1V	H_LYS_44	NZ	L_ASP_86	OD2	2.472
6N1V	H_LYS_44	NZ	L_GLU_106	OE1	3.722
6N1V	H_ARG_138	NH1	L_GLU_214	OE1	2.573
6N1V	H_ARG_138	NH1	L_GLU_214	OE2	3.069
6N1V	H_ARG_138	NH2	L_GLU_214	OE2	3.291
6N1V	H_LYS_218	NZ	L_GLU_127	OE1	3.611
6N1V	Q_ARG_72	NH1	C_ASP_368	OD2	3.927
6N1V	Q_ARG_72	NH2	C_ASP_368	OD2	3.975

Table 1612: Interfacial 6N1V-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6N1W	2_ARG_327	NH2	m_GLU_100I	OE1	3.996
6N1W	2_ARG_504	NH2	d_GLU_657	OE2	3.118
6N1W	3_ARG_100H	NH2	4_ASP_91	OD2	3.241
6N1W	A_ARG_542	NH1	d_GLU_647	OE1	3.516
6N1W	A_ARG_542	NH1	d_GLU_647	OE2	3.474
6N1W	A_ARG_542	NH2	d_GLU_647	OE1	2.848
6N1W	A_ARG_579	NH2	d_GLU_584	OE2	3.464
6N1W	A_LYS_601	NZ	d_GLU_654	OE1	3.802
6N1W	A_LYS_601	NZ	d_GLU_654	OE2	3.060
6N1W	C_ARG_504	NH2	A_GLU_657	OE2	3.221
6N1W	D_ARG_542	NH1	A_GLU_647	OE1	3.273
6N1W	D_ARG_542	NH1	A_GLU_647	OE2	3.289
6N1W	D_ARG_542	NH2	A_GLU_647	OE1	2.942
6N1W	D_ARG_579	NH1	A_GLU_584	OE1	3.854
6N1W	D_ARG_579	NH2	A_GLU_584	OE2	3.567
6N1W	D_LYS_601	NZ	A_GLU_654	OE1	3.837
6N1W	D_LYS_601	NZ	A_GLU_654	OE2	3.044
6N1W	H_ARG_100H	NH2	L_ASP_91	OD2	3.150
6N1W	c_ARG_504	NH2	D_GLU_657	OE2	3.061
6N1W	d_ARG_542	NH1	D_GLU_647	OE1	3.482
6N1W	d_ARG_542	NH1	D_GLU_647	OE2	3.280
6N1W	d_ARG_542	NH2	D_GLU_647	OE1	2.854
6N1W	d_ARG_579	NH1	D_GLU_584	OE1	3.913
6N1W	d_ARG_579	NH2	D_GLU_584	OE2	3.653
6N1W	d_LYS_601	NZ	D_GLU_654	OE1	3.862
6N1W	d_LYS_601	NZ	D_GLU_654	OE2	3.082
6N1W	h_ARG_100H	NH2	L_ASP_91	OD2	3.226

Table 1613: Interfacial 6N1W-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6N5B	H_LYS_149	NZ	L_GLU_128	OE2	3.031
6N5B	H_LYS_214	NZ	L_GLU_127	OE2	3.139

Table 1614: Interfacial 6N5B-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6N5D	C_LYS_149	NZ	D_GLU_127	OE2	2.211
6N5D	C_LYS_215	NZ	D_GLU_126	OE1	3.361
6N5D	C_LYS_215	NZ	D_GLU_126	OE2	3.815
6N5D	E_LYS_149	NZ	F_GLU_127	OE2	3.376
6N5D	L_LYS_149	NZ	N_GLU_127	OE2	2.091
6N5D	L_HIS_170	NE2	N_ASP_141	OD2	3.244

Table 1615: Interfacial 6N5D-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6N5E	H_LYS_217	NZ	I_GLU_126	OE2	2.748
6N5E	E_LYS_217	NZ	D_GLU_126	OE1	2.995
6N5E	E_LYS_217	NZ	D_GLU_126	OE2	2.272
6N5E	E_LYS_222	NZ	D_GLU_126	OE1	3.688
6N5E	G_LYS_217	NZ	F_GLU_126	OE2	3.351

Table 1616: Interfacial 6N5E-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6N6B	A_LYS_296	NZ	L_ASP_28	OD1	3.122
6N6B	A_LYS_296	NZ	L_ASP_28	OD2	3.000
6N6B	A_LYS_296	NZ	L_GLU_68	OE2	2.842
6N6B	A_LYS_431	NZ	K_ASP_101	OD1	3.959
6N6B	A_LYS_431	NZ	K_ASP_101	OD2	3.832
6N6B	K_HIS_169	NE2	L_ASP_167	OD1	3.738
6N6B	K_LYS_213	NZ	L_GLU_123	OE1	2.814
6N6B	K_LYS_213	NZ	L_GLU_123	OE2	3.044

Table 1617: Interfacial 6N6B-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6NB5	H.LYS.223	NZ	L.GLU.126	OE1	3.229
6NB5	H.LYS.223	NZ	L.GLU.126	OE2	2.760
6NB5	I.LYS.157	NZ	M.GLU.127	OE2	3.828
6NB5	I.LYS.223	NZ	M.GLU.126	OE2	3.316

Table 1618: Interfacial 6NB5-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6NB8	H_LYS_223	NZ	L_GLU_128	OE1	2.783
6NB8	H_LYS_223	NZ	L_GLU_128	OE2	3.341
6NB8	L_ARG_51	NH1	H_ASP_113	OD1	2.821
6NB8	L_ARG_51	NH2	H_ASP_113	OD1	3.921
6NB8	L_ARG_51	NH2	H_ASP_115	OD1	3.423

Table 1619: Interfacial 6NB8-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6NC2	A_LYS_46	NZ	B_ASP_636	OD1	3.909
6NC2	A_LYS_500	NZ	I_ASP_664	OD1	2.780
6NC2	A_LYS_500	NZ	I_ASP_664	OD2	3.992
6NC2	A_ARG_503	NH1	B_GLU_654	OE1	3.759
6NC2	A_ARG_503	NH1	B_GLU_654	OE2	3.172
6NC2	B_ARG_542	NH1	I_GLU_647	OE1	2.800
6NC2	B_ARG_542	NH1	I_ASP_648	OD1	3.191
6NC2	B_ARG_542	NH2	I_ASP_648	OD1	3.498
6NC2	B_LYS_574	NZ	A_ASP_107	OD1	2.510
6NC2	B_LYS_574	NZ	A_ASP_107	OD2	3.688
6NC2	H_ARG_96	NH1	L_ASP_50	OD1	3.082
6NC2	H_ARG_96	NH1	L_ASP_50	OD2	3.706
6NC2	H_ARG_96	NH2	L_ASP_50	OD1	3.892
6NC2	H_ARG_96	NH2	L_ASP_50	OD2	3.158
6NC2	C_LYS_46	NZ	I_ASP_636	OD1	3.909
6NC2	C_LYS_500	NZ	J_ASP_664	OD1	2.780
6NC2	C_LYS_500	NZ	J_ASP_664	OD2	3.991
6NC2	C_ARG_503	NH1	I_GLU_654	OE1	3.760
6NC2	C_ARG_503	NH1	I_GLU_654	OE2	3.173
6NC2	I_ARG_542	NH1	J_GLU_647	OE1	2.801
6NC2	I_ARG_542	NH1	J_ASP_648	OD1	3.190
6NC2	I_ARG_542	NH2	J_ASP_648	OD1	3.498
6NC2	I_LYS_574	NZ	C_ASP_107	OD1	2.510
6NC2	I_LYS_574	NZ	C_ASP_107	OD2	3.688
6NC2	O_ARG_96	NH1	T_ASP_50	OD1	3.082
6NC2	O_ARG_96	NH1	T_ASP_50	OD2	3.706
6NC2	O_ARG_96	NH2	T_ASP_50	OD1	3.892
6NC2	O_ARG_96	NH2	T_ASP_50	OD2	3.158
6NC2	D_LYS_46	NZ	J_ASP_636	OD1	3.909
6NC2	D_LYS_500	NZ	B_ASP_664	OD1	2.780
6NC2	D_LYS_500	NZ	B_ASP_664	OD2	3.992
6NC2	D_ARG_503	NH1	J_GLU_654	OE1	3.759
6NC2	D_ARG_503	NH1	J_GLU_654	OE2	3.173
6NC2	J_ARG_542	NH1	B_GLU_647	OE1	2.800
6NC2	J_ARG_542	NH1	B_ASP_648	OD1	3.191
6NC2	J_ARG_542	NH2	B_ASP_648	OD1	3.498
6NC2	J_LYS_574	NZ	D_ASP_107	OD1	2.510
6NC2	J_LYS_574	NZ	D_ASP_107	OD2	3.688
6NC2	P_ARG_96	NH1	U_ASP_50	OD1	3.083
6NC2	P_ARG_96	NH1	U_ASP_50	OD2	3.706
6NC2	P_ARG_96	NH2	U_ASP_50	OD1	3.893
6NC2	P_ARG_96	NH2	U_ASP_50	OD2	3.158
6NC2	E_LYS_46	NZ	K_ASP_636	OD1	3.909
6NC2	E_LYS_500	NZ	M_ASP_664	OD1	2.780
6NC2	E_LYS_500	NZ	M_ASP_664	OD2	3.992
6NC2	E_ARG_503	NH1	K_GLU_654	OE1	3.759
6NC2	E_ARG_503	NH1	K_GLU_654	OE2	3.172
6NC2	K_ARG_542	NH1	M_GLU_647	OE1	2.800
6NC2	K_ARG_542	NH1	M_ASP_648	OD1	3.191
6NC2	K_ARG_542	NH2	M_ASP_648	OD1	3.498
6NC2	K_LYS_574	NZ	E_ASP_107	OD1	2.510
6NC2	K_LYS_574	NZ	E_ASP_107	OD2	3.688
6NC2	Q_ARG_96	NH1	V_ASP_50	OD1	3.082
6NC2	Q_ARG_96	NH1	V_ASP_50	OD2	3.706
6NC2	Q_ARG_96	NH2	V_ASP_50	OD1	3.892
6NC2	Q_ARG_96	NH2	V_ASP_50	OD2	3.158
6NC2	F_LYS_46	NZ	M_ASP_636	OD1	3.909

6NC2	F_LYS_500	NZ	N_ASP_664	OD1	2.780
6NC2	F_LYS_500	NZ	N_ASP_664	OD2	3.991
6NC2	F_ARG_503	NH1	M_GLU_654	OE1	3.759
6NC2	F_ARG_503	NH1	M_GLU_654	OE2	3.173
6NC2	M_ARG_542	NH1	N_GLU_647	OE1	2.801
6NC2	M_ARG_542	NH1	N_ASP_648	OD1	3.191
6NC2	M_ARG_542	NH2	N_ASP_648	OD1	3.498
6NC2	M_LYS_574	NZ	F_ASP_107	OD1	2.510
6NC2	M_LYS_574	NZ	F_ASP_107	OD2	3.688
6NC2	R_ARG_96	NH1	W_ASP_50	OD1	3.082
6NC2	R_ARG_96	NH1	W_ASP_50	OD2	3.706
6NC2	R_ARG_96	NH2	W_ASP_50	OD1	3.892
6NC2	R_ARG_96	NH2	W_ASP_50	OD2	3.157
6NC2	G_LYS_46	NZ	N_ASP_636	OD1	3.909
6NC2	G_LYS_500	NZ	K_ASP_664	OD1	2.780
6NC2	G_LYS_500	NZ	K_ASP_664	OD2	3.992
6NC2	G_ARG_503	NH1	N_GLU_654	OE1	3.759
6NC2	G_ARG_503	NH1	N_GLU_654	OE2	3.173
6NC2	N_ARG_542	NH1	K_GLU_647	OE1	2.800
6NC2	N_ARG_542	NH1	K_ASP_648	OD1	3.191
6NC2	N_ARG_542	NH2	K_ASP_648	OD1	3.498
6NC2	N_LYS_574	NZ	G_ASP_107	OD1	2.510
6NC2	N_LYS_574	NZ	G_ASP_107	OD2	3.688
6NC2	S_ARG_96	NH1	X_ASP_50	OD1	3.082
6NC2	S_ARG_96	NH1	X_ASP_50	OD2	3.706
6NC2	S_ARG_96	NH2	X_ASP_50	OD1	3.892
6NC2	S_ARG_96	NH2	X_ASP_50	OD2	3.158

Table 1620: Interfacial 6NC2-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6NC3	A_LYS_46	NZ	B_ASP_636	OD1	2.912
6NC3	A_LYS_46	NZ	B_ASP_636	OD2	3.719
6NC3	A_ARG_192	NH2	C_ASP_167	OD1	3.709
6NC3	A_ARG_192	NH2	C_ASP_167	OD2	3.548
6NC3	A_ARG_503	NH2	B_GLU_654	OE1	3.773
6NC3	A_ARG_503	NH2	B_GLU_654	OE2	3.161
6NC3	B_ARG_542	NH2	J_GLU_647	OE1	2.826
6NC3	B_ARG_542	NH2	J_ASP_648	OD1	2.949
6NC3	B_ARG_542	NH2	J_ASP_648	OD2	3.670
6NC3	B_LYS_574	NZ	A_ASP_107	OD1	2.582
6NC3	B_LYS_574	NZ	A_ASP_107	OD2	2.711
6NC3	B_ARG_579	NH1	J_GLU_584	OE2	3.194
6NC3	B_ARG_585	NH2	A_GLU_492	OE1	2.939
6NC3	B_ARG_585	NH2	A_GLU_492	OE2	3.498
6NC3	C_LYS_46	NZ	I_ASP_636	OD1	2.913
6NC3	C_LYS_46	NZ	I_ASP_636	OD2	3.719
6NC3	C_ARG_192	NH2	D_ASP_167	OD1	3.709
6NC3	C_ARG_192	NH2	D_ASP_167	OD2	3.548
6NC3	C_ARG_503	NH2	I_GLU_654	OE1	3.773
6NC3	C_ARG_503	NH2	I_GLU_654	OE2	3.161
6NC3	I_ARG_542	NH2	B_GLU_647	OE1	2.826
6NC3	I_ARG_542	NH2	B_ASP_648	OD1	2.949
6NC3	I_ARG_542	NH2	B_ASP_648	OD2	3.670
6NC3	I_LYS_574	NZ	C_ASP_107	OD1	2.581
6NC3	I_LYS_574	NZ	C_ASP_107	OD2	2.711
6NC3	I_ARG_579	NH1	B_GLU_584	OE2	3.194
6NC3	I_ARG_585	NH2	C_GLU_492	OE1	2.939
6NC3	I_ARG_585	NH2	C_GLU_492	OE2	3.498
6NC3	D_LYS_46	NZ	J_ASP_636	OD1	2.913
6NC3	D_LYS_46	NZ	J_ASP_636	OD2	3.719
6NC3	D_ARG_192	NH2	A_ASP_167	OD1	3.708
6NC3	D_ARG_192	NH2	A_ASP_167	OD2	3.548
6NC3	D_ARG_503	NH2	J_GLU_654	OE1	3.773
6NC3	D_ARG_503	NH2	J_GLU_654	OE2	3.160
6NC3	J_ARG_542	NH2	I_GLU_647	OE1	2.825
6NC3	J_ARG_542	NH2	I_ASP_648	OD1	2.949
6NC3	J_ARG_542	NH2	I_ASP_648	OD2	3.670
6NC3	J_LYS_574	NZ	D_ASP_107	OD1	2.581
6NC3	J_LYS_574	NZ	D_ASP_107	OD2	2.710
6NC3	J_ARG_579	NH1	I_GLU_584	OE2	3.194
6NC3	J_ARG_585	NH2	D_GLU_492	OE1	2.939
6NC3	J_ARG_585	NH2	D_GLU_492	OE2	3.498
6NC3	E_LYS_46	NZ	K_ASP_636	OD1	2.912
6NC3	E_LYS_46	NZ	K_ASP_636	OD2	3.719
6NC3	E_ARG_192	NH2	F_ASP_167	OD1	3.709
6NC3	E_ARG_192	NH2	F_ASP_167	OD2	3.548
6NC3	E_ARG_503	NH2	K_GLU_654	OE1	3.773
6NC3	E_ARG_503	NH2	K_GLU_654	OE2	3.161
6NC3	K_ARG_542	NH2	N_GLU_647	OE1	2.826
6NC3	K_ARG_542	NH2	N_ASP_648	OD1	2.949
6NC3	K_ARG_542	NH2	N_ASP_648	OD2	3.670
6NC3	K_LYS_574	NZ	E_ASP_107	OD1	2.582
6NC3	K_LYS_574	NZ	E_ASP_107	OD2	2.711
6NC3	K_ARG_579	NH1	N_GLU_584	OE2	3.194
6NC3	K_ARG_585	NH2	E_GLU_492	OE1	2.939
6NC3	K_ARG_585	NH2	E_GLU_492	OE2	3.498
6NC3	F_LYS_46	NZ	M_ASP_636	OD1	2.913

6NC3	F_LYS_46	NZ	M_ASP_636	OD2	3.719
6NC3	F_ARG_192	NH2	G_ASP_167	OD1	3.709
6NC3	F_ARG_192	NH2	G_ASP_167	OD2	3.548
6NC3	F_ARG_503	NH2	M_GLU_654	OE1	3.773
6NC3	F_ARG_503	NH2	M_GLU_654	OE2	3.161
6NC3	M_ARG_542	NH2	K_GLU_647	OE1	2.826
6NC3	M_ARG_542	NH2	K_ASP_648	OD1	2.949
6NC3	M_ARG_542	NH2	K_ASP_648	OD2	3.670
6NC3	M_LYS_574	NZ	F_ASP_107	OD1	2.581
6NC3	M_LYS_574	NZ	F_ASP_107	OD2	2.711
6NC3	M_ARG_579	NH1	K_GLU_584	OE2	3.194
6NC3	M_ARG_585	NH2	F_GLU_492	OE1	2.939
6NC3	M_ARG_585	NH2	F_GLU_492	OE2	3.498
6NC3	G_LYS_46	NZ	N_ASP_636	OD1	2.913
6NC3	G_LYS_46	NZ	N_ASP_636	OD2	3.719
6NC3	G_ARG_192	NH2	E_ASP_167	OD1	3.708
6NC3	G_ARG_192	NH2	E_ASP_167	OD2	3.548
6NC3	G_ARG_503	NH2	N_GLU_654	OE1	3.773
6NC3	G_ARG_503	NH2	N_GLU_654	OE2	3.160
6NC3	N_ARG_542	NH2	M_GLU_647	OE1	2.825
6NC3	N_ARG_542	NH2	M_ASP_648	OD1	2.949
6NC3	N_ARG_542	NH2	M_ASP_648	OD2	3.670
6NC3	N_LYS_574	NZ	G_ASP_107	OD1	2.581
6NC3	N_LYS_574	NZ	G_ASP_107	OD2	2.710
6NC3	N_ARG_579	NH1	M_GLU_584	OE2	3.194
6NC3	N_ARG_585	NH2	G_GLU_492	OE1	2.939
6NC3	N_ARG_585	NH2	G_GLU_492	OE2	3.498

Table 1621: Interfacial 6NC3-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6NEX	B_LYS_209	NZ	A_GLU_126	OE2	3.298

Table 1622: Interfacial 6NEX-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6NF2	A_LYS_46	NZ	I_ASP_632	OD2	2.876
6NF2	A_ARG_504	NH2	R_GLU_657	OE2	3.927
6NF2	B_ARG_579	NH1	I_GLU_584	OE2	3.681
6NF2	B_LYS_601	NZ	I_GLU_654	OE1	2.983
6NF2	B_LYS_601	NZ	I_GLU_654	OE2	3.256
6NF2	C_ARG_61	NH1	G_GLU_466	OE1	3.610
6NF2	C_ARG_61	NH2	G_GLU_466	OE2	3.748
6NF2	C_ARG_71	NH2	G_ASP_368	OD1	3.504
6NF2	G_LYS_46	NZ	B_ASP_632	OD2	2.943
6NF2	G_ARG_504	NH2	I_GLU_657	OE2	3.805
6NF2	H_ARG_100F	NH1	L_ASP_50	OD2	2.403
6NF2	H_ARG_100F	NH2	L_ASP_50	OD2	3.926
6NF2	I_ARG_579	NH1	R_GLU_584	OE2	3.624
6NF2	I_LYS_601	NZ	R_GLU_654	OE1	3.068
6NF2	I_LYS_601	NZ	R_GLU_654	OE2	3.333
6NF2	N_ARG_61	NH1	A_GLU_466	OE1	3.592
6NF2	N_ARG_61	NH2	A_GLU_466	OE2	3.737
6NF2	N_ARG_71	NH2	A_ASP_368	OD1	3.532
6NF2	O_ARG_100F	NH1	P_ASP_50	OD2	2.825
6NF2	Q_LYS_46	NZ	R_ASP_632	OD2	2.912
6NF2	Q_ARG_504	NH2	B_GLU_657	OE2	3.920
6NF2	R_ARG_579	NH1	B_GLU_584	OE2	3.657
6NF2	R_LYS_601	NZ	B_GLU_654	OE1	3.130
6NF2	R_LYS_601	NZ	B_GLU_654	OE2	3.363
6NF2	V_ARG_61	NH1	Q_GLU_466	OE1	3.626
6NF2	V_ARG_61	NH2	Q_GLU_466	OE2	3.762
6NF2	V_ARG_71	NH2	Q_ASP_368	OD1	3.511
6NF2	W_ARG_100F	NH1	X_ASP_50	OD2	2.242
6NF2	W_ARG_100F	NH2	X_ASP_50	OD2	3.856

Table 1623: Interfacial 6NF2-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6NF5	A_LYS_46	NZ	B_ASP_632	OD2	2.410
6NF5	A_LYS_137	NZ	L_ASP_51	OD2	2.736
6NF5	A_ARG_192	NH1	J_GLU_164	OE2	3.009
6NF5	A_ARG_192	NH2	J_GLU_164	OE2	3.825
6NF5	B_ARG_542	NH1	D_GLU_647	OE1	3.182
6NF5	B_ARG_542	NH1	D_GLU_647	OE2	3.535
6NF5	B_ARG_542	NH2	D_GLU_647	OE1	3.979
6NF5	B_LYS_574	NZ	A_ASP_107	OD1	2.887
6NF5	B_HIS_585	NE2	A_GLU_492	OE1	3.726
6NF5	B_LYS_601	NZ	D_GLU_657	OE1	3.026
6NF5	K_ARG_53	NH1	B_ASP_659	OD1	3.261
6NF5	K_ARG_53	NH1	B_ASP_659	OD2	3.240
6NF5	K_ARG_53	NH2	B_ASP_659	OD1	3.591
6NF5	K_ARG_53	NH2	B_ASP_659	OD2	2.651
6NF5	C_LYS_46	NZ	D_ASP_632	OD2	2.410
6NF5	C_LYS_137	NZ	F_ASP_51	OD2	2.736
6NF5	C_ARG_192	NH1	A_GLU_164	OE2	3.009
6NF5	C_ARG_192	NH2	A_GLU_164	OE2	3.825
6NF5	D_ARG_542	NH1	M_GLU_647	OE1	3.182
6NF5	D_ARG_542	NH1	M_GLU_647	OE2	3.535
6NF5	D_ARG_542	NH2	M_GLU_647	OE1	3.978
6NF5	D_LYS_574	NZ	C_ASP_107	OD1	2.887
6NF5	D_HIS_585	NE2	C_GLU_492	OE1	3.725
6NF5	D_LYS_601	NZ	M_GLU_657	OE1	3.026
6NF5	G_ARG_53	NH1	D_ASP_659	OD1	3.261
6NF5	G_ARG_53	NH1	D_ASP_659	OD2	3.240
6NF5	G_ARG_53	NH2	D_ASP_659	OD1	3.591
6NF5	G_ARG_53	NH2	D_ASP_659	OD2	2.651
6NF5	J_LYS_46	NZ	M_ASP_632	OD2	2.410
6NF5	J_LYS_137	NZ	P_ASP_51	OD2	2.735
6NF5	J_ARG_192	NH1	C_GLU_164	OE2	3.010
6NF5	J_ARG_192	NH2	C_GLU_164	OE2	3.825
6NF5	M_ARG_542	NH1	B_GLU_647	OE1	3.182
6NF5	M_ARG_542	NH1	B_GLU_647	OE2	3.534
6NF5	M_ARG_542	NH2	B_GLU_647	OE1	3.979
6NF5	M_LYS_574	NZ	J_ASP_107	OD1	2.887
6NF5	M_HIS_585	NE2	J_GLU_492	OE1	3.726
6NF5	M_LYS_601	NZ	B_GLU_657	OE1	3.027
6NF5	Q_ARG_53	NH1	M_ASP_659	OD1	3.262
6NF5	Q_ARG_53	NH1	M_ASP_659	OD2	3.240
6NF5	Q_ARG_53	NH2	M_ASP_659	OD1	3.591
6NF5	Q_ARG_53	NH2	M_ASP_659	OD2	2.650

Table 1624: Interfacial 6NF5-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6NFC	C_ARG_53	NH1	L_ASP_659	OD1	3.890
6NFC	C_ARG_53	NH1	L_ASP_659	OD2	2.842
6NFC	C_ARG_53	NH2	L_ASP_659	OD2	2.675
6NFC	A_LYS_46	NZ	B_ASP_632	OD1	3.913
6NFC	A_LYS_46	NZ	B_ASP_632	OD2	2.455
6NFC	A_LYS_137	NZ	L_ASP_51	OD2	2.690
6NFC	B_ARG_542	NH1	G_GLU_647	OE1	3.297
6NFC	B_ARG_542	NH1	G_GLU_647	OE2	3.640
6NFC	B_LYS_574	NZ	A_GLU_106	OE1	3.608
6NFC	B_LYS_574	NZ	A_GLU_106	OE2	2.473
6NFC	B_ARG_579	NH2	G_GLU_584	OE1	3.071
6NFC	B_ARG_579	NH2	G_GLU_584	OE2	3.850
6NFC	L_LYS_50	NZ	H_GLU_99	OE1	3.024
6NFC	J_ARG_53	NH1	G_ASP_659	OD1	3.783
6NFC	J_ARG_53	NH1	G_ASP_659	OD2	2.774
6NFC	J_ARG_53	NH2	G_ASP_659	OD2	2.735
6NFC	E_LYS_46	NZ	G_ASP_632	OD1	3.927
6NFC	E_LYS_46	NZ	G_ASP_632	OD2	2.442
6NFC	E_ARG_500	NH2	L_ASP_664	OD1	2.950
6NFC	E_ARG_500	NH2	L_ASP_664	OD2	3.747
6NFC	G_ARG_542	NH1	L_GLU_647	OE1	3.321
6NFC	G_ARG_542	NH1	L_GLU_647	OE2	3.884
6NFC	G_LYS_574	NZ	E_GLU_106	OE1	3.312
6NFC	G_LYS_574	NZ	E_GLU_106	OE2	2.741
6NFC	G_ARG_579	NH2	L_GLU_584	OE1	3.032
6NFC	G_ARG_579	NH2	L_GLU_584	OE2	3.885
6NFC	G_LYS_601	NZ	L_GLU_657	OE1	2.933
6NFC	G_LYS_601	NZ	L_GLU_657	OE2	3.730
6NFC	F_LYS_46	NZ	L_ASP_632	OD1	3.960
6NFC	F_LYS_46	NZ	L_ASP_632	OD2	2.474
6NFC	F_LYS_502	NZ	B_ASP_664	OD1	3.023
6NFC	I_ARG_542	NH1	B_GLU_647	OE1	3.339
6NFC	I_ARG_542	NH1	B_GLU_647	OE2	3.856
6NFC	I_LYS_574	NZ	F_ASP_107	OD1	2.742
6NFC	I_ARG_579	NH2	B_GLU_584	OE1	3.222
6NFC	I_ARG_579	NH2	B_GLU_584	OE2	3.762
6NFC	I_LYS_601	NZ	B_GLU_657	OE1	3.945
6NFC	K_ARG_53	NH1	B_ASP_659	OD1	3.915
6NFC	K_ARG_53	NH1	B_ASP_659	OD2	2.784
6NFC	K_ARG_53	NH2	B_ASP_659	OD2	2.738

Table 1625: Interfacial 6NFC-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6NMR	H_LYS_216	NZ	L_GLU_124	OE1	3.273
6NMR	H_LYS_216	NZ	L_GLU_124	OE2	3.010
6NMR	S_ARG_69	NH1	L_GLU_55	OE1	3.247
6NMR	S_ARG_69	NH1	L_GLU_55	OE2	3.038
6NMR	S_ARG_69	NH2	L_GLU_55	OE2	3.173
6NMR	E_ARG_69	NH1	B_GLU_55	OE1	2.733
6NMR	E_ARG_69	NH1	B_GLU_55	OE2	2.469
6NMR	E_ARG_69	NH2	B_GLU_55	OE1	2.510
6NMR	E_ARG_69	NH2	B_GLU_55	OE2	3.637
6NMR	I_ARG_69	NH1	G_GLU_55	OE1	3.183
6NMR	I_ARG_69	NH1	G_GLU_55	OE2	2.119
6NMR	I_ARG_69	NH1	F_ASP_108	OD2	3.629
6NMR	I_ARG_69	NH2	G_GLU_55	OE1	2.639
6NMR	I_ARG_69	NH2	G_GLU_55	OE2	3.327
6NMR	M_ARG_69	NH1	J_ASP_108	OD1	3.945
6NMR	M_ARG_69	NH1	J_ASP_108	OD2	3.140
6NMR	M_ARG_69	NH2	K_GLU_55	OE1	3.608
6NMR	M_ARG_69	NH2	J_ASP_108	OD1	1.901
6NMR	M_ARG_69	NH2	J_ASP_108	OD2	2.331

Table 1626: Interfacial 6NMR-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID residue name residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6NMS	L_ARG_94	NH2	S_GLU_111	OE1	3.728
6NMS	H_ARG_104	NH2	S_GLU_111	OE1	3.455
6NMS	H_ARG_104	NH2	S_GLU_111	OE2	2.500
6NMS	H_LYS_215	NZ	L_GLU_124	OE1	3.565
6NMS	H_LYS_215	NZ	L_GLU_124	OE2	3.270
6NMS	H_LYS_220	NZ	L_GLU_214	OE1	3.397
6NMS	S_LYS_11	NZ	H_ASP_33	OD1	3.001
6NMS	S_LYS_11	NZ	H_GLU_99	OE1	2.549
6NMS	S_HIS_56	ND1	A_ASP_60	OD2	2.658
6NMS	A_ARG_94	NH2	C_GLU_111	OE2	3.453
6NMS	B_ARG_104	NH2	C_GLU_111	OE1	2.703
6NMS	B_ARG_104	NH2	C_GLU_111	OE2	3.000
6NMS	C_LYS_11	NZ	B_ASP_33	OD2	3.490
6NMS	C_LYS_11	NZ	B_GLU_99	OE1	2.892
6NMS	C_ARG_115	NH1	B_GLU_56	OE2	3.579
6NMS	C_ARG_115	NH2	B_GLU_56	OE2	2.699

Table 1627: Interfacial 6NMS-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6NMT	A_ARG_26	NH2	C_ASP_10	OD1	3.433
6NMT	A_ARG_26	NH2	C_ASP_10	OD2	3.182
6NMT	B_ARG_56	NH2	C_GLU_111	OE2	3.542
6NMT	B_LYS_215	NZ	A_GLU_118	OE2	3.496
6NMT	C_LYS_11	NZ	A_ASP_91	OD1	2.678
6NMT	C_LYS_11	NZ	A_ASP_91	OD2	3.319

Table 1628: Interfacial 6NMT-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6NMU	L_LYS_32	NZ	S_ASP_85	OD1	3.326
6NMU	H_ARG_50	NH1	S_GLU_47	OE1	3.597
6NMU	H_ARG_50	NH1	S_GLU_47	OE2	3.084
6NMU	H_ARG_50	NH2	S_GLU_47	OE1	2.989
6NMU	H_ARG_50	NH2	S_GLU_47	OE2	3.577
6NMU	S_ARG_59	NH2	H_ASP_101	OD2	3.444
6NMU	A_LYS_32	NZ	C_ASP_85	OD1	3.635
6NMU	B_ARG_50	NH1	C_GLU_47	OE1	3.989
6NMU	B_ARG_50	NH1	C_GLU_47	OE2	3.035
6NMU	B_ARG_50	NH2	C_GLU_47	OE1	2.804
6NMU	B_ARG_50	NH2	C_GLU_47	OE2	3.091
6NMU	B_LYS_215	NZ	A_GLU_124	OE1	3.494
6NMU	B_LYS_215	NZ	A_GLU_124	OE2	3.379
6NMU	C_ARG_59	NH1	B_ASP_101	OD1	3.720
6NMU	C_ARG_59	NH1	B_ASP_101	OD2	2.808

Table 1629: Interfacial 6NMU-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6O9B	A_ARG_35	NH1	B_ASP_73	OD1	2.773
6O9B	A_ARG_35	NH1	B_ASP_73	OD2	3.974
6O9B	A_ARG_48	NH2	B_ASP_73	OD2	3.479
6O9B	A_HIS_192	ND1	B_ASP_118	OD2	3.864
6O9B	C_LYS_9	NZ	A_ASP_116	OD2	2.706

Table 1630: Interfacial 6O9B-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6O9C	A_ARG_35	NH1	B_ASP_73	OD1	3.395
6O9C	A_HIS_192	NE2	B_ASP_118	OD2	3.199
6O9C	A_ARG_202	NH1	B_ASP_118	OD2	3.014
6O9C	B_LYS_26	NZ	A_GLU_232	OE2	3.913
6O9C	C_LYS_9	NZ	A_ASP_77	OD2	3.855
6O9C	C_LYS_9	NZ	A_ASP_116	OD2	2.984

Table 1631: Interfacial 6O9C-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6OGX	C_LYS_213	NZ	D_GLU_123	OE1	2.791
6OGX	C_LYS_213	NZ	D_GLU_123	OE2	3.773
6OGX	C_LYS_218	NZ	D_ASP_122	OD2	3.785
6OGX	D_ARG_55	NH2	G_ASP_117	OD1	2.990
6OGX	G_ARG_95	NH1	H_ASP_99	OD1	3.462
6OGX	G_ARG_95	NH1	H_ASP_99	OD2	2.833
6OGX	G_ARG_95	NH2	H_ASP_99	OD1	2.923
6OGX	G_ARG_95	NH2	H_ASP_99	OD2	3.646
6OGX	H_ARG_100	NH1	L_GLU_55	OE1	3.516
6OGX	H_ARG_100	NH1	L_GLU_55	OE2	2.787

Table 1632: Interfacial 6OGX-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6OKM	H_ARG_100	NH1	L_GLU_55	OE1	2.851
6OKM	H_HIS_165	NE2	L ASP_167	OD1	3.460
6OKM	H_LYS_210	NZ	L_GLU_123	OE2	3.540
6OKM	H_LYS_215	NZ	L ASP_122	OD1	3.237
6OKM	H_LYS_215	NZ	L ASP_122	OD2	3.538
6OKM	R_ARG_95	NH1	H ASP_99	OD1	3.347
6OKM	R_ARG_95	NH1	H ASP_99	OD2	3.783
6OKM	R_ARG_95	NH2	H ASP_99	OD1	3.371
6OKM	R_ARG_95	NH2	H ASP_99	OD2	2.555

Table 1633: Interfacial 6OKM-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6OKN	A_LYS_213	NZ	B_GLU_123	OE1	3.312
6OKN	A_LYS_213	NZ	B_GLU_123	OE2	2.829
6OKN	C_LYS_213	NZ	D_GLU_123	OE1	3.356
6OKN	C_LYS_213	NZ	D_GLU_123	OE2	2.896
6OKN	C_LYS_218	NZ	D_ASP_122	OD2	3.923

Table 1634: Interfacial 6OKN-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6OOR	A_LYS_148	NZ	H_ASP_55	OD2	3.250
6OOR	B_ARG_12	NH2	A_ASP_242	OD1	3.946
6OOR	B_ARG_12	NH2	A_ASP_242	OD2	2.705
6OOR	B_HIS_34	NE2	A_GLU_97	OE1	2.803
6OOR	B_HIS_34	NE2	A_GLU_97	OE2	3.580
6OOR	H_ARG_109	NH2	A_ASP_80	OD1	2.917
6OOR	H_ARG_109	NH2	A_ASP_80	OD2	3.352
6OOR	H_LYS_220	NZ	L_GLU_128	OE1	2.677
6OOR	H_LYS_220	NZ	L_GLU_128	OE2	2.872

Table 1635: Interfacial 6OOR-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6OSY	2_LYS_282	NZ	8_ASP_100C	OD2	3.941
6OSY	8_ARG_61	NH1	2_GLU_466	OE2	3.827
6OSY	8_ARG_71	NH1	2_ASP_368	OD2	3.948
6OSY	8_ARG_71	NH2	2_ASP_368	OD2	3.279
6OSY	A_ARG_542	NH1	Q_GLU_647	OE2	3.907
6OSY	A_ARG_542	NH2	Q_GLU_647	OE1	3.187
6OSY	A_ARG_542	NH2	Q_GLU_647	OE2	2.660
6OSY	A_ARG_579	NH2	Q_GLU_584	OE1	3.706
6OSY	B_LYS_282	NZ	F_ASP_100C	OD1	3.567
6OSY	B_LYS_282	NZ	F_ASP_100C	OD2	3.346
6OSY	F_ARG_71	NH2	B_ASP_368	OD2	3.635
6OSY	G_ARG_542	NH1	A_GLU_647	OE2	3.983
6OSY	G_ARG_542	NH2	A_GLU_647	OE1	3.165
6OSY	G_ARG_542	NH2	A_GLU_647	OE2	2.705
6OSY	G_ARG_579	NH2	A_GLU_584	OE1	3.899
6OSY	H_ARG_96	NH1	L_GLU_55	OE1	3.662
6OSY	H_HIS_100	ND1	2_GLU_87	OE2	3.031
6OSY	H_HIS_100	NE2	2_GLU_87	OE2	3.785
6OSY	I_ARG_96	NH1	J_GLU_55	OE2	3.419
6OSY	I_HIS_100	ND1	B_GLU_87	OE2	3.029
6OSY	I_HIS_100	NE2	B_GLU_87	OE2	3.781
6OSY	J_ARG_46	NH1	I_ASP_101	OD1	3.411
6OSY	J_ARG_46	NH1	I_ASP_101	OD2	2.599
6OSY	K_LYS_282	NZ	P_ASP_100C	OD2	3.859
6OSY	L_ARG_46	NH1	H_ASP_101	OD1	3.509
6OSY	L_ARG_46	NH1	H_ASP_101	OD2	2.485
6OSY	P_ARG_71	NH1	K_ASP_368	OD2	3.949
6OSY	P_ARG_71	NH2	K_ASP_368	OD2	3.325
6OSY	Q_ARG_542	NH1	G_GLU_647	OE2	3.913
6OSY	Q_ARG_542	NH2	G_GLU_647	OE1	3.228
6OSY	Q_ARG_542	NH2	G_GLU_647	OE2	2.706
6OSY	R_ARG_96	NH1	S_GLU_55	OE2	3.423
6OSY	R_HIS_100	ND1	K_GLU_87	OE1	3.719
6OSY	R_HIS_100	ND1	K_GLU_87	OE2	2.905
6OSY	R_HIS_100	NE2	K_GLU_87	OE1	3.960
6OSY	S_ARG_46	NH1	R_ASP_101	OD1	3.488
6OSY	S_ARG_46	NH1	R_ASP_101	OD2	2.503

Table 1636: Interfacial 6OSY-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6OT1	B_ARG_542	NH2	D_GLU_647	OE1	2.021
6OT1	B_ARG_542	NH2	D_GLU_647	OE2	3.827
6OT1	B_LYS_601	NZ	D_GLU_657	OE1	3.960
6OT1	B_LYS_601	NZ	D_GLU_657	OE2	3.832
6OT1	G_LYS_282	NZ	q_ASP_100C	OD2	3.404
6OT1	G_ARG_327	NH2	m_GLU_100I	OE1	3.817
6OT1	q_ARG_71	NH2	G_ASP_368	OD2	3.596
6OT1	O_ARG_542	NH2	B_GLU_647	OE1	2.048
6OT1	O_ARG_542	NH2	B_GLU_647	OE2	3.874
6OT1	O_LYS_601	NZ	B_GLU_657	OE1	3.934
6OT1	O_LYS_601	NZ	B_GLU_657	OE2	3.759
6OT1	E_LYS_282	NZ	J_ASP_100C	OD2	3.404
6OT1	E_ARG_327	NH2	F_GLU_100I	OE1	3.817
6OT1	J_ARG_71	NH2	E_ASP_368	OD2	3.599
6OT1	D_ARG_542	NH2	O_GLU_647	OE1	2.015
6OT1	D_ARG_542	NH2	O_GLU_647	OE2	3.816
6OT1	D_LYS_601	NZ	O_GLU_657	OE2	3.900
6OT1	P_LYS_282	NZ	S_ASP_100C	OD2	3.405
6OT1	P_ARG_327	NH2	Q_GLU_100I	OE1	3.817
6OT1	S_ARG_71	NH2	P_ASP_368	OD2	3.597

Table 1637: Interfacial 6OT1-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6P62	A_LYS_168	NZ	B_GLU_190	OE2	3.547
6P62	A_ARG_542	NH1	B_GLU_647	OE1	2.629
6P62	A_ARG_542	NH1	B_GLU_647	OE2	3.985
6P62	A_ARG_542	NH2	B_GLU_648	OE2	3.131
6P62	A_ARG_579	NH1	B_GLU_584	OE1	3.453
6P62	A_ARG_579	NH1	B_GLU_584	OE2	2.953
6P62	B_LYS_168	NZ	E_GLU_190	OE2	3.547
6P62	B_ARG_542	NH1	E_GLU_647	OE1	2.630
6P62	B_ARG_542	NH1	E_GLU_647	OE2	3.986
6P62	B_ARG_542	NH2	E_GLU_648	OE2	3.130
6P62	B_ARG_579	NH1	E_GLU_584	OE1	3.454
6P62	B_ARG_579	NH1	E_GLU_584	OE2	2.952
6P62	E_LYS_168	NZ	A_GLU_190	OE2	3.547
6P62	E_ARG_542	NH1	A_GLU_647	OE1	2.629
6P62	E_ARG_542	NH1	A_GLU_647	OE2	3.985
6P62	E_ARG_542	NH2	A_GLU_648	OE2	3.130
6P62	E_ARG_579	NH1	A_GLU_584	OE1	3.453
6P62	E_ARG_579	NH1	A_GLU_584	OE2	2.952

Table 1638: Interfacial 6P62-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6P65	A_ARG_500	NH1	L_GLU_30	OE1	3.144
6P65	A_ARG_500	NH1	L_GLU_30	OE2	3.804
6P65	A_ARG_500	NH2	L_GLU_30	OE1	3.741
6P65	A_ARG_500	NH2	L_GLU_30	OE2	2.979
6P65	A_ARG_542	NH2	B_ASP_648	OD1	3.154
6P65	H_LYS_71	NZ	A_GLU_87	OE1	2.936
6P65	H_LYS_71	NZ	A_GLU_87	OE2	2.864
6P65	H_LYS_100H	NZ	L_ASP_50	OD1	2.708
6P65	H_LYS_100H	NZ	L_ASP_50	OD2	2.597
6P65	B_ARG_500	NH1	D_GLU_30	OE1	3.143
6P65	B_ARG_500	NH1	D_GLU_30	OE2	3.804
6P65	B_ARG_500	NH2	D_GLU_30	OE1	3.741
6P65	B_ARG_500	NH2	D_GLU_30	OE2	2.979
6P65	B_ARG_542	NH2	E_ASP_648	OD1	3.155
6P65	C_LYS_71	NZ	B_GLU_87	OE1	2.936
6P65	C_LYS_71	NZ	B_GLU_87	OE2	2.864
6P65	C_LYS_100H	NZ	D_ASP_50	OD1	2.708
6P65	C_LYS_100H	NZ	D_ASP_50	OD2	2.597
6P65	E_ARG_500	NH1	G_GLU_30	OE1	3.143
6P65	E_ARG_500	NH1	G_GLU_30	OE2	3.804
6P65	E_ARG_500	NH2	G_GLU_30	OE1	3.741
6P65	E_ARG_500	NH2	G_GLU_30	OE2	2.979
6P65	E_ARG_542	NH2	A_ASP_648	OD1	3.154
6P65	F_LYS_71	NZ	E_GLU_87	OE1	2.935
6P65	F_LYS_71	NZ	E_GLU_87	OE2	2.865
6P65	F_LYS_100H	NZ	G_ASP_50	OD1	2.708
6P65	F_LYS_100H	NZ	G_ASP_50	OD2	2.596

Table 1639: Interfacial 6P65-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6PE8	A_LYS_212	NZ	B_GLU_129	OE1	3.617
6PE8	A_LYS_212	NZ	B_GLU_129	OE2	2.921
6PE8	A_LYS_217	NZ	B_ASP_128	OD2	3.408
6PE8	B_LYS_36	NZ	U_GLU_98	OE2	3.943
6PE8	H_LYS_212	NZ	L_GLU_129	OE1	2.763
6PE8	H_LYS_212	NZ	L_GLU_129	OE2	3.237
6PE8	L_LYS_36	NZ	T_GLU_98	OE1	3.975
6PE8	L_LYS_36	NZ	T_GLU_98	OE2	3.494
6PE8	T_ARG_90	NH2	H_ASP_62	OD1	3.932
6PE8	T_LYS_94	NZ	L_ASP_97	OD1	2.502
6PE8	T_LYS_94	NZ	L_ASP_97	OD2	3.872

Table 1640: Interfacial 6PE8-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6PE9	A_LYS_212	NZ	B_GLU_129	OE1	3.227
6PE9	A_LYS_212	NZ	B_GLU_129	OE2	3.311
6PE9	A_LYS_217	NZ	B_ASP_128	OD1	3.061
6PE9	A_LYS_217	NZ	B_ASP_128	OD2	3.113
6PE9	C_LYS_13	NZ	U_GLU_107	OE2	3.461
6PE9	C_LYS_212	NZ	D_GLU_129	OE1	2.716
6PE9	D_LYS_36	NZ	G_GLU_98	OE2	3.800
6PE9	E_LYS_13	NZ	G_GLU_107	OE2	3.510
6PE9	E_LYS_212	NZ	F_GLU_129	OE1	3.511
6PE9	E_LYS_212	NZ	F_GLU_129	OE2	3.915
6PE9	F_LYS_36	NZ	U_GLU_98	OE2	3.769
6PE9	G_ARG_73	NH1	J_GLU_74	OE1	3.140
6PE9	G_ARG_73	NH2	J_GLU_74	OE1	2.423
6PE9	G_ARG_73	NH2	J_GLU_74	OE2	3.851
6PE9	G_LYS_94	NZ	D_ASP_97	OD1	2.957
6PE9	I_LYS_29	NZ	U_ASP_69	OD2	3.034
6PE9	I_ARG_73	NH1	U_GLU_74	OE1	3.681
6PE9	I_ARG_73	NH1	U_GLU_74	OE2	2.345
6PE9	I_ARG_73	NH2	U_GLU_74	OE2	3.507
6PE9	J_ARG_73	NH1	G_GLU_74	OE1	3.931
6PE9	J_ARG_73	NH1	G_GLU_74	OE2	3.429
6PE9	M_LYS_36	NZ	J_GLU_98	OE1	2.716
6PE9	U_LYS_	NZ	L_ASP_	OD2	3.835
6PE9	U_ARG_	NH2	L_GLU_	OE1	3.379
6PE9	U_ARG_	NH2	L_GLU_	OE2	2.907
6PE9	U_LYS_94	NZ	F_ASP_97	OD1	2.940
6PE9	V_ARG_90	NH1	L_ASP_1	OD1	3.701
6PE9	V_ARG_90	NH2	L_ASP_1	OD1	3.047
6PE9	V_LYS_94	NZ	L_ASP_97	OD1	3.203

Table 1641: Interfacial 6PE9-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6PHB	LLYS_43	NZ	D_ASP_27	OD2	2.797
6PHB	LLYS_47	NZ	C_GLU_55	OE1	3.460
6PHB	LLYS_47	NZ	C_GLU_55	OE2	3.396
6PHB	LLYS_47	NZ	D_ASP_105	OD2	2.626
6PHB	C_ARG_95	NH1	L_ASP_28	OD2	3.551
6PHB	C_ARG_95	NH1	L_GLU_39	OE2	3.728
6PHB	D_ARG_50	NH1	L_GLU_39	OE2	3.791
6PHB	D_ARG_50	NH2	L_GLU_39	OE2	2.945
6PHB	D_LYS_213	NZ	C_GLU_124	OE1	2.534
6PHB	D_LYS_213	NZ	C_GLU_124	OE2	3.508
6PHB	E_LYS_43	NZ	B_ASP_27	OD2	3.033
6PHB	E_LYS_47	NZ	A_GLU_55	OE1	3.560
6PHB	E_LYS_47	NZ	A_GLU_55	OE2	3.516
6PHB	E_LYS_47	NZ	B_ASP_105	OD1	2.522
6PHB	A_ARG_95	NH1	E_ASP_28	OD1	3.463
6PHB	A_ARG_95	NH1	E_GLU_39	OE2	3.694
6PHB	B_ARG_50	NH1	E_GLU_39	OE2	3.771
6PHB	B_ARG_50	NH2	E_GLU_39	OE2	2.963
6PHB	B_LYS_213	NZ	A_GLU_124	OE1	3.629
6PHB	B_LYS_213	NZ	A_GLU_124	OE2	2.552

Table 1642: Interfacial 6PHB-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6PHC	I_LYS_2	NZ	A_GLU_96	OE1	3.433
6PHC	A_LYS_209	NZ	B_GLU_122	OE2	3.367
6PHC	E_LYS_2	NZ	C_GLU_96	OE2	3.166
6PHC	C_LYS_75	NZ	A_GLU_1	OE1	3.102
6PHC	C_LYS_209	NZ	D_GLU_122	OE2	3.075

Table 1643: Interfacial 6PHC-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6PHD	H_ARG_52	NH2	C_ASP_131	OD2	3.559
6PHD	H_LYS_158	NZ	L_GLU_128	OE2	2.649
6PHD	H_LYS_224	NZ	L_GLU_127	OE1	2.532
6PHD	H_LYS_224	NZ	L_GLU_127	OE2	2.992
6PHD	C_LYS_118	NZ	H_ASP_109	OD1	3.874
6PHD	C_LYS_135	NZ	L_ASP_51	OD2	3.166

Table 1644: Interfacial 6PHD-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6PHF	A_LYS_63	NZ	C_GLU_89	OE2	2.941
6PHF	A_LYS_150	NZ	B_GLU_123	OE1	3.782
6PHF	A_LYS_216	NZ	B_GLU_122	OE1	2.642
6PHF	A_LYS_216	NZ	B_GLU_122	OE2	2.832
6PHF	G_LYS_130	NZ	A_GLU_59	OE2	2.793
6PHF	G_LYS_135	NZ	B_ASP_48	OD1	3.917
6PHF	G_LYS_135	NZ	B_ASP_48	OD2	2.691
6PHF	B_LYS_50	NZ	G_ASP_160	OD1	3.948
6PHF	B_LYS_50	NZ	G_ASP_160	OD2	3.455
6PHF	C_LYS_63	NZ	A_GLU_89	OE2	3.050
6PHF	C_LYS_150	NZ	D_GLU_123	OE2	2.663
6PHF	C_LYS_216	NZ	D_GLU_122	OE1	2.759
6PHF	C_LYS_216	NZ	D_GLU_122	OE2	3.120
6PHF	E_LYS_130	NZ	C_GLU_59	OE2	2.474
6PHF	E_LYS_135	NZ	D_ASP_48	OD1	3.909
6PHF	E_LYS_135	NZ	D_ASP_48	OD2	2.579

Table 1645: Interfacial 6PHF-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6PHG	A_LYS_221	NZ	B_GLU_126	OE2	3.079

Table 1646: Interfacial 6PHG-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6PHH	C.LYS_76	NZ	A.GLU_1	OE1	3.897
6PHH	A.LYS_76	NZ	C.GLU_1	OE1	3.451
6PHH	A.LYS_221	NZ	B.GLU_126	OE2	3.327

Table 1647: Interfacial 6PHH-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6PI7	B_ARG_67	NH2	A_GLU_345	OE2	3.601
6PI7	C_ARG_105	NH1	A_ASP_334	OD1	2.888
6PI7	F_ARG_105	NH1	D_ASP_334	OD1	3.009
6PI7	G_ARG_4	NH1	A_ASP_385	OD1	3.497
6PI7	G_ARG_4	NH1	A_ASP_385	OD2	3.823
6PI7	G_ARG_4	NH2	A_ASP_385	OD1	3.602
6PI7	G_ARG_4	NH2	A_ASP_385	OD2	3.033
6PI7	G_ARG_6	NH1	A_GLU_433	OE2	2.847
6PI7	G_ARG_6	NH1	A_ASP_437	OD1	3.619
6PI7	G_ARG_6	NH2	A_ASP_437	OD1	2.997
6PI7	G_ARG_6	NH2	A_ASP_440	OD2	2.762

Table 1648: Interfacial 6PI7-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6PYC	H_LYS_208	NZ	L_GLU_124	OE1	2.557
6PYC	H_LYS_208	NZ	L_GLU_124	OE2	3.571
6PYC	L_LYS_108	NZ	B_ASP_32	OD1	2.949
6PYC	A_ARG_99	NH1	B_ASP_91	OD1	3.714
6PYC	B_LYS_53	NZ	L_GLU_17	OE1	3.141
6PYC	B_LYS_53	NZ	L_GLU_17	OE2	3.254

Table 1649: Interfacial 6PYC-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6PYD	H_LYS_213	NZ	L_GLU_127	OE1	3.352
6PYD	A_LYS_213	NZ	B_GLU_127	OE1	3.596

Table 1650: Interfacial 6PYD-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6PZW	A_HIS_98	NE2	B_GLU_214	OE2	3.848
6PZW	A_ARG_253	NH1	K_ASP_53	OD2	2.854
6PZW	A_ARG_253	NH2	K_ASP_53	OD2	2.999
6PZW	A_ARG_419	NH1	B_GLU_214	OE2	3.897
6PZW	K_ARG_97	NH2	L_ASP_50	OD1	2.825
6PZW	K_ARG_97	NH2	L_ASP_50	OD2	3.390
6PZW	D_HIS_98	NE2	A_GLU_214	OE2	3.848
6PZW	D_ARG_253	NH1	F_ASP_53	OD2	2.854
6PZW	D_ARG_253	NH2	F_ASP_53	OD2	2.999
6PZW	D_ARG_419	NH1	A_GLU_214	OE2	3.897
6PZW	F_ARG_97	NH2	E_ASP_50	OD1	2.825
6PZW	F_ARG_97	NH2	E_ASP_50	OD2	3.390
6PZW	J_ARG_97	NH2	G_ASP_50	OD1	2.825
6PZW	J_ARG_97	NH2	G_ASP_50	OD2	3.390
6PZW	C_HIS_98	NE2	D_GLU_214	OE2	3.848
6PZW	C_ARG_253	NH1	J_ASP_53	OD2	2.854
6PZW	C_ARG_253	NH2	J_ASP_53	OD2	2.999
6PZW	C_ARG_419	NH1	D_GLU_214	OE2	3.897
6PZW	B_HIS_98	NE2	C_GLU_214	OE2	3.848
6PZW	B_ARG_253	NH1	H_ASP_53	OD2	2.854
6PZW	B_ARG_253	NH2	H_ASP_53	OD2	2.999
6PZW	B_ARG_419	NH1	C_GLU_214	OE2	3.897
6PZW	H_ARG_97	NH2	L_ASP_50	OD1	2.825
6PZW	H_ARG_97	NH2	L_ASP_50	OD2	3.390

Table 1651: Interfacial 6PZW-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6RPS	A_HIS_34	NE2	B_ASP_102	OD2	3.097
6RPS	A_HIS_64	NE2	H_ASP_54	OD2	2.837
6RPS	A_LYS_170	NZ	H_ASP_54	OD1	3.636
6RPS	A_LYS_170	NZ	H_ASP_54	OD2	2.590
6RPS	A_LYS_170	NZ	H_ASP_56	OD2	2.821
6RPS	A_HIS_234	ND1	H_ASP_56	OD2	3.904
6RPS	A_LYS_250	NZ	B_GLU_13	OE2	2.734
6RPS	B_HIS_64	NE2	N_ASP_54	OD2	2.859
6RPS	B_HIS_103	ND1	A_ASP_36	OD1	3.129
6RPS	B_HIS_103	ND1	A_ASP_36	OD2	3.954
6RPS	B_LYS_170	NZ	N_ASP_54	OD1	3.719
6RPS	B_LYS_170	NZ	N_ASP_54	OD2	2.644
6RPS	B_LYS_170	NZ	N_ASP_56	OD2	2.839
6RPS	B_HIS_234	ND1	N_ASP_56	OD2	3.922
6RPS	B_LYS_250	NZ	A_GLU_13	OE2	2.991
6RPS	N_LYS_214	NZ	M_ASP_122	OD1	3.095
6RPS	N_LYS_214	NZ	M_ASP_122	OD2	3.107
6RPS	H_LYS_209	NZ	L_GLU_123	OE1	2.780
6RPS	H_LYS_209	NZ	L_GLU_123	OE2	3.710

Table 1652: Interfacial 6RPS-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID residue name residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6S3T	A_LYS_49	NZ	C_GLU_158	OE1	3.663
6S3T	B_LYS_49	NZ	L_GLU_158	OE1	3.761
6S3T	D_ARG_35	NH1	S_ASP_332	OD1	3.467
6S3T	D_ARG_35	NH1	S_ASP_332	OD2	2.946
6S3T	D_ARG_35	NH2	S_ASP_332	OD2	3.071
6S3T	D_ARG_35	NH2	S_ASP_334	OD1	3.408
6S3T	D_HIS_171	NE2	C_ASP_171	OD2	3.832
6S3T	D_LYS_215	NZ	C_GLU_127	OE1	2.814
6S3T	D_LYS_215	NZ	C_GLU_127	OE2	3.990
6S3T	E_ARG_35	NH1	T_ASP_332	OD1	3.561
6S3T	E_ARG_35	NH1	T_ASP_332	OD2	3.035
6S3T	E_ARG_35	NH2	T_ASP_332	OD2	3.163
6S3T	E_ARG_35	NH2	T_ASP_334	OD1	3.432
6S3T	E_HIS_171	NE2	L_ASP_171	OD2	3.931
6S3T	E_LYS_215	NZ	L_GLU_127	OE1	3.013
6S3T	N_ARG_35	NH1	A_ASP_332	OD1	3.796
6S3T	N_ARG_35	NH1	A_ASP_332	OD2	3.195
6S3T	N_ARG_35	NH2	A_ASP_332	OD1	3.883
6S3T	N_ARG_35	NH2	A_ASP_332	OD2	2.517
6S3T	N_ARG_35	NH2	A_ASP_334	OD2	3.989
6S3T	N_ARG_73	NH2	S_GLU_44	OE2	2.482
6S3T	N_HIS_171	NE2	M_ASP_171	OD2	3.181
6S3T	N_LYS_215	NZ	M_GLU_127	OE1	2.964
6S3T	N_LYS_215	NZ	M_GLU_127	OE2	3.944
6S3T	R_ARG_35	NH1	B_ASP_332	OD1	3.511
6S3T	R_ARG_35	NH1	B_ASP_332	OD2	2.943
6S3T	R_ARG_35	NH2	B_ASP_332	OD2	2.873
6S3T	R_ARG_35	NH2	B_ASP_334	OD1	3.424
6S3T	R_ARG_73	NH2	T_GLU_44	OE2	2.709
6S3T	R_HIS_171	NE2	Q_ASP_171	OD2	3.265
6S3T	R_LYS_215	NZ	Q_GLU_127	OE1	2.948
6S3T	R_LYS_215	NZ	Q_GLU_127	OE2	3.831

Table 1653: Interfacial 6S3T-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6U02	A_HIS_98	NE2	B_GLU_214	OE2	3.838
6U02	A_ARG_209	NH1	J_GLU_128	OE2	3.226
6U02	A_ARG_210	NH2	J_ASP_412	OD1	3.355
6U02	A_ARG_210	NH2	J_ASP_412	OD2	3.535
6U02	A_ARG_419	NH1	B_GLU_214	OE2	3.906
6U02	B_HIS_98	NE2	E_GLU_214	OE2	3.839
6U02	B_ARG_209	NH1	A_GLU_128	OE2	3.226
6U02	B_ARG_210	NH2	A_ASP_412	OD1	3.355
6U02	B_ARG_210	NH2	A_ASP_412	OD2	3.535
6U02	B_ARG_419	NH1	E_GLU_214	OE2	3.906
6U02	E_HIS_98	NE2	J_GLU_214	OE2	3.838
6U02	E_ARG_209	NH1	B_GLU_128	OE2	3.226
6U02	E_ARG_210	NH2	B_ASP_412	OD1	3.355
6U02	E_ARG_210	NH2	B_ASP_412	OD2	3.536
6U02	E_ARG_419	NH1	J_GLU_214	OE2	3.906
6U02	J_HIS_98	NE2	A_GLU_214	OE2	3.838
6U02	J_ARG_209	NH1	E_GLU_128	OE2	3.226
6U02	J_ARG_210	NH2	E_ASP_412	OD1	3.356
6U02	J_ARG_210	NH2	E_ASP_412	OD2	3.535
6U02	J_ARG_419	NH1	A_GLU_214	OE2	3.906

Table 1654: Interfacial 6U02-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6U59	A.LYS_34	NZ	B.ASP_612	OD1	2.489
6U59	A_ARG_504	NH1	I.GLU_662	OE1	3.209
6U59	A_ARG_504	NH1	I.GLU_662	OE2	2.833
6U59	A_ARG_504	NH2	I.GLU_662	OE2	3.911
6U59	B.LYS_574	NZ	A.ASP_107	OD1	2.403
6U59	B_ARG_579	NH2	I.GLU_584	OE1	3.024
6U59	L_ARG_50	NH1	A.GLU_269	OE2	3.175
6U59	L_ARG_50	NH2	A.GLU_268	OE1	2.965
6U59	L_ARG_50	NH2	A.GLU_269	OE2	3.221
6U59	L_ARG_95A	NH1	A.GLU_350	OE2	3.796
6U59	L_ARG_95A	NH2	A.GLU_350	OE1	3.217
6U59	L_ARG_95A	NH2	A.GLU_350	OE2	3.041
6U59	L_ARG_95A	NH2	A.GLU_351	OE1	3.921
6U59	C.LYS_34	NZ	D.ASP_612	OD1	2.489
6U59	C_ARG_504	NH1	B.GLU_662	OE1	3.208
6U59	C_ARG_504	NH1	B.GLU_662	OE2	2.832
6U59	C_ARG_504	NH2	B.GLU_662	OE2	3.910
6U59	D.LYS_574	NZ	C.ASP_107	OD1	2.403
6U59	D_ARG_579	NH2	B.GLU_584	OE1	3.024
6U59	E_ARG_50	NH1	C.GLU_269	OE2	3.175
6U59	E_ARG_50	NH2	C.GLU_268	OE1	2.965
6U59	E_ARG_50	NH2	C.GLU_269	OE2	3.221
6U59	E_ARG_95A	NH1	C.GLU_350	OE2	3.795
6U59	E_ARG_95A	NH2	C.GLU_350	OE1	3.216
6U59	E_ARG_95A	NH2	C.GLU_350	OE2	3.040
6U59	E_ARG_95A	NH2	C.GLU_351	OE1	3.921
6U59	G.LYS_34	NZ	I.ASP_612	OD1	2.489
6U59	G_ARG_504	NH1	D.GLU_662	OE1	3.209
6U59	G_ARG_504	NH1	D.GLU_662	OE2	2.833
6U59	G_ARG_504	NH2	D.GLU_662	OE2	3.910
6U59	I.LYS_574	NZ	G.ASP_107	OD1	2.403
6U59	I_ARG_579	NH2	D.GLU_584	OE1	3.025
6U59	J_ARG_50	NH1	G.GLU_269	OE2	3.175
6U59	J_ARG_50	NH2	G.GLU_268	OE1	2.965
6U59	J_ARG_50	NH2	G.GLU_269	OE2	3.220
6U59	J_ARG_95A	NH1	G.GLU_350	OE2	3.796
6U59	J_ARG_95A	NH2	G.GLU_350	OE1	3.217
6U59	J_ARG_95A	NH2	G.GLU_350	OE2	3.041
6U59	J_ARG_95A	NH2	G.GLU_351	OE1	3.921

Table 1655: Interfacial 6U59-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6UG7	H_HIS_60	NE2	L_GLU_1	OE1	2.854
6UG7	H_HIS_60	NE2	L_GLU_1	OE2	3.808
6UG7	H_LYS_213	NZ	L_GLU_122	OE1	2.927
6UG7	H_LYS_213	NZ	L_GLU_122	OE2	3.960

Table 1656: Interfacial 6UG7-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6UG8	H_HIS_60	NE2	L_GLU_1	OE1	3.688
6UG8	H_LYS_213	NZ	L_GLU_122	OE1	2.779
6UG8	H_LYS_213	NZ	L_GLU_122	OE2	3.811

Table 1657: Interfacial 6UG8-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6UG9	H_HIS_60	NE2	L_GLU_1	OE2	3.673
6UG9	H_LYS_213	NZ	L_GLU_122	OE1	3.853
6UG9	A_HIS_60	NE2	B_GLU_1	OE1	3.507
6UG9	A_LYS_213	NZ	B_GLU_122	OE1	2.877
6UG9	J_HIS_60	NE2	K_GLU_1	OE1	3.585
6UG9	J_LYS_213	NZ	K_GLU_122	OE1	2.648
6UG9	J_LYS_213	NZ	K_GLU_122	OE2	3.296

Table 1658: Interfacial 6UG9-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
6UGA	H_HIS_60	NE2	L_GLU_1	OE1	3.306
6UGA	B_HIS_60	NE2	A_GLU_1	OE2	3.932
6UGA	B_HIS_168	NE2	A_ASP_166	OD1	3.218
6UGA	B_LYS_213	NZ	A_GLU_122	OE1	3.352

Table 1659: Interfacial 6UGA-specific salt bridging networks analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1A14.PDB	O, H.SER_25	N, H.GLN_3	H, H.GLN_3	2.77	1.89	21.99
1A14.PDB	OG, H.SER_25	NE2, H.GLN_5	HE21, H.GLN_5	2.94	2.02	15.87
1A14.PDB	O, H.TYR_90	NE2, H.GLN_6	HE21, H.GLN_6	2.72	1.83	18.57
1A14.PDB	O, H.THR_108	N, H.GLU_10	H, H.GLU_10	2.84	1.94	19.84
1A14.PDB	O, H.THR_110	N, H.VAL_12	H, H.VAL_12	2.96	2.06	20.79
1A14.PDB	O, H.LEU_82C	N, H.GLY_15	H, H.GLY_15	2.91	2.08	27.09
1A14.PDB	O, H.GLN_5	N, H.LYS_23	H, H.LYS_23	2.75	1.80	7.95
1A14.PDB	O, H.ASN_76	N, H.ALA_24	H, H.ALA_24	2.78	1.85	14.53
1A14.PDB	O, H.THR_28	N, H.ASN_31	H, H.ASN_31	2.81	1.88	13.65
1A14.PDB	O, H.PHE_51	N, H.MET_34	H, H.MET_34	2.88	1.94	13.17
1A14.PDB	O, H.ALA_93	N, H.TYR_35	H, H.TYR_35	2.86	1.93	13.77
1A14.PDB	O, H.TYR_91	N, H.VAL_37	H, H.VAL_37	2.95	2.02	16.35
1A14.PDB	O, H.GLU_46	N, H.LYS_38	H, H.LYS_38	2.72	1.78	11.05
1A14.PDB	OE1, L.GLN_38	NE2, H.GLN_39	HE21, H.GLN_39	2.62	1.69	9.24
1A14.PDB	O, H.SER_40	N, H.GLN_43	H, H.GLN_43	2.91	2.06	24.59
1A14.PDB	O, H.TRP_36	N, H.ILE_48	H, H.ILE_48	2.85	1.93	16.00
1A14.PDB	O, H.SER_58	N, H.ILE_50	H, H.ILE_50	2.72	1.81	16.55
1A14.PDB	O, H.MET_34	N, H.PHE_51	H, H.PHE_51	2.91	2.00	17.30
1A14.PDB	O, H.ASP_56	N, H.TYR_52	H, H.TYR_52	2.91	1.96	11.43
1A14.PDB	OD1, H.ASN_54	N, H.ASP_56	H, H.ASP_56	2.82	2.01	27.91
1A14.PDB	O, H.ILE_48	N, H.ASN_60	H, H.ASN_60	2.52	1.70	23.11
1A14.PDB	O, H.TRP_47	ND2, H.ASN_60	HD22, H.ASN_60	2.76	1.87	19.57
1A14.PDB	O, H.PHE_63	N, H.ALA_67	H, H.ALA_67	2.95	1.99	5.88
1A14.PDB	OH, H.TYR_59	N, H.LEU_69	H, H.LEU_69	2.81	1.86	9.44
1A14.PDB	O, H.THR_77	N, H.ASP_72	H, H.ASP_72	2.72	1.79	11.50
1A14.PDB	OD2, H.ASP_72	N, H.SER_75	H, H.SER_75	2.80	1.92	19.95
1A14.PDB	OG1, H.THR_77	OG, H.SER_75	HG, H.SER_75	2.86	2.04	27.11
1A14.PDB	O, H.ASP_72	N, H.THR_77	H, H.THR_77	2.99	2.04	11.91
1A14.PDB	O, H.CYS_22	N, H.ALA_78	H, H.ALA_78	2.74	1.87	21.95
1A14.PDB	O, H.MET_20	N, H.MET_80	H, H.MET_80	2.96	2.07	20.70
1A14.PDB	OE2, H.GLU_85	OG, H.SER_84	HG, H.SER_84	2.91	1.99	12.42
1A14.PDB	O, H.THR_83	N, H.ASP_86	H, H.ASP_86	2.92	1.98	13.36
1A14.PDB	O, H.TYR_102	N, H.ARG_94	H, H.ARG_94	2.71	1.83	20.03
1A14.PDB	OD2, H.ASP_101	NH2, H.ARG_94	HH21, H.ARG_94	2.75	1.83	16.91
1A14.PDB	O, H.GLY_97	N, H.ARG_100	H, H.ARG_100	2.82	1.90	14.18
1A14.PDB	OH, L.TYR_36	N, H.PHE_100E	H, H.PHE_100E	2.73	1.81	13.85
1A14.PDB	OE1, H.GLN_6	N, H.GLY_106	H, H.GLY_106	2.85	1.98	22.46
1A14.PDB	O, H.ALA_88	N, H.VAL_109	H, H.VAL_109	2.80	1.86	11.06
1A14.PDB	O, H.GLU_10	N, H.THR_110	H, H.THR_110	2.78	1.95	26.41
1A14.PDB	O, H.GLU_10	OG1, H.THR_110	HG1, H.THR_110	2.94	1.99	6.65
1A14.PDB	OG, H.SER_87	N, H.VAL_111	H, H.VAL_111	2.68	1.82	20.55

Table 1660: 1A14-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1E6J.PDB	O, H.TYR_94	NE2, H_GLN_6	HE22, H_GLN_6	2.85	1.90	10.79
1E6J.PDB	O, H_GLN_6	NE2, H_GLN_112	HE22, H_GLN_112	2.88	2.04	26.17
1E6J.PDB	O, L.TYR_85	NE2, L_GLN_6	HE22, L_GLN_6	2.85	1.96	20.67
1E6J.PDB	OH, L.TYR_85	NE2, L_GLN_36	HE21, L_GLN_36	2.83	1.87	8.49
1E6J.PDB	OE1, H_GLN_39	NE2, L_GLN_37	HE22, L_GLN_37	2.69	1.84	23.98
1E6J.PDB	OG, L_SER_129	NE2, L_GLN_122	HE22, L_GLN_122	2.94	2.00	13.76
1E6J.PDB	O, L_ILE_104	NE2, L_GLN_164	HE22, L_GLN_164	2.87	1.92	11.35
1E6J.PDB	O, P_GLU_159	NE2, P_GLN_155	HE21, P_GLN_155	2.82	1.93	20.03

Table 1661: 1E6J-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1F3R.PDB	O, A_ASN_68	N, A_TYR_72	H, A_TYR_72	2.96	1.94	7.79
1F3R.PDB	O, B_ASN_230	OH, A_TYR_72	HH, A_TYR_72	2.67	1.70	2.56
1F3R.PDB	O, B_THR_21	N, B_SER_7	H, B_SER_7	2.87	1.87	9.61
1F3R.PDB	O, B_LEU_85	N, B_SER_15	H, B_SER_15	2.82	1.79	2.70
1F3R.PDB	OD1, B_ASN_83	OG1, B_THR_17	HG1, B_THR_17	2.73	1.80	13.32
1F3R.PDB	O, B_LEU_80	N, B_LEU_20	H, B_LEU_20	2.98	2.06	21.36
1F3R.PDB	O, B_VAL_78	N, B_CYS_22	H, B_CYS_22	2.90	1.88	6.63
1F3R.PDB	O, B_ASN_76	N, B_VAL_24	H, B_VAL_24	2.91	1.89	6.46
1F3R.PDB	O, B_SER_28	OG, B_SER_31	HG, B_SER_31	2.64	1.68	8.32
1F3R.PDB	O, B_THR_96	N, B_SER_35	H, B_SER_35	2.97	1.94	2.64
1F3R.PDB	O, B_GLY_49	N, B_TRP_36	H, B_TRP_36	2.92	1.90	3.05
1F3R.PDB	O, B_THR_90	N, B_SER_41	H, B_SER_41	2.88	1.87	9.24
1F3R.PDB	O, B_ARG_38	N, B_GLU_46	H, B_GLU_46	2.92	1.91	7.52
1F3R.PDB	O, B_TRP_36	N, B_MET_48	H, B_MET_48	2.89	1.95	18.67
1F3R.PDB	O, B_ALA_58	N, B_ARG_50	H, B_ARG_50	2.87	1.86	10.08
1F3R.PDB	O, A_GLY_70	NH2, B_ARG_50	HH21, B_ARG_50	2.81	1.79	6.29
1F3R.PDB	O, B_TYR_100	OH, B_TYR_53	HH, B_TYR_53	2.66	1.70	6.56
1F3R.PDB	O, B_LEU_67	OH, B_TYR_59	HH, B_TYR_59	2.69	1.77	15.53
1F3R.PDB	O, B_TRP_47	ND2, B_ASN_60	HD21, B_ASN_60	2.98	1.99	12.26
1F3R.PDB	NE1, A_TRP_67	OG, B_SER_61	HG, B_SER_61	2.86	1.89	6.31
1F3R.PDB	O, B_GLN_77	N, B_ASP_72	H, B_ASP_72	2.95	1.93	8.00
1F3R.PDB	O, B_SER_70	N, B_PHE_79	H, B_PHE_79	2.87	1.91	16.42
1F3R.PDB	O, B_LEU_20	N, B_LEU_80	H, B_LEU_80	2.97	1.97	11.86
1F3R.PDB	O, B_SER_68	N, B_LYS_81	H, B_LYS_81	3.00	2.04	17.31
1F3R.PDB	O, B_LEU_18	N, B_MET_82	H, B_MET_82	2.89	1.88	9.85
1F3R.PDB	O, B_ARG_66	N, B_ASN_83	H, B_ASN_83	2.93	1.91	7.12
1F3R.PDB	O, B_ASP_89	OH, B_TYR_93	HH, B_TYR_93	2.65	1.76	18.66
1F3R.PDB	O, B_VAL_37	N, B_TYR_94	H, B_TYR_94	2.86	1.87	13.22
1F3R.PDB	O, B_SER_35	N, B_THR_96	H, B_THR_96	2.85	1.83	6.85
1F3R.PDB	O, B_PHE_112	N, B_ARG_97	H, B_ARG_97	2.97	1.94	0.13
1F3R.PDB	O, B_TYR_109	N, B_LEU_99	H, B_LEU_99	2.82	1.80	6.09
1F3R.PDB	O, B_LEU_105	OH, B_TYR_100	HH, B_TYR_100	2.81	1.87	9.55
1F3R.PDB	O, B_ARG_97	N, B_ASP_111	H, B_ASP_111	3.00	1.99	8.87
1F3R.PDB	OD2, B_ASP_111	N, B_PHE_112	H, B_PHE_112	2.95	1.99	17.02
1F3R.PDB	O, B_CYS_95	N, B_GLY_114	H, B_GLY_114	2.93	1.91	8.69
1F3R.PDB	O, B_GLY_91	N, B_VAL_119	H, B_VAL_119	2.99	2.03	17.54
1F3R.PDB	O, B_GLY_10	N, B_THR_120	H, B_THR_120	2.83	1.81	7.39
1F3R.PDB	O, B_ASN_257	N, B_LEU_142	H, B_LEU_142	2.85	1.82	6.57
1F3R.PDB	O, B_LYS_162	OG1, B_THR_143	HG1, B_THR_143	2.81	1.98	25.43
1F3R.PDB	O, B_TYR_224	NE2, B_GLN_144	HE22, B_GLN_144	2.91	1.91	11.14
1F3R.PDB	O, B_SER_160	N, B_SER_145	H, B_SER_145	2.97	1.94	2.29
1F3R.PDB	O, B_GLY_238	OG, B_SER_147	HG, B_SER_147	2.70	1.74	5.62
1F3R.PDB	O, B_LEU_216	N, B_GLY_154	H, B_GLY_154	2.96	1.97	13.26
1F3R.PDB	OG1, B_THR_212	OG1, B_THR_158	HG1, B_THR_158	2.80	1.87	11.10
1F3R.PDB	O, B_LEU_211	N, B_LEU_159	H, B_LEU_159	2.93	1.90	5.82
1F3R.PDB	O, B_SER_145	N, B_SER_160	H, B_SER_160	2.85	1.84	8.61
1F3R.PDB	O, B_TYR_209	N, B_CYS_161	H, B_CYS_161	2.83	1.82	9.85
1F3R.PDB	O, B_THR_143	N, B_LYS_162	H, B_LYS_162	2.92	1.94	14.43
1F3R.PDB	O, A_ILE_75	OH, B_TYR_170	HH, B_TYR_170	2.72	1.77	10.88
1F3R.PDB	O, B_ILE_186	N, B_TRP_173	H, B_TRP_173	2.96	1.95	8.06
1F3R.PDB	O, B_PHE_225	N, B_TYR_174	H, B_TYR_174	2.93	1.90	0.94
1F3R.PDB	O, B_LYS_183	N, B_GLN_175	H, B_GLN_175	2.88	1.90	13.28
1F3R.PDB	O, B_THR_223	N, B_GLN_176	H, B_GLN_176	2.93	1.91	6.88
1F3R.PDB	O, B_TRP_173	N, B_LEU_185	H, B_LEU_185	2.95	2.01	19.35
1F3R.PDB	O, B_SER_191	N, B_TYR_187	H, B_TYR_187	2.91	1.92	11.97
1F3R.PDB	O, B_LEU_171	N, B_THR_189	H, B_THR_189	2.92	1.94	15.09
1F3R.PDB	O, B_ASN_169	OG1, B_THR_189	HG1, B_THR_189	2.78	1.86	13.97

1F3R.PDB	O, B_ASN_188	N, B_ASN_190	H, B_ASN_190	2.99	2.10	24.68
1F3R.PDB	O, B_ASN_190	OG, B_SER_191	HG, B_SER_191	2.83	1.89	11.19
1F3R.PDB	O, B_PRO_197	N, B_ARG_199	H, B_ARG_199	2.94	2.05	24.65
1F3R.PDB	OD1, B_ASP_220	NH1, B_ARG_199	HH12, B_ARG_199	2.89	1.98	22.15
1F3R.PDB	O, B_THR_210	N, B_SER_203	H, B_SER_203	2.88	1.86	4.33
1F3R.PDB	O, B_ASN_168	N, B_GLY_206	H, B_GLY_206	2.87	1.85	8.80
1F3R.PDB	O, B_CYS_161	N, B_TYR_209	H, B_TYR_209	2.98	1.97	8.84
1F3R.PDB	O, B_GLY_206	OH, B_TYR_209	HH, B_TYR_209	2.72	1.77	8.74
1F3R.PDB	O, B_SER_203	N, B_THR_210	H, B_THR_210	2.89	1.91	14.26
1F3R.PDB	O, B_SER_203	OG1, B_THR_210	HG1, B_THR_210	2.67	1.72	9.35
1F3R.PDB	O, B_LEU_159	N, B_LEU_211	H, B_LEU_211	2.96	1.94	7.42
1F3R.PDB	O, B_VAL_157	N, B_ILE_213	H, B_ILE_213	2.95	1.95	11.15
1F3R.PDB	O, B_ARG_199	OG, B_SER_214	HG, B_SER_214	2.60	1.65	8.60
1F3R.PDB	OG, B_SER_214	N, B_SER_215	H, B_SER_215	2.99	2.14	28.78
1F3R.PDB	OE1, B_GLN_217	OG, B_SER_215	HG, B_SER_215	2.66	1.72	13.57
1F3R.PDB	O, B_GLN_217	N, B_ASP_220	H, B_ASP_220	2.93	1.97	17.91
1F3R.PDB	O, B_GLN_176	N, B_THR_223	H, B_THR_223	2.88	1.86	6.84
1F3R.PDB	O, B_THR_239	OG1, B_THR_223	HG1, B_THR_223	2.65	1.69	5.79
1F3R.PDB	O, B_ASP_220	OH, B_TYR_224	HH, B_TYR_224	2.64	1.71	12.61
1F3R.PDB	O, B_TYR_174	N, B_PHE_225	H, B_PHE_225	2.92	1.99	20.78
1F3R.PDB	O, B_ALA_172	N, B_TYR_227	H, B_TYR_227	3.00	2.00	11.62
1F3R.PDB	NE1, B_TRP_47	OH, B_TYR_227	HH, B_TYR_227	2.99	2.20	29.73
1F3R.PDB	O, B_TYR_170	N, B_TYR_229	H, B_TYR_229	2.94	1.91	4.24
1F3R.PDB	OD1, B_ASN_188	OH, B_TYR_229	HH, B_TYR_229	2.66	1.70	7.44
1F3R.PDB	OD1, B_ASN_231	N, B_GLY_232	H, B_GLY_232	2.89	1.87	6.19
1F3R.PDB	O, A_ASP_71	OH, B_TYR_233	HH, B_TYR_233	2.71	1.89	25.38
1F3R.PDB	OE1, B_GLN_144	N, B_GLY_238	H, B_GLY_238	2.97	1.99	15.42
1F3R.PDB	O, B_SER_147	N, B_LYS_240	H, B_LYS_240	2.89	1.86	4.01
1F3R.PDB	O, B_LEU_149	OE2, B_GLU_242	HE2, B_GLU_242	2.59	1.65	10.05
1F3R.PDB	O, B_LEU_243	NE2, B_GLN_248	HE21, B_GLN_248	2.97	2.01	16.74
1F3R.PDB	O, B_GLY_136	N, B_ILE_251	H, B_ILE_251	2.88	1.88	10.81
1F3R.PDB	O, B_SER_41	OE2, B_GLU_253	HE2, B_GLU_253	2.63	1.68	6.51
1F3R.PDB	O, B_ASP_139	N, B_ASP_255	H, B_ASP_255	2.95	1.95	13.03

Table 1662: 1F3R-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1HCV.PDB	O, A_THR_110	N, A_VAL_12	H, A_VAL_12	2.93	2.02	18.33
1HCV.PDB	O, A_SER_112	N, A_ALA_14	H, A_ALA_14	2.93	2.13	29.46
1HCV.PDB	O, A_LEU_82C	N, A_GLY_15	H, A_GLY_15	2.71	1.79	13.54
1HCV.PDB	O, A_GLN_13	N, A_GLY_16	H, A_GLY_16	2.86	1.94	16.16
1HCV.PDB	O, A_MET_82	N, A_LEU_18	H, A_LEU_18	2.92	1.99	16.49
1HCV.PDB	O, A_LEU_80	N, A_LEU_20	H, A_LEU_20	2.95	1.97	7.19
1HCV.PDB	O, A_SER_7	N, A_SER_21	H, A_SER_21	2.87	1.92	9.29
1HCV.PDB	O, A_VAL_78	N, A_CYS_22	H, A_CYS_22	2.90	2.03	23.01
1HCV.PDB	O, A_GLN_5	N, A_ALA_23	H, A_ALA_23	2.91	1.94	8.72
1HCV.PDB	O, A_LYS_76	N, A_ALA_24	H, A_ALA_24	2.84	1.87	5.65
1HCV.PDB	O, A_GLY_95	N, A_ASP_33	H, A_ASP_33	2.78	1.82	4.32
1HCV.PDB	O, A_ILE_51	N, A_MET_34	H, A_MET_34	2.93	1.96	6.74
1HCV.PDB	O, A_GLY_93	N, A_GLY_35	H, A_GLY_35	2.81	1.88	14.94
1HCV.PDB	O, A_ALA_49	N, A_TRP_36	H, A_TRP_36	2.79	1.84	9.16
1HCV.PDB	O, A_THR_91	N, A_PHE_37	H, A_PHE_37	2.79	1.88	17.50
1HCV.PDB	O, A_GLU_46	N, A_ARG_38	H, A_ARG_38	2.85	1.92	14.14
1HCV.PDB	OE2, A_GLU_46	NE, A_ARG_38	HE, A_ARG_38	2.98	2.01	4.47
1HCV.PDB	OH, A_TYR_90	NH1, A_ARG_38	HH11, A_ARG_38	2.93	1.98	14.34
1HCV.PDB	OD1, A_ASP_86	NH1, A_ARG_38	HH12, A_ARG_38	2.86	1.90	11.61
1HCV.PDB	O, A_VAL_89	N, A_GLN_39	H, A_GLN_39	2.97	2.07	19.93
1HCV.PDB	O, A_LYS_43	NE2, A_GLN_39	HE22, A_GLN_39	2.89	1.95	12.02
1HCV.PDB	O, A_ALA_40	N, A_LYS_43	H, A_LYS_43	2.92	2.01	18.86
1HCV.PDB	O, A_ARG_38	N, A_GLU_46	H, A_GLU_46	2.84	1.93	16.72
1HCV.PDB	O, A_TRP_36	N, A_VAL_48	H, A_VAL_48	2.86	1.95	18.09
1HCV.PDB	O, A_MET_34	N, A_ILE_51	H, A_ILE_51	2.83	1.91	16.34
1HCV.PDB	O, A_ARG_56	N, A_ASN_52	H, A_ASN_52	2.98	2.06	16.59
1HCV.PDB	O, A_ASN_52	N, A_ALA_55	H, A_ALA_55	2.92	2.11	28.15
1HCV.PDB	O, A_TYR_59	NE, A_ARG_64	HE, A_ARG_64	2.96	2.11	24.27
1HCV.PDB	O, A_TYR_59	NH2, A_ARG_64	HH21, A_ARG_64	2.85	1.95	21.66
1HCV.PDB	O, A_VAL_63	N, A_ARG_66	H, A_ARG_66	2.97	2.05	16.00
1HCV.PDB	O, A_GLN_81	N, A_THR_68	H, A_THR_68	2.89	1.97	16.73
1HCV.PDB	OH, A_TYR_59	N, A_ILE_69	H, A_ILE_69	2.86	1.90	7.83
1HCV.PDB	O, A_TRP_52A	NE, A_ARG_71	HE, A_ARG_71	2.79	1.83	3.79
1HCV.PDB	O, A_THR_77	N, A_ASP_72	H, A_ASP_72	2.82	1.84	2.73
1HCV.PDB	OD1, A_ASP_72	N, A_LYS_75	H, A_LYS_75	2.94	2.05	18.63
1HCV.PDB	O, A_CYS_22	N, A_VAL_78	H, A_VAL_78	2.93	1.97	8.95
1HCV.PDB	O, A_SER_70	N, A_TYR_79	H, A_TYR_79	2.83	1.88	10.07
1HCV.PDB	O, A_LEU_20	N, A_LEU_80	H, A_LEU_80	2.95	2.00	12.10
1HCV.PDB	O, A_THR_68	N, A_GLN_81	H, A_GLN_81	2.77	1.81	7.49
1HCV.PDB	O, A_LEU_18	N, A_MET_82	H, A_MET_82	2.84	1.89	10.75
1HCV.PDB	OD2, A_ASP_86	N, A_LYS_83	H, A_LYS_83	2.81	1.93	18.86
1HCV.PDB	O, A_LYS_83	N, A_ASP_86	H, A_ASP_86	2.78	1.84	11.83
1HCV.PDB	O, A_THR_107	N, A_TYR_90	H, A_TYR_90	2.77	1.82	10.83
1HCV.PDB	O, A_ASP_86	OH, A_TYR_90	HH, A_TYR_90	2.78	1.82	4.95
1HCV.PDB	O, A_PHE_37	N, A_THR_91	H, A_THR_91	2.79	1.83	10.98
1HCV.PDB	OE2, A_GLU_6	N, A_CYS_92	H, A_CYS_92	2.92	1.93	9.32
1HCV.PDB	O, A_GLY_35	N, A_GLY_93	H, A_GLY_93	2.87	1.92	15.71
1HCV.PDB	O, A_ALA_94	N, A_ASP_101	H, A_ASP_101	2.95	2.03	16.44
1HCV.PDB	O, A_CYS_92	N, A_GLY_104	H, A_GLY_104	2.85	1.98	21.84
1HCV.PDB	OE2, A_GLU_6	N, A_GLY_106	H, A_GLY_106	2.97	2.18	29.00
1HCV.PDB	O, A_TYR_90	N, A_THR_107	H, A_THR_107	2.83	1.98	25.29
1HCV.PDB	O, A_GLY_10	N, A_THR_110	H, A_THR_110	2.96	1.98	5.57

Table 1663: 1HCV-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1HGD.PDB	O, B_ILE_140	N, A_ALA_11	H, A_ALA_11	2.90	2.03	23.17
1HGD.PDB	O, B_PHE_138	N, A_LEU_13	H, A_LEU_13	2.95	2.00	13.08
1HGD.PDB	O, B_ARG_25	N, A_CYS_14	H, A_CYS_14	2.89	1.92	6.63
1HGD.PDB	O, B_GLY_136	N, A_LEU_15	H, A_LEU_15	2.87	1.90	8.68
1HGD.PDB	O, B_GLY_23	N, A_GLY_16	H, A_GLY_16	2.93	2.02	18.64
1HGD.PDB	O, A_HIS_18	ND1, A_HIS_17	HD1, A_HIS_17	2.93	2.05	21.54
1HGD.PDB	O, B_TRP_21	N, A_HIS_18	H, A_HIS_18	2.86	2.01	24.44
1HGD.PDB	OD1, A_ASN_322	N, A_VAL_20	H, A_VAL_20	2.77	1.82	9.61
1HGD.PDB	O, A_VAL_36	N, A_THR_24	H, A_THR_24	2.85	1.96	19.97
1HGD.PDB	O, A_ILE_34	N, A_VAL_26	H, A_VAL_26	2.82	1.91	17.04
1HGD.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.80	1.78	9.95
1HGD.PDB	O, A_VAL_26	N, A_ILE_34	H, A_ILE_34	2.88	1.94	11.85
1HGD.PDB	O, A_THR_24	N, A_VAL_36	H, A_VAL_36	2.80	1.84	8.97
1HGD.PDB	O, A_MET_320	N, A_THR_37	H, A_THR_37	2.84	1.87	4.46
1HGD.PDB	O, A_LEU_316	N, A_THR_40	H, A_THR_40	2.81	1.96	24.53
1HGD.PDB	O, A_LEU_314	N, A_LEU_42	H, A_LEU_42	2.82	1.97	25.11
1HGD.PDB	O, A_PHE_294	N, A_GLN_44	H, A_GLN_44	2.82	1.85	6.79
1HGD.PDB	O, A_SER_46	NE2, A_GLN_44	HE22, A_GLN_44	2.87	1.99	21.11
1HGD.PDB	OD2, A_ASP_275	NZ, A_LYS_50	HZ1, A_LYS_50	2.70	1.79	23.99
1HGD.PDB	O, A_PRO_273	N, A_ILE_51	H, A_ILE_51	2.81	1.86	10.46
1HGD.PDB	O, A_ASP_275	N, A_ASN_53	H, A_ASN_53	2.82	1.93	20.82
1HGD.PDB	OD2, A_ASP_85	N, A_ARG_57	H, A_ARG_57	2.86	1.92	12.52
1HGD.PDB	O, A_THR_83	NE, A_ARG_57	HE, A_ARG_57	2.79	1.82	8.87
1HGD.PDB	O, A_LEU_86	N, A_LEU_59	H, A_LEU_59	2.85	1.91	13.74
1HGD.PDB	O, A_VAL_88	N, A_GLY_61	H, A_GLY_61	2.95	2.09	23.46
1HGD.PDB	OD1, A_ASP_60	N, A_ILE_62	H, A_ILE_62	2.87	1.95	16.02
1HGD.PDB	O, A_GLY_61	N, A_CYS_64	H, A_CYS_64	2.88	1.96	16.57
1HGD.PDB	OE2, A_GLU_89	N, A_LEU_66	H, A_LEU_66	2.99	2.02	7.24
1HGD.PDB	O, A_LEU_66	N, A_LEU_70	H, A_LEU_70	2.89	2.00	21.06
1HGD.PDB	O, A_ILE_67	N, A_LEU_71	H, A_LEU_71	2.83	1.86	7.61
1HGD.PDB	O, A_ASP_68	N, A_GLY_72	H, A_GLY_72	2.86	1.93	13.78
1HGD.PDB	OD1, A_ASP_73	N, A_HIS_75	H, A_HIS_75	2.94	2.08	23.98
1HGD.PDB	OD1, A_ASP_73	ND1, A_HIS_75	HD1, A_HIS_75	2.82	1.92	19.21
1HGD.PDB	O, A_ASP_63	NE2, A_HIS_75	HE2, A_HIS_75	2.89	1.98	18.26
1HGD.PDB	O, A_ASP_73	N, A_CYS_76	H, A_CYS_76	2.82	1.87	12.30
1HGD.PDB	O, A_PRO_74	N, A_ASP_77	H, A_ASP_77	2.96	2.01	12.30
1HGD.PDB	OE1, A_GLU_82	N, A_THR_83	H, A_THR_83	2.91	2.00	18.21
1HGD.PDB	O, A_ARG_57	N, A_ASP_85	H, A_ASP_85	2.78	1.87	17.48
1HGD.PDB	O, A_LEU_59	N, A_VAL_88	H, A_VAL_88	2.92	1.95	5.25
1HGD.PDB	O, A_MET_268	N, A_GLU_89	H, A_GLU_89	2.76	1.82	11.67
1HGD.PDB	OD1, A_ASP_60	NE, A_ARG_90	HE, A_ARG_90	2.88	1.91	7.55
1HGD.PDB	O, A_SER_270	NH1, A_ARG_90	HH11, A_ARG_90	2.66	1.79	24.65
1HGD.PDB	O, A_ALA_272	NH1, A_ARG_90	HH12, A_ARG_90	2.63	1.70	17.53
1HGD.PDB	OD2, A_ASP_60	NH2, A_ARG_90	HH21, A_ARG_90	2.80	1.82	10.07
1HGD.PDB	OD1, A_ASP_271	N, A_SER_91	H, A_SER_91	2.89	1.92	6.25
1HGD.PDB	OD1, A_ASP_271	OG, A_SER_91	HG, A_SER_91	2.93	2.12	28.00
1HGD.PDB	OD2, A_ASP_271	OG, A_SER_91	HG, A_SER_91	2.81	1.91	17.78
1HGD.PDB	OD2, A_ASP_68	OG, A_SER_95	HG, A_SER_95	2.92	1.99	16.11
1HGD.PDB	OD2, A_ASP_73	N, A_ASN_96	H, A_ASN_96	2.94	1.97	9.87
1HGD.PDB	OD1, A_ASP_68	OH, A_TYR_100	HH, A_TYR_100	2.88	1.90	0.98
1HGD.PDB	OD2, A_ASP_104	OG, A_SER_107	HG, A_SER_107	2.86	1.96	19.52
1HGD.PDB	O, A_TYR_105	N, A_ARG_109	H, A_ARG_109	2.82	1.85	4.81
1HGD.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.83	1.84	13.41
1HGD.PDB	OD2, F_ASP_79	OG, A_SER_110	HG, A_SER_110	2.92	1.96	11.03
1HGD.PDB	O, A_SER_107	N, A_LEU_111	H, A_LEU_111	2.89	1.94	11.30
1HGD.PDB	O, A_LEU_108	N, A_VAL_112	H, A_VAL_112	2.97	2.01	7.23
1HGD.PDB	O, A_ARG_109	N, A_ALA_113	H, A_ALA_113	2.92	2.01	17.77

1HGD.PDB	O, A_SER_110	N, A_SER_114	H, A_SER_114	2.96	2.05	17.15
1HGD.PDB	OE2, A_GLU_119	OG1, A_THR_117	HG1, A_THR_117	2.87	1.92	9.92
1HGD.PDB	O, A_GLU_82	N, A_LEU_118	H, A_LEU_118	2.91	1.98	15.32
1HGD.PDB	O, A_TYR_257	N, A_ILE_121	H, A_ILE_121	2.85	1.89	7.79
1HGD.PDB	O, A_ARG_255	N, A_GLU_123	H, A_GLU_123	2.91	1.96	11.30
1HGD.PDB	O, A_THR_155	N, A_THR_131	H, A_THR_131	2.76	1.86	18.36
1HGD.PDB	OD1, A_ASN_152	N, A_ASN_133	H, A_ASN_133	2.80	1.88	15.39
1HGD.PDB	O, A_GLY_146	N, A_SER_136	H, A_SER_136	2.72	1.80	14.38
1HGD.PDB	O, A_GLY_144	NZ, A_LYS_140	HZ1, A_LYS_140	2.72	1.75	16.12
1HGD.PDB	OD1, A_ASN_137	NZ, A_LYS_140	HZ2, A_LYS_140	2.76	1.82	19.96
1HGD.PDB	OD2, A_ASP_77	NE, A_ARG_141	HE, A_ARG_141	2.80	1.97	26.87
1HGD.PDB	O, A_PHE_147	NH1, A_ARG_141	HH12, A_ARG_141	2.57	1.62	14.73
1HGD.PDB	OD1, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.86	1.95	21.98
1HGD.PDB	OD2, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.74	1.86	23.87
1HGD.PDB	O, A_GLY_72	NH2, A_ARG_141	HH22, A_ARG_141	2.95	1.97	11.26
1HGD.PDB	O, A_SER_136	N, A_GLY_146	H, A_GLY_146	2.96	2.04	13.96
1HGD.PDB	O, A_GLY_72	N, A_SER_149	H, A_SER_149	2.84	1.94	17.77
1HGD.PDB	O, A_ALA_253	N, A_ASN_152	H, A_ASN_152	2.80	1.94	23.17
1HGD.PDB	OH, A_TYR_195	NE1, A_TRP_153	HE1, A_TRP_153	2.81	1.92	20.45
1HGD.PDB	O, A_LEU_194	N, A_LYS_156	H, A_LYS_156	2.95	2.06	19.92
1HGD.PDB	O, A_SER_193	NZ, A_LYS_156	HZ2, A_LYS_156	2.80	1.80	13.32
1HGD.PDB	O, A_SER_247	N, A_LEU_164	H, A_LEU_164	2.66	1.83	25.34
1HGD.PDB	O, A_ILE_245	N, A_VAL_166	H, A_VAL_166	2.93	1.97	10.28
1HGD.PDB	O, A_LEU_243	OG1, A_THR_167	HG1, A_THR_167	2.93	2.00	13.12
1HGD.PDB	O, A_LEU_243	N, A_MET_168	H, A_MET_168	2.89	1.96	14.94
1HGD.PDB	O, A_ASP_241	N, A_ASN_170	H, A_ASN_170	2.96	1.98	6.23
1HGD.PDB	O, A_PHE_174	ND2, A_ASN_170	HD21, A_ASN_170	2.82	1.87	11.30
1HGD.PDB	O, A_VAL_237	ND2, A_ASN_170	HD22, A_ASN_170	2.83	2.02	27.43
1HGD.PDB	O, A_VAL_237	N, A_LYS_176	H, A_LYS_176	2.97	2.05	17.24
1HGD.PDB	OE2, A_GLU_123	NZ, A_LYS_176	HZ2, A_LYS_176	2.69	1.80	25.20
1HGD.PDB	O, A_THR_235	N, A_TYR_178	H, A_TYR_178	2.79	1.82	5.26
1HGD.PDB	OE1, A_GLU_123	OH, A_TYR_178	HH, A_TYR_178	2.75	1.82	12.48
1HGD.PDB	OG1, A_THR_235	NE1, A_TRP_180	HE1, A_TRP_180	2.94	1.95	4.39
1HGD.PDB	O, A_ASN_250	N, A_HIS_183	H, A_HIS_183	2.86	1.94	16.37
1HGD.PDB	O, A_ARG_229	N, A_HIS_184	H, A_HIS_184	2.80	1.84	6.46
1HGD.PDB	OG, A_SER_231	NE2, A_HIS_184	HE2, A_HIS_184	2.78	1.93	25.06
1HGD.PDB	OE1, A_GLU_190	N, A_SER_186	H, A_SER_186	2.93	1.98	11.85
1HGD.PDB	OG1, A_THR_187	N, A_GLU_190	H, A_GLU_190	2.88	1.93	10.33
1HGD.PDB	O, A_GLN_197	NE2, A_GLN_191	HE22, A_GLN_191	2.88	1.95	15.50
1HGD.PDB	O, A_ASN_188	OG1, A_THR_192	HG1, A_THR_192	2.99	2.04	7.10
1HGD.PDB	O, A_GLN_189	N, A_SER_193	H, A_SER_193	2.80	1.83	3.68
1HGD.PDB	O, A_GLU_190	N, A_LEU_194	H, A_LEU_194	2.97	2.01	9.56
1HGD.PDB	O, A_GLN_191	N, A_TYR_195	H, A_TYR_195	2.77	1.82	9.83
1HGD.PDB	O, A_TYR_161	NE2, A_GLN_197	HE21, A_GLN_197	2.91	1.96	11.57
1HGD.PDB	O, A_ASN_248	NE2, A_GLN_197	HE22, A_GLN_197	2.95	2.02	15.49
1HGD.PDB	OD1, A_ASN_246	NH2, A_ARG_201	HH21, A_ARG_201	2.59	1.75	26.83
1HGD.PDB	O, A_ILE_213	N, A_VAL_202	H, A_VAL_202	3.00	2.02	5.97
1HGD.PDB	O, A_ASN_246	N, A_THR_203	H, A_THR_203	2.83	1.91	16.65
1HGD.PDB	O, A_GLN_211	N, A_VAL_204	H, A_VAL_204	2.85	1.94	18.50
1HGD.PDB	O, A_SER_209	N, A_THR_206	H, A_THR_206	2.89	1.92	7.99
1HGD.PDB	OD1, A_ASP_241	N, A_ARG_207	H, A_ARG_207	2.92	1.95	8.05
1HGD.PDB	OG1, A_THR_206	OG, A_SER_209	HG, A_SER_209	2.90	1.96	11.12
1HGD.PDB	OD1, E_ASP_101	NE2, A_GLN_210	HE22, A_GLN_210	3.00	2.15	26.33
1HGD.PDB	O, A_VAL_204	N, A_GLN_211	H, A_GLN_211	2.82	1.90	17.10
1HGD.PDB	OG1, A_THR_203	OG1, A_THR_212	HG1, A_THR_212	2.90	1.94	6.68
1HGD.PDB	O, A_VAL_202	N, A_ILE_213	H, A_ILE_213	2.87	1.94	15.45
1HGD.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.78	1.86	19.99
1HGD.PDB	O, A_ASN_216	NH2, A_ARG_220	HH22, A_ARG_220	2.74	1.85	22.34

1HGD.PDB	O, A_LEU_226	N, A_VAL_223	H, A_VAL_223	2.88	1.93	9.40
1HGD.PDB	O, A_CYS_97	NE, A_ARG_224	HE, A_ARG_224	2.82	1.98	25.92
1HGD.PDB	O, A_CYS_97	NH2, A_ARG_224	HH21, A_ARG_224	2.84	1.96	24.52
1HGD.PDB	O, A_VAL_223	N, A_LEU_226	H, A_LEU_226	2.93	1.98	11.82
1HGD.PDB	OE2, A_GLU_190	OG, A_SER_228	HG, A_SER_228	2.98	2.00	5.61
1HGD.PDB	O, A_SER_228	NH1, A_ARG_229	HH11, A_ARG_229	2.71	1.76	17.21
1HGD.PDB	O, A_PRO_221	NH2, A_ARG_229	HH22, A_ARG_229	2.60	1.67	16.74
1HGD.PDB	OD1, A_ASP_101	OG, A_SER_231	HG, A_SER_231	2.84	1.88	8.92
1HGD.PDB	O, A_ASP_101	N, A_ILE_232	H, A_ILE_232	2.89	1.95	14.22
1HGD.PDB	O, A_TRP_180	N, A_TYR_233	H, A_TYR_233	2.92	1.95	10.20
1HGD.PDB	O, A_TYR_178	N, A_THR_235	H, A_THR_235	2.88	1.99	20.72
1HGD.PDB	O, A_LYS_176	N, A_VAL_237	H, A_VAL_237	2.78	1.85	14.71
1HGD.PDB	O, F_SER_71	NZ, A_LYS_238	HZ2, A_LYS_238	2.63	1.73	23.20
1HGD.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.93	1.92	13.44
1HGD.PDB	O, A_ASN_170	N, A_GLY_240	H, A_GLY_240	2.86	1.99	22.42
1HGD.PDB	O, A_LYS_238	N, A_ASP_241	H, A_ASP_241	2.97	2.03	13.82
1HGD.PDB	OD1, A_ASP_241	N, A_VAL_242	H, A_VAL_242	2.76	1.95	27.32
1HGD.PDB	O, A_MET_168	N, A_LEU_243	H, A_LEU_243	2.90	1.93	5.35
1HGD.PDB	O, A_SER_205	N, A_VAL_244	H, A_VAL_244	2.96	2.02	12.84
1HGD.PDB	O, A_VAL_166	N, A_ILE_245	H, A_ILE_245	2.91	1.97	12.42
1HGD.PDB	O, A_THR_203	N, A_ASN_246	H, A_ASN_246	2.92	1.96	6.49
1HGD.PDB	OD1, A_ASN_165	ND2, A_ASN_246	HD22, A_ASN_246	2.92	1.97	12.69
1HGD.PDB	O, A_LEU_164	N, A_SER_247	H, A_SER_247	2.92	2.01	18.72
1HGD.PDB	O, A_SER_199	ND2, A_ASN_248	HD21, A_ASN_248	3.00	2.19	29.63
1HGD.PDB	OE1, A_GLN_191	ND2, A_ASN_250	HD21, A_ASN_250	2.94	1.98	9.96
1HGD.PDB	O, A_HIS_183	ND2, A_ASN_250	HD22, A_ASN_250	2.85	1.91	14.80
1HGD.PDB	O, A_ASN_152	N, A_ALA_253	H, A_ALA_253	2.86	1.95	18.07
1HGD.PDB	OD1, A_ASN_133	NH2, A_ARG_255	HH22, A_ARG_255	2.53	1.69	26.82
1HGD.PDB	O, A_ILE_121	N, A_TYR_257	H, A_TYR_257	2.95	2.09	24.12
1HGD.PDB	O, A_LEU_177	N, A_PHE_258	H, A_PHE_258	2.93	1.97	8.57
1HGD.PDB	OE2, A_GLU_119	NH1, A_ARG_261	HH12, A_ARG_261	2.65	1.81	27.93
1HGD.PDB	OE1, A_GLU_119	NH2, A_ARG_261	HH22, A_ARG_261	2.88	1.97	22.77
1HGD.PDB	OD2, A_ASP_85	NZ, A_LYS_264	HZ3, A_LYS_264	2.85	1.86	16.67
1HGD.PDB	O, A_PHE_87	N, A_MET_268	H, A_MET_268	2.83	1.94	19.49
1HGD.PDB	O, A_PRO_284	OG, A_SER_270	HG, A_SER_270	2.85	1.89	8.52
1HGD.PDB	OG, A_SER_270	N, A_ALA_272	H, A_ALA_272	2.92	1.98	12.23
1HGD.PDB	O, A_ILE_51	N, A_ASP_275	H, A_ASP_275	2.87	1.97	19.56
1HGD.PDB	OD1, A_ASP_275	N, A_THR_276	H, A_THR_276	2.83	1.98	24.15
1HGD.PDB	O, A_ASN_54	N, A_SER_279	H, A_SER_279	2.79	1.86	14.12
1HGD.PDB	O, A_TYR_302	N, A_ILE_282	H, A_ILE_282	2.86	1.91	10.03
1HGD.PDB	O, A_THR_283	N, A_GLY_286	H, A_GLY_286	2.82	1.91	15.39
1HGD.PDB	O, A_LYS_50	N, A_SER_287	H, A_SER_287	2.87	1.90	3.72
1HGD.PDB	O, A_ALA_304	ND2, A_ASN_290	HD22, A_ASN_290	2.80	1.90	19.37
1HGD.PDB	OE1, A_GLN_44	NZ, A_LYS_292	HZ1, A_LYS_292	2.71	1.70	11.58
1HGD.PDB	OD2, A_ASP_291	NZ, A_LYS_292	HZ3, A_LYS_292	2.78	1.85	22.68
1HGD.PDB	O, A_LYS_307	N, A_GLN_295	H, A_GLN_295	2.79	1.92	22.70
1HGD.PDB	O, A_ASN_298	NE2, A_GLN_295	HE21, A_GLN_295	2.79	1.82	3.80
1HGD.PDB	O, A_GLN_44	N, A_ASN_296	H, A_ASN_296	2.83	1.90	14.13
1HGD.PDB	OE1, A_GLN_295	N, A_VAL_297	H, A_VAL_297	2.66	1.88	29.86
1HGD.PDB	OD1, A_ASN_285	ND2, A_ASN_298	HD22, A_ASN_298	2.98	2.04	13.52
1HGD.PDB	O, B_LYS_68	NZ, A_LYS_299	HZ2, A_LYS_299	2.96	1.95	12.60
1HGD.PDB	OD1, A_ASN_298	N, A_ILE_300	H, A_ILE_300	2.94	2.01	15.36
1HGD.PDB	O, A_ILE_282	N, A_TYR_302	H, A_TYR_302	2.90	2.05	25.49
1HGD.PDB	O, B_LYS_62	N, A_GLY_303	H, A_GLY_303	2.91	1.96	9.72
1HGD.PDB	O, A_GLN_295	N, A_VAL_309	H, A_VAL_309	2.97	2.17	29.89
1HGD.PDB	OG, B_SER_93	N, A_LYS_310	H, A_LYS_310	2.92	1.97	11.29
1HGD.PDB	OE2, A_GLU_41	N, A_LEU_314	H, A_LEU_314	2.80	1.88	15.00
1HGD.PDB	OE1, A_GLU_41	NZ, A_LYS_315	HZ3, A_LYS_315	2.76	1.81	20.40

1HGD.PDB	O, A_THR_40	N, A_LEU_316	H, A_LEU_316	2.77	1.84	12.70
1HGD.PDB	OD1, B_ASN_104	N, A_ALA_317	H, A_ALA_317	2.78	1.85	14.55
1HGD.PDB	O, A_ASN_38	N, A_THR_318	H, A_THR_318	2.93	2.00	15.92
1HGD.PDB	O, A_VAL_20	ND2, A_ASN_322	HD21, A_ASN_322	2.87	1.96	17.38
1HGD.PDB	OE2, A_GLU_35	ND2, A_ASN_322	HD22, A_ASN_322	2.84	1.97	23.40
1HGD.PDB	O, A_PRO_21	NE2, A_GLN_327	HE22, A_GLN_327	2.81	1.92	20.13
1HGD.PDB	OD2, B_ASP_112	N, B_GLY_1	H2, B_GLY_1	2.82	1.82	14.61
1HGD.PDB	OD1, B_ASP_109	N, B_LEU_2	H, B_LEU_2	2.82	1.95	22.22
1HGD.PDB	OD2, B_ASP_112	N, B_PHE_3	H, B_PHE_3	2.80	1.98	27.04
1HGD.PDB	OD2, B_ASP_112	N, B_GLY_4	H, B_GLY_4	2.93	2.05	20.30
1HGD.PDB	OD1, B_ASP_112	N, B_ALA_5	H, B_ALA_5	2.88	1.99	20.94
1HGD.PDB	O, B_GLY_4	N, B_PHE_9	H, B_PHE_9	2.78	1.84	12.99
1HGD.PDB	O, B_GLY_13	ND2, B_ASN_12	HD22, B_ASN_12	2.80	1.93	22.87
1HGD.PDB	O, A_VAL_323	N, B_GLY_13	H, B_GLY_13	2.71	1.77	11.58
1HGD.PDB	O, A_HIS_17	N, B_TRP_14	H, B_TRP_14	2.85	1.93	15.85
1HGD.PDB	OG1, B_THR_41	N, B_TRP_21	H, B_TRP_21	2.86	1.96	18.16
1HGD.PDB	O, A_GLY_16	N, B_GLY_23	H, B_GLY_23	2.92	1.99	15.76
1HGD.PDB	O, B_ALA_35	N, B_PHE_24	H, B_PHE_24	2.78	1.82	5.68
1HGD.PDB	O, A_CYS_14	N, B_ARG_25	H, B_ARG_25	2.96	2.02	13.01
1HGD.PDB	OE1, B_GLN_34	NE, B_ARG_25	HE, B_ARG_25	2.65	1.77	20.51
1HGD.PDB	O, B_GLY_33	N, B_HIS_26	H, B_HIS_26	2.63	1.81	26.83
1HGD.PDB	O, B_GLY_31	N, B_ASN_28	H, B_ASN_28	2.74	1.82	15.78
1HGD.PDB	O, B_HIS_26	N, B_GLY_33	H, B_GLY_33	2.76	1.88	21.28
1HGD.PDB	O, B_TYR_22	N, B_ASP_37	H, B_ASP_37	2.70	1.77	14.05
1HGD.PDB	OD2, B_ASP_37	N, B_SER_40	H, B_SER_40	2.90	1.95	12.27
1HGD.PDB	O, B_ASP_37	OG1, B_THR_41	HG1, B_THR_41	2.77	1.84	15.28
1HGD.PDB	O, B_LEU_38	N, B_GLN_42	H, B_GLN_42	2.99	2.05	13.49
1HGD.PDB	OD1, B_ASP_46	NE2, B_GLN_42	HE22, B_GLN_42	2.84	1.95	20.63
1HGD.PDB	O, B_LYS_39	N, B_ALA_43	H, B_ALA_43	2.96	2.04	16.02
1HGD.PDB	O, B_SER_40	N, B_ALA_44	H, B_ALA_44	2.96	1.99	5.57
1HGD.PDB	O, B_THR_41	N, B_ILE_45	H, B_ILE_45	2.90	1.93	6.90
1HGD.PDB	O, B_GLN_42	N, B_ASP_46	H, B_ASP_46	2.81	1.84	1.31
1HGD.PDB	O, B_ALA_43	NE2, B_GLN_47	HE22, B_GLN_47	2.89	1.99	19.00
1HGD.PDB	O, B_ILE_45	N, B_ASN_49	H, B_ASN_49	2.87	1.93	13.87
1HGD.PDB	O, B_ASP_46	N, B_GLY_50	H, B_GLY_50	2.87	1.98	20.63
1HGD.PDB	OG1, B_THR_107	NZ, B_LYS_51	HZ1, B_LYS_51	2.96	1.97	16.32
1HGD.PDB	OE1, B_GLU_103	NZ, B_LYS_51	HZ2, B_LYS_51	2.73	1.71	9.93
1HGD.PDB	ND1, B_HIS_106	NZ, B_LYS_51	HZ3, B_LYS_51	2.75	1.79	17.84
1HGD.PDB	O, B_ILE_48	N, B_LEU_52	H, B_LEU_52	2.92	2.00	15.14
1HGD.PDB	O, B_ASN_49	N, B_ASN_53	H, B_ASN_53	2.88	1.92	9.70
1HGD.PDB	OE1, B_GLU_57	NH1, B_ARG_54	HH11, B_ARG_54	2.86	1.87	11.55
1HGD.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.77	1.80	12.79
1HGD.PDB	OE2, B_GLU_61	NZ, B_LYS_58	HZ2, B_LYS_58	2.91	1.88	11.49
1HGD.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ1, B_LYS_62	2.61	1.78	29.53
1HGD.PDB	OD2, F_ASP_90	NZ, B_LYS_62	HZ3, B_LYS_62	2.73	1.84	25.56
1HGD.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.96	2.01	12.34
1HGD.PDB	O, A_LYS_299	NZ, B_LYS_68	HZ1, B_LYS_68	2.92	1.90	10.17
1HGD.PDB	OE2, B_GLU_85	NZ, B_LYS_68	HZ2, B_LYS_68	2.76	1.74	9.73
1HGD.PDB	OG, C_SER_107	N, B_ARG_76	H, B_ARG_76	2.80	1.86	12.47
1HGD.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.88	1.91	8.67
1HGD.PDB	OE2, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.84	1.82	2.51
1HGD.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.71	1.71	6.80
1HGD.PDB	OE1, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.75	1.75	3.21
1HGD.PDB	OE1, B_GLU_74	NE2, B_GLN_78	HE22, B_GLN_78	2.92	1.97	11.55
1HGD.PDB	O, B_GLY_75	N, B_ASP_79	H, B_ASP_79	2.93	1.97	10.45
1HGD.PDB	O, B_GLN_78	N, B_LYS_82	H, B_LYS_82	2.98	2.01	8.27
1HGD.PDB	O, B_ASP_79	N, B_TYR_83	H, B_TYR_83	2.92	1.98	12.82
1HGD.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.65	1.81	23.27

1HGD.PDB	O, B_LEU_80	N, B_VAL_84	H, B_VAL_84	2.91	1.93	4.90
1HGD.PDB	O, B_LYS_82	N, B_ASP_86	H, B_ASP_86	2.94	1.97	5.83
1HGD.PDB	O, B_TYR_83	N, B_THR_87	H, B_THR_87	2.89	1.93	10.17
1HGD.PDB	O, B_VAL_84	N, B_LYS_88	H, B_LYS_88	2.91	1.99	16.72
1HGD.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.76	1.72	5.59
1HGD.PDB	O, B_GLU_85	N, B_ILE_89	H, B_ILE_89	2.85	1.88	3.45
1HGD.PDB	O, B_LYS_88	N, B_TRP_92	H, B_TRP_92	2.96	1.98	5.21
1HGD.PDB	O, B_ILE_89	N, B_SER_93	H, B_SER_93	2.89	1.98	17.56
1HGD.PDB	O, B_ILE_89	OG, B_SER_93	HG, B_SER_93	2.80	1.87	12.12
1HGD.PDB	O, B_ASP_90	N, B_TYR_94	H, B_TYR_94	2.87	1.95	15.58
1HGD.PDB	O, B_TRP_92	N, B_ALA_96	H, B_ALA_96	2.88	1.94	15.13
1HGD.PDB	O, B_SER_93	N, B_GLU_97	H, B_GLU_97	2.98	2.02	8.64
1HGD.PDB	O, B_TYR_94	N, B_LEU_98	H, B_LEU_98	2.95	1.97	4.16
1HGD.PDB	O, B_ASN_95	N, B_LEU_99	H, B_LEU_99	2.94	2.03	17.77
1HGD.PDB	O, B_LEU_98	N, B_LEU_102	H, B_LEU_102	3.00	2.02	4.33
1HGD.PDB	O, B_LEU_99	N, B_GLU_103	H, B_GLU_103	2.95	1.99	9.69
1HGD.PDB	O, B_VAL_100	N, B_ASN_104	H, B_ASN_104	2.89	1.92	9.01
1HGD.PDB	O, A_LYS_27	ND2, B_ASN_104	HD22, B_ASN_104	2.94	1.98	9.01
1HGD.PDB	O, B_LEU_102	N, B_HIS_106	H, B_HIS_106	2.93	1.96	7.40
1HGD.PDB	O, B_GLU_103	N, B_THR_107	H, B_THR_107	2.77	1.89	20.47
1HGD.PDB	O, B_ASN_104	N, B_ILE_108	H, B_ILE_108	2.98	2.01	9.27
1HGD.PDB	O, B_HIS_106	N, B_LEU_110	H, B_LEU_110	2.82	1.87	10.47
1HGD.PDB	O, B_THR_107	OG1, B_THR_111	HG1, B_THR_111	2.97	2.00	4.65
1HGD.PDB	O, B_ASP_109	N, B_SER_113	H, B_SER_113	2.81	1.86	10.44
1HGD.PDB	O, F_LEU_2	OG, B_SER_113	HG, B_SER_113	2.69	1.91	29.59
1HGD.PDB	O, B_SER_113	N, B_LYS_117	H, B_LYS_117	2.72	1.85	22.52
1HGD.PDB	O, B_MET_115	N, B_PHE_119	H, B_PHE_119	3.00	2.05	11.89
1HGD.PDB	O, B_ASN_116	N, B_GLU_120	H, B_GLU_120	2.91	1.94	4.94
1HGD.PDB	O, B_LYS_117	N, B_LYS_121	H, B_LYS_121	2.92	2.03	20.84
1HGD.PDB	O, B_PHE_119	N, B_ARG_123	H, B_ARG_123	2.95	1.99	8.27
1HGD.PDB	OE2, B_GLU_120	NH1, B_ARG_123	HH11, B_ARG_123	2.79	1.91	24.17
1HGD.PDB	O, B_GLU_120	N, B_ARG_124	H, B_ARG_124	2.97	2.00	6.65
1HGD.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.83	2.02	28.17
1HGD.PDB	OE2, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.88	2.01	22.00
1HGD.PDB	O, B_HIS_159	ND2, B_ASN_129	HD21, B_ASN_129	2.97	2.01	9.55
1HGD.PDB	OH, B_TYR_157	ND2, B_ASN_129	HD22, B_ASN_129	2.78	1.83	11.22
1HGD.PDB	O, B_LYS_139	N, B_GLU_131	H, B_GLU_131	2.96	2.05	17.87
1HGD.PDB	O, B_CYS_137	N, B_MET_133	H, B_MET_133	2.86	1.91	11.95
1HGD.PDB	O, A_LEU_13	N, B_PHE_138	H, B_PHE_138	2.71	1.82	20.20
1HGD.PDB	O, B_GLU_131	N, B_LYS_139	H, B_LYS_139	2.85	1.91	12.79
1HGD.PDB	O, A_ALA_11	N, B_ILE_140	H, B_ILE_140	2.81	1.89	16.38
1HGD.PDB	O, B_ASN_129	N, B_TYR_141	H, B_TYR_141	2.94	2.01	16.23
1HGD.PDB	O, B_LYS_143	ND1, B_HIS_142	HD1, B_HIS_142	2.98	2.08	18.98
1HGD.PDB	OE2, B_GLU_165	N, B_LYS_143	H, B_LYS_143	2.93	1.99	13.81
1HGD.PDB	O, B_ASP_145	N, B_ILE_149	H, B_ILE_149	2.84	1.89	10.47
1HGD.PDB	O, B_ASN_146	N, B_GLU_150	H, B_GLU_150	2.92	1.97	11.35
1HGD.PDB	O, B_ALA_147	N, B_SER_151	H, B_SER_151	2.92	2.06	22.74
1HGD.PDB	O, B_CYS_148	OG, B_SER_151	HG, B_SER_151	2.66	1.81	21.47
1HGD.PDB	O, B_GLU_150	N, B_ASN_154	H, B_ASN_154	2.80	1.83	3.48
1HGD.PDB	OE2, B_GLU_150	ND2, B_ASN_154	HD21, B_ASN_154	2.98	2.09	22.34
1HGD.PDB	O, B_SER_151	N, B_THR_156	H, B_THR_156	2.74	1.92	27.01
1HGD.PDB	OD1, B_ASN_154	OG1, B_THR_156	HG1, B_THR_156	2.75	1.84	16.14
1HGD.PDB	OD1, B_ASP_158	N, B_ASP_160	H, B_ASP_160	2.88	2.02	24.02
1HGD.PDB	O, B_HIS_159	N, B_TYR_162	H, B_TYR_162	2.92	2.06	23.47
1HGD.PDB	O, F_ARG_170	NH1, B_ARG_163	HH12, B_ARG_163	2.75	1.79	14.15
1HGD.PDB	O, B_TYR_162	N, B_ALA_166	H, B_ALA_166	2.93	1.95	5.06
1HGD.PDB	O, B_ARG_163	N, B_LEU_167	H, B_LEU_167	2.77	1.81	7.70
1HGD.PDB	O, B_ASP_164	N, B_ASN_168	H, B_ASN_168	2.97	2.02	11.42

1HGD.PDB	O, B_GLU_165	ND2, B_ASN_169	HD22, B_ASN_169	2.96	2.00	8.67
1HGD.PDB	O, B_ALA_166	N, B_ARG_170	H, B_ARG_170	2.80	1.92	20.27
1HGD.PDB	O, B_GLU_128	NE, B_ARG_170	HE, B_ARG_170	2.73	1.86	22.68
1HGD.PDB	OE2, B_GLU_131	NH1, B_ARG_170	HH11, B_ARG_170	2.78	1.79	7.42
1HGD.PDB	O, B_LEU_167	N, B_PHE_171	H, B_PHE_171	2.95	2.04	17.43
1HGD.PDB	O, D_ILE_140	N, C_ALA_11	H, C_ALA_11	2.91	2.01	19.96
1HGD.PDB	O, D_GLN_27	N, C_THR_12	H, C_THR_12	2.92	1.96	10.52
1HGD.PDB	O, D_PHE_138	N, C_LEU_13	H, C_LEU_13	2.98	2.02	9.60
1HGD.PDB	O, D_ARG_25	N, C_CYS_14	H, C_CYS_14	2.74	1.84	19.68
1HGD.PDB	O, D_GLY_136	N, C_LEU_15	H, C_LEU_15	2.88	1.91	5.44
1HGD.PDB	O, D_GLY_23	N, C_GLY_16	H, C_GLY_16	2.97	2.07	19.04
1HGD.PDB	O, C_HIS_18	ND1, C_HIS_17	HD1, C_HIS_17	2.93	2.06	23.26
1HGD.PDB	O, D_TRP_21	N, C_HIS_18	H, C_HIS_18	2.85	1.99	23.00
1HGD.PDB	OD1, C_ASN_322	N, C_VAL_20	H, C_VAL_20	2.80	1.83	3.81
1HGD.PDB	O, C_VAL_36	N, C_THR_24	H, C_THR_24	2.84	1.91	15.31
1HGD.PDB	O, C_ILE_34	N, C_VAL_26	H, C_VAL_26	2.82	1.89	14.49
1HGD.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.80	1.77	7.54
1HGD.PDB	O, C_VAL_26	N, C_ILE_34	H, C_ILE_34	2.89	1.94	12.21
1HGD.PDB	O, C_THR_24	N, C_VAL_36	H, C_VAL_36	2.79	1.83	9.80
1HGD.PDB	O, C_MET_320	N, C_THR_37	H, C_THR_37	2.88	1.90	4.85
1HGD.PDB	O, C_LEU_316	N, C_THR_40	H, C_THR_40	2.84	1.97	22.14
1HGD.PDB	O, C_LEU_314	N, C_LEU_42	H, C_LEU_42	2.78	1.93	24.47
1HGD.PDB	O, C_PHE_294	N, C_GLN_44	H, C_GLN_44	2.79	1.83	6.90
1HGD.PDB	O, C_SER_46	NE2, C_GLN_44	HE22, C_GLN_44	2.85	1.96	21.38
1HGD.PDB	O, C_ASN_285	OG, C_SER_47	HG, C_SER_47	2.81	1.90	15.43
1HGD.PDB	OD2, C_ASP_275	NZ, C_LYS_50	HZ1, C_LYS_50	2.66	1.78	25.77
1HGD.PDB	O, C_PRO_273	N, C_ILE_51	H, C_ILE_51	2.78	1.83	8.71
1HGD.PDB	O, C_ASP_275	N, C_ASN_53	H, C_ASN_53	2.80	1.94	23.81
1HGD.PDB	OD2, C_ASP_85	N, C_ARG_57	H, C_ARG_57	2.85	1.91	10.75
1HGD.PDB	O, C_THR_83	NE, C_ARG_57	HE, C_ARG_57	2.80	1.83	7.46
1HGD.PDB	O, C_LEU_86	N, C_LEU_59	H, C_LEU_59	2.86	1.91	11.22
1HGD.PDB	O, C_VAL_88	N, C_GLY_61	H, C_GLY_61	2.98	2.11	22.39
1HGD.PDB	OD1, C_ASP_60	N, C_ILE_62	H, C_ILE_62	2.86	1.95	16.63
1HGD.PDB	O, C_GLY_61	N, C_CYS_64	H, C_CYS_64	2.87	1.95	15.76
1HGD.PDB	OE2, C_GLU_89	N, C_LEU_66	H, C_LEU_66	2.99	2.02	7.77
1HGD.PDB	O, C_LEU_66	N, C_LEU_70	H, C_LEU_70	2.88	2.00	21.00
1HGD.PDB	O, C_ILE_67	N, C_LEU_71	H, C_LEU_71	2.81	1.86	10.52
1HGD.PDB	O, C_ASP_68	N, C_GLY_72	H, C_GLY_72	2.84	1.91	15.63
1HGD.PDB	OD1, C_ASP_73	N, C_HIS_75	H, C_HIS_75	2.89	2.01	22.22
1HGD.PDB	OD1, C_ASP_73	ND1, C_HIS_75	HD1, C_HIS_75	2.77	1.87	19.67
1HGD.PDB	O, C_ASP_63	NE2, C_HIS_75	HE2, C_HIS_75	2.86	1.94	17.12
1HGD.PDB	O, C_ASP_73	N, C_CYS_76	H, C_CYS_76	2.80	1.86	11.97
1HGD.PDB	O, C_PRO_74	N, C_ASP_77	H, C_ASP_77	2.94	1.99	12.51
1HGD.PDB	O, C_ARG_57	N, C_ASP_85	H, C_ASP_85	2.79	1.90	19.56
1HGD.PDB	O, C_LEU_59	N, C_VAL_88	H, C_VAL_88	2.93	1.95	4.90
1HGD.PDB	O, C_MET_268	N, C_GLU_89	H, C_GLU_89	2.78	1.84	12.72
1HGD.PDB	OD1, C_ASP_60	NE, C_ARG_90	HE, C_ARG_90	2.86	1.89	9.66
1HGD.PDB	O, C_SER_270	NH1, C_ARG_90	HH11, C_ARG_90	2.68	1.81	24.44
1HGD.PDB	O, C_ALA_272	NH1, C_ARG_90	HH12, C_ARG_90	2.62	1.70	17.91
1HGD.PDB	OD2, C_ASP_60	NH2, C_ARG_90	HH21, C_ARG_90	2.78	1.79	10.49
1HGD.PDB	OD1, C_ASP_271	N, C_SER_91	H, C_SER_91	2.89	1.92	5.66
1HGD.PDB	OD1, C_ASP_271	OG, C_SER_91	HG, C_SER_91	2.93	2.11	26.93
1HGD.PDB	OD2, C_ASP_271	OG, C_SER_91	HG, C_SER_91	2.86	1.96	18.80
1HGD.PDB	OD2, C_ASP_68	OG, C_SER_95	HG, C_SER_95	2.88	1.96	15.18
1HGD.PDB	OD2, C_ASP_73	N, C_ASN_96	H, C_ASN_96	2.93	1.97	11.12
1HGD.PDB	OD1, C_ASP_68	OH, C_TYR_100	HH, C_TYR_100	2.89	1.96	14.39
1HGD.PDB	OD2, C_ASP_104	OG, C_SER_107	HG, C_SER_107	2.91	2.00	17.92
1HGD.PDB	O, C_TYR_105	N, C_ARG_109	H, C_ARG_109	2.82	1.85	5.75

1HGD.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.87	1.88	13.44
1HGD.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.73	1.84	19.59
1HGD.PDB	O, C_SER_107	N, C_LEU_111	H, C_LEU_111	2.87	1.93	12.86
1HGD.PDB	O, C_ARG_109	N, C_ALA_113	H, C_ALA_113	2.95	2.03	17.38
1HGD.PDB	OE2, C_GLU_119	OG1, C_THR_117	HG1, C_THR_117	2.86	1.93	10.42
1HGD.PDB	O, C_GLU_82	N, C_LEU_118	H, C_LEU_118	2.89	1.96	15.85
1HGD.PDB	O, C_TYR_257	N, C_ILE_121	H, C_ILE_121	2.88	1.91	7.92
1HGD.PDB	O, C_ARG_255	N, C_GLU_123	H, C_GLU_123	2.91	1.95	11.07
1HGD.PDB	O, C_THR_155	N, C_THR_131	H, C_THR_131	2.77	1.87	18.56
1HGD.PDB	OD1, C_ASN_152	N, C_ASN_133	H, C_ASN_133	2.82	1.89	13.60
1HGD.PDB	O, C_GLY_146	N, C_SER_136	H, C_SER_136	2.73	1.81	14.22
1HGD.PDB	O, C_GLY_144	NZ, C_LYS_140	HZ1, C_LYS_140	2.66	1.71	18.26
1HGD.PDB	OD1, C_ASN_137	NZ, C_LYS_140	HZ2, C_LYS_140	2.78	1.84	20.52
1HGD.PDB	OD2, C_ASP_77	NE, C_ARG_141	HE, C_ARG_141	2.80	1.97	27.06
1HGD.PDB	O, C_PHE_147	NH1, C_ARG_141	HH12, C_ARG_141	2.57	1.62	14.51
1HGD.PDB	OD1, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.87	1.96	21.76
1HGD.PDB	OD2, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.75	1.86	23.93
1HGD.PDB	O, C_GLY_72	NH2, C_ARG_141	HH22, C_ARG_141	2.96	1.99	11.64
1HGD.PDB	OD1, C_ASN_137	OG, C_SER_145	HG, C_SER_145	2.98	2.13	22.87
1HGD.PDB	O, C_SER_136	N, C_GLY_146	H, C_GLY_146	2.97	2.04	13.75
1HGD.PDB	O, C_GLY_72	N, C_SER_149	H, C_SER_149	2.83	1.92	17.38
1HGD.PDB	O, C_ALA_253	N, C_ASN_152	H, C_ASN_152	2.78	1.92	22.70
1HGD.PDB	OH, C_TYR_195	NE1, C_TRP_153	HE1, C_TRP_153	2.80	1.95	24.25
1HGD.PDB	O, C_LEU_194	N, C_LYS_156	H, C_LYS_156	2.95	2.05	20.33
1HGD.PDB	O, C_SER_247	N, C_LEU_164	H, C_LEU_164	2.68	1.84	25.44
1HGD.PDB	O, C_ILE_245	N, C_VAL_166	H, C_VAL_166	2.92	1.97	10.65
1HGD.PDB	O, C_LEU_243	OG1, C_THR_167	HG1, C_THR_167	2.91	2.00	16.96
1HGD.PDB	O, C_LEU_243	N, C_MET_168	H, C_MET_168	2.93	2.00	16.08
1HGD.PDB	O, C_ASP_241	N, C_ASN_170	H, C_ASN_170	2.92	1.95	7.54
1HGD.PDB	O, C_PHE_174	ND2, C_ASN_170	HD21, C_ASN_170	2.81	1.86	10.36
1HGD.PDB	O, C_VAL_237	ND2, C_ASN_170	HD22, C_ASN_170	2.83	2.02	27.86
1HGD.PDB	O, C_VAL_237	N, C_LYS_176	H, C_LYS_176	2.96	2.03	15.89
1HGD.PDB	OE2, C_GLU_123	NZ, C_LYS_176	HZ2, C_LYS_176	2.69	1.80	25.35
1HGD.PDB	O, C_THR_235	N, C_TYR_178	H, C_TYR_178	2.78	1.82	3.58
1HGD.PDB	OE1, C_GLU_123	OH, C_TYR_178	HH, C_TYR_178	2.73	1.80	13.21
1HGD.PDB	OG1, C_THR_235	NE1, C_TRP_180	HE1, C_TRP_180	2.91	1.93	2.97
1HGD.PDB	O, C_ASN_250	N, C_HIS_183	H, C_HIS_183	2.86	1.94	17.04
1HGD.PDB	O, C_ARG_229	N, C_HIS_184	H, C_HIS_184	2.84	1.87	6.25
1HGD.PDB	OG, C_SER_231	NE2, C_HIS_184	HE2, C_HIS_184	2.75	1.91	25.20
1HGD.PDB	OE1, C_GLU_190	N, C_SER_186	H, C_SER_186	2.94	1.99	11.52
1HGD.PDB	OG1, C_THR_187	N, C_GLU_190	H, C_GLU_190	2.91	1.96	11.66
1HGD.PDB	OD1, C_ASN_250	NE2, C_GLN_191	HE21, C_GLN_191	2.98	2.02	9.43
1HGD.PDB	O, C_GLN_197	NE2, C_GLN_191	HE22, C_GLN_191	2.89	1.96	15.69
1HGD.PDB	O, C_GLN_189	OG1, C_THR_192	HG1, C_THR_192	2.81	1.97	23.75
1HGD.PDB	O, C_GLN_189	N, C_SER_193	H, C_SER_193	2.79	1.85	12.90
1HGD.PDB	O, C_GLN_191	N, C_TYR_195	H, C_TYR_195	2.80	1.85	11.05
1HGD.PDB	O, C_TYR_161	NE2, C_GLN_197	HE21, C_GLN_197	2.91	1.96	11.66
1HGD.PDB	O, C_ASN_248	NE2, C_GLN_197	HE22, C_GLN_197	2.97	2.05	15.65
1HGD.PDB	OD1, C_ASN_246	NH2, C_ARG_201	HH21, C_ARG_201	2.60	1.77	27.30
1HGD.PDB	O, C_ILE_213	N, C_VAL_202	H, C_VAL_202	3.00	2.04	9.35
1HGD.PDB	O, C_ASN_246	N, C_THR_203	H, C_THR_203	2.89	1.94	12.58
1HGD.PDB	OG1, C_THR_212	OG1, C_THR_203	HG1, C_THR_203	2.89	1.96	13.30
1HGD.PDB	O, C_GLN_211	N, C_VAL_204	H, C_VAL_204	2.87	1.96	17.77
1HGD.PDB	O, C_SER_209	N, C_THR_206	H, C_THR_206	2.90	1.94	8.48
1HGD.PDB	OD1, C_ASP_241	N, C_ARG_207	H, C_ARG_207	2.91	1.95	9.04
1HGD.PDB	OD2, C_ASP_241	NE, C_ARG_208	HE, C_ARG_208	2.97	2.08	21.42
1HGD.PDB	OG1, C_THR_206	OG, C_SER_209	HG, C_SER_209	2.92	1.98	10.99
1HGD.PDB	OD1, A_ASP_101	NE2, C_GLN_210	HE22, C_GLN_210	2.97	2.13	27.21

1HGD.PDB	O, C_VAL_204	N, C_GLN_211	H, C_GLN_211	2.82	1.89	16.07
1HGD.PDB	O, C_VAL_202	N, C_ILE_213	H, C_ILE_213	2.87	1.94	15.07
1HGD.PDB	O, C_ASN_216	NH1, C_ARG_220	HH12, C_ARG_220	2.88	2.06	29.71
1HGD.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.69	1.80	23.00
1HGD.PDB	O, C_ASN_216	NH2, C_ARG_220	HH22, C_ARG_220	2.74	1.85	22.78
1HGD.PDB	O, C_LEU_226	N, C_VAL_223	H, C_VAL_223	2.86	1.90	8.93
1HGD.PDB	O, C_CYS_97	NE, C_ARG_224	HE, C_ARG_224	2.81	1.97	26.63
1HGD.PDB	O, C_CYS_97	NH2, C_ARG_224	HH21, C_ARG_224	2.83	1.96	24.41
1HGD.PDB	O, C_VAL_223	N, C_LEU_226	H, C_LEU_226	2.96	2.01	12.56
1HGD.PDB	OE2, C_GLU_190	OG, C_SER_228	HG, C_SER_228	3.00	2.02	4.69
1HGD.PDB	O, C_SER_228	NH1, C_ARG_229	HH11, C_ARG_229	2.69	1.75	17.13
1HGD.PDB	O, C_PRO_221	NH2, C_ARG_229	HH22, C_ARG_229	2.59	1.67	18.22
1HGD.PDB	OD1, C_ASP_101	OG, C_SER_231	HG, C_SER_231	2.87	1.90	8.39
1HGD.PDB	O, C_ASP_101	N, C_ILE_232	H, C_ILE_232	2.91	1.97	13.69
1HGD.PDB	O, C_TRP_180	N, C_TYR_233	H, C_TYR_233	2.92	1.96	10.09
1HGD.PDB	O, C_TYR_178	N, C_THR_235	H, C_THR_235	2.86	1.97	20.86
1HGD.PDB	O, C_LYS_176	N, C_VAL_237	H, C_VAL_237	2.76	1.84	16.40
1HGD.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.80	1.83	17.68
1HGD.PDB	O, B_SER_71	NZ, C_LYS_238	HZ3, C_LYS_238	2.57	1.67	23.33
1HGD.PDB	O, C_ASN_170	N, C_GLY_240	H, C_GLY_240	2.86	1.98	22.33
1HGD.PDB	O, C_LYS_238	N, C_ASP_241	H, C_ASP_241	2.97	2.04	14.16
1HGD.PDB	OD1, C_ASP_241	N, C_VAL_242	H, C_VAL_242	2.79	1.97	27.05
1HGD.PDB	O, C_MET_168	N, C_LEU_243	H, C_LEU_243	2.90	1.93	5.78
1HGD.PDB	O, C_SER_205	N, C_VAL_244	H, C_VAL_244	2.99	2.03	11.79
1HGD.PDB	O, C_VAL_166	N, C_ILE_245	H, C_ILE_245	2.96	2.02	13.67
1HGD.PDB	O, C_THR_203	N, C_ASN_246	H, C_ASN_246	2.93	1.96	5.65
1HGD.PDB	OD1, C_ASN_165	ND2, C_ASN_246	HD22, C_ASN_246	2.91	1.96	13.56
1HGD.PDB	O, C_LEU_164	N, C_SER_247	H, C_SER_247	2.95	2.05	18.82
1HGD.PDB	OE1, C_GLN_191	ND2, C_ASN_250	HD21, C_ASN_250	2.90	1.95	10.99
1HGD.PDB	O, C_HIS_183	ND2, C_ASN_250	HD22, C_ASN_250	2.89	1.96	14.74
1HGD.PDB	O, C_ASN_152	N, C_ALA_253	H, C_ALA_253	2.86	1.97	19.68
1HGD.PDB	OD1, C_ASN_133	NH2, C_ARG_255	HH22, C_ARG_255	2.52	1.69	27.35
1HGD.PDB	O, C_ILE_121	N, C_TYR_257	H, C_TYR_257	2.92	2.07	24.63
1HGD.PDB	O, C_LEU_177	N, C_PHE_258	H, C_PHE_258	2.93	1.97	8.49
1HGD.PDB	OE2, C_GLU_119	NH1, C_ARG_261	HH12, C_ARG_261	2.66	1.83	27.96
1HGD.PDB	OE1, C_GLU_119	NH2, C_ARG_261	HH22, C_ARG_261	2.90	2.00	23.32
1HGD.PDB	OD2, C_ASP_85	NZ, C_LYS_264	HZ3, C_LYS_264	2.82	1.84	16.88
1HGD.PDB	O, C_PHE_87	N, C_MET_268	H, C_MET_268	2.82	1.92	19.58
1HGD.PDB	O, C_PRO_284	OG, C_SER_270	HG, C_SER_270	2.86	1.93	14.34
1HGD.PDB	OG, C_SER_270	N, C_ALA_272	H, C_ALA_272	2.88	1.93	11.04
1HGD.PDB	O, C_ILE_51	N, C_ASP_275	H, C_ASP_275	2.89	2.02	21.61
1HGD.PDB	OD1, C_ASP_275	N, C_THR_276	H, C_THR_276	2.82	1.97	24.34
1HGD.PDB	O, C_ASN_54	N, C_SER_279	H, C_SER_279	2.80	1.87	14.30
1HGD.PDB	O, C_TYR_302	N, C_ILE_282	H, C_ILE_282	2.89	1.91	5.26
1HGD.PDB	O, C_THR_283	N, C_GLY_286	H, C_GLY_286	2.83	1.91	15.19
1HGD.PDB	O, C_LYS_50	N, C_SER_287	H, C_SER_287	2.85	1.88	6.04
1HGD.PDB	O, C_ALA_304	ND2, C_ASN_290	HD22, C_ASN_290	2.83	1.94	20.74
1HGD.PDB	OE1, C_GLN_44	NZ, C_LYS_292	HZ1, C_LYS_292	2.73	1.73	12.00
1HGD.PDB	OD2, C_ASP_291	NZ, C_LYS_292	HZ3, C_LYS_292	2.79	1.88	23.81
1HGD.PDB	O, C_LYS_307	N, C_GLN_295	H, C_GLN_295	2.80	1.93	22.24
1HGD.PDB	O, C_ASN_298	NE2, C_GLN_295	HE21, C_GLN_295	2.78	1.81	6.87
1HGD.PDB	O, C_GLN_44	N, C_ASN_296	H, C_ASN_296	2.84	1.92	15.89
1HGD.PDB	OE1, C_GLN_295	N, C_VAL_297	H, C_VAL_297	2.67	1.87	28.66
1HGD.PDB	OD1, C_ASN_285	ND2, C_ASN_298	HD22, C_ASN_298	2.96	2.02	13.09
1HGD.PDB	O, D_LYS_68	NZ, C_LYS_299	HZ2, C_LYS_299	2.97	1.97	13.11
1HGD.PDB	OD1, C_ASN_298	N, C_ILE_300	H, C_ILE_300	2.91	2.01	18.95
1HGD.PDB	O, C_ILE_282	N, C_TYR_302	H, C_TYR_302	2.86	2.02	25.59
1HGD.PDB	O, D_LYS_62	N, C_GLY_303	H, C_GLY_303	2.92	1.97	11.11

1HGD.PDB	O, C_GLN_295	N, C_VAL_309	H, C_VAL_309	2.96	2.15	29.17
1HGD.PDB	OG, D_SER_93	N, C_LYS_310	H, C_LYS_310	2.96	2.01	12.70
1HGD.PDB	OE2, C_GLU_41	N, C_LEU_314	H, C_LEU_314	2.81	1.88	14.84
1HGD.PDB	OE1, C_GLU_41	NZ, C_LYS_315	HZ3, C_LYS_315	2.78	1.84	20.99
1HGD.PDB	O, C_THR_40	N, C_LEU_316	H, C_LEU_316	2.76	1.82	12.19
1HGD.PDB	OD1, D_ASN_104	N, C_ALA_317	H, C_ALA_317	2.76	1.81	11.23
1HGD.PDB	O, C_ASN_38	N, C_THR_318	H, C_THR_318	2.95	2.04	17.98
1HGD.PDB	O, C_VAL_20	ND2, C_ASN_322	HD21, C_ASN_322	2.90	1.99	17.62
1HGD.PDB	OE2, C_GLU_35	ND2, C_ASN_322	HD22, C_ASN_322	2.83	1.94	21.17
1HGD.PDB	OE1, D_GLU_15	NZ, C_LYS_326	HZ1, C_LYS_326	2.78	1.77	11.96
1HGD.PDB	OXT, C_THR_328	NE2, C_GLN_327	HE22, C_GLN_327	2.97	2.03	15.01
1HGD.PDB	OD2, D_ASP_112	N, D_GLY_1	H2, D_GLY_1	2.80	1.80	13.51
1HGD.PDB	OD1, D_ASP_109	N, D_LEU_2	H, D_LEU_2	2.86	1.98	21.55
1HGD.PDB	OD2, D_ASP_112	N, D_PHE_3	H, D_PHE_3	2.84	2.05	29.38
1HGD.PDB	OD2, D_ASP_112	N, D_GLY_4	H, D_GLY_4	2.94	2.04	18.50
1HGD.PDB	OD1, D_ASP_112	N, D_ALA_5	H, D_ALA_5	2.90	2.02	22.02
1HGD.PDB	O, D_GLY_4	N, D_PHE_9	H, D_PHE_9	2.79	1.85	14.03
1HGD.PDB	O, D_GLY_13	ND2, D_ASN_12	HD22, D_ASN_12	2.84	1.96	21.33
1HGD.PDB	O, C_VAL_323	N, D_GLY_13	H, D_GLY_13	2.70	1.78	14.49
1HGD.PDB	O, C_HIS_17	N, D_TRP_14	H, D_TRP_14	2.85	1.91	13.36
1HGD.PDB	OG1, D_THR_41	N, D_TRP_21	H, D_TRP_21	2.90	2.00	19.11
1HGD.PDB	O, C_GLY_16	N, D_GLY_23	H, D_GLY_23	2.93	2.01	16.45
1HGD.PDB	O, D_ALA_35	N, D_PHE_24	H, D_PHE_24	2.81	1.84	5.01
1HGD.PDB	O, C_CYS_14	N, D_ARG_25	H, D_ARG_25	2.91	1.95	9.92
1HGD.PDB	OE1, D_GLN_34	NE, D_ARG_25	HE, D_ARG_25	2.61	1.77	24.43
1HGD.PDB	O, D_GLY_33	N, D_HIS_26	H, D_HIS_26	2.84	1.92	15.70
1HGD.PDB	O, C_THR_12	N, D_GLN_27	H, D_GLN_27	2.91	1.98	16.00
1HGD.PDB	O, D_GLY_31	N, D_ASN_28	H, D_ASN_28	2.90	1.95	12.05
1HGD.PDB	OD1, D_ASN_146	ND2, D_ASN_28	HD21, D_ASN_28	3.00	2.03	9.16
1HGD.PDB	O, D_PHE_24	N, D_ALA_35	H, D_ALA_35	2.79	1.99	28.44
1HGD.PDB	O, D_TYR_22	N, D_ASP_37	H, D_ASP_37	2.70	1.79	16.23
1HGD.PDB	OD2, D_ASP_37	N, D_SER_40	H, D_SER_40	2.91	1.96	11.03
1HGD.PDB	OD2, D_ASP_37	OG, D_SER_40	HG, D_SER_40	2.86	1.96	18.80
1HGD.PDB	O, D_ASP_37	OG1, D_THR_41	HG1, D_THR_41	2.74	1.83	16.22
1HGD.PDB	O, D_LEU_38	N, D_GLN_42	H, D_GLN_42	2.97	2.03	13.89
1HGD.PDB	OD1, D_ASP_46	NE2, D_GLN_42	HE22, D_GLN_42	2.84	1.95	20.82
1HGD.PDB	O, D_LYS_39	N, D_ALA_43	H, D_ALA_43	2.97	2.02	11.21
1HGD.PDB	O, D_SER_40	N, D_ALA_44	H, D_ALA_44	2.97	2.00	5.30
1HGD.PDB	O, D_THR_41	N, D_ILE_45	H, D_ILE_45	2.92	1.97	10.66
1HGD.PDB	O, D_GLN_42	N, D_ASP_46	H, D_ASP_46	2.81	1.84	5.79
1HGD.PDB	O, D_ALA_43	NE2, D_GLN_47	HE22, D_GLN_47	2.86	1.96	18.91
1HGD.PDB	O, D_ILE_45	N, D_ASN_49	H, D_ASN_49	2.87	1.93	14.90
1HGD.PDB	O, D_ASP_46	N, D_GLY_50	H, D_GLY_50	2.89	1.97	17.25
1HGD.PDB	OG1, D_THR_107	NZ, D_LYS_51	HZ1, D_LYS_51	2.96	1.98	16.97
1HGD.PDB	OE1, D_GLU_103	NZ, D_LYS_51	HZ2, D_LYS_51	2.74	1.72	8.47
1HGD.PDB	ND1, D_HIS_106	NZ, D_LYS_51	HZ3, D_LYS_51	2.74	1.78	16.91
1HGD.PDB	O, D_ILE_48	N, D_LEU_52	H, D_LEU_52	2.95	2.04	18.99
1HGD.PDB	O, D_ASN_49	N, D_ASN_53	H, D_ASN_53	2.85	1.90	9.27
1HGD.PDB	O, A_THR_28	NE, D_ARG_54	HE, D_ARG_54	3.00	2.06	13.94
1HGD.PDB	OE1, D_GLU_57	NH1, D_ARG_54	HH11, D_ARG_54	2.85	1.86	12.06
1HGD.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.79	1.82	13.03
1HGD.PDB	OE2, D_GLU_61	NZ, D_LYS_58	HZ2, D_LYS_58	2.90	1.87	10.86
1HGD.PDB	OD2, B_ASP_90	NZ, D_LYS_62	HZ3, D_LYS_62	2.62	1.79	29.99
1HGD.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.96	1.98	5.65
1HGD.PDB	O, C_LYS_299	NZ, D_LYS_68	HZ1, D_LYS_68	2.93	1.92	12.36
1HGD.PDB	OE2, D_GLU_85	NZ, D_LYS_68	HZ2, D_LYS_68	2.78	1.76	10.92
1HGD.PDB	OG, E_SER_107	N, D_ARG_76	H, D_ARG_76	2.86	1.90	9.40
1HGD.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.83	1.87	10.56

1HGD.PDB	OE2, F_GLU.74	NH1, D_ARG.76	HH12, D_ARG.76	2.78	1.77	3.14
1HGD.PDB	OE1, F_GLU.81	NH2, D_ARG.76	HH21, D_ARG.76	2.65	1.67	9.42
1HGD.PDB	OE1, F_GLU.74	NH2, D_ARG.76	HH22, D_ARG.76	2.69	1.70	6.24
1HGD.PDB	OE1, D_GLU.74	NE2, D_GLN.78	HE22, D_GLN.78	2.94	1.97	10.43
1HGD.PDB	O, D_GLY.75	N, D_ASP.79	H, D_ASP.79	2.94	1.98	9.81
1HGD.PDB	O, D_GLN.78	N, D_LYS.82	H, D_LYS.82	2.95	1.98	5.44
1HGD.PDB	O, D_ASP.79	N, D_TYR.83	H, D_TYR.83	2.91	1.98	15.53
1HGD.PDB	OE1, F_GLU.85	OH, D_TYR.83	HH, D_TYR.83	2.57	1.79	29.87
1HGD.PDB	O, D_LEU.80	N, D_VAL.84	H, D_VAL.84	2.86	1.89	6.82
1HGD.PDB	O, D_LYS.82	N, D_ASP.86	H, D_ASP.86	2.94	1.97	2.92
1HGD.PDB	O, D_TYR.83	N, D_THR.87	H, D_THR.87	2.90	1.95	11.15
1HGD.PDB	O, D_VAL.84	N, D_LYS.88	H, D_LYS.88	2.90	2.00	19.38
1HGD.PDB	OH, B_TYR.83	NZ, D_LYS.88	HZ1, D_LYS.88	2.76	1.72	5.75
1HGD.PDB	O, D_GLU.85	N, D_ILE.89	H, D_ILE.89	2.85	1.88	3.25
1HGD.PDB	O, D_LYS.88	N, D_TRP.92	H, D_TRP.92	2.93	1.96	4.18
1HGD.PDB	O, D_ILE.89	N, D_SER.93	H, D_SER.93	2.87	1.96	17.31
1HGD.PDB	O, D_ILE.89	OG, D_SER.93	HG, D_SER.93	2.77	1.86	16.92
1HGD.PDB	O, D_ASP.90	N, D_TYR.94	H, D_TYR.94	2.87	1.97	18.94
1HGD.PDB	O, D_TRP.92	N, D_ALA.96	H, D_ALA.96	2.89	1.94	12.43
1HGD.PDB	O, D_TYR.94	N, D_LEU.98	H, D_LEU.98	2.91	1.95	7.12
1HGD.PDB	O, D_ASN.95	N, D_LEU.99	H, D_LEU.99	2.95	2.03	17.99
1HGD.PDB	O, D_LEU.98	N, D_LEU.102	H, D_LEU.102	2.99	2.01	6.26
1HGD.PDB	O, D_LEU.99	N, D_GLU.103	H, D_GLU.103	2.96	2.00	10.90
1HGD.PDB	O, D_VAL.100	N, D_ASN.104	H, D_ASN.104	2.84	1.88	8.49
1HGD.PDB	O, C_LYS.27	ND2, D_ASN.104	HD22, D_ASN.104	2.96	2.00	10.74
1HGD.PDB	O, D_LEU.102	N, D_HIS.106	H, D_HIS.106	2.92	1.96	8.43
1HGD.PDB	O, D_GLU.103	N, D_THR.107	H, D_THR.107	2.81	1.91	18.55
1HGD.PDB	O, D_ASN.104	N, D_ILE.108	H, D_ILE.108	2.99	2.03	8.56
1HGD.PDB	O, D_HIS.106	N, D_LEU.110	H, D_LEU.110	2.82	1.88	11.88
1HGD.PDB	O, D_ASP.109	N, D_SER.113	H, D_SER.113	2.84	1.89	12.44
1HGD.PDB	O, D_SER.113	N, D_LYS.117	H, D_LYS.117	2.74	1.87	21.85
1HGD.PDB	O, D_MET.115	N, D_PHE.119	H, D_PHE.119	2.99	2.05	13.34
1HGD.PDB	O, D_ASN.116	N, D_GLU.120	H, D_GLU.120	2.89	1.91	1.87
1HGD.PDB	O, D_LYS.117	N, D_LYS.121	H, D_LYS.121	2.92	2.02	19.68
1HGD.PDB	O, D_PHE.119	N, D_ARG.123	H, D_ARG.123	2.95	1.99	11.55
1HGD.PDB	OE2, D_GLU.120	NH1, D_ARG.123	HH11, D_ARG.123	2.80	1.92	24.08
1HGD.PDB	O, D_GLU.120	N, D_ARG.124	H, D_ARG.124	2.98	2.01	7.42
1HGD.PDB	OE1, B_GLU.132	NE, D_ARG.124	HE, D_ARG.124	2.80	2.01	29.31
1HGD.PDB	OE2, B_GLU.132	NE, D_ARG.124	HE, D_ARG.124	2.82	1.95	21.73
1HGD.PDB	O, D_HIS.159	ND2, D_ASN.129	HD21, D_ASN.129	2.95	1.98	9.02
1HGD.PDB	OH, D_TYR.157	ND2, D_ASN.129	HD22, D_ASN.129	2.79	1.82	6.93
1HGD.PDB	O, D_CYS.137	N, D_MET.133	H, D_MET.133	2.89	1.94	11.36
1HGD.PDB	O, C_LEU.13	N, D_PHE.138	H, D_PHE.138	2.74	1.85	19.25
1HGD.PDB	O, D_GLU.131	N, D_LYS.139	H, D_LYS.139	2.83	1.88	9.21
1HGD.PDB	O, C_ALA.11	N, D_ILE.140	H, D_ILE.140	2.85	1.94	17.95
1HGD.PDB	O, D_ASN.129	N, D_TYR.141	H, D_TYR.141	2.95	2.00	12.47
1HGD.PDB	O, D_LYS.143	ND1, D_HIS.142	HD1, D_HIS.142	2.95	2.07	22.42
1HGD.PDB	OE2, D_GLU.165	N, D_LYS.143	H, D_LYS.143	2.98	2.08	20.43
1HGD.PDB	OE2, D_GLU.30	N, D_ASN.146	H, D_ASN.146	2.83	1.93	17.92
1HGD.PDB	O, D_ASP.145	N, D_ILE.149	H, D_ILE.149	2.88	1.92	11.10
1HGD.PDB	O, D_ASN.146	N, D_GLU.150	H, D_GLU.150	2.93	2.00	14.93
1HGD.PDB	O, D_ALA.147	N, D_SER.151	H, D_SER.151	2.95	2.03	16.03
1HGD.PDB	O, D_CYS.148	OG, D_SER.151	HG, D_SER.151	2.69	1.83	21.65
1HGD.PDB	O, D_GLU.150	N, D_ASN.154	H, D_ASN.154	2.80	1.83	6.06
1HGD.PDB	OE2, D_GLU.150	ND2, D_ASN.154	HD21, D_ASN.154	2.88	2.05	27.54
1HGD.PDB	OD1, D_ASN.154	OG1, D_THR.156	HG1, D_THR.156	2.79	1.83	8.53
1HGD.PDB	NE2, D_HIS.142	OH, D_TYR.157	HH, D_TYR.157	2.78	1.89	18.65
1HGD.PDB	OD1, D_ASP.158	N, D_ASP.160	H, D_ASP.160	2.88	2.02	23.43

1HGD.PDB	O, D_HIS_159	N, D_TYR_162	H, D_TYR_162	2.96	2.10	23.77
1HGD.PDB	O, B_ARG_170	NH1, D_ARG_163	HH12, D_ARG_163	2.77	1.79	12.64
1HGD.PDB	O, D_TYR_162	N, D_ALA_166	H, D_ALA_166	2.92	1.95	4.89
1HGD.PDB	O, D_ARG_163	N, D_LEU_167	H, D_LEU_167	2.76	1.80	8.07
1HGD.PDB	O, D_ASP_164	N, D_ASN_168	H, D_ASN_168	2.96	2.00	8.71
1HGD.PDB	O, D_GLU_165	ND2, D_ASN_169	HD22, D_ASN_169	2.94	1.98	8.39
1HGD.PDB	O, D_ALA_166	N, D_ARG_170	H, D_ARG_170	2.81	1.93	20.44
1HGD.PDB	O, D_GLU_128	NE, D_ARG_170	HE, D_ARG_170	2.73	1.86	22.22
1HGD.PDB	OE2, D_GLU_131	NH1, D_ARG_170	HH11, D_ARG_170	2.77	1.78	7.65
1HGD.PDB	O, D_LEU_167	N, D_PHE_171	H, D_PHE_171	2.96	2.02	14.05
1HGD.PDB	O, F_ILE_140	N, E_ALA_11	H, E_ALA_11	2.92	2.03	20.36
1HGD.PDB	O, F_GLN_27	N, E_THR_12	H, E_THR_12	2.97	2.03	14.03
1HGD.PDB	O, F_PHE_138	N, E_LEU_13	H, E_LEU_13	2.98	2.02	11.10
1HGD.PDB	O, F_ARG_25	N, E_CYS_14	H, E_CYS_14	2.65	1.79	21.42
1HGD.PDB	O, F_GLY_136	N, E_LEU_15	H, E_LEU_15	2.85	1.88	5.88
1HGD.PDB	O, F_GLY_23	N, E_GLY_16	H, E_GLY_16	2.93	2.04	20.98
1HGD.PDB	O, E_HIS_18	ND1, E_HIS_17	HD1, E_HIS_17	2.90	2.05	24.96
1HGD.PDB	O, F_TRP_21	N, E_HIS_18	H, E_HIS_18	2.83	1.98	25.03
1HGD.PDB	OD1, E_ASN_322	N, E_VAL_20	H, E_VAL_20	2.79	1.83	7.78
1HGD.PDB	O, E_VAL_36	N, E_THR_24	H, E_THR_24	2.83	1.94	19.94
1HGD.PDB	O, E_ILE_34	N, E_VAL_26	H, E_VAL_26	2.83	1.90	15.73
1HGD.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.79	1.77	8.77
1HGD.PDB	O, E_VAL_26	N, E_ILE_34	H, E_ILE_34	2.86	1.91	10.68
1HGD.PDB	O, E_THR_24	N, E_VAL_36	H, E_VAL_36	2.80	1.85	11.38
1HGD.PDB	O, E_MET_320	N, E_THR_37	H, E_THR_37	2.88	1.91	4.25
1HGD.PDB	O, E_LEU_316	N, E_THR_40	H, E_THR_40	2.82	1.95	22.86
1HGD.PDB	O, E_LEU_314	N, E_LEU_42	H, E_LEU_42	2.82	1.94	21.92
1HGD.PDB	O, E_PHE_294	N, E_GLN_44	H, E_GLN_44	2.85	1.88	5.47
1HGD.PDB	O, E_SER_46	NE2, E_GLN_44	HE22, E_GLN_44	2.85	1.97	21.62
1HGD.PDB	O, E_ASN_285	OG, E_SER_47	HG, E_SER_47	2.85	1.99	21.23
1HGD.PDB	OD2, E_ASP_275	NZ, E_LYS_50	HZ1, E_LYS_50	2.69	1.80	25.14
1HGD.PDB	O, E_PRO_273	N, E_ILE_51	H, E_ILE_51	2.79	1.84	10.59
1HGD.PDB	O, E_ASP_275	N, E_ASN_53	H, E_ASN_53	2.81	1.95	23.64
1HGD.PDB	OD2, E_ASP_85	N, E_ARG_57	H, E_ARG_57	2.85	1.91	12.33
1HGD.PDB	O, E_THR_83	NE, E_ARG_57	HE, E_ARG_57	2.81	1.84	7.04
1HGD.PDB	O, E_LEU_86	N, E_LEU_59	H, E_LEU_59	2.86	1.91	10.61
1HGD.PDB	O, E_VAL_88	N, E_GLY_61	H, E_GLY_61	2.96	2.07	21.18
1HGD.PDB	OD1, E_ASP_60	N, E_ILE_62	H, E_ILE_62	2.88	1.95	15.04
1HGD.PDB	O, E_GLY_61	N, E_CYS_64	H, E_CYS_64	2.89	1.98	17.49
1HGD.PDB	OE2, E_GLU_89	N, E_LEU_66	H, E_LEU_66	2.97	1.99	5.61
1HGD.PDB	O, E_LEU_66	N, E_LEU_70	H, E_LEU_70	2.90	2.02	20.74
1HGD.PDB	O, E_ILE_67	N, E_LEU_71	H, E_LEU_71	2.80	1.84	6.52
1HGD.PDB	O, E_ASP_68	N, E_GLY_72	H, E_GLY_72	2.91	1.98	15.31
1HGD.PDB	OD1, E_ASP_73	N, E_HIS_75	H, E_HIS_75	2.96	2.07	21.14
1HGD.PDB	OD1, E_ASP_73	ND1, E_HIS_75	HD1, E_HIS_75	2.79	1.88	18.25
1HGD.PDB	O, E_ASP_63	NE2, E_HIS_75	HE2, E_HIS_75	2.89	1.97	16.27
1HGD.PDB	O, E_ASP_73	N, E_CYS_76	H, E_CYS_76	2.81	1.87	13.32
1HGD.PDB	O, E_PRO_74	N, E_ASP_77	H, E_ASP_77	2.91	1.96	10.31
1HGD.PDB	O, E_ARG_57	N, E_ASP_85	H, E_ASP_85	2.78	1.89	18.76
1HGD.PDB	O, E_LEU_59	N, E_VAL_88	H, E_VAL_88	2.91	1.94	5.45
1HGD.PDB	O, E_MET_268	N, E_GLU_89	H, E_GLU_89	2.76	1.82	11.82
1HGD.PDB	OD1, E_ASP_60	NE, E_ARG_90	HE, E_ARG_90	2.88	1.91	7.90
1HGD.PDB	O, E_SER_270	NH1, E_ARG_90	HH11, E_ARG_90	2.66	1.80	24.67
1HGD.PDB	O, E_ALA_272	NH1, E_ARG_90	HH12, E_ARG_90	2.60	1.68	18.53
1HGD.PDB	OD2, E_ASP_60	NH2, E_ARG_90	HH21, E_ARG_90	2.82	1.83	10.15
1HGD.PDB	OD1, E_ASP_271	N, E_SER_91	H, E_SER_91	2.88	1.92	9.41
1HGD.PDB	OD1, E_ASP_271	OG, E_SER_91	HG, E_SER_91	2.94	2.13	28.39
1HGD.PDB	OD2, E_ASP_271	OG, E_SER_91	HG, E_SER_91	2.84	1.93	17.47

1HGD.PDB	OD2, E_ASP.68	OG, E_SER.95	HG, E_SER.95	2.91	1.98	14.66
1HGD.PDB	OD2, E_ASP.73	N, E_ASN.96	H, E_ASN.96	2.95	1.99	11.30
1HGD.PDB	OD1, E_ASP.68	OH, E_TYR.100	HH, E_TYR.100	2.86	1.93	14.06
1HGD.PDB	OD2, E_ASP.104	OG, E_SER.107	HG, E_SER.107	2.90	1.98	16.44
1HGD.PDB	O, E_TYR.105	N, E_ARG.109	H, E_ARG.109	2.86	1.88	0.77
1HGD.PDB	OE2, F_GLU.67	NH2, E_ARG.109	HH21, E_ARG.109	2.82	1.85	14.73
1HGD.PDB	OD2, D_ASP.79	OG, E_SER.110	HG, E_SER.110	2.81	1.89	15.50
1HGD.PDB	O, E_SER.107	N, E_LEU.111	H, E_LEU.111	2.92	1.96	10.24
1HGD.PDB	O, E_LEU.108	N, E_VAL.112	H, E_VAL.112	2.98	2.02	7.44
1HGD.PDB	O, E_ARG.109	N, E_ALA.113	H, E_ALA.113	2.92	2.02	18.83
1HGD.PDB	O, E_SER.110	N, E_SER.114	H, E_SER.114	2.98	2.03	12.50
1HGD.PDB	OE2, E_GLU.119	OG1, E_THR.117	HG1, E_THR.117	2.90	1.95	9.79
1HGD.PDB	O, E_GLU.82	N, E_LEU.118	H, E_LEU.118	2.92	1.99	15.84
1HGD.PDB	O, E_TYR.257	N, E_ILE.121	H, E_ILE.121	2.87	1.90	6.59
1HGD.PDB	O, E_ARG.255	N, E_GLU.123	H, E_GLU.123	2.92	1.97	11.75
1HGD.PDB	O, E_THR.155	N, E_THR.131	H, E_THR.131	2.76	1.86	18.28
1HGD.PDB	OD1, E_ASN.152	N, E_ASN.133	H, E_ASN.133	2.85	1.91	14.28
1HGD.PDB	O, E_GLY.146	N, E_SER.136	H, E_SER.136	2.73	1.79	12.16
1HGD.PDB	O, E_GLY.144	NZ, E_LYS.140	HZ1, E_LYS.140	2.69	1.72	15.78
1HGD.PDB	OD1, E_ASN.137	NZ, E_LYS.140	HZ2, E_LYS.140	2.79	1.84	19.51
1HGD.PDB	OD2, E_ASP.77	NE, E_ARG.141	HE, E_ARG.141	2.82	1.98	26.95
1HGD.PDB	O, E_PHE.147	NH1, E_ARG.141	HH12, E_ARG.141	2.57	1.63	15.28
1HGD.PDB	OD1, E_ASP.77	NH2, E_ARG.141	HH21, E_ARG.141	2.88	1.95	21.13
1HGD.PDB	OD2, E_ASP.77	NH2, E_ARG.141	HH21, E_ARG.141	2.75	1.86	24.62
1HGD.PDB	O, E_GLY.72	NH2, E_ARG.141	HH22, E_ARG.141	2.94	1.97	11.68
1HGD.PDB	O, E_SER.136	N, E_GLY.146	H, E_GLY.146	2.97	2.03	13.31
1HGD.PDB	O, E_GLY.72	N, E_SER.149	H, E_SER.149	2.84	1.94	18.94
1HGD.PDB	O, E_ALA.253	N, E_ASN.152	H, E_ASN.152	2.83	1.97	23.36
1HGD.PDB	OH, E_TYR.195	NE1, E_TRP.153	HE1, E_TRP.153	2.82	1.91	19.17
1HGD.PDB	O, E_LEU.194	N, E_LYS.156	H, E_LYS.156	2.96	2.06	18.57
1HGD.PDB	O, E_SER.193	NZ, E_LYS.156	HZ2, E_LYS.156	2.80	1.84	19.27
1HGD.PDB	O, E_SER.247	N, E_LEU.164	H, E_LEU.164	2.67	1.83	24.46
1HGD.PDB	O, E_ILE.245	N, E_VAL.166	H, E_VAL.166	2.95	1.99	10.02
1HGD.PDB	O, E_LEU.243	OG1, E_THR.167	HG1, E_THR.167	2.95	2.08	21.06
1HGD.PDB	O, E_LEU.243	N, E_MET.168	H, E_MET.168	2.92	1.99	16.02
1HGD.PDB	O, E_ASP.241	N, E_ASN.170	H, E_ASN.170	2.93	1.96	7.59
1HGD.PDB	O, E_PHE.174	ND2, E_ASN.170	HD21, E_ASN.170	2.84	1.88	9.66
1HGD.PDB	O, E_VAL.237	ND2, E_ASN.170	HD22, E_ASN.170	2.82	2.02	28.84
1HGD.PDB	O, E_VAL.237	N, E_LYS.176	H, E_LYS.176	2.95	2.02	16.27
1HGD.PDB	OE2, E_GLU.123	NZ, E_LYS.176	HZ2, E_LYS.176	2.69	1.80	25.12
1HGD.PDB	O, E_THR.235	N, E_TYR.178	H, E_TYR.178	2.82	1.85	5.66
1HGD.PDB	OE1, E_GLU.123	OH, E_TYR.178	HH, E_TYR.178	2.75	1.83	13.46
1HGD.PDB	OG1, E_THR.235	NE1, E_TRP.180	HE1, E_TRP.180	2.93	1.94	3.75
1HGD.PDB	O, E_ASN.250	N, E_HIS.183	H, E_HIS.183	2.87	1.97	19.16
1HGD.PDB	O, E_ARG.229	N, E_HIS.184	H, E_HIS.184	2.83	1.87	8.20
1HGD.PDB	OG, E_SER.231	NE2, E_HIS.184	HE2, E_HIS.184	2.80	1.95	25.42
1HGD.PDB	OE1, E_GLU.190	N, E_SER.186	H, E_SER.186	2.91	1.96	11.07
1HGD.PDB	OG1, E_THR.187	N, E_GLU.190	H, E_GLU.190	2.91	1.97	13.39
1HGD.PDB	O, E_GLN.197	NE2, E_GLN.191	HE22, E_GLN.191	2.89	1.97	15.90
1HGD.PDB	O, E_ASN.188	OG1, E_THR.192	HG1, E_THR.192	2.98	2.03	7.22
1HGD.PDB	O, E_GLN.189	N, E_SER.193	H, E_SER.193	2.81	1.84	3.50
1HGD.PDB	O, E_GLU.190	N, E_LEU.194	H, E_LEU.194	2.98	2.02	10.79
1HGD.PDB	O, E_GLN.191	N, E_TYR.195	H, E_TYR.195	2.77	1.82	10.72
1HGD.PDB	O, E_TYR.161	NE2, E_GLN.197	HE21, E_GLN.197	2.91	1.96	10.54
1HGD.PDB	O, E_ASN.248	NE2, E_GLN.197	HE22, E_GLN.197	2.95	2.02	14.25
1HGD.PDB	OD1, E_ASN.246	NH2, E_ARG.201	HH21, E_ARG.201	2.60	1.77	27.54
1HGD.PDB	O, E_ASN.246	N, E_THR.203	H, E_THR.203	2.88	1.92	8.43
1HGD.PDB	OG1, E_THR.212	OG1, E_THR.203	HG1, E_THR.203	2.93	1.99	12.22

1HGD.PDB	O, E_GLN_211	N, E_VAL_204	H, E_VAL_204	2.87	1.96	17.47
1HGD.PDB	O, E_SER_209	N, E_THR_206	H, E_THR_206	2.95	1.99	8.08
1HGD.PDB	OD1, E_ASP_241	N, E_ARG_207	H, E_ARG_207	2.90	1.93	8.79
1HGD.PDB	OG1, E_THR_206	OG, E_SER_209	HG, E_SER_209	2.91	1.97	11.26
1HGD.PDB	OD1, C_ASP_101	NE2, E_GLN_210	HE22, E_GLN_210	2.98	2.14	27.07
1HGD.PDB	O, E_VAL_204	N, E_GLN_211	H, E_GLN_211	2.82	1.90	15.66
1HGD.PDB	O, E_VAL_202	N, E_ILE_213	H, E_ILE_213	2.89	1.96	14.67
1HGD.PDB	O, E_ASN_216	NH1, E_ARG_220	HH12, E_ARG_220	2.89	2.08	29.65
1HGD.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.77	1.90	25.11
1HGD.PDB	O, E_ASN_216	NH2, E_ARG_220	HH22, E_ARG_220	2.74	1.86	23.30
1HGD.PDB	O, E_LEU_226	N, E_VAL_223	H, E_VAL_223	2.87	1.91	7.72
1HGD.PDB	O, E_CYS_97	NE, E_ARG_224	HE, E_ARG_224	2.84	2.00	26.20
1HGD.PDB	O, E_CYS_97	NH2, E_ARG_224	HH21, E_ARG_224	2.84	1.97	24.48
1HGD.PDB	O, E_VAL_223	N, E_LEU_226	H, E_LEU_226	2.93	1.99	12.03
1HGD.PDB	OE2, E_GLU_190	OG, E_SER_228	HG, E_SER_228	2.96	1.98	4.78
1HGD.PDB	O, E_SER_228	NH1, E_ARG_229	HH11, E_ARG_229	2.70	1.76	17.46
1HGD.PDB	O, E_PRO_221	NH2, E_ARG_229	HH22, E_ARG_229	2.58	1.65	17.47
1HGD.PDB	OD1, E_ASP_101	OG, E_SER_231	HG, E_SER_231	2.85	1.91	13.25
1HGD.PDB	O, E_ASP_101	N, E_ILE_232	H, E_ILE_232	2.91	1.98	14.92
1HGD.PDB	O, E_TRP_180	N, E_TYR_233	H, E_TYR_233	2.93	1.97	9.20
1HGD.PDB	O, E_TYR_178	N, E_THR_235	H, E_THR_235	2.86	1.97	20.35
1HGD.PDB	O, E_LYS_176	N, E_VAL_237	H, E_VAL_237	2.77	1.86	16.39
1HGD.PDB	O, D_SER_71	NZ, E_LYS_238	HZ2, E_LYS_238	2.73	1.80	21.39
1HGD.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ3, E_LYS_238	2.87	1.86	13.40
1HGD.PDB	O, E_ASN_170	N, E_GLY_240	H, E_GLY_240	2.89	2.02	22.44
1HGD.PDB	O, E_LYS_238	N, E_ASP_241	H, E_ASP_241	2.96	2.03	13.52
1HGD.PDB	OD1, E_ASP_241	N, E_VAL_242	H, E_VAL_242	2.79	1.95	26.27
1HGD.PDB	O, E_MET_168	N, E_LEU_243	H, E_LEU_243	2.89	1.92	5.48
1HGD.PDB	O, E_VAL_166	N, E_ILE_245	H, E_ILE_245	2.95	2.01	13.26
1HGD.PDB	O, E_THR_203	N, E_ASN_246	H, E_ASN_246	2.94	1.96	4.93
1HGD.PDB	OD1, E_ASN_165	ND2, E_ASN_246	HD22, E_ASN_246	2.91	1.96	12.66
1HGD.PDB	O, E_LEU_164	N, E_SER_247	H, E_SER_247	2.95	2.04	18.22
1HGD.PDB	OE1, E_GLN_191	ND2, E_ASN_250	HD21, E_ASN_250	2.95	1.99	9.92
1HGD.PDB	O, E_HIS_183	ND2, E_ASN_250	HD22, E_ASN_250	2.86	1.93	15.05
1HGD.PDB	O, E_ASN_152	N, E_ALA_253	H, E_ALA_253	2.88	1.99	19.87
1HGD.PDB	OD1, E_ASN_133	NH2, E_ARG_255	HH22, E_ARG_255	2.52	1.69	27.28
1HGD.PDB	O, E_ILE_121	N, E_TYR_257	H, E_TYR_257	2.94	2.11	26.29
1HGD.PDB	O, E_LEU_177	N, E_PHE_258	H, E_PHE_258	2.92	1.95	7.16
1HGD.PDB	OE2, E_GLU_119	NH1, E_ARG_261	HH12, E_ARG_261	2.64	1.81	27.92
1HGD.PDB	OE1, E_GLU_119	NH2, E_ARG_261	HH22, E_ARG_261	2.88	1.97	22.94
1HGD.PDB	OD2, E_ASP_85	NZ, E_LYS_264	HZ3, E_LYS_264	2.87	1.88	16.50
1HGD.PDB	O, E_PHE_87	N, E_MET_268	H, E_MET_268	2.81	1.92	20.02
1HGD.PDB	O, E_PRO_284	OG, E_SER_270	HG, E_SER_270	2.87	1.93	12.39
1HGD.PDB	OG, E_SER_270	N, E_ALA_272	H, E_ALA_272	2.92	1.98	12.12
1HGD.PDB	O, E_ILE_51	N, E_ASP_275	H, E_ASP_275	2.91	2.01	19.96
1HGD.PDB	OD1, E_ASP_275	N, E_THR_276	H, E_THR_276	2.81	1.96	24.15
1HGD.PDB	O, E_ASN_54	N, E_SER_279	H, E_SER_279	2.80	1.87	14.43
1HGD.PDB	O, E_TYR_302	N, E_ILE_282	H, E_ILE_282	2.87	1.90	8.73
1HGD.PDB	O, E_THR_283	N, E_GLY_286	H, E_GLY_286	2.82	1.89	12.51
1HGD.PDB	O, E_LYS_50	N, E_SER_287	H, E_SER_287	2.87	1.90	5.78
1HGD.PDB	O, E_ALA_304	ND2, E_ASN_290	HD22, E_ASN_290	2.83	1.94	19.46
1HGD.PDB	OE1, E_GLN_44	NZ, E_LYS_292	HZ1, E_LYS_292	2.70	1.70	12.87
1HGD.PDB	OD2, E_ASP_291	NZ, E_LYS_292	HZ3, E_LYS_292	2.83	1.91	23.60
1HGD.PDB	O, E_LYS_307	N, E_GLN_295	H, E_GLN_295	2.78	1.92	23.12
1HGD.PDB	O, E_ASN_298	NE2, E_GLN_295	HE21, E_GLN_295	2.76	1.79	7.00
1HGD.PDB	O, E_GLN_44	N, E_ASN_296	H, E_ASN_296	2.84	1.90	13.14
1HGD.PDB	OE1, E_GLN_295	N, E_VAL_297	H, E_VAL_297	2.67	1.86	28.12
1HGD.PDB	OD1, E_ASN_285	ND2, E_ASN_298	HD22, E_ASN_298	2.95	2.01	14.15

1HGD.PDB	O, F_LYS_68	NZ, E_LYS_299	HZ1, E_LYS_299	2.98	1.98	14.54
1HGD.PDB	OD1, E_ASN_298	N, E_ILE_300	H, E_ILE_300	2.90	1.99	17.71
1HGD.PDB	O, E_ILE_282	N, E_TYR_302	H, E_TYR_302	2.88	2.05	26.69
1HGD.PDB	O, E_LYS_264	OH, E_TYR_302	HH, E_TYR_302	2.65	1.86	28.82
1HGD.PDB	O, F_LYS_62	N, E_GLY_303	H, E_GLY_303	2.94	1.98	8.87
1HGD.PDB	O, E_GLN_295	N, E_VAL_309	H, E_VAL_309	2.96	2.15	28.43
1HGD.PDB	OG, F_SER_93	N, E_LYS_310	H, E_LYS_310	2.95	2.00	12.05
1HGD.PDB	OE2, E_GLU_41	N, E_LEU_314	H, E_LEU_314	2.81	1.89	15.95
1HGD.PDB	OE1, E_GLU_41	NZ, E_LYS_315	HZ3, E_LYS_315	2.76	1.83	22.10
1HGD.PDB	O, E_THR_40	N, E_LEU_316	H, E_LEU_316	2.76	1.83	14.34
1HGD.PDB	OD1, F_ASN_104	N, E_ALA_317	H, E_ALA_317	2.79	1.84	10.01
1HGD.PDB	O, E_ASN_38	N, E_THR_318	H, E_THR_318	2.97	2.03	14.24
1HGD.PDB	O, E_VAL_20	ND2, E_ASN_322	HD21, E_ASN_322	2.90	2.00	18.79
1HGD.PDB	OE2, E_GLU_35	ND2, E_ASN_322	HD22, E_ASN_322	2.82	1.95	23.13
1HGD.PDB	OE2, F_GLU_15	N, E_GLU_325	H, E_GLU_325	2.91	2.10	28.29
1HGD.PDB	O, E_GLN_327	NZ, E_LYS_326	HZ1, E_LYS_326	2.81	1.89	22.57
1HGD.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.97	1.97	16.19
1HGD.PDB	O, E_LYS_326	NE2, E_GLN_327	HE22, E_GLN_327	2.85	1.95	19.55
1HGD.PDB	OD2, F_ASP_112	N, F_GLY_1	H2, F_GLY_1	2.81	1.81	13.59
1HGD.PDB	OD1, F_ASP_109	N, F_LEU_2	H, F_LEU_2	2.86	1.96	19.63
1HGD.PDB	OD2, F_ASP_112	N, F_PHE_3	H, F_PHE_3	2.81	2.02	29.56
1HGD.PDB	OD2, F_ASP_112	N, F_GLY_4	H, F_GLY_4	2.92	2.06	23.22
1HGD.PDB	OD1, F_ASP_112	N, F_ALA_5	H, F_ALA_5	2.89	2.02	22.37
1HGD.PDB	O, F_GLY_4	N, F_PHE_9	H, F_PHE_9	2.78	1.84	12.30
1HGD.PDB	O, F_GLY_13	ND2, F_ASN_12	HD22, F_ASN_12	2.80	1.95	24.70
1HGD.PDB	O, E_VAL_323	N, F_GLY_13	H, F_GLY_13	2.71	1.79	15.38
1HGD.PDB	O, E_HIS_17	N, F_TRP_14	H, F_TRP_14	2.87	1.92	12.04
1HGD.PDB	OG1, F_THR_41	N, F_TRP_21	H, F_TRP_21	2.87	1.95	16.02
1HGD.PDB	O, E_GLY_16	N, F_GLY_23	H, F_GLY_23	2.91	2.00	17.89
1HGD.PDB	O, F_ALA_35	N, F_PHE_24	H, F_PHE_24	2.81	1.84	4.26
1HGD.PDB	O, E_CYS_14	N, F_ARG_25	H, F_ARG_25	2.88	1.94	13.26
1HGD.PDB	OE1, F_GLN_34	NE, F_ARG_25	HE, F_ARG_25	2.93	2.07	24.69
1HGD.PDB	OE1, F_GLN_34	NH2, F_ARG_25	HH21, F_ARG_25	2.80	1.89	20.31
1HGD.PDB	O, F_GLY_33	N, F_HIS_26	H, F_HIS_26	2.91	2.03	21.54
1HGD.PDB	O, E_THR_12	N, F_GLN_27	H, F_GLN_27	2.97	2.04	16.25
1HGD.PDB	O, F_GLY_31	N, F_ASN_28	H, F_ASN_28	2.78	1.85	13.40
1HGD.PDB	OD1, F_ASN_146	ND2, F_ASN_28	HD21, F_ASN_28	2.81	1.89	15.27
1HGD.PDB	O, F_CYS_144	ND2, F_ASN_28	HD22, F_ASN_28	2.83	1.93	18.14
1HGD.PDB	O, F_HIS_26	N, F_GLY_33	H, F_GLY_33	2.97	2.11	23.75
1HGD.PDB	O, F_PHE_24	N, F_ALA_35	H, F_ALA_35	2.78	1.98	28.59
1HGD.PDB	O, F_TYR_22	N, F_ASP_37	H, F_ASP_37	2.69	1.77	12.88
1HGD.PDB	OD2, F_ASP_37	N, F_SER_40	H, F_SER_40	2.92	1.96	9.75
1HGD.PDB	OD2, F_ASP_37	OG, F_SER_40	HG, F_SER_40	2.84	1.98	23.42
1HGD.PDB	O, F_ASP_37	OG1, F_THR_41	HG1, F_THR_41	2.75	1.88	21.07
1HGD.PDB	O, F_LEU_38	N, F_GLN_42	H, F_GLN_42	2.93	2.03	18.28
1HGD.PDB	OD1, F_ASP_46	NE2, F_GLN_42	HE22, F_GLN_42	2.83	1.94	21.51
1HGD.PDB	O, F_LYS_39	N, F_ALA_43	H, F_ALA_43	2.93	1.98	11.56
1HGD.PDB	O, F_SER_40	N, F_ALA_44	H, F_ALA_44	2.97	1.99	2.55
1HGD.PDB	O, F_THR_41	N, F_ILE_45	H, F_ILE_45	2.91	1.96	10.99
1HGD.PDB	O, F_GLN_42	N, F_ASP_46	H, F_ASP_46	2.80	1.82	0.60
1HGD.PDB	O, F_ALA_43	NE2, F_GLN_47	HE22, F_GLN_47	2.90	2.01	20.21
1HGD.PDB	O, F_ILE_45	N, F_ASN_49	H, F_ASN_49	2.84	1.94	18.12
1HGD.PDB	O, F_ASP_46	N, F_GLY_50	H, F_GLY_50	2.84	1.95	20.14
1HGD.PDB	OE1, F_GLU_103	NZ, F_LYS_51	HZ2, F_LYS_51	2.72	1.70	8.28
1HGD.PDB	ND1, F_HIS_106	NZ, F_LYS_51	HZ3, F_LYS_51	2.73	1.76	16.89
1HGD.PDB	O, F_ILE_48	N, F_LEU_52	H, F_LEU_52	2.94	2.02	16.22
1HGD.PDB	O, F_ASN_49	N, F_ASN_53	H, F_ASN_53	2.85	1.92	14.75
1HGD.PDB	OE1, F_GLU_57	NH1, F_ARG_54	HH11, F_ARG_54	2.86	1.85	10.37

1HGD.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.72	1.75	12.85
1HGD.PDB	OE2, F_GLU_61	NZ, F_LYS_58	HZ2, F_LYS_58	2.92	1.89	10.22
1HGD.PDB	OD2, D_ASP_90	NZ, F_LYS_62	HZ3, F_LYS_62	2.71	1.86	28.09
1HGD.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.95	1.98	9.92
1HGD.PDB	O, E_LYS_299	NZ, F_LYS_68	HZ1, F_LYS_68	2.97	1.94	5.85
1HGD.PDB	OE2, F_GLU_85	NZ, F_LYS_68	HZ2, F_LYS_68	2.72	1.77	19.94
1HGD.PDB	OG, A_SER_107	N, F_ARG_76	H, F_ARG_76	2.82	1.86	9.34
1HGD.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.86	1.90	10.66
1HGD.PDB	OE2, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.77	1.75	1.42
1HGD.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.64	1.65	5.37
1HGD.PDB	OE1, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.71	1.72	7.42
1HGD.PDB	OE1, F_GLU_74	NE2, F_GLN_78	HE22, F_GLN_78	2.96	1.99	9.91
1HGD.PDB	O, F_GLY_75	N, F_ASP_79	H, F_ASP_79	2.93	1.98	10.55
1HGD.PDB	O, F_GLN_78	N, F_LYS_82	H, F_LYS_82	2.98	2.01	9.35
1HGD.PDB	O, F_ASP_79	N, F_TYR_83	H, F_TYR_83	2.93	1.99	14.99
1HGD.PDB	OE1, B_GLU_85	OH, F_TYR_83	HH, F_TYR_83	2.53	1.75	27.84
1HGD.PDB	O, F_LEU_80	N, F_VAL_84	H, F_VAL_84	2.89	1.92	3.19
1HGD.PDB	O, F_LYS_82	N, F_ASP_86	H, F_ASP_86	2.94	1.97	9.39
1HGD.PDB	O, F_TYR_83	N, F_THR_87	H, F_THR_87	2.90	1.96	11.94
1HGD.PDB	O, F_VAL_84	N, F_LYS_88	H, F_LYS_88	2.92	1.96	11.08
1HGD.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.67	1.66	8.83
1HGD.PDB	O, F_GLU_85	N, F_ILE_89	H, F_ILE_89	2.88	1.90	4.38
1HGD.PDB	O, F_LYS_88	N, F_TRP_92	H, F_TRP_92	2.95	1.98	4.36
1HGD.PDB	O, F_ILE_89	N, F_SER_93	H, F_SER_93	2.85	1.95	19.01
1HGD.PDB	O, F_ILE_89	OG, F_SER_93	HG, F_SER_93	2.82	1.88	12.37
1HGD.PDB	O, F_ASP_90	N, F_TYR_94	H, F_TYR_94	2.87	1.95	17.83
1HGD.PDB	O, F_TRP_92	N, F_ALA_96	H, F_ALA_96	2.93	1.99	13.63
1HGD.PDB	O, F_SER_93	N, F_GLU_97	H, F_GLU_97	2.98	2.03	11.78
1HGD.PDB	O, F_TYR_94	N, F_LEU_98	H, F_LEU_98	2.95	1.97	4.49
1HGD.PDB	O, F_ASN_95	N, F_LEU_99	H, F_LEU_99	2.94	2.01	15.31
1HGD.PDB	O, F_LEU_99	N, F_GLU_103	H, F_GLU_103	2.96	2.00	11.56
1HGD.PDB	O, F_VAL_100	N, F_ASN_104	H, F_ASN_104	2.88	1.92	8.65
1HGD.PDB	O, E_LYS_27	ND2, F_ASN_104	HD22, F_ASN_104	2.95	1.99	8.95
1HGD.PDB	O, F_LEU_102	N, F_HIS_106	H, F_HIS_106	2.94	1.97	6.97
1HGD.PDB	O, F_GLU_103	N, F_THR_107	H, F_THR_107	2.81	1.90	17.76
1HGD.PDB	O, F_ASN_104	N, F_ILE_108	H, F_ILE_108	2.98	2.03	11.71
1HGD.PDB	O, F_HIS_106	N, F_LEU_110	H, F_LEU_110	2.80	1.85	9.01
1HGD.PDB	O, F_ASP_109	N, F_SER_113	H, F_SER_113	2.83	1.87	7.95
1HGD.PDB	O, D_LEU_2	OG, F_SER_113	HG, F_SER_113	2.74	1.91	25.98
1HGD.PDB	O, F_SER_113	N, F_LYS_117	H, F_LYS_117	2.74	1.84	18.35
1HGD.PDB	O, F_MET_115	N, F_PHE_119	H, F_PHE_119	3.00	2.07	16.22
1HGD.PDB	O, F_ASN_116	N, F_GLU_120	H, F_GLU_120	2.89	1.91	4.65
1HGD.PDB	O, F_LYS_117	N, F_LYS_121	H, F_LYS_121	2.95	2.02	15.04
1HGD.PDB	O, F_PHE_119	N, F_ARG_123	H, F_ARG_123	2.94	2.00	14.04
1HGD.PDB	OE2, F_GLU_120	NH1, F_ARG_123	HH11, F_ARG_123	2.77	1.88	23.82
1HGD.PDB	O, F_GLU_120	N, F_ARG_124	H, F_ARG_124	2.95	1.97	3.23
1HGD.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.96	2.14	28.71
1HGD.PDB	OE2, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.94	2.05	20.84
1HGD.PDB	O, F_HIS_159	ND2, F_ASN_129	HD21, F_ASN_129	2.96	2.01	10.95
1HGD.PDB	OH, F_TYR_157	ND2, F_ASN_129	HD22, F_ASN_129	2.80	1.85	12.13
1HGD.PDB	O, F_LYS_139	N, F_GLU_131	H, F_GLU_131	2.97	2.05	16.87
1HGD.PDB	O, F_CYS_137	N, F_MET_133	H, F_MET_133	2.88	1.93	10.80
1HGD.PDB	O, E_LEU_13	N, F_PHE_138	H, F_PHE_138	2.72	1.85	21.62
1HGD.PDB	O, F_GLU_131	N, F_LYS_139	H, F_LYS_139	2.85	1.89	9.90
1HGD.PDB	O, E_ALA_11	N, F_ILE_140	H, F_ILE_140	2.82	1.92	18.45
1HGD.PDB	O, F_ASN_129	N, F_TYR_141	H, F_TYR_141	2.97	2.05	16.46
1HGD.PDB	OE2, F_GLU_165	N, F_LYS_143	H, F_LYS_143	2.96	2.04	17.35
1HGD.PDB	O, F_ASP_145	N, F_ILE_149	H, F_ILE_149	2.86	1.91	11.09

1HGD.PDB	O, F_ASN_146	N, F_GLU_150	H, F_GLU_150	2.91	1.98	15.29
1HGD.PDB	O, F_ALA_147	N, F_SER_151	H, F_SER_151	2.97	2.10	22.90
1HGD.PDB	O, F_CYS_148	OG, F_SER_151	HG, F_SER_151	2.68	1.83	22.68
1HGD.PDB	O, F_GLU_150	N, F_ASN_154	H, F_ASN_154	2.77	1.80	3.19
1HGD.PDB	OD1, F_ASP_158	N, F_ASP_160	H, F_ASP_160	2.93	2.09	25.30
1HGD.PDB	O, F_HIS_159	N, F_TYR_162	H, F_TYR_162	2.96	2.06	19.25
1HGD.PDB	O, D_ARG_170	NH1, F_ARG_163	HH12, F_ARG_163	2.94	1.98	14.11
1HGD.PDB	O, F_TYR_162	N, F_ALA_166	H, F_ALA_166	2.95	1.98	6.51
1HGD.PDB	O, F_ARG_163	N, F_LEU_167	H, F_LEU_167	2.76	1.80	7.00
1HGD.PDB	O, F_ASP_164	N, F_ASN_168	H, F_ASN_168	2.95	1.99	8.58
1HGD.PDB	O, F_GLU_165	ND2, F_ASN_169	HD22, F_ASN_169	3.00	2.04	9.28
1HGD.PDB	O, F_ALA_166	N, F_ARG_170	H, F_ARG_170	2.83	1.97	23.51
1HGD.PDB	O, F_GLU_128	NE, F_ARG_170	HE, F_ARG_170	2.72	1.86	23.45
1HGD.PDB	OE2, F_GLU_131	NH1, F_ARG_170	HH11, F_ARG_170	2.76	1.77	6.97
1HGD.PDB	O, F_LEU_167	N, F_PHE_171	H, F_PHE_171	2.98	2.05	14.52

Table 1664: 1HGD-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1HGE.PDB	O, B_ILE_140	N, A_ALA_11	H, A_ALA_11	2.81	1.93	21.75
1HGE.PDB	O, B_PHE_138	N, A_LEU_13	H, A_LEU_13	2.99	2.04	13.41
1HGE.PDB	O, B_ARG_25	N, A_CYS_14	H, A_CYS_14	2.88	1.92	6.83
1HGE.PDB	O, B_GLY_136	N, A_LEU_15	H, A_LEU_15	2.86	1.90	7.71
1HGE.PDB	O, B_GLY_23	N, A_GLY_16	H, A_GLY_16	2.95	2.03	17.76
1HGE.PDB	O, A_HIS_18	ND1, A_HIS_17	HD1, A_HIS_17	2.99	2.09	20.69
1HGE.PDB	O, B_TRP_21	N, A_HIS_18	H, A_HIS_18	2.85	1.97	21.20
1HGE.PDB	OD1, A_ASN_322	N, A_VAL_20	H, A_VAL_20	2.78	1.83	11.31
1HGE.PDB	O, A_VAL_36	N, A_THR_24	H, A_THR_24	2.84	1.95	19.98
1HGE.PDB	O, A_ILE_34	N, A_VAL_26	H, A_VAL_26	2.81	1.88	13.67
1HGE.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.80	1.78	10.14
1HGE.PDB	O, A_VAL_26	N, A_ILE_34	H, A_ILE_34	2.90	1.96	12.32
1HGE.PDB	O, A_THR_24	N, A_VAL_36	H, A_VAL_36	2.80	1.84	9.48
1HGE.PDB	O, A_MET_320	N, A_THR_37	H, A_THR_37	2.86	1.89	5.71
1HGE.PDB	O, A_LEU_316	N, A_THR_40	H, A_THR_40	2.78	1.95	26.07
1HGE.PDB	O, A_LEU_314	N, A_LEU_42	H, A_LEU_42	2.81	1.99	27.51
1HGE.PDB	O, A_PHE_294	N, A_GLN_44	H, A_GLN_44	2.80	1.84	7.08
1HGE.PDB	O, A_SER_46	NE2, A_GLN_44	HE22, A_GLN_44	2.87	1.99	22.46
1HGE.PDB	OD2, A_ASP_275	NZ, A_LYS_50	HZ1, A_LYS_50	2.75	1.80	21.09
1HGE.PDB	O, A_PRO_273	N, A_ILE_51	H, A_ILE_51	2.81	1.86	12.28
1HGE.PDB	O, A_ASP_275	N, A_ASN_53	H, A_ASN_53	2.79	1.91	21.52
1HGE.PDB	OD2, A_ASP_85	N, A_ARG_57	H, A_ARG_57	2.92	1.99	13.17
1HGE.PDB	O, A_THR_83	NE, A_ARG_57	HE, A_ARG_57	2.79	1.83	9.22
1HGE.PDB	O, A_LEU_86	N, A_LEU_59	H, A_LEU_59	2.90	1.96	12.31
1HGE.PDB	O, A_VAL_88	N, A_GLY_61	H, A_GLY_61	2.97	2.14	26.58
1HGE.PDB	OD1, A_ASP_60	N, A_ILE_62	H, A_ILE_62	2.87	1.94	14.68
1HGE.PDB	O, A_GLY_61	N, A_CYS_64	H, A_CYS_64	2.85	1.93	16.81
1HGE.PDB	O, A_LEU_66	N, A_LEU_70	H, A_LEU_70	2.85	1.96	19.99
1HGE.PDB	O, A_ILE_67	N, A_LEU_71	H, A_LEU_71	2.84	1.88	8.15
1HGE.PDB	O, A_ASP_68	N, A_GLY_72	H, A_GLY_72	2.86	1.94	15.74
1HGE.PDB	OD1, A_ASP_73	ND1, A_HIS_75	HD1, A_HIS_75	2.80	1.89	17.62
1HGE.PDB	O, A_ASP_63	NE2, A_HIS_75	HE2, A_HIS_75	2.86	1.95	18.71
1HGE.PDB	O, A_ASP_73	N, A_CYS_76	H, A_CYS_76	2.78	1.83	10.81
1HGE.PDB	O, A_PRO_74	N, A_ASP_77	H, A_ASP_77	2.92	1.97	11.94
1HGE.PDB	O, A_CYS_76	N, A_PHE_79	H, A_PHE_79	3.00	2.02	2.98
1HGE.PDB	OE1, A_GLU_82	N, A_THR_83	H, A_THR_83	2.93	2.04	19.92
1HGE.PDB	O, A_ARG_57	N, A_ASP_85	H, A_ASP_85	2.80	1.89	17.89
1HGE.PDB	O, A_LEU_59	N, A_VAL_88	H, A_VAL_88	2.95	1.98	5.20
1HGE.PDB	O, A_MET_268	N, A_GLU_89	H, A_GLU_89	2.78	1.83	9.22
1HGE.PDB	OD1, A_ASP_60	NE, A_ARG_90	HE, A_ARG_90	2.85	1.89	7.94
1HGE.PDB	O, A_SER_270	NH1, A_ARG_90	HH11, A_ARG_90	2.62	1.75	23.79
1HGE.PDB	O, A_ALA_272	NH1, A_ARG_90	HH12, A_ARG_90	2.62	1.69	16.06
1HGE.PDB	OD2, A_ASP_60	NH2, A_ARG_90	HH21, A_ARG_90	2.79	1.80	8.90
1HGE.PDB	OD1, A_ASP_271	N, A_SER_91	H, A_SER_91	2.91	1.94	6.37
1HGE.PDB	OD2, A_ASP_271	OG, A_SER_91	HG, A_SER_91	2.81	1.90	18.10
1HGE.PDB	OD2, A_ASP_68	OG, A_SER_95	HG, A_SER_95	2.90	1.97	15.50
1HGE.PDB	OD2, A_ASP_73	N, A_ASN_96	H, A_ASN_96	2.90	1.93	6.89
1HGE.PDB	OD1, A_ASP_68	OH, A_TYR_100	HH, A_TYR_100	2.91	1.93	2.88
1HGE.PDB	O, A_ILE_230	N, A_ASP_101	H, A_ASP_101	3.00	2.11	21.52
1HGE.PDB	OD2, A_ASP_104	OG, A_SER_107	HG, A_SER_107	2.86	1.94	16.59
1HGE.PDB	O, A_TYR_105	N, A_ARG_109	H, A_ARG_109	2.83	1.86	3.58
1HGE.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.74	1.75	12.19
1HGE.PDB	OD2, F_ASP_79	OG, A_SER_110	HG, A_SER_110	2.90	1.95	11.19
1HGE.PDB	O, A_SER_107	N, A_LEU_111	H, A_LEU_111	2.85	1.87	2.87
1HGE.PDB	O, A_LEU_108	N, A_VAL_112	H, A_VAL_112	2.99	2.03	8.13
1HGE.PDB	O, A_ARG_109	N, A_ALA_113	H, A_ALA_113	2.94	2.03	18.27
1HGE.PDB	O, A_SER_110	N, A_SER_114	H, A_SER_114	2.87	1.96	18.01

1HGE.PDB	OE2, A_GLU_119	OG1, A_THR_117	HG1, A_THR_117	2.90	1.95	8.88
1HGE.PDB	O, A_GLU_82	N, A_LEU_118	H, A_LEU_118	2.96	2.03	16.11
1HGE.PDB	O, A_TYR_257	N, A_ILE_121	H, A_ILE_121	2.88	1.91	6.47
1HGE.PDB	O, A_ARG_255	N, A_GLU_123	H, A_GLU_123	2.93	1.98	10.93
1HGE.PDB	O, A_THR_155	N, A_THR_131	H, A_THR_131	2.74	1.84	18.66
1HGE.PDB	OD1, A_ASN_152	N, A_ASN_133	H, A_ASN_133	2.88	1.96	16.29
1HGE.PDB	O, A_TRP_153	N, A_GLY_134	H, A_GLY_134	2.96	2.06	19.55
1HGE.PDB	O, A_GLY_146	N, A_SER_136	H, A_SER_136	2.83	1.88	10.81
1HGE.PDB	OG, A_SER_136	N, A_ALA_138	H, A_ALA_138	2.95	2.01	13.95
1HGE.PDB	O, A_GLY_144	NZ, A_LYS_140	HZ1, A_LYS_140	2.75	1.77	16.24
1HGE.PDB	OD1, A_ASN_137	NZ, A_LYS_140	HZ2, A_LYS_140	2.81	1.83	16.67
1HGE.PDB	OD2, A_ASP_77	NE, A_ARG_141	HE, A_ARG_141	2.81	1.97	26.71
1HGE.PDB	O, A_PHE_147	NH1, A_ARG_141	HH12, A_ARG_141	2.55	1.62	16.38
1HGE.PDB	OD1, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.89	1.98	21.76
1HGE.PDB	OD2, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.75	1.86	23.90
1HGE.PDB	O, A_GLY_72	NH2, A_ARG_141	HH22, A_ARG_141	2.93	1.96	12.25
1HGE.PDB	O, A_GLY_72	N, A_SER_149	H, A_SER_149	2.83	1.92	17.48
1HGE.PDB	O, A_ALA_253	N, A_ASN_152	H, A_ASN_152	2.79	1.91	21.99
1HGE.PDB	OH, A_TYR_195	NE1, A_TRP_153	HE1, A_TRP_153	2.88	1.99	20.14
1HGE.PDB	O, A_LEU_194	N, A_LYS_156	H, A_LYS_156	2.98	2.08	19.15
1HGE.PDB	O, A_SER_193	NZ, A_LYS_156	HZ2, A_LYS_156	2.68	1.68	12.99
1HGE.PDB	O, A_THR_160	N, A_SER_157	H, A_SER_157	2.99	2.09	20.22
1HGE.PDB	O, A_SER_247	N, A_LEU_164	H, A_LEU_164	2.68	1.85	26.14
1HGE.PDB	O, A_ILE_245	N, A_VAL_166	H, A_VAL_166	2.88	1.93	12.18
1HGE.PDB	O, A_LEU_243	OG1, A_THR_167	HG1, A_THR_167	2.88	1.97	16.07
1HGE.PDB	O, A_LEU_243	N, A_MET_168	H, A_MET_168	2.92	1.99	15.75
1HGE.PDB	O, A_ASP_241	N, A_ASN_170	H, A_ASN_170	2.93	1.96	5.62
1HGE.PDB	O, A_PHE_174	ND2, A_ASN_170	HD21, A_ASN_170	2.84	1.88	9.34
1HGE.PDB	O, A_VAL_237	ND2, A_ASN_170	HD22, A_ASN_170	2.86	2.05	28.37
1HGE.PDB	O, A_VAL_237	N, A_LYS_176	H, A_LYS_176	2.98	2.05	15.51
1HGE.PDB	OE2, A_GLU_123	NZ, A_LYS_176	HZ1, A_LYS_176	2.71	1.79	22.78
1HGE.PDB	O, A_THR_235	N, A_TYR_178	H, A_TYR_178	2.82	1.86	5.77
1HGE.PDB	OE1, A_GLU_123	OH, A_TYR_178	HH, A_TYR_178	2.75	1.82	10.80
1HGE.PDB	O, A_TYR_233	N, A_TRP_180	H, A_TRP_180	2.99	2.02	8.32
1HGE.PDB	OG1, A_THR_235	NE1, A_TRP_180	HE1, A_TRP_180	2.92	1.93	3.33
1HGE.PDB	O, A_ASN_250	N, A_HIS_183	H, A_HIS_183	2.92	2.01	18.32
1HGE.PDB	O, A_ARG_229	N, A_HIS_184	H, A_HIS_184	2.86	1.90	8.10
1HGE.PDB	OG, A_SER_231	NE2, A_HIS_184	HE2, A_HIS_184	2.72	1.88	25.40
1HGE.PDB	OG1, A_THR_187	N, A_GLU_190	H, A_GLU_190	2.97	2.02	10.04
1HGE.PDB	O, A_GLN_197	NE2, A_GLN_191	HE22, A_GLN_191	2.96	2.04	16.90
1HGE.PDB	O, A_ASN_188	OG1, A_THR_192	HG1, A_THR_192	3.00	2.04	5.15
1HGE.PDB	O, A_GLN_189	N, A_SER_193	H, A_SER_193	2.84	1.87	3.05
1HGE.PDB	O, A_GLU_190	N, A_LEU_194	H, A_LEU_194	2.96	1.99	8.69
1HGE.PDB	O, A_GLN_191	N, A_TYR_195	H, A_TYR_195	2.77	1.82	9.81
1HGE.PDB	O, A_TYR_161	NE2, A_GLN_197	HE21, A_GLN_197	2.88	1.93	11.11
1HGE.PDB	O, A_ASN_248	NE2, A_GLN_197	HE22, A_GLN_197	2.92	1.99	15.44
1HGE.PDB	OD1, A_ASN_246	NH2, A_ARG_201	HH21, A_ARG_201	2.60	1.73	24.24
1HGE.PDB	O, A_ILE_213	N, A_VAL_202	H, A_VAL_202	2.96	1.99	9.62
1HGE.PDB	O, A_ASN_246	N, A_THR_203	H, A_THR_203	2.84	1.92	16.80
1HGE.PDB	O, A_GLN_211	N, A_VAL_204	H, A_VAL_204	2.83	1.93	18.95
1HGE.PDB	O, A_SER_209	N, A_THR_206	H, A_THR_206	2.97	2.00	7.75
1HGE.PDB	OD1, A_ASP_241	N, A_ARG_207	H, A_ARG_207	2.90	1.93	8.60
1HGE.PDB	OG1, A_THR_206	OG, A_SER_209	HG, A_SER_209	2.97	2.03	10.25
1HGE.PDB	OD1, E_ASP_101	NE2, A_GLN_210	HE22, A_GLN_210	2.91	2.05	24.48
1HGE.PDB	O, A_VAL_204	N, A_GLN_211	H, A_GLN_211	2.84	1.93	17.53
1HGE.PDB	OG1, A_THR_203	OG1, A_THR_212	HG1, A_THR_212	2.85	1.89	3.04
1HGE.PDB	O, A_VAL_202	N, A_ILE_213	H, A_ILE_213	2.83	1.91	16.11
1HGE.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.71	1.78	19.14

1HGE.PDB	O, A_ASN_216	NH2, A_ARG_220	HH22, A_ARG_220	2.65	1.77	22.20
1HGE.PDB	O, A_LEU_226	N, A_VAL_223	H, A_VAL_223	2.87	1.92	10.90
1HGE.PDB	O, A_CYS_97	NE, A_ARG_224	HE, A_ARG_224	2.88	2.06	27.84
1HGE.PDB	O, A_CYS_97	NH2, A_ARG_224	HH21, A_ARG_224	2.81	1.91	22.36
1HGE.PDB	O, A_VAL_223	N, A_LEU_226	H, A_LEU_226	2.91	1.96	11.44
1HGE.PDB	O, A_SER_228	NH1, A_ARG_229	HH11, A_ARG_229	2.68	1.74	17.50
1HGE.PDB	O, A_PRO_221	NH2, A_ARG_229	HH22, A_ARG_229	2.64	1.68	14.09
1HGE.PDB	OD1, A_ASP_101	OG, A_SER_231	HG, A_SER_231	2.85	1.89	7.16
1HGE.PDB	O, A_ASP_101	N, A_ILE_232	H, A_ILE_232	2.93	2.00	16.40
1HGE.PDB	O, A_TRP_180	N, A_TYR_233	H, A_TYR_233	2.87	1.90	8.23
1HGE.PDB	O, A_TYR_178	N, A_THR_235	H, A_THR_235	2.87	1.97	18.03
1HGE.PDB	O, A_LYS_176	N, A_VAL_237	H, A_VAL_237	2.80	1.88	15.84
1HGE.PDB	O, F_SER_71	NZ, A_LYS_238	HZ2, A_LYS_238	2.67	1.73	19.84
1HGE.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.91	1.89	11.73
1HGE.PDB	O, A_ASN_170	N, A_GLY_240	H, A_GLY_240	2.86	1.99	22.30
1HGE.PDB	O, A_LYS_238	N, A_ASP_241	H, A_ASP_241	2.94	2.01	14.08
1HGE.PDB	OD1, A_ASP_241	N, A_VAL_242	H, A_VAL_242	2.76	1.94	27.44
1HGE.PDB	O, A_MET_168	N, A_LEU_243	H, A_LEU_243	2.90	1.93	4.25
1HGE.PDB	O, A_SER_205	N, A_VAL_244	H, A_VAL_244	2.95	2.01	13.31
1HGE.PDB	O, A_VAL_166	N, A_ILE_245	H, A_ILE_245	2.85	1.92	14.45
1HGE.PDB	O, A_THR_203	N, A_ASN_246	H, A_ASN_246	2.90	1.93	7.70
1HGE.PDB	OD1, A_ASN_165	ND2, A_ASN_246	HD22, A_ASN_246	2.88	1.94	13.15
1HGE.PDB	O, A_LEU_164	N, A_SER_247	H, A_SER_247	2.96	2.05	18.81
1HGE.PDB	OE1, A_GLN_191	ND2, A_ASN_250	HD21, A_ASN_250	2.94	1.97	8.25
1HGE.PDB	O, A_HIS_183	ND2, A_ASN_250	HD22, A_ASN_250	2.88	1.92	10.41
1HGE.PDB	O, A_ASN_152	N, A_ALA_253	H, A_ALA_253	2.86	1.98	21.30
1HGE.PDB	OD1, A_ASN_133	NH2, A_ARG_255	HH22, A_ARG_255	2.48	1.67	28.93
1HGE.PDB	O, A_LEU_177	N, A_PHE_258	H, A_PHE_258	2.96	1.99	5.50
1HGE.PDB	OE2, A_GLU_119	NH1, A_ARG_261	HH12, A_ARG_261	2.64	1.81	27.97
1HGE.PDB	OE1, A_GLU_119	NH2, A_ARG_261	HH22, A_ARG_261	2.84	1.95	24.23
1HGE.PDB	OD2, A_ASP_85	NZ, A_LYS_264	HZ3, A_LYS_264	2.77	1.79	16.96
1HGE.PDB	O, A_PHE_87	N, A_MET_268	H, A_MET_268	2.82	1.93	21.12
1HGE.PDB	O, A_PRO_284	OG, A_SER_270	HG, A_SER_270	2.79	1.85	11.32
1HGE.PDB	OG, A_SER_270	N, A_ALA_272	H, A_ALA_272	2.96	2.01	11.61
1HGE.PDB	O, A_ILE_51	N, A_ASP_275	H, A_ASP_275	2.94	2.05	20.45
1HGE.PDB	OD1, A_ASP_275	N, A_THR_276	H, A_THR_276	2.79	1.94	23.69
1HGE.PDB	O, A_ASN_54	N, A_SER_279	H, A_SER_279	2.78	1.85	13.75
1HGE.PDB	O, A_TYR_302	N, A_ILE_282	H, A_ILE_282	2.91	1.94	8.25
1HGE.PDB	O, A_THR_283	N, A_GLY_286	H, A_GLY_286	2.83	1.90	13.31
1HGE.PDB	O, A_LYS_50	N, A_SER_287	H, A_SER_287	2.88	1.91	2.15
1HGE.PDB	O, A_ALA_304	ND2, A_ASN_290	HD22, A_ASN_290	2.81	1.91	18.81
1HGE.PDB	OE1, A_GLN_44	NZ, A_LYS_292	HZ1, A_LYS_292	2.69	1.69	12.67
1HGE.PDB	OD2, A_ASP_291	NZ, A_LYS_292	HZ3, A_LYS_292	2.82	1.86	19.03
1HGE.PDB	O, A_LYS_307	N, A_GLN_295	H, A_GLN_295	2.84	1.95	20.46
1HGE.PDB	O, A_ASN_298	NE2, A_GLN_295	HE21, A_GLN_295	2.75	1.79	6.17
1HGE.PDB	O, A_GLN_44	N, A_ASN_296	H, A_ASN_296	2.80	1.87	13.84
1HGE.PDB	OE1, A_GLN_295	N, A_VAL_297	H, A_VAL_297	2.67	1.87	28.35
1HGE.PDB	O, B_LYS_68	NZ, A_LYS_299	HZ2, A_LYS_299	2.95	1.93	10.27
1HGE.PDB	OD1, A_ASN_298	N, A_ILE_300	H, A_ILE_300	2.94	2.01	15.45
1HGE.PDB	O, A_ILE_282	N, A_TYR_302	H, A_TYR_302	2.95	2.08	23.09
1HGE.PDB	O, B_LYS_62	N, A_GLY_303	H, A_GLY_303	2.95	1.98	8.88
1HGE.PDB	OG, B_SER_93	N, A_LYS_310	H, A_LYS_310	2.91	1.95	10.06
1HGE.PDB	OE2, A_GLU_41	N, A_LEU_314	H, A_LEU_314	2.82	1.89	14.30
1HGE.PDB	OE1, A_GLU_41	NZ, A_LYS_315	HZ3, A_LYS_315	2.82	1.87	21.00
1HGE.PDB	O, A_THR_40	N, A_LEU_316	H, A_LEU_316	2.80	1.85	10.41
1HGE.PDB	OD1, B_ASN_104	N, A_ALA_317	H, A_ALA_317	2.72	1.81	16.15
1HGE.PDB	O, A_ASN_38	N, A_THR_318	H, A_THR_318	2.85	1.93	17.18
1HGE.PDB	O, A_VAL_20	ND2, A_ASN_322	HD21, A_ASN_322	2.93	2.01	15.29

1HGE.PDB	OE2, A_GLU_35	ND2, A_ASN_322	HD22, A_ASN_322	2.88	1.99	21.26
1HGE.PDB	OE1, A_GLU_325	NZ, A_LYS_326	HZ3, A_LYS_326	2.85	1.86	15.04
1HGE.PDB	O, A_PRO_21	NE2, A_GLN_327	HE22, A_GLN_327	2.79	1.93	23.89
1HGE.PDB	OD2, B_ASP_112	N, B_GLY_1	H2, B_GLY_1	2.79	1.81	15.88
1HGE.PDB	OD1, B_ASP_109	N, B_LEU_2	H, B_LEU_2	2.80	1.92	21.49
1HGE.PDB	OD2, B_ASP_112	N, B_PHE_3	H, B_PHE_3	2.74	1.95	29.38
1HGE.PDB	OD2, B_ASP_112	N, B_GLY_4	H, B_GLY_4	2.91	2.02	19.87
1HGE.PDB	OD1, B_ASP_112	N, B_ALA_5	H, B_ALA_5	2.93	2.03	18.95
1HGE.PDB	O, B_GLY_4	N, B_PHE_9	H, B_PHE_9	2.82	1.87	12.40
1HGE.PDB	O, B_GLY_13	ND2, B_ASN_12	HD22, B_ASN_12	2.77	1.94	25.78
1HGE.PDB	O, A_VAL_323	N, B_GLY_13	H, B_GLY_13	2.72	1.79	12.30
1HGE.PDB	O, A_HIS_17	N, B_TRP_14	H, B_TRP_14	2.85	1.92	15.18
1HGE.PDB	OG1, B_THR_41	N, B_TRP_21	H, B_TRP_21	2.88	1.97	18.39
1HGE.PDB	O, A_GLY_16	N, B_GLY_23	H, B_GLY_23	2.92	2.01	18.67
1HGE.PDB	O, B_ALA_35	N, B_PHE_24	H, B_PHE_24	2.78	1.82	3.34
1HGE.PDB	O, A_CYS_14	N, B_ARG_25	H, B_ARG_25	3.00	2.06	13.87
1HGE.PDB	OE1, B_GLN_34	NE, B_ARG_25	HE, B_ARG_25	2.59	1.77	25.60
1HGE.PDB	O, B_GLY_33	N, B_HIS_26	H, B_HIS_26	2.68	1.83	22.72
1HGE.PDB	OG1, B_THR_32	NE2, B_GLN_27	HE22, B_GLN_27	2.99	2.08	18.28
1HGE.PDB	O, B_GLY_31	N, B_ASN_28	H, B_ASN_28	2.82	1.91	16.99
1HGE.PDB	O, B_ASN_28	N, B_GLY_31	H, B_GLY_31	3.00	2.09	18.25
1HGE.PDB	O, B_HIS_26	N, B_GLY_33	H, B_GLY_33	2.86	1.95	17.40
1HGE.PDB	O, B_TYR_22	N, B_ASP_37	H, B_ASP_37	2.72	1.79	12.23
1HGE.PDB	OD2, B_ASP_37	N, B_SER_40	H, B_SER_40	2.87	1.91	9.83
1HGE.PDB	O, B_ASP_37	OG1, B_THR_41	HG1, B_THR_41	2.70	1.82	19.30
1HGE.PDB	O, B_LEU_38	N, B_GLN_42	H, B_GLN_42	2.86	1.93	14.86
1HGE.PDB	OD1, B_ASP_46	NE2, B_GLN_42	HE22, B_GLN_42	2.87	1.96	19.05
1HGE.PDB	O, B_LYS_39	N, B_ALA_43	H, B_ALA_43	2.94	2.00	12.81
1HGE.PDB	O, B_SER_40	N, B_ALA_44	H, B_ALA_44	2.93	1.95	3.59
1HGE.PDB	O, B_GLN_42	N, B_ASP_46	H, B_ASP_46	2.81	1.84	1.45
1HGE.PDB	O, B_ALA_43	NE2, B_GLN_47	HE22, B_GLN_47	2.88	1.96	16.21
1HGE.PDB	O, B_ILE_45	N, B_ASN_49	H, B_ASN_49	2.85	1.89	11.27
1HGE.PDB	O, B_ASP_46	N, B_GLY_50	H, B_GLY_50	2.84	1.93	18.21
1HGE.PDB	OG1, B_THR_107	NZ, B_LYS_51	HZ1, B_LYS_51	2.97	1.99	17.16
1HGE.PDB	OE1, B_GLU_103	NZ, B_LYS_51	HZ2, B_LYS_51	2.76	1.73	6.92
1HGE.PDB	ND1, B_HIS_106	NZ, B_LYS_51	HZ3, B_LYS_51	2.73	1.78	18.14
1HGE.PDB	O, B_ILE_48	N, B_LEU_52	H, B_LEU_52	2.84	1.93	16.73
1HGE.PDB	O, B_ASN_49	N, B_ASN_53	H, B_ASN_53	2.78	1.86	14.52
1HGE.PDB	OE1, B_GLU_57	NH1, B_ARG_54	HH11, B_ARG_54	2.83	1.84	12.19
1HGE.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.84	1.86	12.76
1HGE.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ1, B_LYS_62	2.60	1.76	28.82
1HGE.PDB	OD2, F_ASP_90	NZ, B_LYS_62	HZ3, B_LYS_62	2.69	1.82	26.81
1HGE.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.97	2.02	12.36
1HGE.PDB	O, B_PHE_63	NE2, B_GLN_65	HE22, B_GLN_65	2.99	2.02	6.59
1HGE.PDB	O, A_LYS_299	NZ, B_LYS_68	HZ1, B_LYS_68	2.93	1.92	11.15
1HGE.PDB	OE2, B_GLU_85	NZ, B_LYS_68	HZ2, B_LYS_68	2.78	1.76	9.50
1HGE.PDB	OG, C_SER_107	N, B_ARG_76	H, B_ARG_76	2.82	1.86	9.28
1HGE.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.87	1.91	11.56
1HGE.PDB	OE2, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.84	1.83	5.81
1HGE.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.70	1.70	6.45
1HGE.PDB	OE1, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.79	1.79	3.91
1HGE.PDB	OE1, B_GLU_74	NE2, B_GLN_78	HE22, B_GLN_78	2.97	2.00	7.88
1HGE.PDB	O, B_GLY_75	N, B_ASP_79	H, B_ASP_79	2.91	1.96	12.34
1HGE.PDB	O, B_ILE_77	N, B_GLU_81	H, B_GLU_81	2.94	1.98	9.95
1HGE.PDB	O, B_ASP_79	N, B_TYR_83	H, B_TYR_83	2.93	2.00	15.72
1HGE.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.65	1.81	24.86
1HGE.PDB	O, B_LEU_80	N, B_VAL_84	H, B_VAL_84	2.83	1.87	9.05
1HGE.PDB	O, B_LYS_82	N, B_ASP_86	H, B_ASP_86	2.93	1.97	10.28

1HGE.PDB	O, B_TYR.83	N, B_THR.87	H, B_THR.87	2.93	1.97	8.81
1HGE.PDB	O, B_VAL.84	N, B_LYS.88	H, B_LYS.88	2.94	2.02	16.73
1HGE.PDB	OH, F_TYR.83	NZ, B_LYS.88	HZ1, B_LYS.88	2.75	1.71	5.62
1HGE.PDB	O, B_GLU.85	N, B_ILE.89	H, B_ILE.89	2.88	1.90	4.71
1HGE.PDB	O, B_LYS.88	N, B_TRP.92	H, B_TRP.92	2.97	1.99	5.16
1HGE.PDB	O, B_ILE.89	N, B_SER.93	H, B_SER.93	2.85	1.95	18.50
1HGE.PDB	O, B_ILE.89	OG, B_SER.93	HG, B_SER.93	2.88	1.95	13.07
1HGE.PDB	O, B_ASP.90	N, B_TYR.94	H, B_TYR.94	2.86	1.94	16.10
1HGE.PDB	O, B_TRP.92	N, B_ALA.96	H, B_ALA.96	2.95	2.01	14.83
1HGE.PDB	O, B_TYR.94	N, B_LEU.98	H, B_LEU.98	2.99	2.01	4.40
1HGE.PDB	O, B_ASN.95	N, B_LEU.99	H, B_LEU.99	2.90	1.98	15.69
1HGE.PDB	O, B_LEU.98	N, B_LEU.102	H, B_LEU.102	2.96	1.99	5.20
1HGE.PDB	O, B_LEU.99	N, B_GLU.103	H, B_GLU.103	2.88	1.92	7.57
1HGE.PDB	O, B_VAL.100	N, B_ASN.104	H, B_ASN.104	2.90	1.95	12.33
1HGE.PDB	O, A_LYS.27	ND2, B_ASN.104	HD22, B_ASN.104	2.93	1.97	10.25
1HGE.PDB	O, B_LEU.102	N, B_HIS.106	H, B_HIS.106	2.92	1.96	11.10
1HGE.PDB	O, B_GLU.103	N, B_THR.107	H, B_THR.107	2.81	1.94	21.77
1HGE.PDB	O, B_ASN.104	N, B_ILE.108	H, B_ILE.108	2.89	1.93	10.01
1HGE.PDB	O, B_HIS.106	N, B_LEU.110	H, B_LEU.110	2.83	1.87	9.77
1HGE.PDB	O, B_THR.107	OG1, B_THR.111	HG1, B_THR.111	2.88	1.91	3.54
1HGE.PDB	O, B_ASP.109	N, B_SER.113	H, B_SER.113	2.82	1.87	9.66
1HGE.PDB	O, B_LEU.110	N, B_GLU.114	H, B_GLU.114	2.93	1.98	10.47
1HGE.PDB	O, B_ASP.112	N, B_ASN.116	H, B_ASN.116	2.97	2.00	6.50
1HGE.PDB	O, B_SER.113	N, B_LYS.117	H, B_LYS.117	2.76	1.88	21.74
1HGE.PDB	O, B_GLU.114	N, B_LEU.118	H, B_LEU.118	2.98	2.03	12.99
1HGE.PDB	O, B_MET.115	N, B_PHE.119	H, B_PHE.119	3.00	2.05	11.74
1HGE.PDB	O, B_ASN.116	N, B_GLU.120	H, B_GLU.120	2.94	1.96	5.48
1HGE.PDB	O, B_LYS.117	N, B_LYS.121	H, B_LYS.121	2.93	2.04	20.65
1HGE.PDB	O, B_PHE.119	N, B_ARG.123	H, B_ARG.123	2.92	1.95	6.37
1HGE.PDB	OE2, B_GLU.120	NH1, B_ARG.123	HH11, B_ARG.123	2.84	1.95	23.29
1HGE.PDB	O, B_GLU.120	N, B_ARG.124	H, B_ARG.124	2.99	2.03	10.10
1HGE.PDB	OE1, F_GLU.132	NE, B_ARG.124	HE, B_ARG.124	2.80	1.98	27.36
1HGE.PDB	OE2, F_GLU.132	NE, B_ARG.124	HE, B_ARG.124	2.94	2.06	21.65
1HGE.PDB	O, B_LEU.126	N, B_ASN.129	H, B_ASN.129	2.92	1.98	14.64
1HGE.PDB	O, B_HIS.159	ND2, B_ASN.129	HD21, B_ASN.129	2.96	2.01	10.21
1HGE.PDB	OH, B_TYR.157	ND2, B_ASN.129	HD22, B_ASN.129	2.79	1.85	12.68
1HGE.PDB	O, B_LYS.139	N, B_GLU.131	H, B_GLU.131	2.95	2.03	17.07
1HGE.PDB	O, B_CYS.137	N, B_MET.133	H, B_MET.133	2.86	1.91	11.42
1HGE.PDB	O, A_LEU.13	N, B_PHE.138	H, B_PHE.138	2.71	1.84	21.33
1HGE.PDB	O, B_GLU.131	N, B_LYS.139	H, B_LYS.139	2.81	1.88	12.91
1HGE.PDB	O, A_ALA.11	N, B_ILE.140	H, B_ILE.140	2.75	1.86	18.72
1HGE.PDB	O, B_ASN.129	N, B_TYR.141	H, B_TYR.141	2.86	1.94	15.94
1HGE.PDB	OD2, B_ASP.145	NZ, B_LYS.143	HZ1, B_LYS.143	2.79	1.94	29.42
1HGE.PDB	OE1, B_GLU.30	N, B_ASN.146	H, B_ASN.146	2.97	2.02	12.34
1HGE.PDB	O, B_ASP.145	N, B_ILE.149	H, B_ILE.149	2.91	1.95	10.07
1HGE.PDB	O, B_ASN.146	N, B_GLU.150	H, B_GLU.150	2.95	2.00	12.08
1HGE.PDB	O, B_ALA.147	N, B_SER.151	H, B_SER.151	2.90	2.05	24.74
1HGE.PDB	O, B_CYS.148	OG, B_SER.151	HG, B_SER.151	2.68	1.83	21.90
1HGE.PDB	O, B_GLU.150	N, B_ASN.154	H, B_ASN.154	2.81	1.84	3.57
1HGE.PDB	OE2, B_GLU.150	ND2, B_ASN.154	HD21, B_ASN.154	2.93	2.05	22.48
1HGE.PDB	O, B_SER.151	N, B_THR.156	H, B_THR.156	2.73	1.90	26.23
1HGE.PDB	OD1, B_ASN.154	OG1, B_THR.156	HG1, B_THR.156	2.71	1.82	17.99
1HGE.PDB	OD1, B_ASP.158	N, B_ASP.160	H, B_ASP.160	2.83	1.98	24.58
1HGE.PDB	O, B_HIS.159	N, B_TYR.162	H, B_TYR.162	2.90	2.00	20.06
1HGE.PDB	O, F_ARG.170	NH1, B_ARG.163	HH12, B_ARG.163	2.78	1.81	13.88
1HGE.PDB	O, B_TYR.162	N, B_ALA.166	H, B_ALA.166	2.88	1.91	5.46
1HGE.PDB	O, B_ARG.163	N, B_LEU.167	H, B_LEU.167	2.76	1.81	10.04
1HGE.PDB	O, B_ALA.166	N, B_ARG.170	H, B_ARG.170	2.82	1.95	21.77

1HGE.PDB	O, B_GLU_128	NE, B_ARG_170	HE, B_ARG_170	2.74	1.87	22.54
1HGE.PDB	OE2, B_GLU_131	NH1, B_ARG_170	HH11, B_ARG_170	2.80	1.80	6.47
1HGE.PDB	O, B_LEU_167	N, B_PHE_171	H, B_PHE_171	2.90	1.98	16.40
1HGE.PDB	O, D_ILE_140	N, C_ALA_11	H, C_ALA_11	2.80	1.91	19.98
1HGE.PDB	O, D_PHE_138	N, C_LEU_13	H, C_LEU_13	2.99	2.04	12.20
1HGE.PDB	O, D_ARG_25	N, C_CYS_14	H, C_CYS_14	2.73	1.82	16.85
1HGE.PDB	O, D_GLY_136	N, C_LEU_15	H, C_LEU_15	2.89	1.92	5.03
1HGE.PDB	O, D_GLY_23	N, C_GLY_16	H, C_GLY_16	2.98	2.07	18.60
1HGE.PDB	O, C_HIS_18	ND1, C_HIS_17	HD1, C_HIS_17	3.00	2.12	21.91
1HGE.PDB	O, D_TRP_21	N, C_HIS_18	H, C_HIS_18	2.85	1.96	19.89
1HGE.PDB	OD1, C_ASN_322	N, C_VAL_20	H, C_VAL_20	2.80	1.84	8.99
1HGE.PDB	O, C_VAL_36	N, C_THR_24	H, C_THR_24	2.83	1.91	16.33
1HGE.PDB	O, C_ILE_34	N, C_VAL_26	H, C_VAL_26	2.82	1.87	10.60
1HGE.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.79	1.77	8.74
1HGE.PDB	O, C_VAL_26	N, C_ILE_34	H, C_ILE_34	2.90	1.95	12.39
1HGE.PDB	O, C_THR_24	N, C_VAL_36	H, C_VAL_36	2.79	1.83	9.59
1HGE.PDB	O, C_MET_320	N, C_THR_37	H, C_THR_37	2.87	1.90	5.65
1HGE.PDB	O, C_LEU_316	N, C_THR_40	H, C_THR_40	2.80	1.96	24.94
1HGE.PDB	O, C_LEU_314	N, C_LEU_42	H, C_LEU_42	2.79	1.97	26.99
1HGE.PDB	O, C_PHE_294	N, C_GLN_44	H, C_GLN_44	2.81	1.85	7.78
1HGE.PDB	O, C_SER_46	NE2, C_GLN_44	HE22, C_GLN_44	2.87	1.98	21.20
1HGE.PDB	O, C_ASN_285	OG, C_SER_47	HG, C_SER_47	2.85	1.92	13.60
1HGE.PDB	OG1, C_THR_48	N, C_LYS_50	H, C_LYS_50	2.99	2.04	10.77
1HGE.PDB	OD2, C_ASP_275	NZ, C_LYS_50	HZ1, C_LYS_50	2.70	1.77	22.15
1HGE.PDB	O, C_PRO_273	N, C_ILE_51	H, C_ILE_51	2.80	1.85	11.79
1HGE.PDB	O, C_ASP_275	N, C_ASN_53	H, C_ASN_53	2.75	1.91	24.79
1HGE.PDB	OD2, C_ASP_85	N, C_ARG_57	H, C_ARG_57	2.90	1.96	11.88
1HGE.PDB	O, C_THR_83	NE, C_ARG_57	HE, C_ARG_57	2.79	1.83	9.16
1HGE.PDB	O, C_LEU_86	N, C_LEU_59	H, C_LEU_59	2.93	1.97	10.15
1HGE.PDB	O, C_VAL_88	N, C_GLY_61	H, C_GLY_61	2.98	2.14	25.88
1HGE.PDB	OD1, C_ASP_60	N, C_ILE_62	H, C_ILE_62	2.86	1.94	15.66
1HGE.PDB	O, C_GLY_61	N, C_CYS_64	H, C_CYS_64	2.85	1.93	16.26
1HGE.PDB	O, C_LEU_66	N, C_LEU_70	H, C_LEU_70	2.86	1.97	20.20
1HGE.PDB	O, C_ILE_67	N, C_LEU_71	H, C_LEU_71	2.82	1.86	10.15
1HGE.PDB	O, C_ASP_68	N, C_GLY_72	H, C_GLY_72	2.84	1.92	16.44
1HGE.PDB	OD1, C_ASP_73	ND1, C_HIS_75	HD1, C_HIS_75	2.76	1.85	18.20
1HGE.PDB	O, C_ASP_63	NE2, C_HIS_75	HE2, C_HIS_75	2.82	1.90	17.58
1HGE.PDB	O, C_ASP_73	N, C_CYS_76	H, C_CYS_76	2.77	1.82	10.67
1HGE.PDB	O, C_PRO_74	N, C_ASP_77	H, C_ASP_77	2.88	1.93	11.27
1HGE.PDB	O, C_CYS_76	N, C_PHE_79	H, C_PHE_79	2.99	2.01	4.04
1HGE.PDB	O, C_ARG_57	N, C_ASP_85	H, C_ASP_85	2.79	1.90	19.22
1HGE.PDB	O, C_LEU_59	N, C_VAL_88	H, C_VAL_88	2.96	1.98	5.43
1HGE.PDB	O, C_MET_268	N, C_GLU_89	H, C_GLU_89	2.78	1.83	10.28
1HGE.PDB	OD1, C_ASP_60	NE, C_ARG_90	HE, C_ARG_90	2.84	1.88	10.34
1HGE.PDB	O, C_SER_270	NH1, C_ARG_90	HH11, C_ARG_90	2.64	1.77	24.86
1HGE.PDB	O, C_ALA_272	NH1, C_ARG_90	HH12, C_ARG_90	2.61	1.68	16.52
1HGE.PDB	OD2, C_ASP_60	NH2, C_ARG_90	HH21, C_ARG_90	2.77	1.78	9.61
1HGE.PDB	OD1, C_ASP_271	N, C_SER_91	H, C_SER_91	2.89	1.92	5.94
1HGE.PDB	OD2, C_ASP_271	OG, C_SER_91	HG, C_SER_91	2.80	1.91	19.19
1HGE.PDB	OD2, C_ASP_68	OG, C_SER_95	HG, C_SER_95	2.88	1.95	14.90
1HGE.PDB	OD2, C_ASP_73	N, C_ASN_96	H, C_ASN_96	2.89	1.91	7.72
1HGE.PDB	OD1, C_ASP_68	OH, C_TYR_100	HH, C_TYR_100	2.89	1.97	15.01
1HGE.PDB	O, C_ILE_230	N, C_ASP_101	H, C_ASP_101	2.99	2.10	21.29
1HGE.PDB	OD2, C_ASP_104	OG, C_SER_107	HG, C_SER_107	2.88	1.96	15.70
1HGE.PDB	O, C_TYR_105	N, C_ARG_109	H, C_ARG_109	2.82	1.85	4.05
1HGE.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.78	1.79	11.19
1HGE.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.78	1.86	15.09
1HGE.PDB	O, C_SER_107	N, C_LEU_111	H, C_LEU_111	2.85	1.88	4.99

1HGE.PDB	O, C_ARG_109	N, C_ALA_113	H, C_ALA_113	2.95	2.04	18.55
1HGE.PDB	O, C_SER_110	N, C_SER_114	H, C_SER_114	2.89	1.95	14.50
1HGE.PDB	OE2, C_GLU_119	OG1, C_THR_117	HG1, C_THR_117	2.89	1.94	9.29
1HGE.PDB	O, C_GLU_82	N, C_LEU_118	H, C_LEU_118	2.97	2.03	15.52
1HGE.PDB	O, C_TYR_257	N, C_ILE_121	H, C_ILE_121	2.88	1.91	6.31
1HGE.PDB	O, C_ARG_255	N, C_GLU_123	H, C_GLU_123	2.94	1.98	10.94
1HGE.PDB	O, C_THR_155	N, C_THR_131	H, C_THR_131	2.77	1.87	18.82
1HGE.PDB	OD1, C_ASN_152	N, C_ASN_133	H, C_ASN_133	2.88	1.96	16.12
1HGE.PDB	O, C_TRP_153	N, C_GLY_134	H, C_GLY_134	2.94	2.05	19.45
1HGE.PDB	O, C_GLY_146	N, C_SER_136	H, C_SER_136	2.85	1.90	10.46
1HGE.PDB	OG, C_SER_136	N, C_ALA_138	H, C_ALA_138	2.96	2.02	13.07
1HGE.PDB	O, C_GLY_144	NZ, C_LYS_140	HZ1, C_LYS_140	2.72	1.75	17.13
1HGE.PDB	OD1, C_ASN_137	NZ, C_LYS_140	HZ2, C_LYS_140	2.83	1.86	16.66
1HGE.PDB	OD2, C_ASP_77	NE, C_ARG_141	HE, C_ARG_141	2.80	1.97	26.96
1HGE.PDB	O, C_PHE_147	NH1, C_ARG_141	HH12, C_ARG_141	2.55	1.62	15.87
1HGE.PDB	OD1, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.88	1.96	21.42
1HGE.PDB	OD2, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.74	1.86	24.30
1HGE.PDB	O, C_GLY_72	NH2, C_ARG_141	HH22, C_ARG_141	2.91	1.94	12.79
1HGE.PDB	O, C_GLY_72	N, C_SER_149	H, C_SER_149	2.84	1.92	17.14
1HGE.PDB	O, C_ALA_253	N, C_ASN_152	H, C_ASN_152	2.77	1.90	22.09
1HGE.PDB	OH, C_TYR_195	NE1, C_TRP_153	HE1, C_TRP_153	2.85	1.98	22.78
1HGE.PDB	O, C_LEU_194	N, C_LYS_156	H, C_LYS_156	2.97	2.07	19.03
1HGE.PDB	O, C_THR_160	N, C_SER_157	H, C_SER_157	2.96	2.05	18.03
1HGE.PDB	O, C_SER_247	N, C_LEU_164	H, C_LEU_164	2.70	1.87	25.69
1HGE.PDB	O, C_ILE_245	N, C_VAL_166	H, C_VAL_166	2.88	1.93	12.26
1HGE.PDB	O, C_LEU_243	OG1, C_THR_167	HG1, C_THR_167	2.89	2.00	19.24
1HGE.PDB	O, C_LEU_243	N, C_MET_168	H, C_MET_168	2.95	2.03	16.73
1HGE.PDB	O, C_ASP_241	N, C_ASN_170	H, C_ASN_170	2.90	1.92	6.43
1HGE.PDB	O, C_PHE_174	ND2, C_ASN_170	HD21, C_ASN_170	2.84	1.87	8.31
1HGE.PDB	O, C_VAL_237	ND2, C_ASN_170	HD22, C_ASN_170	2.85	2.06	29.16
1HGE.PDB	O, C_VAL_237	N, C_LYS_176	H, C_LYS_176	2.96	2.03	15.33
1HGE.PDB	OE2, C_GLU_123	NZ, C_LYS_176	HZ1, C_LYS_176	2.71	1.80	23.44
1HGE.PDB	O, C_PHE_258	N, C_LEU_177	H, C_LEU_177	2.95	1.98	5.56
1HGE.PDB	O, C_THR_235	N, C_TYR_178	H, C_TYR_178	2.82	1.85	5.01
1HGE.PDB	OE1, C_GLU_123	OH, C_TYR_178	HH, C_TYR_178	2.73	1.80	12.29
1HGE.PDB	OG1, C_THR_235	NE1, C_TRP_180	HE1, C_TRP_180	2.92	1.93	1.68
1HGE.PDB	O, C_ASN_250	N, C_HIS_183	H, C_HIS_183	2.90	2.00	18.95
1HGE.PDB	O, C_ARG_229	N, C_HIS_184	H, C_HIS_184	2.88	1.92	7.36
1HGE.PDB	OG, C_SER_231	NE2, C_HIS_184	HE2, C_HIS_184	2.71	1.87	25.48
1HGE.PDB	OG1, C_THR_187	N, C_GLU_190	H, C_GLU_190	2.99	2.05	11.81
1HGE.PDB	OD1, C_ASN_250	NE2, C_GLN_191	HE21, C_GLN_191	3.00	2.03	7.73
1HGE.PDB	O, C_GLN_197	NE2, C_GLN_191	HE22, C_GLN_191	2.95	2.03	16.39
1HGE.PDB	O, C_GLN_189	OG1, C_THR_192	HG1, C_THR_192	2.80	1.94	21.49
1HGE.PDB	O, C_GLN_189	N, C_SER_193	H, C_SER_193	2.84	1.90	12.38
1HGE.PDB	O, C_GLU_190	N, C_LEU_194	H, C_LEU_194	3.00	2.03	8.39
1HGE.PDB	O, C_GLN_191	N, C_TYR_195	H, C_TYR_195	2.79	1.84	10.35
1HGE.PDB	O, C_TYR_161	NE2, C_GLN_197	HE21, C_GLN_197	2.87	1.92	10.94
1HGE.PDB	O, C_ASN_248	NE2, C_GLN_197	HE22, C_GLN_197	2.96	2.03	16.11
1HGE.PDB	OD1, C_ASN_246	NH2, C_ARG_201	HH21, C_ARG_201	2.62	1.75	24.53
1HGE.PDB	O, C_ILE_213	N, C_VAL_202	H, C_VAL_202	2.99	2.05	14.11
1HGE.PDB	O, C_ASN_246	N, C_THR_203	H, C_THR_203	2.91	1.96	12.23
1HGE.PDB	OG1, C_THR_212	OG1, C_THR_203	HG1, C_THR_203	2.89	1.94	9.07
1HGE.PDB	O, C_GLN_211	N, C_VAL_204	H, C_VAL_204	2.84	1.94	18.37
1HGE.PDB	O, C_SER_209	N, C_THR_206	H, C_THR_206	2.97	2.00	8.35
1HGE.PDB	OD1, C_ASP_241	N, C_ARG_207	H, C_ARG_207	2.89	1.93	9.60
1HGE.PDB	OG1, C_THR_206	OG, C_SER_209	HG, C_SER_209	2.98	2.03	9.68
1HGE.PDB	OD1, A_ASP_101	NE2, C_GLN_210	HE22, C_GLN_210	2.93	2.07	24.92
1HGE.PDB	O, C_VAL_204	N, C_GLN_211	H, C_GLN_211	2.83	1.91	16.68

1HGE.PDB	O, C_VAL_202	N, C_ILE_213	H, C_ILE_213	2.84	1.91	15.11
1HGE.PDB	ND1, C_HIS_184	N, C_ASN_216	H, C_ASN_216	2.76	1.97	29.84
1HGE.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.64	1.76	23.09
1HGE.PDB	O, C_ASN_216	NH2, C_ARG_220	HH22, C_ARG_220	2.68	1.79	22.17
1HGE.PDB	O, C_LEU_226	N, C_VAL_223	H, C_VAL_223	2.85	1.89	10.14
1HGE.PDB	O, C_CYS_97	NE, C_ARG_224	HE, C_ARG_224	2.86	2.04	28.35
1HGE.PDB	O, C_CYS_97	NH2, C_ARG_224	HH21, C_ARG_224	2.80	1.90	22.90
1HGE.PDB	O, C_VAL_223	N, C_LEU_226	H, C_LEU_226	2.92	1.98	11.69
1HGE.PDB	O, C_SER_228	NH1, C_ARG_229	HH11, C_ARG_229	2.66	1.73	17.65
1HGE.PDB	O, C_PRO_221	NH2, C_ARG_229	HH22, C_ARG_229	2.66	1.70	14.45
1HGE.PDB	OD1, C_ASP_101	OG, C_SER_231	HG, C_SER_231	2.89	1.93	7.03
1HGE.PDB	O, C_ASP_101	N, C_ILE_232	H, C_ILE_232	2.94	2.01	16.06
1HGE.PDB	O, C_TRP_180	N, C_TYR_233	H, C_TYR_233	2.87	1.91	8.74
1HGE.PDB	O, C_TYR_178	N, C_THR_235	H, C_THR_235	2.86	1.95	17.72
1HGE.PDB	O, C_LYS_176	N, C_VAL_237	H, C_VAL_237	2.76	1.86	18.21
1HGE.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.78	1.80	16.75
1HGE.PDB	O, B_SER_71	NZ, C_LYS_238	HZ3, C_LYS_238	2.65	1.71	19.56
1HGE.PDB	O, C_ASN_170	N, C_GLY_240	H, C_GLY_240	2.86	1.99	22.04
1HGE.PDB	O, C_LYS_238	N, C_ASP_241	H, C_ASP_241	2.92	1.99	14.19
1HGE.PDB	OD1, C_ASP_241	N, C_VAL_242	H, C_VAL_242	2.80	1.97	26.99
1HGE.PDB	O, C_MET_168	N, C_LEU_243	H, C_LEU_243	2.92	1.94	4.20
1HGE.PDB	O, C_SER_205	N, C_VAL_244	H, C_VAL_244	2.96	2.01	12.41
1HGE.PDB	O, C_VAL_166	N, C_ILE_245	H, C_ILE_245	2.89	1.96	15.45
1HGE.PDB	O, C_THR_203	N, C_ASN_246	H, C_ASN_246	2.90	1.93	6.52
1HGE.PDB	OD1, C_ASN_165	ND2, C_ASN_246	HD22, C_ASN_246	2.89	1.94	13.09
1HGE.PDB	O, C_LEU_164	N, C_SER_247	H, C_SER_247	2.96	2.05	18.85
1HGE.PDB	O, C_ARG_201	OG, C_SER_247	HG, C_SER_247	2.74	1.95	29.12
1HGE.PDB	OE1, C_GLN_191	ND2, C_ASN_250	HD21, C_ASN_250	2.89	1.93	9.19
1HGE.PDB	O, C_HIS_183	ND2, C_ASN_250	HD22, C_ASN_250	2.90	1.94	11.40
1HGE.PDB	O, C_ASN_152	N, C_ALA_253	H, C_ALA_253	2.88	2.01	23.02
1HGE.PDB	OD1, C_ASN_133	NH2, C_ARG_255	HH22, C_ARG_255	2.48	1.68	29.46
1HGE.PDB	O, C_ILE_121	N, C_TYR_257	H, C_TYR_257	2.98	2.14	25.04
1HGE.PDB	O, C_LEU_177	N, C_PHE_258	H, C_PHE_258	2.95	1.97	4.47
1HGE.PDB	OE2, C_GLU_119	NH1, C_ARG_261	HH12, C_ARG_261	2.65	1.82	27.69
1HGE.PDB	OE1, C_GLU_119	NH2, C_ARG_261	HH22, C_ARG_261	2.84	1.95	24.41
1HGE.PDB	OD2, C_ASP_85	NZ, C_LYS_264	HZ3, C_LYS_264	2.77	1.79	16.79
1HGE.PDB	O, C_PHE_87	N, C_MET_268	H, C_MET_268	2.81	1.93	20.65
1HGE.PDB	O, C_PRO_284	OG, C_SER_270	HG, C_SER_270	2.77	1.85	14.90
1HGE.PDB	OG, C_SER_270	N, C_ALA_272	H, C_ALA_272	2.95	2.00	10.98
1HGE.PDB	O, C_ILE_51	N, C_ASP_275	H, C_ASP_275	2.98	2.09	21.88
1HGE.PDB	OD1, C_ASP_275	N, C_THR_276	H, C_THR_276	2.79	1.93	23.11
1HGE.PDB	O, C_ASN_54	N, C_SER_279	H, C_SER_279	2.78	1.85	13.73
1HGE.PDB	O, C_TYR_302	N, C_ILE_282	H, C_ILE_282	2.90	1.93	4.89
1HGE.PDB	O, C_THR_283	N, C_GLY_286	H, C_GLY_286	2.85	1.91	13.86
1HGE.PDB	O, C_LYS_50	N, C_SER_287	H, C_SER_287	2.85	1.88	3.50
1HGE.PDB	O, C_ALA_304	ND2, C_ASN_290	HD22, C_ASN_290	2.82	1.93	19.75
1HGE.PDB	OE1, C_GLN_44	NZ, C_LYS_292	HZ1, C_LYS_292	2.72	1.72	12.77
1HGE.PDB	OD2, C_ASP_291	NZ, C_LYS_292	HZ3, C_LYS_292	2.84	1.88	19.72
1HGE.PDB	O, C_LYS_307	N, C_GLN_295	H, C_GLN_295	2.83	1.94	20.43
1HGE.PDB	O, C_ASN_298	NE2, C_GLN_295	HE21, C_GLN_295	2.74	1.79	8.05
1HGE.PDB	O, C_GLN_44	N, C_ASN_296	H, C_ASN_296	2.82	1.89	15.19
1HGE.PDB	OE1, C_GLN_295	N, C_VAL_297	H, C_VAL_297	2.70	1.88	26.95
1HGE.PDB	OD1, C_ASN_285	ND2, C_ASN_298	HD22, C_ASN_298	2.99	2.05	12.60
1HGE.PDB	O, D_LYS_68	NZ, C_LYS_299	HZ2, C_LYS_299	2.96	1.94	10.83
1HGE.PDB	OD1, C_ASN_298	N, C_ILE_300	H, C_ILE_300	2.91	2.01	19.01
1HGE.PDB	O, C_ILE_282	N, C_TYR_302	H, C_TYR_302	2.93	2.07	24.01
1HGE.PDB	O, C_LYS_264	OH, C_TYR_302	HH, C_TYR_302	2.65	1.87	29.65
1HGE.PDB	O, D_LYS_62	N, C_GLY_303	H, C_GLY_303	2.94	1.98	10.89

1HGE.PDB	OG, D_SER_93	N, C_LYS_310	H, C_LYS_310	2.92	1.96	11.23
1HGE.PDB	OE2, C_GLU_41	N, C_LEU_314	H, C_LEU_314	2.83	1.89	13.54
1HGE.PDB	OE1, C_GLU_41	NZ, C_LYS_315	HZ3, C_LYS_315	2.82	1.88	21.70
1HGE.PDB	O, C_THR_40	N, C_LEU_316	H, C_LEU_316	2.80	1.84	9.83
1HGE.PDB	OD1, D_ASN_104	N, C_ALA_317	H, C_ALA_317	2.73	1.80	14.37
1HGE.PDB	O, C_ASN_38	N, C_THR_318	H, C_THR_318	2.85	1.95	18.88
1HGE.PDB	O, C_VAL_20	ND2, C_ASN_322	HD21, C_ASN_322	2.96	2.03	15.20
1HGE.PDB	OE2, C_GLU_35	ND2, C_ASN_322	HD22, C_ASN_322	2.89	2.00	20.86
1HGE.PDB	OE1, D_GLU_15	NZ, C_LYS_326	HZ1, C_LYS_326	2.74	1.73	12.73
1HGE.PDB	OXT, C_THR_328	NE2, C_GLN_327	HE22, C_GLN_327	2.97	2.01	12.27
1HGE.PDB	OD2, D_ASP_112	N, D_GLY_1	H2, D_GLY_1	2.75	1.76	15.00
1HGE.PDB	OD1, D_ASP_109	N, D_LEU_2	H, D_LEU_2	2.82	1.93	20.06
1HGE.PDB	OD2, D_ASP_112	N, D_PHE_3	H, D_PHE_3	2.80	2.00	29.38
1HGE.PDB	OD2, D_ASP_112	N, D_GLY_4	H, D_GLY_4	2.92	2.03	19.66
1HGE.PDB	OD1, D_ASP_112	N, D_ALA_5	H, D_ALA_5	2.94	2.04	19.74
1HGE.PDB	O, D_GLY_4	N, D_PHE_9	H, D_PHE_9	2.82	1.88	13.73
1HGE.PDB	O, D_GLY_13	ND2, D_ASN_12	HD22, D_ASN_12	2.81	1.95	23.47
1HGE.PDB	O, C_VAL_323	N, D_GLY_13	H, D_GLY_13	2.71	1.79	14.79
1HGE.PDB	O, C_HIS_17	N, D_TRP_14	H, D_TRP_14	2.88	1.94	13.07
1HGE.PDB	OG1, D_THR_41	N, D_TRP_21	H, D_TRP_21	2.86	1.96	18.92
1HGE.PDB	O, C_GLY_16	N, D_GLY_23	H, D_GLY_23	2.94	2.04	19.95
1HGE.PDB	O, D_ALA_35	N, D_PHE_24	H, D_PHE_24	2.84	1.86	3.41
1HGE.PDB	O, C_CYS_14	N, D_ARG_25	H, D_ARG_25	2.94	1.98	9.40
1HGE.PDB	OE1, D_GLN_34	NE, D_ARG_25	HE, D_ARG_25	2.56	1.76	28.50
1HGE.PDB	O, D_GLY_33	N, D_HIS_26	H, D_HIS_26	2.85	1.95	19.13
1HGE.PDB	O, C_THR_12	N, D_GLN_27	H, D_GLN_27	2.86	1.95	18.04
1HGE.PDB	O, D_GLY_31	N, D_ASN_28	H, D_ASN_28	2.82	1.88	13.03
1HGE.PDB	OD1, D_ASN_28	N, D_GLU_30	H, D_GLU_30	2.96	2.16	29.70
1HGE.PDB	O, D_ASN_28	N, D_GLY_31	H, D_GLY_31	2.97	2.06	18.30
1HGE.PDB	O, D_PHE_24	N, D_ALA_35	H, D_ALA_35	2.79	1.99	28.92
1HGE.PDB	O, D_TYR_22	N, D_ASP_37	H, D_ASP_37	2.72	1.80	13.99
1HGE.PDB	OD2, D_ASP_37	N, D_SER_40	H, D_SER_40	2.88	1.92	10.60
1HGE.PDB	OD2, D_ASP_37	OG, D_SER_40	HG, D_SER_40	2.78	1.93	24.10
1HGE.PDB	O, D_ASP_37	OG1, D_THR_41	HG1, D_THR_41	2.71	1.83	19.19
1HGE.PDB	O, D_LEU_38	N, D_GLN_42	H, D_GLN_42	2.87	1.94	14.92
1HGE.PDB	OD1, D_ASP_46	NE2, D_GLN_42	HE22, D_GLN_42	2.87	1.96	19.33
1HGE.PDB	O, D_LYS_39	N, D_ALA_43	H, D_ALA_43	2.95	2.00	11.25
1HGE.PDB	O, D_SER_40	N, D_ALA_44	H, D_ALA_44	2.93	1.96	3.43
1HGE.PDB	O, D_GLN_42	N, D_ASP_46	H, D_ASP_46	2.80	1.83	3.78
1HGE.PDB	OE2, D_GLU_114	NE2, D_GLN_47	HE21, D_GLN_47	2.99	2.06	16.53
1HGE.PDB	O, D_ALA_43	NE2, D_GLN_47	HE22, D_GLN_47	2.87	1.96	16.48
1HGE.PDB	O, D_ILE_45	N, D_ASN_49	H, D_ASN_49	2.89	1.94	10.31
1HGE.PDB	O, D_ASP_46	N, D_GLY_50	H, D_GLY_50	2.85	1.93	16.23
1HGE.PDB	OG1, D_THR_107	NZ, D_LYS_51	HZ1, D_LYS_51	2.96	1.98	16.83
1HGE.PDB	OE1, D_GLU_103	NZ, D_LYS_51	HZ2, D_LYS_51	2.76	1.73	6.47
1HGE.PDB	ND1, D_HIS_106	NZ, D_LYS_51	HZ3, D_LYS_51	2.77	1.82	18.39
1HGE.PDB	O, D_ILE_48	N, D_LEU_52	H, D_LEU_52	2.84	1.95	19.97
1HGE.PDB	O, D_ASN_49	N, D_ASN_53	H, D_ASN_53	2.80	1.87	13.93
1HGE.PDB	OE1, D_GLU_57	NH1, D_ARG_54	HH11, D_ARG_54	2.82	1.84	12.42
1HGE.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.87	1.89	12.82
1HGE.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.96	1.98	6.23
1HGE.PDB	O, C_LYS_299	NZ, D_LYS_68	HZ1, D_LYS_68	2.92	1.91	12.00
1HGE.PDB	OE2, D_GLU_85	NZ, D_LYS_68	HZ2, D_LYS_68	2.80	1.78	10.75
1HGE.PDB	OG, E_SER_107	N, D_ARG_76	H, D_ARG_76	2.87	1.90	6.58
1HGE.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.79	1.85	14.06
1HGE.PDB	OE2, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.78	1.78	7.91
1HGE.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.63	1.67	11.36
1HGE.PDB	OE1, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.74	1.75	7.04

1HGE.PDB	OE1, D_GLU_74	NE2, D_GLN_78	HE22, D_GLN_78	2.96	1.99	8.03
1HGE.PDB	O, D_GLY_75	N, D_ASP_79	H, D_ASP_79	2.95	2.00	12.34
1HGE.PDB	O, D_ILE_77	N, D_GLU_81	H, D_GLU_81	2.96	2.00	10.54
1HGE.PDB	O, D_ASP_79	N, D_TYR_83	H, D_TYR_83	2.91	1.99	16.75
1HGE.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.58	1.80	29.40
1HGE.PDB	O, D_LEU_80	N, D_VAL_84	H, D_VAL_84	2.82	1.87	12.05
1HGE.PDB	O, D_LYS_82	N, D_ASP_86	H, D_ASP_86	2.94	1.98	8.49
1HGE.PDB	O, D_TYR_83	N, D_THR_87	H, D_THR_87	2.92	1.95	7.61
1HGE.PDB	O, D_VAL_84	N, D_LYS_88	H, D_LYS_88	2.93	2.04	19.95
1HGE.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.71	1.68	6.52
1HGE.PDB	O, D_GLU_85	N, D_ILE_89	H, D_ILE_89	2.88	1.90	2.66
1HGE.PDB	O, D_LYS_88	N, D_TRP_92	H, D_TRP_92	2.96	1.98	4.29
1HGE.PDB	O, D_ILE_89	N, D_SER_93	H, D_SER_93	2.83	1.92	17.54
1HGE.PDB	O, D_ILE_89	OG, D_SER_93	HG, D_SER_93	2.86	1.94	14.79
1HGE.PDB	O, D_ASP_90	N, D_TYR_94	H, D_TYR_94	2.87	1.96	18.12
1HGE.PDB	O, D_TRP_92	N, D_ALA_96	H, D_ALA_96	2.95	2.01	13.60
1HGE.PDB	O, D_TYR_94	N, D_LEU_98	H, D_LEU_98	2.96	1.98	4.20
1HGE.PDB	O, D_ASN_95	N, D_LEU_99	H, D_LEU_99	2.91	1.98	15.66
1HGE.PDB	O, D_LEU_98	N, D_LEU_102	H, D_LEU_102	2.98	2.00	6.37
1HGE.PDB	O, D_LEU_99	N, D_GLU_103	H, D_GLU_103	2.91	1.94	7.56
1HGE.PDB	O, D_VAL_100	N, D_ASN_104	H, D_ASN_104	2.91	1.96	12.51
1HGE.PDB	O, C_LYS_27	ND2, D_ASN_104	HD22, D_ASN_104	2.96	2.00	10.88
1HGE.PDB	O, D_LEU_102	N, D_HIS_106	H, D_HIS_106	2.92	1.97	11.35
1HGE.PDB	O, D_GLU_103	N, D_THR_107	H, D_THR_107	2.85	1.96	20.31
1HGE.PDB	O, D_ASN_104	N, D_ILE_108	H, D_ILE_108	2.91	1.95	9.12
1HGE.PDB	O, D_HIS_106	N, D_LEU_110	H, D_LEU_110	2.80	1.85	9.79
1HGE.PDB	O, D_THR_107	OG1, D_THR_111	HG1, D_THR_111	2.87	1.91	5.65
1HGE.PDB	O, D_ASP_109	N, D_SER_113	H, D_SER_113	2.84	1.89	10.30
1HGE.PDB	O, D_LEU_110	N, D_GLU_114	H, D_GLU_114	2.93	1.97	9.88
1HGE.PDB	O, D_ASP_112	N, D_ASN_116	H, D_ASN_116	2.98	2.01	8.80
1HGE.PDB	O, D_SER_113	N, D_LYS_117	H, D_LYS_117	2.78	1.90	20.87
1HGE.PDB	O, D_MET_115	N, D_PHE_119	H, D_PHE_119	3.00	2.05	13.31
1HGE.PDB	O, D_ASN_116	N, D_GLU_120	H, D_GLU_120	2.94	1.96	2.22
1HGE.PDB	O, D_LYS_117	N, D_LYS_121	H, D_LYS_121	2.93	2.03	20.11
1HGE.PDB	O, D_PHE_119	N, D_ARG_123	H, D_ARG_123	2.91	1.95	8.55
1HGE.PDB	OE2, D_GLU_120	NH1, D_ARG_123	HH11, D_ARG_123	2.83	1.93	23.01
1HGE.PDB	O, D_GLU_120	N, D_ARG_124	H, D_ARG_124	3.00	2.04	10.14
1HGE.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.78	1.98	28.90
1HGE.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.90	2.01	20.41
1HGE.PDB	O, D_LEU_126	N, D_ASN_129	H, D_ASN_129	2.94	1.99	12.91
1HGE.PDB	O, D_HIS_159	ND2, D_ASN_129	HD21, D_ASN_129	2.92	1.97	10.53
1HGE.PDB	OH, D_TYR_157	ND2, D_ASN_129	HD22, D_ASN_129	2.81	1.85	9.24
1HGE.PDB	O, D_LYS_139	N, D_GLU_131	H, D_GLU_131	2.97	2.05	17.56
1HGE.PDB	O, D_CYS_137	N, D_MET_133	H, D_MET_133	2.89	1.93	10.58
1HGE.PDB	O, C_LEU_13	N, D_PHE_138	H, D_PHE_138	2.74	1.87	21.30
1HGE.PDB	O, D_GLU_131	N, D_LYS_139	H, D_LYS_139	2.81	1.87	11.30
1HGE.PDB	O, C_ALA_11	N, D_ILE_140	H, D_ILE_140	2.78	1.88	18.97
1HGE.PDB	O, D_ASN_129	N, D_TYR_141	H, D_TYR_141	2.89	1.95	13.56
1HGE.PDB	OE2, D_GLU_30	N, D_ASN_146	H, D_ASN_146	2.83	1.92	17.98
1HGE.PDB	O, D_ASP_145	N, D_ILE_149	H, D_ILE_149	2.93	1.97	9.93
1HGE.PDB	O, D_ASN_146	N, D_GLU_150	H, D_GLU_150	2.95	2.02	14.34
1HGE.PDB	O, D_ALA_147	N, D_SER_151	H, D_SER_151	2.92	2.03	19.70
1HGE.PDB	O, D_CYS_148	OG, D_SER_151	HG, D_SER_151	2.69	1.84	22.52
1HGE.PDB	O, D_GLU_150	N, D_ASN_154	H, D_ASN_154	2.82	1.85	7.63
1HGE.PDB	O, D_SER_151	N, D_THR_156	H, D_THR_156	2.75	1.94	27.92
1HGE.PDB	OD1, D_ASN_154	OG1, D_THR_156	HG1, D_THR_156	2.74	1.81	12.51
1HGE.PDB	NE2, D_HIS_142	OH, D_TYR_157	HH, D_TYR_157	2.73	1.86	21.01
1HGE.PDB	OD1, D_ASP_158	N, D_ASP_160	H, D_ASP_160	2.84	1.98	23.52

1HGE.PDB	O, D_HIS_159	N, D_TYR_162	H, D_TYR_162	2.91	2.02	20.55
1HGE.PDB	O, D_ASP_160	N, D_ARG_163	H, D_ARG_163	2.99	2.03	9.92
1HGE.PDB	O, B_ARG_170	NH1, D_ARG_163	HH12, D_ARG_163	2.79	1.82	14.16
1HGE.PDB	O, D_TYR_162	N, D_ALA_166	H, D_ALA_166	2.87	1.90	5.91
1HGE.PDB	O, D_ARG_163	N, D_LEU_167	H, D_LEU_167	2.73	1.80	11.73
1HGE.PDB	O, D_ALA_166	N, D_ARG_170	H, D_ARG_170	2.84	1.97	22.00
1HGE.PDB	O, D_GLU_128	NE, D_ARG_170	HE, D_ARG_170	2.74	1.87	22.62
1HGE.PDB	OE2, D_GLU_131	NH1, D_ARG_170	HH11, D_ARG_170	2.79	1.79	6.83
1HGE.PDB	O, D_LEU_167	N, D_PHE_171	H, D_PHE_171	2.89	1.96	14.77
1HGE.PDB	O, F_ILE_140	N, E_ALA_11	H, E_ALA_11	2.82	1.93	19.79
1HGE.PDB	O, F_GLN_27	N, E_THR_12	H, E_THR_12	2.91	1.97	12.43
1HGE.PDB	O, F_PHE_138	N, E_LEU_13	H, E_LEU_13	2.98	2.03	12.93
1HGE.PDB	O, F_ARG_25	N, E_CYS_14	H, E_CYS_14	2.61	1.80	26.88
1HGE.PDB	O, F_GLY_136	N, E_LEU_15	H, E_LEU_15	2.88	1.90	5.56
1HGE.PDB	O, F_GLY_23	N, E_GLY_16	H, E_GLY_16	2.95	2.06	19.95
1HGE.PDB	O, E_HIS_18	ND1, E_HIS_17	HD1, E_HIS_17	2.98	2.10	22.18
1HGE.PDB	O, F_TRP_21	N, E_HIS_18	H, E_HIS_18	2.85	1.97	21.43
1HGE.PDB	OD1, E_ASN_322	N, E_VAL_20	H, E_VAL_20	2.81	1.86	11.30
1HGE.PDB	O, E_VAL_36	N, E_THR_24	H, E_THR_24	2.83	1.94	19.47
1HGE.PDB	O, E_ILE_34	N, E_VAL_26	H, E_VAL_26	2.83	1.88	11.74
1HGE.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.79	1.77	9.75
1HGE.PDB	O, E_LYS_27	OG1, E_THR_28	HG1, E_THR_28	2.99	2.20	29.66
1HGE.PDB	O, E_VAL_26	N, E_ILE_34	H, E_ILE_34	2.89	1.94	12.30
1HGE.PDB	O, E_THR_24	N, E_VAL_36	H, E_VAL_36	2.81	1.85	9.59
1HGE.PDB	O, E_MET_320	N, E_THR_37	H, E_THR_37	2.89	1.91	5.80
1HGE.PDB	O, E_LEU_316	N, E_THR_40	H, E_THR_40	2.78	1.93	24.64
1HGE.PDB	O, E_LEU_314	N, E_LEU_42	H, E_LEU_42	2.80	1.97	26.27
1HGE.PDB	O, E_PHE_294	N, E_GLN_44	H, E_GLN_44	2.81	1.85	6.62
1HGE.PDB	O, E_SER_46	NE2, E_GLN_44	HE22, E_GLN_44	2.85	1.98	22.39
1HGE.PDB	O, E_ASN_285	OG, E_SER_47	HG, E_SER_47	2.87	1.96	16.37
1HGE.PDB	OD2, E_ASP_275	NZ, E_LYS_50	HZ1, E_LYS_50	2.73	1.80	21.86
1HGE.PDB	O, E_PRO_273	N, E_ILE_51	H, E_ILE_51	2.78	1.85	13.53
1HGE.PDB	O, E_ASP_275	N, E_ASN_53	H, E_ASN_53	2.78	1.91	23.30
1HGE.PDB	OD2, E_ASP_85	N, E_ARG_57	H, E_ARG_57	2.91	1.97	12.45
1HGE.PDB	O, E_THR_83	NE, E_ARG_57	HE, E_ARG_57	2.83	1.86	9.17
1HGE.PDB	O, E_LEU_86	N, E_LEU_59	H, E_LEU_59	2.93	1.97	10.59
1HGE.PDB	O, E_VAL_88	N, E_GLY_61	H, E_GLY_61	2.95	2.10	25.32
1HGE.PDB	OD1, E_ASP_60	N, E_ILE_62	H, E_ILE_62	2.86	1.93	15.29
1HGE.PDB	O, E_GLY_61	N, E_CYS_64	H, E_CYS_64	2.87	1.96	17.48
1HGE.PDB	O, E_LEU_66	N, E_LEU_70	H, E_LEU_70	2.86	1.97	20.45
1HGE.PDB	O, E_ILE_67	N, E_LEU_71	H, E_LEU_71	2.83	1.87	6.72
1HGE.PDB	O, E_ASP_68	N, E_GLY_72	H, E_GLY_72	2.87	1.96	17.08
1HGE.PDB	OD1, E_ASP_73	ND1, E_HIS_75	HD1, E_HIS_75	2.77	1.85	16.90
1HGE.PDB	O, E_ASP_63	NE2, E_HIS_75	HE2, E_HIS_75	2.86	1.94	17.47
1HGE.PDB	O, E_ASP_73	N, E_CYS_76	H, E_CYS_76	2.76	1.81	11.37
1HGE.PDB	O, E_PRO_74	N, E_ASP_77	H, E_ASP_77	2.86	1.91	10.86
1HGE.PDB	O, E_CYS_76	N, E_PHE_79	H, E_PHE_79	2.97	1.99	3.02
1HGE.PDB	OE1, E_GLU_82	N, E_THR_83	H, E_THR_83	2.88	1.98	19.27
1HGE.PDB	O, E_ARG_57	N, E_ASP_85	H, E_ASP_85	2.78	1.89	19.36
1HGE.PDB	O, E_LEU_59	N, E_VAL_88	H, E_VAL_88	2.96	1.98	5.16
1HGE.PDB	O, E_MET_268	N, E_GLU_89	H, E_GLU_89	2.77	1.81	8.69
1HGE.PDB	OD1, E_ASP_60	NE, E_ARG_90	HE, E_ARG_90	2.88	1.91	8.59
1HGE.PDB	O, E_SER_270	NH1, E_ARG_90	HH11, E_ARG_90	2.63	1.77	25.17
1HGE.PDB	O, E_ALA_272	NH1, E_ARG_90	HH12, E_ARG_90	2.61	1.68	16.51
1HGE.PDB	OD2, E_ASP_60	NH2, E_ARG_90	HH21, E_ARG_90	2.80	1.80	8.94
1HGE.PDB	OD1, E_ASP_271	N, E_SER_91	H, E_SER_91	2.89	1.92	7.24
1HGE.PDB	OD2, E_ASP_271	OG, E_SER_91	HG, E_SER_91	2.83	1.92	17.26
1HGE.PDB	OD2, E_ASP_68	OG, E_SER_95	HG, E_SER_95	2.91	1.97	13.28

1HGE.PDB	OD2, E_ASP_73	N, E_ASN_96	H, E_ASN_96	2.90	1.94	8.49
1HGE.PDB	OD1, E_ASP_68	OH, E_TYR_100	HH, E_TYR_100	2.88	1.95	14.25
1HGE.PDB	OD2, E_ASP_104	OG, E_SER_107	HG, E_SER_107	2.86	1.93	15.15
1HGE.PDB	O, E_TYR_105	N, E_ARG_109	H, E_ARG_109	2.86	1.88	1.80
1HGE.PDB	OE2, F_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.78	1.79	11.63
1HGE.PDB	OD2, D_ASP_79	OG, E_SER_110	HG, E_SER_110	2.82	1.89	14.19
1HGE.PDB	O, E_SER_107	N, E_LEU_111	H, E_LEU_111	2.87	1.89	3.10
1HGE.PDB	O, E_ARG_109	N, E_ALA_113	H, E_ALA_113	2.93	2.03	20.07
1HGE.PDB	O, E_SER_110	N, E_SER_114	H, E_SER_114	2.88	1.93	13.24
1HGE.PDB	OE2, E_GLU_119	OG1, E_THR_117	HG1, E_THR_117	2.93	1.97	8.29
1HGE.PDB	O, E_GLU_82	N, E_LEU_118	H, E_LEU_118	2.98	2.05	15.39
1HGE.PDB	O, E_TYR_257	N, E_ILE_121	H, E_ILE_121	2.89	1.92	6.39
1HGE.PDB	O, E_ARG_255	N, E_GLU_123	H, E_GLU_123	2.92	1.96	10.72
1HGE.PDB	O, E_THR_155	N, E_THR_131	H, E_THR_131	2.77	1.88	19.94
1HGE.PDB	OD1, E_ASN_152	N, E_ASN_133	H, E_ASN_133	2.90	1.97	15.58
1HGE.PDB	O, E_TRP_153	N, E_GLY_134	H, E_GLY_134	2.95	2.06	19.92
1HGE.PDB	O, E_GLY_146	N, E_SER_136	H, E_SER_136	2.84	1.87	9.56
1HGE.PDB	OG, E_SER_136	N, E_ALA_138	H, E_ALA_138	2.99	2.05	13.25
1HGE.PDB	O, E_GLY_144	NZ, E_LYS_140	HZ1, E_LYS_140	2.71	1.74	16.73
1HGE.PDB	OD1, E_ASN_137	NZ, E_LYS_140	HZ2, E_LYS_140	2.84	1.86	16.83
1HGE.PDB	OD2, E_ASP_77	NE, E_ARG_141	HE, E_ARG_141	2.80	1.96	26.48
1HGE.PDB	O, E_PHE_147	NH1, E_ARG_141	HH12, E_ARG_141	2.55	1.62	17.30
1HGE.PDB	OD1, E_ASP_77	NH2, E_ARG_141	HH21, E_ARG_141	2.91	2.00	21.55
1HGE.PDB	OD2, E_ASP_77	NH2, E_ARG_141	HH21, E_ARG_141	2.75	1.87	24.36
1HGE.PDB	O, E_GLY_72	NH2, E_ARG_141	HH22, E_ARG_141	2.92	1.95	12.66
1HGE.PDB	O, E_GLY_72	N, E_SER_149	H, E_SER_149	2.84	1.93	17.58
1HGE.PDB	OD1, E_ASP_77	OG, E_SER_149	HG, E_SER_149	2.99	2.14	24.93
1HGE.PDB	O, E_ALA_253	N, E_ASN_152	H, E_ASN_152	2.82	1.95	22.18
1HGE.PDB	OH, E_TYR_195	NE1, E_TRP_153	HE1, E_TRP_153	2.90	1.99	18.82
1HGE.PDB	O, E_LEU_194	N, E_LYS_156	H, E_LYS_156	2.96	2.06	18.56
1HGE.PDB	O, E_SER_193	NZ, E_LYS_156	HZ2, E_LYS_156	2.79	1.81	17.51
1HGE.PDB	O, E_THR_160	N, E_SER_157	H, E_SER_157	2.99	2.08	19.06
1HGE.PDB	O, E_SER_247	N, E_LEU_164	H, E_LEU_164	2.69	1.86	25.19
1HGE.PDB	O, E_ILE_245	N, E_VAL_166	H, E_VAL_166	2.91	1.96	12.45
1HGE.PDB	O, E_LEU_243	OG1, E_THR_167	HG1, E_THR_167	2.92	2.05	21.37
1HGE.PDB	O, E_LEU_243	N, E_MET_168	H, E_MET_168	2.94	2.02	16.59
1HGE.PDB	O, E_ASP_241	N, E_ASN_170	H, E_ASN_170	2.92	1.94	6.42
1HGE.PDB	O, E_PHE_174	ND2, E_ASN_170	HD21, E_ASN_170	2.85	1.88	8.67
1HGE.PDB	O, E_VAL_237	ND2, E_ASN_170	HD22, E_ASN_170	2.84	2.05	29.41
1HGE.PDB	O, E_VAL_237	N, E_LYS_176	H, E_LYS_176	2.97	2.04	15.22
1HGE.PDB	OE2, E_GLU_123	NZ, E_LYS_176	HZ1, E_LYS_176	2.73	1.81	23.24
1HGE.PDB	O, E_PHE_258	N, E_LEU_177	H, E_LEU_177	2.99	2.02	5.44
1HGE.PDB	O, E_THR_235	N, E_TYR_178	H, E_TYR_178	2.85	1.89	6.94
1HGE.PDB	OE1, E_GLU_123	OH, E_TYR_178	HH, E_TYR_178	2.75	1.82	12.06
1HGE.PDB	O, E_TYR_233	N, E_TRP_180	H, E_TRP_180	2.98	2.01	9.33
1HGE.PDB	OG1, E_THR_235	NE1, E_TRP_180	HE1, E_TRP_180	2.93	1.94	2.48
1HGE.PDB	O, E_ASN_250	N, E_HIS_183	H, E_HIS_183	2.93	2.02	18.57
1HGE.PDB	O, E_ARG_229	N, E_HIS_184	H, E_HIS_184	2.91	1.95	9.81
1HGE.PDB	OG, E_SER_231	NE2, E_HIS_184	HE2, E_HIS_184	2.75	1.91	25.72
1HGE.PDB	OG1, E_THR_187	N, E_GLU_190	H, E_GLU_190	3.00	2.05	12.79
1HGE.PDB	O, E_GLN_197	NE2, E_GLN_191	HE22, E_GLN_191	2.96	2.04	16.74
1HGE.PDB	O, E_GLN_189	N, E_SER_193	H, E_SER_193	2.85	1.87	3.50
1HGE.PDB	O, E_GLU_190	N, E_LEU_194	H, E_LEU_194	2.96	2.00	9.57
1HGE.PDB	O, E_GLN_191	N, E_TYR_195	H, E_TYR_195	2.77	1.82	10.43
1HGE.PDB	O, E_TYR_161	NE2, E_GLN_197	HE21, E_GLN_197	2.88	1.92	10.46
1HGE.PDB	O, E_ASN_248	NE2, E_GLN_197	HE22, E_GLN_197	2.96	2.02	14.87
1HGE.PDB	OD1, E_ASN_246	NH2, E_ARG_201	HH21, E_ARG_201	2.61	1.75	25.36
1HGE.PDB	O, E_ILE_213	N, E_VAL_202	H, E_VAL_202	2.98	2.03	12.89

1HGE.PDB	O, E_ASN_246	N, E_THR_203	H, E_THR_203	2.89	1.93	9.46
1HGE.PDB	OG1, E_THR_212	OG1, E_THR_203	HG1, E_THR_203	2.89	1.95	10.14
1HGE.PDB	O, E_GLN_211	N, E_VAL_204	H, E_VAL_204	2.86	1.96	18.79
1HGE.PDB	OD1, E_ASP_241	N, E_ARG_207	H, E_ARG_207	2.88	1.92	9.18
1HGE.PDB	OG1, E_THR_206	OG, E_SER_209	HG, E_SER_209	2.98	2.04	10.06
1HGE.PDB	OD1, C_ASP_101	NE2, E_GLN_210	HE22, E_GLN_210	2.89	2.04	25.02
1HGE.PDB	O, E_VAL_204	N, E_GLN_211	H, E_GLN_211	2.84	1.92	15.49
1HGE.PDB	O, E_VAL_202	N, E_ILE_213	H, E_ILE_213	2.85	1.92	15.02
1HGE.PDB	ND1, E_HIS_184	N, E_ASN_216	H, E_ASN_216	2.79	1.98	28.16
1HGE.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.74	1.87	25.04
1HGE.PDB	O, E_ASN_216	NH2, E_ARG_220	HH22, E_ARG_220	2.66	1.79	23.30
1HGE.PDB	O, E_LEU_226	N, E_VAL_223	H, E_VAL_223	2.87	1.91	9.50
1HGE.PDB	O, E_CYS_97	NE, E_ARG_224	HE, E_ARG_224	2.88	2.06	27.97
1HGE.PDB	O, E_CYS_97	NH2, E_ARG_224	HH21, E_ARG_224	2.81	1.92	22.85
1HGE.PDB	O, E_VAL_223	N, E_LEU_226	H, E_LEU_226	2.92	1.97	11.57
1HGE.PDB	O, E_SER_228	NH1, E_ARG_229	HH11, E_ARG_229	2.68	1.75	17.61
1HGE.PDB	O, E_PRO_221	NH2, E_ARG_229	HH22, E_ARG_229	2.62	1.67	14.07
1HGE.PDB	OD1, E_ASP_101	OG, E_SER_231	HG, E_SER_231	2.87	1.92	12.10
1HGE.PDB	O, E_ASP_101	N, E_ILE_232	H, E_ILE_232	2.95	2.02	16.05
1HGE.PDB	O, E_TRP_180	N, E_TYR_233	H, E_TYR_233	2.88	1.91	8.62
1HGE.PDB	O, E_TYR_178	N, E_THR_235	H, E_THR_235	2.87	1.96	17.45
1HGE.PDB	O, E_LYS_176	N, E_VAL_237	H, E_VAL_237	2.79	1.88	17.98
1HGE.PDB	O, D_SER_71	NZ, E_LYS_238	HZ2, E_LYS_238	2.75	1.79	18.19
1HGE.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ3, E_LYS_238	2.85	1.84	12.25
1HGE.PDB	O, E_ASN_170	N, E_GLY_240	H, E_GLY_240	2.89	2.02	22.60
1HGE.PDB	O, E_LYS_238	N, E_ASP_241	H, E_ASP_241	2.92	1.99	13.81
1HGE.PDB	OD1, E_ASP_241	N, E_VAL_242	H, E_VAL_242	2.79	1.97	26.69
1HGE.PDB	O, E_MET_168	N, E_LEU_243	H, E_LEU_243	2.88	1.91	4.05
1HGE.PDB	O, E_SER_205	N, E_VAL_244	H, E_VAL_244	2.98	2.03	12.64
1HGE.PDB	O, E_VAL_166	N, E_ILE_245	H, E_ILE_245	2.88	1.95	14.55
1HGE.PDB	O, E_THR_203	N, E_ASN_246	H, E_ASN_246	2.93	1.96	6.89
1HGE.PDB	OD1, E_ASN_165	ND2, E_ASN_246	HD22, E_ASN_246	2.88	1.93	12.25
1HGE.PDB	O, E_LEU_164	N, E_SER_247	H, E_SER_247	2.96	2.05	17.92
1HGE.PDB	O, E_ARG_201	OG, E_SER_247	HG, E_SER_247	2.74	1.94	28.66
1HGE.PDB	OE1, E_GLN_191	ND2, E_ASN_250	HD21, E_ASN_250	2.94	1.97	8.28
1HGE.PDB	O, E_HIS_183	ND2, E_ASN_250	HD22, E_ASN_250	2.89	1.94	10.81
1HGE.PDB	O, E_ASN_152	N, E_ALA_253	H, E_ALA_253	2.87	2.00	21.77
1HGE.PDB	OD1, E_ASN_133	NH2, E_ARG_255	HH22, E_ARG_255	2.49	1.68	28.65
1HGE.PDB	O, E_ILE_121	N, E_TYR_257	H, E_TYR_257	3.00	2.15	25.48
1HGE.PDB	O, E_LEU_177	N, E_PHE_258	H, E_PHE_258	2.95	1.98	4.40
1HGE.PDB	OE2, E_GLU_119	NH1, E_ARG_261	HH12, E_ARG_261	2.65	1.81	27.82
1HGE.PDB	OE1, E_GLU_119	NH2, E_ARG_261	HH22, E_ARG_261	2.83	1.95	24.52
1HGE.PDB	OD2, E_ASP_85	NZ, E_LYS_264	HZ3, E_LYS_264	2.81	1.83	16.30
1HGE.PDB	O, E_PHE_87	N, E_MET_268	H, E_MET_268	2.79	1.90	20.72
1HGE.PDB	O, E_PRO_284	OG, E_SER_270	HG, E_SER_270	2.79	1.86	13.35
1HGE.PDB	OG, E_SER_270	N, E_ALA_272	H, E_ALA_272	2.97	2.02	11.52
1HGE.PDB	O, E_ILE_51	N, E_ASP_275	H, E_ASP_275	2.97	2.07	20.34
1HGE.PDB	OD1, E_ASP_275	N, E_THR_276	H, E_THR_276	2.78	1.93	23.65
1HGE.PDB	O, E_ASN_54	N, E_SER_279	H, E_SER_279	2.80	1.87	14.21
1HGE.PDB	O, E_TYR_302	N, E_ILE_282	H, E_ILE_282	2.89	1.92	7.96
1HGE.PDB	O, E_THR_283	N, E_GLY_286	H, E_GLY_286	2.82	1.88	11.76
1HGE.PDB	O, E_LYS_50	N, E_SER_287	H, E_SER_287	2.88	1.91	4.05
1HGE.PDB	O, E_ALA_304	ND2, E_ASN_290	HD22, E_ASN_290	2.85	1.96	19.63
1HGE.PDB	OE1, E_GLN_44	NZ, E_LYS_292	HZ1, E_LYS_292	2.72	1.72	11.93
1HGE.PDB	OD2, E_ASP_291	NZ, E_LYS_292	HZ3, E_LYS_292	2.84	1.89	19.87
1HGE.PDB	O, E_LYS_307	N, E_GLN_295	H, E_GLN_295	2.82	1.93	20.26
1HGE.PDB	O, E_ASN_298	NE2, E_GLN_295	HE21, E_GLN_295	2.75	1.80	8.98
1HGE.PDB	O, E_GLN_44	N, E_ASN_296	H, E_ASN_296	2.82	1.88	13.69

1HGE.PDB	OE1, E_GLN_295	N, E_VAL_297	H, E_VAL_297	2.67	1.86	27.79
1HGE.PDB	OD1, E_ASN_285	ND2, E_ASN_298	HD22, E_ASN_298	2.98	2.04	13.10
1HGE.PDB	O, F_LYS_68	NZ, E_LYS_299	HZ2, E_LYS_299	2.95	1.93	11.73
1HGE.PDB	OD1, E_ASN_298	N, E_ILE_300	H, E_ILE_300	2.89	1.97	16.82
1HGE.PDB	O, E_ILE_282	N, E_TYR_302	H, E_TYR_302	2.94	2.07	23.45
1HGE.PDB	O, F_LYS_62	N, E_GLY_303	H, E_GLY_303	2.95	1.98	8.29
1HGE.PDB	OG, F_SER_93	N, E_LYS_310	H, E_LYS_310	2.93	1.97	10.15
1HGE.PDB	OD1, F_ASP_86	NZ, E_LYS_310	HZ3, E_LYS_310	2.86	2.02	29.64
1HGE.PDB	OE2, E_GLU_41	N, E_LEU_314	H, E_LEU_314	2.81	1.89	15.15
1HGE.PDB	OE1, E_GLU_41	NZ, E_LYS_315	HZ3, E_LYS_315	2.80	1.87	22.54
1HGE.PDB	O, E_THR_40	N, E_LEU_316	H, E_LEU_316	2.80	1.85	9.95
1HGE.PDB	OD1, F_ASN_104	N, E_ALA_317	H, E_ALA_317	2.73	1.80	13.22
1HGE.PDB	O, E_ASN_38	N, E_THR_318	H, E_THR_318	2.85	1.93	15.97
1HGE.PDB	O, E_VAL_20	ND2, E_ASN_322	HD21, E_ASN_322	2.99	2.07	17.11
1HGE.PDB	OE2, E_GLU_35	ND2, E_ASN_322	HD22, E_ASN_322	2.87	1.98	21.90
1HGE.PDB	O, E_GLN_327	NZ, E_LYS_326	HZ1, E_LYS_326	2.74	1.86	25.33
1HGE.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.99	2.00	17.08
1HGE.PDB	O, E_LYS_326	NE2, E_GLN_327	HE22, E_GLN_327	2.76	1.89	22.95
1HGE.PDB	OD2, F_ASP_112	N, F_GLY_1	H2, F_GLY_1	2.78	1.80	14.95
1HGE.PDB	OD1, F_ASP_109	N, F_LEU_2	H, F_LEU_2	2.80	1.91	20.53
1HGE.PDB	OD2, F_ASP_112	N, F_GLY_4	H, F_GLY_4	2.92	2.04	21.78
1HGE.PDB	OD1, F_ASP_112	N, F_ALA_5	H, F_ALA_5	2.92	2.02	19.47
1HGE.PDB	O, F_GLY_4	N, F_PHE_9	H, F_PHE_9	2.81	1.87	11.92
1HGE.PDB	O, F_GLY_13	ND2, F_ASN_12	HD22, F_ASN_12	2.79	1.96	26.47
1HGE.PDB	O, E_VAL_323	N, F_GLY_13	H, F_GLY_13	2.72	1.79	12.93
1HGE.PDB	O, E_HIS_17	N, F_TRP_14	H, F_TRP_14	2.85	1.91	12.63
1HGE.PDB	OG1, F_THR_41	N, F_TRP_21	H, F_TRP_21	2.88	1.97	17.81
1HGE.PDB	O, E_GLY_16	N, F_GLY_23	H, F_GLY_23	2.91	2.01	19.90
1HGE.PDB	O, F_ALA_35	N, F_PHE_24	H, F_PHE_24	2.82	1.85	3.58
1HGE.PDB	O, E_CYS_14	N, F_ARG_25	H, F_ARG_25	2.88	1.93	12.79
1HGE.PDB	OE1, F_GLN_34	NE, F_ARG_25	HE, F_ARG_25	2.92	2.07	24.83
1HGE.PDB	OE1, F_GLN_34	NH2, F_ARG_25	HH21, F_ARG_25	2.81	1.90	20.25
1HGE.PDB	O, F_GLY_33	N, F_HIS_26	H, F_HIS_26	2.96	2.07	20.60
1HGE.PDB	O, E_THR_12	N, F_GLN_27	H, F_GLN_27	2.82	1.90	16.16
1HGE.PDB	O, F_GLY_31	N, F_ASN_28	H, F_ASN_28	2.84	1.88	9.14
1HGE.PDB	OD1, F_ASN_146	ND2, F_ASN_28	HD21, F_ASN_28	2.81	1.89	15.75
1HGE.PDB	O, F_CYS_144	ND2, F_ASN_28	HD22, F_ASN_28	2.90	1.97	14.42
1HGE.PDB	O, F_ASN_28	N, F_GLY_31	H, F_GLY_31	2.92	2.08	25.93
1HGE.PDB	O, F_PHE_24	N, F_ALA_35	H, F_ALA_35	2.77	1.97	29.32
1HGE.PDB	O, F_TYR_22	N, F_ASP_37	H, F_ASP_37	2.73	1.79	11.31
1HGE.PDB	OD2, F_ASP_37	N, F_SER_40	H, F_SER_40	2.89	1.93	8.53
1HGE.PDB	OD2, F_ASP_37	OG, F_SER_40	HG, F_SER_40	2.76	1.94	26.96
1HGE.PDB	O, F_ASP_37	OG1, F_THR_41	HG1, F_THR_41	2.69	1.84	22.88
1HGE.PDB	O, F_LEU_38	N, F_GLN_42	H, F_GLN_42	2.83	1.92	17.33
1HGE.PDB	OD1, F_ASP_46	NE2, F_GLN_42	HE22, F_GLN_42	2.86	1.96	19.38
1HGE.PDB	O, F_LYS_39	N, F_ALA_43	H, F_ALA_43	2.93	1.98	9.94
1HGE.PDB	O, F_SER_40	N, F_ALA_44	H, F_ALA_44	2.92	1.94	4.84
1HGE.PDB	O, F_GLN_42	N, F_ASP_46	H, F_ASP_46	2.81	1.84	1.16
1HGE.PDB	OE2, F_GLU_114	NE2, F_GLN_47	HE21, F_GLN_47	3.00	2.09	17.78
1HGE.PDB	O, F_ALA_43	NE2, F_GLN_47	HE22, F_GLN_47	2.91	2.00	18.24
1HGE.PDB	O, F_ILE_45	N, F_ASN_49	H, F_ASN_49	2.83	1.89	13.28
1HGE.PDB	O, F_ASP_46	N, F_GLY_50	H, F_GLY_50	2.83	1.91	17.15
1HGE.PDB	OG1, F_THR_107	NZ, F_LYS_51	HZ1, F_LYS_51	2.97	2.00	18.12
1HGE.PDB	OE1, F_GLU_103	NZ, F_LYS_51	HZ2, F_LYS_51	2.77	1.74	6.40
1HGE.PDB	ND1, F_HIS_106	NZ, F_LYS_51	HZ3, F_LYS_51	2.74	1.79	17.89
1HGE.PDB	O, F_ILE_48	N, F_LEU_52	H, F_LEU_52	2.89	1.97	17.49
1HGE.PDB	O, F_ASN_49	N, F_ASN_53	H, F_ASN_53	2.78	1.88	17.70
1HGE.PDB	OE1, F_GLU_57	NH1, F_ARG_54	HH11, F_ARG_54	2.82	1.83	11.59

1HGE.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.80	1.82	12.52
1HGE.PDB	OD2, D_ASP_90	NZ, F_LYS_62	HZ2, F_LYS_62	2.67	1.83	29.15
1HGE.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.94	1.97	9.11
1HGE.PDB	O, E_LYS_299	NZ, F_LYS_68	HZ1, F_LYS_68	2.97	1.93	4.62
1HGE.PDB	OE2, F_GLU_85	NZ, F_LYS_68	HZ2, F_LYS_68	2.75	1.78	18.51
1HGE.PDB	OG, A_SER_107	N, F_ARG_76	H, F_ARG_76	2.81	1.83	4.38
1HGE.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.85	1.89	11.64
1HGE.PDB	OE2, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.73	1.73	6.19
1HGE.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.65	1.66	5.51
1HGE.PDB	OE1, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.70	1.73	9.07
1HGE.PDB	OE1, F_GLU_74	NE2, F_GLN_78	HE22, F_GLN_78	2.96	1.99	8.87
1HGE.PDB	O, F_GLY_75	N, F_ASP_79	H, F_ASP_79	2.92	1.98	13.37
1HGE.PDB	O, F_ILE_77	N, F_GLU_81	H, F_GLU_81	2.95	1.99	8.53
1HGE.PDB	O, F_ASP_79	N, F_TYR_83	H, F_TYR_83	2.94	2.02	17.09
1HGE.PDB	OE1, B_GLU_85	OH, F_TYR_83	HH, F_TYR_83	2.51	1.76	30.00
1HGE.PDB	O, F_LEU_80	N, F_VAL_84	H, F_VAL_84	2.83	1.87	8.33
1HGE.PDB	O, F_LYS_82	N, F_ASP_86	H, F_ASP_86	2.92	1.97	11.17
1HGE.PDB	O, F_TYR_83	N, F_THR_87	H, F_THR_87	2.93	1.97	9.90
1HGE.PDB	O, F_VAL_84	N, F_LYS_88	H, F_LYS_88	2.95	2.01	12.83
1HGE.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.67	1.65	8.34
1HGE.PDB	O, F_GLU_85	N, F_ILE_89	H, F_ILE_89	2.92	1.94	4.91
1HGE.PDB	O, F_LYS_88	N, F_TRP_92	H, F_TRP_92	2.97	2.00	5.01
1HGE.PDB	O, F_ILE_89	N, F_SER_93	H, F_SER_93	2.84	1.93	17.22
1HGE.PDB	O, F_ILE_89	OG, F_SER_93	HG, F_SER_93	2.85	1.93	13.60
1HGE.PDB	O, F_ASP_90	N, F_TYR_94	H, F_TYR_94	2.85	1.93	16.45
1HGE.PDB	O, F_TYR_94	N, F_LEU_98	H, F_LEU_98	2.97	1.99	3.80
1HGE.PDB	O, F_ASN_95	N, F_LEU_99	H, F_LEU_99	2.92	1.99	14.65
1HGE.PDB	O, F_LEU_98	N, F_LEU_102	H, F_LEU_102	2.96	1.98	4.54
1HGE.PDB	O, F_LEU_99	N, F_GLU_103	H, F_GLU_103	2.90	1.93	9.01
1HGE.PDB	O, F_VAL_100	N, F_ASN_104	H, F_ASN_104	2.88	1.94	12.72
1HGE.PDB	O, E_LYS_27	ND2, F_ASN_104	HD22, F_ASN_104	2.94	1.99	10.01
1HGE.PDB	O, F_LEU_102	N, F_HIS_106	H, F_HIS_106	2.93	1.98	10.60
1HGE.PDB	O, F_GLU_103	N, F_THR_107	H, F_THR_107	2.85	1.95	19.04
1HGE.PDB	O, F_ASN_104	N, F_ILE_108	H, F_ILE_108	2.91	1.95	10.63
1HGE.PDB	O, F_HIS_106	N, F_LEU_110	H, F_LEU_110	2.81	1.84	7.77
1HGE.PDB	O, F_THR_107	OG1, F_THR_111	HG1, F_THR_111	2.90	1.93	1.70
1HGE.PDB	O, F_ASP_109	N, F_SER_113	H, F_SER_113	2.83	1.87	8.23
1HGE.PDB	O, F_LEU_110	N, F_GLU_114	H, F_GLU_114	2.90	1.94	9.48
1HGE.PDB	O, F_SER_113	N, F_LYS_117	H, F_LYS_117	2.79	1.89	18.58
1HGE.PDB	O, F_GLU_114	N, F_LEU_118	H, F_LEU_118	2.97	2.01	10.63
1HGE.PDB	O, F_ASN_116	N, F_GLU_120	H, F_GLU_120	2.93	1.96	5.04
1HGE.PDB	O, F_LYS_117	N, F_LYS_121	H, F_LYS_121	2.93	2.01	16.80
1HGE.PDB	O, F_PHE_119	N, F_ARG_123	H, F_ARG_123	2.92	1.96	9.49
1HGE.PDB	OE2, F_GLU_120	NH1, F_ARG_123	HH11, F_ARG_123	2.81	1.92	23.28
1HGE.PDB	O, F_GLU_120	N, F_ARG_124	H, F_ARG_124	2.97	2.00	7.42
1HGE.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.92	2.09	27.36
1HGE.PDB	O, F_LEU_126	N, F_ASN_129	H, F_ASN_129	2.94	2.00	13.52
1HGE.PDB	O, F_HIS_159	ND2, F_ASN_129	HD21, F_ASN_129	2.95	2.00	10.63
1HGE.PDB	OH, F_TYR_157	ND2, F_ASN_129	HD22, F_ASN_129	2.80	1.87	15.30
1HGE.PDB	O, F_LYS_139	N, F_GLU_131	H, F_GLU_131	2.96	2.04	15.90
1HGE.PDB	O, F_CYS_137	N, F_MET_133	H, F_MET_133	2.88	1.92	10.66
1HGE.PDB	O, E_LEU_13	N, F_PHE_138	H, F_PHE_138	2.73	1.86	22.03
1HGE.PDB	O, F_GLU_131	N, F_LYS_139	H, F_LYS_139	2.82	1.86	10.37
1HGE.PDB	O, E_ALA_11	N, F_ILE_140	H, F_ILE_140	2.75	1.87	19.65
1HGE.PDB	O, F_ASN_129	N, F_TYR_141	H, F_TYR_141	2.90	1.98	16.42
1HGE.PDB	O, F_ASP_145	N, F_ILE_149	H, F_ILE_149	2.91	1.95	10.01
1HGE.PDB	O, F_ASN_146	N, F_GLU_150	H, F_GLU_150	2.93	1.99	14.06
1HGE.PDB	O, F_ALA_147	N, F_SER_151	H, F_SER_151	2.92	2.06	23.67

1HGE.PDB	O, F_CYS_148	OG, F_SER_151	HG, F_SER_151	2.68	1.84	23.64
1HGE.PDB	O, F_GLU_150	N, F_ASN_154	H, F_ASN_154	2.79	1.81	1.42
1HGE.PDB	OD1, F_ASP_158	N, F_ASP_160	H, F_ASP_160	2.88	2.02	24.16
1HGE.PDB	O, F_HIS_159	N, F_TYR_162	H, F_TYR_162	2.92	2.01	17.85
1HGE.PDB	O, D_ARG_170	NH1, F_ARG_163	HH12, F_ARG_163	2.95	1.99	14.32
1HGE.PDB	O, F_TYR_162	N, F_ALA_166	H, F_ALA_166	2.88	1.91	5.83
1HGE.PDB	O, F_ARG_163	N, F_LEU_167	H, F_LEU_167	2.74	1.79	10.43
1HGE.PDB	O, F_ALA_166	N, F_ARG_170	H, F_ARG_170	2.84	1.99	23.33
1HGE.PDB	O, F_GLU_128	NE, F_ARG_170	HE, F_ARG_170	2.74	1.87	22.99
1HGE.PDB	OE2, F_GLU_131	NH1, F_ARG_170	HH11, F_ARG_170	2.78	1.79	6.04
1HGE.PDB	O, F_LEU_167	N, F_PHE_171	H, F_PHE_171	2.91	1.98	14.72

Table 1665: 1HGE-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1HGF.PDB	O, B_ILE_140	N, A_ALA_11	H, A_ALA_11	2.90	2.03	22.48
1HGF.PDB	O, B_PHE_138	N, A_LEU_13	H, A_LEU_13	2.96	1.99	8.07
1HGF.PDB	O, B_ARG_25	N, A_CYS_14	H, A_CYS_14	2.98	2.02	8.89
1HGF.PDB	O, B_GLY_136	N, A_LEU_15	H, A_LEU_15	2.92	1.95	7.83
1HGF.PDB	O, B_GLY_23	N, A_GLY_16	H, A_GLY_16	2.92	2.03	19.80
1HGF.PDB	O, B_TRP_21	N, A_HIS_18	H, A_HIS_18	2.92	2.01	18.08
1HGF.PDB	OD1, A_ASN_322	N, A_VAL_20	H, A_VAL_20	2.80	1.83	7.05
1HGF.PDB	O, A_VAL_36	N, A_THR_24	H, A_THR_24	2.86	1.98	20.85
1HGF.PDB	O, A_ILE_34	N, A_VAL_26	H, A_VAL_26	2.85	1.90	12.10
1HGF.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.79	1.86	21.55
1HGF.PDB	O, A_ASP_31	N, A_THR_28	H, A_THR_28	2.70	1.89	28.68
1HGF.PDB	O, A_VAL_26	N, A_ILE_34	H, A_ILE_34	2.96	2.01	12.92
1HGF.PDB	O, A_THR_24	N, A_VAL_36	H, A_VAL_36	2.81	1.84	5.89
1HGF.PDB	O, A_MET_320	N, A_THR_37	H, A_THR_37	2.89	1.91	4.82
1HGF.PDB	O, A_LEU_316	N, A_THR_40	H, A_THR_40	2.76	1.85	17.44
1HGF.PDB	O, A_LEU_314	N, A_LEU_42	H, A_LEU_42	2.79	1.94	25.04
1HGF.PDB	O, A_PHE_294	N, A_GLN_44	H, A_GLN_44	2.99	2.01	3.16
1HGF.PDB	O, A_SER_46	NE2, A_GLN_44	HE21, A_GLN_44	2.84	1.96	21.79
1HGF.PDB	OD2, A_ASP_275	NZ, A_LYS_50	HZ2, A_LYS_50	2.91	1.91	15.13
1HGF.PDB	O, A_PRO_273	N, A_ILE_51	H, A_ILE_51	2.77	1.81	8.80
1HGF.PDB	O, A_ASP_275	N, A_ASN_53	H, A_ASN_53	2.88	1.94	13.18
1HGF.PDB	OD2, A_ASP_85	N, A_ARG_57	H, A_ARG_57	2.93	1.98	11.29
1HGF.PDB	O, A_THR_83	NE, A_ARG_57	HE, A_ARG_57	2.79	1.82	4.94
1HGF.PDB	O, A_LEU_86	N, A_LEU_59	H, A_LEU_59	2.87	1.93	13.63
1HGF.PDB	OD1, A_ASP_60	N, A_ILE_62	H, A_ILE_62	2.92	1.97	12.05
1HGF.PDB	O, A_GLY_61	N, A_CYS_64	H, A_CYS_64	2.90	1.96	15.17
1HGF.PDB	O, A_LEU_66	N, A_LEU_70	H, A_LEU_70	2.80	1.89	17.51
1HGF.PDB	O, A_ILE_67	N, A_LEU_71	H, A_LEU_71	2.92	1.94	5.50
1HGF.PDB	O, A_ASP_68	N, A_GLY_72	H, A_GLY_72	2.85	1.95	18.27
1HGF.PDB	OD1, A_ASP_73	N, A_HIS_75	H, A_HIS_75	2.98	2.09	20.20
1HGF.PDB	OD1, A_ASP_73	ND1, A_HIS_75	HD1, A_HIS_75	2.84	1.91	15.59
1HGF.PDB	O, A_ASP_63	NE2, A_HIS_75	HE2, A_HIS_75	2.88	1.95	16.02
1HGF.PDB	O, A_ASP_73	N, A_CYS_76	H, A_CYS_76	2.81	1.89	15.96
1HGF.PDB	O, A_PRO_74	N, A_ASP_77	H, A_ASP_77	2.94	1.99	11.05
1HGF.PDB	O, A_CYS_76	N, A_PHE_79	H, A_PHE_79	2.97	2.00	8.63
1HGF.PDB	OE1, A_GLU_82	N, A_THR_83	H, A_THR_83	2.98	2.09	20.75
1HGF.PDB	O, A_ARG_57	N, A_ASP_85	H, A_ASP_85	2.83	1.91	16.22
1HGF.PDB	O, A_MET_268	N, A_GLU_89	H, A_GLU_89	2.80	1.87	13.08
1HGF.PDB	OD1, A_ASP_60	NE, A_ARG_90	HE, A_ARG_90	2.77	1.85	16.11
1HGF.PDB	O, A_SER_270	NH1, A_ARG_90	HH11, A_ARG_90	2.64	1.79	25.97
1HGF.PDB	O, A_ALA_272	NH1, A_ARG_90	HH12, A_ARG_90	2.67	1.74	16.70
1HGF.PDB	OD2, A_ASP_60	NH2, A_ARG_90	HH21, A_ARG_90	2.84	1.84	8.73
1HGF.PDB	OD1, A_ASP_271	N, A_SER_91	H, A_SER_91	2.96	1.99	10.09
1HGF.PDB	OD2, A_ASP_271	OG, A_SER_91	HG, A_SER_91	2.85	1.91	12.59
1HGF.PDB	OD2, A_ASP_73	N, A_ASN_96	H, A_ASN_96	2.89	1.95	14.63
1HGF.PDB	O, A_ILE_230	N, A_ASP_101	H, A_ASP_101	2.99	2.15	25.68
1HGF.PDB	OD2, A_ASP_104	OG, A_SER_107	HG, A_SER_107	2.89	1.97	16.55
1HGF.PDB	O, A_TYR_105	N, A_ARG_109	H, A_ARG_109	2.87	1.89	3.75
1HGF.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.92	1.92	10.51
1HGF.PDB	OD2, F_ASP_79	OG, A_SER_110	HG, A_SER_110	2.82	1.90	15.87
1HGF.PDB	O, A_SER_107	N, A_LEU_111	H, A_LEU_111	2.96	2.00	9.75
1HGF.PDB	O, A_LEU_108	N, A_VAL_112	H, A_VAL_112	2.99	2.02	7.62
1HGF.PDB	O, A_ARG_109	N, A_ALA_113	H, A_ALA_113	2.92	2.00	16.71
1HGF.PDB	O, A_SER_110	N, A_SER_114	H, A_SER_114	2.94	2.06	21.84
1HGF.PDB	OE2, A_GLU_119	OG1, A_THR_117	HG1, A_THR_117	2.95	1.98	3.95
1HGF.PDB	O, A_GLU_82	N, A_LEU_118	H, A_LEU_118	2.98	2.00	4.41
1HGF.PDB	O, A_TYR_257	N, A_ILE_121	H, A_ILE_121	2.82	1.84	1.82

1HGF.PDB	O, A_ARG_255	N, A_GLU_123	H, A_GLU_123	2.84	1.88	9.80
1HGF.PDB	O, A_THR_155	N, A_THR_131	H, A_THR_131	2.73	1.79	9.00
1HGF.PDB	O, A_LYS_156	OG1, A_THR_131	HG1, A_THR_131	2.73	1.79	7.60
1HGF.PDB	ND2, A_ASN_152	NE2, A_GLN_132	HE21, A_GLN_132	2.94	2.00	10.26
1HGF.PDB	OD1, A_ASN_152	N, A_ASN_133	H, A_ASN_133	2.91	1.97	13.50
1HGF.PDB	O, A_TRP_153	N, A_GLY_134	H, A_GLY_134	3.00	2.07	15.59
1HGF.PDB	O, A_GLY_146	N, A_SER_136	H, A_SER_136	2.70	1.84	23.70
1HGF.PDB	O, A_GLY_144	NZ, A_LYS_140	HZ2, A_LYS_140	2.83	1.99	29.88
1HGF.PDB	O, A_GLY_144	N, A_ARG_141	H, A_ARG_141	2.92	2.09	26.49
1HGF.PDB	OD2, A_ASP_77	NE, A_ARG_141	HE, A_ARG_141	2.91	2.06	25.46
1HGF.PDB	O, A_PHE_147	NH1, A_ARG_141	HH12, A_ARG_141	2.58	1.65	16.41
1HGF.PDB	OD1, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.84	1.97	26.05
1HGF.PDB	OD2, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.78	1.86	20.91
1HGF.PDB	O, A_SER_136	N, A_GLY_146	H, A_GLY_146	2.98	2.14	25.61
1HGF.PDB	O, A_GLY_72	N, A_SER_149	H, A_SER_149	2.87	1.95	15.87
1HGF.PDB	O, A_ALA_253	N, A_ASN_152	H, A_ASN_152	2.85	1.95	19.48
1HGF.PDB	OH, A_TYR_195	NE1, A_TRP_153	HE1, A_TRP_153	2.84	1.90	13.02
1HGF.PDB	O, A_THR_131	N, A_THR_155	H, A_THR_155	2.99	2.03	10.01
1HGF.PDB	O, A_LEU_194	N, A_LYS_156	H, A_LYS_156	2.84	1.97	22.10
1HGF.PDB	O, A_THR_160	N, A_SER_157	H, A_SER_157	3.00	2.11	20.90
1HGF.PDB	O, A_SER_247	N, A_LEU_164	H, A_LEU_164	2.70	1.86	25.60
1HGF.PDB	O, A_ILE_245	N, A_VAL_166	H, A_VAL_166	2.89	1.93	10.88
1HGF.PDB	O, A_LEU_243	N, A_MET_168	H, A_MET_168	3.00	2.06	14.85
1HGF.PDB	O, A_ASP_241	N, A_ASN_170	H, A_ASN_170	2.88	1.90	0.71
1HGF.PDB	O, A_PHE_174	ND2, A_ASN_170	HD22, A_ASN_170	2.75	1.81	11.59
1HGF.PDB	O, A_VAL_237	N, A_LYS_176	H, A_LYS_176	2.94	2.04	19.01
1HGF.PDB	OE2, A_GLU_123	NZ, A_LYS_176	HZ1, A_LYS_176	2.72	1.80	23.85
1HGF.PDB	O, A_THR_235	N, A_TYR_178	H, A_TYR_178	2.82	1.85	7.11
1HGF.PDB	OG1, A_THR_235	NE1, A_TRP_180	HE1, A_TRP_180	2.87	1.89	5.46
1HGF.PDB	O, A_ASN_250	N, A_HIS_183	H, A_HIS_183	2.77	1.92	24.91
1HGF.PDB	OH, A_TYR_98	NE2, A_HIS_183	HE2, A_HIS_183	2.90	1.98	15.32
1HGF.PDB	O, A_ARG_229	N, A_HIS_184	H, A_HIS_184	2.84	1.88	9.30
1HGF.PDB	OG, A_SER_231	NE2, A_HIS_184	HE2, A_HIS_184	2.68	1.88	29.05
1HGF.PDB	OD1, A_ASN_250	NE2, A_GLN_191	HE22, A_GLN_191	2.90	1.94	8.27
1HGF.PDB	O, A_ASN_188	N, A_THR_192	H, A_THR_192	2.96	2.06	18.82
1HGF.PDB	O, A_GLN_189	N, A_SER_193	H, A_SER_193	2.83	1.90	13.84
1HGF.PDB	O, A_GLU_190	N, A_LEU_194	H, A_LEU_194	2.93	1.96	8.30
1HGF.PDB	O, A_GLN_191	N, A_TYR_195	H, A_TYR_195	2.75	1.81	10.35
1HGF.PDB	O, A_TYR_195	N, A_GLN_197	H, A_GLN_197	2.73	1.94	29.33
1HGF.PDB	O, A_ASN_248	NE2, A_GLN_197	HE21, A_GLN_197	2.87	2.00	23.13
1HGF.PDB	O, A_TYR_161	NE2, A_GLN_197	HE22, A_GLN_197	2.98	2.03	11.50
1HGF.PDB	O, A_ILE_213	N, A_VAL_202	H, A_VAL_202	2.99	2.02	6.97
1HGF.PDB	O, A_ASN_246	N, A_THR_203	H, A_THR_203	2.96	2.06	19.01
1HGF.PDB	O, A_GLN_211	N, A_VAL_204	H, A_VAL_204	2.92	1.99	15.84
1HGF.PDB	O, A_SER_209	N, A_THR_206	H, A_THR_206	2.95	2.03	15.35
1HGF.PDB	OD1, A_ASP_241	N, A_ARG_207	H, A_ARG_207	2.92	1.95	7.62
1HGF.PDB	O, A_VAL_204	N, A_GLN_211	H, A_GLN_211	2.87	1.98	21.25
1HGF.PDB	OG1, A_THR_203	OG1, A_THR_212	HG1, A_THR_212	2.83	1.91	15.11
1HGF.PDB	O, A_VAL_202	N, A_ILE_213	H, A_ILE_213	2.85	1.94	17.93
1HGF.PDB	ND1, A_HIS_184	N, A_ASN_216	H, A_ASN_216	2.73	1.89	25.27
1HGF.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.64	1.76	23.62
1HGF.PDB	O, A_ASN_216	NH2, A_ARG_220	HH22, A_ARG_220	2.77	1.87	21.15
1HGF.PDB	O, A_LEU_226	N, A_VAL_223	H, A_VAL_223	2.86	1.91	11.57
1HGF.PDB	O, A_CYS_97	NE, A_ARG_224	HE, A_ARG_224	2.81	1.94	23.65
1HGF.PDB	O, A_CYS_97	NH2, A_ARG_224	HH21, A_ARG_224	2.95	2.11	27.74
1HGF.PDB	O, A_VAL_223	N, A_LEU_226	H, A_LEU_226	2.93	1.98	11.09
1HGF.PDB	O, A_SER_228	NH1, A_ARG_229	HH11, A_ARG_229	2.75	1.83	19.84
1HGF.PDB	O, A_PRO_221	NH2, A_ARG_229	HH22, A_ARG_229	2.63	1.68	15.15

1HGF.PDB	O, A_PRO_99	N, A_ILE_230	H, A_ILE_230	2.95	2.09	24.07
1HGF.PDB	OD1, A_ASP_101	OG, A_SER_231	HG, A_SER_231	2.83	1.87	7.29
1HGF.PDB	O, A_ASP_101	N, A_ILE_232	H, A_ILE_232	2.89	1.95	14.12
1HGF.PDB	O, A_TRP_180	N, A_TYR_233	H, A_TYR_233	2.93	1.97	10.39
1HGF.PDB	O, A_TYR_178	N, A_THR_235	H, A_THR_235	2.85	1.97	21.16
1HGF.PDB	O, A_LYS_176	N, A_VAL_237	H, A_VAL_237	2.78	1.84	14.11
1HGF.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ2, A_LYS_238	2.85	1.85	14.58
1HGF.PDB	O, F_SER_71	NZ, A_LYS_238	HZ3, A_LYS_238	2.63	1.67	16.71
1HGF.PDB	O, A_ASN_170	N, A_GLY_240	H, A_GLY_240	2.91	2.09	27.97
1HGF.PDB	O, A_MET_168	N, A_LEU_243	H, A_LEU_243	2.94	1.98	7.98
1HGF.PDB	O, A_SER_205	N, A_VAL_244	H, A_VAL_244	2.89	1.97	15.63
1HGF.PDB	O, A_VAL_166	N, A_ILE_245	H, A_ILE_245	2.94	2.01	15.58
1HGF.PDB	O, A_THR_203	N, A_ASN_246	H, A_ASN_246	2.92	1.96	10.40
1HGF.PDB	OD1, A_ASN_165	ND2, A_ASN_246	HD21, A_ASN_246	2.93	2.03	19.92
1HGF.PDB	O, A_LEU_164	N, A_SER_247	H, A_SER_247	2.90	2.00	19.06
1HGF.PDB	OG, A_SER_247	N, A_GLY_249	H, A_GLY_249	2.99	2.00	4.05
1HGF.PDB	O, A_HIS_183	ND2, A_ASN_250	HD21, A_ASN_250	2.77	1.81	6.63
1HGF.PDB	OE1, A_GLN_191	ND2, A_ASN_250	HD22, A_ASN_250	2.86	1.90	9.57
1HGF.PDB	O, A_ASN_152	N, A_ALA_253	H, A_ALA_253	2.98	2.05	15.63
1HGF.PDB	OD1, A_ASN_133	NH2, A_ARG_255	HH22, A_ARG_255	2.49	1.67	28.52
1HGF.PDB	O, A_LEU_177	N, A_PHE_258	H, A_PHE_258	2.98	2.01	4.56
1HGF.PDB	OE1, A_GLU_119	NH2, A_ARG_261	HH22, A_ARG_261	2.74	1.90	27.76
1HGF.PDB	O, A_PHE_87	N, A_MET_268	H, A_MET_268	2.93	2.03	19.50
1HGF.PDB	O, A_PRO_284	OG, A_SER_270	HG, A_SER_270	2.80	1.83	2.11
1HGF.PDB	OG, A_SER_270	N, A_ALA_272	H, A_ALA_272	2.94	2.02	16.24
1HGF.PDB	O, A_ILE_51	N, A_ASP_275	H, A_ASP_275	2.90	2.00	18.80
1HGF.PDB	OD1, A_ASP_275	N, A_THR_276	H, A_THR_276	2.77	1.92	24.49
1HGF.PDB	O, A_ASN_54	N, A_SER_279	H, A_SER_279	2.78	1.84	13.06
1HGF.PDB	O, A_TYR_302	N, A_ILE_282	H, A_ILE_282	2.94	1.97	5.53
1HGF.PDB	O, A_THR_283	N, A_GLY_286	H, A_GLY_286	2.80	1.86	12.05
1HGF.PDB	O, A_LYS_50	N, A_SER_287	H, A_SER_287	2.81	1.89	15.58
1HGF.PDB	O, A_ALA_304	ND2, A_ASN_290	HD21, A_ASN_290	2.79	1.88	15.92
1HGF.PDB	OE1, A_GLN_44	NZ, A_LYS_292	HZ1, A_LYS_292	2.87	1.83	0.68
1HGF.PDB	OD1, A_ASP_291	NZ, A_LYS_292	HZ2, A_LYS_292	2.86	1.83	8.47
1HGF.PDB	O, A_LYS_307	N, A_GLN_295	H, A_GLN_295	2.82	1.98	25.98
1HGF.PDB	O, A_ASN_298	NE2, A_GLN_295	HE22, A_GLN_295	2.74	1.81	14.12
1HGF.PDB	O, A_GLN_44	N, A_ASN_296	H, A_ASN_296	2.86	1.90	9.96
1HGF.PDB	OD1, A_ASN_298	N, A_ILE_300	H, A_ILE_300	2.89	2.00	19.34
1HGF.PDB	O, A_ILE_282	N, A_TYR_302	H, A_TYR_302	2.80	1.95	24.99
1HGF.PDB	O, B_LYS_62	N, A_GLY_303	H, A_GLY_303	2.90	1.93	4.88
1HGF.PDB	O, A_GLN_295	N, A_VAL_309	H, A_VAL_309	2.94	2.08	24.38
1HGF.PDB	OG, B_SER_93	N, A_LYS_310	H, A_LYS_310	2.89	1.97	16.03
1HGF.PDB	OE1, A_GLU_41	OG1, A_THR_313	HG1, A_THR_313	2.68	1.87	27.57
1HGF.PDB	OE2, A_GLU_41	N, A_LEU_314	H, A_LEU_314	2.78	1.85	12.25
1HGF.PDB	OG1, A_THR_313	NZ, A_LYS_315	HZ2, A_LYS_315	2.95	2.00	20.61
1HGF.PDB	O, A_THR_40	N, A_LEU_316	H, A_LEU_316	2.77	1.84	13.98
1HGF.PDB	OD1, B_ASN_104	N, A_ALA_317	H, A_ALA_317	2.74	1.82	15.07
1HGF.PDB	O, A_ASN_38	N, A_THR_318	H, A_THR_318	2.85	1.92	14.74
1HGF.PDB	OE2, A_GLU_35	ND2, A_ASN_322	HD21, A_ASN_322	2.76	1.93	26.44
1HGF.PDB	O, A_VAL_20	ND2, A_ASN_322	HD22, A_ASN_322	2.95	2.02	15.09
1HGF.PDB	O, A_PRO_21	NE2, A_GLN_327	HE21, A_GLN_327	2.80	2.01	29.67
1HGF.PDB	OD2, B_ASP_112	N, B_GLY_1	H1, B_GLY_1	2.90	1.93	18.51
1HGF.PDB	OD1, B_ASP_109	N, B_LEU_2	H, B_LEU_2	2.91	2.01	19.54
1HGF.PDB	OD2, B_ASP_112	N, B_PHE_3	H, B_PHE_3	2.80	1.99	27.59
1HGF.PDB	OD2, B_ASP_112	N, B_GLY_4	H, B_GLY_4	2.97	2.05	16.11
1HGF.PDB	OD1, B_ASP_112	N, B_ALA_5	H, B_ALA_5	2.98	2.10	21.76
1HGF.PDB	O, B_GLY_4	N, B_PHE_9	H, B_PHE_9	2.80	1.88	14.94
1HGF.PDB	O, B_GLY_13	ND2, B_ASN_12	HD21, B_ASN_12	2.79	1.93	22.97

1HGF.PDB	O, A_VAL_323	N, B_GLY_13	H, B_GLY_13	2.74	1.86	21.47
1HGF.PDB	O, A_HIS_17	N, B_TRP_14	H, B_TRP_14	2.87	1.97	19.18
1HGF.PDB	OG1, B_THR_41	N, B_TRP_21	H, B_TRP_21	2.88	1.96	17.54
1HGF.PDB	O, B_ALA_35	N, B_PHE_24	H, B_PHE_24	2.83	1.86	5.03
1HGF.PDB	O, A_CYS_14	N, B_ARG_25	H, B_ARG_25	2.97	2.03	13.73
1HGF.PDB	OE1, B_GLN_34	NE, B_ARG_25	HE, B_ARG_25	2.64	1.77	20.89
1HGF.PDB	OE1, B_GLN_34	NH2, B_ARG_25	HH21, B_ARG_25	2.81	1.99	28.67
1HGF.PDB	OE2, A_GLU_325	NH2, B_ARG_25	HH22, B_ARG_25	2.99	2.04	16.52
1HGF.PDB	O, B_GLY_31	N, B_ASN_28	H, B_ASN_28	2.76	1.82	13.38
1HGF.PDB	O, B_TYR_22	N, B_ASP_37	H, B_ASP_37	2.72	1.76	1.26
1HGF.PDB	OD2, B_ASP_37	N, B_SER_40	H, B_SER_40	2.89	1.91	1.46
1HGF.PDB	O, B_ASP_37	OG1, B_THR_41	HG1, B_THR_41	2.68	1.88	27.80
1HGF.PDB	O, B_LEU_38	N, B_GLN_42	H, B_GLN_42	2.87	1.93	12.73
1HGF.PDB	OD1, B_ASP_46	NE2, B_GLN_42	HE21, B_GLN_42	2.87	1.99	22.40
1HGF.PDB	O, B_LYS_39	N, B_ALA_43	H, B_ALA_43	2.92	1.97	11.63
1HGF.PDB	O, B_SER_40	N, B_ALA_44	H, B_ALA_44	2.94	1.96	4.26
1HGF.PDB	O, B_GLN_42	N, B_ASP_46	H, B_ASP_46	2.81	1.84	4.31
1HGF.PDB	O, B_ALA_43	NE2, B_GLN_47	HE21, B_GLN_47	2.89	1.94	12.17
1HGF.PDB	O, B_ILE_45	N, B_ASN_49	H, B_ASN_49	2.90	1.97	14.22
1HGF.PDB	O, B_ASP_46	N, B_GLY_50	H, B_GLY_50	2.85	1.93	16.88
1HGF.PDB	O, B_GLN_47	N, B_LYS_51	H, B_LYS_51	2.96	2.00	10.44
1HGF.PDB	OE1, B_GLU_103	NZ, B_LYS_51	HZ1, B_LYS_51	2.74	1.70	5.26
1HGF.PDB	ND1, B_HIS_106	NZ, B_LYS_51	HZ3, B_LYS_51	2.67	1.72	18.38
1HGF.PDB	O, B_ILE_48	N, B_LEU_52	H, B_LEU_52	2.92	2.01	17.60
1HGF.PDB	O, B_ASN_49	N, B_ASN_53	H, B_ASN_53	2.84	1.91	14.80
1HGF.PDB	O, E_THR_28	NE, B_ARG_54	HE, B_ARG_54	2.92	1.94	6.13
1HGF.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.83	1.86	13.50
1HGF.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ2, B_LYS_62	2.71	1.70	11.44
1HGF.PDB	OD2, F_ASP_90	NZ, B_LYS_62	HZ3, B_LYS_62	2.77	1.82	20.37
1HGF.PDB	OG, A_SER_266	ND1, B_HIS_64	HD1, B_HIS_64	2.66	1.79	20.68
1HGF.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.89	1.92	10.70
1HGF.PDB	O, B_PHE_63	NE2, B_GLN_65	HE21, B_GLN_65	2.92	1.95	7.46
1HGF.PDB	OE2, B_GLU_85	NZ, B_LYS_68	HZ1, B_LYS_68	2.67	1.75	22.44
1HGF.PDB	O, A_LYS_299	NZ, B_LYS_68	HZ2, B_LYS_68	2.93	1.89	4.53
1HGF.PDB	OG, C_SER_107	N, B_ARG_76	H, B_ARG_76	2.84	1.90	13.38
1HGF.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.92	1.92	2.47
1HGF.PDB	OE1, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.86	1.84	3.80
1HGF.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.73	1.74	10.29
1HGF.PDB	OE2, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.75	1.74	3.91
1HGF.PDB	O, B_GLY_75	N, B_ASP_79	H, B_ASP_79	2.96	2.00	9.52
1HGF.PDB	O, B_ILE_77	N, B_GLU_81	H, B_GLU_81	2.94	1.98	10.87
1HGF.PDB	O, B_GLN_78	N, B_LYS_82	H, B_LYS_82	3.00	2.09	18.29
1HGF.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.57	1.80	29.66
1HGF.PDB	O, B_LEU_80	N, B_VAL_84	H, B_VAL_84	2.91	1.98	14.24
1HGF.PDB	O, B_LYS_82	N, B_ASP_86	H, B_ASP_86	2.93	1.99	11.73
1HGF.PDB	O, B_TYR_83	N, B_THR_87	H, B_THR_87	2.99	2.04	12.38
1HGF.PDB	O, B_VAL_84	N, B_LYS_88	H, B_LYS_88	2.93	2.07	23.33
1HGF.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.72	1.70	9.91
1HGF.PDB	O, B_GLU_85	N, B_ILE_89	H, B_ILE_89	2.93	1.96	7.36
1HGF.PDB	O, B_LYS_88	N, B_TRP_92	H, B_TRP_92	2.91	1.95	10.80
1HGF.PDB	O, B_ILE_89	N, B_SER_93	H, B_SER_93	2.91	2.02	20.72
1HGF.PDB	O, B_ILE_89	OG, B_SER_93	HG, B_SER_93	2.78	1.94	24.66
1HGF.PDB	O, B_ASP_90	N, B_TYR_94	H, B_TYR_94	3.00	2.07	16.60
1HGF.PDB	O, B_TRP_92	N, B_ALA_96	H, B_ALA_96	2.98	2.04	14.15
1HGF.PDB	O, B_TYR_94	N, B_LEU_98	H, B_LEU_98	2.94	1.99	11.23
1HGF.PDB	O, B_ASN_95	N, B_LEU_99	H, B_LEU_99	3.00	2.03	11.07
1HGF.PDB	O, B_LEU_98	N, B_LEU_102	H, B_LEU_102	2.98	2.01	7.33
1HGF.PDB	O, B_LEU_99	N, B_GLU_103	H, B_GLU_103	2.91	1.94	8.79

1HGF.PDB	O, B_VAL_100	N, B_ASN_104	H, B_ASN_104	2.86	1.91	12.70
1HGF.PDB	O, A_LYS_27	ND2, B_ASN_104	HD21, B_ASN_104	2.88	1.94	13.97
1HGF.PDB	O, B_LEU_102	N, B_HIS_106	H, B_HIS_106	2.90	1.94	9.48
1HGF.PDB	O, B_GLU_103	N, B_THR_107	H, B_THR_107	2.84	1.94	18.07
1HGF.PDB	O, B_ASN_104	N, B_ILE_108	H, B_ILE_108	2.93	1.99	13.61
1HGF.PDB	O, B_HIS_106	N, B_LEU_110	H, B_LEU_110	2.78	1.84	12.67
1HGF.PDB	O, B_ASP_109	N, B_SER_113	H, B_SER_113	2.79	1.85	13.76
1HGF.PDB	O, F_LEU_2	OG, B_SER_113	HG, B_SER_113	2.68	1.90	29.80
1HGF.PDB	O, B_SER_113	N, B_LYS_117	H, B_LYS_117	2.74	1.85	20.16
1HGF.PDB	O, B_GLU_114	N, B_LEU_118	H, B_LEU_118	2.99	2.05	15.07
1HGF.PDB	O, B_MET_115	N, B_PHE_119	H, B_PHE_119	2.97	2.01	9.96
1HGF.PDB	O, B_ASN_116	N, B_GLU_120	H, B_GLU_120	2.92	1.94	1.95
1HGF.PDB	OE2, B_GLU_120	NH1, B_ARG_123	HH11, B_ARG_123	2.78	1.93	26.74
1HGF.PDB	O, B_GLU_120	N, B_ARG_124	H, B_ARG_124	2.96	2.04	16.03
1HGF.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.80	1.86	13.00
1HGF.PDB	OH, B_TYR_157	ND2, B_ASN_129	HD21, B_ASN_129	2.81	1.86	11.58
1HGF.PDB	O, B_HIS_159	ND2, B_ASN_129	HD22, B_ASN_129	2.97	2.06	17.16
1HGF.PDB	O, B_LYS_139	N, B_GLU_131	H, B_GLU_131	2.94	2.04	19.21
1HGF.PDB	O, B_CYS_137	N, B_MET_133	H, B_MET_133	2.88	1.93	11.45
1HGF.PDB	O, A_LEU_13	N, B_PHE_138	H, B_PHE_138	2.73	1.88	23.58
1HGF.PDB	O, B_GLU_131	N, B_LYS_139	H, B_LYS_139	2.85	1.91	11.21
1HGF.PDB	O, A_ALA_11	N, B_ILE_140	H, B_ILE_140	2.80	1.87	14.66
1HGF.PDB	O, B_ASN_129	N, B_TYR_141	H, B_TYR_141	2.87	1.93	12.99
1HGF.PDB	OD2, B_ASP_145	N, B_ALA_147	H, B_ALA_147	2.86	1.98	21.48
1HGF.PDB	O, B_ASP_145	N, B_ILE_149	H, B_ILE_149	2.90	1.94	9.97
1HGF.PDB	O, B_ASN_146	N, B_GLU_150	H, B_GLU_150	2.94	1.99	11.66
1HGF.PDB	O, B_ALA_147	N, B_SER_151	H, B_SER_151	2.85	2.06	29.61
1HGF.PDB	O, B_CYS_148	OG, B_SER_151	HG, B_SER_151	2.68	1.81	19.96
1HGF.PDB	O, B_GLU_150	N, B_ASN_154	H, B_ASN_154	2.87	1.89	5.04
1HGF.PDB	O, B_SER_151	N, B_THR_156	H, B_THR_156	2.77	1.91	23.09
1HGF.PDB	OD1, B_ASN_154	OG1, B_THR_156	HG1, B_THR_156	2.68	1.80	19.09
1HGF.PDB	OD1, B_ASP_158	N, B_ASP_160	H, B_ASP_160	2.97	2.10	23.68
1HGF.PDB	O, B_HIS_159	N, B_TYR_162	H, B_TYR_162	2.85	2.05	29.20
1HGF.PDB	O, F_ARG_170	NH1, B_ARG_163	HH12, B_ARG_163	2.79	1.78	1.27
1HGF.PDB	OE1, F_GLU_131	NH2, B_ARG_163	HH21, B_ARG_163	2.74	1.86	24.20
1HGF.PDB	O, B_TYR_162	N, B_ALA_166	H, B_ALA_166	2.86	1.89	4.35
1HGF.PDB	O, B_ARG_163	N, B_LEU_167	H, B_LEU_167	2.79	1.83	5.57
1HGF.PDB	O, B_GLU_165	ND2, B_ASN_169	HD21, B_ASN_169	3.00	2.06	13.38
1HGF.PDB	O, B_ALA_166	N, B_ARG_170	H, B_ARG_170	2.82	1.94	21.74
1HGF.PDB	O, B_GLU_128	NE, B_ARG_170	HE, B_ARG_170	2.78	1.88	20.28
1HGF.PDB	OE2, B_GLU_131	NH1, B_ARG_170	HH11, B_ARG_170	2.84	1.84	5.96
1HGF.PDB	O, B_LEU_167	N, B_PHE_171	H, B_PHE_171	2.90	1.97	15.47
1HGF.PDB	O, D_ILE_140	N, C_ALA_11	H, C_ALA_11	2.89	2.00	20.42
1HGF.PDB	O, D_GLN_27	N, C_THR_12	H, C_THR_12	2.90	1.96	12.68
1HGF.PDB	O, D_PHE_138	N, C_LEU_13	H, C_LEU_13	2.97	1.99	7.01
1HGF.PDB	O, D_ARG_25	N, C_CYS_14	H, C_CYS_14	2.79	1.86	15.57
1HGF.PDB	O, D_GLY_136	N, C_LEU_15	H, C_LEU_15	2.95	1.97	3.72
1HGF.PDB	O, D_GLY_23	N, C_GLY_16	H, C_GLY_16	2.95	2.05	18.06
1HGF.PDB	O, D_TRP_21	N, C_HIS_18	H, C_HIS_18	2.91	2.01	18.40
1HGF.PDB	OD1, C_ASN_322	N, C_VAL_20	H, C_VAL_20	2.80	1.83	2.80
1HGF.PDB	O, C_VAL_36	N, C_THR_24	H, C_THR_24	2.88	1.97	16.83
1HGF.PDB	O, C_ILE_34	N, C_VAL_26	H, C_VAL_26	2.85	1.90	10.38
1HGF.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.81	1.85	19.93
1HGF.PDB	O, C_ASP_31	N, C_THR_28	H, C_THR_28	2.69	1.91	29.80
1HGF.PDB	O, C_VAL_26	N, C_ILE_34	H, C_ILE_34	2.94	1.99	12.34
1HGF.PDB	O, C_THR_24	N, C_VAL_36	H, C_VAL_36	2.81	1.85	7.51
1HGF.PDB	O, C_MET_320	N, C_THR_37	H, C_THR_37	2.93	1.95	5.43
1HGF.PDB	O, C_LEU_316	N, C_THR_40	H, C_THR_40	2.80	1.89	17.62

1HGF.PDB	O, C_LEU_314	N, C_LEU_42	H, C_LEU_42	2.77	1.92	23.28
1HGF.PDB	O, C_PHE_294	N, C_GLN_44	H, C_GLN_44	2.95	1.98	8.35
1HGF.PDB	O, C_SER_46	NE2, C_GLN_44	HE21, C_GLN_44	2.83	1.96	22.13
1HGF.PDB	O, C_ASN_285	OG, C_SER_47	HG, C_SER_47	2.88	1.94	10.85
1HGF.PDB	OD2, C_ASP_275	NZ, C_LYS_50	HZ2, C_LYS_50	2.88	1.87	13.71
1HGF.PDB	O, C_PRO_273	N, C_ILE_51	H, C_ILE_51	2.76	1.80	7.14
1HGF.PDB	O, C_ASP_275	N, C_ASN_53	H, C_ASN_53	2.87	1.97	19.35
1HGF.PDB	OD2, C_ASP_85	N, C_ARG_57	H, C_ARG_57	2.92	1.96	10.20
1HGF.PDB	O, C_THR_83	NE, C_ARG_57	HE, C_ARG_57	2.76	1.82	12.66
1HGF.PDB	O, C_LEU_86	N, C_LEU_59	H, C_LEU_59	2.88	1.92	8.76
1HGF.PDB	O, C_VAL_88	N, C_GLY_61	H, C_GLY_61	2.99	2.18	28.94
1HGF.PDB	OD1, C_ASP_60	N, C_ILE_62	H, C_ILE_62	2.90	1.96	13.08
1HGF.PDB	O, C_GLY_61	N, C_CYS_64	H, C_CYS_64	2.89	1.95	14.15
1HGF.PDB	O, C_THR_65	N, C_ALA_69	H, C_ALA_69	2.99	2.03	9.48
1HGF.PDB	O, C_LEU_66	N, C_LEU_70	H, C_LEU_70	2.84	1.91	15.42
1HGF.PDB	O, C_ILE_67	N, C_LEU_71	H, C_LEU_71	2.90	1.93	5.47
1HGF.PDB	O, C_ASP_68	N, C_GLY_72	H, C_GLY_72	2.81	1.92	21.42
1HGF.PDB	OD1, C_ASP_73	N, C_HIS_75	H, C_HIS_75	2.97	2.06	19.07
1HGF.PDB	OD1, C_ASP_73	ND1, C_HIS_75	HD1, C_HIS_75	2.84	1.90	12.73
1HGF.PDB	O, C_ASP_63	NE2, C_HIS_75	HE2, C_HIS_75	2.86	1.91	13.30
1HGF.PDB	O, C_ASP_73	N, C_CYS_76	H, C_CYS_76	2.82	1.90	14.90
1HGF.PDB	O, C_PRO_74	N, C_ASP_77	H, C_ASP_77	2.92	1.97	11.55
1HGF.PDB	O, C_CYS_76	N, C_PHE_79	H, C_PHE_79	2.95	1.98	6.66
1HGF.PDB	OE1, C_GLU_82	N, C_THR_83	H, C_THR_83	2.95	2.02	15.89
1HGF.PDB	O, C_ARG_57	N, C_ASP_85	H, C_ASP_85	2.80	1.92	20.17
1HGF.PDB	O, C_MET_268	N, C_GLU_89	H, C_GLU_89	2.83	1.88	10.14
1HGF.PDB	OD1, C_ASP_60	NE, C_ARG_90	HE, C_ARG_90	2.76	1.85	16.46
1HGF.PDB	O, C_SER_270	NH1, C_ARG_90	HH11, C_ARG_90	2.67	1.81	25.78
1HGF.PDB	O, C_ALA_272	NH1, C_ARG_90	HH12, C_ARG_90	2.65	1.72	16.33
1HGF.PDB	OD2, C_ASP_60	NH2, C_ARG_90	HH21, C_ARG_90	2.84	1.85	9.99
1HGF.PDB	OD1, C_ASP_271	N, C_SER_91	H, C_SER_91	2.94	1.98	10.16
1HGF.PDB	OD1, C_ASP_271	OG, C_SER_91	HG, C_SER_91	2.91	2.11	29.01
1HGF.PDB	OD2, C_ASP_271	OG, C_SER_91	HG, C_SER_91	2.86	1.95	16.65
1HGF.PDB	OD2, C_ASP_73	N, C_ASN_96	H, C_ASN_96	2.88	1.95	14.97
1HGF.PDB	SG, C_CYS_97	N, C_TYR_98	H, C_TYR_98	2.99	2.15	25.59
1HGF.PDB	OD1, C_ASP_68	OH, C_TYR_100	HH, C_TYR_100	2.97	2.03	12.15
1HGF.PDB	O, C_ILE_230	N, C_ASP_101	H, C_ASP_101	2.99	2.16	26.80
1HGF.PDB	OD2, C_ASP_104	OG, C_SER_107	HG, C_SER_107	2.91	1.98	14.76
1HGF.PDB	O, C_TYR_105	N, C_ARG_109	H, C_ARG_109	2.87	1.90	5.89
1HGF.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.91	1.92	11.49
1HGF.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.69	1.85	25.37
1HGF.PDB	O, C_SER_107	N, C_LEU_111	H, C_LEU_111	2.95	2.00	12.48
1HGF.PDB	O, C_ARG_109	N, C_ALA_113	H, C_ALA_113	2.94	2.02	17.14
1HGF.PDB	O, C_SER_110	N, C_SER_114	H, C_SER_114	2.95	2.04	18.89
1HGF.PDB	O, C_VAL_112	N, C_GLY_116	H, C_GLY_116	3.00	2.03	6.34
1HGF.PDB	OE2, C_GLU_119	OG1, C_THR_117	HG1, C_THR_117	2.97	2.00	2.16
1HGF.PDB	O, C_GLU_82	N, C_LEU_118	H, C_LEU_118	2.97	2.00	8.06
1HGF.PDB	OD1, C_ASN_81	N, C_PHE_120	H, C_PHE_120	3.00	2.07	15.52
1HGF.PDB	O, C_TYR_257	N, C_ILE_121	H, C_ILE_121	2.83	1.85	1.84
1HGF.PDB	O, C_ARG_255	N, C_GLU_123	H, C_GLU_123	2.86	1.90	9.31
1HGF.PDB	O, C_THR_155	N, C_THR_131	H, C_THR_131	2.75	1.81	11.67
1HGF.PDB	ND2, C_ASN_152	NE2, C_GLN_132	HE21, C_GLN_132	2.94	2.00	12.42
1HGF.PDB	OD1, C_ASN_152	N, C_ASN_133	H, C_ASN_133	2.91	1.95	9.50
1HGF.PDB	O, C_TRP_153	N, C_GLY_134	H, C_GLY_134	2.99	2.07	16.29
1HGF.PDB	O, C_GLY_146	N, C_SER_136	H, C_SER_136	2.71	1.85	23.34
1HGF.PDB	O, C_GLY_144	N, C_ARG_141	H, C_ARG_141	2.89	2.08	28.20
1HGF.PDB	OD2, C_ASP_77	NE, C_ARG_141	HE, C_ARG_141	2.91	2.05	25.56
1HGF.PDB	O, C_PHE_147	NH1, C_ARG_141	HH12, C_ARG_141	2.59	1.66	16.99

1HGF.PDB	OD1, C_ASP.77	NH2, C_ARG.141	HH21, C_ARG.141	2.84	1.98	26.48
1HGF.PDB	OD2, C_ASP.77	NH2, C_ARG.141	HH21, C_ARG.141	2.79	1.86	20.63
1HGF.PDB	O, C_SER.136	N, C_GLY.146	H, C_GLY.146	2.99	2.14	25.31
1HGF.PDB	O, C_GLY.72	N, C_SER.149	H, C_SER.149	2.87	1.95	17.40
1HGF.PDB	O, C_ALA.253	N, C_ASN.152	H, C_ASN.152	2.81	1.90	18.05
1HGF.PDB	OH, C_TYR.195	NE1, C_TRP.153	HE1, C_TRP.153	2.82	1.92	18.47
1HGF.PDB	O, C_LEU.194	N, C_LYS.156	H, C_LYS.156	2.86	2.00	23.97
1HGF.PDB	O, C_THR.160	N, C_SER.157	H, C_SER.157	2.96	2.07	20.42
1HGF.PDB	O, C_SER.247	N, C_LEU.164	H, C_LEU.164	2.70	1.88	26.53
1HGF.PDB	O, C_ILE.245	N, C_VAL.166	H, C_VAL.166	2.89	1.93	11.49
1HGF.PDB	O, C_LEU.243	OG1, C_THR.167	HG1, C_THR.167	2.95	2.01	11.60
1HGF.PDB	O, C_ASP.241	N, C_ASN.170	H, C_ASN.170	2.84	1.87	6.38
1HGF.PDB	O, C_PHE.174	ND2, C_ASN.170	HD22, C_ASN.170	2.74	1.80	12.05
1HGF.PDB	O, C_VAL.237	N, C_LYS.176	H, C_LYS.176	2.93	1.99	14.60
1HGF.PDB	OE2, C_GLU.123	NZ, C_LYS.176	HZ1, C_LYS.176	2.72	1.80	22.47
1HGF.PDB	O, C_THR.235	N, C_TYR.178	H, C_TYR.178	2.78	1.81	4.50
1HGF.PDB	OG1, C_THR.235	NE1, C_TRP.180	HE1, C_TRP.180	2.86	1.88	3.91
1HGF.PDB	O, C_ASN.250	N, C_HIS.183	H, C_HIS.183	2.79	1.92	22.35
1HGF.PDB	OH, C_TYR.98	NE2, C_HIS.183	HE2, C_HIS.183	2.89	1.99	18.89
1HGF.PDB	O, C_ARG.229	N, C_HIS.184	H, C_HIS.184	2.87	1.90	8.03
1HGF.PDB	OG, C_SER.231	NE2, C_HIS.184	HE2, C_HIS.184	2.67	1.86	27.83
1HGF.PDB	OD1, C_ASN.250	NE2, C_GLN.191	HE22, C_GLN.191	2.91	1.94	7.66
1HGF.PDB	O, C_ASN.188	N, C_THR.192	H, C_THR.192	2.94	2.00	14.19
1HGF.PDB	O, C_GLN.189	OG1, C_THR.192	HG1, C_THR.192	2.86	2.05	27.70
1HGF.PDB	O, C_GLN.189	N, C_SER.193	H, C_SER.193	2.81	1.91	19.71
1HGF.PDB	O, C_GLU.190	N, C_LEU.194	H, C_LEU.194	2.96	2.00	9.41
1HGF.PDB	O, C_GLN.191	N, C_TYR.195	H, C_TYR.195	2.79	1.84	10.04
1HGF.PDB	O, C_ASN.248	NE2, C_GLN.197	HE21, C_GLN.197	2.92	2.05	22.87
1HGF.PDB	O, C_TYR.161	NE2, C_GLN.197	HE22, C_GLN.197	2.98	2.03	10.03
1HGF.PDB	OG1, C_THR.212	OG1, C_THR.203	HG1, C_THR.203	2.82	1.90	14.76
1HGF.PDB	O, C_GLN.211	N, C_VAL.204	H, C_VAL.204	2.93	2.00	14.76
1HGF.PDB	O, C_SER.209	N, C_THR.206	H, C_THR.206	2.97	2.04	14.71
1HGF.PDB	OD1, C_ASP.241	N, C_ARG.207	H, C_ARG.207	2.91	1.95	9.01
1HGF.PDB	O, C_VAL.204	N, C_GLN.211	H, C_GLN.211	2.84	1.94	18.99
1HGF.PDB	O, C_VAL.202	N, C_ILE.213	H, C_ILE.213	2.85	1.95	18.52
1HGF.PDB	ND1, C_HIS.184	N, C_ASN.216	H, C_ASN.216	2.71	1.89	26.19
1HGF.PDB	O, C_ASN.216	NH1, C_ARG.220	HH12, C_ARG.220	2.97	2.15	29.93
1HGF.PDB	OE1, E_GLN.210	NH2, C_ARG.220	HH21, C_ARG.220	2.56	1.72	26.72
1HGF.PDB	O, C_ASN.216	NH2, C_ARG.220	HH22, C_ARG.220	2.74	1.84	20.57
1HGF.PDB	O, C_LEU.226	N, C_VAL.223	H, C_VAL.223	2.83	1.89	12.06
1HGF.PDB	O, C_CYS.97	NE, C_ARG.224	HE, C_ARG.224	2.75	1.89	23.47
1HGF.PDB	O, C_CYS.97	NH2, C_ARG.224	HH21, C_ARG.224	2.93	2.09	27.24
1HGF.PDB	O, C_VAL.223	N, C_LEU.226	H, C_LEU.226	2.93	1.99	12.10
1HGF.PDB	O, C_SER.228	NH1, C_ARG.229	HH11, C_ARG.229	2.74	1.82	20.52
1HGF.PDB	O, C_PRO.221	NH2, C_ARG.229	HH22, C_ARG.229	2.64	1.70	16.37
1HGF.PDB	O, C_PRO.99	N, C_ILE.230	H, C_ILE.230	2.97	2.09	21.38
1HGF.PDB	OD1, C_ASP.101	OG, C_SER.231	HG, C_SER.231	2.86	1.89	4.34
1HGF.PDB	O, C_ASP.101	N, C_ILE.232	H, C_ILE.232	2.92	1.98	14.28
1HGF.PDB	O, C_TRP.180	N, C_TYR.233	H, C_TYR.233	2.92	1.97	12.47
1HGF.PDB	O, C_TYR.178	N, C_THR.235	H, C_THR.235	2.83	1.96	22.49
1HGF.PDB	O, C_LYS.176	N, C_VAL.237	H, C_VAL.237	2.78	1.86	15.74
1HGF.PDB	OE1, B_GLU.72	NZ, C_LYS.238	HZ2, C_LYS.238	2.75	1.78	18.48
1HGF.PDB	O, B_SER.71	NZ, C_LYS.238	HZ3, C_LYS.238	2.61	1.62	12.67
1HGF.PDB	O, C_ASN.170	N, C_GLY.240	H, C_GLY.240	2.91	2.11	29.28
1HGF.PDB	O, C_LYS.238	N, C_ASP.241	H, C_ASP.241	2.98	2.06	15.29
1HGF.PDB	O, C_MET.168	N, C_LEU.243	H, C_LEU.243	2.96	1.99	7.32
1HGF.PDB	O, C_SER.205	N, C_VAL.244	H, C_VAL.244	2.94	1.99	13.35
1HGF.PDB	O, C_VAL.166	N, C_ILE.245	H, C_ILE.245	2.97	2.05	16.82

1HGF.PDB	O, C_THR_203	N, C_ASN_246	H, C_ASN_246	2.92	1.97	10.97
1HGF.PDB	OD1, C_ASN_165	ND2, C_ASN_246	HD21, C_ASN_246	2.93	2.04	21.38
1HGF.PDB	O, C_LEU_164	N, C_SER_247	H, C_SER_247	2.93	2.02	18.68
1HGF.PDB	OG, C_SER_247	N, C_GLY_249	H, C_GLY_249	2.99	2.02	6.95
1HGF.PDB	O, C_HIS_183	ND2, C_ASN_250	HD21, C_ASN_250	2.81	1.85	7.16
1HGF.PDB	OE1, C_GLN_191	ND2, C_ASN_250	HD22, C_ASN_250	2.84	1.89	10.62
1HGF.PDB	O, C_ASN_152	N, C_ALA_253	H, C_ALA_253	2.97	2.05	17.09
1HGF.PDB	OD1, C_ASN_133	NH2, C_ARG_255	HH22, C_ARG_255	2.47	1.67	28.90
1HGF.PDB	O, C_ILE_121	N, C_TYR_257	H, C_TYR_257	2.98	2.13	24.91
1HGF.PDB	O, C_LEU_177	N, C_PHE_258	H, C_PHE_258	3.00	2.02	5.00
1HGF.PDB	OE1, C_GLU_119	NH2, C_ARG_261	HH22, C_ARG_261	2.72	1.88	28.14
1HGF.PDB	O, C_PHE_87	N, C_MET_268	H, C_MET_268	2.91	1.98	16.01
1HGF.PDB	OG, C_SER_270	N, C_ALA_272	H, C_ALA_272	2.93	2.02	16.95
1HGF.PDB	O, C_ILE_51	N, C_ASP_275	H, C_ASP_275	2.92	2.05	22.55
1HGF.PDB	OD1, C_ASP_275	N, C_THR_276	H, C_THR_276	2.75	1.92	25.58
1HGF.PDB	O, C_ASN_54	N, C_SER_279	H, C_SER_279	2.77	1.83	12.02
1HGF.PDB	O, C_TYR_302	N, C_ILE_282	H, C_ILE_282	2.94	1.96	4.09
1HGF.PDB	O, C_THR_283	N, C_GLY_286	H, C_GLY_286	2.80	1.85	9.72
1HGF.PDB	O, C_LYS_50	N, C_SER_287	H, C_SER_287	2.77	1.82	8.64
1HGF.PDB	O, C_ALA_304	ND2, C_ASN_290	HD21, C_ASN_290	2.81	1.90	17.53
1HGF.PDB	OE1, C_GLN_44	NZ, C_LYS_292	HZ1, C_LYS_292	2.89	1.84	2.00
1HGF.PDB	OD1, C_ASP_291	NZ, C_LYS_292	HZ2, C_LYS_292	2.88	1.85	8.89
1HGF.PDB	O, C_LYS_307	N, C_GLN_295	H, C_GLN_295	2.79	1.95	25.63
1HGF.PDB	O, C_ASN_298	NE2, C_GLN_295	HE22, C_GLN_295	2.74	1.82	15.41
1HGF.PDB	O, C_GLN_44	N, C_ASN_296	H, C_ASN_296	2.86	1.91	11.96
1HGF.PDB	OD1, C_ASN_298	N, C_ILE_300	H, C_ILE_300	2.86	2.02	25.28
1HGF.PDB	O, C_ILE_282	N, C_TYR_302	H, C_TYR_302	2.79	1.95	25.47
1HGF.PDB	O, D_LYS_62	N, C_GLY_303	H, C_GLY_303	2.91	1.95	8.09
1HGF.PDB	O, C_GLN_295	N, C_VAL_309	H, C_VAL_309	2.90	2.02	21.20
1HGF.PDB	OG, D_SER_93	N, C_LYS_310	H, C_LYS_310	2.89	1.98	17.69
1HGF.PDB	OE1, C_GLU_41	OG1, C_THR_313	HG1, C_THR_313	2.66	1.87	29.10
1HGF.PDB	OE2, C_GLU_41	N, C_LEU_314	H, C_LEU_314	2.78	1.84	12.61
1HGF.PDB	OG1, C_THR_313	NZ, C_LYS_315	HZ2, C_LYS_315	2.92	1.98	21.54
1HGF.PDB	O, C_THR_40	N, C_LEU_316	H, C_LEU_316	2.78	1.85	14.66
1HGF.PDB	OD1, D_ASN_104	N, C_ALA_317	H, C_ALA_317	2.78	1.83	11.25
1HGF.PDB	O, C_ASN_38	N, C_THR_318	H, C_THR_318	2.88	1.93	11.29
1HGF.PDB	OE2, C_GLU_35	ND2, C_ASN_322	HD21, C_ASN_322	2.77	1.93	25.57
1HGF.PDB	O, C_VAL_20	ND2, C_ASN_322	HD22, C_ASN_322	2.97	2.05	15.45
1HGF.PDB	OXT, C_THR_328	NE2, C_GLN_327	HE21, C_GLN_327	2.93	2.09	26.28
1HGF.PDB	OD2, D_ASP_112	N, D_GLY_1	H1, D_GLY_1	2.88	1.90	17.37
1HGF.PDB	OD1, D_ASP_109	N, D_LEU_2	H, D_LEU_2	2.92	2.02	20.08
1HGF.PDB	O, D_GLY_4	N, D_PHE_9	H, D_PHE_9	2.80	1.88	16.46
1HGF.PDB	O, D_GLY_13	ND2, D_ASN_12	HD21, D_ASN_12	2.79	1.92	22.00
1HGF.PDB	O, C_VAL_323	N, D_GLY_13	H, D_GLY_13	2.72	1.85	21.39
1HGF.PDB	O, C_HIS_17	N, D_TRP_14	H, D_TRP_14	2.87	1.96	16.75
1HGF.PDB	OG1, D_THR_41	N, D_TRP_21	H, D_TRP_21	2.91	2.00	17.91
1HGF.PDB	O, D_ALA_35	N, D_PHE_24	H, D_PHE_24	2.85	1.87	3.45
1HGF.PDB	O, C_CYS_14	N, D_ARG_25	H, D_ARG_25	2.90	1.93	7.59
1HGF.PDB	OE1, D_GLN_34	NE, D_ARG_25	HE, D_ARG_25	2.69	1.78	17.17
1HGF.PDB	O, D_GLY_33	N, D_HIS_26	H, D_HIS_26	2.88	2.02	23.62
1HGF.PDB	O, C_THR_12	N, D_GLN_27	H, D_GLN_27	2.86	1.94	17.23
1HGF.PDB	O, D_GLY_31	N, D_ASN_28	H, D_ASN_28	2.96	1.98	6.01
1HGF.PDB	OD1, D_ASN_146	ND2, D_ASN_28	HD22, D_ASN_28	2.89	1.97	17.31
1HGF.PDB	O, D_ASN_28	N, D_GLY_31	H, D_GLY_31	2.88	1.99	19.79
1HGF.PDB	O, D_HIS_26	N, D_GLY_33	H, D_GLY_33	2.97	2.16	28.69
1HGF.PDB	O, D_PHE_24	N, D_ALA_35	H, D_ALA_35	2.78	1.98	29.25
1HGF.PDB	O, D_TYR_22	N, D_ASP_37	H, D_ASP_37	2.72	1.76	4.61
1HGF.PDB	OD2, D_ASP_37	N, D_SER_40	H, D_SER_40	2.90	1.92	1.16

1HGF.PDB	OD2, D_ASP_37	OG, D_SER_40	HG, D_SER_40	2.85	1.95	18.29
1HGF.PDB	O, D_ASP_37	OG1, D_THR_41	HG1, D_THR_41	2.68	1.81	21.66
1HGF.PDB	O, D_LEU_38	N, D_GLN_42	H, D_GLN_42	2.88	1.96	16.52
1HGF.PDB	OD1, D_ASP_46	NE2, D_GLN_42	HE21, D_GLN_42	2.85	1.97	22.40
1HGF.PDB	O, D_LYS_39	N, D_ALA_43	H, D_ALA_43	2.92	1.96	7.79
1HGF.PDB	O, D_SER_40	N, D_ALA_44	H, D_ALA_44	2.95	1.98	3.84
1HGF.PDB	O, D_GLN_42	N, D_ASP_46	H, D_ASP_46	2.80	1.83	2.08
1HGF.PDB	O, D_ALA_43	NE2, D_GLN_47	HE21, D_GLN_47	2.88	1.93	11.54
1HGF.PDB	O, D_ILE_45	N, D_ASN_49	H, D_ASN_49	2.91	1.99	16.85
1HGF.PDB	O, D_ASP_46	N, D_GLY_50	H, D_GLY_50	2.87	1.93	13.85
1HGF.PDB	O, D_GLN_47	N, D_LYS_51	H, D_LYS_51	2.95	1.98	9.03
1HGF.PDB	OE1, D_GLU_103	NZ, D_LYS_51	HZ1, D_LYS_51	2.74	1.71	5.53
1HGF.PDB	ND1, D_HIS_106	NZ, D_LYS_51	HZ3, D_LYS_51	2.69	1.73	17.89
1HGF.PDB	O, D_ILE_48	N, D_LEU_52	H, D_LEU_52	2.91	2.04	22.13
1HGF.PDB	O, D_ASN_49	N, D_ASN_53	H, D_ASN_53	2.86	1.92	13.32
1HGF.PDB	O, A_THR_28	NE, D_ARG_54	HE, D_ARG_54	2.88	1.90	8.46
1HGF.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.84	1.86	12.74
1HGF.PDB	OD2, B_ASP_86	NZ, D_LYS_62	HZ2, D_LYS_62	2.69	1.69	13.49
1HGF.PDB	OD2, B_ASP_90	NZ, D_LYS_62	HZ3, D_LYS_62	2.68	1.77	22.81
1HGF.PDB	OG, C_SER_266	ND1, D_HIS_64	HD1, D_HIS_64	2.64	1.83	27.58
1HGF.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.90	1.92	7.33
1HGF.PDB	O, D_PHE_63	NE2, D_GLN_65	HE21, D_GLN_65	2.97	2.00	7.06
1HGF.PDB	OE2, D_GLU_85	NZ, D_LYS_68	HZ1, D_LYS_68	2.73	1.78	19.48
1HGF.PDB	O, C_LYS_299	NZ, D_LYS_68	HZ2, D_LYS_68	2.93	1.89	4.98
1HGF.PDB	OG, E_SER_107	N, D_ARG_76	H, D_ARG_76	2.91	1.94	7.76
1HGF.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.82	1.85	5.34
1HGF.PDB	OE1, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.79	1.78	3.81
1HGF.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.64	1.68	12.43
1HGF.PDB	OE2, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.70	1.71	7.38
1HGF.PDB	O, D_GLY_75	N, D_ASP_79	H, D_ASP_79	2.98	2.03	12.51
1HGF.PDB	O, D_ILE_77	N, D_GLU_81	H, D_GLU_81	2.96	2.00	8.84
1HGF.PDB	O, D_GLN_78	N, D_LYS_82	H, D_LYS_82	2.96	2.03	15.61
1HGF.PDB	O, D_ASP_79	N, D_TYR_83	H, D_TYR_83	2.99	2.06	16.44
1HGF.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.58	1.80	29.87
1HGF.PDB	O, D_LEU_80	N, D_VAL_84	H, D_VAL_84	2.89	1.96	15.53
1HGF.PDB	O, D_LYS_82	N, D_ASP_86	H, D_ASP_86	2.88	1.93	10.60
1HGF.PDB	O, D_TYR_83	N, D_THR_87	H, D_THR_87	2.98	2.05	15.57
1HGF.PDB	O, D_VAL_84	N, D_LYS_88	H, D_LYS_88	2.92	2.03	20.52
1HGF.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.68	1.69	13.85
1HGF.PDB	O, D_GLU_85	N, D_ILE_89	H, D_ILE_89	2.92	1.94	5.05
1HGF.PDB	O, D_LYS_88	N, D_TRP_92	H, D_TRP_92	2.90	1.93	7.06
1HGF.PDB	O, D_ILE_89	N, D_SER_93	H, D_SER_93	2.93	2.03	18.97
1HGF.PDB	O, D_ILE_89	OG, D_SER_93	HG, D_SER_93	2.79	1.87	14.25
1HGF.PDB	O, D_ASP_90	N, D_TYR_94	H, D_TYR_94	2.98	2.09	20.66
1HGF.PDB	O, D_TRP_92	N, D_ALA_96	H, D_ALA_96	2.99	2.03	9.70
1HGF.PDB	O, D_TYR_94	N, D_LEU_98	H, D_LEU_98	2.90	1.96	13.51
1HGF.PDB	O, D_ASN_95	N, D_LEU_99	H, D_LEU_99	2.97	2.01	11.18
1HGF.PDB	O, D_LEU_98	N, D_LEU_102	H, D_LEU_102	2.98	2.02	11.36
1HGF.PDB	O, D_LEU_99	N, D_GLU_103	H, D_GLU_103	2.92	1.96	10.07
1HGF.PDB	O, D_VAL_100	N, D_ASN_104	H, D_ASN_104	2.84	1.89	11.66
1HGF.PDB	O, C_LYS_27	ND2, D_ASN_104	HD21, D_ASN_104	2.89	1.96	15.72
1HGF.PDB	O, D_LEU_102	N, D_HIS_106	H, D_HIS_106	2.92	1.97	11.28
1HGF.PDB	O, D_GLU_103	N, D_THR_107	H, D_THR_107	2.85	1.92	13.38
1HGF.PDB	O, D_ASN_104	N, D_ILE_108	H, D_ILE_108	2.97	2.03	13.33
1HGF.PDB	O, D_HIS_106	N, D_LEU_110	H, D_LEU_110	2.77	1.83	11.73
1HGF.PDB	O, D_ASP_109	N, D_SER_113	H, D_SER_113	2.82	1.90	15.73
1HGF.PDB	O, D_SER_113	N, D_LYS_117	H, D_LYS_117	2.74	1.83	18.58
1HGF.PDB	O, D_MET_115	N, D_PHE_119	H, D_PHE_119	2.96	2.01	11.81

1HGF.PDB	O, D_ASN_116	N, D_GLU_120	H, D_GLU_120	2.90	1.92	4.93
1HGF.PDB	O, D_PHE_119	N, D_ARG_123	H, D_ARG_123	3.00	2.03	9.49
1HGF.PDB	OE2, D_GLU_120	NH1, D_ARG_123	HH11, D_ARG_123	2.79	1.92	25.71
1HGF.PDB	O, D_GLU_120	N, D_ARG_124	H, D_ARG_124	2.96	2.04	16.78
1HGF.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.79	1.88	16.40
1HGF.PDB	OH, D_TYR_157	ND2, D_ASN_129	HD21, D_ASN_129	2.81	1.84	5.39
1HGF.PDB	O, D_HIS_159	ND2, D_ASN_129	HD22, D_ASN_129	2.94	2.01	14.46
1HGF.PDB	O, D_LYS_139	N, D_GLU_131	H, D_GLU_131	2.98	2.08	19.93
1HGF.PDB	O, D_CYS_137	N, D_MET_133	H, D_MET_133	2.92	1.96	10.87
1HGF.PDB	OD1, D_ASN_135	N, D_CYS_137	H, D_CYS_137	2.83	1.95	20.45
1HGF.PDB	O, C_LEU_13	N, D_PHE_138	H, D_PHE_138	2.75	1.91	24.76
1HGF.PDB	O, D_GLU_131	N, D_LYS_139	H, D_LYS_139	2.83	1.88	9.91
1HGF.PDB	O, C_ALA_11	N, D_ILE_140	H, D_ILE_140	2.82	1.90	15.68
1HGF.PDB	O, D_ASN_129	N, D_TYR_141	H, D_TYR_141	2.87	1.92	10.75
1HGF.PDB	OG, D_SER_29	NZ, D_LYS_143	HZ1, D_LYS_143	2.83	1.89	20.16
1HGF.PDB	OE2, D_GLU_30	N, D_ASN_146	H, D_ASN_146	2.80	1.88	14.92
1HGF.PDB	OD2, D_ASP_145	N, D_ALA_147	H, D_ALA_147	2.87	2.00	23.24
1HGF.PDB	O, D_ASP_145	N, D_ILE_149	H, D_ILE_149	2.93	1.97	10.46
1HGF.PDB	O, D_ASN_146	N, D_GLU_150	H, D_GLU_150	2.94	2.01	15.42
1HGF.PDB	O, D_ALA_147	N, D_SER_151	H, D_SER_151	2.89	2.02	22.93
1HGF.PDB	O, D_CYS_148	OG, D_SER_151	HG, D_SER_151	2.73	1.81	12.37
1HGF.PDB	O, D_GLU_150	N, D_ASN_154	H, D_ASN_154	2.87	1.89	5.22
1HGF.PDB	O, D_SER_151	N, D_THR_156	H, D_THR_156	2.79	1.97	26.84
1HGF.PDB	OD1, D_ASN_154	OG1, D_THR_156	HG1, D_THR_156	2.72	1.80	12.72
1HGF.PDB	NE2, D_HIS_142	OH, D_TYR_157	HH, D_TYR_157	2.72	1.85	19.75
1HGF.PDB	OD1, D_ASP_158	N, D_ASP_160	H, D_ASP_160	3.00	2.13	23.50
1HGF.PDB	O, D_HIS_159	N, D_TYR_162	H, D_TYR_162	2.89	2.08	29.06
1HGF.PDB	O, D_ASP_160	N, D_ARG_163	H, D_ARG_163	3.00	2.09	17.80
1HGF.PDB	O, B_ARG_170	NH1, D_ARG_163	HH12, D_ARG_163	2.84	1.83	3.71
1HGF.PDB	OE1, B_GLU_131	NH2, D_ARG_163	HH21, D_ARG_163	2.70	1.83	24.43
1HGF.PDB	O, D_TYR_162	N, D_ALA_166	H, D_ALA_166	2.86	1.89	3.57
1HGF.PDB	O, D_ARG_163	N, D_LEU_167	H, D_LEU_167	2.79	1.83	4.62
1HGF.PDB	O, D_GLU_165	ND2, D_ASN_169	HD21, D_ASN_169	2.97	2.03	11.99
1HGF.PDB	O, D_ALA_166	N, D_ARG_170	H, D_ARG_170	2.84	1.97	21.75
1HGF.PDB	O, D_GLU_128	NE, D_ARG_170	HE, D_ARG_170	2.76	1.87	20.27
1HGF.PDB	OE2, D_GLU_131	NH1, D_ARG_170	HH11, D_ARG_170	2.84	1.84	5.29
1HGF.PDB	O, D_LEU_167	N, D_PHE_171	H, D_PHE_171	2.90	1.96	12.84
1HGF.PDB	O, F_ILE_140	N, E_ALA_11	H, E_ALA_11	2.95	2.06	20.63
1HGF.PDB	O, F_GLN_27	N, E_THR_12	H, E_THR_12	2.87	1.93	12.24
1HGF.PDB	O, F_PHE_138	N, E_LEU_13	H, E_LEU_13	2.96	1.99	8.43
1HGF.PDB	O, F_ARG_25	N, E_CYS_14	H, E_CYS_14	2.65	1.83	26.13
1HGF.PDB	O, F_GLY_136	N, E_LEU_15	H, E_LEU_15	2.91	1.93	3.45
1HGF.PDB	O, F_GLY_23	N, E_GLY_16	H, E_GLY_16	2.94	2.06	22.45
1HGF.PDB	O, E_HIS_18	ND1, E_HIS_17	HD1, E_HIS_17	2.99	2.14	25.53
1HGF.PDB	O, F_TRP_21	N, E_HIS_18	H, E_HIS_18	2.91	2.00	17.81
1HGF.PDB	OD1, E_ASN_322	N, E_VAL_20	H, E_VAL_20	2.80	1.82	2.55
1HGF.PDB	O, E_VAL_36	N, E_THR_24	H, E_THR_24	2.87	1.98	19.96
1HGF.PDB	O, E_ILE_34	N, E_VAL_26	H, E_VAL_26	2.89	1.93	10.60
1HGF.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.75	1.83	22.30
1HGF.PDB	O, E_VAL_26	N, E_ILE_34	H, E_ILE_34	2.94	1.98	10.18
1HGF.PDB	O, E_THR_24	N, E_VAL_36	H, E_VAL_36	2.81	1.85	7.38
1HGF.PDB	O, E_MET_320	N, E_THR_37	H, E_THR_37	2.91	1.94	5.79
1HGF.PDB	O, E_LEU_316	N, E_THR_40	H, E_THR_40	2.78	1.86	16.07
1HGF.PDB	O, E_LEU_314	N, E_LEU_42	H, E_LEU_42	2.78	1.90	19.77
1HGF.PDB	O, E_PHE_294	N, E_GLN_44	H, E_GLN_44	2.96	1.98	3.65
1HGF.PDB	O, E_SER_46	NE2, E_GLN_44	HE21, E_GLN_44	2.83	1.95	21.77
1HGF.PDB	O, E_ASN_285	OG, E_SER_47	HG, E_SER_47	2.86	1.95	16.70
1HGF.PDB	OD2, E_ASP_275	NZ, E_LYS_50	HZ2, E_LYS_50	2.90	1.90	14.56

1HGF.PDB	O, E_PRO_273	N, E_ILE_51	H, E_ILE_51	2.76	1.81	9.83
1HGF.PDB	O, E_ASP_275	N, E_ASN_53	H, E_ASN_53	2.89	1.97	17.56
1HGF.PDB	OD2, E_ASP_85	N, E_ARG_57	H, E_ARG_57	2.93	1.98	11.47
1HGF.PDB	O, E_THR_83	NE, E_ARG_57	HE, E_ARG_57	2.82	1.86	10.06
1HGF.PDB	O, E_LEU_86	N, E_LEU_59	H, E_LEU_59	2.87	1.91	9.41
1HGF.PDB	OD1, E_ASP_60	N, E_ILE_62	H, E_ILE_62	2.91	1.96	11.31
1HGF.PDB	O, E_GLY_61	N, E_CYS_64	H, E_CYS_64	2.88	1.96	16.75
1HGF.PDB	O, E_THR_65	N, E_ALA_69	H, E_ALA_69	3.00	2.07	14.88
1HGF.PDB	O, E_LEU_66	N, E_LEU_70	H, E_LEU_70	2.82	1.89	15.13
1HGF.PDB	O, E_ILE_67	N, E_LEU_71	H, E_LEU_71	2.91	1.95	6.47
1HGF.PDB	O, E_ASP_68	N, E_GLY_72	H, E_GLY_72	2.87	1.99	21.64
1HGF.PDB	OD1, E_ASP_73	ND1, E_HIS_75	HD1, E_HIS_75	2.85	1.91	12.17
1HGF.PDB	O, E_ASP_63	NE2, E_HIS_75	HE2, E_HIS_75	2.89	1.94	12.08
1HGF.PDB	O, E_ASP_73	N, E_CYS_76	H, E_CYS_76	2.81	1.88	15.29
1HGF.PDB	O, E_PRO_74	N, E_ASP_77	H, E_ASP_77	2.90	1.94	7.27
1HGF.PDB	O, E_CYS_76	N, E_PHE_79	H, E_PHE_79	2.95	1.97	5.01
1HGF.PDB	O, E_ARG_57	N, E_ASP_85	H, E_ASP_85	2.81	1.92	19.34
1HGF.PDB	O, E_MET_268	N, E_GLU_89	H, E_GLU_89	2.79	1.84	8.93
1HGF.PDB	OD1, E_ASP_60	NE, E_ARG_90	HE, E_ARG_90	2.80	1.85	10.51
1HGF.PDB	O, E_SER_270	NH1, E_ARG_90	HH11, E_ARG_90	2.63	1.77	25.28
1HGF.PDB	O, E_ALA_272	NH1, E_ARG_90	HH12, E_ARG_90	2.66	1.73	17.47
1HGF.PDB	OD2, E_ASP_60	NH2, E_ARG_90	HH21, E_ARG_90	2.88	1.89	10.22
1HGF.PDB	OD1, E_ASP_271	N, E_SER_91	H, E_SER_91	2.94	1.98	11.41
1HGF.PDB	OD2, E_ASP_73	N, E_ASN_96	H, E_ASN_96	2.93	1.99	16.05
1HGF.PDB	OD2, E_ASP_104	OG, E_SER_107	HG, E_SER_107	2.88	1.94	12.45
1HGF.PDB	O, E_TYR_105	N, E_ARG_109	H, E_ARG_109	2.91	1.93	1.03
1HGF.PDB	OE2, E_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.88	1.88	11.28
1HGF.PDB	OD2, E_ASP_79	OG, E_SER_110	HG, E_SER_110	2.78	1.90	21.69
1HGF.PDB	O, E_SER_107	N, E_LEU_111	H, E_LEU_111	2.99	2.02	8.11
1HGF.PDB	O, E_ARG_109	N, E_ALA_113	H, E_ALA_113	2.91	2.02	19.90
1HGF.PDB	O, E_SER_110	N, E_SER_114	H, E_SER_114	2.94	2.02	16.55
1HGF.PDB	OE2, E_GLU_119	OG1, E_THR_117	HG1, E_THR_117	2.96	1.99	6.08
1HGF.PDB	O, E_TYR_257	N, E_ILE_121	H, E_ILE_121	2.83	1.86	2.31
1HGF.PDB	O, E_ARG_255	N, E_GLU_123	H, E_GLU_123	2.87	1.92	11.49
1HGF.PDB	O, E_GLU_123	N, E_PHE_125	H, E_PHE_125	2.96	2.16	29.94
1HGF.PDB	O, E_THR_155	N, E_THR_131	H, E_THR_131	2.77	1.83	12.18
1HGF.PDB	ND2, E_ASN_152	NE2, E_GLN_132	HE21, E_GLN_132	2.95	2.01	11.55
1HGF.PDB	OD1, E_ASN_152	N, E_ASN_133	H, E_ASN_133	2.94	1.99	11.33
1HGF.PDB	O, E_TRP_153	N, E_GLY_134	H, E_GLY_134	2.99	2.07	16.55
1HGF.PDB	O, E_GLY_146	N, E_SER_136	H, E_SER_136	2.71	1.82	20.23
1HGF.PDB	OD2, E_ASP_77	NE, E_ARG_141	HE, E_ARG_141	2.92	2.06	25.46
1HGF.PDB	O, E_PHE_147	NH1, E_ARG_141	HH12, E_ARG_141	2.60	1.67	17.74
1HGF.PDB	OD1, E_ASP_77	NH2, E_ARG_141	HH21, E_ARG_141	2.83	1.96	25.41
1HGF.PDB	OD2, E_ASP_77	NH2, E_ARG_141	HH21, E_ARG_141	2.77	1.86	21.24
1HGF.PDB	O, E_SER_136	N, E_GLY_146	H, E_GLY_146	2.98	2.12	24.01
1HGF.PDB	O, E_GLY_72	N, E_SER_149	H, E_SER_149	2.88	1.98	19.21
1HGF.PDB	O, E_ALA_253	N, E_ASN_152	H, E_ASN_152	2.87	1.95	17.97
1HGF.PDB	OH, E_TYR_195	NE1, E_TRP_153	HE1, E_TRP_153	2.83	1.89	12.15
1HGF.PDB	O, E_LEU_194	N, E_LYS_156	H, E_LYS_156	2.87	1.98	19.42
1HGF.PDB	O, E_THR_160	N, E_SER_157	H, E_SER_157	2.99	2.11	21.85
1HGF.PDB	O, E_SER_247	N, E_LEU_164	H, E_LEU_164	2.72	1.84	21.47
1HGF.PDB	O, E_ILE_245	N, E_VAL_166	H, E_VAL_166	2.90	1.96	13.03
1HGF.PDB	O, E_ASP_241	N, E_ASN_170	H, E_ASN_170	2.87	1.90	4.85
1HGF.PDB	O, E_PHE_174	ND2, E_ASN_170	HD22, E_ASN_170	2.77	1.82	9.34
1HGF.PDB	O, E_VAL_237	N, E_LYS_176	H, E_LYS_176	2.92	1.99	15.75
1HGF.PDB	OE2, E_GLU_123	NZ, E_LYS_176	HZ1, E_LYS_176	2.76	1.80	18.44
1HGF.PDB	O, E_THR_235	N, E_TYR_178	H, E_TYR_178	2.83	1.85	2.97
1HGF.PDB	OE1, E_GLU_123	OH, E_TYR_178	HH, E_TYR_178	2.88	1.93	11.71

1HGF.PDB	OG1, E_THR_235	NE1, E_TRP_180	HE1, E_TRP_180	2.85	1.87	2.94
1HGF.PDB	O, E_ASN_250	N, E_HIS_183	H, E_HIS_183	2.80	1.96	25.59
1HGF.PDB	OH, E_TYR_98	NE2, E_HIS_183	HE2, E_HIS_183	2.91	1.99	15.99
1HGF.PDB	O, E_ARG_229	N, E_HIS_184	H, E_HIS_184	2.88	1.94	13.07
1HGF.PDB	OG, E_SER_231	NE2, E_HIS_184	HE2, E_HIS_184	2.70	1.89	28.56
1HGF.PDB	OD1, E_ASN_250	NE2, E_GLN_191	HE22, E_GLN_191	2.96	1.99	7.90
1HGF.PDB	O, E_ASN_188	N, E_THR_192	H, E_THR_192	2.94	2.01	14.37
1HGF.PDB	O, E_GLN_189	N, E_SER_193	H, E_SER_193	2.83	1.90	13.82
1HGF.PDB	O, E_GLU_190	N, E_LEU_194	H, E_LEU_194	2.94	1.99	12.89
1HGF.PDB	O, E_GLN_191	N, E_TYR_195	H, E_TYR_195	2.77	1.83	10.66
1HGF.PDB	O, E_ASN_248	NE2, E_GLN_197	HE21, E_GLN_197	2.89	2.01	21.02
1HGF.PDB	O, E_TYR_161	NE2, E_GLN_197	HE22, E_GLN_197	2.98	2.02	7.72
1HGF.PDB	O, E_ASN_246	N, E_THR_203	H, E_THR_203	2.97	2.01	9.92
1HGF.PDB	OG1, E_THR_212	OG1, E_THR_203	HG1, E_THR_203	2.89	1.95	9.70
1HGF.PDB	O, E_GLN_211	N, E_VAL_204	H, E_VAL_204	2.94	2.02	15.91
1HGF.PDB	OD1, E_ASP_241	N, E_ARG_207	H, E_ARG_207	2.90	1.94	9.22
1HGF.PDB	O, E_VAL_204	N, E_GLN_211	H, E_GLN_211	2.86	1.97	20.41
1HGF.PDB	O, E_VAL_202	N, E_ILE_213	H, E_ILE_213	2.88	1.97	17.74
1HGF.PDB	ND1, E_HIS_184	N, E_ASN_216	H, E_ASN_216	2.74	1.89	23.44
1HGF.PDB	O, E_ASN_216	NH1, E_ARG_220	HH12, E_ARG_220	2.97	2.15	29.37
1HGF.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.65	1.79	25.97
1HGF.PDB	O, E_ASN_216	NH2, E_ARG_220	HH22, E_ARG_220	2.76	1.86	21.47
1HGF.PDB	O, E_LEU_226	N, E_VAL_223	H, E_VAL_223	2.85	1.89	8.19
1HGF.PDB	O, E_CYS_97	NE, E_ARG_224	HE, E_ARG_224	2.78	1.93	24.07
1HGF.PDB	O, E_CYS_97	NH2, E_ARG_224	HH21, E_ARG_224	2.92	2.07	26.92
1HGF.PDB	O, E_VAL_223	N, E_LEU_226	H, E_LEU_226	2.92	1.97	10.75
1HGF.PDB	O, E_SER_228	NH1, E_ARG_229	HH11, E_ARG_229	2.73	1.81	20.22
1HGF.PDB	O, E_PRO_221	NH2, E_ARG_229	HH22, E_ARG_229	2.63	1.68	15.58
1HGF.PDB	O, E_PRO_99	N, E_ILE_230	H, E_ILE_230	2.96	2.12	25.49
1HGF.PDB	OD1, E_ASP_101	OG, E_SER_231	HG, E_SER_231	2.82	1.90	15.36
1HGF.PDB	O, E_ASP_101	N, E_ILE_232	H, E_ILE_232	2.91	1.98	14.67
1HGF.PDB	O, E_TRP_180	N, E_TYR_233	H, E_TYR_233	2.95	1.99	9.60
1HGF.PDB	O, E_TYR_178	N, E_THR_235	H, E_THR_235	2.86	1.98	21.39
1HGF.PDB	O, E_LYS_176	N, E_VAL_237	H, E_VAL_237	2.79	1.87	16.02
1HGF.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ2, E_LYS_238	2.83	1.84	16.42
1HGF.PDB	O, D_SER_71	NZ, E_LYS_238	HZ3, E_LYS_238	2.74	1.75	13.85
1HGF.PDB	O, E_ASN_170	N, E_GLY_240	H, E_GLY_240	2.92	2.12	29.34
1HGF.PDB	O, E_LYS_238	N, E_ASP_241	H, E_ASP_241	2.98	2.04	13.06
1HGF.PDB	OD1, E_ASP_241	N, E_VAL_242	H, E_VAL_242	2.72	1.93	29.38
1HGF.PDB	O, E_MET_168	N, E_LEU_243	H, E_LEU_243	2.94	1.97	6.95
1HGF.PDB	O, E_SER_205	N, E_VAL_244	H, E_VAL_244	2.94	1.98	11.07
1HGF.PDB	O, E_VAL_166	N, E_ILE_245	H, E_ILE_245	2.96	2.03	15.13
1HGF.PDB	O, E_THR_203	N, E_ASN_246	H, E_ASN_246	2.93	1.96	7.07
1HGF.PDB	OD1, E_ASN_165	ND2, E_ASN_246	HD21, E_ASN_246	2.93	2.02	19.67
1HGF.PDB	O, E_LEU_164	N, E_SER_247	H, E_SER_247	2.91	2.00	17.82
1HGF.PDB	O, E_ARG_201	OG, E_SER_247	HG, E_SER_247	2.77	1.98	29.79
1HGF.PDB	OG, E_SER_247	N, E_GLY_249	H, E_GLY_249	3.00	2.01	1.54
1HGF.PDB	O, E_HIS_183	ND2, E_ASN_250	HD21, E_ASN_250	2.78	1.81	7.40
1HGF.PDB	OE1, E_GLN_191	ND2, E_ASN_250	HD22, E_ASN_250	2.87	1.91	8.14
1HGF.PDB	O, E_ASN_152	N, E_ALA_253	H, E_ALA_253	2.95	2.04	17.49
1HGF.PDB	OD1, E_ASN_133	NH2, E_ARG_255	HH22, E_ARG_255	2.47	1.67	29.09
1HGF.PDB	O, E_ILE_121	N, E_TYR_257	H, E_TYR_257	2.99	2.17	27.08
1HGF.PDB	O, E_LEU_177	N, E_PHE_258	H, E_PHE_258	2.97	1.99	6.56
1HGF.PDB	OE1, E_GLU_119	NH2, E_ARG_261	HH22, E_ARG_261	2.73	1.89	28.16
1HGF.PDB	O, E_PHE_87	N, E_MET_268	H, E_MET_268	2.88	1.97	18.30
1HGF.PDB	O, E_PRO_284	OG, E_SER_270	HG, E_SER_270	2.78	1.84	9.58
1HGF.PDB	OG, E_SER_270	N, E_ALA_272	H, E_ALA_272	2.96	2.02	14.55
1HGF.PDB	O, E_ILE_51	N, E_ASP_275	H, E_ASP_275	2.91	2.03	21.67

1HGF.PDB	OD1, E_ASP_275	N, E_THR_276	H, E_THR_276	2.76	1.89	22.50
1HGF.PDB	O, E_ASN_54	N, E_SER_279	H, E_SER_279	2.78	1.83	11.19
1HGF.PDB	O, E_TYR_302	N, E_ILE_282	H, E_ILE_282	2.94	1.96	6.32
1HGF.PDB	O, E_THR_283	N, E_GLY_286	H, E_GLY_286	2.80	1.84	8.27
1HGF.PDB	O, E_LYS_50	N, E_SER_287	H, E_SER_287	2.79	1.82	5.70
1HGF.PDB	O, E_ALA_304	ND2, E_ASN_290	HD21, E_ASN_290	2.83	1.91	16.09
1HGF.PDB	OE1, E_GLN_44	NZ, E_LYS_292	HZ1, E_LYS_292	2.90	1.86	1.40
1HGF.PDB	OD1, E_ASP_291	NZ, E_LYS_292	HZ2, E_LYS_292	2.87	1.84	9.03
1HGF.PDB	O, E_LYS_307	N, E_GLN_295	H, E_GLN_295	2.82	1.98	25.22
1HGF.PDB	O, E_ASN_298	NE2, E_GLN_295	HE22, E_GLN_295	2.75	1.83	15.52
1HGF.PDB	O, E_GLN_44	N, E_ASN_296	H, E_ASN_296	2.89	1.94	10.75
1HGF.PDB	OD1, E_ASN_298	N, E_ILE_300	H, E_ILE_300	2.86	1.98	21.35
1HGF.PDB	O, E_ILE_282	N, E_TYR_302	H, E_TYR_302	2.78	1.95	26.52
1HGF.PDB	O, F_LYS_62	N, E_GLY_303	H, E_GLY_303	2.90	1.93	6.18
1HGF.PDB	O, E_GLN_295	N, E_VAL_309	H, E_VAL_309	2.93	2.06	22.44
1HGF.PDB	OG, F_SER_93	N, E_LYS_310	H, E_LYS_310	2.86	1.93	14.59
1HGF.PDB	OE1, E_GLU_41	OG1, E_THR_313	HG1, E_THR_313	2.68	1.89	29.15
1HGF.PDB	OE2, E_GLU_41	N, E_LEU_314	H, E_LEU_314	2.77	1.85	15.04
1HGF.PDB	OG1, E_THR_313	NZ, E_LYS_315	HZ2, E_LYS_315	2.94	2.00	21.30
1HGF.PDB	O, E_THR_40	N, E_LEU_316	H, E_LEU_316	2.76	1.85	16.85
1HGF.PDB	OD1, F_ASN_104	N, E_ALA_317	H, E_ALA_317	2.72	1.78	10.77
1HGF.PDB	O, E_ASN_38	N, E_THR_318	H, E_THR_318	2.90	1.95	12.98
1HGF.PDB	OE2, E_GLU_35	ND2, E_ASN_322	HD21, E_ASN_322	2.77	1.93	26.11
1HGF.PDB	O, E_VAL_20	ND2, E_ASN_322	HD22, E_ASN_322	2.96	2.04	16.53
1HGF.PDB	O, E_GLN_327	NZ, E_LYS_326	HZ2, E_LYS_326	2.70	1.74	17.93
1HGF.PDB	O, E_LYS_326	NE2, E_GLN_327	HE21, E_GLN_327	2.79	1.87	16.74
1HGF.PDB	OD2, F_ASP_112	N, F_GLY_1	H1, F_GLY_1	2.89	1.91	17.14
1HGF.PDB	OD1, F_ASP_109	N, F_LEU_2	H, F_LEU_2	2.91	2.00	18.77
1HGF.PDB	OD2, F_ASP_112	N, F_GLY_4	H, F_GLY_4	2.97	2.08	20.30
1HGF.PDB	OD1, F_ASP_112	N, F_ALA_5	H, F_ALA_5	2.98	2.11	23.47
1HGF.PDB	O, F_GLY_4	N, F_PHE_9	H, F_PHE_9	2.81	1.86	10.76
1HGF.PDB	O, F_GLY_13	ND2, F_ASN_12	HD21, F_ASN_12	2.77	1.93	24.90
1HGF.PDB	O, E_VAL_323	N, F_GLY_13	H, F_GLY_13	2.75	1.85	19.07
1HGF.PDB	O, E_HIS_17	N, F_TRP_14	H, F_TRP_14	2.87	1.96	16.52
1HGF.PDB	OG1, F_THR_41	N, F_TRP_21	H, F_TRP_21	2.91	1.99	16.39
1HGF.PDB	O, F_ALA_35	N, F_PHE_24	H, F_PHE_24	2.84	1.87	3.09
1HGF.PDB	O, E_CYS_14	N, F_ARG_25	H, F_ARG_25	2.91	1.94	8.25
1HGF.PDB	OE1, F_GLN_34	NE, F_ARG_25	HE, F_ARG_25	2.89	2.02	23.18
1HGF.PDB	OE1, F_GLN_34	NH2, F_ARG_25	HH21, F_ARG_25	2.91	2.03	24.46
1HGF.PDB	O, E_THR_12	N, F_GLN_27	H, F_GLN_27	3.00	2.08	17.91
1HGF.PDB	O, F_GLY_31	N, F_ASN_28	H, F_ASN_28	2.88	1.94	13.45
1HGF.PDB	O, F_CYS_144	ND2, F_ASN_28	HD21, F_ASN_28	2.81	1.91	20.19
1HGF.PDB	OD1, F_ASN_146	ND2, F_ASN_28	HD22, F_ASN_28	2.88	2.02	23.75
1HGF.PDB	O, F_ASN_28	N, F_GLY_31	H, F_GLY_31	2.91	2.04	22.35
1HGF.PDB	O, F_PHE_24	N, F_ALA_35	H, F_ALA_35	2.75	1.95	28.87
1HGF.PDB	O, F_TYR_22	N, F_ASP_37	H, F_ASP_37	2.72	1.77	3.63
1HGF.PDB	OD2, F_ASP_37	N, F_SER_40	H, F_SER_40	2.90	1.92	3.34
1HGF.PDB	O, F_ASP_37	OG1, F_THR_41	HG1, F_THR_41	2.65	1.82	24.28
1HGF.PDB	O, F_LEU_38	N, F_GLN_42	H, F_GLN_42	2.83	1.96	21.43
1HGF.PDB	OD1, F_ASP_46	NE2, F_GLN_42	HE21, F_GLN_42	2.86	1.99	23.71
1HGF.PDB	O, F_LYS_39	N, F_ALA_43	H, F_ALA_43	2.91	1.95	8.37
1HGF.PDB	O, F_SER_40	N, F_ALA_44	H, F_ALA_44	2.92	1.95	0.99
1HGF.PDB	O, F_GLN_42	N, F_ASP_46	H, F_ASP_46	2.79	1.83	7.98
1HGF.PDB	O, F_ALA_43	NE2, F_GLN_47	HE21, F_GLN_47	2.92	1.97	13.01
1HGF.PDB	O, F_ILE_45	N, F_ASN_49	H, F_ASN_49	2.88	1.99	20.58
1HGF.PDB	O, F_ASP_46	N, F_GLY_50	H, F_GLY_50	2.83	1.92	17.00
1HGF.PDB	O, F_GLN_47	N, F_LYS_51	H, F_LYS_51	2.95	1.98	4.87
1HGF.PDB	OE1, F_GLU_103	NZ, F_LYS_51	HZ1, F_LYS_51	2.72	1.69	6.79

1HGF.PDB	ND1, F_HIS_106	NZ, F_LYS_51	HZ3, F_LYS_51	2.66	1.70	17.89
1HGF.PDB	O, F_ILE_48	N, F_LEU_52	H, F_LEU_52	2.92	2.02	18.86
1HGF.PDB	O, F_ASN_49	N, F_ASN_53	H, F_ASN_53	2.83	1.96	22.00
1HGF.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.79	1.81	11.74
1HGF.PDB	OD2, D_ASP_86	NZ, F_LYS_62	HZ2, F_LYS_62	2.67	1.68	13.64
1HGF.PDB	OD2, D_ASP_90	NZ, F_LYS_62	HZ3, F_LYS_62	2.75	1.81	20.23
1HGF.PDB	OG, E_SER_266	ND1, F_HIS_64	HD1, F_HIS_64	2.65	1.77	20.25
1HGF.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.89	1.92	9.46
1HGF.PDB	O, F_PHE_63	NE2, F_GLN_65	HE21, F_GLN_65	2.97	2.00	6.66
1HGF.PDB	OE2, F_GLU_85	NZ, F_LYS_68	HZ1, F_LYS_68	2.64	1.77	26.62
1HGF.PDB	O, E_LYS_299	NZ, F_LYS_68	HZ2, F_LYS_68	2.97	1.95	8.70
1HGF.PDB	OG, A_SER_107	N, F_ARG_76	H, F_ARG_76	2.83	1.87	9.12
1HGF.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.86	1.88	5.84
1HGF.PDB	OE1, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.78	1.77	1.59
1HGF.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.69	1.70	7.61
1HGF.PDB	OE2, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.71	1.73	8.88
1HGF.PDB	O, F_GLY_75	N, F_ASP_79	H, F_ASP_79	2.99	2.05	14.09
1HGF.PDB	O, F_ILE_77	N, F_GLU_81	H, F_GLU_81	2.97	2.01	7.31
1HGF.PDB	O, F_GLN_78	N, F_LYS_82	H, F_LYS_82	2.99	2.12	23.13
1HGF.PDB	O, F_ASP_79	N, F_TYR_83	H, F_TYR_83	2.99	2.06	15.58
1HGF.PDB	O, F_LEU_80	N, F_VAL_84	H, F_VAL_84	2.90	1.94	9.23
1HGF.PDB	O, F_LYS_82	N, F_ASP_86	H, F_ASP_86	2.91	2.00	17.05
1HGF.PDB	O, F_TYR_83	N, F_THR_87	H, F_THR_87	2.99	2.06	14.57
1HGF.PDB	O, F_VAL_84	N, F_LYS_88	H, F_LYS_88	2.93	1.98	10.82
1HGF.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.55	1.63	21.75
1HGF.PDB	O, F_GLU_85	N, F_ILE_89	H, F_ILE_89	2.95	2.00	10.35
1HGF.PDB	O, F_LYS_88	N, F_TRP_92	H, F_TRP_92	2.92	1.96	8.47
1HGF.PDB	O, F_ILE_89	N, F_SER_93	H, F_SER_93	2.89	2.01	22.68
1HGF.PDB	O, F_ASP_90	N, F_TYR_94	H, F_TYR_94	2.99	2.08	18.84
1HGF.PDB	O, F_TRP_92	N, F_ALA_96	H, F_ALA_96	3.00	2.04	10.19
1HGF.PDB	O, F_TYR_94	N, F_LEU_98	H, F_LEU_98	2.95	2.00	11.08
1HGF.PDB	O, F_ASN_95	N, F_LEU_99	H, F_LEU_99	2.97	2.00	8.54
1HGF.PDB	O, F_LEU_98	N, F_LEU_102	H, F_LEU_102	2.99	2.02	4.18
1HGF.PDB	O, F_LEU_99	N, F_GLU_103	H, F_GLU_103	2.91	1.96	12.29
1HGF.PDB	O, F_VAL_100	N, F_ASN_104	H, F_ASN_104	2.82	1.88	14.39
1HGF.PDB	O, E_LYS_27	ND2, F_ASN_104	HD21, F_ASN_104	2.91	1.99	15.12
1HGF.PDB	O, F_LEU_102	N, F_HIS_106	H, F_HIS_106	2.96	1.99	6.92
1HGF.PDB	O, F_GLU_103	N, F_THR_107	H, F_THR_107	2.86	1.92	13.75
1HGF.PDB	O, F_ASN_104	N, F_ILE_108	H, F_ILE_108	2.95	2.03	17.77
1HGF.PDB	O, F_HIS_106	N, F_LEU_110	H, F_LEU_110	2.80	1.84	8.75
1HGF.PDB	O, F_ASP_109	N, F_SER_113	H, F_SER_113	2.83	1.88	9.86
1HGF.PDB	O, D_LEU_2	OG, F_SER_113	HG, F_SER_113	2.73	1.92	27.40
1HGF.PDB	O, F_SER_113	N, F_LYS_117	H, F_LYS_117	2.77	1.85	14.47
1HGF.PDB	O, F_GLU_114	N, F_LEU_118	H, F_LEU_118	2.99	2.05	13.43
1HGF.PDB	O, F_MET_115	N, F_PHE_119	H, F_PHE_119	2.96	2.03	15.65
1HGF.PDB	O, F_ASN_116	N, F_GLU_120	H, F_GLU_120	2.89	1.91	2.90
1HGF.PDB	O, F_PHE_119	N, F_ARG_123	H, F_ARG_123	2.99	2.04	11.96
1HGF.PDB	OE2, F_GLU_120	NH1, F_ARG_123	HH11, F_ARG_123	2.79	1.92	25.30
1HGF.PDB	O, F_GLU_120	N, F_ARG_124	H, F_ARG_124	2.94	1.99	12.33
1HGF.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.90	1.96	15.73
1HGF.PDB	OH, F_TYR_157	ND2, F_ASN_129	HD21, F_ASN_129	2.83	1.89	13.44
1HGF.PDB	O, F_HIS_159	ND2, F_ASN_129	HD22, F_ASN_129	2.96	2.06	18.90
1HGF.PDB	O, F_LYS_139	N, F_GLU_131	H, F_GLU_131	2.97	2.06	18.31
1HGF.PDB	O, F_CYS_137	N, F_MET_133	H, F_MET_133	2.91	1.96	10.70
1HGF.PDB	O, E_LEU_13	N, F_PHE_138	H, F_PHE_138	2.75	1.92	26.04
1HGF.PDB	O, F_GLU_131	N, F_LYS_139	H, F_LYS_139	2.85	1.90	10.44
1HGF.PDB	O, E_ALA_11	N, F_ILE_140	H, F_ILE_140	2.82	1.90	16.36
1HGF.PDB	O, F_ASN_129	N, F_TYR_141	H, F_TYR_141	2.91	1.97	14.31

1HGF.PDB	OD2, F_ASP_145	N, F_ALA_147	H, F_ALA_147	2.85	1.95	18.91
1HGF.PDB	O, F_ASP_145	N, F_ILE_149	H, F_ILE_149	2.92	1.96	9.99
1HGF.PDB	O, F_ASN_146	N, F_GLU_150	H, F_GLU_150	2.92	2.01	16.83
1HGF.PDB	O, F_GLU_150	N, F_ASN_154	H, F_ASN_154	2.85	1.95	19.47
1HGF.PDB	O, F_SER_151	N, F_THR_156	H, F_THR_156	2.79	1.97	27.62
1HGF.PDB	O, F_HIS_159	N, F_TYR_162	H, F_TYR_162	2.90	2.05	24.52
1HGF.PDB	OE1, D_GLU_131	NH2, F_ARG_163	HH21, F_ARG_163	2.69	1.84	27.00
1HGF.PDB	O, F_TYR_162	N, F_ALA_166	H, F_ALA_166	2.88	1.92	7.02
1HGF.PDB	O, F_ARG_163	N, F_LEU_167	H, F_LEU_167	2.80	1.84	8.02
1HGF.PDB	O, F_GLU_165	ND2, F_ASN_169	HD21, F_ASN_169	3.00	2.05	10.68
1HGF.PDB	O, F_ALA_166	N, F_ARG_170	H, F_ARG_170	2.86	2.02	25.68
1HGF.PDB	O, F_GLU_128	NE, F_ARG_170	HE, F_ARG_170	2.79	1.90	20.12
1HGF.PDB	OE2, F_GLU_131	NH1, F_ARG_170	HH11, F_ARG_170	2.85	1.84	3.96
1HGF.PDB	O, F_LEU_167	N, F_PHE_171	H, F_PHE_171	2.90	1.96	11.83

Table 1666: 1HGF-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1HGG.PDB	O, B_ILE_140	N, A_ALA_11	H, A_ALA_11	2.90	1.98	16.87
1HGG.PDB	O, B_PHE_138	N, A_LEU_13	H, A_LEU_13	2.97	2.01	10.10
1HGG.PDB	O, B_ARG_25	N, A_CYS_14	H, A_CYS_14	2.92	1.97	11.02
1HGG.PDB	O, B_GLY_136	N, A_LEU_15	H, A_LEU_15	2.86	1.89	7.78
1HGG.PDB	O, B_GLY_23	N, A_GLY_16	H, A_GLY_16	2.90	2.00	20.11
1HGG.PDB	O, B_TRP_21	N, A_HIS_18	H, A_HIS_18	2.90	1.99	17.50
1HGG.PDB	OD1, A_ASN_322	N, A_VAL_20	H, A_VAL_20	2.82	1.84	4.55
1HGG.PDB	O, A_VAL_36	N, A_THR_24	H, A_THR_24	2.85	1.98	22.87
1HGG.PDB	O, A_ILE_34	N, A_VAL_26	H, A_VAL_26	2.77	1.83	12.78
1HGG.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.90	1.87	9.15
1HGG.PDB	O, A_VAL_26	N, A_ILE_34	H, A_ILE_34	2.94	2.01	14.94
1HGG.PDB	O, A_THR_24	N, A_VAL_36	H, A_VAL_36	2.80	1.84	7.79
1HGG.PDB	O, A_MET_320	N, A_THR_37	H, A_THR_37	2.90	1.93	7.41
1HGG.PDB	O, A_LEU_316	N, A_THR_40	H, A_THR_40	2.81	1.95	23.35
1HGG.PDB	O, A_LEU_314	N, A_LEU_42	H, A_LEU_42	2.87	2.00	23.31
1HGG.PDB	O, A_PHE_294	N, A_GLN_44	H, A_GLN_44	2.82	1.86	8.73
1HGG.PDB	OD2, A_ASP_275	NZ, A_LYS_50	HZ1, A_LYS_50	2.71	1.78	22.40
1HGG.PDB	O, A_PRO_273	N, A_ILE_51	H, A_ILE_51	2.76	1.80	7.18
1HGG.PDB	O, A_ASP_275	N, A_ASN_53	H, A_ASN_53	2.78	1.93	24.69
1HGG.PDB	OD2, A_ASP_85	N, A_ARG_57	H, A_ARG_57	2.88	1.93	11.04
1HGG.PDB	O, A_THR_83	NE, A_ARG_57	HE, A_ARG_57	2.76	1.79	4.99
1HGG.PDB	O, A_LEU_86	N, A_LEU_59	H, A_LEU_59	2.94	1.98	9.64
1HGG.PDB	O, A_VAL_88	N, A_GLY_61	H, A_GLY_61	2.99	2.14	24.72
1HGG.PDB	OD1, A_ASP_60	N, A_ILE_62	H, A_ILE_62	2.86	1.94	14.24
1HGG.PDB	O, A_GLY_61	N, A_CYS_64	H, A_CYS_64	2.94	2.01	15.60
1HGG.PDB	O, A_LEU_66	N, A_LEU_70	H, A_LEU_70	2.85	1.95	18.25
1HGG.PDB	O, A_ILE_67	N, A_LEU_71	H, A_LEU_71	2.83	1.86	6.13
1HGG.PDB	O, A_ASP_68	N, A_GLY_72	H, A_GLY_72	2.84	1.93	17.70
1HGG.PDB	OD1, A_ASP_73	N, A_HIS_75	H, A_HIS_75	2.97	2.06	18.51
1HGG.PDB	OD1, A_ASP_73	ND1, A_HIS_75	HD1, A_HIS_75	2.77	1.87	17.99
1HGG.PDB	O, A_ASP_63	NE2, A_HIS_75	HE2, A_HIS_75	2.83	1.88	12.09
1HGG.PDB	O, A_ASP_73	N, A_CYS_76	H, A_CYS_76	2.73	1.81	15.45
1HGG.PDB	O, A_PRO_74	N, A_ASP_77	H, A_ASP_77	2.92	1.97	11.68
1HGG.PDB	O, A_CYS_76	N, A_PHE_79	H, A_PHE_79	2.99	2.02	6.69
1HGG.PDB	O, A_PHE_79	N, A_GLU_82	H, A_GLU_82	3.00	2.09	17.80
1HGG.PDB	O, A_ARG_57	N, A_ASP_85	H, A_ASP_85	2.86	1.95	17.16
1HGG.PDB	O, A_SER_266	N, A_PHE_87	H, A_PHE_87	2.98	2.05	14.85
1HGG.PDB	O, A_LEU_59	N, A_VAL_88	H, A_VAL_88	2.95	1.98	7.50
1HGG.PDB	O, A_MET_268	N, A_GLU_89	H, A_GLU_89	2.80	1.85	11.55
1HGG.PDB	OD1, A_ASP_60	NE, A_ARG_90	HE, A_ARG_90	2.94	1.96	6.92
1HGG.PDB	O, A_SER_270	NH1, A_ARG_90	HH11, A_ARG_90	2.63	1.77	25.03
1HGG.PDB	O, A_ALA_272	NH1, A_ARG_90	HH12, A_ARG_90	2.66	1.75	18.96
1HGG.PDB	OD2, A_ASP_60	NH2, A_ARG_90	HH21, A_ARG_90	2.79	1.81	10.63
1HGG.PDB	OD1, A_ASP_271	N, A_SER_91	H, A_SER_91	2.92	1.99	16.08
1HGG.PDB	OD1, A_ASP_271	OG, A_SER_91	HG, A_SER_91	2.86	2.03	25.78
1HGG.PDB	OD2, A_ASP_271	OG, A_SER_91	HG, A_SER_91	2.85	1.97	21.46
1HGG.PDB	O, A_ASP_63	N, A_PHE_94	H, A_PHE_94	3.00	2.04	11.56
1HGG.PDB	OD2, A_ASP_68	OG, A_SER_95	HG, A_SER_95	2.94	1.99	11.26
1HGG.PDB	OD2, A_ASP_73	N, A_ASN_96	H, A_ASN_96	2.86	1.92	13.44
1HGG.PDB	SG, A_CYS_97	N, A_TYR_98	H, A_TYR_98	2.99	2.16	26.19
1HGG.PDB	OD1, A_ASP_68	OH, A_TYR_100	HH, A_TYR_100	2.94	1.99	11.28
1HGG.PDB	O, A_ILE_230	N, A_ASP_101	H, A_ASP_101	2.99	2.10	21.45
1HGG.PDB	OD1, A_ASP_104	N, A_SER_107	H, A_SER_107	2.91	2.03	21.37
1HGG.PDB	OD2, A_ASP_104	OG, A_SER_107	HG, A_SER_107	2.84	1.92	16.45
1HGG.PDB	O, A_TYR_105	N, A_ARG_109	H, A_ARG_109	2.79	1.82	3.79
1HGG.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.84	1.86	14.43
1HGG.PDB	OD2, F_ASP_79	OG, A_SER_110	HG, A_SER_110	2.88	1.95	14.29

1HGG.PDB	O, A_SER_107	N, A_LEU_111	H, A_LEU_111	2.81	1.85	7.66
1HGG.PDB	O, A_ARG_109	N, A_ALA_113	H, A_ALA_113	2.89	1.98	17.55
1HGG.PDB	O, A_SER_110	N, A_SER_114	H, A_SER_114	2.94	2.01	15.84
1HGG.PDB	OE2, A_GLU_119	OG1, A_THR_117	HG1, A_THR_117	2.88	1.93	9.58
1HGG.PDB	O, A_TYR_257	N, A_ILE_121	H, A_ILE_121	2.89	1.92	8.73
1HGG.PDB	O, A_ARG_255	N, A_GLU_123	H, A_GLU_123	2.94	2.00	13.79
1HGG.PDB	O, A_THR_155	N, A_THR_131	H, A_THR_131	2.73	1.83	17.36
1HGG.PDB	OD1, A_ASN_152	N, A_ASN_133	H, A_ASN_133	2.89	1.97	16.60
1HGG.PDB	O, A_GLY_146	N, A_SER_136	H, A_SER_136	2.76	1.85	17.88
1HGG.PDB	OG, A_SER_136	N, A_ALA_138	H, A_ALA_138	2.88	1.92	8.65
1HGG.PDB	O, A_GLY_144	NZ, A_LYS_140	HZ1, A_LYS_140	2.89	1.90	15.38
1HGG.PDB	OD1, A_ASN_137	NZ, A_LYS_140	HZ2, A_LYS_140	2.76	1.76	13.87
1HGG.PDB	OD2, A_ASP_77	NE, A_ARG_141	HE, A_ARG_141	2.89	2.07	28.91
1HGG.PDB	O, A_PHE_147	NH1, A_ARG_141	HH12, A_ARG_141	2.49	1.65	25.86
1HGG.PDB	OD1, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.76	1.85	22.03
1HGG.PDB	OD2, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.76	1.87	24.00
1HGG.PDB	O, A_GLY_72	NH2, A_ARG_141	HH22, A_ARG_141	2.92	1.93	7.80
1HGG.PDB	O, A_SER_136	N, A_GLY_146	H, A_GLY_146	2.98	2.09	20.80
1HGG.PDB	O, A_GLY_72	N, A_SER_149	H, A_SER_149	2.90	1.98	16.68
1HGG.PDB	O, A_ALA_253	N, A_ASN_152	H, A_ASN_152	2.72	1.87	24.29
1HGG.PDB	OH, A_TYR_195	NE1, A_TRP_153	HE1, A_TRP_153	2.91	1.96	13.96
1HGG.PDB	O, A_THR_131	N, A_THR_155	H, A_THR_155	2.93	1.99	12.97
1HGG.PDB	O, A_LEU_194	N, A_LYS_156	H, A_LYS_156	2.97	2.08	20.53
1HGG.PDB	O, A_SER_193	NZ, A_LYS_156	HZ2, A_LYS_156	2.65	1.69	18.25
1HGG.PDB	O, A_THR_160	N, A_SER_157	H, A_SER_157	2.97	2.06	18.87
1HGG.PDB	O, A_ILE_245	N, A_VAL_166	H, A_VAL_166	2.87	1.91	9.82
1HGG.PDB	O, A_LEU_243	OG1, A_THR_167	HG1, A_THR_167	2.86	1.98	20.98
1HGG.PDB	O, A_LEU_243	N, A_MET_168	H, A_MET_168	2.89	1.96	15.80
1HGG.PDB	O, A_ASP_241	N, A_ASN_170	H, A_ASN_170	2.91	1.93	5.10
1HGG.PDB	O, A_PHE_174	ND2, A_ASN_170	HD21, A_ASN_170	2.81	1.87	12.89
1HGG.PDB	O, A_VAL_237	ND2, A_ASN_170	HD22, A_ASN_170	2.85	1.98	22.66
1HGG.PDB	O, A_VAL_237	N, A_LYS_176	H, A_LYS_176	2.93	1.99	14.07
1HGG.PDB	OE2, A_GLU_123	NZ, A_LYS_176	HZ1, A_LYS_176	2.65	1.77	25.92
1HGG.PDB	O, A_THR_235	N, A_TYR_178	H, A_TYR_178	2.78	1.81	6.55
1HGG.PDB	OE1, A_GLU_123	OH, A_TYR_178	HH, A_TYR_178	2.78	1.83	8.16
1HGG.PDB	OG1, A_THR_235	NE1, A_TRP_180	HE1, A_TRP_180	2.92	1.93	2.35
1HGG.PDB	O, A_ASN_250	N, A_HIS_183	H, A_HIS_183	2.79	1.91	21.79
1HGG.PDB	O, A_ARG_229	N, A_HIS_184	H, A_HIS_184	2.85	1.88	5.64
1HGG.PDB	OG, A_SER_231	NE2, A_HIS_184	HE2, A_HIS_184	2.80	1.92	21.87
1HGG.PDB	OG1, A_THR_187	N, A_GLU_190	H, A_GLU_190	2.84	1.88	9.16
1HGG.PDB	O, A_THR_187	N, A_GLN_191	H, A_GLN_191	3.00	2.05	11.25
1HGG.PDB	O, A_GLN_197	NE2, A_GLN_191	HE22, A_GLN_191	2.89	1.99	19.48
1HGG.PDB	O, A_ASN_188	OG1, A_THR_192	HG1, A_THR_192	2.94	2.01	12.14
1HGG.PDB	O, A_GLN_189	N, A_SER_193	H, A_SER_193	2.84	1.87	5.56
1HGG.PDB	O, A_GLN_189	OG, A_SER_193	HG, A_SER_193	2.70	1.82	19.80
1HGG.PDB	O, A_GLU_190	N, A_LEU_194	H, A_LEU_194	2.99	2.04	11.68
1HGG.PDB	O, A_GLN_191	N, A_TYR_195	H, A_TYR_195	2.81	1.87	11.54
1HGG.PDB	O, A_THR_192	N, A_VAL_196	H, A_VAL_196	2.94	2.12	27.19
1HGG.PDB	O, A_TYR_161	NE2, A_GLN_197	HE21, A_GLN_197	2.91	1.94	6.31
1HGG.PDB	O, A_ASN_248	NE2, A_GLN_197	HE22, A_GLN_197	2.93	2.04	20.44
1HGG.PDB	OD1, A_ASN_246	NH2, A_ARG_201	HH21, A_ARG_201	2.65	1.72	18.81
1HGG.PDB	O, A_ILE_213	N, A_VAL_202	H, A_VAL_202	2.91	1.94	9.19
1HGG.PDB	O, A_ASN_246	N, A_THR_203	H, A_THR_203	2.82	1.89	14.13
1HGG.PDB	O, A_GLN_211	N, A_VAL_204	H, A_VAL_204	2.88	1.97	18.00
1HGG.PDB	O, A_SER_209	N, A_THR_206	H, A_THR_206	2.97	2.00	7.26
1HGG.PDB	OD1, A_ASP_241	N, A_ARG_207	H, A_ARG_207	2.89	1.94	12.62
1HGG.PDB	OD2, A_ASP_241	NE, A_ARG_208	HE, A_ARG_208	2.96	2.06	20.34
1HGG.PDB	OG1, A_THR_206	OG, A_SER_209	HG, A_SER_209	2.95	2.03	14.98

1HGG.PDB	OD1, E.ASP.101	NE2, A.GLN.210	HE22, A.GLN.210	2.99	2.07	17.95
1HGG.PDB	O, A.VAL.204	N, A.GLN.211	H, A.GLN.211	2.83	1.92	18.11
1HGG.PDB	OG1, A.THR.203	OG1, A.THR.212	HG1, A.THR.212	2.88	1.92	6.20
1HGG.PDB	O, A.VAL.202	N, A.ILE.213	H, A.ILE.213	2.82	1.90	15.67
1HGG.PDB	OE1, C.GLN.210	NH2, A.ARG.220	HH21, A.ARG.220	2.73	1.78	15.93
1HGG.PDB	O, A.ASN.216	NH2, A.ARG.220	HH22, A.ARG.220	2.70	1.79	20.31
1HGG.PDB	O, A.LEU.226	N, A.VAL.223	H, A.VAL.223	2.90	1.94	11.61
1HGG.PDB	O, A.CYS.97	NE, A.ARG.224	HE, A.ARG.224	2.79	1.96	26.10
1HGG.PDB	O, A.CYS.97	NH2, A.ARG.224	HH21, A.ARG.224	2.82	1.96	25.99
1HGG.PDB	O, A.VAL.223	N, A.LEU.226	H, A.LEU.226	2.95	2.01	13.46
1HGG.PDB	O, A.SER.228	NH1, A.ARG.229	HH11, A.ARG.229	2.74	1.81	18.53
1HGG.PDB	O, A.PRO.221	NH2, A.ARG.229	HH22, A.ARG.229	2.60	1.67	16.87
1HGG.PDB	OD1, A.ASP.101	OG, A.SER.231	HG, A.SER.231	2.88	1.92	8.82
1HGG.PDB	O, A.ASP.101	N, A.ILE.232	H, A.ILE.232	2.92	2.00	16.64
1HGG.PDB	O, A.TRP.180	N, A.TYR.233	H, A.TYR.233	2.89	1.93	10.84
1HGG.PDB	O, A.TYR.178	N, A.THR.235	H, A.THR.235	2.90	2.00	18.55
1HGG.PDB	O, A.LYS.176	N, A.VAL.237	H, A.VAL.237	2.81	1.85	9.01
1HGG.PDB	O, F.SER.71	NZ, A.LYS.238	HZ2, A.LYS.238	2.70	1.77	20.55
1HGG.PDB	OE1, F.GLU.72	NZ, A.LYS.238	HZ3, A.LYS.238	2.93	1.93	14.31
1HGG.PDB	OE2, F.GLU.72	NZ, A.LYS.238	HZ3, A.LYS.238	2.74	1.91	29.92
1HGG.PDB	O, A.ASN.170	N, A.GLY.240	H, A.GLY.240	2.85	1.99	23.50
1HGG.PDB	O, A.LYS.238	N, A.ASP.241	H, A.ASP.241	2.97	2.05	16.90
1HGG.PDB	OD1, A.ASP.241	N, A.VAL.242	H, A.VAL.242	2.79	1.98	28.57
1HGG.PDB	O, A.MET.168	N, A.LEU.243	H, A.LEU.243	2.88	1.91	4.58
1HGG.PDB	O, A.SER.205	N, A.VAL.244	H, A.VAL.244	2.92	1.98	13.47
1HGG.PDB	O, A.VAL.166	N, A.ILE.245	H, A.ILE.245	2.93	2.00	14.39
1HGG.PDB	O, A.THR.203	N, A.ASN.246	H, A.ASN.246	2.89	1.94	11.24
1HGG.PDB	OD1, A.ASN.165	ND2, A.ASN.246	HD22, A.ASN.246	2.90	1.98	17.02
1HGG.PDB	O, A.LEU.164	N, A.SER.247	H, A.SER.247	2.90	1.99	18.81
1HGG.PDB	OE1, A.GLN.191	ND2, A.ASN.250	HD21, A.ASN.250	2.92	1.96	11.11
1HGG.PDB	O, A.HIS.183	ND2, A.ASN.250	HD22, A.ASN.250	2.85	1.89	9.48
1HGG.PDB	O, A.ASN.152	N, A.ALA.253	H, A.ALA.253	2.86	1.94	16.70
1HGG.PDB	OD1, A.ASN.133	NH2, A.ARG.255	HH22, A.ARG.255	2.52	1.66	24.50
1HGG.PDB	O, A.ILE.121	N, A.TYR.257	H, A.TYR.257	2.96	2.12	25.89
1HGG.PDB	O, A.LEU.177	N, A.PHE.258	H, A.PHE.258	2.95	2.01	12.69
1HGG.PDB	OG, A.SER.115	N, A.ARG.261	H, A.ARG.261	2.99	2.03	11.53
1HGG.PDB	OE2, A.GLU.119	NH1, A.ARG.261	HH12, A.ARG.261	2.68	1.87	29.79
1HGG.PDB	OE1, A.GLU.119	NH2, A.ARG.261	HH22, A.ARG.261	2.74	1.88	26.75
1HGG.PDB	OH, A.TYR.302	NZ, A.LYS.264	HZ1, A.LYS.264	2.93	1.98	19.58
1HGG.PDB	ND1, A.HIS.56	NZ, A.LYS.264	HZ2, A.LYS.264	2.66	1.73	19.87
1HGG.PDB	OD2, A.ASP.85	NZ, A.LYS.264	HZ3, A.LYS.264	2.83	1.83	12.74
1HGG.PDB	O, A.PHE.87	N, A.MET.268	H, A.MET.268	2.85	1.96	20.36
1HGG.PDB	OE1, B.GLU.67	NH1, A.ARG.269	HH12, A.ARG.269	2.69	1.86	28.34
1HGG.PDB	O, A.PRO.284	OG, A.SER.270	HG, A.SER.270	2.78	1.86	15.49
1HGG.PDB	OG, A.SER.270	N, A.ALA.272	H, A.ALA.272	2.95	2.00	11.38
1HGG.PDB	O, A.ILE.51	N, A.ASP.275	H, A.ASP.275	2.83	1.95	21.40
1HGG.PDB	OD1, A.ASP.275	N, A.THR.276	H, A.THR.276	2.80	1.95	24.62
1HGG.PDB	O, A.ASN.54	N, A.SER.279	H, A.SER.279	2.79	1.85	12.05
1HGG.PDB	O, A.TYR.302	N, A.ILE.282	H, A.ILE.282	2.87	1.93	13.76
1HGG.PDB	O, A.THR.283	N, A.GLY.286	H, A.GLY.286	2.80	1.86	11.09
1HGG.PDB	O, A.LYS.50	N, A.SER.287	H, A.SER.287	2.87	1.90	6.27
1HGG.PDB	O, A.ALA.304	ND2, A.ASN.290	HD22, A.ASN.290	2.86	1.98	20.93
1HGG.PDB	OE1, A.GLN.44	NZ, A.LYS.292	HZ1, A.LYS.292	2.74	1.73	11.51
1HGG.PDB	OD2, A.ASP.291	NZ, A.LYS.292	HZ3, A.LYS.292	2.77	1.90	27.56
1HGG.PDB	O, A.LYS.307	N, A.GLN.295	H, A.GLN.295	2.78	1.90	20.19
1HGG.PDB	O, A.ASN.298	NE2, A.GLN.295	HE21, A.GLN.295	2.82	1.86	7.25
1HGG.PDB	O, A.GLN.44	N, A.ASN.296	H, A.ASN.296	2.89	1.94	10.48
1HGG.PDB	OD1, A.ASN.285	ND2, A.ASN.298	HD22, A.ASN.298	2.97	2.01	11.28

1HGG.PDB	O, B_LYS_68	NZ, A_LYS_299	HZ1, A_LYS_299	2.91	1.88	9.16
1HGG.PDB	OD1, A_ASN_298	N, A_ILE_300	H, A_ILE_300	2.88	1.94	13.01
1HGG.PDB	O, A_ILE_282	N, A_TYR_302	H, A_TYR_302	2.82	1.93	21.11
1HGG.PDB	O, A_LYS_264	OH, A_TYR_302	HH, A_TYR_302	2.68	1.87	27.38
1HGG.PDB	O, B_LYS_62	N, A_GLY_303	H, A_GLY_303	2.91	1.94	6.06
1HGG.PDB	O, A_GLN_295	N, A_VAL_309	H, A_VAL_309	2.91	2.09	27.06
1HGG.PDB	OG, B_SER_93	N, A_LYS_310	H, A_LYS_310	2.89	1.96	14.59
1HGG.PDB	OD1, B_ASP_90	NZ, A_LYS_310	HZ2, A_LYS_310	2.70	1.74	18.08
1HGG.PDB	OE2, A_GLU_41	N, A_LEU_314	H, A_LEU_314	2.82	1.91	16.70
1HGG.PDB	OE1, A_GLU_41	NZ, A_LYS_315	HZ3, A_LYS_315	2.73	1.81	23.14
1HGG.PDB	O, A_THR_40	N, A_LEU_316	H, A_LEU_316	2.77	1.85	15.18
1HGG.PDB	OD1, B_ASN_104	N, A_ALA_317	H, A_ALA_317	2.79	1.88	16.20
1HGG.PDB	O, A_ASN_38	N, A_THR_318	H, A_THR_318	2.90	1.97	14.69
1HGG.PDB	O, A_VAL_20	ND2, A_ASN_322	HD21, A_ASN_322	2.85	1.93	15.64
1HGG.PDB	OE2, A_GLU_35	ND2, A_ASN_322	HD22, A_ASN_322	2.81	1.95	25.01
1HGG.PDB	OE2, B_GLU_15	NZ, A_LYS_326	HZ1, A_LYS_326	2.83	1.89	21.04
1HGG.PDB	OE1, A_GLU_325	NZ, A_LYS_326	HZ3, A_LYS_326	2.82	1.86	18.51
1HGG.PDB	OD2, B_ASP_112	N, B_GLY_1	H2, B_GLY_1	2.70	1.71	13.07
1HGG.PDB	OD1, B_ASP_109	N, B_LEU_2	H, B_LEU_2	2.95	2.05	19.45
1HGG.PDB	OD2, B_ASP_112	N, B_PHE_3	H, B_PHE_3	2.84	2.02	27.93
1HGG.PDB	OD2, B_ASP_112	N, B_GLY_4	H, B_GLY_4	2.94	2.03	17.01
1HGG.PDB	OD1, B_ASP_112	N, B_ALA_5	H, B_ALA_5	2.91	2.04	23.33
1HGG.PDB	O, B_GLY_4	N, B_PHE_9	H, B_PHE_9	2.76	1.84	15.80
1HGG.PDB	O, A_VAL_323	N, B_GLY_13	H, B_GLY_13	2.71	1.78	13.00
1HGG.PDB	O, A_HIS_17	N, B_TRP_14	H, B_TRP_14	2.79	1.88	17.76
1HGG.PDB	OG1, B_THR_41	N, B_TRP_21	H, B_TRP_21	2.85	1.90	11.01
1HGG.PDB	O, A_GLY_16	N, B_GLY_23	H, B_GLY_23	2.99	2.09	20.32
1HGG.PDB	O, B_ALA_35	N, B_PHE_24	H, B_PHE_24	2.82	1.86	7.34
1HGG.PDB	OE1, B_GLN_34	NE, B_ARG_25	HE, B_ARG_25	2.80	1.89	18.36
1HGG.PDB	OE1, B_GLN_34	NH2, B_ARG_25	HH21, B_ARG_25	2.91	2.04	24.97
1HGG.PDB	OE2, A_GLU_325	NH2, B_ARG_25	HH22, B_ARG_25	2.94	1.96	12.23
1HGG.PDB	O, B_GLY_33	N, B_HIS_26	H, B_HIS_26	2.74	1.85	19.00
1HGG.PDB	O, B_GLY_31	N, B_ASN_28	H, B_ASN_28	2.71	1.77	11.36
1HGG.PDB	O, B_ASN_28	N, B_GLY_31	H, B_GLY_31	2.90	1.97	14.90
1HGG.PDB	O, B_PHE_24	N, B_ALA_35	H, B_ALA_35	2.88	2.07	28.80
1HGG.PDB	O, B_TYR_22	N, B_ASP_37	H, B_ASP_37	2.72	1.76	2.83
1HGG.PDB	OD2, B_ASP_37	N, B_SER_40	H, B_SER_40	2.85	1.90	11.78
1HGG.PDB	OD2, B_ASP_37	OG, B_SER_40	HG, B_SER_40	2.80	1.93	21.69
1HGG.PDB	O, B_ASP_37	OG1, B_THR_41	HG1, B_THR_41	2.72	1.82	17.56
1HGG.PDB	O, B_LEU_38	N, B_GLN_42	H, B_GLN_42	2.94	1.99	12.08
1HGG.PDB	OD1, B_ASP_46	NE2, B_GLN_42	HE22, B_GLN_42	2.83	1.95	21.37
1HGG.PDB	O, B_LYS_39	N, B_ALA_43	H, B_ALA_43	2.99	2.02	7.45
1HGG.PDB	O, B_SER_40	N, B_ALA_44	H, B_ALA_44	2.94	1.96	2.17
1HGG.PDB	O, B_THR_41	N, B_ILE_45	H, B_ILE_45	2.95	2.02	15.56
1HGG.PDB	O, B_GLN_42	N, B_ASP_46	H, B_ASP_46	2.79	1.82	3.46
1HGG.PDB	OE2, B_GLU_114	NE2, B_GLN_47	HE21, B_GLN_47	2.96	2.05	17.92
1HGG.PDB	O, B_ALA_43	NE2, B_GLN_47	HE22, B_GLN_47	2.97	2.06	17.51
1HGG.PDB	O, B_ILE_45	N, B_ASN_49	H, B_ASN_49	2.86	1.94	16.30
1HGG.PDB	O, B_ASP_46	N, B_GLY_50	H, B_GLY_50	2.92	2.06	23.80
1HGG.PDB	O, B_GLN_47	N, B_LYS_51	H, B_LYS_51	2.94	1.96	0.16
1HGG.PDB	OG1, B_THR_107	NZ, B_LYS_51	HZ1, B_LYS_51	2.97	2.00	18.19
1HGG.PDB	OE1, B_GLU_103	NZ, B_LYS_51	HZ2, B_LYS_51	2.76	1.73	5.86
1HGG.PDB	ND1, B_HIS_106	NZ, B_LYS_51	HZ3, B_LYS_51	2.77	1.79	14.96
1HGG.PDB	O, B_ILE_48	N, B_LEU_52	H, B_LEU_52	2.89	1.99	19.12
1HGG.PDB	O, B_ASN_49	N, B_ASN_53	H, B_ASN_53	2.89	1.99	19.14
1HGG.PDB	O, E_THR_28	NE, B_ARG_54	HE, B_ARG_54	2.94	1.97	7.82
1HGG.PDB	OE1, B_GLU_57	NH1, B_ARG_54	HH11, B_ARG_54	2.86	1.86	11.23
1HGG.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.75	1.76	9.96

1HGG.PDB	OE2, B_GLU_61	NZ, B_LYS_58	HZ3, B_LYS_58	2.94	1.92	12.53
1HGG.PDB	OD2, F_ASP_90	NZ, B_LYS_62	HZ2, B_LYS_62	2.65	1.82	29.87
1HGG.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ3, B_LYS_62	2.64	1.73	23.35
1HGG.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.90	1.96	14.63
1HGG.PDB	O, B_PHE_63	NE2, B_GLN_65	HE22, B_GLN_65	2.94	1.96	4.34
1HGG.PDB	O, A_LYS_299	NZ, B_LYS_68	HZ1, B_LYS_68	2.86	1.83	9.73
1HGG.PDB	OE2, B_GLU_85	NZ, B_LYS_68	HZ2, B_LYS_68	2.75	1.72	7.06
1HGG.PDB	OE2, B_GLU_72	OG, B_SER_71	HG, B_SER_71	2.84	2.03	27.31
1HGG.PDB	OG, C_SER_107	N, B_ARG_76	H, B_ARG_76	2.77	1.82	10.45
1HGG.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.94	1.96	10.47
1HGG.PDB	OE1, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.88	1.89	10.69
1HGG.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.73	1.73	5.91
1HGG.PDB	OE2, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.82	1.82	7.26
1HGG.PDB	O, B_GLY_75	N, B_ASP_79	H, B_ASP_79	2.85	1.93	16.05
1HGG.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.68	1.80	19.99
1HGG.PDB	O, B_LEU_80	N, B_VAL_84	H, B_VAL_84	2.87	1.91	8.71
1HGG.PDB	O, B_LYS_82	N, B_ASP_86	H, B_ASP_86	2.95	2.00	10.58
1HGG.PDB	O, B_TYR_83	N, B_THR_87	H, B_THR_87	2.90	1.95	10.43
1HGG.PDB	O, B_VAL_84	N, B_LYS_88	H, B_LYS_88	2.87	2.00	23.09
1HGG.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.77	1.73	5.14
1HGG.PDB	O, B_GLU_85	N, B_ILE_89	H, B_ILE_89	2.84	1.88	8.66
1HGG.PDB	O, B_LYS_88	N, B_TRP_92	H, B_TRP_92	2.93	1.96	6.86
1HGG.PDB	O, B_ILE_89	N, B_SER_93	H, B_SER_93	2.84	1.95	20.72
1HGG.PDB	O, B_ILE_89	OG, B_SER_93	HG, B_SER_93	2.79	1.89	17.30
1HGG.PDB	O, B_ASP_90	N, B_TYR_94	H, B_TYR_94	2.97	2.04	15.33
1HGG.PDB	O, B_TRP_92	N, B_ALA_96	H, B_ALA_96	2.98	2.05	15.46
1HGG.PDB	O, B_TYR_94	N, B_LEU_98	H, B_LEU_98	2.95	2.00	9.66
1HGG.PDB	O, B_ASN_95	N, B_LEU_99	H, B_LEU_99	2.89	1.99	18.59
1HGG.PDB	O, B_ALA_96	N, B_VAL_100	H, B_VAL_100	2.98	2.01	8.53
1HGG.PDB	O, B_LEU_98	N, B_LEU_102	H, B_LEU_102	2.92	1.98	12.12
1HGG.PDB	O, B_VAL_100	N, B_ASN_104	H, B_ASN_104	2.85	1.94	17.67
1HGG.PDB	O, A_LYS_27	ND2, B_ASN_104	HD22, B_ASN_104	2.88	1.95	14.60
1HGG.PDB	O, B_LEU_102	N, B_HIS_106	H, B_HIS_106	2.96	2.00	9.47
1HGG.PDB	O, B_GLU_103	N, B_THR_107	H, B_THR_107	2.81	1.95	23.40
1HGG.PDB	O, B_HIS_106	N, B_LEU_110	H, B_LEU_110	2.81	1.86	11.06
1HGG.PDB	O, B_THR_107	N, B_THR_111	H, B_THR_111	2.99	2.04	11.06
1HGG.PDB	O, B_THR_107	OG1, B_THR_111	HG1, B_THR_111	2.84	1.91	11.39
1HGG.PDB	O, B_ASP_109	N, B_SER_113	H, B_SER_113	2.78	1.86	16.47
1HGG.PDB	O, B_SER_113	N, B_LYS_117	H, B_LYS_117	2.73	1.85	21.24
1HGG.PDB	O, B_GLU_114	N, B_LEU_118	H, B_LEU_118	2.99	2.06	15.73
1HGG.PDB	O, B_MET_115	N, B_PHE_119	H, B_PHE_119	3.00	2.05	12.47
1HGG.PDB	O, B_ASN_116	N, B_GLU_120	H, B_GLU_120	2.95	1.97	4.00
1HGG.PDB	O, B_LYS_117	N, B_LYS_121	H, B_LYS_121	2.90	2.02	20.57
1HGG.PDB	O, B_LEU_118	N, B_THR_122	H, B_THR_122	2.96	1.98	6.92
1HGG.PDB	O, B_PHE_119	N, B_ARG_123	H, B_ARG_123	2.91	1.95	9.73
1HGG.PDB	OE2, B_GLU_120	NH1, B_ARG_123	HH11, B_ARG_123	2.73	1.87	25.50
1HGG.PDB	O, B_GLU_120	N, B_ARG_124	H, B_ARG_124	2.98	2.01	8.72
1HGG.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.84	1.98	22.96
1HGG.PDB	OE2, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.81	1.98	25.54
1HGG.PDB	O, B_HIS_159	ND2, B_ASN_129	HD21, B_ASN_129	2.98	2.03	11.68
1HGG.PDB	OH, B_TYR_157	ND2, B_ASN_129	HD22, B_ASN_129	2.80	1.86	13.18
1HGG.PDB	O, B_LYS_139	N, B_GLU_131	H, B_GLU_131	2.96	2.02	13.20
1HGG.PDB	O, B_CYS_137	N, B_MET_133	H, B_MET_133	2.89	1.98	18.42
1HGG.PDB	O, A_LEU_13	N, B_PHE_138	H, B_PHE_138	2.70	1.86	24.49
1HGG.PDB	O, B_GLU_131	N, B_LYS_139	H, B_LYS_139	2.86	1.90	8.51
1HGG.PDB	O, A_ALA_11	N, B_ILE_140	H, B_ILE_140	2.77	1.86	18.05
1HGG.PDB	O, B_ASN_129	N, B_TYR_141	H, B_TYR_141	2.90	1.92	3.10
1HGG.PDB	OE2, B_GLU_165	N, B_LYS_143	H, B_LYS_143	2.97	2.08	21.83

1HGG.PDB	OD1, B.ASP.145	N, B.ALA.147	H, B.ALA.147	2.99	2.19	29.06
1HGG.PDB	O, B.ASP.145	N, B.ILE.149	H, B.ILE.149	2.94	1.98	9.40
1HGG.PDB	O, B.ASN.146	N, B.GLU.150	H, B.GLU.150	2.89	1.95	12.57
1HGG.PDB	O, B.ALA.147	N, B.SER.151	H, B.SER.151	2.85	1.98	22.55
1HGG.PDB	O, B.CYS.148	OG, B.SER.151	HG, B.SER.151	2.71	1.85	21.43
1HGG.PDB	O, B.GLU.150	N, B.ASN.154	H, B.ASN.154	2.84	1.87	3.20
1HGG.PDB	O, B.SER.151	N, B.THR.156	H, B.THR.156	2.76	1.93	25.42
1HGG.PDB	OD1, B.ASN.154	OG1, B.THR.156	HG1, B.THR.156	2.71	1.81	17.64
1HGG.PDB	OD1, B.ASP.158	N, B.ASP.160	H, B.ASP.160	2.97	2.06	18.02
1HGG.PDB	O, B.HIS.159	N, B.TYR.162	H, B.TYR.162	2.94	2.02	17.18
1HGG.PDB	O, B.ASP.160	N, B.ARG.163	H, B.ARG.163	2.91	1.94	6.47
1HGG.PDB	O, F.ARG.170	NH1, B.ARG.163	HH12, B.ARG.163	2.76	1.82	18.13
1HGG.PDB	O, B.TYR.162	N, B.ALA.166	H, B.ALA.166	2.87	1.91	8.33
1HGG.PDB	O, B.ARG.163	N, B.LEU.167	H, B.LEU.167	2.76	1.83	12.88
1HGG.PDB	O, B.ALA.166	N, B.ARG.170	H, B.ARG.170	2.86	1.99	22.15
1HGG.PDB	O, B.GLU.128	NE, B.ARG.170	HE, B.ARG.170	2.71	1.86	24.52
1HGG.PDB	OE2, B.GLU.131	NH1, B.ARG.170	HH11, B.ARG.170	2.85	1.85	6.28
1HGG.PDB	O, B.LEU.167	N, B.PHE.171	H, B.PHE.171	2.94	1.99	10.53
1HGG.PDB	O, D.ILE.140	N, C.ALA.11	H, C.ALA.11	2.88	1.96	16.67
1HGG.PDB	O, D.PHE.138	N, C.LEU.13	H, C.LEU.13	3.00	2.04	10.72
1HGG.PDB	O, D.ARG.25	N, C.CYS.14	H, C.CYS.14	2.73	1.80	13.70
1HGG.PDB	O, D.GLY.136	N, C.LEU.15	H, C.LEU.15	2.90	1.94	8.49
1HGG.PDB	O, D.GLY.23	N, C.GLY.16	H, C.GLY.16	2.91	2.01	20.14
1HGG.PDB	O, D.TRP.21	N, C.HIS.18	H, C.HIS.18	2.90	2.00	17.75
1HGG.PDB	OD1, C.ASN.322	N, C.VAL.20	H, C.VAL.20	2.83	1.86	5.96
1HGG.PDB	O, C.VAL.36	N, C.THR.24	H, C.THR.24	2.85	1.97	21.07
1HGG.PDB	O, C.ILE.34	N, C.VAL.26	H, C.VAL.26	2.78	1.85	13.27
1HGG.PDB	OE2, D.GLU.97	NZ, C.LYS.27	HZ1, C.LYS.27	2.94	1.91	8.28
1HGG.PDB	O, C.VAL.26	N, C.ILE.34	H, C.ILE.34	2.94	2.00	14.30
1HGG.PDB	O, C.THR.24	N, C.VAL.36	H, C.VAL.36	2.78	1.83	9.33
1HGG.PDB	O, C.MET.320	N, C.THR.37	H, C.THR.37	2.95	1.98	6.39
1HGG.PDB	O, C.LEU.316	N, C.THR.40	H, C.THR.40	2.80	1.94	23.65
1HGG.PDB	O, C.LEU.314	N, C.LEU.42	H, C.LEU.42	2.84	1.98	23.25
1HGG.PDB	O, C.PHE.294	N, C.GLN.44	H, C.GLN.44	2.77	1.82	9.57
1HGG.PDB	O, C.ASN.285	OG, C.SER.47	HG, C.SER.47	2.86	1.92	11.28
1HGG.PDB	OD2, C.ASP.275	NZ, C.LYS.50	HZ1, C.LYS.50	2.68	1.77	23.74
1HGG.PDB	O, C.PRO.273	N, C.ILE.51	H, C.ILE.51	2.76	1.81	7.91
1HGG.PDB	O, C.ASP.275	N, C.ASN.53	H, C.ASN.53	2.74	1.92	26.97
1HGG.PDB	OD2, C.ASP.85	N, C.ARG.57	H, C.ARG.57	2.86	1.92	11.42
1HGG.PDB	O, C.THR.83	NE, C.ARG.57	HE, C.ARG.57	2.73	1.76	4.62
1HGG.PDB	OE1, C.GLU.82	NH2, C.ARG.57	HH21, C.ARG.57	2.59	1.77	28.22
1HGG.PDB	O, C.LEU.86	N, C.LEU.59	H, C.LEU.59	2.91	1.94	7.95
1HGG.PDB	O, C.VAL.88	N, C.GLY.61	H, C.GLY.61	2.96	2.11	24.97
1HGG.PDB	OD1, C.ASP.60	N, C.ILE.62	H, C.ILE.62	2.85	1.92	14.37
1HGG.PDB	O, C.GLY.61	N, C.CYS.64	H, C.CYS.64	2.95	2.02	15.64
1HGG.PDB	O, C.LEU.66	N, C.LEU.70	H, C.LEU.70	2.88	1.98	18.83
1HGG.PDB	O, C.ILE.67	N, C.LEU.71	H, C.LEU.71	2.81	1.85	6.57
1HGG.PDB	O, C.ASP.68	N, C.GLY.72	H, C.GLY.72	2.83	1.91	16.32
1HGG.PDB	OD1, C.ASP.73	N, C.HIS.75	H, C.HIS.75	2.95	2.04	19.03
1HGG.PDB	OD1, C.ASP.73	ND1, C.HIS.75	HD1, C.HIS.75	2.72	1.84	20.87
1HGG.PDB	O, C.ASP.63	NE2, C.HIS.75	HE2, C.HIS.75	2.81	1.85	11.39
1HGG.PDB	O, C.ASP.73	N, C.CYS.76	H, C.CYS.76	2.75	1.83	14.81
1HGG.PDB	O, C.PRO.74	N, C.ASP.77	H, C.ASP.77	2.88	1.94	12.22
1HGG.PDB	O, C.PHE.79	N, C.GLU.82	H, C.GLU.82	2.98	2.06	16.43
1HGG.PDB	O, C.ARG.57	N, C.ASP.85	H, C.ASP.85	2.82	1.92	18.11
1HGG.PDB	O, C.LEU.59	N, C.VAL.88	H, C.VAL.88	2.94	1.97	7.31
1HGG.PDB	O, C.MET.268	N, C.GLU.89	H, C.GLU.89	2.84	1.90	11.81
1HGG.PDB	OD1, C.ASP.60	NE, C.ARG.90	HE, C.ARG.90	2.93	1.95	8.71

1HGG.PDB	O, C_SER_270	NH1, C_ARG_90	HH11, C_ARG_90	2.63	1.77	25.40
1HGG.PDB	O, C_ALA_272	NH1, C_ARG_90	HH12, C_ARG_90	2.64	1.73	19.40
1HGG.PDB	OD2, C_ASP_60	NH2, C_ARG_90	HH21, C_ARG_90	2.79	1.80	9.72
1HGG.PDB	OD1, C_ASP_271	N, C_SER_91	H, C_SER_91	2.91	1.98	14.77
1HGG.PDB	OD1, C_ASP_271	OG, C_SER_91	HG, C_SER_91	2.89	2.06	25.85
1HGG.PDB	OD2, C_ASP_271	OG, C_SER_91	HG, C_SER_91	2.90	2.02	21.44
1HGG.PDB	O, C_ASP_63	N, C_PHE_94	H, C_PHE_94	2.99	2.03	11.00
1HGG.PDB	OD2, C_ASP_68	OG, C_SER_95	HG, C_SER_95	2.90	1.95	11.80
1HGG.PDB	OD2, C_ASP_73	N, C_ASN_96	H, C_ASN_96	2.84	1.91	15.44
1HGG.PDB	SG, C_CYS_97	N, C_TYR_98	H, C_TYR_98	2.98	2.13	24.49
1HGG.PDB	OD1, C_ASP_68	OH, C_TYR_100	HH, C_TYR_100	2.93	1.98	11.50
1HGG.PDB	O, C_ILE_230	N, C_ASP_101	H, C_ASP_101	2.95	2.06	21.39
1HGG.PDB	OD1, C_ASP_104	N, C_SER_107	H, C_SER_107	2.96	2.07	20.96
1HGG.PDB	OD2, C_ASP_104	OG, C_SER_107	HG, C_SER_107	2.88	1.95	15.82
1HGG.PDB	O, C_TYR_105	N, C_ARG_109	H, C_ARG_109	2.77	1.80	4.85
1HGG.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.85	1.88	14.56
1HGG.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.76	1.86	17.83
1HGG.PDB	O, C_SER_107	N, C_LEU_111	H, C_LEU_111	2.84	1.88	8.80
1HGG.PDB	O, C_ARG_109	N, C_ALA_113	H, C_ALA_113	2.92	2.01	17.55
1HGG.PDB	O, C_SER_110	N, C_SER_114	H, C_SER_114	2.96	2.00	11.10
1HGG.PDB	OE2, C_GLU_119	OG1, C_THR_117	HG1, C_THR_117	2.92	1.97	8.69
1HGG.PDB	O, C_GLU_82	N, C_LEU_118	H, C_LEU_118	2.98	2.02	11.62
1HGG.PDB	O, C_TYR_257	N, C_ILE_121	H, C_ILE_121	2.89	1.93	9.59
1HGG.PDB	O, C_ARG_255	N, C_GLU_123	H, C_GLU_123	2.97	2.02	13.93
1HGG.PDB	O, C_THR_155	N, C_THR_131	H, C_THR_131	2.76	1.85	16.88
1HGG.PDB	OD1, C_ASN_152	N, C_ASN_133	H, C_ASN_133	2.89	1.97	17.25
1HGG.PDB	O, C_GLY_146	N, C_SER_136	H, C_SER_136	2.76	1.84	16.68
1HGG.PDB	OG, C_SER_136	N, C_ALA_138	H, C_ALA_138	2.90	1.94	8.35
1HGG.PDB	O, C_GLY_144	NZ, C_LYS_140	HZ1, C_LYS_140	2.87	1.89	15.96
1HGG.PDB	OD1, C_ASN_137	NZ, C_LYS_140	HZ2, C_LYS_140	2.78	1.78	13.21
1HGG.PDB	OD2, C_ASP_77	NE, C_ARG_141	HE, C_ARG_141	2.87	2.06	29.23
1HGG.PDB	O, C_PHE_147	NH1, C_ARG_141	HH12, C_ARG_141	2.49	1.65	25.79
1HGG.PDB	OD1, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.76	1.85	22.10
1HGG.PDB	OD2, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.74	1.86	24.28
1HGG.PDB	O, C_GLY_72	NH2, C_ARG_141	HH22, C_ARG_141	2.93	1.94	7.19
1HGG.PDB	OD1, C_ASN_137	OG, C_SER_145	HG, C_SER_145	2.90	2.03	20.82
1HGG.PDB	O, C_SER_136	N, C_GLY_146	H, C_GLY_146	2.99	2.11	21.11
1HGG.PDB	O, C_GLY_72	N, C_SER_149	H, C_SER_149	2.87	1.95	15.72
1HGG.PDB	O, C_ALA_253	N, C_ASN_152	H, C_ASN_152	2.70	1.87	25.79
1HGG.PDB	OH, C_TYR_195	NE1, C_TRP_153	HE1, C_TRP_153	2.90	1.98	17.08
1HGG.PDB	O, C_THR_131	N, C_THR_155	H, C_THR_155	2.97	2.01	10.26
1HGG.PDB	O, C_LEU_194	N, C_LYS_156	H, C_LYS_156	2.96	2.09	22.28
1HGG.PDB	O, C_THR_160	N, C_SER_157	H, C_SER_157	2.94	2.03	17.38
1HGG.PDB	O, C_ILE_245	N, C_VAL_166	H, C_VAL_166	2.88	1.92	11.02
1HGG.PDB	O, C_LEU_243	OG1, C_THR_167	HG1, C_THR_167	2.88	1.99	19.69
1HGG.PDB	O, C_LEU_243	N, C_MET_168	H, C_MET_168	2.95	2.02	15.96
1HGG.PDB	O, C_ASP_241	N, C_ASN_170	H, C_ASN_170	2.87	1.89	5.24
1HGG.PDB	O, C_PHE_174	ND2, C_ASN_170	HD21, C_ASN_170	2.80	1.86	12.52
1HGG.PDB	O, C_VAL_237	ND2, C_ASN_170	HD22, C_ASN_170	2.86	2.00	22.88
1HGG.PDB	O, C_VAL_237	N, C_LYS_176	H, C_LYS_176	2.90	1.97	14.96
1HGG.PDB	OE2, C_GLU_123	NZ, C_LYS_176	HZ1, C_LYS_176	2.63	1.76	26.89
1HGG.PDB	O, C_PHE_258	N, C_LEU_177	H, C_LEU_177	2.95	1.99	9.21
1HGG.PDB	O, C_THR_235	N, C_TYR_178	H, C_TYR_178	2.76	1.80	6.43
1HGG.PDB	OE1, C_GLU_123	OH, C_TYR_178	HH, C_TYR_178	2.78	1.82	5.18
1HGG.PDB	OG1, C_THR_235	NE1, C_TRP_180	HE1, C_TRP_180	2.92	1.93	1.99
1HGG.PDB	O, C_ASN_250	N, C_HIS_183	H, C_HIS_183	2.79	1.93	23.13
1HGG.PDB	O, C_ARG_229	N, C_HIS_184	H, C_HIS_184	2.88	1.91	4.45
1HGG.PDB	OG, C_SER_231	NE2, C_HIS_184	HE2, C_HIS_184	2.79	1.91	21.48

1HGG.PDB	OG1, C_THR_187	N, C_GLU_190	H, C_GLU_190	2.85	1.91	12.50
1HGG.PDB	OD1, C_ASN_250	NE2, C_GLN_191	HE21, C_GLN_191	2.95	1.99	11.16
1HGG.PDB	O, C_GLN_197	NE2, C_GLN_191	HE22, C_GLN_191	2.91	2.02	19.58
1HGG.PDB	O, C_GLN_189	OG1, C_THR_192	HG1, C_THR_192	2.78	1.95	25.67
1HGG.PDB	O, C_GLN_189	N, C_SER_193	H, C_SER_193	2.82	1.90	15.79
1HGG.PDB	O, C_GLN_191	N, C_TYR_195	H, C_TYR_195	2.84	1.90	11.98
1HGG.PDB	O, C_THR_192	N, C_VAL_196	H, C_VAL_196	2.94	2.12	27.31
1HGG.PDB	O, C_TYR_161	NE2, C_GLN_197	HE21, C_GLN_197	2.93	1.96	5.46
1HGG.PDB	O, C_ASN_248	NE2, C_GLN_197	HE22, C_GLN_197	2.96	2.07	20.53
1HGG.PDB	OD1, C_ASN_246	NH2, C_ARG_201	HH21, C_ARG_201	2.66	1.74	19.39
1HGG.PDB	O, C_ILE_213	N, C_VAL_202	H, C_VAL_202	2.95	2.00	11.94
1HGG.PDB	O, C_ASN_246	N, C_THR_203	H, C_THR_203	2.86	1.90	8.48
1HGG.PDB	OG1, C_THR_212	OG1, C_THR_203	HG1, C_THR_203	2.83	1.91	13.70
1HGG.PDB	O, C_GLN_211	N, C_VAL_204	H, C_VAL_204	2.89	1.98	18.00
1HGG.PDB	O, C_SER_209	N, C_THR_206	H, C_THR_206	2.98	2.01	7.02
1HGG.PDB	OD1, C_ASP_241	N, C_ARG_207	H, C_ARG_207	2.89	1.95	13.44
1HGG.PDB	OD2, C_ASP_241	NE, C_ARG_208	HE, C_ARG_208	2.93	2.03	20.59
1HGG.PDB	OG1, C_THR_206	OG, C_SER_209	HG, C_SER_209	2.99	2.06	14.06
1HGG.PDB	O, C_VAL_204	N, C_GLN_211	H, C_GLN_211	2.82	1.90	16.88
1HGG.PDB	O, C_VAL_202	N, C_ILE_213	H, C_ILE_213	2.82	1.89	15.37
1HGG.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.61	1.71	21.26
1HGG.PDB	O, C_ASN_216	NH2, C_ARG_220	HH22, C_ARG_220	2.71	1.81	20.71
1HGG.PDB	O, C_LEU_226	N, C_VAL_223	H, C_VAL_223	2.85	1.90	10.41
1HGG.PDB	O, C_CYS_97	NE, C_ARG_224	HE, C_ARG_224	2.77	1.94	26.89
1HGG.PDB	O, C_CYS_97	NH2, C_ARG_224	HH21, C_ARG_224	2.80	1.94	26.26
1HGG.PDB	O, C_VAL_223	N, C_LEU_226	H, C_LEU_226	2.98	2.05	14.11
1HGG.PDB	O, C_ARG_220	OG, C_SER_227	HG, C_SER_227	2.93	1.98	9.94
1HGG.PDB	O, C_SER_228	NH1, C_ARG_229	HH11, C_ARG_229	2.73	1.79	17.88
1HGG.PDB	O, C_PRO_221	NH2, C_ARG_229	HH22, C_ARG_229	2.58	1.66	18.11
1HGG.PDB	OD1, C_ASP_101	OG, C_SER_231	HG, C_SER_231	2.91	1.95	9.20
1HGG.PDB	O, C_ASP_101	N, C_ILE_232	H, C_ILE_232	2.94	2.02	16.10
1HGG.PDB	O, C_TRP_180	N, C_TYR_233	H, C_TYR_233	2.88	1.93	12.54
1HGG.PDB	O, C_TYR_178	N, C_THR_235	H, C_THR_235	2.88	1.98	19.07
1HGG.PDB	O, C_LYS_176	N, C_VAL_237	H, C_VAL_237	2.77	1.82	10.57
1HGG.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.83	1.86	17.18
1HGG.PDB	OE2, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.70	1.87	29.85
1HGG.PDB	O, B_SER_71	NZ, C_LYS_238	HZ3, C_LYS_238	2.64	1.71	20.39
1HGG.PDB	O, C_ASN_170	N, C_GLY_240	H, C_GLY_240	2.87	2.00	22.99
1HGG.PDB	O, C_LYS_238	N, C_ASP_241	H, C_ASP_241	2.94	2.02	16.73
1HGG.PDB	OD1, C_ASP_241	N, C_VAL_242	H, C_VAL_242	2.79	1.98	28.74
1HGG.PDB	O, C_MET_168	N, C_LEU_243	H, C_LEU_243	2.90	1.93	4.41
1HGG.PDB	O, C_SER_205	N, C_VAL_244	H, C_VAL_244	2.94	1.99	13.16
1HGG.PDB	O, C_VAL_166	N, C_ILE_245	H, C_ILE_245	2.96	2.03	15.63
1HGG.PDB	O, C_THR_203	N, C_ASN_246	H, C_ASN_246	2.89	1.94	11.37
1HGG.PDB	OD1, C_ASN_165	ND2, C_ASN_246	HD22, C_ASN_246	2.88	1.97	17.94
1HGG.PDB	O, C_LEU_164	N, C_SER_247	H, C_SER_247	2.93	2.03	18.95
1HGG.PDB	OE1, C_GLN_191	ND2, C_ASN_250	HD21, C_ASN_250	2.88	1.93	11.32
1HGG.PDB	O, C_HIS_183	ND2, C_ASN_250	HD22, C_ASN_250	2.88	1.92	9.88
1HGG.PDB	O, C_ASN_152	N, C_ALA_253	H, C_ALA_253	2.89	1.98	18.52
1HGG.PDB	OD1, C_ASN_133	NH2, C_ARG_255	HH22, C_ARG_255	2.54	1.68	24.43
1HGG.PDB	O, C_ILE_121	N, C_TYR_257	H, C_TYR_257	2.94	2.10	25.61
1HGG.PDB	O, C_LEU_177	N, C_PHE_258	H, C_PHE_258	2.95	2.00	12.32
1HGG.PDB	OG, C_SER_115	N, C_ARG_261	H, C_ARG_261	2.98	2.02	10.79
1HGG.PDB	OE2, C_GLU_119	NH1, C_ARG_261	HH12, C_ARG_261	2.67	1.86	29.79
1HGG.PDB	OE1, C_GLU_119	NH2, C_ARG_261	HH22, C_ARG_261	2.73	1.87	26.76
1HGG.PDB	OH, C_TYR_302	NZ, C_LYS_264	HZ1, C_LYS_264	2.88	1.92	18.77
1HGG.PDB	ND1, C_HIS_56	NZ, C_LYS_264	HZ2, C_LYS_264	2.66	1.73	19.57
1HGG.PDB	OD2, C_ASP_85	NZ, C_LYS_264	HZ3, C_LYS_264	2.85	1.83	11.83

1HGG.PDB	O, C_PHE_87	N, C_MET_268	H, C_MET_268	2.84	1.93	18.75
1HGG.PDB	OE1, D_GLU_67	NH1, C_ARG_269	HH12, C_ARG_269	2.69	1.85	27.75
1HGG.PDB	O, C_PRO_284	OG, C_SER_270	HG, C_SER_270	2.81	1.87	12.03
1HGG.PDB	OG, C_SER_270	N, C_ALA_272	H, C_ALA_272	2.94	2.00	11.74
1HGG.PDB	O, C_ILE_51	N, C_ASP_275	H, C_ASP_275	2.84	1.97	21.56
1HGG.PDB	OD1, C_ASP_275	N, C_THR_276	H, C_THR_276	2.78	1.93	24.05
1HGG.PDB	O, C_ASN_54	N, C_SER_279	H, C_SER_279	2.77	1.82	11.28
1HGG.PDB	O, C_TYR_302	N, C_ILE_282	H, C_ILE_282	2.90	1.95	12.03
1HGG.PDB	O, C_THR_283	N, C_GLY_286	H, C_GLY_286	2.78	1.84	12.37
1HGG.PDB	O, C_LYS_50	N, C_SER_287	H, C_SER_287	2.83	1.87	6.69
1HGG.PDB	O, C_ALA_304	ND2, C_ASN_290	HD22, C_ASN_290	2.88	2.00	21.32
1HGG.PDB	OE1, C_GLN_44	NZ, C_LYS_292	HZ1, C_LYS_292	2.77	1.76	11.69
1HGG.PDB	OD2, C_ASP_291	NZ, C_LYS_292	HZ3, C_LYS_292	2.78	1.91	27.51
1HGG.PDB	O, C_LYS_307	N, C_GLN_295	H, C_GLN_295	2.80	1.92	20.69
1HGG.PDB	O, C_ASN_298	NE2, C_GLN_295	HE21, C_GLN_295	2.82	1.85	7.30
1HGG.PDB	O, C_GLN_44	N, C_ASN_296	H, C_ASN_296	2.86	1.91	11.10
1HGG.PDB	OD1, C_ASN_285	ND2, C_ASN_298	HD22, C_ASN_298	2.95	2.00	10.88
1HGG.PDB	O, D_LYS_68	NZ, C_LYS_299	HZ1, C_LYS_299	2.94	1.91	9.55
1HGG.PDB	OD1, C_ASN_298	N, C_ILE_300	H, C_ILE_300	2.84	1.92	15.94
1HGG.PDB	O, C_ILE_282	N, C_TYR_302	H, C_TYR_302	2.82	1.94	22.26
1HGG.PDB	O, C_LYS_264	OH, C_TYR_302	HH, C_TYR_302	2.69	1.86	25.98
1HGG.PDB	O, D_LYS_62	N, C_GLY_303	H, C_GLY_303	2.91	1.94	5.10
1HGG.PDB	O, C_GLN_295	N, C_VAL_309	H, C_VAL_309	2.92	2.09	26.95
1HGG.PDB	OG, D_SER_93	N, C_LYS_310	H, C_LYS_310	2.89	1.96	14.95
1HGG.PDB	OD1, D_ASP_90	NZ, C_LYS_310	HZ2, C_LYS_310	2.65	1.73	21.74
1HGG.PDB	OE2, C_GLU_41	N, C_LEU_314	H, C_LEU_314	2.79	1.88	17.71
1HGG.PDB	OE1, C_GLU_41	NZ, C_LYS_315	HZ3, C_LYS_315	2.73	1.82	23.48
1HGG.PDB	O, C_THR_40	N, C_LEU_316	H, C_LEU_316	2.76	1.85	16.07
1HGG.PDB	OD1, D_ASN_104	N, C_ALA_317	H, C_ALA_317	2.78	1.87	17.02
1HGG.PDB	O, C_ASN_38	N, C_THR_318	H, C_THR_318	2.91	1.99	16.68
1HGG.PDB	O, C_VAL_20	ND2, C_ASN_322	HD21, C_ASN_322	2.89	1.97	16.73
1HGG.PDB	OE2, C_GLU_35	ND2, C_ASN_322	HD22, C_ASN_322	2.82	1.96	24.18
1HGG.PDB	OXT, C_THR_328	NE2, C_GLN_327	HE22, C_GLN_327	2.99	2.05	16.22
1HGG.PDB	OD2, D_ASP_112	N, D_GLY_1	H2, D_GLY_1	2.72	1.72	12.91
1HGG.PDB	OD1, D_ASP_109	N, D_LEU_2	H, D_LEU_2	2.98	2.06	18.06
1HGG.PDB	OD2, D_ASP_112	N, D_PHE_3	H, D_PHE_3	2.89	2.07	26.93
1HGG.PDB	OD2, D_ASP_112	N, D_GLY_4	H, D_GLY_4	2.95	2.04	17.54
1HGG.PDB	OD1, D_ASP_112	N, D_ALA_5	H, D_ALA_5	2.93	2.07	23.70
1HGG.PDB	O, D_GLY_4	N, D_PHE_9	H, D_PHE_9	2.79	1.86	14.01
1HGG.PDB	O, C_VAL_323	N, D_GLY_13	H, D_GLY_13	2.71	1.79	13.39
1HGG.PDB	O, C_HIS_17	N, D_TRP_14	H, D_TRP_14	2.80	1.89	17.21
1HGG.PDB	OG1, D_THR_41	N, D_TRP_21	H, D_TRP_21	2.88	1.93	11.49
1HGG.PDB	O, C_GLY_16	N, D_GLY_23	H, D_GLY_23	2.99	2.09	20.18
1HGG.PDB	O, D_ALA_35	N, D_PHE_24	H, D_PHE_24	2.85	1.88	4.85
1HGG.PDB	O, C_CYS_14	N, D_ARG_25	H, D_ARG_25	2.94	1.98	8.24
1HGG.PDB	OE1, D_GLN_34	NE, D_ARG_25	HE, D_ARG_25	2.69	1.81	20.51
1HGG.PDB	OE1, D_GLN_34	NH2, D_ARG_25	HH21, D_ARG_25	2.92	2.08	27.66
1HGG.PDB	O, D_GLY_33	N, D_HIS_26	H, D_HIS_26	2.93	2.01	17.07
1HGG.PDB	O, D_GLY_31	N, D_ASN_28	H, D_ASN_28	2.87	1.91	10.16
1HGG.PDB	OD1, D_ASN_146	ND2, D_ASN_28	HD21, D_ASN_28	2.95	1.98	8.75
1HGG.PDB	O, D_HIS_26	N, D_GLY_33	H, D_GLY_33	2.99	2.09	19.19
1HGG.PDB	O, D_PHE_24	N, D_ALA_35	H, D_ALA_35	2.88	2.07	28.42
1HGG.PDB	O, D_TYR_22	N, D_ASP_37	H, D_ASP_37	2.74	1.77	2.87
1HGG.PDB	OD2, D_ASP_37	N, D_SER_40	H, D_SER_40	2.86	1.92	11.90
1HGG.PDB	OD2, D_ASP_37	OG, D_SER_40	HG, D_SER_40	2.77	1.93	24.58
1HGG.PDB	O, D_ASP_37	OG1, D_THR_41	HG1, D_THR_41	2.70	1.81	19.22
1HGG.PDB	O, D_LEU_38	N, D_GLN_42	H, D_GLN_42	2.95	2.02	14.26
1HGG.PDB	OD1, D_ASP_46	NE2, D_GLN_42	HE22, D_GLN_42	2.85	1.96	21.08

1HGG.PDB	O, D_LYS_39	N, D_ALA_43	H, D_ALA_43	2.99	2.03	8.86
1HGG.PDB	O, D_SER_40	N, D_ALA_44	H, D_ALA_44	2.95	1.97	1.83
1HGG.PDB	O, D_THR_41	N, D_ILE_45	H, D_ILE_45	2.97	2.03	14.64
1HGG.PDB	O, D_GLN_42	N, D_ASP_46	H, D_ASP_46	2.77	1.81	4.12
1HGG.PDB	OE2, D_GLU_114	NE2, D_GLN_47	HE21, D_GLN_47	2.97	2.05	17.17
1HGG.PDB	O, D_ALA_43	NE2, D_GLN_47	HE22, D_GLN_47	2.95	2.03	16.72
1HGG.PDB	O, D_ILE_45	N, D_ASN_49	H, D_ASN_49	2.86	1.93	14.78
1HGG.PDB	O, D_ASP_46	N, D_GLY_50	H, D_GLY_50	2.93	2.07	23.90
1HGG.PDB	O, D_GLN_47	N, D_LYS_51	H, D_LYS_51	2.93	1.95	0.82
1HGG.PDB	OG1, D_THR_107	NZ, D_LYS_51	HZ1, D_LYS_51	2.98	2.00	17.66
1HGG.PDB	OE1, D_GLU_103	NZ, D_LYS_51	HZ2, D_LYS_51	2.77	1.73	6.39
1HGG.PDB	ND1, D_HIS_106	NZ, D_LYS_51	HZ3, D_LYS_51	2.76	1.78	15.09
1HGG.PDB	O, D_ILE_48	N, D_LEU_52	H, D_LEU_52	2.86	1.96	19.21
1HGG.PDB	O, D_ASN_49	N, D_ASN_53	H, D_ASN_53	2.89	1.99	19.47
1HGG.PDB	O, A_THR_28	NE, D_ARG_54	HE, D_ARG_54	2.88	1.91	8.15
1HGG.PDB	OE1, D_GLU_57	NH1, D_ARG_54	HH11, D_ARG_54	2.86	1.86	11.12
1HGG.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.76	1.78	10.56
1HGG.PDB	O, D_ASN_53	N, D_ILE_56	H, D_ILE_56	2.92	2.12	28.93
1HGG.PDB	OE2, D_GLU_61	NZ, D_LYS_58	HZ3, D_LYS_58	2.91	1.89	12.30
1HGG.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.86	1.90	9.42
1HGG.PDB	O, D_PHE_63	NE2, D_GLN_65	HE22, D_GLN_65	2.97	2.00	6.28
1HGG.PDB	O, C_LYS_299	NZ, D_LYS_68	HZ1, D_LYS_68	2.84	1.83	12.46
1HGG.PDB	OE2, D_GLU_85	NZ, D_LYS_68	HZ2, D_LYS_68	2.77	1.74	6.59
1HGG.PDB	OE2, D_GLU_72	OG, D_SER_71	HG, D_SER_71	2.82	2.00	26.77
1HGG.PDB	OG, E_SER_107	N, D_ARG_76	H, D_ARG_76	2.84	1.88	7.98
1HGG.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.86	1.89	9.57
1HGG.PDB	OE1, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.78	1.80	12.10
1HGG.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.67	1.68	6.66
1HGG.PDB	OE2, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.74	1.75	9.29
1HGG.PDB	O, D_GLY_75	N, D_ASP_79	H, D_ASP_79	2.89	1.95	14.50
1HGG.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.59	1.78	26.83
1HGG.PDB	O, D_LEU_80	N, D_VAL_84	H, D_VAL_84	2.86	1.90	9.21
1HGG.PDB	O, D_LYS_82	N, D_ASP_86	H, D_ASP_86	2.98	2.01	8.40
1HGG.PDB	O, D_TYR_83	N, D_THR_87	H, D_THR_87	2.88	1.92	7.85
1HGG.PDB	O, D_VAL_84	N, D_LYS_88	H, D_LYS_88	2.88	2.03	24.81
1HGG.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.73	1.70	8.35
1HGG.PDB	O, D_GLU_85	N, D_ILE_89	H, D_ILE_89	2.83	1.87	9.71
1HGG.PDB	O, D_LYS_88	N, D_TRP_92	H, D_TRP_92	2.89	1.92	6.21
1HGG.PDB	O, D_ILE_89	N, D_SER_93	H, D_SER_93	2.82	1.94	21.49
1HGG.PDB	O, D_ILE_89	OG, D_SER_93	HG, D_SER_93	2.77	1.87	18.00
1HGG.PDB	O, D_ASP_90	N, D_TYR_94	H, D_TYR_94	2.96	2.03	15.50
1HGG.PDB	O, D_TRP_92	N, D_ALA_96	H, D_ALA_96	3.00	2.06	15.10
1HGG.PDB	O, D_TYR_94	N, D_LEU_98	H, D_LEU_98	2.95	1.99	9.12
1HGG.PDB	O, D_ASN_95	N, D_LEU_99	H, D_LEU_99	2.88	1.98	19.51
1HGG.PDB	O, D_ALA_96	N, D_VAL_100	H, D_VAL_100	2.99	2.02	8.75
1HGG.PDB	O, D_LEU_98	N, D_LEU_102	H, D_LEU_102	2.93	1.97	11.16
1HGG.PDB	O, D_VAL_100	N, D_ASN_104	H, D_ASN_104	2.84	1.93	18.38
1HGG.PDB	O, C_LYS_27	ND2, D_ASN_104	HD22, D_ASN_104	2.86	1.93	13.53
1HGG.PDB	O, D_LEU_102	N, D_HIS_106	H, D_HIS_106	2.95	2.00	11.00
1HGG.PDB	O, D_GLU_103	N, D_THR_107	H, D_THR_107	2.82	1.97	24.04
1HGG.PDB	O, D_HIS_106	N, D_LEU_110	H, D_LEU_110	2.77	1.83	11.18
1HGG.PDB	O, D_THR_107	N, D_THR_111	H, D_THR_111	2.98	2.03	10.32
1HGG.PDB	O, D_THR_107	OG1, D_THR_111	HG1, D_THR_111	2.86	1.91	10.45
1HGG.PDB	O, D_ASP_109	N, D_SER_113	H, D_SER_113	2.78	1.86	15.73
1HGG.PDB	O, D_ASP_112	N, D_ASN_116	H, D_ASN_116	3.00	2.01	4.28
1HGG.PDB	O, D_SER_113	N, D_LYS_117	H, D_LYS_117	2.76	1.87	19.86
1HGG.PDB	O, D_ASN_116	N, D_GLU_120	H, D_GLU_120	2.94	1.96	4.15
1HGG.PDB	O, D_LYS_117	N, D_LYS_121	H, D_LYS_121	2.89	1.99	19.16

1HGG.PDB	O, D_LEU_118	N, D_THR_122	H, D_THR_122	2.95	1.98	8.05
1HGG.PDB	O, D_PHE_119	N, D_ARG_123	H, D_ARG_123	2.95	1.99	9.23
1HGG.PDB	OE2, D_GLU_120	NH1, D_ARG_123	HH11, D_ARG_123	2.73	1.87	25.59
1HGG.PDB	O, D_GLU_120	N, D_ARG_124	H, D_ARG_124	2.99	2.02	7.97
1HGG.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.86	2.00	22.57
1HGG.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.78	1.96	26.12
1HGG.PDB	O, D_HIS_159	ND2, D_ASN_129	HD21, D_ASN_129	2.94	1.99	11.72
1HGG.PDB	OH, D_TYR_157	ND2, D_ASN_129	HD22, D_ASN_129	2.80	1.84	10.50
1HGG.PDB	O, D_LYS_139	N, D_GLU_131	H, D_GLU_131	2.99	2.04	13.39
1HGG.PDB	O, D_CYS_137	N, D_MET_133	H, D_MET_133	2.90	1.98	17.30
1HGG.PDB	OD1, D_ASN_135	N, D_CYS_137	H, D_CYS_137	3.00	2.10	19.46
1HGG.PDB	O, C_LEU_13	N, D_PHE_138	H, D_PHE_138	2.73	1.88	23.87
1HGG.PDB	O, D_GLU_131	N, D_LYS_139	H, D_LYS_139	2.86	1.90	10.04
1HGG.PDB	O, C_ALA_11	N, D_ILE_140	H, D_ILE_140	2.80	1.89	17.21
1HGG.PDB	O, D_ASN_129	N, D_TYR_141	H, D_TYR_141	2.89	1.92	4.81
1HGG.PDB	OE2, D_GLU_30	N, D_ASN_146	H, D_ASN_146	2.84	1.92	15.86
1HGG.PDB	O, D_ASP_145	N, D_ILE_149	H, D_ILE_149	2.98	2.02	9.24
1HGG.PDB	O, D_ASN_146	N, D_GLU_150	H, D_GLU_150	2.89	1.95	13.07
1HGG.PDB	O, D_ALA_147	N, D_SER_151	H, D_SER_151	2.89	2.01	20.94
1HGG.PDB	O, D_CYS_148	OG, D_SER_151	HG, D_SER_151	2.72	1.85	20.20
1HGG.PDB	O, D_GLU_150	N, D_ASN_154	H, D_ASN_154	2.84	1.87	4.45
1HGG.PDB	O, D_SER_151	N, D_THR_156	H, D_THR_156	2.78	1.93	25.02
1HGG.PDB	OD1, D_ASN_154	OG1, D_THR_156	HG1, D_THR_156	2.73	1.82	15.46
1HGG.PDB	NE2, D_HIS_142	OH, D_TYR_157	HH, D_TYR_157	2.72	1.85	20.87
1HGG.PDB	OD1, D_ASP_158	N, D_ASP_160	H, D_ASP_160	2.97	2.05	17.87
1HGG.PDB	O, D_HIS_159	N, D_TYR_162	H, D_TYR_162	2.93	2.01	16.79
1HGG.PDB	O, D_ASP_160	N, D_ARG_163	H, D_ARG_163	2.89	1.92	6.62
1HGG.PDB	O, B_ARG_170	NH1, D_ARG_163	HH12, D_ARG_163	2.79	1.85	17.60
1HGG.PDB	O, D_TYR_162	N, D_ALA_166	H, D_ALA_166	2.86	1.90	8.06
1HGG.PDB	O, D_ARG_163	N, D_LEU_167	H, D_LEU_167	2.77	1.84	14.60
1HGG.PDB	O, D_ALA_166	N, D_ARG_170	H, D_ARG_170	2.87	2.00	22.89
1HGG.PDB	O, D_GLU_128	NE, D_ARG_170	HE, D_ARG_170	2.70	1.85	24.63
1HGG.PDB	OE2, D_GLU_131	NH1, D_ARG_170	HH11, D_ARG_170	2.85	1.86	6.70
1HGG.PDB	O, D_LEU_167	N, D_PHE_171	H, D_PHE_171	2.94	1.98	10.64
1HGG.PDB	O, F_ILE_140	N, E_ALA_11	H, E_ALA_11	2.91	1.98	15.76
1HGG.PDB	O, F_GLN_27	N, E_THR_12	H, E_THR_12	2.92	1.99	15.18
1HGG.PDB	O, F_PHE_138	N, E_LEU_13	H, E_LEU_13	2.97	2.01	11.10
1HGG.PDB	O, F_ARG_25	N, E_CYS_14	H, E_CYS_14	2.71	1.83	19.57
1HGG.PDB	O, F_GLY_136	N, E_LEU_15	H, E_LEU_15	2.87	1.90	6.84
1HGG.PDB	O, F_GLY_23	N, E_GLY_16	H, E_GLY_16	2.91	2.01	19.19
1HGG.PDB	O, F_TRP_21	N, E_HIS_18	H, E_HIS_18	2.89	1.99	18.05
1HGG.PDB	OD1, E_ASN_322	N, E_VAL_20	H, E_VAL_20	2.81	1.84	7.14
1HGG.PDB	O, E_VAL_36	N, E_THR_24	H, E_THR_24	2.86	1.99	23.32
1HGG.PDB	O, E_ILE_34	N, E_VAL_26	H, E_VAL_26	2.80	1.86	12.97
1HGG.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.91	1.88	8.89
1HGG.PDB	O, E_VAL_26	N, E_ILE_34	H, E_ILE_34	2.91	1.98	15.06
1HGG.PDB	O, E_THR_24	N, E_VAL_36	H, E_VAL_36	2.79	1.84	9.17
1HGG.PDB	O, E_MET_320	N, E_THR_37	H, E_THR_37	2.93	1.96	8.79
1HGG.PDB	O, E_LEU_316	N, E_THR_40	H, E_THR_40	2.83	1.96	23.13
1HGG.PDB	O, E_LEU_314	N, E_LEU_42	H, E_LEU_42	2.84	1.97	22.62
1HGG.PDB	O, E_PHE_294	N, E_GLN_44	H, E_GLN_44	2.82	1.86	8.10
1HGG.PDB	O, E_ASN_285	OG, E_SER_47	HG, E_SER_47	2.85	1.92	11.49
1HGG.PDB	OD2, E_ASP_275	NZ, E_LYS_50	HZ1, E_LYS_50	2.68	1.77	24.10
1HGG.PDB	O, E_PRO_273	N, E_ILE_51	H, E_ILE_51	2.76	1.80	7.93
1HGG.PDB	O, E_ASP_275	N, E_ASN_53	H, E_ASN_53	2.76	1.93	26.21
1HGG.PDB	OD2, E_ASP_85	N, E_ARG_57	H, E_ARG_57	2.88	1.93	10.58
1HGG.PDB	O, E_THR_83	NE, E_ARG_57	HE, E_ARG_57	2.76	1.79	2.44
1HGG.PDB	O, E_LEU_86	N, E_LEU_59	H, E_LEU_59	2.92	1.95	8.87

1HGG.PDB	O, E_VAL.88	N, E_GLY.61	H, E_GLY.61	2.97	2.12	24.82
1HGG.PDB	OD1, E_ASP.60	N, E_ILE.62	H, E_ILE.62	2.87	1.94	14.20
1HGG.PDB	O, E_GLY.61	N, E_CYS.64	H, E_CYS.64	2.97	2.05	16.18
1HGG.PDB	O, E_LEU.66	N, E_LEU.70	H, E_LEU.70	2.87	1.97	18.30
1HGG.PDB	O, E_ILE.67	N, E_LEU.71	H, E_LEU.71	2.81	1.85	7.87
1HGG.PDB	O, E_ASP.68	N, E_GLY.72	H, E_GLY.72	2.86	1.95	17.48
1HGG.PDB	OD1, E_ASP.73	ND1, E_HIS.75	HD1, E_HIS.75	2.75	1.85	17.34
1HGG.PDB	O, E_ASP.63	NE2, E_HIS.75	HE2, E_HIS.75	2.82	1.87	11.87
1HGG.PDB	O, E_ASP.73	N, E_CYS.76	H, E_CYS.76	2.74	1.82	15.22
1HGG.PDB	O, E_PRO.74	N, E_ASP.77	H, E_ASP.77	2.89	1.94	11.95
1HGG.PDB	O, E_PHE.79	N, E_GLU.82	H, E_GLU.82	3.00	2.09	17.70
1HGG.PDB	OE1, E_GLU.82	N, E_THR.83	H, E_THR.83	2.96	2.07	21.15
1HGG.PDB	O, E_ARG.57	N, E_ASP.85	H, E_ASP.85	2.82	1.91	18.08
1HGG.PDB	O, E_LEU.59	N, E_VAL.88	H, E_VAL.88	2.92	1.95	6.94
1HGG.PDB	O, E_MET.268	N, E_GLU.89	H, E_GLU.89	2.82	1.88	11.27
1HGG.PDB	OD1, E_ASP.60	NE, E_ARG.90	HE, E_ARG.90	2.91	1.94	9.27
1HGG.PDB	O, E_SER.270	NH1, E_ARG.90	HH11, E_ARG.90	2.66	1.80	25.54
1HGG.PDB	O, E_ALA.272	NH1, E_ARG.90	HH12, E_ARG.90	2.63	1.72	18.75
1HGG.PDB	OD2, E_ASP.60	NH2, E_ARG.90	HH21, E_ARG.90	2.83	1.84	9.64
1HGG.PDB	OD1, E_ASP.271	N, E_SER.91	H, E_SER.91	2.89	1.97	16.48
1HGG.PDB	OD1, E_ASP.271	OG, E_SER.91	HG, E_SER.91	2.92	2.07	24.79
1HGG.PDB	OD2, E_ASP.271	OG, E_SER.91	HG, E_SER.91	2.93	2.06	22.08
1HGG.PDB	O, E_ASP.63	N, E_PHE.94	H, E_PHE.94	3.00	2.05	12.31
1HGG.PDB	OD2, E_ASP.68	OG, E_SER.95	HG, E_SER.95	2.93	1.98	13.19
1HGG.PDB	OD2, E_ASP.73	N, E_ASN.96	H, E_ASN.96	2.88	1.94	14.23
1HGG.PDB	SG, E_CYS.97	N, E_TYR.98	H, E_TYR.98	2.97	2.12	24.47
1HGG.PDB	OD1, E_ASP.68	OH, E_TYR.100	HH, E_TYR.100	2.92	1.96	10.90
1HGG.PDB	O, E_ILE.230	N, E_ASP.101	H, E_ASP.101	2.99	2.10	20.87
1HGG.PDB	OD1, E_ASP.104	N, E_SER.107	H, E_SER.107	2.92	2.04	21.12
1HGG.PDB	OD2, E_ASP.104	OG, E_SER.107	HG, E_SER.107	2.85	1.93	15.56
1HGG.PDB	O, E_ASP.104	N, E_LEU.108	H, E_LEU.108	2.97	2.01	9.00
1HGG.PDB	O, E_TYR.105	N, E_ARG.109	H, E_ARG.109	2.81	1.84	2.88
1HGG.PDB	OE2, F_GLU.67	NH2, E_ARG.109	HH21, E_ARG.109	2.88	1.90	14.20
1HGG.PDB	OD2, D_ASP.79	OG, E_SER.110	HG, E_SER.110	2.79	1.88	16.48
1HGG.PDB	O, E_SER.107	N, E_LEU.111	H, E_LEU.111	2.86	1.89	6.99
1HGG.PDB	O, E_ARG.109	N, E_ALA.113	H, E_ALA.113	2.89	1.98	18.53
1HGG.PDB	O, E_SER.110	N, E_SER.114	H, E_SER.114	2.92	1.95	9.29
1HGG.PDB	OE2, E_GLU.119	OG1, E_THR.117	HG1, E_THR.117	2.95	1.99	7.33
1HGG.PDB	O, E_TYR.257	N, E_ILE.121	H, E_ILE.121	2.88	1.93	10.40
1HGG.PDB	O, E_ARG.255	N, E_GLU.123	H, E_GLU.123	2.93	1.99	13.52
1HGG.PDB	O, E_THR.155	N, E_THR.131	H, E_THR.131	2.74	1.86	19.96
1HGG.PDB	OD1, E_ASN.152	N, E_ASN.133	H, E_ASN.133	2.93	2.01	17.35
1HGG.PDB	O, E_GLY.146	N, E_SER.136	H, E_SER.136	2.75	1.83	16.47
1HGG.PDB	OG, E_SER.136	N, E_ALA.138	H, E_ALA.138	2.92	1.95	8.13
1HGG.PDB	O, E_GLY.144	NZ, E_LYS.140	HZ1, E_LYS.140	2.88	1.90	15.75
1HGG.PDB	OD1, E_ASN.137	NZ, E_LYS.140	HZ2, E_LYS.140	2.76	1.76	13.40
1HGG.PDB	OD2, E_ASP.77	NE, E_ARG.141	HE, E_ARG.141	2.90	2.09	29.10
1HGG.PDB	O, E_PHE.147	NH1, E_ARG.141	HH12, E_ARG.141	2.48	1.65	26.20
1HGG.PDB	OD1, E_ASP.77	NH2, E_ARG.141	HH21, E_ARG.141	2.80	1.90	22.17
1HGG.PDB	OD2, E_ASP.77	NH2, E_ARG.141	HH21, E_ARG.141	2.74	1.86	23.74
1HGG.PDB	O, E_GLY.72	NH2, E_ARG.141	HH22, E_ARG.141	2.91	1.92	8.01
1HGG.PDB	OD1, E_ASN.137	OG, E_SER.145	HG, E_SER.145	2.95	2.08	20.42
1HGG.PDB	O, E_SER.136	N, E_GLY.146	H, E_GLY.146	2.98	2.09	20.70
1HGG.PDB	O, E_GLY.72	N, E_SER.149	H, E_SER.149	2.94	2.02	16.43
1HGG.PDB	O, E_ALA.253	N, E_ASN.152	H, E_ASN.152	2.76	1.91	24.30
1HGG.PDB	OH, E_TYR.195	NE1, E_TRP.153	HE1, E_TRP.153	2.91	1.97	14.69
1HGG.PDB	O, E_LEU.194	N, E_LYS.156	H, E_LYS.156	2.96	2.09	22.38
1HGG.PDB	O, E_SER.193	NZ, E_LYS.156	HZ2, E_LYS.156	2.92	2.00	22.42

1HGG.PDB	O, E_THR_160	N, E_SER_157	H, E_SER_157	2.97	2.06	18.55
1HGG.PDB	O, E_ILE_245	N, E_VAL_166	H, E_VAL_166	2.88	1.92	9.84
1HGG.PDB	O, E_LEU_243	OG1, E_THR_167	HG1, E_THR_167	2.89	2.02	20.67
1HGG.PDB	O, E_LEU_243	N, E_MET_168	H, E_MET_168	2.91	1.99	16.43
1HGG.PDB	O, E_ASP_241	N, E_ASN_170	H, E_ASN_170	2.89	1.91	4.36
1HGG.PDB	O, E_PHE_174	ND2, E_ASN_170	HD21, E_ASN_170	2.83	1.89	11.99
1HGG.PDB	O, E_VAL_237	ND2, E_ASN_170	HD22, E_ASN_170	2.85	1.99	23.32
1HGG.PDB	O, E_VAL_237	N, E_LYS_176	H, E_LYS_176	2.89	1.95	13.18
1HGG.PDB	OE2, E_GLU_123	NZ, E_LYS_176	HZ1, E_LYS_176	2.65	1.78	26.50
1HGG.PDB	O, E_THR_235	N, E_TYR_178	H, E_TYR_178	2.81	1.85	6.71
1HGG.PDB	OE1, E_GLU_123	OH, E_TYR_178	HH, E_TYR_178	2.80	1.84	8.47
1HGG.PDB	OG1, E_THR_235	NE1, E_TRP_180	HE1, E_TRP_180	2.93	1.94	2.01
1HGG.PDB	O, E_ASN_250	N, E_HIS_183	H, E_HIS_183	2.79	1.92	22.01
1HGG.PDB	O, E_ARG_229	N, E_HIS_184	H, E_HIS_184	2.88	1.92	7.25
1HGG.PDB	OG, E_SER_231	NE2, E_HIS_184	HE2, E_HIS_184	2.81	1.94	22.49
1HGG.PDB	OG1, E_THR_187	N, E_GLU_190	H, E_GLU_190	2.87	1.93	12.79
1HGG.PDB	O, E_GLN_197	NE2, E_GLN_191	HE22, E_GLN_191	2.91	2.01	19.48
1HGG.PDB	O, E_ASN_188	OG1, E_THR_192	HG1, E_THR_192	2.94	1.99	8.04
1HGG.PDB	O, E_GLN_189	N, E_SER_193	H, E_SER_193	2.85	1.88	6.48
1HGG.PDB	O, E_GLN_191	N, E_TYR_195	H, E_TYR_195	2.82	1.87	11.82
1HGG.PDB	O, E_THR_192	N, E_VAL_196	H, E_VAL_196	2.95	2.13	27.67
1HGG.PDB	O, E_TYR_161	NE2, E_GLN_197	HE21, E_GLN_197	2.93	1.96	5.53
1HGG.PDB	O, E_ASN_248	NE2, E_GLN_197	HE22, E_GLN_197	2.94	2.04	19.72
1HGG.PDB	OD1, E_ASN_246	NH2, E_ARG_201	HH21, E_ARG_201	2.66	1.74	20.08
1HGG.PDB	O, E_ILE_213	N, E_VAL_202	H, E_VAL_202	2.94	1.98	10.96
1HGG.PDB	O, E_ASN_246	N, E_THR_203	H, E_THR_203	2.86	1.89	5.92
1HGG.PDB	OG1, E_THR_212	OG1, E_THR_203	HG1, E_THR_203	2.88	1.95	13.34
1HGG.PDB	O, E_GLN_211	N, E_VAL_204	H, E_VAL_204	2.86	1.96	18.23
1HGG.PDB	OD1, E_ASP_241	N, E_ARG_207	H, E_ARG_207	2.89	1.94	12.68
1HGG.PDB	OD2, E_ASP_241	NE, E_ARG_208	HE, E_ARG_208	2.96	2.05	19.90
1HGG.PDB	OG1, E_THR_206	OG, E_SER_209	HG, E_SER_209	2.99	2.07	14.54
1HGG.PDB	OD1, C_ASP_101	NE2, E_GLN_210	HE22, E_GLN_210	2.96	2.04	17.70
1HGG.PDB	O, E_VAL_204	N, E_GLN_211	H, E_GLN_211	2.83	1.91	15.52
1HGG.PDB	O, E_VAL_202	N, E_ILE_213	H, E_ILE_213	2.83	1.91	15.44
1HGG.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.72	1.80	20.26
1HGG.PDB	O, E_ASN_216	NH2, E_ARG_220	HH22, E_ARG_220	2.70	1.80	21.11
1HGG.PDB	O, E_LEU_226	N, E_VAL_223	H, E_VAL_223	2.87	1.91	9.88
1HGG.PDB	O, E_CYS_97	NE, E_ARG_224	HE, E_ARG_224	2.79	1.95	26.52
1HGG.PDB	O, E_CYS_97	NH2, E_ARG_224	HH21, E_ARG_224	2.81	1.95	25.91
1HGG.PDB	O, E_VAL_223	N, E_LEU_226	H, E_LEU_226	2.99	2.06	14.12
1HGG.PDB	O, E_ARG_220	OG, E_SER_227	HG, E_SER_227	2.91	1.97	11.08
1HGG.PDB	O, E_SER_228	NH1, E_ARG_229	HH11, E_ARG_229	2.74	1.81	18.43
1HGG.PDB	O, E_PRO_221	NH2, E_ARG_229	HH22, E_ARG_229	2.61	1.67	16.25
1HGG.PDB	O, E_ILE_182	N, E_SER_231	H, E_SER_231	3.00	2.12	21.85
1HGG.PDB	OD1, E_ASP_101	OG, E_SER_231	HG, E_SER_231	2.91	1.96	10.31
1HGG.PDB	O, E_ASP_101	N, E_ILE_232	H, E_ILE_232	2.93	2.00	14.76
1HGG.PDB	O, E_TRP_180	N, E_TYR_233	H, E_TYR_233	2.93	1.97	11.34
1HGG.PDB	O, E_TYR_178	N, E_THR_235	H, E_THR_235	2.90	2.00	18.66
1HGG.PDB	O, E_LYS_176	N, E_VAL_237	H, E_VAL_237	2.79	1.84	9.36
1HGG.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ1, E_LYS_238	2.89	1.89	13.93
1HGG.PDB	O, D_SER_71	NZ, E_LYS_238	HZ3, E_LYS_238	2.80	1.86	20.00
1HGG.PDB	O, E_ASN_170	N, E_GLY_240	H, E_GLY_240	2.86	1.99	23.07
1HGG.PDB	O, E_LYS_238	N, E_ASP_241	H, E_ASP_241	2.93	2.02	17.28
1HGG.PDB	OD1, E_ASP_241	N, E_VAL_242	H, E_VAL_242	2.79	1.99	28.45
1HGG.PDB	O, E_MET_168	N, E_LEU_243	H, E_LEU_243	2.88	1.91	4.89
1HGG.PDB	O, E_SER_205	N, E_VAL_244	H, E_VAL_244	2.93	1.99	13.01
1HGG.PDB	O, E_VAL_166	N, E_ILE_245	H, E_ILE_245	2.98	2.06	15.80
1HGG.PDB	O, E_THR_203	N, E_ASN_246	H, E_ASN_246	2.92	1.97	11.38

1HGG.PDB	OD1, E_ASN_165	ND2, E_ASN_246	HD22, E_ASN_246	2.88	1.96	17.66
1HGG.PDB	O, E_LEU_164	N, E_SER_247	H, E_SER_247	2.92	2.01	18.12
1HGG.PDB	OE1, E_GLN_191	ND2, E_ASN_250	HD21, E_ASN_250	2.89	1.94	10.20
1HGG.PDB	O, E_HIS_183	ND2, E_ASN_250	HD22, E_ASN_250	2.88	1.93	10.21
1HGG.PDB	O, E_ASN_152	N, E_ALA_253	H, E_ALA_253	2.90	1.98	17.67
1HGG.PDB	OD1, E_ASN_133	NH2, E_ARG_255	HH22, E_ARG_255	2.55	1.68	24.24
1HGG.PDB	O, E_ILE_121	N, E_TYR_257	H, E_TYR_257	2.94	2.10	26.15
1HGG.PDB	O, E_LEU_177	N, E_PHE_258	H, E_PHE_258	2.94	2.00	12.72
1HGG.PDB	OG, E_SER_115	N, E_ARG_261	H, E_ARG_261	2.99	2.04	12.07
1HGG.PDB	OE2, E_GLU_119	NH1, E_ARG_261	HH12, E_ARG_261	2.69	1.87	29.29
1HGG.PDB	OE1, E_GLU_119	NH2, E_ARG_261	HH22, E_ARG_261	2.74	1.88	26.67
1HGG.PDB	OH, E_TYR_302	NZ, E_LYS_264	HZ1, E_LYS_264	2.90	1.93	18.14
1HGG.PDB	ND1, E_HIS_56	NZ, E_LYS_264	HZ2, E_LYS_264	2.66	1.73	20.09
1HGG.PDB	OD2, E_ASP_85	NZ, E_LYS_264	HZ3, E_LYS_264	2.85	1.83	11.84
1HGG.PDB	O, E_PHE_87	N, E_MET_268	H, E_MET_268	2.81	1.91	19.55
1HGG.PDB	OE1, F_GLU_67	NH1, E_ARG_269	HH12, E_ARG_269	2.69	1.85	27.32
1HGG.PDB	O, E_PRO_284	OG, E_SER_270	HG, E_SER_270	2.76	1.85	15.69
1HGG.PDB	OG, E_SER_270	N, E_ALA_272	H, E_ALA_272	2.95	2.00	11.61
1HGG.PDB	O, E_ILE_51	N, E_ASP_275	H, E_ASP_275	2.87	1.99	21.60
1HGG.PDB	OD1, E_ASP_275	N, E_THR_276	H, E_THR_276	2.79	1.94	24.39
1HGG.PDB	O, E_ASN_54	N, E_SER_279	H, E_SER_279	2.79	1.84	11.36
1HGG.PDB	O, E_TYR_302	N, E_ILE_282	H, E_ILE_282	2.87	1.92	10.52
1HGG.PDB	O, E_THR_283	N, E_GLY_286	H, E_GLY_286	2.79	1.84	9.62
1HGG.PDB	O, E_LYS_50	N, E_SER_287	H, E_SER_287	2.89	1.92	6.20
1HGG.PDB	O, E_ALA_304	ND2, E_ASN_290	HD22, E_ASN_290	2.87	2.00	21.60
1HGG.PDB	OE1, E_GLN_44	NZ, E_LYS_292	HZ1, E_LYS_292	2.77	1.75	10.61
1HGG.PDB	OD2, E_ASP_291	NZ, E_LYS_292	HZ3, E_LYS_292	2.76	1.90	27.94
1HGG.PDB	O, E_LYS_307	N, E_GLN_295	H, E_GLN_295	2.79	1.91	20.65
1HGG.PDB	O, E_ASN_298	NE2, E_GLN_295	HE21, E_GLN_295	2.79	1.83	8.95
1HGG.PDB	O, E_GLN_44	N, E_ASN_296	H, E_ASN_296	2.89	1.93	10.60
1HGG.PDB	OD1, E_ASN_285	ND2, E_ASN_298	HD22, E_ASN_298	2.95	2.00	11.31
1HGG.PDB	O, F_LYS_68	NZ, E_LYS_299	HZ1, E_LYS_299	2.93	1.91	9.86
1HGG.PDB	OD1, E_ASN_298	N, E_ILE_300	H, E_ILE_300	2.82	1.91	16.92
1HGG.PDB	O, E_ILE_282	N, E_TYR_302	H, E_TYR_302	2.82	1.94	21.27
1HGG.PDB	O, E_LYS_264	OH, E_TYR_302	HH, E_TYR_302	2.63	1.84	28.99
1HGG.PDB	O, F_LYS_62	N, E_GLY_303	H, E_GLY_303	2.92	1.95	6.71
1HGG.PDB	O, E_GLN_295	N, E_VAL_309	H, E_VAL_309	2.89	2.05	25.47
1HGG.PDB	OG, F_SER_93	N, E_LYS_310	H, E_LYS_310	2.89	1.95	15.34
1HGG.PDB	OD1, F_ASP_90	NZ, E_LYS_310	HZ2, E_LYS_310	2.64	1.72	22.12
1HGG.PDB	OE2, E_GLU_41	N, E_LEU_314	H, E_LEU_314	2.79	1.89	17.95
1HGG.PDB	OE1, E_GLU_41	NZ, E_LYS_315	HZ3, E_LYS_315	2.68	1.80	26.22
1HGG.PDB	O, E_THR_40	N, E_LEU_316	H, E_LEU_316	2.77	1.85	15.13
1HGG.PDB	OD1, F_ASN_104	N, E_ALA_317	H, E_ALA_317	2.80	1.89	16.99
1HGG.PDB	O, E_ASN_38	N, E_THR_318	H, E_THR_318	2.92	1.99	14.27
1HGG.PDB	O, E_VAL_20	ND2, E_ASN_322	HD21, E_ASN_322	2.88	1.96	16.01
1HGG.PDB	OE2, E_GLU_35	ND2, E_ASN_322	HD22, E_ASN_322	2.79	1.94	25.02
1HGG.PDB	OE2, F_GLU_15	N, E_GLU_325	H, E_GLU_325	2.88	2.08	28.79
1HGG.PDB	O, E_GLN_327	NZ, E_LYS_326	HZ1, E_LYS_326	2.71	1.82	24.99
1HGG.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.98	1.97	15.13
1HGG.PDB	O, E_LYS_326	NE2, E_GLN_327	HE22, E_GLN_327	2.77	1.84	14.97
1HGG.PDB	OD2, F_ASP_112	N, F_GLY_1	H2, F_GLY_1	2.68	1.70	14.41
1HGG.PDB	OD1, F_ASP_109	N, F_LEU_2	H, F_LEU_2	2.94	2.03	18.76
1HGG.PDB	OD2, F_ASP_112	N, F_PHE_3	H, F_PHE_3	2.87	2.05	27.28
1HGG.PDB	OD2, F_ASP_112	N, F_GLY_4	H, F_GLY_4	2.93	2.02	17.67
1HGG.PDB	OD1, F_ASP_112	N, F_ALA_5	H, F_ALA_5	2.93	2.06	23.45
1HGG.PDB	O, F_GLY_4	N, F_PHE_9	H, F_PHE_9	2.76	1.83	14.86
1HGG.PDB	O, E_VAL_323	N, F_GLY_13	H, F_GLY_13	2.73	1.78	9.21
1HGG.PDB	O, E_HIS_17	N, F_TRP_14	H, F_TRP_14	2.81	1.90	18.17

1HGG.PDB	OG1, F_THR_41	N, F_TRP_21	H, F_TRP_21	2.87	1.92	11.28
1HGG.PDB	O, E_GLY_16	N, F_GLY_23	H, F_GLY_23	2.97	2.08	20.37
1HGG.PDB	O, F_ALA_35	N, F_PHE_24	H, F_PHE_24	2.85	1.88	5.77
1HGG.PDB	O, E_CYS_14	N, F_ARG_25	H, F_ARG_25	2.99	2.04	12.72
1HGG.PDB	O, F_GLY_33	N, F_HIS_26	H, F_HIS_26	2.87	1.99	21.57
1HGG.PDB	O, E_THR_12	N, F_GLN_27	H, F_GLN_27	2.98	2.05	15.41
1HGG.PDB	O, F_GLY_31	N, F_ASN_28	H, F_ASN_28	2.80	1.85	12.20
1HGG.PDB	O, F_CYS_144	ND2, F_ASN_28	HD22, F_ASN_28	2.83	1.93	18.95
1HGG.PDB	O, F_PHE_24	N, F_ALA_35	H, F_ALA_35	2.83	2.02	27.51
1HGG.PDB	O, F_TYR_22	N, F_ASP_37	H, F_ASP_37	2.73	1.77	4.79
1HGG.PDB	OD2, F_ASP_37	N, F_SER_40	H, F_SER_40	2.88	1.93	12.27
1HGG.PDB	OD2, F_ASP_37	OG, F_SER_40	HG, F_SER_40	2.74	1.92	26.19
1HGG.PDB	O, F_ASP_37	OG1, F_THR_41	HG1, F_THR_41	2.71	1.82	18.81
1HGG.PDB	O, F_LEU_38	N, F_GLN_42	H, F_GLN_42	2.91	1.98	13.94
1HGG.PDB	OD1, F_ASP_46	NE2, F_GLN_42	HE22, F_GLN_42	2.82	1.94	21.99
1HGG.PDB	O, F_LYS_39	N, F_ALA_43	H, F_ALA_43	2.96	1.99	8.07
1HGG.PDB	O, F_SER_40	N, F_ALA_44	H, F_ALA_44	2.94	1.96	1.69
1HGG.PDB	O, F_THR_41	N, F_ILE_45	H, F_ILE_45	2.95	2.01	14.67
1HGG.PDB	O, F_GLN_42	N, F_ASP_46	H, F_ASP_46	2.77	1.80	0.61
1HGG.PDB	OE2, F_GLU_114	NE2, F_GLN_47	HE21, F_GLN_47	2.97	2.06	18.05
1HGG.PDB	O, F_ALA_43	NE2, F_GLN_47	HE22, F_GLN_47	2.99	2.07	16.84
1HGG.PDB	O, F_ILE_45	N, F_ASN_49	H, F_ASN_49	2.83	1.91	16.15
1HGG.PDB	O, F_ASP_46	N, F_GLY_50	H, F_GLY_50	2.91	2.04	23.57
1HGG.PDB	O, F_GLN_47	N, F_LYS_51	H, F_LYS_51	2.91	1.93	0.37
1HGG.PDB	OG1, F_THR_107	NZ, F_LYS_51	HZ1, F_LYS_51	2.98	2.02	18.55
1HGG.PDB	OE1, F_GLU_103	NZ, F_LYS_51	HZ2, F_LYS_51	2.79	1.76	6.25
1HGG.PDB	ND1, F_HIS_106	NZ, F_LYS_51	HZ3, F_LYS_51	2.72	1.74	15.22
1HGG.PDB	O, F_ILE_48	N, F_LEU_52	H, F_LEU_52	2.90	2.00	18.64
1HGG.PDB	O, F_ASN_49	N, F_ASN_53	H, F_ASN_53	2.88	1.99	19.93
1HGG.PDB	OE1, F_GLU_57	NH1, F_ARG_54	HH11, F_ARG_54	2.85	1.85	10.83
1HGG.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.73	1.74	10.16
1HGG.PDB	O, F_ASN_53	N, F_ILE_56	H, F_ILE_56	2.96	2.16	29.26
1HGG.PDB	OE2, F_GLU_61	NZ, F_LYS_58	HZ3, F_LYS_58	2.94	1.92	12.48
1HGG.PDB	OD2, D_ASP_86	NZ, F_LYS_62	HZ3, F_LYS_62	2.58	1.75	29.01
1HGG.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.87	1.91	10.03
1HGG.PDB	O, F_PHE_63	NE2, F_GLN_65	HE22, F_GLN_65	2.98	2.01	5.05
1HGG.PDB	O, E_LYS_299	NZ, F_LYS_68	HZ1, F_LYS_68	2.85	1.83	8.63
1HGG.PDB	OE2, F_GLU_85	NZ, F_LYS_68	HZ2, F_LYS_68	2.75	1.74	10.05
1HGG.PDB	OE2, F_GLU_72	OG, F_SER_71	HG, F_SER_71	2.86	2.03	26.49
1HGG.PDB	OG, A_SER_107	N, F_ARG_76	H, F_ARG_76	2.79	1.82	4.90
1HGG.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.88	1.92	11.44
1HGG.PDB	OE1, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.75	1.76	9.13
1HGG.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.67	1.68	1.99
1HGG.PDB	OE2, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.79	1.81	10.64
1HGG.PDB	O, F_GLY_75	N, F_ASP_79	H, F_ASP_79	2.85	1.92	13.80
1HGG.PDB	O, F_LEU_80	N, F_VAL_84	H, F_VAL_84	2.86	1.90	9.26
1HGG.PDB	O, F_LYS_82	N, F_ASP_86	H, F_ASP_86	2.94	1.98	10.58
1HGG.PDB	O, F_TYR_83	N, F_THR_87	H, F_THR_87	2.89	1.95	12.08
1HGG.PDB	O, F_VAL_84	N, F_LYS_88	H, F_LYS_88	2.90	2.00	19.38
1HGG.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.68	1.67	10.46
1HGG.PDB	O, F_GLU_85	N, F_ILE_89	H, F_ILE_89	2.87	1.91	8.62
1HGG.PDB	O, F_LYS_88	N, F_TRP_92	H, F_TRP_92	2.93	1.97	10.23
1HGG.PDB	O, F_ILE_89	N, F_SER_93	H, F_SER_93	2.82	1.93	20.13
1HGG.PDB	O, F_ILE_89	OG, F_SER_93	HG, F_SER_93	2.82	1.91	16.61
1HGG.PDB	O, F_ASP_90	N, F_TYR_94	H, F_TYR_94	2.98	2.04	13.91
1HGG.PDB	O, F_TYR_94	N, F_LEU_98	H, F_LEU_98	2.96	1.99	8.41
1HGG.PDB	O, F_ASN_95	N, F_LEU_99	H, F_LEU_99	2.87	1.98	19.54
1HGG.PDB	O, F_LEU_98	N, F_LEU_102	H, F_LEU_102	2.91	1.95	11.26

1HGG.PDB	O, F_VAL_100	N, F_ASN_104	H, F_ASN_104	2.83	1.90	15.88
1HGG.PDB	O, E_LYS_27	ND2, F_ASN_104	HD22, F_ASN_104	2.91	1.98	14.98
1HGG.PDB	O, F_LEU_102	N, F_HIS_106	H, F_HIS_106	2.95	2.00	11.41
1HGG.PDB	O, F_GLU_103	N, F_THR_107	H, F_THR_107	2.84	1.97	22.50
1HGG.PDB	O, F_HIS_106	N, F_LEU_110	H, F_LEU_110	2.81	1.85	10.10
1HGG.PDB	O, F_THR_107	N, F_THR_111	H, F_THR_111	2.97	2.01	8.66
1HGG.PDB	O, F_THR_107	OG1, F_THR_111	HG1, F_THR_111	2.90	1.95	9.89
1HGG.PDB	O, F_ASP_109	N, F_SER_113	H, F_SER_113	2.78	1.87	15.88
1HGG.PDB	O, F_ASP_112	N, F_ASN_116	H, F_ASN_116	2.99	2.01	3.50
1HGG.PDB	O, F_SER_113	N, F_LYS_117	H, F_LYS_117	2.76	1.88	19.98
1HGG.PDB	O, F_ASN_116	N, F_GLU_120	H, F_GLU_120	2.92	1.95	3.79
1HGG.PDB	O, F_LYS_117	N, F_LYS_121	H, F_LYS_121	2.87	1.96	17.48
1HGG.PDB	O, F_LEU_118	N, F_THR_122	H, F_THR_122	2.98	2.04	13.60
1HGG.PDB	O, F_PHE_119	N, F_ARG_123	H, F_ARG_123	2.90	1.95	11.29
1HGG.PDB	OE2, F_GLU_120	NH1, F_ARG_123	HH11, F_ARG_123	2.72	1.86	25.68
1HGG.PDB	O, F_GLU_120	N, F_ARG_124	H, F_ARG_124	2.96	1.99	8.37
1HGG.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.96	2.09	22.59
1HGG.PDB	OE2, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.87	2.01	24.00
1HGG.PDB	O, F_HIS_159	ND2, F_ASN_129	HD21, F_ASN_129	2.99	2.04	11.15
1HGG.PDB	OH, F_TYR_157	ND2, F_ASN_129	HD22, F_ASN_129	2.79	1.86	14.20
1HGG.PDB	O, F_LYS_139	N, F_GLU_131	H, F_GLU_131	2.96	2.01	12.55
1HGG.PDB	O, F_CYS_137	N, F_MET_133	H, F_MET_133	2.88	1.96	16.91
1HGG.PDB	O, E_LEU_13	N, F_PHE_138	H, F_PHE_138	2.72	1.87	23.38
1HGG.PDB	O, F_GLU_131	N, F_LYS_139	H, F_LYS_139	2.84	1.88	8.34
1HGG.PDB	O, E_ALA_11	N, F_ILE_140	H, F_ILE_140	2.79	1.89	17.86
1HGG.PDB	O, F_ASN_129	N, F_TYR_141	H, F_TYR_141	2.91	1.94	4.20
1HGG.PDB	OE2, F_GLU_165	N, F_LYS_143	H, F_LYS_143	2.98	2.11	23.38
1HGG.PDB	OE2, F_GLU_30	N, F_ASN_146	H, F_ASN_146	2.87	1.90	7.26
1HGG.PDB	OD1, F_ASP_145	N, F_ALA_147	H, F_ALA_147	2.98	2.17	28.99
1HGG.PDB	O, F_ASP_145	N, F_ILE_149	H, F_ILE_149	2.98	2.02	9.29
1HGG.PDB	O, F_ASN_146	N, F_GLU_150	H, F_GLU_150	2.88	1.93	11.94
1HGG.PDB	O, F_ALA_147	N, F_SER_151	H, F_SER_151	2.86	1.99	21.94
1HGG.PDB	O, F_CYS_148	OG, F_SER_151	HG, F_SER_151	2.70	1.85	23.21
1HGG.PDB	O, F_GLU_150	N, F_ASN_154	H, F_ASN_154	2.81	1.84	3.77
1HGG.PDB	O, F_HIS_159	N, F_TYR_162	H, F_TYR_162	2.96	2.05	18.31
1HGG.PDB	O, F_ASP_160	N, F_ARG_163	H, F_ARG_163	2.93	1.96	6.26
1HGG.PDB	O, D_ARG_170	NH1, F_ARG_163	HH12, F_ARG_163	2.94	2.00	17.69
1HGG.PDB	O, F_TYR_162	N, F_ALA_166	H, F_ALA_166	2.88	1.92	7.73
1HGG.PDB	O, F_ARG_163	N, F_LEU_167	H, F_LEU_167	2.76	1.84	14.20
1HGG.PDB	O, F_ALA_166	N, F_ARG_170	H, F_ARG_170	2.89	2.02	22.61
1HGG.PDB	O, F_GLU_128	NE, F_ARG_170	HE, F_ARG_170	2.70	1.85	24.72
1HGG.PDB	OE2, F_GLU_131	NH1, F_ARG_170	HH11, F_ARG_170	2.84	1.84	6.38
1HGG.PDB	O, F_LEU_167	N, F_PHE_171	H, F_PHE_171	2.94	1.99	11.68

Table 1667: 1HGG-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1HGH.PDB	O, B_ILE_140	N, A_ALA_11	H, A_ALA_11	2.91	2.03	21.75
1HGH.PDB	O, B_PHE_138	N, A_LEU_13	H, A_LEU_13	2.96	1.99	9.24
1HGH.PDB	O, B_ARG_25	N, A_CYS_14	H, A_CYS_14	2.90	1.93	6.13
1HGH.PDB	O, B_GLY_136	N, A_LEU_15	H, A_LEU_15	2.89	1.92	5.59
1HGH.PDB	O, B_GLY_23	N, A_GLY_16	H, A_GLY_16	2.92	2.07	24.71
1HGH.PDB	O, B_TRP_21	N, A_HIS_18	H, A_HIS_18	2.92	2.03	20.10
1HGH.PDB	OD1, A_ASN_322	N, A_VAL_20	H, A_VAL_20	2.77	1.82	11.72
1HGH.PDB	O, A_VAL_36	N, A_THR_24	H, A_THR_24	2.85	1.96	20.21
1HGH.PDB	O, A_ILE_34	N, A_VAL_26	H, A_VAL_26	2.81	1.89	15.81
1HGH.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.78	1.76	9.03
1HGH.PDB	O, A_ASP_31	N, A_THR_28	H, A_THR_28	2.74	1.91	26.60
1HGH.PDB	O, A_VAL_26	N, A_ILE_34	H, A_ILE_34	2.88	1.93	10.35
1HGH.PDB	O, A_THR_24	N, A_VAL_36	H, A_VAL_36	2.78	1.83	9.24
1HGH.PDB	O, A_MET_320	N, A_THR_37	H, A_THR_37	2.90	1.93	5.37
1HGH.PDB	O, A_LEU_316	N, A_THR_40	H, A_THR_40	2.78	1.95	25.57
1HGH.PDB	O, A_LEU_314	N, A_LEU_42	H, A_LEU_42	2.85	1.99	23.14
1HGH.PDB	O, A_PHE_294	N, A_GLN_44	H, A_GLN_44	2.90	1.92	4.45
1HGH.PDB	O, A_SER_46	NE2, A_GLN_44	HE22, A_GLN_44	2.81	1.96	24.37
1HGH.PDB	OD2, A_ASP_275	NZ, A_LYS_50	HZ1, A_LYS_50	2.79	1.83	19.36
1HGH.PDB	O, A_PRO_273	N, A_ILE_51	H, A_ILE_51	2.82	1.89	14.41
1HGH.PDB	O, A_ASP_275	N, A_ASN_53	H, A_ASN_53	2.86	1.97	20.86
1HGH.PDB	O, A_GLU_280	NE2, A_HIS_56	HE2, A_HIS_56	2.98	2.02	10.58
1HGH.PDB	OD2, A_ASP_85	N, A_ARG_57	H, A_ARG_57	2.81	1.91	18.42
1HGH.PDB	O, A_THR_83	NE, A_ARG_57	HE, A_ARG_57	2.77	1.81	8.25
1HGH.PDB	O, A_LEU_86	N, A_LEU_59	H, A_LEU_59	2.96	2.03	13.96
1HGH.PDB	O, A_VAL_88	N, A_GLY_61	H, A_GLY_61	2.98	2.14	25.31
1HGH.PDB	OD1, A_ASP_60	N, A_ILE_62	H, A_ILE_62	2.86	1.93	13.55
1HGH.PDB	O, A_GLY_61	N, A_CYS_64	H, A_CYS_64	2.88	1.98	19.17
1HGH.PDB	OE2, A_GLU_89	N, A_LEU_66	H, A_LEU_66	2.90	1.95	10.87
1HGH.PDB	O, A_LEU_66	N, A_LEU_70	H, A_LEU_70	2.83	1.95	21.65
1HGH.PDB	O, A_ILE_67	N, A_LEU_71	H, A_LEU_71	2.79	1.83	6.52
1HGH.PDB	O, A_ASP_68	N, A_GLY_72	H, A_GLY_72	2.91	1.99	15.72
1HGH.PDB	OD1, A_ASP_73	ND1, A_HIS_75	HD1, A_HIS_75	2.74	1.85	19.20
1HGH.PDB	O, A_ASP_63	NE2, A_HIS_75	HE2, A_HIS_75	2.75	1.84	17.13
1HGH.PDB	O, A_ASP_73	N, A_CYS_76	H, A_CYS_76	2.78	1.88	17.74
1HGH.PDB	O, A_PRO_74	N, A_ASP_77	H, A_ASP_77	2.92	1.95	6.24
1HGH.PDB	O, A_PHE_79	N, A_GLU_82	H, A_GLU_82	2.94	2.02	16.23
1HGH.PDB	OE1, A_GLU_82	N, A_THR_83	H, A_THR_83	2.95	2.06	20.13
1HGH.PDB	O, A_ARG_57	N, A_ASP_85	H, A_ASP_85	2.82	1.89	15.27
1HGH.PDB	O, A_MET_268	N, A_GLU_89	H, A_GLU_89	2.83	1.89	11.77
1HGH.PDB	OD1, A_ASP_60	NE, A_ARG_90	HE, A_ARG_90	2.85	1.88	8.50
1HGH.PDB	O, A_SER_270	NH1, A_ARG_90	HH11, A_ARG_90	2.64	1.77	24.75
1HGH.PDB	O, A_ALA_272	NH1, A_ARG_90	HH12, A_ARG_90	2.63	1.72	19.06
1HGH.PDB	OD2, A_ASP_60	NH2, A_ARG_90	HH21, A_ARG_90	2.79	1.80	9.33
1HGH.PDB	OD1, A_ASP_271	N, A_SER_91	H, A_SER_91	2.85	1.90	11.89
1HGH.PDB	OD2, A_ASP_271	OG, A_SER_91	HG, A_SER_91	2.76	1.89	21.30
1HGH.PDB	OD2, A_ASP_68	OG, A_SER_95	HG, A_SER_95	2.83	1.95	21.96
1HGH.PDB	OD2, A_ASP_73	N, A_ASN_96	H, A_ASN_96	2.91	1.94	7.26
1HGH.PDB	OD1, A_ASP_68	OH, A_TYR_100	HH, A_TYR_100	2.95	2.07	21.37
1HGH.PDB	O, A_ILE_230	N, A_ASP_101	H, A_ASP_101	2.93	2.05	22.44
1HGH.PDB	OD2, A_ASP_104	OG, A_SER_107	HG, A_SER_107	2.88	1.94	14.34
1HGH.PDB	O, A_TYR_105	N, A_ARG_109	H, A_ARG_109	2.84	1.87	3.70
1HGH.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.86	1.88	13.48
1HGH.PDB	OD2, F_ASP_79	OG, A_SER_110	HG, A_SER_110	2.97	2.01	11.65
1HGH.PDB	O, A_SER_107	N, A_LEU_111	H, A_LEU_111	2.86	1.91	11.39
1HGH.PDB	O, A_LEU_108	N, A_VAL_112	H, A_VAL_112	2.97	2.00	6.33
1HGH.PDB	O, A_ARG_109	N, A_ALA_113	H, A_ALA_113	2.87	1.97	18.74

1HGH.PDB	O, A_SER_110	N, A_SER_114	H, A_SER_114	2.97	2.06	18.17
1HGH.PDB	OE2, A_GLU_119	OG1, A_THR_117	HG1, A_THR_117	2.86	1.91	8.00
1HGH.PDB	O, A_GLU_82	N, A_LEU_118	H, A_LEU_118	2.97	2.03	14.27
1HGH.PDB	O, A_TYR_257	N, A_ILE_121	H, A_ILE_121	2.88	1.93	10.50
1HGH.PDB	O, A_ARG_255	N, A_GLU_123	H, A_GLU_123	2.86	1.91	11.35
1HGH.PDB	O, A_THR_155	N, A_THR_131	H, A_THR_131	2.70	1.82	20.96
1HGH.PDB	O, A_LYS_156	OG1, A_THR_131	HG1, A_THR_131	2.65	1.86	28.53
1HGH.PDB	OD1, A_ASN_152	N, A_ASN_133	H, A_ASN_133	2.91	2.01	19.83
1HGH.PDB	O, A_TRP_153	N, A_GLY_134	H, A_GLY_134	2.97	2.05	15.71
1HGH.PDB	O, A_GLY_146	N, A_SER_136	H, A_SER_136	2.71	1.82	19.78
1HGH.PDB	OG, A_SER_136	N, A_ALA_138	H, A_ALA_138	2.92	1.99	15.62
1HGH.PDB	O, A_GLY_144	NZ, A_LYS_140	HZ1, A_LYS_140	2.88	1.90	16.19
1HGH.PDB	OD1, A_ASN_137	NZ, A_LYS_140	HZ2, A_LYS_140	2.74	1.73	12.09
1HGH.PDB	OD2, A_ASP_77	NE, A_ARG_141	HE, A_ARG_141	2.85	2.03	27.72
1HGH.PDB	O, A_PHE_147	NH1, A_ARG_141	HH12, A_ARG_141	2.57	1.64	17.56
1HGH.PDB	OD1, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.86	1.95	21.78
1HGH.PDB	OD2, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.74	1.85	23.60
1HGH.PDB	O, A_GLY_72	NH2, A_ARG_141	HH22, A_ARG_141	2.97	1.99	11.22
1HGH.PDB	O, A_SER_136	N, A_GLY_146	H, A_GLY_146	2.94	1.99	12.07
1HGH.PDB	O, A_GLY_72	N, A_SER_149	H, A_SER_149	2.87	1.96	17.76
1HGH.PDB	O, A_ALA_253	N, A_ASN_152	H, A_ASN_152	2.72	1.90	27.60
1HGH.PDB	OH, A_TYR_195	NE1, A_TRP_153	HE1, A_TRP_153	2.96	2.05	18.96
1HGH.PDB	O, A_THR_131	N, A_THR_155	H, A_THR_155	2.98	2.04	12.93
1HGH.PDB	O, A_LEU_194	N, A_LYS_156	H, A_LYS_156	2.93	1.99	14.05
1HGH.PDB	O, A_SER_193	NZ, A_LYS_156	HZ2, A_LYS_156	2.80	1.78	10.99
1HGH.PDB	O, A_THR_160	N, A_SER_157	H, A_SER_157	2.94	2.03	18.60
1HGH.PDB	O, A_SER_247	N, A_LEU_164	H, A_LEU_164	2.69	1.86	25.54
1HGH.PDB	O, A_ILE_245	N, A_VAL_166	H, A_VAL_166	2.85	1.89	11.06
1HGH.PDB	O, A_LEU_243	OG1, A_THR_167	HG1, A_THR_167	2.91	1.96	8.56
1HGH.PDB	O, A_LEU_243	N, A_MET_168	H, A_MET_168	2.82	1.89	14.71
1HGH.PDB	O, A_ASP_241	N, A_ASN_170	H, A_ASN_170	2.96	1.99	7.35
1HGH.PDB	O, A_PHE_174	ND2, A_ASN_170	HD21, A_ASN_170	2.81	1.86	12.55
1HGH.PDB	O, A_VAL_237	ND2, A_ASN_170	HD22, A_ASN_170	2.88	2.03	25.05
1HGH.PDB	O, A_VAL_237	N, A_LYS_176	H, A_LYS_176	3.00	2.06	14.88
1HGH.PDB	OE2, A_GLU_123	NZ, A_LYS_176	HZ1, A_LYS_176	2.68	1.79	24.70
1HGH.PDB	O, A_PHE_258	N, A_LEU_177	H, A_LEU_177	2.99	2.01	5.13
1HGH.PDB	O, A_THR_235	N, A_TYR_178	H, A_TYR_178	2.85	1.88	6.04
1HGH.PDB	OE1, A_GLU_123	OH, A_TYR_178	HH, A_TYR_178	2.75	1.81	10.37
1HGH.PDB	OG1, A_THR_235	NE1, A_TRP_180	HE1, A_TRP_180	2.89	1.90	1.65
1HGH.PDB	O, A_ASN_250	N, A_HIS_183	H, A_HIS_183	2.85	1.97	21.49
1HGH.PDB	O, A_ARG_229	N, A_HIS_184	H, A_HIS_184	2.86	1.93	14.05
1HGH.PDB	OG, A_SER_231	NE2, A_HIS_184	HE2, A_HIS_184	2.74	1.90	25.48
1HGH.PDB	OG1, A_THR_187	N, A_GLU_190	H, A_GLU_190	2.92	1.98	12.65
1HGH.PDB	O, A_THR_187	N, A_GLN_191	H, A_GLN_191	2.99	2.03	10.21
1HGH.PDB	OD1, A_ASN_250	NE2, A_GLN_191	HE21, A_GLN_191	2.96	2.00	8.72
1HGH.PDB	O, A_GLN_197	NE2, A_GLN_191	HE22, A_GLN_191	2.95	2.00	12.41
1HGH.PDB	O, A_GLN_189	N, A_SER_193	H, A_SER_193	2.92	1.94	4.94
1HGH.PDB	O, A_GLN_189	OG, A_SER_193	HG, A_SER_193	2.79	2.00	29.43
1HGH.PDB	O, A_GLU_190	N, A_LEU_194	H, A_LEU_194	2.95	1.99	10.19
1HGH.PDB	O, A_GLN_191	N, A_TYR_195	H, A_TYR_195	2.79	1.83	8.10
1HGH.PDB	O, A_TYR_161	NE2, A_GLN_197	HE21, A_GLN_197	2.92	1.97	11.79
1HGH.PDB	O, A_ASN_248	NE2, A_GLN_197	HE22, A_GLN_197	2.87	1.96	16.95
1HGH.PDB	OD1, A_ASN_246	NH2, A_ARG_201	HH21, A_ARG_201	2.63	1.71	19.32
1HGH.PDB	O, A_ILE_213	N, A_VAL_202	H, A_VAL_202	2.95	2.00	12.25
1HGH.PDB	O, A_ASN_246	N, A_THR_203	H, A_THR_203	2.81	1.89	15.97
1HGH.PDB	O, A_GLN_211	N, A_VAL_204	H, A_VAL_204	2.84	1.93	17.60
1HGH.PDB	O, A_SER_209	N, A_THR_206	H, A_THR_206	2.88	1.91	6.84
1HGH.PDB	OD1, A_ASP_241	N, A_ARG_207	H, A_ARG_207	2.88	1.92	8.24

1HGH.PDB	OG1, A_THR.206	OG, A_SER.209	HG, A_SER.209	2.93	1.98	8.14
1HGH.PDB	OD1, E_ASP.101	NE2, A_GLN.210	HE22, A_GLN.210	2.97	2.14	27.61
1HGH.PDB	O, A_VAL.204	N, A_GLN.211	H, A_GLN.211	2.88	1.95	14.72
1HGH.PDB	OG1, A_THR.203	OG1, A_THR.212	HG1, A_THR.212	2.93	1.98	7.92
1HGH.PDB	O, A_VAL.202	N, A_ILE.213	H, A_ILE.213	2.89	1.95	14.76
1HGH.PDB	ND1, A_HIS.184	N, A_ASN.216	H, A_ASN.216	2.75	1.96	29.57
1HGH.PDB	OE1, C_GLN.210	NH2, A_ARG.220	HH21, A_ARG.220	2.66	1.73	18.15
1HGH.PDB	O, A_ASN.216	NH2, A_ARG.220	HH22, A_ARG.220	2.69	1.79	20.62
1HGH.PDB	O, A_LEU.226	N, A_VAL.223	H, A_VAL.223	2.87	1.91	10.54
1HGH.PDB	O, A_CYS.97	NE, A_ARG.224	HE, A_ARG.224	2.80	1.97	26.34
1HGH.PDB	O, A_CYS.97	NH2, A_ARG.224	HH21, A_ARG.224	2.81	1.94	24.94
1HGH.PDB	O, A_VAL.223	N, A_LEU.226	H, A_LEU.226	2.81	1.89	14.05
1HGH.PDB	O, A_SER.228	NH1, A_ARG.229	HH11, A_ARG.229	2.68	1.73	15.83
1HGH.PDB	O, A_PRO.221	NH2, A_ARG.229	HH22, A_ARG.229	2.59	1.64	14.22
1HGH.PDB	OD1, A_ASP.101	OG, A_SER.231	HG, A_SER.231	2.86	1.91	11.01
1HGH.PDB	O, A_ASP.101	N, A_ILE.232	H, A_ILE.232	2.88	1.97	18.41
1HGH.PDB	O, A_TRP.180	N, A_TYR.233	H, A_TYR.233	2.88	1.92	10.18
1HGH.PDB	O, A_TYR.178	N, A_THR.235	H, A_THR.235	2.91	2.01	18.50
1HGH.PDB	O, A_LYS.176	N, A_VAL.237	H, A_VAL.237	2.76	1.84	16.06
1HGH.PDB	O, F_SER.71	NZ, A_LYS.238	HZ2, A_LYS.238	2.69	1.74	19.56
1HGH.PDB	OE1, F_GLU.72	NZ, A_LYS.238	HZ3, A_LYS.238	2.92	1.93	15.64
1HGH.PDB	O, A_ASN.170	N, A_GLY.240	H, A_GLY.240	2.92	2.05	22.76
1HGH.PDB	O, A_LYS.238	N, A_ASP.241	H, A_ASP.241	2.96	2.03	14.77
1HGH.PDB	OD1, A_ASP.241	N, A_VAL.242	H, A_VAL.242	2.75	1.93	27.28
1HGH.PDB	O, A_MET.168	N, A_LEU.243	H, A_LEU.243	2.84	1.87	3.34
1HGH.PDB	O, A_SER.205	N, A_VAL.244	H, A_VAL.244	2.95	2.00	12.06
1HGH.PDB	O, A_VAL.166	N, A_ILE.245	H, A_ILE.245	2.85	1.91	12.74
1HGH.PDB	O, A_THR.203	N, A_ASN.246	H, A_ASN.246	2.92	1.96	9.76
1HGH.PDB	OD1, A_ASN.165	ND2, A_ASN.246	HD22, A_ASN.246	2.95	1.98	10.57
1HGH.PDB	O, A_LEU.164	N, A_SER.247	H, A_SER.247	2.89	1.97	17.06
1HGH.PDB	OE1, A_GLN.191	ND2, A_ASN.250	HD21, A_ASN.250	2.87	1.90	5.96
1HGH.PDB	O, A_HIS.183	ND2, A_ASN.250	HD22, A_ASN.250	2.85	1.88	6.67
1HGH.PDB	O, A_GLY.181	N, A_ILE.252	H, A_ILE.252	2.94	1.99	11.06
1HGH.PDB	O, A_ASN.152	N, A_ALA.253	H, A_ALA.253	2.83	1.93	19.98
1HGH.PDB	O, A_ILE.121	N, A_TYR.257	H, A_TYR.257	3.00	2.13	23.55
1HGH.PDB	O, A_LEU.177	N, A_PHE.258	H, A_PHE.258	2.88	1.93	9.88
1HGH.PDB	OG, A_SER.115	N, A_ARG.261	H, A_ARG.261	2.95	1.99	11.60
1HGH.PDB	OE2, A_GLU.119	NH1, A_ARG.261	HH12, A_ARG.261	2.62	1.81	29.53
1HGH.PDB	OE1, A_GLU.119	NH2, A_ARG.261	HH22, A_ARG.261	2.87	1.97	23.64
1HGH.PDB	OD2, A_ASP.85	NZ, A_LYS.264	HZ3, A_LYS.264	2.81	1.82	15.33
1HGH.PDB	O, A_PHE.87	N, A_MET.268	H, A_MET.268	2.83	1.97	23.14
1HGH.PDB	O, A_GLU.89	N, A_SER.270	H, A_SER.270	3.00	2.03	9.88
1HGH.PDB	O, A_PRO.284	OG, A_SER.270	HG, A_SER.270	2.79	1.85	11.64
1HGH.PDB	OG, A_SER.270	N, A_ALA.272	H, A_ALA.272	2.97	2.03	13.38
1HGH.PDB	O, A_ILE.51	N, A_ASP.275	H, A_ASP.275	2.90	1.99	17.90
1HGH.PDB	OD1, A_ASP.275	N, A_THR.276	H, A_THR.276	2.83	1.96	22.54
1HGH.PDB	O, A_ASN.54	N, A_SER.279	H, A_SER.279	2.78	1.84	12.84
1HGH.PDB	O, A_TYR.302	N, A_ILE.282	H, A_ILE.282	2.85	1.90	11.45
1HGH.PDB	O, A_THR.283	N, A_GLY.286	H, A_GLY.286	2.81	1.91	17.80
1HGH.PDB	O, A_LYS.50	N, A_SER.287	H, A_SER.287	2.92	1.95	4.60
1HGH.PDB	O, A_ALA.304	ND2, A_ASN.290	HD22, A_ASN.290	2.87	1.97	19.64
1HGH.PDB	OE1, A_GLN.44	NZ, A_LYS.292	HZ1, A_LYS.292	2.68	1.67	11.56
1HGH.PDB	OD2, A_ASP.291	NZ, A_LYS.292	HZ3, A_LYS.292	2.82	1.85	18.01
1HGH.PDB	O, A_LYS.307	N, A_GLN.295	H, A_GLN.295	2.87	1.98	21.43
1HGH.PDB	O, A_ASN.298	NE2, A_GLN.295	HE21, A_GLN.295	2.73	1.78	8.62
1HGH.PDB	O, A_GLN.44	N, A_ASN.296	H, A_ASN.296	2.92	1.96	9.49
1HGH.PDB	O, B_LYS.68	NZ, A_LYS.299	HZ1, A_LYS.299	2.98	1.97	13.59
1HGH.PDB	OD1, A_ASN.298	N, A_ILE.300	H, A_ILE.300	2.92	1.97	10.82

1HGH.PDB	O, A_ILE_282	N, A_TYR_302	H, A_TYR_302	2.84	2.02	27.55
1HGH.PDB	O, A_LYS_264	OH, A_TYR_302	HH, A_TYR_302	2.68	1.89	29.18
1HGH.PDB	O, B_LYS_62	N, A_GLY_303	H, A_GLY_303	3.00	2.03	6.35
1HGH.PDB	O, A_GLN_295	N, A_VAL_309	H, A_VAL_309	2.94	2.11	27.12
1HGH.PDB	OG, B_SER_93	N, A_LYS_310	H, A_LYS_310	2.90	1.94	8.41
1HGH.PDB	OD1, B_ASP_86	NZ, A_LYS_310	HZ2, A_LYS_310	2.71	1.84	27.09
1HGH.PDB	OE2, A_GLU_41	N, A_LEU_314	H, A_LEU_314	2.82	1.88	12.85
1HGH.PDB	OE1, A_GLU_41	NZ, A_LYS_315	HZ3, A_LYS_315	2.87	1.90	18.83
1HGH.PDB	O, A_THR_40	N, A_LEU_316	H, A_LEU_316	2.77	1.84	14.60
1HGH.PDB	OD1, B_ASN_104	N, A_ALA_317	H, A_ALA_317	2.74	1.80	10.38
1HGH.PDB	O, A_ASN_38	N, A_THR_318	H, A_THR_318	2.93	1.99	13.50
1HGH.PDB	O, A_GLU_35	N, A_ASN_322	H, A_ASN_322	2.96	1.98	2.64
1HGH.PDB	O, A_VAL_20	ND2, A_ASN_322	HD21, A_ASN_322	2.83	1.91	15.77
1HGH.PDB	OE2, A_GLU_35	ND2, A_ASN_322	HD22, A_ASN_322	2.83	1.93	20.02
1HGH.PDB	OE1, A_GLU_325	NZ, A_LYS_326	HZ3, A_LYS_326	2.84	1.87	17.61
1HGH.PDB	O, A_PRO_21	NE2, A_GLN_327	HE22, A_GLN_327	2.76	1.93	26.05
1HGH.PDB	OD2, B_ASP_112	N, B_GLY_1	H2, B_GLY_1	2.83	1.83	12.80
1HGH.PDB	OD1, B_ASP_109	N, B_LEU_2	H, B_LEU_2	2.87	1.94	15.91
1HGH.PDB	OD2, B_ASP_112	N, B_PHE_3	H, B_PHE_3	2.80	1.99	28.74
1HGH.PDB	OD2, B_ASP_112	N, B_GLY_4	H, B_GLY_4	2.97	2.08	20.13
1HGH.PDB	OD1, B_ASP_112	N, B_ALA_5	H, B_ALA_5	2.90	2.00	18.43
1HGH.PDB	O, B_GLY_4	N, B_PHE_9	H, B_PHE_9	2.83	1.90	13.47
1HGH.PDB	O, B_GLY_13	ND2, B_ASN_12	HD22, B_ASN_12	2.81	1.93	21.84
1HGH.PDB	O, A_VAL_323	N, B_GLY_13	H, B_GLY_13	2.69	1.78	16.40
1HGH.PDB	O, A_HIS_17	N, B_TRP_14	H, B_TRP_14	2.80	1.87	14.18
1HGH.PDB	OG1, B_THR_41	N, B_TRP_21	H, B_TRP_21	2.88	1.96	16.52
1HGH.PDB	O, A_GLY_16	N, B_GLY_23	H, B_GLY_23	2.92	2.01	18.42
1HGH.PDB	O, B_ALA_35	N, B_PHE_24	H, B_PHE_24	2.84	1.87	5.30
1HGH.PDB	O, A_CYS_14	N, B_ARG_25	H, B_ARG_25	2.97	2.02	12.29
1HGH.PDB	OE1, B_GLN_34	NE, B_ARG_25	HE, B_ARG_25	2.67	1.79	21.37
1HGH.PDB	OE1, B_GLN_34	NH2, B_ARG_25	HH21, B_ARG_25	2.91	2.10	29.24
1HGH.PDB	O, B_GLY_33	N, B_HIS_26	H, B_HIS_26	2.69	1.85	24.63
1HGH.PDB	O, B_GLY_31	N, B_ASN_28	H, B_ASN_28	2.77	1.84	14.31
1HGH.PDB	O, B_ASN_28	N, B_GLY_31	H, B_GLY_31	2.97	2.09	21.15
1HGH.PDB	O, B_HIS_26	N, B_GLY_33	H, B_GLY_33	2.87	1.95	17.09
1HGH.PDB	O, B_PHE_24	N, B_ALA_35	H, B_ALA_35	2.82	2.00	27.92
1HGH.PDB	O, B_TYR_22	N, B_ASP_37	H, B_ASP_37	2.71	1.77	10.18
1HGH.PDB	OD2, B_ASP_37	N, B_SER_40	H, B_SER_40	2.86	1.90	7.81
1HGH.PDB	O, B_ASP_37	OG1, B_THR_41	HG1, B_THR_41	2.73	1.82	16.31
1HGH.PDB	O, B_LEU_38	N, B_GLN_42	H, B_GLN_42	2.96	2.02	13.86
1HGH.PDB	OD1, B_ASP_46	NE2, B_GLN_42	HE22, B_GLN_42	2.86	1.97	20.47
1HGH.PDB	O, B_LYS_39	N, B_ALA_43	H, B_ALA_43	2.95	2.01	14.38
1HGH.PDB	O, B_SER_40	N, B_ALA_44	H, B_ALA_44	2.94	1.96	4.02
1HGH.PDB	O, B_THR_41	N, B_ILE_45	H, B_ILE_45	2.92	1.98	12.98
1HGH.PDB	O, B_GLN_42	N, B_ASP_46	H, B_ASP_46	2.79	1.82	1.49
1HGH.PDB	O, B_ALA_43	NE2, B_GLN_47	HE22, B_GLN_47	2.86	1.96	17.99
1HGH.PDB	O, B_ILE_45	N, B_ASN_49	H, B_ASN_49	2.86	1.93	14.26
1HGH.PDB	O, B_ASP_46	N, B_GLY_50	H, B_GLY_50	2.92	2.02	19.62
1HGH.PDB	O, B_GLN_47	N, B_LYS_51	H, B_LYS_51	2.97	2.01	11.02
1HGH.PDB	OE1, B_GLU_103	NZ, B_LYS_51	HZ1, B_LYS_51	2.79	1.76	7.63
1HGH.PDB	ND1, B_HIS_106	NZ, B_LYS_51	HZ2, B_LYS_51	2.80	1.85	18.51
1HGH.PDB	OG1, B_THR_107	NZ, B_LYS_51	HZ3, B_LYS_51	2.89	1.91	15.99
1HGH.PDB	O, B_ILE_48	N, B_LEU_52	H, B_LEU_52	2.93	2.02	17.94
1HGH.PDB	O, B_ASN_49	N, B_ASN_53	H, B_ASN_53	2.82	1.92	18.53
1HGH.PDB	OE1, B_GLU_57	NH1, B_ARG_54	HH11, B_ARG_54	2.86	1.87	11.36
1HGH.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.82	1.86	15.60
1HGH.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ1, B_LYS_62	2.66	1.80	27.71
1HGH.PDB	OD2, F_ASP_90	NZ, B_LYS_62	HZ3, B_LYS_62	2.68	1.82	27.13

1HGH.PDB	OG, A_SER.110	NE2, B_HIS.64	HE2, B_HIS.64	2.87	1.91	11.96
1HGH.PDB	O, B_PHE.63	NE2, B_GLN.65	HE22, B_GLN.65	2.98	2.01	7.37
1HGH.PDB	O, A_LYS.299	NZ, B_LYS.68	HZ1, B_LYS.68	2.89	1.86	6.42
1HGH.PDB	OE2, B_GLU.85	NZ, B_LYS.68	HZ2, B_LYS.68	2.73	1.71	6.94
1HGH.PDB	OG, C_SER.107	N, B_ARG.76	H, B_ARG.76	2.88	1.92	9.13
1HGH.PDB	OE2, D_GLU.81	NE, B_ARG.76	HE, B_ARG.76	2.87	1.90	9.70
1HGH.PDB	OE2, D_GLU.74	NH1, B_ARG.76	HH12, B_ARG.76	2.91	1.90	8.45
1HGH.PDB	OE1, D_GLU.81	NH2, B_ARG.76	HH21, B_ARG.76	2.77	1.76	5.47
1HGH.PDB	OE1, D_GLU.74	NH2, B_ARG.76	HH22, B_ARG.76	2.89	1.87	2.83
1HGH.PDB	O, B_GLU.72	NE2, B_GLN.78	HE21, B_GLN.78	2.94	1.96	7.72
1HGH.PDB	OE1, B_GLU.74	NE2, B_GLN.78	HE22, B_GLN.78	2.91	1.95	10.12
1HGH.PDB	O, B_GLY.75	N, B_ASP.79	H, B_ASP.79	2.86	1.93	16.21
1HGH.PDB	O, B_ASP.79	N, B_TYR.83	H, B_TYR.83	2.90	2.00	19.79
1HGH.PDB	OE1, D_GLU.85	OH, B_TYR.83	HH, B_TYR.83	2.69	1.84	23.96
1HGH.PDB	O, B_LEU.80	N, B_VAL.84	H, B_VAL.84	2.72	1.80	14.22
1HGH.PDB	O, B_LYS.82	N, B_ASP.86	H, B_ASP.86	2.94	2.00	12.60
1HGH.PDB	OH, F_TYR.83	NZ, B_LYS.88	HZ1, B_LYS.88	2.74	1.71	7.44
1HGH.PDB	O, B_GLU.85	N, B_ILE.89	H, B_ILE.89	2.85	1.87	2.68
1HGH.PDB	O, B_LYS.88	N, B_TRP.92	H, B_TRP.92	2.92	1.94	4.60
1HGH.PDB	O, B_ILE.89	N, B_SER.93	H, B_SER.93	2.91	2.02	21.18
1HGH.PDB	O, B_ILE.89	OG, B_SER.93	HG, B_SER.93	2.79	1.87	15.47
1HGH.PDB	O, B_ASP.90	N, B_TYR.94	H, B_TYR.94	2.88	1.97	17.78
1HGH.PDB	O, B_LEU.91	N, B_ASN.95	H, B_ASN.95	3.00	2.02	1.45
1HGH.PDB	O, B_TRP.92	N, B_ALA.96	H, B_ALA.96	2.97	2.04	15.59
1HGH.PDB	O, B_TYR.94	N, B_LEU.98	H, B_LEU.98	2.93	1.96	5.82
1HGH.PDB	O, B_ASN.95	N, B_LEU.99	H, B_LEU.99	2.94	2.02	15.77
1HGH.PDB	O, B_VAL.100	N, B_ASN.104	H, B_ASN.104	2.89	1.94	12.26
1HGH.PDB	O, A_LYS.27	ND2, B_ASN.104	HD22, B_ASN.104	2.88	1.93	11.07
1HGH.PDB	O, B_LEU.102	N, B_HIS.106	H, B_HIS.106	2.96	1.99	8.01
1HGH.PDB	O, B_GLU.103	N, B_THR.107	H, B_THR.107	2.84	1.93	17.70
1HGH.PDB	O, B_HIS.106	N, B_LEU.110	H, B_LEU.110	2.80	1.84	8.73
1HGH.PDB	O, B_THR.107	OG1, B_THR.111	HG1, B_THR.111	2.85	1.90	7.42
1HGH.PDB	O, B_ASP.109	N, B_SER.113	H, B_SER.113	2.77	1.82	9.55
1HGH.PDB	O, B_ASP.112	N, B_ASN.116	H, B_ASN.116	3.00	2.02	6.31
1HGH.PDB	O, B_SER.113	N, B_LYS.117	H, B_LYS.117	2.71	1.89	26.84
1HGH.PDB	O, B_GLU.114	N, B_LEU.118	H, B_LEU.118	2.99	2.02	7.88
1HGH.PDB	O, B_ASN.116	N, B_GLU.120	H, B_GLU.120	2.94	1.96	2.10
1HGH.PDB	O, B_LYS.117	N, B_LYS.121	H, B_LYS.121	2.86	1.96	18.76
1HGH.PDB	O, B_LEU.118	N, B_THR.122	H, B_THR.122	2.99	2.01	4.84
1HGH.PDB	O, B_PHE.119	N, B_ARG.123	H, B_ARG.123	2.90	1.94	9.49
1HGH.PDB	OE2, B_GLU.120	NH1, B_ARG.123	HH11, B_ARG.123	2.74	1.85	22.74
1HGH.PDB	O, B_GLU.120	N, B_ARG.124	H, B_ARG.124	2.98	2.02	10.15
1HGH.PDB	OE1, F_GLU.132	NE, B_ARG.124	HE, B_ARG.124	2.76	1.94	26.47
1HGH.PDB	OE2, F_GLU.132	NE, B_ARG.124	HE, B_ARG.124	2.83	1.98	23.62
1HGH.PDB	O, B_LEU.126	N, B_ASN.129	H, B_ASN.129	2.97	2.04	14.58
1HGH.PDB	OH, B_TYR.157	ND2, B_ASN.129	HD22, B_ASN.129	2.83	1.87	11.09
1HGH.PDB	O, B_LYS.139	N, B_GLU.131	H, B_GLU.131	2.93	2.01	16.63
1HGH.PDB	O, B_CYS.137	N, B_MET.133	H, B_MET.133	2.84	1.90	13.58
1HGH.PDB	O, A_LEU.13	N, B_PHE.138	H, B_PHE.138	2.71	1.82	19.17
1HGH.PDB	O, B_GLU.131	N, B_LYS.139	H, B_LYS.139	2.85	1.89	6.05
1HGH.PDB	O, A_ALA.11	N, B_ILE.140	H, B_ILE.140	2.77	1.85	16.34
1HGH.PDB	O, B_ASN.129	N, B_TYR.141	H, B_TYR.141	2.84	1.90	13.40
1HGH.PDB	O, B_ILE.140	N, B_HIS.142	H, B_HIS.142	3.00	2.21	29.95
1HGH.PDB	OE2, B_GLU.165	N, B_LYS.143	H, B_LYS.143	2.98	2.03	13.49
1HGH.PDB	OE1, B_GLU.30	N, B_ASN.146	H, B_ASN.146	2.90	1.99	19.37
1HGH.PDB	O, B_ASP.145	N, B_ILE.149	H, B_ILE.149	2.89	1.93	10.45
1HGH.PDB	O, B_ASN.146	N, B_GLU.150	H, B_GLU.150	2.91	1.99	15.45
1HGH.PDB	O, B_ALA.147	N, B_SER.151	H, B_SER.151	2.92	2.08	25.20

1HGH.PDB	O, B_CYS_148	OG, B_SER_151	HG, B_SER_151	2.72	1.85	19.70
1HGH.PDB	O, B_GLU_150	N, B_ASN_154	H, B_ASN_154	2.82	1.84	0.36
1HGH.PDB	OE2, B_GLU_150	ND2, B_ASN_154	HD21, B_ASN_154	2.97	2.10	23.74
1HGH.PDB	O, B_SER_151	N, B_THR_156	H, B_THR_156	2.77	1.95	26.55
1HGH.PDB	OD1, B_ASN_154	OG1, B_THR_156	HG1, B_THR_156	2.66	1.78	19.28
1HGH.PDB	OD1, B_ASP_158	N, B_ASP_160	H, B_ASP_160	2.94	2.06	21.76
1HGH.PDB	O, B_HIS_159	N, B_TYR_162	H, B_TYR_162	2.90	2.01	20.57
1HGH.PDB	O, F_ARG_170	NH1, B_ARG_163	HH12, B_ARG_163	2.69	1.71	10.72
1HGH.PDB	O, B_TYR_162	N, B_ALA_166	H, B_ALA_166	2.89	1.91	4.63
1HGH.PDB	O, B_ARG_163	N, B_LEU_167	H, B_LEU_167	2.82	1.86	7.93
1HGH.PDB	O, B_GLU_165	ND2, B_ASN_169	HD22, B_ASN_169	2.96	1.99	6.61
1HGH.PDB	O, B_ALA_166	N, B_ARG_170	H, B_ARG_170	2.78	1.91	21.64
1HGH.PDB	O, B_GLU_128	NE, B_ARG_170	HE, B_ARG_170	2.74	1.88	23.26
1HGH.PDB	OE2, B_GLU_131	NH1, B_ARG_170	HH11, B_ARG_170	2.83	1.83	5.81
1HGH.PDB	O, B_LEU_167	N, B_PHE_171	H, B_PHE_171	2.96	2.03	15.44
1HGH.PDB	O, D_ILE_140	N, C_ALA_11	H, C_ALA_11	2.90	2.02	21.17
1HGH.PDB	O, D_GLN_27	N, C_THR_12	H, C_THR_12	2.94	1.99	10.37
1HGH.PDB	O, D_PHE_138	N, C_LEU_13	H, C_LEU_13	2.98	2.01	8.63
1HGH.PDB	O, D_ARG_25	N, C_CYS_14	H, C_CYS_14	2.74	1.80	11.01
1HGH.PDB	O, D_GLY_136	N, C_LEU_15	H, C_LEU_15	2.92	1.95	6.34
1HGH.PDB	O, D_GLY_23	N, C_GLY_16	H, C_GLY_16	2.95	2.08	23.40
1HGH.PDB	O, D_TRP_21	N, C_HIS_18	H, C_HIS_18	2.93	2.04	20.66
1HGH.PDB	OD1, C_ASN_322	N, C_VAL_20	H, C_VAL_20	2.77	1.84	13.32
1HGH.PDB	O, C_VAL_36	N, C_THR_24	H, C_THR_24	2.84	1.94	18.88
1HGH.PDB	O, C_ILE_34	N, C_VAL_26	H, C_VAL_26	2.81	1.89	15.19
1HGH.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.82	1.78	7.61
1HGH.PDB	O, C_ASP_31	N, C_THR_28	H, C_THR_28	2.72	1.89	26.38
1HGH.PDB	O, C_VAL_26	N, C_ILE_34	H, C_ILE_34	2.87	1.91	10.12
1HGH.PDB	O, C_THR_24	N, C_VAL_36	H, C_VAL_36	2.79	1.83	8.93
1HGH.PDB	O, C_MET_320	N, C_THR_37	H, C_THR_37	2.94	1.96	4.71
1HGH.PDB	O, C_LEU_316	N, C_THR_40	H, C_THR_40	2.84	2.01	25.77
1HGH.PDB	O, C_LEU_314	N, C_LEU_42	H, C_LEU_42	2.83	1.98	24.51
1HGH.PDB	O, C_PHE_294	N, C_GLN_44	H, C_GLN_44	2.92	1.94	4.18
1HGH.PDB	O, C_SER_46	NE2, C_GLN_44	HE22, C_GLN_44	2.81	1.95	23.93
1HGH.PDB	O, C_ASN_285	OG, C_SER_47	HG, C_SER_47	2.78	1.85	12.35
1HGH.PDB	OD2, C_ASP_275	NZ, C_LYS_50	HZ1, C_LYS_50	2.77	1.81	19.74
1HGH.PDB	O, C_PRO_273	N, C_ILE_51	H, C_ILE_51	2.79	1.88	17.33
1HGH.PDB	O, C_ASP_275	N, C_ASN_53	H, C_ASN_53	2.82	1.92	18.86
1HGH.PDB	O, C_GLU_280	NE2, C_HIS_56	HE2, C_HIS_56	2.96	2.00	11.12
1HGH.PDB	OD2, C_ASP_85	N, C_ARG_57	H, C_ARG_57	2.82	1.94	21.49
1HGH.PDB	O, C_THR_83	NE, C_ARG_57	HE, C_ARG_57	2.74	1.79	9.49
1HGH.PDB	O, C_LEU_86	N, C_LEU_59	H, C_LEU_59	2.97	2.04	15.48
1HGH.PDB	O, C_VAL_88	N, C_GLY_61	H, C_GLY_61	2.96	2.15	28.24
1HGH.PDB	OD1, C_ASP_60	N, C_ILE_62	H, C_ILE_62	2.88	1.94	12.53
1HGH.PDB	O, C_GLY_61	N, C_CYS_64	H, C_CYS_64	2.87	1.98	20.97
1HGH.PDB	OE2, C_GLU_89	N, C_LEU_66	H, C_LEU_66	2.91	1.94	8.58
1HGH.PDB	O, C_LEU_66	N, C_LEU_70	H, C_LEU_70	2.86	2.00	23.48
1HGH.PDB	O, C_ILE_67	N, C_LEU_71	H, C_LEU_71	2.80	1.84	8.28
1HGH.PDB	O, C_ASP_68	N, C_GLY_72	H, C_GLY_72	2.90	1.96	13.34
1HGH.PDB	OD1, C_ASP_73	ND1, C_HIS_75	HD1, C_HIS_75	2.71	1.84	22.23
1HGH.PDB	O, C_ASP_63	NE2, C_HIS_75	HE2, C_HIS_75	2.74	1.84	19.08
1HGH.PDB	O, C_ASP_73	N, C_CYS_76	H, C_CYS_76	2.76	1.88	21.08
1HGH.PDB	O, C_PRO_74	N, C_ASP_77	H, C_ASP_77	2.92	1.94	6.05
1HGH.PDB	O, C_CYS_76	N, C_PHE_79	H, C_PHE_79	2.99	2.01	3.05
1HGH.PDB	O, C_PHE_79	N, C_GLU_82	H, C_GLU_82	2.96	2.04	15.86
1HGH.PDB	OE1, C_GLU_82	N, C_THR_83	H, C_THR_83	2.89	2.00	20.79
1HGH.PDB	O, C_ARG_57	N, C_ASP_85	H, C_ASP_85	2.82	1.87	10.67
1HGH.PDB	O, C_MET_268	N, C_GLU_89	H, C_GLU_89	2.85	1.91	11.22

1HGH.PDB	OD1, C_ASP.60	NE, C_ARG.90	HE, C_ARG.90	2.80	1.87	15.44
1HGH.PDB	O, C_SER.270	NH1, C_ARG.90	HH11, C_ARG.90	2.64	1.80	26.46
1HGH.PDB	O, C_ALA.272	NH1, C_ARG.90	HH12, C_ARG.90	2.63	1.73	20.12
1HGH.PDB	OD2, C_ASP.60	NH2, C_ARG.90	HH21, C_ARG.90	2.76	1.77	8.79
1HGH.PDB	OD1, C_ASP.271	N, C_SER.91	H, C_SER.91	2.85	1.89	10.15
1HGH.PDB	OD2, C_ASP.271	OG, C_SER.91	HG, C_SER.91	2.80	1.87	12.62
1HGH.PDB	OD2, C_ASP.68	OG, C_SER.95	HG, C_SER.95	2.83	1.92	18.04
1HGH.PDB	OD2, C_ASP.73	N, C_ASN.96	H, C_ASN.96	2.88	1.92	9.38
1HGH.PDB	OD1, C_ASP.68	OH, C_TYR.100	HH, C_TYR.100	2.94	2.01	15.20
1HGH.PDB	O, C_ILE.230	N, C_ASP.101	H, C_ASP.101	2.88	2.00	21.91
1HGH.PDB	OD2, C_ASP.104	OG, C_SER.107	HG, C_SER.107	2.88	1.96	17.02
1HGH.PDB	O, C_TYR.105	N, C_ARG.109	H, C_ARG.109	2.83	1.86	3.16
1HGH.PDB	OE2, D_GLU.67	NH2, C_ARG.109	HH21, C_ARG.109	2.86	1.88	13.66
1HGH.PDB	OD2, B_ASP.79	OG, C_SER.110	HG, C_SER.110	2.78	1.85	13.87
1HGH.PDB	O, C_SER.107	N, C_LEU.111	H, C_LEU.111	2.85	1.90	10.01
1HGH.PDB	O, C_ARG.109	N, C_ALA.113	H, C_ALA.113	2.90	1.99	17.86
1HGH.PDB	O, C_SER.110	N, C_SER.114	H, C_SER.114	2.98	2.02	11.21
1HGH.PDB	OE2, C_GLU.119	OG1, C_THR.117	HG1, C_THR.117	2.87	1.92	8.14
1HGH.PDB	O, C_GLU.82	N, C_LEU.118	H, C_LEU.118	2.94	1.98	9.54
1HGH.PDB	O, C_TYR.257	N, C_ILE.121	H, C_ILE.121	2.91	1.96	13.11
1HGH.PDB	O, C_ARG.255	N, C_GLU.123	H, C_GLU.123	2.84	1.89	11.27
1HGH.PDB	O, C_THR.155	N, C_THR.131	H, C_THR.131	2.73	1.84	19.41
1HGH.PDB	OD1, C_ASN.152	N, C_ASN.133	H, C_ASN.133	2.88	2.02	23.07
1HGH.PDB	O, C_TRP.153	N, C_GLY.134	H, C_GLY.134	3.00	2.07	15.16
1HGH.PDB	O, C_GLY.146	N, C_SER.136	H, C_SER.136	2.72	1.83	18.30
1HGH.PDB	OG, C_SER.136	N, C_ALA.138	H, C_ALA.138	2.92	2.02	18.99
1HGH.PDB	O, C_GLY.144	NZ, C_LYS.140	HZ1, C_LYS.140	2.84	1.87	16.40
1HGH.PDB	OD1, C_ASN.137	NZ, C_LYS.140	HZ2, C_LYS.140	2.76	1.74	10.11
1HGH.PDB	OD2, C_ASP.77	NE, C_ARG.141	HE, C_ARG.141	2.85	2.02	26.86
1HGH.PDB	O, C_PHE.147	NH1, C_ARG.141	HH12, C_ARG.141	2.56	1.64	18.32
1HGH.PDB	OD1, C_ASP.77	NH2, C_ARG.141	HH21, C_ARG.141	2.88	1.98	22.59
1HGH.PDB	OD2, C_ASP.77	NH2, C_ARG.141	HH21, C_ARG.141	2.75	1.86	23.43
1HGH.PDB	O, C_GLY.72	NH2, C_ARG.141	HH22, C_ARG.141	2.92	1.95	11.58
1HGH.PDB	OD1, C_ASN.137	OG, C_SER.145	HG, C_SER.145	2.89	2.04	23.42
1HGH.PDB	O, C_SER.136	N, C_GLY.146	H, C_GLY.146	2.94	2.00	12.32
1HGH.PDB	O, C_GLY.72	N, C_SER.149	H, C_SER.149	2.86	1.93	14.59
1HGH.PDB	OH, C_TYR.195	NE1, C_TRP.153	HE1, C_TRP.153	2.92	2.00	17.94
1HGH.PDB	O, C_LEU.194	N, C_LYS.156	H, C_LYS.156	2.95	2.02	15.17
1HGH.PDB	O, C_THR.160	N, C_SER.157	H, C_SER.157	2.91	1.98	14.73
1HGH.PDB	O, C_SER.247	N, C_LEU.164	H, C_LEU.164	2.74	1.91	26.14
1HGH.PDB	O, C_ILE.245	N, C_VAL.166	H, C_VAL.166	2.84	1.89	12.07
1HGH.PDB	O, C_LEU.243	OG1, C_THR.167	HG1, C_THR.167	2.87	1.97	18.05
1HGH.PDB	O, C_LEU.243	N, C_MET.168	H, C_MET.168	2.84	1.91	14.36
1HGH.PDB	O, C_ASP.241	N, C_ASN.170	H, C_ASN.170	2.92	1.95	6.13
1HGH.PDB	O, C_PHE.174	ND2, C_ASN.170	HD21, C_ASN.170	2.82	1.87	11.99
1HGH.PDB	O, C_VAL.237	ND2, C_ASN.170	HD22, C_ASN.170	2.87	2.05	26.77
1HGH.PDB	O, C_VAL.237	N, C_LYS.176	H, C_LYS.176	2.98	2.08	18.97
1HGH.PDB	OE2, C_GLU.123	NZ, C_LYS.176	HZ1, C_LYS.176	2.65	1.80	28.51
1HGH.PDB	O, C_PHE.258	N, C_LEU.177	H, C_LEU.177	2.96	1.98	4.25
1HGH.PDB	O, C_THR.235	N, C_TYR.178	H, C_TYR.178	2.84	1.89	11.44
1HGH.PDB	OE1, C_GLU.123	OH, C_TYR.178	HH, C_TYR.178	2.74	1.81	11.36
1HGH.PDB	OG1, C_THR.235	NE1, C_TRP.180	HE1, C_TRP.180	2.88	1.89	0.71
1HGH.PDB	O, C_ASN.250	N, C_HIS.183	H, C_HIS.183	2.86	2.01	24.69
1HGH.PDB	O, C_ARG.229	N, C_HIS.184	H, C_HIS.184	2.88	1.93	10.57
1HGH.PDB	OG, C_SER.231	NE2, C_HIS.184	HE2, C_HIS.184	2.77	1.92	24.69
1HGH.PDB	OG1, C_THR.187	N, C_GLU.190	H, C_GLU.190	2.94	2.00	12.64
1HGH.PDB	OD1, C_ASN.250	NE2, C_GLN.191	HE21, C_GLN.191	2.95	1.99	9.46
1HGH.PDB	O, C_GLN.197	NE2, C_GLN.191	HE22, C_GLN.191	2.94	1.99	11.67

1HGH.PDB	O, C_GLN_189	OG1, C_THR_192	HG1, C_THR_192	2.82	1.90	13.51
1HGH.PDB	O, C_GLN_189	N, C_SER_193	H, C_SER_193	2.90	1.95	11.34
1HGH.PDB	O, C_GLU_190	N, C_LEU_194	H, C_LEU_194	2.97	1.99	6.33
1HGH.PDB	O, C_GLN_191	N, C_TYR_195	H, C_TYR_195	2.80	1.84	8.79
1HGH.PDB	O, C_TYR_195	N, C_GLN_197	H, C_GLN_197	2.68	1.90	29.95
1HGH.PDB	O, C_TYR_161	NE2, C_GLN_197	HE21, C_GLN_197	2.92	1.98	11.92
1HGH.PDB	O, C_ASN_248	NE2, C_GLN_197	HE22, C_GLN_197	2.88	1.96	16.62
1HGH.PDB	OD1, C_ASN_246	NH2, C_ARG_201	HH21, C_ARG_201	2.65	1.73	20.02
1HGH.PDB	O, C_ILE_213	N, C_VAL_202	H, C_VAL_202	2.96	2.02	14.06
1HGH.PDB	O, C_ASN_246	N, C_THR_203	H, C_THR_203	2.85	1.89	9.27
1HGH.PDB	OG1, C_THR_212	OG1, C_THR_203	HG1, C_THR_203	2.92	1.98	11.43
1HGH.PDB	O, C_GLN_211	N, C_VAL_204	H, C_VAL_204	2.86	1.95	18.48
1HGH.PDB	O, C_SER_209	N, C_THR_206	H, C_THR_206	2.88	1.91	6.25
1HGH.PDB	OD1, C_ASP_241	N, C_ARG_207	H, C_ARG_207	2.87	1.91	10.07
1HGH.PDB	OD2, C_ASP_241	NE, C_ARG_208	HE, C_ARG_208	2.97	2.08	22.63
1HGH.PDB	OG1, C_THR_206	OG, C_SER_209	HG, C_SER_209	2.95	2.00	8.11
1HGH.PDB	OD1, A_ASP_101	NE2, C_GLN_210	HE22, C_GLN_210	2.93	2.07	24.87
1HGH.PDB	O, C_VAL_204	N, C_GLN_211	H, C_GLN_211	2.87	1.94	15.75
1HGH.PDB	O, C_VAL_202	N, C_ILE_213	H, C_ILE_213	2.87	1.94	14.37
1HGH.PDB	ND1, C_HIS_184	N, C_ASN_216	H, C_ASN_216	2.74	1.94	28.49
1HGH.PDB	O, C_ASN_216	NH1, C_ARG_220	HH12, C_ARG_220	2.90	2.08	29.68
1HGH.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.57	1.72	26.03
1HGH.PDB	O, C_ASN_216	NH2, C_ARG_220	HH22, C_ARG_220	2.69	1.80	21.79
1HGH.PDB	O, C_LEU_226	N, C_VAL_223	H, C_VAL_223	2.85	1.88	8.82
1HGH.PDB	O, C_CYS_97	NE, C_ARG_224	HE, C_ARG_224	2.79	1.97	28.26
1HGH.PDB	O, C_CYS_97	NH2, C_ARG_224	HH21, C_ARG_224	2.81	1.96	27.50
1HGH.PDB	O, C_VAL_223	N, C_LEU_226	H, C_LEU_226	2.85	1.93	15.63
1HGH.PDB	O, C_ARG_220	OG, C_SER_227	HG, C_SER_227	2.97	2.04	13.65
1HGH.PDB	O, C_SER_228	NH1, C_ARG_229	HH11, C_ARG_229	2.65	1.70	16.09
1HGH.PDB	O, C_PRO_221	NH2, C_ARG_229	HH22, C_ARG_229	2.62	1.66	13.46
1HGH.PDB	OD1, C_ASP_101	OG, C_SER_231	HG, C_SER_231	2.86	1.92	12.68
1HGH.PDB	O, C_ASP_101	N, C_ILE_232	H, C_ILE_232	2.90	1.98	16.86
1HGH.PDB	O, C_TRP_180	N, C_TYR_233	H, C_TYR_233	2.89	1.92	6.98
1HGH.PDB	O, C_TYR_178	N, C_THR_235	H, C_THR_235	2.90	1.98	17.23
1HGH.PDB	O, C_LYS_176	N, C_VAL_237	H, C_VAL_237	2.74	1.82	16.60
1HGH.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.71	1.80	22.72
1HGH.PDB	O, B_SER_71	NZ, C_LYS_238	HZ3, C_LYS_238	2.68	1.75	20.57
1HGH.PDB	O, C_ASN_170	N, C_GLY_240	H, C_GLY_240	2.92	2.04	20.96
1HGH.PDB	O, C_LYS_238	N, C_ASP_241	H, C_ASP_241	2.93	1.99	14.39
1HGH.PDB	OD1, C_ASP_241	N, C_VAL_242	H, C_VAL_242	2.78	1.96	27.73
1HGH.PDB	O, C_MET_168	N, C_LEU_243	H, C_LEU_243	2.86	1.89	2.64
1HGH.PDB	O, C_SER_205	N, C_VAL_244	H, C_VAL_244	2.96	2.02	14.40
1HGH.PDB	O, C_VAL_166	N, C_ILE_245	H, C_ILE_245	2.87	1.93	13.03
1HGH.PDB	O, C_THR_203	N, C_ASN_246	H, C_ASN_246	2.89	1.95	12.42
1HGH.PDB	OD1, C_ASN_165	ND2, C_ASN_246	HD22, C_ASN_246	2.97	2.00	10.03
1HGH.PDB	O, C_LEU_164	N, C_SER_247	H, C_SER_247	2.91	2.00	17.54
1HGH.PDB	O, C_ARG_201	OG, C_SER_247	HG, C_SER_247	2.73	1.94	29.65
1HGH.PDB	OE1, C_GLN_191	ND2, C_ASN_250	HD21, C_ASN_250	2.86	1.89	6.98
1HGH.PDB	O, C_HIS_183	ND2, C_ASN_250	HD22, C_ASN_250	2.87	1.90	8.13
1HGH.PDB	O, C_GLY_181	N, C_ILE_252	H, C_ILE_252	2.97	2.02	11.25
1HGH.PDB	O, C_ASN_152	N, C_ALA_253	H, C_ALA_253	2.87	2.00	22.06
1HGH.PDB	O, C_ILE_121	N, C_TYR_257	H, C_TYR_257	2.97	2.09	21.43
1HGH.PDB	O, C_LEU_177	N, C_PHE_258	H, C_PHE_258	2.89	1.95	13.32
1HGH.PDB	O, C_GLU_119	N, C_LYS_259	H, C_LYS_259	2.98	2.10	21.28
1HGH.PDB	OG, C_SER_115	N, C_ARG_261	H, C_ARG_261	2.95	2.00	12.02
1HGH.PDB	OE2, C_GLU_119	NH1, C_ARG_261	HH12, C_ARG_261	2.64	1.82	29.37
1HGH.PDB	OE1, C_GLU_119	NH2, C_ARG_261	HH22, C_ARG_261	2.85	1.97	24.44
1HGH.PDB	OD2, C_ASP_85	NZ, C_LYS_264	HZ3, C_LYS_264	2.79	1.81	15.90

1HGH.PDB	O, C_PHE_87	N, C_MET_268	H, C_MET_268	2.82	1.96	23.69
1HGH.PDB	O, C_GLU_89	N, C_SER_270	H, C_SER_270	2.99	2.02	9.99
1HGH.PDB	O, C_PRO_284	OG, C_SER_270	HG, C_SER_270	2.79	1.83	6.01
1HGH.PDB	OG, C_SER_270	N, C_ALA_272	H, C_ALA_272	2.92	1.99	14.61
1HGH.PDB	O, C_ILE_51	N, C_ASP_275	H, C_ASP_275	2.92	1.99	15.40
1HGH.PDB	OD1, C_ASP_275	N, C_THR_276	H, C_THR_276	2.82	1.95	22.45
1HGH.PDB	O, C_ASN_54	N, C_SER_279	H, C_SER_279	2.78	1.84	13.60
1HGH.PDB	O, C_TYR_302	N, C_ILE_282	H, C_ILE_282	2.88	1.95	15.61
1HGH.PDB	O, C_THR_283	N, C_GLY_286	H, C_GLY_286	2.83	1.94	19.20
1HGH.PDB	O, C_LYS_50	N, C_SER_287	H, C_SER_287	2.85	1.88	2.68
1HGH.PDB	O, C_ALA_304	ND2, C_ASN_290	HD22, C_ASN_290	2.89	2.00	20.66
1HGH.PDB	OE1, C_GLN_44	NZ, C_LYS_292	HZ1, C_LYS_292	2.68	1.68	11.00
1HGH.PDB	OD2, C_ASP_291	NZ, C_LYS_292	HZ3, C_LYS_292	2.82	1.84	17.38
1HGH.PDB	O, C_LYS_307	N, C_GLN_295	H, C_GLN_295	2.85	2.00	24.78
1HGH.PDB	O, C_ASN_298	NE2, C_GLN_295	HE21, C_GLN_295	2.73	1.77	6.42
1HGH.PDB	O, C_GLN_44	N, C_ASN_296	H, C_ASN_296	2.89	1.94	9.83
1HGH.PDB	OD1, C_ASN_285	ND2, C_ASN_298	HD22, C_ASN_298	2.99	2.06	14.92
1HGH.PDB	OD1, C_ASN_298	N, C_ILE_300	H, C_ILE_300	2.90	1.96	12.51
1HGH.PDB	O, C_ILE_282	N, C_TYR_302	H, C_TYR_302	2.82	1.98	25.76
1HGH.PDB	O, C_GLN_295	N, C_VAL_309	H, C_VAL_309	2.93	2.12	28.37
1HGH.PDB	OG, D_SER_93	N, C_LYS_310	H, C_LYS_310	2.93	1.96	8.29
1HGH.PDB	OD1, D_ASP_86	NZ, C_LYS_310	HZ2, C_LYS_310	2.73	1.85	26.20
1HGH.PDB	OE2, C_GLU_41	N, C_LEU_314	H, C_LEU_314	2.81	1.86	11.11
1HGH.PDB	OE1, C_GLU_41	NZ, C_LYS_315	HZ3, C_LYS_315	2.87	1.91	19.47
1HGH.PDB	O, C_THR_40	N, C_LEU_316	H, C_LEU_316	2.77	1.83	12.11
1HGH.PDB	OD1, D_ASN_104	N, C_ALA_317	H, C_ALA_317	2.74	1.81	14.42
1HGH.PDB	O, C_ASN_38	N, C_THR_318	H, C_THR_318	2.94	1.99	12.96
1HGH.PDB	O, C_GLU_35	N, C_ASN_322	H, C_ASN_322	2.96	1.98	1.89
1HGH.PDB	O, C_VAL_20	ND2, C_ASN_322	HD21, C_ASN_322	2.84	1.92	16.39
1HGH.PDB	OE2, C_GLU_35	ND2, C_ASN_322	HD22, C_ASN_322	2.82	1.91	18.57
1HGH.PDB	OE1, D_GLU_15	NZ, C_LYS_326	HZ1, C_LYS_326	2.77	1.75	11.00
1HGH.PDB	OXT, C_THR_328	NE2, C_GLN_327	HE22, C_GLN_327	2.93	1.99	14.57
1HGH.PDB	OD2, D_ASP_112	N, D_GLY_1	H2, D_GLY_1	2.82	1.82	12.93
1HGH.PDB	OD1, D_ASP_109	N, D_LEU_2	H, D_LEU_2	2.90	1.96	14.04
1HGH.PDB	OD2, D_ASP_112	N, D_PHE_3	H, D_PHE_3	2.83	2.03	28.69
1HGH.PDB	OD2, D_ASP_112	N, D_GLY_4	H, D_GLY_4	2.96	2.09	21.45
1HGH.PDB	OD1, D_ASP_112	N, D_ALA_5	H, D_ALA_5	2.95	2.04	18.20
1HGH.PDB	O, D_GLY_4	N, D_PHE_9	H, D_PHE_9	2.82	1.88	12.35
1HGH.PDB	O, D_GLY_13	ND2, D_ASN_12	HD22, D_ASN_12	2.83	1.93	18.16
1HGH.PDB	O, C_VAL_323	N, D_GLY_13	H, D_GLY_13	2.68	1.77	15.36
1HGH.PDB	O, C_HIS_17	N, D_TRP_14	H, D_TRP_14	2.80	1.87	13.64
1HGH.PDB	OG1, D_THR_41	N, D_TRP_21	H, D_TRP_21	2.88	1.96	16.44
1HGH.PDB	O, C_GLY_16	N, D_GLY_23	H, D_GLY_23	2.92	2.01	18.18
1HGH.PDB	O, D_ALA_35	N, D_PHE_24	H, D_PHE_24	2.87	1.90	5.65
1HGH.PDB	O, C_CYS_14	N, D_ARG_25	H, D_ARG_25	2.90	1.94	10.42
1HGH.PDB	OE1, D_GLN_34	NE, D_ARG_25	HE, D_ARG_25	2.91	1.96	12.36
1HGH.PDB	O, D_GLY_33	N, D_HIS_26	H, D_HIS_26	2.85	1.94	18.22
1HGH.PDB	O, C_THR_12	N, D_GLN_27	H, D_GLN_27	2.91	1.98	14.85
1HGH.PDB	O, D_GLY_31	N, D_ASN_28	H, D_ASN_28	2.93	1.97	10.70
1HGH.PDB	OD1, D_ASN_28	N, D_GLU_30	H, D_GLU_30	2.88	2.06	26.85
1HGH.PDB	O, D_HIS_26	N, D_GLY_33	H, D_GLY_33	2.86	2.05	27.85
1HGH.PDB	O, D_PHE_24	N, D_ALA_35	H, D_ALA_35	2.81	1.99	27.43
1HGH.PDB	O, D_TYR_22	N, D_ASP_37	H, D_ASP_37	2.72	1.78	9.80
1HGH.PDB	OD2, D_ASP_37	N, D_SER_40	H, D_SER_40	2.86	1.91	10.58
1HGH.PDB	OD2, D_ASP_37	OG, D_SER_40	HG, D_SER_40	2.74	1.93	27.28
1HGH.PDB	O, D_ASP_37	OG1, D_THR_41	HG1, D_THR_41	2.73	1.83	18.40
1HGH.PDB	O, D_LEU_38	N, D_GLN_42	H, D_GLN_42	2.92	1.99	14.71
1HGH.PDB	OD1, D_ASP_46	NE2, D_GLN_42	HE22, D_GLN_42	2.87	1.96	19.71

1HGH.PDB	O, D_LYS_39	N, D_ALA_43	H, D_ALA_43	2.95	2.04	17.64
1HGH.PDB	O, D_SER_40	N, D_ALA_44	H, D_ALA_44	2.94	1.96	3.83
1HGH.PDB	O, D_THR_41	N, D_ILE_45	H, D_ILE_45	2.94	1.99	10.18
1HGH.PDB	O, D_GLN_42	N, D_ASP_46	H, D_ASP_46	2.79	1.82	1.60
1HGH.PDB	O, D_ALA_43	NE2, D_GLN_47	HE22, D_GLN_47	2.84	1.94	17.94
1HGH.PDB	O, D_ILE_45	N, D_ASN_49	H, D_ASN_49	2.88	1.92	10.54
1HGH.PDB	O, D_ASP_46	N, D_GLY_50	H, D_GLY_50	2.97	2.07	20.28
1HGH.PDB	O, D_GLN_47	N, D_LYS_51	H, D_LYS_51	2.96	2.00	10.33
1HGH.PDB	OE1, D_GLU_103	NZ, D_LYS_51	HZ1, D_LYS_51	2.74	1.72	7.43
1HGH.PDB	ND1, D_HIS_106	NZ, D_LYS_51	HZ2, D_LYS_51	2.80	1.84	18.41
1HGH.PDB	OG1, D_THR_107	NZ, D_LYS_51	HZ3, D_LYS_51	2.90	1.93	16.98
1HGH.PDB	O, D_ILE_48	N, D_LEU_52	H, D_LEU_52	2.94	2.02	16.46
1HGH.PDB	O, D_ASN_49	N, D_ASN_53	H, D_ASN_53	2.80	1.89	17.97
1HGH.PDB	O, A_THR_28	NE, D_ARG_54	HE, D_ARG_54	2.96	1.98	3.97
1HGH.PDB	OE1, D_GLU_57	NH1, D_ARG_54	HH11, D_ARG_54	2.86	1.86	11.45
1HGH.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.80	1.85	16.64
1HGH.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.84	1.88	10.18
1HGH.PDB	O, C_LYS_299	NZ, D_LYS_68	HZ1, D_LYS_68	2.88	1.85	6.67
1HGH.PDB	OE2, D_GLU_85	NZ, D_LYS_68	HZ2, D_LYS_68	2.75	1.73	9.37
1HGH.PDB	OG, E_SER_107	N, D_ARG_76	H, D_ARG_76	2.91	1.94	8.23
1HGH.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.79	1.84	10.45
1HGH.PDB	OE2, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.77	1.77	10.38
1HGH.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.70	1.70	6.41
1HGH.PDB	OE1, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.75	1.75	5.88
1HGH.PDB	O, D_GLU_72	NE2, D_GLN_78	HE21, D_GLN_78	2.93	1.96	8.18
1HGH.PDB	OE1, D_GLU_74	NE2, D_GLN_78	HE22, D_GLN_78	2.92	1.96	9.79
1HGH.PDB	O, D_GLY_75	N, D_ASP_79	H, D_ASP_79	2.84	1.88	10.94
1HGH.PDB	O, D_ASP_79	N, D_TYR_83	H, D_TYR_83	2.86	1.93	15.47
1HGH.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.59	1.81	29.86
1HGH.PDB	O, D_LEU_80	N, D_VAL_84	H, D_VAL_84	2.71	1.80	16.30
1HGH.PDB	O, D_LYS_82	N, D_ASP_86	H, D_ASP_86	2.95	1.99	9.46
1HGH.PDB	O, D_VAL_84	N, D_LYS_88	H, D_LYS_88	2.98	2.09	19.67
1HGH.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.66	1.64	7.83
1HGH.PDB	O, D_GLU_85	N, D_ILE_89	H, D_ILE_89	2.85	1.88	5.79
1HGH.PDB	O, D_LYS_88	N, D_TRP_92	H, D_TRP_92	2.90	1.92	5.72
1HGH.PDB	O, D_ILE_89	N, D_SER_93	H, D_SER_93	2.89	1.99	19.16
1HGH.PDB	O, D_ILE_89	OG, D_SER_93	HG, D_SER_93	2.76	1.84	13.71
1HGH.PDB	O, D_ASP_90	N, D_TYR_94	H, D_TYR_94	2.86	1.93	14.89
1HGH.PDB	O, D_LEU_91	N, D_ASN_95	H, D_ASN_95	3.00	2.01	2.40
1HGH.PDB	O, D_TRP_92	N, D_ALA_96	H, D_ALA_96	2.97	2.07	19.88
1HGH.PDB	O, D_TYR_94	N, D_LEU_98	H, D_LEU_98	2.95	1.98	4.96
1HGH.PDB	O, D_ASN_95	N, D_LEU_99	H, D_LEU_99	2.96	2.05	17.05
1HGH.PDB	O, D_VAL_100	N, D_ASN_104	H, D_ASN_104	2.87	1.94	14.58
1HGH.PDB	O, C_LYS_27	ND2, D_ASN_104	HD22, D_ASN_104	2.89	1.94	11.70
1HGH.PDB	O, D_LEU_102	N, D_HIS_106	H, D_HIS_106	2.95	1.98	8.89
1HGH.PDB	O, D_GLU_103	N, D_THR_107	H, D_THR_107	2.84	1.94	18.36
1HGH.PDB	O, D_HIS_106	N, D_LEU_110	H, D_LEU_110	2.82	1.86	9.68
1HGH.PDB	O, D_THR_107	OG1, D_THR_111	HG1, D_THR_111	2.89	1.92	2.49
1HGH.PDB	O, D_ASP_109	N, D_SER_113	H, D_SER_113	2.77	1.82	8.06
1HGH.PDB	O, D_ASP_112	N, D_ASN_116	H, D_ASN_116	2.96	1.98	6.25
1HGH.PDB	O, D_SER_113	N, D_LYS_117	H, D_LYS_117	2.75	1.92	25.56
1HGH.PDB	O, D_GLU_114	N, D_LEU_118	H, D_LEU_118	3.00	2.03	9.32
1HGH.PDB	O, D_ASN_116	N, D_GLU_120	H, D_GLU_120	2.93	1.95	1.97
1HGH.PDB	O, D_LYS_117	N, D_LYS_121	H, D_LYS_121	2.85	1.95	19.21
1HGH.PDB	O, D_LEU_118	N, D_THR_122	H, D_THR_122	2.98	2.00	5.78
1HGH.PDB	O, D_PHE_119	N, D_ARG_123	H, D_ARG_123	2.89	1.93	8.77
1HGH.PDB	OE2, D_GLU_120	NH1, D_ARG_123	HH11, D_ARG_123	2.77	1.87	22.36
1HGH.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.80	1.98	26.35

1HGH.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.84	1.99	23.38
1HGH.PDB	O, D_LEU_126	N, D_ASN_129	H, D_ASN_129	2.98	2.04	13.91
1HGH.PDB	O, D_HIS_159	ND2, D_ASN_129	HD21, D_ASN_129	2.99	2.06	14.65
1HGH.PDB	OH, D_TYR_157	ND2, D_ASN_129	HD22, D_ASN_129	2.83	1.87	7.67
1HGH.PDB	O, D_LYS_139	N, D_GLU_131	H, D_GLU_131	2.96	2.04	16.55
1HGH.PDB	O, D_CYS_137	N, D_MET_133	H, D_MET_133	2.85	1.91	13.04
1HGH.PDB	OD1, D_ASN_135	N, D_CYS_137	H, D_CYS_137	2.95	2.05	19.26
1HGH.PDB	O, C_LEU_13	N, D_PHE_138	H, D_PHE_138	2.75	1.85	18.05
1HGH.PDB	O, D_GLU_131	N, D_LYS_139	H, D_LYS_139	2.80	1.84	6.99
1HGH.PDB	O, C_ALA_11	N, D_ILE_140	H, D_ILE_140	2.83	1.90	15.57
1HGH.PDB	O, D_ASN_129	N, D_TYR_141	H, D_TYR_141	2.84	1.91	14.49
1HGH.PDB	OE2, D_GLU_30	N, D_ASN_146	H, D_ASN_146	2.90	1.97	15.32
1HGH.PDB	O, D_ASP_145	N, D_ILE_149	H, D_ILE_149	2.92	1.97	10.33
1HGH.PDB	O, D_ASN_146	N, D_GLU_150	H, D_GLU_150	2.92	1.99	14.54
1HGH.PDB	O, D_ALA_147	N, D_SER_151	H, D_SER_151	2.94	2.07	23.02
1HGH.PDB	O, D_CYS_148	OG, D_SER_151	HG, D_SER_151	2.73	1.84	17.19
1HGH.PDB	O, D_GLU_150	N, D_ASN_154	H, D_ASN_154	2.82	1.84	3.73
1HGH.PDB	O, D_SER_151	N, D_THR_156	H, D_THR_156	2.80	1.97	26.19
1HGH.PDB	OD1, D_ASN_154	OG1, D_THR_156	HG1, D_THR_156	2.69	1.80	16.96
1HGH.PDB	NE2, D_HIS_142	OH, D_TYR_157	HH, D_TYR_157	2.68	1.87	26.02
1HGH.PDB	OD1, D_ASP_158	N, D_ASP_160	H, D_ASP_160	2.94	2.07	22.26
1HGH.PDB	O, D_HIS_159	N, D_TYR_162	H, D_TYR_162	2.94	2.06	20.90
1HGH.PDB	O, B_ARG_170	NH1, D_ARG_163	HH12, D_ARG_163	2.75	1.77	10.76
1HGH.PDB	O, D_TYR_162	N, D_ALA_166	H, D_ALA_166	2.89	1.92	5.05
1HGH.PDB	O, D_ARG_163	N, D_LEU_167	H, D_LEU_167	2.82	1.86	8.99
1HGH.PDB	O, D_ASP_164	N, D_ASN_168	H, D_ASN_168	2.99	2.02	7.50
1HGH.PDB	O, D_GLU_165	ND2, D_ASN_169	HD22, D_ASN_169	2.97	2.00	7.05
1HGH.PDB	O, D_ALA_166	N, D_ARG_170	H, D_ARG_170	2.80	1.93	21.90
1HGH.PDB	O, D_GLU_128	NE, D_ARG_170	HE, D_ARG_170	2.74	1.87	23.06
1HGH.PDB	OE2, D_GLU_131	NH1, D_ARG_170	HH11, D_ARG_170	2.83	1.83	5.85
1HGH.PDB	O, D_LEU_167	N, D_PHE_171	H, D_PHE_171	2.95	2.02	15.80
1HGH.PDB	O, F_ILE_140	N, E_ALA_11	H, E_ALA_11	2.92	2.02	19.53
1HGH.PDB	O, F_PHE_138	N, E_LEU_13	H, E_LEU_13	2.96	1.99	9.34
1HGH.PDB	O, F_ARG_25	N, E_CYS_14	H, E_CYS_14	2.64	1.78	21.59
1HGH.PDB	O, F_GLY_136	N, E_LEU_15	H, E_LEU_15	2.90	1.93	5.74
1HGH.PDB	O, F_GLY_23	N, E_GLY_16	H, E_GLY_16	2.92	2.05	22.72
1HGH.PDB	O, E_HIS_18	ND1, E_HIS_17	HD1, E_HIS_17	2.99	2.08	18.51
1HGH.PDB	O, F_TRP_21	N, E_HIS_18	H, E_HIS_18	2.92	2.03	19.54
1HGH.PDB	OD1, E_ASN_322	N, E_VAL_20	H, E_VAL_20	2.74	1.82	16.04
1HGH.PDB	O, E_VAL_36	N, E_THR_24	H, E_THR_24	2.82	1.93	20.03
1HGH.PDB	O, E_ILE_34	N, E_VAL_26	H, E_VAL_26	2.82	1.88	13.02
1HGH.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.77	1.74	8.08
1HGH.PDB	O, E_ASP_31	N, E_THR_28	H, E_THR_28	2.77	1.94	26.92
1HGH.PDB	O, E_VAL_26	N, E_ILE_34	H, E_ILE_34	2.87	1.92	12.72
1HGH.PDB	O, E_THR_24	N, E_VAL_36	H, E_VAL_36	2.79	1.83	5.74
1HGH.PDB	O, E_MET_320	N, E_THR_37	H, E_THR_37	2.91	1.94	5.98
1HGH.PDB	O, E_LEU_316	N, E_THR_40	H, E_THR_40	2.81	1.97	25.58
1HGH.PDB	O, E_LEU_314	N, E_LEU_42	H, E_LEU_42	2.86	1.99	23.51
1HGH.PDB	O, E_PHE_294	N, E_GLN_44	H, E_GLN_44	2.90	1.92	3.60
1HGH.PDB	O, E_SER_46	NE2, E_GLN_44	HE22, E_GLN_44	2.79	1.94	24.07
1HGH.PDB	O, E_ASN_285	OG, E_SER_47	HG, E_SER_47	2.82	1.86	5.68
1HGH.PDB	OD2, E_ASP_275	NZ, E_LYS_50	HZ1, E_LYS_50	2.78	1.83	20.38
1HGH.PDB	O, E_PRO_273	N, E_ILE_51	H, E_ILE_51	2.79	1.86	14.05
1HGH.PDB	O, E_ASP_275	N, E_ASN_53	H, E_ASN_53	2.84	1.95	20.03
1HGH.PDB	O, E_GLU_280	NE2, E_HIS_56	HE2, E_HIS_56	3.00	2.04	11.75
1HGH.PDB	OD2, E_ASP_85	N, E_ARG_57	H, E_ARG_57	2.80	1.92	20.20
1HGH.PDB	O, E_THR_83	NE, E_ARG_57	HE, E_ARG_57	2.76	1.81	9.61
1HGH.PDB	O, E_LEU_86	N, E_LEU_59	H, E_LEU_59	2.94	2.02	16.24

1HGH.PDB	O, E_VAL.88	N, E_GLY.61	H, E_GLY.61	2.97	2.17	29.53
1HGH.PDB	OD1, E_ASP.60	N, E_ILE.62	H, E_ILE.62	2.88	1.95	12.63
1HGH.PDB	O, E_GLY.61	N, E_CYS.64	H, E_CYS.64	2.91	2.01	19.21
1HGH.PDB	OE2, E_GLU.89	N, E_LEU.66	H, E_LEU.66	2.90	1.94	8.52
1HGH.PDB	O, E_LEU.66	N, E_LEU.70	H, E_LEU.70	2.83	1.96	22.59
1HGH.PDB	O, E_ILE.67	N, E_LEU.71	H, E_LEU.71	2.80	1.85	10.15
1HGH.PDB	O, E_ASP.68	N, E_GLY.72	H, E_GLY.72	2.92	1.98	13.98
1HGH.PDB	OD1, E_ASP.73	ND1, E_HIS.75	HD1, E_HIS.75	2.70	1.83	21.52
1HGH.PDB	O, E_ASP.63	NE2, E_HIS.75	HE2, E_HIS.75	2.76	1.85	18.40
1HGH.PDB	O, E_ASP.73	N, E_CYS.76	H, E_CYS.76	2.77	1.88	19.19
1HGH.PDB	O, E_PRO.74	N, E_ASP.77	H, E_ASP.77	2.89	1.93	8.73
1HGH.PDB	O, E_CYS.76	N, E_PHE.79	H, E_PHE.79	2.99	2.02	3.39
1HGH.PDB	O, E_PHE.79	N, E_GLU.82	H, E_GLU.82	2.96	2.03	14.49
1HGH.PDB	OE1, E_GLU.82	N, E_THR.83	H, E_THR.83	2.87	2.01	22.92
1HGH.PDB	O, E_ARG.57	N, E_ASP.85	H, E_ASP.85	2.80	1.87	13.06
1HGH.PDB	O, E_MET.268	N, E_GLU.89	H, E_GLU.89	2.80	1.86	11.55
1HGH.PDB	OD1, E_ASP.60	NE, E_ARG.90	HE, E_ARG.90	2.82	1.87	13.57
1HGH.PDB	O, E_SER.270	NH1, E_ARG.90	HH11, E_ARG.90	2.65	1.80	26.29
1HGH.PDB	O, E_ALA.272	NH1, E_ARG.90	HH12, E_ARG.90	2.63	1.72	19.05
1HGH.PDB	OD2, E_ASP.60	NH2, E_ARG.90	HH21, E_ARG.90	2.82	1.82	8.69
1HGH.PDB	OD1, E_ASP.271	N, E_SER.91	H, E_SER.91	2.82	1.87	11.20
1HGH.PDB	OD2, E_ASP.271	OG, E_SER.91	HG, E_SER.91	2.81	1.88	14.87
1HGH.PDB	OD2, E_ASP.68	OG, E_SER.95	HG, E_SER.95	2.88	1.94	13.28
1HGH.PDB	OD2, E_ASP.73	N, E_ASN.96	H, E_ASN.96	2.91	1.94	6.86
1HGH.PDB	OD1, E_ASP.68	OH, E_TYR.100	HH, E_TYR.100	2.91	1.97	12.96
1HGH.PDB	O, E_ILE.230	N, E_ASP.101	H, E_ASP.101	2.92	2.05	22.42
1HGH.PDB	OD2, E_ASP.104	OG, E_SER.107	HG, E_SER.107	2.88	1.97	18.12
1HGH.PDB	O, E_TYR.105	N, E_ARG.109	H, E_ARG.109	2.86	1.89	4.60
1HGH.PDB	OE2, F_GLU.67	NH2, E_ARG.109	HH21, E_ARG.109	2.88	1.90	13.56
1HGH.PDB	OD2, D_ASP.79	OG, E_SER.110	HG, E_SER.110	2.90	1.94	9.49
1HGH.PDB	O, E_SER.107	N, E_LEU.111	H, E_LEU.111	2.88	1.93	12.85
1HGH.PDB	O, E_ARG.109	N, E_ALA.113	H, E_ALA.113	2.87	1.96	17.46
1HGH.PDB	O, E_SER.110	N, E_SER.114	H, E_SER.114	2.96	2.00	10.70
1HGH.PDB	OE2, E_GLU.119	OG1, E_THR.117	HG1, E_THR.117	2.88	1.94	11.16
1HGH.PDB	O, E_GLU.82	N, E_LEU.118	H, E_LEU.118	2.97	2.01	10.67
1HGH.PDB	O, E_TYR.257	N, E_ILE.121	H, E_ILE.121	2.91	1.96	12.67
1HGH.PDB	O, E_ARG.255	N, E_GLU.123	H, E_GLU.123	2.88	1.92	10.98
1HGH.PDB	O, E_THR.155	N, E_THR.131	H, E_THR.131	2.72	1.85	21.27
1HGH.PDB	OD1, E_ASN.152	N, E_ASN.133	H, E_ASN.133	2.90	2.03	22.25
1HGH.PDB	O, E_TRP.153	N, E_GLY.134	H, E_GLY.134	2.97	2.04	15.57
1HGH.PDB	O, E_GLY.146	N, E_SER.136	H, E_SER.136	2.72	1.83	19.86
1HGH.PDB	OG, E_SER.136	N, E_ALA.138	H, E_ALA.138	2.95	2.04	18.21
1HGH.PDB	O, E_GLY.144	NZ, E_LYS.140	HZ1, E_LYS.140	2.90	1.92	16.43
1HGH.PDB	OD1, E_ASN.137	NZ, E_LYS.140	HZ2, E_LYS.140	2.75	1.75	11.91
1HGH.PDB	OD2, E_ASP.77	NE, E_ARG.141	HE, E_ARG.141	2.85	2.01	27.16
1HGH.PDB	O, E_PHE.147	NH1, E_ARG.141	HH12, E_ARG.141	2.56	1.64	18.71
1HGH.PDB	OD1, E_ASP.77	NH2, E_ARG.141	HH21, E_ARG.141	2.89	1.99	22.46
1HGH.PDB	OD2, E_ASP.77	NH2, E_ARG.141	HH21, E_ARG.141	2.74	1.84	23.25
1HGH.PDB	O, E_GLY.72	NH2, E_ARG.141	HH22, E_ARG.141	2.94	1.96	11.25
1HGH.PDB	OD1, E_ASN.137	OG, E_SER.145	HG, E_SER.145	2.98	2.07	15.03
1HGH.PDB	O, E_SER.136	N, E_GLY.146	H, E_GLY.146	2.94	1.99	13.35
1HGH.PDB	O, E_GLY.72	N, E_SER.149	H, E_SER.149	2.91	1.97	14.68
1HGH.PDB	O, E_ALA.253	N, E_ASN.152	H, E_ASN.152	2.75	1.96	29.93
1HGH.PDB	OH, E_TYR.195	NE1, E_TRP.153	HE1, E_TRP.153	2.94	2.03	18.49
1HGH.PDB	O, E_LEU.194	N, E_LYS.156	H, E_LYS.156	2.95	2.04	17.92
1HGH.PDB	O, E_SER.193	NZ, E_LYS.156	HZ2, E_LYS.156	2.74	1.77	17.07
1HGH.PDB	O, E_THR.160	N, E_SER.157	H, E_SER.157	2.95	2.02	16.56
1HGH.PDB	O, E_SER.247	N, E_LEU.164	H, E_LEU.164	2.73	1.90	26.43

1HGH.PDB	O, E_ILE.245	N, E_VAL.166	H, E_VAL.166	2.87	1.94	14.01
1HGH.PDB	O, E_LEU.243	OG1, E_THR.167	HG1, E_THR.167	2.95	2.02	14.19
1HGH.PDB	O, E_LEU.243	N, E_MET.168	H, E_MET.168	2.85	1.92	14.04
1HGH.PDB	O, E_ASP.241	N, E_ASN.170	H, E_ASN.170	2.95	1.97	5.59
1HGH.PDB	O, E_PHE.174	ND2, E_ASN.170	HD21, E_ASN.170	2.82	1.88	12.75
1HGH.PDB	O, E_VAL.237	ND2, E_ASN.170	HD22, E_ASN.170	2.89	2.06	25.88
1HGH.PDB	O, E_VAL.237	N, E_LYS.176	H, E_LYS.176	2.98	2.06	17.00
1HGH.PDB	OE2, E_GLU.123	NZ, E_LYS.176	HZ1, E_LYS.176	2.69	1.82	26.87
1HGH.PDB	O, E_PHE.258	N, E_LEU.177	H, E_LEU.177	2.97	2.00	4.18
1HGH.PDB	O, E_THR.235	N, E_TYR.178	H, E_TYR.178	2.86	1.90	10.67
1HGH.PDB	OE1, E_GLU.123	OH, E_TYR.178	HH, E_TYR.178	2.77	1.82	8.79
1HGH.PDB	OG1, E_THR.235	NE1, E_TRP.180	HE1, E_TRP.180	2.88	1.89	0.99
1HGH.PDB	O, E_ASN.250	N, E_HIS.183	H, E_HIS.183	2.86	1.99	21.99
1HGH.PDB	O, E_ARG.229	N, E_HIS.184	H, E_HIS.184	2.88	1.94	12.21
1HGH.PDB	OG, E_SER.231	NE2, E_HIS.184	HE2, E_HIS.184	2.78	1.93	25.10
1HGH.PDB	OG1, E_THR.187	N, E_GLU.190	H, E_GLU.190	2.95	2.00	11.05
1HGH.PDB	OD1, E_ASN.250	NE2, E_GLN.191	HE21, E_GLN.191	2.99	2.02	8.22
1HGH.PDB	O, E_GLN.197	NE2, E_GLN.191	HE22, E_GLN.191	2.93	1.98	11.58
1HGH.PDB	O, E_GLN.189	N, E_SER.193	H, E_SER.193	2.93	1.94	3.87
1HGH.PDB	O, E_GLU.190	N, E_LEU.194	H, E_LEU.194	2.96	1.97	5.03
1HGH.PDB	O, E_GLN.191	N, E_TYR.195	H, E_TYR.195	2.79	1.83	8.93
1HGH.PDB	O, E_TYR.195	N, E_GLN.197	H, E_GLN.197	2.65	1.86	29.33
1HGH.PDB	O, E_TYR.161	NE2, E_GLN.197	HE21, E_GLN.197	2.94	1.99	11.18
1HGH.PDB	O, E_ASN.248	NE2, E_GLN.197	HE22, E_GLN.197	2.86	1.94	17.19
1HGH.PDB	OD1, E_ASN.246	NH2, E_ARG.201	HH21, E_ARG.201	2.64	1.73	21.41
1HGH.PDB	O, E_ILE.213	N, E_VAL.202	H, E_VAL.202	2.96	2.00	10.60
1HGH.PDB	O, E_ASN.246	N, E_THR.203	H, E_THR.203	2.87	1.91	9.98
1HGH.PDB	OG1, E_THR.212	OG1, E_THR.203	HG1, E_THR.203	2.98	2.08	17.30
1HGH.PDB	O, E_GLN.211	N, E_VAL.204	H, E_VAL.204	2.87	1.97	20.15
1HGH.PDB	O, E_SER.209	N, E_THR.206	H, E_THR.206	2.92	1.96	6.97
1HGH.PDB	OD1, E_ASP.241	N, E_ARG.207	H, E_ARG.207	2.86	1.90	9.49
1HGH.PDB	OG1, E_THR.206	OG, E_SER.209	HG, E_SER.209	2.95	2.00	8.64
1HGH.PDB	OD1, C_ASP.101	NE2, E_GLN.210	HE22, E_GLN.210	2.95	2.09	25.33
1HGH.PDB	O, E_VAL.204	N, E_GLN.211	H, E_GLN.211	2.89	1.95	12.74
1HGH.PDB	O, E_VAL.202	N, E_ILE.213	H, E_ILE.213	2.90	1.97	14.56
1HGH.PDB	ND1, E_HIS.184	N, E_ASN.216	H, E_ASN.216	2.77	1.96	27.61
1HGH.PDB	OE1, A_GLN.210	NH2, E_ARG.220	HH21, E_ARG.220	2.68	1.79	22.30
1HGH.PDB	O, E_ASN.216	NH2, E_ARG.220	HH22, E_ARG.220	2.67	1.78	21.90
1HGH.PDB	O, E_LEU.226	N, E_VAL.223	H, E_VAL.223	2.86	1.90	9.88
1HGH.PDB	O, E_CYS.97	NE, E_ARG.224	HE, E_ARG.224	2.82	1.98	26.83
1HGH.PDB	O, E_CYS.97	NH2, E_ARG.224	HH21, E_ARG.224	2.83	1.97	26.23
1HGH.PDB	O, E_VAL.223	N, E_LEU.226	H, E_LEU.226	2.83	1.91	14.82
1HGH.PDB	O, E_ARG.220	OG, E_SER.227	HG, E_SER.227	2.98	2.06	16.39
1HGH.PDB	O, E_SER.228	NH1, E_ARG.229	HH11, E_ARG.229	2.68	1.73	16.77
1HGH.PDB	O, E_PRO.221	NH2, E_ARG.229	HH22, E_ARG.229	2.59	1.64	14.71
1HGH.PDB	OD1, E_ASP.101	OG, E_SER.231	HG, E_SER.231	2.86	1.91	11.78
1HGH.PDB	O, E_ASP.101	N, E_ILE.232	H, E_ILE.232	2.89	1.97	15.99
1HGH.PDB	O, E_TRP.180	N, E_TYR.233	H, E_TYR.233	2.91	1.95	8.91
1HGH.PDB	O, E_TYR.178	N, E_THR.235	H, E_THR.235	2.90	1.99	17.41
1HGH.PDB	O, E_LYS.176	N, E_VAL.237	H, E_VAL.237	2.74	1.82	15.90
1HGH.PDB	O, D_SER.71	NZ, E_LYS.238	HZ2, E_LYS.238	2.84	1.88	19.22
1HGH.PDB	OE1, D_GLU.72	NZ, E_LYS.238	HZ3, E_LYS.238	2.87	1.88	15.42
1HGH.PDB	O, E_ASN.170	N, E_GLY.240	H, E_GLY.240	2.93	2.05	21.68
1HGH.PDB	O, E_LYS.238	N, E_ASP.241	H, E_ASP.241	2.93	2.01	15.54
1HGH.PDB	OD1, E_ASP.241	N, E_VAL.242	H, E_VAL.242	2.78	1.96	27.21
1HGH.PDB	O, E_MET.168	N, E_LEU.243	H, E_LEU.243	2.84	1.87	3.13
1HGH.PDB	O, E_SER.205	N, E_VAL.244	H, E_VAL.244	2.97	2.03	14.34
1HGH.PDB	O, E_VAL.166	N, E_ILE.245	H, E_ILE.245	2.86	1.92	13.73

1HGH.PDB	O, E_THR_203	N, E_ASN_246	H, E_ASN_246	2.93	2.00	14.46
1HGH.PDB	OD1, E_ASN_165	ND2, E_ASN_246	HD22, E_ASN_246	2.98	2.01	10.13
1HGH.PDB	O, E_LEU_164	N, E_SER_247	H, E_SER_247	2.90	1.99	17.74
1HGH.PDB	OE1, E_GLN_191	ND2, E_ASN_250	HD21, E_ASN_250	2.89	1.92	6.88
1HGH.PDB	O, E_HIS_183	ND2, E_ASN_250	HD22, E_ASN_250	2.85	1.88	7.17
1HGH.PDB	O, E_GLY_181	N, E_ILE_252	H, E_ILE_252	2.96	2.00	10.43
1HGH.PDB	O, E_ASN_152	N, E_ALA_253	H, E_ALA_253	2.86	1.96	18.53
1HGH.PDB	O, E_ILE_121	N, E_TYR_257	H, E_TYR_257	2.97	2.09	21.21
1HGH.PDB	O, E_LEU_177	N, E_PHE_258	H, E_PHE_258	2.87	1.92	12.22
1HGH.PDB	OG, E_SER_115	N, E_ARG_261	H, E_ARG_261	2.96	2.00	11.47
1HGH.PDB	OE2, E_GLU_119	NH1, E_ARG_261	HH12, E_ARG_261	2.63	1.81	29.30
1HGH.PDB	OE1, E_GLU_119	NH2, E_ARG_261	HH22, E_ARG_261	2.85	1.96	24.42
1HGH.PDB	OD2, E_ASP_85	NZ, E_LYS_264	HZ3, E_LYS_264	2.81	1.82	14.94
1HGH.PDB	O, E_PHE_87	N, E_MET_268	H, E_MET_268	2.82	1.95	22.70
1HGH.PDB	OE1, F_GLU_67	NH1, E_ARG_269	HH12, E_ARG_269	2.71	1.88	29.19
1HGH.PDB	O, E_GLU_89	N, E_SER_270	H, E_SER_270	2.97	2.01	10.37
1HGH.PDB	O, E_PRO_284	OG, E_SER_270	HG, E_SER_270	2.79	1.83	6.34
1HGH.PDB	OG, E_SER_270	N, E_ALA_272	H, E_ALA_272	2.93	2.00	13.96
1HGH.PDB	O, E_ILE_51	N, E_ASP_275	H, E_ASP_275	2.89	1.98	17.07
1HGH.PDB	OD1, E_ASP_275	N, E_THR_276	H, E_THR_276	2.81	1.94	22.67
1HGH.PDB	O, E_ASN_54	N, E_SER_279	H, E_SER_279	2.79	1.85	12.96
1HGH.PDB	O, E_TYR_302	N, E_ILE_282	H, E_ILE_282	2.90	1.96	14.02
1HGH.PDB	O, E_THR_283	N, E_GLY_286	H, E_GLY_286	2.82	1.92	18.13
1HGH.PDB	O, E_LYS_50	N, E_SER_287	H, E_SER_287	2.89	1.92	2.42
1HGH.PDB	O, E_ALA_304	ND2, E_ASN_290	HD22, E_ASN_290	2.86	1.98	20.69
1HGH.PDB	OE1, E_GLN_44	NZ, E_LYS_292	HZ1, E_LYS_292	2.67	1.66	10.24
1HGH.PDB	OD2, E_ASP_291	NZ, E_LYS_292	HZ3, E_LYS_292	2.84	1.86	17.36
1HGH.PDB	O, E_LYS_307	N, E_GLN_295	H, E_GLN_295	2.84	1.97	22.67
1HGH.PDB	O, E_ASN_298	NE2, E_GLN_295	HE21, E_GLN_295	2.75	1.79	8.52
1HGH.PDB	O, E_GLN_44	N, E_ASN_296	H, E_ASN_296	2.90	1.94	9.06
1HGH.PDB	OD1, E_ASN_298	N, E_ILE_300	H, E_ILE_300	2.92	1.98	13.95
1HGH.PDB	O, E_ILE_282	N, E_TYR_302	H, E_TYR_302	2.84	2.00	26.34
1HGH.PDB	O, F_LYS_62	N, E_GLY_303	H, E_GLY_303	2.98	2.01	7.92
1HGH.PDB	O, E_PRO_293	N, E_LYS_307	H, E_LYS_307	3.00	2.03	9.04
1HGH.PDB	O, E_GLN_295	N, E_VAL_309	H, E_VAL_309	2.91	2.07	25.95
1HGH.PDB	OG, F_SER_93	N, E_LYS_310	H, E_LYS_310	2.93	1.97	10.42
1HGH.PDB	OD1, F_ASP_86	NZ, E_LYS_310	HZ2, E_LYS_310	2.74	1.87	26.77
1HGH.PDB	O, F_SER_93	NE2, E_GLN_311	HE21, E_GLN_311	2.99	2.02	4.65
1HGH.PDB	OE2, E_GLU_41	N, E_LEU_314	H, E_LEU_314	2.81	1.87	11.19
1HGH.PDB	OE1, E_GLU_41	NZ, E_LYS_315	HZ3, E_LYS_315	2.85	1.89	19.70
1HGH.PDB	O, E_THR_40	N, E_LEU_316	H, E_LEU_316	2.77	1.82	9.99
1HGH.PDB	OD1, F_ASN_104	N, E_ALA_317	H, E_ALA_317	2.75	1.81	11.69
1HGH.PDB	O, E_ASN_38	N, E_THR_318	H, E_THR_318	2.95	2.00	12.19
1HGH.PDB	O, E_GLU_35	N, E_ASN_322	H, E_ASN_322	2.96	1.98	2.25
1HGH.PDB	O, E_VAL_20	ND2, E_ASN_322	HD21, E_ASN_322	2.82	1.91	16.60
1HGH.PDB	OE2, E_GLU_35	ND2, E_ASN_322	HD22, E_ASN_322	2.80	1.90	19.14
1HGH.PDB	OE2, F_GLU_15	N, E_GLU_325	H, E_GLU_325	2.97	2.16	28.37
1HGH.PDB	O, E_GLN_327	NZ, E_LYS_326	HZ1, E_LYS_326	2.85	1.92	22.31
1HGH.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.90	1.89	12.96
1HGH.PDB	O, E_LYS_326	NE2, E_GLN_327	HE22, E_GLN_327	2.81	1.89	16.48
1HGH.PDB	OD2, F_ASP_112	N, F_GLY_1	H2, F_GLY_1	2.82	1.82	13.22
1HGH.PDB	OD1, F_ASP_109	N, F_LEU_2	H, F_LEU_2	2.91	1.98	15.54
1HGH.PDB	OD2, F_ASP_112	N, F_PHE_3	H, F_PHE_3	2.80	2.01	28.96
1HGH.PDB	OD2, F_ASP_112	N, F_GLY_4	H, F_GLY_4	2.95	2.06	19.48
1HGH.PDB	OD1, F_ASP_112	N, F_ALA_5	H, F_ALA_5	2.92	2.00	17.34
1HGH.PDB	O, F_GLY_4	N, F_PHE_9	H, F_PHE_9	2.86	1.91	12.98
1HGH.PDB	O, F_GLY_13	ND2, F_ASN_12	HD22, F_ASN_12	2.80	1.92	21.14
1HGH.PDB	O, E_VAL_323	N, F_GLY_13	H, F_GLY_13	2.70	1.77	11.97

1HGH.PDB	O, E_HIS_17	N, F_TRP_14	H, F_TRP_14	2.81	1.87	12.50
1HGH.PDB	OG1, F_THR_41	N, F_TRP_21	H, F_TRP_21	2.88	1.96	16.20
1HGH.PDB	O, E_GLY_16	N, F_GLY_23	H, F_GLY_23	2.91	2.00	17.53
1HGH.PDB	O, F_ALA_35	N, F_PHE_24	H, F_PHE_24	2.86	1.89	4.90
1HGH.PDB	O, E_CYS_14	N, F_ARG_25	H, F_ARG_25	2.90	1.98	16.77
1HGH.PDB	OE1, F_GLN_34	NH2, F_ARG_25	HH21, F_ARG_25	2.92	2.03	23.48
1HGH.PDB	O, F_GLY_33	N, F_HIS_26	H, F_HIS_26	2.90	2.03	21.65
1HGH.PDB	O, E_THR_12	N, F_GLN_27	H, F_GLN_27	2.91	2.03	20.46
1HGH.PDB	O, F_GLY_31	N, F_ASN_28	H, F_ASN_28	2.72	1.81	16.52
1HGH.PDB	OD1, F_ASN_146	ND2, F_ASN_28	HD21, F_ASN_28	2.91	1.96	12.69
1HGH.PDB	O, F_CYS_144	ND2, F_ASN_28	HD22, F_ASN_28	2.96	2.10	23.78
1HGH.PDB	O, F_PHE_24	N, F_ALA_35	H, F_ALA_35	2.81	2.00	28.47
1HGH.PDB	O, F_TYR_22	N, F_ASP_37	H, F_ASP_37	2.69	1.76	12.03
1HGH.PDB	OD2, F_ASP_37	N, F_SER_40	H, F_SER_40	2.86	1.90	9.36
1HGH.PDB	OD2, F_ASP_37	OG, F_SER_40	HG, F_SER_40	2.73	1.92	26.94
1HGH.PDB	O, F_ASP_37	OG1, F_THR_41	HG1, F_THR_41	2.73	1.82	16.92
1HGH.PDB	O, F_LEU_38	N, F_GLN_42	H, F_GLN_42	2.93	1.99	14.39
1HGH.PDB	OD1, F_ASP_46	NE2, F_GLN_42	HE22, F_GLN_42	2.85	1.95	20.25
1HGH.PDB	O, F_LYS_39	N, F_ALA_43	H, F_ALA_43	2.92	1.99	14.06
1HGH.PDB	O, F_SER_40	N, F_ALA_44	H, F_ALA_44	2.94	1.96	3.72
1HGH.PDB	O, F_THR_41	N, F_ILE_45	H, F_ILE_45	2.94	2.00	13.08
1HGH.PDB	O, F_GLN_42	N, F_ASP_46	H, F_ASP_46	2.77	1.80	1.50
1HGH.PDB	OE2, F_GLU_114	NE2, F_GLN_47	HE21, F_GLN_47	2.99	2.08	19.28
1HGH.PDB	O, F_ALA_43	NE2, F_GLN_47	HE22, F_GLN_47	2.86	1.96	18.47
1HGH.PDB	O, F_ILE_45	N, F_ASN_49	H, F_ASN_49	2.86	1.91	11.74
1HGH.PDB	O, F_ASP_46	N, F_GLY_50	H, F_GLY_50	2.93	2.01	18.13
1HGH.PDB	O, F_GLN_47	N, F_LYS_51	H, F_LYS_51	2.95	2.01	12.39
1HGH.PDB	OE1, F_GLU_103	NZ, F_LYS_51	HZ1, F_LYS_51	2.75	1.72	7.02
1HGH.PDB	ND1, F_HIS_106	NZ, F_LYS_51	HZ2, F_LYS_51	2.77	1.82	19.11
1HGH.PDB	OG1, F_THR_107	NZ, F_LYS_51	HZ3, F_LYS_51	2.93	1.96	17.40
1HGH.PDB	O, F_ILE_48	N, F_LEU_52	H, F_LEU_52	2.94	2.03	18.13
1HGH.PDB	O, F_ASN_49	N, F_ASN_53	H, F_ASN_53	2.82	1.91	17.65
1HGH.PDB	OE1, F_GLU_57	NH1, F_ARG_54	HH11, F_ARG_54	2.88	1.88	10.86
1HGH.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.72	1.77	15.67
1HGH.PDB	OD2, D_ASP_90	NZ, F_LYS_62	HZ2, F_LYS_62	2.68	1.83	28.02
1HGH.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.87	1.91	9.23
1HGH.PDB	O, E_LYS_299	NZ, F_LYS_68	HZ1, F_LYS_68	2.91	1.87	1.37
1HGH.PDB	OE2, F_GLU_85	NZ, F_LYS_68	HZ2, F_LYS_68	2.73	1.74	15.07
1HGH.PDB	OG, A_SER_107	N, F_ARG_76	H, F_ARG_76	2.80	1.83	4.45
1HGH.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.84	1.87	10.72
1HGH.PDB	OE2, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.73	1.73	5.34
1HGH.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.71	1.70	1.21
1HGH.PDB	OE1, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.78	1.78	7.19
1HGH.PDB	O, F_GLU_72	NE2, F_GLN_78	HE21, F_GLN_78	2.90	1.94	9.41
1HGH.PDB	OE1, F_GLU_74	NE2, F_GLN_78	HE22, F_GLN_78	2.92	1.95	8.97
1HGH.PDB	O, F_GLY_75	N, F_ASP_79	H, F_ASP_79	2.84	1.89	11.67
1HGH.PDB	O, F_ASP_79	N, F_TYR_83	H, F_TYR_83	2.85	1.92	14.40
1HGH.PDB	OE1, B_GLU_85	OH, F_TYR_83	HH, F_TYR_83	2.53	1.74	27.23
1HGH.PDB	O, F_LEU_80	N, F_VAL_84	H, F_VAL_84	2.73	1.81	14.79
1HGH.PDB	O, F_LYS_82	N, F_ASP_86	H, F_ASP_86	2.93	1.98	9.76
1HGH.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.65	1.63	9.88
1HGH.PDB	O, F_GLU_85	N, F_ILE_89	H, F_ILE_89	2.87	1.89	5.28
1HGH.PDB	O, F_LYS_88	N, F_TRP_92	H, F_TRP_92	2.94	1.97	7.63
1HGH.PDB	O, F_ILE_89	N, F_SER_93	H, F_SER_93	2.86	1.97	18.83
1HGH.PDB	O, F_ILE_89	OG, F_SER_93	HG, F_SER_93	2.78	1.88	16.61
1HGH.PDB	O, F_ASP_90	N, F_TYR_94	H, F_TYR_94	2.84	1.92	15.99
1HGH.PDB	O, F_LEU_91	N, F_ASN_95	H, F_ASN_95	3.00	2.02	3.46
1HGH.PDB	O, F_TRP_92	N, F_ALA_96	H, F_ALA_96	2.98	2.07	17.48

1HGH.PDB	O, F_TYR_94	N, F_LEU_98	H, F_LEU_98	2.95	1.97	6.50
1HGH.PDB	O, F_ASN_95	N, F_LEU_99	H, F_LEU_99	2.94	2.05	19.69
1HGH.PDB	O, F_LEU_98	N, F_LEU_102	H, F_LEU_102	3.00	2.02	4.44
1HGH.PDB	O, F_VAL_100	N, F_ASN_104	H, F_ASN_104	2.88	1.93	12.02
1HGH.PDB	O, E_LYS_27	ND2, F_ASN_104	HD22, F_ASN_104	2.90	1.95	12.28
1HGH.PDB	O, F_LEU_102	N, F_HIS_106	H, F_HIS_106	2.96	2.00	11.13
1HGH.PDB	O, F_GLU_103	N, F_THR_107	H, F_THR_107	2.86	1.95	17.81
1HGH.PDB	O, F_HIS_106	N, F_LEU_110	H, F_LEU_110	2.81	1.86	10.81
1HGH.PDB	O, F_THR_107	OG1, F_THR_111	HG1, F_THR_111	2.90	1.94	2.05
1HGH.PDB	O, F_ASP_109	N, F_SER_113	H, F_SER_113	2.77	1.83	10.08
1HGH.PDB	O, F_ASP_112	N, F_ASN_116	H, F_ASN_116	2.97	1.99	5.76
1HGH.PDB	O, F_SER_113	N, F_LYS_117	H, F_LYS_117	2.73	1.90	25.90
1HGH.PDB	O, F_GLU_114	N, F_LEU_118	H, F_LEU_118	2.99	2.02	8.75
1HGH.PDB	O, F_ASN_116	N, F_GLU_120	H, F_GLU_120	2.90	1.92	2.56
1HGH.PDB	O, F_LYS_117	N, F_LYS_121	H, F_LYS_121	2.86	1.95	17.55
1HGH.PDB	O, F_LEU_118	N, F_THR_122	H, F_THR_122	3.00	2.04	9.77
1HGH.PDB	O, F_PHE_119	N, F_ARG_123	H, F_ARG_123	2.88	1.91	8.40
1HGH.PDB	OE2, F_GLU_120	NH1, F_ARG_123	HH11, F_ARG_123	2.74	1.84	22.63
1HGH.PDB	O, F_GLU_120	N, F_ARG_124	H, F_ARG_124	2.97	2.00	8.45
1HGH.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.89	2.06	26.55
1HGH.PDB	OE2, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.92	2.03	21.52
1HGH.PDB	O, F_LEU_126	N, F_ASN_129	H, F_ASN_129	2.97	2.04	14.05
1HGH.PDB	OH, F_TYR_157	ND2, F_ASN_129	HD22, F_ASN_129	2.82	1.88	14.11
1HGH.PDB	O, F_LYS_139	N, F_GLU_131	H, F_GLU_131	2.96	2.04	16.53
1HGH.PDB	O, F_CYS_137	N, F_MET_133	H, F_MET_133	2.86	1.92	14.22
1HGH.PDB	O, E_LEU_13	N, F_PHE_138	H, F_PHE_138	2.71	1.82	18.02
1HGH.PDB	O, F_GLU_131	N, F_LYS_139	H, F_LYS_139	2.82	1.86	5.73
1HGH.PDB	O, E_ALA_11	N, F_ILE_140	H, F_ILE_140	2.79	1.87	15.45
1HGH.PDB	O, F_ASN_129	N, F_TYR_141	H, F_TYR_141	2.86	1.92	14.36
1HGH.PDB	OE2, F_GLU_165	N, F_LYS_143	H, F_LYS_143	2.98	2.04	16.16
1HGH.PDB	O, F_ASP_145	N, F_ILE_149	H, F_ILE_149	2.90	1.94	10.21
1HGH.PDB	O, F_ASN_146	N, F_GLU_150	H, F_GLU_150	2.92	1.99	14.40
1HGH.PDB	O, F_ALA_147	N, F_SER_151	H, F_SER_151	2.95	2.08	22.59
1HGH.PDB	O, F_CYS_148	OG, F_SER_151	HG, F_SER_151	2.76	1.89	20.46
1HGH.PDB	O, F_GLU_150	N, F_ASN_154	H, F_ASN_154	2.79	1.82	2.73
1HGH.PDB	OD1, F_ASP_158	N, F_ASP_160	H, F_ASP_160	2.98	2.10	21.90
1HGH.PDB	O, F_HIS_159	N, F_TYR_162	H, F_TYR_162	2.95	2.07	22.27
1HGH.PDB	O, D_ARG_170	NH1, F_ARG_163	HH12, F_ARG_163	2.89	1.90	10.67
1HGH.PDB	O, F_TYR_162	N, F_ALA_166	H, F_ALA_166	2.94	1.96	4.91
1HGH.PDB	O, F_ARG_163	N, F_LEU_167	H, F_LEU_167	2.82	1.86	8.96
1HGH.PDB	O, F_GLU_165	ND2, F_ASN_169	HD22, F_ASN_169	2.99	2.03	7.50
1HGH.PDB	O, F_ALA_166	N, F_ARG_170	H, F_ARG_170	2.83	1.95	20.78
1HGH.PDB	O, F_GLU_128	NE, F_ARG_170	HE, F_ARG_170	2.76	1.89	22.46
1HGH.PDB	OE2, F_GLU_131	NH1, F_ARG_170	HH11, F_ARG_170	2.84	1.84	5.40
1HGH.PDB	O, F_LEU_167	N, F_PHE_171	H, F_PHE_171	2.96	2.05	17.03

Table 1668: 1HGH-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1HGI.PDB	O, B_ILE_140	N, A_ALA_11	H, A_ALA_11	2.84	1.92	15.59
1HGI.PDB	O, B_PHE_138	N, A_LEU_13	H, A_LEU_13	3.00	2.03	9.98
1HGI.PDB	O, B_ARG_25	N, A_CYS_14	H, A_CYS_14	2.96	2.03	15.50
1HGI.PDB	O, B_GLY_136	N, A_LEU_15	H, A_LEU_15	2.93	1.96	7.25
1HGI.PDB	O, B_GLY_23	N, A_GLY_16	H, A_GLY_16	2.98	2.12	23.40
1HGI.PDB	O, A_HIS_18	ND1, A_HIS_17	HD1, A_HIS_17	2.95	2.05	20.26
1HGI.PDB	O, B_TRP_21	N, A_HIS_18	H, A_HIS_18	2.89	1.98	18.40
1HGI.PDB	OD1, A_ASN_322	N, A_VAL_20	H, A_VAL_20	2.77	1.82	10.44
1HGI.PDB	O, A_VAL_36	N, A_THR_24	H, A_THR_24	2.83	1.89	12.49
1HGI.PDB	O, A_ILE_34	N, A_VAL_26	H, A_VAL_26	2.77	1.82	9.67
1HGI.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.90	1.86	7.66
1HGI.PDB	O, A_ASP_31	N, A_THR_28	H, A_THR_28	2.78	1.96	27.36
1HGI.PDB	O, A_VAL_26	N, A_ILE_34	H, A_ILE_34	2.91	2.01	18.80
1HGI.PDB	O, A_THR_24	N, A_VAL_36	H, A_VAL_36	2.78	1.82	5.76
1HGI.PDB	O, A_MET_320	N, A_THR_37	H, A_THR_37	2.84	1.88	8.46
1HGI.PDB	O, A_LEU_316	N, A_THR_40	H, A_THR_40	2.88	2.01	22.14
1HGI.PDB	O, A_LEU_314	N, A_LEU_42	H, A_LEU_42	2.85	1.98	22.93
1HGI.PDB	OE2, A_GLU_41	N, A_VAL_43	H, A_VAL_43	2.99	2.05	14.68
1HGI.PDB	O, A_PHE_294	N, A_GLN_44	H, A_GLN_44	2.83	1.87	6.80
1HGI.PDB	O, A_SER_46	NE2, A_GLN_44	HE22, A_GLN_44	2.80	1.99	27.53
1HGI.PDB	OD2, A_ASP_275	NZ, A_LYS_50	HZ1, A_LYS_50	2.71	1.78	22.79
1HGI.PDB	O, A_PRO_273	N, A_ILE_51	H, A_ILE_51	2.80	1.85	10.62
1HGI.PDB	O, A_ASP_275	N, A_ASN_53	H, A_ASN_53	2.87	2.01	23.36
1HGI.PDB	O, A_GLU_280	NE2, A_HIS_56	HE2, A_HIS_56	2.99	2.05	14.61
1HGI.PDB	OD2, A_ASP_85	N, A_ARG_57	H, A_ARG_57	2.87	1.92	11.71
1HGI.PDB	O, A_THR_83	NE, A_ARG_57	HE, A_ARG_57	2.85	1.87	3.06
1HGI.PDB	O, A_LEU_86	N, A_LEU_59	H, A_LEU_59	2.86	1.91	10.36
1HGI.PDB	O, A_VAL_88	N, A_GLY_61	H, A_GLY_61	2.97	2.12	24.22
1HGI.PDB	OD1, A_ASP_60	N, A_ILE_62	H, A_ILE_62	2.84	1.91	13.27
1HGI.PDB	O, A_GLY_61	N, A_CYS_64	H, A_CYS_64	2.89	1.98	18.14
1HGI.PDB	OE2, A_GLU_89	N, A_LEU_66	H, A_LEU_66	3.00	2.06	15.37
1HGI.PDB	O, A_LEU_66	N, A_LEU_70	H, A_LEU_70	2.81	1.92	20.22
1HGI.PDB	O, A_ILE_67	N, A_LEU_71	H, A_LEU_71	2.84	1.88	6.23
1HGI.PDB	O, A_ASP_68	N, A_GLY_72	H, A_GLY_72	2.79	1.85	12.70
1HGI.PDB	OD1, A_ASP_73	ND1, A_HIS_75	HD1, A_HIS_75	2.90	1.96	15.34
1HGI.PDB	O, A_ASP_63	NE2, A_HIS_75	HE2, A_HIS_75	2.84	1.90	14.11
1HGI.PDB	O, A_ASP_73	N, A_CYS_76	H, A_CYS_76	2.75	1.84	16.03
1HGI.PDB	O, A_PRO_74	N, A_ASP_77	H, A_ASP_77	2.94	1.98	10.08
1HGI.PDB	O, A_CYS_76	N, A_PHE_79	H, A_PHE_79	2.96	1.99	3.40
1HGI.PDB	OE1, A_GLU_82	N, A_THR_83	H, A_THR_83	2.96	2.07	20.90
1HGI.PDB	O, A_ARG_57	N, A_ASP_85	H, A_ASP_85	2.81	1.90	17.53
1HGI.PDB	O, A_MET_268	N, A_GLU_89	H, A_GLU_89	2.81	1.85	7.54
1HGI.PDB	OD1, A_ASP_60	NE, A_ARG_90	HE, A_ARG_90	2.89	1.91	4.93
1HGI.PDB	O, A_SER_270	NH1, A_ARG_90	HH11, A_ARG_90	2.65	1.78	23.88
1HGI.PDB	O, A_ALA_272	NH1, A_ARG_90	HH12, A_ARG_90	2.62	1.72	20.22
1HGI.PDB	OD2, A_ASP_60	NH2, A_ARG_90	HH21, A_ARG_90	2.83	1.85	11.60
1HGI.PDB	OD1, A_ASP_271	N, A_SER_91	H, A_SER_91	2.91	1.95	10.73
1HGI.PDB	OD1, A_ASP_271	OG, A_SER_91	HG, A_SER_91	2.93	2.10	25.86
1HGI.PDB	OD2, A_ASP_271	OG, A_SER_91	HG, A_SER_91	2.80	1.92	20.51
1HGI.PDB	OD2, A_ASP_68	OG, A_SER_95	HG, A_SER_95	2.89	1.96	14.00
1HGI.PDB	OD2, A_ASP_73	N, A_ASN_96	H, A_ASN_96	2.87	1.92	13.04
1HGI.PDB	OD1, A_ASP_68	OH, A_TYR_100	HH, A_TYR_100	2.99	2.05	13.08
1HGI.PDB	OD2, A_ASP_104	OG, A_SER_107	HG, A_SER_107	2.89	1.96	15.23
1HGI.PDB	O, A_TYR_105	N, A_ARG_109	H, A_ARG_109	2.86	1.88	3.08
1HGI.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.80	1.81	13.24
1HGI.PDB	O, A_SER_107	N, A_LEU_111	H, A_LEU_111	2.85	1.89	7.63
1HGI.PDB	O, A_LEU_108	N, A_VAL_112	H, A_VAL_112	2.97	1.99	2.18

1HGI.PDB	O, A_ARG_109	N, A_ALA_113	H, A_ALA_113	2.95	2.04	17.40
1HGI.PDB	O, A_SER_110	N, A_SER_114	H, A_SER_114	2.94	2.06	20.96
1HGI.PDB	OE2, A_GLU_119	OG1, A_THR_117	HG1, A_THR_117	2.93	2.01	15.43
1HGI.PDB	O, A_GLU_82	N, A_LEU_118	H, A_LEU_118	2.94	2.01	15.84
1HGI.PDB	O, A_TYR_257	N, A_ILE_121	H, A_ILE_121	2.92	1.95	6.91
1HGI.PDB	O, A_ARG_255	N, A_GLU_123	H, A_GLU_123	2.88	1.93	11.84
1HGI.PDB	O, A_THR_155	N, A_THR_131	H, A_THR_131	2.73	1.85	20.63
1HGI.PDB	OD1, A_ASN_152	N, A_ASN_133	H, A_ASN_133	2.84	1.92	17.02
1HGI.PDB	O, A_GLY_146	N, A_SER_136	H, A_SER_136	2.75	1.87	20.99
1HGI.PDB	OG, A_SER_136	N, A_ALA_138	H, A_ALA_138	2.84	1.93	17.99
1HGI.PDB	O, A_GLY_144	NZ, A_LYS_140	HZ1, A_LYS_140	2.89	1.92	16.20
1HGI.PDB	OD1, A_ASN_137	NZ, A_LYS_140	HZ2, A_LYS_140	2.79	1.79	13.01
1HGI.PDB	OD2, A_ASP_77	NE, A_ARG_141	HE, A_ARG_141	2.82	2.01	29.43
1HGI.PDB	O, A_PHE_147	NH1, A_ARG_141	HH12, A_ARG_141	2.56	1.66	20.36
1HGI.PDB	OD1, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.93	2.01	20.43
1HGI.PDB	OD2, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.69	1.82	24.99
1HGI.PDB	O, A_GLY_72	NH2, A_ARG_141	HH22, A_ARG_141	3.00	2.01	9.22
1HGI.PDB	O, A_SER_136	N, A_GLY_146	H, A_GLY_146	2.98	2.04	14.64
1HGI.PDB	O, A_GLY_72	N, A_SER_149	H, A_SER_149	2.91	1.98	15.28
1HGI.PDB	O, A_ALA_253	N, A_ASN_152	H, A_ASN_152	2.76	1.90	23.60
1HGI.PDB	OH, A_TYR_195	NE1, A_TRP_153	HE1, A_TRP_153	2.87	1.98	21.02
1HGI.PDB	O, A_THR_131	N, A_THR_155	H, A_THR_155	2.95	1.99	10.46
1HGI.PDB	O, A_LEU_194	N, A_LYS_156	H, A_LYS_156	2.87	1.97	18.02
1HGI.PDB	O, A_SER_193	NZ, A_LYS_156	HZ2, A_LYS_156	2.75	1.76	15.14
1HGI.PDB	O, A_THR_160	N, A_SER_157	H, A_SER_157	2.90	2.01	20.69
1HGI.PDB	OG1, A_THR_131	OG, A_SER_157	HG, A_SER_157	2.97	2.02	9.12
1HGI.PDB	O, A_SER_247	N, A_LEU_164	H, A_LEU_164	2.71	1.88	25.60
1HGI.PDB	O, A_ILE_245	N, A_VAL_166	H, A_VAL_166	2.88	1.93	12.13
1HGI.PDB	O, A_LEU_243	OG1, A_THR_167	HG1, A_THR_167	2.87	2.00	20.84
1HGI.PDB	O, A_LEU_243	N, A_MET_168	H, A_MET_168	2.94	2.01	15.31
1HGI.PDB	O, A_ASP_241	N, A_ASN_170	H, A_ASN_170	2.98	2.00	3.78
1HGI.PDB	O, A_PHE_174	ND2, A_ASN_170	HD21, A_ASN_170	2.83	1.88	13.11
1HGI.PDB	O, A_VAL_237	ND2, A_ASN_170	HD22, A_ASN_170	2.97	2.11	23.66
1HGI.PDB	O, A_VAL_237	N, A_LYS_176	H, A_LYS_176	2.96	2.02	13.33
1HGI.PDB	OE2, A_GLU_123	NZ, A_LYS_176	HZ1, A_LYS_176	2.68	1.79	25.50
1HGI.PDB	O, A_THR_235	N, A_TYR_178	H, A_TYR_178	2.83	1.86	3.17
1HGI.PDB	OE1, A_GLU_123	OH, A_TYR_178	HH, A_TYR_178	2.78	1.82	7.33
1HGI.PDB	OG1, A_THR_235	NE1, A_TRP_180	HE1, A_TRP_180	2.85	1.87	3.02
1HGI.PDB	O, A_ILE_252	N, A_GLY_181	H, A_GLY_181	2.99	2.17	27.41
1HGI.PDB	O, A_ASN_250	N, A_HIS_183	H, A_HIS_183	2.91	2.02	20.40
1HGI.PDB	O, A_ARG_229	N, A_HIS_184	H, A_HIS_184	2.87	1.91	8.12
1HGI.PDB	OG, A_SER_231	NE2, A_HIS_184	HE2, A_HIS_184	2.81	1.93	22.19
1HGI.PDB	OE1, A_GLU_190	N, A_SER_186	H, A_SER_186	2.97	2.07	20.08
1HGI.PDB	OD1, A_ASN_250	NE2, A_GLN_191	HE21, A_GLN_191	2.93	1.97	11.19
1HGI.PDB	O, A_GLN_197	NE2, A_GLN_191	HE22, A_GLN_191	2.94	1.98	10.63
1HGI.PDB	O, A_ASN_188	N, A_THR_192	H, A_THR_192	2.97	2.03	12.91
1HGI.PDB	O, A_ASN_188	OG1, A_THR_192	HG1, A_THR_192	2.95	1.99	5.36
1HGI.PDB	O, A_GLN_189	N, A_SER_193	H, A_SER_193	2.83	1.86	5.01
1HGI.PDB	O, A_GLN_191	N, A_TYR_195	H, A_TYR_195	2.74	1.78	5.84
1HGI.PDB	O, A_TYR_161	NE2, A_GLN_197	HE21, A_GLN_197	2.98	2.02	10.94
1HGI.PDB	O, A_ASN_248	NE2, A_GLN_197	HE22, A_GLN_197	2.92	2.01	18.40
1HGI.PDB	OD1, A_ASN_246	NH2, A_ARG_201	HH21, A_ARG_201	2.54	1.71	26.99
1HGI.PDB	O, A_ILE_213	N, A_VAL_202	H, A_VAL_202	2.93	1.95	5.55
1HGI.PDB	O, A_ASN_246	N, A_THR_203	H, A_THR_203	2.85	1.91	12.85
1HGI.PDB	O, A_GLN_211	N, A_VAL_204	H, A_VAL_204	2.83	1.91	15.32
1HGI.PDB	O, A_VAL_244	N, A_SER_205	H, A_SER_205	2.95	2.02	15.55
1HGI.PDB	O, A_SER_209	N, A_THR_206	H, A_THR_206	2.90	1.93	7.39
1HGI.PDB	OD1, A_ASP_241	N, A_ARG_207	H, A_ARG_207	2.92	1.95	9.91

1HGI.PDB	OD2, A_ASP_241	NE, A_ARG_208	HE, A_ARG_208	2.96	2.05	19.55
1HGI.PDB	O, A_VAL_204	N, A_GLN_211	H, A_GLN_211	2.90	1.98	16.08
1HGI.PDB	OG1, A_THR_203	OG1, A_THR_212	HG1, A_THR_212	2.96	2.00	2.15
1HGI.PDB	O, A_VAL_202	N, A_ILE_213	H, A_ILE_213	2.83	1.91	15.65
1HGI.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.65	1.73	18.55
1HGI.PDB	O, A_ASN_216	NH2, A_ARG_220	HH22, A_ARG_220	2.69	1.79	20.57
1HGI.PDB	O, A_LEU_226	N, A_VAL_223	H, A_VAL_223	2.88	1.91	8.35
1HGI.PDB	O, A_CYS_97	NE, A_ARG_224	HE, A_ARG_224	2.78	1.93	25.49
1HGI.PDB	O, A_CYS_97	NH2, A_ARG_224	HH21, A_ARG_224	2.83	1.97	25.33
1HGI.PDB	O, A_VAL_223	N, A_LEU_226	H, A_LEU_226	2.93	2.00	15.45
1HGI.PDB	O, A_SER_228	NH1, A_ARG_229	HH11, A_ARG_229	2.68	1.75	18.52
1HGI.PDB	O, A_PRO_221	NH2, A_ARG_229	HH22, A_ARG_229	2.62	1.67	14.70
1HGI.PDB	O, A_PRO_99	N, A_ILE_230	H, A_ILE_230	2.99	2.15	25.83
1HGI.PDB	O, A_ILE_182	N, A_SER_231	H, A_SER_231	2.99	2.14	24.63
1HGI.PDB	OD1, A_ASP_101	OG, A_SER_231	HG, A_SER_231	2.96	2.01	11.74
1HGI.PDB	O, A_ASP_101	N, A_ILE_232	H, A_ILE_232	2.92	1.99	15.11
1HGI.PDB	O, A_TRP_180	N, A_TYR_233	H, A_TYR_233	2.89	1.92	9.03
1HGI.PDB	O, A_TYR_178	N, A_THR_235	H, A_THR_235	2.82	1.93	19.14
1HGI.PDB	O, A_LYS_176	N, A_VAL_237	H, A_VAL_237	2.80	1.86	12.56
1HGI.PDB	O, F_SER_71	NZ, A_LYS_238	HZ2, A_LYS_238	2.65	1.80	28.67
1HGI.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.85	1.85	15.00
1HGI.PDB	O, A_ASN_170	N, A_GLY_240	H, A_GLY_240	2.91	2.07	25.35
1HGI.PDB	OD1, A_ASP_241	N, A_VAL_242	H, A_VAL_242	2.74	1.94	29.06
1HGI.PDB	O, A_MET_168	N, A_LEU_243	H, A_LEU_243	2.93	1.96	6.54
1HGI.PDB	O, A_SER_205	N, A_VAL_244	H, A_VAL_244	2.95	2.00	12.56
1HGI.PDB	O, A_VAL_166	N, A_ILE_245	H, A_ILE_245	2.98	2.04	14.27
1HGI.PDB	O, A_THR_203	N, A_ASN_246	H, A_ASN_246	2.86	1.93	15.27
1HGI.PDB	O, A_LEU_164	N, A_SER_247	H, A_SER_247	2.86	1.96	18.93
1HGI.PDB	O, A_ARG_201	OG, A_SER_247	HG, A_SER_247	2.80	2.00	29.04
1HGI.PDB	OE1, A_GLN_191	ND2, A_ASN_250	HD21, A_ASN_250	2.89	1.93	10.00
1HGI.PDB	O, A_HIS_183	ND2, A_ASN_250	HD22, A_ASN_250	2.85	1.88	5.42
1HGI.PDB	O, A_GLY_181	N, A_ILE_252	H, A_ILE_252	2.93	1.97	10.35
1HGI.PDB	O, A_ASN_152	N, A_ALA_253	H, A_ALA_253	2.80	1.92	21.29
1HGI.PDB	O, A_LEU_177	N, A_PHE_258	H, A_PHE_258	2.93	1.97	9.46
1HGI.PDB	OE2, A_GLU_119	NH1, A_ARG_261	HH12, A_ARG_261	2.66	1.83	28.46
1HGI.PDB	OE1, A_GLU_119	NH2, A_ARG_261	HH22, A_ARG_261	2.85	1.99	27.12
1HGI.PDB	OD2, A_ASP_85	NZ, A_LYS_264	HZ3, A_LYS_264	2.82	1.85	17.23
1HGI.PDB	O, A_PHE_87	N, A_MET_268	H, A_MET_268	2.89	2.01	22.03
1HGI.PDB	O, A_PRO_284	OG, A_SER_270	HG, A_SER_270	2.81	1.87	11.59
1HGI.PDB	OG, A_SER_270	N, A_ALA_272	H, A_ALA_272	2.98	2.03	12.37
1HGI.PDB	O, A_ILE_51	N, A_ASP_275	H, A_ASP_275	2.92	2.02	19.41
1HGI.PDB	OD1, A_ASP_275	N, A_THR_276	H, A_THR_276	2.85	2.00	24.58
1HGI.PDB	O, A_ASN_54	N, A_SER_279	H, A_SER_279	2.79	1.86	13.88
1HGI.PDB	O, A_TYR_302	N, A_ILE_282	H, A_ILE_282	2.88	1.92	8.64
1HGI.PDB	O, A_THR_283	N, A_GLY_286	H, A_GLY_286	2.81	1.89	14.79
1HGI.PDB	O, A_LYS_50	N, A_SER_287	H, A_SER_287	2.89	1.91	3.39
1HGI.PDB	O, A_ALA_304	ND2, A_ASN_290	HD22, A_ASN_290	2.73	1.85	20.49
1HGI.PDB	OE1, A_GLN_44	NZ, A_LYS_292	HZ1, A_LYS_292	2.74	1.74	11.73
1HGI.PDB	OD2, A_ASP_291	NZ, A_LYS_292	HZ3, A_LYS_292	2.81	1.89	23.33
1HGI.PDB	O, A_LYS_307	N, A_GLN_295	H, A_GLN_295	2.85	1.96	20.30
1HGI.PDB	O, A_ASN_298	NE2, A_GLN_295	HE21, A_GLN_295	2.82	1.86	9.08
1HGI.PDB	O, A_GLN_44	N, A_ASN_296	H, A_ASN_296	2.91	1.97	13.42
1HGI.PDB	OE1, A_GLN_295	N, A_VAL_297	H, A_VAL_297	2.73	1.93	28.60
1HGI.PDB	OD1, A_ASN_298	N, A_ILE_300	H, A_ILE_300	2.93	1.98	12.80
1HGI.PDB	O, A_ILE_282	N, A_TYR_302	H, A_TYR_302	2.98	2.09	21.95
1HGI.PDB	O, A_LYS_264	OH, A_TYR_302	HH, A_TYR_302	2.75	1.94	27.71
1HGI.PDB	O, B_LYS_62	N, A_GLY_303	H, A_GLY_303	2.96	1.99	7.07
1HGI.PDB	O, A_GLN_295	N, A_VAL_309	H, A_VAL_309	2.99	2.14	25.08

1HGI.PDB	OG, B_SER_93	N, A_LYS_310	H, A_LYS_310	2.98	2.05	15.58
1HGI.PDB	OD1, B_ASP_86	NZ, A_LYS_310	HZ3, A_LYS_310	2.76	1.92	29.34
1HGI.PDB	OE2, A_GLU_41	N, A_LEU_314	H, A_LEU_314	2.86	1.90	8.56
1HGI.PDB	OE1, A_GLU_41	NZ, A_LYS_315	HZ3, A_LYS_315	2.77	1.82	19.86
1HGI.PDB	O, A_THR_40	N, A_LEU_316	H, A_LEU_316	2.86	1.94	16.90
1HGI.PDB	OD1, B_ASN_104	N, A_ALA_317	H, A_ALA_317	2.74	1.83	15.76
1HGI.PDB	O, A_ASN_38	N, A_THR_318	H, A_THR_318	2.82	1.93	19.87
1HGI.PDB	O, A_VAL_20	ND2, A_ASN_322	HD21, A_ASN_322	2.87	1.93	13.77
1HGI.PDB	OE2, A_GLU_35	ND2, A_ASN_322	HD22, A_ASN_322	2.93	1.97	12.34
1HGI.PDB	OE2, B_GLU_15	NZ, A_LYS_326	HZ1, A_LYS_326	2.79	1.93	27.33
1HGI.PDB	OE1, A_GLU_325	NZ, A_LYS_326	HZ3, A_LYS_326	2.91	1.94	17.77
1HGI.PDB	OE1, B_GLU_15	N, A_THR_328	H, A_THR_328	2.87	1.93	12.65
1HGI.PDB	OD2, B_ASP_112	N, B_GLY_1	H2, B_GLY_1	2.79	1.78	11.80
1HGI.PDB	OD1, B_ASP_109	N, B_LEU_2	H, B_LEU_2	2.89	1.95	13.58
1HGI.PDB	OD2, B_ASP_112	N, B_PHE_3	H, B_PHE_3	2.82	2.00	27.10
1HGI.PDB	OD2, B_ASP_112	N, B_GLY_4	H, B_GLY_4	2.93	2.02	17.65
1HGI.PDB	OD1, B_ASP_112	N, B_ALA_5	H, B_ALA_5	2.82	1.90	16.18
1HGI.PDB	O, B_GLY_4	N, B_PHE_9	H, B_PHE_9	2.84	1.90	12.47
1HGI.PDB	O, B_GLY_13	ND2, B_ASN_12	HD22, B_ASN_12	2.81	1.91	19.43
1HGI.PDB	O, A_VAL_323	N, B_GLY_13	H, B_GLY_13	2.68	1.79	18.45
1HGI.PDB	O, A_HIS_17	N, B_TRP_14	H, B_TRP_14	2.78	1.88	17.65
1HGI.PDB	OG1, B_THR_41	N, B_TRP_21	H, B_TRP_21	2.98	2.13	25.10
1HGI.PDB	O, A_GLY_16	N, B_GLY_23	H, B_GLY_23	2.97	2.06	17.58
1HGI.PDB	O, B_ALA_35	N, B_PHE_24	H, B_PHE_24	2.80	1.84	7.18
1HGI.PDB	OE1, B_GLN_34	NE, B_ARG_25	HE, B_ARG_25	2.60	1.78	26.17
1HGI.PDB	OE1, B_GLN_34	NH2, B_ARG_25	HH21, B_ARG_25	2.75	1.92	27.98
1HGI.PDB	OE2, A_GLU_325	NH2, B_ARG_25	HH22, B_ARG_25	2.93	1.95	13.46
1HGI.PDB	O, B_GLY_33	N, B_HIS_26	H, B_HIS_26	2.73	1.82	16.37
1HGI.PDB	O, B_GLY_31	N, B_ASN_28	H, B_ASN_28	2.73	1.84	19.89
1HGI.PDB	O, B_ASN_28	N, B_GLY_31	H, B_GLY_31	2.85	2.01	25.49
1HGI.PDB	O, B_PHE_24	N, B_ALA_35	H, B_ALA_35	2.80	2.01	29.31
1HGI.PDB	O, B_TYR_22	N, B_ASP_37	H, B_ASP_37	2.70	1.78	14.64
1HGI.PDB	OD2, B_ASP_37	N, B_SER_40	H, B_SER_40	2.90	1.93	5.57
1HGI.PDB	O, B_ASP_37	OG1, B_THR_41	HG1, B_THR_41	2.74	1.83	15.44
1HGI.PDB	OD1, B_ASP_46	NE2, B_GLN_42	HE22, B_GLN_42	2.89	2.02	23.36
1HGI.PDB	O, B_SER_40	N, B_ALA_44	H, B_ALA_44	2.95	1.97	3.32
1HGI.PDB	O, B_THR_41	N, B_ILE_45	H, B_ILE_45	2.96	2.03	14.49
1HGI.PDB	O, B_GLN_42	N, B_ASP_46	H, B_ASP_46	2.71	1.76	6.05
1HGI.PDB	O, B_ALA_43	NE2, B_GLN_47	HE22, B_GLN_47	2.94	2.02	16.15
1HGI.PDB	O, B_ILE_45	N, B_ASN_49	H, B_ASN_49	2.87	1.98	20.49
1HGI.PDB	O, B_ASP_46	N, B_GLY_50	H, B_GLY_50	2.94	2.01	16.14
1HGI.PDB	O, B_GLN_47	N, B_LYS_51	H, B_LYS_51	3.00	2.02	5.35
1HGI.PDB	OG1, B_THR_107	NZ, B_LYS_51	HZ1, B_LYS_51	2.96	1.97	15.88
1HGI.PDB	OE1, B_GLU_103	NZ, B_LYS_51	HZ2, B_LYS_51	2.82	1.78	6.88
1HGI.PDB	ND1, B_HIS_106	NZ, B_LYS_51	HZ3, B_LYS_51	2.81	1.87	19.52
1HGI.PDB	O, B_ILE_48	N, B_LEU_52	H, B_LEU_52	2.94	2.01	15.10
1HGI.PDB	O, B_ASN_49	N, B_ASN_53	H, B_ASN_53	2.79	1.92	22.20
1HGI.PDB	O, E_THR_28	NE, B_ARG_54	HE, B_ARG_54	2.88	1.92	10.21
1HGI.PDB	OE1, B_GLU_57	NH1, B_ARG_54	HH11, B_ARG_54	2.86	1.87	11.02
1HGI.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.81	1.84	14.63
1HGI.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ1, B_LYS_62	2.67	1.78	25.75
1HGI.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.87	1.89	8.13
1HGI.PDB	O, B_PHE_63	NE2, B_GLN_65	HE22, B_GLN_65	2.93	1.95	3.70
1HGI.PDB	O, A_LYS_299	NZ, B_LYS_68	HZ1, B_LYS_68	2.81	1.78	9.15
1HGI.PDB	OE2, B_GLU_85	NZ, B_LYS_68	HZ2, B_LYS_68	2.79	1.75	2.13
1HGI.PDB	OG, C_SER_107	N, B_ARG_76	H, B_ARG_76	2.85	1.90	10.66
1HGI.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.86	1.89	7.04
1HGI.PDB	OE2, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.92	1.89	1.72

1HGI.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.71	1.72	8.42
1HGI.PDB	OE1, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.86	1.86	6.93
1HGI.PDB	O, B_GLU_72	NE2, B_GLN_78	HE21, B_GLN_78	2.96	1.98	5.26
1HGI.PDB	OE1, B_GLU_74	NE2, B_GLN_78	HE22, B_GLN_78	2.94	1.97	8.23
1HGI.PDB	O, B_ASP_79	N, B_TYR_83	H, B_TYR_83	2.91	2.00	18.32
1HGI.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.78	1.84	13.46
1HGI.PDB	O, B_LEU_80	N, B_VAL_84	H, B_VAL_84	2.75	1.83	14.22
1HGI.PDB	O, B_LYS_82	N, B_ASP_86	H, B_ASP_86	2.90	1.94	10.51
1HGI.PDB	O, B_TYR_83	N, B_THR_87	H, B_THR_87	2.96	2.01	11.07
1HGI.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.65	1.64	9.94
1HGI.PDB	O, B_GLU_85	N, B_ILE_89	H, B_ILE_89	2.86	1.89	9.56
1HGI.PDB	O, B_LYS_88	N, B_TRP_92	H, B_TRP_92	2.97	1.99	6.73
1HGI.PDB	O, B_ILE_89	N, B_SER_93	H, B_SER_93	2.87	1.94	14.62
1HGI.PDB	O, B_ILE_89	OG, B_SER_93	HG, B_SER_93	2.83	1.94	18.39
1HGI.PDB	O, B_ASP_90	N, B_TYR_94	H, B_TYR_94	2.94	2.02	16.85
1HGI.PDB	O, B_TRP_92	N, B_ALA_96	H, B_ALA_96	2.90	1.95	10.47
1HGI.PDB	O, B_TYR_94	N, B_LEU_98	H, B_LEU_98	2.90	1.94	9.73
1HGI.PDB	O, B_ASN_95	N, B_LEU_99	H, B_LEU_99	2.85	1.96	19.61
1HGI.PDB	O, B_ALA_96	N, B_VAL_100	H, B_VAL_100	2.99	2.03	8.76
1HGI.PDB	O, B_LEU_98	N, B_LEU_102	H, B_LEU_102	2.99	2.01	3.39
1HGI.PDB	O, B_LEU_99	N, B_GLU_103	H, B_GLU_103	2.93	1.96	7.47
1HGI.PDB	O, B_VAL_100	N, B_ASN_104	H, B_ASN_104	2.87	1.90	6.79
1HGI.PDB	O, A_LYS_27	ND2, B_ASN_104	HD22, B_ASN_104	2.86	1.90	10.00
1HGI.PDB	O, B_LEU_102	N, B_HIS_106	H, B_HIS_106	2.92	1.98	15.03
1HGI.PDB	O, B_GLU_103	N, B_THR_107	H, B_THR_107	2.76	1.89	21.30
1HGI.PDB	O, B_ASN_104	N, B_ILE_108	H, B_ILE_108	2.93	1.97	9.63
1HGI.PDB	O, B_HIS_106	N, B_LEU_110	H, B_LEU_110	2.81	1.86	12.25
1HGI.PDB	O, B_THR_107	OG1, B_THR_111	HG1, B_THR_111	2.94	1.97	3.25
1HGI.PDB	O, B_ASP_109	N, B_SER_113	H, B_SER_113	2.80	1.86	12.43
1HGI.PDB	O, F_LEU_2	OG, B_SER_113	HG, B_SER_113	2.77	1.90	22.05
1HGI.PDB	O, B_LEU_110	N, B_GLU_114	H, B_GLU_114	2.95	1.99	9.30
1HGI.PDB	O, B_ASP_112	N, B_ASN_116	H, B_ASN_116	2.96	2.02	13.43
1HGI.PDB	O, B_SER_113	N, B_LYS_117	H, B_LYS_117	2.68	1.82	23.27
1HGI.PDB	O, B_ASN_116	N, B_GLU_120	H, B_GLU_120	2.93	1.95	4.31
1HGI.PDB	O, B_LYS_117	N, B_LYS_121	H, B_LYS_121	2.92	2.00	16.22
1HGI.PDB	OE2, B_GLU_120	NH1, B_ARG_123	HH11, B_ARG_123	2.84	1.97	25.22
1HGI.PDB	O, B_GLU_120	N, B_ARG_124	H, B_ARG_124	2.91	1.93	5.01
1HGI.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.81	1.96	23.50
1HGI.PDB	OE2, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.86	2.02	24.92
1HGI.PDB	O, B_LEU_126	N, B_ASN_129	H, B_ASN_129	2.99	2.06	15.00
1HGI.PDB	O, B_HIS_159	ND2, B_ASN_129	HD21, B_ASN_129	3.00	2.06	13.30
1HGI.PDB	OH, B_TYR_157	ND2, B_ASN_129	HD22, B_ASN_129	2.81	1.86	9.72
1HGI.PDB	O, B_LYS_139	N, B_GLU_131	H, B_GLU_131	2.91	1.98	14.55
1HGI.PDB	O, B_CYS_137	N, B_MET_133	H, B_MET_133	2.81	1.88	13.30
1HGI.PDB	O, A_LEU_13	N, B_PHE_138	H, B_PHE_138	2.74	1.89	23.78
1HGI.PDB	O, B_GLU_131	N, B_LYS_139	H, B_LYS_139	2.82	1.86	8.55
1HGI.PDB	O, A_ALA_11	N, B_ILE_140	H, B_ILE_140	2.77	1.87	18.46
1HGI.PDB	O, B_ASN_129	N, B_TYR_141	H, B_TYR_141	2.82	1.85	4.69
1HGI.PDB	OE2, B_GLU_165	N, B_LYS_143	H, B_LYS_143	2.87	1.93	14.38
1HGI.PDB	OE1, B_GLU_30	N, B_ASN_146	H, B_ASN_146	2.95	2.07	23.02
1HGI.PDB	O, B_ASP_145	N, B_ILE_149	H, B_ILE_149	2.90	1.94	7.96
1HGI.PDB	O, B_ASN_146	N, B_GLU_150	H, B_GLU_150	2.83	1.92	17.44
1HGI.PDB	O, B_ALA_147	N, B_SER_151	H, B_SER_151	2.90	2.01	20.08
1HGI.PDB	O, B_CYS_148	OG, B_SER_151	HG, B_SER_151	2.68	1.84	23.42
1HGI.PDB	O, B_GLU_150	N, B_ASN_154	H, B_ASN_154	2.81	1.83	1.94
1HGI.PDB	OE2, B_GLU_150	ND2, B_ASN_154	HD21, B_ASN_154	2.84	2.01	27.47
1HGI.PDB	O, B_SER_151	N, B_THR_156	H, B_THR_156	2.77	1.94	25.73
1HGI.PDB	OD1, B_ASN_154	OG1, B_THR_156	HG1, B_THR_156	2.64	1.78	21.15

1HGI.PDB	O, B_HIS_159	N, B_TYR_162	H, B_TYR_162	2.88	2.01	22.48
1HGI.PDB	O, F_ARG_170	NH1, B_ARG_163	HH12, B_ARG_163	2.73	1.76	13.86
1HGI.PDB	O, B_TYR_162	N, B_ALA_166	H, B_ALA_166	2.86	1.88	1.82
1HGI.PDB	O, B_ARG_163	N, B_LEU_167	H, B_LEU_167	2.77	1.81	5.67
1HGI.PDB	O, B_ALA_166	N, B_ARG_170	H, B_ARG_170	2.78	1.90	21.33
1HGI.PDB	O, B_GLU_128	NE, B_ARG_170	HE, B_ARG_170	2.72	1.88	25.72
1HGI.PDB	OE2, B_GLU_131	NH1, B_ARG_170	HH11, B_ARG_170	2.77	1.77	6.54
1HGI.PDB	O, B_LEU_167	N, B_PHE_171	H, B_PHE_171	2.90	1.96	12.85
1HGI.PDB	O, D_ILE_140	N, C_ALA_11	H, C_ALA_11	2.86	1.93	15.33
1HGI.PDB	O, D_GLN_27	N, C_THR_12	H, C_THR_12	2.98	2.01	4.69
1HGI.PDB	O, D_PHE_138	N, C_LEU_13	H, C_LEU_13	2.99	2.03	9.93
1HGI.PDB	O, D_ARG_25	N, C_CYS_14	H, C_CYS_14	2.67	1.83	24.75
1HGI.PDB	O, D_GLY_136	N, C_LEU_15	H, C_LEU_15	2.95	1.98	7.51
1HGI.PDB	O, D_GLY_23	N, C_GLY_16	H, C_GLY_16	2.99	2.12	22.96
1HGI.PDB	O, C_HIS_18	ND1, C_HIS_17	HD1, C_HIS_17	2.96	2.07	20.32
1HGI.PDB	O, D_TRP_21	N, C_HIS_18	H, C_HIS_18	2.88	1.97	18.12
1HGI.PDB	OD1, C_ASN_322	N, C_VAL_20	H, C_VAL_20	2.78	1.82	9.40
1HGI.PDB	O, C_VAL_36	N, C_THR_24	H, C_THR_24	2.85	1.90	11.53
1HGI.PDB	O, C_ILE_34	N, C_VAL_26	H, C_VAL_26	2.78	1.84	11.07
1HGI.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.88	1.83	6.58
1HGI.PDB	O, C_ASP_31	N, C_THR_28	H, C_THR_28	2.76	1.94	27.36
1HGI.PDB	O, C_VAL_26	N, C_ILE_34	H, C_ILE_34	2.92	2.01	18.98
1HGI.PDB	O, C_THR_24	N, C_VAL_36	H, C_VAL_36	2.78	1.82	7.09
1HGI.PDB	O, C_MET_320	N, C_THR_37	H, C_THR_37	2.89	1.92	7.75
1HGI.PDB	O, C_LEU_316	N, C_THR_40	H, C_THR_40	2.92	2.04	21.59
1HGI.PDB	O, C_LEU_314	N, C_LEU_42	H, C_LEU_42	2.81	1.95	23.61
1HGI.PDB	OE2, C_GLU_41	N, C_VAL_43	H, C_VAL_43	2.99	2.05	14.73
1HGI.PDB	O, C_PHE_294	N, C_GLN_44	H, C_GLN_44	2.82	1.86	6.96
1HGI.PDB	O, C_SER_46	NE2, C_GLN_44	HE22, C_GLN_44	2.83	2.00	26.47
1HGI.PDB	O, C_ASN_285	OG, C_SER_47	HG, C_SER_47	2.79	1.92	20.46
1HGI.PDB	OD2, C_ASP_275	NZ, C_LYS_50	HZ1, C_LYS_50	2.68	1.77	23.91
1HGI.PDB	O, C_PRO_273	N, C_ILE_51	H, C_ILE_51	2.79	1.84	11.72
1HGI.PDB	O, C_ASP_275	N, C_ASN_53	H, C_ASN_53	2.84	1.98	23.59
1HGI.PDB	O, C_GLU_280	NE2, C_HIS_56	HE2, C_HIS_56	3.00	2.06	15.07
1HGI.PDB	OD2, C_ASP_85	N, C_ARG_57	H, C_ARG_57	2.85	1.91	11.94
1HGI.PDB	O, C_THR_83	NE, C_ARG_57	HE, C_ARG_57	2.81	1.84	5.65
1HGI.PDB	O, C_LEU_86	N, C_LEU_59	H, C_LEU_59	2.86	1.90	10.05
1HGI.PDB	O, C_VAL_88	N, C_GLY_61	H, C_GLY_61	2.94	2.11	25.94
1HGI.PDB	OD1, C_ASP_60	N, C_ILE_62	H, C_ILE_62	2.85	1.91	12.59
1HGI.PDB	O, C_GLY_61	N, C_CYS_64	H, C_CYS_64	2.89	1.99	19.13
1HGI.PDB	O, C_LEU_66	N, C_LEU_70	H, C_LEU_70	2.83	1.94	20.67
1HGI.PDB	O, C_ILE_67	N, C_LEU_71	H, C_LEU_71	2.84	1.87	6.00
1HGI.PDB	O, C_ASP_68	N, C_GLY_72	H, C_GLY_72	2.79	1.85	12.61
1HGI.PDB	OD1, C_ASP_73	ND1, C_HIS_75	HD1, C_HIS_75	2.88	1.94	15.46
1HGI.PDB	O, C_ASP_63	NE2, C_HIS_75	HE2, C_HIS_75	2.82	1.88	14.02
1HGI.PDB	O, C_ASP_73	N, C_CYS_76	H, C_CYS_76	2.75	1.84	16.01
1HGI.PDB	O, C_PRO_74	N, C_ASP_77	H, C_ASP_77	2.91	1.96	10.58
1HGI.PDB	O, C_CYS_76	N, C_PHE_79	H, C_PHE_79	2.94	1.96	2.92
1HGI.PDB	OE1, C_GLU_82	N, C_THR_83	H, C_THR_83	2.93	2.02	17.21
1HGI.PDB	O, C_ARG_57	N, C_ASP_85	H, C_ASP_85	2.81	1.91	18.21
1HGI.PDB	O, C_MET_268	N, C_GLU_89	H, C_GLU_89	2.80	1.84	7.26
1HGI.PDB	OD1, C_ASP_60	NE, C_ARG_90	HE, C_ARG_90	2.83	1.88	11.13
1HGI.PDB	O, C_SER_270	NH1, C_ARG_90	HH11, C_ARG_90	2.67	1.81	25.47
1HGI.PDB	O, C_ALA_272	NH1, C_ARG_90	HH12, C_ARG_90	2.60	1.70	21.36
1HGI.PDB	OD2, C_ASP_60	NH2, C_ARG_90	HH21, C_ARG_90	2.77	1.79	11.02
1HGI.PDB	OD1, C_ASP_271	N, C_SER_91	H, C_SER_91	2.90	1.94	8.90
1HGI.PDB	OD1, C_ASP_271	OG, C_SER_91	HG, C_SER_91	2.95	2.13	27.22
1HGI.PDB	OD2, C_ASP_271	OG, C_SER_91	HG, C_SER_91	2.83	1.94	19.64

1HGI.PDB	OD2, C_ASP_68	OG, C_SER_95	HG, C_SER_95	2.89	1.96	14.85
1HGI.PDB	OD2, C_ASP_73	N, C_ASN_96	H, C_ASN_96	2.88	1.93	14.25
1HGI.PDB	OD1, C_ASP_68	OH, C_TYR_100	HH, C_TYR_100	2.94	1.99	10.92
1HGI.PDB	OD2, C_ASP_104	OG, C_SER_107	HG, C_SER_107	2.90	1.96	13.90
1HGI.PDB	O, C_TYR_105	N, C_ARG_109	H, C_ARG_109	2.86	1.89	3.57
1HGI.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.82	1.84	15.02
1HGI.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.85	1.90	11.29
1HGI.PDB	O, C_SER_107	N, C_LEU_111	H, C_LEU_111	2.85	1.89	7.56
1HGI.PDB	O, C_LEU_108	N, C_VAL_112	H, C_VAL_112	3.00	2.02	3.49
1HGI.PDB	O, C_ARG_109	N, C_ALA_113	H, C_ALA_113	2.96	2.06	18.71
1HGI.PDB	O, C_SER_110	N, C_SER_114	H, C_SER_114	2.95	2.00	13.25
1HGI.PDB	OE2, C_GLU_119	OG1, C_THR_117	HG1, C_THR_117	2.95	2.03	14.67
1HGI.PDB	O, C_GLU_82	N, C_LEU_118	H, C_LEU_118	2.88	1.95	16.18
1HGI.PDB	O, C_TYR_257	N, C_ILE_121	H, C_ILE_121	2.94	1.97	6.04
1HGI.PDB	O, C_ARG_255	N, C_GLU_123	H, C_GLU_123	2.89	1.94	11.68
1HGI.PDB	O, C_THR_155	N, C_THR_131	H, C_THR_131	2.76	1.87	19.24
1HGI.PDB	OD1, C_ASN_152	N, C_ASN_133	H, C_ASN_133	2.83	1.91	16.95
1HGI.PDB	O, C_GLY_146	N, C_SER_136	H, C_SER_136	2.76	1.88	20.67
1HGI.PDB	OG, C_SER_136	N, C_ALA_138	H, C_ALA_138	2.86	1.95	18.03
1HGI.PDB	O, C_GLY_144	NZ, C_LYS_140	HZ1, C_LYS_140	2.86	1.89	16.83
1HGI.PDB	OD1, C_ASN_137	NZ, C_LYS_140	HZ2, C_LYS_140	2.83	1.83	12.62
1HGI.PDB	OD2, C_ASP_77	NE, C_ARG_141	HE, C_ARG_141	2.83	2.02	29.40
1HGI.PDB	O, C_PHE_147	NH1, C_ARG_141	HH12, C_ARG_141	2.56	1.65	20.19
1HGI.PDB	OD1, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.93	2.01	20.50
1HGI.PDB	OD2, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.70	1.83	25.10
1HGI.PDB	O, C_GLY_72	NH2, C_ARG_141	HH22, C_ARG_141	2.97	1.99	9.60
1HGI.PDB	O, C_SER_136	N, C_GLY_146	H, C_GLY_146	2.99	2.05	14.57
1HGI.PDB	O, C_GLY_72	N, C_SER_149	H, C_SER_149	2.90	1.97	15.40
1HGI.PDB	O, C_ALA_253	N, C_ASN_152	H, C_ASN_152	2.73	1.88	24.43
1HGI.PDB	OH, C_TYR_195	NE1, C_TRP_153	HE1, C_TRP_153	2.82	1.96	22.98
1HGI.PDB	O, C_LEU_194	N, C_LYS_156	H, C_LYS_156	2.88	1.99	20.12
1HGI.PDB	O, C_THR_160	N, C_SER_157	H, C_SER_157	2.87	1.98	19.55
1HGI.PDB	O, C_SER_247	N, C_LEU_164	H, C_LEU_164	2.73	1.90	26.15
1HGI.PDB	O, C_ILE_245	N, C_VAL_166	H, C_VAL_166	2.88	1.93	12.15
1HGI.PDB	O, C_LEU_243	OG1, C_THR_167	HG1, C_THR_167	2.85	1.95	18.23
1HGI.PDB	O, C_LEU_243	N, C_MET_168	H, C_MET_168	2.97	2.05	16.15
1HGI.PDB	O, C_ASP_241	N, C_ASN_170	H, C_ASN_170	2.92	1.94	4.90
1HGI.PDB	O, C_PHE_174	ND2, C_ASN_170	HD21, C_ASN_170	2.83	1.88	12.32
1HGI.PDB	O, C_VAL_237	ND2, C_ASN_170	HD22, C_ASN_170	2.96	2.10	24.31
1HGI.PDB	O, C_VAL_237	N, C_LYS_176	H, C_LYS_176	2.94	2.00	13.35
1HGI.PDB	OE2, C_GLU_123	NZ, C_LYS_176	HZ1, C_LYS_176	2.68	1.80	26.11
1HGI.PDB	O, C_PHE_258	N, C_LEU_177	H, C_LEU_177	2.96	1.99	8.81
1HGI.PDB	O, C_THR_235	N, C_TYR_178	H, C_TYR_178	2.82	1.85	3.86
1HGI.PDB	OE1, C_GLU_123	OH, C_TYR_178	HH, C_TYR_178	2.75	1.80	7.25
1HGI.PDB	OG1, C_THR_235	NE1, C_TRP_180	HE1, C_TRP_180	2.84	1.86	3.22
1HGI.PDB	O, C_ILE_252	N, C_GLY_181	H, C_GLY_181	2.98	2.16	27.47
1HGI.PDB	O, C_ASN_250	N, C_HIS_183	H, C_HIS_183	2.91	2.02	20.05
1HGI.PDB	O, C_ARG_229	N, C_HIS_184	H, C_HIS_184	2.89	1.92	8.40
1HGI.PDB	OG, C_SER_231	NE2, C_HIS_184	HE2, C_HIS_184	2.81	1.93	22.34
1HGI.PDB	OE1, C_GLU_190	N, C_SER_186	H, C_SER_186	3.00	2.10	20.23
1HGI.PDB	OD1, C_ASN_250	NE2, C_GLN_191	HE21, C_GLN_191	2.86	1.91	10.94
1HGI.PDB	O, C_GLN_197	NE2, C_GLN_191	HE22, C_GLN_191	2.97	2.02	11.67
1HGI.PDB	O, C_ASN_188	N, C_THR_192	H, C_THR_192	2.98	2.00	5.60
1HGI.PDB	O, C_GLN_189	OG1, C_THR_192	HG1, C_THR_192	2.81	1.90	15.34
1HGI.PDB	O, C_GLN_189	N, C_SER_193	H, C_SER_193	2.84	1.90	13.29
1HGI.PDB	O, C_GLN_191	N, C_TYR_195	H, C_TYR_195	2.76	1.80	7.13
1HGI.PDB	O, C_TYR_161	NE2, C_GLN_197	HE21, C_GLN_197	2.96	2.01	11.19
1HGI.PDB	O, C_ASN_248	NE2, C_GLN_197	HE22, C_GLN_197	2.92	2.02	18.87

1HGI.PDB	OD1, C_ASN_246	NH2, C_ARG_201	HH21, C_ARG_201	2.55	1.72	27.61
1HGI.PDB	O, C_ILE_213	N, C_VAL_202	H, C_VAL_202	2.94	1.98	9.08
1HGI.PDB	O, C_ASN_246	N, C_THR_203	H, C_THR_203	2.86	1.89	7.88
1HGI.PDB	OG1, C_THR_212	OG1, C_THR_203	HG1, C_THR_203	2.94	2.00	11.06
1HGI.PDB	O, C_GLN_211	N, C_VAL_204	H, C_VAL_204	2.84	1.92	15.35
1HGI.PDB	O, C_VAL_244	N, C_SER_205	H, C_SER_205	2.96	2.05	17.13
1HGI.PDB	O, C_SER_209	N, C_THR_206	H, C_THR_206	2.90	1.93	7.31
1HGI.PDB	OD1, C_ASP_241	N, C_ARG_207	H, C_ARG_207	2.90	1.95	10.96
1HGI.PDB	OD2, C_ASP_241	NE, C_ARG_208	HE, C_ARG_208	2.92	2.01	19.66
1HGI.PDB	O, C_VAL_204	N, C_GLN_211	H, C_GLN_211	2.87	1.93	14.30
1HGI.PDB	O, C_VAL_202	N, C_ILE_213	H, C_ILE_213	2.82	1.89	14.72
1HGI.PDB	O, C_ASN_216	NH1, C_ARG_220	HH12, C_ARG_220	2.89	2.08	29.98
1HGI.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.62	1.75	23.70
1HGI.PDB	O, C_ASN_216	NH2, C_ARG_220	HH22, C_ARG_220	2.69	1.79	20.70
1HGI.PDB	O, C_LEU_226	N, C_VAL_223	H, C_VAL_223	2.85	1.88	6.86
1HGI.PDB	O, C_CYS_97	NE, C_ARG_224	HE, C_ARG_224	2.75	1.92	26.67
1HGI.PDB	O, C_CYS_97	NH2, C_ARG_224	HH21, C_ARG_224	2.83	1.98	26.45
1HGI.PDB	O, C_VAL_223	N, C_LEU_226	H, C_LEU_226	2.94	2.02	16.27
1HGI.PDB	O, C_SER_228	NH1, C_ARG_229	HH11, C_ARG_229	2.65	1.73	19.05
1HGI.PDB	O, C_PRO_221	NH2, C_ARG_229	HH22, C_ARG_229	2.65	1.69	14.06
1HGI.PDB	OD1, C_ASP_101	OG, C_SER_231	HG, C_SER_231	2.97	2.02	12.14
1HGI.PDB	O, C_ASP_101	N, C_ILE_232	H, C_ILE_232	2.92	1.98	14.17
1HGI.PDB	O, C_TRP_180	N, C_TYR_233	H, C_TYR_233	2.88	1.92	9.12
1HGI.PDB	O, C_TYR_178	N, C_THR_235	H, C_THR_235	2.81	1.91	19.71
1HGI.PDB	O, C_LYS_176	N, C_VAL_237	H, C_VAL_237	2.80	1.87	14.88
1HGI.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.67	1.77	23.68
1HGI.PDB	O, B_SER_71	NZ, C_LYS_238	HZ3, C_LYS_238	2.57	1.73	28.43
1HGI.PDB	O, C_ASN_170	N, C_GLY_240	H, C_GLY_240	2.88	2.03	25.25
1HGI.PDB	OD1, C_ASP_241	N, C_VAL_242	H, C_VAL_242	2.77	1.97	28.83
1HGI.PDB	O, C_MET_168	N, C_LEU_243	H, C_LEU_243	2.92	1.95	6.19
1HGI.PDB	O, C_SER_205	N, C_VAL_244	H, C_VAL_244	2.97	2.02	12.13
1HGI.PDB	O, C_VAL_166	N, C_ILE_245	H, C_ILE_245	2.97	2.04	14.87
1HGI.PDB	O, C_THR_203	N, C_ASN_246	H, C_ASN_246	2.85	1.92	14.46
1HGI.PDB	O, C_LEU_164	N, C_SER_247	H, C_SER_247	2.86	1.95	18.44
1HGI.PDB	O, C_ARG_201	OG, C_SER_247	HG, C_SER_247	2.81	2.01	28.50
1HGI.PDB	OE1, C_GLN_191	ND2, C_ASN_250	HD21, C_ASN_250	2.87	1.92	11.00
1HGI.PDB	O, C_HIS_183	ND2, C_ASN_250	HD22, C_ASN_250	2.85	1.88	5.75
1HGI.PDB	O, C_ASN_152	N, C_ALA_253	H, C_ALA_253	2.82	1.96	22.89
1HGI.PDB	O, C_ILE_121	N, C_TYR_257	H, C_TYR_257	2.97	2.10	23.39
1HGI.PDB	O, C_LEU_177	N, C_PHE_258	H, C_PHE_258	2.92	1.96	9.71
1HGI.PDB	OE2, C_GLU_119	NH1, C_ARG_261	HH12, C_ARG_261	2.66	1.84	29.01
1HGI.PDB	OE1, C_GLU_119	NH2, C_ARG_261	HH22, C_ARG_261	2.84	1.99	27.78
1HGI.PDB	OD2, C_ASP_85	NZ, C_LYS_264	HZ3, C_LYS_264	2.83	1.86	17.28
1HGI.PDB	O, C_PHE_87	N, C_MET_268	H, C_MET_268	2.86	1.97	20.48
1HGI.PDB	O, C_PRO_284	OG, C_SER_270	HG, C_SER_270	2.81	1.86	9.17
1HGI.PDB	OG, C_SER_270	N, C_ALA_272	H, C_ALA_272	2.97	2.03	11.96
1HGI.PDB	O, C_ILE_51	N, C_ASP_275	H, C_ASP_275	2.97	2.06	19.21
1HGI.PDB	OD1, C_ASP_275	N, C_THR_276	H, C_THR_276	2.80	1.96	24.61
1HGI.PDB	O, C_ASN_54	N, C_SER_279	H, C_SER_279	2.76	1.83	13.77
1HGI.PDB	O, C_TYR_302	N, C_ILE_282	H, C_ILE_282	2.89	1.93	9.00
1HGI.PDB	O, C_THR_283	N, C_GLY_286	H, C_GLY_286	2.81	1.89	16.23
1HGI.PDB	O, C_LYS_50	N, C_SER_287	H, C_SER_287	2.84	1.87	3.21
1HGI.PDB	O, C_ALA_304	ND2, C_ASN_290	HD22, C_ASN_290	2.76	1.88	20.58
1HGI.PDB	OE1, C_GLN_44	NZ, C_LYS_292	HZ1, C_LYS_292	2.75	1.75	12.02
1HGI.PDB	OD2, C_ASP_291	NZ, C_LYS_292	HZ3, C_LYS_292	2.82	1.90	23.36
1HGI.PDB	O, C_LYS_307	N, C_GLN_295	H, C_GLN_295	2.80	1.92	20.79
1HGI.PDB	O, C_ASN_298	NE2, C_GLN_295	HE21, C_GLN_295	2.79	1.83	9.85
1HGI.PDB	O, C_GLN_44	N, C_ASN_296	H, C_ASN_296	2.86	1.93	14.90

1HGI.PDB	OE1, C_GLN_295	N, C_VAL_297	H, C_VAL_297	2.80	1.98	27.59
1HGI.PDB	OD1, C_ASN_285	ND2, C_ASN_298	HD22, C_ASN_298	3.00	2.03	7.73
1HGI.PDB	OD1, C_ASN_298	N, C_ILE_300	H, C_ILE_300	2.91	2.01	18.61
1HGI.PDB	O, C_ILE_282	N, C_TYR_302	H, C_TYR_302	2.94	2.06	21.76
1HGI.PDB	O, C_LYS_264	OH, C_TYR_302	HH, C_TYR_302	2.75	1.95	27.81
1HGI.PDB	O, D_LYS_62	N, C_GLY_303	H, C_GLY_303	2.97	2.00	7.92
1HGI.PDB	O, C_PRO_293	N, C_LYS_307	H, C_LYS_307	2.99	2.03	8.70
1HGI.PDB	O, C_GLN_295	N, C_VAL_309	H, C_VAL_309	2.93	2.08	24.45
1HGI.PDB	OD1, D_ASP_86	NZ, C_LYS_310	HZ3, C_LYS_310	2.77	1.93	29.51
1HGI.PDB	OE2, C_GLU_41	N, C_LEU_314	H, C_LEU_314	2.83	1.87	8.52
1HGI.PDB	OE1, C_GLU_41	NZ, C_LYS_315	HZ3, C_LYS_315	2.75	1.80	20.43
1HGI.PDB	O, C_THR_40	N, C_LEU_316	H, C_LEU_316	2.83	1.90	15.29
1HGI.PDB	OD1, D_ASN_104	N, C_ALA_317	H, C_ALA_317	2.74	1.83	16.29
1HGI.PDB	O, C_ASN_38	N, C_THR_318	H, C_THR_318	2.87	1.98	20.30
1HGI.PDB	O, C_VAL_20	ND2, C_ASN_322	HD21, C_ASN_322	2.87	1.94	14.86
1HGI.PDB	OE2, C_GLU_35	ND2, C_ASN_322	HD22, C_ASN_322	2.90	1.95	11.70
1HGI.PDB	OE1, D_GLU_15	NZ, C_LYS_326	HZ1, C_LYS_326	2.83	1.84	16.25
1HGI.PDB	OD2, D_ASP_112	N, D_GLY_1	H1, D_GLY_1	2.77	1.76	11.64
1HGI.PDB	OD1, D_ASP_109	N, D_LEU_2	H, D_LEU_2	2.92	1.97	13.20
1HGI.PDB	OD2, D_ASP_112	N, D_PHE_3	H, D_PHE_3	2.88	2.06	26.84
1HGI.PDB	OD2, D_ASP_112	N, D_GLY_4	H, D_GLY_4	2.95	2.06	19.72
1HGI.PDB	OD1, D_ASP_112	N, D_ALA_5	H, D_ALA_5	2.82	1.91	16.74
1HGI.PDB	O, D_GLY_4	N, D_PHE_9	H, D_PHE_9	2.83	1.89	12.42
1HGI.PDB	O, D_GLY_13	ND2, D_ASN_12	HD22, D_ASN_12	2.80	1.89	16.05
1HGI.PDB	O, C_VAL_323	N, D_GLY_13	H, D_GLY_13	2.65	1.77	19.23
1HGI.PDB	O, C_HIS_17	N, D_TRP_14	H, D_TRP_14	2.83	1.92	16.86
1HGI.PDB	OG1, D_THR_41	N, D_TRP_21	H, D_TRP_21	2.98	2.14	26.03
1HGI.PDB	O, C_GLY_16	N, D_GLY_23	H, D_GLY_23	2.94	2.02	16.89
1HGI.PDB	O, D_ALA_35	N, D_PHE_24	H, D_PHE_24	2.82	1.86	6.63
1HGI.PDB	O, C_CYS_14	N, D_ARG_25	H, D_ARG_25	2.88	1.94	13.44
1HGI.PDB	OE1, D_GLN_34	NE, D_ARG_25	HE, D_ARG_25	2.62	1.78	23.70
1HGI.PDB	O, D_GLY_33	N, D_HIS_26	H, D_HIS_26	2.88	1.93	11.28
1HGI.PDB	O, C_THR_12	N, D_GLN_27	H, D_GLN_27	2.95	2.00	13.47
1HGI.PDB	O, D_GLY_31	N, D_ASN_28	H, D_ASN_28	2.97	2.06	18.59
1HGI.PDB	OD1, D_ASN_146	ND2, D_ASN_28	HD21, D_ASN_28	2.93	1.98	12.39
1HGI.PDB	OD1, D_ASN_28	N, D_GLU_30	H, D_GLU_30	2.83	1.95	21.69
1HGI.PDB	O, D_HIS_26	N, D_GLY_33	H, D_GLY_33	2.99	2.10	20.01
1HGI.PDB	O, D_PHE_24	N, D_ALA_35	H, D_ALA_35	2.80	1.98	27.73
1HGI.PDB	O, D_TYR_22	N, D_ASP_37	H, D_ASP_37	2.72	1.78	11.42
1HGI.PDB	OD2, D_ASP_37	N, D_SER_40	H, D_SER_40	2.89	1.92	6.59
1HGI.PDB	OD2, D_ASP_37	OG, D_SER_40	HG, D_SER_40	2.78	1.93	23.19
1HGI.PDB	O, D_ASP_37	OG1, D_THR_41	HG1, D_THR_41	2.73	1.82	16.18
1HGI.PDB	OD1, D_ASP_46	NE2, D_GLN_42	HE22, D_GLN_42	2.88	2.01	23.38
1HGI.PDB	O, D_SER_40	N, D_ALA_44	H, D_ALA_44	2.93	1.95	3.19
1HGI.PDB	O, D_THR_41	N, D_ILE_45	H, D_ILE_45	2.97	2.03	13.52
1HGI.PDB	O, D_GLN_42	N, D_ASP_46	H, D_ASP_46	2.71	1.76	6.20
1HGI.PDB	O, D_ALA_43	NE2, D_GLN_47	HE22, D_GLN_47	2.88	1.96	16.19
1HGI.PDB	O, D_ILE_45	N, D_ASN_49	H, D_ASN_49	2.89	1.98	17.77
1HGI.PDB	O, D_ASP_46	N, D_GLY_50	H, D_GLY_50	2.98	2.04	15.66
1HGI.PDB	O, D_GLN_47	N, D_LYS_51	H, D_LYS_51	2.98	2.01	5.63
1HGI.PDB	OE1, D_GLU_103	NZ, D_LYS_51	HZ2, D_LYS_51	2.81	1.77	5.89
1HGI.PDB	ND1, D_HIS_106	NZ, D_LYS_51	HZ3, D_LYS_51	2.78	1.83	18.78
1HGI.PDB	O, D_ILE_48	N, D_LEU_52	H, D_LEU_52	2.93	2.01	16.44
1HGI.PDB	O, D_ASN_49	N, D_ASN_53	H, D_ASN_53	2.77	1.91	22.51
1HGI.PDB	O, A_THR_28	NE, D_ARG_54	HE, D_ARG_54	2.83	1.87	10.21
1HGI.PDB	OE1, D_GLU_57	NH1, D_ARG_54	HH11, D_ARG_54	2.85	1.86	11.80
1HGI.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.81	1.85	15.40
1HGI.PDB	OE2, D_GLU_61	NZ, D_LYS_58	HZ2, D_LYS_58	3.00	2.01	17.14

1HGI.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.83	1.85	2.78
1HGI.PDB	O, D_PHE_63	NE2, D_GLN_65	HE22, D_GLN_65	2.98	2.00	3.57
1HGI.PDB	O, C_LYS_299	NZ, D_LYS_68	HZ1, D_LYS_68	2.79	1.78	10.55
1HGI.PDB	OE2, D_GLU_85	NZ, D_LYS_68	HZ2, D_LYS_68	2.81	1.76	2.16
1HGI.PDB	OG, E_SER_107	N, D_ARG_76	H, D_ARG_76	2.89	1.92	9.17
1HGI.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.80	1.82	5.40
1HGI.PDB	OE2, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.78	1.76	4.18
1HGI.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.61	1.67	15.38
1HGI.PDB	OE1, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.76	1.77	8.75
1HGI.PDB	O, D_GLU_72	NE2, D_GLN_78	HE21, D_GLN_78	2.97	2.00	4.85
1HGI.PDB	OE1, D_GLU_74	NE2, D_GLN_78	HE22, D_GLN_78	2.92	1.95	8.47
1HGI.PDB	O, D_ASP_79	N, D_TYR_83	H, D_TYR_83	2.89	2.00	19.78
1HGI.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.69	1.81	20.41
1HGI.PDB	O, D_LEU_80	N, D_VAL_84	H, D_VAL_84	2.72	1.83	17.89
1HGI.PDB	O, D_LYS_82	N, D_ASP_86	H, D_ASP_86	2.90	1.94	8.30
1HGI.PDB	O, D_TYR_83	N, D_THR_87	H, D_THR_87	2.92	1.96	7.87
1HGI.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.66	1.64	7.30
1HGI.PDB	O, D_GLU_85	N, D_ILE_89	H, D_ILE_89	2.88	1.92	10.07
1HGI.PDB	O, D_ASP_86	N, D_ASP_90	H, D_ASP_90	2.97	2.00	6.24
1HGI.PDB	O, D_LYS_88	N, D_TRP_92	H, D_TRP_92	2.97	2.00	6.54
1HGI.PDB	O, D_ILE_89	N, D_SER_93	H, D_SER_93	2.87	1.94	14.13
1HGI.PDB	O, D_ILE_89	OG, D_SER_93	HG, D_SER_93	2.80	1.92	19.66
1HGI.PDB	O, D_ASP_90	N, D_TYR_94	H, D_TYR_94	2.93	2.00	16.49
1HGI.PDB	O, D_TRP_92	N, D_ALA_96	H, D_ALA_96	2.93	1.97	9.70
1HGI.PDB	O, D_TYR_94	N, D_LEU_98	H, D_LEU_98	2.90	1.94	9.34
1HGI.PDB	O, D_ASN_95	N, D_LEU_99	H, D_LEU_99	2.84	1.96	21.05
1HGI.PDB	O, D_LEU_98	N, D_LEU_102	H, D_LEU_102	2.99	2.02	4.46
1HGI.PDB	O, D_LEU_99	N, D_GLU_103	H, D_GLU_103	2.97	2.00	7.39
1HGI.PDB	O, D_VAL_100	N, D_ASN_104	H, D_ASN_104	2.87	1.91	10.16
1HGI.PDB	O, C_LYS_27	ND2, D_ASN_104	HD22, D_ASN_104	2.83	1.88	11.60
1HGI.PDB	O, D_LEU_102	N, D_HIS_106	H, D_HIS_106	2.93	2.00	15.62
1HGI.PDB	O, D_GLU_103	N, D_THR_107	H, D_THR_107	2.78	1.91	22.01
1HGI.PDB	O, D_ASN_104	N, D_ILE_108	H, D_ILE_108	2.95	2.00	10.44
1HGI.PDB	O, D_HIS_106	N, D_LEU_110	H, D_LEU_110	2.81	1.86	10.24
1HGI.PDB	O, D_THR_107	OG1, D_THR_111	HG1, D_THR_111	2.94	1.97	4.08
1HGI.PDB	O, D_ASP_109	N, D_SER_113	H, D_SER_113	2.82	1.87	9.43
1HGI.PDB	O, B_LEU_2	OG, D_SER_113	HG, D_SER_113	2.77	1.91	22.96
1HGI.PDB	O, D_LEU_110	N, D_GLU_114	H, D_GLU_114	2.96	2.00	9.06
1HGI.PDB	O, D_ASP_112	N, D_ASN_116	H, D_ASN_116	2.95	2.00	13.00
1HGI.PDB	O, D_SER_113	N, D_LYS_117	H, D_LYS_117	2.70	1.83	21.74
1HGI.PDB	O, D_ASN_116	N, D_GLU_120	H, D_GLU_120	2.92	1.95	4.03
1HGI.PDB	O, D_LYS_117	N, D_LYS_121	H, D_LYS_121	2.93	2.00	15.48
1HGI.PDB	OE2, D_GLU_120	NH1, D_ARG_123	HH11, D_ARG_123	2.83	1.97	25.69
1HGI.PDB	O, D_GLU_120	N, D_ARG_124	H, D_ARG_124	2.93	1.95	3.12
1HGI.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.84	1.98	23.95
1HGI.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.88	2.03	24.96
1HGI.PDB	O, D_LEU_126	N, D_ASN_129	H, D_ASN_129	3.00	2.06	14.34
1HGI.PDB	O, D_HIS_159	ND2, D_ASN_129	HD21, D_ASN_129	2.99	2.04	12.91
1HGI.PDB	OH, D_TYR_157	ND2, D_ASN_129	HD22, D_ASN_129	2.81	1.84	5.40
1HGI.PDB	O, D_LYS_139	N, D_GLU_131	H, D_GLU_131	2.93	2.00	14.77
1HGI.PDB	O, D_CYS_137	N, D_MET_133	H, D_MET_133	2.81	1.87	12.15
1HGI.PDB	OD1, D_ASN_135	N, D_CYS_137	H, D_CYS_137	2.87	1.99	20.31
1HGI.PDB	O, C_LEU_13	N, D_PHE_138	H, D_PHE_138	2.79	1.92	22.46
1HGI.PDB	O, D_GLU_131	N, D_LYS_139	H, D_LYS_139	2.79	1.84	9.37
1HGI.PDB	O, C_ALA_11	N, D_ILE_140	H, D_ILE_140	2.81	1.91	18.30
1HGI.PDB	O, D_ASN_129	N, D_TYR_141	H, D_TYR_141	2.85	1.88	4.18
1HGI.PDB	OE2, D_GLU_165	N, D_LYS_143	H, D_LYS_143	2.89	1.96	16.92
1HGI.PDB	OE2, D_GLU_30	N, D_ASN_146	H, D_ASN_146	2.90	1.95	12.47

1HGI.PDB	O, D_ASP_145	N, D_ILE_149	H, D_ILE_149	2.94	1.98	8.42
1HGI.PDB	O, D_ASN_146	N, D_GLU_150	H, D_GLU_150	2.83	1.93	18.07
1HGI.PDB	O, D_ALA_147	N, D_SER_151	H, D_SER_151	2.92	2.00	16.50
1HGI.PDB	O, D_CYS_148	OG, D_SER_151	HG, D_SER_151	2.71	1.85	21.05
1HGI.PDB	O, D_GLU_150	N, D_ASN_154	H, D_ASN_154	2.81	1.83	1.56
1HGI.PDB	O, D_SER_151	N, D_THR_156	H, D_THR_156	2.80	1.97	25.47
1HGI.PDB	OD1, D_ASN_154	OG1, D_THR_156	HG1, D_THR_156	2.68	1.79	17.62
1HGI.PDB	NE2, D_HIS_142	OH, D_TYR_157	HH, D_TYR_157	2.72	1.85	20.80
1HGI.PDB	O, D_HIS_159	N, D_TYR_162	H, D_TYR_162	2.90	2.02	21.56
1HGI.PDB	O, B_ARG_170	NH1, D_ARG_163	HH12, D_ARG_163	2.80	1.83	13.94
1HGI.PDB	O, D_TYR_162	N, D_ALA_166	H, D_ALA_166	2.86	1.89	1.04
1HGI.PDB	O, D_ARG_163	N, D_LEU_167	H, D_LEU_167	2.77	1.81	6.36
1HGI.PDB	O, D_ALA_166	N, D_ARG_170	H, D_ARG_170	2.80	1.93	22.25
1HGI.PDB	O, D_GLU_128	NE, D_ARG_170	HE, D_ARG_170	2.72	1.87	25.38
1HGI.PDB	OE2, D_GLU_131	NH1, D_ARG_170	HH11, D_ARG_170	2.77	1.78	6.80
1HGI.PDB	O, D_LEU_167	N, D_PHE_171	H, D_PHE_171	2.90	1.96	13.08
1HGI.PDB	O, F_ILE_140	N, E_ALA_11	H, E_ALA_11	2.89	1.95	14.83
1HGI.PDB	O, F_GLN_27	N, E_THR_12	H, E_THR_12	2.94	2.00	13.31
1HGI.PDB	O, F_PHE_138	N, E_LEU_13	H, E_LEU_13	2.97	2.02	11.46
1HGI.PDB	O, F_ARG_25	N, E_CYS_14	H, E_CYS_14	2.66	1.84	26.53
1HGI.PDB	O, F_GLY_136	N, E_LEU_15	H, E_LEU_15	2.92	1.95	6.28
1HGI.PDB	O, F_GLY_23	N, E_GLY_16	H, E_GLY_16	2.99	2.12	22.78
1HGI.PDB	O, E_HIS_18	ND1, E_HIS_17	HD1, E_HIS_17	2.91	2.01	19.98
1HGI.PDB	O, F_TRP_21	N, E_HIS_18	H, E_HIS_18	2.89	1.99	19.14
1HGI.PDB	OD1, E_ASN_322	N, E_VAL_20	H, E_VAL_20	2.75	1.81	12.01
1HGI.PDB	O, E_VAL_36	N, E_THR_24	H, E_THR_24	2.83	1.90	13.27
1HGI.PDB	O, E_ILE_34	N, E_VAL_26	H, E_VAL_26	2.80	1.85	10.53
1HGI.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.86	1.82	7.44
1HGI.PDB	O, E_ASP_31	N, E_THR_28	H, E_THR_28	2.81	2.00	28.11
1HGI.PDB	O, E_VAL_26	N, E_ILE_34	H, E_ILE_34	2.91	2.01	19.08
1HGI.PDB	O, E_THR_24	N, E_VAL_36	H, E_VAL_36	2.78	1.82	6.19
1HGI.PDB	O, E_MET_320	N, E_THR_37	H, E_THR_37	2.83	1.86	7.80
1HGI.PDB	O, E_LEU_316	N, E_THR_40	H, E_THR_40	2.86	1.98	21.93
1HGI.PDB	O, E_LEU_314	N, E_LEU_42	H, E_LEU_42	2.82	1.95	22.62
1HGI.PDB	O, E_PHE_294	N, E_GLN_44	H, E_GLN_44	2.83	1.86	6.11
1HGI.PDB	O, E_SER_46	NE2, E_GLN_44	HE22, E_GLN_44	2.78	1.97	27.44
1HGI.PDB	O, E_ASN_285	OG, E_SER_47	HG, E_SER_47	2.82	1.91	15.52
1HGI.PDB	OD2, E_ASP_275	NZ, E_LYS_50	HZ1, E_LYS_50	2.70	1.78	22.89
1HGI.PDB	O, E_PRO_273	N, E_ILE_51	H, E_ILE_51	2.78	1.83	10.95
1HGI.PDB	O, E_ASP_275	N, E_ASN_53	H, E_ASN_53	2.86	2.00	23.91
1HGI.PDB	O, E_GLU_280	NE2, E_HIS_56	HE2, E_HIS_56	3.00	2.06	15.06
1HGI.PDB	OD2, E_ASP_85	N, E_ARG_57	H, E_ARG_57	2.84	1.90	11.96
1HGI.PDB	O, E_THR_83	NE, E_ARG_57	HE, E_ARG_57	2.81	1.83	5.10
1HGI.PDB	O, E_LEU_86	N, E_LEU_59	H, E_LEU_59	2.85	1.89	9.90
1HGI.PDB	O, E_VAL_88	N, E_GLY_61	H, E_GLY_61	2.94	2.11	26.55
1HGI.PDB	OD1, E_ASP_60	N, E_ILE_62	H, E_ILE_62	2.85	1.91	12.99
1HGI.PDB	O, E_GLY_61	N, E_CYS_64	H, E_CYS_64	2.89	1.99	18.65
1HGI.PDB	OE2, E_GLU_89	N, E_LEU_66	H, E_LEU_66	2.99	2.04	13.34
1HGI.PDB	O, E_LEU_66	N, E_LEU_70	H, E_LEU_70	2.83	1.95	21.53
1HGI.PDB	O, E_ILE_67	N, E_LEU_71	H, E_LEU_71	2.87	1.90	5.23
1HGI.PDB	O, E_ASP_68	N, E_GLY_72	H, E_GLY_72	2.81	1.87	13.53
1HGI.PDB	OD1, E_ASP_73	ND1, E_HIS_75	HD1, E_HIS_75	2.87	1.94	15.26
1HGI.PDB	O, E_ASP_63	NE2, E_HIS_75	HE2, E_HIS_75	2.82	1.88	13.89
1HGI.PDB	O, E_ASP_73	N, E_CYS_76	H, E_CYS_76	2.75	1.83	16.25
1HGI.PDB	O, E_PRO_74	N, E_ASP_77	H, E_ASP_77	2.91	1.96	9.76
1HGI.PDB	O, E_CYS_76	N, E_PHE_79	H, E_PHE_79	2.93	1.96	3.56
1HGI.PDB	OE1, E_GLU_82	N, E_THR_83	H, E_THR_83	2.89	2.00	21.36
1HGI.PDB	O, E_ARG_57	N, E_ASP_85	H, E_ASP_85	2.76	1.87	19.11

1HGI.PDB	O, E_MET.268	N, E_GLU.89	H, E_GLU.89	2.77	1.81	7.27
1HGI.PDB	OD1, E_ASP.60	NE, E_ARG.90	HE, E_ARG.90	2.89	1.92	8.33
1HGI.PDB	O, E_SER.270	NH1, E_ARG.90	HH11, E_ARG.90	2.67	1.80	24.87
1HGI.PDB	O, E_ALA.272	NH1, E_ARG.90	HH12, E_ARG.90	2.58	1.69	21.42
1HGI.PDB	OD2, E_ASP.60	NH2, E_ARG.90	HH21, E_ARG.90	2.84	1.85	10.04
1HGI.PDB	OD1, E_ASP.271	N, E_SER.91	H, E_SER.91	2.90	1.95	11.41
1HGI.PDB	OD1, E_ASP.271	OG, E_SER.91	HG, E_SER.91	2.94	2.11	26.21
1HGI.PDB	OD2, E_ASP.271	OG, E_SER.91	HG, E_SER.91	2.82	1.93	20.43
1HGI.PDB	OD2, E_ASP.68	OG, E_SER.95	HG, E_SER.95	2.90	1.96	13.54
1HGI.PDB	OD2, E_ASP.73	N, E_ASN.96	H, E_ASN.96	2.90	1.96	13.19
1HGI.PDB	OD1, E_ASP.68	OH, E_TYR.100	HH, E_TYR.100	2.94	1.98	8.32
1HGI.PDB	OD2, E_ASP.104	OG, E_SER.107	HG, E_SER.107	2.91	1.98	14.52
1HGI.PDB	O, E_TYR.105	N, E_ARG.109	H, E_ARG.109	2.90	1.93	4.30
1HGI.PDB	OE2, F_GLU.67	NH2, E_ARG.109	HH21, E_ARG.109	2.78	1.80	14.37
1HGI.PDB	OD2, D_ASP.79	OG, E_SER.110	HG, E_SER.110	2.90	1.94	10.08
1HGI.PDB	O, E_SER.107	N, E_LEU.111	H, E_LEU.111	2.87	1.91	6.91
1HGI.PDB	O, E_LEU.108	N, E_VAL.112	H, E_VAL.112	2.97	1.99	3.20
1HGI.PDB	O, E_ARG.109	N, E_ALA.113	H, E_ALA.113	2.98	2.07	18.10
1HGI.PDB	O, E_SER.110	N, E_SER.114	H, E_SER.114	2.94	2.00	13.83
1HGI.PDB	OE2, E_GLU.119	OG1, E_THR.117	HG1, E_THR.117	2.98	2.05	12.54
1HGI.PDB	O, E_GLU.82	N, E_LEU.118	H, E_LEU.118	2.91	1.97	15.20
1HGI.PDB	O, E_TYR.257	N, E_ILE.121	H, E_ILE.121	2.92	1.95	7.25
1HGI.PDB	O, E_ARG.255	N, E_GLU.123	H, E_GLU.123	2.89	1.94	11.77
1HGI.PDB	O, E_THR.155	N, E_THR.131	H, E_THR.131	2.77	1.89	21.32
1HGI.PDB	OD1, E_ASN.152	N, E_ASN.133	H, E_ASN.133	2.84	1.93	17.00
1HGI.PDB	O, E_GLY.146	N, E_SER.136	H, E_SER.136	2.77	1.88	19.62
1HGI.PDB	OG, E_SER.136	N, E_ALA.138	H, E_ALA.138	2.87	1.96	18.10
1HGI.PDB	O, E_GLY.144	NZ, E_LYS.140	HZ1, E_LYS.140	2.89	1.92	16.40
1HGI.PDB	OD1, E_ASN.137	NZ, E_LYS.140	HZ2, E_LYS.140	2.83	1.82	12.93
1HGI.PDB	OD2, E_ASP.77	NE, E_ARG.141	HE, E_ARG.141	2.83	2.01	29.05
1HGI.PDB	O, E_PHE.147	NH1, E_ARG.141	HH12, E_ARG.141	2.55	1.65	20.15
1HGI.PDB	OD1, E_ASP.77	NH2, E_ARG.141	HH21, E_ARG.141	2.94	2.01	20.45
1HGI.PDB	OD2, E_ASP.77	NH2, E_ARG.141	HH21, E_ARG.141	2.70	1.83	24.80
1HGI.PDB	O, E_GLY.72	NH2, E_ARG.141	HH22, E_ARG.141	2.98	2.00	9.93
1HGI.PDB	OD1, E_ASN.137	OG, E_SER.145	HG, E_SER.145	2.92	2.15	29.94
1HGI.PDB	O, E_SER.136	N, E_GLY.146	H, E_GLY.146	2.98	2.04	14.06
1HGI.PDB	O, E_GLY.72	N, E_SER.149	H, E_SER.149	2.92	1.99	15.35
1HGI.PDB	O, E_ALA.253	N, E_ASN.152	H, E_ASN.152	2.77	1.92	24.49
1HGI.PDB	OH, E_TYR.195	NE1, E_TRP.153	HE1, E_TRP.153	2.87	1.98	20.67
1HGI.PDB	O, E_LEU.194	N, E_LYS.156	H, E_LYS.156	2.89	2.00	19.98
1HGI.PDB	O, E_SER.193	NZ, E_LYS.156	HZ2, E_LYS.156	2.74	1.75	15.56
1HGI.PDB	O, E_THR.160	N, E_SER.157	H, E_SER.157	2.90	2.00	19.80
1HGI.PDB	O, E_SER.247	N, E_LEU.164	H, E_LEU.164	2.73	1.89	25.21
1HGI.PDB	O, E_ILE.245	N, E_VAL.166	H, E_VAL.166	2.92	1.98	12.27
1HGI.PDB	O, E_LEU.243	OG1, E_THR.167	HG1, E_THR.167	2.89	2.00	19.18
1HGI.PDB	O, E_LEU.243	N, E_MET.168	H, E_MET.168	2.98	2.05	15.68
1HGI.PDB	O, E_ASP.241	N, E_ASN.170	H, E_ASN.170	2.96	1.98	4.05
1HGI.PDB	O, E_PHE.174	ND2, E_ASN.170	HD21, E_ASN.170	2.85	1.90	12.31
1HGI.PDB	O, E_VAL.237	ND2, E_ASN.170	HD22, E_ASN.170	2.95	2.11	25.03
1HGI.PDB	O, E_VAL.237	N, E_LYS.176	H, E_LYS.176	2.94	2.00	12.53
1HGI.PDB	OE2, E_GLU.123	NZ, E_LYS.176	HZ1, E_LYS.176	2.69	1.80	25.89
1HGI.PDB	O, E_PHE.258	N, E_LEU.177	H, E_LEU.177	2.98	2.01	8.00
1HGI.PDB	O, E_THR.235	N, E_TYR.178	H, E_TYR.178	2.83	1.86	3.40
1HGI.PDB	OE1, E_GLU.123	OH, E_TYR.178	HH, E_TYR.178	2.77	1.82	8.27
1HGI.PDB	OG1, E_THR.235	NE1, E_TRP.180	HE1, E_TRP.180	2.85	1.87	2.03
1HGI.PDB	O, E_ASN.250	N, E_HIS.183	H, E_HIS.183	2.94	2.04	20.19
1HGI.PDB	O, E_ARG.229	N, E_HIS.184	H, E_HIS.184	2.89	1.93	8.27
1HGI.PDB	OG, E_SER.231	NE2, E_HIS.184	HE2, E_HIS.184	2.81	1.95	23.57

1HGI.PDB	OD1, E_ASN_250	NE2, E_GLN_191	HE21, E_GLN_191	2.93	1.97	10.64
1HGI.PDB	O, E_GLN_197	NE2, E_GLN_191	HE22, E_GLN_191	2.95	1.99	10.71
1HGI.PDB	O, E_ASN_188	N, E_THR_192	H, E_THR_192	2.98	2.03	12.25
1HGI.PDB	O, E_ASN_188	OG1, E_THR_192	HG1, E_THR_192	2.95	1.99	2.99
1HGI.PDB	O, E_GLN_189	N, E_SER_193	H, E_SER_193	2.85	1.88	3.98
1HGI.PDB	O, E_GLN_191	N, E_TYR_195	H, E_TYR_195	2.76	1.80	5.82
1HGI.PDB	O, E_TYR_161	NE2, E_GLN_197	HE21, E_GLN_197	3.00	2.04	10.17
1HGI.PDB	O, E_ASN_248	NE2, E_GLN_197	HE22, E_GLN_197	2.91	2.00	18.24
1HGI.PDB	OD1, E_ASN_246	NH2, E_ARG_201	HH21, E_ARG_201	2.57	1.74	27.51
1HGI.PDB	O, E_ILE_213	N, E_VAL_202	H, E_VAL_202	2.95	1.98	8.47
1HGI.PDB	O, E_ASN_246	N, E_THR_203	H, E_THR_203	2.89	1.92	4.39
1HGI.PDB	O, E_GLN_211	N, E_VAL_204	H, E_VAL_204	2.85	1.92	15.24
1HGI.PDB	O, E_VAL_244	N, E_SER_205	H, E_SER_205	2.97	2.05	16.25
1HGI.PDB	O, E_SER_209	N, E_THR_206	H, E_THR_206	2.94	1.97	8.14
1HGI.PDB	OD1, E_ASP_241	N, E_ARG_207	H, E_ARG_207	2.91	1.95	10.57
1HGI.PDB	OD2, E_ASP_241	NE, E_ARG_208	HE, E_ARG_208	2.98	2.07	19.52
1HGI.PDB	O, E_VAL_204	N, E_GLN_211	H, E_GLN_211	2.91	1.97	13.40
1HGI.PDB	O, E_VAL_202	N, E_ILE_213	H, E_ILE_213	2.85	1.92	15.12
1HGI.PDB	ND1, E_HIS_184	N, E_ASN_216	H, E_ASN_216	2.74	1.94	28.99
1HGI.PDB	O, E_ASN_216	NH1, E_ARG_220	HH12, E_ARG_220	2.87	2.06	29.75
1HGI.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.69	1.80	23.03
1HGI.PDB	O, E_ASN_216	NH2, E_ARG_220	HH22, E_ARG_220	2.70	1.80	21.47
1HGI.PDB	O, E_LEU_226	N, E_VAL_223	H, E_VAL_223	2.88	1.90	5.13
1HGI.PDB	O, E_CYS_97	NE, E_ARG_224	HE, E_ARG_224	2.81	1.97	26.09
1HGI.PDB	O, E_CYS_97	NH2, E_ARG_224	HH21, E_ARG_224	2.85	1.99	25.73
1HGI.PDB	O, E_VAL_223	N, E_LEU_226	H, E_LEU_226	2.93	2.00	15.87
1HGI.PDB	O, E_SER_228	NH1, E_ARG_229	HH11, E_ARG_229	2.68	1.75	18.51
1HGI.PDB	O, E_PRO_221	NH2, E_ARG_229	HH22, E_ARG_229	2.66	1.70	13.51
1HGI.PDB	OD1, E_ASP_101	OG, E_SER_231	HG, E_SER_231	2.99	2.05	12.53
1HGI.PDB	O, E_ASP_101	N, E_ILE_232	H, E_ILE_232	2.94	2.00	13.40
1HGI.PDB	O, E_TRP_180	N, E_TYR_233	H, E_TYR_233	2.90	1.93	7.29
1HGI.PDB	O, E_TYR_178	N, E_THR_235	H, E_THR_235	2.82	1.92	19.31
1HGI.PDB	O, E_LYS_176	N, E_VAL_237	H, E_VAL_237	2.80	1.86	13.21
1HGI.PDB	O, D_SER_71	NZ, E_LYS_238	HZ2, E_LYS_238	2.75	1.87	26.62
1HGI.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ3, E_LYS_238	2.80	1.81	15.90
1HGI.PDB	O, E_ASN_170	N, E_GLY_240	H, E_GLY_240	2.90	2.05	25.02
1HGI.PDB	OD1, E_ASP_241	N, E_VAL_242	H, E_VAL_242	2.76	1.96	28.65
1HGI.PDB	O, E_MET_168	N, E_LEU_243	H, E_LEU_243	2.92	1.95	5.56
1HGI.PDB	O, E_SER_205	N, E_VAL_244	H, E_VAL_244	2.99	2.04	11.95
1HGI.PDB	O, E_THR_203	N, E_ASN_246	H, E_ASN_246	2.86	1.93	15.06
1HGI.PDB	O, E_LEU_164	N, E_SER_247	H, E_SER_247	2.89	1.98	17.96
1HGI.PDB	O, E_ARG_201	OG, E_SER_247	HG, E_SER_247	2.86	2.05	28.14
1HGI.PDB	OE1, E_GLN_191	ND2, E_ASN_250	HD21, E_ASN_250	2.90	1.94	10.02
1HGI.PDB	O, E_HIS_183	ND2, E_ASN_250	HD22, E_ASN_250	2.84	1.87	6.39
1HGI.PDB	O, E_ASN_152	N, E_ALA_253	H, E_ALA_253	2.82	1.94	21.84
1HGI.PDB	O, E_ILE_121	N, E_TYR_257	H, E_TYR_257	2.96	2.09	22.80
1HGI.PDB	O, E_LEU_177	N, E_PHE_258	H, E_PHE_258	2.90	1.94	8.58
1HGI.PDB	OE2, E_GLU_119	NH1, E_ARG_261	HH12, E_ARG_261	2.65	1.83	28.50
1HGI.PDB	OE1, E_GLU_119	NH2, E_ARG_261	HH22, E_ARG_261	2.84	1.99	27.52
1HGI.PDB	OD2, E_ASP_85	NZ, E_LYS_264	HZ3, E_LYS_264	2.86	1.87	16.39
1HGI.PDB	O, E_ASP_85	N, E_SER_266	H, E_SER_266	2.99	2.14	25.54
1HGI.PDB	O, E_PHE_87	N, E_MET_268	H, E_MET_268	2.85	1.97	21.63
1HGI.PDB	O, E_PRO_284	OG, E_SER_270	HG, E_SER_270	2.79	1.85	10.23
1HGI.PDB	OG, E_SER_270	N, E_ALA_272	H, E_ALA_272	2.98	2.03	12.01
1HGI.PDB	O, E_ILE_51	N, E_ASP_275	H, E_ASP_275	2.93	2.03	19.68
1HGI.PDB	OD1, E_ASP_275	N, E_THR_276	H, E_THR_276	2.83	1.98	25.02
1HGI.PDB	O, E_ASN_54	N, E_SER_279	H, E_SER_279	2.79	1.86	14.40
1HGI.PDB	O, E_TYR_302	N, E_ILE_282	H, E_ILE_282	2.87	1.91	9.87

1HGI.PDB	O, E_THR_283	N, E_GLY_286	H, E_GLY_286	2.80	1.87	13.74
1HGI.PDB	O, E_LYS_50	N, E_SER_287	H, E_SER_287	2.85	1.88	3.05
1HGI.PDB	O, E_ALA_304	ND2, E_ASN_290	HD22, E_ASN_290	2.75	1.86	20.40
1HGI.PDB	OE1, E_GLN_44	NZ, E_LYS_292	HZ1, E_LYS_292	2.73	1.72	12.13
1HGI.PDB	OD2, E_ASP_291	NZ, E_LYS_292	HZ3, E_LYS_292	2.87	1.94	23.09
1HGI.PDB	O, E_LYS_307	N, E_GLN_295	H, E_GLN_295	2.79	1.91	21.81
1HGI.PDB	O, E_ASN_298	NE2, E_GLN_295	HE21, E_GLN_295	2.78	1.83	10.67
1HGI.PDB	O, E_GLN_44	N, E_ASN_296	H, E_ASN_296	2.87	1.95	15.01
1HGI.PDB	OE1, E_GLN_295	N, E_VAL_297	H, E_VAL_297	2.74	1.92	27.74
1HGI.PDB	OD1, E_ASN_285	ND2, E_ASN_298	HD22, E_ASN_298	2.97	2.00	7.97
1HGI.PDB	OD1, E_ASN_298	N, E_ILE_300	H, E_ILE_300	2.91	1.99	17.07
1HGI.PDB	O, E_ILE_282	N, E_TYR_302	H, E_TYR_302	2.94	2.05	21.12
1HGI.PDB	O, E_LYS_264	OH, E_TYR_302	HH, E_TYR_302	2.73	1.93	27.81
1HGI.PDB	O, F_LYS_62	N, E_GLY_303	H, E_GLY_303	2.93	1.96	6.65
1HGI.PDB	O, E_PRO_293	N, E_LYS_307	H, E_LYS_307	2.98	2.02	9.39
1HGI.PDB	O, E_GLN_295	N, E_VAL_309	H, E_VAL_309	2.93	2.07	24.14
1HGI.PDB	OG, F_SER_93	N, E_LYS_310	H, E_LYS_310	2.99	2.05	13.79
1HGI.PDB	OD1, F_ASP_86	NZ, E_LYS_310	HZ3, E_LYS_310	2.76	1.91	29.16
1HGI.PDB	OE2, E_GLU_41	N, E_LEU_314	H, E_LEU_314	2.84	1.88	8.62
1HGI.PDB	OE1, E_GLU_41	NZ, E_LYS_315	HZ3, E_LYS_315	2.74	1.81	21.50
1HGI.PDB	O, E_THR_40	N, E_LEU_316	H, E_LEU_316	2.81	1.89	15.98
1HGI.PDB	OD1, F_ASN_104	N, E_ALA_317	H, E_ALA_317	2.72	1.81	15.78
1HGI.PDB	O, E_ASN_38	N, E_THR_318	H, E_THR_318	2.88	1.97	18.20
1HGI.PDB	O, E_VAL_20	ND2, E_ASN_322	HD21, E_ASN_322	2.90	1.97	15.71
1HGI.PDB	OE2, E_GLU_35	ND2, E_ASN_322	HD22, E_ASN_322	2.92	1.96	12.59
1HGI.PDB	O, E_GLN_327	NZ, E_LYS_326	HZ1, E_LYS_326	2.69	1.77	22.48
1HGI.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.88	1.86	11.05
1HGI.PDB	O, E_LYS_326	NE2, E_GLN_327	HE22, E_GLN_327	2.82	1.87	11.22
1HGI.PDB	OD2, F_ASP_112	N, F_GLY_1	H1, F_GLY_1	2.78	1.77	11.25
1HGI.PDB	OD1, F_ASP_109	N, F_LEU_2	H, F_LEU_2	2.91	1.97	13.16
1HGI.PDB	OD2, F_ASP_112	N, F_PHE_3	H, F_PHE_3	2.84	2.03	27.46
1HGI.PDB	OD2, F_ASP_112	N, F_GLY_4	H, F_GLY_4	2.93	2.03	18.14
1HGI.PDB	OD1, F_ASP_112	N, F_ALA_5	H, F_ALA_5	2.81	1.90	16.38
1HGI.PDB	O, F_GLY_4	N, F_PHE_9	H, F_PHE_9	2.85	1.90	11.24
1HGI.PDB	O, F_GLY_13	ND2, F_ASN_12	HD22, F_ASN_12	2.79	1.91	21.41
1HGI.PDB	O, E_VAL_323	N, F_GLY_13	H, F_GLY_13	2.66	1.77	18.62
1HGI.PDB	O, E_HIS_17	N, F_TRP_14	H, F_TRP_14	2.84	1.93	16.42
1HGI.PDB	OG1, F_THR_41	N, F_TRP_21	H, F_TRP_21	2.99	2.14	24.96
1HGI.PDB	O, E_GLY_16	N, F_GLY_23	H, F_GLY_23	2.97	2.05	16.89
1HGI.PDB	O, F_ALA_35	N, F_PHE_24	H, F_PHE_24	2.82	1.85	6.25
1HGI.PDB	O, E_CYS_14	N, F_ARG_25	H, F_ARG_25	2.91	2.04	22.96
1HGI.PDB	OE1, F_GLN_34	NH2, F_ARG_25	HH21, F_ARG_25	2.91	1.98	18.85
1HGI.PDB	O, F_GLY_33	N, F_HIS_26	H, F_HIS_26	2.85	1.94	17.98
1HGI.PDB	O, E_THR_12	N, F_GLN_27	H, F_GLN_27	2.93	1.99	14.92
1HGI.PDB	O, F_GLY_31	N, F_ASN_28	H, F_ASN_28	2.87	1.90	8.27
1HGI.PDB	OD1, F_ASN_146	ND2, F_ASN_28	HD21, F_ASN_28	2.93	2.01	16.48
1HGI.PDB	O, F_CYS_144	ND2, F_ASN_28	HD22, F_ASN_28	3.00	2.14	23.86
1HGI.PDB	O, F_PHE_24	N, F_ALA_35	H, F_ALA_35	2.77	1.97	29.03
1HGI.PDB	O, F_TYR_22	N, F_ASP_37	H, F_ASP_37	2.70	1.78	13.02
1HGI.PDB	OD2, F_ASP_37	N, F_SER_40	H, F_SER_40	2.93	1.96	6.56
1HGI.PDB	OD2, F_ASP_37	OG, F_SER_40	HG, F_SER_40	2.76	1.92	24.70
1HGI.PDB	O, F_ASP_37	OG1, F_THR_41	HG1, F_THR_41	2.70	1.81	18.66
1HGI.PDB	O, F_LEU_38	N, F_GLN_42	H, F_GLN_42	3.00	2.08	17.54
1HGI.PDB	OD1, F_ASP_46	NE2, F_GLN_42	HE22, F_GLN_42	2.86	1.99	23.93
1HGI.PDB	O, F_LYS_39	N, F_ALA_43	H, F_ALA_43	2.96	2.00	7.28
1HGI.PDB	O, F_SER_40	N, F_ALA_44	H, F_ALA_44	2.94	1.96	3.55
1HGI.PDB	O, F_THR_41	N, F_ILE_45	H, F_ILE_45	2.94	2.00	13.26
1HGI.PDB	O, F_GLN_42	N, F_ASP_46	H, F_ASP_46	2.71	1.76	8.22

1HGI.PDB	O, F_ALA_43	NE2, F_GLN_47	HE22, F_GLN_47	2.92	1.99	15.42
1HGI.PDB	O, F_ILE_45	N, F_ASN_49	H, F_ASN_49	2.88	1.98	19.70
1HGI.PDB	O, F_ASP_46	N, F_GLY_50	H, F_GLY_50	2.94	2.01	15.37
1HGI.PDB	OE1, F_GLU_103	NZ, F_LYS_51	HZ2, F_LYS_51	2.80	1.76	5.82
1HGI.PDB	ND1, F_HIS_106	NZ, F_LYS_51	HZ3, F_LYS_51	2.75	1.80	19.60
1HGI.PDB	O, F_ILE_48	N, F_LEU_52	H, F_LEU_52	2.96	2.03	15.82
1HGI.PDB	O, F_ASN_49	N, F_ASN_53	H, F_ASN_53	2.80	1.95	24.38
1HGI.PDB	O, C_THR_28	NE, F_ARG_54	HE, F_ARG_54	2.95	1.99	9.70
1HGI.PDB	OE1, F_GLU_57	NH1, F_ARG_54	HH11, F_ARG_54	2.83	1.84	11.68
1HGI.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.75	1.79	14.82
1HGI.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.84	1.87	3.62
1HGI.PDB	O, E_LYS_299	NZ, F_LYS_68	HZ1, F_LYS_68	2.80	1.76	2.37
1HGI.PDB	OE2, F_GLU_85	NZ, F_LYS_68	HZ2, F_LYS_68	2.74	1.72	8.70
1HGI.PDB	OG, A_SER_107	N, F_ARG_76	H, F_ARG_76	2.79	1.83	7.22
1HGI.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.85	1.88	7.37
1HGI.PDB	OE2, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.77	1.76	3.93
1HGI.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.64	1.66	4.79
1HGI.PDB	OE1, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.76	1.78	10.40
1HGI.PDB	O, F_GLU_72	NE2, F_GLN_78	HE21, F_GLN_78	2.93	1.96	6.67
1HGI.PDB	OE1, F_GLU_74	NE2, F_GLN_78	HE22, F_GLN_78	2.95	1.98	8.40
1HGI.PDB	O, F_ASP_79	N, F_TYR_83	H, F_TYR_83	2.90	1.99	17.92
1HGI.PDB	OE1, B_GLU_85	OH, F_TYR_83	HH, F_TYR_83	2.58	1.75	24.06
1HGI.PDB	O, F_LEU_80	N, F_VAL_84	H, F_VAL_84	2.77	1.86	16.15
1HGI.PDB	O, F_LYS_82	N, F_ASP_86	H, F_ASP_86	2.91	1.96	11.16
1HGI.PDB	O, F_TYR_83	N, F_THR_87	H, F_THR_87	2.92	1.97	10.81
1HGI.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.61	1.62	12.49
1HGI.PDB	O, F_GLU_85	N, F_ILE_89	H, F_ILE_89	2.88	1.92	9.04
1HGI.PDB	O, F_LYS_88	N, F_TRP_92	H, F_TRP_92	2.96	1.99	7.36
1HGI.PDB	O, F_ILE_89	N, F_SER_93	H, F_SER_93	2.88	1.94	13.75
1HGI.PDB	O, F_ILE_89	OG, F_SER_93	HG, F_SER_93	2.83	1.94	18.22
1HGI.PDB	O, F_ASP_90	N, F_TYR_94	H, F_TYR_94	2.93	2.00	16.36
1HGI.PDB	O, F_TRP_92	N, F_ALA_96	H, F_ALA_96	2.93	1.97	9.62
1HGI.PDB	O, F_TYR_94	N, F_LEU_98	H, F_LEU_98	2.91	1.95	9.75
1HGI.PDB	O, F_ASN_95	N, F_LEU_99	H, F_LEU_99	2.85	1.97	20.80
1HGI.PDB	O, F_LEU_99	N, F_GLU_103	H, F_GLU_103	2.93	1.96	7.51
1HGI.PDB	O, F_VAL_100	N, F_ASN_104	H, F_ASN_104	2.86	1.89	6.57
1HGI.PDB	O, E_LYS_27	ND2, F_ASN_104	HD22, F_ASN_104	2.88	1.93	10.77
1HGI.PDB	O, F_LEU_102	N, F_HIS_106	H, F_HIS_106	2.94	2.01	16.17
1HGI.PDB	O, F_GLU_103	N, F_THR_107	H, F_THR_107	2.77	1.88	20.29
1HGI.PDB	O, F_ASN_104	N, F_ILE_108	H, F_ILE_108	2.98	2.02	10.32
1HGI.PDB	O, F_HIS_106	N, F_LEU_110	H, F_LEU_110	2.83	1.87	10.55
1HGI.PDB	O, F_THR_107	OG1, F_THR_111	HG1, F_THR_111	2.97	2.00	2.90
1HGI.PDB	O, F_ASP_109	N, F_SER_113	H, F_SER_113	2.84	1.88	8.44
1HGI.PDB	O, D_LEU_2	OG, F_SER_113	HG, F_SER_113	2.78	1.94	24.17
1HGI.PDB	O, F_LEU_110	N, F_GLU_114	H, F_GLU_114	2.93	1.97	9.47
1HGI.PDB	O, F_THR_111	N, F_MET_115	H, F_MET_115	3.00	2.05	12.25
1HGI.PDB	O, F_ASP_112	N, F_ASN_116	H, F_ASN_116	2.97	2.03	13.76
1HGI.PDB	O, F_SER_113	N, F_LYS_117	H, F_LYS_117	2.72	1.85	21.38
1HGI.PDB	O, F_GLU_114	N, F_LEU_118	H, F_LEU_118	2.97	2.00	4.23
1HGI.PDB	O, F_ASN_116	N, F_GLU_120	H, F_GLU_120	2.90	1.92	4.14
1HGI.PDB	O, F_LYS_117	N, F_LYS_121	H, F_LYS_121	2.95	2.01	14.18
1HGI.PDB	O, F_LEU_118	OG1, F_THR_122	HG1, F_THR_122	2.94	1.99	9.77
1HGI.PDB	OE2, F_GLU_120	NH1, F_ARG_123	HH11, F_ARG_123	2.81	1.95	25.91
1HGI.PDB	O, F_GLU_120	N, F_ARG_124	H, F_ARG_124	2.91	1.93	3.14
1HGI.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.96	2.09	23.50
1HGI.PDB	OE2, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.96	2.09	23.34
1HGI.PDB	O, F_LEU_126	N, F_ASN_129	H, F_ASN_129	2.99	2.06	14.77
1HGI.PDB	OH, F_TYR_157	ND2, F_ASN_129	HD22, F_ASN_129	2.81	1.86	11.53

1HGI.PDB	O, F_LYS_139	N, F_GLU_131	H, F_GLU_131	2.91	1.97	13.98
1HGI.PDB	O, F_CYS_137	N, F_MET_133	H, F_MET_133	2.82	1.88	11.89
1HGI.PDB	O, E_LEU_13	N, F_PHE_138	H, F_PHE_138	2.75	1.89	22.82
1HGI.PDB	O, F_GLU_131	N, F_LYS_139	H, F_LYS_139	2.80	1.85	8.12
1HGI.PDB	O, E_ALA_11	N, F_ILE_140	H, F_ILE_140	2.78	1.89	18.92
1HGI.PDB	O, F_ASN_129	N, F_TYR_141	H, F_TYR_141	2.85	1.88	5.59
1HGI.PDB	OE2, F_GLU_165	N, F_LYS_143	H, F_LYS_143	2.88	1.95	16.12
1HGI.PDB	OE1, F_GLU_30	N, F_ASN_146	H, F_ASN_146	2.87	1.93	13.21
1HGI.PDB	O, F_ASP_145	N, F_ILE_149	H, F_ILE_149	2.92	1.96	7.67
1HGI.PDB	O, F_ASN_146	N, F_GLU_150	H, F_GLU_150	2.82	1.91	17.13
1HGI.PDB	O, F_ALA_147	N, F_SER_151	H, F_SER_151	2.94	2.03	17.96
1HGI.PDB	O, F_CYS_148	OG, F_SER_151	HG, F_SER_151	2.72	1.86	20.78
1HGI.PDB	O, F_GLU_150	N, F_ASN_154	H, F_ASN_154	2.78	1.81	2.53
1HGI.PDB	O, F_HIS_159	N, F_TYR_162	H, F_TYR_162	2.91	2.05	22.85
1HGI.PDB	O, D_ARG_170	NH1, F_ARG_163	HH12, F_ARG_163	2.92	1.95	13.55
1HGI.PDB	OE2, D_GLU_131	NH2, F_ARG_163	HH22, F_ARG_163	2.69	1.85	26.81
1HGI.PDB	O, F_TYR_162	N, F_ALA_166	H, F_ALA_166	2.89	1.91	1.45
1HGI.PDB	O, F_ARG_163	N, F_LEU_167	H, F_LEU_167	2.78	1.81	5.41
1HGI.PDB	O, F_ALA_166	N, F_ARG_170	H, F_ARG_170	2.82	1.95	21.63
1HGI.PDB	O, F_GLU_128	NE, F_ARG_170	HE, F_ARG_170	2.73	1.88	25.04
1HGI.PDB	OE2, F_GLU_131	NH1, F_ARG_170	HH11, F_ARG_170	2.75	1.76	6.67
1HGI.PDB	O, F_LEU_167	N, F_PHE_171	H, F_PHE_171	2.92	1.98	13.87

Table 1669: 1HGI-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1HGJ.PDB	O, B_ILE_140	N, A_ALA_11	H, A_ALA_11	2.85	1.95	18.97
1HGJ.PDB	O, B_PHE_138	N, A_LEU_13	H, A_LEU_13	2.97	2.00	8.62
1HGJ.PDB	O, B_ARG_25	N, A_CYS_14	H, A_CYS_14	2.88	1.94	12.89
1HGJ.PDB	O, B_GLY_136	N, A_LEU_15	H, A_LEU_15	2.93	1.95	2.37
1HGJ.PDB	O, B_GLY_23	N, A_GLY_16	H, A_GLY_16	2.86	1.96	18.97
1HGJ.PDB	O, A_HIS_18	ND1, A_HIS_17	HD1, A_HIS_17	2.94	2.07	22.50
1HGJ.PDB	O, B_TRP_21	N, A_HIS_18	H, A_HIS_18	2.85	1.98	21.54
1HGJ.PDB	OD1, A_ASN_322	N, A_VAL_20	H, A_VAL_20	2.76	1.81	10.35
1HGJ.PDB	O, A_VAL_36	N, A_THR_24	H, A_THR_24	2.86	1.95	16.84
1HGJ.PDB	O, A_ILE_34	N, A_VAL_26	H, A_VAL_26	2.80	1.86	12.04
1HGJ.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.81	1.78	9.30
1HGJ.PDB	O, A_ASP_31	N, A_THR_28	H, A_THR_28	2.73	1.88	24.26
1HGJ.PDB	O, A_VAL_26	N, A_ILE_34	H, A_ILE_34	2.90	1.95	11.45
1HGJ.PDB	O, A_THR_24	N, A_VAL_36	H, A_VAL_36	2.81	1.84	5.48
1HGJ.PDB	O, A_MET_320	N, A_THR_37	H, A_THR_37	2.87	1.90	7.32
1HGJ.PDB	O, A_LEU_316	N, A_THR_40	H, A_THR_40	2.84	2.00	24.78
1HGJ.PDB	O, A_LEU_314	N, A_LEU_42	H, A_LEU_42	2.83	1.95	21.41
1HGJ.PDB	O, A_PHE_294	N, A_GLN_44	H, A_GLN_44	2.83	1.86	6.97
1HGJ.PDB	O, A_SER_46	NE2, A_GLN_44	HE22, A_GLN_44	2.92	2.02	20.25
1HGJ.PDB	OD2, A_ASP_275	NZ, A_LYS_50	HZ1, A_LYS_50	2.74	1.82	22.91
1HGJ.PDB	O, A_PRO_273	N, A_ILE_51	H, A_ILE_51	2.86	1.90	9.76
1HGJ.PDB	O, A_ASP_275	N, A_ASN_53	H, A_ASN_53	2.80	1.95	24.33
1HGJ.PDB	O, A_GLU_280	NE2, A_HIS_56	HE2, A_HIS_56	2.97	2.05	17.77
1HGJ.PDB	OD2, A_ASP_85	N, A_ARG_57	H, A_ARG_57	2.86	1.92	12.38
1HGJ.PDB	O, A_THR_83	NE, A_ARG_57	HE, A_ARG_57	2.77	1.80	8.03
1HGJ.PDB	O, A_LEU_86	N, A_LEU_59	H, A_LEU_59	2.86	1.91	11.37
1HGJ.PDB	O, A_VAL_88	N, A_GLY_61	H, A_GLY_61	2.97	2.09	22.25
1HGJ.PDB	OD1, A_ASP_60	N, A_ILE_62	H, A_ILE_62	2.87	1.94	15.09
1HGJ.PDB	O, A_GLY_61	N, A_CYS_64	H, A_CYS_64	2.89	1.97	17.07
1HGJ.PDB	O, A_LEU_66	N, A_LEU_70	H, A_LEU_70	2.88	1.99	19.66
1HGJ.PDB	O, A_ILE_67	N, A_LEU_71	H, A_LEU_71	2.83	1.87	6.71
1HGJ.PDB	O, A_ASP_68	N, A_GLY_72	H, A_GLY_72	2.88	1.97	18.26
1HGJ.PDB	OD1, A_ASP_73	N, A_HIS_75	H, A_HIS_75	2.98	2.07	18.75
1HGJ.PDB	OD1, A_ASP_73	ND1, A_HIS_75	HD1, A_HIS_75	2.83	1.91	17.40
1HGJ.PDB	O, A_ASP_63	NE2, A_HIS_75	HE2, A_HIS_75	2.85	1.95	19.40
1HGJ.PDB	O, A_ASP_73	N, A_CYS_76	H, A_CYS_76	2.78	1.84	13.08
1HGJ.PDB	O, A_PRO_74	N, A_ASP_77	H, A_ASP_77	2.97	2.01	11.14
1HGJ.PDB	O, A_ARG_57	N, A_ASP_85	H, A_ASP_85	2.81	1.89	16.54
1HGJ.PDB	O, A_LEU_59	N, A_VAL_88	H, A_VAL_88	2.98	2.01	7.07
1HGJ.PDB	O, A_MET_268	N, A_GLU_89	H, A_GLU_89	2.79	1.84	8.85
1HGJ.PDB	OD1, A_ASP_60	NE, A_ARG_90	HE, A_ARG_90	2.88	1.91	7.56
1HGJ.PDB	O, A_SER_270	NH1, A_ARG_90	HH11, A_ARG_90	2.70	1.81	23.07
1HGJ.PDB	O, A_ALA_272	NH1, A_ARG_90	HH12, A_ARG_90	2.62	1.70	17.78
1HGJ.PDB	OD2, A_ASP_60	NH2, A_ARG_90	HH21, A_ARG_90	2.81	1.82	10.05
1HGJ.PDB	OD1, A_ASP_271	N, A_SER_91	H, A_SER_91	2.92	1.95	7.81
1HGJ.PDB	OD1, A_ASP_271	OG, A_SER_91	HG, A_SER_91	2.98	2.13	24.27
1HGJ.PDB	OD2, A_ASP_271	OG, A_SER_91	HG, A_SER_91	2.78	1.90	20.01
1HGJ.PDB	OD2, A_ASP_68	OG, A_SER_95	HG, A_SER_95	2.95	2.05	19.19
1HGJ.PDB	OD2, A_ASP_73	N, A_ASN_96	H, A_ASN_96	2.89	1.93	9.91
1HGJ.PDB	O, A_ILE_230	N, A_ASP_101	H, A_ASP_101	2.95	2.08	23.05
1HGJ.PDB	OD2, A_ASP_104	OG, A_SER_107	HG, A_SER_107	2.84	1.95	18.85
1HGJ.PDB	O, A_TYR_105	N, A_ARG_109	H, A_ARG_109	2.84	1.86	2.92
1HGJ.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.75	1.77	12.07
1HGJ.PDB	OD2, F_ASP_79	OG, A_SER_110	HG, A_SER_110	2.94	1.98	10.39
1HGJ.PDB	O, A_SER_107	N, A_LEU_111	H, A_LEU_111	2.86	1.89	5.37
1HGJ.PDB	O, A_ARG_109	N, A_ALA_113	H, A_ALA_113	2.93	2.03	18.98
1HGJ.PDB	O, A_SER_110	N, A_SER_114	H, A_SER_114	2.89	1.97	15.80

1HGJ.PDB	OE2, A_GLU_119	OG1, A_THR_117	HG1, A_THR_117	2.87	1.94	12.44
1HGJ.PDB	O, A_GLU_82	N, A_LEU_118	H, A_LEU_118	2.93	2.00	16.05
1HGJ.PDB	O, A_TYR_257	N, A_ILE_121	H, A_ILE_121	2.85	1.88	7.23
1HGJ.PDB	O, A_ARG_255	N, A_GLU_123	H, A_GLU_123	2.94	1.98	10.39
1HGJ.PDB	O, A_THR_155	N, A_THR_131	H, A_THR_131	2.71	1.83	19.42
1HGJ.PDB	OD1, A_ASN_152	N, A_ASN_133	H, A_ASN_133	2.86	1.94	16.50
1HGJ.PDB	O, A_GLY_146	N, A_SER_136	H, A_SER_136	2.74	1.85	19.18
1HGJ.PDB	OG, A_SER_136	N, A_ALA_138	H, A_ALA_138	2.90	1.96	14.29
1HGJ.PDB	O, A_GLY_144	NZ, A_LYS_140	HZ1, A_LYS_140	2.76	1.78	16.23
1HGJ.PDB	OD1, A_ASN_137	NZ, A_LYS_140	HZ2, A_LYS_140	2.70	1.70	13.62
1HGJ.PDB	OD2, A_ASP_77	NE, A_ARG_141	HE, A_ARG_141	2.82	1.99	27.09
1HGJ.PDB	O, A_PHE_147	NH1, A_ARG_141	HH12, A_ARG_141	2.55	1.62	16.97
1HGJ.PDB	OD1, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.82	1.90	21.48
1HGJ.PDB	OD2, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.75	1.86	24.28
1HGJ.PDB	O, A_GLY_72	NH2, A_ARG_141	HH22, A_ARG_141	2.89	1.91	10.49
1HGJ.PDB	O, A_SER_136	N, A_GLY_146	H, A_GLY_146	2.92	1.99	15.16
1HGJ.PDB	O, A_GLY_72	N, A_SER_149	H, A_SER_149	2.81	1.92	19.89
1HGJ.PDB	O, A_ALA_253	N, A_ASN_152	H, A_ASN_152	2.77	1.94	25.94
1HGJ.PDB	OH, A_TYR_195	NE1, A_TRP_153	HE1, A_TRP_153	2.85	1.94	18.91
1HGJ.PDB	O, A_THR_131	N, A_THR_155	H, A_THR_155	2.98	2.03	13.10
1HGJ.PDB	O, A_LEU_194	N, A_LYS_156	H, A_LYS_156	2.96	2.04	16.82
1HGJ.PDB	O, A_SER_193	NZ, A_LYS_156	HZ2, A_LYS_156	2.76	1.77	15.28
1HGJ.PDB	O, A_SER_247	N, A_LEU_164	H, A_LEU_164	2.71	1.86	23.94
1HGJ.PDB	O, A_ILE_245	N, A_VAL_166	H, A_VAL_166	2.96	2.01	11.11
1HGJ.PDB	O, A_LEU_243	OG1, A_THR_167	HG1, A_THR_167	2.95	2.00	7.14
1HGJ.PDB	O, A_LEU_243	N, A_MET_168	H, A_MET_168	2.88	1.96	15.85
1HGJ.PDB	O, A_ASP_241	N, A_ASN_170	H, A_ASN_170	2.94	1.97	10.04
1HGJ.PDB	O, A_PHE_174	ND2, A_ASN_170	HD21, A_ASN_170	2.85	1.90	10.43
1HGJ.PDB	O, A_VAL_237	ND2, A_ASN_170	HD22, A_ASN_170	2.88	2.05	26.57
1HGJ.PDB	O, A_VAL_237	N, A_LYS_176	H, A_LYS_176	2.93	1.99	13.19
1HGJ.PDB	OE2, A_GLU_123	NZ, A_LYS_176	HZ1, A_LYS_176	2.68	1.78	24.65
1HGJ.PDB	O, A_THR_235	N, A_TYR_178	H, A_TYR_178	2.81	1.83	1.66
1HGJ.PDB	OE1, A_GLU_123	OH, A_TYR_178	HH, A_TYR_178	2.79	1.84	8.91
1HGJ.PDB	OG1, A_THR_235	NE1, A_TRP_180	HE1, A_TRP_180	2.92	1.93	4.44
1HGJ.PDB	O, A_ASN_250	N, A_HIS_183	H, A_HIS_183	2.90	1.98	16.84
1HGJ.PDB	O, A_ARG_229	N, A_HIS_184	H, A_HIS_184	2.83	1.87	9.59
1HGJ.PDB	OG, A_SER_231	NE2, A_HIS_184	HE2, A_HIS_184	2.75	1.92	26.36
1HGJ.PDB	OG1, A_THR_187	N, A_GLU_190	H, A_GLU_190	2.88	1.93	10.33
1HGJ.PDB	O, A_GLN_197	NE2, A_GLN_191	HE22, A_GLN_191	2.90	1.98	16.92
1HGJ.PDB	O, A_ASN_188	OG1, A_THR_192	HG1, A_THR_192	2.97	2.01	7.08
1HGJ.PDB	O, A_GLN_189	N, A_SER_193	H, A_SER_193	2.85	1.87	2.99
1HGJ.PDB	O, A_GLU_190	N, A_LEU_194	H, A_LEU_194	2.97	2.00	9.61
1HGJ.PDB	O, A_GLN_191	N, A_TYR_195	H, A_TYR_195	2.80	1.85	9.60
1HGJ.PDB	O, A_TYR_161	NE2, A_GLN_197	HE21, A_GLN_197	2.87	1.93	12.14
1HGJ.PDB	O, A_ASN_248	NE2, A_GLN_197	HE22, A_GLN_197	2.87	1.94	14.83
1HGJ.PDB	OD1, A_ASN_246	NH2, A_ARG_201	HH21, A_ARG_201	2.58	1.73	25.49
1HGJ.PDB	O, A_ILE_213	N, A_VAL_202	H, A_VAL_202	2.97	2.02	12.20
1HGJ.PDB	O, A_ASN_246	N, A_THR_203	H, A_THR_203	2.90	1.99	17.82
1HGJ.PDB	O, A_GLN_211	N, A_VAL_204	H, A_VAL_204	2.83	1.93	18.94
1HGJ.PDB	O, A_SER_209	N, A_THR_206	H, A_THR_206	2.89	1.93	8.74
1HGJ.PDB	OD1, A_ASP_241	N, A_ARG_207	H, A_ARG_207	2.88	1.92	9.03
1HGJ.PDB	OG1, A_THR_206	OG, A_SER_209	HG, A_SER_209	3.00	2.04	8.15
1HGJ.PDB	O, A_VAL_204	N, A_GLN_211	H, A_GLN_211	2.91	2.00	17.89
1HGJ.PDB	OG1, A_THR_203	OG1, A_THR_212	HG1, A_THR_212	2.89	1.93	3.12
1HGJ.PDB	O, A_VAL_202	N, A_ILE_213	H, A_ILE_213	2.84	1.92	16.69
1HGJ.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.67	1.78	22.50
1HGJ.PDB	O, A_ASN_216	NH2, A_ARG_220	HH22, A_ARG_220	2.78	1.89	22.30
1HGJ.PDB	O, A_LEU_226	N, A_VAL_223	H, A_VAL_223	2.84	1.88	10.14

1HGJ.PDB	O, A_CYS_97	NE, A_ARG_224	HE, A_ARG_224	2.80	1.95	24.47
1HGJ.PDB	O, A_CYS_97	NH2, A_ARG_224	HH21, A_ARG_224	2.93	2.07	26.25
1HGJ.PDB	O, A_VAL_223	N, A_LEU_226	H, A_LEU_226	2.91	1.97	13.14
1HGJ.PDB	O, A_SER_228	NH1, A_ARG_229	HH11, A_ARG_229	2.72	1.77	16.65
1HGJ.PDB	O, A_PRO_221	NH2, A_ARG_229	HH22, A_ARG_229	2.62	1.66	13.73
1HGJ.PDB	OD1, A_ASP_101	OG, A_SER_231	HG, A_SER_231	2.87	1.91	9.73
1HGJ.PDB	O, A_ASP_101	N, A_ILE_232	H, A_ILE_232	2.86	1.94	17.01
1HGJ.PDB	O, A_TRP_180	N, A_TYR_233	H, A_TYR_233	2.94	1.96	7.60
1HGJ.PDB	O, A_TYR_178	N, A_THR_235	H, A_THR_235	2.91	2.02	19.93
1HGJ.PDB	O, A_LYS_176	N, A_VAL_237	H, A_VAL_237	2.80	1.86	14.26
1HGJ.PDB	O, F_SER_71	NZ, A_LYS_238	HZ2, A_LYS_238	2.62	1.72	23.44
1HGJ.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.90	1.90	13.91
1HGJ.PDB	O, A_ASN_170	N, A_GLY_240	H, A_GLY_240	2.83	1.97	23.20
1HGJ.PDB	OD1, A_ASP_241	N, A_VAL_242	H, A_VAL_242	2.77	1.93	25.51
1HGJ.PDB	O, A_MET_168	N, A_LEU_243	H, A_LEU_243	2.93	1.96	5.60
1HGJ.PDB	O, A_SER_205	N, A_VAL_244	H, A_VAL_244	2.98	2.03	12.76
1HGJ.PDB	O, A_VAL_166	N, A_ILE_245	H, A_ILE_245	2.88	1.93	13.19
1HGJ.PDB	O, A_THR_203	N, A_ASN_246	H, A_ASN_246	2.93	1.96	5.50
1HGJ.PDB	OD1, A_ASN_165	ND2, A_ASN_246	HD22, A_ASN_246	2.91	1.95	11.26
1HGJ.PDB	O, A_LEU_164	N, A_SER_247	H, A_SER_247	2.91	2.00	18.09
1HGJ.PDB	O, A_HIS_183	ND2, A_ASN_250	HD22, A_ASN_250	2.81	1.86	11.47
1HGJ.PDB	O, A_GLY_181	N, A_ILE_252	H, A_ILE_252	2.95	1.99	11.10
1HGJ.PDB	O, A_ASN_152	N, A_ALA_253	H, A_ALA_253	2.89	2.00	20.87
1HGJ.PDB	OD1, A_ASN_133	NH2, A_ARG_255	HH22, A_ARG_255	2.53	1.70	27.52
1HGJ.PDB	O, A_ILE_121	N, A_TYR_257	H, A_TYR_257	2.95	2.11	25.99
1HGJ.PDB	O, A_LEU_177	N, A_PHE_258	H, A_PHE_258	2.93	1.97	8.17
1HGJ.PDB	OG, A_SER_115	N, A_ARG_261	H, A_ARG_261	2.93	1.99	14.40
1HGJ.PDB	OE2, A_GLU_119	NH1, A_ARG_261	HH12, A_ARG_261	2.65	1.82	28.35
1HGJ.PDB	OE1, A_GLU_119	NH2, A_ARG_261	HH22, A_ARG_261	2.90	1.99	23.18
1HGJ.PDB	OD2, A_ASP_85	NZ, A_LYS_264	HZ3, A_LYS_264	2.84	1.85	15.53
1HGJ.PDB	O, A_PHE_87	N, A_MET_268	H, A_MET_268	2.87	1.96	18.47
1HGJ.PDB	O, A_PRO_284	OG, A_SER_270	HG, A_SER_270	2.82	1.88	11.71
1HGJ.PDB	OG, A_SER_270	N, A_ALA_272	H, A_ALA_272	2.99	2.05	13.78
1HGJ.PDB	O, A_ILE_51	N, A_ASP_275	H, A_ASP_275	2.92	2.02	19.32
1HGJ.PDB	OD1, A_ASP_275	N, A_THR_276	H, A_THR_276	2.81	1.96	23.63
1HGJ.PDB	O, A_ASN_54	N, A_SER_279	H, A_SER_279	2.81	1.88	14.91
1HGJ.PDB	O, A_TYR_302	N, A_ILE_282	H, A_ILE_282	2.92	1.95	7.78
1HGJ.PDB	O, A_THR_283	N, A_GLY_286	H, A_GLY_286	2.78	1.86	14.62
1HGJ.PDB	O, A_LYS_50	N, A_SER_287	H, A_SER_287	2.84	1.87	6.72
1HGJ.PDB	O, A_ALA_304	ND2, A_ASN_290	HD22, A_ASN_290	2.82	1.91	18.14
1HGJ.PDB	OE1, A_GLN_44	NZ, A_LYS_292	HZ1, A_LYS_292	2.71	1.70	11.30
1HGJ.PDB	OD2, A_ASP_291	NZ, A_LYS_292	HZ3, A_LYS_292	2.80	1.82	17.27
1HGJ.PDB	O, A_LYS_307	N, A_GLN_295	H, A_GLN_295	2.89	1.99	19.47
1HGJ.PDB	O, A_ASN_298	NE2, A_GLN_295	HE21, A_GLN_295	2.78	1.82	8.78
1HGJ.PDB	O, A_GLN_44	N, A_ASN_296	H, A_ASN_296	2.84	1.91	14.48
1HGJ.PDB	OE1, A_GLN_295	N, A_VAL_297	H, A_VAL_297	2.74	1.95	29.44
1HGJ.PDB	O, B_LYS_68	NZ, A_LYS_299	HZ2, A_LYS_299	2.95	1.96	14.91
1HGJ.PDB	OD1, A_ASN_298	N, A_ILE_300	H, A_ILE_300	2.86	1.95	16.95
1HGJ.PDB	O, A_ILE_282	N, A_TYR_302	H, A_TYR_302	2.88	2.05	26.62
1HGJ.PDB	O, A_LYS_264	OH, A_TYR_302	HH, A_TYR_302	2.66	1.88	29.88
1HGJ.PDB	O, B_LYS_62	N, A_GLY_303	H, A_GLY_303	2.93	1.97	8.41
1HGJ.PDB	O, A_GLN_295	N, A_VAL_309	H, A_VAL_309	2.92	2.10	27.87
1HGJ.PDB	OE2, A_GLU_41	N, A_LEU_314	H, A_LEU_314	2.79	1.86	13.81
1HGJ.PDB	OE1, A_GLU_41	NZ, A_LYS_315	HZ3, A_LYS_315	2.85	1.90	20.12
1HGJ.PDB	O, A_THR_40	N, A_LEU_316	H, A_LEU_316	2.80	1.86	11.89
1HGJ.PDB	OD1, B_ASN_104	N, A_ALA_317	H, A_ALA_317	2.74	1.81	13.01
1HGJ.PDB	O, A_ASN_38	N, A_THR_318	H, A_THR_318	2.86	1.94	16.91
1HGJ.PDB	O, A_VAL_20	ND2, A_ASN_322	HD21, A_ASN_322	2.87	1.93	14.22

1HGJ.PDB	OE2, A_GLU_35	ND2, A_ASN_322	HD22, A_ASN_322	2.88	1.99	20.96
1HGJ.PDB	OE1, A_GLU_325	NZ, A_LYS_326	HZ3, A_LYS_326	2.92	1.93	15.95
1HGJ.PDB	O, A_PRO_21	NE2, A_GLN_327	HE22, A_GLN_327	2.76	1.91	24.52
1HGJ.PDB	OE1, B_GLU_15	N, A_THR_328	H, A_THR_328	2.99	2.03	9.44
1HGJ.PDB	OD2, B_ASP_112	N, B_GLY_1	H2, B_GLY_1	2.78	1.79	13.86
1HGJ.PDB	OD1, B_ASP_109	N, B_LEU_2	H, B_LEU_2	2.86	1.98	21.89
1HGJ.PDB	OD2, B_ASP_112	N, B_PHE_3	H, B_PHE_3	2.78	1.97	28.02
1HGJ.PDB	OD2, B_ASP_112	N, B_GLY_4	H, B_GLY_4	2.88	1.96	16.60
1HGJ.PDB	OD1, B_ASP_112	N, B_ALA_5	H, B_ALA_5	2.84	1.99	24.18
1HGJ.PDB	OD1, B_ASP_112	N, B_ILE_6	H, B_ILE_6	3.00	2.08	16.65
1HGJ.PDB	O, B_GLY_4	N, B_PHE_9	H, B_PHE_9	2.78	1.85	13.96
1HGJ.PDB	O, B_GLY_13	ND2, B_ASN_12	HD22, B_ASN_12	2.87	1.99	21.80
1HGJ.PDB	O, A_VAL_323	N, B_GLY_13	H, B_GLY_13	2.69	1.76	11.68
1HGJ.PDB	O, A_HIS_17	N, B_TRP_14	H, B_TRP_14	2.84	1.89	12.22
1HGJ.PDB	OG1, B_THR_41	N, B_TRP_21	H, B_TRP_21	2.94	2.02	16.97
1HGJ.PDB	O, A_GLY_16	N, B_GLY_23	H, B_GLY_23	2.94	2.02	17.07
1HGJ.PDB	O, B_ALA_35	N, B_PHE_24	H, B_PHE_24	2.82	1.86	8.22
1HGJ.PDB	O, A_CYS_14	N, B_ARG_25	H, B_ARG_25	2.98	2.05	15.51
1HGJ.PDB	OE1, B_GLN_34	NE, B_ARG_25	HE, B_ARG_25	2.57	1.79	29.34
1HGJ.PDB	OE2, A_GLU_325	NH2, B_ARG_25	HH22, B_ARG_25	2.97	2.01	15.94
1HGJ.PDB	O, B_GLY_33	N, B_HIS_26	H, B_HIS_26	2.69	1.82	21.72
1HGJ.PDB	O, B_GLY_31	N, B_ASN_28	H, B_ASN_28	2.73	1.80	14.27
1HGJ.PDB	O, B_ASN_28	N, B_GLY_31	H, B_GLY_31	2.95	2.06	20.54
1HGJ.PDB	O, B_HIS_26	N, B_GLY_33	H, B_GLY_33	2.91	1.99	16.91
1HGJ.PDB	O, B_PHE_24	N, B_ALA_35	H, B_ALA_35	2.77	1.91	23.35
1HGJ.PDB	O, B_TYR_22	N, B_ASP_37	H, B_ASP_37	2.68	1.76	13.66
1HGJ.PDB	OD2, B_ASP_37	N, B_SER_40	H, B_SER_40	2.93	1.96	8.36
1HGJ.PDB	O, B_ASP_37	OG1, B_THR_41	HG1, B_THR_41	2.75	1.82	13.86
1HGJ.PDB	O, B_LEU_38	N, B_GLN_42	H, B_GLN_42	2.95	2.02	15.28
1HGJ.PDB	OD1, B_ASP_46	NE2, B_GLN_42	HE22, B_GLN_42	2.81	1.92	21.14
1HGJ.PDB	O, B_LYS_39	N, B_ALA_43	H, B_ALA_43	2.97	2.02	10.62
1HGJ.PDB	O, B_SER_40	N, B_ALA_44	H, B_ALA_44	2.96	1.98	1.15
1HGJ.PDB	O, B_THR_41	N, B_ILE_45	H, B_ILE_45	2.88	1.92	10.00
1HGJ.PDB	O, B_GLN_42	N, B_ASP_46	H, B_ASP_46	2.77	1.81	2.39
1HGJ.PDB	OE2, B_GLU_114	NE2, B_GLN_47	HE21, B_GLN_47	2.96	2.05	17.93
1HGJ.PDB	O, B_ALA_43	NE2, B_GLN_47	HE22, B_GLN_47	2.92	2.04	21.05
1HGJ.PDB	O, B_ILE_45	N, B_ASN_49	H, B_ASN_49	2.87	1.94	16.22
1HGJ.PDB	O, B_ASP_46	N, B_GLY_50	H, B_GLY_50	2.84	1.96	21.96
1HGJ.PDB	OG1, B_THR_107	NZ, B_LYS_51	HZ1, B_LYS_51	2.96	1.99	17.76
1HGJ.PDB	OE1, B_GLU_103	NZ, B_LYS_51	HZ2, B_LYS_51	2.78	1.74	6.16
1HGJ.PDB	ND1, B_HIS_106	NZ, B_LYS_51	HZ3, B_LYS_51	2.79	1.82	16.46
1HGJ.PDB	O, B_ILE_48	N, B_LEU_52	H, B_LEU_52	2.87	1.97	17.59
1HGJ.PDB	O, B_ASN_49	N, B_ASN_53	H, B_ASN_53	2.88	1.95	13.58
1HGJ.PDB	O, E_THR_28	NE, B_ARG_54	HE, B_ARG_54	3.00	2.04	10.82
1HGJ.PDB	OE1, B_GLU_57	NH1, B_ARG_54	HH11, B_ARG_54	2.87	1.87	9.43
1HGJ.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.77	1.81	15.09
1HGJ.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ1, B_LYS_62	2.65	1.75	23.55
1HGJ.PDB	OD2, F_ASP_90	NZ, B_LYS_62	HZ3, B_LYS_62	2.74	1.89	28.52
1HGJ.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.89	1.93	11.21
1HGJ.PDB	O, A_LYS_299	NZ, B_LYS_68	HZ1, B_LYS_68	2.90	1.89	11.39
1HGJ.PDB	OE2, B_GLU_85	NZ, B_LYS_68	HZ2, B_LYS_68	2.78	1.76	8.72
1HGJ.PDB	OG, C_SER_107	N, B_ARG_76	H, B_ARG_76	2.84	1.89	10.24
1HGJ.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.90	1.93	10.80
1HGJ.PDB	OE2, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.88	1.87	5.28
1HGJ.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.72	1.72	3.64
1HGJ.PDB	OE1, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.85	1.84	3.19
1HGJ.PDB	OE1, B_GLU_74	NE2, B_GLN_78	HE22, B_GLN_78	2.90	1.95	12.93
1HGJ.PDB	O, B_GLY_75	N, B_ASP_79	H, B_ASP_79	2.93	2.00	14.44

1HGJ.PDB	O, B_ILE_77	N, B_GLU_81	H, B_GLU_81	2.99	2.02	6.22
1HGJ.PDB	O, B_GLN_78	N, B_LYS_82	H, B_LYS_82	2.95	1.99	7.96
1HGJ.PDB	O, B_ASP_79	N, B_TYR_83	H, B_TYR_83	2.84	1.90	13.83
1HGJ.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.67	1.83	24.12
1HGJ.PDB	O, B_LEU_80	N, B_VAL_84	H, B_VAL_84	2.83	1.86	5.05
1HGJ.PDB	O, B_LYS_82	N, B_ASP_86	H, B_ASP_86	2.93	1.98	11.14
1HGJ.PDB	O, B_TYR_83	N, B_THR_87	H, B_THR_87	2.88	1.94	13.57
1HGJ.PDB	O, B_VAL_84	N, B_LYS_88	H, B_LYS_88	2.97	2.03	12.68
1HGJ.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.78	1.75	7.42
1HGJ.PDB	O, B_GLU_85	N, B_ILE_89	H, B_ILE_89	2.86	1.88	2.57
1HGJ.PDB	O, B_LYS_88	N, B_TRP_92	H, B_TRP_92	2.95	1.97	4.34
1HGJ.PDB	O, B_ILE_89	N, B_SER_93	H, B_SER_93	2.84	1.96	21.34
1HGJ.PDB	O, B_ILE_89	OG, B_SER_93	HG, B_SER_93	2.85	1.94	16.10
1HGJ.PDB	O, B_ASP_90	N, B_TYR_94	H, B_TYR_94	2.84	1.94	19.37
1HGJ.PDB	O, B_TRP_92	N, B_ALA_96	H, B_ALA_96	2.98	2.03	11.55
1HGJ.PDB	O, B_TYR_94	N, B_LEU_98	H, B_LEU_98	2.96	1.99	5.51
1HGJ.PDB	O, B_ASN_95	N, B_LEU_99	H, B_LEU_99	2.87	1.95	16.33
1HGJ.PDB	O, B_LEU_98	N, B_LEU_102	H, B_LEU_102	2.95	1.98	7.34
1HGJ.PDB	O, B_LEU_99	N, B_GLU_103	H, B_GLU_103	2.95	1.99	9.27
1HGJ.PDB	O, B_VAL_100	N, B_ASN_104	H, B_ASN_104	2.84	1.88	10.60
1HGJ.PDB	O, A_LYS_27	ND2, B_ASN_104	HD22, B_ASN_104	2.89	1.94	10.52
1HGJ.PDB	O, B_LEU_102	N, B_HIS_106	H, B_HIS_106	2.93	1.97	8.51
1HGJ.PDB	O, B_GLU_103	N, B_THR_107	H, B_THR_107	2.83	1.93	19.44
1HGJ.PDB	O, B_HIS_106	N, B_LEU_110	H, B_LEU_110	2.81	1.85	8.24
1HGJ.PDB	O, B_THR_107	OG1, B_THR_111	HG1, B_THR_111	2.81	1.92	19.54
1HGJ.PDB	O, B_ASP_109	N, B_SER_113	H, B_SER_113	2.79	1.83	7.83
1HGJ.PDB	O, F_LEU_2	OG, B_SER_113	HG, B_SER_113	2.74	1.91	25.16
1HGJ.PDB	O, B_LEU_110	N, B_GLU_114	H, B_GLU_114	2.95	1.99	10.32
1HGJ.PDB	O, B_ASP_112	N, B_ASN_116	H, B_ASN_116	2.97	2.01	9.78
1HGJ.PDB	O, B_SER_113	N, B_LYS_117	H, B_LYS_117	2.71	1.84	21.48
1HGJ.PDB	O, B_GLU_114	N, B_LEU_118	H, B_LEU_118	2.97	2.01	9.85
1HGJ.PDB	O, B_ASN_116	N, B_GLU_120	H, B_GLU_120	2.95	1.98	2.37
1HGJ.PDB	O, B_LYS_117	N, B_LYS_121	H, B_LYS_121	2.92	2.02	19.46
1HGJ.PDB	O, B_PHE_119	N, B_ARG_123	H, B_ARG_123	2.95	1.98	8.48
1HGJ.PDB	OE2, B_GLU_120	NH1, B_ARG_123	HH11, B_ARG_123	2.74	1.86	23.95
1HGJ.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.82	2.00	27.29
1HGJ.PDB	OE2, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.91	2.02	20.91
1HGJ.PDB	O, B_HIS_159	ND2, B_ASN_129	HD21, B_ASN_129	2.96	2.00	9.85
1HGJ.PDB	OH, B_TYR_157	ND2, B_ASN_129	HD22, B_ASN_129	2.77	1.84	15.18
1HGJ.PDB	O, B_LYS_139	N, B_GLU_131	H, B_GLU_131	2.92	1.98	12.78
1HGJ.PDB	O, B_CYS_137	N, B_MET_133	H, B_MET_133	2.85	1.92	15.10
1HGJ.PDB	O, A_LEU_13	N, B_PHE_138	H, B_PHE_138	2.71	1.86	23.78
1HGJ.PDB	O, B_GLU_131	N, B_LYS_139	H, B_LYS_139	2.83	1.87	8.18
1HGJ.PDB	O, A_ALA_11	N, B_ILE_140	H, B_ILE_140	2.77	1.86	16.77
1HGJ.PDB	O, B_ASN_129	N, B_TYR_141	H, B_TYR_141	2.93	1.98	12.18
1HGJ.PDB	OE2, B_GLU_165	N, B_LYS_143	H, B_LYS_143	2.97	2.02	13.21
1HGJ.PDB	OE1, B_GLU_30	N, B_ASN_146	H, B_ASN_146	2.90	1.96	14.42
1HGJ.PDB	O, B_ASP_145	N, B_ILE_149	H, B_ILE_149	2.89	1.94	10.22
1HGJ.PDB	O, B_ASN_146	N, B_GLU_150	H, B_GLU_150	2.88	1.95	15.40
1HGJ.PDB	O, B_ALA_147	N, B_SER_151	H, B_SER_151	2.86	1.97	19.97
1HGJ.PDB	O, B_CYS_148	OG, B_SER_151	HG, B_SER_151	2.69	1.85	23.77
1HGJ.PDB	O, B_GLU_150	N, B_ASN_154	H, B_ASN_154	2.80	1.82	1.74
1HGJ.PDB	OE2, B_GLU_150	ND2, B_ASN_154	HD21, B_ASN_154	2.81	2.00	28.55
1HGJ.PDB	O, B_SER_151	N, B_THR_156	H, B_THR_156	2.71	1.89	26.64
1HGJ.PDB	OD1, B_ASN_154	OG1, B_THR_156	HG1, B_THR_156	2.67	1.80	19.98
1HGJ.PDB	OD1, B_ASP_158	N, B_ASP_160	H, B_ASP_160	2.91	2.05	23.96
1HGJ.PDB	O, B_HIS_159	N, B_TYR_162	H, B_TYR_162	2.94	2.06	21.10
1HGJ.PDB	O, F_ARG_170	NH1, B_ARG_163	HH12, B_ARG_163	2.72	1.75	12.61

1HGJ.PDB	O, B_TYR_162	N, B_ALA_166	H, B_ALA_166	2.86	1.89	2.61
1HGJ.PDB	O, B_ARG_163	N, B_LEU_167	H, B_LEU_167	2.77	1.81	8.42
1HGJ.PDB	O, B_ALA_166	N, B_ARG_170	H, B_ARG_170	2.83	1.95	21.36
1HGJ.PDB	O, B_GLU_128	NE, B_ARG_170	HE, B_ARG_170	2.79	1.92	22.95
1HGJ.PDB	OE2, B_GLU_131	NH1, B_ARG_170	HH11, B_ARG_170	2.80	1.80	6.39
1HGJ.PDB	O, B_LEU_167	N, B_PHE_171	H, B_PHE_171	2.93	2.01	16.69
1HGJ.PDB	O, D_ILE_140	N, C_ALA_11	H, C_ALA_11	2.85	1.95	19.06
1HGJ.PDB	O, D_GLN_27	N, C_THR_12	H, C_THR_12	2.99	2.03	8.05
1HGJ.PDB	O, D_PHE_138	N, C_LEU_13	H, C_LEU_13	2.99	2.02	7.89
1HGJ.PDB	O, D_ARG_25	N, C_CYS_14	H, C_CYS_14	2.76	1.85	16.80
1HGJ.PDB	O, D_GLY_136	N, C_LEU_15	H, C_LEU_15	2.95	1.97	3.95
1HGJ.PDB	O, D_GLY_23	N, C_GLY_16	H, C_GLY_16	2.89	1.98	18.54
1HGJ.PDB	O, C_HIS_18	ND1, C_HIS_17	HD1, C_HIS_17	2.94	2.08	23.78
1HGJ.PDB	O, D_TRP_21	N, C_HIS_18	H, C_HIS_18	2.86	1.97	20.63
1HGJ.PDB	OD1, C_ASN_322	N, C_VAL_20	H, C_VAL_20	2.78	1.82	9.76
1HGJ.PDB	O, C_VAL_36	N, C_THR_24	H, C_THR_24	2.86	1.93	13.58
1HGJ.PDB	O, C_ILE_34	N, C_VAL_26	H, C_VAL_26	2.80	1.85	11.08
1HGJ.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.82	1.80	8.63
1HGJ.PDB	O, C_ASP_31	N, C_THR_28	H, C_THR_28	2.73	1.88	23.51
1HGJ.PDB	O, C_VAL_26	N, C_ILE_34	H, C_ILE_34	2.90	1.95	12.50
1HGJ.PDB	O, C_THR_24	N, C_VAL_36	H, C_VAL_36	2.82	1.85	5.74
1HGJ.PDB	O, C_MET_320	N, C_THR_37	H, C_THR_37	2.89	1.92	6.83
1HGJ.PDB	O, C_LEU_316	N, C_THR_40	H, C_THR_40	2.90	2.05	25.12
1HGJ.PDB	O, C_LEU_314	N, C_LEU_42	H, C_LEU_42	2.80	1.93	22.39
1HGJ.PDB	O, C_PHE_294	N, C_GLN_44	H, C_GLN_44	2.82	1.85	7.42
1HGJ.PDB	O, C_SER_46	NE2, C_GLN_44	HE22, C_GLN_44	2.90	2.00	19.73
1HGJ.PDB	O, C_ASN_285	OG, C_SER_47	HG, C_SER_47	2.83	1.92	15.29
1HGJ.PDB	OD2, C_ASP_275	NZ, C_LYS_50	HZ1, C_LYS_50	2.74	1.82	22.76
1HGJ.PDB	O, C_PRO_273	N, C_ILE_51	H, C_ILE_51	2.85	1.89	9.03
1HGJ.PDB	O, C_ASP_275	N, C_ASN_53	H, C_ASN_53	2.78	1.94	25.31
1HGJ.PDB	O, C_GLU_280	NE2, C_HIS_56	HE2, C_HIS_56	2.97	2.05	17.85
1HGJ.PDB	OD2, C_ASP_85	N, C_ARG_57	H, C_ARG_57	2.84	1.90	12.58
1HGJ.PDB	O, C_THR_83	NE, C_ARG_57	HE, C_ARG_57	2.76	1.80	8.04
1HGJ.PDB	O, C_LEU_86	N, C_LEU_59	H, C_LEU_59	2.87	1.92	10.21
1HGJ.PDB	O, C_VAL_88	N, C_GLY_61	H, C_GLY_61	2.97	2.10	22.49
1HGJ.PDB	OD1, C_ASP_60	N, C_ILE_62	H, C_ILE_62	2.85	1.93	15.07
1HGJ.PDB	O, C_GLY_61	N, C_CYS_64	H, C_CYS_64	2.87	1.96	17.46
1HGJ.PDB	O, C_LEU_66	N, C_LEU_70	H, C_LEU_70	2.89	2.00	19.99
1HGJ.PDB	O, C_ILE_67	N, C_LEU_71	H, C_LEU_71	2.82	1.86	8.52
1HGJ.PDB	O, C_ASP_68	N, C_GLY_72	H, C_GLY_72	2.86	1.96	18.14
1HGJ.PDB	OD1, C_ASP_73	N, C_HIS_75	H, C_HIS_75	2.96	2.05	18.04
1HGJ.PDB	OD1, C_ASP_73	ND1, C_HIS_75	HD1, C_HIS_75	2.80	1.89	17.49
1HGJ.PDB	O, C_ASP_63	NE2, C_HIS_75	HE2, C_HIS_75	2.82	1.92	19.39
1HGJ.PDB	O, C_ASP_73	N, C_CYS_76	H, C_CYS_76	2.78	1.84	12.95
1HGJ.PDB	O, C_PRO_74	N, C_ASP_77	H, C_ASP_77	2.96	2.00	11.06
1HGJ.PDB	O, C_ARG_57	N, C_ASP_85	H, C_ASP_85	2.81	1.90	16.89
1HGJ.PDB	O, C_LEU_59	N, C_VAL_88	H, C_VAL_88	2.97	2.00	6.49
1HGJ.PDB	O, C_MET_268	N, C_GLU_89	H, C_GLU_89	2.80	1.85	10.39
1HGJ.PDB	OD1, C_ASP_60	NE, C_ARG_90	HE, C_ARG_90	2.88	1.91	9.03
1HGJ.PDB	O, C_SER_270	NH1, C_ARG_90	HH11, C_ARG_90	2.68	1.80	24.07
1HGJ.PDB	O, C_ALA_272	NH1, C_ARG_90	HH12, C_ARG_90	2.62	1.70	18.50
1HGJ.PDB	OD2, C_ASP_60	NH2, C_ARG_90	HH21, C_ARG_90	2.78	1.79	9.66
1HGJ.PDB	OD1, C_ASP_271	N, C_SER_91	H, C_SER_91	2.92	1.95	7.70
1HGJ.PDB	OD1, C_ASP_271	OG, C_SER_91	HG, C_SER_91	2.99	2.16	26.38
1HGJ.PDB	OD2, C_ASP_271	OG, C_SER_91	HG, C_SER_91	2.81	1.92	18.67
1HGJ.PDB	OD2, C_ASP_68	OG, C_SER_95	HG, C_SER_95	2.93	1.99	14.68
1HGJ.PDB	OD2, C_ASP_73	N, C_ASN_96	H, C_ASN_96	2.87	1.92	11.70
1HGJ.PDB	OD1, C_ASP_68	OH, C_TYR_100	HH, C_TYR_100	2.88	1.95	14.58

1HGJ.PDB	O, C_ILE_230	N, C_ASP_101	H, C_ASP_101	2.91	2.04	23.02
1HGJ.PDB	OD2, C_ASP_104	OG, C_SER_107	HG, C_SER_107	2.90	1.99	17.96
1HGJ.PDB	O, C_TYR_105	N, C_ARG_109	H, C_ARG_109	2.82	1.85	3.87
1HGJ.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.76	1.78	13.33
1HGJ.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.79	1.87	14.95
1HGJ.PDB	O, C_SER_107	N, C_LEU_111	H, C_LEU_111	2.85	1.89	7.06
1HGJ.PDB	O, C_ARG_109	N, C_ALA_113	H, C_ALA_113	2.95	2.06	19.71
1HGJ.PDB	O, C_SER_110	N, C_SER_114	H, C_SER_114	2.92	1.97	12.30
1HGJ.PDB	OE2, C_GLU_119	OG1, C_THR_117	HG1, C_THR_117	2.88	1.94	11.85
1HGJ.PDB	O, C_GLU_82	N, C_LEU_118	H, C_LEU_118	2.91	1.97	15.15
1HGJ.PDB	O, C_TYR_257	N, C_ILE_121	H, C_ILE_121	2.86	1.89	7.41
1HGJ.PDB	O, C_ARG_255	N, C_GLU_123	H, C_GLU_123	2.93	1.97	10.38
1HGJ.PDB	O, C_THR_155	N, C_THR_131	H, C_THR_131	2.74	1.84	18.58
1HGJ.PDB	OD1, C_ASN_152	N, C_ASN_133	H, C_ASN_133	2.86	1.94	15.99
1HGJ.PDB	O, C_GLY_146	N, C_SER_136	H, C_SER_136	2.75	1.85	18.24
1HGJ.PDB	OG, C_SER_136	N, C_ALA_138	H, C_ALA_138	2.91	1.97	13.65
1HGJ.PDB	O, C_GLY_144	NZ, C_LYS_140	HZ1, C_LYS_140	2.72	1.76	17.33
1HGJ.PDB	OD1, C_ASN_137	NZ, C_LYS_140	HZ2, C_LYS_140	2.71	1.72	13.24
1HGJ.PDB	OD2, C_ASP_77	NE, C_ARG_141	HE, C_ARG_141	2.82	1.99	27.42
1HGJ.PDB	O, C_PHE_147	NH1, C_ARG_141	HH12, C_ARG_141	2.55	1.62	17.29
1HGJ.PDB	OD1, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.81	1.89	21.37
1HGJ.PDB	OD2, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.74	1.86	24.47
1HGJ.PDB	O, C_GLY_72	NH2, C_ARG_141	HH22, C_ARG_141	2.89	1.91	10.48
1HGJ.PDB	OD1, C_ASN_137	OG, C_SER_145	HG, C_SER_145	2.92	2.08	24.33
1HGJ.PDB	O, C_SER_136	N, C_GLY_146	H, C_GLY_146	2.93	2.00	15.25
1HGJ.PDB	O, C_GLY_72	N, C_SER_149	H, C_SER_149	2.81	1.91	18.87
1HGJ.PDB	O, C_ALA_253	N, C_ASN_152	H, C_ASN_152	2.77	1.94	26.39
1HGJ.PDB	OH, C_TYR_195	NE1, C_TRP_153	HE1, C_TRP_153	2.84	1.96	21.72
1HGJ.PDB	O, C_THR_131	N, C_THR_155	H, C_THR_155	2.99	2.03	9.79
1HGJ.PDB	O, C_LEU_194	N, C_LYS_156	H, C_LYS_156	2.97	2.05	16.86
1HGJ.PDB	O, C_SER_247	N, C_LEU_164	H, C_LEU_164	2.72	1.87	24.03
1HGJ.PDB	O, C_ILE_245	N, C_VAL_166	H, C_VAL_166	2.96	2.01	10.78
1HGJ.PDB	O, C_LEU_243	OG1, C_THR_167	HG1, C_THR_167	2.93	2.04	19.65
1HGJ.PDB	O, C_LEU_243	N, C_MET_168	H, C_MET_168	2.91	1.99	17.19
1HGJ.PDB	O, C_ASP_241	N, C_ASN_170	H, C_ASN_170	2.89	1.92	9.78
1HGJ.PDB	O, C_PHE_174	ND2, C_ASN_170	HD21, C_ASN_170	2.84	1.88	9.63
1HGJ.PDB	O, C_VAL_237	ND2, C_ASN_170	HD22, C_ASN_170	2.87	2.05	26.94
1HGJ.PDB	O, C_VAL_237	N, C_LYS_176	H, C_LYS_176	2.90	1.97	14.44
1HGJ.PDB	OE2, C_GLU_123	NZ, C_LYS_176	HZ1, C_LYS_176	2.69	1.80	24.96
1HGJ.PDB	O, C_PHE_258	N, C_LEU_177	H, C_LEU_177	2.97	2.00	6.71
1HGJ.PDB	O, C_THR_235	N, C_TYR_178	H, C_TYR_178	2.79	1.83	4.13
1HGJ.PDB	OE1, C_GLU_123	OH, C_TYR_178	HH, C_TYR_178	2.77	1.82	8.51
1HGJ.PDB	OG1, C_THR_235	NE1, C_TRP_180	HE1, C_TRP_180	2.91	1.92	4.72
1HGJ.PDB	O, C_ASN_250	N, C_HIS_183	H, C_HIS_183	2.91	2.00	17.12
1HGJ.PDB	O, C_ARG_229	N, C_HIS_184	H, C_HIS_184	2.88	1.92	8.64
1HGJ.PDB	OG, C_SER_231	NE2, C_HIS_184	HE2, C_HIS_184	2.74	1.91	26.34
1HGJ.PDB	OG1, C_THR_187	N, C_GLU_190	H, C_GLU_190	2.91	1.96	12.15
1HGJ.PDB	OD1, C_ASN_250	NE2, C_GLN_191	HE21, C_GLN_191	2.99	2.02	8.22
1HGJ.PDB	O, C_GLN_197	NE2, C_GLN_191	HE22, C_GLN_191	2.89	1.97	17.35
1HGJ.PDB	O, C_GLN_189	OG1, C_THR_192	HG1, C_THR_192	2.84	1.97	20.14
1HGJ.PDB	O, C_GLN_189	N, C_SER_193	H, C_SER_193	2.85	1.90	9.95
1HGJ.PDB	O, C_GLN_191	N, C_TYR_195	H, C_TYR_195	2.82	1.86	10.13
1HGJ.PDB	O, C_TYR_161	NE2, C_GLN_197	HE21, C_GLN_197	2.90	1.95	11.26
1HGJ.PDB	O, C_ASN_248	NE2, C_GLN_197	HE22, C_GLN_197	2.87	1.94	15.42
1HGJ.PDB	OD1, C_ASN_246	NH2, C_ARG_201	HH21, C_ARG_201	2.59	1.74	25.86
1HGJ.PDB	O, C_ILE_213	N, C_VAL_202	H, C_VAL_202	2.99	2.07	16.15
1HGJ.PDB	O, C_ASN_246	N, C_THR_203	H, C_THR_203	2.94	2.00	13.61
1HGJ.PDB	OG1, C_THR_212	OG1, C_THR_203	HG1, C_THR_203	2.89	1.94	9.95

1HGJ.PDB	O, C_GLN_211	N, C_VAL_204	H, C_VAL_204	2.83	1.93	19.04
1HGJ.PDB	O, C_SER_209	N, C_THR_206	H, C_THR_206	2.91	1.95	8.75
1HGJ.PDB	OD1, C_ASP_241	N, C_ARG_207	H, C_ARG_207	2.88	1.92	10.11
1HGJ.PDB	O, C_VAL_204	N, C_GLN_211	H, C_GLN_211	2.90	1.98	16.77
1HGJ.PDB	O, C_VAL_202	N, C_ILE_213	H, C_ILE_213	2.84	1.92	15.65
1HGJ.PDB	O, C_ASN_216	NH1, C_ARG_220	HH12, C_ARG_220	2.91	2.10	29.44
1HGJ.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.66	1.82	26.85
1HGJ.PDB	O, C_ASN_216	NH2, C_ARG_220	HH22, C_ARG_220	2.76	1.88	22.85
1HGJ.PDB	O, C_LEU_226	N, C_VAL_223	H, C_VAL_223	2.82	1.86	9.59
1HGJ.PDB	O, C_CYS_97	NE, C_ARG_224	HE, C_ARG_224	2.77	1.91	24.59
1HGJ.PDB	O, C_CYS_97	NH2, C_ARG_224	HH21, C_ARG_224	2.94	2.09	27.65
1HGJ.PDB	O, C_VAL_223	N, C_LEU_226	H, C_LEU_226	2.93	1.99	13.69
1HGJ.PDB	O, C_SER_228	NH1, C_ARG_229	HH11, C_ARG_229	2.68	1.74	16.79
1HGJ.PDB	O, C_PRO_221	NH2, C_ARG_229	HH22, C_ARG_229	2.63	1.67	13.79
1HGJ.PDB	OD1, C_ASP_101	OG, C_SER_231	HG, C_SER_231	2.91	1.95	9.37
1HGJ.PDB	O, C_ASP_101	N, C_ILE_232	H, C_ILE_232	2.88	1.96	16.46
1HGJ.PDB	O, C_TRP_180	N, C_TYR_233	H, C_TYR_233	2.93	1.96	7.62
1HGJ.PDB	O, C_TYR_178	N, C_THR_235	H, C_THR_235	2.88	1.98	19.28
1HGJ.PDB	O, C_LYS_176	N, C_VAL_237	H, C_VAL_237	2.78	1.87	16.51
1HGJ.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.75	1.79	18.67
1HGJ.PDB	O, B_SER_71	NZ, C_LYS_238	HZ3, C_LYS_238	2.55	1.67	24.42
1HGJ.PDB	O, C_ASN_170	N, C_GLY_240	H, C_GLY_240	2.83	1.96	22.49
1HGJ.PDB	O, C_LYS_238	N, C_ASP_241	H, C_ASP_241	3.00	2.07	14.48
1HGJ.PDB	OD1, C_ASP_241	N, C_VAL_242	H, C_VAL_242	2.79	1.95	25.43
1HGJ.PDB	O, C_MET_168	N, C_LEU_243	H, C_LEU_243	2.93	1.95	4.94
1HGJ.PDB	O, C_SER_205	N, C_VAL_244	H, C_VAL_244	2.99	2.04	12.22
1HGJ.PDB	O, C_VAL_166	N, C_ILE_245	H, C_ILE_245	2.91	1.98	14.47
1HGJ.PDB	O, C_THR_203	N, C_ASN_246	H, C_ASN_246	2.94	1.97	6.29
1HGJ.PDB	OD1, C_ASN_165	ND2, C_ASN_246	HD22, C_ASN_246	2.89	1.93	12.15
1HGJ.PDB	O, C_LEU_164	N, C_SER_247	H, C_SER_247	2.92	2.00	17.46
1HGJ.PDB	O, C_HIS_183	ND2, C_ASN_250	HD22, C_ASN_250	2.86	1.91	11.73
1HGJ.PDB	O, C_GLY_181	N, C_ILE_252	H, C_ILE_252	3.00	2.04	10.63
1HGJ.PDB	O, C_ASN_152	N, C_ALA_253	H, C_ALA_253	2.89	2.00	20.86
1HGJ.PDB	OD1, C_ASN_133	NH2, C_ARG_255	HH22, C_ARG_255	2.54	1.71	27.08
1HGJ.PDB	O, C_ILE_121	N, C_TYR_257	H, C_TYR_257	2.90	2.06	24.92
1HGJ.PDB	O, C_LEU_177	N, C_PHE_258	H, C_PHE_258	2.92	1.95	7.10
1HGJ.PDB	OG, C_SER_115	N, C_ARG_261	H, C_ARG_261	2.96	2.02	14.08
1HGJ.PDB	OE2, C_GLU_119	NH1, C_ARG_261	HH12, C_ARG_261	2.65	1.83	28.56
1HGJ.PDB	OE1, C_GLU_119	NH2, C_ARG_261	HH22, C_ARG_261	2.92	2.03	23.97
1HGJ.PDB	OD2, C_ASP_85	NZ, C_LYS_264	HZ3, C_LYS_264	2.82	1.83	14.94
1HGJ.PDB	O, C_PHE_87	N, C_MET_268	H, C_MET_268	2.85	1.94	18.47
1HGJ.PDB	O, C_PRO_284	OG, C_SER_270	HG, C_SER_270	2.82	1.88	11.05
1HGJ.PDB	O, C_ILE_51	N, C_ASP_275	H, C_ASP_275	2.97	2.06	19.32
1HGJ.PDB	OD1, C_ASP_275	N, C_THR_276	H, C_THR_276	2.79	1.94	23.72
1HGJ.PDB	O, C_ASN_54	N, C_SER_279	H, C_SER_279	2.79	1.87	15.26
1HGJ.PDB	O, C_TYR_302	N, C_ILE_282	H, C_ILE_282	2.92	1.95	6.05
1HGJ.PDB	O, C_THR_283	N, C_GLY_286	H, C_GLY_286	2.79	1.87	14.96
1HGJ.PDB	O, C_LYS_50	N, C_SER_287	H, C_SER_287	2.81	1.85	7.28
1HGJ.PDB	O, C_ALA_304	ND2, C_ASN_290	HD22, C_ASN_290	2.84	1.93	18.26
1HGJ.PDB	OE1, C_GLN_44	NZ, C_LYS_292	HZ1, C_LYS_292	2.73	1.72	10.59
1HGJ.PDB	OD2, C_ASP_291	NZ, C_LYS_292	HZ3, C_LYS_292	2.82	1.84	16.66
1HGJ.PDB	O, C_LYS_307	N, C_GLN_295	H, C_GLN_295	2.91	2.01	20.39
1HGJ.PDB	O, C_ASN_298	NE2, C_GLN_295	HE21, C_GLN_295	2.78	1.83	8.19
1HGJ.PDB	O, C_GLN_44	N, C_ASN_296	H, C_ASN_296	2.84	1.91	13.62
1HGJ.PDB	OE1, C_GLN_295	N, C_VAL_297	H, C_VAL_297	2.75	1.95	28.92
1HGJ.PDB	O, D_LYS_68	NZ, C_LYS_299	HZ2, C_LYS_299	2.96	1.96	14.80
1HGJ.PDB	OD1, C_ASN_298	N, C_ILE_300	H, C_ILE_300	2.82	1.93	19.65
1HGJ.PDB	O, C_ILE_282	N, C_TYR_302	H, C_TYR_302	2.87	2.05	27.80

1HGJ.PDB	O, C_LYS_264	OH, C_TYR_302	HH, C_TYR_302	2.65	1.87	29.71
1HGJ.PDB	O, D_LYS_62	N, C_GLY_303	H, C_GLY_303	2.93	1.98	10.54
1HGJ.PDB	O, C_GLN_295	N, C_VAL_309	H, C_VAL_309	2.88	2.06	26.91
1HGJ.PDB	OG, D_SER_93	N, C_LYS_310	H, C_LYS_310	3.00	2.04	11.61
1HGJ.PDB	OD1, D_ASP_86	NZ, C_LYS_310	HZ3, C_LYS_310	2.94	2.10	29.37
1HGJ.PDB	OE2, C_GLU_41	N, C_LEU_314	H, C_LEU_314	2.78	1.85	13.27
1HGJ.PDB	OE1, C_GLU_41	NZ, C_LYS_315	HZ3, C_LYS_315	2.86	1.91	20.22
1HGJ.PDB	O, C_THR_40	N, C_LEU_316	H, C_LEU_316	2.82	1.87	11.05
1HGJ.PDB	OD1, D_ASN_104	N, C_ALA_317	H, C_ALA_317	2.74	1.82	13.77
1HGJ.PDB	O, C_ASN_38	N, C_THR_318	H, C_THR_318	2.92	2.00	16.68
1HGJ.PDB	O, C_VAL_20	ND2, C_ASN_322	HD21, C_ASN_322	2.87	1.94	14.85
1HGJ.PDB	OE2, C_GLU_35	ND2, C_ASN_322	HD22, C_ASN_322	2.88	1.97	19.99
1HGJ.PDB	OE1, D_GLU_15	NZ, C_LYS_326	HZ1, C_LYS_326	2.91	1.86	5.48
1HGJ.PDB	OD2, D_ASP_112	N, D_GLY_1	H2, D_GLY_1	2.78	1.78	13.54
1HGJ.PDB	OD1, D_ASP_109	N, D_LEU_2	H, D_LEU_2	2.88	1.99	20.57
1HGJ.PDB	OD2, D_ASP_112	N, D_PHE_3	H, D_PHE_3	2.81	2.00	27.45
1HGJ.PDB	OD2, D_ASP_112	N, D_GLY_4	H, D_GLY_4	2.87	1.96	16.53
1HGJ.PDB	OD1, D_ASP_112	N, D_ALA_5	H, D_ALA_5	2.85	1.99	23.99
1HGJ.PDB	O, D_GLY_4	N, D_PHE_9	H, D_PHE_9	2.80	1.87	14.24
1HGJ.PDB	O, D_GLY_13	ND2, D_ASN_12	HD22, D_ASN_12	2.90	2.01	19.14
1HGJ.PDB	O, C_VAL_323	N, D_GLY_13	H, D_GLY_13	2.70	1.77	13.01
1HGJ.PDB	O, C_HIS_17	N, D_TRP_14	H, D_TRP_14	2.84	1.88	10.47
1HGJ.PDB	OG1, D_THR_41	N, D_TRP_21	H, D_TRP_21	2.94	2.03	16.88
1HGJ.PDB	O, C_GLY_16	N, D_GLY_23	H, D_GLY_23	2.95	2.03	16.60
1HGJ.PDB	O, D_ALA_35	N, D_PHE_24	H, D_PHE_24	2.84	1.87	6.75
1HGJ.PDB	O, C_CYS_14	N, D_ARG_25	H, D_ARG_25	2.96	2.03	15.69
1HGJ.PDB	OE1, D_GLN_34	NE, D_ARG_25	HE, D_ARG_25	2.65	1.80	23.08
1HGJ.PDB	O, D_GLY_33	N, D_HIS_26	H, D_HIS_26	2.87	1.95	17.26
1HGJ.PDB	O, C_THR_12	N, D_GLN_27	H, D_GLN_27	2.96	2.04	16.68
1HGJ.PDB	O, D_GLY_31	N, D_ASN_28	H, D_ASN_28	2.92	1.97	10.77
1HGJ.PDB	OD1, D_ASN_146	ND2, D_ASN_28	HD21, D_ASN_28	2.98	2.03	11.81
1HGJ.PDB	OD1, D_ASN_28	N, D_GLU_30	H, D_GLU_30	2.82	1.99	26.55
1HGJ.PDB	O, D_HIS_26	N, D_GLY_33	H, D_GLY_33	2.97	2.10	23.23
1HGJ.PDB	O, D_PHE_24	N, D_ALA_35	H, D_ALA_35	2.80	1.92	21.75
1HGJ.PDB	O, D_TYR_22	N, D_ASP_37	H, D_ASP_37	2.70	1.76	11.08
1HGJ.PDB	OD2, D_ASP_37	N, D_SER_40	H, D_SER_40	2.95	1.99	9.26
1HGJ.PDB	OD2, D_ASP_37	OG, D_SER_40	HG, D_SER_40	2.82	1.96	22.49
1HGJ.PDB	O, D_ASP_37	OG1, D_THR_41	HG1, D_THR_41	2.76	1.85	16.95
1HGJ.PDB	O, D_LEU_38	N, D_GLN_42	H, D_GLN_42	2.96	2.03	15.57
1HGJ.PDB	OD1, D_ASP_46	NE2, D_GLN_42	HE22, D_GLN_42	2.81	1.92	21.12
1HGJ.PDB	O, D_LYS_39	N, D_ALA_43	H, D_ALA_43	2.97	2.01	10.81
1HGJ.PDB	O, D_SER_40	N, D_ALA_44	H, D_ALA_44	2.97	1.99	1.97
1HGJ.PDB	O, D_THR_41	N, D_ILE_45	H, D_ILE_45	2.89	1.93	10.07
1HGJ.PDB	O, D_GLN_42	N, D_ASP_46	H, D_ASP_46	2.76	1.79	4.41
1HGJ.PDB	OE2, D_GLU_114	NE2, D_GLN_47	HE21, D_GLN_47	2.94	2.03	18.44
1HGJ.PDB	O, D_ALA_43	NE2, D_GLN_47	HE22, D_GLN_47	2.90	2.02	20.80
1HGJ.PDB	O, D_ILE_45	N, D_ASN_49	H, D_ASN_49	2.90	1.96	15.06
1HGJ.PDB	O, D_ASP_46	N, D_GLY_50	H, D_GLY_50	2.88	2.00	21.98
1HGJ.PDB	OG1, D_THR_107	NZ, D_LYS_51	HZ1, D_LYS_51	2.97	1.99	16.18
1HGJ.PDB	OE1, D_GLU_103	NZ, D_LYS_51	HZ2, D_LYS_51	2.80	1.76	6.89
1HGJ.PDB	ND1, D_HIS_106	NZ, D_LYS_51	HZ3, D_LYS_51	2.79	1.82	16.80
1HGJ.PDB	O, D_ILE_48	N, D_LEU_52	H, D_LEU_52	2.89	1.98	17.52
1HGJ.PDB	O, D_ASN_49	N, D_ASN_53	H, D_ASN_53	2.86	1.92	13.12
1HGJ.PDB	O, A_THR_28	NE, D_ARG_54	HE, D_ARG_54	2.94	1.98	10.71
1HGJ.PDB	OE1, D_GLU_57	NH1, D_ARG_54	HH11, D_ARG_54	2.87	1.86	9.17
1HGJ.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.84	1.88	15.58
1HGJ.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.89	1.91	5.59
1HGJ.PDB	O, C_LYS_299	NZ, D_LYS_68	HZ1, D_LYS_68	2.93	1.91	11.63

1HGJ.PDB	OE2, D_GLU_85	NZ, D_LYS_68	HZ2, D_LYS_68	2.82	1.80	11.23
1HGJ.PDB	OG, E_SER_107	N, D_ARG_76	H, D_ARG_76	2.86	1.90	9.67
1HGJ.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.85	1.89	10.87
1HGJ.PDB	OE2, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.76	1.76	7.89
1HGJ.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.68	1.69	5.65
1HGJ.PDB	OE1, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.71	1.72	5.59
1HGJ.PDB	OE1, D_GLU_74	NE2, D_GLN_78	HE22, D_GLN_78	2.88	1.94	14.79
1HGJ.PDB	O, D_GLY_75	N, D_ASP_79	H, D_ASP_79	2.96	2.02	12.85
1HGJ.PDB	O, D_GLN_78	N, D_LYS_82	H, D_LYS_82	2.93	1.96	6.74
1HGJ.PDB	O, D_ASP_79	N, D_TYR_83	H, D_TYR_83	2.85	1.90	12.33
1HGJ.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.63	1.81	25.72
1HGJ.PDB	O, D_LEU_80	N, D_VAL_84	H, D_VAL_84	2.81	1.84	7.09
1HGJ.PDB	O, D_LYS_82	N, D_ASP_86	H, D_ASP_86	2.93	1.96	7.56
1HGJ.PDB	O, D_TYR_83	N, D_THR_87	H, D_THR_87	2.89	1.94	10.26
1HGJ.PDB	O, D_VAL_84	N, D_LYS_88	H, D_LYS_88	2.98	2.07	17.30
1HGJ.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.75	1.72	7.31
1HGJ.PDB	O, D_GLU_85	N, D_ILE_89	H, D_ILE_89	2.85	1.88	2.88
1HGJ.PDB	O, D_LYS_88	N, D_TRP_92	H, D_TRP_92	2.93	1.96	4.62
1HGJ.PDB	O, D_ILE_89	N, D_SER_93	H, D_SER_93	2.81	1.94	21.33
1HGJ.PDB	O, D_ILE_89	OG, D_SER_93	HG, D_SER_93	2.87	1.95	15.74
1HGJ.PDB	O, D_ASP_90	N, D_TYR_94	H, D_TYR_94	2.84	1.94	18.59
1HGJ.PDB	O, D_LEU_91	N, D_ASN_95	H, D_ASN_95	2.98	2.00	5.61
1HGJ.PDB	O, D_TYR_94	N, D_LEU_98	H, D_LEU_98	2.94	1.97	5.79
1HGJ.PDB	O, D_ASN_95	N, D_LEU_99	H, D_LEU_99	2.89	1.98	17.69
1HGJ.PDB	O, D_LEU_98	N, D_LEU_102	H, D_LEU_102	2.94	1.98	8.88
1HGJ.PDB	O, D_LEU_99	N, D_GLU_103	H, D_GLU_103	2.96	1.99	8.34
1HGJ.PDB	O, D_VAL_100	N, D_ASN_104	H, D_ASN_104	2.80	1.86	13.01
1HGJ.PDB	O, C_LYS_27	ND2, D_ASN_104	HD22, D_ASN_104	2.90	1.94	10.67
1HGJ.PDB	O, D_LEU_102	N, D_HIS_106	H, D_HIS_106	2.93	1.97	8.46
1HGJ.PDB	O, D_GLU_103	N, D_THR_107	H, D_THR_107	2.85	1.96	20.31
1HGJ.PDB	O, D_HIS_106	N, D_LEU_110	H, D_LEU_110	2.79	1.83	9.65
1HGJ.PDB	O, D_THR_107	OG1, D_THR_111	HG1, D_THR_111	2.84	1.88	5.73
1HGJ.PDB	O, D_ASP_109	N, D_SER_113	H, D_SER_113	2.82	1.86	7.21
1HGJ.PDB	O, B_LEU_2	OG, D_SER_113	HG, D_SER_113	2.68	1.87	27.58
1HGJ.PDB	O, D_LEU_110	N, D_GLU_114	H, D_GLU_114	2.94	1.99	11.05
1HGJ.PDB	O, D_ASP_112	N, D_ASN_116	H, D_ASN_116	2.97	2.01	9.82
1HGJ.PDB	O, D_SER_113	N, D_LYS_117	H, D_LYS_117	2.74	1.86	21.58
1HGJ.PDB	O, D_GLU_114	N, D_LEU_118	H, D_LEU_118	2.99	2.04	11.08
1HGJ.PDB	O, D_ASN_116	N, D_GLU_120	H, D_GLU_120	2.94	1.96	1.58
1HGJ.PDB	O, D_LYS_117	N, D_LYS_121	H, D_LYS_121	2.92	2.02	18.90
1HGJ.PDB	O, D_PHE_119	N, D_ARG_123	H, D_ARG_123	2.94	1.98	8.81
1HGJ.PDB	OE2, D_GLU_120	NH1, D_ARG_123	HH11, D_ARG_123	2.74	1.85	23.39
1HGJ.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.80	1.98	27.33
1HGJ.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.87	2.00	21.99
1HGJ.PDB	OH, B_TYR_141	NH1, D_ARG_127	HH12, D_ARG_127	2.99	2.02	12.89
1HGJ.PDB	O, D_HIS_159	ND2, D_ASN_129	HD21, D_ASN_129	2.95	1.99	10.63
1HGJ.PDB	OH, D_TYR_157	ND2, D_ASN_129	HD22, D_ASN_129	2.79	1.84	10.20
1HGJ.PDB	O, D_LYS_139	N, D_GLU_131	H, D_GLU_131	2.95	2.01	13.86
1HGJ.PDB	O, D_CYS_137	N, D_MET_133	H, D_MET_133	2.85	1.92	14.74
1HGJ.PDB	OD1, D_ASN_135	N, D_CYS_137	H, D_CYS_137	2.89	1.99	19.26
1HGJ.PDB	O, C_LEU_13	N, D_PHE_138	H, D_PHE_138	2.74	1.87	22.25
1HGJ.PDB	O, D_GLU_131	N, D_LYS_139	H, D_LYS_139	2.81	1.86	10.15
1HGJ.PDB	O, C_ALA_11	N, D_ILE_140	H, D_ILE_140	2.80	1.87	15.19
1HGJ.PDB	O, D_ASN_129	N, D_TYR_141	H, D_TYR_141	2.96	2.02	12.67
1HGJ.PDB	OE2, D_GLU_30	N, D_ASN_146	H, D_ASN_146	2.86	1.92	14.29
1HGJ.PDB	O, D_ASP_145	N, D_ILE_149	H, D_ILE_149	2.91	1.96	10.44
1HGJ.PDB	O, D_ASN_146	N, D_GLU_150	H, D_GLU_150	2.91	1.98	15.92
1HGJ.PDB	O, D_ALA_147	N, D_SER_151	H, D_SER_151	2.90	1.98	17.07

1HGJ.PDB	O, D_CYS_148	OG, D_SER_151	HG, D_SER_151	2.70	1.86	22.84
1HGJ.PDB	O, D_GLU_150	N, D_ASN_154	H, D_ASN_154	2.80	1.83	5.11
1HGJ.PDB	O, D_SER_151	N, D_THR_156	H, D_THR_156	2.73	1.90	25.93
1HGJ.PDB	OD1, D_ASN_154	OG1, D_THR_156	HG1, D_THR_156	2.71	1.81	16.75
1HGJ.PDB	NE2, D_HIS_142	OH, D_TYR_157	HH, D_TYR_157	2.78	1.88	18.06
1HGJ.PDB	OD1, D_ASP_158	N, D_ASP_160	H, D_ASP_160	2.92	2.05	23.79
1HGJ.PDB	O, D_HIS_159	N, D_TYR_162	H, D_TYR_162	2.94	2.05	20.16
1HGJ.PDB	O, B_ARG_170	NH1, D_ARG_163	HH12, D_ARG_163	2.74	1.76	11.80
1HGJ.PDB	O, D_TYR_162	N, D_ALA_166	H, D_ALA_166	2.85	1.88	3.22
1HGJ.PDB	O, D_ARG_163	N, D_LEU_167	H, D_LEU_167	2.76	1.82	10.09
1HGJ.PDB	O, D_ASP_164	N, D_ASN_168	H, D_ASN_168	3.00	2.04	9.26
1HGJ.PDB	O, D_ALA_166	N, D_ARG_170	H, D_ARG_170	2.83	1.97	22.68
1HGJ.PDB	O, D_GLU_128	NE, D_ARG_170	HE, D_ARG_170	2.77	1.90	22.62
1HGJ.PDB	OE2, D_GLU_131	NH1, D_ARG_170	HH11, D_ARG_170	2.79	1.80	6.55
1HGJ.PDB	O, D_LEU_167	N, D_PHE_171	H, D_PHE_171	2.92	2.00	16.37
1HGJ.PDB	O, F_ILE_140	N, E_ALA_11	H, E_ALA_11	2.86	1.96	18.18
1HGJ.PDB	O, F_GLN_27	N, E_THR_12	H, E_THR_12	2.93	2.00	15.55
1HGJ.PDB	O, F_PHE_138	N, E_LEU_13	H, E_LEU_13	2.96	1.99	8.56
1HGJ.PDB	O, F_ARG_25	N, E_CYS_14	H, E_CYS_14	2.66	1.82	24.90
1HGJ.PDB	O, F_GLY_136	N, E_LEU_15	H, E_LEU_15	2.91	1.94	3.68
1HGJ.PDB	O, F_GLY_23	N, E_GLY_16	H, E_GLY_16	2.87	1.96	18.32
1HGJ.PDB	O, E_HIS_18	ND1, E_HIS_17	HD1, E_HIS_17	2.90	2.02	21.78
1HGJ.PDB	O, F_TRP_21	N, E_HIS_18	H, E_HIS_18	2.83	1.96	22.19
1HGJ.PDB	OD1, E_ASN_322	N, E_VAL_20	H, E_VAL_20	2.78	1.83	10.50
1HGJ.PDB	O, E_VAL_36	N, E_THR_24	H, E_THR_24	2.85	1.93	16.11
1HGJ.PDB	O, E_ILE_34	N, E_VAL_26	H, E_VAL_26	2.82	1.87	11.16
1HGJ.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.81	1.79	8.50
1HGJ.PDB	O, E_ASP_31	N, E_THR_28	H, E_THR_28	2.74	1.89	24.59
1HGJ.PDB	O, E_VAL_26	N, E_ILE_34	H, E_ILE_34	2.87	1.93	12.94
1HGJ.PDB	O, E_THR_24	N, E_VAL_36	H, E_VAL_36	2.82	1.85	5.68
1HGJ.PDB	O, E_MET_320	N, E_THR_37	H, E_THR_37	2.86	1.90	7.27
1HGJ.PDB	O, E_LEU_316	N, E_THR_40	H, E_THR_40	2.85	2.00	25.13
1HGJ.PDB	O, E_LEU_314	N, E_LEU_42	H, E_LEU_42	2.82	1.95	22.41
1HGJ.PDB	O, E_PHE_294	N, E_GLN_44	H, E_GLN_44	2.85	1.88	6.55
1HGJ.PDB	O, E_SER_46	NE2, E_GLN_44	HE22, E_GLN_44	2.90	2.00	19.51
1HGJ.PDB	O, E_ASN_285	OG, E_SER_47	HG, E_SER_47	2.83	1.92	15.25
1HGJ.PDB	OD2, E_ASP_275	NZ, E_LYS_50	HZ1, E_LYS_50	2.74	1.82	22.90
1HGJ.PDB	O, E_PRO_273	N, E_ILE_51	H, E_ILE_51	2.84	1.88	9.36
1HGJ.PDB	O, E_ASP_275	N, E_ASN_53	H, E_ASN_53	2.80	1.95	24.30
1HGJ.PDB	O, E_GLU_280	NE2, E_HIS_56	HE2, E_HIS_56	2.98	2.06	17.67
1HGJ.PDB	OD2, E_ASP_85	N, E_ARG_57	H, E_ARG_57	2.82	1.89	13.47
1HGJ.PDB	O, E_THR_83	NE, E_ARG_57	HE, E_ARG_57	2.78	1.81	7.69
1HGJ.PDB	O, E_LEU_86	N, E_LEU_59	H, E_LEU_59	2.87	1.91	10.09
1HGJ.PDB	O, E_VAL_88	N, E_GLY_61	H, E_GLY_61	2.97	2.10	22.60
1HGJ.PDB	OD1, E_ASP_60	N, E_ILE_62	H, E_ILE_62	2.86	1.94	15.40
1HGJ.PDB	O, E_GLY_61	N, E_CYS_64	H, E_CYS_64	2.90	1.99	17.47
1HGJ.PDB	O, E_LEU_66	N, E_LEU_70	H, E_LEU_70	2.91	2.02	20.49
1HGJ.PDB	O, E_ILE_67	N, E_LEU_71	H, E_LEU_71	2.82	1.86	7.76
1HGJ.PDB	O, E_ASP_68	N, E_GLY_72	H, E_GLY_72	2.90	1.99	18.41
1HGJ.PDB	OD1, E_ASP_73	ND1, E_HIS_75	HD1, E_HIS_75	2.80	1.88	17.19
1HGJ.PDB	O, E_ASP_63	NE2, E_HIS_75	HE2, E_HIS_75	2.86	1.95	19.12
1HGJ.PDB	O, E_ASP_73	N, E_CYS_76	H, E_CYS_76	2.76	1.82	13.01
1HGJ.PDB	O, E_PRO_74	N, E_ASP_77	H, E_ASP_77	2.93	1.97	10.57
1HGJ.PDB	O, E_CYS_76	N, E_PHE_79	H, E_PHE_79	2.99	2.02	4.96
1HGJ.PDB	O, E_ARG_57	N, E_ASP_85	H, E_ASP_85	2.80	1.90	17.59
1HGJ.PDB	O, E_LEU_59	N, E_VAL_88	H, E_VAL_88	2.98	2.01	5.78
1HGJ.PDB	O, E_MET_268	N, E_GLU_89	H, E_GLU_89	2.79	1.83	9.12
1HGJ.PDB	OD1, E_ASP_60	NE, E_ARG_90	HE, E_ARG_90	2.91	1.94	8.87

1HGJ.PDB	O, E_SER.270	NH1, E_ARG.90	HH11, E_ARG.90	2.71	1.84	24.06
1HGJ.PDB	O, E_ALA.272	NH1, E_ARG.90	HH12, E_ARG.90	2.60	1.68	18.01
1HGJ.PDB	OD2, E_ASP.60	NH2, E_ARG.90	HH21, E_ARG.90	2.83	1.83	8.62
1HGJ.PDB	OD1, E_ASP.271	N, E_SER.91	H, E_SER.91	2.91	1.94	8.21
1HGJ.PDB	OD1, E_ASP.271	OG, E_SER.91	HG, E_SER.91	2.99	2.15	25.95
1HGJ.PDB	OD2, E_ASP.271	OG, E_SER.91	HG, E_SER.91	2.82	1.92	18.47
1HGJ.PDB	OD2, E_ASP.68	OG, E_SER.95	HG, E_SER.95	2.94	2.00	13.81
1HGJ.PDB	OD2, E_ASP.73	N, E_ASN.96	H, E_ASN.96	2.91	1.95	10.69
1HGJ.PDB	OD1, E_ASP.68	OH, E_TYR.100	HH, E_TYR.100	2.88	1.94	12.28
1HGJ.PDB	O, E_ILE.230	N, E_ASP.101	H, E_ASP.101	2.96	2.10	23.29
1HGJ.PDB	OD2, E_ASP.104	OG, E_SER.107	HG, E_SER.107	2.85	1.94	18.67
1HGJ.PDB	O, E_TYR.105	N, E_ARG.109	H, E_ARG.109	2.87	1.90	3.75
1HGJ.PDB	OE2, F_GLU.67	NH2, E_ARG.109	HH21, E_ARG.109	2.76	1.77	12.82
1HGJ.PDB	OD2, D_ASP.79	OG, E_SER.110	HG, E_SER.110	2.79	1.87	15.96
1HGJ.PDB	O, E_SER.107	N, E_LEU.111	H, E_LEU.111	2.87	1.90	6.50
1HGJ.PDB	O, E_ARG.109	N, E_ALA.113	H, E_ALA.113	2.94	2.05	20.26
1HGJ.PDB	O, E_SER.110	N, E_SER.114	H, E_SER.114	2.90	1.95	11.85
1HGJ.PDB	OE2, E_GLU.119	OG1, E_THR.117	HG1, E_THR.117	2.91	1.96	10.96
1HGJ.PDB	O, E_GLU.82	N, E_LEU.118	H, E_LEU.118	2.93	2.00	15.98
1HGJ.PDB	O, E_TYR.257	N, E_ILE.121	H, E_ILE.121	2.86	1.90	7.59
1HGJ.PDB	O, E_ARG.255	N, E_GLU.123	H, E_GLU.123	2.95	1.98	9.79
1HGJ.PDB	O, E_THR.155	N, E_THR.131	H, E_THR.131	2.73	1.86	21.20
1HGJ.PDB	OD1, E_ASN.152	N, E_ASN.133	H, E_ASN.133	2.87	1.94	15.99
1HGJ.PDB	O, E_GLY.146	N, E_SER.136	H, E_SER.136	2.74	1.83	17.73
1HGJ.PDB	OG, E_SER.136	N, E_ALA.138	H, E_ALA.138	2.94	2.00	14.03
1HGJ.PDB	O, E_GLY.144	NZ, E_LYS.140	HZ1, E_LYS.140	2.75	1.78	16.45
1HGJ.PDB	OD1, E_ASN.137	NZ, E_LYS.140	HZ2, E_LYS.140	2.71	1.72	13.56
1HGJ.PDB	OD2, E_ASP.77	NE, E_ARG.141	HE, E_ARG.141	2.84	2.00	27.31
1HGJ.PDB	O, E_PHE.147	NH1, E_ARG.141	HH12, E_ARG.141	2.54	1.62	17.41
1HGJ.PDB	OD1, E_ASP.77	NH2, E_ARG.141	HH21, E_ARG.141	2.84	1.92	21.35
1HGJ.PDB	OD2, E_ASP.77	NH2, E_ARG.141	HH21, E_ARG.141	2.75	1.86	24.32
1HGJ.PDB	O, E_GLY.72	NH2, E_ARG.141	HH22, E_ARG.141	2.88	1.90	10.71
1HGJ.PDB	OD1, E_ASN.137	OG, E_SER.145	HG, E_SER.145	2.96	2.12	24.46
1HGJ.PDB	O, E_SER.136	N, E_GLY.146	H, E_GLY.146	2.92	1.99	15.20
1HGJ.PDB	O, E_GLY.72	N, E_SER.149	H, E_SER.149	2.83	1.94	19.83
1HGJ.PDB	O, E_ALA.253	N, E_ASN.152	H, E_ASN.152	2.81	1.98	26.27
1HGJ.PDB	OH, E_TYR.195	NE1, E_TRP.153	HE1, E_TRP.153	2.83	1.93	19.26
1HGJ.PDB	O, E_LEU.194	N, E_LYS.156	H, E_LYS.156	2.96	2.04	16.52
1HGJ.PDB	O, E_SER.193	NZ, E_LYS.156	HZ2, E_LYS.156	2.72	1.80	21.90
1HGJ.PDB	O, E_SER.247	N, E_LEU.164	H, E_LEU.164	2.72	1.87	23.95
1HGJ.PDB	O, E_ILE.245	N, E_VAL.166	H, E_VAL.166	2.99	2.04	11.20
1HGJ.PDB	O, E_LEU.243	OG1, E_THR.167	HG1, E_THR.167	2.97	2.09	21.09
1HGJ.PDB	O, E_LEU.243	N, E_MET.168	H, E_MET.168	2.90	1.98	16.52
1HGJ.PDB	O, E_ASP.241	N, E_ASN.170	H, E_ASN.170	2.90	1.94	11.02
1HGJ.PDB	O, E_PHE.174	ND2, E_ASN.170	HD21, E_ASN.170	2.85	1.90	10.04
1HGJ.PDB	O, E_VAL.237	ND2, E_ASN.170	HD22, E_ASN.170	2.87	2.05	27.43
1HGJ.PDB	O, E_VAL.237	N, E_LYS.176	H, E_LYS.176	2.91	1.97	13.40
1HGJ.PDB	OE2, E_GLU.123	NZ, E_LYS.176	HZ1, E_LYS.176	2.69	1.80	25.95
1HGJ.PDB	O, E_PHE.258	N, E_LEU.177	H, E_LEU.177	2.99	2.02	6.31
1HGJ.PDB	O, E_THR.235	N, E_TYR.178	H, E_TYR.178	2.83	1.86	3.63
1HGJ.PDB	OE1, E_GLU.123	OH, E_TYR.178	HH, E_TYR.178	2.77	1.83	11.08
1HGJ.PDB	OG1, E_THR.235	NE1, E_TRP.180	HE1, E_TRP.180	2.94	1.96	4.45
1HGJ.PDB	O, E_ASN.250	N, E_HIS.183	H, E_HIS.183	2.92	2.00	17.04
1HGJ.PDB	O, E_ARG.229	N, E_HIS.184	H, E_HIS.184	2.87	1.92	10.49
1HGJ.PDB	OG, E_SER.231	NE2, E_HIS.184	HE2, E_HIS.184	2.75	1.92	26.56
1HGJ.PDB	OG1, E_THR.187	N, E_GLU.190	H, E_GLU.190	2.90	1.96	12.58
1HGJ.PDB	O, E_GLN.197	NE2, E_GLN.191	HE22, E_GLN.191	2.91	1.99	17.51
1HGJ.PDB	O, E_ASN.188	OG1, E_THR.192	HG1, E_THR.192	2.94	1.98	6.07

1HGJ.PDB	O, E_GLN_189	N, E_SER_193	H, E_SER_193	2.85	1.87	2.13
1HGJ.PDB	O, E_GLU_190	N, E_LEU_194	H, E_LEU_194	2.97	2.00	9.20
1HGJ.PDB	O, E_GLN_191	N, E_TYR_195	H, E_TYR_195	2.80	1.85	9.91
1HGJ.PDB	O, E_TYR_195	N, E_GLN_197	H, E_GLN_197	2.71	1.92	29.63
1HGJ.PDB	O, E_TYR_161	NE2, E_GLN_197	HE21, E_GLN_197	2.91	1.96	10.54
1HGJ.PDB	O, E_ASN_248	NE2, E_GLN_197	HE22, E_GLN_197	2.87	1.94	14.62
1HGJ.PDB	OD1, E_ASN_246	NH2, E_ARG_201	HH21, E_ARG_201	2.59	1.74	26.30
1HGJ.PDB	O, E_ILE_213	N, E_VAL_202	H, E_VAL_202	3.00	2.07	14.91
1HGJ.PDB	O, E_ASN_246	N, E_THR_203	H, E_THR_203	2.93	1.98	11.44
1HGJ.PDB	OG1, E_THR_212	OG1, E_THR_203	HG1, E_THR_203	2.93	1.99	12.00
1HGJ.PDB	O, E_GLN_211	N, E_VAL_204	H, E_VAL_204	2.84	1.94	19.22
1HGJ.PDB	O, E_SER_209	N, E_THR_206	H, E_THR_206	2.94	1.97	8.33
1HGJ.PDB	OD1, E_ASP_241	N, E_ARG_207	H, E_ARG_207	2.88	1.92	9.33
1HGJ.PDB	OD1, C_ASP_101	NE2, E_GLN_210	HE22, E_GLN_210	2.94	2.10	26.45
1HGJ.PDB	O, E_VAL_204	N, E_GLN_211	H, E_GLN_211	2.90	1.97	16.00
1HGJ.PDB	O, E_VAL_202	N, E_ILE_213	H, E_ILE_213	2.86	1.94	15.90
1HGJ.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.69	1.86	28.41
1HGJ.PDB	O, E_ASN_216	NH2, E_ARG_220	HH22, E_ARG_220	2.77	1.90	23.93
1HGJ.PDB	O, E_LEU_226	N, E_VAL_223	H, E_VAL_223	2.82	1.86	9.44
1HGJ.PDB	O, E_CYS_97	NE, E_ARG_224	HE, E_ARG_224	2.81	1.96	24.68
1HGJ.PDB	O, E_CYS_97	NH2, E_ARG_224	HH21, E_ARG_224	2.94	2.09	27.02
1HGJ.PDB	O, E_VAL_223	N, E_LEU_226	H, E_LEU_226	2.92	1.98	13.32
1HGJ.PDB	O, E_SER_228	NH1, E_ARG_229	HH11, E_ARG_229	2.73	1.78	16.61
1HGJ.PDB	O, E_PRO_221	NH2, E_ARG_229	HH22, E_ARG_229	2.62	1.66	13.20
1HGJ.PDB	OD1, E_ASP_101	OG, E_SER_231	HG, E_SER_231	2.90	1.95	11.36
1HGJ.PDB	O, E_ASP_101	N, E_ILE_232	H, E_ILE_232	2.88	1.96	15.95
1HGJ.PDB	O, E_TRP_180	N, E_TYR_233	H, E_TYR_233	2.94	1.97	6.84
1HGJ.PDB	O, E_TYR_178	N, E_THR_235	H, E_THR_235	2.90	2.00	19.30
1HGJ.PDB	O, E_LYS_176	N, E_VAL_237	H, E_VAL_237	2.80	1.88	15.33
1HGJ.PDB	O, D_SER_71	NZ, E_LYS_238	HZ2, E_LYS_238	2.65	1.73	22.71
1HGJ.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ3, E_LYS_238	2.87	1.86	13.82
1HGJ.PDB	O, E_ASN_170	N, E_GLY_240	H, E_GLY_240	2.85	1.98	22.38
1HGJ.PDB	OD1, E_ASP_241	N, E_VAL_242	H, E_VAL_242	2.79	1.95	25.35
1HGJ.PDB	O, E_MET_168	N, E_LEU_243	H, E_LEU_243	2.92	1.95	5.02
1HGJ.PDB	O, E_VAL_166	N, E_ILE_245	H, E_ILE_245	2.90	1.96	13.71
1HGJ.PDB	O, E_THR_203	N, E_ASN_246	H, E_ASN_246	2.96	1.99	5.52
1HGJ.PDB	OD1, E_ASN_165	ND2, E_ASN_246	HD22, E_ASN_246	2.89	1.94	11.88
1HGJ.PDB	O, E_LEU_164	N, E_SER_247	H, E_SER_247	2.94	2.02	17.47
1HGJ.PDB	O, E_HIS_183	ND2, E_ASN_250	HD22, E_ASN_250	2.83	1.88	12.22
1HGJ.PDB	O, E_ASN_152	N, E_ALA_253	H, E_ALA_253	2.89	2.00	20.06
1HGJ.PDB	OD1, E_ASN_133	NH2, E_ARG_255	HH22, E_ARG_255	2.55	1.71	26.62
1HGJ.PDB	O, E_ILE_121	N, E_TYR_257	H, E_TYR_257	2.92	2.08	25.41
1HGJ.PDB	O, E_LEU_177	N, E_PHE_258	H, E_PHE_258	2.92	1.95	7.34
1HGJ.PDB	OG, E_SER_115	N, E_ARG_261	H, E_ARG_261	2.94	2.00	14.60
1HGJ.PDB	OE2, E_GLU_119	NH1, E_ARG_261	HH12, E_ARG_261	2.65	1.82	28.15
1HGJ.PDB	OE1, E_GLU_119	NH2, E_ARG_261	HH22, E_ARG_261	2.91	2.01	23.66
1HGJ.PDB	OD2, E_ASP_85	NZ, E_LYS_264	HZ3, E_LYS_264	2.86	1.86	15.01
1HGJ.PDB	O, E_PHE_87	N, E_MET_268	H, E_MET_268	2.83	1.92	18.18
1HGJ.PDB	O, E_PRO_284	OG, E_SER_270	HG, E_SER_270	2.82	1.88	11.49
1HGJ.PDB	OG, E_SER_270	N, E_ALA_272	H, E_ALA_272	2.99	2.05	12.84
1HGJ.PDB	O, E_ILE_51	N, E_ASP_275	H, E_ASP_275	2.93	2.03	19.50
1HGJ.PDB	OD1, E_ASP_275	N, E_THR_276	H, E_THR_276	2.79	1.94	24.04
1HGJ.PDB	O, E_ASN_54	N, E_SER_279	H, E_SER_279	2.81	1.88	14.80
1HGJ.PDB	O, E_TYR_302	N, E_ILE_282	H, E_ILE_282	2.91	1.94	6.79
1HGJ.PDB	O, E_THR_283	N, E_GLY_286	H, E_GLY_286	2.81	1.88	13.99
1HGJ.PDB	O, E_LYS_50	N, E_SER_287	H, E_SER_287	2.83	1.86	7.05
1HGJ.PDB	O, E_ALA_304	ND2, E_ASN_290	HD22, E_ASN_290	2.82	1.92	17.80
1HGJ.PDB	OE1, E_GLN_44	NZ, E_LYS_292	HZ1, E_LYS_292	2.72	1.70	10.33

1HGJ.PDB	OD2, E_ASP_291	NZ, E_LYS_292	HZ3, E_LYS_292	2.83	1.86	17.49
1HGJ.PDB	O, E_LYS_307	N, E_GLN_295	H, E_GLN_295	2.87	1.98	20.11
1HGJ.PDB	O, E_ASN_298	NE2, E_GLN_295	HE21, E_GLN_295	2.74	1.78	8.06
1HGJ.PDB	O, E_GLN_44	N, E_ASN_296	H, E_ASN_296	2.84	1.90	13.41
1HGJ.PDB	OE1, E_GLN_295	N, E_VAL_297	H, E_VAL_297	2.70	1.91	29.61
1HGJ.PDB	O, F_LYS_68	NZ, E_LYS_299	HZ1, E_LYS_299	2.94	1.95	15.31
1HGJ.PDB	OD1, E_ASN_298	N, E_ILE_300	H, E_ILE_300	2.84	1.96	20.15
1HGJ.PDB	O, E_ILE_282	N, E_TYR_302	H, E_TYR_302	2.88	2.04	26.30
1HGJ.PDB	O, E_LYS_264	OH, E_TYR_302	HH, E_TYR_302	2.66	1.88	29.67
1HGJ.PDB	O, F_LYS_62	N, E_GLY_303	H, E_GLY_303	2.92	1.96	9.12
1HGJ.PDB	O, E_GLN_295	N, E_VAL_309	H, E_VAL_309	2.91	2.08	26.42
1HGJ.PDB	OG, F_SER_93	N, E_LYS_310	H, E_LYS_310	2.99	2.03	10.38
1HGJ.PDB	OD1, F_ASP_86	NZ, E_LYS_310	HZ3, E_LYS_310	2.93	2.08	29.22
1HGJ.PDB	OE2, E_GLU_41	N, E_LEU_314	H, E_LEU_314	2.79	1.86	13.14
1HGJ.PDB	OE1, E_GLU_41	NZ, E_LYS_315	HZ3, E_LYS_315	2.86	1.91	20.65
1HGJ.PDB	O, E_THR_40	N, E_LEU_316	H, E_LEU_316	2.79	1.84	10.66
1HGJ.PDB	OD1, F_ASN_104	N, E_ALA_317	H, E_ALA_317	2.73	1.80	11.35
1HGJ.PDB	O, E_ASN_38	N, E_THR_318	H, E_THR_318	2.91	1.98	16.58
1HGJ.PDB	O, E_VAL_20	ND2, E_ASN_322	HD21, E_ASN_322	2.87	1.94	14.58
1HGJ.PDB	OE2, E_GLU_35	ND2, E_ASN_322	HD22, E_ASN_322	2.86	1.96	20.74
1HGJ.PDB	OE2, F_GLU_15	N, E_GLU_325	H, E_GLU_325	2.88	2.08	29.65
1HGJ.PDB	O, E_GLN_327	NZ, E_LYS_326	HZ1, E_LYS_326	2.81	1.90	23.82
1HGJ.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.87	1.86	12.83
1HGJ.PDB	O, E_LYS_326	NE2, E_GLN_327	HE22, E_GLN_327	2.82	1.90	17.58
1HGJ.PDB	OD2, F_ASP_112	N, F_GLY_1	H2, F_GLY_1	2.75	1.76	14.31
1HGJ.PDB	OD1, F_ASP_109	N, F_LEU_2	H, F_LEU_2	2.87	1.99	21.90
1HGJ.PDB	OD2, F_ASP_112	N, F_PHE_3	H, F_PHE_3	2.83	2.02	27.46
1HGJ.PDB	OD2, F_ASP_112	N, F_GLY_4	H, F_GLY_4	2.87	1.95	16.24
1HGJ.PDB	OD1, F_ASP_112	N, F_ALA_5	H, F_ALA_5	2.84	1.98	23.38
1HGJ.PDB	OD1, F_ASP_112	N, F_ILE_6	H, F_ILE_6	3.00	2.08	18.28
1HGJ.PDB	O, F_GLY_4	N, F_PHE_9	H, F_PHE_9	2.79	1.86	13.96
1HGJ.PDB	O, F_GLY_13	ND2, F_ASN_12	HD22, F_ASN_12	2.89	2.02	22.28
1HGJ.PDB	O, E_VAL_323	N, F_GLY_13	H, F_GLY_13	2.69	1.76	10.96
1HGJ.PDB	O, E_HIS_17	N, F_TRP_14	H, F_TRP_14	2.84	1.89	11.67
1HGJ.PDB	OG1, F_THR_41	N, F_TRP_21	H, F_TRP_21	2.96	2.04	16.61
1HGJ.PDB	O, E_GLY_16	N, F_GLY_23	H, F_GLY_23	2.93	2.01	16.90
1HGJ.PDB	O, F_ALA_35	N, F_PHE_24	H, F_PHE_24	2.82	1.85	6.05
1HGJ.PDB	O, E_CYS_14	N, F_ARG_25	H, F_ARG_25	2.87	1.99	20.85
1HGJ.PDB	OE1, F_GLN_34	NE, F_ARG_25	HE, F_ARG_25	2.86	2.05	28.42
1HGJ.PDB	OE1, F_GLN_34	NH2, F_ARG_25	HH21, F_ARG_25	2.64	1.73	20.69
1HGJ.PDB	O, F_GLY_33	N, F_HIS_26	H, F_HIS_26	2.93	2.04	19.59
1HGJ.PDB	O, E_THR_12	N, F_GLN_27	H, F_GLN_27	2.89	1.97	15.73
1HGJ.PDB	O, F_GLY_31	N, F_ASN_28	H, F_ASN_28	2.76	1.81	11.08
1HGJ.PDB	OD1, F_ASN_146	ND2, F_ASN_28	HD21, F_ASN_28	2.81	1.89	16.64
1HGJ.PDB	O, F_CYS_144	ND2, F_ASN_28	HD22, F_ASN_28	2.86	1.94	16.87
1HGJ.PDB	O, F_PHE_24	N, F_ALA_35	H, F_ALA_35	2.77	1.91	22.75
1HGJ.PDB	O, F_TYR_22	N, F_ASP_37	H, F_ASP_37	2.70	1.77	12.58
1HGJ.PDB	OD2, F_ASP_37	N, F_SER_40	H, F_SER_40	2.96	1.99	8.62
1HGJ.PDB	OD2, F_ASP_37	OG, F_SER_40	HG, F_SER_40	2.80	1.95	24.06
1HGJ.PDB	O, F_ASP_37	OG1, F_THR_41	HG1, F_THR_41	2.72	1.84	19.21
1HGJ.PDB	O, F_LEU_38	N, F_GLN_42	H, F_GLN_42	2.93	2.00	15.35
1HGJ.PDB	OD1, F_ASP_46	NE2, F_GLN_42	HE22, F_GLN_42	2.80	1.92	21.18
1HGJ.PDB	O, F_LYS_39	N, F_ALA_43	H, F_ALA_43	2.93	1.97	8.45
1HGJ.PDB	O, F_SER_40	N, F_ALA_44	H, F_ALA_44	2.96	1.98	2.14
1HGJ.PDB	O, F_THR_41	N, F_ILE_45	H, F_ILE_45	2.88	1.94	11.66
1HGJ.PDB	O, F_GLN_42	N, F_ASP_46	H, F_ASP_46	2.77	1.80	2.95
1HGJ.PDB	OE2, F_GLU_114	NE2, F_GLN_47	HE21, F_GLN_47	2.95	2.04	18.06
1HGJ.PDB	O, F_ALA_43	NE2, F_GLN_47	HE22, F_GLN_47	2.95	2.07	21.45

1HGJ.PDB	O, F_ILE.45	N, F_ASN.49	H, F_ASN.49	2.87	1.94	15.82
1HGJ.PDB	O, F_ASP.46	N, F_GLY.50	H, F_GLY.50	2.83	1.94	20.73
1HGJ.PDB	OE1, F_GLU.103	NZ, F_LYS.51	HZ2, F_LYS.51	2.79	1.75	5.77
1HGJ.PDB	ND1, F_HIS.106	NZ, F_LYS.51	HZ3, F_LYS.51	2.75	1.79	17.21
1HGJ.PDB	O, F_ILE.48	N, F_LEU.52	H, F_LEU.52	2.90	1.98	16.71
1HGJ.PDB	O, F_ASN.49	N, F_ASN.53	H, F_ASN.53	2.87	1.94	13.91
1HGJ.PDB	OE1, F_GLU.57	NH1, F_ARG.54	HH11, F_ARG.54	2.86	1.86	9.70
1HGJ.PDB	OE2, D_GLU.97	NH2, F_ARG.54	HH22, F_ARG.54	2.77	1.81	14.54
1HGJ.PDB	OG, E_SER.110	NE2, F_HIS.64	HE2, F_HIS.64	2.90	1.93	7.02
1HGJ.PDB	O, E_LYS.299	NZ, F_LYS.68	HZ1, F_LYS.68	2.93	1.90	4.77
1HGJ.PDB	OE2, F_GLU.85	NZ, F_LYS.68	HZ2, F_LYS.68	2.74	1.77	18.09
1HGJ.PDB	OG, A_SER.107	N, F_ARG.76	H, F_ARG.76	2.85	1.88	6.29
1HGJ.PDB	OE2, B_GLU.81	NE, F_ARG.76	HE, F_ARG.76	2.85	1.89	12.57
1HGJ.PDB	OE2, B_GLU.74	NH1, F_ARG.76	HH12, F_ARG.76	2.70	1.70	4.55
1HGJ.PDB	OE1, B_GLU.81	NH2, F_ARG.76	HH21, F_ARG.76	2.65	1.66	2.84
1HGJ.PDB	OE1, B_GLU.74	NH2, F_ARG.76	HH22, F_ARG.76	2.72	1.73	7.95
1HGJ.PDB	OE1, F_GLU.74	NE2, F_GLN.78	HE22, F_GLN.78	2.92	1.97	13.10
1HGJ.PDB	O, F_GLY.75	N, F_ASP.79	H, F_ASP.79	2.96	2.02	12.63
1HGJ.PDB	O, F_GLN.78	N, F_LYS.82	H, F_LYS.82	2.96	1.99	6.52
1HGJ.PDB	O, F_ASP.79	N, F_TYR.83	H, F_TYR.83	2.83	1.89	13.63
1HGJ.PDB	OE1, B_GLU.85	OH, F_TYR.83	HH, F_TYR.83	2.53	1.75	28.54
1HGJ.PDB	O, F_LEU.80	N, F_VAL.84	H, F_VAL.84	2.82	1.86	7.45
1HGJ.PDB	O, F_LYS.82	N, F_ASP.86	H, F_ASP.86	2.93	1.97	9.90
1HGJ.PDB	O, F_TYR.83	N, F_THR.87	H, F_THR.87	2.88	1.95	13.71
1HGJ.PDB	O, F_VAL.84	N, F_LYS.88	H, F_LYS.88	2.98	2.03	12.44
1HGJ.PDB	OH, D_TYR.83	NZ, F_LYS.88	HZ1, F_LYS.88	2.70	1.68	8.19
1HGJ.PDB	O, F_GLU.85	N, F_ILE.89	H, F_ILE.89	2.86	1.88	2.87
1HGJ.PDB	O, F_LYS.88	N, F_TRP.92	H, F_TRP.92	2.93	1.96	5.23
1HGJ.PDB	O, F_ILE.89	N, F_SER.93	H, F_SER.93	2.83	1.94	19.77
1HGJ.PDB	O, F_ILE.89	OG, F_SER.93	HG, F_SER.93	2.86	1.95	15.80
1HGJ.PDB	O, F_ASP.90	N, F_TYR.94	H, F_TYR.94	2.83	1.93	19.07
1HGJ.PDB	O, F_TYR.94	N, F_LEU.98	H, F_LEU.98	2.95	1.98	6.19
1HGJ.PDB	O, F_ASN.95	N, F_LEU.99	H, F_LEU.99	2.87	1.97	18.16
1HGJ.PDB	O, F_LEU.98	N, F_LEU.102	H, F_LEU.102	2.95	1.98	8.07
1HGJ.PDB	O, F_LEU.99	N, F_GLU.103	H, F_GLU.103	2.95	1.99	9.09
1HGJ.PDB	O, F_VAL.100	N, F_ASN.104	H, F_ASN.104	2.81	1.86	11.07
1HGJ.PDB	O, E_LYS.27	ND2, F_ASN.104	HD22, F_ASN.104	2.91	1.96	11.78
1HGJ.PDB	O, F_LEU.102	N, F_HIS.106	H, F_HIS.106	2.94	1.98	8.79
1HGJ.PDB	O, F_GLU.103	N, F_THR.107	H, F_THR.107	2.86	1.95	17.68
1HGJ.PDB	O, F_HIS.106	N, F_LEU.110	H, F_LEU.110	2.80	1.84	7.98
1HGJ.PDB	O, F_THR.107	OG1, F_THR.111	HG1, F_THR.111	2.89	1.92	1.87
1HGJ.PDB	O, F_ASP.109	N, F_SER.113	H, F_SER.113	2.81	1.84	6.27
1HGJ.PDB	O, D_LEU.2	OG, F_SER.113	HG, F_SER.113	2.74	1.92	26.51
1HGJ.PDB	O, F_LEU.110	N, F_GLU.114	H, F_GLU.114	2.93	1.97	10.83
1HGJ.PDB	O, F_ASP.112	N, F_ASN.116	H, F_ASN.116	2.99	2.03	9.83
1HGJ.PDB	O, F_SER.113	N, F_LYS.117	H, F_LYS.117	2.74	1.86	21.34
1HGJ.PDB	O, F_GLU.114	N, F_LEU.118	H, F_LEU.118	2.96	2.00	9.84
1HGJ.PDB	O, F_ASN.116	N, F_GLU.120	H, F_GLU.120	2.93	1.95	2.43
1HGJ.PDB	O, F_LYS.117	N, F_LYS.121	H, F_LYS.121	2.95	2.03	16.46
1HGJ.PDB	O, F_PHE.119	N, F_ARG.123	H, F_ARG.123	2.92	1.97	10.33
1HGJ.PDB	OE2, F_GLU.120	NH1, F_ARG.123	HH11, F_ARG.123	2.73	1.86	24.44
1HGJ.PDB	OE1, D_GLU.132	NE, F_ARG.124	HE, F_ARG.124	2.92	2.09	27.65
1HGJ.PDB	OE2, D_GLU.132	NE, F_ARG.124	HE, F_ARG.124	2.96	2.06	20.98
1HGJ.PDB	O, F_HIS.159	ND2, F_ASN.129	HD21, F_ASN.129	2.97	2.01	8.92
1HGJ.PDB	OH, F_TYR.157	ND2, F_ASN.129	HD22, F_ASN.129	2.75	1.85	17.65
1HGJ.PDB	O, F_LYS.139	N, F_GLU.131	H, F_GLU.131	2.94	1.99	12.85
1HGJ.PDB	O, F_CYS.137	N, F_MET.133	H, F_MET.133	2.84	1.91	14.51
1HGJ.PDB	OD1, F_ASN.135	N, F_CYS.137	H, F_CYS.137	2.98	2.16	26.53

1HGJ.PDB	O, E_LEU_13	N, F_PHE_138	H, F_PHE_138	2.73	1.87	22.18
1HGJ.PDB	O, F_GLU_131	N, F_LYS_139	H, F_LYS_139	2.81	1.86	9.38
1HGJ.PDB	O, E_ALA_11	N, F_ILE_140	H, F_ILE_140	2.78	1.87	17.89
1HGJ.PDB	O, F_ASN_129	N, F_TYR_141	H, F_TYR_141	2.96	2.03	14.20
1HGJ.PDB	OE2, F_GLU_165	N, F_LYS_143	H, F_LYS_143	2.99	2.05	14.57
1HGJ.PDB	O, F_ASP_145	N, F_ILE_149	H, F_ILE_149	2.90	1.95	10.28
1HGJ.PDB	O, F_ASN_146	N, F_GLU_150	H, F_GLU_150	2.89	1.95	14.81
1HGJ.PDB	O, F_ALA_147	N, F_SER_151	H, F_SER_151	2.90	2.00	18.77
1HGJ.PDB	O, F_CYS_148	OG, F_SER_151	HG, F_SER_151	2.72	1.92	27.65
1HGJ.PDB	O, F_GLU_150	N, F_ASN_154	H, F_ASN_154	2.78	1.81	1.94
1HGJ.PDB	OD1, F_ASP_158	N, F_ASP_160	H, F_ASP_160	2.95	2.08	23.42
1HGJ.PDB	O, F_HIS_159	N, F_TYR_162	H, F_TYR_162	2.96	2.07	20.30
1HGJ.PDB	O, D_ARG_170	NH1, F_ARG_163	HH12, F_ARG_163	2.89	1.91	11.37
1HGJ.PDB	O, F_TYR_162	N, F_ALA_166	H, F_ALA_166	2.89	1.92	3.44
1HGJ.PDB	O, F_ARG_163	N, F_LEU_167	H, F_LEU_167	2.76	1.81	9.28
1HGJ.PDB	O, F_ASP_164	N, F_ASN_168	H, F_ASN_168	2.99	2.03	9.70
1HGJ.PDB	O, F_ALA_166	N, F_ARG_170	H, F_ARG_170	2.86	1.98	21.69
1HGJ.PDB	O, F_GLU_128	NE, F_ARG_170	HE, F_ARG_170	2.77	1.90	22.39
1HGJ.PDB	OE2, F_GLU_131	NH1, F_ARG_170	HH11, F_ARG_170	2.79	1.80	6.77
1HGJ.PDB	O, F_LEU_167	N, F_PHE_171	H, F_PHE_171	2.94	2.02	16.73

Table 1670: 1HGJ-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1OSP.PDB	OG, L.SER.26	N, L.GLN.3	H, L.GLN.3	2.70	1.79	13.92
1OSP.PDB	O, L.LYS.24	N, L.SER.5	H, L.SER.5	2.66	1.74	13.88
1OSP.PDB	O, L.TYR.86	NE2, L.GLN.6	HE21, L.GLN.6	2.96	2.00	8.59
1OSP.PDB	O, L.LYS.103	N, L.PHE.11	H, L.PHE.11	2.89	1.98	18.16
1OSP.PDB	O, L.GLU.105	N, L.VAL.13	H, L.VAL.13	2.80	1.85	11.83
1OSP.PDB	O, L.LEU.78	N, L.GLY.16	H, L.GLY.16	2.67	1.75	12.23
1OSP.PDB	OD1, L.ASP.17	N, L.ARG.18	H, L.ARG.18	2.90	2.10	29.03
1OSP.PDB	O, L.ILE.75	N, L.VAL.19	H, L.VAL.19	2.73	1.79	10.56
1OSP.PDB	O, L.LEU.73	N, L.ILE.21	H, L.ILE.21	2.79	1.84	10.88
1OSP.PDB	O, L.TYR.71	N, L.CYS.23	H, L.CYS.23	2.71	1.82	18.30
1OSP.PDB	O, L.SER.5	N, L.LYS.24	H, L.LYS.24	2.95	2.04	17.66
1OSP.PDB	OH, L.TYR.71	N, L.SER.31	H, L.SER.31	2.95	2.08	22.39
1OSP.PDB	O, L.TYR.30	NH1, L.ARG.32	HH11, L.ARG.32	2.63	1.69	15.15
1OSP.PDB	O, O.LYS.44	NH1, L.ARG.32	HH12, L.ARG.32	2.98	2.09	22.73
1OSP.PDB	O, O.SER.43	NH2, L.ARG.32	HH22, L.ARG.32	2.91	1.93	9.19
1OSP.PDB	O, L.SER.31	N, L.LEU.33	H, L.LEU.33	2.98	2.14	25.04
1OSP.PDB	O, L.GLN.89	N, L.ALA.34	H, L.ALA.34	2.77	1.82	10.76
1OSP.PDB	O, L.ILE.48	N, L.TRP.35	H, L.TRP.35	2.95	2.03	16.19
1OSP.PDB	O, L.PHE.87	N, L.TYR.36	H, L.TYR.36	2.75	1.89	22.90
1OSP.PDB	OE1, L.GLN.89	OH, L.TYR.36	HH, L.TYR.36	2.81	1.86	10.05
1OSP.PDB	O, L.ARG.45	N, L.GLN.37	H, L.GLN.37	2.92	1.98	13.78
1OSP.PDB	O, L.THR.85	N, L.GLN.38	H, L.GLN.38	2.68	1.77	15.79
1OSP.PDB	O, L.ASN.42	NE2, L.GLN.38	HE22, L.GLN.38	2.84	1.91	14.33
1OSP.PDB	O, L.GLN.37	N, L.ARG.45	H, L.ARG.45	2.71	1.86	23.84
1OSP.PDB	O, L.TRP.35	N, L.LEU.47	H, L.LEU.47	2.77	1.81	8.27
1OSP.PDB	O, L.SER.53	N, L.SER.49	H, L.SER.49	2.83	1.86	5.93
1OSP.PDB	OH, L.TYR.91	N, L.GLY.50	H, L.GLY.50	2.94	2.04	18.66
1OSP.PDB	O, L.LEU.33	N, L.ALA.51	H, L.ALA.51	2.85	1.96	19.10
1OSP.PDB	O, L.GLY.50	N, L.THR.52	H, L.THR.52	2.84	2.01	25.88
1OSP.PDB	O, L.SER.49	N, L.SER.53	H, L.SER.53	2.91	2.11	29.67
1OSP.PDB	O, L.LEU.47	N, L.GLU.55	H, L.GLU.55	2.98	2.09	21.52
1OSP.PDB	O, L.LEU.46	NE1, L.TRP.57	HE1, L.TRP.57	2.86	1.90	10.61
1OSP.PDB	O, L.SER.74	N, L.SER.63	H, L.SER.63	2.92	2.11	28.83
1OSP.PDB	O, L.THR.72	N, L.SER.65	H, L.SER.65	2.98	2.07	17.30
1OSP.PDB	O, L.CYS.23	N, L.TYR.71	H, L.TYR.71	2.86	1.98	20.08
1OSP.PDB	O, L.ILE.21	N, L.LEU.73	H, L.LEU.73	2.87	1.98	20.14
1OSP.PDB	O, L.SER.63	N, L.SER.74	H, L.SER.74	2.74	1.79	7.99
1OSP.PDB	O, L.VAL.19	N, L.ILE.75	H, L.ILE.75	2.84	1.89	12.51
1OSP.PDB	O, L.ASP.17	N, L.LEU.78	H, L.LEU.78	2.81	1.87	13.11
1OSP.PDB	O, L.GLN.79	N, L.ASP.82	H, L.ASP.82	2.86	1.91	11.93
1OSP.PDB	O, L.GLN.38	N, L.THR.85	H, L.THR.85	2.92	1.95	4.18
1OSP.PDB	O, L.THR.102	N, L.TYR.86	H, L.TYR.86	2.89	1.93	8.08
1OSP.PDB	O, L.ASP.82	OH, L.TYR.86	HH, L.TYR.86	2.85	1.91	12.11
1OSP.PDB	O, L.TYR.36	N, L.PHE.87	H, L.PHE.87	2.96	2.01	13.11
1OSP.PDB	O, L.ALA.34	N, L.GLN.89	H, L.GLN.89	2.85	2.04	28.87
1OSP.PDB	O, L.GLN.90	NE2, L.GLN.89	HE22, L.GLN.89	2.86	2.00	23.53
1OSP.PDB	O, L.THR.97	N, L.GLN.90	H, L.GLN.90	2.93	2.01	16.17
1OSP.PDB	O, L.SER.93	NE2, L.GLN.90	HE21, L.GLN.90	2.98	2.01	7.86
1OSP.PDB	OG1, L.THR.97	NE2, L.GLN.90	HE22, L.GLN.90	3.00	2.06	15.72
1OSP.PDB	O, L.ARG.32	N, L.TYR.91	H, L.TYR.91	2.95	1.99	9.54
1OSP.PDB	OE1, L.GLN.90	N, L.TRP.92	H, L.TRP.92	2.79	1.98	27.96
1OSP.PDB	O, L.CYS.88	N, L.GLY.99	H, L.GLY.99	2.75	1.80	9.69
1OSP.PDB	OE1, L.GLN.6	N, L.GLY.101	H, L.GLY.101	2.85	1.99	22.93
1OSP.PDB	O, L.TYR.86	N, L.THR.102	H, L.THR.102	2.94	2.02	17.58
1OSP.PDB	O, L.SER.8	OG1, L.THR.102	HG1, L.THR.102	2.69	1.79	17.03
1OSP.PDB	O, L.SER.9	N, L.LYS.103	H, L.LYS.103	2.69	1.74	5.66
1OSP.PDB	O, L.ALA.84	N, L.LEU.104	H, L.LEU.104	2.92	2.02	18.72

1OSP.PDB	O, L_PHE.11	N, L_GLU.105	H, L_GLU.105	2.91	2.04	22.49
1OSP.PDB	OE1, L_GLN.166	N, L_ILE.106	H, L_ILE.106	2.92	1.96	10.71
1OSP.PDB	O, L_VAL.13	N, L_LYS.107	H, L_LYS.107	2.80	1.92	21.29
1OSP.PDB	O, L_ALA.109	NE, L_ARG.108	HE, L_ARG.108	2.74	1.82	13.78
1OSP.PDB	O, L_ASP.170	NH1, L_ARG.108	HH11, L_ARG.108	2.91	1.95	11.72
1OSP.PDB	O, L_TYR.140	N, L_ALA.111	H, L_ALA.111	2.99	2.03	8.54
1OSP.PDB	O, L_ASN.137	N, L_THR.114	H, L_THR.114	2.83	1.86	3.43
1OSP.PDB	O, L_PHE.135	N, L_SER.116	H, L_SER.116	2.91	2.00	18.69
1OSP.PDB	O, L_VAL.133	N, L_PHE.118	H, L_PHE.118	2.70	1.85	23.89
1OSP.PDB	O, L_SER.122	N, L_THR.126	H, L_THR.126	2.83	1.95	20.51
1OSP.PDB	O, L_SER.122	OG1, L_THR.126	HG1, L_THR.126	2.68	1.79	17.62
1OSP.PDB	O, L_LEU.125	N, L_GLY.128	H, L_GLY.128	2.89	1.98	18.00
1OSP.PDB	OE1, L_GLN.124	N, L_SER.131	H, L_SER.131	2.84	2.03	28.15
1OSP.PDB	O, L_LEU.179	N, L_VAL.132	H, L_VAL.132	2.99	2.03	9.27
1OSP.PDB	O, L_PHE.118	N, L_VAL.133	H, L_VAL.133	2.94	1.99	10.25
1OSP.PDB	O, L_SER.177	N, L_CYS.134	H, L_CYS.134	2.87	1.96	17.37
1OSP.PDB	O, L_SER.116	N, L_PHE.135	H, L_PHE.135	2.92	2.02	19.40
1OSP.PDB	O, L_MET.175	N, L_LEU.136	H, L_LEU.136	2.84	1.89	10.42
1OSP.PDB	O, L_THR.114	N, L_ASN.137	H, L_ASN.137	2.82	1.87	10.96
1OSP.PDB	O, L_TYR.173	N, L_PHE.139	H, L_PHE.139	2.82	1.85	4.99
1OSP.PDB	OE1, L_GLU.105	OH, L_TYR.140	HH, L_TYR.140	2.90	2.03	21.23
1OSP.PDB	O, L_THR.197	N, L_ASN.145	H, L_ASN.145	2.93	2.05	21.16
1OSP.PDB	O, L_GLU.195	N, L_LYS.147	H, L_LYS.147	2.84	1.90	13.83
1OSP.PDB	OG, L_SER.177	NE1, L_TRP.148	HE1, L_TRP.148	2.94	1.97	6.03
1OSP.PDB	O, L_THR.193	N, L_LYS.149	H, L_LYS.149	2.86	1.89	5.27
1OSP.PDB	O, L_SER.153	N, L_ILE.150	H, L_ILE.150	2.73	1.84	20.13
1OSP.PDB	O, L_SER.191	N, L_ASP.151	H, L_ASP.151	2.90	1.94	7.97
1OSP.PDB	O, L_TRP.148	N, L_ARG.155	H, L_ARG.155	2.67	1.85	27.49
1OSP.PDB	O, L_SER.176	N, L_SER.162	H, L_SER.162	2.90	1.97	13.57
1OSP.PDB	O, L_ILE.106	NE2, L_GLN.166	HE21, L_GLN.166	2.72	1.85	21.90
1OSP.PDB	OD1, L_ASP.167	N, L_LYS.169	H, L_LYS.169	2.91	2.06	23.22
1OSP.PDB	OD1, L_ASP.167	N, L_ASP.170	H, L_ASP.170	2.97	2.06	17.28
1OSP.PDB	OD1, L_ASP.170	N, L_THR.172	H, L_THR.172	2.93	1.99	11.17
1OSP.PDB	O, L_PHE.139	N, L_TYR.173	H, L_TYR.173	2.78	1.85	13.38
1OSP.PDB	O, L_LEU.136	N, L_MET.175	H, L_MET.175	2.90	2.00	19.13
1OSP.PDB	O, L_SER.162	N, L_SER.176	H, L_SER.176	2.94	1.99	10.89
1OSP.PDB	O, L_CYS.134	N, L_SER.177	H, L_SER.177	2.92	1.98	13.57
1OSP.PDB	O, L_LEU.160	N, L_THR.178	H, L_THR.178	2.95	1.99	8.96
1OSP.PDB	O, L_VAL.132	N, L_LEU.179	H, L_LEU.179	2.86	1.89	6.54
1OSP.PDB	O, L_GLY.158	N, L_THR.180	H, L_THR.180	2.81	1.87	11.29
1OSP.PDB	OG, L_SER.131	OG1, L_THR.180	HG1, L_THR.180	2.85	1.92	11.66
1OSP.PDB	O, L_ALA.130	N, L_LEU.181	H, L_LEU.181	2.78	1.82	7.56
1OSP.PDB	O, L_GLY.128	N, L_LYS.183	H, L_LYS.183	2.85	1.89	9.20
1OSP.PDB	O, L_THR.182	N, L_TYR.186	H, L_TYR.186	2.97	2.01	7.10
1OSP.PDB	O, L_LYS.183	N, L_GLU.187	H, L_GLU.187	2.92	1.97	10.78
1OSP.PDB	O, L_GLU.185	N, L_ARG.188	H, L_ARG.188	2.88	2.00	21.14
1OSP.PDB	O, L_PHE.209	N, L_TYR.192	H, L_TYR.192	2.89	1.92	5.15
1OSP.PDB	O, L_LYS.207	N, L_CYS.194	H, L_CYS.194	3.00	2.06	13.98
1OSP.PDB	O, L_LYS.147	N, L_GLU.195	H, L_GLU.195	2.86	1.93	14.83
1OSP.PDB	O, L_ILE.205	N, L_ALA.196	H, L_ALA.196	2.74	1.78	0.99
1OSP.PDB	O, L_ASN.145	N, L_THR.197	H, L_THR.197	2.74	1.79	7.28
1OSP.PDB	OD2, L_ASP.110	NZ, L_LYS.199	HZ3, L_LYS.199	2.64	1.82	29.88
1OSP.PDB	O, L_ALA.196	N, L_ILE.205	H, L_ILE.205	2.88	2.01	22.87
1OSP.PDB	O, L_TYR.192	N, L_PHE.209	H, L_PHE.209	2.99	2.09	20.05
1OSP.PDB	O, L_ASN.190	N, L_ARG.211	H, L_ARG.211	2.57	1.73	22.30
1OSP.PDB	OD1, L_ASN.190	N, L_ASN.212	H, L_ASN.212	2.63	1.70	14.44
1OSP.PDB	O, H_THR.25	N, H_GLN.3	H, H_GLN.3	2.84	1.98	24.33
1OSP.PDB	O, H_THR.21	N, H_SER.7	H, H_SER.7	2.81	1.95	22.81

1OSP.PDB	O, H_THR_117	N, H_VAL_12	H, H_VAL_12	2.94	2.00	13.37
1OSP.PDB	O, H_VAL_85	N, H_SER_15	H, H_SER_15	2.92	1.95	6.64
1OSP.PDB	O, H_LYS_13	N, H_GLN_16	H, H_GLN_16	3.00	2.09	18.64
1OSP.PDB	OD1, H_ASN_83	OG1, H_THR_17	HG1, H_THR_17	2.79	1.95	24.49
1OSP.PDB	O, H_LEU_82	N, H_LEU_18	H, H_LEU_18	2.68	1.78	16.36
1OSP.PDB	O, H_LEU_80	N, H_LEU_20	H, H_LEU_20	2.94	1.99	11.52
1OSP.PDB	O, H_SER_7	N, H_THR_21	H, H_THR_21	2.82	1.88	11.48
1OSP.PDB	O, H_TYR_78	N, H_CYS_22	H, H_CYS_22	2.86	1.91	11.66
1OSP.PDB	O, H_GLN_5	N, H_SER_23	H, H_SER_23	2.89	1.92	6.27
1OSP.PDB	O, H_GLN_3	N, H_THR_25	H, H_THR_25	2.88	1.93	10.50
1OSP.PDB	OD1, H_ASN_76	N, H_ILE_29	H, H_ILE_29	2.92	1.99	15.63
1OSP.PDB	O, H_ILE_51	N, H_TRP_34	H, H_TRP_34	2.95	1.99	10.12
1OSP.PDB	O, H_SER_31	NE1, H_TRP_34	HE1, H_TRP_34	2.85	1.98	23.03
1OSP.PDB	O, H_ALA_96	N, H_ASP_35	H, H_ASP_35	2.77	1.81	7.66
1OSP.PDB	O, H_GLY_49	N, H_TRP_36	H, H_TRP_36	2.89	2.03	23.14
1OSP.PDB	O, H_TYR_94	N, H_ILE_37	H, H_ILE_37	2.84	1.87	8.13
1OSP.PDB	O, H_GLU_46	N, H_ARG_38	H, H_ARG_38	2.95	1.99	11.63
1OSP.PDB	OE1, H_GLU_46	NH1, H_ARG_38	HH11, H_ARG_38	2.77	1.80	9.20
1OSP.PDB	OH, H_TYR_93	NH2, H_ARG_38	HH21, H_ARG_38	2.83	1.87	12.82
1OSP.PDB	OD1, H_ASP_89	NH2, H_ARG_38	HH22, H_ARG_38	2.83	1.91	19.07
1OSP.PDB	O, H_THR_92	N, H_LYS_39	H, H_LYS_39	2.72	1.83	19.36
1OSP.PDB	O, H_LYS_44	N, H_PHE_40	H, H_PHE_40	2.72	1.83	18.74
1OSP.PDB	O, H_PHE_40	N, H_ASN_43	H, H_ASN_43	2.74	1.91	24.90
1OSP.PDB	O, H_ARG_38	N, H_GLU_46	H, H_GLU_46	2.94	2.08	24.27
1OSP.PDB	O, H_TRP_36	N, H_MET_48	H, H_MET_48	2.82	1.92	18.56
1OSP.PDB	O, H_TRP_34	N, H_ILE_51	H, H_ILE_51	2.94	2.01	16.05
1OSP.PDB	O, H_GLY_56	N, H_ARG_52	H, H_ARG_52	2.70	1.82	20.54
1OSP.PDB	O, H_ARG_52	N, H_GLY_55	H, H_GLY_55	2.98	2.16	28.05
1OSP.PDB	O, H_MET_48	N, H_ASN_60	H, H_ASN_60	2.81	1.84	4.94
1OSP.PDB	O, H_PHE_47	ND2, H_ASN_60	HD22, H_ASN_60	2.80	1.84	6.91
1OSP.PDB	OD1, H_ASN_60	N, H_SER_62	H, H_SER_62	2.92	1.99	15.17
1OSP.PDB	OD2, L_ASP_1	OG, H_SER_62	HG, H_SER_62	2.98	2.17	26.53
1OSP.PDB	O, H_GLN_81	N, H_SER_68	H, H_SER_68	2.92	2.02	18.77
1OSP.PDB	OH, H_TYR_59	N, H_ILE_69	H, H_ILE_69	2.83	1.90	13.21
1OSP.PDB	O, H_HIS_77	N, H_ASP_72	H, H_ASP_72	2.76	1.83	13.63
1OSP.PDB	OD1, H_ASP_72	N, H_LYS_75	H, H_LYS_75	2.98	2.11	21.21
1OSP.PDB	O, H_GLU_27	ND2, H_ASN_76	HD21, H_ASN_76	2.87	1.93	13.17
1OSP.PDB	O, H_VAL_24	ND2, H_ASN_76	HD22, H_ASN_76	2.88	1.97	18.51
1OSP.PDB	O, H_ASN_76	ND1, H_HIS_77	HD1, H_HIS_77	2.92	1.96	10.26
1OSP.PDB	O, H_THR_70	N, H_TYR_79	H, H_TYR_79	2.78	1.83	9.64
1OSP.PDB	O, H_SER_68	N, H_GLN_81	H, H_GLN_81	2.98	2.10	21.73
1OSP.PDB	O, H_LEU_18	N, H_LEU_82	H, H_LEU_82	2.92	1.99	15.92
1OSP.PDB	O, H_GLN_16	N, H_VAL_85	H, H_VAL_85	2.82	1.85	6.22
1OSP.PDB	OD2, H_ASP_89	N, H_VAL_86	H, H_VAL_86	2.80	1.88	11.59
1OSP.PDB	O, H_VAL_86	N, H_ASP_89	H, H_ASP_89	2.89	1.96	13.81
1OSP.PDB	O, H_THR_114	N, H_TYR_93	H, H_TYR_93	2.83	1.88	11.95
1OSP.PDB	O, H_ASP_89	OH, H_TYR_93	HH, H_TYR_93	2.70	1.77	11.96
1OSP.PDB	O, H_ILE_37	N, H_TYR_94	H, H_TYR_94	2.68	1.76	13.41
1OSP.PDB	OE2, H_GLU_6	N, H_CYS_95	H, H_CYS_95	2.95	2.01	11.90
1OSP.PDB	O, H_PHE_109	N, H_ARG_97	H, H_ARG_97	2.87	1.96	17.07
1OSP.PDB	O, H_PHE_33	N, H_SER_98	H, H_SER_98	2.89	1.95	12.66
1OSP.PDB	O, H_GLY_106	N, H_ARG_99	H, H_ARG_99	2.65	1.77	20.05
1OSP.PDB	OG, H_SER_105	N, H_ASP_100	H, H_ASP_100	2.96	2.05	15.15
1OSP.PDB	O, O_ASP_93	N, H_TYR_101	H, H_TYR_101	2.96	2.00	9.88
1OSP.PDB	OH, L_TYR_36	N, H_PHE_107	H, H_PHE_107	2.90	1.92	4.68
1OSP.PDB	O, H_PHE_107	NE1, H_TRP_110	HE1, H_TRP_110	2.73	1.93	28.89
1OSP.PDB	OE1, H_GLU_6	N, H_GLY_113	H, H_GLY_113	2.71	1.88	24.91
1OSP.PDB	O, H_ALA_91	N, H_VAL_116	H, H_VAL_116	2.85	1.88	5.20

1OSP.PDB	O, H_SER.10	N, H_THR.117	H, H_THR.117	2.78	1.82	8.67
1OSP.PDB	O, H_LYS.150	N, H_SER.127	H, H_SER.127	2.92	1.96	10.41
1OSP.PDB	O, H_LEU.148	N, H_TYR.129	H, H_TYR.129	2.81	1.85	8.10
1OSP.PDB	O, H_GLY.146	N, H_LEU.131	H, H_LEU.131	2.76	1.84	15.39
1OSP.PDB	O, H_VAL.190	N, H_VAL.143	H, H_VAL.143	2.73	1.81	13.86
1OSP.PDB	O, H_VAL.188	N, H_LEU.145	H, H_LEU.145	2.82	1.87	9.83
1OSP.PDB	O, H_LEU.131	N, H_GLY.146	H, H_GLY.146	2.94	2.07	22.39
1OSP.PDB	O, H_SER.186	N, H_CYS.147	H, H_CYS.147	3.00	2.12	21.82
1OSP.PDB	O, H_TYR.129	N, H_LEU.148	H, H_LEU.148	2.83	1.89	14.70
1OSP.PDB	O, H_MET.184	N, H_VAL.149	H, H_VAL.149	2.83	1.86	7.67
1OSP.PDB	O, H_SER.127	N, H_LYS.150	H, H_LYS.150	2.86	1.89	5.15
1OSP.PDB	O, H_THR.124	N, H_PHE.153	H, H_PHE.153	2.99	2.11	20.08
1OSP.PDB	OE1, H_GLU.155	N, H_SER.156	H, H_SER.156	2.82	1.96	21.80
1OSP.PDB	O, H_SER.203	N, H_THR.160	H, H_THR.160	2.81	1.86	11.32
1OSP.PDB	OG, H_SER.186	NE1, H_TRP.161	HE1, H_TRP.161	2.94	1.96	6.92
1OSP.PDB	O, H_SER.187	N, H_HIS.171	H, H_HIS.171	2.90	1.95	12.27
1OSP.PDB	O, H_SER.185	N, H_PHE.173	H, H_PHE.173	2.83	1.89	14.13
1OSP.PDB	O, H_LEU.181	N, H_GLN.178	H, H_GLN.178	2.99	2.02	8.47
1OSP.PDB	O, H_TYR.152	N, H_TYR.182	H, H_TYR.182	2.70	1.78	13.65
1OSP.PDB	O, H_VAL.149	N, H_MET.184	H, H_MET.184	2.88	1.94	12.78
1OSP.PDB	OG, L_SER.176	OG, H_SER.185	HG, H_SER.185	2.74	1.91	24.72
1OSP.PDB	O, H_HIS.171	N, H_SER.187	H, H_SER.187	2.79	1.91	19.94
1OSP.PDB	O, H_LEU.145	N, H_VAL.188	H, H_VAL.188	2.91	1.95	10.57
1OSP.PDB	O, H_SER.169	N, H_THR.189	H, H_THR.189	2.97	2.10	22.89
1OSP.PDB	O, H_VAL.143	N, H_VAL.190	H, H_VAL.190	2.87	1.94	15.00
1OSP.PDB	O, H_SER.141	N, H_SER.192	H, H_SER.192	2.75	1.80	9.03
1OSP.PDB	O, H_PRO.191	N, H_THR.194	H, H_THR.194	2.85	1.95	18.47
1OSP.PDB	O, H_PRO.191	OG1, H_THR.194	HG1, H_THR.194	2.70	1.91	28.34
1OSP.PDB	O, H_ASN.162	N, H_THR.201	H, H_THR.201	2.71	1.81	16.91
1OSP.PDB	O, H_LYS.215	N, H_CYS.202	H, H_CYS.202	2.91	1.95	9.86
1OSP.PDB	O, H_THR.160	N, H_SER.203	H, H_SER.203	2.69	1.78	14.42
1OSP.PDB	O, H_VAL.213	N, H_VAL.204	H, H_VAL.204	2.76	1.80	5.73
1OSP.PDB	O, H_THR.158	N, H_ALA.205	H, H_ALA.205	2.97	2.01	9.69
1OSP.PDB	O, H_THR.211	N, H_HIS.206	H, H_HIS.206	2.87	1.90	7.50
1OSP.PDB	OG, H_SER.209	ND1, H_HIS.206	HD1, H_HIS.206	2.73	1.88	25.05
1OSP.PDB	O, H_PRO.154	NE2, H_HIS.206	HE2, H_HIS.206	2.71	1.78	13.27
1OSP.PDB	O, H_PRO.207	N, H_SER.210	H, H_SER.210	2.91	1.98	12.92
1OSP.PDB	O, H_VAL.204	N, H_VAL.213	H, H_VAL.213	2.78	1.87	17.04
1OSP.PDB	O, H_CYS.202	N, H_LYS.215	H, H_LYS.215	2.75	1.83	14.50
1OSP.PDB	OE1, L_GLU.123	NZ, H_LYS.215	HZ2, H_LYS.215	2.78	1.85	20.53
1OSP.PDB	O, H_VAL.200	N, H_LEU.217	H, H_LEU.217	2.88	1.93	11.66
1OSP.PDB	O, O_ASP.25	OG, O_SER.29	HG, O_SER.29	2.96	2.06	17.60
1OSP.PDB	O, O_VAL.42	N, O_VAL.30	H, O_VAL.30	2.74	1.80	11.57
1OSP.PDB	O, O_VAL.40	N, O_VAL.32	H, O_VAL.32	2.79	1.86	14.04
1OSP.PDB	O, O_MET.38	N, O_LEU.34	H, O_LEU.34	2.77	1.93	25.21
1OSP.PDB	OD1, O_ASP.33	NZ, O_LYS.39	HZ2, O_LYS.39	2.81	1.85	17.76
1OSP.PDB	O, O_VAL.32	N, O_VAL.40	H, O_VAL.40	2.85	1.95	18.60
1OSP.PDB	O, O_ILE.55	N, O_LEU.41	H, O_LEU.41	2.73	1.77	2.80
1OSP.PDB	O, O_VAL.30	N, O_VAL.42	H, O_VAL.42	2.79	1.83	5.03
1OSP.PDB	O, O_LYS.51	N, O_ASN.47	H, O_ASN.47	2.68	1.74	7.05
1OSP.PDB	OD1, O_ASN.47	N, O_ASP.49	H, O_ASP.49	2.77	1.90	22.03
1OSP.PDB	O, O_ASN.47	N, O_GLY.50	H, O_GLY.50	2.81	1.86	10.63
1OSP.PDB	OD1, O_ASN.47	N, O_LYS.51	H, O_LYS.51	2.98	2.06	16.48
1OSP.PDB	O, O_SER.67	N, O_TYR.52	H, O_TYR.52	2.69	1.80	18.76
1OSP.PDB	OG, O_SER.43	N, O_ASP.53	H, O_ASP.53	2.84	1.87	5.15
1OSP.PDB	O, O_GLY.65	N, O_LEU.54	H, O_LEU.54	2.75	1.89	23.21
1OSP.PDB	O, O_LEU.61	N, O_VAL.58	H, O_VAL.58	2.83	1.87	9.77
1OSP.PDB	O, O_ALA.56	N, O_LEU.63	H, O_LEU.63	2.76	1.81	6.30

1OSP.PDB	O, O_GLU_77	N, O_LYS_64	H, O_LYS_64	2.80	1.86	12.67
1OSP.PDB	O, O_TYR_52	N, O_SER_67	H, O_SER_67	2.91	2.05	23.91
1OSP.PDB	O, O_LEU_88	N, O_LEU_76	H, O_LEU_76	2.81	1.86	9.34
1OSP.PDB	O, O_LYS_64	N, O_GLU_77	H, O_GLU_77	2.89	2.01	22.35
1OSP.PDB	O, O_VAL_86	N, O_GLY_78	H, O_GLY_78	2.92	2.04	22.03
1OSP.PDB	O, O_CYS_84	N, O_LYS_80	H, O_LYS_80	2.88	1.91	7.18
1OSP.PDB	O, O_LYS_80	N, O_LYS_83	H, O_LYS_83	2.97	2.11	23.34
1OSP.PDB	OD1, O_ASP_82	N, O_CYS_84	H, O_CYS_84	2.94	2.02	12.85
1OSP.PDB	O, O_GLY_78	N, O_VAL_86	H, O_VAL_86	2.78	1.82	7.53
1OSP.PDB	O, O_GLU_100	N, O_LYS_87	H, O_LYS_87	2.83	1.86	6.51
1OSP.PDB	O, O_LEU_76	N, O_LEU_88	H, O_LEU_88	2.85	1.88	3.67
1OSP.PDB	O, O_THR_98	N, O_THR_89	H, O_THR_89	2.87	1.91	8.56
1OSP.PDB	O, O_GLY_74	N, O_ILE_90	H, O_ILE_90	2.80	1.83	2.30
1OSP.PDB	O, O_GLN_96	N, O_SER_91	H, O_SER_91	2.90	1.92	4.64
1OSP.PDB	O, O_SER_91	N, O_LEU_94	H, O_LEU_94	2.77	1.86	16.57
1OSP.PDB	O, O_THR_115	N, O_THR_97	H, O_THR_97	2.95	2.01	13.77
1OSP.PDB	O, O_THR_89	N, O_THR_98	H, O_THR_98	2.94	2.04	19.56
1OSP.PDB	O, O_LYS_113	N, O_LEU_99	H, O_LEU_99	2.95	1.99	7.52
1OSP.PDB	O, O_LYS_87	N, O_GLU_100	H, O_GLU_100	2.86	1.89	3.85
1OSP.PDB	O, O_LYS_85	N, O_PHE_102	H, O_PHE_102	2.73	1.77	4.67
1OSP.PDB	O, O_THR_108	N, O_LYS_103	H, O_LYS_103	2.81	1.88	14.70
1OSP.PDB	O, O_LYS_103	N, O_GLY_106	H, O_GLY_106	2.79	1.88	17.21
1OSP.PDB	O, O_VAL_101	N, O_VAL_110	H, O_VAL_110	2.84	1.89	11.58
1OSP.PDB	O, O_GLU_124	N, O_LYS_112	H, O_LYS_112	2.97	2.14	27.43
1OSP.PDB	O, O_LEU_99	N, O_LYS_113	H, O_LYS_113	2.94	1.98	9.26
1OSP.PDB	O, O_THR_122	N, O_VAL_114	H, O_VAL_114	2.91	1.95	10.05
1OSP.PDB	O, O_THR_97	N, O_THR_115	H, O_THR_115	2.93	1.98	12.74
1OSP.PDB	O, O_SER_120	N, O_SER_116	H, O_SER_116	2.84	1.87	6.23
1OSP.PDB	O, O_GLY_95	N, O_LYS_117	H, O_LYS_117	2.85	2.02	26.58
1OSP.PDB	O, O_SER_116	N, O_LYS_119	H, O_LYS_119	3.00	2.13	23.54
1OSP.PDB	OD1, O_ASP_118	N, O_SER_120	H, O_SER_120	2.97	2.05	14.24
1OSP.PDB	O, O_THR_138	N, O_SER_121	H, O_SER_121	2.84	1.93	17.68
1OSP.PDB	O, O_VAL_114	N, O_THR_122	H, O_THR_122	2.89	1.97	16.41
1OSP.PDB	O, O_ILE_136	N, O_GLU_123	H, O_GLU_123	2.84	1.88	8.73
1OSP.PDB	O, O_LYS_112	N, O_GLU_124	H, O_GLU_124	2.76	1.80	4.84
1OSP.PDB	O, O_GLU_134	N, O_LYS_125	H, O_LYS_125	2.97	2.02	11.11
1OSP.PDB	O, O_GLU_131	N, O_ASN_127	H, O_ASN_127	2.72	1.91	28.14
1OSP.PDB	OD1, O_ASN_127	N, O_LYS_129	H, O_LYS_129	2.89	2.06	25.72
1OSP.PDB	O, O_ASN_127	N, O_GLY_130	H, O_GLY_130	2.88	1.93	10.26
1OSP.PDB	OD1, O_ASN_127	N, O_GLU_131	H, O_GLU_131	2.98	2.04	13.29
1OSP.PDB	O, O_LYS_125	N, O_SER_133	H, O_SER_133	2.75	1.83	15.11
1OSP.PDB	O, O_TYR_147	N, O_LYS_135	H, O_LYS_135	2.89	1.94	12.24
1OSP.PDB	O, O_GLU_123	N, O_ILE_136	H, O_ILE_136	2.91	1.99	16.85
1OSP.PDB	O, O_LEU_145	N, O_ILE_137	H, O_ILE_137	2.93	1.95	4.82
1OSP.PDB	O, O_SER_121	N, O_THR_138	H, O_THR_138	2.76	1.86	18.89
1OSP.PDB	O, O_THR_143	N, O_ARG_139	H, O_ARG_139	2.90	1.93	8.66
1OSP.PDB	OG1, O_THR_143	NH1, O_ARG_139	HH11, O_ARG_139	2.73	1.78	14.74
1OSP.PDB	OE2, O_GLU_160	NH2, O_ARG_139	HH22, O_ARG_139	2.96	2.05	19.95
1OSP.PDB	O, O_ARG_139	N, O_GLY_142	H, O_GLY_142	2.82	1.89	14.20
1OSP.PDB	O, O_VAL_161	N, O_ARG_144	H, O_ARG_144	2.86	1.92	11.75
1OSP.PDB	O, O_LYS_159	N, O_GLU_146	H, O_GLU_146	2.74	1.79	9.08
1OSP.PDB	O, O_LYS_135	N, O_TYR_147	H, O_TYR_147	2.76	1.82	11.54
1OSP.PDB	O, O_SER_155	N, O_LYS_151	H, O_LYS_151	2.82	1.90	16.12
1OSP.PDB	O, O_LYS_151	N, O_GLY_154	H, O_GLY_154	3.00	2.15	24.39
1OSP.PDB	O, O_THR_148	N, O_LYS_157	H, O_LYS_157	2.96	2.06	18.52
1OSP.PDB	O, O_GLU_146	N, O_LYS_159	H, O_LYS_159	2.90	2.10	29.35
1OSP.PDB	O, O_LEU_167	N, O_GLU_160	H, O_GLU_160	2.80	1.84	8.36
1OSP.PDB	O, O_ARG_144	N, O_VAL_161	H, O_VAL_161	2.67	1.80	21.27

1OSP.PDB	O, O_TYR_165	N, O_LEU_162	H, O_LEU_162	2.97	2.08	19.74
1OSP.PDB	O, O_GLU_160	N, O_LEU_167	H, O_LEU_167	2.98	2.02	8.76
1OSP.PDB	O, O_THR_177	N, O_THR_170	H, O_THR_170	2.94	2.08	23.59
1OSP.PDB	O, O_GLY_156	N, O_LEU_171	H, O_LEU_171	2.97	2.15	28.04
1OSP.PDB	O, O_ILE_191	N, O_THR_176	H, O_THR_176	2.77	1.81	7.44
1OSP.PDB	O, O_THR_170	N, O_THR_177	H, O_THR_177	2.90	1.94	8.28
1OSP.PDB	O, O_LYS_189	N, O_LEU_178	H, O_LEU_178	2.85	1.91	12.14
1OSP.PDB	O, O_GLU_168	N, O_VAL_179	H, O_VAL_179	2.80	1.83	5.32
1OSP.PDB	O, O_LEU_187	N, O_VAL_180	H, O_VAL_180	2.82	1.89	14.25
1OSP.PDB	O, O_GLU_182	N, O_VAL_185	H, O_VAL_185	2.98	2.06	16.93
1OSP.PDB	O, O_ASN_202	N, O_THR_186	H, O_THR_186	2.75	1.80	6.91
1OSP.PDB	O, O_VAL_180	N, O_LEU_187	H, O_LEU_187	2.73	1.77	7.01
1OSP.PDB	O, O_GLU_200	N, O_SER_188	H, O_SER_188	2.94	1.96	4.07
1OSP.PDB	O, O_LEU_178	N, O_LYS_189	H, O_LYS_189	2.81	1.84	6.92
1OSP.PDB	OE1, O_GLU_160	NZ, O_LYS_189	HZ1, O_LYS_189	2.95	1.93	9.44
1OSP.PDB	O, O_SER_198	N, O_ASN_190	H, O_ASN_190	2.85	1.88	7.09
1OSP.PDB	OG, O_SER_198	ND2, O_ASN_190	HD22, O_ASN_190	2.97	2.02	11.75
1OSP.PDB	O, O_THR_176	N, O_ILE_191	H, O_ILE_191	2.86	1.92	14.23
1OSP.PDB	O, O_GLU_196	N, O_SER_192	H, O_SER_192	2.84	1.90	12.51
1OSP.PDB	O, O_SER_192	N, O_GLY_195	H, O_GLY_195	2.80	1.87	14.11
1OSP.PDB	O, O_THR_186	N, O_ASN_202	H, O_ASN_202	2.98	2.04	13.31
1OSP.PDB	O, O_THR_184	N, O_THR_204	H, O_THR_204	2.90	1.95	13.33
1OSP.PDB	OD1, O_ASP_203	N, O_ASP_205	H, O_ASP_205	2.93	2.02	16.29
1OSP.PDB	O, O_SER_207	N, O_THR_210	H, O_THR_210	2.99	2.05	13.36
1OSP.PDB	OD2, O_ASP_203	N, O_LYS_212	H, O_LYS_212	2.91	1.95	1.32
1OSP.PDB	O, O_THR_210	NZ, O_LYS_212	HZ1, O_LYS_212	2.94	1.97	16.29
1OSP.PDB	O, O_THR_224	N, O_ALA_215	H, O_ALA_215	2.95	2.06	20.55
1OSP.PDB	O, O_THR_222	N, O_ASN_217	H, O_ASN_217	2.94	2.00	14.86
1OSP.PDB	O, O_SER_218	N, O_SER_221	H, O_SER_221	2.93	2.08	24.26
1OSP.PDB	O, O_LEU_235	N, O_LEU_223	H, O_LEU_223	2.82	1.86	8.38
1OSP.PDB	O, O_ALA_215	N, O_THR_224	H, O_THR_224	2.90	1.97	14.17
1OSP.PDB	OD1, O_ASP_234	OG1, O_THR_224	HG1, O_THR_224	2.71	1.92	27.50
1OSP.PDB	O, O_LYS_233	N, O_ILE_225	H, O_ILE_225	2.88	1.93	10.58
1OSP.PDB	O, O_THR_213	N, O_THR_226	H, O_THR_226	2.78	1.85	13.98
1OSP.PDB	O, O_LYS_230	N, O_VAL_227	H, O_VAL_227	2.89	1.96	15.17
1OSP.PDB	O, O_VAL_227	N, O_LYS_230	H, O_LYS_230	2.93	2.00	15.15
1OSP.PDB	O, O_SER_250	NZ, O_LYS_230	HZ1, O_LYS_230	2.95	1.95	11.76
1OSP.PDB	O, O_ILE_225	N, O_THR_232	H, O_THR_232	2.81	1.85	8.22
1OSP.PDB	O, O_GLN_246	N, O_ASP_234	H, O_ASP_234	2.97	2.05	16.64
1OSP.PDB	O, O_LEU_223	N, O_LEU_235	H, O_LEU_235	2.73	1.78	7.98
1OSP.PDB	O, O_THR_244	N, O_VAL_236	H, O_VAL_236	2.90	1.94	9.91
1OSP.PDB	O, O_SER_221	N, O_PHE_237	H, O_PHE_237	2.91	1.92	1.81
1OSP.PDB	O, O_VAL_236	N, O_THR_244	H, O_THR_244	2.91	2.01	19.80
1OSP.PDB	O, O_VAL_260	N, O_VAL_245	H, O_VAL_245	2.75	1.81	11.28
1OSP.PDB	O, O_GLU_256	NE2, O_GLN_246	HE22, O_GLN_246	2.92	1.95	7.48
1OSP.PDB	O, O_THR_232	N, O_TYR_248	H, O_TYR_248	2.90	2.01	20.77
1OSP.PDB	OD1, O_ASP_234	OH, O_TYR_248	HH, O_TYR_248	2.73	1.90	24.06
1OSP.PDB	O, O_LYS_254	N, O_ASP_249	H, O_ASP_249	2.87	1.94	14.75
1OSP.PDB	O, O_ASP_249	N, O_GLY_252	H, O_GLY_252	2.85	1.98	21.02
1OSP.PDB	OD2, O_ASP_249	N, O_LYS_254	H, O_LYS_254	2.80	1.86	5.31
1OSP.PDB	O, O_GLN_247	N, O_GLU_256	H, O_GLU_256	2.93	1.98	13.89
1OSP.PDB	O, O_VAL_245	N, O_VAL_260	H, O_VAL_260	2.77	1.81	5.97
1OSP.PDB	O, O_ILE_243	N, O_ILE_262	H, O_ILE_262	2.80	1.83	3.81
1OSP.PDB	OE1, O_GLU_267	N, O_THR_263	H, O_THR_263	2.83	1.90	11.29
1OSP.PDB	O, O_ASP_266	N, O_ASN_270	H, O_ASN_270	2.79	1.90	19.11

Table 1671: 1OSP-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1PSK.PDB	O, L_TYR_85	NE2, L_GLN_6	HE21, L_GLN_6	2.81	1.89	16.29
1PSK.PDB	O, L_LYS_102	N, L_MET_11	H, L_MET_11	2.72	1.89	26.00
1PSK.PDB	O, L_GLU_104	N, L_ALA_13	H, L_ALA_13	2.83	1.92	17.43
1PSK.PDB	O, L_MET_77	N, L_GLY_16	H, L_GLY_16	2.73	1.77	6.44
1PSK.PDB	O, L_ILE_74	N, L_VAL_19	H, L_VAL_19	2.88	2.00	21.06
1PSK.PDB	O, L_LEU_72	N, L_ILE_21	H, L_ILE_21	2.81	1.98	26.09
1PSK.PDB	O, L_SER_7	N, L_THR_22	H, L_THR_22	2.98	2.05	14.20
1PSK.PDB	O, L_TYR_70	N, L_CYS_23	H, L_CYS_23	2.74	1.94	28.83
1PSK.PDB	O, L_THR_68	N, L_ALA_25	H, L_ALA_25	2.80	1.83	4.30
1PSK.PDB	O, L_VAL_3	N, L_SER_26	H, L_SER_26	2.84	1.92	15.77
1PSK.PDB	O, L_GLN_88	N, L_HIS_33	H, L_HIS_33	2.77	1.93	24.90
1PSK.PDB	O, L_ILE_47	N, L_TRP_34	H, L_TRP_34	2.73	1.83	16.95
1PSK.PDB	O, L_TYR_86	N, L_PHE_35	H, L_PHE_35	2.70	1.82	20.29
1PSK.PDB	O, L_LYS_44	N, L_GLN_36	H, L_GLN_36	2.74	1.81	13.25
1PSK.PDB	O, L_THR_41	NE2, L_GLN_37	HE22, L_GLN_37	2.64	1.76	19.44
1PSK.PDB	O, L_GLU_80	NZ, L_LYS_38	HZ2, L_LYS_38	2.69	1.82	26.34
1PSK.PDB	O, L_LYS_38	N, L_THR_41	H, L_THR_41	2.90	1.99	18.24
1PSK.PDB	O, L_TRP_34	N, L_TRP_46	H, L_TRP_46	2.75	1.83	15.53
1PSK.PDB	O, L_THR_52	N, L_TYR_48	H, L_TYR_48	2.90	2.05	25.41
1PSK.PDB	O, L_ILE_32	N, L_THR_50	H, L_THR_50	2.83	2.01	27.59
1PSK.PDB	O, L_SER_49	N, L_SER_51	H, L_SER_51	2.81	1.95	22.62
1PSK.PDB	O, L_SER_71	N, L_SER_64	H, L_SER_64	2.93	2.00	15.47
1PSK.PDB	O, L_SER_69	N, L_SER_66	H, L_SER_66	2.87	2.04	26.16
1PSK.PDB	O, L_CYS_23	N, L_TYR_70	H, L_TYR_70	2.88	1.92	9.26
1PSK.PDB	O, L_SER_64	N, L_SER_71	H, L_SER_71	2.83	1.87	10.56
1PSK.PDB	O, L_ILE_21	N, L_LEU_72	H, L_LEU_72	2.84	1.87	7.12
1PSK.PDB	O, L_VAL_19	N, L_ILE_74	H, L_ILE_74	2.66	1.77	18.08
1PSK.PDB	O, L_ARG_60	N, L_SER_75	H, L_SER_75	2.95	2.02	15.07
1PSK.PDB	O, L_GLU_17	N, L_MET_77	H, L_MET_77	2.56	1.73	24.40
1PSK.PDB	O, L_THR_101	N, L_TYR_85	H, L_TYR_85	2.97	2.05	16.35
1PSK.PDB	O, L_PHE_35	N, L_TYR_86	H, L_TYR_86	2.89	2.04	24.71
1PSK.PDB	OE1, L_GLN_6	N, L_CYS_87	H, L_CYS_87	2.90	2.04	23.69
1PSK.PDB	O, L_HIS_33	N, L_GLN_88	H, L_GLN_88	2.64	1.77	19.96
1PSK.PDB	O, L_ALA_9	N, L_LYS_102	H, L_LYS_102	2.79	1.82	7.68
1PSK.PDB	O, L_ALA_83	N, L_LEU_103	H, L_LEU_103	2.67	1.77	17.39
1PSK.PDB	O, L_MET_11	N, L_GLU_104	H, L_GLU_104	2.63	1.81	26.11
1PSK.PDB	O, L_ALA_13	N, L_LYS_106	H, L_LYS_106	2.86	1.91	10.19
1PSK.PDB	O, L_ALA_108	NE, L_ARG_107	HE, L_ARG_107	2.69	1.87	26.11
1PSK.PDB	O, L ASP_169	NH1, L_ARG_107	HH11, L_ARG_107	2.89	1.94	13.94
1PSK.PDB	O, L_ALA_108	NH2, L_ARG_107	HH21, L_ARG_107	2.77	1.96	29.27
1PSK.PDB	O, L_TYR_139	N, L_ALA_110	H, L_ALA_110	2.80	1.90	19.51
1PSK.PDB	O, L ASN_136	N, L_THR_113	H, L_THR_113	2.79	1.85	11.43
1PSK.PDB	O, L_SER_120	N, L_LEU_124	H, L_LEU_124	2.82	1.86	7.62
1PSK.PDB	O, L_SER_121	N, L_THR_125	H, L_THR_125	2.73	1.80	12.63
1PSK.PDB	O, L_SER_121	OG1, L_THR_125	HG1, L_THR_125	2.84	1.90	10.36
1PSK.PDB	O, L_GLU_122	OG, L_SER_126	HG, L_SER_126	2.94	2.08	22.24
1PSK.PDB	O, L_LEU_180	N, L_ALA_129	H, L_ALA_129	2.84	1.94	18.85
1PSK.PDB	O, L_LEU_178	N, L_VAL_131	H, L_VAL_131	2.87	2.03	25.59
1PSK.PDB	OG, L_SER_173	N, L ASN_137	H, L ASN_137	2.92	1.98	12.28
1PSK.PDB	O, L_TYR_172	N, L_PHE_138	H, L_PHE_138	2.85	1.88	6.49
1PSK.PDB	O, L_GLU_194	N, L_LYS_146	H, L_LYS_146	2.97	2.01	10.09
1PSK.PDB	OG, L_SER_176	NE1, L_TRP_147	HE1, L_TRP_147	2.73	1.78	10.14
1PSK.PDB	O, L_THR_192	N, L_LYS_148	H, L_LYS_148	2.68	1.78	17.05
1PSK.PDB	O, L_SER_152	N, L_ILE_149	H, L_ILE_149	2.76	1.81	9.00
1PSK.PDB	O, L_SER_190	N, L ASP_150	H, L ASP_150	2.82	1.85	2.71
1PSK.PDB	O, L_ILE_149	N, L_SER_152	H, L_SER_152	2.78	1.90	20.78
1PSK.PDB	OE1, L_GLN_155	N, L ASN_156	H, L ASN_156	2.98	2.05	13.77

1PSK.PDB	O, L_THR_177	N, L_LEU_159	H, L_LEU_159	2.87	2.02	24.21
1PSK.PDB	O, H_PRO_168	OG, L_SER_161	HG, L_SER_161	2.76	1.90	22.64
1PSK.PDB	O, L_ILE_105	NE2, L_GLN_165	HE21, L_GLN_165	2.92	2.00	17.26
1PSK.PDB	O, L_THR_171	N, L_ASP_166	H, L_ASP_166	2.81	1.87	10.96
1PSK.PDB	OD2, L_ASP_166	N, L_ASP_169	H, L_ASP_169	2.99	2.04	7.95
1PSK.PDB	O, L_PHE_138	N, L_TYR_172	H, L_TYR_172	2.85	1.92	14.74
1PSK.PDB	O, L_LEU_135	N, L_MET_174	H, L_MET_174	2.76	1.79	2.98
1PSK.PDB	O, L_CYS_133	N, L_SER_176	H, L_SER_176	2.88	1.92	9.72
1PSK.PDB	OD1, L_ASN_160	OG, L_SER_176	HG, L_SER_176	2.79	1.87	14.99
1PSK.PDB	O, L_GLY_157	N, L_THR_179	H, L_THR_179	2.95	2.12	26.59
1PSK.PDB	O, L_ALA_129	N, L_LEU_180	H, L_LEU_180	2.80	1.83	2.82
1PSK.PDB	O, L_THR_181	N, L_TYR_185	H, L_TYR_185	2.95	2.01	13.19
1PSK.PDB	O, L_LYS_182	N, L_GLU_186	H, L_GLU_186	2.95	1.99	9.74
1PSK.PDB	O, L_PHE_208	N, L_TYR_191	H, L_TYR_191	2.94	1.97	6.75
1PSK.PDB	O, L_LYS_148	N, L_THR_192	H, L_THR_192	2.84	1.87	6.81
1PSK.PDB	O, L_LYS_146	N, L_GLU_194	H, L_GLU_194	2.94	2.02	16.13
1PSK.PDB	O, L_ILE_204	N, L_ALA_195	H, L_ALA_195	2.94	2.01	15.37
1PSK.PDB	O, L_ASN_144	N, L_THR_196	H, L_THR_196	2.65	1.83	27.50
1PSK.PDB	O, L_TYR_191	N, L_PHE_208	H, L_PHE_208	2.94	2.02	17.53
1PSK.PDB	O, L_ASN_189	N, L_ARG_210	H, L_ARG_210	2.72	1.78	9.08
1PSK.PDB	O, L_HIS_188	NH1, L_ARG_210	HH11, L_ARG_210	2.85	1.95	20.39
1PSK.PDB	O, H_TYR_94	NE2, H_GLN_6	HE21, H_GLN_6	2.75	1.83	14.83
1PSK.PDB	O, H_THR_109	N, H_GLU_10	H, H_GLU_10	2.94	2.04	19.11
1PSK.PDB	O, H_THR_111	N, H_VAL_12	H, H_VAL_12	2.75	1.86	19.89
1PSK.PDB	O, H_LYS_13	N, H_ALA_16	H, H_ALA_16	2.98	2.05	15.84
1PSK.PDB	O, H_LEU_83	N, H_VAL_18	H, H_VAL_18	2.94	2.01	16.46
1PSK.PDB	OG, H_SER_7	N, H_SER_21	H, H_SER_21	2.91	1.95	7.05
1PSK.PDB	O, H_THR_77	N, H_THR_24	H, H_THR_24	2.84	1.91	14.03
1PSK.PDB	O, H_THR_97	N, H_HIS_35	H, H_HIS_35	2.81	1.88	13.42
1PSK.PDB	NE1, H_TRP_47	ND1, H_HIS_35	HD1, H_HIS_35	2.92	2.03	20.19
1PSK.PDB	O, H_TYR_95	N, H_VAL_37	H, H_VAL_37	2.78	1.85	13.12
1PSK.PDB	O, H_GLU_46	N, H_LYS_38	H, H_LYS_38	2.74	1.81	11.82
1PSK.PDB	O, H_VAL_93	N, H_GLN_39	H, H_GLN_39	2.70	1.83	20.61
1PSK.PDB	O, H_SER_40	NE2, H_GLN_39	HE22, H_GLN_39	2.98	2.06	16.51
1PSK.PDB	O, H_SER_44	N, H_SER_40	H, H_SER_40	2.86	1.90	10.36
1PSK.PDB	O, H_LYS_38	N, H_GLU_46	H, H_GLU_46	2.72	1.82	17.92
1PSK.PDB	O, H_TRP_36	N, H_ILE_48	H, H_ILE_48	2.97	2.07	18.37
1PSK.PDB	O, H_ASN_59	N, H_ASP_50	H, H_ASP_50	2.89	1.96	16.23
1PSK.PDB	O, H_GLY_57	N, H_ASN_52	H, H_ASN_52	2.75	1.93	27.30
1PSK.PDB	O, H_PRO_53	N, H_ASN_55	H, H_ASN_55	2.75	1.87	20.51
1PSK.PDB	O, H_PRO_53	ND2, H_ASN_55	HD22, H_ASN_55	2.76	1.94	26.77
1PSK.PDB	O, H_ILE_48	N, H_ASN_61	H, H_ASN_61	2.93	2.02	18.42
1PSK.PDB	O, H_TRP_47	ND2, H_ASN_61	HD22, H_ASN_61	2.88	1.97	18.24
1PSK.PDB	OD1, H_ASN_61	N, H_LYS_63	H, H_LYS_63	2.93	2.01	16.11
1PSK.PDB	O, H_PHE_64	N, H_ALA_68	H, H_ALA_68	2.83	1.93	18.74
1PSK.PDB	OH, H_TYR_60	N, H_LEU_70	H, H_LEU_70	2.73	1.84	18.80
1PSK.PDB	O, H_THR_78	N, H_HIS_73	H, H_HIS_73	2.82	2.01	28.97
1PSK.PDB	OG1, H_THR_78	OG, H_SER_76	HG, H_SER_76	2.94	2.03	16.27
1PSK.PDB	O, H_THR_71	N, H_TYR_80	H, H_TYR_80	2.94	2.09	24.76
1PSK.PDB	O, H_VAL_18	N, H_LEU_83	H, H_LEU_83	2.81	1.85	9.28
1PSK.PDB	OD2, H_ASP_90	N, H_THR_87	H, H_THR_87	2.99	2.12	22.62
1PSK.PDB	O, H_THR_87	N, H_ASP_90	H, H_ASP_90	2.83	1.90	13.61
1PSK.PDB	O, H_SER_88	OG, H_SER_91	HG, H_SER_91	2.90	1.97	12.52
1PSK.PDB	O, H_GLN_39	N, H_VAL_93	H, H_VAL_93	2.97	1.99	0.74
1PSK.PDB	O, H_THR_108	N, H_TYR_94	H, H_TYR_94	2.81	1.89	15.61
1PSK.PDB	O, H_ASP_90	OH, H_TYR_94	HH, H_TYR_94	2.77	1.87	17.15
1PSK.PDB	O, H_VAL_37	N, H_TYR_95	H, H_TYR_95	2.95	1.97	7.17
1PSK.PDB	O, H_HIS_35	N, H_THR_97	H, H_THR_97	2.81	1.92	20.68

1PSK.PDB	O, H_TYR_103	N, H_SER_98	H, H_SER_98	2.80	1.88	15.11
1PSK.PDB	OH, H_TYR_27	OG, H_SER_98	HG, H_SER_98	2.95	2.06	19.06
1PSK.PDB	O, H_TYR_94	N, H_THR_108	H, H_THR_108	2.86	2.00	23.11
1PSK.PDB	O, H_SER_7	OG1, H_THR_108	HG1, H_THR_108	2.62	1.79	24.94
1PSK.PDB	O, H_ALA_92	N, H_LEU_110	H, H_LEU_110	2.97	2.02	12.06
1PSK.PDB	O, H_GLU_10	N, H_THR_111	H, H_THR_111	2.77	1.82	9.08
1PSK.PDB	O, H_LYS_144	N, H_SER_121	H, H_SER_121	2.81	1.84	4.61
1PSK.PDB	O, H_LEU_142	N, H_TYR_123	H, H_TYR_123	2.75	1.89	23.66
1PSK.PDB	O, H_GLY_140	N, H_LEU_125	H, H_LEU_125	2.83	1.96	22.70
1PSK.PDB	O, H_VAL_182	N, H_LEU_139	H, H_LEU_139	2.94	1.97	6.89
1PSK.PDB	O, H_SER_180	N, H_CYS_141	H, H_CYS_141	2.84	1.96	21.90
1PSK.PDB	O, H_TYR_123	N, H_LEU_142	H, H_LEU_142	2.94	1.96	5.65
1PSK.PDB	O, H_LEU_178	N, H_VAL_143	H, H_VAL_143	2.80	1.85	10.99
1PSK.PDB	O, H_SER_121	N, H_LYS_144	H, H_LYS_144	2.73	1.77	7.35
1PSK.PDB	O, H_LEU_175	N, H_GLN_172	H, H_GLN_172	2.99	2.02	7.12
1PSK.PDB	O, H_TYR_146	N, H_TYR_176	H, H_TYR_176	2.73	1.77	6.58
1PSK.PDB	O, H_VAL_170	N, H_THR_177	H, H_THR_177	3.00	2.15	24.71
1PSK.PDB	O, H_HIS_165	N, H_SER_181	H, H_SER_181	2.93	1.97	9.97
1PSK.PDB	O, H_GLY_163	N, H_THR_183	H, H_THR_183	2.96	2.11	24.27
1PSK.PDB	O, H_VAL_137	N, H_VAL_184	H, H_VAL_184	2.80	1.88	17.57
1PSK.PDB	O, H_THR_188	N, H_GLN_192	H, H_GLN_192	2.60	1.80	26.98
1PSK.PDB	OD1, H_ASN_156	N, H_THR_195	H, H_THR_195	2.91	1.95	9.28
1PSK.PDB	O, H_THR_154	N, H_ASN_197	H, H_ASN_197	2.76	1.83	13.92
1PSK.PDB	O, H_LYS_206	N, H_VAL_198	H, H_VAL_198	2.73	1.84	18.50
1PSK.PDB	O, H_HIS_200	N, H_SER_204	H, H_SER_204	2.75	1.84	15.81
1PSK.PDB	O, H_VAL_198	N, H_LYS_206	H, H_LYS_206	2.77	1.84	13.06
1PSK.PDB	O, H_PRO_120	NZ, H_LYS_206	HZ1, H_LYS_206	2.63	1.80	29.01

Table 1672: 1PSK-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1R21-1.PDB	O, A_ARG.96	N, A_VAL.8	H, A_VAL.8	2.92	2.11	28.07
1R21-1.PDB	O, A_ILE.51	N, A_CYS.27	H, A_CYS.27	2.73	1.80	13.77
1R21-1.PDB	O, A_CYS.49	N, A_PHE.29	H, A_PHE.29	2.63	1.76	21.39
1R21-1.PDB	O, A_GLY.32	N, A_CYS.35	H, A_CYS.35	2.97	2.04	15.31
1R21-1.PDB	O, A_LEU.28	N, A_ILE.37	H, A_ILE.37	2.58	1.63	11.44
1R21-1.PDB	O, A_CYS.27	N, A_ILE.51	H, A_ILE.51	2.59	1.74	23.78
1R21-1.PDB	O, A_ILE.59	N, A_GLU.52	H, A_GLU.52	2.42	1.47	10.01
1R21-1.PDB	O, A_SER.25	N, A_ILE.53	H, A_ILE.53	2.91	2.02	20.16
1R21-1.PDB	O, A_GLU.57	N, A_HIS.54	H, A_HIS.54	2.41	1.54	20.64
1R21-1.PDB	O, A_GLU.52	N, A_ILE.59	H, A_ILE.59	2.67	1.74	15.06
1R21-1.PDB	OG1, A_THR.69	ND2, A_ASN.62	HD21, A_ASN.62	2.86	1.99	21.79
1R21-1.PDB	ND2, A_ASN.62	N, A_THR.69	H, A_THR.69	2.75	1.81	12.35
1R21-1.PDB	O, A_THR.89	N, A_GLN.70	H, A_GLN.70	2.50	1.71	28.49
1R21-1.PDB	O, A_SER.74	N, A_VAL.71	H, A_VAL.71	2.82	1.84	3.74
1R21-1.PDB	O, A_VAL.87	N, A_ASN.72	H, A_ASN.72	2.95	2.00	10.39
1R21-1.PDB	O, A_VAL.71	N, A_SER.74	H, A_SER.74	2.47	1.61	23.41
1R21-1.PDB	OD2, A_ASP.86	N, A_LYS.83	H, A_LYS.83	2.35	1.40	9.85
1R21-1.PDB	O, A_TYR.97	N, A_GLY.85	H, A_GLY.85	2.98	2.05	14.93
1R21-1.PDB	O, A_PHE.95	N, A_ILE.88	H, A_ILE.88	2.64	1.67	7.14
1R21-1.PDB	O, A_GLN.70	N, A_THR.89	H, A_THR.89	2.52	1.55	4.70
1R21-1.PDB	O, A_ARG.93	N, A_ILE.90	H, A_ILE.90	2.76	1.81	12.04
1R21-1.PDB	O, A_ILE.88	N, A_PHE.95	H, A_PHE.95	2.52	1.55	6.84
1R21-1.PDB	O, A_VAL.8	N, A_ARG.96	H, A_ARG.96	2.54	1.67	21.94
1R21-1.PDB	O, A_ARG.6	N, A_GLU.98	H, A_GLU.98	2.97	1.99	7.38
1R21-1.PDB	ND1, A_HIS.84	N, A_ASN.99	H, A_ASN.99	2.78	1.83	11.23
1R21-10.PDB	O, A_PHE.20	N, A_LEU.7	H, A_LEU.7	2.54	1.63	17.03
1R21-10.PDB	O, A_ARG.96	N, A_VAL.8	H, A_VAL.8	2.88	1.97	16.93
1R21-10.PDB	O, A_PRO.18	N, A_THR.9	H, A_THR.9	2.64	1.77	22.03
1R21-10.PDB	O, A_ARG.5	N, A_LEU.22	H, A_LEU.22	2.90	2.07	26.17
1R21-10.PDB	O, A_ILE.51	N, A_CYS.27	H, A_CYS.27	2.90	1.97	15.62
1R21-10.PDB	O, A_CYS.49	N, A_PHE.29	H, A_PHE.29	2.63	1.76	20.96
1R21-10.PDB	O, A_LEU.28	N, A_ILE.37	H, A_ILE.37	2.61	1.66	11.11
1R21-10.PDB	O, A_GLY.30	N, A_ILE.39	H, A_ILE.39	2.86	1.97	19.93
1R21-10.PDB	O, A_LEU.41	N, A_VAL.44	H, A_VAL.44	2.90	2.09	27.66
1R21-10.PDB	O, A_CYS.27	N, A_ILE.51	H, A_ILE.51	2.67	1.79	22.06
1R21-10.PDB	O, A_ILE.59	N, A_GLU.52	H, A_GLU.52	2.49	1.61	19.99
1R21-10.PDB	O, A_GLU.57	N, A_HIS.54	H, A_HIS.54	2.63	1.74	19.91
1R21-10.PDB	O, A_GLU.52	N, A_ILE.59	H, A_ILE.59	2.58	1.65	14.41
1R21-10.PDB	O, A_VAL.80	N, A_LEU.60	H, A_LEU.60	2.98	2.07	18.84
1R21-10.PDB	OG1, A_THR.69	ND2, A_ASN.62	HD21, A_ASN.62	2.90	2.06	25.22
1R21-10.PDB	ND2, A_ASN.62	N, A_THR.69	H, A_THR.69	2.86	1.92	14.24
1R21-10.PDB	O, A_SER.74	N, A_VAL.71	H, A_VAL.71	2.72	1.74	5.16
1R21-10.PDB	O, A_VAL.87	N, A_ASN.72	H, A_ASN.72	2.98	2.03	12.85
1R21-10.PDB	O, A_VAL.71	N, A_SER.74	H, A_SER.74	2.40	1.47	14.75
1R21-10.PDB	O, A_THR.69	N, A_ILE.76	H, A_ILE.76	2.93	2.09	24.54
1R21-10.PDB	O, A_ALA.58	N, A_LEU.82	H, A_LEU.82	2.93	2.12	28.18
1R21-10.PDB	OD2, A_ASP.86	N, A_LYS.83	H, A_LYS.83	2.34	1.37	8.83
1R21-10.PDB	O, A_TYR.97	N, A_GLY.85	H, A_GLY.85	2.85	2.03	27.50
1R21-10.PDB	O, A_LYS.83	N, A_ASP.86	H, A_ASP.86	2.93	2.10	26.57
1R21-10.PDB	O, A_PHE.95	N, A_ILE.88	H, A_ILE.88	2.55	1.60	10.99
1R21-10.PDB	O, A_GLN.70	N, A_THR.89	H, A_THR.89	2.70	1.75	9.37
1R21-10.PDB	O, A_ARG.93	N, A_ILE.90	H, A_ILE.90	2.66	1.70	9.59
1R21-10.PDB	O, A_ILE.88	N, A_PHE.95	H, A_PHE.95	2.60	1.73	21.06
1R21-10.PDB	O, A_VAL.8	N, A_ARG.96	H, A_ARG.96	2.52	1.64	21.43
1R21-10.PDB	ND1, A_HIS.84	N, A_ASN.99	H, A_ASN.99	2.77	1.80	7.83
1R21-11.PDB	O, A_LEU.7	N, A_PHE.20	H, A_PHE.20	2.62	1.83	29.77
1R21-11.PDB	O, A_ILE.51	N, A_CYS.27	H, A_CYS.27	2.93	1.97	9.94

1R21-11.PDB	O, A_CYS_49	N, A_PHE_29	H, A_PHE_29	2.82	1.94	21.59
1R21-11.PDB	O, A_LEU_28	N, A_ILE_37	H, A_ILE_37	2.67	1.76	16.89
1R21-11.PDB	O, A_GLY_30	N, A_ILE_39	H, A_ILE_39	2.89	1.99	18.61
1R21-11.PDB	O, A_LEU_41	N, A_VAL_44	H, A_VAL_44	2.87	2.01	24.14
1R21-11.PDB	O, A_CYS_27	N, A_ILE_51	H, A_ILE_51	2.91	2.09	27.62
1R21-11.PDB	O, A_ILE_59	N, A_GLU_52	H, A_GLU_52	2.50	1.54	7.92
1R21-11.PDB	O, A_GLU_57	N, A_HIS_54	H, A_HIS_54	2.47	1.52	11.34
1R21-11.PDB	O, A_GLU_52	N, A_ILE_59	H, A_ILE_59	2.50	1.53	7.38
1R21-11.PDB	O, A_LYS_50	N, A_HIS_61	H, A_HIS_61	2.34	1.55	28.69
1R21-11.PDB	OG, A_SER_64	ND2, A_ASN_62	HD22, A_ASN_62	2.35	1.48	21.77
1R21-11.PDB	ND2, A_ASN_62	N, A_THR_69	H, A_THR_69	2.87	1.91	9.38
1R21-11.PDB	O, A_THR_89	N, A_GLN_70	H, A_GLN_70	2.52	1.62	18.25
1R21-11.PDB	O, A_VAL_71	N, A_SER_74	H, A_SER_74	2.43	1.53	18.84
1R21-11.PDB	O, A_VAL_71	OG, A_SER_74	HG, A_SER_74	2.65	1.87	28.98
1R21-11.PDB	N, A_GLY_85	ND1, A_HIS_84	HD1, A_HIS_84	2.62	1.77	24.61
1R21-11.PDB	O, A_LYS_83	N, A_ASP_86	H, A_ASP_86	2.93	2.08	25.03
1R21-11.PDB	O, A_PHE_95	N, A_ILE_88	H, A_ILE_88	2.49	1.58	17.48
1R21-11.PDB	O, A_GLN_70	N, A_THR_89	H, A_THR_89	2.50	1.53	3.27
1R21-11.PDB	O, A_ARG_93	N, A_ILE_90	H, A_ILE_90	2.78	1.90	20.94
1R21-11.PDB	O, A_ILE_88	N, A_PHE_95	H, A_PHE_95	2.50	1.61	19.58
1R21-11.PDB	O, A_VAL_8	N, A_ARG_96	H, A_ARG_96	2.62	1.79	25.65
1R21-11.PDB	O, A_ASP_86	N, A_TYR_97	H, A_TYR_97	2.89	1.91	5.12
1R21-12.PDB	O, A_HIS_54	NH1, A_ARG_5	HH12, A_ARG_5	2.35	1.46	20.98
1R21-12.PDB	O, A_ASP_16	N, A_LYS_11	H, A_LYS_11	2.75	1.92	26.57
1R21-12.PDB	O, A_LEU_7	N, A_PHE_20	H, A_PHE_20	2.75	1.93	26.79
1R21-12.PDB	O, A_ILE_51	N, A_CYS_27	H, A_CYS_27	2.63	1.69	14.10
1R21-12.PDB	O, A_CYS_49	N, A_PHE_29	H, A_PHE_29	2.60	1.71	19.44
1R21-12.PDB	O, A_LEU_28	N, A_ILE_37	H, A_ILE_37	2.57	1.63	12.93
1R21-12.PDB	O, A_LEU_41	N, A_VAL_44	H, A_VAL_44	2.87	2.03	25.37
1R21-12.PDB	O, A_CYS_27	N, A_ILE_51	H, A_ILE_51	2.54	1.72	26.76
1R21-12.PDB	O, A_ILE_59	N, A_GLU_52	H, A_GLU_52	2.50	1.60	18.41
1R21-12.PDB	O, A_SER_25	N, A_ILE_53	H, A_ILE_53	2.75	1.90	23.58
1R21-12.PDB	O, A_GLU_57	N, A_HIS_54	H, A_HIS_54	2.53	1.59	12.83
1R21-12.PDB	O, A_GLU_52	N, A_ILE_59	H, A_ILE_59	2.53	1.55	3.06
1R21-12.PDB	OD1, A_ASN_67	OG1, A_THR_66	HG1, A_THR_66	2.34	1.38	3.67
1R21-12.PDB	ND2, A_ASN_62	N, A_THR_69	H, A_THR_69	2.95	1.98	4.80
1R21-12.PDB	O, A_SER_74	N, A_VAL_71	H, A_VAL_71	2.74	1.76	4.25
1R21-12.PDB	O, A_VAL_87	N, A_ASN_72	H, A_ASN_72	2.97	2.02	11.55
1R21-12.PDB	O, A_VAL_71	N, A_SER_74	H, A_SER_74	2.46	1.58	19.54
1R21-12.PDB	O, A_TYR_97	N, A_GLY_85	H, A_GLY_85	2.87	2.02	24.88
1R21-12.PDB	O, A_PHE_95	N, A_ILE_88	H, A_ILE_88	2.84	1.89	12.15
1R21-12.PDB	O, A_GLN_70	N, A_THR_89	H, A_THR_89	2.50	1.53	5.45
1R21-12.PDB	O, A_ARG_93	N, A_ILE_90	H, A_ILE_90	2.66	1.75	17.37
1R21-12.PDB	O, A_ILE_88	N, A_PHE_95	H, A_PHE_95	2.61	1.63	4.84
1R21-12.PDB	O, A_VAL_8	N, A_ARG_96	H, A_ARG_96	2.92	2.06	24.15
1R21-12.PDB	ND1, A_HIS_84	N, A_ASN_99	H, A_ASN_99	2.78	1.81	6.29
1R21-13.PDB	O, A_PHE_20	N, A_LEU_7	H, A_LEU_7	2.91	1.96	10.96
1R21-13.PDB	O, A_LEU_7	N, A_PHE_20	H, A_PHE_20	2.60	1.77	25.97
1R21-13.PDB	O, A_ILE_51	N, A_CYS_27	H, A_CYS_27	2.75	1.81	13.78
1R21-13.PDB	O, A_CYS_49	N, A_PHE_29	H, A_PHE_29	2.85	1.88	7.67
1R21-13.PDB	O, A_GLY_32	N, A_CYS_35	H, A_CYS_35	2.95	2.05	19.20
1R21-13.PDB	O, A_LEU_28	N, A_ILE_37	H, A_ILE_37	2.62	1.65	8.44
1R21-13.PDB	OG, A_SER_45	N, A_GLN_47	H, A_GLN_47	2.99	2.17	27.24
1R21-13.PDB	O, A_CYS_27	N, A_ILE_51	H, A_ILE_51	2.43	1.49	12.20
1R21-13.PDB	O, A_ILE_59	N, A_GLU_52	H, A_GLU_52	2.43	1.54	19.61
1R21-13.PDB	O, A_GLU_57	N, A_HIS_54	H, A_HIS_54	2.39	1.45	12.69
1R21-13.PDB	O, A_GLU_52	N, A_ILE_59	H, A_ILE_59	2.60	1.64	9.03
1R21-13.PDB	O, A_LYS_50	N, A_HIS_61	H, A_HIS_61	2.72	1.77	12.00

1R21-13.PDB	OG1, A_THR_69	ND2, A_ASN_62	HD22, A_ASN_62	2.50	1.62	19.65
1R21-13.PDB	O, A_HIS_48	N, A_PHE_63	H, A_PHE_63	2.98	2.08	19.86
1R21-13.PDB	O, A_HIS_48	N, A_SER_64	H, A_SER_64	3.00	2.09	18.58
1R21-13.PDB	O, A_THR_89	N, A_GLN_70	H, A_GLN_70	2.61	1.74	22.03
1R21-13.PDB	O, A_SER_74	N, A_VAL_71	H, A_VAL_71	2.72	1.81	16.96
1R21-13.PDB	O, A_VAL_71	N, A_SER_74	H, A_SER_74	2.42	1.47	9.86
1R21-13.PDB	O, A_PHE_95	N, A_ILE_88	H, A_ILE_88	2.49	1.53	9.17
1R21-13.PDB	O, A_GLN_70	N, A_THR_89	H, A_THR_89	2.84	1.88	8.15
1R21-13.PDB	O, A_ARG_93	N, A_ILE_90	H, A_ILE_90	2.77	1.79	2.62
1R21-13.PDB	O, A_ILE_88	N, A_PHE_95	H, A_PHE_95	2.53	1.57	8.67
1R21-13.PDB	O, A_VAL_8	N, A_ARG_96	H, A_ARG_96	2.67	1.79	21.65
1R21-13.PDB	ND1, A_HIS_84	N, A_ASN_99	H, A_ASN_99	2.75	1.78	6.35
1R21-13.PDB	OH, A_TYR_97	ND2, A_ASN_99	HD21, A_ASN_99	2.51	1.54	7.69
1R21-14.PDB	O, A_LYS_11	N, A_GLY_14	H, A_GLY_14	2.87	1.98	19.78
1R21-14.PDB	O, A_LEU_7	N, A_PHE_20	H, A_PHE_20	2.54	1.58	9.83
1R21-14.PDB	O, A_ILE_51	N, A_CYS_27	H, A_CYS_27	2.51	1.56	10.89
1R21-14.PDB	O, A_CYS_49	N, A_PHE_29	H, A_PHE_29	2.67	1.74	15.50
1R21-14.PDB	O, A_LEU_28	N, A_ILE_37	H, A_ILE_37	2.59	1.64	10.66
1R21-14.PDB	O, A_GLY_30	N, A_ILE_39	H, A_ILE_39	2.98	2.01	7.49
1R21-14.PDB	O, A_CYS_27	N, A_ILE_51	H, A_ILE_51	2.41	1.51	18.34
1R21-14.PDB	O, A_ILE_59	N, A_GLU_52	H, A_GLU_52	2.40	1.49	17.73
1R21-14.PDB	O, A_GLU_57	N, A_HIS_54	H, A_HIS_54	2.54	1.66	20.37
1R21-14.PDB	O, A_GLU_52	N, A_ILE_59	H, A_ILE_59	2.44	1.48	8.49
1R21-14.PDB	OG1, A_THR_69	ND2, A_ASN_62	HD21, A_ASN_62	2.52	1.57	12.09
1R21-14.PDB	ND2, A_ASN_62	N, A_THR_69	H, A_THR_69	2.79	1.90	20.15
1R21-14.PDB	O, A_SER_74	N, A_VAL_71	H, A_VAL_71	2.76	1.80	9.73
1R21-14.PDB	O, A_VAL_71	N, A_SER_74	H, A_SER_74	2.68	1.86	26.85
1R21-14.PDB	O, A_THR_69	N, A_ILE_76	H, A_ILE_76	2.74	1.79	12.00
1R21-14.PDB	OE1, A_GLU_57	NE, A_ARG_81	HE, A_ARG_81	2.82	2.02	29.06
1R21-14.PDB	OE2, A_GLU_57	NH2, A_ARG_81	HH21, A_ARG_81	2.46	1.50	12.90
1R21-14.PDB	O, A_LYS_83	N, A ASP_86	H, A ASP_86	2.90	2.01	20.84
1R21-14.PDB	O, A_PHE_95	N, A_ILE_88	H, A_ILE_88	2.88	1.96	15.69
1R21-14.PDB	O, A_GLN_70	N, A_THR_89	H, A_THR_89	2.35	1.46	19.02
1R21-14.PDB	O, A_ARG_93	N, A_ILE_90	H, A_ILE_90	2.73	1.76	5.94
1R21-14.PDB	O, A_ILE_88	N, A_PHE_95	H, A_PHE_95	2.68	1.71	6.73
1R21-14.PDB	O, A_VAL_8	N, A_ARG_96	H, A_ARG_96	2.64	1.79	24.33
1R21-14.PDB	ND1, A_HIS_84	N, A_ASN_99	H, A_ASN_99	2.72	1.75	7.22
1R21-14.PDB	OH, A_TYR_97	ND2, A_ASN_99	HD22, A_ASN_99	2.66	1.70	8.32
1R21-14.PDB	O, A_THR_4	N, A_GLU_100	H, A_GLU_100	2.70	1.78	16.06
1R21-15.PDB	O, A_ARG_96	N, A_VAL_8	H, A_VAL_8	2.88	1.93	10.65
1R21-15.PDB	O, A_SER_13	N, A_VAL_15	H, A_VAL_15	2.35	1.44	16.35
1R21-15.PDB	O, A_LEU_7	N, A_PHE_20	H, A_PHE_20	2.72	1.80	16.28
1R21-15.PDB	O, A_ILE_51	N, A_CYS_27	H, A_CYS_27	2.61	1.66	12.03
1R21-15.PDB	O, A_CYS_49	N, A_PHE_29	H, A_PHE_29	2.69	1.83	22.46
1R21-15.PDB	O, A_LEU_28	N, A_ILE_37	H, A_ILE_37	2.63	1.74	19.85
1R21-15.PDB	O, A_GLY_30	N, A_ILE_39	H, A_ILE_39	2.35	1.52	25.02
1R21-15.PDB	O, A_LEU_41	N, A_VAL_44	H, A_VAL_44	2.84	1.98	24.12
1R21-15.PDB	O, A_CYS_27	N, A_ILE_51	H, A_ILE_51	2.47	1.55	15.28
1R21-15.PDB	O, A_ILE_59	N, A_GLU_52	H, A_GLU_52	2.51	1.64	21.23
1R21-15.PDB	O, A_SER_25	N, A_ILE_53	H, A_ILE_53	2.58	1.68	18.87
1R21-15.PDB	O, A_GLU_57	N, A_HIS_54	H, A_HIS_54	2.77	1.90	21.35
1R21-15.PDB	O, A_GLU_52	N, A_ILE_59	H, A_ILE_59	2.58	1.61	8.20
1R21-15.PDB	ND2, A_ASN_62	N, A_THR_69	H, A_THR_69	2.81	1.84	7.15
1R21-15.PDB	O, A_THR_89	N, A_GLN_70	H, A_GLN_70	2.43	1.52	17.31
1R21-15.PDB	O, A_SER_74	N, A_VAL_71	H, A_VAL_71	2.74	1.76	5.74
1R21-15.PDB	O, A_VAL_87	N, A_ASN_72	H, A_ASN_72	2.86	1.91	10.94
1R21-15.PDB	O, A_VAL_71	N, A_SER_74	H, A_SER_74	2.38	1.51	21.59
1R21-15.PDB	O, A_LYS_83	N, A ASP_86	H, A ASP_86	2.97	2.11	23.04

1R21-15.PDB	O, A_PHE.95	N, A_ILE.88	H, A_ILE.88	2.57	1.60	8.14
1R21-15.PDB	O, A_GLN.70	N, A_THR.89	H, A_THR.89	2.38	1.41	5.21
1R21-15.PDB	O, A_ARG.93	N, A_ILE.90	H, A_ILE.90	2.86	1.91	12.34
1R21-15.PDB	O, A_ILE.88	N, A_PHE.95	H, A_PHE.95	2.57	1.60	6.79
1R21-15.PDB	O, A_VAL.8	N, A_ARG.96	H, A_ARG.96	2.52	1.57	12.45
1R21-15.PDB	O, A_ASP.86	N, A_TYR.97	H, A_TYR.97	2.93	1.95	3.90
1R21-15.PDB	ND1, A_HIS.84	N, A_ASN.99	H, A_ASN.99	2.69	1.85	25.22
1R21-16.PDB	O, A_GLN.56	NH2, A_ARG.5	HH22, A_ARG.5	2.34	1.43	18.03
1R21-16.PDB	O, A_PRO.18	N, A_THR.9	H, A_THR.9	2.87	1.96	17.95
1R21-16.PDB	O, A_LEU.7	N, A_PHE.20	H, A_PHE.20	2.79	1.90	20.16
1R21-16.PDB	O, A_ILE.51	N, A_CYS.27	H, A_CYS.27	2.97	2.01	9.41
1R21-16.PDB	O, A_CYS.49	N, A_PHE.29	H, A_PHE.29	2.70	1.82	20.83
1R21-16.PDB	O, A_LEU.28	N, A_ILE.37	H, A_ILE.37	2.64	1.66	6.75
1R21-16.PDB	O, A_GLY.30	N, A_ILE.39	H, A_ILE.39	2.92	2.04	21.29
1R21-16.PDB	O, A_LEU.41	N, A_VAL.44	H, A_VAL.44	2.78	1.86	16.48
1R21-16.PDB	N, A_LYS.50	SG, A_CYS.49	HG, A_CYS.49	2.71	1.94	29.78
1R21-16.PDB	O, A_CYS.27	N, A_ILE.51	H, A_ILE.51	2.66	1.76	18.43
1R21-16.PDB	O, A_ILE.59	N, A_GLU.52	H, A_GLU.52	2.35	1.42	13.61
1R21-16.PDB	O, A_GLU.57	N, A_HIS.54	H, A_HIS.54	2.48	1.61	21.21
1R21-16.PDB	O, A_GLU.52	N, A_ILE.59	H, A_ILE.59	2.45	1.49	8.62
1R21-16.PDB	O, A_LYS.50	N, A_HIS.61	H, A_HIS.61	2.79	1.86	14.54
1R21-16.PDB	O, A_ASN.67	OG, A_SER.64	HG, A_SER.64	2.30	1.47	23.15
1R21-16.PDB	ND2, A_ASN.62	N, A_THR.69	H, A_THR.69	2.78	1.82	9.93
1R21-16.PDB	O, A_THR.89	N, A_GLN.70	H, A_GLN.70	2.50	1.67	25.41
1R21-16.PDB	O, A_SER.74	N, A_VAL.71	H, A_VAL.71	2.80	1.83	8.69
1R21-16.PDB	O, A_VAL.87	N, A_ASN.72	H, A_ASN.72	2.98	2.02	10.53
1R21-16.PDB	O, A_VAL.71	N, A_SER.74	H, A_SER.74	2.44	1.53	16.98
1R21-16.PDB	OE1, A_GLU.57	NE, A_ARG.81	HE, A_ARG.81	2.43	1.60	25.79
1R21-16.PDB	OD2, A_ASP.86	N, A_LYS.83	H, A_LYS.83	2.35	1.45	17.98
1R21-16.PDB	O, A_PHE.95	N, A_ILE.88	H, A_ILE.88	2.63	1.69	13.56
1R21-16.PDB	O, A_GLN.70	N, A_THR.89	H, A_THR.89	2.63	1.67	7.81
1R21-16.PDB	O, A_ARG.93	N, A_ILE.90	H, A_ILE.90	2.81	1.86	12.00
1R21-16.PDB	O, A_ILE.88	N, A_PHE.95	H, A_PHE.95	2.55	1.60	9.47
1R21-16.PDB	O, A_VAL.8	N, A_ARG.96	H, A_ARG.96	2.56	1.67	20.20
1R21-16.PDB	ND1, A_HIS.84	N, A_ASN.99	H, A_ASN.99	2.73	1.80	13.70
1R21-17.PDB	ND2, A_ASN.99	NE, A_ARG.5	HE, A_ARG.5	2.79	1.84	10.87
1R21-17.PDB	O, A_MET.1	NH2, A_ARG.6	HH21, A_ARG.6	2.74	1.87	24.11
1R21-17.PDB	O, A_LYS.11	N, A_GLY.14	H, A_GLY.14	2.90	2.08	27.87
1R21-17.PDB	O, A_ILE.51	N, A_CYS.27	H, A_CYS.27	2.92	1.99	13.70
1R21-17.PDB	O, A_CYS.49	N, A_PHE.29	H, A_PHE.29	2.53	1.61	15.83
1R21-17.PDB	O, A_LEU.28	N, A_ILE.37	H, A_ILE.37	2.62	1.67	11.05
1R21-17.PDB	O, A_LEU.41	N, A_VAL.44	H, A_VAL.44	2.81	1.91	19.33
1R21-17.PDB	N, A_LYS.50	SG, A_CYS.49	HG, A_CYS.49	2.88	2.09	29.10
1R21-17.PDB	O, A_CYS.27	N, A_ILE.51	H, A_ILE.51	2.65	1.79	22.63
1R21-17.PDB	O, A_ILE.59	N, A_GLU.52	H, A_GLU.52	2.52	1.59	14.29
1R21-17.PDB	O, A_GLU.57	N, A_HIS.54	H, A_HIS.54	2.65	1.75	18.68
1R21-17.PDB	OH, A_TYR.97	N, A_ALA.58	H, A_ALA.58	2.72	1.89	26.01
1R21-17.PDB	O, A_GLU.52	N, A_ILE.59	H, A_ILE.59	2.54	1.61	14.09
1R21-17.PDB	ND2, A_ASN.62	N, A_THR.69	H, A_THR.69	2.79	1.83	10.71
1R21-17.PDB	O, A_THR.89	N, A_GLN.70	H, A_GLN.70	2.59	1.75	25.37
1R21-17.PDB	O, A_SER.74	N, A_VAL.71	H, A_VAL.71	2.94	1.96	5.72
1R21-17.PDB	O, A_VAL.71	N, A_SER.74	H, A_SER.74	2.46	1.58	20.03
1R21-17.PDB	OD2, A_ASP.86	N, A_LYS.83	H, A_LYS.83	2.55	1.59	9.81
1R21-17.PDB	O, A_LYS.83	N, A_ASP.86	H, A_ASP.86	2.89	2.09	28.87
1R21-17.PDB	O, A_GLN.70	N, A_THR.89	H, A_THR.89	2.44	1.48	5.59
1R21-17.PDB	OG, A_SER.94	OG1, A_THR.89	HG1, A_THR.89	2.85	1.94	16.35
1R21-17.PDB	O, A_ARG.93	N, A_ILE.90	H, A_ILE.90	2.85	1.87	5.40
1R21-17.PDB	O, A_ILE.88	N, A_PHE.95	H, A_PHE.95	2.73	1.78	13.00

1R21-17.PDB	O, A_VAL.8	N, A_ARG.96	H, A_ARG.96	2.69	1.78	16.86
1R21-17.PDB	ND1, A_HIS.84	N, A_ASN.99	H, A_ASN.99	2.76	1.87	19.62
1R21-18.PDB	O, A_ARG.96	N, A_VAL.8	H, A_VAL.8	2.73	1.79	13.70
1R21-18.PDB	O, A_LEU.7	N, A_PHE.20	H, A_PHE.20	2.72	1.86	23.59
1R21-18.PDB	O, A_ILE.51	N, A_CYS.27	H, A_CYS.27	2.72	1.82	18.54
1R21-18.PDB	O, A_CYS.49	N, A_PHE.29	H, A_PHE.29	2.70	1.85	23.94
1R21-18.PDB	O, A_LEU.28	N, A_ILE.37	H, A_ILE.37	2.69	1.74	12.20
1R21-18.PDB	O, A_LEU.41	N, A_VAL.44	H, A_VAL.44	2.84	2.03	28.77
1R21-18.PDB	O, A_CYS.27	N, A_ILE.51	H, A_ILE.51	2.61	1.76	24.32
1R21-18.PDB	O, A_ILE.59	N, A_GLU.52	H, A_GLU.52	2.43	1.48	11.54
1R21-18.PDB	O, A_GLU.57	N, A_HIS.54	H, A_HIS.54	2.49	1.54	10.72
1R21-18.PDB	O, A_GLU.52	N, A_ILE.59	H, A_ILE.59	2.56	1.66	18.64
1R21-18.PDB	OD1, A_ASN.67	OG1, A_THR.66	HG1, A_THR.66	2.60	1.66	10.07
1R21-18.PDB	ND2, A_ASN.62	N, A_THR.69	H, A_THR.69	2.83	1.90	12.87
1R21-18.PDB	O, A_THR.89	N, A_GLN.70	H, A_GLN.70	2.37	1.53	24.51
1R21-18.PDB	O, A_SER.74	N, A_VAL.71	H, A_VAL.71	2.79	1.82	9.69
1R21-18.PDB	O, A_VAL.71	N, A_SER.74	H, A_SER.74	2.46	1.62	24.85
1R21-18.PDB	OE2, A_GLU.100	NE2, A_HIS.84	HE2, A_HIS.84	2.44	1.60	25.14
1R21-18.PDB	O, A_PHE.95	N, A_ILE.88	H, A_ILE.88	2.60	1.64	8.44
1R21-18.PDB	O, A_GLN.70	N, A_THR.89	H, A_THR.89	2.43	1.45	2.51
1R21-18.PDB	O, A_ARG.93	N, A_ILE.90	H, A_ILE.90	2.78	1.81	6.62
1R21-18.PDB	O, A_ILE.88	N, A_PHE.95	H, A_PHE.95	2.57	1.60	5.68
1R21-18.PDB	O, A_VAL.8	N, A_ARG.96	H, A_ARG.96	2.51	1.63	20.84
1R21-18.PDB	ND1, A_HIS.84	N, A_ASN.99	H, A_ASN.99	2.90	1.93	9.14
1R21-19.PDB	O, A_ARG.96	N, A_VAL.8	H, A_VAL.8	2.99	2.07	17.19
1R21-19.PDB	O, A_LEU.7	N, A_PHE.20	H, A_PHE.20	2.60	1.69	17.39
1R21-19.PDB	O, A_ILE.51	N, A_CYS.27	H, A_CYS.27	2.92	1.99	15.89
1R21-19.PDB	O, A_CYS.49	N, A_PHE.29	H, A_PHE.29	2.60	1.72	21.65
1R21-19.PDB	O, A_LEU.28	N, A_ILE.37	H, A_ILE.37	2.59	1.64	12.32
1R21-19.PDB	OE2, A_GLU.34	NE2, A_GLN.47	HE21, A_GLN.47	2.80	1.93	22.82
1R21-19.PDB	O, A_CYS.27	N, A_ILE.51	H, A_ILE.51	2.77	1.98	29.09
1R21-19.PDB	O, A_ILE.59	N, A_GLU.52	H, A_GLU.52	2.43	1.48	11.27
1R21-19.PDB	O, A_GLU.57	N, A_HIS.54	H, A_HIS.54	2.56	1.64	15.53
1R21-19.PDB	OH, A_TYR.97	N, A_ALA.58	H, A_ALA.58	2.88	2.06	27.15
1R21-19.PDB	O, A_GLU.52	N, A_ILE.59	H, A_ILE.59	2.44	1.53	17.22
1R21-19.PDB	OG1, A_THR.69	ND2, A_ASN.62	HD21, A_ASN.62	2.83	2.03	29.57
1R21-19.PDB	ND2, A_ASN.62	N, A_THR.69	H, A_THR.69	2.67	1.78	19.68
1R21-19.PDB	O, A_THR.89	N, A_GLN.70	H, A_GLN.70	2.64	1.78	22.36
1R21-19.PDB	O, A_SER.74	N, A_VAL.71	H, A_VAL.71	2.64	1.69	11.33
1R21-19.PDB	O, A_VAL.71	N, A_SER.74	H, A_SER.74	2.48	1.59	19.12
1R21-19.PDB	O, A_THR.69	N, A_ILE.76	H, A_ILE.76	2.76	1.93	26.34
1R21-19.PDB	O, A_LYS.83	N, A_ASP.86	H, A_ASP.86	2.90	2.02	21.05
1R21-19.PDB	O, A_PHE.95	N, A_ILE.88	H, A_ILE.88	2.84	1.95	19.79
1R21-19.PDB	O, A_GLN.70	N, A_THR.89	H, A_THR.89	2.66	1.69	6.71
1R21-19.PDB	O, A_ARG.93	N, A_ILE.90	H, A_ILE.90	2.72	1.76	8.86
1R21-19.PDB	O, A_ILE.88	N, A_PHE.95	H, A_PHE.95	2.54	1.63	17.83
1R21-19.PDB	O, A_VAL.8	N, A_ARG.96	H, A_ARG.96	2.59	1.69	17.99
1R21-19.PDB	ND1, A_HIS.84	N, A_ASN.99	H, A_ASN.99	2.84	1.89	10.70
1R21-2.PDB	N, A_ARG.5	OG1, A_THR.4	HG1, A_THR.4	2.74	1.85	17.56
1R21-2.PDB	O, A_PHE.20	N, A_LEU.7	H, A_LEU.7	2.95	1.98	8.03
1R21-2.PDB	O, A_LEU.7	N, A_PHE.20	H, A_PHE.20	2.59	1.74	24.59
1R21-2.PDB	O, A_CYS.49	N, A_PHE.29	H, A_PHE.29	2.72	1.83	19.71
1R21-2.PDB	O, A_LEU.28	N, A_ILE.37	H, A_ILE.37	2.57	1.60	6.95
1R21-2.PDB	OE2, A_GLU.34	NE2, A_GLN.47	HE21, A_GLN.47	2.62	1.65	7.42
1R21-2.PDB	O, A_CYS.27	N, A_ILE.51	H, A_ILE.51	2.67	1.82	25.05
1R21-2.PDB	O, A_ILE.59	N, A_GLU.52	H, A_GLU.52	2.42	1.55	22.16
1R21-2.PDB	O, A_GLU.57	N, A_HIS.54	H, A_HIS.54	2.50	1.69	27.80
1R21-2.PDB	O, A_GLU.52	N, A_ILE.59	H, A_ILE.59	2.46	1.49	3.05

1R21-2.PDB	OG1, A_THR_69	ND2, A_ASN_62	HD21, A_ASN_62	2.81	1.92	20.56
1R21-2.PDB	OG, A_SER_64	ND2, A_ASN_62	HD22, A_ASN_62	2.42	1.53	18.22
1R21-2.PDB	ND2, A_ASN_62	N, A_THR_69	H, A_THR_69	2.76	1.81	12.74
1R21-2.PDB	O, A_THR_89	N, A_GLN_70	H, A_GLN_70	2.51	1.65	23.32
1R21-2.PDB	O, A_VAL_87	N, A_ASN_72	H, A_ASN_72	2.97	2.02	10.02
1R21-2.PDB	O, A_VAL_71	N, A_SER_74	H, A_SER_74	2.58	1.65	14.58
1R21-2.PDB	OD2, A_ASP_86	N, A_LYS_83	H, A_LYS_83	2.34	1.53	27.15
1R21-2.PDB	O, A_TYR_97	N, A_GLY_85	H, A_GLY_85	2.88	2.06	27.73
1R21-2.PDB	O, A_PHE_95	N, A_ILE_88	H, A_ILE_88	2.71	1.73	6.39
1R21-2.PDB	O, A_GLN_70	N, A_THR_89	H, A_THR_89	2.55	1.58	6.68
1R21-2.PDB	OG, A_SER_94	OG1, A_THR_89	HG1, A_THR_89	2.98	2.02	6.58
1R21-2.PDB	O, A_ARG_93	N, A_ILE_90	H, A_ILE_90	2.82	1.89	14.80
1R21-2.PDB	O, A_ILE_88	N, A_PHE_95	H, A_PHE_95	2.61	1.65	9.22
1R21-2.PDB	O, A_VAL_8	N, A_ARG_96	H, A_ARG_96	2.61	1.75	22.96
1R21-2.PDB	OD2, A_ASP_16	NH1, A_ARG_96	HH12, A_ARG_96	2.71	1.87	26.03
1R21-2.PDB	ND1, A_HIS_84	N, A_ASN_99	H, A_ASN_99	2.71	1.73	1.63
1R21-20.PDB	O, A_PHE_20	N, A_LEU_7	H, A_LEU_7	2.89	1.97	16.40
1R21-20.PDB	O, A_LEU_7	N, A_PHE_20	H, A_PHE_20	2.54	1.59	11.23
1R21-20.PDB	O, A_ILE_51	N, A_CYS_27	H, A_CYS_27	2.71	1.75	9.33
1R21-20.PDB	O, A_CYS_49	N, A_PHE_29	H, A_PHE_29	2.67	1.77	18.32
1R21-20.PDB	O, A_LEU_28	N, A_ILE_37	H, A_ILE_37	2.61	1.64	6.85
1R21-20.PDB	N, A_LYS_46	OG, A_SER_45	HG, A_SER_45	2.70	1.79	15.25
1R21-20.PDB	O, A_CYS_27	N, A_ILE_51	H, A_ILE_51	2.42	1.58	23.81
1R21-20.PDB	O, A_ILE_59	N, A_GLU_52	H, A_GLU_52	2.32	1.45	21.34
1R21-20.PDB	O, A_GLU_57	N, A_HIS_54	H, A_HIS_54	2.45	1.51	12.30
1R21-20.PDB	O, A_GLU_52	N, A_ILE_59	H, A_ILE_59	2.48	1.51	4.91
1R21-20.PDB	O, A_VAL_80	N, A_LEU_60	H, A_LEU_60	2.94	1.97	6.46
1R21-20.PDB	O, A_LYS_50	N, A_HIS_61	H, A_HIS_61	2.71	1.83	20.97
1R21-20.PDB	ND2, A_ASN_62	N, A_THR_69	H, A_THR_69	2.81	1.85	8.55
1R21-20.PDB	O, A_THR_89	N, A_GLN_70	H, A_GLN_70	2.55	1.71	24.95
1R21-20.PDB	O, A_VAL_87	N, A_ASN_72	H, A_ASN_72	2.84	1.89	10.53
1R21-20.PDB	O, A_VAL_71	N, A_SER_74	H, A_SER_74	2.53	1.62	17.33
1R21-20.PDB	O, A_VAL_71	OG, A_SER_74	HG, A_SER_74	2.49	1.70	27.88
1R21-20.PDB	O, A_PHE_95	N, A_ILE_88	H, A_ILE_88	2.46	1.49	5.80
1R21-20.PDB	O, A_GLN_70	N, A_THR_89	H, A_THR_89	2.46	1.50	7.24
1R21-20.PDB	O, A_ARG_93	N, A_ILE_90	H, A_ILE_90	2.66	1.69	6.47
1R21-20.PDB	O, A_ILE_88	N, A_PHE_95	H, A_PHE_95	2.54	1.58	8.65
1R21-20.PDB	O, A_VAL_8	N, A_ARG_96	H, A_ARG_96	2.64	1.79	24.11
1R21-20.PDB	ND1, A_HIS_84	N, A_ASN_99	H, A_ASN_99	2.96	2.01	12.19
1R21-21.PDB	O, A_PHE_20	N, A_LEU_7	H, A_LEU_7	2.96	2.07	20.84
1R21-21.PDB	O, A_ARG_96	N, A_VAL_8	H, A_VAL_8	2.59	1.62	4.25
1R21-21.PDB	O, A_LEU_7	N, A_PHE_20	H, A_PHE_20	2.61	1.64	5.69
1R21-21.PDB	O, A_ILE_51	N, A_CYS_27	H, A_CYS_27	2.91	1.95	10.90
1R21-21.PDB	O, A_CYS_49	N, A_PHE_29	H, A_PHE_29	2.68	1.81	22.17
1R21-21.PDB	O, A_LEU_28	N, A_ILE_37	H, A_ILE_37	2.56	1.62	13.05
1R21-21.PDB	O, A_LEU_41	N, A_VAL_44	H, A_VAL_44	2.91	2.06	24.25
1R21-21.PDB	O, A_CYS_27	N, A_ILE_51	H, A_ILE_51	2.73	1.89	24.96
1R21-21.PDB	O, A_ILE_59	N, A_GLU_52	H, A_GLU_52	2.35	1.50	22.81
1R21-21.PDB	O, A_GLU_57	N, A_HIS_54	H, A_HIS_54	2.92	1.97	10.24
1R21-21.PDB	O, A_GLU_52	N, A_ILE_59	H, A_ILE_59	2.54	1.70	24.70
1R21-21.PDB	ND2, A_ASN_62	N, A_THR_69	H, A_THR_69	2.75	1.85	18.29
1R21-21.PDB	O, A_THR_89	N, A_GLN_70	H, A_GLN_70	2.65	1.74	16.82
1R21-21.PDB	O, A_SER_74	N, A_VAL_71	H, A_VAL_71	2.64	1.68	10.54
1R21-21.PDB	O, A_VAL_87	N, A_ASN_72	H, A_ASN_72	2.70	1.73	7.44
1R21-21.PDB	O, A_VAL_71	N, A_SER_74	H, A_SER_74	2.70	1.91	29.55
1R21-21.PDB	OD2, A_ASP_86	N, A_LYS_83	H, A_LYS_83	2.35	1.45	17.97
1R21-21.PDB	OD1, A_ASN_72	N, A_VAL_87	H, A_VAL_87	2.99	2.03	10.40
1R21-21.PDB	O, A_PHE_95	N, A_ILE_88	H, A_ILE_88	2.42	1.51	16.26

1R21-21.PDB	O, A_GLN_70	N, A_THR_89	H, A_THR_89	2.52	1.56	6.68
1R21-21.PDB	O, A_ARG_93	N, A_ILE_90	H, A_ILE_90	2.78	1.92	23.35
1R21-21.PDB	O, A_ILE_88	N, A_PHE_95	H, A_PHE_95	2.32	1.44	19.20
1R21-21.PDB	O, A_VAL_8	N, A_ARG_96	H, A_ARG_96	2.40	1.50	17.53
1R21-21.PDB	ND1, A_HIS_84	N, A_ASN_99	H, A_ASN_99	2.69	1.78	18.43
1R21-22.PDB	O, A_LYS_11	N, A_GLY_14	H, A_GLY_14	2.92	1.99	15.41
1R21-22.PDB	OD1, A_ASP_16	N, A_GLY_17	H, A_GLY_17	2.32	1.45	19.59
1R21-22.PDB	O, A_LEU_7	N, A_PHE_20	H, A_PHE_20	2.61	1.65	9.53
1R21-22.PDB	O, A_ILE_51	N, A_CYS_27	H, A_CYS_27	2.87	1.96	17.01
1R21-22.PDB	O, A_CYS_49	N, A_PHE_29	H, A_PHE_29	2.60	1.70	18.19
1R21-22.PDB	O, A_VAL_44	NH1, A_ARG_31	HH11, A_ARG_31	2.32	1.43	20.44
1R21-22.PDB	O, A_LEU_28	N, A_ILE_37	H, A_ILE_37	2.50	1.57	14.67
1R21-22.PDB	O, A_GLY_30	N, A_ILE_39	H, A_ILE_39	2.87	1.93	13.15
1R21-22.PDB	O, A_CYS_27	N, A_ILE_51	H, A_ILE_51	2.68	1.88	28.33
1R21-22.PDB	O, A_ILE_59	N, A_GLU_52	H, A_GLU_52	2.35	1.46	18.95
1R21-22.PDB	O, A_SER_25	N, A_ILE_53	H, A_ILE_53	2.75	1.92	25.97
1R21-22.PDB	O, A_GLU_57	N, A_HIS_54	H, A_HIS_54	2.43	1.49	13.42
1R21-22.PDB	O, A_GLU_52	N, A_ILE_59	H, A_ILE_59	2.51	1.56	11.28
1R21-22.PDB	OG, A_SER_64	ND2, A_ASN_62	HD22, A_ASN_62	2.37	1.45	16.21
1R21-22.PDB	ND2, A_ASN_62	N, A_THR_69	H, A_THR_69	2.75	1.81	13.92
1R21-22.PDB	O, A_THR_89	N, A_GLN_70	H, A_GLN_70	2.39	1.49	18.52
1R21-22.PDB	O, A_SER_74	N, A_VAL_71	H, A_VAL_71	2.73	1.76	7.13
1R21-22.PDB	O, A_VAL_71	N, A_SER_74	H, A_SER_74	2.40	1.54	22.50
1R21-22.PDB	OD2, A_ASP_86	N, A_LYS_83	H, A_LYS_83	2.34	1.47	21.74
1R21-22.PDB	O, A_TYR_97	N, A_GLY_85	H, A_GLY_85	2.95	2.10	24.40
1R21-22.PDB	O, A_PHE_95	N, A_ILE_88	H, A_ILE_88	2.63	1.67	6.98
1R21-22.PDB	O, A_GLN_70	N, A_THR_89	H, A_THR_89	2.41	1.52	18.90
1R21-22.PDB	O, A_ARG_93	N, A_ILE_90	H, A_ILE_90	2.74	1.77	6.10
1R21-22.PDB	O, A_ILE_88	N, A_PHE_95	H, A_PHE_95	2.64	1.72	15.76
1R21-22.PDB	O, A_VAL_8	N, A_ARG_96	H, A_ARG_96	2.37	1.47	18.14
1R21-22.PDB	O, A_ASP_86	N, A_TYR_97	H, A_TYR_97	2.99	2.03	9.81
1R21-22.PDB	ND1, A_HIS_84	N, A_ASN_99	H, A_ASN_99	2.84	1.90	14.56
1R21-23.PDB	O, A_ARG_96	N, A_VAL_8	H, A_VAL_8	2.86	1.92	13.31
1R21-23.PDB	O, A_CYS_49	N, A_PHE_29	H, A_PHE_29	2.64	1.75	19.18
1R21-23.PDB	O, A_LEU_28	N, A_ILE_37	H, A_ILE_37	2.58	1.62	9.88
1R21-23.PDB	O, A_CYS_27	N, A_ILE_51	H, A_ILE_51	2.71	1.91	29.18
1R21-23.PDB	O, A_SER_25	N, A_ILE_53	H, A_ILE_53	2.69	1.85	24.46
1R21-23.PDB	O, A_GLU_57	N, A_HIS_54	H, A_HIS_54	2.99	2.01	4.94
1R21-23.PDB	ND1, A_HIS_54	N, A_GLU_57	H, A_GLU_57	2.90	2.03	23.13
1R21-23.PDB	O, A_GLU_52	N, A_ILE_59	H, A_ILE_59	2.62	1.77	23.57
1R21-23.PDB	ND2, A_ASN_62	N, A_THR_69	H, A_THR_69	2.86	1.89	7.90
1R21-23.PDB	O, A_VAL_71	N, A_SER_74	H, A_SER_74	2.40	1.48	15.27
1R21-23.PDB	OE1, A_GLU_57	NE, A_ARG_81	HE, A_ARG_81	2.65	1.70	11.54
1R21-23.PDB	OD2, A_ASP_86	N, A_LYS_83	H, A_LYS_83	2.56	1.66	17.59
1R21-23.PDB	O, A_PHE_95	N, A_ILE_88	H, A_ILE_88	2.67	1.71	9.77
1R21-23.PDB	O, A_GLN_70	N, A_THR_89	H, A_THR_89	2.44	1.47	4.21
1R21-23.PDB	O, A_ARG_93	N, A_ILE_90	H, A_ILE_90	2.77	1.83	11.81
1R21-23.PDB	O, A_ILE_88	N, A_PHE_95	H, A_PHE_95	2.62	1.66	9.26
1R21-23.PDB	O, A_VAL_8	N, A_ARG_96	H, A_ARG_96	2.53	1.67	22.54
1R21-23.PDB	ND1, A_HIS_84	N, A_ASN_99	H, A_ASN_99	2.78	1.83	12.42
1R21-3.PDB	O, A_PRO_18	N, A_THR_9	H, A_THR_9	2.75	1.82	15.55
1R21-3.PDB	OD1, A_ASP_16	NE2, A_HIS_19	HE2, A_HIS_19	2.71	1.85	23.51
1R21-3.PDB	O, A_LEU_7	N, A_PHE_20	H, A_PHE_20	2.81	2.01	29.61
1R21-3.PDB	O, A_ILE_51	N, A_CYS_27	H, A_CYS_27	2.79	1.88	18.32
1R21-3.PDB	O, A_CYS_49	N, A_PHE_29	H, A_PHE_29	2.76	1.82	13.22
1R21-3.PDB	O, A_LEU_28	N, A_ILE_37	H, A_ILE_37	2.65	1.72	14.66
1R21-3.PDB	O, A_GLY_30	N, A_ILE_39	H, A_ILE_39	2.90	1.94	10.95
1R21-3.PDB	OE2, A_GLU_34	NE2, A_GLN_47	HE22, A_GLN_47	2.72	1.92	29.24

1R21-3.PDB	O, A_ILE_59	N, A_GLU_52	H, A_GLU_52	2.41	1.46	10.14
1R21-3.PDB	O, A_SER_25	N, A_ILE_53	H, A_ILE_53	2.44	1.55	19.50
1R21-3.PDB	O, A_GLU_57	N, A_HIS_54	H, A_HIS_54	2.46	1.55	16.84
1R21-3.PDB	O, A_GLU_52	N, A_ILE_59	H, A_ILE_59	2.65	1.70	10.74
1R21-3.PDB	O, A_LYS_50	N, A_HIS_61	H, A_HIS_61	2.72	1.91	28.48
1R21-3.PDB	OG1, A_THR_69	ND2, A_ASN_62	HD21, A_ASN_62	2.87	2.01	23.40
1R21-3.PDB	O, A_HIS_48	N, A_PHE_63	H, A_PHE_63	2.66	1.74	15.84
1R21-3.PDB	ND2, A_ASN_62	N, A_THR_69	H, A_THR_69	2.80	1.85	9.14
1R21-3.PDB	O, A_SER_74	N, A_VAL_71	H, A_VAL_71	2.76	1.79	6.23
1R21-3.PDB	O, A_VAL_87	N, A_ASN_72	H, A_ASN_72	2.81	1.87	12.50
1R21-3.PDB	O, A_VAL_71	N, A_SER_74	H, A_SER_74	2.52	1.65	22.26
1R21-3.PDB	O, A_PHE_95	N, A_ILE_88	H, A_ILE_88	2.38	1.42	9.04
1R21-3.PDB	O, A_GLN_70	N, A_THR_89	H, A_THR_89	2.58	1.62	7.30
1R21-3.PDB	O, A_ARG_93	N, A_ILE_90	H, A_ILE_90	2.88	1.98	18.52
1R21-3.PDB	O, A_ILE_88	N, A_PHE_95	H, A_PHE_95	2.49	1.52	2.60
1R21-3.PDB	O, A_VAL_8	N, A_ARG_96	H, A_ARG_96	2.86	1.93	15.31
1R21-3.PDB	ND1, A_HIS_84	N, A_ASN_99	H, A_ASN_99	2.73	1.81	16.46
1R21-4.PDB	O, A_GLN_56	NH2, A_ARG_5	HH21, A_ARG_5	2.90	2.09	29.83
1R21-4.PDB	O, A_LEU_7	N, A_PHE_20	H, A_PHE_20	2.67	1.82	24.01
1R21-4.PDB	O, A_ILE_51	N, A_CYS_27	H, A_CYS_27	2.66	1.75	17.27
1R21-4.PDB	O, A_CYS_49	N, A_PHE_29	H, A_PHE_29	2.65	1.73	16.15
1R21-4.PDB	O, A_LEU_28	N, A_ILE_37	H, A_ILE_37	2.58	1.63	11.12
1R21-4.PDB	O, A_GLY_30	N, A_ILE_39	H, A_ILE_39	2.96	2.02	14.09
1R21-4.PDB	O, A_LEU_41	N, A_VAL_44	H, A_VAL_44	2.78	1.93	24.60
1R21-4.PDB	O, A_CYS_27	N, A_ILE_51	H, A_ILE_51	2.64	1.83	27.83
1R21-4.PDB	O, A_ILE_59	N, A_GLU_52	H, A_GLU_52	2.49	1.57	16.14
1R21-4.PDB	O, A_SER_25	N, A_ILE_53	H, A_ILE_53	2.85	2.00	24.05
1R21-4.PDB	N, A_GLU_55	ND1, A_HIS_54	HD1, A_HIS_54	2.58	1.78	28.52
1R21-4.PDB	O, A_GLU_52	N, A_ILE_59	H, A_ILE_59	2.59	1.66	14.45
1R21-4.PDB	OD1, A_ASN_67	OG1, A_THR_66	HG1, A_THR_66	2.40	1.45	5.76
1R21-4.PDB	ND2, A_ASN_62	N, A_THR_69	H, A_THR_69	2.80	1.85	11.39
1R21-4.PDB	O, A_THR_89	N, A_GLN_70	H, A_GLN_70	2.55	1.67	20.25
1R21-4.PDB	O, A_SER_74	N, A_VAL_71	H, A_VAL_71	2.68	1.77	17.57
1R21-4.PDB	O, A_VAL_71	N, A_SER_74	H, A_SER_74	2.43	1.52	16.62
1R21-4.PDB	OE1, A_GLU_57	NE, A_ARG_81	HE, A_ARG_81	2.76	1.87	19.46
1R21-4.PDB	OE1, A_GLU_57	NH2, A_ARG_81	HH21, A_ARG_81	2.93	2.10	27.48
1R21-4.PDB	OD2, A_ASP_86	N, A_LYS_83	H, A_LYS_83	2.52	1.72	28.30
1R21-4.PDB	O, A_PHE_95	N, A_ILE_88	H, A_ILE_88	2.41	1.51	17.89
1R21-4.PDB	O, A_GLN_70	N, A_THR_89	H, A_THR_89	2.59	1.62	4.11
1R21-4.PDB	O, A_ARG_93	N, A_ILE_90	H, A_ILE_90	2.76	1.91	24.78
1R21-4.PDB	O, A_ILE_88	N, A_PHE_95	H, A_PHE_95	2.36	1.44	14.85
1R21-4.PDB	ND1, A_HIS_84	N, A_ASN_99	H, A_ASN_99	2.80	1.85	12.02
1R21-5.PDB	O, A_VAL_15	N, A_LYS_11	H, A_LYS_11	2.78	1.94	24.72
1R21-5.PDB	O, A_LYS_11	N, A_GLY_14	H, A_GLY_14	2.58	1.71	22.29
1R21-5.PDB	O, A_LEU_7	N, A_PHE_20	H, A_PHE_20	2.74	1.95	29.42
1R21-5.PDB	O, A_ILE_51	N, A_CYS_27	H, A_CYS_27	2.96	2.03	16.24
1R21-5.PDB	O, A_CYS_49	N, A_PHE_29	H, A_PHE_29	2.56	1.68	20.60
1R21-5.PDB	O, A_GLY_32	N, A_CYS_35	H, A_CYS_35	3.00	2.10	20.00
1R21-5.PDB	O, A_LEU_28	N, A_ILE_37	H, A_ILE_37	2.63	1.66	7.71
1R21-5.PDB	O, A_CYS_27	N, A_ILE_51	H, A_ILE_51	2.67	1.84	25.60
1R21-5.PDB	O, A_ILE_59	N, A_GLU_52	H, A_GLU_52	2.45	1.51	13.28
1R21-5.PDB	O, A_SER_25	N, A_ILE_53	H, A_ILE_53	2.88	2.00	20.92
1R21-5.PDB	O, A_GLU_57	N, A_HIS_54	H, A_HIS_54	2.45	1.55	17.67
1R21-5.PDB	O, A_GLU_52	N, A_ILE_59	H, A_ILE_59	2.73	1.80	15.41
1R21-5.PDB	OG1, A_THR_69	ND2, A_ASN_62	HD22, A_ASN_62	2.62	1.75	21.48
1R21-5.PDB	O, A_THR_89	N, A_GLN_70	H, A_GLN_70	2.61	1.83	29.99
1R21-5.PDB	O, A_VAL_87	N, A_ASN_72	H, A_ASN_72	2.99	2.02	8.39
1R21-5.PDB	O, A_VAL_71	N, A_SER_74	H, A_SER_74	2.41	1.47	13.31

1R21-5.PDB	OD2, A_ASP_86	N, A_LYS_83	H, A_LYS_83	2.31	1.52	27.57
1R21-5.PDB	O, A_PHE_95	N, A_ILE_88	H, A_ILE_88	2.66	1.72	14.09
1R21-5.PDB	O, A_GLN_70	N, A_THR_89	H, A_THR_89	2.73	1.76	5.33
1R21-5.PDB	O, A_ARG_93	N, A_ILE_90	H, A_ILE_90	2.64	1.71	14.23
1R21-5.PDB	O, A_ILE_88	N, A_PHE_95	H, A_PHE_95	2.55	1.58	4.54
1R21-5.PDB	O, A_VAL_8	N, A_ARG_96	H, A_ARG_96	2.68	1.85	26.28
1R21-5.PDB	ND1, A_HIS_84	N, A_ASN_99	H, A_ASN_99	2.79	1.81	1.91
1R21-6.PDB	O, A_LEU_7	N, A_PHE_20	H, A_PHE_20	2.66	1.77	20.35
1R21-6.PDB	O, A_CYS_49	N, A_PHE_29	H, A_PHE_29	2.75	1.83	16.30
1R21-6.PDB	O, A_LEU_28	N, A_ILE_37	H, A_ILE_37	2.59	1.63	9.82
1R21-6.PDB	O, A_GLY_30	N, A_ILE_39	H, A_ILE_39	2.91	2.07	25.97
1R21-6.PDB	O, A_LEU_41	N, A_VAL_44	H, A_VAL_44	2.95	2.04	17.93
1R21-6.PDB	N, A_LYS_50	SG, A_CYS_49	HG, A_CYS_49	2.71	1.89	25.56
1R21-6.PDB	O, A_CYS_27	N, A_ILE_51	H, A_ILE_51	2.75	1.91	25.39
1R21-6.PDB	O, A_ILE_59	N, A_GLU_52	H, A_GLU_52	2.40	1.53	21.67
1R21-6.PDB	O, A_GLU_57	N, A_HIS_54	H, A_HIS_54	2.79	1.89	19.06
1R21-6.PDB	O, A_GLU_52	N, A_ILE_59	H, A_ILE_59	2.58	1.61	5.50
1R21-6.PDB	OG1, A_THR_69	ND2, A_ASN_62	HD21, A_ASN_62	2.81	1.95	22.23
1R21-6.PDB	OD1, A_ASN_67	OG1, A_THR_66	HG1, A_THR_66	2.30	1.42	18.29
1R21-6.PDB	ND2, A_ASN_62	N, A_THR_69	H, A_THR_69	2.77	1.82	9.89
1R21-6.PDB	O, A_THR_89	N, A_GLN_70	H, A_GLN_70	2.74	1.83	16.28
1R21-6.PDB	O, A_SER_74	N, A_VAL_71	H, A_VAL_71	2.71	1.73	5.25
1R21-6.PDB	O, A_VAL_87	N, A_ASN_72	H, A_ASN_72	2.81	1.83	4.97
1R21-6.PDB	O, A_VAL_71	N, A_SER_74	H, A_SER_74	2.47	1.57	18.72
1R21-6.PDB	O, A_TYR_97	N, A_GLY_85	H, A_GLY_85	2.85	1.98	22.19
1R21-6.PDB	O, A_PHE_95	N, A_ILE_88	H, A_ILE_88	2.58	1.60	5.92
1R21-6.PDB	O, A_GLN_70	N, A_THR_89	H, A_THR_89	2.72	1.76	7.04
1R21-6.PDB	O, A_ARG_93	N, A_ILE_90	H, A_ILE_90	2.73	1.78	11.89
1R21-6.PDB	O, A_ILE_88	N, A_PHE_95	H, A_PHE_95	2.50	1.55	9.80
1R21-6.PDB	O, A_VAL_8	N, A_ARG_96	H, A_ARG_96	2.94	2.02	15.77
1R21-6.PDB	ND1, A_HIS_84	N, A_ASN_99	H, A_ASN_99	2.78	1.82	10.56
1R21-6.PDB	O, A_THR_4	N, A_GLU_100	H, A_GLU_100	2.69	1.89	28.90
1R21-7.PDB	O, A_ARG_96	N, A_VAL_8	H, A_VAL_8	2.93	2.00	14.50
1R21-7.PDB	O, A_SER_94	N, A_ILE_10	H, A_ILE_10	2.75	1.83	17.27
1R21-7.PDB	O, A_LEU_7	N, A_PHE_20	H, A_PHE_20	2.62	1.73	19.92
1R21-7.PDB	O, A_ILE_51	N, A_CYS_27	H, A_CYS_27	2.70	1.75	13.12
1R21-7.PDB	O, A_CYS_49	N, A_PHE_29	H, A_PHE_29	2.69	1.79	18.19
1R21-7.PDB	O, A_LEU_28	N, A_ILE_37	H, A_ILE_37	2.66	1.71	12.73
1R21-7.PDB	O, A_GLY_30	N, A_ILE_39	H, A_ILE_39	2.93	2.03	19.31
1R21-7.PDB	O, A_CYS_27	N, A_ILE_51	H, A_ILE_51	2.59	1.76	25.78
1R21-7.PDB	O, A_ILE_59	N, A_GLU_52	H, A_GLU_52	2.42	1.57	22.98
1R21-7.PDB	O, A_SER_25	N, A_ILE_53	H, A_ILE_53	2.58	1.70	20.39
1R21-7.PDB	O, A_GLU_57	N, A_HIS_54	H, A_HIS_54	2.55	1.59	6.66
1R21-7.PDB	O, A_GLU_52	N, A_ILE_59	H, A_ILE_59	2.51	1.62	19.11
1R21-7.PDB	OD1, A_ASN_67	OG1, A_THR_66	HG1, A_THR_66	2.91	2.05	21.54
1R21-7.PDB	ND2, A_ASN_62	N, A_THR_69	H, A_THR_69	2.80	1.87	14.50
1R21-7.PDB	O, A_THR_89	N, A_GLN_70	H, A_GLN_70	2.81	2.02	29.36
1R21-7.PDB	O, A_SER_74	N, A_VAL_71	H, A_VAL_71	2.67	1.70	5.32
1R21-7.PDB	O, A_VAL_71	N, A_SER_74	H, A_SER_74	2.40	1.46	12.46
1R21-7.PDB	O, A_PHE_95	N, A_ILE_88	H, A_ILE_88	2.42	1.50	16.16
1R21-7.PDB	O, A_GLN_70	N, A_THR_89	H, A_THR_89	2.72	1.75	6.96
1R21-7.PDB	O, A_ARG_93	N, A_ILE_90	H, A_ILE_90	2.79	1.96	26.27
1R21-7.PDB	O, A_ILE_88	N, A_PHE_95	H, A_PHE_95	2.39	1.47	15.58
1R21-7.PDB	O, A_VAL_8	N, A_ARG_96	H, A_ARG_96	2.62	1.75	22.19
1R21-7.PDB	O, A_ASP_86	N, A_TYR_97	H, A_TYR_97	2.95	1.97	3.22
1R21-7.PDB	ND1, A_HIS_84	N, A_ASN_99	H, A_ASN_99	2.74	1.77	3.18
1R21-7.PDB	O, A_THR_4	N, A_GLU_100	H, A_GLU_100	2.96	1.98	1.07
1R21-8.PDB	O, A_LEU_7	N, A_PHE_20	H, A_PHE_20	2.64	1.67	5.83

1R21-8.PDB	O, A_ILE.51	N, A_CYS.27	H, A_CYS.27	2.97	2.06	18.29
1R21-8.PDB	O, A_CYS.49	N, A_PHE.29	H, A_PHE.29	2.74	1.82	17.14
1R21-8.PDB	O, A_GLY.32	N, A_CYS.35	H, A_CYS.35	2.97	2.06	17.41
1R21-8.PDB	O, A_LEU.28	N, A_ILE.37	H, A_ILE.37	2.56	1.64	16.71
1R21-8.PDB	O, A_CYS.27	N, A_ILE.51	H, A_ILE.51	2.90	2.08	27.50
1R21-8.PDB	O, A_ILE.59	N, A_GLU.52	H, A_GLU.52	2.39	1.51	20.05
1R21-8.PDB	O, A_SER.25	N, A_ILE.53	H, A_ILE.53	2.86	1.97	19.70
1R21-8.PDB	O, A_GLU.57	N, A_HIS.54	H, A_HIS.54	2.63	1.73	17.57
1R21-8.PDB	O, A_GLU.52	N, A_ILE.59	H, A_ILE.59	2.67	1.74	13.79
1R21-8.PDB	O, A_HIS.48	N, A_PHE.63	H, A_PHE.63	2.95	1.99	8.40
1R21-8.PDB	ND2, A_ASN.62	N, A_THR.69	H, A_THR.69	2.77	1.82	11.69
1R21-8.PDB	O, A_THR.89	N, A_GLN.70	H, A_GLN.70	2.54	1.69	23.06
1R21-8.PDB	O, A_SER.74	N, A_VAL.71	H, A_VAL.71	2.87	1.96	17.78
1R21-8.PDB	O, A_VAL.87	N, A_ASN.72	H, A_ASN.72	2.79	1.84	10.06
1R21-8.PDB	O, A_VAL.71	N, A_SER.74	H, A_SER.74	2.39	1.49	18.17
1R21-8.PDB	OD2, A_ASP.86	N, A_LYS.83	H, A_LYS.83	2.70	1.83	21.74
1R21-8.PDB	O, A_LYS.83	N, A_ASP.86	H, A_ASP.86	2.99	2.13	23.27
1R21-8.PDB	O, A_PHE.95	N, A_ILE.88	H, A_ILE.88	2.50	1.64	22.70
1R21-8.PDB	O, A_GLN.70	N, A_THR.89	H, A_THR.89	2.52	1.55	4.58
1R21-8.PDB	O, A_ARG.93	N, A_ILE.90	H, A_ILE.90	2.80	1.96	25.17
1R21-8.PDB	O, A_ILE.88	N, A_PHE.95	H, A_PHE.95	2.40	1.51	18.62
1R21-8.PDB	O, A_VAL.8	N, A_ARG.96	H, A_ARG.96	2.59	1.64	10.89
1R21-8.PDB	ND1, A_HIS.84	N, A_ASN.99	H, A_ASN.99	2.79	1.82	9.29
1R21-9.PDB	O, A_ARG.96	N, A_VAL.8	H, A_VAL.8	2.95	2.02	15.16
1R21-9.PDB	O, A_VAL.15	N, A_LYS.11	H, A_LYS.11	2.46	1.54	16.41
1R21-9.PDB	O, A_LYS.11	N, A_GLY.14	H, A_GLY.14	2.77	1.83	13.31
1R21-9.PDB	O, A_THR.9	N, A_GLY.17	H, A_GLY.17	2.92	2.09	26.43
1R21-9.PDB	O, A_LEU.7	N, A_PHE.20	H, A_PHE.20	2.73	1.90	26.46
1R21-9.PDB	O, A_ILE.51	N, A_CYS.27	H, A_CYS.27	2.80	1.95	24.06
1R21-9.PDB	O, A_CYS.49	N, A_PHE.29	H, A_PHE.29	2.58	1.68	18.54
1R21-9.PDB	O, A_LEU.28	N, A_ILE.37	H, A_ILE.37	2.61	1.66	11.75
1R21-9.PDB	O, A_GLY.30	N, A_ILE.39	H, A_ILE.39	2.95	2.00	11.86
1R21-9.PDB	O, A_CYS.27	N, A_ILE.51	H, A_ILE.51	2.58	1.76	26.53
1R21-9.PDB	O, A_ILE.59	N, A_GLU.52	H, A_GLU.52	2.41	1.49	15.40
1R21-9.PDB	O, A_GLU.57	N, A_HIS.54	H, A_HIS.54	2.39	1.49	17.88
1R21-9.PDB	O, A_GLU.52	N, A_ILE.59	H, A_ILE.59	2.53	1.64	19.17
1R21-9.PDB	OG1, A_THR.69	ND2, A_ASN.62	HD21, A_ASN.62	2.59	1.65	13.02
1R21-9.PDB	ND2, A_ASN.62	N, A_THR.69	H, A_THR.69	2.80	1.88	16.74
1R21-9.PDB	O, A_THR.89	N, A_GLN.70	H, A_GLN.70	2.54	1.65	19.35
1R21-9.PDB	O, A_SER.74	N, A_VAL.71	H, A_VAL.71	2.88	1.97	18.35
1R21-9.PDB	O, A_VAL.71	N, A_SER.74	H, A_SER.74	2.82	1.99	26.19
1R21-9.PDB	O, A_LYS.83	N, A_ASP.86	H, A_ASP.86	2.95	2.09	23.46
1R21-9.PDB	O, A_PHE.95	N, A_ILE.88	H, A_ILE.88	2.79	1.83	9.96
1R21-9.PDB	O, A_GLN.70	N, A_THR.89	H, A_THR.89	2.38	1.46	15.43
1R21-9.PDB	O, A_ARG.93	N, A_ILE.90	H, A_ILE.90	2.76	1.79	6.89
1R21-9.PDB	O, A_ILE.88	N, A_PHE.95	H, A_PHE.95	2.67	1.69	5.04
1R21-9.PDB	O, A_VAL.8	N, A_ARG.96	H, A_ARG.96	2.57	1.73	25.04
1R21-9.PDB	ND1, A_HIS.84	N, A_ASN.99	H, A_ASN.99	2.74	1.83	17.89

Table 1673: 1R21-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1S4H-8.PDB	OE1, A_GLU_2	N, A_GLU_1	H3, A_GLU_1	3.00	2.12	26.52

Table 1674: 1S4H-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1S4J-1.PDB	O, A_MET_7	N, A_SER_3	H, A_SER_3	2.68	1.88	28.39
1S4J-10.PDB	O, A_MET_7	N, A_SER_3	H, A_SER_3	2.70	1.89	28.31
1S4J-10.PDB	OD2, A_ASP_5	N, A_LEU_11	H, A_LEU_11	2.97	2.11	23.51
1S4J-11.PDB	O, A_MET_7	N, A_SER_3	H, A_SER_3	2.71	1.88	26.65
1S4J-12.PDB	O, A_MET_7	N, A_SER_3	H, A_SER_3	2.58	1.69	19.82
1S4J-14.PDB	O, A_MET_7	N, A_SER_3	H, A_SER_3	2.62	1.79	26.02
1S4J-14.PDB	OD2, A_ASP_5	N, A_LEU_11	H, A_LEU_11	2.83	2.00	26.13
1S4J-15.PDB	O, A_MET_7	N, A_SER_3	H, A_SER_3	2.73	1.91	26.73
1S4J-16.PDB	O, A_MET_7	N, A_SER_3	H, A_SER_3	2.76	1.95	28.49
1S4J-17.PDB	O, A_MET_7	N, A_SER_3	H, A_SER_3	2.73	1.90	26.91
1S4J-18.PDB	O, A_MET_7	N, A_SER_3	H, A_SER_3	2.72	1.86	23.67
1S4J-19.PDB	O, A_MET_7	N, A_SER_3	H, A_SER_3	2.72	1.87	24.36
1S4J-2.PDB	O, A_MET_7	N, A_SER_3	H, A_SER_3	2.72	1.90	26.68
1S4J-20.PDB	O, A_MET_7	N, A_SER_3	H, A_SER_3	2.77	1.95	27.92
1S4J-20.PDB	O, A_GLY_10	N, A_PHE_12	H, A_PHE_12	2.84	1.99	23.23
1S4J-3.PDB	O, A_MET_7	N, A_SER_3	H, A_SER_3	2.75	1.93	27.51
1S4J-5.PDB	O, A_MET_7	N, A_SER_3	H, A_SER_3	2.72	1.90	26.53
1S4J-6.PDB	O, A_MET_7	N, A_SER_3	H, A_SER_3	2.73	1.90	26.66
1S4J-7.PDB	O, A_MET_7	N, A_SER_3	H, A_SER_3	2.73	1.90	26.44
1S4J-8.PDB	O, A_MET_7	N, A_SER_3	H, A_SER_3	2.73	1.90	26.61
1S4J-9.PDB	O, A_MET_7	N, A_SER_3	H, A_SER_3	2.64	1.83	27.37
1S4J-9.PDB	OD2, A_ASP_5	N, A_LEU_11	H, A_LEU_11	2.83	2.00	25.25

Table 1675: 1S4J-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1TOR-5.PDB	O, A_ASN_2	N, A_ASP_5	H, A_ASP_5	2.95	2.03	21.29

Table 1676: 1TOR-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1TOS-2.PDB	O, A_ASN_2	N, A_ASP_5	H, A_ASP_5	2.88	1.98	23.42

Table 1677: 1TOS-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1VFB.PDB	OG, A_SER_26	N, A_VAL_3	H, A_VAL_3	2.94	1.97	6.30
1VFB.PDB	O, A_ARG_24	N, A_THR_5	H, A_THR_5	2.90	1.93	5.77
1VFB.PDB	O, A_THR_22	N, A_SER_7	H, A_SER_7	2.99	2.11	22.15
1VFB.PDB	O, A_LYS_103	N, A_LEU_11	H, A_LEU_11	2.94	2.05	20.26
1VFB.PDB	O, A_GLU_105	N, A_ALA_13	H, A_ALA_13	2.80	1.93	21.73
1VFB.PDB	O, A_LEU_78	N, A_GLY_16	H, A_GLY_16	2.82	1.99	26.99
1VFB.PDB	O, A_LEU_73	N, A_ILE_21	H, A_ILE_21	2.85	1.95	18.65
1VFB.PDB	O, A_SER_7	N, A_THR_22	H, A_THR_22	2.95	1.97	3.77
1VFB.PDB	O, A_TYR_71	N, A_CYS_23	H, A_CYS_23	2.89	1.95	12.19
1VFB.PDB	O, A_THR_5	N, A_ARG_24	H, A_ARG_24	2.86	1.97	19.64
1VFB.PDB	O, A_THR_69	N, A_ALA_25	H, A_ALA_25	2.80	1.83	9.00
1VFB.PDB	OD1, A_ASN_28	N, A_HIS_30	H, A_HIS_30	2.87	2.03	25.94
1VFB.PDB	O, A_GLN_89	N, A_ALA_34	H, A_ALA_34	2.86	1.95	17.31
1VFB.PDB	O, A_VAL_48	N, A_TRP_35	H, A_TRP_35	2.90	1.96	12.47
1VFB.PDB	O, A_TYR_87	N, A_TYR_36	H, A_TYR_36	2.90	1.97	14.82
1VFB.PDB	OE1, A_GLN_89	OH, A_TYR_36	HH, A_TYR_36	2.84	2.00	25.31
1VFB.PDB	O, A_GLN_45	N, A_GLN_37	H, A_GLN_37	2.94	2.00	11.43
1VFB.PDB	O, A_SER_85	N, A_GLN_38	H, A_GLN_38	2.78	1.86	16.10
1VFB.PDB	O, A_LYS_42	NE2, A_GLN_38	HE22, A_GLN_38	2.95	2.03	15.93
1VFB.PDB	O, A_LYS_39	N, A_LYS_42	H, A_LYS_42	2.94	2.06	21.86
1VFB.PDB	O, A_GLN_37	N, A_GLN_45	H, A_GLN_45	2.83	1.94	20.43
1VFB.PDB	O, A_TRP_35	N, A_LEU_47	H, A_LEU_47	2.87	1.94	14.84
1VFB.PDB	O, A_THR_53	N, A_TYR_49	H, A_TYR_49	2.88	1.94	13.56
1VFB.PDB	O, A_TYR_49	N, A_THR_53	H, A_THR_53	2.96	2.04	16.01
1VFB.PDB	O, A_LEU_47	N, A_ALA_55	H, A_ALA_55	2.84	1.93	17.83
1VFB.PDB	OD2, A_ASP_82	NE, A_ARG_61	HE, A_ARG_61	2.88	1.96	15.15
1VFB.PDB	OD1, A_ASP_82	NH2, A_ARG_61	HH21, A_ARG_61	2.85	1.87	9.42
1VFB.PDB	O, A_LYS_74	N, A_SER_63	H, A_SER_63	2.88	1.93	11.55
1VFB.PDB	O, A_SER_72	N, A_SER_65	H, A_SER_65	2.96	2.03	16.59
1VFB.PDB	O, A_CYS_23	N, A_TYR_71	H, A_TYR_71	2.90	2.02	21.95
1VFB.PDB	O, A_GLY_68	OH, A_TYR_71	HH, A_TYR_71	2.83	1.87	7.60
1VFB.PDB	O, A_SER_65	N, A_SER_72	H, A_SER_72	2.93	1.97	9.57
1VFB.PDB	O, A_ILE_21	N, A_LEU_73	H, A_LEU_73	2.93	1.98	10.05
1VFB.PDB	O, A_SER_63	N, A_LYS_74	H, A_LYS_74	2.78	1.85	14.93
1VFB.PDB	O, A_VAL_19	N, A_ILE_75	H, A_ILE_75	3.00	2.05	11.89
1VFB.PDB	O, A_ARG_61	N, A_ASN_76	H, A_ASN_76	2.94	1.97	4.92
1VFB.PDB	O, A_GLU_17	N, A_LEU_78	H, A_LEU_78	2.98	2.01	6.59
1VFB.PDB	OD2, A_ASP_82	N, A_GLN_79	H, A_GLN_79	2.99	2.09	19.33
1VFB.PDB	O, A_GLN_79	N, A_ASP_82	H, A_ASP_82	2.90	1.94	8.94
1VFB.PDB	O, A_GLN_38	N, A_SER_85	H, A_SER_85	2.92	1.96	9.01
1VFB.PDB	O, A_THR_102	N, A_TYR_86	H, A_TYR_86	2.97	2.09	22.04
1VFB.PDB	O, A_ASP_82	OH, A_TYR_86	HH, A_TYR_86	2.70	1.75	6.61
1VFB.PDB	O, A_ALA_34	N, A_GLN_89	H, A_GLN_89	2.89	2.00	22.07
1VFB.PDB	O, A_TYR_32	N, A_PHE_91	H, A_PHE_91	2.82	1.88	13.65
1VFB.PDB	OE1, C_GLN_121	N, A_SER_93	H, A_SER_93	2.89	1.92	8.17
1VFB.PDB	OE1, B_GLU_98	NH1, A_ARG_96	HH12, A_ARG_96	2.82	1.84	8.38
1VFB.PDB	OE2, B_GLU_98	NH2, A_ARG_96	HH22, A_ARG_96	2.81	1.85	10.74
1VFB.PDB	O, A_CYS_88	N, A_GLY_99	H, A_GLY_99	2.78	1.86	15.50
1VFB.PDB	O, A_TYR_86	N, A_THR_102	H, A_THR_102	2.95	2.08	22.50
1VFB.PDB	O, A_PRO_8	OG1, A_THR_102	HG1, A_THR_102	2.77	1.85	14.39
1VFB.PDB	O, A_ALA_9	N, A_LYS_103	H, A_LYS_103	2.90	1.93	7.79
1VFB.PDB	O, A_GLY_84	N, A_LEU_104	H, A_LEU_104	2.88	1.91	5.85
1VFB.PDB	O, A_LEU_11	N, A_GLU_105	H, A_GLU_105	2.89	1.94	12.21
1VFB.PDB	O, B_SER_25	N, B_GLN_3	H, B_GLN_3	2.88	1.92	9.87
1VFB.PDB	O, B_THR_23	N, B_GLN_5	H, B_GLN_5	2.98	2.10	21.16
1VFB.PDB	O, B_THR_21	N, B_SER_7	H, B_SER_7	2.85	2.00	24.61
1VFB.PDB	O, B_PRO_9	N, B_LEU_11	H, B_LEU_11	2.92	2.13	29.55

1VFB.PDB	OE1, B_GLN_16	N, B_ALA_13	H, B_ALA_13	2.78	1.85	14.74
1VFB.PDB	O, B_ALA_13	N, B_GLN_16	H, B_GLN_16	2.90	1.97	15.84
1VFB.PDB	O, B_MET_82	N, B_LEU_18	H, B_LEU_18	2.72	1.87	23.78
1VFB.PDB	O, B_LEU_80	N, B_ILE_20	H, B_ILE_20	2.91	2.00	17.66
1VFB.PDB	O, B_SER_7	N, B_THR_21	H, B_THR_21	2.89	1.93	9.84
1VFB.PDB	O, B_VAL_78	N, B_CYS_22	H, B_CYS_22	2.86	1.89	3.27
1VFB.PDB	O, B_GLN_5	N, B_THR_23	H, B_THR_23	2.86	1.92	12.65
1VFB.PDB	O, B_SER_76	N, B_VAL_24	H, B_VAL_24	2.97	2.00	3.39
1VFB.PDB	O, B_GLN_3	N, B_SER_25	H, B_SER_25	2.93	2.07	23.55
1VFB.PDB	OG, B_SER_28	OG1, B_THR_30	HG1, B_THR_30	2.97	2.08	19.82
1VFB.PDB	O, B_ILE_51	N, B_VAL_34	H, B_VAL_34	2.91	2.01	18.80
1VFB.PDB	O, B_ALA_96	N, B_ASN_35	H, B_ASN_35	2.89	1.92	5.93
1VFB.PDB	OE1, B_GLU_98	ND2, B_ASN_35	HD21, B_ASN_35	2.85	2.00	23.37
1VFB.PDB	O, B_GLY_49	N, B_TRP_36	H, B_TRP_36	2.96	2.02	15.17
1VFB.PDB	O, B_TYR_94	N, B_VAL_37	H, B_VAL_37	2.92	1.95	9.63
1VFB.PDB	O, B_GLU_46	N, B_ARG_38	H, B_ARG_38	2.89	1.95	14.15
1VFB.PDB	OD1, B_ASP_89	NH1, B_ARG_38	HH12, B_ARG_38	3.00	2.07	17.31
1VFB.PDB	O, B_ARG_92	N, B_GLN_39	H, B_GLN_39	2.82	1.90	16.49
1VFB.PDB	OE1, A_GLN_38	NE2, B_GLN_39	HE21, B_GLN_39	2.95	1.98	8.04
1VFB.PDB	O, B_LYS_43	NE2, B_GLN_39	HE22, B_GLN_39	2.95	2.05	19.96
1VFB.PDB	O, B_PRO_40	N, B_LYS_43	H, B_LYS_43	2.85	1.98	21.72
1VFB.PDB	O, B_ARG_38	N, B_GLU_46	H, B_GLU_46	2.84	1.96	21.55
1VFB.PDB	OD1, B_ASN_35	NE1, B_TRP_47	HE1, B_TRP_47	2.80	1.83	5.78
1VFB.PDB	O, B_TRP_36	N, B_LEU_48	H, B_LEU_48	2.92	1.98	13.84
1VFB.PDB	O, B_ASP_58	N, B_MET_50	H, B_MET_50	2.89	1.97	17.18
1VFB.PDB	O, B_ASN_56	N, B_TRP_52	H, B_TRP_52	2.90	1.95	9.28
1VFB.PDB	O, B_TRP_52	N, B_GLY_55	H, B_GLY_55	2.85	1.92	14.57
1VFB.PDB	O, B_LEU_48	N, B_ASN_60	H, B_ASN_60	2.94	1.98	8.25
1VFB.PDB	O, B_TRP_47	ND2, B_ASN_60	HD22, B_ASN_60	2.87	1.90	6.16
1VFB.PDB	OD1, B_ASN_60	N, B_ALA_62	H, B_ALA_62	2.90	2.08	27.74
1VFB.PDB	O, B_LEU_63	N, B_ARG_66	H, B_ARG_66	2.99	2.04	12.74
1VFB.PDB	OD2, B_ASP_89	NH1, B_ARG_66	HH12, B_ARG_66	2.89	1.97	19.13
1VFB.PDB	OD1, B_ASP_89	NH2, B_ARG_66	HH22, B_ARG_66	2.93	1.93	3.85
1VFB.PDB	O, B_LYS_81	N, B_SER_68	H, B_SER_68	2.97	2.10	22.66
1VFB.PDB	OH, B_TYR_59	N, B_ILE_69	H, B_ILE_69	2.97	2.01	7.63
1VFB.PDB	OD1, B_ASN_73	NZ, B_LYS_71	HZ1, B_LYS_71	2.93	2.08	28.65
1VFB.PDB	O, B_GLY_53	NZ, B_LYS_71	HZ3, B_LYS_71	2.92	2.04	25.68
1VFB.PDB	O, B_GLN_77	N, B_ASP_72	H, B_ASP_72	2.85	1.88	5.90
1VFB.PDB	O, B_CYS_22	N, B_VAL_78	H, B_VAL_78	2.96	2.07	20.13
1VFB.PDB	O, B_SER_70	N, B_PHE_79	H, B_PHE_79	2.82	1.89	14.11
1VFB.PDB	O, B_SER_68	N, B_LYS_81	H, B_LYS_81	2.78	1.89	20.09
1VFB.PDB	OG, B_SER_70	NZ, B_LYS_81	HZ2, B_LYS_81	2.92	2.05	26.58
1VFB.PDB	O, B_LEU_18	N, B_MET_82	H, B_MET_82	2.84	1.92	15.27
1VFB.PDB	OD1, B_ASN_83	OG, B_SER_84	HG, B_SER_84	2.99	2.04	8.51
1VFB.PDB	OD2, B_ASP_89	N, B_HIS_86	H, B_HIS_86	3.00	2.17	27.32
1VFB.PDB	O, B_THR_87	OG1, B_THR_90	HG1, B_THR_90	2.90	1.94	9.38
1VFB.PDB	O, B_GLN_39	N, B_ARG_92	H, B_ARG_92	2.99	2.02	2.81
1VFB.PDB	O, B_THR_110	N, B_TYR_93	H, B_TYR_93	2.83	1.90	15.51
1VFB.PDB	OE2, B_GLU_6	N, B_CYS_95	H, B_CYS_95	2.85	2.00	23.74
1VFB.PDB	O, B_ASN_35	N, B_ALA_96	H, B_ALA_96	2.98	2.12	24.00
1VFB.PDB	O, B_TYR_105	N, B_ARG_97	H, B_ARG_97	2.78	1.93	24.54
1VFB.PDB	OD1, B_ASP_104	NE, B_ARG_97	HE, B_ARG_97	2.99	2.02	4.50
1VFB.PDB	OD2, B_ASP_104	NH2, B_ARG_97	HH21, B_ARG_97	2.86	1.87	3.52
1VFB.PDB	O, B_GLY_33	N, B_GLU_98	H, B_GLU_98	2.83	1.86	4.19
1VFB.PDB	O, B_ARG_102	N, B_ARG_99	H, B_ARG_99	2.95	2.00	10.93
1VFB.PDB	O, B_ASP_100	NH1, B_ARG_102	HH11, B_ARG_102	3.00	2.15	26.78
1VFB.PDB	O, C_GLY_22	NH1, B_ARG_102	HH12, B_ARG_102	2.82	1.90	18.81
1VFB.PDB	O, B_CYS_95	N, B_GLY_107	H, B_GLY_107	2.97	2.01	8.78

1VFB.PDB	OE1, B_GLU_6	N, B_GLY_109	H, B_GLY_109	2.89	1.99	17.04
1VFB.PDB	O, B_TYR_93	N, B_THR_110	H, B_THR_110	2.94	2.04	19.36
1VFB.PDB	O, B_ALA_91	N, B_LEU_112	H, B_LEU_112	2.81	1.84	5.13
1VFB.PDB	O, B_GLY_10	N, B_THR_113	H, B_THR_113	2.88	1.92	9.03
1VFB.PDB	OG1, B_THR_90	N, B_VAL_114	H, B_VAL_114	2.95	1.97	3.76
1VFB.PDB	O, B_VAL_12	N, B_SER_115	H, B_SER_115	2.89	1.92	7.04
1VFB.PDB	OG1, C_THR_40	N, C_LYS_1	H1, C_LYS_1	2.88	1.92	18.01
1VFB.PDB	O, C_PHE_38	N, C_PHE_3	H, C_PHE_3	2.97	2.01	11.57
1VFB.PDB	O, C_ARG_5	N, C_ALA_9	H, C_ALA_9	2.93	1.95	4.49
1VFB.PDB	O, C_CYS_6	N, C_ALA_10	H, C_ALA_10	2.92	1.95	7.61
1VFB.PDB	O, C_LEU_8	N, C_MET_12	H, C_MET_12	2.84	1.91	15.62
1VFB.PDB	O, C_ALA_9	N, C_LYS_13	H, C_LYS_13	2.90	1.96	13.16
1VFB.PDB	O, C_ALA_11	ND1, C_HIS_15	HD1, C_HIS_15	2.83	1.90	15.15
1VFB.PDB	OG1, C_THR_89	NE2, C_HIS_15	HE2, C_HIS_15	2.84	1.94	19.37
1VFB.PDB	O, C_ASN_19	N, C_GLY_22	H, C_GLY_22	2.99	2.09	19.97
1VFB.PDB	O, C_TYR_20	N, C_TYR_23	H, C_TYR_23	2.95	1.99	10.86
1VFB.PDB	OD2, B_ASP_100	N, C_SER_24	H, C_SER_24	2.91	2.09	27.47
1VFB.PDB	O, C_GLY_26	N, C_CYS_30	H, C_CYS_30	2.84	1.96	21.71
1VFB.PDB	O, C_ASN_27	N, C_ALA_31	H, C_ALA_31	2.91	1.97	11.60
1VFB.PDB	O, C_ALA_31	N, C_GLU_35	H, C_GLU_35	2.82	1.95	22.11
1VFB.PDB	O, C_ALA_32	N, C_SER_36	H, C_SER_36	2.95	2.06	19.79
1VFB.PDB	O, C_ILE_55	OG, C_SER_36	HG, C_SER_36	2.79	1.88	15.77
1VFB.PDB	O, C_LYS_1	N, C_THR_40	H, C_THR_40	2.90	1.95	9.98
1VFB.PDB	OE1, C_GLN_41	OG1, C_THR_40	HG1, C_THR_40	2.88	1.98	18.75
1VFB.PDB	OD1, C_ASN_39	N, C_GLN_41	H, C_GLN_41	2.92	2.01	18.23
1VFB.PDB	O, C_LEU_84	NE2, C_GLN_41	HE21, C_GLN_41	2.78	1.99	29.59
1VFB.PDB	O, C_ASP_52	N, C_ASN_44	H, C_ASN_44	2.91	2.02	19.92
1VFB.PDB	O, C_SER_50	ND2, C_ASN_46	HD22, C_ASN_46	2.86	1.97	19.52
1VFB.PDB	O, C_ASN_46	N, C_ASP_48	H, C_ASP_48	2.84	1.95	20.51
1VFB.PDB	OG, C_SER_60	N, C_THR_51	H, C_THR_51	2.85	1.89	9.75
1VFB.PDB	O, C_ASN_44	N, C_ASP_52	H, C_ASP_52	2.77	1.89	21.40
1VFB.PDB	O, C_ILE_58	N, C_TYR_53	H, C_TYR_53	2.84	1.91	14.87
1VFB.PDB	O, C_ALA_42	N, C_GLY_54	H, C_GLY_54	2.75	1.87	21.13
1VFB.PDB	O, C_GLY_54	NE2, C_GLN_57	HE22, C_GLN_57	2.80	1.83	6.26
1VFB.PDB	OG1, C_THR_69	OG, C_SER_60	HG, C_SER_60	2.78	1.84	10.98
1VFB.PDB	O, C_PRO_70	NE, C_ARG_61	HE, C_ARG_61	2.72	1.91	27.72
1VFB.PDB	O, C_ILE_78	N, C_ASN_65	H, C_ASN_65	2.88	1.94	12.38
1VFB.PDB	O, C_SER_60	OG, C_SER_72	HG, C_SER_72	2.95	1.99	6.61
1VFB.PDB	O, C_ARG_61	N, C_ARG_73	H, C_ARG_73	2.84	1.87	6.21
1VFB.PDB	O, C_TRP_62	N, C_LEU_75	H, C_LEU_75	2.82	1.88	12.22
1VFB.PDB	O, C_TRP_63	N, C_CYS_76	H, C_CYS_76	2.88	1.99	20.44
1VFB.PDB	O, C_ASN_74	N, C_ASN_77	H, C_ASN_77	2.92	2.10	27.67
1VFB.PDB	O, C_ASN_65	N, C_CYS_80	H, C_CYS_80	2.95	1.99	9.67
1VFB.PDB	O, C_PRO_79	N, C_ALA_82	H, C_ALA_82	2.89	1.99	18.39
1VFB.PDB	O, C_ILE_88	N, C_VAL_92	H, C_VAL_92	2.91	2.06	24.26
1VFB.PDB	O, C_THR_89	N, C_ASN_93	H, C_ASN_93	2.88	1.92	8.98
1VFB.PDB	O, C_VAL_92	N, C_LYS_96	H, C_LYS_96	2.88	1.94	14.28
1VFB.PDB	O, C_ALA_95	N, C_VAL_99	H, C_VAL_99	2.93	2.05	20.53
1VFB.PDB	O, C_ASP_101	N, C_GLY_104	H, C_GLY_104	2.99	2.10	19.98
1VFB.PDB	O, C_LEU_56	NE1, C_TRP_108	HE1, C_TRP_108	2.75	1.86	21.02
1VFB.PDB	OD1, C_ASN_27	NE1, C_TRP_111	HE1, C_TRP_111	2.95	2.01	14.04
1VFB.PDB	O, C_VAL_109	N, C_ASN_113	H, C_ASN_113	2.97	2.00	6.92
1VFB.PDB	O, C_ALA_110	N, C_ARG_114	H, C_ARG_114	2.73	1.86	21.81
1VFB.PDB	O, C_TRP_111	N, C_CYS_115	H, C_CYS_115	2.84	1.99	24.09
1VFB.PDB	O, C_TRP_111	N, C_LYS_116	H, C_LYS_116	2.81	1.93	20.73
1VFB.PDB	O, C_CYS_115	N, C_THR_118	H, C_THR_118	2.99	2.13	23.03
1VFB.PDB	O, C_CYS_115	OG1, C_THR_118	HG1, C_THR_118	2.73	1.80	11.89
1VFB.PDB	O, C_THR_118	N, C_VAL_120	H, C_VAL_120	2.89	2.08	27.51

1VFB.PDB	O, A_PHE_91	NE2, C_GLN_121	HE21, C_GLN_121	2.82	1.88	14.37
1VFB.PDB	O, C_GLN_121	N, C_ILE_124	H, C_ILE_124	2.94	2.00	13.68
1VFB.PDB	OE1, C_GLN_121	NH1, C_ARG_125	HH11, C_ARG_125	2.96	2.02	16.36

Table 1678: 1VFB-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
2MKL-1.PDB	O, C_VAL_32	N, C_SER_8	H, C_SER_8	2.87	1.94	15.13
2MKL-1.PDB	O, C_GLU_30	N, C_SER_10	H, C_SER_10	2.78	1.81	7.07
2MKL-1.PDB	O, C_VAL_28	N, C_LEU_12	H, C_LEU_12	2.85	1.96	21.36
2MKL-1.PDB	OXT, C_ALA_105	NZ, C_LYS_13	HZ3, C_LYS_13	2.65	1.63	10.83
2MKL-1.PDB	OD1, C_ASP_80	OG1, C_THR_21	HG1, C_THR_21	2.65	1.79	22.35
2MKL-1.PDB	OD2, C_ASP_80	NE2, C_GLN_22	HE21, C_GLN_22	2.86	1.96	18.61
2MKL-1.PDB	O, C_VAL_74	OG1, C_THR_24	HG1, C_THR_24	2.53	1.57	5.32
2MKL-1.PDB	O, C_LEU_72	N, C_ILE_27	H, C_ILE_27	2.90	1.93	8.25
2MKL-1.PDB	O, C_SER_70	N, C_CYS_29	H, C_CYS_29	2.74	1.79	13.45
2MKL-1.PDB	O, C_SER_10	N, C_GLU_30	H, C_GLU_30	2.74	1.77	7.68
2MKL-1.PDB	O, C_ILE_68	N, C_ILE_31	H, C_ILE_31	2.71	1.73	3.33
2MKL-1.PDB	O, C_SER_8	N, C_VAL_32	H, C_VAL_32	2.86	1.94	16.02
2MKL-1.PDB	O, C_SER_66	N, C_TYR_33	H, C_TYR_33	2.96	2.02	12.76
2MKL-1.PDB	O, C_GLU_90	N, C_LYS_40	H, C_LYS_40	2.75	1.77	6.32
2MKL-1.PDB	O, C_LEU_88	N, C_PHE_42	H, C_PHE_42	2.83	1.96	23.06
2MKL-1.PDB	O, C_VAL_86	N, C_GLN_44	H, C_GLN_44	2.98	2.06	17.99
2MKL-1.PDB	O, C_VAL_48	N, C_VAL_45	H, C_VAL_45	2.89	1.93	11.14
2MKL-1.PDB	O, C_VAL_45	N, C_VAL_48	H, C_VAL_48	2.85	1.96	20.78
2MKL-1.PDB	O, C_TRP_43	NH1, C_ARG_50	HH11, C_ARG_50	2.73	1.80	17.42
2MKL-1.PDB	O, C_LYS_71	N, C_GLU_55	H, C_GLU_55	2.87	2.01	24.71
2MKL-1.PDB	O, C_VAL_69	N, C_GLN_57	H, C_GLN_57	2.76	1.79	7.63
2MKL-1.PDB	O, C_THR_67	N, C_GLU_60	H, C_GLU_60	2.78	1.84	14.09
2MKL-1.PDB	O, C_LYS_65	N, C_SER_62	H, C_SER_62	2.90	1.94	10.66
2MKL-1.PDB	O, C_SER_62	N, C_LYS_65	H, C_LYS_65	2.95	2.06	20.90
2MKL-1.PDB	OG, C_SER_34	NZ, C_LYS_65	HZ2, C_LYS_65	2.81	1.84	16.47
2MKL-1.PDB	O, C_TYR_33	N, C_SER_66	H, C_SER_66	2.85	2.01	24.96
2MKL-1.PDB	O, C_GLU_60	N, C_THR_67	H, C_THR_67	2.81	1.89	17.79
2MKL-1.PDB	O, C_ILE_31	N, C_ILE_68	H, C_ILE_68	2.81	1.84	9.32
2MKL-1.PDB	O, C_CYS_29	N, C_SER_70	H, C_SER_70	2.78	1.84	15.75
2MKL-1.PDB	O, C_GLU_55	N, C_LYS_71	H, C_LYS_71	2.94	2.02	16.84
2MKL-1.PDB	O, C_ILE_27	N, C_LEU_72	H, C_LEU_72	2.65	1.82	25.39
2MKL-1.PDB	O, C_GLY_53	N, C_LYS_73	H, C_LYS_73	2.72	1.81	18.13
2MKL-1.PDB	O, C_ALA_25	NZ, C_LYS_73	HZ3, C_LYS_73	2.77	1.77	11.66
2MKL-1.PDB	O, C_ALA_76	N, C_ASP_80	H, C_ASP_80	2.69	1.74	10.81
2MKL-1.PDB	O, C_GLU_78	N, C_SER_81	H, C_SER_81	2.94	2.13	29.26
2MKL-1.PDB	O, C_TRP_79	N, C_GLY_82	H, C_GLY_82	2.98	2.06	17.42
2MKL-1.PDB	OE1, C_GLU_78	OG1, C_THR_83	HG1, C_THR_83	2.66	1.70	8.48
2MKL-1.PDB	O, C_ALA_100	N, C_CYS_87	H, C_CYS_87	2.70	1.74	9.85
2MKL-1.PDB	O, C_PHE_42	N, C_LEU_88	H, C_LEU_88	2.74	1.76	6.64
2MKL-1.PDB	O, C_VAL_98	N, C_VAL_89	H, C_VAL_89	2.86	1.96	19.19
2MKL-1.PDB	O, C_LYS_40	N, C_GLU_90	H, C_GLU_90	2.85	1.91	13.13
2MKL-1.PDB	OD2, C_ASP_91	N, C_GLU_93	H, C_GLU_93	2.91	2.06	25.41
2MKL-1.PDB	O, C_ASP_91	N, C_LEU_94	H, C_LEU_94	2.97	2.04	16.30
2MKL-1.PDB	O, C_CYS_87	N, C_ALA_100	H, C_ALA_100	2.87	2.07	29.58
2MKL-1.PDB	O, C_TYR_85	N, C_ILE_102	H, C_ILE_102	2.75	1.93	27.29
2MKL-1.PDB	OD1, C_ASP_80	NZ, C_LYS_104	HZ1, C_LYS_104	2.72	1.78	20.43
2MKL-1.PDB	O, C_ASP_80	NZ, C_LYS_104	HZ3, C_LYS_104	2.71	1.81	23.71
2MKL-10.PDB	O, C_VAL_32	N, C_SER_8	H, C_SER_8	2.91	1.92	0.91
2MKL-10.PDB	O, C_GLU_30	N, C_SER_10	H, C_SER_10	2.77	1.80	6.96
2MKL-10.PDB	O, C_VAL_28	N, C_LEU_12	H, C_LEU_12	2.68	1.71	4.93
2MKL-10.PDB	O, C_PRO_15	NE2, C_GLN_22	HE21, C_GLN_22	2.70	1.72	5.44
2MKL-10.PDB	O, C_LEU_72	OG1, C_THR_26	HG1, C_THR_26	2.68	1.73	10.60
2MKL-10.PDB	O, C_LEU_72	N, C_ILE_27	H, C_ILE_27	2.84	2.02	27.43
2MKL-10.PDB	O, C_LEU_12	N, C_VAL_28	H, C_VAL_28	2.99	2.05	14.29
2MKL-10.PDB	O, C_SER_70	N, C_CYS_29	H, C_CYS_29	2.68	1.70	4.32
2MKL-10.PDB	O, C_SER_10	N, C_GLU_30	H, C_GLU_30	2.73	1.81	16.56
2MKL-10.PDB	O, C_SER_8	N, C_VAL_32	H, C_VAL_32	2.77	1.79	4.04

2MKL-10.PDB	O, C_SER.66	N, C_TYR.33	H, C_TYR.33	2.97	2.01	10.13
2MKL-10.PDB	OD1, C_ASP.91	N, C_GLU.37	H, C_GLU.37	2.80	1.93	22.75
2MKL-10.PDB	O, C_GLU.90	N, C_LYS.40	H, C_LYS.40	2.92	1.97	11.19
2MKL-10.PDB	OE2, C_GLU.90	NZ, C_LYS.40	HZ2, C_LYS.40	2.58	1.67	23.06
2MKL-10.PDB	O, C_LEU.88	N, C_PHE.42	H, C_PHE.42	2.92	1.94	6.40
2MKL-10.PDB	O, C_VAL.48	N, C_VAL.45	H, C_VAL.45	2.84	1.89	12.91
2MKL-10.PDB	O, C_VAL.45	N, C_VAL.48	H, C_VAL.48	2.85	2.01	25.64
2MKL-10.PDB	O, C_LYS.71	N, C_GLU.55	H, C_GLU.55	2.68	1.75	14.91
2MKL-10.PDB	O, C_VAL.69	N, C_GLN.57	H, C_GLN.57	2.86	1.90	10.97
2MKL-10.PDB	O, C_THR.67	N, C_GLU.60	H, C_GLU.60	2.97	2.01	8.51
2MKL-10.PDB	O, C_SER.62	N, C_LYS.65	H, C_LYS.65	2.88	1.95	14.30
2MKL-10.PDB	O, C_TYR.33	N, C_SER.66	H, C_SER.66	2.72	1.86	23.25
2MKL-10.PDB	OG, C_SER.62	OG1, C_THR.67	HG1, C_THR.67	2.83	1.88	6.13
2MKL-10.PDB	O, C_CYS.29	N, C_SER.70	H, C_SER.70	2.83	1.85	7.06
2MKL-10.PDB	O, C_GLU.55	N, C_LYS.71	H, C_LYS.71	2.73	1.76	7.85
2MKL-10.PDB	O, C_ILE.27	N, C_LEU.72	H, C_LEU.72	2.69	1.71	7.54
2MKL-10.PDB	O, C_GLY.53	N, C_LYS.73	H, C_LYS.73	2.74	1.76	5.67
2MKL-10.PDB	O, C_ALA.76	N, C_ASP.80	H, C_ASP.80	2.74	1.79	12.95
2MKL-10.PDB	O, C_GLU.78	N, C_SER.81	H, C_SER.81	2.92	2.10	27.95
2MKL-10.PDB	O, C_TRP.79	N, C_GLY.82	H, C_GLY.82	2.95	2.02	15.81
2MKL-10.PDB	O, C_ALA.100	N, C_CYS.87	H, C_CYS.87	2.74	1.76	5.71
2MKL-10.PDB	O, C_PHE.42	N, C_LEU.88	H, C_LEU.88	2.71	1.75	9.91
2MKL-10.PDB	O, C_VAL.98	N, C_VAL.89	H, C_VAL.89	2.70	1.81	20.27
2MKL-10.PDB	O, C_LYS.40	N, C_GLU.90	H, C_GLU.90	2.78	1.93	24.87
2MKL-10.PDB	OD2, C_ASP.91	N, C_GLU.93	H, C_GLU.93	2.71	1.82	20.62
2MKL-10.PDB	O, C_VAL.89	N, C_VAL.98	H, C_VAL.98	2.95	1.97	2.47
2MKL-10.PDB	O, C_CYS.87	N, C_ALA.100	H, C_ALA.100	2.90	2.06	26.13
2MKL-10.PDB	O, C_TYR.85	N, C_ILE.102	H, C_ILE.102	2.78	1.86	16.84
2MKL-10.PDB	OXT, C_ALA.105	NZ, C_LYS.104	HZ3, C_LYS.104	2.68	1.72	17.77
2MKL-2.PDB	OD1, C_ASP.6	N, C_GLY.2	H, C_GLY.2	2.76	1.77	3.72
2MKL-2.PDB	O, C_ARG.3	N, C_THR.5	H, C_THR.5	2.70	1.90	29.18
2MKL-2.PDB	O, C_VAL.32	N, C_SER.8	H, C_SER.8	2.91	1.93	2.96
2MKL-2.PDB	O, C_GLU.30	N, C_SER.10	H, C_SER.10	2.85	1.91	14.14
2MKL-2.PDB	O, C_VAL.28	N, C_LEU.12	H, C_LEU.12	2.67	1.73	13.23
2MKL-2.PDB	OXT, C_ALA.105	NZ, C_LYS.13	HZ3, C_LYS.13	2.61	1.67	20.57
2MKL-2.PDB	O, C_PRO.14	N, C_PHE.16	H, C_PHE.16	2.68	1.84	24.86
2MKL-2.PDB	O, C_THR.24	N, C_THR.26	H, C_THR.26	2.87	2.01	23.54
2MKL-2.PDB	O, C_LEU.72	OG1, C_THR.26	HG1, C_THR.26	2.63	1.69	10.64
2MKL-2.PDB	O, C_LEU.72	N, C_ILE.27	H, C_ILE.27	2.90	2.08	27.91
2MKL-2.PDB	O, C_SER.70	N, C_CYS.29	H, C_CYS.29	2.73	1.79	13.27
2MKL-2.PDB	O, C_SER.10	N, C_GLU.30	H, C_GLU.30	2.88	1.96	17.58
2MKL-2.PDB	O, C_ILE.68	N, C_ILE.31	H, C_ILE.31	2.87	1.90	7.16
2MKL-2.PDB	O, C_SER.8	N, C_VAL.32	H, C_VAL.32	2.78	1.81	9.22
2MKL-2.PDB	O, C_SER.66	N, C_TYR.33	H, C_TYR.33	2.94	2.00	12.67
2MKL-2.PDB	OD1, C_ASP.35	OG, C_SER.34	HG, C_SER.34	2.77	1.81	5.76
2MKL-2.PDB	O, C_GLU.90	N, C_LYS.40	H, C_LYS.40	2.89	1.95	12.75
2MKL-2.PDB	O, C_LEU.88	N, C_PHE.42	H, C_PHE.42	2.81	1.85	8.44
2MKL-2.PDB	O, C_VAL.48	N, C_VAL.45	H, C_VAL.45	2.78	1.87	17.34
2MKL-2.PDB	O, C_VAL.45	N, C_VAL.48	H, C_VAL.48	2.84	2.02	27.01
2MKL-2.PDB	OH, C_TYR.85	NH1, C_ARG.50	HH11, C_ARG.50	2.66	1.70	14.67
2MKL-2.PDB	OE2, C_GLU.78	NH1, C_ARG.50	HH12, C_ARG.50	2.73	1.79	17.34
2MKL-2.PDB	O, C_LYS.71	N, C_GLU.55	H, C_GLU.55	2.70	1.82	21.14
2MKL-2.PDB	O, C_THR.67	N, C_GLU.60	H, C_GLU.60	2.77	1.81	9.91
2MKL-2.PDB	O, C_SER.62	N, C_LYS.65	H, C_LYS.65	2.89	2.03	23.66
2MKL-2.PDB	O, C_TYR.33	N, C_SER.66	H, C_SER.66	2.85	2.01	26.03
2MKL-2.PDB	O, C_GLU.60	N, C_THR.67	H, C_THR.67	2.83	1.98	24.85
2MKL-2.PDB	O, C_ILE.31	N, C_ILE.68	H, C_ILE.68	2.88	1.91	9.29
2MKL-2.PDB	O, C_CYS.29	N, C_SER.70	H, C_SER.70	2.83	1.87	10.79

2MKL-2.PDB	O, C_GLU_55	N, C_LYS_71	H, C_LYS_71	2.73	1.79	13.88
2MKL-2.PDB	OE1, C_GLU_55	NZ, C_LYS_71	HZ1, C_LYS_71	2.72	1.71	11.97
2MKL-2.PDB	O, C_ILE_27	N, C_LEU_72	H, C_LEU_72	2.68	1.70	2.15
2MKL-2.PDB	O, C_GLY_53	N, C_LYS_73	H, C_LYS_73	2.69	1.73	8.58
2MKL-2.PDB	O, C_ALA_76	N, C_ASP_80	H, C_ASP_80	2.99	2.07	17.02
2MKL-2.PDB	O, C_SER_77	OG, C_SER_81	HG, C_SER_81	2.59	1.64	9.12
2MKL-2.PDB	O, C_TRP_79	N, C_GLY_82	H, C_GLY_82	2.99	2.06	16.33
2MKL-2.PDB	OD1, C_ASN_46	OG1, C_THR_83	HG1, C_THR_83	2.72	1.91	26.52
2MKL-2.PDB	O, C_GLN_44	N, C_VAL_86	H, C_VAL_86	2.87	1.99	21.54
2MKL-2.PDB	O, C_ALA_100	N, C_CYS_87	H, C_CYS_87	2.71	1.74	6.36
2MKL-2.PDB	O, C_PHE_42	N, C_LEU_88	H, C_LEU_88	2.70	1.72	2.99
2MKL-2.PDB	O, C_VAL_98	N, C_VAL_89	H, C_VAL_89	2.79	1.88	17.49
2MKL-2.PDB	OD2, C_ASP_91	N, C_GLU_93	H, C_GLU_93	2.95	2.05	18.82
2MKL-2.PDB	O, C_ASP_91	N, C_LEU_94	H, C_LEU_94	2.91	2.01	20.37
2MKL-2.PDB	O, C_VAL_89	N, C_VAL_98	H, C_VAL_98	2.92	1.98	13.93
2MKL-2.PDB	O, C_CYS_87	N, C_ALA_100	H, C_ALA_100	2.93	2.10	27.00
2MKL-2.PDB	O, C_TYR_85	OG, C_SER_101	HG, C_SER_101	2.98	2.03	8.67
2MKL-2.PDB	O, C_TYR_85	N, C_ILE_102	H, C_ILE_102	2.79	1.86	15.51
2MKL-3.PDB	OE1, C_GLU_93	NH1, C_ARG_3	HH12, C_ARG_3	2.68	1.70	11.24
2MKL-3.PDB	O, C_VAL_32	N, C_SER_8	H, C_SER_8	2.88	1.97	17.61
2MKL-3.PDB	O, C_GLU_30	N, C_SER_10	H, C_SER_10	2.89	1.92	6.89
2MKL-3.PDB	O, C_VAL_28	N, C_LEU_12	H, C_LEU_12	2.65	1.67	5.19
2MKL-3.PDB	OXT, C_ALA_105	NZ, C_LYS_13	HZ1, C_LYS_13	2.67	1.72	19.52
2MKL-3.PDB	O, C_TRP_20	OG1, C_THR_21	HG1, C_THR_21	2.91	1.97	13.27
2MKL-3.PDB	O, C_THR_24	N, C_THR_26	H, C_THR_26	2.76	1.91	24.64
2MKL-3.PDB	O, C_LEU_72	OG1, C_THR_26	HG1, C_THR_26	2.58	1.64	12.96
2MKL-3.PDB	O, C_SER_70	N, C_CYS_29	H, C_CYS_29	2.68	1.74	12.62
2MKL-3.PDB	O, C_SER_10	N, C_GLU_30	H, C_GLU_30	2.90	1.95	12.95
2MKL-3.PDB	O, C_ILE_68	N, C_ILE_31	H, C_ILE_31	2.92	1.94	7.65
2MKL-3.PDB	O, C_SER_8	N, C_VAL_32	H, C_VAL_32	2.84	1.90	14.60
2MKL-3.PDB	O, C_SER_66	N, C_TYR_33	H, C_TYR_33	2.81	1.86	12.33
2MKL-3.PDB	OD1, C_ASP_91	N, C_GLU_37	H, C_GLU_37	2.74	1.89	24.66
2MKL-3.PDB	O, C_GLU_90	N, C_LYS_40	H, C_LYS_40	2.97	1.99	6.05
2MKL-3.PDB	O, C_LEU_88	N, C_PHE_42	H, C_PHE_42	2.73	1.79	14.89
2MKL-3.PDB	OE2, C_GLU_84	N, C_GLY_47	H, C_GLY_47	2.89	2.08	28.18
2MKL-3.PDB	O, C_VAL_45	N, C_VAL_48	H, C_VAL_48	2.92	2.02	19.65
2MKL-3.PDB	O, C_LYS_71	N, C_GLU_55	H, C_GLU_55	2.68	1.79	20.49
2MKL-3.PDB	O, C_VAL_69	N, C_GLN_57	H, C_GLN_57	2.76	1.79	7.77
2MKL-3.PDB	O, C_GLY_63	NE1, C_TRP_61	HE1, C_TRP_61	2.71	1.80	19.18
2MKL-3.PDB	O, C_LYS_65	N, C_SER_62	H, C_SER_62	2.68	1.70	4.43
2MKL-3.PDB	O, C_SER_62	N, C_LYS_65	H, C_LYS_65	2.91	1.97	14.37
2MKL-3.PDB	OG, C_SER_34	NZ, C_LYS_65	HZ3, C_LYS_65	2.80	1.76	6.92
2MKL-3.PDB	O, C_TYR_33	N, C_SER_66	H, C_SER_66	2.69	1.79	19.81
2MKL-3.PDB	O, C_GLU_60	N, C_THR_67	H, C_THR_67	2.89	1.96	15.80
2MKL-3.PDB	O, C_ILE_31	N, C_ILE_68	H, C_ILE_68	2.71	1.77	14.66
2MKL-3.PDB	O, C_CYS_29	N, C_SER_70	H, C_SER_70	2.78	1.85	15.96
2MKL-3.PDB	O, C_GLU_55	N, C_LYS_71	H, C_LYS_71	2.82	1.90	15.66
2MKL-3.PDB	OE2, C_GLU_55	NZ, C_LYS_71	HZ1, C_LYS_71	2.64	1.59	1.73
2MKL-3.PDB	OG1, C_THR_26	NZ, C_LYS_71	HZ3, C_LYS_71	2.86	1.95	23.23
2MKL-3.PDB	O, C_ILE_27	N, C_LEU_72	H, C_LEU_72	2.71	1.73	2.63
2MKL-3.PDB	O, C_GLY_53	N, C_LYS_73	H, C_LYS_73	2.74	1.75	3.68
2MKL-3.PDB	O, C_ALA_76	N, C_ASP_80	H, C_ASP_80	2.72	1.79	14.15
2MKL-3.PDB	O, C_GLU_78	N, C_SER_81	H, C_SER_81	2.92	2.06	23.97
2MKL-3.PDB	O, C_TRP_79	N, C_GLY_82	H, C_GLY_82	2.95	2.01	14.70
2MKL-3.PDB	OD1, C_ASN_46	OG1, C_THR_83	HG1, C_THR_83	2.91	1.97	11.57
2MKL-3.PDB	O, C_ALA_100	N, C_CYS_87	H, C_CYS_87	2.69	1.73	11.27
2MKL-3.PDB	O, C_PHE_42	N, C_LEU_88	H, C_LEU_88	2.93	2.02	18.64
2MKL-3.PDB	O, C_VAL_98	N, C_VAL_89	H, C_VAL_89	2.70	1.79	17.71

2MKL-3.PDB	O, C_LYS_40	N, C_GLU_90	H, C_GLU_90	2.89	1.98	17.88
2MKL-3.PDB	OD2, C_ASP_91	N, C_GLU_93	H, C_GLU_93	2.68	1.74	15.47
2MKL-3.PDB	O, C_ASP_91	N, C_LEU_94	H, C_LEU_94	2.96	2.02	14.82
2MKL-3.PDB	O, C_VAL_89	N, C_VAL_98	H, C_VAL_98	2.70	1.73	7.23
2MKL-3.PDB	O, C_TYR_85	N, C_ILE_102	H, C_ILE_102	2.70	1.82	21.56
2MKL-3.PDB	OD1, C_ASP_80	NZ, C_LYS_104	HZ2, C_LYS_104	2.61	1.56	1.39
2MKL-4.PDB	OD1, C_ASP_6	N, C_GLY_2	H, C_GLY_2	2.67	1.68	4.84
2MKL-4.PDB	O, C_VAL_32	N, C_SER_8	H, C_SER_8	2.78	1.82	11.31
2MKL-4.PDB	O, C_GLU_30	N, C_SER_10	H, C_SER_10	2.90	2.00	20.41
2MKL-4.PDB	O, C_VAL_28	N, C_LEU_12	H, C_LEU_12	2.69	1.71	3.92
2MKL-4.PDB	O, C_ALA_105	NZ, C_LYS_13	HZ1, C_LYS_13	2.63	1.64	14.05
2MKL-4.PDB	OE1, C_GLU_17	NE1, C_TRP_20	HE1, C_TRP_20	2.69	1.70	6.61
2MKL-4.PDB	O, C_THR_24	N, C_THR_26	H, C_THR_26	2.90	2.07	26.74
2MKL-4.PDB	O, C_LEU_72	OG1, C_THR_26	HG1, C_THR_26	2.72	1.81	15.12
2MKL-4.PDB	O, C_SER_70	N, C_CYS_29	H, C_CYS_29	2.72	1.78	13.99
2MKL-4.PDB	O, C_SER_10	N, C_GLU_30	H, C_GLU_30	2.82	1.87	12.27
2MKL-4.PDB	O, C_ILE_68	N, C_ILE_31	H, C_ILE_31	2.81	1.83	5.53
2MKL-4.PDB	O, C_SER_8	N, C_VAL_32	H, C_VAL_32	2.75	1.77	3.26
2MKL-4.PDB	O, C_SER_66	N, C_TYR_33	H, C_TYR_33	2.94	1.97	7.56
2MKL-4.PDB	O, C_SER_64	OG, C_SER_34	HG, C_SER_34	2.77	1.80	1.75
2MKL-4.PDB	OE1, C_GLU_37	ND2, C_ASN_38	HD21, C_ASN_38	2.75	1.84	18.89
2MKL-4.PDB	O, C_LEU_88	N, C_PHE_42	H, C_PHE_42	2.69	1.73	9.14
2MKL-4.PDB	O, C_VAL_48	N, C_VAL_45	H, C_VAL_45	2.71	1.78	15.12
2MKL-4.PDB	OE1, C_GLU_84	ND2, C_ASN_46	HD21, C_ASN_46	2.79	1.87	17.49
2MKL-4.PDB	O, C_VAL_45	N, C_VAL_48	H, C_VAL_48	2.77	1.89	22.69
2MKL-4.PDB	OH, C_TYR_85	NE, C_ARG_50	HE, C_ARG_50	2.95	2.07	22.98
2MKL-4.PDB	OE1, C_GLU_78	NH2, C_ARG_50	HH21, C_ARG_50	2.70	1.74	15.78
2MKL-4.PDB	O, C_LYS_71	N, C_GLU_55	H, C_GLU_55	2.71	1.81	18.61
2MKL-4.PDB	O, C_VAL_69	N, C_GLN_57	H, C_GLN_57	2.73	1.78	11.53
2MKL-4.PDB	O, C_SER_62	N, C_LYS_65	H, C_LYS_65	2.84	1.85	4.44
2MKL-4.PDB	O, C_TYR_33	N, C_SER_66	H, C_SER_66	2.69	1.77	16.96
2MKL-4.PDB	O, C_ILE_31	N, C_ILE_68	H, C_ILE_68	2.81	1.88	14.11
2MKL-4.PDB	O, C_CYS_29	N, C_SER_70	H, C_SER_70	2.73	1.81	16.08
2MKL-4.PDB	O, C_GLU_55	N, C_LYS_71	H, C_LYS_71	2.71	1.78	13.91
2MKL-4.PDB	OE2, C_GLU_55	NZ, C_LYS_71	HZ1, C_LYS_71	2.65	1.66	15.29
2MKL-4.PDB	O, C_ILE_27	N, C_LEU_72	H, C_LEU_72	2.71	1.73	8.37
2MKL-4.PDB	O, C_GLY_53	N, C_LYS_73	H, C_LYS_73	2.76	1.78	6.24
2MKL-4.PDB	OE1, C_GLU_78	N, C_MET_75	H, C_MET_75	2.82	1.87	13.55
2MKL-4.PDB	O, C_ALA_76	N, C_ASP_80	H, C_ASP_80	2.90	2.02	21.07
2MKL-4.PDB	O, C_TRP_79	N, C_GLY_82	H, C_GLY_82	2.93	2.03	19.45
2MKL-4.PDB	O, C_ALA_100	N, C_CYS_87	H, C_CYS_87	2.67	1.71	9.36
2MKL-4.PDB	O, C_PHE_42	N, C_LEU_88	H, C_LEU_88	2.83	2.00	27.21
2MKL-4.PDB	O, C_VAL_98	N, C_VAL_89	H, C_VAL_89	2.69	1.75	13.90
2MKL-4.PDB	O, C_LYS_40	N, C_GLU_90	H, C_GLU_90	2.95	1.97	6.05
2MKL-4.PDB	OD2, C_ASP_91	N, C_GLU_93	H, C_GLU_93	2.83	1.95	21.47
2MKL-4.PDB	O, C_VAL_89	N, C_VAL_98	H, C_VAL_98	2.84	1.87	7.29
2MKL-4.PDB	O, C_TYR_85	N, C_ILE_102	H, C_ILE_102	2.72	1.78	13.87
2MKL-5.PDB	OG1, C_THR_5	NE2, C_GLN_4	HE21, C_GLN_4	2.80	1.92	21.71
2MKL-5.PDB	O, C_VAL_32	N, C_SER_8	H, C_SER_8	2.85	1.89	10.14
2MKL-5.PDB	O, C_GLU_30	N, C_SER_10	H, C_SER_10	2.70	1.73	5.85
2MKL-5.PDB	O, C_VAL_28	N, C_LEU_12	H, C_LEU_12	2.69	1.72	7.27
2MKL-5.PDB	O, C_ALA_105	NZ, C_LYS_13	HZ2, C_LYS_13	2.70	1.67	8.50
2MKL-5.PDB	O, C_LEU_72	N, C_ILE_27	H, C_ILE_27	2.84	2.03	28.89
2MKL-5.PDB	O, C_SER_70	N, C_CYS_29	H, C_CYS_29	2.69	1.72	7.41
2MKL-5.PDB	O, C_SER_10	N, C_GLU_30	H, C_GLU_30	2.79	1.82	7.58
2MKL-5.PDB	O, C_ILE_68	N, C_ILE_31	H, C_ILE_31	2.79	1.81	2.50
2MKL-5.PDB	O, C_SER_8	N, C_VAL_32	H, C_VAL_32	2.80	1.83	9.41
2MKL-5.PDB	O, C_SER_66	N, C_TYR_33	H, C_TYR_33	2.93	1.97	10.84

2MKL-5.PDB	OD1, C_ASP_35	OG, C_SER_34	HG, C_SER_34	2.85	1.91	12.30
2MKL-5.PDB	O, C_GLU_90	N, C_LYS_40	H, C_LYS_40	2.94	1.96	3.61
2MKL-5.PDB	O, C_LEU_88	N, C_PHE_42	H, C_PHE_42	2.90	1.95	11.88
2MKL-5.PDB	O, C_VAL_48	N, C_VAL_45	H, C_VAL_45	2.81	1.90	17.99
2MKL-5.PDB	O, C_VAL_45	N, C_VAL_48	H, C_VAL_48	2.85	1.99	24.39
2MKL-5.PDB	OE1, C_GLU_78	NH2, C_ARG_50	HH22, C_ARG_50	2.76	1.81	16.18
2MKL-5.PDB	O, C_LYS_71	N, C_GLU_55	H, C_GLU_55	2.78	1.82	12.33
2MKL-5.PDB	O, C_VAL_69	N, C_GLN_57	H, C_GLN_57	2.78	1.80	6.57
2MKL-5.PDB	O, C_THR_67	N, C_GLU_60	H, C_GLU_60	2.84	1.94	20.40
2MKL-5.PDB	O, C_SER_62	N, C_SER_64	H, C_SER_64	2.53	1.70	25.66
2MKL-5.PDB	OD2, C_ASP_6	NZ, C_LYS_65	HZ2, C_LYS_65	2.68	1.69	14.66
2MKL-5.PDB	O, C_TYR_33	N, C_SER_66	H, C_SER_66	2.80	1.91	20.20
2MKL-5.PDB	O, C_ILE_31	N, C_ILE_68	H, C_ILE_68	2.76	1.80	8.71
2MKL-5.PDB	O, C_CYS_29	N, C_SER_70	H, C_SER_70	2.77	1.81	10.20
2MKL-5.PDB	O, C_GLU_55	N, C_LYS_71	H, C_LYS_71	2.74	1.78	6.80
2MKL-5.PDB	O, C_ILE_27	N, C_LEU_72	H, C_LEU_72	2.68	1.70	3.69
2MKL-5.PDB	O, C_GLY_53	N, C_LYS_73	H, C_LYS_73	2.68	1.72	8.29
2MKL-5.PDB	O, C_ALA_76	N, C_ASP_80	H, C_ASP_80	2.74	1.77	7.96
2MKL-5.PDB	O, C_TRP_79	N, C_GLY_82	H, C_GLY_82	2.89	1.97	17.29
2MKL-5.PDB	OE2, C_GLU_78	OG1, C_THR_83	HG1, C_THR_83	2.81	1.87	12.01
2MKL-5.PDB	O, C_ALA_100	N, C_CYS_87	H, C_CYS_87	2.72	1.76	9.78
2MKL-5.PDB	O, C_PHE_42	N, C_LEU_88	H, C_LEU_88	2.71	1.74	7.08
2MKL-5.PDB	O, C_VAL_98	N, C_VAL_89	H, C_VAL_89	2.71	1.78	15.68
2MKL-5.PDB	OD2, C_ASP_91	N, C_GLU_93	H, C_GLU_93	2.93	2.06	22.91
2MKL-5.PDB	O, C_VAL_89	N, C_VAL_98	H, C_VAL_98	2.95	1.98	7.21
2MKL-5.PDB	O, C_CYS_87	N, C_ALA_100	H, C_ALA_100	2.91	2.10	28.19
2MKL-5.PDB	O, C_TYR_85	N, C_ILE_102	H, C_ILE_102	2.65	1.75	17.77
2MKL-5.PDB	OXT, C_ALA_105	NZ, C_LYS_104	HZ2, C_LYS_104	2.74	1.74	13.81
2MKL-6.PDB	O, C_VAL_32	N, C_SER_8	H, C_SER_8	2.70	1.80	19.33
2MKL-6.PDB	O, C_VAL_28	N, C_LEU_12	H, C_LEU_12	2.64	1.67	9.36
2MKL-6.PDB	OXT, C_ALA_105	NZ, C_LYS_13	HZ2, C_LYS_13	2.64	1.69	18.78
2MKL-6.PDB	OE2, C_GLU_17	NZ, C_LYS_13	HZ3, C_LYS_13	2.63	1.59	5.83
2MKL-6.PDB	O, C_VAL_74	OG1, C_THR_24	HG1, C_THR_24	2.63	1.68	6.20
2MKL-6.PDB	O, C_LEU_72	N, C_ILE_27	H, C_ILE_27	2.81	1.83	4.74
2MKL-6.PDB	O, C_SER_70	N, C_CYS_29	H, C_CYS_29	2.68	1.72	9.63
2MKL-6.PDB	O, C_SER_10	N, C_GLU_30	H, C_GLU_30	2.74	1.79	11.80
2MKL-6.PDB	O, C_SER_8	N, C_VAL_32	H, C_VAL_32	2.94	1.99	13.64
2MKL-6.PDB	O, C_SER_66	N, C_TYR_33	H, C_TYR_33	2.94	1.99	12.36
2MKL-6.PDB	OD2, C_ASP_91	N, C_GLU_37	H, C_GLU_37	2.93	1.96	8.54
2MKL-6.PDB	O, C_GLU_90	N, C_LYS_40	H, C_LYS_40	2.93	1.96	4.64
2MKL-6.PDB	O, C_LEU_88	N, C_PHE_42	H, C_PHE_42	2.84	1.91	15.28
2MKL-6.PDB	O, C_GLY_47	NE2, C_GLN_44	HE21, C_GLN_44	2.88	2.02	23.44
2MKL-6.PDB	O, C_VAL_48	N, C_VAL_45	H, C_VAL_45	2.83	1.89	14.07
2MKL-6.PDB	OE1, C_GLU_84	ND2, C_ASN_46	HD21, C_ASN_46	2.90	1.97	15.36
2MKL-6.PDB	O, C_VAL_45	N, C_VAL_48	H, C_VAL_48	2.91	2.02	21.18
2MKL-6.PDB	OE2, C_GLU_78	NH2, C_ARG_50	HH22, C_ARG_50	2.72	1.70	3.73
2MKL-6.PDB	O, C_LYS_71	N, C_GLU_55	H, C_GLU_55	2.82	1.99	26.45
2MKL-6.PDB	O, C_VAL_69	N, C_GLN_57	H, C_GLN_57	2.71	1.75	9.51
2MKL-6.PDB	O, C_THR_67	N, C_GLU_60	H, C_GLU_60	2.83	1.87	9.90
2MKL-6.PDB	O, C_LYS_65	N, C_SER_62	H, C_SER_62	2.99	2.02	8.78
2MKL-6.PDB	O, C_SER_62	N, C_LYS_65	H, C_LYS_65	2.93	2.00	16.12
2MKL-6.PDB	OD2, C_ASP_6	NZ, C_LYS_65	HZ3, C_LYS_65	2.59	1.63	17.95
2MKL-6.PDB	O, C_TYR_33	N, C_SER_66	H, C_SER_66	2.80	1.88	16.03
2MKL-6.PDB	O, C_GLU_60	N, C_THR_67	H, C_THR_67	2.90	2.10	28.48
2MKL-6.PDB	O, C_ILE_31	N, C_ILE_68	H, C_ILE_68	2.89	1.92	9.05
2MKL-6.PDB	O, C_CYS_29	N, C_SER_70	H, C_SER_70	2.88	1.94	13.67
2MKL-6.PDB	O, C_GLU_55	N, C_LYS_71	H, C_LYS_71	2.76	1.80	10.17
2MKL-6.PDB	OE2, C_GLU_55	NZ, C_LYS_71	HZ1, C_LYS_71	2.70	1.72	16.34

2MKL-6.PDB	O, C_ILE_27	N, C_LEU_72	H, C_LEU_72	2.65	1.75	19.43
2MKL-6.PDB	O, C_GLY_53	N, C_LYS_73	H, C_LYS_73	2.75	1.77	6.62
2MKL-6.PDB	O, C_ALA_76	N, C_ASP_80	H, C_ASP_80	2.70	1.73	7.99
2MKL-6.PDB	O, C_TRP_79	N, C_GLY_82	H, C_GLY_82	2.93	2.02	19.18
2MKL-6.PDB	OD1, C_ASN_46	OG1, C_THR_83	HG1, C_THR_83	2.65	1.71	11.83
2MKL-6.PDB	O, C_ALA_100	N, C_CYS_87	H, C_CYS_87	2.74	1.76	5.40
2MKL-6.PDB	O, C_PHE_42	N, C_LEU_88	H, C_LEU_88	2.76	1.79	7.22
2MKL-6.PDB	O, C_VAL_98	N, C_VAL_89	H, C_VAL_89	2.69	1.77	16.78
2MKL-6.PDB	O, C_VAL_89	N, C_VAL_98	H, C_VAL_98	2.99	2.01	1.37
2MKL-6.PDB	O, C_CYS_87	N, C_ALA_100	H, C_ALA_100	2.94	2.11	26.98
2MKL-6.PDB	O, C_TYR_85	N, C_ILE_102	H, C_ILE_102	2.75	1.80	12.64
2MKL-6.PDB	OD1, C_ASP_80	NZ, C_LYS_104	HZ1, C_LYS_104	2.64	1.71	20.84
2MKL-7.PDB	OD1, C_ASP_6	NE, C_ARG_3	HE, C_ARG_3	2.80	1.90	20.83
2MKL-7.PDB	OD2, C_ASP_6	NE, C_ARG_3	HE, C_ARG_3	2.95	2.13	27.86
2MKL-7.PDB	OD2, C_ASP_6	NH2, C_ARG_3	HH21, C_ARG_3	2.72	1.79	18.49
2MKL-7.PDB	O, C_GLY_2	N, C_GLN_4	H, C_GLN_4	2.91	2.07	25.29
2MKL-7.PDB	O, C_VAL_32	N, C_SER_8	H, C_SER_8	2.86	1.92	13.37
2MKL-7.PDB	O, C_GLU_30	N, C_SER_10	H, C_SER_10	2.76	1.78	0.59
2MKL-7.PDB	O, C_VAL_28	N, C_LEU_12	H, C_LEU_12	2.69	1.70	3.11
2MKL-7.PDB	O, C_PRO_14	N, C_PHE_16	H, C_PHE_16	2.65	1.73	16.96
2MKL-7.PDB	O, C_PHE_16	N, C_GLU_18	H, C_GLU_18	2.58	1.74	25.12
2MKL-7.PDB	O, C_PHE_16	N, C_TRP_20	H, C_TRP_20	2.98	2.12	23.41
2MKL-7.PDB	O, C_GLN_22	N, C_THR_24	H, C_THR_24	2.67	1.86	27.69
2MKL-7.PDB	O, C_LEU_72	OG1, C_THR_26	HG1, C_THR_26	2.61	1.71	16.80
2MKL-7.PDB	O, C_LEU_72	N, C_ILE_27	H, C_ILE_27	2.83	2.01	27.24
2MKL-7.PDB	O, C_SER_70	N, C_CYS_29	H, C_CYS_29	2.71	1.75	8.90
2MKL-7.PDB	O, C_SER_10	N, C_GLU_30	H, C_GLU_30	2.79	1.83	10.18
2MKL-7.PDB	O, C_ILE_68	N, C_ILE_31	H, C_ILE_31	2.98	2.00	2.29
2MKL-7.PDB	O, C_SER_8	N, C_VAL_32	H, C_VAL_32	2.74	1.76	3.52
2MKL-7.PDB	O, C_SER_66	N, C_TYR_33	H, C_TYR_33	2.95	2.00	12.03
2MKL-7.PDB	O, C_SER_64	OG, C_SER_34	HG, C_SER_34	2.66	1.69	4.53
2MKL-7.PDB	O, C_LEU_88	N, C_PHE_42	H, C_PHE_42	2.87	1.89	4.70
2MKL-7.PDB	O, C_VAL_45	N, C_VAL_48	H, C_VAL_48	2.96	2.07	20.95
2MKL-7.PDB	O, C_VAL_54	NZ, C_LYS_52	HZ1, C_LYS_52	2.71	1.68	7.22
2MKL-7.PDB	O, C_LYS_71	N, C_GLU_55	H, C_GLU_55	2.76	1.91	24.53
2MKL-7.PDB	O, C_VAL_69	N, C_GLN_57	H, C_GLN_57	2.73	1.77	10.49
2MKL-7.PDB	O, C_THR_67	N, C_GLU_60	H, C_GLU_60	2.81	1.87	13.84
2MKL-7.PDB	OE1, C_GLU_60	N, C_TRP_61	H, C_TRP_61	2.86	1.94	17.90
2MKL-7.PDB	O, C_LYS_65	N, C_SER_62	H, C_SER_62	2.88	1.90	4.45
2MKL-7.PDB	O, C_SER_62	N, C_LYS_65	H, C_LYS_65	2.88	1.96	16.75
2MKL-7.PDB	OD1, C_ASP_6	NZ, C_LYS_65	HZ2, C_LYS_65	2.61	1.57	4.07
2MKL-7.PDB	O, C_TYR_33	N, C_SER_66	H, C_SER_66	2.78	1.94	25.87
2MKL-7.PDB	O, C_GLU_60	N, C_THR_67	H, C_THR_67	2.69	1.81	21.94
2MKL-7.PDB	O, C_ILE_31	N, C_ILE_68	H, C_ILE_68	2.96	1.98	7.22
2MKL-7.PDB	O, C_CYS_29	N, C_SER_70	H, C_SER_70	2.75	1.80	11.18
2MKL-7.PDB	O, C_GLU_55	N, C_LYS_71	H, C_LYS_71	2.75	1.91	24.82
2MKL-7.PDB	O, C_ILE_27	N, C_LEU_72	H, C_LEU_72	2.67	1.73	13.09
2MKL-7.PDB	O, C_GLY_53	N, C_LYS_73	H, C_LYS_73	2.80	1.82	6.40
2MKL-7.PDB	OG1, C_THR_24	NZ, C_LYS_73	HZ1, C_LYS_73	2.79	1.84	19.74
2MKL-7.PDB	O, C_ALA_76	N, C_ASP_80	H, C_ASP_80	2.73	1.79	13.61
2MKL-7.PDB	O, C_GLU_78	N, C_SER_81	H, C_SER_81	2.92	2.09	26.88
2MKL-7.PDB	O, C_TRP_79	N, C_GLY_82	H, C_GLY_82	2.96	2.03	15.54
2MKL-7.PDB	OE2, C_GLU_78	OG1, C_THR_83	HG1, C_THR_83	2.59	1.64	9.74
2MKL-7.PDB	O, C_ALA_100	N, C_CYS_87	H, C_CYS_87	2.73	1.75	2.91
2MKL-7.PDB	O, C_PHE_42	N, C_LEU_88	H, C_LEU_88	2.67	1.75	17.26
2MKL-7.PDB	O, C_VAL_98	N, C_VAL_89	H, C_VAL_89	2.85	1.96	20.95
2MKL-7.PDB	OD2, C_ASP_91	N, C_GLU_93	H, C_GLU_93	2.83	1.89	14.21
2MKL-7.PDB	O, C_VAL_89	N, C_VAL_98	H, C_VAL_98	2.92	1.95	4.26

2MKL-7.PDB	O, C_CYS_87	N, C_ALA_100	H, C_ALA_100	2.86	2.03	26.56
2MKL-7.PDB	O, C_TYR_85	N, C_ILE_102	H, C_ILE_102	2.82	1.93	20.79
2MKL-7.PDB	O, C_ALA_105	NZ, C_LYS_104	HZ3, C_LYS_104	2.60	1.63	17.04
2MKL-8.PDB	O, C_VAL_32	N, C_SER_8	H, C_SER_8	2.76	1.79	7.90
2MKL-8.PDB	O, C_GLU_30	N, C_SER_10	H, C_SER_10	2.88	1.92	12.44
2MKL-8.PDB	O, C_VAL_28	N, C_LEU_12	H, C_LEU_12	2.63	1.65	4.98
2MKL-8.PDB	O, C_ALA_105	NZ, C_LYS_13	HZ2, C_LYS_13	2.61	1.57	5.41
2MKL-8.PDB	OE2, C_GLU_17	N, C_GLU_18	H, C_GLU_18	2.97	2.09	21.14
2MKL-8.PDB	O, C_LEU_72	OG1, C_THR_26	HG1, C_THR_26	2.97	2.06	16.54
2MKL-8.PDB	O, C_LEU_72	N, C_ILE_27	H, C_ILE_27	2.76	1.84	17.21
2MKL-8.PDB	O, C_SER_70	N, C_CYS_29	H, C_CYS_29	2.80	1.87	15.66
2MKL-8.PDB	O, C_SER_10	N, C_GLU_30	H, C_GLU_30	2.74	1.81	16.35
2MKL-8.PDB	O, C_ILE_68	N, C_ILE_31	H, C_ILE_31	2.87	1.90	7.35
2MKL-8.PDB	O, C_SER_8	N, C_VAL_32	H, C_VAL_32	2.73	1.75	6.64
2MKL-8.PDB	O, C_SER_64	OG, C_SER_34	HG, C_SER_34	2.72	1.87	22.15
2MKL-8.PDB	OD2, C_ASP_91	N, C_ASN_38	H, C_ASN_38	2.62	1.64	4.38
2MKL-8.PDB	O, C_GLU_37	ND2, C_ASN_38	HD21, C_ASN_38	2.58	1.65	16.81
2MKL-8.PDB	O, C_LEU_88	N, C_PHE_42	H, C_PHE_42	2.73	1.76	7.97
2MKL-8.PDB	OG, C_SER_70	NE1, C_TRP_43	HE1, C_TRP_43	2.82	1.83	2.10
2MKL-8.PDB	O, C_VAL_86	N, C_GLN_44	H, C_GLN_44	3.00	2.07	16.25
2MKL-8.PDB	O, C_VAL_48	N, C_VAL_45	H, C_VAL_45	2.73	1.82	17.50
2MKL-8.PDB	O, C_VAL_45	N, C_VAL_48	H, C_VAL_48	2.98	2.08	19.95
2MKL-8.PDB	OE2, C_GLU_78	NH1, C_ARG_50	HH12, C_ARG_50	2.63	1.62	3.58
2MKL-8.PDB	O, C_LYS_73	NH2, C_ARG_50	HH21, C_ARG_50	2.93	1.96	12.60
2MKL-8.PDB	O, C_GLU_49	NZ, C_LYS_51	HZ2, C_LYS_51	2.93	1.94	14.57
2MKL-8.PDB	O, C_LYS_71	N, C_GLU_55	H, C_GLU_55	2.75	1.82	14.98
2MKL-8.PDB	O, C_VAL_69	N, C_GLN_57	H, C_GLN_57	2.96	2.01	12.37
2MKL-8.PDB	O, C_THR_67	N, C_GLU_60	H, C_GLU_60	2.98	2.10	22.35
2MKL-8.PDB	O, C_SER_62	N, C_LYS_65	H, C_LYS_65	2.98	2.01	8.55
2MKL-8.PDB	OD2, C_ASP_6	NZ, C_LYS_65	HZ3, C_LYS_65	2.64	1.68	18.41
2MKL-8.PDB	O, C_TYR_33	N, C_SER_66	H, C_SER_66	2.73	1.81	16.99
2MKL-8.PDB	O, C_ILE_31	N, C_ILE_68	H, C_ILE_68	2.80	1.84	10.07
2MKL-8.PDB	O, C_CYS_29	N, C_SER_70	H, C_SER_70	2.86	1.88	5.47
2MKL-8.PDB	O, C_GLU_55	N, C_LYS_71	H, C_LYS_71	2.77	1.80	6.52
2MKL-8.PDB	O, C_ILE_27	N, C_LEU_72	H, C_LEU_72	2.69	1.74	12.28
2MKL-8.PDB	O, C_GLY_53	N, C_LYS_73	H, C_LYS_73	2.71	1.74	7.49
2MKL-8.PDB	O, C_ALA_25	N, C_VAL_74	H, C_VAL_74	2.97	2.03	14.41
2MKL-8.PDB	OE1, C_GLU_78	N, C_MET_75	H, C_MET_75	2.72	1.76	9.33
2MKL-8.PDB	O, C_ALA_76	N, C_ASP_80	H, C_ASP_80	2.65	1.71	13.15
2MKL-8.PDB	O, C_GLU_78	N, C_SER_81	H, C_SER_81	2.97	2.14	27.36
2MKL-8.PDB	O, C_SER_77	OG, C_SER_81	HG, C_SER_81	2.56	1.60	6.14
2MKL-8.PDB	O, C_TRP_79	N, C_GLY_82	H, C_GLY_82	2.98	2.06	16.79
2MKL-8.PDB	O, C_ALA_100	N, C_CYS_87	H, C_CYS_87	2.71	1.76	12.28
2MKL-8.PDB	O, C_PHE_42	N, C_LEU_88	H, C_LEU_88	2.77	1.80	5.62
2MKL-8.PDB	O, C_LYS_40	N, C_GLU_90	H, C_GLU_90	2.83	1.87	9.17
2MKL-8.PDB	OD1, C_ASP_91	N, C_GLU_93	H, C_GLU_93	2.62	1.67	12.30
2MKL-8.PDB	O, C_CYS_87	N, C_ALA_100	H, C_ALA_100	2.89	2.08	28.20
2MKL-8.PDB	O, C_TYR_85	N, C_ILE_102	H, C_ILE_102	2.83	1.93	19.99
2MKL-8.PDB	O, C_GLY_82	NH1, C_ARG_103	HH11, C_ARG_103	2.70	1.75	16.11
2MKL-8.PDB	OD1, C_ASP_80	NZ, C_LYS_104	HZ1, C_LYS_104	2.61	1.59	9.01
2MKL-9.PDB	OG1, C_THR_96	N, C_MET_1	H2, C_MET_1	2.76	1.75	11.34
2MKL-9.PDB	O, C_VAL_9	OG, C_SER_10	HG, C_SER_10	2.88	1.94	11.21
2MKL-9.PDB	O, C_VAL_28	N, C_LEU_12	H, C_LEU_12	2.61	1.63	7.07
2MKL-9.PDB	O, C_THR_24	N, C_THR_26	H, C_THR_26	2.89	2.03	23.40
2MKL-9.PDB	O, C_LEU_72	OG1, C_THR_26	HG1, C_THR_26	2.65	1.69	6.28
2MKL-9.PDB	O, C_LEU_72	N, C_ILE_27	H, C_ILE_27	2.89	2.04	24.93
2MKL-9.PDB	O, C_SER_70	N, C_CYS_29	H, C_CYS_29	2.74	1.78	9.84
2MKL-9.PDB	O, C_SER_10	N, C_GLU_30	H, C_GLU_30	2.88	1.91	6.77

2MKL-9.PDB	O, C_ILE_68	N, C_ILE_31	H, C_ILE_31	2.89	1.92	7.18
2MKL-9.PDB	O, C_SER_8	N, C_VAL_32	H, C_VAL_32	2.76	1.81	11.14
2MKL-9.PDB	O, C_SER_66	N, C_TYR_33	H, C_TYR_33	2.98	2.04	15.18
2MKL-9.PDB	O, C_LEU_88	N, C_PHE_42	H, C_PHE_42	2.92	1.99	16.26
2MKL-9.PDB	O, C_GLY_47	NE2, C_GLN_44	HE21, C_GLN_44	2.91	2.11	28.91
2MKL-9.PDB	O, C_VAL_48	N, C_VAL_45	H, C_VAL_45	2.81	1.87	13.63
2MKL-9.PDB	O, C_VAL_45	N, C_VAL_48	H, C_VAL_48	2.87	2.01	23.76
2MKL-9.PDB	OE2, C_GLU_78	NH2, C_ARG_50	HH22, C_ARG_50	2.68	1.69	8.63
2MKL-9.PDB	O, C_LYS_71	N, C_GLU_55	H, C_GLU_55	2.70	1.82	21.75
2MKL-9.PDB	O, C_THR_67	N, C_GLU_60	H, C_GLU_60	2.71	1.77	13.93
2MKL-9.PDB	O, C_LYS_65	N, C_SER_62	H, C_SER_62	2.85	1.92	15.49
2MKL-9.PDB	O, C_SER_62	N, C_LYS_65	H, C_LYS_65	2.77	1.83	13.89
2MKL-9.PDB	OD2, C_ASP_6	NZ, C_LYS_65	HZ2, C_LYS_65	2.75	1.71	7.05
2MKL-9.PDB	O, C_ILE_31	N, C_ILE_68	H, C_ILE_68	2.77	1.81	8.93
2MKL-9.PDB	O, C_CYS_29	N, C_SER_70	H, C_SER_70	2.85	1.87	7.34
2MKL-9.PDB	O, C_GLU_55	N, C_LYS_71	H, C_LYS_71	2.73	1.77	9.92
2MKL-9.PDB	O, C_ILE_27	N, C_LEU_72	H, C_LEU_72	2.68	1.70	5.96
2MKL-9.PDB	O, C_GLY_53	N, C_LYS_73	H, C_LYS_73	2.69	1.71	1.06
2MKL-9.PDB	O, C_ALA_76	N, C_ASP_80	H, C_ASP_80	2.94	2.03	18.41
2MKL-9.PDB	O, C_GLU_78	N, C_SER_81	H, C_SER_81	2.94	2.11	27.71
2MKL-9.PDB	O, C_TRP_79	N, C_GLY_82	H, C_GLY_82	2.94	2.01	15.71
2MKL-9.PDB	O, C_ALA_100	N, C_CYS_87	H, C_CYS_87	2.71	1.74	7.57
2MKL-9.PDB	O, C_PHE_42	N, C_LEU_88	H, C_LEU_88	2.76	1.77	3.30
2MKL-9.PDB	O, C_VAL_98	N, C_VAL_89	H, C_VAL_89	2.84	1.93	17.52
2MKL-9.PDB	OE2, C_GLU_37	OG, C_SER_92	HG, C_SER_92	3.00	2.20	28.49
2MKL-9.PDB	O, C_ASP_91	N, C_LEU_94	H, C_LEU_94	2.98	2.06	17.03
2MKL-9.PDB	O, C_CYS_87	N, C_ALA_100	H, C_ALA_100	2.97	2.14	27.19
2MKL-9.PDB	O, C_TYR_85	OG, C_SER_101	HG, C_SER_101	2.85	1.92	13.62
2MKL-9.PDB	O, C_TYR_85	N, C_ILE_102	H, C_ILE_102	2.74	1.79	13.03

Table 1679: 2MKL-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
2RLL.PDB	O, A_PRO_8	N, A_ASP_11	H, A_ASP_11	2.97	2.17	28.89

Table 1680: 2RLL-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
3SE8.PDB	OE2, G_GLU_91	NE1, G_TRP_45	HE1, G_TRP_45	2.78	2.03	24.08
3SE8.PDB	OE1, G_GLN_103	N, G_LEU_52	H, G_LEU_52	2.91	2.05	3.20
3SE8.PDB	O, G_HIS_216	N, G_ALA_55	H, G_ALA_55	2.90	2.11	20.01
3SE8.PDB	O, G_VAL_75	N, G_SER_56	H, G_SER_56	2.97	2.22	24.79
3SE8.PDB	OD1, G_ASN_67	N, G_LYS_59	H, G_LYS_59	2.79	1.96	12.33
3SE8.PDB	O, G_SER_209	N, G_VAL_65	H, G_VAL_65	2.99	2.15	12.16
3SE8.PDB	OE2, G_GLU_64	N, G_HIS_66	H, G_HIS_66	2.94	2.09	3.80
3SE8.PDB	OE2, G_GLU_64	ND1, G_HIS_66	HD1, G_HIS_66	2.82	1.98	11.41
3SE8.PDB	OE1, G_GLU_64	N, G_ASN_67	H, G_ASN_67	2.93	2.14	18.64
3SE8.PDB	OE1, G_GLU_64	ND2, G_ASN_67	HD22, G_ASN_67	2.82	2.00	14.84
3SE8.PDB	O, G_HIS_66	N, G_ALA_70	H, G_ALA_70	2.99	2.14	6.51
3SE8.PDB	O, G_ASN_67	N, G_THR_71	H, G_THR_71	2.92	2.13	19.42
3SE8.PDB	O, G_ALA_70	N, G_CYS_74	H, G_CYS_74	2.70	1.91	18.43
3SE8.PDB	O, G_CYS_54	N, G_VAL_75	H, G_VAL_75	2.88	2.07	16.86
3SE8.PDB	OD1, G_ASP_78	N, G_ASN_80	H, G_ASN_80	2.97	2.17	18.12
3SE8.PDB	O, G_SER_244	N, G_ILE_84	H, G_ILE_84	2.94	2.12	14.64
3SE8.PDB	O, G_VAL_242	N, G_LEU_86	H, G_LEU_86	2.80	1.94	0.64
3SE8.PDB	O, G_CYS_239	N, G_GLU_91	H, G_GLU_91	2.91	2.11	18.25
3SE8.PDB	O, G_GLY_237	N, G_PHE_93	H, G_PHE_93	2.87	2.06	15.53
3SE8.PDB	O, G_GLY_235	N, G_MET_95	H, G_MET_95	2.80	1.96	10.44
3SE8.PDB	O, G_ASN_94	N, G_LYS_97	H, G_LYS_97	2.95	2.11	10.82
3SE8.PDB	O, G_ASN_98	N, G_VAL_101	H, G_VAL_101	2.85	2.03	14.99
3SE8.PDB	O, G_THR_50	NE2, G_GLN_103	HE21, G_GLN_103	2.73	1.97	22.93
3SE8.PDB	OD1, G_ASN_99	NE2, G_GLN_103	HE22, G_GLN_103	2.99	2.17	14.68
3SE8.PDB	O, G_VAL_101	N, G_GLN_105	H, G_GLN_105	2.96	2.12	10.76
3SE8.PDB	O, G_MET_104	N, G_VAL_108	H, G_VAL_108	2.93	2.11	15.74
3SE8.PDB	O, G_GLN_105	N, G_ILE_109	H, G_ILE_109	2.97	2.12	7.19
3SE8.PDB	O, G_GLU_106	N, G_SER_110	H, G_SER_110	2.87	2.05	13.15
3SE8.PDB	O, G_ASP_107	N, G_LEU_111	H, G_LEU_111	2.87	2.07	18.28
3SE8.PDB	O, G_VAL_108	N, G_TRP_112	H, G_TRP_112	2.94	2.10	9.73
3SE8.PDB	O, G_ILE_109	N, G_ASP_113	H, G_ASP_113	2.91	2.13	20.04
3SE8.PDB	O, G_TRP_112	N, G_LEU_116	H, G_LEU_116	2.87	2.03	11.15
3SE8.PDB	O, G_ILE_201	N, G_LYS_121	H, G_LYS_121	2.84	2.08	23.60
3SE8.PDB	O, G_GLN_432	N, G_LEU_122	H, G_LEU_122	2.84	1.98	3.70
3SE8.PDB	OE2, G_GLU_381	NZ, G_LYS_207	HZ2, G_LYS_207	2.74	1.86	4.82
3SE8.PDB	OE2, G_GLU_64	N, G_ASP_211	H, G_ASP_211	2.86	2.06	17.85
3SE8.PDB	O, G_ILE_251	N, G_ILE_215	H, G_ILE_215	2.86	2.03	14.34
3SE8.PDB	O, G_ALA_55	N, G_HIS_216	H, G_HIS_216	2.88	2.03	9.08
3SE8.PDB	O, G_THR_248	ND1, G_HIS_216	HD1, G_HIS_216	2.90	2.07	13.28
3SE8.PDB	O, G_PHE_53	N, G_CYS_218	H, G_CYS_218	2.89	2.13	22.85
3SE8.PDB	O, G_VAL_489	N, G_VAL_224	H, G_VAL_224	2.98	2.17	16.77
3SE8.PDB	O, G_LYS_487	N, G_LEU_226	H, G_LEU_226	2.72	1.91	15.99
3SE8.PDB	O, G_SER_243	N, G_LYS_227	H, G_LYS_227	2.80	1.97	12.53
3SE8.PDB	O, G_LYS_485	N, G_CYS_228	H, G_CYS_228	2.74	1.93	16.67
3SE8.PDB	O, G_ASN_241	N, G_ASN_229	H, G_ASN_229	2.73	1.90	11.23
3SE8.PDB	O, G_GLU_91	N, G_CYS_239	H, G_CYS_239	2.59	1.79	18.72
3SE8.PDB	OD2, G_ASP_230	N, G_LYS_240	H, G_LYS_240	2.98	2.13	6.94
3SE8.PDB	OD1, G_ASP_230	N, G_ASN_241	H, G_ASN_241	2.67	1.87	17.74
3SE8.PDB	O, G_LYS_227	N, G_SER_243	H, G_SER_243	2.97	2.15	15.16
3SE8.PDB	OE2, G_GLU_83	OG, G_SER_243	HG, G_SER_243	2.64	1.83	7.57
3SE8.PDB	O, G_ILE_84	N, G_SER_244	H, G_SER_244	2.68	1.89	18.10
3SE8.PDB	O, G_ILE_225	N, G_VAL_245	H, G_VAL_245	2.90	2.07	10.51
3SE8.PDB	O, G_TYR_217	N, G_THR_248	H, G_THR_248	2.72	1.92	16.92
3SE8.PDB	OH, G_TYR_486	ND1, G_HIS_249	HD1, G_HIS_249	2.64	1.81	12.83
3SE8.PDB	OE1, G_GLU_482	NE2, G_HIS_249	HE2, G_HIS_249	3.00	2.16	9.93
3SE8.PDB	O, G_ILE_215	N, G_ILE_251	H, G_ILE_251	2.96	2.12	9.55
3SE8.PDB	O, G_HIS_375	N, G_THR_257	H, G_THR_257	2.97	2.23	26.05

3SE8.PDB	O, G_THR_257	N, G_LEU_259	H, G_LEU_259	2.81	2.06	25.63
3SE8.PDB	O, G_GLY_451	N, G_LEU_260	H, G_LEU_260	2.87	2.03	11.95
3SE8.PDB	O, G_ASN_448	N, G_ASN_262	H, G_ASN_262	2.71	1.88	12.07
3SE8.PDB	OE2, G_GLU_482	N, G_SER_264	H, G_SER_264	2.73	1.91	13.91
3SE8.PDB	O, G_LEU_288	N, G_ALA_266	H, G_ALA_266	2.78	2.00	20.85
3SE8.PDB	O, G_ILE_285	N, G_ARG_273	H, G_ARG_273	2.79	1.98	16.42
3SE8.PDB	O, G_PHE_233	NH2, G_ARG_273	HH22, G_ARG_273	2.82	2.02	18.59
3SE8.PDB	O, G_ASN_276	N, G_ASN_279	H, G_ASN_279	2.78	1.96	14.69
3SE8.PDB	OD1, G_ASN_279	N, G_ALA_281	H, G_ALA_281	2.86	2.06	17.39
3SE8.PDB	O, G_LEU_454	N, G_ILE_284	H, G_ILE_284	2.84	1.98	2.93
3SE8.PDB	O, G_ARG_273	N, G_ILE_285	H, G_ILE_285	2.70	1.87	12.33
3SE8.PDB	O, G_ILE_452	N, G_VAL_286	H, G_VAL_286	2.88	2.04	10.30
3SE8.PDB	O, G_ILE_271	N, G_HIS_287	H, G_HIS_287	2.82	1.96	3.43
3SE8.PDB	O, G_SER_264	NE2, G_HIS_287	HE2, G_HIS_287	2.67	1.83	10.99
3SE8.PDB	O, G_SER_447	N, G_ILE_294	H, G_ILE_294	2.75	1.94	17.22
3SE8.PDB	O, G_GLU_332	N, G_ASN_295	H, G_ASN_295	2.93	2.13	18.46
3SE8.PDB	O, G_TYR_330	N, G_THR_297	H, G_THR_297	2.85	2.02	13.88
3SE8.PDB	O, G_ILE_443	N, G_ARG_298	H, G_ARG_298	2.74	1.91	12.06
3SE8.PDB	O, G_ILE_326	NH1, G_ARG_298	HH11, G_ARG_298	2.83	2.00	11.83
3SE8.PDB	O, G_GLY_441	NH2, G_ARG_298	HH21, G_ARG_298	2.55	1.70	4.64
3SE8.PDB	O, G_ILE_439	NH2, G_ARG_298	HH22, G_ARG_298	2.90	2.10	18.34
3SE8.PDB	O, G_CYS_418	N, G_ALA_329	H, G_ALA_329	2.90	2.06	11.88
3SE8.PDB	O, G_LEU_416	N, G_CYS_331	H, G_CYS_331	2.98	2.19	20.31
3SE8.PDB	O, G_ASN_295	N, G_GLU_332	H, G_GLU_332	2.74	1.92	15.11
3SE8.PDB	O, G_ILE_414	N, G_ILE_333	H, G_ILE_333	2.90	2.08	15.80
3SE8.PDB	O, G_GLY_412	N, G_GLY_335	H, G_GLY_335	2.61	1.86	25.24
3SE8.PDB	OD1, G_ASN_334	N, G_LYS_337	H, G_LYS_337	2.85	2.02	13.75
3SE8.PDB	O, G_ASN_334	N, G_TRP_338	H, G_TRP_338	2.85	2.04	16.18
3SE8.PDB	O, G_LEU_390	NE1, G_TRP_338	HE1, G_TRP_338	2.58	1.76	15.13
3SE8.PDB	O, G_GLY_335	N, G_ASN_339	H, G_ASN_339	2.74	1.88	4.81
3SE8.PDB	O, G_TRP_338	N, G_LEU_342	H, G_LEU_342	2.77	1.94	11.71
3SE8.PDB	O, G_VAL_341	N, G_VAL_345	H, G_VAL_345	2.89	2.13	23.16
3SE8.PDB	O, G_LEU_342	N, G_THR_346	H, G_THR_346	2.94	2.12	14.67
3SE8.PDB	O, G_LYS_343	OG1, G_THR_346	HG1, G_THR_346	2.65	1.92	23.05
3SE8.PDB	O, G_LYS_343	N, G_GLU_347	H, G_GLU_347	3.00	2.22	21.50
3SE8.PDB	O, G_GLN_344	N, G_LYS_348	H, G_LYS_348	2.99	2.19	18.12
3SE8.PDB	OE2, G_GLU_269	NZ, G_LYS_348	HZ1, G_LYS_348	2.90	2.14	25.94
3SE8.PDB	OE1, G_GLU_351	NZ, G_LYS_348	HZ3, G_LYS_348	2.96	2.10	14.00
3SE8.PDB	O, G_VAL_345	N, G_LEU_349	H, G_LEU_349	2.94	2.12	15.13
3SE8.PDB	O, G_LYS_350	N, G_ASN_355	H, G_ASN_355	2.97	2.13	9.29
3SE8.PDB	O, G_PHE_353	N, G_LYS_357	H, G_LYS_357	2.81	1.95	2.88
3SE8.PDB	OD1, G_ASN_393	N, G_PHE_361	H, G_PHE_361	2.89	2.04	5.90
3SE8.PDB	O, G_PHE_468	N, G_GLN_362	H, G_GLN_362	2.83	2.01	15.06
3SE8.PDB	O, H_TRP_54	N, G_ASP_368	H, G_ASP_368	2.75	1.91	10.72
3SE8.PDB	O, G_LEU_369	N, G_MET_373	H, G_MET_373	3.00	2.23	22.44
3SE8.PDB	O, G_CYS_385	N, G_HIS_374	H, G_HIS_374	2.81	2.03	21.55
3SE8.PDB	O, G_THR_257	ND1, G_HIS_374	HD1, G_HIS_374	2.91	2.06	7.53
3SE8.PDB	O, G_PHE_383	ND1, G_HIS_375	HD1, G_HIS_375	2.96	2.19	22.53
3SE8.PDB	O, G_GLU_381	N, G_CYS_378	H, G_CYS_378	2.90	2.12	21.09
3SE8.PDB	O, G_CYS_378	N, G_GLU_381	H, G_GLU_381	2.88	2.03	7.72
3SE8.PDB	O, G_PHE_376	N, G_PHE_383	H, G_PHE_383	2.77	1.95	13.43
3SE8.PDB	O, G_HIS_374	N, G_CYS_385	H, G_CYS_385	2.80	1.98	13.95
3SE8.PDB	OD1, G_ASN_386	N, G_THR_388	H, G_THR_388	2.94	2.09	9.87
3SE8.PDB	O, G_THR_387	N, G_LEU_390	H, G_LEU_390	2.83	2.03	19.01
3SE8.PDB	O, G_PHE_361	ND2, G_ASN_393	HD22, G_ASN_393	2.82	1.99	12.21
3SE8.PDB	OD1, G_ASN_392	N, G_THR_394	H, G_THR_394	2.97	2.24	26.64
3SE8.PDB	O, G_ILE_333	N, G_ILE_414	H, G_ILE_414	2.79	2.00	18.93
3SE8.PDB	O, G_CYS_331	N, G_LEU_416	H, G_LEU_416	2.80	2.05	24.46

3SE8.PDB	O, G_ALA_329	N, G_CYS_418	H, G_CYS_418	2.89	2.04	8.98
3SE8.PDB	O, G_TYR_384	N, G_LYS_419	H, G_LYS_419	2.92	2.14	22.08
3SE8.PDB	O, G_ARG_327	N, G_ILE_420	H, G_ILE_420	2.82	2.00	14.23
3SE8.PDB	O, G_ALA_433	N, G_ILE_424	H, G_ILE_424	2.88	2.06	14.47
3SE8.PDB	OE2, G_GLU_370	N, G_ASN_425	H, G_ASN_425	2.74	1.89	6.23
3SE8.PDB	O, G_GLY_431	N, G_MET_426	H, G_MET_426	2.76	1.90	1.16
3SE8.PDB	O, G_MET_426	N, G_GLY_429	H, G_GLY_429	2.90	2.07	12.32
3SE8.PDB	O, G_ILE_424	N, G_ALA_433	H, G_ALA_433	2.84	2.01	13.80
3SE8.PDB	O, G_VAL_120	N, G_MET_434	H, G_MET_434	2.89	2.08	16.32
3SE8.PDB	O, G_GLN_422	N, G_TYR_435	H, G_TYR_435	2.70	1.89	15.98
3SE8.PDB	OD1, G_ASN_295	ND2, G_ASN_444	HD21, G_ASN_444	2.87	2.12	25.11
3SE8.PDB	OG1, G_THR_297	ND2, G_ASN_444	HD22, G_ASN_444	2.77	1.99	20.73
3SE8.PDB	O, G_ILE_294	N, G_SER_447	H, G_SER_447	2.93	2.10	11.64
3SE8.PDB	O, G_LEU_260	N, G_THR_450	H, G_THR_450	2.91	2.08	13.27
3SE8.PDB	O, G_VAL_286	N, G_ILE_452	H, G_ILE_452	3.00	2.20	19.52
3SE8.PDB	O, G_GLN_258	N, G_LEU_453	H, G_LEU_453	2.85	2.00	5.65
3SE8.PDB	O, G_ILE_284	N, G_LEU_454	H, G_LEU_454	2.99	2.16	13.70
3SE8.PDB	O, G_ARG_469	N, G_THR_455	H, G_THR_455	2.90	2.07	11.48
3SE8.PDB	O, G_THR_467	N, G_ASP_457	H, G_ASP_457	2.94	2.11	12.90
3SE8.PDB	OE2, L_GLU_96	N, G_GLY_459	H, G_GLY_459	2.81	1.99	15.35
3SE8.PDB	O, G_THR_358	N, G_GLU_466	H, G_GLU_466	2.85	2.09	22.90
3SE8.PDB	O, G_ILE_360	N, G_PHE_468	H, G_PHE_468	2.81	2.00	17.29
3SE8.PDB	O, G_THR_455	N, G_ARG_469	H, G_ARG_469	2.91	2.11	19.07
3SE8.PDB	OD2, G_ASP_457	NE, G_ARG_469	HE, G_ARG_469	2.90	2.06	8.93
3SE8.PDB	O, G_PRO_363	NH1, G_ARG_469	HH11, G_ARG_469	2.85	2.03	15.65
3SE8.PDB	OD1, G_ASP_457	NH2, G_ARG_469	HH21, G_ARG_469	2.93	2.11	16.29
3SE8.PDB	O, G_ASN_474	N, G_ASP_477	H, G_ASP_477	2.86	2.03	13.09
3SE8.PDB	OE1, G_GLN_105	NE1, G_TRP_479	HE1, G_TRP_479	2.68	1.92	22.70
3SE8.PDB	O, G_LYS_476	N, G_ARG_480	H, G_ARG_480	2.90	2.07	12.50
3SE8.PDB	O, G_ASP_477	N, G_SER_481	H, G_SER_481	2.99	2.24	26.03
3SE8.PDB	O, G_TRP_479	N, G_LEU_483	H, G_LEU_483	2.88	2.12	23.01
3SE8.PDB	O, G_LEU_226	N, G_LYS_487	H, G_LYS_487	2.94	2.15	19.58
3SE8.PDB	OE1, G_GLU_91	NZ, G_LYS_487	HZ1, G_LYS_487	2.58	1.77	20.55
3SE8.PDB	OD1, G_ASP_47	NZ, G_LYS_487	HZ2, G_LYS_487	2.90	2.08	19.02
3SE8.PDB	O, G_ASN_92	NZ, G_LYS_487	HZ3, G_LYS_487	2.95	2.08	10.80
3SE8.PDB	O, G_VAL_224	N, G_VAL_489	H, G_VAL_489	2.91	2.06	7.65
3SE8.PDB	O, G_LYS_46	N, G_GLN_490	H, G_GLN_490	2.88	2.05	12.76
3SE8.PDB	O, H_SER_25	N, H_GLN_3	H, H_GLN_3	2.90	2.11	20.10
3SE8.PDB	O, H_ARG_23	N, H_VAL_5	H, H_VAL_5	2.88	2.06	15.74
3SE8.PDB	OE1, H_GLN_105	N, H_GLN_6	H, H_GLN_6	2.87	2.02	5.14
3SE8.PDB	O, H_TYR_90	NE2, H_GLN_6	HE22, H_GLN_6	2.89	2.04	7.71
3SE8.PDB	O, H_VAL_110	N, H_LYS_12	H, H_LYS_12	2.75	1.91	10.56
3SE8.PDB	O, H_LEU_82C	N, H_GLY_15	H, H_GLY_15	2.89	2.09	17.72
3SE8.PDB	O, H_THR_13	N, H_SER_16	H, H_SER_16	2.97	2.16	15.50
3SE8.PDB	O, H_PHE_82	N, H_VAL_18	H, H_VAL_18	2.79	1.98	16.37
3SE8.PDB	O, H_MET_80	N, H_ILE_20	H, H_ILE_20	2.76	1.91	7.97
3SE8.PDB	O, H_ALA_78	N, H_CYS_22	H, H_CYS_22	2.72	2.02	29.24
3SE8.PDB	O, H_VAL_5	N, H_ARG_23	H, H_ARG_23	2.79	1.98	14.71
3SE8.PDB	O, H_GLY_76G	N, H_ALA_24	H, H_ALA_24	2.79	1.93	5.97
3SE8.PDB	O, H_GLN_3	N, H_SER_25	H, H_SER_25	2.94	2.16	21.94
3SE8.PDB	O, H_ASP_76E	N, H_PHE_29	H, H_PHE_29	2.78	1.95	13.33
3SE8.PDB	O, H_ILE_51	N, H_ILE_34	H, H_ILE_34	3.00	2.20	18.68
3SE8.PDB	O, H_VAL_93	N, H_HIS_35	H, H_HIS_35	2.89	2.07	13.75
3SE8.PDB	O, H_GLY_49	N, H_TRP_36	H, H_TRP_36	2.94	2.13	16.16
3SE8.PDB	O, H_PHE_91	N, H_VAL_37	H, H_VAL_37	2.86	2.04	15.75
3SE8.PDB	O, H_GLU_46	N, H_ARG_38	H, H_ARG_38	2.88	2.04	10.56
3SE8.PDB	OE1, H_GLU_46	NH1, H_ARG_38	HH11, H_ARG_38	2.64	1.78	1.94
3SE8.PDB	OH, H_TYR_90	NH2, H_ARG_38	HH21, H_ARG_38	2.79	1.95	9.66

3SE8.PDB	OD1, H_ASP_86	NH2, H_ARG_38	HH22, H_ARG_38	2.67	1.83	8.41
3SE8.PDB	O, H_GLU_89	N, H_LEU_39	H, H_LEU_39	2.83	1.99	10.37
3SE8.PDB	O, H_GLY_44	N, H_ILE_40	H, H_ILE_40	2.78	1.93	4.45
3SE8.PDB	O, H_ILE_40	N, H_LYS_43	H, H_LYS_43	2.97	2.13	10.43
3SE8.PDB	O, H_ILE_40	N, H_GLY_44	H, H_GLY_44	2.89	2.10	18.47
3SE8.PDB	O, H_ARG_38	N, H_GLU_46	H, H_GLU_46	2.75	1.95	18.36
3SE8.PDB	O, H_TRP_36	N, H_ILE_48	H, H_ILE_48	2.84	1.99	6.89
3SE8.PDB	O, H_SER_58	N, H_TRP_50	H, H_TRP_50	2.96	2.22	26.23
3SE8.PDB	OD1, G_ASN_280	NE1, H_TRP_50	HE1, H_TRP_50	3.00	2.21	20.49
3SE8.PDB	O, H_ILE_34	N, H_ILE_51	H, H_ILE_51	2.93	2.15	20.77
3SE8.PDB	O, H_ALA_56	N, H_LYS_52	H, H_LYS_52	2.80	1.97	14.43
3SE8.PDB	O, G_GLY_473	NE1, H_TRP_54	HE1, H_TRP_54	2.82	1.98	10.03
3SE8.PDB	O, H_ILE_48	N, H_ALA_60	H, H_ALA_60	2.88	2.02	4.64
3SE8.PDB	O, G_GLY_458	N, H_ARG_61	H, H_ARG_61	2.91	2.08	12.24
3SE8.PDB	OE2, H_GLU_46	NE2, H_GLN_62	HE21, H_GLN_62	2.91	2.06	7.60
3SE8.PDB	O, H_ALA_60	N, H_LEU_63	H, H_LEU_63	2.83	1.99	9.80
3SE8.PDB	OD1, G_ASP_457	NE2, H_GLN_64	HE22, H_GLN_64	2.94	2.12	14.23
3SE8.PDB	O, H_LEU_63	N, H_ARG_66	H, H_ARG_66	2.92	2.10	15.21
3SE8.PDB	OD2, H_ASP_86	NH2, H_ARG_66	HH22, H_ARG_66	2.60	1.84	23.72
3SE8.PDB	O, H_GLU_81	N, H_SER_68	H, H_SER_68	2.93	2.16	21.80
3SE8.PDB	OH, H_TYR_59	N, H_MET_69	H, H_MET_69	2.92	2.08	11.45
3SE8.PDB	O, H_PRO_52A	NE, H_ARG_71	HE, H_ARG_71	2.71	2.00	28.51
3SE8.PDB	OD2, G_ASP_368	NH2, H_ARG_71	HH22, H_ARG_71	2.91	2.05	6.24
3SE8.PDB	O, H_VAL_77	N, H_GLN_72	H, H_GLN_72	2.77	1.96	16.92
3SE8.PDB	O, H_ASP_76C	OG, H_SER_74	HG, H_SER_74	2.69	1.89	9.03
3SE8.PDB	O, H_GLN_72	N, H_VAL_77	H, H_VAL_77	2.77	1.94	13.20
3SE8.PDB	O, H_CYS_22	N, H_ALA_78	H, H_ALA_78	2.93	2.10	11.74
3SE8.PDB	O, H_THR_70	N, H_TYR_79	H, H_TYR_79	2.81	1.96	9.20
3SE8.PDB	O, H_ILE_20	N, H_MET_80	H, H_MET_80	2.83	2.02	15.19
3SE8.PDB	O, H_SER_68	N, H_GLU_81	H, H_GLU_81	2.84	2.00	11.16
3SE8.PDB	O, H_VAL_18	N, H_PHE_82	H, H_PHE_82	2.77	1.96	15.74
3SE8.PDB	O, H_ARG_66	N, H_SER_82A	H, H_SER_82A	2.80	2.01	18.90
3SE8.PDB	OD2, H_ASP_86	N, H_THR_83	H, H_THR_83	2.93	2.13	19.14
3SE8.PDB	O, H_THR_83	N, H_ASP_86	H, H_ASP_86	2.81	1.97	9.27
3SE8.PDB	O, H_PRO_84	N, H_THR_87	H, H_THR_87	2.98	2.14	8.29
3SE8.PDB	O, H_THR_107	N, H_TYR_90	H, H_TYR_90	2.78	1.92	6.22
3SE8.PDB	O, H_VAL_37	N, H_PHE_91	H, H_PHE_91	2.68	1.83	4.53
3SE8.PDB	O, H_HIS_35	N, H_VAL_93	H, H_VAL_93	2.86	2.07	20.12
3SE8.PDB	O, H_TYR_102	N, H_ARG_94	H, H_ARG_94	2.96	2.18	21.24
3SE8.PDB	O, H_ARG_95	NE, H_ARG_94	HE, H_ARG_94	2.79	1.97	14.73
3SE8.PDB	OH, L_TYR_36	N, H_TRP_100F	H, H_TRP_100F	2.89	2.04	6.32
3SE8.PDB	O, H_CYS_92	N, H_CYS_104	H, H_CYS_104	2.93	2.08	5.94
3SE8.PDB	O, H_TYR_90	N, H_THR_107	H, H_THR_107	2.73	1.94	19.33
3SE8.PDB	O, H_ALA_88	N, H_VAL_109	H, H_VAL_109	2.95	2.10	5.90
3SE8.PDB	O, H_LYS_12	N, H_SER_112	H, H_SER_112	2.88	2.11	21.39
3SE8.PDB	OG, H_SER_112	N, H_ALA_114	H, H_ALA_114	2.93	2.08	8.21
3SE8.PDB	O, H_PHE_146	N, H_LYS_117	H, H_LYS_117	2.70	1.88	13.27
3SE8.PDB	O, H_ASP_144	NZ, H_LYS_117	HZ2, H_LYS_117	2.77	2.03	28.12
3SE8.PDB	O, H_LYS_143	N, H_SER_120	H, H_SER_120	2.76	1.96	18.99
3SE8.PDB	O, H_LEU_141	N, H_PHE_122	H, H_PHE_122	2.84	2.01	11.61
3SE8.PDB	O, H_GLY_139	N, H_LEU_124	H, H_LEU_124	2.75	1.90	4.08
3SE8.PDB	O, H_VAL_184	N, H_ALA_136	H, H_ALA_136	2.84	2.00	9.22
3SE8.PDB	O, H_LEU_124	N, H_GLY_139	H, H_GLY_139	2.85	2.13	28.46
3SE8.PDB	O, H_SER_180	N, H_CYS_140	H, H_CYS_140	2.74	1.94	18.37
3SE8.PDB	O, H_PHE_122	N, H_LEU_141	H, H_LEU_141	2.66	1.82	9.87
3SE8.PDB	O, H_LEU_178	N, H_VAL_142	H, H_VAL_142	2.68	1.85	13.60
3SE8.PDB	O, H_SER_120	N, H_LYS_143	H, H_LYS_143	2.76	1.90	5.34
3SE8.PDB	O, H_LYS_117	N, H_PHE_146	H, H_PHE_146	2.83	2.03	17.73

3SE8.PDB	O, H.ASN.199	N, H.THR.151	H, H.THR.151	2.89	2.07	15.54
3SE8.PDB	O, H.ASN.197	N, H.SER.153	H, H.SER.153	2.93	2.14	19.75
3SE8.PDB	OG, H.SER.180	NE1, H.TRP.154	HE1, H.TRP.154	2.94	2.09	7.62
3SE8.PDB	O, H.ILE.195	N, H.ASN.155	H, H.ASN.155	2.71	1.87	10.52
3SE8.PDB	OD1, H.ASN.197	N, H.SER.156	H, H.SER.156	2.66	1.83	13.48
3SE8.PDB	O, H.TRP.154	N, H.GLY.157	H, H.GLY.157	2.82	2.03	19.36
3SE8.PDB	O, H.VAL.181	N, H.HIS.164	H, H.HIS.164	2.78	1.96	13.60
3SE8.PDB	O, H.SER.179	N, H.PHE.166	H, H.PHE.166	2.99	2.15	9.97
3SE8.PDB	O, H.SER.177	N, H.VAL.169	H, H.VAL.169	2.82	1.98	12.77
3SE8.PDB	O, H.LEU.175	N, H.GLN.171	H, H.GLN.171	2.92	2.07	8.88
3SE8.PDB	OD1, H.ASP.144	NE2, H.GLN.171	HE22, H.GLN.171	2.79	1.98	16.20
3SE8.PDB	O, H.GLN.171	N, H.GLY.174	H, H.GLY.174	2.99	2.14	9.14
3SE8.PDB	O, H.TYR.145	N, H.TYR.176	H, H.TYR.176	2.78	1.96	14.03
3SE8.PDB	O, H.VAL.169	N, H.SER.177	H, H.SER.177	2.95	2.22	27.00
3SE8.PDB	O, H.VAL.142	N, H.LEU.178	H, H.LEU.178	2.89	2.07	14.62
3SE8.PDB	O, H.CYS.140	N, H.SER.180	H, H.SER.180	2.90	2.08	15.09
3SE8.PDB	O, H.HIS.164	N, H.VAL.181	H, H.VAL.181	2.92	2.09	11.34
3SE8.PDB	O, H.LEU.138	N, H.VAL.182	H, H.VAL.182	2.88	2.09	19.86
3SE8.PDB	O, H.ALA.136	N, H.VAL.184	H, H.VAL.184	2.91	2.10	16.13
3SE8.PDB	O, H.SER.188	N, H.GLN.192	H, H.GLN.192	2.74	1.90	10.09
3SE8.PDB	OD1, H.ASN.155	N, H.ILE.195	H, H.ILE.195	2.81	2.01	16.89
3SE8.PDB	O, H.LYS.209	N, H.CYS.196	H, H.CYS.196	2.96	2.16	17.85
3SE8.PDB	O, H.SER.153	N, H.ASN.197	H, H.ASN.197	2.75	1.91	9.58
3SE8.PDB	O, H.VAL.207	N, H.VAL.198	H, H.VAL.198	2.77	1.92	5.89
3SE8.PDB	O, H.THR.151	N, H.ASN.199	H, H.ASN.199	2.84	2.01	12.61
3SE8.PDB	O, H.THR.205	N, H.HIS.200	H, H.HIS.200	2.70	1.84	5.53
3SE8.PDB	OG, H.SER.203	ND1, H.HIS.200	HD1, H.HIS.200	2.45	1.61	10.75
3SE8.PDB	O, H.PRO.147	NE2, H.HIS.200	HE2, H.HIS.200	2.78	1.97	17.41
3SE8.PDB	O, H.LYS.201	N, H.ASN.204	H, H.ASN.204	2.85	2.06	18.91
3SE8.PDB	O, H.HIS.200	N, H.THR.205	H, H.THR.205	2.88	2.03	7.09
3SE8.PDB	O, H.VAL.198	N, H.VAL.207	H, H.VAL.207	2.80	1.98	15.00
3SE8.PDB	O, H.CYS.196	N, H.LYS.209	H, H.LYS.209	2.95	2.10	10.01
3SE8.PDB	O, H.TYR.194	N, H.VAL.211	H, H.VAL.211	2.83	1.97	6.68
3SE8.PDB	OG, L.SER.26	N, L.VAL.3	H, L.VAL.3	2.82	1.96	2.57
3SE8.PDB	O, L.LYS.24	N, L.THR.5	H, L.THR.5	2.89	2.05	11.05
3SE8.PDB	O, L.TYR.86	NE2, L.GLN.6	HE22, L.GLN.6	2.87	2.04	13.32
3SE8.PDB	O, L.GLU.103	N, L.LEU.11	H, L.LEU.11	2.80	1.97	11.47
3SE8.PDB	OE1, L.GLU.17	N, L.SER.14	H, L.SER.14	2.71	1.87	8.08
3SE8.PDB	O, L.LEU.78	N, L.GLY.16	H, L.GLY.16	2.93	2.19	25.85
3SE8.PDB	O, L.ILE.75	N, L.ALA.19	H, L.ALA.19	2.95	2.15	18.92
3SE8.PDB	O, L.LEU.73	N, L.LEU.21	H, L.LEU.21	2.86	2.04	13.81
3SE8.PDB	O, L.SER.7	N, L.PHE.22	H, L.PHE.22	2.87	2.02	8.84
3SE8.PDB	O, L.PHE.71	N, L.CYS.23	H, L.CYS.23	2.82	2.00	14.57
3SE8.PDB	O, L.THR.5	N, L.LYS.24	H, L.LYS.24	2.96	2.11	8.02
3SE8.PDB	OD1, L.ASP.70	NZ, L.LYS.24	HZ3, L.LYS.24	2.62	1.80	18.41
3SE8.PDB	O, L.THR.69	N, L.ALA.25	H, L.ALA.25	2.86	2.08	21.04
3SE8.PDB	OG1, L.THR.51	N, L.MET.33	H, L.MET.33	2.91	2.13	21.08
3SE8.PDB	O, L.ILE.48	N, L.TRP.35	H, L.TRP.35	2.90	2.11	18.66
3SE8.PDB	O, L.TYR.87	N, L.TYR.36	H, L.TYR.36	2.80	1.98	13.67
3SE8.PDB	O, L.ARG.45	N, L.GLN.37	H, L.GLN.37	2.76	1.94	13.35
3SE8.PDB	OH, L.TYR.86	NE2, L.GLN.37	HE21, L.GLN.37	2.98	2.15	12.85
3SE8.PDB	O, L.VAL.85	N, L.LYS.38	H, L.LYS.38	2.76	1.91	8.80
3SE8.PDB	O, L.ARG.39	N, L.GLN.42	H, L.GLN.42	2.97	2.15	14.92
3SE8.PDB	O, L.GLN.37	N, L.ARG.45	H, L.ARG.45	2.81	2.02	18.98
3SE8.PDB	O, L.TRP.35	N, L.LEU.47	H, L.LEU.47	2.85	1.99	4.76
3SE8.PDB	O, L.ARG.53	N, L.TYR.49	H, L.TYR.49	2.85	2.04	17.02
3SE8.PDB	O, L.MET.33	N, L.THR.51	H, L.THR.51	2.77	1.98	19.97
3SE8.PDB	O, L.ASP.50	N, L.SER.52	H, L.SER.52	2.85	2.14	29.05

3SE8.PDB	O, L.TYR_49	N, L.ARG_53	H, L.ARG_53	2.91	2.09	16.37
3SE8.PDB	OD2, L.ASP_50	NE, L.ARG_53	HE, L.ARG_53	2.87	2.02	8.47
3SE8.PDB	O, L.VAL_58	NH1, L.ARG_54	HH11, L.ARG_54	2.73	1.98	24.33
3SE8.PDB	O, L.LEU_47	N, L.ALA_55	H, L.ALA_55	2.80	1.97	13.40
3SE8.PDB	OE1, H.GLN_101	N, L.SER_56	H, L.SER_56	2.97	2.12	7.63
3SE8.PDB	OD2, L.ASP_82	NE, L.ARG_61	HE, L.ARG_61	2.91	2.18	26.35
3SE8.PDB	OD1, L.ASP_82	NH2, L.ARG_61	HH21, L.ARG_61	2.77	1.91	2.48
3SE8.PDB	O, L.THR_74	N, L.VAL_63	H, L.VAL_63	2.77	1.99	20.80
3SE8.PDB	O, L.ASP_70	N, L.SER_67	H, L.SER_67	2.93	2.14	19.36
3SE8.PDB	O, L.CYS_23	N, L.PHE_71	H, L.PHE_71	2.87	2.10	23.31
3SE8.PDB	O, L.SER_65	N, L.PHE_72	H, L.PHE_72	2.87	2.05	15.57
3SE8.PDB	O, L.LEU_21	N, L.LEU_73	H, L.LEU_73	2.88	2.10	20.44
3SE8.PDB	O, L.VAL_63	N, L.THR_74	H, L.THR_74	2.77	1.92	5.55
3SE8.PDB	O, L.ALA_19	N, L.ILE_75	H, L.ILE_75	2.87	2.05	14.86
3SE8.PDB	O, L.ARG_61	N, L.ASN_76	H, L.ASN_76	2.80	1.97	11.69
3SE8.PDB	O, L.GLU_17	N, L.LEU_78	H, L.LEU_78	2.85	2.02	13.66
3SE8.PDB	OD2, L.ASP_82	N, L.ASP_79	H, L.ASP_79	2.69	1.83	4.70
3SE8.PDB	OD2, L.ASP_79	N, L.GLU_81	H, L.GLU_81	2.90	2.04	2.10
3SE8.PDB	O, L.ASP_79	N, L.ASP_82	H, L.ASP_82	2.84	2.00	9.57
3SE8.PDB	O, L.SER_102	N, L.TYR_86	H, L.TYR_86	2.84	2.02	14.87
3SE8.PDB	O, L.TYR_36	N, L.TYR_87	H, L.TYR_87	2.95	2.14	16.13
3SE8.PDB	O, L.THR_34	N, L.GLN_89	H, L.GLN_89	2.91	2.20	29.11
3SE8.PDB	O, L.PHE_97	N, L.GLN_90	H, L.GLN_90	2.96	2.20	22.66
3SE8.PDB	O, L.GLN_90	N, L.PHE_97	H, L.PHE_97	2.91	2.07	11.26
3SE8.PDB	O, L.CYS_88	N, L.GLY_99	H, L.GLY_99	2.90	2.07	12.93
3SE8.PDB	OE1, L.GLN_6	N, L.GLY_101	H, L.GLY_101	2.82	2.11	29.29
3SE8.PDB	O, L.TYR_86	N, L.SER_102	H, L.SER_102	2.87	2.06	17.39
3SE8.PDB	O, L.GLY_9	N, L.GLU_103	H, L.GLU_103	2.90	2.06	7.87
3SE8.PDB	O, L.ALA_84	N, L.LEU_104	H, L.LEU_104	2.85	2.00	5.96
3SE8.PDB	O, L.LEU_11	N, L.GLU_105	H, L.GLU_105	2.77	1.92	5.93
3SE8.PDB	O, L.LEU_13	N, L.HIS_107	H, L.HIS_107	2.81	1.97	8.56
3SE8.PDB	O, L.THR_109	NE, L.ARG_108	HE, L.ARG_108	2.88	2.04	10.14
3SE8.PDB	O, L.ASP_170	NH1, L.ARG_108	HH11, L.ARG_108	2.96	2.12	9.70
3SE8.PDB	O, L.TYR_140	N, L.ALA_111	H, L.ALA_111	2.78	1.95	13.81
3SE8.PDB	O, L.LEU_135	N, L.PHE_116	H, L.PHE_116	2.96	2.16	19.15
3SE8.PDB	O, L.VAL_133	N, L.PHE_118	H, L.PHE_118	2.81	2.01	18.69
3SE8.PDB	OG, L.SER_131	NE2, L.GLN_124	HE22, L.GLN_124	2.53	1.70	11.07
3SE8.PDB	O, L.ASP_122	N, L.LYS_126	H, L.LYS_126	2.78	1.93	8.17
3SE8.PDB	O, L.GLN_124	N, L.SER_127	H, L.SER_127	2.84	2.04	18.54
3SE8.PDB	O, L.LEU_125	N, L.GLY_128	H, L.GLY_128	2.82	1.97	6.06
3SE8.PDB	O, L.LEU_181	N, L.ALA_130	H, L.ALA_130	2.63	1.79	9.50
3SE8.PDB	OE1, L.GLN_124	N, L.SER_131	H, L.SER_131	2.86	2.08	21.14
3SE8.PDB	O, L.LEU_179	N, L.VAL_132	H, L.VAL_132	2.81	1.96	9.07
3SE8.PDB	O, L.SER_177	N, L.CYS_134	H, L.CYS_134	2.82	1.99	11.76
3SE8.PDB	O, L.PHE_116	N, L.LEU_135	H, L.LEU_135	2.83	2.00	13.84
3SE8.PDB	O, L.LEU_175	N, L.LEU_136	H, L.LEU_136	2.76	1.91	3.24
3SE8.PDB	O, L.SER_114	N, L.ASN_137	H, L.ASN_137	2.82	1.98	11.18
3SE8.PDB	O, L.TYR_173	N, L.PHE_139	H, L.PHE_139	2.79	1.99	16.94
3SE8.PDB	O, L.ALA_111	N, L.TYR_140	H, L.TYR_140	2.99	2.17	14.53
3SE8.PDB	OE2, L.GLU_103	NH2, L.ARG_142	HH22, L.ARG_142	2.84	2.00	11.39
3SE8.PDB	O, L.THR_197	N, L.LYS_145	H, L.LYS_145	2.99	2.15	9.49
3SE8.PDB	O, L.GLU_195	N, L.GLN_147	H, L.GLN_147	2.92	2.09	11.46
3SE8.PDB	OE1, L.GLU_195	NE2, L.GLN_147	HE21, L.GLN_147	2.66	1.93	26.32
3SE8.PDB	OG, L.SER_177	NE1, L.TRP_148	HE1, L.TRP_148	2.88	2.08	18.18
3SE8.PDB	O, L.ALA_193	N, L.LYS_149	H, L.LYS_149	2.82	1.98	10.28
3SE8.PDB	O, L.ALA_153	N, L.VAL_150	H, L.VAL_150	2.96	2.16	18.37
3SE8.PDB	O, L.VAL_191	N, L.ASP_151	H, L.ASP_151	2.77	1.95	13.90
3SE8.PDB	O, L.TRP_148	N, L.GLN_155	H, L.GLN_155	2.82	1.99	12.31

3SE8.PDB	O, L_ALA_153	NE2, L_GLN_155	HE21, L_GLN_155	2.94	2.12	14.25
3SE8.PDB	O, L_SER_176	N, L_SER_162	H, L_SER_162	2.99	2.21	20.46
3SE8.PDB	O, H_PRO_167	OG, L_SER_162	HG, L_SER_162	2.71	1.98	23.05
3SE8.PDB	O, L_SER_174	N, L_THR_164	H, L_THR_164	2.92	2.10	13.88
3SE8.PDB	O, L_SER_171	NE2, L_GLN_166	HE21, L_GLN_166	2.94	2.11	13.32
3SE8.PDB	O, L_VAL_106	NE2, L_GLN_166	HE22, L_GLN_166	2.84	2.02	15.85
3SE8.PDB	O, L_THR_172	N, L_ASP_167	H, L_ASP_167	2.84	1.99	3.58
3SE8.PDB	OD2, L_ASP_167	N, L_LYS_169	H, L_LYS_169	2.88	2.07	16.82
3SE8.PDB	OD2, L_ASP_167	N, L_ASP_170	H, L_ASP_170	2.87	2.05	15.65
3SE8.PDB	OD1, L_ASP_170	N, L_THR_172	H, L_THR_172	2.93	2.11	15.74
3SE8.PDB	OD1, L_ASP_170	OG1, L_THR_172	HG1, L_THR_172	2.49	1.68	7.38
3SE8.PDB	O, L_PHE_139	N, L_TYR_173	H, L_TYR_173	2.84	2.00	11.94
3SE8.PDB	OG1, L_THR_164	N, L_SER_174	H, L_SER_174	2.99	2.17	15.57
3SE8.PDB	O, L_LEU_136	N, L_LEU_175	H, L_LEU_175	2.83	2.02	17.07
3SE8.PDB	O, L_SER_162	N, L_SER_176	H, L_SER_176	2.98	2.17	16.25
3SE8.PDB	O, L_CYS_134	N, L_SER_177	H, L_SER_177	2.87	2.05	14.69
3SE8.PDB	O, L_GLN_160	N, L_THR_178	H, L_THR_178	2.92	2.11	17.07
3SE8.PDB	O, L_VAL_132	N, L_LEU_179	H, L_LEU_179	2.77	2.01	22.55
3SE8.PDB	O, L_ASN_158	N, L_THR_180	H, L_THR_180	2.97	2.13	11.98
3SE8.PDB	O, L_ALA_130	N, L_LEU_181	H, L_LEU_181	2.83	1.98	9.00
3SE8.PDB	O, L_GLY_128	N, L_LYS_183	H, L_LYS_183	2.93	2.10	13.14
3SE8.PDB	O, L_SER_182	N, L_TYR_186	H, L_TYR_186	2.84	2.00	10.56
3SE8.PDB	O, L_LYS_183	N, L_GLU_187	H, L_GLU_187	2.94	2.13	17.20
3SE8.PDB	OD1, L_ASP_151	N, L_VAL_191	H, L_VAL_191	2.92	2.06	1.84
3SE8.PDB	O, L_PHE_209	N, L_TYR_192	H, L_TYR_192	2.97	2.12	6.17
3SE8.PDB	O, L_LYS_149	N, L_ALA_193	H, L_ALA_193	2.91	2.16	23.94
3SE8.PDB	O, L_LYS_207	N, L_CYS_194	H, L_CYS_194	2.97	2.16	16.78
3SE8.PDB	O, L_GLN_147	N, L_GLU_195	H, L_GLU_195	2.83	1.99	10.05
3SE8.PDB	O, L_VAL_205	N, L_VAL_196	H, L_VAL_196	2.74	1.90	10.53
3SE8.PDB	O, L_LYS_145	N, L_THR_197	H, L_THR_197	2.83	2.01	13.35
3SE8.PDB	O, L_PRO_141	NE2, L_HIS_198	HE2, L_HIS_198	2.98	2.16	13.12
3SE8.PDB	ND1, L_HIS_198	N, L_GLY_200	H, L_GLY_200	2.98	2.13	8.19
3SE8.PDB	O, L_HIS_198	N, L_LEU_201	H, L_LEU_201	2.88	2.03	8.01
3SE8.PDB	O, L_VAL_196	N, L_VAL_205	H, L_VAL_205	2.94	2.17	21.99
3SE8.PDB	O, L_TYR_192	N, L_PHE_209	H, L_PHE_209	2.99	2.20	20.60
3SE8.PDB	O, L_LYS_190	N, L_ARG_211	H, L_ARG_211	2.70	1.88	14.42
3SE8.PDB	O, L_HIS_189	NE, L_ARG_211	HE, L_ARG_211	2.74	1.90	11.40

Table 1681: 3SE8-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
3SE9.PDB	OE1, G_GLN_103	N, G_LEU_52	H, G_LEU_52	2.89	2.03	2.17
3SE9.PDB	O, G_CYS_218	N, G_PHE_53	H, G_PHE_53	2.97	2.17	17.99
3SE9.PDB	O, G_HIS_216	N, G_ALA_55	H, G_ALA_55	2.87	2.11	23.70
3SE9.PDB	O, G_VAL_75	N, G_SER_56	H, G_SER_56	2.93	2.15	21.60
3SE9.PDB	OG, G_SER_56	N, G_ALA_58	H, G_ALA_58	2.98	2.14	10.37
3SE9.PDB	OD1, G_ASN_67	N, G_LYS_59	H, G_LYS_59	2.90	2.07	12.58
3SE9.PDB	OE2, G_GLU_62	N, G_GLU_64	H, G_GLU_64	2.88	2.04	11.06
3SE9.PDB	O, G_SER_209	N, G_VAL_65	H, G_VAL_65	2.97	2.18	19.43
3SE9.PDB	OE2, G_GLU_64	ND1, G_HIS_66	HD1, G_HIS_66	2.73	1.88	8.47
3SE9.PDB	OE1, G_GLU_64	N, G_ASN_67	H, G_ASN_67	2.81	1.99	14.35
3SE9.PDB	OE1, G_GLU_64	ND2, G_ASN_67	HD21, G_ASN_67	2.83	2.01	14.03
3SE9.PDB	O, G_VAL_65	N, G_TRP_69	H, G_TRP_69	2.98	2.13	9.76
3SE9.PDB	O, G_HIS_66	N, G_ALA_70	H, G_ALA_70	2.90	2.08	14.89
3SE9.PDB	O, G_ASN_67	N, G_THR_71	H, G_THR_71	2.96	2.22	26.00
3SE9.PDB	O, G_TRP_69	N, G_ALA_73	H, G_ALA_73	2.87	2.02	9.06
3SE9.PDB	O, G_ALA_70	N, G_CYS_74	H, G_CYS_74	2.89	2.10	19.93
3SE9.PDB	O, G_CYS_54	N, G_VAL_75	H, G_VAL_75	2.97	2.15	14.48
3SE9.PDB	OD2, G_ASP_78	N, G_ASN_80	H, G_ASN_80	2.89	2.12	23.01
3SE9.PDB	O, G_SER_244	N, G_ILE_84	H, G_ILE_84	2.90	2.12	20.23
3SE9.PDB	O, G_VAL_242	N, G_LEU_86	H, G_LEU_86	2.84	1.98	4.71
3SE9.PDB	O, G_GLY_237	N, G_PHE_93	H, G_PHE_93	2.80	1.98	13.97
3SE9.PDB	O, G_GLY_235	N, G_MET_95	H, G_MET_95	2.84	2.07	22.25
3SE9.PDB	O, G_ASN_98	N, G_VAL_101	H, G_VAL_101	2.89	2.09	18.37
3SE9.PDB	OD1, G_ASN_99	NE2, G_GLN_103	HE21, G_GLN_103	2.75	1.96	19.57
3SE9.PDB	O, G_THR_50	NE2, G_GLN_103	HE22, G_GLN_103	2.73	1.94	19.46
3SE9.PDB	O, G_VAL_101	N, G_GLN_105	H, G_GLN_105	2.94	2.12	13.43
3SE9.PDB	O, G_MET_104	N, G_VAL_108	H, G_VAL_108	2.99	2.15	12.10
3SE9.PDB	O, G_GLN_105	N, G_ILE_109	H, G_ILE_109	2.94	2.09	6.88
3SE9.PDB	O, G_GLU_106	N, G_SER_110	H, G_SER_110	2.94	2.14	17.70
3SE9.PDB	O, G_ASP_107	N, G_LEU_111	H, G_LEU_111	2.78	1.94	10.68
3SE9.PDB	O, G_VAL_108	N, G_TRP_112	H, G_TRP_112	2.98	2.14	9.89
3SE9.PDB	O, G_ILE_109	N, G_ASP_113	H, G_ASP_113	2.94	2.20	25.93
3SE9.PDB	O, G_TRP_112	N, G_LEU_116	H, G_LEU_116	2.84	2.03	15.60
3SE9.PDB	O, G_ILE_201	N, G_LYS_121	H, G_LYS_121	2.90	2.06	12.24
3SE9.PDB	OE1, G_GLN_117	NZ, G_LYS_121	HZ3, G_LYS_121	2.58	1.83	27.32
3SE9.PDB	O, G_GLN_432	N, G_LEU_122	H, G_LEU_122	2.88	2.03	6.48
3SE9.PDB	O, G_LYS_121	N, G_ILE_201	H, G_ILE_201	2.95	2.11	10.92
3SE9.PDB	O, G_PRO_437	NZ, G_LYS_207	HZ2, G_LYS_207	2.83	2.09	27.83
3SE9.PDB	OE2, G_GLU_64	N, G_ASP_211	H, G_ASP_211	2.75	1.90	8.78
3SE9.PDB	O, G_ILE_251	N, G_ILE_215	H, G_ILE_215	2.82	1.98	12.02
3SE9.PDB	O, G_ALA_55	N, G_HIS_216	H, G_HIS_216	2.77	1.91	2.26
3SE9.PDB	OG1, G_THR_248	N, G_TYR_217	H, G_TYR_217	2.95	2.09	2.54
3SE9.PDB	O, G_PHE_53	N, G_CYS_218	H, G_CYS_218	2.85	2.07	20.62
3SE9.PDB	O, G_VAL_489	N, G_VAL_224	H, G_VAL_224	2.98	2.16	15.19
3SE9.PDB	O, G_LYS_487	N, G_LEU_226	H, G_LEU_226	2.88	2.08	18.00
3SE9.PDB	O, G_SER_243	N, G_LYS_227	H, G_LYS_227	2.60	1.80	16.43
3SE9.PDB	O, G_LYS_485	N, G_CYS_228	H, G_CYS_228	2.85	2.03	14.69
3SE9.PDB	O, G_ASN_241	N, G_ASN_229	H, G_ASN_229	2.78	1.96	14.08
3SE9.PDB	O, G_PHE_93	N, G_GLY_237	H, G_GLY_237	2.96	2.25	29.34
3SE9.PDB	O, G_GLU_91	N, G_CYS_239	H, G_CYS_239	2.74	2.00	26.00
3SE9.PDB	OD2, G_ASP_230	N, G_LYS_240	H, G_LYS_240	2.84	2.00	11.61
3SE9.PDB	OD1, G_ASP_230	N, G_ASN_241	H, G_ASN_241	2.75	2.01	25.57
3SE9.PDB	O, G_LYS_227	N, G_SER_243	H, G_SER_243	2.98	2.15	13.38
3SE9.PDB	OE2, G_GLU_83	OG, G_SER_243	HG, G_SER_243	2.65	1.89	17.63
3SE9.PDB	O, G_ILE_84	N, G_SER_244	H, G_SER_244	2.82	2.02	19.32
3SE9.PDB	O, G_ILE_225	N, G_VAL_245	H, G_VAL_245	2.83	2.01	13.24
3SE9.PDB	O, G_TYR_217	N, G_THR_248	H, G_THR_248	2.73	1.92	16.59

3SE9.PDB	OH, G_TYR_486	ND1, G_HIS_249	HD1, G_HIS_249	2.73	1.91	13.84
3SE9.PDB	O, G_ILE_215	N, G_ILE_251	H, G_ILE_251	2.80	1.94	2.64
3SE9.PDB	O, G_LYS_252	N, G_VAL_254	H, G_VAL_254	2.91	2.20	29.72
3SE9.PDB	O, G_HIS_375	N, G_THR_257	H, G_THR_257	3.00	2.26	26.89
3SE9.PDB	O, G_GLU_370	OG1, G_THR_257	HG1, G_THR_257	2.66	1.88	15.46
3SE9.PDB	O, G_ILE_371	NE2, G_GLN_258	HE22, G_GLN_258	2.86	2.01	8.57
3SE9.PDB	O, G_THR_257	N, G_LEU_259	H, G_LEU_259	2.60	1.87	26.09
3SE9.PDB	O, G_GLY_451	N, G_LEU_260	H, G_LEU_260	2.95	2.15	18.25
3SE9.PDB	O, G_ASN_448	N, G_ASN_262	H, G_ASN_262	2.69	1.86	13.26
3SE9.PDB	OE2, G_GLU_482	N, G_SER_264	H, G_SER_264	2.65	1.82	11.12
3SE9.PDB	O, G_LEU_288	N, G_ALA_266	H, G_ALA_266	2.85	2.12	26.29
3SE9.PDB	O, G_ILE_285	N, G_ARG_273	H, G_ARG_273	2.81	2.03	21.22
3SE9.PDB	O, G_ASN_276	N, G_ASN_279	H, G_ASN_279	2.76	1.96	18.81
3SE9.PDB	OD1, G_ASN_279	N, G_ALA_281	H, G_ALA_281	2.99	2.19	18.54
3SE9.PDB	O, G_ASN_279	N, G_LYS_282	H, G_LYS_282	2.89	2.04	7.99
3SE9.PDB	O, G_LEU_454	N, G_ILE_284	H, G_ILE_284	2.90	2.04	2.40
3SE9.PDB	O, G_ARG_273	N, G_ILE_285	H, G_ILE_285	2.83	1.99	11.82
3SE9.PDB	O, G_ILE_452	N, G_VAL_286	H, G_VAL_286	2.83	1.98	5.93
3SE9.PDB	O, G_ILE_271	N, G_HIS_287	H, G_HIS_287	2.81	1.96	6.79
3SE9.PDB	O, G_SER_264	NE2, G_HIS_287	HE2, G_HIS_287	2.74	1.92	14.77
3SE9.PDB	O, G_THR_450	N, G_LEU_288	H, G_LEU_288	3.00	2.19	16.95
3SE9.PDB	O, G_SER_447	N, G_ILE_294	H, G_ILE_294	2.94	2.13	15.34
3SE9.PDB	O, G_GLU_332	N, G_ASN_295	H, G_ASN_295	2.88	2.07	17.19
3SE9.PDB	O, G_TYR_330	N, G_THR_297	H, G_THR_297	2.76	1.95	15.38
3SE9.PDB	O, G_ILE_443	N, G_ARG_298	H, G_ARG_298	2.81	1.99	16.03
3SE9.PDB	O, G_ILE_326	NH1, G_ARG_298	HH11, G_ARG_298	2.73	1.91	14.56
3SE9.PDB	O, G_GLY_441	NH2, G_ARG_298	HH21, G_ARG_298	2.64	1.78	1.00
3SE9.PDB	O, G_ILE_439	NH2, G_ARG_298	HH22, G_ARG_298	2.74	1.95	20.11
3SE9.PDB	OD1, G_ASP_325	N, G_ARG_327	H, G_ARG_327	2.97	2.13	12.25
3SE9.PDB	OE1, G_GLN_422	NH1, G_ARG_327	HH11, G_ARG_327	2.62	1.84	19.91
3SE9.PDB	O, G_THR_297	N, G_TYR_330	H, G_TYR_330	2.97	2.18	20.21
3SE9.PDB	O, G_LEU_416	N, G_CYS_331	H, G_CYS_331	2.98	2.20	20.74
3SE9.PDB	O, G_ASN_295	N, G_GLU_332	H, G_GLU_332	2.81	1.99	12.99
3SE9.PDB	O, G_ILE_414	N, G_ILE_333	H, G_ILE_333	2.98	2.19	19.45
3SE9.PDB	O, G_ASN_334	N, G_TRP_338	H, G_TRP_338	2.98	2.12	4.45
3SE9.PDB	O, G_LEU_390	NE1, G_TRP_338	HE1, G_TRP_338	2.40	1.59	15.54
3SE9.PDB	O, G_GLY_335	N, G_ASN_339	H, G_ASN_339	2.97	2.13	11.25
3SE9.PDB	O, G_TRP_338	N, G_LEU_342	H, G_LEU_342	2.95	2.13	14.49
3SE9.PDB	O, G_ASN_339	N, G_LYS_343	H, G_LYS_343	2.90	2.16	25.67
3SE9.PDB	O, G_VAL_341	N, G_VAL_345	H, G_VAL_345	2.84	2.07	22.06
3SE9.PDB	O, G_GLN_344	N, G_LYS_348	H, G_LYS_348	2.93	2.17	23.65
3SE9.PDB	O, G_VAL_345	N, G_LEU_349	H, G_LEU_349	2.90	2.08	13.64
3SE9.PDB	O, G_THR_346	N, G_LYS_350	H, G_LYS_350	2.84	2.03	16.44
3SE9.PDB	O, G_LEU_349	N, G_HIS_352	H, G_HIS_352	2.89	2.18	29.71
3SE9.PDB	O, G_LYS_350	N, G_ASN_355	H, G_ASN_355	2.78	1.99	18.73
3SE9.PDB	O, G_PHE_353	N, G_LYS_357	H, G_LYS_357	2.82	1.98	9.00
3SE9.PDB	O, G_GLU_466	N, G_ILE_360	H, G_ILE_360	2.86	2.07	19.89
3SE9.PDB	OD1, G_ASN_393	N, G_PHE_361	H, G_PHE_361	2.87	2.02	7.09
3SE9.PDB	O, G_PHE_468	N, G_GLN_362	H, G_GLN_362	2.86	2.06	18.17
3SE9.PDB	O, G_PHE_361	NE2, G_GLN_362	HE22, G_GLN_362	2.61	1.80	15.95
3SE9.PDB	O, H_THR_53	N, G_ASP_368	H, G_ASP_368	2.97	2.15	15.24
3SE9.PDB	O, G_ASP_368	N, G_ILE_371	H, G_ILE_371	2.96	2.14	15.47
3SE9.PDB	O, G_ASP_368	N, G_THR_372	H, G_THR_372	2.96	2.15	17.04
3SE9.PDB	O, G_CYS_385	N, G_HIS_374	H, G_HIS_374	2.80	2.04	23.10
3SE9.PDB	O, G_THR_257	ND1, G_HIS_374	HD1, G_HIS_374	2.94	2.14	18.49
3SE9.PDB	O, G_GLU_381	N, G_CYS_378	H, G_CYS_378	2.81	2.03	21.46
3SE9.PDB	O, G_CYS_378	N, G_GLU_381	H, G_GLU_381	2.91	2.07	11.74
3SE9.PDB	O, G_PHE_376	N, G_PHE_383	H, G_PHE_383	2.77	1.93	9.82

3SE9.PDB	O, G_LYS_419	N, G_TYR_384	H, G_TYR_384	2.88	2.12	23.39
3SE9.PDB	O, G_HIS_374	N, G_CYS_385	H, G_CYS_385	2.82	2.01	16.28
3SE9.PDB	OD1, G_ASN_386	N, G_THR_388	H, G_THR_388	2.98	2.13	7.03
3SE9.PDB	O, G_THR_415	NE2, G_GLN_389	HE21, G_GLN_389	2.67	1.89	20.77
3SE9.PDB	O, G_THR_387	N, G_LEU_390	H, G_LEU_390	2.79	2.00	19.51
3SE9.PDB	O, G_PHE_361	ND2, G_ASN_393	HD21, G_ASN_393	2.74	1.88	3.74
3SE9.PDB	O, G_ILE_333	N, G_ILE_414	H, G_ILE_414	2.79	1.93	6.04
3SE9.PDB	O, G_CYS_331	N, G_LEU_416	H, G_LEU_416	2.86	2.03	11.55
3SE9.PDB	O, G_ALA_329	N, G_CYS_418	H, G_CYS_418	2.84	2.00	9.75
3SE9.PDB	O, G_TYR_384	N, G_LYS_419	H, G_LYS_419	2.88	2.10	21.78
3SE9.PDB	O, G_ARG_327	N, G_ILE_420	H, G_ILE_420	2.87	2.06	16.89
3SE9.PDB	O, G_ALA_433	N, G_ILE_424	H, G_ILE_424	2.96	2.14	15.31
3SE9.PDB	OE2, G_GLU_370	N, G_ASN_425	H, G_ASN_425	2.82	1.97	7.07
3SE9.PDB	OE1, G_GLU_370	ND2, G_ASN_425	HD21, G_ASN_425	2.86	2.02	9.78
3SE9.PDB	O, G_GLY_431	N, G_MET_426	H, G_MET_426	2.79	1.93	2.68
3SE9.PDB	O, G_MET_426	N, G_GLY_429	H, G_GLY_429	2.72	1.88	8.66
3SE9.PDB	O, G_ILE_424	N, G_ALA_433	H, G_ALA_433	2.93	2.10	11.85
3SE9.PDB	O, G_VAL_120	N, G_MET_434	H, G_MET_434	2.93	2.19	26.00
3SE9.PDB	O, G_GLN_422	N, G_TYR_435	H, G_TYR_435	2.67	1.86	16.15
3SE9.PDB	O, G_ARG_298	N, G_ILE_443	H, G_ILE_443	2.97	2.13	10.43
3SE9.PDB	OD1, G_ASN_295	ND2, G_ASN_444	HD21, G_ASN_444	2.93	2.17	24.18
3SE9.PDB	OG1, G_THR_297	ND2, G_ASN_444	HD22, G_ASN_444	2.97	2.23	26.41
3SE9.PDB	O, G_ILE_294	N, G_SER_447	H, G_SER_447	2.99	2.16	12.03
3SE9.PDB	O, G_VAL_292	N, G_ILE_449	H, G_ILE_449	2.90	2.05	8.11
3SE9.PDB	O, G_VAL_286	N, G_ILE_452	H, G_ILE_452	2.96	2.20	22.66
3SE9.PDB	O, G_GLN_258	N, G_LEU_453	H, G_LEU_453	2.91	2.06	4.64
3SE9.PDB	O, G_ILE_284	N, G_LEU_454	H, G_LEU_454	2.88	2.08	17.98
3SE9.PDB	O, G_ARG_469	N, G_THR_455	H, G_THR_455	2.88	2.05	12.96
3SE9.PDB	OE2, G_GLU_466	NH1, G_ARG_456	HH11, G_ARG_456	2.71	1.88	12.87
3SE9.PDB	O, G_THR_467	N, G_ASP_457	H, G_ASP_457	2.81	1.96	8.69
3SE9.PDB	O, G_THR_358	N, G_GLU_466	H, G_GLU_466	2.63	1.83	17.35
3SE9.PDB	O, G_ILE_360	N, G_PHE_468	H, G_PHE_468	2.76	1.94	14.82
3SE9.PDB	O, G_THR_455	N, G_ARG_469	H, G_ARG_469	2.95	2.15	17.67
3SE9.PDB	O, G_LEU_453	N, G_GLY_471	H, G_GLY_471	2.80	2.02	20.51
3SE9.PDB	OE1, G_GLN_105	NE1, G_TRP_479	HE1, G_TRP_479	2.69	1.89	17.56
3SE9.PDB	O, G_LYS_476	N, G_ARG_480	H, G_ARG_480	2.94	2.14	18.76
3SE9.PDB	O, G_ASP_477	N, G_SER_481	H, G_SER_481	2.99	2.25	26.30
3SE9.PDB	O, G_TRP_479	N, G_LEU_483	H, G_LEU_483	2.82	2.04	21.47
3SE9.PDB	O, G_LEU_483	N, G_TYR_486	H, G_TYR_486	2.94	2.11	13.26
3SE9.PDB	O, G_ASN_92	NZ, G_LYS_487	HZ2, G_LYS_487	2.93	2.06	7.72
3SE9.PDB	OE1, G_GLU_91	NZ, G_LYS_487	HZ3, G_LYS_487	2.63	1.86	24.78
3SE9.PDB	O, G_VAL_224	N, G_VAL_489	H, G_VAL_489	2.96	2.10	4.39
3SE9.PDB	O, G_LYS_46	N, G_GLN_490	H, G_GLN_490	2.80	1.98	15.13
3SE9.PDB	O, G_GLY_222	N, G_ILE_491	H, G_ILE_491	2.99	2.20	21.02
3SE9.PDB	O, G_VAL_44	N, G_GLU_492	H, G_GLU_492	2.87	2.09	21.24
3SE9.PDB	O, H_TRP_23	N, H_VAL_5	H, H_VAL_5	2.93	2.09	11.74
3SE9.PDB	O, H_TYR_90	NE2, H_GLN_6	HE21, H_GLN_6	2.96	2.10	4.89
3SE9.PDB	O, H_LEU_108	N, H_GLY_10	H, H_GLY_10	2.94	2.16	21.74
3SE9.PDB	O, H_VAL_110	N, H_LYS_12	H, H_LYS_12	2.90	2.09	15.31
3SE9.PDB	O, H_LEU_82C	N, H_GLY_15	H, H_GLY_15	2.64	1.84	17.68
3SE9.PDB	O, H_ILE_82	N, H_VAL_18	H, H_VAL_18	2.83	2.05	20.43
3SE9.PDB	OD1, H_ASP_81	NE, H_ARG_19	HE, H_ARG_19	2.75	1.91	10.76
3SE9.PDB	O, H_MET_80	N, H_VAL_20	H, H_VAL_20	2.85	2.01	10.21
3SE9.PDB	OG, H_SER_7	N, H_SER_21	H, H_SER_21	2.77	1.92	7.84
3SE9.PDB	O, H_VAL_5	N, H_TRP_23	H, H_TRP_23	2.93	2.15	21.94
3SE9.PDB	O, H_SER_25	N, H_PHE_29	H, H_PHE_29	2.88	2.03	6.53
3SE9.PDB	O, H_GLU_26	N, H_GLU_30	H, H_GLU_30	2.87	2.05	15.53
3SE9.PDB	O, H_GLN_95	N, H_GLU_33	H, H_GLU_33	2.91	2.13	21.88

3SE9.PDB	O, H_VAL_51	N, H_ILE_35	H, H_ILE_35	2.94	2.15	19.12
3SE9.PDB	O, H_ALA_93	N, H_HIS_35A	H, H_HIS_35A	2.77	1.93	10.56
3SE9.PDB	O, H_GLY_49	N, H_TRP_36	H, H_TRP_36	2.93	2.09	11.34
3SE9.PDB	O, H_PHE_91	N, H_VAL_37	H, H_VAL_37	2.94	2.12	14.35
3SE9.PDB	O, H_GLU_46	N, H_ARG_38	H, H_ARG_38	2.93	2.12	16.03
3SE9.PDB	OH, H_TYR_90	NH1, H_ARG_38	HH11, H_ARG_38	2.99	2.21	21.73
3SE9.PDB	OD1, H_ASP_86	NH1, H_ARG_38	HH12, H_ARG_38	2.86	2.03	12.66
3SE9.PDB	O, H_THR_89	N, H_GLN_39	H, H_GLN_39	2.91	2.10	16.25
3SE9.PDB	O, H_GLN_43	NE2, H_GLN_39	HE21, H_GLN_39	2.88	2.07	16.30
3SE9.PDB	O, H_ALA_40	N, H_GLN_43	H, H_GLN_43	2.88	2.07	16.77
3SE9.PDB	O, H_ARG_38	N, H_GLU_46	H, H_GLU_46	2.90	2.11	20.67
3SE9.PDB	O, H_TRP_36	N, H_ILE_48	H, H_ILE_48	2.76	1.91	8.76
3SE9.PDB	O, H_ASN_57	N, H_TRP_50	H, H_TRP_50	2.97	2.24	26.24
3SE9.PDB	OD1, G_ASN_280	NE1, H_TRP_50	HE1, H_TRP_50	2.86	2.03	11.46
3SE9.PDB	O, H_ALA_55	N, H_LYS_52	H, H_LYS_52	2.82	2.02	18.64
3SE9.PDB	O, H_GLU_33	N, H_THR_52A	H, H_THR_52A	2.97	2.15	15.80
3SE9.PDB	O, H_LYS_52	N, H_GLY_54	H, H_GLY_54	2.87	2.11	23.24
3SE9.PDB	O, G_ARG_456	ND2, H_ASN_57	HD22, H_ASN_57	2.82	1.98	10.42
3SE9.PDB	O, H_ILE_48	N, H_GLY_59	H, H_GLY_59	2.88	2.11	22.31
3SE9.PDB	O, H_SER_60	N, H_ARG_64	H, H_ARG_64	2.81	1.98	12.96
3SE9.PDB	OG, G_SER_365	NH1, H_ARG_64	HH11, H_ARG_64	2.81	2.04	21.79
3SE9.PDB	O, H_PRO_61	N, H_GLN_65	H, H_GLN_65	2.78	2.04	25.46
3SE9.PDB	O, H_ASP_62	N, H_ARG_66	H, H_ARG_66	2.94	2.23	28.48
3SE9.PDB	OD2, H_ASP_86	NH2, H_ARG_66	HH22, H_ARG_66	2.37	1.62	23.34
3SE9.PDB	O, H_PHE_63	N, H_VAL_67	H, H_VAL_67	2.84	2.04	18.39
3SE9.PDB	O, H_ASP_81	N, H_SER_68	H, H_SER_68	2.86	2.04	15.98
3SE9.PDB	O, H_THR_52A	NE, H_ARG_71	HE, H_ARG_71	2.71	1.89	14.64
3SE9.PDB	OD2, G_ASP_368	NH1, H_ARG_71	HH12, H_ARG_71	2.77	1.92	7.25
3SE9.PDB	O, H_THR_77	N, H_ASP_72	H, H_ASP_72	2.80	1.97	12.39
3SE9.PDB	O, G_GLY_429	NH1, H_ARG_73	HH12, H_ARG_73	2.99	2.23	23.32
3SE9.PDB	O, H_LEU_75	OG1, H_THR_77	HG1, H_THR_77	2.67	1.90	16.77
3SE9.PDB	O, H_CYS_22	N, H_ALA_78	H, H_ALA_78	2.72	1.89	13.13
3SE9.PDB	O, H_THR_70	N, H_HIS_79	H, H_HIS_79	2.97	2.14	11.35
3SE9.PDB	OG, H_SER_21	ND1, H_HIS_79	HD1, H_HIS_79	2.69	1.93	23.16
3SE9.PDB	O, H_VAL_20	N, H_MET_80	H, H_MET_80	2.71	1.86	8.21
3SE9.PDB	O, H_SER_68	N, H_ASP_81	H, H_ASP_81	2.93	2.09	10.84
3SE9.PDB	O, H_VAL_18	N, H_ILE_82	H, H_ILE_82	2.83	2.01	14.83
3SE9.PDB	OG, H_SER_68	NH1, H_ARG_82A	HH12, H_ARG_82A	2.84	2.02	15.25
3SE9.PDB	OD2, H_ASP_86	N, H_THR_83	H, H_THR_83	2.88	2.05	13.61
3SE9.PDB	O, H_THR_83	N, H_ASP_86	H, H_ASP_86	2.95	2.11	10.53
3SE9.PDB	O, H_GLN_39	N, H_THR_89	H, H_THR_89	2.98	2.19	19.31
3SE9.PDB	O, H_THR_107	N, H_TYR_90	H, H_TYR_90	2.82	1.97	6.56
3SE9.PDB	O, H_VAL_37	N, H_PHE_91	H, H_PHE_91	2.71	1.86	7.71
3SE9.PDB	OE1, H_GLN_6	N, H_CYS_92	H, H_CYS_92	2.90	2.06	12.06
3SE9.PDB	O, H_HIS_35A	N, H_ALA_93	H, H_ALA_93	2.82	2.09	27.40
3SE9.PDB	O, H_LEU_102	N, H_ARG_94	H, H_ARG_94	2.99	2.16	14.50
3SE9.PDB	OD1, H_ASP_101	NH2, H_ARG_94	HH21, H_ARG_94	2.74	1.90	10.49
3SE9.PDB	O, H_LEU_34	N, H_GLN_95	H, H_GLN_95	2.93	2.08	7.14
3SE9.PDB	OH, H_TYR_100E	NE2, H_GLN_100B	HE22, H_GLN_100B	2.88	2.05	12.80
3SE9.PDB	OD1, G_ASN_279	NE1, H_TRP_100D	HE1, H_TRP_100D	2.86	2.13	26.83
3SE9.PDB	OH, L_TYR_36	N, H_PHE_100F	H, H_PHE_100F	2.88	2.05	11.59
3SE9.PDB	O, H_CYS_92	N, H_GLY_104	H, H_GLY_104	2.87	2.02	7.22
3SE9.PDB	O, H_GLN_6	NH2, H_ARG_105	HH21, H_ARG_105	2.67	1.92	23.91
3SE9.PDB	O, H_TYR_90	N, H_THR_107	H, H_THR_107	2.73	1.92	16.56
3SE9.PDB	OG, H_SER_9	N, H_LEU_108	H, H_LEU_108	2.69	1.93	23.13
3SE9.PDB	O, H_ALA_88	N, H_ILE_109	H, H_ILE_109	2.93	2.07	6.87
3SE9.PDB	OG1, H_THR_87	N, H_VAL_111	H, H_VAL_111	2.93	2.08	7.05
3SE9.PDB	OG, H_SER_112	N, H_ALA_114	H, H_ALA_114	2.96	2.13	12.08

3SE9.PDB	O, H_PHE_146	N, H_LYS_117	H, H_LYS_117	2.71	1.88	12.05
3SE9.PDB	O, H_ASP_144	NZ, H_LYS_117	HZ2, H_LYS_117	2.71	1.95	26.51
3SE9.PDB	O, H_LYS_143	N, H_SER_120	H, H_SER_120	2.94	2.18	23.30
3SE9.PDB	O, H_LEU_141	N, H_PHE_122	H, H_PHE_122	2.83	1.99	10.34
3SE9.PDB	O, H_GLY_139	N, H_LEU_124	H, H_LEU_124	2.72	1.86	7.35
3SE9.PDB	O, H_VAL_184	N, H_ALA_136	H, H_ALA_136	2.58	1.73	7.05
3SE9.PDB	O, H_VAL_182	N, H_LEU_138	H, H_LEU_138	2.98	2.14	9.89
3SE9.PDB	O, H_SER_180	N, H_CYS_140	H, H_CYS_140	2.81	2.02	19.42
3SE9.PDB	O, H_PHE_122	N, H_LEU_141	H, H_LEU_141	2.71	1.87	9.85
3SE9.PDB	O, H_LEU_178	N, H_VAL_142	H, H_VAL_142	2.67	1.83	9.14
3SE9.PDB	O, H_SER_120	N, H_LYS_143	H, H_LYS_143	2.81	1.96	4.58
3SE9.PDB	O, H_LYS_117	N, H_PHE_146	H, H_PHE_146	2.83	2.04	19.01
3SE9.PDB	O, H_ASN_199	N, H_THR_151	H, H_THR_151	2.82	2.01	15.51
3SE9.PDB	OG, H_SER_180	NE1, H_TRP_154	HE1, H_TRP_154	2.83	2.00	12.34
3SE9.PDB	O, H_ILE_195	N, H_ASN_155	H, H_ASN_155	2.72	1.88	10.78
3SE9.PDB	OD1, H_ASN_197	N, H_SER_156	H, H_SER_156	2.63	1.82	16.31
3SE9.PDB	O, H_TRP_154	N, H_GLY_157	H, H_GLY_157	2.94	2.17	22.03
3SE9.PDB	O, H_VAL_181	N, H_HIS_164	H, H_HIS_164	2.79	1.95	10.78
3SE9.PDB	OD1, L_ASN_138	NE2, H_HIS_164	HE2, H_HIS_164	2.87	2.10	22.18
3SE9.PDB	O, H_SER_179	N, H_PHE_166	H, H_PHE_166	2.83	1.98	8.83
3SE9.PDB	O, H_SER_177	N, H_VAL_169	H, H_VAL_169	2.79	1.97	15.38
3SE9.PDB	O, H_LEU_175	N, H_GLN_171	H, H_GLN_171	2.88	2.03	9.89
3SE9.PDB	OD1, H_ASP_144	NE2, H_GLN_171	HE22, H_GLN_171	2.70	1.89	15.22
3SE9.PDB	O, H_GLN_171	N, H_GLY_174	H, H_GLY_174	2.82	1.98	10.33
3SE9.PDB	O, H_TYR_145	N, H_TYR_176	H, H_TYR_176	2.80	1.95	9.52
3SE9.PDB	O, H_VAL_169	N, H_SER_177	H, H_SER_177	2.92	2.11	17.68
3SE9.PDB	O, H_VAL_142	N, H_LEU_178	H, H_LEU_178	2.84	2.05	18.79
3SE9.PDB	O, H_HIS_164	N, H_VAL_181	H, H_VAL_181	2.77	1.93	11.77
3SE9.PDB	O, H_LEU_138	N, H_VAL_182	H, H_VAL_182	2.73	1.91	15.41
3SE9.PDB	O, H_ALA_136	N, H_VAL_184	H, H_VAL_184	2.65	1.82	11.73
3SE9.PDB	O, H_GLY_134	N, H_SER_186	H, H_SER_186	2.77	1.92	8.30
3SE9.PDB	O, H_PRO_185	N, H_SER_188	H, H_SER_188	2.84	2.03	16.03
3SE9.PDB	OD1, H_ASN_155	N, H_ILE_195	H, H_ILE_195	2.88	2.07	17.09
3SE9.PDB	O, H_SER_153	N, H_ASN_197	H, H_ASN_197	2.68	1.83	7.88
3SE9.PDB	OD1, H_ASP_208	ND2, H_ASN_197	HD21, H_ASN_197	2.90	2.07	13.74
3SE9.PDB	O, H_VAL_207	N, H_VAL_198	H, H_VAL_198	2.67	1.81	3.24
3SE9.PDB	O, H_THR_151	N, H_ASN_199	H, H_ASN_199	2.88	2.05	12.73
3SE9.PDB	O, H_THR_205	N, H_HIS_200	H, H_HIS_200	2.70	1.85	4.09
3SE9.PDB	OG, H_SER_203	ND1, H_HIS_200	HD1, H_HIS_200	2.68	1.84	9.59
3SE9.PDB	O, H_PRO_147	NE2, H_HIS_200	HE2, H_HIS_200	2.74	1.92	15.55
3SE9.PDB	O, H_LYS_201	N, H_ASN_204	H, H_ASN_204	2.85	2.04	15.88
3SE9.PDB	O, H_VAL_198	N, H_VAL_207	H, H_VAL_207	2.76	1.95	16.29
3SE9.PDB	O, H_CYS_196	N, H_LYS_209	H, H_LYS_209	2.96	2.13	12.56
3SE9.PDB	O, H_TYR_194	N, H_VAL_211	H, H_VAL_211	2.84	1.98	5.32
3SE9.PDB	OE1, L_GLN_100	N, L_GLN_6	H, L_GLN_6	2.87	2.05	13.27
3SE9.PDB	O, L_TYR_86	NE2, L_GLN_6	HE21, L_GLN_6	2.65	1.87	19.42
3SE9.PDB	O, L_SER_22	N, L_SER_7	H, L_SER_7	2.91	2.10	15.22
3SE9.PDB	O, L_ARG_103	N, L_LEU_11	H, L_LEU_11	2.81	2.03	20.07
3SE9.PDB	OE2, L_GLU_17	N, L_SER_14	H, L_SER_14	2.75	1.90	8.71
3SE9.PDB	O, L_MET_78	N, L_GLY_16	H, L_GLY_16	2.86	2.12	26.24
3SE9.PDB	O, L_SER_14	N, L_GLU_17	H, L_GLU_17	3.00	2.15	9.67
3SE9.PDB	O, L_ILE_75	N, L_ALA_19	H, L_ALA_19	2.75	1.95	18.77
3SE9.PDB	O, L_LEU_73	N, L_LEU_21	H, L_LEU_21	2.92	2.06	4.08
3SE9.PDB	O, L_SER_7	N, L_SER_22	H, L_SER_22	2.90	2.04	6.45
3SE9.PDB	O, L_TYR_71	N, L_CYS_23	H, L_CYS_23	2.61	1.79	13.38
3SE9.PDB	O, L_THR_5	N, L_THR_24	H, L_THR_24	2.87	2.04	10.61
3SE9.PDB	O, L_VAL_3	N, L_ALA_26	H, L_ALA_26	2.84	2.01	13.56
3SE9.PDB	OH, L_TYR_71	N, L_GLY_31	H, L_GLY_31	2.83	1.99	8.85

3SE9.PDB	O, L_GLN_89	N, L_THR_34	H, L_THR_34	2.89	2.12	22.07
3SE9.PDB	O, L_ILE_48	N, L_TRP_35	H, L_TRP_35	2.92	2.14	20.82
3SE9.PDB	O, L_TYR_87	N, L_TYR_36	H, L_TYR_36	2.80	1.96	11.38
3SE9.PDB	O, L_LYS_45	N, L_GLN_37	H, L_GLN_37	2.89	2.10	19.91
3SE9.PDB	O, L_ARG_85	N, L_LYS_38	H, L_LYS_38	2.86	2.11	24.20
3SE9.PDB	O, L_GLN_42	NZ, L_LYS_38	HZ2, L_LYS_38	2.69	1.95	28.64
3SE9.PDB	O, L_GLU_81	NZ, L_LYS_39	HZ3, L_LYS_39	2.86	2.10	26.41
3SE9.PDB	O, L_GLN_37	N, L_LYS_45	H, L_LYS_45	2.78	1.95	13.05
3SE9.PDB	O, L_TRP_35	N, L_LEU_47	H, L_LEU_47	2.87	2.05	13.50
3SE9.PDB	O, L_LYS_53	N, L_PHE_49	H, L_PHE_49	2.83	2.01	14.47
3SE9.PDB	O, L_MET_33	N, L_THR_51	H, L_THR_51	2.85	2.05	18.27
3SE9.PDB	O, L_ALA_50	N, L_SER_52	H, L_SER_52	2.77	2.03	26.37
3SE9.PDB	O, L_PHE_49	N, L_LYS_53	H, L_LYS_53	2.88	2.12	23.41
3SE9.PDB	O, L_THR_74	N, L_SER_63	H, L_SER_63	2.83	2.02	16.49
3SE9.PDB	O, L_GLY_68	NE2, L_GLN_66	HE21, L_GLN_66	2.85	2.01	10.87
3SE9.PDB	O, L_GLN_70	N, L_PHE_67	H, L_PHE_67	2.77	1.98	19.75
3SE9.PDB	O, L_PHE_67	N, L_GLN_70	H, L_GLN_70	2.81	1.99	14.85
3SE9.PDB	O, L_CYS_23	N, L_TYR_71	H, L_TYR_71	2.90	2.05	8.86
3SE9.PDB	O, L_SER_65	N, L_THR_72	H, L_THR_72	2.92	2.08	10.66
3SE9.PDB	O, L_LEU_21	N, L_LEU_73	H, L_LEU_73	2.70	1.90	17.14
3SE9.PDB	O, L_SER_63	N, L_THR_74	H, L_THR_74	2.72	1.87	5.98
3SE9.PDB	O, L_GLU_17	N, L_MET_78	H, L_MET_78	2.89	2.06	12.71
3SE9.PDB	OD2, L ASP_82	N, L_GLU_79	H, L_GLU_79	2.83	1.97	2.91
3SE9.PDB	O, L_GLU_79	N, L ASP_82	H, L ASP_82	2.98	2.15	13.63
3SE9.PDB	O, L_THR_102	N, L_TYR_86	H, L_TYR_86	2.81	2.08	27.06
3SE9.PDB	O, L_THR_34	N, L_GLN_89	H, L_GLN_89	2.81	2.01	18.78
3SE9.PDB	O, L_LEU_91	NE2, L_GLN_89	HE22, L_GLN_89	2.88	2.12	24.17
3SE9.PDB	O, L_PHE_97	N, L_GLN_90	H, L_GLN_90	2.90	2.18	28.93
3SE9.PDB	O, L_SER_27	NE2, L_GLN_90	HE21, L_GLN_90	2.99	2.17	16.35
3SE9.PDB	O, L_CYS_88	N, L_GLY_99	H, L_GLY_99	2.80	1.97	11.46
3SE9.PDB	O, L_TYR_86	N, L_THR_102	H, L_THR_102	2.76	1.99	22.12
3SE9.PDB	O, L_ALA_84	N, L_LEU_104	H, L_LEU_104	2.90	2.05	7.67
3SE9.PDB	O, L_LEU_11	N, L_GLU_105	H, L_GLU_105	2.83	2.02	16.12
3SE9.PDB	OE1, L_GLN_166	N, L_ILE_106	H, L_ILE_106	2.83	2.02	16.05
3SE9.PDB	O, L_LEU_13	N, L_ARG_107	H, L_ARG_107	2.82	1.98	9.67
3SE9.PDB	O, L_TYR_140	N, L_ALA_111	H, L_ALA_111	2.91	2.10	17.28
3SE9.PDB	O, L_VAL_133	N, L_PHE_118	H, L_PHE_118	2.77	1.97	18.18
3SE9.PDB	OG, L_SER_131	NE2, L_GLN_124	HE21, L_GLN_124	2.87	2.02	8.09
3SE9.PDB	O, L_GLN_124	N, L_SER_127	H, L_SER_127	2.85	2.11	25.81
3SE9.PDB	O, L_LEU_125	N, L_GLY_128	H, L_GLY_128	2.77	1.93	7.72
3SE9.PDB	O, L_LEU_181	N, L_ALA_130	H, L_ALA_130	2.85	2.00	6.88
3SE9.PDB	O, L_LEU_179	N, L_VAL_132	H, L_VAL_132	2.65	1.81	8.60
3SE9.PDB	O, L_SER_177	N, L_CYS_134	H, L_CYS_134	2.87	2.03	11.55
3SE9.PDB	O, L_PHE_116	N, L_LEU_135	H, L_LEU_135	2.83	2.01	13.22
3SE9.PDB	O, L_LEU_175	N, L_LEU_136	H, L_LEU_136	2.80	1.94	5.67
3SE9.PDB	O, L_SER_114	N, L ASN_137	H, L ASN_137	2.87	2.06	16.53
3SE9.PDB	OG, L_SER_174	N, L ASN_138	H, L ASN_138	2.87	2.02	6.61
3SE9.PDB	O, L_TYR_173	N, L_PHE_139	H, L_PHE_139	2.71	1.88	11.74
3SE9.PDB	O, L_ALA_111	N, L_TYR_140	H, L_TYR_140	2.97	2.14	13.63
3SE9.PDB	O, L_GLU_195	N, L_GLN_147	H, L_GLN_147	2.88	2.05	13.30
3SE9.PDB	OG, L_SER_177	NE1, L_TRP_148	HE1, L_TRP_148	2.88	2.05	13.01
3SE9.PDB	O, L_ALA_193	N, L_LYS_149	H, L_LYS_149	2.85	2.03	13.91
3SE9.PDB	O, L_ALA_153	N, L_VAL_150	H, L_VAL_150	2.92	2.10	13.17
3SE9.PDB	O, L_VAL_191	N, L ASP_151	H, L ASP_151	2.74	1.91	13.52
3SE9.PDB	O, L_VAL_150	N, L_ALA_153	H, L_ALA_153	2.87	2.02	9.15
3SE9.PDB	O, L_TRP_148	N, L_GLN_155	H, L_GLN_155	3.00	2.16	10.91
3SE9.PDB	O, L_THR_178	N, L_GLN_160	H, L_GLN_160	2.99	2.20	19.65
3SE9.PDB	O, L_SER_176	N, L_SER_162	H, L_SER_162	2.81	2.05	22.68

3SE9.PDB	O, H_PRO_167	OG, L_SER_162	HG, L_SER_162	2.60	1.89	25.20
3SE9.PDB	O, L_SER_174	N, L_THR_164	H, L_THR_164	2.97	2.14	12.76
3SE9.PDB	O, L_ILE_106	NE2, L_GLN_166	HE21, L_GLN_166	2.82	2.03	19.63
3SE9.PDB	O, L_SER_171	NE2, L_GLN_166	HE22, L_GLN_166	2.91	2.08	11.92
3SE9.PDB	O, L_THR_172	N, L_ASP_167	H, L_ASP_167	2.88	2.05	12.43
3SE9.PDB	OD2, L_ASP_167	N, L_LYS_169	H, L_LYS_169	2.73	1.98	24.54
3SE9.PDB	OD2, L_ASP_167	N, L_ASP_170	H, L_ASP_170	2.87	2.10	21.70
3SE9.PDB	OD1, L_ASP_170	OG1, L_THR_172	HG1, L_THR_172	2.48	1.71	16.29
3SE9.PDB	O, L_PHE_139	N, L_TYR_173	H, L_TYR_173	2.70	1.86	11.73
3SE9.PDB	O, L_LEU_136	N, L_LEU_175	H, L_LEU_175	2.79	1.97	15.48
3SE9.PDB	O, L_SER_162	N, L_SER_176	H, L_SER_176	2.85	2.02	11.18
3SE9.PDB	O, L_CYS_134	N, L_SER_177	H, L_SER_177	2.95	2.11	11.27
3SE9.PDB	O, L_GLN_160	N, L_THR_178	H, L_THR_178	2.80	1.96	9.46
3SE9.PDB	O, L_VAL_132	N, L_LEU_179	H, L_LEU_179	2.70	1.87	12.38
3SE9.PDB	O, L_ASN_158	N, L_THR_180	H, L_THR_180	3.00	2.16	11.07
3SE9.PDB	O, L_ALA_130	N, L_LEU_181	H, L_LEU_181	2.86	2.02	11.27
3SE9.PDB	O, L_GLY_128	N, L_LYS_183	H, L_LYS_183	2.82	2.01	15.80
3SE9.PDB	OE1, L_GLU_187	NZ, L_LYS_183	HZ3, L_LYS_183	2.82	2.09	29.82
3SE9.PDB	O, L_LYS_183	N, L_GLU_187	H, L_GLU_187	2.93	2.13	19.51
3SE9.PDB	OD2, L_ASP_151	ND1, L_HIS_189	HD1, L_HIS_189	2.89	2.18	29.99
3SE9.PDB	OD1, L_ASP_151	N, L_VAL_191	H, L_VAL_191	2.92	2.06	1.45
3SE9.PDB	O, L_PHE_209	N, L_TYR_192	H, L_TYR_192	2.96	2.10	3.54
3SE9.PDB	O, L_LYS_149	N, L_ALA_193	H, L_ALA_193	2.83	2.03	17.72
3SE9.PDB	O, L_LYS_207	N, L_CYS_194	H, L_CYS_194	2.79	1.94	6.54
3SE9.PDB	O, L_GLN_147	N, L_GLU_195	H, L_GLU_195	2.78	1.93	8.55
3SE9.PDB	O, L_VAL_205	N, L_VAL_196	H, L_VAL_196	2.74	1.90	9.26
3SE9.PDB	O, L_LYS_145	N, L_THR_197	H, L_THR_197	2.89	2.05	9.75
3SE9.PDB	ND1, L_HIS_198	N, L_GLY_200	H, L_GLY_200	3.00	2.16	11.89
3SE9.PDB	O, L_HIS_198	N, L_LEU_201	H, L_LEU_201	2.74	1.90	9.36
3SE9.PDB	O, L_VAL_196	N, L_VAL_205	H, L_VAL_205	2.96	2.24	27.95
3SE9.PDB	O, L_CYS_194	N, L_LYS_207	H, L_LYS_207	2.92	2.12	17.78
3SE9.PDB	O, L_TYR_192	N, L_PHE_209	H, L_PHE_209	2.89	2.14	24.10
3SE9.PDB	O, L_LYS_190	N, L_ARG_211	H, L_ARG_211	2.77	1.94	11.39

Table 1682: 3SE9-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
3THM.PDB	N, L_VAL_3	OG, L_SER_2	HG, L_SER_2	2.83	2.12	25.75
3THM.PDB	OG, L_SER_2	N, L_LEU_4	H, L_LEU_4	2.87	2.06	16.74
3THM.PDB	O, L_SER_23	N, L_THR_5	H, L_THR_5	2.87	2.03	10.68
3THM.PDB	O, L_TYR_87	NE2, L_GLN_6	HE21, L_GLN_6	2.88	2.03	6.32
3THM.PDB	OE1, L_GLU_12	N, L_ALA_13	H, L_ALA_13	2.70	1.91	19.84
3THM.PDB	O, L_LEU_79	N, L_ARG_15	H, L_ARG_15	2.74	1.88	4.28
3THM.PDB	O, L_LEU_74	N, L_ILE_20	H, L_ILE_20	2.80	1.96	9.35
3THM.PDB	O, L_THR_5	N, L_SER_23	H, L_SER_23	2.90	2.09	16.08
3THM.PDB	O, L_THR_70	N, L_GLY_24	H, L_GLY_24	2.84	2.07	23.10
3THM.PDB	OD1, L_ASN_28	N, L_ASN_25	H, L_ASN_25	2.96	2.18	18.32
3THM.PDB	OD1, L_ASP_93	ND2, L_ASN_28	HD21, L_ASN_28	2.85	2.01	9.28
3THM.PDB	OD1, L_ASN_28	N, L_ILE_29	H, L_ILE_29	2.67	1.87	18.36
3THM.PDB	O, L_ASN_25	N, L_GLY_30	H, L_GLY_30	2.96	2.12	9.14
3THM.PDB	O, L_ASN_28	N, L_TYR_32	H, L_TYR_32	2.89	2.11	20.74
3THM.PDB	OD2, L_ASP_52	N, L_VAL_34	H, L_VAL_34	2.76	2.01	24.28
3THM.PDB	O, L_SER_90	N, L_ASN_35	H, L_ASN_35	2.89	2.07	14.41
3THM.PDB	O, H_ALA_117	ND2, L_ASN_35	HD21, L_ASN_35	2.77	1.97	17.79
3THM.PDB	O, L_ILE_49	N, L_TRP_36	H, L_TRP_36	2.81	1.98	12.62
3THM.PDB	O, L_TYR_88	N, L_TYR_37	H, L_TYR_37	2.84	2.02	14.79
3THM.PDB	O, L_LYS_46	N, L_GLN_38	H, L_GLN_38	2.87	2.08	19.68
3THM.PDB	OH, L_TYR_87	NE2, L_GLN_38	HE21, L_GLN_38	2.86	2.05	16.36
3THM.PDB	O, L_ASP_86	N, L_GLN_39	H, L_GLN_39	2.67	1.81	4.75
3THM.PDB	O, L_LEU_40	N, L_LYS_43	H, L_LYS_43	2.88	2.04	10.22
3THM.PDB	O, L_GLN_38	N, L_LYS_46	H, L_LYS_46	2.84	2.05	18.96
3THM.PDB	O, L_TRP_36	N, L_LEU_48	H, L_LEU_48	2.82	1.98	12.51
3THM.PDB	O, L_LEU_54	N, L_TYR_50	H, L_TYR_50	2.87	2.06	17.25
3THM.PDB	OD1, L_ASN_35	N, L_SER_51	H, L_SER_51	2.98	2.18	17.87
3THM.PDB	O, L_VAL_34	N, L_ASP_52	H, L_ASP_52	2.82	1.98	11.63
3THM.PDB	O, L_ASP_61	NH2, L_ARG_55	HH21, L_ARG_55	2.95	2.23	28.54
3THM.PDB	OD1, L_ASP_83	NE, L_ARG_62	HE, L_ARG_62	2.86	2.03	12.52
3THM.PDB	OD2, L_ASP_83	NH2, L_ARG_62	HH21, L_ARG_62	2.63	1.79	10.74
3THM.PDB	O, L_ALA_75	N, L_SER_64	H, L_SER_64	2.96	2.14	13.06
3THM.PDB	O, L_SER_73	N, L_SER_66	H, L_SER_66	2.95	2.17	20.65
3THM.PDB	O, L_THR_71	N, L_SER_68	H, L_SER_68	2.93	2.09	7.96
3THM.PDB	O, L_SER_68	N, L_THR_71	H, L_THR_71	2.94	2.09	5.15
3THM.PDB	O, L_CYS_22	N, L_ALA_72	H, L_ALA_72	2.80	1.98	14.59
3THM.PDB	O, L_SER_66	N, L_SER_73	H, L_SER_73	2.76	1.91	7.29
3THM.PDB	O, L_ILE_20	N, L_LEU_74	H, L_LEU_74	2.97	2.15	14.37
3THM.PDB	O, L_SER_64	N, L_ALA_75	H, L_ALA_75	2.82	2.00	15.44
3THM.PDB	O, L_VAL_18	N, L_ILE_76	H, L_ILE_76	2.90	2.07	11.54
3THM.PDB	OD2, L_ASP_78	NH1, L_ARG_77	HH11, L_ARG_77	2.79	2.00	19.01
3THM.PDB	O, L_GLN_16	N, L_LEU_79	H, L_LEU_79	2.98	2.13	4.45
3THM.PDB	OD1, L_ASP_83	N, L_LEU_80	H, L_LEU_80	2.94	2.09	0.76
3THM.PDB	O, L_LEU_80	N, L_ASP_83	H, L_ASP_83	2.90	2.06	10.43
3THM.PDB	O, L_GLN_39	N, L_ASP_86	H, L_ASP_86	2.98	2.17	16.25
3THM.PDB	O, L_THR_105	N, L_TYR_87	H, L_TYR_87	2.83	2.01	15.92
3THM.PDB	O, L_TYR_37	N, L_TYR_88	H, L_TYR_88	2.90	2.08	14.37
3THM.PDB	O, L_SER_27	N, L_ASP_94	H, L_ASP_94	2.91	2.10	16.82
3THM.PDB	OD2, L_ASP_93	N, L_THR_95	H, L_THR_95	2.93	2.14	20.81
3THM.PDB	OD2, L_ASP_93	N, L_LEU_96	H, L_LEU_96	2.88	2.03	8.57
3THM.PDB	O, L_THR_91	N, L_VAL_100	H, L_VAL_100	2.85	2.00	6.96
3THM.PDB	O, L_CYS_89	N, L_GLY_102	H, L_GLY_102	2.91	2.09	13.69
3THM.PDB	O, L_TYR_87	N, L_THR_105	H, L_THR_105	2.90	2.14	23.36
3THM.PDB	O, L_PRO_8	N, L_LYS_106	H, L_LYS_106	2.93	2.09	11.49
3THM.PDB	O, L_ALA_85	N, L_VAL_107	H, L_VAL_107	2.85	2.01	9.33
3THM.PDB	OE1, L_GLU_84	N, L_VAL_109	H, L_VAL_109	2.88	2.08	17.71
3THM.PDB	O, L_GLU_12	N, L_LEU_110	H, L_LEU_110	2.93	2.10	11.26

3THM.PDB	OH, L_TYR_144	N, L_GLY_111	H, L_GLY_111	2.94	2.13	15.64
3THM.PDB	O, L_TYR_144	N, L_ALA_115	H, L_ALA_115	2.97	2.15	12.90
3THM.PDB	O, L_SER_141	N, L_SER_118	H, L_SER_118	2.88	2.05	12.08
3THM.PDB	O, L_LEU_139	N, L_THR_120	H, L_THR_120	2.88	2.06	14.03
3THM.PDB	O, L_VAL_137	N, L_PHE_122	H, L_PHE_122	2.87	2.03	12.38
3THM.PDB	O, L_LEU_129	N, L_ASN_132	H, L_ASN_132	2.78	1.99	19.66
3THM.PDB	OE1, L_GLU_128	N, L_THR_135	H, L_THR_135	2.71	1.92	18.59
3THM.PDB	O, L_LEU_182	N, L_LEU_136	H, L_LEU_136	2.87	2.02	9.82
3THM.PDB	O, L_SER_180	N, L_CYS_138	H, L_CYS_138	2.84	1.98	5.42
3THM.PDB	O, L_THR_120	N, L_LEU_139	H, L_LEU_139	2.76	1.90	6.56
3THM.PDB	O, L_ALA_178	N, L_ILE_140	H, L_ILE_140	2.89	2.15	25.14
3THM.PDB	O, L_SER_118	N, L_SER_141	H, L_SER_141	2.99	2.18	16.95
3THM.PDB	O, L_THR_200	N, L_THR_149	H, L_THR_149	2.96	2.13	13.40
3THM.PDB	O, L_GLN_198	N, L_ALA_151	H, L_ALA_151	2.90	2.07	13.36
3THM.PDB	OG, L_SER_180	NE1, L_TRP_152	HE1, L_TRP_152	2.84	1.99	7.64
3THM.PDB	O, L_SER_196	N, L_LYS_153	H, L_LYS_153	2.89	2.09	18.48
3THM.PDB	O, L_SER_157	N, L_ALA_154	H, L_ALA_154	2.77	1.99	21.42
3THM.PDB	O, L_SER_194	N, L_ASP_155	H, L_ASP_155	2.71	1.86	0.53
3THM.PDB	O, L_ALA_154	N, L_SER_157	H, L_SER_157	2.85	2.02	12.03
3THM.PDB	O, L_TYR_181	N, L_GLU_164	H, L_GLU_164	2.88	2.07	15.71
3THM.PDB	O, L_SER_179	N, L_THR_166	H, L_THR_166	2.84	2.02	13.98
3THM.PDB	O, L_ALA_177	N, L_SER_169	H, L_SER_169	2.84	2.02	15.98
3THM.PDB	O, L_LYS_175	N, L_GLN_171	H, L_GLN_171	2.63	1.80	12.05
3THM.PDB	OD1, L_ASP_142	NE2, L_GLN_171	HE22, L_GLN_171	2.87	2.03	8.80
3THM.PDB	O, L_GLN_171	N, L_ASN_174	H, L_ASN_174	2.95	2.14	16.29
3THM.PDB	OD1, L_ASN_173	N, L_LYS_175	H, L_LYS_175	2.86	2.05	16.58
3THM.PDB	O, L_SER_169	N, L_ALA_177	H, L_ALA_177	2.84	2.05	18.78
3THM.PDB	O, L_ILE_140	N, L_ALA_178	H, L_ALA_178	2.72	1.90	14.30
3THM.PDB	OG1, L_THR_166	N, L_SER_179	H, L_SER_179	2.86	2.02	12.53
3THM.PDB	O, L_CYS_138	N, L_SER_180	H, L_SER_180	2.89	2.07	15.30
3THM.PDB	O, L_GLU_164	N, L_TYR_181	H, L_TYR_181	2.72	1.88	12.14
3THM.PDB	O, L_GLY_162	N, L_SER_183	H, L_SER_183	2.89	2.05	9.19
3THM.PDB	O, L_ALA_134	N, L_LEU_184	H, L_LEU_184	2.75	1.90	5.72
3THM.PDB	OD1, L_ASP_155	ND1, L_HIS_192	HD1, L_HIS_192	2.84	1.98	0.83
3THM.PDB	O, L_LYS_153	N, L_SER_196	H, L_SER_196	2.82	2.02	17.68
3THM.PDB	O, L_LYS_208	N, L_CYS_197	H, L_CYS_197	2.89	2.14	23.69
3THM.PDB	O, L_ALA_151	N, L_GLN_198	H, L_GLN_198	2.69	1.85	10.52
3THM.PDB	O, L_VAL_206	N, L_VAL_199	H, L_VAL_199	2.87	2.03	11.90
3THM.PDB	O, L_THR_149	N, L_THR_200	H, L_THR_200	2.80	1.94	5.73
3THM.PDB	OG1, L_THR_205	OG1, L_THR_200	HG1, L_THR_200	2.83	2.04	14.40
3THM.PDB	O, L_SER_204	N, L_HIS_201	H, L_HIS_201	2.89	2.07	13.82
3THM.PDB	O, L_PRO_145	NE2, L_HIS_201	HE2, L_HIS_201	2.93	2.13	17.58
3THM.PDB	O, L_CYS_197	N, L_LYS_208	H, L_LYS_208	3.00	2.18	15.53
3THM.PDB	O, L_TYR_195	N, L_VAL_210	H, L_VAL_210	2.99	2.18	15.60
3THM.PDB	O, H_THR_21	N, H_SER_7	H, H_SER_7	2.99	2.26	26.55
3THM.PDB	O, H_PRO_9	N, H_LEU_11	H, H_LEU_11	2.71	1.97	25.47
3THM.PDB	O, H_THR_129	N, H_VAL_12	H, H_VAL_12	2.92	2.10	14.43
3THM.PDB	O, H_VAL_92	N, H_SER_15	H, H_SER_15	2.84	2.00	9.85
3THM.PDB	O, H_LEU_89	N, H_LEU_18	H, H_LEU_18	2.73	1.90	12.52
3THM.PDB	O, H_LEU_87	N, H_LEU_20	H, H_LEU_20	2.81	1.97	10.10
3THM.PDB	O, H_VAL_85	N, H_CYS_22	H, H_CYS_22	2.69	1.90	18.57
3THM.PDB	O, H_GLN_5	N, H_THR_23	H, H_THR_23	2.91	2.06	9.33
3THM.PDB	O, H_ASN_83	N, H_VAL_24	H, H_VAL_24	2.95	2.09	5.07
3THM.PDB	O, H_GLN_3	N, H_SER_25	H, H_SER_25	2.97	2.14	12.04
3THM.PDB	OD1, H_ASN_83	N, H_ILE_29	H, H_ILE_29	2.98	2.13	8.25
3THM.PDB	O, H_TYR_55	N, H_TYR_34	H, H_TYR_34	2.87	2.06	17.59
3THM.PDB	O, H_ILE_53	N, H_GLY_36	H, H_GLY_36	2.90	2.14	23.00
3THM.PDB	O, H_ALA_103	N, H_VAL_37	H, H_VAL_37	2.92	2.10	13.94

3THM.PDB	O, H_TYR_101	N, H_VAL_39	H, H_VAL_39	2.92	2.10	14.86
3THM.PDB	O, H_GLU_48	N, H_ARG_40	H, H_ARG_40	2.87	2.07	18.62
3THM.PDB	OE1, H_GLU_48	NE, H_ARG_40	HE, H_ARG_40	2.92	2.11	16.36
3THM.PDB	OD1, H_ASP_96	NH1, H_ARG_40	HH12, H_ARG_40	2.76	1.92	9.45
3THM.PDB	O, H_LEU_99	N, H_GLN_41	H, H_GLN_41	2.75	1.96	19.23
3THM.PDB	OE1, L_GLN_39	NE2, H_GLN_41	HE22, H_GLN_41	2.98	2.14	9.35
3THM.PDB	O, H_SER_42	N, H_LYS_45	H, H_LYS_45	2.83	2.00	12.10
3THM.PDB	O, H_ARG_40	N, H_GLU_48	H, H_GLU_48	2.98	2.23	24.84
3THM.PDB	OG, H_SER_52	NE1, H_TRP_49	HE1, H_TRP_49	2.98	2.27	29.23
3THM.PDB	O, H_TRP_38	N, H_VAL_50	H, H_VAL_50	2.78	1.93	5.54
3THM.PDB	O, H_GLY_36	N, H_ILE_53	H, H_ILE_53	2.92	2.11	15.71
3THM.PDB	O, H_SER_63	N, H_ALA_54	H, H_ALA_54	2.85	2.03	14.59
3THM.PDB	O, H_TYR_34	N, H_TYR_55	H, H_TYR_55	2.70	1.86	8.19
3THM.PDB	O, H_SER_61	N, H_ARG_56	H, H_ARG_56	2.79	1.94	3.04
3THM.PDB	O, H_TRP_49	ND2, H_ASN_67	HD21, H_ASN_67	2.99	2.17	14.54
3THM.PDB	OD1, H_ASN_67	N, H_SER_69	H, H_SER_69	2.88	2.04	9.73
3THM.PDB	O, H_PRO_68	N, H_LYS_71	H, H_LYS_71	2.99	2.15	9.73
3THM.PDB	O, H_LEU_70	N, H_ARG_73	H, H_ARG_73	2.98	2.17	16.28
3THM.PDB	O, H_THR_90	NH1, H_ARG_73	HH11, H_ARG_73	2.99	2.22	21.63
3THM.PDB	OD1, H_ASP_96	NH2, H_ARG_73	HH22, H_ARG_73	2.91	2.05	3.20
3THM.PDB	O, H_ARG_88	N, H_THR_75	H, H_THR_75	2.81	1.99	15.03
3THM.PDB	OH, H_TYR_66	N, H_VAL_76	H, H_VAL_76	2.75	1.94	15.65
3THM.PDB	O, H_GLN_84	N, H_ASP_79	H, H_ASP_79	2.81	1.97	8.52
3THM.PDB	O, H_ALA_27	ND2, H_ASN_83	HD21, H_ASN_83	2.72	1.92	17.02
3THM.PDB	O, H_VAL_24	ND2, H_ASN_83	HD22, H_ASN_83	2.73	1.93	16.56
3THM.PDB	O, H_CYS_22	N, H_VAL_85	H, H_VAL_85	2.95	2.13	13.75
3THM.PDB	O, H_SER_77	N, H_SER_86	H, H_SER_86	2.75	1.94	17.86
3THM.PDB	O, H_LEU_20	N, H_LEU_87	H, H_LEU_87	2.98	2.17	15.66
3THM.PDB	O, H_THR_75	N, H_ARG_88	H, H_ARG_88	2.85	2.03	14.81
3THM.PDB	O, H_LEU_18	N, H_LEU_89	H, H_LEU_89	2.80	2.02	20.86
3THM.PDB	O, H_ARG_73	N, H_THR_90	H, H_THR_90	2.97	2.15	16.37
3THM.PDB	OD2, H_ASP_96	N, H_THR_93	H, H_THR_93	2.92	2.12	16.99
3THM.PDB	O, H_THR_93	N, H_ASP_96	H, H_ASP_96	2.87	2.02	6.72
3THM.PDB	O, H_VAL_128	N, H_ALA_98	H, H_ALA_98	2.97	2.18	20.37
3THM.PDB	O, H_GLN_41	N, H_LEU_99	H, H_LEU_99	2.82	2.04	20.70
3THM.PDB	O, H_THR_126	N, H_TYR_100	H, H_TYR_100	2.79	1.94	6.57
3THM.PDB	O, H_VAL_39	N, H_TYR_101	H, H_TYR_101	2.82	1.97	6.69
3THM.PDB	OE2, H_GLU_6	N, H_CYS_102	H, H_CYS_102	2.91	2.11	17.93
3THM.PDB	O, H_VAL_37	N, H_ALA_103	H, H_ALA_103	2.92	2.15	22.20
3THM.PDB	O, H_VAL_121	N, H_ARG_104	H, H_ARG_104	2.93	2.16	22.36
3THM.PDB	OD1, H_ASP_120	NE, H_ARG_104	HE, H_ARG_104	2.94	2.10	9.96
3THM.PDB	OD2, H_ASP_120	NH2, H_ARG_104	HH21, H_ARG_104	2.75	2.00	25.31
3THM.PDB	O, H_TYR_35	N, H_ARG_105	H, H_ARG_105	2.94	2.12	13.20
3THM.PDB	O, F_CYS_43	NH1, H_ARG_105	HH12, H_ARG_105	2.85	2.05	18.46
3THM.PDB	O, H_ALA_118	N, H_GLN_106	H, H_GLN_106	2.92	2.09	11.12
3THM.PDB	O, H_TRP_116	N, H_LEU_108	H, H_LEU_108	2.87	2.01	4.97
3THM.PDB	O, H_TYR_114	N, H_ASP_110	H, H_ASP_110	2.97	2.20	22.11
3THM.PDB	OD2, H_ASP_110	N, H_THR_112	H, H_THR_112	2.71	1.90	15.44
3THM.PDB	OD2, H_ASP_110	OG1, H_THR_112	HG1, H_THR_112	2.76	1.95	7.38
3THM.PDB	OD1, H_ASP_109	NE2, H_GLN_115	HE21, H_GLN_115	2.80	1.96	11.40
3THM.PDB	O, H_CYS_102	N, H_GLY_123	H, H_GLY_123	2.94	2.12	14.27
3THM.PDB	OE1, H_GLU_6	N, H_GLY_125	H, H_GLY_125	2.63	1.81	15.46
3THM.PDB	O, H_TYR_100	N, H_THR_126	H, H_THR_126	2.88	2.07	16.47
3THM.PDB	O, H_ALA_98	N, H_VAL_128	H, H_VAL_128	2.86	2.04	14.39
3THM.PDB	O, H_GLY_10	N, H_THR_129	H, H_THR_129	2.91	2.10	17.08
3THM.PDB	OG1, H_THR_97	N, H_VAL_130	H, H_VAL_130	2.80	1.94	1.61
3THM.PDB	O, H_VAL_12	N, H_SER_131	H, H_SER_131	2.82	2.03	20.60
3THM.PDB	OG, H_SER_131	N, H_ALA_133	H, H_ALA_133	2.89	2.06	13.32

3THM.PDB	O, H_PHE.165	N, H_LYS.136	H, H_LYS.136	2.85	2.08	21.01
3THM.PDB	O, H_LYS.162	N, H_SER.139	H, H_SER.139	2.99	2.21	21.41
3THM.PDB	O, H_LEU.160	N, H_PHE.141	H, H_PHE.141	2.90	2.07	13.94
3THM.PDB	O, H_GLY.158	N, H_LEU.143	H, H_LEU.143	2.66	1.82	10.00
3THM.PDB	O, H_LEU.143	N, H_GLY.158	H, H_GLY.158	2.93	2.12	16.47
3THM.PDB	O, H_SER.199	N, H_ACYS.159	H, H_ACYS.159	2.87	2.09	19.75
3THM.PDB	O, H_SER.199	N, H_BCYS.159	H, H_BCYS.159	2.93	2.18	25.13
3THM.PDB	O, H_PHE.141	N, H_LEU.160	H, H_LEU.160	2.78	1.98	17.74
3THM.PDB	O, H_LEU.197	N, H_VAL.161	H, H_VAL.161	2.77	1.93	8.59
3THM.PDB	O, H_SER.139	N, H_LYS.162	H, H_LYS.162	2.85	2.00	5.79
3THM.PDB	OG, L_SER.183	NZ, H_LYS.162	HZ1, H_LYS.162	2.77	1.97	21.34
3THM.PDB	OG1, L_THR.135	NZ, H_LYS.162	HZ2, H_LYS.162	2.85	2.02	17.75
3THM.PDB	OG, H_SER.196	N, H_ASP.163	H, H_ASP.163	2.90	2.06	10.60
3THM.PDB	O, H_TYR.195	N, H_TYR.164	H, H_TYR.164	2.87	2.08	20.27
3THM.PDB	OG, H_SER.199	NE1, H_TRP.173	HE1, H_TRP.173	3.00	2.15	7.78
3THM.PDB	O, H_ILE.214	N, H_ASN.174	H, H_ASN.174	2.65	1.83	15.08
3THM.PDB	OD1, H_ASN.216	N, H_SER.175	H, H_SER.175	2.77	2.04	26.97
3THM.PDB	O, H_TRP.173	N, H_GLY.176	H, H_GLY.176	2.79	2.00	19.31
3THM.PDB	O, H_ASN.174	N, H_ALA.177	H, H_ALA.177	2.93	2.12	16.59
3THM.PDB	O, H_VAL.200	N, H_HIS.183	H, H_HIS.183	2.68	1.84	8.83
3THM.PDB	O, H_SER.198	N, H_PHE.185	H, H_PHE.185	2.88	2.05	11.29
3THM.PDB	O, H_SER.196	N, H_VAL.188	H, H_VAL.188	2.78	2.06	27.88
3THM.PDB	O, H_LEU.194	N, H_GLN.190	H, H_GLN.190	2.87	2.07	17.50
3THM.PDB	O, H_GLN.190	N, H_GLY.193	H, H_GLY.193	2.85	2.01	11.86
3THM.PDB	O, H_TYR.164	N, H_TYR.195	H, H_TYR.195	2.86	2.01	9.29
3THM.PDB	O, H_VAL.188	N, H_SER.196	H, H_SER.196	2.94	2.15	19.84
3THM.PDB	O, H_VAL.161	N, H_LEU.197	H, H_LEU.197	2.93	2.14	18.92
3THM.PDB	O, H_HIS.183	N, H_VAL.200	H, H_VAL.200	2.86	2.01	9.19
3THM.PDB	O, H_LEU.157	N, H_VAL.201	H, H_VAL.201	2.69	1.85	11.90
3THM.PDB	O, H_GLY.181	N, H_THR.202	H, H_THR.202	3.00	2.19	16.64
3THM.PDB	O, H_PRO.204	N, H_SER.207	H, H_SER.207	2.96	2.23	27.46
3THM.PDB	O, H_SER.207	N, H_GLN.211	H, H_GLN.211	2.68	1.84	9.21
3THM.PDB	OD1, H_ASN.174	N, H_ILE.214	H, H_ILE.214	2.87	2.13	26.27
3THM.PDB	O, H_LYS.228	N, H_CYS.215	H, H_CYS.215	2.84	2.07	22.53
3THM.PDB	O, H_SER.172	N, H_ASN.216	H, H_ASN.216	2.73	1.89	10.25
3THM.PDB	OD1, H_ASP.227	ND2, H_ASN.216	HD22, H_ASN.216	2.86	2.03	14.19
3THM.PDB	O, H_VAL.226	N, H_VAL.217	H, H_VAL.217	2.70	1.86	9.29
3THM.PDB	O, H_THR.170	N, H_ASN.218	H, H_ASN.218	2.97	2.15	14.77
3THM.PDB	O, H_THR.224	N, H_HIS.219	H, H_HIS.219	2.94	2.09	7.91
3THM.PDB	OG, H_SER.222	ND1, H_HIS.219	HD1, H_HIS.219	2.82	2.08	24.90
3THM.PDB	O, H_PRO.166	NE2, H_HIS.219	HE2, H_HIS.219	2.71	1.87	10.58
3THM.PDB	O, H_LYS.220	N, H_ASN.223	H, H_ASN.223	2.76	2.01	25.66
3THM.PDB	O, H_VAL.217	N, H_VAL.226	H, H_VAL.226	2.74	1.90	11.00
3THM.PDB	O, H_CYS.215	N, H_LYS.228	H, H_LYS.228	2.89	2.06	14.00
3THM.PDB	O, H_TYR.213	N, H_VAL.230	H, H_VAL.230	2.80	1.96	9.90
3THM.PDB	OD2, F_ASP.56	ND1, F_HIS.38	HD1, F_HIS.38	2.77	1.98	19.59
3THM.PDB	O, F_GLY.40	N, F_CYS.43	H, F_CYS.43	2.96	2.13	13.45
3THM.PDB	OE2, F_GLU.63	N, F_HIS.44	H, F_HIS.44	2.86	2.00	4.98
3THM.PDB	OH, H_TYR.35	ND1, F_HIS.44	HD1, F_HIS.44	2.69	1.83	5.98
3THM.PDB	OG, H_SER.63	NE2, F_HIS.44	HE2, F_HIS.44	2.83	2.07	23.36
3THM.PDB	OE1, F_GLU.63	N, F_LYS.45	H, F_LYS.45	2.81	1.99	14.79
3THM.PDB	O, F_HIS.80	N, F_CYS.47	H, F_CYS.47	2.76	1.92	10.08
3THM.PDB	OG1, F_THR.76	N, F_GLY.50	H, F_GLY.50	2.93	2.22	29.13
3THM.PDB	O, F_VAL.67	N, F_ARG.52	H, F_ARG.52	2.76	2.01	24.49
3THM.PDB	O, F_ASP.65	N, F_ALA.54	H, F_ALA.54	2.91	2.11	18.55
3THM.PDB	OG1, F_THR.58	N, F_GLY.61	H, F_GLY.61	2.96	2.22	26.61
3THM.PDB	O, F_ARG.52	N, F_VAL.67	H, F_VAL.67	2.78	1.94	11.01
3THM.PDB	O, F_GLY.50	N, F_CYS.69	H, F_CYS.69	2.95	2.13	14.13

3THM.PDB	O, F_GLN_70	N, F_LYS_73	H, F_LYS_73	2.88	2.05	12.43
3THM.PDB	O, F_GLN_70	N, F_GLU_74	H, F_GLU_74	2.89	2.05	11.11
3THM.PDB	O, F_ARG_86	N, F_TYR_75	H, F_TYR_75	2.78	2.03	24.45
3THM.PDB	O, F_ARG_105	N, F_THR_76	H, F_THR_76	2.94	2.15	19.85
3THM.PDB	O, L_SER_51	NZ, F_LYS_78	HZ2, F_LYS_78	3.00	2.15	15.09
3THM.PDB	O, F_GLU_51	NE2, F_HIS_80	HE2, F_HIS_80	2.76	1.91	6.66
3THM.PDB	O, F_TYR_75	N, F_ARG_86	H, F_ARG_86	2.77	1.94	13.51
3THM.PDB	O, F_LYS_73	N, F_CYS_88	H, F_CYS_88	2.79	1.94	5.08
3THM.PDB	OD1, F_ASN_108	N, F_ARG_89	H, F_ARG_89	2.64	1.87	22.68
3THM.PDB	O, F_GLN_107	N, F_THR_104	H, F_THR_104	2.82	1.99	12.71

Table 1683: 3THM-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
3TJE.PDB	OG, L_SER_2	N, L_LEU_4	H, L_LEU_4	2.98	2.19	19.51
3TJE.PDB	O, L_SER_23	N, L_THR_5	H, L_THR_5	2.89	2.05	11.59
3TJE.PDB	O, L_TYR_87	NE2, L_GLN_6	HE21, L_GLN_6	2.84	2.01	11.61
3TJE.PDB	O, L_LYS_106	N, L_VAL_10	H, L_VAL_10	2.95	2.15	17.08
3TJE.PDB	OE1, L_GLU_12	N, L_ALA_13	H, L_ALA_13	2.73	1.95	20.14
3TJE.PDB	O, L_LEU_79	N, L_ARG_15	H, L_ARG_15	2.84	2.01	13.10
3TJE.PDB	O, L_LEU_74	N, L_ILE_20	H, L_ILE_20	2.71	1.88	13.42
3TJE.PDB	O, L_THR_5	N, L_SER_23	H, L_SER_23	2.97	2.17	18.20
3TJE.PDB	O, L_THR_70	N, L_GLY_24	H, L_GLY_24	2.81	1.98	12.07
3TJE.PDB	OD1, L_ASN_28	N, L_ASN_25	H, L_ASN_25	2.88	2.06	15.65
3TJE.PDB	OD1, L_ASN_25	N, L_PHE_27	H, L_PHE_27	2.67	1.88	19.71
3TJE.PDB	OD1, L_ASP_93	ND2, L_ASN_28	HD21, L_ASN_28	2.73	1.89	10.95
3TJE.PDB	OD1, L_ASN_28	N, L_ILE_29	H, L_ILE_29	2.67	1.87	18.78
3TJE.PDB	O, L_ASN_25	N, L_GLY_30	H, L_GLY_30	2.98	2.19	18.64
3TJE.PDB	O, L_ASN_28	N, L_ARG_31	H, L_ARG_31	2.87	2.03	11.14
3TJE.PDB	OD1, L_ASP_94	NH1, L_ARG_31	HH11, L_ARG_31	2.81	2.04	22.49
3TJE.PDB	O, L_ASN_28	N, L_TYR_32	H, L_TYR_32	2.86	2.10	23.81
3TJE.PDB	OD1, L_ASN_52	N, L_VAL_34	H, L_VAL_34	2.85	2.02	12.87
3TJE.PDB	O, L_SER_90	N, L_ASN_35	H, L_ASN_35	2.92	2.09	12.93
3TJE.PDB	O, H_ALA_117	ND2, L_ASN_35	HD21, L_ASN_35	2.81	2.01	17.88
3TJE.PDB	O, L_ILE_49	N, L_TRP_36	H, L_TRP_36	2.75	1.91	11.08
3TJE.PDB	O, L_TYR_88	N, L_TYR_37	H, L_TYR_37	2.81	1.99	14.58
3TJE.PDB	O, L_LYS_46	N, L_GLN_38	H, L_GLN_38	2.87	2.07	18.73
3TJE.PDB	OH, L_TYR_87	NE2, L_GLN_38	HE21, L_GLN_38	2.91	2.10	17.00
3TJE.PDB	O, L_ASP_86	N, L_GLN_39	H, L_GLN_39	2.75	1.92	11.44
3TJE.PDB	O, L_LYS_43	NE2, L_GLN_39	HE21, L_GLN_39	2.96	2.17	20.11
3TJE.PDB	O, L_LEU_40	N, L_LYS_43	H, L_LYS_43	2.81	1.96	7.60
3TJE.PDB	O, L_GLN_38	N, L_LYS_46	H, L_LYS_46	2.89	2.11	21.83
3TJE.PDB	O, L_TRP_36	N, L_LEU_48	H, L_LEU_48	2.96	2.15	16.44
3TJE.PDB	O, L_LEU_54	N, L_TYR_50	H, L_TYR_50	2.88	2.07	15.46
3TJE.PDB	O, L_VAL_34	N, L_ASN_52	H, L_ASN_52	2.84	2.00	11.32
3TJE.PDB	O, L_TYR_51	N, L_ASN_53	H, L_ASN_53	2.85	2.14	29.08
3TJE.PDB	O, L_TYR_50	N, L_LEU_54	H, L_LEU_54	2.99	2.17	16.15
3TJE.PDB	O, L_PHE_63	NH1, L_ARG_55	HH11, L_ARG_55	2.88	2.12	23.88
3TJE.PDB	OD2, L_ASP_83	NH1, L_ARG_62	HH12, L_ARG_62	2.77	1.98	19.25
3TJE.PDB	OD1, L_ASP_83	NH2, L_ARG_62	HH22, L_ARG_62	2.87	2.01	3.19
3TJE.PDB	O, L_ASP_73	N, L_SER_66	H, L_SER_66	2.91	2.14	21.13
3TJE.PDB	O, L_BSER_73	N, L_SER_66	H, L_SER_66	2.91	2.13	20.97
3TJE.PDB	O, L_TYR_32	NZ, L_LYS_67	HZ2, L_LYS_67	2.82	2.02	22.26
3TJE.PDB	O, L_SER_71	N, L_SER_68	H, L_SER_68	2.88	2.03	8.39
3TJE.PDB	O, L_SER_68	N, L_SER_71	H, L_SER_71	2.99	2.15	8.41
3TJE.PDB	O, L_CYS_22	N, L_ALA_72	H, L_ALA_72	2.87	2.04	13.56
3TJE.PDB	O, L_SER_66	N, L_ASP_73	H, L_ASP_73	2.83	2.04	18.54
3TJE.PDB	O, L_SER_66	N, L_BSER_73	H, L_BSER_73	2.85	2.06	19.36
3TJE.PDB	O, L_ILE_20	N, L_LEU_74	H, L_LEU_74	2.94	2.12	13.68
3TJE.PDB	O, L_SER_64	N, L_ALA_75	H, L_ALA_75	2.88	2.03	9.17
3TJE.PDB	O, L_VAL_18	N, L_ILE_76	H, L_ILE_76	2.93	2.11	14.42
3TJE.PDB	OD2, L_ASP_78	NH1, L_ARG_77	HH11, L_ARG_77	2.74	1.93	16.91
3TJE.PDB	O, L_GLN_16	N, L_LEU_79	H, L_LEU_79	2.98	2.14	10.89
3TJE.PDB	OD2, L_ASP_83	N, L_LEU_80	H, L_LEU_80	2.81	1.96	7.20
3TJE.PDB	O, L_LEU_80	N, L_ASP_83	H, L_ASP_83	2.88	2.03	9.91
3TJE.PDB	O, L_THR_105	N, L_TYR_87	H, L_TYR_87	2.92	2.12	18.00
3TJE.PDB	O, L_TYR_37	N, L_TYR_88	H, L_TYR_88	2.91	2.09	14.23
3TJE.PDB	O, L_PRO_33	OG1, L_THR_91	HG1, L_THR_91	2.76	2.04	23.18
3TJE.PDB	O, L_GLY_98	N, L_ASP_93	H, L_ASP_93	2.88	2.03	9.26
3TJE.PDB	O, L_PHE_27	N, L_ASP_94	H, L_ASP_94	2.94	2.09	6.58
3TJE.PDB	OD2, L_ASP_93	N, L_LEU_96	H, L_LEU_96	2.80	2.01	19.19

3TJE.PDB	O, L_THR_91	N, L_VAL_100	H, L_VAL_100	2.77	1.92	9.60
3TJE.PDB	O, L_CYS_89	N, L_GLY_102	H, L_GLY_102	2.86	2.05	17.43
3TJE.PDB	O, L_TYR_87	N, L_THR_105	H, L_THR_105	2.85	2.08	21.91
3TJE.PDB	O, L_PRO_7	OG1, L_THR_105	HG1, L_THR_105	2.71	1.92	11.71
3TJE.PDB	O, L_PRO_8	N, L_LYS_106	H, L_LYS_106	2.83	1.98	10.06
3TJE.PDB	O, L_ALA_85	N, L_VAL_107	H, L_VAL_107	2.95	2.10	8.53
3TJE.PDB	OE2, L_GLU_84	N, L_VAL_109	H, L_VAL_109	2.88	2.05	12.54
3TJE.PDB	O, L_GLU_12	N, L_LEU_110	H, L_LEU_110	2.90	2.08	14.25
3TJE.PDB	OH, L_TYR_144	N, L_GLY_111	H, L_GLY_111	2.92	2.12	17.61
3TJE.PDB	O, L_TYR_144	N, L_ALA_115	H, L_ALA_115	2.80	2.00	16.96
3TJE.PDB	O, L_SER_141	N, L_SER_118	H, L_SER_118	2.91	2.14	22.45
3TJE.PDB	O, L_LEU_139	N, L_THR_120	H, L_THR_120	2.96	2.12	10.98
3TJE.PDB	O, L_VAL_137	N, L_PHE_122	H, L_PHE_122	2.77	1.92	8.56
3TJE.PDB	O, L_LEU_129	N, L_ASN_132	H, L_ASN_132	2.97	2.15	16.34
3TJE.PDB	OE2, L_GLU_128	OG1, L_THR_135	HG1, L_THR_135	2.52	1.76	18.95
3TJE.PDB	O, L_LEU_182	N, L_LEU_136	H, L_LEU_136	2.82	1.99	11.01
3TJE.PDB	O, L_SER_180	N, L_CYS_138	H, L_CYS_138	2.78	1.93	6.24
3TJE.PDB	O, L_THR_120	N, L_LEU_139	H, L_LEU_139	2.87	2.03	10.47
3TJE.PDB	O, L_ALA_178	N, L_ILE_140	H, L_ILE_140	2.83	2.07	23.88
3TJE.PDB	OE1, L_GLN_171	N, L_ASP_142	H, L_ASP_142	2.90	2.05	8.27
3TJE.PDB	O, L_ALA_115	N, L_TYR_144	H, L_TYR_144	2.95	2.16	19.36
3TJE.PDB	O, L_THR_200	N, L_THR_149	H, L_THR_149	2.90	2.10	17.11
3TJE.PDB	O, L_GLN_198	N, L_ALA_151	H, L_ALA_151	2.89	2.08	16.72
3TJE.PDB	OG, L_SER_180	NE1, L_TRP_152	HE1, L_TRP_152	2.95	2.10	8.91
3TJE.PDB	O, L_SER_157	N, L_ALA_154	H, L_ALA_154	2.87	2.03	11.03
3TJE.PDB	O, L_SER_194	N, L_ASP_155	H, L_ASP_155	2.88	2.03	6.45
3TJE.PDB	O, L_ALA_154	N, L_SER_157	H, L_SER_157	2.84	2.00	9.67
3TJE.PDB	O, L_SER_179	N, L_THR_166	H, L_THR_166	2.85	2.03	14.19
3TJE.PDB	O, L_ALA_177	N, L_SER_169	H, L_SER_169	2.80	1.99	16.63
3TJE.PDB	O, L_LYS_175	N, L_GLN_171	H, L_GLN_171	2.71	1.85	3.49
3TJE.PDB	OD1, L_ASP_142	NE2, L_GLN_171	HE21, L_GLN_171	2.80	1.98	15.09
3TJE.PDB	O, L_GLN_171	N, L_ASN_174	H, L_ASN_174	2.96	2.12	11.80
3TJE.PDB	OD1, L_ASN_173	N, L_LYS_175	H, L_LYS_175	2.90	2.05	7.85
3TJE.PDB	O, L_PHE_143	N, L_TYR_176	H, L_TYR_176	2.84	2.01	10.88
3TJE.PDB	O, L_SER_169	N, L_ALA_177	H, L_ALA_177	2.94	2.12	14.89
3TJE.PDB	O, L_ILE_140	N, L_ALA_178	H, L_ALA_178	2.67	1.87	18.00
3TJE.PDB	OG1, L_THR_166	N, L_SER_179	H, L_SER_179	2.90	2.10	18.20
3TJE.PDB	O, L_CYS_138	N, L_SER_180	H, L_SER_180	2.89	2.09	17.42
3TJE.PDB	O, L_GLU_164	N, L_TYR_181	H, L_TYR_181	2.81	1.99	15.18
3TJE.PDB	O, L_LEU_136	N, L_LEU_182	H, L_LEU_182	2.96	2.15	16.77
3TJE.PDB	O, L_GLY_162	N, L_SER_183	H, L_SER_183	2.95	2.11	9.60
3TJE.PDB	O, L_ALA_134	N, L_LEU_184	H, L_LEU_184	2.91	2.06	5.00
3TJE.PDB	OG1, L_THR_185	N, L_GLN_188	H, L_GLN_188	2.93	2.09	10.43
3TJE.PDB	O, L_THR_185	N, L_TRP_189	H, L_TRP_189	2.96	2.12	11.25
3TJE.PDB	O, L_VAL_210	N, L_TYR_195	H, L_TYR_195	2.89	2.08	15.12
3TJE.PDB	O, L_LYS_153	N, L_SER_196	H, L_SER_196	2.96	2.16	17.59
3TJE.PDB	O, L_LYS_208	N, L_CYS_197	H, L_CYS_197	2.95	2.14	16.29
3TJE.PDB	O, L_ALA_151	N, L_GLN_198	H, L_GLN_198	2.79	1.94	4.13
3TJE.PDB	O, L_VAL_206	N, L_VAL_199	H, L_VAL_199	2.84	2.01	12.78
3TJE.PDB	O, L_THR_149	N, L_THR_200	H, L_THR_200	2.81	1.96	9.64
3TJE.PDB	OG1, L_THR_205	OG1, L_THR_200	HG1, L_THR_200	2.75	1.97	15.90
3TJE.PDB	O, L_SER_204	N, L_HIS_201	H, L_HIS_201	2.96	2.13	12.24
3TJE.PDB	O, L_PRO_145	NE2, L_HIS_201	HE2, L_HIS_201	2.93	2.12	17.78
3TJE.PDB	O, L_TYR_195	N, L_VAL_210	H, L_VAL_210	2.98	2.16	15.92
3TJE.PDB	O, H_SER_25	N, H_GLN_3	H, H_GLN_3	2.88	2.06	14.24
3TJE.PDB	O, H_THR_21	N, H_SER_7	H, H_SER_7	2.87	2.11	23.93
3TJE.PDB	O, H_THR_129	N, H_VAL_12	H, H_VAL_12	2.84	2.01	13.76
3TJE.PDB	O, H_VAL_92	N, H_SER_15	H, H_SER_15	2.99	2.17	15.06

3TJE.PDB	O, H.LEU_89	N, H.LEU_18	H, H.LEU_18	2.80	1.97	12.54
3TJE.PDB	O, H.LEU_87	N, H.LEU_20	H, H.LEU_20	2.91	2.09	15.75
3TJE.PDB	O, H.SER_7	N, H.THR_21	H, H.THR_21	2.91	2.07	9.29
3TJE.PDB	O, H.VAL_85	N, H.CYS_22	H, H.CYS_22	2.64	1.80	12.14
3TJE.PDB	O, H.GLN_5	N, H.THR_23	H, H.THR_23	2.80	1.95	6.62
3TJE.PDB	O, H.ASN_83	N, H.VAL_24	H, H.VAL_24	2.83	1.97	5.09
3TJE.PDB	O, H.GLN_3	N, H.SER_25	H, H.SER_25	2.89	2.05	10.07
3TJE.PDB	OD1, H.ASN_83	N, H.ILE_29	H, H.ILE_29	2.95	2.10	5.57
3TJE.PDB	O, H.TYR_55	N, H.TYR_34	H, H.TYR_34	2.89	2.10	20.67
3TJE.PDB	O, H.ILE_53	N, H.GLY_36	H, H.GLY_36	2.94	2.15	19.40
3TJE.PDB	O, H.ALA_103	N, H.VAL_37	H, H.VAL_37	2.90	2.07	11.42
3TJE.PDB	O, H.TYR_101	N, H.VAL_39	H, H.VAL_39	2.86	2.03	12.06
3TJE.PDB	O, H.GLU_48	N, H.ARG_40	H, H.ARG_40	2.80	1.98	14.17
3TJE.PDB	OE1, H.GLU_48	NE, H.ARG_40	HE, H.ARG_40	2.72	1.90	14.58
3TJE.PDB	OD1, H.ASP_96	NH1, H.ARG_40	HH12, H.ARG_40	2.84	2.01	12.94
3TJE.PDB	O, H.LEU_99	N, H.GLN_41	H, H.GLN_41	2.86	2.14	27.68
3TJE.PDB	OE1, L.GLN_39	NE2, H.GLN_41	HE21, H.GLN_41	2.98	2.15	10.85
3TJE.PDB	O, H.LYS_45	NE2, H.GLN_41	HE22, H.GLN_41	2.99	2.23	24.37
3TJE.PDB	O, H.SER_42	N, H.LYS_45	H, H.LYS_45	2.68	1.88	17.77
3TJE.PDB	O, H.ARG_40	N, H.GLU_48	H, H.GLU_48	2.85	2.11	26.04
3TJE.PDB	O, H.TRP_38	N, H.VAL_50	H, H.VAL_50	2.78	1.93	6.45
3TJE.PDB	O, H.GLY_36	N, H.ILE_53	H, H.ILE_53	2.93	2.12	17.64
3TJE.PDB	O, H.SER_63	N, H.ALA_54	H, H.ALA_54	2.78	1.96	13.18
3TJE.PDB	O, H.TYR_34	N, H.TYR_55	H, H.TYR_55	2.89	2.08	16.16
3TJE.PDB	O, H.SER_61	N, H.ARG_56	H, H.ARG_56	2.85	1.99	1.86
3TJE.PDB	O, H.ALA_54	N, H.SER_63	H, H.SER_63	2.78	2.05	26.84
3TJE.PDB	O, H.VAL_50	N, H.ASN_67	H, H.ASN_67	2.97	2.11	4.12
3TJE.PDB	O, H.TRP_49	ND2, H.ASN_67	HD21, H.ASN_67	2.89	2.04	7.41
3TJE.PDB	OD1, H.ASN_67	N, H.SER_69	H, H.SER_69	2.97	2.12	5.43
3TJE.PDB	O, H.LEU_70	N, H.ARG_73	H, H.ARG_73	2.89	2.05	11.17
3TJE.PDB	OD2, H.ASP_96	NH1, H.ARG_73	HH12, H.ARG_73	2.84	2.09	24.31
3TJE.PDB	OD1, H.ASP_96	NH2, H.ARG_73	HH22, H.ARG_73	2.94	2.09	3.77
3TJE.PDB	O, H.ARG_88	N, H.THR_75	H, H.THR_75	2.86	2.06	17.69
3TJE.PDB	OH, H.TYR_66	N, H.VAL_76	H, H.VAL_76	2.78	1.97	16.41
3TJE.PDB	O, H.GLN_84	N, H.ASP_79	H, H.ASP_79	2.90	2.07	12.81
3TJE.PDB	OD2, H.ASP_79	OG, H.SER_81	HG, H.SER_81	2.85	2.15	27.35
3TJE.PDB	O, H.ALA_27	ND2, H.ASN_83	HD21, H.ASN_83	2.68	1.91	21.50
3TJE.PDB	O, H.VAL_24	ND2, H.ASN_83	HD22, H.ASN_83	2.83	2.02	14.94
3TJE.PDB	O, H.CYS_22	N, H.VAL_85	H, H.VAL_85	2.88	2.08	16.90
3TJE.PDB	O, H.SER_77	N, H.SER_86	H, H.SER_86	2.83	2.01	15.98
3TJE.PDB	O, H.LEU_20	N, H.LEU_87	H, H.LEU_87	2.94	2.13	16.25
3TJE.PDB	O, H.THR_75	N, H.ARG_88	H, H.ARG_88	2.86	2.03	13.96
3TJE.PDB	O, H.LEU_18	N, H.LEU_89	H, H.LEU_89	2.84	2.02	14.49
3TJE.PDB	O, H.ARG_73	N, H.THR_90	H, H.THR_90	2.85	2.04	16.07
3TJE.PDB	O, H.THR_93	N, H.ASP_96	H, H.ASP_96	2.94	2.10	9.54
3TJE.PDB	O, H.GLN_41	N, H.LEU_99	H, H.LEU_99	2.74	1.92	14.43
3TJE.PDB	O, H.THR_126	N, H.TYR_100	H, H.TYR_100	2.79	1.93	2.67
3TJE.PDB	O, H.VAL_39	N, H.TYR_101	H, H.TYR_101	2.77	1.93	10.43
3TJE.PDB	OE2, H.GLU_6	N, H.CYS_102	H, H.CYS_102	2.72	1.91	15.94
3TJE.PDB	O, H.VAL_121	N, H.ARG_104	H, H.ARG_104	2.91	2.13	21.28
3TJE.PDB	OD1, H.ASP_120	NE, H.ARG_104	HE, H.ARG_104	2.87	2.06	15.55
3TJE.PDB	OD2, H.ASP_120	NH2, H.ARG_104	HH21, H.ARG_104	2.68	1.96	27.63
3TJE.PDB	O, H.TYR_35	N, H.ARG_105	H, H.ARG_105	2.94	2.12	13.39
3TJE.PDB	O, F_CYS_43	NH1, H.ARG_105	HH12, H.ARG_105	2.85	2.08	23.11
3TJE.PDB	O, H.ALA_118	N, H.GLN_106	H, H.GLN_106	2.87	2.03	10.40
3TJE.PDB	O, H.TRP_116	N, H.LEU_108	H, H.LEU_108	2.87	2.02	4.86
3TJE.PDB	O, H.TYR_114	N, H.ASP_110	H, H.ASP_110	2.92	2.19	27.17
3TJE.PDB	OD2, H.ASP_110	N, H.THR_112	H, H.THR_112	3.00	2.17	12.16

3TJE.PDB	O, H_LEU_108	N, H_TRP_116	H, H_TRP_116	3.00	2.21	20.70
3TJE.PDB	OH, L_TYR_37	N, H_PHE_119	H, H_PHE_119	2.96	2.10	4.74
3TJE.PDB	O, H_CYS_102	N, H_GLY_123	H, H_GLY_123	2.82	2.01	17.20
3TJE.PDB	OE1, H_GLU_6	N, H_GLY_125	H, H_GLY_125	2.75	1.92	11.39
3TJE.PDB	O, H_TYR_100	N, H_THR_126	H, H_THR_126	2.90	2.10	17.97
3TJE.PDB	O, H_ALA_98	N, H_VAL_128	H, H_VAL_128	2.90	2.08	14.31
3TJE.PDB	O, H_GLY_10	N, H_THR_129	H, H_THR_129	2.80	1.96	9.76
3TJE.PDB	O, H_VAL_12	N, H_SER_131	H, H_SER_131	3.00	2.24	24.52
3TJE.PDB	O, H_PHE_165	N, H_LYS_136	H, H_LYS_136	2.83	2.02	16.58
3TJE.PDB	O, H_ASP_163	NZ, H_LYS_136	HZ2, H_LYS_136	2.77	1.97	20.93
3TJE.PDB	O, H_LEU_160	N, H_PHE_141	H, H_PHE_141	2.88	2.04	12.24
3TJE.PDB	O, H_GLY_158	N, H_LEU_143	H, H_LEU_143	2.57	1.72	7.54
3TJE.PDB	O, H_VAL_203	N, H_ALA_155	H, H_ALA_155	2.69	1.91	20.72
3TJE.PDB	O, H_LEU_143	N, H_GLY_158	H, H_GLY_158	2.85	2.05	18.58
3TJE.PDB	O, H_SER_199	N, H_CYS_159	H, H_CYS_159	2.99	2.22	22.42
3TJE.PDB	O, H_PHE_141	N, H_LEU_160	H, H_LEU_160	2.79	1.97	14.71
3TJE.PDB	O, H_LEU_197	N, H_VAL_161	H, H_VAL_161	2.81	1.97	8.46
3TJE.PDB	O, H_SER_139	N, H_ALYS_162	H, H_ALYS_162	2.77	1.93	9.67
3TJE.PDB	O, H_SER_139	N, H_BLYS_162	H, H_BLYS_162	2.78	1.95	10.83
3TJE.PDB	N, H_ALYS_162	N, H_BLYS_162	H, H_BLYS_162	0.01	0.85	29.33
3TJE.PDB	O, H_TYR_195	N, H_TYR_164	H, H_TYR_164	2.92	2.13	20.02
3TJE.PDB	OG, H_SER_199	NE1, H_TRP_173	HE1, H_TRP_173	2.95	2.10	8.21
3TJE.PDB	O, H_ILE_214	N, H_ASN_174	H, H_ASN_174	2.64	1.81	12.80
3TJE.PDB	O, H_THR_212	ND2, H_ASN_174	HD21, H_ASN_174	2.99	2.18	18.13
3TJE.PDB	OD1, H_ASN_216	N, H_SER_175	H, H_SER_175	2.79	2.01	20.02
3TJE.PDB	O, H_TRP_173	N, H_GLY_176	H, H_GLY_176	2.73	1.90	13.59
3TJE.PDB	O, H_VAL_200	N, H_HIS_183	H, H_HIS_183	2.76	1.93	13.04
3TJE.PDB	O, H_SER_198	N, H_PHE_185	H, H_PHE_185	2.93	2.09	11.93
3TJE.PDB	O, H_SER_196	N, H_VAL_188	H, H_VAL_188	2.92	2.13	19.94
3TJE.PDB	O, H_LEU_194	N, H_GLN_190	H, H_GLN_190	2.89	2.03	2.73
3TJE.PDB	OD1, H_ASP_163	NE2, H_GLN_190	HE21, H_GLN_190	2.74	1.93	16.43
3TJE.PDB	O, H_LEU_194	NE2, H_GLN_190	HE22, H_GLN_190	2.91	2.07	10.67
3TJE.PDB	O, H_GLN_190	N, H_GLY_193	H, H_GLY_193	2.82	1.99	10.97
3TJE.PDB	O, H_TYR_164	N, H_TYR_195	H, H_TYR_195	2.85	2.00	9.32
3TJE.PDB	O, H_HIS_183	N, H_VAL_200	H, H_VAL_200	2.82	2.00	16.33
3TJE.PDB	O, H_LEU_157	N, H_VAL_201	H, H_VAL_201	2.89	2.05	10.36
3TJE.PDB	O, H_ALA_155	N, H_VAL_203	H, H_VAL_203	2.94	2.10	10.75
3TJE.PDB	O, H_GLY_153	N, H_SER_205	H, H_SER_205	2.57	1.73	10.17
3TJE.PDB	OD1, H_ASN_174	N, H_ILE_214	H, H_ILE_214	2.72	1.92	17.15
3TJE.PDB	O, H_SER_172	N, H_ASN_216	H, H_ASN_216	2.85	2.03	15.86
3TJE.PDB	OD1, H_ASP_227	ND2, H_ASN_216	HD22, H_ASN_216	2.79	1.98	17.28
3TJE.PDB	O, H_VAL_226	N, H_VAL_217	H, H_VAL_217	2.75	1.89	4.56
3TJE.PDB	O, H_THR_170	N, H_AASN_218	H, H_AASN_218	2.99	2.16	12.40
3TJE.PDB	O, H_THR_170	N, H_BASN_218	H, H_BASN_218	2.97	2.14	13.28
3TJE.PDB	O, H_PRO_166	NE2, H_HIS_219	HE2, H_HIS_219	2.74	1.90	8.90
3TJE.PDB	O, H_LYS_220	N, H_ASN_223	H, H_ASN_223	2.92	2.10	14.79
3TJE.PDB	OG, H_SER_222	OG1, H_THR_224	HG1, H_THR_224	2.65	1.92	22.20
3TJE.PDB	O, H_VAL_217	N, H_VAL_226	H, H_VAL_226	2.85	2.02	13.83
3TJE.PDB	O, H_CYS_215	N, H_LYS_228	H, H_LYS_228	2.90	2.09	15.61
3TJE.PDB	O, H_TYR_213	N, H_VAL_230	H, H_VAL_230	2.88	2.03	8.45
3TJE.PDB	O, F_GLY_40	N, F_CYS_43	H, F_CYS_43	2.88	2.06	15.38
3TJE.PDB	OE2, F_GLU_63	N, F_HIS_44	H, F_HIS_44	2.91	2.05	1.72
3TJE.PDB	OH, H_TYR_35	ND1, F_HIS_44	HD1, F_HIS_44	2.56	1.70	3.69
3TJE.PDB	OE1, F_GLU_63	N, F_LYS_45	H, F_LYS_45	2.91	2.10	15.27
3TJE.PDB	O, F_HIS_80	N, F_CYS_47	H, F_CYS_47	2.82	1.98	10.44
3TJE.PDB	OG1, F_THR_76	N, F_GLY_50	H, F_GLY_50	2.74	2.01	27.76
3TJE.PDB	O, F_VAL_67	N, F_ARG_52	H, F_ARG_52	2.89	2.17	27.83
3TJE.PDB	O, F_SER_82	N, F_LYS_53	H, F_LYS_53	2.94	2.10	9.60

3TJE.PDB	O, F_ASP_65	N, F_ALA_54	H, F_ALA_54	2.88	2.07	15.43
3TJE.PDB	O, F_ARG_52	N, F_VAL_67	H, F_VAL_67	2.77	1.94	11.91
3TJE.PDB	O, F_GLY_50	N, F_CYS_69	H, F_CYS_69	2.96	2.12	10.65
3TJE.PDB	O, F_GLN_70	N, F_LYS_73	H, F_LYS_73	2.97	2.14	11.31
3TJE.PDB	O, F_GLN_70	N, F_GLU_74	H, F_GLU_74	2.91	2.06	7.91
3TJE.PDB	O, F_ARG_86	N, F_TYR_75	H, F_TYR_75	2.68	1.90	20.37
3TJE.PDB	O, F_ARG_105	N, F_THR_76	H, F_THR_76	2.92	2.12	18.47
3TJE.PDB	O, F_GLU_51	NE2, F_HIS_80	HE2, F_HIS_80	2.72	1.86	5.72
3TJE.PDB	O, F_TYR_75	N, F_ARG_86	H, F_ARG_86	2.68	1.83	6.97
3TJE.PDB	O, F_LYS_73	N, F_CYS_88	H, F_CYS_88	2.78	1.92	5.80
3TJE.PDB	OD1, F_ASN_108	N, F_AARG_89	H, F_AARG_89	2.87	2.04	11.64
3TJE.PDB	OD1, F_ASN_108	N, F_BARG_89	H, F_BARG_89	2.83	1.98	7.34
3TJE.PDB	OD1, F_ASP_92	N, F_GLY_94	H, F_GLY_94	2.84	2.05	19.77
3TJE.PDB	O, F_ASP_92	N, F_HIS_95	H, F_HIS_95	2.97	2.16	18.09
3TJE.PDB	O, F_GLU_93	N, F_GLY_96	H, F_GLY_96	2.71	1.88	12.35
3TJE.PDB	O, F_ARG_112	N, F_GLU_98	H, F_GLU_98	2.94	2.15	19.49
3TJE.PDB	O, F_LYS_110	N, F_GLU_100	H, F_GLU_100	2.61	1.76	9.32
3TJE.PDB	O, F_GLN_107	N, F_THR_104	H, F_THR_104	2.82	1.98	10.85
3TJE.PDB	O, F_ILE_101	N, F_LYS_110	H, F_LYS_110	2.83	1.99	9.81
3TJE.PDB	OE2, F_GLU_98	NE, F_ARG_112	HE, F_ARG_112	2.97	2.20	22.98
3TJE.PDB	O, F_GLY_96	N, F_LYS_114	H, F_LYS_114	2.92	2.14	21.07
3TJE.PDB	O, F_LYS_114	N, F_PHE_117	H, F_PHE_117	2.97	2.13	10.64
3TJE.PDB	O, F_ASP_128	N, F_PHE_118	H, F_PHE_118	2.93	2.18	24.79
3TJE.PDB	O, F_HIS_95	N, F_CYS_127	H, F_CYS_127	2.92	2.09	13.51

Table 1684: 3TJE-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
3U2S.PDB	O, H.SER.25	N, H.ARG.3	H, H.ARG.3	2.89	2.07	15.49
3U2S.PDB	O, H.SER.21	N, H.SER.7	H, H.SER.7	2.84	2.05	19.48
3U2S.PDB	O, H.THR.110	N, H.VAL.12	H, H.VAL.12	2.86	2.03	11.16
3U2S.PDB	O, H.LEU.82C	N, H.GLY.15	H, H.GLY.15	2.74	1.93	16.73
3U2S.PDB	O, H.MET.82	N, H.LEU.18	H, H.LEU.18	2.81	2.03	20.52
3U2S.PDB	O, H.LEU.80	N, H.LEU.20	H, H.LEU.20	2.85	2.03	14.92
3U2S.PDB	O, H.SER.7	N, H.SER.21	H, H.SER.21	2.93	2.09	10.95
3U2S.PDB	O, H.VAL.5	N, H.ALA.23	H, H.ALA.23	2.92	2.11	16.83
3U2S.PDB	O, H.ASP.76	N, H.ALA.24	H, H.ALA.24	2.96	2.10	4.40
3U2S.PDB	O, H.ASP.100L	NE, H.ARG.31	HE, H.ARG.31	2.89	2.12	21.23
3U2S.PDB	O, H.ASP.100L	NH2, H.ARG.31	HH21, H.ARG.31	2.93	2.18	24.99
3U2S.PDB	O, H.VAL.93	N, H.HIS.35	H, H.HIS.35	2.77	1.93	11.33
3U2S.PDB	OE1, H.GLU.95	NE2, H.HIS.35	HE2, H.HIS.35	2.64	1.80	11.05
3U2S.PDB	O, H.ALA.49	N, H.TRP.36	H, H.TRP.36	2.96	2.24	28.24
3U2S.PDB	O, H.TYR.79	NE1, H.TRP.36	HE1, H.TRP.36	2.98	2.22	24.67
3U2S.PDB	O, H.PHE.91	N, H.VAL.37	H, H.VAL.37	2.97	2.15	14.01
3U2S.PDB	O, H.GLU.46	N, H.ARG.38	H, H.ARG.38	2.90	2.05	8.68
3U2S.PDB	OE2, H.GLU.46	NE, H.ARG.38	HE, H.ARG.38	2.80	2.01	18.34
3U2S.PDB	OD1, H.ASP.86	NH1, H.ARG.38	HH12, H.ARG.38	2.84	2.00	11.28
3U2S.PDB	OE2, H.GLU.46	NH2, H.ARG.38	HH21, H.ARG.38	2.92	2.18	25.81
3U2S.PDB	O, H.THR.89	N, H.GLN.39	H, H.GLN.39	2.85	2.11	25.60
3U2S.PDB	OE1, H.GLN.38	NE2, H.GLN.39	HE22, H.GLN.39	2.89	2.04	8.55
3U2S.PDB	O, H.ALA.40	N, H.GLN.43	H, H.GLN.43	2.91	2.10	16.74
3U2S.PDB	O, H.ARG.38	N, H.GLU.46	H, H.GLU.46	2.82	2.01	17.41
3U2S.PDB	O, H.TRP.36	N, H.VAL.48	H, H.VAL.48	2.95	2.12	14.22
3U2S.PDB	O, H.TYR.58	N, H.PHE.50	H, H.PHE.50	2.96	2.16	17.41
3U2S.PDB	O, H.MET.34	N, H.ILE.51	H, H.ILE.51	2.86	2.05	16.44
3U2S.PDB	O, H.GLU.56	N, H.LYS.52	H, H.LYS.52	2.94	2.08	3.51
3U2S.PDB	O, H.PHE.100J	OH, H.TYR.52A	HH, H.TYR.52A	2.62	1.87	20.61
3U2S.PDB	O, H.LYS.52	N, H.GLY.54	H, H.GLY.54	2.83	2.01	14.33
3U2S.PDB	O, H.PHE.50	N, H.TYR.58	H, H.TYR.58	2.91	2.10	17.46
3U2S.PDB	O, H.VAL.48	N, H.ALA.60	H, H.ALA.60	2.97	2.15	15.16
3U2S.PDB	OE1, H.GLU.46	OG, H.SER.62	HG, H.SER.62	2.75	1.94	7.42
3U2S.PDB	O, H.VAL.63	N, H.ARG.66	H, H.ARG.66	2.80	2.00	17.44
3U2S.PDB	OD2, H.ASP.86	NH1, H.ARG.66	HH12, H.ARG.66	2.53	1.74	19.65
3U2S.PDB	OD1, H.ASP.86	NH2, H.ARG.66	HH22, H.ARG.66	2.93	2.08	7.53
3U2S.PDB	O, H.VAL.63	N, H.LEU.67	H, H.LEU.67	2.93	2.08	6.74
3U2S.PDB	O, H.GLN.81	N, H.SER.68	H, H.SER.68	2.87	2.07	17.94
3U2S.PDB	OD1, H.ASN.73	NE, H.ARG.71	HE, H.ARG.71	2.77	1.98	19.66
3U2S.PDB	O, H.GLN.32	NH1, H.ARG.71	HH12, H.ARG.71	2.91	2.17	26.10
3U2S.PDB	O, H.THR.77	N, H.ASP.72	H, H.ASP.72	2.85	2.01	9.05
3U2S.PDB	O, H.TYR.52A	ND2, H.ASN.73	HD22, H.ASN.73	2.99	2.13	6.14
3U2S.PDB	O, H.LYS.75	OG1, H.THR.77	HG1, H.THR.77	2.81	2.01	11.82
3U2S.PDB	O, H.CYS.22	N, H.LEU.78	H, H.LEU.78	2.95	2.13	14.49
3U2S.PDB	O, H.SER.70	N, H.TYR.79	H, H.TYR.79	2.84	1.99	5.70
3U2S.PDB	O, H.LEU.20	N, H.LEU.80	H, H.LEU.80	2.94	2.14	17.83
3U2S.PDB	O, H.SER.68	N, H.GLN.81	H, H.GLN.81	2.80	1.98	14.94
3U2S.PDB	O, H.LEU.18	N, H.MET.82	H, H.MET.82	2.77	1.95	13.17
3U2S.PDB	O, H.ARG.66	N, H.ASN.82A	H, H.ASN.82A	2.84	2.00	7.73
3U2S.PDB	OD2, H.ASP.86	N, H.ARG.83	H, H.ARG.83	2.90	2.08	14.43
3U2S.PDB	O, H.ARG.83	N, H.ASP.86	H, H.ASP.86	2.86	2.02	10.14
3U2S.PDB	O, H.VAL.84	N, H.THR.87	H, H.THR.87	2.92	2.08	10.30
3U2S.PDB	O, H.VAL.109	N, H.ALA.88	H, H.ALA.88	2.93	2.20	26.51
3U2S.PDB	O, H.GLN.39	N, H.THR.89	H, H.THR.89	2.92	2.16	23.30
3U2S.PDB	O, H.THR.107	N, H.TYR.90	H, H.TYR.90	2.86	2.02	9.16
3U2S.PDB	O, H.VAL.37	N, H.PHE.91	H, H.PHE.91	2.69	1.83	4.03
3U2S.PDB	OE2, H.GLU.6	N, H.CYS.92	H, H.CYS.92	2.82	1.99	11.94

3U2S.PDB	O, H.HIS_35	N, H.VAL_93	H, H.VAL_93	2.98	2.21	22.76
3U2S.PDB	O, H.VAL_102	N, H.ARG_94	H, H.ARG_94	2.86	2.04	14.82
3U2S.PDB	OD1, H.ASP_101	NE, H.ARG_94	HE, H.ARG_94	2.95	2.09	2.87
3U2S.PDB	OD2, H.ASP_101	NH2, H.ARG_94	HH21, H.ARG_94	2.85	2.03	14.60
3U2S.PDB	O, H.TYR_100S	N, H.ALA_96	H, H.ALA_96	2.80	1.96	10.51
3U2S.PDB	O, H.TYR_100E	N, H.ARG_100B	H, H.ARG_100B	2.95	2.16	20.33
3U2S.PDB	O, H.ARG_100B	N, H.TYR_100E	H, H.TYR_100E	2.87	2.03	10.02
3U2S.PDB	O, H.GLY_100M	N, H.ASP_100I	H, H.ASP_100I	2.85	2.06	18.58
3U2S.PDB	OD1, H.ASP_100I	N, H.PHE_100J	H, H.PHE_100J	2.74	2.00	25.64
3U2S.PDB	O, H.ARG_31	N, H.TYR_100N	H, H.TYR_100N	2.93	2.08	7.40
3U2S.PDB	O, H.GLY_98	N, H.TYR_100O	H, H.TYR_100O	2.86	2.13	27.57
3U2S.PDB	O, H.ALA_96	N, H.TYR_100Q	H, H.TYR_100Q	2.80	1.95	7.01
3U2S.PDB	OH, L.TYR_36	N, H.MET_100T	H, H.MET_100T	2.95	2.15	18.41
3U2S.PDB	OE1, H.GLU_6	N, H.GLY_106	H, H.GLY_106	2.86	2.05	16.47
3U2S.PDB	O, H.TYR_90	N, H.THR_107	H, H.THR_107	2.97	2.17	19.03
3U2S.PDB	O, H.ALA_88	N, H.VAL_109	H, H.VAL_109	2.87	2.02	6.55
3U2S.PDB	O, H.GLY_10	N, H.THR_110	H, H.THR_110	2.97	2.13	11.00
3U2S.PDB	OG1, H.THR_87	N, H.VAL_111	H, H.VAL_111	2.85	1.99	5.74
3U2S.PDB	O, H.VAL_12	N, H.SER_112	H, H.SER_112	2.94	2.12	13.79
3U2S.PDB	OG, H.SER_112	N, H.ALA_114	H, H.ALA_114	2.87	2.03	9.67
3U2S.PDB	O, H.PHE_146	N, H.LYS_117	H, H.LYS_117	2.83	1.99	11.04
3U2S.PDB	O, H.ASP_144	NZ, H.LYS_117	HZ2, H.LYS_117	2.56	1.71	13.65
3U2S.PDB	O, H.LYS_143	N, H.SER_120	H, H.SER_120	2.85	2.04	16.72
3U2S.PDB	O, H.LEU_141	N, H.PHE_122	H, H.PHE_122	2.95	2.11	11.99
3U2S.PDB	O, H.GLY_139	N, H.LEU_124	H, H.LEU_124	2.81	1.97	10.93
3U2S.PDB	O, H.VAL_184	N, H.ALA_136	H, H.ALA_136	2.85	2.04	17.15
3U2S.PDB	O, H.SER_180	N, H.CYS_140	H, H.CYS_140	2.86	2.06	19.17
3U2S.PDB	O, H.PHE_122	N, H.LEU_141	H, H.LEU_141	2.84	2.00	10.39
3U2S.PDB	O, H.LEU_178	N, H.VAL_142	H, H.VAL_142	2.75	1.92	11.05
3U2S.PDB	O, H.SER_120	N, H.LYS_143	H, H.LYS_143	2.79	1.93	5.65
3U2S.PDB	O, H.LYS_117	N, H.PHE_146	H, H.PHE_146	2.94	2.13	15.74
3U2S.PDB	O, H.ASN_199	N, H.THR_151	H, H.THR_151	2.99	2.18	16.40
3U2S.PDB	O, H.ASN_197	N, H.SER_153	H, H.SER_153	2.95	2.14	16.70
3U2S.PDB	OG, H.SER_180	NE1, H.TRP_154	HE1, H.TRP_154	2.93	2.08	7.46
3U2S.PDB	O, H.ILE_195	N, H.ASN_155	H, H.ASN_155	2.79	1.95	11.05
3U2S.PDB	OD1, H.ASN_197	N, H.SER_156	H, H.SER_156	2.71	1.93	20.75
3U2S.PDB	O, H.TRP_154	N, H.GLY_157	H, H.GLY_157	2.86	2.13	26.48
3U2S.PDB	O, H.ASN_155	N, H.ALA_158	H, H.ALA_158	2.95	2.09	5.38
3U2S.PDB	O, H.VAL_181	N, H.HIS_164	H, H.HIS_164	2.77	1.95	14.28
3U2S.PDB	OG, L.SER_165	NE2, H.HIS_164	HE2, H.HIS_164	2.93	2.12	16.97
3U2S.PDB	O, H.SER_179	N, H.PHE_166	H, H.PHE_166	2.88	2.02	1.67
3U2S.PDB	O, H.SER_177	N, H.VAL_169	H, H.VAL_169	2.82	2.01	16.07
3U2S.PDB	O, H.LEU_175	NE2, H.GLN_171	HE21, H.GLN_171	2.97	2.11	6.21
3U2S.PDB	OD2, H.ASP_144	NE2, H.GLN_171	HE22, H.GLN_171	2.87	2.09	20.57
3U2S.PDB	O, H.GLN_171	N, H.GLY_174	H, H.GLY_174	2.90	2.05	6.90
3U2S.PDB	O, H.TYR_145	N, H.TYR_176	H, H.TYR_176	2.78	1.93	7.16
3U2S.PDB	O, H.VAL_169	N, H.SER_177	H, H.SER_177	2.99	2.22	22.23
3U2S.PDB	O, H.VAL_142	N, H.LEU_178	H, H.LEU_178	2.92	2.13	19.87
3U2S.PDB	O, H.CYS_140	N, H.SER_180	H, H.SER_180	2.96	2.15	15.32
3U2S.PDB	O, H.HIS_164	N, H.VAL_181	H, H.VAL_181	2.88	2.05	12.91
3U2S.PDB	O, H.LEU_138	N, H.VAL_182	H, H.VAL_182	2.85	2.03	14.42
3U2S.PDB	O, H.ALA_136	N, H.VAL_184	H, H.VAL_184	2.90	2.07	11.08
3U2S.PDB	O, H.PRO_185	N, H.SER_188	H, H.SER_188	2.91	2.12	19.48
3U2S.PDB	O, H.SER_188	N, H.GLN_192	H, H.GLN_192	2.76	1.90	4.37
3U2S.PDB	OD1, H.ASN_155	N, H.ILE_195	H, H.ILE_195	2.89	2.08	16.84
3U2S.PDB	O, H.LYS_209	N, H.CYS_196	H, H.CYS_196	2.96	2.19	21.56
3U2S.PDB	O, H.SER_153	N, H.ASN_197	H, H.ASN_197	2.74	1.90	9.86
3U2S.PDB	OD2, H.ASP_208	ND2, H.ASN_197	HD21, H.ASN_197	2.76	1.92	10.02

3U2S.PDB	O, H.VAL_207	N, H.VAL_198	H, H.VAL_198	2.74	1.88	1.51
3U2S.PDB	O, H.THR_151	N, H.ASN_199	H, H.ASN_199	2.98	2.15	13.83
3U2S.PDB	O, H.THR_205	N, H.HIS_200	H, H.HIS_200	2.86	2.01	7.91
3U2S.PDB	OG, H.SER_203	ND1, H.HIS_200	HD1, H.HIS_200	2.77	1.92	6.39
3U2S.PDB	O, H.PRO_147	NE2, H.HIS_200	HE2, H.HIS_200	2.63	1.80	12.76
3U2S.PDB	O, H.LYS_201	N, H.ASN_204	H, H.ASN_204	2.93	2.10	12.81
3U2S.PDB	O, H.VAL_198	N, H.VAL_207	H, H.VAL_207	2.81	1.98	12.69
3U2S.PDB	O, H.CYS_196	N, H.LYS_209	H, H.LYS_209	2.98	2.15	13.52
3U2S.PDB	O, H.TYR_194	N, H.VAL_211	H, H.VAL_211	2.76	1.91	7.74
3U2S.PDB	O, L.GLN_24	N, L.THR_5	H, L.THR_5	2.92	2.09	11.98
3U2S.PDB	O, L.TYR_86	NE2, L.GLN_6	HE22, L.GLN_6	2.90	2.07	12.85
3U2S.PDB	O, L.LYS_103	N, L.VAL_11	H, L.VAL_11	2.95	2.14	17.04
3U2S.PDB	O, L.LEU_78	N, L.GLY_16	H, L.GLY_16	2.87	2.09	21.13
3U2S.PDB	O, L.ILE_75	N, L.ILE_19	H, L.ILE_19	3.00	2.19	17.55
3U2S.PDB	OG1, L.THR_74	OG1, L.THR_20	HG1, L.THR_20	2.83	2.11	23.78
3U2S.PDB	O, L.LEU_73	N, L.ILE_21	H, L.ILE_21	2.80	1.99	15.96
3U2S.PDB	O, L.THR_5	N, L.GLN_24	H, L.GLN_24	2.89	2.07	13.09
3U2S.PDB	O, L.ASN_69	N, L.GLY_25	H, L.GLY_25	2.76	1.90	2.23
3U2S.PDB	OD1, L.ASP_27B	N, L.THR_26	H, L.THR_26	2.75	1.92	10.72
3U2S.PDB	OD2, L.ASP_27B	OG1, L.THR_26	HG1, L.THR_26	2.86	2.11	19.40
3U2S.PDB	OD1, L.ASP_27B	N, L.VAL_27C	H, L.VAL_27C	2.60	1.80	17.74
3U2S.PDB	O, L.THR_26	N, L.GLY_28	H, L.GLY_28	2.91	2.07	11.04
3U2S.PDB	O, L.ASP_27B	N, L.GLY_29	H, L.GLY_29	2.99	2.17	15.01
3U2S.PDB	O, L.LYS_89	N, L.SER_34	H, L.SER_34	2.88	2.09	20.40
3U2S.PDB	O, L.ILE_48	N, L.TRP_35	H, L.TRP_35	2.79	1.99	17.98
3U2S.PDB	O, L.TYR_87	N, L.TYR_36	H, L.TYR_36	2.86	2.11	24.00
3U2S.PDB	O, L.LYS_45	N, L.GLN_37	H, L.GLN_37	2.86	2.04	13.48
3U2S.PDB	OH, L.TYR_86	NE2, L.GLN_37	HE21, L.GLN_37	2.82	1.97	2.95
3U2S.PDB	O, L.ASP_85	N, L.GLN_38	H, L.GLN_38	2.74	1.95	19.17
3U2S.PDB	O, L.LYS_42	NE2, L.GLN_38	HE21, L.GLN_38	2.89	2.06	12.72
3U2S.PDB	OE1, H.GLN_39	NE2, L.GLN_38	HE22, L.GLN_38	2.91	2.09	13.75
3U2S.PDB	O, L.GLN_37	N, L.LYS_45	H, L.LYS_45	2.88	2.16	27.52
3U2S.PDB	O, L.TRP_35	N, L.VAL_47	H, L.VAL_47	2.82	1.99	13.03
3U2S.PDB	O, L.LYS_53	N, L.TYR_49	H, L.TYR_49	2.89	2.08	17.33
3U2S.PDB	O, L.VAL_33	N, L.VAL_51	H, L.VAL_51	2.83	1.98	6.67
3U2S.PDB	O, L.ASP_50	N, L.SER_52	H, L.SER_52	2.90	2.20	29.99
3U2S.PDB	O, L.TYR_49	N, L.LYS_53	H, L.LYS_53	2.86	2.03	13.95
3U2S.PDB	OD2, L.ASP_50	NZ, L.LYS_53	HZ2, L.LYS_53	2.84	1.96	4.63
3U2S.PDB	O, L.PHE_62	NH1, L.ARG_54	HH11, L.ARG_54	2.99	2.19	18.54
3U2S.PDB	OD2, C.ASP_167	ND2, L.ASN_60	HD22, L.ASN_60	2.90	2.14	22.76
3U2S.PDB	OD2, L.ASP_82	NH1, L.ARG_61	HH12, L.ARG_61	2.86	2.09	21.77
3U2S.PDB	OD1, L.ASP_82	NH2, L.ARG_61	HH22, L.ARG_61	2.97	2.11	4.14
3U2S.PDB	O, L.THR_74	N, L.SER_63	H, L.SER_63	2.98	2.16	15.11
3U2S.PDB	O, L.SER_72	N, L.SER_65	H, L.SER_65	2.99	2.19	18.65
3U2S.PDB	OE2, L.GLU_31	NZ, L.LYS_66	HZ1, L.LYS_66	2.99	2.15	15.69
3U2S.PDB	O, L.VAL_27C	NZ, L.LYS_66	HZ3, L.LYS_66	2.87	2.07	20.96
3U2S.PDB	O, L.THR_70	N, L.SER_67	H, L.SER_67	2.98	2.14	11.28
3U2S.PDB	O, L.CYS_23	N, L.ALA_71	H, L.ALA_71	2.87	2.04	13.61
3U2S.PDB	O, L.SER_65	N, L.SER_72	H, L.SER_72	2.80	1.98	13.45
3U2S.PDB	O, L.ILE_21	N, L.LEU_73	H, L.LEU_73	2.88	2.06	14.21
3U2S.PDB	O, L.SER_63	N, L.THR_74	H, L.THR_74	2.87	2.03	10.26
3U2S.PDB	O, L.ILE_19	N, L.ILE_75	H, L.ILE_75	2.92	2.10	15.07
3U2S.PDB	O, L.GLN_17	N, L.LEU_78	H, L.LEU_78	2.99	2.15	10.36
3U2S.PDB	OD2, L.ASP_82	N, L.GLN_79	H, L.GLN_79	2.81	1.96	8.38
3U2S.PDB	O, L.GLN_79	N, L.ASP_82	H, L.ASP_82	2.92	2.07	8.13
3U2S.PDB	O, L.GLN_38	N, L.ASP_85	H, L.ASP_85	2.89	2.05	8.81
3U2S.PDB	O, L.THR_102	N, L.TYR_86	H, L.TYR_86	2.77	1.96	15.94
3U2S.PDB	OE1, L.GLN_6	N, L.CYS_88	H, L.CYS_88	2.99	2.16	12.72

3U2S.PDB	O, L-ARG_95A	N, L-THR_92	H, L-THR_92	2.99	2.23	24.29
3U2S.PDB	O, L-THR_92	N, L-ARG_95	H, L-ARG_95	2.97	2.16	16.66
3U2S.PDB	OD1, H-ASP_61	NH2, L-ARG_95A	HH22, L-ARG_95A	2.34	1.58	22.53
3U2S.PDB	OE2, H-GLU_95	NH2, L-ARG_96	HH21, L-ARG_96	2.87	2.05	15.72
3U2S.PDB	O, L-CYS_88	N, L-GLY_99	H, L-GLY_99	2.79	1.97	14.65
3U2S.PDB	O, L-TYR_86	N, L-THR_102	H, L-THR_102	2.76	2.00	23.00
3U2S.PDB	O, L-PRO_7	OG1, L-THR_102	HG1, L-THR_102	2.63	1.82	4.45
3U2S.PDB	O, L-ALA_8	N, L-LYS_103	H, L-LYS_103	2.97	2.12	6.71
3U2S.PDB	O, L-GLY_84	N, L-LEU_104	H, L-LEU_104	2.88	2.02	5.05
3U2S.PDB	O, L-VAL_11	N, L-THR_105	H, L-THR_105	2.95	2.13	14.49
3U2S.PDB	OE1, L-GLU_83	N, L-VAL_106	H, L-VAL_106	2.89	2.07	15.38
3U2S.PDB	O, L-GLY_13	N, L-LEU_106A	H, L-LEU_106A	2.94	2.12	14.62
3U2S.PDB	O, L-TYR_140	N, L-ALA_111	H, L-ALA_111	2.82	1.98	11.85
3U2S.PDB	O, L-SER_137	N, L-SER_114	H, L-SER_114	2.77	1.94	12.77
3U2S.PDB	O, L-LEU_135	N, L-THR_116	H, L-THR_116	2.87	2.04	11.07
3U2S.PDB	O, L-VAL_133	N, L-PHE_118	H, L-PHE_118	2.76	1.92	9.67
3U2S.PDB	O, L-SER_122	N, L-GLN_126	H, L-GLN_126	2.90	2.12	21.06
3U2S.PDB	O, L-GLU_124	N, L-ALA_127	H, L-ALA_127	2.91	2.17	26.56
3U2S.PDB	O, L-LEU_125	N, L-ASN_128	H, L-ASN_128	2.96	2.14	16.25
3U2S.PDB	OE2, L-GLU_124	OG1, L-THR_131	HG1, L-THR_131	2.54	1.83	25.31
3U2S.PDB	O, L-LEU_178	N, L-LEU_132	H, L-LEU_132	2.88	2.05	12.78
3U2S.PDB	O, L-SER_176	N, L-CYS_134	H, L-CYS_134	2.76	1.90	1.60
3U2S.PDB	O, L-THR_116	N, L-LEU_135	H, L-LEU_135	2.74	1.89	1.47
3U2S.PDB	O, L-ALA_174	N, L-ILE_136	H, L-ILE_136	2.84	2.02	15.96
3U2S.PDB	O, L-SER_114	N, L-SER_137	H, L-SER_137	2.84	2.03	17.34
3U2S.PDB	OE1, L-GLN_167	N, L-ASP_138	H, L-ASP_138	2.90	2.06	11.00
3U2S.PDB	O, L-ALA_111	N, L-TYR_140	H, L-TYR_140	2.92	2.12	18.95
3U2S.PDB	O, L-PRO_141	N, L-ALA_143	H, L-ALA_143	2.92	2.21	29.24
3U2S.PDB	O, L-THR_196	N, L-THR_145	H, L-THR_145	2.91	2.08	11.19
3U2S.PDB	O, L-GLN_194	N, L-ALA_147	H, L-ALA_147	2.84	2.02	14.58
3U2S.PDB	OG, L-SER_176	NE1, L-TRP_148	HE1, L-TRP_148	2.93	2.09	11.15
3U2S.PDB	O, L-SER_192	N, L-LYS_149	H, L-LYS_149	2.92	2.14	21.71
3U2S.PDB	O, L-SER_153	N, L-ALA_150	H, L-ALA_150	2.77	2.00	21.57
3U2S.PDB	O, L-SER_190	N, L-ASP_151	H, L-ASP_151	2.62	1.78	11.93
3U2S.PDB	O, L-TRP_148	N, L-VAL_155	H, L-VAL_155	2.98	2.16	15.40
3U2S.PDB	O, L-SER_175	N, L-THR_162	H, L-THR_162	2.82	2.00	14.91
3U2S.PDB	O, L-ALA_173	N, L-SER_165	H, L-SER_165	2.74	1.91	13.98
3U2S.PDB	O, L-LYS_171	N, L-GLN_167	H, L-GLN_167	2.73	1.88	8.55
3U2S.PDB	OD1, L-ASP_138	NE2, L-GLN_167	HE22, L-GLN_167	2.82	2.00	15.99
3U2S.PDB	OD1, L-ASP_138	ND2, L-ASN_169	HD22, L-ASN_169	2.92	2.10	15.30
3U2S.PDB	O, L-GLN_167	N, L-ASN_170	H, L-ASN_170	2.88	2.04	11.78
3U2S.PDB	OD1, L-ASN_169	N, L-LYS_171	H, L-LYS_171	2.91	2.07	8.70
3U2S.PDB	O, L-PHE_139	N, L-TYR_172	H, L-TYR_172	2.84	2.05	19.75
3U2S.PDB	O, L-SER_165	N, L-ALA_173	H, L-ALA_173	2.93	2.10	13.60
3U2S.PDB	O, L-ILE_136	N, L-ALA_174	H, L-ALA_174	2.74	1.97	22.21
3U2S.PDB	OG1, L-THR_162	N, L-SER_175	H, L-SER_175	2.92	2.13	19.21
3U2S.PDB	O, L-CYS_134	N, L-SER_176	H, L-SER_176	2.86	2.05	17.04
3U2S.PDB	O, L-GLU_160	N, L-TYR_177	H, L-TYR_177	2.73	1.94	18.58
3U2S.PDB	O, L-GLY_158	N, L-SER_179	H, L-SER_179	2.88	2.05	11.87
3U2S.PDB	O, L-ALA_130	N, L-LEU_180	H, L-LEU_180	2.86	2.01	7.38
3U2S.PDB	OE1, L-GLN_184	N, L-THR_181	H, L-THR_181	2.99	2.19	18.35
3U2S.PDB	O, L-VAL_206	N, L-TYR_191	H, L-TYR_191	2.95	2.11	11.29
3U2S.PDB	O, L-LYS_149	N, L-SER_192	H, L-SER_192	2.91	2.11	17.67
3U2S.PDB	O, L-ALA_147	N, L-GLN_194	H, L-GLN_194	2.75	1.91	11.28
3U2S.PDB	O, L-VAL_202	N, L-VAL_195	H, L-VAL_195	2.80	1.94	3.08
3U2S.PDB	O, L-THR_145	N, L-THR_196	H, L-THR_196	2.78	1.97	15.99
3U2S.PDB	OG1, L-THR_201	OG1, L-THR_196	HG1, L-THR_196	2.99	2.20	12.41
3U2S.PDB	O, L-SER_200	N, L-HIS_197	H, L-HIS_197	2.83	1.99	8.72

3U2S.PDB	O, L.PRO_141	NE2, L.HIS_197	HE2, L.HIS_197	2.95	2.17	20.02
3U2S.PDB	O, L.HIS_197	N, L.SER_200	H, L.SER_200	2.95	2.10	9.03
3U2S.PDB	O, L.VAL_195	N, L.VAL_202	H, L.VAL_202	2.82	1.99	11.70
3U2S.PDB	O, L.VAL_115	NZ, L.LYS_204	HZ2, L.LYS_204	2.85	2.09	26.22
3U2S.PDB	O, L.TYR_191	N, L.VAL_206	H, L.VAL_206	2.98	2.18	18.28
3U2S.PDB	O, G.THR_201	N, G.PHE_121	H, G.PHE_121	2.70	1.87	12.95
3U2S.PDB	O, G.PHE_235	N, G.ALA_124	H, G.ALA_124	2.87	2.04	12.10
3U2S.PDB	O, G.GLN_197	N, G.ALA_125	H, G.ALA_125	2.88	2.10	21.74
3U2S.PDB	O, G.VAL_237	N, G.CYS_126	H, G.CYS_126	2.73	1.95	20.04
3U2S.PDB	O, G.SER_195	N, G.VAL_127	H, G.VAL_127	2.86	2.06	17.61
3U2S.PDB	O, G.LEU_193	N, G.LEU_129	H, G.LEU_129	2.74	1.88	2.50
3U2S.PDB	O, G.TYR_191	N, G.CYS_131	H, G.CYS_131	2.75	1.91	8.80
3U2S.PDB	O, G.HIS_156	N, G.THR_132	H, G.THR_132	2.82	2.00	14.90
3U2S.PDB	O, G.PHE_176	N, G.LYS_155	H, G.LYS_155	2.81	1.97	9.94
3U2S.PDB	O, G.ALA_174	N, G.CYS_157	H, G.CYS_157	2.84	2.08	23.82
3U2S.PDB	O, G.GLN_170	N, G.ILE_161	H, G.ILE_161	2.99	2.16	11.12
3U2S.PDB	O, H.ASN_100F	N, G.LYS_169	H, G.LYS_169	2.84	1.99	7.68
3U2S.PDB	O, G.ILE_161	N, G.GLN_170	H, G.GLN_170	2.91	2.11	17.48
3U2S.PDB	O, G.PHE_159	N, G.VAL_172	H, G.VAL_172	2.63	1.79	10.86
3U2S.PDB	OH, H.TYR_100K	ND2, G.ASN_173	HD21, G.ASN_173	2.97	2.13	8.87
3U2S.PDB	O, G.LYS_155	N, G.PHE_176	H, G.PHE_176	2.95	2.13	15.03
3U2S.PDB	O, G.CYS_131	N, G.TYR_191	H, G.TYR_191	2.70	1.86	8.47
3U2S.PDB	O, G.LEU_129	N, G.LEU_193	H, G.LEU_193	2.86	2.06	17.04
3U2S.PDB	O, G.VAL_127	N, G.SER_195	H, G.SER_195	2.90	2.06	10.61
3U2S.PDB	O, G.ALA_125	N, G.GLN_197	H, G.GLN_197	2.97	2.17	17.81
3U2S.PDB	O, G.ALA_209	N, G.PHE_213	H, G.PHE_213	2.92	2.06	4.30
3U2S.PDB	O, G.ALA_210	N, G.LYS_214	H, G.LYS_214	2.72	1.91	16.83
3U2S.PDB	O, G.VAL_212	N, G.TYR_216	H, G.TYR_216	2.98	2.15	13.12
3U2S.PDB	O, G.LYS_214	N, G.ASN_218	H, G.ASN_218	2.94	2.11	12.77
3U2S.PDB	O, G.GLN_215	N, G.ASP_219	H, G.ASP_219	2.86	2.06	18.20
3U2S.PDB	O, G.THR_232	OG1, G.THR_234	HG1, G.THR_234	2.83	2.05	16.75
3U2S.PDB	O, G.LYS_122	N, G.PHE_235	H, G.PHE_235	2.85	2.08	22.39
3U2S.PDB	O, G.THR_227	N, G.THR_236	H, G.THR_236	2.90	2.11	19.48
3U2S.PDB	O, G.ALA_124	N, G.VAL_237	H, G.VAL_237	2.94	2.12	15.29
3U2S.PDB	O, G.CYS_126	N, G.GLU_239	H, G.GLU_239	2.92	2.11	16.99
3U2S.PDB	O, A.SER_25	N, A.ARG_3	H, A.ARG_3	2.90	2.11	19.62
3U2S.PDB	O, A.ALA_23	N, A.VAL_5	H, A.VAL_5	2.99	2.20	19.87
3U2S.PDB	O, A.SER_21	N, A.SER_7	H, A.SER_7	2.83	2.05	20.30
3U2S.PDB	O, A.THR_110	N, A.VAL_12	H, A.VAL_12	2.89	2.06	13.20
3U2S.PDB	O, A.LEU_82C	N, A.GLY_15	H, A.GLY_15	2.82	2.05	22.09
3U2S.PDB	O, A.MET_82	N, A.LEU_18	H, A.LEU_18	2.86	2.07	19.99
3U2S.PDB	OE1, A.GLN_81	NH1, A.ARG_19	HH11, A.ARG_19	2.87	2.10	22.03
3U2S.PDB	O, A.LEU_80	N, A.LEU_20	H, A.LEU_20	2.84	2.01	14.35
3U2S.PDB	O, A.SER_7	N, A.SER_21	H, A.SER_21	2.96	2.12	10.61
3U2S.PDB	O, A.VAL_5	N, A.ALA_23	H, A.ALA_23	2.92	2.09	13.34
3U2S.PDB	O, A.ASP_76	N, A.ALA_24	H, A.ALA_24	2.97	2.11	3.15
3U2S.PDB	O, A.ARG_3	N, A.SER_25	H, A.SER_25	2.95	2.14	17.02
3U2S.PDB	O, A.ASP_100L	NE, A.ARG_31	HE, A.ARG_31	2.88	2.08	17.86
3U2S.PDB	O, A.VAL_93	N, A.HIS_35	H, A.HIS_35	2.73	1.90	11.49
3U2S.PDB	OE1, A.GLU_95	NE2, A.HIS_35	HE2, A.HIS_35	2.70	1.86	8.94
3U2S.PDB	O, A.ALA_49	N, A.TRP_36	H, A.TRP_36	3.00	2.25	25.82
3U2S.PDB	O, A.TYR_79	NE1, A.TRP_36	HE1, A.TRP_36	2.96	2.23	27.73
3U2S.PDB	O, A.PHE_91	N, A.VAL_37	H, A.VAL_37	2.92	2.09	14.10
3U2S.PDB	O, A.GLU_46	N, A.ARG_38	H, A.ARG_38	2.87	2.03	8.46
3U2S.PDB	OE2, A.GLU_46	NE, A.ARG_38	HE, A.ARG_38	2.74	1.98	23.65
3U2S.PDB	OH, A.TYR_90	NH1, A.ARG_38	HH11, A.ARG_38	2.88	2.07	17.44
3U2S.PDB	OD1, A.ASP_86	NH1, A.ARG_38	HH12, A.ARG_38	2.89	2.04	8.28
3U2S.PDB	OE2, A.GLU_46	NH2, A.ARG_38	HH21, A.ARG_38	2.90	2.18	27.83

3U2S.PDB	O, A_THR_89	N, A_GLN_39	H, A_GLN_39	2.91	2.16	24.75
3U2S.PDB	OE1, B_GLN_38	NE2, A_GLN_39	HE22, A_GLN_39	2.92	2.07	7.34
3U2S.PDB	O, A_ALA_40	N, A_GLN_43	H, A_GLN_43	2.87	2.06	15.56
3U2S.PDB	O, A_ARG_38	N, A_GLU_46	H, A_GLU_46	2.76	1.99	21.51
3U2S.PDB	O, A_TYR_58	N, A_PHE_50	H, A_PHE_50	2.89	2.09	18.19
3U2S.PDB	O, A_MET_34	N, A_ILE_51	H, A_ILE_51	2.92	2.12	18.53
3U2S.PDB	O, A_GLU_56	N, A_LYS_52	H, A_LYS_52	2.97	2.12	7.01
3U2S.PDB	O, A_PHE_100J	OH, A_TYR_52A	HH, A_TYR_52A	2.59	1.88	24.42
3U2S.PDB	O, A_LYS_52	N, A_GLY_54	H, A_GLY_54	2.87	2.03	9.21
3U2S.PDB	OD2, A_ASP_53	N, A_SER_55	H, A_SER_55	2.98	2.16	14.39
3U2S.PDB	O, A_PHE_50	N, A_TYR_58	H, A_TYR_58	2.79	1.96	13.05
3U2S.PDB	O, A_VAL_48	N, A_ALA_60	H, A_ALA_60	2.95	2.13	13.20
3U2S.PDB	O, A_VAL_63	N, A_ARG_66	H, A_ARG_66	2.73	1.88	9.69
3U2S.PDB	OD2, A_ASP_86	NH1, A_ARG_66	HH12, A_ARG_66	2.48	1.66	13.42
3U2S.PDB	O, A_VAL_63	N, A_LEU_67	H, A_LEU_67	2.90	2.05	9.26
3U2S.PDB	O, A_GLN_81	N, A_SER_68	H, A_SER_68	2.85	2.08	21.35
3U2S.PDB	OD1, A_ASN_73	NE, A_ARG_71	HE, A_ARG_71	2.81	2.03	20.92
3U2S.PDB	O, A_GLN_32	NH1, A_ARG_71	HH12, A_ARG_71	2.95	2.21	26.35
3U2S.PDB	O, A_THR_77	N, A_ASP_72	H, A_ASP_72	2.91	2.06	7.19
3U2S.PDB	O, A_TYR_52A	ND2, A_ASN_73	HD22, A_ASN_73	2.92	2.06	5.19
3U2S.PDB	O, A_LYS_75	OG1, A_THR_77	HG1, A_THR_77	2.85	2.08	17.09
3U2S.PDB	O, A_CYS_22	N, A_LEU_78	H, A_LEU_78	2.91	2.12	18.34
3U2S.PDB	O, A_SER_70	N, A_TYR_79	H, A_TYR_79	2.82	1.97	5.95
3U2S.PDB	O, A_LEU_20	N, A_LEU_80	H, A_LEU_80	2.92	2.11	16.81
3U2S.PDB	O, A_SER_68	N, A_GLN_81	H, A_GLN_81	2.79	1.96	12.01
3U2S.PDB	O, A_LEU_18	N, A_MET_82	H, A_MET_82	2.72	1.90	13.43
3U2S.PDB	O, A_ARG_66	N, A_ASN_82A	H, A_ASN_82A	2.72	1.94	20.65
3U2S.PDB	OD2, A_ASP_86	N, A_ARG_83	H, A_ARG_83	2.76	1.95	16.59
3U2S.PDB	OE1, A_GLU_85	NH1, A_ARG_83	HH11, A_ARG_83	2.91	2.14	21.39
3U2S.PDB	O, A_ARG_83	N, A_ASP_86	H, A_ASP_86	2.84	2.01	13.57
3U2S.PDB	O, A_VAL_84	N, A_THR_87	H, A_THR_87	2.99	2.15	12.03
3U2S.PDB	O, A_VAL_84	OG1, A_THR_87	HG1, A_THR_87	2.79	2.12	29.92
3U2S.PDB	O, A_GLN_39	N, A_THR_89	H, A_THR_89	2.88	2.07	17.15
3U2S.PDB	O, A_THR_107	N, A_TYR_90	H, A_TYR_90	2.83	1.98	6.95
3U2S.PDB	O, A_VAL_37	N, A_PHE_91	H, A_PHE_91	2.67	1.82	6.67
3U2S.PDB	OE2, A_GLU_6	N, A_CYS_92	H, A_CYS_92	2.72	1.89	13.80
3U2S.PDB	O, A_HIS_35	N, A_VAL_93	H, A_VAL_93	2.96	2.18	20.19
3U2S.PDB	O, A_VAL_102	N, A_ARG_94	H, A_ARG_94	2.84	2.03	15.63
3U2S.PDB	OD1, A_ASP_101	NE, A_ARG_94	HE, A_ARG_94	2.84	1.98	4.74
3U2S.PDB	OD2, A_ASP_101	NH2, A_ARG_94	HH21, A_ARG_94	2.90	2.12	20.79
3U2S.PDB	O, A_TYR_100S	N, A_ALA_96	H, A_ALA_96	2.80	1.96	10.95
3U2S.PDB	O, A_TYR_100E	N, A_ARG_100B	H, A_ARG_100B	2.98	2.15	11.35
3U2S.PDB	O, A_ARG_100B	N, A_TYR_100E	H, A_TYR_100E	2.79	1.94	7.07
3U2S.PDB	O, C_ASP_167	N, A_ASN_100F	H, A_ASN_100F	2.97	2.14	14.21
3U2S.PDB	O, A_GLY_100M	N, A_ASP_100I	H, A_ASP_100I	2.82	1.97	9.87
3U2S.PDB	OD1, A_ASP_100I	N, A_PHE_100J	H, A_PHE_100J	2.78	2.05	27.11
3U2S.PDB	O, A_ARG_31	N, A_TYR_100N	H, A_TYR_100N	2.94	2.09	8.42
3U2S.PDB	O, A_GLY_98	N, A_TYR_100O	H, A_TYR_100O	2.92	2.19	26.39
3U2S.PDB	O, A_ALA_96	N, A_TYR_100Q	H, A_TYR_100Q	2.75	1.90	9.19
3U2S.PDB	OE1, A_GLU_6	N, A_GLY_106	H, A_GLY_106	2.86	2.06	17.09
3U2S.PDB	O, A_TYR_90	N, A_THR_107	H, A_THR_107	2.98	2.19	19.53
3U2S.PDB	O, A_ALA_88	N, A_VAL_109	H, A_VAL_109	2.92	2.07	4.29
3U2S.PDB	O, A_GLY_10	N, A_THR_110	H, A_THR_110	2.86	2.01	7.11
3U2S.PDB	OG1, A_THR_87	N, A_VAL_111	H, A_VAL_111	2.87	2.02	8.59
3U2S.PDB	O, A_VAL_12	N, A_SER_112	H, A_SER_112	2.92	2.11	15.36
3U2S.PDB	O, A_PHE_146	N, A_LYS_117	H, A_LYS_117	2.83	2.02	16.74
3U2S.PDB	O, A_ASP_144	NZ, A_LYS_117	HZ2, A_LYS_117	2.78	2.05	29.01
3U2S.PDB	O, A_LYS_143	N, A_SER_120	H, A_SER_120	2.88	2.06	14.03

3U2S.PDB	O, A_GLY_139	N, A_LEU_124	H, A_LEU_124	2.65	1.84	16.74
3U2S.PDB	O, A_LEU_124	N, A_GLY_139	H, A_GLY_139	2.96	2.16	18.70
3U2S.PDB	O, A_SER_180	N, A_CYS_140	H, A_CYS_140	2.75	1.94	16.77
3U2S.PDB	O, A_PHE_122	N, A_LEU_141	H, A_LEU_141	2.88	2.03	7.64
3U2S.PDB	O, A_LEU_178	N, A_VAL_142	H, A_VAL_142	2.79	1.98	17.03
3U2S.PDB	O, A_SER_120	N, A_LYS_143	H, A_LYS_143	2.78	1.92	1.74
3U2S.PDB	OG1, B_THR_131	NZ, A_LYS_143	HZ2, A_LYS_143	2.41	1.67	27.35
3U2S.PDB	O, A_TYR_176	N, A_TYR_145	H, A_TYR_145	2.98	2.17	17.16
3U2S.PDB	O, A_LYS_117	N, A_PHE_146	H, A_PHE_146	2.95	2.17	21.41
3U2S.PDB	O, A_ASN_199	N, A_THR_151	H, A_THR_151	2.98	2.16	15.19
3U2S.PDB	O, A_ILE_195	N, A_ASN_155	H, A_ASN_155	2.78	1.93	7.52
3U2S.PDB	O, A_VAL_181	N, A_HIS_164	H, A_HIS_164	2.87	2.03	10.09
3U2S.PDB	O, A_SER_179	N, A_PHE_166	H, A_PHE_166	2.98	2.12	5.94
3U2S.PDB	O, A_SER_177	N, A_VAL_169	H, A_VAL_169	2.72	1.90	14.55
3U2S.PDB	OD2, A_ASP_144	NE2, A_GLN_171	HE22, A_GLN_171	2.82	1.98	10.06
3U2S.PDB	O, A_GLN_171	N, A_GLY_174	H, A_GLY_174	2.97	2.11	5.23
3U2S.PDB	O, A_TYR_145	N, A_TYR_176	H, A_TYR_176	2.71	1.86	5.46
3U2S.PDB	O, A_VAL_169	N, A_SER_177	H, A_SER_177	2.96	2.16	18.03
3U2S.PDB	O, A_VAL_142	N, A_LEU_178	H, A_LEU_178	2.98	2.19	18.64
3U2S.PDB	O, A_CYS_140	N, A_SER_180	H, A_SER_180	2.98	2.18	18.33
3U2S.PDB	O, A_LEU_138	N, A_VAL_182	H, A_VAL_182	2.84	2.04	17.50
3U2S.PDB	O, A_GLY_162	N, A_THR_183	H, A_THR_183	2.90	2.11	19.30
3U2S.PDB	O, A_SER_153	N, A_ASN_197	H, A_ASN_197	2.76	1.95	14.90
3U2S.PDB	O, A_VAL_207	N, A_VAL_198	H, A_VAL_198	2.76	1.93	12.35
3U2S.PDB	O, A_THR_151	N, A_ASN_199	H, A_ASN_199	2.98	2.16	15.76
3U2S.PDB	O, A_THR_205	N, A_HIS_200	H, A_HIS_200	2.74	1.90	9.41
3U2S.PDB	OG, A_SER_203	ND1, A_HIS_200	HD1, A_HIS_200	2.63	1.78	5.16
3U2S.PDB	O, A_PRO_147	NE2, A_HIS_200	HE2, A_HIS_200	2.75	1.94	15.51
3U2S.PDB	O, A_VAL_198	N, A_VAL_207	H, A_VAL_207	2.82	1.98	12.41
3U2S.PDB	O, A_TYR_194	N, A_VAL_211	H, A_VAL_211	2.94	2.09	7.62
3U2S.PDB	O, B_GLN_24	N, B_THR_5	H, B_THR_5	2.92	2.09	11.05
3U2S.PDB	O, B_TYR_86	NE2, B_GLN_6	HE22, B_GLN_6	2.85	2.02	13.19
3U2S.PDB	O, B_LYS_103	N, B_VAL_11	H, B_VAL_11	2.85	2.04	16.11
3U2S.PDB	OE1, B_GLN_17	N, B_SER_14	H, B_SER_14	2.92	2.13	20.55
3U2S.PDB	O, B_LEU_78	N, B_GLY_16	H, B_GLY_16	2.87	2.07	17.65
3U2S.PDB	O, B_ILE_75	N, B_ILE_19	H, B_ILE_19	2.93	2.15	21.26
3U2S.PDB	OG1, B_THR_74	OG1, B_THR_20	HG1, B_THR_20	2.88	2.16	24.36
3U2S.PDB	O, B_LEU_73	N, B_ILE_21	H, B_ILE_21	2.82	2.00	14.83
3U2S.PDB	O, B_THR_5	N, B_GLN_24	H, B_GLN_24	2.91	2.09	15.35
3U2S.PDB	O, B_ASN_69	N, B_GLY_25	H, B_GLY_25	2.73	1.88	3.63
3U2S.PDB	OD1, B_ASP_27B	N, B_THR_26	H, B_THR_26	2.84	2.02	14.26
3U2S.PDB	OD2, B_ASP_27B	OG1, B_THR_26	HG1, B_THR_26	2.89	2.14	20.81
3U2S.PDB	OD1, B_ASP_27B	N, B_VAL_27C	H, B_VAL_27C	2.70	1.91	19.64
3U2S.PDB	O, B_THR_26	N, B_GLY_28	H, B_GLY_28	2.91	2.08	12.42
3U2S.PDB	O, B_ASP_27B	N, B_GLY_29	H, B_GLY_29	2.89	2.05	10.78
3U2S.PDB	O, B_LYS_89	N, B_SER_34	H, B_SER_34	2.84	2.04	18.48
3U2S.PDB	O, B_ILE_48	N, B_TRP_35	H, B_TRP_35	2.89	2.10	19.01
3U2S.PDB	O, B_TYR_87	N, B_TYR_36	H, B_TYR_36	2.89	2.14	24.66
3U2S.PDB	O, B_LYS_45	N, B_GLN_37	H, B_GLN_37	2.82	2.00	13.80
3U2S.PDB	OH, B_TYR_86	NE2, B_GLN_37	HE21, B_GLN_37	2.88	2.02	1.18
3U2S.PDB	O, B_ASP_85	N, B_GLN_38	H, B_GLN_38	2.78	1.98	17.35
3U2S.PDB	O, B_LYS_42	NE2, B_GLN_38	HE21, B_GLN_38	2.90	2.07	13.31
3U2S.PDB	OE1, A_GLN_39	NE2, B_GLN_38	HE22, B_GLN_38	2.92	2.08	10.61
3U2S.PDB	O, B_GLN_37	N, B_LYS_45	H, B_LYS_45	2.81	2.08	26.63
3U2S.PDB	O, B_TRP_35	N, B_VAL_47	H, B_VAL_47	2.86	2.02	10.13
3U2S.PDB	O, B_LYS_53	N, B_TYR_49	H, B_TYR_49	2.92	2.11	17.26
3U2S.PDB	O, B_VAL_33	N, B_VAL_51	H, B_VAL_51	2.86	2.01	7.74
3U2S.PDB	O, B_ASP_50	N, B_SER_52	H, B_SER_52	2.89	2.18	28.89

3U2S.PDB	O, B.TYR_49	N, B.LYS_53	H, B.LYS_53	2.90	2.09	16.83
3U2S.PDB	OD2, B.ASP_50	NZ, B.LYS_53	HZ2, B.LYS_53	2.75	1.88	8.80
3U2S.PDB	O, B.VAL_58	NH1, B.ARG_54	HH11, B.ARG_54	2.92	2.11	16.82
3U2S.PDB	O, B.SER_76	NH1, B.ARG_61	HH11, B.ARG_61	2.99	2.17	14.44
3U2S.PDB	OD2, B.ASP_82	NH1, B.ARG_61	HH12, B.ARG_61	2.78	1.98	19.10
3U2S.PDB	OD1, B.ASP_82	NH2, B.ARG_61	HH22, B.ARG_61	2.93	2.07	0.82
3U2S.PDB	O, B.VAL_27C	NZ, B.LYS_66	HZ3, B.LYS_66	2.85	2.03	18.40
3U2S.PDB	O, B.THR_70	N, B.SER_67	H, B.SER_67	2.96	2.13	11.57
3U2S.PDB	O, B.CYS_23	N, B.ALA_71	H, B.ALA_71	2.85	2.05	17.45
3U2S.PDB	O, B.SER_65	N, B.SER_72	H, B.SER_72	2.89	2.07	15.07
3U2S.PDB	O, B.ILE_21	N, B.LEU_73	H, B.LEU_73	2.90	2.08	14.34
3U2S.PDB	O, B.SER_63	N, B.THR_74	H, B.THR_74	2.87	2.04	12.52
3U2S.PDB	O, B.ILE_19	N, B.ILE_75	H, B.ILE_75	2.92	2.11	16.75
3U2S.PDB	O, B.ARG_61	N, B.SER_76	H, B.SER_76	2.95	2.11	12.03
3U2S.PDB	O, B.GLN_17	N, B.LEU_78	H, B.LEU_78	2.82	1.97	8.22
3U2S.PDB	OD2, B.ASP_82	N, B.GLN_79	H, B.GLN_79	2.84	2.01	11.59
3U2S.PDB	OG1, H.THR_160	N, B.ALA_80	H, B.ALA_80	2.90	2.08	14.44
3U2S.PDB	O, B.GLN_79	N, B.ASP_82	H, B.ASP_82	2.90	2.05	8.49
3U2S.PDB	O, B.ALA_80	N, B.GLU_83	H, B.GLU_83	2.99	2.13	4.82
3U2S.PDB	O, B.THR_102	N, B.TYR_86	H, B.TYR_86	2.83	2.04	18.67
3U2S.PDB	O, B.ARG_95A	N, B.THR_92	H, B.THR_92	2.98	2.24	26.76
3U2S.PDB	O, B.THR_92	N, B.ARG_95	H, B.ARG_95	2.98	2.15	13.06
3U2S.PDB	OD1, A.ASP_61	NH1, B.ARG_95A	HH12, B.ARG_95A	2.63	1.91	26.97
3U2S.PDB	OE2, A.GLU_95	NH2, B.ARG_96	HH21, B.ARG_96	2.98	2.16	13.77
3U2S.PDB	O, B.CYS_88	N, B.GLY_99	H, B.GLY_99	2.84	2.02	13.65
3U2S.PDB	O, B.TYR_86	N, B.THR_102	H, B.THR_102	2.88	2.13	24.78
3U2S.PDB	O, B.PRO_7	OG1, B.THR_102	HG1, B.THR_102	2.64	1.82	5.54
3U2S.PDB	O, B.GLY_84	N, B.LEU_104	H, B.LEU_104	2.79	1.94	4.02
3U2S.PDB	O, B.VAL_11	N, B.THR_105	H, B.THR_105	2.99	2.17	14.21
3U2S.PDB	OH, B.TYR_140	N, B.GLY_107	H, B.GLY_107	2.85	2.06	20.14
3U2S.PDB	O, B.TYR_140	N, B.ALA_111	H, B.ALA_111	2.98	2.14	10.58
3U2S.PDB	O, B.SER_137	N, B.SER_114	H, B.SER_114	2.93	2.10	13.38
3U2S.PDB	O, B.LEU_135	N, B.THR_116	H, B.THR_116	2.97	2.16	15.84
3U2S.PDB	O, B.VAL_133	N, B.PHE_118	H, B.PHE_118	2.87	2.04	12.26
3U2S.PDB	O, B.LEU_125	N, B.ASN_128	H, B.ASN_128	2.97	2.18	18.83
3U2S.PDB	O, B.SER_176	N, B.CYS_134	H, B.CYS_134	2.86	2.01	7.06
3U2S.PDB	O, B.THR_116	N, B.LEU_135	H, B.LEU_135	2.78	1.93	5.65
3U2S.PDB	O, B.ALA_174	N, B.ILE_136	H, B.ILE_136	2.93	2.14	18.97
3U2S.PDB	O, B.SER_114	N, B.SER_137	H, B.SER_137	2.99	2.19	18.33
3U2S.PDB	OE1, B.GLN_167	N, B.ASP_138	H, B.ASP_138	2.95	2.17	20.82
3U2S.PDB	O, B.ALA_111	N, B.TYR_140	H, B.TYR_140	2.94	2.14	17.27
3U2S.PDB	O, B.PRO_141	N, B.ALA_143	H, B.ALA_143	3.00	2.29	29.69
3U2S.PDB	O, B.GLN_194	N, B.ALA_147	H, B.ALA_147	2.93	2.10	11.92
3U2S.PDB	OG, B.SER_176	NE1, B.TRP_148	HE1, B.TRP_148	2.87	2.03	9.65
3U2S.PDB	O, B.SER_190	N, B.ASP_151	H, B.ASP_151	2.76	1.91	5.32
3U2S.PDB	O, B.TRP_148	N, B.VAL_155	H, B.VAL_155	2.92	2.16	22.91
3U2S.PDB	O, B.TYR_177	N, B.GLU_160	H, B.GLU_160	2.79	1.97	13.97
3U2S.PDB	O, B.SER_175	N, B.THR_162	H, B.THR_162	2.92	2.09	12.18
3U2S.PDB	O, B.ALA_173	N, B.SER_165	H, B.SER_165	2.94	2.13	16.38
3U2S.PDB	O, B.LYS_171	N, B.GLN_167	H, B.GLN_167	2.56	1.71	7.13
3U2S.PDB	OD1, B.ASN_169	NE2, B.GLN_167	HE21, B.GLN_167	2.93	2.16	22.14
3U2S.PDB	OD1, B.ASP_138	NE2, B.GLN_167	HE22, B.GLN_167	2.75	1.90	7.18
3U2S.PDB	OD1, B.ASN_169	N, B.LYS_171	H, B.LYS_171	2.90	2.06	11.66
3U2S.PDB	O, B.PHE_139	N, B.TYR_172	H, B.TYR_172	2.94	2.14	18.70
3U2S.PDB	O, B.SER_165	N, B.ALA_173	H, B.ALA_173	2.91	2.10	18.16
3U2S.PDB	O, B.ILE_136	N, B.ALA_174	H, B.ALA_174	2.80	1.97	12.77
3U2S.PDB	O, B.CYS_134	N, B.SER_176	H, B.SER_176	2.86	2.06	18.58
3U2S.PDB	O, B.GLU_160	N, B.TYR_177	H, B.TYR_177	2.64	1.81	12.56

3U2S.PDB	O, B_GLY_158	N, B_SER_179	H, B_SER_179	2.87	2.03	11.48
3U2S.PDB	O, B_ALA_130	N, B_LEU_180	H, B_LEU_180	2.96	2.11	5.53
3U2S.PDB	O, B_PRO_182	N, B_LYS_186	H, B_LYS_186	2.96	2.16	17.55
3U2S.PDB	OD1, B_ASP_151	N, B_SER_190	H, B_SER_190	2.97	2.20	22.59
3U2S.PDB	O, B_VAL_206	N, B_TYR_191	H, B_TYR_191	2.92	2.10	13.48
3U2S.PDB	O, B_LYS_149	N, B_SER_192	H, B_SER_192	2.99	2.21	20.57
3U2S.PDB	O, B_LYS_204	N, B_CYS_193	H, B_CYS_193	2.92	2.14	21.01
3U2S.PDB	O, B_ALA_147	N, B_GLN_194	H, B_GLN_194	2.80	1.97	13.29
3U2S.PDB	O, B_VAL_202	N, B_VAL_195	H, B_VAL_195	2.78	1.93	3.68
3U2S.PDB	O, B_THR_145	N, B_THR_196	H, B_THR_196	2.86	2.00	5.33
3U2S.PDB	OG1, B_THR_201	OG1, B_THR_196	HG1, B_THR_196	2.79	1.99	11.66
3U2S.PDB	O, B_SER_200	N, B_HIS_197	H, B_HIS_197	2.90	2.05	7.61
3U2S.PDB	O, B_PRO_141	NE2, B_HIS_197	HE2, B_HIS_197	2.83	2.07	23.66
3U2S.PDB	O, B_HIS_197	N, B_SER_200	H, B_SER_200	2.92	2.07	5.55
3U2S.PDB	O, B_VAL_195	N, B_VAL_202	H, B_VAL_202	2.72	1.88	10.92
3U2S.PDB	O, B_TYR_191	N, B_VAL_206	H, B_VAL_206	2.88	2.06	14.38
3U2S.PDB	O, C_THR_201	N, C_PHE_121	H, C_PHE_121	2.92	2.06	2.96
3U2S.PDB	O, C_LYS_233	N, C_LYS_122	H, C_LYS_122	2.76	1.94	13.22
3U2S.PDB	O, C_THR_199	N, C_LEU_123	H, C_LEU_123	2.83	2.01	15.42
3U2S.PDB	O, C_PHE_235	N, C_ALA_124	H, C_ALA_124	2.96	2.15	16.72
3U2S.PDB	O, C_GLN_197	N, C_ALA_125	H, C_ALA_125	2.97	2.18	19.36
3U2S.PDB	O, C_VAL_237	N, C_CYS_126	H, C_CYS_126	2.89	2.18	29.45
3U2S.PDB	O, C_SER_195	N, C_VAL_127	H, C_VAL_127	2.78	2.00	19.73
3U2S.PDB	O, C_LEU_193	N, C_LEU_129	H, C_LEU_129	2.58	1.72	4.21
3U2S.PDB	O, C_SER_158	N, C_ALA_130	H, C_ALA_130	2.91	2.07	10.47
3U2S.PDB	O, C_TYR_191	N, C_CYS_131	H, C_CYS_131	2.97	2.14	13.58
3U2S.PDB	O, C_HIS_156	N, C_THR_132	H, C_THR_132	2.87	2.10	22.75
3U2S.PDB	O, C_PHE_176	N, C_LYS_155	H, C_LYS_155	2.92	2.08	9.76
3U2S.PDB	O, C_ALA_174	N, C_CYS_157	H, C_CYS_157	2.85	2.01	11.36
3U2S.PDB	O, C_GLN_170	N, C_ILE_161	H, C_ILE_161	2.98	2.15	12.25
3U2S.PDB	OG1, C_THR_163	N, C_VAL_165	H, C_VAL_165	2.97	2.12	10.44
3U2S.PDB	O, A_ASN_100F	N, C_LYS_169	H, C_LYS_169	2.91	2.08	13.24
3U2S.PDB	O, C_ILE_161	N, C_GLN_170	H, C_GLN_170	2.89	2.09	17.25
3U2S.PDB	O, C_PHE_159	N, C_VAL_172	H, C_VAL_172	2.73	1.89	10.39
3U2S.PDB	O, C_LYS_155	N, C_PHE_176	H, C_PHE_176	2.99	2.16	12.58
3U2S.PDB	O, C_CYS_131	N, C_TYR_191	H, C_TYR_191	2.87	2.05	15.43
3U2S.PDB	O, C_LEU_129	N, C_LEU_193	H, C_LEU_193	2.96	2.21	25.28
3U2S.PDB	O, C_VAL_127	N, C_SER_195	H, C_SER_195	2.88	2.02	5.76
3U2S.PDB	O, C_ALA_125	N, C_GLN_197	H, C_GLN_197	2.93	2.12	15.95
3U2S.PDB	O, C_LEU_123	N, C_THR_199	H, C_THR_199	2.87	2.07	18.73
3U2S.PDB	O, C_ALA_206	N, C_ALA_210	H, C_ALA_210	2.93	2.14	20.34
3U2S.PDB	O, C_THR_232	OG1, C_THR_234	HG1, C_THR_234	2.76	1.97	14.48
3U2S.PDB	O, C_LYS_122	N, C_PHE_235	H, C_PHE_235	2.66	1.87	18.30
3U2S.PDB	O, C_THR_227	N, C_THR_236	H, C_THR_236	2.92	2.14	20.62
3U2S.PDB	O, C_ALA_124	N, C_VAL_237	H, C_VAL_237	2.99	2.14	7.85

Table 1685: 3U2S-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
3UYR.PDB	O, H.THR.23	N, H.VAL.5	H, H.VAL.5	2.87	2.05	15.70
3UYR.PDB	O, H.SER.21	N, H.SER.7	H, H.SER.7	2.82	2.03	20.07
3UYR.PDB	O, H.THR.112	N, H.GLY.10	H, H.GLY.10	2.77	1.94	13.13
3UYR.PDB	O, H.THR.114	N, H.VAL.12	H, H.VAL.12	2.88	2.07	16.54
3UYR.PDB	O, H.LEU.86	N, H.GLY.15	H, H.GLY.15	2.68	1.86	14.42
3UYR.PDB	O, H.MET.83	N, H.MET.18	H, H.MET.18	2.83	2.00	14.86
3UYR.PDB	O, H.LEU.81	N, H.LEU.20	H, H.LEU.20	2.86	2.03	15.99
3UYR.PDB	OG, H.SER.7	N, H.SER.21	H, H.SER.21	2.96	2.12	9.95
3UYR.PDB	O, H.VAL.5	N, H.THR.23	H, H.THR.23	2.80	1.98	14.92
3UYR.PDB	O, H.THR.28	N, H.ASP.31	H, H.ASP.31	2.78	1.97	17.10
3UYR.PDB	O, H.ILE.51	N, H.MET.34	H, H.MET.34	2.92	2.09	17.05
3UYR.PDB	O, H.ALA.97	N, H.ALA.35	H, H.ALA.35	2.83	2.02	16.97
3UYR.PDB	O, H.ALA.49	N, H.TRP.36	H, H.TRP.36	2.81	2.00	15.63
3UYR.PDB	O, H.TYR.95	N, H.VAL.37	H, H.VAL.37	2.95	2.10	10.85
3UYR.PDB	O, H.GLU.46	N, H.ARG.38	H, H.ARG.38	2.89	2.05	12.16
3UYR.PDB	OE1, H.GLU.46	NE, H.ARG.38	HE, H.ARG.38	2.84	2.03	16.92
3UYR.PDB	O, H.THR.93	N, H.GLN.39	H, H.GLN.39	2.74	1.95	18.61
3UYR.PDB	O, H.ARG.38	N, H.GLU.46	H, H.GLU.46	2.90	2.11	20.15
3UYR.PDB	OD1, H.ASN.50	NE1, H.TRP.47	HE1, H.TRP.47	2.95	2.18	22.72
3UYR.PDB	O, H.TRP.36	N, H.VAL.48	H, H.VAL.48	2.89	2.08	15.29
3UYR.PDB	O, H.TYR.59	N, H.ASN.50	H, H.ASN.50	2.85	2.06	20.39
3UYR.PDB	O, H.MET.34	N, H.ILE.51	H, H.ILE.51	2.84	2.04	20.05
3UYR.PDB	OD1, H.ASP.54	N, H.SER.56	H, H.SER.56	3.00	2.18	14.88
3UYR.PDB	O, H.ASN.50	N, H.TYR.59	H, H.TYR.59	2.85	2.02	13.64
3UYR.PDB	O, H.VAL.48	N, H.LEU.61	H, H.LEU.61	2.98	2.13	7.86
3UYR.PDB	O, H.ASP.62	N, H.LYS.65	H, H.LYS.65	2.99	2.13	4.39
3UYR.PDB	O, H.LEU.64	N, H.ARG.67	H, H.ARG.67	2.98	2.13	8.99
3UYR.PDB	O, H.SER.84	NH1, H.ARG.67	HH11, H.ARG.67	2.94	2.14	18.03
3UYR.PDB	O, H.GLN.82	N, H.ILE.69	H, H.ILE.69	2.76	1.97	19.91
3UYR.PDB	OH, H.TYR.60	N, H.ILE.70	H, H.ILE.70	2.89	2.08	16.21
3UYR.PDB	O, H.TYR.32	NH1, H.ARG.72	HH12, H.ARG.72	2.89	2.11	20.18
3UYR.PDB	O, H.ILE.78	N, H.ASP.73	H, H.ASP.73	2.70	1.96	26.09
3UYR.PDB	OD1, H.ASP.73	N, H.ALA.75	H, H.ALA.75	3.00	2.29	29.64
3UYR.PDB	O, H.ASP.73	N, H.ILE.78	H, H.ILE.78	2.94	2.08	11.87
3UYR.PDB	O, H.CYS.22	N, H.LEU.79	H, H.LEU.79	2.83	1.98	6.29
3UYR.PDB	O, H.SER.71	N, H.TYR.80	H, H.TYR.80	2.75	1.91	7.16
3UYR.PDB	O, H.LEU.20	N, H.LEU.81	H, H.LEU.81	2.86	2.02	12.02
3UYR.PDB	O, H.ILE.69	N, H.GLN.82	H, H.GLN.82	2.78	1.98	18.27
3UYR.PDB	O, H.MET.18	N, H.MET.83	H, H.MET.83	2.76	1.93	11.89
3UYR.PDB	O, H.SER.16	N, H.LEU.86	H, H.LEU.86	2.97	2.14	12.64
3UYR.PDB	O, H.SER.85	NH1, H.ARG.87	HH11, H.ARG.87	2.82	2.10	28.67
3UYR.PDB	O, H.ARG.87	N, H.ASP.90	H, H.ASP.90	2.99	2.14	6.54
3UYR.PDB	O, H.VAL.113	N, H.ALA.92	H, H.ALA.92	2.99	2.22	22.62
3UYR.PDB	O, H.GLN.39	N, H.THR.93	H, H.THR.93	2.87	2.02	7.65
3UYR.PDB	O, H.THR.111	N, H.TYR.94	H, H.TYR.94	2.77	1.93	7.70
3UYR.PDB	O, H.VAL.37	N, H.TYR.95	H, H.TYR.95	2.76	1.92	4.33
3UYR.PDB	OE2, H.GLU.6	N, H.CYS.96	H, H.CYS.96	2.87	2.06	15.59
3UYR.PDB	O, H.ALA.35	N, H.ALA.97	H, H.ALA.97	2.87	2.05	15.28
3UYR.PDB	O, H.VAL.106	N, H.ARG.98	H, H.ARG.98	2.80	2.00	18.41
3UYR.PDB	OD1, H.ASP.105	NE, H.ARG.98	HE, H.ARG.98	2.98	2.16	14.38
3UYR.PDB	OD2, H.ASP.105	NH2, H.ARG.98	HH21, H.ARG.98	2.92	2.07	8.84
3UYR.PDB	O, H.TYR.103	N, H.THR.100	H, H.THR.100	2.82	1.97	9.07
3UYR.PDB	OE1, P_GLN.48	N, H.ASN.101	H, H.ASN.101	2.90	2.08	14.57
3UYR.PDB	O, H.THR.100	N, H.TYR.103	H, H.TYR.103	2.94	2.08	4.35
3UYR.PDB	OH, L.TYR.41	N, H.LEU.104	H, H.LEU.104	2.91	2.05	4.02
3UYR.PDB	O, H.CYS.96	N, H.GLY.108	H, H.GLY.108	2.80	1.99	17.37
3UYR.PDB	O, H.TYR.94	N, H.THR.111	H, H.THR.111	2.80	2.01	19.20

3UYR.PDB	O, H_ALA_92	N, H_VAL_113	H, H_VAL_113	2.86	2.03	11.74
3UYR.PDB	O, H_GLY_10	N, H_THR_114	H, H_THR_114	2.91	2.06	9.85
3UYR.PDB	OG1, H_THR_91	N, H_VAL_115	H, H_VAL_115	2.95	2.09	4.97
3UYR.PDB	O, H_VAL_12	N, H_SER_116	H, H_SER_116	2.87	2.10	23.24
3UYR.PDB	O, H_PHE_150	N, H_THR_121	H, H_THR_121	2.88	2.05	13.74
3UYR.PDB	O, H_LYS_147	N, H_SER_124	H, H_SER_124	2.80	1.96	9.50
3UYR.PDB	O, H_LEU_145	N, H_TYR_126	H, H_TYR_126	2.81	1.98	12.02
3UYR.PDB	O, H_GLY_143	N, H_LEU_128	H, H_LEU_128	2.77	1.99	20.76
3UYR.PDB	O, H_VAL_187	N, H_VAL_140	H, H_VAL_140	2.79	1.98	16.70
3UYR.PDB	O, H_VAL_185	N, H_LEU_142	H, H_LEU_142	2.82	1.97	8.16
3UYR.PDB	O, H_LEU_128	N, H_GLY_143	H, H_GLY_143	2.84	2.04	17.93
3UYR.PDB	O, H_SER_183	N, H_CYS_144	H, H_CYS_144	2.83	2.03	18.84
3UYR.PDB	O, H_TYR_126	N, H_LEU_145	H, H_LEU_145	2.83	1.98	9.31
3UYR.PDB	O, H_MET_181	N, H_VAL_146	H, H_VAL_146	2.78	1.94	7.21
3UYR.PDB	O, H_SER_124	N, H_LYS_147	H, H_LYS_147	2.85	2.00	9.15
3UYR.PDB	O, H_THR_121	N, H_PHE_150	H, H_PHE_150	2.94	2.13	17.37
3UYR.PDB	O, H_ALA_202	N, H_THR_155	H, H_THR_155	2.91	2.09	17.68
3UYR.PDB	O, H_SER_200	N, H_THR_157	H, H_THR_157	2.85	2.03	15.50
3UYR.PDB	OG, H_SER_183	NE1, H_TRP_158	HE1, H_TRP_158	2.93	2.08	7.42
3UYR.PDB	O, H_THR_198	N, H_ASN_159	H, H_ASN_159	2.85	2.00	6.81
3UYR.PDB	O, H_THR_196	ND2, H_ASN_159	HD21, H_ASN_159	2.99	2.16	12.25
3UYR.PDB	O, H_SER_184	N, H_HIS_168	H, H_HIS_168	2.82	2.01	16.83
3UYR.PDB	O, H_SER_182	N, H_PHE_170	H, H_PHE_170	2.87	2.01	1.94
3UYR.PDB	O, H_THR_180	N, H_LEU_173	H, H_LEU_173	2.80	1.98	14.35
3UYR.PDB	O, H_LEU_178	N, H_GLU_175	H, H_GLU_175	2.86	2.02	11.60
3UYR.PDB	O, H_TYR_149	N, H_TYR_179	H, H_TYR_179	2.88	2.02	4.66
3UYR.PDB	O, H_LEU_173	N, H_THR_180	H, H_THR_180	2.85	2.02	14.69
3UYR.PDB	O, H_VAL_146	N, H_MET_181	H, H_MET_181	2.84	2.01	13.98
3UYR.PDB	O, H_CYS_144	N, H_SER_183	H, H_SER_183	2.93	2.11	17.38
3UYR.PDB	O, H_HIS_168	N, H_SER_184	H, H_SER_184	2.81	2.00	15.83
3UYR.PDB	O, H_LEU_142	N, H_VAL_185	H, H_VAL_185	2.88	2.04	12.88
3UYR.PDB	O, H_VAL_140	N, H_VAL_187	H, H_VAL_187	2.92	2.09	16.07
3UYR.PDB	O, H_SER_138	N, H_SER_189	H, H_SER_189	2.93	2.08	7.47
3UYR.PDB	O, H_THR_191	N, H_GLN_195	H, H_GLN_195	2.89	2.08	16.64
3UYR.PDB	OD1, H_ASN_159	N, H_THR_198	H, H_THR_198	2.89	2.14	25.42
3UYR.PDB	O, H_LYS_212	N, H_CYS_199	H, H_CYS_199	2.82	2.04	21.76
3UYR.PDB	O, H_THR_157	N, H_SER_200	H, H_SER_200	2.77	1.94	8.80
3UYR.PDB	O, H_VAL_210	N, H_VAL_201	H, H_VAL_201	2.74	1.93	14.32
3UYR.PDB	O, H_THR_155	N, H_ALA_202	H, H_ALA_202	2.84	2.00	11.25
3UYR.PDB	O, H_THR_208	N, H_HIS_203	H, H_HIS_203	2.84	2.01	11.63
3UYR.PDB	OG, H_SER_206	ND1, H_HIS_203	HD1, H_HIS_203	2.81	2.06	24.47
3UYR.PDB	O, H_PRO_151	NE2, H_HIS_203	HE2, H_HIS_203	2.78	1.95	12.82
3UYR.PDB	O, H_PRO_204	N, H_SER_207	H, H_SER_207	2.93	2.11	16.45
3UYR.PDB	O, H_SER_206	OG1, H_THR_208	HG1, H_THR_208	2.92	2.11	9.83
3UYR.PDB	O, H_VAL_201	N, H_VAL_210	H, H_VAL_210	2.82	2.01	15.56
3UYR.PDB	O, H_CYS_199	N, H_LYS_212	H, H_LYS_212	2.72	1.97	24.25
3UYR.PDB	OE2, L_GLU_127	NZ, H_LYS_212	HZ3, H_LYS_212	2.87	2.08	23.12
3UYR.PDB	O, H_VAL_197	N, H_LEU_214	H, H_LEU_214	2.84	1.98	4.90
3UYR.PDB	OG, L_SER_26	N, L_VAL_3	H, L_VAL_3	2.88	2.07	15.64
3UYR.PDB	O, L_ARG_24	N, L_THR_5	H, L_THR_5	2.82	1.98	11.17
3UYR.PDB	O, L_TYR_91	NE2, L_GLN_6	HE21, L_GLN_6	2.91	2.06	4.88
3UYR.PDB	O, L_SER_22	N, L_THR_7	H, L_THR_7	2.88	2.05	13.60
3UYR.PDB	O, L_LYS_107	N, L_LEU_11	H, L_LEU_11	2.78	1.95	12.54
3UYR.PDB	O, L_GLU_109	N, L_VAL_13	H, L_VAL_13	2.83	2.02	17.58
3UYR.PDB	O, L_VAL_83	N, L_GLY_16	H, L_GLY_16	2.85	2.01	12.40
3UYR.PDB	O, L_ILE_80	N, L_ALA_19	H, L_ALA_19	2.80	1.98	15.31
3UYR.PDB	O, L_LEU_78	N, L_ILE_21	H, L_ILE_21	2.80	1.97	13.25
3UYR.PDB	O, L_THR_7	N, L_SER_22	H, L_SER_22	2.80	1.95	7.59

3UYR.PDB	O, L_PHE_76	N, L_CYS_23	H, L_CYS_23	2.89	2.03	7.24
3UYR.PDB	O, L_THR_5	N, L_ARG_24	H, L_ARG_24	2.90	2.05	9.82
3UYR.PDB	O, L_THR_74	N, L_SER_25	H, L_SER_25	2.93	2.14	19.27
3UYR.PDB	O, L_GLY_73	N, L_LEU_29	H, L_LEU_29	2.94	2.10	10.63
3UYR.PDB	O, L_ASN_35	N, L_HIS_31	H, L_HIS_31	2.79	1.96	11.60
3UYR.PDB	O, P_PRO_50	NE2, L_HIS_31	HE2, L_HIS_31	2.91	2.13	21.00
3UYR.PDB	O, L_HIS_31	N, L_GLY_34	H, L_GLY_34	2.88	2.04	11.36
3UYR.PDB	OD1, L_ASN_33	N, L_ASN_35	H, L_ASN_35	2.92	2.06	4.57
3UYR.PDB	O, L_SER_94	N, L_HIS_39	H, L_HIS_39	2.84	2.01	14.97
3UYR.PDB	O, L_ILE_53	N, L_TRP_40	H, L_TRP_40	2.74	1.91	12.06
3UYR.PDB	O, L_PHE_92	N, L_TYR_41	H, L_TYR_41	2.85	1.99	7.67
3UYR.PDB	O, L_ASN_50	N, L_LEU_42	H, L_LEU_42	2.87	2.07	16.83
3UYR.PDB	O, L_VAL_90	N, L_GLN_43	H, L_GLN_43	2.80	1.95	5.26
3UYR.PDB	O, L_LEU_42	N, L_ASN_50	H, L_ASN_50	2.86	2.10	23.14
3UYR.PDB	O, L_TRP_40	N, L_LEU_52	H, L_LEU_52	2.84	2.01	12.79
3UYR.PDB	O, L_ASN_58	N, L_TYR_54	H, L_TYR_54	2.84	2.05	19.87
3UYR.PDB	O, L_LEU_38	N, L_VAL_56	H, L_VAL_56	2.77	1.91	6.14
3UYR.PDB	O, L_LYS_55	N, L_SER_57	H, L_SER_57	2.83	2.11	28.35
3UYR.PDB	O, L_TYR_54	N, L_ASN_58	H, L_ASN_58	3.00	2.19	16.78
3UYR.PDB	O, L_LEU_52	N, L_PHE_60	H, L_PHE_60	2.97	2.11	3.95
3UYR.PDB	O, L_PHE_60	N, L_VAL_63	H, L_VAL_63	2.97	2.12	9.01
3UYR.PDB	OD2, L_ASP_87	NH1, L_ARG_66	HH12, L_ARG_66	2.92	2.12	17.99
3UYR.PDB	O, L_LYS_79	N, L_SER_68	H, L_SER_68	2.85	2.02	11.95
3UYR.PDB	O, L_THR_77	N, L_SER_70	H, L_SER_70	2.85	2.05	19.01
3UYR.PDB	O, L_ASP_75	N, L_SER_72	H, L_SER_72	2.90	2.11	22.40
3UYR.PDB	O, L_SER_72	N, L_ASP_75	H, L_ASP_75	2.99	2.11	2.04
3UYR.PDB	O, L_CYS_23	N, L_PHE_76	H, L_PHE_76	2.88	2.06	17.75
3UYR.PDB	O, L_SER_70	N, L_THR_77	H, L_THR_77	2.91	2.06	11.18
3UYR.PDB	O, L_ILE_21	N, L_LEU_78	H, L_LEU_78	2.85	2.02	13.64
3UYR.PDB	O, L_SER_68	N, L_LYS_79	H, L_LYS_79	2.81	1.95	3.66
3UYR.PDB	O, L_ALA_19	N, L_ILE_80	H, L_ILE_80	2.83	2.00	12.62
3UYR.PDB	O, L_ARG_66	N, L_SER_81	H, L_SER_81	2.98	2.14	10.19
3UYR.PDB	O, L_ASP_17	N, L_VAL_83	H, L_VAL_83	2.95	2.10	8.86
3UYR.PDB	OD2, L_ASP_87	N, L_GLU_84	H, L_GLU_84	2.89	2.03	6.75
3UYR.PDB	O, L_GLU_84	N, L_ASP_87	H, L_ASP_87	2.87	2.03	9.35
3UYR.PDB	O, L_GLN_43	N, L_VAL_90	H, L_VAL_90	2.88	2.03	9.40
3UYR.PDB	O, L_THR_106	N, L_TYR_91	H, L_TYR_91	2.84	1.99	8.33
3UYR.PDB	O, L_TYR_41	N, L_PHE_92	H, L_PHE_92	2.86	2.03	13.68
3UYR.PDB	OE1, L_GLN_6	N, L_CYS_93	H, L_CYS_93	3.00	2.19	17.32
3UYR.PDB	O, L_HIS_39	N, L_SER_94	H, L_SER_94	2.83	2.06	23.28
3UYR.PDB	O, L_THR_101	N, L_GLN_95	H, L_GLN_95	2.94	2.12	15.68
3UYR.PDB	O, L_TYR_37	N, L_SER_96	H, L_SER_96	2.94	2.15	18.38
3UYR.PDB	OE1, L_GLN_95	N, L_HIS_98	H, L_HIS_98	2.95	2.09	2.48
3UYR.PDB	O, L_SER_28	NE2, L_HIS_98	HE2, L_HIS_98	2.88	2.05	12.63
3UYR.PDB	O, L_CYS_93	N, L_GLY_103	H, L_GLY_103	2.78	1.93	6.25
3UYR.PDB	O, L_TYR_91	N, L_THR_106	H, L_THR_106	2.84	2.03	18.62
3UYR.PDB	O, L_GLY_89	N, L_LEU_108	H, L_LEU_108	2.94	2.13	16.80
3UYR.PDB	O, L_LEU_11	N, L_GLU_109	H, L_GLU_109	2.82	1.97	7.29
3UYR.PDB	OE1, L_GLN_170	N, L_ILE_110	H, L_ILE_110	2.98	2.14	10.85
3UYR.PDB	O, L_VAL_13	N, L_LYS_111	H, L_LYS_111	2.91	2.06	8.31
3UYR.PDB	O, L_ALA_113	NE, L_ARG_112	HE, L_ARG_112	2.77	1.91	2.87
3UYR.PDB	O, L_ASP_174	NH1, L_ARG_112	HH11, L_ARG_112	2.84	2.02	14.52
3UYR.PDB	O, L_TYR_144	N, L_ALA_115	H, L_ALA_115	2.82	2.03	20.71
3UYR.PDB	O, L_ASN_141	N, L_THR_118	H, L_THR_118	2.86	2.01	9.08
3UYR.PDB	O, L_PHE_139	N, L_SER_120	H, L_SER_120	2.86	2.03	15.20
3UYR.PDB	O, L_VAL_137	N, L_PHE_122	H, L_PHE_122	2.78	2.00	21.33
3UYR.PDB	OG, L_SER_135	NE2, L_GLN_128	HE22, L_GLN_128	2.97	2.12	5.23
3UYR.PDB	O, L_SER_126	N, L_THR_130	H, L_THR_130	2.82	2.00	15.78

3UYR.PDB	O, L_GLN_128	N, L_SER_131	H, L_SER_131	2.96	2.14	14.42
3UYR.PDB	O, L_LEU_185	N, L_ALA_134	H, L_ALA_134	2.87	2.07	19.29
3UYR.PDB	OE1, L_GLN_128	N, L_SER_135	H, L_SER_135	2.90	2.07	13.80
3UYR.PDB	O, L_LEU_183	N, L_VAL_136	H, L_VAL_136	2.80	1.97	12.38
3UYR.PDB	O, L_PHE_122	N, L_VAL_137	H, L_VAL_137	2.95	2.10	12.15
3UYR.PDB	O, L_SER_181	N, L_CYS_138	H, L_CYS_138	2.83	1.98	8.48
3UYR.PDB	O, L_SER_120	N, L_PHE_139	H, L_PHE_139	2.80	2.03	23.03
3UYR.PDB	O, L_MET_179	N, L_LEU_140	H, L_LEU_140	2.85	1.99	0.89
3UYR.PDB	O, L_THR_118	N, L_ASN_141	H, L_ASN_141	2.83	1.99	11.90
3UYR.PDB	OG, L_SER_178	N, L_ASN_142	H, L_ASN_142	2.99	2.15	11.11
3UYR.PDB	O, L_TYR_177	N, L_PHE_143	H, L_PHE_143	2.85	2.04	16.59
3UYR.PDB	O, L_ALA_115	N, L_TYR_144	H, L_TYR_144	2.91	2.10	16.84
3UYR.PDB	O, L_THR_201	N, L_ASN_149	H, L_ASN_149	2.86	2.00	8.27
3UYR.PDB	O, L_GLU_199	N, L_LYS_151	H, L_LYS_151	2.82	2.00	15.42
3UYR.PDB	O, L_THR_197	N, L_LYS_153	H, L_LYS_153	2.84	2.01	13.66
3UYR.PDB	O, L_SER_157	N, L_ILE_154	H, L_ILE_154	2.87	2.03	11.53
3UYR.PDB	O, L_SER_195	N, L_ASP_155	H, L_ASP_155	2.87	2.05	15.34
3UYR.PDB	O, L_ILE_154	N, L_SER_157	H, L_SER_157	2.89	2.05	8.75
3UYR.PDB	O, L_THR_182	N, L_LEU_164	H, L_LEU_164	2.83	2.00	12.39
3UYR.PDB	O, L_SER_180	N, L_SER_166	H, L_SER_166	2.84	2.01	13.00
3UYR.PDB	O, H_PRO_171	OG, L_SER_166	HG, L_SER_166	2.72	1.97	20.46
3UYR.PDB	O, L_SER_178	N, L_THR_168	H, L_THR_168	2.87	2.04	12.69
3UYR.PDB	O, L_ILE_110	NE2, L_GLN_170	HE21, L_GLN_170	2.74	1.92	14.96
3UYR.PDB	O, L_SER_175	NE2, L_GLN_170	HE22, L_GLN_170	2.95	2.10	7.23
3UYR.PDB	O, L_THR_176	N, L_ASP_171	H, L_ASP_171	2.94	2.09	6.43
3UYR.PDB	OD1, L_ASP_174	OG1, L_THR_176	HG1, L_THR_176	2.78	1.97	7.90
3UYR.PDB	O, L_PHE_143	N, L_TYR_177	H, L_TYR_177	2.87	2.01	4.97
3UYR.PDB	O, L_LEU_140	N, L_MET_179	H, L_MET_179	2.90	2.09	17.57
3UYR.PDB	O, L_SER_166	N, L_SER_180	H, L_SER_180	2.83	2.01	15.72
3UYR.PDB	O, L_CYS_138	N, L_SER_181	H, L_SER_181	2.84	1.99	8.90
3UYR.PDB	O, L_LEU_164	N, L_THR_182	H, L_THR_182	2.82	1.99	13.16
3UYR.PDB	O, L_VAL_136	N, L_LEU_183	H, L_LEU_183	2.83	1.99	11.27
3UYR.PDB	O, L_ALA_134	N, L_LEU_185	H, L_LEU_185	2.79	1.94	5.06
3UYR.PDB	O, L_THR_186	N, L_TYR_190	H, L_TYR_190	2.96	2.12	12.41
3UYR.PDB	O, L_LYS_187	N, L_GLU_191	H, L_GLU_191	2.81	2.00	16.98
3UYR.PDB	OD2, L_ASP_155	ND1, L_HIS_193	HD1, L_HIS_193	2.93	2.16	21.52
3UYR.PDB	ND2, L_ASN_216	ND2, L_ASN_194	HD22, L_ASN_194	2.90	2.18	28.48
3UYR.PDB	O, L_PHE_213	N, L_TYR_196	H, L_TYR_196	2.86	2.00	4.60
3UYR.PDB	O, L_LYS_153	N, L_THR_197	H, L_THR_197	2.91	2.08	15.26
3UYR.PDB	O, L_LYS_211	N, L_CYS_198	H, L_CYS_198	2.83	2.02	16.54
3UYR.PDB	O, L_LYS_151	N, L_GLU_199	H, L_GLU_199	2.79	1.98	16.73
3UYR.PDB	O, L_ILE_209	N, L_ALA_200	H, L_ALA_200	2.74	1.92	13.71
3UYR.PDB	O, L_ASN_149	N, L_THR_201	H, L_THR_201	2.78	1.96	14.01
3UYR.PDB	OG1, L_THR_204	ND1, L_HIS_202	HD1, L_HIS_202	2.78	1.93	6.06
3UYR.PDB	O, L_ALA_200	N, L_ILE_209	H, L_ILE_209	2.92	2.18	25.89
3UYR.PDB	O, L_CYS_198	N, L_LYS_211	H, L_LYS_211	2.90	2.05	8.10
3UYR.PDB	O, L_TYR_196	N, L_PHE_213	H, L_PHE_213	2.87	2.05	16.74
3UYR.PDB	O, L_ASN_194	N, L_ARG_215	H, L_ARG_215	2.75	1.97	21.32
3UYR.PDB	O, L_HIS_193	NE, L_ARG_215	HE, L_ARG_215	2.87	2.04	12.99
3UYR.PDB	OD1, H_ASN_101	NE2, P_GLN_48	HE22, P_GLN_48	2.57	1.87	29.89

Table 1686: 3UYR-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
3X0E.PDB	O, A_PHE.198	NZ, A_LYS.116	HZ3, A_LYS.116	2.72	1.88	16.62
3X0E.PDB	OD1, A_ASP.122	NE2, A_GLN.118	HE21, A_GLN.118	2.93	2.22	29.07
3X0E.PDB	O, A_ASN.115	N, A_ILE.119	H, A_ILE.119	2.94	2.11	11.48
3X0E.PDB	O, A_GLN.118	N, A_ASP.122	H, A_ASP.122	2.95	2.12	13.26
3X0E.PDB	O, A_ILE.119	N, A_VAL.123	H, A_VAL.123	2.88	2.05	13.75
3X0E.PDB	OD2, A_ASP.195	NZ, A_LYS.124	HZ1, A_LYS.124	3.00	2.19	21.32
3X0E.PDB	O, A_ASP.122	N, A_PHE.126	H, A_PHE.126	2.90	2.08	15.30
3X0E.PDB	O, A_VAL.123	N, A_TYR.127	H, A_TYR.127	2.95	2.12	11.57
3X0E.PDB	O, A_LYS.124	N, A_ASP.128	H, A_ASP.128	2.92	2.07	7.55
3X0E.PDB	O, A_GLN.125	N, A_GLN.129	H, A_GLN.129	2.88	2.03	7.18
3X0E.PDB	O, A_TYR.127	N, A_LEU.131	H, A_LEU.131	2.82	2.00	14.74
3X0E.PDB	O, A_ASP.128	N, A_GLN.132	H, A_GLN.132	2.95	2.12	11.27
3X0E.PDB	O, A_ALA.130	N, A_ALA.134	H, A_ALA.134	2.77	1.95	14.29
3X0E.PDB	O, A_GLN.133	N, A_ASP.137	H, A_ASP.137	2.92	2.17	25.03
3X0E.PDB	O, A_ASN.141	N, A_ALA.145	H, A_ALA.145	2.97	2.17	18.25
3X0E.PDB	O, A_ASN.142	N, A_VAL.146	H, A_VAL.146	2.81	1.98	12.77
3X0E.PDB	O, A_LYS.144	N, A_LYS.148	H, A_LYS.148	2.95	2.10	7.95
3X0E.PDB	O, A_ALA.145	N, A_THR.149	H, A_THR.149	2.85	2.06	19.27
3X0E.PDB	O, A_VAL.146	N, A_PHE.150	H, A_PHE.150	2.92	2.09	13.09
3X0E.PDB	O, A_VAL.147	N, A_HIS.151	H, A_HIS.151	2.86	2.05	17.72
3X0E.PDB	O, A_LEU.174	ND1, A_HIS.151	HD1, A_HIS.151	2.63	1.79	9.32
3X0E.PDB	O, A_THR.149	N, A_THR.153	H, A_THR.153	2.90	2.06	11.00
3X0E.PDB	O, A_PHE.150	N, A_LEU.154	H, A_LEU.154	2.90	2.06	10.44
3X0E.PDB	OD2, A_ASP.189	N, A_SER.160	H, A_SER.160	2.87	2.16	28.56
3X0E.PDB	OD2, A_ASP.128	OG1, A_THR.161	HG1, A_THR.161	2.92	2.13	12.66
3X0E.PDB	O, A_LEU.162	N, A_LEU.165	H, A_LEU.165	2.87	2.07	18.34
3X0E.PDB	O, A_SER.168	N, A_ASN.172	H, A_ASN.172	2.80	2.05	24.69
3X0E.PDB	O, A_SER.168	ND2, A_ASN.172	HD22, A_ASN.172	2.72	1.93	18.83
3X0E.PDB	O, A_LEU.170	N, A_ASN.173	H, A_ASN.173	2.82	1.98	11.48
3X0E.PDB	O, A_PRO.176	N, A_SER.179	H, A_SER.179	2.96	2.12	10.85
3X0E.PDB	O, A_CYS.157	ND2, A_ASN.184	HD21, A_ASN.184	2.90	2.04	5.52
3X0E.PDB	OD1, A_ASP.155	NZ, A_LYS.187	HZ1, A_LYS.187	2.84	2.07	26.10
3X0E.PDB	OD2, A_ASP.189	N, A_HIS.191	H, A_HIS.191	2.94	2.18	22.64
3X0E.PDB	O, A_CYS.190	N, A_ILE.194	H, A_ILE.194	2.84	2.02	14.86
3X0E.PDB	O, A_HIS.191	N, A_ASP.195	H, A_ASP.195	2.95	2.12	12.91
3X0E.PDB	O, A_GLN.192	N, A_ASP.196	H, A_ASP.196	2.86	2.06	18.82
3X0E.PDB	O, A_ASP.196	N, A_LYS.201	H, A_LYS.201	2.89	2.07	14.52
3X0E.PDB	OD1, B_ASN.115	N, B_GLN.118	H, B_GLN.118	2.83	2.07	23.69
3X0E.PDB	O, B_LYS.116	N, B_ALA.120	H, B_ALA.120	2.96	2.13	11.70
3X0E.PDB	O, B_GLN.118	N, B_ASP.122	H, B_ASP.122	2.91	2.08	11.40
3X0E.PDB	O, B_ILE.119	N, B_VAL.123	H, B_VAL.123	2.88	2.07	15.19
3X0E.PDB	O, B_ALA.120	N, B_LYS.124	H, B_LYS.124	2.98	2.18	17.57
3X0E.PDB	OD1, B_ASP.195	NZ, B_LYS.124	HZ1, B_LYS.124	2.75	2.02	29.74
3X0E.PDB	O, B_VAL.123	N, B_TYR.127	H, B_TYR.127	2.87	2.05	14.21
3X0E.PDB	O, B_LYS.124	N, B_ASP.128	H, B_ASP.128	2.82	1.97	7.12
3X0E.PDB	O, B_GLN.125	N, B_GLN.129	H, B_GLN.129	2.95	2.09	4.29
3X0E.PDB	O, B_TYR.127	N, B_LEU.131	H, B_LEU.131	2.80	2.02	19.97
3X0E.PDB	O, B_GLN.129	N, B_GLN.133	H, B_GLN.133	2.90	2.04	5.41
3X0E.PDB	O, B_ALA.130	N, B_ALA.134	H, B_ALA.134	2.78	2.05	26.00
3X0E.PDB	O, B_GLN.132	N, B_VAL.136	H, B_VAL.136	2.97	2.12	6.76
3X0E.PDB	O, B_LYS.144	N, B_LYS.148	H, B_LYS.148	2.88	2.03	4.95
3X0E.PDB	O, B_ALA.145	N, B_THR.149	H, B_THR.149	2.96	2.14	15.45
3X0E.PDB	O, B_ALA.145	OG1, B_THR.149	HG1, B_THR.149	2.91	2.17	22.45
3X0E.PDB	O, B_VAL.146	N, B_PHE.150	H, B_PHE.150	2.95	2.10	9.14
3X0E.PDB	O, B_VAL.147	N, B_HIS.151	H, B_HIS.151	2.89	2.04	9.03
3X0E.PDB	O, B_LEU.174	ND1, B_HIS.151	HD1, B_HIS.151	2.75	1.90	7.86
3X0E.PDB	O, B_LYS.148	N, B_GLU.152	H, B_GLU.152	2.88	2.06	15.18

3X0E.PDB	O, B_THR_149	N, B_THR_153	H, B_THR_153	2.82	1.98	10.07
3X0E.PDB	O, B_PHE_150	N, B_LEU_154	H, B_LEU_154	2.87	2.04	11.99
3X0E.PDB	OG1, B_THR_166	N, B_SER_159	H, B_SER_159	2.96	2.14	15.38
3X0E.PDB	OD2, B_ASP_189	N, B_SER_160	H, B_SER_160	2.78	1.93	3.69
3X0E.PDB	OG, B_SER_159	OG1, B_THR_161	HG1, B_THR_161	2.79	1.98	7.89
3X0E.PDB	O, B_SER_159	N, B_LEU_162	H, B_LEU_162	2.92	2.08	12.42
3X0E.PDB	O, B_LEU_162	N, B_THR_166	H, B_THR_166	2.94	2.18	23.20
3X0E.PDB	O, B_LEU_162	OG1, B_THR_166	HG1, B_THR_166	2.88	2.11	16.63
3X0E.PDB	O, B_THR_163	N, B_THR_167	H, B_THR_167	2.85	2.03	14.83
3X0E.PDB	O, B_LEU_165	N, B_VAL_169	H, B_VAL_169	2.94	2.17	21.85
3X0E.PDB	O, B_THR_166	N, B_LEU_170	H, B_LEU_170	2.95	2.19	24.26
3X0E.PDB	O, B_THR_167	N, B_LYS_171	H, B_LYS_171	2.99	2.15	11.05
3X0E.PDB	O, B_ASN_184	N, B_GLU_188	H, B_GLU_188	2.89	2.05	8.79
3X0E.PDB	OD1, B_ASP_128	NE2, B_HIS_191	HE2, B_HIS_191	2.68	1.83	6.07
3X0E.PDB	OD1, B_ASP_189	N, B_GLN_192	H, B_GLN_192	2.88	2.05	11.35
3X0E.PDB	O, B_ASP_189	N, B_LYS_193	H, B_LYS_193	2.99	2.20	19.70
3X0E.PDB	O, B_CYS_190	N, B_ILE_194	H, B_ILE_194	2.95	2.13	14.03
3X0E.PDB	O, B_GLN_192	N, B_ASP_196	H, B_ASP_196	2.94	2.14	18.40
3X0E.PDB	O, B_LYS_193	N, B_LEU_197	H, B_LEU_197	2.89	2.17	28.98
3X0E.PDB	O, B_ASP_196	N, B_LYS_201	H, B_LYS_201	2.91	2.09	15.23

Table 1687: 3X0E-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
3X0F.PDB	OD1, A_ASN.115	N, A_ASP.117	H, A_ASP.117	2.76	2.05	29.22
3X0F.PDB	O, A_LYS.116	N, A_ALA.120	H, A_ALA.120	2.96	2.10	6.18
3X0F.PDB	O, A_GLN.118	N, A_ASP.122	H, A_ASP.122	2.90	2.09	15.79
3X0F.PDB	O, A_ILE.119	N, A_VAL.123	H, A_VAL.123	2.92	2.11	16.68
3X0F.PDB	O, A_ALA.120	N, A_LYS.124	H, A_LYS.124	2.96	2.13	12.80
3X0F.PDB	OD1, A_ASP.195	NZ, A_LYS.124	HZ3, A_LYS.124	2.91	2.03	6.30
3X0F.PDB	O, A_ASP.122	N, A_PHE.126	H, A_PHE.126	2.92	2.10	14.97
3X0F.PDB	O, A_VAL.123	N, A_TYR.127	H, A_TYR.127	2.88	2.05	12.59
3X0F.PDB	O, A_LYS.124	N, A_ASP.128	H, A_ASP.128	2.89	2.08	15.92
3X0F.PDB	O, A_TYR.127	N, A_LEU.131	H, A_LEU.131	2.80	1.98	14.29
3X0F.PDB	O, A_ALA.130	N, A_ALA.134	H, A_ALA.134	2.84	2.00	11.20
3X0F.PDB	O, A_GLN.133	N, A_ASP.137	H, A_ASP.137	2.91	2.07	8.58
3X0F.PDB	OD1, A_ASP.137	N, A_ASP.139	H, A_ASP.139	2.85	1.99	3.86
3X0F.PDB	O, A_ALA.140	N, A_LYS.144	H, A_LYS.144	2.97	2.14	11.74
3X0F.PDB	O, A_ALA.134	NZ, A_LYS.144	HZ3, A_LYS.144	2.61	1.87	27.66
3X0F.PDB	O, A_ASN.142	N, A_VAL.146	H, A_VAL.146	2.93	2.09	11.09
3X0F.PDB	O, A_ALA.143	N, A_VAL.147	H, A_VAL.147	2.89	2.04	7.77
3X0F.PDB	O, A_LYS.144	N, A_LYS.148	H, A_LYS.148	2.90	2.05	7.59
3X0F.PDB	O, A_SER.173	NZ, A_LYS.148	HZ3, A_LYS.148	2.88	2.00	7.58
3X0F.PDB	O, A_ALA.145	OG1, A_THR.149	HG1, A_THR.149	2.91	2.14	15.86
3X0F.PDB	O, A_VAL.147	N, A_HIS.151	H, A_HIS.151	2.90	2.06	9.89
3X0F.PDB	O, A_LEU.174	ND1, A_HIS.151	HD1, A_HIS.151	2.77	1.98	20.06
3X0F.PDB	O, A_LYS.148	N, A_GLU.152	H, A_GLU.152	2.93	2.09	11.11
3X0F.PDB	O, A_THR.149	N, A_THR.153	H, A_THR.153	2.90	2.09	16.44
3X0F.PDB	O, A_PHE.150	N, A_LEU.154	H, A_LEU.154	2.81	2.01	18.57
3X0F.PDB	OG1, A_THR.163	N, A_ASN.160	H, A_ASN.160	2.95	2.21	26.42
3X0F.PDB	OG, A_SER.159	OG1, A_THR.163	HG1, A_THR.163	2.77	1.96	7.35
3X0F.PDB	O, A_ASN.160	N, A_THR.164	H, A_THR.164	2.88	2.07	16.97
3X0F.PDB	O, A_ASN.160	OG1, A_THR.164	HG1, A_THR.164	2.73	2.01	24.68
3X0F.PDB	O, A_LEU.162	N, A_THR.166	H, A_THR.166	2.92	2.10	13.93
3X0F.PDB	O, A_THR.163	OG1, A_THR.167	HG1, A_THR.167	2.89	2.12	16.26
3X0F.PDB	O, A_THR.166	N, A_LEU.170	H, A_LEU.170	2.90	2.06	12.50
3X0F.PDB	O, A_THR.167	N, A_ARG.171	H, A_ARG.171	2.82	2.01	17.53
3X0F.PDB	O, A_ARG.171	N, A_LEU.174	H, A_LEU.174	2.93	2.08	5.89
3X0F.PDB	O, A_ASN.172	N, A_CYS.175	H, A_CYS.175	3.00	2.20	18.23
3X0F.PDB	OG1, A_THR.183	N, A_ASN.180	H, A_ASN.180	2.96	2.18	19.92
3X0F.PDB	OD1, A_ASN.180	N, A_LEU.182	H, A_LEU.182	2.45	1.71	25.25
3X0F.PDB	O, A_THR.183	N, A_LEU.186	H, A_LEU.186	2.99	2.15	11.85
3X0F.PDB	O, A_PRO.184	N, A_GLN.187	H, A_GLN.187	2.97	2.13	7.84
3X0F.PDB	OE1, A_GLN.192	N, A_ASP.189	H, A_ASP.189	2.95	2.17	21.65
3X0F.PDB	O, A_GLY.158	N, A_CYS.190	H, A_CYS.190	2.80	1.94	6.85
3X0F.PDB	OD1, A_ASP.128	NE2, A_HIS.191	HE2, A_HIS.191	2.65	1.83	14.50
3X0F.PDB	OD1, A_ASP.189	N, A_GLN.192	H, A_GLN.192	2.76	1.93	12.98
3X0F.PDB	O, A_CYS.190	N, A_ILE.194	H, A_ILE.194	2.92	2.08	11.33
3X0F.PDB	O, A_HIS.191	N, A_ASP.195	H, A_ASP.195	2.89	2.05	8.32
3X0F.PDB	OD1, B_ASN.115	N, B_ASP.117	H, B_ASP.117	2.83	2.09	25.59
3X0F.PDB	O, B_ILE.119	N, B_VAL.123	H, B_VAL.123	2.90	2.08	14.90
3X0F.PDB	O, B_ALA.120	N, B_LYS.124	H, B_LYS.124	2.96	2.13	14.11
3X0F.PDB	O, B_ASP.122	N, B_PHE.126	H, B_PHE.126	2.92	2.10	15.77
3X0F.PDB	O, B_VAL.123	N, B_TYR.127	H, B_TYR.127	2.83	1.99	10.66
3X0F.PDB	O, B_LYS.124	N, B_ASP.128	H, B_ASP.128	2.91	2.10	15.77
3X0F.PDB	O, B_TYR.127	N, B_LEU.131	H, B_LEU.131	2.83	2.00	14.03
3X0F.PDB	O, B_ASP.128	N, B_GLN.132	H, B_GLN.132	2.94	2.11	13.87
3X0F.PDB	O, B_ALA.130	N, B_ALA.134	H, B_ALA.134	2.84	1.99	5.94
3X0F.PDB	O, B_GLN.133	N, B_ASP.137	H, B_ASP.137	2.83	1.99	9.88
3X0F.PDB	OD1, B_ASP.137	N, B_ASP.139	H, B_ASP.139	2.78	1.95	12.28
3X0F.PDB	O, B_ASN.141	N, B_ALA.145	H, B_ALA.145	2.98	2.19	18.75

3X0F.PDB	O, B_ASN_142	N, B_VAL_146	H, B_VAL_146	2.93	2.10	14.03
3X0F.PDB	O, B_ALA_143	N, B_VAL_147	H, B_VAL_147	2.90	2.05	8.67
3X0F.PDB	O, B_LYS_144	N, B_LYS_148	H, B_LYS_148	2.93	2.08	6.49
3X0F.PDB	O, B_ALA_145	OG1, B_THR_149	HG1, B_THR_149	2.77	1.99	16.05
3X0F.PDB	O, B_VAL_147	N, B_HIS_151	H, B_HIS_151	2.84	2.00	10.99
3X0F.PDB	O, B_LEU_174	ND1, B_HIS_151	HD1, B_HIS_151	2.65	1.84	15.99
3X0F.PDB	OH, B_TYR_127	NE2, B_HIS_151	HE2, B_HIS_151	2.81	2.02	19.67
3X0F.PDB	O, B_LYS_148	N, B_GLU_152	H, B_GLU_152	2.77	1.92	6.84
3X0F.PDB	O, B_THR_149	N, B_THR_153	H, B_THR_153	2.95	2.13	14.83
3X0F.PDB	O, B_PHE_150	N, B_LEU_154	H, B_LEU_154	2.85	2.04	17.17
3X0F.PDB	OG1, B_THR_163	OG, B_SER_159	HG, B_SER_159	2.96	2.16	10.94
3X0F.PDB	O, B_ASN_160	OG1, B_THR_164	HG1, B_THR_164	2.57	1.80	16.52
3X0F.PDB	O, B_LEU_162	N, B_THR_166	H, B_THR_166	2.76	1.93	11.31
3X0F.PDB	O, B_THR_163	N, B_THR_167	H, B_THR_167	2.99	2.18	15.60
3X0F.PDB	O, B_THR_166	N, B_LEU_170	H, B_LEU_170	2.87	2.06	18.01
3X0F.PDB	O, B_GLY_158	N, B_CYS_190	H, B_CYS_190	2.83	2.05	20.10
3X0F.PDB	OD1, B_ASP_128	NE2, B_HIS_191	HE2, B_HIS_191	2.69	1.83	1.74
3X0F.PDB	O, B_CYS_190	N, B_ILE_194	H, B_ILE_194	2.81	1.97	10.56
3X0F.PDB	O, B_GLN_192	N, B_GLU_196	H, B_GLU_196	2.96	2.13	13.52
3X0F.PDB	O, B_LYS_193	N, B_LEU_197	H, B_LEU_197	2.98	2.18	18.16
3X0F.PDB	O, B_ILE_194	N, B_PHE_198	H, B_PHE_198	2.87	2.06	16.88
3X0F.PDB	O, B_ASP_195	N, B_SER_199	H, B_SER_199	2.79	2.06	26.20

Table 1688: 3X0F-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4F33.PDB	OG, A.SER.27	N, A.GLU.4	H, A.GLU.4	2.93	2.12	15.90
4F33.PDB	O, A.SER.25	N, A.THR.6	H, A.THR.6	2.82	1.97	4.01
4F33.PDB	O, A.TYR.86	NE2, A.GLN.7	HE22, A.GLN.7	2.87	2.09	21.54
4F33.PDB	O, A.THR.23	N, A.SER.8	H, A.SER.8	2.88	2.08	17.40
4F33.PDB	O, A.LYS.103	N, A.MET.12	H, A.MET.12	2.89	2.08	17.33
4F33.PDB	OE2, A.GLU.18	N, A.SER.15	H, A.SER.15	2.97	2.12	6.98
4F33.PDB	O, A.VAL.78	N, A.GLY.17	H, A.GLY.17	2.85	2.06	20.41
4F33.PDB	O, A.ILE.75	N, A.VAL.20	H, A.VAL.20	2.97	2.17	19.12
4F33.PDB	O, A.LEU.73	N, A.MET.22	H, A.MET.22	2.86	2.02	10.29
4F33.PDB	O, A.SER.8	N, A.THR.23	H, A.THR.23	2.78	1.93	7.24
4F33.PDB	O, A.TYR.71	N, A.CYS.24	H, A.CYS.24	2.78	1.93	6.93
4F33.PDB	O, A.THR.6	N, A.SER.25	H, A.SER.25	2.80	1.94	5.80
4F33.PDB	O, A.ASN.69	N, A.ALA.26	H, A.ALA.26	2.83	1.99	8.87
4F33.PDB	O, A.ILE.48	N, A.TRP.35	H, A.TRP.35	2.69	1.86	13.25
4F33.PDB	O, A.TYR.87	N, A.TYR.36	H, A.TYR.36	2.79	1.98	16.56
4F33.PDB	O, A.LYS.45	N, A.GLN.37	H, A.GLN.37	2.93	2.17	24.56
4F33.PDB	O, A.THR.85	N, A.GLN.38	H, A.GLN.38	2.78	1.94	8.77
4F33.PDB	O, A.THR.42	NE2, A.GLN.38	HE21, A.GLN.38	2.85	2.01	10.50
4F33.PDB	OE1, B.GLN.39	NE2, A.GLN.38	HE22, A.GLN.38	2.96	2.13	12.75
4F33.PDB	O, A.GLU.81	NZ, A.LYS.39	HZ1, A.LYS.39	2.81	1.96	14.34
4F33.PDB	O, A.ASP.83	NZ, A.LYS.39	HZ3, A.LYS.39	2.88	2.10	24.06
4F33.PDB	O, A.LYS.39	OG1, A.THR.42	HG1, A.THR.42	2.81	1.99	3.65
4F33.PDB	O, B.GLY.110	OG, A.SER.43	HG, A.SER.43	2.65	1.95	25.99
4F33.PDB	O, A.GLN.37	N, A.LYS.45	H, A.LYS.45	2.79	1.96	13.89
4F33.PDB	O, B.ARG.104	NH1, A.ARG.46	HH11, A.ARG.46	2.62	1.83	18.99
4F33.PDB	O, A.TRP.35	N, A.TRP.47	H, A.TRP.47	2.84	2.05	19.82
4F33.PDB	O, A.LYS.53	N, A.TYR.49	H, A.TYR.49	2.79	1.99	16.95
4F33.PDB	O, A.MET.33	N, A.THR.51	H, A.THR.51	2.74	1.92	15.06
4F33.PDB	O, A.ASP.50	N, A.SER.52	H, A.SER.52	2.84	2.12	28.76
4F33.PDB	O, A.TYR.49	N, A.LYS.53	H, A.LYS.53	2.87	2.05	15.09
4F33.PDB	OD2, A.ASP.82	NE, A.ARG.61	HE, A.ARG.61	2.81	2.09	28.09
4F33.PDB	OD1, A.ASP.82	NH2, A.ARG.61	HH21, A.ARG.61	2.71	1.85	4.82
4F33.PDB	O, A.THR.74	N, A.SER.63	H, A.SER.63	2.91	2.14	22.09
4F33.PDB	O, A.ALA.26	ND2, A.ASN.69	HD21, A.ASN.69	2.95	2.09	2.58
4F33.PDB	O, A.SER.67	N, A.SER.70	H, A.SER.70	2.98	2.12	3.48
4F33.PDB	O, A.CYS.24	N, A.TYR.71	H, A.TYR.71	2.94	2.09	7.81
4F33.PDB	O, A.VAL.30	OH, A.TYR.71	HH, A.TYR.71	2.83	2.13	26.33
4F33.PDB	O, A.SER.65	N, A.SER.72	H, A.SER.72	2.82	1.99	12.37
4F33.PDB	O, A.MET.22	N, A.LEU.73	H, A.LEU.73	2.90	2.08	15.13
4F33.PDB	O, A.SER.63	N, A.THR.74	H, A.THR.74	2.86	2.01	8.97
4F33.PDB	OG1, A.THR.21	OG1, A.THR.74	HG1, A.THR.74	2.73	1.99	21.82
4F33.PDB	O, A.VAL.20	N, A.ILE.75	H, A.ILE.75	2.86	2.05	16.70
4F33.PDB	O, A.ARG.61	N, A.SER.76	H, A.SER.76	2.74	1.93	15.27
4F33.PDB	O, A.GLU.18	N, A.VAL.78	H, A.VAL.78	2.98	2.22	23.09
4F33.PDB	OD2, A.ASP.82	N, A.GLU.79	H, A.GLU.79	2.83	1.97	5.35
4F33.PDB	O, A.GLU.79	N, A.ASP.82	H, A.ASP.82	2.82	1.98	10.48
4F33.PDB	O, A.GLN.38	N, A.THR.85	H, A.THR.85	2.93	2.09	10.56
4F33.PDB	O, A.THR.102	N, A.TYR.86	H, A.TYR.86	2.88	2.05	12.33
4F33.PDB	O, A.TYR.36	N, A.TYR.87	H, A.TYR.87	2.86	2.04	15.05
4F33.PDB	OG1, A.THR.97	NE2, A.GLN.90	HE21, A.GLN.90	2.97	2.15	14.62
4F33.PDB	O, A.TYR.32	NE1, A.TRP.91	HE1, A.TRP.91	2.74	1.96	21.98
4F33.PDB	O, A.ILE.3	OG1, A.THR.97	HG1, A.THR.97	2.86	2.07	13.11
4F33.PDB	O, A.CYS.88	N, A.GLY.99	H, A.GLY.99	2.86	2.04	15.33
4F33.PDB	OE1, A.GLN.7	N, A.GLY.101	H, A.GLY.101	2.83	2.06	22.47
4F33.PDB	O, A.TYR.86	N, A.THR.102	H, A.THR.102	2.93	2.11	14.73
4F33.PDB	O, A.PRO.9	OG1, A.THR.102	HG1, A.THR.102	2.73	1.96	15.99
4F33.PDB	O, A.ALA.10	N, A.LYS.103	H, A.LYS.103	2.90	2.06	9.01

4F33.PDB	O, A_ALA_84	N, A_VAL_104	H, A_VAL_104	2.88	2.03	4.65
4F33.PDB	O, A_MET_12	N, A_GLU_105	H, A_GLU_105	2.79	1.94	7.59
4F33.PDB	OE1, A_GLN_166	N, A_ILE_106	H, A_ILE_106	2.90	2.05	6.64
4F33.PDB	O, A_ALA_14	N, A_LYS_107	H, A_LYS_107	2.83	2.00	10.77
4F33.PDB	OG, A_SER_13	NZ, A_LYS_107	HZ3, A_LYS_107	2.94	2.07	9.78
4F33.PDB	O, A_THR_109	NE, A_ARG_108	HE, A_ARG_108	2.77	1.91	3.92
4F33.PDB	O, A_ASP_170	NH1, A_ARG_108	HH11, A_ARG_108	2.95	2.12	11.15
4F33.PDB	O, A_TYR_140	N, A_ALA_111	H, A_ALA_111	2.85	2.01	10.73
4F33.PDB	O, A_LEU_135	N, A_PHE_116	H, A_PHE_116	2.94	2.15	19.06
4F33.PDB	O, A_VAL_133	N, A_PHE_118	H, A_PHE_118	2.80	2.01	19.24
4F33.PDB	OG, A_SER_131	NE2, A_GLN_124	HE22, A_GLN_124	2.81	1.96	5.54
4F33.PDB	O, A_LEU_125	N, A_GLY_128	H, A_GLY_128	2.79	1.95	9.52
4F33.PDB	O, A_LEU_181	N, A_ALA_130	H, A_ALA_130	2.76	1.92	9.83
4F33.PDB	OE1, A_GLN_124	N, A_SER_131	H, A_SER_131	2.96	2.15	16.54
4F33.PDB	O, A_LEU_179	N, A_VAL_132	H, A_VAL_132	2.82	1.98	11.91
4F33.PDB	O, A_SER_177	N, A_CYS_134	H, A_CYS_134	2.86	2.01	7.49
4F33.PDB	O, A_PHE_116	N, A_LEU_135	H, A_LEU_135	2.76	1.92	8.98
4F33.PDB	O, A_LEU_175	N, A_LEU_136	H, A_LEU_136	2.76	1.90	4.04
4F33.PDB	O, A_SER_114	N, A_ASN_137	H, A_ASN_137	2.84	2.02	13.99
4F33.PDB	O, A_TYR_173	N, A_PHE_139	H, A_PHE_139	2.85	2.04	16.43
4F33.PDB	O, A_ALA_111	N, A_TYR_140	H, A_TYR_140	2.90	2.09	16.65
4F33.PDB	O, A_THR_197	N, A_LYS_145	H, A_LYS_145	2.98	2.16	14.92
4F33.PDB	O, A_GLU_195	N, A_GLN_147	H, A_GLN_147	2.86	2.02	11.34
4F33.PDB	OG, A_SER_177	NE1, A_TRP_148	HE1, A_TRP_148	2.91	2.09	14.52
4F33.PDB	O, A_ALA_193	N, A_LYS_149	H, A_LYS_149	2.87	2.03	10.60
4F33.PDB	OE1, A_GLU_195	NZ, A_LYS_149	HZ2, A_LYS_149	2.59	1.85	28.21
4F33.PDB	O, A_VAL_191	N, A_ASP_151	H, A_ASP_151	2.75	1.92	13.23
4F33.PDB	O, A_VAL_150	N, A_ALA_153	H, A_ALA_153	2.85	2.00	6.45
4F33.PDB	O, A_TRP_148	N, A_GLN_155	H, A_GLN_155	2.92	2.11	17.54
4F33.PDB	OE1, A_GLN_155	ND2, A_ASN_158	HD22, A_ASN_158	2.89	2.06	12.00
4F33.PDB	O, A_THR_178	N, A_GLN_160	H, A_GLN_160	2.98	2.22	22.84
4F33.PDB	O, A_SER_176	N, A_SER_162	H, A_SER_162	2.94	2.15	19.03
4F33.PDB	O, B_PRO_173	OG, A_SER_162	HG, A_SER_162	2.76	2.03	23.18
4F33.PDB	O, A_SER_174	N, A_THR_164	H, A_THR_164	2.92	2.09	12.25
4F33.PDB	O, A_SER_171	NE2, A_GLN_166	HE21, A_GLN_166	2.92	2.09	13.24
4F33.PDB	O, A_ILE_106	NE2, A_GLN_166	HE22, A_GLN_166	2.72	1.92	18.36
4F33.PDB	OD1, A_ASP_167	N, A_LYS_169	H, A_LYS_169	2.65	1.81	10.48
4F33.PDB	O, A_ASP_167	N, A_SER_171	H, A_SER_171	2.90	2.19	29.27
4F33.PDB	OD1, A_ASP_170	N, A_THR_172	H, A_THR_172	2.86	2.04	14.41
4F33.PDB	OD1, A_ASP_170	OG1, A_THR_172	HG1, A_THR_172	2.68	1.86	4.02
4F33.PDB	O, A_PHE_139	N, A_TYR_173	H, A_TYR_173	2.78	1.94	7.95
4F33.PDB	OG1, A_THR_164	N, A_SER_174	H, A_SER_174	2.96	2.13	11.32
4F33.PDB	O, A_LEU_136	N, A_LEU_175	H, A_LEU_175	2.82	2.01	16.11
4F33.PDB	O, A_SER_162	N, A_SER_176	H, A_SER_176	2.89	2.07	14.35
4F33.PDB	O, A_CYS_134	N, A_SER_177	H, A_SER_177	2.92	2.09	13.76
4F33.PDB	O, A_GLN_160	N, A_THR_178	H, A_THR_178	2.88	2.04	10.18
4F33.PDB	O, A_VAL_132	N, A_LEU_179	H, A_LEU_179	2.84	2.02	14.45
4F33.PDB	O, A_ASN_158	N, A_THR_180	H, A_THR_180	2.95	2.12	11.92
4F33.PDB	O, A_ALA_130	N, A_LEU_181	H, A_LEU_181	2.88	2.05	13.17
4F33.PDB	O, A_GLY_128	N, A_LYS_183	H, A_LYS_183	2.98	2.19	19.73
4F33.PDB	OG, A_SER_182	N, A_ASP_185	H, A_ASP_185	2.87	2.04	12.72
4F33.PDB	O, A_SER_182	N, A_TYR_186	H, A_TYR_186	2.80	1.98	14.27
4F33.PDB	O, A_LYS_183	N, A_GLU_187	H, A_GLU_187	2.86	2.04	14.84
4F33.PDB	OD2, A_ASP_151	N, A_LYS_190	H, A_LYS_190	2.95	2.15	18.90
4F33.PDB	OD1, A_ASP_151	N, A_VAL_191	H, A_VAL_191	2.83	1.98	4.63
4F33.PDB	O, A_PHE_209	N, A_TYR_192	H, A_TYR_192	2.96	2.11	7.57
4F33.PDB	O, A_LYS_149	N, A_ALA_193	H, A_ALA_193	2.92	2.11	16.79
4F33.PDB	O, A_LYS_207	N, A_CYS_194	H, A_CYS_194	2.99	2.20	20.51

4F33.PDB	O, A_GLN_147	N, A_GLU_195	H, A_GLU_195	2.80	1.96	10.16
4F33.PDB	O, A_VAL_205	N, A_VAL_196	H, A_VAL_196	2.72	1.89	12.89
4F33.PDB	O, A_LYS_145	N, A_THR_197	H, A_THR_197	2.87	2.04	14.20
4F33.PDB	O, A_HIS_198	N, A_LEU_201	H, A_LEU_201	2.83	1.98	4.49
4F33.PDB	O, A_VAL_196	N, A_VAL_205	H, A_VAL_205	2.93	2.11	14.32
4F33.PDB	O, A_TYR_192	N, A_PHE_209	H, A_PHE_209	2.97	2.19	21.09
4F33.PDB	O, A_LYS_190	N, A_ARG_211	H, A_ARG_211	2.77	1.94	10.87
4F33.PDB	O, A_HIS_189	NE, A_ARG_211	HE, A_ARG_211	2.95	2.11	10.88
4F33.PDB	O, B_LYS_23	N, B_GLN_5	H, B_GLN_5	2.89	2.04	6.23
4F33.PDB	O, B_TYR_94	NE2, B_GLN_6	HE22, B_GLN_6	2.91	2.10	17.22
4F33.PDB	O, B_SER_21	N, B_SER_7	H, B_SER_7	2.99	2.26	27.49
4F33.PDB	O, B_PRO_114	N, B_GLU_10	H, B_GLU_10	2.94	2.16	20.47
4F33.PDB	O, B_LEU_86	N, B_GLY_15	H, B_GLY_15	2.71	1.91	16.40
4F33.PDB	O, B_LEU_83	N, B_VAL_18	H, B_VAL_18	2.93	2.17	23.19
4F33.PDB	O, B_MET_81	N, B_ILE_20	H, B_ILE_20	2.82	1.99	11.32
4F33.PDB	OG, B_SER_7	N, B_SER_21	H, B_SER_21	2.96	2.11	7.69
4F33.PDB	O, B_ALA_79	N, B_CYS_22	H, B_CYS_22	2.82	2.06	23.47
4F33.PDB	O, B_GLN_5	N, B_LYS_23	H, B_LYS_23	2.73	1.90	11.88
4F33.PDB	O, B_SER_77	N, B_ALA_24	H, B_ALA_24	2.97	2.12	8.25
4F33.PDB	O, B_GLN_3	N, B_SER_25	H, B_SER_25	2.93	2.12	17.16
4F33.PDB	O, B_SER_28	N, B_GLY_31	H, B_GLY_31	2.98	2.12	6.95
4F33.PDB	O, B_GLY_99	N, B_THR_33	H, B_THR_33	2.98	2.22	23.44
4F33.PDB	O, B_ALA_97	N, B_ASN_35	H, B_ASN_35	2.80	1.95	8.88
4F33.PDB	O, B_PHE_95	N, B_VAL_37	H, B_VAL_37	2.85	2.06	19.95
4F33.PDB	O, B_GLU_46	N, B_LYS_38	H, B_LYS_38	2.82	2.01	16.68
4F33.PDB	O, B_GLU_89	NZ, B_LYS_38	HZ1, B_LYS_38	2.86	1.98	5.39
4F33.PDB	O, B_VAL_93	N, B_GLN_39	H, B_GLN_39	2.87	2.01	5.84
4F33.PDB	OE1, A_GLN_38	NE2, B_GLN_39	HE22, B_GLN_39	2.82	1.97	5.31
4F33.PDB	O, B_SER_40	N, B_LYS_43	H, B_LYS_43	2.88	2.06	15.26
4F33.PDB	O, B_LYS_38	N, B_GLU_46	H, B_GLU_46	2.87	2.06	16.90
4F33.PDB	O, B_TRP_36	N, B_ILE_48	H, B_ILE_48	2.80	1.95	7.15
4F33.PDB	O, B_SER_59	N, B_LEU_50	H, B_LEU_50	2.87	2.08	19.32
4F33.PDB	O, B_MET_34	N, B_ILE_51	H, B_ILE_51	2.89	2.09	18.35
4F33.PDB	O, B_ALA_57	N, B_THR_52	H, B_THR_52	2.92	2.09	13.37
4F33.PDB	O, B_THR_52	N, B_GLY_56	H, B_GLY_56	2.89	2.15	26.20
4F33.PDB	OD1, B_ASN_55	N, B_ALA_57	H, B_ALA_57	2.85	2.00	7.05
4F33.PDB	O, B_LEU_50	N, B_SER_59	H, B_SER_59	2.88	2.09	19.09
4F33.PDB	O, B_ILE_48	N, B_ASN_61	H, B_ASN_61	2.90	2.09	17.36
4F33.PDB	O, B_TRP_47	ND2, B_ASN_61	HD21, B_ASN_61	2.94	2.11	14.44
4F33.PDB	OE2, B_GLU_46	NZ, B_LYS_63	HZ3, B_LYS_63	2.70	1.89	19.35
4F33.PDB	O, B_ASN_61	N, B_PHE_64	H, B_PHE_64	2.77	1.93	12.05
4F33.PDB	OD2, B_ASP_90	NZ, B_LYS_67	HZ2, B_LYS_67	2.73	1.86	7.48
4F33.PDB	O, B_LEU_84	NZ, B_LYS_67	HZ3, B_LYS_67	2.85	2.01	15.38
4F33.PDB	O, B_PHE_64	N, B_ALA_68	H, B_ALA_68	2.93	2.14	19.80
4F33.PDB	O, B_ASP_82	N, B_THR_69	H, B_THR_69	2.92	2.16	23.54
4F33.PDB	OH, B_TYR_60	N, B_LEU_70	H, B_LEU_70	2.92	2.07	9.07
4F33.PDB	O, B_THR_78	N, B_ASP_73	H, B_ASP_73	2.75	1.91	10.75
4F33.PDB	O, B_CYS_22	N, B_ALA_79	H, B_ALA_79	2.91	2.08	13.58
4F33.PDB	O, B_THR_71	N, B_TYR_80	H, B_TYR_80	2.83	1.97	4.70
4F33.PDB	O, B_ILE_20	N, B_MET_81	H, B_MET_81	2.96	2.15	15.91
4F33.PDB	O, B_THR_69	N, B_ASP_82	H, B_ASP_82	2.88	2.06	13.69
4F33.PDB	O, B_VAL_18	N, B_LEU_83	H, B_LEU_83	2.80	1.96	11.41
4F33.PDB	O, B_LYS_67	N, B_LEU_84	H, B_LEU_84	2.92	2.11	17.58
4F33.PDB	O, B_ALA_16	N, B_LEU_86	H, B_LEU_86	2.87	2.02	6.19
4F33.PDB	OD2, B_ASP_90	N, B_THR_87	H, B_THR_87	2.83	2.02	16.35
4F33.PDB	O, B_THR_87	N, B_ASP_90	H, B_ASP_90	2.88	2.04	10.12
4F33.PDB	O, B_SER_88	N, B_SER_91	H, B_SER_91	2.97	2.12	6.19
4F33.PDB	O, B_VAL_115	N, B_ALA_92	H, B_ALA_92	2.98	2.25	27.22

4F33.PDB	O, B_GLN_39	N, B_VAL_93	H, B_VAL_93	2.95	2.11	9.70
4F33.PDB	O, B_THR_113	N, B_TYR_94	H, B_TYR_94	2.86	2.02	9.76
4F33.PDB	O, B_VAL_37	N, B_PHE_95	H, B_PHE_95	2.79	1.94	9.71
4F33.PDB	O, B_ASN_35	N, B_ALA_97	H, B_ALA_97	2.79	2.04	25.47
4F33.PDB	O, B_TYR_108	N, B_ARG_98	H, B_ARG_98	2.80	2.01	18.50
4F33.PDB	OD2, B_ASP_107	NH2, B_ARG_98	HH21, B_ARG_98	2.74	1.88	6.50
4F33.PDB	O, B_THR_33	N, B_GLY_99	H, B_GLY_99	2.94	2.10	10.07
4F33.PDB	OD1, B_ASP_102	NE, B_ARG_104	HE, B_ARG_104	2.87	2.03	8.81
4F33.PDB	OD2, B_ASP_107	NH1, B_ARG_104	HH11, B_ARG_104	2.78	1.96	13.74
4F33.PDB	OD2, B_ASP_102	NH2, B_ARG_104	HH21, B_ARG_104	2.87	2.08	19.19
4F33.PDB	OH, A_TYR_36	N, B_PHE_106	H, B_PHE_106	2.97	2.12	7.79
4F33.PDB	O, B_CYS_96	N, B_GLY_110	H, B_GLY_110	2.83	1.98	5.16
4F33.PDB	OE1, B_GLN_6	N, B_GLY_112	H, B_GLY_112	2.90	2.10	18.34
4F33.PDB	O, B_TYR_94	N, B_THR_113	H, B_THR_113	2.81	1.99	14.66
4F33.PDB	O, B_SER_7	OG1, B_THR_113	HG1, B_THR_113	2.83	2.05	14.68
4F33.PDB	O, B_ALA_92	N, B_VAL_115	H, B_VAL_115	2.84	1.99	7.09
4F33.PDB	OG, B_SER_91	N, B_VAL_117	H, B_VAL_117	2.86	2.01	9.50
4F33.PDB	O, B_GLU_12	N, B_SER_118	H, B_SER_118	2.87	2.07	16.95
4F33.PDB	O, B_PHE_152	N, B_LYS_123	H, B_LYS_123	2.81	1.98	13.03
4F33.PDB	O, B_ASP_150	NZ, B_LYS_123	HZ2, B_LYS_123	2.83	2.00	16.92
4F33.PDB	O, B_GLY_124	NZ, B_LYS_123	HZ3, B_LYS_123	2.99	2.25	28.99
4F33.PDB	OE2, G_GLU_123	N, B_GLY_124	H, B_GLY_124	2.73	1.87	2.75
4F33.PDB	O, B_LYS_149	N, B_SER_126	H, B_SER_126	2.95	2.16	19.58
4F33.PDB	O, B_LEU_147	N, B_PHE_128	H, B_PHE_128	2.87	2.05	14.02
4F33.PDB	O, B_GLY_145	N, B_LEU_130	H, B_LEU_130	2.71	1.85	5.41
4F33.PDB	OG, B_SER_136	N, B_SER_133	H, B_SER_133	2.90	2.08	15.18
4F33.PDB	OG, B_SER_133	N, B_LYS_135	H, B_LYS_135	2.89	2.11	19.85
4F33.PDB	O, B_SER_133	OG1, B_THR_137	HG1, B_THR_137	2.92	2.21	25.24
4F33.PDB	O, B_SER_138	N, B_THR_141	H, B_THR_141	2.82	1.98	11.03
4F33.PDB	O, B_VAL_190	N, B_ALA_142	H, B_ALA_142	2.81	1.95	3.27
4F33.PDB	O, B_SER_136	N, B_ALA_143	H, B_ALA_143	2.75	1.93	14.52
4F33.PDB	O, B_LEU_130	N, B_GLY_145	H, B_GLY_145	2.97	2.22	25.31
4F33.PDB	O, B_PHE_128	N, B_LEU_147	H, B_LEU_147	2.81	1.97	10.25
4F33.PDB	O, B_LEU_184	N, B_VAL_148	H, B_VAL_148	2.76	1.91	7.90
4F33.PDB	O, B_SER_126	N, B_LYS_149	H, B_LYS_149	2.79	1.93	4.11
4F33.PDB	O, B_LYS_123	N, B_PHE_152	H, B_PHE_152	2.89	2.09	18.27
4F33.PDB	O, B_ASN_203	N, B_SER_159	H, B_SER_159	2.96	2.15	17.06
4F33.PDB	OG, B_SER_186	NE1, B_TRP_160	HE1, B_TRP_160	2.97	2.13	10.43
4F33.PDB	O, B_ILE_201	N, B_ASN_161	H, B_ASN_161	2.81	1.97	10.56
4F33.PDB	OD1, B_ASN_203	N, B_SER_162	H, B_SER_162	2.81	2.00	15.00
4F33.PDB	O, B_TRP_160	N, B_GLY_163	H, B_GLY_163	2.93	2.14	20.08
4F33.PDB	O, B_VAL_187	N, B_HIS_170	H, B_HIS_170	2.81	1.98	12.68
4F33.PDB	O, B_SER_185	N, B_PHE_172	H, B_PHE_172	3.00	2.14	5.14
4F33.PDB	O, B_SER_183	N, B_VAL_175	H, B_VAL_175	2.90	2.08	14.90
4F33.PDB	O, B_LEU_181	N, B_GLN_177	H, B_GLN_177	2.81	1.96	6.18
4F33.PDB	OD1, B_ASP_150	NE2, B_GLN_177	HE22, B_GLN_177	2.84	2.07	21.15
4F33.PDB	O, B_TYR_151	N, B_TYR_182	H, B_TYR_182	2.85	2.02	11.23
4F33.PDB	O, B_VAL_148	N, B_LEU_184	H, B_LEU_184	2.91	2.10	17.00
4F33.PDB	O, B_CYS_146	N, B_SER_186	H, B_SER_186	2.97	2.15	14.23
4F33.PDB	O, B_HIS_170	N, B_VAL_187	H, B_VAL_187	2.83	1.99	10.23
4F33.PDB	O, B_LEU_144	N, B_VAL_188	H, B_VAL_188	2.83	2.04	19.81
4F33.PDB	O, B_ALA_142	N, B_VAL_190	H, B_VAL_190	2.79	1.97	14.47
4F33.PDB	O, B_GLY_140	N, B_SER_192	H, B_SER_192	2.87	2.03	10.06
4F33.PDB	O, B_PRO_191	N, B_SER_194	H, B_SER_194	2.87	2.02	9.35
4F33.PDB	O, B_SER_194	N, B_GLN_198	H, B_GLN_198	2.75	1.90	4.61
4F33.PDB	O, B_THR_199	NE2, B_GLN_198	HE21, B_GLN_198	2.96	2.10	2.10
4F33.PDB	OD1, B_ASN_161	N, B_ILE_201	H, B_ILE_201	2.82	2.00	13.45
4F33.PDB	O, B_LYS_215	N, B_CYS_202	H, B_CYS_202	2.94	2.15	19.46

4F33.PDB	O, B.SER_159	N, B.ASN_203	H, B.ASN_203	2.77	1.92	6.83
4F33.PDB	OD1, B.ASP_214	ND2, B.ASN_203	HD21, B.ASN_203	2.97	2.12	8.15
4F33.PDB	O, B.VAL_213	N, B.VAL_204	H, B.VAL_204	2.74	1.90	9.17
4F33.PDB	O, B.THR_157	N, B.ASN_205	H, B.ASN_205	2.86	2.01	7.37
4F33.PDB	O, B.THR_211	N, B.HIS_206	H, B.HIS_206	2.85	2.00	6.46
4F33.PDB	OG, B.SER_209	ND1, B.HIS_206	HD1, B.HIS_206	2.61	1.78	12.57
4F33.PDB	O, B.PRO_153	NE2, B.HIS_206	HE2, B.HIS_206	2.85	2.02	12.89
4F33.PDB	O, B.LYS_207	N, B.ASN_210	H, B.ASN_210	2.94	2.11	13.00
4F33.PDB	O, H.ASP_214	N, B.LYS_212	H, B.LYS_212	2.81	2.00	15.02
4F33.PDB	O, B.VAL_204	N, B.VAL_213	H, B.VAL_213	2.80	1.98	15.11
4F33.PDB	O, H.LYS_212	N, B.ASP_214	H, B.ASP_214	2.84	2.02	15.98
4F33.PDB	O, B.CYS_202	N, B.LYS_215	H, B.LYS_215	2.91	2.09	16.20
4F33.PDB	OE1, A.GLU_123	NZ, B.LYS_215	HZ1, B.LYS_215	2.68	1.82	12.44
4F33.PDB	OG1, H.THR_211	NZ, B.LYS_215	HZ2, B.LYS_215	2.83	1.95	7.37
4F33.PDB	O, B.TYR_200	N, B.VAL_217	H, B.VAL_217	2.89	2.04	8.29
4F33.PDB	OG, C.SER_27	N, C.GLU_4	H, C.GLU_4	2.91	2.10	15.68
4F33.PDB	O, C.SER_25	N, C.THR_6	H, C.THR_6	2.79	1.94	4.69
4F33.PDB	O, C.TYR_86	NE2, C.GLN_7	HE22, C.GLN_7	2.91	2.14	22.16
4F33.PDB	O, C.THR_23	N, C.SER_8	H, C.SER_8	2.94	2.13	16.69
4F33.PDB	O, C.LYS_103	N, C.MET_12	H, C.MET_12	2.88	2.06	16.35
4F33.PDB	OE2, C.GLU_18	N, C.SER_15	H, C.SER_15	2.79	1.94	9.08
4F33.PDB	O, C.VAL_78	N, C.GLY_17	H, C.GLY_17	2.81	2.02	19.83
4F33.PDB	O, C.LEU_73	N, C.MET_22	H, C.MET_22	2.85	2.01	10.93
4F33.PDB	O, C.SER_8	N, C.THR_23	H, C.THR_23	2.77	1.93	10.15
4F33.PDB	O, C.TYR_71	N, C.CYS_24	H, C.CYS_24	2.75	1.90	8.61
4F33.PDB	O, C.THR_6	N, C.SER_25	H, C.SER_25	2.79	1.94	6.02
4F33.PDB	O, C.ASN_69	N, C.ALA_26	H, C.ALA_26	2.82	1.97	9.46
4F33.PDB	O, C.GLN_89	N, C.HIS_34	H, C.HIS_34	2.95	2.09	1.08
4F33.PDB	O, C.ILE_48	N, C.TRP_35	H, C.TRP_35	2.66	1.84	15.50
4F33.PDB	O, C.TYR_87	N, C.TYR_36	H, C.TYR_36	2.75	1.94	16.72
4F33.PDB	O, C.LYS_45	N, C.GLN_37	H, C.GLN_37	2.94	2.17	21.42
4F33.PDB	O, C.THR_85	N, C.GLN_38	H, C.GLN_38	2.81	1.97	10.54
4F33.PDB	O, C.THR_42	NE2, C.GLN_38	HE21, C.GLN_38	2.84	2.00	10.36
4F33.PDB	O, C.GLU_81	NZ, C.LYS_39	HZ1, C.LYS_39	2.82	1.94	9.21
4F33.PDB	O, C.ASP_83	NZ, C.LYS_39	HZ3, C.LYS_39	2.78	1.95	17.23
4F33.PDB	O, C.LYS_39	OG1, C.THR_42	HG1, C.THR_42	2.80	1.99	2.97
4F33.PDB	O, D.GLY_110	OG, C.SER_43	HG, C.SER_43	2.70	1.98	23.76
4F33.PDB	O, C.GLN_37	N, C.LYS_45	H, C.LYS_45	2.82	2.00	13.68
4F33.PDB	O, D.ARG_104	NH1, C.ARG_46	HH11, C.ARG_46	2.70	1.92	20.25
4F33.PDB	O, C.TRP_35	N, C.TRP_47	H, C.TRP_47	2.85	2.05	17.44
4F33.PDB	O, C.LYS_53	N, C.TYR_49	H, C.TYR_49	2.78	1.99	18.60
4F33.PDB	O, C.MET_33	N, C.THR_51	H, C.THR_51	2.75	1.94	16.16
4F33.PDB	O, C.ASP_50	N, C.SER_52	H, C.SER_52	2.86	2.16	29.76
4F33.PDB	O, C.TYR_49	N, C.LYS_53	H, C.LYS_53	2.90	2.09	16.92
4F33.PDB	OD2, C.ASP_82	NE, C.ARG_61	HE, C.ARG_61	2.88	2.06	14.32
4F33.PDB	OD1, C.ASP_82	NH2, C.ARG_61	HH21, C.ARG_61	2.91	2.08	14.25
4F33.PDB	O, C.THR_74	N, C.SER_63	H, C.SER_63	2.94	2.17	23.62
4F33.PDB	O, C.ALA_26	ND2, C.ASN_69	HD21, C.ASN_69	2.94	2.09	4.35
4F33.PDB	O, C.CYS_24	N, C.TYR_71	H, C.TYR_71	2.98	2.13	6.28
4F33.PDB	O, C.VAL_30	OH, C.TYR_71	HH, C.TYR_71	2.83	2.11	24.09
4F33.PDB	O, C.SER_65	N, C.SER_72	H, C.SER_72	2.76	1.92	10.63
4F33.PDB	O, C.MET_22	N, C.LEU_73	H, C.LEU_73	2.91	2.10	15.81
4F33.PDB	O, C.SER_63	N, C.THR_74	H, C.THR_74	2.85	2.00	8.73
4F33.PDB	OG1, C.THR_21	OG1, C.THR_74	HG1, C.THR_74	2.68	1.93	19.90
4F33.PDB	O, C.VAL_20	N, C.ILE_75	H, C.ILE_75	2.88	2.07	17.51
4F33.PDB	O, C.ARG_61	N, C.SER_76	H, C.SER_76	2.77	1.94	14.06
4F33.PDB	O, C.GLU_18	N, C.VAL_78	H, C.VAL_78	2.97	2.17	18.03
4F33.PDB	OD2, C.ASP_82	N, C.GLU_79	H, C.GLU_79	2.86	2.02	10.29

4F33.PDB	O, C_GLU_79	N, C_ASP_82	H, C_ASP_82	2.89	2.04	7.80
4F33.PDB	O, C_GLN_38	N, C_THR_85	H, C_THR_85	2.95	2.11	9.52
4F33.PDB	O, C_THR_102	N, C_TYR_86	H, C_TYR_86	2.85	2.02	13.04
4F33.PDB	O, C_TYR_36	N, C_TYR_87	H, C_TYR_87	2.85	2.03	14.78
4F33.PDB	O, C_TYR_32	NE1, C_TRP_91	HE1, C_TRP_91	2.75	1.98	22.25
4F33.PDB	O, D_TYR_60	NE2, C_HIS_94	HE2, C_HIS_94	2.75	2.00	24.62
4F33.PDB	O, C_ILE_3	OG1, C_THR_97	HG1, C_THR_97	2.89	2.10	13.01
4F33.PDB	O, C_CYS_88	N, C_GLY_99	H, C_GLY_99	2.82	2.00	15.41
4F33.PDB	OE1, C_GLN_7	N, C_GLY_101	H, C_GLY_101	2.82	2.04	21.32
4F33.PDB	O, C_TYR_86	N, C_THR_102	H, C_THR_102	2.90	2.08	14.65
4F33.PDB	O, C_PRO_9	OG1, C_THR_102	HG1, C_THR_102	2.73	1.96	16.75
4F33.PDB	O, C_ALA_10	N, C_LYS_103	H, C_LYS_103	2.87	2.02	9.78
4F33.PDB	O, C_ALA_84	N, C_VAL_104	H, C_VAL_104	2.85	1.99	3.00
4F33.PDB	O, C_MET_12	N, C_GLU_105	H, C_GLU_105	2.79	1.94	5.03
4F33.PDB	OE1, C_GLN_166	N, C_ILE_106	H, C_ILE_106	2.86	2.01	8.73
4F33.PDB	O, C_ALA_14	N, C_LYS_107	H, C_LYS_107	2.76	1.93	12.89
4F33.PDB	OG, C_SER_13	NZ, C_LYS_107	HZ3, C_LYS_107	2.78	1.89	2.73
4F33.PDB	O, C_THR_109	NE, C_ARG_108	HE, C_ARG_108	2.78	1.92	5.15
4F33.PDB	O, C_ASP_170	NH1, C_ARG_108	HH11, C_ARG_108	2.94	2.11	12.58
4F33.PDB	O, C_TYR_140	N, C_ALA_111	H, C_ALA_111	2.88	2.05	12.17
4F33.PDB	O, C_LEU_135	N, C_PHE_116	H, C_PHE_116	2.88	2.08	18.08
4F33.PDB	O, C_VAL_133	N, C_PHE_118	H, C_PHE_118	2.80	1.99	16.53
4F33.PDB	OG, C_SER_131	NE2, C_GLN_124	HE22, C_GLN_124	2.83	1.97	4.97
4F33.PDB	O, C_GLN_124	N, C_SER_127	H, C_SER_127	2.84	2.05	19.55
4F33.PDB	O, C_LEU_125	N, C_GLY_128	H, C_GLY_128	2.88	2.04	11.07
4F33.PDB	O, C_LEU_181	N, C_ALA_130	H, C_ALA_130	2.79	1.95	9.71
4F33.PDB	OE1, C_GLN_124	N, C_SER_131	H, C_SER_131	2.98	2.18	18.03
4F33.PDB	O, C_LEU_179	N, C_VAL_132	H, C_VAL_132	2.83	2.00	12.70
4F33.PDB	O, C_SER_177	N, C_CYS_134	H, C_CYS_134	2.82	1.97	5.76
4F33.PDB	O, C_PHE_116	N, C_LEU_135	H, C_LEU_135	2.74	1.89	9.47
4F33.PDB	O, C_LEU_175	N, C_LEU_136	H, C_LEU_136	2.76	1.91	7.00
4F33.PDB	O, C_SER_114	N, C_ASN_137	H, C_ASN_137	2.81	1.98	13.13
4F33.PDB	O, C_TYR_173	N, C_PHE_139	H, C_PHE_139	2.86	2.04	15.11
4F33.PDB	O, C_ALA_111	N, C_TYR_140	H, C_TYR_140	2.92	2.12	17.57
4F33.PDB	O, C_GLU_195	N, C_GLN_147	H, C_GLN_147	2.86	2.02	11.56
4F33.PDB	OG, C_SER_177	NE1, C_TRP_148	HE1, C_TRP_148	2.93	2.10	14.22
4F33.PDB	O, C_ALA_193	N, C_LYS_149	H, C_LYS_149	2.87	2.03	10.70
4F33.PDB	OE1, C_GLU_195	NZ, C_LYS_149	HZ2, C_LYS_149	2.67	1.88	22.11
4F33.PDB	O, C_VAL_191	N, C_ASP_151	H, C_ASP_151	2.76	1.93	12.00
4F33.PDB	O, C_VAL_150	N, C_ALA_153	H, C_ALA_153	2.82	1.97	7.87
4F33.PDB	O, C_TRP_148	N, C_GLN_155	H, C_GLN_155	2.94	2.10	11.34
4F33.PDB	OE1, C_GLN_155	ND2, C_ASN_158	HD22, C_ASN_158	2.91	2.09	15.33
4F33.PDB	O, C_SER_176	N, C_SER_162	H, C_SER_162	2.97	2.18	19.59
4F33.PDB	O, D_PRO_173	OG, C_SER_162	HG, C_SER_162	2.78	2.07	25.83
4F33.PDB	O, C_SER_174	N, C_THR_164	H, C_THR_164	2.96	2.13	12.36
4F33.PDB	O, C_SER_171	NE2, C_GLN_166	HE21, C_GLN_166	2.98	2.16	14.32
4F33.PDB	O, C_ILE_106	NE2, C_GLN_166	HE22, C_GLN_166	2.67	1.89	20.30
4F33.PDB	O, C_THR_172	N, C_ASP_167	H, C_ASP_167	2.93	2.09	7.56
4F33.PDB	OD1, C_ASP_167	N, C_LYS_169	H, C_LYS_169	2.61	1.77	10.10
4F33.PDB	OD1, C_ASP_170	N, C_THR_172	H, C_THR_172	2.87	2.04	12.16
4F33.PDB	OD1, C_ASP_170	OG1, C_THR_172	HG1, C_THR_172	2.72	1.91	5.07
4F33.PDB	O, C_PHE_139	N, C_TYR_173	H, C_TYR_173	2.83	2.00	13.92
4F33.PDB	OG1, C_THR_164	N, C_SER_174	H, C_SER_174	2.96	2.12	9.60
4F33.PDB	O, C_LEU_136	N, C_LEU_175	H, C_LEU_175	2.83	2.02	15.79
4F33.PDB	O, C_SER_162	N, C_SER_176	H, C_SER_176	2.89	2.07	14.79
4F33.PDB	O, C_CYS_134	N, C_SER_177	H, C_SER_177	2.90	2.08	14.93
4F33.PDB	O, C_GLN_160	N, C_THR_178	H, C_THR_178	2.90	2.07	13.20
4F33.PDB	O, C_VAL_132	N, C_LEU_179	H, C_LEU_179	2.84	2.04	17.52

4F33.PDB	O, C.ASN_158	N, C.THR_180	H, C.THR_180	2.93	2.09	10.99
4F33.PDB	O, C.ALA_130	N, C.LEU_181	H, C.LEU_181	2.89	2.06	12.78
4F33.PDB	O, C.GLY_128	N, C.LYS_183	H, C.LYS_183	2.87	2.02	7.20
4F33.PDB	OG, C.SER_182	N, C.ASP_185	H, C.ASP_185	2.76	1.98	21.47
4F33.PDB	O, C.SER_182	N, C.TYR_186	H, C.TYR_186	2.81	1.98	11.89
4F33.PDB	OD2, C.ASP_151	N, C.LYS_190	H, C.LYS_190	2.88	2.06	14.40
4F33.PDB	OD1, C.ASP_151	N, C.VAL_191	H, C.VAL_191	2.83	1.97	2.95
4F33.PDB	O, C.PHE_209	N, C.TYR_192	H, C.TYR_192	2.95	2.11	11.22
4F33.PDB	O, C.LYS_149	N, C.ALA_193	H, C.ALA_193	2.88	2.09	19.06
4F33.PDB	O, C.LYS_207	N, C.CYS_194	H, C.CYS_194	2.93	2.15	21.61
4F33.PDB	O, C.GLN_147	N, C.GLU_195	H, C.GLU_195	2.81	1.98	11.88
4F33.PDB	O, C.VAL_205	N, C.VAL_196	H, C.VAL_196	2.70	1.88	13.56
4F33.PDB	O, C.LYS_145	N, C.THR_197	H, C.THR_197	2.85	2.02	13.13
4F33.PDB	O, C.HIS_198	N, C.LEU_201	H, C.LEU_201	2.84	1.98	4.52
4F33.PDB	O, C.VAL_196	N, C.VAL_205	H, C.VAL_205	2.89	2.08	16.55
4F33.PDB	O, C.TYR_192	N, C.PHE_209	H, C.PHE_209	2.97	2.18	20.47
4F33.PDB	O, C.LYS_190	N, C.ARG_211	H, C.ARG_211	2.85	2.00	9.23
4F33.PDB	O, C.HIS_189	NE, C.ARG_211	HE, C.ARG_211	2.85	2.00	3.91
4F33.PDB	O, D.SER_25	N, D.GLN_3	H, D.GLN_3	2.93	2.12	15.40
4F33.PDB	O, D.LYS_23	N, D.GLN_5	H, D.GLN_5	2.87	2.02	5.59
4F33.PDB	O, D.TYR_94	NE2, D.GLN_6	HE22, D.GLN_6	2.88	2.07	16.36
4F33.PDB	O, D.PRO_114	N, D.GLU_10	H, D.GLU_10	2.90	2.11	19.09
4F33.PDB	O, D.THR_116	N, D.GLU_12	H, D.GLU_12	2.98	2.19	19.88
4F33.PDB	O, D.LEU_86	N, D.GLY_15	H, D.GLY_15	2.74	1.92	14.74
4F33.PDB	O, D.LEU_83	N, D.VAL_18	H, D.VAL_18	2.96	2.19	22.61
4F33.PDB	O, D.MET_81	N, D.ILE_20	H, D.ILE_20	2.89	2.06	12.32
4F33.PDB	OG, D.SER_7	N, D.SER_21	H, D.SER_21	2.90	2.06	8.88
4F33.PDB	O, D.ALA_79	N, D.CYS_22	H, D.CYS_22	2.83	2.09	25.29
4F33.PDB	O, D.GLN_5	N, D.LYS_23	H, D.LYS_23	2.75	1.91	10.41
4F33.PDB	O, D.SER_77	N, D.ALA_24	H, D.ALA_24	2.92	2.07	4.90
4F33.PDB	O, D.GLN_3	N, D.SER_25	H, D.SER_25	2.94	2.12	15.81
4F33.PDB	O, D.SER_28	N, D.GLY_31	H, D.GLY_31	2.96	2.11	6.44
4F33.PDB	O, D.GLY_99	N, D.THR_33	H, D.THR_33	2.96	2.15	17.63
4F33.PDB	O, D.ALA_97	N, D.ASN_35	H, D.ASN_35	2.79	1.98	15.45
4F33.PDB	O, D.PHE_95	N, D.VAL_37	H, D.VAL_37	2.84	2.04	17.56
4F33.PDB	O, D.GLU_46	N, D.LYS_38	H, D.LYS_38	2.82	2.00	14.83
4F33.PDB	O, D.GLU_89	NZ, D.LYS_38	HZ1, D.LYS_38	2.95	2.06	6.08
4F33.PDB	O, D.VAL_93	N, D.GLN_39	H, D.GLN_39	2.83	1.98	3.65
4F33.PDB	OE1, C.GLN_38	NE2, D.GLN_39	HE22, D.GLN_39	2.89	2.03	5.23
4F33.PDB	O, D.SER_40	N, D.LYS_43	H, D.LYS_43	2.91	2.09	14.92
4F33.PDB	O, D.LYS_38	N, D.GLU_46	H, D.GLU_46	2.91	2.09	16.01
4F33.PDB	O, D.TRP_36	N, D.ILE_48	H, D.ILE_48	2.86	2.02	11.41
4F33.PDB	O, D.SER_59	N, D.LEU_50	H, D.LEU_50	2.88	2.10	20.07
4F33.PDB	O, D.MET_34	N, D.ILE_51	H, D.ILE_51	2.90	2.09	16.54
4F33.PDB	O, D.ALA_57	N, D.THR_52	H, D.THR_52	2.93	2.11	14.70
4F33.PDB	O, D.THR_52	N, D.GLY_56	H, D.GLY_56	2.90	2.15	24.29
4F33.PDB	OD1, D.ASN_55	N, D.ALA_57	H, D.ALA_57	2.90	2.05	6.42
4F33.PDB	O, D.LEU_50	N, D.SER_59	H, D.SER_59	2.88	2.07	17.59
4F33.PDB	O, D.ILE_48	N, D.ASN_61	H, D.ASN_61	2.92	2.10	15.21
4F33.PDB	O, D.TRP_47	ND2, D.ASN_61	HD21, D.ASN_61	2.96	2.14	14.14
4F33.PDB	OE2, D.GLU_46	NZ, D.LYS_63	HZ3, D.LYS_63	2.60	1.76	15.82
4F33.PDB	O, D.ASN_61	N, D.PHE_64	H, D.PHE_64	2.75	1.91	9.55
4F33.PDB	OD2, D.ASP_90	NZ, D.LYS_67	HZ2, D.LYS_67	2.76	2.03	29.11
4F33.PDB	O, D.PHE_64	N, D.ALA_68	H, D.ALA_68	2.91	2.10	17.71
4F33.PDB	O, D.ASP_82	N, D.THR_69	H, D.THR_69	2.88	2.12	23.04
4F33.PDB	OH, D.TYR_60	N, D.LEU_70	H, D.LEU_70	2.83	1.99	10.08
4F33.PDB	O, D.THR_78	N, D.ASP_73	H, D.ASP_73	2.75	1.92	11.81
4F33.PDB	O, D.CYS_22	N, D.ALA_79	H, D.ALA_79	2.88	2.07	15.38

4F33.PDB	O, D_THR_71	N, D_TYR_80	H, D_TYR_80	2.77	1.92	5.85
4F33.PDB	O, D_ILE_20	N, D_MET_81	H, D_MET_81	2.97	2.15	15.01
4F33.PDB	O, D_THR_69	N, D_ASP_82	H, D_ASP_82	2.90	2.08	13.98
4F33.PDB	O, D_VAL_18	N, D_LEU_83	H, D_LEU_83	2.77	1.94	12.96
4F33.PDB	O, D_LYS_67	N, D_LEU_84	H, D_LEU_84	2.92	2.10	15.11
4F33.PDB	O, D_ALA_16	N, D_LEU_86	H, D_LEU_86	2.90	2.05	7.92
4F33.PDB	OD2, D_ASP_90	N, D_THR_87	H, D_THR_87	2.84	2.02	15.18
4F33.PDB	O, D_THR_87	N, D_ASP_90	H, D_ASP_90	2.90	2.06	10.57
4F33.PDB	O, D_SER_88	N, D_SER_91	H, D_SER_91	2.97	2.12	5.73
4F33.PDB	O, D_VAL_115	N, D_ALA_92	H, D_ALA_92	2.97	2.21	24.68
4F33.PDB	O, D_THR_113	N, D_TYR_94	H, D_TYR_94	2.85	2.00	9.44
4F33.PDB	O, D_VAL_37	N, D_PHE_95	H, D_PHE_95	2.78	1.94	9.26
4F33.PDB	O, D_ASN_35	N, D_ALA_97	H, D_ALA_97	2.87	2.11	23.35
4F33.PDB	O, D_TYR_108	N, D_ARG_98	H, D_ARG_98	2.83	2.05	21.19
4F33.PDB	OD2, D_ASP_107	NH2, D_ARG_98	HH21, D_ARG_98	2.74	1.89	7.29
4F33.PDB	O, D_THR_33	N, D_GLY_99	H, D_GLY_99	2.93	2.09	9.33
4F33.PDB	OD1, D_ASP_102	NE, D_ARG_104	HE, D_ARG_104	2.89	2.05	10.59
4F33.PDB	OD2, D_ASP_107	NH1, D_ARG_104	HH11, D_ARG_104	2.83	2.01	15.77
4F33.PDB	OD2, D_ASP_102	NH2, D_ARG_104	HH21, D_ARG_104	2.91	2.10	15.53
4F33.PDB	O, D_CYS_96	N, D_GLY_110	H, D_GLY_110	2.76	1.90	5.93
4F33.PDB	OE1, D_GLN_6	N, D_GLY_112	H, D_GLY_112	2.92	2.15	21.82
4F33.PDB	O, D_TYR_94	N, D_THR_113	H, D_THR_113	2.83	2.03	18.15
4F33.PDB	O, D_SER_7	OG1, D_THR_113	HG1, D_THR_113	2.79	2.01	15.83
4F33.PDB	O, D_ALA_92	N, D_VAL_115	H, D_VAL_115	2.80	1.95	9.13
4F33.PDB	O, D_GLU_10	N, D_THR_116	H, D_THR_116	2.95	2.12	11.31
4F33.PDB	OG, D_SER_91	N, D_VAL_117	H, D_VAL_117	2.81	1.98	11.24
4F33.PDB	O, D_GLU_12	N, D_SER_118	H, D_SER_118	2.89	2.09	17.84
4F33.PDB	O, D_PHE_152	N, D_LYS_123	H, D_LYS_123	2.79	1.97	13.96
4F33.PDB	O, D_ASP_150	NZ, D_LYS_123	HZ2, D_LYS_123	2.85	2.02	18.34
4F33.PDB	OE2, E_GLU_123	N, D_GLY_124	H, D_GLY_124	2.84	1.99	7.85
4F33.PDB	O, D_LYS_149	N, D_SER_126	H, D_SER_126	2.92	2.12	17.54
4F33.PDB	O, D_LEU_147	N, D_PHE_128	H, D_PHE_128	2.91	2.07	11.82
4F33.PDB	O, D_GLY_145	N, D_LEU_130	H, D_LEU_130	2.69	1.84	6.30
4F33.PDB	OG, D_SER_136	N, D_SER_133	H, D_SER_133	2.93	2.12	15.23
4F33.PDB	OG, D_SER_133	N, D_LYS_135	H, D_LYS_135	2.86	2.06	18.00
4F33.PDB	O, D_SER_133	OG1, D_THR_137	HG1, D_THR_137	2.93	2.22	24.93
4F33.PDB	O, D_SER_138	N, D_THR_141	H, D_THR_141	2.86	2.02	10.67
4F33.PDB	O, D_VAL_190	N, D_ALA_142	H, D_ALA_142	2.79	1.94	3.93
4F33.PDB	O, D_SER_136	N, D_ALA_143	H, D_ALA_143	2.80	1.98	13.96
4F33.PDB	O, D_VAL_188	N, D_LEU_144	H, D_LEU_144	2.99	2.17	15.33
4F33.PDB	O, D_LEU_130	N, D_GLY_145	H, D_GLY_145	2.95	2.17	22.25
4F33.PDB	O, D_PHE_128	N, D_LEU_147	H, D_LEU_147	2.85	2.01	10.25
4F33.PDB	O, D_LEU_184	N, D_VAL_148	H, D_VAL_148	2.76	1.91	9.22
4F33.PDB	O, D_SER_126	N, D_LYS_149	H, D_LYS_149	2.79	1.93	3.93
4F33.PDB	O, D_LYS_123	N, D_PHE_152	H, D_PHE_152	2.96	2.17	18.86
4F33.PDB	O, D_ASN_203	N, D_SER_159	H, D_SER_159	2.92	2.12	18.15
4F33.PDB	OG, D_SER_186	NE1, D_TRP_160	HE1, D_TRP_160	3.00	2.15	9.78
4F33.PDB	O, D_ILE_201	N, D_ASN_161	H, D_ASN_161	2.81	1.96	10.06
4F33.PDB	OD1, D_ASN_203	N, D_SER_162	H, D_SER_162	2.79	1.98	16.60
4F33.PDB	O, D_TRP_160	N, D_GLY_163	H, D_GLY_163	2.90	2.14	23.00
4F33.PDB	O, D_VAL_187	N, D_HIS_170	H, D_HIS_170	2.79	1.95	11.73
4F33.PDB	O, D_SER_185	N, D_PHE_172	H, D_PHE_172	2.98	2.14	9.15
4F33.PDB	O, D_SER_183	N, D_VAL_175	H, D_VAL_175	2.91	2.09	14.44
4F33.PDB	O, D_LEU_181	N, D_GLN_177	H, D_GLN_177	2.85	2.00	7.10
4F33.PDB	OD1, D_ASP_150	NE2, D_GLN_177	HE22, D_GLN_177	2.86	2.09	21.57
4F33.PDB	O, D_TYR_151	N, D_TYR_182	H, D_TYR_182	2.82	1.97	7.39
4F33.PDB	O, D_VAL_148	N, D_LEU_184	H, D_LEU_184	2.89	2.08	17.21
4F33.PDB	O, D_CYS_146	N, D_SER_186	H, D_SER_186	2.93	2.11	15.37

4F33.PDB	O, D_HIS_170	N, D_VAL_187	H, D_VAL_187	2.83	2.00	11.95
4F33.PDB	O, D_LEU_144	N, D_VAL_188	H, D_VAL_188	2.81	2.00	17.23
4F33.PDB	O, D_ALA_142	N, D_VAL_190	H, D_VAL_190	2.77	1.95	14.72
4F33.PDB	O, D_GLY_140	N, D_SER_192	H, D_SER_192	2.86	2.02	8.26
4F33.PDB	O, D_PRO_191	N, D_SER_194	H, D_SER_194	2.92	2.08	9.17
4F33.PDB	O, D_SER_194	N, D_GLN_198	H, D_GLN_198	2.75	1.89	2.92
4F33.PDB	OD1, D_ASN_161	N, D_ILE_201	H, D_ILE_201	2.80	1.96	10.93
4F33.PDB	O, D_LYS_215	N, D_CYS_202	H, D_CYS_202	2.93	2.15	21.05
4F33.PDB	O, D_SER_159	N, D_ASN_203	H, D_ASN_203	2.77	1.92	5.28
4F33.PDB	O, D_VAL_213	N, D_VAL_204	H, D_VAL_204	2.77	1.93	9.54
4F33.PDB	O, D_THR_157	N, D_ASN_205	H, D_ASN_205	2.87	2.02	7.57
4F33.PDB	O, D_THR_211	N, D_HIS_206	H, D_HIS_206	2.84	1.99	6.89
4F33.PDB	O, D_PRO_153	NE2, D_HIS_206	HE2, D_HIS_206	2.81	1.97	10.37
4F33.PDB	O, D_LYS_207	N, D_ASN_210	H, D_ASN_210	2.91	2.08	12.71
4F33.PDB	O, F_ASP_214	N, D_LYS_212	H, D_LYS_212	2.98	2.15	12.10
4F33.PDB	O, D_VAL_204	N, D_VAL_213	H, D_VAL_213	2.79	1.97	13.65
4F33.PDB	O, F_LYS_212	N, D_ASP_214	H, D_ASP_214	2.85	2.03	14.94
4F33.PDB	O, D_CYS_202	N, D_LYS_215	H, D_LYS_215	2.96	2.16	17.33
4F33.PDB	OE1, C_GLU_123	NZ, D_LYS_215	HZ1, D_LYS_215	2.79	1.99	22.47
4F33.PDB	OG1, F_THR_211	NZ, D_LYS_215	HZ2, D_LYS_215	2.86	1.99	10.67
4F33.PDB	O, F_ASN_210	N, D_LYS_216	H, D_LYS_216	2.98	2.16	15.42
4F33.PDB	O, D_TYR_200	N, D_VAL_217	H, D_VAL_217	2.85	2.00	8.55
4F33.PDB	OG, E_SER_27	N, E_GLU_4	H, E_GLU_4	2.92	2.11	16.14
4F33.PDB	O, E_SER_25	N, E_THR_6	H, E_THR_6	2.78	1.92	4.96
4F33.PDB	O, E_TYR_86	NE2, E_GLN_7	HE22, E_GLN_7	2.94	2.17	22.59
4F33.PDB	O, E_THR_23	N, E_SER_8	H, E_SER_8	2.92	2.12	16.81
4F33.PDB	O, E_LYS_103	N, E_MET_12	H, E_MET_12	2.82	1.98	10.01
4F33.PDB	O, E_GLU_105	N, E_ALA_14	H, E_ALA_14	2.97	2.16	16.60
4F33.PDB	OE2, E_GLU_18	N, E_SER_15	H, E_SER_15	2.79	1.94	7.58
4F33.PDB	O, E_VAL_78	N, E_GLY_17	H, E_GLY_17	2.81	2.00	17.52
4F33.PDB	OG1, E_THR_74	OG1, E_THR_21	HG1, E_THR_21	2.80	2.03	17.05
4F33.PDB	O, E_LEU_73	N, E_MET_22	H, E_MET_22	2.92	2.09	12.31
4F33.PDB	O, E_SER_8	N, E_THR_23	H, E_THR_23	2.82	1.97	8.66
4F33.PDB	O, E_TYR_71	N, E_CYS_24	H, E_CYS_24	2.67	1.82	5.57
4F33.PDB	O, E_THR_6	N, E_SER_25	H, E_SER_25	2.85	2.00	8.30
4F33.PDB	O, E_ASN_69	N, E_ALA_26	H, E_ALA_26	2.80	1.95	9.70
4F33.PDB	O, E_GLN_89	N, E_HIS_34	H, E_HIS_34	2.94	2.08	4.58
4F33.PDB	O, E_ILE_48	N, E_TRP_35	H, E_TRP_35	2.69	1.88	16.85
4F33.PDB	O, E_TYR_87	N, E_TYR_36	H, E_TYR_36	2.80	1.97	13.97
4F33.PDB	O, E_LYS_45	N, E_GLN_37	H, E_GLN_37	2.87	2.09	20.05
4F33.PDB	O, E_THR_85	N, E_GLN_38	H, E_GLN_38	2.87	2.05	13.42
4F33.PDB	O, E_THR_42	NE2, E_GLN_38	HE21, E_GLN_38	2.90	2.07	12.17
4F33.PDB	O, E_GLU_81	NZ, E_LYS_39	HZ1, E_LYS_39	2.82	1.96	12.79
4F33.PDB	O, E_ASP_83	NZ, E_LYS_39	HZ3, E_LYS_39	2.75	1.95	21.71
4F33.PDB	O, E_LYS_39	OG1, E_THR_42	HG1, E_THR_42	2.99	2.17	4.21
4F33.PDB	O, F_GLY_110	OG, E_SER_43	HG, E_SER_43	2.52	1.83	27.97
4F33.PDB	O, E_GLN_37	N, E_LYS_45	H, E_LYS_45	2.74	1.96	19.86
4F33.PDB	O, F_ARG_104	NH1, E_ARG_46	HH11, E_ARG_46	2.85	2.03	15.38
4F33.PDB	O, E_TRP_35	N, E_TRP_47	H, E_TRP_47	2.82	2.04	19.57
4F33.PDB	O, E_LYS_53	N, E_TYR_49	H, E_TYR_49	2.74	1.93	17.49
4F33.PDB	O, E_MET_33	N, E_THR_51	H, E_THR_51	2.76	1.93	12.30
4F33.PDB	O, E_ASP_50	N, E_SER_52	H, E_SER_52	2.85	2.14	29.22
4F33.PDB	O, E_TYR_49	N, E_LYS_53	H, E_LYS_53	2.87	2.09	20.53
4F33.PDB	O, E_TRP_47	N, E_ALA_55	H, E_ALA_55	2.97	2.11	5.56
4F33.PDB	OD2, E_ASP_82	NE, E_ARG_61	HE, E_ARG_61	2.93	2.08	6.42
4F33.PDB	OD1, E_ASP_82	NH2, E_ARG_61	HH21, E_ARG_61	2.82	1.98	9.42
4F33.PDB	O, E_THR_74	N, E_SER_63	H, E_SER_63	2.96	2.20	24.19
4F33.PDB	O, E_ALA_26	ND2, E_ASN_69	HD21, E_ASN_69	2.90	2.05	3.08

4F33.PDB	O, E_CYS_24	N, E_TYR_71	H, E_TYR_71	2.86	2.02	8.43
4F33.PDB	O, E_VAL_30	OH, E_TYR_71	HH, E_TYR_71	2.89	2.18	25.55
4F33.PDB	O, E_SER_65	N, E_SER_72	H, E_SER_72	2.76	1.93	12.78
4F33.PDB	O, E_SER_63	N, E_THR_74	H, E_THR_74	2.80	1.96	11.27
4F33.PDB	O, E_VAL_20	N, E_ILE_75	H, E_ILE_75	2.91	2.09	15.96
4F33.PDB	O, E_ARG_61	N, E_SER_76	H, E_SER_76	2.77	1.96	15.82
4F33.PDB	O, E_GLU_18	N, E_VAL_78	H, E_VAL_78	2.84	2.06	21.38
4F33.PDB	OD2, E_ASP_82	N, E_GLU_79	H, E_GLU_79	2.86	2.00	3.08
4F33.PDB	O, E_GLU_79	N, E_ASP_82	H, E_ASP_82	2.87	2.03	9.88
4F33.PDB	O, E_GLN_38	N, E_THR_85	H, E_THR_85	2.88	2.04	8.55
4F33.PDB	O, E_THR_102	N, E_TYR_86	H, E_TYR_86	2.86	2.02	10.02
4F33.PDB	O, E_TYR_36	N, E_TYR_87	H, E_TYR_87	2.88	2.07	16.48
4F33.PDB	OG1, E_THR_97	NE2, E_GLN_90	HE21, E_GLN_90	2.99	2.17	14.98
4F33.PDB	O, E_TYR_32	NE1, E_TRP_91	HE1, E_TRP_91	2.73	1.95	21.71
4F33.PDB	O, E_ILE_3	OG1, E_THR_97	HG1, E_THR_97	2.76	1.96	11.49
4F33.PDB	O, E_CYS_88	N, E_GLY_99	H, E_GLY_99	2.76	1.93	12.97
4F33.PDB	OE1, E_GLN_7	N, E_GLY_101	H, E_GLY_101	2.77	2.01	24.02
4F33.PDB	O, E_TYR_86	N, E_THR_102	H, E_THR_102	2.88	2.06	14.06
4F33.PDB	O, E_PRO_9	OG1, E_THR_102	HG1, E_THR_102	2.74	1.97	16.27
4F33.PDB	O, E_ALA_10	N, E_LYS_103	H, E_LYS_103	2.83	1.99	8.80
4F33.PDB	O, E_ALA_84	N, E_VAL_104	H, E_VAL_104	2.84	1.98	6.54
4F33.PDB	O, E_MET_12	N, E_GLU_105	H, E_GLU_105	2.75	1.90	5.61
4F33.PDB	OE1, E_GLN_166	N, E_ILE_106	H, E_ILE_106	2.88	2.05	11.13
4F33.PDB	O, E_ALA_14	N, E_LYS_107	H, E_LYS_107	2.77	1.92	7.71
4F33.PDB	O, E_THR_109	NE, E_ARG_108	HE, E_ARG_108	2.78	1.92	2.02
4F33.PDB	O, E_ASP_170	NH1, E_ARG_108	HH11, E_ARG_108	2.88	2.05	12.27
4F33.PDB	O, E_TYR_140	N, E_ALA_111	H, E_ALA_111	2.93	2.09	9.90
4F33.PDB	O, E_LEU_135	N, E_PHE_116	H, E_PHE_116	2.88	2.07	17.28
4F33.PDB	O, E_VAL_133	N, E_PHE_118	H, E_PHE_118	2.80	2.05	23.65
4F33.PDB	OG, E_SER_131	NE2, E_GLN_124	HE22, E_GLN_124	2.81	1.95	4.17
4F33.PDB	O, E_GLN_124	N, E_SER_127	H, E_SER_127	2.86	2.13	27.30
4F33.PDB	O, E_LEU_125	N, E_GLY_128	H, E_GLY_128	2.83	1.98	9.86
4F33.PDB	O, E_LEU_181	N, E_ALA_130	H, E_ALA_130	2.74	1.89	8.05
4F33.PDB	O, E_LEU_179	N, E_VAL_132	H, E_VAL_132	2.80	1.98	14.92
4F33.PDB	O, E_SER_177	N, E_CYS_134	H, E_CYS_134	2.85	2.00	9.73
4F33.PDB	O, E_PHE_116	N, E_LEU_135	H, E_LEU_135	2.83	1.99	7.95
4F33.PDB	O, E_LEU_175	N, E_LEU_136	H, E_LEU_136	2.79	1.94	6.94
4F33.PDB	O, E_SER_114	N, E_ASN_137	H, E_ASN_137	2.80	1.99	16.39
4F33.PDB	O, E_TYR_173	N, E_PHE_139	H, E_PHE_139	2.88	2.07	16.01
4F33.PDB	O, E_ALA_111	N, E_TYR_140	H, E_TYR_140	2.90	2.10	17.94
4F33.PDB	O, E_GLU_195	N, E_GLN_147	H, E_GLN_147	2.86	2.03	12.56
4F33.PDB	OG, E_SER_177	NE1, E_TRP_148	HE1, E_TRP_148	2.88	2.05	13.86
4F33.PDB	O, E_ALA_193	N, E_LYS_149	H, E_LYS_149	2.81	1.97	9.94
4F33.PDB	OE1, E_GLU_195	NZ, E_LYS_149	HZ2, E_LYS_149	2.77	1.97	22.37
4F33.PDB	O, E_VAL_191	N, E_ASP_151	H, E_ASP_151	2.76	1.93	11.74
4F33.PDB	O, E_VAL_150	N, E_ALA_153	H, E_ALA_153	2.93	2.08	7.11
4F33.PDB	O, E_TRP_148	N, E_GLN_155	H, E_GLN_155	2.90	2.06	11.04
4F33.PDB	OE1, E_GLN_155	ND2, E_ASN_158	HD22, E_ASN_158	2.91	2.08	12.67
4F33.PDB	O, F_LEU_176	NE2, E_GLN_160	HE22, E_GLN_160	2.93	2.08	4.21
4F33.PDB	O, E_SER_176	N, E_SER_162	H, E_SER_162	2.99	2.20	20.78
4F33.PDB	O, F_PRO_173	OG, E_SER_162	HG, E_SER_162	2.63	1.89	21.98
4F33.PDB	O, E_SER_174	N, E_THR_164	H, E_THR_164	2.96	2.13	13.63
4F33.PDB	O, E_SER_171	NE2, E_GLN_166	HE21, E_GLN_166	2.92	2.10	16.16
4F33.PDB	O, E_ILE_106	NE2, E_GLN_166	HE22, E_GLN_166	2.70	1.91	18.56
4F33.PDB	O, E_THR_172	N, E_ASP_167	H, E_ASP_167	2.96	2.11	9.67
4F33.PDB	OD1, E_ASP_170	N, E_THR_172	H, E_THR_172	2.87	2.07	17.42
4F33.PDB	OD1, E_ASP_170	OG1, E_THR_172	HG1, E_THR_172	2.66	1.85	7.41
4F33.PDB	O, E_PHE_139	N, E_TYR_173	H, E_TYR_173	2.81	1.97	10.48

4F33.PDB	OG1, E_THR_164	N, E_SER_174	H, E_SER_174	3.00	2.15	8.96
4F33.PDB	O, E_LEU_136	N, E_LEU_175	H, E_LEU_175	2.88	2.07	16.14
4F33.PDB	O, E_SER_162	N, E_SER_176	H, E_SER_176	2.95	2.12	13.93
4F33.PDB	O, E_CYS_134	N, E_SER_177	H, E_SER_177	2.89	2.07	14.26
4F33.PDB	O, E_GLN_160	N, E_THR_178	H, E_THR_178	2.90	2.07	12.50
4F33.PDB	O, E_VAL_132	N, E_LEU_179	H, E_LEU_179	2.83	2.00	13.32
4F33.PDB	O, E_ASN_158	N, E_THR_180	H, E_THR_180	2.97	2.13	9.98
4F33.PDB	O, E_ALA_130	N, E_LEU_181	H, E_LEU_181	2.88	2.04	11.81
4F33.PDB	O, E_GLY_128	N, E_LYS_183	H, E_LYS_183	2.91	2.08	11.41
4F33.PDB	OG, E_SER_182	N, E_ASP_185	H, E_ASP_185	2.89	2.05	12.49
4F33.PDB	O, E_SER_182	N, E_TYR_186	H, E_TYR_186	2.82	2.00	13.68
4F33.PDB	O, E_LYS_183	N, E_GLU_187	H, E_GLU_187	2.88	2.09	19.35
4F33.PDB	OD1, E_ASP_151	N, E_VAL_191	H, E_VAL_191	2.77	1.93	8.77
4F33.PDB	O, E_PHE_209	N, E_TYR_192	H, E_TYR_192	2.98	2.13	8.15
4F33.PDB	O, E_LYS_149	N, E_ALA_193	H, E_ALA_193	2.88	2.08	18.56
4F33.PDB	O, E_LYS_207	N, E_CYS_194	H, E_CYS_194	2.96	2.17	20.79
4F33.PDB	O, E_GLN_147	N, E_GLU_195	H, E_GLU_195	2.74	1.90	10.88
4F33.PDB	O, E_VAL_205	N, E_VAL_196	H, E_VAL_196	2.72	1.89	12.46
4F33.PDB	ND1, E_HIS_198	N, E_GLY_200	H, E_GLY_200	2.98	2.12	5.22
4F33.PDB	O, E_HIS_198	N, E_LEU_201	H, E_LEU_201	2.84	1.99	5.31
4F33.PDB	O, E_VAL_196	N, E_VAL_205	H, E_VAL_205	2.92	2.09	13.32
4F33.PDB	O, E_TYR_192	N, E_PHE_209	H, E_PHE_209	2.94	2.17	22.18
4F33.PDB	O, E_LYS_190	N, E_ARG_211	H, E_ARG_211	2.74	1.94	17.57
4F33.PDB	O, E_HIS_189	NE, E_ARG_211	HE, E_ARG_211	2.92	2.09	14.00
4F33.PDB	O, F_SER_25	N, F_GLN_3	H, F_GLN_3	2.92	2.09	11.79
4F33.PDB	O, F_LYS_23	N, F_GLN_5	H, F_GLN_5	2.85	2.00	7.55
4F33.PDB	O, F_TYR_94	NE2, F_GLN_6	HE22, F_GLN_6	2.86	2.05	16.42
4F33.PDB	O, F_PRO_114	N, F_GLU_10	H, F_GLU_10	2.96	2.18	21.47
4F33.PDB	O, F_THR_116	N, F_GLU_12	H, F_GLU_12	2.95	2.15	17.10
4F33.PDB	O, F_LEU_86	N, F_GLY_15	H, F_GLY_15	2.68	1.85	13.71
4F33.PDB	O, F_LEU_83	N, F_VAL_18	H, F_VAL_18	2.99	2.22	23.08
4F33.PDB	O, F_MET_81	N, F_ILE_20	H, F_ILE_20	2.85	2.01	12.08
4F33.PDB	OG, F_SER_7	N, F_SER_21	H, F_SER_21	2.96	2.12	10.03
4F33.PDB	O, F_GLN_5	N, F_LYS_23	H, F_LYS_23	2.77	1.93	10.80
4F33.PDB	O, F_SER_77	N, F_ALA_24	H, F_ALA_24	2.90	2.05	6.06
4F33.PDB	O, F_GLN_3	N, F_SER_25	H, F_SER_25	2.87	2.06	15.90
4F33.PDB	O, A_GLY_60	N, F_PHE_29	H, F_PHE_29	2.97	2.18	20.00
4F33.PDB	O, F_GLY_99	N, F_THR_33	H, F_THR_33	2.87	2.06	15.66
4F33.PDB	O, F_ALA_97	N, F_ASN_35	H, F_ASN_35	2.80	1.96	10.72
4F33.PDB	O, F_PHE_95	N, F_VAL_37	H, F_VAL_37	2.82	2.02	18.07
4F33.PDB	O, F_GLU_46	N, F_LYS_38	H, F_LYS_38	2.79	1.98	16.31
4F33.PDB	O, F_GLU_89	NZ, F_LYS_38	HZ1, F_LYS_38	2.88	2.00	2.60
4F33.PDB	O, F_VAL_93	N, F_GLN_39	H, F_GLN_39	2.84	1.98	5.27
4F33.PDB	OE1, E_GLN_38	NE2, F_GLN_39	HE22, F_GLN_39	2.92	2.06	5.53
4F33.PDB	O, F_SER_40	N, F_LYS_43	H, F_LYS_43	2.90	2.09	15.21
4F33.PDB	O, F_LYS_38	N, F_GLU_46	H, F_GLU_46	2.89	2.10	18.91
4F33.PDB	O, F_TRP_36	N, F_ILE_48	H, F_ILE_48	2.82	1.97	6.48
4F33.PDB	O, F_SER_59	N, F_LEU_50	H, F_LEU_50	2.90	2.11	20.04
4F33.PDB	O, F_MET_34	N, F_ILE_51	H, F_ILE_51	2.90	2.10	17.75
4F33.PDB	O, F_ALA_57	N, F_THR_52	H, F_THR_52	2.97	2.15	14.94
4F33.PDB	O, F_THR_52	N, F_GLY_56	H, F_GLY_56	2.93	2.22	29.15
4F33.PDB	OD1, F_ASN_55	N, F_ALA_57	H, F_ALA_57	2.86	2.00	3.80
4F33.PDB	O, F_LEU_50	N, F_SER_59	H, F_SER_59	2.89	2.09	17.90
4F33.PDB	O, F_ILE_48	N, F_ASN_61	H, F_ASN_61	2.97	2.17	18.69
4F33.PDB	O, F_TRP_47	ND2, F_ASN_61	HD21, F_ASN_61	2.90	2.07	11.50
4F33.PDB	OE2, F_GLU_46	NZ, F_LYS_63	HZ3, F_LYS_63	2.68	1.79	3.79
4F33.PDB	O, F_ASN_61	N, F_PHE_64	H, F_PHE_64	2.81	1.98	12.75
4F33.PDB	OD2, F_ASP_90	NZ, F_LYS_67	HZ2, F_LYS_67	2.98	2.09	4.59

4F33.PDB	O, F_LEU_84	NZ, F_LYS_67	HZ3, F_LYS_67	2.88	2.01	9.79
4F33.PDB	O, F_PHE_64	N, F_ALA_68	H, F_ALA_68	2.89	2.09	17.94
4F33.PDB	O, F ASP_82	N, F_THR_69	H, F_THR_69	2.89	2.11	21.20
4F33.PDB	OH, F_TYR_60	N, F_LEU_70	H, F_LEU_70	2.85	2.00	7.63
4F33.PDB	O, F_THR_78	N, F ASP_73	H, F ASP_73	2.73	1.90	11.77
4F33.PDB	O, F_CYS_22	N, F_ALA_79	H, F_ALA_79	2.88	2.06	15.43
4F33.PDB	O, F_THR_71	N, F_TYR_80	H, F_TYR_80	2.81	1.96	9.04
4F33.PDB	O, F_ILE_20	N, F_MET_81	H, F_MET_81	2.93	2.11	15.35
4F33.PDB	O, F_THR_69	N, F ASP_82	H, F ASP_82	2.94	2.10	11.40
4F33.PDB	O, F_VAL_18	N, F_LEU_83	H, F_LEU_83	2.81	1.97	10.47
4F33.PDB	O, F_LYS_67	N, F_LEU_84	H, F_LEU_84	2.89	2.09	17.45
4F33.PDB	O, F_ALA_16	N, F_LEU_86	H, F_LEU_86	2.91	2.07	9.18
4F33.PDB	OD2, F ASP_90	N, F_THR_87	H, F_THR_87	2.85	2.02	12.72
4F33.PDB	O, F_THR_87	N, F ASP_90	H, F ASP_90	2.83	1.99	10.62
4F33.PDB	O, F_VAL_115	N, F_ALA_92	H, F_ALA_92	2.97	2.26	28.93
4F33.PDB	O, F_THR_113	N, F_TYR_94	H, F_TYR_94	2.92	2.08	8.53
4F33.PDB	O, F_VAL_37	N, F_PHE_95	H, F_PHE_95	2.78	1.94	9.71
4F33.PDB	O, F ASN_35	N, F_ALA_97	H, F_ALA_97	2.84	2.08	24.00
4F33.PDB	O, F_TYR_108	N, F ARG_98	H, F ARG_98	2.82	2.03	20.08
4F33.PDB	OD1, F ASP_107	NE, F ARG_98	HE, F ARG_98	2.99	2.13	4.74
4F33.PDB	OD2, F ASP_107	NH2, F ARG_98	HH21, F ARG_98	2.77	1.91	5.42
4F33.PDB	O, F_THR_33	N, F_GLY_99	H, F_GLY_99	2.97	2.13	11.08
4F33.PDB	OD1, F ASP_102	NE, F ARG_104	HE, F ARG_104	2.84	1.99	7.33
4F33.PDB	OD2, F ASP_107	NH1, F ARG_104	HH11, F ARG_104	2.84	2.02	14.35
4F33.PDB	OD2, F ASP_102	NH2, F ARG_104	HH21, F ARG_104	2.90	2.10	17.22
4F33.PDB	OH, E_TYR_36	N, F_PHE_106	H, F_PHE_106	2.80	1.96	9.30
4F33.PDB	O, F_CYS_96	N, F_GLY_110	H, F_GLY_110	2.75	1.90	3.11
4F33.PDB	OE1, F_GLN_6	N, F_GLY_112	H, F_GLY_112	2.83	2.05	20.58
4F33.PDB	O, F_THR_94	N, F_THR_113	H, F_THR_113	2.80	2.02	20.38
4F33.PDB	O, F_SER_7	OG1, F_THR_113	HG1, F_THR_113	2.84	2.08	18.41
4F33.PDB	O, F_ALA_92	N, F_VAL_115	H, F_VAL_115	2.82	1.98	10.24
4F33.PDB	OG, F_SER_91	N, F_VAL_117	H, F_VAL_117	2.84	2.00	11.18
4F33.PDB	O, F_GLU_12	N, F_SER_118	H, F_SER_118	2.89	2.09	17.44
4F33.PDB	O, F_PHE_152	N, F_LYS_123	H, F_LYS_123	2.81	1.98	13.07
4F33.PDB	O, F ASP_150	NZ, F_LYS_123	HZ2, F_LYS_123	2.85	2.01	15.13
4F33.PDB	OE2, C_GLU_123	N, F_GLY_124	H, F_GLY_124	2.81	1.96	5.00
4F33.PDB	O, F_LYS_149	N, F_SER_126	H, F_SER_126	2.90	2.09	15.48
4F33.PDB	O, F_LEU_147	N, F_PHE_128	H, F_PHE_128	2.87	2.04	12.96
4F33.PDB	O, F_GLY_145	N, F_LEU_130	H, F_LEU_130	2.73	1.88	6.31
4F33.PDB	OG, F_SER_136	N, F_SER_133	H, F_SER_133	2.95	2.13	15.24
4F33.PDB	OG, F_SER_133	N, F_LYS_135	H, F_LYS_135	2.90	2.11	20.53
4F33.PDB	O, F_SER_133	OG1, F_THR_137	HG1, F_THR_137	2.95	2.23	24.52
4F33.PDB	O, F_SER_138	N, F_THR_141	H, F_THR_141	2.81	1.97	11.04
4F33.PDB	O, F_VAL_190	N, F_ALA_142	H, F_ALA_142	2.77	1.91	4.10
4F33.PDB	O, F_SER_136	N, F_ALA_143	H, F_ALA_143	2.80	1.97	12.99
4F33.PDB	O, F_LEU_130	N, F_GLY_145	H, F_GLY_145	2.92	2.16	24.09
4F33.PDB	O, F_PHE_128	N, F_LEU_147	H, F_LEU_147	2.82	1.98	9.09
4F33.PDB	O, F_LEU_184	N, F_VAL_148	H, F_VAL_148	2.76	1.91	9.03
4F33.PDB	O, F_SER_126	N, F_LYS_149	H, F_LYS_149	2.76	1.90	3.32
4F33.PDB	O, F_LYS_123	N, F_PHE_152	H, F_PHE_152	2.93	2.12	17.02
4F33.PDB	O, F ASN_203	N, F_SER_159	H, F_SER_159	2.97	2.16	16.38
4F33.PDB	OG, F_SER_186	NE1, F_TRP_160	HE1, F_TRP_160	3.00	2.15	9.04
4F33.PDB	O, F_ILE_201	N, F ASN_161	H, F ASN_161	2.83	1.99	9.71
4F33.PDB	OD1, F ASN_203	N, F_SER_162	H, F_SER_162	2.79	1.98	16.87
4F33.PDB	O, F_TRP_160	N, F_GLY_163	H, F_GLY_163	2.90	2.14	23.82
4F33.PDB	O, F_VAL_187	N, F_HIS_170	H, F_HIS_170	2.79	1.95	11.88
4F33.PDB	O, F_SER_185	N, F_PHE_172	H, F_PHE_172	2.94	2.09	4.01
4F33.PDB	O, F_SER_183	N, F_VAL_175	H, F_VAL_175	2.90	2.08	14.72

4F33.PDB	O, F.LEU_181	N, F.GLN_177	H, F.GLN_177	2.83	1.98	7.25
4F33.PDB	OD1, F.ASP_150	NE2, F.GLN_177	HE22, F.GLN_177	2.82	2.02	17.76
4F33.PDB	O, F.TYR_151	N, F.TYR_182	H, F.TYR_182	2.79	1.93	3.62
4F33.PDB	O, F.VAL_148	N, F.LEU_184	H, F.LEU_184	2.91	2.11	17.32
4F33.PDB	O, F.CYS_146	N, F.SER_186	H, F.SER_186	2.97	2.15	15.30
4F33.PDB	O, F.HIS_170	N, F.VAL_187	H, F.VAL_187	2.89	2.06	12.38
4F33.PDB	O, F.LEU_144	N, F.VAL_188	H, F.VAL_188	2.81	2.01	17.82
4F33.PDB	O, F.ALA_142	N, F.VAL_190	H, F.VAL_190	2.77	1.95	15.08
4F33.PDB	O, F.GLY_140	N, F.SER_192	H, F.SER_192	2.89	2.04	8.47
4F33.PDB	O, F.PRO_191	N, F.SER_194	H, F.SER_194	2.94	2.10	10.73
4F33.PDB	O, F.SER_194	N, F.GLN_198	H, F.GLN_198	2.74	1.88	2.67
4F33.PDB	O, F.THR_199	NE2, F.GLN_198	HE21, F.GLN_198	2.92	2.06	2.83
4F33.PDB	OD1, F.ASN_161	N, F.ILE_201	H, F.ILE_201	2.77	1.94	13.18
4F33.PDB	O, F.LYS_215	N, F.CYS_202	H, F.CYS_202	2.93	2.14	19.72
4F33.PDB	O, F.SER_159	N, F.ASN_203	H, F.ASN_203	2.82	1.96	5.68
4F33.PDB	OD1, F.ASP_214	ND2, F.ASN_203	HD21, F.ASN_203	2.95	2.10	8.40
4F33.PDB	O, F.VAL_213	N, F.VAL_204	H, F.VAL_204	2.74	1.89	7.26
4F33.PDB	O, F.THR_157	N, F.ASN_205	H, F.ASN_205	2.87	2.02	8.95
4F33.PDB	O, F.THR_211	N, F.HIS_206	H, F.HIS_206	2.87	2.02	7.60
4F33.PDB	OG, F.SER_209	ND1, F.HIS_206	HD1, F.HIS_206	2.64	1.82	13.68
4F33.PDB	O, F.PRO_153	NE2, F.HIS_206	HE2, F.HIS_206	2.81	1.97	9.86
4F33.PDB	O, F.LYS_207	N, F.ASN_210	H, F.ASN_210	2.97	2.15	14.98
4F33.PDB	O, D.ASP_214	N, F.LYS_212	H, F.LYS_212	2.94	2.11	12.64
4F33.PDB	O, F.VAL_204	N, F.VAL_213	H, F.VAL_213	2.85	2.02	13.27
4F33.PDB	O, D.LYS_212	N, F.ASP_214	H, F.ASP_214	2.84	2.02	14.84
4F33.PDB	O, F.CYS_202	N, F.LYS_215	H, F.LYS_215	2.92	2.10	15.07
4F33.PDB	OE1, E.GLU_123	NZ, F.LYS_215	HZ1, F.LYS_215	2.61	1.84	24.34
4F33.PDB	OG1, D.THR_211	NZ, F.LYS_215	HZ2, F.LYS_215	2.92	2.04	7.71
4F33.PDB	O, F.TYR_200	N, F.VAL_217	H, F.VAL_217	2.89	2.04	9.32
4F33.PDB	OG, G.SER_27	N, G.GLU_4	H, G.GLU_4	2.95	2.12	14.03
4F33.PDB	O, G.SER_25	N, G.THR_6	H, G.THR_6	2.78	1.93	4.59
4F33.PDB	O, G.TYR_86	NE2, G.GLN_7	HE22, G.GLN_7	2.90	2.13	22.62
4F33.PDB	O, G.THR_23	N, G.SER_8	H, G.SER_8	2.90	2.09	16.80
4F33.PDB	O, G.LYS_103	N, G.MET_12	H, G.MET_12	2.76	1.93	13.02
4F33.PDB	O, G.GLU_105	N, G.ALA_14	H, G.ALA_14	2.97	2.16	16.65
4F33.PDB	OE2, G.GLU_18	N, G.SER_15	H, G.SER_15	2.71	1.86	9.24
4F33.PDB	O, G.VAL_78	N, G.GLY_17	H, G.GLY_17	2.81	2.01	18.15
4F33.PDB	O, G.ILE_75	N, G.VAL_20	H, G.VAL_20	2.96	2.19	21.57
4F33.PDB	OG1, G.THR_74	OG1, G.THR_21	HG1, G.THR_21	2.73	1.97	18.47
4F33.PDB	O, G.SER_8	OG1, G.THR_23	H, G.THR_23	2.83	1.99	8.78
4F33.PDB	O, G.TYR_71	N, G.CYS_24	H, G.CYS_24	2.68	1.82	4.01
4F33.PDB	O, G.THR_6	N, G.SER_25	H, G.SER_25	2.81	1.96	7.25
4F33.PDB	O, G.ASN_69	N, G.ALA_26	H, G.ALA_26	2.79	1.95	9.77
4F33.PDB	O, G.GLN_89	N, G.HIS_34	H, G.HIS_34	2.98	2.11	0.46
4F33.PDB	O, G.ILE_48	N, G.TRP_35	H, G.TRP_35	2.66	1.84	13.67
4F33.PDB	O, G.TYR_87	N, G.TYR_36	H, G.TYR_36	2.77	1.96	14.84
4F33.PDB	O, G.LYS_45	N, G.GLN_37	H, G.GLN_37	2.88	2.13	24.53
4F33.PDB	O, G.THR_85	N, G.GLN_38	H, G.GLN_38	2.82	1.98	9.18
4F33.PDB	O, G.THR_42	NE2, G.GLN_38	HE21, G.GLN_38	2.88	2.05	12.56
4F33.PDB	O, G.GLU_81	NZ, G.LYS_39	HZ1, G.LYS_39	2.81	1.93	9.10
4F33.PDB	O, G.ASP_83	NZ, G.LYS_39	HZ3, G.LYS_39	2.78	1.91	11.96
4F33.PDB	O, G.GLN_37	N, G.LYS_45	H, G.LYS_45	2.77	1.97	18.28
4F33.PDB	O, G.TRP_35	N, G.TRP_47	H, G.TRP_47	2.83	2.03	17.67
4F33.PDB	O, G.LYS_53	N, G.TYR_49	H, G.TYR_49	2.75	1.94	15.45
4F33.PDB	O, G.MET_33	N, G.THR_51	H, G.THR_51	2.73	1.90	12.70
4F33.PDB	O, G.ASP_50	N, G.SER_52	H, G.SER_52	2.85	2.13	28.17
4F33.PDB	O, G.TYR_49	N, G.LYS_53	H, G.LYS_53	2.86	2.08	20.69
4F33.PDB	O, G.TRP_47	N, G.ALA_55	H, G.ALA_55	2.97	2.12	4.41

4F33.PDB	OD1, G_ASP_82	NH2, G_ARG_61	HH21, G_ARG_61	2.73	1.89	8.68
4F33.PDB	OE2, G_GLU_81	NH2, G_ARG_61	HH22, G_ARG_61	2.96	2.16	17.92
4F33.PDB	O, G_THR_74	N, G_SER_63	H, G_SER_63	2.95	2.19	22.57
4F33.PDB	O, G_ALA_26	ND2, G_ASN_69	HD21, G_ASN_69	2.91	2.05	4.65
4F33.PDB	O, G_SER_67	N, G_SER_70	H, G_SER_70	2.98	2.13	6.01
4F33.PDB	O, G_CYS_24	N, G_TYR_71	H, G_TYR_71	2.90	2.05	8.92
4F33.PDB	O, G_VAL_30	OH, G_TYR_71	HH, G_TYR_71	2.88	2.15	24.02
4F33.PDB	O, G_SER_65	N, G_SER_72	H, G_SER_72	2.77	1.93	11.28
4F33.PDB	O, G_SER_63	N, G_THR_74	H, G_THR_74	2.79	1.96	12.22
4F33.PDB	O, G_VAL_20	N, G_ILE_75	H, G_ILE_75	2.92	2.11	16.41
4F33.PDB	O, G_ARG_61	N, G_SER_76	H, G_SER_76	2.80	1.98	14.52
4F33.PDB	O, G_GLU_18	N, G_VAL_78	H, G_VAL_78	2.74	1.99	24.30
4F33.PDB	OD2, G_ASP_82	N, G_GLU_79	H, G_GLU_79	2.87	2.02	5.18
4F33.PDB	O, G_GLU_79	N, G_ASP_82	H, G_ASP_82	2.87	2.04	11.79
4F33.PDB	O, G_GLN_38	N, G_THR_85	H, G_THR_85	2.89	2.05	11.10
4F33.PDB	O, G_THR_102	N, G_TYR_86	H, G_TYR_86	2.86	2.02	10.07
4F33.PDB	O, G_TYR_36	N, G_TYR_87	H, G_TYR_87	2.88	2.07	16.64
4F33.PDB	O, G_TYR_32	NE1, G_TRP_91	HE1, G_TRP_91	2.74	1.97	22.30
4F33.PDB	OE1, G_GLN_90	N, G_LYS_93	H, G_LYS_93	2.98	2.15	12.47
4F33.PDB	O, H_TYR_60	NE2, G_HIS_94	HE2, G_HIS_94	2.97	2.17	17.68
4F33.PDB	O, G_ILE_3	OG1, G_THR_97	HG1, G_THR_97	2.79	1.99	11.42
4F33.PDB	O, G_CYS_88	N, G_GLY_99	H, G_GLY_99	2.79	1.97	13.30
4F33.PDB	OE1, G_GLN_7	N, G_GLY_101	H, G_GLY_101	2.78	2.01	21.97
4F33.PDB	O, G_TYR_86	N, G_THR_102	H, G_THR_102	2.90	2.07	12.97
4F33.PDB	O, G_PRO_9	OG1, G_THR_102	HG1, G_THR_102	2.80	2.04	18.20
4F33.PDB	O, G_ALA_10	N, G_LYS_103	H, G_LYS_103	2.82	1.98	10.32
4F33.PDB	O, G_ALA_84	N, G_VAL_104	H, G_VAL_104	2.84	1.98	2.92
4F33.PDB	O, G_MET_12	N, G_GLU_105	H, G_GLU_105	2.77	1.92	6.46
4F33.PDB	OE1, G_GLN_166	N, G_ILE_106	H, G_ILE_106	2.88	2.04	11.50
4F33.PDB	O, G_ALA_14	N, G_LYS_107	H, G_LYS_107	2.80	1.96	9.94
4F33.PDB	O, G_THR_109	NE, G_ARG_108	HE, G_ARG_108	2.74	1.88	3.40
4F33.PDB	O, G_ASP_170	NH1, G_ARG_108	HH11, G_ARG_108	2.91	2.09	13.89
4F33.PDB	O, G_TYR_140	N, G_ALA_111	H, G_ALA_111	2.91	2.07	11.81
4F33.PDB	O, G_LEU_135	N, G_PHE_116	H, G_PHE_116	2.84	2.01	14.03
4F33.PDB	O, G_VAL_133	N, G_PHE_118	H, G_PHE_118	2.82	2.01	17.24
4F33.PDB	OG, G_SER_131	NE2, G_GLN_124	HE22, G_GLN_124	2.79	1.93	5.18
4F33.PDB	O, G_GLN_124	N, G_SER_127	H, G_SER_127	2.82	2.03	19.57
4F33.PDB	O, G_LEU_125	N, G_GLY_128	H, G_GLY_128	2.86	2.03	13.69
4F33.PDB	O, G_LEU_181	N, G_ALA_130	H, G_ALA_130	2.79	1.94	9.03
4F33.PDB	O, G_LEU_179	N, G_VAL_132	H, G_VAL_132	2.82	1.99	12.45
4F33.PDB	O, G_SER_177	N, G_CYS_134	H, G_CYS_134	2.82	1.98	10.53
4F33.PDB	O, G_PHE_116	N, G_LEU_135	H, G_LEU_135	2.78	1.93	9.33
4F33.PDB	O, G_LEU_175	N, G_LEU_136	H, G_LEU_136	2.79	1.94	5.85
4F33.PDB	O, G_SER_114	N, G_ASN_137	H, G_ASN_137	2.85	2.02	14.57
4F33.PDB	O, G_TYR_173	N, G_PHE_139	H, G_PHE_139	2.87	2.06	16.25
4F33.PDB	O, G_ALA_111	N, G_TYR_140	H, G_TYR_140	2.87	2.06	17.58
4F33.PDB	O, G_GLU_195	N, G_GLN_147	H, G_GLN_147	2.86	2.03	12.62
4F33.PDB	OG, G_SER_177	NE1, G_TRP_148	HE1, G_TRP_148	2.87	2.04	13.06
4F33.PDB	O, G_ALA_193	N, G_LYS_149	H, G_LYS_149	2.82	1.98	9.73
4F33.PDB	O, G_VAL_191	N, G_ASP_151	H, G_ASP_151	2.80	1.96	11.61
4F33.PDB	O, G_VAL_150	N, G_ALA_153	H, G_ALA_153	2.97	2.12	7.09
4F33.PDB	O, G_TRP_148	N, G_GLN_155	H, G_GLN_155	2.87	2.02	6.80
4F33.PDB	OE1, G_GLN_155	ND2, G_ASN_158	HD22, G_ASN_158	2.92	2.10	14.66
4F33.PDB	O, H_LEU_176	NE2, G_GLN_160	HE22, G_GLN_160	2.89	2.04	8.42
4F33.PDB	O, G_SER_176	N, G_SER_162	H, G_SER_162	2.99	2.22	21.55
4F33.PDB	O, H_PRO_173	OG, G_SER_162	HG, G_SER_162	2.65	1.94	25.59
4F33.PDB	O, G_SER_174	N, G_THR_164	H, G_THR_164	3.00	2.17	13.79
4F33.PDB	O, G_SER_171	NE2, G_GLN_166	HE21, G_GLN_166	2.92	2.09	14.25

4F33.PDB	O, G_ILE_106	NE2, G_GLN_166	HE22, G_GLN_166	2.78	2.00	21.03
4F33.PDB	O, G_THR_172	N, G_ASP_167	H, G_ASP_167	3.00	2.15	7.80
4F33.PDB	OD1, G_ASP_167	N, G_LYS_169	H, G_LYS_169	2.59	1.77	13.16
4F33.PDB	OD1, G_ASP_170	N, G_THR_172	H, G_THR_172	2.88	2.07	16.47
4F33.PDB	OD1, G_ASP_170	OG1, G_THR_172	HG1, G_THR_172	2.69	1.89	8.34
4F33.PDB	O, G_PHE_139	N, G_TYR_173	H, G_TYR_173	2.81	1.97	8.53
4F33.PDB	OG1, G_THR_164	N, G_SER_174	H, G_SER_174	2.96	2.14	13.32
4F33.PDB	O, G_LEU_136	N, G_LEU_175	H, G_LEU_175	2.80	1.99	16.36
4F33.PDB	O, G_SER_162	N, G_SER_176	H, G_SER_176	2.93	2.11	14.30
4F33.PDB	O, G_CYS_134	N, G_SER_177	H, G_SER_177	2.88	2.06	13.62
4F33.PDB	O, G_GLN_160	N, G_THR_178	H, G_THR_178	2.92	2.10	14.24
4F33.PDB	O, G_VAL_132	N, G_LEU_179	H, G_LEU_179	2.85	2.02	12.70
4F33.PDB	O, G_ASN_158	N, G_THR_180	H, G_THR_180	2.97	2.14	11.60
4F33.PDB	O, G_ALA_130	N, G_LEU_181	H, G_LEU_181	2.90	2.07	12.18
4F33.PDB	O, G_GLY_128	N, G_LYS_183	H, G_LYS_183	2.88	2.04	9.29
4F33.PDB	OG, G_SER_182	N, G_ASP_185	H, G_ASP_185	2.89	2.09	18.06
4F33.PDB	O, G_SER_182	N, G_TYR_186	H, G_TYR_186	2.85	2.00	5.00
4F33.PDB	O, G_LYS_183	N, G_GLU_187	H, G_GLU_187	2.98	2.20	20.06
4F33.PDB	O, G_ASP_185	N, G_LYS_188	H, G_LYS_188	2.67	1.90	21.28
4F33.PDB	OD2, G_ASP_151	ND1, G_HIS_189	HD1, G_HIS_189	2.86	2.09	22.44
4F33.PDB	OD1, G_ASP_151	N, G_VAL_191	H, G_VAL_191	2.83	1.98	7.69
4F33.PDB	O, G_PHE_209	N, G_TYR_192	H, G_TYR_192	2.93	2.08	7.39
4F33.PDB	O, G_LYS_149	N, G_ALA_193	H, G_ALA_193	2.92	2.11	16.65
4F33.PDB	O, G_LYS_207	N, G_CYS_194	H, G_CYS_194	2.88	2.10	20.64
4F33.PDB	O, G_GLN_147	N, G_GLU_195	H, G_GLU_195	2.75	1.91	11.05
4F33.PDB	O, G_VAL_205	N, G_VAL_196	H, G_VAL_196	2.75	1.92	11.23
4F33.PDB	ND1, G_HIS_198	N, G_GLY_200	H, G_GLY_200	2.95	2.10	7.40
4F33.PDB	O, G_HIS_198	N, G_LEU_201	H, G_LEU_201	2.95	2.09	6.07
4F33.PDB	O, G_VAL_196	N, G_VAL_205	H, G_VAL_205	2.94	2.12	15.56
4F33.PDB	O, G_TYR_192	N, G_PHE_209	H, G_PHE_209	2.97	2.19	21.65
4F33.PDB	O, G_LYS_190	N, G_ARG_211	H, G_ARG_211	2.69	1.87	14.60
4F33.PDB	O, G_HIS_189	NE, G_ARG_211	HE, G_ARG_211	2.61	1.80	15.33
4F33.PDB	O, H_SER_25	N, H_GLN_3	H, H_GLN_3	2.95	2.13	15.35
4F33.PDB	O, H_LYS_23	N, H_GLN_5	H, H_GLN_5	2.86	2.00	5.15
4F33.PDB	O, H_TYR_94	NE2, H_GLN_6	HE22, H_GLN_6	2.90	2.09	16.65
4F33.PDB	O, H_SER_21	N, H_SER_7	H, H_SER_7	2.94	2.20	26.21
4F33.PDB	O, H_PRO_114	N, H_GLU_10	H, H_GLU_10	2.90	2.11	19.39
4F33.PDB	O, H_LEU_86	N, H_GLY_15	H, H_GLY_15	2.71	1.88	13.48
4F33.PDB	O, H_LEU_83	N, H_VAL_18	H, H_VAL_18	2.99	2.23	23.20
4F33.PDB	O, H_MET_81	N, H_ILE_20	H, H_ILE_20	2.88	2.05	13.37
4F33.PDB	O, H_GLN_5	N, H_LYS_23	H, H_LYS_23	2.75	1.91	8.98
4F33.PDB	O, H_SER_77	N, H_ALA_24	H, H_ALA_24	2.91	2.05	3.04
4F33.PDB	O, H_GLN_3	N, H_SER_25	H, H_SER_25	2.89	2.07	15.25
4F33.PDB	O, C_GLY_60	N, H_PHE_29	H, H_PHE_29	2.96	2.15	17.00
4F33.PDB	O, H_SER_28	N, H_GLY_31	H, H_GLY_31	3.00	2.15	9.57
4F33.PDB	O, H_GLY_99	N, H_THR_33	H, H_THR_33	2.95	2.14	17.33
4F33.PDB	O, H_ALA_97	N, H_ASN_35	H, H_ASN_35	2.77	1.93	11.02
4F33.PDB	O, H_PHE_95	N, H_VAL_37	H, H_VAL_37	2.79	1.98	16.38
4F33.PDB	O, H_GLU_46	N, H_LYS_38	H, H_LYS_38	2.77	1.95	13.91
4F33.PDB	O, H_GLU_89	NZ, H_LYS_38	HZ1, H_LYS_38	2.83	1.95	4.26
4F33.PDB	O, H_VAL_93	N, H_GLN_39	H, H_GLN_39	2.79	1.93	3.64
4F33.PDB	O, H_SER_40	N, H_LYS_43	H, H_LYS_43	2.96	2.14	14.33
4F33.PDB	O, H_LYS_38	N, H_GLU_46	H, H_GLU_46	2.92	2.12	18.59
4F33.PDB	O, H_TRP_36	N, H_ILE_48	H, H_ILE_48	2.85	2.00	7.74
4F33.PDB	O, H_SER_59	N, H_LEU_50	H, H_LEU_50	2.90	2.12	20.46
4F33.PDB	O, H_MET_34	N, H_ILE_51	H, H_ILE_51	2.91	2.11	17.46
4F33.PDB	O, H_ALA_57	N, H_THR_52	H, H_THR_52	2.92	2.10	14.38
4F33.PDB	O, H_THR_52	N, H_GLY_56	H, H_GLY_56	2.89	2.18	28.64

4F33.PDB	OD1, H_ASN_55	N, H_ALA_57	H, H_ALA_57	2.90	2.05	3.80
4F33.PDB	O, H_LEU_50	N, H_SER_59	H, H_SER_59	2.92	2.11	17.14
4F33.PDB	O, H_ILE_48	N, H_ASN_61	H, H_ASN_61	2.88	2.05	13.78
4F33.PDB	O, H_TRP_47	ND2, H_ASN_61	HD21, H_ASN_61	2.94	2.11	13.13
4F33.PDB	OE2, H_GLU_46	NZ, H_LYS_63	HZ3, H_LYS_63	2.72	1.93	23.08
4F33.PDB	O, H_ASN_61	N, H_PHE_64	H, H_PHE_64	2.76	1.93	12.08
4F33.PDB	O, H_PHE_64	N, H_LYS_67	H, H_LYS_67	2.99	2.27	28.17
4F33.PDB	OD2, H_ASP_90	NZ, H_LYS_67	HZ2, H_LYS_67	2.82	1.98	16.29
4F33.PDB	O, H_LEU_84	NZ, H_LYS_67	HZ3, H_LYS_67	2.97	2.18	23.42
4F33.PDB	O, H_PHE_64	N, H_ALA_68	H, H_ALA_68	2.90	2.09	16.52
4F33.PDB	O, H_ASP_82	N, H_THR_69	H, H_THR_69	2.92	2.16	23.47
4F33.PDB	OH, H_TYR_60	N, H_LEU_70	H, H_LEU_70	2.87	2.03	9.16
4F33.PDB	O, H_THR_78	N, H_ASP_73	H, H_ASP_73	2.76	1.93	11.64
4F33.PDB	O, H_CYS_22	N, H_ALA_79	H, H_ALA_79	2.86	2.05	15.52
4F33.PDB	O, H_THR_71	N, H_TYR_80	H, H_TYR_80	2.82	1.96	4.65
4F33.PDB	O, H_ILE_20	N, H_MET_81	H, H_MET_81	2.94	2.11	14.01
4F33.PDB	O, H_THR_69	N, H_ASP_82	H, H_ASP_82	2.90	2.07	11.71
4F33.PDB	O, H_VAL_18	N, H_LEU_83	H, H_LEU_83	2.79	1.96	11.28
4F33.PDB	O, H_LYS_67	N, H_LEU_84	H, H_LEU_84	2.89	2.08	16.65
4F33.PDB	O, H_ALA_16	N, H_LEU_86	H, H_LEU_86	2.90	2.06	8.91
4F33.PDB	OD2, H_ASP_90	N, H_THR_87	H, H_THR_87	2.84	2.01	13.54
4F33.PDB	O, H_THR_87	N, H_ASP_90	H, H_ASP_90	2.82	1.98	9.38
4F33.PDB	O, H_SER_88	N, H_SER_91	H, H_SER_91	2.94	2.08	5.94
4F33.PDB	O, H_VAL_115	N, H_ALA_92	H, H_ALA_92	2.98	2.25	27.64
4F33.PDB	O, H_THR_113	N, H_TYR_94	H, H_TYR_94	2.93	2.08	7.56
4F33.PDB	O, H_VAL_37	N, H_PHE_95	H, H_PHE_95	2.76	1.92	9.09
4F33.PDB	O, H_ASN_35	N, H_ALA_97	H, H_ALA_97	2.85	2.09	23.41
4F33.PDB	O, H_TYR_108	N, H_ARG_98	H, H_ARG_98	2.84	2.07	21.36
4F33.PDB	OD1, H_ASP_107	NE, H_ARG_98	HE, H_ARG_98	2.95	2.15	18.92
4F33.PDB	OD2, H_ASP_107	NH2, H_ARG_98	HH21, H_ARG_98	2.79	1.95	8.93
4F33.PDB	O, H_THR_33	N, H_GLY_99	H, H_GLY_99	2.98	2.14	10.15
4F33.PDB	OD1, H_ASP_102	NE, H_ARG_104	HE, H_ARG_104	2.85	2.00	6.80
4F33.PDB	OD2, H_ASP_107	NH1, H_ARG_104	HH11, H_ARG_104	2.85	2.04	16.23
4F33.PDB	OD2, H_ASP_102	NH2, H_ARG_104	HH21, H_ARG_104	2.93	2.12	16.50
4F33.PDB	OH, G_TYR_36	N, H_PHE_106	H, H_PHE_106	2.74	1.89	7.07
4F33.PDB	O, H_CYS_96	N, H_GLY_110	H, H_GLY_110	2.73	1.87	4.66
4F33.PDB	OE1, H_GLN_6	N, H_GLY_112	H, H_GLY_112	2.84	2.08	23.08
4F33.PDB	O, H_TYR_94	N, H_THR_113	H, H_THR_113	2.79	2.00	19.33
4F33.PDB	O, H_SER_7	OG1, H_THR_113	HG1, H_THR_113	2.86	2.10	18.89
4F33.PDB	O, H_ALA_92	N, H_VAL_115	H, H_VAL_115	2.81	1.98	12.26
4F33.PDB	OG, H_SER_91	N, H_VAL_117	H, H_VAL_117	2.86	2.06	16.73
4F33.PDB	O, H_GLU_12	N, H_SER_118	H, H_SER_118	2.89	2.08	15.90
4F33.PDB	O, H_PHE_152	N, H_LYS_123	H, H_LYS_123	2.83	2.00	12.24
4F33.PDB	O, H_ASP_150	NZ, H_LYS_123	HZ2, H_LYS_123	2.81	1.95	12.86
4F33.PDB	OE2, A_GLU_123	N, H_GLY_124	H, H_GLY_124	2.97	2.12	7.35
4F33.PDB	O, H_LYS_149	N, H_SER_126	H, H_SER_126	2.87	2.05	14.54
4F33.PDB	O, H_LEU_147	N, H_PHE_128	H, H_PHE_128	2.88	2.06	14.55
4F33.PDB	O, H_GLY_145	N, H_LEU_130	H, H_LEU_130	2.75	1.90	6.63
4F33.PDB	OG, H_SER_136	N, H_SER_133	H, H_SER_133	2.96	2.15	16.37
4F33.PDB	OG, H_SER_133	N, H_LYS_135	H, H_LYS_135	2.86	2.08	20.02
4F33.PDB	O, G_SER_208	NZ, H_LYS_135	HZ3, H_LYS_135	2.85	1.99	13.05
4F33.PDB	O, H_SER_133	OG1, H_THR_137	HG1, H_THR_137	2.95	2.25	26.10
4F33.PDB	O, H_SER_138	N, H_THR_141	H, H_THR_141	2.82	1.99	10.59
4F33.PDB	O, H_VAL_190	N, H_ALA_142	H, H_ALA_142	2.80	1.95	4.86
4F33.PDB	O, H_SER_136	N, H_ALA_143	H, H_ALA_143	2.78	1.96	14.14
4F33.PDB	O, H_VAL_188	N, H_LEU_144	H, H_LEU_144	2.99	2.16	14.52
4F33.PDB	O, H_LEU_130	N, H_GLY_145	H, H_GLY_145	2.92	2.15	21.74
4F33.PDB	O, H_PHE_128	N, H_LEU_147	H, H_LEU_147	2.83	1.99	10.04

4F33.PDB	O, H.LEU.184	N, H.VAL.148	H, H.VAL.148	2.77	1.93	9.98
4F33.PDB	O, H.SER.126	N, H.LYS.149	H, H.LYS.149	2.81	1.96	4.12
4F33.PDB	O, H.LYS.123	N, H.PHE.152	H, H.PHE.152	2.92	2.12	18.54
4F33.PDB	OG, H.SER.186	NE1, H.TRP.160	HE1, H.TRP.160	2.99	2.15	10.12
4F33.PDB	O, H.ILE.201	N, H.ASN.161	H, H.ASN.161	2.75	1.91	10.53
4F33.PDB	OD1, H.ASN.203	N, H.SER.162	H, H.SER.162	2.80	1.99	16.84
4F33.PDB	O, H.TRP.160	N, H.GLY.163	H, H.GLY.163	2.91	2.16	25.30
4F33.PDB	O, H.ASN.161	N, H.ALA.164	H, H.ALA.164	2.99	2.13	5.75
4F33.PDB	O, H.VAL.187	N, H.HIS.170	H, H.HIS.170	2.76	1.93	12.16
4F33.PDB	O, H.SER.185	N, H.PHE.172	H, H.PHE.172	2.96	2.11	6.73
4F33.PDB	O, H.SER.183	N, H.VAL.175	H, H.VAL.175	2.88	2.06	12.99
4F33.PDB	O, H.LEU.181	N, H.GLN.177	H, H.GLN.177	2.85	2.00	6.78
4F33.PDB	OD1, H.ASP.150	NE2, H.GLN.177	HE22, H.GLN.177	2.83	2.04	19.22
4F33.PDB	O, H.GLN.177	N, H.GLY.180	H, H.GLY.180	2.96	2.10	4.33
4F33.PDB	O, H.TYR.151	N, H.TYR.182	H, H.TYR.182	2.83	1.98	4.16
4F33.PDB	O, H.VAL.148	N, H.LEU.184	H, H.LEU.184	2.93	2.14	19.17
4F33.PDB	O, H.CYS.146	N, H.SER.186	H, H.SER.186	2.99	2.19	16.98
4F33.PDB	O, H.HIS.170	N, H.VAL.187	H, H.VAL.187	2.86	2.03	12.28
4F33.PDB	O, H.LEU.144	N, H.VAL.188	H, H.VAL.188	2.79	1.98	17.58
4F33.PDB	O, H.ALA.142	N, H.VAL.190	H, H.VAL.190	2.80	1.99	14.89
4F33.PDB	O, H.GLY.140	N, H.SER.192	H, H.SER.192	2.85	2.00	7.56
4F33.PDB	O, H.SER.194	N, H.GLN.198	H, H.GLN.198	2.75	1.90	3.78
4F33.PDB	O, H.THR.199	NE2, H.GLN.198	HE21, H.GLN.198	2.90	2.04	2.16
4F33.PDB	OD1, H.ASN.161	N, H.ILE.201	H, H.ILE.201	2.74	1.91	10.89
4F33.PDB	O, H.LYS.215	N, H.CYS.202	H, H.CYS.202	2.98	2.20	21.56
4F33.PDB	O, H.SER.159	N, H.ASN.203	H, H.ASN.203	2.79	1.94	8.15
4F33.PDB	OD1, H.ASP.214	ND2, H.ASN.203	HD21, H.ASN.203	2.91	2.05	5.75
4F33.PDB	O, H.VAL.213	N, H.VAL.204	H, H.VAL.204	2.77	1.91	5.12
4F33.PDB	O, H.THR.157	N, H.ASN.205	H, H.ASN.205	2.86	2.02	8.69
4F33.PDB	O, H.THR.211	N, H.HIS.206	H, H.HIS.206	2.87	2.02	7.96
4F33.PDB	O, H.PRO.153	NE2, H.HIS.206	HE2, H.HIS.206	2.85	2.00	9.82
4F33.PDB	O, H.LYS.207	N, H.ASN.210	H, H.ASN.210	2.94	2.11	13.37
4F33.PDB	O, H.SER.209	OG1, H.THR.211	HG1, H.THR.211	2.98	2.28	27.00
4F33.PDB	O, H.VAL.204	N, H.VAL.213	H, H.VAL.213	2.84	2.02	14.41
4F33.PDB	O, B.LYS.212	N, H.ASP.214	H, H.ASP.214	2.71	1.89	15.00
4F33.PDB	O, H.CYS.202	N, H.LYS.215	H, H.LYS.215	2.98	2.18	17.82
4F33.PDB	OE1, G.GLU.123	NZ, H.LYS.215	HZ1, H.LYS.215	2.97	2.19	24.10
4F33.PDB	OG1, B.THR.211	NZ, H.LYS.215	HZ2, H.LYS.215	2.80	1.95	14.49
4F33.PDB	O, B.ASN.210	N, H.LYS.216	H, H.LYS.216	2.82	2.01	16.40
4F33.PDB	O, H.TYR.200	N, H.VAL.217	H, H.VAL.217	2.85	2.01	9.04

Table 1689: 4F33-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4F3F.PDB	O, A_SER_25	N, A_THR_6	H, A_THR_6	2.85	2.00	8.09
4F3F.PDB	O, A_THR_23	N, A_SER_8	H, A_SER_8	2.94	2.15	20.13
4F3F.PDB	O, A_LYS_103	N, A_MET_12	H, A_MET_12	2.79	1.97	13.63
4F3F.PDB	O, A_GLU_105	N, A_ALA_14	H, A_ALA_14	2.99	2.22	22.34
4F3F.PDB	O, A_VAL_78	N, A_GLY_17	H, A_GLY_17	2.86	2.04	14.29
4F3F.PDB	O, A_SER_15	N, A_GLU_18	H, A_GLU_18	3.00	2.16	11.55
4F3F.PDB	O, A_ILE_75	N, A_VAL_20	H, A_VAL_20	2.94	2.13	15.17
4F3F.PDB	O, A_LEU_73	N, A_MET_22	H, A_MET_22	2.83	2.00	12.74
4F3F.PDB	O, A_SER_8	N, A_THR_23	H, A_THR_23	2.79	1.94	4.31
4F3F.PDB	O, A_TYR_71	N, A_CYS_24	H, A_CYS_24	2.77	1.94	12.44
4F3F.PDB	O, A_THR_6	N, A_SER_25	H, A_SER_25	2.94	2.11	13.40
4F3F.PDB	O, A_ASN_69	N, A_ALA_26	H, A_ALA_26	2.80	1.96	8.83
4F3F.PDB	O, A_GLU_4	N, A_SER_27	H, A_SER_27	2.90	2.18	27.52
4F3F.PDB	O, A_GLN_89	N, A_HIS_34	H, A_HIS_34	2.93	2.11	13.52
4F3F.PDB	O, A_ILE_48	N, A_TRP_35	H, A_TRP_35	2.83	2.01	14.96
4F3F.PDB	O, A_TYR_87	N, A_TYR_36	H, A_TYR_36	2.88	2.12	23.08
4F3F.PDB	O, A_LYS_45	N, A_GLN_37	H, A_GLN_37	2.83	2.04	20.59
4F3F.PDB	O, A_THR_85	N, A_GLN_38	H, A_GLN_38	2.89	2.06	12.49
4F3F.PDB	O, A_THR_42	NE2, A_GLN_38	HE21, A_GLN_38	2.97	2.19	20.06
4F3F.PDB	OE1, B_GLN_39	NE2, A_GLN_38	HE22, A_GLN_38	2.88	2.04	8.75
4F3F.PDB	O, A_GLU_81	NZ, A_LYS_39	HZ1, A_LYS_39	2.81	1.98	18.05
4F3F.PDB	O, A_LYS_39	OG1, A_THR_42	HG1, A_THR_42	3.00	2.19	8.01
4F3F.PDB	O, A_GLN_37	N, A_LYS_45	H, A_LYS_45	2.76	2.04	27.53
4F3F.PDB	O, B_ARG_104	NH1, A_ARG_46	HH11, A_ARG_46	2.93	2.16	22.46
4F3F.PDB	O, A_TRP_35	N, A_TRP_47	H, A_TRP_47	2.80	1.94	4.03
4F3F.PDB	O, A_LYS_53	N, A_TYR_49	H, A_TYR_49	2.96	2.17	19.74
4F3F.PDB	ND1, A_HIS_34	N, A_ASP_50	H, A_ASP_50	2.97	2.24	27.25
4F3F.PDB	O, A_MET_33	N, A_THR_51	H, A_THR_51	2.64	1.85	18.18
4F3F.PDB	OD1, A_ASP_82	NH2, A_ARG_61	HH21, A_ARG_61	2.60	1.79	16.27
4F3F.PDB	OE2, A_GLU_81	NH2, A_ARG_61	HH22, A_ARG_61	2.95	2.12	13.66
4F3F.PDB	O, A_THR_74	N, A_SER_63	H, A_SER_63	2.85	2.05	18.09
4F3F.PDB	O, A_CYS_24	N, A_TYR_71	H, A_TYR_71	2.90	2.04	4.79
4F3F.PDB	O, A_SER_65	N, A_SER_72	H, A_SER_72	2.82	1.98	10.66
4F3F.PDB	O, A_MET_22	N, A_LEU_73	H, A_LEU_73	2.92	2.10	15.06
4F3F.PDB	O, A_SER_63	N, A_THR_74	H, A_THR_74	2.88	2.03	8.55
4F3F.PDB	OG1, A_THR_21	OG1, A_THR_74	HG1, A_THR_74	2.77	2.04	22.11
4F3F.PDB	O, A_VAL_20	N, A_ILE_75	H, A_ILE_75	2.85	2.01	11.39
4F3F.PDB	O, A_ARG_61	N, A_SER_76	H, A_SER_76	2.86	2.02	10.12
4F3F.PDB	O, A_GLU_18	N, A_VAL_78	H, A_VAL_78	2.86	2.14	28.13
4F3F.PDB	O, A_GLU_79	N, A_ASP_82	H, A_ASP_82	2.80	1.94	6.21
4F3F.PDB	O, A_GLN_38	N, A_THR_85	H, A_THR_85	2.92	2.06	3.36
4F3F.PDB	O, A_TYR_36	N, A_TYR_87	H, A_TYR_87	2.93	2.15	21.63
4F3F.PDB	O, A_LYS_93	NE2, A_GLN_90	HE22, A_GLN_90	2.99	2.13	6.87
4F3F.PDB	OE1, A_GLN_90	N, A_LYS_93	H, A_LYS_93	2.97	2.13	10.10
4F3F.PDB	OG, B_SER_59	NE2, A_HIS_94	HE2, A_HIS_94	2.82	2.03	19.68
4F3F.PDB	O, A_ILE_3	OG1, A_THR_97	HG1, A_THR_97	2.80	2.02	14.86
4F3F.PDB	O, A_CYS_88	N, A_GLY_99	H, A_GLY_99	2.99	2.20	20.16
4F3F.PDB	OE1, A_GLN_7	N, A_GLY_101	H, A_GLY_101	2.71	1.99	27.52
4F3F.PDB	O, A_TYR_86	N, A_THR_102	H, A_THR_102	2.92	2.11	15.50
4F3F.PDB	O, A_PRO_9	OG1, A_THR_102	HG1, A_THR_102	2.92	2.17	21.04
4F3F.PDB	O, A_ALA_10	N, A_LYS_103	H, A_LYS_103	2.75	1.91	11.21
4F3F.PDB	O, A_ALA_84	N, A_VAL_104	H, A_VAL_104	2.95	2.11	8.56
4F3F.PDB	O, A_MET_12	N, A_GLU_105	H, A_GLU_105	2.87	2.10	22.23
4F3F.PDB	OE1, A_GLN_166	N, A_ILE_106	H, A_ILE_106	2.99	2.18	16.49
4F3F.PDB	O, A_ALA_14	N, A_LYS_107	H, A_LYS_107	2.82	1.98	10.57
4F3F.PDB	O, A_THR_109	NE, A_ARG_108	HE, A_ARG_108	2.88	2.12	22.89
4F3F.PDB	O, A_ASP_170	NH1, A_ARG_108	HH11, A_ARG_108	2.89	2.10	20.47

4F3F.PDB	O, A_TYR_140	N, A_ALA_111	H, A_ALA_111	2.92	2.09	12.11
4F3F.PDB	O, A_LEU_135	N, A_PHE_116	H, A_PHE_116	2.90	2.08	13.90
4F3F.PDB	O, A_VAL_133	N, A_PHE_118	H, A_PHE_118	2.78	1.95	12.67
4F3F.PDB	OG, A_SER_131	NE2, A_GLN_124	HE22, A_GLN_124	2.84	2.05	19.05
4F3F.PDB	O, A_LEU_181	N, A_ALA_130	H, A_ALA_130	2.80	1.96	8.40
4F3F.PDB	O, A_LEU_179	N, A_VAL_132	H, A_VAL_132	2.96	2.17	19.13
4F3F.PDB	O, A_SER_177	N, A_CYS_134	H, A_CYS_134	2.84	2.04	17.70
4F3F.PDB	O, A_PHE_116	N, A_LEU_135	H, A_LEU_135	2.66	1.81	8.41
4F3F.PDB	O, A_LEU_175	N, A_LEU_136	H, A_LEU_136	2.88	2.03	5.32
4F3F.PDB	O, A_SER_114	N, A_ASN_137	H, A_ASN_137	2.75	1.89	4.10
4F3F.PDB	O, A_TYR_173	N, A_PHE_139	H, A_PHE_139	2.82	2.03	20.49
4F3F.PDB	O, A_ALA_111	N, A_TYR_140	H, A_TYR_140	2.95	2.18	22.48
4F3F.PDB	O, A_ALA_193	N, A_LYS_149	H, A_LYS_149	3.00	2.22	21.52
4F3F.PDB	O, A_VAL_191	N, A_ASP_151	H, A_ASP_151	2.71	1.88	11.67
4F3F.PDB	O, A_VAL_150	N, A_ALA_153	H, A_ALA_153	2.83	2.03	17.81
4F3F.PDB	O, A_TRP_148	N, A_GLN_155	H, A_GLN_155	2.92	2.17	25.11
4F3F.PDB	O, A_SER_176	N, A_SER_162	H, A_SER_162	2.98	2.24	25.07
4F3F.PDB	O, A_SER_174	N, A_THR_164	H, A_THR_164	2.92	2.10	15.13
4F3F.PDB	O, A_THR_172	N, A_ASP_167	H, A_ASP_167	2.94	2.11	11.83
4F3F.PDB	OD1, A_ASP_167	N, A_LYS_169	H, A_LYS_169	2.79	1.96	13.81
4F3F.PDB	OD1, A_ASP_170	OG1, A_THR_172	HG1, A_THR_172	2.85	2.05	10.97
4F3F.PDB	O, A_PHE_139	N, A_TYR_173	H, A_TYR_173	2.86	2.03	12.73
4F3F.PDB	O, A_SER_162	N, A_SER_176	H, A_SER_176	2.91	2.10	15.82
4F3F.PDB	O, A_CYS_134	N, A_SER_177	H, A_SER_177	2.93	2.13	19.09
4F3F.PDB	O, A_GLN_160	N, A_THR_178	H, A_THR_178	2.92	2.12	17.96
4F3F.PDB	O, A_VAL_132	N, A_LEU_179	H, A_LEU_179	2.93	2.14	19.16
4F3F.PDB	O, A_ALA_130	N, A_LEU_181	H, A_LEU_181	2.80	1.95	8.13
4F3F.PDB	O, A_SER_182	N, A_TYR_186	H, A_TYR_186	2.99	2.15	10.88
4F3F.PDB	OD1, A_ASP_151	N, A_VAL_191	H, A_VAL_191	2.94	2.11	13.49
4F3F.PDB	O, A_PHE_209	N, A_TYR_192	H, A_TYR_192	2.94	2.10	9.21
4F3F.PDB	O, A_GLN_147	N, A_GLU_195	H, A_GLU_195	2.80	1.99	16.60
4F3F.PDB	O, A_VAL_205	N, A_VAL_196	H, A_VAL_196	2.78	1.93	8.20
4F3F.PDB	ND1, A_HIS_198	N, A_GLY_200	H, A_GLY_200	2.95	2.12	12.01
4F3F.PDB	O, A_HIS_198	N, A_LEU_201	H, A_LEU_201	2.90	2.07	12.31
4F3F.PDB	O, B_TYR_94	NE2, B_GLN_6	HE22, B_GLN_6	2.92	2.11	17.10
4F3F.PDB	O, B_PRO_114	N, B_GLU_10	H, B_GLU_10	2.98	2.18	17.64
4F3F.PDB	O, B_LEU_86	N, B_GLY_15	H, B_GLY_15	2.56	1.75	16.93
4F3F.PDB	O, B_LYS_13	N, B_ALA_16	H, B_ALA_16	2.90	2.04	5.29
4F3F.PDB	O, B_LEU_83	N, B_VAL_18	H, B_VAL_18	2.95	2.18	22.39
4F3F.PDB	O, B_GLN_5	N, B_LYS_23	H, B_LYS_23	2.93	2.10	13.11
4F3F.PDB	O, B_SER_77	N, B_ALA_24	H, B_ALA_24	2.82	2.01	16.18
4F3F.PDB	O, B_GLN_3	N, B_SER_25	H, B_SER_25	3.00	2.19	16.92
4F3F.PDB	O, B_SER_28	N, B_GLY_31	H, B_GLY_31	2.71	1.95	22.79
4F3F.PDB	O, B_ALA_97	N, B_ASN_35	H, B_ASN_35	2.89	2.09	18.86
4F3F.PDB	O, B_GLY_49	N, B_TRP_36	H, B_TRP_36	3.00	2.19	17.54
4F3F.PDB	O, B_PHE_95	N, B_VAL_37	H, B_VAL_37	2.87	2.08	19.73
4F3F.PDB	O, B_GLU_46	N, B_LYS_38	H, B_LYS_38	2.87	2.05	15.48
4F3F.PDB	O, B_GLU_89	NZ, B_LYS_38	HZ1, B_LYS_38	2.93	2.08	14.15
4F3F.PDB	O, B_VAL_93	N, B_GLN_39	H, B_GLN_39	2.84	2.02	15.17
4F3F.PDB	OD1, B_ASN_35	NE1, B_TRP_47	HE1, B_TRP_47	2.99	2.19	19.59
4F3F.PDB	O, B_TRP_36	N, B_ILE_48	H, B_ILE_48	2.96	2.11	6.75
4F3F.PDB	O, B_SER_59	N, B_LEU_50	H, B_LEU_50	2.89	2.11	20.92
4F3F.PDB	O, B_MET_34	N, B_ILE_51	H, B_ILE_51	2.99	2.27	27.72
4F3F.PDB	O, B_THR_52	N, B_GLY_56	H, B_GLY_56	2.97	2.22	25.34
4F3F.PDB	OD1, B_ASN_55	N, B_ALA_57	H, B_ALA_57	2.90	2.06	10.30
4F3F.PDB	O, B_LEU_50	N, B_SER_59	H, B_SER_59	2.93	2.13	17.76
4F3F.PDB	O, B_ILE_48	N, B_ASN_61	H, B_ASN_61	2.87	2.04	12.30
4F3F.PDB	O, B_TRP_47	ND2, B_ASN_61	HD21, B_ASN_61	2.71	1.89	13.91

4F3F.PDB	O, B_ASN_61	N, B_PHE_64	H, B_PHE_64	2.78	1.97	15.06
4F3F.PDB	O, B_GLN_62	N, B_ARG_65	H, B_ARG_65	2.89	2.05	11.05
4F3F.PDB	OD2, B_ASP_90	NZ, B_LYS_67	HZ2, B_LYS_67	2.92	2.05	9.99
4F3F.PDB	O, B_PHE_64	N, B_ALA_68	H, B_ALA_68	2.96	2.20	23.34
4F3F.PDB	O, B_ASP_82	N, B_THR_69	H, B_THR_69	2.93	2.18	24.51
4F3F.PDB	O, B_THR_78	N, B_ASP_73	H, B_ASP_73	2.77	1.93	10.54
4F3F.PDB	O, B_TYR_54	NZ, B_LYS_74	HZ2, B_LYS_74	2.82	1.94	9.19
4F3F.PDB	O, B_LYS_74	N, B_SER_77	H, B_SER_77	2.92	2.08	10.24
4F3F.PDB	O, B_SER_76	OG1, B_THR_78	HG1, B_THR_78	2.88	2.12	18.89
4F3F.PDB	O, B_CYS_22	N, B_ALA_79	H, B_ALA_79	2.86	2.03	14.35
4F3F.PDB	O, B_THR_71	N, B_TYR_80	H, B_TYR_80	2.91	2.08	12.13
4F3F.PDB	O, B_ILE_20	N, B_MET_81	H, B_MET_81	2.89	2.08	15.65
4F3F.PDB	O, B_THR_69	N, B_ASP_82	H, B_ASP_82	2.91	2.07	10.66
4F3F.PDB	O, B_VAL_18	N, B_LEU_83	H, B_LEU_83	2.87	2.02	5.50
4F3F.PDB	O, B_LYS_67	N, B_LEU_84	H, B_LEU_84	2.90	2.07	12.20
4F3F.PDB	O, B_ALA_16	N, B_LEU_86	H, B_LEU_86	2.91	2.08	13.35
4F3F.PDB	OD2, B_ASP_90	N, B_THR_87	H, B_THR_87	2.74	1.92	13.61
4F3F.PDB	O, B_THR_87	N, B_ASP_90	H, B_ASP_90	2.93	2.08	9.70
4F3F.PDB	O, B_VAL_115	N, B_ALA_92	H, B_ALA_92	2.95	2.23	27.95
4F3F.PDB	O, B_THR_113	N, B_TYR_94	H, B_TYR_94	2.79	1.96	11.98
4F3F.PDB	O, B_VAL_37	N, B_PHE_95	H, B_PHE_95	2.81	2.00	16.62
4F3F.PDB	O, B_ASN_35	N, B_ALA_97	H, B_ALA_97	2.93	2.17	24.23
4F3F.PDB	O, B_TYR_108	N, B_ARG_98	H, B_ARG_98	2.77	2.02	24.77
4F3F.PDB	OD2, B_ASP_107	NH2, B_ARG_98	HH21, B_ARG_98	2.79	1.95	9.80
4F3F.PDB	O, B_GLY_105	N, B_GLY_100	H, B_GLY_100	2.89	2.13	23.94
4F3F.PDB	OE1, C_GLU_52	N, B_ASP_102	H, B_ASP_102	2.88	2.08	17.53
4F3F.PDB	O, B_GLY_103	N, B_GLY_105	H, B_GLY_105	2.80	2.09	28.59
4F3F.PDB	OH, A_TYR_36	N, B_PHE_106	H, B_PHE_106	2.71	1.88	12.56
4F3F.PDB	O, B_CYS_96	N, B_GLY_110	H, B_GLY_110	2.79	1.94	7.86
4F3F.PDB	OE1, B_GLN_6	N, B_GLY_112	H, B_GLY_112	2.83	2.12	28.70
4F3F.PDB	O, B_TYR_94	N, B_THR_113	H, B_THR_113	2.82	2.00	14.66
4F3F.PDB	O, B_SER_7	OG1, B_THR_113	HG1, B_THR_113	2.72	1.93	13.91
4F3F.PDB	O, B_ALA_92	N, B_VAL_115	H, B_VAL_115	2.81	1.96	5.43
4F3F.PDB	OG, B_SER_91	N, B_VAL_117	H, B_VAL_117	2.69	1.83	2.50
4F3F.PDB	OG, B_SER_118	N, B_ALA_120	H, B_ALA_120	2.75	2.02	26.82
4F3F.PDB	O, B_PHE_152	N, B_LYS_123	H, B_LYS_123	2.85	2.11	25.39
4F3F.PDB	O, B_LEU_147	N, B_PHE_128	H, B_PHE_128	2.79	2.01	20.40
4F3F.PDB	O, B_GLY_145	N, B_LEU_130	H, B_LEU_130	2.57	1.73	11.24
4F3F.PDB	O, B_LEU_130	N, B_GLY_145	H, B_GLY_145	2.80	2.01	19.86
4F3F.PDB	O, B_SER_186	N, B_CYS_146	H, B_CYS_146	2.73	1.98	24.62
4F3F.PDB	O, B_PHE_128	N, B_LEU_147	H, B_LEU_147	2.70	1.84	3.31
4F3F.PDB	O, B_LEU_184	N, B_VAL_148	H, B_VAL_148	2.84	2.01	12.24
4F3F.PDB	O, B_SER_126	N, B_LYS_149	H, B_LYS_149	2.81	2.00	15.44
4F3F.PDB	O, B_LYS_123	N, B_PHE_152	H, B_PHE_152	2.80	2.03	23.11
4F3F.PDB	O, B_ASN_205	N, B_THR_157	H, B_THR_157	2.70	1.85	8.13
4F3F.PDB	O, B_ILE_201	N, B_ASN_161	H, B_ASN_161	2.74	1.89	7.43
4F3F.PDB	O, B_ASN_161	N, B_ALA_164	H, B_ALA_164	2.98	2.15	14.27
4F3F.PDB	O, B_VAL_187	N, B_HIS_170	H, B_HIS_170	2.83	1.99	10.01
4F3F.PDB	OD1, A_ASN_138	NE2, B_HIS_170	HE2, B_HIS_170	2.82	2.05	21.56
4F3F.PDB	O, B_SER_185	N, B_PHE_172	H, B_PHE_172	2.99	2.14	4.25
4F3F.PDB	O, B_SER_183	N, B_VAL_175	H, B_VAL_175	2.79	1.99	18.03
4F3F.PDB	O, B_LEU_181	N, B_GLN_177	H, B_GLN_177	2.69	1.88	16.92
4F3F.PDB	OD1, B_ASP_150	NE2, B_GLN_177	HE22, B_GLN_177	2.87	2.13	25.54
4F3F.PDB	O, B_GLN_177	N, B_GLY_180	H, B_GLY_180	2.83	2.02	16.47
4F3F.PDB	O, B_TYR_151	N, B_TYR_182	H, B_TYR_182	2.87	2.02	3.69
4F3F.PDB	O, B_CYS_146	N, B_SER_186	H, B_SER_186	2.83	2.01	14.97
4F3F.PDB	O, B_HIS_170	N, B_VAL_187	H, B_VAL_187	2.77	1.93	9.44
4F3F.PDB	O, B_LEU_144	N, B_VAL_188	H, B_VAL_188	2.86	2.09	23.17

4F3F.PDB	O, B_ALA_142	N, B_VAL_190	H, B_VAL_190	2.86	2.06	18.75
4F3F.PDB	OD1, B_ASN_161	N, B_ILE_201	H, B_ILE_201	2.88	2.06	14.25
4F3F.PDB	O, B_SER_159	N, B_ASN_203	H, B_ASN_203	2.81	1.96	4.97
4F3F.PDB	O, B_VAL_213	N, B_VAL_204	H, B_VAL_204	2.70	1.90	17.22
4F3F.PDB	O, B_THR_211	N, B_HIS_206	H, B_HIS_206	2.82	2.01	16.21
4F3F.PDB	OG, B_SER_209	ND1, B_HIS_206	HD1, B_HIS_206	2.43	1.61	13.98
4F3F.PDB	O, B_PRO_153	NE2, B_HIS_206	HE2, B_HIS_206	2.65	1.82	11.74
4F3F.PDB	OE1, C_GLN_40	N, C_ILE_16	H, C_ILE_16	2.59	1.73	3.34
4F3F.PDB	OE1, C_GLU_27	N, C_LYS_24	H, C_LYS_24	2.86	2.05	15.66
4F3F.PDB	O, B_ASP_102	NZ, C_LYS_24	HZ2, C_LYS_24	2.85	2.03	18.08
4F3F.PDB	OD1, B_ASP_102	N, C_LYS_25	H, C_LYS_25	2.86	2.02	9.58
4F3F.PDB	OH, B_TYR_101	NZ, C_LYS_25	HZ3, C_LYS_25	2.87	2.11	26.18
4F3F.PDB	OH, A_TYR_32	NE1, C_TRP_26	HE1, C_TRP_26	2.97	2.17	18.16
4F3F.PDB	O, C_LYS_24	N, C_LEU_28	H, C_LEU_28	2.97	2.15	14.14
4F3F.PDB	O, C_LEU_28	N, C_CYS_31	H, C_CYS_31	2.99	2.25	25.66
4F3F.PDB	OD1, C_ASP_33	N, C_LEU_36	H, C_LEU_36	2.84	2.00	10.02
4F3F.PDB	O, C_ALA_34	N, C_ALA_38	H, C_ALA_38	2.78	1.99	18.86
4F3F.PDB	O, C_LEU_36	OG1, C_THR_39	HG1, C_THR_39	2.91	2.17	21.49
4F3F.PDB	OE2, C_GLU_15	NH2, C_ARG_43	HH21, C_ARG_43	2.88	2.04	9.30
4F3F.PDB	O, C_VAL_44	N, C_ILE_47	H, C_ILE_47	2.93	2.16	22.22
4F3F.PDB	O, C_ILE_47	N, C_PHE_49	H, C_PHE_49	2.71	1.99	27.94
4F3F.PDB	OE1, C_GLN_53	N, C_THR_50	H, C_THR_50	2.83	2.01	14.01
4F3F.PDB	O, C_TYR_23	NE2, C_GLN_53	HE21, C_GLN_53	2.91	2.11	17.04
4F3F.PDB	O, C_ILE_21	NE2, C_GLN_53	HE22, C_GLN_53	2.85	2.03	15.04
4F3F.PDB	O, C_THR_50	N, C_LEU_54	H, C_LEU_54	2.77	1.94	11.60
4F3F.PDB	O, C_TYR_51	N, C_ASP_55	H, C_ASP_55	2.90	2.12	22.28
4F3F.PDB	O, C_LEU_54	N, C_LYS_58	H, C_LYS_58	2.82	2.01	16.54
4F3F.PDB	O, C_ASP_55	N, C_HIS_59	H, C_HIS_59	2.98	2.22	24.03
4F3F.PDB	O, C_GLU_29	NZ, C_LYS_60	HZ1, C_LYS_60	2.68	1.83	14.40
4F3F.PDB	O, C_HIS_59	N, C_ASP_62	H, C_ASP_62	2.90	2.16	25.96
4F3F.PDB	O, C_HIS_59	N, C_GLU_63	H, C_GLU_63	2.98	2.18	17.58

Table 1690: 4F3F-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4JAM.PDB	O, H_SER_25	N, H_GLN_3	H, H_GLN_3	2.94	2.14	17.76
4JAM.PDB	O, H_THR_23	N, H_GLN_5	H, H_GLN_5	3.00	2.20	17.90
4JAM.PDB	O, H_THR_21	N, H_SER_7	H, H_SER_7	2.81	2.01	18.59
4JAM.PDB	O, H_VAL_82C	N, H_SER_15	H, H_SER_15	2.81	1.98	12.83
4JAM.PDB	O, H_LYS_13	N, H_GLU_16	H, H_GLU_16	3.00	2.20	18.36
4JAM.PDB	O, H_LEU_82	N, H_LEU_18	H, H_LEU_18	2.84	2.06	21.67
4JAM.PDB	O, H_LEU_80	N, H_LEU_20	H, H_LEU_20	2.89	2.05	11.57
4JAM.PDB	O, H_PHE_78	N, H_CYS_22	H, H_CYS_22	2.73	1.91	13.99
4JAM.PDB	O, H_GLN_5	N, H_THR_23	H, H_THR_23	2.84	2.01	12.14
4JAM.PDB	O, H_ASP_76	N, H_VAL_24	H, H_VAL_24	2.88	2.03	6.27
4JAM.PDB	O, H_GLN_3	N, H_SER_25	H, H_SER_25	2.95	2.17	20.66
4JAM.PDB	O, H_GLY_30	OG1, H_THR_32	HG1, H_THR_32	2.84	2.06	16.49
4JAM.PDB	O, H_LEU_95	N, H_TYR_33	H, H_TYR_33	2.76	1.93	13.12
4JAM.PDB	O, H_ILE_51	N, H_TRP_34	H, H_TRP_34	2.84	2.05	18.90
4JAM.PDB	O, H_MET_29	NE1, H_TRP_34	HE1, H_TRP_34	2.94	2.08	6.03
4JAM.PDB	O, H_ALA_93	N, H_SER_35	H, H_SER_35	2.84	2.00	9.25
4JAM.PDB	O, H_GLY_49	N, H_TRP_36	H, H_TRP_36	2.94	2.10	11.93
4JAM.PDB	O, H_PHE_91	N, H_LEU_37	H, H_LEU_37	2.84	2.01	12.67
4JAM.PDB	O, H_GLU_46	N, H_ARG_38	H, H_ARG_38	2.86	2.06	18.02
4JAM.PDB	OE2, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.93	2.10	13.53
4JAM.PDB	OH, H_TYR_90	NH1, H_ARG_38	HH11, H_ARG_38	2.92	2.12	17.99
4JAM.PDB	OD1, H_ASP_86	NH1, H_ARG_38	HH12, H_ARG_38	2.91	2.07	10.41
4JAM.PDB	O, H_VAL_89	N, H_LEU_39	H, H_LEU_39	2.84	2.08	24.06
4JAM.PDB	O, H_ARG_38	N, H_GLU_46	H, H_GLU_46	2.84	2.01	13.22
4JAM.PDB	O, H_TRP_36	N, H_ILE_48	H, H_ILE_48	2.87	2.03	11.32
4JAM.PDB	O, H_ASN_58	N, H_TYR_50	H, H_TYR_50	2.84	2.06	20.47
4JAM.PDB	O, H_TRP_34	N, H_ILE_51	H, H_ILE_51	2.88	2.15	26.94
4JAM.PDB	O, H_GLU_56	N, H_PHE_52	H, H_PHE_52	2.96	2.12	11.30
4JAM.PDB	O, H_PHE_52	N, H_GLY_55	H, H_GLY_55	2.76	1.91	7.28
4JAM.PDB	O, H_TYR_50	N, H_ASN_58	H, H_ASN_58	2.98	2.17	16.49
4JAM.PDB	O, H_ILE_48	N, H_SER_60	H, H_SER_60	2.89	2.04	4.59
4JAM.PDB	O, H_LEU_63	N, H_ARG_66	H, H_ARG_66	2.96	2.10	3.45
4JAM.PDB	O, H_ARG_82A	NH1, H_ARG_66	HH11, H_ARG_66	2.94	2.15	19.87
4JAM.PDB	OD1, H_ASP_86	NH2, H_ARG_66	HH22, H_ARG_66	2.96	2.12	9.52
4JAM.PDB	O, H_ARG_81	N, H_SER_68	H, H_SER_68	2.89	2.11	20.79
4JAM.PDB	OH, H_TYR_59	N, H_ILE_69	H, H_ILE_69	2.96	2.15	16.37
4JAM.PDB	O, H_GLN_77	N, H_ASP_72	H, H_ASP_72	2.79	1.94	5.32
4JAM.PDB	OD1, H_ASP_72	N, H_SER_74	H, H_SER_74	2.98	2.20	21.77
4JAM.PDB	OD1, H_ASP_72	N, H_GLU_75	H, H_GLU_75	2.97	2.14	12.50
4JAM.PDB	O, H_CYS_22	N, H_PHE_78	H, H_PHE_78	2.92	2.11	17.57
4JAM.PDB	O, H_SER_70	N, H_SER_79	H, H_SER_79	2.91	2.12	20.02
4JAM.PDB	O, H_LEU_20	N, H_LEU_80	H, H_LEU_80	2.92	2.08	12.05
4JAM.PDB	O, H_SER_68	N, H_ARG_81	H, H_ARG_81	2.90	2.07	12.47
4JAM.PDB	O, H_LEU_18	N, H_LEU_82	H, H_LEU_82	2.90	2.10	17.80
4JAM.PDB	O, H_ARG_66	N, H_ARG_82A	H, H_ARG_82A	2.87	2.03	10.53
4JAM.PDB	OD2, H_ASP_86	N, H_THR_83	H, H_THR_83	2.93	2.14	18.89
4JAM.PDB	O, H_THR_83	N, H_ASP_86	H, H_ASP_86	2.85	2.00	7.55
4JAM.PDB	O, H_ALA_84	N, H_THR_87	H, H_THR_87	2.98	2.13	7.55
4JAM.PDB	O, H_LEU_39	N, H_VAL_89	H, H_VAL_89	2.92	2.09	11.66
4JAM.PDB	O, H_SER_107	N, H_TYR_90	H, H_TYR_90	2.92	2.07	8.56
4JAM.PDB	O, H_LEU_37	N, H_PHE_91	H, H_PHE_91	2.79	1.93	6.64
4JAM.PDB	O, H_SER_35	N, H_ALA_93	H, H_ALA_93	2.97	2.20	22.59
4JAM.PDB	O, H_ARG_101	N, H_SER_94	H, H_SER_94	2.87	2.08	19.41
4JAM.PDB	O, H_GLY_31	N, H_ARG_97	H, H_ARG_97	2.96	2.11	7.24
4JAM.PDB	O, H_LEU_100	N, H_ALA_100C	H, H_ALA_100C	3.00	2.15	9.56
4JAM.PDB	OH, L_TYR_36	N, H_PHE_100E	H, H_PHE_100E	2.85	2.03	15.20
4JAM.PDB	O, H_SER_94	N, H_ARG_101	H, H_ARG_101	2.76	1.92	10.57

4JAM.PDB	O, H_CYS_92	N, H_GLY_104	H, H_GLY_104	2.85	2.01	11.27
4JAM.PDB	O, H_TYR_90	N, H_SER_107	H, H_SER_107	2.95	2.16	20.47
4JAM.PDB	O, H_SER_7	OG, H_SER_107	HG, H_SER_107	2.70	1.93	17.20
4JAM.PDB	O, H_ALA_88	N, H_VAL_109	H, H_VAL_109	2.86	2.01	8.44
4JAM.PDB	OG1, H_THR_87	N, H_VAL_111	H, H_VAL_111	2.96	2.11	6.95
4JAM.PDB	O, H_PHE_146	N, H_LYS_117	H, H_LYS_117	2.84	2.00	10.63
4JAM.PDB	O, H_ASP_144	NZ, H_LYS_117	HZ2, H_LYS_117	2.90	2.10	21.43
4JAM.PDB	O, H_LYS_143	N, H_SER_120	H, H_SER_120	2.96	2.16	18.52
4JAM.PDB	O, H_LEU_141	N, H_PHE_122	H, H_PHE_122	2.88	2.04	12.44
4JAM.PDB	O, H_GLY_139	N, H_LEU_124	H, H_LEU_124	2.76	1.91	9.61
4JAM.PDB	OG, H_SER_127	N, H_LYS_129	H, H_LYS_129	2.99	2.25	26.12
4JAM.PDB	O, H_VAL_184	N, H_ALA_136	H, H_ALA_136	2.89	2.08	16.20
4JAM.PDB	O, H_LEU_124	N, H_GLY_139	H, H_GLY_139	2.92	2.13	20.18
4JAM.PDB	O, H_SER_180	N, H_CYS_140	H, H_CYS_140	2.84	2.07	21.53
4JAM.PDB	O, H_PHE_122	N, H_LEU_141	H, H_LEU_141	2.77	1.93	9.15
4JAM.PDB	O, H_LEU_178	N, H_VAL_142	H, H_VAL_142	2.76	1.91	9.10
4JAM.PDB	O, H_SER_120	N, H_LYS_143	H, H_LYS_143	2.77	1.92	7.28
4JAM.PDB	OD1, H_ASP_144	NZ, H_LYS_143	HZ2, H_LYS_143	3.00	2.12	8.81
4JAM.PDB	O, H_TYR_176	N, H_TYR_145	H, H_TYR_145	2.91	2.10	17.24
4JAM.PDB	O, H_LYS_117	N, H_PHE_146	H, H_PHE_146	2.94	2.14	18.10
4JAM.PDB	O, H_ASN_197	N, H_SER_153	H, H_SER_153	2.89	2.07	14.46
4JAM.PDB	OG, H_SER_180	NE1, H_TRP_154	HE1, H_TRP_154	2.95	2.10	8.20
4JAM.PDB	O, H_ILE_195	N, H_ASN_155	H, H_ASN_155	2.94	2.10	11.47
4JAM.PDB	OD1, H_ASN_197	N, H_SER_156	H, H_SER_156	2.74	1.93	17.72
4JAM.PDB	O, H_TRP_154	N, H_GLY_157	H, H_GLY_157	2.90	2.12	19.88
4JAM.PDB	O, H_VAL_181	N, H_HIS_164	H, H_HIS_164	2.85	2.02	12.88
4JAM.PDB	OG, H_SER_180	OG1, H_THR_165	HG1, H_THR_165	2.85	2.09	18.68
4JAM.PDB	O, H_SER_179	N, H_PHE_166	H, H_PHE_166	2.96	2.10	3.06
4JAM.PDB	O, H_SER_177	N, H_VAL_169	H, H_VAL_169	2.88	2.09	20.11
4JAM.PDB	O, H_LEU_175	N, H_GLN_171	H, H_GLN_171	2.88	2.02	6.22
4JAM.PDB	O, H_GLN_171	N, H_GLY_174	H, H_GLY_174	2.89	2.04	7.16
4JAM.PDB	O, H_TYR_145	N, H_TYR_176	H, H_TYR_176	2.77	1.92	3.97
4JAM.PDB	O, H_VAL_142	N, H_LEU_178	H, H_LEU_178	2.91	2.13	21.00
4JAM.PDB	O, H_CYS_140	N, H_SER_180	H, H_SER_180	3.00	2.18	15.61
4JAM.PDB	O, H_HIS_164	N, H_VAL_181	H, H_VAL_181	2.91	2.06	7.14
4JAM.PDB	O, H_LEU_138	N, H_VAL_182	H, H_VAL_182	2.78	1.95	12.87
4JAM.PDB	O, H_GLY_162	N, H_THR_183	H, H_THR_183	2.94	2.15	19.24
4JAM.PDB	O, H_GLY_134	N, H_SER_186	H, H_SER_186	2.99	2.13	1.16
4JAM.PDB	O, H_PRO_185	N, H_SER_188	H, H_SER_188	2.94	2.11	13.31
4JAM.PDB	O, H_SER_188	N, H_GLN_192	H, H_GLN_192	2.79	1.94	7.97
4JAM.PDB	OD1, H_ASN_155	N, H_ILE_195	H, H_ILE_195	2.97	2.17	18.26
4JAM.PDB	O, H_LYS_209	N, H_CYS_196	H, H_CYS_196	2.89	2.09	19.00
4JAM.PDB	O, H_SER_153	N, H_ASN_197	H, H_ASN_197	2.82	1.97	5.10
4JAM.PDB	O, H_VAL_207	N, H_VAL_198	H, H_VAL_198	2.79	1.94	6.21
4JAM.PDB	O, H_THR_151	N, H_ASN_199	H, H_ASN_199	2.92	2.08	11.31
4JAM.PDB	O, H_THR_205	N, H_HIS_200	H, H_HIS_200	2.85	1.99	2.37
4JAM.PDB	OG, H_SER_203	ND1, H_HIS_200	HD1, H_HIS_200	2.70	1.91	20.45
4JAM.PDB	O, H_PRO_147	NE2, H_HIS_200	HE2, H_HIS_200	2.80	1.96	10.13
4JAM.PDB	O, H_LYS_201	N, H_ASN_204	H, H_ASN_204	2.95	2.12	12.20
4JAM.PDB	O, H_VAL_198	N, H_VAL_207	H, H_VAL_207	2.89	2.08	17.27
4JAM.PDB	O, H_CYS_196	N, H_LYS_209	H, H_LYS_209	2.97	2.17	17.34
4JAM.PDB	O, H_TYR_194	N, H_VAL_211	H, H_VAL_211	2.86	2.01	8.16
4JAM.PDB	O, L_TYR_86	NE2, L_GLN_6	HE22, L_GLN_6	2.86	2.03	12.40
4JAM.PDB	O, L_GLN_103	N, L_VAL_11	H, L_VAL_11	2.91	2.06	8.42
4JAM.PDB	OE1, L_GLN_17	N, L_SER_14	H, L_SER_14	2.84	2.00	10.61
4JAM.PDB	O, L_ILE_75	N, L_ALA_19	H, L_ALA_19	2.99	2.17	15.72
4JAM.PDB	O, L_LEU_73	N, L_ILE_21	H, L_ILE_21	2.83	1.99	10.81
4JAM.PDB	O, L_ALA_71	N, L_CYS_23	H, L_CYS_23	2.74	2.01	26.68

4JAM.PDB	O, L_THR_5	N, L_SER_24	H, L_SER_24	2.92	2.08	11.35
4JAM.PDB	O, L_SER_69	N, L_ALA_26	H, L_ALA_26	2.89	2.06	12.83
4JAM.PDB	OD1, H_ASN_100B	ND2, L_ASN_32	HD21, L_ASN_32	2.96	2.21	25.94
4JAM.PDB	OD1, L_ASN_51	N, L_VAL_33	H, L_VAL_33	2.88	2.05	13.33
4JAM.PDB	O, L_ILE_48	N, L_TRP_35	H, L_TRP_35	2.89	2.14	24.66
4JAM.PDB	O, L_TYR_87	N, L_TYR_36	H, L_TYR_36	2.84	2.01	12.44
4JAM.PDB	O, L_GLU_45	N, L_GLN_37	H, L_GLN_37	2.80	1.97	12.63
4JAM.PDB	OH, L_TYR_86	NE2, L_GLN_37	HE21, L_GLN_37	2.92	2.07	7.82
4JAM.PDB	O, L_ASP_85	N, L_VAL_38	H, L_VAL_38	2.71	1.87	12.07
4JAM.PDB	O, L_ILE_81	NZ, L_LYS_39	HZ3, L_LYS_39	2.71	1.89	18.99
4JAM.PDB	O, L_TRP_35	N, L_VAL_47	H, L_VAL_47	2.89	2.06	14.03
4JAM.PDB	O, L_LYS_53	N, L_PHE_49	H, L_PHE_49	2.86	2.03	12.66
4JAM.PDB	O, L_VAL_33	N, L_ASN_51	H, L_ASN_51	2.91	2.07	10.53
4JAM.PDB	O, L_GLU_50	N, L_TYR_52	H, L_TYR_52	2.89	2.17	28.38
4JAM.PDB	O, L_PHE_49	N, L_LYS_53	H, L_LYS_53	2.85	2.05	18.62
4JAM.PDB	OE1, L_GLU_50	NZ, L_LYS_53	HZ1, L_LYS_53	2.81	1.96	13.53
4JAM.PDB	OD2, L_ASP_82	NE, L_ARG_61	HE, L_ARG_61	2.81	2.02	19.36
4JAM.PDB	OD1, L_ASP_82	NH2, L_ARG_61	HH21, L_ARG_61	2.93	2.10	13.29
4JAM.PDB	O, L_THR_74	N, L_SER_63	H, L_SER_63	2.92	2.09	12.30
4JAM.PDB	O, L_ALA_26	NZ, L_LYS_66	HZ1, L_LYS_66	2.91	2.11	21.70
4JAM.PDB	O, L_GLY_68	NZ, L_LYS_66	HZ3, L_LYS_66	2.98	2.22	27.29
4JAM.PDB	O, L_CYS_23	N, L_ALA_71	H, L_ALA_71	2.82	2.01	15.87
4JAM.PDB	O, L_SER_65	N, L_THR_72	H, L_THR_72	2.77	1.93	11.94
4JAM.PDB	O, L_ILE_21	N, L_LEU_73	H, L_LEU_73	2.77	1.96	15.27
4JAM.PDB	O, L_SER_63	N, L_THR_74	H, L_THR_74	2.90	2.05	4.48
4JAM.PDB	O, L_ALA_19	N, L_ILE_75	H, L_ILE_75	2.91	2.09	14.28
4JAM.PDB	OD2, L_ASP_82	N, L_GLN_79	H, L_GLN_79	2.89	2.04	5.61
4JAM.PDB	O, L_GLN_79	N, L_ASP_82	H, L_ASP_82	2.89	2.09	18.18
4JAM.PDB	O, L_VAL_38	N, L_ASP_85	H, L_ASP_85	2.90	2.08	16.10
4JAM.PDB	O, L_THR_102	N, L_TYR_86	H, L_TYR_86	2.86	2.04	14.55
4JAM.PDB	O, L_TYR_36	N, L_TYR_87	H, L_TYR_87	2.99	2.18	17.93
4JAM.PDB	O, L_VAL_97	N, L_VAL_90	H, L_VAL_90	2.92	2.09	13.43
4JAM.PDB	O, L_THR_95A	N, L_ASP_92	H, L_ASP_92	2.92	2.16	23.57
4JAM.PDB	OD1, L_ASP_92	N, L_PHE_94	H, L_PHE_94	2.87	2.09	20.85
4JAM.PDB	OD1, L_ASP_92	N, L_SER_95	H, L_SER_95	2.87	2.05	13.98
4JAM.PDB	O, L_SER_95	N, L_PHE_96	H, L_PHE_96	2.80	2.09	28.58
4JAM.PDB	O, L_VAL_90	N, L_VAL_97	H, L_VAL_97	2.88	2.03	5.98
4JAM.PDB	O, L_CYS_88	N, L_GLY_99	H, L_GLY_99	2.82	1.99	13.21
4JAM.PDB	O, L_TYR_86	N, L_THR_102	H, L_THR_102	2.90	2.13	22.21
4JAM.PDB	O, L_PRO_7	OG1, L_THR_102	HG1, L_THR_102	2.58	1.77	7.88
4JAM.PDB	O, L_PRO_8	N, L_GLN_103	H, L_GLN_103	2.91	2.06	9.20
4JAM.PDB	O, L_ALA_84	N, L_VAL_104	H, L_VAL_104	2.83	1.97	5.25
4JAM.PDB	OE1, L_GLU_83	N, L_VAL_106	H, L_VAL_106	2.88	2.04	10.37
4JAM.PDB	O, L_VAL_13	N, L_LEU_106A	H, L_LEU_106A	2.89	2.06	12.78
4JAM.PDB	OH, L_TYR_172	NH2, L_ARG_107	HH22, L_ARG_107	2.87	2.14	27.08
4JAM.PDB	O, L_ASN_170	NE2, L_GLN_108	HE22, L_GLN_108	2.96	2.17	20.42
4JAM.PDB	OE1, L_GLU_198	NZ, L_LYS_110	HZ2, L_LYS_110	2.60	1.75	13.04
4JAM.PDB	O, L_TYR_140	N, L_ALA_111	H, L_ALA_111	2.92	2.08	10.21
4JAM.PDB	O, L_SER_137	N, L_THR_114	H, L_THR_114	2.88	2.05	12.38
4JAM.PDB	O, L_LEU_135	N, L_THR_116	H, L_THR_116	2.92	2.09	14.50
4JAM.PDB	O, L_VAL_133	N, L_PHE_118	H, L_PHE_118	2.86	2.02	11.47
4JAM.PDB	O, L_SER_122	N, L_GLN_126	H, L_GLN_126	2.95	2.16	20.22
4JAM.PDB	O, L_LEU_125	N, L_ASN_128	H, L_ASN_128	2.93	2.12	17.43
4JAM.PDB	OE2, L_GLU_124	OG1, L_THR_131	HG1, L_THR_131	2.56	1.86	25.46
4JAM.PDB	O, L_LEU_178	N, L_LEU_132	H, L_LEU_132	2.88	2.05	11.45
4JAM.PDB	O, L_SER_176	N, L_CYS_134	H, L_CYS_134	2.82	1.98	10.00
4JAM.PDB	O, L_THR_116	N, L_LEU_135	H, L_LEU_135	2.80	1.96	9.63
4JAM.PDB	O, L_ALA_174	N, L_ILE_136	H, L_ILE_136	2.86	2.07	20.07

4JAM.PDB	O, L_THR_114	N, L_SER_137	H, L_SER_137	2.99	2.19	17.72
4JAM.PDB	OE1, L_GLN_167	N, L_ASP_138	H, L_ASP_138	2.84	2.00	8.06
4JAM.PDB	O, L_ALA_111	N, L_TYR_140	H, L_TYR_140	2.99	2.16	14.54
4JAM.PDB	O, L_GLN_194	N, L_ALA_147	H, L_ALA_147	2.82	1.99	11.47
4JAM.PDB	OG, L_SER_176	NE1, L_TRP_148	HE1, L_TRP_148	2.87	2.03	8.58
4JAM.PDB	O, L_SER_192	N, L_LYS_149	H, L_LYS_149	2.97	2.15	15.62
4JAM.PDB	OE1, L_GLU_203	NZ, L_LYS_149	HZ2, L_LYS_149	2.76	1.94	19.38
4JAM.PDB	O, L_SER_153	N, L_ALA_150	H, L_ALA_150	2.77	1.99	21.36
4JAM.PDB	O, L_SER_190	N, L_ASP_151	H, L_ASP_151	2.76	1.91	6.56
4JAM.PDB	O, L_ALA_150	N, L_SER_153	H, L_SER_153	2.98	2.14	10.89
4JAM.PDB	O, L_TRP_148	N, L_VAL_155	H, L_VAL_155	2.93	2.10	14.25
4JAM.PDB	O, L_TYR_177	N, L_GLU_160	H, L_GLU_160	2.98	2.18	18.13
4JAM.PDB	O, L_SER_175	N, L_THR_162	H, L_THR_162	2.83	2.01	13.96
4JAM.PDB	O, L_ALA_173	N, L_SER_165	H, L_SER_165	2.87	2.08	18.46
4JAM.PDB	O, L_LYS_171	N, L_GLN_167	H, L_GLN_167	2.72	1.88	10.56
4JAM.PDB	OD1, L_ASN_169	N, L_LYS_171	H, L_LYS_171	2.95	2.10	8.57
4JAM.PDB	O, L_PHE_139	N, L_TYR_172	H, L_TYR_172	2.85	2.06	19.58
4JAM.PDB	O, L_SER_165	N, L_ALA_173	H, L_ALA_173	2.90	2.09	17.11
4JAM.PDB	O, L_ILE_136	N, L_ALA_174	H, L_ALA_174	2.73	1.92	17.17
4JAM.PDB	OG1, L_THR_162	N, L_SER_175	H, L_SER_175	2.85	2.04	16.03
4JAM.PDB	O, L_CYS_134	N, L_SER_176	H, L_SER_176	2.90	2.09	17.03
4JAM.PDB	O, L_GLU_160	N, L_TYR_177	H, L_TYR_177	2.83	2.06	21.58
4JAM.PDB	O, L_GLY_158	N, L_SER_179	H, L_SER_179	2.81	1.99	14.68
4JAM.PDB	OE1, L_GLN_184	N, L_THR_181	H, L_THR_181	2.99	2.16	13.42
4JAM.PDB	OG1, L_THR_181	N, L_GLN_184	H, L_GLN_184	2.98	2.15	12.48
4JAM.PDB	O, L_PRO_182	N, L_LYS_186	H, L_LYS_186	2.91	2.10	17.39
4JAM.PDB	O, L_GLN_184	ND1, L_HIS_188	HD1, L_HIS_188	2.79	1.96	11.98
4JAM.PDB	O, L_VAL_206	N, L_TYR_191	H, L_TYR_191	2.94	2.12	15.63
4JAM.PDB	O, L_LYS_149	N, L_SER_192	H, L_SER_192	2.93	2.14	19.54
4JAM.PDB	O, L_LYS_204	N, L_CYS_193	H, L_CYS_193	2.94	2.17	21.83
4JAM.PDB	O, L_ALA_147	N, L_GLN_194	H, L_GLN_194	2.78	1.94	10.07
4JAM.PDB	O, L_VAL_202	N, L_VAL_195	H, L_VAL_195	2.79	1.94	8.00
4JAM.PDB	O, L_THR_145	N, L_THR_196	H, L_THR_196	2.89	2.05	11.25
4JAM.PDB	O, L_SER_200	N, L_HIS_197	H, L_HIS_197	2.89	2.06	12.19
4JAM.PDB	O, L_PRO_141	NE2, L_HIS_197	HE2, L_HIS_197	2.88	2.09	19.08
4JAM.PDB	O, L_HIS_197	N, L_SER_200	H, L_SER_200	2.90	2.08	13.58
4JAM.PDB	O, B_THR_201	N, L_THR_201	H, L_THR_201	2.84	2.04	18.18
4JAM.PDB	O, L_VAL_195	N, L_VAL_202	H, L_VAL_202	2.85	2.05	16.95
4JAM.PDB	O, B_GLY_199	N, L_GLU_203	H, L_GLU_203	2.91	2.13	21.03
4JAM.PDB	O, L_CYS_193	N, L_LYS_204	H, L_LYS_204	2.98	2.16	14.76
4JAM.PDB	OG, L_SER_192	OG1, L_THR_205	HG1, L_THR_205	2.80	2.01	12.51
4JAM.PDB	O, L_TYR_191	N, L_VAL_206	H, L_VAL_206	2.94	2.11	11.22
4JAM.PDB	O, A_SER_25	N, A_GLN_3	H, A_GLN_3	2.94	2.10	9.95
4JAM.PDB	O, A_THR_23	N, A_GLN_5	H, A_GLN_5	2.89	2.07	13.60
4JAM.PDB	O, A_THR_21	N, A_SER_7	H, A_SER_7	2.82	2.01	14.85
4JAM.PDB	O, A_SER_110	N, A_VAL_12	H, A_VAL_12	2.99	2.19	18.50
4JAM.PDB	O, A_THR_112	N, A_SER_14	H, A_SER_14	2.90	2.06	9.18
4JAM.PDB	O, A_VAL_82C	N, A_SER_15	H, A_SER_15	2.89	2.08	16.29
4JAM.PDB	O, A_LEU_82	N, A_LEU_18	H, A_LEU_18	2.70	1.88	14.19
4JAM.PDB	O, A_LEU_80	N, A_LEU_20	H, A_LEU_20	2.81	1.98	11.56
4JAM.PDB	O, A_PHE_78	N, A_CYS_22	H, A_CYS_22	2.83	2.07	24.51
4JAM.PDB	O, A_GLN_5	N, A_THR_23	H, A_THR_23	2.83	1.99	10.35
4JAM.PDB	O, A_ASP_76	N, A_VAL_24	H, A_VAL_24	2.78	1.94	10.44
4JAM.PDB	O, A_GLN_3	N, A_SER_25	H, A_SER_25	2.88	2.06	13.90
4JAM.PDB	O, A_LEU_95	N, A_TYR_33	H, A_TYR_33	2.74	1.91	11.80
4JAM.PDB	O, A_ILE_51	N, A_TRP_34	H, A_TRP_34	2.90	2.16	25.25
4JAM.PDB	OE1, A_GLU_75	NE1, A_TRP_34	HE1, A_TRP_34	2.65	1.81	8.69
4JAM.PDB	O, A_ALA_93	N, A_SER_35	H, A_SER_35	2.81	1.97	10.90

4JAM.PDB	O, A_GLY_49	N, A_TRP_36	H, A_TRP_36	2.88	2.06	14.67
4JAM.PDB	O, A_PHE_91	N, A_LEU_37	H, A_LEU_37	2.78	1.96	15.17
4JAM.PDB	O, A_GLU_46	N, A_ARG_38	H, A_ARG_38	2.85	2.04	17.56
4JAM.PDB	OH, A_TYR_90	NH1, A_ARG_38	HH11, A_ARG_38	2.87	2.07	18.01
4JAM.PDB	OD1, A_ASP_86	NH1, A_ARG_38	HH12, A_ARG_38	2.79	1.96	13.17
4JAM.PDB	O, A_VAL_89	N, A_LEU_39	H, A_LEU_39	2.82	2.05	21.84
4JAM.PDB	OG, A_SER_40	N, A_LYS_43	H, A_LYS_43	2.68	1.90	20.68
4JAM.PDB	O, A_SER_40	N, A_GLY_44	H, A_GLY_44	2.72	2.01	28.80
4JAM.PDB	O, A_ARG_38	N, A_GLU_46	H, A_GLU_46	2.77	1.99	21.09
4JAM.PDB	O, A_TRP_36	N, A_ILE_48	H, A_ILE_48	2.90	2.07	12.30
4JAM.PDB	O, A_ASN_58	N, A_TYR_50	H, A_TYR_50	2.95	2.18	21.50
4JAM.PDB	O, A_TRP_34	N, A_ILE_51	H, A_ILE_51	2.90	2.16	25.67
4JAM.PDB	O, A_GLU_56	N, A_PHE_52	H, A_PHE_52	2.91	2.08	12.28
4JAM.PDB	O, A_PHE_52	N, A_GLY_55	H, A_GLY_55	2.79	1.95	9.90
4JAM.PDB	O, A_ILE_48	N, A_SER_60	H, A_SER_60	2.88	2.02	3.37
4JAM.PDB	O, A_SER_60	N, A_LEU_63	H, A_LEU_63	2.89	2.04	9.01
4JAM.PDB	O, A_ARG_82A	NE, A_ARG_66	HE, A_ARG_66	2.88	2.02	3.98
4JAM.PDB	OD2, A_ASP_86	NH2, A_ARG_66	HH22, A_ARG_66	2.34	1.63	27.75
4JAM.PDB	O, A_ARG_81	N, A_SER_68	H, A_SER_68	2.87	2.07	18.65
4JAM.PDB	OH, A_TYR_59	N, A_ILE_69	H, A_ILE_69	2.97	2.13	12.03
4JAM.PDB	O, A_ASP_72	N, A_GLU_75	H, A_GLU_75	2.93	2.09	9.42
4JAM.PDB	O, A_CYS_22	N, A_PHE_78	H, A_PHE_78	2.92	2.13	18.49
4JAM.PDB	O, A_SER_70	N, A_SER_79	H, A_SER_79	2.85	2.07	21.83
4JAM.PDB	O, A_LEU_20	N, A_LEU_80	H, A_LEU_80	2.84	2.00	11.63
4JAM.PDB	O, A_SER_68	N, A_ARG_81	H, A_ARG_81	2.88	2.05	14.04
4JAM.PDB	O, A_LEU_18	N, A_LEU_82	H, A_LEU_82	2.75	1.94	16.17
4JAM.PDB	O, A_ARG_66	N, A_ARG_82A	H, A_ARG_82A	2.95	2.11	11.99
4JAM.PDB	OD2, A_ASP_86	N, A_THR_83	H, A_THR_83	2.96	2.22	25.50
4JAM.PDB	O, A_THR_83	N, A_ASP_86	H, A_ASP_86	2.86	2.09	22.70
4JAM.PDB	O, A_SER_107	N, A_TYR_90	H, A_TYR_90	2.85	2.01	8.55
4JAM.PDB	O, A_LEU_37	N, A_PHE_91	H, A_PHE_91	2.75	1.90	5.20
4JAM.PDB	O, A_SER_35	N, A_ALA_93	H, A_ALA_93	2.93	2.20	27.04
4JAM.PDB	O, A_TYR_33	N, A_LEU_95	H, A_LEU_95	3.00	2.25	25.86
4JAM.PDB	O, A_GLY_31	N, A_ARG_97	H, A_ARG_97	2.91	2.06	7.51
4JAM.PDB	OH, B_TYR_36	N, A_PHE_100E	H, A_PHE_100E	2.90	2.09	16.41
4JAM.PDB	O, A_CYS_92	N, A_GLY_104	H, A_GLY_104	2.77	1.93	10.11
4JAM.PDB	O, A_TYR_90	N, A_SER_107	H, A_SER_107	2.89	2.11	20.38
4JAM.PDB	O, A_SER_7	OG, A_SER_107	HG, A_SER_107	2.54	1.76	15.69
4JAM.PDB	O, A_ALA_88	N, A_VAL_109	H, A_VAL_109	2.91	2.06	7.84
4JAM.PDB	O, A_GLY_10	N, A_SER_110	H, A_SER_110	2.93	2.15	20.41
4JAM.PDB	OG1, A_THR_87	N, A_VAL_111	H, A_VAL_111	2.97	2.12	7.94
4JAM.PDB	O, A_PHE_146	N, A_LYS_117	H, A_LYS_117	2.85	2.02	10.61
4JAM.PDB	O, A_ASP_144	NZ, A_LYS_117	HZ2, A_LYS_117	2.79	1.99	21.27
4JAM.PDB	O, A_LYS_143	N, A_SER_120	H, A_SER_120	2.98	2.15	12.51
4JAM.PDB	O, A_LEU_141	N, A_PHE_122	H, A_PHE_122	2.89	2.06	12.92
4JAM.PDB	O, A_GLY_139	N, A_LEU_124	H, A_LEU_124	2.77	1.92	5.35
4JAM.PDB	O, A_THR_131	N, A_GLY_134	H, A_GLY_134	2.80	2.06	25.22
4JAM.PDB	O, A_VAL_184	N, A_ALA_136	H, A_ALA_136	2.84	2.01	14.16
4JAM.PDB	O, A_LEU_124	N, A_GLY_139	H, A_GLY_139	2.85	2.09	22.70
4JAM.PDB	O, A_SER_180	N, A_CYS_140	H, A_CYS_140	2.87	2.09	20.45
4JAM.PDB	O, A_PHE_122	N, A_LEU_141	H, A_LEU_141	2.78	1.94	10.64
4JAM.PDB	O, A_LEU_178	N, A_VAL_142	H, A_VAL_142	2.76	1.91	7.10
4JAM.PDB	O, A_SER_120	N, A_LYS_143	H, A_LYS_143	2.81	1.96	7.64
4JAM.PDB	O, A_TYR_176	N, A_TYR_145	H, A_TYR_145	2.94	2.13	16.66
4JAM.PDB	O, A_LYS_117	N, A_PHE_146	H, A_PHE_146	2.87	2.06	16.70
4JAM.PDB	O, A_ASN_199	N, A_THR_151	H, A_THR_151	2.95	2.15	18.15
4JAM.PDB	O, A_ASN_197	N, A_SER_153	H, A_SER_153	2.87	2.06	16.36
4JAM.PDB	OG, A_SER_180	NE1, A_TRP_154	HE1, A_TRP_154	2.95	2.10	7.51

4JAM.PDB	O, A_ILE_195	N, A_ASN_155	H, A_ASN_155	2.80	1.97	12.29
4JAM.PDB	O, A_THR_193	ND2, A_ASN_155	HD22, A_ASN_155	2.86	2.05	16.16
4JAM.PDB	OD1, A_ASN_197	N, A_SER_156	H, A_SER_156	2.73	1.93	18.38
4JAM.PDB	O, A_TRP_154	N, A_GLY_157	H, A_GLY_157	2.96	2.18	20.46
4JAM.PDB	O, A_VAL_181	N, A_HIS_164	H, A_HIS_164	2.77	1.93	10.79
4JAM.PDB	O, A_SER_179	N, A_PHE_166	H, A_PHE_166	2.88	2.02	6.82
4JAM.PDB	O, A_SER_177	N, A_VAL_169	H, A_VAL_169	2.89	2.12	22.70
4JAM.PDB	O, A_LEU_175	N, A_GLN_171	H, A_GLN_171	2.93	2.09	10.51
4JAM.PDB	O, A_TYR_145	N, A_TYR_176	H, A_TYR_176	2.79	1.94	7.72
4JAM.PDB	O, A_VAL_142	N, A_LEU_178	H, A_LEU_178	2.85	2.07	20.92
4JAM.PDB	O, A_HIS_164	N, A_VAL_181	H, A_VAL_181	2.86	2.02	11.33
4JAM.PDB	O, A_LEU_138	N, A_VAL_182	H, A_VAL_182	2.71	1.88	13.50
4JAM.PDB	O, A_GLY_162	N, A_THR_183	H, A_THR_183	2.84	2.03	17.10
4JAM.PDB	O, A_ALA_136	N, A_VAL_184	H, A_VAL_184	2.93	2.09	11.23
4JAM.PDB	O, A_PRO_185	N, A_SER_188	H, A_SER_188	2.84	2.02	14.21
4JAM.PDB	O, A_SER_188	N, A_GLN_192	H, A_GLN_192	2.88	2.11	21.94
4JAM.PDB	OD1, A_ASN_155	N, A_ILE_195	H, A_ILE_195	2.80	2.00	18.20
4JAM.PDB	O, A_LYS_209	N, A_CYS_196	H, A_CYS_196	2.93	2.15	20.80
4JAM.PDB	O, A_SER_153	N, A_ASN_197	H, A_ASN_197	2.73	1.88	7.40
4JAM.PDB	OD1, A_ASP_208	ND2, A_ASN_197	HD21, A_ASN_197	2.90	2.10	17.20
4JAM.PDB	O, A_VAL_207	N, A_VAL_198	H, A_VAL_198	2.77	1.91	4.34
4JAM.PDB	O, A_THR_151	N, A_ASN_199	H, A_ASN_199	2.89	2.04	9.44
4JAM.PDB	O, A_THR_205	N, A_HIS_200	H, A_HIS_200	2.91	2.05	2.97
4JAM.PDB	OG, A_SER_203	ND1, A_HIS_200	HD1, A_HIS_200	2.74	1.92	14.00
4JAM.PDB	O, A_PRO_147	NE2, A_HIS_200	HE2, A_HIS_200	2.78	1.94	11.18
4JAM.PDB	O, A_LYS_201	N, A_ASN_204	H, A_ASN_204	2.92	2.09	11.42
4JAM.PDB	O, A_VAL_198	N, A_VAL_207	H, A_VAL_207	2.80	2.00	17.03
4JAM.PDB	O, A_TYR_194	N, A_VAL_211	H, A_VAL_211	2.81	1.96	8.45
4JAM.PDB	O, B_TYR_86	NE2, B_GLN_6	HE22, B_GLN_6	2.90	2.06	9.94
4JAM.PDB	O, B_GLN_103	N, B_VAL_11	H, B_VAL_11	2.89	2.06	12.76
4JAM.PDB	O, B_THR_105	N, B_VAL_13	H, B_VAL_13	2.98	2.16	14.79
4JAM.PDB	OE1, B_GLN_17	N, B_SER_14	H, B_SER_14	2.99	2.15	10.22
4JAM.PDB	O, B_THR_78	N, B_GLY_16	H, B_GLY_16	2.84	2.02	14.85
4JAM.PDB	O, B_ILE_75	N, B_ALA_19	H, B_ALA_19	2.87	2.07	18.88
4JAM.PDB	O, B_LEU_73	N, B_ILE_21	H, B_ILE_21	2.84	2.01	13.27
4JAM.PDB	O, B_ALA_71	N, B_CYS_23	H, B_CYS_23	2.84	2.13	29.21
4JAM.PDB	O, B_THR_5	N, B_SER_24	H, B_SER_24	2.89	2.07	16.00
4JAM.PDB	O, B_SER_69	N, B_ALA_26	H, B_ALA_26	2.97	2.15	14.49
4JAM.PDB	OD1, B_ASN_51	N, B_VAL_33	H, B_VAL_33	2.90	2.09	17.62
4JAM.PDB	O, B_ILE_48	N, B_TRP_35	H, B_TRP_35	2.87	2.06	17.28
4JAM.PDB	O, B_TYR_87	N, B_TYR_36	H, B_TYR_36	2.80	1.98	15.33
4JAM.PDB	O, B_GLU_45	N, B_GLN_37	H, B_GLN_37	2.84	2.00	10.11
4JAM.PDB	O, B_ASP_85	N, B_VAL_38	H, B_VAL_38	2.74	1.98	24.01
4JAM.PDB	O, B_TRP_35	N, B_VAL_47	H, B_VAL_47	2.91	2.08	11.41
4JAM.PDB	O, B_LYS_53	N, B_PHE_49	H, B_PHE_49	2.82	2.00	15.86
4JAM.PDB	O, B_VAL_33	N, B_ASN_51	H, B_ASN_51	2.89	2.05	8.66
4JAM.PDB	O, B_PHE_49	N, B_LYS_53	H, B_LYS_53	2.88	2.08	17.59
4JAM.PDB	OE1, B_GLU_50	NZ, B_LYS_53	HZ1, B_LYS_53	2.75	1.92	17.48
4JAM.PDB	OD2, B_ASP_82	NE, B_ARG_61	HE, B_ARG_61	2.84	2.00	9.73
4JAM.PDB	OD1, B_ASP_82	NH2, B_ARG_61	HH21, B_ARG_61	2.90	2.08	13.97
4JAM.PDB	O, B_THR_74	N, B_SER_63	H, B_SER_63	2.90	2.11	18.40
4JAM.PDB	O, B_THR_72	N, B_SER_65	H, B_SER_65	2.98	2.21	22.62
4JAM.PDB	O, B_GLY_68	NZ, B_LYS_66	HZ2, B_LYS_66	2.76	1.98	23.05
4JAM.PDB	O, B_ALA_26	NZ, B_LYS_66	HZ3, B_LYS_66	2.92	2.09	18.23
4JAM.PDB	O, B_THR_70	N, B_SER_67	H, B_SER_67	2.96	2.13	11.34
4JAM.PDB	O, B_CYS_23	N, B_ALA_71	H, B_ALA_71	2.82	1.99	11.72
4JAM.PDB	O, B_SER_65	N, B_THR_72	H, B_THR_72	2.73	1.91	13.48
4JAM.PDB	O, B_ILE_21	N, B_LEU_73	H, B_LEU_73	2.73	1.91	13.67

4JAM.PDB	O, B_SER_63	N, B_THR_74	H, B_THR_74	2.81	1.96	4.99
4JAM.PDB	O, B_ALA_19	N, B_ILE_75	H, B_ILE_75	2.81	1.98	12.21
4JAM.PDB	O, B_ARG_61	N, B_ARG_76	H, B_ARG_76	2.93	2.11	14.36
4JAM.PDB	O, B_GLN_17	OG1, B_THR_78	HG1, B_THR_78	2.80	2.08	24.26
4JAM.PDB	OD2, B_ASP_82	N, B_GLN_79	H, B_GLN_79	2.86	2.01	7.86
4JAM.PDB	O, B_GLN_79	N, B_ASP_82	H, B_ASP_82	2.76	1.93	12.45
4JAM.PDB	O, B_VAL_38	N, B_ASP_85	H, B_ASP_85	2.95	2.11	9.64
4JAM.PDB	O, B_THR_102	N, B_TYR_86	H, B_TYR_86	2.85	2.02	14.13
4JAM.PDB	O, B_TYR_36	N, B_TYR_87	H, B_TYR_87	2.90	2.10	18.08
4JAM.PDB	O, B_VAL_97	N, B_VAL_90	H, B_VAL_90	2.97	2.14	13.94
4JAM.PDB	O, B_THR_95A	N, B_ASP_92	H, B_ASP_92	2.89	2.11	20.40
4JAM.PDB	OD2, B_ASP_92	N, B_PHE_94	H, B_PHE_94	3.00	2.22	21.54
4JAM.PDB	OD2, B_ASP_92	N, B_SER_95	H, B_SER_95	2.88	2.04	10.50
4JAM.PDB	O, B_CYS_88	N, B_GLY_99	H, B_GLY_99	2.86	2.06	17.89
4JAM.PDB	O, B_TYR_86	N, B_THR_102	H, B_THR_102	2.89	2.09	19.07
4JAM.PDB	O, B_PRO_7	OG1, B_THR_102	HG1, B_THR_102	2.60	1.79	5.95
4JAM.PDB	O, B_PRO_8	N, B_GLN_103	H, B_GLN_103	2.92	2.06	5.49
4JAM.PDB	O, B_ALA_84	N, B_VAL_104	H, B_VAL_104	2.91	2.06	7.09
4JAM.PDB	O, B_VAL_11	N, B_THR_105	H, B_THR_105	2.91	2.10	16.07
4JAM.PDB	OE2, B_GLU_83	N, B_VAL_106	H, B_VAL_106	2.95	2.13	15.31
4JAM.PDB	O, B_VAL_13	N, B_LEU_106A	H, B_LEU_106A	2.82	1.99	13.48
4JAM.PDB	O, B_TYR_140	N, B_ALA_111	H, B_ALA_111	2.90	2.06	11.74
4JAM.PDB	O, B_SER_137	N, B_THR_114	H, B_THR_114	2.85	2.03	14.77
4JAM.PDB	O, B_LEU_135	N, B_THR_116	H, B_THR_116	2.92	2.10	15.29
4JAM.PDB	O, B_VAL_133	N, B_PHE_118	H, B_PHE_118	2.84	2.00	12.03
4JAM.PDB	O, B_SER_122	N, B_GLN_126	H, B_GLN_126	2.94	2.16	20.43
4JAM.PDB	O, B_LEU_125	N, B_ASN_128	H, B_ASN_128	2.88	2.08	18.55
4JAM.PDB	OE2, B_GLU_124	OG1, B_THR_131	HG1, B_THR_131	2.53	1.82	24.30
4JAM.PDB	O, B_LEU_178	N, B_LEU_132	H, B_LEU_132	2.89	2.06	12.17
4JAM.PDB	O, B_SER_176	N, B_CYS_134	H, B_CYS_134	2.78	1.93	7.29
4JAM.PDB	O, B_THR_116	N, B_LEU_135	H, B_LEU_135	2.79	1.95	9.74
4JAM.PDB	O, B_ALA_174	N, B_ILE_136	H, B_ILE_136	2.88	2.07	16.56
4JAM.PDB	O, B_THR_114	N, B_SER_137	H, B_SER_137	2.91	2.10	17.42
4JAM.PDB	OE1, B_GLN_167	N, B_ASP_138	H, B_ASP_138	2.91	2.10	16.41
4JAM.PDB	O, B_ALA_111	N, B_TYR_140	H, B_TYR_140	2.91	2.10	17.01
4JAM.PDB	O, B_PRO_141	N, B_ALA_143	H, B_ALA_143	2.99	2.27	28.43
4JAM.PDB	O, B_THR_196	N, B_THR_145	H, B_THR_145	2.96	2.12	11.72
4JAM.PDB	O, B_GLN_194	N, B_ALA_147	H, B_ALA_147	2.86	2.01	7.10
4JAM.PDB	OG, B_SER_176	NE1, B_TRP_148	HE1, B_TRP_148	2.84	1.99	9.50
4JAM.PDB	O, B_SER_192	N, B_LYS_149	H, B_LYS_149	2.91	2.11	17.98
4JAM.PDB	O, B_SER_153	N, B_ALA_150	H, B_ALA_150	2.77	1.99	21.31
4JAM.PDB	O, B_SER_190	N, B_ASP_151	H, B_ASP_151	2.80	1.95	5.68
4JAM.PDB	O, B_ALA_150	N, B_SER_153	H, B_SER_153	2.93	2.09	10.65
4JAM.PDB	O, B_TRP_148	N, B_VAL_155	H, B_VAL_155	2.88	2.08	19.02
4JAM.PDB	O, B_SER_175	N, B_THR_162	H, B_THR_162	2.91	2.09	13.86
4JAM.PDB	O, B_ALA_173	N, B_SER_165	H, B_SER_165	2.90	2.11	18.23
4JAM.PDB	O, B_LYS_171	N, B_GLN_167	H, B_GLN_167	2.72	1.89	12.32
4JAM.PDB	OD1, B_ASP_138	ND2, B_ASN_169	HD22, B_ASN_169	2.93	2.14	18.27
4JAM.PDB	O, B_GLN_167	N, B_ASN_170	H, B_ASN_170	2.86	2.04	15.66
4JAM.PDB	OD1, B_ASN_169	N, B_LYS_171	H, B_LYS_171	2.94	2.09	7.42
4JAM.PDB	O, B_PHE_139	N, B_TYR_172	H, B_TYR_172	2.86	2.05	16.14
4JAM.PDB	O, B_SER_165	N, B_ALA_173	H, B_ALA_173	2.83	2.03	18.01
4JAM.PDB	O, B_ILE_136	N, B_ALA_174	H, B_ALA_174	2.80	2.00	17.84
4JAM.PDB	OG1, B_THR_162	N, B_SER_175	H, B_SER_175	2.99	2.18	15.84
4JAM.PDB	O, B_CYS_134	N, B_SER_176	H, B_SER_176	2.83	2.04	19.01
4JAM.PDB	O, B_GLU_160	N, B_TYR_177	H, B_TYR_177	2.83	2.05	21.00
4JAM.PDB	O, B_GLY_158	N, B_SER_179	H, B_SER_179	2.85	2.02	11.54
4JAM.PDB	O, B_ALA_130	N, B_LEU_180	H, B_LEU_180	2.95	2.10	4.88

4JAM.PDB	OE1, B_GLN_184	N, B_THR_181	H, B_THR_181	2.84	2.01	11.32
4JAM.PDB	O, B_PRO_182	N, B_LYS_186	H, B_LYS_186	2.96	2.16	18.74
4JAM.PDB	O, B_GLN_184	ND1, B_HIS_188	HD1, B_HIS_188	2.78	1.95	11.73
4JAM.PDB	O, B_VAL_206	N, B_TYR_191	H, B_TYR_191	2.95	2.12	13.13
4JAM.PDB	O, B_LYS_149	N, B_SER_192	H, B_SER_192	2.94	2.14	18.61
4JAM.PDB	O, B_LYS_204	N, B_CYS_193	H, B_CYS_193	2.89	2.12	22.37
4JAM.PDB	O, B_ALA_147	N, B_GLN_194	H, B_GLN_194	2.78	1.93	7.25
4JAM.PDB	O, B_VAL_202	N, B_VAL_195	H, B_VAL_195	2.76	1.91	7.42
4JAM.PDB	O, B_THR_145	N, B_THR_196	H, B_THR_196	2.80	1.97	12.47
4JAM.PDB	O, B_SER_200	N, B_HIS_197	H, B_HIS_197	2.88	2.04	11.03
4JAM.PDB	O, B_ALA_143	ND1, B_HIS_197	HD1, B_HIS_197	2.86	2.07	19.34
4JAM.PDB	O, B_TYR_140	NE2, B_HIS_197	HE2, B_HIS_197	2.99	2.21	20.59
4JAM.PDB	O, L_THR_201	N, B_THR_201	H, B_THR_201	2.77	1.96	16.15
4JAM.PDB	O, B_VAL_195	N, B_VAL_202	H, B_VAL_202	2.88	2.09	18.94
4JAM.PDB	O, L_GLY_199	N, B_GLU_203	H, B_GLU_203	2.79	1.99	17.96
4JAM.PDB	O, B_CYS_193	N, B_LYS_204	H, B_LYS_204	2.99	2.16	13.66
4JAM.PDB	OG, B_SER_192	OG1, B_THR_205	HG1, B_THR_205	2.64	1.83	8.66
4JAM.PDB	O, B_TYR_191	N, B_VAL_206	H, B_VAL_206	2.87	2.04	12.78

Table 1691: 4JAM-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4JAN.PDB	O, G_LEU_369	OG1, G_THR_373	HG1, G_THR_373	2.74	1.94	9.78
4JAN.PDB	OD2, G_ASP_457	NE, G_ARG_469	HE, G_ARG_469	2.84	2.10	25.29
4JAN.PDB	O, H_LEU_82	N, H_LEU_18	H, H_LEU_18	2.99	2.15	11.38
4JAN.PDB	O, H_LEU_80	N, H_LEU_20	H, H_LEU_20	2.91	2.08	12.99
4JAN.PDB	O, H_PHE_78	N, H_CYS_22	H, H_CYS_22	2.95	2.11	8.83
4JAN.PDB	O, H_LEU_95	N, H_TYR_33	H, H_TYR_33	2.93	2.08	3.54
4JAN.PDB	O, H_ALA_93	N, H_SER_35	H, H_SER_35	2.92	2.06	5.78
4JAN.PDB	O, H_GLY_49	N, H_TRP_36	H, H_TRP_36	2.83	2.01	15.38
4JAN.PDB	OE1, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.76	1.94	14.56
4JAN.PDB	O, H_GLU_56	N, H_PHE_52	H, H_PHE_52	2.90	2.07	12.88
4JAN.PDB	O, H_ILE_48	N, H_SER_60	H, H_SER_60	2.96	2.18	20.49
4JAN.PDB	O, H_ARG_81	N, H_SER_68	H, H_SER_68	2.97	2.23	25.47
4JAN.PDB	O, H_SER_70	N, H_SER_79	H, H_SER_79	2.76	2.01	24.12
4JAN.PDB	O, H_SER_68	N, H_ARG_81	H, H_ARG_81	2.78	1.96	15.76
4JAN.PDB	O, H_LEU_18	N, H_LEU_82	H, H_LEU_82	2.84	2.03	16.49
4JAN.PDB	O, H_ARG_66	N, H_ARG_82A	H, H_ARG_82A	2.86	2.03	11.31
4JAN.PDB	OD2, H_ASP_86	N, H_THR_83	H, H_THR_83	2.81	2.03	20.96
4JAN.PDB	O, H_LEU_39	N, H_VAL_89	H, H_VAL_89	2.99	2.16	12.27
4JAN.PDB	O, H_LEU_37	N, H_PHE_91	H, H_PHE_91	2.53	1.78	23.52
4JAN.PDB	O, H_SER_35	N, H_ALA_93	H, H_ALA_93	3.00	2.21	20.09
4JAN.PDB	O, H_ARG_101	N, H_SER_94	H, H_SER_94	2.78	1.97	15.85
4JAN.PDB	OH, L_TYR_36	N, H_PHE_100E	H, H_PHE_100E	2.91	2.16	24.28
4JAN.PDB	O, H_GLY_10	N, H_SER_110	H, H_SER_110	2.97	2.13	11.49
4JAN.PDB	OG1, H_THR_87	N, H_VAL_111	H, H_VAL_111	2.78	1.99	19.23
4JAN.PDB	O, H_LYS_143	N, H_SER_120	H, H_SER_120	3.00	2.19	17.41
4JAN.PDB	O, H_GLY_139	N, H_LEU_124	H, H_LEU_124	2.67	1.88	19.71
4JAN.PDB	O, H_SER_180	N, H_CYS_140	H, H_CYS_140	2.89	2.12	21.89
4JAN.PDB	O, H_PHE_122	N, H_LEU_141	H, H_LEU_141	2.69	1.97	27.64
4JAN.PDB	O, H_LEU_178	N, H_VAL_142	H, H_VAL_142	2.93	2.19	25.68
4JAN.PDB	O, H_SER_120	N, H_LYS_143	H, H_LYS_143	2.88	2.07	16.97
4JAN.PDB	OG, H_SER_177	N, H_ASP_144	H, H_ASP_144	2.98	2.22	23.77
4JAN.PDB	O, H_TYR_176	N, H_TYR_145	H, H_TYR_145	2.92	2.12	17.16
4JAN.PDB	O, H_ASN_197	N, H_SER_153	H, H_SER_153	2.94	2.18	23.25
4JAN.PDB	OG, H_SER_180	NE1, H_TRP_154	HE1, H_TRP_154	2.82	2.02	18.56
4JAN.PDB	O, H_ILE_195	N, H_ASN_155	H, H_ASN_155	2.83	2.00	12.78
4JAN.PDB	OD2, B_ASP_92	OG, H_SER_156	HG, H_SER_156	2.50	1.78	23.90
4JAN.PDB	O, H_ASN_155	N, H_ALA_158	H, H_ALA_158	2.83	2.01	13.54
4JAN.PDB	O, H_VAL_181	N, H_HIS_164	H, H_HIS_164	2.84	2.13	28.95
4JAN.PDB	O, H_SER_179	N, H_PHE_166	H, H_PHE_166	2.95	2.11	10.08
4JAN.PDB	O, H_SER_177	N, H_VAL_169	H, H_VAL_169	2.63	1.81	14.24
4JAN.PDB	O, H_LEU_175	N, H_GLN_171	H, H_GLN_171	2.71	1.98	26.37
4JAN.PDB	O, H_GLN_171	N, H_GLY_174	H, H_GLY_174	2.90	2.07	12.23
4JAN.PDB	O, H_TYR_145	N, H_TYR_176	H, H_TYR_176	2.70	1.90	16.76
4JAN.PDB	O, H_TYR_176	OG, H_SER_177	HG, H_SER_177	2.89	2.11	14.84
4JAN.PDB	O, H_VAL_142	N, H_LEU_178	H, H_LEU_178	3.00	2.25	25.78
4JAN.PDB	O, H_LEU_138	N, H_VAL_182	H, H_VAL_182	2.90	2.08	14.87
4JAN.PDB	O, H_ALA_136	N, H_VAL_184	H, H_VAL_184	2.78	2.07	28.36
4JAN.PDB	OD1, H_ASN_155	N, H_ILE_195	H, H_ILE_195	2.84	2.00	11.14
4JAN.PDB	O, H_SER_153	N, H_ASN_197	H, H_ASN_197	2.60	1.74	3.05
4JAN.PDB	O, H_VAL_207	N, H_VAL_198	H, H_VAL_198	2.76	1.92	8.31
4JAN.PDB	O, H_THR_205	N, H_HIS_200	H, H_HIS_200	2.76	1.93	11.54
4JAN.PDB	OG, H_SER_203	ND1, H_HIS_200	HD1, H_HIS_200	2.81	1.96	7.87
4JAN.PDB	O, H_PRO_147	NE2, H_HIS_200	HE2, H_HIS_200	2.77	1.95	14.57
4JAN.PDB	OD1, H_ASN_199	NZ, H_LYS_201	HZ2, H_LYS_201	2.90	2.05	14.58
4JAN.PDB	O, H_LYS_201	N, H_ASN_204	H, H_ASN_204	2.80	1.95	7.81
4JAN.PDB	OE1, L_GLU_123	NZ, H_LYS_209	HZ1, H_LYS_209	2.89	2.13	26.71
4JAN.PDB	O, L_SER_24	N, L_THR_5	H, L_THR_5	2.90	2.04	2.68

4JAN.PDB	OG1, L_THR_102	NE2, L_GLN_6	HE21, L_GLN_6	2.82	2.05	22.18
4JAN.PDB	O, L_THR_5	N, L_SER_24	H, L_SER_24	2.97	2.16	17.64
4JAN.PDB	OD1, H_ASN_100B	ND2, L_ASN_32	HD21, L_ASN_32	2.76	1.91	6.44
4JAN.PDB	OD1, L_ASN_51	N, L_VAL_33	H, L_VAL_33	2.69	1.88	15.86
4JAN.PDB	O, L_ILE_48	N, L_TRP_35	H, L_TRP_35	2.76	1.98	21.52
4JAN.PDB	O, L_TYR_87	N, L_TYR_36	H, L_TYR_36	2.91	2.21	29.89
4JAN.PDB	N, L_GLU_45	N, L_GLN_37	H, L_GLN_37	2.95	2.11	10.30
4JAN.PDB	OH, L_TYR_86	NE2, L_GLN_37	HE21, L_GLN_37	2.95	2.09	6.42
4JAN.PDB	O, L_ASP_85	N, L_VAL_38	H, L_VAL_38	2.79	2.03	23.50
4JAN.PDB	O, L_LYS_53	N, L_PHE_49	H, L_PHE_49	2.88	2.09	19.26
4JAN.PDB	O, L_VAL_33	N, L_ASN_51	H, L_ASN_51	2.69	1.87	15.52
4JAN.PDB	O, L_GLU_50	N, L_TYR_52	H, L_TYR_52	2.84	2.11	27.26
4JAN.PDB	O, L_THR_70	N, L_SER_67	H, L_SER_67	3.00	2.15	8.93
4JAN.PDB	O, L_ILE_21	N, L_LEU_73	H, L_LEU_73	2.82	1.99	12.33
4JAN.PDB	O, L_THR_102	N, L_TYR_86	H, L_TYR_86	2.80	1.98	15.29
4JAN.PDB	O, L_TYR_36	N, L_TYR_87	H, L_TYR_87	2.98	2.17	16.36
4JAN.PDB	OE1, L_GLN_6	N, L_CYS_88	H, L_CYS_88	2.79	1.93	6.67
4JAN.PDB	O, L_CYS_34	N, L_GLN_89	H, L_GLN_89	2.97	2.18	19.32
4JAN.PDB	O, L_VAL_97	N, L_VAL_90	H, L_VAL_90	2.89	2.10	20.39
4JAN.PDB	OD2, L_ASP_92	N, L_PHE_94	H, L_PHE_94	2.63	1.85	20.98
4JAN.PDB	O, L_SER_95	N, L_PHE_96	H, L_PHE_96	2.69	1.97	28.39
4JAN.PDB	O, L_VAL_90	N, L_VAL_97	H, L_VAL_97	2.99	2.15	10.31
4JAN.PDB	O, L_CYS_88	N, L_GLY_99	H, L_GLY_99	2.82	2.06	23.88
4JAN.PDB	O, L_TYR_86	N, L_THR_102	H, L_THR_102	2.93	2.11	14.91
4JAN.PDB	O, L_PRO_7	OG1, L_THR_102	HG1, L_THR_102	2.82	2.04	15.16
4JAN.PDB	O, L_PRO_8	N, L_GLN_103	H, L_GLN_103	2.82	2.06	23.53
4JAN.PDB	O, L_TYR_140	N, L_ALA_111	H, L_ALA_111	2.97	2.14	13.46
4JAN.PDB	O, L_SER_137	N, L_THR_114	H, L_THR_114	2.99	2.13	3.09
4JAN.PDB	O, L_VAL_133	N, L_PHE_118	H, L_PHE_118	2.93	2.14	19.05
4JAN.PDB	O, L_LEU_125	N, L_ASN_128	H, L_ASN_128	2.78	1.96	14.81
4JAN.PDB	O, L_LEU_178	N, L_LEU_132	H, L_LEU_132	2.97	2.12	8.13
4JAN.PDB	O, L_SER_176	N, L_CYS_134	H, L_CYS_134	2.87	2.02	8.60
4JAN.PDB	O, L_THR_116	N, L_LEU_135	H, L_LEU_135	2.88	2.10	20.45
4JAN.PDB	O, L_ALA_174	N, L_ILE_136	H, L_ILE_136	2.97	2.14	12.22
4JAN.PDB	O, L_GLN_194	N, L_ALA_147	H, L_ALA_147	2.83	2.00	13.79
4JAN.PDB	OG, L_SER_176	NE1, L_TRP_148	HE1, L_TRP_148	2.88	2.04	9.05
4JAN.PDB	O, L_SER_192	N, L_LYS_149	H, L_LYS_149	2.99	2.18	15.44
4JAN.PDB	O, L_SER_153	N, L_ALA_150	H, L_ALA_150	2.78	2.08	29.85
4JAN.PDB	O, L_ALA_150	N, L_SER_153	H, L_SER_153	2.82	2.11	29.31
4JAN.PDB	O, L_TYR_177	N, L_GLU_160	H, L_GLU_160	2.87	2.05	14.31
4JAN.PDB	O, L_LYS_171	N, L_GLN_167	H, L_GLN_167	2.85	2.01	10.38
4JAN.PDB	O, L_ILE_136	N, L_ALA_174	H, L_ALA_174	2.73	1.95	20.72
4JAN.PDB	O, L_CYS_134	N, L_SER_176	H, L_SER_176	2.88	2.05	13.75
4JAN.PDB	O, L_GLU_160	N, L_TYR_177	H, L_TYR_177	2.73	1.90	14.38
4JAN.PDB	O, L_GLY_158	N, L_SER_179	H, L_SER_179	2.92	2.09	12.76
4JAN.PDB	O, L_ALA_130	N, L_LEU_180	H, L_LEU_180	2.75	1.90	5.66
4JAN.PDB	O, L_GLN_184	ND1, L_HIS_188	HD1, L_HIS_188	2.96	2.12	10.76
4JAN.PDB	OD1, L_ASP_151	N, L_ARG_189	H, L_ARG_189	3.00	2.16	11.57
4JAN.PDB	O, L_LYS_149	N, L_SER_192	H, L_SER_192	2.84	2.11	26.53
4JAN.PDB	O, L_LYS_204	N, L_CYS_193	H, L_CYS_193	2.87	2.03	10.09
4JAN.PDB	O, L_ALA_147	N, L_GLN_194	H, L_GLN_194	2.87	2.02	4.62
4JAN.PDB	O, L_VAL_202	N, L_VAL_195	H, L_VAL_195	2.90	2.06	10.52
4JAN.PDB	O, L_THR_145	N, L_THR_196	H, L_THR_196	2.87	2.04	12.50
4JAN.PDB	O, L_SER_200	N, L_HIS_197	H, L_HIS_197	2.86	2.00	3.42
4JAN.PDB	O, L_ASP_368	OG1, L_THR_372	HG1, L_THR_372	2.92	2.17	20.42
4JAN.PDB	O, A_THR_21	N, A_SER_7	H, A_SER_7	2.83	1.99	9.81
4JAN.PDB	O, A_THR_112	N, A_SER_14	H, A_SER_14	2.81	2.04	22.68
4JAN.PDB	O, A_LEU_80	N, A_LEU_20	H, A_LEU_20	2.96	2.16	17.44

4JAN.PDB	O, A_PHE_78	N, A_CYS_22	H, A_CYS_22	2.83	1.97	0.81
4JAN.PDB	O, A_GLN_5	N, A_THR_23	H, A_THR_23	2.99	2.16	14.12
4JAN.PDB	O, A_GLN_3	N, A_SER_25	H, A_SER_25	2.86	2.06	18.82
4JAN.PDB	O, A_LEU_95	N, A_TYR_33	H, A_TYR_33	2.88	2.02	1.62
4JAN.PDB	O, A_ILE_51	N, A_TRP_34	H, A_TRP_34	2.83	2.04	18.86
4JAN.PDB	O, A_MET_29	NE1, A_TRP_34	HE1, A_TRP_34	2.96	2.14	15.47
4JAN.PDB	O, A_ALA_93	N, A_SER_35	H, A_SER_35	2.87	2.01	0.65
4JAN.PDB	O, A_GLY_49	N, A_TRP_36	H, A_TRP_36	2.82	2.06	23.18
4JAN.PDB	O, A_GLY_44	N, A_SER_40	H, A_SER_40	2.94	2.14	17.50
4JAN.PDB	O, A_ARG_38	N, A_GLU_46	H, A_GLU_46	2.99	2.17	14.48
4JAN.PDB	O, A_TRP_36	N, A_ILE_48	H, A_ILE_48	2.86	2.04	16.32
4JAN.PDB	O, A_GLU_56	N, A_PHE_52	H, A_PHE_52	2.98	2.16	16.12
4JAN.PDB	O, A_ILE_48	N, A_SER_60	H, A_SER_60	2.99	2.18	16.95
4JAN.PDB	O, A_SER_60	N, A_LEU_63	H, A_LEU_63	2.80	1.99	16.81
4JAN.PDB	O, A_SER_68	N, A_ARG_81	H, A_ARG_81	2.93	2.10	13.34
4JAN.PDB	O, A_LEU_18	N, A_LEU_82	H, A_LEU_82	2.69	1.85	10.39
4JAN.PDB	O, A_GLU_16	N, A_VAL_82C	H, A_VAL_82C	3.00	2.21	20.36
4JAN.PDB	OD2, A_ASP_86	N, A_THR_83	H, A_THR_83	2.88	2.09	19.27
4JAN.PDB	O, A_THR_83	N, A_ASP_86	H, A_ASP_86	2.91	2.07	9.93
4JAN.PDB	O, A_SER_107	N, A_TYR_90	H, A_TYR_90	2.97	2.13	10.15
4JAN.PDB	O, A_LEU_37	N, A_PHE_91	H, A_PHE_91	2.69	1.88	17.21
4JAN.PDB	O, A_ARG_101	N, A_SER_94	H, A_SER_94	2.99	2.21	21.56
4JAN.PDB	OH, B_TYR_36	N, A_PHE_100E	H, A_PHE_100E	2.74	1.90	10.14
4JAN.PDB	OE1, A_GLU_6	N, A_GLY_106	H, A_GLY_106	2.61	1.75	6.59
4JAN.PDB	O, A_TYR_90	N, A_SER_107	H, A_SER_107	2.97	2.13	8.67
4JAN.PDB	O, A_ALA_88	N, A_VAL_109	H, A_VAL_109	2.99	2.18	17.96
4JAN.PDB	O, A_PHE_146	N, A_LYS_117	H, A_LYS_117	2.69	1.91	19.93
4JAN.PDB	O, A_LYS_143	N, A_SER_120	H, A_SER_120	2.98	2.15	12.62
4JAN.PDB	O, A_GLY_139	N, A_LEU_124	H, A_LEU_124	2.71	1.91	18.55
4JAN.PDB	O, A_SER_180	N, A_CYS_140	H, A_CYS_140	2.65	1.92	25.79
4JAN.PDB	O, A_PHE_122	N, A_LEU_141	H, A_LEU_141	2.77	1.98	18.97
4JAN.PDB	O, A_SER_120	N, A_LYS_143	H, A_LYS_143	2.80	1.94	2.87
4JAN.PDB	OG, A_SER_177	N, A_ASP_144	H, A_ASP_144	2.90	2.06	12.00
4JAN.PDB	O, A_LYS_117	N, A_PHE_146	H, A_PHE_146	2.99	2.19	18.95
4JAN.PDB	OG, A_SER_180	NE1, A_TRP_154	HE1, A_TRP_154	2.82	2.05	22.21
4JAN.PDB	O, A_ILE_195	N, A_ASN_155	H, A_ASN_155	2.74	1.91	12.38
4JAN.PDB	O, A_ASN_155	N, A_ALA_158	H, A_ALA_158	2.86	2.02	8.83
4JAN.PDB	O, A_THR_160	N, A_VAL_163	H, A_VAL_163	2.86	2.07	19.66
4JAN.PDB	O, A_VAL_181	N, A_HIS_164	H, A_HIS_164	2.90	2.04	3.65
4JAN.PDB	O, A_SER_177	N, A_VAL_169	H, A_VAL_169	2.73	1.92	17.07
4JAN.PDB	O, A_LEU_175	N, A_GLN_171	H, A_GLN_171	2.97	2.21	23.74
4JAN.PDB	O, A_TYR_145	N, A_TYR_176	H, A_TYR_176	2.83	2.03	16.73
4JAN.PDB	O, A_HIS_164	N, A_VAL_181	H, A_VAL_181	2.91	2.06	6.75
4JAN.PDB	O, A_LEU_138	N, A_VAL_182	H, A_VAL_182	2.71	1.89	15.22
4JAN.PDB	O, A_GLY_162	N, A_THR_183	H, A_THR_183	2.93	2.11	13.23
4JAN.PDB	O, A_SER_153	N, A_ASN_197	H, A_ASN_197	2.67	1.82	8.22
4JAN.PDB	O, A_VAL_207	N, A_VAL_198	H, A_VAL_198	2.88	2.07	16.65
4JAN.PDB	O, A_THR_205	N, A_HIS_200	H, A_HIS_200	2.71	1.87	10.96
4JAN.PDB	O, A_PRO_147	NE2, A_HIS_200	HE2, A_HIS_200	2.55	1.74	15.97
4JAN.PDB	O, A_LYS_201	N, A_ASN_204	H, A_ASN_204	2.88	2.07	15.76
4JAN.PDB	OG, B_SER_100	N, B_GLN_6	H, B_GLN_6	3.00	2.16	10.47
4JAN.PDB	O, B_TYR_86	NE2, B_GLN_6	HE22, B_GLN_6	2.99	2.19	18.54
4JAN.PDB	O, B_LEU_73	N, B_ILE_21	H, B_ILE_21	2.96	2.14	15.25
4JAN.PDB	O, B_SER_69	N, B_GLY_25	H, B_GLY_25	2.72	1.94	20.09
4JAN.PDB	O, I_GLY_458	ND2, B_ASN_32	HD22, B_ASN_32	2.86	2.11	24.85
4JAN.PDB	OD1, B_ASN_51	N, B_VAL_33	H, B_VAL_33	2.78	2.02	23.53
4JAN.PDB	O, B_ILE_48	N, B_TRP_35	H, B_TRP_35	2.62	1.79	12.25
4JAN.PDB	O, B_TYR_87	N, B_TYR_36	H, B_TYR_36	2.76	1.97	19.04

4JAN.PDB	O, B_GLU_45	N, B_GLN_37	H, B_GLN_37	2.98	2.12	6.36
4JAN.PDB	O, B_LYS_39	N, B_GLN_42	H, B_GLN_42	2.91	2.08	12.48
4JAN.PDB	O, B_GLN_37	N, B_GLU_45	H, B_GLU_45	2.95	2.21	25.79
4JAN.PDB	O, B_LYS_53	N, B_PHE_49	H, B_PHE_49	2.84	2.05	19.11
4JAN.PDB	O, B_VAL_33	N, B_ASN_51	H, B_ASN_51	2.74	1.89	7.92
4JAN.PDB	O, B_GLU_50	N, B_TYR_52	H, B_TYR_52	2.69	1.94	24.45
4JAN.PDB	O, B_ILE_58	NH1, B_ARG_54	HH11, B_ARG_54	2.92	2.17	24.41
4JAN.PDB	O, B_SER_65	N, B_THR_72	H, B_THR_72	2.86	2.07	20.13
4JAN.PDB	O, B_ILE_21	N, B_LEU_73	H, B_LEU_73	2.97	2.14	12.90
4JAN.PDB	O, B_SER_63	N, B_THR_74	H, B_THR_74	2.68	1.89	18.45
4JAN.PDB	O, B_ALA_19	N, B_ILE_75	H, B_ILE_75	2.83	1.99	8.89
4JAN.PDB	OD2, B_ASP_82	N, B_GLN_79	H, B_GLN_79	2.99	2.13	4.57
4JAN.PDB	O, B_GLY_77	NE2, B_GLN_79	HE21, B_GLN_79	2.96	2.14	15.90
4JAN.PDB	O, B_GLN_79	N, B_ASP_82	H, B_ASP_82	2.87	2.03	10.85
4JAN.PDB	O, B_THR_102	N, B_TYR_86	H, B_TYR_86	2.79	1.98	17.36
4JAN.PDB	O, B_TYR_36	N, B_TYR_87	H, B_TYR_87	2.95	2.16	19.18
4JAN.PDB	OE1, B_GLN_6	N, B_CYS_88	H, B_CYS_88	2.99	2.13	6.44
4JAN.PDB	O, B_VAL_97	N, B_VAL_90	H, B_VAL_90	2.92	2.10	15.26
4JAN.PDB	O, B_THR_95A	N, B_ASP_92	H, B_ASP_92	2.97	2.19	21.06
4JAN.PDB	OD1, B_ASP_92	N, B_SER_95	H, B_SER_95	2.95	2.11	10.76
4JAN.PDB	O, B_CYS_88	N, B_GLY_99	H, B_GLY_99	2.83	2.06	22.19
4JAN.PDB	O, B_PRO_7	OG1, B_THR_102	HG1, B_THR_102	2.80	2.02	16.54
4JAN.PDB	O, B_ALA_84	N, B_VAL_104	H, B_VAL_104	2.98	2.27	29.44
4JAN.PDB	O, B_SER_137	N, B_THR_114	H, B_THR_114	2.85	2.04	16.89
4JAN.PDB	O, B_LEU_135	N, B_THR_116	H, B_THR_116	2.95	2.14	16.39
4JAN.PDB	O, B_VAL_133	N, B_PHE_118	H, B_PHE_118	2.86	2.07	20.55
4JAN.PDB	O, B_LEU_125	N, B_ASN_128	H, B_ASN_128	2.72	1.91	16.63
4JAN.PDB	O, B_GLU_124	N, B_LYS_129	H, B_LYS_129	2.87	2.08	18.91
4JAN.PDB	OE2, B_GLU_124	OG1, B_THR_131	HG1, B_THR_131	2.64	1.97	29.01
4JAN.PDB	O, B_THR_116	N, B_LEU_135	H, B_LEU_135	2.75	1.97	21.41
4JAN.PDB	O, B_ALA_174	N, B_ILE_136	H, B_ILE_136	2.78	1.97	16.45
4JAN.PDB	OG, B_SER_176	NE1, B_TRP_148	HE1, B_TRP_148	2.83	1.98	7.29
4JAN.PDB	O, B_SER_192	N, B_LYS_149	H, B_LYS_149	2.90	2.11	19.36
4JAN.PDB	O, B_SER_190	N, B_ASP_151	H, B_ASP_151	2.88	2.10	21.97
4JAN.PDB	O, B_TRP_148	N, B_VAL_155	H, B_VAL_155	2.98	2.17	15.79
4JAN.PDB	O, B_SER_175	N, B_THR_162	H, B_THR_162	2.94	2.10	11.27
4JAN.PDB	O, B_ALA_173	N, B_SER_165	H, B_SER_165	2.74	1.89	5.66
4JAN.PDB	O, B_SER_165	N, B_ALA_173	H, B_ALA_173	2.84	2.14	29.64
4JAN.PDB	O, B_ILE_136	N, B_ALA_174	H, B_ALA_174	2.68	1.83	6.81
4JAN.PDB	OG1, B_THR_162	N, B_SER_175	H, B_SER_175	2.88	2.10	20.76
4JAN.PDB	O, B_CYS_134	N, B_SER_176	H, B_SER_176	2.98	2.17	16.97
4JAN.PDB	O, B_GLU_160	N, B_TYR_177	H, B_TYR_177	2.73	1.89	11.82
4JAN.PDB	O, B_GLY_158	N, B_SER_179	H, B_SER_179	2.67	1.83	10.89
4JAN.PDB	O, B_ALA_130	N, B_LEU_180	H, B_LEU_180	2.91	2.07	11.05
4JAN.PDB	O, B_GLN_184	ND1, B_HIS_188	HD1, B_HIS_188	2.88	2.12	24.08
4JAN.PDB	O, B_VAL_206	N, B_TYR_191	H, B_TYR_191	2.91	2.11	18.32
4JAN.PDB	O, B_LYS_149	N, B_SER_192	H, B_SER_192	2.92	2.08	10.84
4JAN.PDB	O, B_LYS_204	N, B_CYS_193	H, B_CYS_193	2.89	2.08	17.27
4JAN.PDB	O, B_THR_145	N, B_THR_196	H, B_THR_196	2.81	1.98	12.47
4JAN.PDB	O, B_TYR_191	N, B_VAL_206	H, B_VAL_206	2.97	2.16	15.65

Table 1692: 4JAN-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4KRM.PDB	OG1, A_THR_339	N, A_LYS_311	H, A_LYS_311	2.92	2.20	28.58
4KRM.PDB	O, A_SER_340	N, A_CYS_313	H, A_CYS_313	2.94	2.14	18.43
4KRM.PDB	O, A_PHE_321	N, A_GLY_317	H, A_GLY_317	2.69	1.98	27.87
4KRM.PDB	O, A_ILE_318	N, A_PHE_321	H, A_PHE_321	2.88	2.03	7.40
4KRM.PDB	O, A_ILE_327	OG, A_SER_326	HG, A_SER_326	2.93	2.13	14.37
4KRM.PDB	O, A_HIS_346	N, A_ILE_327	H, A_ILE_327	2.90	2.07	14.21
4KRM.PDB	OD1, A_ASN_331	N, A_ASN_328	H, A_ASN_328	2.99	2.15	12.11
4KRM.PDB	OD1, A_ASN_328	N, A_ASN_331	H, A_ASN_331	2.99	2.22	23.18
4KRM.PDB	O, A_ASN_328	N, A_ILE_332	H, A_ILE_332	2.91	2.20	29.98
4KRM.PDB	O, A_LYS_311	N, A_THR_339	H, A_THR_339	2.88	2.02	6.29
4KRM.PDB	O, A_GLU_376	N, A_ILE_341	H, A_ILE_341	2.94	2.11	11.47
4KRM.PDB	O, A_CYS_313	N, A_SER_342	H, A_SER_342	2.76	1.95	16.34
4KRM.PDB	O, A_LEU_382	N, A_ILE_347	H, A_ILE_347	2.79	1.99	18.25
4KRM.PDB	OG, A_SER_326	N, A_LEU_348	H, A_LEU_348	2.83	2.02	16.65
4KRM.PDB	OE1, B_GLU_110	NH1, A_ARG_353	HH11, A_ARG_353	2.81	2.05	22.81
4KRM.PDB	O, B_GLU_110	NH1, A_ARG_353	HH12, A_ARG_353	2.55	1.85	29.89
4KRM.PDB	O, B_ALA_100	NH2, A_ARG_353	HH21, A_ARG_353	2.89	2.04	4.33
4KRM.PDB	O, A_THR_360	N, A_ASP_355	H, A_ASP_355	2.66	1.81	5.35
4KRM.PDB	OD2, A_ASP_355	OG1, A_THR_358	HG1, A_THR_358	2.65	1.94	26.40
4KRM.PDB	O, A_SER_356	N, A_HIS_359	H, A_HIS_359	2.84	2.01	13.45
4KRM.PDB	O, A_ASP_355	N, A_THR_360	H, A_THR_360	2.91	2.05	3.38
4KRM.PDB	O, A_ALA_351	N, A_LEU_363	H, A_LEU_363	2.79	2.01	20.09
4KRM.PDB	O, A_LEU_368	N, A_LEU_371	H, A_LEU_371	2.89	2.04	5.32
4KRM.PDB	O, A_CYS_338	OG1, A_THR_373	HG1, A_THR_373	2.68	1.93	22.17
4KRM.PDB	O, A_LEU_371	N, A_VAL_374	H, A_VAL_374	2.85	2.00	7.81
4KRM.PDB	O, A_THR_339	N, A_LYS_375	H, A_LYS_375	2.66	1.83	11.99
4KRM.PDB	O, A_ILE_401	N, A_ILE_377	H, A_ILE_377	2.94	2.18	24.17
4KRM.PDB	OD1, A_ASP_344	N, A_PHE_380	H, A_PHE_380	2.98	2.20	21.02
4KRM.PDB	O, A_SER_413	N, A_LEU_381	H, A_LEU_381	2.78	1.97	16.41
4KRM.PDB	O, A_LEU_345	N, A_LEU_382	H, A_LEU_382	2.88	2.02	4.02
4KRM.PDB	O, A_ALA_415	N, A_ILE_383	H, A_ILE_383	2.77	1.92	6.18
4KRM.PDB	O, A_ILE_347	N, A_GLN_384	H, A_GLN_384	2.86	2.00	5.29
4KRM.PDB	O, B_ASP_112	NE2, A_GLN_384	HE22, A_GLN_384	2.93	2.19	25.19
4KRM.PDB	O, A_ASP_392	NE1, A_TRP_386	HE1, A_TRP_386	2.99	2.28	29.76
4KRM.PDB	O, A_LEU_424	N, A_LEU_393	H, A_LEU_393	2.91	2.10	16.43
4KRM.PDB	O, A_LEU_393	N, A_PHE_396	H, A_PHE_396	2.71	1.87	10.13
4KRM.PDB	O, A_HIS_394	N, A_GLU_397	H, A_GLU_397	2.91	2.12	20.07
4KRM.PDB	O, A_LYS_372	ND2, A_ASN_398	HD22, A_ASN_398	2.93	2.13	18.65
4KRM.PDB	O, A_LYS_375	N, A_GLU_400	H, A_GLU_400	2.70	1.87	10.88
4KRM.PDB	O, A_ILE_377	N, A_ARG_403	H, A_ARG_403	2.78	1.94	11.49
4KRM.PDB	OE1, A_GLU_376	NE, A_ARG_403	HE, A_ARG_403	2.51	1.78	27.17
4KRM.PDB	O, A_THR_378	N, A_ARG_405	H, A_ARG_405	2.85	2.00	9.02
4KRM.PDB	OD1, A_ASP_434	NZ, A_LYS_407	HZ1, A_LYS_407	2.92	2.12	20.92
4KRM.PDB	O, A_PHE_412	N, A_GLN_408	H, A_GLN_408	2.63	1.80	13.69
4KRM.PDB	O, A_GLN_408	N, A_GLN_411	H, A_GLN_411	2.82	1.96	5.62
4KRM.PDB	O, A_GLN_408	N, A_PHE_412	H, A_PHE_412	2.94	2.09	8.70
4KRM.PDB	O, A_ASP_436	N, A_SER_413	H, A_SER_413	2.93	2.11	15.55
4KRM.PDB	O, A_LEU_381	N, A_ALA_415	H, A_ALA_415	2.80	1.97	12.88
4KRM.PDB	O, A_ILE_438	N, A_VAL_416	H, A_VAL_416	2.99	2.16	12.80
4KRM.PDB	O, A_ILE_383	N, A_VAL_417	H, A_VAL_417	2.95	2.13	13.97
4KRM.PDB	OD1, A_ASN_442	N, A_LEU_419	H, A_LEU_419	2.76	1.92	9.88
4KRM.PDB	O, A_THR_391	N, A_THR_422	H, A_THR_422	2.81	2.00	16.60
4KRM.PDB	O, A_GLU_400	N, A_LYS_430	H, A_LYS_430	2.90	2.04	3.76
4KRM.PDB	O, A_LEU_456	N, A_ILE_432	H, A_ILE_432	2.57	1.76	16.64
4KRM.PDB	O, A_ILE_402	N, A_SER_433	H, A_SER_433	2.90	2.16	25.97
4KRM.PDB	OE2, A_GLU_431	OG, A_SER_433	HG, A_SER_433	2.82	2.09	25.22
4KRM.PDB	O, A_GLN_411	N, A_ASP_436	H, A_ASP_436	2.93	2.08	7.26

4KRM.PDB	O, A_LYS_465	N, A_ILE_439	H, A_ILE_439	2.96	2.14	14.27
4KRM.PDB	O, A_ASN_442	N, A_LEU_445	H, A_LEU_445	2.98	2.12	2.89
4KRM.PDB	O, A_THR_422	N, A_CYS_446	H, A_CYS_446	2.97	2.11	5.38
4KRM.PDB	O, A_TYR_447	OG1, A_THR_450	HG1, A_THR_450	2.75	1.92	8.55
4KRM.PDB	O, A_TRP_453	N, A_LEU_456	H, A_LEU_456	2.93	2.12	17.80
4KRM.PDB	OE1, A_GLN_462	N, A_GLY_458	H, A_GLY_458	2.69	1.84	7.86
4KRM.PDB	OE1, A_GLN_462	N, A_THR_459	H, A_THR_459	2.99	2.16	12.73
4KRM.PDB	O, A_GLY_435	NE2, A_GLN_462	HE21, A_GLN_462	2.63	1.77	3.27
4KRM.PDB	OD1, A_ASP_436	N, A_LYS_463	H, A_LYS_463	2.91	2.06	8.47
4KRM.PDB	O, A_VAL_437	N, A_LYS_465	H, A_LYS_465	2.78	2.01	22.88
4KRM.PDB	O, A_ILE_439	ND2, A_ASN_469	HD21, A_ASN_469	2.85	2.08	21.76
4KRM.PDB	O, A_GLY_471	N, A_CYS_475	H, A_CYS_475	2.79	2.04	24.90
4KRM.PDB	O, A_GLU_472	N, A_LYS_476	H, A_LYS_476	2.77	1.94	13.13
4KRM.PDB	O, A_ASN_473	N, A_ALA_477	H, A_ALA_477	2.66	1.88	21.43
4KRM.PDB	O, A_HIS_483	N, A_CYS_486	H, A_CYS_486	2.87	2.03	10.18
4KRM.PDB	O, A_SER_501	N, A_SER_487	H, A_SER_487	2.90	2.07	12.52
4KRM.PDB	OG, A_SER_487	N, A_GLU_489	H, A_GLU_489	2.96	2.14	13.27
4KRM.PDB	OG1, A_THR_450	N, A_CYS_491	H, A_CYS_491	2.91	2.10	16.18
4KRM.PDB	O, A_ASP_498	N, A_TRP_492	H, A_TRP_492	2.86	2.05	15.11
4KRM.PDB	O, A_GLU_495	N, A_ASP_498	H, A_ASP_498	2.80	2.03	22.83
4KRM.PDB	O, A_LEU_485	N, A_ARG_503	H, A_ARG_503	2.76	1.90	4.21
4KRM.PDB	O, B_SER_25	N, B_LYS_3	H, B_LYS_3	2.91	2.07	11.33
4KRM.PDB	O, B_ALA_23	N, B_GLU_5	H, B_GLU_5	2.96	2.22	26.70
4KRM.PDB	O, B_THR_21	N, B_SER_7	H, B_SER_7	2.88	2.10	21.31
4KRM.PDB	O, B_THR_121	N, B_VAL_12	H, B_VAL_12	2.77	2.07	29.25
4KRM.PDB	O, B_SER_123	N, B_THR_14	H, B_THR_14	2.68	1.96	28.32
4KRM.PDB	O, B_SER_123	OG1, B_THR_14	HG1, B_THR_14	2.82	1.99	5.72
4KRM.PDB	O, B_LEU_86	N, B_GLY_15	H, B_GLY_15	2.91	2.05	5.95
4KRM.PDB	O, B_GLN_13	N, B_GLY_16	H, B_GLY_16	2.98	2.16	15.73
4KRM.PDB	O, B_MET_83	N, B_LEU_18	H, B_LEU_18	2.71	1.92	20.37
4KRM.PDB	OD1, B_ASP_80	NE, B_ARG_19	HE, B_ARG_19	2.67	1.85	15.03
4KRM.PDB	O, B_SER_7	N, B_THR_21	H, B_THR_21	2.89	2.05	10.43
4KRM.PDB	O, B_VAL_79	N, B_CYS_22	H, B_CYS_22	2.79	2.06	26.42
4KRM.PDB	O, B_GLU_5	N, B_ALA_23	H, B_ALA_23	2.89	2.05	11.71
4KRM.PDB	O, B_LYS_3	N, B_SER_25	H, B_SER_25	2.88	2.12	23.79
4KRM.PDB	O, B_SER_31	NH2, B_ARG_30	HH21, B_ARG_30	2.67	1.86	15.52
4KRM.PDB	O, B_ILE_51	N, B_MET_34	H, B_MET_34	2.89	2.11	20.74
4KRM.PDB	O, B_ALA_97	N, B_GLY_35	H, B_GLY_35	2.89	2.06	13.98
4KRM.PDB	O, B_SER_49	N, B_TRP_36	H, B_TRP_36	2.64	1.81	13.98
4KRM.PDB	O, B_TYR_95	N, B_PHE_37	H, B_PHE_37	2.76	1.91	6.76
4KRM.PDB	O, B_GLU_46	N, B_ARG_38	H, B_ARG_38	2.99	2.20	20.36
4KRM.PDB	OH, B_TYR_94	NH1, B_ARG_38	HH11, B_ARG_38	2.87	2.05	14.24
4KRM.PDB	OD2, B_ASP_90	NH1, B_ARG_38	HH12, B_ARG_38	2.85	2.02	12.95
4KRM.PDB	O, B_ILE_93	N, B_GLN_39	H, B_GLN_39	2.92	2.13	20.36
4KRM.PDB	O, B_ARG_38	N, B_GLU_46	H, B_GLU_46	2.95	2.11	11.02
4KRM.PDB	O, B_TRP_36	N, B_VAL_48	H, B_VAL_48	2.79	1.99	17.02
4KRM.PDB	O, B_GLY_59	OG, B_SER_49	HG, B_SER_49	3.00	2.27	25.42
4KRM.PDB	O, B_GLY_59	N, B_GLY_50	H, B_GLY_50	2.98	2.19	19.85
4KRM.PDB	O, B_MET_34	N, B_ILE_51	H, B_ILE_51	2.75	1.95	18.18
4KRM.PDB	O, B_SER_57	N, B_SER_52	H, B_SER_52	2.88	2.11	21.64
4KRM.PDB	O, B_SER_102	N, B_TRP_53	H, B_TRP_53	2.88	2.06	15.16
4KRM.PDB	O, C_LYS_310	N, B_THR_58	H, B_THR_58	2.99	2.17	13.91
4KRM.PDB	O, B_GLY_50	N, B_GLY_59	H, B_GLY_59	2.89	2.09	18.08
4KRM.PDB	O, C_GLU_308	N, B_TYR_60	H, B_TYR_60	2.75	1.96	19.67
4KRM.PDB	O, B_VAL_48	N, B_ALA_61	H, B_ALA_61	2.97	2.14	11.48
4KRM.PDB	O, B_GLN_82	N, B_THR_69	H, B_THR_69	2.86	2.07	20.15
4KRM.PDB	OH, B_TYR_60	N, B_ILE_70	H, B_ILE_70	2.77	1.93	11.16
4KRM.PDB	O, B_TYR_32	NH1, B_ARG_72	HH12, B_ARG_72	2.74	1.92	15.98

4KRM.PDB	O, B_THR_78	N, B_ASP_73	H, B_ASP_73	2.94	2.13	15.69
4KRM.PDB	O, B_TRP_53	ND2, B_ASN_74	HD21, B_ASN_74	2.77	1.97	18.80
4KRM.PDB	OD2, B_ASP_73	N, B_LYS_76	H, B_LYS_76	2.99	2.16	13.15
4KRM.PDB	O, B_CYS_22	N, B_VAL_79	H, B_VAL_79	2.99	2.26	27.32
4KRM.PDB	O, B_SER_71	N, B_ASP_80	H, B_ASP_80	2.86	2.11	25.20
4KRM.PDB	O, B_LEU_20	N, B_LEU_81	H, B_LEU_81	2.80	1.98	15.20
4KRM.PDB	O, B_THR_69	N, B_GLN_82	H, B_GLN_82	2.74	1.94	17.70
4KRM.PDB	O, B_LEU_18	N, B_MET_83	H, B_MET_83	2.77	1.93	11.70
4KRM.PDB	OD1, B_ASP_90	N, B_LYS_87	H, B_LYS_87	2.76	1.93	11.52
4KRM.PDB	O, B_LYS_87	N, B_ASP_90	H, B_ASP_90	2.96	2.12	11.27
4KRM.PDB	O, B_THR_118	N, B_TYR_94	H, B_TYR_94	2.77	1.94	12.66
4KRM.PDB	O, B_ASP_90	OH, B_TYR_94	HH, B_TYR_94	2.84	2.02	10.29
4KRM.PDB	O, B_PHE_37	N, B_TYR_95	H, B_TYR_95	2.82	2.03	20.26
4KRM.PDB	OE2, B_GLU_6	N, B_CYS_96	H, B_CYS_96	2.72	1.87	8.28
4KRM.PDB	O, B_GLY_35	N, B_ALA_97	H, B_ALA_97	2.96	2.23	26.81
4KRM.PDB	O, B_TYR_113	N, B_ALA_98	H, B_ALA_98	2.91	2.10	17.25
4KRM.PDB	O, B_GLY_33	N, B_ALA_99	H, B_ALA_99	2.85	2.03	15.87
4KRM.PDB	OD2, B_ASP_112	N, B_ALA_100	H, B_ALA_100	2.80	1.99	16.77
4KRM.PDB	OH, B_TYR_111	N, B_TYR_105	H, B_TYR_105	2.90	2.06	10.42
4KRM.PDB	O, B_TYR_105	OH, B_TYR_111	HH, B_TYR_111	2.48	1.64	3.96
4KRM.PDB	O, B_ALA_98	N, B_ASP_112	H, B_ASP_112	2.84	2.11	26.99
4KRM.PDB	O, B_CYS_96	N, B_GLY_115	H, B_GLY_115	2.90	2.14	23.95
4KRM.PDB	OE1, B_GLU_6	N, B_GLY_117	H, B_GLY_117	2.78	1.97	15.53
4KRM.PDB	O, B_ALA_92	N, B_VAL_120	H, B_VAL_120	2.95	2.13	14.97
4KRM.PDB	O, B_GLY_10	N, B_THR_121	H, B_THR_121	2.89	2.05	10.22
4KRM.PDB	O, B_VAL_12	N, B_SER_123	H, B_SER_123	2.95	2.12	14.13
4KRM.PDB	O, B_TYR_60	N, C_GLU_308	H, C_GLU_308	2.91	2.19	28.33
4KRM.PDB	O, B_THR_58	N, C_LYS_310	H, C_LYS_310	2.88	2.06	14.23
4KRM.PDB	OG1, C_THR_339	N, C_LYS_311	H, C_LYS_311	2.77	2.04	26.62
4KRM.PDB	O, B_ASP_56	N, C_VAL_312	H, C_VAL_312	2.73	1.89	9.64
4KRM.PDB	O, C_SER_340	N, C_CYS_313	H, C_CYS_313	2.90	2.07	13.28
4KRM.PDB	O, C_PHE_321	N, C_GLY_317	H, C_GLY_317	2.70	1.87	11.98
4KRM.PDB	OD1, C_ASN_331	N, C_ASN_328	H, C_ASN_328	2.83	1.99	10.78
4KRM.PDB	O, C_ASN_328	N, C_ILE_332	H, C_ILE_332	3.00	2.27	27.38
4KRM.PDB	O, C_ILE_332	N, C_PHE_335	H, C_PHE_335	2.93	2.08	7.41
4KRM.PDB	O, C_LYS_311	N, C_THR_339	H, C_THR_339	2.74	1.92	14.57
4KRM.PDB	O, C_GLU_376	N, C_ILE_341	H, C_ILE_341	2.82	2.00	14.90
4KRM.PDB	O, C_CYS_313	N, C_SER_342	H, C_SER_342	2.83	2.04	19.53
4KRM.PDB	OG1, C_THR_378	N, C_GLY_343	H, C_GLY_343	2.77	2.01	23.25
4KRM.PDB	O, C_LEU_382	N, C_ILE_347	H, C_ILE_347	2.86	2.08	21.12
4KRM.PDB	O, C_LEU_348	N, C_ALA_351	H, C_ALA_351	2.96	2.12	10.17
4KRM.PDB	OE1, D_GLU_110	NH1, C_ARG_353	HH11, C_ARG_353	2.87	2.05	16.15
4KRM.PDB	O, D_ALA_100	NH2, C_ARG_353	HH21, C_ARG_353	2.80	2.00	16.96
4KRM.PDB	O, C_VAL_350	N, C_GLY_354	H, C_GLY_354	2.77	2.02	24.08
4KRM.PDB	O, C_THR_360	N, C_ASP_355	H, C_ASP_355	2.65	1.83	13.88
4KRM.PDB	OD2, C_ASP_355	OG1, C_THR_358	HG1, C_THR_358	2.75	2.00	22.12
4KRM.PDB	O, C_SER_356	N, C_HIS_359	H, C_HIS_359	2.67	1.84	12.90
4KRM.PDB	O, C_ASP_355	N, C_THR_360	H, C_THR_360	2.84	1.99	7.14
4KRM.PDB	O, C_ALA_351	N, C_LEU_363	H, C_LEU_363	2.78	2.07	28.76
4KRM.PDB	O, C_ASP_364	N, C_GLU_367	H, C_GLU_367	2.87	2.07	17.30
4KRM.PDB	O, C_CYS_338	OG1, C_THR_373	HG1, C_THR_373	2.60	1.90	27.53
4KRM.PDB	O, C_LEU_371	N, C_VAL_374	H, C_VAL_374	3.00	2.15	9.63
4KRM.PDB	O, C_THR_339	N, C_LYS_375	H, C_LYS_375	2.73	1.87	2.04
4KRM.PDB	O, C_ILE_401	N, C_ILE_377	H, C_ILE_377	2.94	2.12	15.55
4KRM.PDB	O, C_ILE_341	N, C_THR_378	H, C_THR_378	2.99	2.14	8.37
4KRM.PDB	O, C_GLY_343	N, C_GLY_379	H, C_GLY_379	2.96	2.24	28.09
4KRM.PDB	OD1, C_ASP_344	N, C_PHE_380	H, C_PHE_380	2.87	2.06	16.59
4KRM.PDB	O, C_SER_413	N, C_LEU_381	H, C_LEU_381	2.85	2.05	18.05

4KRM.PDB	O, C_LEU_345	N, C_LEU_382	H, C_LEU_382	2.85	2.00	6.50
4KRM.PDB	O, C_ALA_415	N, C_ILE_383	H, C_ILE_383	2.86	2.06	18.11
4KRM.PDB	O, C_ILE_347	N, C_GLN_384	H, C_GLN_384	2.79	2.00	19.39
4KRM.PDB	O, C_ASP_392	NE1, C_TRP_386	HE1, C_TRP_386	2.82	2.06	23.80
4KRM.PDB	O, C_LEU_424	N, C_LEU_393	H, C_LEU_393	2.90	2.09	16.80
4KRM.PDB	O, C_LEU_393	N, C_PHE_396	H, C_PHE_396	2.95	2.11	10.22
4KRM.PDB	O, C_HIS_394	N, C_GLU_397	H, C_GLU_397	2.85	2.06	19.79
4KRM.PDB	O, C_LYS_372	ND2, C_ASN_398	HD22, C_ASN_398	2.65	1.81	9.39
4KRM.PDB	O, C_LYS_375	N, C_GLU_400	H, C_GLU_400	2.97	2.13	10.86
4KRM.PDB	O, C_GLU_431	N, C_ILE_402	H, C_ILE_402	2.98	2.16	15.59
4KRM.PDB	O, C_ILE_377	N, C_ARG_403	H, C_ARG_403	2.88	2.07	17.91
4KRM.PDB	OE1, C_GLU_376	NH1, C_ARG_403	HH11, C_ARG_403	3.00	2.18	16.51
4KRM.PDB	O, C_THR_378	N, C_ARG_405	H, C_ARG_405	2.81	1.97	9.73
4KRM.PDB	O, C_PHE_412	N, C_GLN_408	H, C_GLN_408	2.69	1.89	18.44
4KRM.PDB	O, C_GLN_408	N, C_GLN_411	H, C_GLN_411	2.85	2.01	8.79
4KRM.PDB	O, C_GLN_408	N, C_PHE_412	H, C_PHE_412	2.93	2.08	8.35
4KRM.PDB	O, C_ASP_436	N, C_SER_413	H, C_SER_413	2.81	1.98	12.74
4KRM.PDB	O, C_LEU_381	N, C_ALA_415	H, C_ALA_415	2.86	2.01	6.79
4KRM.PDB	O, C_ILE_438	N, C_VAL_416	H, C_VAL_416	2.91	2.08	11.96
4KRM.PDB	OD1, C_ASN_442	N, C_LEU_419	H, C_LEU_419	2.87	2.05	14.54
4KRM.PDB	O, C_THR_391	N, C_THR_422	H, C_THR_422	2.92	2.14	20.64
4KRM.PDB	OD1, C_ASP_498	NH2, C_ARG_427	HH21, C_ARG_427	2.43	1.69	25.29
4KRM.PDB	O, C_GLU_400	N, C_LYS_430	H, C_LYS_430	2.87	2.01	1.36
4KRM.PDB	O, C_LEU_456	N, C_ILE_432	H, C_ILE_432	2.84	1.99	8.13
4KRM.PDB	O, C_ILE_402	N, C_SER_433	H, C_SER_433	2.88	2.13	25.53
4KRM.PDB	OE2, C_GLU_431	OG, C_SER_433	HG, C_SER_433	2.86	2.06	14.79
4KRM.PDB	O, C_GLN_411	N, C_ASP_436	H, C_ASP_436	2.86	2.00	4.00
4KRM.PDB	O, C_LEU_414	N, C_ILE_438	H, C_ILE_438	2.90	2.08	13.19
4KRM.PDB	O, C_LYS_465	N, C_ILE_439	H, C_ILE_439	2.99	2.17	14.81
4KRM.PDB	OD1, C_ASN_469	N, C_ASN_442	H, C_ASN_442	2.74	1.97	21.04
4KRM.PDB	O, C_ASN_442	N, C_LEU_445	H, C_LEU_445	2.89	2.04	5.71
4KRM.PDB	O, C_TYR_447	N, C_THR_450	H, C_THR_450	2.94	2.09	7.41
4KRM.PDB	O, C_TYR_447	OG1, C_THR_450	HG1, C_THR_450	2.78	1.97	12.32
4KRM.PDB	OE1, C_GLU_489	NZ, C_LYS_455	HZ2, C_LYS_455	2.73	1.95	24.04
4KRM.PDB	O, C_TRP_453	N, C_LEU_456	H, C_LEU_456	2.87	2.15	27.86
4KRM.PDB	OE1, C_GLN_462	N, C_THR_459	H, C_THR_459	2.63	1.78	3.39
4KRM.PDB	O, C_SER_433	OG1, C_THR_459	HG1, C_THR_459	2.93	2.13	15.18
4KRM.PDB	O, C_GLY_435	NE2, C_GLN_462	HE21, C_GLN_462	2.88	2.03	7.30
4KRM.PDB	O, C_ILE_432	NE2, C_GLN_462	HE22, C_GLN_462	2.87	2.04	12.71
4KRM.PDB	OD1, C_ASP_436	N, C_LYS_463	H, C_LYS_463	2.83	1.97	7.15
4KRM.PDB	O, C_VAL_437	N, C_LYS_465	H, C_LYS_465	2.86	2.07	19.53
4KRM.PDB	O, C_ILE_439	ND2, C_ASN_469	HD21, C_ASN_469	2.82	2.06	23.01
4KRM.PDB	O, C_GLY_471	N, C_CYS_475	H, C_CYS_475	2.80	1.97	13.89
4KRM.PDB	O, C_GLU_472	N, C_LYS_476	H, C_LYS_476	2.76	1.96	18.66
4KRM.PDB	O, C_SER_501	N, C_SER_487	H, C_SER_487	2.90	2.08	13.40
4KRM.PDB	O, C_ASP_498	N, C_TRP_492	H, C_TRP_492	2.81	1.98	12.84
4KRM.PDB	O, C_PRO_496	N, C_CYS_499	H, C_CYS_499	2.91	2.08	13.02
4KRM.PDB	O, C_ALA_484	NE, C_ARG_503	HE, C_ARG_503	2.52	1.76	22.72
4KRM.PDB	O, D_SER_25	N, D_LYS_3	H, D_LYS_3	2.82	1.97	7.73
4KRM.PDB	O, D_ALA_23	N, D_GLU_5	H, D_GLU_5	2.92	2.10	13.79
4KRM.PDB	O, D_THR_121	N, D_VAL_12	H, D_VAL_12	2.95	2.18	23.16
4KRM.PDB	O, D_LEU_86	N, D_GLY_15	H, D_GLY_15	2.70	1.87	11.51
4KRM.PDB	O, D_GLN_13	N, D_GLY_16	H, D_GLY_16	2.72	1.98	26.19
4KRM.PDB	O, D_MET_83	N, D_LEU_18	H, D_LEU_18	3.00	2.20	18.58
4KRM.PDB	OE1, D_GLN_82	NH1, D_ARG_19	HH11, D_ARG_19	2.94	2.12	14.24
4KRM.PDB	O, D_LEU_81	N, D_LEU_20	H, D_LEU_20	2.98	2.19	20.30
4KRM.PDB	O, D_SER_7	N, D_THR_21	H, D_THR_21	2.83	1.99	11.71
4KRM.PDB	O, D_VAL_79	N, D_CYS_22	H, D_CYS_22	2.91	2.16	23.74

4KRM.PDB	O, D_GLU_5	N, D_ALA_23	H, D_ALA_23	2.86	2.02	10.32
4KRM.PDB	O, D_LYS_3	N, D_SER_25	H, D_SER_25	2.93	2.11	14.36
4KRM.PDB	OD2, C_ASP_355	NH1, D_ARG_30	HH12, D_ARG_30	2.45	1.63	13.53
4KRM.PDB	O, D_ALA_99	N, D_GLY_33	H, D_GLY_33	2.93	2.16	22.74
4KRM.PDB	O, D_ALA_97	N, D_GLY_35	H, D_GLY_35	2.86	2.06	17.94
4KRM.PDB	O, D_SER_49	N, D_TRP_36	H, D_TRP_36	2.77	1.94	12.95
4KRM.PDB	O, D_TYR_95	N, D_PHE_37	H, D_PHE_37	2.83	2.00	11.67
4KRM.PDB	O, D_GLU_46	N, D_ARG_38	H, D_ARG_38	2.89	2.09	17.91
4KRM.PDB	OE1, D_GLU_46	NE, D_ARG_38	HE, D_ARG_38	2.79	1.96	12.48
4KRM.PDB	O, D_ILE_93	N, D_GLN_39	H, D_GLN_39	2.91	2.12	19.63
4KRM.PDB	O, D_ARG_38	N, D_GLU_46	H, D_GLU_46	2.85	2.02	11.19
4KRM.PDB	O, D_TRP_36	N, D_VAL_48	H, D_VAL_48	2.93	2.16	21.89
4KRM.PDB	O, D_GLY_59	OG, D_SER_49	HG, D_SER_49	2.87	2.17	28.65
4KRM.PDB	O, D_GLY_59	N, D_GLY_50	H, D_GLY_50	2.97	2.17	17.64
4KRM.PDB	O, D_MET_34	N, D_ILE_51	H, D_ILE_51	2.91	2.12	20.05
4KRM.PDB	O, D_SER_102	N, D_TRP_53	H, D_TRP_53	2.83	2.01	14.56
4KRM.PDB	O, D_GLY_50	N, D_GLY_59	H, D_GLY_59	2.80	2.03	22.40
4KRM.PDB	O, E_GLU_308	N, D_TYR_60	H, D_TYR_60	2.82	2.08	26.84
4KRM.PDB	O, D_VAL_48	N, D_ALA_61	H, D_ALA_61	2.93	2.14	18.86
4KRM.PDB	O, D_GLN_82	N, D_THR_69	H, D_THR_69	2.93	2.16	22.84
4KRM.PDB	OH, D_TYR_60	N, D_ILE_70	H, D_ILE_70	2.85	2.02	13.28
4KRM.PDB	O, D_TYR_32	NH2, D_ARG_72	HH22, D_ARG_72	2.68	1.86	14.70
4KRM.PDB	O, D_TRP_53	ND2, D_ASN_74	HD21, D_ASN_74	2.93	2.13	17.25
4KRM.PDB	O, D_SER_71	N, D_ASP_80	H, D_ASP_80	2.68	1.90	20.52
4KRM.PDB	O, D_LEU_20	N, D_LEU_81	H, D_LEU_81	2.87	2.07	19.11
4KRM.PDB	O, D_THR_69	N, D_GLN_82	H, D_GLN_82	2.77	1.93	7.52
4KRM.PDB	O, D_LEU_18	N, D_MET_83	H, D_MET_83	2.74	1.89	9.04
4KRM.PDB	OD1, D_ASP_90	N, D_LYS_87	H, D_LYS_87	2.86	2.02	10.59
4KRM.PDB	O, D_THR_118	N, D_TYR_94	H, D_TYR_94	2.80	1.95	8.02
4KRM.PDB	O, D_ASP_90	OH, D_TYR_94	HH, D_TYR_94	2.74	1.90	2.03
4KRM.PDB	O, D_PHE_37	N, D_TYR_95	H, D_TYR_95	2.75	1.94	16.71
4KRM.PDB	OE2, D_GLU_6	N, D_CYS_96	H, D_CYS_96	2.74	1.90	11.31
4KRM.PDB	O, D_TYR_113	N, D_ALA_98	H, D_ALA_98	2.88	2.08	18.17
4KRM.PDB	O, D_GLY_33	N, D_ALA_99	H, D_ALA_99	2.73	1.90	13.15
4KRM.PDB	OD2, D_ASP_112	N, D_ALA_100	H, D_ALA_100	2.90	2.08	15.09
4KRM.PDB	O, D_SER_31	N, D_GLY_101	H, D_GLY_101	2.79	1.93	3.06
4KRM.PDB	O, D_TYR_105	OH, D_TYR_111	HH, D_TYR_111	2.68	1.86	10.32
4KRM.PDB	O, D_ALA_98	N, D_ASP_112	H, D_ASP_112	2.84	2.03	16.97
4KRM.PDB	O, D_ALA_92	N, D_VAL_120	H, D_VAL_120	2.94	2.12	14.83
4KRM.PDB	O, D_GLY_10	N, D_THR_121	H, D_THR_121	2.87	2.04	11.88
4KRM.PDB	OG1, D_THR_91	N, D_VAL_122	H, D_VAL_122	2.88	2.06	14.21
4KRM.PDB	O, D_THR_58	N, E_LYS_310	H, E_LYS_310	2.79	2.02	22.01
4KRM.PDB	O, E_SER_340	N, E_CYS_313	H, E_CYS_313	2.94	2.14	19.13
4KRM.PDB	O, E_PHE_321	N, E_GLY_317	H, E_GLY_317	2.77	1.95	14.36
4KRM.PDB	O, E_GLY_319	N, E_LYS_322	H, E_LYS_322	2.82	2.09	27.17
4KRM.PDB	O, E_ILE_327	OG, E_SER_326	HG, E_SER_326	2.91	2.09	10.66
4KRM.PDB	O, E_HIS_346	N, E_ILE_327	H, E_ILE_327	2.96	2.13	12.07
4KRM.PDB	OD1, E_ASN_331	N, E_ASN_328	H, E_ASN_328	2.92	2.08	11.06
4KRM.PDB	OD1, E_ASN_328	N, E_ASN_331	H, E_ASN_331	2.76	1.96	17.47
4KRM.PDB	O, E_LYS_311	N, E_THR_339	H, E_THR_339	2.88	2.04	8.53
4KRM.PDB	O, E_GLU_376	N, E_ILE_341	H, E_ILE_341	2.83	1.99	10.53
4KRM.PDB	O, E_CYS_313	N, E_SER_342	H, E_SER_342	2.81	2.01	18.67
4KRM.PDB	OG1, E_THR_378	N, E_GLY_343	H, E_GLY_343	2.67	1.96	28.18
4KRM.PDB	O, E_PHE_380	N, E_LEU_345	H, E_LEU_345	2.98	2.16	13.52
4KRM.PDB	O, E_LEU_382	N, E_ILE_347	H, E_ILE_347	2.93	2.15	21.34
4KRM.PDB	OG, E_SER_326	N, E_LEU_348	H, E_LEU_348	2.89	2.06	13.76
4KRM.PDB	O, E_LEU_348	N, E_ALA_351	H, E_ALA_351	2.93	2.15	20.83
4KRM.PDB	O, E_PRO_349	N, E_ARG_353	H, E_ARG_353	2.97	2.21	24.57

4KRM.PDB	OE1, F_GLU_110	NH1, E_ARG_353	HH11, E_ARG_353	2.85	2.03	14.34
4KRM.PDB	O, F_GLU_110	NH1, E_ARG_353	HH12, E_ARG_353	2.46	1.72	24.77
4KRM.PDB	O, F_ALA_100	NH2, E_ARG_353	HH21, E_ARG_353	2.81	1.99	15.85
4KRM.PDB	OD2, F_ASP_112	NH2, E_ARG_353	HH22, E_ARG_353	2.96	2.18	20.33
4KRM.PDB	O, E_VAL_350	N, E_GLY_354	H, E_GLY_354	2.78	1.95	14.18
4KRM.PDB	O, E_THR_360	N, E_ASP_355	H, E_ASP_355	2.77	1.92	5.02
4KRM.PDB	OD2, E_ASP_355	OG1, E_THR_358	HG1, E_THR_358	2.55	1.85	27.90
4KRM.PDB	O, E_SER_356	N, E_HIS_359	H, E_HIS_359	2.96	2.14	15.14
4KRM.PDB	O, E_ASP_355	N, E_THR_360	H, E_THR_360	2.89	2.04	8.71
4KRM.PDB	O, E_LEU_368	N, E_LEU_371	H, E_LEU_371	2.96	2.11	6.62
4KRM.PDB	O, E_CYS_338	OG1, E_THR_373	HG1, E_THR_373	2.65	1.89	21.62
4KRM.PDB	O, E_LEU_371	N, E_VAL_374	H, E_VAL_374	2.87	2.03	11.52
4KRM.PDB	O, E_THR_339	N, E_LYS_375	H, E_LYS_375	2.80	1.95	3.65
4KRM.PDB	O, E_ILE_341	N, E_THR_378	H, E_THR_378	2.99	2.16	11.77
4KRM.PDB	O, E_GLY_343	N, E_GLY_379	H, E_GLY_379	2.96	2.26	29.80
4KRM.PDB	O, E_SER_413	N, E_LEU_381	H, E_LEU_381	2.89	2.08	16.67
4KRM.PDB	O, E_LEU_345	N, E_LEU_382	H, E_LEU_382	2.95	2.10	8.54
4KRM.PDB	O, E_ALA_415	N, E_ILE_383	H, E_ILE_383	2.79	1.94	5.21
4KRM.PDB	O, F_ASP_112	NE2, E_GLN_384	HE22, E_GLN_384	2.82	2.10	28.13
4KRM.PDB	O, E_LEU_424	N, E_LEU_393	H, E_LEU_393	2.88	2.06	14.51
4KRM.PDB	O, E_LEU_393	N, E_PHE_396	H, E_PHE_396	2.99	2.16	13.86
4KRM.PDB	O, E_HIS_394	N, E_GLU_397	H, E_GLU_397	2.82	2.04	20.64
4KRM.PDB	O, E_LYS_372	ND2, E_ASN_398	HD22, E_ASN_398	2.92	2.11	15.20
4KRM.PDB	O, E_LYS_375	N, E_GLU_400	H, E_GLU_400	2.81	1.96	8.49
4KRM.PDB	O, E_ILE_377	N, E_ARG_403	H, E_ARG_403	2.94	2.11	13.50
4KRM.PDB	O, E_THR_378	N, E_ARG_405	H, E_ARG_405	2.98	2.15	12.71
4KRM.PDB	OD1, E_ASP_434	NZ, E_LYS_407	HZ1, E_LYS_407	2.65	1.88	23.95
4KRM.PDB	O, E_PHE_412	N, E_GLN_408	H, E_GLN_408	2.79	1.99	17.99
4KRM.PDB	O, E_LYS_407	N, E_GLY_410	H, E_GLY_410	2.97	2.18	18.85
4KRM.PDB	O, E_GLN_408	N, E_GLN_411	H, E_GLN_411	2.93	2.08	6.71
4KRM.PDB	O, E_ASP_436	N, E_SER_413	H, E_SER_413	2.91	2.10	16.30
4KRM.PDB	O, E_LEU_381	N, E_ALA_415	H, E_ALA_415	2.85	2.12	26.97
4KRM.PDB	O, E_ILE_383	N, E_VAL_417	H, E_VAL_417	2.90	2.05	7.33
4KRM.PDB	O, E_SER_440	N, E_SER_418	H, E_SER_418	2.92	2.12	18.48
4KRM.PDB	OD1, E_ASN_442	N, E_LEU_419	H, E_LEU_419	2.67	1.86	14.59
4KRM.PDB	O, E_THR_391	N, E_THR_422	H, E_THR_422	2.80	2.00	17.36
4KRM.PDB	O, E_LEU_456	N, E_ILE_432	H, E_ILE_432	2.68	1.84	9.53
4KRM.PDB	O, E_ILE_402	N, E_SER_433	H, E_SER_433	2.93	2.19	25.97
4KRM.PDB	OE2, E_GLU_431	OG, E_SER_433	HG, E_SER_433	2.91	2.17	23.57
4KRM.PDB	O, E_GLN_411	N, E_ASP_436	H, E_ASP_436	2.85	1.99	3.30
4KRM.PDB	O, E_LYS_465	N, E_ILE_439	H, E_ILE_439	2.87	2.04	13.60
4KRM.PDB	O, E_ASN_442	N, E_LEU_445	H, E_LEU_445	2.93	2.08	7.42
4KRM.PDB	O, E_THR_422	N, E_CYS_446	H, E_CYS_446	2.91	2.06	4.97
4KRM.PDB	O, E_TYR_447	N, E_THR_450	H, E_THR_450	2.98	2.15	11.59
4KRM.PDB	O, E_TYR_447	OG1, E_THR_450	HG1, E_THR_450	2.73	1.91	9.86
4KRM.PDB	O, E_GLU_489	N, E_ASN_452	H, E_ASN_452	2.85	2.08	22.47
4KRM.PDB	OE1, E_GLN_462	N, E_GLY_458	H, E_GLY_458	2.67	1.84	13.21
4KRM.PDB	OE1, E_GLN_462	N, E_THR_459	H, E_THR_459	2.93	2.08	6.67
4KRM.PDB	O, E_GLY_435	NE2, E_GLN_462	HE21, E_GLN_462	2.81	1.97	10.34
4KRM.PDB	OD1, E_ASP_436	N, E_LYS_463	H, E_LYS_463	2.74	1.90	10.82
4KRM.PDB	O, E_VAL_437	N, E_LYS_465	H, E_LYS_465	2.73	1.90	11.45
4KRM.PDB	O, E_ILE_439	ND2, E_ASN_469	HD21, E_ASN_469	2.99	2.18	18.20
4KRM.PDB	O, E_GLY_471	N, E_CYS_475	H, E_CYS_475	2.86	2.02	8.70
4KRM.PDB	O, E_GLU_472	N, E_LYS_476	H, E_LYS_476	2.70	1.86	10.04
4KRM.PDB	O, E_SER_501	N, E_SER_487	H, E_SER_487	2.92	2.08	12.18
4KRM.PDB	OG, E_SER_487	N, E_GLU_489	H, E_GLU_489	2.96	2.14	14.73
4KRM.PDB	OG1, E_THR_450	N, E_CYS_491	H, E_CYS_491	2.93	2.14	19.72
4KRM.PDB	O, E_ASP_498	N, E_TRP_492	H, E_TRP_492	2.80	1.98	14.94

4KRM.PDB	OD2, E_ASP.498	N, E_GLU.495	H, E_GLU.495	2.92	2.09	11.64
4KRM.PDB	O, E_GLU.495	N, E_ASP.498	H, E_ASP.498	2.98	2.18	17.73
4KRM.PDB	O, E_LEU.485	N, E_ARG.503	H, E_ARG.503	2.88	2.12	23.79
4KRM.PDB	O, F_SER.25	N, F_LYS.3	H, F_LYS.3	2.86	2.05	17.09
4KRM.PDB	O, F_THR.21	N, F_SER.7	H, F_SER.7	2.95	2.13	15.30
4KRM.PDB	O, F_SER.7	N, F_THR.21	H, F_THR.21	2.73	1.87	2.52
4KRM.PDB	O, F_LYS.3	N, F_SER.25	H, F_SER.25	2.98	2.15	11.96
4KRM.PDB	O, F_SER.31	NH2, F_ARG.30	HH21, F_ARG.30	2.61	1.79	15.83
4KRM.PDB	O, F_ALA.99	N, F_GLY.33	H, F_GLY.33	2.82	2.07	24.40
4KRM.PDB	O, F_ILE.51	N, F_MET.34	H, F_MET.34	2.93	2.11	15.70
4KRM.PDB	O, F_ALA.97	N, F_GLY.35	H, F_GLY.35	2.80	1.97	12.17
4KRM.PDB	O, F_SER.49	N, F_TRP.36	H, F_TRP.36	2.73	1.89	10.21
4KRM.PDB	O, F_TYR.95	N, F_PHE.37	H, F_PHE.37	2.81	1.97	10.88
4KRM.PDB	O, F_GLU.46	N, F_ARG.38	H, F_ARG.38	2.90	2.09	16.96
4KRM.PDB	OE1, F_GLU.46	NE, F_ARG.38	HE, F_ARG.38	2.74	1.95	18.99
4KRM.PDB	OD2, F_ASP.90	NH1, F_ARG.38	HH12, F_ARG.38	2.95	2.22	27.79
4KRM.PDB	OE1, F_GLU.46	NH2, F_ARG.38	HH21, F_ARG.38	2.97	2.26	28.90
4KRM.PDB	O, F_ILE.93	N, F_GLN.39	H, F_GLN.39	2.82	2.04	20.98
4KRM.PDB	O, F_ARG.38	N, F_GLU.46	H, F_GLU.46	2.90	2.06	10.12
4KRM.PDB	O, F_TRP.36	N, F_VAL.48	H, F_VAL.48	2.88	2.06	14.02
4KRM.PDB	O, F_GLY.59	OG, F_SER.49	HG, F_SER.49	2.88	2.11	18.96
4KRM.PDB	O, F_MET.34	N, F_ILE.51	H, F_ILE.51	2.74	1.95	19.38
4KRM.PDB	O, F_SER.57	N, F_SER.52	H, F_SER.52	2.97	2.18	19.50
4KRM.PDB	O, F_SER.102	N, F_TRP.53	H, F_TRP.53	2.81	2.02	19.56
4KRM.PDB	O, F_GLY.50	N, F_GLY.59	H, F_GLY.59	2.97	2.21	23.47
4KRM.PDB	O, F_VAL.48	N, F_ALA.61	H, F_ALA.61	2.76	1.97	19.40
4KRM.PDB	O, F_ALA.61	N, F_VAL.64	H, F_VAL.64	2.98	2.13	8.69
4KRM.PDB	O, F_GLN.82	N, F_THR.69	H, F_THR.69	2.91	2.11	18.52
4KRM.PDB	OH, F_TYR.60	N, F_ILE.70	H, F_ILE.70	2.89	2.06	11.48
4KRM.PDB	O, F_TYR.32	NH2, F_ARG.72	HH22, F_ARG.72	2.78	1.95	12.55
4KRM.PDB	O, F_THR.78	N, F_ASP.73	H, F_ASP.73	2.80	1.97	13.02
4KRM.PDB	O, F_TRP.53	ND2, F_ASN.74	HD21, F_ASN.74	2.93	2.12	16.19
4KRM.PDB	O, F_SER.71	N, F_ASP.80	H, F_ASP.80	2.70	1.92	21.61
4KRM.PDB	O, F_LEU.20	N, F_LEU.81	H, F_LEU.81	2.76	1.99	22.17
4KRM.PDB	O, F_THR.69	N, F_GLN.82	H, F_GLN.82	2.76	1.97	19.23
4KRM.PDB	O, F_LEU.18	N, F_MET.83	H, F_MET.83	2.64	1.79	6.89
4KRM.PDB	O, F_LYS.87	N, F_ASP.90	H, F_ASP.90	2.98	2.21	22.29
4KRM.PDB	O, F_VAL.120	N, F_ALA.92	H, F_ALA.92	2.97	2.23	25.76
4KRM.PDB	O, F_GLN.39	N, F_ILE.93	H, F_ILE.93	2.94	2.10	11.68
4KRM.PDB	O, F_THR.118	N, F_TYR.94	H, F_TYR.94	2.68	1.91	22.25
4KRM.PDB	O, F_PHE.37	N, F_TYR.95	H, F_TYR.95	2.61	1.83	20.76
4KRM.PDB	OE2, F_GLU.6	N, F_CYS.96	H, F_CYS.96	2.70	1.85	6.40
4KRM.PDB	O, F_TYR.113	N, F_ALA.98	H, F_ALA.98	2.93	2.11	13.82
4KRM.PDB	O, F_GLY.33	N, F_ALA.99	H, F_ALA.99	2.73	1.91	15.09
4KRM.PDB	OD2, F_ASP.112	N, F_ALA.100	H, F_ALA.100	2.76	1.94	15.63
4KRM.PDB	O, F_SER.31	N, F_GLY.101	H, F_GLY.101	2.75	1.91	9.93
4KRM.PDB	OG, F_SER.57	NE1, F_TRP.104	HE1, F_TRP.104	3.00	2.20	18.23
4KRM.PDB	OH, F_TYR.111	N, F_TYR.105	H, F_TYR.105	2.96	2.11	6.28
4KRM.PDB	O, F_TYR.105	OH, F_TYR.111	HH, F_TYR.111	2.59	1.76	7.82
4KRM.PDB	O, F_ALA.98	N, F_ASP.112	H, F_ASP.112	2.76	1.97	19.53
4KRM.PDB	O, F_ALA.92	N, F_VAL.120	H, F_VAL.120	2.87	2.04	13.51
4KRM.PDB	O, J_THR.58	N, G_LYS.310	H, G_LYS.310	2.73	1.87	4.39
4KRM.PDB	OG1, G_THR.339	N, G_LYS.311	H, G_LYS.311	2.65	1.81	9.30
4KRM.PDB	O, J_ASP.56	N, G_VAL.312	H, G_VAL.312	2.86	2.02	9.25
4KRM.PDB	O, G_SER.340	N, G_CYS.313	H, G_CYS.313	2.95	2.13	14.37
4KRM.PDB	OE2, G_GLU.320	ND2, G_ASN.314	HD22, G_ASN.314	2.93	2.08	7.68
4KRM.PDB	O, G_PHE.321	N, G_GLY.317	H, G_GLY.317	2.53	1.78	24.02
4KRM.PDB	O, G_ILE.318	N, G_PHE.321	H, G_PHE.321	2.93	2.11	15.10

4KRM.PDB	O, G_ILE_327	OG, G_SER_326	HG, G_SER_326	2.75	1.93	11.46
4KRM.PDB	OD1, G_ASN_331	N, G_ASN_328	H, G_ASN_328	2.74	1.90	10.28
4KRM.PDB	OD1, G_ASN_328	N, G_THR_330	H, G_THR_330	2.95	2.20	24.53
4KRM.PDB	O, G_LYS_311	N, G_THR_339	H, G_THR_339	2.89	2.05	9.34
4KRM.PDB	O, G_GLU_376	N, G_ILE_341	H, G_ILE_341	2.80	1.96	11.60
4KRM.PDB	O, G_CYS_313	N, G_SER_342	H, G_SER_342	2.82	1.98	11.49
4KRM.PDB	O, G_PHE_380	N, G_LEU_345	H, G_LEU_345	2.93	2.10	13.53
4KRM.PDB	O, G_LEU_382	N, G_ILE_347	H, G_ILE_347	2.70	1.92	20.05
4KRM.PDB	OD1, H_ASP_112	N, G_VAL_350	H, G_VAL_350	2.96	2.25	28.54
4KRM.PDB	O, H_GLU_110	NH1, G_ARG_353	HH12, G_ARG_353	2.56	1.83	26.87
4KRM.PDB	O, H_ALA_100	NH2, G_ARG_353	HH21, G_ARG_353	2.51	1.75	22.59
4KRM.PDB	O, G_THR_360	N, G_ASP_355	H, G_ASP_355	2.70	1.88	14.64
4KRM.PDB	OD2, G_ASP_355	OG1, G_THR_358	HG1, G_THR_358	2.44	1.73	26.83
4KRM.PDB	O, G_SER_356	N, G_HIS_359	H, G_HIS_359	2.93	2.09	11.16
4KRM.PDB	O, G_ASP_355	N, G_THR_360	H, G_THR_360	2.97	2.12	5.02
4KRM.PDB	O, G_ALA_351	N, G_LEU_363	H, G_LEU_363	2.76	1.95	17.12
4KRM.PDB	O, G_ASP_364	N, G_GLU_367	H, G_GLU_367	2.88	2.09	19.30
4KRM.PDB	O, G_CYS_338	OG1, G_THR_373	HG1, G_THR_373	2.73	2.02	27.50
4KRM.PDB	O, G_LEU_371	N, G_VAL_374	H, G_VAL_374	2.85	2.01	8.31
4KRM.PDB	O, G_THR_339	N, G_LYS_375	H, G_LYS_375	2.65	1.80	5.93
4KRM.PDB	O, G_ILE_401	N, G_ILE_377	H, G_ILE_377	2.87	2.09	20.96
4KRM.PDB	O, G_ILE_341	N, G_THR_378	H, G_THR_378	2.88	2.03	7.65
4KRM.PDB	O, G_GLY_343	N, G_GLY_379	H, G_GLY_379	2.80	2.07	27.17
4KRM.PDB	O, G_SER_413	N, G_LEU_381	H, G_LEU_381	2.90	2.12	21.15
4KRM.PDB	O, G_LEU_345	N, G_LEU_382	H, G_LEU_382	2.83	1.99	8.73
4KRM.PDB	O, G_ALA_415	N, G_ILE_383	H, G_ILE_383	2.86	2.01	8.40
4KRM.PDB	O, G_ILE_347	N, G_GLN_384	H, G_GLN_384	2.81	1.95	0.88
4KRM.PDB	O, G_LEU_424	N, G_LEU_393	H, G_LEU_393	2.77	1.94	12.00
4KRM.PDB	O, G_ASP_392	N, G_HIS_394	H, G_HIS_394	2.93	2.22	28.78
4KRM.PDB	O, G_LEU_393	N, G_PHE_396	H, G_PHE_396	2.92	2.10	14.77
4KRM.PDB	O, G_HIS_394	N, G_GLU_397	H, G_GLU_397	2.97	2.19	21.14
4KRM.PDB	O, G_LYS_372	ND2, G_ASN_398	HD22, G_ASN_398	2.84	2.00	11.57
4KRM.PDB	O, G_LYS_375	N, G_GLU_400	H, G_GLU_400	2.78	1.96	14.21
4KRM.PDB	O, G_LYS_375	N, G_ILE_401	H, G_ILE_401	2.99	2.20	20.10
4KRM.PDB	O, G_GLU_431	N, G_ILE_402	H, G_ILE_402	2.97	2.14	13.48
4KRM.PDB	O, G_ILE_377	N, G_ARG_403	H, G_ARG_403	2.93	2.11	14.81
4KRM.PDB	OE2, B_GLU_5	NZ, G_LYS_407	HZ1, G_LYS_407	2.98	2.17	20.60
4KRM.PDB	O, G_PHE_412	N, G_GLN_408	H, G_GLN_408	2.76	2.01	23.83
4KRM.PDB	O, G_LYS_407	N, G_GLY_410	H, G_GLY_410	2.94	2.22	27.68
4KRM.PDB	O, G_GLN_408	N, G_GLN_411	H, G_GLN_411	2.79	2.01	20.58
4KRM.PDB	O, G_ASP_436	N, G_SER_413	H, G_SER_413	2.85	2.07	21.98
4KRM.PDB	O, G_LEU_381	N, G_ALA_415	H, G_ALA_415	2.89	2.06	13.22
4KRM.PDB	O, G_ILE_438	N, G_VAL_416	H, G_VAL_416	2.96	2.13	13.42
4KRM.PDB	O, G_ILE_383	N, G_VAL_417	H, G_VAL_417	2.92	2.07	10.01
4KRM.PDB	O, G_SER_440	N, G_SER_418	H, G_SER_418	2.92	2.13	19.69
4KRM.PDB	OD1, G_ASN_442	N, G_LEU_419	H, G_LEU_419	2.75	1.90	7.74
4KRM.PDB	O, G_THR_391	N, G_THR_422	H, G_THR_422	2.76	1.99	22.35
4KRM.PDB	OD1, G_ASP_498	NE, G_ARG_427	HE, G_ARG_427	2.63	1.82	16.62
4KRM.PDB	O, G_GLU_400	N, G_LYS_430	H, G_LYS_430	2.83	2.00	11.28
4KRM.PDB	O, G_LEU_456	N, G_ILE_432	H, G_ILE_432	2.61	1.79	15.19
4KRM.PDB	O, G_ILE_402	N, G_SER_433	H, G_SER_433	2.83	2.10	26.95
4KRM.PDB	OE2, G_GLU_431	OG, G_SER_433	HG, G_SER_433	2.90	2.13	19.38
4KRM.PDB	O, G_GLN_411	N, G_ASP_436	H, G_ASP_436	2.84	1.99	7.12
4KRM.PDB	O, G_LEU_414	N, G_ILE_438	H, G_ILE_438	2.99	2.16	12.24
4KRM.PDB	O, G_LYS_465	N, G_ILE_439	H, G_ILE_439	2.85	2.05	16.86
4KRM.PDB	O, G_THR_422	N, G_CYS_446	H, G_CYS_446	2.95	2.09	5.98
4KRM.PDB	O, G_TYR_447	OG1, G_THR_450	HG1, G_THR_450	2.91	2.12	17.41
4KRM.PDB	O, G_TRP_453	N, G_LEU_456	H, G_LEU_456	2.82	2.02	18.78

4KRM.PDB	OE1, G_GLN_462	N, G_GLY_458	H, G_GLY_458	2.58	1.75	11.60
4KRM.PDB	OE1, G_GLN_462	N, G_THR_459	H, G_THR_459	2.66	1.85	16.39
4KRM.PDB	O, G_ILE_432	NE2, G_GLN_462	HE22, G_GLN_462	2.98	2.14	10.37
4KRM.PDB	OD2, G_ASP_436	NZ, G_LYS_463	HZ3, G_LYS_463	2.68	1.83	13.12
4KRM.PDB	O, G_VAL_437	N, G_LYS_465	H, G_LYS_465	2.68	1.91	21.58
4KRM.PDB	O, G_ILE_439	ND2, G_ASN_469	HD21, G_ASN_469	2.98	2.19	20.07
4KRM.PDB	O, G_GLY_479	N, G_VAL_481	H, G_VAL_481	2.78	2.05	26.86
4KRM.PDB	O, G_HIS_483	N, G_CYS_486	H, G_CYS_486	2.82	1.98	11.71
4KRM.PDB	O, G_SER_501	N, G_SER_487	H, G_SER_487	2.97	2.12	8.14
4KRM.PDB	OG1, G_THR_450	N, G_CYS_491	H, G_CYS_491	2.97	2.16	16.33
4KRM.PDB	O, G_ASP_498	N, G_TRP_492	H, G_TRP_492	2.74	1.91	11.68
4KRM.PDB	OD2, G_ASP_498	N, G_GLU_495	H, G_GLU_495	2.95	2.14	15.12
4KRM.PDB	O, G_GLU_495	N, G_ASP_498	H, G_ASP_498	2.86	2.09	21.75
4KRM.PDB	O, H_SER_25	N, H_LYS_3	H, H_LYS_3	2.79	1.95	8.78
4KRM.PDB	O, H_THR_121	N, H_VAL_12	H, H_VAL_12	2.78	2.06	27.37
4KRM.PDB	O, H_LEU_86	N, H_GLY_15	H, H_GLY_15	2.81	1.97	8.46
4KRM.PDB	O, H_GLN_13	N, H_GLY_16	H, H_GLY_16	2.88	2.10	20.19
4KRM.PDB	O, H_MET_83	N, H_LEU_18	H, H_LEU_18	2.86	2.12	25.13
4KRM.PDB	O, H_LEU_81	N, H_LEU_20	H, H_LEU_20	2.99	2.19	18.49
4KRM.PDB	O, H_SER_7	N, H_THR_21	H, H_THR_21	2.95	2.12	12.95
4KRM.PDB	OD1, H_ASP_80	OG1, H_THR_21	HG1, H_THR_21	2.86	2.06	13.63
4KRM.PDB	O, H_VAL_79	N, H_CYS_22	H, H_CYS_22	2.70	1.88	14.06
4KRM.PDB	O, H_GLU_5	N, H_ALA_23	H, H_ALA_23	2.89	2.06	12.94
4KRM.PDB	O, H_LYS_3	N, H_SER_25	H, H_SER_25	2.91	2.09	13.71
4KRM.PDB	O, H_GLN_1	N, H_ARG_27	H, H_ARG_27	2.48	1.77	28.35
4KRM.PDB	OD2, G_ASP_355	NH1, H_ARG_30	HH12, H_ARG_30	2.45	1.69	23.45
4KRM.PDB	O, H_SER_31	NH2, H_ARG_30	HH21, H_ARG_30	2.78	1.93	7.41
4KRM.PDB	O, H_ALA_99	N, H_GLY_33	H, H_GLY_33	2.86	2.05	16.44
4KRM.PDB	O, H_ALA_97	N, H_GLY_35	H, H_GLY_35	2.94	2.11	13.58
4KRM.PDB	O, H_SER_49	N, H_TRP_36	H, H_TRP_36	2.62	1.77	8.75
4KRM.PDB	O, H_TYR_95	N, H_PHE_37	H, H_PHE_37	2.89	2.05	9.66
4KRM.PDB	O, H_GLU_46	N, H_ARG_38	H, H_ARG_38	2.94	2.12	14.51
4KRM.PDB	OH, H_TYR_94	NH1, H_ARG_38	HH11, H_ARG_38	2.96	2.15	17.21
4KRM.PDB	OD2, H_ASP_90	NH1, H_ARG_38	HH12, H_ARG_38	2.78	1.94	11.87
4KRM.PDB	O, H_ILE_93	N, H_GLN_39	H, H_GLN_39	2.82	2.05	22.91
4KRM.PDB	O, H_ARG_38	N, H_GLU_46	H, H_GLU_46	2.85	2.00	7.03
4KRM.PDB	O, H_TRP_36	N, H_VAL_48	H, H_VAL_48	2.89	2.09	19.35
4KRM.PDB	O, H_GLY_59	OG, H_SER_49	HG, H_SER_49	2.79	2.01	17.53
4KRM.PDB	O, H_SER_57	N, H_SER_52	H, H_SER_52	2.91	2.10	15.97
4KRM.PDB	O, H_SER_102	N, H_TRP_53	H, H_TRP_53	2.86	2.06	18.40
4KRM.PDB	O, H_GLY_50	N, H_GLY_59	H, H_GLY_59	2.99	2.18	17.15
4KRM.PDB	O, H_VAL_48	N, H_ALA_61	H, H_ALA_61	2.83	2.04	18.74
4KRM.PDB	O, H_GLN_82	N, H_THR_69	H, H_THR_69	2.90	2.15	24.65
4KRM.PDB	OH, H_TYR_60	N, H_ILE_70	H, H_ILE_70	2.79	1.97	14.83
4KRM.PDB	O, H_ASP_80	N, H_SER_71	H, H_SER_71	3.00	2.23	22.57
4KRM.PDB	O, H_TRP_53	ND2, H_ASN_74	HD21, H_ASN_74	2.76	1.95	15.85
4KRM.PDB	OD2, H_ASP_73	N, H_LYS_76	H, H_LYS_76	2.90	2.09	16.51
4KRM.PDB	O, H_CYS_22	N, H_VAL_79	H, H_VAL_79	2.88	2.15	26.91
4KRM.PDB	O, H_SER_71	N, H_ASP_80	H, H_ASP_80	2.65	1.83	14.09
4KRM.PDB	O, H_LEU_20	N, H_LEU_81	H, H_LEU_81	2.81	2.00	15.97
4KRM.PDB	O, H_THR_69	N, H_GLN_82	H, H_GLN_82	2.88	2.06	13.12
4KRM.PDB	O, H_LEU_18	N, H_MET_83	H, H_MET_83	2.85	2.06	18.92
4KRM.PDB	OD1, H_ASP_90	N, H_LYS_87	H, H_LYS_87	2.94	2.18	22.86
4KRM.PDB	O, H_LYS_87	N, H_ASP_90	H, H_ASP_90	2.96	2.13	11.70
4KRM.PDB	O, H_VAL_120	N, H_ALA_92	H, H_ALA_92	2.96	2.18	20.64
4KRM.PDB	O, H_THR_118	N, H_TYR_94	H, H_TYR_94	2.81	1.97	10.96
4KRM.PDB	O, H_ASP_90	OH, H_TYR_94	HH, H_TYR_94	2.70	1.86	4.54
4KRM.PDB	O, H_PHE_37	N, H_TYR_95	H, H_TYR_95	2.58	1.73	7.75

4KRM.PDB	OE2, H_GLU_6	N, H_CYS_96	H, H_CYS_96	2.89	2.06	12.97
4KRM.PDB	O, H_TYR_113	N, H_ALA_98	H, H_ALA_98	2.83	2.01	14.92
4KRM.PDB	O, H_GLY_33	N, H_ALA_99	H, H_ALA_99	2.76	1.95	17.06
4KRM.PDB	OD2, H_ASP_112	N, H_ALA_100	H, H_ALA_100	2.90	2.11	20.56
4KRM.PDB	OH, H_TYR_111	N, H_TYR_105	H, H_TYR_105	3.00	2.17	13.07
4KRM.PDB	O, H_TYR_105	OH, H_TYR_111	HH, H_TYR_111	2.65	1.82	7.16
4KRM.PDB	O, H_ALA_98	N, H_ASP_112	H, H_ASP_112	2.68	1.89	19.59
4KRM.PDB	O, H_CYS_96	N, H_GLY_115	H, H_GLY_115	2.91	2.11	18.40
4KRM.PDB	O, H_ALA_92	N, H_VAL_120	H, H_VAL_120	2.84	1.98	5.98
4KRM.PDB	O, H_GLY_10	N, H_THR_121	H, H_THR_121	2.98	2.20	20.73
4KRM.PDB	O, H_VAL_12	N, H_SER_123	H, H_SER_123	2.98	2.16	13.88
4KRM.PDB	O, L_TYR_60	N, L_GLU_308	H, L_GLU_308	2.69	1.88	16.25
4KRM.PDB	O, L_THR_58	N, L_LYS_310	H, L_LYS_310	2.70	1.84	3.45
4KRM.PDB	OG1, L_THR_339	N, L_LYS_311	H, L_LYS_311	2.88	2.03	10.00
4KRM.PDB	O, L_ASP_56	N, L_VAL_312	H, L_VAL_312	2.83	1.98	8.53
4KRM.PDB	O, L_SER_340	N, L_CYS_313	H, L_CYS_313	2.89	2.06	11.76
4KRM.PDB	O, L_ASP_344	N, L_ILE_316	H, L_ILE_316	2.80	2.09	29.01
4KRM.PDB	O, L_PHE_321	N, L_GLY_317	H, L_GLY_317	2.73	1.96	22.99
4KRM.PDB	O, L_ILE_318	N, L_PHE_321	H, L_PHE_321	2.93	2.10	12.75
4KRM.PDB	O, L_ILE_327	OG, L_SER_326	HG, L_SER_326	2.89	2.08	11.44
4KRM.PDB	OD1, L_ASN_331	N, L_ASN_328	H, L_ASN_328	2.82	1.98	9.33
4KRM.PDB	OD1, L_ASN_328	N, L_ASN_331	H, L_ASN_331	2.99	2.20	19.62
4KRM.PDB	O, L_SER_326	ND2, L_ASN_331	HD21, L_ASN_331	2.92	2.07	8.49
4KRM.PDB	O, L_ILE_332	N, L_PHE_335	H, L_PHE_335	2.95	2.11	11.07
4KRM.PDB	O, L_LYS_311	N, L_THR_339	H, L_THR_339	2.90	2.09	16.73
4KRM.PDB	O, L_GLU_376	N, L_ILE_341	H, L_ILE_341	2.71	1.87	11.39
4KRM.PDB	O, L_CYS_313	N, L_SER_342	H, L_SER_342	2.80	1.99	16.11
4KRM.PDB	OD1, J_ASP_112	N, L_VAL_350	H, L_VAL_350	2.88	2.05	13.27
4KRM.PDB	O, L_PRO_349	N, L_PHE_352	H, L_PHE_352	2.95	2.25	30.00
4KRM.PDB	OE1, J_GLU_110	NH1, L_ARG_353	HH11, L_ARG_353	2.86	2.07	18.90
4KRM.PDB	O, J_ALA_100	NH2, L_ARG_353	HH21, L_ARG_353	2.97	2.14	13.62
4KRM.PDB	OD2, J_ASP_112	NH2, L_ARG_353	HH22, L_ARG_353	3.00	2.19	17.61
4KRM.PDB	O, L_VAL_350	N, L_GLY_354	H, L_GLY_354	2.71	1.89	14.51
4KRM.PDB	O, L_THR_360	N, L_ASP_355	H, L_ASP_355	2.71	1.86	7.14
4KRM.PDB	O, L_SER_356	N, L_HIS_359	H, L_HIS_359	2.93	2.08	7.30
4KRM.PDB	O, L_ASP_355	N, L_THR_360	H, L_THR_360	2.86	2.01	5.45
4KRM.PDB	O, L_ALA_351	N, L_LEU_363	H, L_LEU_363	2.78	1.95	13.31
4KRM.PDB	O, L_ASP_364	N, L_GLU_367	H, L_GLU_367	2.93	2.21	27.86
4KRM.PDB	O, L_GLN_366	N, L_ASP_369	H, L_ASP_369	2.86	2.00	2.35
4KRM.PDB	O, L_CYS_338	OG1, L_THR_373	HG1, L_THR_373	2.82	2.09	25.50
4KRM.PDB	O, L_THR_339	N, L_LYS_375	H, L_LYS_375	2.71	1.85	3.93
4KRM.PDB	O, L_ILE_401	N, L_ILE_377	H, L_ILE_377	2.89	2.07	14.58
4KRM.PDB	O, L_ILE_341	N, L_THR_378	H, L_THR_378	2.93	2.08	9.23
4KRM.PDB	O, L_SER_413	N, L_LEU_381	H, L_LEU_381	2.75	1.94	16.75
4KRM.PDB	O, L_LEU_345	N, L_LEU_382	H, L_LEU_382	2.90	2.05	7.20
4KRM.PDB	O, L_ALA_415	N, L_ILE_383	H, L_ILE_383	2.86	2.06	17.70
4KRM.PDB	O, L_ILE_347	N, L_GLN_384	H, L_GLN_384	2.86	2.01	5.31
4KRM.PDB	O, L_ASP_392	NE1, L_TRP_386	HE1, L_TRP_386	2.95	2.22	27.18
4KRM.PDB	O, L_LEU_424	N, L_LEU_393	H, L_LEU_393	2.95	2.14	17.35
4KRM.PDB	O, L_LEU_393	N, L_PHE_396	H, L_PHE_396	2.98	2.13	9.44
4KRM.PDB	O, L_HIS_394	N, L_GLU_397	H, L_GLU_397	2.79	2.02	21.70
4KRM.PDB	O, L_LYS_372	ND2, L_ASN_398	HD22, L_ASN_398	2.66	1.85	16.79
4KRM.PDB	O, L_GLU_431	N, L_ILE_402	H, L_ILE_402	2.98	2.16	14.32
4KRM.PDB	O, L_ILE_377	N, L_ARG_403	H, L_ARG_403	2.74	1.92	14.23
4KRM.PDB	OE1, L_GLU_376	NH1, L_ARG_403	HH11, L_ARG_403	2.44	1.73	28.52
4KRM.PDB	O, L_THR_378	N, L_ARG_405	H, L_ARG_405	2.76	1.91	6.37
4KRM.PDB	O, L_PHE_412	N, L_GLN_408	H, L_GLN_408	2.70	1.95	24.36
4KRM.PDB	O, L_GLN_408	N, L_GLN_411	H, L_GLN_411	2.99	2.13	5.39

4KRM.PDB	O, I_GLN_408	N, I_PHE_412	H, I_PHE_412	2.93	2.08	4.67
4KRM.PDB	O, I_ASP_436	N, I_SER_413	H, I_SER_413	2.86	2.02	12.03
4KRM.PDB	O, I_LEU_381	N, I_ALA_415	H, I_ALA_415	2.85	2.03	14.56
4KRM.PDB	O, I_ILE_438	N, I_VAL_416	H, I_VAL_416	2.89	2.05	11.42
4KRM.PDB	O, I_ILE_383	N, I_VAL_417	H, I_VAL_417	2.89	2.03	5.24
4KRM.PDB	OD1, I_ASN_442	N, I_LEU_419	H, I_LEU_419	2.81	1.99	14.43
4KRM.PDB	O, I_THR_391	N, I_THR_422	H, I_THR_422	2.89	2.08	17.87
4KRM.PDB	O, I_GLU_400	N, I_LYS_430	H, I_LYS_430	2.98	2.13	8.06
4KRM.PDB	O, I_LEU_456	N, I_ILE_432	H, I_ILE_432	2.75	1.92	11.71
4KRM.PDB	O, I_ILE_402	N, I_SER_433	H, I_SER_433	2.89	2.14	24.79
4KRM.PDB	OE2, I_GLU_431	OG, I_SER_433	HG, I_SER_433	2.91	2.09	9.73
4KRM.PDB	OD1, I_ASP_434	N, I_GLY_435	H, I_GLY_435	2.61	1.88	26.82
4KRM.PDB	O, I_GLN_411	N, I_ASP_436	H, I_ASP_436	2.81	1.95	4.03
4KRM.PDB	O, I_LEU_414	N, I_ILE_438	H, I_ILE_438	2.94	2.11	13.80
4KRM.PDB	OD1, I_ASN_469	ND2, I_ASN_442	HD22, I_ASN_442	2.76	1.93	12.03
4KRM.PDB	O, I_THR_422	N, I_CYS_446	H, I_CYS_446	2.73	1.88	7.27
4KRM.PDB	O, I_TYR_447	OG1, I_THR_450	HG1, I_THR_450	2.88	2.08	15.87
4KRM.PDB	OE1, I_GLN_462	N, I_GLY_458	H, I_GLY_458	2.63	1.77	6.16
4KRM.PDB	OE1, I_GLN_462	N, I_THR_459	H, I_THR_459	2.73	1.99	24.99
4KRM.PDB	O, I_ILE_432	NE2, I_GLN_462	HE22, I_GLN_462	2.64	1.79	3.75
4KRM.PDB	O, I_VAL_437	N, I_LYS_465	H, I_LYS_465	2.80	2.00	17.16
4KRM.PDB	O, I_ILE_439	ND2, I_ASN_469	HD21, I_ASN_469	2.82	2.04	21.05
4KRM.PDB	OD1, I_ASN_473	OG, I_SER_474	HG, I_SER_474	2.73	1.91	11.26
4KRM.PDB	O, I_GLY_479	N, I_VAL_481	H, I_VAL_481	2.96	2.25	29.56
4KRM.PDB	OG1, I_THR_450	N, I_CYS_491	H, I_CYS_491	2.81	1.99	15.75
4KRM.PDB	O, I_ASP_498	N, I_TRP_492	H, I_TRP_492	2.78	1.96	14.16
4KRM.PDB	O, I_PRO_496	N, I_CYS_499	H, I_CYS_499	2.92	2.09	12.35
4KRM.PDB	O, J_SER_25	N, J_LYS_3	H, J_LYS_3	2.85	2.01	8.57
4KRM.PDB	O, J_ALA_23	N, J_GLU_5	H, J_GLU_5	2.99	2.16	13.86
4KRM.PDB	O, J_THR_121	N, J_VAL_12	H, J_VAL_12	3.00	2.24	24.14
4KRM.PDB	O, J_LEU_86	N, J_GLY_15	H, J_GLY_15	2.66	1.81	6.69
4KRM.PDB	O, J_GLN_13	N, J_GLY_16	H, J_GLY_16	2.94	2.17	21.17
4KRM.PDB	OD1, J_ASP_80	NE, J_ARG_19	HE, J_ARG_19	2.78	1.97	16.74
4KRM.PDB	O, J_LEU_81	N, J_LEU_20	H, J_LEU_20	2.96	2.15	16.27
4KRM.PDB	O, J_SER_7	N, J_THR_21	H, J_THR_21	2.87	2.05	15.09
4KRM.PDB	O, J_VAL_79	N, J_CYS_22	H, J_CYS_22	2.95	2.23	28.38
4KRM.PDB	O, J_GLU_5	N, J_ALA_23	H, J_ALA_23	2.89	2.08	15.16
4KRM.PDB	O, J_GLN_1	N, J_ARG_27	H, J_ARG_27	2.63	1.91	27.25
4KRM.PDB	O, J_THR_28	N, J_ARG_30	H, J_ARG_30	2.80	2.09	29.22
4KRM.PDB	O, J_SER_31	NH2, J_ARG_30	HH21, J_ARG_30	2.53	1.73	17.55
4KRM.PDB	O, J_ALA_99	N, J_GLY_33	H, J_GLY_33	2.86	2.12	25.08
4KRM.PDB	O, J_ILE_51	N, J_MET_34	H, J_MET_34	2.99	2.28	29.29
4KRM.PDB	O, J_ALA_97	N, J_GLY_35	H, J_GLY_35	2.84	2.04	17.40
4KRM.PDB	O, J_SER_49	N, J_TRP_36	H, J_TRP_36	2.70	1.86	9.65
4KRM.PDB	O, J_TYR_95	N, J_PHE_37	H, J_PHE_37	2.82	1.99	12.49
4KRM.PDB	O, J_GLU_46	N, J_ARG_38	H, J_ARG_38	2.92	2.10	15.90
4KRM.PDB	OH, J_TYR_94	NH1, J_ARG_38	HH11, J_ARG_38	2.85	2.02	12.10
4KRM.PDB	OD2, J_ASP_90	NH1, J_ARG_38	HH12, J_ARG_38	2.97	2.15	14.05
4KRM.PDB	O, J_ILE_93	N, J_GLN_39	H, J_GLN_39	2.89	2.11	20.97
4KRM.PDB	O, J_ARG_38	N, J_GLU_46	H, J_GLU_46	2.86	2.02	11.35
4KRM.PDB	O, J_TRP_36	N, J_VAL_48	H, J_VAL_48	2.89	2.09	18.44
4KRM.PDB	O, J_MET_34	N, J_ILE_51	H, J_ILE_51	2.84	2.02	15.75
4KRM.PDB	O, J_SER_57	N, J_SER_52	H, J_SER_52	2.88	2.10	20.91
4KRM.PDB	O, J_SER_102	N, J_TRP_53	H, J_TRP_53	2.92	2.12	18.19
4KRM.PDB	O, J_GLY_50	N, J_GLY_59	H, J_GLY_59	2.99	2.18	16.04
4KRM.PDB	O, G_GLU_308	N, J_TYR_60	H, J_TYR_60	2.74	1.97	22.05
4KRM.PDB	O, J_VAL_48	N, J_ALA_61	H, J_ALA_61	2.78	1.94	11.47
4KRM.PDB	O, J_SER_63	NH1, J_ARG_67	HH11, J_ARG_67	2.71	1.87	10.55

4KRM.PDB	OD1, J_ASP_90	NH2, J_ARG_67	HH22, J_ARG_67	2.61	1.77	10.49
4KRM.PDB	O, J_GLN_82	N, J_THR_69	H, J_THR_69	2.92	2.13	20.56
4KRM.PDB	OH, J_TYR_60	N, J_ILE_70	H, J_ILE_70	2.83	2.01	15.28
4KRM.PDB	OD1, J_ASN_74	NE, J_ARG_72	HE, J_ARG_72	2.67	1.87	16.97
4KRM.PDB	O, J_TYR_32	NH1, J_ARG_72	HH12, J_ARG_72	2.75	1.96	19.64
4KRM.PDB	O, J_TYR_32	NH2, J_ARG_72	HH22, J_ARG_72	2.98	2.27	29.63
4KRM.PDB	O, J_TRP_53	ND2, J_ASN_74	HD21, J_ASN_74	2.64	1.92	27.41
4KRM.PDB	O, J_SER_71	N, J_ASP_80	H, J_ASP_80	2.70	1.90	17.63
4KRM.PDB	O, J_LEU_20	N, J_LEU_81	H, J_LEU_81	2.84	2.06	20.27
4KRM.PDB	O, J_THR_69	N, J_GLN_82	H, J_GLN_82	2.78	1.99	19.54
4KRM.PDB	O, J_LEU_18	N, J_MET_83	H, J_MET_83	2.71	1.90	15.45
4KRM.PDB	OD1, J_ASP_90	N, J_LYS_87	H, J_LYS_87	2.95	2.13	13.64
4KRM.PDB	O, J_LYS_87	N, J_ASP_90	H, J_ASP_90	2.61	1.76	7.15
4KRM.PDB	O, J_ASP_90	OH, J_TYR_94	HH, J_TYR_94	2.63	1.80	7.10
4KRM.PDB	O, J_PHE_37	N, J_TYR_95	H, J_TYR_95	2.62	1.79	12.04
4KRM.PDB	OE2, J_GLU_6	N, J_CYS_96	H, J_CYS_96	2.75	1.91	8.89
4KRM.PDB	O, J_TYR_113	N, J_ALA_98	H, J_ALA_98	3.00	2.20	18.29
4KRM.PDB	O, J_GLY_33	N, J_ALA_99	H, J_ALA_99	2.77	1.94	13.41
4KRM.PDB	OD2, J_ASP_112	N, J_ALA_100	H, J_ALA_100	2.99	2.17	16.23
4KRM.PDB	O, J_SER_31	N, J_GLY_101	H, J_GLY_101	2.93	2.08	6.19
4KRM.PDB	OG, J_SER_57	NE1, J_TRP_104	HE1, J_TRP_104	2.98	2.26	28.43
4KRM.PDB	OH, J_TYR_111	N, J_TYR_105	H, J_TYR_105	2.99	2.14	8.48
4KRM.PDB	O, J_TYR_105	OH, J_TYR_111	HH, J_TYR_111	2.76	1.92	3.09
4KRM.PDB	O, J_ALA_98	N, J_ASP_112	H, J_ASP_112	2.80	2.02	20.50
4KRM.PDB	OE1, J_GLU_6	N, J_GLY_117	H, J_GLY_117	2.88	2.04	11.43
4KRM.PDB	O, J_ALA_92	N, J_VAL_120	H, J_VAL_120	2.87	2.03	9.32
4KRM.PDB	O, J_GLY_10	N, J_THR_121	H, J_THR_121	2.81	1.98	11.54
4KRM.PDB	OG1, J_THR_91	N, J_VAL_122	H, J_VAL_122	2.77	1.92	7.72
4KRM.PDB	O, K_SER_340	N, K_CYS_313	H, K_CYS_313	2.84	2.01	12.83
4KRM.PDB	O, K_ASP_344	N, K_ILE_316	H, K_ILE_316	3.00	2.29	29.47
4KRM.PDB	O, K_PHE_321	N, K_GLY_317	H, K_GLY_317	2.69	1.90	19.46
4KRM.PDB	OD1, K_ASN_331	N, K_ASN_328	H, K_ASN_328	2.83	1.99	11.57
4KRM.PDB	OD1, K_ASN_328	N, K_THR_330	H, K_THR_330	2.89	2.17	28.13
4KRM.PDB	O, K_SER_326	ND2, K_ASN_331	HD21, K_ASN_331	2.93	2.14	20.17
4KRM.PDB	O, K_LYS_311	N, K_THR_339	H, K_THR_339	2.88	2.03	7.02
4KRM.PDB	O, K_GLU_376	N, K_ILE_341	H, K_ILE_341	2.75	1.92	10.64
4KRM.PDB	O, K_CYS_313	N, K_SER_342	H, K_SER_342	2.81	1.98	11.90
4KRM.PDB	O, K_PHE_380	N, K_LEU_345	H, K_LEU_345	2.95	2.14	16.87
4KRM.PDB	O, K_LEU_382	N, K_ILE_347	H, K_ILE_347	2.87	2.09	20.57
4KRM.PDB	OD1, L_ASP_112	N, K_VAL_350	H, K_VAL_350	2.89	2.07	15.44
4KRM.PDB	O, K_LEU_348	N, K_ALA_351	H, K_ALA_351	2.98	2.18	17.67
4KRM.PDB	O, K_PRO_349	N, K_PHE_352	H, K_PHE_352	2.94	2.16	21.68
4KRM.PDB	OE1, L_GLU_110	NH1, K_ARG_353	HH11, K_ARG_353	2.89	2.06	12.41
4KRM.PDB	O, L_GLU_110	NH1, K_ARG_353	HH12, K_ARG_353	2.54	1.80	24.42
4KRM.PDB	O, L_ALA_100	NH2, K_ARG_353	HH21, K_ARG_353	2.92	2.14	20.95
4KRM.PDB	OD2, L_ASP_112	NH2, K_ARG_353	HH22, K_ARG_353	2.89	2.07	13.96
4KRM.PDB	O, K_VAL_350	N, K_GLY_354	H, K_GLY_354	2.71	1.91	17.56
4KRM.PDB	O, K_THR_360	N, K_ASP_355	H, K_ASP_355	2.67	1.85	14.28
4KRM.PDB	O, K_ASP_355	N, K_THR_358	H, K_THR_358	2.95	2.19	22.97
4KRM.PDB	OD2, K_ASP_355	OG1, K_THR_358	HG1, K_THR_358	2.91	2.21	28.73
4KRM.PDB	O, K_ASP_355	N, K_THR_360	H, K_THR_360	2.96	2.12	9.53
4KRM.PDB	O, K_ALA_351	N, K_LEU_363	H, K_LEU_363	2.66	1.89	22.52
4KRM.PDB	O, K_ASP_364	N, K_GLU_367	H, K_GLU_367	2.81	1.97	10.44
4KRM.PDB	O, K_LEU_368	N, K_LEU_371	H, K_LEU_371	2.97	2.12	7.39
4KRM.PDB	O, K_THR_339	N, K_LYS_375	H, K_LYS_375	2.86	2.00	4.75
4KRM.PDB	O, K_ILE_401	N, K_ILE_377	H, K_ILE_377	2.86	2.06	18.35
4KRM.PDB	O, K_SER_413	N, K_LEU_381	H, K_LEU_381	2.86	2.05	17.20
4KRM.PDB	O, K_LEU_345	N, K_LEU_382	H, K_LEU_382	2.82	1.96	1.57

4KRM.PDB	O, K_ALA_415	N, K_ILE_383	H, K_ILE_383	2.80	1.95	7.54
4KRM.PDB	O, K_ILE_347	N, K_GLN_384	H, K_GLN_384	2.96	2.17	19.38
4KRM.PDB	O, K_LYS_375	N, K_GLU_400	H, K_GLU_400	2.90	2.08	14.24
4KRM.PDB	O, K_LYS_375	N, K_ILE_401	H, K_ILE_401	2.95	2.14	17.68
4KRM.PDB	O, K_ILE_377	N, K_ARG_403	H, K_ARG_403	2.74	1.95	18.26
4KRM.PDB	O, K_THR_378	N, K_ARG_405	H, K_ARG_405	2.74	1.91	12.90
4KRM.PDB	O, K_PHE_412	N, K_GLN_408	H, K_GLN_408	2.74	1.94	17.95
4KRM.PDB	O, K_ASP_436	N, K_SER_413	H, K_SER_413	2.84	2.02	13.83
4KRM.PDB	O, K_LEU_381	N, K_ALA_415	H, K_ALA_415	2.89	2.12	21.80
4KRM.PDB	O, K_SER_440	N, K_SER_418	H, K_SER_418	2.83	1.99	11.88
4KRM.PDB	O, K_THR_391	N, K_THR_422	H, K_THR_422	2.85	2.06	19.39
4KRM.PDB	O, K_GLU_400	N, K_LYS_430	H, K_LYS_430	2.91	2.08	12.04
4KRM.PDB	O, K_LEU_456	N, K_ILE_432	H, K_ILE_432	2.65	1.80	6.86
4KRM.PDB	OD2, K_ASP_434	N, K_GLY_435	H, K_GLY_435	2.55	1.82	26.56
4KRM.PDB	O, K_GLN_411	N, K_ASP_436	H, K_ASP_436	2.63	1.81	13.73
4KRM.PDB	O, K_LYS_465	N, K_ILE_439	H, K_ILE_439	2.92	2.09	12.95
4KRM.PDB	OD1, K_ASN_469	N, K_ASN_442	H, K_ASN_442	2.83	2.07	23.19
4KRM.PDB	O, K_THR_422	N, K_CYS_446	H, K_CYS_446	2.91	2.07	11.69
4KRM.PDB	O, K_TYR_447	OG1, K_THR_450	HG1, K_THR_450	2.66	1.87	18.01
4KRM.PDB	OE1, K_GLN_462	N, K_GLY_458	H, K_GLY_458	2.63	1.78	7.92
4KRM.PDB	OE1, K_GLN_462	N, K_THR_459	H, K_THR_459	2.89	2.13	24.15
4KRM.PDB	O, K_GLY_435	NE2, K_GLN_462	HE21, K_GLN_462	2.96	2.10	5.79
4KRM.PDB	O, K_ILE_432	NE2, K_GLN_462	HE22, K_GLN_462	2.88	2.05	10.71
4KRM.PDB	OD1, K_ASP_436	N, K_LYS_463	H, K_LYS_463	2.88	2.03	6.44
4KRM.PDB	O, K_VAL_437	N, K_LYS_465	H, K_LYS_465	2.84	2.14	29.81
4KRM.PDB	O, K_ILE_439	ND2, K_ASN_469	HD21, K_ASN_469	2.65	1.81	9.31
4KRM.PDB	O, K_HIS_483	N, K_CYS_486	H, K_CYS_486	2.95	2.11	10.23
4KRM.PDB	O, K_SER_501	N, K_SER_487	H, K_SER_487	2.75	1.90	8.02
4KRM.PDB	O, K_ASP_498	N, K_TRP_492	H, K_TRP_492	2.71	1.86	9.15
4KRM.PDB	OD2, K_ASP_498	N, K_GLU_495	H, K_GLU_495	2.88	2.09	20.84
4KRM.PDB	O, K_GLU_495	N, K_ASP_498	H, K_ASP_498	2.85	2.04	15.93
4KRM.PDB	O, L_SER_25	N, L_LYS_3	H, L_LYS_3	2.83	2.01	14.97
4KRM.PDB	O, L_THR_121	N, L_VAL_12	H, L_VAL_12	2.91	2.16	24.48
4KRM.PDB	O, L_SER_123	OG1, L_THR_14	HG1, L_THR_14	2.67	1.86	12.28
4KRM.PDB	O, L_LEU_86	N, L_GLY_15	H, L_GLY_15	2.91	2.05	2.74
4KRM.PDB	O, L_GLN_13	N, L_GLY_16	H, L_GLY_16	2.82	2.02	18.09
4KRM.PDB	O, L_MET_83	N, L_LEU_18	H, L_LEU_18	2.78	1.98	18.62
4KRM.PDB	OD1, L_ASP_80	NE, L_ARG_19	HE, L_ARG_19	2.96	2.10	5.59
4KRM.PDB	O, L_SER_7	N, L_THR_21	H, L_THR_21	2.74	1.90	9.36
4KRM.PDB	O, L_GLN_1	N, L_ARG_27	H, L_ARG_27	2.68	1.97	28.48
4KRM.PDB	OD2, K_ASP_355	NH1, L_ARG_30	HH12, L_ARG_30	2.44	1.65	18.93
4KRM.PDB	O, L_SER_31	NH2, L_ARG_30	HH21, L_ARG_30	2.82	1.99	12.91
4KRM.PDB	O, L_ALA_99	N, L_GLY_33	H, L_GLY_33	2.77	2.03	25.95
4KRM.PDB	O, L_ILE_51	N, L_MET_34	H, L_MET_34	2.99	2.20	19.18
4KRM.PDB	O, L_SER_49	N, L_TRP_36	H, L_TRP_36	2.68	1.84	10.36
4KRM.PDB	O, L_TYR_95	N, L_PHE_37	H, L_PHE_37	2.91	2.07	10.93
4KRM.PDB	O, L_GLU_46	N, L_ARG_38	H, L_ARG_38	2.90	2.07	13.98
4KRM.PDB	OE1, L_GLU_46	NE, L_ARG_38	HE, L_ARG_38	2.86	2.01	10.17
4KRM.PDB	O, L_ARG_38	N, L_GLU_46	H, L_GLU_46	2.74	1.90	10.16
4KRM.PDB	O, L_GLY_59	OG, L_SER_49	HG, L_SER_49	2.90	2.14	20.97
4KRM.PDB	O, L_MET_34	N, L_ILE_51	H, L_ILE_51	2.78	1.94	10.92
4KRM.PDB	O, L_SER_57	N, L_SER_52	H, L_SER_52	2.96	2.15	16.80
4KRM.PDB	O, L_SER_102	N, L_TRP_53	H, L_TRP_53	3.00	2.20	17.87
4KRM.PDB	O, L_LYS_310	N, L_THR_58	H, L_THR_58	2.98	2.15	12.69
4KRM.PDB	O, L_GLY_50	N, L_GLY_59	H, L_GLY_59	2.79	1.99	18.05
4KRM.PDB	O, L_GLU_308	N, L_TYR_60	H, L_TYR_60	2.75	2.02	27.31
4KRM.PDB	O, L_VAL_48	N, L_ALA_61	H, L_ALA_61	2.83	1.98	9.16
4KRM.PDB	O, L_VAL_64	N, L_ARG_67	H, L_ARG_67	3.00	2.22	21.09

4KRM.PDB	O, L_SER_63	NH1, L_ARG_67	HH11, L_ARG_67	2.44	1.68	23.68
4KRM.PDB	OD1, L_ASP_90	NH2, L_ARG_67	HH22, L_ARG_67	2.60	1.80	17.17
4KRM.PDB	O, L_GLN_82	N, L_THR_69	H, L_THR_69	2.84	2.07	22.44
4KRM.PDB	OH, L_TYR_60	N, L_ILE_70	H, L_ILE_70	2.86	2.03	11.87
4KRM.PDB	O, L_SER_71	N, L_ASP_80	H, L_ASP_80	2.67	1.93	24.67
4KRM.PDB	O, L_LEU_20	N, L_LEU_81	H, L_LEU_81	2.93	2.20	26.65
4KRM.PDB	O, L_THR_69	N, L_GLN_82	H, L_GLN_82	2.79	2.06	26.22
4KRM.PDB	O, L_LEU_18	N, L_MET_83	H, L_MET_83	2.64	1.78	5.27
4KRM.PDB	OD1, L_ASP_90	N, L_LYS_87	H, L_LYS_87	2.83	2.05	20.17
4KRM.PDB	O, L_LYS_87	N, L_ASP_90	H, L_ASP_90	2.74	1.91	10.51
4KRM.PDB	O, L_VAL_120	N, L_ALA_92	H, L_ALA_92	2.86	2.07	19.77
4KRM.PDB	O, L_THR_118	N, L_TYR_94	H, L_TYR_94	2.84	2.02	14.78
4KRM.PDB	O, L_ASP_90	OH, L_TYR_94	HH, L_TYR_94	2.64	1.81	6.78
4KRM.PDB	O, L_PHE_37	N, L_TYR_95	H, L_TYR_95	2.71	1.89	15.70
4KRM.PDB	OE2, L_GLU_6	N, L_CYS_96	H, L_CYS_96	2.72	1.88	9.52
4KRM.PDB	O, L_TYR_113	N, L_ALA_98	H, L_ALA_98	2.86	2.11	25.39
4KRM.PDB	O, L_GLY_33	N, L_ALA_99	H, L_ALA_99	2.67	1.81	5.83
4KRM.PDB	O, L_SER_31	N, L_GLY_101	H, L_GLY_101	2.99	2.14	7.82
4KRM.PDB	O, L_TYR_105	OH, L_TYR_111	HH, L_TYR_111	2.61	1.77	5.19
4KRM.PDB	O, L_ALA_98	N, L_ASP_112	H, L_ASP_112	2.77	2.00	22.02
4KRM.PDB	O, L_ALA_92	N, L_VAL_120	H, L_VAL_120	2.77	1.92	3.01
4KRM.PDB	O, L_GLY_10	N, L_THR_121	H, L_THR_121	2.92	2.12	18.79
4KRM.PDB	OG1, L_THR_91	N, L_VAL_122	H, L_VAL_122	2.76	1.92	9.29

Table 1693: 4KRM-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4KRO.PDB	O, A_LYS_5	N, A_GLU_35	H, A_GLU_35	2.92	2.11	16.47
4KRO.PDB	O, A_VAL_268	N, A_TYR_261	H, A_TYR_261	2.78	2.04	26.05
4KRO.PDB	O, A_VAL_284	N, A_VAL_276	H, A_VAL_276	2.65	1.87	20.75
4KRO.PDB	O, A_SER_282	N, A_THR_278	H, A_THR_278	2.79	1.96	11.51
4KRO.PDB	OG1, A_THR_278	OG, A_SER_282	HG, A_SER_282	2.99	2.27	26.50
4KRO.PDB	O, A_SER_262	N, A_CYS_283	H, A_CYS_283	2.82	2.04	21.13
4KRO.PDB	O, A_VAL_276	N, A_VAL_284	H, A_VAL_284	2.74	2.03	29.17
4KRO.PDB	O, A_LYS_303	N, A_TYR_292	H, A_TYR_292	2.85	1.99	3.19
4KRO.PDB	O, A_LYS_301	N, A_MET_294	H, A_MET_294	2.78	1.96	14.61
4KRO.PDB	OE2, A_GLU_376	NH2, A_ARG_310	HH21, A_ARG_310	2.98	2.18	18.33
4KRO.PDB	OG1, A_THR_339	N, A_LYS_311	H, A_LYS_311	2.69	1.85	11.41
4KRO.PDB	O, A_LYS_336	NZ, A_LYS_311	HZ2, A_LYS_311	2.69	1.83	12.56
4KRO.PDB	O, A_ASP_344	N, A_ILE_316	H, A_ILE_316	2.97	2.17	18.52
4KRO.PDB	O, A_ILE_318	N, A_PHE_321	H, A_PHE_321	2.93	2.07	5.85
4KRO.PDB	OD1, A_ASN_331	N, A_ASN_328	H, A_ASN_328	2.73	1.96	22.23
4KRO.PDB	OD1, A_ASN_328	N, A_ASN_331	H, A_ASN_331	2.87	2.05	14.42
4KRO.PDB	O, A_ASN_331	N, A_HIS_334	H, A_HIS_334	2.89	2.11	21.52
4KRO.PDB	O, A_LYS_311	N, A_THR_339	H, A_THR_339	2.87	2.02	7.89
4KRO.PDB	O, A_CYS_313	N, A_SER_342	H, A_SER_342	2.88	2.10	20.40
4KRO.PDB	OG1, A_THR_378	N, A_GLY_343	H, A_GLY_343	2.79	1.97	15.18
4KRO.PDB	O, A_PHE_380	N, A_LEU_345	H, A_LEU_345	2.94	2.19	25.43
4KRO.PDB	O, A_LEU_382	N, A_ILE_347	H, A_ILE_347	2.91	2.17	26.62
4KRO.PDB	O, D_GLY_54	NH1, A_ARG_353	HH12, A_ARG_353	2.81	1.97	9.47
4KRO.PDB	O, A_VAL_350	N, A_GLY_354	H, A_GLY_354	2.70	1.97	26.74
4KRO.PDB	O, A_THR_360	N, A_ASP_355	H, A_ASP_355	2.94	2.16	20.76
4KRO.PDB	OD2, A_ASP_355	OG1, A_THR_358	HG1, A_THR_358	2.98	2.18	14.96
4KRO.PDB	O, A_SER_356	N, A_HIS_359	H, A_HIS_359	2.50	1.76	24.87
4KRO.PDB	O, A_ALA_351	N, A_LEU_363	H, A_LEU_363	2.64	1.78	3.26
4KRO.PDB	O, A_ASP_364	N, A_GLU_367	H, A_GLU_367	2.99	2.20	18.77
4KRO.PDB	O, A_LEU_368	N, A_LEU_371	H, A_LEU_371	2.92	2.07	9.49
4KRO.PDB	O, A_ASP_369	N, A_LYS_372	H, A_LYS_372	2.82	1.98	9.49
4KRO.PDB	O, A_CYS_338	OG1, A_THR_373	HG1, A_THR_373	2.91	2.20	27.34
4KRO.PDB	O, A_THR_339	N, A_LYS_375	H, A_LYS_375	2.64	1.78	1.90
4KRO.PDB	OG, B_SER_103	NZ, A_LYS_375	HZ2, A_LYS_375	2.61	1.76	15.34
4KRO.PDB	O, A_ILE_401	N, A_ILE_377	H, A_ILE_377	2.94	2.13	16.36
4KRO.PDB	OD1, A_ASP_344	N, A_PHE_380	H, A_PHE_380	2.92	2.14	21.56
4KRO.PDB	O, A_SER_413	N, A_LEU_381	H, A_LEU_381	2.80	2.00	16.89
4KRO.PDB	O, A_LEU_345	N, A_LEU_382	H, A_LEU_382	2.86	2.00	3.58
4KRO.PDB	O, A_ALA_415	N, A_ILE_383	H, A_ILE_383	2.88	2.04	11.10
4KRO.PDB	O, A_ILE_347	N, A_GLN_384	H, A_GLN_384	2.90	2.16	25.76
4KRO.PDB	OH, D_TYR_102	NE2, A_GLN_384	HE21, A_GLN_384	2.87	2.16	29.24
4KRO.PDB	O, A_LEU_424	N, A_LEU_393	H, A_LEU_393	2.79	1.95	10.09
4KRO.PDB	O, A_ASP_392	N, A_HIS_394	H, A_HIS_394	2.67	1.93	25.23
4KRO.PDB	O, A_LEU_393	N, A_PHE_396	H, A_PHE_396	2.83	1.98	8.97
4KRO.PDB	O, A_HIS_394	N, A_GLU_397	H, A_GLU_397	2.93	2.19	26.10
4KRO.PDB	O, A_LYS_375	N, A_GLU_400	H, A_GLU_400	2.79	1.95	10.25
4KRO.PDB	O, A_GLU_431	N, A_ILE_402	H, A_ILE_402	2.98	2.18	17.20
4KRO.PDB	O, A_ILE_377	N, A_ARG_403	H, A_ARG_403	2.73	1.91	14.33
4KRO.PDB	O, B_TYR_100	NH2, A_ARG_403	HH22, A_ARG_403	2.57	1.73	11.63
4KRO.PDB	O, A_GLY_379	N, A_GLY_404	H, A_GLY_404	2.93	2.20	27.61
4KRO.PDB	O, A_THR_378	N, A_ARG_405	H, A_ARG_405	2.90	2.05	8.12
4KRO.PDB	OD1, B_ASP_118	NE, A_ARG_405	HE, A_ARG_405	2.72	1.93	19.48
4KRO.PDB	O, A_PHE_412	N, A_GLN_408	H, A_GLN_408	2.80	2.00	17.98
4KRO.PDB	O, A_GLN_408	N, A_GLN_411	H, A_GLN_411	2.81	2.01	18.21
4KRO.PDB	O, A_GLN_408	N, A_PHE_412	H, A_PHE_412	2.97	2.14	13.47
4KRO.PDB	O, A_ASP_436	N, A_SER_413	H, A_SER_413	2.98	2.23	25.46
4KRO.PDB	O, A_ILE_438	N, A_VAL_416	H, A_VAL_416	2.84	2.03	15.03

4KRO.PDB	O, A_SER_440	N, A_SER_418	H, A_SER_418	2.77	2.00	21.19
4KRO.PDB	OD1, A_ASN_442	N, A_LEU_419	H, A_LEU_419	2.67	1.82	7.73
4KRO.PDB	O, A_THR_391	N, A_THR_422	H, A_THR_422	2.54	1.70	10.95
4KRO.PDB	OD1, A_ASP_498	NH2, A_ARG_427	HH21, A_ARG_427	2.62	1.82	18.67
4KRO.PDB	O, A_GLU_400	N, A_LYS_430	H, A_LYS_430	2.73	1.88	4.94
4KRO.PDB	O, A_GLN_411	N, A_ASP_436	H, A_ASP_436	2.89	2.06	12.84
4KRO.PDB	O, A_LEU_414	N, A_ILE_438	H, A_ILE_438	2.87	2.04	13.24
4KRO.PDB	O, A_LYS_465	N, A_ILE_439	H, A_ILE_439	2.84	1.99	6.10
4KRO.PDB	OD1, A_ASN_469	ND2, A_ASN_442	HD22, A_ASN_442	2.75	1.96	18.83
4KRO.PDB	O, A_THR_422	N, A_CYS_446	H, A_CYS_446	2.88	2.05	14.08
4KRO.PDB	O, A_TRP_453	N, A_LEU_456	H, A_LEU_456	2.81	2.03	20.74
4KRO.PDB	O, A_SER_433	OG1, A_THR_459	HG1, A_THR_459	2.64	1.93	27.14
4KRO.PDB	O, A_GLY_435	NE2, A_GLN_462	HE21, A_GLN_462	2.56	1.71	6.56
4KRO.PDB	OD1, A_ASP_436	N, A_LYS_463	H, A_LYS_463	2.76	1.91	6.26
4KRO.PDB	O, A_VAL_437	N, A_LYS_465	H, A_LYS_465	2.89	2.08	15.96
4KRO.PDB	O, A_ILE_439	N, A_ILE_467	H, A_ILE_467	2.90	2.11	19.76
4KRO.PDB	O, A_GLU_472	N, A_LYS_476	H, A_LYS_476	2.82	2.01	16.80
4KRO.PDB	O, A_HIS_483	N, A_CYS_486	H, A_CYS_486	3.00	2.18	14.93
4KRO.PDB	O, A_SER_501	N, A_SER_487	H, A_SER_487	2.94	2.09	7.57
4KRO.PDB	OG, A_SER_501	OG, A_SER_487	HG, A_SER_487	2.37	1.68	29.03
4KRO.PDB	OG, A_SER_487	N, A_GLU_489	H, A_GLU_489	2.96	2.12	10.12
4KRO.PDB	O, A_ASP_498	N, A_TRP_492	H, A_TRP_492	2.74	1.90	10.17
4KRO.PDB	O, A_GLY_490	N, A_VAL_500	H, A_VAL_500	2.91	2.13	19.89
4KRO.PDB	O, A_LEU_485	N, A_ARG_503	H, A_ARG_503	2.90	2.06	9.38
4KRO.PDB	OD1, A_ASN_504	NH1, A_ARG_503	HH11, A_ARG_503	2.52	1.76	23.61
4KRO.PDB	O, A_VAL_505	N, A_VAL_512	H, A_VAL_512	2.94	2.11	13.63
4KRO.PDB	OE1, A_GLU_524	N, A_ASN_516	H, A_ASN_516	2.81	1.95	3.86
4KRO.PDB	O, A_CYS_515	N, A_LEU_517	H, A_LEU_517	2.67	1.93	26.36
4KRO.PDB	O, A_LEU_517	N, A_GLU_519	H, A_GLU_519	2.78	2.04	26.41
4KRO.PDB	O, A_GLY_520	NH1, A_ARG_523	HH11, A_ARG_523	2.75	2.02	27.17
4KRO.PDB	O, A_ILE_532	N, A_PHE_525	H, A_PHE_525	2.85	2.07	20.01
4KRO.PDB	O, A_PHE_525	N, A_ILE_532	H, A_ILE_532	2.90	2.06	11.44
4KRO.PDB	O, A_ARG_523	N, A_CYS_534	H, A_CYS_534	2.64	1.78	1.35
4KRO.PDB	O, A_PRO_536	N, A_CYS_538	H, A_CYS_538	2.84	2.10	26.42
4KRO.PDB	O, A_GLN_557	N, A_LEU_539	H, A_LEU_539	2.89	2.11	20.92
4KRO.PDB	O, A_LEU_539	NE2, A_GLN_541	HE21, A_GLN_541	2.61	1.79	15.38
4KRO.PDB	O, A_ASN_554	N, A_THR_548	H, A_THR_548	2.75	1.93	14.66
4KRO.PDB	OG1, A_THR_548	ND2, A_ASN_554	HD22, A_ASN_554	2.92	2.13	19.09
4KRO.PDB	O, A_VAL_568	N, A_TYR_561	H, A_TYR_561	2.97	2.17	17.83
4KRO.PDB	O, A_GLY_458	N, B_VAL_2	H, B_VAL_2	2.76	1.93	12.61
4KRO.PDB	O, B_SER_25	N, B_GLN_3	H, B_GLN_3	2.75	1.92	13.69
4KRO.PDB	O, B_THR_77	N, B_ALA_24	H, B_ALA_24	2.76	1.99	21.77
4KRO.PDB	O, B_THR_99	N, B_ALA_33	H, B_ALA_33	2.78	2.00	21.37
4KRO.PDB	O, B_ILE_51	N, B_MET_34	H, B_MET_34	2.93	2.11	14.97
4KRO.PDB	O, B_GLY_55	N, B_TYR_57	H, B_TYR_57	2.52	1.78	25.18
4KRO.PDB	O, B_TYR_119	N, B_ALA_98	H, B_ALA_98	2.93	2.19	26.24
4KRO.PDB	O, B_SER_31	N, B_LEU_101	H, B_LEU_101	2.95	2.17	21.67
4KRO.PDB	O, B_SER_102	N, B_TYR_105	H, B_TYR_105	2.87	2.05	13.73
4KRO.PDB	O, B_PRO_114	N, B_TYR_117	H, B_TYR_117	2.95	2.10	5.45
4KRO.PDB	O, B_PRO_111	OH, B_TYR_117	HH, B_TYR_117	2.59	1.81	17.04
4KRO.PDB	O, C_ARG_24	N, C_THR_5	H, C_THR_5	2.91	2.15	23.49
4KRO.PDB	O, C_GLU_105	N, C_VAL_13	H, C_VAL_13	3.00	2.29	29.53
4KRO.PDB	O, C_LEU_73	N, C_PHE_21	H, C_PHE_21	2.68	1.86	14.19
4KRO.PDB	O, C_PHE_71	N, C_CYS_23	H, C_CYS_23	2.97	2.13	10.71
4KRO.PDB	O, C_THR_5	N, C_ARG_24	H, C_ARG_24	2.88	2.05	12.65
4KRO.PDB	O, C_THR_69	N, C_ALA_25	H, C_ALA_25	2.78	1.97	17.42
4KRO.PDB	O, C_GLY_68	N, C_ILE_29	H, C_ILE_29	2.76	1.93	13.88
4KRO.PDB	O, C_THR_31	N, C_ILE_33	H, C_ILE_33	2.83	2.11	27.53

4KRO.PDB	O, C_GLN_89	N, C_HIS_34	H, C_HIS_34	2.73	1.95	19.98
4KRO.PDB	O, C_ILE_48	N, C_TRP_35	H, C_TRP_35	2.83	2.00	11.93
4KRO.PDB	O, C_TYR_87	N, C_TYR_36	H, C_TYR_36	2.69	1.90	19.38
4KRO.PDB	OE1, C_GLN_89	OH, C_TYR_36	HH, C_TYR_36	2.63	1.80	6.46
4KRO.PDB	O, C_ARG_45	N, C_GLN_37	H, C_GLN_37	2.62	1.80	13.58
4KRO.PDB	OH, C_TYR_86	NE2, C_GLN_37	HE21, C_GLN_37	2.94	2.13	16.57
4KRO.PDB	O, C_ASP_85	N, C_GLN_38	H, C_GLN_38	2.68	1.83	9.02
4KRO.PDB	OE1, D_GLN_39	NE2, C_GLN_38	HE22, C_GLN_38	2.85	2.00	7.50
4KRO.PDB	O, C_GLN_37	N, C_ARG_45	H, C_ARG_45	2.41	1.69	27.50
4KRO.PDB	O, C_TRP_35	N, C_LEU_47	H, C_LEU_47	2.85	1.99	3.81
4KRO.PDB	O, C_GLU_53	N, C_LYS_49	H, C_LYS_49	2.98	2.17	16.10
4KRO.PDB	OD2, D_ASP_103	OH, C_TYR_50	HH, C_TYR_50	2.49	1.72	20.15
4KRO.PDB	O, C_ILE_33	N, C_ALA_51	H, C_ALA_51	2.88	2.14	26.02
4KRO.PDB	OD1, C_ASP_82	NH2, C_ARG_61	HH21, C_ARG_61	2.64	1.81	12.76
4KRO.PDB	O, C_GLY_30	N, C_GLY_68	H, C_GLY_68	2.70	1.96	25.34
4KRO.PDB	O, C_CYS_23	N, C_PHE_71	H, C_PHE_71	2.97	2.22	24.26
4KRO.PDB	O, C_SER_63	N, C_SER_74	H, C_SER_74	2.78	1.94	9.14
4KRO.PDB	O, C_VAL_19	N, C_ILE_75	H, C_ILE_75	2.80	2.05	24.74
4KRO.PDB	OD2, C_ASP_82	N, C_GLU_79	H, C_GLU_79	2.59	1.74	8.25
4KRO.PDB	O, C_GLU_79	N, C_ASP_82	H, C_ASP_82	2.82	1.98	10.41
4KRO.PDB	O, C_GLN_38	N, C_ASP_85	H, C_ASP_85	2.89	2.07	15.87
4KRO.PDB	O, C_THR_102	N, C_TYR_86	H, C_TYR_86	2.96	2.19	22.34
4KRO.PDB	O, C_ASP_82	OH, C_TYR_86	HH, C_TYR_86	2.61	1.78	7.16
4KRO.PDB	O, C_TYR_36	N, C_TYR_87	H, C_TYR_87	2.90	2.11	19.86
4KRO.PDB	O, D_TYR_104	NE2, C_GLN_89	HE22, C_GLN_89	3.00	2.19	16.80
4KRO.PDB	OD1, D_ASP_103	ND2, C_ASN_91	HD21, C_ASN_91	2.93	2.12	16.18
4KRO.PDB	OE1, C_GLN_90	N, C_ASN_92	H, C_ASN_92	2.89	2.15	26.36
4KRO.PDB	OD1, C_ASN_32	ND2, C_ASN_92	HD22, C_ASN_92	2.97	2.20	23.59
4KRO.PDB	O, A_ASN_469	N, C_TRP_94	H, C_TRP_94	2.75	1.95	19.24
4KRO.PDB	OD2, D_ASP_58	NE1, C_TRP_94	HE1, C_TRP_94	2.80	2.10	29.15
4KRO.PDB	O, C_CYS_88	N, C_GLY_99	H, C_GLY_99	2.89	2.12	21.60
4KRO.PDB	OE1, C_GLN_6	N, C_GLY_101	H, C_GLY_101	2.92	2.21	28.54
4KRO.PDB	O, C_TYR_86	N, C_THR_102	H, C_THR_102	2.97	2.19	21.52
4KRO.PDB	O, C_PRO_8	OG1, C_THR_102	HG1, C_THR_102	2.68	1.90	18.51
4KRO.PDB	O, C_VAL_9	N, C_LYS_103	H, C_LYS_103	2.98	2.14	9.34
4KRO.PDB	O, C_VAL_13	N, C_LYS_107	H, C_LYS_107	2.95	2.13	15.77
4KRO.PDB	O, C_TYR_140	N, C_ALA_111	H, C_ALA_111	2.89	2.03	3.33
4KRO.PDB	O, C_LEU_135	N, C_PHE_116	H, C_PHE_116	2.87	2.15	27.51
4KRO.PDB	O, C_VAL_133	N, C_PHE_118	H, C_PHE_118	2.79	2.04	24.19
4KRO.PDB	OG, C_SER_121	N, C_GLN_124	H, C_GLN_124	2.92	2.16	22.95
4KRO.PDB	OG, C_SER_131	NE2, C_GLN_124	HE22, C_GLN_124	2.85	2.00	6.78
4KRO.PDB	OE1, C_GLN_124	N, C_SER_131	H, C_SER_131	2.94	2.16	21.66
4KRO.PDB	O, C_LEU_179	N, C_VAL_132	H, C_VAL_132	2.76	1.90	3.17
4KRO.PDB	O, C_SER_177	N, C_CYS_134	H, C_CYS_134	2.88	2.05	12.39
4KRO.PDB	O, C_PHE_116	N, C_LEU_135	H, C_LEU_135	2.91	2.11	17.23
4KRO.PDB	O, C_LEU_175	N, C_LEU_136	H, C_LEU_136	2.87	2.05	14.62
4KRO.PDB	O, C_SER_114	N, C_ASN_137	H, C_ASN_137	2.91	2.13	21.13
4KRO.PDB	O, C_TYR_173	N, C_PHE_139	H, C_PHE_139	2.69	1.92	21.18
4KRO.PDB	O, C_ALA_111	N, C_TYR_140	H, C_TYR_140	2.84	1.99	7.77
4KRO.PDB	O, C_GLU_195	N, C_GLN_147	H, C_GLN_147	2.74	1.94	17.18
4KRO.PDB	OG, C_SER_177	NE1, C_TRP_148	HE1, C_TRP_148	2.83	2.01	15.90
4KRO.PDB	O, C_VAL_150	N, C_ALA_153	H, C_ALA_153	3.00	2.29	29.91
4KRO.PDB	O, C_TRP_148	N, C_GLN_155	H, C_GLN_155	2.90	2.07	11.42
4KRO.PDB	OE1, C_GLN_155	ND2, C_ASN_158	HD21, C_ASN_158	2.72	1.97	24.54
4KRO.PDB	O, D_LEU_176	NE2, C_GLN_160	HE22, C_GLN_160	2.74	1.92	15.89
4KRO.PDB	O, C_SER_174	N, C_THR_164	H, C_THR_164	2.94	2.12	15.62
4KRO.PDB	O, C_LEU_106	NE2, C_GLN_166	HE22, C_GLN_166	2.49	1.66	13.43
4KRO.PDB	OD1, C_ASP_167	N, C_LYS_169	H, C_LYS_169	2.54	1.73	16.83

4KRO.PDB	OD1, C_ASP_167	N, C_ASP_170	H, C_ASP_170	2.97	2.21	22.78
4KRO.PDB	OD1, C_ASP_170	OG1, C_THR_172	HG1, C_THR_172	2.68	1.86	11.97
4KRO.PDB	O, C_PHE_139	N, C_TYR_173	H, C_TYR_173	2.66	1.84	12.86
4KRO.PDB	O, C_LEU_136	N, C_LEU_175	H, C_LEU_175	2.88	2.06	14.51
4KRO.PDB	O, C_SER_162	N, C_SER_176	H, C_SER_176	2.82	2.00	14.99
4KRO.PDB	O, C_GLN_160	N, C_THR_178	H, C_THR_178	2.80	2.08	27.64
4KRO.PDB	O, C_VAL_132	N, C_LEU_179	H, C_LEU_179	2.78	2.01	22.37
4KRO.PDB	OG, C_SER_182	N, C_ASP_185	H, C_ASP_185	2.76	1.91	3.71
4KRO.PDB	O, C_SER_182	N, C_TYR_186	H, C_TYR_186	2.63	1.82	15.93
4KRO.PDB	O, C_LYS_183	N, C_GLU_187	H, C_GLU_187	2.89	2.10	19.45
4KRO.PDB	O, C_ASP_185	ND1, C_HIS_189	HD1, C_HIS_189	2.98	2.14	11.48
4KRO.PDB	O, C_TYR_186	OH, C_TYR_192	HH, C_TYR_192	2.55	1.84	27.09
4KRO.PDB	O, C_LYS_149	N, C_ALA_193	H, C_ALA_193	2.99	2.27	28.68
4KRO.PDB	O, C_GLN_147	N, C_GLU_195	H, C_GLU_195	2.80	2.05	25.03
4KRO.PDB	O, C_PRO_141	NE2, C_HIS_198	HE2, C_HIS_198	2.93	2.09	10.93
4KRO.PDB	O, D_SER_25	N, D_GLN_3	H, D_GLN_3	2.73	1.89	10.77
4KRO.PDB	O, D_THR_23	N, D_LYS_5	H, D_LYS_5	2.94	2.08	5.53
4KRO.PDB	OE1, D_GLN_111	N, D_GLN_6	H, D_GLN_6	2.70	1.86	8.92
4KRO.PDB	O, D_TYR_93	NE2, D_GLN_6	HE22, D_GLN_6	2.93	2.12	16.83
4KRO.PDB	O, D_THR_116	N, D_VAL_12	H, D_VAL_12	2.92	2.09	13.60
4KRO.PDB	O, D_LEU_85	N, D_SER_15	H, D_SER_15	2.92	2.10	15.76
4KRO.PDB	O, D_MET_82	N, D_LEU_18	H, D_LEU_18	2.86	2.03	12.27
4KRO.PDB	O, D_SER_7	N, D_THR_21	H, D_THR_21	2.91	2.14	22.32
4KRO.PDB	O, D_VAL_78	N, D_CYS_22	H, D_CYS_22	2.84	2.11	27.17
4KRO.PDB	O, D_LYS_5	N, D_THR_23	H, D_THR_23	2.75	1.97	20.91
4KRO.PDB	O, D_SER_76	N, D_VAL_24	H, D_VAL_24	2.87	2.01	5.71
4KRO.PDB	O, D_GLN_3	N, D_SER_25	H, D_SER_25	2.95	2.20	25.22
4KRO.PDB	OG, D_SER_28	N, D_THR_30	H, D_THR_30	2.84	2.00	11.38
4KRO.PDB	O, D_ALA_96	N, D_HIS_35	H, D_HIS_35	2.82	2.00	14.36
4KRO.PDB	O, D_GLY_49	N, D_TRP_36	H, D_TRP_36	2.85	2.06	19.08
4KRO.PDB	O, D_GLU_46	N, D_ARG_38	H, D_ARG_38	2.89	2.07	15.74
4KRO.PDB	OE1, D_GLU_46	NE, D_ARG_38	HE, D_ARG_38	3.00	2.22	20.92
4KRO.PDB	OH, D_TYR_93	NH1, D_ARG_38	HH11, D_ARG_38	2.92	2.15	22.16
4KRO.PDB	OE1, D_GLU_46	NH2, D_ARG_38	HH21, D_ARG_38	2.98	2.22	22.99
4KRO.PDB	O, D_ILE_92	N, D_GLN_39	H, D_GLN_39	2.94	2.21	27.13
4KRO.PDB	OE1, C_GLN_38	NE2, D_GLN_39	HE22, D_GLN_39	2.80	1.94	4.32
4KRO.PDB	OG, D_SER_40	N, D_GLY_42	H, D_GLY_42	2.92	2.07	6.19
4KRO.PDB	OG, D_SER_40	N, D_LYS_43	H, D_LYS_43	2.94	2.09	7.22
4KRO.PDB	O, D_ARG_38	N, D_GLU_46	H, D_GLU_46	2.75	1.90	6.17
4KRO.PDB	O, D_TRP_36	N, D_LEU_48	H, D_LEU_48	2.73	1.89	10.02
4KRO.PDB	O, D_ASP_58	N, D_VAL_50	H, D_VAL_50	2.87	2.09	21.92
4KRO.PDB	O, D_ASN_56	N, D_TRP_52	H, D_TRP_52	2.99	2.23	23.03
4KRO.PDB	O, D_TRP_52	N, D_GLY_55	H, D_GLY_55	2.93	2.09	9.77
4KRO.PDB	OH, D_TYR_59	OG1, D_THR_57	HG1, D_THR_57	2.96	2.15	12.78
4KRO.PDB	O, D_LEU_48	N, D_ASN_60	H, D_ASN_60	2.85	2.00	4.84
4KRO.PDB	O, D_TRP_47	ND2, D_ASN_60	HD22, D_ASN_60	2.96	2.11	6.97
4KRO.PDB	O, D_ASN_60	N, D_PHE_63	H, D_PHE_63	2.78	2.00	21.76
4KRO.PDB	O, D_ASN_83	NH1, D_ARG_66	HH11, D_ARG_66	2.85	2.14	29.21
4KRO.PDB	O, D_LYS_81	N, D_SER_68	H, D_SER_68	2.97	2.25	28.54
4KRO.PDB	OH, D_TYR_59	N, D_ILE_69	H, D_ILE_69	2.89	2.06	12.12
4KRO.PDB	O, D_SER_53	NZ, D_LYS_71	HZ1, D_LYS_71	2.91	2.02	5.81
4KRO.PDB	O, D_GLN_77	N, D_ASP_72	H, D_ASP_72	2.90	2.08	14.73
4KRO.PDB	OD1, D_ASP_72	N, D_LYS_75	H, D_LYS_75	2.48	1.64	10.83
4KRO.PDB	O, D_CYS_22	N, D_VAL_78	H, D_VAL_78	2.93	2.12	17.21
4KRO.PDB	O, D_ASN_70	N, D_PHE_79	H, D_PHE_79	2.77	1.91	3.73
4KRO.PDB	O, D_ILE_20	N, D_PHE_80	H, D_PHE_80	2.90	2.07	13.53
4KRO.PDB	O, D_ARG_66	N, D_ASN_83	H, D_ASN_83	2.97	2.16	16.89
4KRO.PDB	O, D_GLN_16	N, D_LEU_85	H, D_LEU_85	2.55	1.73	12.99

4KRO.PDB	OD2, D_ASP_89	N, D_GLN_86	H, D_GLN_86	2.43	1.70	25.84
4KRO.PDB	O, D_GLN_86	N, D_ASP_89	H, D_ASP_89	2.86	2.03	12.89
4KRO.PDB	O, D_SER_87	N, D_THR_90	H, D_THR_90	2.89	2.04	5.88
4KRO.PDB	O, D_SER_87	OG1, D_THR_90	HG1, D_THR_90	2.62	1.82	14.65
4KRO.PDB	O, D_THR_113	N, D_TYR_93	H, D_TYR_93	2.85	2.02	14.16
4KRO.PDB	O, D_ASP_89	OH, D_TYR_93	HH, D_TYR_93	2.82	1.98	1.28
4KRO.PDB	O, D_VAL_37	N, D_TYR_94	H, D_TYR_94	2.63	1.78	8.56
4KRO.PDB	OE1, D_GLN_6	N, D_CYS_95	H, D_CYS_95	2.92	2.20	28.43
4KRO.PDB	O, D_HIS_35	N, D_ALA_96	H, D_ALA_96	2.91	2.11	17.80
4KRO.PDB	O, D_TYR_108	N, D_ARG_97	H, D_ARG_97	2.79	1.98	15.74
4KRO.PDB	O, D_ALA_98	NE, D_ARG_97	HE, D_ARG_97	2.79	2.01	20.72
4KRO.PDB	O, D_ALA_98	NH2, D_ARG_97	HH21, D_ARG_97	2.94	2.23	29.79
4KRO.PDB	O, D_GLU_105	N, D_LEU_99	H, D_LEU_99	2.85	2.03	14.43
4KRO.PDB	OE1, A_GLN_408	OH, D_TYR_102	HH, D_TYR_102	2.75	1.97	18.39
4KRO.PDB	OD1, D_ASP_103	N, D_TYR_104	H, D_TYR_104	2.55	1.84	28.26
4KRO.PDB	OH, C_TYR_36	N, D_PHE_106	H, D_PHE_106	2.93	2.08	9.34
4KRO.PDB	O, D_CYS_95	N, D_GLY_110	H, D_GLY_110	2.62	1.82	17.46
4KRO.PDB	O, D_GLN_6	NE2, D_GLN_111	HE22, D_GLN_111	2.78	2.02	23.66
4KRO.PDB	O, D_TYR_93	N, D_THR_113	H, D_THR_113	2.89	2.15	25.46
4KRO.PDB	O, D_ALA_91	N, D_VAL_115	H, D_VAL_115	2.99	2.15	11.01
4KRO.PDB	OG, D_SER_118	N, D_ALA_120	H, D_ALA_120	2.76	1.99	21.72
4KRO.PDB	O, D_PHE_152	N, D_LYS_123	H, D_LYS_123	2.82	1.99	13.07
4KRO.PDB	O, D_LEU_147	N, D_PHE_128	H, D_PHE_128	2.92	2.17	24.83
4KRO.PDB	O, D_GLY_145	N, D_LEU_130	H, D_LEU_130	2.69	1.85	11.60
4KRO.PDB	O, D_VAL_190	N, D_ALA_142	H, D_ALA_142	2.67	1.84	12.02
4KRO.PDB	O, D_SER_186	N, D_CYS_146	H, D_CYS_146	2.74	1.92	15.98
4KRO.PDB	O, D_PHE_128	N, D_LEU_147	H, D_LEU_147	2.84	2.06	20.81
4KRO.PDB	O, D_LEU_184	N, D_VAL_148	H, D_VAL_148	2.86	2.09	22.97
4KRO.PDB	O, D_SER_126	N, D_LYS_149	H, D_LYS_149	2.93	2.10	12.69
4KRO.PDB	O, D_TYR_182	N, D_TYR_151	H, D_TYR_151	2.83	2.02	15.76
4KRO.PDB	O, D_LYS_123	N, D_PHE_152	H, D_PHE_152	2.93	2.11	15.98
4KRO.PDB	O, D_ASN_203	N, D_SER_159	H, D_SER_159	2.92	2.10	15.23
4KRO.PDB	O, D_ILE_201	N, D_ASN_161	H, D_ASN_161	2.76	1.94	14.37
4KRO.PDB	O, D_ASN_161	N, D_ALA_164	H, D_ALA_164	2.84	2.02	14.35
4KRO.PDB	O, D_VAL_187	N, D_HIS_170	H, D_HIS_170	2.69	1.86	10.95
4KRO.PDB	O, D_SER_185	N, D_PHE_172	H, D_PHE_172	2.85	2.00	6.56
4KRO.PDB	O, D_SER_183	N, D_VAL_175	H, D_VAL_175	2.75	1.89	4.87
4KRO.PDB	O, D_LEU_181	N, D_GLN_177	H, D_GLN_177	2.93	2.08	7.13
4KRO.PDB	O, D_TYR_151	N, D_TYR_182	H, D_TYR_182	2.50	1.65	4.99
4KRO.PDB	O, D_VAL_148	N, D_LEU_184	H, D_LEU_184	2.76	1.92	11.80
4KRO.PDB	O, D_HIS_170	N, D_VAL_187	H, D_VAL_187	2.73	1.92	16.55
4KRO.PDB	O, D_LEU_144	N, D_VAL_188	H, D_VAL_188	2.75	1.91	11.62
4KRO.PDB	O, D_ALA_142	N, D_VAL_190	H, D_VAL_190	2.86	2.04	15.25
4KRO.PDB	O, D_PRO_191	N, D_SER_194	H, D_SER_194	2.76	1.94	14.19
4KRO.PDB	O, D_PRO_191	OG, D_SER_194	HG, D_SER_194	2.46	1.63	8.00
4KRO.PDB	O, D_SER_194	N, D_GLN_198	H, D_GLN_198	2.58	1.74	10.02
4KRO.PDB	OD1, D_ASN_161	N, D_ILE_201	H, D_ILE_201	2.82	1.96	5.92
4KRO.PDB	O, D_SER_159	N, D_ASN_203	H, D_ASN_203	2.69	1.89	17.41
4KRO.PDB	O, D_VAL_213	N, D_VAL_204	H, D_VAL_204	2.66	1.81	8.41
4KRO.PDB	O, D_THR_211	N, D_HIS_206	H, D_HIS_206	2.94	2.10	11.11
4KRO.PDB	OG, D_SER_209	ND1, D_HIS_206	HD1, D_HIS_206	2.71	1.87	9.56
4KRO.PDB	O, D_PRO_153	NE2, D_HIS_206	HE2, D_HIS_206	2.79	1.99	18.14
4KRO.PDB	O, D_LYS_207	N, D_ASN_210	H, D_ASN_210	2.94	2.16	21.67
4KRO.PDB	O, D_VAL_204	N, D_VAL_213	H, D_VAL_213	2.73	1.93	18.78
4KRO.PDB	O, D_TYR_200	N, D_VAL_217	H, D_VAL_217	2.94	2.10	7.76

Table 1694: 4KRO-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4KRP.PDB	OE2, A_GLU_376	NH2, A_ARG_310	HH21, A_ARG_310	2.93	2.09	9.81
4KRP.PDB	OG1, A_THR_339	N, A_LYS_311	H, A_LYS_311	2.83	2.07	23.53
4KRP.PDB	O, A_SER_340	N, A_CYS_313	H, A_CYS_313	2.79	2.04	24.55
4KRP.PDB	O, A_ILE_318	N, A_PHE_321	H, A_PHE_321	2.70	1.86	11.77
4KRP.PDB	OD1, A_ASN_331	N, A_ASN_328	H, A_ASN_328	2.72	1.98	25.49
4KRP.PDB	OD1, A_ASN_328	N, A_ASN_331	H, A_ASN_331	2.86	2.01	7.83
4KRP.PDB	O, A_SER_326	ND2, A_ASN_331	HD21, A_ASN_331	2.94	2.16	20.31
4KRP.PDB	O, A_LYS_311	N, A_THR_339	H, A_THR_339	2.82	1.97	9.55
4KRP.PDB	O, A_CYS_313	N, A_SER_342	H, A_SER_342	2.72	1.88	10.06
4KRP.PDB	O, A_PHE_380	N, A_LEU_345	H, A_LEU_345	3.00	2.26	26.76
4KRP.PDB	O, A_LEU_382	N, A_ILE_347	H, A_ILE_347	2.72	1.92	18.37
4KRP.PDB	O, A_PRO_349	N, A_PHE_352	H, A_PHE_352	2.78	2.03	24.55
4KRP.PDB	O, D_GLY_54	NH2, A_ARG_353	HH22, A_ARG_353	2.83	1.98	6.79
4KRP.PDB	O, A_VAL_350	N, A_GLY_354	H, A_GLY_354	2.64	1.84	18.31
4KRP.PDB	O, A_SER_356	N, A_HIS_359	H, A_HIS_359	2.65	1.82	11.74
4KRP.PDB	O, A_ASP_355	N, A_THR_360	H, A_THR_360	2.92	2.06	3.09
4KRP.PDB	O, A_ALA_351	N, A_LEU_363	H, A_LEU_363	2.92	2.16	23.72
4KRP.PDB	O, A_ASP_364	N, A_GLU_367	H, A_GLU_367	2.97	2.11	4.06
4KRP.PDB	O, A_LEU_368	N, A_LEU_371	H, A_LEU_371	2.87	2.01	5.39
4KRP.PDB	O, A_ASP_369	N, A_LYS_372	H, A_LYS_372	2.94	2.10	8.68
4KRP.PDB	O, A_LEU_371	N, A_VAL_374	H, A_VAL_374	2.92	2.07	7.73
4KRP.PDB	O, A_THR_339	N, A_LYS_375	H, A_LYS_375	2.78	1.92	1.18
4KRP.PDB	O, A_GLY_343	N, A_GLY_379	H, A_GLY_379	2.76	2.04	28.24
4KRP.PDB	O, A_SER_413	N, A_LEU_381	H, A_LEU_381	2.81	2.01	17.34
4KRP.PDB	O, A_LEU_345	N, A_LEU_382	H, A_LEU_382	2.80	1.94	4.00
4KRP.PDB	O, A_ILE_347	N, A_GLN_384	H, A_GLN_384	2.84	2.01	12.43
4KRP.PDB	O, A_LEU_424	N, A_LEU_393	H, A_LEU_393	2.97	2.16	16.10
4KRP.PDB	O, A_HIS_394	N, A_GLU_397	H, A_GLU_397	2.88	2.13	24.87
4KRP.PDB	O, A_LYS_375	N, A_GLU_400	H, A_GLU_400	2.71	1.87	9.05
4KRP.PDB	O, A_ILE_377	N, A_ARG_403	H, A_ARG_403	2.92	2.09	14.20
4KRP.PDB	O, A_THR_378	N, A_ARG_405	H, A_ARG_405	2.67	1.81	2.52
4KRP.PDB	OD1, B_ASP_115	NH2, A_ARG_405	HH21, A_ARG_405	2.63	1.81	15.48
4KRP.PDB	O, A_PHE_412	N, A_GLN_408	H, A_GLN_408	2.79	2.03	23.31
4KRP.PDB	O, A_LYS_407	N, A_GLY_410	H, A_GLY_410	2.86	2.05	17.53
4KRP.PDB	O, A_GLN_408	N, A_GLN_411	H, A_GLN_411	2.78	2.00	20.78
4KRP.PDB	O, A_ASP_436	N, A_SER_413	H, A_SER_413	2.87	2.07	17.71
4KRP.PDB	O, A_ILE_438	N, A_VAL_416	H, A_VAL_416	2.90	2.08	16.39
4KRP.PDB	O, A_SER_440	N, A_SER_418	H, A_SER_418	2.95	2.20	24.18
4KRP.PDB	OD1, A_ASN_442	N, A_LEU_419	H, A_LEU_419	2.73	1.91	15.19
4KRP.PDB	O, A_THR_391	N, A_THR_422	H, A_THR_422	2.73	1.88	8.32
4KRP.PDB	OD1, A_ASP_498	NE, A_ARG_427	HE, A_ARG_427	2.55	1.82	26.18
4KRP.PDB	OD1, A_ASP_498	NH2, A_ARG_427	HH21, A_ARG_427	2.59	1.89	29.61
4KRP.PDB	O, A_LEU_426	N, A_LEU_429	H, A_LEU_429	3.00	2.18	15.49
4KRP.PDB	O, A_GLU_400	N, A_LYS_430	H, A_LYS_430	2.88	2.03	9.97
4KRP.PDB	O, A_LEU_456	N, A_ILE_432	H, A_ILE_432	2.71	1.86	9.38
4KRP.PDB	OE2, A_GLU_431	OG, A_SER_433	HG, A_SER_433	2.69	1.90	15.48
4KRP.PDB	O, A_GLN_411	N, A_ASP_436	H, A_ASP_436	2.90	2.06	8.63
4KRP.PDB	O, A_LEU_414	N, A_ILE_438	H, A_ILE_438	2.88	2.06	16.00
4KRP.PDB	O, A_LYS_465	N, A_ILE_439	H, A_ILE_439	2.90	2.09	17.29
4KRP.PDB	O, A_VAL_416	N, A_SER_440	H, A_SER_440	2.97	2.14	13.77
4KRP.PDB	O, D_TYR_102	OG, A_SER_440	HG, A_SER_440	2.65	1.82	4.10
4KRP.PDB	OD1, A_ASN_469	N, A_ASN_442	H, A_ASN_442	2.97	2.19	20.16
4KRP.PDB	OD1, A_ASN_469	ND2, A_ASN_442	HD22, A_ASN_442	2.94	2.17	23.18
4KRP.PDB	OD1, D_ASP_58	NZ, A_LYS_443	HZ1, A_LYS_443	2.65	1.82	17.69
4KRP.PDB	O, A_ASN_442	N, A_LEU_445	H, A_LEU_445	2.90	2.04	7.12
4KRP.PDB	O, A_THR_422	N, A_CYS_446	H, A_CYS_446	2.71	1.90	15.25
4KRP.PDB	O, A_TYR_447	N, A_ASN_449	H, A_ASN_449	2.43	1.66	21.82

4KRP.PDB	OE1, A_GLU_489	NZ, A_LYS_455	HZ2, A_LYS_455	2.95	2.19	25.72
4KRP.PDB	O, A_TRP_453	N, A_LEU_456	H, A_LEU_456	2.87	2.09	20.64
4KRP.PDB	OE1, A_GLN_462	N, A_THR_459	H, A_THR_459	2.95	2.18	22.01
4KRP.PDB	O, A_SER_433	OG1, A_THR_459	HG1, A_THR_459	2.66	1.97	29.29
4KRP.PDB	O, A_GLY_435	NE2, A_GLN_462	HE21, A_GLN_462	2.76	1.90	2.70
4KRP.PDB	O, A_ILE_432	NE2, A_GLN_462	HE22, A_GLN_462	2.97	2.15	14.48
4KRP.PDB	O, A_VAL_437	N, A_LYS_465	H, A_LYS_465	2.75	1.95	18.20
4KRP.PDB	OD2, D_ASP_103	NZ, A_LYS_465	HZ2, A_LYS_465	2.93	2.05	5.06
4KRP.PDB	O, A_ILE_439	N, A_ILE_467	H, A_ILE_467	2.93	2.10	12.53
4KRP.PDB	OG, A_SER_474	NE, A_ARG_470	HE, A_ARG_470	2.76	1.96	18.13
4KRP.PDB	O, A_LYS_476	N, A_GLY_479	H, A_GLY_479	2.71	1.88	12.77
4KRP.PDB	O, A_CYS_475	N, A_GLN_480	H, A_GLN_480	2.77	1.95	13.73
4KRP.PDB	O, A_SER_501	N, A_SER_487	H, A_SER_487	2.89	2.04	7.18
4KRP.PDB	OG, A_SER_501	OG, A_SER_487	HG, A_SER_487	2.45	1.66	16.67
4KRP.PDB	O, A_ASP_498	N, A_TRP_492	H, A_TRP_492	2.79	1.96	13.24
4KRP.PDB	OE1, A_GLU_495	NE, A_ARG_497	HE, A_ARG_497	2.60	1.79	14.71
4KRP.PDB	O, A_GLU_495	N, A_ASP_498	H, A_ASP_498	2.96	2.15	17.44
4KRP.PDB	O, A_GLY_490	N, A_VAL_500	H, A_VAL_500	2.88	2.04	9.24
4KRP.PDB	O, A_LEU_485	N, A_ARG_503	H, A_ARG_503	2.76	1.97	19.17
4KRP.PDB	O, A_GLU_510	N, A_ARG_507	H, A_ARG_507	2.85	2.07	20.90
4KRP.PDB	OE1, A_GLU_524	NE, A_ARG_507	HE, A_ARG_507	2.83	2.04	19.78
4KRP.PDB	O, A_VAL_505	N, A_VAL_512	H, A_VAL_512	2.78	1.98	18.78
4KRP.PDB	O, A_GLY_520	NH1, A_ARG_523	HH11, A_ARG_523	2.96	2.22	25.33
4KRP.PDB	O, A_ASN_516	N, A_GLU_524	H, A_GLU_524	2.98	2.17	17.27
4KRP.PDB	O, A_ILE_532	N, A_PHE_525	H, A_PHE_525	2.83	2.06	21.15
4KRP.PDB	O, A_GLU_530	N, A_GLU_527	H, A_GLU_527	2.83	2.00	14.02
4KRP.PDB	O, A_SER_506	N, A_CYS_531	H, A_CYS_531	2.79	1.96	12.76
4KRP.PDB	O, A_PHE_525	N, A_ILE_532	H, A_ILE_532	2.70	1.90	17.86
4KRP.PDB	O, A_ARG_523	N, A_CYS_534	H, A_CYS_534	2.73	1.90	12.34
4KRP.PDB	O, A_HIS_535	N, A_CYS_538	H, A_CYS_538	2.99	2.17	14.86
4KRP.PDB	O, A_GLN_557	N, A_LEU_539	H, A_LEU_539	2.68	1.97	29.21
4KRP.PDB	O, A_LEU_539	NE2, A_GLN_541	HE21, A_GLN_541	2.85	2.01	8.93
4KRP.PDB	OD1, A_ASN_544	N, A_ILE_545	H, A_ILE_545	2.79	2.04	25.27
4KRP.PDB	OE2, A_GLU_527	NH2, A_ARG_550	HH22, A_ARG_550	2.54	1.76	21.10
4KRP.PDB	O, A_GLU_537	N, A_ALA_559	H, A_ALA_559	2.74	1.88	1.56
4KRP.PDB	O, A_ALA_559	ND1, A_HIS_560	HD1, A_HIS_560	2.61	1.91	29.44
4KRP.PDB	O, A_HIS_566	N, A_ASP_563	H, A_ASP_563	2.73	1.89	10.58
4KRP.PDB	O, A_TYR_561	N, A_VAL_568	H, A_VAL_568	2.97	2.14	13.62
4KRP.PDB	OG, C_SER_26	N, C_LEU_3	H, C_LEU_3	2.98	2.13	7.00
4KRP.PDB	O, C_ARG_24	N, C_THR_5	H, C_THR_5	2.78	1.93	4.32
4KRP.PDB	O, C_TYR_86	NE2, C_GLN_6	HE22, C_GLN_6	2.90	2.07	11.06
4KRP.PDB	O, C_SER_22	N, C_SER_7	H, C_SER_7	2.93	2.12	15.95
4KRP.PDB	O, C_LYS_103	N, C_LEU_11	H, C_LEU_11	2.74	2.00	25.88
4KRP.PDB	OE1, C_GLU_17	N, C_SER_14	H, C_SER_14	2.90	2.05	7.83
4KRP.PDB	O, C_VAL_78	N, C_GLY_16	H, C_GLY_16	2.86	2.04	14.86
4KRP.PDB	O, C_ILE_75	N, C_VAL_19	H, C_VAL_19	2.92	2.12	19.12
4KRP.PDB	O, C_LEU_73	N, C_PHE_21	H, C_PHE_21	2.85	2.02	11.22
4KRP.PDB	O, C_SER_7	N, C_SER_22	H, C_SER_22	2.96	2.13	12.93
4KRP.PDB	O, C_THR_5	N, C_ARG_24	H, C_ARG_24	2.76	1.98	20.70
4KRP.PDB	O, C_THR_69	N, C_ALA_25	H, C_ALA_25	2.58	1.76	13.74
4KRP.PDB	O, C_LEU_3	N, C_SER_26	H, C_SER_26	2.90	2.10	18.68
4KRP.PDB	O, C_GLY_68	N, C_ILE_29	H, C_ILE_29	2.84	2.01	12.74
4KRP.PDB	OD1, C_ASN_92	ND2, C_ASN_32	HD22, C_ASN_32	2.85	2.14	29.38
4KRP.PDB	O, C_THR_31	N, C_ILE_33	H, C_ILE_33	2.75	2.02	26.66
4KRP.PDB	O, C_GLN_89	N, C_HIS_34	H, C_HIS_34	2.86	2.05	15.92
4KRP.PDB	O, C_ILE_48	N, C_TRP_35	H, C_TRP_35	2.96	2.13	11.92
4KRP.PDB	O, C_TYR_87	N, C_TYR_36	H, C_TYR_36	2.77	1.96	16.47
4KRP.PDB	OE1, C_GLN_89	OH, C_TYR_36	HH, C_TYR_36	2.33	1.50	6.36

4KRP.PDB	O, C_ARG_45	N, C_GLN_37	H, C_GLN_37	2.82	2.00	14.50
4KRP.PDB	OH, C_TYR_86	NE2, C_GLN_37	HE21, C_GLN_37	2.85	2.02	13.51
4KRP.PDB	O, C_ASP_85	N, C_GLN_38	H, C_GLN_38	2.84	2.04	18.23
4KRP.PDB	OE1, D_GLN_39	NE2, C_GLN_38	HE22, C_GLN_38	2.70	1.84	6.09
4KRP.PDB	O, C_ARG_39	N, C_GLY_42	H, C_GLY_42	2.94	2.19	25.37
4KRP.PDB	O, C_GLN_37	N, C_ARG_45	H, C_ARG_45	2.51	1.81	29.63
4KRP.PDB	O, C_TRP_35	N, C_LEU_47	H, C_LEU_47	2.88	2.04	8.47
4KRP.PDB	O, C_GLU_53	N, C_LYS_49	H, C_LYS_49	2.92	2.08	11.40
4KRP.PDB	OE1, C_GLU_53	NZ, C_LYS_49	HZ3, C_LYS_49	2.81	1.93	8.64
4KRP.PDB	OD2, D_ASP_103	OH, C_TYR_50	HH, C_TYR_50	2.43	1.66	18.96
4KRP.PDB	O, C_ILE_33	N, C_ALA_51	H, C_ALA_51	2.69	1.90	19.00
4KRP.PDB	OD1, C_ASP_82	NH2, C_ARG_61	HH21, C_ARG_61	2.79	1.98	15.39
4KRP.PDB	O, C_SER_74	N, C_SER_63	H, C_SER_63	2.89	2.12	22.33
4KRP.PDB	O, C_THR_72	N, C_SER_65	H, C_SER_65	2.82	2.03	19.74
4KRP.PDB	O, C_GLY_30	N, C_GLY_68	H, C_GLY_68	2.65	1.84	16.72
4KRP.PDB	O, C_CYS_23	N, C_PHE_71	H, C_PHE_71	2.92	2.13	19.47
4KRP.PDB	O, C_SER_65	N, C_THR_72	H, C_THR_72	2.85	2.06	18.53
4KRP.PDB	O, C_SER_63	N, C_SER_74	H, C_SER_74	2.53	1.70	12.96
4KRP.PDB	O, C_VAL_19	N, C_ILE_75	H, C_ILE_75	2.98	2.18	17.84
4KRP.PDB	OD2, C_ASP_82	N, C_GLU_79	H, C_GLU_79	2.97	2.11	4.01
4KRP.PDB	O, C_GLN_38	N, C_ASP_85	H, C_ASP_85	2.96	2.14	13.68
4KRP.PDB	O, C_THR_102	N, C_TYR_86	H, C_TYR_86	2.85	2.05	17.70
4KRP.PDB	O, C_ASP_82	OH, C_TYR_86	HH, C_TYR_86	2.56	1.73	8.98
4KRP.PDB	O, C_HIS_34	N, C_GLN_89	H, C_GLN_89	2.79	2.03	23.96
4KRP.PDB	OG1, C_THR_96	NE2, C_GLN_89	HE21, C_GLN_89	2.69	1.93	23.74
4KRP.PDB	O, C_ASN_93	NE2, C_GLN_90	HE22, C_GLN_90	2.65	1.80	8.11
4KRP.PDB	O, C_ASN_32	N, C_ASN_91	H, C_ASN_91	2.95	2.16	18.97
4KRP.PDB	OD1, D_ASP_103	ND2, C_ASN_91	HD21, C_ASN_91	2.77	1.91	6.24
4KRP.PDB	OD1, C_ASN_93	ND2, C_ASN_92	HD22, C_ASN_92	2.69	1.97	27.74
4KRP.PDB	OE1, C_GLN_90	N, C_ASN_93	H, C_ASN_93	2.83	2.02	15.94
4KRP.PDB	O, A_ASN_469	N, C_TRP_94	H, C_TRP_94	2.68	1.89	19.97
4KRP.PDB	OD2, D_ASP_58	NE1, C_TRP_94	HE1, C_TRP_94	2.98	2.17	17.26
4KRP.PDB	O, C_GLN_90	OG1, C_THR_96	HG1, C_THR_96	2.81	1.98	6.89
4KRP.PDB	O, C_CYS_88	N, C_GLY_99	H, C_GLY_99	2.82	1.98	10.72
4KRP.PDB	OE1, C_GLN_6	N, C_GLY_101	H, C_GLY_101	2.99	2.26	27.03
4KRP.PDB	O, C_TYR_86	N, C_THR_102	H, C_THR_102	2.99	2.27	27.64
4KRP.PDB	O, C_PRO_8	OG1, C_THR_102	HG1, C_THR_102	2.64	1.87	19.11
4KRP.PDB	O, C_VAL_9	N, C_LYS_103	H, C_LYS_103	2.82	2.01	15.16
4KRP.PDB	OE2, C_GLU_105	NZ, C_LYS_103	HZ1, C_LYS_103	2.82	2.05	25.15
4KRP.PDB	O, C_ALA_84	N, C_LEU_104	H, C_LEU_104	2.94	2.09	2.60
4KRP.PDB	O, C_VAL_13	N, C_LYS_107	H, C_LYS_107	2.79	1.98	15.54
4KRP.PDB	O, C_TYR_140	N, C_ALA_111	H, C_ALA_111	2.77	1.92	7.65
4KRP.PDB	O, C_LEU_135	N, C_PHE_116	H, C_PHE_116	2.88	2.06	15.19
4KRP.PDB	O, C_VAL_133	N, C_PHE_118	H, C_PHE_118	2.72	1.89	12.07
4KRP.PDB	OG, C_SER_131	NE2, C_GLN_124	HE22, C_GLN_124	2.89	2.10	19.98
4KRP.PDB	O, C_GLN_124	N, C_SER_127	H, C_SER_127	2.75	2.03	27.79
4KRP.PDB	O, C_LEU_125	N, C_GLY_128	H, C_GLY_128	2.99	2.19	18.71
4KRP.PDB	O, C_LEU_179	N, C_VAL_132	H, C_VAL_132	2.64	1.85	19.72
4KRP.PDB	O, C_SER_177	N, C_CYS_134	H, C_CYS_134	2.73	1.88	7.44
4KRP.PDB	O, C_PHE_116	N, C_LEU_135	H, C_LEU_135	2.66	1.81	8.16
4KRP.PDB	O, C_LEU_175	N, C_LEU_136	H, C_LEU_136	2.74	1.88	6.29
4KRP.PDB	O, C_SER_114	N, C_ASN_137	H, C_ASN_137	2.81	1.97	10.83
4KRP.PDB	OG, C_SER_174	N, C_ASN_138	H, C_ASN_138	2.97	2.11	3.04
4KRP.PDB	O, C_TYR_173	N, C_PHE_139	H, C_PHE_139	2.73	1.95	19.51
4KRP.PDB	O, C_ALA_111	N, C_TYR_140	H, C_TYR_140	2.91	2.08	13.77
4KRP.PDB	O, C_THR_197	N, C_LYS_145	H, C_LYS_145	2.91	2.06	4.69
4KRP.PDB	O, C_GLU_195	N, C_GLN_147	H, C_GLN_147	2.81	1.96	9.38
4KRP.PDB	O, C_ALA_193	N, C_LYS_149	H, C_LYS_149	2.85	2.05	18.63

4KRP.PDB	O, C_ALA_153	NE2, C_GLN_155	HE21, C_GLN_155	2.95	2.09	2.78
4KRP.PDB	OE1, C_GLN_155	ND2, C_ASN_158	HD21, C_ASN_158	2.83	2.12	29.23
4KRP.PDB	O, D_LEU_176	NE2, C_GLN_160	HE22, C_GLN_160	2.56	1.80	22.58
4KRP.PDB	O, C_SER_176	N, C_SER_162	H, C_SER_162	2.90	2.19	29.40
4KRP.PDB	O, D_PRO_173	OG, C_SER_162	HG, C_SER_162	2.80	2.10	28.74
4KRP.PDB	O, C_SER_174	N, C_THR_164	H, C_THR_164	2.91	2.07	10.69
4KRP.PDB	O, C_LEU_106	NE2, C_GLN_166	HE22, C_GLN_166	2.63	1.89	25.54
4KRP.PDB	OD2, C_ASP_167	N, C_LYS_169	H, C_LYS_169	2.96	2.14	15.63
4KRP.PDB	OD1, C_ASP_170	N, C_THR_172	H, C_THR_172	2.88	2.10	20.13
4KRP.PDB	OD1, C_ASP_170	OG1, C_THR_172	HG1, C_THR_172	2.53	1.69	5.91
4KRP.PDB	O, C_PHE_139	N, C_TYR_173	H, C_TYR_173	2.71	1.87	11.75
4KRP.PDB	O, C_LEU_136	N, C_LEU_175	H, C_LEU_175	2.80	2.00	17.17
4KRP.PDB	O, C_SER_162	N, C_SER_176	H, C_SER_176	2.91	2.09	14.35
4KRP.PDB	O, C_CYS_134	N, C_SER_177	H, C_SER_177	2.80	1.97	12.12
4KRP.PDB	O, C_GLN_160	N, C_THR_178	H, C_THR_178	2.94	2.21	26.85
4KRP.PDB	O, C_VAL_132	N, C_LEU_179	H, C_LEU_179	2.74	1.93	15.89
4KRP.PDB	O, C_ALA_130	N, C_LEU_181	H, C_LEU_181	2.98	2.18	18.35
4KRP.PDB	O, C_SER_182	N, C_TYR_186	H, C_TYR_186	2.78	1.98	17.36
4KRP.PDB	O, C_LYS_183	N, C_GLU_187	H, C_GLU_187	2.89	2.07	14.82
4KRP.PDB	O, C_ASP_185	ND1, C_HIS_189	HD1, C_HIS_189	2.74	1.90	11.57
4KRP.PDB	OD1, C_ASP_151	N, C_VAL_191	H, C_VAL_191	2.89	2.04	6.74
4KRP.PDB	O, C_TYR_186	OH, C_TYR_192	HH, C_TYR_192	2.61	1.88	24.84
4KRP.PDB	O, C_LYS_149	N, C_ALA_193	H, C_ALA_193	2.84	2.08	22.88
4KRP.PDB	O, C_LYS_207	N, C_CYS_194	H, C_CYS_194	2.89	2.06	14.21
4KRP.PDB	O, C_GLN_147	N, C_GLU_195	H, C_GLU_195	2.73	1.87	5.27
4KRP.PDB	O, C_VAL_205	N, C_VAL_196	H, C_VAL_196	2.64	1.80	9.51
4KRP.PDB	O, C_LYS_145	N, C_THR_197	H, C_THR_197	2.81	1.98	11.85
4KRP.PDB	O, C_PRO_141	NE2, C_HIS_198	HE2, C_HIS_198	2.87	2.02	6.17
4KRP.PDB	O, C_LYS_190	N, C_ARG_211	H, C_ARG_211	2.85	2.03	15.20
4KRP.PDB	O, C_HIS_189	NE, C_ARG_211	HE, C_ARG_211	2.71	1.90	16.56
4KRP.PDB	O, D_SER_25	N, D_GLN_3	H, D_GLN_3	2.74	1.91	10.35
4KRP.PDB	O, D_THR_23	N, D_LYS_5	H, D_LYS_5	2.97	2.12	3.88
4KRP.PDB	OE1, D_GLN_111	N, D_GLN_6	H, D_GLN_6	2.91	2.08	12.88
4KRP.PDB	OG1, D_THR_113	NE2, D_GLN_6	HE21, D_GLN_6	2.88	2.03	4.76
4KRP.PDB	O, D_TYR_93	NE2, D_GLN_6	HE22, D_GLN_6	2.91	2.18	26.39
4KRP.PDB	O, D_THR_21	N, D_SER_7	H, D_SER_7	2.78	1.98	17.63
4KRP.PDB	O, D_LEU_85	N, D_SER_15	H, D_SER_15	2.66	1.85	14.89
4KRP.PDB	O, D_GLN_13	N, D_GLN_16	H, D_GLN_16	2.90	2.10	17.19
4KRP.PDB	O, D_MET_82	N, D_LEU_18	H, D_LEU_18	2.72	1.90	13.60
4KRP.PDB	O, D_SER_7	N, D_THR_21	H, D_THR_21	2.80	1.94	2.06
4KRP.PDB	O, D_VAL_78	N, D_CYS_22	H, D_CYS_22	2.79	1.97	15.13
4KRP.PDB	O, D_LYS_5	N, D_THR_23	H, D_THR_23	2.64	1.81	12.04
4KRP.PDB	O, D_SER_76	N, D_VAL_24	H, D_VAL_24	2.93	2.08	8.52
4KRP.PDB	OG, D_SER_28	N, D_THR_30	H, D_THR_30	2.95	2.11	10.64
4KRP.PDB	O, D_ALA_96	N, D_HIS_35	H, D_HIS_35	2.75	1.91	9.74
4KRP.PDB	O, D_GLY_49	N, D_TRP_36	H, D_TRP_36	2.84	2.06	19.69
4KRP.PDB	O, D_TYR_94	N, D_VAL_37	H, D_VAL_37	2.90	2.08	13.15
4KRP.PDB	O, D_GLU_46	N, D_ARG_38	H, D_ARG_38	2.87	2.05	14.44
4KRP.PDB	OH, D_TYR_93	NH1, D_ARG_38	HH11, D_ARG_38	2.96	2.18	20.80
4KRP.PDB	OD1, D_ASP_89	NH1, D_ARG_38	HH12, D_ARG_38	2.91	2.06	7.49
4KRP.PDB	OE1, C_GLN_38	NE2, D_GLN_39	HE22, D_GLN_39	2.72	1.87	5.47
4KRP.PDB	O, D_ARG_38	N, D_GLU_46	H, D_GLU_46	2.84	2.01	12.31
4KRP.PDB	O, D_TRP_36	N, D_LEU_48	H, D_LEU_48	2.81	1.97	10.41
4KRP.PDB	O, D_ASP_58	N, D_VAL_50	H, D_VAL_50	2.83	2.10	26.44
4KRP.PDB	O, D_ASN_56	N, D_TRP_52	H, D_TRP_52	2.85	2.04	16.32
4KRP.PDB	O, D_LEU_48	N, D_ASN_60	H, D_ASN_60	2.81	1.96	6.79
4KRP.PDB	O, D_TRP_47	ND2, D_ASN_60	HD22, D_ASN_60	2.84	2.05	19.17
4KRP.PDB	O, D_ASN_60	N, D_PHE_63	H, D_PHE_63	2.99	2.23	24.51

4KRP.PDB	OD1, D_ASP_89	NH2, D_ARG_66	HH22, D_ARG_66	2.59	1.74	9.60
4KRP.PDB	O, D_LYS_81	N, D_SER_68	H, D_SER_68	2.89	2.07	14.89
4KRP.PDB	OH, D_TYR_59	N, D_ILE_69	H, D_ILE_69	2.90	2.09	15.54
4KRP.PDB	O, D_CYS_22	N, D_VAL_78	H, D_VAL_78	2.72	1.92	18.23
4KRP.PDB	O, D_ASN_70	N, D_PHE_79	H, D_PHE_79	2.97	2.12	3.62
4KRP.PDB	O, D_ILE_20	N, D_PHE_80	H, D_PHE_80	2.75	1.92	12.16
4KRP.PDB	O, D_ARG_66	N, D_ASN_83	H, D_ASN_83	2.96	2.20	23.47
4KRP.PDB	O, D_GLN_16	N, D_LEU_85	H, D_LEU_85	2.88	2.04	9.71
4KRP.PDB	O, D_GLN_86	N, D_ASP_89	H, D_ASP_89	2.99	2.19	16.67
4KRP.PDB	O, D_SER_87	N, D_THR_90	H, D_THR_90	2.99	2.16	13.47
4KRP.PDB	O, D_SER_87	OG1, D_THR_90	HG1, D_THR_90	2.81	2.08	24.26
4KRP.PDB	O, D_ASP_89	OH, D_TYR_93	HH, D_TYR_93	2.65	1.83	9.74
4KRP.PDB	O, D_VAL_37	N, D_TYR_94	H, D_TYR_94	2.57	1.74	12.70
4KRP.PDB	O, D_HIS_35	N, D_ALA_96	H, D_ALA_96	2.75	1.98	21.78
4KRP.PDB	O, D_TYR_108	N, D_ARG_97	H, D_ARG_97	2.89	2.07	13.85
4KRP.PDB	O, D_ALA_98	NE, D_ARG_97	HE, D_ARG_97	2.79	1.94	9.03
4KRP.PDB	OE1, A_GLN_408	OH, D_TYR_102	HH, D_TYR_102	2.56	1.74	10.00
4KRP.PDB	OD1, D_ASP_103	N, D_TYR_104	H, D_TYR_104	2.53	1.80	26.58
4KRP.PDB	OG, A_SER_440	OH, D_TYR_104	HH, D_TYR_104	2.94	2.22	25.72
4KRP.PDB	OH, C_TYR_36	N, D_PHE_106	H, D_PHE_106	2.89	2.11	20.61
4KRP.PDB	O, D_PHE_106	NE1, D_TRP_109	HE1, D_TRP_109	2.74	2.02	27.52
4KRP.PDB	O, D_CYS_95	N, D_GLY_110	H, D_GLY_110	2.83	1.97	4.87
4KRP.PDB	O, D_TYR_93	N, D_THR_113	H, D_THR_113	2.79	2.00	19.35
4KRP.PDB	O, D_ALA_91	N, D_VAL_115	H, D_VAL_115	2.94	2.21	27.64
4KRP.PDB	O, D_GLY_10	N, D_THR_116	H, D_THR_116	2.48	1.64	10.06
4KRP.PDB	OG, D_SER_118	N, D_ALA_120	H, D_ALA_120	2.80	1.99	15.68
4KRP.PDB	O, D_PHE_152	N, D_LYS_123	H, D_LYS_123	2.61	1.84	21.89
4KRP.PDB	O, D_ASP_150	NZ, D_LYS_123	HZ2, D_LYS_123	2.97	2.10	10.97
4KRP.PDB	O, D_LYS_149	N, D_SER_126	H, D_SER_126	2.93	2.09	12.06
4KRP.PDB	O, D_LEU_147	N, D_PHE_128	H, D_PHE_128	2.93	2.14	18.89
4KRP.PDB	O, D_GLY_145	N, D_LEU_130	H, D_LEU_130	2.60	1.75	6.78
4KRP.PDB	O, D_VAL_190	N, D_ALA_142	H, D_ALA_142	2.58	1.73	8.25
4KRP.PDB	O, D_LEU_130	N, D_GLY_145	H, D_GLY_145	2.97	2.21	23.33
4KRP.PDB	O, D_SER_186	N, D_CYS_146	H, D_CYS_146	2.72	1.92	18.42
4KRP.PDB	O, D_PHE_128	N, D_LEU_147	H, D_LEU_147	2.61	1.77	10.44
4KRP.PDB	O, D_LEU_184	N, D_VAL_148	H, D_VAL_148	2.60	1.80	18.24
4KRP.PDB	O, D_TYR_182	N, D_TYR_151	H, D_TYR_151	2.99	2.17	14.93
4KRP.PDB	O, D_LYS_123	N, D_PHE_152	H, D_PHE_152	2.86	2.03	12.67
4KRP.PDB	O, D_ASN_205	N, D_THR_157	H, D_THR_157	2.80	1.97	11.71
4KRP.PDB	O, D_ILE_201	N, D_ASN_161	H, D_ASN_161	2.77	1.93	9.15
4KRP.PDB	OD1, D_ASN_203	N, D_SER_162	H, D_SER_162	2.69	1.90	19.84
4KRP.PDB	O, D_VAL_187	N, D_HIS_170	H, D_HIS_170	2.77	1.95	15.10
4KRP.PDB	O, D_SER_185	N, D_PHE_172	H, D_PHE_172	2.95	2.10	7.75
4KRP.PDB	O, D_LEU_181	N, D_GLN_177	H, D_GLN_177	2.91	2.07	9.36
4KRP.PDB	O, D_GLN_177	N, D_GLY_180	H, D_GLY_180	2.74	1.90	10.27
4KRP.PDB	OG, D_SER_179	N, D_LEU_181	H, D_LEU_181	2.98	2.17	16.32
4KRP.PDB	O, D_TYR_151	N, D_TYR_182	H, D_TYR_182	2.66	1.81	7.88
4KRP.PDB	O, D_VAL_148	N, D_LEU_184	H, D_LEU_184	2.65	1.91	24.40
4KRP.PDB	O, D_CYS_146	N, D_SER_186	H, D_SER_186	2.92	2.10	15.79
4KRP.PDB	O, D_HIS_170	N, D_VAL_187	H, D_VAL_187	2.99	2.16	13.15
4KRP.PDB	O, D_LEU_144	N, D_VAL_188	H, D_VAL_188	2.79	2.00	19.05
4KRP.PDB	O, D_ALA_142	N, D_VAL_190	H, D_VAL_190	2.74	1.92	13.51
4KRP.PDB	O, D_SER_192	N, D_SER_194	H, D_SER_194	2.72	1.97	24.52
4KRP.PDB	O, D_SER_194	N, D_THR_197	H, D_THR_197	2.83	2.02	16.59
4KRP.PDB	O, D_SER_194	N, D_GLN_198	H, D_GLN_198	2.63	1.78	8.20
4KRP.PDB	O, D_SER_159	N, D_ASN_203	H, D_ASN_203	2.84	2.01	11.39
4KRP.PDB	OD1, D_ASP_214	ND2, D_ASN_203	HD22, D_ASN_203	2.70	1.84	4.78
4KRP.PDB	O, D_VAL_213	N, D_VAL_204	H, D_VAL_204	2.74	1.92	15.13

4KRP.PDB	O, D_THR_157	N, D_ASN_205	H, D_ASN_205	2.79	1.96	11.86
4KRP.PDB	O, D_THR_211	N, D_HIS_206	H, D_HIS_206	2.93	2.14	19.62
4KRP.PDB	OG, D_SER_209	ND1, D_HIS_206	HD1, D_HIS_206	2.94	2.08	3.63
4KRP.PDB	O, D_PRO_153	NE2, D_HIS_206	HE2, D_HIS_206	2.75	1.91	8.08
4KRP.PDB	O, D_LYS_207	N, D_ASN_210	H, D_ASN_210	2.60	1.84	22.95
4KRP.PDB	OG, D_SER_209	OG1, D_THR_211	HG1, D_THR_211	2.56	1.87	28.78
4KRP.PDB	O, D_VAL_204	N, D_VAL_213	H, D_VAL_213	2.73	1.88	7.94
4KRP.PDB	O, D_TYR_200	N, D_VAL_217	H, D_VAL_217	2.90	2.06	11.80
4KRP.PDB	O, B_SER_25	N, B_GLN_3	H, B_GLN_3	2.91	2.07	9.08
4KRP.PDB	O, B_ALA_23	N, B_VAL_5	H, B_VAL_5	2.88	2.02	5.91
4KRP.PDB	OE1, A_GLU_431	OH, B_TYR_32	HH, B_TYR_32	2.59	1.78	7.49
4KRP.PDB	O, B_GLY_99	N, B_ALA_33	H, B_ALA_33	2.82	2.06	24.31
4KRP.PDB	O, B_MET_34	N, B_ILE_51	H, B_ILE_51	2.92	2.20	27.79
4KRP.PDB	O, B_SER_104	ND2, B_ASN_52	HD21, B_ASN_52	2.66	1.89	21.34
4KRP.PDB	O, B_ALA_50	N, B_TYR_59	H, B_TYR_59	2.95	2.11	9.44
4KRP.PDB	O, B_TYR_116	N, B_ALA_98	H, B_ALA_98	2.91	2.18	26.96
4KRP.PDB	OE1, A_GLU_400	OH, B_TYR_100	HH, B_TYR_100	2.94	2.13	13.29
4KRP.PDB	OE2, A_GLU_431	OH, B_TYR_116	HH, B_TYR_116	2.43	1.75	29.09

Table 1695: 4KRP-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4NZR.PDB	O, H.SER.25	N, H.GLN.3	H, H.GLN.3	2.88	2.05	13.11
4NZR.PDB	O, H.THR.23	N, H.GLN.5	H, H.GLN.5	2.98	2.24	25.71
4NZR.PDB	O, H.SER.21	N, H.SER.7	H, H.SER.7	2.82	2.05	20.97
4NZR.PDB	O, H.THR.110	N, H.VAL.12	H, H.VAL.12	2.90	2.11	18.80
4NZR.PDB	OE1, H.GLU.16	N, H.LYS.13	H, H.LYS.13	2.94	2.09	8.37
4NZR.PDB	O, H.VAL.82C	N, H.SER.15	H, H.SER.15	2.76	1.92	10.81
4NZR.PDB	O, H.LEU.82	N, H.LEU.18	H, H.LEU.18	2.85	2.05	16.86
4NZR.PDB	O, H.LEU.80	N, H.LEU.20	H, H.LEU.20	2.86	2.03	13.74
4NZR.PDB	O, H.PHE.78	N, H.CYS.22	H, H.CYS.22	2.79	1.97	15.99
4NZR.PDB	O, H.GLN.5	N, H.THR.23	H, H.THR.23	2.93	2.12	16.85
4NZR.PDB	O, H.ASN.76	N, H.VAL.24	H, H.VAL.24	2.94	2.10	8.87
4NZR.PDB	O, H.GLN.3	N, H.SER.25	H, H.SER.25	2.82	1.99	12.13
4NZR.PDB	OD1, H.ASN.76	N, H.ILE.29	H, H.ILE.29	2.97	2.16	16.56
4NZR.PDB	O, H.ASP.31E	N, H.GLY.31A	H, H.GLY.31A	2.95	2.12	14.61
4NZR.PDB	O, H.GLU.31B	N, H.ASP.31E	H, H.ASP.31E	2.99	2.13	1.38
4NZR.PDB	O, H.ALA.93	N, H.GLY.35	H, H.GLY.35	2.82	1.96	6.32
4NZR.PDB	O, H.GLY.49	N, H.TRP.36	H, H.TRP.36	2.93	2.18	24.86
4NZR.PDB	O, H.PHE.91	N, H.VAL.37	H, H.VAL.37	2.89	2.07	13.63
4NZR.PDB	O, H.GLU.46	N, H.ARG.38	H, H.ARG.38	2.82	2.00	14.96
4NZR.PDB	OE1, H.GLU.46	NE, H.ARG.38	HE, H.ARG.38	2.83	2.07	23.07
4NZR.PDB	OH, H.TYR.90	NH1, H.ARG.38	HH11, H.ARG.38	2.96	2.16	17.91
4NZR.PDB	OD1, H.ASP.86	NH1, H.ARG.38	HH12, H.ARG.38	2.73	1.88	7.20
4NZR.PDB	OE1, H.GLU.46	NH2, H.ARG.38	HH21, H.ARG.38	2.78	2.02	22.98
4NZR.PDB	O, H.VAL.89	N, H.HIS.39	H, H.HIS.39	2.78	1.96	14.92
4NZR.PDB	O, H.SER.40	N, H.LYS.43	H, H.LYS.43	2.77	1.94	13.14
4NZR.PDB	O, H.ARG.38	N, H.GLU.46	H, H.GLU.46	2.92	2.12	17.91
4NZR.PDB	OG, H.SER.50	NE1, H.TRP.47	HE1, H.TRP.47	2.87	2.03	11.63
4NZR.PDB	O, H.TRP.36	N, H.ILE.48	H, H.ILE.48	2.93	2.07	4.55
4NZR.PDB	O, H.HIS.58	N, H.SER.50	H, H.SER.50	2.85	2.04	14.94
4NZR.PDB	O, H.TRP.34	N, H.ILE.51	H, H.ILE.51	2.79	1.98	16.48
4NZR.PDB	O, H.THR.56	N, H.HIS.52	H, H.HIS.52	2.85	2.01	9.46
4NZR.PDB	OD1, H.ASP.31G	NE2, H.HIS.52	HE2, H.HIS.52	2.60	1.83	22.01
4NZR.PDB	OD1, H.ASP.31G	NE1, H.TRP.53	HE1, H.TRP.53	2.92	2.20	28.43
4NZR.PDB	O, H.HIS.52	N, H.GLY.55	H, H.GLY.55	2.84	2.03	16.32
4NZR.PDB	O, H.SER.50	N, H.HIS.58	H, H.HIS.58	2.89	2.05	10.67
4NZR.PDB	O, H.ILE.48	N, H.LYS.60	H, H.LYS.60	2.87	2.02	5.64
4NZR.PDB	O, H.LYS.60	N, H.LEU.63	H, H.LEU.63	2.86	2.08	20.68
4NZR.PDB	O, H.LEU.63	N, H.ARG.66	H, H.ARG.66	2.78	1.94	10.08
4NZR.PDB	O, H.ALA.82A	NH1, H.ARG.66	HH11, H.ARG.66	2.95	2.12	13.91
4NZR.PDB	OD2, H.ASP.86	NH1, H.ARG.66	HH12, H.ARG.66	2.98	2.20	21.88
4NZR.PDB	O, H.ARG.81	N, H.SER.68	H, H.SER.68	2.95	2.16	19.71
4NZR.PDB	O, H.TRP.77	N, H.ASP.72	H, H.ASP.72	2.90	2.05	4.26
4NZR.PDB	O, H.ASP.27	ND2, H.ASN.76	HD21, H.ASN.76	2.81	2.01	17.45
4NZR.PDB	O, H.VAL.24	ND2, H.ASN.76	HD22, H.ASN.76	2.87	2.02	7.45
4NZR.PDB	O, H.SER.70	N, H.SER.79	H, H.SER.79	2.92	2.13	19.56
4NZR.PDB	O, H.LEU.20	N, H.LEU.80	H, H.LEU.80	2.88	2.05	13.30
4NZR.PDB	O, H.SER.68	N, H.ARG.81	H, H.ARG.81	2.79	1.94	8.27
4NZR.PDB	O, H.LEU.18	N, H.LEU.82	H, H.LEU.82	2.82	2.00	14.32
4NZR.PDB	O, H.ARG.66	N, H.ALA.82A	H, H.ALA.82A	2.75	1.90	8.50
4NZR.PDB	O, H.THR.83	N, H.ASP.86	H, H.ASP.86	2.82	1.97	8.78
4NZR.PDB	O, H.ALA.84	N, H.THR.87	H, H.THR.87	2.95	2.10	9.57
4NZR.PDB	O, H.HIS.39	N, H.VAL.89	H, H.VAL.89	2.90	2.08	15.32
4NZR.PDB	O, H.VAL.107	N, H.TYR.90	H, H.TYR.90	2.84	2.00	11.61
4NZR.PDB	O, H.VAL.37	N, H.PHE.91	H, H.PHE.91	2.75	1.91	10.12
4NZR.PDB	OE2, H.GLU.6	N, H.CYS.92	H, H.CYS.92	2.87	2.06	15.61
4NZR.PDB	O, H.GLY.35	N, H.ALA.93	H, H.ALA.93	2.84	2.09	24.53
4NZR.PDB	O, H.VAL.102	N, H.ARG.94	H, H.ARG.94	2.90	2.15	25.02

4NZR.PDB	OD1, H_ASP_101	NE, H_ARG_94	HE, H_ARG_94	2.90	2.05	5.79
4NZR.PDB	OD2, H_ASP_101	NH2, H_ARG_94	HH21, H_ARG_94	2.73	1.90	13.79
4NZR.PDB	O, H_HIS_33	N, H_HIS_95	H, H_HIS_95	2.85	2.00	2.84
4NZR.PDB	OG, H_SER_50	ND1, H_HIS_95	HD1, H_HIS_95	2.67	1.84	11.69
4NZR.PDB	O, H_GLY_100H	NE2, H_HIS_95	HE2, H_HIS_95	2.92	2.20	27.79
4NZR.PDB	O, H_TRP_100I	N, H_ARG_96	H, H_ARG_96	2.84	2.03	17.11
4NZR.PDB	O, H_ARG_96	N, H_GLY_100H	H, H_GLY_100H	2.83	2.09	26.32
4NZR.PDB	O, H_ARG_96	N, H_TRP_100I	H, H_TRP_100I	2.87	2.13	26.51
4NZR.PDB	OH, L_TYR_36	N, H_PHE_100J	H, H_PHE_100J	2.96	2.11	8.14
4NZR.PDB	O, H_PHE_100J	NE1, H_TRP_103	HE1, H_TRP_103	2.95	2.19	23.88
4NZR.PDB	O, H_CYS_92	N, H_GLY_104	H, H_GLY_104	2.86	2.04	15.44
4NZR.PDB	OE1, H_GLU_6	N, H_GLY_106	H, H_GLY_106	2.82	2.04	21.27
4NZR.PDB	O, H_TYR_90	N, H_VAL_107	H, H_VAL_107	2.93	2.12	16.92
4NZR.PDB	O, H_ALA_88	N, H_VAL_109	H, H_VAL_109	2.86	2.00	1.82
4NZR.PDB	O, H_GLY_10	N, H_THR_110	H, H_THR_110	2.80	1.95	8.91
4NZR.PDB	OG1, H_THR_87	N, H_VAL_111	H, H_VAL_111	2.87	2.02	10.02
4NZR.PDB	O, H_VAL_12	N, H_SER_112	H, H_SER_112	2.92	2.12	18.68
4NZR.PDB	O, H_PHE_148	N, H_LYS_117	H, H_LYS_117	2.83	1.99	10.22
4NZR.PDB	O, H_ASP_146	NZ, H_LYS_117	HZ2, H_LYS_117	2.85	2.05	22.38
4NZR.PDB	O, H_LYS_145	N, H_SER_120	H, H_SER_120	2.88	2.07	16.11
4NZR.PDB	O, H_LEU_143	N, H_PHE_122	H, H_PHE_122	2.83	2.00	12.46
4NZR.PDB	O, H_GLY_141	N, H_LEU_124	H, H_LEU_124	2.75	1.90	5.12
4NZR.PDB	O, H_VAL_193	N, H_ALA_138	H, H_ALA_138	2.76	1.91	7.40
4NZR.PDB	O, H_VAL_191	N, H_LEU_140	H, H_LEU_140	2.93	2.10	13.85
4NZR.PDB	O, H_LEU_124	N, H_GLY_141	H, H_GLY_141	2.91	2.17	26.54
4NZR.PDB	O, H_SER_189	N, H_CYS_142	H, H_CYS_142	2.86	2.07	19.75
4NZR.PDB	O, H_PHE_122	N, H_LEU_143	H, H_LEU_143	2.77	1.93	12.58
4NZR.PDB	O, H_LEU_187	N, H_VAL_144	H, H_VAL_144	2.76	1.91	5.81
4NZR.PDB	O, H_SER_120	N, H_LYS_145	H, H_LYS_145	2.83	1.98	8.06
4NZR.PDB	O, H_LYS_117	N, H_PHE_148	H, H_PHE_148	2.88	2.08	18.10
4NZR.PDB	O, H_ASN_211	N, H_THR_153	H, H_THR_153	2.86	2.04	14.37
4NZR.PDB	O, H_ASN_209	N, H_SER_156	H, H_SER_156	2.93	2.11	14.90
4NZR.PDB	O, H_ILE_207	N, H_ASN_162	H, H_ASN_162	2.83	1.99	8.33
4NZR.PDB	OD1, H_ASN_209	N, H_SER_163	H, H_SER_163	2.78	2.01	22.06
4NZR.PDB	O, H_VAL_190	N, H_HIS_172	H, H_HIS_172	2.89	2.06	13.96
4NZR.PDB	O, H_SER_188	N, H_PHE_174	H, H_PHE_174	2.98	2.13	5.13
4NZR.PDB	O, H_SER_186	N, H_VAL_177	H, H_VAL_177	2.84	2.01	12.47
4NZR.PDB	O, H_LEU_184	N, H_GLN_179	H, H_GLN_179	2.83	1.98	4.97
4NZR.PDB	OD1, H_ASP_146	NE2, H_GLN_179	HE22, H_GLN_179	2.89	2.12	22.14
4NZR.PDB	O, H_GLN_179	N, H_GLY_183	H, H_GLY_183	2.81	1.99	13.79
4NZR.PDB	O, H_TYR_147	N, H_TYR_185	H, H_TYR_185	2.76	1.91	6.87
4NZR.PDB	O, H_VAL_177	N, H_SER_186	H, H_SER_186	2.92	2.15	22.72
4NZR.PDB	O, H_VAL_144	N, H_LEU_187	H, H_LEU_187	2.86	2.05	15.45
4NZR.PDB	OG, L_SER_176	OG, H_SER_188	HG, H_SER_188	2.88	2.16	24.46
4NZR.PDB	O, H_CYS_142	N, H_SER_189	H, H_SER_189	2.99	2.16	13.39
4NZR.PDB	O, H_HIS_172	N, H_VAL_190	H, H_VAL_190	2.81	1.98	14.14
4NZR.PDB	O, H_LEU_140	N, H_VAL_191	H, H_VAL_191	2.76	1.94	15.00
4NZR.PDB	O, H_ALA_138	N, H_VAL_193	H, H_VAL_193	2.76	1.96	16.51
4NZR.PDB	O, H_GLY_136	N, H_SER_195	H, H_SER_195	2.71	1.87	10.73
4NZR.PDB	O, H_PRO_194	N, H_SER_197	H, H_SER_197	2.94	2.08	6.12
4NZR.PDB	O, H_SER_197	N, H_GLN_203	H, H_GLN_203	2.86	2.05	15.22
4NZR.PDB	OD1, H_ASN_162	N, H_ILE_207	H, H_ILE_207	2.78	1.97	16.55
4NZR.PDB	O, H_SER_156	N, H_ASN_209	H, H_ASN_209	2.81	1.96	7.21
4NZR.PDB	OD1, H_ASP_220	ND2, H_ASN_209	HD22, H_ASN_209	2.89	2.06	12.07
4NZR.PDB	O, H_VAL_219	N, H_VAL_210	H, H_VAL_210	2.75	1.90	7.71
4NZR.PDB	O, H_THR_153	N, H_ASN_211	H, H_ASN_211	2.89	2.07	14.75
4NZR.PDB	OG, H_SER_215	ND1, H_HIS_212	HD1, H_HIS_212	2.80	1.99	17.07
4NZR.PDB	O, H_PRO_149	NE2, H_HIS_212	HE2, H_HIS_212	2.62	1.78	7.68

4NZR.PDB	O, H.LYS_213	N, H.ASN_216	H, H.ASN_216	2.95	2.12	11.20
4NZR.PDB	O, H.VAL_210	N, H.VAL_219	H, H.VAL_219	2.94	2.10	10.72
4NZR.PDB	O, H.CYS_208	N, H.LYS_221	H, H.LYS_221	2.90	2.08	14.73
4NZR.PDB	OE2, L.GLU_123	NZ, H.LYS_221	HZ2, H.LYS_221	2.99	2.10	2.00
4NZR.PDB	OE2, H.GLU_226	NE, H.ARG_222	HE, H.ARG_222	2.65	1.93	27.41
4NZR.PDB	O, H.TYR_206	N, H.VAL_225	H, H.VAL_225	2.90	2.05	6.78
4NZR.PDB	OG, L.SER_26	N, L.VAL_3	H, L.VAL_3	2.89	2.07	14.71
4NZR.PDB	O, L.ARG_24	N, L.THR_5	H, L.THR_5	2.79	1.95	10.02
4NZR.PDB	OE1, L.GLN_100	N, L.GLN_6	H, L.GLN_6	2.88	2.02	5.19
4NZR.PDB	O, L.TYR_86	NE2, L.GLN_6	HE22, L.GLN_6	2.88	2.05	12.91
4NZR.PDB	O, L.LYS_103	N, L.LEU_11	H, L.LEU_11	2.85	2.09	23.33
4NZR.PDB	OE2, L.GLU_17	N, L.SER_14	H, L.SER_14	2.82	1.98	9.91
4NZR.PDB	O, M.PRO_119	OG, L.SER_14	HG, L.SER_14	2.76	2.00	18.37
4NZR.PDB	O, L.MET_78	N, L.GLY_16	H, L.GLY_16	2.77	1.93	12.23
4NZR.PDB	OG1, M.THR_110	N, L.THR_18	H, L.THR_18	2.82	2.00	15.23
4NZR.PDB	O, L.ILE_75	N, L.VAL_19	H, L.VAL_19	2.83	2.05	21.72
4NZR.PDB	O, L.LEU_73	N, L.LEU_21	H, L.LEU_21	2.87	2.02	8.50
4NZR.PDB	O, L.SER_7	N, L.SER_22	H, L.SER_22	2.89	2.05	9.28
4NZR.PDB	O, L.PHE_71	N, L.CYS_23	H, L.CYS_23	2.92	2.12	16.99
4NZR.PDB	O, L.THR_5	N, L.ARG_24	H, L.ARG_24	2.83	2.01	13.32
4NZR.PDB	O, L.THR_69	N, L.ALA_25	H, L.ALA_25	2.94	2.14	18.04
4NZR.PDB	O, L.GLY_68	N, L.ILE_29	H, L.ILE_29	2.91	2.06	8.12
4NZR.PDB	OD1, L.ASN_28	N, L.ASN_30	H, L.ASN_30	2.80	1.97	11.83
4NZR.PDB	OE1, L.GLU_92	ND2, L.ASN_30	HD22, L.ASN_30	2.94	2.10	10.05
4NZR.PDB	OH, L.TYR_52	NZ, L.LYS_31	HZ1, L.LYS_31	2.57	1.77	21.34
4NZR.PDB	O, L.ILE_29	N, L.ASN_32	H, L.ASN_32	2.86	2.02	10.39
4NZR.PDB	O, L.GLN_89	N, L.ALA_34	H, L.ALA_34	2.87	2.04	11.97
4NZR.PDB	O, L.ILE_48	N, L.TRP_35	H, L.TRP_35	2.93	2.13	19.22
4NZR.PDB	O, L.TYR_87	N, L.TYR_36	H, L.TYR_36	2.69	1.88	17.31
4NZR.PDB	O, L.ARG_45	N, L.GLN_37	H, L.GLN_37	2.90	2.09	17.34
4NZR.PDB	OH, L.TYR_86	NE2, L.GLN_37	HE21, L.GLN_37	2.96	2.11	9.58
4NZR.PDB	O, L.VAL_85	N, L.TYR_38	H, L.TYR_38	2.76	1.97	19.78
4NZR.PDB	O, L.GLN_37	N, L.ARG_45	H, L.ARG_45	2.86	2.09	21.39
4NZR.PDB	O, L.TRP_35	N, L.VAL_47	H, L.VAL_47	2.91	2.05	2.37
4NZR.PDB	O, L.SER_53	N, L.PHE_49	H, L.PHE_49	2.86	2.07	19.76
4NZR.PDB	OH, L.TYR_91	N, L.GLU_50	H, L.GLU_50	2.96	2.25	29.60
4NZR.PDB	O, L.LEU_33	N, L.THR_51	H, L.THR_51	2.80	1.96	10.12
4NZR.PDB	O, L.LYS_31	OG1, L.THR_51	HG1, L.THR_51	2.80	2.02	13.30
4NZR.PDB	O, L.GLU_50	N, L.TYR_52	H, L.TYR_52	2.75	2.01	25.67
4NZR.PDB	O, L.PHE_49	N, L.SER_53	H, L.SER_53	2.90	2.12	21.06
4NZR.PDB	OH, M.TYR_444	N, L.LYS_54	H, L.LYS_54	2.91	2.06	4.85
4NZR.PDB	OD2, L.ASP_82	NH1, L.ARG_61	HH12, L.ARG_61	2.70	1.89	15.31
4NZR.PDB	O, M.ALA_391	NH2, L.ARG_61	HH21, L.ARG_61	2.90	2.11	19.46
4NZR.PDB	OD1, L.ASP_82	NH2, L.ARG_61	HH22, L.ARG_61	2.85	2.01	9.02
4NZR.PDB	O, L.THR_74	N, L.VAL_63	H, L.VAL_63	2.91	2.08	12.21
4NZR.PDB	O, L.THR_72	N, L.SER_65	H, L.SER_65	2.90	2.08	15.21
4NZR.PDB	O, L.GLU_70	N, L.SER_67	H, L.SER_67	2.94	2.16	20.85
4NZR.PDB	O, L.CYS_23	N, L.PHE_71	H, L.PHE_71	2.88	2.14	25.90
4NZR.PDB	O, L.SER_65	N, L.THR_72	H, L.THR_72	2.94	2.11	12.62
4NZR.PDB	O, L.LEU_21	N, L.LEU_73	H, L.LEU_73	2.84	2.03	16.61
4NZR.PDB	O, L.VAL_63	N, L.THR_74	H, L.THR_74	2.76	1.90	4.94
4NZR.PDB	O, L.VAL_19	N, L.ILE_75	H, L.ILE_75	2.77	1.98	19.82
4NZR.PDB	O, L.ARG_61	ND2, L.ASN_76	HD22, L.ASN_76	2.96	2.12	12.10
4NZR.PDB	OG, M.SER_106	N, L.ASN_77	H, L.ASN_77	2.86	2.01	5.30
4NZR.PDB	O, L.GLU_17	N, L.MET_78	H, L.MET_78	2.92	2.06	6.39
4NZR.PDB	OD2, L.ASP_82	N, L.GLN_79	H, L.GLN_79	2.85	2.01	8.63
4NZR.PDB	O, L.ASN_77	NE2, L.GLN_79	HE21, L.GLN_79	2.79	1.94	9.45
4NZR.PDB	O, L.GLN_79	N, L.ASP_82	H, L.ASP_82	2.93	2.08	8.91

4NZR.PDB	O, L_TYR_38	N, L_VAL_85	H, L_VAL_85	2.95	2.10	5.38
4NZR.PDB	O, L_THR_102	N, L_TYR_86	H, L_TYR_86	2.91	2.07	11.72
4NZR.PDB	O, L_TYR_36	N, L_TYR_87	H, L_TYR_87	2.86	2.04	15.92
4NZR.PDB	O, L_THR_97	N, L_GLN_90	H, L_GLN_90	2.96	2.18	20.60
4NZR.PDB	O, H_ALA_100G	NE, L_ARG_96	HE, L_ARG_96	2.83	2.08	23.79
4NZR.PDB	O, L_GLU_93	NH1, L_ARG_96	HH11, L_ARG_96	2.92	2.18	26.23
4NZR.PDB	O, H_ALA_100G	NH2, L_ARG_96	HH21, L_ARG_96	2.80	2.05	24.03
4NZR.PDB	O, L_ILE_2	OG1, L_THR_97	HG1, L_THR_97	2.76	1.95	5.21
4NZR.PDB	O, L_CYS_88	N, L_GLY_99	H, L_GLY_99	2.96	2.18	21.78
4NZR.PDB	O, L_GLN_6	NE2, L_GLN_100	HE22, L_GLN_100	2.65	1.87	20.23
4NZR.PDB	OE1, L_GLN_6	N, L_GLY_101	H, L_GLY_101	2.96	2.20	24.19
4NZR.PDB	O, L_TYR_86	N, L_THR_102	H, L_THR_102	2.92	2.12	16.99
4NZR.PDB	O, L_PRO_8	OG1, L_THR_102	HG1, L_THR_102	2.71	2.03	28.62
4NZR.PDB	O, L ASP_9	N, L_LYS_103	H, L_LYS_103	2.97	2.17	18.66
4NZR.PDB	O, L_ALA_84	N, L_VAL_104	H, L_VAL_104	2.92	2.09	11.20
4NZR.PDB	O, L_LEU_11	N, L ASP_105	H, L ASP_105	2.92	2.08	10.70
4NZR.PDB	O, L_VAL_13	N, L_LYS_107	H, L_LYS_107	2.87	2.06	16.88
4NZR.PDB	O, L_THR_109	NE, L_ARG_108	HE, L_ARG_108	2.88	2.03	6.39
4NZR.PDB	O, L ASP_170	NH1, L_ARG_108	HH11, L_ARG_108	2.85	2.01	10.32
4NZR.PDB	O, M ASN_177	NH2, L_ARG_108	HH22, L_ARG_108	2.82	2.05	22.21
4NZR.PDB	O, M_GLY_178	N, L_THR_109	H, L_THR_109	2.92	2.07	5.99
4NZR.PDB	O, M_GLY_178	OG1, L_THR_109	HG1, L_THR_109	2.88	2.17	26.23
4NZR.PDB	O, M ASP_117	N, L_VAL_110	H, L_VAL_110	2.96	2.14	15.09
4NZR.PDB	O, L_TYR_140	N, L_ALA_111	H, L_ALA_111	2.82	1.99	12.32
4NZR.PDB	O, L_LEU_135	N, L_PHE_116	H, L_PHE_116	2.94	2.12	15.43
4NZR.PDB	O, L_VAL_133	N, L_PHE_118	H, L_PHE_118	2.81	1.99	14.02
4NZR.PDB	OG, L_SER_121	N, L_GLN_124	H, L_GLN_124	2.99	2.17	16.25
4NZR.PDB	OG, L_SER_131	NE2, L_GLN_124	HE22, L_GLN_124	2.90	2.04	4.21
4NZR.PDB	O, L_GLN_124	N, L_SER_127	H, L_SER_127	2.85	2.12	26.70
4NZR.PDB	O, L_LEU_125	N, L_GLY_128	H, L_GLY_128	2.99	2.18	17.68
4NZR.PDB	O, L_LEU_181	N, L_ALA_130	H, L_ALA_130	2.81	2.02	18.51
4NZR.PDB	OE1, L_GLN_124	N, L_SER_131	H, L_SER_131	2.91	2.10	17.17
4NZR.PDB	O, L_LEU_179	N, L_VAL_132	H, L_VAL_132	2.79	1.95	10.51
4NZR.PDB	O, L_SER_177	N, L_CYS_134	H, L_CYS_134	2.78	1.94	10.51
4NZR.PDB	O, L_PHE_116	N, L_LEU_135	H, L_LEU_135	2.78	1.93	7.68
4NZR.PDB	O, L_LEU_175	N, L_LEU_136	H, L_LEU_136	2.79	1.93	3.71
4NZR.PDB	O, L_SER_114	N, L ASN_137	H, L ASN_137	2.76	1.93	13.32
4NZR.PDB	OG, L_SER_174	N, L ASN_138	H, L ASN_138	2.97	2.12	9.18
4NZR.PDB	O, L_TYR_173	N, L_PHE_139	H, L_PHE_139	2.80	1.98	13.87
4NZR.PDB	O, L_ALA_111	N, L_TYR_140	H, L_TYR_140	2.94	2.14	17.85
4NZR.PDB	O, L_GLU_195	N, L_GLN_147	H, L_GLN_147	2.85	2.04	15.79
4NZR.PDB	OG, L_SER_177	NE1, L_TRP_148	HE1, L_TRP_148	2.91	2.07	10.59
4NZR.PDB	O, L_ALA_193	N, L_LYS_149	H, L_LYS_149	2.88	2.05	12.05
4NZR.PDB	O, L_VAL_191	N, L ASP_151	H, L ASP_151	2.81	1.98	13.22
4NZR.PDB	O, L_VAL_150	N, L_ALA_153	H, L_ALA_153	2.92	2.07	7.66
4NZR.PDB	O, L_TRP_148	N, L_GLN_155	H, L_GLN_155	2.84	2.00	9.48
4NZR.PDB	O, L_ALA_153	NE2, L_GLN_155	HE21, L_GLN_155	2.97	2.11	2.73
4NZR.PDB	OE1, L_GLN_155	ND2, L ASN_158	HD21, L ASN_158	2.96	2.11	9.14
4NZR.PDB	O, H_LEU_178	NE2, L_GLN_160	HE22, L_GLN_160	2.86	2.01	7.83
4NZR.PDB	O, L_SER_176	N, L_SER_162	H, L_SER_162	2.96	2.18	20.83
4NZR.PDB	O, H_PRO_175	OG, L_SER_162	HG, L_SER_162	2.79	1.98	7.14
4NZR.PDB	O, L_SER_174	N, L_THR_164	H, L_THR_164	2.96	2.15	15.87
4NZR.PDB	O, L_SER_171	NE2, L_GLN_166	HE21, L_GLN_166	2.93	2.09	7.84
4NZR.PDB	O, L_ILE_106	NE2, L_GLN_166	HE22, L_GLN_166	2.71	1.88	13.12
4NZR.PDB	O, L_THR_172	N, L ASP_167	H, L ASP_167	2.77	1.92	9.43
4NZR.PDB	OD1, L ASP_167	N, L_LYS_169	H, L_LYS_169	2.86	2.01	8.70
4NZR.PDB	O, L ASP_167	N, L_SER_171	H, L_SER_171	2.75	2.00	24.50
4NZR.PDB	OD1, L ASP_170	OG1, L_THR_172	HG1, L_THR_172	2.70	1.89	6.41

4NZR.PDB	O, L_PHE_139	N, L_TYR_173	H, L_TYR_173	2.82	1.99	11.40
4NZR.PDB	OG1, L_THR_164	N, L_SER_174	H, L_SER_174	2.94	2.15	19.12
4NZR.PDB	O, L_LEU_136	N, L_LEU_175	H, L_LEU_175	2.89	2.12	21.67
4NZR.PDB	O, L_SER_162	N, L_SER_176	H, L_SER_176	2.97	2.14	13.36
4NZR.PDB	OG, H_SER_188	OG, L_SER_176	HG, L_SER_176	2.88	2.09	13.66
4NZR.PDB	O, L_CYS_134	N, L_SER_177	H, L_SER_177	2.86	2.02	10.25
4NZR.PDB	O, L_GLN_160	N, L_THR_178	H, L_THR_178	2.83	2.00	11.32
4NZR.PDB	O, L_VAL_132	N, L_LEU_179	H, L_LEU_179	2.78	1.96	14.30
4NZR.PDB	O, L_ASN_158	N, L_THR_180	H, L_THR_180	2.97	2.13	10.64
4NZR.PDB	O, L_ALA_130	N, L_LEU_181	H, L_LEU_181	2.88	2.04	10.13
4NZR.PDB	O, L_GLY_128	N, L_LYS_183	H, L_LYS_183	2.93	2.11	14.95
4NZR.PDB	O, L_SER_182	N, L_TYR_186	H, L_TYR_186	2.96	2.11	6.64
4NZR.PDB	O, L_LYS_183	N, L_GLU_187	H, L_GLU_187	3.00	2.19	17.62
4NZR.PDB	O, L_ASP_185	N, L_LYS_188	H, L_LYS_188	2.95	2.13	13.06
4NZR.PDB	OD2, L_ASP_151	ND1, L_HIS_189	HD1, L_HIS_189	2.85	2.11	26.53
4NZR.PDB	OD1, L_ASP_151	N, L_VAL_191	H, L_VAL_191	2.94	2.08	3.42
4NZR.PDB	O, L_PHE_209	N, L_TYR_192	H, L_TYR_192	2.93	2.08	7.61
4NZR.PDB	O, L_LYS_149	N, L_ALA_193	H, L_ALA_193	2.88	2.09	18.86
4NZR.PDB	O, L_LYS_207	N, L_CYS_194	H, L_CYS_194	2.85	2.01	12.39
4NZR.PDB	O, L_VAL_205	N, L_VAL_196	H, L_VAL_196	2.71	1.89	14.56
4NZR.PDB	O, L_LYS_145	N, L_THR_197	H, L_THR_197	2.92	2.09	11.99
4NZR.PDB	O, L_PRO_141	NE2, L_HIS_198	HE2, L_HIS_198	2.90	2.07	12.26
4NZR.PDB	ND1, L_HIS_198	N, L_GLY_200	H, L_GLY_200	2.94	2.09	6.73
4NZR.PDB	O, L_HIS_198	N, L_LEU_201	H, L_LEU_201	2.89	2.04	8.10
4NZR.PDB	O, L_VAL_196	N, L_VAL_205	H, L_VAL_205	2.92	2.14	20.36
4NZR.PDB	O, L_CYS_194	N, L_LYS_207	H, L_LYS_207	2.92	2.14	21.11
4NZR.PDB	O, L_TYR_192	N, L_PHE_209	H, L_PHE_209	2.96	2.19	21.79
4NZR.PDB	O, L_LYS_190	N, L_ARG_211	H, L_ARG_211	2.70	1.87	12.15
4NZR.PDB	O, L_HIS_189	NE, L_ARG_211	HE, L_ARG_211	2.80	2.03	21.60
4NZR.PDB	O, M_GLU_124	N, M_TYR_82	H, M_TYR_82	2.96	2.13	13.02
4NZR.PDB	O, M_SER_126	N, M_SER_84	H, M_SER_84	2.98	2.15	13.57
4NZR.PDB	O, M_LEU_128	N, M_ILE_86	H, M_ILE_86	2.86	2.05	17.30
4NZR.PDB	O, M_LYS_130	N, M_LEU_88	H, M_LEU_88	2.84	1.99	7.85
4NZR.PDB	OD1, M_ASP_87	N, M_SER_89	H, M_SER_89	2.86	2.02	8.48
4NZR.PDB	OD1, M_ASN_378	NH1, M_ARG_95	HH12, M_ARG_95	2.71	1.91	18.53
4NZR.PDB	O, M_PHE_94	N, M_PHE_98	H, M_PHE_98	2.87	2.04	11.19
4NZR.PDB	O, M_ARG_95	N, M_ARG_99	H, M_ARG_99	2.91	2.10	16.79
4NZR.PDB	O, M_PHE_98	N, M_ALA_102	H, M_ALA_102	2.82	1.99	13.59
4NZR.PDB	O, M_ARG_99	N, M_ASN_103	H, M_ASN_103	2.77	1.95	14.29
4NZR.PDB	O, M_ALA_102	N, M_SER_106	H, M_SER_106	2.84	2.02	14.09
4NZR.PDB	O, M_ASN_103	N, M_GLU_107	H, M_GLU_107	2.90	2.10	17.39
4NZR.PDB	O, M_GLU_104	N, M_ALA_108	H, M_ALA_108	2.97	2.17	17.15
4NZR.PDB	O, M_LEU_105	N, M_ILE_109	H, M_ILE_109	2.94	2.17	22.50
4NZR.PDB	O, M_SER_106	N, M_THR_110	H, M_THR_110	2.95	2.12	14.11
4NZR.PDB	O, M_SER_106	OG1, M_THR_110	HG1, M_THR_110	2.74	1.95	13.19
4NZR.PDB	O, M_GLU_107	N, M_ASN_111	H, M_ASN_111	2.94	2.16	21.46
4NZR.PDB	O, M_SER_112	NZ, M_LYS_114	HZ1, M_LYS_114	2.69	1.82	10.18
4NZR.PDB	O, M_VAL_120	N, M_GLY_115	H, M_GLY_115	2.93	2.17	24.30
4NZR.PDB	O, M_SER_156	NE, M_ARG_118	HE, M_ARG_118	3.00	2.25	25.81
4NZR.PDB	O, M_SER_156	NH2, M_ARG_118	HH21, M_ARG_118	2.85	2.07	20.58
4NZR.PDB	O, M_ARG_118	N, M_VAL_120	H, M_VAL_120	2.76	2.02	26.00
4NZR.PDB	O, M_TYR_144	N, M_ILE_125	H, M_ILE_125	2.88	2.09	19.38
4NZR.PDB	O, M_TYR_82	N, M_SER_126	H, M_SER_126	2.89	2.07	14.81
4NZR.PDB	OE2, M_GLU_124	OG, M_SER_126	HG, M_SER_126	2.49	1.81	27.79
4NZR.PDB	O, M_ALA_142	N, M_GLY_127	H, M_GLY_127	2.88	2.07	15.98
4NZR.PDB	O, M_SER_84	N, M_LEU_128	H, M_LEU_128	2.81	1.97	11.35
4NZR.PDB	O, M_PHE_140	N, M_ILE_129	H, M_ILE_129	2.77	1.91	2.60
4NZR.PDB	O, M_ILE_86	N, M_LYS_130	H, M_LYS_130	2.86	2.00	2.42

4NZR.PDB	O, M_THR_137	OG1, M_THR_131	HG1, M_THR_131	2.69	1.93	17.31
4NZR.PDB	O, M_TYR_379	N, M_ILE_136	H, M_ILE_136	2.91	2.08	13.78
4NZR.PDB	O, M_ILE_129	N, M_PHE_140	H, M_PHE_140	2.99	2.21	21.20
4NZR.PDB	OE2, M_GLU_124	NZ, M_LYS_141	HZ2, M_LYS_141	2.96	2.15	21.57
4NZR.PDB	O, M_GLY_127	N, M_ALA_142	H, M_ALA_142	2.80	1.95	6.73
4NZR.PDB	O, M_GLN_159	N, M_GLY_143	H, M_GLY_143	2.82	2.00	13.14
4NZR.PDB	O, M_ILE_125	N, M_TYR_144	H, M_TYR_144	2.80	2.04	23.22
4NZR.PDB	O, M_LEU_155	N, M_HIS_147	H, M_HIS_147	2.85	2.01	10.85
4NZR.PDB	O, M_SER_153	N, M_ALA_149	H, M_ALA_149	2.76	1.91	5.90
4NZR.PDB	O, M_ALA_149	N, M_GLY_152	H, M_GLY_152	2.79	1.94	8.29
4NZR.PDB	O, M_LEU_180	N, M_TYR_158	H, M_TYR_158	2.83	1.99	9.68
4NZR.PDB	O, M_GLY_143	N, M_GLN_159	H, M_GLN_159	2.87	2.04	13.27
4NZR.PDB	O, M_PHE_382	N, M_PHE_164	H, M_PHE_164	2.85	2.03	14.98
4NZR.PDB	O, M_TYR_338	ND2, M_ASN_165	HD21, M_ASN_165	2.81	2.03	20.49
4NZR.PDB	O, M_ASN_183	ND2, M_ASN_165	HD22, M_ASN_165	2.99	2.16	11.12
4NZR.PDB	OD1, M_ASN_335	ND2, M_ASN_166	HD22, M_ASN_166	2.95	2.13	14.03
4NZR.PDB	OD1, M_ASN_183	NE, M_ARG_167	HE, M_ARG_167	2.87	2.09	20.21
4NZR.PDB	OD1, M_ASP_339	NH2, M_ARG_167	HH22, M_ARG_167	2.84	2.05	19.40
4NZR.PDB	OE2, M_GLU_311	N, M_LEU_169	H, M_LEU_169	2.70	1.87	11.59
4NZR.PDB	OE2, M_GLU_311	N, M_MET_170	H, M_MET_170	2.91	2.07	11.26
4NZR.PDB	O, M_SER_198	N, M_LEU_173	H, M_LEU_173	2.95	2.10	5.86
4NZR.PDB	OD1, M_ASN_177	N, M_THR_179	H, M_THR_179	2.81	1.95	3.90
4NZR.PDB	OD1, M_ASN_177	OG1, M_THR_179	HG1, M_THR_179	2.75	1.94	6.81
4NZR.PDB	O, M_TYR_158	N, M_ALA_182	H, M_ALA_182	2.88	2.03	6.05
4NZR.PDB	OE1, M_GLN_174	N, M_ASN_183	H, M_ASN_183	2.83	2.00	12.26
4NZR.PDB	O, M_ASN_165	ND2, M_ASN_183	HD21, M_ASN_183	2.83	2.00	11.27
4NZR.PDB	O, M_TYR_187	N, M_PHE_191	H, M_PHE_191	2.90	2.07	12.39
4NZR.PDB	O, M_ASP_189	N, M_SER_196	H, M_SER_196	2.84	2.04	18.29
4NZR.PDB	O, M_PHE_197	N, M_TRP_200	H, M_TRP_200	2.82	1.97	10.31
4NZR.PDB	O, M_PRO_171	NE1, M_TRP_200	HE1, M_TRP_200	2.83	1.99	8.99
4NZR.PDB	O, M_PHE_222	N, M_SER_201	H, M_SER_201	2.78	1.94	12.33
4NZR.PDB	O, M_THR_203	ND2, M_ASN_202	HD22, M_ASN_202	2.86	2.06	17.05
4NZR.PDB	O, M_THR_220	N, M_THR_203	H, M_THR_203	2.86	2.05	16.26
4NZR.PDB	OD1, M_ASP_217	OG1, M_THR_207	HG1, M_THR_207	2.72	1.90	1.28
4NZR.PDB	O, M_TYR_216	N, M_VAL_208	H, M_VAL_208	2.71	1.87	8.33
4NZR.PDB	O, M_LEU_214	N, M_THR_210	H, M_THR_210	2.96	2.14	13.71
4NZR.PDB	O, M_ALA_245	N, M_ASP_217	H, M_ASP_217	2.93	2.09	9.77
4NZR.PDB	O, M_THR_206	N, M_LYS_218	H, M_LYS_218	2.92	2.13	20.21
4NZR.PDB	OG1, M_THR_203	N, M_THR_220	H, M_THR_220	2.85	2.05	18.11
4NZR.PDB	O, M_VAL_241	N, M_TYR_221	H, M_TYR_221	2.93	2.11	14.30
4NZR.PDB	O, M_SER_201	N, M_PHE_222	H, M_PHE_222	2.88	2.09	19.39
4NZR.PDB	O, M_ALA_224	N, M_SER_227	H, M_SER_227	2.86	2.03	13.10
4NZR.PDB	O, M_PRO_228	N, M_SER_232	H, M_SER_232	2.88	2.10	20.88
4NZR.PDB	O, M_LEU_229	N, M_TYR_233	H, M_TYR_233	2.92	2.16	23.55
4NZR.PDB	O, M_TYR_221	N, M_VAL_241	H, M_VAL_241	2.87	2.02	7.27
4NZR.PDB	OE1, M_GLU_261	NZ, M_LYS_242	HZ1, M_LYS_242	2.96	2.22	28.06
4NZR.PDB	O, M_GLU_261	NZ, M_LYS_242	HZ3, M_LYS_242	2.55	1.69	11.67
4NZR.PDB	O, M_TRP_219	N, M_THR_243	H, M_THR_243	2.79	1.95	10.59
4NZR.PDB	O, M_ASP_217	N, M_ALA_245	H, M_ALA_245	2.89	2.07	14.41
4NZR.PDB	O, M_ILE_267	N, M_ILE_246	H, M_ILE_246	2.96	2.14	14.76
4NZR.PDB	O, M_ARG_269	N, M_ALA_248	H, M_ALA_248	2.78	1.96	15.32
4NZR.PDB	OD1, M_ASP_247	N, M_LYS_249	H, M_LYS_249	2.95	2.10	5.78
4NZR.PDB	OD1, M_ASP_250	NZ, M_LYS_249	HZ2, M_LYS_249	2.93	2.05	7.77
4NZR.PDB	O, M_ASP_247	N, M_ASP_250	H, M_ASP_250	2.94	2.10	10.81
4NZR.PDB	O, M_ASP_250	N, M_LEU_254	H, M_LEU_254	2.89	2.16	27.92
4NZR.PDB	NE2, M_GLN_282	NZ, M_LYS_255	HZ2, M_LYS_255	2.97	2.08	5.26
4NZR.PDB	O, M_LEU_254	N, M_ILE_258	H, M_ILE_258	2.84	1.99	9.84
4NZR.PDB	O, M_THR_257	N, M_GLU_261	H, M_GLU_261	2.89	2.08	16.34

4NZR.PDB	O, M.ILE.258	N, M.LYS.262	H, M.LYS.262	2.89	2.11	21.82
4NZR.PDB	O, M.LYS.289	N, M.LEU.266	H, M.LEU.266	2.92	2.10	13.96
4NZR.PDB	O, M.LEU.244	N, M.ILE.267	H, M.ILE.267	2.88	2.03	7.52
4NZR.PDB	O, M.SER.291	N, M.ILE.268	H, M.ILE.268	2.95	2.09	5.10
4NZR.PDB	O, M.ILE.246	N, M.ARG.269	H, M.ARG.269	2.83	1.98	9.70
4NZR.PDB	OD2, M.ASP.217	NH1, M.ARG.269	HH12, M.ARG.269	2.82	1.99	14.04
4NZR.PDB	O, M.GLN.193	NH2, M.ARG.269	HH21, M.ARG.269	2.90	2.20	29.55
4NZR.PDB	O, M.TYR.293	N, M.LEU.271	H, M.LEU.271	2.91	2.07	10.40
4NZR.PDB	O, M.GLY.275	N, M.LEU.278	H, M.LEU.278	2.93	2.08	6.63
4NZR.PDB	O, M.SER.276	N, M.ASN.279	H, M.ASN.279	2.87	2.04	13.20
4NZR.PDB	O, M.LEU.278	N, M.LEU.281	H, M.LEU.281	3.00	2.14	5.40
4NZR.PDB	O, M.THR.264	N, M.LYS.288	H, M.LYS.288	2.79	2.01	19.89
4NZR.PDB	OE2, M.GLU.313	NZ, M.LYS.289	HZ1, M.LYS.289	2.70	1.96	27.41
4NZR.PDB	OE1, M.GLU.311	NZ, M.LYS.289	HZ3, M.LYS.289	2.89	2.00	2.29
4NZR.PDB	O, M.GLU.313	N, M.LEU.292	H, M.LEU.292	2.92	2.08	9.41
4NZR.PDB	O, M.ILE.268	N, M.TYR.293	H, M.TYR.293	2.81	1.96	5.69
4NZR.PDB	O, M.GLY.273	N, M.THR.297	H, M.THR.297	2.74	1.93	16.92
4NZR.PDB	O, M.ASN.274	N, M.ASN.300	H, M.ASN.300	2.77	1.96	17.19
4NZR.PDB	O, M.LEU.330	NE2, M.GLN.304	HE21, M.GLN.304	2.93	2.09	8.97
4NZR.PDB	O, M.VAL.329	N, M.PHE.306	H, M.PHE.306	2.92	2.13	19.27
4NZR.PDB	O, M.LYS.288	N, M.VAL.310	H, M.VAL.310	2.73	1.91	14.16
4NZR.PDB	O, M.ASN.335	N, M.LEU.312	H, M.LEU.312	2.83	2.09	26.31
4NZR.PDB	O, M.LEU.292	N, M.TYR.315	H, M.TYR.315	2.81	2.05	23.22
4NZR.PDB	O, M.GLY.294	N, M.THR.317	H, M.THR.317	2.77	1.95	15.24
4NZR.PDB	O, M.VAL.299	N, M.ASN.326	H, M.ASN.326	2.99	2.14	6.61
4NZR.PDB	O, M.VAL.309	OG1, M.THR.334	HG1, M.THR.334	2.89	2.12	15.85
4NZR.PDB	O, M.VAL.310	N, M.ASN.335	H, M.ASN.335	2.95	2.14	16.98
4NZR.PDB	O, M.VAL.310	ND2, M.ASN.335	HD22, M.ASN.335	2.97	2.16	17.87
4NZR.PDB	OE2, M.GLU.383	N, M.VAL.336	H, M.VAL.336	2.87	2.03	8.95
4NZR.PDB	O, M.LEU.312	N, M.ILE.337	H, M.ILE.337	2.90	2.08	14.00
4NZR.PDB	OD1, M.ASN.165	N, M.TYR.338	H, M.TYR.338	2.85	2.02	11.20
4NZR.PDB	OG, M.SER.343	N, M.ASP.339	H, M.ASP.339	2.88	2.05	13.57
4NZR.PDB	OD1, M.ASN.184	N, M.LEU.340	H, M.LEU.340	2.86	2.02	9.90
4NZR.PDB	O, M.ASP.339	N, M.SER.343	H, M.SER.343	2.85	2.02	12.90
4NZR.PDB	O, M.ALA.320	NZ, M.LYS.344	HZ1, M.LYS.344	2.76	1.89	11.48
4NZR.PDB	O, M.SER.318	NZ, M.LYS.344	HZ3, M.LYS.344	2.90	2.04	12.02
4NZR.PDB	O, M.PHE.323	N, M.THR.347	H, M.THR.347	2.86	2.04	13.38
4NZR.PDB	O, M.PHE.325	N, M.ASP.350	H, M.ASP.350	2.77	1.92	5.83
4NZR.PDB	O, M.LEU.399	N, M.LEU.351	H, M.LEU.351	2.77	1.98	19.72
4NZR.PDB	OD1, M.ASP.350	N, M.THR.352	H, M.THR.352	2.94	2.11	11.48
4NZR.PDB	OD1, M.ASP.350	OG1, M.THR.352	HG1, M.THR.352	2.69	1.93	19.00
4NZR.PDB	O, M.LEU.351	N, M.VAL.354	H, M.VAL.354	2.99	2.17	14.74
4NZR.PDB	O, M.ALA.363	N, M.ASN.358	H, M.ASN.358	2.83	2.00	12.67
4NZR.PDB	O, M.LEU.356	N, M.ASP.365	H, M.ASP.365	2.81	1.96	8.63
4NZR.PDB	O, M.GLN.357	NZ, M.LYS.368	HZ2, M.LYS.368	2.90	2.01	4.14
4NZR.PDB	O, M.ALA.366	N, M.LYS.370	H, M.LYS.370	2.94	2.09	7.76
4NZR.PDB	OE1, M.GLU.420	NZ, M.LYS.370	HZ2, M.LYS.370	2.61	1.80	20.02
4NZR.PDB	O, M.ASN.367	N, M.GLN.371	H, M.GLN.371	2.96	2.16	18.23
4NZR.PDB	OD1, M.ASP.375	NE2, M.GLN.371	HE21, M.GLN.371	2.92	2.12	18.76
4NZR.PDB	O, M.LEU.369	N, M.VAL.373	H, M.VAL.373	2.99	2.14	9.69
4NZR.PDB	O, M.LYS.370	N, M.GLY.374	H, M.GLY.374	2.80	1.98	14.26
4NZR.PDB	O, M.GLN.371	N, M.ASP.375	H, M.ASP.375	2.91	2.15	24.37
4NZR.PDB	O, M.VAL.373	N, M.ILE.376	H, M.ILE.376	2.99	2.25	26.03
4NZR.PDB	O, M.VAL.373	N, M.TYR.377	H, M.TYR.377	2.78	1.92	4.41
4NZR.PDB	O, M.GLY.374	N, M.ASN.378	H, M.ASN.378	2.88	2.07	16.83
4NZR.PDB	O, M.GLY.374	N, M.TYR.379	H, M.TYR.379	2.99	2.17	15.14
4NZR.PDB	OE1, M.GLU.383	NH1, M.ARG.380	HH11, M.ARG.380	2.65	1.84	14.74
4NZR.PDB	O, M.THR.334	NH1, M.ARG.380	HH12, M.ARG.380	2.93	2.14	19.06

4NZR.PDB	O, M_GLU_162	NH1, M_ARG_381	HH12, M_ARG_381	2.93	2.20	26.71
4NZR.PDB	OE1, M_GLU_162	NH2, M_ARG_381	HH22, M_ARG_381	3.00	2.22	21.24
4NZR.PDB	OE1, L_GLU_81	NE, M_ARG_384	HE, M_ARG_384	2.93	2.09	10.37
4NZR.PDB	O, M_GLY_388	NH1, M_ARG_384	HH12, M_ARG_384	2.81	2.01	18.07
4NZR.PDB	O, M_LYS_344	NE2, M_GLN_385	HE22, M_GLN_385	2.71	1.92	19.06
4NZR.PDB	O, M_GLU_383	N, M_PHE_386	H, M_PHE_386	2.99	2.17	16.23
4NZR.PDB	O, M_ARG_384	N, M_GLN_387	H, M_GLN_387	2.98	2.13	8.94
4NZR.PDB	O, M_ARG_381	NE2, M_GLN_387	HE21, M_GLN_387	2.77	1.96	17.54
4NZR.PDB	O, M_GLU_162	NE2, M_GLN_387	HE22, M_GLN_387	2.83	2.04	18.31
4NZR.PDB	OE1, M_GLN_387	N, M_GLY_392	H, M_GLY_392	2.78	1.95	10.56
4NZR.PDB	O, M_PHE_390	N, M_GLY_393	H, M_GLY_393	2.93	2.13	18.34
4NZR.PDB	OD1, M_ASP_396	NZ, M_LYS_397	HZ1, M_LYS_397	2.90	2.03	10.85
4NZR.PDB	O, M_TYR_437	N, M_TYR_398	H, M_TYR_398	2.93	2.11	14.24
4NZR.PDB	O, M_ILE_349	N, M_LEU_399	H, M_LEU_399	2.84	2.00	10.68
4NZR.PDB	O, M_THR_435	N, M_VAL_400	H, M_VAL_400	2.89	2.06	12.03
4NZR.PDB	OD2, M_ASP_410	ND2, M_ASN_402	HD22, M_ASN_402	2.93	2.14	18.97
4NZR.PDB	OD2, M_ASP_410	N, M_VAL_403	H, M_VAL_403	2.81	2.04	21.61
4NZR.PDB	OD1, M_ASN_404	N, M_ASN_406	H, M_ASN_406	2.87	2.04	12.77
4NZR.PDB	O, M_LYS_407	N, M_ASP_411	H, M_ASP_411	2.97	2.15	15.64
4NZR.PDB	O, M_ASP_408	N, M_ASP_412	H, M_ASP_412	2.92	2.12	19.03
4NZR.PDB	O, M_SER_409	N, M_LEU_413	H, M_LEU_413	2.93	2.10	12.24
4NZR.PDB	O, M_ASP_410	N, M_VAL_414	H, M_VAL_414	2.89	2.06	12.64
4NZR.PDB	O, M_ASP_411	N, M_TYR_415	H, M_TYR_415	2.83	1.98	9.53
4NZR.PDB	O, M_ASP_412	N, M_ARG_416	H, M_ARG_416	2.86	2.01	9.04
4NZR.PDB	OE2, M_GLU_464	NH1, M_ARG_416	HH12, M_ARG_416	2.68	1.83	5.86
4NZR.PDB	OE1, M_GLU_464	NH2, M_ARG_416	HH22, M_ARG_416	2.88	2.03	6.77
4NZR.PDB	O, M_LEU_413	N, M_SER_417	H, M_SER_417	2.88	2.05	11.51
4NZR.PDB	O, M_VAL_414	N, M_LEU_418	H, M_LEU_418	2.92	2.09	12.46
4NZR.PDB	O, M_LEU_418	N, M_LEU_421	H, M_LEU_421	2.84	2.06	20.21
4NZR.PDB	O, M_LYS_419	N, M_ASN_422	H, M_ASN_422	2.91	2.11	18.90
4NZR.PDB	O, M_LEU_418	N, M_LEU_423	H, M_LEU_423	2.97	2.13	11.14
4NZR.PDB	O, M_ASN_440	N, M_HIS_424	H, M_HIS_424	2.82	2.03	19.83
4NZR.PDB	O, M_ARG_438	N, M_GLU_426	H, M_GLU_426	2.73	1.89	8.53
4NZR.PDB	O, M_TYR_436	N, M_TYR_429	H, M_TYR_429	2.86	2.01	8.90
4NZR.PDB	OD1, M_ASP_411	NH1, M_ARG_430	HH12, M_ARG_430	2.84	2.06	21.86
4NZR.PDB	O, M_ASN_434	N, M_GLU_431	H, M_GLU_431	2.87	2.02	8.65
4NZR.PDB	O, M_VAL_400	N, M_THR_435	H, M_THR_435	2.80	1.99	16.75
4NZR.PDB	OD1, M_ASN_402	OG1, M_THR_435	HG1, M_THR_435	2.74	1.98	18.44
4NZR.PDB	O, M_TYR_429	N, M_TYR_436	H, M_TYR_436	2.75	1.91	12.60
4NZR.PDB	O, M_TYR_398	N, M_TYR_437	H, M_TYR_437	2.80	1.95	5.61
4NZR.PDB	O, M_GLU_427	N, M_ARG_438	H, M_ARG_438	2.92	2.08	10.71
4NZR.PDB	OD2, M_ASP_396	NE, M_ARG_438	HE, M_ARG_438	2.86	2.00	5.29
4NZR.PDB	O, M_ASP_396	N, M_VAL_439	H, M_VAL_439	2.78	2.00	20.99
4NZR.PDB	O, M_HIS_424	N, M_ASN_440	H, M_ASN_440	2.91	2.07	11.96
4NZR.PDB	OE2, M_GLU_426	ND2, M_ASN_440	HD22, M_ASN_440	2.87	2.05	14.71
4NZR.PDB	OH, M_TYR_394	N, M_GLU_441	H, M_GLU_441	2.91	2.08	11.38
4NZR.PDB	OD1, M_ASN_440	N, M_ASN_442	H, M_ASN_442	2.86	2.01	10.00
4NZR.PDB	O, M_GLU_426	N, M_TYR_450	H, M_TYR_450	2.94	2.10	8.91
4NZR.PDB	OG, M_SER_448	N, M_GLU_451	H, M_GLU_451	3.00	2.15	7.42
4NZR.PDB	O, M_SER_448	N, M_ASN_452	H, M_ASN_452	2.99	2.16	12.61
4NZR.PDB	O, M_GLY_446	ND2, M_ASN_452	HD22, M_ASN_452	2.95	2.14	17.61
4NZR.PDB	O, M_ILE_449	N, M_GLU_453	H, M_GLU_453	2.90	2.04	6.17
4NZR.PDB	OD1, M_ASP_412	NH1, M_ARG_454	HH12, M_ARG_454	2.79	1.98	15.66
4NZR.PDB	O, M_GLU_451	N, M_ALA_455	H, M_ALA_455	2.80	1.96	11.85
4NZR.PDB	O, M_GLU_453	NH1, M_ARG_457	HH11, M_ARG_457	2.87	2.09	20.01
4NZR.PDB	OD1, H_ASP_31E	NH1, M_ARG_457	HH12, M_ARG_457	2.96	2.12	11.27
4NZR.PDB	OD2, H_ASP_31E	NH2, M_ARG_457	HH22, M_ARG_457	2.55	1.75	17.03
4NZR.PDB	O, M_ARG_454	N, M_ASP_458	H, M_ASP_458	2.91	2.20	29.30

4NZR.PDB	O, M_ASP_458	N, M_GLN_462	H, M_GLN_462	2.90	2.06	11.58
4NZR.PDB	O, M_SER_459	N, M_ASN_463	H, M_ASN_463	2.97	2.15	14.56
4NZR.PDB	O, M_GLU_460	N, M_GLU_464	H, M_GLU_464	2.94	2.12	14.76
4NZR.PDB	O, M_PHE_461	N, M_ILE_465	H, M_ILE_465	2.92	2.11	16.00
4NZR.PDB	O, M_ASN_463	N, M_LYS_467	H, M_LYS_467	2.98	2.13	6.16
4NZR.PDB	O, M_GLU_464	N, M_ARG_468	H, M_ARG_468	2.90	2.06	11.94

Table 1696: 4NZR-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4NZU.PDB	OG, L.SER.26	N, L.GLU.3	H, L.GLU.3	2.85	2.00	7.06
4NZU.PDB	O, L.GLN.24	N, L.THR.5	H, L.THR.5	2.89	2.06	12.85
4NZU.PDB	O, L.LYS.103	N, L.LEU.11	H, L.LEU.11	2.89	2.11	20.24
4NZU.PDB	O, L.GLU.105	N, L.ALA.13	H, L.ALA.13	2.97	2.15	15.91
4NZU.PDB	OD2, L.ASP.17	N, L.SER.14	H, L.SER.14	2.85	2.00	6.08
4NZU.PDB	O, L.LEU.78	N, L.GLY.16	H, L.GLY.16	2.75	1.92	11.17
4NZU.PDB	O, L.ILE.75	N, L.VAL.19	H, L.VAL.19	2.93	2.10	12.37
4NZU.PDB	O, L.PHE.73	N, L.ILE.21	H, L.ILE.21	2.89	2.06	11.61
4NZU.PDB	O, L.SER.7	N, L.THR.22	H, L.THR.22	2.86	2.01	5.56
4NZU.PDB	O, L.PHE.71	N, L.CYS.23	H, L.CYS.23	2.91	2.09	15.17
4NZU.PDB	O, L.THR.5	N, L.GLN.24	H, L.GLN.24	2.88	2.07	16.80
4NZU.PDB	O, L.THR.69	N, L.ALA.25	H, L.ALA.25	2.86	2.06	18.12
4NZU.PDB	O, L.GLY.68	N, L.ILE.29	H, L.ILE.29	2.87	2.02	6.63
4NZU.PDB	O, L.ILE.29	N, L.PHE.32	H, L.PHE.32	2.88	2.03	7.32
4NZU.PDB	O, L.GLN.89	N, L.ASP.34	H, L.ASP.34	2.88	2.05	12.07
4NZU.PDB	O, L.ILE.48	N, L.TRP.35	H, L.TRP.35	2.86	2.02	11.26
4NZU.PDB	O, L.TYR.87	N, L.TYR.36	H, L.TYR.36	2.84	2.02	14.90
4NZU.PDB	O, L.LYS.45	N, L.GLN.37	H, L.GLN.37	2.88	2.06	16.18
4NZU.PDB	O, L.VAL.85	N, L.GLN.38	H, L.GLN.38	2.81	2.00	16.84
4NZU.PDB	O, L.GLU.81	NE, L.ARG.39	HE, L.ARG.39	2.82	1.89	12.62
4NZU.PDB	O, L.ARG.39	N, L.LYS.42	H, L.LYS.42	2.98	2.17	16.62
4NZU.PDB	O, L.GLN.37	N, L.LYS.45	H, L.LYS.45	2.86	2.08	21.32
4NZU.PDB	O, L.TRP.35	N, L.LEU.47	H, L.LEU.47	2.90	2.05	4.96
4NZU.PDB	O, L.ASN.53	N, L.TYR.49	H, L.TYR.49	2.92	2.13	19.67
4NZU.PDB	O, L.LEU.33	N, L.ALA.51	H, L.ALA.51	2.73	1.91	14.91
4NZU.PDB	O, L.ASP.50	N, L.SER.52	H, L.SER.52	2.85	2.15	29.96
4NZU.PDB	O, L.TYR.49	N, L.ASN.53	H, L.ASN.53	2.95	2.12	14.12
4NZU.PDB	O, L.LEU.47	N, L.ALA.55	H, L.ALA.55	2.95	2.09	3.99
4NZU.PDB	OD2, L.ASP.82	NE, L.ARG.61	HE, L.ARG.61	2.83	2.03	27.68
4NZU.PDB	OD1, L.ASP.82	NH2, L.ARG.61	HH21, L.ARG.61	2.85	2.00	7.18
4NZU.PDB	O, L.THR.72	N, L.SER.65	H, L.SER.65	2.93	2.14	18.79
4NZU.PDB	O, L.ALA.30	N, L.GLY.68	H, L.GLY.68	2.88	2.07	17.47
4NZU.PDB	O, L.CYS.23	N, L.PHE.71	H, L.PHE.71	2.88	2.07	16.98
4NZU.PDB	O, L.SER.65	N, L.THR.72	H, L.THR.72	2.92	2.09	12.57
4NZU.PDB	O, L.ILE.21	N, L.PHE.73	H, L.PHE.73	2.91	2.08	12.35
4NZU.PDB	O, L.THR.63	N, L.THR.74	H, L.THR.74	2.88	2.05	11.92
4NZU.PDB	O, L.VAL.19	N, L.ILE.75	H, L.ILE.75	2.89	2.09	18.00
4NZU.PDB	O, L.ARG.61	N, L.SER.76	H, L.SER.76	2.83	2.03	17.44
4NZU.PDB	O, L.ASP.17	N, L.LEU.78	H, L.LEU.78	2.83	2.04	19.06
4NZU.PDB	OD2, L.ASP.82	N, L.GLN.79	H, L.GLN.79	2.91	2.07	9.01
4NZU.PDB	O, L.GLN.79	N, L.ASP.82	H, L.ASP.82	2.86	2.03	11.16
4NZU.PDB	O, L.THR.102	N, L.TYR.86	H, L.TYR.86	2.95	2.13	15.14
4NZU.PDB	O, L.TYR.36	N, L.TYR.87	H, L.TYR.87	2.92	2.11	16.96
4NZU.PDB	O, L.PHE.32	N, L.TYR.91	H, L.TYR.91	2.96	2.16	17.93
4NZU.PDB	O, L.CYS.88	N, L.GLY.99	H, L.GLY.99	2.83	2.03	18.33
4NZU.PDB	OE1, L.GLN.6	N, L.GLY.101	H, L.GLY.101	2.96	2.20	24.47
4NZU.PDB	O, L.TYR.86	N, L.THR.102	H, L.THR.102	2.91	2.10	16.25
4NZU.PDB	O, L.ALA.84	N, L.LEU.104	H, L.LEU.104	2.96	2.10	5.58
4NZU.PDB	O, L.LEU.11	N, L.GLU.105	H, L.GLU.105	2.96	2.15	17.50
4NZU.PDB	OE1, L.GLN.166	N, L.THR.106	H, L.THR.106	2.83	1.99	8.58
4NZU.PDB	O, L.ALA.13	N, L.LYS.107	H, L.LYS.107	2.88	2.05	13.69
4NZU.PDB	O, L.THR.109	NE, L.ARG.108	HE, L.ARG.108	2.81	1.86	9.52
4NZU.PDB	O, L.ASP.170	NH1, L.ARG.108	HH11, L.ARG.108	2.81	1.98	12.07
4NZU.PDB	O, L.TYR.140	N, L.ALA.111	H, L.ALA.111	2.88	2.04	11.37
4NZU.PDB	O, L.LEU.135	N, L.PHE.116	H, L.PHE.116	2.95	2.18	22.98
4NZU.PDB	O, L.VAL.133	N, L.PHE.118	H, L.PHE.118	2.80	2.00	18.01
4NZU.PDB	OG, L.SER.121	N, L.GLN.124	H, L.GLN.124	2.94	2.11	13.38

4NZU.PDB	O, L_LEU_181	N, L_ALA_130	H, L_ALA_130	2.90	2.05	9.45
4NZU.PDB	NE2, L_GLN_124	N, L_SER_131	H, L_SER_131	2.97	2.20	21.35
4NZU.PDB	O, L_LEU_179	N, L_VAL_132	H, L_VAL_132	2.90	2.07	11.76
4NZU.PDB	O, L_SER_177	N, L_CYS_134	H, L_CYS_134	2.87	2.04	13.69
4NZU.PDB	O, L_PHE_116	N, L_LEU_135	H, L_LEU_135	2.83	2.00	10.89
4NZU.PDB	O, L_LEU_175	N, L_LEU_136	H, L_LEU_136	2.84	1.99	6.57
4NZU.PDB	O, L_SER_114	N, L_ASN_137	H, L_ASN_137	2.79	1.96	12.42
4NZU.PDB	O, L_TYR_173	N, L_PHE_139	H, L_PHE_139	2.81	1.98	12.12
4NZU.PDB	O, L_ALA_111	N, L_TYR_140	H, L_TYR_140	2.98	2.17	16.59
4NZU.PDB	O, L_GLU_195	N, L_GLN_147	H, L_GLN_147	2.80	1.97	12.05
4NZU.PDB	OG, L_SER_177	NE1, L_TRP_148	HE1, L_TRP_148	2.90	1.89	11.12
4NZU.PDB	O, L_ALA_193	N, L_LYS_149	H, L_LYS_149	2.86	2.04	14.54
4NZU.PDB	O, L_VAL_191	N, L_ASP_151	H, L_ASP_151	2.81	1.98	13.30
4NZU.PDB	O, L_VAL_150	N, L_ALA_153	H, L_ALA_153	2.89	2.05	9.67
4NZU.PDB	O, L_TRP_148	N, L_GLN_155	H, L_GLN_155	2.91	2.07	10.18
4NZU.PDB	O, L_SER_176	N, L_SER_162	H, L_SER_162	2.96	2.18	20.50
4NZU.PDB	O, L_SER_174	N, L_THR_164	H, L_THR_164	2.99	2.18	16.93
4NZU.PDB	O, L_THR_172	N, L_ASP_167	H, L_ASP_167	2.80	1.96	8.83
4NZU.PDB	OD2, L_ASP_167	N, L_LYS_169	H, L_LYS_169	2.96	2.24	28.01
4NZU.PDB	OD2, L_ASP_167	N, L_ASP_170	H, L_ASP_170	2.95	2.13	14.40
4NZU.PDB	O, L_ASP_167	N, L_SER_171	H, L_SER_171	2.96	2.22	25.63
4NZU.PDB	OD1, L_ASP_170	N, L_THR_172	H, L_THR_172	2.94	2.13	16.20
4NZU.PDB	O, L_PHE_139	N, L_TYR_173	H, L_TYR_173	2.83	1.98	8.20
4NZU.PDB	O, L_LEU_136	N, L_LEU_175	H, L_LEU_175	2.85	2.05	17.53
4NZU.PDB	O, L_SER_162	N, L_SER_176	H, L_SER_176	2.96	2.14	14.63
4NZU.PDB	O, L_CYS_134	N, L_SER_177	H, L_SER_177	2.92	2.08	12.73
4NZU.PDB	O, L_GLN_160	N, L_THR_178	H, L_THR_178	2.85	2.02	12.21
4NZU.PDB	O, L_VAL_132	N, L_LEU_179	H, L_LEU_179	2.78	1.95	11.28
4NZU.PDB	O, L_ASN_158	N, L_THR_180	H, L_THR_180	2.89	2.04	7.97
4NZU.PDB	O, L_ALA_130	N, L_LEU_181	H, L_LEU_181	2.89	2.03	5.02
4NZU.PDB	O, L_GLY_128	N, L_LYS_183	H, L_LYS_183	2.93	2.08	7.57
4NZU.PDB	OG, L_SER_182	N, L_ASP_185	H, L_ASP_185	2.98	2.15	12.85
4NZU.PDB	O, L_SER_182	N, L_TYR_186	H, L_TYR_186	2.98	2.14	10.93
4NZU.PDB	O, L_LYS_183	N, L_GLU_187	H, L_GLU_187	2.86	2.03	12.51
4NZU.PDB	OD1, L_ASP_151	N, L_LYS_190	H, L_LYS_190	2.93	2.09	10.09
4NZU.PDB	OD1, L_ASP_151	N, L_VAL_191	H, L_VAL_191	2.97	2.13	9.29
4NZU.PDB	O, L_PHE_209	N, L_TYR_192	H, L_TYR_192	2.93	2.08	5.07
4NZU.PDB	O, L_LYS_149	N, L_ALA_193	H, L_ALA_193	2.96	2.16	18.28
4NZU.PDB	O, L_LYS_207	N, L_CYS_194	H, L_CYS_194	2.90	2.07	13.44
4NZU.PDB	O, L_GLN_147	N, L_GLU_195	H, L_GLU_195	2.85	2.00	7.85
4NZU.PDB	O, L_VAL_205	N, L_VAL_196	H, L_VAL_196	2.76	1.93	12.73
4NZU.PDB	O, L_LYS_145	N, L_THR_197	H, L_THR_197	2.96	2.14	13.76
4NZU.PDB	ND1, L_HIS_198	N, L_GLY_200	H, L_GLY_200	2.95	2.10	4.09
4NZU.PDB	O, L_HIS_198	N, L_LEU_201	H, L_LEU_201	2.91	2.06	7.34
4NZU.PDB	O, L_VAL_196	N, L_VAL_205	H, L_VAL_205	2.97	2.18	19.82
4NZU.PDB	O, L_TYR_192	N, L_PHE_209	H, L_PHE_209	2.95	2.17	20.95
4NZU.PDB	O, L_LYS_190	N, L_ARG_211	H, L_ARG_211	2.79	1.96	13.34
4NZU.PDB	O, L_HIS_189	NE, L_ARG_211	HE, L_ARG_211	2.83	1.95	20.09
4NZU.PDB	O, H_SER_25	N, H_SER_3	H, H_SER_3	2.94	2.15	18.68
4NZU.PDB	O, H_ALA_23	N, H_VAL_5	H, H_VAL_5	2.94	2.11	12.25
4NZU.PDB	OE1, H_GLN_105	N, H_GLU_6	H, H_GLU_6	2.88	2.02	2.55
4NZU.PDB	O, H_SER_21	N, H_SER_7	H, H_SER_7	2.91	2.11	18.23
4NZU.PDB	O, H_THR_110	N, H_VAL_12	H, H_VAL_12	2.93	2.20	26.91
4NZU.PDB	O, H_LEU_82C	N, H_GLY_15	H, H_GLY_15	2.72	1.86	1.10
4NZU.PDB	O, H_MET_82	N, H_LEU_18	H, H_LEU_18	2.87	2.07	18.95
4NZU.PDB	O, H_LEU_80	N, H_LEU_20	H, H_LEU_20	2.89	2.06	11.46
4NZU.PDB	O, H_SER_7	N, H_SER_21	H, H_SER_21	2.98	2.14	9.55
4NZU.PDB	O, H_LEU_78	N, H_CYS_22	H, H_CYS_22	2.82	2.04	21.59

4NZU.PDB	O, H_VAL_5	N, H_ALA_23	H, H_ALA_23	2.82	1.97	8.42
4NZU.PDB	O, H_ASN_76	N, H_ALA_24	H, H_ALA_24	2.93	2.07	4.56
4NZU.PDB	O, H_SER_3	N, H_SER_25	H, H_SER_25	2.99	2.20	20.90
4NZU.PDB	O, H_ALA_93	N, H_HIS_35	H, H_HIS_35	2.93	2.12	16.07
4NZU.PDB	O, H_ALA_49	N, H_TRP_36	H, H_TRP_36	2.92	2.14	21.04
4NZU.PDB	O, H_TYR_91	N, H_VAL_37	H, H_VAL_37	2.88	2.05	13.75
4NZU.PDB	O, H_GLU_46	N, H_ARG_38	H, H_ARG_38	2.81	1.97	10.17
4NZU.PDB	OE2, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.81	1.92	18.37
4NZU.PDB	OD1, H_ASP_86	NH1, H_ARG_38	HH12, H_ARG_38	2.87	2.03	8.91
4NZU.PDB	O, H_VAL_89	N, H_GLN_39	H, H_GLN_39	2.85	2.12	26.56
4NZU.PDB	O, H_ALA_40	N, H_ASP_43	H, H_ASP_43	2.95	2.13	14.09
4NZU.PDB	O, H_ARG_38	N, H_GLU_46	H, H_GLU_46	2.83	2.07	24.02
4NZU.PDB	O, H_TRP_36	N, H_VAL_48	H, H_VAL_48	2.86	2.04	15.06
4NZU.PDB	O, H_TYR_58	N, H_PHE_50	H, H_PHE_50	2.88	2.08	16.89
4NZU.PDB	O, H_PHE_34	N, H_ILE_51	H, H_ILE_51	2.88	2.05	13.34
4NZU.PDB	O, H_SER_56	N, H_SER_52	H, H_SER_52	2.92	2.10	13.95
4NZU.PDB	O, H_SER_52	N, H_GLY_54	H, H_GLY_54	2.94	2.14	17.16
4NZU.PDB	O, H_VAL_48	N, H_ALA_60	H, H_ALA_60	2.91	2.08	13.02
4NZU.PDB	O, H_SER_82B	NH1, H_ARG_66	HH11, H_ARG_66	2.99	2.16	13.59
4NZU.PDB	OD2, H_ASP_86	NH1, H_ARG_66	HH12, H_ARG_66	2.80	1.94	3.46
4NZU.PDB	O, H_GLN_81	N, H_THR_68	H, H_THR_68	2.85	2.05	17.96
4NZU.PDB	OH, H_TYR_59	N, H_ILE_69	H, H_ILE_69	2.96	2.13	12.69
4NZU.PDB	O, H_TYR_32	NH1, H_ARG_71	HH12, H_ARG_71	2.89	2.14	25.08
4NZU.PDB	O, H_TYR_32	NH2, H_ARG_71	HH22, H_ARG_71	2.94	2.22	27.85
4NZU.PDB	O, H_THR_77	N, H_ASP_72	H, H_ASP_72	2.87	2.04	12.43
4NZU.PDB	O, H_CYS_22	N, H_LEU_78	H, H_LEU_78	2.86	2.03	13.04
4NZU.PDB	O, H_SER_70	N, H_SER_79	H, H_SER_79	2.89	2.05	11.36
4NZU.PDB	O, H_LEU_20	N, H_LEU_80	H, H_LEU_80	2.94	2.13	15.87
4NZU.PDB	O, H_THR_68	N, H_GLN_81	H, H_GLN_81	2.89	2.05	10.75
4NZU.PDB	O, H_LEU_18	N, H_MET_82	H, H_MET_82	2.85	2.01	9.41
4NZU.PDB	O, H_ARG_66	N, H_ASN_82A	H, H_ASN_82A	2.85	2.04	16.30
4NZU.PDB	OD2, H_ASP_86	N, H_LYS_83	H, H_LYS_83	2.86	2.03	12.94
4NZU.PDB	O, H_LYS_83	N, H_ASP_86	H, H_ASP_86	2.84	2.02	13.61
4NZU.PDB	O, H_GLN_39	N, H_VAL_89	H, H_VAL_89	2.90	2.11	18.38
4NZU.PDB	O, H_THR_107	N, H_TYR_90	H, H_TYR_90	2.88	2.04	8.85
4NZU.PDB	O, H_VAL_37	N, H_TYR_91	H, H_TYR_91	2.73	1.88	6.70
4NZU.PDB	O, H_HIS_35	N, H_ALA_93	H, H_ALA_93	2.90	2.19	28.63
4NZU.PDB	O, H_TYR_102	N, H_ARG_94	H, H_ARG_94	2.97	2.19	21.23
4NZU.PDB	O, H_ALA_95	NE, H_ARG_94	HE, H_ARG_94	2.86	2.03	25.77
4NZU.PDB	O, H_ALA_95	NH2, H_ARG_94	HH21, H_ARG_94	2.85	2.09	22.83
4NZU.PDB	OD1, H_ASP_97	NH2, H_ARG_94	HH22, H_ARG_94	2.85	2.02	14.02
4NZU.PDB	O, H_SER_31	N, H_CYS_100C	H, H_CYS_100C	2.76	1.91	5.59
4NZU.PDB	O, H_LYS_100E	N, H_ALA_100G	H, H_ALA_100G	2.86	2.15	29.42
4NZU.PDB	OH, L_TYR_36	N, H_PHE_100H	H, H_PHE_100H	2.86	2.04	13.13
4NZU.PDB	O, H_PHE_100H	NE1, H_TRP_103	HE1, H_TRP_103	2.88	2.03	28.43
4NZU.PDB	O, H_CYS_92	N, H_GLY_104	H, H_GLY_104	2.88	2.05	13.50
4NZU.PDB	OE2, H_GLU_6	N, H_GLY_106	H, H_GLY_106	2.99	2.21	21.44
4NZU.PDB	O, H_ALA_88	N, H_VAL_109	H, H_VAL_109	2.91	2.05	3.91
4NZU.PDB	OG1, H_THR_87	N, H_VAL_111	H, H_VAL_111	2.93	2.07	3.36
4NZU.PDB	O, H_VAL_12	N, H_SER_112	H, H_SER_112	2.95	2.14	16.38
4NZU.PDB	OG, H_SER_112	N, H_ALA_114	H, H_ALA_114	2.91	2.06	8.79
4NZU.PDB	O, H_PHE_148	N, H_LYS_117	H, H_LYS_117	2.88	2.05	12.81
4NZU.PDB	O, H_LYS_145	N, H_SER_120	H, H_SER_120	2.90	2.12	21.09
4NZU.PDB	O, H_LEU_143	N, H_PHE_122	H, H_PHE_122	2.87	2.03	9.52
4NZU.PDB	O, H_GLY_141	N, H_LEU_124	H, H_LEU_124	2.81	1.96	5.22
4NZU.PDB	OG, H_SER_195	N, H_GLY_135	H, H_GLY_135	2.91	2.20	29.13
4NZU.PDB	O, H_VAL_193	N, H_ALA_138	H, H_ALA_138	2.83	2.01	14.25
4NZU.PDB	O, H_VAL_191	N, H_LEU_140	H, H_LEU_140	2.93	2.10	13.71

4NZU.PDB	O, H_LEU_124	N, H_GLY_141	H, H_GLY_141	2.82	2.09	26.80
4NZU.PDB	O, H_SER_189	N, H_CYS_142	H, H_CYS_142	2.85	2.07	19.90
4NZU.PDB	O, H_PHE_122	N, H_LEU_143	H, H_LEU_143	2.81	1.97	11.58
4NZU.PDB	O, H_LEU_187	N, H_VAL_144	H, H_VAL_144	2.71	1.85	5.98
4NZU.PDB	O, H_SER_120	N, H_LYS_145	H, H_LYS_145	2.81	1.96	5.69
4NZU.PDB	O, H_LYS_117	N, H_PHE_148	H, H_PHE_148	2.88	2.08	17.45
4NZU.PDB	O, H_ASN_209	N, H_SER_156	H, H_SER_156	2.95	2.15	17.06
4NZU.PDB	OG, H_SER_189	NE1, H_TRP_157	HE1, H_TRP_157	2.92	1.90	9.04
4NZU.PDB	O, H_ILE_207	N, H_ASN_162	H, H_ASN_162	2.83	1.99	9.99
4NZU.PDB	OD1, H_ASN_209	N, H_SER_163	H, H_SER_163	2.80	1.99	15.68
4NZU.PDB	O, H_TRP_157	N, H_GLY_164	H, H_GLY_164	2.93	2.20	26.82
4NZU.PDB	O, H_VAL_190	N, H_HIS_172	H, H_HIS_172	2.83	2.02	16.48
4NZU.PDB	O, H_SER_188	N, H_PHE_174	H, H_PHE_174	2.92	2.06	3.04
4NZU.PDB	O, H_SER_186	N, H_VAL_177	H, H_VAL_177	2.90	2.09	15.20
4NZU.PDB	O, H_LEU_184	N, H_GLN_179	H, H_GLN_179	2.86	2.01	8.15
4NZU.PDB	O, H_GLN_179	N, H_GLY_183	H, H_GLY_183	2.91	2.06	7.56
4NZU.PDB	O, H_TYR_147	N, H_TYR_185	H, H_TYR_185	2.80	1.95	8.98
4NZU.PDB	O, H_VAL_144	N, H_LEU_187	H, H_LEU_187	2.87	2.07	16.93
4NZU.PDB	O, H_CYS_142	N, H_SER_189	H, H_SER_189	2.99	2.16	14.04
4NZU.PDB	O, H_HIS_172	N, H_VAL_190	H, H_VAL_190	2.85	2.02	12.23
4NZU.PDB	O, H_LEU_140	N, H_VAL_191	H, H_VAL_191	2.86	2.05	16.60
4NZU.PDB	O, H_ALA_138	N, H_VAL_193	H, H_VAL_193	2.91	2.09	14.81
4NZU.PDB	O, H_GLY_136	N, H_SER_195	H, H_SER_195	2.96	2.15	15.58
4NZU.PDB	O, H_PRO_194	N, H_SER_197	H, H_SER_197	2.90	2.09	16.91
4NZU.PDB	OH, H_TYR_206	OG, H_BSER_197	HG, H_BSER_197	2.82	2.05	15.42
4NZU.PDB	O, H_SER_197	N, H_GLN_203	H, H_GLN_203	2.89	2.06	13.09
4NZU.PDB	OD1, H_ASN_162	N, H_ILE_207	H, H_ILE_207	2.90	2.10	18.98
4NZU.PDB	O, H_LYS_221	N, H_CYS_208	H, H_CYS_208	2.94	2.14	18.10
4NZU.PDB	O, H_SER_156	N, H_ASN_209	H, H_ASN_209	2.80	1.94	7.24
4NZU.PDB	O, H_VAL_219	N, H_VAL_210	H, H_VAL_210	2.79	1.93	4.11
4NZU.PDB	O, H_THR_153	N, H_ASN_211	H, H_ASN_211	2.98	2.16	14.35
4NZU.PDB	O, H_THR_217	N, H_HIS_212	H, H_HIS_212	2.78	1.93	6.91
4NZU.PDB	O, H_VAL_210	N, H_VAL_219	H, H_VAL_219	2.89	2.07	13.72
4NZU.PDB	O, H_CYS_208	N, H_LYS_221	H, H_LYS_221	2.90	2.08	13.19
4NZU.PDB	O, H_TYR_206	N, H_VAL_223	H, H_VAL_223	2.82	1.97	6.85

Table 1697: 4NZU-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4QEX.PDB	OD2, A_ASP_414	NH2, A_ARG_349	HH21, A_ARG_349	3.00	2.26	27.00
4QEX.PDB	O, A_PHE_316	N, A_ASN_356	H, A_ASN_356	2.87	2.04	13.53
4QEX.PDB	O, H_ALA_78	N, H_CYS_22	H, H_CYS_22	2.89	2.13	23.77
4QEX.PDB	O, H_ILE_51	N, H_MET_34	H, H_MET_34	2.99	2.24	24.56
4QEX.PDB	O, H_MET_34	N, H_ILE_51	H, H_ILE_51	2.88	2.12	24.11
4QEX.PDB	O, H_VAL_37	N, H_TYR_91	H, H_TYR_91	2.94	2.16	21.47
4QEX.PDB	OD2, B_ASP_414	NH2, B_ARG_349	HH21, B_ARG_349	2.99	2.26	27.25
4QEX.PDB	O, B_PHE_316	N, B_ASN_356	H, B_ASN_356	2.87	2.04	13.77
4QEX.PDB	O, I_ALA_78	N, I_CYS_22	H, I_CYS_22	2.89	2.13	24.05
4QEX.PDB	O, I_ILE_51	N, I_MET_34	H, I_MET_34	2.98	2.23	24.63
4QEX.PDB	O, I_TYR_91	N, I_VAL_37	H, I_VAL_37	3.00	2.18	14.72
4QEX.PDB	O, I_MET_34	N, I_ILE_51	H, I_ILE_51	2.88	2.13	24.11
4QEX.PDB	O, I_VAL_37	N, I_TYR_91	H, I_TYR_91	2.96	2.15	17.39

Table 1698: 4QEX-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4WUU.PDB	OD2, A_ASP_29	ND1, A_HIS_3	HD1, A_HIS_3	2.93	2.13	17.75
4WUU.PDB	O, A_TYR_99	N, A_TYR_7	H, A_TYR_7	2.76	1.92	10.35
4WUU.PDB	O, A_VAL_25	N, A_PHE_8	H, A_PHE_8	2.96	2.14	14.63
4WUU.PDB	O, A_ARG_97	N, A_PHE_9	H, A_PHE_9	2.76	2.00	23.12
4WUU.PDB	O, A_ILE_23	N, A_THR_10	H, A_THR_10	2.77	1.94	11.62
4WUU.PDB	O, A_HIS_93	N, A_SER_13	H, A_SER_13	2.94	2.18	22.69
4WUU.PDB	OG, A_SER_38	N, A_PHE_22	H, A_PHE_22	2.99	2.28	28.95
4WUU.PDB	O, A_THR_10	N, A_ILE_23	H, A_ILE_23	2.73	1.91	14.53
4WUU.PDB	O, A_PHE_36	N, A_ALA_24	H, A_ALA_24	2.98	2.17	16.88
4WUU.PDB	O, A_PHE_8	N, A_VAL_25	H, A_VAL_25	2.92	2.13	19.23
4WUU.PDB	O, A_ARG_6	N, A_TYR_27	H, A_TYR_27	2.91	2.07	7.74
4WUU.PDB	O, A_THR_31	N, A_VAL_28	H, A_VAL_28	2.84	2.03	16.38
4WUU.PDB	O, A_SER_4	N, A_ASP_29	H, A_ASP_29	2.78	1.95	12.60
4WUU.PDB	O, A_VAL_28	N, A_THR_31	H, A_THR_31	2.84	1.99	7.07
4WUU.PDB	OE1, A_GLU_46	NE, A_ARG_35	HE, A_ARG_35	2.77	1.96	15.11
4WUU.PDB	O, A_ALA_24	N, A_PHE_36	H, A_PHE_36	2.92	2.14	20.69
4WUU.PDB	O, A_PHE_22	N, A_SER_38	H, A_SER_38	2.95	2.16	19.48
4WUU.PDB	OD1, A_ASP_37	N, A_ASP_39	H, A_ASP_39	2.77	1.98	19.65
4WUU.PDB	OE2, A_GLU_46	OG, A_SER_42	HG, A_SER_42	2.85	2.07	18.95
4WUU.PDB	O, A_ARG_35	N, A_GLU_46	H, A_GLU_46	2.99	2.17	14.81
4WUU.PDB	O, A_PHE_33	N, A_ARG_48	H, A_ARG_48	2.89	2.07	14.83
4WUU.PDB	OD2, B_ASP_53	NE, A_ARG_48	HE, A_ARG_48	2.84	2.13	29.12
4WUU.PDB	OH, A_TYR_171	OH, A_TYR_59	HH, A_TYR_59	2.71	1.89	11.34
4WUU.PDB	O, A_PRO_57	N, A_ASP_61	H, A_ASP_61	2.71	1.85	6.09
4WUU.PDB	O, A_GLU_58	N, A_GLY_62	H, A_GLY_62	2.94	2.16	20.28
4WUU.PDB	O, A_TYR_59	N, A_GLU_63	H, A_GLU_63	2.86	2.00	6.81
4WUU.PDB	O, A_TRP_60	N, A_THR_64	H, A_THR_64	2.90	2.08	14.57
4WUU.PDB	OH, E_TYR_104	NZ, A_LYS_66	HZ3, A_LYS_66	2.89	2.02	10.84
4WUU.PDB	O, A_GLU_63	N, A_VAL_67	H, A_VAL_67	2.84	2.02	14.98
4WUU.PDB	O, A_ARG_65	N, A_ALA_69	H, A_ALA_69	3.00	2.14	3.72
4WUU.PDB	O, A_LYS_68	OG, A_SER_71	HG, A_SER_71	2.82	2.03	15.69
4WUU.PDB	O, A_ALA_69	OG1, A_THR_73	HG1, A_THR_73	3.00	2.20	14.54
4WUU.PDB	O, A_HIS_70	N, A_HIS_74	H, A_HIS_74	2.95	2.14	15.71
4WUU.PDB	O, A_SER_71	N, A_ARG_75	H, A_ARG_75	2.82	2.00	14.92
4WUU.PDB	O, A_THR_73	N, A_ASP_77	H, A_ASP_77	2.79	1.98	16.13
4WUU.PDB	O, A_VAL_76	N, A_THR_80	H, A_THR_80	2.88	2.08	19.21
4WUU.PDB	O, A_ASP_77	N, A_LEU_81	H, A_LEU_81	2.80	2.01	18.94
4WUU.PDB	OXT, C_LEU_9	OH, A_TYR_84	HH, A_TYR_84	2.64	1.82	12.17
4WUU.PDB	OD2, A_ASP_137	OH, A_TYR_85	HH, A_TYR_85	2.79	1.98	13.39
4WUU.PDB	O, A_SER_13	OG, A_SER_92	HG, A_SER_92	2.55	1.73	10.54
4WUU.PDB	OG, A_SER_13	N, A_HIS_93	H, A_HIS_93	2.78	1.95	13.85
4WUU.PDB	OD1, A_ASP_119	N, A_THR_94	H, A_THR_94	2.87	2.10	22.46
4WUU.PDB	O, A_SER_11	N, A_VAL_95	H, A_VAL_95	2.78	1.96	15.83
4WUU.PDB	O, A_ALA_117	N, A_GLN_96	H, A_GLN_96	2.85	2.05	18.30
4WUU.PDB	O, B_TRP_60	NE2, A_GLN_96	HE22, A_GLN_96	2.78	1.93	8.81
4WUU.PDB	O, A_PHE_9	N, A_ARG_97	H, A_ARG_97	2.92	2.14	20.57
4WUU.PDB	O, A_GLN_115	N, A_MET_98	H, A_MET_98	2.92	2.09	12.67
4WUU.PDB	O, A_MET_5	N, A_CYS_101	H, A_CYS_101	2.91	2.19	28.90
4WUU.PDB	O, A_ARG_111	N, A_ASP_102	H, A_ASP_102	2.81	1.99	13.14
4WUU.PDB	O, A_HIS_3	N, A_VAL_103	H, A_VAL_103	2.85	2.00	5.54
4WUU.PDB	O, A_ARG_108	N, A_GLY_104	H, A_GLY_104	2.96	2.19	22.29
4WUU.PDB	O, A_GLY_104	N, A_TRP_107	H, A_TRP_107	2.80	2.02	20.77
4WUU.PDB	O, A_ASP_102	N, A_LEU_110	H, A_LEU_110	2.72	1.90	14.82
4WUU.PDB	O, A_MET_98	N, A_GLN_115	H, A_GLN_115	2.70	1.87	13.07
4WUU.PDB	O, A_ILE_124	N, A_TYR_116	H, A_TYR_116	2.79	1.93	4.70
4WUU.PDB	OE1, A_GLN_87	OH, A_TYR_118	HH, A_TYR_118	2.94	2.13	11.47
4WUU.PDB	O, A_THR_94	N, A_ASP_119	H, A_ASP_119	2.71	1.87	9.67

4WUU.PDB	OG1, A_THR_143	OH, A_TYR_123	HH, A_TYR_123	2.74	1.95	17.32
4WUU.PDB	O, A_THR_134	N, A_ALA_125	H, A_ALA_125	2.79	2.07	26.99
4WUU.PDB	O, A_ALA_125	N, A_THR_134	H, A_THR_134	2.73	1.89	10.54
4WUU.PDB	O, A_ALA_140	N, A_LYS_144	H, A_LYS_144	2.66	1.82	11.78
4WUU.PDB	O, C_LEU_9	NZ, A_LYS_146	HZ3, A_LYS_146	2.76	1.90	13.68
4WUU.PDB	O, C_TYR_8	NE1, A_TRP_147	HE1, A_TRP_147	2.81	1.99	15.97
4WUU.PDB	O, A_LYS_146	N, A_ALA_150	H, A_ALA_150	2.92	2.13	20.13
4WUU.PDB	O, A_TRP_147	N, A_VAL_152	H, A_VAL_152	2.94	2.08	3.18
4WUU.PDB	O, A_VAL_152	N, A_LEU_156	H, A_LEU_156	2.97	2.15	15.29
4WUU.PDB	O, A_ALA_153	N, A_ARG_157	H, A_ARG_157	2.89	2.04	9.86
4WUU.PDB	O, C_ARG_1	OH, A_TYR_159	HH, A_TYR_159	2.86	2.02	6.39
4WUU.PDB	O, A_LEU_156	N, A_LEU_160	H, A_LEU_160	2.72	1.88	9.29
4WUU.PDB	O, A_TYR_159	N, A_CYS_164	H, A_CYS_164	2.62	1.77	6.61
4WUU.PDB	O, A_CYS_164	N, A_LEU_168	H, A_LEU_168	2.93	2.10	13.84
4WUU.PDB	O, A_VAL_165	N, A_ARG_169	H, A_ARG_169	2.89	2.05	8.58
4WUU.PDB	O, A_TRP_107	NE, A_ARG_169	HE, A_ARG_169	2.99	2.28	29.58
4WUU.PDB	O, A_TRP_107	NH2, A_ARG_169	HH21, A_ARG_169	2.90	2.19	28.46
4WUU.PDB	OE2, A_GLU_55	NE, A_ARG_170	HE, A_ARG_170	2.89	2.03	3.82
4WUU.PDB	O, A_TRP_167	N, A_TYR_171	H, A_TYR_171	2.90	2.05	5.21
4WUU.PDB	O, A_LEU_168	N, A_LEU_172	H, A_LEU_172	2.90	2.13	22.30
4WUU.PDB	O, A_ARG_170	N, A_ASN_174	H, A_ASN_174	2.98	2.15	11.94
4WUU.PDB	O, A_TYR_171	N, A_GLY_175	H, A_GLY_175	2.88	2.04	8.17
4WUU.PDB	O, A_GLY_175	N, A_LEU_179	H, A_LEU_179	2.67	1.82	8.19
4WUU.PDB	O, A_THR_178	NH2, A_ARG_181	HH21, A_ARG_181	2.71	1.91	17.26
4WUU.PDB	O, A_HIS_188	N, A_TRP_204	H, A_TRP_204	2.78	1.93	9.00
4WUU.PDB	O, A_LYS_186	N, A_LEU_206	H, A_LEU_206	2.86	2.04	15.38
4WUU.PDB	O, A_ASP_183	N, A_TYR_209	H, A_TYR_209	2.76	1.98	20.63
4WUU.PDB	O, A_ALA_245	NE1, A_TRP_217	HE1, A_TRP_217	2.84	2.09	23.84
4WUU.PDB	O, A_GLN_242	N, A_ARG_234	H, A_ARG_234	2.84	2.02	15.28
4WUU.PDB	OE1, B_GLN_8	NH1, A_ARG_234	HH11, A_ARG_234	2.79	2.07	27.49
4WUU.PDB	OE1, A_GLN_242	NH2, A_ARG_234	HH21, A_ARG_234	3.00	2.27	27.42
4WUU.PDB	O, A_THR_240	N, A_ALA_236	H, A_ALA_236	2.92	2.07	7.39
4WUU.PDB	OD1, A_ASP_238	OG1, A_THR_240	HG1, A_THR_240	2.61	1.79	8.96
4WUU.PDB	O, A_ARG_234	N, A_GLN_242	H, A_GLN_242	2.75	1.97	20.96
4WUU.PDB	O, B_HIS_31	N, B_ARG_3	H, B_ARG_3	2.86	2.03	11.56
4WUU.PDB	OG1, B_THR_86	OG1, B_THR_4	HG1, B_THR_4	2.90	2.14	21.40
4WUU.PDB	O, B_SER_28	N, B_LYS_6	H, B_LYS_6	2.87	2.05	15.60
4WUU.PDB	O, A_PRO_235	OH, B_TYR_10	HH, B_TYR_10	2.61	1.79	11.75
4WUU.PDB	O, B_PHE_22	N, B_ARG_12	H, B_ARG_12	2.79	2.03	23.74
4WUU.PDB	OD1, B_ASN_21	N, B_HIS_13	H, B_HIS_13	2.89	2.04	5.58
4WUU.PDB	O, B_PRO_72	N, B_GLY_18	H, B_GLY_18	2.92	2.11	17.66
4WUU.PDB	O, B_GLU_16	N, B_LYS_19	H, B_LYS_19	2.97	2.20	22.07
4WUU.PDB	O, B_PHE_70	N, B_ASN_21	H, B_ASN_21	2.81	2.00	16.15
4WUU.PDB	O, B_HIS_13	ND2, B_ASN_21	HD21, B_ASN_21	2.56	1.73	12.09
4WUU.PDB	OD1, B_ASN_21	N, B_PHE_22	H, B_PHE_22	2.97	2.25	28.82
4WUU.PDB	O, B_THR_68	N, B_LEU_23	H, B_LEU_23	2.82	1.98	11.92
4WUU.PDB	O, B_TYR_10	N, B_ASN_24	H, B_ASN_24	2.72	1.90	14.68
4WUU.PDB	O, A_ALA_236	ND2, B_ASN_24	HD21, B_ASN_24	2.81	2.05	22.96
4WUU.PDB	O, B_TYR_66	N, B_CYS_25	H, B_CYS_25	2.71	1.87	10.19
4WUU.PDB	O, B_GLN_8	N, B_TYR_26	H, B_TYR_26	2.86	2.05	15.75
4WUU.PDB	OE1, A_GLU_232	OH, B_TYR_26	HH, B_TYR_26	2.95	2.14	13.27
4WUU.PDB	O, B_LEU_64	N, B_VAL_27	H, B_VAL_27	2.92	2.11	17.06
4WUU.PDB	O, B_LYS_6	N, B_SER_28	H, B_SER_28	2.97	2.17	19.07
4WUU.PDB	O, B_ARG_3	N, B_HIS_31	H, B_HIS_31	2.97	2.16	15.90
4WUU.PDB	O, B_GLU_44	N, B_LYS_41	H, B_LYS_41	2.88	2.07	16.59
4WUU.PDB	O, B_GLU_77	N, B_ASN_42	H, B_ASN_42	2.51	1.66	6.56
4WUU.PDB	OD1, B_ASP_38	NE, B_ARG_45	HE, B_ARG_45	2.54	1.82	27.34
4WUU.PDB	O, B_LEU_65	N, B_SER_52	H, B_SER_52	2.79	2.01	20.88

4WUU.PDB	O, B.SER_61	N, B.SER_57	H, B.SER_57	2.89	2.12	21.85
4WUU.PDB	O, B.SER_57	N, B.TRP_60	H, B.TRP_60	2.99	2.16	14.14
4WUU.PDB	O, B.PHE_30	N, B.PHE_62	H, B.PHE_62	2.98	2.14	10.04
4WUU.PDB	OG, B.SER_52	N, B.LEU_65	H, B.LEU_65	2.96	2.16	18.95
4WUU.PDB	O, B.CYS_25	N, B.TYR_66	H, B.TYR_66	2.90	2.12	19.74
4WUU.PDB	OD1, B.ASN_42	N, B.GLU_77	H, B.GLU_77	2.71	1.88	11.42
4WUU.PDB	O, B.ASP_38	N, B.ARG_81	H, B.ARG_81	2.83	1.98	5.14
4WUU.PDB	O, B.LYS_91	N, B.VAL_82	H, B.VAL_82	2.78	1.94	11.03
4WUU.PDB	O, B.GLU_36	N, B.ASN_83	H, B.ASN_83	2.81	1.99	15.23
4WUU.PDB	O, B.PRO_32	NE2, B.HIS_84	HE2, B.HIS_84	2.79	1.94	7.34
4WUU.PDB	ND1, B.HIS_84	OG1, B.THR_86	HG1, B.THR_86	2.95	2.20	22.57
4WUU.PDB	O, B.CYS_80	N, B.VAL_93	H, B.VAL_93	2.90	2.07	14.26
4WUU.PDB	O, B.TYR_78	N, B.TRP_95	H, B.TRP_95	2.84	2.01	11.88
4WUU.PDB	OH, A.TYR_171	N, C.ARG_1	H1, C.ARG_1	2.79	2.03	25.96
4WUU.PDB	OE2, A.GLU_63	N, C.MET_2	H, C.MET_2	2.90	2.09	16.21
4WUU.PDB	O, D.TYR_87	NE2, D.GLN_6	HE22, D.GLN_6	2.71	1.90	15.76
4WUU.PDB	O, D.LYS_106	N, D.ALA_10	H, D.ALA_10	2.90	2.14	24.22
4WUU.PDB	OE1, D.GLN_16	N, D.THR_13	H, D.THR_13	2.67	1.88	19.99
4WUU.PDB	O, D.LEU_74	N, D.ILE_20	H, D.ILE_20	2.74	1.99	24.99
4WUU.PDB	O, D.THR_5	N, D.SER_23	H, D.SER_23	2.85	2.04	15.21
4WUU.PDB	O, D.THR_70	N, D.GLY_24	H, D.GLY_24	2.81	1.97	11.14
4WUU.PDB	OD1, D.ASN_28	N, D.SER_25	H, D.SER_25	2.82	2.03	19.32
4WUU.PDB	OD1, D.ASN_28	N, D.ILE_29	H, D.ILE_29	2.67	1.86	15.71
4WUU.PDB	O, D.SER_25	N, D.GLY_30	H, D.GLY_30	2.74	2.02	28.00
4WUU.PDB	OD1, D.ASN_52	N, D.VAL_34	H, D.VAL_34	2.65	1.82	10.44
4WUU.PDB	O, D.ILE_49	N, D.TRP_36	H, D.TRP_36	2.74	1.90	10.94
4WUU.PDB	O, D.TYR_88	N, D.TYR_37	H, D.TYR_37	2.74	1.93	16.60
4WUU.PDB	O, D.LYS_46	N, D.GLN_38	H, D.GLN_38	2.85	2.06	19.88
4WUU.PDB	O, D.ASP_86	N, D.GLN_39	H, D.GLN_39	2.86	2.07	20.09
4WUU.PDB	OE1, E.GLN_39	NE2, D.GLN_39	HE22, D.GLN_39	2.94	2.18	23.53
4WUU.PDB	O, D.GLN_38	N, D.LYS_46	H, D.LYS_46	2.66	1.91	24.48
4WUU.PDB	O, D.TRP_36	N, D.LEU_48	H, D.LEU_48	2.81	1.96	9.20
4WUU.PDB	O, D.VAL_34	N, D.ASN_52	H, D.ASN_52	2.71	1.91	17.51
4WUU.PDB	O, D.TYR_50	N, D.GLN_54	H, D.GLN_54	2.84	2.03	17.63
4WUU.PDB	OD2, D.ASP_83	NE, D.ARG_62	HE, D.ARG_62	2.79	2.08	28.83
4WUU.PDB	OD1, D.ASP_83	NH2, D.ARG_62	HH21, D.ARG_62	2.86	2.00	2.74
4WUU.PDB	O, D.SER_73	N, D.SER_66	H, D.SER_66	2.98	2.20	21.24
4WUU.PDB	O, D.SER_71	N, D.SER_68	H, D.SER_68	2.91	2.13	20.74
4WUU.PDB	O, D.CYS_22	N, D.ALA_72	H, D.ALA_72	2.80	1.97	12.36
4WUU.PDB	O, D.SER_64	N, D.ALA_75	H, D.ALA_75	2.67	1.84	13.24
4WUU.PDB	O, D.ARG_62	N, D.SER_77	H, D.SER_77	2.87	2.05	15.21
4WUU.PDB	O, D.GLN_16	N, D.GLY_78	H, D.GLY_78	2.83	2.06	22.13
4WUU.PDB	O, D.GLN_16	N, D.LEU_79	H, D.LEU_79	2.99	2.26	27.65
4WUU.PDB	O, D.GLY_78	NE2, D.GLN_80	HE21, D.GLN_80	2.75	1.96	20.10
4WUU.PDB	O, D.THR_105	N, D.TYR_87	H, D.TYR_87	2.90	2.13	23.52
4WUU.PDB	O, D.ASP_83	OH, D.TYR_87	HH, D.TYR_87	2.68	1.84	6.34
4WUU.PDB	O, D.TYR_37	N, D.TYR_88	H, D.TYR_88	2.89	2.07	13.58
4WUU.PDB	OE1, D.GLN_6	N, D.CYS_89	H, D.CYS_89	2.99	2.19	19.58
4WUU.PDB	O, D.GLY_98	N, D.ASP_93	H, D.ASP_93	2.75	1.89	0.36
4WUU.PDB	OD1, E.ASP_106	NE1, D.TRP_99	HE1, D.TRP_99	2.95	2.19	24.35
4WUU.PDB	O, D.ALA_91	N, D.VAL_100	H, D.VAL_100	2.97	2.13	10.77
4WUU.PDB	O, D.TYR_87	N, D.THR_105	H, D.THR_105	2.86	2.16	29.98
4WUU.PDB	O, D.PRO_7	OG1, D.THR_105	HG1, D.THR_105	2.43	1.60	5.47
4WUU.PDB	O, D.PRO_8	N, D.LYS_106	H, D.LYS_106	2.54	1.73	16.46
4WUU.PDB	O, D.ALA_10	N, D.THR_108	H, D.THR_108	2.87	2.05	14.29
4WUU.PDB	O, D.VAL_137	N, D.PHE_122	H, D.PHE_122	2.93	2.13	18.73
4WUU.PDB	O, D.ILE_140	OG, D.SER_141	HG, D.SER_141	2.39	1.64	20.74
4WUU.PDB	O, D.CYS_138	N, D.SER_180	H, D.SER_180	2.83	2.03	17.76

4WUU.PDB	OG1, D_THR_165	OG, D_SER_180	HG, D_SER_180	3.00	2.24	22.62
4WUU.PDB	O, D_GLU_164	N, D_TYR_181	H, D_TYR_181	2.94	2.09	6.97
4WUU.PDB	O, E_LYS_23	N, E_VAL_5	H, E_VAL_5	2.91	2.08	12.06
4WUU.PDB	O, E_TYR_94	NE2, E_GLN_6	HE22, E_GLN_6	2.66	1.82	10.49
4WUU.PDB	O, E_LEU_116	N, E_GLU_10	H, E_GLU_10	2.74	1.93	15.88
4WUU.PDB	O, E_THR_118	N, E_LYS_12	H, E_LYS_12	2.72	1.97	24.94
4WUU.PDB	O, E_LEU_81	N, E_ILE_20	H, E_ILE_20	2.99	2.27	27.77
4WUU.PDB	O, E_ALA_79	N, E_CYS_22	H, E_CYS_22	2.79	2.05	26.43
4WUU.PDB	O, E_VAL_5	N, E_LYS_23	H, E_LYS_23	2.85	2.00	7.51
4WUU.PDB	O, E_SER_77	N, E_GLY_24	H, E_GLY_24	2.96	2.13	14.07
4WUU.PDB	O, E_ALA_97	N, E_SER_35	H, E_SER_35	2.86	2.01	6.50
4WUU.PDB	O, E_TYR_95	N, E_VAL_37	H, E_VAL_37	2.60	1.79	15.34
4WUU.PDB	O, E_GLU_46	N, E_ARG_38	H, E_ARG_38	2.74	1.93	15.84
4WUU.PDB	O, E_MET_93	N, E_GLN_39	H, E_GLN_39	2.93	2.14	19.90
4WUU.PDB	OE1, D_GLN_39	NE2, E_GLN_39	HE22, E_GLN_39	2.55	1.73	14.29
4WUU.PDB	O, E_MET_40	N, E_LYS_43	H, E_LYS_43	2.92	2.08	8.65
4WUU.PDB	O, E_ARG_38	N, E_GLU_46	H, E_GLU_46	2.81	2.04	21.42
4WUU.PDB	O, E_TRP_36	N, E_MET_48	H, E_MET_48	2.85	2.01	9.52
4WUU.PDB	O, E_THR_59	N, E_ARG_50	H, E_ARG_50	2.92	2.11	16.22
4WUU.PDB	OE2, A_GLU_166	NH2, E_ARG_50	HH22, E_ARG_50	2.67	1.88	18.69
4WUU.PDB	O, E_ILE_34	N, E_VAL_51	H, E_VAL_51	2.91	2.10	17.37
4WUU.PDB	O, E_TYR_57	N, E_ASP_52	H, E_ASP_52	2.77	1.94	11.78
4WUU.PDB	OD1, E_ASP_52	N, E_GLY_54	H, E_GLY_54	2.93	2.22	29.55
4WUU.PDB	O, E_ILE_70	OG, E_SER_58	HG, E_SER_58	2.56	1.77	16.65
4WUU.PDB	O, E_MET_48	N, E_SER_61	H, E_SER_61	3.00	2.19	16.66
4WUU.PDB	O, E_SER_61	N, E_PHE_64	H, E_PHE_64	2.90	2.08	14.75
4WUU.PDB	O, E_GLN_82	N, E_THR_69	H, E_THR_69	2.86	2.06	17.27
4WUU.PDB	OH, E_TYR_60	N, E_ILE_70	H, E_ILE_70	2.95	2.13	13.50
4WUU.PDB	O, E_THR_78	N, E_ASP_73	H, E_ASP_73	2.72	1.95	22.66
4WUU.PDB	OD1, E_ASP_73	OG, E_SER_75	HG, E_SER_75	2.93	2.16	19.72
4WUU.PDB	O, E_CYS_22	N, E_ALA_79	H, E_ALA_79	2.74	1.89	8.78
4WUU.PDB	O, E_SER_71	N, E_TYR_80	H, E_TYR_80	2.97	2.17	17.59
4WUU.PDB	O, E_THR_69	N, E_GLN_82	H, E_GLN_82	2.93	2.22	28.66
4WUU.PDB	O, E_LEU_18	N, E_TRP_83	H, E_TRP_83	2.80	1.95	10.15
4WUU.PDB	OD2, E_ASP_90	N, E_LYS_87	H, E_LYS_87	2.81	1.97	9.45
4WUU.PDB	O, E_THR_115	N, E_TYR_94	H, E_TYR_94	2.93	2.16	22.48
4WUU.PDB	O, E_ASP_90	OH, E_TYR_94	HH, E_TYR_94	2.62	1.78	4.11
4WUU.PDB	O, E_VAL_37	N, E_TYR_95	H, E_TYR_95	2.78	2.01	21.75
4WUU.PDB	O, E_PRO_110	N, E_ARG_98	H, E_ARG_98	2.98	2.16	15.09
4WUU.PDB	OE1, A_GLU_63	OH, E_TYR_104	HH, E_TYR_104	2.59	1.76	7.82
4WUU.PDB	OE1, A_GLU_58	N, E_TYR_105	H, E_TYR_105	2.88	2.05	12.40
4WUU.PDB	OE1, A_GLU_55	OH, E_TYR_105	HH, E_TYR_105	2.47	1.79	29.86
4WUU.PDB	O, E_CYS_96	N, E_GLY_112	H, E_GLY_112	2.73	1.88	6.91
4WUU.PDB	O, E_SER_7	OG1, E_THR_115	HG1, E_THR_115	2.87	2.12	21.80
4WUU.PDB	O, E_ALA_92	N, E_VAL_117	H, E_VAL_117	2.94	2.09	9.12
4WUU.PDB	O, E_GLU_10	N, E_THR_118	H, E_THR_118	2.81	2.08	26.12
4WUU.PDB	OG1, E_THR_91	N, E_VAL_119	H, E_VAL_119	2.69	1.92	22.07
4WUU.PDB	O, E_SER_188	N, E_CYS_148	H, E_CYS_148	2.84	2.07	21.15
4WUU.PDB	O, E_PHE_130	N, E_LEU_149	H, E_LEU_149	2.81	2.09	28.03
4WUU.PDB	O, E_TYR_184	N, E_TYR_153	H, E_TYR_153	2.99	2.17	14.59
4WUU.PDB	OE1, E_GLU_156	OH, E_TYR_153	HH, E_TYR_153	2.97	2.18	16.08
4WUU.PDB	O, E_LYS_125	N, E_PHE_154	H, E_PHE_154	2.79	1.96	12.82
4WUU.PDB	O, E_TYR_153	N, E_TYR_184	H, E_TYR_184	2.70	1.85	7.96

Table 1699: 4WUU-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4Z0X.PDB	O, A.ASP_25	OH, A.TYR_2	HH, A.TYR_2	2.80	1.97	6.75
4Z0X.PDB	O, A.SER_23	N, A.THR_5	H, A.THR_5	2.85	2.02	14.04
4Z0X.PDB	OG1, A.THR_101	NE2, A.GLN_6	HE21, A.GLN_6	2.98	2.23	24.64
4Z0X.PDB	O, A.TYR_85	NE2, A.GLN_6	HE22, A.GLN_6	2.80	1.95	8.09
4Z0X.PDB	O, A.THR_104	N, A.VAL_12	H, A.VAL_12	2.52	1.67	7.35
4Z0X.PDB	OG1, A.THR_77	N, A.GLY_15	H, A.GLY_15	2.67	1.88	19.17
4Z0X.PDB	OE1, A.GLN_16	OG1, A.THR_17	HG1, A.THR_17	2.97	2.23	24.46
4Z0X.PDB	O, A.LEU_72	N, A.ILE_20	H, A.ILE_20	2.77	1.96	17.57
4Z0X.PDB	O, A.ALA_70	N, A.CYS_22	H, A.CYS_22	2.77	1.99	21.67
4Z0X.PDB	O, A.THR_5	N, A.SER_23	H, A.SER_23	2.81	2.00	16.58
4Z0X.PDB	O, A.ASN_68	N, A.GLY_24	H, A.GLY_24	2.89	2.08	17.57
4Z0X.PDB	O, A.LEU_27	N, A.LYS_30	H, A.LYS_30	2.84	2.00	9.85
4Z0X.PDB	OD1, A.ASP_50	N, A.VAL_32	H, A.VAL_32	2.87	2.04	13.49
4Z0X.PDB	O, A.LEU_47	N, A.TRP_34	H, A.TRP_34	2.79	1.98	15.57
4Z0X.PDB	O, A.TYR_86	N, A.TYR_35	H, A.TYR_35	2.82	2.01	16.09
4Z0X.PDB	OE1, A.GLN_88	OH, A.TYR_35	HH, A.TYR_35	2.99	2.19	16.02
4Z0X.PDB	O, A.VAL_44	N, A.GLN_36	H, A.GLN_36	2.60	1.77	13.39
4Z0X.PDB	O, A.ASP_84	N, A.GLN_37	H, A.GLN_37	2.88	2.08	17.37
4Z0X.PDB	OE1, B.GLN_64	NE2, A.GLN_37	HE22, A.GLN_37	2.75	1.99	23.41
4Z0X.PDB	O, A.GLN_36	N, A.VAL_44	H, A.VAL_44	2.70	1.89	16.44
4Z0X.PDB	O, A.TRP_34	N, A.VAL_46	H, A.VAL_46	2.99	2.14	7.42
4Z0X.PDB	O, A.LYS_52	N, A.TYR_48	H, A.TYR_48	2.81	1.99	14.31
4Z0X.PDB	O, A.VAL_32	N, A.ASP_50	H, A.ASP_50	2.74	1.91	13.42
4Z0X.PDB	O, A.GLN_49	N, A.SER_51	H, A.SER_51	2.75	2.01	26.59
4Z0X.PDB	O, A.TYR_48	N, A.LYS_52	H, A.LYS_52	2.96	2.19	22.52
4Z0X.PDB	O, A.PHE_61	NE, A.ARG_53	HE, A.ARG_53	2.38	1.60	20.12
4Z0X.PDB	OD2, A.ASP_81	NH1, A.ARG_60	HH12, A.ARG_60	2.72	1.91	16.22
4Z0X.PDB	O, A.THR_73	N, A.SER_62	H, A.SER_62	2.83	2.01	14.05
4Z0X.PDB	O, A.THR_69	N, A.SER_66	H, A.SER_66	2.92	2.06	6.16
4Z0X.PDB	O, A.SER_66	N, A.THR_69	H, A.THR_69	2.80	1.94	3.16
4Z0X.PDB	OD1, A.ASN_68	OG1, A.THR_69	HG1, A.THR_69	2.91	2.09	9.92
4Z0X.PDB	O, A.CYS_22	N, A.ALA_70	H, A.ALA_70	2.78	1.96	14.70
4Z0X.PDB	O, A.SER_64	N, A.THR_71	H, A.THR_71	2.92	2.10	14.49
4Z0X.PDB	O, A.ILE_20	N, A.LEU_72	H, A.LEU_72	2.78	1.96	14.72
4Z0X.PDB	O, A.SER_62	N, A.THR_73	H, A.THR_73	2.73	1.87	2.53
4Z0X.PDB	O, A.ALA_18	N, A.ILE_74	H, A.ILE_74	2.71	1.87	12.36
4Z0X.PDB	O, A.ARG_60	N, A.SER_75	H, A.SER_75	2.66	1.92	25.71
4Z0X.PDB	O, A.GLN_78	N, A.ASP_81	H, A.ASP_81	2.82	2.02	19.19
4Z0X.PDB	O, A.GLN_37	N, A.ASP_84	H, A.ASP_84	2.80	1.95	9.61
4Z0X.PDB	O, A.THR_101	N, A.TYR_85	H, A.TYR_85	2.95	2.11	9.72
4Z0X.PDB	O, A.ASP_81	OH, A.TYR_85	HH, A.TYR_85	2.69	1.90	17.09
4Z0X.PDB	O, B.GLY_129	NE2, A.GLN_88	HE22, A.GLN_88	2.63	1.87	22.97
4Z0X.PDB	O, B.GLY_129	NE1, A.TRP_90	HE1, A.TRP_90	2.96	2.14	15.73
4Z0X.PDB	O, A.ALA_94	N, A.ASP_91	H, A.ASP_91	2.88	2.04	11.61
4Z0X.PDB	OH, C.TYR_443	N, A.SER_93	H, A.SER_93	2.99	2.17	13.42
4Z0X.PDB	O, A.ALA_89	N, A.VAL_96	H, A.VAL_96	2.88	2.05	11.58
4Z0X.PDB	O, A.CYS_87	N, A.GLY_98	H, A.GLY_98	2.99	2.16	12.80
4Z0X.PDB	O, A.TYR_85	N, A.THR_101	H, A.THR_101	2.96	2.16	18.49
4Z0X.PDB	O, A.PRO_7	OG1, A.THR_101	HG1, A.THR_101	2.61	1.78	9.78
4Z0X.PDB	O, A.PRO_8	N, A.LYS_102	H, A.LYS_102	2.94	2.08	5.27
4Z0X.PDB	O, A.ALA_83	N, A.LEU_103	H, A.LEU_103	2.90	2.08	13.84
4Z0X.PDB	O, A.VAL_10	N, A.THR_104	H, A.THR_104	2.88	2.05	13.22
4Z0X.PDB	O, A.VAL_12	N, A.LEU_106	H, A.LEU_106	2.44	1.64	16.67
4Z0X.PDB	O, B.LEU_139	N, B.GLU_35	H, B.GLU_35	2.78	1.95	12.53
4Z0X.PDB	O, B.LEU_111	N, B.GLY_40	H, B.GLY_40	2.87	2.06	15.69
4Z0X.PDB	O, B.LYS_38	N, B.SER_41	H, B.SER_41	2.91	2.07	11.45
4Z0X.PDB	O, B.LYS_38	OG, B.SER_41	HG, B.SER_41	2.46	1.70	19.33

4Z0X.PDB	OE2, B_GLU_107	OG, B_SER_42	HG, B_SER_42	2.96	2.17	17.40
4Z0X.PDB	O, B_MET_106	N, B_VAL_45	H, B_VAL_45	2.73	1.90	11.31
4Z0X.PDB	OE1, B_GLN_31	N, B_SER_46	H, B_SER_46	2.95	2.11	10.80
4Z0X.PDB	OE1, B_GLN_31	OG, B_SER_46	HG, B_SER_46	2.75	1.93	11.18
4Z0X.PDB	O, B_ALA_104	N, B_CYS_47	H, B_CYS_47	2.48	1.72	23.24
4Z0X.PDB	O, B_PHE_76	N, B_ILE_59	H, B_ILE_59	2.75	1.91	10.64
4Z0X.PDB	O, B_ALA_122	N, B_THR_60	H, B_THR_60	2.78	2.00	20.86
4Z0X.PDB	O, B_GLY_74	N, B_TRP_61	H, B_TRP_61	2.88	2.03	5.31
4Z0X.PDB	O, B_TYR_120	N, B_VAL_62	H, B_VAL_62	2.96	2.12	9.50
4Z0X.PDB	OE2, B_GLU_71	NE, B_ARG_63	HE, B_ARG_63	2.78	1.94	9.25
4Z0X.PDB	OD1, B_ASP_115	NH1, B_ARG_63	HH12, B_ARG_63	3.00	2.15	8.77
4Z0X.PDB	O, B_VAL_118	N, B_GLN_64	H, B_GLN_64	2.70	1.91	18.82
4Z0X.PDB	O, B_TRP_61	N, B_MET_73	H, B_MET_73	2.89	2.05	11.27
4Z0X.PDB	O, B_MET_84	N, B_GLY_75	H, B_GLY_75	2.80	2.00	19.09
4Z0X.PDB	O, B_ILE_59	N, B_PHE_76	H, B_PHE_76	2.84	2.02	13.51
4Z0X.PDB	O, B_GLY_75	N, B_MET_84	H, B_MET_84	2.91	2.08	13.54
4Z0X.PDB	OE1, B_GLN_90	NE, B_ARG_92	HE, B_ARG_92	2.75	1.97	21.20
4Z0X.PDB	OD2, B_ASP_115	NH1, B_ARG_92	HH12, B_ARG_92	2.90	2.09	15.11
4Z0X.PDB	OD1, B_ASP_115	NH2, B_ARG_92	HH22, B_ARG_92	2.68	1.87	17.08
4Z0X.PDB	O, B_GLU_107	N, B_THR_94	H, B_THR_94	2.93	2.14	19.73
4Z0X.PDB	O, B_TYR_105	N, B_THR_96	H, B_THR_96	2.98	2.17	16.27
4Z0X.PDB	O, B_SER_100	OG, B_SER_102	HG, B_SER_102	2.77	1.99	18.26
4Z0X.PDB	O, B_THR_96	N, B_TYR_105	H, B_TYR_105	2.64	1.82	13.50
4Z0X.PDB	O, B_VAL_45	N, B_MET_106	H, B_MET_106	2.83	1.98	6.79
4Z0X.PDB	O, B_THR_94	N, B_GLU_107	H, B_GLU_107	2.90	2.05	7.24
4Z0X.PDB	O, B_VAL_43	N, B_LEU_108	H, B_LEU_108	2.96	2.14	15.47
4Z0X.PDB	O, B_ARG_92	N, B_THR_109	H, B_THR_109	2.97	2.14	11.99
4Z0X.PDB	O, B_SER_41	N, B_LEU_111	H, B_LEU_111	2.94	2.09	6.29
4Z0X.PDB	OD2, B_ASP_115	N, B_ARG_112	H, B_ARG_112	2.72	1.96	22.70
4Z0X.PDB	O, B_ARG_112	N, B_ASP_115	H, B_ASP_115	2.66	1.82	10.17
4Z0X.PDB	O, B_THR_138	N, B_TYR_119	H, B_TYR_119	2.87	2.02	7.83
4Z0X.PDB	O, B_ASP_115	OH, B_TYR_119	HH, B_TYR_119	2.68	1.89	16.10
4Z0X.PDB	O, B_VAL_62	N, B_TYR_120	H, B_TYR_120	2.59	1.74	8.64
4Z0X.PDB	OE1, B_GLN_64	OH, B_TYR_120	HH, B_TYR_120	2.91	2.08	8.45
4Z0X.PDB	O, B_THR_60	N, B_ALA_122	H, B_ALA_122	2.71	1.91	17.66
4Z0X.PDB	O, B_TYR_133	N, B_ARG_123	H, B_ARG_123	2.79	1.95	10.77
4Z0X.PDB	O, B_VAL_27	NE, B_ARG_123	HE, B_ARG_123	2.62	1.82	18.21
4Z0X.PDB	O, C_LEU_441	N, B_SER_127	H, B_SER_127	2.61	1.82	19.78
4Z0X.PDB	OH, A_TYR_35	N, B_TYR_131	H, B_TYR_131	2.85	2.09	23.16
4Z0X.PDB	O, B_SER_32	OG1, B_THR_138	HG1, B_THR_138	2.51	1.69	7.93
4Z0X.PDB	O, B_ALA_117	N, B_VAL_140	H, B_VAL_140	2.85	1.99	6.27
4Z0X.PDB	O, B_GLU_35	N, B_THR_141	H, B_THR_141	2.88	2.05	13.44
4Z0X.PDB	O, C_ALA_439	N, C_TYR_443	H, C_TYR_443	2.86	2.01	7.86

Table 1700: 4Z0X-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5I76.PDB	OG, A_SER.26	N, A_LEU.3	H, A_LEU.3	2.93	2.11	13.63
5I76.PDB	O, A_ARG.24	N, A_THR.5	H, A_THR.5	2.85	2.02	11.85
5I76.PDB	O, A_TYR.86	NE2, A_GLN.6	HE22, A_GLN.6	2.97	2.18	18.78
5I76.PDB	O, A_LYS.103	N, A_LEU.11	H, A_LEU.11	2.81	1.99	15.02
5I76.PDB	O, A_VAL.78	N, A_GLY.16	H, A_GLY.16	2.83	1.97	5.42
5I76.PDB	OD1, A_ASN.76	NH1, A_ARG.18	HH11, A_ARG.18	2.77	1.94	12.53
5I76.PDB	O, A_ILE.75	N, A_VAL.19	H, A_VAL.19	2.92	2.11	15.94
5I76.PDB	O, A_LEU.73	N, A_PHE.21	H, A_PHE.21	2.75	1.92	12.31
5I76.PDB	O, A_PHE.71	N, A_CYS.23	H, A_CYS.23	2.97	2.12	7.46
5I76.PDB	O, A_THR.5	N, A_ARG.24	H, A_ARG.24	2.95	2.13	14.78
5I76.PDB	O, A_THR.69	N, A_ALA.25	H, A_ALA.25	2.95	2.17	21.21
5I76.PDB	O, A_GLY.68	N, A_ILE.29	H, A_ILE.29	2.89	2.05	11.68
5I76.PDB	O, A_ILE.29	N, A_ASN.32	H, A_ASN.32	2.93	2.08	6.67
5I76.PDB	O, A_THR.31	N, A_ILE.33	H, A_ILE.33	2.92	2.20	28.68
5I76.PDB	O, A_GLN.89	N, A_HIS.34	H, A_HIS.34	2.81	1.99	14.63
5I76.PDB	O, A_ILE.48	N, A_TRP.35	H, A_TRP.35	2.92	2.10	13.82
5I76.PDB	O, A_TYR.87	N, A_TYR.36	H, A_TYR.36	2.81	2.01	17.84
5I76.PDB	OE1, A_GLN.89	OH, A_TYR.36	HH, A_TYR.36	2.60	1.77	6.74
5I76.PDB	O, A_ARG.45	N, A_GLN.37	H, A_GLN.37	2.91	2.08	14.58
5I76.PDB	OH, A_TYR.86	NE2, A_GLN.37	HE21, A_GLN.37	2.93	2.09	10.63
5I76.PDB	O, A_ASP.85	N, A_GLN.38	H, A_GLN.38	2.79	1.98	15.97
5I76.PDB	OE1, B_GLN.39	NE2, A_GLN.38	HE22, A_GLN.38	2.94	2.10	10.68
5I76.PDB	O, A_ARG.39	N, A_GLY.42	H, A_GLY.42	2.91	2.09	15.47
5I76.PDB	O, B_GLY.110	OG, A_SER.43	HG, A_SER.43	2.73	2.02	27.09
5I76.PDB	O, A_TRP.35	N, A_LEU.47	H, A_LEU.47	2.79	1.93	2.43
5I76.PDB	OE1, A_GLU.53	NZ, A_LYS.49	HZ2, A_LYS.49	2.94	2.09	13.35
5I76.PDB	OD2, B_ASP.103	OH, A_TYR.50	HH, A_TYR.50	2.64	1.88	21.01
5I76.PDB	O, A_ILE.33	N, A_ALA.51	H, A_ALA.51	2.67	1.85	13.57
5I76.PDB	O, A_TYR.50	N, A_SER.52	H, A_SER.52	2.77	2.05	27.32
5I76.PDB	O, A_LYS.49	N, A_GLU.53	H, A_GLU.53	2.80	2.00	17.59
5I76.PDB	OD1, A_ASP.82	NH2, A_ARG.61	HH21, A_ARG.61	2.77	1.93	10.41
5I76.PDB	OE2, A_GLU.81	NH2, A_ARG.61	HH22, A_ARG.61	2.77	1.92	8.54
5I76.PDB	O, A_SER.74	N, A_SER.63	H, A_SER.63	2.94	2.14	18.34
5I76.PDB	O, A_THR.72	N, A_SER.65	H, A_SER.65	2.92	2.10	15.80
5I76.PDB	O, A_GLY.30	N, A_GLY.68	H, A_GLY.68	2.79	2.04	24.26
5I76.PDB	O, A_SER.65	N, A_THR.72	H, A_THR.72	2.94	2.12	13.74
5I76.PDB	O, A_PHE.21	N, A_LEU.73	H, A_LEU.73	3.00	2.22	21.96
5I76.PDB	O, A_SER.63	N, A_SER.74	H, A_SER.74	2.85	1.99	4.51
5I76.PDB	O, A_VAL.19	N, A_ILE.75	H, A_ILE.75	2.85	2.03	15.69
5I76.PDB	O, A_ARG.61	N, A_ASN.76	H, A_ASN.76	2.79	1.97	14.79
5I76.PDB	O, A_GLU.17	N, A_VAL.78	H, A_VAL.78	2.96	2.12	10.44
5I76.PDB	OD2, A_ASP.82	N, A_GLU.79	H, A_GLU.79	2.95	2.11	11.60
5I76.PDB	O, A_GLU.79	N, A_ASP.82	H, A_ASP.82	2.78	1.95	11.07
5I76.PDB	O, A_GLN.38	N, A_ASP.85	H, A_ASP.85	2.93	2.13	17.77
5I76.PDB	O, A_THR.102	N, A_TYR.86	H, A_TYR.86	2.91	2.14	23.37
5I76.PDB	O, A_ASP.82	OH, A_TYR.86	HH, A_TYR.86	2.55	1.72	9.51
5I76.PDB	O, A_TYR.36	N, A_TYR.87	H, A_TYR.87	2.89	2.08	16.03
5I76.PDB	OG1, A_THR.96	NE2, A_GLN.89	HE21, A_GLN.89	2.89	2.08	16.62
5I76.PDB	O, A_THR.97	N, A_GLN.90	H, A_GLN.90	2.93	2.15	21.05
5I76.PDB	OD1, A_ASN.93	ND2, A_ASN.92	HD22, A_ASN.92	2.89	2.06	14.53
5I76.PDB	O, A_GLN.90	OG1, A_THR.96	HG1, A_THR.96	2.66	1.94	25.05
5I76.PDB	O, A_ILE.2	OG1, A_THR.97	HG1, A_THR.97	2.88	2.08	14.12
5I76.PDB	O, A_CYS.88	N, A_GLY.99	H, A_GLY.99	2.80	1.99	16.49
5I76.PDB	OE1, A_GLN.6	N, A_GLY.101	H, A_GLY.101	2.95	2.25	29.58
5I76.PDB	O, A_TYR.86	N, A_THR.102	H, A_THR.102	2.91	2.11	17.28
5I76.PDB	O, A_PRO.8	OG1, A_THR.102	HG1, A_THR.102	2.77	2.04	24.64
5I76.PDB	O, A_VAL.9	N, A_LYS.103	H, A_LYS.103	2.97	2.12	8.09

5I76.PDB	O, A_ALA_84	N, A_LEU_104	H, A_LEU_104	2.94	2.08	1.76
5I76.PDB	O, A_LEU_11	N, A_GLU_105	H, A_GLU_105	2.78	1.93	6.87
5I76.PDB	O, A_VAL_13	N, A_LYS_107	H, A_LYS_107	2.80	1.97	11.70
5I76.PDB	OG, A_SER_12	NZ, A_LYS_107	HZ3, A_LYS_107	2.75	1.89	12.15
5I76.PDB	O, A_TYR_140	N, A_ALA_111	H, A_ALA_111	2.82	2.00	15.73
5I76.PDB	O, A_LEU_135	N, A_PHE_116	H, A_PHE_116	2.95	2.18	23.57
5I76.PDB	O, A_VAL_133	N, A_PHE_118	H, A_PHE_118	2.81	2.04	21.46
5I76.PDB	OG, A_SER_131	NE2, A_GLN_124	HE22, A_GLN_124	2.78	1.92	5.16
5I76.PDB	O, A_GLN_124	N, A_SER_127	H, A_SER_127	2.80	1.97	11.43
5I76.PDB	O, A_GLN_124	OG, A_SER_127	HG, A_SER_127	2.76	1.92	5.99
5I76.PDB	O, A_LEU_181	N, A_ALA_130	H, A_ALA_130	2.88	2.06	14.29
5I76.PDB	OE1, A_GLN_124	N, A_SER_131	H, A_SER_131	2.93	2.12	16.06
5I76.PDB	O, A_LEU_179	N, A_VAL_132	H, A_VAL_132	2.86	2.02	10.93
5I76.PDB	O, A_SER_177	N, A_CYS_134	H, A_CYS_134	2.84	1.99	8.38
5I76.PDB	O, A_PHE_116	N, A_LEU_135	H, A_LEU_135	2.80	1.96	8.13
5I76.PDB	O, A_LEU_175	N, A_LEU_136	H, A_LEU_136	2.86	2.01	4.38
5I76.PDB	O, A_SER_114	N, A_ASN_137	H, A_ASN_137	2.78	1.96	14.88
5I76.PDB	OG, A_SER_174	N, A_ASN_138	H, A_ASN_138	2.99	2.15	10.62
5I76.PDB	O, A_TYR_173	N, A_PHE_139	H, A_PHE_139	2.85	2.03	14.64
5I76.PDB	O, A_ALA_111	N, A_TYR_140	H, A_TYR_140	2.84	2.04	18.07
5I76.PDB	OE2, A_GLU_143	NZ, A_LYS_145	HZ3, A_LYS_145	2.87	2.06	20.39
5I76.PDB	O, A_GLU_195	N, A_GLN_147	H, A_GLN_147	2.83	2.01	15.29
5I76.PDB	OG, A_SER_177	NE1, A_TRP_148	HE1, A_TRP_148	2.97	2.15	13.90
5I76.PDB	O, A_ALA_193	N, A_LYS_149	H, A_LYS_149	2.89	2.04	9.43
5I76.PDB	O, A_VAL_191	N, A_ASP_151	H, A_ASP_151	2.77	1.94	12.86
5I76.PDB	O, A_TRP_148	N, A_GLN_155	H, A_GLN_155	2.81	1.97	9.99
5I76.PDB	O, A_ALA_153	NE2, A_GLN_155	HE21, A_GLN_155	2.93	2.08	7.12
5I76.PDB	O, A_THR_178	N, A_GLN_160	H, A_GLN_160	2.97	2.20	22.65
5I76.PDB	O, A_SER_176	N, A_SER_162	H, A_SER_162	2.82	2.02	18.15
5I76.PDB	O, B_PRO_173	OG, A_SER_162	HG, A_SER_162	2.48	1.79	28.75
5I76.PDB	O, A_SER_174	N, A_THR_164	H, A_THR_164	2.85	2.02	12.10
5I76.PDB	O, A_SER_171	NE2, A_GLN_166	HE21, A_GLN_166	2.90	2.05	6.30
5I76.PDB	O, A_LEU_106	NE2, A_GLN_166	HE22, A_GLN_166	2.72	1.91	17.00
5I76.PDB	O, A_THR_172	N, A_ASP_167	H, A_ASP_167	2.78	1.95	11.68
5I76.PDB	OD1, A_ASP_167	N, A_LYS_169	H, A_LYS_169	2.67	1.87	18.00
5I76.PDB	O, A_ASP_167	N, A_SER_171	H, A_SER_171	2.85	2.10	24.64
5I76.PDB	OD1, A_ASP_170	OG1, A_THR_172	HG1, A_THR_172	2.65	1.83	9.24
5I76.PDB	O, A_PHE_139	N, A_TYR_173	H, A_TYR_173	2.85	2.00	5.15
5I76.PDB	OE2, A_GLU_105	OH, A_TYR_173	HH, A_TYR_173	2.42	1.66	21.73
5I76.PDB	OG1, A_THR_164	N, A_SER_174	H, A_SER_174	2.83	2.01	15.67
5I76.PDB	O, A_LEU_136	N, A_LEU_175	H, A_LEU_175	2.85	2.05	17.34
5I76.PDB	O, A_SER_162	N, A_SER_176	H, A_SER_176	2.84	2.01	11.93
5I76.PDB	O, A_CYS_134	N, A_SER_177	H, A_SER_177	2.92	2.08	10.24
5I76.PDB	O, A_GLN_160	N, A_THR_178	H, A_THR_178	2.84	2.01	11.67
5I76.PDB	O, A_VAL_132	N, A_LEU_179	H, A_LEU_179	2.88	2.05	12.69
5I76.PDB	O, A_ALA_130	N, A_LEU_181	H, A_LEU_181	2.89	2.05	10.41
5I76.PDB	O, A_GLY_128	N, A_LYS_183	H, A_LYS_183	2.99	2.14	6.01
5I76.PDB	OG, A_SER_182	N, A_ASP_185	H, A_ASP_185	2.96	2.11	8.88
5I76.PDB	O, A_SER_182	N, A_TYR_186	H, A_TYR_186	2.77	1.92	7.00
5I76.PDB	O, A_LYS_183	N, A_GLU_187	H, A_GLU_187	2.88	2.08	18.36
5I76.PDB	O, A_ASP_185	N, A_LYS_188	H, A_LYS_188	2.97	2.19	21.73
5I76.PDB	OD1, A_ASP_151	N, A_VAL_191	H, A_VAL_191	2.98	2.13	9.38
5I76.PDB	O, A_PHE_209	N, A_TYR_192	H, A_TYR_192	2.92	2.08	9.60
5I76.PDB	O, A_LYS_149	N, A_ALA_193	H, A_ALA_193	2.91	2.19	28.01
5I76.PDB	O, A_LYS_207	N, A_CYS_194	H, A_CYS_194	2.85	2.00	8.12
5I76.PDB	O, A_GLN_147	N, A_GLU_195	H, A_GLU_195	2.84	1.99	7.10
5I76.PDB	O, A_VAL_205	N, A_VAL_196	H, A_VAL_196	2.79	2.00	20.45
5I76.PDB	O, A_LYS_145	N, A_THR_197	H, A_THR_197	2.98	2.16	15.25

5I76.PDB	O, A_PRO.141	NE2, A_HIS.198	HE2, A_HIS.198	2.94	2.11	12.28
5I76.PDB	ND1, A_HIS.198	N, A_GLY.200	H, A_GLY.200	2.85	1.99	1.58
5I76.PDB	O, A_HIS.198	N, A_LEU.201	H, A_LEU.201	2.86	2.01	7.02
5I76.PDB	O, A_CYS.194	N, A_LYS.207	H, A_LYS.207	2.92	2.10	16.09
5I76.PDB	O, A_TYR.192	N, A_PHE.209	H, A_PHE.209	2.90	2.13	22.49
5I76.PDB	O, A_LYS.190	N, A_ARG.211	H, A_ARG.211	2.76	1.93	12.12
5I76.PDB	O, A_HIS.189	NE, A_ARG.211	HE, A_ARG.211	2.68	1.86	13.91
5I76.PDB	O, B_SER.25	N, B_GLN.3	H, B_GLN.3	2.91	2.09	13.09
5I76.PDB	O, B_THR.23	N, B_LYS.5	H, B_LYS.5	2.90	2.14	23.54
5I76.PDB	OE1, B_GLN.111	N, B_GLN.6	H, B_GLN.6	2.83	2.01	14.84
5I76.PDB	O, B_TYR.93	NE2, B_GLN.6	HE22, B_GLN.6	2.84	1.99	7.48
5I76.PDB	O, B_THR.21	N, B_SER.7	H, B_SER.7	2.98	2.22	22.91
5I76.PDB	O, B_THR.116	N, B_VAL.12	H, B_VAL.12	2.86	2.03	11.02
5I76.PDB	O, B_LEU.85	N, B_SER.15	H, B_SER.15	2.72	1.87	6.27
5I76.PDB	O, B_PRO.14	OG, B_SER.15	HG, B_SER.15	2.58	1.82	21.55
5I76.PDB	O, B_GLN.13	N, B_GLN.16	H, B_GLN.16	2.98	2.13	9.97
5I76.PDB	O, B_MET.82	N, B_LEU.18	H, B_LEU.18	2.89	2.08	17.80
5I76.PDB	O, B_PHE.80	N, B_ILE.20	H, B_ILE.20	2.83	2.01	14.78
5I76.PDB	OG, B_SER.7	N, B_THR.21	H, B_THR.21	2.99	2.15	11.92
5I76.PDB	O, B_VAL.78	N, B_CYS.22	H, B_CYS.22	2.85	2.00	8.90
5I76.PDB	O, B_LYS.5	N, B_THR.23	H, B_THR.23	2.85	2.00	7.48
5I76.PDB	O, B_SER.76	N, B_VAL.24	H, B_VAL.24	2.97	2.13	10.77
5I76.PDB	O, B_GLN.3	N, B_SER.25	H, B_SER.25	2.89	2.10	18.84
5I76.PDB	O, B_SER.28	N, B_ASN.31	H, B_ASN.31	2.98	2.14	8.72
5I76.PDB	O, B_ILE.51	N, B_VAL.34	H, B_VAL.34	2.93	2.14	19.88
5I76.PDB	O, B_ALA.96	N, B_HIS.35	H, B_HIS.35	2.88	2.03	7.93
5I76.PDB	O, B_GLY.49	N, B_TRP.36	H, B_TRP.36	2.91	2.12	19.85
5I76.PDB	O, B_TYR.94	N, B_VAL.37	H, B_VAL.37	2.91	2.08	14.52
5I76.PDB	O, B_GLU.46	N, B_ARG.38	H, B_ARG.38	2.84	2.03	16.24
5I76.PDB	OD1, B_ASP.89	NH1, B_ARG.38	HH12, B_ARG.38	2.81	1.96	5.27
5I76.PDB	O, B_ILE.92	N, B_GLN.39	H, B_GLN.39	2.86	2.11	24.85
5I76.PDB	OE1, A_GLN.38	NE2, B_GLN.39	HE22, B_GLN.39	2.80	1.95	6.66
5I76.PDB	O, B_ARG.38	N, B_GLU.46	H, B_GLU.46	2.80	2.03	22.07
5I76.PDB	O, B_TRP.36	N, B_LEU.48	H, B_LEU.48	2.83	1.97	5.22
5I76.PDB	O, B_ASP.58	N, B_VAL.50	H, B_VAL.50	2.90	2.16	26.66
5I76.PDB	O, B_VAL.34	N, B_ILE.51	H, B_ILE.51	2.98	2.17	16.74
5I76.PDB	O, B_ASN.56	N, B_TRP.52	H, B_TRP.52	2.85	1.99	5.55
5I76.PDB	OD2, B_ASP.58	NE1, B_TRP.52	HE1, B_TRP.52	2.79	1.94	5.91
5I76.PDB	O, B_TRP.52	N, B_GLY.55	H, B_GLY.55	2.86	2.04	14.33
5I76.PDB	O, B_LEU.48	N, B_ASN.60	H, B_ASN.60	2.81	1.96	6.22
5I76.PDB	O, B_TRP.47	ND2, B_ASN.60	HD22, B_ASN.60	2.78	1.99	18.30
5I76.PDB	O, B_ASN.60	N, B_PHE.63	H, B_PHE.63	2.84	1.99	7.17
5I76.PDB	OD2, B_ASP.89	NH1, B_ARG.66	HH12, B_ARG.66	2.96	2.17	19.36
5I76.PDB	OD1, B_ASP.89	NH2, B_ARG.66	HH22, B_ARG.66	2.84	1.99	7.50
5I76.PDB	O, B_LYS.81	N, B_SER.68	H, B_SER.68	2.86	2.02	9.98
5I76.PDB	OH, B_TYR.59	N, B_ILE.69	H, B_ILE.69	3.00	2.17	14.31
5I76.PDB	O, B_SER.53	NZ, B_LYS.71	HZ1, B_LYS.71	2.77	1.91	12.10
5I76.PDB	O, B_GLN.77	N, B_ASP.72	H, B_ASP.72	2.80	1.95	9.05
5I76.PDB	OD1, B_ASP.72	OG, B_SER.74	HG, B_SER.74	2.49	1.80	29.35
5I76.PDB	O, B_CYS.22	N, B_VAL.78	H, B_VAL.78	2.83	1.99	12.58
5I76.PDB	O, B_ASN.70	N, B_PHE.79	H, B_PHE.79	2.80	1.94	1.15
5I76.PDB	O, B_ILE.20	N, B_PHE.80	H, B_PHE.80	2.88	2.02	3.13
5I76.PDB	O, B_SER.68	N, B_LYS.81	H, B_LYS.81	2.91	2.14	22.98
5I76.PDB	O, B_LEU.18	N, B_MET.82	H, B_MET.82	2.97	2.19	21.42
5I76.PDB	O, B_ARG.66	N, B_ASN.83	H, B_ASN.83	2.85	2.05	18.95
5I76.PDB	OD2, B_ASP.89	N, B_GLN.86	H, B_GLN.86	2.84	2.01	11.92
5I76.PDB	O, B_GLN.86	N, B_ASP.89	H, B_ASP.89	2.79	1.94	8.58
5I76.PDB	O, B_SER.87	N, B_THR.90	H, B_THR.90	2.93	2.07	2.10

5I76.PDB	O, B_GLN_39	N, B_ILE_92	H, B_ILE_92	2.94	2.12	13.61
5I76.PDB	O, B_THR_113	N, B_TYR_93	H, B_TYR_93	2.91	2.07	10.02
5I76.PDB	O, B_ASP_89	OH, B_TYR_93	HH, B_TYR_93	2.75	1.94	12.69
5I76.PDB	O, B_VAL_37	N, B_TYR_94	H, B_TYR_94	2.72	1.88	9.49
5I76.PDB	O, B_TYR_108	N, B_ARG_97	H, B_ARG_97	2.86	2.06	17.77
5I76.PDB	O, B_ALA_98	NH1, B_ARG_97	HH11, B_ARG_97	2.98	2.16	15.13
5I76.PDB	OD1, B_ASP_103	N, B_TYR_104	H, B_TYR_104	2.65	1.89	23.73
5I76.PDB	O, B_PHE_106	NE1, B_TRP_109	HE1, B_TRP_109	2.83	2.11	27.98
5I76.PDB	O, B_CYS_95	N, B_GLY_110	H, B_GLY_110	2.95	2.10	8.84
5I76.PDB	O, B_GLN_6	NE2, B_GLN_111	HE22, B_GLN_111	2.97	2.18	20.05
5I76.PDB	O, B_TYR_93	N, B_THR_113	H, B_THR_113	2.81	2.08	26.53
5I76.PDB	O, B_ALA_91	N, B_VAL_115	H, B_VAL_115	2.97	2.13	9.34
5I76.PDB	OG1, B_THR_90	N, B_VAL_117	H, B_VAL_117	2.78	1.93	4.58
5I76.PDB	O, B_PHE_152	N, B_LYS_123	H, B_LYS_123	2.83	1.99	11.39
5I76.PDB	O, B_ASP_150	NZ, B_LYS_123	HZ2, B_LYS_123	2.87	2.07	21.60
5I76.PDB	O, B_LYS_149	N, B_SER_126	H, B_SER_126	2.91	2.10	15.91
5I76.PDB	O, B_LEU_147	N, B_PHE_128	H, B_PHE_128	2.88	2.05	13.67
5I76.PDB	O, B_GLY_145	N, B_LEU_130	H, B_LEU_130	2.86	2.03	13.19
5I76.PDB	O, B_SER_134	OG1, B_THR_137	HG1, B_THR_137	2.81	2.01	14.63
5I76.PDB	O, B_VAL_190	N, B_ALA_142	H, B_ALA_142	2.82	1.97	8.01
5I76.PDB	O, B_LEU_130	N, B_GLY_145	H, B_GLY_145	2.93	2.14	20.40
5I76.PDB	O, B_SER_186	N, B_CYS_146	H, B_CYS_146	2.85	2.05	18.23
5I76.PDB	O, B_PHE_128	N, B_LEU_147	H, B_LEU_147	2.85	2.03	14.76
5I76.PDB	O, B_LEU_184	N, B_VAL_148	H, B_VAL_148	2.78	1.93	4.33
5I76.PDB	O, B_SER_126	N, B_LYS_149	H, B_LYS_149	2.80	1.95	7.51
5I76.PDB	O, B_LYS_123	N, B_PHE_152	H, B_PHE_152	2.84	2.02	15.64
5I76.PDB	O, B_ASN_205	N, B_THR_157	H, B_THR_157	2.93	2.11	15.41
5I76.PDB	O, B_ASN_203	N, B_SER_159	H, B_SER_159	2.90	2.10	17.76
5I76.PDB	OD1, B_ASN_203	OG, B_SER_159	HG, B_SER_159	2.82	2.04	17.93
5I76.PDB	OG, B_SER_186	NE1, B_TRP_160	HE1, B_TRP_160	2.99	2.15	11.06
5I76.PDB	O, B_ILE_201	N, B_ASN_161	H, B_ASN_161	2.78	1.93	9.08
5I76.PDB	OD1, B_ASN_203	N, B_SER_162	H, B_SER_162	2.79	2.01	21.54
5I76.PDB	O, B_TRP_160	N, B_GLY_163	H, B_GLY_163	2.88	2.13	24.26
5I76.PDB	O, B_ASN_161	N, B_ALA_164	H, B_ALA_164	2.99	2.14	8.06
5I76.PDB	O, B_VAL_187	N, B_HIS_170	H, B_HIS_170	2.79	1.96	12.00
5I76.PDB	O, B_SER_185	N, B_PHE_172	H, B_PHE_172	2.91	2.06	5.99
5I76.PDB	O, B_SER_183	N, B_VAL_175	H, B_VAL_175	2.87	2.03	11.83
5I76.PDB	O, B_LEU_181	N, B_GLN_177	H, B_GLN_177	2.84	2.00	8.84
5I76.PDB	OD1, B_ASP_150	NE2, B_GLN_177	HE22, B_GLN_177	2.79	2.00	19.18
5I76.PDB	O, B_GLN_177	N, B_GLY_180	H, B_GLY_180	2.82	1.98	9.91
5I76.PDB	O, B_TYR_151	N, B_TYR_182	H, B_TYR_182	2.72	1.88	9.69
5I76.PDB	O, B_VAL_148	N, B_LEU_184	H, B_LEU_184	2.84	2.03	15.91
5I76.PDB	OG, A_SER_176	OG, B_SER_185	HG, B_SER_185	2.89	2.15	23.05
5I76.PDB	O, B_CYS_146	N, B_SER_186	H, B_SER_186	2.93	2.10	13.63
5I76.PDB	O, B_HIS_170	N, B_VAL_187	H, B_VAL_187	2.94	2.11	13.31
5I76.PDB	O, B_LEU_144	N, B_VAL_188	H, B_VAL_188	2.83	2.02	16.59
5I76.PDB	O, B_ALA_142	N, B_VAL_190	H, B_VAL_190	2.85	2.05	17.07
5I76.PDB	O, B_GLY_140	N, B_SER_192	H, B_SER_192	2.92	2.09	13.75
5I76.PDB	O, B_PRO_191	OG, B_SER_194	HG, B_SER_194	2.91	2.11	15.99
5I76.PDB	O, B_SER_194	N, B_GLN_198	H, B_GLN_198	2.93	2.07	2.43
5I76.PDB	OG, B_SER_194	OH, B_TYR_200	HH, B_TYR_200	2.81	2.03	18.26
5I76.PDB	OD1, B_ASN_161	N, B_ILE_201	H, B_ILE_201	2.82	2.02	18.20
5I76.PDB	O, B_LYS_215	N, B_CYS_202	H, B_CYS_202	2.96	2.17	19.90
5I76.PDB	O, B_SER_159	N, B_ASN_203	H, B_ASN_203	2.80	1.94	5.79
5I76.PDB	OD1, B_ASP_214	ND2, B_ASN_203	HD22, B_ASN_203	2.90	2.11	19.71
5I76.PDB	O, B_VAL_213	N, B_VAL_204	H, B_VAL_204	2.78	1.92	4.35
5I76.PDB	O, B_THR_157	N, B_ASN_205	H, B_ASN_205	2.91	2.08	13.35
5I76.PDB	O, B_THR_211	N, B_HIS_206	H, B_HIS_206	2.85	2.00	6.66

5I76.PDB	O, B.LYS_207	N, B.ASN_210	H, B.ASN_210	2.96	2.11	7.92
5I76.PDB	O, B.VAL_204	N, B.VAL_213	H, B.VAL_213	2.87	2.05	15.17
5I76.PDB	O, B.CYS_202	N, B.LYS_215	H, B.LYS_215	2.91	2.13	20.69
5I76.PDB	OE1, A.GLU_123	NZ, B.LYS_215	HZ1, B.LYS_215	2.73	1.96	24.68
5I76.PDB	OE2, A.GLU_123	NZ, B.LYS_215	HZ1, B.LYS_215	2.89	2.11	24.69
5I76.PDB	OE1, B.GLU_218	NE, B.ARG_216	HE, B.ARG_216	2.64	1.90	25.25
5I76.PDB	OE1, B.GLU_218	NH2, B.ARG_216	HH21, B.ARG_216	2.69	1.98	29.12
5I76.PDB	O, B.TYR_200	N, B.VAL_217	H, B.VAL_217	2.83	1.99	10.82
5I76.PDB	O, C.ARG_24	N, C.THR_5	H, C.THR_5	2.87	2.03	8.25
5I76.PDB	O, C.TYR_86	NE2, C.GLN_6	HE22, C.GLN_6	2.86	2.05	16.89
5I76.PDB	O, C.LYS_103	N, C.LEU_11	H, C.LEU_11	2.75	1.91	12.00
5I76.PDB	O, C.GLU_105	N, C.VAL_13	H, C.VAL_13	2.98	2.20	22.09
5I76.PDB	OE1, C.GLU_17	N, C.SER_14	H, C.SER_14	3.00	2.15	7.87
5I76.PDB	O, C.VAL_78	N, C.GLY_16	H, C.GLY_16	2.98	2.12	1.61
5I76.PDB	O, C.ILE_75	N, C.VAL_19	H, C.VAL_19	2.86	2.02	11.04
5I76.PDB	O, C.LEU_73	N, C.PHE_21	H, C.PHE_21	2.77	1.93	10.26
5I76.PDB	O, C.PHE_71	N, C.CYS_23	H, C.CYS_23	2.95	2.11	10.08
5I76.PDB	O, C.THR_5	N, C.ARG_24	H, C.ARG_24	2.99	2.18	17.88
5I76.PDB	OD2, A.ASP_70	NH1, C.ARG_24	HH12, C.ARG_24	2.95	2.23	28.81
5I76.PDB	O, C.THR_69	N, C.ALA_25	H, C.ALA_25	2.74	1.96	20.09
5I76.PDB	O, C.GLY_68	N, C.ILE_29	H, C.ILE_29	2.91	2.08	12.56
5I76.PDB	O, C.ILE_29	N, C.ASN_32	H, C.ASN_32	2.96	2.11	6.37
5I76.PDB	O, C.THR_31	N, C.ILE_33	H, C.ILE_33	2.97	2.26	29.60
5I76.PDB	O, C.GLN_89	N, C.HIS_34	H, C.HIS_34	2.87	2.06	16.27
5I76.PDB	O, C.ILE_48	N, C.TRP_35	H, C.TRP_35	2.95	2.13	14.67
5I76.PDB	O, C.TYR_87	N, C.TYR_36	H, C.TYR_36	2.85	2.04	16.51
5I76.PDB	OE1, C.GLN_89	OH, C.TYR_36	HH, C.TYR_36	2.73	1.90	7.00
5I76.PDB	O, C.ARG_45	N, C.GLN_37	H, C.GLN_37	2.82	2.01	17.23
5I76.PDB	OH, C.TYR_86	NE2, C.GLN_37	HE21, C.GLN_37	2.93	2.09	9.49
5I76.PDB	O, C.ASP_85	N, C.GLN_38	H, C.GLN_38	2.82	1.99	13.89
5I76.PDB	O, C.GLY_42	NE2, C.GLN_38	HE21, C.GLN_38	3.00	2.24	24.26
5I76.PDB	O, C.ARG_39	N, C.GLY_42	H, C.GLY_42	2.88	2.09	19.43
5I76.PDB	O, D.GLY_110	OG, C.SER_43	HG, C.SER_43	2.84	2.15	29.22
5I76.PDB	O, C.GLN_37	N, C.ARG_45	H, C.ARG_45	2.65	1.95	29.24
5I76.PDB	OE1, C.GLN_37	NH1, C.ARG_45	HH11, C.ARG_45	2.96	2.15	17.42
5I76.PDB	O, C.TRP_35	N, C.LEU_47	H, C.LEU_47	2.79	1.93	2.36
5I76.PDB	O, C.GLU_53	N, C.LYS_49	H, C.LYS_49	2.99	2.18	15.56
5I76.PDB	OE1, C.GLU_53	NZ, C.LYS_49	HZ2, C.LYS_49	2.64	1.79	13.55
5I76.PDB	OD2, D.ASP_103	OH, C.TYR_50	HH, C.TYR_50	2.76	1.95	12.40
5I76.PDB	O, C.ILE_33	N, C.ALA_51	H, C.ALA_51	2.70	1.88	13.82
5I76.PDB	O, C.TYR_50	N, C.SER_52	H, C.SER_52	2.78	2.06	27.37
5I76.PDB	O, C.LYS_49	N, C.GLU_53	H, C.GLU_53	2.82	2.02	19.04
5I76.PDB	OD1, C.ASP_82	NH2, C.ARG_61	HH21, C.ARG_61	2.76	1.93	11.41
5I76.PDB	OE2, C.GLU_81	NH2, C.ARG_61	HH22, C.ARG_61	2.83	2.01	16.02
5I76.PDB	O, C.SER_74	N, C.SER_63	H, C.SER_63	2.93	2.13	17.96
5I76.PDB	O, C.THR_72	N, C.SER_65	H, C.SER_65	2.91	2.11	19.14
5I76.PDB	O, C.GLY_30	N, C.GLY_68	H, C.GLY_68	2.72	1.97	23.76
5I76.PDB	O, C.CYS_23	N, C.PHE_71	H, C.PHE_71	2.89	2.16	27.04
5I76.PDB	O, C.SER_65	N, C.THR_72	H, C.THR_72	2.94	2.10	11.42
5I76.PDB	O, C.PHE_21	N, C.LEU_73	H, C.LEU_73	2.99	2.22	23.12
5I76.PDB	O, C.SER_63	N, C.SER_74	H, C.SER_74	2.84	1.98	5.34
5I76.PDB	O, C.VAL_19	N, C.ILE_75	H, C.ILE_75	2.92	2.11	17.51
5I76.PDB	O, C.ARG_61	N, C.ASN_76	H, C.ASN_76	2.86	2.03	12.61
5I76.PDB	O, C.GLU_17	N, C.VAL_78	H, C.VAL_78	2.96	2.15	17.03
5I76.PDB	OD2, C.ASP_82	N, C.GLU_79	H, C.GLU_79	2.90	2.06	11.12
5I76.PDB	OG, C.SER_171	OG, C.SER_80	HG, C.SER_80	2.59	1.79	14.57
5I76.PDB	O, C.GLU_79	N, C.ASP_82	H, C.ASP_82	2.91	2.09	15.61
5I76.PDB	O, C.GLN_38	N, C.ASP_85	H, C.ASP_85	2.95	2.16	19.54

5I76.PDB	O, C.THR.102	N, C.TYR.86	H, C.TYR.86	2.85	2.08	22.66
5I76.PDB	O, C.ASP.82	OH, C.TYR.86	HH, C.TYR.86	2.60	1.79	11.86
5I76.PDB	O, C.TYR.36	N, C.TYR.87	H, C.TYR.87	2.91	2.10	16.52
5I76.PDB	OG1, C.THR.96	NE2, C.GLN.89	HE21, C.GLN.89	2.74	1.92	15.47
5I76.PDB	O, C.THR.97	N, C.GLN.90	H, C.GLN.90	2.85	2.07	20.66
5I76.PDB	O, C.ASN.93	NE2, C.GLN.90	HE22, C.GLN.90	2.93	2.08	7.37
5I76.PDB	OD1, C.ASN.93	ND2, C.ASN.92	HD22, C.ASN.92	2.84	2.03	16.29
5I76.PDB	O, C.GLN.90	OG1, C.THR.96	HG1, C.THR.96	2.71	1.98	25.42
5I76.PDB	O, C.ILE.2	OG1, C.THR.97	HG1, C.THR.97	2.79	1.98	12.72
5I76.PDB	O, C.CYS.88	N, C.GLY.99	H, C.GLY.99	2.86	2.07	19.65
5I76.PDB	O, C.TYR.86	N, C.THR.102	H, C.THR.102	2.98	2.17	16.60
5I76.PDB	O, C.PRO.8	OG1, C.THR.102	HG1, C.THR.102	2.70	1.91	16.81
5I76.PDB	O, C.VAL.9	N, C.LYS.103	H, C.LYS.103	2.92	2.08	9.07
5I76.PDB	O, C.ALA.84	N, C.LEU.104	H, C.LEU.104	3.00	2.14	2.26
5I76.PDB	O, C.LEU.11	N, C.GLU.105	H, C.GLU.105	2.83	1.99	8.86
5I76.PDB	O, C.VAL.13	N, C.LYS.107	H, C.LYS.107	2.70	1.85	8.61
5I76.PDB	O, C.THR.109	NE, C.ARG.108	HE, C.ARG.108	2.76	1.94	14.16
5I76.PDB	O, C.ASP.170	NH1, C.ARG.108	HH11, C.ARG.108	2.86	2.03	13.35
5I76.PDB	O, C.TYR.140	N, C.ALA.111	H, C.ALA.111	2.87	2.03	11.62
5I76.PDB	O, C.LEU.135	N, C.PHE.116	H, C.PHE.116	2.94	2.17	22.55
5I76.PDB	O, C.VAL.133	N, C.PHE.118	H, C.PHE.118	2.80	1.99	16.08
5I76.PDB	OG, C.SER.131	NE2, C.GLN.124	HE22, C.GLN.124	2.87	2.02	5.94
5I76.PDB	O, C.ASP.122	N, C.LYS.126	H, C.LYS.126	2.96	2.16	17.90
5I76.PDB	O, C.GLN.124	N, C.SER.127	H, C.SER.127	2.86	2.07	20.07
5I76.PDB	O, C.GLN.124	OG, C.SER.127	HG, C.SER.127	2.65	1.87	17.60
5I76.PDB	O, C.LEU.125	N, C.GLY.128	H, C.GLY.128	2.88	2.03	8.22
5I76.PDB	O, C.LEU.181	N, C.ALA.130	H, C.ALA.130	2.83	2.02	16.04
5I76.PDB	OE1, C.GLN.124	N, C.SER.131	H, C.SER.131	2.91	2.10	16.13
5I76.PDB	OG1, C.THR.180	OG, C.SER.131	HG, C.SER.131	2.93	2.13	14.64
5I76.PDB	O, C.LEU.179	N, C.VAL.132	H, C.VAL.132	2.79	1.93	4.92
5I76.PDB	O, C.SER.177	N, C.CYS.134	H, C.CYS.134	2.78	1.93	7.78
5I76.PDB	O, C.PHE.116	N, C.LEU.135	H, C.LEU.135	2.83	1.98	7.23
5I76.PDB	O, C.LEU.175	N, C.LEU.136	H, C.LEU.136	2.87	2.03	8.14
5I76.PDB	O, C.SER.114	N, C.ASN.137	H, C.ASN.137	2.83	1.99	9.65
5I76.PDB	O, C.TYR.173	N, C.PHE.139	H, C.PHE.139	2.81	1.98	14.22
5I76.PDB	O, C.ALA.111	N, C.TYR.140	H, C.TYR.140	2.97	2.16	16.55
5I76.PDB	OE1, C.GLU.105	OH, C.TYR.140	HH, C.TYR.140	2.89	2.14	22.51
5I76.PDB	O, C.THR.197	N, C.LYS.145	H, C.LYS.145	2.98	2.14	9.58
5I76.PDB	O, C.GLU.195	N, C.GLN.147	H, C.GLN.147	2.87	2.05	14.85
5I76.PDB	O, A.SER.202	NE2, C.GLN.147	HE22, C.GLN.147	2.78	1.96	13.33
5I76.PDB	OG, C.SER.177	NE1, C.TRP.148	HE1, C.TRP.148	2.90	2.11	19.54
5I76.PDB	O, C.ALA.193	N, C.LYS.149	H, C.LYS.149	2.90	2.07	12.57
5I76.PDB	O, C.ALA.153	N, C.VAL.150	H, C.VAL.150	2.94	2.13	15.93
5I76.PDB	O, C.VAL.191	N, C.ASP.151	H, C.ASP.151	2.91	2.07	12.19
5I76.PDB	O, C.VAL.150	N, C.ALA.153	H, C.ALA.153	2.82	1.97	8.28
5I76.PDB	O, C.TRP.148	N, C.GLN.155	H, C.GLN.155	2.85	2.01	11.31
5I76.PDB	O, C.ALA.153	NE2, C.GLN.155	HE21, C.GLN.155	2.94	2.09	9.82
5I76.PDB	OE1, C.GLN.155	ND2, C.ASN.158	HD22, C.ASN.158	2.96	2.21	25.95
5I76.PDB	O, C.THR.178	N, C.GLN.160	H, C.GLN.160	2.96	2.16	17.81
5I76.PDB	O, C.SER.176	N, C.SER.162	H, C.SER.162	2.87	2.08	18.90
5I76.PDB	O, C.SER.174	N, C.THR.164	H, C.THR.164	2.96	2.12	9.89
5I76.PDB	O, C.SER.171	NE2, C.GLN.166	HE21, C.GLN.166	2.93	2.09	11.05
5I76.PDB	O, C.LEU.106	NE2, C.GLN.166	HE22, C.GLN.166	2.76	1.97	19.15
5I76.PDB	O, C.THR.172	N, C.ASP.167	H, C.ASP.167	2.84	2.05	19.17
5I76.PDB	OD2, C.ASP.167	N, C.LYS.169	H, C.LYS.169	2.81	2.03	20.18
5I76.PDB	OD2, C.ASP.167	N, C.ASP.170	H, C.ASP.170	2.96	2.19	22.65
5I76.PDB	O, C.ASP.167	N, C.SER.171	H, C.SER.171	2.79	2.03	23.14
5I76.PDB	OD1, C.ASP.170	N, C.THR.172	H, C.THR.172	2.98	2.17	15.09

5I76.PDB	OD1, C_ASP_170	OG1, C_THR_172	HG1, C_THR_172	2.79	1.97	11.52
5I76.PDB	O, C_PHE_139	N, C_TYR_173	H, C_TYR_173	2.84	1.99	6.46
5I76.PDB	OE2, C_GLU_105	OH, C_TYR_173	HH, C_TYR_173	2.72	1.89	6.26
5I76.PDB	O, C_LEU_136	N, C_LEU_175	H, C_LEU_175	2.89	2.11	21.04
5I76.PDB	O, C_SER_162	N, C_SER_176	H, C_SER_176	2.87	2.04	12.82
5I76.PDB	O, C_CYS_134	N, C_SER_177	H, C_SER_177	2.86	2.04	15.37
5I76.PDB	O, C_GLN_160	N, C_THR_178	H, C_THR_178	2.89	2.09	17.26
5I76.PDB	O, C_VAL_132	N, C_LEU_179	H, C_LEU_179	2.86	2.02	11.05
5I76.PDB	O, C_ALA_130	N, C_LEU_181	H, C_LEU_181	2.86	2.03	12.11
5I76.PDB	O, C_SER_182	N, C_TYR_186	H, C_TYR_186	2.80	1.95	6.73
5I76.PDB	O, C_LYS_183	N, C_GLU_187	H, C_GLU_187	2.92	2.12	19.05
5I76.PDB	O, C_ASP_185	N, C_LYS_188	H, C_LYS_188	2.99	2.16	13.62
5I76.PDB	OD2, C_ASP_151	ND1, C_HIS_189	HD1, C_HIS_189	2.35	1.61	24.33
5I76.PDB	OD1, C_ASP_151	N, C_VAL_191	H, C_VAL_191	2.92	2.09	11.65
5I76.PDB	O, C_PHE_209	N, C_TYR_192	H, C_TYR_192	2.96	2.11	8.01
5I76.PDB	O, C_LYS_149	N, C_ALA_193	H, C_ALA_193	2.98	2.25	27.79
5I76.PDB	O, C_LYS_207	N, C_CYS_194	H, C_CYS_194	2.84	1.98	5.34
5I76.PDB	O, C_GLN_147	N, C_GLU_195	H, C_GLU_195	2.83	1.99	10.59
5I76.PDB	O, C_VAL_205	N, C_VAL_196	H, C_VAL_196	2.75	1.95	18.04
5I76.PDB	O, C_LYS_145	N, C_THR_197	H, C_THR_197	2.93	2.12	16.49
5I76.PDB	ND1, C_HIS_198	N, C_GLY_200	H, C_GLY_200	2.94	2.08	6.54
5I76.PDB	O, C_HIS_198	N, C_LEU_201	H, C_LEU_201	2.84	1.98	6.14
5I76.PDB	O, C_VAL_196	N, C_VAL_205	H, C_VAL_205	2.92	2.11	16.84
5I76.PDB	O, C_CYS_194	N, C_LYS_207	H, C_LYS_207	2.90	2.08	15.23
5I76.PDB	O, C_TYR_192	N, C_PHE_209	H, C_PHE_209	2.92	2.14	20.73
5I76.PDB	O, C_LYS_190	N, C_ARG_211	H, C_ARG_211	2.72	1.88	9.66
5I76.PDB	O, C_HIS_189	NE, C_ARG_211	HE, C_ARG_211	2.72	1.86	2.35
5I76.PDB	O, D_SER_25	N, D_GLN_3	H, D_GLN_3	2.94	2.11	12.93
5I76.PDB	O, D_THR_23	N, D_LYS_5	H, D_LYS_5	2.88	2.10	20.15
5I76.PDB	OE1, D_GLN_111	N, D_GLN_6	H, D_GLN_6	2.88	2.06	13.61
5I76.PDB	O, D_TYR_93	NE2, D_GLN_6	HE22, D_GLN_6	2.83	1.97	5.03
5I76.PDB	O, D_THR_21	N, D_SER_7	H, D_SER_7	2.93	2.18	24.73
5I76.PDB	O, D_THR_116	N, D_VAL_12	H, D_VAL_12	2.82	1.99	13.27
5I76.PDB	O, D_LEU_85	N, D_SER_15	H, D_SER_15	2.74	1.90	9.28
5I76.PDB	O, D_GLN_13	N, D_GLN_16	H, D_GLN_16	2.92	2.10	15.02
5I76.PDB	O, D_MET_82	N, D_LEU_18	H, D_LEU_18	2.87	2.04	11.26
5I76.PDB	O, D_PHE_80	N, D_ILE_20	H, D_ILE_20	2.93	2.12	15.50
5I76.PDB	O, D_VAL_78	N, D_CYS_22	H, D_CYS_22	2.82	1.97	8.74
5I76.PDB	O, D_LYS_5	N, D_THR_23	H, D_THR_23	2.84	2.00	7.60
5I76.PDB	O, D_SER_76	N, D_VAL_24	H, D_VAL_24	2.91	2.08	12.63
5I76.PDB	O, D_GLN_3	N, D_SER_25	H, D_SER_25	2.93	2.11	15.90
5I76.PDB	OG, D_SER_28	OG1, D_THR_30	HG1, D_THR_30	2.71	1.88	5.11
5I76.PDB	O, D_SER_28	N, D_ASN_31	H, D_ASN_31	2.99	2.14	9.76
5I76.PDB	O, D_ILE_51	N, D_VAL_34	H, D_VAL_34	2.92	2.14	20.26
5I76.PDB	O, D_ALA_96	N, D_HIS_35	H, D_HIS_35	2.85	2.01	8.24
5I76.PDB	O, D_GLY_49	N, D_TRP_36	H, D_TRP_36	2.85	2.04	16.83
5I76.PDB	O, D_TYR_94	N, D_VAL_37	H, D_VAL_37	2.97	2.15	14.15
5I76.PDB	O, D_GLU_46	N, D_ARG_38	H, D_ARG_38	2.89	2.08	16.88
5I76.PDB	OD1, D_ASP_89	NH1, D_ARG_38	HH12, D_ARG_38	2.88	2.03	7.89
5I76.PDB	O, D_ILE_92	N, D_GLN_39	H, D_GLN_39	2.87	2.14	26.90
5I76.PDB	OE1, C_GLN_38	NE2, D_GLN_39	HE22, D_GLN_39	2.85	2.01	10.98
5I76.PDB	O, D_ARG_38	N, D_GLU_46	H, D_GLU_46	2.89	2.10	19.77
5I76.PDB	O, D_TRP_36	N, D_LEU_48	H, D_LEU_48	2.71	1.86	7.08
5I76.PDB	O, D_ASP_58	N, D_VAL_50	H, D_VAL_50	2.87	2.11	23.52
5I76.PDB	O, D_VAL_34	N, D_ILE_51	H, D_ILE_51	3.00	2.19	16.46
5I76.PDB	O, D_ASN_56	N, D_TRP_52	H, D_TRP_52	2.87	2.02	5.92
5I76.PDB	OD2, D_ASP_58	NE1, D_TRP_52	HE1, D_TRP_52	2.82	1.96	3.64
5I76.PDB	O, D_TRP_52	N, D_GLY_55	H, D_GLY_55	2.86	2.03	12.93

5I76.PDB	O, D_VAL_50	N, D_ASP_58	H, D_ASP_58	2.98	2.17	16.49
5I76.PDB	O, D_LEU_48	N, D_ASN_60	H, D_ASN_60	2.77	1.91	2.03
5I76.PDB	O, D_TRP_47	ND2, D_ASN_60	HD22, D_ASN_60	2.84	2.02	13.85
5I76.PDB	O, D_ASN_60	N, D_PHE_63	H, D_PHE_63	2.84	1.99	9.46
5I76.PDB	OD2, D_ASP_89	NH1, D_ARG_66	HH12, D_ARG_66	2.85	2.02	11.59
5I76.PDB	OD1, D_ASP_89	NH2, D_ARG_66	HH22, D_ARG_66	2.74	1.89	8.51
5I76.PDB	O, D_LYS_81	N, D_SER_68	H, D_SER_68	2.88	2.06	12.89
5I76.PDB	OH, D_TYR_59	N, D_ILE_69	H, D_ILE_69	2.95	2.13	14.70
5I76.PDB	O, D_PHE_79	N, D_ASN_70	H, D_ASN_70	2.95	2.13	15.10
5I76.PDB	O, D_SER_53	NZ, D_LYS_71	HZ1, D_LYS_71	2.72	1.85	9.25
5I76.PDB	O, D_GLN_77	N, D_ASP_72	H, D_ASP_72	2.82	1.99	12.40
5I76.PDB	OD1, D_ASP_72	OG, D_SER_74	HG, D_SER_74	2.71	2.00	26.33
5I76.PDB	O, D_CYS_22	N, D_VAL_78	H, D_VAL_78	2.81	1.98	14.10
5I76.PDB	O, D_ASN_70	N, D_PHE_79	H, D_PHE_79	2.80	1.95	6.90
5I76.PDB	O, D_ILE_20	N, D_PHE_80	H, D_PHE_80	2.86	2.01	4.93
5I76.PDB	O, D_SER_68	N, D_LYS_81	H, D_LYS_81	2.90	2.09	17.14
5I76.PDB	O, D_LEU_18	N, D_MET_82	H, D_MET_82	2.95	2.17	20.62
5I76.PDB	O, D_ARG_66	N, D_ASN_83	H, D_ASN_83	2.77	1.99	20.75
5I76.PDB	OD2, D_ASP_89	N, D_GLN_86	H, D_GLN_86	2.92	2.09	12.09
5I76.PDB	O, D_GLN_86	N, D_ASP_89	H, D_ASP_89	2.77	1.93	7.75
5I76.PDB	O, D_SER_87	N, D_THR_90	H, D_THR_90	3.00	2.14	2.55
5I76.PDB	O, D_GLN_39	N, D_ILE_92	H, D_ILE_92	2.92	2.12	17.89
5I76.PDB	O, D_THR_113	N, D_TYR_93	H, D_TYR_93	2.90	2.07	10.93
5I76.PDB	O, D_ASP_89	OH, D_TYR_93	HH, D_TYR_93	2.67	1.84	7.84
5I76.PDB	O, D_VAL_37	N, D_TYR_94	H, D_TYR_94	2.74	1.91	13.14
5I76.PDB	O, D_TYR_108	N, D_ARG_97	H, D_ARG_97	2.84	2.04	16.66
5I76.PDB	O, D_GLU_105	N, D_LEU_99	H, D_LEU_99	2.74	1.99	24.80
5I76.PDB	OD1, D_ASP_103	N, D_TYR_104	H, D_TYR_104	2.78	2.02	23.34
5I76.PDB	OH, C_TYR_36	N, D_PHE_106	H, D_PHE_106	2.93	2.09	12.40
5I76.PDB	O, D_PHE_106	NE1, D_TRP_109	HE1, D_TRP_109	2.87	2.14	26.78
5I76.PDB	O, D_CYS_95	N, D_GLY_110	H, D_GLY_110	2.79	1.94	6.99
5I76.PDB	O, D_GLN_6	NE2, D_GLN_111	HE22, D_GLN_111	2.93	2.16	22.33
5I76.PDB	O, D_TYR_93	N, D_THR_113	H, D_THR_113	2.81	2.09	27.66
5I76.PDB	O, D_SER_7	OG1, D_THR_113	HG1, D_THR_113	2.96	2.26	28.05
5I76.PDB	O, D_ALA_91	N, D_VAL_115	H, D_VAL_115	2.92	2.06	1.61
5I76.PDB	OG1, D_THR_90	N, D_VAL_117	H, D_VAL_117	2.98	2.15	13.35
5I76.PDB	O, D_PHE_152	N, D_LYS_123	H, D_LYS_123	2.78	1.94	11.09
5I76.PDB	O, D_ASP_150	NZ, D_LYS_123	HZ2, D_LYS_123	2.95	2.13	19.50
5I76.PDB	O, D_LYS_149	N, D_SER_126	H, D_SER_126	2.93	2.12	16.07
5I76.PDB	O, D_LEU_147	N, D_PHE_128	H, D_PHE_128	2.86	2.04	14.01
5I76.PDB	O, D_GLY_145	N, D_LEU_130	H, D_LEU_130	2.76	1.93	12.37
5I76.PDB	O, D_VAL_190	N, D_ALA_142	H, D_ALA_142	2.84	1.99	7.81
5I76.PDB	O, D_VAL_188	N, D_LEU_144	H, D_LEU_144	2.94	2.11	12.57
5I76.PDB	O, D_LEU_130	N, D_GLY_145	H, D_GLY_145	2.87	2.09	20.87
5I76.PDB	O, D_SER_186	N, D_CYS_146	H, D_CYS_146	2.86	2.06	18.05
5I76.PDB	O, D_PHE_128	N, D_LEU_147	H, D_LEU_147	2.79	1.96	12.46
5I76.PDB	O, D_LEU_184	N, D_VAL_148	H, D_VAL_148	2.78	1.92	3.60
5I76.PDB	O, D_SER_126	N, D_LYS_149	H, D_LYS_149	2.86	2.01	8.73
5I76.PDB	OD1, D_ASP_150	NZ, D_LYS_149	HZ3, D_LYS_149	2.86	2.03	16.70
5I76.PDB	OE1, D_GLU_154	OH, D_TYR_151	HH, D_TYR_151	2.91	2.09	9.17
5I76.PDB	O, D_LYS_123	N, D_PHE_152	H, D_PHE_152	2.92	2.10	15.60
5I76.PDB	O, D_ASN_205	N, D_THR_157	H, D_THR_157	2.93	2.10	13.79
5I76.PDB	O, D_ASN_203	N, D_SER_159	H, D_SER_159	2.90	2.10	17.79
5I76.PDB	OD1, D_ASN_203	OG, D_SER_159	HG, D_SER_159	2.84	2.05	16.99
5I76.PDB	OG, D_SER_186	NE1, D_TRP_160	HE1, D_TRP_160	2.92	2.08	9.81
5I76.PDB	O, D_ILE_201	N, D_ASN_161	H, D_ASN_161	2.80	1.97	10.81
5I76.PDB	OD1, D_ASN_203	N, D_SER_162	H, D_SER_162	2.77	1.99	21.35
5I76.PDB	O, D_TRP_160	N, D_GLY_163	H, D_GLY_163	2.92	2.16	23.49

5I76.PDB	O, D_ASN_161	N, D_ALA_164	H, D_ALA_164	2.96	2.12	9.30
5I76.PDB	O, D_VAL_187	N, D_HIS_170	H, D_HIS_170	2.80	1.97	11.03
5I76.PDB	O, D_SER_185	N, D_PHE_172	H, D_PHE_172	2.92	2.07	3.58
5I76.PDB	O, D_LEU_181	N, D_GLN_177	H, D_GLN_177	2.88	2.03	5.94
5I76.PDB	OD1, D_ASP_150	NE2, D_GLN_177	HE22, D_GLN_177	2.71	1.92	19.90
5I76.PDB	O, D_GLN_177	N, D_GLY_180	H, D_GLY_180	2.92	2.07	7.88
5I76.PDB	O, D_TYR_151	N, D_TYR_182	H, D_TYR_182	2.70	1.85	9.44
5I76.PDB	O, D_VAL_148	N, D_LEU_184	H, D_LEU_184	2.93	2.12	16.08
5I76.PDB	O, D_CYS_146	N, D_SER_186	H, D_SER_186	2.93	2.10	13.35
5I76.PDB	O, D_HIS_170	N, D_VAL_187	H, D_VAL_187	2.85	2.02	13.58
5I76.PDB	O, D_LEU_144	N, D_VAL_188	H, D_VAL_188	2.84	2.04	18.13
5I76.PDB	O, D_ALA_142	N, D_VAL_190	H, D_VAL_190	2.88	2.06	15.90
5I76.PDB	O, D_GLY_140	N, D_SER_192	H, D_SER_192	2.66	1.82	10.87
5I76.PDB	O, D_PRO_191	N, D_SER_194	H, D_SER_194	2.93	2.12	17.62
5I76.PDB	O, D_PRO_191	OG, D_SER_194	HG, D_SER_194	2.78	2.01	19.83
5I76.PDB	O, D_SER_194	N, D_GLN_198	H, D_GLN_198	2.92	2.06	3.85
5I76.PDB	O, D_THR_199	NE2, D_GLN_198	HE21, D_GLN_198	2.86	2.01	0.69
5I76.PDB	OG, D_SER_194	OH, D_TYR_200	HH, D_TYR_200	2.69	1.90	16.49
5I76.PDB	OD1, D_ASN_161	N, D_ILE_201	H, D_ILE_201	2.91	2.08	13.96
5I76.PDB	O, D_LYS_215	N, D_CYS_202	H, D_CYS_202	2.93	2.15	21.14
5I76.PDB	O, D_SER_159	N, D_ASN_203	H, D_ASN_203	2.82	1.98	10.06
5I76.PDB	O, D_VAL_213	N, D_VAL_204	H, D_VAL_204	2.81	1.96	3.09
5I76.PDB	O, D_THR_157	N, D_ASN_205	H, D_ASN_205	2.91	2.08	12.09
5I76.PDB	O, D_THR_211	N, D_HIS_206	H, D_HIS_206	2.80	1.95	4.50
5I76.PDB	O, D_PRO_153	NE2, D_HIS_206	HE2, D_HIS_206	2.83	1.99	8.92
5I76.PDB	O, D_LYS_207	N, D_ASN_210	H, D_ASN_210	2.86	2.01	9.18
5I76.PDB	O, D_VAL_204	N, D_VAL_213	H, D_VAL_213	2.96	2.15	16.50
5I76.PDB	O, D_CYS_202	N, D_LYS_215	H, D_LYS_215	2.92	2.10	13.71
5I76.PDB	OE1, C_GLU_123	NZ, D_LYS_215	HZ1, D_LYS_215	2.60	1.73	11.40
5I76.PDB	O, D_TYR_200	N, D_VAL_217	H, D_VAL_217	2.83	1.98	9.45

Table 1701: 5I76-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5JO5.PDB	O, H.SER_25	N, H.GLN_3	H, H.GLN_3	2.86	2.02	10.87
5JO5.PDB	O, H.ALA_23	N, H.VAL_5	H, H.VAL_5	2.97	2.20	22.57
5JO5.PDB	O, H.SER_21	N, H.SER_7	H, H.SER_7	2.83	2.06	22.33
5JO5.PDB	OG1, H.THR_107	N, H.GLY_9	H, H.GLY_9	2.92	2.18	25.94
5JO5.PDB	O, H.THR_110	N, H.VAL_12	H, H.VAL_12	2.95	2.16	19.95
5JO5.PDB	O, H.LEU_82C	N, H.GLY_15	H, H.GLY_15	2.87	2.03	10.84
5JO5.PDB	O, H.LYS_13	N, H.GLY_16	H, H.GLY_16	2.89	2.08	16.43
5JO5.PDB	O, H.MET_82	N, H.LEU_18	H, H.LEU_18	2.85	2.08	21.54
5JO5.PDB	O, H.LEU_80	N, H.LEU_20	H, H.LEU_20	2.83	1.98	7.63
5JO5.PDB	O, H.SER_7	N, H.SER_21	H, H.SER_21	2.95	2.11	11.17
5JO5.PDB	O, H.LEU_78	N, H.CYS_22	H, H.CYS_22	2.71	1.93	21.85
5JO5.PDB	O, H.ASN_76	N, H.ALA_24	H, H.ALA_24	2.98	2.24	25.87
5JO5.PDB	O, H.GLN_3	N, H.SER_25	H, H.SER_25	2.97	2.18	20.13
5JO5.PDB	OD2, H.ASP_53	NE1, H.TRP_33	HE1, H.TRP_33	2.93	2.17	24.23
5JO5.PDB	O, H.ALA_93	N, H.SER_35	H, H.SER_35	2.89	2.05	12.04
5JO5.PDB	OG1, H.THR_95	OG, H.SER_35	HG, H.SER_35	2.68	1.99	28.91
5JO5.PDB	O, H.GLY_49	N, H.TRP_36	H, H.TRP_36	2.91	2.11	18.39
5JO5.PDB	O, H.TYR_91	N, H.VAL_37	H, H.VAL_37	2.87	2.05	15.23
5JO5.PDB	O, H.GLU_46	N, H.ARG_38	H, H.ARG_38	2.84	1.99	8.78
5JO5.PDB	OE1, H.GLU_46	NE, H.ARG_38	HE, H.ARG_38	2.82	2.00	14.74
5JO5.PDB	OH, H.TYR_90	NH1, H.ARG_38	HH11, H.ARG_38	2.91	2.09	14.97
5JO5.PDB	OD1, H.ASP_86	NH1, H.ARG_38	HH12, H.ARG_38	2.87	2.05	14.25
5JO5.PDB	O, H.VAL_89	N, H.GLN_39	H, H.GLN_39	2.85	2.14	29.27
5JO5.PDB	O, H.LYS_43	NE2, H.GLN_39	HE21, H.GLN_39	2.97	2.25	28.76
5JO5.PDB	OE1, H.GLN_38	NE2, H.GLN_39	HE22, H.GLN_39	2.84	2.00	9.38
5JO5.PDB	O, H.ALA_40	N, H.LYS_43	H, H.LYS_43	2.90	2.09	16.35
5JO5.PDB	O, H.ARG_38	N, H.GLU_46	H, H.GLU_46	2.79	2.02	21.68
5JO5.PDB	O, H.TRP_36	N, H.VAL_48	H, H.VAL_48	2.94	2.11	12.31
5JO5.PDB	OE1, H.GLU_100J	NE, H.ARG_50	HE, H.ARG_50	2.77	2.00	22.35
5JO5.PDB	OD2, H.ASP_58	NH2, H.ARG_50	HH22, H.ARG_50	2.84	2.00	11.12
5JO5.PDB	O, H.MET_34	N, H.ILE_51	H, H.ILE_51	2.83	2.00	12.12
5JO5.PDB	O, H.THR_56	N, H.LYS_52	H, H.LYS_52	2.88	2.07	15.53
5JO5.PDB	O, H.LYS_52B	N, H.GLY_54	H, H.GLY_54	2.98	2.13	6.95
5JO5.PDB	O, H.SER_52A	N, H.GLY_55	H, H.GLY_55	2.78	2.06	28.32
5JO5.PDB	O, H.VAL_48	N, H.ALA_60	H, H.ALA_60	2.93	2.08	7.36
5JO5.PDB	O, H.VAL_63	N, H.ARG_66	H, H.ARG_66	2.94	2.10	10.09
5JO5.PDB	OD2, H.ASP_86	NH1, H.ARG_66	HH12, H.ARG_66	2.78	1.94	11.10
5JO5.PDB	O, H.PRO_62	NH2, H.ARG_66	HH21, H.ARG_66	2.88	2.03	7.86
5JO5.PDB	O, H.GLN_81	N, H.THR_68	H, H.THR_68	2.80	1.99	17.53
5JO5.PDB	OH, H.TYR_59	N, H.ILE_69	H, H.ILE_69	2.86	2.01	7.98
5JO5.PDB	OD1, H.ASP_73	NE, H.ARG_71	HE, H.ARG_71	2.85	2.05	17.58
5JO5.PDB	O, H.ALA_32	NH1, H.ARG_71	HH12, H.ARG_71	2.86	2.11	24.42
5JO5.PDB	O, H.ALA_32	NH2, H.ARG_71	HH22, H.ARG_71	2.83	2.07	23.03
5JO5.PDB	O, H.THR_77	N, H.ASP_72	H, H.ASP_72	2.89	2.04	7.72
5JO5.PDB	OD1, H.ASP_72	OG, H.SER_74	HG, H.SER_74	2.59	1.76	4.73
5JO5.PDB	O, H.LYS_75	OG1, H.THR_77	HG1, H.THR_77	2.84	2.04	15.24
5JO5.PDB	O, H.CYS_22	N, H.LEU_78	H, H.LEU_78	2.85	2.02	12.40
5JO5.PDB	O, H.SER_70	N, H.TYR_79	H, H.TYR_79	2.84	2.00	10.37
5JO5.PDB	O, H.LEU_20	N, H.LEU_80	H, H.LEU_80	2.99	2.17	15.30
5JO5.PDB	O, H.THR_68	N, H.GLN_81	H, H.GLN_81	2.80	1.97	11.82
5JO5.PDB	O, H.LEU_18	N, H.MET_82	H, H.MET_82	2.68	1.83	6.72
5JO5.PDB	O, H.ARG_66	N, H.ASN_82A	H, H.ASN_82A	2.89	2.08	16.66
5JO5.PDB	OD2, H.ASP_86	N, H.LYS_83	H, H.LYS_83	2.83	2.01	15.00
5JO5.PDB	O, H.LYS_83	N, H.ASP_86	H, H.ASP_86	2.89	2.04	9.43
5JO5.PDB	O, H.VAL_109	N, H.ALA_88	H, H.ALA_88	2.98	2.20	21.19
5JO5.PDB	O, H.GLN_39	N, H.VAL_89	H, H.VAL_89	2.91	2.12	19.27
5JO5.PDB	O, H.THR_107	N, H.TYR_90	H, H.TYR_90	2.80	1.96	8.92

5JO5.PDB	O, H_ASP_86	OH, H_TYR_90	HH, H_TYR_90	2.72	1.89	9.52
5JO5.PDB	O, H_VAL_37	N, H_TYR_91	H, H_TYR_91	2.60	1.74	3.84
5JO5.PDB	OE2, H_GLU_6	N, H_CYS_92	H, H_CYS_92	2.73	1.88	6.94
5JO5.PDB	O, H_SER_35	N, H_ALA_93	H, H_ALA_93	2.87	2.09	21.23
5JO5.PDB	OD2, H_ASP_102	NE, H_ARG_94	HE, H_ARG_94	2.81	2.07	25.27
5JO5.PDB	OD2, H_ASP_102	NH1, H_ARG_94	HH11, H_ARG_94	2.70	1.93	22.67
5JO5.PDB	O, H_TRP_33	N, H_THR_95	H, H_THR_95	2.84	2.02	13.21
5JO5.PDB	O, H_TYR_100K	N, H_GLY_96	H, H_GLY_96	2.75	2.04	28.69
5JO5.PDB	OH, L_TYR_36	N, H_PHE_100L	H, H_PHE_100L	2.79	1.96	12.88
5JO5.PDB	O, H_ARG_94	N, H_GLN_101	H, H_GLN_101	2.75	2.02	27.16
5JO5.PDB	O, H_CYS_92	N, H_GLY_104	H, H_GLY_104	2.98	2.18	17.80
5JO5.PDB	O, L_GLY_41	NH2, H_ARG_105	HH22, H_ARG_105	2.85	2.05	18.48
5JO5.PDB	OE1, H_GLU_6	N, H_GLY_106	H, H_GLY_106	2.83	1.97	2.31
5JO5.PDB	O, H_ALA_88	N, H_VAL_109	H, H_VAL_109	2.90	2.04	1.74
5JO5.PDB	OG1, H_THR_87	N, H_VAL_111	H, H_VAL_111	2.87	2.02	7.41
5JO5.PDB	O, H_PHE_146	N, H_LYS_117	H, H_LYS_117	2.78	1.95	14.10
5JO5.PDB	O, H_ASP_144	NZ, H_LYS_117	HZ2, H_LYS_117	2.88	2.15	29.08
5JO5.PDB	O, H_LEU_141	N, H_PHE_122	H, H_PHE_122	2.87	2.06	15.46
5JO5.PDB	O, H_GLY_139	N, H_LEU_124	H, H_LEU_124	2.83	1.98	8.83
5JO5.PDB	O, H_THR_135	N, H_SER_132	H, H_SER_132	2.79	2.00	20.13
5JO5.PDB	O, H_VAL_184	N, H_ALA_136	H, H_ALA_136	2.77	1.96	15.59
5JO5.PDB	O, H_LEU_124	N, H_GLY_139	H, H_GLY_139	2.94	2.17	22.16
5JO5.PDB	O, H_SER_180	N, H_CYS_140	H, H_CYS_140	2.79	2.01	20.41
5JO5.PDB	O, H_PHE_122	N, H_LEU_141	H, H_LEU_141	2.81	1.96	8.37
5JO5.PDB	O, H_LEU_178	N, H_VAL_142	H, H_VAL_142	2.78	1.93	4.91
5JO5.PDB	O, H_SER_120	N, H_LYS_143	H, H_LYS_143	2.78	1.93	7.38
5JO5.PDB	OE2, L_GLU_124	NZ, H_LYS_143	HZ2, H_LYS_143	2.46	1.63	17.05
5JO5.PDB	O, H_TYR_176	N, H_TYR_145	H, H_TYR_145	2.93	2.12	18.01
5JO5.PDB	O, H_LYS_117	N, H_PHE_146	H, H_PHE_146	2.91	2.11	18.36
5JO5.PDB	O, H_ASN_197	N, H_SER_153	H, H_SER_153	2.98	2.17	17.36
5JO5.PDB	OD1, H_ASN_197	OG, H_SER_153	HG, H_SER_153	2.83	2.04	17.75
5JO5.PDB	OG, H_SER_180	NE1, H_TRP_154	HE1, H_TRP_154	2.93	2.09	10.13
5JO5.PDB	O, H_ILE_195	N, H_ASN_155	H, H_ASN_155	2.79	1.95	11.56
5JO5.PDB	OD1, H_ASN_197	N, H_SER_156	H, H_SER_156	2.79	1.98	16.54
5JO5.PDB	O, H_VAL_181	N, H_HIS_164	H, H_HIS_164	2.87	2.04	11.88
5JO5.PDB	O, H_SER_179	N, H_PHE_166	H, H_PHE_166	2.94	2.09	7.03
5JO5.PDB	O, H_SER_177	N, H_VAL_169	H, H_VAL_169	2.82	1.99	13.61
5JO5.PDB	O, H_LEU_175	N, H_GLN_171	H, H_GLN_171	2.90	2.04	2.90
5JO5.PDB	OD1, H_ASP_144	NE2, H_GLN_171	HE22, H_GLN_171	2.85	2.05	18.06
5JO5.PDB	O, H_GLN_171	N, H_GLY_174	H, H_GLY_174	2.76	1.91	7.94
5JO5.PDB	O, H_TYR_145	N, H_TYR_176	H, H_TYR_176	2.87	2.01	3.19
5JO5.PDB	O, H_VAL_142	N, H_LEU_178	H, H_LEU_178	2.88	2.10	20.17
5JO5.PDB	OH, L_TYR_177	OG, H_SER_179	HG, H_SER_179	2.73	2.00	25.96
5JO5.PDB	O, H_CYS_140	N, H_SER_180	H, H_SER_180	2.97	2.15	16.14
5JO5.PDB	O, H_HIS_164	N, H_VAL_181	H, H_VAL_181	2.90	2.05	10.33
5JO5.PDB	O, H_LEU_138	N, H_VAL_182	H, H_VAL_182	2.81	1.98	13.21
5JO5.PDB	O, H_ALA_136	N, H_VAL_184	H, H_VAL_184	2.93	2.09	11.13
5JO5.PDB	O, H_GLY_134	N, H_SER_186	H, H_SER_186	2.74	1.90	11.33
5JO5.PDB	O, H_PRO_185	N, H_SER_188	H, H_SER_188	2.93	2.12	16.10
5JO5.PDB	O, H_PRO_185	OG, H_SER_188	HG, H_SER_188	2.69	1.85	3.24
5JO5.PDB	O, H_SER_188	N, H_GLN_192	H, H_GLN_192	2.64	1.80	8.80
5JO5.PDB	O, H_THR_193	NE2, H_GLN_192	HE21, H_GLN_192	2.95	2.13	13.81
5JO5.PDB	OG, H_SER_188	OH, H_TYR_194	HH, H_TYR_194	2.61	1.85	20.74
5JO5.PDB	OD1, H_ASN_155	N, H_ILE_195	H, H_ILE_195	2.90	2.09	16.29
5JO5.PDB	O, H_LYS_209	N, H_CYS_196	H, H_CYS_196	2.98	2.20	20.49
5JO5.PDB	O, H_SER_153	N, H_ASN_197	H, H_ASN_197	2.76	1.91	7.31
5JO5.PDB	OD1, H_ASP_208	ND2, H_ASN_197	HD22, H_ASN_197	2.91	2.06	7.04
5JO5.PDB	O, H_VAL_207	N, H_VAL_198	H, H_VAL_198	2.73	1.88	4.89

5JO5.PDB	O, H_THR_205	N, H_HIS_200	H, H_HIS_200	2.87	2.01	1.84
5JO5.PDB	O, H_PRO_147	NE2, H_HIS_200	HE2, H_HIS_200	2.76	1.91	9.60
5JO5.PDB	O, H_LYS_201	N, H_ASN_204	H, H_ASN_204	2.99	2.16	10.85
5JO5.PDB	O, H_VAL_198	N, H_VAL_207	H, H_VAL_207	2.80	1.98	14.15
5JO5.PDB	O, H_TYR_194	N, H_VAL_211	H, H_VAL_211	2.90	2.06	10.21
5JO5.PDB	O, L_GLN_24	N, L_THR_5	H, L_THR_5	2.86	2.04	14.84
5JO5.PDB	O, L_TYR_86	NE2, L_GLN_6	HE22, L_GLN_6	2.96	2.12	10.37
5JO5.PDB	O, L_LYS_103	N, L_VAL_11	H, L_VAL_11	2.96	2.14	15.21
5JO5.PDB	O, L_THR_105	N, L_VAL_13	H, L_VAL_13	2.96	2.22	26.22
5JO5.PDB	O, L_ALA_78	N, L_GLY_16	H, L_GLY_16	2.86	2.00	4.99
5JO5.PDB	O, L_ILE_75	N, L_VAL_19	H, L_VAL_19	2.97	2.17	18.95
5JO5.PDB	O, L_LEU_73	N, L_ILE_21	H, L_ILE_21	2.80	1.96	10.07
5JO5.PDB	O, L_ALA_71	N, L_CYS_23	H, L_CYS_23	2.65	1.81	9.51
5JO5.PDB	O, L_THR_5	N, L_GLN_24	H, L_GLN_24	2.94	2.18	24.54
5JO5.PDB	O, L_ASN_69	N, L_GLY_25	H, L_GLY_25	2.97	2.14	12.74
5JO5.PDB	O, L_ARG_91	OG, L_SER_27	HG, L_SER_27	2.58	1.79	15.77
5JO5.PDB	OE1, D_GLN_24	OG, L_SER_30	HG, L_SER_30	2.84	2.07	18.45
5JO5.PDB	O, L_SER_89	N, L_SER_34	H, L_SER_34	2.96	2.20	23.71
5JO5.PDB	O, L_ILE_48	N, L_TRP_35	H, L_TRP_35	2.92	2.12	18.40
5JO5.PDB	O, L_TYR_87	N, L_TYR_36	H, L_TYR_36	2.82	2.06	23.68
5JO5.PDB	O, L_VAL_45	N, L_GLN_37	H, L_GLN_37	2.90	2.07	14.26
5JO5.PDB	OH, L_TYR_86	NE2, L_GLN_37	HE21, L_GLN_37	2.94	2.08	4.10
5JO5.PDB	O, L_ASP_85	N, L_GLN_38	H, L_GLN_38	2.78	1.99	19.05
5JO5.PDB	OE1, H_GLN_39	NE2, L_GLN_38	HE22, L_GLN_38	2.83	2.00	13.03
5JO5.PDB	O, L_LYS_39	N, L_GLN_42	H, L_GLN_42	2.99	2.18	16.76
5JO5.PDB	O, L_GLN_37	N, L_VAL_45	H, L_VAL_45	2.86	2.09	22.29
5JO5.PDB	O, L_TRP_35	N, L_VAL_47	H, L_VAL_47	2.87	2.01	3.07
5JO5.PDB	OD1, L_ASN_52	NE, L_ARG_54	HE, L_ARG_54	2.95	2.15	18.15
5JO5.PDB	OD1, L_ASP_82	NH2, L_ARG_61	HH21, L_ARG_61	2.75	1.92	13.56
5JO5.PDB	OE2, L_GLU_81	NH2, L_ARG_61	HH22, L_ARG_61	2.98	2.17	16.30
5JO5.PDB	O, L_THR_74	N, L_SER_63	H, L_SER_63	2.91	2.14	22.21
5JO5.PDB	OD1, L_ASN_52	N, L_GLY_64	H, L_GLY_64	2.74	1.93	16.44
5JO5.PDB	O, L_SER_72	N, L_SER_65	H, L_SER_65	2.99	2.21	21.03
5JO5.PDB	O, L_THR_70	N, L_SER_67	H, L_SER_67	2.96	2.13	12.51
5JO5.PDB	O, L_SER_67	N, L_THR_70	H, L_THR_70	2.95	2.13	15.77
5JO5.PDB	O, L_SER_67	OG1, L_THR_70	HG1, L_THR_70	2.76	1.95	12.31
5JO5.PDB	O, L_CYS_23	N, L_ALA_71	H, L_ALA_71	2.78	1.96	15.50
5JO5.PDB	O, L_SER_65	N, L_SER_72	H, L_SER_72	2.85	2.01	11.19
5JO5.PDB	O, L_ILE_21	N, L_LEU_73	H, L_LEU_73	2.77	1.95	14.84
5JO5.PDB	O, L_SER_63	N, L_THR_74	H, L_THR_74	2.81	1.96	6.34
5JO5.PDB	O, L_VAL_19	N, L_ILE_75	H, L_ILE_75	2.92	2.10	14.23
5JO5.PDB	O, L_ARG_61	N, L_THR_76	H, L_THR_76	3.00	2.18	15.65
5JO5.PDB	O, L_GLN_17	N, L_ALA_78	H, L_ALA_78	2.90	2.06	10.41
5JO5.PDB	OD2, L_ASP_82	N, L_GLN_79	H, L_GLN_79	2.88	2.03	7.63
5JO5.PDB	O, L_GLN_79	N, L_ASP_82	H, L_ASP_82	2.84	1.99	8.17
5JO5.PDB	O, L_GLN_38	N, L_ASP_85	H, L_ASP_85	2.85	2.02	13.72
5JO5.PDB	O, L_THR_102	N, L_TYR_86	H, L_TYR_86	2.82	2.00	14.85
5JO5.PDB	O, L_ASP_82	OH, L_TYR_86	HH, L_TYR_86	2.63	1.81	7.96
5JO5.PDB	O, L_TYR_36	N, L_TYR_87	H, L_TYR_87	2.95	2.15	18.69
5JO5.PDB	O, L_SER_34	N, L_SER_89	H, L_SER_89	2.88	2.15	26.79
5JO5.PDB	O, L_VAL_97	OG, L_SER_89	HG, L_SER_89	2.82	2.06	20.46
5JO5.PDB	OE2, H_GLU_100J	NH2, L_ARG_91	HH22, L_ARG_91	2.69	1.84	7.26
5JO5.PDB	OH, L_TYR_31	N, L_GLY_95	H, L_GLY_95	2.78	1.95	11.57
5JO5.PDB	OD1, L_ASP_92	OG, L_SER_95A	HG, L_SER_95A	2.53	1.76	19.87
5JO5.PDB	OD1, H_ASP_58	NE, L_ARG_95B	HE, L_ARG_95B	2.95	2.13	14.76
5JO5.PDB	OG, L_SER_95A	N, L_LEU_95C	H, L_LEU_95C	2.90	2.07	11.01
5JO5.PDB	O, L_SER_90	N, L_VAL_97	H, L_VAL_97	2.91	2.08	13.54
5JO5.PDB	O, L_CYS_88	N, L_GLY_99	H, L_GLY_99	2.86	2.04	15.85

5JO5.PDB	OE1, L_GLN_6	N, L_GLY_101	H, L_GLY_101	2.93	2.15	20.63
5JO5.PDB	O, L_TYR_86	N, L_THR_102	H, L_THR_102	2.83	2.05	21.30
5JO5.PDB	O, L ASP_7	OG1, L_THR_102	HG1, L_THR_102	2.55	1.71	2.52
5JO5.PDB	O, L_PRO_8	N, L_LYS_103	H, L_LYS_103	2.89	2.05	8.92
5JO5.PDB	O, L_ALA_84	N, L_LEU_104	H, L_LEU_104	2.87	2.03	9.56
5JO5.PDB	OE2, L_GLU_83	N, L_VAL_106	H, L_VAL_106	2.95	2.18	22.86
5JO5.PDB	O, L_VAL_13	N, L_LEU_106A	H, L_LEU_106A	2.88	2.04	12.25
5JO5.PDB	OH, L_TYR_140	N, L_SER_107	H, L_SER_107	2.96	2.15	15.96
5JO5.PDB	OE1, L_GLU_198	NZ, L_LYS_110	HZ3, L_LYS_110	2.94	2.09	14.01
5JO5.PDB	O, L_TYR_140	N, L_ALA_111	H, L_ALA_111	2.75	1.91	11.65
5JO5.PDB	O, L_SER_137	N, L_SER_114	H, L_SER_114	2.88	2.08	18.09
5JO5.PDB	O, L_LEU_135	N, L_THR_116	H, L_THR_116	2.97	2.14	11.76
5JO5.PDB	O, L_VAL_133	N, L_PHE_118	H, L_PHE_118	2.81	1.95	5.47
5JO5.PDB	OE2, L_GLU_124	OG1, L_THR_131	HG1, L_THR_131	2.52	1.80	26.33
5JO5.PDB	O, L_LEU_178	N, L_LEU_132	H, L_LEU_132	2.86	2.05	15.80
5JO5.PDB	O, L_SER_176	N, L_CYS_134	H, L_CYS_134	2.82	1.97	8.12
5JO5.PDB	O, L_THR_116	N, L_LEU_135	H, L_LEU_135	2.90	2.05	8.63
5JO5.PDB	O, L_ALA_174	N, L_ILE_136	H, L_ILE_136	2.88	2.10	21.82
5JO5.PDB	O, L_SER_114	N, L_SER_137	H, L_SER_137	2.94	2.15	19.51
5JO5.PDB	OE1, L_GLN_167	N, L ASP_138	H, L ASP_138	2.79	2.02	21.93
5JO5.PDB	O, L_PRO_141	N, L_ALA_143	H, L_ALA_143	2.87	2.16	29.13
5JO5.PDB	O, L_GLN_194	N, L_ALA_147	H, L_ALA_147	2.86	2.03	12.40
5JO5.PDB	OG, L_SER_176	NE1, L_TRP_148	HE1, L_TRP_148	2.93	2.09	9.40
5JO5.PDB	O, L_SER_192	N, L_LYS_149	H, L_LYS_149	2.97	2.16	17.57
5JO5.PDB	O, L_SER_153	N, L_ALA_150	H, L_ALA_150	2.83	2.05	20.73
5JO5.PDB	O, L_TRP_148	N, L_VAL_155	H, L_VAL_155	2.95	2.13	15.00
5JO5.PDB	O, L_SER_175	N, L_THR_162	H, L_THR_162	2.86	2.04	15.42
5JO5.PDB	O, H_GLY_42	OG1, L_THR_163	HG1, L_THR_163	2.52	1.79	25.04
5JO5.PDB	O, L_LYS_171	N, L_GLN_167	H, L_GLN_167	2.64	1.79	5.56
5JO5.PDB	OD1, L ASN_169	NE2, L_GLN_167	HE21, L_GLN_167	2.89	2.12	21.54
5JO5.PDB	O, L_PHE_139	N, L_TYR_172	H, L_TYR_172	2.91	2.12	19.98
5JO5.PDB	O, L_SER_165	N, L_ALA_173	H, L_ALA_173	2.99	2.18	16.79
5JO5.PDB	O, L_ILE_136	N, L_ALA_174	H, L_ALA_174	2.74	1.94	17.43
5JO5.PDB	OG1, L_THR_162	OG, L_SER_175	HG, L_SER_175	2.94	2.19	22.64
5JO5.PDB	O, L_CYS_134	N, L_SER_176	H, L_SER_176	2.92	2.13	20.19
5JO5.PDB	OG1, L_THR_161	OG, L_SER_176	HG, L_SER_176	2.79	2.07	26.34
5JO5.PDB	O, L_GLU_160	N, L_TYR_177	H, L_TYR_177	2.76	1.95	17.14
5JO5.PDB	O, L_LEU_132	N, L_LEU_178	H, L_LEU_178	2.97	2.16	15.14
5JO5.PDB	O, L_GLY_158	N, L_SER_179	H, L_SER_179	2.93	2.10	12.81
5JO5.PDB	O, L_ALA_130	N, L_LEU_180	H, L_LEU_180	2.74	1.88	1.66
5JO5.PDB	OE1, L_GLN_184	N, L_THR_181	H, L_THR_181	2.79	1.96	12.16
5JO5.PDB	O, L_LYS_149	N, L_SER_192	H, L_SER_192	2.91	2.12	19.77
5JO5.PDB	OG1, L_THR_205	OG, L_SER_192	HG, L_SER_192	2.82	2.12	28.14
5JO5.PDB	O, L_LYS_204	N, L_CYS_193	H, L_CYS_193	2.89	2.08	16.55
5JO5.PDB	O, L_ALA_147	N, L_GLN_194	H, L_GLN_194	2.74	1.89	6.08
5JO5.PDB	O, L_VAL_202	N, L_VAL_195	H, L_VAL_195	2.92	2.09	13.64
5JO5.PDB	O, L_THR_145	N, L_THR_196	H, L_THR_196	2.99	2.14	7.48
5JO5.PDB	O, L_SER_200	N, L_HIS_197	H, L_HIS_197	2.70	1.87	12.42
5JO5.PDB	O, L_PRO_141	NE2, L_HIS_197	HE2, L_HIS_197	2.84	2.04	18.51
5JO5.PDB	O, L_HIS_197	N, L_SER_200	H, L_SER_200	2.99	2.16	11.48
5JO5.PDB	OG1, L_THR_196	OG1, L_THR_201	HG1, L_THR_201	2.95	2.20	22.04
5JO5.PDB	O, L_VAL_195	N, L_VAL_202	H, L_VAL_202	2.93	2.11	14.66
5JO5.PDB	O, L_TYR_191	N, L_VAL_206	H, L_VAL_206	2.84	2.01	13.12
5JO5.PDB	O, A_SER_25	N, A_GLN_3	H, A_GLN_3	2.86	2.01	9.97
5JO5.PDB	O, A_ALA_23	N, A_VAL_5	H, A_VAL_5	3.00	2.23	23.15
5JO5.PDB	O, A_SER_21	N, A_SER_7	H, A_SER_7	2.80	2.01	19.59
5JO5.PDB	OG1, A_THR_107	N, A_GLY_9	H, A_GLY_9	2.93	2.20	27.02
5JO5.PDB	O, A_THR_110	N, A_VAL_12	H, A_VAL_12	2.89	2.09	18.23

5JO5.PDB	O, A_LEU_82C	N, A_GLY_15	H, A_GLY_15	2.79	1.96	12.62
5JO5.PDB	O, A_LYS_13	N, A_GLY_16	H, A_GLY_16	2.95	2.13	15.67
5JO5.PDB	O, A_MET_82	N, A_LEU_18	H, A_LEU_18	2.94	2.14	18.28
5JO5.PDB	O, A_LEU_80	N, A_LEU_20	H, A_LEU_20	2.82	2.00	14.35
5JO5.PDB	O, A_SER_7	N, A_SER_21	H, A_SER_21	2.92	2.08	11.20
5JO5.PDB	O, A_LEU_78	N, A_CYS_22	H, A_CYS_22	2.77	2.01	23.44
5JO5.PDB	O, A_VAL_5	N, A_ALA_23	H, A_ALA_23	2.96	2.14	16.35
5JO5.PDB	O, A_PHE_29	N, A_ALA_32	H, A_ALA_32	2.94	2.09	3.75
5JO5.PDB	OD2, A_ASP_53	NE1, A_TRP_33	HE1, A_TRP_33	2.82	2.05	21.67
5JO5.PDB	O, A_ALA_93	N, A_SER_35	H, A_SER_35	2.92	2.09	13.78
5JO5.PDB	O, A_GLY_49	N, A_TRP_36	H, A_TRP_36	2.89	2.08	17.21
5JO5.PDB	O, A_TYR_91	N, A_VAL_37	H, A_VAL_37	2.83	2.00	13.43
5JO5.PDB	O, A_GLU_46	N, A_ARG_38	H, A_ARG_38	2.87	2.02	9.33
5JO5.PDB	OE1, A_GLU_46	NE, A_ARG_38	HE, A_ARG_38	2.78	1.97	16.63
5JO5.PDB	OD1, A_ASP_86	NH1, A_ARG_38	HH12, A_ARG_38	2.83	2.01	14.60
5JO5.PDB	OE1, B_GLN_38	NE2, A_GLN_39	HE22, A_GLN_39	2.87	2.02	8.31
5JO5.PDB	O, A_ALA_40	N, A_LYS_43	H, A_LYS_43	2.86	2.03	13.20
5JO5.PDB	O, A_ARG_38	N, A_GLU_46	H, A_GLU_46	2.79	2.01	20.62
5JO5.PDB	O, A_TRP_36	N, A_VAL_48	H, A_VAL_48	2.91	2.08	13.09
5JO5.PDB	OE1, A_GLU_100J	NE, A_ARG_50	HE, A_ARG_50	2.88	2.11	22.13
5JO5.PDB	OE2, A_GLU_100J	NH1, A_ARG_50	HH11, A_ARG_50	2.91	2.07	11.34
5JO5.PDB	OD2, A_ASP_58	NH2, A_ARG_50	HH22, A_ARG_50	2.88	2.05	13.39
5JO5.PDB	O, A_MET_34	N, A_ILE_51	H, A_ILE_51	2.86	2.02	11.89
5JO5.PDB	O, A_THR_56	N, A_LYS_52	H, A_LYS_52	2.85	2.02	13.45
5JO5.PDB	O, A_LYS_52B	N, A_GLY_54	H, A_GLY_54	2.90	2.06	8.56
5JO5.PDB	O, A_SER_52A	N, A_GLY_55	H, A_GLY_55	2.85	2.06	18.80
5JO5.PDB	O, A_VAL_48	N, A_ALA_60	H, A_ALA_60	2.97	2.12	7.83
5JO5.PDB	O, A_VAL_63	N, A_ARG_66	H, A_ARG_66	2.94	2.11	11.71
5JO5.PDB	O, A_SER_82B	NH1, A_ARG_66	HH11, A_ARG_66	2.94	2.23	29.90
5JO5.PDB	OD2, A_ASP_86	NH1, A_ARG_66	HH12, A_ARG_66	2.80	1.98	14.11
5JO5.PDB	O, A_PRO_62	NH2, A_ARG_66	HH21, A_ARG_66	2.96	2.10	6.17
5JO5.PDB	O, A_GLN_81	N, A_THR_68	H, A_THR_68	2.83	2.01	13.97
5JO5.PDB	OH, A_TYR_59	N, A_ILE_69	H, A_ILE_69	2.85	2.01	8.90
5JO5.PDB	OD1, A_ASP_73	NE, A_ARG_71	HE, A_ARG_71	2.86	2.09	22.09
5JO5.PDB	O, A_ALA_32	NH1, A_ARG_71	HH12, A_ARG_71	2.93	2.18	24.18
5JO5.PDB	O, A_ALA_32	NH2, A_ARG_71	HH22, A_ARG_71	2.90	2.14	22.88
5JO5.PDB	O, A_THR_77	N, A_ASP_72	H, A_ASP_72	2.96	2.10	6.62
5JO5.PDB	OD1, A_ASP_72	OG, A_SER_74	HG, A_SER_74	2.54	1.80	22.83
5JO5.PDB	O, A_LYS_75	OG1, A_THR_77	HG1, A_THR_77	2.92	2.11	13.47
5JO5.PDB	O, A_CYS_22	N, A_LEU_78	H, A_LEU_78	2.92	2.08	10.42
5JO5.PDB	O, A_SER_70	N, A_TYR_79	H, A_TYR_79	2.88	2.05	13.41
5JO5.PDB	O, A_THR_68	N, A_GLN_81	H, A_GLN_81	2.75	1.92	12.07
5JO5.PDB	O, A_LEU_18	N, A_MET_82	H, A_MET_82	2.76	1.91	7.81
5JO5.PDB	OD2, A_ASP_86	N, A_LYS_83	H, A_LYS_83	2.81	1.98	13.27
5JO5.PDB	O, A_LYS_83	N, A_ASP_86	H, A_ASP_86	2.81	1.98	12.37
5JO5.PDB	O, A_GLN_39	N, A_VAL_89	H, A_VAL_89	2.91	2.12	19.76
5JO5.PDB	O, A_THR_107	N, A_TYR_90	H, A_TYR_90	2.80	1.95	9.44
5JO5.PDB	O, A_ASP_86	OH, A_TYR_90	HH, A_TYR_90	2.68	1.87	12.71
5JO5.PDB	O, A_VAL_37	N, A_TYR_91	H, A_TYR_91	2.64	1.78	2.28
5JO5.PDB	OE2, A_GLU_6	N, A_CYS_92	H, A_CYS_92	2.84	2.03	15.70
5JO5.PDB	O, A_SER_35	N, A_ALA_93	H, A_ALA_93	2.90	2.14	23.25
5JO5.PDB	OD2, A_ASP_102	NE, A_ARG_94	HE, A_ARG_94	2.86	2.14	28.73
5JO5.PDB	OD2, A_ASP_102	NH1, A_ARG_94	HH11, A_ARG_94	2.58	1.79	19.06
5JO5.PDB	O, A_TRP_33	N, A_THR_95	H, A_THR_95	2.83	2.01	14.93
5JO5.PDB	O, A_TYR_100K	N, A_GLY_96	H, A_GLY_96	2.84	2.07	22.90
5JO5.PDB	O, A_GLU_100I	N, A_TYR_98	H, A_TYR_98	2.88	2.03	8.11
5JO5.PDB	O, A_GLY_96	N, A_TYR_100K	H, A_TYR_100K	2.90	2.10	17.32
5JO5.PDB	OH, B_TYR_36	N, A_PHE_100L	H, A_PHE_100L	2.86	2.06	18.12

5JO5.PDB	O, A_ARG_94	N, A_GLN_101	H, A_GLN_101	2.84	2.09	25.14
5JO5.PDB	O, B_GLY_41	NH1, A_ARG_105	HH12, A_ARG_105	2.66	1.82	9.49
5JO5.PDB	OE1, A_GLU_6	N, A_GLY_106	H, A_GLY_106	2.88	2.02	1.10
5JO5.PDB	O, A_ALA_88	N, A_VAL_109	H, A_VAL_109	2.93	2.07	3.98
5JO5.PDB	OG1, A_THR_87	N, A_VAL_111	H, A_VAL_111	2.98	2.14	10.40
5JO5.PDB	O, A_PHE_146	N, A_LYS_117	H, A_LYS_117	2.76	1.96	17.53
5JO5.PDB	O, A_ASP_144	NZ, A_LYS_117	HZ2, A_LYS_117	2.76	2.02	28.39
5JO5.PDB	O, A_LEU_141	N, A_PHE_122	H, A_PHE_122	2.89	2.09	16.71
5JO5.PDB	O, A_GLY_139	N, A_LEU_124	H, A_LEU_124	2.85	2.00	8.87
5JO5.PDB	O, A_SER_132	N, A_THR_135	H, A_THR_135	3.00	2.15	8.03
5JO5.PDB	O, A_VAL_184	N, A_ALA_136	H, A_ALA_136	2.76	1.95	16.74
5JO5.PDB	O, A_SER_180	N, A_CYS_140	H, A_CYS_140	2.83	2.05	19.65
5JO5.PDB	O, A_PHE_122	N, A_LEU_141	H, A_LEU_141	2.83	1.98	7.04
5JO5.PDB	O, A_LEU_178	N, A_VAL_142	H, A_VAL_142	2.79	1.93	5.86
5JO5.PDB	O, A_SER_120	N, A_LYS_143	H, A_LYS_143	2.78	1.93	6.54
5JO5.PDB	OE2, B_GLU_124	NZ, A_LYS_143	HZ2, A_LYS_143	2.62	1.83	23.29
5JO5.PDB	O, A_TYR_176	N, A_TYR_145	H, A_TYR_145	2.91	2.11	17.73
5JO5.PDB	O, A_LYS_117	N, A_PHE_146	H, A_PHE_146	2.93	2.13	18.00
5JO5.PDB	O, A_ASN_197	N, A_SER_153	H, A_SER_153	2.99	2.18	16.28
5JO5.PDB	OD1, A_ASN_197	OG, A_SER_153	HG, A_SER_153	2.78	2.00	18.34
5JO5.PDB	OG, A_SER_180	NE1, A_TRP_154	HE1, A_TRP_154	2.89	2.05	11.45
5JO5.PDB	O, A_ILE_195	N, A_ASN_155	H, A_ASN_155	2.78	1.95	12.63
5JO5.PDB	OD1, A_ASN_197	N, A_SER_156	H, A_SER_156	2.75	1.94	16.25
5JO5.PDB	O, A_TRP_154	N, A_GLY_157	H, A_GLY_157	2.98	2.18	18.25
5JO5.PDB	O, A_VAL_181	N, A_HIS_164	H, A_HIS_164	2.84	2.01	12.57
5JO5.PDB	O, A_SER_179	N, A_PHE_166	H, A_PHE_166	2.92	2.07	5.08
5JO5.PDB	O, A_SER_177	N, A_VAL_169	H, A_VAL_169	2.79	1.96	14.12
5JO5.PDB	O, A_LEU_175	N, A_GLN_171	H, A_GLN_171	2.92	2.06	3.13
5JO5.PDB	OD1, A_ASP_144	NE2, A_GLN_171	HE22, A_GLN_171	2.80	2.01	18.53
5JO5.PDB	O, A_GLN_171	N, A_GLY_174	H, A_GLY_174	2.84	1.99	4.07
5JO5.PDB	O, A_TYR_145	N, A_TYR_176	H, A_TYR_176	2.86	2.00	3.44
5JO5.PDB	O, A_VAL_142	N, A_LEU_178	H, A_LEU_178	2.89	2.11	20.35
5JO5.PDB	OH, B_TYR_177	OG, A_SER_179	HG, A_SER_179	2.83	2.10	25.21
5JO5.PDB	O, A_CYS_140	N, A_SER_180	H, A_SER_180	2.96	2.14	14.89
5JO5.PDB	O, A_HIS_164	N, A_VAL_181	H, A_VAL_181	2.88	2.06	14.86
5JO5.PDB	O, A_LEU_138	N, A_VAL_182	H, A_VAL_182	2.81	1.98	12.72
5JO5.PDB	O, A_ALA_136	N, A_VAL_184	H, A_VAL_184	2.85	2.03	14.13
5JO5.PDB	O, A_GLY_134	N, A_SER_186	H, A_SER_186	2.73	1.88	8.68
5JO5.PDB	O, A_PRO_185	N, A_SER_188	H, A_SER_188	2.87	2.11	23.16
5JO5.PDB	O, A_PRO_185	OG, A_SER_188	HG, A_SER_188	2.64	1.81	7.89
5JO5.PDB	O, A_SER_188	N, A_THR_191	H, A_THR_191	2.98	2.17	16.73
5JO5.PDB	O, A_SER_188	N, A_GLN_192	H, A_GLN_192	2.81	1.96	9.04
5JO5.PDB	OG, A_SER_188	OH, A_TYR_194	HH, A_TYR_194	2.69	1.94	22.27
5JO5.PDB	OD1, A_ASN_155	N, A_ILE_195	H, A_ILE_195	2.85	2.04	16.46
5JO5.PDB	O, A_LYS_209	N, A_CYS_196	H, A_CYS_196	2.97	2.19	19.93
5JO5.PDB	O, A_SER_153	N, A_ASN_197	H, A_ASN_197	2.77	1.92	7.59
5JO5.PDB	O, A_VAL_207	N, A_VAL_198	H, A_VAL_198	2.69	1.83	4.66
5JO5.PDB	OG, A_SER_203	ND1, A_HIS_200	HD1, A_HIS_200	2.79	2.03	23.43
5JO5.PDB	O, A_PRO_147	NE2, A_HIS_200	HE2, A_HIS_200	2.73	1.88	6.85
5JO5.PDB	O, A_SER_203	OG1, A_THR_205	HG1, A_THR_205	2.95	2.24	27.28
5JO5.PDB	O, A_VAL_198	N, A_VAL_207	H, A_VAL_207	2.77	1.95	15.31
5JO5.PDB	O, A_CYS_196	N, A_LYS_209	H, A_LYS_209	2.98	2.17	16.36
5JO5.PDB	OE2, B_GLU_123	NZ, A_LYS_209	HZ1, A_LYS_209	2.55	1.68	10.64
5JO5.PDB	O, A_TYR_194	N, A_VAL_211	H, A_VAL_211	2.93	2.09	10.38
5JO5.PDB	O, B_GLN_24	N, B_THR_5	H, B_THR_5	2.82	1.99	13.54
5JO5.PDB	O, B_TYR_86	NE2, B_GLN_6	HE22, B_GLN_6	2.95	2.13	14.24
5JO5.PDB	O, B_LYS_103	N, B_VAL_11	H, B_VAL_11	2.99	2.17	14.79
5JO5.PDB	O, B_THR_105	N, B_VAL_13	H, B_VAL_13	2.91	2.14	21.54

5JO5.PDB	O, B.ALA.78	N, B.GLY.16	H, B.GLY.16	2.80	1.95	6.96
5JO5.PDB	O, B.ALA.14	N, B.GLN.17	H, B.GLN.17	3.00	2.14	6.45
5JO5.PDB	O, B.ILE.75	N, B.VAL.19	H, B.VAL.19	2.94	2.13	16.92
5JO5.PDB	O, B.LEU.73	N, B.ILE.21	H, B.ILE.21	2.77	1.92	7.42
5JO5.PDB	O, B.ALA.71	N, B.CYS.23	H, B.CYS.23	2.73	1.95	21.25
5JO5.PDB	O, B.THR.5	N, B.GLN.24	H, B.GLN.24	2.88	2.15	26.17
5JO5.PDB	O, B.ASN.69	N, B.GLY.25	H, B.GLY.25	2.95	2.12	12.16
5JO5.PDB	O, B.ARG.91	OG, B.SER.27	HG, B.SER.27	2.69	1.95	23.94
5JO5.PDB	O, B.GLY.25	N, B.LEU.28	H, B.LEU.28	2.92	2.12	17.50
5JO5.PDB	O, B.SER.27	N, B.SER.30	H, B.SER.30	2.94	2.12	14.59
5JO5.PDB	O, B.SER.89	N, B.SER.34	H, B.SER.34	2.95	2.14	17.48
5JO5.PDB	O, B.ILE.48	N, B.TRP.35	H, B.TRP.35	2.82	2.01	17.71
5JO5.PDB	O, B.TYR.87	N, B.TYR.36	H, B.TYR.36	2.80	2.06	24.94
5JO5.PDB	O, B.VAL.45	N, B.GLN.37	H, B.GLN.37	2.88	2.07	16.60
5JO5.PDB	OH, B.TYR.86	NE2, B.GLN.37	HE21, B.GLN.37	2.95	2.09	5.48
5JO5.PDB	O, B.ASP.85	N, B.GLN.38	H, B.GLN.38	2.79	2.00	18.67
5JO5.PDB	OE1, A.GLN.39	NE2, B.GLN.38	HE22, B.GLN.38	2.90	2.07	12.43
5JO5.PDB	O, B.GLN.37	N, B.VAL.45	H, B.VAL.45	2.85	2.08	22.23
5JO5.PDB	O, B.TRP.35	N, B.VAL.47	H, B.VAL.47	2.80	1.94	1.50
5JO5.PDB	O, B.ASN.53	N, B.TYR.49	H, B.TYR.49	2.95	2.14	16.79
5JO5.PDB	O, B.ASP.60	NH1, B.ARG.54	HH12, B.ARG.54	2.83	2.07	22.75
5JO5.PDB	OD1, B.ASP.82	NH2, B.ARG.61	HH21, B.ARG.61	2.66	1.83	11.88
5JO5.PDB	O, B.THR.74	N, B.SER.63	H, B.SER.63	2.95	2.17	20.44
5JO5.PDB	OD1, B.ASN.52	N, B.GLY.64	H, B.GLY.64	2.76	1.93	12.24
5JO5.PDB	O, F.ARG.29	ND2, B.ASN.69	HD21, B.ASN.69	2.80	1.99	16.03
5JO5.PDB	O, B.SER.67	N, B.THR.70	H, B.THR.70	2.93	2.12	15.05
5JO5.PDB	O, B.SER.67	OG1, B.THR.70	HG1, B.THR.70	2.62	1.83	17.02
5JO5.PDB	O, B.CYS.23	N, B.ALA.71	H, B.ALA.71	2.77	1.96	16.51
5JO5.PDB	O, B.SER.65	N, B.SER.72	H, B.SER.72	2.94	2.10	12.05
5JO5.PDB	O, B.ILE.21	N, B.LEU.73	H, B.LEU.73	2.80	2.00	18.00
5JO5.PDB	O, B.SER.63	N, B.THR.74	H, B.THR.74	2.83	1.99	8.11
5JO5.PDB	O, B.VAL.19	N, B.ILE.75	H, B.ILE.75	2.88	2.05	12.36
5JO5.PDB	O, B.GLN.17	N, B.ALA.78	H, B.ALA.78	2.88	2.04	9.27
5JO5.PDB	OD2, B.ASP.82	N, B.GLN.79	H, B.GLN.79	2.90	2.05	7.32
5JO5.PDB	O, B.GLN.79	N, B.ASP.82	H, B.ASP.82	2.86	2.02	10.30
5JO5.PDB	O, B.GLN.38	N, B.ASP.85	H, B.ASP.85	2.90	2.08	13.72
5JO5.PDB	O, B.THR.102	N, B.TYR.86	H, B.TYR.86	2.83	2.01	15.48
5JO5.PDB	O, B.ASP.82	OH, B.TYR.86	HH, B.TYR.86	2.63	1.81	9.87
5JO5.PDB	O, B.TYR.36	N, B.TYR.87	H, B.TYR.87	2.92	2.12	17.35
5JO5.PDB	O, B.SER.34	N, B.SER.89	H, B.SER.89	2.90	2.16	26.65
5JO5.PDB	O, B.VAL.97	OG, B.SER.89	HG, B.SER.89	2.80	2.03	20.14
5JO5.PDB	O, A.GLY.100H	NE, B.ARG.91	HE, B.ARG.91	2.94	2.09	9.41
5JO5.PDB	OH, B.TYR.31	N, B.GLY.95	H, B.GLY.95	2.85	2.01	11.73
5JO5.PDB	OD1, B.ASP.92	OG, B.SER.95A	HG, B.SER.95A	2.47	1.67	15.14
5JO5.PDB	OG, B.SER.95A	N, B.LEU.95C	H, B.LEU.95C	2.98	2.13	6.04
5JO5.PDB	O, B.SER.90	N, B.VAL.97	H, B.VAL.97	2.93	2.11	13.52
5JO5.PDB	O, B.CYS.88	N, B.GLY.99	H, B.GLY.99	2.87	2.07	18.58
5JO5.PDB	O, B.TYR.86	N, B.THR.102	H, B.THR.102	2.85	2.06	19.16
5JO5.PDB	O, B.ASP.7	OG1, B.THR.102	HG1, B.THR.102	2.67	1.84	6.53
5JO5.PDB	O, B.PRO.8	N, B.LYS.103	H, B.LYS.103	2.86	2.01	7.04
5JO5.PDB	O, B.ALA.84	N, B.LEU.104	H, B.LEU.104	2.88	2.04	10.34
5JO5.PDB	O, B.VAL.11	N, B.THR.105	H, B.THR.105	2.98	2.17	16.12
5JO5.PDB	OE2, B.GLU.83	N, B.VAL.106	H, B.VAL.106	2.94	2.17	22.79
5JO5.PDB	O, B.VAL.13	N, B.LEU.106A	H, B.LEU.106A	2.84	2.01	13.15
5JO5.PDB	OH, B.TYR.140	N, B.SER.107	H, B.SER.107	2.96	2.17	18.24
5JO5.PDB	O, B.TYR.140	N, B.ALA.111	H, B.ALA.111	2.79	1.96	11.97
5JO5.PDB	O, B.SER.137	N, B.SER.114	H, B.SER.114	2.91	2.11	17.49
5JO5.PDB	O, B.LEU.135	N, B.THR.116	H, B.THR.116	2.96	2.13	12.67

5JO5.PDB	O, B.VAL_133	N, B.PHE_118	H, B.PHE_118	2.80	1.94	5.22
5JO5.PDB	O, B.LEU_125	N, B.ASN_128	H, B.ASN_128	2.88	2.06	15.38
5JO5.PDB	OE1, B.GLU_124	N, B.THR_131	H, B.THR_131	2.94	2.22	28.36
5JO5.PDB	OE2, B.GLU_124	OG1, B.THR_131	HG1, B.THR_131	2.59	1.86	24.88
5JO5.PDB	O, B.LEU_178	N, B.LEU_132	H, B.LEU_132	2.93	2.11	15.51
5JO5.PDB	O, B.SER_176	N, B.CYS_134	H, B.CYS_134	2.82	1.97	4.20
5JO5.PDB	O, B.THR_116	N, B.LEU_135	H, B.LEU_135	2.91	2.08	12.22
5JO5.PDB	O, B.ALA_174	N, B.ILE_136	H, B.ILE_136	2.90	2.13	23.29
5JO5.PDB	O, B.SER_114	N, B.SER_137	H, B.SER_137	2.93	2.15	21.86
5JO5.PDB	OE1, B.GLN_167	N, B.ASP_138	H, B.ASP_138	2.85	2.08	22.86
5JO5.PDB	O, B.ALA_111	N, B.TYR_140	H, B.TYR_140	2.99	2.17	16.28
5JO5.PDB	O, B.GLN_194	N, B.ALA_147	H, B.ALA_147	2.88	2.05	13.99
5JO5.PDB	OG, B.SER_176	NE1, B.TRP_148	HE1, B.TRP_148	2.89	2.05	10.46
5JO5.PDB	O, B.SER_192	N, B.LYS_149	H, B.LYS_149	2.94	2.16	21.00
5JO5.PDB	O, B.SER_153	N, B.ALA_150	H, B.ALA_150	2.80	1.98	15.92
5JO5.PDB	O, B.SER_190	N, B.ASP_151	H, B.ASP_151	2.96	2.12	10.60
5JO5.PDB	O, B.ALA_150	N, B.SER_153	H, B.SER_153	2.85	2.01	8.39
5JO5.PDB	O, B.TYR_177	N, B.GLU_160	H, B.GLU_160	2.99	2.19	18.42
5JO5.PDB	O, B.SER_175	N, B.THR_162	H, B.THR_162	2.83	2.00	12.84
5JO5.PDB	O, A.GLY_42	OG1, B.THR_163	HG1, B.THR_163	2.48	1.73	21.87
5JO5.PDB	O, B.LYS_171	N, B.GLN_167	H, B.GLN_167	2.72	1.87	6.72
5JO5.PDB	OD1, B.ASN_169	NE2, B.GLN_167	HE21, B.GLN_167	2.98	2.24	26.40
5JO5.PDB	OD1, B.ASP_138	NE2, B.GLN_167	HE22, B.GLN_167	2.99	2.14	6.65
5JO5.PDB	O, B.PHE_139	N, B.TYR_172	H, B.TYR_172	2.89	2.09	16.64
5JO5.PDB	O, B.ILE_136	N, B.ALA_174	H, B.ALA_174	2.78	1.99	18.28
5JO5.PDB	OG1, B.THR_162	N, B.SER_175	H, B.SER_175	2.97	2.18	20.62
5JO5.PDB	OG1, B.THR_162	OG, B.SER_175	HG, B.SER_175	2.87	2.11	21.53
5JO5.PDB	O, B.CYS_134	N, B.SER_176	H, B.SER_176	2.89	2.09	18.62
5JO5.PDB	OG1, B.THR_161	OG, B.SER_176	HG, B.SER_176	2.78	2.05	24.57
5JO5.PDB	O, B.GLU_160	N, B.TYR_177	H, B.TYR_177	2.74	1.95	18.78
5JO5.PDB	O, B.LEU_132	N, B.LEU_178	H, B.LEU_178	2.98	2.16	14.96
5JO5.PDB	O, B.GLY_158	N, B.SER_179	H, B.SER_179	2.79	1.95	12.09
5JO5.PDB	O, B.ALA_130	N, B.LEU_180	H, B.LEU_180	2.84	1.98	3.06
5JO5.PDB	OE1, B.GLN_184	N, B.THR_181	H, B.THR_181	2.98	2.15	11.97
5JO5.PDB	O, B.GLN_184	OG, B.SER_187	HG, B.SER_187	2.84	2.02	9.83
5JO5.PDB	OD1, B.ASP_151	N, B.ARG_189	H, B.ARG_189	2.77	1.99	21.06
5JO5.PDB	O, B.VAL_206	N, B.TYR_191	H, B.TYR_191	2.97	2.14	12.35
5JO5.PDB	O, B.LYS_149	N, B.SER_192	H, B.SER_192	2.94	2.15	19.79
5JO5.PDB	OG1, B.THR_205	OG, B.SER_192	HG, B.SER_192	2.59	1.90	29.12
5JO5.PDB	O, B.LYS_204	N, B.CYS_193	H, B.CYS_193	2.85	2.06	19.97
5JO5.PDB	O, B.ALA_147	N, B.GLN_194	H, B.GLN_194	2.76	1.91	8.07
5JO5.PDB	OE2, B.GLU_203	NE2, B.GLN_194	HE21, B.GLN_194	2.60	1.77	11.97
5JO5.PDB	O, B.VAL_202	N, B.VAL_195	H, B.VAL_195	2.87	2.03	10.67
5JO5.PDB	O, B.THR_145	N, B.THR_196	H, B.THR_196	2.94	2.09	7.84
5JO5.PDB	O, B.SER_200	N, B.HIS_197	H, B.HIS_197	2.84	2.00	11.99
5JO5.PDB	O, B.PRO_141	NE2, B.HIS_197	HE2, B.HIS_197	2.91	2.14	22.84
5JO5.PDB	OG1, B.THR_196	OG1, B.THR_201	HG1, B.THR_201	2.97	2.21	22.11
5JO5.PDB	O, B.VAL_195	N, B.VAL_202	H, B.VAL_202	2.91	2.09	14.85
5JO5.PDB	O, B.TYR_191	N, B.VAL_206	H, B.VAL_206	2.88	2.07	15.96
5JO5.PDB	O, C.SER_25	N, C.GLN_3	H, C.GLN_3	2.95	2.10	9.50
5JO5.PDB	O, C.SER_21	N, C.SER_7	H, C.SER_7	2.80	2.03	21.56
5JO5.PDB	OG1, C.THR_107	N, C.GLY_9	H, C.GLY_9	2.94	2.21	27.65
5JO5.PDB	O, C.THR_110	N, C.VAL_12	H, C.VAL_12	2.90	2.11	19.33
5JO5.PDB	O, C.LEU_82C	N, C.GLY_15	H, C.GLY_15	2.77	1.95	13.95
5JO5.PDB	O, C.LYS_13	N, C.GLY_16	H, C.GLY_16	2.93	2.13	17.72
5JO5.PDB	O, C.MET_82	N, C.LEU_18	H, C.LEU_18	2.90	2.11	18.94
5JO5.PDB	O, C.LEU_80	N, C.LEU_20	H, C.LEU_20	2.76	1.94	13.93
5JO5.PDB	O, C.SER_7	N, C.SER_21	H, C.SER_21	2.94	2.10	10.42

5JO5.PDB	O, C.LEU_78	N, C.CYS_22	H, C.CYS_22	2.73	1.95	21.22
5JO5.PDB	O, C.VAL_5	N, C.ALA_23	H, C.ALA_23	2.95	2.13	13.78
5JO5.PDB	O, C.PHE_29	N, C.ALA_32	H, C.ALA_32	2.90	2.05	5.82
5JO5.PDB	OD2, C.ASP_53	NE1, C.TRP_33	HE1, C.TRP_33	2.84	2.06	21.35
5JO5.PDB	O, C.ALA_93	N, C.SER_35	H, C.SER_35	2.93	2.11	13.64
5JO5.PDB	O, C.GLY_49	N, C.TRP_36	H, C.TRP_36	2.89	2.07	16.12
5JO5.PDB	O, C.TYR_91	N, C.VAL_37	H, C.VAL_37	2.87	2.05	13.46
5JO5.PDB	O, C.GLU_46	N, C.ARG_38	H, C.ARG_38	2.87	2.03	9.28
5JO5.PDB	OE1, C.GLU_46	NE, C.ARG_38	HE, C.ARG_38	2.77	1.97	17.97
5JO5.PDB	OH, C.TYR_90	NH1, C.ARG_38	HH11, C.ARG_38	3.00	2.18	14.70
5JO5.PDB	OD1, C.ASP_86	NH1, C.ARG_38	HH12, C.ARG_38	2.85	2.02	13.98
5JO5.PDB	OE1, D.GLN_38	NE2, C.GLN_39	HE22, C.GLN_39	2.86	2.02	9.45
5JO5.PDB	O, C.ALA_40	N, C.LYS_43	H, C.LYS_43	2.88	2.04	10.48
5JO5.PDB	O, C.ARG_38	N, C.GLU_46	H, C.GLU_46	2.77	1.99	20.78
5JO5.PDB	O, C.TRP_36	N, C.VAL_48	H, C.VAL_48	2.90	2.07	13.17
5JO5.PDB	OE1, C.GLU_100J	NE, C.ARG_50	HE, C.ARG_50	2.87	2.09	20.20
5JO5.PDB	OD2, C.ASP_58	NH1, C.ARG_50	HH12, C.ARG_50	2.77	1.94	11.94
5JO5.PDB	OE2, C.GLU_100J	NH2, C.ARG_50	HH21, C.ARG_50	2.86	2.02	10.69
5JO5.PDB	O, C.MET_34	N, C.ILE_51	H, C.ILE_51	2.83	1.99	11.56
5JO5.PDB	O, C.THR_56	N, C.LYS_52	H, C.LYS_52	2.95	2.12	13.78
5JO5.PDB	O, C.SER_52A	N, C.ASP_53	H, C.ASP_53	2.94	2.23	29.56
5JO5.PDB	O, C.LYS_52B	N, C.GLY_54	H, C.GLY_54	3.00	2.15	9.38
5JO5.PDB	O, C.SER_52A	N, C.GLY_55	H, C.GLY_55	2.78	2.00	20.47
5JO5.PDB	O, C.VAL_48	N, C.ALA_60	H, C.ALA_60	2.89	2.04	7.94
5JO5.PDB	O, C.VAL_63	N, C.ARG_66	H, C.ARG_66	2.93	2.09	10.54
5JO5.PDB	OD2, C.ASP_86	NH1, C.ARG_66	HH12, C.ARG_66	2.83	2.01	15.29
5JO5.PDB	O, C.PRO_62	NH2, C.ARG_66	HH21, C.ARG_66	2.87	2.02	7.14
5JO5.PDB	O, C.GLN_81	N, C.THR_68	H, C.THR_68	2.82	2.00	14.42
5JO5.PDB	OH, C.TYR_59	N, C.ILE_69	H, C.ILE_69	2.82	1.97	9.17
5JO5.PDB	OD1, C.ASP_73	NE, C.ARG_71	HE, C.ARG_71	2.90	2.12	21.25
5JO5.PDB	O, C.ALA_32	NH1, C.ARG_71	HH12, C.ARG_71	2.94	2.19	24.89
5JO5.PDB	O, C.ALA_32	NH2, C.ARG_71	HH22, C.ARG_71	2.89	2.13	22.77
5JO5.PDB	O, C.THR_77	N, C.ASP_72	H, C.ASP_72	2.91	2.06	7.23
5JO5.PDB	OD1, C.ASP_72	OG, C.SER_74	HG, C.SER_74	2.61	1.84	20.06
5JO5.PDB	O, C.CYS_22	N, C.LEU_78	H, C.LEU_78	2.88	2.05	11.40
5JO5.PDB	O, C.SER_70	N, C.TYR_79	H, C.TYR_79	2.85	2.00	9.09
5JO5.PDB	O, C.THR_68	N, C.GLN_81	H, C.GLN_81	2.76	1.93	12.88
5JO5.PDB	OD2, C.ASP_86	N, C.LYS_83	H, C.LYS_83	2.79	1.97	14.63
5JO5.PDB	O, C.LYS_83	N, C.ASP_86	H, C.ASP_86	2.83	2.00	13.05
5JO5.PDB	O, C.VAL_109	N, C.ALA_88	H, C.ALA_88	2.97	2.19	21.73
5JO5.PDB	O, C.GLN_39	N, C.VAL_89	H, C.VAL_89	2.92	2.12	17.72
5JO5.PDB	O, C.THR_107	N, C.TYR_90	H, C.TYR_90	2.82	1.97	9.30
5JO5.PDB	O, C.ASP_86	OH, C.TYR_90	HH, C.TYR_90	2.68	1.88	13.76
5JO5.PDB	O, C.VAL_37	N, C.TYR_91	H, C.TYR_91	2.60	1.74	2.45
5JO5.PDB	OE2, C.GLU_6	N, C.CYS_92	H, C.CYS_92	2.75	1.90	6.95
5JO5.PDB	O, C.SER_35	N, C.ALA_93	H, C.ALA_93	2.91	2.13	21.34
5JO5.PDB	OD2, C.ASP_102	NE, C.ARG_94	HE, C.ARG_94	2.79	2.08	28.98
5JO5.PDB	OD2, C.ASP_102	NH1, C.ARG_94	HH11, C.ARG_94	2.55	1.78	21.18
5JO5.PDB	O, C.TYR_100K	N, C.GLY_96	H, C.GLY_96	2.82	2.05	21.49
5JO5.PDB	O, C.GLU_100I	N, C.TYR_98	H, C.TYR_98	2.79	1.95	9.02
5JO5.PDB	O, C.GLY_96	N, C.TYR_100K	H, C.TYR_100K	2.91	2.11	17.91
5JO5.PDB	OH, D.TYR_36	N, C.PHE_100L	H, C.PHE_100L	2.87	2.08	19.05
5JO5.PDB	O, C.ARG_94	N, C.GLN_101	H, C.GLN_101	2.81	2.06	25.18
5JO5.PDB	O, C.CYS_92	N, C.GLY_104	H, C.GLY_104	2.86	2.05	16.43
5JO5.PDB	OE1, C.GLU_6	N, C.ARG_105	H, C.ARG_105	2.82	2.06	23.52
5JO5.PDB	OE1, C.GLU_6	N, C.GLY_106	H, C.GLY_106	2.82	1.96	3.31
5JO5.PDB	O, C.ALA_88	N, C.VAL_109	H, C.VAL_109	2.90	2.04	2.47
5JO5.PDB	OG1, C.THR_87	N, C.VAL_111	H, C.VAL_111	2.92	2.08	9.87

5JO5.PDB	O, C_PHE.146	N, C_LYS.117	H, C_LYS.117	2.76	1.94	13.75
5JO5.PDB	O, C_ASP.144	NZ, C_LYS.117	HZ2, C_LYS.117	2.78	2.05	29.84
5JO5.PDB	O, C_LEU.141	N, C_PHE.122	H, C_PHE.122	2.86	2.03	12.84
5JO5.PDB	O, C_GLY.139	N, C_LEU.124	H, C_LEU.124	2.85	2.00	9.59
5JO5.PDB	O, C_VAL.184	N, C_ALA.136	H, C_ALA.136	2.67	1.87	17.12
5JO5.PDB	O, C_VAL.182	N, C_LEU.138	H, C_LEU.138	2.99	2.15	10.96
5JO5.PDB	O, C_SER.180	N, C_CYS.140	H, C_CYS.140	2.84	2.06	20.26
5JO5.PDB	O, C_PHE.122	N, C_LEU.141	H, C_LEU.141	2.78	1.93	7.78
5JO5.PDB	O, C_LEU.178	N, C_VAL.142	H, C_VAL.142	2.81	1.96	6.47
5JO5.PDB	O, C_SER.120	N, C_LYS.143	H, C_LYS.143	2.82	1.98	11.11
5JO5.PDB	OE2, D_GLU.124	NZ, C_LYS.143	HZ2, C_LYS.143	2.79	1.92	10.71
5JO5.PDB	O, C_TYR.176	N, C_TYR.145	H, C_TYR.145	2.94	2.13	17.07
5JO5.PDB	O, C_LYS.117	N, C_PHE.146	H, C_PHE.146	2.94	2.13	16.66
5JO5.PDB	OD1, C_ASN.197	OG, C_SER.153	HG, C_SER.153	2.81	2.01	15.61
5JO5.PDB	OG, C_SER.180	NE1, C_TRP.154	HE1, C_TRP.154	2.96	2.13	11.76
5JO5.PDB	O, C_ILE.195	N, C_ASN.155	H, C_ASN.155	2.75	1.92	12.18
5JO5.PDB	OD1, C_ASN.197	N, C_SER.156	H, C_SER.156	2.79	1.97	14.38
5JO5.PDB	O, C_VAL.181	N, C_HIS.164	H, C_HIS.164	2.89	2.06	13.61
5JO5.PDB	O, C_SER.179	N, C_PHE.166	H, C_PHE.166	2.91	2.06	6.29
5JO5.PDB	OD1, C_ASP.144	NE2, C_GLN.171	HE22, C_GLN.171	2.92	2.12	18.22
5JO5.PDB	O, C_GLN.171	N, C_GLY.174	H, C_GLY.174	2.78	1.92	5.07
5JO5.PDB	O, C_TYR.145	N, C_TYR.176	H, C_TYR.176	2.90	2.05	5.55
5JO5.PDB	O, C_VAL.142	N, C_LEU.178	H, C_LEU.178	2.87	2.09	20.32
5JO5.PDB	OH, D_TYR.177	OG, C_SER.179	HG, C_SER.179	2.71	1.97	23.23
5JO5.PDB	O, C_HIS.164	N, C_VAL.181	H, C_VAL.181	2.89	2.06	14.17
5JO5.PDB	O, C_LEU.138	N, C_VAL.182	H, C_VAL.182	2.77	1.94	12.20
5JO5.PDB	O, C_ALA.136	N, C_VAL.184	H, C_VAL.184	2.81	1.98	13.68
5JO5.PDB	O, C_GLY.134	N, C_SER.186	H, C_SER.186	2.64	1.80	9.61
5JO5.PDB	O, C_PRO.185	OG, C_SER.188	HG, C_SER.188	2.73	1.93	15.82
5JO5.PDB	OG, C_SER.188	OH, C_TYR.194	HH, C_TYR.194	2.62	1.86	20.70
5JO5.PDB	OD1, C_ASN.155	N, C_ILE.195	H, C_ILE.195	2.85	2.02	13.84
5JO5.PDB	O, C_LYS.209	N, C_CYS.196	H, C_CYS.196	2.96	2.18	21.34
5JO5.PDB	O, C_SER.153	N, C_ASN.197	H, C_ASN.197	2.74	1.89	6.97
5JO5.PDB	OD1, C_ASP.208	ND2, C_ASN.197	HD22, C_ASN.197	2.98	2.12	6.27
5JO5.PDB	O, C_VAL.207	N, C_VAL.198	H, C_VAL.198	2.78	1.92	1.89
5JO5.PDB	OG, C_SER.203	ND1, C_HIS.200	HD1, C_HIS.200	2.85	2.10	24.59
5JO5.PDB	O, C_PRO.147	NE2, C_HIS.200	HE2, C_HIS.200	2.76	1.92	8.00
5JO5.PDB	O, C_LYS.201	N, C_ASN.204	H, C_ASN.204	2.96	2.12	10.38
5JO5.PDB	O, C_SER.203	OG1, C_THR.205	HG1, C_THR.205	2.94	2.25	29.40
5JO5.PDB	O, C_VAL.198	N, C_VAL.207	H, C_VAL.207	2.82	2.00	14.71
5JO5.PDB	O, C_CYS.196	N, C_LYS.209	H, C_LYS.209	3.00	2.20	18.19
5JO5.PDB	OE2, D_GLU.123	NZ, C_LYS.209	HZ1, C_LYS.209	2.58	1.72	11.28
5JO5.PDB	O, C_TYR.194	N, C_VAL.211	H, C_VAL.211	2.92	2.08	10.11
5JO5.PDB	O, D_LEU.4	OG, D_SER.2	HG, D_SER.2	2.63	1.95	29.82
5JO5.PDB	O, D_GLN.24	N, D_THR.5	H, D_THR.5	2.84	2.03	16.14
5JO5.PDB	O, D_TYR.86	NE2, D_GLN.6	HE22, D_GLN.6	3.00	2.19	16.22
5JO5.PDB	O, D_LYS.103	N, D_VAL.11	H, D_VAL.11	2.98	2.16	13.76
5JO5.PDB	O, D_THR.105	N, D_VAL.13	H, D_VAL.13	2.89	2.13	23.23
5JO5.PDB	O, D_ALA.78	N, D_GLY.16	H, D_GLY.16	2.84	1.98	3.58
5JO5.PDB	O, D_ILE.75	N, D_VAL.19	H, D_VAL.19	2.97	2.17	17.08
5JO5.PDB	O, D_LEU.73	N, D_ILE.21	H, D_ILE.21	2.92	2.07	8.03
5JO5.PDB	O, D_ALA.71	N, D_CYS.23	H, D_CYS.23	2.70	1.92	20.84
5JO5.PDB	O, D_THR.5	N, D_GLN.24	H, D_GLN.24	2.92	2.17	25.43
5JO5.PDB	O, D_ASN.69	N, D_GLY.25	H, D_GLY.25	2.96	2.12	12.19
5JO5.PDB	O, D_ARG.91	OG, D_SER.27	HG, D_SER.27	2.66	1.91	22.45
5JO5.PDB	O, D_GLY.25	N, D_LEU.28	H, D_LEU.28	2.92	2.11	17.85
5JO5.PDB	O, D_SER.27	N, D_SER.30	H, D_SER.30	2.96	2.14	14.55
5JO5.PDB	O, D_SER.89	N, D_SER.34	H, D_SER.34	2.92	2.12	18.05

5JO5.PDB	O, D_ILE_48	N, D_TRP_35	H, D_TRP_35	2.78	1.99	19.58
5JO5.PDB	O, D_TYR_87	N, D_TYR_36	H, D_TYR_36	2.78	2.03	24.47
5JO5.PDB	OG, D_SER_34	OH, D_TYR_36	HH, D_TYR_36	2.76	2.07	29.85
5JO5.PDB	O, D_VAL_45	N, D_GLN_37	H, D_GLN_37	2.86	2.04	14.87
5JO5.PDB	OH, D_TYR_86	NE2, D_GLN_37	HE21, D_GLN_37	2.93	2.09	8.87
5JO5.PDB	O, D_ASP_85	N, D_GLN_38	H, D_GLN_38	2.81	2.02	20.05
5JO5.PDB	OE1, C_GLN_39	NE2, D_GLN_38	HE22, D_GLN_38	2.92	2.09	12.72
5JO5.PDB	O, D_GLN_37	N, D_VAL_45	H, D_VAL_45	2.80	2.03	21.65
5JO5.PDB	O, D_TRP_35	N, D_VAL_47	H, D_VAL_47	2.89	2.03	2.23
5JO5.PDB	O, D_ASN_53	N, D_TYR_49	H, D_TYR_49	2.99	2.18	15.70
5JO5.PDB	OD1, D_ASP_82	NH2, D_ARG_61	HH21, D_ARG_61	2.88	2.03	6.97
5JO5.PDB	O, D_THR_74	N, D_SER_63	H, D_SER_63	2.94	2.16	21.20
5JO5.PDB	OD1, D_ASN_52	N, D_GLY_64	H, D_GLY_64	2.96	2.14	14.40
5JO5.PDB	O, D_SER_72	N, D_SER_65	H, D_SER_65	2.95	2.18	22.43
5JO5.PDB	O, L_ARG_29	ND2, D_ASN_69	HD21, D_ASN_69	2.86	2.03	13.06
5JO5.PDB	O, D_SER_67	N, D_THR_70	H, D_THR_70	2.94	2.12	15.68
5JO5.PDB	O, D_SER_67	OG1, D_THR_70	HG1, D_THR_70	2.67	1.87	14.98
5JO5.PDB	O, D_CYS_23	N, D_ALA_71	H, D_ALA_71	2.75	1.94	16.72
5JO5.PDB	O, D_SER_65	N, D_SER_72	H, D_SER_72	2.85	2.02	12.10
5JO5.PDB	O, D_ILE_21	N, D_LEU_73	H, D_LEU_73	2.82	2.05	22.07
5JO5.PDB	O, D_SER_63	N, D_THR_74	H, D_THR_74	2.79	1.94	10.27
5JO5.PDB	O, D_VAL_19	N, D_ILE_75	H, D_ILE_75	2.89	2.06	12.55
5JO5.PDB	O, D_GLN_17	N, D_ALA_78	H, D_ALA_78	2.90	2.06	11.54
5JO5.PDB	OD2, D_ASP_82	N, D_GLN_79	H, D_GLN_79	2.86	2.00	5.70
5JO5.PDB	O, D_GLN_79	N, D_ASP_82	H, D_ASP_82	2.84	2.00	10.08
5JO5.PDB	O, D_GLN_38	N, D_ASP_85	H, D_ASP_85	2.92	2.10	13.46
5JO5.PDB	O, D_THR_102	N, D_TYR_86	H, D_TYR_86	2.83	2.01	15.81
5JO5.PDB	O, D_ASP_82	OH, D_TYR_86	HH, D_TYR_86	2.68	1.86	10.68
5JO5.PDB	O, D_TYR_36	N, D_TYR_87	H, D_TYR_87	2.93	2.13	17.76
5JO5.PDB	O, D_SER_34	N, D_SER_89	H, D_SER_89	2.89	2.16	27.05
5JO5.PDB	O, D_VAL_97	OG, D_SER_89	HG, D_SER_89	2.81	2.05	20.40
5JO5.PDB	OH, D_TYR_31	N, D_GLY_95	H, D_GLY_95	2.87	2.05	14.54
5JO5.PDB	OD1, D_ASP_92	OG, D_SER_95A	HG, D_SER_95A	2.53	1.74	15.88
5JO5.PDB	OD1, C_ASP_58	NE, D_ARG_95B	HE, D_ARG_95B	2.94	2.10	11.64
5JO5.PDB	OG, D_SER_95A	N, D_LEU_95C	H, D_LEU_95C	2.96	2.11	7.06
5JO5.PDB	O, D_SER_90	N, D_VAL_97	H, D_VAL_97	2.96	2.13	12.85
5JO5.PDB	O, D_CYS_88	N, D_GLY_99	H, D_GLY_99	2.87	2.08	18.28
5JO5.PDB	O, D_TYR_86	N, D_THR_102	H, D_THR_102	2.86	2.06	18.86
5JO5.PDB	O, D_ASP_7	OG1, D_THR_102	HG1, D_THR_102	2.66	1.83	6.75
5JO5.PDB	O, D_PRO_8	N, D_LYS_103	H, D_LYS_103	2.88	2.03	8.03
5JO5.PDB	O, D_ALA_84	N, D_LEU_104	H, D_LEU_104	2.86	2.02	9.74
5JO5.PDB	O, D_VAL_11	N, D_THR_105	H, D_THR_105	2.94	2.13	15.68
5JO5.PDB	OE2, D_GLU_83	N, D_VAL_106	H, D_VAL_106	2.99	2.26	27.16
5JO5.PDB	O, D_VAL_13	N, D_LEU_106A	H, D_LEU_106A	2.85	2.03	13.72
5JO5.PDB	OH, D_TYR_140	N, D_SER_107	H, D_SER_107	2.99	2.19	18.62
5JO5.PDB	O, D_TYR_140	N, D_ALA_111	H, D_ALA_111	2.83	2.00	12.24
5JO5.PDB	O, D_SER_137	N, D_SER_114	H, D_SER_114	2.93	2.12	17.17
5JO5.PDB	O, D_LEU_135	N, D_THR_116	H, D_THR_116	2.99	2.15	12.62
5JO5.PDB	O, D_VAL_133	N, D_PHE_118	H, D_PHE_118	2.76	1.91	6.01
5JO5.PDB	O, D_LEU_125	N, D_ASN_128	H, D_ASN_128	3.00	2.17	13.92
5JO5.PDB	OE1, D_GLU_124	N, D_THR_131	H, D_THR_131	2.94	2.20	26.30
5JO5.PDB	OE2, D_GLU_124	OG1, D_THR_131	HG1, D_THR_131	2.53	1.79	22.99
5JO5.PDB	O, D_LEU_178	N, D_LEU_132	H, D_LEU_132	2.92	2.11	16.22
5JO5.PDB	O, D_SER_176	N, D_CYS_134	H, D_CYS_134	2.87	2.02	3.73
5JO5.PDB	O, D_THR_116	N, D_LEU_135	H, D_LEU_135	2.89	2.05	10.60
5JO5.PDB	O, D_ALA_174	N, D_ILE_136	H, D_ILE_136	2.85	2.08	22.19
5JO5.PDB	O, D_SER_114	N, D_SER_137	H, D_SER_137	2.94	2.16	20.21
5JO5.PDB	OE1, D_GLN_167	N, D_ASP_138	H, D_ASP_138	2.90	2.13	21.66

5JO5.PDB	O, D_ALA_111	N, D_TYR_140	H, D_TYR_140	2.95	2.14	16.49
5JO5.PDB	O, D_PRO_141	N, D_ALA_143	H, D_ALA_143	2.91	2.20	29.22
5JO5.PDB	O, D_GLN_194	N, D_ALA_147	H, D_ALA_147	2.87	2.05	14.86
5JO5.PDB	OG, D_SER_176	NE1, D_TRP_148	HE1, D_TRP_148	2.85	2.01	9.98
5JO5.PDB	O, D_SER_153	N, D_ALA_150	H, D_ALA_150	2.82	2.02	17.16
5JO5.PDB	O, D_SER_190	N, D_ASP_151	H, D_ASP_151	2.91	2.08	10.80
5JO5.PDB	O, D_ALA_150	N, D_SER_153	H, D_SER_153	2.91	2.07	9.74
5JO5.PDB	O, D_TYR_177	N, D_GLU_160	H, D_GLU_160	2.99	2.19	18.70
5JO5.PDB	O, D_SER_175	N, D_THR_162	H, D_THR_162	2.86	2.03	12.76
5JO5.PDB	O, C_GLY_42	OG1, D_THR_163	HG1, D_THR_163	2.56	1.81	22.64
5JO5.PDB	O, D_LYS_171	N, D_GLN_167	H, D_GLN_167	2.61	1.77	8.91
5JO5.PDB	OD1, D_ASN_169	NE2, D_GLN_167	HE21, D_GLN_167	2.91	2.12	19.40
5JO5.PDB	OD1, D_ASP_138	NE2, D_GLN_167	HE22, D_GLN_167	2.88	2.03	6.31
5JO5.PDB	O, D_GLN_167	N, D_ASN_170	H, D_ASN_170	2.90	2.07	12.77
5JO5.PDB	O, D_PHE_139	N, D_TYR_172	H, D_TYR_172	2.94	2.13	17.51
5JO5.PDB	O, D_ILE_136	N, D_ALA_174	H, D_ALA_174	2.70	1.89	16.69
5JO5.PDB	OG1, D_THR_162	N, D_SER_175	H, D_SER_175	2.99	2.19	18.15
5JO5.PDB	O, D_CYS_134	N, D_SER_176	H, D_SER_176	2.88	2.10	20.17
5JO5.PDB	OG1, D_THR_161	OG, D_SER_176	HG, D_SER_176	2.78	2.01	20.04
5JO5.PDB	O, D_GLU_160	N, D_TYR_177	H, D_TYR_177	2.73	1.94	18.28
5JO5.PDB	O, D_LEU_132	N, D_LEU_178	H, D_LEU_178	3.00	2.17	13.80
5JO5.PDB	O, D_GLY_158	N, D_SER_179	H, D_SER_179	2.79	1.96	12.81
5JO5.PDB	O, D_ALA_130	N, D_LEU_180	H, D_LEU_180	2.83	1.97	3.34
5JO5.PDB	OD2, D_ASP_151	ND1, D_HIS_188	HD1, D_HIS_188	2.67	1.86	16.19
5JO5.PDB	O, D_VAL_206	N, D_TYR_191	H, D_TYR_191	2.99	2.16	11.55
5JO5.PDB	O, D_GLN_184	OH, D_TYR_191	HH, D_TYR_191	2.98	2.21	19.53
5JO5.PDB	O, D_LYS_149	N, D_SER_192	H, D_SER_192	2.91	2.12	19.04
5JO5.PDB	OG1, D_THR_205	OG, D_SER_192	HG, D_SER_192	2.76	2.06	27.74
5JO5.PDB	O, D_LYS_204	N, D_CYS_193	H, D_CYS_193	2.83	2.03	16.94
5JO5.PDB	O, D_ALA_147	N, D_GLN_194	H, D_GLN_194	2.79	1.95	9.12
5JO5.PDB	OE2, D_GLU_203	NE2, D_GLN_194	HE21, D_GLN_194	2.41	1.67	25.54
5JO5.PDB	O, D_VAL_202	N, D_VAL_195	H, D_VAL_195	2.84	2.00	11.51
5JO5.PDB	O, D_THR_145	N, D_THR_196	H, D_THR_196	2.90	2.05	9.26
5JO5.PDB	O, D_SER_200	N, D_HIS_197	H, D_HIS_197	2.74	1.91	13.29
5JO5.PDB	O, D_PRO_141	NE2, D_HIS_197	HE2, D_HIS_197	2.94	2.17	22.03
5JO5.PDB	O, D_HIS_197	N, D_SER_200	H, D_SER_200	2.99	2.14	6.86
5JO5.PDB	O, D_VAL_195	N, D_VAL_202	H, D_VAL_202	2.92	2.09	14.26
5JO5.PDB	O, D_TYR_191	N, D_VAL_206	H, D_VAL_206	2.89	2.07	14.82
5JO5.PDB	O, E_SER_25	N, E_GLN_3	H, E_GLN_3	2.86	2.02	10.81
5JO5.PDB	O, E_SER_21	N, E_SER_7	H, E_SER_7	2.79	2.01	21.43
5JO5.PDB	OG1, E_THR_107	N, E_GLY_9	H, E_GLY_9	2.94	2.20	26.14
5JO5.PDB	O, E_THR_110	N, E_VAL_12	H, E_VAL_12	2.91	2.13	20.76
5JO5.PDB	O, E_LEU_82C	N, E_GLY_15	H, E_GLY_15	2.84	2.01	12.49
5JO5.PDB	O, E_LYS_13	N, E_GLY_16	H, E_GLY_16	2.85	2.02	13.81
5JO5.PDB	O, E_MET_82	N, E_LEU_18	H, E_LEU_18	2.89	2.11	20.71
5JO5.PDB	O, E_LEU_80	N, E_LEU_20	H, E_LEU_20	2.82	1.97	8.28
5JO5.PDB	O, E_SER_7	N, E_SER_21	H, E_SER_21	2.95	2.12	12.48
5JO5.PDB	O, E_LEU_78	N, E_CYS_22	H, E_CYS_22	2.73	1.97	22.79
5JO5.PDB	O, E_ASN_76	N, E_ALA_24	H, E_ALA_24	2.94	2.16	21.70
5JO5.PDB	O, E_GLN_3	N, E_SER_25	H, E_SER_25	2.98	2.18	19.36
5JO5.PDB	OD2, E_ASP_53	NE1, E_TRP_33	HE1, E_TRP_33	2.89	2.14	24.08
5JO5.PDB	O, E_ALA_93	N, E_SER_35	H, E_SER_35	2.93	2.11	14.57
5JO5.PDB	OG1, E_THR_95	OG, E_SER_35	HG, E_SER_35	2.65	1.97	29.96
5JO5.PDB	O, E_GLY_49	N, E_TRP_36	H, E_TRP_36	2.88	2.07	17.60
5JO5.PDB	O, E_TYR_91	N, E_VAL_37	H, E_VAL_37	2.87	2.04	13.44
5JO5.PDB	O, E_GLU_46	N, E_ARG_38	H, E_ARG_38	2.86	2.02	8.76
5JO5.PDB	OE1, E_GLU_46	NE, E_ARG_38	HE, E_ARG_38	2.75	1.95	17.65
5JO5.PDB	OH, E_TYR_90	NH1, E_ARG_38	HH11, E_ARG_38	2.94	2.11	14.05

5JO5.PDB	OD1, E_ASP_86	NH1, E_ARG_38	HH12, E_ARG_38	2.82	2.00	15.16
5JO5.PDB	O, E_LYS_43	NE2, E_GLN_39	HE21, E_GLN_39	2.97	2.27	29.74
5JO5.PDB	OE1, F_GLN_38	NE2, E_GLN_39	HE22, E_GLN_39	2.90	2.06	10.70
5JO5.PDB	O, E_ALA_40	N, E_LYS_43	H, E_LYS_43	2.91	2.07	11.48
5JO5.PDB	O, E_ARG_38	N, E_GLU_46	H, E_GLU_46	2.82	2.03	20.58
5JO5.PDB	O, E_TRP_36	N, E_VAL_48	H, E_VAL_48	2.91	2.08	12.92
5JO5.PDB	OE1, E_GLU_100J	NE, E_ARG_50	HE, E_ARG_50	2.82	2.06	22.79
5JO5.PDB	OD2, E_ASP_58	NH1, E_ARG_50	HH12, E_ARG_50	2.78	1.94	10.17
5JO5.PDB	OE2, E_GLU_100J	NH2, E_ARG_50	HH21, E_ARG_50	2.98	2.13	7.82
5JO5.PDB	O, E_MET_34	N, E_ILE_51	H, E_ILE_51	2.82	1.99	12.16
5JO5.PDB	O, E_THR_56	N, E_LYS_52	H, E_LYS_52	2.88	2.06	15.44
5JO5.PDB	O, E_SER_52A	N, E_GLY_55	H, E_GLY_55	2.77	2.05	28.25
5JO5.PDB	O, E_VAL_48	N, E_ALA_60	H, E_ALA_60	2.92	2.07	6.71
5JO5.PDB	O, E_VAL_63	N, E_ARG_66	H, E_ARG_66	2.94	2.10	9.43
5JO5.PDB	OD2, E_ASP_86	NH1, E_ARG_66	HH12, E_ARG_66	2.75	1.91	9.04
5JO5.PDB	O, E_PRO_62	NH2, E_ARG_66	HH21, E_ARG_66	2.89	2.04	7.82
5JO5.PDB	O, E_GLN_81	N, E_THR_68	H, E_THR_68	2.78	1.96	15.96
5JO5.PDB	OH, E_TYR_59	N, E_ILE_69	H, E_ILE_69	2.86	2.02	8.94
5JO5.PDB	OD1, E_ASP_73	NE, E_ARG_71	HE, E_ARG_71	2.89	2.11	20.53
5JO5.PDB	O, E_ALA_32	NH1, E_ARG_71	HH12, E_ARG_71	2.87	2.12	24.62
5JO5.PDB	O, E_ALA_32	NH2, E_ARG_71	HH22, E_ARG_71	2.83	2.06	22.60
5JO5.PDB	O, E_THR_77	N, E_ASP_72	H, E_ASP_72	2.94	2.10	9.13
5JO5.PDB	OD1, E_ASP_72	OG, E_SER_74	HG, E_SER_74	2.60	1.77	6.90
5JO5.PDB	O, E_ASP_72	N, E_LYS_75	H, E_LYS_75	2.92	2.11	15.84
5JO5.PDB	O, E_LYS_75	OG1, E_THR_77	HG1, E_THR_77	2.87	2.06	11.81
5JO5.PDB	O, E_CYS_22	N, E_LEU_78	H, E_LEU_78	2.84	2.01	12.18
5JO5.PDB	O, E_SER_70	N, E_TYR_79	H, E_TYR_79	2.79	1.96	14.25
5JO5.PDB	O, E_LEU_20	N, E_LEU_80	H, E_LEU_80	2.96	2.14	14.05
5JO5.PDB	O, E_THR_68	N, E_GLN_81	H, E_GLN_81	2.80	1.97	12.32
5JO5.PDB	O, E_LEU_18	N, E_MET_82	H, E_MET_82	2.73	1.87	5.04
5JO5.PDB	O, E_ARG_66	N, E_ASN_82A	H, E_ASN_82A	2.93	2.10	12.92
5JO5.PDB	OD2, E_ASP_86	N, E_LYS_83	H, E_LYS_83	2.87	2.04	12.63
5JO5.PDB	O, E_LYS_83	N, E_ASP_86	H, E_ASP_86	2.88	2.03	9.99
5JO5.PDB	O, E_VAL_109	N, E_ALA_88	H, E_ALA_88	3.00	2.22	22.40
5JO5.PDB	O, E_GLN_39	N, E_VAL_89	H, E_VAL_89	2.94	2.14	17.80
5JO5.PDB	O, E_THR_107	N, E_TYR_90	H, E_TYR_90	2.81	1.97	10.34
5JO5.PDB	O, E_ASP_86	OH, E_TYR_90	HH, E_TYR_90	2.76	1.94	9.78
5JO5.PDB	O, E_VAL_37	N, E_TYR_91	H, E_TYR_91	2.62	1.76	3.70
5JO5.PDB	OE2, E_GLU_6	N, E_CYS_92	H, E_CYS_92	2.83	2.01	14.83
5JO5.PDB	O, E_SER_35	N, E_ALA_93	H, E_ALA_93	2.90	2.13	22.60
5JO5.PDB	OD2, E_ASP_102	NE, E_ARG_94	HE, E_ARG_94	2.83	2.08	25.07
5JO5.PDB	OD2, E_ASP_102	NH2, E_ARG_94	HH21, E_ARG_94	2.73	1.97	23.25
5JO5.PDB	O, E_TRP_33	N, E_THR_95	H, E_THR_95	2.81	1.99	14.28
5JO5.PDB	O, E_TYR_100K	N, E_GLY_96	H, E_GLY_96	2.75	2.03	27.94
5JO5.PDB	O, E_GLY_96	N, E_TYR_100K	H, E_TYR_100K	2.92	2.10	14.59
5JO5.PDB	OH, F_TYR_36	N, E_PHE_100L	H, E_PHE_100L	2.79	1.96	13.04
5JO5.PDB	O, E_ARG_94	N, E_GLN_101	H, E_GLN_101	2.75	2.03	27.51
5JO5.PDB	O, F_GLY_41	NH2, E_ARG_105	HH22, E_ARG_105	2.92	2.13	19.96
5JO5.PDB	OE1, E_GLU_6	N, E_GLY_106	H, E_GLY_106	2.88	2.02	0.89
5JO5.PDB	O, E_ALA_88	N, E_VAL_109	H, E_VAL_109	2.88	2.03	1.87
5JO5.PDB	OG1, E_THR_87	N, E_VAL_111	H, E_VAL_111	2.92	2.06	5.86
5JO5.PDB	O, E_VAL_12	N, E_SER_112	H, E_SER_112	2.97	2.21	23.58
5JO5.PDB	O, E_PHE_146	N, E_LYS_117	H, E_LYS_117	2.75	1.93	13.93
5JO5.PDB	O, E_ASP_144	NZ, E_LYS_117	HZ2, E_LYS_117	2.91	2.14	25.25
5JO5.PDB	O, E_LEU_141	N, E_PHE_122	H, E_PHE_122	2.90	2.08	14.62
5JO5.PDB	O, E_GLY_139	N, E_LEU_124	H, E_LEU_124	2.87	2.02	7.60
5JO5.PDB	O, E_VAL_184	N, E_ALA_136	H, E_ALA_136	2.71	1.90	16.68
5JO5.PDB	O, E_LEU_124	N, E_GLY_139	H, E_GLY_139	2.98	2.20	21.04

5JO5.PDB	O, E_SER.180	N, E_CYS.140	H, E_CYS.140	2.80	2.01	20.63
5JO5.PDB	O, E_PHE.122	N, E_LEU.141	H, E_LEU.141	2.82	1.97	5.54
5JO5.PDB	O, E_LEU.178	N, E_VAL.142	H, E_VAL.142	2.80	1.95	6.99
5JO5.PDB	O, E_SER.120	N, E_LYS.143	H, E_LYS.143	2.77	1.93	10.34
5JO5.PDB	OE2, F_GLU.124	NZ, E_LYS.143	HZ2, E_LYS.143	2.55	1.75	21.57
5JO5.PDB	O, E_TYR.176	N, E_TYR.145	H, E_TYR.145	2.90	2.11	20.23
5JO5.PDB	O, E_LYS.117	N, E_PHE.146	H, E_PHE.146	2.89	2.08	16.85
5JO5.PDB	O, E_ASN.197	N, E_SER.153	H, E_SER.153	2.97	2.16	17.92
5JO5.PDB	OD1, E_ASN.197	OG, E_SER.153	HG, E_SER.153	2.80	2.02	18.49
5JO5.PDB	OG, E_SER.180	NE1, E_TRP.154	HE1, E_TRP.154	2.96	2.13	12.27
5JO5.PDB	O, E_ILE.195	N, E_ASN.155	H, E_ASN.155	2.72	1.89	11.94
5JO5.PDB	OD1, E_ASN.197	N, E_SER.156	H, E_SER.156	2.66	1.84	15.32
5JO5.PDB	O, E_VAL.181	N, E_HIS.164	H, E_HIS.164	2.85	2.02	11.29
5JO5.PDB	O, E_SER.179	N, E_PHE.166	H, E_PHE.166	2.89	2.04	5.07
5JO5.PDB	O, E_SER.177	N, E_VAL.169	H, E_VAL.169	2.81	2.02	19.59
5JO5.PDB	OD1, E_ASP.144	NE2, E_GLN.171	HE22, E_GLN.171	2.83	2.02	16.42
5JO5.PDB	O, E_GLN.171	N, E_GLY.174	H, E_GLY.174	2.76	1.91	5.26
5JO5.PDB	O, E_TYR.145	N, E_TYR.176	H, E_TYR.176	2.86	2.00	3.93
5JO5.PDB	O, E_VAL.142	N, E_LEU.178	H, E_LEU.178	2.85	2.07	21.31
5JO5.PDB	OH, F_TYR.177	OG, E_SER.179	HG, E_SER.179	2.58	1.87	27.02
5JO5.PDB	O, E_CYS.140	N, E_SER.180	H, E_SER.180	2.98	2.17	15.74
5JO5.PDB	O, E_HIS.164	N, E_VAL.181	H, E_VAL.181	2.86	2.02	9.16
5JO5.PDB	O, E_LEU.138	N, E_VAL.182	H, E_VAL.182	2.76	1.93	11.92
5JO5.PDB	O, E_ALA.136	N, E_VAL.184	H, E_VAL.184	2.83	2.00	12.03
5JO5.PDB	O, E_GLY.134	N, E_SER.186	H, E_SER.186	2.88	2.03	8.01
5JO5.PDB	O, E_GLY.133	OG, E_SER.186	HG, E_SER.186	2.97	2.22	21.72
5JO5.PDB	O, E_PRO.185	N, E_SER.188	H, E_SER.188	2.97	2.20	23.16
5JO5.PDB	O, E_PRO.185	OG, E_SER.188	HG, E_SER.188	2.59	1.76	5.13
5JO5.PDB	O, E_SER.188	N, E_THR.191	H, E_THR.191	2.90	2.15	24.49
5JO5.PDB	O, E_SER.188	N, E_GLN.192	H, E_GLN.192	2.68	1.83	7.38
5JO5.PDB	OG, E_SER.188	OH, E_TYR.194	HH, E_TYR.194	2.65	1.91	23.44
5JO5.PDB	OD1, E_ASN.155	N, E_ILE.195	H, E_ILE.195	2.79	1.96	12.66
5JO5.PDB	O, E_LYS.209	N, E_CYS.196	H, E_CYS.196	2.95	2.16	19.80
5JO5.PDB	O, E_SER.153	N, E_ASN.197	H, E_ASN.197	2.69	1.84	6.11
5JO5.PDB	OD1, E_ASP.208	ND2, E_ASN.197	HD22, E_ASN.197	2.93	2.08	6.74
5JO5.PDB	O, E_VAL.207	N, E_VAL.198	H, E_VAL.198	2.75	1.89	4.70
5JO5.PDB	O, E_THR.151	N, E_ASN.199	H, E_ASN.199	2.87	2.02	5.85
5JO5.PDB	O, E_THR.205	N, E_HIS.200	H, E_HIS.200	2.87	2.01	4.48
5JO5.PDB	O, E_PRO.147	NE2, E_HIS.200	HE2, E_HIS.200	2.80	1.96	10.29
5JO5.PDB	O, E_LYS.201	N, E_ASN.204	H, E_ASN.204	2.97	2.13	10.21
5JO5.PDB	O, E_SER.203	OG1, E_THR.205	HG1, E_THR.205	2.99	2.30	29.09
5JO5.PDB	O, E_VAL.198	N, E_VAL.207	H, E_VAL.207	2.77	1.95	14.33
5JO5.PDB	OE2, F_GLU.123	NZ, E_LYS.209	HZ1, E_LYS.209	2.57	1.74	17.62
5JO5.PDB	O, E_TYR.194	N, E_VAL.211	H, E_VAL.211	2.91	2.07	9.99
5JO5.PDB	O, F_GLN.24	N, F_THR.5	H, F_THR.5	2.85	2.04	16.07
5JO5.PDB	O, F_TYR.86	NE2, F_GLN.6	HE22, F_GLN.6	2.95	2.11	10.68
5JO5.PDB	O, F_LYS.103	N, F_VAL.11	H, F_VAL.11	2.95	2.12	12.95
5JO5.PDB	O, F_THR.105	N, F_VAL.13	H, F_VAL.13	2.93	2.19	26.75
5JO5.PDB	O, F_ALA.78	N, F_GLY.16	H, F_GLY.16	2.88	2.02	3.27
5JO5.PDB	O, F_ALA.14	N, F_GLN.17	H, F_GLN.17	2.98	2.13	8.18
5JO5.PDB	O, F_ILE.75	N, F_VAL.19	H, F_VAL.19	2.97	2.17	17.62
5JO5.PDB	O, F_LEU.73	N, F_ILE.21	H, F_ILE.21	2.79	1.95	9.82
5JO5.PDB	O, F_ALA.71	N, F_CYS.23	H, F_CYS.23	2.65	1.81	10.82
5JO5.PDB	O, F_THR.5	N, F_GLN.24	H, F_GLN.24	2.96	2.22	25.96
5JO5.PDB	O, F_ASN.69	N, F_GLY.25	H, F_GLY.25	2.99	2.16	12.96
5JO5.PDB	O, F_ARG.91	OG, F_SER.27	HG, F_SER.27	2.61	1.83	18.13
5JO5.PDB	O, F_SER.27	N, F_SER.30	H, F_SER.30	2.99	2.17	15.08
5JO5.PDB	OE1, B_GLN.24	OG, F_SER.30	HG, F_SER.30	2.88	2.11	20.15

5JO5.PDB	O, F_SER.89	N, F_SER.34	H, F_SER.34	2.96	2.19	21.82
5JO5.PDB	O, F_ILE.48	N, F_TRP.35	H, F_TRP.35	2.86	2.07	19.30
5JO5.PDB	O, F_TYR.87	N, F_TYR.36	H, F_TYR.36	2.85	2.11	26.39
5JO5.PDB	O, F_VAL.45	N, F_GLN.37	H, F_GLN.37	2.90	2.07	14.11
5JO5.PDB	OH, F_TYR.86	NE2, F_GLN.37	HE21, F_GLN.37	2.98	2.12	5.01
5JO5.PDB	O, F_ASP.85	N, F_GLN.38	H, F_GLN.38	2.82	2.06	22.85
5JO5.PDB	OE1, E_GLN.39	NE2, F_GLN.38	HE22, F_GLN.38	2.85	2.02	12.75
5JO5.PDB	O, F_GLN.37	N, F_VAL.45	H, F_VAL.45	2.82	2.05	21.93
5JO5.PDB	OD2, F_ASP.82	NE, F_ARG.61	HE, F_ARG.61	2.99	2.15	12.18
5JO5.PDB	OD1, F_ASP.82	NH2, F_ARG.61	HH21, F_ARG.61	2.81	1.97	11.97
5JO5.PDB	O, F_THR.74	N, F_SER.63	H, F_SER.63	2.98	2.21	22.42
5JO5.PDB	OD1, F_ASN.52	N, F_GLY.64	H, F_GLY.64	2.75	1.92	12.61
5JO5.PDB	O, F_SER.72	N, F_SER.65	H, F_SER.65	2.99	2.19	19.46
5JO5.PDB	O, F_THR.70	N, F_SER.67	H, F_SER.67	2.97	2.14	12.81
5JO5.PDB	O, F_SER.67	N, F_THR.70	H, F_THR.70	2.94	2.14	18.28
5JO5.PDB	O, F_SER.67	OG1, F_THR.70	HG1, F_THR.70	2.69	1.87	11.09
5JO5.PDB	O, F_CYS.23	N, F_ALA.71	H, F_ALA.71	2.78	1.96	15.69
5JO5.PDB	O, F_SER.65	N, F_SER.72	H, F_SER.72	2.89	2.05	10.31
5JO5.PDB	O, F_ILE.21	N, F_LEU.73	H, F_LEU.73	2.79	1.97	15.26
5JO5.PDB	O, F_SER.63	N, F_THR.74	H, F_THR.74	2.85	2.00	6.83
5JO5.PDB	O, F_VAL.19	N, F_ILE.75	H, F_ILE.75	2.91	2.08	12.77
5JO5.PDB	O, F_GLN.17	N, F_ALA.78	H, F_ALA.78	2.92	2.08	9.70
5JO5.PDB	OD2, F_ASP.82	N, F_GLN.79	H, F_GLN.79	2.94	2.10	8.41
5JO5.PDB	O, F_GLN.79	N, F_ASP.82	H, F_ASP.82	2.82	1.98	9.27
5JO5.PDB	O, F_GLN.38	N, F_ASP.85	H, F_ASP.85	2.86	2.02	11.88
5JO5.PDB	O, F_THR.102	N, F_TYR.86	H, F_TYR.86	2.82	2.01	15.14
5JO5.PDB	O, F_ASP.82	OH, F_TYR.86	HH, F_TYR.86	2.63	1.82	11.29
5JO5.PDB	O, F_TYR.36	N, F_TYR.87	H, F_TYR.87	2.95	2.15	18.80
5JO5.PDB	O, F_SER.34	N, F_SER.89	H, F_SER.89	2.90	2.17	27.32
5JO5.PDB	O, F_VAL.97	OG, F_SER.89	HG, F_SER.89	2.78	2.02	20.17
5JO5.PDB	OE2, E_GLU.100J	NH2, F_ARG.91	HH22, F_ARG.91	2.72	1.87	5.99
5JO5.PDB	OH, F_TYR.31	N, F_GLY.95	H, F_GLY.95	2.74	1.89	6.32
5JO5.PDB	OD1, F_ASP.92	OG, F_SER.95A	HG, F_SER.95A	2.58	1.83	23.06
5JO5.PDB	OD1, E_ASP.58	NE, F_ARG.95B	HE, F_ARG.95B	2.92	2.09	12.47
5JO5.PDB	OG, F_SER.95A	N, F_LEU.95C	H, F_LEU.95C	2.90	2.05	9.93
5JO5.PDB	O, F_SER.90	N, F_VAL.97	H, F_VAL.97	2.91	2.09	15.13
5JO5.PDB	O, F_CYS.88	N, F_GLY.99	H, F_GLY.99	2.87	2.06	15.92
5JO5.PDB	OE1, F_GLN.6	N, F_GLY.101	H, F_GLY.101	2.94	2.16	20.91
5JO5.PDB	O, F_TYR.86	N, F_THR.102	H, F_THR.102	2.82	2.02	18.81
5JO5.PDB	O, F_ASP.7	OG1, F_THR.102	HG1, F_THR.102	2.62	1.78	2.80
5JO5.PDB	O, F_PRO.8	N, F_LYS.103	H, F_LYS.103	2.89	2.04	8.00
5JO5.PDB	O, F_ALA.84	N, F_LEU.104	H, F_LEU.104	2.87	2.02	9.37
5JO5.PDB	O, F_VAL.11	N, F_THR.105	H, F_THR.105	2.99	2.16	14.54
5JO5.PDB	OE2, F_GLU.83	N, F_VAL.106	H, F_VAL.106	3.00	2.24	24.21
5JO5.PDB	O, F_VAL.13	N, F_LEU.106A	H, F_LEU.106A	2.87	2.04	14.03
5JO5.PDB	OH, F_TYR.140	N, F_SER.107	H, F_SER.107	2.93	2.11	14.82
5JO5.PDB	OE1, F_GLU.198	NZ, F_LYS.110	HZ3, F_LYS.110	2.97	2.11	10.79
5JO5.PDB	O, F_TYR.140	N, F_ALA.111	H, F_ALA.111	2.81	1.99	13.38
5JO5.PDB	O, F_SER.137	N, F_SER.114	H, F_SER.114	2.87	2.06	17.12
5JO5.PDB	O, F_LEU.135	N, F_THR.116	H, F_THR.116	2.97	2.14	11.95
5JO5.PDB	O, F_VAL.133	N, F_PHE.118	H, F_PHE.118	2.79	1.95	9.20
5JO5.PDB	O, F_LEU.125	N, F_ASN.128	H, F_ASN.128	2.88	2.07	17.11
5JO5.PDB	OE1, F_GLU.124	N, F_THR.131	H, F_THR.131	2.94	2.22	28.54
5JO5.PDB	OE2, F_GLU.124	OG1, F_THR.131	HG1, F_THR.131	2.49	1.76	24.10
5JO5.PDB	O, F_LEU.178	N, F_LEU.132	H, F_LEU.132	2.91	2.08	13.23
5JO5.PDB	O, F_SER.176	N, F_CYS.134	H, F_CYS.134	2.83	1.97	3.69
5JO5.PDB	O, F_THR.116	N, F_LEU.135	H, F_LEU.135	2.88	2.04	11.11
5JO5.PDB	O, F_ALA.174	N, F_ILE.136	H, F_ILE.136	2.89	2.10	19.87

5JO5.PDB	O, F_SER_114	N, F_SER_137	H, F_SER_137	2.91	2.12	19.22
5JO5.PDB	OE1, F_GLN_167	N, F_ASP_138	H, F_ASP_138	2.81	2.05	22.81
5JO5.PDB	O, F_PRO_141	N, F_ALA_143	H, F_ALA_143	2.90	2.19	29.08
5JO5.PDB	O, F_GLN_194	N, F_ALA_147	H, F_ALA_147	2.81	1.99	13.22
5JO5.PDB	OG, F_SER_176	NE1, F_TRP_148	HE1, F_TRP_148	2.88	2.03	9.94
5JO5.PDB	O, F_SER_192	N, F_LYS_149	H, F_LYS_149	2.88	2.06	15.62
5JO5.PDB	O, F_SER_153	N, F_ALA_150	H, F_ALA_150	2.80	1.99	15.96
5JO5.PDB	O, F_SER_190	N, F_ASP_151	H, F_ASP_151	2.90	2.06	10.54
5JO5.PDB	O, F_TRP_148	N, F_VAL_155	H, F_VAL_155	2.94	2.14	18.31
5JO5.PDB	O, F_TYR_177	N, F_GLU_160	H, F_GLU_160	2.97	2.17	17.39
5JO5.PDB	O, F_SER_175	N, F_THR_162	H, F_THR_162	2.87	2.04	13.17
5JO5.PDB	O, E_GLY_42	OG1, F_THR_163	HG1, F_THR_163	2.55	1.80	22.10
5JO5.PDB	O, F_ALA_173	N, F_SER_165	H, F_SER_165	2.89	2.07	14.19
5JO5.PDB	O, F_LYS_171	N, F_GLN_167	H, F_GLN_167	2.66	1.81	8.80
5JO5.PDB	OD1, F_ASN_169	NE2, F_GLN_167	HE21, F_GLN_167	2.87	2.13	25.80
5JO5.PDB	OD1, F_ASP_138	NE2, F_GLN_167	HE22, F_GLN_167	2.86	2.01	8.07
5JO5.PDB	OD1, F_ASN_169	N, F_LYS_171	H, F_LYS_171	2.94	2.09	6.57
5JO5.PDB	O, F_PHE_139	N, F_TYR_172	H, F_TYR_172	2.89	2.07	14.51
5JO5.PDB	O, F_SER_165	N, F_ALA_173	H, F_ALA_173	2.87	2.08	18.80
5JO5.PDB	O, F_ILE_136	N, F_ALA_174	H, F_ALA_174	2.75	1.95	16.67
5JO5.PDB	O, F_CYS_134	N, F_SER_176	H, F_SER_176	2.88	2.10	19.67
5JO5.PDB	OG1, F_THR_161	OG, F_SER_176	HG, F_SER_176	2.84	2.06	17.97
5JO5.PDB	O, F_GLU_160	N, F_TYR_177	H, F_TYR_177	2.70	1.88	14.68
5JO5.PDB	O, F_LEU_132	N, F_LEU_178	H, F_LEU_178	2.95	2.12	12.77
5JO5.PDB	O, F_GLY_158	N, F_SER_179	H, F_SER_179	2.85	2.02	11.91
5JO5.PDB	O, F_ALA_130	N, F_LEU_180	H, F_LEU_180	2.77	1.91	5.50
5JO5.PDB	OE1, F_GLN_184	N, F_THR_181	H, F_THR_181	2.91	2.08	13.75
5JO5.PDB	OG1, F_THR_181	N, F_GLN_184	H, F_GLN_184	2.92	2.09	12.10
5JO5.PDB	O, F_THR_181	N, F_TRP_185	H, F_TRP_185	2.95	2.13	14.97
5JO5.PDB	O, F_GLN_184	OG, F_SER_187	HG, F_SER_187	2.92	2.14	19.66
5JO5.PDB	OD1, F_ASP_151	N, F_ARG_189	H, F_ARG_189	2.70	1.97	26.16
5JO5.PDB	O, F_VAL_206	N, F_TYR_191	H, F_TYR_191	2.98	2.14	9.84
5JO5.PDB	O, F_GLN_184	OH, F_TYR_191	HH, F_TYR_191	2.85	2.14	27.44
5JO5.PDB	O, F_LYS_149	N, F_SER_192	H, F_SER_192	2.93	2.14	18.88
5JO5.PDB	O, F_LYS_204	N, F_CYS_193	H, F_CYS_193	2.94	2.14	19.38
5JO5.PDB	O, F_ALA_147	N, F_GLN_194	H, F_GLN_194	2.69	1.84	5.08
5JO5.PDB	OE2, F_GLU_203	NE2, F_GLN_194	HE21, F_GLN_194	2.48	1.75	26.23
5JO5.PDB	O, F_VAL_202	N, F_VAL_195	H, F_VAL_195	2.88	2.05	13.06
5JO5.PDB	O, F_THR_145	N, F_THR_196	H, F_THR_196	2.95	2.10	7.48
5JO5.PDB	O, F_SER_200	N, F_HIS_197	H, F_HIS_197	2.74	1.91	11.69
5JO5.PDB	O, F_PRO_141	NE2, F_HIS_197	HE2, F_HIS_197	2.87	2.10	22.42
5JO5.PDB	O, F_HIS_197	N, F_SER_200	H, F_SER_200	2.97	2.13	8.27
5JO5.PDB	O, F_VAL_195	N, F_VAL_202	H, F_VAL_202	2.91	2.07	12.06
5JO5.PDB	O, F_TYR_191	N, F_VAL_206	H, F_VAL_206	2.91	2.09	15.37

Table 1702: 5JO5-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5JR1.PDB	O, H_SER_21	N, H_SER_7	H, H_SER_7	2.87	2.09	21.13
5JR1.PDB	O, H_THR_110	N, H_VAL_12	H, H_VAL_12	2.96	2.15	17.17
5JR1.PDB	O, H_LEU_82C	N, H_GLY_15	H, H_GLY_15	2.79	1.94	9.64
5JR1.PDB	O, H_LYS_13	N, H_GLY_16	H, H_GLY_16	2.88	2.07	16.51
5JR1.PDB	O, H_MET_82	N, H_LEU_18	H, H_LEU_18	2.78	2.00	19.93
5JR1.PDB	O, H_LEU_80	N, H_LEU_20	H, H_LEU_20	2.79	1.95	10.03
5JR1.PDB	O, H_LEU_78	N, H_CYS_22	H, H_CYS_22	2.73	2.00	26.48
5JR1.PDB	O, H_ASN_76	N, H_ALA_24	H, H_ALA_24	2.94	2.10	11.00
5JR1.PDB	O, H_PHE_29	N, H_ALA_32	H, H_ALA_32	2.90	2.05	7.28
5JR1.PDB	O, H_ALA_93	N, H_SER_35	H, H_SER_35	2.81	1.99	14.30
5JR1.PDB	O, H_GLY_49	N, H_TRP_36	H, H_TRP_36	2.95	2.15	18.51
5JR1.PDB	O, H_TYR_91	N, H_VAL_37	H, H_VAL_37	2.90	2.08	14.88
5JR1.PDB	O, H_GLU_46	N, H_ARG_38	H, H_ARG_38	2.79	1.96	12.39
5JR1.PDB	OE2, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.66	1.91	24.18
5JR1.PDB	OH, H_TYR_90	NH1, H_ARG_38	HH11, H_ARG_38	2.93	2.12	16.05
5JR1.PDB	OD1, H_ASP_86	NH1, H_ARG_38	HH12, H_ARG_38	2.94	2.11	12.77
5JR1.PDB	OE2, H_GLU_46	NH2, H_ARG_38	HH21, H_ARG_38	2.68	1.95	27.48
5JR1.PDB	O, H_VAL_89	N, H_GLN_39	H, H_GLN_39	2.80	2.04	23.21
5JR1.PDB	O, H_ALA_40	N, H_LYS_43	H, H_LYS_43	2.97	2.14	12.77
5JR1.PDB	O, H_TRP_36	N, H_VAL_48	H, H_VAL_48	2.78	1.94	10.30
5JR1.PDB	O, H_ASP_58	N, H_ARG_50	H, H_ARG_50	2.97	2.19	21.36
5JR1.PDB	O, H_MET_34	N, H_ILE_51	H, H_ILE_51	2.89	2.08	16.37
5JR1.PDB	O, H_THR_56	N, H_LYS_52	H, H_LYS_52	2.98	2.15	12.98
5JR1.PDB	OD1, H_ASP_53	N, H_GLY_54	H, H_GLY_54	2.21	1.48	25.64
5JR1.PDB	O, H_VAL_48	N, H_ALA_60	H, H_ALA_60	2.91	2.06	6.87
5JR1.PDB	OD2, H_ASP_86	NH1, H_ARG_66	HH12, H_ARG_66	2.72	1.87	9.50
5JR1.PDB	O, H_PRO_62	NH2, H_ARG_66	HH21, H_ARG_66	2.78	1.93	7.41
5JR1.PDB	O, H_GLN_81	N, H_THR_68	H, H_THR_68	2.82	2.01	16.76
5JR1.PDB	OH, H_TYR_59	N, H_ILE_69	H, H_ILE_69	2.78	1.93	7.40
5JR1.PDB	OD1, H_ASP_73	NE, H_ARG_71	HE, H_ARG_71	2.99	2.20	19.01
5JR1.PDB	O, H_ALA_32	NH1, H_ARG_71	HH12, H_ARG_71	2.98	2.22	23.48
5JR1.PDB	O, H_ALA_32	NH2, H_ARG_71	HH22, H_ARG_71	2.99	2.24	24.05
5JR1.PDB	O, H_THR_77	N, H_ASP_72	H, H_ASP_72	2.92	2.10	14.47
5JR1.PDB	OD1, H_ASP_72	OG, H_SER_74	HG, H_SER_74	2.50	1.70	14.47
5JR1.PDB	O, H_LYS_75	OG1, H_THR_77	HG1, H_THR_77	2.91	2.09	10.97
5JR1.PDB	O, H_CYS_22	N, H_LEU_78	H, H_LEU_78	2.87	2.04	11.82
5JR1.PDB	O, H_SER_70	N, H_TYR_79	H, H_TYR_79	2.85	2.00	9.75
5JR1.PDB	O, H_LEU_20	N, H_LEU_80	H, H_LEU_80	2.93	2.12	16.09
5JR1.PDB	O, H_THR_68	N, H_GLN_81	H, H_GLN_81	2.82	1.98	10.53
5JR1.PDB	O, H_LEU_18	N, H_MET_82	H, H_MET_82	2.76	1.92	9.12
5JR1.PDB	OD2, H_ASP_86	N, H_LYS_83	H, H_LYS_83	2.82	1.96	6.84
5JR1.PDB	O, H_LYS_83	N, H_ASP_86	H, H_ASP_86	2.64	1.79	6.68
5JR1.PDB	O, H_VAL_109	N, H_ALA_88	H, H_ALA_88	2.98	2.19	19.05
5JR1.PDB	O, H_GLN_39	N, H_VAL_89	H, H_VAL_89	2.83	2.04	19.63
5JR1.PDB	O, H_THR_107	N, H_TYR_90	H, H_TYR_90	2.85	2.00	7.31
5JR1.PDB	O, H_ASP_86	OH, H_TYR_90	HH, H_TYR_90	2.69	1.86	8.47
5JR1.PDB	O, H_VAL_37	N, H_TYR_91	H, H_TYR_91	2.66	1.80	1.80
5JR1.PDB	OE2, H_GLU_6	N, H_CYS_92	H, H_CYS_92	2.70	1.87	12.64
5JR1.PDB	O, H_SER_35	N, H_ALA_93	H, H_ALA_93	2.93	2.15	21.88
5JR1.PDB	O, H_ASP_102	N, H_ARG_94	H, H_ARG_94	2.91	2.18	27.54
5JR1.PDB	O, H_TRP_33	N, H_THR_95	H, H_THR_95	2.98	2.15	11.92
5JR1.PDB	O, H_TYR_100K	N, H_GLY_96	H, H_GLY_96	2.88	2.07	15.19
5JR1.PDB	O, H_GLU_100I	N, H_TYR_98	H, H_TYR_98	2.97	2.17	18.39
5JR1.PDB	O, H_TYR_98	N, H_GLU_100I	H, H_GLU_100I	2.76	1.96	17.68
5JR1.PDB	O, H_GLY_96	N, H_TYR_100K	H, H_TYR_100K	2.85	2.09	23.20
5JR1.PDB	OH, L_TYR_36	N, H_PHE_100L	H, H_PHE_100L	2.93	2.14	18.24
5JR1.PDB	O, H_ARG_94	N, H_GLN_101	H, H_GLN_101	2.77	2.05	27.74

5JR1.PDB	O, L_GLY_41	NH1, H_ARG_105	HH11, H_ARG_105	2.58	1.82	23.25
5JR1.PDB	OE1, H_GLU_6	N, H_GLY_106	H, H_GLY_106	2.84	2.01	12.28
5JR1.PDB	O, H_TYR_90	N, H_THR_107	H, H_THR_107	2.99	2.28	29.77
5JR1.PDB	O, H_ALA_88	N, H_VAL_109	H, H_VAL_109	2.92	2.07	7.11
5JR1.PDB	OG1, H_THR_87	N, H_BVAL_111	H, H_BVAL_111	3.00	2.15	5.58
5JR1.PDB	O, H_PHE_146	N, H_LYS_117	H, H_LYS_117	2.82	1.99	13.52
5JR1.PDB	O, H_ASP_144	NZ, H_LYS_117	HZ2, H_LYS_117	2.92	2.10	18.09
5JR1.PDB	O, H_LYS_143	N, H_SER_120	H, H_SER_120	2.94	2.13	15.86
5JR1.PDB	O, H_LEU_141	N, H_PHE_122	H, H_PHE_122	2.88	2.05	12.08
5JR1.PDB	O, H_GLY_139	N, H_LEU_124	H, H_LEU_124	2.79	1.94	8.07
5JR1.PDB	O, H_VAL_184	N, H_ALA_136	H, H_ALA_136	2.78	1.96	15.67
5JR1.PDB	O, H_LEU_124	N, H_GLY_139	H, H_GLY_139	2.92	2.11	16.29
5JR1.PDB	O, H_SER_180	N, H_CYS_140	H, H_CYS_140	2.94	2.15	19.79
5JR1.PDB	O, H_PHE_122	N, H_LEU_141	H, H_LEU_141	2.84	1.99	9.59
5JR1.PDB	O, H_LEU_178	N, H_VAL_142	H, H_VAL_142	2.76	1.90	4.75
5JR1.PDB	O, H_SER_120	N, H_LYS_143	H, H_LYS_143	2.77	1.93	8.90
5JR1.PDB	O, H_TYR_176	N, H_TYR_145	H, H_TYR_145	2.95	2.14	16.52
5JR1.PDB	O, H_LYS_117	N, H_PHE_146	H, H_PHE_146	2.89	2.08	16.28
5JR1.PDB	O, H_ASN_199	N, H_THR_151	H, H_THR_151	2.93	2.09	11.48
5JR1.PDB	O, H_ASN_197	N, H_SER_153	H, H_SER_153	2.90	2.09	17.08
5JR1.PDB	OD1, H_ASN_197	OG, H_SER_153	HG, H_SER_153	2.85	2.04	12.85
5JR1.PDB	OG, H_SER_180	NE1, H_TRP_154	HE1, H_TRP_154	2.87	2.02	7.55
5JR1.PDB	O, H_ILE_195	N, H_ASN_155	H, H_ASN_155	2.82	1.98	10.05
5JR1.PDB	OD1, H_ASN_197	N, H_SER_156	H, H_SER_156	2.76	1.96	17.23
5JR1.PDB	O, H_VAL_181	N, H_HIS_164	H, H_HIS_164	2.82	1.99	11.94
5JR1.PDB	O, H_SER_179	N, H_PHE_166	H, H_PHE_166	2.91	2.06	3.95
5JR1.PDB	O, H_SER_177	N, H_VAL_169	H, H_VAL_169	2.84	2.03	16.11
5JR1.PDB	O, H_LEU_175	N, H_GLN_171	H, H_GLN_171	2.92	2.06	5.15
5JR1.PDB	OD1, H_ASP_144	NE2, H_GLN_171	HE22, H_GLN_171	2.73	1.95	20.99
5JR1.PDB	O, H_GLN_171	N, H_GLY_174	H, H_GLY_174	2.88	2.05	12.35
5JR1.PDB	O, H_TYR_145	N, H_TYR_176	H, H_TYR_176	2.81	1.96	8.57
5JR1.PDB	OE1, H_GLN_171	OG, H_SER_177	HG, H_SER_177	2.71	1.98	25.79
5JR1.PDB	O, H_VAL_142	N, H_LEU_178	H, H_LEU_178	2.91	2.11	17.70
5JR1.PDB	OH, L_TYR_178	OG, H_SER_179	HG, H_SER_179	2.83	2.03	15.88
5JR1.PDB	O, H_HIS_164	N, H_VAL_181	H, H_VAL_181	2.79	1.96	12.10
5JR1.PDB	O, H_LEU_138	N, H_VAL_182	H, H_VAL_182	2.82	2.00	14.39
5JR1.PDB	O, H_ALA_136	N, H_VAL_184	H, H_VAL_184	2.80	1.97	12.21
5JR1.PDB	O, H_GLY_134	N, H_SER_186	H, H_SER_186	2.82	1.97	7.53
5JR1.PDB	O, H_PRO_185	OG, H_SER_188	HG, H_SER_188	2.70	1.86	3.21
5JR1.PDB	O, H_SER_188	N, H_GLN_192	H, H_GLN_192	2.88	2.04	10.77
5JR1.PDB	OG, H_SER_188	OH, H_TYR_194	HH, H_TYR_194	2.70	1.94	20.59
5JR1.PDB	OD1, H_ASN_155	N, H_ILE_195	H, H_ILE_195	2.86	2.03	13.39
5JR1.PDB	O, H_LYS_209	N, H_CYS_196	H, H_CYS_196	2.96	2.17	19.83
5JR1.PDB	O, H_SER_153	N, H_ASN_197	H, H_ASN_197	2.79	1.95	7.76
5JR1.PDB	O, H_VAL_207	N, H_VAL_198	H, H_VAL_198	2.80	1.97	13.81
5JR1.PDB	O, H_THR_151	N, H_ASN_199	H, H_ASN_199	2.88	2.05	14.08
5JR1.PDB	O, H_THR_205	N, H_HIS_200	H, H_HIS_200	2.87	2.03	10.85
5JR1.PDB	O, H_PRO_147	NE2, H_HIS_200	HE2, H_HIS_200	2.86	2.02	11.05
5JR1.PDB	O, H_LYS_201	N, H_ASN_204	H, H_ASN_204	2.97	2.13	9.90
5JR1.PDB	O, H_VAL_198	N, H_VAL_207	H, H_VAL_207	2.90	2.09	16.74
5JR1.PDB	O, H_CYS_196	N, H_LYS_209	H, H_LYS_209	2.83	2.04	19.23
5JR1.PDB	OE2, H_GLU_212	NE, H_BARG_210	HE, H_BARG_210	2.40	1.64	22.83
5JR1.PDB	O, H_TYR_194	N, H_VAL_211	H, H_VAL_211	2.98	2.15	13.77
5JR1.PDB	O, L_ARG_24	N, L_THR_5	H, L_THR_5	2.88	2.05	12.05
5JR1.PDB	O, L_TYR_86	NE2, L_GLN_6	HE22, L_GLN_6	2.95	2.16	19.38
5JR1.PDB	O, L_LYS_103	N, L_VAL_11	H, L_VAL_11	2.92	2.11	16.33
5JR1.PDB	O, L_ALA_78	N, L_GLY_16	H, L_GLY_16	2.86	2.01	7.27
5JR1.PDB	O, L_LEU_73	N, L_ILE_21	H, L_ILE_21	2.79	1.95	10.20

5JR1.PDB	O, L_ALA_71	N, L_CYS_23	H, L_CYS_23	2.79	1.94	9.36
5JR1.PDB	O, L_THR_5	N, L_ARG_24	H, L_ARG_24	2.91	2.12	20.30
5JR1.PDB	O, L_GLY_25	N, L_LEU_28	H, L_LEU_28	2.91	2.14	22.06
5JR1.PDB	O, L_SER_89	N, L_SER_34	H, L_SER_34	2.85	2.04	16.48
5JR1.PDB	O, L_PHE_48	N, L_TRP_35	H, L_TRP_35	2.89	2.09	17.65
5JR1.PDB	O, L_TYR_87	N, L_TYR_36	H, L_TYR_36	2.89	2.07	15.48
5JR1.PDB	N, H_PHE_100L	OH, L_TYR_36	HH, L_TYR_36	2.93	2.21	26.41
5JR1.PDB	O, L_ILE_45	N, L_GLN_37	H, L_GLN_37	2.91	2.11	18.13
5JR1.PDB	OH, L_TYR_86	NE2, L_GLN_37	HE21, L_GLN_37	2.92	2.08	10.60
5JR1.PDB	O, L_GLU_85	N, L_LYS_38	H, L_LYS_38	2.75	1.91	11.42
5JR1.PDB	O, L_GLN_37	N, L_ILE_45	H, L_ILE_45	2.81	1.99	14.72
5JR1.PDB	O, L_TRP_35	N, L_LEU_47	H, L_LEU_47	2.80	1.95	7.57
5JR1.PDB	O, L_ASN_53	N, L_TYR_49	H, L_TYR_49	2.89	2.10	19.62
5JR1.PDB	O, L_PHE_62	NE, L_ARG_54	HE, L_ARG_54	2.79	2.02	21.45
5JR1.PDB	O, L_PHE_62	NH2, L_ARG_54	HH21, L_ARG_54	2.91	2.19	28.02
5JR1.PDB	OD2, L_ASP_82	NE, L_ARG_61	HE, L_ARG_61	2.81	2.00	15.72
5JR1.PDB	OD1, L_ASP_82	NH2, L_ARG_61	HH21, L_ARG_61	2.74	1.90	11.09
5JR1.PDB	O, L_THR_74	N, L_SER_63	H, L_SER_63	2.98	2.19	19.40
5JR1.PDB	O, L_SER_72	N, L_SER_65	H, L_SER_65	2.90	2.12	21.18
5JR1.PDB	O, L_SER_67	N, L_ARG_70	H, L_ARG_70	2.86	2.02	9.85
5JR1.PDB	O, L_CYS_23	N, L_ALA_71	H, L_ALA_71	2.91	2.10	16.23
5JR1.PDB	O, L_SER_65	N, L_SER_72	H, L_SER_72	2.84	2.01	12.34
5JR1.PDB	O, L_ILE_21	N, L_LEU_73	H, L_LEU_73	2.78	1.95	12.54
5JR1.PDB	O, L_SER_63	N, L_THR_74	H, L_THR_74	2.78	1.93	7.21
5JR1.PDB	OG1, L_THR_20	OG1, L_THR_74	HG1, L_THR_74	2.96	2.15	13.12
5JR1.PDB	O, L_VAL_19	N, L_ILE_75	H, L_ILE_75	2.80	1.99	13.64
5JR1.PDB	O, L_ARG_61	N, L_SER_76	H, L_SER_76	2.98	2.17	14.63
5JR1.PDB	O, L_ARG_17	N, L_ALA_78	H, L_ALA_78	2.83	2.04	17.38
5JR1.PDB	OD2, L_ASP_82	N, L_GLN_79	H, L_GLN_79	2.91	2.06	9.01
5JR1.PDB	O, L_GLN_79	N, L_ASP_82	H, L_ASP_82	2.90	2.05	8.33
5JR1.PDB	O, L_LYS_38	N, L_GLU_85	H, L_GLU_85	2.91	2.07	8.57
5JR1.PDB	O, L_THR_102	N, L_TYR_86	H, L_TYR_86	2.84	2.05	20.14
5JR1.PDB	O, L_ASP_82	OH, L_TYR_86	HH, L_TYR_86	2.65	1.82	8.64
5JR1.PDB	O, L_TYR_36	N, L_TYR_87	H, L_TYR_87	2.94	2.12	15.76
5JR1.PDB	O, L_VAL_97	OG, L_SER_89	HG, L_SER_89	2.81	2.07	23.50
5JR1.PDB	O, L_TYR_32	OG, L_SER_90	HG, L_SER_90	2.84	2.07	19.10
5JR1.PDB	O, L_SER_95A	NE, L_ARG_91	HE, L_ARG_91	2.92	2.13	19.73
5JR1.PDB	O, L_GLY_95	NH1, L_ARG_91	HH11, L_ARG_91	2.58	1.80	19.50
5JR1.PDB	O, H_PRO_100F	NH1, L_ARG_91	HH12, L_ARG_91	2.89	2.18	29.36
5JR1.PDB	O, H_PRO_100F	NH2, L_ARG_91	HH22, L_ARG_91	2.82	2.09	26.91
5JR1.PDB	O, L_LEU_95C	N, L_ASP_92	H, L_ASP_92	2.85	2.03	14.49
5JR1.PDB	OD2, L_ASP_92	N, L_SER_94	H, L_SER_94	2.66	1.84	13.82
5JR1.PDB	OD2, L_ASP_92	OG, L_SER_94	HG, L_SER_94	2.41	1.66	21.72
5JR1.PDB	O, L_ASP_92	N, L_GLY_95	H, L_GLY_95	2.95	2.09	5.43
5JR1.PDB	OD2, L_ASP_58	NH2, L_ARG_95B	HH22, L_ARG_95B	2.47	1.67	16.99
5JR1.PDB	O, L_SER_90	N, L_VAL_97	H, L_VAL_97	2.83	1.98	7.91
5JR1.PDB	O, L_CYS_88	N, L_GLY_99	H, L_GLY_99	2.88	2.08	16.95
5JR1.PDB	O, L_TYR_86	N, L_THR_102	H, L_THR_102	2.89	2.09	17.99
5JR1.PDB	O, L_GLU_7	OG1, L_THR_102	HG1, L_THR_102	2.75	1.92	9.86
5JR1.PDB	O, L_THR_8	N, L_LYS_103	H, L_LYS_103	2.87	2.02	7.49
5JR1.PDB	O, L_ALA_84	N, L_LEU_104	H, L_LEU_104	2.86	2.02	10.37
5JR1.PDB	O, L_VAL_11	N, L_THR_105	H, L_THR_105	2.95	2.12	13.22
5JR1.PDB	OD1, L_ASP_83	N, L_VAL_106	H, L_VAL_106	2.52	1.67	7.56
5JR1.PDB	O, L_VAL_13	N, L_LEU_106A	H, L_LEU_106A	2.86	2.04	13.99
5JR1.PDB	OH, L_TYR_141	N, L_SER_107	H, L_SER_107	2.98	2.19	19.63
5JR1.PDB	OE1, L_GLU_199	NZ, L_LYS_110	HZ3, L_LYS_110	2.77	1.91	11.53
5JR1.PDB	O, L_TYR_141	N, L_ALA_111	H, L_ALA_111	2.82	1.98	10.35
5JR1.PDB	O, L_SER_138	N, L_SER_114	H, L_SER_114	2.83	1.98	5.37

5JR1.PDB	O, L_LEU_136	N, L_THR_116	H, L_THR_116	2.93	2.12	15.66
5JR1.PDB	O, L_VAL_134	N, L_PHE_118	H, L_PHE_118	2.82	1.99	11.01
5JR1.PDB	O, L_SER_122	N, L_LEU_126	H, L_LEU_126	2.98	2.14	8.64
5JR1.PDB	O, L_LEU_126	N, L_ASN_129	H, L_ASN_129	2.85	2.04	16.99
5JR1.PDB	OE2, L_GLU_125	OG1, L_THR_132	HG1, L_THR_132	2.53	1.79	23.02
5JR1.PDB	O, L_LEU_179	N, L_LEU_133	H, L_LEU_133	2.87	2.06	17.19
5JR1.PDB	O, L_SER_177	N, L_CYS_135	H, L_CYS_135	2.87	2.01	4.08
5JR1.PDB	O, L_THR_116	N, L_LEU_136	H, L_LEU_136	2.82	1.96	6.02
5JR1.PDB	O, L_ALA_175	N, L_ILE_137	H, L_ILE_137	2.93	2.15	21.12
5JR1.PDB	O, L_SER_114	N, L_SER_138	H, L_SER_138	2.87	2.07	19.40
5JR1.PDB	OE1, L_GLN_168	N, L_ASP_139	H, L_ASP_139	2.93	2.12	16.63
5JR1.PDB	O, L_ALA_111	N, L_TYR_141	H, L_TYR_141	2.90	2.08	15.02
5JR1.PDB	O, L_GLN_195	N, L_ALA_148	H, L_ALA_148	2.93	2.11	16.11
5JR1.PDB	OG, L_SER_177	NE1, L_TRP_149	HE1, L_TRP_149	2.84	1.99	9.64
5JR1.PDB	O, L_SER_193	N, L_LYS_150	H, L_LYS_150	2.91	2.10	16.78
5JR1.PDB	OE1, L_GLN_195	NZ, L_LYS_150	HZ3, L_LYS_150	2.79	1.91	7.52
5JR1.PDB	O, L_SER_154	N, L_ALA_151	H, L_ALA_151	2.97	2.15	14.89
5JR1.PDB	O, L_ALA_151	N, L_SER_154	H, L_SER_154	2.85	2.01	8.48
5JR1.PDB	O, L_TRP_149	N, L_VAL_156	H, L_VAL_156	2.98	2.14	8.84
5JR1.PDB	O, L_TYR_178	N, L_GLU_161	H, L_GLU_161	2.96	2.15	17.71
5JR1.PDB	O, L_SER_176	N, L_THR_163	H, L_THR_163	2.91	2.08	11.01
5JR1.PDB	O, L_ALA_174	N, L_SER_166	H, L_SER_166	2.98	2.16	14.11
5JR1.PDB	O, L_LYS_172	N, L_GLN_168	H, L_GLN_168	2.54	1.68	1.19
5JR1.PDB	OD1, L_ASN_170	NE2, L_GLN_168	HE21, L_GLN_168	2.60	1.77	13.13
5JR1.PDB	OD1, L_ASP_139	NE2, L_GLN_168	HE22, L_GLN_168	2.73	1.87	5.77
5JR1.PDB	O, L_GLN_168	N, L_ASN_171	H, L_ASN_171	2.91	2.08	14.01
5JR1.PDB	O, L_PHE_140	N, L_TYR_173	H, L_TYR_173	2.88	2.05	13.43
5JR1.PDB	O, L_SER_166	N, L_ALA_174	H, L_ALA_174	2.94	2.15	19.09
5JR1.PDB	O, L_ILE_137	N, L_ALA_175	H, L_ALA_175	2.81	2.00	16.74
5JR1.PDB	O, L_CYS_135	N, L_SER_177	H, L_SER_177	2.92	2.12	17.27
5JR1.PDB	O, L_GLU_161	N, L_TYR_178	H, L_TYR_178	2.78	1.97	16.16
5JR1.PDB	O, L_LEU_133	N, L_LEU_179	H, L_LEU_179	2.98	2.17	15.29
5JR1.PDB	O, L_GLY_159	N, L_SER_180	H, L_SER_180	2.73	1.89	11.54
5JR1.PDB	O, L_ALA_131	N, L_LEU_181	H, L_LEU_181	2.95	2.10	6.67
5JR1.PDB	OE1, L_GLN_185	N, L_THR_182	H, L_THR_182	2.93	2.10	11.07
5JR1.PDB	OG1, L_THR_182	N, L_GLN_185	H, L_GLN_185	2.88	2.04	12.03
5JR1.PDB	O, L_THR_182	N, L_TRP_186	H, L_TRP_186	2.96	2.13	12.66
5JR1.PDB	O, L_VAL_207	N, L_TYR_192	H, L_TYR_192	2.92	2.08	9.44
5JR1.PDB	O, L_LYS_150	N, L_SER_193	H, L_SER_193	2.81	1.99	15.01
5JR1.PDB	O, L_LYS_205	N, L_CYS_194	H, L_CYS_194	2.96	2.17	19.17
5JR1.PDB	O, L_ALA_148	N, L_GLN_195	H, L_GLN_195	2.75	1.89	4.07
5JR1.PDB	OE2, L_GLU_204	NE2, L_GLN_195	HE21, L_GLN_195	2.95	2.12	11.81
5JR1.PDB	O, L_VAL_203	N, L_VAL_196	H, L_VAL_196	2.75	1.89	4.95
5JR1.PDB	O, L_THR_146	N, L_THR_197	H, L_THR_197	2.80	1.96	10.45
5JR1.PDB	O, L_SER_201	N, L_HIS_198	H, L_HIS_198	2.87	2.03	9.19
5JR1.PDB	O, L_PRO_142	NE2, L_HIS_198	HE2, L_HIS_198	2.88	2.11	21.70
5JR1.PDB	O, L_HIS_198	N, L_SER_201	H, L_SER_201	2.99	2.18	15.98
5JR1.PDB	OG1, L_THR_197	OG1, L_THR_202	HG1, L_THR_202	2.77	1.97	14.73
5JR1.PDB	O, L_VAL_196	N, L_VAL_203	H, L_VAL_203	2.77	1.92	8.70
5JR1.PDB	O, L_TYR_192	N, L_VAL_207	H, L_VAL_207	2.92	2.11	16.47

Table 1703: 5JR1-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5JUE.PDB	OG, L_SER_26	N, L_VAL_3	H, L_VAL_3	2.98	2.17	16.79
5JUE.PDB	O, L_ARG_24	N, L_THR_5	H, L_THR_5	2.79	1.95	8.65
5JUE.PDB	O, L_TYR_86	NE2, L_GLN_6	HE22, L_GLN_6	2.67	1.82	7.14
5JUE.PDB	O, L_LYS_103	N, L_LEU_11	H, L_LEU_11	2.83	2.02	15.60
5JUE.PDB	O, L_ASP_105	N, L_VAL_13	H, L_VAL_13	2.59	1.84	24.65
5JUE.PDB	O, L_VAL_78	N, L_GLY_16	H, L_GLY_16	2.91	2.08	13.41
5JUE.PDB	O, L_ILE_75	N, L_ALA_19	H, L_ALA_19	2.83	2.04	19.69
5JUE.PDB	O, L_LEU_73	N, L_ILE_21	H, L_ILE_21	2.80	1.97	12.30
5JUE.PDB	O, L_PHE_71	N, L_CYS_23	H, L_CYS_23	2.87	2.07	17.94
5JUE.PDB	O, L_THR_5	N, L_ARG_24	H, L_ARG_24	2.84	2.02	16.32
5JUE.PDB	O, L_THR_69	N, L_SER_25	H, L_SER_25	2.87	2.09	20.67
5JUE.PDB	O, L_GLY_68	N, L_LEU_27B	H, L_LEU_27B	2.95	2.09	6.56
5JUE.PDB	O, L_ASN_30	N, L_HIS_27D	H, L_HIS_27D	2.78	1.95	11.98
5JUE.PDB	O, L_HIS_27D	N, L_GLY_29	H, L_GLY_29	2.92	2.07	9.18
5JUE.PDB	OD1, L_ASN_28	N, L_ASN_30	H, L_ASN_30	2.82	1.98	7.63
5JUE.PDB	O, L_SER_89	N, L_HIS_34	H, L_HIS_34	2.90	2.08	14.05
5JUE.PDB	O, L_ILE_48	N, L_TRP_35	H, L_TRP_35	2.88	2.05	13.75
5JUE.PDB	O, L_PHE_87	N, L_TYR_36	H, L_TYR_36	2.82	2.02	18.65
5JUE.PDB	O, H_MET_100E	OH, L_TYR_36	HH, L_TYR_36	2.57	1.73	1.94
5JUE.PDB	O, L_LYS_45	N, L_LEU_37	H, L_LEU_37	2.94	2.13	17.21
5JUE.PDB	O, L_VAL_85	N, L_GLN_38	H, L_GLN_38	2.76	1.91	8.75
5JUE.PDB	OH, H_TYR_91	NE2, L_GLN_38	HE22, L_GLN_38	2.57	1.77	17.09
5JUE.PDB	O, L_LEU_37	N, L_LYS_45	H, L_LYS_45	2.82	2.01	16.77
5JUE.PDB	O, L_TRP_35	N, L_LEU_47	H, L_LEU_47	2.92	2.07	6.45
5JUE.PDB	O, L_ASN_53	N, L_TYR_49	H, L_TYR_49	2.77	1.96	16.15
5JUE.PDB	O, L_LEU_33	N, L_VAL_51	H, L_VAL_51	2.73	1.88	3.35
5JUE.PDB	O, L_LYS_50	N, L_SER_52	H, L_SER_52	2.82	2.09	27.26
5JUE.PDB	O, L_TYR_49	N, L_ASN_53	H, L_ASN_53	2.91	2.09	15.10
5JUE.PDB	O, L_LEU_47	N, L_PHE_55	H, L_PHE_55	2.94	2.09	7.35
5JUE.PDB	OD1, L_ASP_82	NH1, L_ARG_61	HH12, L_ARG_61	2.84	1.98	1.66
5JUE.PDB	OD2, L_ASP_82	NH2, L_ARG_61	HH22, L_ARG_61	2.58	1.76	15.54
5JUE.PDB	O, L_LYS_74	N, L_SER_63	H, L_SER_63	2.99	2.17	15.39
5JUE.PDB	O, L_THR_72	N, L_SER_65	H, L_SER_65	2.99	2.19	17.98
5JUE.PDB	O, L_CYS_23	N, L_PHE_71	H, L_PHE_71	2.91	2.13	20.93
5JUE.PDB	O, L_SER_65	N, L_THR_72	H, L_THR_72	3.00	2.17	13.38
5JUE.PDB	O, L_ILE_21	N, L_LEU_73	H, L_LEU_73	2.72	1.90	13.66
5JUE.PDB	O, L_SER_63	N, L_LYS_74	H, L_LYS_74	2.85	1.99	5.09
5JUE.PDB	O, L_ALA_19	N, L_ILE_75	H, L_ILE_75	2.85	2.02	11.67
5JUE.PDB	O, L_ARG_61	N, L_SER_76	H, L_SER_76	2.90	2.06	8.87
5JUE.PDB	OD2, L_ASP_82	N, L_GLU_79	H, L_GLU_79	2.91	2.07	10.58
5JUE.PDB	O, L_GLN_38	N, L_VAL_85	H, L_VAL_85	2.89	2.03	2.65
5JUE.PDB	O, L_THR_102	N, L_TYR_86	H, L_TYR_86	2.84	1.99	9.23
5JUE.PDB	O, L_ASP_82	OH, L_TYR_86	HH, L_TYR_86	2.44	1.73	27.01
5JUE.PDB	O, L_HIS_34	N, L_SER_89	H, L_SER_89	2.89	2.13	24.06
5JUE.PDB	O, L_HIS_93	NE2, L_GLN_90	HE22, L_GLN_90	2.99	2.13	3.59
5JUE.PDB	O, L_LEU_27B	OG1, L_THR_92	HG1, L_THR_92	2.74	1.96	18.74
5JUE.PDB	OE1, L_GLN_90	N, L_HIS_93	H, L_HIS_93	2.98	2.13	5.06
5JUE.PDB	O, L_VAL_2	OG1, L_THR_97	HG1, L_THR_97	2.62	1.84	18.25
5JUE.PDB	O, L_CYS_88	N, L_GLY_99	H, L_GLY_99	2.87	2.05	14.91
5JUE.PDB	OE1, L_GLN_6	N, L_GLY_101	H, L_GLY_101	2.93	2.15	21.08
5JUE.PDB	O, L_TYR_86	N, L_THR_102	H, L_THR_102	2.79	2.00	18.87
5JUE.PDB	O, L_PRO_8	OG1, L_THR_102	HG1, L_THR_102	2.72	1.95	19.56
5JUE.PDB	O, L_LEU_9	N, L_LYS_103	H, L_LYS_103	2.97	2.12	8.91
5JUE.PDB	O, L_LEU_11	N, L_ASP_105	H, L_ASP_105	2.72	1.89	12.81
5JUE.PDB	OE1, L_GLN_166	N, L_ILE_106	H, L_ILE_106	2.97	2.13	9.61
5JUE.PDB	O, L_VAL_13	N, L_LYS_107	H, L_LYS_107	2.92	2.11	17.64
5JUE.PDB	O, L_ALA_109	NE, L_ARG_108	HE, L_ARG_108	2.71	1.88	11.79

5JUE.PDB	O, L_ASP_170	NH1, L_ARG_108	HH11, L_ARG_108	2.89	2.05	10.58
5JUE.PDB	O, L_TYR_140	N, L_ALA_111	H, L_ALA_111	2.90	2.07	11.29
5JUE.PDB	O, L_ASN_137	N, L_THR_114	H, L_THR_114	2.87	2.02	7.17
5JUE.PDB	O, L_VAL_133	N, L_PHE_118	H, L_PHE_118	2.73	1.99	26.03
5JUE.PDB	OG, L_SER_121	N, L_GLN_124	H, L_GLN_124	2.96	2.13	13.41
5JUE.PDB	OG, L_SER_131	NE2, L_GLN_124	HE22, L_GLN_124	2.87	2.01	1.74
5JUE.PDB	O, L_SER_122	N, L_THR_126	H, L_THR_126	2.98	2.17	17.04
5JUE.PDB	OE1, L_GLN_124	N, L_SER_131	H, L_SER_131	2.85	2.11	26.16
5JUE.PDB	O, L_LEU_179	N, L_VAL_132	H, L_VAL_132	2.77	1.93	11.31
5JUE.PDB	O, L_SER_177	N, L_CYS_134	H, L_CYS_134	2.80	1.98	14.40
5JUE.PDB	O, L_SER_116	N, L_PHE_135	H, L_PHE_135	2.88	2.09	19.24
5JUE.PDB	O, L_MET_175	N, L_LEU_136	H, L_LEU_136	2.81	1.96	4.25
5JUE.PDB	O, L_THR_114	N, L_ASN_137	H, L_ASN_137	2.86	2.04	14.67
5JUE.PDB	O, L_TYR_173	N, L_PHE_139	H, L_PHE_139	2.85	2.03	14.35
5JUE.PDB	OD2, L_ASP_105	OH, L_TYR_140	HH, L_TYR_140	2.73	1.90	9.39
5JUE.PDB	O, L_GLU_195	N, L_LYS_147	H, L_LYS_147	2.84	2.04	18.72
5JUE.PDB	OG, L_SER_177	NE1, L_TRP_148	HE1, L_TRP_148	2.84	1.99	8.07
5JUE.PDB	O, L_THR_193	N, L_LYS_149	H, L_LYS_149	2.96	2.16	18.02
5JUE.PDB	OE2, L_GLU_195	NZ, L_LYS_149	HZ1, L_LYS_149	2.94	2.11	18.07
5JUE.PDB	O, L_SER_153	N, L_ILE_150	H, L_ILE_150	2.87	2.09	21.73
5JUE.PDB	O, L_SER_191	N, L_ASP_151	H, L_ASP_151	2.80	1.96	9.61
5JUE.PDB	O, L_ILE_150	N, L_SER_153	H, L_SER_153	2.88	2.02	3.01
5JUE.PDB	O, L_TRP_148	N, L_ARG_155	H, L_ARG_155	2.83	2.02	17.08
5JUE.PDB	OE1, L_GLU_185	NH1, L_ARG_155	HH12, L_ARG_155	2.98	2.13	8.18
5JUE.PDB	O, L_THR_178	N, L_LEU_160	H, L_LEU_160	2.89	2.07	14.30
5JUE.PDB	O, L_SER_176	N, L_SER_162	H, L_SER_162	2.89	2.09	18.60
5JUE.PDB	O, H_PRO_167	OG, L_SER_162	HG, L_SER_162	2.70	1.95	22.84
5JUE.PDB	O, L_SER_174	N, L_THR_164	H, L_THR_164	2.96	2.13	11.82
5JUE.PDB	O, L_ILE_106	NE2, L_GLN_166	HE22, L_GLN_166	2.89	2.10	19.76
5JUE.PDB	O, L_THR_172	N, L_ASP_167	H, L_ASP_167	2.82	1.99	14.34
5JUE.PDB	OD2, L_ASP_167	N, L_ASP_170	H, L_ASP_170	2.89	2.09	18.48
5JUE.PDB	O, L_ASP_167	N, L_SER_171	H, L_SER_171	2.91	2.19	28.73
5JUE.PDB	OD1, L_ASP_170	N, L_THR_172	H, L_THR_172	2.88	2.05	13.18
5JUE.PDB	OD1, L_ASP_170	OG1, L_THR_172	HG1, L_THR_172	2.65	1.84	10.43
5JUE.PDB	O, L_PHE_139	N, L_TYR_173	H, L_TYR_173	2.81	1.98	12.09
5JUE.PDB	OD1, L_ASP_105	OH, L_TYR_173	HH, L_TYR_173	2.53	1.79	22.81
5JUE.PDB	O, L_LEU_136	N, L_MET_175	H, L_MET_175	2.80	2.04	23.93
5JUE.PDB	O, L_SER_162	N, L_SER_176	H, L_SER_176	2.85	2.01	10.71
5JUE.PDB	OG, H_SER_178	OG, L_SER_176	HG, L_SER_176	2.78	1.94	3.13
5JUE.PDB	O, L_CYS_134	N, L_SER_177	H, L_SER_177	2.87	2.03	11.31
5JUE.PDB	OD1, L_ASN_161	OG, L_SER_177	HG, L_SER_177	2.61	1.88	24.46
5JUE.PDB	O, L_LEU_160	N, L_THR_178	H, L_THR_178	2.82	1.98	12.12
5JUE.PDB	O, L_VAL_132	N, L_LEU_179	H, L_LEU_179	2.82	2.00	15.30
5JUE.PDB	O, L_GLY_158	N, L_THR_180	H, L_THR_180	2.90	2.06	10.37
5JUE.PDB	O, L_ALA_130	N, L_LEU_181	H, L_LEU_181	2.87	2.02	8.71
5JUE.PDB	OG1, L_THR_182	N, L_GLU_185	H, L_GLU_185	2.89	2.08	16.50
5JUE.PDB	O, L_THR_182	N, L_TYR_186	H, L_TYR_186	2.88	2.04	12.09
5JUE.PDB	O, L_LYS_183	N, L_GLU_187	H, L_GLU_187	2.97	2.16	17.18
5JUE.PDB	OD1, L_ASP_184	NE, L_ARG_188	HE, L_ARG_188	2.70	1.93	22.77
5JUE.PDB	OD1, L_ASP_151	N, L_SER_191	H, L_SER_191	2.84	1.99	8.55
5JUE.PDB	OG, L_SER_208	OG1, L_THR_193	HG1, L_THR_193	2.92	2.19	25.67
5JUE.PDB	O, L_LYS_207	N, L_CYS_194	H, L_CYS_194	2.90	2.07	13.15
5JUE.PDB	O, L_LYS_147	N, L_GLU_195	H, L_GLU_195	2.80	2.03	21.10
5JUE.PDB	O, L_ILE_205	N, L_ALA_196	H, L_ALA_196	2.77	1.93	11.01
5JUE.PDB	O, L_ASN_145	N, L_THR_197	H, L_THR_197	2.81	1.97	10.17
5JUE.PDB	ND1, L_HIS_198	OG1, L_THR_200	HG1, L_THR_200	2.88	2.17	27.29
5JUE.PDB	O, L_HIS_198	N, L_SER_201	H, L_SER_201	2.99	2.13	4.28
5JUE.PDB	O, L_ALA_196	N, L_ILE_205	H, L_ILE_205	2.89	2.16	26.61

5JUE.PDB	O, L_CYS_194	N, L_LYS_207	H, L_LYS_207	2.98	2.13	8.08
5JUE.PDB	O, L_TYR_192	OG, L_SER_208	HG, L_SER_208	2.94	2.25	29.37
5JUE.PDB	O, L_TYR_192	N, L_PHE_209	H, L_PHE_209	2.97	2.18	20.14
5JUE.PDB	O, L_ASN_190	N, L_ARG_211	H, L_ARG_211	2.82	2.02	17.54
5JUE.PDB	O, L_HIS_189	NH1, L_ARG_211	HH11, L_ARG_211	2.81	2.00	16.77
5JUE.PDB	O, H_LYS_23	N, H_GLN_5	H, H_GLN_5	2.85	2.00	7.87
5JUE.PDB	OE1, H_GLN_105	N, H_GLU_6	H, H_GLU_6	2.79	1.93	4.85
5JUE.PDB	O, H_THR_108	N, H_GLU_10	H, H_GLU_10	2.90	2.06	10.22
5JUE.PDB	O, H_THR_110	N, H_VAL_12	H, H_VAL_12	2.87	2.05	14.20
5JUE.PDB	O, H_LEU_82C	N, H_GLY_15	H, H_GLY_15	2.69	1.84	3.78
5JUE.PDB	O, H_PHE_82	N, H_VAL_18	H, H_VAL_18	2.89	2.15	25.49
5JUE.PDB	O, H_MET_80	N, H_ILE_20	H, H_ILE_20	2.88	2.05	14.33
5JUE.PDB	OG, H_SER_7	N, H_SER_21	H, H_SER_21	2.95	2.10	6.39
5JUE.PDB	O, H_GLN_5	N, H_LYS_23	H, H_LYS_23	2.86	2.01	5.12
5JUE.PDB	O, H_SER_76	N, H_ALA_24	H, H_ALA_24	2.79	1.93	3.59
5JUE.PDB	O, H_LEU_95	N, H_TYR_33	H, H_TYR_33	2.75	1.97	21.10
5JUE.PDB	O, H_ILE_51	N, H_ILE_34	H, H_ILE_34	2.95	2.13	14.74
5JUE.PDB	O, H_ALA_93	N, H_HIS_35	H, H_HIS_35	2.70	1.87	12.64
5JUE.PDB	O, H_GLY_49	N, H_TRP_36	H, H_TRP_36	2.96	2.14	14.80
5JUE.PDB	O, H_TYR_91	N, H_VAL_37	H, H_VAL_37	2.90	2.12	21.72
5JUE.PDB	O, H_GLU_46	N, H_LYS_38	H, H_LYS_38	2.77	1.91	6.07
5JUE.PDB	O, H_GLU_85	NZ, H_LYS_38	HZ3, H_LYS_38	2.96	2.18	24.16
5JUE.PDB	O, H_VAL_89	N, H_GLN_39	H, H_GLN_39	2.71	1.95	22.82
5JUE.PDB	O, H_LYS_38	N, H_GLU_46	H, H_GLU_46	2.82	2.03	19.41
5JUE.PDB	ND1, H_HIS_35	NE1, H_TRP_47	HE1, H_TRP_47	2.93	2.15	20.72
5JUE.PDB	O, H_TRP_36	N, H_ILE_48	H, H_ILE_48	2.82	1.97	8.50
5JUE.PDB	O, H_PHE_58	N, H_PHE_50	H, H_PHE_50	2.95	2.18	21.32
5JUE.PDB	O, H_ILE_34	N, H_ILE_51	H, H_ILE_51	2.91	2.08	13.15
5JUE.PDB	O, H_ALA_56	N, H_SER_52	H, H_SER_52	2.80	1.98	14.65
5JUE.PDB	O, H_TYR_32	N, H_CYS_52A	H, H_CYS_52A	2.96	2.15	16.57
5JUE.PDB	O, H_SER_52	N, H_GLY_55	H, H_GLY_55	2.82	2.07	24.44
5JUE.PDB	O, H_ILE_48	N, H_ASN_60	H, H_ASN_60	2.84	2.02	15.39
5JUE.PDB	O, H_TRP_47	ND2, H_ASN_60	HD22, H_ASN_60	2.96	2.15	16.53
5JUE.PDB	O, H_ASN_60	N, H_PHE_63	H, H_PHE_63	2.69	1.86	13.05
5JUE.PDB	O, H_PHE_63	N, H_LYS_66	H, H_LYS_66	2.88	2.11	21.18
5JUE.PDB	OD2, H_ASP_86	NZ, H_LYS_66	HZ1, H_LYS_66	2.76	1.87	4.19
5JUE.PDB	O, H_LYS_81	N, H_THR_68	H, H_THR_68	2.79	2.01	20.33
5JUE.PDB	OH, H_TYR_59	N, H_PHE_69	H, H_PHE_69	2.85	2.00	6.71
5JUE.PDB	O, H_THR_77	N, H_ASP_72	H, H_ASP_72	2.79	1.96	13.59
5JUE.PDB	O, H_SER_75	OG1, H_THR_77	HG1, H_THR_77	2.86	2.10	21.30
5JUE.PDB	O, H_CYS_22	N, H_ALA_78	H, H_ALA_78	2.84	2.01	12.71
5JUE.PDB	O, H_THR_70	N, H_TYR_79	H, H_TYR_79	2.81	1.97	11.04
5JUE.PDB	O, H_ILE_20	N, H_MET_80	H, H_MET_80	2.90	2.08	15.24
5JUE.PDB	O, H_THR_68	N, H_LYS_81	H, H_LYS_81	2.77	1.92	8.40
5JUE.PDB	O, H_VAL_18	N, H_PHE_82	H, H_PHE_82	2.76	1.93	11.48
5JUE.PDB	O, H_ALA_16	N, H_LEU_82C	H, H_LEU_82C	2.95	2.10	6.09
5JUE.PDB	OD2, H_ASP_86	N, H_THR_83	H, H_THR_83	2.87	2.09	20.55
5JUE.PDB	O, H_THR_83	N, H_ASP_86	H, H_ASP_86	2.75	1.95	17.05
5JUE.PDB	O, H_PHE_84	N, H_SER_87	H, H_SER_87	2.98	2.14	9.08
5JUE.PDB	O, H_GLN_39	N, H_VAL_89	H, H_VAL_89	2.93	2.09	11.76
5JUE.PDB	O, H_THR_107	N, H_TYR_90	H, H_TYR_90	2.88	2.04	10.67
5JUE.PDB	O, H_ASP_86	OH, H_TYR_90	HH, H_TYR_90	2.63	1.81	11.12
5JUE.PDB	O, H_VAL_37	N, H_TYR_91	H, H_TYR_91	2.79	1.95	9.11
5JUE.PDB	OE1, H_GLN_39	OH, H_TYR_91	HH, H_TYR_91	2.83	2.02	11.19
5JUE.PDB	O, H_HIS_35	N, H_ALA_93	H, H_ALA_93	2.84	2.10	26.47
5JUE.PDB	O, H_TYR_102	N, H_ARG_94	H, H_ARG_94	2.91	2.11	17.26
5JUE.PDB	OD1, H_ASP_101	NE, H_ARG_94	HE, H_ARG_94	2.72	1.88	8.15
5JUE.PDB	OD2, H_ASP_101	NH2, H_ARG_94	HH21, H_ARG_94	2.85	2.02	12.42

5JUE.PDB	O, H_TYR_33	N, H_LEU_95	H, H_LEU_95	2.78	2.01	21.79
5JUE.PDB	O, H_CYS_92	N, H_GLY_104	H, H_GLY_104	2.87	2.02	8.85
5JUE.PDB	O, H_GLU_6	NE2, H_GLN_105	HE22, H_GLN_105	2.95	2.22	27.22
5JUE.PDB	OE1, H_GLU_6	N, H_GLY_106	H, H_GLY_106	2.94	2.16	21.03
5JUE.PDB	O, H_TYR_90	N, H_THR_107	H, H_THR_107	2.85	2.05	17.16
5JUE.PDB	O, H_SER_7	OG1, H_THR_107	HG1, H_THR_107	2.75	1.97	19.56
5JUE.PDB	O, H_ALA_88	N, H_VAL_109	H, H_VAL_109	2.87	2.01	4.42
5JUE.PDB	O, H_GLU_10	N, H_THR_110	H, H_THR_110	2.93	2.09	10.96
5JUE.PDB	OG, H_SER_87	N, H_VAL_111	H, H_VAL_111	2.90	2.07	12.94
5JUE.PDB	OG, H_SER_112	N, H_ALA_114	H, H_ALA_114	2.93	2.07	5.78
5JUE.PDB	O, H_PHE_146	N, H_THR_117	H, H_THR_117	2.86	2.04	14.00
5JUE.PDB	O, H_LYS_115	OG1, H_THR_117	HG1, H_THR_117	2.86	2.06	13.74
5JUE.PDB	O, H_LYS_143	N, H_SER_120	H, H_SER_120	2.92	2.10	14.44
5JUE.PDB	O, H_LEU_141	N, H_TYR_122	H, H_TYR_122	2.78	1.95	12.46
5JUE.PDB	O, H_GLY_139	N, H_LEU_124	H, H_LEU_124	2.76	1.94	15.50
5JUE.PDB	O, H_VAL_183	N, H_VAL_136	H, H_VAL_136	2.78	1.97	15.84
5JUE.PDB	O, H_VAL_181	N, H_LEU_138	H, H_LEU_138	2.83	1.98	9.69
5JUE.PDB	O, H_LEU_124	N, H_GLY_139	H, H_GLY_139	2.92	2.12	17.53
5JUE.PDB	O, H_SER_179	N, H_CYS_140	H, H_CYS_140	2.90	2.16	25.88
5JUE.PDB	O, H_TYR_122	N, H_LEU_141	H, H_LEU_141	2.90	2.05	9.18
5JUE.PDB	O, H_LEU_177	N, H_VAL_142	H, H_VAL_142	2.80	1.96	9.80
5JUE.PDB	O, H_SER_120	N, H_LYS_143	H, H_LYS_143	2.83	1.99	8.41
5JUE.PDB	OE2, H_GLU_148	OH, H_TYR_145	HH, H_TYR_145	2.72	1.89	3.03
5JUE.PDB	O, H_THR_117	N, H_PHE_146	H, H_PHE_146	2.99	2.19	18.30
5JUE.PDB	O, H_ALA_198	N, H_THR_151	H, H_THR_151	2.83	2.01	15.90
5JUE.PDB	O, H_ASN_196	N, H_THR_153	H, H_THR_153	2.83	2.02	15.46
5JUE.PDB	OD1, H_ASN_196	OG1, H_THR_153	HG1, H_THR_153	2.74	1.98	20.12
5JUE.PDB	O, H_THR_194	N, H_ASN_155	H, H_ASN_155	2.82	1.98	9.66
5JUE.PDB	OD1, H_ASN_196	N, H_SER_156	H, H_SER_156	2.76	1.93	12.37
5JUE.PDB	O, H_ASN_155	N, H_SER_158	H, H_SER_158	2.96	2.12	11.60
5JUE.PDB	O, H_SER_180	N, H_HIS_164	H, H_HIS_164	2.88	2.06	15.45
5JUE.PDB	O, H_SER_178	N, H_PHE_166	H, H_PHE_166	2.91	2.05	0.92
5JUE.PDB	O, H_THR_176	N, H_VAL_169	H, H_VAL_169	2.91	2.09	14.10
5JUE.PDB	O, H_LEU_174	N, H_GLN_171	H, H_GLN_171	2.86	2.02	11.81
5JUE.PDB	O, H_TYR_145	N, H_TYR_175	H, H_TYR_175	2.78	1.92	3.54
5JUE.PDB	O, H_VAL_169	N, H_THR_176	H, H_THR_176	2.91	2.13	21.19
5JUE.PDB	O, H_VAL_142	N, H_LEU_177	H, H_LEU_177	2.89	2.07	15.29
5JUE.PDB	O, H_CYS_140	N, H_SER_179	H, H_SER_179	2.96	2.18	21.41
5JUE.PDB	O, H_HIS_164	N, H_SER_180	H, H_SER_180	2.77	1.97	17.64
5JUE.PDB	O, H_LEU_138	N, H_VAL_181	H, H_VAL_181	2.85	2.04	16.39
5JUE.PDB	O, H_GLY_162	N, H_THR_182	H, H_THR_182	2.95	2.18	23.27
5JUE.PDB	OG1, H_THR_137	OG1, H_THR_182	HG1, H_THR_182	2.77	2.00	20.14
5JUE.PDB	O, H_VAL_136	N, H_VAL_183	H, H_VAL_183	2.99	2.18	15.82
5JUE.PDB	O, H_SER_134	N, H_SER_185	H, H_SER_185	2.84	2.01	11.66
5JUE.PDB	O, H_THR_184	N, H_THR_187	H, H_THR_187	2.89	2.07	14.43
5JUE.PDB	OG1, H_THR_184	OG1, H_THR_187	HG1, H_THR_187	2.67	1.90	19.94
5JUE.PDB	O, H_THR_187	N, H_GLN_191	H, H_GLN_191	2.84	2.07	22.35
5JUE.PDB	OD1, H_ASN_155	N, H_THR_194	H, H_THR_194	2.84	2.06	20.75
5JUE.PDB	O, H_LYS_208	N, H_CYS_195	H, H_CYS_195	2.98	2.17	16.43
5JUE.PDB	O, H_THR_153	N, H_ASN_196	H, H_ASN_196	2.77	1.92	6.43
5JUE.PDB	O, H_VAL_206	N, H_VAL_197	H, H_VAL_197	2.87	2.03	11.32
5JUE.PDB	O, H_THR_151	N, H_ALA_198	H, H_ALA_198	2.82	2.00	15.03
5JUE.PDB	ND1, H_HIS_199	OG, H_SER_202	HG, H_SER_202	2.87	2.13	24.10
5JUE.PDB	O, H_PRO_200	N, H_SER_203	H, H_SER_203	2.74	1.98	23.65
5JUE.PDB	O, H_VAL_197	N, H_VAL_206	H, H_VAL_206	2.85	2.02	12.25
5JUE.PDB	O, H_CYS_195	N, H_LYS_208	H, H_LYS_208	2.96	2.13	13.25
5JUE.PDB	OE1, L_GLU_123	NZ, H_LYS_208	HZ1, H_LYS_208	2.81	1.98	17.66
5JUE.PDB	O, H_ILE_193	N, H_ILE_210	H, H_ILE_210	2.91	2.05	5.10

5JUE.PDB	O, H_ALA_125	NE, H_ARG_213	HE, H_ARG_213	2.97	2.21	22.96
5JUE.PDB	O, H_ALA_125	NH1, H_ARG_213	HH11, H_ARG_213	2.91	2.14	23.09
5JUE.PDB	O, L_PRO_119	NH1, H_ARG_213	HH12, H_ARG_213	2.84	2.13	29.21
5JUE.PDB	O, L_PRO_120	NH2, H_ARG_213	HH22, H_ARG_213	2.94	2.13	15.93

Table 1704: 5JUE-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5JXA.PDB	OE1, H_GLN_105	N, H_GLN_6	H, H_GLN_6	2.84	1.98	2.17
5JXA.PDB	O, H_TYR_90	NE2, H_GLN_6	HE22, H_GLN_6	2.90	2.05	7.37
5JXA.PDB	O, H_VAL_110	N, H_LYS_12	H, H_LYS_12	2.83	2.00	13.73
5JXA.PDB	O, H_LEU_82C	N, H_GLY_15	H, H_GLY_15	2.72	1.89	11.76
5JXA.PDB	O, H_THR_13	OG, H_SER_16	HG, H_SER_16	2.64	1.85	16.20
5JXA.PDB	O, H_PHE_82	N, H_VAL_18	H, H_VAL_18	3.00	2.19	17.49
5JXA.PDB	O, H_MET_80	N, H_ILE_20	H, H_ILE_20	2.90	2.05	7.33
5JXA.PDB	O, H_ALA_78	N, H_CYS_22	H, H_CYS_22	2.76	2.06	29.69
5JXA.PDB	O, H_GLY_76G	N, H_ALA_24	H, H_ALA_24	2.81	1.96	7.69
5JXA.PDB	OD1, H_ASN_28	N, H_ARG_30	H, H_ARG_30	2.98	2.23	24.67
5JXA.PDB	O, H_SER_74	NH2, H_ARG_30	HH22, H_ARG_30	2.90	2.07	12.90
5JXA.PDB	O, H_ASN_28	N, H_ASP_31	H, H_ASP_31	2.98	2.13	8.21
5JXA.PDB	O, H_ILE_51	N, H_ILE_34	H, H_ILE_34	2.89	2.08	16.53
5JXA.PDB	O, H_GLY_49	N, H_TRP_36	H, H_TRP_36	2.93	2.16	21.63
5JXA.PDB	O, H_PHE_91	N, H_VAL_37	H, H_VAL_37	3.00	2.19	17.03
5JXA.PDB	O, H_GLU_46	N, H_ARG_38	H, H_ARG_38	2.95	2.12	11.49
5JXA.PDB	OE1, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.80	2.04	23.29
5JXA.PDB	OD1, H_ASP_86	NH1, H_ARG_38	HH12, H_ARG_38	2.74	1.88	4.26
5JXA.PDB	OE1, H_GLU_46	NH2, H_ARG_38	HH21, H_ARG_38	2.76	2.00	23.95
5JXA.PDB	O, H_GLU_89	N, H_LEU_39	H, H_LEU_39	2.77	1.93	11.85
5JXA.PDB	O, H_GLY_44	N, H_ILE_40	H, H_ILE_40	2.91	2.05	5.76
5JXA.PDB	O, H_ILE_40	N, H_GLY_44	H, H_GLY_44	2.97	2.17	18.25
5JXA.PDB	O, H_ARG_38	N, H_GLU_46	H, H_GLU_46	2.79	2.00	19.09
5JXA.PDB	O, H_TRP_36	N, H_ILE_48	H, H_ILE_48	2.83	1.98	7.19
5JXA.PDB	O, H_SER_58	N, H_TRP_50	H, H_TRP_50	2.83	2.05	20.31
5JXA.PDB	O, H_ILE_34	N, H_ILE_51	H, H_ILE_51	2.86	2.05	16.90
5JXA.PDB	O, H_ALA_56	N, H_LYS_52	H, H_LYS_52	2.85	2.02	13.26
5JXA.PDB	O, H_TRP_50	N, H_SER_58	H, H_SER_58	2.99	2.19	18.18
5JXA.PDB	O, H_ILE_48	N, H_ALA_60	H, H_ALA_60	2.91	2.07	7.65
5JXA.PDB	OE2, H_GLU_46	NE2, H_GLN_62	HE21, H_GLN_62	2.86	2.00	1.72
5JXA.PDB	O, H_ALA_60	N, H_LEU_63	H, H_LEU_63	2.91	2.10	16.09
5JXA.PDB	O, H_LEU_63	N, H_ARG_66	H, H_ARG_66	2.89	2.06	11.35
5JXA.PDB	OD1, H_ASP_86	NH2, H_ARG_66	HH22, H_ARG_66	2.96	2.11	6.31
5JXA.PDB	O, H_GLU_81	N, H_SER_68	H, H_SER_68	2.87	2.09	21.34
5JXA.PDB	OH, H_TYR_59	N, H_MET_69	H, H_MET_69	2.89	2.04	7.98
5JXA.PDB	O, H_PRO_52A	NE, H_ARG_71	HE, H_ARG_71	2.75	1.92	12.12
5JXA.PDB	O, H_ASP_76C	OG, H_SER_74	HG, H_SER_74	2.75	1.97	16.95
5JXA.PDB	OD1, H_ASP_76	N, H_ASP_76B	H, H_ASP_76B	2.44	1.62	14.02
5JXA.PDB	O, H_ASP_76	N, H_ASP_76C	H, H_ASP_76C	2.97	2.14	13.17
5JXA.PDB	OD2, H_ASP_76C	NE1, H_TRP_76F	HE1, H_TRP_76F	2.87	2.15	28.04
5JXA.PDB	O, H_CYS_22	N, H_ALA_78	H, H_ALA_78	2.89	2.05	10.11
5JXA.PDB	O, H_THR_70	N, H_TYR_79	H, H_TYR_79	2.80	1.95	8.03
5JXA.PDB	O, H_SER_68	N, H_GLU_81	H, H_GLU_81	2.76	1.90	6.10
5JXA.PDB	O, H_VAL_18	N, H_PHE_82	H, H_PHE_82	2.84	2.03	16.50
5JXA.PDB	O, H_ARG_66	N, H_SER_82A	H, H_SER_82A	2.80	1.99	17.15
5JXA.PDB	OD2, H_ASP_86	N, H_THR_83	H, H_THR_83	2.91	2.10	15.72
5JXA.PDB	O, H_THR_83	N, H_ASP_86	H, H_ASP_86	2.85	2.00	7.33
5JXA.PDB	O, H_THR_107	N, H_TYR_90	H, H_TYR_90	2.86	2.00	7.75
5JXA.PDB	O, H_VAL_37	N, H_PHE_91	H, H_PHE_91	2.82	1.95	8.59
5JXA.PDB	O, H_HIS_35	N, H_VAL_93	H, H_VAL_93	2.91	2.05	12.82
5JXA.PDB	O, H_TYR_102	N, H_ARG_94	H, H_ARG_94	2.93	2.09	18.47
5JXA.PDB	O, H_GLY_96	NE, H_ARG_95	HE, H_ARG_95	2.87	2.08	18.29
5JXA.PDB	O, H_GLY_96	NH2, H_ARG_95	HH21, H_ARG_95	2.95	2.20	24.49
5JXA.PDB	OD1, H_ASP_99	NH2, H_ARG_95	HH22, H_ARG_95	2.95	2.09	5.23
5JXA.PDB	OD2, L_ASP_50	OH, H_TYR_100	HH, H_TYR_100	2.57	1.75	11.76
5JXA.PDB	OH, L_TYR_36	N, H_TRP_100F	H, H_TRP_100F	2.85	2.00	7.52
5JXA.PDB	O, H_CYS_92	N, H_GLY_104	H, H_GLY_104	2.82	1.96	4.16

5JXA.PDB	O, H_GLN_6	NE2, H_GLN_105	HE22, H_GLN_105	2.97	2.19	21.71
5JXA.PDB	O, H_TYR_90	N, H_THR_107	H, H_THR_107	2.79	2.05	25.50
5JXA.PDB	O, H_SER_7	OG1, H_THR_107	HG1, H_THR_107	2.82	2.10	26.24
5JXA.PDB	O, H_ALA_88	N, H_VAL_109	H, H_VAL_109	2.99	2.13	5.29
5JXA.PDB	OG1, H_THR_87	N, H_VAL_111	H, H_VAL_111	2.97	2.11	2.98
5JXA.PDB	O, H_LYS_12	N, H_SER_112	H, H_SER_112	2.81	2.01	17.72
5JXA.PDB	OG, H_SER_112	N, H_ALA_114	H, H_ALA_114	2.92	2.06	5.24
5JXA.PDB	O, H_PHE_146	N, H_LYS_117	H, H_LYS_117	2.81	2.00	15.52
5JXA.PDB	O, H_ASP_144	NZ, H_LYS_117	HZ2, H_LYS_117	2.76	2.00	26.54
5JXA.PDB	O, H_LYS_143	N, H_SER_120	H, H_SER_120	2.88	2.02	13.76
5JXA.PDB	O, H_LEU_141	N, H_PHE_122	H, H_PHE_122	2.87	2.05	13.14
5JXA.PDB	O, H_GLY_139	N, H_LEU_124	H, H_LEU_124	2.78	1.93	6.72
5JXA.PDB	O, H_VAL_184	N, H_ALA_136	H, H_ALA_136	2.62	1.77	9.09
5JXA.PDB	O, H_LEU_124	N, H_GLY_139	H, H_GLY_139	2.90	2.16	25.91
5JXA.PDB	O, H_SER_180	N, H_CYS_140	H, H_CYS_140	2.84	2.03	17.78
5JXA.PDB	O, H_PHE_122	N, H_LEU_141	H, H_LEU_141	2.80	1.96	10.45
5JXA.PDB	O, H_LEU_178	N, H_VAL_142	H, H_VAL_142	2.71	1.86	8.75
5JXA.PDB	O, H_SER_120	N, H_LYS_143	H, H_LYS_143	2.86	2.01	6.05
5JXA.PDB	OD1, H_ASP_144	NZ, H_LYS_143	HZ3, H_LYS_143	2.92	2.12	22.30
5JXA.PDB	O, H_LYS_117	N, H_PHE_146	H, H_PHE_146	2.93	2.11	14.00
5JXA.PDB	O, H_ASN_199	N, H_THR_151	H, H_THR_151	2.95	2.12	13.67
5JXA.PDB	O, H_ASN_197	N, H_SER_153	H, H_SER_153	2.94	2.13	16.37
5JXA.PDB	OD1, H_ASN_197	OG, H_SER_153	HG, H_SER_153	2.75	1.96	17.62
5JXA.PDB	OG, H_SER_180	NE1, H_TRP_154	HE1, H_TRP_154	2.96	2.12	10.70
5JXA.PDB	O, H_ILE_195	N, H_ASN_155	H, H_ASN_155	2.75	1.91	9.52
5JXA.PDB	OD1, H_ASN_197	N, H_SER_156	H, H_SER_156	2.77	1.96	16.97
5JXA.PDB	O, H_VAL_181	N, H_HIS_164	H, H_HIS_164	2.83	2.00	13.86
5JXA.PDB	O, H_SER_179	N, H_PHE_166	H, H_PHE_166	3.00	2.16	10.32
5JXA.PDB	O, H_SER_177	N, H_VAL_169	H, H_VAL_169	2.97	2.15	15.76
5JXA.PDB	O, H_LEU_175	N, H_GLN_171	H, H_GLN_171	2.96	2.12	8.09
5JXA.PDB	O, H_LEU_175	NE2, H_GLN_171	HE21, H_GLN_171	2.90	2.06	9.29
5JXA.PDB	OD1, H_ASP_144	NE2, H_GLN_171	HE22, H_GLN_171	2.86	2.05	16.31
5JXA.PDB	O, H_GLN_171	N, H_GLY_174	H, H_GLY_174	2.95	2.10	7.88
5JXA.PDB	O, H_TYR_145	N, H_TYR_176	H, H_TYR_176	2.75	1.91	10.32
5JXA.PDB	O, H_VAL_142	N, H_LEU_178	H, H_LEU_178	2.89	2.08	16.18
5JXA.PDB	O, H_CYS_140	N, H_SER_180	H, H_SER_180	2.89	2.07	14.12
5JXA.PDB	O, H_HIS_164	N, H_VAL_181	H, H_VAL_181	2.89	2.06	12.60
5JXA.PDB	O, H_LEU_138	N, H_VAL_182	H, H_VAL_182	2.88	2.09	18.88
5JXA.PDB	O, H_ALA_136	N, H_VAL_184	H, H_VAL_184	2.85	2.04	16.24
5JXA.PDB	O, H_GLY_134	N, H_SER_186	H, H_SER_186	2.13	1.27	5.45
5JXA.PDB	O, H_PRO_185	OG, H_SER_188	HG, H_SER_188	2.58	1.75	4.20
5JXA.PDB	O, H_SER_188	N, H_GLN_192	H, H_GLN_192	2.82	1.97	8.59
5JXA.PDB	O, H_THR_193	NE2, H_GLN_192	HE21, H_GLN_192	2.91	2.09	13.40
5JXA.PDB	OG, H_SER_188	OH, H_TYR_194	HH, H_TYR_194	2.92	2.22	28.67
5JXA.PDB	OD1, H_ASN_155	N, H_ILE_195	H, H_ILE_195	2.81	2.00	16.75
5JXA.PDB	O, H_LYS_209	N, H_CYS_196	H, H_CYS_196	2.97	2.21	23.72
5JXA.PDB	O, H_SER_153	N, H_ASN_197	H, H_ASN_197	2.71	1.87	7.78
5JXA.PDB	O, H_VAL_207	N, H_VAL_198	H, H_VAL_198	2.72	1.86	4.76
5JXA.PDB	O, H_THR_151	N, H_ASN_199	H, H_ASN_199	2.95	2.11	11.96
5JXA.PDB	O, H_THR_205	N, H_HIS_200	H, H_HIS_200	2.85	2.00	9.64
5JXA.PDB	O, H_PRO_147	NE2, H_HIS_200	HE2, H_HIS_200	2.71	1.87	10.25
5JXA.PDB	ND1, H_HIS_200	OG, H_SER_203	HG, H_SER_203	2.82	2.10	26.44
5JXA.PDB	O, H_LYS_201	N, H_ASN_204	H, H_ASN_204	2.83	2.01	13.96
5JXA.PDB	O, H_VAL_198	N, H_VAL_207	H, H_VAL_207	2.84	2.02	14.35
5JXA.PDB	O, H_CYS_196	N, H_LYS_209	H, H_LYS_209	2.96	2.14	15.80
5JXA.PDB	O, H_TYR_194	N, H_VAL_211	H, H_VAL_211	2.90	2.05	6.52
5JXA.PDB	OG, L_SER_26	N, L_VAL_3	H, L_VAL_3	2.90	2.06	10.44
5JXA.PDB	O, L_LYS_24	N, L_THR_5	H, L_THR_5	2.81	1.98	12.20

5JXA.PDB	O, L_TYR_86	NE2, L_GLN_6	HE22, L_GLN_6	2.89	2.07	15.63
5JXA.PDB	O, L_GLU_103	N, L_LEU_11	H, L_LEU_11	2.77	1.93	11.05
5JXA.PDB	OE1, L_GLU_17	N, L_SER_14	H, L_SER_14	2.78	1.95	10.28
5JXA.PDB	O, L_LEU_78	N, L_GLY_16	H, L_GLY_16	2.83	2.05	20.59
5JXA.PDB	O, L_SER_14	N, L_GLU_17	H, L_GLU_17	2.99	2.14	6.52
5JXA.PDB	O, L_ILE_75	N, L_ALA_19	H, L_ALA_19	2.95	2.13	15.15
5JXA.PDB	O, L_LEU_73	N, L_LEU_21	H, L_LEU_21	2.85	2.01	11.82
5JXA.PDB	O, L_SER_7	N, L_PHE_22	H, L_PHE_22	2.93	2.08	9.65
5JXA.PDB	O, L_PHE_71	N, L_CYS_23	H, L_CYS_23	2.86	2.02	10.81
5JXA.PDB	O, L_THR_5	N, L_LYS_24	H, L_LYS_24	2.95	2.10	7.38
5JXA.PDB	O, L_THR_69	N, L_ALA_25	H, L_ALA_25	2.83	2.00	12.63
5JXA.PDB	O, L_ILE_48	N, L_TRP_35	H, L_TRP_35	2.93	2.10	13.22
5JXA.PDB	O, L_TYR_87	N, L_TYR_36	H, L_TYR_36	2.78	1.95	13.00
5JXA.PDB	OE1, L_GLN_89	OH, L_TYR_36	HH, L_TYR_36	2.71	1.91	14.07
5JXA.PDB	O, L_ARG_45	N, L_GLN_37	H, L_GLN_37	2.89	2.06	13.47
5JXA.PDB	OH, L_TYR_86	NE2, L_GLN_37	HE21, L_GLN_37	2.99	2.15	10.29
5JXA.PDB	O, L_VAL_85	N, L_LYS_38	H, L_LYS_38	2.75	1.89	4.40
5JXA.PDB	O, L_GLN_42	NZ, L_LYS_38	HZ3, L_LYS_38	2.71	1.90	27.32
5JXA.PDB	O, L_GLU_81	NE, L_ARG_39	HE, L_ARG_39	2.78	1.86	16.81
5JXA.PDB	O, L_ARG_39	N, L_GLN_42	H, L_GLN_42	2.96	2.14	14.42
5JXA.PDB	O, L_GLN_37	N, L_ARG_45	H, L_ARG_45	2.85	2.09	23.31
5JXA.PDB	O, L_TRP_35	N, L_LEU_47	H, L_LEU_47	2.90	2.06	9.03
5JXA.PDB	O, L_ARG_53	N, L_TYR_49	H, L_TYR_49	2.87	2.07	17.25
5JXA.PDB	O, L_MET_33	N, L_THR_51	H, L_THR_51	2.75	1.91	11.49
5JXA.PDB	O, L_TYR_49	N, L_ARG_53	H, L_ARG_53	2.88	2.10	22.06
5JXA.PDB	OH, H_TYR_100	NH2, L_ARG_53	HH21, L_ARG_53	2.89	2.07	18.12
5JXA.PDB	O, L_LEU_47	N, L_ALA_55	H, L_ALA_55	2.99	2.14	7.32
5JXA.PDB	OD2, L_ASP_82	NE, L_ARG_61	HE, L_ARG_61	2.88	2.15	27.19
5JXA.PDB	OD1, L_ASP_82	NH2, L_ARG_61	HH21, L_ARG_61	2.84	1.98	2.45
5JXA.PDB	O, L_THR_74	N, L_VAL_63	H, L_VAL_63	2.82	1.99	13.39
5JXA.PDB	O, L_PHE_72	N, L_SER_65	H, L_SER_65	2.91	2.10	15.27
5JXA.PDB	OD1, L_ASP_70	OG1, L_THR_69	HG1, L_THR_69	2.92	2.09	7.50
5JXA.PDB	O, L_CYS_23	N, L_PHE_71	H, L_PHE_71	2.96	2.17	20.10
5JXA.PDB	O, L_SER_65	N, L_PHE_72	H, L_PHE_72	2.92	2.09	12.41
5JXA.PDB	O, L_LEU_21	N, L_LEU_73	H, L_LEU_73	2.92	2.12	19.36
5JXA.PDB	O, L_VAL_63	N, L_THR_74	H, L_THR_74	2.86	2.00	5.29
5JXA.PDB	O, L_ALA_19	N, L_ILE_75	H, L_ILE_75	2.87	2.05	14.95
5JXA.PDB	O, L_ARG_61	N, L_ASN_76	H, L_ASN_76	2.88	2.03	8.54
5JXA.PDB	O, L_GLU_17	N, L_LEU_78	H, L_LEU_78	2.83	2.01	13.81
5JXA.PDB	OD2, L_ASP_82	N, L_ASP_79	H, L_ASP_79	2.65	1.79	5.80
5JXA.PDB	OD2, L_ASP_79	N, L_GLU_81	H, L_GLU_81	2.94	2.08	2.69
5JXA.PDB	O, L_ASP_79	N, L_ASP_82	H, L_ASP_82	2.79	1.95	7.93
5JXA.PDB	O, L_SER_102	N, L_TYR_86	H, L_TYR_86	2.86	2.03	12.51
5JXA.PDB	O, L_ASP_82	OH, L_TYR_86	HH, L_TYR_86	2.60	1.79	10.99
5JXA.PDB	O, L_TYR_36	N, L_TYR_87	H, L_TYR_87	2.95	2.13	15.47
5JXA.PDB	O, L_THR_34	N, L_GLN_89	H, L_GLN_89	2.89	2.18	29.17
5JXA.PDB	O, L_PHE_97	N, L_GLN_90	H, L_GLN_90	2.95	2.17	21.39
5JXA.PDB	O, L_GLN_90	N, L_PHE_97	H, L_PHE_97	2.85	2.03	15.63
5JXA.PDB	O, L_CYS_88	N, L_GLY_99	H, L_GLY_99	2.94	2.12	17.39
5JXA.PDB	OE1, L_GLN_6	N, L_GLY_101	H, L_GLY_101	2.89	2.15	26.61
5JXA.PDB	O, L_TYR_86	N, L_SER_102	H, L_SER_102	2.89	2.08	16.76
5JXA.PDB	O, L_PRO_8	OG, L_SER_102	HG, L_SER_102	2.69	2.00	29.55
5JXA.PDB	O, L_GLY_9	N, L_GLU_103	H, L_GLU_103	2.89	2.04	6.77
5JXA.PDB	O, L_ALA_84	N, L_LEU_104	H, L_LEU_104	2.88	2.04	11.59
5JXA.PDB	O, L_LEU_11	N, L_GLU_105	H, L_GLU_105	2.90	2.07	12.41
5JXA.PDB	OE1, L_GLN_166	N, L_VAL_106	H, L_VAL_106	2.98	2.12	4.21
5JXA.PDB	O, L_LEU_13	N, L_HIS_107	H, L_HIS_107	2.92	2.09	12.00
5JXA.PDB	O, L_THR_109	NE, L_ARG_108	HE, L_ARG_108	2.85	2.02	11.20

5JXA.PDB	O, L_ASP_170	NH1, L_ARG_108	HH11, L_ARG_108	2.90	2.05	7.50
5JXA.PDB	O, L_TYR_140	N, L_ALA_111	H, L_ALA_111	2.88	2.04	11.67
5JXA.PDB	O, L_LEU_135	N, L_PHE_116	H, L_PHE_116	2.95	2.16	18.98
5JXA.PDB	O, L_VAL_133	N, L_PHE_118	H, L_PHE_118	2.79	1.99	17.84
5JXA.PDB	OG, L_SER_131	NE2, L_GLN_124	HE22, L_GLN_124	2.80	1.95	4.80
5JXA.PDB	O, L_GLN_124	N, L_SER_127	H, L_SER_127	2.78	1.98	17.11
5JXA.PDB	O, L_LEU_125	N, L_GLY_128	H, L_GLY_128	2.90	2.04	5.48
5JXA.PDB	O, L_LEU_181	N, L_ALA_130	H, L_ALA_130	2.76	1.92	10.28
5JXA.PDB	OE1, L_GLN_124	N, L_SER_131	H, L_SER_131	3.00	2.18	14.97
5JXA.PDB	O, L_LEU_179	N, L_VAL_132	H, L_VAL_132	2.83	1.99	9.70
5JXA.PDB	O, L_SER_177	N, L_CYS_134	H, L_CYS_134	2.84	2.01	12.61
5JXA.PDB	O, L_PHE_116	N, L_LEU_135	H, L_LEU_135	2.76	1.91	8.80
5JXA.PDB	O, L_LEU_175	N, L_LEU_136	H, L_LEU_136	2.76	1.91	4.29
5JXA.PDB	O, L_SER_114	N, L_ASN_137	H, L_ASN_137	2.86	2.06	16.81
5JXA.PDB	O, L_TYR_173	N, L_PHE_139	H, L_PHE_139	2.83	2.00	12.08
5JXA.PDB	O, L_ALA_111	N, L_TYR_140	H, L_TYR_140	2.95	2.14	16.31
5JXA.PDB	OE1, L_GLU_105	OH, L_TYR_140	HH, L_TYR_140	2.43	1.65	17.73
5JXA.PDB	OE1, L_GLU_103	NH1, L_ARG_142	HH12, L_ARG_142	2.87	2.05	14.46
5JXA.PDB	OH, L_TYR_173	NH2, L_ARG_142	HH21, L_ARG_142	2.84	2.07	21.88
5JXA.PDB	OE2, L_GLU_103	NH2, L_ARG_142	HH22, L_ARG_142	2.79	1.94	8.50
5JXA.PDB	O, L_THR_197	N, L_LYS_145	H, L_LYS_145	2.95	2.11	9.81
5JXA.PDB	O, L_GLU_195	N, L_GLN_147	H, L_GLN_147	2.80	1.97	13.47
5JXA.PDB	O, L_TRP_148	NE2, L_GLN_147	HE21, L_GLN_147	2.90	2.05	7.67
5JXA.PDB	OG, L_SER_177	NE1, L_TRP_148	HE1, L_TRP_148	2.86	2.05	17.07
5JXA.PDB	O, L_ALA_193	N, L_LYS_149	H, L_LYS_149	2.88	2.05	13.32
5JXA.PDB	O, L_ALA_153	N, L_VAL_150	H, L_VAL_150	3.00	2.18	15.98
5JXA.PDB	O, L_VAL_191	N, L_ASP_151	H, L_ASP_151	2.79	1.95	10.19
5JXA.PDB	O, L_VAL_150	N, L_ALA_153	H, L_ALA_153	2.90	2.07	13.09
5JXA.PDB	O, L_TRP_148	N, L_GLN_155	H, L_GLN_155	2.93	2.09	9.40
5JXA.PDB	OE1, L_GLN_155	ND2, L_ASN_158	HD21, L_ASN_158	2.94	2.10	10.59
5JXA.PDB	O, H_LEU_170	NE2, L_GLN_160	HE22, L_GLN_160	2.84	1.99	4.55
5JXA.PDB	O, L_SER_176	N, L_SER_162	H, L_SER_162	2.98	2.19	20.08
5JXA.PDB	O, H_PRO_167	OG, L_SER_162	HG, L_SER_162	2.69	1.94	23.37
5JXA.PDB	O, L_SER_171	NE2, L_GLN_166	HE21, L_GLN_166	2.90	2.05	9.75
5JXA.PDB	O, L_VAL_106	NE2, L_GLN_166	HE22, L_GLN_166	2.89	2.10	19.46
5JXA.PDB	O, L_THR_172	N, L_ASP_167	H, L_ASP_167	2.83	2.01	13.03
5JXA.PDB	OD2, L_ASP_167	N, L_LYS_169	H, L_LYS_169	2.81	2.02	19.97
5JXA.PDB	OD2, L_ASP_167	N, L_ASP_170	H, L_ASP_170	2.85	2.02	14.37
5JXA.PDB	O, L_ASP_167	N, L_SER_171	H, L_SER_171	2.99	2.25	26.24
5JXA.PDB	OD1, L_ASP_170	N, L_THR_172	H, L_THR_172	2.91	2.07	10.06
5JXA.PDB	OD1, L_ASP_170	OG1, L_THR_172	HG1, L_THR_172	2.69	1.87	10.60
5JXA.PDB	O, L_PHE_139	N, L_TYR_173	H, L_TYR_173	2.81	1.97	11.11
5JXA.PDB	OE2, L_GLU_105	OH, L_TYR_173	HH, L_TYR_173	2.63	1.83	14.46
5JXA.PDB	OG1, L_THR_164	N, L_SER_174	H, L_SER_174	2.99	2.15	10.27
5JXA.PDB	O, L_LEU_136	N, L_LEU_175	H, L_LEU_175	2.81	2.01	18.94
5JXA.PDB	O, L_SER_162	N, L_SER_176	H, L_SER_176	2.93	2.11	14.73
5JXA.PDB	O, L_CYS_134	N, L_SER_177	H, L_SER_177	2.85	2.03	14.72
5JXA.PDB	O, L_GLN_160	N, L_THR_178	H, L_THR_178	2.87	2.05	14.07
5JXA.PDB	O, L_VAL_132	N, L_LEU_179	H, L_LEU_179	2.77	1.94	12.42
5JXA.PDB	O, L_ALA_130	N, L_LEU_181	H, L_LEU_181	2.90	2.06	10.98
5JXA.PDB	O, L_GLY_128	N, L_LYS_183	H, L_LYS_183	2.84	2.03	16.09
5JXA.PDB	O, L_SER_182	N, L_TYR_186	H, L_TYR_186	2.88	2.05	12.31
5JXA.PDB	O, L_LYS_183	N, L_GLU_187	H, L_GLU_187	2.94	2.15	20.11
5JXA.PDB	OD1, L_ASP_185	NZ, L_LYS_188	HZ2, L_LYS_188	2.85	2.03	19.98
5JXA.PDB	OD1, L_ASP_151	N, L_VAL_191	H, L_VAL_191	2.74	1.89	7.60
5JXA.PDB	O, L_PHE_209	N, L_TYR_192	H, L_TYR_192	2.93	2.07	4.78
5JXA.PDB	O, L_LYS_149	N, L_ALA_193	H, L_ALA_193	2.95	2.14	18.10
5JXA.PDB	O, L_LYS_207	N, L_CYS_194	H, L_CYS_194	2.83	1.98	9.36

5JXA.PDB	O, L_GLN_147	N, L_GLU_195	H, L_GLU_195	2.80	1.95	6.91
5JXA.PDB	O, L_VAL_205	N, L_VAL_196	H, L_VAL_196	2.78	1.95	10.55
5JXA.PDB	O, L_LYS_145	N, L_THR_197	H, L_THR_197	2.82	1.99	11.86
5JXA.PDB	O, L_PRO_141	NE2, L_HIS_198	HE2, L_HIS_198	2.88	2.05	12.53
5JXA.PDB	ND1, L_HIS_198	N, L_GLY_200	H, L_GLY_200	2.95	2.09	3.68
5JXA.PDB	O, L_HIS_198	N, L_LEU_201	H, L_LEU_201	2.92	2.08	9.11
5JXA.PDB	O, L_TYR_192	N, L_PHE_209	H, L_PHE_209	2.96	2.19	22.81
5JXA.PDB	OE2, L_GLU_213	ND2, L_ASN_210	HD22, L_ASN_210	2.76	1.93	12.84
5JXA.PDB	O, L_LYS_190	N, L_ARG_211	H, L_ARG_211	2.77	1.93	11.49
5JXA.PDB	O, L_HIS_189	NE, L_ARG_211	HE, L_ARG_211	2.81	1.95	5.90
5JXA.PDB	O, L_ASN_210	N, L_GLU_213	H, L_GLU_213	2.99	2.18	16.84

Table 1705: 5JXA-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5M2C.PDB	OD1, A_ASN.115	N, A_GLN.118	H, A_GLN.118	2.65	1.88	23.04
5M2C.PDB	O, A_LYS.116	N, A_ALA.120	H, A_ALA.120	2.80	1.94	5.96
5M2C.PDB	O, A_ASP.117	N, A_LYS.121	H, A_LYS.121	2.93	2.08	6.70
5M2C.PDB	O, A_GLN.118	N, A_ASP.122	H, A_ASP.122	2.87	2.05	16.09
5M2C.PDB	O, A_ILE.119	N, A_VAL.123	H, A_VAL.123	2.90	2.07	12.20
5M2C.PDB	O, A_ALA.120	N, A_LYS.124	H, A_LYS.124	2.89	2.06	12.17
5M2C.PDB	OD1, A_ASP.195	NZ, A_LYS.124	HZ1, A_LYS.124	2.99	2.26	29.03
5M2C.PDB	O, A_LYS.121	N, A_GLN.125	H, A_GLN.125	2.83	2.00	12.74
5M2C.PDB	O, A_ASP.122	N, A_PHE.126	H, A_PHE.126	2.85	2.04	15.29
5M2C.PDB	O, A_VAL.123	N, A_TYR.127	H, A_TYR.127	2.79	1.94	7.39
5M2C.PDB	O, A_LYS.124	N, A_ASP.128	H, A_ASP.128	2.86	2.06	18.46
5M2C.PDB	O, A_TYR.127	N, A_LEU.131	H, A_LEU.131	2.86	2.03	12.22
5M2C.PDB	O, A_ALA.130	N, A_ALA.134	H, A_ALA.134	2.83	2.04	19.67
5M2C.PDB	O, A_ASN.142	N, A_VAL.146	H, A_VAL.146	2.94	2.13	15.93
5M2C.PDB	O, A_ALA.143	N, A_VAL.147	H, A_VAL.147	2.90	2.05	6.08
5M2C.PDB	O, A_LYS.144	N, A_LYS.148	H, A_LYS.148	2.93	2.10	12.46
5M2C.PDB	O, A_VAL.146	N, A_PHE.150	H, A_PHE.150	2.92	2.07	6.77
5M2C.PDB	O, A_VAL.147	N, A_HIS.151	H, A_HIS.151	2.88	2.04	10.85
5M2C.PDB	O, A_LEU.174	ND1, A_HIS.151	HD1, A_HIS.151	2.73	1.92	15.82
5M2C.PDB	OH, A_TYR.127	NE2, A_HIS.151	HE2, A_HIS.151	2.61	1.77	12.06
5M2C.PDB	O, A_LYS.148	N, A_GLU.152	H, A_GLU.152	2.86	2.05	15.70
5M2C.PDB	O, A_THR.149	N, A_THR.153	H, A_THR.153	2.91	2.10	16.77
5M2C.PDB	O, A_THR.149	OG1, A_THR.153	HG1, A_THR.153	2.64	1.94	28.18
5M2C.PDB	O, A_PHE.150	N, A_LEU.154	H, A_LEU.154	2.87	2.06	17.25
5M2C.PDB	OG1, A_THR.163	N, A_SER.160	H, A_SER.160	2.95	2.16	19.89
5M2C.PDB	OG, A_SER.159	OG1, A_THR.163	HG1, A_THR.163	2.88	2.07	13.51
5M2C.PDB	O, A_SER.160	N, A_ALA.164	H, A_ALA.164	2.88	2.08	17.84
5M2C.PDB	O, A_THR.163	N, A_THR.167	H, A_THR.167	3.00	2.16	10.84
5M2C.PDB	O, A_THR.163	OG1, A_THR.167	HG1, A_THR.167	2.60	1.83	18.83
5M2C.PDB	O, A_ALA.164	N, A_SER.168	H, A_SER.168	2.91	2.11	17.88
5M2C.PDB	O, A_LEU.165	N, A_VAL.169	H, A_VAL.169	2.99	2.26	28.05
5M2C.PDB	O, A_THR.166	N, A_LEU.170	H, A_LEU.170	2.75	1.89	5.46
5M2C.PDB	O, A_THR.167	N, A_LYS.171	H, A_LYS.171	2.68	1.86	14.38
5M2C.PDB	O, A_LYS.171	N, A_LEU.174	H, A_LEU.174	2.89	2.03	5.60
5M2C.PDB	O, A_ASN.172	N, A_CYS.175	H, A_CYS.175	2.92	2.11	15.91
5M2C.PDB	O, A_PRO.176	N, A_SER.179	H, A_SER.179	2.98	2.16	15.63
5M2C.PDB	O, A_PRO.176	OG, A_SER.179	HG, A_SER.179	2.63	1.93	27.89
5M2C.PDB	OG, A_SER.183	N, A_ASN.180	H, A_ASN.180	2.83	2.08	25.30
5M2C.PDB	O, A_ASN.180	N, A_ASN.184	H, A_ASN.184	2.95	2.10	7.28
5M2C.PDB	OG, A_SER.179	ND2, A_ASN.184	HD21, A_ASN.184	2.93	2.13	18.24
5M2C.PDB	O, A_SER.183	N, A_PHE.186	H, A_PHE.186	2.77	1.95	13.31
5M2C.PDB	O, A_GLY.158	N, A_CYS.190	H, A_CYS.190	2.73	1.87	5.91
5M2C.PDB	OD2, A_ASP.128	NE2, A_HIS.191	HE2, A_HIS.191	2.69	1.84	6.13
5M2C.PDB	OD2, A_ASP.189	N, A_GLN.192	H, A_GLN.192	2.84	2.00	11.08
5M2C.PDB	O, A_CYS.190	N, A_ILE.194	H, A_ILE.194	2.93	2.11	15.42
5M2C.PDB	O, A_HIS.191	N, A_ASP.195	H, A_ASP.195	2.87	2.03	10.69
5M2C.PDB	O, A_GLN.192	N, A_ASP.196	H, A_ASP.196	2.80	2.05	24.04
5M2C.PDB	O, A_LYS.193	N, A_LEU.197	H, A_LEU.197	2.95	2.18	21.85
5M2C.PDB	O, A_ASP.195	OG, A_SER.199	HG, A_SER.199	2.79	2.04	23.21
5M2C.PDB	O, A_ASP.196	N, A_LYS.201	H, A_LYS.201	2.85	2.04	17.50
5M2C.PDB	OD1, B_ASN.115	N, B_GLN.118	H, B_GLN.118	2.50	1.70	17.47
5M2C.PDB	O, B_LYS.116	N, B_ALA.120	H, B_ALA.120	2.85	2.00	7.33
5M2C.PDB	O, B_ASP.117	N, B_LYS.121	H, B_LYS.121	2.86	2.01	8.98
5M2C.PDB	O, B_GLN.118	N, B_ASP.122	H, B_ASP.122	2.84	2.03	16.46
5M2C.PDB	O, B_ILE.119	N, B_VAL.123	H, B_VAL.123	2.89	2.07	14.86
5M2C.PDB	O, B_ALA.120	N, B_LYS.124	H, B_LYS.124	2.93	2.08	10.04
5M2C.PDB	O, B_LYS.121	N, B_GLN.125	H, B_GLN.125	2.84	2.01	12.48

5M2C.PDB	O, B_ASP_122	N, B_PHE_126	H, B_PHE_126	2.86	2.06	18.89
5M2C.PDB	O, B_VAL_123	N, B_TYR_127	H, B_TYR_127	2.81	1.97	10.19
5M2C.PDB	O, B_LYS_124	N, B_ASP_128	H, B_ASP_128	2.88	2.10	21.63
5M2C.PDB	O, B_TYR_127	N, B_LEU_131	H, B_LEU_131	2.85	2.02	11.94
5M2C.PDB	O, B_ALA_130	N, B_ALA_134	H, B_ALA_134	2.90	2.12	20.23
5M2C.PDB	O, B_ASN_142	N, B_VAL_146	H, B_VAL_146	2.99	2.15	11.45
5M2C.PDB	O, B_ALA_143	N, B_VAL_147	H, B_VAL_147	2.91	2.05	3.26
5M2C.PDB	O, B_LYS_144	N, B_LYS_148	H, B_LYS_148	2.96	2.14	15.99
5M2C.PDB	O, B_ALA_145	N, B_THR_149	H, B_THR_149	2.98	2.21	21.80
5M2C.PDB	O, B_ALA_145	OG1, B_THR_149	HG1, B_THR_149	2.78	1.99	18.17
5M2C.PDB	O, B_VAL_146	N, B_PHE_150	H, B_PHE_150	2.91	2.07	8.81
5M2C.PDB	O, B_VAL_147	N, B_HIS_151	H, B_HIS_151	2.89	2.07	14.41
5M2C.PDB	O, B_LEU_174	ND1, B_HIS_151	HD1, B_HIS_151	2.73	1.93	16.98
5M2C.PDB	OH, B_TYR_127	NE2, B_HIS_151	HE2, B_HIS_151	2.61	1.78	13.01
5M2C.PDB	O, B_LYS_148	N, B_GLU_152	H, B_GLU_152	2.84	2.02	14.19
5M2C.PDB	O, B_THR_149	N, B_THR_153	H, B_THR_153	2.90	2.09	15.77
5M2C.PDB	O, B_PHE_150	N, B_LEU_154	H, B_LEU_154	2.88	2.08	18.38
5M2C.PDB	O, B_SER_160	N, B_ALA_164	H, B_ALA_164	2.89	2.09	18.03
5M2C.PDB	O, B_THR_163	N, B_THR_167	H, B_THR_167	2.99	2.16	11.49
5M2C.PDB	O, B_THR_163	OG1, B_THR_167	HG1, B_THR_167	2.57	1.79	17.65
5M2C.PDB	O, B_ALA_164	N, B_SER_168	H, B_SER_168	2.89	2.09	18.74
5M2C.PDB	O, B_LEU_165	N, B_VAL_169	H, B_VAL_169	2.94	2.15	19.39
5M2C.PDB	O, B_THR_166	N, B_LEU_170	H, B_LEU_170	2.77	1.92	7.49
5M2C.PDB	O, B_THR_167	N, B_LYS_171	H, B_LYS_171	2.70	1.89	16.35
5M2C.PDB	O, B_LYS_171	N, B_LEU_174	H, B_LEU_174	2.94	2.09	4.41
5M2C.PDB	O, B_ASN_172	N, B_CYS_175	H, B_CYS_175	2.97	2.15	14.80
5M2C.PDB	O, B_PRO_176	OG, B_SER_179	HG, B_SER_179	2.63	1.92	26.26
5M2C.PDB	OG, B_SER_183	N, B_ASN_180	H, B_ASN_180	2.76	1.98	21.29
5M2C.PDB	O, B_ASN_180	N, B_ASN_184	H, B_ASN_184	2.89	2.04	8.95
5M2C.PDB	OG, B_SER_179	ND2, B_ASN_184	HD21, B_ASN_184	2.89	2.10	19.97
5M2C.PDB	O, B_SER_183	N, B_PHE_186	H, B_PHE_186	2.92	2.09	13.99
5M2C.PDB	O, B_GLY_158	N, B_CYS_190	H, B_CYS_190	2.71	1.85	3.39
5M2C.PDB	OD2, B_ASP_128	NE2, B_HIS_191	HE2, B_HIS_191	2.71	1.86	7.63
5M2C.PDB	OD2, B_ASP_189	N, B_GLN_192	H, B_GLN_192	2.90	2.07	13.53
5M2C.PDB	O, B_CYS_190	N, B_ILE_194	H, B_ILE_194	2.91	2.10	17.50
5M2C.PDB	O, B_HIS_191	N, B_ASP_195	H, B_ASP_195	2.87	2.03	11.04
5M2C.PDB	O, B_GLN_192	N, B_ASP_196	H, B_ASP_196	2.81	2.05	23.43
5M2C.PDB	O, B_ASP_195	N, B_SER_199	H, B_SER_199	2.98	2.26	28.48
5M2C.PDB	O, B_ASP_195	OG, B_SER_199	HG, B_SER_199	2.85	2.13	27.00
5M2C.PDB	O, B_ASP_196	N, B_LYS_201	H, B_LYS_201	2.97	2.16	15.75

Table 1706: 5M2C-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5M33.PDB	O, A_GLU_110	N, A_PHE_113	H, A_PHE_113	2.89	2.13	23.34
5M33.PDB	OD1, A_ASN_115	N, A_GLN_118	H, A_GLN_118	2.87	2.05	15.86
5M33.PDB	OD1, A_ASP_122	NE2, A_GLN_118	HE21, A_GLN_118	2.92	2.20	28.21
5M33.PDB	O, A_GLN_118	N, A_ASP_122	H, A_ASP_122	2.91	2.09	14.98
5M33.PDB	O, A_ILE_119	N, A_VAL_123	H, A_VAL_123	2.90	2.08	14.75
5M33.PDB	O, A_ALA_120	N, A_LYS_124	H, A_LYS_124	2.97	2.13	9.03
5M33.PDB	OD1, A_ASP_195	NZ, A_LYS_124	HZ3, A_LYS_124	2.81	2.00	20.18
5M33.PDB	O, A_LYS_121	N, A_GLN_125	H, A_GLN_125	2.95	2.14	15.95
5M33.PDB	O, A_ASP_122	N, A_PHE_126	H, A_PHE_126	2.85	2.02	12.96
5M33.PDB	O, A_VAL_123	N, A_TYR_127	H, A_TYR_127	2.90	2.06	8.97
5M33.PDB	NE2, A_HIS_151	OH, A_TYR_127	HH, A_TYR_127	2.74	1.90	5.54
5M33.PDB	O, A_LYS_124	N, A_ASP_128	H, A_ASP_128	2.96	2.14	15.35
5M33.PDB	O, A_GLN_125	N, A_GLN_129	H, A_GLN_129	2.89	2.05	10.97
5M33.PDB	O, A_TYR_127	N, A_LEU_131	H, A_LEU_131	2.85	2.03	13.94
5M33.PDB	O, A_ALA_130	N, A_ALA_134	H, A_ALA_134	2.84	2.03	15.90
5M33.PDB	O, A_GLN_133	N, A_ASP_137	H, A_ASP_137	2.89	2.12	21.46
5M33.PDB	O, A_ASP_139	N, A_ASN_141	H, A_ASN_141	2.85	2.12	27.58
5M33.PDB	O, A_ALA_140	N, A_LYS_144	H, A_LYS_144	2.99	2.14	7.21
5M33.PDB	O, A_ALA_134	NZ, A_LYS_144	HZ1, A_LYS_144	2.63	1.88	27.02
5M33.PDB	O, A_ASN_142	N, A_VAL_146	H, A_VAL_146	2.83	2.01	15.56
5M33.PDB	O, A_LYS_144	N, A_LYS_148	H, A_LYS_148	2.98	2.13	8.41
5M33.PDB	O, A_ALA_145	N, A_THR_149	H, A_THR_149	2.97	2.14	13.99
5M33.PDB	O, A_ALA_145	OG1, A_THR_149	HG1, A_THR_149	2.90	2.10	14.64
5M33.PDB	O, A_VAL_146	N, A_PHE_150	H, A_PHE_150	2.90	2.07	12.70
5M33.PDB	O, A_VAL_147	N, A_HIS_151	H, A_HIS_151	2.86	2.03	12.68
5M33.PDB	O, A_LEU_174	ND1, A_HIS_151	HD1, A_HIS_151	2.74	1.89	6.51
5M33.PDB	O, A_LYS_148	N, A_GLU_152	H, A_GLU_152	2.94	2.12	14.44
5M33.PDB	O, A_THR_149	N, A_THR_153	H, A_THR_153	2.89	2.04	7.79
5M33.PDB	O, A_PHE_150	N, A_LEU_154	H, A_LEU_154	2.88	2.05	10.83
5M33.PDB	OD2, A_ASP_189	N, A_SER_160	H, A_SER_160	2.83	2.06	21.68
5M33.PDB	O, A_LEU_162	N, A_LEU_165	H, A_LEU_165	2.91	2.09	16.07
5M33.PDB	O, A_LEU_165	N, A_VAL_169	H, A_VAL_169	2.92	2.13	19.68
5M33.PDB	O, A_THR_166	N, A_LEU_170	H, A_LEU_170	2.91	2.09	13.68
5M33.PDB	O, A_PRO_176	N, A_SER_179	H, A_SER_179	2.93	2.10	12.30
5M33.PDB	O, A_ASN_180	N, A_ASN_184	H, A_ASN_184	2.90	2.08	14.21
5M33.PDB	O, A_CYS_157	ND2, A_ASN_184	HD21, A_ASN_184	2.88	2.04	11.64
5M33.PDB	OD1, A_ASP_155	NZ, A_LYS_187	HZ1, A_LYS_187	2.82	1.95	10.61
5M33.PDB	O, A_GLY_158	N, A_CYS_190	H, A_CYS_190	2.93	2.07	4.56
5M33.PDB	OD2, A_ASP_189	N, A_HIS_191	H, A_HIS_191	2.98	2.19	19.93
5M33.PDB	OD2, A_ASP_128	NE2, A_HIS_191	HE2, A_HIS_191	2.76	2.00	23.16
5M33.PDB	OD1, A_ASP_196	NE2, A_GLN_192	HE21, A_GLN_192	2.98	2.18	18.41
5M33.PDB	OE1, A_GLU_188	NZ, A_LYS_193	HZ2, A_LYS_193	2.93	2.07	12.47
5M33.PDB	O, A_CYS_190	N, A_ILE_194	H, A_ILE_194	2.89	2.07	15.58
5M33.PDB	O, A_HIS_191	N, A_ASP_195	H, A_ASP_195	2.97	2.13	8.98
5M33.PDB	O, A_GLN_192	N, A_ASP_196	H, A_ASP_196	2.88	2.06	14.98
5M33.PDB	O, A_ASP_195	N, A_SER_199	H, A_SER_199	2.93	2.19	25.46
5M33.PDB	O, A_ASP_196	N, A_LYS_201	H, A_LYS_201	2.86	2.03	14.10
5M33.PDB	OE1, A_GLN_129	N, B_VAL_114	H, B_VAL_114	2.67	1.84	13.32
5M33.PDB	OD1, B_ASN_115	N, B_GLN_118	H, B_GLN_118	2.98	2.19	19.82
5M33.PDB	OD1, B_ASP_122	NE2, B_GLN_118	HE21, B_GLN_118	2.96	2.19	23.61
5M33.PDB	O, B_GLN_118	N, B_ASP_122	H, B_ASP_122	2.94	2.12	14.74
5M33.PDB	O, B_ILE_119	N, B_VAL_123	H, B_VAL_123	2.92	2.09	14.21
5M33.PDB	O, B_ALA_120	N, B_LYS_124	H, B_LYS_124	2.95	2.13	13.05
5M33.PDB	O, B_LYS_121	N, B_GLN_125	H, B_GLN_125	2.97	2.15	14.67
5M33.PDB	O, B_ASP_122	N, B_PHE_126	H, B_PHE_126	2.83	2.02	16.58
5M33.PDB	O, B_VAL_123	N, B_TYR_127	H, B_TYR_127	2.90	2.05	7.34
5M33.PDB	NE2, B_HIS_151	OH, B_TYR_127	HH, B_TYR_127	2.78	1.94	5.42

5M33.PDB	O, B_LYS_124	N, B_ASP_128	H, B_ASP_128	2.88	2.07	15.69
5M33.PDB	O, B_GLN_125	N, B_GLN_129	H, B_GLN_129	3.00	2.18	15.70
5M33.PDB	OE1, B_GLN_133	NE2, B_GLN_129	HE22, B_GLN_129	2.83	2.06	21.87
5M33.PDB	O, B_TYR_127	N, B_LEU_131	H, B_LEU_131	2.88	2.05	11.48
5M33.PDB	O, B_GLN_129	N, B_GLN_133	H, B_GLN_133	2.98	2.15	12.11
5M33.PDB	O, B_ALA_130	N, B_ALA_134	H, B_ALA_134	2.83	2.07	24.03
5M33.PDB	O, B_ALA_134	NZ, B_LYS_144	HZ2, B_LYS_144	2.73	1.99	28.33
5M33.PDB	O, B_ALA_143	N, B_VAL_147	H, B_VAL_147	2.84	1.99	5.95
5M33.PDB	O, B_LYS_144	N, B_LYS_148	H, B_LYS_148	2.93	2.08	9.25
5M33.PDB	O, B_ALA_145	N, B_THR_149	H, B_THR_149	2.93	2.11	14.19
5M33.PDB	O, B_ALA_145	OG1, B_THR_149	HG1, B_THR_149	2.85	2.11	23.29
5M33.PDB	O, B_VAL_146	N, B_PHE_150	H, B_PHE_150	2.93	2.09	9.45
5M33.PDB	O, B_VAL_147	N, B_HIS_151	H, B_HIS_151	2.93	2.09	11.38
5M33.PDB	O, B_LEU_174	ND1, B_HIS_151	HD1, B_HIS_151	2.74	1.90	9.06
5M33.PDB	O, B_LYS_148	N, B_GLU_152	H, B_GLU_152	2.91	2.08	12.10
5M33.PDB	O, B_THR_149	N, B_THR_153	H, B_THR_153	2.90	2.07	12.38
5M33.PDB	O, B_PHE_150	N, B_LEU_154	H, B_LEU_154	2.87	2.02	7.88
5M33.PDB	OD1, B_ASP_189	N, B_SER_160	H, B_SER_160	2.83	1.97	1.56
5M33.PDB	OD1, B_ASP_189	OG, B_SER_160	HG, B_SER_160	2.86	2.13	25.03
5M33.PDB	O, B_SER_159	N, B_LEU_162	H, B_LEU_162	2.96	2.12	9.23
5M33.PDB	O, B_LEU_162	OG1, B_THR_166	HG1, B_THR_166	2.89	2.08	13.11
5M33.PDB	O, B_THR_163	N, B_THR_167	H, B_THR_167	2.93	2.11	14.74
5M33.PDB	O, B_LEU_165	N, B_VAL_169	H, B_VAL_169	2.98	2.16	14.43
5M33.PDB	O, B_THR_167	N, B_LYS_171	H, B_LYS_171	2.99	2.26	27.58
5M33.PDB	O, B_SER_179	N, B_SER_183	H, B_SER_183	2.82	1.97	7.48
5M33.PDB	O, B_GLY_158	N, B_CYS_190	H, B_CYS_190	2.96	2.12	9.28
5M33.PDB	OD2, B_ASP_128	NE2, B_HIS_191	HE2, B_HIS_191	2.69	1.83	4.41
5M33.PDB	OD2, B_ASP_189	N, B_GLN_192	H, B_GLN_192	2.97	2.16	16.91
5M33.PDB	OD1, B_ASP_196	NE2, B_GLN_192	HE21, B_GLN_192	2.92	2.12	17.81
5M33.PDB	O, B_CYS_190	N, B_ILE_194	H, B_ILE_194	2.95	2.13	14.36
5M33.PDB	O, B_HIS_191	N, B_ASP_195	H, B_ASP_195	2.95	2.10	7.27
5M33.PDB	O, B_GLN_192	N, B_ASP_196	H, B_ASP_196	2.83	2.01	15.81
5M33.PDB	O, B_LYS_193	N, B_LEU_197	H, B_LEU_197	2.94	2.16	20.67
5M33.PDB	O, B_ASP_195	N, B_SER_199	H, B_SER_199	2.93	2.22	28.83
5M33.PDB	O, B_ASP_196	N, B_LYS_201	H, B_LYS_201	2.98	2.26	27.91

Table 1707: 5M33-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5M3D.PDB	O, A.ASP.117	N, A.LYS.121	H, A.LYS.121	2.91	2.07	9.22
5M3D.PDB	O, A.GLN.118	N, A.ASP.122	H, A.ASP.122	2.83	1.99	10.35
5M3D.PDB	O, A.ILE.119	N, A.VAL.123	H, A.VAL.123	2.80	2.00	16.75
5M3D.PDB	O, A.ALA.120	N, A.LYS.124	H, A.LYS.124	2.87	2.02	7.87
5M3D.PDB	OD2, A.ASP.195	NZ, A.LYS.124	HZ1, A.LYS.124	2.68	1.86	18.64
5M3D.PDB	O, A.LYS.121	N, A.GLN.125	H, A.GLN.125	2.82	1.99	11.95
5M3D.PDB	O, A.ASP.122	N, A.PHE.126	H, A.PHE.126	2.97	2.13	10.05
5M3D.PDB	O, A.VAL.123	N, A.TYR.127	H, A.TYR.127	2.86	2.04	15.68
5M3D.PDB	NE2, A.HIS.151	OH, A.TYR.127	HH, A.TYR.127	2.90	2.07	7.76
5M3D.PDB	O, A.LYS.124	N, A.ASP.128	H, A.ASP.128	2.81	1.97	10.20
5M3D.PDB	O, A.TYR.127	N, A.LEU.131	H, A.LEU.131	2.85	2.06	19.33
5M3D.PDB	O, A.ASP.128	N, A.GLN.132	H, A.GLN.132	2.90	2.05	6.60
5M3D.PDB	O, A.ALA.130	N, A.ALA.134	H, A.ALA.134	2.87	2.13	25.45
5M3D.PDB	O, A.LEU.131	N, A.VAL.135	H, A.VAL.135	2.91	2.18	26.93
5M3D.PDB	O, A.ALA.143	N, A.VAL.147	H, A.VAL.147	2.83	1.97	0.49
5M3D.PDB	O, A.LYS.144	N, A.LYS.148	H, A.LYS.148	2.78	1.93	2.97
5M3D.PDB	O, A.ALA.145	N, A.THR.149	H, A.THR.149	2.94	2.20	26.27
5M3D.PDB	O, A.VAL.146	N, A.PHE.150	H, A.PHE.150	2.81	1.96	8.90
5M3D.PDB	O, A.VAL.147	N, A.HIS.151	H, A.HIS.151	2.83	2.03	18.07
5M3D.PDB	O, A.LEU.174	ND1, A.HIS.151	HD1, A.HIS.151	2.54	1.70	10.32
5M3D.PDB	O, A.LYS.148	N, A.GLU.152	H, A.GLU.152	2.91	2.05	3.90
5M3D.PDB	O, A.THR.149	N, A.THR.153	H, A.THR.153	2.94	2.14	17.42
5M3D.PDB	O, A.THR.149	OG1, A.THR.153	HG1, A.THR.153	2.71	1.99	26.30
5M3D.PDB	O, A.PHE.150	N, A.LEU.154	H, A.LEU.154	2.82	2.01	16.30
5M3D.PDB	OG1, A.THR.163	N, A.SER.160	H, A.SER.160	2.68	1.93	24.41
5M3D.PDB	OG, A.SER.159	OG1, A.THR.163	HG1, A.THR.163	2.65	1.81	3.28
5M3D.PDB	O, A.SER.160	N, A.ALA.164	H, A.ALA.164	2.68	1.86	13.35
5M3D.PDB	O, A.LEU.162	N, A.THR.166	H, A.THR.166	2.92	2.11	17.03
5M3D.PDB	O, A.THR.163	N, A.THR.167	H, A.THR.167	2.80	1.97	12.32
5M3D.PDB	O, A.THR.163	OG1, A.THR.167	HG1, A.THR.167	2.52	1.70	11.15
5M3D.PDB	O, A.ALA.164	N, A.SER.168	H, A.SER.168	2.89	2.05	8.46
5M3D.PDB	O, A.LEU.165	OG, A.SER.168	HG, A.SER.168	2.61	1.86	22.97
5M3D.PDB	O, A.THR.166	N, A.LEU.170	H, A.LEU.170	2.78	1.95	12.52
5M3D.PDB	O, A.THR.167	N, A.LYS.171	H, A.LYS.171	2.87	2.05	15.75
5M3D.PDB	O, A.ASN.172	N, A.CYS.175	H, A.CYS.175	2.95	2.10	9.28
5M3D.PDB	OE2, A.GLU.152	N, A.SER.177	H, A.SER.177	2.77	2.02	24.92
5M3D.PDB	O, A.PRO.176	N, A.SER.179	H, A.SER.179	2.91	2.14	22.27
5M3D.PDB	O, A.GLY.158	N, A.CYS.190	H, A.CYS.190	2.75	1.91	12.01
5M3D.PDB	OD2, A.ASP.128	NE2, A.HIS.191	HE2, A.HIS.191	2.68	1.84	10.19
5M3D.PDB	OD2, A.ASP.189	N, A.GLN.192	H, A.GLN.192	2.94	2.11	13.24
5M3D.PDB	O, A.CYS.190	N, A.ILE.194	H, A.ILE.194	2.85	2.02	12.94
5M3D.PDB	O, A.GLN.192	N, A.ASP.196	H, A.ASP.196	2.98	2.19	20.53
5M3D.PDB	O, A.LYS.193	N, A.LEU.197	H, A.LEU.197	2.95	2.19	23.68
5M3D.PDB	O, A.ASP.196	N, A.GLY.200	H, A.GLY.200	2.84	2.13	29.15
5M3D.PDB	O, A.ASP.196	N, A.LYS.201	H, A.LYS.201	2.79	1.95	11.59
5M3D.PDB	O, B.ASP.117	N, B.LYS.121	H, B.LYS.121	2.91	2.06	7.49
5M3D.PDB	O, B.GLN.118	N, B.ASP.122	H, B.ASP.122	2.85	2.04	15.98
5M3D.PDB	O, B.ILE.119	N, B.VAL.123	H, B.VAL.123	2.79	2.02	22.71
5M3D.PDB	O, B.ALA.120	N, B.LYS.124	H, B.LYS.124	2.98	2.14	9.81
5M3D.PDB	O, B.LYS.121	N, B.GLN.125	H, B.GLN.125	2.85	2.02	12.96
5M3D.PDB	O, B.VAL.123	N, B.TYR.127	H, B.TYR.127	2.75	1.92	13.65
5M3D.PDB	O, B.LYS.124	N, B.ASP.128	H, B.ASP.128	2.78	1.96	14.20
5M3D.PDB	O, B.TYR.127	N, B.LEU.131	H, B.LEU.131	2.91	2.12	19.44
5M3D.PDB	O, B.ASP.128	N, B.GLN.132	H, B.GLN.132	2.94	2.09	6.13
5M3D.PDB	O, B.LEU.131	N, B.VAL.135	H, B.VAL.135	2.87	2.11	24.04
5M3D.PDB	O, B.GLN.133	N, B.ASP.137	H, B.ASP.137	2.97	2.23	25.98
5M3D.PDB	O, B.ALA.140	N, B.LYS.144	H, B.LYS.144	2.98	2.14	8.88

5M3D.PDB	O, B.ALA.143	N, B.VAL.147	H, B.VAL.147	2.86	2.01	7.67
5M3D.PDB	O, B.LYS.144	N, B.LYS.148	H, B.LYS.148	2.88	2.04	10.53
5M3D.PDB	O, B.ALA.145	N, B.THR.149	H, B.THR.149	2.92	2.16	24.76
5M3D.PDB	O, B.ALA.145	OG1, B.THR.149	HG1, B.THR.149	2.92	2.10	9.10
5M3D.PDB	O, B.VAL.146	N, B.PHE.150	H, B.PHE.150	2.87	2.03	11.14
5M3D.PDB	O, B.VAL.147	N, B.HIS.151	H, B.HIS.151	2.90	2.05	8.21
5M3D.PDB	O, B.LEU.174	ND1, B.HIS.151	HD1, B.HIS.151	2.69	1.87	15.29
5M3D.PDB	O, B.LYS.148	N, B.GLU.152	H, B.GLU.152	2.90	2.06	9.45
5M3D.PDB	O, B.THR.149	N, B.THR.153	H, B.THR.153	2.76	1.95	16.27
5M3D.PDB	O, B.THR.149	OG1, B.THR.153	HG1, B.THR.153	2.68	1.93	21.92
5M3D.PDB	O, B.PHE.150	N, B.LEU.154	H, B.LEU.154	2.72	1.93	19.17
5M3D.PDB	OG1, B.THR.163	N, B.SER.160	H, B.SER.160	2.60	1.81	18.90
5M3D.PDB	O, B.SER.160	N, B.ALA.164	H, B.ALA.164	2.64	1.86	20.55
5M3D.PDB	O, B.LEU.162	N, B.THR.166	H, B.THR.166	2.88	2.06	14.51
5M3D.PDB	O, B.THR.163	N, B.THR.167	H, B.THR.167	2.95	2.11	9.70
5M3D.PDB	O, B.THR.163	OG1, B.THR.167	HG1, B.THR.167	2.62	1.82	14.83
5M3D.PDB	O, B.ALA.164	N, B.SER.168	H, B.SER.168	2.95	2.12	11.19
5M3D.PDB	O, B.LEU.165	N, B.VAL.169	H, B.VAL.169	2.95	2.20	25.38
5M3D.PDB	O, B.THR.166	N, B.LEU.170	H, B.LEU.170	2.72	1.93	19.91
5M3D.PDB	O, B.THR.167	N, B.LYS.171	H, B.LYS.171	2.71	1.87	9.68
5M3D.PDB	O, B.LYS.171	N, B.LEU.174	H, B.LEU.174	2.95	2.14	16.60
5M3D.PDB	O, B.PRO.176	OG, B.SER.179	HG, B.SER.179	2.60	1.81	16.72
5M3D.PDB	O, B.ILE.181	N, B.ASN.184	H, B.ASN.184	2.99	2.21	20.02
5M3D.PDB	O, B.ILE.182	N, B.LEU.185	H, B.LEU.185	2.82	1.98	10.54
5M3D.PDB	O, B.GLY.158	N, B.CYS.190	H, B.CYS.190	2.80	1.94	4.10
5M3D.PDB	OD2, B.ASP.128	NE2, B.HIS.191	HE2, B.HIS.191	2.60	1.78	15.29
5M3D.PDB	OD2, B.ASP.189	N, B.GLN.192	H, B.GLN.192	2.93	2.11	13.82
5M3D.PDB	O, B.CYS.190	N, B.ILE.194	H, B.ILE.194	2.95	2.12	12.39
5M3D.PDB	O, B.GLN.192	N, B.ASP.196	H, B.ASP.196	2.84	2.02	14.80
5M3D.PDB	O, B.LYS.193	N, B.LEU.197	H, B.LEU.197	2.93	2.17	22.99
5M3D.PDB	O, B.ASP.195	N, B.SER.199	H, B.SER.199	2.86	2.15	29.72
5M3D.PDB	O, B.ASP.195	OG, B.SER.199	HG, B.SER.199	2.55	1.74	13.09
5M3D.PDB	O, B.ASP.196	N, B.LYS.201	H, B.LYS.201	2.86	2.06	19.17
5M3D.PDB	OD1, C.ASN.115	N, C.ASP.117	H, C.ASP.117	2.96	2.17	19.69
5M3D.PDB	O, C.ILE.119	N, C.VAL.123	H, C.VAL.123	2.94	2.22	28.48
5M3D.PDB	O, C.ALA.120	N, C.LYS.124	H, C.LYS.124	2.91	2.07	9.91
5M3D.PDB	O, C.LYS.121	N, C.GLN.125	H, C.GLN.125	2.85	2.05	17.95
5M3D.PDB	O, C.VAL.123	N, C.TYR.127	H, C.TYR.127	2.85	2.00	5.96
5M3D.PDB	O, C.LYS.124	N, C.ASP.128	H, C.ASP.128	2.86	2.05	16.00
5M3D.PDB	O, C.GLN.125	N, C.GLN.129	H, C.GLN.129	2.82	2.03	19.59
5M3D.PDB	O, C.TYR.127	N, C.LEU.131	H, C.LEU.131	2.81	1.98	13.11
5M3D.PDB	O, C.ASP.128	N, C.GLN.132	H, C.GLN.132	2.89	2.04	7.47
5M3D.PDB	O, C.ALA.130	N, C.ALA.134	H, C.ALA.134	2.74	1.97	21.94
5M3D.PDB	O, C.LEU.131	N, C.VAL.135	H, C.VAL.135	2.89	2.05	11.04
5M3D.PDB	O, C.ALA.134	N, C.ASP.137	H, C.ASP.137	2.88	2.05	12.98
5M3D.PDB	O, C.ASP.139	N, C.ASN.142	H, C.ASN.142	2.98	2.16	15.52
5M3D.PDB	O, C.ALA.143	N, C.VAL.147	H, C.VAL.147	2.88	2.05	12.04
5M3D.PDB	O, C.ALA.145	N, C.THR.149	H, C.THR.149	2.76	1.97	19.10
5M3D.PDB	O, C.ALA.145	OG1, C.THR.149	HG1, C.THR.149	2.85	2.04	10.77
5M3D.PDB	O, C.VAL.146	N, C.PHE.150	H, C.PHE.150	2.86	2.02	10.98
5M3D.PDB	O, C.VAL.147	N, C.HIS.151	H, C.HIS.151	2.93	2.10	13.09
5M3D.PDB	O, C.LEU.174	ND1, C.HIS.151	HD1, C.HIS.151	2.77	1.93	9.75
5M3D.PDB	OH, C.TYR.127	NE2, C.HIS.151	HE2, C.HIS.151	2.47	1.64	11.96
5M3D.PDB	O, C.LYS.148	N, C.GLU.152	H, C.GLU.152	2.93	2.07	6.86
5M3D.PDB	O, C.THR.149	N, C.THR.153	H, C.THR.153	2.90	2.09	16.64
5M3D.PDB	O, C.THR.149	OG1, C.THR.153	HG1, C.THR.153	2.82	2.11	26.57
5M3D.PDB	O, C.PHE.150	N, C.LEU.154	H, C.LEU.154	2.84	2.09	25.26
5M3D.PDB	O, C.SER.160	N, C.ALA.164	H, C.ALA.164	2.77	1.96	15.47

5M3D.PDB	O, C.THR.161	N, C.LEU.165	H, C.LEU.165	2.92	2.11	16.78
5M3D.PDB	O, C.LEU.162	N, C.THR.166	H, C.THR.166	2.96	2.13	14.34
5M3D.PDB	O, C.LEU.162	OG1, C.THR.166	HG1, C.THR.166	2.66	1.88	17.50
5M3D.PDB	O, C.THR.163	N, C.THR.167	H, C.THR.167	2.83	2.02	16.33
5M3D.PDB	O, C.ALA.164	N, C.SER.168	H, C.SER.168	2.89	2.05	9.74
5M3D.PDB	O, C.LEU.165	N, C.VAL.169	H, C.VAL.169	2.92	2.16	23.23
5M3D.PDB	O, C.THR.166	N, C.LEU.170	H, C.LEU.170	2.78	2.00	20.88
5M3D.PDB	O, C.THR.167	N, C.LYS.171	H, C.LYS.171	2.57	1.75	15.04
5M3D.PDB	O, C.LYS.171	N, C.LEU.174	H, C.LEU.174	2.84	1.99	6.87
5M3D.PDB	OE2, C.GLU.152	N, C.SER.177	H, C.SER.177	2.69	1.86	11.04
5M3D.PDB	O, C.PRO.176	N, C.SER.179	H, C.SER.179	2.93	2.13	18.85
5M3D.PDB	O, C.SER.183	N, C.LYS.187	H, C.LYS.187	2.80	1.94	3.39
5M3D.PDB	O, C.GLY.158	N, C.CYS.190	H, C.CYS.190	2.73	1.88	7.85
5M3D.PDB	OD2, C.ASP.128	NE2, C.HIS.191	HE2, C.HIS.191	2.54	1.74	17.73
5M3D.PDB	OD2, C.ASP.189	N, C.GLN.192	H, C.GLN.192	2.80	1.97	13.12
5M3D.PDB	O, C.CYS.190	N, C.ILE.194	H, C.ILE.194	2.91	2.07	10.39
5M3D.PDB	O, C.GLN.192	N, C.ASP.196	H, C.ASP.196	3.00	2.18	15.71
5M3D.PDB	O, C.LYS.193	N, C.LEU.197	H, C.LEU.197	2.84	2.09	24.23
5M3D.PDB	O, C.ILE.194	N, C.PHE.198	H, C.PHE.198	2.99	2.20	19.69
5M3D.PDB	O, C.ASP.195	N, C.SER.199	H, C.SER.199	2.70	2.00	29.60
5M3D.PDB	O, C.ASP.196	N, C.GLY.200	H, C.GLY.200	2.91	2.19	27.12
5M3D.PDB	O, C.ASP.196	N, C.LYS.201	H, C.LYS.201	2.94	2.12	15.69
5M3D.PDB	O, D.LYS.116	N, D.ALA.120	H, D.ALA.120	2.96	2.12	9.84
5M3D.PDB	O, D.ASP.117	N, D.LYS.121	H, D.LYS.121	2.91	2.07	10.71
5M3D.PDB	O, D.GLN.118	N, D.ASP.122	H, D.ASP.122	2.91	2.16	24.90
5M3D.PDB	O, D.ILE.119	N, D.VAL.123	H, D.VAL.123	2.93	2.21	28.37
5M3D.PDB	O, D.LYS.121	N, D.GLN.125	H, D.GLN.125	2.91	2.11	17.36
5M3D.PDB	O, D.ASP.122	N, D.PHE.126	H, D.PHE.126	2.97	2.18	20.39
5M3D.PDB	O, D.VAL.123	N, D.TYR.127	H, D.TYR.127	2.77	1.93	9.04
5M3D.PDB	O, D.LYS.124	N, D.ASP.128	H, D.ASP.128	2.88	2.02	2.98
5M3D.PDB	O, D.GLN.125	N, D.GLN.129	H, D.GLN.129	2.86	2.07	19.17
5M3D.PDB	O, D.TYR.127	N, D.LEU.131	H, D.LEU.131	2.78	1.93	8.17
5M3D.PDB	O, D.ASP.128	N, D.GLN.132	H, D.GLN.132	2.90	2.06	10.99
5M3D.PDB	O, D.ALA.130	N, D.ALA.134	H, D.ALA.134	2.62	1.92	29.22
5M3D.PDB	O, D.ALA.134	N, D.ASP.137	H, D.ASP.137	2.77	1.92	5.77
5M3D.PDB	OD1, D.ASP.139	N, D.LYS.144	H, D.LYS.144	2.75	1.89	6.98
5M3D.PDB	O, D.ALA.143	N, D.VAL.147	H, D.VAL.147	2.90	2.06	10.59
5M3D.PDB	O, D.ALA.145	N, D.THR.149	H, D.THR.149	2.80	2.05	24.05
5M3D.PDB	O, D.ALA.145	OG1, D.THR.149	HG1, D.THR.149	2.76	1.96	14.72
5M3D.PDB	O, D.VAL.146	N, D.PHE.150	H, D.PHE.150	2.91	2.07	9.79
5M3D.PDB	O, D.VAL.147	N, D.HIS.151	H, D.HIS.151	2.81	1.99	13.17
5M3D.PDB	O, D.LEU.174	ND1, D.HIS.151	HD1, D.HIS.151	2.86	2.05	15.14
5M3D.PDB	O, D.THR.149	N, D.THR.153	H, D.THR.153	2.95	2.11	9.66
5M3D.PDB	O, D.THR.149	OG1, D.THR.153	HG1, D.THR.153	2.80	2.08	26.61
5M3D.PDB	O, D.PHE.150	N, D.LEU.154	H, D.LEU.154	2.86	2.05	16.07
5M3D.PDB	O, D.SER.160	N, D.ALA.164	H, D.ALA.164	2.69	1.86	12.75
5M3D.PDB	O, D.THR.161	N, D.LEU.165	H, D.LEU.165	2.89	2.08	15.84
5M3D.PDB	O, D.LEU.162	N, D.THR.166	H, D.THR.166	2.90	2.06	10.23
5M3D.PDB	O, D.THR.163	N, D.THR.167	H, D.THR.167	2.74	1.91	11.96
5M3D.PDB	O, D.THR.163	OG1, D.THR.167	HG1, D.THR.167	2.95	2.24	27.05
5M3D.PDB	O, D.ALA.164	N, D.SER.168	H, D.SER.168	2.84	2.03	16.52
5M3D.PDB	O, D.LEU.165	N, D.VAL.169	H, D.VAL.169	2.95	2.18	22.42
5M3D.PDB	O, D.THR.166	N, D.LEU.170	H, D.LEU.170	2.84	2.04	17.12
5M3D.PDB	O, D.THR.167	N, D.LYS.171	H, D.LYS.171	2.56	1.77	19.83
5M3D.PDB	O, D.LYS.171	N, D.LEU.174	H, D.LEU.174	2.77	1.92	4.36
5M3D.PDB	O, D.PRO.176	OG, D.SER.179	HG, D.SER.179	2.66	1.84	11.66
5M3D.PDB	O, D.ASN.180	OG, D.SER.183	HG, D.SER.183	2.86	2.12	23.28
5M3D.PDB	O, D.ILE.182	N, D.LEU.185	H, D.LEU.185	2.97	2.13	11.47

5M3D.PDB	O, D_SER_183	N, D_LYS_187	H, D_LYS_187	2.96	2.10	3.55
5M3D.PDB	OE1, D_GLN_192	N, D_ASP_189	H, D_ASP_189	2.76	1.94	13.89
5M3D.PDB	O, D_GLY_158	N, D_CYS_190	H, D_CYS_190	2.79	1.94	7.19
5M3D.PDB	OD2, D_ASP_128	NE2, D_HIS_191	HE2, D_HIS_191	2.53	1.71	14.84
5M3D.PDB	OD2, D_ASP_189	N, D_GLN_192	H, D_GLN_192	2.82	1.99	12.15
5M3D.PDB	O, D_CYS_190	N, D_ILE_194	H, D_ILE_194	2.85	2.03	13.91
5M3D.PDB	O, D_GLN_192	N, D_ASP_196	H, D_ASP_196	2.90	2.15	24.84
5M3D.PDB	O, D_LYS_193	N, D_LEU_197	H, D_LEU_197	2.84	2.06	21.13
5M3D.PDB	O, D_ASP_196	N, D_GLY_200	H, D_GLY_200	2.79	2.05	26.33
5M3D.PDB	O, D_ASP_196	N, D_LYS_201	H, D_LYS_201	2.96	2.14	14.32

Table 1708: 5M3D-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5M3T.PDB	O, A.ASN.115	N, A.ILE.119	H, A.ILE.119	2.94	2.13	16.30
5M3T.PDB	O, A.GLN.118	N, A.ASP.122	H, A.ASP.122	2.97	2.19	21.02
5M3T.PDB	O, A.ILE.119	N, A.VAL.123	H, A.VAL.123	2.95	2.14	16.63
5M3T.PDB	O, A.ASP.122	N, A.PHE.126	H, A.PHE.126	2.88	2.06	13.64
5M3T.PDB	O, A.VAL.123	N, A.TYR.127	H, A.TYR.127	2.88	2.09	19.10
5M3T.PDB	NE2, A.HIS.151	OH, A.TYR.127	HH, A.TYR.127	2.73	1.92	14.40
5M3T.PDB	O, A.LYS.124	N, A.ASP.128	H, A.ASP.128	2.86	2.07	18.62
5M3T.PDB	O, A.GLN.125	N, A.GLN.129	H, A.GLN.129	2.97	2.16	16.06
5M3T.PDB	O, A.TYR.127	N, A.LEU.131	H, A.LEU.131	2.89	2.07	15.58
5M3T.PDB	O, A.ALA.130	N, A.ALA.134	H, A.ALA.134	2.77	2.03	25.75
5M3T.PDB	O, A.ALA.140	N, A.LYS.144	H, A.LYS.144	2.98	2.17	17.68
5M3T.PDB	O, A.ASN.142	N, A.VAL.146	H, A.VAL.146	2.80	1.98	15.12
5M3T.PDB	O, A.ALA.143	N, A.VAL.147	H, A.VAL.147	2.84	1.99	7.75
5M3T.PDB	O, A.LYS.144	N, A.LYS.148	H, A.LYS.148	2.91	2.07	11.07
5M3T.PDB	O, A.ALA.145	N, A.THR.149	H, A.THR.149	2.85	2.06	19.94
5M3T.PDB	O, A.ALA.145	OG1, A.THR.149	HG1, A.THR.149	2.69	1.91	17.48
5M3T.PDB	O, A.VAL.146	N, A.PHE.150	H, A.PHE.150	2.91	2.08	11.96
5M3T.PDB	O, A.VAL.147	N, A.HIS.151	H, A.HIS.151	2.93	2.10	13.01
5M3T.PDB	O, A.LEU.174	ND1, A.HIS.151	HD1, A.HIS.151	2.75	1.93	15.38
5M3T.PDB	O, A.LYS.148	N, A.GLU.152	H, A.GLU.152	2.97	2.16	17.30
5M3T.PDB	O, A.THR.149	N, A.THR.153	H, A.THR.153	2.89	2.07	15.13
5M3T.PDB	O, A.THR.149	OG1, A.THR.153	HG1, A.THR.153	2.85	2.15	27.69
5M3T.PDB	O, A.GLU.188	N, A.CYS.157	H, A.CYS.157	2.99	2.17	14.35
5M3T.PDB	OD2, A.ASP.189	N, A.SER.160	H, A.SER.160	2.80	1.94	2.42
5M3T.PDB	OG, A.SER.159	OG1, A.THR.161	HG1, A.THR.161	2.93	2.10	8.83
5M3T.PDB	O, A.SER.159	N, A.LEU.162	H, A.LEU.162	3.00	2.15	8.92
5M3T.PDB	O, A.LEU.162	N, A.THR.166	H, A.THR.166	2.96	2.13	13.96
5M3T.PDB	O, A.LEU.162	OG1, A.THR.166	HG1, A.THR.166	2.89	2.11	19.45
5M3T.PDB	O, A.THR.163	N, A.THR.167	H, A.THR.167	2.97	2.15	13.47
5M3T.PDB	O, A.LEU.165	N, A.VAL.169	H, A.VAL.169	2.96	2.14	13.88
5M3T.PDB	O, A.THR.166	N, A.LEU.170	H, A.LEU.170	2.99	2.16	12.64
5M3T.PDB	O, A.VAL.169	N, A.LEU.174	H, A.LEU.174	2.96	2.11	5.74
5M3T.PDB	O, A.ILE.182	N, A.PHE.186	H, A.PHE.186	2.70	1.92	20.08
5M3T.PDB	O, A.GLY.158	N, A.CYS.190	H, A.CYS.190	2.89	2.03	5.47
5M3T.PDB	OD1, A.ASP.189	N, A.HIS.191	H, A.HIS.191	2.81	2.03	20.34
5M3T.PDB	OD1, A.ASP.128	NE2, A.HIS.191	HE2, A.HIS.191	2.70	1.84	4.47
5M3T.PDB	O, A.ASP.189	N, A.LYS.193	H, A.LYS.193	3.00	2.19	17.82
5M3T.PDB	O, A.ASP.155	NZ, A.LYS.193	HZ1, A.LYS.193	2.94	2.21	29.02
5M3T.PDB	O, A.CYS.190	N, A.ILE.194	H, A.ILE.194	2.88	2.04	11.45
5M3T.PDB	O, A.HIS.191	N, A.ASP.195	H, A.ASP.195	2.95	2.12	14.00
5M3T.PDB	O, A.GLN.192	N, A.ASP.196	H, A.ASP.196	2.79	2.00	19.02
5M3T.PDB	O, A.LYS.193	N, A.LEU.197	H, A.LEU.197	2.95	2.23	28.39
5M3T.PDB	O, B.ILE.119	N, B.VAL.123	H, B.VAL.123	2.98	2.18	17.74
5M3T.PDB	OD2, B.ASP.195	NZ, B.LYS.124	HZ1, B.LYS.124	2.94	2.15	23.24
5M3T.PDB	O, B.ASP.122	N, B.PHE.126	H, B.PHE.126	2.88	2.07	16.55
5M3T.PDB	O, B.VAL.123	N, B.TYR.127	H, B.TYR.127	2.81	1.99	15.05
5M3T.PDB	NE2, B.HIS.151	OH, B.TYR.127	HH, B.TYR.127	2.86	2.03	6.62
5M3T.PDB	O, B.LYS.124	N, B.ASP.128	H, B.ASP.128	2.79	1.96	14.44
5M3T.PDB	O, B.TYR.127	N, B.LEU.131	H, B.LEU.131	2.74	1.91	11.63
5M3T.PDB	O, B.ASP.128	N, B.GLN.132	H, B.GLN.132	2.93	2.08	4.43
5M3T.PDB	O, B.ALA.130	N, B.ALA.134	H, B.ALA.134	2.82	2.01	17.03
5M3T.PDB	O, B.LEU.131	N, B.VAL.135	H, B.VAL.135	2.93	2.13	18.76
5M3T.PDB	O, B.ALA.140	N, B.LYS.144	H, B.LYS.144	2.99	2.13	5.84
5M3T.PDB	O, B.ASN.142	N, B.VAL.146	H, B.VAL.146	2.82	1.98	10.01
5M3T.PDB	O, B.ALA.143	N, B.VAL.147	H, B.VAL.147	2.79	1.96	12.14
5M3T.PDB	O, B.LYS.144	N, B.LYS.148	H, B.LYS.148	2.86	2.03	12.94
5M3T.PDB	O, B.CYS.175	NZ, B.LYS.148	HZ1, B.LYS.148	2.54	1.78	25.33

5M3T.PDB	O, B_ASN_173	NZ, B_LYS_148	HZ2, B_LYS_148	2.88	2.03	13.59
5M3T.PDB	O, B_ALA_145	N, B_THR_149	H, B_THR_149	2.96	2.15	16.07
5M3T.PDB	O, B_ALA_145	OG1, B_THR_149	HG1, B_THR_149	2.88	2.12	22.32
5M3T.PDB	O, B_VAL_146	N, B_PHE_150	H, B_PHE_150	2.92	2.09	12.17
5M3T.PDB	O, B_VAL_147	N, B_HIS_151	H, B_HIS_151	2.86	2.03	12.60
5M3T.PDB	O, B_LEU_174	ND1, B_HIS_151	HD1, B_HIS_151	2.62	1.77	9.06
5M3T.PDB	O, B_LYS_148	N, B_GLU_152	H, B_GLU_152	2.91	2.09	13.59
5M3T.PDB	O, B_THR_149	N, B_THR_153	H, B_THR_153	2.94	2.11	13.14
5M3T.PDB	O, B_THR_149	OG1, B_THR_153	HG1, B_THR_153	2.80	2.10	28.85
5M3T.PDB	O, B_PHE_150	N, B_LEU_154	H, B_LEU_154	2.95	2.15	17.32
5M3T.PDB	OG1, B_THR_163	N, B_SER_160	H, B_SER_160	2.86	2.05	16.20
5M3T.PDB	O, B_SER_160	N, B_ALA_164	H, B_ALA_164	2.90	2.11	19.32
5M3T.PDB	O, B_THR_161	N, B_LEU_165	H, B_LEU_165	2.94	2.12	14.02
5M3T.PDB	O, B_LEU_162	N, B_THR_166	H, B_THR_166	2.99	2.17	13.93
5M3T.PDB	O, B_LEU_162	OG1, B_THR_166	HG1, B_THR_166	2.94	2.16	18.55
5M3T.PDB	O, B_THR_163	N, B_THR_167	H, B_THR_167	2.90	2.06	9.78
5M3T.PDB	O, B_THR_163	OG1, B_THR_167	HG1, B_THR_167	2.66	1.89	19.90
5M3T.PDB	O, B_ALA_164	N, B_SER_168	H, B_SER_168	2.96	2.19	22.50
5M3T.PDB	O, B_LEU_165	OG, B_SER_168	HG, B_SER_168	2.85	2.06	16.49
5M3T.PDB	O, B_THR_166	N, B_LEU_170	H, B_LEU_170	2.88	2.10	19.82
5M3T.PDB	O, B_THR_167	N, B_LYS_171	H, B_LYS_171	2.76	1.95	17.26
5M3T.PDB	O, B_SER_168	ND2, B_ASN_172	HD21, B_ASN_172	2.93	2.11	14.38
5M3T.PDB	O, B_ASN_172	N, B_CYS_175	H, B_CYS_175	2.85	2.01	8.34
5M3T.PDB	O, B_ILE_181	N, B_ASN_184	H, B_ASN_184	2.85	2.05	18.46
5M3T.PDB	O, B_SER_183	N, B_LYS_187	H, B_LYS_187	2.83	2.00	12.69
5M3T.PDB	OE1, B_GLN_192	N, B_ASP_189	H, B_ASP_189	2.94	2.14	17.48
5M3T.PDB	O, B_GLY_158	N, B_CYS_190	H, B_CYS_190	2.83	1.97	6.16
5M3T.PDB	OD1, B_ASP_128	NE2, B_HIS_191	HE2, B_HIS_191	2.76	1.92	11.16
5M3T.PDB	OD1, B_ASP_189	N, B_GLN_192	H, B_GLN_192	2.85	2.02	14.15
5M3T.PDB	O, B_LEU_154	NZ, B_LYS_193	HZ2, B_LYS_193	2.66	1.92	28.24
5M3T.PDB	O, B_CYS_190	N, B_ILE_194	H, B_ILE_194	2.86	2.09	22.77
5M3T.PDB	O, B_HIS_191	N, B_ASP_195	H, B_ASP_195	2.99	2.18	15.97
5M3T.PDB	O, B_GLN_192	N, B_ASP_196	H, B_ASP_196	2.98	2.18	17.63
5M3T.PDB	O, B_ASP_195	OG, B_SER_199	HG, B_SER_199	2.82	2.09	24.74

Table 1709: 5M3T-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5M4R.PDB	OG1, A_THR_163	N, A_SER_160	H, A_SER_160	2.97	2.12	8.70
5M4R.PDB	OG, A_SER_159	OG1, A_THR_163	HG1, A_THR_163	2.93	2.14	15.31
5M4R.PDB	O, A_SER_160	N, A_ALA_164	H, A_ALA_164	2.56	1.75	15.32
5M4R.PDB	O, A_GLY_158	N, A_CYS_190	H, A_CYS_190	2.82	1.96	5.83
5M4R.PDB	OD2, A_ASP_128	NE2, A_HIS_191	HE2, A_HIS_191	2.54	1.73	17.27
5M4R.PDB	O, A_CYS_190	N, A_ILE_194	H, A_ILE_194	2.79	2.00	18.71
5M4R.PDB	O, A_HIS_191	N, A_ASP_195	H, A_ASP_195	2.85	2.00	5.80
5M4R.PDB	O, B_LYS_121	N, B_GLN_125	H, B_GLN_125	2.88	2.03	8.53
5M4R.PDB	O, B_LYS_124	N, B_ASP_128	H, B_ASP_128	2.83	1.99	10.44
5M4R.PDB	O, B_VAL_146	N, B_PHE_150	H, B_PHE_150	2.87	2.04	11.41
5M4R.PDB	O, B_VAL_147	N, B_HIS_151	H, B_HIS_151	2.85	2.02	12.74
5M4R.PDB	O, B_LYS_148	N, B_GLU_152	H, B_GLU_152	2.83	2.00	11.22
5M4R.PDB	O, B_THR_149	N, B_THR_153	H, B_THR_153	2.76	1.93	11.52
5M4R.PDB	O, B_THR_149	OG1, B_THR_153	HG1, B_THR_153	2.73	2.03	28.15
5M4R.PDB	OG1, B_THR_163	N, B_SER_160	H, B_SER_160	2.82	2.01	15.84
5M4R.PDB	OG, B_SER_159	OG1, B_THR_163	HG1, B_THR_163	2.85	2.02	5.63
5M4R.PDB	O, B_SER_160	N, B_ALA_164	H, B_ALA_164	2.76	2.02	25.53
5M4R.PDB	O, B_THR_161	N, B_LEU_165	H, B_LEU_165	2.85	2.00	9.07
5M4R.PDB	O, B_LEU_162	N, B_THR_166	H, B_THR_166	2.80	1.95	8.30
5M4R.PDB	O, B_LEU_162	OG1, B_THR_166	HG1, B_THR_166	2.92	2.11	12.23
5M4R.PDB	O, B_THR_163	N, B_THR_167	H, B_THR_167	2.81	1.99	13.82
5M4R.PDB	O, B_ALA_164	N, B_SER_168	H, B_SER_168	2.85	2.04	17.78
5M4R.PDB	O, B_LEU_165	N, B_VAL_169	H, B_VAL_169	2.67	1.97	29.59
5M4R.PDB	O, C_ASP_117	N, C_LYS_121	H, C_LYS_121	2.88	2.04	8.52
5M4R.PDB	O, C_ALA_120	N, C_LYS_124	H, C_LYS_124	2.90	2.05	8.18
5M4R.PDB	O, C_LYS_121	N, C_GLN_125	H, C_GLN_125	2.88	2.04	12.44
5M4R.PDB	O, C_ASP_122	N, C_PHE_126	H, C_PHE_126	2.84	1.99	7.74
5M4R.PDB	O, C_VAL_123	N, C_TYR_127	H, C_TYR_127	2.85	2.01	7.89
5M4R.PDB	O, C_LYS_124	N, C_ASP_128	H, C_ASP_128	2.85	2.01	11.99
5M4R.PDB	O, C_GLN_125	N, C_GLN_129	H, C_GLN_129	2.90	2.06	10.04
5M4R.PDB	O, C_PHE_126	N, C_ALA_130	H, C_ALA_130	2.92	2.07	6.44
5M4R.PDB	O, C_TYR_127	N, C_LEU_131	H, C_LEU_131	2.76	1.97	18.98
5M4R.PDB	O, C_ASP_128	N, C_GLN_132	H, C_GLN_132	2.86	2.01	6.65
5M4R.PDB	O, C_LEU_131	N, C_VAL_135	H, C_VAL_135	2.86	2.02	10.05
5M4R.PDB	O, C_ALA_143	N, C_VAL_147	H, C_VAL_147	2.83	1.98	7.24
5M4R.PDB	O, C_ALA_145	N, C_THR_149	H, C_THR_149	2.85	2.02	12.51
5M4R.PDB	O, C_VAL_146	N, C_PHE_150	H, C_PHE_150	2.86	2.02	10.77
5M4R.PDB	O, C_VAL_147	N, C_HIS_151	H, C_HIS_151	2.82	2.00	14.15
5M4R.PDB	O, C_THR_149	OG1, C_THR_153	HG1, C_THR_153	2.74	2.04	29.05
5M4R.PDB	O, C_PHE_150	N, C_LEU_154	H, C_LEU_154	2.89	2.07	13.98
5M4R.PDB	OG1, C_THR_163	N, C_SER_160	H, C_SER_160	2.80	1.95	7.20
5M4R.PDB	OG, C_SER_159	OG1, C_THR_163	HG1, C_THR_163	2.95	2.12	7.91
5M4R.PDB	O, C_SER_160	N, C_ALA_164	H, C_ALA_164	2.84	2.04	18.04
5M4R.PDB	O, C_THR_161	N, C_LEU_165	H, C_LEU_165	2.77	1.94	14.09
5M4R.PDB	O, C_LEU_162	OG1, C_THR_166	HG1, C_THR_166	2.73	1.97	21.05
5M4R.PDB	O, C_THR_163	N, C_THR_167	H, C_THR_167	2.86	2.02	10.18
5M4R.PDB	O, C_THR_163	OG1, C_THR_167	HG1, C_THR_167	2.56	1.86	28.52
5M4R.PDB	O, C_LEU_165	N, C_VAL_169	H, C_VAL_169	2.81	2.04	22.87
5M4R.PDB	OD2, C_ASP_189	N, C_GLN_192	H, C_GLN_192	2.75	1.90	7.52
5M4R.PDB	O, C_CYS_190	N, C_ILE_194	H, C_ILE_194	2.79	1.99	17.52
5M4R.PDB	O, C_HIS_191	N, C_ASP_195	H, C_ASP_195	2.83	1.98	6.12
5M4R.PDB	O, C_GLN_192	N, C_ASP_196	H, C_ASP_196	2.81	1.97	12.51
5M4R.PDB	O, C_LYS_193	N, C_LEU_197	H, C_LEU_197	2.74	1.99	24.89
5M4R.PDB	O, D_THR_149	N, D_THR_153	H, D_THR_153	2.76	1.94	13.90
5M4R.PDB	O, D_CYS_190	N, D_ILE_194	H, D_ILE_194	2.80	1.98	16.24
5M4R.PDB	O, D_ILE_194	N, D_PHE_198	H, D_PHE_198	2.90	2.07	14.01
5M4R.PDB	O, E_ALA_145	N, E_THR_149	H, E_THR_149	2.84	2.01	12.20

5M4R.PDB	O, E_VAL_147	N, E_HIS_151	H, E_HIS_151	2.82	1.99	11.67
5M4R.PDB	O, E_LYS_148	N, E_GLU_152	H, E_GLU_152	2.81	1.99	14.86
5M4R.PDB	O, E_THR_149	N, E_THR_153	H, E_THR_153	2.77	1.95	13.19
5M4R.PDB	O, E_THR_149	OG1, E_THR_153	HG1, E_THR_153	2.73	2.03	28.19
5M4R.PDB	O, E_PHE_150	N, E_LEU_154	H, E_LEU_154	2.88	2.06	14.16
5M4R.PDB	OG1, E_THR_163	N, E_SER_160	H, E_SER_160	2.70	1.88	13.56
5M4R.PDB	O, E_SER_160	N, E_ALA_164	H, E_ALA_164	2.73	1.96	22.03
5M4R.PDB	OD2, E_ASP_128	NE2, E_HIS_191	HE2, E_HIS_191	2.53	1.73	17.17
5M4R.PDB	O, E_CYS_190	N, E_ILE_194	H, E_ILE_194	2.78	1.97	15.37

Table 1710: 5M4R-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5T6P.PDB	OG, A_SER.26	N, A_LEU.3	H, A_LEU.3	2.84	1.99	5.70
5T6P.PDB	O, A_ARG.24	N, A_THR.5	H, A_THR.5	2.80	1.96	9.75
5T6P.PDB	O, A_TYR.91	NE2, A_GLN.6	HE22, A_GLN.6	2.77	1.91	5.02
5T6P.PDB	O, A_SER.22	N, A_THR.7	H, A_THR.7	2.80	1.98	15.63
5T6P.PDB	O, A_LYS.108	N, A_LEU.11	H, A_LEU.11	2.86	2.14	28.05
5T6P.PDB	O, A_GLU.110	N, A_VAL.13	H, A_VAL.13	2.92	2.18	25.74
5T6P.PDB	O, A_ILE.80	N, A_ALA.19	H, A_ALA.19	2.98	2.15	13.33
5T6P.PDB	O, A_LEU.78	N, A_ILE.21	H, A_ILE.21	2.78	1.94	11.87
5T6P.PDB	O, A_THR.7	N, A_SER.22	H, A_SER.22	2.67	1.82	5.62
5T6P.PDB	O, A_PHE.76	N, A_CYS.23	H, A_CYS.23	2.67	1.84	13.46
5T6P.PDB	O, A_THR.5	N, A_ARG.24	H, A_ARG.24	2.81	2.01	17.15
5T6P.PDB	OD1, A_ASP.75	NE, A_ARG.24	HE, A_ARG.24	2.87	2.06	16.15
5T6P.PDB	O, A_THR.74	N, A_SER.25	H, A_SER.25	2.92	2.15	21.71
5T6P.PDB	O, A_LYS.35	N, A_HIS.31	H, A_HIS.31	2.71	1.85	5.88
5T6P.PDB	O, A_HIS.31	N, A_GLY.34	H, A_GLY.34	2.72	1.87	7.51
5T6P.PDB	OD1, A_ASN.33	N, A_LYS.35	H, A_LYS.35	2.79	1.96	11.94
5T6P.PDB	O, A_PHE.94	N, A_GLU.39	H, A_GLU.39	2.82	1.99	13.41
5T6P.PDB	O, A_ILE.53	N, A_TRP.40	H, A_TRP.40	2.93	2.13	18.35
5T6P.PDB	O, A_TYR.92	N, A_TYR.41	H, A_TYR.41	2.73	1.89	11.55
5T6P.PDB	O, A_LYS.50	N, A_LEU.42	H, A_LEU.42	2.88	2.08	18.93
5T6P.PDB	O, A_VAL.90	N, A_GLN.43	H, A_GLN.43	2.78	1.94	8.75
5T6P.PDB	O, A_GLN.47	NE2, A_GLN.43	HE21, A_GLN.43	2.91	2.07	10.44
5T6P.PDB	O, B_GLY.107	OG, A_SER.48	HG, A_SER.48	2.52	1.72	14.73
5T6P.PDB	O, A_LEU.42	N, A_LYS.50	H, A_LYS.50	2.76	2.01	25.02
5T6P.PDB	O, A_TRP.40	N, A_LEU.52	H, A_LEU.52	2.89	2.04	6.78
5T6P.PDB	O, A_LYS.58	N, A_TYR.54	H, A_TYR.54	2.88	2.08	17.82
5T6P.PDB	O, A_ILE.36	NE, A_ARG.55	HE, A_ARG.55	2.95	2.12	13.12
5T6P.PDB	O, A_LEU.38	N, A_VAL.56	H, A_VAL.56	2.81	1.97	8.99
5T6P.PDB	O, A_ARG.55	N, A_SER.57	H, A_SER.57	2.79	2.06	26.54
5T6P.PDB	O, A_TYR.54	N, A_LYS.58	H, A_LYS.58	2.92	2.13	19.37
5T6P.PDB	O, A_LEU.52	N, A_PHE.60	H, A_PHE.60	2.86	2.00	6.63
5T6P.PDB	OD1, A_ASP.87	NH2, A_ARG.66	HH22, A_ARG.66	2.87	2.03	10.92
5T6P.PDB	O, A_LYS.79	N, A_SER.68	H, A_SER.68	2.87	2.04	13.46
5T6P.PDB	O, A_CYS.23	N, A_PHE.76	H, A_PHE.76	2.81	1.99	14.73
5T6P.PDB	O, A_SER.70	N, A_THR.77	H, A_THR.77	2.96	2.14	16.18
5T6P.PDB	O, A_ILE.21	N, A_LEU.78	H, A_LEU.78	2.87	2.08	19.36
5T6P.PDB	O, A_SER.68	N, A_LYS.79	H, A_LYS.79	2.72	1.88	9.62
5T6P.PDB	O, A_ALA.19	N, A_ILE.80	H, A_ILE.80	2.82	1.98	10.03
5T6P.PDB	O, A_GLN.43	N, A_VAL.90	H, A_VAL.90	2.99	2.16	12.00
5T6P.PDB	O, A_THR.107	N, A_TYR.91	H, A_TYR.91	2.97	2.12	9.83
5T6P.PDB	O, A_ASP.87	OH, A_TYR.91	HH, A_TYR.91	2.67	1.98	29.62
5T6P.PDB	O, A_TYR.41	N, A_TYR.92	H, A_TYR.92	2.76	1.93	13.16
5T6P.PDB	OE1, A_GLN.6	N, A_CYS.93	H, A_CYS.93	2.94	2.12	14.92
5T6P.PDB	O, A_THR.102	N, A_GLN.95	H, A_GLN.95	2.94	2.13	17.40
5T6P.PDB	O, A_HIS.98	NE2, A_GLN.95	HE22, A_GLN.95	2.68	1.87	14.95
5T6P.PDB	O, A_TYR.37	N, A_GLY.96	H, A_GLY.96	2.73	1.90	11.23
5T6P.PDB	O, A_ILE.29	OG, A_SER.97	HG, A_SER.97	2.65	1.82	7.55
5T6P.PDB	OE1, A_GLN.95	N, A_HIS.98	H, A_HIS.98	2.88	2.02	3.19
5T6P.PDB	O, A_VAL.2	OG1, A_THR.102	HG1, A_THR.102	2.83	2.02	12.78
5T6P.PDB	O, A_CYS.93	N, A_GLY.104	H, A_GLY.104	2.64	1.79	9.16
5T6P.PDB	O, A_TYR.91	N, A_THR.107	H, A_THR.107	2.98	2.24	26.12
5T6P.PDB	O, A_PRO.8	OG1, A_THR.107	HG1, A_THR.107	2.63	1.91	24.93
5T6P.PDB	O, A_GLY.89	N, A_LEU.109	H, A_LEU.109	2.81	1.95	2.82
5T6P.PDB	O, A_VAL.13	N, A_LYS.112	H, A_LYS.112	2.81	1.97	10.01
5T6P.PDB	O, A_TYR.145	N, A_ALA.116	H, A_ALA.116	2.79	1.99	17.20
5T6P.PDB	O, A_ASN.142	N, A_THR.119	H, A_THR.119	2.97	2.14	12.03
5T6P.PDB	O, A_VAL.138	N, A_PHE.123	H, A_PHE.123	2.88	2.11	21.78

5T6P.PDB	OG, A_SER.136	NE2, A_GLN.129	HE22, A_GLN.129	2.81	1.96	6.44
5T6P.PDB	O, A_GLN.129	OG, A_SER.132	HG, A_SER.132	2.72	1.92	13.31
5T6P.PDB	O, A_LEU.130	N, A_GLY.133	H, A_GLY.133	2.98	2.20	21.49
5T6P.PDB	OE1, A_GLN.129	N, A_SER.136	H, A_SER.136	2.79	1.94	7.05
5T6P.PDB	O, A_LEU.184	N, A_VAL.137	H, A_VAL.137	2.71	1.87	10.57
5T6P.PDB	O, A_SER.182	N, A_CYS.139	H, A_CYS.139	2.76	2.04	28.21
5T6P.PDB	O, A_SER.121	N, A_PHE.140	H, A_PHE.140	2.76	1.97	19.62
5T6P.PDB	O, A_MET.180	N, A_LEU.141	H, A_LEU.141	2.79	1.94	5.89
5T6P.PDB	OG, A_SER.179	N, A_ASN.143	H, A_ASN.143	2.90	2.08	15.40
5T6P.PDB	O, A_TYR.178	N, A_PHE.144	H, A_PHE.144	2.81	1.97	9.66
5T6P.PDB	O, A_ALA.116	N, A_TYR.145	H, A_TYR.145	2.97	2.15	15.15
5T6P.PDB	O, A_GLU.200	N, A_LYS.152	H, A_LYS.152	2.97	2.17	16.98
5T6P.PDB	OG, A_SER.182	NE1, A_TRP.153	HE1, A_TRP.153	2.84	2.00	11.05
5T6P.PDB	O, A_THR.198	N, A_LYS.154	H, A_LYS.154	2.71	1.93	21.47
5T6P.PDB	O, A_SER.196	N, A_ASP.156	H, A_ASP.156	2.70	1.86	10.47
5T6P.PDB	O, A_TRP.153	N, A_ARG.160	H, A_ARG.160	2.85	2.08	22.60
5T6P.PDB	O, A_SER.181	N, A_SER.167	H, A_SER.167	2.92	2.15	23.07
5T6P.PDB	O, B_PRO.170	OG, A_SER.167	HG, A_SER.167	2.98	2.14	3.80
5T6P.PDB	O, A_LYS.147	NE1, A_TRP.168	HE1, A_TRP.168	2.99	2.28	29.51
5T6P.PDB	O, A_SER.179	N, A_THR.169	H, A_THR.169	2.77	1.93	8.31
5T6P.PDB	O, A_ASP.170	OG1, A_THR.169	HG1, A_THR.169	2.93	2.19	24.31
5T6P.PDB	O, A_THR.177	N, A_ASP.172	H, A_ASP.172	2.83	2.02	16.18
5T6P.PDB	OD1, A_ASP.172	N, A_LYS.174	H, A_LYS.174	2.80	1.97	12.91
5T6P.PDB	O, A_ASP.172	N, A_SER.176	H, A_SER.176	2.74	2.02	27.29
5T6P.PDB	OD1, A_ASP.175	OG1, A_THR.177	HG1, A_THR.177	2.59	1.78	13.64
5T6P.PDB	O, A_PHE.144	N, A_TYR.178	H, A_TYR.178	2.77	1.93	7.97
5T6P.PDB	O, A_LEU.141	N, A_MET.180	H, A_MET.180	2.77	1.96	16.22
5T6P.PDB	O, A_SER.167	N, A_SER.181	H, A_SER.181	2.83	2.04	19.51
5T6P.PDB	O, A_CYS.139	N, A_SER.182	H, A_SER.182	2.79	1.96	11.39
5T6P.PDB	OD1, A_ASN.166	OG, A_SER.182	HG, A_SER.182	2.54	1.72	9.61
5T6P.PDB	O, A_LEU.165	N, A_THR.183	H, A_THR.183	2.87	2.06	15.52
5T6P.PDB	O, A_VAL.137	N, A_LEU.184	H, A_LEU.184	2.77	1.97	18.32
5T6P.PDB	O, A_GLY.163	N, A_THR.185	H, A_THR.185	2.97	2.14	12.81
5T6P.PDB	O, A_ALA.135	N, A_LEU.186	H, A_LEU.186	2.78	1.96	13.71
5T6P.PDB	O, A_GLY.133	N, A_LYS.188	H, A_LYS.188	2.86	2.01	2.28
5T6P.PDB	OG1, A_THR.187	N, A_GLU.190	H, A_GLU.190	2.92	2.08	10.76
5T6P.PDB	O, A_THR.187	N, A_TYR.191	H, A_TYR.191	2.82	1.98	9.18
5T6P.PDB	OD1, A_ASP.156	N, A_SER.196	H, A_SER.196	2.91	2.06	3.81
5T6P.PDB	O, A_LYS.152	N, A_GLU.200	H, A_GLU.200	2.95	2.17	21.10
5T6P.PDB	O, A_ILE.210	N, A_ALA.201	H, A_ALA.201	2.76	1.98	21.19
5T6P.PDB	O, A_ASN.150	N, A_THR.202	H, A_THR.202	2.73	1.90	13.59
5T6P.PDB	OG, A_SER.206	N, A_SER.208	H, A_SER.208	2.93	2.13	18.20
5T6P.PDB	O, A_ALA.201	N, A_ILE.210	H, A_ILE.210	2.83	2.04	19.01
5T6P.PDB	O, B_SER.25	N, B_LYS.3	H, B_LYS.3	2.92	2.08	9.95
5T6P.PDB	O, B_ALA.23	N, B_VAL.5	H, B_VAL.5	2.98	2.21	22.28
5T6P.PDB	O, B_SER.21	N, B_SER.7	H, B_SER.7	2.97	2.22	25.31
5T6P.PDB	O, B_THR.113	N, B_VAL.12	H, B_VAL.12	2.78	2.02	23.72
5T6P.PDB	O, B_LEU.86	N, B_GLY.15	H, B_GLY.15	2.71	1.85	6.92
5T6P.PDB	O, B_ALA.13	N, B_GLY.16	H, B_GLY.16	2.97	2.19	21.44
5T6P.PDB	O, B_LEU.81	N, B_LEU.20	H, B_LEU.20	2.89	2.07	14.31
5T6P.PDB	O, B_VAL.5	N, B_ALA.23	H, B_ALA.23	2.70	1.89	15.98
5T6P.PDB	O, B_LYS.3	N, B_SER.25	H, B_SER.25	2.98	2.28	29.57
5T6P.PDB	O, B_ILE.51	N, B_MET.34	H, B_MET.34	2.95	2.13	15.81
5T6P.PDB	O, B_ALA.49	N, B_TRP.36	H, B_TRP.36	2.99	2.18	18.20
5T6P.PDB	O, B_GLU.46	N, B_ARG.38	H, B_ARG.38	2.93	2.09	10.53
5T6P.PDB	OE1, B_GLU.46	NE, B_ARG.38	HE, B_ARG.38	2.70	1.96	26.33
5T6P.PDB	O, B_ILE.93	N, B_GLN.39	H, B_GLN.39	2.73	1.94	18.82
5T6P.PDB	OE1, A_GLN.43	NE2, B_GLN.39	HE22, B_GLN.39	2.71	1.86	5.14

5T6P.PDB	O, B_ARG_44	N, B_THR_40	H, B_THR_40	2.94	2.13	17.68
5T6P.PDB	O, B_THR_40	N, B_LYS_43	H, B_LYS_43	2.81	1.99	15.16
5T6P.PDB	O, B_ARG_38	N, B_GLU_46	H, B_GLU_46	2.91	2.09	13.32
5T6P.PDB	O, B_TYR_59	N, B_TYR_50	H, B_TYR_50	2.85	2.14	28.28
5T6P.PDB	O, B_MET_34	N, B_ILE_51	H, B_ILE_51	3.00	2.23	23.58
5T6P.PDB	O, B_GLY_56	N, B_ASN_52	H, B_ASN_52	2.85	1.99	5.44
5T6P.PDB	O, B_ASN_52	N, B_GLY_55	H, B_GLY_55	2.99	2.14	4.85
5T6P.PDB	OD1, B_ASN_52	N, B_GLY_56	H, B_GLY_56	2.63	1.80	11.54
5T6P.PDB	O, F_PRO_8	ND2, B_ASN_57	HD21, B_ASN_57	2.91	2.07	9.74
5T6P.PDB	O, B_TYR_50	N, B_TYR_59	H, B_TYR_59	2.93	2.14	20.03
5T6P.PDB	O, B_GLN_82	N, B_THR_69	H, B_THR_69	2.67	1.94	26.83
5T6P.PDB	OD1, B_ASN_74	NE, B_ARG_72	HE, B_ARG_72	2.87	2.14	26.22
5T6P.PDB	O, B_THR_78	N, B_ASP_73	H, B_ASP_73	2.91	2.10	15.58
5T6P.PDB	O, B_LYS_76	OG1, B_THR_78	HG1, B_THR_78	2.86	2.09	20.72
5T6P.PDB	O, B_SER_71	N, B_TYR_80	H, B_TYR_80	2.84	1.99	6.51
5T6P.PDB	O, B_THR_69	N, B_GLN_82	H, B_GLN_82	2.81	1.97	9.07
5T6P.PDB	O, B_LEU_18	N, B_MET_83	H, B_MET_83	2.79	1.99	17.97
5T6P.PDB	O, B_ARG_67	OG, B_SER_84	HG, B_SER_84	2.97	2.16	13.27
5T6P.PDB	O, B_GLN_39	N, B_ILE_93	H, B_ILE_93	2.90	2.11	19.97
5T6P.PDB	O, B_THR_110	N, B_TYR_94	H, B_TYR_94	2.94	2.08	2.28
5T6P.PDB	O, B_ASP_90	OH, B_TYR_94	HH, B_TYR_94	2.68	1.86	11.38
5T6P.PDB	O, B_VAL_37	N, B_TYR_95	H, B_TYR_95	2.64	1.79	3.58
5T6P.PDB	O, B_PRO_33	N, B_GLN_99	H, B_GLN_99	2.96	2.14	14.24
5T6P.PDB	O, B_GLY_102	N, B_TYR_100	H, B_TYR_100	2.99	2.25	25.89
5T6P.PDB	OD1, B_ASP_104	N, B_GLY_102	H, B_GLY_102	2.80	1.95	8.41
5T6P.PDB	O, B_PHE_103	NE1, B_TRP_106	HE1, B_TRP_106	2.96	2.22	25.91
5T6P.PDB	O, B_CYS_96	N, B_GLY_107	H, B_GLY_107	2.84	2.03	15.83
5T6P.PDB	OE1, B_GLU_6	N, B_GLY_109	H, B_GLY_109	2.80	1.98	13.61
5T6P.PDB	O, B_ALA_92	N, B_LEU_112	H, B_LEU_112	2.89	2.04	9.43
5T6P.PDB	O, B_GLY_10	N, B_THR_113	H, B_THR_113	2.91	2.09	14.72
5T6P.PDB	O, B_VAL_12	N, B_SER_115	H, B_SER_115	2.80	2.05	24.92
5T6P.PDB	O, B_PHE_149	N, B_THR_120	H, B_THR_120	2.75	1.91	11.84
5T6P.PDB	O, B_LEU_144	N, B_TYR_125	H, B_TYR_125	2.91	2.10	16.22
5T6P.PDB	O, B_VAL_186	N, B_VAL_139	H, B_VAL_139	2.78	1.95	11.66
5T6P.PDB	O, B_VAL_184	N, B_LEU_141	H, B_LEU_141	2.63	1.79	9.20
5T6P.PDB	O, B_SER_182	N, B_CYS_143	H, B_CYS_143	2.65	1.86	19.42
5T6P.PDB	O, B_TYR_125	N, B_LEU_144	H, B_LEU_144	2.95	2.09	2.74
5T6P.PDB	O, B_LEU_180	N, B_VAL_145	H, B_VAL_145	2.75	1.91	7.82
5T6P.PDB	O, B_TYR_178	N, B_TYR_148	H, B_TYR_148	2.98	2.19	19.53
5T6P.PDB	O, B_THR_120	N, B_PHE_149	H, B_PHE_149	2.83	2.02	15.93
5T6P.PDB	O, B_ALA_201	N, B_THR_154	H, B_THR_154	2.97	2.17	18.38
5T6P.PDB	O, B_ASN_199	N, B_THR_156	H, B_THR_156	2.88	2.07	16.23
5T6P.PDB	O, B_THR_197	N, B_ASN_158	H, B_ASN_158	2.90	2.09	16.11
5T6P.PDB	O, B_SER_181	N, B_PHE_169	H, B_PHE_169	2.91	2.06	6.94
5T6P.PDB	O, B_LEU_177	N, B_GLN_174	H, B_GLN_174	2.84	1.98	4.57
5T6P.PDB	O, B_GLN_174	N, B_LEU_177	H, B_LEU_177	2.93	2.14	19.22
5T6P.PDB	O, B_TYR_148	N, B_TYR_178	H, B_TYR_178	2.71	1.85	6.27
5T6P.PDB	O, B_VAL_145	N, B_LEU_180	H, B_LEU_180	2.86	2.04	15.49
5T6P.PDB	O, B_CYS_143	N, B_SER_182	H, B_SER_182	2.70	1.91	18.91
5T6P.PDB	O, B_LEU_141	N, B_VAL_184	H, B_VAL_184	2.73	1.88	7.12
5T6P.PDB	O, B_VAL_139	N, B_VAL_186	H, B_VAL_186	2.85	2.02	12.50
5T6P.PDB	OD1, B_ASN_158	N, B_THR_197	H, B_THR_197	2.89	2.12	22.97
5T6P.PDB	O, B_LYS_211	N, B_CYS_198	H, B_CYS_198	2.83	2.00	11.79
5T6P.PDB	O, B_THR_156	N, B_ASN_199	H, B_ASN_199	2.83	1.97	3.18
5T6P.PDB	O, B_VAL_209	N, B_VAL_200	H, B_VAL_200	2.85	2.02	12.35
5T6P.PDB	O, B_THR_154	N, B_ALA_201	H, B_ALA_201	2.90	2.12	21.54
5T6P.PDB	O, B_PRO_150	NE2, B_HIS_202	HE2, B_HIS_202	2.71	1.86	4.81
5T6P.PDB	O, B_VAL_200	N, B_VAL_209	H, B_VAL_209	2.85	2.04	16.15

5T6P.PDB	O, B_CYS_198	N, B_LYS_211	H, B_LYS_211	2.86	2.05	16.75
5T6P.PDB	O, B_VAL_196	N, B_ILE_213	H, B_ILE_213	2.82	1.97	6.68
5T6P.PDB	OG, C_SER_26	N, C_LEU_3	H, C_LEU_3	2.79	1.93	4.03
5T6P.PDB	O, C_ARG_24	N, C_THR_5	H, C_THR_5	2.86	2.03	11.46
5T6P.PDB	O, C_TYR_91	NE2, C_GLN_6	HE22, C_GLN_6	2.75	1.89	3.04
5T6P.PDB	O, C_SER_22	N, C_THR_7	H, C_THR_7	2.88	2.06	14.16
5T6P.PDB	O, C_LYS_108	N, C_LEU_11	H, C_LEU_11	2.88	2.16	28.19
5T6P.PDB	O, C_GLU_110	N, C_VAL_13	H, C_VAL_13	2.97	2.24	26.82
5T6P.PDB	O, C_ILE_80	N, C_ALA_19	H, C_ALA_19	3.00	2.17	14.18
5T6P.PDB	O, C_LEU_78	N, C_ILE_21	H, C_ILE_21	2.76	1.92	12.06
5T6P.PDB	O, C_THR_7	N, C_SER_22	H, C_SER_22	2.70	1.85	6.95
5T6P.PDB	O, C_PHE_76	N, C_CYS_23	H, C_CYS_23	2.70	1.86	10.98
5T6P.PDB	O, C_THR_5	N, C_ARG_24	H, C_ARG_24	2.81	2.00	15.67
5T6P.PDB	OD1, C_ASP_75	NE, C_ARG_24	HE, C_ARG_24	2.92	2.14	20.59
5T6P.PDB	OD1, C_ASP_75	NH2, C_ARG_24	HH21, C_ARG_24	2.94	2.18	23.70
5T6P.PDB	O, C_HIS_31	N, C_GLY_34	H, C_GLY_34	2.90	2.04	3.71
5T6P.PDB	OD1, C_ASN_33	N, C_LYS_35	H, C_LYS_35	2.76	1.93	12.01
5T6P.PDB	O, C_PHE_94	N, C_GLU_39	H, C_GLU_39	2.84	2.01	13.22
5T6P.PDB	O, C_ILE_53	N, C_TRP_40	H, C_TRP_40	2.81	2.01	18.58
5T6P.PDB	O, C_TYR_92	N, C_TYR_41	H, C_TYR_41	2.76	1.92	9.44
5T6P.PDB	O, C_LYS_50	N, C_LEU_42	H, C_LEU_42	2.99	2.19	18.71
5T6P.PDB	O, C_VAL_90	N, C_GLN_43	H, C_GLN_43	2.75	1.90	8.01
5T6P.PDB	OE1, D_GLN_39	NE2, C_GLN_43	HE22, C_GLN_43	3.00	2.17	12.88
5T6P.PDB	O, D_GLY_107	OG, C_SER_48	HG, C_SER_48	2.66	1.94	25.38
5T6P.PDB	O, C_LEU_42	N, C_LYS_50	H, C_LYS_50	2.87	2.11	23.73
5T6P.PDB	O, C_TRP_40	N, C_LEU_52	H, C_LEU_52	2.81	1.96	6.06
5T6P.PDB	O, C_LYS_58	N, C_TYR_54	H, C_TYR_54	2.92	2.10	15.01
5T6P.PDB	O, C_LEU_38	N, C_VAL_56	H, C_VAL_56	2.88	2.04	8.48
5T6P.PDB	O, C_ARG_55	N, C_SER_57	H, C_SER_57	2.66	1.91	24.23
5T6P.PDB	O, C_TYR_54	N, C_LYS_58	H, C_LYS_58	2.91	2.14	22.42
5T6P.PDB	O, C_LEU_52	N, C_PHE_60	H, C_PHE_60	2.93	2.07	3.44
5T6P.PDB	O, C_LYS_79	N, C_SER_68	H, C_SER_68	2.83	1.99	10.51
5T6P.PDB	O, C_CYS_23	N, C_PHE_76	H, C_PHE_76	2.93	2.11	14.43
5T6P.PDB	O, C_ILE_21	N, C_LEU_78	H, C_LEU_78	2.76	1.99	21.57
5T6P.PDB	O, C_SER_68	N, C_LYS_79	H, C_LYS_79	2.78	1.92	4.56
5T6P.PDB	O, C_ALA_19	N, C_ILE_80	H, C_ILE_80	2.92	2.08	10.76
5T6P.PDB	O, C_GLN_43	N, C_VAL_90	H, C_VAL_90	2.95	2.12	13.12
5T6P.PDB	O, C_THR_107	N, C_TYR_91	H, C_TYR_91	2.80	1.96	9.61
5T6P.PDB	O, C_TYR_41	N, C_TYR_92	H, C_TYR_92	2.74	1.93	15.61
5T6P.PDB	O, C_HIS_98	NE2, C_GLN_95	HE22, C_GLN_95	2.72	1.90	15.32
5T6P.PDB	O, C_TYR_37	N, C_GLY_96	H, C_GLY_96	2.80	1.96	11.65
5T6P.PDB	O, C_ILE_29	OG, C_SER_97	HG, C_SER_97	2.80	1.98	12.04
5T6P.PDB	OE1, C_GLN_95	N, C_HIS_98	H, C_HIS_98	2.87	2.02	5.84
5T6P.PDB	O, C_VAL_2	OG1, C_THR_102	HG1, C_THR_102	2.71	1.89	10.27
5T6P.PDB	O, C_CYS_93	N, C_GLY_104	H, C_GLY_104	2.76	1.92	10.56
5T6P.PDB	OE1, C_GLN_6	N, C_GLY_106	H, C_GLY_106	2.99	2.28	28.82
5T6P.PDB	O, C_TYR_91	N, C_THR_107	H, C_THR_107	2.87	2.11	24.01
5T6P.PDB	O, C_PRO_8	OG1, C_THR_107	HG1, C_THR_107	2.74	2.02	25.98
5T6P.PDB	O, C_GLY_89	N, C_LEU_109	H, C_LEU_109	2.77	1.92	5.68
5T6P.PDB	OE1, C_GLN_171	N, C_ILE_111	H, C_ILE_111	2.98	2.15	12.64
5T6P.PDB	O, C_VAL_13	N, C_LYS_112	H, C_LYS_112	2.85	2.02	11.60
5T6P.PDB	O, C_ASP_175	NE, C_ARG_113	HE, C_ARG_113	2.48	1.76	27.03
5T6P.PDB	O, C_TYR_145	N, C_ALA_116	H, C_ALA_116	2.84	2.04	18.21
5T6P.PDB	O, C_ASN_142	N, C_THR_119	H, C_THR_119	2.93	2.10	12.42
5T6P.PDB	O, C_VAL_138	N, C_PHE_123	H, C_PHE_123	2.72	1.95	21.08
5T6P.PDB	OG, C_SER_136	NE2, C_GLN_129	HE22, C_GLN_129	2.79	1.95	11.34
5T6P.PDB	O, C_SER_127	N, C_THR_131	H, C_THR_131	2.98	2.17	16.75
5T6P.PDB	O, C_SER_127	OG1, C_THR_131	HG1, C_THR_131	2.92	2.09	7.67

5T6P.PDB	O, C_GLN_129	OG, C_SER_132	HG, C_SER_132	2.59	1.78	13.08
5T6P.PDB	O, C_LEU_130	N, C_GLY_133	H, C_GLY_133	2.95	2.18	22.40
5T6P.PDB	O, C_LEU_184	N, C_VAL_137	H, C_VAL_137	2.75	1.91	11.06
5T6P.PDB	O, C_SER_182	N, C_CYS_139	H, C_CYS_139	2.88	2.16	27.24
5T6P.PDB	O, C_SER_121	N, C_PHE_140	H, C_PHE_140	2.80	2.02	21.09
5T6P.PDB	O, C_MET_180	N, C_LEU_141	H, C_LEU_141	2.85	2.01	8.82
5T6P.PDB	OG, C_SER_179	N, C_ASN_143	H, C_ASN_143	2.94	2.10	9.85
5T6P.PDB	O, C_TYR_178	N, C_PHE_144	H, C_PHE_144	2.77	1.92	8.13
5T6P.PDB	OG, C_SER_182	NE1, C_TRP_153	HE1, C_TRP_153	2.89	2.07	15.50
5T6P.PDB	O, C_THR_198	N, C_LYS_154	H, C_LYS_154	2.75	1.96	18.48
5T6P.PDB	O, C_SER_196	N, C_ASP_156	H, C_ASP_156	2.70	1.86	10.78
5T6P.PDB	O, C_TRP_153	N, C_ARG_160	H, C_ARG_160	2.72	1.94	21.43
5T6P.PDB	O, C_SER_181	N, C_SER_167	H, C_SER_167	2.91	2.15	22.92
5T6P.PDB	O, C_LYS_147	NE1, C_TRP_168	HE1, C_TRP_168	3.00	2.28	28.07
5T6P.PDB	O, C_SER_179	N, C_THR_169	H, C_THR_169	2.70	1.86	8.97
5T6P.PDB	O, C_ASP_170	OG1, C_THR_169	HG1, C_THR_169	2.94	2.20	24.83
5T6P.PDB	O, C_SER_176	NE2, C_GLN_171	HE21, C_GLN_171	2.89	2.05	12.01
5T6P.PDB	O, C_ILE_111	NE2, C_GLN_171	HE22, C_GLN_171	2.85	2.04	15.54
5T6P.PDB	O, C_THR_177	N, C_ASP_172	H, C_ASP_172	2.94	2.12	14.22
5T6P.PDB	OD1, C_ASP_172	N, C_LYS_174	H, C_LYS_174	2.89	2.05	10.44
5T6P.PDB	O, C_ASP_172	N, C_SER_176	H, C_SER_176	2.80	2.08	27.25
5T6P.PDB	OD1, C_ASP_175	N, C_THR_177	H, C_THR_177	2.99	2.17	14.08
5T6P.PDB	OD1, C_ASP_175	OG1, C_THR_177	HG1, C_THR_177	2.69	1.86	7.21
5T6P.PDB	O, C_PHE_144	N, C_TYR_178	H, C_TYR_178	2.70	1.84	4.46
5T6P.PDB	O, C_LEU_141	N, C_MET_180	H, C_MET_180	2.84	2.02	15.41
5T6P.PDB	O, C_SER_167	N, C_SER_181	H, C_SER_181	2.79	2.00	19.18
5T6P.PDB	O, C_CYS_139	N, C_SER_182	H, C_SER_182	2.88	2.03	8.59
5T6P.PDB	OD1, C_ASN_166	OG, C_SER_182	HG, C_SER_182	2.45	1.64	11.11
5T6P.PDB	O, C_VAL_137	N, C_LEU_184	H, C_LEU_184	2.79	1.98	16.51
5T6P.PDB	O, C_ALA_135	N, C_LEU_186	H, C_LEU_186	2.93	2.10	13.93
5T6P.PDB	O, C_GLY_133	N, C_LYS_188	H, C_LYS_188	2.95	2.12	12.53
5T6P.PDB	O, C_THR_187	N, C_TYR_191	H, C_TYR_191	2.98	2.13	6.59
5T6P.PDB	OD1, C_ASP_156	N, C_SER_196	H, C_SER_196	2.87	2.02	6.00
5T6P.PDB	OG, C_SER_213	OG1, C_THR_198	HG1, C_THR_198	3.00	2.20	14.46
5T6P.PDB	O, C_ILE_210	N, C_ALA_201	H, C_ALA_201	2.94	2.14	17.24
5T6P.PDB	O, C_ASN_150	N, C_THR_202	H, C_THR_202	2.84	2.03	16.39
5T6P.PDB	O, C_ALA_201	N, C_ILE_210	H, C_ILE_210	2.99	2.24	25.62
5T6P.PDB	O, D_SER_25	N, D_LYS_3	H, D_LYS_3	2.88	2.06	14.17
5T6P.PDB	O, D_THR_113	N, D_VAL_12	H, D_VAL_12	2.73	1.95	21.29
5T6P.PDB	O, D_LEU_86	N, D_GLY_15	H, D_GLY_15	2.72	1.86	4.08
5T6P.PDB	O, D_ALA_13	N, D_GLY_16	H, D_GLY_16	2.92	2.16	22.99
5T6P.PDB	O, D_MET_83	N, D_LEU_18	H, D_LEU_18	2.98	2.18	18.81
5T6P.PDB	O, D_LEU_81	N, D_LEU_20	H, D_LEU_20	2.99	2.15	11.31
5T6P.PDB	O, D_VAL_5	N, D_ALA_23	H, D_ALA_23	2.75	1.94	16.20
5T6P.PDB	O, D_LYS_3	N, D_SER_25	H, D_SER_25	2.97	2.23	25.58
5T6P.PDB	O, D_ILE_51	N, D_MET_34	H, D_MET_34	2.96	2.14	15.76
5T6P.PDB	O, D_GLU_46	N, D_ARG_38	H, D_ARG_38	2.85	2.01	11.39
5T6P.PDB	O, D_ILE_93	N, D_GLN_39	H, D_GLN_39	2.72	1.93	19.22
5T6P.PDB	OE1, C_GLN_43	NE2, D_GLN_39	HE22, D_GLN_39	2.79	1.94	7.20
5T6P.PDB	O, D_THR_40	N, D_LYS_43	H, D_LYS_43	2.74	1.92	14.91
5T6P.PDB	O, D_ARG_38	N, D_GLU_46	H, D_GLU_46	2.87	2.03	9.75
5T6P.PDB	O, D_GLY_56	N, D_ASN_52	H, D_ASN_52	2.87	2.01	5.61
5T6P.PDB	OD1, D_ASN_52	N, D_GLY_56	H, D_GLY_56	2.70	1.88	14.82
5T6P.PDB	O, D_VAL_64	N, D_ARG_67	H, D_ARG_67	2.94	2.10	10.62
5T6P.PDB	O, D_GLN_82	N, D_THR_69	H, D_THR_69	2.84	2.13	29.43
5T6P.PDB	OD1, D_ASN_74	NE, D_ARG_72	HE, D_ARG_72	2.79	2.07	27.15
5T6P.PDB	O, D_TYR_32	NH2, D_ARG_72	HH22, D_ARG_72	3.00	2.24	24.48
5T6P.PDB	O, D_THR_78	N, D_ASP_73	H, D_ASP_73	2.80	1.97	14.04

5T6P.PDB	O, D_ASN_53	ND2, D_ASN_74	HD21, D_ASN_74	3.00	2.17	13.41
5T6P.PDB	O, D_LYS_76	OG1, D_THR_78	HG1, D_THR_78	2.82	2.06	20.07
5T6P.PDB	O, D_SER_71	N, D_TYR_80	H, D_TYR_80	2.80	1.95	7.50
5T6P.PDB	O, D_THR_69	N, D_GLN_82	H, D_GLN_82	2.94	2.10	10.42
5T6P.PDB	O, D_LEU_18	N, D_MET_83	H, D_MET_83	2.78	1.94	10.80
5T6P.PDB	O, D_ARG_67	OG, D_SER_84	HG, D_SER_84	2.89	2.11	18.15
5T6P.PDB	O, D_GLN_39	N, D_ILE_93	H, D_ILE_93	2.95	2.17	20.82
5T6P.PDB	O, D_ASP_90	OH, D_TYR_94	HH, D_TYR_94	2.82	2.01	12.26
5T6P.PDB	O, D_VAL_37	N, D_TYR_95	H, D_TYR_95	2.61	1.75	6.47
5T6P.PDB	O, D_TYR_105	N, D_ARG_98	H, D_ARG_98	2.94	2.21	27.44
5T6P.PDB	OD1, D_ASP_104	N, D_GLY_102	H, D_GLY_102	2.73	1.88	6.65
5T6P.PDB	OH, C_TYR_41	N, D_PHE_103	H, D_PHE_103	2.95	2.09	5.85
5T6P.PDB	O, D_PHE_103	NE1, D_TRP_106	HE1, D_TRP_106	2.89	2.15	26.36
5T6P.PDB	O, D_CYS_96	N, D_GLY_107	H, D_GLY_107	2.78	1.98	18.45
5T6P.PDB	OE1, D_GLU_6	N, D_GLY_109	H, D_GLY_109	2.82	1.98	11.29
5T6P.PDB	O, D_ALA_92	N, D_LEU_112	H, D_LEU_112	2.91	2.08	13.48
5T6P.PDB	O, D_GLY_10	N, D_THR_113	H, D_THR_113	2.98	2.16	15.81
5T6P.PDB	O, D_VAL_12	N, D_SER_115	H, D_SER_115	2.63	1.84	18.22
5T6P.PDB	OG, D_SER_115	N, D_ALA_117	H, D_ALA_117	2.99	2.16	13.20
5T6P.PDB	O, D_PHE_149	N, D_THR_120	H, D_THR_120	2.64	1.82	13.09
5T6P.PDB	O, D_LEU_144	N, D_TYR_125	H, D_TYR_125	2.84	2.03	17.31
5T6P.PDB	O, D_GLY_142	N, D_LEU_127	H, D_LEU_127	2.66	1.91	24.44
5T6P.PDB	O, D_VAL_184	N, D_LEU_141	H, D_LEU_141	2.71	1.86	8.53
5T6P.PDB	O, D_LEU_127	N, D_GLY_142	H, D_GLY_142	2.95	2.21	25.85
5T6P.PDB	O, D_SER_182	N, D_CYS_143	H, D_CYS_143	2.92	2.13	19.17
5T6P.PDB	O, D_TYR_125	N, D_LEU_144	H, D_LEU_144	2.68	1.83	6.73
5T6P.PDB	O, D_LEU_180	N, D_VAL_145	H, D_VAL_145	2.89	2.05	11.52
5T6P.PDB	O, D_TYR_178	N, D_GLY_147	H, D_GLY_147	2.78	2.07	29.34
5T6P.PDB	O, D_THR_120	N, D_PHE_149	H, D_PHE_149	2.69	1.86	13.14
5T6P.PDB	O, D_ASN_199	N, D_THR_156	H, D_THR_156	2.86	2.04	16.17
5T6P.PDB	OG, D_SER_182	NE1, D_TRP_157	HE1, D_TRP_157	2.97	2.13	11.56
5T6P.PDB	O, D_THR_197	N, D_ASN_158	H, D_ASN_158	2.80	1.97	13.62
5T6P.PDB	OD1, D_ASN_199	N, D_SER_159	H, D_SER_159	2.76	1.93	12.39
5T6P.PDB	O, D_SER_181	N, D_PHE_169	H, D_PHE_169	2.92	2.06	6.74
5T6P.PDB	O, D_LEU_177	N, D_GLN_174	H, D_GLN_174	2.90	2.05	9.77
5T6P.PDB	O, D_VAL_145	N, D_LEU_180	H, D_LEU_180	2.92	2.09	12.70
5T6P.PDB	O, D_CYS_143	N, D_SER_182	H, D_SER_182	2.99	2.18	17.49
5T6P.PDB	O, D_LEU_141	N, D_VAL_184	H, D_VAL_184	2.83	2.00	11.08
5T6P.PDB	O, D_VAL_139	N, D_VAL_186	H, D_VAL_186	2.98	2.17	17.79
5T6P.PDB	N, D_MET_138	OG, D_SER_188	HG, D_SER_188	2.81	2.08	24.12
5T6P.PDB	O, D_LYS_211	N, D_CYS_198	H, D_CYS_198	2.89	2.04	10.05
5T6P.PDB	O, D_THR_156	N, D_ASN_199	H, D_ASN_199	2.84	1.98	3.08
5T6P.PDB	O, D_THR_207	N, D_HIS_202	H, D_HIS_202	2.87	2.08	19.72
5T6P.PDB	O, D_PRO_150	NE2, D_HIS_202	HE2, D_HIS_202	2.50	1.66	9.39
5T6P.PDB	O, D_PRO_203	N, D_SER_206	H, D_SER_206	3.00	2.24	23.51
5T6P.PDB	O, D_HIS_202	N, D_THR_207	H, D_THR_207	2.78	1.92	6.54
5T6P.PDB	O, D_VAL_200	N, D_VAL_209	H, D_VAL_209	2.88	2.09	19.68
5T6P.PDB	O, D_CYS_198	N, D_LYS_211	H, D_LYS_211	2.87	2.05	13.61
5T6P.PDB	OE1, C_GLU_39	NE, E_ARG_5	HE, E_ARG_5	2.86	2.02	10.72

Table 1711: 5T6P-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5T78.PDB	OD1, C.ASN.150	N, A.ASP.1	H1, A.ASP.1	2.85	2.07	23.76
5T78.PDB	OG, A.SER.26	N, A.LEU.3	H, A.LEU.3	2.77	1.92	5.16
5T78.PDB	O, A.ARG.24	N, A.THR.5	H, A.THR.5	2.76	1.94	14.03
5T78.PDB	O, A.SER.22	N, A.THR.7	H, A.THR.7	2.99	2.18	17.34
5T78.PDB	O, A.LYS.108	N, A.LEU.11	H, A.LEU.11	2.88	2.17	29.09
5T78.PDB	O, A.VAL.83	N, A.GLY.16	H, A.GLY.16	2.89	2.04	7.22
5T78.PDB	O, A.LEU.78	N, A.ILE.21	H, A.ILE.21	2.93	2.10	12.51
5T78.PDB	O, A.THR.7	N, A.SER.22	H, A.SER.22	2.70	1.84	3.93
5T78.PDB	O, A.PHE.76	N, A.CYS.23	H, A.CYS.23	2.77	1.99	20.04
5T78.PDB	O, A.THR.5	N, A.ARG.24	H, A.ARG.24	2.73	1.95	21.00
5T78.PDB	O, A.THR.74	N, A.SER.25	H, A.SER.25	2.93	2.13	18.34
5T78.PDB	O, A.LYS.35	N, A.HIS.31	H, A.HIS.31	2.86	2.05	16.92
5T78.PDB	O, A.HIS.31	N, A.GLY.34	H, A.GLY.34	2.98	2.13	5.88
5T78.PDB	OD1, A.ASN.33	N, A.LYS.35	H, A.LYS.35	2.95	2.11	11.40
5T78.PDB	O, A.PHE.94	N, A.GLU.39	H, A.GLU.39	2.67	1.85	14.17
5T78.PDB	O, A.ILE.53	N, A.TRP.40	H, A.TRP.40	2.80	1.98	14.47
5T78.PDB	O, A.TYR.92	N, A.TYR.41	H, A.TYR.41	2.83	2.00	12.62
5T78.PDB	O, A.LYS.50	N, A.LEU.42	H, A.LEU.42	2.94	2.12	15.79
5T78.PDB	O, A.VAL.90	N, A.GLN.43	H, A.GLN.43	2.75	1.91	9.96
5T78.PDB	O, A.GLN.47	NE2, A.GLN.43	HE21, A.GLN.43	2.87	2.05	14.69
5T78.PDB	OE1, B.GLN.39	NE2, A.GLN.43	HE22, A.GLN.43	2.92	2.08	9.79
5T78.PDB	O, A.LYS.44	N, A.GLN.47	H, A.GLN.47	2.88	2.11	22.48
5T78.PDB	O, B.GLY.107	OG, A.SER.48	HG, A.SER.48	2.44	1.64	14.53
5T78.PDB	O, A.LEU.42	N, A.LYS.50	H, A.LYS.50	2.92	2.18	25.97
5T78.PDB	O, A.TRP.40	N, A.LEU.52	H, A.LEU.52	2.90	2.04	3.31
5T78.PDB	O, A.LYS.58	N, A.TYR.54	H, A.TYR.54	2.94	2.12	16.14
5T78.PDB	O, A.LEU.38	N, A.VAL.56	H, A.VAL.56	2.99	2.14	9.64
5T78.PDB	O, A.ARG.55	N, A.SER.57	H, A.SER.57	2.65	1.91	25.85
5T78.PDB	O, A.TYR.54	N, A.LYS.58	H, A.LYS.58	2.90	2.09	16.26
5T78.PDB	O, A.LEU.52	N, A.PHE.60	H, A.PHE.60	2.85	2.03	15.54
5T78.PDB	OD2, A.ASP.87	NH1, A.ARG.66	HH12, A.ARG.66	2.55	1.80	24.29
5T78.PDB	OD1, A.ASP.87	NH2, A.ARG.66	HH22, A.ARG.66	2.87	2.03	11.23
5T78.PDB	O, A.LYS.79	N, A.SER.68	H, A.SER.68	2.94	2.13	16.71
5T78.PDB	O, A.THR.77	N, A.SER.70	H, A.SER.70	2.85	2.11	25.59
5T78.PDB	O, A.CYS.23	N, A.PHE.76	H, A.PHE.76	2.95	2.11	10.95
5T78.PDB	O, A.SER.70	N, A.THR.77	H, A.THR.77	2.83	2.03	18.36
5T78.PDB	O, A.ILE.21	N, A.LEU.78	H, A.LEU.78	2.90	2.07	13.51
5T78.PDB	O, A.SER.68	N, A.LYS.79	H, A.LYS.79	2.71	1.87	11.82
5T78.PDB	O, A.ALA.19	N, A.ILE.80	H, A.ILE.80	2.96	2.14	14.84
5T78.PDB	OD2, A.ASP.87	N, A.GLU.84	H, A.GLU.84	2.82	1.98	8.50
5T78.PDB	O, A.GLU.84	N, A.ASP.87	H, A.ASP.87	2.85	2.00	6.16
5T78.PDB	O, A.GLN.43	N, A.VAL.90	H, A.VAL.90	2.81	1.97	10.43
5T78.PDB	O, A.THR.107	N, A.TYR.91	H, A.TYR.91	2.77	1.92	8.36
5T78.PDB	O, A.ASP.87	OH, A.TYR.91	HH, A.TYR.91	2.69	1.98	27.33
5T78.PDB	O, A.TYR.41	N, A.TYR.92	H, A.TYR.92	2.75	1.92	13.82
5T78.PDB	O, B.LYS.43	OH, A.TYR.92	HH, A.TYR.92	2.74	2.03	27.20
5T78.PDB	O, A.HIS.98	NE2, A.GLN.95	HE22, A.GLN.95	2.92	2.12	18.53
5T78.PDB	O, A.TYR.37	N, A.GLY.96	H, A.GLY.96	2.69	1.89	17.50
5T78.PDB	O, A.ILE.29	OG, A.SER.97	HG, A.SER.97	2.60	1.77	8.73
5T78.PDB	OE1, A.GLN.95	N, A.HIS.98	H, A.HIS.98	2.98	2.13	5.45
5T78.PDB	O, A.VAL.2	OG1, A.THR.102	HG1, A.THR.102	2.90	2.09	13.47
5T78.PDB	O, A.CYS.93	N, A.GLY.104	H, A.GLY.104	2.80	1.97	11.96
5T78.PDB	O, A.TYR.91	N, A.THR.107	H, A.THR.107	2.90	2.14	23.68
5T78.PDB	O, A.PRO.8	OG1, A.THR.107	HG1, A.THR.107	2.83	2.13	28.32
5T78.PDB	O, A.GLY.89	N, A.LEU.109	H, A.LEU.109	2.84	2.00	8.45
5T78.PDB	O, A.LEU.11	N, A.GLU.110	H, A.GLU.110	2.89	2.03	4.85
5T78.PDB	OE1, A.GLN.171	N, A.ILE.111	H, A.ILE.111	2.97	2.14	12.35

5T78.PDB	O, A_VAL_13	N, A_LYS_112	H, A_LYS_112	2.85	2.01	10.13
5T78.PDB	O, A_ASP_175	NE, A_ARG_113	HE, A_ARG_113	2.74	2.03	29.28
5T78.PDB	O, A_TYR_145	N, A_ALA_116	H, A_ALA_116	2.81	1.98	12.42
5T78.PDB	O, A_ASN_142	N, A_THR_119	H, A_THR_119	2.97	2.16	15.94
5T78.PDB	O, A_VAL_138	N, A_PHE_123	H, A_PHE_123	2.72	1.95	21.36
5T78.PDB	OG, A_SER_136	NE2, A_GLN_129	HE22, A_GLN_129	2.86	2.01	3.70
5T78.PDB	OE1, A_GLN_129	N, A_SER_136	H, A_SER_136	2.91	2.06	8.11
5T78.PDB	O, A_LEU_184	N, A_VAL_137	H, A_VAL_137	2.77	1.93	11.05
5T78.PDB	O, A_SER_182	N, A_CYS_139	H, A_CYS_139	2.88	2.10	21.11
5T78.PDB	O, A_SER_121	N, A_PHE_140	H, A_PHE_140	2.83	2.07	23.10
5T78.PDB	O, A_MET_180	N, A_LEU_141	H, A_LEU_141	2.79	1.93	5.17
5T78.PDB	OG, A_SER_179	N, A_ASN_143	H, A_ASN_143	2.98	2.18	18.51
5T78.PDB	O, A_TYR_178	N, A_PHE_144	H, A_PHE_144	2.83	2.00	10.95
5T78.PDB	O, A_GLU_200	N, A_LYS_152	H, A_LYS_152	2.93	2.13	17.83
5T78.PDB	OG, A_SER_182	NE1, A_TRP_153	HE1, A_TRP_153	2.68	1.86	12.79
5T78.PDB	O, A_THR_198	N, A_LYS_154	H, A_LYS_154	2.86	2.06	17.77
5T78.PDB	O, A_SER_158	N, A_ILE_155	H, A_ILE_155	2.71	1.89	15.55
5T78.PDB	O, A_SER_196	N, A_ASP_156	H, A_ASP_156	2.87	2.03	11.28
5T78.PDB	O, A_THR_183	N, A_LEU_165	H, A_LEU_165	2.87	2.15	28.15
5T78.PDB	O, A_SER_181	N, A_SER_167	H, A_SER_167	2.88	2.13	24.95
5T78.PDB	O, B_PRO_170	OG, A_SER_167	HG, A_SER_167	2.91	2.11	14.54
5T78.PDB	O, A_SER_179	N, A_THR_169	H, A_THR_169	2.90	2.06	10.39
5T78.PDB	O, A_ASP_170	OG1, A_THR_169	HG1, A_THR_169	2.92	2.23	29.63
5T78.PDB	O, A_ILE_111	NE2, A_GLN_171	HE22, A_GLN_171	2.73	1.91	15.69
5T78.PDB	O, A_THR_177	N, A_ASP_172	H, A_ASP_172	2.80	1.95	9.74
5T78.PDB	OD1, A_ASP_172	N, A_LYS_174	H, A_LYS_174	2.78	1.98	17.25
5T78.PDB	OD1, A_ASP_175	N, A_THR_177	H, A_THR_177	2.96	2.13	13.21
5T78.PDB	OD1, A_ASP_175	OG1, A_THR_177	HG1, A_THR_177	2.57	1.74	7.68
5T78.PDB	O, A_PHE_144	N, A_TYR_178	H, A_TYR_178	2.78	1.93	4.54
5T78.PDB	O, A_LEU_141	N, A_MET_180	H, A_MET_180	2.83	2.03	17.69
5T78.PDB	O, A_SER_167	N, A_SER_181	H, A_SER_181	2.92	2.13	19.33
5T78.PDB	O, A_CYS_139	N, A_SER_182	H, A_SER_182	2.91	2.07	11.51
5T78.PDB	OD1, A_ASN_166	OG, A_SER_182	HG, A_SER_182	2.63	1.89	23.17
5T78.PDB	O, A_LEU_165	N, A_THR_183	H, A_THR_183	2.82	2.01	15.88
5T78.PDB	O, A_VAL_137	N, A_LEU_184	H, A_LEU_184	2.80	1.99	16.92
5T78.PDB	O, A_GLY_163	N, A_THR_185	H, A_THR_185	2.94	2.10	11.69
5T78.PDB	O, A_ALA_135	N, A_LEU_186	H, A_LEU_186	2.79	1.97	14.73
5T78.PDB	O, A_GLY_133	N, A_LYS_188	H, A_LYS_188	2.91	2.08	12.09
5T78.PDB	OD2, A_ASP_156	ND1, A_HIS_194	HD1, A_HIS_194	2.73	1.92	16.43
5T78.PDB	O, A_LYS_154	N, A_THR_198	H, A_THR_198	2.92	2.19	26.56
5T78.PDB	O, A_LYS_152	N, A_GLU_200	H, A_GLU_200	2.90	2.08	15.52
5T78.PDB	O, A_ILE_210	N, A_ALA_201	H, A_ALA_201	2.96	2.16	17.21
5T78.PDB	O, A_ASN_150	N, A_THR_202	H, A_THR_202	2.72	1.89	13.21
5T78.PDB	ND1, A_HIS_203	OG1, A_THR_205	HG1, A_THR_205	2.99	2.26	25.09
5T78.PDB	O, A_ALA_201	N, A_ILE_210	H, A_ILE_210	2.84	2.02	14.61
5T78.PDB	OG1, A_THR_198	OG, A_SER_213	HG, A_SER_213	2.76	1.99	20.46
5T78.PDB	O, B_SER_21	N, B_SER_7	H, B_SER_7	2.89	2.16	26.40
5T78.PDB	O, B_THR_113	N, B_VAL_12	H, B_VAL_12	2.88	2.08	18.22
5T78.PDB	O, B_LEU_86	N, B_GLY_15	H, B_GLY_15	2.82	1.98	8.23
5T78.PDB	O, B_LEU_81	N, B_LEU_20	H, B_LEU_20	2.77	1.95	14.38
5T78.PDB	O, B_VAL_5	N, B_ALA_23	H, B_ALA_23	2.79	1.96	12.99
5T78.PDB	O, B_ASN_77	N, B_ALA_24	H, B_ALA_24	2.95	2.10	5.61
5T78.PDB	O, B_ILE_97	N, B_SER_35	H, B_SER_35	3.00	2.17	14.65
5T78.PDB	O, B_ALA_49	N, B_TRP_36	H, B_TRP_36	2.97	2.18	20.26
5T78.PDB	O, B_GLU_46	N, B_ARG_38	H, B_ARG_38	2.72	1.88	9.22
5T78.PDB	OE1, B_GLU_46	NE, B_ARG_38	HE, B_ARG_38	2.94	2.16	20.63
5T78.PDB	OH, B_TYR_94	NH1, B_ARG_38	HH11, B_ARG_38	2.90	2.09	15.42
5T78.PDB	OD1, B_ASP_90	NH1, B_ARG_38	HH12, B_ARG_38	2.89	2.09	17.62

5T78.PDB	O, B_ILE.93	N, B_GLN.39	H, B_GLN.39	2.78	1.98	17.72
5T78.PDB	OE1, A_GLN.43	NE2, B_GLN.39	HE22, B_GLN.39	2.63	1.78	5.56
5T78.PDB	O, B_THR.40	N, B_LYS.43	H, B_LYS.43	2.64	1.83	15.69
5T78.PDB	O, B_ARG.38	N, B_GLU.46	H, B_GLU.46	2.78	1.95	11.59
5T78.PDB	O, B_TRP.36	N, B_VAL.48	H, B_VAL.48	2.96	2.11	4.39
5T78.PDB	O, B_GLN.82	N, B_THR.69	H, B_THR.69	2.84	2.05	19.71
5T78.PDB	OH, B_TYR.60	N, B_ILE.70	H, B_ILE.70	2.81	2.01	18.63
5T78.PDB	OD1, B_ASN.74	NE, B_ARG.72	HE, B_ARG.72	2.69	1.95	25.68
5T78.PDB	O, B_THR.78	N, B_ASP.73	H, B_ASP.73	3.00	2.15	8.98
5T78.PDB	O, B_CYS.22	N, B_LEU.79	H, B_LEU.79	2.95	2.15	18.76
5T78.PDB	O, B_SER.71	N, B_TYR.80	H, B_TYR.80	2.82	1.97	8.86
5T78.PDB	O, B_LEU.20	N, B_LEU.81	H, B_LEU.81	2.97	2.19	21.07
5T78.PDB	O, B_THR.69	N, B_GLN.82	H, B_GLN.82	2.85	2.05	17.58
5T78.PDB	O, B_LEU.18	N, B_MET.83	H, B_MET.83	2.74	1.98	23.26
5T78.PDB	OD2, B_ASP.90	N, B_LYS.87	H, B_LYS.87	2.78	1.92	2.04
5T78.PDB	O, B_GLN.39	N, B_ILE.93	H, B_ILE.93	2.84	2.04	18.32
5T78.PDB	O, B_THR.110	N, B_TYR.94	H, B_TYR.94	2.77	1.91	3.39
5T78.PDB	O, B_ASP.90	OH, B_TYR.94	HH, B_TYR.94	2.74	1.93	12.66
5T78.PDB	O, B_VAL.37	N, B_TYR.95	H, B_TYR.95	2.67	1.82	4.17
5T78.PDB	OE1, B_GLN.39	OH, B_TYR.95	HH, B_TYR.95	2.91	2.11	14.46
5T78.PDB	OE2, B_GLU.6	N, B_CYS.96	H, B_CYS.96	2.65	1.81	8.49
5T78.PDB	OD1, B_ASP.104	N, B_GLY.102	H, B_GLY.102	2.93	2.09	9.46
5T78.PDB	OH, A_TYR.41	N, B_PHE.103	H, B_PHE.103	2.85	2.00	5.24
5T78.PDB	O, B_PHE.103	NE1, B_TRP.106	HE1, B_TRP.106	2.89	2.16	27.37
5T78.PDB	O, B_CYS.96	N, B_GLY.107	H, B_GLY.107	2.88	2.05	11.81
5T78.PDB	O, B_ALA.92	N, B_LEU.112	H, B_LEU.112	2.91	2.10	16.63
5T78.PDB	OG1, B_THR.91	N, B_VAL.114	H, B_VAL.114	2.84	1.98	4.39
5T78.PDB	O, B_PHE.149	N, B_THR.120	H, B_THR.120	2.84	2.00	10.54
5T78.PDB	O, B_LYS.146	N, B_SER.123	H, B_SER.123	2.99	2.18	17.27
5T78.PDB	O, B_LEU.144	N, B_TYR.125	H, B_TYR.125	2.88	2.07	16.65
5T78.PDB	O, B_GLY.142	N, B_LEU.127	H, B_LEU.127	2.85	2.06	19.67
5T78.PDB	O, B_VAL.186	N, B_VAL.139	H, B_VAL.139	2.76	1.90	4.98
5T78.PDB	OG1, B_THR.185	OG1, B_THR.140	HG1, B_THR.140	2.97	2.14	5.19
5T78.PDB	O, B_VAL.184	N, B_LEU.141	H, B_LEU.141	2.73	1.89	10.61
5T78.PDB	O, B_SER.182	N, B_CYS.143	H, B_CYS.143	2.99	2.23	23.48
5T78.PDB	O, B_TYR.125	N, B_LEU.144	H, B_LEU.144	2.79	1.95	10.28
5T78.PDB	O, B_LEU.180	N, B_VAL.145	H, B_VAL.145	2.91	2.07	9.52
5T78.PDB	O, B_SER.123	N, B_LYS.146	H, B_LYS.146	2.85	2.01	7.84
5T78.PDB	O, B_THR.120	N, B_PHE.149	H, B_PHE.149	2.90	2.09	17.04
5T78.PDB	O, B_ALA.201	N, B_THR.154	H, B_THR.154	3.00	2.21	19.88
5T78.PDB	O, B_ASN.199	N, B_THR.156	H, B_THR.156	2.81	1.98	11.68
5T78.PDB	O, B_THR.197	N, B_ASN.158	H, B_ASN.158	2.82	1.98	10.92
5T78.PDB	OD1, B_ASN.199	N, B_SER.159	H, B_SER.159	2.70	1.89	14.93
5T78.PDB	O, B_TRP.157	N, B_GLY.160	H, B_GLY.160	2.98	2.17	16.73
5T78.PDB	O, B_SER.181	N, B_PHE.169	H, B_PHE.169	2.81	1.96	6.40
5T78.PDB	O, B_LEU.177	N, B_GLN.174	H, B_GLN.174	2.94	2.10	10.35
5T78.PDB	O, B_TYR.148	N, B_TYR.178	H, B_TYR.178	2.83	1.97	1.07
5T78.PDB	O, B_VAL.172	N, B_THR.179	H, B_THR.179	2.95	2.19	24.45
5T78.PDB	O, B_VAL.145	N, B_LEU.180	H, B_LEU.180	2.94	2.12	15.28
5T78.PDB	O, B_HIS.167	N, B_SER.183	H, B_SER.183	2.99	2.13	4.09
5T78.PDB	O, B_LEU.141	N, B_VAL.184	H, B_VAL.184	2.95	2.11	9.47
5T78.PDB	O, B_GLY.165	N, B_THR.185	H, B_THR.185	2.86	2.16	29.53
5T78.PDB	O, B_VAL.139	N, B_VAL.186	H, B_VAL.186	2.86	2.08	20.52
5T78.PDB	OD1, B_ASN.158	N, B_THR.197	H, B_THR.197	2.72	1.93	18.91
5T78.PDB	O, B_LYS.211	N, B_CYS.198	H, B_CYS.198	2.79	1.94	3.58
5T78.PDB	O, B_THR.156	N, B_ASN.199	H, B_ASN.199	2.75	1.89	4.63
5T78.PDB	O, B_VAL.209	N, B_VAL.200	H, B_VAL.200	2.85	2.01	8.95
5T78.PDB	O, B_THR.154	N, B_ALA.201	H, B_ALA.201	2.91	2.08	12.90

5T78.PDB	O, B_THR_207	N, B_HIS_202	H, B_HIS_202	2.79	1.94	7.70
5T78.PDB	O, B_PRO_150	NE2, B_HIS_202	HE2, B_HIS_202	2.74	1.92	14.58
5T78.PDB	O, B_PRO_203	N, B_SER_206	H, B_SER_206	2.79	2.01	21.34
5T78.PDB	O, B_VAL_200	N, B_VAL_209	H, B_VAL_209	2.83	2.00	12.26
5T78.PDB	O, B_CYS_198	N, B_LYS_211	H, B_LYS_211	2.91	2.09	14.58
5T78.PDB	O, B_VAL_196	N, B_ILE_213	H, B_ILE_213	2.98	2.13	8.16
5T78.PDB	OE1, A_GLU_39	NH1, F_ARG_5	HH11, F_ARG_5	2.68	1.83	9.33
5T78.PDB	OG, C_SER_26	N, C_LEU_3	H, C_LEU_3	2.73	1.88	4.61
5T78.PDB	O, C_ARG_24	N, C_THR_5	H, C_THR_5	2.78	1.95	10.72
5T78.PDB	O, C_TYR_91	NE2, C_GLN_6	HE22, C_GLN_6	2.96	2.13	12.54
5T78.PDB	O, C_SER_22	N, C_THR_7	H, C_THR_7	2.88	2.10	19.87
5T78.PDB	O, C_LYS_108	N, C_LEU_11	H, C_LEU_11	2.84	2.11	26.95
5T78.PDB	O, C_VAL_83	N, C_GLY_16	H, C_GLY_16	2.91	2.06	6.60
5T78.PDB	O, C_ILE_80	N, C_ALA_19	H, C_ALA_19	2.84	2.03	15.95
5T78.PDB	O, C_LEU_78	N, C_ILE_21	H, C_ILE_21	2.99	2.16	13.69
5T78.PDB	O, C_THR_7	N, C_SER_22	H, C_SER_22	2.73	1.88	3.18
5T78.PDB	O, C_PHE_76	N, C_CYS_23	H, C_CYS_23	2.75	1.96	19.40
5T78.PDB	O, C_THR_5	N, C_ARG_24	H, C_ARG_24	2.63	1.83	18.67
5T78.PDB	OD1, C_ASP_75	NE, C_ARG_24	HE, C_ARG_24	2.96	2.16	17.61
5T78.PDB	O, C_THR_74	N, C_SER_25	H, C_SER_25	2.94	2.15	19.26
5T78.PDB	O, C_LYS_35	N, C_HIS_31	H, C_HIS_31	2.92	2.13	19.70
5T78.PDB	OH, C_TYR_37	ND2, C_ASN_33	HD21, C_ASN_33	2.96	2.18	21.06
5T78.PDB	O, C_HIS_31	N, C_GLY_34	H, C_GLY_34	3.00	2.15	8.88
5T78.PDB	OD1, C_ASN_33	N, C_LYS_35	H, C_LYS_35	2.89	2.07	15.44
5T78.PDB	O, C_PHE_94	N, C_GLU_39	H, C_GLU_39	2.80	1.97	13.19
5T78.PDB	O, C_ILE_53	N, C_TRP_40	H, C_TRP_40	2.85	2.04	17.58
5T78.PDB	O, C_TYR_92	N, C_TYR_41	H, C_TYR_41	2.86	2.04	13.58
5T78.PDB	O, C_LYS_50	N, C_LEU_42	H, C_LEU_42	2.96	2.15	16.18
5T78.PDB	O, C_VAL_90	N, C_GLN_43	H, C_GLN_43	2.84	2.01	10.96
5T78.PDB	O, C_LYS_44	N, C_GLN_47	H, C_GLN_47	2.91	2.11	19.11
5T78.PDB	O, D_GLY_107	OG, C_SER_48	HG, C_SER_48	2.59	1.80	15.22
5T78.PDB	O, C_LEU_42	N, C_LYS_50	H, C_LYS_50	2.85	2.10	25.26
5T78.PDB	O, C_TRP_40	N, C_LEU_52	H, C_LEU_52	2.91	2.06	6.20
5T78.PDB	O, C_LYS_58	N, C_TYR_54	H, C_TYR_54	2.95	2.13	15.51
5T78.PDB	O, C_LEU_38	N, C_VAL_56	H, C_VAL_56	2.84	1.99	9.09
5T78.PDB	O, C_ARG_55	N, C_SER_57	H, C_SER_57	2.67	1.95	28.00
5T78.PDB	O, C_TYR_54	N, C_LYS_58	H, C_LYS_58	2.92	2.10	14.52
5T78.PDB	O, C_LEU_52	N, C_PHE_60	H, C_PHE_60	2.96	2.14	14.24
5T78.PDB	OD2, C_ASP_87	NH1, C_ARG_66	HH12, C_ARG_66	2.35	1.56	19.31
5T78.PDB	O, C_LYS_79	N, C_SER_68	H, C_SER_68	2.84	2.06	20.21
5T78.PDB	O, C_THR_77	N, C_SER_70	H, C_SER_70	2.99	2.25	25.43
5T78.PDB	O, C_CYS_23	N, C_PHE_76	H, C_PHE_76	2.98	2.15	10.91
5T78.PDB	O, C_SER_70	N, C_THR_77	H, C_THR_77	2.95	2.14	16.22
5T78.PDB	O, C_ILE_21	N, C_LEU_78	H, C_LEU_78	2.92	2.09	12.26
5T78.PDB	O, C_SER_68	N, C_LYS_79	H, C_LYS_79	2.69	1.86	12.12
5T78.PDB	O, C_ALA_19	N, C_ILE_80	H, C_ILE_80	2.92	2.10	14.89
5T78.PDB	O, C_ASP_17	N, C_VAL_83	H, C_VAL_83	2.96	2.10	6.35
5T78.PDB	O, C_GLU_84	N, C_ASP_87	H, C_ASP_87	2.96	2.11	8.35
5T78.PDB	O, C_GLN_43	N, C_VAL_90	H, C_VAL_90	2.89	2.05	10.76
5T78.PDB	O, C_THR_107	N, C_TYR_91	H, C_TYR_91	2.71	1.86	8.50
5T78.PDB	O, C_ASP_87	OH, C_TYR_91	HH, C_TYR_91	2.69	1.94	21.91
5T78.PDB	O, C_TYR_41	N, C_TYR_92	H, C_TYR_92	2.85	2.03	14.75
5T78.PDB	O, D_LYS_43	OH, C_TYR_92	HH, C_TYR_92	2.90	2.21	29.37
5T78.PDB	O, C_HIS_98	NE2, C_GLN_95	HE22, C_GLN_95	2.74	1.90	10.22
5T78.PDB	O, C_TYR_37	N, C_GLY_96	H, C_GLY_96	2.72	1.93	19.30
5T78.PDB	O, C_ILE_29	OG, C_SER_97	HG, C_SER_97	2.56	1.73	9.58
5T78.PDB	O, C_VAL_2	OG1, C_THR_102	HG1, C_THR_102	2.90	2.09	14.58
5T78.PDB	O, C_CYS_93	N, C_GLY_104	H, C_GLY_104	2.78	1.94	9.79

5T78.PDB	O, C_TYR_91	N, C_THR_107	H, C_THR_107	2.86	2.08	22.08
5T78.PDB	O, C_PRO_8	OG1, C_THR_107	HG1, C_THR_107	2.85	2.11	24.36
5T78.PDB	O, C_GLY_89	N, C_LEU_109	H, C_LEU_109	2.72	1.88	8.68
5T78.PDB	O, C_LEU_11	N, C_GLU_110	H, C_GLU_110	2.94	2.09	6.48
5T78.PDB	OE1, C_GLN_171	N, C_ILE_111	H, C_ILE_111	2.92	2.08	10.11
5T78.PDB	O, C_VAL_13	N, C_LYS_112	H, C_LYS_112	2.91	2.09	13.64
5T78.PDB	O, C_ASP_175	NE, C_ARG_113	HE, C_ARG_113	2.82	2.03	19.01
5T78.PDB	O, C_TYR_145	N, C_ALA_116	H, C_ALA_116	2.82	1.99	13.51
5T78.PDB	O, C_ASN_142	N, C_THR_119	H, C_THR_119	2.98	2.18	17.98
5T78.PDB	O, C_VAL_138	N, C_PHE_123	H, C_PHE_123	2.72	1.94	20.98
5T78.PDB	O, C_GLN_129	OG, C_SER_132	HG, C_SER_132	2.70	1.96	24.09
5T78.PDB	OE1, C_GLN_129	N, C_SER_136	H, C_SER_136	2.96	2.13	13.97
5T78.PDB	O, C_LEU_184	N, C_VAL_137	H, C_VAL_137	2.85	2.01	9.76
5T78.PDB	O, C_SER_182	N, C_CYS_139	H, C_CYS_139	2.88	2.10	20.35
5T78.PDB	O, C_SER_121	N, C_PHE_140	H, C_PHE_140	2.89	2.10	20.29
5T78.PDB	O, C_MET_180	N, C_LEU_141	H, C_LEU_141	2.83	1.97	5.00
5T78.PDB	OG, C_SER_179	N, C_ASN_143	H, C_ASN_143	2.76	1.98	21.20
5T78.PDB	O, C_TYR_178	N, C_PHE_144	H, C_PHE_144	2.82	2.00	13.31
5T78.PDB	OG, C_SER_182	NE1, C_TRP_153	HE1, C_TRP_153	2.84	2.01	13.01
5T78.PDB	O, C_THR_198	N, C_LYS_154	H, C_LYS_154	2.79	1.99	17.84
5T78.PDB	O, C_SER_158	N, C_ILE_155	H, C_ILE_155	2.77	1.97	16.65
5T78.PDB	O, C_SER_196	N, C_ASP_156	H, C_ASP_156	2.85	2.02	12.83
5T78.PDB	O, A_SER_26	N, C_ASN_166	H, C_ASN_166	2.63	1.86	20.95
5T78.PDB	O, D_PRO_170	OG, C_SER_167	HG, C_SER_167	2.87	2.05	10.83
5T78.PDB	O, C_LYS_147	NE1, C_TRP_168	HE1, C_TRP_168	2.87	2.16	29.23
5T78.PDB	O, C_SER_179	N, C_THR_169	H, C_THR_169	2.97	2.13	10.91
5T78.PDB	O, C_ILE_111	NE2, C_GLN_171	HE22, C_GLN_171	2.61	1.79	14.42
5T78.PDB	O, C_THR_177	N, C_ASP_172	H, C_ASP_172	2.84	2.00	11.78
5T78.PDB	OD1, C_ASP_175	OG1, C_THR_177	HG1, C_THR_177	2.53	1.70	9.09
5T78.PDB	O, C_PHE_144	N, C_TYR_178	H, C_TYR_178	2.83	1.97	6.87
5T78.PDB	O, C_LEU_141	N, C_MET_180	H, C_MET_180	2.81	2.01	18.22
5T78.PDB	O, C_SER_167	N, C_SER_181	H, C_SER_181	3.00	2.20	18.36
5T78.PDB	O, C_CYS_139	N, C_SER_182	H, C_SER_182	2.90	2.06	10.20
5T78.PDB	OD1, C_ASN_166	OG, C_SER_182	HG, C_SER_182	2.85	2.09	21.73
5T78.PDB	O, C_LEU_165	N, C_THR_183	H, C_THR_183	2.96	2.12	11.56
5T78.PDB	O, C_VAL_137	N, C_LEU_184	H, C_LEU_184	2.88	2.07	16.37
5T78.PDB	O, C_ALA_135	N, C_LEU_186	H, C_LEU_186	2.77	1.93	10.86
5T78.PDB	O, C_GLY_133	N, C_LYS_188	H, C_LYS_188	2.96	2.15	17.19
5T78.PDB	OG1, C_THR_187	N, C_GLU_190	H, C_GLU_190	2.96	2.14	14.63
5T78.PDB	OD2, C_ASP_156	ND1, C_HIS_194	HD1, C_HIS_194	2.58	1.78	18.23
5T78.PDB	O, C_LYS_152	N, C_GLU_200	H, C_GLU_200	2.99	2.19	18.60
5T78.PDB	O, C_ILE_210	N, C_ALA_201	H, C_ALA_201	2.91	2.11	18.88
5T78.PDB	O, C_ASN_150	N, C_THR_202	H, C_THR_202	2.79	1.96	11.41
5T78.PDB	O, C_PRO_146	NE2, C_HIS_203	HE2, C_HIS_203	2.99	2.15	9.93
5T78.PDB	ND1, C_HIS_203	OG1, C_THR_205	HG1, C_THR_205	3.00	2.26	23.83
5T78.PDB	O, C_ALA_201	N, C_ILE_210	H, C_ILE_210	2.84	2.01	13.72
5T78.PDB	O, C_ASN_195	N, C_ARG_216	H, C_ARG_216	2.82	2.00	14.32
5T78.PDB	O, D_SER_25	N, D_LYS_3	H, D_LYS_3	2.88	2.06	16.00
5T78.PDB	O, D_SER_21	N, D_SER_7	H, D_SER_7	2.77	2.07	29.94
5T78.PDB	O, D_THR_113	N, D_VAL_12	H, D_VAL_12	2.94	2.15	19.31
5T78.PDB	O, D_LEU_86	N, D_GLY_15	H, D_GLY_15	2.80	1.95	6.77
5T78.PDB	O, D_ALA_13	N, D_GLY_16	H, D_GLY_16	2.96	2.14	15.77
5T78.PDB	O, D_MET_83	N, D_LEU_18	H, D_LEU_18	2.98	2.18	18.13
5T78.PDB	O, D_LEU_81	N, D_LEU_20	H, D_LEU_20	2.82	2.00	15.18
5T78.PDB	O, D_VAL_5	N, D_ALA_23	H, D_ALA_23	2.89	2.09	16.85
5T78.PDB	O, D_ASN_77	N, D_ALA_24	H, D_ALA_24	2.81	1.96	7.81
5T78.PDB	O, D_ILE_97	N, D_SER_35	H, D_SER_35	2.90	2.09	16.41
5T78.PDB	O, D_ALA_49	N, D_TRP_36	H, D_TRP_36	2.96	2.19	21.68

5T78.PDB	O, D_GLU_46	N, D_ARG_38	H, D_ARG_38	2.84	1.99	7.93
5T78.PDB	OE1, D_GLU_46	NE, D_ARG_38	HE, D_ARG_38	2.65	1.91	25.36
5T78.PDB	OH, D_TYR_94	NH1, D_ARG_38	HH11, D_ARG_38	2.88	2.06	14.14
5T78.PDB	OD1, D_ASP_90	NH1, D_ARG_38	HH12, D_ARG_38	2.85	2.05	16.93
5T78.PDB	O, D_ILE_93	N, D_GLN_39	H, D_GLN_39	2.73	1.94	19.04
5T78.PDB	OE1, C_GLN_43	NE2, D_GLN_39	HE22, D_GLN_39	2.72	1.87	5.23
5T78.PDB	O, D_ARG_44	N, D_THR_40	H, D_THR_40	2.98	2.18	19.30
5T78.PDB	O, D_THR_40	N, D_LYS_43	H, D_LYS_43	2.67	1.84	13.85
5T78.PDB	O, D_ARG_38	N, D_GLU_46	H, D_GLU_46	2.84	2.01	12.67
5T78.PDB	O, D_TRP_36	N, D_VAL_48	H, D_VAL_48	2.98	2.12	3.28
5T78.PDB	O, D_MET_34	N, D_ILE_51	H, D_ILE_51	2.95	2.17	21.24
5T78.PDB	OD1, D_ASN_52	N, D_GLY_56	H, D_GLY_56	2.75	1.95	18.27
5T78.PDB	O, D_GLN_82	N, D_THR_69	H, D_THR_69	2.80	2.05	24.68
5T78.PDB	OH, D_TYR_60	N, D_ILE_70	H, D_ILE_70	2.81	2.01	18.25
5T78.PDB	OD1, D_ASN_74	NE, D_ARG_72	HE, D_ARG_72	2.71	2.01	29.42
5T78.PDB	O, D_TYR_32	NH1, D_ARG_72	HH12, D_ARG_72	2.98	2.17	17.20
5T78.PDB	O, D_CYS_22	N, D_LEU_79	H, D_LEU_79	2.88	2.07	17.29
5T78.PDB	O, D_SER_71	N, D_TYR_80	H, D_TYR_80	2.89	2.04	9.91
5T78.PDB	O, D_LEU_20	N, D_LEU_81	H, D_LEU_81	2.95	2.20	24.69
5T78.PDB	O, D_THR_69	N, D_GLN_82	H, D_GLN_82	2.94	2.12	15.46
5T78.PDB	O, D_LEU_18	N, D_MET_83	H, D_MET_83	2.79	2.00	20.15
5T78.PDB	OD2, D_ASP_90	N, D_LYS_87	H, D_LYS_87	2.89	2.04	6.02
5T78.PDB	O, D_LEU_112	N, D_ALA_92	H, D_ALA_92	2.85	2.07	20.10
5T78.PDB	O, D_GLN_39	N, D_ILE_93	H, D_ILE_93	2.93	2.16	22.14
5T78.PDB	O, D_THR_110	N, D_TYR_94	H, D_TYR_94	2.81	1.96	2.19
5T78.PDB	O, D_ASP_90	OH, D_TYR_94	HH, D_TYR_94	2.65	1.83	8.83
5T78.PDB	O, D_VAL_37	N, D_TYR_95	H, D_TYR_95	2.63	1.78	4.62
5T78.PDB	OE1, D_GLN_39	OH, D_TYR_95	HH, D_TYR_95	2.98	2.17	11.35
5T78.PDB	OE2, D_GLU_6	N, D_CYS_96	H, D_CYS_96	2.78	1.93	7.90
5T78.PDB	OD1, D_ASP_104	N, D_GLY_102	H, D_GLY_102	2.77	1.92	7.47
5T78.PDB	OH, C_TYR_41	N, D_PHE_103	H, D_PHE_103	2.85	2.00	7.54
5T78.PDB	O, D_CYS_96	N, D_GLY_107	H, D_GLY_107	2.94	2.10	10.44
5T78.PDB	OE1, D_GLU_6	N, D_GLY_109	H, D_GLY_109	2.82	1.99	12.53
5T78.PDB	O, D_ALA_92	N, D_LEU_112	H, D_LEU_112	2.76	1.94	15.02
5T78.PDB	OG1, D_THR_91	N, D_VAL_114	H, D_VAL_114	2.86	2.01	6.88
5T78.PDB	O, D_PHE_149	N, D_THR_120	H, D_THR_120	2.81	1.96	9.17
5T78.PDB	O, D_LYS_146	N, D_SER_123	H, D_SER_123	2.97	2.17	17.75
5T78.PDB	O, D_LEU_144	N, D_TYR_125	H, D_TYR_125	2.89	2.08	16.53
5T78.PDB	O, D_GLY_142	N, D_LEU_127	H, D_LEU_127	2.90	2.13	23.33
5T78.PDB	O, D_VAL_186	N, D_VAL_139	H, D_VAL_139	2.83	1.97	3.34
5T78.PDB	O, D_VAL_184	N, D_LEU_141	H, D_LEU_141	2.81	1.99	15.70
5T78.PDB	O, D_SER_182	N, D_CYS_143	H, D_CYS_143	2.95	2.18	22.37
5T78.PDB	O, D_TYR_125	N, D_LEU_144	H, D_LEU_144	2.93	2.09	9.92
5T78.PDB	O, D_LEU_180	N, D_VAL_145	H, D_VAL_145	2.81	1.97	7.59
5T78.PDB	O, D_SER_123	N, D_LYS_146	H, D_LYS_146	2.94	2.10	9.29
5T78.PDB	O, D_THR_120	N, D_PHE_149	H, D_PHE_149	2.90	2.10	18.43
5T78.PDB	O, D_ASN_199	N, D_THR_156	H, D_THR_156	2.94	2.10	10.47
5T78.PDB	OG, D_SER_182	NE1, D_TRP_157	HE1, D_TRP_157	2.99	2.19	18.03
5T78.PDB	O, D_THR_197	N, D_ASN_158	H, D_ASN_158	2.89	2.04	8.58
5T78.PDB	OD1, D_ASN_199	N, D_SER_159	H, D_SER_159	2.73	1.89	10.93
5T78.PDB	O, D_TRP_157	N, D_GLY_160	H, D_GLY_160	2.79	1.98	17.29
5T78.PDB	OD1, C_ASN_142	NE2, D_HIS_167	HE2, D_HIS_167	2.85	2.00	9.68
5T78.PDB	O, D_SER_181	N, D_PHE_169	H, D_PHE_169	2.91	2.06	5.50
5T78.PDB	O, D_THR_179	N, D_VAL_172	H, D_VAL_172	2.97	2.16	16.66
5T78.PDB	O, D_LEU_177	N, D_GLN_174	H, D_GLN_174	2.91	2.06	7.53
5T78.PDB	OD2, A_ASP_75	N, D_SER_175	H, D_SER_175	2.84	2.00	10.93
5T78.PDB	O, D_TYR_148	N, D_TYR_178	H, D_TYR_178	2.82	1.96	2.75
5T78.PDB	O, D_VAL_172	N, D_THR_179	H, D_THR_179	2.97	2.22	24.34

5T78.PDB	O, D_VAL_145	N, D_LEU_180	H, D_LEU_180	2.85	2.03	14.78
5T78.PDB	O, D_CYS_143	N, D_SER_182	H, D_SER_182	2.99	2.19	18.10
5T78.PDB	O, D_HIS_167	N, D_SER_183	H, D_SER_183	2.87	2.01	1.62
5T78.PDB	O, D_LEU_141	N, D_VAL_184	H, D_VAL_184	2.93	2.08	8.26
5T78.PDB	O, D_VAL_139	N, D_VAL_186	H, D_VAL_186	2.97	2.19	20.48
5T78.PDB	OD1, D_ASN_158	N, D_THR_197	H, D_THR_197	2.81	2.01	18.23
5T78.PDB	O, D_LYS_211	N, D_CYS_198	H, D_CYS_198	2.82	1.96	5.03
5T78.PDB	O, D_THR_156	N, D_ASN_199	H, D_ASN_199	2.88	2.02	1.38
5T78.PDB	O, D_VAL_209	N, D_VAL_200	H, D_VAL_200	2.81	1.96	8.46
5T78.PDB	O, D_THR_154	N, D_ALA_201	H, D_ALA_201	2.98	2.16	13.25
5T78.PDB	O, D_THR_207	N, D_HIS_202	H, D_HIS_202	2.80	1.95	7.22
5T78.PDB	O, D_PRO_150	NE2, D_HIS_202	HE2, D_HIS_202	2.66	1.84	14.06
5T78.PDB	O, D_PRO_203	N, D_SER_206	H, D_SER_206	2.91	2.12	19.46
5T78.PDB	O, D_VAL_200	N, D_VAL_209	H, D_VAL_209	2.85	2.03	14.24
5T78.PDB	O, D_CYS_198	N, D_LYS_211	H, D_LYS_211	2.85	2.05	18.38
5T78.PDB	OE1, C_GLU_39	NH1, E_ARG_5	HH11, E_ARG_5	2.69	1.87	13.16

Table 1712: 5T78-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5U3J.PDB	O, H.LEU.82C	N, H.GLY.15	H, H.GLY.15	2.68	1.83	3.74
5U3J.PDB	O, H.LYS.13	N, H.GLY.16	H, H.GLY.16	2.99	2.15	12.62
5U3J.PDB	O, H.MET.82	N, H.LEU.18	H, H.LEU.18	2.68	1.88	17.05
5U3J.PDB	OE1, H.GLN.81	NE, H.ARG.19	HE, H.ARG.19	2.98	2.21	22.79
5U3J.PDB	O, H.LEU.80	N, H.LEU.20	H, H.LEU.20	2.96	2.14	16.12
5U3J.PDB	O, H.LEU.78	N, H.CYS.22	H, H.CYS.22	2.77	1.97	17.66
5U3J.PDB	O, H.THR.28	OG1, H.THR.32	HG1, H.THR.32	2.71	2.00	27.44
5U3J.PDB	OD2, H.ASP.53	NE1, H.TRP.33	HE1, H.TRP.33	2.97	2.22	24.73
5U3J.PDB	O, H.THR.93	N, H.SER.35	H, H.SER.35	2.87	2.05	14.77
5U3J.PDB	O, H.GLY.49	N, H.TRP.36	H, H.TRP.36	2.81	1.99	15.09
5U3J.PDB	O, H.PHE.91	N, H.VAL.37	H, H.VAL.37	2.90	2.06	9.69
5U3J.PDB	OE1, H.GLU.46	NE, H.ARG.38	HE, H.ARG.38	2.88	2.05	13.82
5U3J.PDB	OD1, H.ASP.86	NH1, H.ARG.38	HH12, H.ARG.38	2.85	2.09	23.00
5U3J.PDB	OG, H.SER.35	NE1, H.TRP.47	HE1, H.TRP.47	2.44	1.73	27.73
5U3J.PDB	O, H.TRP.36	N, H.VAL.48	H, H.VAL.48	2.91	2.09	13.49
5U3J.PDB	O, H.GLU.58	N, H.ARG.50	H, H.ARG.50	2.88	2.07	16.55
5U3J.PDB	OE1, H.GLU.58	NE, H.ARG.50	HE, H.ARG.50	2.83	2.12	29.07
5U3J.PDB	OE1, H.GLU.58	NH2, H.ARG.50	HH21, H.ARG.50	2.79	2.08	29.38
5U3J.PDB	O, H.MET.34	N, H.ILE.51	H, H.ILE.51	2.70	1.90	17.80
5U3J.PDB	O, H.ASN.52B	N, H.GLY.54	H, H.GLY.54	2.97	2.17	18.44
5U3J.PDB	O, H.VAL.48	N, H.ALA.60	H, H.ALA.60	2.71	1.92	19.22
5U3J.PDB	O, H.VAL.63	N, H.ARG.66	H, H.ARG.66	2.99	2.15	10.50
5U3J.PDB	OD2, H.ASP.86	NH1, H.ARG.66	HH12, H.ARG.66	2.57	1.73	9.26
5U3J.PDB	OD1, H.ASP.86	NH2, H.ARG.66	HH22, H.ARG.66	2.89	2.04	5.32
5U3J.PDB	O, H.GLN.81	N, H.THR.68	H, H.THR.68	2.98	2.27	28.87
5U3J.PDB	OH, H.TYR.59	N, H.ILE.69	H, H.ILE.69	2.88	2.05	11.11
5U3J.PDB	O, H.THR.32	NH1, H.ARG.71	HH12, H.ARG.71	2.85	2.04	17.00
5U3J.PDB	O, H.THR.77	N, H.ASP.72	H, H.ASP.72	2.83	2.04	19.14
5U3J.PDB	O, H.ASP.72	N, H.ARG.75	H, H.ARG.75	2.96	2.12	10.52
5U3J.PDB	O, H.ARG.75	OG1, H.THR.77	HG1, H.THR.77	2.85	2.06	17.00
5U3J.PDB	O, H.CYS.22	N, H.LEU.78	H, H.LEU.78	2.84	2.02	14.17
5U3J.PDB	O, H.SER.70	N, H.TYR.79	H, H.TYR.79	2.89	2.05	10.03
5U3J.PDB	O, H.THR.68	N, H.GLN.81	H, H.GLN.81	2.76	1.91	9.85
5U3J.PDB	O, H.LEU.18	N, H.MET.82	H, H.MET.82	2.72	1.89	13.44
5U3J.PDB	O, H.ARG.66	OG1, H.THR.82A	HG1, H.THR.82A	2.74	1.94	14.02
5U3J.PDB	O, H.GLY.16	N, H.LEU.82C	H, H.LEU.82C	2.98	2.20	20.11
5U3J.PDB	OD2, H.ASP.86	N, H.LYS.83	H, H.LYS.83	2.93	2.08	5.84
5U3J.PDB	O, H.GLN.39	N, H.ARG.89	H, H.ARG.89	2.74	1.90	10.05
5U3J.PDB	O, H.THR.107	N, H.TYR.90	H, H.TYR.90	2.95	2.11	11.30
5U3J.PDB	O, H.ASP.86	OH, H.TYR.90	HH, H.TYR.90	2.53	1.71	8.74
5U3J.PDB	O, H.VAL.37	N, H.PHE.91	H, H.PHE.91	2.51	1.68	10.84
5U3J.PDB	OE2, H.GLU.6	N, H.CYS.92	H, H.CYS.92	2.75	1.89	6.53
5U3J.PDB	O, H.TRP.33	N, H.ASP.95	H, H.ASP.95	2.77	1.92	6.84
5U3J.PDB	O, H.TYR.100K	N, H.GLU.98	H, H.GLU.98	2.94	2.22	28.79
5U3J.PDB	O, H.PHE.100D	N, H.TRP.100G	H, H.TRP.100G	2.86	2.01	6.48
5U3J.PDB	O, H.GLU.100F	OG, H.SER.100I	HG, H.SER.100I	2.76	1.95	12.70
5U3J.PDB	O, H.GLU.98	N, H.TYR.100K	H, H.TYR.100K	2.86	2.12	25.47
5U3J.PDB	OD1, L.ASP.31	OH, H.TYR.100K	HH, H.TYR.100K	2.88	2.04	5.22
5U3J.PDB	OH, L.TYR.36	N, H.MET.100N	H, H.MET.100N	2.75	1.92	13.09
5U3J.PDB	OE1, H.GLU.6	N, H.GLY.106	H, H.GLY.106	2.94	2.10	10.69
5U3J.PDB	O, H.GLY.88	N, H.VAL.109	H, H.VAL.109	2.80	1.95	8.22
5U3J.PDB	O, H.GLY.10	N, H.THR.110	H, H.THR.110	2.98	2.17	17.31
5U3J.PDB	OG, H.SER.87	N, H.VAL.111	H, H.VAL.111	2.79	1.95	7.31
5U3J.PDB	O, H.PHE.146	N, H.LYS.117	H, H.LYS.117	2.94	2.12	14.80
5U3J.PDB	O, H.LYS.143	N, H.SER.120	H, H.SER.120	2.97	2.12	7.20
5U3J.PDB	O, H.LEU.141	N, H.PHE.122	H, H.PHE.122	2.79	2.02	22.59
5U3J.PDB	O, H.GLY.139	N, H.LEU.124	H, H.LEU.124	2.74	1.98	23.31

5U3J.PDB	O, H.SER.130	N, H.ALA.137	H, H.ALA.137	2.87	2.16	29.44
5U3J.PDB	O, H.SER.180	N, H.CYS.140	H, H.CYS.140	2.63	1.85	19.83
5U3J.PDB	O, H.PHE.122	N, H.LEU.141	H, H.LEU.141	2.71	1.86	7.01
5U3J.PDB	O, H.LEU.178	N, H.VAL.142	H, H.VAL.142	2.96	2.22	26.19
5U3J.PDB	O, H.LYS.117	N, H.PHE.146	H, H.PHE.146	2.97	2.25	28.41
5U3J.PDB	O, H.ASN.197	N, H.SER.153	H, H.SER.153	2.96	2.15	16.40
5U3J.PDB	OG, H.SER.180	NE1, H.TRP.154	HE1, H.TRP.154	2.98	2.15	12.85
5U3J.PDB	O, H.SER.177	N, H.VAL.169	H, H.VAL.169	2.87	2.08	18.96
5U3J.PDB	O, H.LEU.175	N, H.GLN.171	H, H.GLN.171	2.85	2.01	9.90
5U3J.PDB	O, H.GLN.171	N, H.GLY.174	H, H.GLY.174	2.81	1.98	10.98
5U3J.PDB	O, H.TYR.145	N, H.TYR.176	H, H.TYR.176	2.90	2.05	6.56
5U3J.PDB	O, H.VAL.142	N, H.LEU.178	H, H.LEU.178	2.95	2.16	18.81
5U3J.PDB	O, H.HIS.164	N, H.VAL.181	H, H.VAL.181	2.91	2.08	14.09
5U3J.PDB	O, H.LEU.138	N, H.VAL.182	H, H.VAL.182	2.66	1.85	17.24
5U3J.PDB	OD1, H.ASN.155	N, H.ILE.195	H, H.ILE.195	2.70	1.88	13.20
5U3J.PDB	O, H.SER.153	N, H.ASN.197	H, H.ASN.197	2.90	2.15	24.53
5U3J.PDB	O, H.VAL.207	N, H.VAL.198	H, H.VAL.198	2.82	1.98	9.42
5U3J.PDB	O, H.PRO.147	NE2, H.HIS.200	HE2, H.HIS.200	2.98	2.14	11.71
5U3J.PDB	O, H.VAL.198	N, H.VAL.207	H, H.VAL.207	2.90	2.10	17.28
5U3J.PDB	O, L.TYR.86	NE2, L.GLN.6	HE22, L.GLN.6	2.61	1.91	29.28
5U3J.PDB	O, L.ILE.29	N, L.TYR.32	H, L.TYR.32	2.94	2.08	3.56
5U3J.PDB	OE1, H.GLU.100F	OH, L.TYR.32	HH, L.TYR.32	2.62	1.91	27.84
5U3J.PDB	O, L.ILE.48	N, L.TRP.35	H, L.TRP.35	2.59	1.80	18.85
5U3J.PDB	O, L.TYR.87	N, L.TYR.36	H, L.TYR.36	2.81	2.00	16.97
5U3J.PDB	OE1, L.GLN.89	OH, L.TYR.36	HH, L.TYR.36	2.74	1.93	13.79
5U3J.PDB	O, L.LYS.45	N, L.GLN.37	H, L.GLN.37	2.91	2.10	17.84
5U3J.PDB	OE1, H.GLN.39	NE2, L.GLN.38	HE22, L.GLN.38	2.66	1.83	12.57
5U3J.PDB	O, L.GLN.37	N, L.LYS.45	H, L.LYS.45	2.58	1.77	16.56
5U3J.PDB	O, L.LYS.53	N, L.TYR.49	H, L.TYR.49	2.83	2.07	23.24
5U3J.PDB	O, L.ASP.82	OH, L.TYR.86	HH, L.TYR.86	2.92	2.16	22.19
5U3J.PDB	O, L.ASN.34	N, L.GLN.89	H, L.GLN.89	2.94	2.19	25.35
5U3J.PDB	O, L.VAL.133	N, L.PHE.118	H, L.PHE.118	2.97	2.15	14.78
5U3J.PDB	OG, L.SER.131	NE2, L.GLN.124	HE22, L.GLN.124	2.67	1.82	7.69
5U3J.PDB	O, L.LEU.181	N, L.ALA.130	H, L.ALA.130	2.68	1.95	26.74
5U3J.PDB	O, L.LEU.179	N, L.VAL.132	H, L.VAL.132	2.84	2.01	12.36
5U3J.PDB	O, L.GLU.195	N, L.GLN.147	H, L.GLN.147	2.91	2.06	7.51
5U3J.PDB	OG, L.SER.177	NE1, L.TRP.148	HE1, L.TRP.148	2.81	2.02	19.92
5U3J.PDB	O, L.TRP.148	N, L.GLN.155	H, L.GLN.155	2.85	2.01	10.26
5U3J.PDB	O, H.PRO.167	OG, L.SER.162	HG, L.SER.162	2.90	2.16	24.21
5U3J.PDB	O, L.LEU.136	N, L.LEU.175	H, L.LEU.175	2.78	2.04	25.99
5U3J.PDB	O, L.SER.162	N, L.SER.176	H, L.SER.176	2.81	2.07	25.43
5U3J.PDB	O, L.GLN.160	N, L.THR.178	H, L.THR.178	2.90	2.05	9.65
5U3J.PDB	O, L.VAL.132	N, L.LEU.179	H, L.LEU.179	2.58	1.74	8.42
5U3J.PDB	O, L.ALA.130	N, L.LEU.181	H, L.LEU.181	2.90	2.18	27.62
5U3J.PDB	O, L.SER.182	N, L.TYR.186	H, L.TYR.186	2.73	1.97	23.20
5U3J.PDB	O, L.LYS.183	N, L.GLU.187	H, L.GLU.187	2.87	2.13	25.64
5U3J.PDB	O, L.VAL.205	N, L.VAL.196	H, L.VAL.196	2.92	2.06	3.44
5U3J.PDB	O, A.PHE.673	OG1, A.THR.676	HG1, A.THR.676	2.55	1.85	27.32
5U3J.PDB	O, A.ASP.674	N, A.TRP.678	H, A.TRP.678	2.96	2.23	26.81
5U3J.PDB	O, A.ILE.675	N, A.LEU.679	H, A.LEU.679	2.98	2.15	11.89
5U3J.PDB	O, A.THR.676	N, A.TRP.680	H, A.TRP.680	2.90	2.12	20.48
5U3J.PDB	O, A.ASN.677	N, A.TYR.681	H, A.TYR.681	2.74	1.96	21.09
5U3J.PDB	O, A.TRP.678	N, A.ILE.682	H, A.ILE.682	2.63	1.81	13.86

Table 1713: 5U3J-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5U3N.PDB	O, H_VAL_23	N, H_VAL_5	H, H_VAL_5	2.91	2.06	7.34
5U3N.PDB	O, H_TYR_90	NE2, H_GLN_6	HE22, H_GLN_6	2.83	2.00	12.08
5U3N.PDB	O, H_LEU_82C	N, H_GLY_15	H, H_GLY_15	2.69	1.84	5.70
5U3N.PDB	O, H_LYS_13	N, H_GLY_16	H, H_GLY_16	2.84	2.03	16.66
5U3N.PDB	O, H_MET_82	N, H_LEU_18	H, H_LEU_18	2.86	2.07	19.50
5U3N.PDB	OG, H_SER_7	N, H_SER_21	H, H_SER_21	2.86	2.03	12.74
5U3N.PDB	O, H_VAL_5	N, H_VAL_23	H, H_VAL_23	2.81	1.99	14.35
5U3N.PDB	O, H_ASN_76	N, H_THR_24	H, H_THR_24	2.94	2.15	18.71
5U3N.PDB	O, H_GLN_3	N, H_SER_25	H, H_SER_25	2.99	2.20	19.07
5U3N.PDB	O, H_THR_28	OG1, H_THR_32	HG1, H_THR_32	2.86	2.15	27.61
5U3N.PDB	O, H_ILE_51	N, H_MET_34	H, H_MET_34	2.95	2.12	13.00
5U3N.PDB	O, H_ALA_49	N, H_TRP_36	H, H_TRP_36	2.81	2.02	19.03
5U3N.PDB	O, H_TYR_91	N, H_VAL_37	H, H_VAL_37	2.87	2.04	12.29
5U3N.PDB	O, H_GLU_46	N, H_ARG_38	H, H_ARG_38	2.84	1.99	7.64
5U3N.PDB	OE1, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.91	2.07	9.07
5U3N.PDB	OH, H_TYR_90	NH1, H_ARG_38	HH11, H_ARG_38	3.00	2.21	20.04
5U3N.PDB	O, H_VAL_89	N, H_GLN_39	H, H_GLN_39	2.83	2.04	20.47
5U3N.PDB	O, H_ARG_38	N, H_GLU_46	H, H_GLU_46	2.85	2.12	27.26
5U3N.PDB	O, H_TRP_36	N, H_VAL_48	H, H_VAL_48	2.79	1.97	13.99
5U3N.PDB	OD2, H_ASP_58	NE, H_ARG_50	HE, H_ARG_50	2.78	1.98	18.36
5U3N.PDB	O, H_MET_34	N, H_ILE_51	H, H_ILE_51	2.79	1.99	18.29
5U3N.PDB	O, H_ILE_56	N, H_SER_52	H, H_SER_52	2.99	2.26	27.62
5U3N.PDB	OD2, H_ASP_674	NH1, H_ARG_52A	HH12, H_ARG_52A	3.00	2.24	24.41
5U3N.PDB	OD1, H_ASP_53	NH2, H_ARG_52A	HH21, H_ARG_52A	2.93	2.18	25.35
5U3N.PDB	O, H_ARG_52A	N, H_ASP_53	H, H_ASP_53	2.99	2.21	21.52
5U3N.PDB	OG, H_SER_52	N, H_ILE_56	H, H_ILE_56	2.80	2.06	25.80
5U3N.PDB	O, H_VAL_48	N, H_ALA_60	H, H_ALA_60	2.80	1.95	7.61
5U3N.PDB	O, H_VAL_63	N, H_ARG_66	H, H_ARG_66	3.00	2.17	13.97
5U3N.PDB	OD2, H_ASP_86	NH1, H_ARG_66	HH12, H_ARG_66	2.73	1.91	14.46
5U3N.PDB	O, H_PRO_62	NH2, H_ARG_66	HH21, H_ARG_66	2.95	2.10	7.27
5U3N.PDB	O, H_HIS_81	N, H_ILE_68	H, H_ILE_68	2.90	2.10	18.72
5U3N.PDB	OH, H_TYR_59	N, H_ILE_69	H, H_ILE_69	2.92	2.12	19.11
5U3N.PDB	OD1, H_ASP_73	NE, H_ARG_71	HE, H_ARG_71	2.93	2.13	17.92
5U3N.PDB	O, H_THR_32	NH1, H_ARG_71	HH12, H_ARG_71	2.85	2.04	16.27
5U3N.PDB	O, H_THR_77	N, H_ASP_72	H, H_ASP_72	2.83	1.99	11.84
5U3N.PDB	O, H_CYS_22	N, H_LEU_78	H, H_LEU_78	2.84	2.00	10.39
5U3N.PDB	O, H_SER_70	N, H_PHE_79	H, H_PHE_79	2.80	1.94	3.12
5U3N.PDB	O, H_ILE_68	N, H_HIS_81	H, H_HIS_81	2.75	1.95	17.72
5U3N.PDB	O, H_LEU_18	N, H_MET_82	H, H_MET_82	2.59	1.75	10.08
5U3N.PDB	OD2, H_ASP_86	N, H_LYS_83	H, H_LYS_83	2.93	2.12	15.88
5U3N.PDB	O, H_LYS_83	N, H_ASP_86	H, H_ASP_86	2.78	1.94	11.41
5U3N.PDB	O, H_THR_107	N, H_TYR_90	H, H_TYR_90	2.72	1.88	9.30
5U3N.PDB	O, H_ASP_86	OH, H_TYR_90	HH, H_TYR_90	2.67	1.88	16.73
5U3N.PDB	O, H_VAL_37	N, H_TYR_91	H, H_TYR_91	2.62	1.77	5.09
5U3N.PDB	O, H_SER_35	N, H_THR_93	H, H_THR_93	2.88	2.10	21.23
5U3N.PDB	O, H_TRP_33	N, H_ASP_95	H, H_ASP_95	2.83	1.98	5.13
5U3N.PDB	O, H_TYR_100L	N, H_GLU_96	H, H_GLU_96	2.96	2.15	16.42
5U3N.PDB	O, H_ASN_100J	N, H_ALA_98	H, H_ALA_98	2.86	2.02	10.29
5U3N.PDB	OE1, H_GLU_100E	NE, H_ARG_100B	HE, H_ARG_100B	2.83	1.97	4.42
5U3N.PDB	OE2, H_GLU_100E	NH2, H_ARG_100B	HH21, H_ARG_100B	2.91	2.08	12.18
5U3N.PDB	OD1, L_ASP_31	NH2, H_ARG_100B	HH22, H_ARG_100B	2.97	2.15	14.50
5U3N.PDB	O, H_ARG_100B	N, H_GLU_100E	H, H_GLU_100E	2.83	2.05	20.60
5U3N.PDB	O, H_PHE_100C	N, H_TRP_100F	H, H_TRP_100F	2.93	2.08	6.81
5U3N.PDB	O, H_LEU_100A	NE1, H_TRP_100F	HE1, H_TRP_100F	2.88	2.10	19.92
5U3N.PDB	O, H_GLU_100E	N, H_TYR_100H	H, H_TYR_100H	2.96	2.12	9.41
5U3N.PDB	O, H_ALA_98	N, H_ASN_100J	H, H_ASN_100J	2.93	2.10	13.13
5U3N.PDB	OD1, L_ASN_34	ND2, H_ASN_100J	HD21, H_ASN_100J	2.72	1.86	2.61

5U3N.PDB	O, H_GLU_96	N, H_TYR_100L	H, H_TYR_100L	2.88	2.05	12.56
5U3N.PDB	OH, L_TYR_36	N, H_MET_100M	H, H_MET_100M	2.99	2.13	5.54
5U3N.PDB	O, H_ALA_94	N, H_ASP_101	H, H_ASP_101	2.74	1.99	25.37
5U3N.PDB	O, H_CYS_92	N, H_GLY_104	H, H_GLY_104	2.82	1.98	9.77
5U3N.PDB	OE1, H_GLN_6	N, H_GLY_106	H, H_GLY_106	2.96	2.22	25.98
5U3N.PDB	O, H_TYR_90	N, H_THR_107	H, H_THR_107	2.85	2.08	22.78
5U3N.PDB	O, H_ALA_88	N, H_VAL_109	H, H_VAL_109	2.88	2.03	6.16
5U3N.PDB	O, H_GLY_10	N, H_ILE_110	H, H_ILE_110	2.94	2.09	6.89
5U3N.PDB	OG1, H_THR_87	N, H_VAL_111	H, H_VAL_111	2.89	2.03	4.98
5U3N.PDB	O, H_VAL_12	N, H_SER_112	H, H_SER_112	2.98	2.17	17.21
5U3N.PDB	O, H_PHE_146	N, H_LYS_117	H, H_LYS_117	2.78	1.97	16.03
5U3N.PDB	O, H_GLY_139	N, H_LEU_124	H, H_LEU_124	2.86	2.00	5.63
5U3N.PDB	O, H_VAL_184	N, H_ALA_136	H, H_ALA_136	2.84	1.99	5.94
5U3N.PDB	O, H_LEU_124	N, H_GLY_139	H, H_GLY_139	3.00	2.25	25.48
5U3N.PDB	O, H_SER_180	N, H_CYS_140	H, H_CYS_140	2.82	2.02	17.61
5U3N.PDB	O, H_PHE_122	N, H_LEU_141	H, H_LEU_141	2.79	1.95	10.76
5U3N.PDB	O, H_LEU_178	N, H_VAL_142	H, H_VAL_142	2.71	1.86	7.20
5U3N.PDB	O, H_SER_120	N, H_LYS_143	H, H_LYS_143	2.84	1.99	7.21
5U3N.PDB	O, H_LYS_117	N, H_PHE_146	H, H_PHE_146	2.94	2.13	16.41
5U3N.PDB	O, H_ASN_199	N, H_THR_151	H, H_THR_151	3.00	2.17	12.79
5U3N.PDB	OG, H_SER_180	NE1, H_TRP_154	HE1, H_TRP_154	2.95	2.11	9.10
5U3N.PDB	O, H_ILE_195	N, H_ASN_155	H, H_ASN_155	2.79	1.95	11.06
5U3N.PDB	OD1, H_ASN_197	N, H_SER_156	H, H_SER_156	2.62	1.82	17.28
5U3N.PDB	O, H_TRP_154	N, H_GLY_157	H, H_GLY_157	2.98	2.26	27.93
5U3N.PDB	OD1, L_ASN_138	NE2, H_HIS_164	HE2, H_HIS_164	2.92	2.21	29.54
5U3N.PDB	O, H_SER_179	N, H_PHE_166	H, H_PHE_166	2.96	2.11	6.98
5U3N.PDB	O, H_SER_177	N, H_VAL_169	H, H_VAL_169	2.89	2.05	12.11
5U3N.PDB	O, H_LEU_175	N, H_GLN_171	H, H_GLN_171	2.79	1.96	11.18
5U3N.PDB	O, H_LEU_175	NE2, H_GLN_171	HE21, H_GLN_171	2.95	2.10	7.82
5U3N.PDB	OD1, H_ASP_144	NE2, H_GLN_171	HE22, H_GLN_171	2.99	2.19	18.08
5U3N.PDB	O, H_GLN_171	N, H_GLY_174	H, H_GLY_174	2.89	2.04	7.78
5U3N.PDB	O, H_TYR_145	N, H_TYR_176	H, H_TYR_176	2.81	1.96	5.90
5U3N.PDB	O, H_VAL_169	N, H_SER_177	H, H_SER_177	2.98	2.23	24.19
5U3N.PDB	O, H_VAL_142	N, H_LEU_178	H, H_LEU_178	2.86	2.04	15.63
5U3N.PDB	O, H_HIS_164	N, H_VAL_181	H, H_VAL_181	2.83	1.99	10.90
5U3N.PDB	O, H_LEU_138	N, H_VAL_182	H, H_VAL_182	2.84	2.03	16.03
5U3N.PDB	O, H_ALA_136	N, H_VAL_184	H, H_VAL_184	2.89	2.08	16.51
5U3N.PDB	O, H_GLY_134	N, H_SER_186	H, H_SER_186	2.89	2.05	9.68
5U3N.PDB	O, H_PRO_185	N, H_SER_188	H, H_SER_188	2.86	2.07	20.15
5U3N.PDB	O, H_SER_188	N, H_GLN_192	H, H_GLN_192	2.98	2.15	13.47
5U3N.PDB	OD1, H_ASN_155	N, H_ILE_195	H, H_ILE_195	2.89	2.08	15.15
5U3N.PDB	O, H_LYS_209	N, H_CYS_196	H, H_CYS_196	2.96	2.17	20.77
5U3N.PDB	O, H_SER_153	N, H_ASN_197	H, H_ASN_197	2.66	1.82	9.65
5U3N.PDB	O, H_VAL_207	N, H_VAL_198	H, H_VAL_198	2.77	1.91	0.90
5U3N.PDB	O, H_THR_205	N, H_HIS_200	H, H_HIS_200	2.79	1.93	4.87
5U3N.PDB	O, H_PRO_147	NE2, H_HIS_200	HE2, H_HIS_200	2.62	1.78	9.36
5U3N.PDB	O, H_VAL_198	N, H_VAL_207	H, H_VAL_207	2.91	2.08	14.15
5U3N.PDB	O, H_TYR_194	N, H_AVAL_211	H, H_AVAL_211	2.89	2.05	9.34
5U3N.PDB	O, H_TYR_194	N, H_BVAL_211	H, H_BVAL_211	2.89	2.05	9.13
5U3N.PDB	O, H_PRO_126	N, H_LYS_214	H, H_LYS_214	2.98	2.16	14.79
5U3N.PDB	OG, L_SER_26	N, L_ARG_3	H, L_ARG_3	2.86	2.02	10.52
5U3N.PDB	O, L_ARG_24	N, L_THR_5	H, L_THR_5	2.80	1.98	16.09
5U3N.PDB	O, L_TYR_86	NE2, L_GLN_6	HE22, L_GLN_6	2.86	2.00	3.53
5U3N.PDB	O, L_LYS_103	N, L_LEU_11	H, L_LEU_11	2.90	2.11	18.99
5U3N.PDB	OH, L_TYR_140	OG, L_SER_12	HG, L_SER_12	2.60	1.87	23.71
5U3N.PDB	O, L_ASP_105	N, L_ALA_13	H, L_ALA_13	2.97	2.13	11.36
5U3N.PDB	OD2, L_ASP_17	N, L_SER_14	H, L_SER_14	2.75	1.96	18.71
5U3N.PDB	O, L_LEU_78	N, L_GLY_16	H, L_GLY_16	2.68	1.90	20.67

5U3N.PDB	O, L_ILE_75	N, L_ILE_19	H, L_ILE_19	2.79	1.95	9.47
5U3N.PDB	O, L_LEU_73	N, L_ILE_21	H, L_ILE_21	2.95	2.11	10.95
5U3N.PDB	O, L_PHE_71	N, L_CYS_23	H, L_CYS_23	2.87	2.04	13.33
5U3N.PDB	O, L_THR_5	N, L_ARG_24	H, L_ARG_24	2.75	1.90	7.83
5U3N.PDB	O, L_SER_69	N, L_ALA_25	H, L_ALA_25	2.85	2.03	14.92
5U3N.PDB	O, L_ARG_3	N, L_SER_26	H, L_SER_26	2.91	2.13	20.77
5U3N.PDB	O, L_GLY_68	N, L_ILE_29	H, L_ILE_29	2.69	1.85	10.61
5U3N.PDB	O, L_ILE_29	N, L_TYR_32	H, L_TYR_32	2.96	2.12	12.33
5U3N.PDB	O, L_ASP_31	N, L_LEU_33	H, L_LEU_33	2.77	2.05	28.04
5U3N.PDB	O, L_GLN_89	N, L_ASN_34	H, L_ASN_34	2.83	2.03	18.28
5U3N.PDB	OE1, L_GLN_89	ND2, L_ASN_34	HD22, L_ASN_34	2.99	2.18	18.14
5U3N.PDB	O, L_ILE_48	N, L_TRP_35	H, L_TRP_35	2.81	1.99	14.14
5U3N.PDB	O, L_TYR_87	N, L_TYR_36	H, L_TYR_36	2.79	1.96	13.76
5U3N.PDB	OE1, L_GLN_89	OH, L_TYR_36	HH, L_TYR_36	2.64	1.80	1.88
5U3N.PDB	O, L_LYS_45	N, L_LYS_37	H, L_LYS_37	2.84	2.01	13.10
5U3N.PDB	O, L_THR_85	N, L_HIS_38	H, L_HIS_38	2.80	2.03	21.49
5U3N.PDB	O, L_LYS_37	N, L_LYS_45	H, L_LYS_45	2.88	2.10	20.13
5U3N.PDB	O, L_TRP_35	N, L_LEU_47	H, L_LEU_47	2.79	1.93	3.84
5U3N.PDB	O, L_LYS_53	N, L_TYR_49	H, L_TYR_49	2.82	2.01	15.81
5U3N.PDB	OD1, L_ASN_34	N, L_SER_50	H, L_SER_50	2.96	2.18	21.09
5U3N.PDB	O, L_LEU_33	N, L_ALA_51	H, L_ALA_51	2.71	1.90	16.24
5U3N.PDB	O, L_TYR_49	N, L_LYS_53	H, L_LYS_53	2.83	2.03	18.60
5U3N.PDB	O, L_THR_72	N, L_SER_65	H, L_SER_65	2.95	2.15	18.23
5U3N.PDB	O, L_LYS_30	N, L_GLY_68	H, L_GLY_68	2.91	2.07	11.47
5U3N.PDB	O, L_CYS_23	N, L_PHE_71	H, L_PHE_71	2.92	2.08	10.20
5U3N.PDB	O, L_SER_65	N, L_THR_72	H, L_THR_72	2.89	2.07	15.08
5U3N.PDB	O, L_ILE_21	N, L_LEU_73	H, L_LEU_73	2.84	2.01	12.13
5U3N.PDB	O, L_SER_63	N, L_THR_74	H, L_THR_74	2.80	1.97	11.07
5U3N.PDB	O, L_ILE_19	N, L_ILE_75	H, L_ILE_75	2.86	2.08	19.78
5U3N.PDB	O, L_ARG_61	N, L_SER_76	H, L_SER_76	2.96	2.19	23.24
5U3N.PDB	O, L_ASP_17	N, L_LEU_78	H, L_LEU_78	2.72	1.92	19.04
5U3N.PDB	OD2, L_ASP_82	N, L_GLN_79	H, L_GLN_79	3.00	2.14	4.35
5U3N.PDB	O, L_GLN_79	N, L_ASP_82	H, L_ASP_82	2.83	1.99	10.16
5U3N.PDB	O, L_THR_102	N, L_TYR_86	H, L_TYR_86	2.90	2.10	17.67
5U3N.PDB	O, L_ASP_82	OH, L_TYR_86	HH, L_TYR_86	2.60	1.78	10.78
5U3N.PDB	O, L_TYR_36	N, L_TYR_87	H, L_TYR_87	2.92	2.10	15.56
5U3N.PDB	OE2, L_GLU_90	N, L_TYR_92	H, L_TYR_92	2.85	2.02	13.73
5U3N.PDB	O, L_CYS_88	N, L_GLY_99	H, L_GLY_99	2.82	2.02	16.99
5U3N.PDB	O, L_TYR_86	N, L_THR_102	H, L_THR_102	2.93	2.13	18.82
5U3N.PDB	O, L_PRO_8	OG1, L_THR_102	HG1, L_THR_102	2.67	1.96	27.26
5U3N.PDB	O, L_ALA_84	N, L_VAL_104	H, L_VAL_104	2.83	1.97	3.89
5U3N.PDB	O, L_LEU_11	N, L_ASP_105	H, L_ASP_105	2.98	2.15	13.92
5U3N.PDB	O, L_ALA_13	N, L_LYS_107	H, L_LYS_107	2.81	1.99	14.79
5U3N.PDB	O, L_THR_109	NE, L_ARG_108	HE, L_ARG_108	2.80	1.97	12.49
5U3N.PDB	O, L_ASP_170	NH1, L_ARG_108	HH11, L_ARG_108	2.97	2.15	15.13
5U3N.PDB	O, L_TYR_140	N, L_ALA_111	H, L_ALA_111	2.86	2.03	12.00
5U3N.PDB	O, L_LEU_135	N, L_PHE_116	H, L_PHE_116	2.88	2.09	19.79
5U3N.PDB	O, L_VAL_133	N, L_PHE_118	H, L_PHE_118	2.74	1.97	21.45
5U3N.PDB	OG, L_SER_131	NE2, L_GLN_124	HE22, L_GLN_124	2.80	1.94	3.81
5U3N.PDB	O, L_GLN_124	N, L_SER_127	H, L_SER_127	2.78	1.95	13.25
5U3N.PDB	O, L_GLN_124	OG, L_SER_127	HG, L_SER_127	2.63	1.79	4.63
5U3N.PDB	O, L_LEU_181	N, L_ALA_130	H, L_ALA_130	2.78	1.96	14.77
5U3N.PDB	OE1, L_GLN_124	N, L_SER_131	H, L_SER_131	2.94	2.15	18.69
5U3N.PDB	O, L_LEU_179	N, L_VAL_132	H, L_VAL_132	2.83	2.00	12.34
5U3N.PDB	O, L_SER_177	N, L_CYS_134	H, L_CYS_134	2.80	1.96	9.76
5U3N.PDB	O, L_PHE_116	N, L_LEU_135	H, L_LEU_135	2.72	1.88	11.53
5U3N.PDB	O, L_LEU_175	N, L_LEU_136	H, L_LEU_136	2.80	1.95	6.87
5U3N.PDB	O, L_SER_114	N, L_ASN_137	H, L_ASN_137	2.88	2.07	16.62

5U3N.PDB	OG, L.SER.174	N, L.ASN.138	H, L.ASN.138	2.99	2.16	12.45
5U3N.PDB	O, L.TYR.173	N, L.PHE.139	H, L.PHE.139	2.79	1.97	14.75
5U3N.PDB	O, L.ALA.111	N, L.TYR.140	H, L.TYR.140	2.87	2.08	18.95
5U3N.PDB	OD1, L.ASP.105	OH, L.TYR.140	HH, L.TYR.140	2.61	1.87	24.55
5U3N.PDB	O, L.GLU.195	N, L.GLN.147	H, L.GLN.147	2.84	2.01	12.00
5U3N.PDB	OG, L.SER.177	NE1, L.TRP.148	HE1, L.TRP.148	2.84	2.01	13.43
5U3N.PDB	O, L.ALA.193	N, L.LYS.149	H, L.LYS.149	2.84	2.00	9.94
5U3N.PDB	O, L.ALA.153	N, L.VAL.150	H, L.VAL.150	2.99	2.18	15.96
5U3N.PDB	O, L.AVAL.191	N, L.ASP.151	H, L.ASP.151	2.86	2.04	14.13
5U3N.PDB	O, L.BVAL.191	N, L.ASP.151	H, L.ASP.151	2.89	2.08	16.42
5U3N.PDB	O, L.VAL.150	N, L.ALA.153	H, L.ALA.153	2.90	2.05	8.35
5U3N.PDB	O, L.TRP.148	N, L.GLN.155	H, L.GLN.155	2.90	2.06	8.61
5U3N.PDB	O, L.ALA.153	NE2, L.GLN.155	HE21, L.GLN.155	2.97	2.12	8.23
5U3N.PDB	O, L.SER.176	N, L.SER.162	H, L.SER.162	2.95	2.15	17.97
5U3N.PDB	O, H.PRO.167	OG, L.SER.162	HG, L.SER.162	2.77	1.98	17.29
5U3N.PDB	O, L.SER.174	N, L.THR.164	H, L.THR.164	2.94	2.11	13.10
5U3N.PDB	O, L.SER.171	NE2, L.GLN.166	HE21, L.GLN.166	2.97	2.12	7.09
5U3N.PDB	O, L.LEU.106	NE2, L.GLN.166	HE22, L.GLN.166	2.79	2.02	22.69
5U3N.PDB	O, L.THR.172	N, L.ASP.167	H, L.ASP.167	2.90	2.10	16.69
5U3N.PDB	OD1, L.ASP.170	N, L.THR.172	H, L.THR.172	2.98	2.17	16.32
5U3N.PDB	OD1, L.ASP.170	OG1, L.THR.172	HG1, L.THR.172	2.63	1.80	7.71
5U3N.PDB	O, L.PHE.139	N, L.TYR.173	H, L.TYR.173	2.80	1.96	11.34
5U3N.PDB	OD2, L.ASP.105	OH, L.TYR.173	HH, L.TYR.173	2.66	1.88	16.93
5U3N.PDB	OG1, L.THR.164	N, L.SER.174	H, L.SER.174	2.99	2.17	14.48
5U3N.PDB	O, L.LEU.136	N, L.LEU.175	H, L.LEU.175	2.82	2.02	18.65
5U3N.PDB	O, L.SER.162	N, L.SER.176	H, L.SER.176	2.90	2.07	13.04
5U3N.PDB	O, L.CYS.134	N, L.SER.177	H, L.SER.177	2.88	2.05	10.58
5U3N.PDB	O, L.GLN.160	N, L.THR.178	H, L.THR.178	2.93	2.10	13.26
5U3N.PDB	O, L.VAL.132	N, L.LEU.179	H, L.LEU.179	2.72	1.91	15.62
5U3N.PDB	O, L.ASN.158	N, L.ATHR.180	H, L.ATHR.180	2.96	2.10	5.76
5U3N.PDB	O, L.ASN.158	N, L.BTHR.180	H, L.BTHR.180	2.98	2.13	8.23
5U3N.PDB	O, L.GLY.128	N, L.LYS.183	H, L.LYS.183	2.89	2.05	8.75
5U3N.PDB	O, L.SER.182	N, L.TYR.186	H, L.TYR.186	2.90	2.05	6.90
5U3N.PDB	O, L.LYS.183	N, L.GLU.187	H, L.GLU.187	2.91	2.12	19.43
5U3N.PDB	O, L.ASP.185	ND1, L.HIS.189	HD1, L.HIS.189	2.98	2.23	25.25
5U3N.PDB	OD1, L.ASP.151	N, L.BVAL.191	H, L.BVAL.191	3.00	2.14	6.33
5U3N.PDB	O, L.LYS.149	N, L.ALA.193	H, L.ALA.193	2.88	2.14	25.73
5U3N.PDB	O, L.LYS.207	N, L.CYS.194	H, L.CYS.194	2.96	2.16	18.86
5U3N.PDB	O, L.GLN.147	N, L.GLU.195	H, L.GLU.195	2.72	1.89	12.68
5U3N.PDB	O, L.VAL.205	N, L.VAL.196	H, L.VAL.196	2.76	1.95	15.71
5U3N.PDB	O, L.PRO.141	NE2, L.HIS.198	HE2, L.HIS.198	2.82	1.99	12.93
5U3N.PDB	O, L.HIS.198	N, L.LEU.201	H, L.LEU.201	2.79	1.94	8.84
5U3N.PDB	O, L.VAL.196	N, L.VAL.205	H, L.VAL.205	2.95	2.17	20.32
5U3N.PDB	O, L.TYR.192	N, L.PHE.209	H, L.PHE.209	2.95	2.17	22.09
5U3N.PDB	O, L.LYS.190	N, L.ARG.211	H, L.ARG.211	2.79	1.98	15.41
5U3N.PDB	O, L.HIS.189	NE, L.ARG.211	HE, L.ARG.211	2.72	1.88	11.65
5U3N.PDB	OD1, A.ASP.664	N, A.TRP.666	H, A.TRP.666	2.85	1.99	5.09
5U3N.PDB	OD2, A.ASP.674	N, A.ASN.671	H, A.ASN.671	2.89	2.10	19.70
5U3N.PDB	O, A.ASP.674	N, A.TRP.678	H, A.TRP.678	2.91	2.12	19.94
5U3N.PDB	O, A.ILE.675	N, A.LEU.679	H, A.LEU.679	2.85	2.02	12.95
5U3N.PDB	O, A.THR.676	N, A.TRP.680	H, A.TRP.680	2.88	2.03	5.54
5U3N.PDB	O, A.ASN.677	N, A.TYR.681	H, A.TYR.681	2.92	2.08	9.34
5U3N.PDB	O, A.TRP.678	N, A.ILE.682	H, A.ILE.682	2.84	2.11	26.86
5U3N.PDB	O, A.TRP.680	N, A.LYS.684	H, A.LYS.684	2.96	2.10	3.54

Table 1714: 5U3N-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5UCB.PDB	O, H.SER_25	N, H.GLN_3	H, H.GLN_3	2.99	2.18	16.58
5UCB.PDB	O, H.SER_21	N, H.SER_7	H, H.SER_7	2.88	2.10	20.32
5UCB.PDB	O, H.THR_110	N, H.VAL_12	H, H.VAL_12	2.93	2.15	21.18
5UCB.PDB	O, H.LEU_82C	N, H.GLY_15	H, H.GLY_15	2.80	1.96	10.79
5UCB.PDB	O, H.GLN_13	N, H.GLY_16	H, H.GLY_16	2.96	2.13	13.46
5UCB.PDB	O, H.MET_82	N, H.LEU_18	H, H.LEU_18	2.96	2.17	20.10
5UCB.PDB	O, H.LEU_80	N, H.LEU_20	H, H.LEU_20	2.83	2.01	13.56
5UCB.PDB	O, H.SER_7	N, H.SER_21	H, H.SER_21	2.92	2.09	11.91
5UCB.PDB	O, H.ALA_78	N, H.CYS_22	H, H.CYS_22	2.76	2.02	25.89
5UCB.PDB	O, H.VAL_5	N, H.ALA_23	H, H.ALA_23	2.98	2.15	12.17
5UCB.PDB	O, H.GLN_3	N, H.SER_25	H, H.SER_25	2.87	2.02	8.54
5UCB.PDB	OD1, H.ASN_76	N, H.VAL_29	H, H.VAL_29	2.79	1.95	9.36
5UCB.PDB	OD1, H.ASN_28	N, H.SER_30	H, H.SER_30	2.95	2.10	6.39
5UCB.PDB	O, H.ALA_93	N, H.HIS_35	H, H.HIS_35	2.87	2.12	24.96
5UCB.PDB	OG, H.SER_33	NE2, H.HIS_35	HE2, H.HIS_35	2.88	2.09	19.50
5UCB.PDB	O, H.ALA_49	N, H.TRP_36	H, H.TRP_36	2.86	2.03	11.66
5UCB.PDB	O, H.TYR_91	N, H.VAL_37	H, H.VAL_37	2.92	2.10	13.93
5UCB.PDB	O, H.GLU_46	N, H.ARG_38	H, H.ARG_38	2.80	1.96	9.03
5UCB.PDB	OE1, H.GLU_46	NE, H.ARG_38	HE, H.ARG_38	2.85	2.03	15.54
5UCB.PDB	OH, H.TYR_90	NH1, H.ARG_38	HH11, H.ARG_38	2.94	2.12	15.88
5UCB.PDB	OD1, H.ASP_86	NH1, H.ARG_38	HH12, H.ARG_38	2.88	2.08	18.54
5UCB.PDB	O, H.VAL_89	N, H.GLN_39	H, H.GLN_39	2.83	2.10	26.74
5UCB.PDB	O, H.LYS_43	NE2, H.GLN_39	HE21, H.GLN_39	2.97	2.21	23.38
5UCB.PDB	OE1, L.GLN_38	NE2, H.GLN_39	HE22, H.GLN_39	2.96	2.12	9.92
5UCB.PDB	O, H.ALA_40	N, H.LYS_43	H, H.LYS_43	2.94	2.10	10.79
5UCB.PDB	O, H.ARG_38	N, H.GLU_46	H, H.GLU_46	2.82	2.01	15.90
5UCB.PDB	OG, H.SER_50	NE1, H.TRP_47	HE1, H.TRP_47	2.72	1.98	25.90
5UCB.PDB	O, H.TRP_36	N, H.VAL_48	H, H.VAL_48	2.90	2.07	12.31
5UCB.PDB	O, H.SER_58	N, H.SER_50	H, H.SER_50	2.91	2.11	18.26
5UCB.PDB	O, H.ILE_34	N, H.ILE_51	H, H.ILE_51	2.92	2.10	14.85
5UCB.PDB	O, H.SER_56	N, H.TYR_52	H, H.TYR_52	2.91	2.14	22.03
5UCB.PDB	O, B.LEU_5	OH, H.TYR_53	HH, H.TYR_53	2.73	1.99	23.03
5UCB.PDB	O, H.PRO_52A	N, H.TYR_54	H, H.TYR_54	2.76	2.01	24.37
5UCB.PDB	O, H.SER_50	N, H.SER_58	H, H.SER_58	2.97	2.16	17.28
5UCB.PDB	O, H.VAL_48	N, H.ALA_60	H, H.ALA_60	2.97	2.12	8.58
5UCB.PDB	O, H.VAL_63	N, H.ARG_66	H, H.ARG_66	2.93	2.10	10.67
5UCB.PDB	O, H.SER_82B	NH1, H.ARG_66	HH11, H.ARG_66	2.96	2.19	22.84
5UCB.PDB	OD2, H.ASP_86	NH1, H.ARG_66	HH12, H.ARG_66	2.75	1.90	5.99
5UCB.PDB	O, H.SER_62	NH2, H.ARG_66	HH21, H.ARG_66	2.91	2.06	4.12
5UCB.PDB	O, H.GLN_81	N, H.THR_68	H, H.THR_68	2.89	2.10	19.31
5UCB.PDB	OH, H.TYR_59	N, H.ILE_69	H, H.ILE_69	2.89	2.08	15.94
5UCB.PDB	O, H.THR_77	N, H.ASP_72	H, H.ASP_72	2.91	2.07	9.90
5UCB.PDB	OD1, H.ASP_72	OG, H.SER_74	HG, H.SER_74	2.60	1.83	20.07
5UCB.PDB	O, H.PHE_27	ND2, H.ASN_76	HD21, H.ASN_76	2.86	2.00	2.63
5UCB.PDB	O, H.LYS_75	OG1, H.THR_77	HG1, H.THR_77	2.96	2.13	8.72
5UCB.PDB	O, H.CYS_22	N, H.ALA_78	H, H.ALA_78	2.91	2.09	14.01
5UCB.PDB	O, H.SER_70	N, H.TYR_79	H, H.TYR_79	2.82	2.01	17.30
5UCB.PDB	O, H.LEU_20	N, H.LEU_80	H, H.LEU_80	2.93	2.12	15.92
5UCB.PDB	O, H.THR_68	N, H.GLN_81	H, H.GLN_81	2.85	2.03	14.25
5UCB.PDB	O, H.LEU_18	N, H.MET_82	H, H.MET_82	2.76	1.91	5.48
5UCB.PDB	OD2, H.ASP_86	N, H.ARG_83	H, H.ARG_83	2.84	2.02	15.13
5UCB.PDB	O, H.ARG_83	N, H.ASP_86	H, H.ASP_86	2.85	2.00	6.49
5UCB.PDB	O, H.GLN_39	N, H.VAL_89	H, H.VAL_89	2.94	2.15	19.65
5UCB.PDB	O, H.THR_107	N, H.TYR_90	H, H.TYR_90	2.82	1.97	6.43
5UCB.PDB	O, H.ASP_86	OH, H.TYR_90	HH, H.TYR_90	2.71	1.87	3.56
5UCB.PDB	O, H.VAL_37	N, H.TYR_91	H, H.TYR_91	2.75	1.90	8.79
5UCB.PDB	OE2, H.GLU_6	N, H.CYS_92	H, H.CYS_92	2.86	2.03	11.54

5UCB.PDB	O, H_HIS_35	N, H_ALA_93	H, H_ALA_93	2.82	2.03	19.85
5UCB.PDB	O, H_TYR_102	N, H_ARG_94	H, H_ARG_94	2.90	2.09	15.76
5UCB.PDB	O, H_SER_33	N, H_GLY_95	H, H_GLY_95	2.82	1.97	6.39
5UCB.PDB	O, H_ALA_99	N, H_TYR_96	H, H_TYR_96	2.79	1.94	8.94
5UCB.PDB	O, B_VAL_145	N, H_GLY_97	H, H_GLY_97	2.90	2.05	8.98
5UCB.PDB	O, H_TYR_96	N, H_ALA_99	H, H_ALA_99	2.86	2.03	11.06
5UCB.PDB	O, H_ARG_94	N, H_ASP_101	H, H_ASP_101	2.97	2.22	25.01
5UCB.PDB	O, H_CYS_92	N, H_GLY_104	H, H_GLY_104	2.92	2.08	11.62
5UCB.PDB	OE1, H_GLU_6	N, H_GLY_106	H, H_GLY_106	2.84	2.01	12.83
5UCB.PDB	O, H_TYR_90	N, H_THR_107	H, H_THR_107	2.95	2.15	17.03
5UCB.PDB	O, H_ALA_88	N, H_VAL_109	H, H_VAL_109	2.93	2.08	2.47
5UCB.PDB	OG1, H_THR_87	N, H_VAL_111	H, H_VAL_111	2.96	2.11	5.78
5UCB.PDB	O, H_VAL_12	N, H_PHE_112	H, H_PHE_112	2.91	2.15	23.15
5UCB.PDB	O, H_PHE_146	N, H_LYS_116	H, H_LYS_116	2.86	2.03	11.25
5UCB.PDB	O, H_LYS_143	N, H_SER_120	H, H_SER_120	2.97	2.14	12.13
5UCB.PDB	O, H_LEU_141	N, H_PHE_122	H, H_PHE_122	2.87	2.04	11.40
5UCB.PDB	O, H_GLY_139	N, H_LEU_124	H, H_LEU_124	2.78	1.92	6.23
5UCB.PDB	OG, H_SER_127	N, H_LYS_129	H, H_LYS_129	2.96	2.13	12.32
5UCB.PDB	O, L_SER_208	NZ, H_LYS_129	HZ2, H_LYS_129	2.83	2.06	25.53
5UCB.PDB	O, H_SER_127	N, H_SER_130	H, H_SER_130	2.91	2.06	7.11
5UCB.PDB	O, H_SER_132	N, H_THR_135	H, H_THR_135	2.95	2.10	8.67
5UCB.PDB	O, H_VAL_184	N, H_ALA_136	H, H_ALA_136	2.78	1.98	18.51
5UCB.PDB	O, H_SER_130	N, H_ALA_137	H, H_ALA_137	2.85	2.03	15.53
5UCB.PDB	O, H_VAL_182	N, H_LEU_138	H, H_LEU_138	2.99	2.18	16.62
5UCB.PDB	O, H_LEU_124	N, H_GLY_139	H, H_GLY_139	2.94	2.17	22.56
5UCB.PDB	O, H_SER_180	N, H_CYS_140	H, H_CYS_140	2.83	2.03	18.28
5UCB.PDB	O, H_PHE_122	N, H_LEU_141	H, H_LEU_141	2.79	1.94	8.33
5UCB.PDB	O, H_LEU_178	N, H_VAL_142	H, H_VAL_142	2.74	1.88	4.14
5UCB.PDB	O, H_SER_120	N, H_LYS_143	H, H_LYS_143	2.78	1.93	5.09
5UCB.PDB	O, H_LYS_116	N, H_PHE_146	H, H_PHE_146	2.95	2.14	16.58
5UCB.PDB	O, H_ASN_199	N, H_THR_151	H, H_THR_151	2.98	2.16	14.61
5UCB.PDB	O, H_ASN_197	N, H_SER_153	H, H_SER_153	2.95	2.14	16.54
5UCB.PDB	OD1, H_ASN_197	OG, H_SER_153	HG, H_SER_153	2.85	2.06	15.76
5UCB.PDB	OG, H_SER_180	NE1, H_TRP_154	HE1, H_TRP_154	2.92	2.07	7.16
5UCB.PDB	O, H_ILE_195	N, H_ASN_155	H, H_ASN_155	2.78	1.94	9.76
5UCB.PDB	OD1, H_ASN_197	N, H_SER_156	H, H_SER_156	2.74	1.94	17.37
5UCB.PDB	O, H_TRP_154	N, H_GLY_157	H, H_GLY_157	2.95	2.22	27.37
5UCB.PDB	O, H_VAL_181	N, H_HIS_164	H, H_HIS_164	2.82	1.99	13.79
5UCB.PDB	O, H_SER_179	N, H_PHE_166	H, H_PHE_166	2.94	2.09	6.35
5UCB.PDB	O, H_SER_177	N, H_VAL_169	H, H_VAL_169	2.90	2.07	11.28
5UCB.PDB	O, H_LEU_175	N, H_GLN_171	H, H_GLN_171	2.90	2.06	8.51
5UCB.PDB	OD1, H_ASP_144	NE2, H_GLN_171	HE22, H_GLN_171	2.78	1.99	18.86
5UCB.PDB	O, H_GLN_171	N, H_GLY_174	H, H_GLY_174	2.86	2.01	8.15
5UCB.PDB	O, H_TYR_145	N, H_TYR_176	H, H_TYR_176	2.86	2.01	5.39
5UCB.PDB	O, H_VAL_142	N, H_LEU_178	H, H_LEU_178	2.87	2.06	16.64
5UCB.PDB	O, H_HIS_164	N, H_VAL_181	H, H_VAL_181	2.87	2.03	11.87
5UCB.PDB	O, H_LEU_138	N, H_VAL_182	H, H_VAL_182	2.82	2.02	16.97
5UCB.PDB	O, H_ALA_136	N, H_VAL_184	H, H_VAL_184	2.90	2.07	12.53
5UCB.PDB	O, H_GLY_134	N, H_SER_186	H, H_SER_186	2.94	2.10	11.37
5UCB.PDB	O, H_PRO_185	N, H_SER_188	H, H_SER_188	2.97	2.14	13.02
5UCB.PDB	O, H_PRO_185	OG, H_SER_188	HG, H_SER_188	2.68	1.85	4.71
5UCB.PDB	O, H_THR_193	NE2, H_GLN_192	HE21, H_GLN_192	2.94	2.08	2.24
5UCB.PDB	OG, H_SER_188	OH, H_TYR_194	HH, H_TYR_194	2.72	1.90	9.93
5UCB.PDB	OD1, H_ASN_155	N, H_ILE_195	H, H_ILE_195	2.82	2.03	19.24
5UCB.PDB	O, H_LYS_209	N, H_CYS_196	H, H_CYS_196	2.98	2.19	20.71
5UCB.PDB	O, H_SER_153	N, H_ASN_197	H, H_ASN_197	2.75	1.90	8.02
5UCB.PDB	OD1, H_ASP_208	ND2, H_ASN_197	HD22, H_ASN_197	2.80	1.95	7.44
5UCB.PDB	O, H_VAL_207	N, H_VAL_198	H, H_VAL_198	2.80	1.95	7.37

5UCB.PDB	O, H.THR.151	N, H.ASN.199	H, H.ASN.199	2.96	2.13	12.40
5UCB.PDB	O, H.THR.205	N, H.HIS.200	H, H.HIS.200	2.86	2.02	9.86
5UCB.PDB	O, H.PRO.147	NE2, H.HIS.200	HE2, H.HIS.200	2.80	1.97	12.02
5UCB.PDB	O, H.VAL.198	N, H.VAL.207	H, H.VAL.207	2.86	2.03	11.55
5UCB.PDB	O, H.CYS.196	N, H.LYS.209	H, H.LYS.209	2.99	2.16	13.99
5UCB.PDB	O, H.TYR.194	N, H.VAL.211	H, H.VAL.211	2.90	2.04	4.78
5UCB.PDB	O, L.TYR.86	NE2, L.GLN.6	HE22, L.GLN.6	2.81	2.01	17.50
5UCB.PDB	O, L.LYS.103	N, L.LEU.11	H, L.LEU.11	2.85	2.05	18.74
5UCB.PDB	O, L.GLU.105	N, L.ALA.13	H, L.ALA.13	2.91	2.12	19.40
5UCB.PDB	OD2, L.ASP.17	N, L.SER.14	H, L.SER.14	2.85	2.00	7.52
5UCB.PDB	O, L.LEU.78	N, L.GLY.16	H, L.GLY.16	2.86	2.04	14.88
5UCB.PDB	O, L.SER.14	N, L.ASP.17	H, L.ASP.17	2.92	2.09	12.95
5UCB.PDB	O, L.LEU.73	N, L.ILE.21	H, L.ILE.21	2.89	2.08	16.55
5UCB.PDB	O, L.TYR.71	N, L.CYS.23	H, L.CYS.23	2.80	1.98	13.36
5UCB.PDB	O, L.THR.5	N, L.ARG.24	H, L.ARG.24	2.82	2.03	19.90
5UCB.PDB	O, L.THR.69	N, L.ALA.25	H, L.ALA.25	2.83	1.98	7.34
5UCB.PDB	OE1, L.GLN.3	OG, L.SER.26	HG, L.SER.26	2.61	1.78	7.17
5UCB.PDB	OD2, B.ASP.51	OG, L.SER.30	HG, L.SER.30	2.58	1.81	20.19
5UCB.PDB	O, L.ILE.48	N, L.TRP.35	H, L.TRP.35	2.89	2.09	17.06
5UCB.PDB	O, L.TYR.87	N, L.TYR.36	H, L.TYR.36	2.82	2.03	19.85
5UCB.PDB	OE1, L.GLN.89	OH, L.TYR.36	HH, L.TYR.36	2.64	1.84	15.57
5UCB.PDB	O, L.LYS.45	N, L.GLN.37	H, L.GLN.37	2.91	2.09	14.54
5UCB.PDB	OH, L.TYR.86	NE2, L.GLN.37	HE21, L.GLN.37	2.99	2.15	9.80
5UCB.PDB	O, L.THR.85	N, L.GLN.38	H, L.GLN.38	2.74	1.93	16.51
5UCB.PDB	O, L.LYS.42	NE2, L.GLN.38	HE21, L.GLN.38	2.88	2.08	17.97
5UCB.PDB	OE1, H.GLN.39	NE2, L.GLN.38	HE22, L.GLN.38	2.95	2.13	14.86
5UCB.PDB	O, L.GLU.81	NZ, L.LYS.39	HZ1, L.LYS.39	2.69	1.90	22.19
5UCB.PDB	O, L.GLN.37	N, L.LYS.45	H, L.LYS.45	2.84	2.05	19.57
5UCB.PDB	O, L.TRP.35	N, L.LEU.47	H, L.LEU.47	2.82	1.97	5.85
5UCB.PDB	O, L.SER.53	N, L.TYR.49	H, L.TYR.49	2.87	2.07	17.59
5UCB.PDB	O, L.VAL.33	N, L.ALA.51	H, L.ALA.51	2.85	2.02	11.41
5UCB.PDB	O, L.TYR.49	N, L.SER.53	H, L.SER.53	2.93	2.12	15.91
5UCB.PDB	O, L.LEU.47	N, L.TYR.55	H, L.TYR.55	2.94	2.08	2.44
5UCB.PDB	OD2, L.ASP.82	NE, L.ARG.61	HE, L.ARG.61	2.82	2.01	16.79
5UCB.PDB	OD1, L.ASP.82	NH2, L.ARG.61	HH21, L.ARG.61	2.85	1.99	4.65
5UCB.PDB	O, L.THR.74	N, L.SER.63	H, L.SER.63	2.97	2.19	19.92
5UCB.PDB	O, L.THR.72	N, L.SER.65	H, L.SER.65	2.97	2.20	22.80
5UCB.PDB	O, B.SER.47	NH1, L.ARG.66	HH12, L.ARG.66	2.77	1.99	21.64
5UCB.PDB	O, B.SER.47	NH2, L.ARG.66	HH22, L.ARG.66	2.89	2.16	27.12
5UCB.PDB	O, L.ASP.70	N, L.SER.67	H, L.SER.67	2.84	2.01	11.95
5UCB.PDB	O, B.ARG.48	N, L.GLY.68	H, L.GLY.68	2.79	1.95	9.02
5UCB.PDB	O, L.SER.67	N, L.ASP.70	H, L.ASP.70	2.95	2.11	10.96
5UCB.PDB	O, L.CYS.23	N, L.TYR.71	H, L.TYR.71	2.85	2.00	7.89
5UCB.PDB	O, L.SER.65	N, L.THR.72	H, L.THR.72	2.92	2.09	12.93
5UCB.PDB	OG1, L.THR.22	OG1, L.THR.72	HG1, L.THR.72	2.96	2.18	19.19
5UCB.PDB	O, L.ILE.21	N, L.LEU.73	H, L.LEU.73	2.82	2.02	18.31
5UCB.PDB	O, L.SER.63	N, L.THR.74	H, L.THR.74	2.88	2.03	7.94
5UCB.PDB	O, L.VAL.19	N, L.ILE.75	H, L.ILE.75	2.85	2.02	13.35
5UCB.PDB	O, L.ARG.61	N, L.SER.76	H, L.SER.76	2.93	2.12	17.13
5UCB.PDB	O, L.ASP.17	N, L.LEU.78	H, L.LEU.78	2.83	2.04	19.24
5UCB.PDB	OD2, L.ASP.82	N, L.GLN.79	H, L.GLN.79	2.81	1.95	4.90
5UCB.PDB	O, L.GLN.79	N, L.ASP.82	H, L.ASP.82	2.94	2.09	7.96
5UCB.PDB	O, L.GLN.38	N, L.THR.85	H, L.THR.85	2.95	2.11	8.28
5UCB.PDB	O, L.THR.102	N, L.TYR.86	H, L.TYR.86	2.88	2.06	15.79
5UCB.PDB	O, L.ASP.82	OH, L.TYR.86	HH, L.TYR.86	2.68	1.86	10.64
5UCB.PDB	O, L.TYR.36	N, L.TYR.87	H, L.TYR.87	2.88	2.06	15.19
5UCB.PDB	O, L.ALA.32	N, L.ASP.91	H, L.ASP.91	2.84	1.99	7.27
5UCB.PDB	O, L.LEU.95	N, L.GLY.92	H, L.GLY.92	2.81	2.01	17.89

5UCB.PDB	O, L_GLN_90	N, L_THR_97	H, L_THR_97	2.89	2.07	13.99
5UCB.PDB	O, L_CYS_88	N, L_GLY_99	H, L_GLY_99	2.87	2.06	16.05
5UCB.PDB	O, L_GLN_6	NE2, L_GLN_100	HE21, L_GLN_100	2.96	2.10	3.33
5UCB.PDB	O, L_TYR_86	N, L_THR_102	H, L_THR_102	2.91	2.11	19.06
5UCB.PDB	O, L_PRO_8	OG1, L_THR_102	HG1, L_THR_102	2.64	1.82	9.17
5UCB.PDB	O, L_SER_9	N, L_LYS_103	H, L_LYS_103	2.86	2.02	9.83
5UCB.PDB	OE1, L_GLU_165	NZ, L_LYS_103	HZ3, L_LYS_103	2.77	1.90	9.89
5UCB.PDB	O, L_ALA_84	N, L_VAL_104	H, L_VAL_104	2.92	2.06	4.48
5UCB.PDB	O, L_LEU_11	N, L_GLU_105	H, L_GLU_105	2.83	1.98	7.22
5UCB.PDB	OE1, L_GLN_166	N, L_ILE_106	H, L_ILE_106	2.97	2.14	12.29
5UCB.PDB	O, L_ALA_13	N, L_LYS_107	H, L_LYS_107	2.94	2.14	17.97
5UCB.PDB	O, L_THR_109	NE, L_ARG_108	HE, L_ARG_108	2.81	1.98	12.46
5UCB.PDB	O, L_ASP_170	NH1, L_ARG_108	HH11, L_ARG_108	2.96	2.13	10.72
5UCB.PDB	O, L_TYR_140	N, L_ALA_111	H, L_ALA_111	2.86	2.03	12.05
5UCB.PDB	O, L_LEU_135	N, L_PHE_116	H, L_PHE_116	2.91	2.10	16.52
5UCB.PDB	O, L_VAL_133	N, L_PHE_118	H, L_PHE_118	2.84	2.06	20.95
5UCB.PDB	OG, L_SER_131	NE2, L_GLN_124	HE22, L_GLN_124	2.73	1.87	2.66
5UCB.PDB	O, L_GLN_124	N, L_SER_127	H, L_SER_127	2.84	2.11	27.03
5UCB.PDB	O, L_GLN_124	OG, L_SER_127	HG, L_SER_127	2.54	1.72	9.22
5UCB.PDB	O, L_LEU_125	N, L_GLY_128	H, L_GLY_128	2.90	2.09	16.29
5UCB.PDB	O, L_LEU_181	N, L_ALA_130	H, L_ALA_130	2.86	2.04	14.78
5UCB.PDB	OE1, L_GLN_124	N, L_SER_131	H, L_SER_131	2.91	2.10	16.27
5UCB.PDB	O, L_LEU_179	N, L_VAL_132	H, L_VAL_132	2.80	1.95	9.72
5UCB.PDB	O, L_SER_177	N, L_CYS_134	H, L_CYS_134	2.81	1.97	8.89
5UCB.PDB	O, L_PHE_116	N, L_LEU_135	H, L_LEU_135	2.84	2.00	9.91
5UCB.PDB	O, L_LEU_175	N, L_LEU_136	H, L_LEU_136	2.82	1.97	6.91
5UCB.PDB	O, L_SER_114	N, L_ASN_137	H, L_ASN_137	2.82	2.00	13.64
5UCB.PDB	OG, L_SER_174	N, L_ASN_138	H, L_ASN_138	3.00	2.18	14.73
5UCB.PDB	O, L_TYR_173	N, L_PHE_139	H, L_PHE_139	2.80	1.98	15.50
5UCB.PDB	O, L_ALA_111	N, L_TYR_140	H, L_TYR_140	2.92	2.11	16.50
5UCB.PDB	O, L_GLU_195	N, L_GLN_147	H, L_GLN_147	2.87	2.02	9.88
5UCB.PDB	OG, L_SER_177	NE1, L_TRP_148	HE1, L_TRP_148	2.92	2.09	12.30
5UCB.PDB	O, L_ALA_193	N, L_LYS_149	H, L_LYS_149	2.92	2.09	12.63
5UCB.PDB	O, L_ALA_153	N, L_VAL_150	H, L_VAL_150	2.98	2.16	16.04
5UCB.PDB	O, L_VAL_191	N, L_ASP_151	H, L_ASP_151	2.74	1.90	10.65
5UCB.PDB	O, L_VAL_150	N, L_ALA_153	H, L_ALA_153	2.91	2.06	8.01
5UCB.PDB	O, L_TRP_148	N, L_GLN_155	H, L_GLN_155	2.94	2.12	14.17
5UCB.PDB	O, L_ALA_153	NE2, L_GLN_155	HE21, L_GLN_155	2.97	2.12	7.54
5UCB.PDB	OE1, L_GLN_155	ND2, L_ASN_158	HD21, L_ASN_158	2.98	2.15	12.35
5UCB.PDB	O, L_LEU_170	NE2, L_GLN_160	HE22, L_GLN_160	2.99	2.13	5.75
5UCB.PDB	O, L_SER_176	N, L_SER_162	H, L_SER_162	2.95	2.16	19.90
5UCB.PDB	O, H_PRO_167	OG, L_SER_162	HG, L_SER_162	2.68	1.94	24.13
5UCB.PDB	O, L_SER_174	N, L_THR_164	H, L_THR_164	2.94	2.12	14.57
5UCB.PDB	O, L_SER_171	NE2, L_GLN_166	HE21, L_GLN_166	2.94	2.17	23.45
5UCB.PDB	O, L_ILE_106	NE2, L_GLN_166	HE22, L_GLN_166	2.80	1.96	9.36
5UCB.PDB	O, L_THR_172	N, L_ASP_167	H, L_ASP_167	2.83	2.01	14.08
5UCB.PDB	OD2, L_ASP_167	N, L_ASP_170	H, L_ASP_170	2.95	2.15	18.34
5UCB.PDB	O, L_ASP_167	N, L_SER_171	H, L_SER_171	2.83	2.10	27.38
5UCB.PDB	OD1, L_ASP_170	N, L_THR_172	H, L_THR_172	2.93	2.09	9.94
5UCB.PDB	OD1, L_ASP_170	OG1, L_THR_172	HG1, L_THR_172	2.71	1.89	8.99
5UCB.PDB	O, L_PHE_139	N, L_TYR_173	H, L_TYR_173	2.82	1.97	6.86
5UCB.PDB	OE2, L_GLU_105	OH, L_TYR_173	HH, L_TYR_173	2.61	1.81	15.35
5UCB.PDB	O, L_LEU_136	N, L_LEU_175	H, L_LEU_175	2.88	2.08	17.16
5UCB.PDB	O, L_SER_162	N, L_SER_176	H, L_SER_176	2.94	2.12	15.24
5UCB.PDB	O, L_CYS_134	N, L_SER_177	H, L_SER_177	2.86	2.02	11.18
5UCB.PDB	O, L_GLN_160	N, L_THR_178	H, L_THR_178	2.87	2.04	12.63
5UCB.PDB	O, L_VAL_132	N, L_LEU_179	H, L_LEU_179	2.79	1.97	14.56
5UCB.PDB	O, L_ASN_158	N, L_THR_180	H, L_THR_180	2.97	2.12	9.36

5UCB.PDB	O, L_ALA_130	N, L_LEU_181	H, L_LEU_181	2.88	2.04	9.45
5UCB.PDB	OG, L_SER_182	N, L_ASP_185	H, L_ASP_185	3.00	2.15	7.40
5UCB.PDB	O, L_SER_182	N, L_TYR_186	H, L_TYR_186	2.90	2.06	11.13
5UCB.PDB	O, L_LYS_183	N, L_GLU_187	H, L_GLU_187	2.89	2.04	6.84
5UCB.PDB	OD1, L_ASP_151	N, L_VAL_191	H, L_VAL_191	2.90	2.05	6.39
5UCB.PDB	O, L_PHE_209	N, L_TYR_192	H, L_TYR_192	2.96	2.11	7.95
5UCB.PDB	O, L_LYS_149	N, L_ALA_193	H, L_ALA_193	2.91	2.10	16.38
5UCB.PDB	O, L_LYS_207	N, L_CYS_194	H, L_CYS_194	2.82	1.97	8.63
5UCB.PDB	O, L_GLN_147	N, L_GLU_195	H, L_GLU_195	2.82	1.97	7.58
5UCB.PDB	O, L_VAL_205	N, L_VAL_196	H, L_VAL_196	2.73	1.91	15.27
5UCB.PDB	O, L_LYS_145	N, L_THR_197	H, L_THR_197	2.87	2.03	10.61
5UCB.PDB	O, L_PRO_141	NE2, L_HIS_198	HE2, L_HIS_198	2.90	2.07	14.06
5UCB.PDB	ND1, L_HIS_198	N, L_GLY_200	H, L_GLY_200	2.97	2.11	4.92
5UCB.PDB	O, L_HIS_198	N, L_LEU_201	H, L_LEU_201	2.92	2.08	10.11
5UCB.PDB	O, L_VAL_196	N, L_VAL_205	H, L_VAL_205	2.94	2.22	28.63
5UCB.PDB	O, L_CYS_194	N, L_LYS_207	H, L_LYS_207	2.89	2.07	14.81
5UCB.PDB	O, L_TYR_192	N, L_PHE_209	H, L_PHE_209	2.96	2.17	21.00
5UCB.PDB	O, L_LYS_190	N, L_ARG_211	H, L_ARG_211	2.83	2.11	27.52
5UCB.PDB	O, B_GLU_28	N, B_SER_4	H, B_SER_4	2.92	2.10	13.37
5UCB.PDB	O, B_THR_26	N, B_LEU_6	H, B_LEU_6	2.81	1.99	15.67
5UCB.PDB	O, B_GLU_24	N, B_LYS_9	H, B_LYS_9	2.95	2.17	21.44
5UCB.PDB	O, B_GLU_22	N, B_LEU_11	H, B_LEU_11	2.84	1.99	8.95
5UCB.PDB	O, B_PRO_20	ND2, B_ASN_12	HD21, B_ASN_12	2.86	2.03	12.12
5UCB.PDB	O, B_ILE_138	ND2, B_ASN_13	HD21, B_ASN_13	2.86	2.13	26.24
5UCB.PDB	O, B_ARG_136	N, B_ALA_15	H, B_ALA_15	3.00	2.19	16.91
5UCB.PDB	OD1, B_ASP_132	NZ, B_LYS_16	HZ1, B_LYS_16	2.90	2.15	27.66
5UCB.PDB	O, B_ILE_134	N, B_PHE_17	H, B_PHE_17	2.94	2.10	10.85
5UCB.PDB	O, B_LYS_16	N, B_ASP_19	H, B_ASP_19	2.97	2.13	10.34
5UCB.PDB	O, B_ALA_75	N, B_TYR_21	H, B_TYR_21	2.82	2.02	17.42
5UCB.PDB	O, B_PHE_73	N, B_PHE_23	H, B_PHE_23	2.94	2.09	7.26
5UCB.PDB	O, B_LYS_9	N, B_GLU_24	H, B_GLU_24	2.80	1.98	14.46
5UCB.PDB	O, B_PHE_71	N, B_ILE_25	H, B_ILE_25	2.84	1.99	6.56
5UCB.PDB	O, B_GLY_7	N, B_THR_26	H, B_THR_26	2.95	2.10	4.53
5UCB.PDB	O, B_ASN_69	N, B_PHE_27	H, B_PHE_27	2.94	2.11	13.13
5UCB.PDB	O, B_SER_4	N, B_GLU_28	H, B_GLU_28	2.91	2.10	17.54
5UCB.PDB	O, B_GLY_67	N, B_CYS_29	H, B_CYS_29	2.96	2.14	15.57
5UCB.PDB	O, B_ILE_2	N, B_LEU_30	H, B_LEU_30	2.83	2.00	11.91
5UCB.PDB	OD2, B_ASP_153	N, B_LYS_34	H, B_LYS_34	2.94	2.14	18.44
5UCB.PDB	OH, B_TYR_100	N, B_HIS_35	H, B_HIS_35	2.93	2.15	21.81
5UCB.PDB	O, B_VAL_61	N, B_LEU_37	H, B_LEU_37	2.93	2.13	18.65
5UCB.PDB	O, B_ILE_59	N, B_TRP_39	H, B_TRP_39	2.91	2.12	19.76
5UCB.PDB	O, B_SER_97	N, B_LYS_40	H, B_LYS_40	2.88	2.06	15.75
5UCB.PDB	O, B_LEU_95	N, B_THR_42	H, B_THR_42	2.88	2.09	19.90
5UCB.PDB	O, B_GLN_54	N, B_TYR_43	H, B_TYR_43	2.83	2.01	14.02
5UCB.PDB	OE2, B_GLU_87	OH, B_TYR_43	HH, B_TYR_43	2.72	1.91	12.68
5UCB.PDB	O, B_VAL_93	N, B_VAL_44	H, B_VAL_44	2.93	2.08	6.15
5UCB.PDB	O, B_HIS_52	N, B_GLY_45	H, B_GLY_45	2.82	1.98	9.81
5UCB.PDB	OD1, B_ASP_51	OG, B_SER_46	HG, B_SER_46	2.83	2.02	12.78
5UCB.PDB	O, B_LEU_50	N, B_SER_47	H, B_SER_47	2.94	2.21	27.12
5UCB.PDB	OE1, B_GLU_87	OG, B_SER_47	HG, B_SER_47	2.62	1.82	14.05
5UCB.PDB	O, B_GLY_45	N, B_HIS_52	H, B_HIS_52	2.75	1.95	17.98
5UCB.PDB	O, B_TYR_43	N, B_GLN_54	H, B_GLN_54	2.99	2.21	20.44
5UCB.PDB	O, B_LEU_41	N, B_LEU_56	H, B_LEU_56	2.80	2.03	22.15
5UCB.PDB	O, B_TRP_39	N, B_ILE_59	H, B_ILE_59	2.85	2.07	20.70
5UCB.PDB	O, B_LEU_37	N, B_VAL_61	H, B_VAL_61	2.83	1.99	11.73
5UCB.PDB	O, B_CYS_29	N, B_GLY_67	H, B_GLY_67	2.83	1.97	6.62
5UCB.PDB	O, B_PHE_27	N, B_ASN_69	H, B_ASN_69	2.76	1.99	22.57
5UCB.PDB	O, B_PHE_23	N, B_PHE_73	H, B_PHE_73	2.79	1.98	16.10

5UCB.PDB	O, B_TYR_21	N, B_ALA_75	H, B_ALA_75	2.81	1.98	12.45
5UCB.PDB	OD2, B_ASP_57	N, B_ASP_76	H, B_ASP_76	2.88	2.07	15.78
5UCB.PDB	OE1, B_GLN_54	N, B_SER_79	H, B_SER_79	2.94	2.10	11.73
5UCB.PDB	O, B_ALA_80	N, B_ILE_83	H, B_ILE_83	3.00	2.16	12.13
5UCB.PDB	O, B_PRO_84	N, B_GLU_87	H, B_GLU_87	2.81	2.08	26.69
5UCB.PDB	O, B_GLU_87	OG, B_SER_90	HG, B_SER_90	2.87	2.04	8.25
5UCB.PDB	O, B_VAL_112	N, B_THR_92	H, B_THR_92	2.86	2.03	12.64
5UCB.PDB	O, B_THR_42	N, B_LEU_95	H, B_LEU_95	2.81	2.01	16.51
5UCB.PDB	O, B_VAL_108	N, B_LEU_96	H, B_LEU_96	2.80	1.97	10.47
5UCB.PDB	O, B_LYS_40	N, B_SER_97	H, B_SER_97	2.90	2.07	12.23
5UCB.PDB	O, B_GLU_38	N, B_SER_99	H, B_SER_99	2.90	2.12	21.40
5UCB.PDB	O, B_ARG_103	N, B_TYR_100	H, B_TYR_100	2.86	2.06	17.81
5UCB.PDB	OD1, B_ASP_153	OH, B_TYR_100	HH, B_TYR_100	2.55	1.73	8.75
5UCB.PDB	O, B_TYR_100	N, B_ARG_103	H, B_ARG_103	2.90	2.08	14.68
5UCB.PDB	O, B_VAL_151	NE, B_ARG_103	HE, B_ARG_103	2.81	2.01	18.23
5UCB.PDB	OD2, B_ASP_101	NH1, B_ARG_103	HH12, B_ARG_103	2.89	2.11	20.47
5UCB.PDB	O, B_THR_146	N, B_ARG_107	H, B_ARG_107	2.85	2.07	20.33
5UCB.PDB	OE2, B_GLU_104	NE, B_ARG_107	HE, B_ARG_107	2.91	2.05	4.26
5UCB.PDB	O, B_LEU_96	N, B_VAL_108	H, B_VAL_108	2.68	1.84	10.31
5UCB.PDB	O, B_ARG_144	N, B_GLY_109	H, B_GLY_109	2.80	1.96	9.36
5UCB.PDB	O, B_ILE_94	N, B_TYR_110	H, B_TYR_110	2.92	2.13	18.74
5UCB.PDB	O, L_ASP_91	OH, B_TYR_111	HH, B_TYR_111	2.57	1.75	11.11
5UCB.PDB	O, B_THR_92	N, B_VAL_112	H, B_VAL_112	2.87	2.09	21.11
5UCB.PDB	O, B_ASN_137	N, B_ASN_113	H, B_ASN_113	2.89	2.05	9.00
5UCB.PDB	O, B_SER_90	ND2, B_ASN_114	HD22, B_ASN_114	2.97	2.13	9.19
5UCB.PDB	O, B_GLU_118	N, B_ARG_122	H, B_ARG_122	2.99	2.17	14.84
5UCB.PDB	O, B_TYR_116	NH1, B_ARG_122	HH11, B_ARG_122	2.93	2.10	12.81
5UCB.PDB	O, B_GLU_120	N, B_ASN_124	H, B_ASN_124	2.98	2.27	29.44
5UCB.PDB	O, B_VAL_129	NZ, B_LYS_128	HZ2, B_LYS_128	2.82	1.95	9.37
5UCB.PDB	O, B_GLN_130	N, B_HIS_133	H, B_HIS_133	2.98	2.14	9.05
5UCB.PDB	OD1, B_ASP_117	ND1, B_HIS_133	HD1, B_HIS_133	2.95	2.15	18.23
5UCB.PDB	O, B_GLU_115	N, B_VAL_135	H, B_VAL_135	2.83	1.97	4.10
5UCB.PDB	O, B_ALA_15	N, B_ARG_136	H, B_ARG_136	2.79	1.98	17.55
5UCB.PDB	O, B_ASP_19	NH1, B_ARG_136	HH12, B_ARG_136	2.88	2.07	16.59
5UCB.PDB	O, B_ASN_113	N, B_ASN_137	H, B_ASN_137	2.81	2.02	19.05
5UCB.PDB	OD1, B_ASN_13	N, B_ILE_138	H, B_ILE_138	2.88	2.04	12.14
5UCB.PDB	O, B_TYR_111	N, B_LEU_139	H, B_LEU_139	2.86	2.01	7.51
5UCB.PDB	OG, H_SER_58	NZ, B_LYS_142	HZ3, B_LYS_142	2.83	1.96	8.82
5UCB.PDB	O, B_GLY_109	N, B_ARG_144	H, B_ARG_144	2.81	1.96	8.55
5UCB.PDB	O, B_LYS_142	NH1, B_ARG_144	HH11, B_ARG_144	2.91	2.12	19.24
5UCB.PDB	OD1, L_ASP_91	NH2, B_ARG_144	HH21, B_ARG_144	2.84	2.03	16.18
5UCB.PDB	O, B_ARG_107	N, B_THR_146	H, B_THR_146	2.81	1.98	11.97
5UCB.PDB	O, B_PHE_105	N, B_PHE_148	H, B_PHE_148	2.97	2.13	9.82

Table 1715: 5UCB-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5UJZ.PDB	OD2, B.ASP.612	N, B.PHE.503	H, B.PHE.503	2.82	1.98	9.98
5UJZ.PDB	OE1, B.GLU.574	N, B.ASN.571	H, B.ASN.571	2.73	1.96	22.10
5UJZ.PDB	OD1, B.ASN.571	N, B.LEU.573	H, B.LEU.573	2.86	2.10	22.42
5UJZ.PDB	O, B.ARG.575	N, B.ASN.579	H, B.ASN.579	2.92	2.06	2.26
5UJZ.PDB	O, B.ARG.576	N, B.LEU.580	H, B.LEU.580	2.88	2.06	14.57
5UJZ.PDB	O, B.MET.577	N, B.ASN.581	H, B.ASN.581	2.87	2.02	8.14
5UJZ.PDB	O, B.GLU.578	N, B.LYS.582	H, B.LYS.582	2.88	2.03	6.05
5UJZ.PDB	O, B.ASN.579	N, B.LYS.583	H, B.LYS.583	2.96	2.20	23.30
5UJZ.PDB	O, B.LEU.580	N, B.VAL.584	H, B.VAL.584	2.77	1.95	12.45
5UJZ.PDB	O, B.LYS.583	N, B.GLY.587	H, B.GLY.587	2.90	2.12	21.34
5UJZ.PDB	O, B.VAL.584	N, B.PHE.588	H, B.PHE.588	2.97	2.16	15.91
5UJZ.PDB	O, B.PHE.588	N, B.TRP.592	H, B.TRP.592	2.95	2.10	7.22
5UJZ.PDB	O, B.ASP.590	N, B.TYR.594	H, B.TYR.594	2.86	2.06	18.30
5UJZ.PDB	O, B.ILE.591	N, B.ASN.595	H, B.ASN.595	2.96	2.11	4.50
5UJZ.PDB	O, B.TRP.592	N, B.ALA.596	H, B.ALA.596	2.92	2.09	14.14
5UJZ.PDB	O, B.THR.593	N, B.GLU.597	H, B.GLU.597	2.94	2.13	17.13
5UJZ.PDB	O, B.ASN.595	N, B.LEU.599	H, B.LEU.599	2.92	2.21	29.47
5UJZ.PDB	O, B.ALA.596	N, B.VAL.600	H, B.VAL.600	2.90	2.16	25.76
5UJZ.PDB	O, B.LEU.598	N, B.LEU.602	H, B.LEU.602	2.89	2.04	6.88
5UJZ.PDB	O, B.LEU.599	N, B.GLU.603	H, B.GLU.603	2.89	2.05	10.08
5UJZ.PDB	O, B.VAL.600	N, B.ASN.604	H, B.ASN.604	2.99	2.17	14.45
5UJZ.PDB	O, B.LEU.602	N, B.ARG.606	H, B.ARG.606	2.86	2.03	11.15
5UJZ.PDB	O, B.ASN.604	N, B.LEU.608	H, B.LEU.608	2.98	2.16	15.31
5UJZ.PDB	O, B.LEU.608	N, B.ASP.612	H, B.ASP.612	2.95	2.10	4.89
5UJZ.PDB	OE1, D.GLU.574	N, D.ASN.571	H, D.ASN.571	2.73	1.96	22.20
5UJZ.PDB	OD1, D.ASN.571	N, D.LEU.573	H, D.LEU.573	2.86	2.10	22.20
5UJZ.PDB	O, D.ARG.575	N, D.ASN.579	H, D.ASN.579	2.92	2.06	2.09
5UJZ.PDB	O, D.ARG.576	N, D.LEU.580	H, D.LEU.580	2.88	2.06	14.50
5UJZ.PDB	O, D.MET.577	N, D.ASN.581	H, D.ASN.581	2.87	2.02	7.86
5UJZ.PDB	O, D.GLU.578	N, D.LYS.582	H, D.LYS.582	2.88	2.03	5.99
5UJZ.PDB	O, D.ASN.579	N, D.LYS.583	H, D.LYS.583	2.96	2.20	23.42
5UJZ.PDB	O, D.LEU.580	N, D.VAL.584	H, D.VAL.584	2.77	1.95	12.36
5UJZ.PDB	O, D.ASN.581	N, D.ASP.585	H, D.ASP.585	2.93	2.09	8.97
5UJZ.PDB	O, D.LYS.583	N, D.GLY.587	H, D.GLY.587	2.90	2.12	21.44
5UJZ.PDB	O, D.VAL.584	N, D.PHE.588	H, D.PHE.588	2.97	2.16	15.92
5UJZ.PDB	O, D.ASP.585	N, D.ILE.589	H, D.ILE.589	2.87	2.03	9.83
5UJZ.PDB	O, D.PHE.588	N, D.TRP.592	H, D.TRP.592	2.95	2.10	7.33
5UJZ.PDB	O, D.TRP.592	N, D.ALA.596	H, D.ALA.596	2.92	2.09	14.04
5UJZ.PDB	O, D.ASN.595	N, D.LEU.599	H, D.LEU.599	2.91	2.21	29.48
5UJZ.PDB	OE1, F.GLU.574	N, F.ASN.571	H, F.ASN.571	2.73	1.96	22.15
5UJZ.PDB	OD1, F.ASN.571	N, F.LEU.573	H, F.LEU.573	2.86	2.10	22.13
5UJZ.PDB	O, F.ARG.575	N, F.ASN.579	H, F.ASN.579	2.92	2.05	1.88
5UJZ.PDB	O, F.ARG.576	N, F.LEU.580	H, F.LEU.580	2.88	2.06	14.64
5UJZ.PDB	O, F.MET.577	N, F.ASN.581	H, F.ASN.581	2.87	2.02	7.56
5UJZ.PDB	O, F.GLU.578	N, F.LYS.582	H, F.LYS.582	2.88	2.03	5.84
5UJZ.PDB	O, F.ASN.579	N, F.LYS.583	H, F.LYS.583	2.96	2.20	23.60
5UJZ.PDB	O, F.LEU.580	N, F.VAL.584	H, F.VAL.584	2.77	1.95	12.39
5UJZ.PDB	O, F.ASN.581	N, F.ASP.585	H, F.ASP.585	2.93	2.09	8.86
5UJZ.PDB	O, F.LYS.582	N, F.ASP.586	H, F.ASP.586	2.90	2.06	8.24
5UJZ.PDB	O, F.LYS.583	N, F.GLY.587	H, F.GLY.587	2.90	2.12	21.41
5UJZ.PDB	O, F.VAL.584	N, F.PHE.588	H, F.PHE.588	2.97	2.16	15.90
5UJZ.PDB	O, F.ASP.585	N, F.ILE.589	H, F.ILE.589	2.87	2.03	9.71
5UJZ.PDB	O, F.ASP.586	N, F.ASP.590	H, F.ASP.590	2.94	2.13	16.67
5UJZ.PDB	O, F.PHE.588	N, F.TRP.592	H, F.TRP.592	2.95	2.10	7.36
5UJZ.PDB	O, F.ILE.589	N, F.THR.593	H, F.THR.593	2.94	2.15	21.05
5UJZ.PDB	O, F.ASP.590	N, F.TYR.594	H, F.TYR.594	2.86	2.06	18.69
5UJZ.PDB	O, F.ILE.591	N, F.ASN.595	H, F.ASN.595	2.96	2.11	4.41

5UJZ.PDB	O, F_TRP_592	N, F_ALA_596	H, F_ALA_596	2.92	2.09	13.92
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Table 1716: 5UJZ-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5UK0.PDB	O, A_THR_235	N, A_VAL_178	H, A_VAL_178	3.00	2.15	9.10
5UK0.PDB	O, A_TYR_233	N, A_TRP_180	H, A_TRP_180	2.83	2.06	22.85
5UK0.PDB	O, A_HIS_98	N, A_TYR_232	H, A_TYR_232	2.76	1.93	13.46
5UK0.PDB	O, A_TRP_180	N, A_TYR_233	H, A_TYR_233	2.86	2.01	7.16
5UK0.PDB	O, A_ALA_100	NE1, A_TRP_234	HE1, A_TRP_234	2.75	1.95	17.16
5UK0.PDB	O, A_VAL_178	N, A_THR_235	H, A_THR_235	2.96	2.15	14.92
5UK0.PDB	OD2, B_ASP_612	N, B_PHE_503	H, B_PHE_503	2.70	1.87	11.32
5UK0.PDB	O, B_ALA_505	N, B_GLY_508	H, B_GLY_508	2.62	1.89	25.83
5UK0.PDB	O, B_GLY_504	N, B_PHE_509	H, B_PHE_509	2.72	1.93	19.32
5UK0.PDB	O, B_ALA_535	N, B_TYR_524	H, B_TYR_524	2.87	2.06	16.06
5UK0.PDB	O, B_GLY_533	N, B_HIS_526	H, B_HIS_526	2.86	2.15	29.56
5UK0.PDB	O, B_TYR_524	N, B_ALA_535	H, B_ALA_535	2.96	2.18	21.03
5UK0.PDB	O, B_TYR_522	N, B_ASP_537	H, B_ASP_537	2.88	2.08	16.70
5UK0.PDB	O, B_GLN_538	N, B_GLN_542	H, B_GLN_542	2.87	2.06	16.85
5UK0.PDB	O, B_LYS_539	N, B_ASN_543	H, B_ASN_543	2.98	2.18	18.23
5UK0.PDB	O, B_SER_540	N, B_ALA_544	H, B_ALA_544	2.92	2.10	14.62
5UK0.PDB	O, B_THR_541	N, B_ILE_545	H, B_ILE_545	2.93	2.14	18.92
5UK0.PDB	O, B_GLN_542	N, B_ASN_546	H, B_ASN_546	2.90	2.07	13.85
5UK0.PDB	O, B_ILE_545	N, B_THR_549	H, B_THR_549	2.91	2.09	13.10
5UK0.PDB	O, B_ASN_546	N, B_ASN_550	H, B_ASN_550	2.97	2.16	16.74
5UK0.PDB	O, B_GLY_547	N, B_LYS_551	H, B_LYS_551	2.90	2.15	24.65
5UK0.PDB	O, B_ILE_548	N, B_VAL_552	H, B_VAL_552	2.98	2.14	11.61
5UK0.PDB	O, B_THR_549	N, B_ASN_553	H, B_ASN_553	2.96	2.10	2.11
5UK0.PDB	O, B_ASN_550	N, B_SER_554	H, B_SER_554	2.98	2.23	25.37
5UK0.PDB	O, B_VAL_552	N, B_ILE_556	H, B_ILE_556	2.99	2.17	15.52
5UK0.PDB	OD1, F_ASP_590	ND2, B_ASN_560	HD22, B_ASN_560	2.72	1.94	19.72
5UK0.PDB	O, B_GLU_574	N, B_GLU_578	H, B_GLU_578	2.95	2.23	28.27
5UK0.PDB	O, B_ARG_575	N, B_ASN_579	H, B_ASN_579	2.86	2.00	5.28
5UK0.PDB	O, B_ARG_576	N, B_LEU_580	H, B_LEU_580	2.90	2.08	14.14
5UK0.PDB	O, B_MET_577	N, B_ASN_581	H, B_ASN_581	2.90	2.05	9.42
5UK0.PDB	O, B_GLU_578	N, B_LYS_582	H, B_LYS_582	2.89	2.04	6.59
5UK0.PDB	O, B_ASN_579	N, B_LYS_583	H, B_LYS_583	2.99	2.19	17.96
5UK0.PDB	O, B_LEU_580	N, B_VAL_584	H, B_VAL_584	2.79	1.97	14.76
5UK0.PDB	O, B_ASN_581	N, B_ASP_585	H, B_ASP_585	2.96	2.12	8.51
5UK0.PDB	O, B_LYS_582	N, B_ASP_586	H, B_ASP_586	2.88	2.03	6.06
5UK0.PDB	O, B_LYS_583	N, B_GLY_587	H, B_GLY_587	2.88	2.11	21.69
5UK0.PDB	O, B_ASP_585	N, B_ILE_589	H, B_ILE_589	2.91	2.09	14.38
5UK0.PDB	O, B_ASP_586	N, B_ASP_590	H, B_ASP_590	2.91	2.09	14.55
5UK0.PDB	O, B_PHE_588	N, B_TRP_592	H, B_TRP_592	2.93	2.08	6.61
5UK0.PDB	O, B_ILE_589	N, B_THR_593	H, B_THR_593	2.96	2.20	24.14
5UK0.PDB	O, B_ASP_590	N, B_TYR_594	H, B_TYR_594	2.90	2.12	20.32
5UK0.PDB	O, B_ILE_591	N, B_ASN_595	H, B_ASN_595	2.98	2.13	3.96
5UK0.PDB	O, B_TRP_592	N, B_ALA_596	H, B_ALA_596	2.89	2.07	14.01
5UK0.PDB	O, B_THR_593	N, B_GLU_597	H, B_GLU_597	2.94	2.15	19.17
5UK0.PDB	O, B_ASN_595	N, B_LEU_599	H, B_LEU_599	2.94	2.22	27.64
5UK0.PDB	O, B_ALA_596	N, B_VAL_600	H, B_VAL_600	2.93	2.19	26.06
5UK0.PDB	O, B_LEU_598	N, B_LEU_602	H, B_LEU_602	2.93	2.09	10.30
5UK0.PDB	O, B_LEU_599	N, B_GLU_603	H, B_GLU_603	2.87	2.04	13.58
5UK0.PDB	O, B_VAL_600	N, B_ASN_604	H, B_ASN_604	2.99	2.17	14.76
5UK0.PDB	O, B_LEU_601	N, B_GLU_605	H, B_GLU_605	2.98	2.18	18.00
5UK0.PDB	O, B_LEU_602	N, B_ARG_606	H, B_ARG_606	2.85	2.01	10.65
5UK0.PDB	O, B_ASN_604	N, B_LEU_608	H, B_LEU_608	2.96	2.16	17.86
5UK0.PDB	O, B_GLU_605	N, B_ASP_609	H, B_ASP_609	2.94	2.14	18.33
5UK0.PDB	O, B_THR_607	N, B_HIS_611	H, B_HIS_611	2.95	2.15	17.84
5UK0.PDB	O, B_LEU_608	N, B_ASP_612	H, B_ASP_612	2.94	2.09	8.40
5UK0.PDB	O, B_ASP_609	N, B_SER_613	H, B_SER_613	2.89	2.09	18.36
5UK0.PDB	O, B_HIS_611	N, B_VAL_615	H, B_VAL_615	2.99	2.17	12.43

5UK0.PDB	O, B_SER_613	N, B_ASN_617	H, B_ASN_617	2.86	2.04	15.11
5UK0.PDB	O, F_LEU_502	ND2, B_ASN_617	HD22, B_ASN_617	2.60	1.80	16.74
5UK0.PDB	O, B_ASN_614	N, B_LEU_618	H, B_LEU_618	2.97	2.17	18.23
5UK0.PDB	O, B_VAL_615	N, B_TYR_619	H, B_TYR_619	2.89	2.08	17.73
5UK0.PDB	O, B_ASN_617	N, B_LYS_621	H, B_LYS_621	2.91	2.19	28.31
5UK0.PDB	O, B_LEU_618	N, B_VAL_622	H, B_VAL_622	2.91	2.12	20.36
5UK0.PDB	O, B_TYR_619	N, B_LYS_623	H, B_LYS_623	2.95	2.14	15.77
5UK0.PDB	O, B_GLU_639	N, B_LYS_631	H, B_LYS_631	2.93	2.13	17.90
5UK0.PDB	OD1, C_ASN_231	N, C_HIS_98	H, C_HIS_98	2.89	2.08	15.31
5UK0.PDB	O, C_ASP_101	N, C_LEU_105	H, C_LEU_105	2.95	2.14	16.91
5UK0.PDB	O, C_LEU_105	N, C_LEU_109	H, C_LEU_109	2.87	2.07	17.71
5UK0.PDB	O, C_THR_131	N, C_THR_155	H, C_THR_155	2.70	1.87	11.80
5UK0.PDB	O, C_THR_235	N, C_VAL_178	H, C_VAL_178	2.99	2.15	8.93
5UK0.PDB	O, C_TYR_233	N, C_TRP_180	H, C_TRP_180	2.83	2.06	22.92
5UK0.PDB	O, C_ILE_252	N, C_GLY_181	H, C_GLY_181	2.96	2.20	23.53
5UK0.PDB	O, C_ASN_231	N, C_VAL_182	H, C_VAL_182	2.94	2.21	26.92
5UK0.PDB	O, C_ASN_250	N, C_HIS_183	H, C_HIS_183	2.90	2.10	17.87
5UK0.PDB	O, C_HIS_98	N, C_TYR_232	H, C_TYR_232	2.75	1.93	13.38
5UK0.PDB	O, C_TRP_180	N, C_TYR_233	H, C_TYR_233	2.86	2.01	7.20
5UK0.PDB	O, C_ALA_100	NE1, C_TRP_234	HE1, C_TRP_234	2.75	1.95	17.15
5UK0.PDB	O, C_VAL_178	N, C_THR_235	H, C_THR_235	2.96	2.15	14.97
5UK0.PDB	O, C_VAL_176	N, C_LEU_237	H, C_LEU_237	2.90	2.14	23.70
5UK0.PDB	O, C_GLY_181	N, C_ILE_252	H, C_ILE_252	2.86	2.07	19.19
5UK0.PDB	OD1, D_ASP_586	NH2, C_ARG_311	HH22, C_ARG_311	2.98	2.20	18.56
5UK0.PDB	OD2, D_ASP_612	N, D_PHE_503	H, D_PHE_503	2.70	1.87	11.03
5UK0.PDB	O, D_ALA_505	N, D_GLY_508	H, D_GLY_508	2.63	1.89	25.56
5UK0.PDB	O, D_GLY_504	N, D_PHE_509	H, D_PHE_509	2.72	1.93	19.19
5UK0.PDB	O, D_ALA_535	N, D_TYR_524	H, D_TYR_524	2.87	2.06	15.73
5UK0.PDB	O, D_TYR_524	N, D_ALA_535	H, D_ALA_535	2.96	2.18	21.51
5UK0.PDB	O, D_TYR_522	N, D_ASP_537	H, D_ASP_537	2.88	2.07	16.56
5UK0.PDB	O, D_GLN_538	N, D_GLN_542	H, D_GLN_542	2.87	2.06	16.50
5UK0.PDB	O, D_LYS_539	N, D_ASN_543	H, D_ASN_543	2.98	2.18	18.20
5UK0.PDB	O, D_SER_540	N, D_ALA_544	H, D_ALA_544	2.93	2.11	14.85
5UK0.PDB	O, D_THR_541	N, D_ILE_545	H, D_ILE_545	2.93	2.14	18.87
5UK0.PDB	O, D_GLN_542	N, D_ASN_546	H, D_ASN_546	2.90	2.07	13.58
5UK0.PDB	O, D_ILE_545	N, D_THR_549	H, D_THR_549	2.91	2.09	12.94
5UK0.PDB	O, D_ASN_546	N, D_ASN_550	H, D_ASN_550	2.97	2.16	16.37
5UK0.PDB	O, D_GLY_547	N, D_LYS_551	H, D_LYS_551	2.90	2.15	24.73
5UK0.PDB	O, D_ILE_548	N, D_VAL_552	H, D_VAL_552	2.98	2.14	11.77
5UK0.PDB	O, D_THR_549	N, D_ASN_553	H, D_ASN_553	2.96	2.10	2.11
5UK0.PDB	O, D_ASN_550	N, D_SER_554	H, D_SER_554	2.98	2.23	25.34
5UK0.PDB	O, D_VAL_552	N, D_ILE_556	H, D_ILE_556	2.99	2.17	15.75
5UK0.PDB	OD1, B_ASP_590	ND2, D_ASN_560	HD22, D_ASN_560	2.73	1.95	20.06
5UK0.PDB	O, D_GLU_574	N, D_GLU_578	H, D_GLU_578	2.95	2.23	28.68
5UK0.PDB	O, D_ARG_575	N, D_ASN_579	H, D_ASN_579	2.86	2.00	3.72
5UK0.PDB	O, D_ARG_576	N, D_LEU_580	H, D_LEU_580	2.90	2.07	13.93
5UK0.PDB	O, D_MET_577	N, D_ASN_581	H, D_ASN_581	2.90	2.05	9.24
5UK0.PDB	O, D_GLU_578	N, D_LYS_582	H, D_LYS_582	2.89	2.04	7.42
5UK0.PDB	O, D_ASN_579	N, D_LYS_583	H, D_LYS_583	2.99	2.19	18.48
5UK0.PDB	O, D_LEU_580	N, D_VAL_584	H, D_VAL_584	2.79	1.97	14.60
5UK0.PDB	O, D_ASN_581	N, D_ASP_585	H, D_ASP_585	2.96	2.12	8.30
5UK0.PDB	O, D_LYS_582	N, D_ASP_586	H, D_ASP_586	2.88	2.03	7.07
5UK0.PDB	O, D_LYS_583	N, D_GLY_587	H, D_GLY_587	2.88	2.11	21.76
5UK0.PDB	O, D_ASP_585	N, D_ILE_589	H, D_ILE_589	2.91	2.09	14.41
5UK0.PDB	O, D_ASP_586	N, D_ASP_590	H, D_ASP_590	2.91	2.09	15.63
5UK0.PDB	O, D_PHE_588	N, D_TRP_592	H, D_TRP_592	2.93	2.08	6.27
5UK0.PDB	O, D_ILE_589	N, D_THR_593	H, D_THR_593	2.96	2.21	24.62
5UK0.PDB	O, D_ASP_590	N, D_TYR_594	H, D_TYR_594	2.90	2.12	21.14

5UK0.PDB	O, D_ILE_591	N, D_ASN_595	H, D_ASN_595	2.98	2.12	3.15
5UK0.PDB	O, D_TRP_592	N, D_ALA_596	H, D_ALA_596	2.89	2.07	14.15
5UK0.PDB	O, D_THR_593	N, D_GLU_597	H, D_GLU_597	2.94	2.15	19.89
5UK0.PDB	O, D_ASN_595	N, D_LEU_599	H, D_LEU_599	2.94	2.21	26.82
5UK0.PDB	O, D_ALA_596	N, D_VAL_600	H, D_VAL_600	2.93	2.19	25.78
5UK0.PDB	O, D_LEU_598	N, D_LEU_602	H, D_LEU_602	2.93	2.09	10.12
5UK0.PDB	O, D_LEU_599	N, D_GLU_603	H, D_GLU_603	2.86	2.04	13.30
5UK0.PDB	O, D_VAL_600	N, D_ASN_604	H, D_ASN_604	2.99	2.17	15.08
5UK0.PDB	O, D_LEU_601	N, D_GLU_605	H, D_GLU_605	2.98	2.18	18.56
5UK0.PDB	O, D_LEU_602	N, D_ARG_606	H, D_ARG_606	2.85	2.01	10.50
5UK0.PDB	O, D_ASN_604	N, D_LEU_608	H, D_LEU_608	2.96	2.16	18.11
5UK0.PDB	O, D_GLU_605	N, D_ASP_609	H, D_ASP_609	2.94	2.14	18.44
5UK0.PDB	O, D_THR_607	N, D_HIS_611	H, D_HIS_611	2.95	2.15	17.74
5UK0.PDB	O, D_LEU_608	N, D_ASP_612	H, D_ASP_612	2.94	2.09	8.59
5UK0.PDB	O, D_ASP_609	N, D_SER_613	H, D_SER_613	2.89	2.09	18.51
5UK0.PDB	O, D_HIS_611	N, D_VAL_615	H, D_VAL_615	2.99	2.17	12.24
5UK0.PDB	O, D_SER_613	N, D_ASN_617	H, D_ASN_617	2.86	2.05	15.31
5UK0.PDB	O, B_LEU_502	ND2, D_ASN_617	HD22, D_ASN_617	2.62	1.80	13.03
5UK0.PDB	O, D_ASN_614	N, D_LEU_618	H, D_LEU_618	2.97	2.17	17.99
5UK0.PDB	O, D_VAL_615	N, D_TYR_619	H, D_TYR_619	2.89	2.08	17.58
5UK0.PDB	O, D_ASN_617	N, D_LYS_621	H, D_LYS_621	2.91	2.19	28.69
5UK0.PDB	O, D_LEU_618	N, D_VAL_622	H, D_VAL_622	2.91	2.12	19.99
5UK0.PDB	O, D_TYR_619	N, D_LYS_623	H, D_LYS_623	2.95	2.14	15.66
5UK0.PDB	OH, D_TYR_659	ND2, D_ASN_628	HD22, D_ASN_628	2.78	1.98	17.11
5UK0.PDB	O, D_GLU_639	N, D_LYS_631	H, D_LYS_631	2.93	2.13	17.74
5UK0.PDB	OD1, E_ASN_231	N, E_HIS_98	H, E_HIS_98	2.89	2.08	15.58
5UK0.PDB	O, E_ASP_101	N, E_LEU_105	H, E_LEU_105	2.95	2.14	17.24
5UK0.PDB	O, E_ALA_253	N, E_LEU_152	H, E_LEU_152	2.92	2.19	27.06
5UK0.PDB	O, E_THR_235	N, E_VAL_178	H, E_VAL_178	2.99	2.15	9.16
5UK0.PDB	O, E_TYR_233	N, E_TRP_180	H, E_TRP_180	2.83	2.07	23.11
5UK0.PDB	O, E_ILE_252	N, E_GLY_181	H, E_GLY_181	2.96	2.20	23.58
5UK0.PDB	O, E_ASN_231	N, E_VAL_182	H, E_VAL_182	2.94	2.21	26.82
5UK0.PDB	O, E_ASN_250	N, E_HIS_183	H, E_HIS_183	2.90	2.10	17.70
5UK0.PDB	O, E_HIS_98	N, E_TYR_232	H, E_TYR_232	2.75	1.93	13.43
5UK0.PDB	O, E_TRP_180	N, E_TYR_233	H, E_TYR_233	2.86	2.01	7.32
5UK0.PDB	O, E_ALA_100	NE1, E_TRP_234	HE1, E_TRP_234	2.75	1.95	17.13
5UK0.PDB	O, E_VAL_178	N, E_THR_235	H, E_THR_235	2.96	2.15	14.95
5UK0.PDB	O, E_GLY_181	N, E_ILE_252	H, E_ILE_252	2.86	2.06	19.00
5UK0.PDB	O, E_LEU_152	N, E_ALA_253	H, E_ALA_253	2.98	2.15	13.22
5UK0.PDB	OD2, F_ASP_612	N, F_PHE_503	H, F_PHE_503	2.70	1.87	11.30
5UK0.PDB	O, F_ALA_505	N, F_GLY_508	H, F_GLY_508	2.62	1.89	25.82
5UK0.PDB	O, F_GLY_504	N, F_PHE_509	H, F_PHE_509	2.72	1.93	19.29
5UK0.PDB	O, F_TYR_522	N, F_ASP_537	H, F_ASP_537	2.88	2.08	16.77
5UK0.PDB	O, F_GLN_538	N, F_GLN_542	H, F_GLN_542	2.87	2.06	16.85
5UK0.PDB	O, F_LYS_539	N, F_ASN_543	H, F_ASN_543	2.98	2.18	18.15
5UK0.PDB	O, F_SER_540	N, F_ALA_544	H, F_ALA_544	2.92	2.10	14.52
5UK0.PDB	O, F_THR_541	N, F_ILE_545	H, F_ILE_545	2.93	2.14	19.01
5UK0.PDB	O, F_GLN_542	N, F_ASN_546	H, F_ASN_546	2.90	2.07	13.91
5UK0.PDB	O, F_ILE_545	N, F_THR_549	H, F_THR_549	2.91	2.09	13.20
5UK0.PDB	O, F_GLY_547	N, F_LYS_551	H, F_LYS_551	2.90	2.15	24.70
5UK0.PDB	O, F_ILE_548	N, F_VAL_552	H, F_VAL_552	2.98	2.14	11.60
5UK0.PDB	O, F_THR_549	N, F_ASN_553	H, F_ASN_553	2.96	2.10	2.17
5UK0.PDB	O, F_GLU_574	N, F_GLU_578	H, F_GLU_578	2.95	2.23	28.18
5UK0.PDB	O, F_ARG_575	N, F_ASN_579	H, F_ASN_579	2.86	2.00	5.11
5UK0.PDB	O, F_ARG_576	N, F_LEU_580	H, F_LEU_580	2.90	2.08	14.08
5UK0.PDB	O, F_MET_577	N, F_ASN_581	H, F_ASN_581	2.90	2.05	9.26
5UK0.PDB	O, F_GLU_578	N, F_LYS_582	H, F_LYS_582	2.89	2.04	6.55
5UK0.PDB	O, F_ASN_579	N, F_LYS_583	H, F_LYS_583	2.99	2.19	17.94

5UK0.PDB	O, F_LEU_580	N, F_VAL_584	H, F_VAL_584	2.79	1.97	14.87
5UK0.PDB	O, F_ASN_581	N, F_ASP_585	H, F_ASP_585	2.96	2.12	8.36
5UK0.PDB	O, F_LYS_582	N, F_ASP_586	H, F_ASP_586	2.88	2.03	6.16
5UK0.PDB	O, F_LYS_583	N, F_GLY_587	H, F_GLY_587	2.88	2.11	21.80
5UK0.PDB	O, F_ASP_585	N, F_ILE_589	H, F_ILE_589	2.91	2.09	14.50
5UK0.PDB	O, F_ASP_586	N, F_ASP_590	H, F_ASP_590	2.91	2.09	14.81
5UK0.PDB	O, F_PHE_588	N, F_TRP_592	H, F_TRP_592	2.93	2.08	6.51
5UK0.PDB	O, F_ILE_589	N, F_THR_593	H, F_THR_593	2.96	2.20	24.02
5UK0.PDB	O, F_ASP_590	N, F_TYR_594	H, F_TYR_594	2.90	2.12	20.53
5UK0.PDB	O, F_ILE_591	N, F_ASN_595	H, F_ASN_595	2.98	2.13	3.84
5UK0.PDB	O, F_TRP_592	N, F_ALA_596	H, F_ALA_596	2.89	2.07	13.98
5UK0.PDB	O, F_THR_593	N, F_GLU_597	H, F_GLU_597	2.94	2.15	19.04
5UK0.PDB	O, F_ASN_595	N, F_LEU_599	H, F_LEU_599	2.94	2.22	27.60
5UK0.PDB	O, F_ALA_596	N, F_VAL_600	H, F_VAL_600	2.93	2.19	26.00
5UK0.PDB	O, F_LEU_598	N, F_LEU_602	H, F_LEU_602	2.93	2.09	10.36
5UK0.PDB	O, F_LEU_599	N, F_GLU_603	H, F_GLU_603	2.87	2.04	13.60
5UK0.PDB	O, F_VAL_600	N, F_ASN_604	H, F_ASN_604	2.99	2.17	14.81
5UK0.PDB	O, F_LEU_601	N, F_GLU_605	H, F_GLU_605	2.98	2.18	18.18
5UK0.PDB	O, F_LEU_602	N, F_ARG_606	H, F_ARG_606	2.84	2.01	10.64
5UK0.PDB	O, F_ASN_604	N, F_LEU_608	H, F_LEU_608	2.96	2.16	17.90
5UK0.PDB	O, F_GLU_605	N, F_ASP_609	H, F_ASP_609	2.94	2.14	18.42
5UK0.PDB	O, F_THR_607	N, F_HIS_611	H, F_HIS_611	2.95	2.15	17.79
5UK0.PDB	O, F_LEU_608	N, F_ASP_612	H, F_ASP_612	2.94	2.09	8.54
5UK0.PDB	O, F_ASP_609	N, F_SER_613	H, F_SER_613	2.89	2.09	18.54
5UK0.PDB	O, F_HIS_611	N, F_VAL_615	H, F_VAL_615	2.99	2.17	12.51
5UK0.PDB	O, F_SER_613	N, F_ASN_617	H, F_ASN_617	2.86	2.04	15.17
5UK0.PDB	O, D_LEU_502	ND2, F_ASN_617	HD22, F_ASN_617	2.71	1.89	14.40
5UK0.PDB	O, F_ASN_614	N, F_LEU_618	H, F_LEU_618	2.97	2.17	18.13
5UK0.PDB	O, F_VAL_615	N, F_TYR_619	H, F_TYR_619	2.89	2.08	17.81
5UK0.PDB	O, F_ASN_617	N, F_LYS_621	H, F_LYS_621	2.91	2.19	28.37
5UK0.PDB	O, F_LEU_618	N, F_VAL_622	H, F_VAL_622	2.91	2.12	20.33
5UK0.PDB	O, F_TYR_619	N, F_LYS_623	H, F_LYS_623	2.95	2.14	15.82

Table 1717: 5UK0-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5UK1.PDB	O, D_VAL_552	N, D_ILE_556	H, D_ILE_556	2.96	2.12	11.93
5UK1.PDB	OE1, F_GLU_574	N, F_ASN_571	H, F_ASN_571	2.86	2.03	13.31
5UK1.PDB	O, F_GLU_574	N, F_GLU_578	H, F_GLU_578	2.94	2.20	25.93
5UK1.PDB	O, F_ARG_575	N, F_ASN_579	H, F_ASN_579	2.86	2.00	2.72
5UK1.PDB	O, F_ARG_576	N, F_LEU_580	H, F_LEU_580	2.81	1.99	13.05
5UK1.PDB	O, F_MET_577	N, F_ASN_581	H, F_ASN_581	2.86	2.02	9.83
5UK1.PDB	O, F_GLU_578	N, F_LYS_582	H, F_LYS_582	2.87	2.01	5.13
5UK1.PDB	O, F_ASN_579	N, F_LYS_583	H, F_LYS_583	2.94	2.18	22.71
5UK1.PDB	O, F_LEU_580	N, F_VAL_584	H, F_VAL_584	2.76	1.97	18.59
5UK1.PDB	O, F_ASN_581	N, F_ASP_585	H, F_ASP_585	2.97	2.13	10.07
5UK1.PDB	O, F_VAL_584	N, F_PHE_588	H, F_PHE_588	2.96	2.20	23.32

Table 1718: 5UK1-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5UK2.PDB	O, A_ALA_100	NE1, A_TRP_234	HE1, A_TRP_234	2.78	1.96	13.46
5UK2.PDB	OE1, B_GLU_574	N, B_ASN_571	H, B_ASN_571	2.96	2.16	19.53
5UK2.PDB	OD1, B_ASN_571	N, B_LEU_573	H, B_LEU_573	2.85	2.08	22.03
5UK2.PDB	O, B_ARG_575	N, B_ASN_579	H, B_ASN_579	2.99	2.13	2.73
5UK2.PDB	O, B_ARG_576	N, B_LEU_580	H, B_LEU_580	2.91	2.11	18.12
5UK2.PDB	O, B_MET_577	N, B_ASN_581	H, B_ASN_581	2.88	2.04	8.65
5UK2.PDB	O, B_GLU_578	N, B_LYS_582	H, B_LYS_582	2.97	2.11	2.97
5UK2.PDB	O, B_ASN_579	N, B_LYS_583	H, B_LYS_583	2.97	2.22	23.65
5UK2.PDB	O, B_LEU_580	N, B_VAL_584	H, B_VAL_584	2.78	1.98	15.70
5UK2.PDB	O, B_ASN_581	N, B_ASP_585	H, B_ASP_585	2.99	2.14	7.89
5UK2.PDB	O, B_LYS_583	N, B_GLY_587	H, B_GLY_587	2.91	2.15	22.85
5UK2.PDB	O, B_VAL_584	N, B_PHE_588	H, B_PHE_588	2.97	2.15	13.63
5UK2.PDB	O, B_ASP_585	N, B_ILE_589	H, B_ILE_589	2.86	2.03	12.99
5UK2.PDB	O, B_PHE_588	N, B_TRP_592	H, B_TRP_592	2.95	2.11	9.98
5UK2.PDB	O, B_ILE_589	N, B_THR_593	H, B_THR_593	2.97	2.20	23.17
5UK2.PDB	O, B_ASP_590	N, B_TYR_594	H, B_TYR_594	2.88	2.12	22.46
5UK2.PDB	O, B_ILE_591	N, B_ASN_595	H, B_ASN_595	2.96	2.11	4.99
5UK2.PDB	O, B_TRP_592	N, B_ALA_596	H, B_ALA_596	2.93	2.11	15.16
5UK2.PDB	OE1, F_GLU_574	N, F_ASN_571	H, F_ASN_571	2.96	2.16	19.49
5UK2.PDB	OD1, F_ASN_571	N, F_LEU_573	H, F_LEU_573	2.85	2.08	21.74
5UK2.PDB	O, F_ARG_575	N, F_ASN_579	H, F_ASN_579	2.99	2.13	2.69
5UK2.PDB	O, F_ARG_576	N, F_LEU_580	H, F_LEU_580	2.91	2.11	18.05
5UK2.PDB	O, F_MET_577	N, F_ASN_581	H, F_ASN_581	2.88	2.04	8.63
5UK2.PDB	O, F_ASN_579	N, F_LYS_583	H, F_LYS_583	2.97	2.22	23.60
5UK2.PDB	O, F_LEU_580	N, F_VAL_584	H, F_VAL_584	2.78	1.98	15.73
5UK2.PDB	O, F_VAL_584	N, F_PHE_588	H, F_PHE_588	2.97	2.15	13.56

Table 1719: 5UK2-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5VXJ.PDB	O, A_VAL.41	N, A_THR.45	H, A_THR.45	2.85	2.03	14.33
5VXJ.PDB	O, A_SER.43	N, A_LEU.47	H, A_LEU.47	2.92	2.09	14.12
5VXJ.PDB	O, A_MET.46	N, A_THR.50	H, A_THR.50	2.71	1.87	10.48
5VXJ.PDB	O, A_MET.46	OG1, A_THR.50	HG1, A_THR.50	2.73	1.96	20.05
5VXJ.PDB	O, A_LEU.47	N, A_LEU.51	H, A_LEU.51	2.75	1.90	3.64
5VXJ.PDB	OD2, A_ASP.309	NH2, A_ARG.55	HH21, A_ARG.55	2.90	2.12	21.39
5VXJ.PDB	O, A_ASN.53	N, A_THR.57	H, A_THR.57	2.92	2.09	13.03
5VXJ.PDB	O, A_ILE.54	N, A_ASN.58	H, A_ASN.58	2.76	1.94	14.78
5VXJ.PDB	O, A_THR.57	N, A_LEU.61	H, A_LEU.61	2.95	2.16	20.24
5VXJ.PDB	O, A_ASN.58	N, A_LYS.62	H, A_LYS.62	2.92	2.08	10.15
5VXJ.PDB	OG, A_SER.302	NZ, A_LYS.62	HZ2, A_LYS.62	2.77	1.91	12.44
5VXJ.PDB	OG, A_SER.306	NZ, A_LYS.62	HZ3, A_LYS.62	2.75	1.92	16.95
5VXJ.PDB	O, A_LEU.61	N, A_LEU.65	H, A_LEU.65	2.88	2.04	11.05
5VXJ.PDB	O, A_THR.73	N, A_GLU.77	H, A_GLU.77	2.92	2.15	21.99
5VXJ.PDB	O, A_SER.74	N, A_ILE.78	H, A_ILE.78	2.84	1.99	6.65
5VXJ.PDB	O, A_GLU.77	N, A_HIS.81	H, A_HIS.81	2.96	2.12	10.84
5VXJ.PDB	O, A_ILE.78	N, A_SER.82	H, A_SER.82	2.74	1.89	4.58
5VXJ.PDB	O, A_ALA.79	N, A_SER.83	H, A_SER.83	2.95	2.13	16.02
5VXJ.PDB	O, A_LEU.80	N, A_GLN.84	H, A_GLN.84	2.97	2.17	18.25
5VXJ.PDB	O, A_HIS.81	N, A_ILE.85	H, A_ILE.85	2.84	2.00	10.73
5VXJ.PDB	O, A_SER.82	N, A_SER.86	H, A_SER.86	2.95	2.09	3.63
5VXJ.PDB	O, A_SER.83	N, A_MET.87	H, A_MET.87	2.90	2.08	16.45
5VXJ.PDB	O, A_ILE.85	N, A_VAL.89	H, A_VAL.89	2.68	1.83	6.60
5VXJ.PDB	O, A_SER.86	N, A_ASN.90	H, A_ASN.90	2.83	2.04	19.63
5VXJ.PDB	O, A_ASP.88	N, A_SER.92	H, A_SER.92	2.88	2.03	7.69
5VXJ.PDB	O, A_VAL.89	N, A_ALA.93	H, A_ALA.93	2.95	2.14	16.09
5VXJ.PDB	O, A_LYS.91	N, A_LEU.95	H, A_LEU.95	2.93	2.12	16.80
5VXJ.PDB	O, A_SER.92	N, A_LEU.96	H, A_LEU.96	2.83	1.97	3.74
5VXJ.PDB	O, A_ALA.93	N, A_ASP.97	H, A_ASP.97	2.81	2.03	20.86
5VXJ.PDB	O, A_LEU.96	N, A_SER.100	H, A_SER.100	2.98	2.27	29.77
5VXJ.PDB	O, A_ARG.132	OG, A_SER.100	HG, A_SER.100	2.62	1.84	18.43
5VXJ.PDB	OD2, A_ASP.97	NE, A_ARG.101	HE, A_ARG.101	2.80	1.97	13.39
5VXJ.PDB	O, A_ILE.98	N, A_ASN.102	H, A_ASN.102	2.95	2.11	10.28
5VXJ.PDB	O, A_SER.100	N, A_GLU.103	H, A_GLU.103	2.99	2.22	22.55
5VXJ.PDB	O, A_LEU.99	N, A_TYR.104	H, A_TYR.104	2.95	2.14	17.03
5VXJ.PDB	O, A_ILE.129	NH1, A_ARG.111	HH12, A_ARG.111	2.61	1.80	16.87
5VXJ.PDB	O, A_LEU.113	N, A_SER.116	H, A_SER.116	2.99	2.17	13.81
5VXJ.PDB	O, A_LEU.114	N, A_ALA.117	H, A_ALA.117	2.91	2.07	9.65
5VXJ.PDB	O, A_LYS.119	N, A_GLU.122	H, A_GLU.122	2.96	2.17	19.32
5VXJ.PDB	O, A_SER.130	N, A_LEU.134	H, A_LEU.134	2.99	2.20	18.86
5VXJ.PDB	O, A_TYR.104	NE1, A_TRP.135	HE1, A_TRP.135	2.84	2.08	23.47
5VXJ.PDB	O, A_GLU.133	N, A_LYS.137	H, A_LYS.137	2.97	2.16	17.73
5VXJ.PDB	O, A_LEU.134	N, A_ILE.138	H, A_ILE.138	2.93	2.16	21.74
5VXJ.PDB	O, A_TRP.135	N, A_ALA.139	H, A_ALA.139	2.99	2.16	12.41
5VXJ.PDB	O, A_ALA.136	N, A_ASN.140	H, A_ASN.140	2.89	2.04	5.99
5VXJ.PDB	O, A_LYS.137	N, A_SER.141	H, A_SER.141	2.86	2.11	24.60
5VXJ.PDB	O, A_ALA.121	OG, A_SER.141	HG, A_SER.141	2.90	2.17	24.63
5VXJ.PDB	O, A_ILE.138	N, A_ILE.142	H, A_ILE.142	2.98	2.14	10.65
5VXJ.PDB	O, A_ASN.140	N, A_ASP.144	H, A_ASP.144	2.74	1.94	18.04
5VXJ.PDB	O, A_SER.141	N, A_ILE.145	H, A_ILE.145	2.97	2.12	7.63
5VXJ.PDB	O, A_ASP.144	N, A_GLN.148	H, A_GLN.148	2.73	1.88	8.38
5VXJ.PDB	O, A_ILE.145	N, A_LEU.150	H, A_LEU.150	2.96	2.11	7.42
5VXJ.PDB	O, A_ASN.146	N, A_LYS.151	H, A_LYS.151	2.96	2.16	18.68
5VXJ.PDB	OE2, A_GLU.229	OH, A_TYR.153	HH, A_TYR.153	2.70	1.94	21.05
5VXJ.PDB	O, A_GLU.154	N, A_SER.158	H, A_SER.158	2.90	2.09	15.89
5VXJ.PDB	O, A_HIS.155	N, A_SER.159	H, A_SER.159	2.80	1.96	9.42
5VXJ.PDB	O, A_VAL.157	N, A_THR.161	H, A_THR.161	2.82	1.98	11.00

5VXJ.PDB	O, A_VAL_157	OG1, A_THR_161	HG1, A_THR_161	2.60	1.90	27.90
5VXJ.PDB	O, A_TYR_160	N, A_TYR_164	H, A_TYR_164	2.91	2.09	14.34
5VXJ.PDB	OD1, A_ASP_287	OH, A_TYR_164	HH, A_TYR_164	2.72	1.96	22.05
5VXJ.PDB	O, A_THR_161	N, A_GLN_165	H, A_GLN_165	2.84	2.05	19.22
5VXJ.PDB	O, A_GLN_162	N, A_ASP_166	H, A_ASP_166	2.94	2.09	8.93
5VXJ.PDB	O, A_MET_163	N, A_PHE_167	H, A_PHE_167	2.91	2.10	17.54
5VXJ.PDB	O, A_TYR_164	N, A_SER_168	H, A_SER_168	2.81	2.03	20.85
5VXJ.PDB	O, A_TYR_164	OG, A_SER_168	HG, A_SER_168	2.89	2.09	13.52
5VXJ.PDB	O, A_SER_168	N, A_SER_172	H, A_SER_172	2.98	2.21	21.86
5VXJ.PDB	O, A_LEU_174	N, A_TRP_177	H, A_TRP_177	2.99	2.26	27.17
5VXJ.PDB	OD1, A_ASP_184	N, A_ASN_186	H, A_ASN_186	2.76	1.91	7.29
5VXJ.PDB	O, A_LEU_271	N, A_VAL_188	H, A_VAL_188	2.87	2.09	19.88
5VXJ.PDB	O, A_SER_179	N, A_LYS_189	H, A_LYS_189	2.61	1.75	6.27
5VXJ.PDB	O, A_VAL_269	N, A_LEU_190	H, A_LEU_190	2.84	2.02	14.05
5VXJ.PDB	O, A_TRP_177	N, A_GLN_191	H, A_GLN_191	2.95	2.15	19.06
5VXJ.PDB	OE2, A_GLU_268	NE2, A_GLN_191	HE22, A_GLN_191	2.93	2.12	16.99
5VXJ.PDB	O, A_VAL_192	N, A_LYS_196	H, A_LYS_196	2.67	1.82	7.56
5VXJ.PDB	O, A_ASN_193	N, A_LYS_197	H, A_LYS_197	2.75	1.93	14.74
5VXJ.PDB	O, A_LYS_196	N, A_GLU_200	H, A_GLU_200	2.98	2.16	13.97
5VXJ.PDB	O, A_ALA_198	N, A_LEU_202	H, A_LEU_202	2.92	2.14	21.59
5VXJ.PDB	OD1, A_ASP_254	NZ, A_LYS_203	HZ2, A_LYS_203	2.48	1.62	10.37
5VXJ.PDB	O, A_GLU_201	N, A_LYS_205	H, A_LYS_205	2.84	2.05	19.85
5VXJ.PDB	OD2, A_ASP_166	NZ, A_LYS_205	HZ2, A_LYS_205	2.60	1.73	10.82
5VXJ.PDB	OD2, A_ASP_166	OH, A_TYR_206	HH, A_TYR_206	2.59	1.78	13.29
5VXJ.PDB	O, A_TYR_244	N, A_VAL_218	H, A_VAL_218	2.97	2.15	14.20
5VXJ.PDB	OG, A_SER_219	N, A_GLN_222	H, A_GLN_222	2.99	2.14	8.32
5VXJ.PDB	O, A_SER_219	N, A_ALA_223	H, A_ALA_223	2.98	2.15	10.83
5VXJ.PDB	O, A_GLN_220	N, A_ASN_224	H, A_ASN_224	2.96	2.18	20.88
5VXJ.PDB	O, A_ALA_223	N, A_LEU_227	H, A_LEU_227	2.92	2.16	24.23
5VXJ.PDB	O, A_TRP_226	N, A_LEU_230	H, A_LEU_230	2.82	1.96	5.43
5VXJ.PDB	O, A_LEU_227	N, A_GLY_231	H, A_GLY_231	2.79	1.94	7.11
5VXJ.PDB	O, A_VAL_245	N, A_SER_238	H, A_SER_238	2.93	2.14	18.31
5VXJ.PDB	O, A_SER_238	N, A_VAL_245	H, A_VAL_245	2.90	2.09	17.18
5VXJ.PDB	O, A_TYR_212	N, A_VAL_246	H, A_VAL_246	2.63	1.77	2.37
5VXJ.PDB	O, A_LYS_236	N, A_SER_247	H, A_SER_247	2.73	1.99	25.54
5VXJ.PDB	O, A_ILE_234	N, A_ASN_249	H, A_ASN_249	2.99	2.14	5.52
5VXJ.PDB	OD1, A_ASN_249	N, A_THR_251	H, A_THR_251	2.98	2.14	12.09
5VXJ.PDB	OD1, A_ASN_249	OG1, A_THR_251	HG1, A_THR_251	2.61	1.88	24.99
5VXJ.PDB	O, A_THR_251	N, A_ASN_255	H, A_ASN_255	2.72	1.90	15.38
5VXJ.PDB	O, A_PRO_252	N, A_MET_256	H, A_MET_256	2.93	2.09	10.06
5VXJ.PDB	O, A_ILE_253	N, A_LEU_257	H, A_LEU_257	2.89	2.11	21.11
5VXJ.PDB	O, A_ASP_254	N, A_LYS_258	H, A_LYS_258	2.89	2.05	10.53
5VXJ.PDB	O, A_ASN_255	N, A_SER_259	H, A_SER_259	2.85	2.05	18.21
5VXJ.PDB	O, A_MET_256	N, A_LEU_260	H, A_LEU_260	2.88	2.06	15.58
5VXJ.PDB	O, A_LEU_260	N, A_LEU_263	H, A_LEU_263	2.93	2.08	8.28
5VXJ.PDB	O, A_VAL_188	N, A_LEU_271	H, A_LEU_271	2.79	1.96	13.97
5VXJ.PDB	OD1, A_ASP_272	N, A_LYS_275	H, A_LYS_275	2.71	1.87	8.42
5VXJ.PDB	O, A_ASP_272	N, A_TYR_276	H, A_TYR_276	2.96	2.18	20.66
5VXJ.PDB	O, A_ASN_273	N, A_GLN_277	H, A_GLN_277	2.93	2.09	9.71
5VXJ.PDB	O, A_ALA_274	N, A_ALA_278	H, A_ALA_278	2.97	2.14	12.65
5VXJ.PDB	O, A_TYR_276	N, A_ASN_280	H, A_ASN_280	2.81	1.95	2.97
5VXJ.PDB	O, A_GLN_277	N, A_ALA_281	H, A_ALA_281	2.86	2.07	19.09
5VXJ.PDB	O, A_TRP_279	N, A_PHE_283	H, A_PHE_283	2.88	2.07	15.81
5VXJ.PDB	O, A_ASN_280	N, A_SER_284	H, A_SER_284	2.76	1.91	8.04
5VXJ.PDB	O, A_ASN_280	OG, A_SER_284	HG, A_SER_284	2.99	2.26	24.82
5VXJ.PDB	O, A_ALA_281	N, A_ALA_285	H, A_ALA_285	2.96	2.19	22.09
5VXJ.PDB	O, A_SER_284	N, A_GLU_288	H, A_GLU_288	2.97	2.15	15.81
5VXJ.PDB	O, A_ALA_285	N, A_THR_289	H, A_THR_289	2.87	2.12	24.45

5VXJ.PDB	O, A_ALA_285	OG1, A_THR_289	HG1, A_THR_289	2.86	2.03	7.57
5VXJ.PDB	O, A_ASP_287	N, A_LYS_291	H, A_LYS_291	2.93	2.09	9.56
5VXJ.PDB	O, A_GLU_288	N, A_ASN_292	H, A_ASN_292	2.87	2.05	14.52
5VXJ.PDB	O, A_THR_289	N, A_ASN_293	H, A_ASN_293	2.90	2.09	17.21
5VXJ.PDB	O, A_MET_290	N, A_LEU_294	H, A_LEU_294	2.92	2.07	7.82
5VXJ.PDB	O, A_LYS_291	N, A_GLN_295	H, A_GLN_295	2.99	2.14	9.97
5VXJ.PDB	O, A_ASN_292	N, A_THR_296	H, A_THR_296	2.84	2.08	24.09
5VXJ.PDB	O, A_LEU_294	N, A_VAL_298	H, A_VAL_298	2.91	2.08	13.79
5VXJ.PDB	O, A_LEU_297	N, A_TYR_301	H, A_TYR_301	2.90	2.05	7.11
5VXJ.PDB	O, A_VAL_298	N, A_SER_302	H, A_SER_302	2.79	1.95	9.28
5VXJ.PDB	O, A_GLN_299	N, A_ASN_303	H, A_ASN_303	2.74	1.90	10.18
5VXJ.PDB	O, A_LYS_300	N, A_ALA_304	H, A_ALA_304	2.86	2.05	16.63
5VXJ.PDB	O, A_TYR_301	N, A_ASN_305	H, A_ASN_305	2.97	2.18	19.72
5VXJ.PDB	OD1, A_ASN_58	ND2, A_ASN_305	HD21, A_ASN_305	2.96	2.14	16.38
5VXJ.PDB	O, A_ALA_304	N, A_PHE_308	H, A_PHE_308	2.88	2.04	10.22
5VXJ.PDB	O, A_ASN_305	N, A_ASP_309	H, A_ASP_309	2.74	1.94	18.74
5VXJ.PDB	O, A_SER_306	N, A_ASN_310	H, A_ASN_310	2.77	1.99	20.96
5VXJ.PDB	O, A_ASP_309	N, A_LYS_313	H, A_LYS_313	2.88	2.04	10.21
5VXJ.PDB	O, A_ASN_310	N, A_VAL_314	H, A_VAL_314	2.93	2.11	13.42
5VXJ.PDB	O, A_LEU_311	N, A_LEU_315	H, A_LEU_315	2.74	1.89	8.56
5VXJ.PDB	O, A_VAL_312	N, A_SER_316	H, A_SER_316	2.85	2.04	14.90
5VXJ.PDB	O, A_VAL_314	OG1, A_THR_318	HG1, A_THR_318	2.99	2.16	6.68
5VXJ.PDB	O, A_LEU_315	N, A_ILE_319	H, A_ILE_319	2.97	2.18	20.05
5VXJ.PDB	O, A_SER_316	N, A_SER_320	H, A_SER_320	3.00	2.17	14.20
5VXJ.PDB	O, A_THR_318	OG, A_SER_322	HG, A_SER_322	2.97	2.21	21.62
5VXJ.PDB	O, B_SER_25	N, B_GLN_3	H, B_GLN_3	2.86	2.03	13.37
5VXJ.PDB	O, B_ALA_23	N, B_ALA_5	H, B_ALA_5	2.95	2.16	20.65
5VXJ.PDB	O, B_GLN_114	N, B_GLY_10	H, B_GLY_10	2.78	1.93	4.26
5VXJ.PDB	O, B_THR_116	N, B_ALA_12	H, B_ALA_12	2.97	2.27	29.86
5VXJ.PDB	O, B_LEU_86	N, B_GLY_15	H, B_GLY_15	2.80	1.97	12.25
5VXJ.PDB	O, B_GLN_13	N, B_GLY_16	H, B_GLY_16	2.89	2.07	14.89
5VXJ.PDB	O, B_MET_83	N, B_LEU_18	H, B_LEU_18	2.81	2.01	18.59
5VXJ.PDB	OE1, B_GLN_82	NE, B_ARG_19	HE, B_ARG_19	2.47	1.66	15.76
5VXJ.PDB	O, B_THR_7	N, B_SER_21	H, B_SER_21	2.89	2.13	23.79
5VXJ.PDB	O, B_VAL_79	N, B_CYS_22	H, B_CYS_22	2.97	2.22	24.17
5VXJ.PDB	O, B_ALA_5	N, B_ALA_23	H, B_ALA_23	2.85	2.01	10.80
5VXJ.PDB	O, B_ASN_77	N, B_ALA_24	H, B_ALA_24	2.89	2.04	8.57
5VXJ.PDB	O, B_THR_28	N, B_ARG_31	H, B_ARG_31	2.95	2.13	14.81
5VXJ.PDB	O, B_GLY_99	N, B_VAL_33	H, B_VAL_33	2.85	2.06	20.75
5VXJ.PDB	O, B_ASN_97	N, B_ASN_35	H, B_ASN_35	2.73	1.92	16.35
5VXJ.PDB	O, B_VAL_95	N, B_TYR_37	H, B_TYR_37	2.74	1.89	6.02
5VXJ.PDB	OE2, B_GLU_46	NE, B_ARG_38	HE, B_ARG_38	2.93	2.12	17.64
5VXJ.PDB	OH, B_TYR_94	NH1, B_ARG_38	HH11, B_ARG_38	2.80	1.98	13.19
5VXJ.PDB	OD1, B_ASP_90	NH1, B_ARG_38	HH12, B_ARG_38	2.76	1.91	7.08
5VXJ.PDB	O, B_ARG_38	N, B_GLU_46	H, B_GLU_46	2.92	2.08	10.18
5VXJ.PDB	O, B_TRP_36	N, B_VAL_48	H, B_VAL_48	2.83	2.04	19.58
5VXJ.PDB	OD1, B_ASN_35	NE, B_ARG_50	HE, B_ARG_50	2.65	1.82	11.22
5VXJ.PDB	OE1, I_GLU_200	NH1, B_ARG_50	HH12, B_ARG_50	2.92	2.07	7.25
5VXJ.PDB	O, B_SER_30	OH, B_TYR_52	HH, B_TYR_52	2.72	1.93	15.55
5VXJ.PDB	OD1, B_ASP_53	N, B_GLY_55	H, B_GLY_55	2.72	1.91	16.35
5VXJ.PDB	O, B_ARG_50	N, B_SER_59	H, B_SER_59	2.55	1.72	12.05
5VXJ.PDB	O, B_VAL_48	N, B_ALA_61	H, B_ALA_61	2.78	1.92	5.65
5VXJ.PDB	OD2, B_ASP_90	NH1, B_ARG_67	HH12, B_ARG_67	2.82	2.01	16.67
5VXJ.PDB	OD1, B_ASP_90	NH2, B_ARG_67	HH22, B_ARG_67	2.96	2.12	11.06
5VXJ.PDB	O, B_VAL_64	N, B_PHE_68	H, B_PHE_68	2.90	2.06	11.49
5VXJ.PDB	O, B_GLN_82	N, B_THR_69	H, B_THR_69	2.99	2.19	17.88
5VXJ.PDB	O, B_HIS_80	N, B_SER_71	H, B_SER_71	2.98	2.19	19.14
5VXJ.PDB	O, B_ALA_32	NH2, B_ARG_72	HH22, B_ARG_72	2.73	1.87	6.16

5VXJ.PDB	O, B_THR_78	N, B_ASP_73	H, B_ASP_73	2.88	2.03	8.84
5VXJ.PDB	O, B_SER_71	N, B_HIS_80	H, B_HIS_80	2.94	2.16	21.65
5VXJ.PDB	O, B_LEU_20	N, B_LEU_81	H, B_LEU_81	2.93	2.12	17.56
5VXJ.PDB	O, B_THR_69	N, B_GLN_82	H, B_GLN_82	2.77	2.03	25.51
5VXJ.PDB	OD1, B_ASN_84	NE2, B_GLN_82	HE21, B_GLN_82	2.95	2.09	2.81
5VXJ.PDB	O, B_LEU_18	N, B_MET_83	H, B_MET_83	2.63	1.77	6.35
5VXJ.PDB	O, B_LYS_87	N, B_ASP_90	H, B_ASP_90	2.82	2.01	16.00
5VXJ.PDB	O, B_THR_113	N, B_TYR_94	H, B_TYR_94	2.87	2.08	19.12
5VXJ.PDB	O, B_ASP_90	OH, B_TYR_94	HH, B_TYR_94	2.68	1.86	10.06
5VXJ.PDB	O, B_TYR_37	N, B_VAL_95	H, B_VAL_95	3.00	2.17	13.97
5VXJ.PDB	O, B_ASN_35	N, B_ASN_97	H, B_ASN_97	2.80	2.07	26.52
5VXJ.PDB	OG1, B_THR_107	ND2, B_ASN_97	HD21, B_ASN_97	2.64	1.86	19.39
5VXJ.PDB	O, B_VAL_33	N, B_GLY_99	H, B_GLY_99	2.75	1.91	8.60
5VXJ.PDB	O, B_ARG_106	N, B_ILE_100	H, B_ILE_100	2.81	1.95	1.78
5VXJ.PDB	O, B_ASN_104	N, B_ASP_102	H, B_ASP_102	2.92	2.07	4.41
5VXJ.PDB	OE1, I_GLU_201	OH, B_TYR_105	HH, B_TYR_105	2.51	1.70	12.69
5VXJ.PDB	O, B_ALA_98	OG1, B_THR_107	HG1, B_THR_107	2.89	2.18	28.04
5VXJ.PDB	OE1, B_GLU_6	N, B_GLY_112	H, B_GLY_112	2.87	2.05	14.11
5VXJ.PDB	O, B_TYR_94	N, B_THR_113	H, B_THR_113	2.58	1.76	13.84
5VXJ.PDB	O, B_GLY_10	N, B_THR_116	H, B_THR_116	2.97	2.14	11.68
5VXJ.PDB	O, C_THR_45	N, C_ASP_49	H, C_ASP_49	3.00	2.16	11.23
5VXJ.PDB	O, C_MET_46	N, C_THR_50	H, C_THR_50	2.75	1.93	15.42
5VXJ.PDB	O, C_MET_46	OG1, C_THR_50	HG1, C_THR_50	2.84	2.05	16.87
5VXJ.PDB	O, C_LEU_47	N, C_LEU_51	H, C_LEU_51	2.66	1.82	9.17
5VXJ.PDB	OD2, C_ASP_309	NH2, C_ARG_55	HH21, C_ARG_55	2.97	2.17	18.00
5VXJ.PDB	O, C_HIS_52	N, C_THR_56	H, C_THR_56	2.83	2.00	14.10
5VXJ.PDB	O, C_ASN_53	N, C_THR_57	H, C_THR_57	2.88	2.05	12.91
5VXJ.PDB	O, C_ILE_54	N, C_ASN_58	H, C_ASN_58	2.78	2.03	23.87
5VXJ.PDB	O, C_THR_57	N, C_LEU_61	H, C_LEU_61	2.97	2.16	17.22
5VXJ.PDB	O, C_ASN_58	N, C_LYS_62	H, C_LYS_62	2.91	2.07	10.71
5VXJ.PDB	OG, C_SER_302	NZ, C_LYS_62	HZ2, C_LYS_62	2.61	1.73	6.54
5VXJ.PDB	O, C_THR_73	N, C_GLU_77	H, C_GLU_77	2.89	2.05	10.72
5VXJ.PDB	O, C_SER_74	N, C_ILE_78	H, C_ILE_78	2.75	1.91	9.49
5VXJ.PDB	O, C_LEU_75	N, C_ALA_79	H, C_ALA_79	2.88	2.03	7.76
5VXJ.PDB	O, C_GLU_76	N, C_LEU_80	H, C_LEU_80	2.83	1.99	11.70
5VXJ.PDB	O, C_GLU_77	N, C_HIS_81	H, C_HIS_81	2.88	2.03	8.46
5VXJ.PDB	O, C_ILE_78	N, C_SER_82	H, C_SER_82	2.83	2.00	12.85
5VXJ.PDB	OE2, C_GLU_154	OG, C_SER_82	HG, C_SER_82	2.58	1.81	19.25
5VXJ.PDB	O, C_ALA_79	N, C_SER_83	H, C_SER_83	2.82	1.99	12.64
5VXJ.PDB	O, C_HIS_81	N, C_ILE_85	H, C_ILE_85	2.92	2.10	14.49
5VXJ.PDB	O, C_SER_82	N, C_SER_86	H, C_SER_86	2.94	2.09	6.22
5VXJ.PDB	O, C_SER_83	N, C_MET_87	H, C_MET_87	2.90	2.13	22.48
5VXJ.PDB	O, C_ILE_85	N, C_VAL_89	H, C_VAL_89	2.71	1.95	23.99
5VXJ.PDB	O, C_SER_86	N, C_ASN_90	H, C_ASN_90	2.95	2.14	17.73
5VXJ.PDB	O, C_ASP_88	OG, C_SER_92	HG, C_SER_92	2.81	2.10	26.84
5VXJ.PDB	O, C_VAL_89	N, C_ALA_93	H, C_ALA_93	2.99	2.18	16.35
5VXJ.PDB	O, C_ASN_90	N, C_GLN_94	H, C_GLN_94	2.93	2.09	10.71
5VXJ.PDB	O, C_LYS_91	N, C_LEU_95	H, C_LEU_95	2.99	2.16	11.86
5VXJ.PDB	O, C_SER_92	N, C_LEU_96	H, C_LEU_96	2.76	1.91	4.52
5VXJ.PDB	O, C_ALA_93	N, C_ASP_97	H, C_ASP_97	2.67	1.87	17.34
5VXJ.PDB	O, C_GLN_94	N, C_ILE_98	H, C_ILE_98	2.93	2.20	27.48
5VXJ.PDB	O, C_LEU_95	N, C_LEU_99	H, C_LEU_99	2.86	2.06	16.81
5VXJ.PDB	O, C_LEU_96	N, C_SER_100	H, C_SER_100	2.97	2.19	20.79
5VXJ.PDB	O, C_ARG_132	OG, C_SER_100	HG, C_SER_100	2.62	1.83	15.07
5VXJ.PDB	OD2, C_ASP_97	NE, C_ARG_101	HE, C_ARG_101	2.84	2.03	16.71
5VXJ.PDB	O, C_ILE_98	N, C_ASN_102	H, C_ASN_102	2.93	2.10	11.46
5VXJ.PDB	OD1, C_ASN_107	N, C_ALA_110	H, C_ALA_110	2.74	1.90	11.07
5VXJ.PDB	O, C_ILE_106	NE, C_ARG_111	HE, C_ARG_111	2.84	2.08	23.05

5VXJ.PDB	O, C_ILE_129	NH1, C_ARG_111	HH12, C_ARG_111	2.70	1.99	28.89
5VXJ.PDB	O, C_ILE_129	NH2, C_ARG_111	HH22, C_ARG_111	2.67	1.95	27.54
5VXJ.PDB	O, C_LEU_113	N, C_SER_116	H, C_SER_116	2.74	1.92	13.94
5VXJ.PDB	O, C_PRO_118	N, C_ALA_121	H, C_ALA_121	2.93	2.09	9.05
5VXJ.PDB	O, C_LYS_119	N, C_GLU_122	H, C_GLU_122	2.93	2.12	17.73
5VXJ.PDB	O, D_GLY_56	NH2, C_ARG_132	HH22, C_ARG_132	2.97	2.20	22.55
5VXJ.PDB	O, C_SER_130	N, C_LEU_134	H, C_LEU_134	2.95	2.18	22.13
5VXJ.PDB	O, C_HIS_131	N, C_TRP_135	H, C_TRP_135	2.90	2.05	5.85
5VXJ.PDB	O, C_TYR_104	NE1, C_TRP_135	HE1, C_TRP_135	2.72	1.92	17.01
5VXJ.PDB	O, C_TRP_135	N, C_ALA_139	H, C_ALA_139	2.83	1.99	9.11
5VXJ.PDB	O, C_ALA_136	N, C_ASN_140	H, C_ASN_140	2.88	2.08	18.03
5VXJ.PDB	O, C_LYS_137	N, C_SER_141	H, C_SER_141	2.84	2.09	25.00
5VXJ.PDB	O, C_ALA_121	OG, C_SER_141	HG, C_SER_141	2.69	1.99	27.96
5VXJ.PDB	O, C_ASN_140	N, C_ASP_144	H, C_ASP_144	2.68	1.84	11.11
5VXJ.PDB	O, C_SER_141	N, C_ILE_145	H, C_ILE_145	2.98	2.16	13.90
5VXJ.PDB	O, C_ASP_144	N, C_GLN_148	H, C_GLN_148	2.81	1.97	10.25
5VXJ.PDB	O, C_ILE_145	N, C_LEU_150	H, C_LEU_150	2.99	2.16	11.96
5VXJ.PDB	O, C_ASN_146	N, C_LYS_151	H, C_LYS_151	2.89	2.07	15.50
5VXJ.PDB	O, C_TYR_153	N, C_VAL_157	H, C_VAL_157	2.98	2.14	11.48
5VXJ.PDB	O, C_GLU_154	N, C_SER_158	H, C_SER_158	2.91	2.10	16.58
5VXJ.PDB	O, C_HIS_155	N, C_SER_159	H, C_SER_159	2.84	2.04	18.93
5VXJ.PDB	O, C_VAL_157	N, C_THR_161	H, C_THR_161	2.84	2.01	12.19
5VXJ.PDB	O, C_TYR_160	N, C_TYR_164	H, C_TYR_164	2.88	2.06	13.58
5VXJ.PDB	OD1, C_ASP_287	OH, C_TYR_164	HH, C_TYR_164	2.77	1.96	12.03
5VXJ.PDB	O, C_THR_161	N, C_GLN_165	H, C_GLN_165	2.79	1.97	15.66
5VXJ.PDB	O, C_TYR_164	N, C_SER_168	H, C_SER_168	2.76	1.95	16.85
5VXJ.PDB	O, C_TYR_164	OG, C_SER_168	HG, C_SER_168	2.78	1.96	10.71
5VXJ.PDB	O, C_PHE_167	N, C_LEU_171	H, C_LEU_171	2.81	2.03	19.93
5VXJ.PDB	O, C_SER_168	N, C_SER_172	H, C_SER_172	2.88	2.13	25.56
5VXJ.PDB	O, C_LEU_271	N, C_VAL_188	H, C_VAL_188	2.99	2.14	7.19
5VXJ.PDB	O, C_SER_179	N, C_LYS_189	H, C_LYS_189	2.75	1.90	6.70
5VXJ.PDB	O, C_VAL_269	N, C_LEU_190	H, C_LEU_190	2.85	2.06	18.77
5VXJ.PDB	O, C_TRP_177	N, C_GLN_191	H, C_GLN_191	2.92	2.10	14.50
5VXJ.PDB	OE2, C_GLU_268	NE2, C_GLN_191	HE22, C_GLN_191	2.80	1.97	12.09
5VXJ.PDB	O, C_VAL_192	N, C_LYS_196	H, C_LYS_196	2.64	1.80	8.82
5VXJ.PDB	O, C_ASN_193	N, C_LYS_197	H, C_LYS_197	2.77	1.95	14.40
5VXJ.PDB	OE1, C_GLU_201	NZ, C_LYS_197	HZ3, C_LYS_197	2.59	1.85	27.46
5VXJ.PDB	O, C_LYS_196	N, C_GLU_200	H, C_GLU_200	2.98	2.14	10.98
5VXJ.PDB	O, C_ALA_198	N, C_LEU_202	H, C_LEU_202	2.84	2.10	25.29
5VXJ.PDB	OD1, C_ASP_254	NZ, C_LYS_203	HZ2, C_LYS_203	2.69	1.87	19.49
5VXJ.PDB	O, C_GLU_201	N, C_LYS_205	H, C_LYS_205	2.93	2.15	21.77
5VXJ.PDB	OD2, C_ASP_166	NZ, C_LYS_205	HZ2, C_LYS_205	2.85	1.99	12.15
5VXJ.PDB	OD2, C_ASP_166	OH, C_TYR_206	HH, C_TYR_206	2.58	1.76	10.37
5VXJ.PDB	O, C_TYR_244	N, C_VAL_218	H, C_VAL_218	2.89	2.05	9.55
5VXJ.PDB	O, C_SER_219	N, C_ALA_223	H, C_ALA_223	2.91	2.08	14.53
5VXJ.PDB	O, C_GLN_220	N, C_ASN_224	H, C_ASN_224	2.98	2.12	5.55
5VXJ.PDB	O, C_GLN_220	ND2, C_ASN_224	HD22, C_ASN_224	2.76	2.00	23.07
5VXJ.PDB	O, C_GLU_221	N, C_LYS_225	H, C_LYS_225	2.88	2.10	20.87
5VXJ.PDB	O, C_ALA_223	N, C_LEU_227	H, C_LEU_227	2.84	2.04	17.85
5VXJ.PDB	O, C_TRP_226	N, C_LEU_230	H, C_LEU_230	2.93	2.16	22.32
5VXJ.PDB	O, C_LEU_227	N, C_GLY_231	H, C_GLY_231	2.79	1.97	15.24
5VXJ.PDB	O, C_SER_247	N, C_LYS_236	H, C_LYS_236	2.90	2.15	23.83
5VXJ.PDB	O, C_VAL_245	N, C_SER_238	H, C_SER_238	2.96	2.16	18.06
5VXJ.PDB	O, C_SER_238	N, C_VAL_245	H, C_VAL_245	2.79	1.99	18.55
5VXJ.PDB	O, C_TYR_212	N, C_VAL_246	H, C_VAL_246	2.73	1.88	6.99
5VXJ.PDB	O, C_ILE_234	N, C_ASN_249	H, C_ASN_249	2.93	2.08	8.15
5VXJ.PDB	OD1, C_ASN_249	N, C_THR_251	H, C_THR_251	2.83	2.01	13.51
5VXJ.PDB	OD1, C_ASN_249	OG1, C_THR_251	HG1, C_THR_251	2.56	1.78	18.84

5VXJ.PDB	O, C_MET_250	N, C_ASP_254	H, C_ASP_254	2.97	2.14	14.27
5VXJ.PDB	O, C_THR_251	N, C_ASN_255	H, C_ASN_255	2.90	2.11	19.57
5VXJ.PDB	O, C_ASN_255	N, C_SER_259	H, C_SER_259	2.82	1.98	10.57
5VXJ.PDB	O, C_LEU_257	N, C_ASP_261	H, C_ASP_261	2.89	2.05	9.73
5VXJ.PDB	O, C_VAL_188	N, C_LEU_271	H, C_LEU_271	2.72	1.88	10.23
5VXJ.PDB	OD1, C_ASP_272	N, C_LYS_275	H, C_LYS_275	2.76	1.96	18.08
5VXJ.PDB	O, C_ASP_272	N, C_TYR_276	H, C_TYR_276	2.98	2.15	12.87
5VXJ.PDB	O, C_ASN_273	N, C_GLN_277	H, C_GLN_277	2.97	2.12	5.77
5VXJ.PDB	O, C_LYS_275	N, C_TRP_279	H, C_TRP_279	3.00	2.19	17.09
5VXJ.PDB	O, C_TYR_276	N, C_ASN_280	H, C_ASN_280	2.84	2.00	8.68
5VXJ.PDB	O, C_GLN_277	N, C_ALA_281	H, C_ALA_281	2.95	2.16	19.58
5VXJ.PDB	O, C_TRP_279	N, C_PHE_283	H, C_PHE_283	2.80	1.97	11.54
5VXJ.PDB	O, C_ASN_280	N, C_SER_284	H, C_SER_284	2.86	2.05	17.29
5VXJ.PDB	O, C_ALA_281	N, C_ALA_285	H, C_ALA_285	2.97	2.22	25.52
5VXJ.PDB	O, C_SER_284	N, C_GLU_288	H, C_GLU_288	2.90	2.09	16.06
5VXJ.PDB	O, C_ASP_287	N, C_LYS_291	H, C_LYS_291	2.96	2.16	17.42
5VXJ.PDB	O, C_GLU_288	N, C_ASN_292	H, C_ASN_292	2.78	1.93	7.30
5VXJ.PDB	O, C_MET_290	N, C_LEU_294	H, C_LEU_294	2.96	2.14	14.65
5VXJ.PDB	O, C_LYS_291	N, C_GLN_295	H, C_GLN_295	2.93	2.08	7.49
5VXJ.PDB	O, C_ASN_292	N, C_THR_296	H, C_THR_296	2.81	1.96	6.25
5VXJ.PDB	O, C_ASN_293	N, C_LEU_297	H, C_LEU_297	2.87	2.03	9.84
5VXJ.PDB	O, C_LEU_294	N, C_VAL_298	H, C_VAL_298	2.89	2.07	16.24
5VXJ.PDB	O, C_GLN_295	N, C_GLN_299	H, C_GLN_299	2.96	2.18	20.39
5VXJ.PDB	O, C_THR_296	N, C_LYS_300	H, C_LYS_300	2.95	2.12	12.60
5VXJ.PDB	O, C_VAL_298	N, C_SER_302	H, C_SER_302	2.91	2.17	26.05
5VXJ.PDB	O, C_GLN_299	N, C_ASN_303	H, C_ASN_303	2.83	2.01	12.96
5VXJ.PDB	O, C_LYS_300	N, C_ALA_304	H, C_ALA_304	2.95	2.16	19.44
5VXJ.PDB	OD1, C_ASN_58	ND2, C_ASN_305	HD21, C_ASN_305	2.84	2.04	17.79
5VXJ.PDB	O, C_ALA_304	N, C_PHE_308	H, C_PHE_308	2.91	2.07	9.64
5VXJ.PDB	O, C_ASN_305	N, C_ASP_309	H, C_ASP_309	2.81	2.07	26.01
5VXJ.PDB	O, C_SER_306	N, C_ASN_310	H, C_ASN_310	2.67	1.91	23.54
5VXJ.PDB	O, C_ASP_309	N, C_LYS_313	H, C_LYS_313	2.90	2.07	12.85
5VXJ.PDB	O, C_ASN_310	N, C_VAL_314	H, C_VAL_314	2.90	2.06	10.88
5VXJ.PDB	O, C_LEU_311	N, C_LEU_315	H, C_LEU_315	2.75	1.90	6.64
5VXJ.PDB	O, C_VAL_312	N, C_SER_316	H, C_SER_316	2.93	2.11	14.92
5VXJ.PDB	O, C_VAL_314	OG, C_SER_317	HG, C_SER_317	2.65	1.90	22.58
5VXJ.PDB	O, C_LEU_315	OG1, C_THR_318	HG1, C_THR_318	2.63	1.83	14.36
5VXJ.PDB	O, D_SER_25	N, D_GLN_3	H, D_GLN_3	2.83	2.04	19.53
5VXJ.PDB	O, D_ALA_23	N, D_ALA_5	H, D_ALA_5	2.92	2.12	17.92
5VXJ.PDB	O, D_SER_21	N, D_THR_7	H, D_THR_7	2.92	2.12	17.84
5VXJ.PDB	O, D_GLN_114	N, D_GLY_10	H, D_GLY_10	2.92	2.10	13.53
5VXJ.PDB	O, D_THR_116	N, D_ALA_12	H, D_ALA_12	2.90	2.14	23.36
5VXJ.PDB	O, D_LEU_86	N, D_GLY_15	H, D_GLY_15	2.64	1.81	11.28
5VXJ.PDB	O, D_GLN_13	N, D_GLY_16	H, D_GLY_16	2.82	2.06	23.83
5VXJ.PDB	O, D_MET_83	N, D_LEU_18	H, D_LEU_18	2.89	2.09	18.27
5VXJ.PDB	OD1, C_ASN_140	NE, D_ARG_19	HE, D_ARG_19	2.55	1.80	23.66
5VXJ.PDB	OE1, D_GLN_82	NH1, D_ARG_19	HH11, D_ARG_19	2.94	2.14	18.04
5VXJ.PDB	O, D_THR_7	N, D_SER_21	H, D_SER_21	2.99	2.14	7.08
5VXJ.PDB	O, D_ALA_5	N, D_ALA_23	H, D_ALA_23	2.87	2.03	10.49
5VXJ.PDB	O, D_ASN_77	N, D_ALA_24	H, D_ALA_24	2.92	2.08	9.76
5VXJ.PDB	O, D_THR_28	N, D_ARG_31	H, D_ARG_31	2.98	2.15	11.20
5VXJ.PDB	O, D_GLY_99	N, D_VAL_33	H, D_VAL_33	2.95	2.15	17.67
5VXJ.PDB	O, D_ASN_97	N, D_ASN_35	H, D_ASN_35	2.69	1.87	14.00
5VXJ.PDB	O, D_VAL_95	N, D_TYR_37	H, D_TYR_37	2.62	1.77	8.93
5VXJ.PDB	O, D_GLU_46	N, D_ARG_38	H, D_ARG_38	2.97	2.17	18.09
5VXJ.PDB	OE2, D_GLU_46	NE, D_ARG_38	HE, D_ARG_38	2.46	1.69	20.96
5VXJ.PDB	OD1, D_ASP_90	NH1, D_ARG_38	HH12, D_ARG_38	2.86	2.04	15.32
5VXJ.PDB	O, D_ARG_38	N, D_GLU_46	H, D_GLU_46	2.89	2.05	10.29

5VXJ.PDB	O, D_TRP_36	N, D_VAL_48	H, D_VAL_48	2.77	1.94	12.94
5VXJ.PDB	OD1, D_ASN_35	NE, D_ARG_50	HE, D_ARG_50	2.89	2.08	17.01
5VXJ.PDB	O, D_SER_30	OH, D_TYR_52	HH, D_TYR_52	2.65	1.82	6.70
5VXJ.PDB	OD1, D_ASP_53	N, D_GLY_55	H, D_GLY_55	2.89	2.10	19.66
5VXJ.PDB	O, D_ASP_53	N, D_GLY_56	H, D_GLY_56	2.97	2.13	9.23
5VXJ.PDB	O, D_ARG_50	N, D_SER_59	H, D_SER_59	2.64	1.81	11.93
5VXJ.PDB	O, D_VAL_48	N, D_ALA_61	H, D_ALA_61	2.74	1.98	23.42
5VXJ.PDB	OD2, D_ASP_90	NH1, D_ARG_67	HH12, D_ARG_67	2.76	1.94	14.49
5VXJ.PDB	OD1, D_ASP_90	NH2, D_ARG_67	HH22, D_ARG_67	2.92	2.07	6.62
5VXJ.PDB	O, D_VAL_64	N, D_PHE_68	H, D_PHE_68	2.99	2.19	16.85
5VXJ.PDB	O, D_GLN_82	N, D_THR_69	H, D_THR_69	2.99	2.18	16.88
5VXJ.PDB	O, D_HIS_80	N, D_SER_71	H, D_SER_71	2.95	2.13	13.86
5VXJ.PDB	OD1, D_ASN_74	NE, D_ARG_72	HE, D_ARG_72	2.76	1.91	6.10
5VXJ.PDB	O, D_THR_78	N, D_ASP_73	H, D_ASP_73	2.97	2.14	12.70
5VXJ.PDB	OD1, D_ASP_73	N, D_LYS_76	H, D_LYS_76	2.99	2.16	13.54
5VXJ.PDB	O, D_LEU_20	N, D_LEU_81	H, D_LEU_81	2.96	2.19	22.26
5VXJ.PDB	OD1, D_ASN_84	NE2, D_GLN_82	HE21, D_GLN_82	2.80	1.94	4.20
5VXJ.PDB	O, D_LEU_18	N, D_MET_83	H, D_MET_83	2.68	1.83	7.86
5VXJ.PDB	O, D_ARG_67	N, D_ASN_84	H, D_ASN_84	2.94	2.13	15.75
5VXJ.PDB	O, D_LYS_87	N, D_ASP_90	H, D_ASP_90	2.78	1.93	7.73
5VXJ.PDB	O, D_VAL_115	N, D_ALA_92	H, D_ALA_92	2.97	2.20	22.44
5VXJ.PDB	O, D_THR_113	N, D_TYR_94	H, D_TYR_94	2.96	2.15	16.57
5VXJ.PDB	O, D_ASP_90	OH, D_TYR_94	HH, D_TYR_94	2.94	2.12	10.43
5VXJ.PDB	O, D_TYR_37	N, D_VAL_95	H, D_VAL_95	2.83	2.02	15.84
5VXJ.PDB	O, D_ASN_35	N, D_ASN_97	H, D_ASN_97	2.86	2.07	19.41
5VXJ.PDB	OG1, D_THR_107	ND2, D_ASN_97	HD21, D_ASN_97	2.71	1.91	17.78
5VXJ.PDB	O, D_VAL_33	N, D_GLY_99	H, D_GLY_99	2.78	1.95	12.57
5VXJ.PDB	O, D_ARG_106	N, D_ILE_100	H, D_ILE_100	2.91	2.05	5.49
5VXJ.PDB	O, D_ARG_31	N, D_PHE_101	H, D_PHE_101	2.74	1.90	10.09
5VXJ.PDB	OE1, E_GLU_201	OH, D_TYR_105	HH, D_TYR_105	2.53	1.70	8.84
5VXJ.PDB	O, D_ALA_98	OG1, D_THR_107	HG1, D_THR_107	2.97	2.23	23.46
5VXJ.PDB	O, D_TYR_94	N, D_THR_113	H, D_THR_113	2.79	1.97	15.52
5VXJ.PDB	O, D_GLY_8	OG1, D_THR_113	HG1, D_THR_113	2.58	1.83	22.66
5VXJ.PDB	O, D_ALA_92	N, D_VAL_115	H, D_VAL_115	2.94	2.08	3.33
5VXJ.PDB	O, D_ALA_12	N, D_SER_118	H, D_SER_118	2.88	2.09	19.39
5VXJ.PDB	O, E_SER_42	OG1, E_THR_45	HG1, E_THR_45	2.81	2.08	25.17
5VXJ.PDB	O, E_SER_43	N, E_LEU_47	H, E_LEU_47	2.99	2.22	22.05
5VXJ.PDB	O, E_LEU_44	N, E_ASN_48	H, E_ASN_48	2.99	2.18	16.94
5VXJ.PDB	O, E_LEU_47	N, E_LEU_51	H, E_LEU_51	2.95	2.10	6.68
5VXJ.PDB	O, E_ASP_49	N, E_ASN_53	H, E_ASN_53	2.84	2.02	14.73
5VXJ.PDB	O, E_THR_50	N, E_ILE_54	H, E_ILE_54	2.90	2.13	22.19
5VXJ.PDB	OD2, E_ASP_309	NH2, E_ARG_55	HH21, E_ARG_55	2.82	2.06	24.28
5VXJ.PDB	O, E_HIS_52	N, E_THR_56	H, E_THR_56	2.95	2.14	17.58
5VXJ.PDB	O, E_ILE_54	N, E_ASN_58	H, E_ASN_58	2.86	2.04	14.78
5VXJ.PDB	O, E_THR_57	N, E_LEU_61	H, E_LEU_61	2.88	2.07	15.00
5VXJ.PDB	O, E_ASN_58	N, E_LYS_62	H, E_LYS_62	2.72	1.87	6.56
5VXJ.PDB	OG, E_SER_306	NZ, E_LYS_62	HZ1, E_LYS_62	2.46	1.61	13.80
5VXJ.PDB	O, E_GLN_59	N, E_LYS_63	H, E_LYS_63	2.92	2.13	20.33
5VXJ.PDB	OG, E_SER_74	N, E_THR_71	H, E_THR_71	2.92	2.17	24.42
5VXJ.PDB	O, E_THR_73	N, E_GLU_77	H, E_GLU_77	2.99	2.15	11.35
5VXJ.PDB	O, E_LEU_75	N, E_ALA_79	H, E_ALA_79	2.96	2.12	10.44
5VXJ.PDB	O, E_GLU_76	N, E_LEU_80	H, E_LEU_80	2.99	2.17	14.62
5VXJ.PDB	O, E_GLU_77	N, E_HIS_81	H, E_HIS_81	2.87	2.01	3.03
5VXJ.PDB	O, E_ILE_78	N, E_SER_82	H, E_SER_82	2.71	1.88	13.72
5VXJ.PDB	O, E_ALA_79	N, E_SER_83	H, E_SER_83	2.74	1.90	10.07
5VXJ.PDB	O, E_LEU_80	N, E_GLN_84	H, E_GLN_84	2.86	2.13	27.19
5VXJ.PDB	O, E_HIS_81	N, E_ILE_85	H, E_ILE_85	2.94	2.14	18.50
5VXJ.PDB	O, E_ILE_85	N, E_VAL_89	H, E_VAL_89	2.68	1.84	9.90

5VXJ.PDB	O, E_SER_86	N, E_ASN_90	H, E_ASN_90	2.92	2.12	17.55
5VXJ.PDB	O, E_ASP_88	N, E_SER_92	H, E_SER_92	2.75	1.92	13.99
5VXJ.PDB	O, E_VAL_89	N, E_ALA_93	H, E_ALA_93	2.83	2.00	12.43
5VXJ.PDB	O, E_ASN_90	N, E_GLN_94	H, E_GLN_94	2.83	2.00	12.46
5VXJ.PDB	O, E_LYS_91	N, E_LEU_95	H, E_LEU_95	2.99	2.16	12.05
5VXJ.PDB	O, E_SER_92	N, E_LEU_96	H, E_LEU_96	2.76	1.90	1.16
5VXJ.PDB	O, E_ALA_93	N, E_ASP_97	H, E_ASP_97	2.76	2.00	23.32
5VXJ.PDB	O, E_ARG_132	OG, E_SER_100	HG, E_SER_100	2.69	1.91	17.95
5VXJ.PDB	O, E_ILE_98	N, E_ASN_102	H, E_ASN_102	2.86	2.01	8.88
5VXJ.PDB	O, E_SER_100	N, E_GLU_103	H, E_GLU_103	2.97	2.19	21.11
5VXJ.PDB	O, E_LEU_99	N, E_TYR_104	H, E_TYR_104	2.98	2.17	15.50
5VXJ.PDB	OD1, E_ASN_107	N, E_ALA_110	H, E_ALA_110	2.69	1.84	7.11
5VXJ.PDB	O, E_ILE_106	NE, E_ARG_111	HE, E_ARG_111	2.78	2.02	23.50
5VXJ.PDB	O, E_LEU_113	OG, E_SER_116	HG, E_SER_116	2.58	1.78	13.78
5VXJ.PDB	O, E_LEU_114	N, E_ALA_117	H, E_ALA_117	2.86	2.02	11.54
5VXJ.PDB	O, E_PRO_118	N, E_ALA_121	H, E_ALA_121	2.98	2.15	11.22
5VXJ.PDB	O, E_LYS_119	N, E_GLU_122	H, E_GLU_122	2.92	2.14	21.73
5VXJ.PDB	O, E_TYR_104	NE1, E_TRP_135	HE1, E_TRP_135	2.71	1.94	22.95
5VXJ.PDB	O, E_GLU_133	N, E_LYS_137	H, E_LYS_137	2.86	2.07	19.63
5VXJ.PDB	OD2, F_ASP_73	NZ, E_LYS_137	HZ2, E_LYS_137	2.77	1.96	20.15
5VXJ.PDB	O, E_LEU_134	N, E_ILE_138	H, E_ILE_138	2.98	2.17	17.01
5VXJ.PDB	O, E_TRP_135	N, E_ALA_139	H, E_ALA_139	2.97	2.13	10.92
5VXJ.PDB	O, E_ALA_136	N, E_ASN_140	H, E_ASN_140	2.93	2.08	7.93
5VXJ.PDB	O, E_LYS_137	N, E_SER_141	H, E_SER_141	2.81	2.07	25.81
5VXJ.PDB	O, E_ALA_121	OG, E_SER_141	HG, E_SER_141	2.98	2.28	28.49
5VXJ.PDB	O, E_ASN_140	N, E_ASP_144	H, E_ASP_144	2.69	1.88	16.68
5VXJ.PDB	O, E_SER_141	N, E_ILE_145	H, E_ILE_145	2.84	2.00	9.07
5VXJ.PDB	O, E_ASP_144	N, E_GLN_148	H, E_GLN_148	2.78	1.95	12.00
5VXJ.PDB	O, E_ILE_145	N, E_LEU_150	H, E_LEU_150	2.93	2.08	9.20
5VXJ.PDB	O, E_ASN_146	N, E_LYS_151	H, E_LYS_151	2.91	2.08	12.08
5VXJ.PDB	O, E_TYR_153	N, E_VAL_157	H, E_VAL_157	2.91	2.06	8.11
5VXJ.PDB	O, E_GLU_154	N, E_SER_158	H, E_SER_158	2.80	1.95	8.74
5VXJ.PDB	O, E_HIS_155	N, E_SER_159	H, E_SER_159	2.71	1.87	11.62
5VXJ.PDB	O, E_ALA_156	N, E_TYR_160	H, E_TYR_160	2.93	2.08	7.60
5VXJ.PDB	O, E_VAL_157	N, E_THR_161	H, E_THR_161	2.81	1.98	13.79
5VXJ.PDB	O, E_VAL_157	OG1, E_THR_161	HG1, E_THR_161	2.55	1.80	22.47
5VXJ.PDB	O, E_TYR_160	N, E_TYR_164	H, E_TYR_164	3.00	2.18	15.88
5VXJ.PDB	OD1, E_ASP_287	OH, E_TYR_164	HH, E_TYR_164	2.85	2.09	21.13
5VXJ.PDB	O, E_THR_161	N, E_GLN_165	H, E_GLN_165	2.75	1.91	9.80
5VXJ.PDB	O, E_LEU_70	NE2, E_GLN_165	HE21, E_GLN_165	2.84	2.05	19.77
5VXJ.PDB	O, E_GLN_162	N, E_ASP_166	H, E_ASP_166	2.97	2.14	14.36
5VXJ.PDB	O, E_MET_163	N, E_PHE_167	H, E_PHE_167	2.92	2.13	18.67
5VXJ.PDB	O, E_TYR_164	N, E_SER_168	H, E_SER_168	2.77	1.96	15.85
5VXJ.PDB	O, E_TYR_164	OG, E_SER_168	HG, E_SER_168	2.89	2.07	10.15
5VXJ.PDB	O, E_PHE_167	N, E_LEU_171	H, E_LEU_171	2.80	2.00	18.45
5VXJ.PDB	O, E_SER_168	N, E_SER_172	H, E_SER_172	2.82	2.04	21.33
5VXJ.PDB	O, D_TYR_105	OG, E_SER_173	HG, E_SER_173	2.87	2.17	28.40
5VXJ.PDB	O, E_LEU_271	N, E_VAL_188	H, E_VAL_188	2.72	1.89	11.17
5VXJ.PDB	O, E_SER_179	N, E_LYS_189	H, E_LYS_189	2.74	1.89	6.16
5VXJ.PDB	O, E_VAL_269	N, E_LEU_190	H, E_LEU_190	2.84	2.05	20.49
5VXJ.PDB	O, E_TRP_177	N, E_GLN_191	H, E_GLN_191	2.94	2.12	14.86
5VXJ.PDB	O, E_VAL_192	N, E_LYS_196	H, E_LYS_196	2.75	1.91	8.80
5VXJ.PDB	O, E_ASN_193	N, E_LYS_197	H, E_LYS_197	2.71	1.85	6.12
5VXJ.PDB	OD1, D_ASN_97	NZ, E_LYS_197	HZ1, E_LYS_197	2.80	1.95	14.72
5VXJ.PDB	OE2, E_GLU_201	NZ, E_LYS_197	HZ3, E_LYS_197	2.47	1.71	25.42
5VXJ.PDB	O, E_LEU_195	N, E_LEU_199	H, E_LEU_199	3.00	2.17	13.11
5VXJ.PDB	O, E_LYS_196	N, E_GLU_200	H, E_GLU_200	2.76	1.92	10.71
5VXJ.PDB	O, E_ALA_198	N, E_LEU_202	H, E_LEU_202	2.95	2.17	21.29

5VXJ.PDB	OD1, E_ASP_254	NZ, E_LYS_203	HZ2, E_LYS_203	2.55	1.67	5.69
5VXJ.PDB	O, E_GLU_201	N, E_LYS_205	H, E_LYS_205	2.76	2.01	23.93
5VXJ.PDB	OD2, E_ASP_166	NZ, E_LYS_205	HZ2, E_LYS_205	2.79	1.95	15.80
5VXJ.PDB	OD2, E_ASP_166	OH, E_TYR_206	HH, E_TYR_206	2.80	1.99	13.17
5VXJ.PDB	O, F_GLY_112	ND2, E_ASN_216	HD21, E_ASN_216	2.68	1.91	21.74
5VXJ.PDB	O, E_TYR_244	N, E_VAL_218	H, E_VAL_218	2.90	2.07	12.38
5VXJ.PDB	O, E_SER_219	N, E_ALA_223	H, E_ALA_223	2.85	2.02	12.36
5VXJ.PDB	O, E_GLN_220	N, E_ASN_224	H, E_ASN_224	2.92	2.12	17.22
5VXJ.PDB	O, E_GLU_221	N, E_LYS_225	H, E_LYS_225	2.83	2.07	23.55
5VXJ.PDB	O, E_ALA_223	N, E_LEU_227	H, E_LEU_227	2.90	2.08	14.99
5VXJ.PDB	O, E_TRP_226	N, E_LEU_230	H, E_LEU_230	2.79	1.93	5.43
5VXJ.PDB	O, E_SER_247	N, E_LYS_236	H, E_LYS_236	2.89	2.18	29.32
5VXJ.PDB	O, E_GLY_243	N, E_LYS_240	H, E_LYS_240	2.92	2.06	6.86
5VXJ.PDB	O, E_VAL_218	N, E_TYR_244	H, E_TYR_244	2.83	2.10	27.72
5VXJ.PDB	O, E_SER_238	N, E_VAL_245	H, E_VAL_245	2.99	2.17	14.78
5VXJ.PDB	O, E_TYR_212	N, E_VAL_246	H, E_VAL_246	2.78	1.92	1.28
5VXJ.PDB	O, E_ILE_234	N, E_ASN_249	H, E_ASN_249	2.95	2.10	8.04
5VXJ.PDB	OD1, E_ASN_249	N, E_THR_251	H, E_THR_251	2.92	2.09	11.77
5VXJ.PDB	OD1, E_ASN_249	OG1, E_THR_251	HG1, E_THR_251	2.55	1.84	26.63
5VXJ.PDB	O, E_MET_250	N, E_ASP_254	H, E_ASP_254	2.99	2.17	15.41
5VXJ.PDB	O, E_THR_251	N, E_ASN_255	H, E_ASN_255	2.75	1.94	15.61
5VXJ.PDB	O, E_MET_256	N, E_LEU_260	H, E_LEU_260	2.96	2.20	24.13
5VXJ.PDB	O, E_LYS_258	N, E_ASN_262	H, E_ASN_262	2.93	2.19	25.85
5VXJ.PDB	O, E_VAL_188	N, E_LEU_271	H, E_LEU_271	2.71	1.86	9.01
5VXJ.PDB	O, E_ASN_273	N, E_GLN_277	H, E_GLN_277	2.93	2.08	8.17
5VXJ.PDB	O, E_LYS_275	N, E_TRP_279	H, E_TRP_279	2.94	2.10	8.60
5VXJ.PDB	O, E_TYR_276	N, E_ASN_280	H, E_ASN_280	2.69	1.83	1.86
5VXJ.PDB	O, E_TRP_279	N, E_PHE_283	H, E_PHE_283	2.90	2.06	8.44
5VXJ.PDB	O, E_GLU_288	N, E_ASN_292	H, E_ASN_292	2.93	2.09	10.24
5VXJ.PDB	O, E_THR_289	N, E_ASN_293	H, E_ASN_293	2.93	2.09	10.01
5VXJ.PDB	O, E_MET_290	N, E_LEU_294	H, E_LEU_294	2.94	2.11	13.11
5VXJ.PDB	O, E_LYS_291	N, E_GLN_295	H, E_GLN_295	2.83	1.98	7.53
5VXJ.PDB	O, E_ASN_292	N, E_THR_296	H, E_THR_296	2.78	2.01	22.46
5VXJ.PDB	O, E_LEU_294	N, E_VAL_298	H, E_VAL_298	2.95	2.10	6.64
5VXJ.PDB	O, E_THR_296	N, E_LYS_300	H, E_LYS_300	2.96	2.14	14.74
5VXJ.PDB	O, E_LEU_297	N, E_TYR_301	H, E_TYR_301	2.79	1.94	8.70
5VXJ.PDB	O, E_VAL_298	N, E_SER_302	H, E_SER_302	2.84	2.02	14.64
5VXJ.PDB	O, E_GLN_299	N, E_ASN_303	H, E_ASN_303	2.93	2.07	5.66
5VXJ.PDB	O, E_LYS_300	N, E_ALA_304	H, E_ALA_304	2.85	2.08	22.30
5VXJ.PDB	OD1, E_ASN_58	ND2, E_ASN_305	HD21, E_ASN_305	2.80	1.98	14.83
5VXJ.PDB	O, E_ALA_304	N, E_PHE_308	H, E_PHE_308	2.93	2.09	11.91
5VXJ.PDB	O, E_ASN_305	N, E_ASP_309	H, E_ASP_309	2.75	1.92	13.10
5VXJ.PDB	O, E_SER_306	N, E_ASN_310	H, E_ASN_310	2.83	2.05	20.17
5VXJ.PDB	O, E_LEU_311	N, E_LEU_315	H, E_LEU_315	2.80	1.98	13.54
5VXJ.PDB	O, E_VAL_312	N, E_SER_316	H, E_SER_316	2.92	2.08	10.70
5VXJ.PDB	O, E_LYS_313	OG, E_SER_316	HG, E_SER_316	2.95	2.17	17.14
5VXJ.PDB	O, E_VAL_314	N, E_THR_318	H, E_THR_318	2.84	2.03	16.20
5VXJ.PDB	O, E_LEU_315	N, E_ILE_319	H, E_ILE_319	2.87	2.09	21.51
5VXJ.PDB	O, E_SER_316	OG, E_SER_320	HG, E_SER_320	2.93	2.11	9.97
5VXJ.PDB	O, F_SER_25	N, F_GLN_3	H, F_GLN_3	2.86	2.05	17.85
5VXJ.PDB	O, F_ALA_23	N, F_ALA_5	H, F_ALA_5	2.98	2.24	26.74
5VXJ.PDB	O, F_SER_21	N, F_THR_7	H, F_THR_7	2.94	2.17	21.96
5VXJ.PDB	O, F_GLN_114	N, F_GLY_10	H, F_GLY_10	2.72	1.87	6.47
5VXJ.PDB	O, F_THR_116	N, F_ALA_12	H, F_ALA_12	2.88	2.15	27.23
5VXJ.PDB	O, F_LEU_86	N, F_GLY_15	H, F_GLY_15	2.89	2.06	12.09
5VXJ.PDB	O, F_GLN_13	N, F_GLY_16	H, F_GLY_16	2.90	2.06	10.07
5VXJ.PDB	O, F_MET_83	N, F_LEU_18	H, F_LEU_18	2.85	2.06	20.12
5VXJ.PDB	OE1, F_GLN_82	NE, F_ARG_19	HE, F_ARG_19	2.82	1.96	3.39

5VXJ.PDB	O, F_THR_7	N, F_SER_21	H, F_SER_21	2.85	2.05	18.37
5VXJ.PDB	O, F_VAL_79	N, F_CYS_22	H, F_CYS_22	2.95	2.15	19.55
5VXJ.PDB	O, F_ALA_5	N, F_ALA_23	H, F_ALA_23	2.80	1.96	10.17
5VXJ.PDB	O, F_ASN_77	N, F_ALA_24	H, F_ALA_24	2.80	1.95	4.41
5VXJ.PDB	O, F_GLY_99	N, F_VAL_33	H, F_VAL_33	2.72	1.90	15.23
5VXJ.PDB	O, F_ASN_97	N, F_ASN_35	H, F_ASN_35	2.71	1.87	10.04
5VXJ.PDB	OD1, F_ASN_97	ND2, F_ASN_35	HD22, F_ASN_35	2.86	2.08	21.21
5VXJ.PDB	O, F_ALA_49	N, F_TRP_36	H, F_TRP_36	2.90	2.07	13.72
5VXJ.PDB	O, F_VAL_95	N, F_TYR_37	H, F_TYR_37	2.88	2.02	2.78
5VXJ.PDB	OD1, F_ASP_90	NH1, F_ARG_38	HH12, F_ARG_38	2.92	2.20	28.14
5VXJ.PDB	OE2, F_GLU_46	NH2, F_ARG_38	HH21, F_ARG_38	2.73	1.93	18.99
5VXJ.PDB	OE1, F_GLU_44	N, F_ARG_45	H, F_ARG_45	2.62	1.85	20.92
5VXJ.PDB	O, F_ARG_38	N, F_GLU_46	H, F_GLU_46	2.92	2.09	11.31
5VXJ.PDB	O, F_TRP_36	N, F_VAL_48	H, F_VAL_48	2.74	1.91	14.11
5VXJ.PDB	O, F_SER_59	N, F_ARG_50	H, F_ARG_50	2.88	2.09	20.53
5VXJ.PDB	OE1, G_GLU_200	NH2, F_ARG_50	HH22, F_ARG_50	2.70	1.89	15.49
5VXJ.PDB	O, F_SER_30	OH, F_TYR_52	HH, F_TYR_52	2.69	1.86	8.38
5VXJ.PDB	OD1, F_ASP_53	N, F_GLY_55	H, F_GLY_55	2.61	1.87	25.39
5VXJ.PDB	O, F_ARG_50	N, F_SER_59	H, F_SER_59	2.82	2.00	14.71
5VXJ.PDB	O, F_SER_85	NH1, F_ARG_67	HH11, F_ARG_67	2.83	2.08	24.34
5VXJ.PDB	OD2, F_ASP_90	NH1, F_ARG_67	HH12, F_ARG_67	2.83	1.99	10.41
5VXJ.PDB	OD1, F_ASN_74	NE, F_ARG_72	HE, F_ARG_72	2.72	1.88	10.50
5VXJ.PDB	O, F_ALA_32	NH1, F_ARG_72	HH12, F_ARG_72	2.99	2.18	16.73
5VXJ.PDB	O, F_LEU_18	N, F_MET_83	H, F_MET_83	2.56	1.71	7.06
5VXJ.PDB	OD2, F_ASP_90	N, F_LYS_87	H, F_LYS_87	2.92	2.15	21.40
5VXJ.PDB	O, F_LYS_87	N, F_ASP_90	H, F_ASP_90	2.85	2.01	12.44
5VXJ.PDB	O, F_PRO_88	N, F_THR_91	H, F_THR_91	2.99	2.14	6.98
5VXJ.PDB	O, F_VAL_115	N, F_ALA_92	H, F_ALA_92	2.99	2.23	23.19
5VXJ.PDB	O, F_GLN_39	N, F_MET_93	H, F_MET_93	2.76	1.90	4.39
5VXJ.PDB	O, F_THR_113	N, F_TYR_94	H, F_TYR_94	2.89	2.09	17.19
5VXJ.PDB	O, F_ASP_90	OH, F_TYR_94	HH, F_TYR_94	2.65	1.83	9.35
5VXJ.PDB	OE2, F_GLU_6	N, F_CYS_96	H, F_CYS_96	2.48	1.64	10.12
5VXJ.PDB	O, F_ASN_35	N, F_ASN_97	H, F_ASN_97	2.96	2.17	18.94
5VXJ.PDB	OG1, F_THR_107	ND2, F_ASN_97	HD21, F_ASN_97	2.73	1.95	21.26
5VXJ.PDB	O, F_VAL_33	N, F_GLY_99	H, F_GLY_99	2.77	1.92	6.76
5VXJ.PDB	O, F_ARG_106	N, F_ILE_100	H, F_ILE_100	2.81	1.97	10.04
5VXJ.PDB	O, F_ARG_31	N, F_PHE_101	H, F_PHE_101	2.72	1.87	8.92
5VXJ.PDB	OE1, G_GLU_201	OH, F_TYR_105	HH, F_TYR_105	2.57	1.75	11.97
5VXJ.PDB	O, F_CYS_96	N, F_GLY_110	H, F_GLY_110	2.87	2.09	20.49
5VXJ.PDB	O, E_THR_217	NE2, F_GLN_111	HE22, F_GLN_111	2.98	2.12	6.26
5VXJ.PDB	OE1, F_GLU_6	N, F_GLY_112	H, F_GLY_112	2.49	1.66	12.35
5VXJ.PDB	O, F_TYR_94	N, F_THR_113	H, F_THR_113	2.80	1.99	17.44
5VXJ.PDB	O, F_ALA_92	N, F_VAL_115	H, F_VAL_115	2.94	2.08	6.59
5VXJ.PDB	OG1, F_THR_91	N, F_VAL_117	H, F_VAL_117	2.91	2.05	1.59
5VXJ.PDB	O, G_LEU_47	N, G_LEU_51	H, G_LEU_51	2.82	2.00	14.56
5VXJ.PDB	O, G_ASP_49	N, G_ASN_53	H, G_ASN_53	2.43	1.60	12.48
5VXJ.PDB	O, G_HIS_52	N, G_THR_56	H, G_THR_56	2.92	2.09	13.87
5VXJ.PDB	O, G_ARG_55	N, G_THR_57	H, G_THR_57	2.92	2.19	26.60
5VXJ.PDB	O, G_THR_57	N, G_LEU_61	H, G_LEU_61	2.82	1.99	11.74
5VXJ.PDB	O, G_ASN_58	N, G_LYS_62	H, G_LYS_62	2.82	1.97	8.16
5VXJ.PDB	O, G_LEU_61	N, G_LEU_65	H, G_LEU_65	2.93	2.16	22.32
5VXJ.PDB	O, G_LYS_62	OG, G_SER_66	HG, G_SER_66	2.76	1.97	15.54
5VXJ.PDB	O, G_ALA_79	N, G_SER_83	H, G_SER_83	2.87	2.11	23.33
5VXJ.PDB	O, G_LEU_80	N, G_GLN_84	H, G_GLN_84	2.88	2.12	24.02
5VXJ.PDB	O, G_HIS_81	N, G_ILE_85	H, G_ILE_85	2.98	2.19	19.61
5VXJ.PDB	O, G_ILE_85	N, G_VAL_89	H, G_VAL_89	2.81	2.00	16.83
5VXJ.PDB	O, G_ASP_88	N, G_SER_92	H, G_SER_92	2.63	1.80	11.22
5VXJ.PDB	O, G_ASP_88	OG, G_SER_92	HG, G_SER_92	2.83	2.07	20.88

5VXJ.PDB	O, G_VAL_89	N, G_ALA_93	H, G_ALA_93	2.81	1.99	14.69
5VXJ.PDB	O, G_SER_92	N, G_LEU_96	H, G_LEU_96	2.87	2.02	7.93
5VXJ.PDB	O, G_ALA_93	N, G_ASP_97	H, G_ASP_97	2.78	1.96	13.95
5VXJ.PDB	O, G_GLN_94	N, G_ILE_98	H, G_ILE_98	2.75	1.95	17.07
5VXJ.PDB	O, G_LEU_95	N, G_LEU_99	H, G_LEU_99	2.95	2.15	17.03
5VXJ.PDB	O, G_LEU_96	N, G_SER_100	H, G_SER_100	2.90	2.14	23.00
5VXJ.PDB	O, G_ARG_132	OG, G_SER_100	HG, G_SER_100	2.76	1.96	15.44
5VXJ.PDB	O, G_ASP_97	N, G_ARG_101	H, G_ARG_101	2.92	2.09	13.45
5VXJ.PDB	OD2, G_ASP_97	NE, G_ARG_101	HE, G_ARG_101	2.67	1.82	7.54
5VXJ.PDB	O, G_ILE_98	N, G_ASN_102	H, G_ASN_102	2.95	2.14	17.00
5VXJ.PDB	O, G_LEU_113	OG, G_SER_116	HG, G_SER_116	2.49	1.72	19.82
5VXJ.PDB	O, G_PRO_118	N, G_ALA_121	H, G_ALA_121	2.99	2.21	20.79
5VXJ.PDB	O, G_LYS_119	N, G_GLU_122	H, G_GLU_122	2.97	2.13	11.69
5VXJ.PDB	O, H_GLY_56	NH2, G_ARG_132	HH22, G_ARG_132	2.94	2.20	26.37
5VXJ.PDB	O, G_TYR_104	NE1, G_TRP_135	HE1, G_TRP_135	2.73	1.97	23.31
5VXJ.PDB	O, G_GLU_133	N, G_LYS_137	H, G_LYS_137	2.98	2.20	21.62
5VXJ.PDB	O, G_LEU_134	N, G_ILE_138	H, G_ILE_138	2.96	2.21	25.46
5VXJ.PDB	O, G_TRP_135	N, G_ALA_139	H, G_ALA_139	2.77	1.93	7.72
5VXJ.PDB	O, G_ALA_136	N, G_ASN_140	H, G_ASN_140	2.82	1.97	8.22
5VXJ.PDB	O, G_LYS_137	N, G_SER_141	H, G_SER_141	3.00	2.27	27.08
5VXJ.PDB	O, G_ALA_121	OG, G_SER_141	HG, G_SER_141	2.84	2.05	16.77
5VXJ.PDB	O, G_ASN_140	N, G_ASP_144	H, G_ASP_144	2.65	1.83	15.34
5VXJ.PDB	O, G_SER_141	N, G_ILE_145	H, G_ILE_145	2.98	2.15	13.01
5VXJ.PDB	O, G_ASP_144	N, G_GLN_148	H, G_GLN_148	2.87	2.03	9.64
5VXJ.PDB	O, G_ILE_145	N, G_LEU_150	H, G_LEU_150	2.93	2.09	11.15
5VXJ.PDB	O, G_ASN_146	N, G_LYS_151	H, G_LYS_151	2.69	1.86	11.46
5VXJ.PDB	O, G_LYS_151	N, G_HIS_155	H, G_HIS_155	2.94	2.14	18.38
5VXJ.PDB	O, G_VAL_152	N, G_ALA_156	H, G_ALA_156	2.99	2.15	9.93
5VXJ.PDB	O, G_TYR_153	N, G_VAL_157	H, G_VAL_157	2.97	2.12	8.52
5VXJ.PDB	O, G_GLU_154	N, G_SER_158	H, G_SER_158	2.89	2.07	14.41
5VXJ.PDB	O, G_HIS_155	N, G_SER_159	H, G_SER_159	2.67	1.82	8.29
5VXJ.PDB	O, G_ALA_156	N, G_TYR_160	H, G_TYR_160	2.95	2.09	4.91
5VXJ.PDB	O, G_VAL_157	N, G_THR_161	H, G_THR_161	2.89	2.06	12.73
5VXJ.PDB	O, G_VAL_157	OG1, G_THR_161	HG1, G_THR_161	2.73	2.03	28.26
5VXJ.PDB	O, G_TYR_160	N, G_TYR_164	H, G_TYR_164	2.94	2.13	15.80
5VXJ.PDB	OD1, G_ASP_287	OH, G_TYR_164	HH, G_TYR_164	2.79	1.99	15.03
5VXJ.PDB	O, G_THR_161	N, G_GLN_165	H, G_GLN_165	2.71	1.89	15.11
5VXJ.PDB	O, G_GLN_162	N, G_ASP_166	H, G_ASP_166	2.86	2.02	10.34
5VXJ.PDB	O, G_MET_163	N, G_PHE_167	H, G_PHE_167	2.94	2.13	15.85
5VXJ.PDB	O, G_TYR_164	N, G_SER_168	H, G_SER_168	2.76	1.96	17.74
5VXJ.PDB	O, G_PHE_167	N, G_LEU_171	H, G_LEU_171	2.92	2.14	21.89
5VXJ.PDB	O, F_TYR_105	OG, G_SER_173	HG, G_SER_173	2.88	2.16	26.33
5VXJ.PDB	OD1, I_ASN_292	N, G_GLY_176	H, G_GLY_176	2.76	2.01	25.37
5VXJ.PDB	O, G_LYS_189	N, G_SER_179	H, G_SER_179	2.93	2.15	21.27
5VXJ.PDB	O, G_SER_187	N, G_GLY_181	H, G_GLY_181	2.82	1.96	3.25
5VXJ.PDB	O, G_LEU_271	N, G_VAL_188	H, G_VAL_188	2.64	1.80	10.40
5VXJ.PDB	O, G_SER_179	N, G_LYS_189	H, G_LYS_189	2.74	1.88	0.48
5VXJ.PDB	O, G_VAL_269	N, G_LEU_190	H, G_LEU_190	2.94	2.10	11.59
5VXJ.PDB	O, G_TRP_177	N, G_GLN_191	H, G_GLN_191	2.89	2.06	12.28
5VXJ.PDB	O, G_VAL_192	N, G_LYS_196	H, G_LYS_196	2.73	1.88	6.19
5VXJ.PDB	O, G_ASN_193	N, G_LYS_197	H, G_LYS_197	2.77	1.93	12.03
5VXJ.PDB	OE2, G_GLU_201	NZ, G_LYS_197	HZ3, G_LYS_197	2.59	1.86	28.64
5VXJ.PDB	O, G_LYS_196	N, G_GLU_200	H, G_GLU_200	2.89	2.03	3.65
5VXJ.PDB	O, G_ALA_198	N, G_LEU_202	H, G_LEU_202	2.82	2.06	23.29
5VXJ.PDB	OD1, G_ASP_254	NZ, G_LYS_203	HZ2, G_LYS_203	2.49	1.62	9.92
5VXJ.PDB	O, G_GLU_201	N, G_LYS_205	H, G_LYS_205	2.90	2.17	27.16
5VXJ.PDB	OD2, G_ASP_166	NZ, G_LYS_205	HZ2, G_LYS_205	2.82	1.96	12.05
5VXJ.PDB	OD2, G_ASP_166	OH, G_TYR_206	HH, G_TYR_206	2.52	1.70	11.57

5VXJ.PDB	OE1, H_GLN_111	OG1, G_THR_217	HG1, G_THR_217	2.86	2.17	29.58
5VXJ.PDB	O, G_TYR_244	N, G_VAL_218	H, G_VAL_218	2.86	2.06	17.78
5VXJ.PDB	O, G_SER_219	N, G_ALA_223	H, G_ALA_223	2.97	2.15	15.26
5VXJ.PDB	O, G_ALA_223	N, G_LEU_227	H, G_LEU_227	2.91	2.13	21.40
5VXJ.PDB	O, G_ASN_224	N, G_THR_228	H, G_THR_228	2.94	2.09	5.59
5VXJ.PDB	O, G_TRP_226	N, G_LEU_230	H, G_LEU_230	2.80	1.99	15.37
5VXJ.PDB	O, G_SER_247	N, G_LYS_236	H, G_LYS_236	2.91	2.21	29.46
5VXJ.PDB	O, G_GLY_243	N, G_LYS_240	H, G_LYS_240	2.93	2.08	7.36
5VXJ.PDB	O, G_VAL_218	N, G_TYR_244	H, G_TYR_244	2.68	1.96	27.92
5VXJ.PDB	O, G_TYR_212	N, G_VAL_246	H, G_VAL_246	2.69	1.84	4.47
5VXJ.PDB	O, G_ILE_234	N, G_ASN_249	H, G_ASN_249	2.98	2.13	6.76
5VXJ.PDB	OD1, G_ASN_249	N, G_THR_251	H, G_THR_251	2.80	1.95	8.59
5VXJ.PDB	O, G_MET_250	N, G_ASP_254	H, G_ASP_254	2.98	2.15	13.88
5VXJ.PDB	O, G_THR_251	N, G_ASN_255	H, G_ASN_255	2.80	1.98	15.19
5VXJ.PDB	O, G_ILE_253	N, G_LEU_257	H, G_LEU_257	2.98	2.19	19.77
5VXJ.PDB	O, G_ASP_254	N, G_LYS_258	H, G_LYS_258	2.96	2.13	13.32
5VXJ.PDB	O, G_ASN_255	N, G_SER_259	H, G_SER_259	2.97	2.13	11.23
5VXJ.PDB	O, G_MET_256	N, G_LEU_260	H, G_LEU_260	2.98	2.17	16.38
5VXJ.PDB	O, G_LEU_257	N, G_ASP_261	H, G_ASP_261	2.95	2.11	10.36
5VXJ.PDB	O, G_VAL_188	N, G_LEU_271	H, G_LEU_271	2.72	1.88	11.49
5VXJ.PDB	OD1, G_ASP_272	N, G_LYS_275	H, G_LYS_275	2.67	1.82	9.36
5VXJ.PDB	O, G_ASN_273	N, G_GLN_277	H, G_GLN_277	2.90	2.04	4.56
5VXJ.PDB	O, G_TYR_276	N, G_ASN_280	H, G_ASN_280	2.80	1.95	8.62
5VXJ.PDB	O, G_TRP_279	N, G_PHE_283	H, G_PHE_283	2.87	2.07	17.67
5VXJ.PDB	O, G_ASN_280	N, G_SER_284	H, G_SER_284	2.95	2.13	14.24
5VXJ.PDB	O, G_ASN_280	OG, G_SER_284	HG, G_SER_284	2.97	2.24	25.76
5VXJ.PDB	O, G_SER_284	N, G_GLU_288	H, G_GLU_288	2.91	2.15	23.37
5VXJ.PDB	O, G_GLU_288	N, G_ASN_292	H, G_ASN_292	2.83	1.99	8.91
5VXJ.PDB	O, G_THR_289	N, G_ASN_293	H, G_ASN_293	2.94	2.09	6.63
5VXJ.PDB	O, G_LYS_291	N, G_GLN_295	H, G_GLN_295	2.97	2.14	12.50
5VXJ.PDB	O, G_ASN_292	N, G_THR_296	H, G_THR_296	2.78	1.97	17.22
5VXJ.PDB	O, G_ASN_293	N, G_LEU_297	H, G_LEU_297	2.97	2.15	14.27
5VXJ.PDB	O, G_LEU_294	N, G_VAL_298	H, G_VAL_298	2.94	2.10	8.59
5VXJ.PDB	O, G_THR_296	N, G_LYS_300	H, G_LYS_300	2.93	2.11	14.54
5VXJ.PDB	O, G_LEU_297	N, G_TYR_301	H, G_TYR_301	2.79	1.93	5.96
5VXJ.PDB	O, G_VAL_298	N, G_SER_302	H, G_SER_302	2.92	2.18	25.79
5VXJ.PDB	O, G_GLN_299	N, G_ASN_303	H, G_ASN_303	2.89	2.06	11.76
5VXJ.PDB	O, G_LYS_300	N, G_ALA_304	H, G_ALA_304	2.91	2.09	15.09
5VXJ.PDB	O, G_ASN_305	N, G_ASP_309	H, G_ASP_309	2.86	2.10	23.50
5VXJ.PDB	O, G_ASN_310	N, G_VAL_314	H, G_VAL_314	2.93	2.09	9.81
5VXJ.PDB	O, G_LEU_311	N, G_LEU_315	H, G_LEU_315	2.80	1.98	14.79
5VXJ.PDB	O, G_VAL_312	N, G_SER_316	H, G_SER_316	2.85	2.00	7.85
5VXJ.PDB	O, G_VAL_314	OG, G_SER_317	HG, G_SER_317	2.91	2.15	20.46
5VXJ.PDB	OE1, H_GLN_1	N, H_VAL_2	H, H_VAL_2	2.95	2.22	27.04
5VXJ.PDB	O, H_SER_25	N, H_GLN_3	H, H_GLN_3	2.91	2.09	16.25
5VXJ.PDB	O, H_ALA_23	N, H_ALA_5	H, H_ALA_5	2.99	2.18	17.17
5VXJ.PDB	O, H_SER_21	N, H_THR_7	H, H_THR_7	2.88	2.14	25.14
5VXJ.PDB	O, H_GLN_114	N, H_GLY_10	H, H_GLY_10	2.91	2.07	10.18
5VXJ.PDB	O, H_THR_116	N, H_ALA_12	H, H_ALA_12	2.81	2.11	29.16
5VXJ.PDB	O, H_LEU_86	N, H_GLY_15	H, H_GLY_15	2.89	2.09	19.18
5VXJ.PDB	O, H_GLN_13	N, H_GLY_16	H, H_GLY_16	2.90	2.08	13.33
5VXJ.PDB	O, H_MET_83	N, H_LEU_18	H, H_LEU_18	2.94	2.15	20.85
5VXJ.PDB	OE1, H_GLN_82	NE, H_ARG_19	HE, H_ARG_19	2.76	1.91	8.69
5VXJ.PDB	O, H_LEU_81	N, H_LEU_20	H, H_LEU_20	2.81	2.00	16.24
5VXJ.PDB	O, H_THR_7	N, H_SER_21	H, H_SER_21	2.81	2.01	17.25
5VXJ.PDB	O, H_VAL_79	N, H_CYS_22	H, H_CYS_22	2.93	2.10	13.46
5VXJ.PDB	O, H_ALA_5	N, H_ALA_23	H, H_ALA_23	2.89	2.09	18.03
5VXJ.PDB	O, H_ASN_77	N, H_ALA_24	H, H_ALA_24	2.87	2.01	2.06

5VXJ.PDB	O, H_THR_28	N, H_ARG_31	H, H_ARG_31	2.95	2.12	13.87
5VXJ.PDB	O, H_GLY_99	N, H_VAL_33	H, H_VAL_33	2.75	1.93	14.82
5VXJ.PDB	O, H_ASN_97	N, H_ASN_35	H, H_ASN_35	2.70	1.89	16.43
5VXJ.PDB	OD1, H_ASN_97	ND2, H_ASN_35	HD22, H_ASN_35	2.85	2.10	23.91
5VXJ.PDB	O, H_ALA_49	N, H_TRP_36	H, H_TRP_36	2.96	2.13	12.43
5VXJ.PDB	O, H_VAL_95	N, H_TYR_37	H, H_TYR_37	2.93	2.07	4.40
5VXJ.PDB	O, H_GLU_46	N, H_ARG_38	H, H_ARG_38	3.00	2.20	19.46
5VXJ.PDB	OD1, H_ASP_90	NH1, H_ARG_38	HH12, H_ARG_38	3.00	2.16	12.34
5VXJ.PDB	O, H_LYS_43	NE2, H_GLN_39	HE21, H_GLN_39	2.90	2.07	12.82
5VXJ.PDB	O, H_ALA_40	N, H_LYS_43	H, H_LYS_43	2.85	2.05	18.19
5VXJ.PDB	O, H_TRP_36	N, H_VAL_48	H, H_VAL_48	2.81	1.99	14.82
5VXJ.PDB	OD1, H_ASN_35	NE, H_ARG_50	HE, H_ARG_50	2.75	1.93	14.53
5VXJ.PDB	O, H_SER_30	OH, H_TYR_52	HH, H_TYR_52	2.54	1.73	12.01
5VXJ.PDB	O, H_ARG_50	N, H_SER_59	H, H_SER_59	2.65	1.83	14.48
5VXJ.PDB	O, H_VAL_48	N, H_ALA_61	H, H_ALA_61	2.92	2.06	6.45
5VXJ.PDB	OD2, H_ASP_90	NH1, H_ARG_67	HH12, H_ARG_67	2.89	2.05	9.62
5VXJ.PDB	O, H_VAL_64	N, H_PHE_68	H, H_PHE_68	2.94	2.11	12.01
5VXJ.PDB	O, H_GLN_82	N, H_THR_69	H, H_THR_69	2.98	2.17	16.65
5VXJ.PDB	O, H_HIS_80	N, H_SER_71	H, H_SER_71	2.96	2.17	19.86
5VXJ.PDB	OD1, H_ASN_74	NE, H_ARG_72	HE, H_ARG_72	2.76	1.95	17.61
5VXJ.PDB	O, H_THR_78	N, H_ASP_73	H, H_ASP_73	2.94	2.10	8.61
5VXJ.PDB	OD1, H_ASP_73	N, H_ALA_75	H, H_ALA_75	2.98	2.24	26.47
5VXJ.PDB	O, H_LEU_20	N, H_LEU_81	H, H_LEU_81	2.92	2.17	25.39
5VXJ.PDB	O, H_THR_69	N, H_GLN_82	H, H_GLN_82	2.80	2.01	19.49
5VXJ.PDB	OD1, H_ASN_84	NE2, H_GLN_82	HE21, H_GLN_82	2.86	2.05	16.57
5VXJ.PDB	O, H_LEU_18	N, H_MET_83	H, H_MET_83	2.73	1.88	6.75
5VXJ.PDB	OD2, H_ASP_90	N, H_LYS_87	H, H_LYS_87	2.78	1.93	8.81
5VXJ.PDB	O, H_LYS_87	N, H_ASP_90	H, H_ASP_90	2.91	2.12	18.68
5VXJ.PDB	O, H_PRO_88	OG1, H_THR_91	HG1, H_THR_91	2.87	2.17	28.10
5VXJ.PDB	O, H_GLN_39	N, H_MET_93	H, H_MET_93	2.94	2.08	2.62
5VXJ.PDB	O, H_THR_113	N, H_TYR_94	H, H_TYR_94	2.90	2.08	15.59
5VXJ.PDB	O, H_ASP_90	OH, H_TYR_94	HH, H_TYR_94	2.76	1.93	4.55
5VXJ.PDB	OE2, H_GLU_6	N, H_CYS_96	H, H_CYS_96	2.77	1.93	11.06
5VXJ.PDB	O, H_ASN_35	N, H_ASN_97	H, H_ASN_97	3.00	2.18	14.80
5VXJ.PDB	OG1, H_THR_107	ND2, H_ASN_97	HD21, H_ASN_97	2.53	1.81	26.67
5VXJ.PDB	O, H_VAL_33	N, H_GLY_99	H, H_GLY_99	2.83	1.97	3.41
5VXJ.PDB	O, H_ARG_31	N, H_PHE_101	H, H_PHE_101	2.92	2.07	4.69
5VXJ.PDB	O, H_ALA_98	OG1, H_THR_107	HG1, H_THR_107	2.78	2.00	18.25
5VXJ.PDB	O, H_TYR_94	N, H_THR_113	H, H_THR_113	2.71	1.88	13.43
5VXJ.PDB	O, H_ALA_92	N, H_VAL_115	H, H_VAL_115	2.99	2.14	8.76
5VXJ.PDB	O, I_HIS_52	N, I_THR_56	H, I_THR_56	3.00	2.25	25.56
5VXJ.PDB	O, I_ILE_54	N, I_ASN_58	H, I_ASN_58	2.85	2.04	16.92
5VXJ.PDB	OD1, I_ASP_309	ND2, I_ASN_58	HD22, I_ASN_58	2.73	1.88	5.94
5VXJ.PDB	O, I_THR_57	N, I_LEU_61	H, I_LEU_61	2.75	1.93	14.25
5VXJ.PDB	O, I_SER_74	N, I_ILE_78	H, I_ILE_78	2.96	2.17	19.05
5VXJ.PDB	O, I_ILE_78	N, I_SER_82	H, I_SER_82	2.89	2.03	4.23
5VXJ.PDB	OE1, I_GLU_154	OG, I_SER_82	HG, I_SER_82	2.52	1.79	24.33
5VXJ.PDB	O, I_ALA_79	N, I_SER_83	H, I_SER_83	2.97	2.17	18.99
5VXJ.PDB	O, I_LEU_80	N, I_GLN_84	H, I_GLN_84	2.85	2.09	23.46
5VXJ.PDB	O, I_HIS_81	N, I_ILE_85	H, I_ILE_85	2.91	2.07	9.50
5VXJ.PDB	O, I_SER_82	N, I_SER_86	H, I_SER_86	2.96	2.13	13.40
5VXJ.PDB	O, I_ILE_85	N, I_VAL_89	H, I_VAL_89	2.75	1.92	11.99
5VXJ.PDB	O, I_SER_86	N, I_ASN_90	H, I_ASN_90	2.87	2.05	14.01
5VXJ.PDB	O, I_ASP_88	N, I_SER_92	H, I_SER_92	2.88	2.08	18.99
5VXJ.PDB	O, I_VAL_89	N, I_ALA_93	H, I_ALA_93	2.77	1.96	17.15
5VXJ.PDB	O, I_SER_92	N, I_LEU_96	H, I_LEU_96	2.85	1.99	1.66
5VXJ.PDB	O, I_ALA_93	N, I_ASP_97	H, I_ASP_97	2.73	1.95	20.17
5VXJ.PDB	O, I_ARG_132	OG, I_SER_100	HG, I_SER_100	2.62	1.86	20.59

5VXJ.PDB	OD2, I_ASP_97	NE, I_ARG_101	HE, I_ARG_101	2.83	2.07	23.56
5VXJ.PDB	O, I_ILE_98	N, I_ASN_102	H, I_ASN_102	2.91	2.10	16.45
5VXJ.PDB	O, I_ILE_129	NH2, I_ARG_111	HH22, I_ARG_111	2.55	1.83	26.80
5VXJ.PDB	O, I_GLU_112	N, I_HIS_115	H, I_HIS_115	2.95	2.18	22.09
5VXJ.PDB	O, I_LEU_113	N, I_SER_116	H, I_SER_116	2.82	1.99	12.68
5VXJ.PDB	O, I_LEU_114	N, I_ALA_117	H, I_ALA_117	2.81	1.96	7.97
5VXJ.PDB	O, I_HIS_131	N, I_TRP_135	H, I_TRP_135	2.86	2.01	6.63
5VXJ.PDB	O, I_TYR_104	NE1, I_TRP_135	HE1, I_TRP_135	2.77	2.01	23.99
5VXJ.PDB	OD2, J_ASP_73	NZ, I_LYS_137	HZ3, I_LYS_137	2.90	2.17	29.52
5VXJ.PDB	O, I_TRP_135	N, I_ALA_139	H, I_ALA_139	2.88	2.02	5.33
5VXJ.PDB	O, I_ALA_136	N, I_ASN_140	H, I_ASN_140	2.79	1.94	7.31
5VXJ.PDB	O, I_ASN_140	N, I_ASP_144	H, I_ASP_144	2.67	1.82	9.22
5VXJ.PDB	O, I_SER_141	N, I_ILE_145	H, I_ILE_145	2.92	2.09	14.16
5VXJ.PDB	O, I_ASP_144	N, I_GLN_148	H, I_GLN_148	2.87	2.03	10.58
5VXJ.PDB	O, I_ASN_146	N, I_LYS_151	H, I_LYS_151	2.96	2.13	13.63
5VXJ.PDB	O, I_GLU_154	N, I_SER_158	H, I_SER_158	2.91	2.08	12.92
5VXJ.PDB	O, I_HIS_155	N, I_SER_159	H, I_SER_159	2.86	2.02	8.08
5VXJ.PDB	O, I_VAL_157	N, I_THR_161	H, I_THR_161	2.74	1.90	11.36
5VXJ.PDB	O, I_SER_158	N, I_GLN_162	H, I_GLN_162	2.99	2.14	8.77
5VXJ.PDB	O, I_TYR_160	N, I_TYR_164	H, I_TYR_164	2.94	2.12	14.36
5VXJ.PDB	OD1, I_ASP_287	OH, I_TYR_164	HH, I_TYR_164	2.95	2.16	17.45
5VXJ.PDB	O, I_THR_161	N, I_GLN_165	H, I_GLN_165	2.73	1.92	16.54
5VXJ.PDB	O, I_GLN_162	N, I_ASP_166	H, I_ASP_166	2.98	2.15	13.40
5VXJ.PDB	O, I_MET_163	N, I_PHE_167	H, I_PHE_167	2.92	2.10	14.46
5VXJ.PDB	O, I_TYR_164	N, I_SER_168	H, I_SER_168	2.79	1.99	18.69
5VXJ.PDB	O, I_TYR_164	OG, I_SER_168	HG, I_SER_168	2.84	2.02	10.56
5VXJ.PDB	O, I_PHE_167	N, I_LEU_171	H, I_LEU_171	2.88	2.09	18.97
5VXJ.PDB	O, I_SER_168	N, I_SER_172	H, I_SER_172	2.93	2.14	20.32
5VXJ.PDB	O, I_LEU_171	N, I_LEU_174	H, I_LEU_174	2.98	2.15	13.51
5VXJ.PDB	O, I_LYS_189	N, I_SER_179	H, I_SER_179	2.95	2.20	24.93
5VXJ.PDB	O, I_SER_187	N, I_GLY_181	H, I_GLY_181	2.71	1.95	23.30
5VXJ.PDB	O, I_LEU_271	N, I_VAL_188	H, I_VAL_188	2.51	1.65	3.63
5VXJ.PDB	O, I_SER_179	N, I_LYS_189	H, I_LYS_189	2.57	1.72	7.44
5VXJ.PDB	O, I_VAL_269	N, I_LEU_190	H, I_LEU_190	2.88	2.08	17.76
5VXJ.PDB	O, I_TRP_177	N, I_GLN_191	H, I_GLN_191	2.84	2.00	11.79
5VXJ.PDB	O, I_VAL_192	N, I_LYS_196	H, I_LYS_196	2.80	1.94	4.24
5VXJ.PDB	O, I_ASN_193	N, I_LYS_197	H, I_LYS_197	2.85	2.02	13.07
5VXJ.PDB	OD1, B_ASN_97	NZ, I_LYS_197	HZ1, I_LYS_197	2.68	1.88	21.92
5VXJ.PDB	O, I_LEU_195	N, I_LEU_199	H, I_LEU_199	3.00	2.18	15.17
5VXJ.PDB	O, I_LYS_196	N, I_GLU_200	H, I_GLU_200	2.81	1.96	9.14
5VXJ.PDB	O, I_LYS_197	N, I_GLU_201	H, I_GLU_201	2.97	2.16	16.25
5VXJ.PDB	O, I_ALA_198	N, I_LEU_202	H, I_LEU_202	3.00	2.21	19.76
5VXJ.PDB	OD1, I_ASP_254	NZ, I_LYS_203	HZ2, I_LYS_203	2.60	1.74	12.72
5VXJ.PDB	O, I_GLU_201	N, I_LYS_205	H, I_LYS_205	2.75	1.96	18.48
5VXJ.PDB	OD2, I_ASP_166	NZ, I_LYS_205	HZ2, I_LYS_205	2.77	1.91	10.79
5VXJ.PDB	OD2, I_ASP_166	OH, I_TYR_206	HH, I_TYR_206	2.50	1.67	8.28
5VXJ.PDB	O, I_VAL_246	N, I_LEU_211	H, I_LEU_211	2.81	2.10	28.98
5VXJ.PDB	O, I_SER_219	N, I_ALA_223	H, I_ALA_223	2.88	2.07	17.36
5VXJ.PDB	O, I_GLN_220	N, I_ASN_224	H, I_ASN_224	2.91	2.06	6.82
5VXJ.PDB	O, I_GLU_221	N, I_LYS_225	H, I_LYS_225	2.94	2.21	26.90
5VXJ.PDB	O, I_ALA_223	N, I_LEU_227	H, I_LEU_227	2.90	2.08	14.48
5VXJ.PDB	O, I_TRP_226	N, I_LEU_230	H, I_LEU_230	2.81	1.97	9.92
5VXJ.PDB	O, I_GLY_231	N, I_ILE_234	H, I_ILE_234	2.96	2.14	14.73
5VXJ.PDB	O, I_VAL_245	N, I_SER_238	H, I_SER_238	2.98	2.16	15.04
5VXJ.PDB	O, I_TYR_212	N, I_VAL_246	H, I_VAL_246	2.76	1.90	2.08
5VXJ.PDB	O, I_ILE_234	N, I_ASN_249	H, I_ASN_249	2.85	2.02	12.88
5VXJ.PDB	OD1, I_ASN_249	N, I_THR_251	H, I_THR_251	2.98	2.14	10.78
5VXJ.PDB	OD1, I_ASN_249	OG1, I_THR_251	HG1, I_THR_251	2.69	1.98	27.82

5VXJ.PDB	O, I_THR_251	N, I_ASN_255	H, I_ASN_255	2.72	1.91	16.03
5VXJ.PDB	O, I_PRO_252	N, I_MET_256	H, I_MET_256	2.98	2.15	12.95
5VXJ.PDB	O, I_ILE_253	N, I_LEU_257	H, I_LEU_257	2.86	2.03	13.56
5VXJ.PDB	O, I_ASP_254	N, I_LYS_258	H, I_LYS_258	2.91	2.07	10.53
5VXJ.PDB	O, I_ASN_255	N, I_SER_259	H, I_SER_259	2.91	2.10	16.35
5VXJ.PDB	O, I_MET_256	N, I_LEU_260	H, I_LEU_260	2.77	2.06	28.49
5VXJ.PDB	O, I_LEU_257	N, I_ASP_261	H, I_ASP_261	2.89	2.05	10.23
5VXJ.PDB	O, I_VAL_188	N, I_LEU_271	H, I_LEU_271	2.63	1.80	11.88
5VXJ.PDB	O, I_LYS_275	N, I_TRP_279	H, I_TRP_279	2.89	2.08	15.60
5VXJ.PDB	O, I_TYR_276	N, I_ASN_280	H, I_ASN_280	2.72	1.88	10.70
5VXJ.PDB	O, I_TRP_279	N, I_PHE_283	H, I_PHE_283	2.84	1.99	5.52
5VXJ.PDB	O, I_ASN_280	N, I_SER_284	H, I_SER_284	2.88	2.09	19.38
5VXJ.PDB	O, I_ASN_280	OG, I_SER_284	HG, I_SER_284	2.54	1.77	19.23
5VXJ.PDB	O, I_ALA_281	N, I_ALA_285	H, I_ALA_285	2.96	2.25	29.29
5VXJ.PDB	O, I_SER_284	N, I_GLU_288	H, I_GLU_288	2.89	2.11	20.80
5VXJ.PDB	O, I_THR_289	N, I_ASN_293	H, I_ASN_293	2.83	2.00	11.34
5VXJ.PDB	O, I_MET_290	N, I_LEU_294	H, I_LEU_294	2.91	2.07	11.98
5VXJ.PDB	O, I_ASN_292	N, I_THR_296	H, I_THR_296	2.91	2.10	15.19
5VXJ.PDB	O, I_LEU_294	N, I_VAL_298	H, I_VAL_298	2.97	2.13	11.40
5VXJ.PDB	O, I_GLN_295	N, I_GLN_299	H, I_GLN_299	2.67	1.83	9.61
5VXJ.PDB	O, I_THR_296	N, I_LYS_300	H, I_LYS_300	2.79	1.96	13.56
5VXJ.PDB	O, I_LEU_297	N, I_TYR_301	H, I_TYR_301	2.86	2.02	11.85
5VXJ.PDB	O, I_VAL_298	N, I_SER_302	H, I_SER_302	2.89	2.10	19.67
5VXJ.PDB	O, I_ASN_303	N, I_ILE_307	H, I_ILE_307	2.99	2.15	10.86
5VXJ.PDB	O, I_ALA_304	N, I_PHE_308	H, I_PHE_308	2.90	2.15	24.75
5VXJ.PDB	O, I_ASN_305	N, I_ASP_309	H, I_ASP_309	2.79	2.00	19.69
5VXJ.PDB	O, I_SER_306	N, I_ASN_310	H, I_ASN_310	2.75	1.93	13.59
5VXJ.PDB	O, I_ASP_309	N, I_LYS_313	H, I_LYS_313	2.84	2.05	19.66
5VXJ.PDB	O, I_LEU_311	N, I_LEU_315	H, I_LEU_315	2.80	1.96	10.49
5VXJ.PDB	O, I_VAL_312	N, I_SER_316	H, I_SER_316	3.00	2.19	16.29
5VXJ.PDB	O, I_LEU_315	OG1, I_THR_318	HG1, I_THR_318	2.75	2.04	26.52
5VXJ.PDB	O, I_LEU_315	N, I_ILE_319	H, I_ILE_319	2.98	2.22	23.66
5VXJ.PDB	O, J_SER_25	N, J_GLN_3	H, J_GLN_3	2.93	2.12	17.29
5VXJ.PDB	O, J_ALA_23	N, J_ALA_5	H, J_ALA_5	2.99	2.25	25.24
5VXJ.PDB	O, J_SER_21	N, J_THR_7	H, J_THR_7	2.92	2.17	25.75
5VXJ.PDB	O, J_GLN_114	N, J_GLY_10	H, J_GLY_10	2.89	2.04	6.92
5VXJ.PDB	O, J_THR_116	N, J_ALA_12	H, J_ALA_12	2.87	2.12	24.55
5VXJ.PDB	O, J_LEU_86	N, J_GLY_15	H, J_GLY_15	2.84	2.02	14.92
5VXJ.PDB	O, J_GLN_13	N, J_GLY_16	H, J_GLY_16	2.95	2.13	13.71
5VXJ.PDB	O, J_MET_83	N, J_LEU_18	H, J_LEU_18	2.83	2.07	23.77
5VXJ.PDB	OE1, J_GLN_82	NE, J_ARG_19	HE, J_ARG_19	2.52	1.72	17.43
5VXJ.PDB	O, J_THR_7	N, J_SER_21	H, J_SER_21	2.88	2.09	20.19
5VXJ.PDB	O, J_ASN_77	N, J_ALA_24	H, J_ALA_24	2.97	2.12	7.90
5VXJ.PDB	O, J_GLY_99	N, J_VAL_33	H, J_VAL_33	2.92	2.10	15.57
5VXJ.PDB	O, J_ASN_97	N, J_ASN_35	H, J_ASN_35	2.70	1.87	12.63
5VXJ.PDB	OD1, J_ASN_97	ND2, J_ASN_35	HD22, J_ASN_35	3.00	2.21	19.94
5VXJ.PDB	O, J_ALA_49	N, J_TRP_36	H, J_TRP_36	2.88	2.04	12.12
5VXJ.PDB	O, J_VAL_95	N, J_TYR_37	H, J_TYR_37	2.66	1.81	6.37
5VXJ.PDB	OD1, J_ASP_90	NH1, J_ARG_38	HH12, J_ARG_38	2.89	2.13	23.59
5VXJ.PDB	OE2, J_GLU_46	NH2, J_ARG_38	HH21, J_ARG_38	2.77	1.96	16.80
5VXJ.PDB	O, J_ARG_38	N, J_GLU_46	H, J_GLU_46	2.68	1.85	12.20
5VXJ.PDB	O, J_TRP_36	N, J_VAL_48	H, J_VAL_48	2.83	2.01	13.87
5VXJ.PDB	O, J_SER_59	N, J_ARG_50	H, J_ARG_50	2.92	2.18	25.84
5VXJ.PDB	OD1, J_ASN_35	NE, J_ARG_50	HE, J_ARG_50	2.74	1.91	11.68
5VXJ.PDB	O, J_SER_30	OH, J_TYR_52	HH, J_TYR_52	2.67	1.83	3.11
5VXJ.PDB	OD1, J_ASP_53	N, J_GLY_55	H, J_GLY_55	2.81	1.99	15.68
5VXJ.PDB	O, J_ARG_50	N, J_SER_59	H, J_SER_59	2.68	1.87	16.27
5VXJ.PDB	O, J_VAL_48	N, J_ALA_61	H, J_ALA_61	2.84	2.03	16.19

5VXJ.PDB	O, J_VAL_64	N, J_ARG_67	H, J_ARG_67	2.97	2.13	10.41
5VXJ.PDB	O, J_SER_85	NH1, J_ARG_67	HH11, J_ARG_67	2.90	2.16	26.24
5VXJ.PDB	OD2, J_ASP_90	NH1, J_ARG_67	HH12, J_ARG_67	2.55	1.74	16.72
5VXJ.PDB	OD1, J_ASP_90	NH2, J_ARG_67	HH22, J_ARG_67	2.84	1.98	5.11
5VXJ.PDB	O, J_VAL_64	N, J_PHE_68	H, J_PHE_68	2.99	2.15	10.61
5VXJ.PDB	O, J_HIS_80	N, J_SER_71	H, J_SER_71	2.98	2.20	21.12
5VXJ.PDB	O, J_ALA_32	NH2, J_ARG_72	HH22, J_ARG_72	2.52	1.69	13.12
5VXJ.PDB	O, J_THR_78	N, J_ASP_73	H, J_ASP_73	2.84	2.00	9.78
5VXJ.PDB	O, J_SER_71	N, J_HIS_80	H, J_HIS_80	2.97	2.18	20.55
5VXJ.PDB	O, J_THR_69	N, J_GLN_82	H, J_GLN_82	2.81	2.10	29.71
5VXJ.PDB	OD1, J_ASN_84	NE2, J_GLN_82	HE21, J_GLN_82	2.94	2.08	3.32
5VXJ.PDB	O, J_LEU_18	N, J_MET_83	H, J_MET_83	2.68	1.83	7.41
5VXJ.PDB	OD2, J_ASP_90	N, J_LYS_87	H, J_LYS_87	2.89	2.11	21.60
5VXJ.PDB	O, J_GLN_39	N, J_MET_93	H, J_MET_93	2.84	2.02	15.68
5VXJ.PDB	O, J_THR_113	N, J_TYR_94	H, J_TYR_94	2.95	2.11	9.77
5VXJ.PDB	O, J_ASP_90	OH, J_TYR_94	HH, J_TYR_94	2.90	2.08	7.74
5VXJ.PDB	O, J_ASN_35	N, J_ASN_97	H, J_ASN_97	2.69	1.93	22.73
5VXJ.PDB	OG1, J_THR_107	ND2, J_ASN_97	HD21, J_ASN_97	2.57	1.77	17.56
5VXJ.PDB	O, J_VAL_33	N, J_GLY_99	H, J_GLY_99	2.77	1.92	8.58
5VXJ.PDB	O, J_ARG_106	N, J_ILE_100	H, J_ILE_100	2.88	2.03	4.95
5VXJ.PDB	O, J_ARG_31	N, J_PHE_101	H, J_PHE_101	2.81	1.97	10.82
5VXJ.PDB	O, J_ALA_98	OG1, J_THR_107	HG1, J_THR_107	2.84	2.12	25.86
5VXJ.PDB	O, I_THR_217	NE2, J_GLN_111	HE22, J_GLN_111	2.92	2.11	16.33
5VXJ.PDB	OE1, J_GLU_6	N, J_GLY_112	H, J_GLY_112	2.94	2.09	6.96
5VXJ.PDB	O, J_TYR_94	N, J_THR_113	H, J_THR_113	2.80	1.97	13.72
5VXJ.PDB	OG1, J_THR_91	N, J_VAL_117	H, J_VAL_117	2.75	1.90	8.09

Table 1720: 5VXJ-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5VXK.PDB	O, B_SER_21	N, B_SER_7	H, B_SER_7	2.86	2.13	26.17
5VXK.PDB	O, B_GLN_13	N, B_GLY_16	H, B_GLY_16	2.95	2.16	18.88
5VXK.PDB	O, B_MET_83	N, B_LEU_18	H, B_LEU_18	2.96	2.15	15.77
5VXK.PDB	O, B_LEU_81	N, B_LEU_20	H, B_LEU_20	2.96	2.23	26.63
5VXK.PDB	O, B_VAL_79	N, B_CYS_22	H, B_CYS_22	2.62	1.80	13.05
5VXK.PDB	O, B_VAL_5	N, B_ALA_23	H, B_ALA_23	2.80	1.94	5.13
5VXK.PDB	OD1, B_ASN_77	N, B_LEU_29	H, B_LEU_29	2.87	2.10	22.34
5VXK.PDB	O, B_SER_49	N, B_TRP_36	H, B_TRP_36	2.81	1.99	12.98
5VXK.PDB	O, B_TYR_95	N, B_PHE_37	H, B_PHE_37	2.70	1.90	18.05
5VXK.PDB	O, B_GLU_46	N, B_ARG_38	H, B_ARG_38	2.93	2.12	16.27
5VXK.PDB	O, B_ARG_38	N, B_GLU_46	H, B_GLU_46	2.99	2.14	5.94
5VXK.PDB	O, B_TRP_36	N, B_VAL_48	H, B_VAL_48	2.67	1.86	15.37
5VXK.PDB	O, B_SER_59	N, B_CYS_50	H, B_CYS_50	2.88	2.12	22.90
5VXK.PDB	O, B_ILE_34	N, B_ILE_51	H, B_ILE_51	2.91	2.11	17.59
5VXK.PDB	O, B_THR_57	N, B_SER_52	H, B_SER_52	2.96	2.19	22.56
5VXK.PDB	O, B_GLN_106	OG1, B_THR_57	HG1, B_THR_57	2.72	2.03	28.93
5VXK.PDB	O, B_CYS_50	N, B_SER_59	H, B_SER_59	2.94	2.13	16.19
5VXK.PDB	O, B_VAL_48	N, B_SER_61	H, B_SER_61	2.73	1.90	12.27
5VXK.PDB	OD2, B_ASP_90	NH2, B_ARG_67	HH22, B_ARG_67	2.27	1.58	28.79
5VXK.PDB	OH, B_TYR_60	N, B_ILE_70	H, B_ILE_70	2.93	2.10	13.23
5VXK.PDB	O, B_SER_52	NH1, B_ARG_72	HH11, B_ARG_72	2.49	1.76	25.78
5VXK.PDB	O, B_ARG_78	N, B_ASP_73	H, B_ASP_73	2.58	1.73	6.46
5VXK.PDB	O, B_ASP_73	N, B_ARG_78	H, B_ARG_78	2.89	2.11	20.69
5VXK.PDB	O, B_CYS_22	N, B_VAL_79	H, B_VAL_79	2.94	2.14	17.09
5VXK.PDB	O, B_LEU_20	N, B_LEU_81	H, B_LEU_81	2.95	2.13	15.57
5VXK.PDB	O, B_THR_69	N, B_GLN_82	H, B_GLN_82	2.72	1.89	13.34
5VXK.PDB	O, B_LEU_18	N, B_MET_83	H, B_MET_83	2.84	2.03	16.84
5VXK.PDB	O, B_VAL_124	N, B_ALA_92	H, B_ALA_92	2.95	2.21	25.44
5VXK.PDB	O, B_PHE_37	N, B_TYR_95	H, B_TYR_95	2.71	1.89	14.49
5VXK.PDB	O, B_ALA_35	N, B_ALA_97	H, B_ALA_97	2.83	2.02	15.30
5VXK.PDB	O, B_VAL_117	N, B_ALA_98	H, B_ALA_98	2.99	2.21	21.08
5VXK.PDB	OD1, A_ASN_280	N, B_SER_103	H, B_SER_103	2.64	1.78	2.03
5VXK.PDB	OD1, A_ASN_280	N, B_VAL_104	H, B_VAL_104	2.84	2.01	12.48
5VXK.PDB	OG, A_SER_168	NE2, B_GLN_106	HE21, B_GLN_106	2.99	2.23	24.43
5VXK.PDB	OD2, A_ASP_287	NE2, B_GLN_106	HE22, B_GLN_106	2.77	1.94	12.81
5VXK.PDB	O, B_ILE_111	ND1, B_HIS_115	HD1, B_HIS_115	2.77	2.01	23.21
5VXK.PDB	O, B_GLY_113	NE, B_ARG_116	HE, B_ARG_116	2.86	2.06	17.67
5VXK.PDB	O, B_HIS_115	NE1, B_TRP_118	HE1, B_TRP_118	2.75	1.99	22.39
5VXK.PDB	OE1, B_GLU_6	N, B_GLY_121	H, B_GLY_121	2.76	1.92	11.78
5VXK.PDB	O, B_ALA_92	N, B_VAL_124	H, B_VAL_124	2.96	2.14	13.72
5VXK.PDB	OG1, B_THR_91	N, B_VAL_126	H, B_VAL_126	2.92	2.13	18.63
5VXK.PDB	O, A_LEU_44	N, A_ASN_48	H, A_ASN_48	2.73	1.91	14.91
5VXK.PDB	O, A_MET_46	N, A_THR_50	H, A_THR_50	2.82	1.97	7.12
5VXK.PDB	O, A_MET_46	OG1, A_THR_50	HG1, A_THR_50	2.68	1.85	7.57
5VXK.PDB	O, A_LEU_47	N, A_LEU_51	H, A_LEU_51	2.82	2.05	22.07
5VXK.PDB	O, A_ASP_49	N, A_ASN_53	H, A_ASN_53	2.90	2.05	9.25
5VXK.PDB	O, A_ASN_53	OG1, A_THR_57	HG1, A_THR_57	2.98	2.23	23.33
5VXK.PDB	O, A_ILE_54	N, A_ASN_58	H, A_ASN_58	2.93	2.11	14.43
5VXK.PDB	O, A_THR_56	N, A_ALA_60	H, A_ALA_60	2.98	2.15	13.11
5VXK.PDB	O, A_THR_57	N, A_LEU_61	H, A_LEU_61	2.94	2.13	16.68
5VXK.PDB	O, A_THR_71	N, A_LEU_75	H, A_LEU_75	2.95	2.14	16.00
5VXK.PDB	O, A_SER_74	N, A_ILE_78	H, A_ILE_78	2.92	2.06	5.83
5VXK.PDB	O, A_LEU_75	N, A_ALA_79	H, A_ALA_79	2.85	2.04	15.25
5VXK.PDB	O, A_GLU_77	N, A_HIS_81	H, A_HIS_81	2.98	2.14	8.61
5VXK.PDB	O, A_HIS_81	N, A_ILE_85	H, A_ILE_85	2.94	2.14	17.36
5VXK.PDB	O, A_SER_82	N, A_SER_86	H, A_SER_86	2.95	2.11	11.27
5VXK.PDB	O, A_SER_83	N, A_MET_87	H, A_MET_87	2.97	2.19	21.87

5VXK.PDB	O, A_ILE_85	N, A_VAL_89	H, A_VAL_89	2.79	2.01	20.21
5VXK.PDB	O, A_SER_86	N, A_ASN_90	H, A_ASN_90	2.99	2.14	5.84
5VXK.PDB	O, A_ASP_88	N, A_SER_92	H, A_SER_92	2.74	1.93	15.12
5VXK.PDB	O, A_ASP_88	OG, A_SER_92	HG, A_SER_92	3.00	2.29	28.37
5VXK.PDB	O, A_VAL_89	N, A_ALA_93	H, A_ALA_93	2.64	1.84	17.64
5VXK.PDB	O, A_SER_92	N, A_LEU_96	H, A_LEU_96	2.92	2.12	17.09
5VXK.PDB	O, A_LEU_96	N, A_SER_100	H, A_SER_100	2.70	1.93	21.92
5VXK.PDB	O, A_ARG_132	OG, A_SER_100	HG, A_SER_100	2.56	1.76	14.48
5VXK.PDB	O, A_ILE_98	N, A_ASN_102	H, A_ASN_102	2.91	2.05	5.88
5VXK.PDB	O, A_ILE_129	NH1, A_ARG_111	HH12, A_ARG_111	2.59	1.79	17.96
5VXK.PDB	O, A_ARG_111	N, A_LEU_114	H, A_LEU_114	2.85	2.05	18.01
5VXK.PDB	O, A_LEU_114	N, A_ALA_117	H, A_ALA_117	2.88	2.04	10.22
5VXK.PDB	O, A_TYR_104	NE1, A_TRP_135	HE1, A_TRP_135	2.54	1.70	9.79
5VXK.PDB	O, A_GLU_133	N, A_LYS_137	H, A_LYS_137	2.56	1.75	16.84
5VXK.PDB	O, A_LEU_134	N, A_ILE_138	H, A_ILE_138	2.73	1.96	22.76
5VXK.PDB	O, A_ALA_136	N, A_ASN_140	H, A_ASN_140	2.97	2.13	10.71
5VXK.PDB	O, A_ASN_140	N, A_ASP_144	H, A_ASP_144	2.65	1.81	8.85
5VXK.PDB	O, A_ASN_143	N, A_GLU_147	H, A_GLU_147	2.75	1.98	21.76
5VXK.PDB	O, A_ASP_144	N, A_GLN_148	H, A_GLN_148	2.72	1.87	4.64
5VXK.PDB	O, A_ASN_146	N, A_LYS_151	H, A_LYS_151	2.89	2.03	2.48
5VXK.PDB	O, A_LEU_150	N, A_GLU_154	H, A_GLU_154	2.80	1.99	16.19
5VXK.PDB	O, A_TYR_153	N, A_VAL_157	H, A_VAL_157	2.98	2.12	4.91
5VXK.PDB	O, A_HIS_155	N, A_SER_159	H, A_SER_159	2.74	1.89	9.23
5VXK.PDB	O, A_ALA_156	N, A_TYR_160	H, A_TYR_160	2.93	2.08	2.62
5VXK.PDB	O, A_VAL_157	N, A_THR_161	H, A_THR_161	2.80	1.98	15.42
5VXK.PDB	O, A_VAL_157	OG1, A_THR_161	HG1, A_THR_161	2.57	1.86	27.02
5VXK.PDB	O, A_SER_158	N, A_GLN_162	H, A_GLN_162	2.99	2.13	2.67
5VXK.PDB	O, A_TYR_160	N, A_TYR_164	H, A_TYR_164	2.84	2.00	11.73
5VXK.PDB	OD2, A_ASP_287	OH, A_TYR_164	HH, A_TYR_164	2.91	2.21	28.15
5VXK.PDB	O, A_THR_161	N, A_GLN_165	H, A_GLN_165	2.79	1.96	12.75
5VXK.PDB	O, A_MET_163	N, A_PHE_167	H, A_PHE_167	2.79	1.98	16.43
5VXK.PDB	O, A_TYR_164	N, A_SER_168	H, A_SER_168	2.63	1.79	8.68
5VXK.PDB	O, A_GLN_165	N, A_ALA_169	H, A_ALA_169	2.96	2.21	24.63
5VXK.PDB	O, A_SER_168	N, A_SER_172	H, A_SER_172	2.96	2.20	23.46
5VXK.PDB	O, A_LYS_189	N, A_SER_179	H, A_SER_179	2.81	2.06	25.54
5VXK.PDB	O, A_LEU_271	N, A_VAL_188	H, A_VAL_188	2.72	1.94	20.48
5VXK.PDB	O, A_SER_179	N, A_LYS_189	H, A_LYS_189	2.77	1.93	11.30
5VXK.PDB	O, A_VAL_269	N, A_LEU_190	H, A_LEU_190	2.98	2.14	11.69
5VXK.PDB	O, A_TRP_177	N, A_GLN_191	H, A_GLN_191	2.79	1.96	11.53
5VXK.PDB	O, A_GLN_191	N, A_LEU_195	H, A_LEU_195	2.98	2.12	0.40
5VXK.PDB	O, A_VAL_192	N, A_LYS_196	H, A_LYS_196	2.70	1.92	21.14
5VXK.PDB	OD2, A_ASP_261	NZ, A_LYS_196	HZ3, A_LYS_196	2.74	1.87	9.57
5VXK.PDB	O, A_ASN_193	N, A_LYS_197	H, A_LYS_197	2.84	1.99	8.82
5VXK.PDB	O, A_SER_194	N, A_ALA_198	H, A_ALA_198	2.95	2.12	13.78
5VXK.PDB	O, A_LYS_196	N, A_GLU_200	H, A_GLU_200	2.92	2.18	26.73
5VXK.PDB	O, A_LYS_197	N, A_GLU_201	H, A_GLU_201	2.99	2.17	14.72
5VXK.PDB	O, A_GLU_200	N, A_GLU_204	H, A_GLU_204	2.87	2.03	10.71
5VXK.PDB	O, A_VAL_246	N, A_LEU_211	H, A_LEU_211	2.69	1.92	21.70
5VXK.PDB	O, A_SER_219	N, A_ALA_223	H, A_ALA_223	2.87	2.01	6.41
5VXK.PDB	O, A_GLN_222	N, A_TRP_226	H, A_TRP_226	2.85	2.07	21.25
5VXK.PDB	O, A_ASN_224	N, A_THR_228	H, A_THR_228	2.67	1.85	13.34
5VXK.PDB	O, A_GLY_231	N, A_THR_233	H, A_THR_233	2.55	1.79	23.98
5VXK.PDB	O, A_SER_247	N, A_LYS_236	H, A_LYS_236	2.76	1.98	20.26
5VXK.PDB	O, A_VAL_245	N, A_SER_238	H, A_SER_238	2.92	2.13	19.88
5VXK.PDB	O, A_TYR_212	N, A_VAL_246	H, A_VAL_246	2.83	1.98	7.21
5VXK.PDB	O, A_LYS_236	N, A_SER_247	H, A_SER_247	2.77	1.95	15.51
5VXK.PDB	O, A_ILE_234	N, A_ASN_249	H, A_ASN_249	2.90	2.07	12.40
5VXK.PDB	OD1, A_ASN_249	N, A_THR_251	H, A_THR_251	2.95	2.10	9.19

5VXK.PDB	O, A_MET.250	N, A_ASP.254	H, A_ASP.254	2.78	1.96	13.63
5VXK.PDB	O, A_THR.251	N, A_ASN.255	H, A_ASN.255	2.70	1.89	17.04
5VXK.PDB	O, A_ASP.254	N, A_LYS.258	H, A_LYS.258	2.95	2.18	22.11
5VXK.PDB	O, A_ASN.255	N, A_SER.259	H, A_SER.259	2.99	2.21	21.36
5VXK.PDB	O, A_MET.256	OG, A_SER.259	HG, A_SER.259	2.72	1.88	2.53
5VXK.PDB	O, A_LEU.257	N, A_ASP.261	H, A_ASP.261	2.96	2.15	15.35
5VXK.PDB	O, A_LYS.258	N, A_ASN.262	H, A_ASN.262	3.00	2.20	18.58
5VXK.PDB	O, A_VAL.188	N, A_LEU.271	H, A_LEU.271	2.82	1.97	7.95
5VXK.PDB	O, A_ASN.186	N, A_ASN.273	H, A_ASN.273	2.88	2.14	26.01
5VXK.PDB	O, A_ASP.272	N, A_TYR.276	H, A_TYR.276	2.84	2.01	12.24
5VXK.PDB	OG1, B_THR.102	OH, A_TYR.276	HH, A_TYR.276	2.57	1.73	6.50
5VXK.PDB	O, A_ASN.273	N, A_GLN.277	H, A_GLN.277	2.84	2.02	14.45
5VXK.PDB	O, A_LYS.275	N, A_TRP.279	H, A_TRP.279	2.92	2.06	3.36
5VXK.PDB	O, A_TYR.276	N, A_ASN.280	H, A_ASN.280	2.71	1.86	7.15
5VXK.PDB	O, A_GLN.277	N, A_ALA.281	H, A_ALA.281	2.91	2.11	18.24
5VXK.PDB	O, A_ALA.281	N, A_ALA.285	H, A_ALA.285	2.89	2.13	23.89
5VXK.PDB	O, A_ASP.287	N, A_LYS.291	H, A_LYS.291	2.81	1.95	4.20
5VXK.PDB	O, A_GLU.288	N, A_ASN.292	H, A_ASN.292	2.77	1.96	17.31
5VXK.PDB	O, A_THR.289	N, A_ASN.293	H, A_ASN.293	2.79	1.96	12.40
5VXK.PDB	OH, A_TYR.160	ND2, A_ASN.293	HD22, A_ASN.293	2.77	1.97	18.05
5VXK.PDB	O, A_MET.290	N, A_LEU.294	H, A_LEU.294	2.88	2.05	13.48
5VXK.PDB	O, A_ASN.292	N, A_THR.296	H, A_THR.296	2.98	2.19	19.74
5VXK.PDB	O, A_LEU.294	N, A_VAL.298	H, A_VAL.298	2.93	2.09	11.47
5VXK.PDB	O, A_GLN.295	N, A_GLN.299	H, A_GLN.299	2.92	2.19	26.68
5VXK.PDB	O, A_THR.296	N, A_LYS.300	H, A_LYS.300	2.95	2.12	13.38
5VXK.PDB	O, A_LEU.297	N, A_TYR.301	H, A_TYR.301	2.89	2.06	12.10
5VXK.PDB	O, A_VAL.298	N, A_SER.302	H, A_SER.302	2.77	1.95	14.37
5VXK.PDB	O, A_GLN.299	N, A_ASN.303	H, A_ASN.303	2.69	1.84	7.73
5VXK.PDB	O, A_ALA.304	N, A_PHE.308	H, A_PHE.308	2.91	2.07	9.74
5VXK.PDB	O, A_ASN.305	N, A_ASP.309	H, A_ASP.309	2.69	1.83	5.55
5VXK.PDB	O, A_SER.306	N, A_ASN.310	H, A_ASN.310	2.96	2.11	5.89
5VXK.PDB	O, A_PHE.308	N, A_VAL.312	H, A_VAL.312	2.89	2.04	4.79
5VXK.PDB	O, A_ASP.309	N, A_LYS.313	H, A_LYS.313	2.99	2.14	4.76
5VXK.PDB	O, A_LEU.311	N, A_LEU.315	H, A_LEU.315	2.77	1.95	15.34
5VXK.PDB	O, A_VAL.312	N, A_SER.316	H, A_SER.316	2.86	2.04	13.60
5VXK.PDB	O, A_VAL.314	N, A_THR.318	H, A_THR.318	2.93	2.12	16.50
5VXK.PDB	O, A_LEU.315	N, A_ILE.319	H, A_ILE.319	2.77	1.92	6.38
5VXK.PDB	O, A_SER.316	N, A_SER.320	H, A_SER.320	2.83	1.98	7.77
5VXK.PDB	O, A_SER.316	OG, A_SER.320	HG, A_SER.320	2.92	2.19	24.37
5VXK.PDB	O, A_SER.317	OG, A_SER.321	HG, A_SER.321	2.91	2.13	18.92

Table 1721: 5VXK-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5VXL.PDB	O, A_SER_42	N, A_MET_46	H, A_MET_46	2.87	2.01	3.50
5VXL.PDB	O, A_LEU_44	N, A_ASN_48	H, A_ASN_48	2.76	1.92	10.16
5VXL.PDB	O, A_THR_45	N, A_ASP_49	H, A_ASP_49	2.99	2.15	12.53
5VXL.PDB	O, A_MET_46	OG1, A_THR_50	HG1, A_THR_50	2.62	1.82	14.28
5VXL.PDB	O, A_LEU_47	N, A_LEU_51	H, A_LEU_51	2.90	2.10	17.57
5VXL.PDB	O, A_HIS_52	N, A_THR_56	H, A_THR_56	2.90	2.15	24.51
5VXL.PDB	O, A_ILE_54	N, A_ASN_58	H, A_ASN_58	2.71	1.88	13.56
5VXL.PDB	OD1, A_ASP_309	ND2, A_ASN_58	HD22, A_ASN_58	2.92	2.09	13.70
5VXL.PDB	O, A_THR_57	N, A_LEU_61	H, A_LEU_61	2.89	2.12	22.63
5VXL.PDB	O, A_THR_73	N, A_GLU_77	H, A_GLU_77	2.82	2.00	14.04
5VXL.PDB	O, A_SER_74	N, A_ILE_78	H, A_ILE_78	2.96	2.13	11.95
5VXL.PDB	OE1, A_GLU_154	OG, A_SER_82	HG, A_SER_82	2.52	1.77	21.68
5VXL.PDB	O, A_ALA_79	N, A_SER_83	H, A_SER_83	2.92	2.10	15.30
5VXL.PDB	O, A_LEU_80	N, A_GLN_84	H, A_GLN_84	2.91	2.12	19.31
5VXL.PDB	OD2, A_ASP_88	NE2, A_GLN_84	HE21, A_GLN_84	2.89	2.16	27.92
5VXL.PDB	O, A_HIS_81	N, A_ILE_85	H, A_ILE_85	2.85	2.01	10.10
5VXL.PDB	O, A_SER_82	N, A_SER_86	H, A_SER_86	2.94	2.14	18.49
5VXL.PDB	O, A_SER_82	OG, A_SER_86	HG, A_SER_86	2.79	1.98	12.76
5VXL.PDB	O, A_GLN_84	N, A_ASP_88	H, A_ASP_88	2.93	2.10	13.48
5VXL.PDB	O, A_ILE_85	N, A_VAL_89	H, A_VAL_89	2.78	1.95	11.84
5VXL.PDB	O, A_ASP_88	N, A_SER_92	H, A_SER_92	2.92	2.08	10.89
5VXL.PDB	O, A_ASP_88	OG, A_SER_92	HG, A_SER_92	2.87	2.05	11.00
5VXL.PDB	O, A_VAL_89	N, A_ALA_93	H, A_ALA_93	2.95	2.11	11.37
5VXL.PDB	O, A_LYS_91	N, A_LEU_95	H, A_LEU_95	2.97	2.17	17.92
5VXL.PDB	O, A_SER_92	N, A_LEU_96	H, A_LEU_96	2.63	1.78	7.72
5VXL.PDB	O, A_ALA_93	N, A_ASP_97	H, A_ASP_97	2.67	1.89	19.80
5VXL.PDB	O, A_SER_100	N, A_GLU_103	H, A_GLU_103	2.79	2.00	19.85
5VXL.PDB	O, A_PRO_118	N, A_ALA_121	H, A_ALA_121	2.84	2.03	15.32
5VXL.PDB	O, A_TYR_104	NE1, A_TRP_135	HE1, A_TRP_135	2.90	2.05	6.79
5VXL.PDB	O, A_GLU_133	N, A_LYS_137	H, A_LYS_137	2.91	2.15	23.30
5VXL.PDB	O, A_ALA_136	ND2, A_ASN_140	HD22, A_ASN_140	2.52	1.69	13.57
5VXL.PDB	O, A_ILE_138	N, A_ILE_142	H, A_ILE_142	2.68	1.84	10.96
5VXL.PDB	O, A_ASN_140	N, A_ASP_144	H, A_ASP_144	2.65	1.82	12.29
5VXL.PDB	O, A_SER_141	N, A_ILE_145	H, A_ILE_145	2.85	2.02	11.93
5VXL.PDB	O, A_ILE_145	N, A_LEU_150	H, A_LEU_150	2.86	2.08	21.09
5VXL.PDB	O, A_ASN_146	N, A_LYS_151	H, A_LYS_151	2.72	1.87	8.33
5VXL.PDB	O, A_TYR_153	N, A_VAL_157	H, A_VAL_157	2.99	2.14	9.15
5VXL.PDB	O, A_HIS_155	OG, A_SER_158	HG, A_SER_158	2.93	2.15	19.18
5VXL.PDB	O, A_HIS_155	N, A_SER_159	H, A_SER_159	2.66	1.80	3.85
5VXL.PDB	O, A_HIS_155	OG, A_SER_159	HG, A_SER_159	2.90	2.17	24.99
5VXL.PDB	O, A_ALA_156	N, A_TYR_160	H, A_TYR_160	2.93	2.09	8.00
5VXL.PDB	O, A_VAL_157	N, A_THR_161	H, A_THR_161	2.60	1.78	15.33
5VXL.PDB	O, A_VAL_157	OG1, A_THR_161	HG1, A_THR_161	2.46	1.70	20.64
5VXL.PDB	O, A_SER_158	N, A_GLN_162	H, A_GLN_162	2.84	1.98	1.63
5VXL.PDB	O, A_TYR_160	N, A_TYR_164	H, A_TYR_164	2.84	2.00	8.81
5VXL.PDB	O, A_THR_161	N, A_GLN_165	H, A_GLN_165	2.72	1.90	14.74
5VXL.PDB	O, A_TYR_164	N, A_SER_168	H, A_SER_168	2.87	2.04	11.91
5VXL.PDB	O, A_TYR_164	OG, A_SER_168	HG, A_SER_168	2.96	2.15	13.58
5VXL.PDB	O, A_PHE_167	N, A_LEU_171	H, A_LEU_171	2.92	2.16	23.19
5VXL.PDB	O, A_SER_168	N, A_SER_172	H, A_SER_172	2.92	2.12	18.79
5VXL.PDB	O, A_LYS_189	N, A_SER_179	H, A_SER_179	2.93	2.11	16.24
5VXL.PDB	O, A_SER_187	N, A_GLY_181	H, A_GLY_181	2.88	2.06	15.19
5VXL.PDB	O, A_SER_179	N, A_LYS_189	H, A_LYS_189	2.63	1.86	21.36
5VXL.PDB	O, A_VAL_269	N, A_LEU_190	H, A_LEU_190	2.66	1.92	26.28
5VXL.PDB	O, A_TRP_177	N, A_GLN_191	H, A_GLN_191	2.89	2.06	12.45
5VXL.PDB	O, A_VAL_192	N, A_LYS_196	H, A_LYS_196	2.82	1.98	9.06
5VXL.PDB	O, A_ASN_193	N, A_LYS_197	H, A_LYS_197	2.99	2.13	1.38

5VXL.PDB	O, A_LEU_195	N, A_LEU_199	H, A_LEU_199	2.96	2.13	13.84
5VXL.PDB	O, A_LYS_196	N, A_GLU_200	H, A_GLU_200	2.68	1.83	8.42
5VXL.PDB	O, A_LYS_197	N, A_GLU_201	H, A_GLU_201	2.99	2.18	15.98
5VXL.PDB	OD1, A ASP_254	NZ, A_LYS_203	HZ3, A_LYS_203	2.55	1.71	15.49
5VXL.PDB	O, A_GLU_201	N, A_LYS_205	H, A_LYS_205	2.94	2.16	21.06
5VXL.PDB	OD2, B ASP_52	NZ, A_LYS_205	HZ1, A_LYS_205	3.00	2.13	10.69
5VXL.PDB	OD2, A ASP_166	OH, A_TYR_206	HH, A_TYR_206	2.43	1.61	11.33
5VXL.PDB	O, A_SER_219	N, A_ALA_223	H, A_ALA_223	2.65	1.81	10.36
5VXL.PDB	O, A_GLN_220	N, A_ASN_224	H, A_ASN_224	2.69	1.83	3.86
5VXL.PDB	OE1, A_GLN_148	NE1, A_TRP_226	HE1, A_TRP_226	2.87	2.02	9.28
5VXL.PDB	O, A_ALA_223	N, A_LEU_227	H, A_LEU_227	2.81	2.00	17.07
5VXL.PDB	O, A_TRP_226	N, A_LEU_230	H, A_LEU_230	2.94	2.11	10.97
5VXL.PDB	O, A_LEU_227	N, A_GLY_231	H, A_GLY_231	2.69	1.85	9.90
5VXL.PDB	O, A_GLY_243	N, A_LYS_240	H, A_LYS_240	2.98	2.14	10.92
5VXL.PDB	O, A_VAL_218	N, A_TYR_244	H, A_TYR_244	2.96	2.11	6.92
5VXL.PDB	O, A_SER_238	N, A_VAL_245	H, A_VAL_245	2.99	2.26	27.20
5VXL.PDB	O, A_TYR_212	N, A_VAL_246	H, A_VAL_246	2.52	1.74	20.61
5VXL.PDB	O, A_ILE_234	N, A_ASN_249	H, A_ASN_249	2.93	2.09	9.83
5VXL.PDB	OD1, A_ASN_249	N, A_THR_251	H, A_THR_251	2.75	1.91	9.14
5VXL.PDB	O, A_MET_250	N, A ASP_254	H, A ASP_254	2.85	2.02	11.68
5VXL.PDB	O, A_THR_251	N, A_ASN_255	H, A_ASN_255	2.77	1.94	13.53
5VXL.PDB	OE2, A_GLU_286	ND2, A_ASN_255	HD22, A_ASN_255	2.74	1.94	17.54
5VXL.PDB	O, A_ILE_253	N, A_LEU_257	H, A_LEU_257	2.98	2.15	14.50
5VXL.PDB	O, A ASP_254	N, A_LYS_258	H, A_LYS_258	2.99	2.17	14.91
5VXL.PDB	O, A_ASN_255	N, A_SER_259	H, A_SER_259	2.97	2.14	13.88
5VXL.PDB	O, A_MET_256	N, A_LEU_260	H, A_LEU_260	2.88	2.07	16.61
5VXL.PDB	O, A_LEU_257	N, A ASP_261	H, A ASP_261	2.97	2.13	9.61
5VXL.PDB	O, A_LEU_260	N, A_LEU_263	H, A_LEU_263	2.99	2.27	28.32
5VXL.PDB	O, A_LEU_190	N, A_VAL_269	H, A_VAL_269	2.90	2.08	13.99
5VXL.PDB	O, A_VAL_188	N, A_LEU_271	H, A_LEU_271	2.85	2.02	11.38
5VXL.PDB	OD1, A ASP_272	N, A_ASN_273	H, A_ASN_273	2.65	1.95	29.16
5VXL.PDB	O, A_TYR_276	N, A_ASN_280	H, A_ASN_280	2.86	2.01	4.96
5VXL.PDB	O, A_TRP_279	N, A_PHE_283	H, A_PHE_283	2.89	2.08	16.09
5VXL.PDB	O, A_ASN_280	N, A_SER_284	H, A_SER_284	2.73	1.94	20.02
5VXL.PDB	O, A_ASN_280	OG, A_SER_284	HG, A_SER_284	2.71	1.94	20.16
5VXL.PDB	O, A_ALA_281	N, A_ALA_285	H, A_ALA_285	2.78	2.01	22.25
5VXL.PDB	O, A_ALA_285	N, A_THR_289	H, A_THR_289	2.98	2.16	14.81
5VXL.PDB	O, A ASP_287	N, A_LYS_291	H, A_LYS_291	2.89	2.06	14.03
5VXL.PDB	O, A_GLU_288	N, A_ASN_292	H, A_ASN_292	2.65	1.85	17.95
5VXL.PDB	O, A_THR_289	N, A_ASN_293	H, A_ASN_293	2.72	1.88	9.66
5VXL.PDB	O, A_MET_290	N, A_LEU_294	H, A_LEU_294	2.92	2.12	18.98
5VXL.PDB	O, A_ASN_292	N, A_THR_296	H, A_THR_296	2.80	2.02	20.58
5VXL.PDB	O, A_ASN_292	OG1, A_THR_296	HG1, A_THR_296	2.92	2.11	12.62
5VXL.PDB	O, A_LEU_294	N, A_VAL_298	H, A_VAL_298	2.97	2.14	12.75
5VXL.PDB	O, A_THR_296	N, A_LYS_300	H, A_LYS_300	2.96	2.11	7.04
5VXL.PDB	O, A_LEU_297	N, A_TYR_301	H, A_TYR_301	2.75	2.04	28.78
5VXL.PDB	O, A_VAL_298	N, A_SER_302	H, A_SER_302	2.75	1.91	8.45
5VXL.PDB	O, A_GLN_299	N, A_ASN_303	H, A_ASN_303	2.84	2.01	12.17
5VXL.PDB	O, A_TYR_301	N, A_ASN_305	H, A_ASN_305	2.82	2.10	28.03
5VXL.PDB	O, A_SER_302	N, A_SER_306	H, A_SER_306	2.92	2.14	21.23
5VXL.PDB	O, A_ASN_303	N, A_ILE_307	H, A_ILE_307	2.92	2.13	18.78
5VXL.PDB	O, A_ASN_305	N, A ASP_309	H, A ASP_309	2.71	1.93	21.31
5VXL.PDB	O, A_ILE_307	N, A_LEU_311	H, A_LEU_311	2.89	2.07	14.43
5VXL.PDB	O, A ASP_309	N, A_LYS_313	H, A_LYS_313	2.80	1.99	16.36
5VXL.PDB	O, A_ASN_310	N, A_VAL_314	H, A_VAL_314	2.86	2.01	5.31
5VXL.PDB	O, A_VAL_312	N, A_SER_316	H, A_SER_316	2.63	1.77	5.33
5VXL.PDB	O, A_VAL_314	OG1, A_THR_318	HG1, A_THR_318	2.55	1.72	7.64
5VXL.PDB	O, B_SER_25	N, B_GLN_3	H, B_GLN_3	2.70	1.85	6.65

5VXL.PDB	O, B_SER_21	N, B_SER_7	H, B_SER_7	2.62	1.81	16.40
5VXL.PDB	O, B_THR_114	N, B_VAL_12	H, B_VAL_12	2.86	2.04	13.69
5VXL.PDB	O, B_LEU_87	N, B_GLY_15	H, B_GLY_15	2.66	1.82	8.14
5VXL.PDB	O, B_GLN_13	N, B_GLY_16	H, B_GLY_16	2.79	1.96	12.54
5VXL.PDB	O, B_MET_84	N, B_LEU_18	H, B_LEU_18	2.84	2.08	22.47
5VXL.PDB	O, B_LEU_18	NH1, B_ARG_19	HH11, B_ARG_19	2.76	1.99	23.14
5VXL.PDB	O, B_SER_7	N, B_SER_21	H, B_SER_21	2.79	1.97	15.64
5VXL.PDB	O, B_VAL_80	N, B_CYS_22	H, B_CYS_22	2.67	1.84	12.31
5VXL.PDB	O, B_GLN_3	N, B_SER_25	H, B_SER_25	2.94	2.16	21.35
5VXL.PDB	O, B_ILE_51	N, B_MET_34	H, B_MET_34	2.85	2.13	28.16
5VXL.PDB	O, B_ASN_98	N, B_GLY_35	H, B_GLY_35	2.93	2.19	27.03
5VXL.PDB	O, B_TYR_96	N, B_TYR_37	H, B_TYR_37	2.76	1.92	10.99
5VXL.PDB	O, B_GLU_46	N, B_ARG_38	H, B_ARG_38	2.91	2.11	17.69
5VXL.PDB	OD1, B_ASP_91	NH1, B_ARG_38	HH12, B_ARG_38	2.97	2.23	26.01
5VXL.PDB	O, B_MET_34	N, B_ILE_51	H, B_ILE_51	2.82	1.98	9.96
5VXL.PDB	O, B_ILE_30	N, B_TYR_54	H, B_TYR_54	2.87	2.10	22.14
5VXL.PDB	O, A_ALA_198	OH, B_TYR_54	HH, B_TYR_54	2.38	1.67	27.03
5VXL.PDB	OD1, A_ASP_166	N, B_SER_55	H, B_SER_55	2.91	2.18	28.04
5VXL.PDB	OD1, A_ASP_166	OG, B_SER_55	HG, B_SER_55	2.56	1.73	4.68
5VXL.PDB	O, B_ALA_62	N, B_VAL_65	H, B_VAL_65	2.93	2.21	29.05
5VXL.PDB	OD2, B_ASP_91	NH1, B_ARG_68	HH12, B_ARG_68	2.83	2.06	22.74
5VXL.PDB	O, B_SER_64	NH2, B_ARG_68	HH21, B_ARG_68	2.89	2.07	15.16
5VXL.PDB	OD1, B_ASN_75	NE, B_ARG_73	HE, B_ARG_73	2.98	2.26	28.00
5VXL.PDB	O, B_TYR_32	NH1, B_ARG_73	HH12, B_ARG_73	2.99	2.21	21.42
5VXL.PDB	O, B_ARG_79	N, B_ASP_74	H, B_ASP_74	2.83	1.98	9.00
5VXL.PDB	OH, B_TYR_81	NE, B_ARG_79	HE, B_ARG_79	2.96	2.14	13.15
5VXL.PDB	O, B_CYS_22	N, B_VAL_80	H, B_VAL_80	2.66	1.84	14.02
5VXL.PDB	O, B_SER_72	N, B_TYR_81	H, B_TYR_81	2.82	1.97	3.12
5VXL.PDB	O, B_LEU_20	N, B_LEU_82	H, B_LEU_82	2.80	2.00	19.11
5VXL.PDB	O, B_LEU_18	N, B_MET_84	H, B_MET_84	2.92	2.06	5.88
5VXL.PDB	O, B_ARG_68	N, B_ASN_85	H, B_ASN_85	2.99	2.16	13.78
5VXL.PDB	O, B_GLY_16	N, B_LEU_87	H, B_LEU_87	2.89	2.07	14.28
5VXL.PDB	OD2, B_ASP_91	N, B_LYS_88	H, B_LYS_88	2.92	2.07	3.13
5VXL.PDB	O, B_LYS_88	N, B_ASP_91	H, B_ASP_91	2.90	2.09	15.76
5VXL.PDB	O, B_PRO_89	N, B_THR_92	H, B_THR_92	2.97	2.23	25.58
5VXL.PDB	O, B_VAL_113	N, B_ALA_93	H, B_ALA_93	2.99	2.24	25.85
5VXL.PDB	O, B_THR_111	N, B_TYR_95	H, B_TYR_95	2.79	2.00	19.66
5VXL.PDB	O, B_ASP_91	OH, B_TYR_95	HH, B_TYR_95	2.70	1.86	0.59
5VXL.PDB	O, B_TYR_37	N, B_TYR_96	H, B_TYR_96	2.76	2.02	25.56
5VXL.PDB	OE2, B_GLU_6	N, B_CYS_97	H, B_CYS_97	2.88	2.07	15.37
5VXL.PDB	O, B_GLY_35	N, B_ASN_98	H, B_ASN_98	2.73	1.91	13.08
5VXL.PDB	O, B_TYR_106	N, B_ALA_99	H, B_ALA_99	2.92	2.09	12.87
5VXL.PDB	O, B_ASN_33	N, B_ASN_100	H, B_ASN_100	2.79	2.01	20.69
5VXL.PDB	O, B_ASN_104	N, B_LEU_101	H, B_LEU_101	2.93	2.12	16.88
5VXL.PDB	OE2, A_GLU_201	NH2, B_ARG_102	HH22, B_ARG_102	2.87	2.08	20.03
5VXL.PDB	O, B_LEU_101	N, B_ASN_104	H, B_ASN_104	2.99	2.18	16.70
5VXL.PDB	O, B_ALA_99	N, B_TYR_106	H, B_TYR_106	2.85	2.08	22.40
5VXL.PDB	OE1, B_GLU_6	N, B_GLY_110	H, B_GLY_110	2.56	1.79	21.05
5VXL.PDB	O, B_ALA_93	N, B_VAL_113	H, B_VAL_113	2.86	2.05	16.79

Table 1722: 5VXL-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5VXM.PDB	O, A.SER.43	N, A.LEU.47	H, A.LEU.47	2.98	2.17	15.99
5VXM.PDB	O, A.THR.45	N, A.ASP.49	H, A.ASP.49	2.87	2.12	24.84
5VXM.PDB	O, A.LEU.47	N, A.LEU.51	H, A.LEU.51	2.78	1.93	8.20
5VXM.PDB	O, A.ASN.48	N, A.HIS.52	H, A.HIS.52	2.97	2.22	25.09
5VXM.PDB	O, A.HIS.52	OG1, A.THR.56	HG1, A.THR.56	2.93	2.14	17.08
5VXM.PDB	O, A.ILE.54	N, A.ASN.58	H, A.ASN.58	2.67	1.83	11.82
5VXM.PDB	OD1, A.ASP.309	ND2, A.ASN.58	HD22, A.ASN.58	2.74	1.89	5.63
5VXM.PDB	O, A.ARG.55	N, A.GLN.59	H, A.GLN.59	2.87	2.11	23.42
5VXM.PDB	O, A.THR.57	N, A.LEU.61	H, A.LEU.61	2.81	1.96	8.36
5VXM.PDB	O, A.ASN.58	N, A.LYS.62	H, A.LYS.62	2.92	2.12	18.24
5VXM.PDB	O, A.LYS.63	OG, A.SER.66	HG, A.SER.66	2.80	2.08	26.74
5VXM.PDB	O, A.THR.71	N, A.LEU.75	H, A.LEU.75	2.95	2.16	20.11
5VXM.PDB	O, A.SER.74	N, A.ILE.78	H, A.ILE.78	2.99	2.18	16.60
5VXM.PDB	O, A.LEU.75	N, A.ALA.79	H, A.ALA.79	2.89	2.06	11.29
5VXM.PDB	O, A.ILE.78	N, A.SER.82	H, A.SER.82	2.98	2.13	10.08
5VXM.PDB	O, A.ILE.78	OG, A.SER.82	HG, A.SER.82	2.83	2.02	14.46
5VXM.PDB	O, A.ALA.79	N, A.SER.83	H, A.SER.83	2.84	2.05	18.67
5VXM.PDB	O, A.LEU.80	N, A.GLN.84	H, A.GLN.84	2.64	1.80	8.82
5VXM.PDB	OD1, A.ASP.88	NE2, A.GLN.84	HE21, A.GLN.84	2.60	1.75	9.62
5VXM.PDB	O, A.HIS.81	N, A.ILE.85	H, A.ILE.85	2.65	1.82	12.85
5VXM.PDB	O, A.SER.82	OG, A.SER.86	HG, A.SER.86	2.97	2.14	6.66
5VXM.PDB	O, A.ILE.85	N, A.VAL.89	H, A.VAL.89	2.86	2.05	15.94
5VXM.PDB	O, A.MET.87	N, A.LYS.91	H, A.LYS.91	2.99	2.19	17.82
5VXM.PDB	O, A.ASP.88	N, A.SER.92	H, A.SER.92	2.77	1.94	12.57
5VXM.PDB	O, A.ILE.145	N, A.LEU.150	H, A.LEU.150	2.92	2.12	18.38
5VXM.PDB	O, A.ASN.146	N, A.LYS.151	H, A.LYS.151	2.86	2.02	9.54
5VXM.PDB	O, A.LEU.150	N, A.GLU.154	H, A.GLU.154	2.97	2.16	16.91
5VXM.PDB	O, A.VAL.152	N, A.ALA.156	H, A.ALA.156	2.98	2.13	8.33
5VXM.PDB	O, A.TYR.153	N, A.VAL.157	H, A.VAL.157	2.93	2.11	15.35
5VXM.PDB	O, A.GLU.154	N, A.SER.158	H, A.SER.158	2.98	2.18	17.97
5VXM.PDB	O, A.HIS.155	N, A.SER.159	H, A.SER.159	2.95	2.10	8.74
5VXM.PDB	O, A.VAL.157	N, A.THR.161	H, A.THR.161	2.89	2.06	13.47
5VXM.PDB	O, A.VAL.157	OG1, A.THR.161	HG1, A.THR.161	2.43	1.69	23.26
5VXM.PDB	O, A.SER.158	N, A.GLN.162	H, A.GLN.162	2.97	2.13	9.45
5VXM.PDB	O, A.SER.159	N, A.MET.163	H, A.MET.163	2.98	2.14	9.28
5VXM.PDB	O, A.TYR.160	N, A.TYR.164	H, A.TYR.164	2.84	2.00	11.12
5VXM.PDB	OD1, A.ASP.287	OH, A.TYR.164	HH, A.TYR.164	2.66	1.84	11.86
5VXM.PDB	O, A.THR.161	N, A.GLN.165	H, A.GLN.165	2.81	1.96	8.47
5VXM.PDB	O, A.LEU.70	NE2, A.GLN.165	HE21, A.GLN.165	2.72	1.96	23.75
5VXM.PDB	O, A.GLN.162	N, A.ASP.166	H, A.ASP.166	2.96	2.12	10.69
5VXM.PDB	O, A.MET.163	N, A.PHE.167	H, A.PHE.167	2.81	2.01	18.58
5VXM.PDB	O, A.TYR.164	N, A.SER.168	H, A.SER.168	2.79	2.00	19.99
5VXM.PDB	O, A.TYR.164	OG, A.SER.168	HG, A.SER.168	2.87	2.02	0.77
5VXM.PDB	O, A.SER.168	N, A.SER.172	H, A.SER.172	2.86	2.05	16.01
5VXM.PDB	O, A.LEU.171	N, A.LEU.174	H, A.LEU.174	2.94	2.11	13.11
5VXM.PDB	O, A.LEU.174	N, A.TRP.177	H, A.TRP.177	2.78	1.95	10.80
5VXM.PDB	OE2, B.GLU.111	NE1, A.TRP.177	HE1, A.TRP.177	2.76	1.97	19.61
5VXM.PDB	O, A.SER.187	N, A.GLY.181	H, A.GLY.181	2.97	2.17	18.19
5VXM.PDB	O, A.LEU.271	N, A.VAL.188	H, A.VAL.188	2.81	1.98	12.86
5VXM.PDB	O, A.SER.179	N, A.LYS.189	H, A.LYS.189	2.57	1.73	10.12
5VXM.PDB	O, A.VAL.269	N, A.LEU.190	H, A.LEU.190	2.87	2.05	15.09
5VXM.PDB	O, A.TRP.177	N, A.GLN.191	H, A.GLN.191	2.93	2.13	18.42
5VXM.PDB	O, A.VAL.192	N, A.LYS.196	H, A.LYS.196	2.81	1.97	10.63
5VXM.PDB	O, A.ASN.193	N, A.LYS.197	H, A.LYS.197	2.96	2.10	4.46
5VXM.PDB	O, A.LYS.196	N, A.GLU.200	H, A.GLU.200	2.84	2.04	17.32
5VXM.PDB	O, A.LEU.199	N, A.LYS.203	H, A.LYS.203	2.98	2.17	15.17
5VXM.PDB	O, A.GLU.200	N, A.GLU.204	H, A.GLU.204	2.89	2.04	8.12

5VXM.PDB	O, A_GLU_201	N, A_LYS_205	H, A_LYS_205	2.81	2.04	22.11
5VXM.PDB	OD2, A_ASP_166	NZ, A_LYS_205	HZ3, A_LYS_205	2.79	1.92	8.41
5VXM.PDB	OD2, A_ASP_166	OH, A_TYR_206	HH, A_TYR_206	2.53	1.73	14.26
5VXM.PDB	O, A_TYR_244	N, A_VAL_218	H, A_VAL_218	2.98	2.15	13.66
5VXM.PDB	O, A_SER_219	N, A_ALA_223	H, A_ALA_223	2.76	1.93	12.38
5VXM.PDB	O, A_GLN_220	ND2, A_ASN_224	HD22, A_ASN_224	2.78	1.96	13.87
5VXM.PDB	O, A_GLU_221	N, A_LYS_225	H, A_LYS_225	2.92	2.09	12.89
5VXM.PDB	O, A_ALA_223	N, A_LEU_227	H, A_LEU_227	2.97	2.23	26.22
5VXM.PDB	O, A_TRP_226	N, A_LEU_230	H, A_LEU_230	2.84	2.13	28.15
5VXM.PDB	O, A_LEU_227	N, A_GLY_231	H, A_GLY_231	2.67	1.83	9.65
5VXM.PDB	O, A_SER_247	N, A_LYS_236	H, A_LYS_236	2.94	2.17	23.09
5VXM.PDB	O, A_VAL_245	N, A_SER_238	H, A_SER_238	2.82	2.00	14.23
5VXM.PDB	O, A_GLY_243	N, A_LYS_240	H, A_LYS_240	2.90	2.05	7.30
5VXM.PDB	O, A_VAL_218	N, A_TYR_244	H, A_TYR_244	2.94	2.13	17.51
5VXM.PDB	O, A_TYR_212	N, A_VAL_246	H, A_VAL_246	2.67	1.83	9.46
5VXM.PDB	O, A_LYS_236	N, A_SER_247	H, A_SER_247	2.73	1.97	23.18
5VXM.PDB	O, A_ILE_234	N, A_ASN_249	H, A_ASN_249	2.66	1.81	8.12
5VXM.PDB	O, A_GLY_232	ND2, A_ASN_249	HD22, A_ASN_249	2.93	2.16	22.59
5VXM.PDB	OD1, A_ASN_249	N, A_THR_251	H, A_THR_251	2.92	2.07	8.88
5VXM.PDB	O, A_MET_250	N, A_ASP_254	H, A_ASP_254	2.82	1.99	10.70
5VXM.PDB	O, A_THR_251	N, A_ASN_255	H, A_ASN_255	2.65	1.83	15.00
5VXM.PDB	O, A_ILE_253	N, A_LEU_257	H, A_LEU_257	2.90	2.05	9.48
5VXM.PDB	O, A_ASP_254	N, A_LYS_258	H, A_LYS_258	2.93	2.08	4.06
5VXM.PDB	O, A_ASN_255	OG, A_SER_259	HG, A_SER_259	2.90	2.14	20.43
5VXM.PDB	O, A_MET_256	N, A_LEU_260	H, A_LEU_260	2.87	2.06	16.67
5VXM.PDB	O, A_LEU_257	N, A_ASP_261	H, A_ASP_261	2.90	2.07	12.51
5VXM.PDB	O, A_VAL_188	N, A_LEU_271	H, A_LEU_271	2.70	1.86	11.12
5VXM.PDB	O, A_TYR_276	N, A_ASN_280	H, A_ASN_280	2.79	1.94	7.45
5VXM.PDB	O, A_ALA_278	N, A_GLY_282	H, A_GLY_282	2.93	2.21	27.83
5VXM.PDB	O, A_TRP_279	N, A_PHE_283	H, A_PHE_283	2.71	1.90	16.14
5VXM.PDB	O, A_ALA_281	N, A_ALA_285	H, A_ALA_285	2.95	2.16	20.45
5VXM.PDB	O, A_GLY_282	N, A_GLU_286	H, A_GLU_286	2.89	2.04	9.37
5VXM.PDB	O, A_ALA_285	N, A_THR_289	H, A_THR_289	2.85	2.02	13.32
5VXM.PDB	O, A_GLU_286	N, A_MET_290	H, A_MET_290	2.99	2.16	12.67
5VXM.PDB	O, A_ASP_287	N, A_LYS_291	H, A_LYS_291	2.81	1.96	6.90
5VXM.PDB	OE2, A_GLU_288	NZ, A_LYS_291	HZ1, A_LYS_291	2.70	1.90	22.27
5VXM.PDB	O, A_GLU_288	N, A_ASN_292	H, A_ASN_292	2.85	2.03	14.40
5VXM.PDB	O, A_THR_289	N, A_ASN_293	H, A_ASN_293	2.86	2.04	14.91
5VXM.PDB	O, A_MET_290	N, A_LEU_294	H, A_LEU_294	2.98	2.18	17.50
5VXM.PDB	O, A_LYS_291	N, A_GLN_295	H, A_GLN_295	2.91	2.06	10.25
5VXM.PDB	O, A_ASN_292	N, A_THR_296	H, A_THR_296	2.99	2.15	11.78
5VXM.PDB	O, A_ASN_292	OG1, A_THR_296	HG1, A_THR_296	2.95	2.17	19.47
5VXM.PDB	O, A_LEU_294	N, A_VAL_298	H, A_VAL_298	2.79	1.95	9.51
5VXM.PDB	O, A_GLN_295	N, A_GLN_299	H, A_GLN_299	2.83	2.05	20.38
5VXM.PDB	O, A_VAL_298	N, A_SER_302	H, A_SER_302	2.97	2.12	8.83
5VXM.PDB	O, A_GLN_299	N, A_ASN_303	H, A_ASN_303	2.91	2.08	12.38
5VXM.PDB	O, A_LYS_300	N, A_ALA_304	H, A_ALA_304	2.94	2.10	8.88
5VXM.PDB	O, A_TYR_301	N, A_ASN_305	H, A_ASN_305	2.83	2.00	12.81
5VXM.PDB	O, A_SER_302	N, A_SER_306	H, A_SER_306	2.82	2.09	26.84
5VXM.PDB	O, A_ASN_303	N, A_ILE_307	H, A_ILE_307	2.93	2.12	16.79
5VXM.PDB	O, A_ALA_304	N, A_PHE_308	H, A_PHE_308	2.85	2.02	14.30
5VXM.PDB	O, A_ASN_305	N, A_ASP_309	H, A_ASP_309	2.84	2.05	19.19
5VXM.PDB	O, A_ASP_309	N, A_LYS_313	H, A_LYS_313	2.76	1.93	13.42
5VXM.PDB	O, B_SER_25	N, B_GLN_3	H, B_GLN_3	2.54	1.70	8.57
5VXM.PDB	O, B_SER_21	N, B_SER_7	H, B_SER_7	2.84	2.04	16.92
5VXM.PDB	O, B_LEU_86	N, B_GLY_15	H, B_GLY_15	2.69	1.85	9.47
5VXM.PDB	O, B_GLN_13	N, B_GLY_16	H, B_GLY_16	2.77	1.93	10.62
5VXM.PDB	O, B_MET_83	N, B_LEU_18	H, B_LEU_18	2.79	2.00	18.93

5VXM.PDB	O, B.LEU_81	N, B.LEU_20	H, B.LEU_20	2.91	2.09	14.06
5VXM.PDB	O, B.SER_7	N, B.SER_21	H, B.SER_21	2.77	1.94	13.53
5VXM.PDB	O, B.VAL_79	N, B.CYS_22	H, B.CYS_22	2.80	2.05	25.06
5VXM.PDB	O, B.VAL_5	N, B.ALA_23	H, B.ALA_23	2.85	2.03	14.23
5VXM.PDB	O, B.ASN_77	N, B.VAL_24	H, B.VAL_24	2.90	2.04	1.76
5VXM.PDB	O, B.GLN_3	N, B.SER_25	H, B.SER_25	2.84	2.00	10.15
5VXM.PDB	O, B.ALA_97	N, B.GLY_35	H, B.GLY_35	2.79	1.95	10.70
5VXM.PDB	O, B.SER_49	N, B.TRP_36	H, B.TRP_36	2.71	1.90	16.74
5VXM.PDB	O, B.PHE_95	N, B.PHE_37	H, B.PHE_37	2.88	2.07	17.02
5VXM.PDB	O, B.GLU_46	N, B.ARG_38	H, B.ARG_38	2.87	2.06	16.90
5VXM.PDB	OH, B.TYR_94	NH1, B.ARG_38	HH11, B.ARG_38	2.95	2.12	12.47
5VXM.PDB	OD1, B.ASP_90	NH1, B.ARG_38	HH12, B.ARG_38	2.77	1.97	17.13
5VXM.PDB	O, B.VAL_93	N, B.GLN_39	H, B.GLN_39	2.84	2.06	21.66
5VXM.PDB	O, B.ARG_38	N, B.GLU_46	H, B.GLU_46	2.82	2.11	29.28
5VXM.PDB	O, B.TRP_36	N, B.VAL_48	H, B.VAL_48	2.81	2.02	19.40
5VXM.PDB	O, B.ARG_59	OG, B.SER_49	HG, B.SER_49	2.90	2.19	27.71
5VXM.PDB	O, B.ARG_59	N, B.CYS_50	H, B.CYS_50	2.95	2.17	21.36
5VXM.PDB	O, B.ILE_34	N, B.ILE_51	H, B.ILE_51	2.96	2.19	22.03
5VXM.PDB	O, B.ASN_52	N, B.GLY_55	H, B.GLY_55	2.92	2.12	17.73
5VXM.PDB	OD1, B.ASP_54	OG, B.SER_56	HG, B.SER_56	2.63	1.84	17.09
5VXM.PDB	O, B.CYS_50	N, B.ARG_59	H, B.ARG_59	2.78	1.95	11.90
5VXM.PDB	O, B.VAL_48	N, B.ALA_61	H, B.ALA_61	2.94	2.11	11.33
5VXM.PDB	O, B.ALA_61	N, B.VAL_64	H, B.VAL_64	2.99	2.14	7.44
5VXM.PDB	OD2, B.ASP_90	NH1, B.ARG_67	HH12, B.ARG_67	2.75	1.92	11.95
5VXM.PDB	O, B.SER_63	NH2, B.ARG_67	HH21, B.ARG_67	2.79	1.93	1.60
5VXM.PDB	O, B.GLN_82	N, B.THR_69	H, B.THR_69	2.89	2.14	25.06
5VXM.PDB	OH, B.TYR_60	N, B.ILE_70	H, B.ILE_70	2.83	1.99	10.74
5VXM.PDB	O, B.THR_78	N, B.ASP_73	H, B.ASP_73	2.82	1.98	10.27
5VXM.PDB	O, B.LYS_76	OG1, B.THR_78	HG1, B.THR_78	2.89	2.13	21.00
5VXM.PDB	O, B.SER_71	N, B.TYR_80	H, B.TYR_80	2.70	1.86	9.68
5VXM.PDB	O, B.LEU_20	N, B.LEU_81	H, B.LEU_81	2.93	2.11	15.49
5VXM.PDB	O, B.THR_69	N, B.GLN_82	H, B.GLN_82	2.76	1.95	17.35
5VXM.PDB	OD1, B.ASN_84	NE2, B.GLN_82	HE21, B.GLN_82	2.81	1.97	10.38
5VXM.PDB	O, B.LEU_18	N, B.MET_83	H, B.MET_83	2.67	1.83	10.89
5VXM.PDB	OD2, B.ASP_90	N, B.LYS_87	H, B.LYS_87	2.82	1.98	12.23
5VXM.PDB	O, B.LYS_87	N, B.ASP_90	H, B.ASP_90	2.83	2.00	13.54
5VXM.PDB	O, B.VAL_121	N, B.ALA_92	H, B.ALA_92	2.97	2.16	16.91
5VXM.PDB	O, B.THR_119	N, B.TYR_94	H, B.TYR_94	2.86	2.01	6.10
5VXM.PDB	O, B.ASP_90	OH, B.TYR_94	HH, B.TYR_94	2.85	2.04	12.05
5VXM.PDB	O, B.PHE_37	N, B.PHE_95	H, B.PHE_95	2.68	1.84	10.79
5VXM.PDB	OE2, B.GLU_6	N, B.CYS_96	H, B.CYS_96	2.76	1.91	7.11
5VXM.PDB	O, B.GLY_35	N, B.ALA_97	H, B.ALA_97	2.99	2.18	17.54
5VXM.PDB	O, B.SER_114	N, B.ALA_98	H, B.ALA_98	2.98	2.19	20.00
5VXM.PDB	O, B.ALA_33	N, B.LYS_99	H, B.LYS_99	2.92	2.09	12.04
5VXM.PDB	O, B.CYS_104	NZ, B.LYS_99	HZ2, B.LYS_99	2.88	2.13	28.17
5VXM.PDB	O, B.PHE_103	NZ, B.LYS_99	HZ3, B.LYS_99	2.88	2.06	19.18
5VXM.PDB	O, A.ASP_166	NE1, B.TRP_102	HE1, B.TRP_102	2.92	2.09	13.88
5VXM.PDB	OE2, A.GLU_201	N, B.CYS_104	H, B.CYS_104	2.85	2.02	10.45
5VXM.PDB	OE1, A.GLU_201	N, B.SER_105	H, B.SER_105	2.58	1.74	9.22
5VXM.PDB	O, B.ALA_98	N, B.ASN_113	H, B.ASN_113	2.61	1.89	26.80
5VXM.PDB	O, B.CYS_96	N, B.GLY_116	H, B.GLY_116	2.83	2.02	17.26
5VXM.PDB	O, B.TYR_94	N, B.THR_119	H, B.THR_119	2.94	2.16	20.89
5VXM.PDB	O, B.ALA_92	N, B.VAL_121	H, B.VAL_121	2.99	2.14	5.92
5VXM.PDB	O, B.GLY_10	N, B.THR_122	H, B.THR_122	2.99	2.17	15.52
5VXM.PDB	OG1, B.THR_91	N, B.VAL_123	H, B.VAL_123	2.86	2.00	4.07

Table 1723: 5VXM-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5VXR.PDB	O, H_THR_25	N, H_GLN_3	H, H_GLN_3	2.92	1.95	14.37
5VXR.PDB	O, H_THR_21	N, H_SER_7	H, H_SER_7	2.88	2.02	26.36
5VXR.PDB	O, H_THR_116	N, H_VAL_12	H, H_VAL_12	2.94	2.01	19.87
5VXR.PDB	O, H_VAL_85	N, H_SER_15	H, H_SER_15	2.75	1.75	7.98
5VXR.PDB	O, H_LEU_82	N, H_LEU_18	H, H_LEU_18	2.86	1.91	16.47
5VXR.PDB	O, H_LEU_80	N, H_LEU_20	H, H_LEU_20	2.86	1.87	11.91
5VXR.PDB	O, H_SER_7	N, H_THR_21	H, H_THR_21	2.94	1.94	9.22
5VXR.PDB	O, H_TYR_78	N, H_CYS_22	H, H_CYS_22	2.74	1.74	4.96
5VXR.PDB	O, H_GLN_5	N, H_SER_23	H, H_SER_23	2.92	1.94	11.80
5VXR.PDB	O, H_GLN_3	N, H_THR_25	H, H_THR_25	2.97	2.00	12.94
5VXR.PDB	OD1, H_ASN_76	N, H_ILE_29	H, H_ILE_29	2.90	1.95	16.89
5VXR.PDB	OH, H_TYR_100	N, H_GLY_32	H, H_GLY_32	2.89	1.92	12.65
5VXR.PDB	O, H_MET_98	N, H_TYR_33	H, H_TYR_33	2.88	1.88	9.69
5VXR.PDB	O, H_ILE_51	N, H_TRP_34	H, H_TRP_34	2.94	1.99	17.07
5VXR.PDB	O, H_SER_31	NE1, H_TRP_34	HE1, H_TRP_34	2.87	2.00	25.22
5VXR.PDB	O, H_ALA_96	N, H_ASN_35	H, H_ASN_35	2.84	1.89	16.00
5VXR.PDB	O, H_ALA_96	ND2, H_ASN_35	HD22, H_ASN_35	2.93	1.96	14.02
5VXR.PDB	O, H_GLY_49	N, H_TRP_36	H, H_TRP_36	2.83	1.89	18.36
5VXR.PDB	O, H_TYR_94	N, H_ILE_37	H, H_ILE_37	2.90	1.96	17.84
5VXR.PDB	O, H_GLU_46	N, H_ARG_38	H, H_ARG_38	2.92	1.95	13.24
5VXR.PDB	OE1, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.74	1.86	23.26
5VXR.PDB	OH, H_TYR_93	NH1, H_ARG_38	HH11, H_ARG_38	2.95	1.99	15.54
5VXR.PDB	OD1, H_ASP_89	NH1, H_ARG_38	HH12, H_ARG_38	2.81	1.80	4.81
5VXR.PDB	OE1, H_GLU_46	NH2, H_ARG_38	HH21, H_ARG_38	2.83	2.01	29.32
5VXR.PDB	O, H_THR_92	N, H_LYS_39	H, H_LYS_39	2.79	1.85	17.39
5VXR.PDB	OE1, L_GLN_38	NZ, H_LYS_39	HZ2, H_LYS_39	2.72	1.76	14.94
5VXR.PDB	O, H_LYS_44	N, H_PHE_40	H, H_PHE_40	2.95	2.01	17.78
5VXR.PDB	O, H_ARG_38	N, H_GLU_46	H, H_GLU_46	2.82	1.86	15.19
5VXR.PDB	OD1, H_ASN_35	OH, H_TYR_47	HH, H_TYR_47	2.72	1.74	8.88
5VXR.PDB	O, H_TRP_36	N, H_VAL_48	H, H_VAL_48	2.92	1.97	16.43
5VXR.PDB	O, H_TYR_58	N, H_TYR_50	H, H_TYR_50	2.82	1.91	21.30
5VXR.PDB	OD1, P_ASN_415	OH, H_TYR_50	HH, H_TYR_50	2.71	1.82	21.79
5VXR.PDB	O, H_TRP_34	N, H_ILE_51	H, H_ILE_51	2.89	1.95	17.36
5VXR.PDB	O, H_ASP_56	N, H_SER_52	H, H_SER_52	2.72	1.75	13.95
5VXR.PDB	O, H_SER_52	N, H_GLY_55	H, H_GLY_55	2.89	1.89	5.97
5VXR.PDB	O, H_VAL_48	N, H_ASN_60	H, H_ASN_60	2.87	1.86	4.40
5VXR.PDB	O, H_TYR_47	ND2, H_ASN_60	HD22, H_ASN_60	2.79	1.80	10.72
5VXR.PDB	OD1, H_ASN_60	N, H_SER_62	H, H_SER_62	2.94	2.03	22.09
5VXR.PDB	O, H_ASN_60	N, H_LEU_63	H, H_LEU_63	2.95	1.98	13.61
5VXR.PDB	O, H_LEU_63	N, H_ARG_66	H, H_ARG_66	2.91	1.93	12.44
5VXR.PDB	O, H_ASN_83	NH1, H_ARG_66	HH11, H_ARG_66	2.95	1.98	13.74
5VXR.PDB	OD1, H_ASP_89	NH2, H_ARG_66	HH22, H_ARG_66	2.99	1.98	4.54
5VXR.PDB	O, H_GLN_81	N, H_SER_68	H, H_SER_68	2.99	2.08	21.53
5VXR.PDB	O, H_TYR_53	NH1, H_ARG_71	HH12, H_ARG_71	2.89	2.01	24.28
5VXR.PDB	O, H_GLN_77	N, H_ASP_72	H, H_ASP_72	2.86	1.87	9.03
5VXR.PDB	O, H_ASP_27	ND2, H_ASN_76	HD21, H_ASN_76	2.65	1.73	19.67
5VXR.PDB	O, H_ASN_35	OH, H_TYR_78	HH, H_TYR_78	2.85	1.87	7.07
5VXR.PDB	O, H_THR_70	N, H_TYR_79	H, H_TYR_79	2.84	1.90	18.23
5VXR.PDB	OE1, H_GLN_77	OH, H_TYR_79	HH, H_TYR_79	2.72	1.76	12.10
5VXR.PDB	O, H_LEU_20	N, H_LEU_80	H, H_LEU_80	2.93	1.97	15.68
5VXR.PDB	O, H_SER_68	N, H_GLN_81	H, H_GLN_81	2.89	1.91	12.77
5VXR.PDB	O, H_LEU_18	N, H_LEU_82	H, H_LEU_82	2.90	1.93	13.50
5VXR.PDB	O, H_ARG_66	N, H_ASN_83	H, H_ASN_83	2.85	1.86	10.37
5VXR.PDB	O, H_THR_86	N, H_ASP_89	H, H_ASP_89	2.84	1.84	7.21
5VXR.PDB	O, H_LYS_39	N, H_THR_92	H, H_THR_92	2.80	1.83	13.98
5VXR.PDB	O, H_THR_113	N, H_TYR_93	H, H_TYR_93	2.85	1.85	8.50
5VXR.PDB	O, H_ASP_89	OH, H_TYR_93	HH, H_TYR_93	2.69	1.71	5.93

5VXR.PDB	O, H_ILE_37	N, H_TYR_94	H, H_TYR_94	2.75	1.75	6.84
5VXR.PDB	OE2, H_GLU_6	N, H_CYS_95	H, H_CYS_95	2.78	1.84	17.15
5VXR.PDB	O, H_SER_108	N, H_ARG_97	H, H_ARG_97	2.83	1.90	18.04
5VXR.PDB	O, H_TYR_33	N, H_MET_98	H, H_MET_98	2.92	1.95	14.04
5VXR.PDB	O, H_TYR_100	N, H_GLN_103	H, H_GLN_103	2.92	2.02	21.61
5VXR.PDB	OH, L_TYR_36	N, H_PHE_106	H, H_PHE_106	2.92	1.92	7.59
5VXR.PDB	O, H_CYS_95	N, H_GLY_110	H, H_GLY_110	2.91	1.93	12.29
5VXR.PDB	OE1, H_GLU_6	N, H_GLY_112	H, H_GLY_112	2.87	1.90	13.05
5VXR.PDB	O, H_TYR_93	N, H_THR_113	H, H_THR_113	2.95	2.02	20.05
5VXR.PDB	O, H_ALA_91	N, H_VAL_115	H, H_VAL_115	2.97	1.97	6.59
5VXR.PDB	O, H_SER_10	N, H_THR_116	H, H_THR_116	2.95	1.96	9.99
5VXR.PDB	OG1, H_THR_90	N, H_VAL_117	H, H_VAL_117	2.94	1.93	5.04
5VXR.PDB	O, H_VAL_12	N, H_SER_118	H, H_SER_118	2.98	2.10	24.14
5VXR.PDB	OG, H_SER_118	N, H_ALA_120	H, H_ALA_120	2.97	2.00	14.42
5VXR.PDB	O, H_PHE_152	N, H_THR_123	H, H_THR_123	2.88	1.92	15.25
5VXR.PDB	O, H_LYS_149	N, H_SER_126	H, H_SER_126	2.81	1.84	13.35
5VXR.PDB	O, H_LEU_147	N, H_TYR_128	H, H_TYR_128	2.83	1.83	9.66
5VXR.PDB	O, H_GLY_145	N, H_LEU_130	H, H_LEU_130	2.83	1.90	19.03
5VXR.PDB	O, H_VAL_189	N, H_VAL_142	H, H_VAL_142	2.94	1.98	15.04
5VXR.PDB	O, H_VAL_187	N, H_LEU_144	H, H_LEU_144	2.89	1.92	13.91
5VXR.PDB	O, H_LEU_130	N, H_GLY_145	H, H_GLY_145	2.93	2.02	21.14
5VXR.PDB	O, H_SER_185	N, H_CYS_146	H, H_CYS_146	2.89	1.97	20.23
5VXR.PDB	O, H_TYR_128	N, H_LEU_147	H, H_LEU_147	2.91	1.92	10.17
5VXR.PDB	O, H_MET_183	N, H_VAL_148	H, H_VAL_148	2.86	1.85	4.57
5VXR.PDB	O, H_SER_126	N, H_LYS_149	H, H_LYS_149	2.87	1.88	10.16
5VXR.PDB	OE2, H_GLU_154	OH, H_TYR_151	HH, H_TYR_151	2.81	1.83	6.84
5VXR.PDB	O, H_THR_123	N, H_PHE_152	H, H_PHE_152	2.98	2.05	18.35
5VXR.PDB	O, H_SER_202	N, H_THR_159	H, H_THR_159	2.91	1.94	14.94
5VXR.PDB	OG, H_SER_185	NE1, H_TRP_160	HE1, H_TRP_160	2.93	1.93	7.21
5VXR.PDB	O, H_THR_188	OG, H_SER_168	HG, H_SER_168	2.72	1.82	20.67
5VXR.PDB	O, H_SER_186	N, H_HIS_170	H, H_HIS_170	2.94	2.01	18.18
5VXR.PDB	OD1, L_ASN_138	NE2, H_HIS_170	HE2, H_HIS_170	2.89	1.98	20.57
5VXR.PDB	O, H_SER_184	N, H_PHE_172	H, H_PHE_172	2.89	1.89	7.85
5VXR.PDB	O, H_THR_182	N, H_LEU_175	H, H_LEU_175	2.96	2.01	16.29
5VXR.PDB	O, H_GLN_177	OG, H_SER_178	HG, H_SER_178	2.93	2.03	20.61
5VXR.PDB	O, H_TYR_151	N, H_TYR_181	H, H_TYR_181	2.81	1.80	4.32
5VXR.PDB	O, H_VAL_148	N, H_MET_183	H, H_MET_183	2.89	1.92	13.39
5VXR.PDB	O, H_LEU_144	N, H_VAL_187	H, H_VAL_187	2.82	1.86	14.30
5VXR.PDB	OG1, H_THR_143	OG1, H_THR_188	HG1, H_THR_188	2.81	1.84	10.15
5VXR.PDB	O, H_GLY_139	OG, H_SER_191	HG, H_SER_191	2.77	1.88	20.92
5VXR.PDB	O, H_GLY_139	OG, H_BSER_191	HG, H_BSER_191	2.77	1.86	19.71
5VXR.PDB	O, H_PRO_190	N, H_THR_193	H, H_THR_193	2.87	1.87	5.97
5VXR.PDB	O, H_THR_193	N, H_GLN_197	H, H_GLN_197	2.93	2.07	26.39
5VXR.PDB	OD1, H_ASN_161	N, H_THR_200	H, H_THR_200	2.97	2.02	17.18
5VXR.PDB	O, H_THR_159	N, H_SER_202	H, H_SER_202	2.75	1.75	5.74
5VXR.PDB	O, H_VAL_212	N, H_VAL_203	H, H_VAL_203	2.81	1.81	7.96
5VXR.PDB	O, H_THR_157	N, H_ALA_204	H, H_ALA_204	2.86	1.90	13.85
5VXR.PDB	O, H_THR_210	N, H_HIS_205	H, H_HIS_205	2.82	1.84	11.68
5VXR.PDB	O, H_PRO_153	NE2, H_HIS_205	HE2, H_HIS_205	2.81	1.82	9.76
5VXR.PDB	O, H_PRO_206	N, H_SER_209	H, H_SER_209	2.98	2.02	13.76
5VXR.PDB	O, H_SER_208	OG1, H_THR_210	HG1, H_THR_210	2.87	2.03	26.51
5VXR.PDB	O, H_VAL_203	N, H_VAL_212	H, H_VAL_212	2.95	2.00	16.98
5VXR.PDB	O, H_CYS_201	N, H_LYS_214	H, H_LYS_214	2.91	2.01	22.37
5VXR.PDB	OE2, L_GLU_123	NZ, H_LYS_214	HZ1, H_LYS_214	2.93	1.98	15.97
5VXR.PDB	O, H_VAL_199	N, H_LEU_216	H, H_LEU_216	2.90	1.89	4.43
5VXR.PDB	OG, L_SER_26	N, L_VAL_3	H, L_VAL_3	2.91	1.91	7.32
5VXR.PDB	O, L_ARG_24	N, L_THR_5	H, L_THR_5	2.78	1.77	4.90
5VXR.PDB	O, L_TYR_86	NE2, L_GLN_6	HE22, L_GLN_6	2.89	1.89	8.04

5VXR.PDB	O, L_SER_22	N, L_SER_7	H, L_SER_7	2.95	2.03	19.63
5VXR.PDB	O, L_LYS_103	N, L_LEU_11	H, L_LEU_11	2.93	2.01	19.94
5VXR.PDB	O, L_GLU_105	N, L_VAL_13	H, L_VAL_13	2.91	1.98	18.79
5VXR.PDB	O, L_VAL_78	N, L_GLY_16	H, L_GLY_16	2.93	1.93	8.01
5VXR.PDB	O, L_ILE_75	N, L_ALA_19	H, L_ALA_19	2.83	1.83	8.13
5VXR.PDB	O, L_SER_7	N, L_SER_22	H, L_SER_22	2.84	1.82	1.96
5VXR.PDB	O, L_PHE_71	N, L_CYS_23	H, L_CYS_23	2.89	1.92	13.55
5VXR.PDB	O, L_THR_5	N, L_ARG_24	H, L_ARG_24	2.90	1.89	4.93
5VXR.PDB	OD1, L_ASP_70	NE, L_ARG_24	HE, L_ARG_24	2.94	2.08	26.80
5VXR.PDB	O, L_THR_69	N, L_ALA_25	H, L_ALA_25	2.84	1.89	15.97
5VXR.PDB	O, L_LYS_30	N, L_SER_27D	H, L_SER_27D	2.97	2.06	21.07
5VXR.PDB	OD1, L_ASN_92	OG, L_SER_27D	HG, L_SER_27D	2.79	1.83	11.69
5VXR.PDB	O, L_SER_27D	N, L_LYS_30	H, L_LYS_30	3.00	2.02	13.12
5VXR.PDB	O, H_GLY_101	NZ, L_LYS_30	HZ1, L_LYS_30	2.83	1.85	13.06
5VXR.PDB	O, L_GLN_89	N, L_HIS_34	H, L_HIS_34	2.88	1.90	13.39
5VXR.PDB	OD1, L_ASN_91	NE2, L_HIS_34	HE2, L_HIS_34	2.77	1.79	12.93
5VXR.PDB	O, L_ILE_48	N, L_TRP_35	H, L_TRP_35	2.81	1.84	13.58
5VXR.PDB	O, L_TYR_87	N, L_TYR_36	H, L_TYR_36	2.86	1.93	18.12
5VXR.PDB	OE1, L_GLN_89	OH, L_TYR_36	HH, L_TYR_36	2.69	1.74	13.43
5VXR.PDB	O, L_LYS_45	N, L_GLN_37	H, L_GLN_37	2.88	1.93	17.34
5VXR.PDB	OH, L_TYR_86	NE2, L_GLN_37	HE21, L_GLN_37	2.98	1.98	9.70
5VXR.PDB	O, L_THR_85	N, L_GLN_38	H, L_GLN_38	2.78	1.82	15.10
5VXR.PDB	O, L_GLN_42	NE2, L_GLN_38	HE21, L_GLN_38	2.91	1.92	11.28
5VXR.PDB	O, L_ASP_81	NZ, L_LYS_39	HZ3, L_LYS_39	2.63	1.68	15.29
5VXR.PDB	O, L_GLN_37	N, L_LYS_45	H, L_LYS_45	2.79	1.86	19.53
5VXR.PDB	O, L_TRP_35	N, L_LEU_47	H, L_LEU_47	2.83	1.83	6.37
5VXR.PDB	O, L_ASN_53	N, L_TYR_49	H, L_TYR_49	2.88	1.93	17.74
5VXR.PDB	O, L_LEU_33	N, L_ALA_51	H, L_ALA_51	2.80	1.87	18.75
5VXR.PDB	O, L_TYR_49	N, L_ASN_53	H, L_ASN_53	2.90	1.93	14.40
5VXR.PDB	O, L_LEU_47	N, L_GLU_55	H, L_GLU_55	2.95	1.94	3.22
5VXR.PDB	O, L_PRO_59	N, L_ARG_61	H, L_ARG_61	2.78	1.96	29.25
5VXR.PDB	O, L_PRO_77	NH1, L_ARG_61	HH11, L_ARG_61	2.81	1.92	23.49
5VXR.PDB	OD2, L_ASP_82	NH1, L_ARG_61	HH12, L_ARG_61	2.75	1.79	15.16
5VXR.PDB	OD1, L_ASP_82	NH2, L_ARG_61	HH22, L_ARG_61	2.82	1.82	7.27
5VXR.PDB	O, L_THR_74	N, L_SER_63	H, L_SER_63	2.98	2.05	19.15
5VXR.PDB	O, L_THR_72	N, L_SER_65	H, L_SER_65	2.96	2.02	18.59
5VXR.PDB	OD1, L_ASP_27C	N, L_ARG_68	H, L_ARG_68	2.98	2.08	21.58
5VXR.PDB	O, L_CYS_23	N, L_PHE_71	H, L_PHE_71	2.90	2.01	23.31
5VXR.PDB	O, L_SER_65	N, L_THR_72	H, L_THR_72	2.91	1.95	14.63
5VXR.PDB	O, L_ILE_21	N, L_LEU_73	H, L_LEU_73	2.86	1.89	14.64
5VXR.PDB	O, L_SER_63	N, L_THR_74	H, L_THR_74	2.84	1.84	5.95
5VXR.PDB	O, L_ALA_19	N, L_ILE_75	H, L_ILE_75	2.86	1.89	14.39
5VXR.PDB	O, L_ARG_61	N, L_ASP_76	H, L_ASP_76	2.76	1.80	14.69
5VXR.PDB	O, L_GLN_17	N, L_VAL_78	H, L_VAL_78	2.93	1.95	13.22
5VXR.PDB	OD2, L_ASP_82	N, L_GLU_79	H, L_GLU_79	2.85	1.85	8.34
5VXR.PDB	O, L_GLU_79	N, L_ASP_82	H, L_ASP_82	2.97	1.97	6.55
5VXR.PDB	O, L_THR_102	N, L_TYR_86	H, L_TYR_86	2.91	1.93	13.41
5VXR.PDB	O, L_ASP_82	OH, L_TYR_86	HH, L_TYR_86	2.70	1.78	16.73
5VXR.PDB	O, L_TYR_36	N, L_TYR_87	H, L_TYR_87	2.90	1.95	16.78
5VXR.PDB	O, L_THR_97	N, L_HIS_90	H, L_HIS_90	2.99	2.05	18.83
5VXR.PDB	O, P_GLY_418	NE1, L_TRP_96	HE1, L_TRP_96	2.88	1.87	5.74
5VXR.PDB	O, L_ILE_2	OG1, L_THR_97	HG1, L_THR_97	2.97	2.02	14.29
5VXR.PDB	O, L_CYS_88	N, L_GLY_99	H, L_GLY_99	2.83	1.83	7.30
5VXR.PDB	O, L_TYR_86	N, L_THR_102	H, L_THR_102	2.94	2.03	21.75
5VXR.PDB	O, L_PRO_8	OG1, L_THR_102	HG1, L_THR_102	2.75	1.79	11.72
5VXR.PDB	O, L_ALA_84	N, L_LEU_104	H, L_LEU_104	2.91	1.89	2.60
5VXR.PDB	OE1, L_GLN_166	N, L_ILE_106	H, L_ILE_106	2.84	1.85	9.18
5VXR.PDB	O, L_VAL_13	N, L_LYS_107	H, L_LYS_107	2.81	1.82	9.46

5VXR.PDB	O, L_ALA_109	NE, L_ARG_108	HE, L_ARG_108	2.87	1.86	6.94
5VXR.PDB	O, L_ASP_170	NH1, L_ARG_108	HH11, L_ARG_108	2.81	1.81	8.28
5VXR.PDB	O, L_TYR_140	N, L_ALA_111	H, L_ALA_111	2.89	1.90	8.41
5VXR.PDB	O, L_ASN_137	N, L_THR_114	H, L_THR_114	2.87	1.88	8.25
5VXR.PDB	O, L_PHE_135	N, L_SER_116	H, L_SER_116	2.96	2.02	17.37
5VXR.PDB	O, L_VAL_133	N, L_PHE_118	H, L_PHE_118	2.78	1.90	24.38
5VXR.PDB	OG, L_SER_131	NE2, L_GLN_124	HE22, L_GLN_124	2.92	1.91	5.03
5VXR.PDB	O, L_SER_122	N, L_THR_126	H, L_THR_126	2.91	1.96	16.41
5VXR.PDB	O, L_GLN_124	OG, L_SER_127	HG, L_SER_127	2.77	1.86	18.69
5VXR.PDB	O, L_LEU_181	N, L_ALA_130	H, L_ALA_130	2.92	2.02	22.78
5VXR.PDB	OE1, L_GLN_124	N, L_SER_131	H, L_SER_131	2.86	1.94	21.02
5VXR.PDB	O, L_LEU_179	N, L_VAL_132	H, L_VAL_132	2.84	1.88	14.58
5VXR.PDB	O, L_SER_116	N, L_PHE_135	H, L_PHE_135	2.89	1.98	20.99
5VXR.PDB	O, L_MET_175	N, L_LEU_136	H, L_LEU_136	2.88	1.87	5.63
5VXR.PDB	O, L_THR_114	N, L_ASN_137	H, L_ASN_137	2.89	1.90	10.32
5VXR.PDB	OG, L_SER_174	N, L_ASN_138	H, L_ASN_138	2.95	1.98	14.50
5VXR.PDB	O, L_TYR_173	N, L_PHE_139	H, L_PHE_139	2.83	1.84	11.10
5VXR.PDB	O, L_ALA_111	N, L_TYR_140	H, L_TYR_140	2.94	1.98	15.41
5VXR.PDB	O, L_GLU_195	N, L_LYS_147	H, L_LYS_147	2.93	1.98	16.97
5VXR.PDB	OG, L_SER_177	NE1, L_TRP_148	HE1, L_TRP_148	2.80	1.85	16.41
5VXR.PDB	O, L_THR_193	N, L_LYS_149	H, L_LYS_149	2.85	1.88	14.14
5VXR.PDB	O, L_SER_153	N, L_ILE_150	H, L_ILE_150	2.93	1.98	15.57
5VXR.PDB	O, L_SER_191	N, L_ASP_151	H, L_ASP_151	2.78	1.80	12.18
5VXR.PDB	O, L_ILE_150	N, L_SER_153	H, L_SER_153	2.99	1.99	4.98
5VXR.PDB	O, L_TRP_148	N, L_ARG_155	H, L_ARG_155	2.93	1.99	17.51
5VXR.PDB	O, L_THR_178	N, L_LEU_160	H, L_LEU_160	2.91	1.98	18.71
5VXR.PDB	O, L_SER_176	N, L_SER_162	H, L_SER_162	2.83	1.87	15.71
5VXR.PDB	O, L_SER_174	N, L_THR_164	H, L_THR_164	2.88	1.88	8.76
5VXR.PDB	O, L_SER_171	NE2, L_GLN_166	HE21, L_GLN_166	2.83	1.86	12.46
5VXR.PDB	O, L_ILE_106	NE2, L_GLN_166	HE22, L_GLN_166	2.77	1.85	20.51
5VXR.PDB	O, L_THR_172	N, L_ASP_167	H, L_ASP_167	2.85	1.85	9.35
5VXR.PDB	OD2, L_ASP_167	N, L_LYS_169	H, L_LYS_169	2.90	1.99	21.19
5VXR.PDB	OD2, L_ASP_167	N, L_ASP_170	H, L_ASP_170	2.84	1.89	16.19
5VXR.PDB	OD1, L_ASP_170	N, L_THR_172	H, L_THR_172	2.96	2.00	16.34
5VXR.PDB	OD1, L_ASP_170	OG1, L_THR_172	HG1, L_THR_172	2.70	1.76	15.44
5VXR.PDB	O, L_PHE_139	N, L_TYR_173	H, L_TYR_173	2.85	1.84	7.73
5VXR.PDB	O, L_LEU_136	N, L_MET_175	H, L_MET_175	2.84	1.91	18.20
5VXR.PDB	O, L_SER_162	N, L_SER_176	H, L_SER_176	2.88	1.94	17.54
5VXR.PDB	OG, H_SER_184	OG, L_SER_176	HG, L_SER_176	2.79	1.86	17.30
5VXR.PDB	O, L_CYS_134	N, L_SER_177	H, L_SER_177	2.91	1.91	10.22
5VXR.PDB	OD1, L_ASN_161	OG, L_SER_177	HG, L_SER_177	2.64	1.73	19.24
5VXR.PDB	O, L_LEU_160	N, L_THR_178	H, L_THR_178	2.85	1.91	18.48
5VXR.PDB	O, L_VAL_132	N, L_LEU_179	H, L_LEU_179	2.78	1.81	13.39
5VXR.PDB	O, L_GLY_158	N, L_THR_180	H, L_THR_180	2.83	1.86	14.32
5VXR.PDB	OG, L_SER_131	OG1, L_THR_180	HG1, L_THR_180	2.88	2.00	21.77
5VXR.PDB	O, L_ALA_130	N, L_LEU_181	H, L_LEU_181	2.83	1.84	9.97
5VXR.PDB	O, L_GLY_128	N, L_LYS_183	H, L_LYS_183	2.94	1.97	12.73
5VXR.PDB	O, L_THR_182	N, L_TYR_186	H, L_TYR_186	2.95	1.95	8.11
5VXR.PDB	O, L_LYS_183	N, L_GLU_187	H, L_GLU_187	3.00	2.08	21.03
5VXR.PDB	OD2, L_ASP_151	ND1, L_HIS_189	HD1, L_HIS_189	2.73	1.79	17.03
5VXR.PDB	OD1, L_ASP_151	N, L_SER_191	H, L_SER_191	2.90	1.90	6.70
5VXR.PDB	O, L_PHE_209	N, L_TYR_192	H, L_TYR_192	2.97	1.97	6.50
5VXR.PDB	O, L_LYS_149	N, L_THR_193	H, L_THR_193	2.96	2.06	22.36
5VXR.PDB	O, L_LYS_147	N, L_GLU_195	H, L_GLU_195	2.79	1.85	17.75
5VXR.PDB	O, L_ILE_205	N, L_ALA_196	H, L_ALA_196	2.78	1.81	13.90
5VXR.PDB	O, L_ASN_145	N, L_THR_197	H, L_THR_197	2.84	1.85	9.75
5VXR.PDB	O, L_PRO_141	NE2, L_HIS_198	HE2, L_HIS_198	2.90	1.90	7.27
5VXR.PDB	ND1, L_HIS_198	OG1, L_THR_200	HG1, L_THR_200	2.74	1.84	20.28

5VXR.PDB	O, L_SER_203	OG, L_SER_201	HG, L_SER_201	2.73	1.78	13.42
5VXR.PDB	O, L_ALA_196	N, L_ILE_205	H, L_ILE_205	2.98	2.07	22.00
5VXR.PDB	O, L_ASN_190	N, L_ARG_211	H, L_ARG_211	2.77	1.80	14.86
5VXR.PDB	O, L_HIS_189	NE, L_ARG_211	HE, L_ARG_211	2.85	1.85	8.53
5VXR.PDB	O, P_HIS_421	N, P_ILE_414	H, P_ILE_414	2.99	2.01	11.82
5VXR.PDB	OH, H_TYR_33	N, P_ASN_415	H, P_ASN_415	2.82	1.94	24.20
5VXR.PDB	O, P_SER_419	N, P_THR_416	H, P_THR_416	2.88	1.93	15.75
5VXR.PDB	NE2, P_HIS_421	OG1, P_THR_416	HG1, P_THR_416	2.72	1.87	24.94
5VXR.PDB	O, L_ASN_91	NE1, P_TRP_420	HE1, P_TRP_420	2.80	1.97	28.78
5VXR.PDB	O, P_ILE_414	N, P_HIS_421	H, P_HIS_421	2.91	2.04	25.40

Table 1724: 5VXR-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5WKQ.PDB	O, A.ASN.74	N, A.GLN.78	H, A.GLN.78	2.98	2.14	9.16
5WKQ.PDB	O, A.ALA.75	N, A.LEU.79	H, A.LEU.79	2.93	2.08	8.87
5WKQ.PDB	O, A.SER.76	OG1, A.THR.80	HG1, A.THR.80	2.93	2.13	16.27
5WKQ.PDB	O, A.GLN.78	N, A.LEU.82	H, A.LEU.82	2.82	2.00	15.52
5WKQ.PDB	O, A.LEU.79	N, A.ILE.83	H, A.ILE.83	2.90	2.05	7.59
5WKQ.PDB	O, A.LEU.81	N, A.ASN.85	H, A.ASN.85	2.92	2.07	7.63
5WKQ.PDB	O, A.ILE.83	N, A.ILE.87	H, A.ILE.87	2.92	2.08	9.62
5WKQ.PDB	O, A.LEU.86	N, A.LEU.90	H, A.LEU.90	2.92	2.07	6.38
5WKQ.PDB	O, A.ILE.87	N, A.GLY.91	H, A.GLY.91	2.97	2.16	15.88
5WKQ.PDB	O, A.GLY.91	OG, A.SER.94	HG, A.SER.94	2.98	2.17	13.97
5WKQ.PDB	O, A.LEU.95	N, A.THR.99	H, A.THR.99	2.87	2.01	5.83
5WKQ.PDB	O, A.THR.96	N, A.ASN.100	H, A.ASN.100	2.93	2.14	18.75
5WKQ.PDB	O, A.LEU.98	N, A.ILE.102	H, A.ILE.102	2.87	2.09	20.92
5WKQ.PDB	O, A.THR.99	N, A.THR.103	H, A.THR.103	2.97	2.15	15.29
5WKQ.PDB	O, A.LYS.101	N, A.TRP.105	H, A.TRP.105	2.97	2.17	18.38
5WKQ.PDB	OG1, A.THR.80	NZ, A.LYS.106	HZ1, A.LYS.106	2.47	1.72	27.03
5WKQ.PDB	O, A.ALA.104	N, A.GLN.108	H, A.GLN.108	2.95	2.11	11.57
5WKQ.PDB	O, A.TRP.105	N, A.GLN.109	H, A.GLN.109	2.89	2.04	3.84
5WKQ.PDB	O, A.LYS.106	N, A.GLN.110	H, A.GLN.110	2.89	2.05	11.19
5WKQ.PDB	O, A.SER.107	N, A.ALA.111	H, A.ALA.111	3.00	2.17	13.35
5WKQ.PDB	O, A.GLN.108	N, A.ARG.112	H, A.ARG.112	2.98	2.16	14.92
5WKQ.PDB	O, A.GLN.109	N, A.GLN.113	H, A.GLN.113	2.94	2.10	9.80
5WKQ.PDB	O, A.ARG.112	N, A.ASN.116	H, A.ASN.116	2.83	1.99	11.00
5WKQ.PDB	O, A.GLN.113	N, A.LEU.117	H, A.LEU.117	2.99	2.18	16.36
5WKQ.PDB	O, A.LYS.115	N, A.PHE.119	H, A.PHE.119	2.80	1.98	13.76
5WKQ.PDB	O, A.ASN.116	N, A.SER.120	H, A.SER.120	2.81	1.97	9.85
5WKQ.PDB	O, A.PHE.119	N, A.ILE.123	H, A.ILE.123	2.99	2.14	9.43
5WKQ.PDB	O, A.SER.120	N, A.ASN.124	H, A.ASN.124	2.97	2.14	13.74
5WKQ.PDB	O, A.ILE.123	N, A.LEU.127	H, A.LEU.127	2.86	2.03	12.46
5WKQ.PDB	O, A.THR.125	N, A.GLU.129	H, A.GLU.129	2.89	2.06	14.27
5WKQ.PDB	O, A.LEU.126	N, A.THR.130	H, A.THR.130	2.85	2.02	13.06
5WKQ.PDB	O, A.LEU.127	N, A.GLU.131	H, A.GLU.131	2.91	2.07	8.81
5WKQ.PDB	O, A.SER.128	N, A.GLY.132	H, A.GLY.132	2.95	2.11	11.67
5WKQ.PDB	O, A.THR.130	N, A.THR.134	H, A.THR.134	2.86	2.03	13.70
5WKQ.PDB	O, A.THR.130	OG1, A.THR.134	HG1, A.THR.134	2.90	2.17	24.55
5WKQ.PDB	O, A.GLU.131	N, A.ARG.135	H, A.ARG.135	2.96	2.15	15.46
5WKQ.PDB	OG, B.SER.208	NH2, A.ARG.135	HH21, A.ARG.135	2.89	2.06	11.87
5WKQ.PDB	O, A.LEU.133	N, A.TYR.137	H, A.TYR.137	2.86	2.07	19.86
5WKQ.PDB	O, A.THR.134	N, A.GLU.138	H, A.GLU.138	2.82	1.98	11.30
5WKQ.PDB	O, A.TYR.137	N, A.ILE.141	H, A.ILE.141	2.92	2.07	6.24
5WKQ.PDB	O, A.GLN.140	N, A.LEU.144	H, A.LEU.144	2.76	1.98	19.80
5WKQ.PDB	O, A.ILE.141	N, A.LYS.145	H, A.LYS.145	2.95	2.17	21.49
5WKQ.PDB	O, A.LYS.143	N, A.ALA.147	H, A.ALA.147	2.98	2.17	16.58
5WKQ.PDB	O, A.LEU.144	N, A.ASP.148	H, A.ASP.148	2.92	2.09	13.80
5WKQ.PDB	O, A.ALA.147	N, A.ILE.151	H, A.ILE.151	3.00	2.18	14.31
5WKQ.PDB	O, A.SER.149	N, A.ASP.153	H, A.ASP.153	2.97	2.14	11.92
5WKQ.PDB	O, A.ILE.151	N, A.GLU.155	H, A.GLU.155	2.91	2.05	3.54
5WKQ.PDB	O, A.LYS.152	N, A.ASN.156	H, A.ASN.156	2.94	2.16	21.59
5WKQ.PDB	O, A.ASP.153	N, A.LYS.157	H, A.LYS.157	2.91	2.13	20.82
5WKQ.PDB	O, A.LEU.154	N, A.ILE.158	H, A.ILE.158	2.88	2.06	14.11
5WKQ.PDB	O, A.GLU.155	N, A.ASN.159	H, A.ASN.159	2.95	2.11	10.87
5WKQ.PDB	O, A.LYS.157	N, A.ILE.161	H, A.ILE.161	2.96	2.13	11.39
5WKQ.PDB	O, A.ILE.158	N, A.GLN.162	H, A.GLN.162	2.96	2.16	19.47
5WKQ.PDB	OE2, A.GLU.182	NE2, A.GLN.162	HE21, A.GLN.162	2.71	1.89	15.15
5WKQ.PDB	O, A.ILE.161	N, A.LEU.165	H, A.LEU.165	2.83	2.01	14.76
5WKQ.PDB	O, A.THR.163	OG, A.SER.166	HG, A.SER.166	2.82	1.99	6.15
5WKQ.PDB	O, A.ARG.164	N, A.GLU.167	H, A.GLU.167	2.98	2.16	15.01

5WKQ.PDB	O, A_LYS_175	N, A_SER_179	H, A_SER_179	2.81	1.95	0.77
5WKQ.PDB	O, A_LYS_177	N, A_GLU_181	H, A_GLU_181	2.97	2.17	18.02
5WKQ.PDB	O, A_LEU_178	N, A_GLU_182	H, A_GLU_182	2.79	1.97	15.96
5WKQ.PDB	O, A_SER_179	N, A_ILE_183	H, A_ILE_183	2.86	2.03	12.39
5WKQ.PDB	O, A_GLU_182	N, A_THR_186	H, A_THR_186	2.96	2.16	17.62
5WKQ.PDB	O, A_GLU_182	OG1, A_THR_186	HG1, A_THR_186	2.95	2.25	28.98
5WKQ.PDB	O, A_LEU_185	N, A_LYS_189	H, A_LYS_189	2.81	2.00	16.47
5WKQ.PDB	O, A_THR_186	N, A_ASP_190	H, A_ASP_190	2.80	1.95	5.67
5WKQ.PDB	O, A_LYS_188	N, A_ALA_192	H, A_ALA_192	2.92	2.13	19.91
5WKQ.PDB	O, A_LYS_189	N, A_VAL_193	H, A_VAL_193	2.85	2.05	18.34
5WKQ.PDB	O, A_ALA_192	N, A_ARG_196	H, A_ARG_196	2.85	2.00	8.33
5WKQ.PDB	O, A_ASP_195	N, A_ILE_199	H, A_ILE_199	2.97	2.14	13.27
5WKQ.PDB	O, A_ARG_196	N, A_GLU_200	H, A_GLU_200	2.87	2.01	4.50
5WKQ.PDB	O, A_LEU_198	N, A_LYS_202	H, A_LYS_202	2.90	2.10	18.39
5WKQ.PDB	O, A_ILE_199	N, A_THR_203	H, A_THR_203	2.80	1.96	10.08
5WKQ.PDB	O, A_ILE_199	OG1, A_THR_203	HG1, A_THR_203	2.97	2.24	25.20
5WKQ.PDB	O, A_LEU_204	N, A_SER_208	H, A_SER_208	2.96	2.20	23.33
5WKQ.PDB	O, A_ILE_206	N, A_LEU_210	H, A_LEU_210	2.92	2.12	17.69
5WKQ.PDB	O, A_HIS_207	N, A_THR_211	H, A_THR_211	3.00	2.23	23.43
5WKQ.PDB	O, A_SER_208	N, A_ASP_212	H, A_ASP_212	2.86	2.05	16.07
5WKQ.PDB	O, A_LYS_209	N, A_LYS_213	H, A_LYS_213	2.99	2.21	20.73
5WKQ.PDB	O, A_LEU_210	N, A_SER_214	H, A_SER_214	2.99	2.17	15.42
5WKQ.PDB	O, A_THR_211	OG, A_SER_214	HG, A_SER_214	2.74	1.93	13.01
5WKQ.PDB	O, A_ASP_212	N, A_GLN_216	H, A_GLN_216	2.85	2.04	17.18
5WKQ.PDB	O, A_LYS_213	N, A_LEU_217	H, A_LEU_217	2.82	1.99	14.07
5WKQ.PDB	O, A_MET_215	N, A_LYS_219	H, A_LYS_219	2.99	2.17	15.70
5WKQ.PDB	O, A_LEU_217	N, A_ILE_221	H, A_ILE_221	3.00	2.19	17.23
5WKQ.PDB	O, A_GLU_218	N, A_ASP_222	H, A_ASP_222	2.93	2.08	8.56
5WKQ.PDB	O, A_LYS_219	N, A_SER_223	H, A_SER_223	2.82	2.02	17.93
5WKQ.PDB	O, A_GLU_220	N, A_PHE_224	H, A_PHE_224	2.96	2.16	19.24
5WKQ.PDB	O, A_ILE_221	N, A_SER_225	H, A_SER_225	2.98	2.15	11.85
5WKQ.PDB	O, A_ASP_222	N, A_ALA_226	H, A_ALA_226	2.92	2.10	14.82
5WKQ.PDB	O, A_PHE_224	N, A_SER_228	H, A_SER_228	2.81	1.98	13.22
5WKQ.PDB	O, A_SER_225	N, A_ASN_229	H, A_ASN_229	2.97	2.17	18.32
5WKQ.PDB	O, A_ALA_226	OG1, A_THR_230	HG1, A_THR_230	3.00	2.17	9.26
5WKQ.PDB	O, A_SER_228	NE2, A_GLN_235	HE22, A_GLN_235	2.83	2.08	24.75
5WKQ.PDB	O, B_ALA_75	N, B_LEU_79	H, B_LEU_79	2.76	1.93	13.13
5WKQ.PDB	O, B_SER_76	N, B_THR_80	H, B_THR_80	3.00	2.21	19.48
5WKQ.PDB	O, B_GLN_78	N, B_LEU_82	H, B_LEU_82	2.90	2.10	19.38
5WKQ.PDB	O, B_LEU_79	N, B_ILE_83	H, B_ILE_83	2.90	2.06	11.95
5WKQ.PDB	O, B_LEU_81	N, B_ASN_85	H, B_ASN_85	2.99	2.16	14.14
5WKQ.PDB	O, B_LEU_82	N, B_LEU_86	H, B_LEU_86	2.93	2.11	15.27
5WKQ.PDB	O, B_ILE_83	N, B_ILE_87	H, B_ILE_87	2.80	1.97	13.54
5WKQ.PDB	O, B_GLY_84	N, B_GLN_88	H, B_GLN_88	2.92	2.15	21.64
5WKQ.PDB	O, B_LEU_86	N, B_LEU_90	H, B_LEU_90	2.83	1.98	8.98
5WKQ.PDB	O, B_ILE_87	N, B_GLY_91	H, B_GLY_91	2.92	2.09	13.90
5WKQ.PDB	O, B_LEU_95	N, B_THR_99	H, B_THR_99	2.78	1.92	3.48
5WKQ.PDB	O, B_THR_96	N, B_ASN_100	H, B_ASN_100	2.89	2.06	14.47
5WKQ.PDB	O, B_ALA_97	N, B_LYS_101	H, B_LYS_101	2.94	2.10	8.27
5WKQ.PDB	O, B_LEU_98	N, B_ILE_102	H, B_ILE_102	2.87	2.10	23.41
5WKQ.PDB	O, B_THR_99	N, B_THR_103	H, B_THR_103	2.98	2.14	12.40
5WKQ.PDB	O, B_LYS_101	N, B_TRP_105	H, B_TRP_105	2.85	2.02	12.87
5WKQ.PDB	O, B_ILE_102	N, B_LYS_106	H, B_LYS_106	2.89	2.08	17.14
5WKQ.PDB	O, B_TRP_105	N, B_GLN_109	H, B_GLN_109	2.93	2.12	16.73
5WKQ.PDB	O, B_LYS_106	N, B_GLN_110	H, B_GLN_110	2.89	2.09	18.27
5WKQ.PDB	O, B_SER_107	N, B_ALA_111	H, B_ALA_111	2.92	2.12	17.32
5WKQ.PDB	O, B_GLN_108	N, B_ARG_112	H, B_ARG_112	2.99	2.14	6.98
5WKQ.PDB	O, B_GLN_109	N, B_GLN_113	H, B_GLN_113	2.90	2.09	16.25

5WKQ.PDB	O, B_GLN_110	N, B_GLN_114	H, B_GLN_114	2.91	2.09	15.83
5WKQ.PDB	O, B_ALA_111	N, B_LYS_115	H, B_LYS_115	2.90	2.07	13.13
5WKQ.PDB	O, B_ARG_112	N, B_ASN_116	H, B_ASN_116	2.85	2.03	15.38
5WKQ.PDB	O, B_GLN_114	N, B_GLU_118	H, B_GLU_118	2.95	2.12	11.18
5WKQ.PDB	O, B_LYS_115	N, B_PHE_119	H, B_PHE_119	2.93	2.08	7.47
5WKQ.PDB	O, B_ASN_116	N, B_SER_120	H, B_SER_120	2.96	2.11	7.40
5WKQ.PDB	O, B_LEU_117	N, B_ASP_121	H, B_ASP_121	2.93	2.09	10.56
5WKQ.PDB	O, B_GLU_118	N, B_LYS_122	H, B_LYS_122	2.95	2.15	18.53
5WKQ.PDB	O, B_PHE_119	N, B_ILE_123	H, B_ILE_123	2.84	2.00	11.79
5WKQ.PDB	O, B_LYS_122	N, B_LEU_126	H, B_LEU_126	2.94	2.08	4.26
5WKQ.PDB	O, B_ILE_123	N, B_LEU_127	H, B_LEU_127	2.80	2.00	17.69
5WKQ.PDB	O, B_THR_125	N, B_GLU_129	H, B_GLU_129	2.91	2.08	11.09
5WKQ.PDB	O, B_LEU_126	N, B_THR_130	H, B_THR_130	2.83	2.00	12.55
5WKQ.PDB	O, B_LEU_127	N, B_GLU_131	H, B_GLU_131	2.89	2.05	10.95
5WKQ.PDB	O, B_THR_130	N, B_THR_134	H, B_THR_134	2.79	1.98	16.24
5WKQ.PDB	O, B_THR_130	OG1, B_THR_134	HG1, B_THR_134	2.99	2.22	19.25
5WKQ.PDB	O, B_GLY_132	N, B_ASP_136	H, B_ASP_136	2.99	2.18	16.20
5WKQ.PDB	O, B_LEU_133	N, B_TYR_137	H, B_TYR_137	2.84	2.01	13.19
5WKQ.PDB	O, B_THR_134	N, B_GLU_138	H, B_GLU_138	2.98	2.16	14.73
5WKQ.PDB	O, B_TYR_137	N, B_ILE_141	H, B_ILE_141	2.98	2.19	19.03
5WKQ.PDB	O, B_GLN_140	N, B_LEU_144	H, B_LEU_144	2.86	2.11	25.33
5WKQ.PDB	O, B_ILE_141	N, B_LYS_145	H, B_LYS_145	2.89	2.08	15.46
5WKQ.PDB	O, B_LYS_143	N, B_ALA_147	H, B_ALA_147	2.95	2.16	20.04
5WKQ.PDB	O, B_LEU_144	N, B_ASP_148	H, B_ASP_148	2.84	1.99	5.61
5WKQ.PDB	O, B_LYS_145	N, B_SER_149	H, B_SER_149	2.97	2.17	18.50
5WKQ.PDB	O, B_ASN_146	N, B_LYS_150	H, B_LYS_150	2.94	2.13	17.77
5WKQ.PDB	O, B_ALA_147	N, B_ILE_151	H, B_ILE_151	2.98	2.16	14.66
5WKQ.PDB	O, B_ASP_148	N, B_LYS_152	H, B_LYS_152	2.91	2.07	10.46
5WKQ.PDB	O, B_ILE_151	N, B_GLU_155	H, B_GLU_155	2.85	2.01	9.24
5WKQ.PDB	O, B_LYS_152	N, B_ASN_156	H, B_ASN_156	2.87	2.10	22.12
5WKQ.PDB	O, B_LEU_154	N, B_ILE_158	H, B_ILE_158	2.84	2.00	9.55
5WKQ.PDB	O, B_ASN_156	N, B_GLN_160	H, B_GLN_160	2.98	2.15	12.59
5WKQ.PDB	O, B_LYS_157	N, B_ILE_161	H, B_ILE_161	2.99	2.17	15.50
5WKQ.PDB	OE2, B_GLU_182	NE2, B_GLN_162	HE21, B_GLN_162	2.63	1.85	20.38
5WKQ.PDB	O, B_ASN_159	N, B_THR_163	H, B_THR_163	2.97	2.13	11.47
5WKQ.PDB	O, B_GLN_160	N, B_ARG_164	H, B_ARG_164	2.79	1.95	8.04
5WKQ.PDB	O, B_ILE_161	N, B_LEU_165	H, B_LEU_165	2.73	1.95	20.16
5WKQ.PDB	O, B_THR_163	OG, B_SER_166	HG, B_SER_166	2.84	2.00	2.60
5WKQ.PDB	O, B_GLU_182	N, B_THR_186	H, B_THR_186	2.91	2.09	14.89
5WKQ.PDB	O, B_LEU_185	N, B_LYS_189	H, B_LYS_189	2.88	2.10	21.13
5WKQ.PDB	O, B_THR_186	N, B_ASP_190	H, B_ASP_190	2.94	2.09	7.09
5WKQ.PDB	O, B_LYS_189	N, B_VAL_193	H, B_VAL_193	2.86	2.07	19.28
5WKQ.PDB	O, B_ALA_191	N, B_ASP_195	H, B_ASP_195	2.76	1.92	9.36
5WKQ.PDB	O, B_ALA_192	N, B_ARG_196	H, B_ARG_196	2.80	2.02	20.33
5WKQ.PDB	OD1, B_ASP_148	NH1, B_ARG_196	HH11, B_ARG_196	2.87	2.13	25.83
5WKQ.PDB	O, B_VAL_193	N, B_THR_197	H, B_THR_197	2.86	2.02	10.23
5WKQ.PDB	O, B_ARG_196	N, B_GLU_200	H, B_GLU_200	2.88	2.05	12.74
5WKQ.PDB	O, B_THR_197	N, B_GLN_201	H, B_GLN_201	2.89	2.05	8.57
5WKQ.PDB	O, B_ILE_199	N, B_THR_203	H, B_THR_203	2.92	2.14	20.25
5WKQ.PDB	O, B_ILE_199	OG1, B_THR_203	HG1, B_THR_203	2.75	2.02	24.53
5WKQ.PDB	O, B_GLU_200	N, B_LEU_204	H, B_LEU_204	2.93	2.09	11.16
5WKQ.PDB	O, B_THR_203	N, B_HIS_207	H, B_HIS_207	2.92	2.07	7.74
5WKQ.PDB	OE2, A_GLU_131	ND1, B_HIS_207	HD1, B_HIS_207	2.65	1.88	22.26
5WKQ.PDB	O, B_LEU_204	N, B_SER_208	H, B_SER_208	2.87	2.08	18.92
5WKQ.PDB	O, B_SER_205	N, B_LYS_209	H, B_LYS_209	2.90	2.09	16.81
5WKQ.PDB	O, B_ILE_206	N, B_LEU_210	H, B_LEU_210	2.88	2.10	21.93
5WKQ.PDB	O, B_HIS_207	N, B_THR_211	H, B_THR_211	2.88	2.05	12.96
5WKQ.PDB	OE1, A_GLU_131	OG1, B_THR_211	HG1, B_THR_211	2.63	1.86	19.68

5WKQ.PDB	O, B.SER_208	N, B.ASP_212	H, B.ASP_212	2.88	2.08	18.34
5WKQ.PDB	O, B.LYS_209	N, B.LYS_213	H, B.LYS_213	2.97	2.19	21.54
5WKQ.PDB	O, B.THR_211	OG, B.SER_214	HG, B.SER_214	2.63	1.88	22.05
5WKQ.PDB	O, B.ASP_212	N, B.GLN_216	H, B.GLN_216	2.92	2.09	13.17
5WKQ.PDB	O, B.LYS_213	N, B.LEU_217	H, B.LEU_217	2.89	2.06	14.20
5WKQ.PDB	O, B.MET_215	N, B.LYS_219	H, B.LYS_219	2.89	2.07	14.81
5WKQ.PDB	O, B.GLN_216	N, B.GLU_220	H, B.GLU_220	2.97	2.15	14.12
5WKQ.PDB	O, B.LEU_217	N, B.ILE_221	H, B.ILE_221	2.90	2.10	17.72
5WKQ.PDB	O, B.GLU_218	N, B.ASP_222	H, B.ASP_222	2.89	2.07	14.28
5WKQ.PDB	O, B.LYS_219	N, B.SER_223	H, B.SER_223	2.87	2.04	11.53
5WKQ.PDB	O, B.ASP_222	N, B.ALA_226	H, B.ALA_226	2.87	2.09	21.47
5WKQ.PDB	O, B.SER_223	N, B.PHE_227	H, B.PHE_227	2.88	2.09	20.68

Table 1725: 5WKQ-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5WN9.PDB	OE1, H_GLN_1	NE2, H_GLN_3	HE21, H_GLN_3	2.70	1.88	14.43
5WN9.PDB	O, H_LYS_23	N, H_VAL_5	H, H_VAL_5	2.93	2.10	13.33
5WN9.PDB	OE1, H_GLN_116	N, H_GLN_6	H, H_GLN_6	2.83	1.97	4.77
5WN9.PDB	O, H_TYR_94	NE2, H_GLN_6	HE22, H_GLN_6	2.87	2.09	20.35
5WN9.PDB	O, H_LEU_119	N, H_GLU_10	H, H_GLU_10	2.95	2.12	13.96
5WN9.PDB	O, H_THR_121	N, H_LYS_12	H, H_LYS_12	2.90	2.09	16.60
5WN9.PDB	O, H_LEU_86	N, H_GLY_15	H, H_GLY_15	2.76	1.92	11.25
5WN9.PDB	O, H_LEU_83	N, H_VAL_18	H, H_VAL_18	2.97	2.16	16.04
5WN9.PDB	O, H_MET_81	N, H_LEU_20	H, H_LEU_20	2.76	1.92	9.07
5WN9.PDB	O, H_VAL_5	N, H_LYS_23	H, H_LYS_23	2.84	1.99	8.74
5WN9.PDB	O, H_ASN_77	N, H_ALA_24	H, H_ALA_24	2.85	2.00	2.73
5WN9.PDB	O, H_GLN_3	N, H_SER_25	H, H_SER_25	2.91	2.11	19.22
5WN9.PDB	O, H_GLY_97	N, H_SER_35	H, H_SER_35	2.98	2.16	11.85
5WN9.PDB	O, H_TYR_95	N, H_VAL_37	H, H_VAL_37	2.89	2.08	15.19
5WN9.PDB	O, H_GLU_46	N, H_ARG_38	H, H_ARG_38	2.88	2.07	17.27
5WN9.PDB	OE1, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.78	2.00	20.76
5WN9.PDB	OH, H_TYR_94	NH2, H_ARG_38	HH21, H_ARG_38	2.96	2.17	18.48
5WN9.PDB	OD1, H_ASP_90	NH2, H_ARG_38	HH22, H_ARG_38	2.91	2.07	9.36
5WN9.PDB	O, H_VAL_93	N, H_GLN_39	H, H_GLN_39	2.85	2.11	25.52
5WN9.PDB	OE1, H_GLN_182	NE2, H_GLN_39	HE22, H_GLN_39	2.96	2.11	8.81
5WN9.PDB	O, H_ARG_38	N, H_GLU_46	H, H_GLU_46	2.90	2.11	19.48
5WN9.PDB	O, H_TRP_36	N, H_MET_48	H, H_MET_48	2.86	2.02	9.08
5WN9.PDB	O, H_TYR_59	N, H_TRP_50	H, H_TRP_50	2.87	2.08	18.82
5WN9.PDB	O, H_ALA_106	NE1, H_TRP_50	HE1, H_TRP_50	2.91	2.13	20.34
5WN9.PDB	O, H_VAL_34	N, H_SER_51	H, H_SER_51	2.88	2.09	18.45
5WN9.PDB	O, H_VAL_34	OG, H_SER_51	HG, H_SER_51	2.85	2.13	25.31
5WN9.PDB	O, H_ASN_57	N, H_SER_52	H, H_SER_52	2.90	2.09	17.84
5WN9.PDB	O, H_SER_52	N, H_GLY_56	H, H_GLY_56	2.91	2.13	21.69
5WN9.PDB	OD1, H_ASN_55	N, H_ASN_57	H, H_ASN_57	2.95	2.11	6.76
5WN9.PDB	O, H_TRP_50	N, H_TYR_59	H, H_TYR_59	2.96	2.17	19.00
5WN9.PDB	O, H_MET_48	N, H_ALA_61	H, H_ALA_61	2.91	2.07	8.09
5WN9.PDB	O, H_ALA_61	N, H_LEU_64	H, H_LEU_64	2.94	2.13	15.81
5WN9.PDB	O, H_LEU_64	N, H_ARG_67	H, H_ARG_67	2.91	2.19	28.27
5WN9.PDB	OD2, H_ASP_90	NH1, H_ARG_67	HH12, H_ARG_67	2.27	1.51	22.67
5WN9.PDB	O, H_GLU_82	N, H_THR_69	H, H_THR_69	2.97	2.19	21.04
5WN9.PDB	OH, H_TYR_60	N, H_MET_70	H, H_MET_70	2.89	2.04	9.93
5WN9.PDB	O, H_THR_78	N, H_ASP_73	H, H_ASP_73	2.77	1.94	12.50
5WN9.PDB	OD1, H_ASP_73	N, H_SER_75	H, H_SER_75	2.97	2.21	23.09
5WN9.PDB	OD1, H_ASP_73	OG, H_SER_75	HG, H_SER_75	2.58	1.79	16.04
5WN9.PDB	O, H_CYS_22	N, H_ALA_79	H, H_ALA_79	2.83	1.99	10.49
5WN9.PDB	O, H_THR_71	N, H_TYR_80	H, H_TYR_80	2.85	2.01	11.64
5WN9.PDB	O, H_LEU_20	N, H_MET_81	H, H_MET_81	2.95	2.14	16.70
5WN9.PDB	O, H_THR_69	N, H_GLU_82	H, H_GLU_82	2.85	2.02	12.09
5WN9.PDB	O, H_VAL_18	N, H_LEU_83	H, H_LEU_83	2.91	2.12	19.85
5WN9.PDB	O, H_ARG_67	N, H_ARG_84	H, H_ARG_84	2.80	1.98	15.10
5WN9.PDB	OG1, H_THR_69	NH1, H_ARG_84	HH12, H_ARG_84	2.83	2.06	21.62
5WN9.PDB	O, H_ALA_66	NH2, H_ARG_84	HH21, H_ARG_84	2.99	2.24	24.04
5WN9.PDB	O, H_ALA_16	N, H_LEU_86	H, H_LEU_86	2.99	2.14	2.07
5WN9.PDB	OD2, H_ASP_90	N, H_ARG_87	H, H_ARG_87	2.89	2.10	17.07
5WN9.PDB	O, H_SER_85	NH1, H_ARG_87	HH11, H_ARG_87	2.78	2.03	24.21
5WN9.PDB	O, H_ARG_87	N, H_ASP_90	H, H_ASP_90	2.92	2.07	9.16
5WN9.PDB	O, H_GLN_39	N, H_VAL_93	H, H_VAL_93	2.93	2.14	19.95
5WN9.PDB	O, H_THR_118	N, H_TYR_94	H, H_TYR_94	2.77	1.92	7.11
5WN9.PDB	O, H_ASP_90	OH, H_TYR_94	HH, H_TYR_94	2.64	1.81	7.80
5WN9.PDB	O, H_VAL_37	N, H_TYR_95	H, H_TYR_95	2.71	1.86	4.49
5WN9.PDB	O, H_SER_35	N, H_GLY_97	H, H_GLY_97	2.90	2.14	23.59
5WN9.PDB	O, H_SER_113	N, H_ARG_98	H, H_ARG_98	2.91	2.10	16.03

5WN9.PDB	OD1, H_ASP_112	NE, H_ARG_98	HE, H_ARG_98	2.94	2.13	15.87
5WN9.PDB	OD2, H_ASP_112	NH1, H_ARG_98	HH11, H_ARG_98	2.84	2.01	13.12
5WN9.PDB	O, H_PRO_110	N, H_MET_100	H, H_MET_100	2.87	2.05	15.00
5WN9.PDB	OD1, H_ASP_99	N, H_GLY_109	H, H_GLY_109	2.84	2.01	13.27
5WN9.PDB	OH, H_TYR_180	N, H_PHE_111	H, H_PHE_111	2.98	2.20	19.41
5WN9.PDB	O, H_CYS_96	N, H_GLY_115	H, H_GLY_115	2.86	2.02	9.77
5WN9.PDB	O, H_GLN_6	NE2, H_GLN_116	HE22, H_GLN_116	2.88	2.05	14.44
5WN9.PDB	OE1, H_GLN_6	N, H_GLY_117	H, H_GLY_117	2.99	2.25	25.16
5WN9.PDB	O, H_TYR_94	N, H_THR_118	H, H_THR_118	2.78	1.97	14.98
5WN9.PDB	O, H_SER_7	OG1, H_THR_118	HG1, H_THR_118	2.77	2.03	24.19
5WN9.PDB	O, H_ALA_92	N, H_VAL_120	H, H_VAL_120	2.95	2.10	8.42
5WN9.PDB	O, H_GLU_10	N, H_THR_121	H, H_THR_121	2.91	2.06	8.28
5WN9.PDB	OG1, H_THR_91	N, H_VAL_122	H, H_VAL_122	2.90	2.05	5.63
5WN9.PDB	O, H_LYS_12	N, H_SER_123	H, H_SER_123	2.75	1.94	16.31
5WN9.PDB	O, H_ARG_168	N, H_THR_149	H, H_THR_149	2.97	2.13	11.46
5WN9.PDB	O, H_TYR_230	NE2, H_GLN_150	HE22, H_GLN_150	2.99	2.13	4.72
5WN9.PDB	O, H_SER_166	N, H_SER_151	H, H_SER_151	2.95	2.15	17.82
5WN9.PDB	O, H_LYS_247	N, H_VAL_155	H, H_VAL_155	2.96	2.17	20.07
5WN9.PDB	O, H_GLU_249	N, H_ALA_157	H, H_ALA_157	2.97	2.20	22.22
5WN9.PDB	OD2, H_ASP_161	N, H_SER_158	H, H_SER_158	2.85	2.00	7.54
5WN9.PDB	O, H_LEU_222	N, H_GLY_160	H, H_GLY_160	2.71	1.90	15.63
5WN9.PDB	OG1, H_THR_218	NH2, H_ARG_162	HH21, H_ARG_162	2.83	2.04	19.79
5WN9.PDB	O, H_LEU_217	N, H_ILE_165	H, H_ILE_165	2.79	1.95	8.96
5WN9.PDB	O, H_SER_151	N, H_SER_166	H, H_SER_166	2.82	1.97	7.02
5WN9.PDB	O, H_PHE_215	N, H_CYS_167	H, H_CYS_167	2.89	2.04	8.23
5WN9.PDB	O, H_THR_149	N, H_ARG_168	H, H_ARG_168	2.89	2.06	13.39
5WN9.PDB	O, H_THR_213	N, H_ALA_169	H, H_ALA_169	2.83	2.01	14.31
5WN9.PDB	O, H_GLY_212	N, H_ILE_173	H, H_ILE_173	2.92	2.09	10.87
5WN9.PDB	O, H_ILE_173	N, H_SER_176	H, H_SER_176	2.94	2.08	5.22
5WN9.PDB	O, H_GLN_233	N, H_ALA_178	H, H_ALA_178	2.89	2.06	12.90
5WN9.PDB	O, H_ILE_192	N, H_TRP_179	H, H_TRP_179	2.88	2.07	16.13
5WN9.PDB	O, H_TYR_231	N, H_TYR_180	H, H_TYR_180	2.81	2.00	16.41
5WN9.PDB	OE1, H_GLN_233	OH, H_TYR_180	HH, H_TYR_180	2.70	1.87	8.37
5WN9.PDB	O, H_GLN_189	N, H_GLN_181	H, H_GLN_181	2.87	2.05	15.50
5WN9.PDB	O, H_THR_229	N, H_GLN_182	H, H_GLN_182	2.73	1.91	15.73
5WN9.PDB	O, H_LYS_186	NE2, H_GLN_182	HE21, H_GLN_182	2.95	2.15	17.69
5WN9.PDB	OE1, H_GLN_39	NE2, H_GLN_182	HE22, H_GLN_182	2.85	2.00	9.41
5WN9.PDB	O, H_GLN_181	N, H_GLN_189	H, H_GLN_189	2.76	1.98	20.74
5WN9.PDB	O, H_TRP_179	N, H_LEU_191	H, H_LEU_191	2.80	1.95	5.76
5WN9.PDB	O, H_SER_197	N, H_TYR_193	H, H_TYR_193	2.93	2.13	18.06
5WN9.PDB	O, H_LEU_177	N, H_ALA_195	H, H_ALA_195	2.82	2.00	13.79
5WN9.PDB	O, H_GLY_208	OG, H_BSER_196	HG, H_BSER_196	2.95	2.19	21.28
5WN9.PDB	O, H_TYR_193	N, H_SER_197	H, H_SER_197	2.88	2.08	19.19
5WN9.PDB	O, H_LEU_191	N, H_GLN_199	H, H_GLN_199	2.93	2.07	0.47
5WN9.PDB	OD2, H_ASP_226	NE, H_ARG_205	HE, H_ARG_205	2.80	1.99	17.36
5WN9.PDB	OD1, H_ASP_226	NH1, H_ARG_205	HH11, H_ARG_205	2.89	2.03	4.48
5WN9.PDB	O, H_THR_216	N, H_SER_209	H, H_SER_209	3.00	2.21	19.73
5WN9.PDB	O, H_SER_174	N, H_GLY_212	H, H_GLY_212	2.91	2.07	9.42
5WN9.PDB	O, H_CYS_167	N, H_PHE_215	H, H_PHE_215	2.93	2.12	15.69
5WN9.PDB	O, H_ILE_165	N, H_LEU_217	H, H_LEU_217	2.91	2.09	15.07
5WN9.PDB	O, H_SER_207	N, H_THR_218	H, H_THR_218	2.92	2.08	10.72
5WN9.PDB	OG1, H_THR_164	OG1, H_THR_218	HG1, H_THR_218	2.96	2.26	28.62
5WN9.PDB	O, H_VAL_163	N, H_ILE_219	H, H_ILE_219	2.79	1.97	14.91
5WN9.PDB	O, H_ARG_205	N, H_SER_220	H, H_SER_220	2.99	2.21	20.02
5WN9.PDB	O, H_ASP_161	N, H_LEU_222	H, H_LEU_222	2.76	1.97	18.80
5WN9.PDB	OD2, H_ASP_226	N, H_GLN_223	H, H_GLN_223	2.93	2.08	7.95
5WN9.PDB	O, H_GLN_223	N, H_ASP_226	H, H_ASP_226	2.82	1.98	8.91
5WN9.PDB	O, H_THR_246	N, H_TYR_230	H, H_TYR_230	2.87	2.06	16.33

5WN9.PDB	O, H_ASP_226	OH, H_TYR_230	HH, H_TYR_230	2.62	1.80	10.05
5WN9.PDB	O, H_TYR_180	N, H_TYR_231	H, H_TYR_231	2.93	2.12	16.57
5WN9.PDB	O, H_THR_241	N, H_GLN_234	H, H_GLN_234	2.95	2.18	23.47
5WN9.PDB	O, H_THR_146	OG1, H_THR_241	HG1, H_THR_241	2.72	1.91	13.19
5WN9.PDB	O, H_CYS_232	N, H_GLY_243	H, H_GLY_243	2.91	2.11	17.20
5WN9.PDB	O, H_TYR_230	N, H_THR_246	H, H_THR_246	2.86	2.08	20.56
5WN9.PDB	O, H_PRO_152	OG1, H_THR_246	HG1, H_THR_246	2.65	1.95	28.58
5WN9.PDB	O, H_SER_153	N, H_LYS_247	H, H_LYS_247	2.96	2.15	15.87
5WN9.PDB	O, H_ALA_228	N, H_VAL_248	H, H_VAL_248	2.90	2.04	3.82
5WN9.PDB	O, H_VAL_155	N, H_GLU_249	H, H_GLU_249	2.87	2.03	10.19
5WN9.PDB	O, A_LYS_187	N, A_CYS_173	H, A_CYS_173	2.97	2.18	19.66
5WN9.PDB	O, A_CYS_176	N, A_ASN_179	H, A_ASN_179	2.99	2.15	7.83
5WN9.PDB	O, A_SER_177	NE1, A_TRP_183	HE1, A_TRP_183	2.88	2.03	4.80
5WN9.PDB	O, A_VAL_171	N, A_LYS_187	H, A_LYS_187	2.85	2.04	15.74
5WN9.PDB	OD1, H_ASN_57	NE, A_ARG_188	HE, A_ARG_188	2.58	1.61	2.15

Table 1726: 5WN9-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1A14.PDB	OG, H_SER_25	NE2, H_GLN_5	HE21, H_GLN_5	2.94	2.02	15.87
1A14.PDB	OE1, L_GLN_38	NE2, H_GLN_39	HE21, H_GLN_39	2.62	1.69	9.24
1A14.PDB	OG1, H_THR_77	OG, H_SER_75	HG, H_SER_75	2.86	2.04	27.11
1A14.PDB	OE2, H_GLU_85	OG, H_SER_84	HG, H_SER_84	2.91	1.99	12.42
1A14.PDB	OD2, H_ASP_101	NH2, H_ARG_94	HH21, H_ARG_94	2.75	1.83	16.91

Table 1727: 1A14-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1E6J.PDB	OH, L-TYR_85	NE2, L-GLN_36	HE21, L-GLN_36	2.83	1.87	8.49
1E6J.PDB	OE1, H-GLN_39	NE2, L-GLN_37	HE22, L-GLN_37	2.69	1.84	23.98
1E6J.PDB	OG, L-SER_129	NE2, L-GLN_122	HE22, L-GLN_122	2.94	2.00	13.76

Table 1728: 1E6J-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1F3R.PDB	OD1, B_ASN_83	OG1, B_THR_17	HG1, B_THR_17	2.73	1.80	13.32
1F3R.PDB	NE1, A_TRP_67	OG, B_SER_61	HG, B_SER_61	2.86	1.89	6.31
1F3R.PDB	OG1, B_THR_212	OG1, B_THR_158	HG1, B_THR_158	2.80	1.87	11.10
1F3R.PDB	OD1, B_ASP_220	NH1, B_ARG_199	HH12, B_ARG_199	2.89	1.98	22.15
1F3R.PDB	OE1, B_GLN_217	OG, B_SER_215	HG, B_SER_215	2.66	1.72	13.57
1F3R.PDB	NE1, B_TRP_47	OH, B_TYR_227	HH, B_TYR_227	2.99	2.20	29.73
1F3R.PDB	OD1, B_ASN_188	OH, B_TYR_229	HH, B_TYR_229	2.66	1.70	7.44

Table 1729: 1F3R-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1HCV.PDB	OE2, A_GLU_46	NE, A_ARG_38	HE, A_ARG_38	2.98	2.01	4.47
1HCV.PDB	OH, A_TYR_90	NH1, A_ARG_38	HH11, A_ARG_38	2.93	1.98	14.34
1HCV.PDB	OD1, A_ASP_86	NH1, A_ARG_38	HH12, A_ARG_38	2.86	1.90	11.61

Table 1730: 1HCV-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1HGD.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.80	1.78	9.95
1HGD.PDB	OD2, A_ASP_275	NZ, A_LYS_50	HZ1, A_LYS_50	2.70	1.79	23.99
1HGD.PDB	OD1, A_ASP_73	ND1, A_HIS_75	HD1, A_HIS_75	2.82	1.92	19.21
1HGD.PDB	OD1, A_ASP_60	NE, A_ARG_90	HE, A_ARG_90	2.88	1.91	7.55
1HGD.PDB	OD2, A_ASP_60	NH2, A_ARG_90	HH21, A_ARG_90	2.80	1.82	10.07
1HGD.PDB	OD1, A_ASP_271	OG, A_SER_91	HG, A_SER_91	2.93	2.12	28.00
1HGD.PDB	OD2, A_ASP_271	OG, A_SER_91	HG, A_SER_91	2.81	1.91	17.78
1HGD.PDB	OD2, A_ASP_68	OG, A_SER_95	HG, A_SER_95	2.92	1.99	16.11
1HGD.PDB	OD1, A_ASP_68	OH, A_TYR_100	HH, A_TYR_100	2.88	1.90	0.98
1HGD.PDB	OD2, A_ASP_104	OG, A_SER_107	HG, A_SER_107	2.86	1.96	19.52
1HGD.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.83	1.84	13.41
1HGD.PDB	OD2, F_ASP_79	OG, A_SER_110	HG, A_SER_110	2.92	1.96	11.03
1HGD.PDB	OE2, A_GLU_119	OG1, A_THR_117	HG1, A_THR_117	2.87	1.92	9.92
1HGD.PDB	OD1, A_ASN_137	NZ, A_LYS_140	HZ2, A_LYS_140	2.76	1.82	19.96
1HGD.PDB	OD2, A_ASP_77	NE, A_ARG_141	HE, A_ARG_141	2.80	1.97	26.87
1HGD.PDB	OD1, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.86	1.95	21.98
1HGD.PDB	OD2, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.74	1.86	23.87
1HGD.PDB	OH, A_TYR_195	NE1, A_TRP_153	HE1, A_TRP_153	2.81	1.92	20.45
1HGD.PDB	OE2, A_GLU_123	NZ, A_LYS_176	HZ2, A_LYS_176	2.69	1.80	25.20
1HGD.PDB	OE1, A_GLU_123	OH, A_TYR_178	HH, A_TYR_178	2.75	1.82	12.48
1HGD.PDB	OG1, A_THR_235	NE1, A_TRP_180	HE1, A_TRP_180	2.94	1.95	4.39
1HGD.PDB	OG, A_SER_231	NE2, A_HIS_184	HE2, A_HIS_184	2.78	1.93	25.06
1HGD.PDB	OD1, A_ASN_246	NH2, A_ARG_201	HH21, A_ARG_201	2.59	1.75	26.83
1HGD.PDB	OG1, A_THR_206	OG, A_SER_209	HG, A_SER_209	2.90	1.96	11.12
1HGD.PDB	OD1, E_ASP_101	NE2, A_GLN_210	HE22, A_GLN_210	3.00	2.15	26.33
1HGD.PDB	OG1, A_THR_203	OG1, A_THR_212	HG1, A_THR_212	2.90	1.94	6.68
1HGD.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.78	1.86	19.99
1HGD.PDB	OE2, A_GLU_190	OG, A_SER_228	HG, A_SER_228	2.98	2.00	5.61
1HGD.PDB	OD1, A_ASP_101	OG, A_SER_231	HG, A_SER_231	2.84	1.88	8.92
1HGD.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.93	1.92	13.44
1HGD.PDB	OD1, A_ASN_165	ND2, A_ASN_246	HD22, A_ASN_246	2.92	1.97	12.69
1HGD.PDB	OE1, A_GLN_191	ND2, A_ASN_250	HD21, A_ASN_250	2.94	1.98	9.96
1HGD.PDB	OD1, A_ASN_133	NH2, A_ARG_255	HH22, A_ARG_255	2.53	1.69	26.82
1HGD.PDB	OE2, A_GLU_119	NH1, A_ARG_261	HH12, A_ARG_261	2.65	1.81	27.93
1HGD.PDB	OE1, A_GLU_119	NH2, A_ARG_261	HH22, A_ARG_261	2.88	1.97	22.77
1HGD.PDB	OD2, A_ASP_85	NZ, A_LYS_264	HZ3, A_LYS_264	2.85	1.86	16.67
1HGD.PDB	OE1, A_GLN_44	NZ, A_LYS_292	HZ1, A_LYS_292	2.71	1.70	11.58
1HGD.PDB	OD2, A_ASP_291	NZ, A_LYS_292	HZ3, A_LYS_292	2.78	1.85	22.68
1HGD.PDB	OD1, A_ASN_285	ND2, A_ASN_298	HD22, A_ASN_298	2.98	2.04	13.52
1HGD.PDB	OE1, A_GLU_41	NZ, A_LYS_315	HZ3, A_LYS_315	2.76	1.81	20.40
1HGD.PDB	OE2, A_GLU_35	ND2, A_ASN_322	HD22, A_ASN_322	2.84	1.97	23.40
1HGD.PDB	OE1, B_GLN_34	NE, B_ARG_25	HE, B_ARG_25	2.65	1.77	20.51
1HGD.PDB	OD1, B_ASP_46	NE2, B_GLN_42	HE22, B_GLN_42	2.84	1.95	20.63
1HGD.PDB	OG1, B_THR_107	NZ, B_LYS_51	HZ1, B_LYS_51	2.96	1.97	16.32
1HGD.PDB	OE1, B_GLU_103	NZ, B_LYS_51	HZ2, B_LYS_51	2.73	1.71	9.93
1HGD.PDB	ND1, B_HIS_106	NZ, B_LYS_51	HZ3, B_LYS_51	2.75	1.79	17.84
1HGD.PDB	OE1, B_GLU_57	NH1, B_ARG_54	HH11, B_ARG_54	2.86	1.87	11.55
1HGD.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.77	1.80	12.79
1HGD.PDB	OE2, B_GLU_61	NZ, B_LYS_58	HZ2, B_LYS_58	2.91	1.88	11.49
1HGD.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ1, B_LYS_62	2.61	1.78	29.53
1HGD.PDB	OD2, F_ASP_90	NZ, B_LYS_62	HZ3, B_LYS_62	2.73	1.84	25.56
1HGD.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.96	2.01	12.34
1HGD.PDB	OE2, B_GLU_85	NZ, B_LYS_68	HZ2, B_LYS_68	2.76	1.74	9.73
1HGD.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.88	1.91	8.67
1HGD.PDB	OE2, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.84	1.82	2.51
1HGD.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.71	1.71	6.80
1HGD.PDB	OE1, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.75	1.75	3.21

1HGD.PDB	OE1, B_GLU_74	NE2, B_GLN_78	HE22, B_GLN_78	2.92	1.97	11.55
1HGD.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.65	1.81	23.27
1HGD.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.76	1.72	5.59
1HGD.PDB	OE2, B_GLU_120	NH1, B_ARG_123	HH11, B_ARG_123	2.79	1.91	24.17
1HGD.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.83	2.02	28.17
1HGD.PDB	OE2, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.88	2.01	22.00
1HGD.PDB	OH, B_TYR_157	ND2, B_ASN_129	HD22, B_ASN_129	2.78	1.83	11.22
1HGD.PDB	OE2, B_GLU_150	ND2, B_ASN_154	HD21, B_ASN_154	2.98	2.09	22.34
1HGD.PDB	OD1, B_ASN_154	OG1, B_THR_156	HG1, B_THR_156	2.75	1.84	16.14
1HGD.PDB	OE2, B_GLU_131	NH1, B_ARG_170	HH11, B_ARG_170	2.78	1.79	7.42
1HGD.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.80	1.77	7.54
1HGD.PDB	OD2, C_ASP_275	NZ, C_LYS_50	HZ1, C_LYS_50	2.66	1.78	25.77
1HGD.PDB	OD1, C_ASP_73	ND1, C_HIS_75	HD1, C_HIS_75	2.77	1.87	19.67
1HGD.PDB	OD1, C_ASP_60	NE, C_ARG_90	HE, C_ARG_90	2.86	1.89	9.66
1HGD.PDB	OD2, C_ASP_60	NH2, C_ARG_90	HH21, C_ARG_90	2.78	1.79	10.49
1HGD.PDB	OD1, C_ASP_271	OG, C_SER_91	HG, C_SER_91	2.93	2.11	26.93
1HGD.PDB	OD2, C_ASP_271	OG, C_SER_91	HG, C_SER_91	2.86	1.96	18.80
1HGD.PDB	OD2, C_ASP_68	OG, C_SER_95	HG, C_SER_95	2.88	1.96	15.18
1HGD.PDB	OD1, C_ASP_68	OH, C_TYR_100	HH, C_TYR_100	2.89	1.96	14.39
1HGD.PDB	OD2, C_ASP_104	OG, C_SER_107	HG, C_SER_107	2.91	2.00	17.92
1HGD.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.87	1.88	13.44
1HGD.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.73	1.84	19.59
1HGD.PDB	OE2, C_GLU_119	OG1, C_THR_117	HG1, C_THR_117	2.86	1.93	10.42
1HGD.PDB	OD1, C_ASN_137	NZ, C_LYS_140	HZ2, C_LYS_140	2.78	1.84	20.52
1HGD.PDB	OD2, C_ASP_77	NE, C_ARG_141	HE, C_ARG_141	2.80	1.97	27.06
1HGD.PDB	OD1, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.87	1.96	21.76
1HGD.PDB	OD2, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.75	1.86	23.93
1HGD.PDB	OD1, C_ASN_137	OG, C_SER_145	HG, C_SER_145	2.98	2.13	22.87
1HGD.PDB	OH, C_TYR_195	NE1, C_TRP_153	HE1, C_TRP_153	2.80	1.95	24.25
1HGD.PDB	OE2, C_GLU_123	NZ, C_LYS_176	HZ2, C_LYS_176	2.69	1.80	25.35
1HGD.PDB	OE1, C_GLU_123	OH, C_TYR_178	HH, C_TYR_178	2.73	1.80	13.21
1HGD.PDB	OG1, C_THR_235	NE1, C_TRP_180	HE1, C_TRP_180	2.91	1.93	2.97
1HGD.PDB	OG, C_SER_231	NE2, C_HIS_184	HE2, C_HIS_184	2.75	1.91	25.20
1HGD.PDB	OD1, C_ASN_250	NE2, C_GLN_191	HE21, C_GLN_191	2.98	2.02	9.43
1HGD.PDB	OD1, C_ASN_246	NH2, C_ARG_201	HH21, C_ARG_201	2.60	1.77	27.30
1HGD.PDB	OG1, C_THR_212	OG1, C_THR_203	HG1, C_THR_203	2.89	1.96	13.30
1HGD.PDB	OD2, C_ASP_241	NE, C_ARG_208	HE, C_ARG_208	2.97	2.08	21.42
1HGD.PDB	OG1, C_THR_206	OG, C_SER_209	HG, C_SER_209	2.92	1.98	10.99
1HGD.PDB	OD1, A_ASP_101	NE2, C_GLN_210	HE22, C_GLN_210	2.97	2.13	27.21
1HGD.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.69	1.80	23.00
1HGD.PDB	OE2, C_GLU_190	OG, C_SER_228	HG, C_SER_228	3.00	2.02	4.69
1HGD.PDB	OD1, C_ASP_101	OG, C_SER_231	HG, C_SER_231	2.87	1.90	8.39
1HGD.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.80	1.83	17.68
1HGD.PDB	OD1, C_ASN_165	ND2, C_ASN_246	HD22, C_ASN_246	2.91	1.96	13.56
1HGD.PDB	OE1, C_GLN_191	ND2, C_ASN_250	HD21, C_ASN_250	2.90	1.95	10.99
1HGD.PDB	OD1, C_ASN_133	NH2, C_ARG_255	HH22, C_ARG_255	2.52	1.69	27.35
1HGD.PDB	OE2, C_GLU_119	NH1, C_ARG_261	HH12, C_ARG_261	2.66	1.83	27.96
1HGD.PDB	OE1, C_GLU_119	NH2, C_ARG_261	HH22, C_ARG_261	2.90	2.00	23.32
1HGD.PDB	OD2, C_ASP_85	NZ, C_LYS_264	HZ3, C_LYS_264	2.82	1.84	16.88
1HGD.PDB	OE1, C_GLN_44	NZ, C_LYS_292	HZ1, C_LYS_292	2.73	1.73	12.00
1HGD.PDB	OD2, C_ASP_291	NZ, C_LYS_292	HZ3, C_LYS_292	2.79	1.88	23.81
1HGD.PDB	OD1, C_ASN_285	ND2, C_ASN_298	HD22, C_ASN_298	2.96	2.02	13.09
1HGD.PDB	OE1, C_GLU_41	NZ, C_LYS_315	HZ3, C_LYS_315	2.78	1.84	20.99
1HGD.PDB	OE2, C_GLU_35	ND2, C_ASN_322	HD22, C_ASN_322	2.83	1.94	21.17
1HGD.PDB	OE1, D_GLU_15	NZ, C_LYS_326	HZ1, C_LYS_326	2.78	1.77	11.96
1HGD.PDB	OXT, C_THR_328	NE2, C_GLN_327	HE22, C_GLN_327	2.97	2.03	15.01
1HGD.PDB	OE1, D_GLN_34	NE, D_ARG_25	HE, D_ARG_25	2.61	1.77	24.43
1HGD.PDB	OD1, D_ASN_146	ND2, D_ASN_28	HD21, D_ASN_28	3.00	2.03	9.16

1HGD.PDB	OD2, D_ASP_37	OG, D_SER_40	HG, D_SER_40	2.86	1.96	18.80
1HGD.PDB	OD1, D_ASP_46	NE2, D_GLN_42	HE22, D_GLN_42	2.84	1.95	20.82
1HGD.PDB	OG1, D_THR_107	NZ, D_LYS_51	HZ1, D_LYS_51	2.96	1.98	16.97
1HGD.PDB	OE1, D_GLU_103	NZ, D_LYS_51	HZ2, D_LYS_51	2.74	1.72	8.47
1HGD.PDB	ND1, D_HIS_106	NZ, D_LYS_51	HZ3, D_LYS_51	2.74	1.78	16.91
1HGD.PDB	OE1, D_GLU_57	NH1, D_ARG_54	HH11, D_ARG_54	2.85	1.86	12.06
1HGD.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.79	1.82	13.03
1HGD.PDB	OE2, D_GLU_61	NZ, D_LYS_58	HZ2, D_LYS_58	2.90	1.87	10.86
1HGD.PDB	OD2, B_ASP_90	NZ, D_LYS_62	HZ3, D_LYS_62	2.62	1.79	29.99
1HGD.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.96	1.98	5.65
1HGD.PDB	OE2, D_GLU_85	NZ, D_LYS_68	HZ2, D_LYS_68	2.78	1.76	10.92
1HGD.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.83	1.87	10.56
1HGD.PDB	OE2, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.78	1.77	3.14
1HGD.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.65	1.67	9.42
1HGD.PDB	OE1, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.69	1.70	6.24
1HGD.PDB	OE1, D_GLU_74	NE2, D_GLN_78	HE22, D_GLN_78	2.94	1.97	10.43
1HGD.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.57	1.79	29.87
1HGD.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.76	1.72	5.75
1HGD.PDB	OE2, D_GLU_120	NH1, D_ARG_123	HH11, D_ARG_123	2.80	1.92	24.08
1HGD.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.80	2.01	29.31
1HGD.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.82	1.95	21.73
1HGD.PDB	OH, D_TYR_157	ND2, D_ASN_129	HD22, D_ASN_129	2.79	1.82	6.93
1HGD.PDB	OE2, D_GLU_150	ND2, D_ASN_154	HD21, D_ASN_154	2.88	2.05	27.54
1HGD.PDB	OD1, D_ASN_154	OG1, D_THR_156	HG1, D_THR_156	2.79	1.83	8.53
1HGD.PDB	NE2, D_HIS_142	OH, D_TYR_157	HH, D_TYR_157	2.78	1.89	18.65
1HGD.PDB	OE2, D_GLU_131	NH1, D_ARG_170	HH11, D_ARG_170	2.77	1.78	7.65
1HGD.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.79	1.77	8.77
1HGD.PDB	OD2, E_ASP_275	NZ, E_LYS_50	HZ1, E_LYS_50	2.69	1.80	25.14
1HGD.PDB	OD1, E_ASP_73	ND1, E_HIS_75	HD1, E_HIS_75	2.79	1.88	18.25
1HGD.PDB	OD1, E_ASP_60	NE, E_ARG_90	HE, E_ARG_90	2.88	1.91	7.90
1HGD.PDB	OD2, E_ASP_60	NH2, E_ARG_90	HH21, E_ARG_90	2.82	1.83	10.15
1HGD.PDB	OD1, E_ASP_271	OG, E_SER_91	HG, E_SER_91	2.94	2.13	28.39
1HGD.PDB	OD2, E_ASP_271	OG, E_SER_91	HG, E_SER_91	2.84	1.93	17.47
1HGD.PDB	OD2, E_ASP_68	OG, E_SER_95	HG, E_SER_95	2.91	1.98	14.66
1HGD.PDB	OD1, E_ASP_68	OH, E_TYR_100	HH, E_TYR_100	2.86	1.93	14.06
1HGD.PDB	OD2, E_ASP_104	OG, E_SER_107	HG, E_SER_107	2.90	1.98	16.44
1HGD.PDB	OE2, F_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.82	1.85	14.73
1HGD.PDB	OD2, D_ASP_79	OG, E_SER_110	HG, E_SER_110	2.81	1.89	15.50
1HGD.PDB	OE2, E_GLU_119	OG1, E_THR_117	HG1, E_THR_117	2.90	1.95	9.79
1HGD.PDB	OD1, E_ASN_137	NZ, E_LYS_140	HZ2, E_LYS_140	2.79	1.84	19.51
1HGD.PDB	OD2, E_ASP_77	NE, E_ARG_141	HE, E_ARG_141	2.82	1.98	26.95
1HGD.PDB	OD1, E_ASP_77	NH2, E_ARG_141	HH21, E_ARG_141	2.88	1.95	21.13
1HGD.PDB	OD2, E_ASP_77	NH2, E_ARG_141	HH21, E_ARG_141	2.75	1.86	24.62
1HGD.PDB	OH, E_TYR_195	NE1, E_TRP_153	HE1, E_TRP_153	2.82	1.91	19.17
1HGD.PDB	OE2, E_GLU_123	NZ, E_LYS_176	HZ2, E_LYS_176	2.69	1.80	25.12
1HGD.PDB	OE1, E_GLU_123	OH, E_TYR_178	HH, E_TYR_178	2.75	1.83	13.46
1HGD.PDB	OG1, E_THR_235	NE1, E_TRP_180	HE1, E_TRP_180	2.93	1.94	3.75
1HGD.PDB	OG, E_SER_231	NE2, E_HIS_184	HE2, E_HIS_184	2.80	1.95	25.42
1HGD.PDB	OD1, E_ASN_246	NH2, E_ARG_201	HH21, E_ARG_201	2.60	1.77	27.54
1HGD.PDB	OG1, E_THR_212	OG1, E_THR_203	HG1, E_THR_203	2.93	1.99	12.22
1HGD.PDB	OG1, E_THR_206	OG, E_SER_209	HG, E_SER_209	2.91	1.97	11.26
1HGD.PDB	OD1, C_ASP_101	NE2, E_GLN_210	HE22, E_GLN_210	2.98	2.14	27.07
1HGD.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.77	1.90	25.11
1HGD.PDB	OE2, E_GLU_190	OG, E_SER_228	HG, E_SER_228	2.96	1.98	4.78
1HGD.PDB	OD1, E_ASP_101	OG, E_SER_231	HG, E_SER_231	2.85	1.91	13.25
1HGD.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ3, E_LYS_238	2.87	1.86	13.40
1HGD.PDB	OD1, E_ASN_165	ND2, E_ASN_246	HD22, E_ASN_246	2.91	1.96	12.66
1HGD.PDB	OE1, E_GLN_191	ND2, E_ASN_250	HD21, E_ASN_250	2.95	1.99	9.92

1HGD.PDB	OD1, E_ASN_133	NH2, E_ARG_255	HH22, E_ARG_255	2.52	1.69	27.28
1HGD.PDB	OE2, E_GLU_119	NH1, E_ARG_261	HH12, E_ARG_261	2.64	1.81	27.92
1HGD.PDB	OE1, E_GLU_119	NH2, E_ARG_261	HH22, E_ARG_261	2.88	1.97	22.94
1HGD.PDB	OD2, E_ASP_85	NZ, E_LYS_264	HZ3, E_LYS_264	2.87	1.88	16.50
1HGD.PDB	OE1, E_GLN_44	NZ, E_LYS_292	HZ1, E_LYS_292	2.70	1.70	12.87
1HGD.PDB	OD2, E_ASP_291	NZ, E_LYS_292	HZ3, E_LYS_292	2.83	1.91	23.60
1HGD.PDB	OD1, E_ASN_285	ND2, E_ASN_298	HD22, E_ASN_298	2.95	2.01	14.15
1HGD.PDB	OE1, E_GLU_41	NZ, E_LYS_315	HZ3, E_LYS_315	2.76	1.83	22.10
1HGD.PDB	OE2, E_GLU_35	ND2, E_ASN_322	HD22, E_ASN_322	2.82	1.95	23.13
1HGD.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.97	1.97	16.19
1HGD.PDB	OE1, F_GLN_34	NE, F_ARG_25	HE, F_ARG_25	2.93	2.07	24.69
1HGD.PDB	OE1, F_GLN_34	NH2, F_ARG_25	HH21, F_ARG_25	2.80	1.89	20.31
1HGD.PDB	OD1, F_ASN_146	ND2, F_ASN_28	HD21, F_ASN_28	2.81	1.89	15.27
1HGD.PDB	OD2, F_ASP_37	OG, F_SER_40	HG, F_SER_40	2.84	1.98	23.42
1HGD.PDB	OD1, F_ASP_46	NE2, F_GLN_42	HE22, F_GLN_42	2.83	1.94	21.51
1HGD.PDB	OE1, F_GLU_103	NZ, F_LYS_51	HZ2, F_LYS_51	2.72	1.70	8.28
1HGD.PDB	ND1, F_HIS_106	NZ, F_LYS_51	HZ3, F_LYS_51	2.73	1.76	16.89
1HGD.PDB	OE1, F_GLU_57	NH1, F_ARG_54	HH11, F_ARG_54	2.86	1.85	10.37
1HGD.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.72	1.75	12.85
1HGD.PDB	OE2, F_GLU_61	NZ, F_LYS_58	HZ2, F_LYS_58	2.92	1.89	10.22
1HGD.PDB	OD2, D_ASP_90	NZ, F_LYS_62	HZ3, F_LYS_62	2.71	1.86	28.09
1HGD.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.95	1.98	9.92
1HGD.PDB	OE2, F_GLU_85	NZ, F_LYS_68	HZ2, F_LYS_68	2.72	1.77	19.94
1HGD.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.86	1.90	10.66
1HGD.PDB	OE2, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.77	1.75	1.42
1HGD.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.64	1.65	5.37
1HGD.PDB	OE1, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.71	1.72	7.42
1HGD.PDB	OE1, F_GLU_74	NE2, F_GLN_78	HE22, F_GLN_78	2.96	1.99	9.91
1HGD.PDB	OE1, B_GLU_85	OH, F_TYR_83	HH, F_TYR_83	2.53	1.75	27.84
1HGD.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.67	1.66	8.83
1HGD.PDB	OE2, F_GLU_120	NH1, F_ARG_123	HH11, F_ARG_123	2.77	1.88	23.82
1HGD.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.96	2.14	28.71
1HGD.PDB	OE2, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.94	2.05	20.84
1HGD.PDB	OH, F_TYR_157	ND2, F_ASN_129	HD22, F_ASN_129	2.80	1.85	12.13
1HGD.PDB	OE2, F_GLU_131	NH1, F_ARG_170	HH11, F_ARG_170	2.76	1.77	6.97

Table 1731: 1HGD-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1HGE.PDB	OE2, B.GLU.97	NZ, A.LYS.27	HZ1, A.LYS.27	2.80	1.78	10.14
1HGE.PDB	OD2, A.ASP.275	NZ, A.LYS.50	HZ1, A.LYS.50	2.75	1.80	21.09
1HGE.PDB	OD1, A.ASP.73	ND1, A.HIS.75	HD1, A.HIS.75	2.80	1.89	17.62
1HGE.PDB	OD1, A.ASP.60	NE, A.ARG.90	HE, A.ARG.90	2.85	1.89	7.94
1HGE.PDB	OD2, A.ASP.60	NH2, A.ARG.90	HH21, A.ARG.90	2.79	1.80	8.90
1HGE.PDB	OD2, A.ASP.271	OG, A.SER.91	HG, A.SER.91	2.81	1.90	18.10
1HGE.PDB	OD2, A.ASP.68	OG, A.SER.95	HG, A.SER.95	2.90	1.97	15.50
1HGE.PDB	OD1, A.ASP.68	OH, A.TYR.100	HH, A.TYR.100	2.91	1.93	2.88
1HGE.PDB	OD2, A.ASP.104	OG, A.SER.107	HG, A.SER.107	2.86	1.94	16.59
1HGE.PDB	OE2, B.GLU.67	NH2, A.ARG.109	HH21, A.ARG.109	2.74	1.75	12.19
1HGE.PDB	OD2, F.ASP.79	OG, A.SER.110	HG, A.SER.110	2.90	1.95	11.19
1HGE.PDB	OE2, A.GLU.119	OG1, A.THR.117	HG1, A.THR.117	2.90	1.95	8.88
1HGE.PDB	OD1, A.ASN.137	NZ, A.LYS.140	HZ2, A.LYS.140	2.81	1.83	16.67
1HGE.PDB	OD2, A.ASP.77	NE, A.ARG.141	HE, A.ARG.141	2.81	1.97	26.71
1HGE.PDB	OD1, A.ASP.77	NH2, A.ARG.141	HH21, A.ARG.141	2.89	1.98	21.76
1HGE.PDB	OD2, A.ASP.77	NH2, A.ARG.141	HH21, A.ARG.141	2.75	1.86	23.90
1HGE.PDB	OH, A.TYR.195	NE1, A.TRP.153	HE1, A.TRP.153	2.88	1.99	20.14
1HGE.PDB	OE2, A.GLU.123	NZ, A.LYS.176	HZ1, A.LYS.176	2.71	1.79	22.78
1HGE.PDB	OE1, A.GLU.123	OH, A.TYR.178	HH, A.TYR.178	2.75	1.82	10.80
1HGE.PDB	OG1, A.THR.235	NE1, A.TRP.180	HE1, A.TRP.180	2.92	1.93	3.33
1HGE.PDB	OG, A.SER.231	NE2, A.HIS.184	HE2, A.HIS.184	2.72	1.88	25.40
1HGE.PDB	OD1, A.ASN.246	NH2, A.ARG.201	HH21, A.ARG.201	2.60	1.73	24.24
1HGE.PDB	OG1, A.THR.206	OG, A.SER.209	HG, A.SER.209	2.97	2.03	10.25
1HGE.PDB	OD1, E.ASP.101	NE2, A.GLN.210	HE22, A.GLN.210	2.91	2.05	24.48
1HGE.PDB	OG1, A.THR.203	OG1, A.THR.212	HG1, A.THR.212	2.85	1.89	3.04
1HGE.PDB	OE1, C.GLN.210	NH2, A.ARG.220	HH21, A.ARG.220	2.71	1.78	19.14
1HGE.PDB	OD1, A.ASP.101	OG, A.SER.231	HG, A.SER.231	2.85	1.89	7.16
1HGE.PDB	OE1, F.GLU.72	NZ, A.LYS.238	HZ3, A.LYS.238	2.91	1.89	11.73
1HGE.PDB	OD1, A.ASN.165	ND2, A.ASN.246	HD22, A.ASN.246	2.88	1.94	13.15
1HGE.PDB	OE1, A.GLN.191	ND2, A.ASN.250	HD21, A.ASN.250	2.94	1.97	8.25
1HGE.PDB	OD1, A.ASN.133	NH2, A.ARG.255	HH22, A.ARG.255	2.48	1.67	28.93
1HGE.PDB	OE2, A.GLU.119	NH1, A.ARG.261	HH12, A.ARG.261	2.64	1.81	27.97
1HGE.PDB	OE1, A.GLU.119	NH2, A.ARG.261	HH22, A.ARG.261	2.84	1.95	24.23
1HGE.PDB	OD2, A.ASP.85	NZ, A.LYS.264	HZ3, A.LYS.264	2.77	1.79	16.96
1HGE.PDB	OE1, A.GLN.44	NZ, A.LYS.292	HZ1, A.LYS.292	2.69	1.69	12.67
1HGE.PDB	OD2, A.ASP.291	NZ, A.LYS.292	HZ3, A.LYS.292	2.82	1.86	19.03
1HGE.PDB	OE1, A.GLU.41	NZ, A.LYS.315	HZ3, A.LYS.315	2.82	1.87	21.00
1HGE.PDB	OE2, A.GLU.35	ND2, A.ASN.322	HD22, A.ASN.322	2.88	1.99	21.26
1HGE.PDB	OE1, A.GLU.325	NZ, A.LYS.326	HZ3, A.LYS.326	2.85	1.86	15.04
1HGE.PDB	OE1, B.GLN.34	NE, B.ARG.25	HE, B.ARG.25	2.59	1.77	25.60
1HGE.PDB	OG1, B.THR.32	NE2, B.GLN.27	HE22, B.GLN.27	2.99	2.08	18.28
1HGE.PDB	OD1, B.ASP.46	NE2, B.GLN.42	HE22, B.GLN.42	2.87	1.96	19.05
1HGE.PDB	OG1, B.THR.107	NZ, B.LYS.51	HZ1, B.LYS.51	2.97	1.99	17.16
1HGE.PDB	OE1, B.GLU.103	NZ, B.LYS.51	HZ2, B.LYS.51	2.76	1.73	6.92
1HGE.PDB	ND1, B.HIS.106	NZ, B.LYS.51	HZ3, B.LYS.51	2.73	1.78	18.14
1HGE.PDB	OE1, B.GLU.57	NH1, B.ARG.54	HH11, B.ARG.54	2.83	1.84	12.19
1HGE.PDB	OE2, F.GLU.97	NH2, B.ARG.54	HH22, B.ARG.54	2.84	1.86	12.76
1HGE.PDB	OD2, F.ASP.86	NZ, B.LYS.62	HZ1, B.LYS.62	2.60	1.76	28.82
1HGE.PDB	OD2, F.ASP.90	NZ, B.LYS.62	HZ3, B.LYS.62	2.69	1.82	26.81
1HGE.PDB	OG, A.SER.110	NE2, B.HIS.64	HE2, B.HIS.64	2.97	2.02	12.36
1HGE.PDB	OE2, B.GLU.85	NZ, B.LYS.68	HZ2, B.LYS.68	2.78	1.76	9.50
1HGE.PDB	OE2, D.GLU.81	NE, B.ARG.76	HE, B.ARG.76	2.87	1.91	11.56
1HGE.PDB	OE2, D.GLU.74	NH1, B.ARG.76	HH12, B.ARG.76	2.84	1.83	5.81
1HGE.PDB	OE1, D.GLU.81	NH2, B.ARG.76	HH21, B.ARG.76	2.70	1.70	6.45
1HGE.PDB	OE1, D.GLU.74	NH2, B.ARG.76	HH22, B.ARG.76	2.79	1.79	3.91
1HGE.PDB	OE1, B.GLU.74	NE2, B.GLN.78	HE22, B.GLN.78	2.97	2.00	7.88
1HGE.PDB	OE1, D.GLU.85	OH, B.TYR.83	HH, B.TYR.83	2.65	1.81	24.86

1HGE.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.75	1.71	5.62
1HGE.PDB	OE2, B_GLU_120	NH1, B_ARG_123	HH11, B_ARG_123	2.84	1.95	23.29
1HGE.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.80	1.98	27.36
1HGE.PDB	OE2, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.94	2.06	21.65
1HGE.PDB	OH, B_TYR_157	ND2, B_ASN_129	HD22, B_ASN_129	2.79	1.85	12.68
1HGE.PDB	OD2, B_ASP_145	NZ, B_LYS_143	HZ1, B_LYS_143	2.79	1.94	29.42
1HGE.PDB	OE2, B_GLU_150	ND2, B_ASN_154	HD21, B_ASN_154	2.93	2.05	22.48
1HGE.PDB	OD1, B_ASN_154	OG1, B_THR_156	HG1, B_THR_156	2.71	1.82	17.99
1HGE.PDB	OE2, B_GLU_131	NH1, B_ARG_170	HH11, B_ARG_170	2.80	1.80	6.47
1HGE.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.79	1.77	8.74
1HGE.PDB	OD2, C_ASP_275	NZ, C_LYS_50	HZ1, C_LYS_50	2.70	1.77	22.15
1HGE.PDB	OD1, C_ASP_73	ND1, C_HIS_75	HD1, C_HIS_75	2.76	1.85	18.20
1HGE.PDB	OD1, C_ASP_60	NE, C_ARG_90	HE, C_ARG_90	2.84	1.88	10.34
1HGE.PDB	OD2, C_ASP_60	NH2, C_ARG_90	HH21, C_ARG_90	2.77	1.78	9.61
1HGE.PDB	OD2, C_ASP_271	OG, C_SER_91	HG, C_SER_91	2.80	1.91	19.19
1HGE.PDB	OD2, C_ASP_68	OG, C_SER_95	HG, C_SER_95	2.88	1.95	14.90
1HGE.PDB	OD1, C_ASP_68	OH, C_TYR_100	HH, C_TYR_100	2.89	1.97	15.01
1HGE.PDB	OD2, C_ASP_104	OG, C_SER_107	HG, C_SER_107	2.88	1.96	15.70
1HGE.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.78	1.79	11.19
1HGE.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.78	1.86	15.09
1HGE.PDB	OE2, C_GLU_119	OG1, C_THR_117	HG1, C_THR_117	2.89	1.94	9.29
1HGE.PDB	OD1, C_ASN_137	NZ, C_LYS_140	HZ2, C_LYS_140	2.83	1.86	16.66
1HGE.PDB	OD2, C_ASP_77	NE, C_ARG_141	HE, C_ARG_141	2.80	1.97	26.96
1HGE.PDB	OD1, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.88	1.96	21.42
1HGE.PDB	OD2, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.74	1.86	24.30
1HGE.PDB	OH, C_TYR_195	NE1, C_TRP_153	HE1, C_TRP_153	2.85	1.98	22.78
1HGE.PDB	OE2, C_GLU_123	NZ, C_LYS_176	HZ1, C_LYS_176	2.71	1.80	23.44
1HGE.PDB	OE1, C_GLU_123	OH, C_TYR_178	HH, C_TYR_178	2.73	1.80	12.29
1HGE.PDB	OG1, C_THR_235	NE1, C_TRP_180	HE1, C_TRP_180	2.92	1.93	1.68
1HGE.PDB	OG, C_SER_231	NE2, C_HIS_184	HE2, C_HIS_184	2.71	1.87	25.48
1HGE.PDB	OD1, C_ASN_250	NE2, C_GLN_191	HE21, C_GLN_191	3.00	2.03	7.73
1HGE.PDB	OD1, C_ASN_246	NH2, C_ARG_201	HH21, C_ARG_201	2.62	1.75	24.53
1HGE.PDB	OG1, C_THR_212	OG1, C_THR_203	HG1, C_THR_203	2.89	1.94	9.07
1HGE.PDB	OG1, C_THR_206	OG, C_SER_209	HG, C_SER_209	2.98	2.03	9.68
1HGE.PDB	OD1, A_ASP_101	NE2, C_GLN_210	HE22, C_GLN_210	2.93	2.07	24.92
1HGE.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.64	1.76	23.09
1HGE.PDB	OD1, C_ASP_101	OG, C_SER_231	HG, C_SER_231	2.89	1.93	7.03
1HGE.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.78	1.80	16.75
1HGE.PDB	OD1, C_ASN_165	ND2, C_ASN_246	HD22, C_ASN_246	2.89	1.94	13.09
1HGE.PDB	OE1, C_GLN_191	ND2, C_ASN_250	HD21, C_ASN_250	2.89	1.93	9.19
1HGE.PDB	OD1, C_ASN_133	NH2, C_ARG_255	HH22, C_ARG_255	2.48	1.68	29.46
1HGE.PDB	OE2, C_GLU_119	NH1, C_ARG_261	HH12, C_ARG_261	2.65	1.82	27.69
1HGE.PDB	OE1, C_GLU_119	NH2, C_ARG_261	HH22, C_ARG_261	2.84	1.95	24.41
1HGE.PDB	OD2, C_ASP_85	NZ, C_LYS_264	HZ3, C_LYS_264	2.77	1.79	16.79
1HGE.PDB	OE1, C_GLN_44	NZ, C_LYS_292	HZ1, C_LYS_292	2.72	1.72	12.77
1HGE.PDB	OD2, C_ASP_291	NZ, C_LYS_292	HZ3, C_LYS_292	2.84	1.88	19.72
1HGE.PDB	OD1, C_ASN_285	ND2, C_ASN_298	HD22, C_ASN_298	2.99	2.05	12.60
1HGE.PDB	OE1, C_GLU_41	NZ, C_LYS_315	HZ3, C_LYS_315	2.82	1.88	21.70
1HGE.PDB	OE2, C_GLU_35	ND2, C_ASN_322	HD22, C_ASN_322	2.89	2.00	20.86
1HGE.PDB	OE1, D_GLU_15	NZ, C_LYS_326	HZ1, C_LYS_326	2.74	1.73	12.73
1HGE.PDB	OXT, C_THR_328	NE2, C_GLN_327	HE22, C_GLN_327	2.97	2.01	12.27
1HGE.PDB	OE1, D_GLN_34	NE, D_ARG_25	HE, D_ARG_25	2.56	1.76	28.50
1HGE.PDB	OD2, D_ASP_37	OG, D_SER_40	HG, D_SER_40	2.78	1.93	24.10
1HGE.PDB	OD1, D_ASP_46	NE2, D_GLN_42	HE22, D_GLN_42	2.87	1.96	19.33
1HGE.PDB	OE2, D_GLU_114	NE2, D_GLN_47	HE21, D_GLN_47	2.99	2.06	16.53
1HGE.PDB	OG1, D_THR_107	NZ, D_LYS_51	HZ1, D_LYS_51	2.96	1.98	16.83
1HGE.PDB	OE1, D_GLU_103	NZ, D_LYS_51	HZ2, D_LYS_51	2.76	1.73	6.47
1HGE.PDB	ND1, D_HIS_106	NZ, D_LYS_51	HZ3, D_LYS_51	2.77	1.82	18.39

1HGE.PDB	OE1, D_GLU_57	NH1, D_ARG_54	HH11, D_ARG_54	2.82	1.84	12.42
1HGE.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.87	1.89	12.82
1HGE.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.96	1.98	6.23
1HGE.PDB	OE2, D_GLU_85	NZ, D_LYS_68	HZ2, D_LYS_68	2.80	1.78	10.75
1HGE.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.79	1.85	14.06
1HGE.PDB	OE2, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.78	1.78	7.91
1HGE.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.63	1.67	11.36
1HGE.PDB	OE1, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.74	1.75	7.04
1HGE.PDB	OE1, D_GLU_74	NE2, D_GLN_78	HE22, D_GLN_78	2.96	1.99	8.03
1HGE.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.58	1.80	29.40
1HGE.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.71	1.68	6.52
1HGE.PDB	OE2, D_GLU_120	NH1, D_ARG_123	HH11, D_ARG_123	2.83	1.93	23.01
1HGE.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.78	1.98	28.90
1HGE.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.90	2.01	20.41
1HGE.PDB	OH, D_TYR_157	ND2, D_ASN_129	HD22, D_ASN_129	2.81	1.85	9.24
1HGE.PDB	OD1, D_ASN_154	OG1, D_THR_156	HG1, D_THR_156	2.74	1.81	12.51
1HGE.PDB	NE2, D_HIS_142	OH, D_TYR_157	HH, D_TYR_157	2.73	1.86	21.01
1HGE.PDB	OE2, D_GLU_131	NH1, D_ARG_170	HH11, D_ARG_170	2.79	1.79	6.83
1HGE.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.79	1.77	9.75
1HGE.PDB	OD2, E_ASP_275	NZ, E_LYS_50	HZ1, E_LYS_50	2.73	1.80	21.86
1HGE.PDB	OD1, E_ASP_73	ND1, E_HIS_75	HD1, E_HIS_75	2.77	1.85	16.90
1HGE.PDB	OD1, E_ASP_60	NE, E_ARG_90	HE, E_ARG_90	2.88	1.91	8.59
1HGE.PDB	OD2, E_ASP_60	NH2, E_ARG_90	HH21, E_ARG_90	2.80	1.80	8.94
1HGE.PDB	OD2, E_ASP_271	OG, E_SER_91	HG, E_SER_91	2.83	1.92	17.26
1HGE.PDB	OD2, E_ASP_68	OG, E_SER_95	HG, E_SER_95	2.91	1.97	13.28
1HGE.PDB	OD1, E_ASP_68	OH, E_TYR_100	HH, E_TYR_100	2.88	1.95	14.25
1HGE.PDB	OD2, E_ASP_104	OG, E_SER_107	HG, E_SER_107	2.86	1.93	15.15
1HGE.PDB	OE2, F_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.78	1.79	11.63
1HGE.PDB	OD2, D_ASP_79	OG, E_SER_110	HG, E_SER_110	2.82	1.89	14.19
1HGE.PDB	OE2, E_GLU_119	OG1, E_THR_117	HG1, E_THR_117	2.93	1.97	8.29
1HGE.PDB	OD1, E_ASN_137	NZ, E_LYS_140	HZ2, E_LYS_140	2.84	1.86	16.83
1HGE.PDB	OD2, E_ASP_77	NE, E_ARG_141	HE, E_ARG_141	2.80	1.96	26.48
1HGE.PDB	OD1, E_ASP_77	NH2, E_ARG_141	HH21, E_ARG_141	2.91	2.00	21.55
1HGE.PDB	OD2, E_ASP_77	NH2, E_ARG_141	HH21, E_ARG_141	2.75	1.87	24.36
1HGE.PDB	OD1, E_ASP_77	OG, E_SER_149	HG, E_SER_149	2.99	2.14	24.93
1HGE.PDB	OH, E_TYR_195	NE1, E_TRP_153	HE1, E_TRP_153	2.90	1.99	18.82
1HGE.PDB	OE2, E_GLU_123	NZ, E_LYS_176	HZ1, E_LYS_176	2.73	1.81	23.24
1HGE.PDB	OE1, E_GLU_123	OH, E_TYR_178	HH, E_TYR_178	2.75	1.82	12.06
1HGE.PDB	OG1, E_THR_235	NE1, E_TRP_180	HE1, E_TRP_180	2.93	1.94	2.48
1HGE.PDB	OG, E_SER_231	NE2, E_HIS_184	HE2, E_HIS_184	2.75	1.91	25.72
1HGE.PDB	OD1, E_ASN_246	NH2, E_ARG_201	HH21, E_ARG_201	2.61	1.75	25.36
1HGE.PDB	OG1, E_THR_212	OG1, E_THR_203	HG1, E_THR_203	2.89	1.95	10.14
1HGE.PDB	OG1, E_THR_206	OG, E_SER_209	HG, E_SER_209	2.98	2.04	10.06
1HGE.PDB	OD1, C_ASP_101	NE2, E_GLN_210	HE22, E_GLN_210	2.89	2.04	25.02
1HGE.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.74	1.87	25.04
1HGE.PDB	OD1, E_ASP_101	OG, E_SER_231	HG, E_SER_231	2.87	1.92	12.10
1HGE.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ3, E_LYS_238	2.85	1.84	12.25
1HGE.PDB	OD1, E_ASN_165	ND2, E_ASN_246	HD22, E_ASN_246	2.88	1.93	12.25
1HGE.PDB	OE1, E_GLN_191	ND2, E_ASN_250	HD21, E_ASN_250	2.94	1.97	8.28
1HGE.PDB	OD1, E_ASN_133	NH2, E_ARG_255	HH22, E_ARG_255	2.49	1.68	28.65
1HGE.PDB	OE2, E_GLU_119	NH1, E_ARG_261	HH12, E_ARG_261	2.65	1.81	27.82
1HGE.PDB	OE1, E_GLU_119	NH2, E_ARG_261	HH22, E_ARG_261	2.83	1.95	24.52
1HGE.PDB	OD2, E_ASP_85	NZ, E_LYS_264	HZ3, E_LYS_264	2.81	1.83	16.30
1HGE.PDB	OE1, E_GLN_44	NZ, E_LYS_292	HZ1, E_LYS_292	2.72	1.72	11.93
1HGE.PDB	OD2, E_ASP_291	NZ, E_LYS_292	HZ3, E_LYS_292	2.84	1.89	19.87
1HGE.PDB	OD1, E_ASN_285	ND2, E_ASN_298	HD22, E_ASN_298	2.98	2.04	13.10
1HGE.PDB	OD1, F_ASP_86	NZ, E_LYS_310	HZ3, E_LYS_310	2.86	2.02	29.64
1HGE.PDB	OE1, E_GLU_41	NZ, E_LYS_315	HZ3, E_LYS_315	2.80	1.87	22.54

1HGE.PDB	OE2, E_GLU_35	ND2, E_ASN_322	HD22, E_ASN_322	2.87	1.98	21.90
1HGE.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.99	2.00	17.08
1HGE.PDB	OE1, F_GLN_34	NE, F_ARG_25	HE, F_ARG_25	2.92	2.07	24.83
1HGE.PDB	OE1, F_GLN_34	NH2, F_ARG_25	HH21, F_ARG_25	2.81	1.90	20.25
1HGE.PDB	OD1, F_ASN_146	ND2, F_ASN_28	HD21, F_ASN_28	2.81	1.89	15.75
1HGE.PDB	OD2, F_ASP_37	OG, F_SER_40	HG, F_SER_40	2.76	1.94	26.96
1HGE.PDB	OD1, F_ASP_46	NE2, F_GLN_42	HE22, F_GLN_42	2.86	1.96	19.38
1HGE.PDB	OE2, F_GLU_114	NE2, F_GLN_47	HE21, F_GLN_47	3.00	2.09	17.78
1HGE.PDB	OG1, F_THR_107	NZ, F_LYS_51	HZ1, F_LYS_51	2.97	2.00	18.12
1HGE.PDB	OE1, F_GLU_103	NZ, F_LYS_51	HZ2, F_LYS_51	2.77	1.74	6.40
1HGE.PDB	ND1, F_HIS_106	NZ, F_LYS_51	HZ3, F_LYS_51	2.74	1.79	17.89
1HGE.PDB	OE1, F_GLU_57	NH1, F_ARG_54	HH11, F_ARG_54	2.82	1.83	11.59
1HGE.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.80	1.82	12.52
1HGE.PDB	OD2, D_ASP_90	NZ, F_LYS_62	HZ2, F_LYS_62	2.67	1.83	29.15
1HGE.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.94	1.97	9.11
1HGE.PDB	OE2, F_GLU_85	NZ, F_LYS_68	HZ2, F_LYS_68	2.75	1.78	18.51
1HGE.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.85	1.89	11.64
1HGE.PDB	OE2, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.73	1.73	6.19
1HGE.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.65	1.66	5.51
1HGE.PDB	OE1, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.70	1.73	9.07
1HGE.PDB	OE1, F_GLU_74	NE2, F_GLN_78	HE22, F_GLN_78	2.96	1.99	8.87
1HGE.PDB	OE1, B_GLU_85	OH, F_TYR_83	HH, F_TYR_83	2.51	1.76	30.00
1HGE.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.67	1.65	8.34
1HGE.PDB	OE2, F_GLU_120	NH1, F_ARG_123	HH11, F_ARG_123	2.81	1.92	23.28
1HGE.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.92	2.09	27.36
1HGE.PDB	OH, F_TYR_157	ND2, F_ASN_129	HD22, F_ASN_129	2.80	1.87	15.30
1HGE.PDB	OE2, F_GLU_131	NH1, F_ARG_170	HH11, F_ARG_170	2.78	1.79	6.04

Table 1732: 1HGE-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1HGF.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.79	1.86	21.55
1HGF.PDB	OD2, A_ASP_275	NZ, A_LYS_50	HZ2, A_LYS_50	2.91	1.91	15.13
1HGF.PDB	OD1, A_ASP_73	ND1, A_HIS_75	HD1, A_HIS_75	2.84	1.91	15.59
1HGF.PDB	OD1, A_ASP_60	NE, A_ARG_90	HE, A_ARG_90	2.77	1.85	16.11
1HGF.PDB	OD2, A_ASP_60	NH2, A_ARG_90	HH21, A_ARG_90	2.84	1.84	8.73
1HGF.PDB	OD2, A_ASP_271	OG, A_SER_91	HG, A_SER_91	2.85	1.91	12.59
1HGF.PDB	OD2, A_ASP_104	OG, A_SER_107	HG, A_SER_107	2.89	1.97	16.55
1HGF.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.92	1.92	10.51
1HGF.PDB	OD2, F_ASP_79	OG, A_SER_110	HG, A_SER_110	2.82	1.90	15.87
1HGF.PDB	OE2, A_GLU_119	OG1, A_THR_117	HG1, A_THR_117	2.95	1.98	3.95
1HGF.PDB	ND2, A_ASN_152	NE2, A_GLN_132	HE21, A_GLN_132	2.94	2.00	10.26
1HGF.PDB	OD2, A_ASP_77	NE, A_ARG_141	HE, A_ARG_141	2.91	2.06	25.46
1HGF.PDB	OD1, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.84	1.97	26.05
1HGF.PDB	OD2, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.78	1.86	20.91
1HGF.PDB	OH, A_TYR_195	NE1, A_TRP_153	HE1, A_TRP_153	2.84	1.90	13.02
1HGF.PDB	OE2, A_GLU_123	NZ, A_LYS_176	HZ1, A_LYS_176	2.72	1.80	23.85
1HGF.PDB	OG1, A_THR_235	NE1, A_TRP_180	HE1, A_TRP_180	2.87	1.89	5.46
1HGF.PDB	OH, A_TYR_98	NE2, A_HIS_183	HE2, A_HIS_183	2.90	1.98	15.32
1HGF.PDB	OG, A_SER_231	NE2, A_HIS_184	HE2, A_HIS_184	2.68	1.88	29.05
1HGF.PDB	OD1, A_ASN_250	NE2, A_GLN_191	HE22, A_GLN_191	2.90	1.94	8.27
1HGF.PDB	OG1, A_THR_203	OG1, A_THR_212	HG1, A_THR_212	2.83	1.91	15.11
1HGF.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.64	1.76	23.62
1HGF.PDB	OD1, A_ASP_101	OG, A_SER_231	HG, A_SER_231	2.83	1.87	7.29
1HGF.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ2, A_LYS_238	2.85	1.85	14.58
1HGF.PDB	OD1, A_ASN_165	ND2, A_ASN_246	HD21, A_ASN_246	2.93	2.03	19.92
1HGF.PDB	OE1, A_GLN_191	ND2, A_ASN_250	HD22, A_ASN_250	2.86	1.90	9.57
1HGF.PDB	OD1, A_ASN_133	NH2, A_ARG_255	HH22, A_ARG_255	2.49	1.67	28.52
1HGF.PDB	OE1, A_GLU_119	NH2, A_ARG_261	HH22, A_ARG_261	2.74	1.90	27.76
1HGF.PDB	OE1, A_GLN_44	NZ, A_LYS_292	HZ1, A_LYS_292	2.87	1.83	0.68
1HGF.PDB	OD1, A_ASP_291	NZ, A_LYS_292	HZ2, A_LYS_292	2.86	1.83	8.47
1HGF.PDB	OE1, A_GLU_41	OG1, A_THR_313	HG1, A_THR_313	2.68	1.87	27.57
1HGF.PDB	OG1, A_THR_313	NZ, A_LYS_315	HZ2, A_LYS_315	2.95	2.00	20.61
1HGF.PDB	OE2, A_GLU_35	ND2, A_ASN_322	HD21, A_ASN_322	2.76	1.93	26.44
1HGF.PDB	OE1, B_GLN_34	NE, B_ARG_25	HE, B_ARG_25	2.64	1.77	20.89
1HGF.PDB	OE1, B_GLN_34	NH2, B_ARG_25	HH21, B_ARG_25	2.81	1.99	28.67
1HGF.PDB	OE2, A_GLU_325	NH2, B_ARG_25	HH22, B_ARG_25	2.99	2.04	16.52
1HGF.PDB	OD1, B_ASP_46	NE2, B_GLN_42	HE21, B_GLN_42	2.87	1.99	22.40
1HGF.PDB	OE1, B_GLU_103	NZ, B_LYS_51	HZ1, B_LYS_51	2.74	1.70	5.26
1HGF.PDB	ND1, B_HIS_106	NZ, B_LYS_51	HZ3, B_LYS_51	2.67	1.72	18.38
1HGF.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.83	1.86	13.50
1HGF.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ2, B_LYS_62	2.71	1.70	11.44
1HGF.PDB	OD2, F_ASP_90	NZ, B_LYS_62	HZ3, B_LYS_62	2.77	1.82	20.37
1HGF.PDB	OG, A_SER_266	ND1, B_HIS_64	HD1, B_HIS_64	2.66	1.79	20.68
1HGF.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.89	1.92	10.70
1HGF.PDB	OE2, B_GLU_85	NZ, B_LYS_68	HZ1, B_LYS_68	2.67	1.75	22.44
1HGF.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.92	1.92	2.47
1HGF.PDB	OE1, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.86	1.84	3.80
1HGF.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.73	1.74	10.29
1HGF.PDB	OE2, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.75	1.74	3.91
1HGF.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.57	1.80	29.66
1HGF.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.72	1.70	9.91
1HGF.PDB	OE2, B_GLU_120	NH1, B_ARG_123	HH11, B_ARG_123	2.78	1.93	26.74
1HGF.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.80	1.86	13.00
1HGF.PDB	OH, B_TYR_157	ND2, B_ASN_129	HD21, B_ASN_129	2.81	1.86	11.58
1HGF.PDB	OD1, B_ASN_154	OG1, B_THR_156	HG1, B_THR_156	2.68	1.80	19.09
1HGF.PDB	OE1, F_GLU_131	NH2, B_ARG_163	HH21, B_ARG_163	2.74	1.86	24.20
1HGF.PDB	OE2, B_GLU_131	NH1, B_ARG_170	HH11, B_ARG_170	2.84	1.84	5.96

1HGF.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.81	1.85	19.93
1HGF.PDB	OD2, C_ASP_275	NZ, C_LYS_50	HZ2, C_LYS_50	2.88	1.87	13.71
1HGF.PDB	OD1, C_ASP_73	ND1, C_HIS_75	HD1, C_HIS_75	2.84	1.90	12.73
1HGF.PDB	OD1, C_ASP_60	NE, C_ARG_90	HE, C_ARG_90	2.76	1.85	16.46
1HGF.PDB	OD2, C_ASP_60	NH2, C_ARG_90	HH21, C_ARG_90	2.84	1.85	9.99
1HGF.PDB	OD1, C_ASP_271	OG, C_SER_91	HG, C_SER_91	2.91	2.11	29.01
1HGF.PDB	OD2, C_ASP_271	OG, C_SER_91	HG, C_SER_91	2.86	1.95	16.65
1HGF.PDB	OD1, C_ASP_68	OH, C_TYR_100	HH, C_TYR_100	2.97	2.03	12.15
1HGF.PDB	OD2, C_ASP_104	OG, C_SER_107	HG, C_SER_107	2.91	1.98	14.76
1HGF.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.91	1.92	11.49
1HGF.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.69	1.85	25.37
1HGF.PDB	OE2, C_GLU_119	OG1, C_THR_117	HG1, C_THR_117	2.97	2.00	2.16
1HGF.PDB	ND2, C_ASN_152	NE2, C_GLN_132	HE21, C_GLN_132	2.94	2.00	12.42
1HGF.PDB	OD2, C_ASP_77	NE, C_ARG_141	HE, C_ARG_141	2.91	2.05	25.56
1HGF.PDB	OD1, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.84	1.98	26.48
1HGF.PDB	OD2, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.79	1.86	20.63
1HGF.PDB	OH, C_TYR_195	NE1, C_TRP_153	HE1, C_TRP_153	2.82	1.92	18.47
1HGF.PDB	OE2, C_GLU_123	NZ, C_LYS_176	HZ1, C_LYS_176	2.72	1.80	22.47
1HGF.PDB	OG1, C_THR_235	NE1, C_TRP_180	HE1, C_TRP_180	2.86	1.88	3.91
1HGF.PDB	OH, C_TYR_98	NE2, C_HIS_183	HE2, C_HIS_183	2.89	1.99	18.89
1HGF.PDB	OG, C_SER_231	NE2, C_HIS_184	HE2, C_HIS_184	2.67	1.86	27.83
1HGF.PDB	OD1, C_ASN_250	NE2, C_GLN_191	HE22, C_GLN_191	2.91	1.94	7.66
1HGF.PDB	OG1, C_THR_212	OG1, C_THR_203	HG1, C_THR_203	2.82	1.90	14.76
1HGF.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.56	1.72	26.72
1HGF.PDB	OD1, C_ASP_101	OG, C_SER_231	HG, C_SER_231	2.86	1.89	4.34
1HGF.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ2, C_LYS_238	2.75	1.78	18.48
1HGF.PDB	OD1, C_ASN_165	ND2, C_ASN_246	HD21, C_ASN_246	2.93	2.04	21.38
1HGF.PDB	OE1, C_GLN_191	ND2, C_ASN_250	HD22, C_ASN_250	2.84	1.89	10.62
1HGF.PDB	OD1, C_ASN_133	NH2, C_ARG_255	HH22, C_ARG_255	2.47	1.67	28.90
1HGF.PDB	OE1, C_GLU_119	NH2, C_ARG_261	HH22, C_ARG_261	2.72	1.88	28.14
1HGF.PDB	OE1, C_GLN_44	NZ, C_LYS_292	HZ1, C_LYS_292	2.89	1.84	2.00
1HGF.PDB	OD1, C_ASP_291	NZ, C_LYS_292	HZ2, C_LYS_292	2.88	1.85	8.89
1HGF.PDB	OE1, C_GLU_41	OG1, C_THR_313	HG1, C_THR_313	2.66	1.87	29.10
1HGF.PDB	OG1, C_THR_313	NZ, C_LYS_315	HZ2, C_LYS_315	2.92	1.98	21.54
1HGF.PDB	OE2, C_GLU_35	ND2, C_ASN_322	HD21, C_ASN_322	2.77	1.93	25.57
1HGF.PDB	OXT, C_THR_328	NE2, C_GLN_327	HE21, C_GLN_327	2.93	2.09	26.28
1HGF.PDB	OE1, D_GLN_34	NE, D_ARG_25	HE, D_ARG_25	2.69	1.78	17.17
1HGF.PDB	OD1, D_ASN_146	ND2, D_ASN_28	HD22, D_ASN_28	2.89	1.97	17.31
1HGF.PDB	OD2, D_ASP_37	OG, D_SER_40	HG, D_SER_40	2.85	1.95	18.29
1HGF.PDB	OD1, D_ASP_46	NE2, D_GLN_42	HE21, D_GLN_42	2.85	1.97	22.40
1HGF.PDB	OE1, D_GLU_103	NZ, D_LYS_51	HZ1, D_LYS_51	2.74	1.71	5.53
1HGF.PDB	ND1, D_HIS_106	NZ, D_LYS_51	HZ3, D_LYS_51	2.69	1.73	17.89
1HGF.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.84	1.86	12.74
1HGF.PDB	OD2, B_ASP_86	NZ, D_LYS_62	HZ2, D_LYS_62	2.69	1.69	13.49
1HGF.PDB	OD2, B_ASP_90	NZ, D_LYS_62	HZ3, D_LYS_62	2.68	1.77	22.81
1HGF.PDB	OG, C_SER_266	ND1, D_HIS_64	HD1, D_HIS_64	2.64	1.83	27.58
1HGF.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.90	1.92	7.33
1HGF.PDB	OE2, D_GLU_85	NZ, D_LYS_68	HZ1, D_LYS_68	2.73	1.78	19.48
1HGF.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.82	1.85	5.34
1HGF.PDB	OE1, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.79	1.78	3.81
1HGF.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.64	1.68	12.43
1HGF.PDB	OE2, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.70	1.71	7.38
1HGF.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.58	1.80	29.87
1HGF.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.68	1.69	13.85
1HGF.PDB	OE2, D_GLU_120	NH1, D_ARG_123	HH11, D_ARG_123	2.79	1.92	25.71
1HGF.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.79	1.88	16.40
1HGF.PDB	OH, D_TYR_157	ND2, D_ASN_129	HD21, D_ASN_129	2.81	1.84	5.39
1HGF.PDB	OG, D_SER_29	NZ, D_LYS_143	HZ1, D_LYS_143	2.83	1.89	20.16

1HGF.PDB	OD1, D_ASN.154	OG1, D_THR.156	HG1, D_THR.156	2.72	1.80	12.72
1HGF.PDB	NE2, D_HIS.142	OH, D_TYR.157	HH, D_TYR.157	2.72	1.85	19.75
1HGF.PDB	OE1, B_GLU.131	NH2, D_ARG.163	HH21, D_ARG.163	2.70	1.83	24.43
1HGF.PDB	OE2, D_GLU.131	NH1, D_ARG.170	HH11, D_ARG.170	2.84	1.84	5.29
1HGF.PDB	OE2, F_GLU.97	NZ, E_LYS.27	HZ1, E_LYS.27	2.75	1.83	22.30
1HGF.PDB	OD2, E_ASP.275	NZ, E_LYS.50	HZ2, E_LYS.50	2.90	1.90	14.56
1HGF.PDB	OD1, E_ASP.73	ND1, E_HIS.75	HD1, E_HIS.75	2.85	1.91	12.17
1HGF.PDB	OD1, E_ASP.60	NE, E_ARG.90	HE, E_ARG.90	2.80	1.85	10.51
1HGF.PDB	OD2, E_ASP.60	NH2, E_ARG.90	HH21, E_ARG.90	2.88	1.89	10.22
1HGF.PDB	OD2, E_ASP.104	OG, E_SER.107	HG, E_SER.107	2.88	1.94	12.45
1HGF.PDB	OE2, F_GLU.67	NH2, E_ARG.109	HH21, E_ARG.109	2.88	1.88	11.28
1HGF.PDB	OD2, D_ASP.79	OG, E_SER.110	HG, E_SER.110	2.78	1.90	21.69
1HGF.PDB	OE2, E_GLU.119	OG1, E_THR.117	HG1, E_THR.117	2.96	1.99	6.08
1HGF.PDB	ND2, E_ASN.152	NE2, E_GLN.132	HE21, E_GLN.132	2.95	2.01	11.55
1HGF.PDB	OD2, E_ASP.77	NE, E_ARG.141	HE, E_ARG.141	2.92	2.06	25.46
1HGF.PDB	OD1, E_ASP.77	NH2, E_ARG.141	HH21, E_ARG.141	2.83	1.96	25.41
1HGF.PDB	OD2, E_ASP.77	NH2, E_ARG.141	HH21, E_ARG.141	2.77	1.86	21.24
1HGF.PDB	OH, E_TYR.195	NE1, E_TRP.153	HE1, E_TRP.153	2.83	1.89	12.15
1HGF.PDB	OE2, E_GLU.123	NZ, E_LYS.176	HZ1, E_LYS.176	2.76	1.80	18.44
1HGF.PDB	OE1, E_GLU.123	OH, E_TYR.178	HH, E_TYR.178	2.88	1.93	11.71
1HGF.PDB	OG1, E_THR.235	NE1, E_TRP.180	HE1, E_TRP.180	2.85	1.87	2.94
1HGF.PDB	OH, E_TYR.98	NE2, E_HIS.183	HE2, E_HIS.183	2.91	1.99	15.99
1HGF.PDB	OG, E_SER.231	NE2, E_HIS.184	HE2, E_HIS.184	2.70	1.89	28.56
1HGF.PDB	OD1, E_ASN.250	NE2, E_GLN.191	HE22, E_GLN.191	2.96	1.99	7.90
1HGF.PDB	OG1, E_THR.212	OG1, E_THR.203	HG1, E_THR.203	2.89	1.95	9.70
1HGF.PDB	OE1, A_GLN.210	NH2, E_ARG.220	HH21, E_ARG.220	2.65	1.79	25.97
1HGF.PDB	OD1, E_ASP.101	OG, E_SER.231	HG, E_SER.231	2.82	1.90	15.36
1HGF.PDB	OE1, D_GLU.72	NZ, E_LYS.238	HZ2, E_LYS.238	2.83	1.84	16.42
1HGF.PDB	OD1, E_ASN.165	ND2, E_ASN.246	HD21, E_ASN.246	2.93	2.02	19.67
1HGF.PDB	OE1, E_GLN.191	ND2, E_ASN.250	HD22, E_ASN.250	2.87	1.91	8.14
1HGF.PDB	OD1, E_ASN.133	NH2, E_ARG.255	HH22, E_ARG.255	2.47	1.67	29.09
1HGF.PDB	OE1, E_GLU.119	NH2, E_ARG.261	HH22, E_ARG.261	2.73	1.89	28.16
1HGF.PDB	OE1, E_GLN.44	NZ, E_LYS.292	HZ1, E_LYS.292	2.90	1.86	1.40
1HGF.PDB	OD1, E_ASP.291	NZ, E_LYS.292	HZ2, E_LYS.292	2.87	1.84	9.03
1HGF.PDB	OE1, E_GLU.41	OG1, E_THR.313	HG1, E_THR.313	2.68	1.89	29.15
1HGF.PDB	OG1, E_THR.313	NZ, E_LYS.315	HZ2, E_LYS.315	2.94	2.00	21.30
1HGF.PDB	OE2, E_GLU.35	ND2, E_ASN.322	HD21, E_ASN.322	2.77	1.93	26.11
1HGF.PDB	OE1, F_GLN.34	NE, F_ARG.25	HE, F_ARG.25	2.89	2.02	23.18
1HGF.PDB	OE1, F_GLN.34	NH2, F_ARG.25	HH21, F_ARG.25	2.91	2.03	24.46
1HGF.PDB	OD1, F_ASN.146	ND2, F_ASN.28	HD22, F_ASN.28	2.88	2.02	23.75
1HGF.PDB	OD1, F_ASP.46	NE2, F_GLN.42	HE21, F_GLN.42	2.86	1.99	23.71
1HGF.PDB	OE1, F_GLU.103	NZ, F_LYS.51	HZ1, F_LYS.51	2.72	1.69	6.79
1HGF.PDB	ND1, F_HIS.106	NZ, F_LYS.51	HZ3, F_LYS.51	2.66	1.70	17.89
1HGF.PDB	OE2, D_GLU.97	NH2, F_ARG.54	HH22, F_ARG.54	2.79	1.81	11.74
1HGF.PDB	OD2, D_ASP.86	NZ, F_LYS.62	HZ2, F_LYS.62	2.67	1.68	13.64
1HGF.PDB	OD2, D_ASP.90	NZ, F_LYS.62	HZ3, F_LYS.62	2.75	1.81	20.23
1HGF.PDB	OG, E_SER.266	ND1, F_HIS.64	HD1, F_HIS.64	2.65	1.77	20.25
1HGF.PDB	OG, E_SER.110	NE2, F_HIS.64	HE2, F_HIS.64	2.89	1.92	9.46
1HGF.PDB	OE2, F_GLU.85	NZ, F_LYS.68	HZ1, F_LYS.68	2.64	1.77	26.62
1HGF.PDB	OE2, B_GLU.81	NE, F_ARG.76	HE, F_ARG.76	2.86	1.88	5.84
1HGF.PDB	OE1, B_GLU.74	NH1, F_ARG.76	HH12, F_ARG.76	2.78	1.77	1.59
1HGF.PDB	OE1, B_GLU.81	NH2, F_ARG.76	HH21, F_ARG.76	2.69	1.70	7.61
1HGF.PDB	OE2, B_GLU.74	NH2, F_ARG.76	HH22, F_ARG.76	2.71	1.73	8.88
1HGF.PDB	OH, D_TYR.83	NZ, F_LYS.88	HZ1, F_LYS.88	2.55	1.63	21.75
1HGF.PDB	OE2, F_GLU.120	NH1, F_ARG.123	HH11, F_ARG.123	2.79	1.92	25.30
1HGF.PDB	OE1, D_GLU.132	NE, F_ARG.124	HE, F_ARG.124	2.90	1.96	15.73
1HGF.PDB	OH, F_TYR.157	ND2, F_ASN.129	HD21, F_ASN.129	2.83	1.89	13.44
1HGF.PDB	OE1, D_GLU.131	NH2, F_ARG.163	HH21, F_ARG.163	2.69	1.84	27.00

1HGF.PDB	OE2, F_GLU_131	NH1, F_ARG_170	HH11, F_ARG_170	2.85	1.84	3.96
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Table 1733: 1HGF-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1HGG.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.90	1.87	9.15
1HGG.PDB	OD2, A_ASP_275	NZ, A_LYS_50	HZ1, A_LYS_50	2.71	1.78	22.40
1HGG.PDB	OD1, A_ASP_73	ND1, A_HIS_75	HD1, A_HIS_75	2.77	1.87	17.99
1HGG.PDB	OD1, A_ASP_60	NE, A_ARG_90	HE, A_ARG_90	2.94	1.96	6.92
1HGG.PDB	OD2, A_ASP_60	NH2, A_ARG_90	HH21, A_ARG_90	2.79	1.81	10.63
1HGG.PDB	OD1, A_ASP_271	OG, A_SER_91	HG, A_SER_91	2.86	2.03	25.78
1HGG.PDB	OD2, A_ASP_271	OG, A_SER_91	HG, A_SER_91	2.85	1.97	21.46
1HGG.PDB	OD2, A_ASP_68	OG, A_SER_95	HG, A_SER_95	2.94	1.99	11.26
1HGG.PDB	OD1, A_ASP_68	OH, A_TYR_100	HH, A_TYR_100	2.94	1.99	11.28
1HGG.PDB	OD2, A_ASP_104	OG, A_SER_107	HG, A_SER_107	2.84	1.92	16.45
1HGG.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.84	1.86	14.43
1HGG.PDB	OD2, F_ASP_79	OG, A_SER_110	HG, A_SER_110	2.88	1.95	14.29
1HGG.PDB	OE2, A_GLU_119	OG1, A_THR_117	HG1, A_THR_117	2.88	1.93	9.58
1HGG.PDB	OD1, A_ASN_137	NZ, A_LYS_140	HZ2, A_LYS_140	2.76	1.76	13.87
1HGG.PDB	OD2, A_ASP_77	NE, A_ARG_141	HE, A_ARG_141	2.89	2.07	28.91
1HGG.PDB	OD1, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.76	1.85	22.03
1HGG.PDB	OD2, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.76	1.87	24.00
1HGG.PDB	OH, A_TYR_195	NE1, A_TRP_153	HE1, A_TRP_153	2.91	1.96	13.96
1HGG.PDB	OE2, A_GLU_123	NZ, A_LYS_176	HZ1, A_LYS_176	2.65	1.77	25.92
1HGG.PDB	OE1, A_GLU_123	OH, A_TYR_178	HH, A_TYR_178	2.78	1.83	8.16
1HGG.PDB	OG1, A_THR_235	NE1, A_TRP_180	HE1, A_TRP_180	2.92	1.93	2.35
1HGG.PDB	OG, A_SER_231	NE2, A_HIS_184	HE2, A_HIS_184	2.80	1.92	21.87
1HGG.PDB	OD1, A_ASN_246	NH2, A_ARG_201	HH21, A_ARG_201	2.65	1.72	18.81
1HGG.PDB	OD2, A_ASP_241	NE, A_ARG_208	HE, A_ARG_208	2.96	2.06	20.34
1HGG.PDB	OG1, A_THR_206	OG, A_SER_209	HG, A_SER_209	2.95	2.03	14.98
1HGG.PDB	OD1, E_ASP_101	NE2, A_GLN_210	HE22, A_GLN_210	2.99	2.07	17.95
1HGG.PDB	OG1, A_THR_203	OG1, A_THR_212	HG1, A_THR_212	2.88	1.92	6.20
1HGG.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.73	1.78	15.93
1HGG.PDB	OD1, A_ASP_101	OG, A_SER_231	HG, A_SER_231	2.88	1.92	8.82
1HGG.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.93	1.93	14.31
1HGG.PDB	OE2, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.74	1.91	29.92
1HGG.PDB	OD1, A_ASN_165	ND2, A_ASN_246	HD22, A_ASN_246	2.90	1.98	17.02
1HGG.PDB	OE1, A_GLN_191	ND2, A_ASN_250	HD21, A_ASN_250	2.92	1.96	11.11
1HGG.PDB	OD1, A_ASN_133	NH2, A_ARG_255	HH22, A_ARG_255	2.52	1.66	24.50
1HGG.PDB	OE2, A_GLU_119	NH1, A_ARG_261	HH12, A_ARG_261	2.68	1.87	29.79
1HGG.PDB	OE1, A_GLU_119	NH2, A_ARG_261	HH22, A_ARG_261	2.74	1.88	26.75
1HGG.PDB	OH, A_TYR_302	NZ, A_LYS_264	HZ1, A_LYS_264	2.93	1.98	19.58
1HGG.PDB	ND1, A_HIS_56	NZ, A_LYS_264	HZ2, A_LYS_264	2.66	1.73	19.87
1HGG.PDB	OD2, A_ASP_85	NZ, A_LYS_264	HZ3, A_LYS_264	2.83	1.83	12.74
1HGG.PDB	OE1, B_GLU_67	NH1, A_ARG_269	HH12, A_ARG_269	2.69	1.86	28.34
1HGG.PDB	OE1, A_GLN_44	NZ, A_LYS_292	HZ1, A_LYS_292	2.74	1.73	11.51
1HGG.PDB	OD2, A_ASP_291	NZ, A_LYS_292	HZ3, A_LYS_292	2.77	1.90	27.56
1HGG.PDB	OD1, A_ASN_285	ND2, A_ASN_298	HD22, A_ASN_298	2.97	2.01	11.28
1HGG.PDB	OD1, B_ASP_90	NZ, A_LYS_310	HZ2, A_LYS_310	2.70	1.74	18.08
1HGG.PDB	OE1, A_GLU_41	NZ, A_LYS_315	HZ3, A_LYS_315	2.73	1.81	23.14
1HGG.PDB	OE2, A_GLU_35	ND2, A_ASN_322	HD22, A_ASN_322	2.81	1.95	25.01
1HGG.PDB	OE2, B_GLU_15	NZ, A_LYS_326	HZ1, A_LYS_326	2.83	1.89	21.04
1HGG.PDB	OE1, A_GLU_325	NZ, A_LYS_326	HZ3, A_LYS_326	2.82	1.86	18.51
1HGG.PDB	OE1, B_GLN_34	NE, B_ARG_25	HE, B_ARG_25	2.80	1.89	18.36
1HGG.PDB	OE1, B_GLN_34	NH2, B_ARG_25	HH21, B_ARG_25	2.91	2.04	24.97
1HGG.PDB	OE2, A_GLU_325	NH2, B_ARG_25	HH22, B_ARG_25	2.94	1.96	12.23
1HGG.PDB	OD2, B_ASP_37	OG, B_SER_40	HG, B_SER_40	2.80	1.93	21.69
1HGG.PDB	OD1, B_ASP_46	NE2, B_GLN_42	HE22, B_GLN_42	2.83	1.95	21.37
1HGG.PDB	OE2, B_GLU_114	NE2, B_GLN_47	HE21, B_GLN_47	2.96	2.05	17.92
1HGG.PDB	OG1, B_THR_107	NZ, B_LYS_51	HZ1, B_LYS_51	2.97	2.00	18.19
1HGG.PDB	OE1, B_GLU_103	NZ, B_LYS_51	HZ2, B_LYS_51	2.76	1.73	5.86
1HGG.PDB	ND1, B_HIS_106	NZ, B_LYS_51	HZ3, B_LYS_51	2.77	1.79	14.96

1HGG.PDB	OE1, B_GLU.57	NH1, B_ARG.54	HH11, B_ARG.54	2.86	1.86	11.23
1HGG.PDB	OE2, F_GLU.97	NH2, B_ARG.54	HH22, B_ARG.54	2.75	1.76	9.96
1HGG.PDB	OE2, B_GLU.61	NZ, B_LYS.58	HZ3, B_LYS.58	2.94	1.92	12.53
1HGG.PDB	OD2, F_ASP.90	NZ, B_LYS.62	HZ2, B_LYS.62	2.65	1.82	29.87
1HGG.PDB	OD2, F_ASP.86	NZ, B_LYS.62	HZ3, B_LYS.62	2.64	1.73	23.35
1HGG.PDB	OG, A_SER.110	NE2, B_HIS.64	HE2, B_HIS.64	2.90	1.96	14.63
1HGG.PDB	OE2, B_GLU.85	NZ, B_LYS.68	HZ2, B_LYS.68	2.75	1.72	7.06
1HGG.PDB	OE2, B_GLU.72	OG, B_SER.71	HG, B_SER.71	2.84	2.03	27.31
1HGG.PDB	OE2, D_GLU.81	NE, B_ARG.76	HE, B_ARG.76	2.94	1.96	10.47
1HGG.PDB	OE1, D_GLU.74	NH1, B_ARG.76	HH12, B_ARG.76	2.88	1.89	10.69
1HGG.PDB	OE1, D_GLU.81	NH2, B_ARG.76	HH21, B_ARG.76	2.73	1.73	5.91
1HGG.PDB	OE2, D_GLU.74	NH2, B_ARG.76	HH22, B_ARG.76	2.82	1.82	7.26
1HGG.PDB	OE1, D_GLU.85	OH, B_TYR.83	HH, B_TYR.83	2.68	1.80	19.99
1HGG.PDB	OH, F_TYR.83	NZ, B_LYS.88	HZ1, B_LYS.88	2.77	1.73	5.14
1HGG.PDB	OE2, B_GLU.120	NH1, B_ARG.123	HH11, B_ARG.123	2.73	1.87	25.50
1HGG.PDB	OE1, F_GLU.132	NE, B_ARG.124	HE, B_ARG.124	2.84	1.98	22.96
1HGG.PDB	OE2, F_GLU.132	NE, B_ARG.124	HE, B_ARG.124	2.81	1.98	25.54
1HGG.PDB	OH, B_TYR.157	ND2, B_ASN.129	HD22, B_ASN.129	2.80	1.86	13.18
1HGG.PDB	OD1, B_ASN.154	OG1, B_THR.156	HG1, B_THR.156	2.71	1.81	17.64
1HGG.PDB	OE2, B_GLU.131	NH1, B_ARG.170	HH11, B_ARG.170	2.85	1.85	6.28
1HGG.PDB	OE2, D_GLU.97	NZ, C_LYS.27	HZ1, C_LYS.27	2.94	1.91	8.28
1HGG.PDB	OD2, C_ASP.275	NZ, C_LYS.50	HZ1, C_LYS.50	2.68	1.77	23.74
1HGG.PDB	OE1, C_GLU.82	NH2, C_ARG.57	HH21, C_ARG.57	2.59	1.77	28.22
1HGG.PDB	OD1, C_ASP.73	ND1, C_HIS.75	HD1, C_HIS.75	2.72	1.84	20.87
1HGG.PDB	OD1, C_ASP.60	NE, C_ARG.90	HE, C_ARG.90	2.93	1.95	8.71
1HGG.PDB	OD2, C_ASP.60	NH2, C_ARG.90	HH21, C_ARG.90	2.79	1.80	9.72
1HGG.PDB	OD1, C_ASP.271	OG, C_SER.91	HG, C_SER.91	2.89	2.06	25.85
1HGG.PDB	OD2, C_ASP.271	OG, C_SER.91	HG, C_SER.91	2.90	2.02	21.44
1HGG.PDB	OD2, C_ASP.68	OG, C_SER.95	HG, C_SER.95	2.90	1.95	11.80
1HGG.PDB	OD1, C_ASP.68	OH, C_TYR.100	HH, C_TYR.100	2.93	1.98	11.50
1HGG.PDB	OD2, C_ASP.104	OG, C_SER.107	HG, C_SER.107	2.88	1.95	15.82
1HGG.PDB	OE2, D_GLU.67	NH2, C_ARG.109	HH21, C_ARG.109	2.85	1.88	14.56
1HGG.PDB	OD2, B_ASP.79	OG, C_SER.110	HG, C_SER.110	2.76	1.86	17.83
1HGG.PDB	OE2, C_GLU.119	OG1, C_THR.117	HG1, C_THR.117	2.92	1.97	8.69
1HGG.PDB	OD1, C_ASN.137	NZ, C_LYS.140	HZ2, C_LYS.140	2.78	1.78	13.21
1HGG.PDB	OD2, C_ASP.77	NE, C_ARG.141	HE, C_ARG.141	2.87	2.06	29.23
1HGG.PDB	OD1, C_ASP.77	NH2, C_ARG.141	HH21, C_ARG.141	2.76	1.85	22.10
1HGG.PDB	OD2, C_ASP.77	NH2, C_ARG.141	HH21, C_ARG.141	2.74	1.86	24.28
1HGG.PDB	OD1, C_ASN.137	OG, C_SER.145	HG, C_SER.145	2.90	2.03	20.82
1HGG.PDB	OH, C_TYR.195	NE1, C_TRP.153	HE1, C_TRP.153	2.90	1.98	17.08
1HGG.PDB	OE2, C_GLU.123	NZ, C_LYS.176	HZ1, C_LYS.176	2.63	1.76	26.89
1HGG.PDB	OE1, C_GLU.123	OH, C_TYR.178	HH, C_TYR.178	2.78	1.82	5.18
1HGG.PDB	OG1, C_THR.235	NE1, C_TRP.180	HE1, C_TRP.180	2.92	1.93	1.99
1HGG.PDB	OG, C_SER.231	NE2, C_HIS.184	HE2, C_HIS.184	2.79	1.91	21.48
1HGG.PDB	OD1, C_ASN.250	NE2, C_GLN.191	HE21, C_GLN.191	2.95	1.99	11.16
1HGG.PDB	OD1, C_ASN.246	NH2, C_ARG.201	HH21, C_ARG.201	2.66	1.74	19.39
1HGG.PDB	OG1, C_THR.212	OG1, C_THR.203	HG1, C_THR.203	2.83	1.91	13.70
1HGG.PDB	OD2, C_ASP.241	NE, C_ARG.208	HE, C_ARG.208	2.93	2.03	20.59
1HGG.PDB	OG1, C_THR.206	OG, C_SER.209	HG, C_SER.209	2.99	2.06	14.06
1HGG.PDB	OE1, E_GLN.210	NH2, C_ARG.220	HH21, C_ARG.220	2.61	1.71	21.26
1HGG.PDB	OD1, C_ASP.101	OG, C_SER.231	HG, C_SER.231	2.91	1.95	9.20
1HGG.PDB	OE1, B_GLU.72	NZ, C_LYS.238	HZ1, C_LYS.238	2.83	1.86	17.18
1HGG.PDB	OE2, B_GLU.72	NZ, C_LYS.238	HZ1, C_LYS.238	2.70	1.87	29.85
1HGG.PDB	OD1, C_ASN.165	ND2, C_ASN.246	HD22, C_ASN.246	2.88	1.97	17.94
1HGG.PDB	OE1, C_GLN.191	ND2, C_ASN.250	HD21, C_ASN.250	2.88	1.93	11.32
1HGG.PDB	OD1, C_ASN.133	NH2, C_ARG.255	HH22, C_ARG.255	2.54	1.68	24.43
1HGG.PDB	OE2, C_GLU.119	NH1, C_ARG.261	HH12, C_ARG.261	2.67	1.86	29.79
1HGG.PDB	OE1, C_GLU.119	NH2, C_ARG.261	HH22, C_ARG.261	2.73	1.87	26.76

1HGG.PDB	OH, C_TYR_302	NZ, C_LYS_264	HZ1, C_LYS_264	2.88	1.92	18.77
1HGG.PDB	ND1, C_HIS_56	NZ, C_LYS_264	HZ2, C_LYS_264	2.66	1.73	19.57
1HGG.PDB	OD2, C_ASP_85	NZ, C_LYS_264	HZ3, C_LYS_264	2.85	1.83	11.83
1HGG.PDB	OE1, D_GLU_67	NH1, C_ARG_269	HH12, C_ARG_269	2.69	1.85	27.75
1HGG.PDB	OE1, C_GLN_44	NZ, C_LYS_292	HZ1, C_LYS_292	2.77	1.76	11.69
1HGG.PDB	OD2, C_ASP_291	NZ, C_LYS_292	HZ3, C_LYS_292	2.78	1.91	27.51
1HGG.PDB	OD1, C_ASN_285	ND2, C_ASN_298	HD22, C_ASN_298	2.95	2.00	10.88
1HGG.PDB	OD1, D_ASP_90	NZ, C_LYS_310	HZ2, C_LYS_310	2.65	1.73	21.74
1HGG.PDB	OE1, C_GLU_41	NZ, C_LYS_315	HZ3, C_LYS_315	2.73	1.82	23.48
1HGG.PDB	OE2, C_GLU_35	ND2, C_ASN_322	HD22, C_ASN_322	2.82	1.96	24.18
1HGG.PDB	OXT, C_THR_328	NE2, C_GLN_327	HE22, C_GLN_327	2.99	2.05	16.22
1HGG.PDB	OE1, D_GLN_34	NE, D_ARG_25	HE, D_ARG_25	2.69	1.81	20.51
1HGG.PDB	OE1, D_GLN_34	NH2, D_ARG_25	HH21, D_ARG_25	2.92	2.08	27.66
1HGG.PDB	OD1, D_ASN_146	ND2, D_ASN_28	HD21, D_ASN_28	2.95	1.98	8.75
1HGG.PDB	OD2, D_ASP_37	OG, D_SER_40	HG, D_SER_40	2.77	1.93	24.58
1HGG.PDB	OD1, D_ASP_46	NE2, D_GLN_42	HE22, D_GLN_42	2.85	1.96	21.08
1HGG.PDB	OE2, D_GLU_114	NE2, D_GLN_47	HE21, D_GLN_47	2.97	2.05	17.17
1HGG.PDB	OG1, D_THR_107	NZ, D_LYS_51	HZ1, D_LYS_51	2.98	2.00	17.66
1HGG.PDB	OE1, D_GLU_103	NZ, D_LYS_51	HZ2, D_LYS_51	2.77	1.73	6.39
1HGG.PDB	ND1, D_HIS_106	NZ, D_LYS_51	HZ3, D_LYS_51	2.76	1.78	15.09
1HGG.PDB	OE1, D_GLU_57	NH1, D_ARG_54	HH11, D_ARG_54	2.86	1.86	11.12
1HGG.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.76	1.78	10.56
1HGG.PDB	OE2, D_GLU_61	NZ, D_LYS_58	HZ3, D_LYS_58	2.91	1.89	12.30
1HGG.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.86	1.90	9.42
1HGG.PDB	OE2, D_GLU_85	NZ, D_LYS_68	HZ2, D_LYS_68	2.77	1.74	6.59
1HGG.PDB	OE2, D_GLU_72	OG, D_SER_71	HG, D_SER_71	2.82	2.00	26.77
1HGG.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.86	1.89	9.57
1HGG.PDB	OE1, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.78	1.80	12.10
1HGG.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.67	1.68	6.66
1HGG.PDB	OE2, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.74	1.75	9.29
1HGG.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.59	1.78	26.83
1HGG.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.73	1.70	8.35
1HGG.PDB	OE2, D_GLU_120	NH1, D_ARG_123	HH11, D_ARG_123	2.73	1.87	25.59
1HGG.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.86	2.00	22.57
1HGG.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.78	1.96	26.12
1HGG.PDB	OH, D_TYR_157	ND2, D_ASN_129	HD22, D_ASN_129	2.80	1.84	10.50
1HGG.PDB	OD1, D_ASN_154	OG1, D_THR_156	HG1, D_THR_156	2.73	1.82	15.46
1HGG.PDB	NE2, D_HIS_142	OH, D_TYR_157	HH, D_TYR_157	2.72	1.85	20.87
1HGG.PDB	OE2, D_GLU_131	NH1, D_ARG_170	HH11, D_ARG_170	2.85	1.86	6.70
1HGG.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.91	1.88	8.89
1HGG.PDB	OD2, E_ASP_275	NZ, E_LYS_50	HZ1, E_LYS_50	2.68	1.77	24.10
1HGG.PDB	OD1, E_ASP_73	ND1, E_HIS_75	HD1, E_HIS_75	2.75	1.85	17.34
1HGG.PDB	OD1, E_ASP_60	NE, E_ARG_90	HE, E_ARG_90	2.91	1.94	9.27
1HGG.PDB	OD2, E_ASP_60	NH2, E_ARG_90	HH21, E_ARG_90	2.83	1.84	9.64
1HGG.PDB	OD1, E_ASP_271	OG, E_SER_91	HG, E_SER_91	2.92	2.07	24.79
1HGG.PDB	OD2, E_ASP_271	OG, E_SER_91	HG, E_SER_91	2.93	2.06	22.08
1HGG.PDB	OD2, E_ASP_68	OG, E_SER_95	HG, E_SER_95	2.93	1.98	13.19
1HGG.PDB	OD1, E_ASP_68	OH, E_TYR_100	HH, E_TYR_100	2.92	1.96	10.90
1HGG.PDB	OD2, E_ASP_104	OG, E_SER_107	HG, E_SER_107	2.85	1.93	15.56
1HGG.PDB	OE2, F_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.88	1.90	14.20
1HGG.PDB	OD2, D_ASP_79	OG, E_SER_110	HG, E_SER_110	2.79	1.88	16.48
1HGG.PDB	OE2, E_GLU_119	OG1, E_THR_117	HG1, E_THR_117	2.95	1.99	7.33
1HGG.PDB	OD1, E_ASN_137	NZ, E_LYS_140	HZ2, E_LYS_140	2.76	1.76	13.40
1HGG.PDB	OD2, E_ASP_77	NE, E_ARG_141	HE, E_ARG_141	2.90	2.09	29.10
1HGG.PDB	OD1, E_ASP_77	NH2, E_ARG_141	HH21, E_ARG_141	2.80	1.90	22.17
1HGG.PDB	OD2, E_ASP_77	NH2, E_ARG_141	HH21, E_ARG_141	2.74	1.86	23.74
1HGG.PDB	OD1, E_ASN_137	OG, E_SER_145	HG, E_SER_145	2.95	2.08	20.42
1HGG.PDB	OH, E_TYR_195	NE1, E_TRP_153	HE1, E_TRP_153	2.91	1.97	14.69

1HGG.PDB	OE2, E_GLU_123	NZ, E_LYS_176	HZ1, E_LYS_176	2.65	1.78	26.50
1HGG.PDB	OE1, E_GLU_123	OH, E_TYR_178	HH, E_TYR_178	2.80	1.84	8.47
1HGG.PDB	OG1, E_THR_235	NE1, E_TRP_180	HE1, E_TRP_180	2.93	1.94	2.01
1HGG.PDB	OG, E_SER_231	NE2, E_HIS_184	HE2, E_HIS_184	2.81	1.94	22.49
1HGG.PDB	OD1, E_ASN_246	NH2, E_ARG_201	HH21, E_ARG_201	2.66	1.74	20.08
1HGG.PDB	OG1, E_THR_212	OG1, E_THR_203	HG1, E_THR_203	2.88	1.95	13.34
1HGG.PDB	OD2, E_ASP_241	NE, E_ARG_208	HE, E_ARG_208	2.96	2.05	19.90
1HGG.PDB	OG1, E_THR_206	OG, E_SER_209	HG, E_SER_209	2.99	2.07	14.54
1HGG.PDB	OD1, C_ASP_101	NE2, E_GLN_210	HE22, E_GLN_210	2.96	2.04	17.70
1HGG.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.72	1.80	20.26
1HGG.PDB	OD1, E_ASP_101	OG, E_SER_231	HG, E_SER_231	2.91	1.96	10.31
1HGG.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ1, E_LYS_238	2.89	1.89	13.93
1HGG.PDB	OD1, E_ASN_165	ND2, E_ASN_246	HD22, E_ASN_246	2.88	1.96	17.66
1HGG.PDB	OE1, E_GLN_191	ND2, E_ASN_250	HD21, E_ASN_250	2.89	1.94	10.20
1HGG.PDB	OD1, E_ASN_133	NH2, E_ARG_255	HH22, E_ARG_255	2.55	1.68	24.24
1HGG.PDB	OE2, E_GLU_119	NH1, E_ARG_261	HH12, E_ARG_261	2.69	1.87	29.29
1HGG.PDB	OE1, E_GLU_119	NH2, E_ARG_261	HH22, E_ARG_261	2.74	1.88	26.67
1HGG.PDB	OH, E_TYR_302	NZ, E_LYS_264	HZ1, E_LYS_264	2.90	1.93	18.14
1HGG.PDB	ND1, E_HIS_56	NZ, E_LYS_264	HZ2, E_LYS_264	2.66	1.73	20.09
1HGG.PDB	OD2, E_ASP_85	NZ, E_LYS_264	HZ3, E_LYS_264	2.85	1.83	11.84
1HGG.PDB	OE1, F_GLU_67	NH1, E_ARG_269	HH12, E_ARG_269	2.69	1.85	27.32
1HGG.PDB	OE1, E_GLN_44	NZ, E_LYS_292	HZ1, E_LYS_292	2.77	1.75	10.61
1HGG.PDB	OD2, E_ASP_291	NZ, E_LYS_292	HZ3, E_LYS_292	2.76	1.90	27.94
1HGG.PDB	OD1, E_ASN_285	ND2, E_ASN_298	HD22, E_ASN_298	2.95	2.00	11.31
1HGG.PDB	OD1, F_ASP_90	NZ, E_LYS_310	HZ2, E_LYS_310	2.64	1.72	22.12
1HGG.PDB	OE1, E_GLU_41	NZ, E_LYS_315	HZ3, E_LYS_315	2.68	1.80	26.22
1HGG.PDB	OE2, E_GLU_35	ND2, E_ASN_322	HD22, E_ASN_322	2.79	1.94	25.02
1HGG.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.98	1.97	15.13
1HGG.PDB	OD2, F_ASP_37	OG, F_SER_40	HG, F_SER_40	2.74	1.92	26.19
1HGG.PDB	OD1, F_ASP_46	NE2, F_GLN_42	HE22, F_GLN_42	2.82	1.94	21.99
1HGG.PDB	OE2, F_GLU_114	NE2, F_GLN_47	HE21, F_GLN_47	2.97	2.06	18.05
1HGG.PDB	OG1, F_THR_107	NZ, F_LYS_51	HZ1, F_LYS_51	2.98	2.02	18.55
1HGG.PDB	OE1, F_GLU_103	NZ, F_LYS_51	HZ2, F_LYS_51	2.79	1.76	6.25
1HGG.PDB	ND1, F_HIS_106	NZ, F_LYS_51	HZ3, F_LYS_51	2.72	1.74	15.22
1HGG.PDB	OE1, F_GLU_57	NH1, F_ARG_54	HH11, F_ARG_54	2.85	1.85	10.83
1HGG.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.73	1.74	10.16
1HGG.PDB	OE2, F_GLU_61	NZ, F_LYS_58	HZ3, F_LYS_58	2.94	1.92	12.48
1HGG.PDB	OD2, D_ASP_86	NZ, F_LYS_62	HZ3, F_LYS_62	2.58	1.75	29.01
1HGG.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.87	1.91	10.03
1HGG.PDB	OE2, F_GLU_85	NZ, F_LYS_68	HZ2, F_LYS_68	2.75	1.74	10.05
1HGG.PDB	OE2, F_GLU_72	OG, F_SER_71	HG, F_SER_71	2.86	2.03	26.49
1HGG.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.88	1.92	11.44
1HGG.PDB	OE1, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.75	1.76	9.13
1HGG.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.67	1.68	1.99
1HGG.PDB	OE2, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.79	1.81	10.64
1HGG.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.68	1.67	10.46
1HGG.PDB	OE2, F_GLU_120	NH1, F_ARG_123	HH11, F_ARG_123	2.72	1.86	25.68
1HGG.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.96	2.09	22.59
1HGG.PDB	OE2, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.87	2.01	24.00
1HGG.PDB	OH, F_TYR_157	ND2, F_ASN_129	HD22, F_ASN_129	2.79	1.86	14.20
1HGG.PDB	OE2, F_GLU_131	NH1, F_ARG_170	HH11, F_ARG_170	2.84	1.84	6.38

Table 1734: 1HGG-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1HGH.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.78	1.76	9.03
1HGH.PDB	OD2, A_ASP_275	NZ, A_LYS_50	HZ1, A_LYS_50	2.79	1.83	19.36
1HGH.PDB	OD1, A_ASP_73	ND1, A_HIS_75	HD1, A_HIS_75	2.74	1.85	19.20
1HGH.PDB	OD1, A_ASP_60	NE, A_ARG_90	HE, A_ARG_90	2.85	1.88	8.50
1HGH.PDB	OD2, A_ASP_60	NH2, A_ARG_90	HH21, A_ARG_90	2.79	1.80	9.33
1HGH.PDB	OD2, A_ASP_271	OG, A_SER_91	HG, A_SER_91	2.76	1.89	21.30
1HGH.PDB	OD2, A_ASP_68	OG, A_SER_95	HG, A_SER_95	2.83	1.95	21.96
1HGH.PDB	OD1, A_ASP_68	OH, A_TYR_100	HH, A_TYR_100	2.95	2.07	21.37
1HGH.PDB	OD2, A_ASP_104	OG, A_SER_107	HG, A_SER_107	2.88	1.94	14.34
1HGH.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.86	1.88	13.48
1HGH.PDB	OD2, F_ASP_79	OG, A_SER_110	HG, A_SER_110	2.97	2.01	11.65
1HGH.PDB	OE2, A_GLU_119	OG1, A_THR_117	HG1, A_THR_117	2.86	1.91	8.00
1HGH.PDB	OD1, A_ASN_137	NZ, A_LYS_140	HZ2, A_LYS_140	2.74	1.73	12.09
1HGH.PDB	OD2, A_ASP_77	NE, A_ARG_141	HE, A_ARG_141	2.85	2.03	27.72
1HGH.PDB	OD1, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.86	1.95	21.78
1HGH.PDB	OD2, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.74	1.85	23.60
1HGH.PDB	OH, A_TYR_195	NE1, A_TRP_153	HE1, A_TRP_153	2.96	2.05	18.96
1HGH.PDB	OE2, A_GLU_123	NZ, A_LYS_176	HZ1, A_LYS_176	2.68	1.79	24.70
1HGH.PDB	OE1, A_GLU_123	OH, A_TYR_178	HH, A_TYR_178	2.75	1.81	10.37
1HGH.PDB	OG1, A_THR_235	NE1, A_TRP_180	HE1, A_TRP_180	2.89	1.90	1.65
1HGH.PDB	OG, A_SER_231	NE2, A_HIS_184	HE2, A_HIS_184	2.74	1.90	25.48
1HGH.PDB	OD1, A_ASN_250	NE2, A_GLN_191	HE21, A_GLN_191	2.96	2.00	8.72
1HGH.PDB	OD1, A_ASN_246	NH2, A_ARG_201	HH21, A_ARG_201	2.63	1.71	19.32
1HGH.PDB	OG1, A_THR_206	OG, A_SER_209	HG, A_SER_209	2.93	1.98	8.14
1HGH.PDB	OD1, E_ASP_101	NE2, A_GLN_210	HE22, A_GLN_210	2.97	2.14	27.61
1HGH.PDB	OG1, A_THR_203	OG1, A_THR_212	HG1, A_THR_212	2.93	1.98	7.92
1HGH.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.66	1.73	18.15
1HGH.PDB	OD1, A_ASP_101	OG, A_SER_231	HG, A_SER_231	2.86	1.91	11.01
1HGH.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.92	1.93	15.64
1HGH.PDB	OD1, A_ASN_165	ND2, A_ASN_246	HD22, A_ASN_246	2.95	1.98	10.57
1HGH.PDB	OE1, A_GLN_191	ND2, A_ASN_250	HD21, A_ASN_250	2.87	1.90	5.96
1HGH.PDB	OE2, A_GLU_119	NH1, A_ARG_261	HH12, A_ARG_261	2.62	1.81	29.53
1HGH.PDB	OE1, A_GLU_119	NH2, A_ARG_261	HH22, A_ARG_261	2.87	1.97	23.64
1HGH.PDB	OD2, A_ASP_85	NZ, A_LYS_264	HZ3, A_LYS_264	2.81	1.82	15.33
1HGH.PDB	OE1, A_GLN_44	NZ, A_LYS_292	HZ1, A_LYS_292	2.68	1.67	11.56
1HGH.PDB	OD2, A_ASP_291	NZ, A_LYS_292	HZ3, A_LYS_292	2.82	1.85	18.01
1HGH.PDB	OD1, B_ASP_86	NZ, A_LYS_310	HZ2, A_LYS_310	2.71	1.84	27.09
1HGH.PDB	OE1, A_GLU_41	NZ, A_LYS_315	HZ3, A_LYS_315	2.87	1.90	18.83
1HGH.PDB	OE2, A_GLU_35	ND2, A_ASN_322	HD22, A_ASN_322	2.83	1.93	20.02
1HGH.PDB	OE1, A_GLU_325	NZ, A_LYS_326	HZ3, A_LYS_326	2.84	1.87	17.61
1HGH.PDB	OE1, B_GLN_34	NE, B_ARG_25	HE, B_ARG_25	2.67	1.79	21.37
1HGH.PDB	OE1, B_GLN_34	NH2, B_ARG_25	HH21, B_ARG_25	2.91	2.10	29.24
1HGH.PDB	OD1, B_ASP_46	NE2, B_GLN_42	HE22, B_GLN_42	2.86	1.97	20.47
1HGH.PDB	OE1, B_GLU_103	NZ, B_LYS_51	HZ1, B_LYS_51	2.79	1.76	7.63
1HGH.PDB	ND1, B_HIS_106	NZ, B_LYS_51	HZ2, B_LYS_51	2.80	1.85	18.51
1HGH.PDB	OG1, B_THR_107	NZ, B_LYS_51	HZ3, B_LYS_51	2.89	1.91	15.99
1HGH.PDB	OE1, B_GLU_57	NH1, B_ARG_54	HH11, B_ARG_54	2.86	1.87	11.36
1HGH.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.82	1.86	15.60
1HGH.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ1, B_LYS_62	2.66	1.80	27.71
1HGH.PDB	OD2, F_ASP_90	NZ, B_LYS_62	HZ3, B_LYS_62	2.68	1.82	27.13
1HGH.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.87	1.91	11.96
1HGH.PDB	OE2, B_GLU_85	NZ, B_LYS_68	HZ2, B_LYS_68	2.73	1.71	6.94
1HGH.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.87	1.90	9.70
1HGH.PDB	OE2, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.91	1.90	8.45
1HGH.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.77	1.76	5.47
1HGH.PDB	OE1, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.89	1.87	2.83
1HGH.PDB	OE1, B_GLU_74	NE2, B_GLN_78	HE22, B_GLN_78	2.91	1.95	10.12

1HGH.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.69	1.84	23.96
1HGH.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.74	1.71	7.44
1HGH.PDB	OE2, B_GLU_120	NH1, B_ARG_123	HH11, B_ARG_123	2.74	1.85	22.74
1HGH.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.76	1.94	26.47
1HGH.PDB	OE2, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.83	1.98	23.62
1HGH.PDB	OH, B_TYR_157	ND2, B_ASN_129	HD22, B_ASN_129	2.83	1.87	11.09
1HGH.PDB	OE2, B_GLU_150	ND2, B_ASN_154	HD21, B_ASN_154	2.97	2.10	23.74
1HGH.PDB	OD1, B_ASN_154	OG1, B_THR_156	HG1, B_THR_156	2.66	1.78	19.28
1HGH.PDB	OE2, B_GLU_131	NH1, B_ARG_170	HH11, B_ARG_170	2.83	1.83	5.81
1HGH.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.82	1.78	7.61
1HGH.PDB	OD2, C_ASP_275	NZ, C_LYS_50	HZ1, C_LYS_50	2.77	1.81	19.74
1HGH.PDB	OD1, C_ASP_73	ND1, C_HIS_75	HD1, C_HIS_75	2.71	1.84	22.23
1HGH.PDB	OD1, C_ASP_60	NE, C_ARG_90	HE, C_ARG_90	2.80	1.87	15.44
1HGH.PDB	OD2, C_ASP_60	NH2, C_ARG_90	HH21, C_ARG_90	2.76	1.77	8.79
1HGH.PDB	OD2, C_ASP_271	OG, C_SER_91	HG, C_SER_91	2.80	1.87	12.62
1HGH.PDB	OD2, C_ASP_68	OG, C_SER_95	HG, C_SER_95	2.83	1.92	18.04
1HGH.PDB	OD1, C_ASP_68	OH, C_TYR_100	HH, C_TYR_100	2.94	2.01	15.20
1HGH.PDB	OD2, C_ASP_104	OG, C_SER_107	HG, C_SER_107	2.88	1.96	17.02
1HGH.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.86	1.88	13.66
1HGH.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.78	1.85	13.87
1HGH.PDB	OE2, C_GLU_119	OG1, C_THR_117	HG1, C_THR_117	2.87	1.92	8.14
1HGH.PDB	OD1, C_ASN_137	NZ, C_LYS_140	HZ2, C_LYS_140	2.76	1.74	10.11
1HGH.PDB	OD2, C_ASP_77	NE, C_ARG_141	HE, C_ARG_141	2.85	2.02	26.86
1HGH.PDB	OD1, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.88	1.98	22.59
1HGH.PDB	OD2, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.75	1.86	23.43
1HGH.PDB	OD1, C_ASN_137	OG, C_SER_145	HG, C_SER_145	2.89	2.04	23.42
1HGH.PDB	OH, C_TYR_195	NE1, C_TRP_153	HE1, C_TRP_153	2.92	2.00	17.94
1HGH.PDB	OE2, C_GLU_123	NZ, C_LYS_176	HZ1, C_LYS_176	2.65	1.80	28.51
1HGH.PDB	OE1, C_GLU_123	OH, C_TYR_178	HH, C_TYR_178	2.74	1.81	11.36
1HGH.PDB	OG1, C_THR_235	NE1, C_TRP_180	HE1, C_TRP_180	2.88	1.89	0.71
1HGH.PDB	OG, C_SER_231	NE2, C_HIS_184	HE2, C_HIS_184	2.77	1.92	24.69
1HGH.PDB	OD1, C_ASN_250	NE2, C_GLN_191	HE21, C_GLN_191	2.95	1.99	9.46
1HGH.PDB	OD1, C_ASN_246	NH2, C_ARG_201	HH21, C_ARG_201	2.65	1.73	20.02
1HGH.PDB	OG1, C_THR_212	OG1, C_THR_203	HG1, C_THR_203	2.92	1.98	11.43
1HGH.PDB	OD2, C_ASP_241	NE, C_ARG_208	HE, C_ARG_208	2.97	2.08	22.63
1HGH.PDB	OG1, C_THR_206	OG, C_SER_209	HG, C_SER_209	2.95	2.00	8.11
1HGH.PDB	OD1, A_ASP_101	NE2, C_GLN_210	HE22, C_GLN_210	2.93	2.07	24.87
1HGH.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.57	1.72	26.03
1HGH.PDB	OD1, C_ASP_101	OG, C_SER_231	HG, C_SER_231	2.86	1.92	12.68
1HGH.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.71	1.80	22.72
1HGH.PDB	OD1, C_ASN_165	ND2, C_ASN_246	HD22, C_ASN_246	2.97	2.00	10.03
1HGH.PDB	OE1, C_GLN_191	ND2, C_ASN_250	HD21, C_ASN_250	2.86	1.89	6.98
1HGH.PDB	OE2, C_GLU_119	NH1, C_ARG_261	HH12, C_ARG_261	2.64	1.82	29.37
1HGH.PDB	OE1, C_GLU_119	NH2, C_ARG_261	HH22, C_ARG_261	2.85	1.97	24.44
1HGH.PDB	OD2, C_ASP_85	NZ, C_LYS_264	HZ3, C_LYS_264	2.79	1.81	15.90
1HGH.PDB	OE1, C_GLN_44	NZ, C_LYS_292	HZ1, C_LYS_292	2.68	1.68	11.00
1HGH.PDB	OD2, C_ASP_291	NZ, C_LYS_292	HZ3, C_LYS_292	2.82	1.84	17.38
1HGH.PDB	OD1, C_ASN_285	ND2, C_ASN_298	HD22, C_ASN_298	2.99	2.06	14.92
1HGH.PDB	OD1, D_ASP_86	NZ, C_LYS_310	HZ2, C_LYS_310	2.73	1.85	26.20
1HGH.PDB	OE1, C_GLU_41	NZ, C_LYS_315	HZ3, C_LYS_315	2.87	1.91	19.47
1HGH.PDB	OE2, C_GLU_35	ND2, C_ASN_322	HD22, C_ASN_322	2.82	1.91	18.57
1HGH.PDB	OE1, D_GLU_15	NZ, C_LYS_326	HZ1, C_LYS_326	2.77	1.75	11.00
1HGH.PDB	OXT, C_THR_328	NE2, C_GLN_327	HE22, C_GLN_327	2.93	1.99	14.57
1HGH.PDB	OE1, D_GLN_34	NE, D_ARG_25	HE, D_ARG_25	2.91	1.96	12.36
1HGH.PDB	OD2, D_ASP_37	OG, D_SER_40	HG, D_SER_40	2.74	1.93	27.28
1HGH.PDB	OD1, D_ASP_46	NE2, D_GLN_42	HE22, D_GLN_42	2.87	1.96	19.71
1HGH.PDB	OE1, D_GLU_103	NZ, D_LYS_51	HZ1, D_LYS_51	2.74	1.72	7.43
1HGH.PDB	ND1, D_HIS_106	NZ, D_LYS_51	HZ2, D_LYS_51	2.80	1.84	18.41

1HGH.PDB	OG1, D_THR_107	NZ, D_LYS_51	HZ3, D_LYS_51	2.90	1.93	16.98
1HGH.PDB	OE1, D_GLU_57	NH1, D_ARG_54	HH11, D_ARG_54	2.86	1.86	11.45
1HGH.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.80	1.85	16.64
1HGH.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.84	1.88	10.18
1HGH.PDB	OE2, D_GLU_85	NZ, D_LYS_68	HZ2, D_LYS_68	2.75	1.73	9.37
1HGH.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.79	1.84	10.45
1HGH.PDB	OE2, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.77	1.77	10.38
1HGH.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.70	1.70	6.41
1HGH.PDB	OE1, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.75	1.75	5.88
1HGH.PDB	OE1, D_GLU_74	NE2, D_GLN_78	HE22, D_GLN_78	2.92	1.96	9.79
1HGH.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.59	1.81	29.86
1HGH.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.66	1.64	7.83
1HGH.PDB	OE2, D_GLU_120	NH1, D_ARG_123	HH11, D_ARG_123	2.77	1.87	22.36
1HGH.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.80	1.98	26.35
1HGH.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.84	1.99	23.38
1HGH.PDB	OH, D_TYR_157	ND2, D_ASN_129	HD22, D_ASN_129	2.83	1.87	7.67
1HGH.PDB	OD1, D_ASN_154	OG1, D_THR_156	HG1, D_THR_156	2.69	1.80	16.96
1HGH.PDB	NE2, D_HIS_142	OH, D_TYR_157	HH, D_TYR_157	2.68	1.87	26.02
1HGH.PDB	OE2, D_GLU_131	NH1, D_ARG_170	HH11, D_ARG_170	2.83	1.83	5.85
1HGH.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.77	1.74	8.08
1HGH.PDB	OD2, E_ASP_275	NZ, E_LYS_50	HZ1, E_LYS_50	2.78	1.83	20.38
1HGH.PDB	OD1, E_ASP_73	ND1, E_HIS_75	HD1, E_HIS_75	2.70	1.83	21.52
1HGH.PDB	OD1, E_ASP_60	NE, E_ARG_90	HE, E_ARG_90	2.82	1.87	13.57
1HGH.PDB	OD2, E_ASP_60	NH2, E_ARG_90	HH21, E_ARG_90	2.82	1.82	8.69
1HGH.PDB	OD2, E_ASP_271	OG, E_SER_91	HG, E_SER_91	2.81	1.88	14.87
1HGH.PDB	OD2, E_ASP_68	OG, E_SER_95	HG, E_SER_95	2.88	1.94	13.28
1HGH.PDB	OD1, E_ASP_68	OH, E_TYR_100	HH, E_TYR_100	2.91	1.97	12.96
1HGH.PDB	OD2, E_ASP_104	OG, E_SER_107	HG, E_SER_107	2.88	1.97	18.12
1HGH.PDB	OE2, F_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.88	1.90	13.56
1HGH.PDB	OD2, D_ASP_79	OG, E_SER_110	HG, E_SER_110	2.90	1.94	9.49
1HGH.PDB	OE2, E_GLU_119	OG1, E_THR_117	HG1, E_THR_117	2.88	1.94	11.16
1HGH.PDB	OD1, E_ASN_137	NZ, E_LYS_140	HZ2, E_LYS_140	2.75	1.75	11.91
1HGH.PDB	OD2, E_ASP_77	NE, E_ARG_141	HE, E_ARG_141	2.85	2.01	27.16
1HGH.PDB	OD1, E_ASP_77	NH2, E_ARG_141	HH21, E_ARG_141	2.89	1.99	22.46
1HGH.PDB	OD2, E_ASP_77	NH2, E_ARG_141	HH21, E_ARG_141	2.74	1.84	23.25
1HGH.PDB	OD1, E_ASN_137	OG, E_SER_145	HG, E_SER_145	2.98	2.07	15.03
1HGH.PDB	OH, E_TYR_195	NE1, E_TRP_153	HE1, E_TRP_153	2.94	2.03	18.49
1HGH.PDB	OE2, E_GLU_123	NZ, E_LYS_176	HZ1, E_LYS_176	2.69	1.82	26.87
1HGH.PDB	OE1, E_GLU_123	OH, E_TYR_178	HH, E_TYR_178	2.77	1.82	8.79
1HGH.PDB	OG1, E_THR_235	NE1, E_TRP_180	HE1, E_TRP_180	2.88	1.89	0.99
1HGH.PDB	OG, E_SER_231	NE2, E_HIS_184	HE2, E_HIS_184	2.78	1.93	25.10
1HGH.PDB	OD1, E_ASN_250	NE2, E_GLN_191	HE21, E_GLN_191	2.99	2.02	8.22
1HGH.PDB	OD1, E_ASN_246	NH2, E_ARG_201	HH21, E_ARG_201	2.64	1.73	21.41
1HGH.PDB	OG1, E_THR_212	OG1, E_THR_203	HG1, E_THR_203	2.98	2.08	17.30
1HGH.PDB	OG1, E_THR_206	OG, E_SER_209	HG, E_SER_209	2.95	2.00	8.64
1HGH.PDB	OD1, C_ASP_101	NE2, E_GLN_210	HE22, E_GLN_210	2.95	2.09	25.33
1HGH.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.68	1.79	22.30
1HGH.PDB	OD1, E_ASP_101	OG, E_SER_231	HG, E_SER_231	2.86	1.91	11.78
1HGH.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ3, E_LYS_238	2.87	1.88	15.42
1HGH.PDB	OD1, E_ASN_165	ND2, E_ASN_246	HD22, E_ASN_246	2.98	2.01	10.13
1HGH.PDB	OE1, E_GLN_191	ND2, E_ASN_250	HD21, E_ASN_250	2.89	1.92	6.88
1HGH.PDB	OE2, E_GLU_119	NH1, E_ARG_261	HH12, E_ARG_261	2.63	1.81	29.30
1HGH.PDB	OE1, E_GLU_119	NH2, E_ARG_261	HH22, E_ARG_261	2.85	1.96	24.42
1HGH.PDB	OD2, E_ASP_85	NZ, E_LYS_264	HZ3, E_LYS_264	2.81	1.82	14.94
1HGH.PDB	OE1, F_GLU_67	NH1, E_ARG_269	HH12, E_ARG_269	2.71	1.88	29.19
1HGH.PDB	OE1, E_GLN_44	NZ, E_LYS_292	HZ1, E_LYS_292	2.67	1.66	10.24
1HGH.PDB	OD2, E_ASP_291	NZ, E_LYS_292	HZ3, E_LYS_292	2.84	1.86	17.36
1HGH.PDB	OD1, F_ASP_86	NZ, E_LYS_310	HZ2, E_LYS_310	2.74	1.87	26.77

1HGH.PDB	OE1, E_GLU_41	NZ, E_LYS_315	HZ3, E_LYS_315	2.85	1.89	19.70
1HGH.PDB	OE2, E_GLU_35	ND2, E_ASN_322	HD22, E_ASN_322	2.80	1.90	19.14
1HGH.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.90	1.89	12.96
1HGH.PDB	OE1, F_GLN_34	NH2, F_ARG_25	HH21, F_ARG_25	2.92	2.03	23.48
1HGH.PDB	OD1, F_ASN_146	ND2, F_ASN_28	HD21, F_ASN_28	2.91	1.96	12.69
1HGH.PDB	OD2, F_ASP_37	OG, F_SER_40	HG, F_SER_40	2.73	1.92	26.94
1HGH.PDB	OD1, F_ASP_46	NE2, F_GLN_42	HE22, F_GLN_42	2.85	1.95	20.25
1HGH.PDB	OE2, F_GLU_114	NE2, F_GLN_47	HE21, F_GLN_47	2.99	2.08	19.28
1HGH.PDB	OE1, F_GLU_103	NZ, F_LYS_51	HZ1, F_LYS_51	2.75	1.72	7.02
1HGH.PDB	ND1, F_HIS_106	NZ, F_LYS_51	HZ2, F_LYS_51	2.77	1.82	19.11
1HGH.PDB	OG1, F_THR_107	NZ, F_LYS_51	HZ3, F_LYS_51	2.93	1.96	17.40
1HGH.PDB	OE1, F_GLU_57	NH1, F_ARG_54	HH11, F_ARG_54	2.88	1.88	10.86
1HGH.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.72	1.77	15.67
1HGH.PDB	OD2, D_ASP_90	NZ, F_LYS_62	HZ2, F_LYS_62	2.68	1.83	28.02
1HGH.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.87	1.91	9.23
1HGH.PDB	OE2, F_GLU_85	NZ, F_LYS_68	HZ2, F_LYS_68	2.73	1.74	15.07
1HGH.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.84	1.87	10.72
1HGH.PDB	OE2, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.73	1.73	5.34
1HGH.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.71	1.70	1.21
1HGH.PDB	OE1, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.78	1.78	7.19
1HGH.PDB	OE1, F_GLU_74	NE2, F_GLN_78	HE22, F_GLN_78	2.92	1.95	8.97
1HGH.PDB	OE1, B_GLU_85	OH, F_TYR_83	HH, F_TYR_83	2.53	1.74	27.23
1HGH.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.65	1.63	9.88
1HGH.PDB	OE2, F_GLU_120	NH1, F_ARG_123	HH11, F_ARG_123	2.74	1.84	22.63
1HGH.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.89	2.06	26.55
1HGH.PDB	OE2, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.92	2.03	21.52
1HGH.PDB	OH, F_TYR_157	ND2, F_ASN_129	HD22, F_ASN_129	2.82	1.88	14.11
1HGH.PDB	OE2, F_GLU_131	NH1, F_ARG_170	HH11, F_ARG_170	2.84	1.84	5.40

Table 1735: 1HGH-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1HGI.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.90	1.86	7.66
1HGI.PDB	OD2, A_ASP_275	NZ, A_LYS_50	HZ1, A_LYS_50	2.71	1.78	22.79
1HGI.PDB	OD1, A_ASP_73	ND1, A_HIS_75	HD1, A_HIS_75	2.90	1.96	15.34
1HGI.PDB	OD1, A_ASP_60	NE, A_ARG_90	HE, A_ARG_90	2.89	1.91	4.93
1HGI.PDB	OD2, A_ASP_60	NH2, A_ARG_90	HH21, A_ARG_90	2.83	1.85	11.60
1HGI.PDB	OD1, A_ASP_271	OG, A_SER_91	HG, A_SER_91	2.93	2.10	25.86
1HGI.PDB	OD2, A_ASP_271	OG, A_SER_91	HG, A_SER_91	2.80	1.92	20.51
1HGI.PDB	OD2, A_ASP_68	OG, A_SER_95	HG, A_SER_95	2.89	1.96	14.00
1HGI.PDB	OD1, A_ASP_68	OH, A_TYR_100	HH, A_TYR_100	2.99	2.05	13.08
1HGI.PDB	OD2, A_ASP_104	OG, A_SER_107	HG, A_SER_107	2.89	1.96	15.23
1HGI.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.80	1.81	13.24
1HGI.PDB	OE2, A_GLU_119	OG1, A_THR_117	HG1, A_THR_117	2.93	2.01	15.43
1HGI.PDB	OD1, A_ASN_137	NZ, A_LYS_140	HZ2, A_LYS_140	2.79	1.79	13.01
1HGI.PDB	OD2, A_ASP_77	NE, A_ARG_141	HE, A_ARG_141	2.82	2.01	29.43
1HGI.PDB	OD1, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.93	2.01	20.43
1HGI.PDB	OD2, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.69	1.82	24.99
1HGI.PDB	OH, A_TYR_195	NE1, A_TRP_153	HE1, A_TRP_153	2.87	1.98	21.02
1HGI.PDB	OG1, A_THR_131	OG, A_SER_157	HG, A_SER_157	2.97	2.02	9.12
1HGI.PDB	OE2, A_GLU_123	NZ, A_LYS_176	HZ1, A_LYS_176	2.68	1.79	25.50
1HGI.PDB	OE1, A_GLU_123	OH, A_TYR_178	HH, A_TYR_178	2.78	1.82	7.33
1HGI.PDB	OG1, A_THR_235	NE1, A_TRP_180	HE1, A_TRP_180	2.85	1.87	3.02
1HGI.PDB	OG, A_SER_231	NE2, A_HIS_184	HE2, A_HIS_184	2.81	1.93	22.19
1HGI.PDB	OD1, A_ASN_250	NE2, A_GLN_191	HE21, A_GLN_191	2.93	1.97	11.19
1HGI.PDB	OD1, A_ASN_246	NH2, A_ARG_201	HH21, A_ARG_201	2.54	1.71	26.99
1HGI.PDB	OD2, A_ASP_241	NE, A_ARG_208	HE, A_ARG_208	2.96	2.05	19.55
1HGI.PDB	OG1, A_THR_203	OG1, A_THR_212	HG1, A_THR_212	2.96	2.00	2.15
1HGI.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.65	1.73	18.55
1HGI.PDB	OD1, A_ASP_101	OG, A_SER_231	HG, A_SER_231	2.96	2.01	11.74
1HGI.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.85	1.85	15.00
1HGI.PDB	OE1, A_GLN_191	ND2, A_ASN_250	HD21, A_ASN_250	2.89	1.93	10.00
1HGI.PDB	OE2, A_GLU_119	NH1, A_ARG_261	HH12, A_ARG_261	2.66	1.83	28.46
1HGI.PDB	OE1, A_GLU_119	NH2, A_ARG_261	HH22, A_ARG_261	2.85	1.99	27.12
1HGI.PDB	OD2, A_ASP_85	NZ, A_LYS_264	HZ3, A_LYS_264	2.82	1.85	17.23
1HGI.PDB	OE1, A_GLN_44	NZ, A_LYS_292	HZ1, A_LYS_292	2.74	1.74	11.73
1HGI.PDB	OD2, A_ASP_291	NZ, A_LYS_292	HZ3, A_LYS_292	2.81	1.89	23.33
1HGI.PDB	OD1, B_ASP_86	NZ, A_LYS_310	HZ3, A_LYS_310	2.76	1.92	29.34
1HGI.PDB	OE1, A_GLU_41	NZ, A_LYS_315	HZ3, A_LYS_315	2.77	1.82	19.86
1HGI.PDB	OE2, A_GLU_35	ND2, A_ASN_322	HD22, A_ASN_322	2.93	1.97	12.34
1HGI.PDB	OE2, B_GLU_15	NZ, A_LYS_326	HZ1, A_LYS_326	2.79	1.93	27.33
1HGI.PDB	OE1, A_GLU_325	NZ, A_LYS_326	HZ3, A_LYS_326	2.91	1.94	17.77
1HGI.PDB	OE1, B_GLN_34	NE, B_ARG_25	HE, B_ARG_25	2.60	1.78	26.17
1HGI.PDB	OE1, B_GLN_34	NH2, B_ARG_25	HH21, B_ARG_25	2.75	1.92	27.98
1HGI.PDB	OE2, A_GLU_325	NH2, B_ARG_25	HH22, B_ARG_25	2.93	1.95	13.46
1HGI.PDB	OD1, B_ASP_46	NE2, B_GLN_42	HE22, B_GLN_42	2.89	2.02	23.36
1HGI.PDB	OG1, B_THR_107	NZ, B_LYS_51	HZ1, B_LYS_51	2.96	1.97	15.88
1HGI.PDB	OE1, B_GLU_103	NZ, B_LYS_51	HZ2, B_LYS_51	2.82	1.78	6.88
1HGI.PDB	ND1, B_HIS_106	NZ, B_LYS_51	HZ3, B_LYS_51	2.81	1.87	19.52
1HGI.PDB	OE1, B_GLU_57	NH1, B_ARG_54	HH11, B_ARG_54	2.86	1.87	11.02
1HGI.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.81	1.84	14.63
1HGI.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ1, B_LYS_62	2.67	1.78	25.75
1HGI.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.87	1.89	8.13
1HGI.PDB	OE2, B_GLU_85	NZ, B_LYS_68	HZ2, B_LYS_68	2.79	1.75	2.13
1HGI.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.86	1.89	7.04
1HGI.PDB	OE2, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.92	1.89	1.72
1HGI.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.71	1.72	8.42
1HGI.PDB	OE1, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.86	1.86	6.93
1HGI.PDB	OE1, B_GLU_74	NE2, B_GLN_78	HE22, B_GLN_78	2.94	1.97	8.23

1HGI.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.78	1.84	13.46
1HGI.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.65	1.64	9.94
1HGI.PDB	OE2, B_GLU_120	NH1, B_ARG_123	HH11, B_ARG_123	2.84	1.97	25.22
1HGI.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.81	1.96	23.50
1HGI.PDB	OE2, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.86	2.02	24.92
1HGI.PDB	OH, B_TYR_157	ND2, B_ASN_129	HD22, B_ASN_129	2.81	1.86	9.72
1HGI.PDB	OE2, B_GLU_150	ND2, B_ASN_154	HD21, B_ASN_154	2.84	2.01	27.47
1HGI.PDB	OD1, B_ASN_154	OG1, B_THR_156	HG1, B_THR_156	2.64	1.78	21.15
1HGI.PDB	OE2, B_GLU_131	NH1, B_ARG_170	HH11, B_ARG_170	2.77	1.77	6.54
1HGI.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.88	1.83	6.58
1HGI.PDB	OD2, C_ASP_275	NZ, C_LYS_50	HZ1, C_LYS_50	2.68	1.77	23.91
1HGI.PDB	OD1, C_ASP_73	ND1, C_HIS_75	HD1, C_HIS_75	2.88	1.94	15.46
1HGI.PDB	OD1, C_ASP_60	NE, C_ARG_90	HE, C_ARG_90	2.83	1.88	11.13
1HGI.PDB	OD2, C_ASP_60	NH2, C_ARG_90	HH21, C_ARG_90	2.77	1.79	11.02
1HGI.PDB	OD1, C_ASP_271	OG, C_SER_91	HG, C_SER_91	2.95	2.13	27.22
1HGI.PDB	OD2, C_ASP_271	OG, C_SER_91	HG, C_SER_91	2.83	1.94	19.64
1HGI.PDB	OD2, C_ASP_68	OG, C_SER_95	HG, C_SER_95	2.89	1.96	14.85
1HGI.PDB	OD1, C_ASP_68	OH, C_TYR_100	HH, C_TYR_100	2.94	1.99	10.92
1HGI.PDB	OD2, C_ASP_104	OG, C_SER_107	HG, C_SER_107	2.90	1.96	13.90
1HGI.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.82	1.84	15.02
1HGI.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.85	1.90	11.29
1HGI.PDB	OE2, C_GLU_119	OG1, C_THR_117	HG1, C_THR_117	2.95	2.03	14.67
1HGI.PDB	OD1, C_ASN_137	NZ, C_LYS_140	HZ2, C_LYS_140	2.83	1.83	12.62
1HGI.PDB	OD2, C_ASP_77	NE, C_ARG_141	HE, C_ARG_141	2.83	2.02	29.40
1HGI.PDB	OD1, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.93	2.01	20.50
1HGI.PDB	OD2, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.70	1.83	25.10
1HGI.PDB	OH, C_TYR_195	NE1, C_TRP_153	HE1, C_TRP_153	2.82	1.96	22.98
1HGI.PDB	OE2, C_GLU_123	NZ, C_LYS_176	HZ1, C_LYS_176	2.68	1.80	26.11
1HGI.PDB	OE1, C_GLU_123	OH, C_TYR_178	HH, C_TYR_178	2.75	1.80	7.25
1HGI.PDB	OG1, C_THR_235	NE1, C_TRP_180	HE1, C_TRP_180	2.84	1.86	3.22
1HGI.PDB	OG, C_SER_231	NE2, C_HIS_184	HE2, C_HIS_184	2.81	1.93	22.34
1HGI.PDB	OD1, C_ASN_250	NE2, C_GLN_191	HE21, C_GLN_191	2.86	1.91	10.94
1HGI.PDB	OD1, C_ASN_246	NH2, C_ARG_201	HH21, C_ARG_201	2.55	1.72	27.61
1HGI.PDB	OG1, C_THR_212	OG1, C_THR_203	HG1, C_THR_203	2.94	2.00	11.06
1HGI.PDB	OD2, C_ASP_241	NE, C_ARG_208	HE, C_ARG_208	2.92	2.01	19.66
1HGI.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.62	1.75	23.70
1HGI.PDB	OD1, C_ASP_101	OG, C_SER_231	HG, C_SER_231	2.97	2.02	12.14
1HGI.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.67	1.77	23.68
1HGI.PDB	OE1, C_GLN_191	ND2, C_ASN_250	HD21, C_ASN_250	2.87	1.92	11.00
1HGI.PDB	OE2, C_GLU_119	NH1, C_ARG_261	HH12, C_ARG_261	2.66	1.84	29.01
1HGI.PDB	OE1, C_GLU_119	NH2, C_ARG_261	HH22, C_ARG_261	2.84	1.99	27.78
1HGI.PDB	OD2, C_ASP_85	NZ, C_LYS_264	HZ3, C_LYS_264	2.83	1.86	17.28
1HGI.PDB	OE1, C_GLN_44	NZ, C_LYS_292	HZ1, C_LYS_292	2.75	1.75	12.02
1HGI.PDB	OD2, C_ASP_291	NZ, C_LYS_292	HZ3, C_LYS_292	2.82	1.90	23.36
1HGI.PDB	OD1, C_ASN_285	ND2, C_ASN_298	HD22, C_ASN_298	3.00	2.03	7.73
1HGI.PDB	OD1, D_ASP_86	NZ, C_LYS_310	HZ3, C_LYS_310	2.77	1.93	29.51
1HGI.PDB	OE1, C_GLU_41	NZ, C_LYS_315	HZ3, C_LYS_315	2.75	1.80	20.43
1HGI.PDB	OE2, C_GLU_35	ND2, C_ASN_322	HD22, C_ASN_322	2.90	1.95	11.70
1HGI.PDB	OE1, D_GLU_15	NZ, C_LYS_326	HZ1, C_LYS_326	2.83	1.84	16.25
1HGI.PDB	OE1, D_GLN_34	NE, D_ARG_25	HE, D_ARG_25	2.62	1.78	23.70
1HGI.PDB	OD1, D_ASN_146	ND2, D_ASN_28	HD21, D_ASN_28	2.93	1.98	12.39
1HGI.PDB	OD2, D_ASP_37	OG, D_SER_40	HG, D_SER_40	2.78	1.93	23.19
1HGI.PDB	OD1, D_ASP_46	NE2, D_GLN_42	HE22, D_GLN_42	2.88	2.01	23.38
1HGI.PDB	OE1, D_GLU_103	NZ, D_LYS_51	HZ2, D_LYS_51	2.81	1.77	5.89
1HGI.PDB	ND1, D_HIS_106	NZ, D_LYS_51	HZ3, D_LYS_51	2.78	1.83	18.78
1HGI.PDB	OE1, D_GLU_57	NH1, D_ARG_54	HH11, D_ARG_54	2.85	1.86	11.80
1HGI.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.81	1.85	15.40
1HGI.PDB	OE2, D_GLU_61	NZ, D_LYS_58	HZ2, D_LYS_58	3.00	2.01	17.14

1HGI.PDB	OG, C_SER.110	NE2, D_HIS.64	HE2, D_HIS.64	2.83	1.85	2.78
1HGI.PDB	OE2, D_GLU.85	NZ, D_LYS.68	HZ2, D_LYS.68	2.81	1.76	2.16
1HGI.PDB	OE2, F_GLU.81	NE, D_ARG.76	HE, D_ARG.76	2.80	1.82	5.40
1HGI.PDB	OE2, F_GLU.74	NH1, D_ARG.76	HH12, D_ARG.76	2.78	1.76	4.18
1HGI.PDB	OE1, F_GLU.81	NH2, D_ARG.76	HH21, D_ARG.76	2.61	1.67	15.38
1HGI.PDB	OE1, F_GLU.74	NH2, D_ARG.76	HH22, D_ARG.76	2.76	1.77	8.75
1HGI.PDB	OE1, D_GLU.74	NE2, D_GLN.78	HE22, D_GLN.78	2.92	1.95	8.47
1HGI.PDB	OE1, F_GLU.85	OH, D_TYR.83	HH, D_TYR.83	2.69	1.81	20.41
1HGI.PDB	OH, B_TYR.83	NZ, D_LYS.88	HZ1, D_LYS.88	2.66	1.64	7.30
1HGI.PDB	OE2, D_GLU.120	NH1, D_ARG.123	HH11, D_ARG.123	2.83	1.97	25.69
1HGI.PDB	OE1, B_GLU.132	NE, D_ARG.124	HE, D_ARG.124	2.84	1.98	23.95
1HGI.PDB	OE2, B_GLU.132	NE, D_ARG.124	HE, D_ARG.124	2.88	2.03	24.96
1HGI.PDB	OH, D_TYR.157	ND2, D_ASN.129	HD22, D_ASN.129	2.81	1.84	5.40
1HGI.PDB	OD1, D_ASN.154	OG1, D_THR.156	HG1, D_THR.156	2.68	1.79	17.62
1HGI.PDB	NE2, D_HIS.142	OH, D_TYR.157	HH, D_TYR.157	2.72	1.85	20.80
1HGI.PDB	OE2, D_GLU.131	NH1, D_ARG.170	HH11, D_ARG.170	2.77	1.78	6.80
1HGI.PDB	OE2, F_GLU.97	NZ, E_LYS.27	HZ1, E_LYS.27	2.86	1.82	7.44
1HGI.PDB	OD2, E_ASP.275	NZ, E_LYS.50	HZ1, E_LYS.50	2.70	1.78	22.89
1HGI.PDB	OD1, E_ASP.73	ND1, E_HIS.75	HD1, E_HIS.75	2.87	1.94	15.26
1HGI.PDB	OD1, E_ASP.60	NE, E_ARG.90	HE, E_ARG.90	2.89	1.92	8.33
1HGI.PDB	OD2, E_ASP.60	NH2, E_ARG.90	HH21, E_ARG.90	2.84	1.85	10.04
1HGI.PDB	OD1, E_ASP.271	OG, E_SER.91	HG, E_SER.91	2.94	2.11	26.21
1HGI.PDB	OD2, E_ASP.271	OG, E_SER.91	HG, E_SER.91	2.82	1.93	20.43
1HGI.PDB	OD2, E_ASP.68	OG, E_SER.95	HG, E_SER.95	2.90	1.96	13.54
1HGI.PDB	OD1, E_ASP.68	OH, E_TYR.100	HH, E_TYR.100	2.94	1.98	8.32
1HGI.PDB	OD2, E_ASP.104	OG, E_SER.107	HG, E_SER.107	2.91	1.98	14.52
1HGI.PDB	OE2, F_GLU.67	NH2, E_ARG.109	HH21, E_ARG.109	2.78	1.80	14.37
1HGI.PDB	OD2, D_ASP.79	OG, E_SER.110	HG, E_SER.110	2.90	1.94	10.08
1HGI.PDB	OE2, E_GLU.119	OG1, E_THR.117	HG1, E_THR.117	2.98	2.05	12.54
1HGI.PDB	OD1, E_ASN.137	NZ, E_LYS.140	HZ2, E_LYS.140	2.83	1.82	12.93
1HGI.PDB	OD2, E_ASP.77	NE, E_ARG.141	HE, E_ARG.141	2.83	2.01	29.05
1HGI.PDB	OD1, E_ASP.77	NH2, E_ARG.141	HH21, E_ARG.141	2.94	2.01	20.45
1HGI.PDB	OD2, E_ASP.77	NH2, E_ARG.141	HH21, E_ARG.141	2.70	1.83	24.80
1HGI.PDB	OD1, E_ASN.137	OG, E_SER.145	HG, E_SER.145	2.92	2.15	29.94
1HGI.PDB	OH, E_TYR.195	NE1, E_TRP.153	HE1, E_TRP.153	2.87	1.98	20.67
1HGI.PDB	OE2, E_GLU.123	NZ, E_LYS.176	HZ1, E_LYS.176	2.69	1.80	25.89
1HGI.PDB	OE1, E_GLU.123	OH, E_TYR.178	HH, E_TYR.178	2.77	1.82	8.27
1HGI.PDB	OG1, E_THR.235	NE1, E_TRP.180	HE1, E_TRP.180	2.85	1.87	2.03
1HGI.PDB	OG, E_SER.231	NE2, E_HIS.184	HE2, E_HIS.184	2.81	1.95	23.57
1HGI.PDB	OD1, E_ASN.250	NE2, E_GLN.191	HE21, E_GLN.191	2.93	1.97	10.64
1HGI.PDB	OD1, E_ASN.246	NH2, E_ARG.201	HH21, E_ARG.201	2.57	1.74	27.51
1HGI.PDB	OD2, E_ASP.241	NE, E_ARG.208	HE, E_ARG.208	2.98	2.07	19.52
1HGI.PDB	OE1, A_GLN.210	NH2, E_ARG.220	HH21, E_ARG.220	2.69	1.80	23.03
1HGI.PDB	OD1, E_ASP.101	OG, E_SER.231	HG, E_SER.231	2.99	2.05	12.53
1HGI.PDB	OE1, D_GLU.72	NZ, E_LYS.238	HZ3, E_LYS.238	2.80	1.81	15.90
1HGI.PDB	OE1, E_GLN.191	ND2, E_ASN.250	HD21, E_ASN.250	2.90	1.94	10.02
1HGI.PDB	OE2, E_GLU.119	NH1, E_ARG.261	HH12, E_ARG.261	2.65	1.83	28.50
1HGI.PDB	OE1, E_GLU.119	NH2, E_ARG.261	HH22, E_ARG.261	2.84	1.99	27.52
1HGI.PDB	OD2, E_ASP.85	NZ, E_LYS.264	HZ3, E_LYS.264	2.86	1.87	16.39
1HGI.PDB	OE1, E_GLN.44	NZ, E_LYS.292	HZ1, E_LYS.292	2.73	1.72	12.13
1HGI.PDB	OD2, E_ASP.291	NZ, E_LYS.292	HZ3, E_LYS.292	2.87	1.94	23.09
1HGI.PDB	OD1, E_ASN.285	ND2, E_ASN.298	HD22, E_ASN.298	2.97	2.00	7.97
1HGI.PDB	OD1, F_ASP.86	NZ, E_LYS.310	HZ3, E_LYS.310	2.76	1.91	29.16
1HGI.PDB	OE1, E_GLU.41	NZ, E_LYS.315	HZ3, E_LYS.315	2.74	1.81	21.50
1HGI.PDB	OE2, E_GLU.35	ND2, E_ASN.322	HD22, E_ASN.322	2.92	1.96	12.59
1HGI.PDB	OE1, F_GLU.15	NZ, E_LYS.326	HZ3, E_LYS.326	2.88	1.86	11.05
1HGI.PDB	OE1, F_GLN.34	NH2, F_ARG.25	HH21, F_ARG.25	2.91	1.98	18.85
1HGI.PDB	OD1, F_ASN.146	ND2, F_ASN.28	HD21, F_ASN.28	2.93	2.01	16.48

1HGI.PDB	OD2, F_ASP_37	OG, F_SER_40	HG, F_SER_40	2.76	1.92	24.70
1HGI.PDB	OD1, F_ASP_46	NE2, F_GLN_42	HE22, F_GLN_42	2.86	1.99	23.93
1HGI.PDB	OE1, F_GLU_103	NZ, F_LYS_51	HZ2, F_LYS_51	2.80	1.76	5.82
1HGI.PDB	ND1, F_HIS_106	NZ, F_LYS_51	HZ3, F_LYS_51	2.75	1.80	19.60
1HGI.PDB	OE1, F_GLU_57	NH1, F_ARG_54	HH11, F_ARG_54	2.83	1.84	11.68
1HGI.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.75	1.79	14.82
1HGI.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.84	1.87	3.62
1HGI.PDB	OE2, F_GLU_85	NZ, F_LYS_68	HZ2, F_LYS_68	2.74	1.72	8.70
1HGI.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.85	1.88	7.37
1HGI.PDB	OE2, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.77	1.76	3.93
1HGI.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.64	1.66	4.79
1HGI.PDB	OE1, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.76	1.78	10.40
1HGI.PDB	OE1, F_GLU_74	NE2, F_GLN_78	HE22, F_GLN_78	2.95	1.98	8.40
1HGI.PDB	OE1, B_GLU_85	OH, F_TYR_83	HH, F_TYR_83	2.58	1.75	24.06
1HGI.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.61	1.62	12.49
1HGI.PDB	OE2, F_GLU_120	NH1, F_ARG_123	HH11, F_ARG_123	2.81	1.95	25.91
1HGI.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.96	2.09	23.50
1HGI.PDB	OE2, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.96	2.09	23.34
1HGI.PDB	OH, F_TYR_157	ND2, F_ASN_129	HD22, F_ASN_129	2.81	1.86	11.53
1HGI.PDB	OE2, D_GLU_131	NH2, F_ARG_163	HH22, F_ARG_163	2.69	1.85	26.81
1HGI.PDB	OE2, F_GLU_131	NH1, F_ARG_170	HH11, F_ARG_170	2.75	1.76	6.67

Table 1736: 1HGI-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1HGJ.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.81	1.78	9.30
1HGJ.PDB	OD2, A_ASP_275	NZ, A_LYS_50	HZ1, A_LYS_50	2.74	1.82	22.91
1HGJ.PDB	OD1, A_ASP_73	ND1, A_HIS_75	HD1, A_HIS_75	2.83	1.91	17.40
1HGJ.PDB	OD1, A_ASP_60	NE, A_ARG_90	HE, A_ARG_90	2.88	1.91	7.56
1HGJ.PDB	OD2, A_ASP_60	NH2, A_ARG_90	HH21, A_ARG_90	2.81	1.82	10.05
1HGJ.PDB	OD1, A_ASP_271	OG, A_SER_91	HG, A_SER_91	2.98	2.13	24.27
1HGJ.PDB	OD2, A_ASP_271	OG, A_SER_91	HG, A_SER_91	2.78	1.90	20.01
1HGJ.PDB	OD2, A_ASP_68	OG, A_SER_95	HG, A_SER_95	2.95	2.05	19.19
1HGJ.PDB	OD2, A_ASP_104	OG, A_SER_107	HG, A_SER_107	2.84	1.95	18.85
1HGJ.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.75	1.77	12.07
1HGJ.PDB	OD2, F_ASP_79	OG, A_SER_110	HG, A_SER_110	2.94	1.98	10.39
1HGJ.PDB	OE2, A_GLU_119	OG1, A_THR_117	HG1, A_THR_117	2.87	1.94	12.44
1HGJ.PDB	OD1, A_ASN_137	NZ, A_LYS_140	HZ2, A_LYS_140	2.70	1.70	13.62
1HGJ.PDB	OD2, A_ASP_77	NE, A_ARG_141	HE, A_ARG_141	2.82	1.99	27.09
1HGJ.PDB	OD1, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.82	1.90	21.48
1HGJ.PDB	OD2, A_ASP_77	NH2, A_ARG_141	HH21, A_ARG_141	2.75	1.86	24.28
1HGJ.PDB	OH, A_TYR_195	NE1, A_TRP_153	HE1, A_TRP_153	2.85	1.94	18.91
1HGJ.PDB	OE2, A_GLU_123	NZ, A_LYS_176	HZ1, A_LYS_176	2.68	1.78	24.65
1HGJ.PDB	OE1, A_GLU_123	OH, A_TYR_178	HH, A_TYR_178	2.79	1.84	8.91
1HGJ.PDB	OG1, A_THR_235	NE1, A_TRP_180	HE1, A_TRP_180	2.92	1.93	4.44
1HGJ.PDB	OG, A_SER_231	NE2, A_HIS_184	HE2, A_HIS_184	2.75	1.92	26.36
1HGJ.PDB	OD1, A_ASN_246	NH2, A_ARG_201	HH21, A_ARG_201	2.58	1.73	25.49
1HGJ.PDB	OG1, A_THR_206	OG, A_SER_209	HG, A_SER_209	3.00	2.04	8.15
1HGJ.PDB	OG1, A_THR_203	OG1, A_THR_212	HG1, A_THR_212	2.89	1.93	3.12
1HGJ.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.67	1.78	22.50
1HGJ.PDB	OD1, A_ASP_101	OG, A_SER_231	HG, A_SER_231	2.87	1.91	9.73
1HGJ.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.90	1.90	13.91
1HGJ.PDB	OD1, A_ASN_165	ND2, A_ASN_246	HD22, A_ASN_246	2.91	1.95	11.26
1HGJ.PDB	OD1, A_ASN_133	NH2, A_ARG_255	HH22, A_ARG_255	2.53	1.70	27.52
1HGJ.PDB	OE2, A_GLU_119	NH1, A_ARG_261	HH12, A_ARG_261	2.65	1.82	28.35
1HGJ.PDB	OE1, A_GLU_119	NH2, A_ARG_261	HH22, A_ARG_261	2.90	1.99	23.18
1HGJ.PDB	OD2, A_ASP_85	NZ, A_LYS_264	HZ3, A_LYS_264	2.84	1.85	15.53
1HGJ.PDB	OE1, A_GLN_44	NZ, A_LYS_292	HZ1, A_LYS_292	2.71	1.70	11.30
1HGJ.PDB	OD2, A_ASP_291	NZ, A_LYS_292	HZ3, A_LYS_292	2.80	1.82	17.27
1HGJ.PDB	OE1, A_GLU_41	NZ, A_LYS_315	HZ3, A_LYS_315	2.85	1.90	20.12
1HGJ.PDB	OE2, A_GLU_35	ND2, A_ASN_322	HD22, A_ASN_322	2.88	1.99	20.96
1HGJ.PDB	OE1, A_GLU_325	NZ, A_LYS_326	HZ3, A_LYS_326	2.92	1.93	15.95
1HGJ.PDB	OE1, B_GLN_34	NE, B_ARG_25	HE, B_ARG_25	2.57	1.79	29.34
1HGJ.PDB	OE2, A_GLU_325	NH2, B_ARG_25	HH22, B_ARG_25	2.97	2.01	15.94
1HGJ.PDB	OD1, B_ASP_46	NE2, B_GLN_42	HE22, B_GLN_42	2.81	1.92	21.14
1HGJ.PDB	OE2, B_GLU_114	NE2, B_GLN_47	HE21, B_GLN_47	2.96	2.05	17.93
1HGJ.PDB	OG1, B_THR_107	NZ, B_LYS_51	HZ1, B_LYS_51	2.96	1.99	17.76
1HGJ.PDB	OE1, B_GLU_103	NZ, B_LYS_51	HZ2, B_LYS_51	2.78	1.74	6.16
1HGJ.PDB	ND1, B_HIS_106	NZ, B_LYS_51	HZ3, B_LYS_51	2.79	1.82	16.46
1HGJ.PDB	OE1, B_GLU_57	NH1, B_ARG_54	HH11, B_ARG_54	2.87	1.87	9.43
1HGJ.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.77	1.81	15.09
1HGJ.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ1, B_LYS_62	2.65	1.75	23.55
1HGJ.PDB	OD2, F_ASP_90	NZ, B_LYS_62	HZ3, B_LYS_62	2.74	1.89	28.52
1HGJ.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.89	1.93	11.21
1HGJ.PDB	OE2, B_GLU_85	NZ, B_LYS_68	HZ2, B_LYS_68	2.78	1.76	8.72
1HGJ.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.90	1.93	10.80
1HGJ.PDB	OE2, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.88	1.87	5.28
1HGJ.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.72	1.72	3.64
1HGJ.PDB	OE1, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.85	1.84	3.19
1HGJ.PDB	OE1, B_GLU_74	NE2, B_GLN_78	HE22, B_GLN_78	2.90	1.95	12.93
1HGJ.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.67	1.83	24.12
1HGJ.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.78	1.75	7.42

1HGJ.PDB	OE2, B_GLU_120	NH1, B_ARG_123	HH11, B_ARG_123	2.74	1.86	23.95
1HGJ.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.82	2.00	27.29
1HGJ.PDB	OE2, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.91	2.02	20.91
1HGJ.PDB	OH, B_TYR_157	ND2, B_ASN_129	HD22, B_ASN_129	2.77	1.84	15.18
1HGJ.PDB	OE2, B_GLU_150	ND2, B_ASN_154	HD21, B_ASN_154	2.81	2.00	28.55
1HGJ.PDB	OD1, B_ASN_154	OG1, B_THR_156	HG1, B_THR_156	2.67	1.80	19.98
1HGJ.PDB	OE2, B_GLU_131	NH1, B_ARG_170	HH11, B_ARG_170	2.80	1.80	6.39
1HGJ.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.82	1.80	8.63
1HGJ.PDB	OD2, C_ASP_275	NZ, C_LYS_50	HZ1, C_LYS_50	2.74	1.82	22.76
1HGJ.PDB	OD1, C_ASP_73	ND1, C_HIS_75	HD1, C_HIS_75	2.80	1.89	17.49
1HGJ.PDB	OD1, C_ASP_60	NE, C_ARG_90	HE, C_ARG_90	2.88	1.91	9.03
1HGJ.PDB	OD2, C_ASP_60	NH2, C_ARG_90	HH21, C_ARG_90	2.78	1.79	9.66
1HGJ.PDB	OD1, C_ASP_271	OG, C_SER_91	HG, C_SER_91	2.99	2.16	26.38
1HGJ.PDB	OD2, C_ASP_271	OG, C_SER_91	HG, C_SER_91	2.81	1.92	18.67
1HGJ.PDB	OD2, C_ASP_68	OG, C_SER_95	HG, C_SER_95	2.93	1.99	14.68
1HGJ.PDB	OD1, C_ASP_68	OH, C_TYR_100	HH, C_TYR_100	2.88	1.95	14.58
1HGJ.PDB	OD2, C_ASP_104	OG, C_SER_107	HG, C_SER_107	2.90	1.99	17.96
1HGJ.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.76	1.78	13.33
1HGJ.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.79	1.87	14.95
1HGJ.PDB	OE2, C_GLU_119	OG1, C_THR_117	HG1, C_THR_117	2.88	1.94	11.85
1HGJ.PDB	OD1, C_ASN_137	NZ, C_LYS_140	HZ2, C_LYS_140	2.71	1.72	13.24
1HGJ.PDB	OD2, C_ASP_77	NE, C_ARG_141	HE, C_ARG_141	2.82	1.99	27.42
1HGJ.PDB	OD1, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.81	1.89	21.37
1HGJ.PDB	OD2, C_ASP_77	NH2, C_ARG_141	HH21, C_ARG_141	2.74	1.86	24.47
1HGJ.PDB	OD1, C_ASN_137	OG, C_SER_145	HG, C_SER_145	2.92	2.08	24.33
1HGJ.PDB	OH, C_TYR_195	NE1, C_TRP_153	HE1, C_TRP_153	2.84	1.96	21.72
1HGJ.PDB	OE2, C_GLU_123	NZ, C_LYS_176	HZ1, C_LYS_176	2.69	1.80	24.96
1HGJ.PDB	OE1, C_GLU_123	OH, C_TYR_178	HH, C_TYR_178	2.77	1.82	8.51
1HGJ.PDB	OG1, C_THR_235	NE1, C_TRP_180	HE1, C_TRP_180	2.91	1.92	4.72
1HGJ.PDB	OG, C_SER_231	NE2, C_HIS_184	HE2, C_HIS_184	2.74	1.91	26.34
1HGJ.PDB	OD1, C_ASN_250	NE2, C_GLN_191	HE21, C_GLN_191	2.99	2.02	8.22
1HGJ.PDB	OD1, C_ASN_246	NH2, C_ARG_201	HH21, C_ARG_201	2.59	1.74	25.86
1HGJ.PDB	OG1, C_THR_212	OG1, C_THR_203	HG1, C_THR_203	2.89	1.94	9.95
1HGJ.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.66	1.82	26.85
1HGJ.PDB	OD1, C_ASP_101	OG, C_SER_231	HG, C_SER_231	2.91	1.95	9.37
1HGJ.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.75	1.79	18.67
1HGJ.PDB	OD1, C_ASN_165	ND2, C_ASN_246	HD22, C_ASN_246	2.89	1.93	12.15
1HGJ.PDB	OD1, C_ASN_133	NH2, C_ARG_255	HH22, C_ARG_255	2.54	1.71	27.08
1HGJ.PDB	OE2, C_GLU_119	NH1, C_ARG_261	HH12, C_ARG_261	2.65	1.83	28.56
1HGJ.PDB	OE1, C_GLU_119	NH2, C_ARG_261	HH22, C_ARG_261	2.92	2.03	23.97
1HGJ.PDB	OD2, C_ASP_85	NZ, C_LYS_264	HZ3, C_LYS_264	2.82	1.83	14.94
1HGJ.PDB	OE1, C_GLN_44	NZ, C_LYS_292	HZ1, C_LYS_292	2.73	1.72	10.59
1HGJ.PDB	OD2, C_ASP_291	NZ, C_LYS_292	HZ3, C_LYS_292	2.82	1.84	16.66
1HGJ.PDB	OD1, D_ASP_86	NZ, C_LYS_310	HZ3, C_LYS_310	2.94	2.10	29.37
1HGJ.PDB	OE1, C_GLU_41	NZ, C_LYS_315	HZ3, C_LYS_315	2.86	1.91	20.22
1HGJ.PDB	OE2, C_GLU_35	ND2, C_ASN_322	HD22, C_ASN_322	2.88	1.97	19.99
1HGJ.PDB	OE1, D_GLU_15	NZ, C_LYS_326	HZ1, C_LYS_326	2.91	1.86	5.48
1HGJ.PDB	OE1, D_GLN_34	NE, D_ARG_25	HE, D_ARG_25	2.65	1.80	23.08
1HGJ.PDB	OD1, D_ASN_146	ND2, D_ASN_28	HD21, D_ASN_28	2.98	2.03	11.81
1HGJ.PDB	OD2, D_ASP_37	OG, D_SER_40	HG, D_SER_40	2.82	1.96	22.49
1HGJ.PDB	OD1, D_ASP_46	NE2, D_GLN_42	HE22, D_GLN_42	2.81	1.92	21.12
1HGJ.PDB	OE2, D_GLU_114	NE2, D_GLN_47	HE21, D_GLN_47	2.94	2.03	18.44
1HGJ.PDB	OG1, D_THR_107	NZ, D_LYS_51	HZ1, D_LYS_51	2.97	1.99	16.18
1HGJ.PDB	OE1, D_GLU_103	NZ, D_LYS_51	HZ2, D_LYS_51	2.80	1.76	6.89
1HGJ.PDB	ND1, D_HIS_106	NZ, D_LYS_51	HZ3, D_LYS_51	2.79	1.82	16.80
1HGJ.PDB	OE1, D_GLU_57	NH1, D_ARG_54	HH11, D_ARG_54	2.87	1.86	9.17
1HGJ.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.84	1.88	15.58
1HGJ.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.89	1.91	5.59

1HGJ.PDB	OE2, D_GLU_85	NZ, D_LYS_68	HZ2, D_LYS_68	2.82	1.80	11.23
1HGJ.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.85	1.89	10.87
1HGJ.PDB	OE2, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.76	1.76	7.89
1HGJ.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.68	1.69	5.65
1HGJ.PDB	OE1, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.71	1.72	5.59
1HGJ.PDB	OE1, D_GLU_74	NE2, D_GLN_78	HE22, D_GLN_78	2.88	1.94	14.79
1HGJ.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.63	1.81	25.72
1HGJ.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.75	1.72	7.31
1HGJ.PDB	OE2, D_GLU_120	NH1, D_ARG_123	HH11, D_ARG_123	2.74	1.85	23.39
1HGJ.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.80	1.98	27.33
1HGJ.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.87	2.00	21.99
1HGJ.PDB	OH, B_TYR_141	NH1, D_ARG_127	HH12, D_ARG_127	2.99	2.02	12.89
1HGJ.PDB	OH, D_TYR_157	ND2, D_ASN_129	HD22, D_ASN_129	2.79	1.84	10.20
1HGJ.PDB	OD1, D_ASN_154	OG1, D_THR_156	HG1, D_THR_156	2.71	1.81	16.75
1HGJ.PDB	NE2, D_HIS_142	OH, D_TYR_157	HH, D_TYR_157	2.78	1.88	18.06
1HGJ.PDB	OE2, D_GLU_131	NH1, D_ARG_170	HH11, D_ARG_170	2.79	1.80	6.55
1HGJ.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.81	1.79	8.50
1HGJ.PDB	OD2, E_ASP_275	NZ, E_LYS_50	HZ1, E_LYS_50	2.74	1.82	22.90
1HGJ.PDB	OD1, E_ASP_73	ND1, E_HIS_75	HD1, E_HIS_75	2.80	1.88	17.19
1HGJ.PDB	OD1, E_ASP_60	NE, E_ARG_90	HE, E_ARG_90	2.91	1.94	8.87
1HGJ.PDB	OD2, E_ASP_60	NH2, E_ARG_90	HH21, E_ARG_90	2.83	1.83	8.62
1HGJ.PDB	OD1, E_ASP_271	OG, E_SER_91	HG, E_SER_91	2.99	2.15	25.95
1HGJ.PDB	OD2, E_ASP_271	OG, E_SER_91	HG, E_SER_91	2.82	1.92	18.47
1HGJ.PDB	OD2, E_ASP_68	OG, E_SER_95	HG, E_SER_95	2.94	2.00	13.81
1HGJ.PDB	OD1, E_ASP_68	OH, E_TYR_100	HH, E_TYR_100	2.88	1.94	12.28
1HGJ.PDB	OD2, E_ASP_104	OG, E_SER_107	HG, E_SER_107	2.85	1.94	18.67
1HGJ.PDB	OE2, F_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.76	1.77	12.82
1HGJ.PDB	OD2, D_ASP_79	OG, E_SER_110	HG, E_SER_110	2.79	1.87	15.96
1HGJ.PDB	OE2, E_GLU_119	OG1, E_THR_117	HG1, E_THR_117	2.91	1.96	10.96
1HGJ.PDB	OD1, E_ASN_137	NZ, E_LYS_140	HZ2, E_LYS_140	2.71	1.72	13.56
1HGJ.PDB	OD2, E_ASP_77	NE, E_ARG_141	HE, E_ARG_141	2.84	2.00	27.31
1HGJ.PDB	OD1, E_ASP_77	NH2, E_ARG_141	HH21, E_ARG_141	2.84	1.92	21.35
1HGJ.PDB	OD2, E_ASP_77	NH2, E_ARG_141	HH21, E_ARG_141	2.75	1.86	24.32
1HGJ.PDB	OD1, E_ASN_137	OG, E_SER_145	HG, E_SER_145	2.96	2.12	24.46
1HGJ.PDB	OH, E_TYR_195	NE1, E_TRP_153	HE1, E_TRP_153	2.83	1.93	19.26
1HGJ.PDB	OE2, E_GLU_123	NZ, E_LYS_176	HZ1, E_LYS_176	2.69	1.80	25.95
1HGJ.PDB	OE1, E_GLU_123	OH, E_TYR_178	HH, E_TYR_178	2.77	1.83	11.08
1HGJ.PDB	OG1, E_THR_235	NE1, E_TRP_180	HE1, E_TRP_180	2.94	1.96	4.45
1HGJ.PDB	OG, E_SER_231	NE2, E_HIS_184	HE2, E_HIS_184	2.75	1.92	26.56
1HGJ.PDB	OD1, E_ASN_246	NH2, E_ARG_201	HH21, E_ARG_201	2.59	1.74	26.30
1HGJ.PDB	OG1, E_THR_212	OG1, E_THR_203	HG1, E_THR_203	2.93	1.99	12.00
1HGJ.PDB	OD1, C_ASP_101	NE2, E_GLN_210	HE22, E_GLN_210	2.94	2.10	26.45
1HGJ.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.69	1.86	28.41
1HGJ.PDB	OD1, E_ASP_101	OG, E_SER_231	HG, E_SER_231	2.90	1.95	11.36
1HGJ.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ3, E_LYS_238	2.87	1.86	13.82
1HGJ.PDB	OD1, E_ASN_165	ND2, E_ASN_246	HD22, E_ASN_246	2.89	1.94	11.88
1HGJ.PDB	OD1, E_ASN_133	NH2, E_ARG_255	HH22, E_ARG_255	2.55	1.71	26.62
1HGJ.PDB	OE2, E_GLU_119	NH1, E_ARG_261	HH12, E_ARG_261	2.65	1.82	28.15
1HGJ.PDB	OE1, E_GLU_119	NH2, E_ARG_261	HH22, E_ARG_261	2.91	2.01	23.66
1HGJ.PDB	OD2, E_ASP_85	NZ, E_LYS_264	HZ3, E_LYS_264	2.86	1.86	15.01
1HGJ.PDB	OE1, E_GLN_44	NZ, E_LYS_292	HZ1, E_LYS_292	2.72	1.70	10.33
1HGJ.PDB	OD2, E_ASP_291	NZ, E_LYS_292	HZ3, E_LYS_292	2.83	1.86	17.49
1HGJ.PDB	OD1, F_ASP_86	NZ, E_LYS_310	HZ3, E_LYS_310	2.93	2.08	29.22
1HGJ.PDB	OE1, E_GLU_41	NZ, E_LYS_315	HZ3, E_LYS_315	2.86	1.91	20.65
1HGJ.PDB	OE2, E_GLU_35	ND2, E_ASN_322	HD22, E_ASN_322	2.86	1.96	20.74
1HGJ.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.87	1.86	12.83
1HGJ.PDB	OE1, F_GLN_34	NE, F_ARG_25	HE, F_ARG_25	2.86	2.05	28.42
1HGJ.PDB	OE1, F_GLN_34	NH2, F_ARG_25	HH21, F_ARG_25	2.64	1.73	20.69

1HGJ.PDB	OD1, F_ASN_146	ND2, F_ASN_28	HD21, F_ASN_28	2.81	1.89	16.64
1HGJ.PDB	OD2, F_ASP_37	OG, F_SER_40	HG, F_SER_40	2.80	1.95	24.06
1HGJ.PDB	OD1, F_ASP_46	NE2, F_GLN_42	HE22, F_GLN_42	2.80	1.92	21.18
1HGJ.PDB	OE2, F_GLU_114	NE2, F_GLN_47	HE21, F_GLN_47	2.95	2.04	18.06
1HGJ.PDB	OE1, F_GLU_103	NZ, F_LYS_51	HZ2, F_LYS_51	2.79	1.75	5.77
1HGJ.PDB	ND1, F_HIS_106	NZ, F_LYS_51	HZ3, F_LYS_51	2.75	1.79	17.21
1HGJ.PDB	OE1, F_GLU_57	NH1, F_ARG_54	HH11, F_ARG_54	2.86	1.86	9.70
1HGJ.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.77	1.81	14.54
1HGJ.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.90	1.93	7.02
1HGJ.PDB	OE2, F_GLU_85	NZ, F_LYS_68	HZ2, F_LYS_68	2.74	1.77	18.09
1HGJ.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.85	1.89	12.57
1HGJ.PDB	OE2, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.70	1.70	4.55
1HGJ.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.65	1.66	2.84
1HGJ.PDB	OE1, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.72	1.73	7.95
1HGJ.PDB	OE1, F_GLU_74	NE2, F_GLN_78	HE22, F_GLN_78	2.92	1.97	13.10
1HGJ.PDB	OE1, B_GLU_85	OH, F_TYR_83	HH, F_TYR_83	2.53	1.75	28.54
1HGJ.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.70	1.68	8.19
1HGJ.PDB	OE2, F_GLU_120	NH1, F_ARG_123	HH11, F_ARG_123	2.73	1.86	24.44
1HGJ.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.92	2.09	27.65
1HGJ.PDB	OE2, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.96	2.06	20.98
1HGJ.PDB	OH, F_TYR_157	ND2, F_ASN_129	HD22, F_ASN_129	2.75	1.85	17.65
1HGJ.PDB	OE2, F_GLU_131	NH1, F_ARG_170	HH11, F_ARG_170	2.79	1.80	6.77

Table 1737: 1HGJ-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1OSP.PDB	OE1, L_GLN_89	OH, L_TYR_36	HH, L_TYR_36	2.81	1.86	10.05
1OSP.PDB	OG1, L_THR_97	NE2, L_GLN_90	HE22, L_GLN_90	3.00	2.06	15.72
1OSP.PDB	OE1, L_GLU_105	OH, L_TYR_140	HH, L_TYR_140	2.90	2.03	21.23
1OSP.PDB	OG, L_SER_177	NE1, L_TRP_148	HE1, L_TRP_148	2.94	1.97	6.03
1OSP.PDB	OG, L_SER_131	OG1, L_THR_180	HG1, L_THR_180	2.85	1.92	11.66
1OSP.PDB	OD2, L_ASP_110	NZ, L_LYS_199	HZ3, L_LYS_199	2.64	1.82	29.88
1OSP.PDB	OD1, H_ASN_83	OG1, H_THR_17	HG1, H_THR_17	2.79	1.95	24.49
1OSP.PDB	OE1, H_GLU_46	NH1, H_ARG_38	HH11, H_ARG_38	2.77	1.80	9.20
1OSP.PDB	OH, H_TYR_93	NH2, H_ARG_38	HH21, H_ARG_38	2.83	1.87	12.82
1OSP.PDB	OD1, H_ASP_89	NH2, H_ARG_38	HH22, H_ARG_38	2.83	1.91	19.07
1OSP.PDB	OD2, L_ASP_1	OG, H_SER_62	HG, H_SER_62	2.98	2.17	26.53
1OSP.PDB	OG, H_SER_186	NE1, H_TRP_161	HE1, H_TRP_161	2.94	1.96	6.92
1OSP.PDB	OG, L_SER_176	OG, H_SER_185	HG, H_SER_185	2.74	1.91	24.72
1OSP.PDB	OG, H_SER_209	ND1, H_HIS_206	HD1, H_HIS_206	2.73	1.88	25.05
1OSP.PDB	OE1, L_GLU_123	NZ, H_LYS_215	HZ2, H_LYS_215	2.78	1.85	20.53
1OSP.PDB	OD1, O_ASP_33	NZ, O_LYS_39	HZ2, O_LYS_39	2.81	1.85	17.76
1OSP.PDB	OG1, O_THR_143	NH1, O_ARG_139	HH11, O_ARG_139	2.73	1.78	14.74
1OSP.PDB	OE2, O_GLU_160	NH2, O_ARG_139	HH22, O_ARG_139	2.96	2.05	19.95
1OSP.PDB	OE1, O_GLU_160	NZ, O_LYS_189	HZ1, O_LYS_189	2.95	1.93	9.44
1OSP.PDB	OG, O_SER_198	ND2, O_ASN_190	HD22, O_ASN_190	2.97	2.02	11.75
1OSP.PDB	OD1, O_ASP_234	OG1, O_THR_224	HG1, O_THR_224	2.71	1.92	27.50
1OSP.PDB	OD1, O_ASP_234	OH, O_TYR_248	HH, O_TYR_248	2.73	1.90	24.06

Table 1738: 1OSP-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1PSK.PDB	OG, L_SER_176	NE1, L_TRP_147	HE1, L_TRP_147	2.73	1.78	10.14
1PSK.PDB	OD1, L_ASN_160	OG, L_SER_176	HG, L_SER_176	2.79	1.87	14.99
1PSK.PDB	NE1, H_TRP_47	ND1, H_HIS_35	HD1, H_HIS_35	2.92	2.03	20.19
1PSK.PDB	OG1, H_THR_78	OG, H_SER_76	HG, H_SER_76	2.94	2.03	16.27
1PSK.PDB	OH, H_TYR_27	OG, H_SER_98	HG, H_SER_98	2.95	2.06	19.06

Table 1739: 1PSK-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1R21-1.PDB	OG1, A_THR_69	ND2, A_ASN_62	HD21, A_ASN_62	2.86	1.99	21.79
1R21-10.PDB	OG1, A_THR_69	ND2, A_ASN_62	HD21, A_ASN_62	2.90	2.06	25.22
1R21-11.PDB	OG, A_SER_64	ND2, A_ASN_62	HD22, A_ASN_62	2.35	1.48	21.77
1R21-12.PDB	OD1, A_ASN_67	OG1, A_THR_66	HG1, A_THR_66	2.34	1.38	3.67
1R21-13.PDB	OG1, A_THR_69	ND2, A_ASN_62	HD22, A_ASN_62	2.50	1.62	19.65
1R21-13.PDB	OH, A_TYR_97	ND2, A_ASN_99	HD21, A_ASN_99	2.51	1.54	7.69
1R21-14.PDB	OG1, A_THR_69	ND2, A_ASN_62	HD21, A_ASN_62	2.52	1.57	12.09
1R21-14.PDB	OE1, A_GLU_57	NE, A_ARG_81	HE, A_ARG_81	2.82	2.02	29.06
1R21-14.PDB	OE2, A_GLU_57	NH2, A_ARG_81	HH21, A_ARG_81	2.46	1.50	12.90
1R21-14.PDB	OH, A_TYR_97	ND2, A_ASN_99	HD22, A_ASN_99	2.66	1.70	8.32
1R21-16.PDB	OE1, A_GLU_57	NE, A_ARG_81	HE, A_ARG_81	2.43	1.60	25.79
1R21-17.PDB	ND2, A_ASN_99	NE, A_ARG_5	HE, A_ARG_5	2.79	1.84	10.87
1R21-17.PDB	OG, A_SER_94	OG1, A_THR_89	HG1, A_THR_89	2.85	1.94	16.35
1R21-18.PDB	OD1, A_ASN_67	OG1, A_THR_66	HG1, A_THR_66	2.60	1.66	10.07
1R21-18.PDB	OE2, A_GLU_100	NE2, A_HIS_84	HE2, A_HIS_84	2.44	1.60	25.14
1R21-19.PDB	OE2, A_GLU_34	NE2, A_GLN_47	HE21, A_GLN_47	2.80	1.93	22.82
1R21-19.PDB	OG1, A_THR_69	ND2, A_ASN_62	HD21, A_ASN_62	2.83	2.03	29.57
1R21-2.PDB	OE2, A_GLU_34	NE2, A_GLN_47	HE21, A_GLN_47	2.62	1.65	7.42
1R21-2.PDB	OG1, A_THR_69	ND2, A_ASN_62	HD21, A_ASN_62	2.81	1.92	20.56
1R21-2.PDB	OG, A_SER_64	ND2, A_ASN_62	HD22, A_ASN_62	2.42	1.53	18.22
1R21-2.PDB	OG, A_SER_94	OG1, A_THR_89	HG1, A_THR_89	2.98	2.02	6.58
1R21-2.PDB	OD2, A_ASP_16	NH1, A_ARG_96	HH12, A_ARG_96	2.71	1.87	26.03
1R21-22.PDB	OG, A_SER_64	ND2, A_ASN_62	HD22, A_ASN_62	2.37	1.45	16.21
1R21-23.PDB	OE1, A_GLU_57	NE, A_ARG_81	HE, A_ARG_81	2.65	1.70	11.54
1R21-3.PDB	OD1, A_ASP_16	NE2, A_HIS_19	HE2, A_HIS_19	2.71	1.85	23.51
1R21-3.PDB	OE2, A_GLU_34	NE2, A_GLN_47	HE22, A_GLN_47	2.72	1.92	29.24
1R21-3.PDB	OG1, A_THR_69	ND2, A_ASN_62	HD21, A_ASN_62	2.87	2.01	23.40
1R21-4.PDB	OD1, A_ASN_67	OG1, A_THR_66	HG1, A_THR_66	2.40	1.45	5.76
1R21-4.PDB	OE1, A_GLU_57	NE, A_ARG_81	HE, A_ARG_81	2.76	1.87	19.46
1R21-4.PDB	OE1, A_GLU_57	NH2, A_ARG_81	HH21, A_ARG_81	2.93	2.10	27.48
1R21-5.PDB	OG1, A_THR_69	ND2, A_ASN_62	HD22, A_ASN_62	2.62	1.75	21.48
1R21-6.PDB	OG1, A_THR_69	ND2, A_ASN_62	HD21, A_ASN_62	2.81	1.95	22.23
1R21-6.PDB	OD1, A_ASN_67	OG1, A_THR_66	HG1, A_THR_66	2.30	1.42	18.29
1R21-7.PDB	OD1, A_ASN_67	OG1, A_THR_66	HG1, A_THR_66	2.91	2.05	21.54
1R21-9.PDB	OG1, A_THR_69	ND2, A_ASN_62	HD21, A_ASN_62	2.59	1.65	13.02

Table 1740: 1R21-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1VFB.PDB	OE1, A_GLN_89	OH, A_TYR_36	HH, A_TYR_36	2.84	2.00	25.31
1VFB.PDB	OD2, A_ASP_82	NE, A_ARG_61	HE, A_ARG_61	2.88	1.96	15.15
1VFB.PDB	OD1, A_ASP_82	NH2, A_ARG_61	HH21, A_ARG_61	2.85	1.87	9.42
1VFB.PDB	OE1, B_GLU_98	NH1, A_ARG_96	HH12, A_ARG_96	2.82	1.84	8.38
1VFB.PDB	OE2, B_GLU_98	NH2, A_ARG_96	HH22, A_ARG_96	2.81	1.85	10.74
1VFB.PDB	OG, B_SER_28	OG1, B_THR_30	HG1, B_THR_30	2.97	2.08	19.82
1VFB.PDB	OE1, B_GLU_98	ND2, B_ASN_35	HD21, B_ASN_35	2.85	2.00	23.37
1VFB.PDB	OD1, B_ASP_89	NH1, B_ARG_38	HH12, B_ARG_38	3.00	2.07	17.31
1VFB.PDB	OE1, A_GLN_38	NE2, B_GLN_39	HE21, B_GLN_39	2.95	1.98	8.04
1VFB.PDB	OD1, B_ASN_35	NE1, B_TRP_47	HE1, B_TRP_47	2.80	1.83	5.78
1VFB.PDB	OD2, B_ASP_89	NH1, B_ARG_66	HH12, B_ARG_66	2.89	1.97	19.13
1VFB.PDB	OD1, B_ASP_89	NH2, B_ARG_66	HH22, B_ARG_66	2.93	1.93	3.85
1VFB.PDB	OD1, B_ASN_73	NZ, B_LYS_71	HZ1, B_LYS_71	2.93	2.08	28.65
1VFB.PDB	OG, B_SER_70	NZ, B_LYS_81	HZ2, B_LYS_81	2.92	2.05	26.58
1VFB.PDB	OD1, B_ASN_83	OG, B_SER_84	HG, B_SER_84	2.99	2.04	8.51
1VFB.PDB	OD1, B_ASP_104	NE, B_ARG_97	HE, B_ARG_97	2.99	2.02	4.50
1VFB.PDB	OD2, B_ASP_104	NH2, B_ARG_97	HH21, B_ARG_97	2.86	1.87	3.52
1VFB.PDB	OG1, C_THR_89	NE2, C_HIS_15	HE2, C_HIS_15	2.84	1.94	19.37
1VFB.PDB	OE1, C_GLN_41	OG1, C_THR_40	HG1, C_THR_40	2.88	1.98	18.75
1VFB.PDB	OG1, C_THR_69	OG, C_SER_60	HG, C_SER_60	2.78	1.84	10.98
1VFB.PDB	OD1, C_ASN_27	NE1, C_TRP_111	HE1, C_TRP_111	2.95	2.01	14.04
1VFB.PDB	OE1, C_GLN_121	NH1, C_ARG_125	HH11, C_ARG_125	2.96	2.02	16.36

Table 1741: 1VFB-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
2MKL-1.PDB	OXT, C_ALA_105	NZ, C_LYS_13	HZ3, C_LYS_13	2.65	1.63	10.83
2MKL-1.PDB	OD1, C_ASP_80	OG1, C_THR_21	HG1, C_THR_21	2.65	1.79	22.35
2MKL-1.PDB	OD2, C_ASP_80	NE2, C_GLN_22	HE21, C_GLN_22	2.86	1.96	18.61
2MKL-1.PDB	OG, C_SER_34	NZ, C_LYS_65	HZ2, C_LYS_65	2.81	1.84	16.47
2MKL-1.PDB	OE1, C_GLU_78	OG1, C_THR_83	HG1, C_THR_83	2.66	1.70	8.48
2MKL-1.PDB	OD1, C_ASP_80	NZ, C_LYS_104	HZ1, C_LYS_104	2.72	1.78	20.43
2MKL-10.PDB	OE2, C_GLU_90	NZ, C_LYS_40	HZ2, C_LYS_40	2.58	1.67	23.06
2MKL-10.PDB	OG, C_SER_62	OG1, C_THR_67	HG1, C_THR_67	2.83	1.88	6.13
2MKL-10.PDB	OXT, C_ALA_105	NZ, C_LYS_104	HZ3, C_LYS_104	2.68	1.72	17.77
2MKL-2.PDB	OXT, C_ALA_105	NZ, C_LYS_13	HZ3, C_LYS_13	2.61	1.67	20.57
2MKL-2.PDB	OD1, C_ASP_35	OG, C_SER_34	HG, C_SER_34	2.77	1.81	5.76
2MKL-2.PDB	OH, C_TYR_85	NH1, C_ARG_50	HH11, C_ARG_50	2.66	1.70	14.67
2MKL-2.PDB	OE2, C_GLU_78	NH1, C_ARG_50	HH12, C_ARG_50	2.73	1.79	17.34
2MKL-2.PDB	OE1, C_GLU_55	NZ, C_LYS_71	HZ1, C_LYS_71	2.72	1.71	11.97
2MKL-2.PDB	OD1, C_ASN_46	OG1, C_THR_83	HG1, C_THR_83	2.72	1.91	26.52
2MKL-3.PDB	OE1, C_GLU_93	NH1, C_ARG_3	HH12, C_ARG_3	2.68	1.70	11.24
2MKL-3.PDB	OXT, C_ALA_105	NZ, C_LYS_13	HZ1, C_LYS_13	2.67	1.72	19.52
2MKL-3.PDB	OG, C_SER_34	NZ, C_LYS_65	HZ3, C_LYS_65	2.80	1.76	6.92
2MKL-3.PDB	OE2, C_GLU_55	NZ, C_LYS_71	HZ1, C_LYS_71	2.64	1.59	1.73
2MKL-3.PDB	OG1, C_THR_26	NZ, C_LYS_71	HZ3, C_LYS_71	2.86	1.95	23.23
2MKL-3.PDB	OD1, C_ASN_46	OG1, C_THR_83	HG1, C_THR_83	2.91	1.97	11.57
2MKL-3.PDB	OD1, C_ASP_80	NZ, C_LYS_104	HZ2, C_LYS_104	2.61	1.56	1.39
2MKL-4.PDB	OE1, C_GLU_17	NE1, C_TRP_20	HE1, C_TRP_20	2.69	1.70	6.61
2MKL-4.PDB	OE1, C_GLU_37	ND2, C_ASN_38	HD21, C_ASN_38	2.75	1.84	18.89
2MKL-4.PDB	OE1, C_GLU_84	ND2, C_ASN_46	HD21, C_ASN_46	2.79	1.87	17.49
2MKL-4.PDB	OH, C_TYR_85	NE, C_ARG_50	HE, C_ARG_50	2.95	2.07	22.98
2MKL-4.PDB	OE1, C_GLU_78	NH2, C_ARG_50	HH21, C_ARG_50	2.70	1.74	15.78
2MKL-4.PDB	OE2, C_GLU_55	NZ, C_LYS_71	HZ1, C_LYS_71	2.65	1.66	15.29
2MKL-5.PDB	OG1, C_THR_5	NE2, C_GLN_4	HE21, C_GLN_4	2.80	1.92	21.71
2MKL-5.PDB	OD1, C_ASP_35	OG, C_SER_34	HG, C_SER_34	2.85	1.91	12.30
2MKL-5.PDB	OE1, C_GLU_78	NH2, C_ARG_50	HH22, C_ARG_50	2.76	1.81	16.18
2MKL-5.PDB	OD2, C_ASP_6	NZ, C_LYS_65	HZ2, C_LYS_65	2.68	1.69	14.66
2MKL-5.PDB	OE2, C_GLU_78	OG1, C_THR_83	HG1, C_THR_83	2.81	1.87	12.01
2MKL-5.PDB	OXT, C_ALA_105	NZ, C_LYS_104	HZ2, C_LYS_104	2.74	1.74	13.81
2MKL-6.PDB	OXT, C_ALA_105	NZ, C_LYS_13	HZ2, C_LYS_13	2.64	1.69	18.78
2MKL-6.PDB	OE2, C_GLU_17	NZ, C_LYS_13	HZ3, C_LYS_13	2.63	1.59	5.83
2MKL-6.PDB	OE1, C_GLU_84	ND2, C_ASN_46	HD21, C_ASN_46	2.90	1.97	15.36
2MKL-6.PDB	OE2, C_GLU_78	NH2, C_ARG_50	HH22, C_ARG_50	2.72	1.70	3.73
2MKL-6.PDB	OD2, C_ASP_6	NZ, C_LYS_65	HZ3, C_LYS_65	2.59	1.63	17.95
2MKL-6.PDB	OE2, C_GLU_55	NZ, C_LYS_71	HZ1, C_LYS_71	2.70	1.72	16.34
2MKL-6.PDB	OD1, C_ASN_46	OG1, C_THR_83	HG1, C_THR_83	2.65	1.71	11.83
2MKL-6.PDB	OD1, C_ASP_80	NZ, C_LYS_104	HZ1, C_LYS_104	2.64	1.71	20.84
2MKL-7.PDB	OD1, C_ASP_6	NE, C_ARG_3	HE, C_ARG_3	2.80	1.90	20.83
2MKL-7.PDB	OD2, C_ASP_6	NE, C_ARG_3	HE, C_ARG_3	2.95	2.13	27.86
2MKL-7.PDB	OD2, C_ASP_6	NH2, C_ARG_3	HH21, C_ARG_3	2.72	1.79	18.49
2MKL-7.PDB	OD1, C_ASP_6	NZ, C_LYS_65	HZ2, C_LYS_65	2.61	1.57	4.07
2MKL-7.PDB	OG1, C_THR_24	NZ, C_LYS_73	HZ1, C_LYS_73	2.79	1.84	19.74
2MKL-7.PDB	OE2, C_GLU_78	OG1, C_THR_83	HG1, C_THR_83	2.59	1.64	9.74
2MKL-8.PDB	OG, C_SER_70	NE1, C_TRP_43	HE1, C_TRP_43	2.82	1.83	2.10
2MKL-8.PDB	OE2, C_GLU_78	NH1, C_ARG_50	HH12, C_ARG_50	2.63	1.62	3.58
2MKL-8.PDB	OD2, C_ASP_6	NZ, C_LYS_65	HZ3, C_LYS_65	2.64	1.68	18.41
2MKL-8.PDB	OD1, C_ASP_80	NZ, C_LYS_104	HZ1, C_LYS_104	2.61	1.59	9.01
2MKL-9.PDB	OE2, C_GLU_78	NH2, C_ARG_50	HH22, C_ARG_50	2.68	1.69	8.63
2MKL-9.PDB	OD2, C_ASP_6	NZ, C_LYS_65	HZ2, C_LYS_65	2.75	1.71	7.05
2MKL-9.PDB	OE2, C_GLU_37	OG, C_SER_92	HG, C_SER_92	3.00	2.20	28.49

Table 1742: 2MKL-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
3SE8.PDB	OE2, G_GLU_91	NE1, G_TRP_45	HE1, G_TRP_45	2.78	2.03	24.08
3SE8.PDB	OE2, G_GLU_64	ND1, G_HIS_66	HD1, G_HIS_66	2.82	1.98	11.41
3SE8.PDB	OE1, G_GLU_64	ND2, G_ASN_67	HD22, G_ASN_67	2.82	2.00	14.84
3SE8.PDB	OD1, G_ASN_99	NE2, G_GLN_103	HE22, G_GLN_103	2.99	2.17	14.68
3SE8.PDB	OE2, G_GLU_381	NZ, G_LYS_207	HZ2, G_LYS_207	2.74	1.86	4.82
3SE8.PDB	OE2, G_GLU_83	OG, G_SER_243	HG, G_SER_243	2.64	1.83	7.57
3SE8.PDB	OH, G_TYR_486	ND1, G_HIS_249	HD1, G_HIS_249	2.64	1.81	12.83
3SE8.PDB	OE1, G_GLU_482	NE2, G_HIS_249	HE2, G_HIS_249	3.00	2.16	9.93
3SE8.PDB	OE2, G_GLU_269	NZ, G_LYS_348	HZ1, G_LYS_348	2.90	2.14	25.94
3SE8.PDB	OE1, G_GLU_351	NZ, G_LYS_348	HZ3, G_LYS_348	2.96	2.10	14.00
3SE8.PDB	OD1, G_ASN_295	ND2, G_ASN_444	HD21, G_ASN_444	2.87	2.12	25.11
3SE8.PDB	OG1, G_THR_297	ND2, G_ASN_444	HD22, G_ASN_444	2.77	1.99	20.73
3SE8.PDB	OD2, G_ASP_457	NE, G_ARG_469	HE, G_ARG_469	2.90	2.06	8.93
3SE8.PDB	OD1, G_ASP_457	NH2, G_ARG_469	HH21, G_ARG_469	2.93	2.11	16.29
3SE8.PDB	OE1, G_GLN_105	NE1, G_TRP_479	HE1, G_TRP_479	2.68	1.92	22.70
3SE8.PDB	OE1, G_GLU_91	NZ, G_LYS_487	HZ1, G_LYS_487	2.58	1.77	20.55
3SE8.PDB	OD1, G_ASP_47	NZ, G_LYS_487	HZ2, G_LYS_487	2.90	2.08	19.02
3SE8.PDB	OE1, H_GLU_46	NH1, H_ARG_38	HH11, H_ARG_38	2.64	1.78	1.94
3SE8.PDB	OH, H_TYR_90	NH2, H_ARG_38	HH21, H_ARG_38	2.79	1.95	9.66
3SE8.PDB	OD1, H_ASP_86	NH2, H_ARG_38	HH22, H_ARG_38	2.67	1.83	8.41
3SE8.PDB	OD1, G_ASN_280	NE1, H_TRP_50	HE1, H_TRP_50	3.00	2.21	20.49
3SE8.PDB	OE2, H_GLU_46	NE2, H_GLN_62	HE21, H_GLN_62	2.91	2.06	7.60
3SE8.PDB	OD1, G_ASP_457	NE2, H_GLN_64	HE22, H_GLN_64	2.94	2.12	14.23
3SE8.PDB	OD2, H_ASP_86	NH2, H_ARG_66	HH22, H_ARG_66	2.60	1.84	23.72
3SE8.PDB	OD2, G_ASP_368	NH2, H_ARG_71	HH22, H_ARG_71	2.91	2.05	6.24
3SE8.PDB	OG, H_SER_180	NE1, H_TRP_154	HE1, H_TRP_154	2.94	2.09	7.62
3SE8.PDB	OD1, H_ASP_144	NE2, H_GLN_171	HE22, H_GLN_171	2.79	1.98	16.20
3SE8.PDB	OG, H_SER_203	ND1, H_HIS_200	HD1, H_HIS_200	2.45	1.61	10.75
3SE8.PDB	OD1, L_ASP_70	NZ, L_LYS_24	HZ3, L_LYS_24	2.62	1.80	18.41
3SE8.PDB	OH, L_TYR_86	NE2, L_GLN_37	HE21, L_GLN_37	2.98	2.15	12.85
3SE8.PDB	OD2, L_ASP_50	NE, L_ARG_53	HE, L_ARG_53	2.87	2.02	8.47
3SE8.PDB	OD2, L_ASP_82	NE, L_ARG_61	HE, L_ARG_61	2.91	2.18	26.35
3SE8.PDB	OD1, L_ASP_82	NH2, L_ARG_61	HH21, L_ARG_61	2.77	1.91	2.48
3SE8.PDB	OG, L_SER_131	NE2, L_GLN_124	HE22, L_GLN_124	2.53	1.70	11.07
3SE8.PDB	OE2, L_GLU_103	NH2, L_ARG_142	HH22, L_ARG_142	2.84	2.00	11.39
3SE8.PDB	OE1, L_GLU_195	NE2, L_GLN_147	HE21, L_GLN_147	2.66	1.93	26.32
3SE8.PDB	OG, L_SER_177	NE1, L_TRP_148	HE1, L_TRP_148	2.88	2.08	18.18
3SE8.PDB	OD1, L_ASP_170	OG1, L_THR_172	HG1, L_THR_172	2.49	1.68	7.38

Table 1743: 3SE8-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
3SE9.PDB	OE2, G_GLU_64	ND1, G_HIS_66	HD1, G_HIS_66	2.73	1.88	8.47
3SE9.PDB	OE1, G_GLU_64	ND2, G_ASN_67	HD21, G_ASN_67	2.83	2.01	14.03
3SE9.PDB	OD1, G_ASN_99	NE2, G_GLN_103	HE21, G_GLN_103	2.75	1.96	19.57
3SE9.PDB	OE1, G_GLN_117	NZ, G_LYS_121	HZ3, G_LYS_121	2.58	1.83	27.32
3SE9.PDB	OE2, G_GLU_83	OG, G_SER_243	HG, G_SER_243	2.65	1.89	17.63
3SE9.PDB	OH, G_TYR_486	ND1, G_HIS_249	HD1, G_HIS_249	2.73	1.91	13.84
3SE9.PDB	OE1, G_GLN_422	NH1, G_ARG_327	HH11, G_ARG_327	2.62	1.84	19.91
3SE9.PDB	OE1, G_GLU_370	ND2, G_ASN_425	HD21, G_ASN_425	2.86	2.02	9.78
3SE9.PDB	OD1, G_ASN_295	ND2, G_ASN_444	HD21, G_ASN_444	2.93	2.17	24.18
3SE9.PDB	OG1, G_THR_297	ND2, G_ASN_444	HD22, G_ASN_444	2.97	2.23	26.41
3SE9.PDB	OE2, G_GLU_466	NH1, G_ARG_456	HH11, G_ARG_456	2.71	1.88	12.87
3SE9.PDB	OE1, G_GLN_105	NE1, G_TRP_479	HE1, G_TRP_479	2.69	1.89	17.56
3SE9.PDB	OE1, G_GLU_91	NZ, G_LYS_487	HZ3, G_LYS_487	2.63	1.86	24.78
3SE9.PDB	OD1, H_ASP_81	NE, H_ARG_19	HE, H_ARG_19	2.75	1.91	10.76
3SE9.PDB	OH, H_TYR_90	NH1, H_ARG_38	HH11, H_ARG_38	2.99	2.21	21.73
3SE9.PDB	OD1, H_ASP_86	NH1, H_ARG_38	HH12, H_ARG_38	2.86	2.03	12.66
3SE9.PDB	OD1, G_ASN_280	NE1, H_TRP_50	HE1, H_TRP_50	2.86	2.03	11.46
3SE9.PDB	OG, G_SER_365	NH1, H_ARG_64	HH11, H_ARG_64	2.81	2.04	21.79
3SE9.PDB	OD2, H_ASP_86	NH2, H_ARG_66	HH22, H_ARG_66	2.37	1.62	23.34
3SE9.PDB	OD2, G_ASP_368	NH1, H_ARG_71	HH12, H_ARG_71	2.77	1.92	7.25
3SE9.PDB	OG, H_SER_21	ND1, H_HIS_79	HD1, H_HIS_79	2.69	1.93	23.16
3SE9.PDB	OG, H_SER_68	NH1, H_ARG_82A	HH12, H_ARG_82A	2.84	2.02	15.25
3SE9.PDB	OD1, H_ASP_101	NH2, H_ARG_94	HH21, H_ARG_94	2.74	1.90	10.49
3SE9.PDB	OH, H_TYR_100E	NE2, H_GLN_100B	HE22, H_GLN_100B	2.88	2.05	12.80
3SE9.PDB	OD1, G_ASN_279	NE1, H_TRP_100D	HE1, H_TRP_100D	2.86	2.13	26.83
3SE9.PDB	OG, H_SER_180	NE1, H_TRP_154	HE1, H_TRP_154	2.83	2.00	12.34
3SE9.PDB	OD1, L_ASN_138	NE2, H_HIS_164	HE2, H_HIS_164	2.87	2.10	22.18
3SE9.PDB	OD1, H_ASP_144	NE2, H_GLN_171	HE22, H_GLN_171	2.70	1.89	15.22
3SE9.PDB	OD1, H_ASP_208	ND2, H_ASN_197	HD21, H_ASN_197	2.90	2.07	13.74
3SE9.PDB	OG, H_SER_203	ND1, H_HIS_200	HD1, H_HIS_200	2.68	1.84	9.59
3SE9.PDB	OG, L_SER_131	NE2, L_GLN_124	HE21, L_GLN_124	2.87	2.02	8.09
3SE9.PDB	OG, L_SER_177	NE1, L_TRP_148	HE1, L_TRP_148	2.88	2.05	13.01
3SE9.PDB	OD1, L_ASP_170	OG1, L_THR_172	HG1, L_THR_172	2.48	1.71	16.29
3SE9.PDB	OE1, L_GLU_187	NZ, L_LYS_183	HZ3, L_LYS_183	2.82	2.09	29.82
3SE9.PDB	OD2, L_ASP_151	ND1, L_HIS_189	HD1, L_HIS_189	2.89	2.18	29.99

Table 1744: 3SE9-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
3THM.PDB	OD1, L_ASP_93	ND2, L_ASN_28	HD21, L_ASN_28	2.85	2.01	9.28
3THM.PDB	OH, L_TYR_87	NE2, L_GLN_38	HE21, L_GLN_38	2.86	2.05	16.36
3THM.PDB	OD1, L_ASP_83	NE, L_ARG_62	HE, L_ARG_62	2.86	2.03	12.52
3THM.PDB	OD2, L_ASP_83	NH2, L_ARG_62	HH21, L_ARG_62	2.63	1.79	10.74
3THM.PDB	OD2, L_ASP_78	NH1, L_ARG_77	HH11, L_ARG_77	2.79	2.00	19.01
3THM.PDB	OG, L_SER_180	NE1, L_TRP_152	HE1, L_TRP_152	2.84	1.99	7.64
3THM.PDB	OD1, L_ASP_142	NE2, L_GLN_171	HE22, L_GLN_171	2.87	2.03	8.80
3THM.PDB	OD1, L_ASP_155	ND1, L_HIS_192	HD1, L_HIS_192	2.84	1.98	0.83
3THM.PDB	OG1, L_THR_205	OG1, L_THR_200	HG1, L_THR_200	2.83	2.04	14.40
3THM.PDB	OE1, H_GLU_48	NE, H_ARG_40	HE, H_ARG_40	2.92	2.11	16.36
3THM.PDB	OD1, H_ASP_96	NH1, H_ARG_40	HH12, H_ARG_40	2.76	1.92	9.45
3THM.PDB	OE1, L_GLN_39	NE2, H_GLN_41	HE22, H_GLN_41	2.98	2.14	9.35
3THM.PDB	OG, H_SER_52	NE1, H_TRP_49	HE1, H_TRP_49	2.98	2.27	29.23
3THM.PDB	OD1, H_ASP_96	NH2, H_ARG_73	HH22, H_ARG_73	2.91	2.05	3.20
3THM.PDB	OD1, H_ASP_120	NE, H_ARG_104	HE, H_ARG_104	2.94	2.10	9.96
3THM.PDB	OD2, H_ASP_120	NH2, H_ARG_104	HH21, H_ARG_104	2.75	2.00	25.31
3THM.PDB	OD2, H_ASP_110	OG1, H_THR_112	HG1, H_THR_112	2.76	1.95	7.38
3THM.PDB	OD1, H_ASP_109	NE2, H_GLN_115	HE21, H_GLN_115	2.80	1.96	11.40
3THM.PDB	OG, L_SER_183	NZ, H_LYS_162	HZ1, H_LYS_162	2.77	1.97	21.34
3THM.PDB	OG1, L_THR_135	NZ, H_LYS_162	HZ2, H_LYS_162	2.85	2.02	17.75
3THM.PDB	OG, H_SER_199	NE1, H_TRP_173	HE1, H_TRP_173	3.00	2.15	7.78
3THM.PDB	OD1, H_ASP_227	ND2, H_ASN_216	HD22, H_ASN_216	2.86	2.03	14.19
3THM.PDB	OG, H_SER_222	ND1, H_HIS_219	HD1, H_HIS_219	2.82	2.08	24.90
3THM.PDB	OD2, F_ASP_56	ND1, F_HIS_38	HD1, F_HIS_38	2.77	1.98	19.59
3THM.PDB	OH, H_TYR_35	ND1, F_HIS_44	HD1, F_HIS_44	2.69	1.83	5.98
3THM.PDB	OG, H_SER_63	NE2, F_HIS_44	HE2, F_HIS_44	2.83	2.07	23.36

Table 1745: 3THM-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
3TJE.PDB	OD1, L_ASP_93	ND2, L_ASN_28	HD21, L_ASN_28	2.73	1.89	10.95
3TJE.PDB	OD1, L_ASP_94	NH1, L_ARG_31	HH11, L_ARG_31	2.81	2.04	22.49
3TJE.PDB	OH, L_TYR_87	NE2, L_GLN_38	HE21, L_GLN_38	2.91	2.10	17.00
3TJE.PDB	OD2, L_ASP_83	NH1, L_ARG_62	HH12, L_ARG_62	2.77	1.98	19.25
3TJE.PDB	OD1, L_ASP_83	NH2, L_ARG_62	HH22, L_ARG_62	2.87	2.01	3.19
3TJE.PDB	OD2, L_ASP_78	NH1, L_ARG_77	HH11, L_ARG_77	2.74	1.93	16.91
3TJE.PDB	OE2, L_GLU_128	OG1, L_THR_135	HG1, L_THR_135	2.52	1.76	18.95
3TJE.PDB	OG, L_SER_180	NE1, L_TRP_152	HE1, L_TRP_152	2.95	2.10	8.91
3TJE.PDB	OD1, L_ASP_142	NE2, L_GLN_171	HE21, L_GLN_171	2.80	1.98	15.09
3TJE.PDB	OG1, L_THR_205	OG1, L_THR_200	HG1, L_THR_200	2.75	1.97	15.90
3TJE.PDB	OE1, H_GLU_48	NE, H_ARG_40	HE, H_ARG_40	2.72	1.90	14.58
3TJE.PDB	OD1, H_ASP_96	NH1, H_ARG_40	HH12, H_ARG_40	2.84	2.01	12.94
3TJE.PDB	OE1, L_GLN_39	NE2, H_GLN_41	HE21, H_GLN_41	2.98	2.15	10.85
3TJE.PDB	OD2, H_ASP_96	NH1, H_ARG_73	HH12, H_ARG_73	2.84	2.09	24.31
3TJE.PDB	OD1, H_ASP_96	NH2, H_ARG_73	HH22, H_ARG_73	2.94	2.09	3.77
3TJE.PDB	OD2, H_ASP_79	OG, H_SER_81	HG, H_SER_81	2.85	2.15	27.35
3TJE.PDB	OD1, H_ASP_120	NE, H_ARG_104	HE, H_ARG_104	2.87	2.06	15.55
3TJE.PDB	OD2, H_ASP_120	NH2, H_ARG_104	HH21, H_ARG_104	2.68	1.96	27.63
3TJE.PDB	OG, H_SER_199	NE1, H_TRP_173	HE1, H_TRP_173	2.95	2.10	8.21
3TJE.PDB	OD1, H_ASP_163	NE2, H_GLN_190	HE21, H_GLN_190	2.74	1.93	16.43
3TJE.PDB	OD1, H_ASP_227	ND2, H_ASN_216	HD22, H_ASN_216	2.79	1.98	17.28
3TJE.PDB	OG, H_SER_222	OG1, H_THR_224	HG1, H_THR_224	2.65	1.92	22.20
3TJE.PDB	OH, H_TYR_35	ND1, F_HIS_44	HD1, F_HIS_44	2.56	1.70	3.69
3TJE.PDB	OE2, F_GLU_98	NE, F_ARG_112	HE, F_ARG_112	2.97	2.20	22.98

Table 1746: 3TJE-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
3U2S.PDB	OE1, H_GLU_95	NE2, H_HIS_35	HE2, H_HIS_35	2.64	1.80	11.05
3U2S.PDB	OE2, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.80	2.01	18.34
3U2S.PDB	OD1, H_ASP_86	NH1, H_ARG_38	HH12, H_ARG_38	2.84	2.00	11.28
3U2S.PDB	OE2, H_GLU_46	NH2, H_ARG_38	HH21, H_ARG_38	2.92	2.18	25.81
3U2S.PDB	OE1, L_GLN_38	NE2, H_GLN_39	HE22, H_GLN_39	2.89	2.04	8.55
3U2S.PDB	OE1, H_GLU_46	OG, H_SER_62	HG, H_SER_62	2.75	1.94	7.42
3U2S.PDB	OD2, H_ASP_86	NH1, H_ARG_66	HH12, H_ARG_66	2.53	1.74	19.65
3U2S.PDB	OD1, H_ASP_86	NH2, H_ARG_66	HH22, H_ARG_66	2.93	2.08	7.53
3U2S.PDB	OD1, H_ASN_73	NE, H_ARG_71	HE, H_ARG_71	2.77	1.98	19.66
3U2S.PDB	OD1, H_ASP_101	NE, H_ARG_94	HE, H_ARG_94	2.95	2.09	2.87
3U2S.PDB	OD2, H_ASP_101	NH2, H_ARG_94	HH21, H_ARG_94	2.85	2.03	14.60
3U2S.PDB	OG, H_SER_180	NE1, H_TRP_154	HE1, H_TRP_154	2.93	2.08	7.46
3U2S.PDB	OG, L_SER_165	NE2, H_HIS_164	HE2, H_HIS_164	2.93	2.12	16.97
3U2S.PDB	OD2, H_ASP_144	NE2, H_GLN_171	HE22, H_GLN_171	2.87	2.09	20.57
3U2S.PDB	OD2, H_ASP_208	ND2, H_ASN_197	HD21, H_ASN_197	2.76	1.92	10.02
3U2S.PDB	OG, H_SER_203	ND1, H_HIS_200	HD1, H_HIS_200	2.77	1.92	6.39
3U2S.PDB	OG1, L_THR_74	OG1, L_THR_20	HG1, L_THR_20	2.83	2.11	23.78
3U2S.PDB	OD2, L_ASP_27B	OG1, L_THR_26	HG1, L_THR_26	2.86	2.11	19.40
3U2S.PDB	OH, L_TYR_86	NE2, L_GLN_37	HE21, L_GLN_37	2.82	1.97	2.95
3U2S.PDB	OE1, H_GLN_39	NE2, L_GLN_38	HE22, L_GLN_38	2.91	2.09	13.75
3U2S.PDB	OD2, L_ASP_50	NZ, L_LYS_53	HZ2, L_LYS_53	2.84	1.96	4.63
3U2S.PDB	OD2, C_ASP_167	ND2, L_ASN_60	HD22, L_ASN_60	2.90	2.14	22.76
3U2S.PDB	OD2, L_ASP_82	NH1, L_ARG_61	HH12, L_ARG_61	2.86	2.09	21.77
3U2S.PDB	OD1, L_ASP_82	NH2, L_ARG_61	HH22, L_ARG_61	2.97	2.11	4.14
3U2S.PDB	OE2, L_GLU_31	NZ, L_LYS_66	HZ1, L_LYS_66	2.99	2.15	15.69
3U2S.PDB	OD1, H_ASP_61	NH2, L_ARG_95A	HH22, L_ARG_95A	2.34	1.58	22.53
3U2S.PDB	OE2, H_GLU_95	NH2, L_ARG_96	HH21, L_ARG_96	2.87	2.05	15.72
3U2S.PDB	OE2, L_GLU_124	OG1, L_THR_131	HG1, L_THR_131	2.54	1.83	25.31
3U2S.PDB	OG, L_SER_176	NE1, L_TRP_148	HE1, L_TRP_148	2.93	2.09	11.15
3U2S.PDB	OD1, L_ASP_138	NE2, L_GLN_167	HE22, L_GLN_167	2.82	2.00	15.99
3U2S.PDB	OD1, L_ASP_138	ND2, L_ASN_169	HD22, L_ASN_169	2.92	2.10	15.30
3U2S.PDB	OG1, L_THR_201	OG1, L_THR_196	HG1, L_THR_196	2.99	2.20	12.41
3U2S.PDB	OH, H_TYR_100K	ND2, G_ASN_173	HD21, G_ASN_173	2.97	2.13	8.87
3U2S.PDB	OE1, A_GLN_81	NH1, A_ARG_19	HH11, A_ARG_19	2.87	2.10	22.03
3U2S.PDB	OE1, A_GLU_95	NE2, A_HIS_35	HE2, A_HIS_35	2.70	1.86	8.94
3U2S.PDB	OE2, A_GLU_46	NE, A_ARG_38	HE, A_ARG_38	2.74	1.98	23.65
3U2S.PDB	OH, A_TYR_90	NH1, A_ARG_38	HH11, A_ARG_38	2.88	2.07	17.44
3U2S.PDB	OD1, A_ASP_86	NH1, A_ARG_38	HH12, A_ARG_38	2.89	2.04	8.28
3U2S.PDB	OE2, A_GLU_46	NH2, A_ARG_38	HH21, A_ARG_38	2.90	2.18	27.83
3U2S.PDB	OE1, B_GLN_38	NE2, A_GLN_39	HE22, A_GLN_39	2.92	2.07	7.34
3U2S.PDB	OD2, A_ASP_86	NH1, A_ARG_66	HH12, A_ARG_66	2.48	1.66	13.42
3U2S.PDB	OD1, A_ASN_73	NE, A_ARG_71	HE, A_ARG_71	2.81	2.03	20.92
3U2S.PDB	OE1, A_GLU_85	NH1, A_ARG_83	HH11, A_ARG_83	2.91	2.14	21.39
3U2S.PDB	OD1, A_ASP_101	NE, A_ARG_94	HE, A_ARG_94	2.84	1.98	4.74
3U2S.PDB	OD2, A_ASP_101	NH2, A_ARG_94	HH21, A_ARG_94	2.90	2.12	20.79
3U2S.PDB	OG1, B_THR_131	NZ, A_LYS_143	HZ2, A_LYS_143	2.41	1.67	27.35
3U2S.PDB	OD2, A_ASP_144	NE2, A_GLN_171	HE22, A_GLN_171	2.82	1.98	10.06
3U2S.PDB	OG, A_SER_203	ND1, A_HIS_200	HD1, A_HIS_200	2.63	1.78	5.16
3U2S.PDB	OG1, B_THR_74	OG1, B_THR_20	HG1, B_THR_20	2.88	2.16	24.36
3U2S.PDB	OD2, B_ASP_27B	OG1, B_THR_26	HG1, B_THR_26	2.89	2.14	20.81
3U2S.PDB	OH, B_TYR_86	NE2, B_GLN_37	HE21, B_GLN_37	2.88	2.02	1.18
3U2S.PDB	OE1, A_GLN_39	NE2, B_GLN_38	HE22, B_GLN_38	2.92	2.08	10.61
3U2S.PDB	OD2, B_ASP_50	NZ, B_LYS_53	HZ2, B_LYS_53	2.75	1.88	8.80
3U2S.PDB	OD2, B_ASP_82	NH1, B_ARG_61	HH12, B_ARG_61	2.78	1.98	19.10
3U2S.PDB	OD1, B_ASP_82	NH2, B_ARG_61	HH22, B_ARG_61	2.93	2.07	0.82
3U2S.PDB	OD1, A_ASP_61	NH1, B_ARG_95A	HH12, B_ARG_95A	2.63	1.91	26.97
3U2S.PDB	OE2, A_GLU_95	NH2, B_ARG_96	HH21, B_ARG_96	2.98	2.16	13.77

3U2S.PDB	OG, B_SER_176	NE1, B_TRP_148	HE1, B_TRP_148	2.87	2.03	9.65
3U2S.PDB	OD1, B_ASN_169	NE2, B_GLN_167	HE21, B_GLN_167	2.93	2.16	22.14
3U2S.PDB	OD1, B_ASP_138	NE2, B_GLN_167	HE22, B_GLN_167	2.75	1.90	7.18
3U2S.PDB	OG1, B_THR_201	OG1, B_THR_196	HG1, B_THR_196	2.79	1.99	11.66

Table 1747: 3U2S-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
3UYR.PDB	OE1, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.84	2.03	16.92
3UYR.PDB	OD1, H_ASN_50	NE1, H_TRP_47	HE1, H_TRP_47	2.95	2.18	22.72
3UYR.PDB	OD1, H_ASP_105	NE, H_ARG_98	HE, H_ARG_98	2.98	2.16	14.38
3UYR.PDB	OD2, H_ASP_105	NH2, H_ARG_98	HH21, H_ARG_98	2.92	2.07	8.84
3UYR.PDB	OG, H_SER_183	NE1, H_TRP_158	HE1, H_TRP_158	2.93	2.08	7.42
3UYR.PDB	OG, H_SER_206	ND1, H_HIS_203	HD1, H_HIS_203	2.81	2.06	24.47
3UYR.PDB	OE2, L_GLU_127	NZ, H_LYS_212	HZ3, H_LYS_212	2.87	2.08	23.12
3UYR.PDB	OD2, L_ASP_87	NH1, L_ARG_66	HH12, L_ARG_66	2.92	2.12	17.99
3UYR.PDB	OG, L_SER_135	NE2, L_GLN_128	HE22, L_GLN_128	2.97	2.12	5.23
3UYR.PDB	OD1, L_ASP_174	OG1, L_THR_176	HG1, L_THR_176	2.78	1.97	7.90
3UYR.PDB	OD2, L_ASP_155	ND1, L_HIS_193	HD1, L_HIS_193	2.93	2.16	21.52
3UYR.PDB	ND2, L_ASN_216	ND2, L_ASN_194	HD22, L_ASN_194	2.90	2.18	28.48
3UYR.PDB	OG1, L_THR_204	ND1, L_HIS_202	HD1, L_HIS_202	2.78	1.93	6.06
3UYR.PDB	OD1, H_ASN_101	NE2, P_GLN_48	HE22, P_GLN_48	2.57	1.87	29.89

Table 1748: 3UYR-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
3X0E.PDB	OD1, A_ASP_122	NE2, A_GLN_118	HE21, A_GLN_118	2.93	2.22	29.07
3X0E.PDB	OD2, A_ASP_195	NZ, A_LYS_124	HZ1, A_LYS_124	3.00	2.19	21.32
3X0E.PDB	OD2, A_ASP_128	OG1, A_THR_161	HG1, A_THR_161	2.92	2.13	12.66
3X0E.PDB	OD1, A_ASP_155	NZ, A_LYS_187	HZ1, A_LYS_187	2.84	2.07	26.10
3X0E.PDB	OD1, B_ASP_195	NZ, B_LYS_124	HZ1, B_LYS_124	2.75	2.02	29.74
3X0E.PDB	OG, B_SER_159	OG1, B_THR_161	HG1, B_THR_161	2.79	1.98	7.89
3X0E.PDB	OD1, B_ASP_128	NE2, B_HIS_191	HE2, B_HIS_191	2.68	1.83	6.07

Table 1749: 3X0E-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
3X0F.PDB	OD1, A_ASP_195	NZ, A_LYS_124	HZ3, A_LYS_124	2.91	2.03	6.30
3X0F.PDB	OG, A_SER_159	OG1, A_THR_163	HG1, A_THR_163	2.77	1.96	7.35
3X0F.PDB	OD1, A_ASP_128	NE2, A_HIS_191	HE2, A_HIS_191	2.65	1.83	14.50
3X0F.PDB	OH, B_TYR_127	NE2, B_HIS_151	HE2, B_HIS_151	2.81	2.02	19.67
3X0F.PDB	OG1, B_THR_163	OG, B_SER_159	HG, B_SER_159	2.96	2.16	10.94
3X0F.PDB	OD1, B_ASP_128	NE2, B_HIS_191	HE2, B_HIS_191	2.69	1.83	1.74

Table 1750: 3X0F-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4F33.PDB	OE1, B_GLN_39	NE2, A_GLN_38	HE22, A_GLN_38	2.96	2.13	12.75
4F33.PDB	OD2, A_ASP_82	NE, A_ARG_61	HE, A_ARG_61	2.81	2.09	28.09
4F33.PDB	OD1, A_ASP_82	NH2, A_ARG_61	HH21, A_ARG_61	2.71	1.85	4.82
4F33.PDB	OG1, A_THR_21	OG1, A_THR_74	HG1, A_THR_74	2.73	1.99	21.82
4F33.PDB	OG1, A_THR_97	NE2, A_GLN_90	HE21, A_GLN_90	2.97	2.15	14.62
4F33.PDB	OG, A_SER_13	NZ, A_LYS_107	HZ3, A_LYS_107	2.94	2.07	9.78
4F33.PDB	OG, A_SER_131	NE2, A_GLN_124	HE22, A_GLN_124	2.81	1.96	5.54
4F33.PDB	OG, A_SER_177	NE1, A_TRP_148	HE1, A_TRP_148	2.91	2.09	14.52
4F33.PDB	OE1, A_GLU_195	NZ, A_LYS_149	HZ2, A_LYS_149	2.59	1.85	28.21
4F33.PDB	OE1, A_GLN_155	ND2, A_ASN_158	HD22, A_ASN_158	2.89	2.06	12.00
4F33.PDB	OD1, A_ASP_170	OG1, A_THR_172	HG1, A_THR_172	2.68	1.86	4.02
4F33.PDB	OE1, A_GLN_38	NE2, B_GLN_39	HE22, B_GLN_39	2.82	1.97	5.31
4F33.PDB	OE2, B_GLU_46	NZ, B_LYS_63	HZ3, B_LYS_63	2.70	1.89	19.35
4F33.PDB	OD2, B_ASP_90	NZ, B_LYS_67	HZ2, B_LYS_67	2.73	1.86	7.48
4F33.PDB	OD2, B_ASP_107	NH2, B_ARG_98	HH21, B_ARG_98	2.74	1.88	6.50
4F33.PDB	OD1, B_ASP_102	NE, B_ARG_104	HE, B_ARG_104	2.87	2.03	8.81
4F33.PDB	OD2, B_ASP_107	NH1, B_ARG_104	HH11, B_ARG_104	2.78	1.96	13.74
4F33.PDB	OD2, B_ASP_102	NH2, B_ARG_104	HH21, B_ARG_104	2.87	2.08	19.19
4F33.PDB	OG, B_SER_186	NE1, B_TRP_160	HE1, B_TRP_160	2.97	2.13	10.43
4F33.PDB	OD1, B_ASP_150	NE2, B_GLN_177	HE22, B_GLN_177	2.84	2.07	21.15
4F33.PDB	OD1, B_ASP_214	ND2, B_ASN_203	HD21, B_ASN_203	2.97	2.12	8.15
4F33.PDB	OG, B_SER_209	ND1, B_HIS_206	HD1, B_HIS_206	2.61	1.78	12.57
4F33.PDB	OE1, A_GLU_123	NZ, B_LYS_215	HZ1, B_LYS_215	2.68	1.82	12.44
4F33.PDB	OG1, H_THR_211	NZ, B_LYS_215	HZ2, B_LYS_215	2.83	1.95	7.37
4F33.PDB	OD2, C_ASP_82	NE, C_ARG_61	HE, C_ARG_61	2.88	2.06	14.32
4F33.PDB	OD1, C_ASP_82	NH2, C_ARG_61	HH21, C_ARG_61	2.91	2.08	14.25
4F33.PDB	OG1, C_THR_21	OG1, C_THR_74	HG1, C_THR_74	2.68	1.93	19.90
4F33.PDB	OG, C_SER_13	OG, C_LYS_107	HZ3, C_LYS_107	2.78	1.89	2.73
4F33.PDB	OG, C_SER_131	NE2, C_GLN_124	HE22, C_GLN_124	2.83	1.97	4.97
4F33.PDB	OG, C_SER_177	NE1, C_TRP_148	HE1, C_TRP_148	2.93	2.10	14.22
4F33.PDB	OE1, C_GLU_195	NZ, C_LYS_149	HZ2, C_LYS_149	2.67	1.88	22.11
4F33.PDB	OE1, C_GLN_155	ND2, C_ASN_158	HD22, C_ASN_158	2.91	2.09	15.33
4F33.PDB	OD1, C_ASP_170	OG1, C_THR_172	HG1, C_THR_172	2.72	1.91	5.07
4F33.PDB	OE1, C_GLN_38	NE2, D_GLN_39	HE22, D_GLN_39	2.89	2.03	5.23
4F33.PDB	OE2, D_GLU_46	NZ, D_LYS_63	HZ3, D_LYS_63	2.60	1.76	15.82
4F33.PDB	OD2, D_ASP_90	NZ, D_LYS_67	HZ2, D_LYS_67	2.76	2.03	29.11
4F33.PDB	OD2, D_ASP_107	NH2, D_ARG_98	HH21, D_ARG_98	2.74	1.89	7.29
4F33.PDB	OD1, D_ASP_102	NE, D_ARG_104	HE, D_ARG_104	2.89	2.05	10.59
4F33.PDB	OD2, D_ASP_107	NH1, D_ARG_104	HH11, D_ARG_104	2.83	2.01	15.77
4F33.PDB	OD2, D_ASP_102	NH2, D_ARG_104	HH21, D_ARG_104	2.91	2.10	15.53
4F33.PDB	OG, D_SER_186	NE1, D_TRP_160	HE1, D_TRP_160	3.00	2.15	9.78
4F33.PDB	OD1, D_ASP_150	NE2, D_GLN_177	HE22, D_GLN_177	2.86	2.09	21.57
4F33.PDB	OE1, C_GLU_123	NZ, D_LYS_215	HZ1, D_LYS_215	2.79	1.99	22.47
4F33.PDB	OG1, F_THR_211	NZ, D_LYS_215	HZ2, D_LYS_215	2.86	1.99	10.67
4F33.PDB	OG1, E_THR_74	OG1, E_THR_21	HG1, E_THR_21	2.80	2.03	17.05
4F33.PDB	OD2, E_ASP_82	NE, E_ARG_61	HE, E_ARG_61	2.93	2.08	6.42
4F33.PDB	OD1, E_ASP_82	NH2, E_ARG_61	HH21, E_ARG_61	2.82	1.98	9.42
4F33.PDB	OG1, E_THR_97	NE2, E_GLN_90	HE21, E_GLN_90	2.99	2.17	14.98
4F33.PDB	OG, E_SER_131	NE2, E_GLN_124	HE22, E_GLN_124	2.81	1.95	4.17
4F33.PDB	OG, E_SER_177	NE1, E_TRP_148	HE1, E_TRP_148	2.88	2.05	13.86
4F33.PDB	OE1, E_GLU_195	NZ, E_LYS_149	HZ2, E_LYS_149	2.77	1.97	22.37
4F33.PDB	OE1, E_GLN_155	ND2, E_ASN_158	HD22, E_ASN_158	2.91	2.08	12.67
4F33.PDB	OD1, E_ASP_170	OG1, E_THR_172	HG1, E_THR_172	2.66	1.85	7.41
4F33.PDB	OE1, E_GLN_38	NE2, F_GLN_39	HE22, F_GLN_39	2.92	2.06	5.53
4F33.PDB	OE2, F_GLU_46	NZ, F_LYS_63	HZ3, F_LYS_63	2.68	1.79	3.79
4F33.PDB	OD2, F_ASP_90	NZ, F_LYS_67	HZ2, F_LYS_67	2.98	2.09	4.59
4F33.PDB	OD1, F_ASP_107	NE, F_ARG_98	HE, F_ARG_98	2.99	2.13	4.74

4F33.PDB	OD2, F_ASP_107	NH2, F_ARG_98	HH21, F_ARG_98	2.77	1.91	5.42
4F33.PDB	OD1, F_ASP_102	NE, F_ARG_104	HE, F_ARG_104	2.84	1.99	7.33
4F33.PDB	OD2, F_ASP_107	NH1, F_ARG_104	HH11, F_ARG_104	2.84	2.02	14.35
4F33.PDB	OD2, F_ASP_102	NH2, F_ARG_104	HH21, F_ARG_104	2.90	2.10	17.22
4F33.PDB	OG, F_SER_186	NE1, F_TRP_160	HE1, F_TRP_160	3.00	2.15	9.04
4F33.PDB	OD1, F_ASP_150	NE2, F_GLN_177	HE22, F_GLN_177	2.82	2.02	17.76
4F33.PDB	OD1, F_ASP_214	ND2, F_ASN_203	HD21, F_ASN_203	2.95	2.10	8.40
4F33.PDB	OG, F_SER_209	ND1, F_HIS_206	HD1, F_HIS_206	2.64	1.82	13.68
4F33.PDB	OE1, E_GLU_123	NZ, F_LYS_215	HZ1, F_LYS_215	2.61	1.84	24.34
4F33.PDB	OG1, D_THR_211	NZ, F_LYS_215	HZ2, F_LYS_215	2.92	2.04	7.71
4F33.PDB	OG1, G_THR_74	OG1, G_THR_21	HG1, G_THR_21	2.73	1.97	18.47
4F33.PDB	OD1, G_ASP_82	NH2, G_ARG_61	HH21, G_ARG_61	2.73	1.89	8.68
4F33.PDB	OE2, G_GLU_81	NH2, G_ARG_61	HH22, G_ARG_61	2.96	2.16	17.92
4F33.PDB	OG, G_SER_131	NE2, G_GLN_124	HE22, G_GLN_124	2.79	1.93	5.18
4F33.PDB	OG, G_SER_177	NE1, G_TRP_148	HE1, G_TRP_148	2.87	2.04	13.06
4F33.PDB	OE1, G_GLN_155	ND2, G_ASN_158	HD22, G_ASN_158	2.92	2.10	14.66
4F33.PDB	OD1, G_ASP_170	OG1, G_THR_172	HG1, G_THR_172	2.69	1.89	8.34
4F33.PDB	OD2, G_ASP_151	ND1, G_HIS_189	HD1, G_HIS_189	2.86	2.09	22.44
4F33.PDB	OE2, H_GLU_46	NZ, H_LYS_63	HZ3, H_LYS_63	2.72	1.93	23.08
4F33.PDB	OD2, H_ASP_90	NZ, H_LYS_67	HZ2, H_LYS_67	2.82	1.98	16.29
4F33.PDB	OD1, H_ASP_107	NE, H_ARG_98	HE, H_ARG_98	2.95	2.15	18.92
4F33.PDB	OD2, H_ASP_107	NH2, H_ARG_98	HH21, H_ARG_98	2.79	1.95	8.93
4F33.PDB	OD1, H_ASP_102	NE, H_ARG_104	HE, H_ARG_104	2.85	2.00	6.80
4F33.PDB	OD2, H_ASP_107	NH1, H_ARG_104	HH11, H_ARG_104	2.85	2.04	16.23
4F33.PDB	OD2, H_ASP_102	NH2, H_ARG_104	HH21, H_ARG_104	2.93	2.12	16.50
4F33.PDB	OG, H_SER_186	NE1, H_TRP_160	HE1, H_TRP_160	2.99	2.15	10.12
4F33.PDB	OD1, H_ASP_150	NE2, H_GLN_177	HE22, H_GLN_177	2.83	2.04	19.22
4F33.PDB	OD1, H_ASP_214	ND2, H_ASN_203	HD21, H_ASN_203	2.91	2.05	5.75
4F33.PDB	OE1, G_GLU_123	NZ, H_LYS_215	HZ1, H_LYS_215	2.97	2.19	24.10
4F33.PDB	OG1, B_THR_211	NZ, H_LYS_215	HZ2, H_LYS_215	2.80	1.95	14.49

Table 1751: 4F33-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4F3F.PDB	OE1, B_GLN_39	NE2, A_GLN_38	HE22, A_GLN_38	2.88	2.04	8.75
4F3F.PDB	OD1, A_ASP_82	NH2, A_ARG_61	HH21, A_ARG_61	2.60	1.79	16.27
4F3F.PDB	OE2, A_GLU_81	NH2, A_ARG_61	HH22, A_ARG_61	2.95	2.12	13.66
4F3F.PDB	OG1, A_THR_21	OG1, A_THR_74	HG1, A_THR_74	2.77	2.04	22.11
4F3F.PDB	OG, B_SER_59	NE2, A_HIS_94	HE2, A_HIS_94	2.82	2.03	19.68
4F3F.PDB	OG, A_SER_131	NE2, A_GLN_124	HE22, A_GLN_124	2.84	2.05	19.05
4F3F.PDB	OD1, A_ASP_170	OG1, A_THR_172	HG1, A_THR_172	2.85	2.05	10.97
4F3F.PDB	OD1, B_ASN_35	NE1, B_TRP_47	HE1, B_TRP_47	2.99	2.19	19.59
4F3F.PDB	OD2, B_ASP_90	NZ, B_LYS_67	HZ2, B_LYS_67	2.92	2.05	9.99
4F3F.PDB	OD2, B_ASP_107	NH2, B_ARG_98	HH21, B_ARG_98	2.79	1.95	9.80
4F3F.PDB	OD1, A_ASN_138	NE2, B_HIS_170	HE2, B_HIS_170	2.82	2.05	21.56
4F3F.PDB	OD1, B_ASP_150	NE2, B_GLN_177	HE22, B_GLN_177	2.87	2.13	25.54
4F3F.PDB	OG, B_SER_209	ND1, B_HIS_206	HD1, B_HIS_206	2.43	1.61	13.98
4F3F.PDB	OH, B_TYR_101	NZ, C_LYS_25	HZ3, C_LYS_25	2.87	2.11	26.18
4F3F.PDB	OH, A_TYR_32	NE1, C_TRP_26	HE1, C_TRP_26	2.97	2.17	18.16
4F3F.PDB	OE2, C_GLU_15	NH2, C_ARG_43	HH21, C_ARG_43	2.88	2.04	9.30

Table 1752: 4F3F-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4JAM.PDB	OE2, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.93	2.10	13.53
4JAM.PDB	OH, H_TYR_90	NH1, H_ARG_38	HH11, H_ARG_38	2.92	2.12	17.99
4JAM.PDB	OD1, H_ASP_86	NH1, H_ARG_38	HH12, H_ARG_38	2.91	2.07	10.41
4JAM.PDB	OD1, H_ASP_86	NH2, H_ARG_66	HH22, H_ARG_66	2.96	2.12	9.52
4JAM.PDB	OD1, H_ASP_144	NZ, H_LYS_143	HZ2, H_LYS_143	3.00	2.12	8.81
4JAM.PDB	OG, H_SER_180	NE1, H_TRP_154	HE1, H_TRP_154	2.95	2.10	8.20
4JAM.PDB	OG, H_SER_180	OG1, H_THR_165	HG1, H_THR_165	2.85	2.09	18.68
4JAM.PDB	OG, H_SER_203	ND1, H_HIS_200	HD1, H_HIS_200	2.70	1.91	20.45
4JAM.PDB	OD1, H_ASN_100B	ND2, L_ASN_32	HD21, L_ASN_32	2.96	2.21	25.94
4JAM.PDB	OH, L_TYR_86	NE2, L_GLN_37	HE21, L_GLN_37	2.92	2.07	7.82
4JAM.PDB	OE1, L_GLU_50	NZ, L_LYS_53	HZ1, L_LYS_53	2.81	1.96	13.53
4JAM.PDB	OD2, L_ASP_82	NE, L_ARG_61	HE, L_ARG_61	2.81	2.02	19.36
4JAM.PDB	OD1, L_ASP_82	NH2, L_ARG_61	HH21, L_ARG_61	2.93	2.10	13.29
4JAM.PDB	OH, L_TYR_172	NH2, L_ARG_107	HH22, L_ARG_107	2.87	2.14	27.08
4JAM.PDB	OE1, L_GLU_198	NZ, L_LYS_110	HZ2, L_LYS_110	2.60	1.75	13.04
4JAM.PDB	OE2, L_GLU_124	OG1, L_THR_131	HG1, L_THR_131	2.56	1.86	25.46
4JAM.PDB	OG, L_SER_176	NE1, L_TRP_148	HE1, L_TRP_148	2.87	2.03	8.58
4JAM.PDB	OE1, L_GLU_203	NZ, L_LYS_149	HZ2, L_LYS_149	2.76	1.94	19.38
4JAM.PDB	OG, L_SER_192	OG1, L_THR_205	HG1, L_THR_205	2.80	2.01	12.51
4JAM.PDB	OE1, A_GLU_75	NE1, A_TRP_34	HE1, A_TRP_34	2.65	1.81	8.69
4JAM.PDB	OH, A_TYR_90	NH1, A_ARG_38	HH11, A_ARG_38	2.87	2.07	18.01
4JAM.PDB	OD1, A_ASP_86	NH1, A_ARG_38	HH12, A_ARG_38	2.79	1.96	13.17
4JAM.PDB	OD2, A_ASP_86	NH2, A_ARG_66	HH22, A_ARG_66	2.34	1.63	27.75
4JAM.PDB	OG, A_SER_180	NE1, A_TRP_154	HE1, A_TRP_154	2.95	2.10	7.51
4JAM.PDB	OD1, A_ASP_208	ND2, A_ASN_197	HD21, A_ASN_197	2.90	2.10	17.20
4JAM.PDB	OG, A_SER_203	ND1, A_HIS_200	HD1, A_HIS_200	2.74	1.92	14.00
4JAM.PDB	OE1, B_GLU_50	NZ, B_LYS_53	HZ1, B_LYS_53	2.75	1.92	17.48
4JAM.PDB	OD2, B_ASP_82	NE, B_ARG_61	HE, B_ARG_61	2.84	2.00	9.73
4JAM.PDB	OD1, B_ASP_82	NH2, B_ARG_61	HH21, B_ARG_61	2.90	2.08	13.97
4JAM.PDB	OE2, B_GLU_124	OG1, B_THR_131	HG1, B_THR_131	2.53	1.82	24.30
4JAM.PDB	OG, B_SER_176	NE1, B_TRP_148	HE1, B_TRP_148	2.84	1.99	9.50
4JAM.PDB	OD1, B_ASP_138	ND2, B_ASN_169	HD22, B_ASN_169	2.93	2.14	18.27
4JAM.PDB	OG, B_SER_192	OG1, B_THR_205	HG1, B_THR_205	2.64	1.83	8.66

Table 1753: 4JAM-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4JAN.PDB	OD2, G_ASP_457	NE, G_ARG_469	HE, G_ARG_469	2.84	2.10	25.29
4JAN.PDB	OE1, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.76	1.94	14.56
4JAN.PDB	OG, H_SER_180	NE1, H_TRP_154	HE1, H_TRP_154	2.82	2.02	18.56
4JAN.PDB	OD2, B_ASP_92	OG, H_SER_156	HG, H_SER_156	2.50	1.78	23.90
4JAN.PDB	OG, H_SER_203	ND1, H_HIS_200	HD1, H_HIS_200	2.81	1.96	7.87
4JAN.PDB	OD1, H_ASN_199	NZ, H_LYS_201	HZ2, H_LYS_201	2.90	2.05	14.58
4JAN.PDB	OE1, L_GLU_123	NZ, H_LYS_209	HZ1, H_LYS_209	2.89	2.13	26.71
4JAN.PDB	OG1, L_THR_102	NE2, L_GLN_6	HE21, L_GLN_6	2.82	2.05	22.18
4JAN.PDB	OD1, H_ASN_100B	ND2, L_ASN_32	HD21, L_ASN_32	2.76	1.91	6.44
4JAN.PDB	OH, L_TYR_86	NE2, L_GLN_37	HE21, L_GLN_37	2.95	2.09	6.42
4JAN.PDB	OG, L_SER_176	NE1, L_TRP_148	HE1, L_TRP_148	2.88	2.04	9.05
4JAN.PDB	OG, A_SER_180	NE1, A_TRP_154	HE1, A_TRP_154	2.82	2.05	22.21
4JAN.PDB	OE2, B_GLU_124	OG1, B_THR_131	HG1, B_THR_131	2.64	1.97	29.01
4JAN.PDB	OG, B_SER_176	NE1, B_TRP_148	HE1, B_TRP_148	2.83	1.98	7.29

Table 1754: 4JAN-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4KRM.PDB	OE1, B_GLU_110	NH1, A_ARG_353	HH11, A_ARG_353	2.81	2.05	22.81
4KRM.PDB	OD2, A_ASP_355	OG1, A_THR_358	HG1, A_THR_358	2.65	1.94	26.40
4KRM.PDB	OE1, A_GLU_376	NE, A_ARG_403	HE, A_ARG_403	2.51	1.78	27.17
4KRM.PDB	OD1, A_ASP_434	NZ, A_LYS_407	HZ1, A_LYS_407	2.92	2.12	20.92
4KRM.PDB	OE2, A_GLU_431	OG, A_SER_433	HG, A_SER_433	2.82	2.09	25.22
4KRM.PDB	OD1, B_ASP_80	NE, B_ARG_19	HE, B_ARG_19	2.67	1.85	15.03
4KRM.PDB	OH, B_TYR_94	NH1, B_ARG_38	HH11, B_ARG_38	2.87	2.05	14.24
4KRM.PDB	OD2, B_ASP_90	NH1, B_ARG_38	HH12, B_ARG_38	2.85	2.02	12.95
4KRM.PDB	OE1, D_GLU_110	NH1, C_ARG_353	HH11, C_ARG_353	2.87	2.05	16.15
4KRM.PDB	OD2, C_ASP_355	OG1, C_THR_358	HG1, C_THR_358	2.75	2.00	22.12
4KRM.PDB	OE1, C_GLU_376	NH1, C_ARG_403	HH11, C_ARG_403	3.00	2.18	16.51
4KRM.PDB	OD1, C_ASP_498	NH2, C_ARG_427	HH21, C_ARG_427	2.43	1.69	25.29
4KRM.PDB	OE2, C_GLU_431	OG, C_SER_433	HG, C_SER_433	2.86	2.06	14.79
4KRM.PDB	OE1, C_GLU_489	NZ, C_LYS_455	HZ2, C_LYS_455	2.73	1.95	24.04
4KRM.PDB	OE1, D_GLN_82	NH1, D_ARG_19	HH11, D_ARG_19	2.94	2.12	14.24
4KRM.PDB	OD2, C_ASP_355	NH1, D_ARG_30	HH12, D_ARG_30	2.45	1.63	13.53
4KRM.PDB	OE1, D_GLU_46	NE, D_ARG_38	HE, D_ARG_38	2.79	1.96	12.48
4KRM.PDB	OE1, F_GLU_110	NH1, E_ARG_353	HH11, E_ARG_353	2.85	2.03	14.34
4KRM.PDB	OD2, F_ASP_112	NH2, E_ARG_353	HH22, E_ARG_353	2.96	2.18	20.33
4KRM.PDB	OD2, E_ASP_355	OG1, E_THR_358	HG1, E_THR_358	2.55	1.85	27.90
4KRM.PDB	OD1, E_ASP_434	NZ, E_LYS_407	HZ1, E_LYS_407	2.65	1.88	23.95
4KRM.PDB	OE2, E_GLU_431	OG, E_SER_433	HG, E_SER_433	2.91	2.17	23.57
4KRM.PDB	OE1, F_GLU_46	NE, F_ARG_38	HE, F_ARG_38	2.74	1.95	18.99
4KRM.PDB	OD2, F_ASP_90	NH1, F_ARG_38	HH12, F_ARG_38	2.95	2.22	27.79
4KRM.PDB	OE1, F_GLU_46	NH2, F_ARG_38	HH21, F_ARG_38	2.97	2.26	28.90
4KRM.PDB	OG, F_SER_57	NE1, F_TRP_104	HE1, F_TRP_104	3.00	2.20	18.23
4KRM.PDB	OE2, G_GLU_320	ND2, G_ASN_314	HD22, G_ASN_314	2.93	2.08	7.68
4KRM.PDB	OD2, G_ASP_355	OG1, G_THR_358	HG1, G_THR_358	2.44	1.73	26.83
4KRM.PDB	OE2, B_GLU_5	NZ, G_LYS_407	HZ1, G_LYS_407	2.98	2.17	20.60
4KRM.PDB	OD1, G_ASP_498	NE, G_ARG_427	HE, G_ARG_427	2.63	1.82	16.62
4KRM.PDB	OE2, G_GLU_431	OG, G_SER_433	HG, G_SER_433	2.90	2.13	19.38
4KRM.PDB	OD2, G_ASP_436	NZ, G_LYS_463	HZ3, G_LYS_463	2.68	1.83	13.12
4KRM.PDB	OD1, H_ASP_80	OG1, H_THR_21	HG1, H_THR_21	2.86	2.06	13.63
4KRM.PDB	OD2, G_ASP_355	NH1, H_ARG_30	HH12, H_ARG_30	2.45	1.69	23.45
4KRM.PDB	OH, H_TYR_94	NH1, H_ARG_38	HH11, H_ARG_38	2.96	2.15	17.21
4KRM.PDB	OD2, H_ASP_90	NH1, H_ARG_38	HH12, H_ARG_38	2.78	1.94	11.87
4KRM.PDB	OE1, J_GLU_110	NH1, I_ARG_353	HH11, I_ARG_353	2.86	2.07	18.90
4KRM.PDB	OD2, J_ASP_112	NH2, I_ARG_353	HH22, I_ARG_353	3.00	2.19	17.61
4KRM.PDB	OE1, I_GLU_376	NH1, I_ARG_403	HH11, I_ARG_403	2.44	1.73	28.52
4KRM.PDB	OE2, I_GLU_431	OG, I_SER_433	HG, I_SER_433	2.91	2.09	9.73
4KRM.PDB	OD1, I_ASN_469	ND2, I_ASN_442	HD22, I_ASN_442	2.76	1.93	12.03
4KRM.PDB	OD1, I_ASN_473	OG, I_SER_474	HG, I_SER_474	2.73	1.91	11.26
4KRM.PDB	OD1, J_ASP_80	NE, J_ARG_19	HE, J_ARG_19	2.78	1.97	16.74
4KRM.PDB	OH, J_TYR_94	NH1, J_ARG_38	HH11, J_ARG_38	2.85	2.02	12.10
4KRM.PDB	OD2, J_ASP_90	NH1, J_ARG_38	HH12, J_ARG_38	2.97	2.15	14.05
4KRM.PDB	OD1, J_ASP_90	NH2, J_ARG_67	HH22, J_ARG_67	2.61	1.77	10.49
4KRM.PDB	OD1, J_ASN_74	NE, J_ARG_72	HE, J_ARG_72	2.67	1.87	16.97
4KRM.PDB	OG, J_SER_57	NE1, J_TRP_104	HE1, J_TRP_104	2.98	2.26	28.43
4KRM.PDB	OE1, L_GLU_110	NH1, K_ARG_353	HH11, K_ARG_353	2.89	2.06	12.41
4KRM.PDB	OD2, L_ASP_112	NH2, K_ARG_353	HH22, K_ARG_353	2.89	2.07	13.96
4KRM.PDB	OD2, K_ASP_355	OG1, K_THR_358	HG1, K_THR_358	2.91	2.21	28.73
4KRM.PDB	OD1, L_ASP_80	NE, L_ARG_19	HE, L_ARG_19	2.96	2.10	5.59
4KRM.PDB	OD2, K_ASP_355	NH1, L_ARG_30	HH12, L_ARG_30	2.44	1.65	18.93
4KRM.PDB	OE1, L_GLU_46	NE, L_ARG_38	HE, L_ARG_38	2.86	2.01	10.17
4KRM.PDB	OD1, L_ASP_90	NH2, L_ARG_67	HH22, L_ARG_67	2.60	1.80	17.17

Table 1755: 4KRM-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4KRO.PDB	OG1, A_THR_278	OG, A_SER_282	HG, A_SER_282	2.99	2.27	26.50
4KRO.PDB	OE2, A_GLU_376	NH2, A_ARG_310	HH21, A_ARG_310	2.98	2.18	18.33
4KRO.PDB	OD2, A_ASP_355	OG1, A_THR_358	HG1, A_THR_358	2.98	2.18	14.96
4KRO.PDB	OG, B_SER_103	NZ, A_LYS_375	HZ2, A_LYS_375	2.61	1.76	15.34
4KRO.PDB	OH, D_TYR_102	NE2, A_GLN_384	HE21, A_GLN_384	2.87	2.16	29.24
4KRO.PDB	OD1, B_ASP_118	NE, A_ARG_405	HE, A_ARG_405	2.72	1.93	19.48
4KRO.PDB	OD1, A_ASP_498	NH2, A_ARG_427	HH21, A_ARG_427	2.62	1.82	18.67
4KRO.PDB	OD1, A_ASN_469	ND2, A_ASN_442	HD22, A_ASN_442	2.75	1.96	18.83
4KRO.PDB	OG, A_SER_501	OG, A_SER_487	HG, A_SER_487	2.37	1.68	29.03
4KRO.PDB	OD1, A_ASN_504	NH1, A_ARG_503	HH11, A_ARG_503	2.52	1.76	23.61
4KRO.PDB	OG1, A_THR_548	ND2, A_ASN_554	HD22, A_ASN_554	2.92	2.13	19.09
4KRO.PDB	OE1, C_GLN_89	OH, C_TYR_36	HH, C_TYR_36	2.63	1.80	6.46
4KRO.PDB	OH, C_TYR_86	NE2, C_GLN_37	HE21, C_GLN_37	2.94	2.13	16.57
4KRO.PDB	OE1, D_GLN_39	NE2, C_GLN_38	HE22, C_GLN_38	2.85	2.00	7.50
4KRO.PDB	OD2, D_ASP_103	OH, C_TYR_50	HH, C_TYR_50	2.49	1.72	20.15
4KRO.PDB	OD1, C_ASP_82	NH2, C_ARG_61	HH21, C_ARG_61	2.64	1.81	12.76
4KRO.PDB	OD1, D_ASP_103	ND2, C_ASN_91	HD21, C_ASN_91	2.93	2.12	16.18
4KRO.PDB	OD1, C_ASN_32	ND2, C_ASN_92	HD22, C_ASN_92	2.97	2.20	23.59
4KRO.PDB	OD2, D_ASP_58	NE1, C_TRP_94	HE1, C_TRP_94	2.80	2.10	29.15
4KRO.PDB	OG, C_SER_131	NE2, C_GLN_124	HE22, C_GLN_124	2.85	2.00	6.78
4KRO.PDB	OG, C_SER_177	NE1, C_TRP_148	HE1, C_TRP_148	2.83	2.01	15.90
4KRO.PDB	OE1, C_GLN_155	ND2, C_ASN_158	HD21, C_ASN_158	2.72	1.97	24.54
4KRO.PDB	OD1, C_ASP_170	OG1, C_THR_172	HG1, C_THR_172	2.68	1.86	11.97
4KRO.PDB	OE1, D_GLU_46	NE, D_ARG_38	HE, D_ARG_38	3.00	2.22	20.92
4KRO.PDB	OH, D_TYR_93	NH1, D_ARG_38	HH11, D_ARG_38	2.92	2.15	22.16
4KRO.PDB	OE1, D_GLU_46	NH2, D_ARG_38	HH21, D_ARG_38	2.98	2.22	22.99
4KRO.PDB	OE1, C_GLN_38	NE2, D_GLN_39	HE22, D_GLN_39	2.80	1.94	4.32
4KRO.PDB	OH, D_TYR_59	OG1, D_THR_57	HG1, D_THR_57	2.96	2.15	12.78
4KRO.PDB	OE1, A_GLN_408	OH, D_TYR_102	HH, D_TYR_102	2.75	1.97	18.39
4KRO.PDB	OG, D_SER_209	ND1, D_HIS_206	HD1, D_HIS_206	2.71	1.87	9.56

Table 1756: 4KRO-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4KRP.PDB	OE2, A_GLU_376	NH2, A_ARG_310	HH21, A_ARG_310	2.93	2.09	9.81
4KRP.PDB	OD1, B_ASP_115	NH2, A_ARG_405	HH21, A_ARG_405	2.63	1.81	15.48
4KRP.PDB	OD1, A_ASP_498	NE, A_ARG_427	HE, A_ARG_427	2.55	1.82	26.18
4KRP.PDB	OD1, A_ASP_498	NH2, A_ARG_427	HH21, A_ARG_427	2.59	1.89	29.61
4KRP.PDB	OE2, A_GLU_431	OG, A_SER_433	HG, A_SER_433	2.69	1.90	15.48
4KRP.PDB	OD1, A_ASN_469	ND2, A_ASN_442	HD22, A_ASN_442	2.94	2.17	23.18
4KRP.PDB	OD1, D_ASP_58	NZ, A_LYS_443	HZ1, A_LYS_443	2.65	1.82	17.69
4KRP.PDB	OE1, A_GLU_489	NZ, A_LYS_455	HZ2, A_LYS_455	2.95	2.19	25.72
4KRP.PDB	OD2, D_ASP_103	NZ, A_LYS_465	HZ2, A_LYS_465	2.93	2.05	5.06
4KRP.PDB	OG, A_SER_474	NE, A_ARG_470	HE, A_ARG_470	2.76	1.96	18.13
4KRP.PDB	OG, A_SER_501	OG, A_SER_487	HG, A_SER_487	2.45	1.66	16.67
4KRP.PDB	OE1, A_GLU_495	NE, A_ARG_497	HE, A_ARG_497	2.60	1.79	14.71
4KRP.PDB	OE1, A_GLU_524	NE, A_ARG_507	HE, A_ARG_507	2.83	2.04	19.78
4KRP.PDB	OE2, A_GLU_527	NH2, A_ARG_550	HH22, A_ARG_550	2.54	1.76	21.10
4KRP.PDB	OD1, C_ASN_92	ND2, C_ASN_32	HD22, C_ASN_32	2.85	2.14	29.38
4KRP.PDB	OE1, C_GLN_89	OH, C_TYR_36	HH, C_TYR_36	2.33	1.50	6.36
4KRP.PDB	OH, C_TYR_86	NE2, C_GLN_37	HE21, C_GLN_37	2.85	2.02	13.51
4KRP.PDB	OE1, D_GLN_39	NE2, C_GLN_38	HE22, C_GLN_38	2.70	1.84	6.09
4KRP.PDB	OE1, C_GLU_53	NZ, C_LYS_49	HZ3, C_LYS_49	2.81	1.93	8.64
4KRP.PDB	OD2, D_ASP_103	OH, C_TYR_50	HH, C_TYR_50	2.43	1.66	18.96
4KRP.PDB	OD1, C_ASP_82	NH2, C_ARG_61	HH21, C_ARG_61	2.79	1.98	15.39
4KRP.PDB	OG1, C_THR_96	NE2, C_GLN_89	HE21, C_GLN_89	2.69	1.93	23.74
4KRP.PDB	OD1, D_ASP_103	ND2, C_ASN_91	HD21, C_ASN_91	2.77	1.91	6.24
4KRP.PDB	OD1, C_ASN_93	ND2, C_ASN_92	HD22, C_ASN_92	2.69	1.97	27.74
4KRP.PDB	OD2, D_ASP_58	NE1, C_TRP_94	HE1, C_TRP_94	2.98	2.17	17.26
4KRP.PDB	OE2, C_GLU_105	NZ, C_LYS_103	HZ1, C_LYS_103	2.82	2.05	25.15
4KRP.PDB	OG, C_SER_131	NE2, C_GLN_124	HE22, C_GLN_124	2.89	2.10	19.98
4KRP.PDB	OE1, C_GLN_155	ND2, C_ASN_158	HD21, C_ASN_158	2.83	2.12	29.23
4KRP.PDB	OD1, C_ASP_170	OG1, C_THR_172	HG1, C_THR_172	2.53	1.69	5.91
4KRP.PDB	OG1, D_THR_113	NE2, D_GLN_6	HE21, D_GLN_6	2.88	2.03	4.76
4KRP.PDB	OH, D_TYR_93	NH1, D_ARG_38	HH11, D_ARG_38	2.96	2.18	20.80
4KRP.PDB	OD1, D_ASP_89	NH1, D_ARG_38	HH12, D_ARG_38	2.91	2.06	7.49
4KRP.PDB	OE1, C_GLN_38	NE2, D_GLN_39	HE22, D_GLN_39	2.72	1.87	5.47
4KRP.PDB	OD1, D_ASP_89	NH2, D_ARG_66	HH22, D_ARG_66	2.59	1.74	9.60
4KRP.PDB	OE1, A_GLN_408	OH, D_TYR_102	HH, D_TYR_102	2.56	1.74	10.00
4KRP.PDB	OG, A_SER_440	OH, D_TYR_104	HH, D_TYR_104	2.94	2.22	25.72
4KRP.PDB	OD1, D_ASP_214	ND2, D_ASN_203	HD22, D_ASN_203	2.70	1.84	4.78
4KRP.PDB	OG, D_SER_209	ND1, D_HIS_206	HD1, D_HIS_206	2.94	2.08	3.63
4KRP.PDB	OG, D_SER_209	OG1, D_THR_211	HG1, D_THR_211	2.56	1.87	28.78
4KRP.PDB	OE1, A_GLU_431	OH, B_TYR_32	HH, B_TYR_32	2.59	1.78	7.49
4KRP.PDB	OE1, A_GLU_400	OH, B_TYR_100	HH, B_TYR_100	2.94	2.13	13.29
4KRP.PDB	OE2, A_GLU_431	OH, B_TYR_116	HH, B_TYR_116	2.43	1.75	29.09

Table 1757: 4KRP-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4NZR.PDB	OE1, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.83	2.07	23.07
4NZR.PDB	OH, H_TYR_90	NH1, H_ARG_38	HH11, H_ARG_38	2.96	2.16	17.91
4NZR.PDB	OD1, H_ASP_86	NH1, H_ARG_38	HH12, H_ARG_38	2.73	1.88	7.20
4NZR.PDB	OE1, H_GLU_46	NH2, H_ARG_38	HH21, H_ARG_38	2.78	2.02	22.98
4NZR.PDB	OG, H_SER_50	NE1, H_TRP_47	HE1, H_TRP_47	2.87	2.03	11.63
4NZR.PDB	OD1, H_ASP_31G	NE2, H_HIS_52	HE2, H_HIS_52	2.60	1.83	22.01
4NZR.PDB	OD1, H_ASP_31G	NE1, H_TRP_53	HE1, H_TRP_53	2.92	2.20	28.43
4NZR.PDB	OD2, H_ASP_86	NH1, H_ARG_66	HH12, H_ARG_66	2.98	2.20	21.88
4NZR.PDB	OD1, H_ASP_101	NE, H_ARG_94	HE, H_ARG_94	2.90	2.05	5.79
4NZR.PDB	OD2, H_ASP_101	NH2, H_ARG_94	HH21, H_ARG_94	2.73	1.90	13.79
4NZR.PDB	OG, H_SER_50	ND1, H_HIS_95	HD1, H_HIS_95	2.67	1.84	11.69
4NZR.PDB	OD1, H_ASP_146	NE2, H_GLN_179	HE22, H_GLN_179	2.89	2.12	22.14
4NZR.PDB	OG, L_SER_176	OG, H_SER_188	HG, H_SER_188	2.88	2.16	24.46
4NZR.PDB	OD1, H_ASP_220	ND2, H_ASN_209	HD22, H_ASN_209	2.89	2.06	12.07
4NZR.PDB	OG, H_SER_215	ND1, H_HIS_212	HD1, H_HIS_212	2.80	1.99	17.07
4NZR.PDB	OE2, L_GLU_123	NZ, H_LYS_221	HZ2, H_LYS_221	2.99	2.10	2.00
4NZR.PDB	OE2, H_GLU_226	NE, H_ARG_222	HE, H_ARG_222	2.65	1.93	27.41
4NZR.PDB	OE1, L_GLU_92	ND2, L_ASN_30	HD22, L_ASN_30	2.94	2.10	10.05
4NZR.PDB	OH, L_TYR_52	NZ, L_LYS_31	HZ1, L_LYS_31	2.57	1.77	21.34
4NZR.PDB	OH, L_TYR_86	NE2, L_GLN_37	HE21, L_GLN_37	2.96	2.11	9.58
4NZR.PDB	OD2, L_ASP_82	NH1, L_ARG_61	HH12, L_ARG_61	2.70	1.89	15.31
4NZR.PDB	OD1, L_ASP_82	NH2, L_ARG_61	HH22, L_ARG_61	2.85	2.01	9.02
4NZR.PDB	OG, L_SER_131	NE2, L_GLN_124	HE22, L_GLN_124	2.90	2.04	4.21
4NZR.PDB	OG, L_SER_177	NE1, L_TRP_148	HE1, L_TRP_148	2.91	2.07	10.59
4NZR.PDB	OE1, L_GLN_155	ND2, L_ASN_158	HD21, L_ASN_158	2.96	2.11	9.14
4NZR.PDB	OD1, L_ASP_170	OG1, L_THR_172	HG1, L_THR_172	2.70	1.89	6.41
4NZR.PDB	OG, H_SER_188	OG, L_SER_176	HG, L_SER_176	2.88	2.09	13.66
4NZR.PDB	OD2, L_ASP_151	ND1, L_HIS_189	HD1, L_HIS_189	2.85	2.11	26.53
4NZR.PDB	OD1, M_ASN_378	NH1, M_ARG_95	HH12, M_ARG_95	2.71	1.91	18.53
4NZR.PDB	OE2, M_GLU_124	OG, M_SER_126	HG, M_SER_126	2.49	1.81	27.79
4NZR.PDB	OE2, M_GLU_124	NZ, M_LYS_141	HZ2, M_LYS_141	2.96	2.15	21.57
4NZR.PDB	OD1, M_ASN_335	ND2, M_ASN_166	HD22, M_ASN_166	2.95	2.13	14.03
4NZR.PDB	OD1, M_ASN_183	NE, M_ARG_167	HE, M_ARG_167	2.87	2.09	20.21
4NZR.PDB	OD1, M_ASP_339	NH2, M_ARG_167	HH22, M_ARG_167	2.84	2.05	19.40
4NZR.PDB	OD1, M_ASN_177	OG1, M_THR_179	HG1, M_THR_179	2.75	1.94	6.81
4NZR.PDB	OD1, M_ASP_217	OG1, M_THR_207	HG1, M_THR_207	2.72	1.90	1.28
4NZR.PDB	OE1, M_GLU_261	NZ, M_LYS_242	HZ1, M_LYS_242	2.96	2.22	28.06
4NZR.PDB	OD1, M_ASP_250	NZ, M_LYS_249	HZ2, M_LYS_249	2.93	2.05	7.77
4NZR.PDB	NE2, M_GLN_282	NZ, M_LYS_255	HZ2, M_LYS_255	2.97	2.08	5.26
4NZR.PDB	OD2, M_ASP_217	NH1, M_ARG_269	HH12, M_ARG_269	2.82	1.99	14.04
4NZR.PDB	OE2, M_GLU_313	NZ, M_LYS_289	HZ1, M_LYS_289	2.70	1.96	27.41
4NZR.PDB	OE1, M_GLU_311	NZ, M_LYS_289	HZ3, M_LYS_289	2.89	2.00	2.29
4NZR.PDB	OD1, M_ASP_350	OG1, M_THR_352	HG1, M_THR_352	2.69	1.93	19.00
4NZR.PDB	OE1, M_GLU_420	NZ, M_LYS_370	HZ2, M_LYS_370	2.61	1.80	20.02
4NZR.PDB	OD1, M_ASP_375	NE2, M_GLN_371	HE21, M_GLN_371	2.92	2.12	18.76
4NZR.PDB	OE1, M_GLU_383	NH1, M_ARG_380	HH11, M_ARG_380	2.65	1.84	14.74
4NZR.PDB	OE1, M_GLU_162	NH2, M_ARG_381	HH22, M_ARG_381	3.00	2.22	21.24
4NZR.PDB	OE1, L_GLU_81	NE, M_ARG_384	HE, M_ARG_384	2.93	2.09	10.37
4NZR.PDB	OD1, M_ASP_396	NZ, M_LYS_397	HZ1, M_LYS_397	2.90	2.03	10.85
4NZR.PDB	OD2, M_ASP_410	ND2, M_ASN_402	HD22, M_ASN_402	2.93	2.14	18.97
4NZR.PDB	OE2, M_GLU_464	NH1, M_ARG_416	HH12, M_ARG_416	2.68	1.83	5.86
4NZR.PDB	OE1, M_GLU_464	NH2, M_ARG_416	HH22, M_ARG_416	2.88	2.03	6.77
4NZR.PDB	OD1, M_ASP_411	NH1, M_ARG_430	HH12, M_ARG_430	2.84	2.06	21.86
4NZR.PDB	OD1, M_ASN_402	OG1, M_THR_435	HG1, M_THR_435	2.74	1.98	18.44
4NZR.PDB	OD2, M_ASP_396	NE, M_ARG_438	HE, M_ARG_438	2.86	2.00	5.29
4NZR.PDB	OE2, M_GLU_426	ND2, M_ASN_440	HD22, M_ASN_440	2.87	2.05	14.71
4NZR.PDB	OD1, M_ASP_412	NH1, M_ARG_454	HH12, M_ARG_454	2.79	1.98	15.66

4NZR.PDB	OD1, H_ASP_31E	NH1, M_ARG_457	HH12, M_ARG_457	2.96	2.12	11.27
4NZR.PDB	OD2, H_ASP_31E	NH2, M_ARG_457	HH22, M_ARG_457	2.55	1.75	17.03

Table 1758: 4NZR-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4NZU.PDB	OD2, L_ASP_82	NE, L_ARG_61	HE, L_ARG_61	2.83	2.03	27.68
4NZU.PDB	OD1, L_ASP_82	NH2, L_ARG_61	HH21, L_ARG_61	2.85	2.00	7.18
4NZU.PDB	OG, L_SER_177	NE1, L_TRP_148	HE1, L_TRP_148	2.90	1.89	11.12
4NZU.PDB	OE2, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.81	1.92	18.37
4NZU.PDB	OD1, H_ASP_86	NH1, H_ARG_38	HH12, H_ARG_38	2.87	2.03	8.91
4NZU.PDB	OD2, H_ASP_86	NH1, H_ARG_66	HH12, H_ARG_66	2.80	1.94	3.46
4NZU.PDB	OD1, H_ASP_97	NH2, H_ARG_94	HH22, H_ARG_94	2.85	2.02	14.02
4NZU.PDB	OG, H_SER_189	NE1, H_TRP_157	HE1, H_TRP_157	2.92	1.90	9.04
4NZU.PDB	OH, H_TYR_206	OG, H_BSER_197	HG, H_BSER_197	2.82	2.05	15.42

Table 1759: 4NZU-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4QEX.PDB	OD2, A_ASP_414	NH2, A_ARG_349	HH21, A_ARG_349	3.00	2.26	27.00
4QEX.PDB	OD2, B_ASP_414	NH2, B_ARG_349	HH21, B_ARG_349	2.99	2.26	27.25

Table 1760: 4QEX-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4WUU.PDB	OD2, A_ASP_29	ND1, A_HIS_3	HD1, A_HIS_3	2.93	2.13	17.75
4WUU.PDB	OE1, A_GLU_46	NE, A_ARG_35	HE, A_ARG_35	2.77	1.96	15.11
4WUU.PDB	OE2, A_GLU_46	OG, A_SER_42	HG, A_SER_42	2.85	2.07	18.95
4WUU.PDB	OD2, B_ASP_53	NE, A_ARG_48	HE, A_ARG_48	2.84	2.13	29.12
4WUU.PDB	OH, A_TYR_171	OH, A_TYR_59	HH, A_TYR_59	2.71	1.89	11.34
4WUU.PDB	OH, E_TYR_104	NZ, A_LYS_66	HZ3, A_LYS_66	2.89	2.02	10.84
4WUU.PDB	OXT, C_LEU_9	OH, A_TYR_84	HH, A_TYR_84	2.64	1.82	12.17
4WUU.PDB	OD2, A_ASP_137	OH, A_TYR_85	HH, A_TYR_85	2.79	1.98	13.39
4WUU.PDB	OE1, A_GLN_87	OH, A_TYR_118	HH, A_TYR_118	2.94	2.13	11.47
4WUU.PDB	OG1, A_THR_143	OH, A_TYR_123	HH, A_TYR_123	2.74	1.95	17.32
4WUU.PDB	OE2, A_GLU_55	NE, A_ARG_170	HE, A_ARG_170	2.89	2.03	3.82
4WUU.PDB	OE1, B_GLN_8	NH1, A_ARG_234	HH11, A_ARG_234	2.79	2.07	27.49
4WUU.PDB	OE1, A_GLN_242	NH2, A_ARG_234	HH21, A_ARG_234	3.00	2.27	27.42
4WUU.PDB	OD1, A_ASP_238	OG1, A_THR_240	HG1, A_THR_240	2.61	1.79	8.96
4WUU.PDB	OG1, B_THR_86	OG1, B_THR_4	HG1, B_THR_4	2.90	2.14	21.40
4WUU.PDB	OE1, A_GLU_232	OH, B_TYR_26	HH, B_TYR_26	2.95	2.14	13.27
4WUU.PDB	OD1, B_ASP_38	NE, B_ARG_45	HE, B_ARG_45	2.54	1.82	27.34
4WUU.PDB	ND1, B_HIS_84	OG1, B_THR_86	HG1, B_THR_86	2.95	2.20	22.57
4WUU.PDB	OE1, E_GLN_39	NE2, D_GLN_39	HE22, D_GLN_39	2.94	2.18	23.53
4WUU.PDB	OD2, D_ASP_83	NE, D_ARG_62	HE, D_ARG_62	2.79	2.08	28.83
4WUU.PDB	OD1, D_ASP_83	NH2, D_ARG_62	HH21, D_ARG_62	2.86	2.00	2.74
4WUU.PDB	OD1, E_ASP_106	NE1, D_TRP_99	HE1, D_TRP_99	2.95	2.19	24.35
4WUU.PDB	OG1, D_THR_165	OG, D_SER_180	HG, D_SER_180	3.00	2.24	22.62
4WUU.PDB	OE1, D_GLN_39	NE2, E_GLN_39	HE22, E_GLN_39	2.55	1.73	14.29
4WUU.PDB	OE2, A_GLU_166	NH2, E_ARG_50	HH22, E_ARG_50	2.67	1.88	18.69
4WUU.PDB	OD1, E_ASP_73	OG, E_SER_75	HG, E_SER_75	2.93	2.16	19.72
4WUU.PDB	OE1, A_GLU_63	OH, E_TYR_104	HH, E_TYR_104	2.59	1.76	7.82
4WUU.PDB	OE1, A_GLU_55	OH, E_TYR_105	HH, E_TYR_105	2.47	1.79	29.86
4WUU.PDB	OE1, E_GLU_156	OH, E_TYR_153	HH, E_TYR_153	2.97	2.18	16.08

Table 1761: 4WUU-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4Z0X.PDB	OG1, A_THR_101	NE2, A_GLN_6	HE21, A_GLN_6	2.98	2.23	24.64
4Z0X.PDB	OE1, A_GLN_16	OG1, A_THR_17	HG1, A_THR_17	2.97	2.23	24.46
4Z0X.PDB	OE1, A_GLN_88	OH, A_TYR_35	HH, A_TYR_35	2.99	2.19	16.02
4Z0X.PDB	OE1, B_GLN_64	NE2, A_GLN_37	HE22, A_GLN_37	2.75	1.99	23.41
4Z0X.PDB	OD2, A_ASP_81	NH1, A_ARG_60	HH12, A_ARG_60	2.72	1.91	16.22
4Z0X.PDB	OD1, A_ASN_68	OG1, A_THR_69	HG1, A_THR_69	2.91	2.09	9.92
4Z0X.PDB	OE2, B_GLU_107	OG, B_SER_42	HG, B_SER_42	2.96	2.17	17.40
4Z0X.PDB	OE1, B_GLN_31	OG, B_SER_46	HG, B_SER_46	2.75	1.93	11.18
4Z0X.PDB	OE2, B_GLU_71	NE, B_ARG_63	HE, B_ARG_63	2.78	1.94	9.25
4Z0X.PDB	OD1, B_ASP_115	NH1, B_ARG_63	HH12, B_ARG_63	3.00	2.15	8.77
4Z0X.PDB	OE1, B_GLN_90	NE, B_ARG_92	HE, B_ARG_92	2.75	1.97	21.20
4Z0X.PDB	OD2, B_ASP_115	NH1, B_ARG_92	HH12, B_ARG_92	2.90	2.09	15.11
4Z0X.PDB	OD1, B_ASP_115	NH2, B_ARG_92	HH22, B_ARG_92	2.68	1.87	17.08
4Z0X.PDB	OE1, B_GLN_64	OH, B_TYR_120	HH, B_TYR_120	2.91	2.08	8.45

Table 1762: 4Z0X-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5I76.PDB	OD1, A_ASN_76	NH1, A_ARG_18	HH11, A_ARG_18	2.77	1.94	12.53
5I76.PDB	OE1, A_GLN_89	OH, A_TYR_36	HH, A_TYR_36	2.60	1.77	6.74
5I76.PDB	OH, A_TYR_86	NE2, A_GLN_37	HE21, A_GLN_37	2.93	2.09	10.63
5I76.PDB	OE1, B_GLN_39	NE2, A_GLN_38	HE22, A_GLN_38	2.94	2.10	10.68
5I76.PDB	OE1, A_GLU_53	NZ, A_LYS_49	HZ2, A_LYS_49	2.94	2.09	13.35
5I76.PDB	OD2, B_ASP_103	OH, A_TYR_50	HH, A_TYR_50	2.64	1.88	21.01
5I76.PDB	OD1, A_ASP_82	NH2, A_ARG_61	HH21, A_ARG_61	2.77	1.93	10.41
5I76.PDB	OE2, A_GLU_81	NH2, A_ARG_61	HH22, A_ARG_61	2.77	1.92	8.54
5I76.PDB	OG1, A_THR_96	NE2, A_GLN_89	HE21, A_GLN_89	2.89	2.08	16.62
5I76.PDB	OD1, A_ASN_93	ND2, A_ASN_92	HD22, A_ASN_92	2.89	2.06	14.53
5I76.PDB	OG, A_SER_12	NZ, A_LYS_107	HZ3, A_LYS_107	2.75	1.89	12.15
5I76.PDB	OG, A_SER_131	NE2, A_GLN_124	HE22, A_GLN_124	2.78	1.92	5.16
5I76.PDB	OE2, A_GLU_143	NZ, A_LYS_145	HZ3, A_LYS_145	2.87	2.06	20.39
5I76.PDB	OG, A_SER_177	NE1, A_TRP_148	HE1, A_TRP_148	2.97	2.15	13.90
5I76.PDB	OD1, A_ASP_170	OG1, A_THR_172	HG1, A_THR_172	2.65	1.83	9.24
5I76.PDB	OE2, A_GLU_105	OH, A_TYR_173	HH, A_TYR_173	2.42	1.66	21.73
5I76.PDB	OD1, B_ARG_89	NH1, B_ARG_38	HH12, B_ARG_38	2.81	1.96	5.27
5I76.PDB	OE1, A_GLN_38	NE2, B_GLN_39	HE22, B_GLN_39	2.80	1.95	6.66
5I76.PDB	OD2, B_ASP_58	NE1, B_TRP_52	HE1, B_TRP_52	2.79	1.94	5.91
5I76.PDB	OD2, B_ASP_89	NH1, B_ARG_66	HH12, B_ARG_66	2.96	2.17	19.36
5I76.PDB	OD1, B_ASP_89	NH2, B_ARG_66	HH22, B_ARG_66	2.84	1.99	7.50
5I76.PDB	OD1, B_ASP_72	OG, B_SER_74	HG, B_SER_74	2.49	1.80	29.35
5I76.PDB	OD1, B_ASN_203	OG, B_SER_159	HG, B_SER_159	2.82	2.04	17.93
5I76.PDB	OG, B_SER_186	NE1, B_TRP_160	HE1, B_TRP_160	2.99	2.15	11.06
5I76.PDB	OD1, B_ASP_150	NE2, B_GLN_177	HE22, B_GLN_177	2.79	2.00	19.18
5I76.PDB	OG, A_SER_176	OG, B_SER_185	HG, B_SER_185	2.89	2.15	23.05
5I76.PDB	OG, B_SER_194	OH, B_TYR_200	HH, B_TYR_200	2.81	2.03	18.26
5I76.PDB	OD1, B_ASP_214	ND2, B_ASN_203	HD22, B_ASN_203	2.90	2.11	19.71
5I76.PDB	OE1, A_GLU_123	NZ, B_LYS_215	HZ1, B_LYS_215	2.73	1.96	24.68
5I76.PDB	OE2, A_GLU_123	NZ, B_LYS_215	HZ1, B_LYS_215	2.89	2.11	24.69
5I76.PDB	OE1, B_GLU_218	NE, B_ARG_216	HE, B_ARG_216	2.64	1.90	25.25
5I76.PDB	OE1, B_GLU_218	NH2, B_ARG_216	HH21, B_ARG_216	2.69	1.98	29.12
5I76.PDB	OD2, A_ASP_70	NH1, C_ARG_24	HH12, C_ARG_24	2.95	2.23	28.81
5I76.PDB	OE1, C_GLN_89	OH, C_TYR_36	HH, C_TYR_36	2.73	1.90	7.00
5I76.PDB	OH, C_TYR_86	NE2, C_GLN_37	HE21, C_GLN_37	2.93	2.09	9.49
5I76.PDB	OE1, C_GLN_37	NH1, C_ARG_45	HH11, C_ARG_45	2.96	2.15	17.42
5I76.PDB	OE1, C_GLU_53	NZ, C_LYS_49	HZ2, C_LYS_49	2.64	1.79	13.55
5I76.PDB	OD2, D_ASP_103	OH, C_TYR_50	HH, C_TYR_50	2.76	1.95	12.40
5I76.PDB	OD1, C_ASP_82	NH2, C_ARG_61	HH21, C_ARG_61	2.76	1.93	11.41
5I76.PDB	OE2, C_GLU_81	NH2, C_ARG_61	HH22, C_ARG_61	2.83	2.01	16.02
5I76.PDB	OG, C_SER_171	OG, C_SER_80	HG, C_SER_80	2.59	1.79	14.57
5I76.PDB	OG1, C_THR_96	NE2, C_GLN_89	HE21, C_GLN_89	2.74	1.92	15.47
5I76.PDB	OD1, C_ASN_93	ND2, C_ASN_92	HD22, C_ASN_92	2.84	2.03	16.29
5I76.PDB	OG, C_SER_131	NE2, C_GLN_124	HE22, C_GLN_124	2.87	2.02	5.94
5I76.PDB	OG1, C_THR_180	OG, C_SER_131	HG, C_SER_131	2.93	2.13	14.64
5I76.PDB	OE1, C_GLU_105	OH, C_TYR_140	HH, C_TYR_140	2.89	2.14	22.51
5I76.PDB	OG, C_SER_177	NE1, C_TRP_148	HE1, C_TRP_148	2.90	2.11	19.54
5I76.PDB	OE1, C_GLN_155	ND2, C_ASN_158	HD22, C_ASN_158	2.96	2.21	25.95
5I76.PDB	OD1, C_ASP_170	OG1, C_THR_172	HG1, C_THR_172	2.79	1.97	11.52
5I76.PDB	OE2, C_GLU_105	OH, C_TYR_173	HH, C_TYR_173	2.72	1.89	6.26
5I76.PDB	OD2, C_ASP_151	ND1, C_HIS_189	HD1, C_HIS_189	2.35	1.61	24.33
5I76.PDB	OG, D_SER_28	OG1, D_THR_30	HG1, D_THR_30	2.71	1.88	5.11
5I76.PDB	OD1, D_ASP_89	NH1, D_ARG_38	HH12, D_ARG_38	2.88	2.03	7.89
5I76.PDB	OE1, C_GLN_38	NE2, D_GLN_39	HE22, D_GLN_39	2.85	2.01	10.98
5I76.PDB	OD2, D_ASP_58	NE1, D_TRP_52	HE1, D_TRP_52	2.82	1.96	3.64
5I76.PDB	OD2, D_ASP_89	NH1, D_ARG_66	HH12, D_ARG_66	2.85	2.02	11.59
5I76.PDB	OD1, D_ASP_89	NH2, D_ARG_66	HH22, D_ARG_66	2.74	1.89	8.51

5I76.PDB	OD1, D_ASP_72	OG, D_SER_74	HG, D_SER_74	2.71	2.00	26.33
5I76.PDB	OD1, D_ASP_150	NZ, D_LYS_149	HZ3, D_LYS_149	2.86	2.03	16.70
5I76.PDB	OE1, D_GLU_154	OH, D_TYR_151	HH, D_TYR_151	2.91	2.09	9.17
5I76.PDB	OD1, D_ASN_203	OG, D_SER_159	HG, D_SER_159	2.84	2.05	16.99
5I76.PDB	OG, D_SER_186	NE1, D_TRP_160	HE1, D_TRP_160	2.92	2.08	9.81
5I76.PDB	OD1, D_ASP_150	NE2, D_GLN_177	HE22, D_GLN_177	2.71	1.92	19.90
5I76.PDB	OG, D_SER_194	OH, D_TYR_200	HH, D_TYR_200	2.69	1.90	16.49
5I76.PDB	OE1, C_GLU_123	NZ, D_LYS_215	HZ1, D_LYS_215	2.60	1.73	11.40

Table 1763: 5I76-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5JO5.PDB	OD2, H_ASP_53	NE1, H_TRP_33	HE1, H_TRP_33	2.93	2.17	24.23
5JO5.PDB	OG1, H_THR_95	OG, H_SER_35	HG, H_SER_35	2.68	1.99	28.91
5JO5.PDB	OE1, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.82	2.00	14.74
5JO5.PDB	OH, H_TYR_90	NH1, H_ARG_38	HH11, H_ARG_38	2.91	2.09	14.97
5JO5.PDB	OD1, H_ASP_86	NH1, H_ARG_38	HH12, H_ARG_38	2.87	2.05	14.25
5JO5.PDB	OE1, L_GLN_38	NE2, H_GLN_39	HE22, H_GLN_39	2.84	2.00	9.38
5JO5.PDB	OE1, H_GLU_100J	NE, H_ARG_50	HE, H_ARG_50	2.77	2.00	22.35
5JO5.PDB	OD2, H_ASP_58	NH2, H_ARG_50	HH22, H_ARG_50	2.84	2.00	11.12
5JO5.PDB	OD2, H_ASP_86	NH1, H_ARG_66	HH12, H_ARG_66	2.78	1.94	11.10
5JO5.PDB	OD1, H_ASP_73	NE, H_ARG_71	HE, H_ARG_71	2.85	2.05	17.58
5JO5.PDB	OD1, H_ASP_72	OG, H_SER_74	HG, H_SER_74	2.59	1.76	4.73
5JO5.PDB	OD2, H_ASP_102	NE, H_ARG_94	HE, H_ARG_94	2.81	2.07	25.27
5JO5.PDB	OD2, H_ASP_102	NH1, H_ARG_94	HH11, H_ARG_94	2.70	1.93	22.67
5JO5.PDB	OE2, L_GLU_124	NZ, H_LYS_143	HZ2, H_LYS_143	2.46	1.63	17.05
5JO5.PDB	OD1, H_ASN_197	OG, H_SER_153	HG, H_SER_153	2.83	2.04	17.75
5JO5.PDB	OG, H_SER_180	NE1, H_TRP_154	HE1, H_TRP_154	2.93	2.09	10.13
5JO5.PDB	OD1, H_ASP_144	NE2, H_GLN_171	HE22, H_GLN_171	2.85	2.05	18.06
5JO5.PDB	OH, L_TYR_177	OG, H_SER_179	HG, H_SER_179	2.73	2.00	25.96
5JO5.PDB	OG, H_SER_188	OH, H_TYR_194	HH, H_TYR_194	2.61	1.85	20.74
5JO5.PDB	OD1, H_ASP_208	ND2, H_ASN_197	HD22, H_ASN_197	2.91	2.06	7.04
5JO5.PDB	OE1, D_GLN_24	OG, L_SER_30	HG, L_SER_30	2.84	2.07	18.45
5JO5.PDB	OH, L_TYR_86	NE2, L_GLN_37	HE21, L_GLN_37	2.94	2.08	4.10
5JO5.PDB	OE1, H_GLN_39	NE2, L_GLN_38	HE22, L_GLN_38	2.83	2.00	13.03
5JO5.PDB	OD1, L_ASN_52	NE, L_ARG_54	HE, L_ARG_54	2.95	2.15	18.15
5JO5.PDB	OD1, L_ASP_82	NH2, L_ARG_61	HH21, L_ARG_61	2.75	1.92	13.56
5JO5.PDB	OE2, L_GLU_81	NH2, L_ARG_61	HH22, L_ARG_61	2.98	2.17	16.30
5JO5.PDB	OE2, H_GLU_100J	NH2, L_ARG_91	HH22, L_ARG_91	2.69	1.84	7.26
5JO5.PDB	OD1, L_ASP_92	OG, L_SER_95A	HG, L_SER_95A	2.53	1.76	19.87
5JO5.PDB	OD1, H_ASP_58	NE, L_ARG_95B	HE, L_ARG_95B	2.95	2.13	14.76
5JO5.PDB	OE1, L_GLU_198	NZ, L_LYS_110	HZ3, L_LYS_110	2.94	2.09	14.01
5JO5.PDB	OE2, L_GLU_124	OG1, L_THR_131	HG1, L_THR_131	2.52	1.80	26.33
5JO5.PDB	OG, L_SER_176	NE1, L_TRP_148	HE1, L_TRP_148	2.93	2.09	9.40
5JO5.PDB	OD1, L_ASN_169	NE2, L_GLN_167	HE21, L_GLN_167	2.89	2.12	21.54
5JO5.PDB	OG1, L_THR_162	OG, L_SER_175	HG, L_SER_175	2.94	2.19	22.64
5JO5.PDB	OG1, L_THR_161	OG, L_SER_176	HG, L_SER_176	2.79	2.07	26.34
5JO5.PDB	OG1, L_THR_205	OG, L_SER_192	HG, L_SER_192	2.82	2.12	28.14
5JO5.PDB	OG1, L_THR_196	OG1, L_THR_201	HG1, L_THR_201	2.95	2.20	22.04
5JO5.PDB	OD2, A_ASP_53	NE1, A_TRP_33	HE1, A_TRP_33	2.82	2.05	21.67
5JO5.PDB	OE1, A_GLU_46	NE, A_ARG_38	HE, A_ARG_38	2.78	1.97	16.63
5JO5.PDB	OD1, A_ASP_86	NH1, A_ARG_38	HH12, A_ARG_38	2.83	2.01	14.60
5JO5.PDB	OE1, B_GLN_38	NE2, A_GLN_39	HE22, A_GLN_39	2.87	2.02	8.31
5JO5.PDB	OE1, A_GLU_100J	NE, A_ARG_50	HE, A_ARG_50	2.88	2.11	22.13
5JO5.PDB	OE2, A_GLU_100J	NH1, A_ARG_50	HH11, A_ARG_50	2.91	2.07	11.34
5JO5.PDB	OD2, A_ASP_58	NH2, A_ARG_50	HH22, A_ARG_50	2.88	2.05	13.39
5JO5.PDB	OD2, A_ASP_86	NH1, A_ARG_66	HH12, A_ARG_66	2.80	1.98	14.11
5JO5.PDB	OD1, A_ASP_73	NE, A_ARG_71	HE, A_ARG_71	2.86	2.09	22.09
5JO5.PDB	OD1, A_ASP_72	OG, A_SER_74	HG, A_SER_74	2.54	1.80	22.83
5JO5.PDB	OD2, A_ASP_102	NE, A_ARG_94	HE, A_ARG_94	2.86	2.14	28.73
5JO5.PDB	OD2, A_ASP_102	NH1, A_ARG_94	HH11, A_ARG_94	2.58	1.79	19.06
5JO5.PDB	OE2, B_GLU_124	NZ, A_LYS_143	HZ2, A_LYS_143	2.62	1.83	23.29
5JO5.PDB	OD1, A_ASN_197	OG, A_SER_153	HG, A_SER_153	2.78	2.00	18.34
5JO5.PDB	OG, A_SER_180	NE1, A_TRP_154	HE1, A_TRP_154	2.89	2.05	11.45
5JO5.PDB	OD1, A_ASP_144	NE2, A_GLN_171	HE22, A_GLN_171	2.80	2.01	18.53
5JO5.PDB	OH, B_TYR_177	OG, A_SER_179	HG, A_SER_179	2.83	2.10	25.21
5JO5.PDB	OG, A_SER_188	OH, A_TYR_194	HH, A_TYR_194	2.69	1.94	22.27
5JO5.PDB	OG, A_SER_203	ND1, A_HIS_200	HD1, A_HIS_200	2.79	2.03	23.43
5JO5.PDB	OE2, B_GLU_123	NZ, A_LYS_209	HZ1, A_LYS_209	2.55	1.68	10.64

5JO5.PDB	OH, B_TYR_86	NE2, B_GLN_37	HE21, B_GLN_37	2.95	2.09	5.48
5JO5.PDB	OE1, A_GLN_39	NE2, B_GLN_38	HE22, B_GLN_38	2.90	2.07	12.43
5JO5.PDB	OD1, B_ASP_82	NH2, B_ARG_61	HH21, B_ARG_61	2.66	1.83	11.88
5JO5.PDB	OD1, B_ASP_92	OG, B_SER_95A	HG, B_SER_95A	2.47	1.67	15.14
5JO5.PDB	OE2, B_GLU_124	OG1, B_THR_131	HG1, B_THR_131	2.59	1.86	24.88
5JO5.PDB	OG, B_SER_176	NE1, B_TRP_148	HE1, B_TRP_148	2.89	2.05	10.46
5JO5.PDB	OD1, B_ASN_169	NE2, B_GLN_167	HE21, B_GLN_167	2.98	2.24	26.40
5JO5.PDB	OD1, B_ASP_138	NE2, B_GLN_167	HE22, B_GLN_167	2.99	2.14	6.65
5JO5.PDB	OG1, B_THR_162	OG, B_SER_175	HG, B_SER_175	2.87	2.11	21.53
5JO5.PDB	OG1, B_THR_161	OG, B_SER_176	HG, B_SER_176	2.78	2.05	24.57
5JO5.PDB	OG1, B_THR_205	OG, B_SER_192	HG, B_SER_192	2.59	1.90	29.12
5JO5.PDB	OE2, B_GLU_203	NE2, B_GLN_194	HE21, B_GLN_194	2.60	1.77	11.97
5JO5.PDB	OG1, B_THR_196	OG1, B_THR_201	HG1, B_THR_201	2.97	2.21	22.11
5JO5.PDB	OD2, C_ASP_53	NE1, C_TRP_33	HE1, C_TRP_33	2.84	2.06	21.35
5JO5.PDB	OE1, C_GLU_46	NE, C_ARG_38	HE, C_ARG_38	2.77	1.97	17.97
5JO5.PDB	OH, C_TYR_90	NH1, C_ARG_38	HH11, C_ARG_38	3.00	2.18	14.70
5JO5.PDB	OD1, C_ASP_86	NH1, C_ARG_38	HH12, C_ARG_38	2.85	2.02	13.98
5JO5.PDB	OE1, D_GLN_38	NE2, C_GLN_39	HE22, C_GLN_39	2.86	2.02	9.45
5JO5.PDB	OE1, C_GLU_100J	NE, C_ARG_50	HE, C_ARG_50	2.87	2.09	20.20
5JO5.PDB	OD2, C_ASP_58	NH1, C_ARG_50	HH12, C_ARG_50	2.77	1.94	11.94
5JO5.PDB	OE2, C_GLU_100J	NH2, C_ARG_50	HH21, C_ARG_50	2.86	2.02	10.69
5JO5.PDB	OD2, C_ASP_86	NH1, C_ARG_66	HH12, C_ARG_66	2.83	2.01	15.29
5JO5.PDB	OD1, C_ASP_73	NE, C_ARG_71	HE, C_ARG_71	2.90	2.12	21.25
5JO5.PDB	OD1, C_ASP_72	OG, C_SER_74	HG, C_SER_74	2.61	1.84	20.06
5JO5.PDB	OD2, C_ASP_102	NE, C_ARG_94	HE, C_ARG_94	2.79	2.08	28.98
5JO5.PDB	OD2, C_ASP_102	NH1, C_ARG_94	HH11, C_ARG_94	2.55	1.78	21.18
5JO5.PDB	OE2, D_GLU_124	NZ, C_LYS_143	HZ2, C_LYS_143	2.79	1.92	10.71
5JO5.PDB	OD1, C_ASN_197	OG, C_SER_153	HG, C_SER_153	2.81	2.01	15.61
5JO5.PDB	OG, C_SER_180	NE1, C_TRP_154	HE1, C_TRP_154	2.96	2.13	11.76
5JO5.PDB	OD1, C_ASP_144	NE2, C_GLN_171	HE22, C_GLN_171	2.92	2.12	18.22
5JO5.PDB	OH, D_TYR_177	OG, C_SER_179	HG, C_SER_179	2.71	1.97	23.23
5JO5.PDB	OG, C_SER_188	OH, C_TYR_194	HH, C_TYR_194	2.62	1.86	20.70
5JO5.PDB	OD1, C_ASP_208	ND2, C_ASN_197	HD22, C_ASN_197	2.98	2.12	6.27
5JO5.PDB	OG, C_SER_203	ND1, C_HIS_200	HD1, C_HIS_200	2.85	2.10	24.59
5JO5.PDB	OE2, D_GLU_123	NZ, C_LYS_209	HZ1, C_LYS_209	2.58	1.72	11.28
5JO5.PDB	OG, D_SER_34	OH, D_TYR_36	HH, D_TYR_36	2.76	2.07	29.85
5JO5.PDB	OH, D_TYR_86	NE2, D_GLN_37	HE21, D_GLN_37	2.93	2.09	8.87
5JO5.PDB	OE1, C_GLN_39	NE2, D_GLN_38	HE22, D_GLN_38	2.92	2.09	12.72
5JO5.PDB	OD1, D_ASP_82	NH2, D_ARG_61	HH21, D_ARG_61	2.88	2.03	6.97
5JO5.PDB	OD1, D_ASP_92	OG, D_SER_95A	HG, D_SER_95A	2.53	1.74	15.88
5JO5.PDB	OD1, C_ASP_58	NE, D_ARG_95B	HE, D_ARG_95B	2.94	2.10	11.64
5JO5.PDB	OE2, D_GLU_124	OG1, D_THR_131	HG1, D_THR_131	2.53	1.79	22.99
5JO5.PDB	OG, D_SER_176	NE1, D_TRP_148	HE1, D_TRP_148	2.85	2.01	9.98
5JO5.PDB	OD1, D_ASN_169	NE2, D_GLN_167	HE21, D_GLN_167	2.91	2.12	19.40
5JO5.PDB	OD1, D_ASP_138	NE2, D_GLN_167	HE22, D_GLN_167	2.88	2.03	6.31
5JO5.PDB	OG1, D_THR_161	OG, D_SER_176	HG, D_SER_176	2.78	2.01	20.04
5JO5.PDB	OD2, D_ASP_151	ND1, D_HIS_188	HD1, D_HIS_188	2.67	1.86	16.19
5JO5.PDB	OG1, D_THR_205	OG, D_SER_192	HG, D_SER_192	2.76	2.06	27.74
5JO5.PDB	OE2, D_GLU_203	NE2, D_GLN_194	HE21, D_GLN_194	2.41	1.67	25.54
5JO5.PDB	OD2, E_ASP_53	NE1, E_TRP_33	HE1, E_TRP_33	2.89	2.14	24.08
5JO5.PDB	OG1, E_THR_95	OG, E_SER_35	HG, E_SER_35	2.65	1.97	29.96
5JO5.PDB	OE1, E_GLU_46	NE, E_ARG_38	HE, E_ARG_38	2.75	1.95	17.65
5JO5.PDB	OH, E_TYR_90	NH1, E_ARG_38	HH11, E_ARG_38	2.94	2.11	14.05
5JO5.PDB	OD1, E_ASP_86	NH1, E_ARG_38	HH12, E_ARG_38	2.82	2.00	15.16
5JO5.PDB	OE1, F_GLN_38	NE2, E_GLN_39	HE22, E_GLN_39	2.90	2.06	10.70
5JO5.PDB	OE1, E_GLU_100J	NE, E_ARG_50	HE, E_ARG_50	2.82	2.06	22.79
5JO5.PDB	OD2, E_ASP_58	NH1, E_ARG_50	HH12, E_ARG_50	2.78	1.94	10.17
5JO5.PDB	OE2, E_GLU_100J	NH2, E_ARG_50	HH21, E_ARG_50	2.98	2.13	7.82

5JO5.PDB	OD2, E_ASP_86	NH1, E_ARG_66	HH12, E_ARG_66	2.75	1.91	9.04
5JO5.PDB	OD1, E_ASP_73	NE, E_ARG_71	HE, E_ARG_71	2.89	2.11	20.53
5JO5.PDB	OD1, E_ASP_72	OG, E_SER_74	HG, E_SER_74	2.60	1.77	6.90
5JO5.PDB	OD2, E_ASP_102	NE, E_ARG_94	HE, E_ARG_94	2.83	2.08	25.07
5JO5.PDB	OD2, E_ASP_102	NH2, E_ARG_94	HH21, E_ARG_94	2.73	1.97	23.25
5JO5.PDB	OE2, F_GLU_124	NZ, E_LYS_143	HZ2, E_LYS_143	2.55	1.75	21.57
5JO5.PDB	OD1, E_ASN_197	OG, E_SER_153	HG, E_SER_153	2.80	2.02	18.49
5JO5.PDB	OG, E_SER_180	NE1, E_TRP_154	HE1, E_TRP_154	2.96	2.13	12.27
5JO5.PDB	OD1, E_ASP_144	NE2, E_GLN_171	HE22, E_GLN_171	2.83	2.02	16.42
5JO5.PDB	OH, F_TYR_177	OG, E_SER_179	HG, E_SER_179	2.58	1.87	27.02
5JO5.PDB	OG, E_SER_188	OH, E_TYR_194	HH, E_TYR_194	2.65	1.91	23.44
5JO5.PDB	OD1, E_ASP_208	ND2, E_ASN_197	HD22, E_ASN_197	2.93	2.08	6.74
5JO5.PDB	OE2, F_GLU_123	NZ, E_LYS_209	HZ1, E_LYS_209	2.57	1.74	17.62
5JO5.PDB	OE1, B_GLN_24	OG, F_SER_30	HG, F_SER_30	2.88	2.11	20.15
5JO5.PDB	OH, F_TYR_86	NE2, F_GLN_37	HE21, F_GLN_37	2.98	2.12	5.01
5JO5.PDB	OE1, E_GLN_39	NE2, F_GLN_38	HE22, F_GLN_38	2.85	2.02	12.75
5JO5.PDB	OD2, F_ASP_82	NE, F_ARG_61	HE, F_ARG_61	2.99	2.15	12.18
5JO5.PDB	OD1, F_ASP_82	NH2, F_ARG_61	HH21, F_ARG_61	2.81	1.97	11.97
5JO5.PDB	OE2, E_GLU_100J	NH2, F_ARG_91	HH22, F_ARG_91	2.72	1.87	5.99
5JO5.PDB	OD1, F_ASP_92	OG, F_SER_95A	HG, F_SER_95A	2.58	1.83	23.06
5JO5.PDB	OD1, E_ASP_58	NE, F_ARG_95B	HE, F_ARG_95B	2.92	2.09	12.47
5JO5.PDB	OE1, F_GLU_198	NZ, F_LYS_110	HZ3, F_LYS_110	2.97	2.11	10.79
5JO5.PDB	OE2, F_GLU_124	OG1, F_THR_131	HG1, F_THR_131	2.49	1.76	24.10
5JO5.PDB	OG, F_SER_176	NE1, F_TRP_148	HE1, F_TRP_148	2.88	2.03	9.94
5JO5.PDB	OD1, F_ASN_169	NE2, F_GLN_167	HE21, F_GLN_167	2.87	2.13	25.80
5JO5.PDB	OD1, F_ASP_138	NE2, F_GLN_167	HE22, F_GLN_167	2.86	2.01	8.07
5JO5.PDB	OG1, F_THR_161	OG, F_SER_176	HG, F_SER_176	2.84	2.06	17.97
5JO5.PDB	OE2, F_GLU_203	NE2, F_GLN_194	HE21, F_GLN_194	2.48	1.75	26.23

Table 1764: 5JO5-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5JR1.PDB	OE2, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.66	1.91	24.18
5JR1.PDB	OH, H_TYR_90	NH1, H_ARG_38	HH11, H_ARG_38	2.93	2.12	16.05
5JR1.PDB	OD1, H_ASP_86	NH1, H_ARG_38	HH12, H_ARG_38	2.94	2.11	12.77
5JR1.PDB	OE2, H_GLU_46	NH2, H_ARG_38	HH21, H_ARG_38	2.68	1.95	27.48
5JR1.PDB	OD2, H_ASP_86	NH1, H_ARG_66	HH12, H_ARG_66	2.72	1.87	9.50
5JR1.PDB	OD1, H_ASP_73	NE, H_ARG_71	HE, H_ARG_71	2.99	2.20	19.01
5JR1.PDB	OD1, H_ASP_72	OG, H_SER_74	HG, H_SER_74	2.50	1.70	14.47
5JR1.PDB	OD1, H_ASN_197	OG, H_SER_153	HG, H_SER_153	2.85	2.04	12.85
5JR1.PDB	OG, H_SER_180	NE1, H_TRP_154	HE1, H_TRP_154	2.87	2.02	7.55
5JR1.PDB	OD1, H_ASP_144	NE2, H_GLN_171	HE22, H_GLN_171	2.73	1.95	20.99
5JR1.PDB	OE1, H_GLN_171	OG, H_SER_177	HG, H_SER_177	2.71	1.98	25.79
5JR1.PDB	OH, L_TYR_178	OG, H_SER_179	HG, H_SER_179	2.83	2.03	15.88
5JR1.PDB	OG, H_SER_188	OH, H_TYR_194	HH, H_TYR_194	2.70	1.94	20.59
5JR1.PDB	OE2, H_GLU_212	NE, H_BARG_210	HE, H_BARG_210	2.40	1.64	22.83
5JR1.PDB	OH, L_TYR_86	NE2, L_GLN_37	HE21, L_GLN_37	2.92	2.08	10.60
5JR1.PDB	OD2, L_ASP_82	NE, L_ARG_61	HE, L_ARG_61	2.81	2.00	15.72
5JR1.PDB	OD1, L_ASP_82	NH2, L_ARG_61	HH21, L_ARG_61	2.74	1.90	11.09
5JR1.PDB	OG1, L_THR_20	OG1, L_THR_74	HG1, L_THR_74	2.96	2.15	13.12
5JR1.PDB	OD2, L_ASP_92	OG, L_SER_94	HG, L_SER_94	2.41	1.66	21.72
5JR1.PDB	OD2, H_ASP_58	NH2, L_ARG_95B	HH22, L_ARG_95B	2.47	1.67	16.99
5JR1.PDB	OE1, L_GLU_199	NZ, L_LYS_110	HZ3, L_LYS_110	2.77	1.91	11.53
5JR1.PDB	OE2, L_GLU_125	OG1, L_THR_132	HG1, L_THR_132	2.53	1.79	23.02
5JR1.PDB	OG, L_SER_177	NE1, L_TRP_149	HE1, L_TRP_149	2.84	1.99	9.64
5JR1.PDB	OE1, L_GLN_195	NZ, L_LYS_150	HZ3, L_LYS_150	2.79	1.91	7.52
5JR1.PDB	OD1, L_ASN_170	NE2, L_GLN_168	HE21, L_GLN_168	2.60	1.77	13.13
5JR1.PDB	OD1, L_ASP_139	NE2, L_GLN_168	HE22, L_GLN_168	2.73	1.87	5.77
5JR1.PDB	OE2, L_GLU_204	NE2, L_GLN_195	HE21, L_GLN_195	2.95	2.12	11.81
5JR1.PDB	OG1, L_THR_197	OG1, L_THR_202	HG1, L_THR_202	2.77	1.97	14.73

Table 1765: 5JR1-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5JUE.PDB	OH, H_TYR_91	NE2, L_GLN_38	HE22, L_GLN_38	2.57	1.77	17.09
5JUE.PDB	OD1, L_ASP_82	NH1, L_ARG_61	HH12, L_ARG_61	2.84	1.98	1.66
5JUE.PDB	OD2, L_ASP_82	NH2, L_ARG_61	HH22, L_ARG_61	2.58	1.76	15.54
5JUE.PDB	OG, L_SER_131	NE2, L_GLN_124	HE22, L_GLN_124	2.87	2.01	1.74
5JUE.PDB	OD2, L_ASP_105	OH, L_TYR_140	HH, L_TYR_140	2.73	1.90	9.39
5JUE.PDB	OG, L_SER_177	NE1, L_TRP_148	HE1, L_TRP_148	2.84	1.99	8.07
5JUE.PDB	OE2, L_GLU_195	NZ, L_LYS_149	HZ1, L_LYS_149	2.94	2.11	18.07
5JUE.PDB	OE1, L_GLU_185	NH1, L_ARG_155	HH12, L_ARG_155	2.98	2.13	8.18
5JUE.PDB	OD1, L_ASP_170	OG1, L_THR_172	HG1, L_THR_172	2.65	1.84	10.43
5JUE.PDB	OD1, L_ASP_105	OH, L_TYR_173	HH, L_TYR_173	2.53	1.79	22.81
5JUE.PDB	OG, H_SER_178	OG, L_SER_176	HG, L_SER_176	2.78	1.94	3.13
5JUE.PDB	OD1, L_ASN_161	OG, L_SER_177	HG, L_SER_177	2.61	1.88	24.46
5JUE.PDB	OD1, L_ASP_184	NE, L_ARG_188	HE, L_ARG_188	2.70	1.93	22.77
5JUE.PDB	OG, L_SER_208	OG1, L_THR_193	HG1, L_THR_193	2.92	2.19	25.67
5JUE.PDB	ND1, L_HIS_198	OG1, L_THR_200	HG1, L_THR_200	2.88	2.17	27.29
5JUE.PDB	ND1, H_HIS_35	NE1, H_TRP_47	HE1, H_TRP_47	2.93	2.15	20.72
5JUE.PDB	OD2, H_ASP_86	NZ, H_LYS_66	HZ1, H_LYS_66	2.76	1.87	4.19
5JUE.PDB	OE1, H_GLN_39	OH, H_TYR_91	HH, H_TYR_91	2.83	2.02	11.19
5JUE.PDB	OD1, H_ASP_101	NE, H_ARG_94	HE, H_ARG_94	2.72	1.88	8.15
5JUE.PDB	OD2, H_ASP_101	NH2, H_ARG_94	HH21, H_ARG_94	2.85	2.02	12.42
5JUE.PDB	OE2, H_GLU_148	OH, H_TYR_145	HH, H_TYR_145	2.72	1.89	3.03
5JUE.PDB	OD1, H_ASN_196	OG1, H_THR_153	HG1, H_THR_153	2.74	1.98	20.12
5JUE.PDB	OG1, H_THR_137	OG1, H_THR_182	HG1, H_THR_182	2.77	2.00	20.14
5JUE.PDB	OG1, H_THR_184	OG1, H_THR_187	HG1, H_THR_187	2.67	1.90	19.94
5JUE.PDB	ND1, H_HIS_199	OG, H_SER_202	HG, H_SER_202	2.87	2.13	24.10
5JUE.PDB	OE1, L_GLU_123	NZ, H_LYS_208	HZ1, H_LYS_208	2.81	1.98	17.66

Table 1766: 5JUE-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5JXA.PDB	OE1, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.80	2.04	23.29
5JXA.PDB	OD1, H_ASP_86	NH1, H_ARG_38	HH12, H_ARG_38	2.74	1.88	4.26
5JXA.PDB	OE1, H_GLU_46	NH2, H_ARG_38	HH21, H_ARG_38	2.76	2.00	23.95
5JXA.PDB	OE2, H_GLU_46	NE2, H_GLN_62	HE21, H_GLN_62	2.86	2.00	1.72
5JXA.PDB	OD1, H_ASP_86	NH2, H_ARG_66	HH22, H_ARG_66	2.96	2.11	6.31
5JXA.PDB	OD2, H_ASP_76C	NE1, H_TRP_76F	HE1, H_TRP_76F	2.87	2.15	28.04
5JXA.PDB	OD1, H_ASP_99	NH2, H_ARG_95	HH22, H_ARG_95	2.95	2.09	5.23
5JXA.PDB	OD2, L_ASP_50	OH, H_TYR_100	HH, H_TYR_100	2.57	1.75	11.76
5JXA.PDB	OD1, H_ASP_144	NZ, H_LYS_143	HZ3, H_LYS_143	2.92	2.12	22.30
5JXA.PDB	OD1, H_ASN_197	OG, H_SER_153	HG, H_SER_153	2.75	1.96	17.62
5JXA.PDB	OG, H_SER_180	NE1, H_TRP_154	HE1, H_TRP_154	2.96	2.12	10.70
5JXA.PDB	OD1, H_ASP_144	NE2, H_GLN_171	HE22, H_GLN_171	2.86	2.05	16.31
5JXA.PDB	OG, H_SER_188	OH, H_TYR_194	HH, H_TYR_194	2.92	2.22	28.67
5JXA.PDB	ND1, H_HIS_200	OG, H_SER_203	HG, H_SER_203	2.82	2.10	26.44
5JXA.PDB	OE1, L_GLN_89	OH, L_TYR_36	HH, L_TYR_36	2.71	1.91	14.07
5JXA.PDB	OH, L_TYR_86	NE2, L_GLN_37	HE21, L_GLN_37	2.99	2.15	10.29
5JXA.PDB	OH, H_TYR_100	NH2, L_ARG_53	HH21, L_ARG_53	2.89	2.07	18.12
5JXA.PDB	OD2, L_ASP_82	NE, L_ARG_61	HE, L_ARG_61	2.88	2.15	27.19
5JXA.PDB	OD1, L_ASP_82	NH2, L_ARG_61	HH21, L_ARG_61	2.84	1.98	2.45
5JXA.PDB	OD1, L_ASP_70	OG1, L_THR_69	HG1, L_THR_69	2.92	2.09	7.50
5JXA.PDB	OG, L_SER_131	NE2, L_GLN_124	HE22, L_GLN_124	2.80	1.95	4.80
5JXA.PDB	OE1, L_GLU_105	OH, L_TYR_140	HH, L_TYR_140	2.43	1.65	17.73
5JXA.PDB	OE1, L_GLU_103	NH1, L_ARG_142	HH12, L_ARG_142	2.87	2.05	14.46
5JXA.PDB	OH, L_TYR_173	NH2, L_ARG_142	HH21, L_ARG_142	2.84	2.07	21.88
5JXA.PDB	OE2, L_GLU_103	NH2, L_ARG_142	HH22, L_ARG_142	2.79	1.94	8.50
5JXA.PDB	OG, L_SER_177	NE1, L_TRP_148	HE1, L_TRP_148	2.86	2.05	17.07
5JXA.PDB	OE1, L_GLN_155	ND2, L_ASN_158	HD21, L_ASN_158	2.94	2.10	10.59
5JXA.PDB	OD1, L_ASP_170	OG1, L_THR_172	HG1, L_THR_172	2.69	1.87	10.60
5JXA.PDB	OE2, L_GLU_105	OH, L_TYR_173	HH, L_TYR_173	2.63	1.83	14.46
5JXA.PDB	OD1, L_ASP_185	NZ, L_LYS_188	HZ2, L_LYS_188	2.85	2.03	19.98
5JXA.PDB	OE2, L_GLU_213	ND2, L_ASN_210	HD22, L_ASN_210	2.76	1.93	12.84

Table 1767: 5JXA-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5M2C.PDB	OD1, A_ASP_195	NZ, A_LYS_124	HZ1, A_LYS_124	2.99	2.26	29.03
5M2C.PDB	OH, A_TYR_127	NE2, A_HIS_151	HE2, A_HIS_151	2.61	1.77	12.06
5M2C.PDB	OG, A_SER_159	OG1, A_THR_163	HG1, A_THR_163	2.88	2.07	13.51
5M2C.PDB	OG, A_SER_179	ND2, A_ASN_184	HD21, A_ASN_184	2.93	2.13	18.24
5M2C.PDB	OD2, A_ASP_128	NE2, A_HIS_191	HE2, A_HIS_191	2.69	1.84	6.13
5M2C.PDB	OH, B_TYR_127	NE2, B_HIS_151	HE2, B_HIS_151	2.61	1.78	13.01
5M2C.PDB	OG, B_SER_179	ND2, B_ASN_184	HD21, B_ASN_184	2.89	2.10	19.97
5M2C.PDB	OD2, B_ASP_128	NE2, B_HIS_191	HE2, B_HIS_191	2.71	1.86	7.63

Table 1768: 5M2C-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5M33.PDB	OD1, A_ASP_122	NE2, A_GLN_118	HE21, A_GLN_118	2.92	2.20	28.21
5M33.PDB	OD1, A_ASP_195	NZ, A_LYS_124	HZ3, A_LYS_124	2.81	2.00	20.18
5M33.PDB	NE2, A_HIS_151	OH, A_TYR_127	HH, A_TYR_127	2.74	1.90	5.54
5M33.PDB	OD1, A_ASP_155	NZ, A_LYS_187	HZ1, A_LYS_187	2.82	1.95	10.61
5M33.PDB	OD2, A_ASP_128	NE2, A_HIS_191	HE2, A_HIS_191	2.76	2.00	23.16
5M33.PDB	OD1, A_ASP_196	NE2, A_GLN_192	HE21, A_GLN_192	2.98	2.18	18.41
5M33.PDB	OE1, A_GLU_188	NZ, A_LYS_193	HZ2, A_LYS_193	2.93	2.07	12.47
5M33.PDB	OD1, B_ASP_122	NE2, B_GLN_118	HE21, B_GLN_118	2.96	2.19	23.61
5M33.PDB	NE2, B_HIS_151	OH, B_TYR_127	HH, B_TYR_127	2.78	1.94	5.42
5M33.PDB	OE1, B_GLN_133	NE2, B_GLN_129	HE22, B_GLN_129	2.83	2.06	21.87
5M33.PDB	OD1, B_ASP_189	OG, B_SER_160	HG, B_SER_160	2.86	2.13	25.03
5M33.PDB	OD2, B_ASP_128	NE2, B_HIS_191	HE2, B_HIS_191	2.69	1.83	4.41
5M33.PDB	OD1, B_ASP_196	NE2, B_GLN_192	HE21, B_GLN_192	2.92	2.12	17.81

Table 1769: 5M33-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5M3D.PDB	OD2, A_ASP_195	NZ, A_LYS_124	HZ1, A_LYS_124	2.68	1.86	18.64
5M3D.PDB	NE2, A_HIS_151	OH, A_TYR_127	HH, A_TYR_127	2.90	2.07	7.76
5M3D.PDB	OG1, A_SER_159	OG1, A_THR_163	HG1, A_THR_163	2.65	1.81	3.28
5M3D.PDB	OD2, A_ASP_128	NE2, A_HIS_191	HE2, A_HIS_191	2.68	1.84	10.19
5M3D.PDB	OD2, B_ASP_128	NE2, B_HIS_191	HE2, B_HIS_191	2.60	1.78	15.29
5M3D.PDB	OH, C_TYR_127	NE2, C_HIS_151	HE2, C_HIS_151	2.47	1.64	11.96
5M3D.PDB	OD2, C_ASP_128	NE2, C_HIS_191	HE2, C_HIS_191	2.54	1.74	17.73
5M3D.PDB	OD2, D_ASP_128	NE2, D_HIS_191	HE2, D_HIS_191	2.53	1.71	14.84

Table 1770: 5M3D-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5M3T.PDB	NE2, A_HIS_151	OH, A_TYR_127	HH, A_TYR_127	2.73	1.92	14.40
5M3T.PDB	OG, A_SER_159	OG1, A_THR_161	HG1, A_THR_161	2.93	2.10	8.83
5M3T.PDB	OD1, A_ASP_128	NE2, A_HIS_191	HE2, A_HIS_191	2.70	1.84	4.47
5M3T.PDB	OD2, B_ASP_195	NZ, B_LYS_124	HZ1, B_LYS_124	2.94	2.15	23.24
5M3T.PDB	NE2, B_HIS_151	OH, B_TYR_127	HH, B_TYR_127	2.86	2.03	6.62
5M3T.PDB	OD1, B_ASP_128	NE2, B_HIS_191	HE2, B_HIS_191	2.76	1.92	11.16

Table 1771: 5M3T-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5M4R.PDB	OG, A_SER_159	OG1, A_THR_163	HG1, A_THR_163	2.93	2.14	15.31
5M4R.PDB	OD2, A_ASP_128	NE2, A_HIS_191	HE2, A_HIS_191	2.54	1.73	17.27
5M4R.PDB	OG, B_SER_159	OG1, B_THR_163	HG1, B_THR_163	2.85	2.02	5.63
5M4R.PDB	OG, C_SER_159	OG1, C_THR_163	HG1, C_THR_163	2.95	2.12	7.91
5M4R.PDB	OD2, E_ASP_128	NE2, E_HIS_191	HE2, E_HIS_191	2.53	1.73	17.17

Table 1772: 5M4R-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5T6P.PDB	OD1, A_ASP_75	NE, A_ARG_24	HE, A_ARG_24	2.87	2.06	16.15
5T6P.PDB	OD1, A_ASP_87	NH2, A_ARG_66	HH22, A_ARG_66	2.87	2.03	10.92
5T6P.PDB	OG, A_SER_136	NE2, A_GLN_129	HE22, A_GLN_129	2.81	1.96	6.44
5T6P.PDB	OG, A_SER_182	NE1, A_TRP_153	HE1, A_TRP_153	2.84	2.00	11.05
5T6P.PDB	OD1, A_ASP_175	OG1, A_THR_177	HG1, A_THR_177	2.59	1.78	13.64
5T6P.PDB	OD1, A_ASN_166	OG, A_SER_182	HG, A_SER_182	2.54	1.72	9.61
5T6P.PDB	OE1, B_GLU_46	NE, B_ARG_38	HE, B_ARG_38	2.70	1.96	26.33
5T6P.PDB	OE1, A_GLN_43	NE2, B_GLN_39	HE22, B_GLN_39	2.71	1.86	5.14
5T6P.PDB	OD1, B_ASN_74	NE, B_ARG_72	HE, B_ARG_72	2.87	2.14	26.22
5T6P.PDB	OD1, C_ASP_75	NE, C_ARG_24	HE, C_ARG_24	2.92	2.14	20.59
5T6P.PDB	OD1, C_ASP_75	NH2, C_ARG_24	HH21, C_ARG_24	2.94	2.18	23.70
5T6P.PDB	OE1, D_GLN_39	NE2, C_GLN_43	HE22, C_GLN_43	3.00	2.17	12.88
5T6P.PDB	OG, C_SER_136	NE2, C_GLN_129	HE22, C_GLN_129	2.79	1.95	11.34
5T6P.PDB	OG, C_SER_182	NE1, C_TRP_153	HE1, C_TRP_153	2.89	2.07	15.50
5T6P.PDB	OD1, C_ASP_175	OG1, C_THR_177	HG1, C_THR_177	2.69	1.86	7.21
5T6P.PDB	OD1, C_ASN_166	OG, C_SER_182	HG, C_SER_182	2.45	1.64	11.11
5T6P.PDB	OG, C_SER_213	OG1, C_THR_198	HG1, C_THR_198	3.00	2.20	14.46
5T6P.PDB	OE1, C_GLN_43	NE2, D_GLN_39	HE22, D_GLN_39	2.79	1.94	7.20
5T6P.PDB	OD1, D_ASN_74	NE, D_ARG_72	HE, D_ARG_72	2.79	2.07	27.15
5T6P.PDB	OG, D_SER_182	NE1, D_TRP_157	HE1, D_TRP_157	2.97	2.13	11.56
5T6P.PDB	OE1, C_GLU_39	NE, E_ARG_5	HE, E_ARG_5	2.86	2.02	10.72

Table 1773: 5T6P-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5T78.PDB	OE1, B_GLN_39	NE2, A_GLN_43	HE22, A_GLN_43	2.92	2.08	9.79
5T78.PDB	OD2, A_ASP_87	NH1, A_ARG_66	HH12, A_ARG_66	2.55	1.80	24.29
5T78.PDB	OD1, A_ASP_87	NH2, A_ARG_66	HH22, A_ARG_66	2.87	2.03	11.23
5T78.PDB	OG, A_SER_136	NE2, A_GLN_129	HE22, A_GLN_129	2.86	2.01	3.70
5T78.PDB	OG, A_SER_182	NE1, A_TRP_153	HE1, A_TRP_153	2.68	1.86	12.79
5T78.PDB	OD1, A_ASP_175	OG1, A_THR_177	HG1, A_THR_177	2.57	1.74	7.68
5T78.PDB	OD1, A_ASN_166	OG, A_SER_182	HG, A_SER_182	2.63	1.89	23.17
5T78.PDB	OD2, A_ASP_156	ND1, A_HIS_194	HD1, A_HIS_194	2.73	1.92	16.43
5T78.PDB	ND1, A_HIS_203	OG1, A_THR_205	HG1, A_THR_205	2.99	2.26	25.09
5T78.PDB	OG1, A_THR_198	OG, A_SER_213	HG, A_SER_213	2.76	1.99	20.46
5T78.PDB	OE1, B_GLU_46	NE, B_ARG_38	HE, B_ARG_38	2.94	2.16	20.63
5T78.PDB	OH, B_TYR_94	NH1, B_ARG_38	HH11, B_ARG_38	2.90	2.09	15.42
5T78.PDB	OD1, B_ASP_90	NH1, B_ARG_38	HH12, B_ARG_38	2.89	2.09	17.62
5T78.PDB	OE1, A_GLN_43	NE2, B_GLN_39	HE22, B_GLN_39	2.63	1.78	5.56
5T78.PDB	OD1, B_ASN_74	NE, B_ARG_72	HE, B_ARG_72	2.69	1.95	25.68
5T78.PDB	OE1, B_GLN_39	OH, B_TYR_95	HH, B_TYR_95	2.91	2.11	14.46
5T78.PDB	OG1, B_THR_185	OG1, B_THR_140	HG1, B_THR_140	2.97	2.14	5.19
5T78.PDB	OE1, A_GLU_39	NH1, F_ARG_5	HH11, F_ARG_5	2.68	1.83	9.33
5T78.PDB	OD1, C_ASP_75	NE, C_ARG_24	HE, C_ARG_24	2.96	2.16	17.61
5T78.PDB	OH, C_TYR_37	ND2, C_ASN_33	HD21, C_ASN_33	2.96	2.18	21.06
5T78.PDB	OD2, C_ASP_87	NH1, C_ARG_66	HH12, C_ARG_66	2.35	1.56	19.31
5T78.PDB	OG, C_SER_182	NE1, C_TRP_153	HE1, C_TRP_153	2.84	2.01	13.01
5T78.PDB	OD1, C_ASP_175	OG1, C_THR_177	HG1, C_THR_177	2.53	1.70	9.09
5T78.PDB	OD1, C_ASN_166	OG, C_SER_182	HG, C_SER_182	2.85	2.09	21.73
5T78.PDB	OD2, C_ASP_156	ND1, C_HIS_194	HD1, C_HIS_194	2.58	1.78	18.23
5T78.PDB	ND1, C_HIS_203	OG1, C_THR_205	HG1, C_THR_205	3.00	2.26	23.83
5T78.PDB	OE1, D_GLU_46	NE, D_ARG_38	HE, D_ARG_38	2.65	1.91	25.36
5T78.PDB	OH, D_TYR_94	NH1, D_ARG_38	HH11, D_ARG_38	2.88	2.06	14.14
5T78.PDB	OD1, D_ASP_90	NH1, D_ARG_38	HH12, D_ARG_38	2.85	2.05	16.93
5T78.PDB	OE1, C_GLN_43	NE2, D_GLN_39	HE22, D_GLN_39	2.72	1.87	5.23
5T78.PDB	OD1, D_ASN_74	NE, D_ARG_72	HE, D_ARG_72	2.71	2.01	29.42
5T78.PDB	OE1, D_GLN_39	OH, D_TYR_95	HH, D_TYR_95	2.98	2.17	11.35
5T78.PDB	OG, D_SER_182	NE1, D_TRP_157	HE1, D_TRP_157	2.99	2.19	18.03
5T78.PDB	OD1, C_ASN_142	NE2, D_HIS_167	HE2, D_HIS_167	2.85	2.00	9.68
5T78.PDB	OE1, C_GLU_39	NH1, E_ARG_5	HH11, E_ARG_5	2.69	1.87	13.16

Table 1774: 5T78-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5U3J.PDB	OE1, H_GLN_81	NE, H_ARG_19	HE, H_ARG_19	2.98	2.21	22.79
5U3J.PDB	OD2, H_ASP_53	NE1, H_TRP_33	HE1, H_TRP_33	2.97	2.22	24.73
5U3J.PDB	OE1, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.88	2.05	13.82
5U3J.PDB	OD1, H_ASP_86	NH1, H_ARG_38	HH12, H_ARG_38	2.85	2.09	23.00
5U3J.PDB	OG, H_SER_35	NE1, H_TRP_47	HE1, H_TRP_47	2.44	1.73	27.73
5U3J.PDB	OE1, H_GLU_58	NE, H_ARG_50	HE, H_ARG_50	2.83	2.12	29.07
5U3J.PDB	OE1, H_GLU_58	NH2, H_ARG_50	HH21, H_ARG_50	2.79	2.08	29.38
5U3J.PDB	OD2, H_ASP_86	NH1, H_ARG_66	HH12, H_ARG_66	2.57	1.73	9.26
5U3J.PDB	OD1, H_ASP_86	NH2, H_ARG_66	HH22, H_ARG_66	2.89	2.04	5.32
5U3J.PDB	OD1, L_ASP_31	OH, H_TYR_100K	HH, H_TYR_100K	2.88	2.04	5.22
5U3J.PDB	OG, H_SER_180	NE1, H_TRP_154	HE1, H_TRP_154	2.98	2.15	12.85
5U3J.PDB	OE1, H_GLU_100F	OH, L_TYR_32	HH, L_TYR_32	2.62	1.91	27.84
5U3J.PDB	OE1, L_GLN_89	OH, L_TYR_36	HH, L_TYR_36	2.74	1.93	13.79
5U3J.PDB	OE1, H_GLN_39	NE2, L_GLN_38	HE22, L_GLN_38	2.66	1.83	12.57
5U3J.PDB	OG, L_SER_131	NE2, L_GLN_124	HE22, L_GLN_124	2.67	1.82	7.69
5U3J.PDB	OG, L_SER_177	NE1, L_TRP_148	HE1, L_TRP_148	2.81	2.02	19.92

Table 1775: 5U3J-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5U3N.PDB	OE1, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.91	2.07	9.07
5U3N.PDB	OH, H_TYR_90	NH1, H_ARG_38	HH11, H_ARG_38	3.00	2.21	20.04
5U3N.PDB	OD2, H_ASP_58	NE, H_ARG_50	HE, H_ARG_50	2.78	1.98	18.36
5U3N.PDB	OD2, A_ASP_674	NH1, H_ARG_52A	HH12, H_ARG_52A	3.00	2.24	24.41
5U3N.PDB	OD1, H_ASP_53	NH2, H_ARG_52A	HH21, H_ARG_52A	2.93	2.18	25.35
5U3N.PDB	OD2, H_ASP_86	NH1, H_ARG_66	HH12, H_ARG_66	2.73	1.91	14.46
5U3N.PDB	OD1, H_ASP_73	NE, H_ARG_71	HE, H_ARG_71	2.93	2.13	17.92
5U3N.PDB	OE1, H_GLU_100E	NE, H_ARG_100B	HE, H_ARG_100B	2.83	1.97	4.42
5U3N.PDB	OE2, H_GLU_100E	NH2, H_ARG_100B	HH21, H_ARG_100B	2.91	2.08	12.18
5U3N.PDB	OD1, L_ASP_31	NH2, H_ARG_100B	HH22, H_ARG_100B	2.97	2.15	14.50
5U3N.PDB	OD1, L_ASN_34	ND2, H_ASN_100J	HD21, H_ASN_100J	2.72	1.86	2.61
5U3N.PDB	OG, H_SER_180	NE1, H_TRP_154	HE1, H_TRP_154	2.95	2.11	9.10
5U3N.PDB	OD1, L_ASN_138	NE2, H_HIS_164	HE2, H_HIS_164	2.92	2.21	29.54
5U3N.PDB	OD1, H_ASP_144	NE2, H_GLN_171	HE22, H_GLN_171	2.99	2.19	18.08
5U3N.PDB	OH, L_TYR_140	OG, L_SER_12	HG, L_SER_12	2.60	1.87	23.71
5U3N.PDB	OE1, L_GLN_89	ND2, L_ASN_34	HD22, L_ASN_34	2.99	2.18	18.14
5U3N.PDB	OE1, L_GLN_89	OH, L_TYR_36	HH, L_TYR_36	2.64	1.80	1.88
5U3N.PDB	OG, L_SER_131	NE2, L_GLN_124	HE22, L_GLN_124	2.80	1.94	3.81
5U3N.PDB	OD1, L_ASP_105	OH, L_TYR_140	HH, L_TYR_140	2.61	1.87	24.55
5U3N.PDB	OG, L_SER_177	NE1, L_TRP_148	HE1, L_TRP_148	2.84	2.01	13.43
5U3N.PDB	OD1, L_ASP_170	OG1, L_THR_172	HG1, L_THR_172	2.63	1.80	7.71
5U3N.PDB	OD2, L_ASP_105	OH, L_TYR_173	HH, L_TYR_173	2.66	1.88	16.93

Table 1776: 5U3N-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5UCB.PDB	OG, H_SER_33	NE2, H_HIS_35	HE2, H_HIS_35	2.88	2.09	19.50
5UCB.PDB	OE1, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.85	2.03	15.54
5UCB.PDB	OH, H_TYR_90	NH1, H_ARG_38	HH11, H_ARG_38	2.94	2.12	15.88
5UCB.PDB	OD1, H_ASP_86	NH1, H_ARG_38	HH12, H_ARG_38	2.88	2.08	18.54
5UCB.PDB	OE1, L_GLN_38	NE2, H_GLN_39	HE22, H_GLN_39	2.96	2.12	9.92
5UCB.PDB	OG, H_SER_50	NE1, H_TRP_47	HE1, H_TRP_47	2.72	1.98	25.90
5UCB.PDB	OD2, H_ASP_86	NH1, H_ARG_66	HH12, H_ARG_66	2.75	1.90	5.99
5UCB.PDB	OD1, H_ASP_72	OG, H_SER_74	HG, H_SER_74	2.60	1.83	20.07
5UCB.PDB	OD1, H_ASN_197	OG, H_SER_153	HG, H_SER_153	2.85	2.06	15.76
5UCB.PDB	OG, H_SER_180	NE1, H_TRP_154	HE1, H_TRP_154	2.92	2.07	7.16
5UCB.PDB	OD1, H_ASP_144	NE2, H_GLN_171	HE22, H_GLN_171	2.78	1.99	18.86
5UCB.PDB	OG, H_SER_188	OH, H_TYR_194	HH, H_TYR_194	2.72	1.90	9.93
5UCB.PDB	OD1, H_ASP_208	ND2, H_ASN_197	HD22, H_ASN_197	2.80	1.95	7.44
5UCB.PDB	OE1, L_GLN_3	OG, L_SER_26	HG, L_SER_26	2.61	1.78	7.17
5UCB.PDB	OD2, B_ASP_51	OG, L_SER_30	HG, L_SER_30	2.58	1.81	20.19
5UCB.PDB	OE1, L_GLN_89	OH, L_TYR_36	HH, L_TYR_36	2.64	1.84	15.57
5UCB.PDB	OH, L_TYR_86	NE2, L_GLN_37	HE21, L_GLN_37	2.99	2.15	9.80
5UCB.PDB	OE1, H_GLN_39	NE2, L_GLN_38	HE22, L_GLN_38	2.95	2.13	14.86
5UCB.PDB	OD2, L_ASP_82	NE, L_ARG_61	HE, L_ARG_61	2.82	2.01	16.79
5UCB.PDB	OD1, L_ASP_82	NH2, L_ARG_61	HH21, L_ARG_61	2.85	1.99	4.65
5UCB.PDB	OG1, L_THR_22	OG1, L_THR_72	HG1, L_THR_72	2.96	2.18	19.19
5UCB.PDB	OE1, L_GLU_165	NZ, L_LYS_103	HZ3, L_LYS_103	2.77	1.90	9.89
5UCB.PDB	OG, L_SER_131	NE2, L_GLN_124	HE22, L_GLN_124	2.73	1.87	2.66
5UCB.PDB	OG, L_SER_177	NE1, L_TRP_148	HE1, L_TRP_148	2.92	2.09	12.30
5UCB.PDB	OE1, L_GLN_155	ND2, L_ASN_158	HD21, L_ASN_158	2.98	2.15	12.35
5UCB.PDB	OD1, L_ASP_170	OG1, L_THR_172	HG1, L_THR_172	2.71	1.89	8.99
5UCB.PDB	OE2, L_GLU_105	OH, L_TYR_173	HH, L_TYR_173	2.61	1.81	15.35
5UCB.PDB	OD1, B_ASP_132	NZ, B_LYS_16	HZ1, B_LYS_16	2.90	2.15	27.66
5UCB.PDB	OE2, B_GLU_87	OH, B_TYR_43	HH, B_TYR_43	2.72	1.91	12.68
5UCB.PDB	OD1, B_ASP_51	OG, B_SER_46	HG, B_SER_46	2.83	2.02	12.78
5UCB.PDB	OE1, B_GLU_87	OG, B_SER_47	HG, B_SER_47	2.62	1.82	14.05
5UCB.PDB	OD1, B_ASP_153	OH, B_TYR_100	HH, B_TYR_100	2.55	1.73	8.75
5UCB.PDB	OD2, B_ASP_101	NH1, B_ARG_103	HH12, B_ARG_103	2.89	2.11	20.47
5UCB.PDB	OE2, B_GLU_104	NE, B_ARG_107	HE, B_ARG_107	2.91	2.05	4.26
5UCB.PDB	OD1, B_ASP_117	ND1, B_HIS_133	HD1, B_HIS_133	2.95	2.15	18.23
5UCB.PDB	OG, H_SER_58	NZ, B_LYS_142	HZ3, B_LYS_142	2.83	1.96	8.82
5UCB.PDB	OD1, L_ASP_91	NH2, B_ARG_144	HH21, B_ARG_144	2.84	2.03	16.18

Table 1777: 5UCB-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5UK0.PDB	OD1, F_ASP_590	ND2, B_ASN_560	HD22, B_ASN_560	2.72	1.94	19.72
5UK0.PDB	OD1, D_ASP_586	NH2, C_ARG_311	HH22, C_ARG_311	2.98	2.20	18.56
5UK0.PDB	OD1, B_ASP_590	ND2, D_ASN_560	HD22, D_ASN_560	2.73	1.95	20.06
5UK0.PDB	OH, D_TYR_659	ND2, D_ASN_628	HD22, D_ASN_628	2.78	1.98	17.11

Table 1778: 5UK0-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5VXJ.PDB	OD2, A_ASP_309	NH2, A_ARG_55	HH21, A_ARG_55	2.90	2.12	21.39
5VXJ.PDB	OG, A_SER_302	NZ, A_LYS_62	HZ2, A_LYS_62	2.77	1.91	12.44
5VXJ.PDB	OG, A_SER_306	NZ, A_LYS_62	HZ3, A_LYS_62	2.75	1.92	16.95
5VXJ.PDB	OD2, A_ASP_97	NE, A_ARG_101	HE, A_ARG_101	2.80	1.97	13.39
5VXJ.PDB	OE2, A_GLU_229	OH, A_TYR_153	HH, A_TYR_153	2.70	1.94	21.05
5VXJ.PDB	OD1, A_ASP_287	OH, A_TYR_164	HH, A_TYR_164	2.72	1.96	22.05
5VXJ.PDB	OE2, A_GLU_268	NE2, A_GLN_191	HE22, A_GLN_191	2.93	2.12	16.99
5VXJ.PDB	OD1, A_ASP_254	NZ, A_LYS_203	HZ2, A_LYS_203	2.48	1.62	10.37
5VXJ.PDB	OD2, A_ASP_166	NZ, A_LYS_205	HZ2, A_LYS_205	2.60	1.73	10.82
5VXJ.PDB	OD2, A_ASP_166	OH, A_TYR_206	HH, A_TYR_206	2.59	1.78	13.29
5VXJ.PDB	OD1, A_ASN_249	OG1, A_THR_251	HG1, A_THR_251	2.61	1.88	24.99
5VXJ.PDB	OD1, A_ASN_58	ND2, A_ASN_305	HD21, A_ASN_305	2.96	2.14	16.38
5VXJ.PDB	OE1, B_GLN_82	NE, B_ARG_19	HE, B_ARG_19	2.47	1.66	15.76
5VXJ.PDB	OE2, B_GLU_46	NE, B_ARG_38	HE, B_ARG_38	2.93	2.12	17.64
5VXJ.PDB	OH, B_TYR_94	NH1, B_ARG_38	HH11, B_ARG_38	2.80	1.98	13.19
5VXJ.PDB	OD1, B_ASP_90	NH1, B_ARG_38	HH12, B_ARG_38	2.76	1.91	7.08
5VXJ.PDB	OD1, B_ASN_35	NE, B_ARG_50	HE, B_ARG_50	2.65	1.82	11.22
5VXJ.PDB	OE1, I_GLU_200	NH1, B_ARG_50	HH12, B_ARG_50	2.92	2.07	7.25
5VXJ.PDB	OD2, B_ASP_90	NH1, B_ARG_67	HH12, B_ARG_67	2.82	2.01	16.67
5VXJ.PDB	OD1, B_ASP_90	NH2, B_ARG_67	HH22, B_ARG_67	2.96	2.12	11.06
5VXJ.PDB	OD1, B_ASN_84	NE2, B_GLN_82	HE21, B_GLN_82	2.95	2.09	2.81
5VXJ.PDB	OG1, B_THR_107	ND2, B_ASN_97	HD21, B_ASN_97	2.64	1.86	19.39
5VXJ.PDB	OE1, I_GLU_201	OH, B_TYR_105	HH, B_TYR_105	2.51	1.70	12.69
5VXJ.PDB	OD2, C_ASP_309	NH2, C_ARG_55	HH21, C_ARG_55	2.97	2.17	18.00
5VXJ.PDB	OG, C_SER_302	NZ, C_LYS_62	HZ2, C_LYS_62	2.61	1.73	6.54
5VXJ.PDB	OE2, C_GLU_154	OG, C_SER_82	HG, C_SER_82	2.58	1.81	19.25
5VXJ.PDB	OD2, C_ASP_97	NE, C_ARG_101	HE, C_ARG_101	2.84	2.03	16.71
5VXJ.PDB	OD1, C_ASP_287	OH, C_TYR_164	HH, C_TYR_164	2.77	1.96	12.03
5VXJ.PDB	OE2, C_GLU_268	NE2, C_GLN_191	HE22, C_GLN_191	2.80	1.97	12.09
5VXJ.PDB	OE1, C_GLU_201	NZ, C_LYS_197	HZ3, C_LYS_197	2.59	1.85	27.46
5VXJ.PDB	OD1, C_ASP_254	NZ, C_LYS_203	HZ2, C_LYS_203	2.69	1.87	19.49
5VXJ.PDB	OD2, C_ASP_166	NZ, C_LYS_205	HZ2, C_LYS_205	2.85	1.99	12.15
5VXJ.PDB	OD2, C_ASP_166	OH, C_TYR_206	HH, C_TYR_206	2.58	1.76	10.37
5VXJ.PDB	OD1, C_ASN_249	OG1, C_THR_251	HG1, C_THR_251	2.56	1.78	18.84
5VXJ.PDB	OD1, C_ASN_58	ND2, C_ASN_305	HD21, C_ASN_305	2.84	2.04	17.79
5VXJ.PDB	OD1, C_ASN_140	NE, D_ARG_19	HE, D_ARG_19	2.55	1.80	23.66
5VXJ.PDB	OE1, D_GLN_82	NH1, D_ARG_19	HH11, D_ARG_19	2.94	2.14	18.04
5VXJ.PDB	OE2, D_GLU_46	NE, D_ARG_38	HE, D_ARG_38	2.46	1.69	20.96
5VXJ.PDB	OD1, D_ASP_90	NH1, D_ARG_38	HH12, D_ARG_38	2.86	2.04	15.32
5VXJ.PDB	OD1, D_ASN_35	NE, D_ARG_50	HE, D_ARG_50	2.89	2.08	17.01
5VXJ.PDB	OD2, D_ASP_90	NH1, D_ARG_67	HH12, D_ARG_67	2.76	1.94	14.49
5VXJ.PDB	OD1, D_ASP_90	NH2, D_ARG_67	HH22, D_ARG_67	2.92	2.07	6.62
5VXJ.PDB	OD1, D_ASN_74	NE, D_ARG_72	HE, D_ARG_72	2.76	1.91	6.10
5VXJ.PDB	OD1, D_ASN_84	NE2, D_GLN_82	HE21, D_GLN_82	2.80	1.94	4.20
5VXJ.PDB	OG1, D_THR_107	ND2, D_ASN_97	HD21, D_ASN_97	2.71	1.91	17.78
5VXJ.PDB	OE1, E_GLU_201	OH, D_TYR_105	HH, D_TYR_105	2.53	1.70	8.84
5VXJ.PDB	OD2, E_ASP_309	NH2, E_ARG_55	HH21, E_ARG_55	2.82	2.06	24.28
5VXJ.PDB	OG, E_SER_306	NZ, E_LYS_62	HZ1, E_LYS_62	2.46	1.61	13.80
5VXJ.PDB	OD2, F_ASP_73	NZ, E_LYS_137	HZ2, E_LYS_137	2.77	1.96	20.15
5VXJ.PDB	OD1, E_ASP_287	OH, E_TYR_164	HH, E_TYR_164	2.85	2.09	21.13
5VXJ.PDB	OD1, D_ASN_97	NZ, E_LYS_197	HZ1, E_LYS_197	2.80	1.95	14.72
5VXJ.PDB	OE2, E_GLU_201	NZ, E_LYS_197	HZ3, E_LYS_197	2.47	1.71	25.42
5VXJ.PDB	OD1, E_ASP_254	NZ, E_LYS_203	HZ2, E_LYS_203	2.55	1.67	5.69
5VXJ.PDB	OD2, E_ASP_166	NZ, E_LYS_205	HZ2, E_LYS_205	2.79	1.95	15.80
5VXJ.PDB	OD2, E_ASP_166	OH, E_TYR_206	HH, E_TYR_206	2.80	1.99	13.17
5VXJ.PDB	OD1, E_ASN_249	OG1, E_THR_251	HG1, E_THR_251	2.55	1.84	26.63
5VXJ.PDB	OD1, E_ASN_58	ND2, E_ASN_305	HD21, E_ASN_305	2.80	1.98	14.83

5VXJ.PDB	OE1, F_GLN_82	NE, F_ARG_19	HE, F_ARG_19	2.82	1.96	3.39
5VXJ.PDB	OD1, F_ASN_97	ND2, F_ASN_35	HD22, F_ASN_35	2.86	2.08	21.21
5VXJ.PDB	OD1, F_ASP_90	NH1, F_ARG_38	HH12, F_ARG_38	2.92	2.20	28.14
5VXJ.PDB	OE2, F_GLU_46	NH2, F_ARG_38	HH21, F_ARG_38	2.73	1.93	18.99
5VXJ.PDB	OE1, G_GLU_200	NH2, F_ARG_50	HH22, F_ARG_50	2.70	1.89	15.49
5VXJ.PDB	OD2, F_ASP_90	NH1, F_ARG_67	HH12, F_ARG_67	2.83	1.99	10.41
5VXJ.PDB	OD1, F_ASN_74	NE, F_ARG_72	HE, F_ARG_72	2.72	1.88	10.50
5VXJ.PDB	OG1, F_THR_107	ND2, F_ASN_97	HD21, F_ASN_97	2.73	1.95	21.26
5VXJ.PDB	OE1, G_GLU_201	OH, F_TYR_105	HH, F_TYR_105	2.57	1.75	11.97
5VXJ.PDB	OD2, G_ASP_97	NE, G_ARG_101	HE, G_ARG_101	2.67	1.82	7.54
5VXJ.PDB	OD1, G_ASP_287	OH, G_TYR_164	HH, G_TYR_164	2.79	1.99	15.03
5VXJ.PDB	OE2, G_GLU_201	NZ, G_LYS_197	HZ3, G_LYS_197	2.59	1.86	28.64
5VXJ.PDB	OD1, G_ASP_254	NZ, G_LYS_203	HZ2, G_LYS_203	2.49	1.62	9.92
5VXJ.PDB	OD2, G_ASP_166	NZ, G_LYS_205	HZ2, G_LYS_205	2.82	1.96	12.05
5VXJ.PDB	OD2, G_ASP_166	OH, G_TYR_206	HH, G_TYR_206	2.52	1.70	11.57
5VXJ.PDB	OE1, H_GLN_111	OG1, G_THR_217	HG1, G_THR_217	2.86	2.17	29.58
5VXJ.PDB	OE1, H_GLN_82	NE, H_ARG_19	HE, H_ARG_19	2.76	1.91	8.69
5VXJ.PDB	OD1, H_ASN_97	ND2, H_ASN_35	HD22, H_ASN_35	2.85	2.10	23.91
5VXJ.PDB	OD1, H_ASP_90	NH1, H_ARG_38	HH12, H_ARG_38	3.00	2.16	12.34
5VXJ.PDB	OD1, H_ASN_35	NE, H_ARG_50	HE, H_ARG_50	2.75	1.93	14.53
5VXJ.PDB	OD2, H_ASP_90	NH1, H_ARG_67	HH12, H_ARG_67	2.89	2.05	9.62
5VXJ.PDB	OD1, H_ASN_74	NE, H_ARG_72	HE, H_ARG_72	2.76	1.95	17.61
5VXJ.PDB	OD1, H_ASN_84	NE2, H_GLN_82	HE21, H_GLN_82	2.86	2.05	16.57
5VXJ.PDB	OG1, H_THR_107	ND2, H_ASN_97	HD21, H_ASN_97	2.53	1.81	26.67
5VXJ.PDB	OD1, I_ASP_309	ND2, I_ASN_58	HD22, I_ASN_58	2.73	1.88	5.94
5VXJ.PDB	OE1, I_GLU_154	OG, I_SER_82	HG, I_SER_82	2.52	1.79	24.33
5VXJ.PDB	OD2, I_ASP_97	NE, I_ARG_101	HE, I_ARG_101	2.83	2.07	23.56
5VXJ.PDB	OD2, J_ASP_73	NZ, I_LYS_137	HZ3, I_LYS_137	2.90	2.17	29.52
5VXJ.PDB	OD1, I_ASP_287	OH, I_TYR_164	HH, I_TYR_164	2.95	2.16	17.45
5VXJ.PDB	OD1, B_ASN_97	NZ, I_LYS_197	HZ1, I_LYS_197	2.68	1.88	21.92
5VXJ.PDB	OD1, I_ASP_254	NZ, I_LYS_203	HZ2, I_LYS_203	2.60	1.74	12.72
5VXJ.PDB	OD2, I_ASP_166	NZ, I_LYS_205	HZ2, I_LYS_205	2.77	1.91	10.79
5VXJ.PDB	OD2, I_ASP_166	OH, I_TYR_206	HH, I_TYR_206	2.50	1.67	8.28
5VXJ.PDB	OD1, I_ASN_249	OG1, I_THR_251	HG1, I_THR_251	2.69	1.98	27.82
5VXJ.PDB	OE1, J_GLN_82	NE, J_ARG_19	HE, J_ARG_19	2.52	1.72	17.43
5VXJ.PDB	OD1, J_ASN_97	ND2, J_ASN_35	HD22, J_ASN_35	3.00	2.21	19.94
5VXJ.PDB	OD1, J_ASP_90	NH1, J_ARG_38	HH12, J_ARG_38	2.89	2.13	23.59
5VXJ.PDB	OE2, J_GLU_46	NH2, J_ARG_38	HH21, J_ARG_38	2.77	1.96	16.80
5VXJ.PDB	OD1, J_ASN_35	NE, J_ARG_50	HE, J_ARG_50	2.74	1.91	11.68
5VXJ.PDB	OD2, J_ASP_90	NH1, J_ARG_67	HH12, J_ARG_67	2.55	1.74	16.72
5VXJ.PDB	OD1, J_ASP_90	NH2, J_ARG_67	HH22, J_ARG_67	2.84	1.98	5.11
5VXJ.PDB	OD1, J_ASN_84	NE2, J_GLN_82	HE21, J_GLN_82	2.94	2.08	3.32
5VXJ.PDB	OG1, J_THR_107	ND2, J_ASN_97	HD21, J_ASN_97	2.57	1.77	17.56

Table 1779: 5VXJ-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5VXK.PDB	OD2, B_ASP_90	NH2, B_ARG_67	HH22, B_ARG_67	2.27	1.58	28.79
5VXK.PDB	OG, A_SER_168	NE2, B_GLN_106	HE21, B_GLN_106	2.99	2.23	24.43
5VXK.PDB	OD2, A_ASP_287	NE2, B_GLN_106	HE22, B_GLN_106	2.77	1.94	12.81
5VXK.PDB	OD2, A_ASP_287	OH, A_TYR_164	HH, A_TYR_164	2.91	2.21	28.15
5VXK.PDB	OD2, A_ASP_261	NZ, A_LYS_196	HZ3, A_LYS_196	2.74	1.87	9.57
5VXK.PDB	OG1, B_THR_102	OH, A_TYR_276	HH, A_TYR_276	2.57	1.73	6.50
5VXK.PDB	OH, A_TYR_160	ND2, A_ASN_293	HD22, A_ASN_293	2.77	1.97	18.05

Table 1780: 5VXK-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5VXL.PDB	OD1, A_ASP_309	ND2, A_ASN_58	HD22, A_ASN_58	2.92	2.09	13.70
5VXL.PDB	OE1, A_GLU_154	OG, A_SER_82	HG, A_SER_82	2.52	1.77	21.68
5VXL.PDB	OD2, A_ASP_88	NE2, A_GLN_84	HE21, A_GLN_84	2.89	2.16	27.92
5VXL.PDB	OD1, A_ASP_254	NZ, A_LYS_203	HZ3, A_LYS_203	2.55	1.71	15.49
5VXL.PDB	OD2, B_ASP_52	NZ, A_LYS_205	HZ1, A_LYS_205	3.00	2.13	10.69
5VXL.PDB	OD2, A_ASP_166	OH, A_TYR_206	HH, A_TYR_206	2.43	1.61	11.33
5VXL.PDB	OE1, A_GLN_148	NE1, A_TRP_226	HE1, A_TRP_226	2.87	2.02	9.28
5VXL.PDB	OE2, A_GLU_286	ND2, A_ASN_255	HD22, A_ASN_255	2.74	1.94	17.54
5VXL.PDB	OD1, B_ASP_91	NH1, B_ARG_38	HH12, B_ARG_38	2.97	2.23	26.01
5VXL.PDB	OD1, A_ASP_166	OG, B_SER_55	HG, B_SER_55	2.56	1.73	4.68
5VXL.PDB	OD2, B_ASP_91	NH1, B_ARG_68	HH12, B_ARG_68	2.83	2.06	22.74
5VXL.PDB	OD1, B_ASN_75	NE, B_ARG_73	HE, B_ARG_73	2.98	2.26	28.00
5VXL.PDB	OH, B_TYR_81	NE, B_ARG_79	HE, B_ARG_79	2.96	2.14	13.15
5VXL.PDB	OE2, A_GLU_201	NH2, B_ARG_102	HH22, B_ARG_102	2.87	2.08	20.03

Table 1781: 5VXL-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5VXM.PDB	OD1, A_ASP_309	ND2, A_ASN_58	HD22, A_ASN_58	2.74	1.89	5.63
5VXM.PDB	OD1, A_ASP_88	NE2, A_GLN_84	HE21, A_GLN_84	2.60	1.75	9.62
5VXM.PDB	OD1, A_ASP_287	OH, A_TYR_164	HH, A_TYR_164	2.66	1.84	11.86
5VXM.PDB	OE2, B_GLU_111	NE1, A_TRP_177	HE1, A_TRP_177	2.76	1.97	19.61
5VXM.PDB	OD2, A_ASP_166	NZ, A_LYS_205	HZ3, A_LYS_205	2.79	1.92	8.41
5VXM.PDB	OD2, A_ASP_166	OH, A_TYR_206	HH, A_TYR_206	2.53	1.73	14.26
5VXM.PDB	OE2, A_GLU_288	NZ, A_LYS_291	HZ1, A_LYS_291	2.70	1.90	22.27
5VXM.PDB	OH, B_TYR_94	NH1, B_ARG_38	HH11, B_ARG_38	2.95	2.12	12.47
5VXM.PDB	OD1, B_ASP_90	NH1, B_ARG_38	HH12, B_ARG_38	2.77	1.97	17.13
5VXM.PDB	OD1, B_ASP_54	OG, B_SER_56	HG, B_SER_56	2.63	1.84	17.09
5VXM.PDB	OD2, B_ASP_90	NH1, B_ARG_67	HH12, B_ARG_67	2.75	1.92	11.95
5VXM.PDB	OD1, B_ASN_84	NE2, B_GLN_82	HE21, B_GLN_82	2.81	1.97	10.38

Table 1782: 5VXM-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID residue name residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5VXR.PDB	OE1, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.74	1.86	23.26
5VXR.PDB	OH, H_TYR_93	NH1, H_ARG_38	HH11, H_ARG_38	2.95	1.99	15.54
5VXR.PDB	OD1, H_ASP_89	NH1, H_ARG_38	HH12, H_ARG_38	2.81	1.80	4.81
5VXR.PDB	OE1, H_GLU_46	NH2, H_ARG_38	HH21, H_ARG_38	2.83	2.01	29.32
5VXR.PDB	OE1, L_GLN_38	NZ, H_LYS_39	HZ2, H_LYS_39	2.72	1.76	14.94
5VXR.PDB	OD1, H_ASN_35	OH, H_TYR_47	HH, H_TYR_47	2.72	1.74	8.88
5VXR.PDB	OD1, P_ASN_415	OH, H_TYR_50	HH, H_TYR_50	2.71	1.82	21.79
5VXR.PDB	OD1, H_ASP_89	NH2, H_ARG_66	HH22, H_ARG_66	2.99	1.98	4.54
5VXR.PDB	OE1, H_GLN_77	OH, H_TYR_79	HH, H_TYR_79	2.72	1.76	12.10
5VXR.PDB	OE2, H_GLU_154	OH, H_TYR_151	HH, H_TYR_151	2.81	1.83	6.84
5VXR.PDB	OG, H_SER_185	NE1, H_TRP_160	HE1, H_TRP_160	2.93	1.93	7.21
5VXR.PDB	OD1, L_ASN_138	NE2, H_HIS_170	HE2, H_HIS_170	2.89	1.98	20.57
5VXR.PDB	OG1, H_THR_143	OG1, H_THR_188	HG1, H_THR_188	2.81	1.84	10.15
5VXR.PDB	OE2, L_GLU_123	NZ, H_LYS_214	HZ1, H_LYS_214	2.93	1.98	15.97
5VXR.PDB	OD1, L_ASP_70	NE, L_ARG_24	HE, L_ARG_24	2.94	2.08	26.80
5VXR.PDB	OD1, L_ASN_92	OG, L_SER_27D	HG, L_SER_27D	2.79	1.83	11.69
5VXR.PDB	OD1, L_ASN_91	NE2, L_HIS_34	HE2, L_HIS_34	2.77	1.79	12.93
5VXR.PDB	OE1, L_GLN_89	OH, L_TYR_36	HH, L_TYR_36	2.69	1.74	13.43
5VXR.PDB	OH, L_TYR_86	NE2, L_GLN_37	HE21, L_GLN_37	2.98	1.98	9.70
5VXR.PDB	OD2, L_ASP_82	NH1, L_ARG_61	HH12, L_ARG_61	2.75	1.79	15.16
5VXR.PDB	OD1, L_ASP_82	NH2, L_ARG_61	HH22, L_ARG_61	2.82	1.82	7.27
5VXR.PDB	OG, L_SER_131	NE2, L_GLN_124	HE22, L_GLN_124	2.92	1.91	5.03
5VXR.PDB	OG, L_SER_177	NE1, L_TRP_148	HE1, L_TRP_148	2.80	1.85	16.41
5VXR.PDB	OD1, L_ASP_170	OG1, L_THR_172	HG1, L_THR_172	2.70	1.76	15.44
5VXR.PDB	OG, H_SER_184	OG, L_SER_176	HG, L_SER_176	2.79	1.86	17.30
5VXR.PDB	OD1, L_ASN_161	OG, L_SER_177	HG, L_SER_177	2.64	1.73	19.24
5VXR.PDB	OG, L_SER_131	OG1, L_THR_180	HG1, L_THR_180	2.88	2.00	21.77
5VXR.PDB	OD2, L_ASP_151	ND1, L_HIS_189	HD1, L_HIS_189	2.73	1.79	17.03
5VXR.PDB	ND1, L_HIS_198	OG1, L_THR_200	HG1, L_THR_200	2.74	1.84	20.28
5VXR.PDB	NE2, P_HIS_421	OG1, P_THR_416	HG1, P_THR_416	2.72	1.87	24.94

Table 1783: 5VXR-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5WKQ.PDB	OG1, A_THR_80	NZ, A_LYS_106	HZ1, A_LYS_106	2.47	1.72	27.03
5WKQ.PDB	OG, B_SER_208	NH2, A_ARG_135	HH21, A_ARG_135	2.89	2.06	11.87
5WKQ.PDB	OE2, A_GLU_182	NE2, A_GLN_162	HE21, A_GLN_162	2.71	1.89	15.15
5WKQ.PDB	OE2, B_GLU_182	NE2, B_GLN_162	HE21, B_GLN_162	2.63	1.85	20.38
5WKQ.PDB	OD1, B_ASP_148	NH1, B_ARG_196	HH11, B_ARG_196	2.87	2.13	25.83
5WKQ.PDB	OE2, A_GLU_131	ND1, B_HIS_207	HD1, B_HIS_207	2.65	1.88	22.26
5WKQ.PDB	OE1, A_GLU_131	OG1, B_THR_211	HG1, B_THR_211	2.63	1.86	19.68

Table 1784: 5WKQ-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5WN9.PDB	OE1, H_GLN_1	NE2, H_GLN_3	HE21, H_GLN_3	2.70	1.88	14.43
5WN9.PDB	OE1, H_GLU_46	NE, H_ARG_38	HE, H_ARG_38	2.78	2.00	20.76
5WN9.PDB	OH, H_TYR_94	NH2, H_ARG_38	HH21, H_ARG_38	2.96	2.17	18.48
5WN9.PDB	OD1, H_ASP_90	NH2, H_ARG_38	HH22, H_ARG_38	2.91	2.07	9.36
5WN9.PDB	OE1, H_GLN_182	NE2, H_GLN_39	HE22, H_GLN_39	2.96	2.11	8.81
5WN9.PDB	OD2, H_ASP_90	NH1, H_ARG_67	HH12, H_ARG_67	2.27	1.51	22.67
5WN9.PDB	OD1, H_ASP_73	OG, H_SER_75	HG, H_SER_75	2.58	1.79	16.04
5WN9.PDB	OG1, H_THR_69	NH1, H_ARG_84	HH12, H_ARG_84	2.83	2.06	21.62
5WN9.PDB	OD1, H_ASP_112	NE, H_ARG_98	HE, H_ARG_98	2.94	2.13	15.87
5WN9.PDB	OD2, H_ASP_112	NH1, H_ARG_98	HH11, H_ARG_98	2.84	2.01	13.12
5WN9.PDB	OG1, H_THR_218	NH2, H_ARG_162	HH21, H_ARG_162	2.83	2.04	19.79
5WN9.PDB	OE1, H_GLN_233	OH, H_TYR_180	HH, H_TYR_180	2.70	1.87	8.37
5WN9.PDB	OE1, H_GLN_39	NE2, H_GLN_182	HE22, H_GLN_182	2.85	2.00	9.41
5WN9.PDB	OD2, H_ASP_226	NE, H_ARG_205	HE, H_ARG_205	2.80	1.99	17.36
5WN9.PDB	OD1, H_ASP_226	NH1, H_ARG_205	HH11, H_ARG_205	2.89	2.03	4.48
5WN9.PDB	OG1, H_THR_164	OG1, H_THR_218	HG1, H_THR_218	2.96	2.26	28.62
5WN9.PDB	OD1, H_ASN_57	NE, A_ARG_188	HE, A_ARG_188	2.58	1.61	2.15

Table 1785: 5WN9-specific side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1A14.PDB	OE1, L_GLN_38	NE2, H_GLN_39	HE21, H_GLN_39	2.62	1.69	9.24
1A14.PDB	OH, L_TYR_36	N, H_PHE_100E	H, H_PHE_100E	2.73	1.81	13.85

Table 1786: Interfacial 1A14-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1E6J.PDB	OE1, H_GLN_39	NE2, L_GLN_37	HE22, L_GLN_37	2.69	1.84	23.98

Table 1787: Interfacial 1E6J-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1F3R.PDB	O, B_ASN_230	OH, A_TYR_72	HH, A_TYR_72	2.67	1.70	2.56
1F3R.PDB	O, A_GLY_70	NH2, B_ARG_50	HH21, B_ARG_50	2.81	1.79	6.29
1F3R.PDB	NE1, A_TRP_67	OG, B_SER_61	HG, B_SER_61	2.86	1.89	6.31
1F3R.PDB	O, A_ILE_75	OH, B_TYR_170	HH, B_TYR_170	2.72	1.77	10.88
1F3R.PDB	O, A_ASP_71	OH, B_TYR_233	HH, B_TYR_233	2.71	1.89	25.38

Table 1788: Interfacial 1F3R-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1HGD.PDB	O, B.ILE.140	N, A.ALA.11	H, A.ALA.11	2.90	2.03	23.17
1HGD.PDB	O, B.PHE.138	N, A.LEU.13	H, A.LEU.13	2.95	2.00	13.08
1HGD.PDB	O, B.ARG.25	N, A.CYS.14	H, A.CYS.14	2.89	1.92	6.63
1HGD.PDB	O, B.GLY.136	N, A.LEU.15	H, A.LEU.15	2.87	1.90	8.68
1HGD.PDB	O, B.GLY.23	N, A.GLY.16	H, A.GLY.16	2.93	2.02	18.64
1HGD.PDB	O, B.TRP.21	N, A.HIS.18	H, A.HIS.18	2.86	2.01	24.44
1HGD.PDB	OE2, B.GLU.97	NZ, A.LYS.27	HZ1, A.LYS.27	2.80	1.78	9.95
1HGD.PDB	OE2, B.GLU.67	NH2, A.ARG.109	HH21, A.ARG.109	2.83	1.84	13.41
1HGD.PDB	OD2, F.ASP.79	OG, A.SER.110	HG, A.SER.110	2.92	1.96	11.03
1HGD.PDB	OD1, E.ASP.101	NE2, A.GLN.210	HE22, A.GLN.210	3.00	2.15	26.33
1HGD.PDB	OE1, C.GLN.210	NH2, A.ARG.220	HH21, A.ARG.220	2.78	1.86	19.99
1HGD.PDB	O, F.SER.71	NZ, A.LYS.238	HZ2, A.LYS.238	2.63	1.73	23.20
1HGD.PDB	OE1, F.GLU.72	NZ, A.LYS.238	HZ3, A.LYS.238	2.93	1.92	13.44
1HGD.PDB	O, B.LYS.68	NZ, A.LYS.299	HZ2, A.LYS.299	2.96	1.95	12.60
1HGD.PDB	O, B.LYS.62	N, A.GLY.303	H, A.GLY.303	2.91	1.96	9.72
1HGD.PDB	OG, B.SER.93	N, A.LYS.310	H, A.LYS.310	2.92	1.97	11.29
1HGD.PDB	OD1, B.ASN.104	N, A.ALA.317	H, A.ALA.317	2.78	1.85	14.55
1HGD.PDB	O, A.VAL.323	N, B.GLY.13	H, B.GLY.13	2.71	1.77	11.58
1HGD.PDB	O, A.HIS.17	N, B.TRP.14	H, B.TRP.14	2.85	1.93	15.85
1HGD.PDB	O, A.GLY.16	N, B.GLY.23	H, B.GLY.23	2.92	1.99	15.76
1HGD.PDB	O, A.CYS.14	N, B.ARG.25	H, B.ARG.25	2.96	2.02	13.01
1HGD.PDB	OE2, F.GLU.97	NH2, B.ARG.54	HH22, B.ARG.54	2.77	1.80	12.79
1HGD.PDB	OD2, F.ASP.86	NZ, B.LYS.62	HZ1, B.LYS.62	2.61	1.78	29.53
1HGD.PDB	OD2, F.ASP.90	NZ, B.LYS.62	HZ3, B.LYS.62	2.73	1.84	25.56
1HGD.PDB	OG, A.SER.110	NE2, B.HIS.64	HE2, B.HIS.64	2.96	2.01	12.34
1HGD.PDB	O, A.LYS.299	NZ, B.LYS.68	HZ1, B.LYS.68	2.92	1.90	10.17
1HGD.PDB	OG, C.SER.107	N, B.ARG.76	H, B.ARG.76	2.80	1.86	12.47
1HGD.PDB	OE2, D.GLU.81	NE, B.ARG.76	HE, B.ARG.76	2.88	1.91	8.67
1HGD.PDB	OE2, D.GLU.74	NH1, B.ARG.76	HH12, B.ARG.76	2.84	1.82	2.51
1HGD.PDB	OE1, D.GLU.81	NH2, B.ARG.76	HH21, B.ARG.76	2.71	1.71	6.80
1HGD.PDB	OE1, D.GLU.74	NH2, B.ARG.76	HH22, B.ARG.76	2.75	1.75	3.21
1HGD.PDB	OE1, D.GLU.85	OH, B.TYR.83	HH, B.TYR.83	2.65	1.81	23.27
1HGD.PDB	OH, F.TYR.83	NZ, B.LYS.88	HZ1, B.LYS.88	2.76	1.72	5.59
1HGD.PDB	O, A.LYS.27	ND2, B.ASN.104	HD22, B.ASN.104	2.94	1.98	9.01
1HGD.PDB	O, F.LEU.2	OG, B.SER.113	HG, B.SER.113	2.69	1.91	29.59
1HGD.PDB	OE1, F.GLU.132	NE, B.ARG.124	HE, B.ARG.124	2.83	2.02	28.17
1HGD.PDB	OE2, F.GLU.132	NE, B.ARG.124	HE, B.ARG.124	2.88	2.01	22.00
1HGD.PDB	O, A.LEU.13	N, B.PHE.138	H, B.PHE.138	2.71	1.82	20.20
1HGD.PDB	O, A.ALA.11	N, B.ILE.140	H, B.ILE.140	2.81	1.89	16.38
1HGD.PDB	O, F.ARG.170	NH1, B.ARG.163	HH12, B.ARG.163	2.75	1.79	14.15
1HGD.PDB	O, D.ILE.140	N, C.ALA.11	H, C.ALA.11	2.91	2.01	19.96
1HGD.PDB	O, D.GLN.27	N, C.THR.12	H, C.THR.12	2.92	1.96	10.52
1HGD.PDB	O, D.PHE.138	N, C.LEU.13	H, C.LEU.13	2.98	2.02	9.60
1HGD.PDB	O, D.ARG.25	N, C.CYS.14	H, C.CYS.14	2.74	1.84	19.68
1HGD.PDB	O, D.GLY.136	N, C.LEU.15	H, C.LEU.15	2.88	1.91	5.44
1HGD.PDB	O, D.GLY.23	N, C.GLY.16	H, C.GLY.16	2.97	2.07	19.04
1HGD.PDB	O, D.TRP.21	N, C.HIS.18	H, C.HIS.18	2.85	1.99	23.00
1HGD.PDB	OE2, D.GLU.97	NZ, C.LYS.27	HZ1, C.LYS.27	2.80	1.77	7.54
1HGD.PDB	OE2, D.GLU.67	NH2, C.ARG.109	HH21, C.ARG.109	2.87	1.88	13.44
1HGD.PDB	OD2, B.ASP.79	OG, C.SER.110	HG, C.SER.110	2.73	1.84	19.59
1HGD.PDB	OD1, A.ASP.101	NE2, C.GLN.210	HE22, C.GLN.210	2.97	2.13	27.21
1HGD.PDB	OE1, E.GLN.210	NH2, C.ARG.220	HH21, C.ARG.220	2.69	1.80	23.00
1HGD.PDB	OE1, B.GLU.72	NZ, C.LYS.238	HZ1, C.LYS.238	2.80	1.83	17.68
1HGD.PDB	O, B.SER.71	NZ, C.LYS.238	HZ3, C.LYS.238	2.57	1.67	23.33
1HGD.PDB	O, D.LYS.68	NZ, C.LYS.299	HZ2, C.LYS.299	2.97	1.97	13.11
1HGD.PDB	O, D.LYS.62	N, C.GLY.303	H, C.GLY.303	2.92	1.97	11.11
1HGD.PDB	OG, D.SER.93	N, C.LYS.310	H, C.LYS.310	2.96	2.01	12.70

1HGD.PDB	OD1, D_ASN_104	N, C_ALA_317	H, C_ALA_317	2.76	1.81	11.23
1HGD.PDB	OE1, D_GLU_15	NZ, C_LYS_326	HZ1, C_LYS_326	2.78	1.77	11.96
1HGD.PDB	O, C_VAL_323	N, D_GLY_13	H, D_GLY_13	2.70	1.78	14.49
1HGD.PDB	O, C_HIS_17	N, D_TRP_14	H, D_TRP_14	2.85	1.91	13.36
1HGD.PDB	O, C_GLY_16	N, D_GLY_23	H, D_GLY_23	2.93	2.01	16.45
1HGD.PDB	O, C_CYS_14	N, D_ARG_25	H, D_ARG_25	2.91	1.95	9.92
1HGD.PDB	O, C_THR_12	N, D_GLN_27	H, D_GLN_27	2.91	1.98	16.00
1HGD.PDB	O, A_THR_28	NE, D_ARG_54	HE, D_ARG_54	3.00	2.06	13.94
1HGD.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.79	1.82	13.03
1HGD.PDB	OD2, B_ASP_90	NZ, D_LYS_62	HZ3, D_LYS_62	2.62	1.79	29.99
1HGD.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.96	1.98	5.65
1HGD.PDB	O, C_LYS_299	NZ, D_LYS_68	HZ1, D_LYS_68	2.93	1.92	12.36
1HGD.PDB	OG, E_SER_107	N, D_ARG_76	H, D_ARG_76	2.86	1.90	9.40
1HGD.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.83	1.87	10.56
1HGD.PDB	OE2, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.78	1.77	3.14
1HGD.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.65	1.67	9.42
1HGD.PDB	OE1, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.69	1.70	6.24
1HGD.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.57	1.79	29.87
1HGD.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.76	1.72	5.75
1HGD.PDB	O, C_LYS_27	ND2, D_ASN_104	HD22, D_ASN_104	2.96	2.00	10.74
1HGD.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.80	2.01	29.31
1HGD.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.82	1.95	21.73
1HGD.PDB	O, C_LEU_13	N, D_PHE_138	H, D_PHE_138	2.74	1.85	19.25
1HGD.PDB	O, C_ALA_11	N, D_ILE_140	H, D_ILE_140	2.85	1.94	17.95
1HGD.PDB	O, B_ARG_170	NH1, D_ARG_163	HH12, D_ARG_163	2.77	1.79	12.64
1HGD.PDB	O, F_ILE_140	N, E_ALA_11	H, E_ALA_11	2.92	2.03	20.36
1HGD.PDB	O, F_GLN_27	N, E_THR_12	H, E_THR_12	2.97	2.03	14.03
1HGD.PDB	O, F_PHE_138	N, E_LEU_13	H, E_LEU_13	2.98	2.02	11.10
1HGD.PDB	O, F_ARG_25	N, E_CYS_14	H, E_CYS_14	2.65	1.79	21.42
1HGD.PDB	O, F_GLY_136	N, E_LEU_15	H, E_LEU_15	2.85	1.88	5.88
1HGD.PDB	O, F_GLY_23	N, E_GLY_16	H, E_GLY_16	2.93	2.04	20.98
1HGD.PDB	O, F_TRP_21	N, E_HIS_18	H, E_HIS_18	2.83	1.98	25.03
1HGD.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.79	1.77	8.77
1HGD.PDB	OE2, F_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.82	1.85	14.73
1HGD.PDB	OD2, D_ASP_79	OG, E_SER_110	HG, E_SER_110	2.81	1.89	15.50
1HGD.PDB	OD1, C_ASP_101	NE2, E_GLN_210	HE22, E_GLN_210	2.98	2.14	27.07
1HGD.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.77	1.90	25.11
1HGD.PDB	O, D_SER_71	NZ, E_LYS_238	HZ2, E_LYS_238	2.73	1.80	21.39
1HGD.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ3, E_LYS_238	2.87	1.86	13.40
1HGD.PDB	O, F_LYS_68	NZ, E_LYS_299	HZ1, E_LYS_299	2.98	1.98	14.54
1HGD.PDB	O, F_LYS_62	N, E_GLY_303	H, E_GLY_303	2.94	1.98	8.87
1HGD.PDB	OG, F_SER_93	N, E_LYS_310	H, E_LYS_310	2.95	2.00	12.05
1HGD.PDB	OD1, F_ASN_104	N, E_ALA_317	H, E_ALA_317	2.79	1.84	10.01
1HGD.PDB	OE2, F_GLU_15	N, E_GLU_325	H, E_GLU_325	2.91	2.10	28.29
1HGD.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.97	1.97	16.19
1HGD.PDB	O, E_VAL_323	N, F_GLY_13	H, F_GLY_13	2.71	1.79	15.38
1HGD.PDB	O, E_HIS_17	N, F_TRP_14	H, F_TRP_14	2.87	1.92	12.04
1HGD.PDB	O, E_GLY_16	N, F_GLY_23	H, F_GLY_23	2.91	2.00	17.89
1HGD.PDB	O, E_CYS_14	N, F_ARG_25	H, F_ARG_25	2.88	1.94	13.26
1HGD.PDB	O, E_THR_12	N, F_GLN_27	H, F_GLN_27	2.97	2.04	16.25
1HGD.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.72	1.75	12.85
1HGD.PDB	OD2, D_ASP_90	NZ, F_LYS_62	HZ3, F_LYS_62	2.71	1.86	28.09
1HGD.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.95	1.98	9.92
1HGD.PDB	O, E_LYS_299	NZ, F_LYS_68	HZ1, F_LYS_68	2.97	1.94	5.85
1HGD.PDB	OG, A_SER_107	N, F_ARG_76	H, F_ARG_76	2.82	1.86	9.34
1HGD.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.86	1.90	10.66
1HGD.PDB	OE2, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.77	1.75	1.42
1HGD.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.64	1.65	5.37

1HGD.PDB	OE1, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.71	1.72	7.42
1HGD.PDB	OE1, B_GLU_85	OH, F_TYR_83	HH, F_TYR_83	2.53	1.75	27.84
1HGD.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.67	1.66	8.83
1HGD.PDB	O, E_LYS_27	ND2, F_ASN_104	HD22, F_ASN_104	2.95	1.99	8.95
1HGD.PDB	O, D_LEU_2	OG, F_SER_113	HG, F_SER_113	2.74	1.91	25.98
1HGD.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.96	2.14	28.71
1HGD.PDB	OE2, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.94	2.05	20.84
1HGD.PDB	O, E_LEU_13	N, F_PHE_138	H, F_PHE_138	2.72	1.85	21.62
1HGD.PDB	O, E_ALA_11	N, F_ILE_140	H, F_ILE_140	2.82	1.92	18.45
1HGD.PDB	O, D_ARG_170	NH1, F_ARG_163	HH12, F_ARG_163	2.94	1.98	14.11

Table 1789: Interfacial 1HGD-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1HGE.PDB	O, B.ILE.140	N, A.ALA.11	H, A.ALA.11	2.81	1.93	21.75
1HGE.PDB	O, B.PHE.138	N, A.LEU.13	H, A.LEU.13	2.99	2.04	13.41
1HGE.PDB	O, B.ARG.25	N, A.CYS.14	H, A.CYS.14	2.88	1.92	6.83
1HGE.PDB	O, B.GLY.136	N, A.LEU.15	H, A.LEU.15	2.86	1.90	7.71
1HGE.PDB	O, B.GLY.23	N, A.GLY.16	H, A.GLY.16	2.95	2.03	17.76
1HGE.PDB	O, B.TRP.21	N, A.HIS.18	H, A.HIS.18	2.85	1.97	21.20
1HGE.PDB	OE2, B.GLU.97	NZ, A.LYS.27	HZ1, A.LYS.27	2.80	1.78	10.14
1HGE.PDB	OE2, B.GLU.67	NH2, A.ARG.109	HH21, A.ARG.109	2.74	1.75	12.19
1HGE.PDB	OD2, F.ASP.79	OG, A.SER.110	HG, A.SER.110	2.90	1.95	11.19
1HGE.PDB	OD1, E.ASP.101	NE2, A.GLN.210	HE22, A.GLN.210	2.91	2.05	24.48
1HGE.PDB	OE1, C.GLN.210	NH2, A.ARG.220	HH21, A.ARG.220	2.71	1.78	19.14
1HGE.PDB	O, F.SER.71	NZ, A.LYS.238	HZ2, A.LYS.238	2.67	1.73	19.84
1HGE.PDB	OE1, F.GLU.72	NZ, A.LYS.238	HZ3, A.LYS.238	2.91	1.89	11.73
1HGE.PDB	O, B.LYS.68	NZ, A.LYS.299	HZ2, A.LYS.299	2.95	1.93	10.27
1HGE.PDB	O, B.LYS.62	N, A.GLY.303	H, A.GLY.303	2.95	1.98	8.88
1HGE.PDB	OG, B.SER.93	N, A.LYS.310	H, A.LYS.310	2.91	1.95	10.06
1HGE.PDB	OD1, B.ASN.104	N, A.ALA.317	H, A.ALA.317	2.72	1.81	16.15
1HGE.PDB	O, A.VAL.323	N, B.GLY.13	H, B.GLY.13	2.72	1.79	12.30
1HGE.PDB	O, A.HIS.17	N, B.TRP.14	H, B.TRP.14	2.85	1.92	15.18
1HGE.PDB	O, A.GLY.16	N, B.GLY.23	H, B.GLY.23	2.92	2.01	18.67
1HGE.PDB	O, A.CYS.14	N, B.ARG.25	H, B.ARG.25	3.00	2.06	13.87
1HGE.PDB	OE2, F.GLU.97	NH2, B.ARG.54	HH22, B.ARG.54	2.84	1.86	12.76
1HGE.PDB	OD2, F.ASP.86	NZ, B.LYS.62	HZ1, B.LYS.62	2.60	1.76	28.82
1HGE.PDB	OD2, F.ASP.90	NZ, B.LYS.62	HZ3, B.LYS.62	2.69	1.82	26.81
1HGE.PDB	OG, A.SER.110	NE2, B.HIS.64	HE2, B.HIS.64	2.97	2.02	12.36
1HGE.PDB	O, A.LYS.299	NZ, B.LYS.68	HZ1, B.LYS.68	2.93	1.92	11.15
1HGE.PDB	OG, C.SER.107	N, B.ARG.76	H, B.ARG.76	2.82	1.86	9.28
1HGE.PDB	OE2, D.GLU.81	NE, B.ARG.76	HE, B.ARG.76	2.87	1.91	11.56
1HGE.PDB	OE2, D.GLU.74	NH1, B.ARG.76	HH12, B.ARG.76	2.84	1.83	5.81
1HGE.PDB	OE1, D.GLU.81	NH2, B.ARG.76	HH21, B.ARG.76	2.70	1.70	6.45
1HGE.PDB	OE1, D.GLU.74	NH2, B.ARG.76	HH22, B.ARG.76	2.79	1.79	3.91
1HGE.PDB	OE1, D.GLU.85	OH, B.TYR.83	HH, B.TYR.83	2.65	1.81	24.86
1HGE.PDB	OH, F.TYR.83	NZ, B.LYS.88	HZ1, B.LYS.88	2.75	1.71	5.62
1HGE.PDB	O, A.LYS.27	ND2, B.ASN.104	HD22, B.ASN.104	2.93	1.97	10.25
1HGE.PDB	OE1, F.GLU.132	NE, B.ARG.124	HE, B.ARG.124	2.80	1.98	27.36
1HGE.PDB	OE2, F.GLU.132	NE, B.ARG.124	HE, B.ARG.124	2.94	2.06	21.65
1HGE.PDB	O, A.LEU.13	N, B.PHE.138	H, B.PHE.138	2.71	1.84	21.33
1HGE.PDB	O, A.ALA.11	N, B.ILE.140	H, B.ILE.140	2.75	1.86	18.72
1HGE.PDB	O, F.ARG.170	NH1, B.ARG.163	HH12, B.ARG.163	2.78	1.81	13.88
1HGE.PDB	O, D.ILE.140	N, C.ALA.11	H, C.ALA.11	2.80	1.91	19.98
1HGE.PDB	O, D.PHE.138	N, C.LEU.13	H, C.LEU.13	2.99	2.04	12.20
1HGE.PDB	O, D.ARG.25	N, C.CYS.14	H, C.CYS.14	2.73	1.82	16.85
1HGE.PDB	O, D.GLY.136	N, C.LEU.15	H, C.LEU.15	2.89	1.92	5.03
1HGE.PDB	O, D.GLY.23	N, C.GLY.16	H, C.GLY.16	2.98	2.07	18.60
1HGE.PDB	O, D.TRP.21	N, C.HIS.18	H, C.HIS.18	2.85	1.96	19.89
1HGE.PDB	OE2, D.GLU.97	NZ, C.LYS.27	HZ1, C.LYS.27	2.79	1.77	8.74
1HGE.PDB	OE2, D.GLU.67	NH2, C.ARG.109	HH21, C.ARG.109	2.78	1.79	11.19
1HGE.PDB	OD2, B.ASP.79	OG, C.SER.110	HG, C.SER.110	2.78	1.86	15.09
1HGE.PDB	OD1, A.ASP.101	NE2, C.GLN.210	HE22, C.GLN.210	2.93	2.07	24.92
1HGE.PDB	OE1, E.GLN.210	NH2, C.ARG.220	HH21, C.ARG.220	2.64	1.76	23.09
1HGE.PDB	OE1, B.GLU.72	NZ, C.LYS.238	HZ1, C.LYS.238	2.78	1.80	16.75
1HGE.PDB	O, B.SER.71	NZ, C.LYS.238	HZ3, C.LYS.238	2.65	1.71	19.56
1HGE.PDB	O, D.LYS.68	NZ, C.LYS.299	HZ2, C.LYS.299	2.96	1.94	10.83
1HGE.PDB	O, D.LYS.62	N, C.GLY.303	H, C.GLY.303	2.94	1.98	10.89
1HGE.PDB	OG, D.SER.93	N, C.LYS.310	H, C.LYS.310	2.92	1.96	11.23
1HGE.PDB	OD1, D.ASN.104	N, C.ALA.317	H, C.ALA.317	2.73	1.80	14.37
1HGE.PDB	OE1, D.GLU.15	NZ, C.LYS.326	HZ1, C.LYS.326	2.74	1.73	12.73

1HGE.PDB	O, C_VAL_323	N, D_GLY_13	H, D_GLY_13	2.71	1.79	14.79
1HGE.PDB	O, C_HIS_17	N, D_TRP_14	H, D_TRP_14	2.88	1.94	13.07
1HGE.PDB	O, C_GLY_16	N, D_GLY_23	H, D_GLY_23	2.94	2.04	19.95
1HGE.PDB	O, C_CYS_14	N, D_ARG_25	H, D_ARG_25	2.94	1.98	9.40
1HGE.PDB	O, C_THR_12	N, D_GLN_27	H, D_GLN_27	2.86	1.95	18.04
1HGE.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.87	1.89	12.82
1HGE.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.96	1.98	6.23
1HGE.PDB	O, C_LYS_299	NZ, D_LYS_68	HZ1, D_LYS_68	2.92	1.91	12.00
1HGE.PDB	OG, E_SER_107	N, D_ARG_76	H, D_ARG_76	2.87	1.90	6.58
1HGE.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.79	1.85	14.06
1HGE.PDB	OE2, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.78	1.78	7.91
1HGE.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.63	1.67	11.36
1HGE.PDB	OE1, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.74	1.75	7.04
1HGE.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.58	1.80	29.40
1HGE.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.71	1.68	6.52
1HGE.PDB	O, C_LYS_27	ND2, D_ASN_104	HD22, D_ASN_104	2.96	2.00	10.88
1HGE.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.78	1.98	28.90
1HGE.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.90	2.01	20.41
1HGE.PDB	O, C_LEU_13	N, D_PHE_138	H, D_PHE_138	2.74	1.87	21.30
1HGE.PDB	O, C_ALA_11	N, D_ILE_140	H, D_ILE_140	2.78	1.88	18.97
1HGE.PDB	O, B_ARG_170	NH1, D_ARG_163	HH12, D_ARG_163	2.79	1.82	14.16
1HGE.PDB	O, F_ILE_140	N, E_ALA_11	H, E_ALA_11	2.82	1.93	19.79
1HGE.PDB	O, F_GLN_27	N, E_THR_12	H, E_THR_12	2.91	1.97	12.43
1HGE.PDB	O, F_PHE_138	N, E_LEU_13	H, E_LEU_13	2.98	2.03	12.93
1HGE.PDB	O, F_ARG_25	N, E_CYS_14	H, E_CYS_14	2.61	1.80	26.88
1HGE.PDB	O, F_GLY_136	N, E_LEU_15	H, E_LEU_15	2.88	1.90	5.56
1HGE.PDB	O, F_GLY_23	N, E_GLY_16	H, E_GLY_16	2.95	2.06	19.95
1HGE.PDB	O, F_TRP_21	N, E_HIS_18	H, E_HIS_18	2.85	1.97	21.43
1HGE.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.79	1.77	9.75
1HGE.PDB	OE2, F_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.78	1.79	11.63
1HGE.PDB	OD2, D_ASP_79	OG, E_SER_110	HG, E_SER_110	2.82	1.89	14.19
1HGE.PDB	OD1, C_ASP_101	NE2, E_GLN_210	HE22, E_GLN_210	2.89	2.04	25.02
1HGE.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.74	1.87	25.04
1HGE.PDB	O, D_SER_71	NZ, E_LYS_238	HZ2, E_LYS_238	2.75	1.79	18.19
1HGE.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ3, E_LYS_238	2.85	1.84	12.25
1HGE.PDB	O, F_LYS_68	NZ, E_LYS_299	HZ2, E_LYS_299	2.95	1.93	11.73
1HGE.PDB	O, F_LYS_62	N, E_GLY_303	H, E_GLY_303	2.95	1.98	8.29
1HGE.PDB	OG, F_SER_93	N, E_LYS_310	H, E_LYS_310	2.93	1.97	10.15
1HGE.PDB	OD1, F_ASP_86	NZ, E_LYS_310	HZ3, E_LYS_310	2.86	2.02	29.64
1HGE.PDB	OD1, F_ASN_104	N, E_ALA_317	H, E_ALA_317	2.73	1.80	13.22
1HGE.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.99	2.00	17.08
1HGE.PDB	O, E_VAL_323	N, F_GLY_13	H, F_GLY_13	2.72	1.79	12.93
1HGE.PDB	O, E_HIS_17	N, F_TRP_14	H, F_TRP_14	2.85	1.91	12.63
1HGE.PDB	O, E_GLY_16	N, F_GLY_23	H, F_GLY_23	2.91	2.01	19.90
1HGE.PDB	O, E_CYS_14	N, F_ARG_25	H, F_ARG_25	2.88	1.93	12.79
1HGE.PDB	O, E_THR_12	N, F_GLN_27	H, F_GLN_27	2.82	1.90	16.16
1HGE.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.80	1.82	12.52
1HGE.PDB	OD2, D_ASP_90	NZ, F_LYS_62	HZ2, F_LYS_62	2.67	1.83	29.15
1HGE.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.94	1.97	9.11
1HGE.PDB	O, E_LYS_299	NZ, F_LYS_68	HZ1, F_LYS_68	2.97	1.93	4.62
1HGE.PDB	OG, A_SER_107	N, F_ARG_76	H, F_ARG_76	2.81	1.83	4.38
1HGE.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.85	1.89	11.64
1HGE.PDB	OE2, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.73	1.73	6.19
1HGE.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.65	1.66	5.51
1HGE.PDB	OE1, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.70	1.73	9.07
1HGE.PDB	OE1, B_GLU_85	OH, F_TYR_83	HH, F_TYR_83	2.51	1.76	30.00
1HGE.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.67	1.65	8.34
1HGE.PDB	O, E_LYS_27	ND2, F_ASN_104	HD22, F_ASN_104	2.94	1.99	10.01

1HGE.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.92	2.09	27.36
1HGE.PDB	O, E_LEU_13	N, F_PHE_138	H, F_PHE_138	2.73	1.86	22.03
1HGE.PDB	O, E_ALA_11	N, F_ILE_140	H, F_ILE_140	2.75	1.87	19.65
1HGE.PDB	O, D_ARG_170	NH1, F_ARG_163	HH12, F_ARG_163	2.95	1.99	14.32

Table 1790: Interfacial 1HGE-specific side chain and main chain hydrogen bonding analysis.

In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1HGF.PDB	O, B.ILE.140	N, A.ALA.11	H, A.ALA.11	2.90	2.03	22.48
1HGF.PDB	O, B.PHE.138	N, A.LEU.13	H, A.LEU.13	2.96	1.99	8.07
1HGF.PDB	O, B.ARG.25	N, A.CYS.14	H, A.CYS.14	2.98	2.02	8.89
1HGF.PDB	O, B.GLY.136	N, A.LEU.15	H, A.LEU.15	2.92	1.95	7.83
1HGF.PDB	O, B.GLY.23	N, A.GLY.16	H, A.GLY.16	2.92	2.03	19.80
1HGF.PDB	O, B.TRP.21	N, A.HIS.18	H, A.HIS.18	2.92	2.01	18.08
1HGF.PDB	OE2, B.GLU.97	NZ, A.LYS.27	HZ1, A.LYS.27	2.79	1.86	21.55
1HGF.PDB	OE2, B.GLU.67	NH2, A.ARG.109	HH21, A.ARG.109	2.92	1.92	10.51
1HGF.PDB	OD2, F.ASP.79	OG, A.SER.110	HG, A.SER.110	2.82	1.90	15.87
1HGF.PDB	OE1, C.GLN.210	NH2, A.ARG.220	HH21, A.ARG.220	2.64	1.76	23.62
1HGF.PDB	OE1, F.GLU.72	NZ, A.LYS.238	HZ2, A.LYS.238	2.85	1.85	14.58
1HGF.PDB	O, F.SER.71	NZ, A.LYS.238	HZ3, A.LYS.238	2.63	1.67	16.71
1HGF.PDB	O, B.LYS.62	N, A.GLY.303	H, A.GLY.303	2.90	1.93	4.88
1HGF.PDB	OG, B.SER.93	N, A.LYS.310	H, A.LYS.310	2.89	1.97	16.03
1HGF.PDB	OD1, B.ASN.104	N, A.ALA.317	H, A.ALA.317	2.74	1.82	15.07
1HGF.PDB	O, A.VAL.323	N, B.GLY.13	H, B.GLY.13	2.74	1.86	21.47
1HGF.PDB	O, A.HIS.17	N, B.TRP.14	H, B.TRP.14	2.87	1.97	19.18
1HGF.PDB	O, A.CYS.14	N, B.ARG.25	H, B.ARG.25	2.97	2.03	13.73
1HGF.PDB	OE2, A.GLU.325	NH2, B.ARG.25	HH22, B.ARG.25	2.99	2.04	16.52
1HGF.PDB	O, E.THR.28	NE, B.ARG.54	HE, B.ARG.54	2.92	1.94	6.13
1HGF.PDB	OE2, F.GLU.97	NH2, B.ARG.54	HH22, B.ARG.54	2.83	1.86	13.50
1HGF.PDB	OD2, F.ASP.86	NZ, B.LYS.62	HZ2, B.LYS.62	2.71	1.70	11.44
1HGF.PDB	OD2, F.ASP.90	NZ, B.LYS.62	HZ3, B.LYS.62	2.77	1.82	20.37
1HGF.PDB	OG, A.SER.266	ND1, B.HIS.64	HD1, B.HIS.64	2.66	1.79	20.68
1HGF.PDB	OG, A.SER.110	NE2, B.HIS.64	HE2, B.HIS.64	2.89	1.92	10.70
1HGF.PDB	O, A.LYS.299	NZ, B.LYS.68	HZ2, B.LYS.68	2.93	1.89	4.53
1HGF.PDB	OG, C.SER.107	N, B.ARG.76	H, B.ARG.76	2.84	1.90	13.38
1HGF.PDB	OE2, D.GLU.81	NE, B.ARG.76	HE, B.ARG.76	2.92	1.92	2.47
1HGF.PDB	OE1, D.GLU.74	NH1, B.ARG.76	HH12, B.ARG.76	2.86	1.84	3.80
1HGF.PDB	OE1, D.GLU.81	NH2, B.ARG.76	HH21, B.ARG.76	2.73	1.74	10.29
1HGF.PDB	OE2, D.GLU.74	NH2, B.ARG.76	HH22, B.ARG.76	2.75	1.74	3.91
1HGF.PDB	OE1, D.GLU.85	OH, B.TYR.83	HH, B.TYR.83	2.57	1.80	29.66
1HGF.PDB	OH, F.TYR.83	NZ, B.LYS.88	HZ1, B.LYS.88	2.72	1.70	9.91
1HGF.PDB	O, A.LYS.27	ND2, B.ASN.104	HD21, B.ASN.104	2.88	1.94	13.97
1HGF.PDB	O, F.LEU.2	OG, B.SER.113	HG, B.SER.113	2.68	1.90	29.80
1HGF.PDB	OE1, F.GLU.132	NE, B.ARG.124	HE, B.ARG.124	2.80	1.86	13.00
1HGF.PDB	O, A.LEU.13	N, B.PHE.138	H, B.PHE.138	2.73	1.88	23.58
1HGF.PDB	O, A.ALA.11	N, B.ILE.140	H, B.ILE.140	2.80	1.87	14.66
1HGF.PDB	O, F.ARG.170	NH1, B.ARG.163	HH12, B.ARG.163	2.79	1.78	1.27
1HGF.PDB	OE1, F.GLU.131	NH2, B.ARG.163	HH21, B.ARG.163	2.74	1.86	24.20
1HGF.PDB	O, D.ILE.140	N, C.ALA.11	H, C.ALA.11	2.89	2.00	20.42
1HGF.PDB	O, D.GLN.27	N, C.THR.12	H, C.THR.12	2.90	1.96	12.68
1HGF.PDB	O, D.PHE.138	N, C.LEU.13	H, C.LEU.13	2.97	1.99	7.01
1HGF.PDB	O, D.ARG.25	N, C.CYS.14	H, C.CYS.14	2.79	1.86	15.57
1HGF.PDB	O, D.GLY.136	N, C.LEU.15	H, C.LEU.15	2.95	1.97	3.72
1HGF.PDB	O, D.GLY.23	N, C.GLY.16	H, C.GLY.16	2.95	2.05	18.06
1HGF.PDB	O, D.TRP.21	N, C.HIS.18	H, C.HIS.18	2.91	2.01	18.40
1HGF.PDB	OE2, D.GLU.97	NZ, C.LYS.27	HZ1, C.LYS.27	2.81	1.85	19.93
1HGF.PDB	OE2, D.GLU.67	NH2, C.ARG.109	HH21, C.ARG.109	2.91	1.92	11.49
1HGF.PDB	OD2, B.ASP.79	OG, C.SER.110	HG, C.SER.110	2.69	1.85	25.37
1HGF.PDB	OE1, E.GLN.210	NH2, C.ARG.220	HH21, C.ARG.220	2.56	1.72	26.72
1HGF.PDB	OE1, B.GLU.72	NZ, C.LYS.238	HZ2, C.LYS.238	2.75	1.78	18.48
1HGF.PDB	O, B.SER.71	NZ, C.LYS.238	HZ3, C.LYS.238	2.61	1.62	12.67
1HGF.PDB	O, D.LYS.62	N, C.GLY.303	H, C.GLY.303	2.91	1.95	8.09
1HGF.PDB	OG, D.SER.93	N, C.LYS.310	H, C.LYS.310	2.89	1.98	17.69
1HGF.PDB	OD1, D.ASN.104	N, C.ALA.317	H, C.ALA.317	2.78	1.83	11.25
1HGF.PDB	O, C.VAL.323	N, D.GLY.13	H, D.GLY.13	2.72	1.85	21.39

1HGF.PDB	O, C_HIS_17	N, D_TRP_14	H, D_TRP_14	2.87	1.96	16.75
1HGF.PDB	O, C_CYS_14	N, D_ARG_25	H, D_ARG_25	2.90	1.93	7.59
1HGF.PDB	O, C_THR_12	N, D_GLN_27	H, D_GLN_27	2.86	1.94	17.23
1HGF.PDB	O, A_THR_28	NE, D_ARG_54	HE, D_ARG_54	2.88	1.90	8.46
1HGF.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.84	1.86	12.74
1HGF.PDB	OD2, B_ASP_86	NZ, D_LYS_62	HZ2, D_LYS_62	2.69	1.69	13.49
1HGF.PDB	OD2, B_ASP_90	NZ, D_LYS_62	HZ3, D_LYS_62	2.68	1.77	22.81
1HGF.PDB	OG, C_SER_266	ND1, D_HIS_64	HD1, D_HIS_64	2.64	1.83	27.58
1HGF.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.90	1.92	7.33
1HGF.PDB	O, C_LYS_299	NZ, D_LYS_68	HZ2, D_LYS_68	2.93	1.89	4.98
1HGF.PDB	OG, E_SER_107	N, D_ARG_76	H, D_ARG_76	2.91	1.94	7.76
1HGF.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.82	1.85	5.34
1HGF.PDB	OE1, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.79	1.78	3.81
1HGF.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.64	1.68	12.43
1HGF.PDB	OE2, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.70	1.71	7.38
1HGF.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.58	1.80	29.87
1HGF.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.68	1.69	13.85
1HGF.PDB	O, C_LYS_27	ND2, D_ASN_104	HD21, D_ASN_104	2.89	1.96	15.72
1HGF.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.79	1.88	16.40
1HGF.PDB	O, C_LEU_13	N, D_PHE_138	H, D_PHE_138	2.75	1.91	24.76
1HGF.PDB	O, C_ALA_11	N, D_ILE_140	H, D_ILE_140	2.82	1.90	15.68
1HGF.PDB	O, B_ARG_170	NH1, D_ARG_163	HH12, D_ARG_163	2.84	1.83	3.71
1HGF.PDB	OE1, B_GLU_131	NH2, D_ARG_163	HH21, D_ARG_163	2.70	1.83	24.43
1HGF.PDB	O, F_ILE_140	N, E_ALA_11	H, E_ALA_11	2.95	2.06	20.63
1HGF.PDB	O, F_GLN_27	N, E_THR_12	H, E_THR_12	2.87	1.93	12.24
1HGF.PDB	O, F_PHE_138	N, E_LEU_13	H, E_LEU_13	2.96	1.99	8.43
1HGF.PDB	O, F_ARG_25	N, E_CYS_14	H, E_CYS_14	2.65	1.83	26.13
1HGF.PDB	O, F_GLY_136	N, E_LEU_15	H, E_LEU_15	2.91	1.93	3.45
1HGF.PDB	O, F_GLY_23	N, E_GLY_16	H, E_GLY_16	2.94	2.06	22.45
1HGF.PDB	O, F_TRP_21	N, E_HIS_18	H, E_HIS_18	2.91	2.00	17.81
1HGF.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.75	1.83	22.30
1HGF.PDB	OE2, F_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.88	1.88	11.28
1HGF.PDB	OD2, D_ASP_79	OG, E_SER_110	HG, E_SER_110	2.78	1.90	21.69
1HGF.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.65	1.79	25.97
1HGF.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ2, E_LYS_238	2.83	1.84	16.42
1HGF.PDB	O, D_SER_71	NZ, E_LYS_238	HZ3, E_LYS_238	2.74	1.75	13.85
1HGF.PDB	O, F_LYS_62	N, E_GLY_303	H, E_GLY_303	2.90	1.93	6.18
1HGF.PDB	OG, F_SER_93	N, E_LYS_310	H, E_LYS_310	2.86	1.93	14.59
1HGF.PDB	OD1, F_ASN_104	N, E_ALA_317	H, E_ALA_317	2.72	1.78	10.77
1HGF.PDB	O, E_VAL_323	N, F_GLY_13	H, F_GLY_13	2.75	1.85	19.07
1HGF.PDB	O, E_HIS_17	N, F_TRP_14	H, F_TRP_14	2.87	1.96	16.52
1HGF.PDB	O, E_CYS_14	N, F_ARG_25	H, F_ARG_25	2.91	1.94	8.25
1HGF.PDB	O, E_THR_12	N, F_GLN_27	H, F_GLN_27	3.00	2.08	17.91
1HGF.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.79	1.81	11.74
1HGF.PDB	OD2, D_ASP_86	NZ, F_LYS_62	HZ2, F_LYS_62	2.67	1.68	13.64
1HGF.PDB	OD2, D_ASP_90	NZ, F_LYS_62	HZ3, F_LYS_62	2.75	1.81	20.23
1HGF.PDB	OG, E_SER_266	ND1, F_HIS_64	HD1, F_HIS_64	2.65	1.77	20.25
1HGF.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.89	1.92	9.46
1HGF.PDB	O, E_LYS_299	NZ, F_LYS_68	HZ2, F_LYS_68	2.97	1.95	8.70
1HGF.PDB	OG, A_SER_107	N, F_ARG_76	H, F_ARG_76	2.83	1.87	9.12
1HGF.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.86	1.88	5.84
1HGF.PDB	OE1, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.78	1.77	1.59
1HGF.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.69	1.70	7.61
1HGF.PDB	OE2, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.71	1.73	8.88
1HGF.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.55	1.63	21.75
1HGF.PDB	O, E_LYS_27	ND2, F_ASN_104	HD21, F_ASN_104	2.91	1.99	15.12
1HGF.PDB	O, D_LEU_2	OG, F_SER_113	HG, F_SER_113	2.73	1.92	27.40
1HGF.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.90	1.96	15.73

1HGF.PDB	O, E_LEU_13	N, F_PHE_138	H, F_PHE_138	2.75	1.92	26.04
1HGF.PDB	O, E_ALA_11	N, F_ILE_140	H, F_ILE_140	2.82	1.90	16.36
1HGF.PDB	OE1, D_GLU_131	NH2, F_ARG_163	HH21, F_ARG_163	2.69	1.84	27.00

Table 1791: Interfacial 1HGF-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1HGG.PDB	O, B.ILE.140	N, A.ALA.11	H, A.ALA.11	2.90	1.98	16.87
1HGG.PDB	O, B.PHE.138	N, A.LEU.13	H, A.LEU.13	2.97	2.01	10.10
1HGG.PDB	O, B.ARG.25	N, A.CYS.14	H, A.CYS.14	2.92	1.97	11.02
1HGG.PDB	O, B.GLY.136	N, A.LEU.15	H, A.LEU.15	2.86	1.89	7.78
1HGG.PDB	O, B.GLY.23	N, A.GLY.16	H, A.GLY.16	2.90	2.00	20.11
1HGG.PDB	O, B.TRP.21	N, A.HIS.18	H, A.HIS.18	2.90	1.99	17.50
1HGG.PDB	OE2, B.GLU.97	NZ, A.LYS.27	HZ1, A.LYS.27	2.90	1.87	9.15
1HGG.PDB	OE2, B.GLU.67	NH2, A.ARG.109	HH21, A.ARG.109	2.84	1.86	14.43
1HGG.PDB	OD2, F.ASP.79	OG, A.SER.110	HG, A.SER.110	2.88	1.95	14.29
1HGG.PDB	OD1, E.ASP.101	NE2, A.GLN.210	HE22, A.GLN.210	2.99	2.07	17.95
1HGG.PDB	OE1, C.GLN.210	NH2, A.ARG.220	HH21, A.ARG.220	2.73	1.78	15.93
1HGG.PDB	O, F.SER.71	NZ, A.LYS.238	HZ2, A.LYS.238	2.70	1.77	20.55
1HGG.PDB	OE1, F.GLU.72	NZ, A.LYS.238	HZ3, A.LYS.238	2.93	1.93	14.31
1HGG.PDB	OE2, F.GLU.72	NZ, A.LYS.238	HZ3, A.LYS.238	2.74	1.91	29.92
1HGG.PDB	OE1, B.GLU.67	NH1, A.ARG.269	HH12, A.ARG.269	2.69	1.86	28.34
1HGG.PDB	O, B.LYS.68	NZ, A.LYS.299	HZ1, A.LYS.299	2.91	1.88	9.16
1HGG.PDB	O, B.LYS.62	N, A.GLY.303	H, A.GLY.303	2.91	1.94	6.06
1HGG.PDB	OG, B.SER.93	N, A.LYS.310	H, A.LYS.310	2.89	1.96	14.59
1HGG.PDB	OD1, B.ASP.90	NZ, A.LYS.310	HZ2, A.LYS.310	2.70	1.74	18.08
1HGG.PDB	OD1, B.ASN.104	N, A.ALA.317	H, A.ALA.317	2.79	1.88	16.20
1HGG.PDB	OE2, B.GLU.15	NZ, A.LYS.326	HZ1, A.LYS.326	2.83	1.89	21.04
1HGG.PDB	O, A.VAL.323	N, B.GLY.13	H, B.GLY.13	2.71	1.78	13.00
1HGG.PDB	O, A.HIS.17	N, B.TRP.14	H, B.TRP.14	2.79	1.88	17.76
1HGG.PDB	O, A.GLY.16	N, B.GLY.23	H, B.GLY.23	2.99	2.09	20.32
1HGG.PDB	OE2, A.GLU.325	NH2, B.ARG.25	HH22, B.ARG.25	2.94	1.96	12.23
1HGG.PDB	O, E.THR.28	NE, B.ARG.54	HE, B.ARG.54	2.94	1.97	7.82
1HGG.PDB	OE2, F.GLU.97	NH2, B.ARG.54	HH22, B.ARG.54	2.75	1.76	9.96
1HGG.PDB	OD2, F.ASP.90	NZ, B.LYS.62	HZ2, B.LYS.62	2.65	1.82	29.87
1HGG.PDB	OD2, F.ASP.86	NZ, B.LYS.62	HZ3, B.LYS.62	2.64	1.73	23.35
1HGG.PDB	OG, A.SER.110	NE2, B.HIS.64	HE2, B.HIS.64	2.90	1.96	14.63
1HGG.PDB	O, A.LYS.299	NZ, B.LYS.68	HZ1, B.LYS.68	2.86	1.83	9.73
1HGG.PDB	OG, C.SER.107	N, B.ARG.76	H, B.ARG.76	2.77	1.82	10.45
1HGG.PDB	OE2, D.GLU.81	NE, B.ARG.76	HE, B.ARG.76	2.94	1.96	10.47
1HGG.PDB	OE1, D.GLU.74	NH1, B.ARG.76	HH12, B.ARG.76	2.88	1.89	10.69
1HGG.PDB	OE1, D.GLU.81	NH2, B.ARG.76	HH21, B.ARG.76	2.73	1.73	5.91
1HGG.PDB	OE2, D.GLU.74	NH2, B.ARG.76	HH22, B.ARG.76	2.82	1.82	7.26
1HGG.PDB	OE1, D.GLU.85	OH, B.TYR.83	HH, B.TYR.83	2.68	1.80	19.99
1HGG.PDB	OH, F.TYR.83	NZ, B.LYS.88	HZ1, B.LYS.88	2.77	1.73	5.14
1HGG.PDB	O, A.LYS.27	ND2, B.ASN.104	HD22, B.ASN.104	2.88	1.95	14.60
1HGG.PDB	OE1, F.GLU.132	NE, B.ARG.124	HE, B.ARG.124	2.84	1.98	22.96
1HGG.PDB	OE2, F.GLU.132	NE, B.ARG.124	HE, B.ARG.124	2.81	1.98	25.54
1HGG.PDB	O, A.LEU.13	N, B.PHE.138	H, B.PHE.138	2.70	1.86	24.49
1HGG.PDB	O, A.ALA.11	N, B.ILE.140	H, B.ILE.140	2.77	1.86	18.05
1HGG.PDB	O, F.ARG.170	NH1, B.ARG.163	HH12, B.ARG.163	2.76	1.82	18.13
1HGG.PDB	O, D.ILE.140	N, C.ALA.11	H, C.ALA.11	2.88	1.96	16.67
1HGG.PDB	O, D.PHE.138	N, C.LEU.13	H, C.LEU.13	3.00	2.04	10.72
1HGG.PDB	O, D.ARG.25	N, C.CYS.14	H, C.CYS.14	2.73	1.80	13.70
1HGG.PDB	O, D.GLY.136	N, C.LEU.15	H, C.LEU.15	2.90	1.94	8.49
1HGG.PDB	O, D.GLY.23	N, C.GLY.16	H, C.GLY.16	2.91	2.01	20.14
1HGG.PDB	O, D.TRP.21	N, C.HIS.18	H, C.HIS.18	2.90	2.00	17.75
1HGG.PDB	OE2, D.GLU.97	NZ, C.LYS.27	HZ1, C.LYS.27	2.94	1.91	8.28
1HGG.PDB	OE2, D.GLU.67	NH2, C.ARG.109	HH21, C.ARG.109	2.85	1.88	14.56
1HGG.PDB	OD2, B.ASP.79	OG, C.SER.110	HG, C.SER.110	2.76	1.86	17.83
1HGG.PDB	OE1, E.GLN.210	NH2, C.ARG.220	HH21, C.ARG.220	2.61	1.71	21.26
1HGG.PDB	OE1, B.GLU.72	NZ, C.LYS.238	HZ1, C.LYS.238	2.83	1.86	17.18
1HGG.PDB	OE2, B.GLU.72	NZ, C.LYS.238	HZ1, C.LYS.238	2.70	1.87	29.85
1HGG.PDB	O, B.SER.71	NZ, C.LYS.238	HZ3, C.LYS.238	2.64	1.71	20.39

1HGG.PDB	OE1, D_GLU_67	NH1, C_ARG_269	HH12, C_ARG_269	2.69	1.85	27.75
1HGG.PDB	O, D_LYS_68	NZ, C_LYS_299	HZ1, C_LYS_299	2.94	1.91	9.55
1HGG.PDB	O, D_LYS_62	N, C_GLY_303	H, C_GLY_303	2.91	1.94	5.10
1HGG.PDB	OG, D_SER_93	N, C_LYS_310	H, C_LYS_310	2.89	1.96	14.95
1HGG.PDB	OD1, D_ASP_90	NZ, C_LYS_310	HZ2, C_LYS_310	2.65	1.73	21.74
1HGG.PDB	OD1, D_ASN_104	N, C_ALA_317	H, C_ALA_317	2.78	1.87	17.02
1HGG.PDB	O, C_VAL_323	N, D_GLY_13	H, D_GLY_13	2.71	1.79	13.39
1HGG.PDB	O, C_HIS_17	N, D_TRP_14	H, D_TRP_14	2.80	1.89	17.21
1HGG.PDB	O, C_GLY_16	N, D_GLY_23	H, D_GLY_23	2.99	2.09	20.18
1HGG.PDB	O, C_CYS_14	N, D_ARG_25	H, D_ARG_25	2.94	1.98	8.24
1HGG.PDB	O, A_THR_28	NE, D_ARG_54	HE, D_ARG_54	2.88	1.91	8.15
1HGG.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.76	1.78	10.56
1HGG.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.86	1.90	9.42
1HGG.PDB	O, C_LYS_299	NZ, D_LYS_68	HZ1, D_LYS_68	2.84	1.83	12.46
1HGG.PDB	OG, E_SER_107	N, D_ARG_76	H, D_ARG_76	2.84	1.88	7.98
1HGG.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.86	1.89	9.57
1HGG.PDB	OE1, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.78	1.80	12.10
1HGG.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.67	1.68	6.66
1HGG.PDB	OE2, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.74	1.75	9.29
1HGG.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.59	1.78	26.83
1HGG.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.73	1.70	8.35
1HGG.PDB	O, C_LYS_27	ND2, D_ASN_104	HD22, D_ASN_104	2.86	1.93	13.53
1HGG.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.86	2.00	22.57
1HGG.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.78	1.96	26.12
1HGG.PDB	O, C_LEU_13	N, D_PHE_138	H, D_PHE_138	2.73	1.88	23.87
1HGG.PDB	O, C_ALA_11	N, D_ILE_140	H, D_ILE_140	2.80	1.89	17.21
1HGG.PDB	O, B_ARG_170	NH1, D_ARG_163	HH12, D_ARG_163	2.79	1.85	17.60
1HGG.PDB	O, F_ILE_140	N, E_ALA_11	H, E_ALA_11	2.91	1.98	15.76
1HGG.PDB	O, F_GLN_27	N, E_THR_12	H, E_THR_12	2.92	1.99	15.18
1HGG.PDB	O, F_PHE_138	N, E_LEU_13	H, E_LEU_13	2.97	2.01	11.10
1HGG.PDB	O, F_ARG_25	N, E_CYS_14	H, E_CYS_14	2.71	1.83	19.57
1HGG.PDB	O, F_GLY_136	N, E_LEU_15	H, E_LEU_15	2.87	1.90	6.84
1HGG.PDB	O, F_GLY_23	N, E_GLY_16	H, E_GLY_16	2.91	2.01	19.19
1HGG.PDB	O, F_TRP_21	N, E_HIS_18	H, E_HIS_18	2.89	1.99	18.05
1HGG.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.91	1.88	8.89
1HGG.PDB	OE2, F_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.88	1.90	14.20
1HGG.PDB	OD2, D_ASP_79	OG, E_SER_110	HG, E_SER_110	2.79	1.88	16.48
1HGG.PDB	OD1, C_ASP_101	NE2, E_GLN_210	HE22, E_GLN_210	2.96	2.04	17.70
1HGG.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.72	1.80	20.26
1HGG.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ1, E_LYS_238	2.89	1.89	13.93
1HGG.PDB	O, D_SER_71	NZ, E_LYS_238	HZ3, E_LYS_238	2.80	1.86	20.00
1HGG.PDB	OE1, F_GLU_67	NH1, E_ARG_269	HH12, E_ARG_269	2.69	1.85	27.32
1HGG.PDB	O, F_LYS_68	NZ, E_LYS_299	HZ1, E_LYS_299	2.93	1.91	9.86
1HGG.PDB	O, F_LYS_62	N, E_GLY_303	H, E_GLY_303	2.92	1.95	6.71
1HGG.PDB	OG, F_SER_93	N, E_LYS_310	H, E_LYS_310	2.89	1.95	15.34
1HGG.PDB	OD1, F_ASP_90	NZ, E_LYS_310	HZ2, E_LYS_310	2.64	1.72	22.12
1HGG.PDB	OD1, F_ASN_104	N, E_ALA_317	H, E_ALA_317	2.80	1.89	16.99
1HGG.PDB	OE2, F_GLU_15	N, E_GLU_325	H, E_GLU_325	2.88	2.08	28.79
1HGG.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.98	1.97	15.13
1HGG.PDB	O, E_VAL_323	N, F_GLY_13	H, F_GLY_13	2.73	1.78	9.21
1HGG.PDB	O, E_HIS_17	N, F_TRP_14	H, F_TRP_14	2.81	1.90	18.17
1HGG.PDB	O, E_GLY_16	N, F_GLY_23	H, F_GLY_23	2.97	2.08	20.37
1HGG.PDB	O, E_CYS_14	N, F_ARG_25	H, F_ARG_25	2.99	2.04	12.72
1HGG.PDB	O, E_THR_12	N, F_GLN_27	H, F_GLN_27	2.98	2.05	15.41
1HGG.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.73	1.74	10.16
1HGG.PDB	OD2, D_ASP_86	NZ, F_LYS_62	HZ3, F_LYS_62	2.58	1.75	29.01
1HGG.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.87	1.91	10.03
1HGG.PDB	O, E_LYS_299	NZ, F_LYS_68	HZ1, F_LYS_68	2.85	1.83	8.63

1HGG.PDB	OG, A_SER_107	N, F_ARG_76	H, F_ARG_76	2.79	1.82	4.90
1HGG.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.88	1.92	11.44
1HGG.PDB	OE1, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.75	1.76	9.13
1HGG.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.67	1.68	1.99
1HGG.PDB	OE2, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.79	1.81	10.64
1HGG.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.68	1.67	10.46
1HGG.PDB	O, E_LYS_27	ND2, F_ASN_104	HD22, F_ASN_104	2.91	1.98	14.98
1HGG.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.96	2.09	22.59
1HGG.PDB	OE2, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.87	2.01	24.00
1HGG.PDB	O, E_LEU_13	N, F_PHE_138	H, F_PHE_138	2.72	1.87	23.38
1HGG.PDB	O, E_ALA_11	N, F_ILE_140	H, F_ILE_140	2.79	1.89	17.86
1HGG.PDB	O, D_ARG_170	NH1, F_ARG_163	HH12, F_ARG_163	2.94	2.00	17.69

Table 1792: Interfacial 1HGG-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1HGH.PDB	O, B.ILE.140	N, A.ALA.11	H, A.ALA.11	2.91	2.03	21.75
1HGH.PDB	O, B.PHE.138	N, A.LEU.13	H, A.LEU.13	2.96	1.99	9.24
1HGH.PDB	O, B.ARG.25	N, A.CYS.14	H, A.CYS.14	2.90	1.93	6.13
1HGH.PDB	O, B.GLY.136	N, A.LEU.15	H, A.LEU.15	2.89	1.92	5.59
1HGH.PDB	O, B.GLY.23	N, A.GLY.16	H, A.GLY.16	2.92	2.07	24.71
1HGH.PDB	O, B.TRP.21	N, A.HIS.18	H, A.HIS.18	2.92	2.03	20.10
1HGH.PDB	OE2, B.GLU.97	NZ, A.LYS.27	HZ1, A.LYS.27	2.78	1.76	9.03
1HGH.PDB	OE2, B.GLU.67	NH2, A.ARG.109	HH21, A.ARG.109	2.86	1.88	13.48
1HGH.PDB	OD2, F.ASP.79	OG, A.SER.110	HG, A.SER.110	2.97	2.01	11.65
1HGH.PDB	OD1, E.ASP.101	NE2, A.GLN.210	HE22, A.GLN.210	2.97	2.14	27.61
1HGH.PDB	OE1, C.GLN.210	NH2, A.ARG.220	HH21, A.ARG.220	2.66	1.73	18.15
1HGH.PDB	O, F.SER.71	NZ, A.LYS.238	HZ2, A.LYS.238	2.69	1.74	19.56
1HGH.PDB	OE1, F.GLU.72	NZ, A.LYS.238	HZ3, A.LYS.238	2.92	1.93	15.64
1HGH.PDB	O, B.LYS.68	NZ, A.LYS.299	HZ1, A.LYS.299	2.98	1.97	13.59
1HGH.PDB	O, B.LYS.62	N, A.GLY.303	H, A.GLY.303	3.00	2.03	6.35
1HGH.PDB	OG, B.SER.93	N, A.LYS.310	H, A.LYS.310	2.90	1.94	8.41
1HGH.PDB	OD1, B.ASP.86	NZ, A.LYS.310	HZ2, A.LYS.310	2.71	1.84	27.09
1HGH.PDB	OD1, B.ASN.104	N, A.ALA.317	H, A.ALA.317	2.74	1.80	10.38
1HGH.PDB	O, A.VAL.323	N, B.GLY.13	H, B.GLY.13	2.69	1.78	16.40
1HGH.PDB	O, A.HIS.17	N, B.TRP.14	H, B.TRP.14	2.80	1.87	14.18
1HGH.PDB	O, A.GLY.16	N, B.GLY.23	H, B.GLY.23	2.92	2.01	18.42
1HGH.PDB	O, A.CYS.14	N, B.ARG.25	H, B.ARG.25	2.97	2.02	12.29
1HGH.PDB	OE2, F.GLU.97	NH2, B.ARG.54	HH22, B.ARG.54	2.82	1.86	15.60
1HGH.PDB	OD2, F.ASP.86	NZ, B.LYS.62	HZ1, B.LYS.62	2.66	1.80	27.71
1HGH.PDB	OD2, F.ASP.90	NZ, B.LYS.62	HZ3, B.LYS.62	2.68	1.82	27.13
1HGH.PDB	OG, A.SER.110	NE2, B.HIS.64	HE2, B.HIS.64	2.87	1.91	11.96
1HGH.PDB	O, A.LYS.299	NZ, B.LYS.68	HZ1, B.LYS.68	2.89	1.86	6.42
1HGH.PDB	OG, C.SER.107	N, B.ARG.76	H, B.ARG.76	2.88	1.92	9.13
1HGH.PDB	OE2, D.GLU.81	NE, B.ARG.76	HE, B.ARG.76	2.87	1.90	9.70
1HGH.PDB	OE2, D.GLU.74	NH1, B.ARG.76	HH12, B.ARG.76	2.91	1.90	8.45
1HGH.PDB	OE1, D.GLU.81	NH2, B.ARG.76	HH21, B.ARG.76	2.77	1.76	5.47
1HGH.PDB	OE1, D.GLU.74	NH2, B.ARG.76	HH22, B.ARG.76	2.89	1.87	2.83
1HGH.PDB	OE1, D.GLU.85	OH, B.TYR.83	HH, B.TYR.83	2.69	1.84	23.96
1HGH.PDB	OH, F.TYR.83	NZ, B.LYS.88	HZ1, B.LYS.88	2.74	1.71	7.44
1HGH.PDB	O, A.LYS.27	ND2, B.ASN.104	HD22, B.ASN.104	2.88	1.93	11.07
1HGH.PDB	OE1, F.GLU.132	NE, B.ARG.124	HE, B.ARG.124	2.76	1.94	26.47
1HGH.PDB	OE2, F.GLU.132	NE, B.ARG.124	HE, B.ARG.124	2.83	1.98	23.62
1HGH.PDB	O, A.LEU.13	N, B.PHE.138	H, B.PHE.138	2.71	1.82	19.17
1HGH.PDB	O, A.ALA.11	N, B.ILE.140	H, B.ILE.140	2.77	1.85	16.34
1HGH.PDB	O, F.ARG.170	NH1, B.ARG.163	HH12, B.ARG.163	2.69	1.71	10.72
1HGH.PDB	O, D.ILE.140	N, C.ALA.11	H, C.ALA.11	2.90	2.02	21.17
1HGH.PDB	O, D.GLN.27	N, C.THR.12	H, C.THR.12	2.94	1.99	10.37
1HGH.PDB	O, D.PHE.138	N, C.LEU.13	H, C.LEU.13	2.98	2.01	8.63
1HGH.PDB	O, D.ARG.25	N, C.CYS.14	H, C.CYS.14	2.74	1.80	11.01
1HGH.PDB	O, D.GLY.136	N, C.LEU.15	H, C.LEU.15	2.92	1.95	6.34
1HGH.PDB	O, D.GLY.23	N, C.GLY.16	H, C.GLY.16	2.95	2.08	23.40
1HGH.PDB	O, D.TRP.21	N, C.HIS.18	H, C.HIS.18	2.93	2.04	20.66
1HGH.PDB	OE2, D.GLU.97	NZ, C.LYS.27	HZ1, C.LYS.27	2.82	1.78	7.61
1HGH.PDB	OE2, D.GLU.67	NH2, C.ARG.109	HH21, C.ARG.109	2.86	1.88	13.66
1HGH.PDB	OD2, B.ASP.79	OG, C.SER.110	HG, C.SER.110	2.78	1.85	13.87
1HGH.PDB	OD1, A.ASP.101	NE2, C.GLN.210	HE22, C.GLN.210	2.93	2.07	24.87
1HGH.PDB	OE1, E.GLN.210	NH2, C.ARG.220	HH21, C.ARG.220	2.57	1.72	26.03
1HGH.PDB	OE1, B.GLU.72	NZ, C.LYS.238	HZ1, C.LYS.238	2.71	1.80	22.72
1HGH.PDB	O, B.SER.71	NZ, C.LYS.238	HZ3, C.LYS.238	2.68	1.75	20.57
1HGH.PDB	OG, D.SER.93	N, C.LYS.310	H, C.LYS.310	2.93	1.96	8.29
1HGH.PDB	OD1, D.ASP.86	NZ, C.LYS.310	HZ2, C.LYS.310	2.73	1.85	26.20
1HGH.PDB	OD1, D.ASN.104	N, C.ALA.317	H, C.ALA.317	2.74	1.81	14.42

1HGH.PDB	OE1, D_GLU_15	NZ, C_LYS_326	HZ1, C_LYS_326	2.77	1.75	11.00
1HGH.PDB	O, C_VAL_323	N, D_GLY_13	H, D_GLY_13	2.68	1.77	15.36
1HGH.PDB	O, C_HIS_17	N, D_TRP_14	H, D_TRP_14	2.80	1.87	13.64
1HGH.PDB	O, C_GLY_16	N, D_GLY_23	H, D_GLY_23	2.92	2.01	18.18
1HGH.PDB	O, C_CYS_14	N, D_ARG_25	H, D_ARG_25	2.90	1.94	10.42
1HGH.PDB	O, C_THR_12	N, D_GLN_27	H, D_GLN_27	2.91	1.98	14.85
1HGH.PDB	O, A_THR_28	NE, D_ARG_54	HE, D_ARG_54	2.96	1.98	3.97
1HGH.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.80	1.85	16.64
1HGH.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.84	1.88	10.18
1HGH.PDB	O, C_LYS_299	NZ, D_LYS_68	HZ1, D_LYS_68	2.88	1.85	6.67
1HGH.PDB	OG, E_SER_107	N, D_ARG_76	H, D_ARG_76	2.91	1.94	8.23
1HGH.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.79	1.84	10.45
1HGH.PDB	OE2, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.77	1.77	10.38
1HGH.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.70	1.70	6.41
1HGH.PDB	OE1, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.75	1.75	5.88
1HGH.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.59	1.81	29.86
1HGH.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.66	1.64	7.83
1HGH.PDB	O, C_LYS_27	ND2, D_ASN_104	HD22, D_ASN_104	2.89	1.94	11.70
1HGH.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.80	1.98	26.35
1HGH.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.84	1.99	23.38
1HGH.PDB	O, C_LEU_13	N, D_PHE_138	H, D_PHE_138	2.75	1.85	18.05
1HGH.PDB	O, C_ALA_11	N, D_ILE_140	H, D_ILE_140	2.83	1.90	15.57
1HGH.PDB	O, B_ARG_170	NH1, D_ARG_163	HH12, D_ARG_163	2.75	1.77	10.76
1HGH.PDB	O, F_ILE_140	N, E_ALA_11	H, E_ALA_11	2.92	2.02	19.53
1HGH.PDB	O, F_PHE_138	N, E_LEU_13	H, E_LEU_13	2.96	1.99	9.34
1HGH.PDB	O, F_ARG_25	N, E_CYS_14	H, E_CYS_14	2.64	1.78	21.59
1HGH.PDB	O, F_GLY_136	N, E_LEU_15	H, E_LEU_15	2.90	1.93	5.74
1HGH.PDB	O, F_GLY_23	N, E_GLY_16	H, E_GLY_16	2.92	2.05	22.72
1HGH.PDB	O, F_TRP_21	N, E_HIS_18	H, E_HIS_18	2.92	2.03	19.54
1HGH.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.77	1.74	8.08
1HGH.PDB	OE2, F_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.88	1.90	13.56
1HGH.PDB	OD2, D_ASP_79	OG, E_SER_110	HG, E_SER_110	2.90	1.94	9.49
1HGH.PDB	OD1, C_ASP_101	NE2, E_GLN_210	HE22, E_GLN_210	2.95	2.09	25.33
1HGH.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.68	1.79	22.30
1HGH.PDB	O, D_SER_71	NZ, E_LYS_238	HZ2, E_LYS_238	2.84	1.88	19.22
1HGH.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ3, E_LYS_238	2.87	1.88	15.42
1HGH.PDB	OE1, F_GLU_67	NH1, E_ARG_269	HH12, E_ARG_269	2.71	1.88	29.19
1HGH.PDB	O, F_LYS_62	N, E_GLY_303	H, E_GLY_303	2.98	2.01	7.92
1HGH.PDB	OG, F_SER_93	N, E_LYS_310	H, E_LYS_310	2.93	1.97	10.42
1HGH.PDB	OD1, F_ASP_86	NZ, E_LYS_310	HZ2, E_LYS_310	2.74	1.87	26.77
1HGH.PDB	O, F_SER_93	NE2, E_GLN_311	HE21, E_GLN_311	2.99	2.02	4.65
1HGH.PDB	OD1, F_ASN_104	N, E_ALA_317	H, E_ALA_317	2.75	1.81	11.69
1HGH.PDB	OE2, F_GLU_15	N, E_GLU_325	H, E_GLU_325	2.97	2.16	28.37
1HGH.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.90	1.89	12.96
1HGH.PDB	O, E_VAL_323	N, F_GLY_13	H, F_GLY_13	2.70	1.77	11.97
1HGH.PDB	O, E_HIS_17	N, F_TRP_14	H, F_TRP_14	2.81	1.87	12.50
1HGH.PDB	O, E_GLY_16	N, F_GLY_23	H, F_GLY_23	2.91	2.00	17.53
1HGH.PDB	O, E_CYS_14	N, F_ARG_25	H, F_ARG_25	2.90	1.98	16.77
1HGH.PDB	O, E_THR_12	N, F_GLN_27	H, F_GLN_27	2.91	2.03	20.46
1HGH.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.72	1.77	15.67
1HGH.PDB	OD2, D_ASP_90	NZ, F_LYS_62	HZ2, F_LYS_62	2.68	1.83	28.02
1HGH.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.87	1.91	9.23
1HGH.PDB	O, E_LYS_299	NZ, F_LYS_68	HZ1, F_LYS_68	2.91	1.87	1.37
1HGH.PDB	OG, A_SER_107	N, F_ARG_76	H, F_ARG_76	2.80	1.83	4.45
1HGH.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.84	1.87	10.72
1HGH.PDB	OE2, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.73	1.73	5.34
1HGH.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.71	1.70	1.21
1HGH.PDB	OE1, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.78	1.78	7.19

1HGH.PDB	OE1, B_GLU_85	OH, F_TYR_83	HH, F_TYR_83	2.53	1.74	27.23
1HGH.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.65	1.63	9.88
1HGH.PDB	O, E_LYS_27	ND2, F_ASN_104	HD22, F_ASN_104	2.90	1.95	12.28
1HGH.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.89	2.06	26.55
1HGH.PDB	OE2, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.92	2.03	21.52
1HGH.PDB	O, E_LEU_13	N, F_PHE_138	H, F_PHE_138	2.71	1.82	18.02
1HGH.PDB	O, E_ALA_11	N, F_ILE_140	H, F_ILE_140	2.79	1.87	15.45
1HGH.PDB	O, D_ARG_170	NH1, F_ARG_163	HH12, F_ARG_163	2.89	1.90	10.67

Table 1793: Interfacial 1HGH-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1HGI.PDB	O, B_ILE_140	N, A_ALA_11	H, A_ALA_11	2.84	1.92	15.59
1HGI.PDB	O, B_PHE_138	N, A_LEU_13	H, A_LEU_13	3.00	2.03	9.98
1HGI.PDB	O, B_ARG_25	N, A_CYS_14	H, A_CYS_14	2.96	2.03	15.50
1HGI.PDB	O, B_GLY_136	N, A_LEU_15	H, A_LEU_15	2.93	1.96	7.25
1HGI.PDB	O, B_GLY_23	N, A_GLY_16	H, A_GLY_16	2.98	2.12	23.40
1HGI.PDB	O, B_TRP_21	N, A_HIS_18	H, A_HIS_18	2.89	1.98	18.40
1HGI.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.90	1.86	7.66
1HGI.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.80	1.81	13.24
1HGI.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.65	1.73	18.55
1HGI.PDB	O, F_SER_71	NZ, A_LYS_238	HZ2, A_LYS_238	2.65	1.80	28.67
1HGI.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.85	1.85	15.00
1HGI.PDB	O, B_LYS_62	N, A_GLY_303	H, A_GLY_303	2.96	1.99	7.07
1HGI.PDB	OG, B_SER_93	N, A_LYS_310	H, A_LYS_310	2.98	2.05	15.58
1HGI.PDB	OD1, B_ASP_86	NZ, A_LYS_310	HZ3, A_LYS_310	2.76	1.92	29.34
1HGI.PDB	OD1, B_ASN_104	N, A_ALA_317	H, A_ALA_317	2.74	1.83	15.76
1HGI.PDB	OE2, B_GLU_15	NZ, A_LYS_326	HZ1, A_LYS_326	2.79	1.93	27.33
1HGI.PDB	OE1, B_GLU_15	N, A_THR_328	H, A_THR_328	2.87	1.93	12.65
1HGI.PDB	O, A_VAL_323	N, B_GLY_13	H, B_GLY_13	2.68	1.79	18.45
1HGI.PDB	O, A_HIS_17	N, B_TRP_14	H, B_TRP_14	2.78	1.88	17.65
1HGI.PDB	O, A_GLY_16	N, B_GLY_23	H, B_GLY_23	2.97	2.06	17.58
1HGI.PDB	OE2, A_GLU_325	NH2, B_ARG_25	HH22, B_ARG_25	2.93	1.95	13.46
1HGI.PDB	O, E_THR_28	NE, B_ARG_54	HE, B_ARG_54	2.88	1.92	10.21
1HGI.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.81	1.84	14.63
1HGI.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ1, B_LYS_62	2.67	1.78	25.75
1HGI.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.87	1.89	8.13
1HGI.PDB	O, A_LYS_299	NZ, B_LYS_68	HZ1, B_LYS_68	2.81	1.78	9.15
1HGI.PDB	OG, C_SER_107	N, B_ARG_76	H, B_ARG_76	2.85	1.90	10.66
1HGI.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.86	1.89	7.04
1HGI.PDB	OE2, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.92	1.89	1.72
1HGI.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.71	1.72	8.42
1HGI.PDB	OE1, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.86	1.86	6.93
1HGI.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.78	1.84	13.46
1HGI.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.65	1.64	9.94
1HGI.PDB	O, A_LYS_27	ND2, B_ASN_104	HD22, B_ASN_104	2.86	1.90	10.00
1HGI.PDB	O, F_LEU_2	OG, B_SER_113	HG, B_SER_113	2.77	1.90	22.05
1HGI.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.81	1.96	23.50
1HGI.PDB	OE2, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.86	2.02	24.92
1HGI.PDB	O, A_LEU_13	N, B_PHE_138	H, B_PHE_138	2.74	1.89	23.78
1HGI.PDB	O, A_ALA_11	N, B_ILE_140	H, B_ILE_140	2.77	1.87	18.46
1HGI.PDB	O, F_ARG_170	NH1, B_ARG_163	HH12, B_ARG_163	2.73	1.76	13.86
1HGI.PDB	O, D_ILE_140	N, C_ALA_11	H, C_ALA_11	2.86	1.93	15.33
1HGI.PDB	O, D_GLN_27	N, C_THR_12	H, C_THR_12	2.98	2.01	4.69
1HGI.PDB	O, D_PHE_138	N, C_LEU_13	H, C_LEU_13	2.99	2.03	9.93
1HGI.PDB	O, D_ARG_25	N, C_CYS_14	H, C_CYS_14	2.67	1.83	24.75
1HGI.PDB	O, D_GLY_136	N, C_LEU_15	H, C_LEU_15	2.95	1.98	7.51
1HGI.PDB	O, D_GLY_23	N, C_GLY_16	H, C_GLY_16	2.99	2.12	22.96
1HGI.PDB	O, D_TRP_21	N, C_HIS_18	H, C_HIS_18	2.88	1.97	18.12
1HGI.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.88	1.83	6.58
1HGI.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.82	1.84	15.02
1HGI.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.85	1.90	11.29
1HGI.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.62	1.75	23.70
1HGI.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.67	1.77	23.68
1HGI.PDB	O, B_SER_71	NZ, C_LYS_238	HZ3, C_LYS_238	2.57	1.73	28.43
1HGI.PDB	O, D_LYS_62	N, C_GLY_303	H, C_GLY_303	2.97	2.00	7.92
1HGI.PDB	OD1, D_ASP_86	NZ, C_LYS_310	HZ3, C_LYS_310	2.77	1.93	29.51
1HGI.PDB	OD1, D_ASN_104	N, C_ALA_317	H, C_ALA_317	2.74	1.83	16.29
1HGI.PDB	OE1, D_GLU_15	NZ, C_LYS_326	HZ1, C_LYS_326	2.83	1.84	16.25

1HGI.PDB	O, C_VAL.323	N, D_GLY.13	H, D_GLY.13	2.65	1.77	19.23
1HGI.PDB	O, C_HIS.17	N, D_TRP.14	H, D_TRP.14	2.83	1.92	16.86
1HGI.PDB	O, C_GLY.16	N, D_GLY.23	H, D_GLY.23	2.94	2.02	16.89
1HGI.PDB	O, C_CYS.14	N, D_ARG.25	H, D_ARG.25	2.88	1.94	13.44
1HGI.PDB	O, C_THR.12	N, D_GLN.27	H, D_GLN.27	2.95	2.00	13.47
1HGI.PDB	O, A_THR.28	NE, D_ARG.54	HE, D_ARG.54	2.83	1.87	10.21
1HGI.PDB	OE2, B_GLU.97	NH2, D_ARG.54	HH22, D_ARG.54	2.81	1.85	15.40
1HGI.PDB	OG, C_SER.110	NE2, D_HIS.64	HE2, D_HIS.64	2.83	1.85	2.78
1HGI.PDB	O, C_LYS.299	NZ, D_LYS.68	HZ1, D_LYS.68	2.79	1.78	10.55
1HGI.PDB	OG, E_SER.107	N, D_ARG.76	H, D_ARG.76	2.89	1.92	9.17
1HGI.PDB	OE2, F_GLU.81	NE, D_ARG.76	HE, D_ARG.76	2.80	1.82	5.40
1HGI.PDB	OE2, F_GLU.74	NH1, D_ARG.76	HH12, D_ARG.76	2.78	1.76	4.18
1HGI.PDB	OE1, F_GLU.81	NH2, D_ARG.76	HH21, D_ARG.76	2.61	1.67	15.38
1HGI.PDB	OE1, F_GLU.74	NH2, D_ARG.76	HH22, D_ARG.76	2.76	1.77	8.75
1HGI.PDB	OE1, F_GLU.85	OH, D_TYR.83	HH, D_TYR.83	2.69	1.81	20.41
1HGI.PDB	OH, B_TYR.83	NZ, D_LYS.88	HZ1, D_LYS.88	2.66	1.64	7.30
1HGI.PDB	O, C_LYS.27	ND2, D_ASN.104	HD22, D_ASN.104	2.83	1.88	11.60
1HGI.PDB	O, B_LEU.2	OG, D_SER.113	HG, D_SER.113	2.77	1.91	22.96
1HGI.PDB	OE1, B_GLU.132	NE, D_ARG.124	HE, D_ARG.124	2.84	1.98	23.95
1HGI.PDB	OE2, B_GLU.132	NE, D_ARG.124	HE, D_ARG.124	2.88	2.03	24.96
1HGI.PDB	O, C_LEU.13	N, D_PHE.138	H, D_PHE.138	2.79	1.92	22.46
1HGI.PDB	O, C_ALA.11	N, D_ILE.140	H, D_ILE.140	2.81	1.91	18.30
1HGI.PDB	O, B_ARG.170	NH1, D_ARG.163	HH12, D_ARG.163	2.80	1.83	13.94
1HGI.PDB	O, F_ILE.140	N, E_ALA.11	H, E_ALA.11	2.89	1.95	14.83
1HGI.PDB	O, F_GLN.27	N, E_THR.12	H, E_THR.12	2.94	2.00	13.31
1HGI.PDB	O, F_PHE.138	N, E_LEU.13	H, E_LEU.13	2.97	2.02	11.46
1HGI.PDB	O, F_ARG.25	N, E_CYS.14	H, E_CYS.14	2.66	1.84	26.53
1HGI.PDB	O, F_GLY.136	N, E_LEU.15	H, E_LEU.15	2.92	1.95	6.28
1HGI.PDB	O, F_GLY.23	N, E_GLY.16	H, E_GLY.16	2.99	2.12	22.78
1HGI.PDB	O, F_TRP.21	N, E_HIS.18	H, E_HIS.18	2.89	1.99	19.14
1HGI.PDB	OE2, F_GLU.97	NZ, E_LYS.27	HZ1, E_LYS.27	2.86	1.82	7.44
1HGI.PDB	OE2, F_GLU.67	NH2, E_ARG.109	HH21, E_ARG.109	2.78	1.80	14.37
1HGI.PDB	OD2, D_ASP.79	OG, E_SER.110	HG, E_SER.110	2.90	1.94	10.08
1HGI.PDB	OE1, A_GLN.210	NH2, E_ARG.220	HH21, E_ARG.220	2.69	1.80	23.03
1HGI.PDB	O, D_SER.71	NZ, E_LYS.238	HZ2, E_LYS.238	2.75	1.87	26.62
1HGI.PDB	OE1, D_GLU.72	NZ, E_LYS.238	HZ3, E_LYS.238	2.80	1.81	15.90
1HGI.PDB	O, F_LYS.62	N, E_GLY.303	H, E_GLY.303	2.93	1.96	6.65
1HGI.PDB	OG, F_SER.93	N, E_LYS.310	H, E_LYS.310	2.99	2.05	13.79
1HGI.PDB	OD1, F_ASP.86	NZ, E_LYS.310	HZ3, E_LYS.310	2.76	1.91	29.16
1HGI.PDB	OD1, F_ASN.104	N, E_ALA.317	H, E_ALA.317	2.72	1.81	15.78
1HGI.PDB	OE1, F_GLU.15	NZ, E_LYS.326	HZ3, E_LYS.326	2.88	1.86	11.05
1HGI.PDB	O, E_VAL.323	N, F_GLY.13	H, F_GLY.13	2.66	1.77	18.62
1HGI.PDB	O, E_HIS.17	N, F_TRP.14	H, F_TRP.14	2.84	1.93	16.42
1HGI.PDB	O, E_GLY.16	N, F_GLY.23	H, F_GLY.23	2.97	2.05	16.89
1HGI.PDB	O, E_CYS.14	N, F_ARG.25	H, F_ARG.25	2.91	2.04	22.96
1HGI.PDB	O, E_THR.12	N, F_GLN.27	H, F_GLN.27	2.93	1.99	14.92
1HGI.PDB	O, C_THR.28	NE, F_ARG.54	HE, F_ARG.54	2.95	1.99	9.70
1HGI.PDB	OE2, D_GLU.97	NH2, F_ARG.54	HH22, F_ARG.54	2.75	1.79	14.82
1HGI.PDB	OG, E_SER.110	NE2, F_HIS.64	HE2, F_HIS.64	2.84	1.87	3.62
1HGI.PDB	O, E_LYS.299	NZ, F_LYS.68	HZ1, F_LYS.68	2.80	1.76	2.37
1HGI.PDB	OG, A_SER.107	N, F_ARG.76	H, F_ARG.76	2.79	1.83	7.22
1HGI.PDB	OE2, B_GLU.81	NE, F_ARG.76	HE, F_ARG.76	2.85	1.88	7.37
1HGI.PDB	OE2, B_GLU.74	NH1, F_ARG.76	HH12, F_ARG.76	2.77	1.76	3.93
1HGI.PDB	OE1, B_GLU.81	NH2, F_ARG.76	HH21, F_ARG.76	2.64	1.66	4.79
1HGI.PDB	OE1, B_GLU.74	NH2, F_ARG.76	HH22, F_ARG.76	2.76	1.78	10.40
1HGI.PDB	OE1, B_GLU.85	OH, F_TYR.83	HH, F_TYR.83	2.58	1.75	24.06
1HGI.PDB	OH, D_TYR.83	NZ, F_LYS.88	HZ1, F_LYS.88	2.61	1.62	12.49
1HGI.PDB	O, E_LYS.27	ND2, F_ASN.104	HD22, F_ASN.104	2.88	1.93	10.77

1HGI.PDB	O, D_LEU_2	OG, F_SER_113	HG, F_SER_113	2.78	1.94	24.17
1HGI.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.96	2.09	23.50
1HGI.PDB	OE2, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.96	2.09	23.34
1HGI.PDB	O, E_LEU_13	N, F_PHE_138	H, F_PHE_138	2.75	1.89	22.82
1HGI.PDB	O, E_ALA_11	N, F_ILE_140	H, F_ILE_140	2.78	1.89	18.92
1HGI.PDB	O, D_ARG_170	NH1, F_ARG_163	HH12, F_ARG_163	2.92	1.95	13.55
1HGI.PDB	OE2, D_GLU_131	NH2, F_ARG_163	HH22, F_ARG_163	2.69	1.85	26.81

Table 1794: Interfacial 1HGI-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1HGJ.PDB	O, B.ILE.140	N, A.ALA.11	H, A.ALA.11	2.85	1.95	18.97
1HGJ.PDB	O, B.PHE.138	N, A.LEU.13	H, A.LEU.13	2.97	2.00	8.62
1HGJ.PDB	O, B.ARG.25	N, A.CYS.14	H, A.CYS.14	2.88	1.94	12.89
1HGJ.PDB	O, B.GLY.136	N, A.LEU.15	H, A.LEU.15	2.93	1.95	2.37
1HGJ.PDB	O, B.GLY.23	N, A.GLY.16	H, A.GLY.16	2.86	1.96	18.97
1HGJ.PDB	O, B.TRP.21	N, A.HIS.18	H, A.HIS.18	2.85	1.98	21.54
1HGJ.PDB	OE2, B.GLU.97	NZ, A.LYS.27	HZ1, A.LYS.27	2.81	1.78	9.30
1HGJ.PDB	OE2, B.GLU.67	NH2, A.ARG.109	HH21, A.ARG.109	2.75	1.77	12.07
1HGJ.PDB	OD2, F.ASP.79	OG, A.SER.110	HG, A.SER.110	2.94	1.98	10.39
1HGJ.PDB	OE1, C.GLN.210	NH2, A.ARG.220	HH21, A.ARG.220	2.67	1.78	22.50
1HGJ.PDB	O, F.SER.71	NZ, A.LYS.238	HZ2, A.LYS.238	2.62	1.72	23.44
1HGJ.PDB	OE1, F.GLU.72	NZ, A.LYS.238	HZ3, A.LYS.238	2.90	1.90	13.91
1HGJ.PDB	O, B.LYS.68	NZ, A.LYS.299	HZ2, A.LYS.299	2.95	1.96	14.91
1HGJ.PDB	O, B.LYS.62	N, A.GLY.303	H, A.GLY.303	2.93	1.97	8.41
1HGJ.PDB	OD1, B.ASN.104	N, A.ALA.317	H, A.ALA.317	2.74	1.81	13.01
1HGJ.PDB	OE1, B.GLU.15	N, A.THR.328	H, A.THR.328	2.99	2.03	9.44
1HGJ.PDB	O, A.VAL.323	N, B.GLY.13	H, B.GLY.13	2.69	1.76	11.68
1HGJ.PDB	O, A.HIS.17	N, B.TRP.14	H, B.TRP.14	2.84	1.89	12.22
1HGJ.PDB	O, A.GLY.16	N, B.GLY.23	H, B.GLY.23	2.94	2.02	17.07
1HGJ.PDB	O, A.CYS.14	N, B.ARG.25	H, B.ARG.25	2.98	2.05	15.51
1HGJ.PDB	OE2, A.GLU.325	NH2, B.ARG.25	HH22, B.ARG.25	2.97	2.01	15.94
1HGJ.PDB	O, E.THR.28	NE, B.ARG.54	HE, B.ARG.54	3.00	2.04	10.82
1HGJ.PDB	OE2, F.GLU.97	NH2, B.ARG.54	HH22, B.ARG.54	2.77	1.81	15.09
1HGJ.PDB	OD2, F.ASP.86	NZ, B.LYS.62	HZ1, B.LYS.62	2.65	1.75	23.55
1HGJ.PDB	OD2, F.ASP.90	NZ, B.LYS.62	HZ3, B.LYS.62	2.74	1.89	28.52
1HGJ.PDB	OG, A.SER.110	NE2, B.HIS.64	HE2, B.HIS.64	2.89	1.93	11.21
1HGJ.PDB	O, A.LYS.299	NZ, B.LYS.68	HZ1, B.LYS.68	2.90	1.89	11.39
1HGJ.PDB	OG, C.SER.107	N, B.ARG.76	H, B.ARG.76	2.84	1.89	10.24
1HGJ.PDB	OE2, D.GLU.81	NE, B.ARG.76	HE, B.ARG.76	2.90	1.93	10.80
1HGJ.PDB	OE2, D.GLU.74	NH1, B.ARG.76	HH12, B.ARG.76	2.88	1.87	5.28
1HGJ.PDB	OE1, D.GLU.81	NH2, B.ARG.76	HH21, B.ARG.76	2.72	1.72	3.64
1HGJ.PDB	OE1, D.GLU.74	NH2, B.ARG.76	HH22, B.ARG.76	2.85	1.84	3.19
1HGJ.PDB	OE1, D.GLU.85	OH, B.TYR.83	HH, B.TYR.83	2.67	1.83	24.12
1HGJ.PDB	OH, F.TYR.83	NZ, B.LYS.88	HZ1, B.LYS.88	2.78	1.75	7.42
1HGJ.PDB	O, A.LYS.27	ND2, B.ASN.104	HD22, B.ASN.104	2.89	1.94	10.52
1HGJ.PDB	O, F.LEU.2	OG, B.SER.113	HG, B.SER.113	2.74	1.91	25.16
1HGJ.PDB	OE1, F.GLU.132	NE, B.ARG.124	HE, B.ARG.124	2.82	2.00	27.29
1HGJ.PDB	OE2, F.GLU.132	NE, B.ARG.124	HE, B.ARG.124	2.91	2.02	20.91
1HGJ.PDB	O, A.LEU.13	N, B.PHE.138	H, B.PHE.138	2.71	1.86	23.78
1HGJ.PDB	O, A.ALA.11	N, B.ILE.140	H, B.ILE.140	2.77	1.86	16.77
1HGJ.PDB	O, F.ARG.170	NH1, B.ARG.163	HH12, B.ARG.163	2.72	1.75	12.61
1HGJ.PDB	O, D.ILE.140	N, C.ALA.11	H, C.ALA.11	2.85	1.95	19.06
1HGJ.PDB	O, D.GLN.27	N, C.THR.12	H, C.THR.12	2.99	2.03	8.05
1HGJ.PDB	O, D.PHE.138	N, C.LEU.13	H, C.LEU.13	2.99	2.02	7.89
1HGJ.PDB	O, D.ARG.25	N, C.CYS.14	H, C.CYS.14	2.76	1.85	16.80
1HGJ.PDB	O, D.GLY.136	N, C.LEU.15	H, C.LEU.15	2.95	1.97	3.95
1HGJ.PDB	O, D.GLY.23	N, C.GLY.16	H, C.GLY.16	2.89	1.98	18.54
1HGJ.PDB	O, D.TRP.21	N, C.HIS.18	H, C.HIS.18	2.86	1.97	20.63
1HGJ.PDB	OE2, D.GLU.97	NZ, C.LYS.27	HZ1, C.LYS.27	2.82	1.80	8.63
1HGJ.PDB	OE2, D.GLU.67	NH2, C.ARG.109	HH21, C.ARG.109	2.76	1.78	13.33
1HGJ.PDB	OD2, B.ASP.79	OG, C.SER.110	HG, C.SER.110	2.79	1.87	14.95
1HGJ.PDB	OE1, E.GLN.210	NH2, C.ARG.220	HH21, C.ARG.220	2.66	1.82	26.85
1HGJ.PDB	OE1, B.GLU.72	NZ, C.LYS.238	HZ1, C.LYS.238	2.75	1.79	18.67
1HGJ.PDB	O, B.SER.71	NZ, C.LYS.238	HZ3, C.LYS.238	2.55	1.67	24.42
1HGJ.PDB	O, D.LYS.68	NZ, C.LYS.299	HZ2, C.LYS.299	2.96	1.96	14.80
1HGJ.PDB	O, D.LYS.62	N, C.GLY.303	H, C.GLY.303	2.93	1.98	10.54
1HGJ.PDB	OG, D.SER.93	N, C.LYS.310	H, C.LYS.310	3.00	2.04	11.61

1HGJ.PDB	OD1, D-ASP.86	NZ, C-LYS.310	HZ3, C-LYS.310	2.94	2.10	29.37
1HGJ.PDB	OD1, D-ASN.104	N, C-ALA.317	H, C-ALA.317	2.74	1.82	13.77
1HGJ.PDB	OE1, D-GLU.15	NZ, C-LYS.326	HZ1, C-LYS.326	2.91	1.86	5.48
1HGJ.PDB	O, C-VAL.323	N, D-GLY.13	H, D-GLY.13	2.70	1.77	13.01
1HGJ.PDB	O, C-HIS.17	N, D-TRP.14	H, D-TRP.14	2.84	1.88	10.47
1HGJ.PDB	O, C-GLY.16	N, D-GLY.23	H, D-GLY.23	2.95	2.03	16.60
1HGJ.PDB	O, C-CYS.14	N, D-ARG.25	H, D-ARG.25	2.96	2.03	15.69
1HGJ.PDB	O, C-THR.12	N, D-GLN.27	H, D-GLN.27	2.96	2.04	16.68
1HGJ.PDB	O, A-THR.28	NE, D-ARG.54	HE, D-ARG.54	2.94	1.98	10.71
1HGJ.PDB	OE2, B-GLU.97	NH2, D-ARG.54	HH22, D-ARG.54	2.84	1.88	15.58
1HGJ.PDB	OG, C-SER.110	NE2, D-HIS.64	HE2, D-HIS.64	2.89	1.91	5.59
1HGJ.PDB	O, C-LYS.299	NZ, D-LYS.68	HZ1, D-LYS.68	2.93	1.91	11.63
1HGJ.PDB	OG, E-SER.107	N, D-ARG.76	H, D-ARG.76	2.86	1.90	9.67
1HGJ.PDB	OE2, F-GLU.81	NE, D-ARG.76	HE, D-ARG.76	2.85	1.89	10.87
1HGJ.PDB	OE2, F-GLU.74	NH1, D-ARG.76	HH12, D-ARG.76	2.76	1.76	7.89
1HGJ.PDB	OE1, F-GLU.81	NH2, D-ARG.76	HH21, D-ARG.76	2.68	1.69	5.65
1HGJ.PDB	OE1, F-GLU.74	NH2, D-ARG.76	HH22, D-ARG.76	2.71	1.72	5.59
1HGJ.PDB	OE1, F-GLU.85	OH, D-TYR.83	HH, D-TYR.83	2.63	1.81	25.72
1HGJ.PDB	OH, B-TYR.83	NZ, D-LYS.88	HZ1, D-LYS.88	2.75	1.72	7.31
1HGJ.PDB	O, C-LYS.27	ND2, D-ASN.104	HD22, D-ASN.104	2.90	1.94	10.67
1HGJ.PDB	O, B-LEU.2	OG, D-SER.113	HG, D-SER.113	2.68	1.87	27.58
1HGJ.PDB	OE1, B-GLU.132	NE, D-ARG.124	HE, D-ARG.124	2.80	1.98	27.33
1HGJ.PDB	OE2, B-GLU.132	NE, D-ARG.124	HE, D-ARG.124	2.87	2.00	21.99
1HGJ.PDB	OH, B-TYR.141	NH1, D-ARG.127	HH12, D-ARG.127	2.99	2.02	12.89
1HGJ.PDB	O, C-LEU.13	N, D-PHE.138	H, D-PHE.138	2.74	1.87	22.25
1HGJ.PDB	O, C-ALA.11	N, D-ILE.140	H, D-ILE.140	2.80	1.87	15.19
1HGJ.PDB	O, B-ARG.170	NH1, D-ARG.163	HH12, D-ARG.163	2.74	1.76	11.80
1HGJ.PDB	O, F-ILE.140	N, E-ALA.11	H, E-ALA.11	2.86	1.96	18.18
1HGJ.PDB	O, F-GLN.27	N, E-THR.12	H, E-THR.12	2.93	2.00	15.55
1HGJ.PDB	O, F-PHE.138	N, E-LEU.13	H, E-LEU.13	2.96	1.99	8.56
1HGJ.PDB	O, F-ARG.25	N, E-CYS.14	H, E-CYS.14	2.66	1.82	24.90
1HGJ.PDB	O, F-GLY.136	N, E-LEU.15	H, E-LEU.15	2.91	1.94	3.68
1HGJ.PDB	O, F-GLY.23	N, E-GLY.16	H, E-GLY.16	2.87	1.96	18.32
1HGJ.PDB	O, F-TRP.21	N, E-HIS.18	H, E-HIS.18	2.83	1.96	22.19
1HGJ.PDB	OE2, F-GLU.97	NZ, E-LYS.27	HZ1, E-LYS.27	2.81	1.79	8.50
1HGJ.PDB	OE2, F-GLU.67	NH2, E-ARG.109	HH21, E-ARG.109	2.76	1.77	12.82
1HGJ.PDB	OD2, D-ASP.79	OG, E-SER.110	HG, E-SER.110	2.79	1.87	15.96
1HGJ.PDB	OD1, C-ASP.101	NE2, E-GLN.210	HE22, E-GLN.210	2.94	2.10	26.45
1HGJ.PDB	OE1, A-GLN.210	NH2, E-ARG.220	HH21, E-ARG.220	2.69	1.86	28.41
1HGJ.PDB	O, D-SER.71	NZ, E-LYS.238	HZ2, E-LYS.238	2.65	1.73	22.71
1HGJ.PDB	OE1, D-GLU.72	NZ, E-LYS.238	HZ3, E-LYS.238	2.87	1.86	13.82
1HGJ.PDB	O, F-LYS.68	NZ, E-LYS.299	HZ1, E-LYS.299	2.94	1.95	15.31
1HGJ.PDB	O, F-LYS.62	N, E-GLY.303	H, E-GLY.303	2.92	1.96	9.12
1HGJ.PDB	OG, F-SER.93	N, E-LYS.310	H, E-LYS.310	2.99	2.03	10.38
1HGJ.PDB	OD1, F-ASP.86	NZ, E-LYS.310	HZ3, E-LYS.310	2.93	2.08	29.22
1HGJ.PDB	OD1, F-ASN.104	N, E-ALA.317	H, E-ALA.317	2.73	1.80	11.35
1HGJ.PDB	OE2, F-GLU.15	N, E-GLU.325	H, E-GLU.325	2.88	2.08	29.65
1HGJ.PDB	OE1, F-GLU.15	NZ, E-LYS.326	HZ3, E-LYS.326	2.87	1.86	12.83
1HGJ.PDB	O, E-VAL.323	N, F-GLY.13	H, F-GLY.13	2.69	1.76	10.96
1HGJ.PDB	O, E-HIS.17	N, F-TRP.14	H, F-TRP.14	2.84	1.89	11.67
1HGJ.PDB	O, E-GLY.16	N, F-GLY.23	H, F-GLY.23	2.93	2.01	16.90
1HGJ.PDB	O, E-CYS.14	N, F-ARG.25	H, F-ARG.25	2.87	1.99	20.85
1HGJ.PDB	O, E-THR.12	N, F-GLN.27	H, F-GLN.27	2.89	1.97	15.73
1HGJ.PDB	OE2, D-GLU.97	NH2, F-ARG.54	HH22, F-ARG.54	2.77	1.81	14.54
1HGJ.PDB	OG, E-SER.110	NE2, F-HIS.64	HE2, F-HIS.64	2.90	1.93	7.02
1HGJ.PDB	O, E-LYS.299	NZ, F-LYS.68	HZ1, F-LYS.68	2.93	1.90	4.77
1HGJ.PDB	OG, A-SER.107	N, F-ARG.76	H, F-ARG.76	2.85	1.88	6.29
1HGJ.PDB	OE2, B-GLU.81	NE, F-ARG.76	HE, F-ARG.76	2.85	1.89	12.57

1HGJ.PDB	OE2, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.70	1.70	4.55
1HGJ.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.65	1.66	2.84
1HGJ.PDB	OE1, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.72	1.73	7.95
1HGJ.PDB	OE1, B_GLU_85	OH, F_TYR_83	HH, F_TYR_83	2.53	1.75	28.54
1HGJ.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.70	1.68	8.19
1HGJ.PDB	O, E_LYS_27	ND2, F_ASN_104	HD22, F_ASN_104	2.91	1.96	11.78
1HGJ.PDB	O, D_LEU_2	OG, F_SER_113	HG, F_SER_113	2.74	1.92	26.51
1HGJ.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.92	2.09	27.65
1HGJ.PDB	OE2, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.96	2.06	20.98
1HGJ.PDB	O, E_LEU_13	N, F_PHE_138	H, F_PHE_138	2.73	1.87	22.18
1HGJ.PDB	O, E_ALA_11	N, F_ILE_140	H, F_ILE_140	2.78	1.87	17.89
1HGJ.PDB	O, D_ARG_170	NH1, F_ARG_163	HH12, F_ARG_163	2.89	1.91	11.37

Table 1795: Interfacial 1HGJ-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1OSP.PDB	O, O_LYS_44	NH1, L_ARG_32	HH12, L_ARG_32	2.98	2.09	22.73
1OSP.PDB	O, O_SER_43	NH2, L_ARG_32	HH22, L_ARG_32	2.91	1.93	9.19
1OSP.PDB	OD2, L_ASP_1	OG, H_SER_62	HG, H_SER_62	2.98	2.17	26.53
1OSP.PDB	O, O_ASP_93	N, H_TYR_101	H, H_TYR_101	2.96	2.00	9.88
1OSP.PDB	OH, L_TYR_36	N, H_PHE_107	H, H_PHE_107	2.90	1.92	4.68
1OSP.PDB	OG, L_SER_176	OG, H_SER_185	HG, H_SER_185	2.74	1.91	24.72
1OSP.PDB	OE1, L_GLU_123	NZ, H_LYS_215	HZ2, H_LYS_215	2.78	1.85	20.53

Table 1796: Interfacial 1OSP-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1PSK.PDB	O, H_PRO_168	OG, L_SER_161	HG, L_SER_161	2.76	1.90	22.64

Table 1797: Interfacial 1PSK-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1VFB.PDB	OE1, C_GLN_121	N, A_SER_93	H, A_SER_93	2.89	1.92	8.17
1VFB.PDB	OE1, B_GLU_98	NH1, A_ARG_96	HH12, A_ARG_96	2.82	1.84	8.38
1VFB.PDB	OE2, B_GLU_98	NH2, A_ARG_96	HH22, A_ARG_96	2.81	1.85	10.74
1VFB.PDB	OE1, A_GLN_38	NE2, B_GLN_39	HE21, B_GLN_39	2.95	1.98	8.04
1VFB.PDB	O, C_GLY_22	NH1, B_ARG_102	HH12, B_ARG_102	2.82	1.90	18.81
1VFB.PDB	OD2, B_ASP_100	N, C_SER_24	H, C_SER_24	2.91	2.09	27.47
1VFB.PDB	O, A_PHE_91	NE2, C_GLN_121	HE21, C_GLN_121	2.82	1.88	14.37

Table 1798: Interfacial 1VFB-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
3SE8.PDB	O, H_TRP_54	N, G_ASP_368	H, G_ASP_368	2.75	1.91	10.72
3SE8.PDB	OE2, L_GLU_96	N, G_GLY_459	H, G_GLY_459	2.81	1.99	15.35
3SE8.PDB	OD1, G_ASN_280	NE1, H_TRP_50	HE1, H_TRP_50	3.00	2.21	20.49
3SE8.PDB	O, G_GLY_473	NE1, H_TRP_54	HE1, H_TRP_54	2.82	1.98	10.03
3SE8.PDB	O, G_GLY_458	N, H_ARG_61	H, H_ARG_61	2.91	2.08	12.24
3SE8.PDB	OD1, G_ASP_457	NE2, H_GLN_64	HE22, H_GLN_64	2.94	2.12	14.23
3SE8.PDB	OD2, G_ASP_368	NH2, H_ARG_71	HH22, H_ARG_71	2.91	2.05	6.24
3SE8.PDB	OH, L_TYR_36	N, H_TRP_100F	H, H_TRP_100F	2.89	2.04	6.32
3SE8.PDB	OE1, H_GLN_101	N, L_SER_56	H, L_SER_56	2.97	2.12	7.63
3SE8.PDB	O, H_PRO_167	OG, L_SER_162	HG, L_SER_162	2.71	1.98	23.05

Table 1799: Interfacial 3SE8-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
3SE9.PDB	O, H_THR_53	N, G_ASP_368	H, G_ASP_368	2.97	2.15	15.24
3SE9.PDB	OD1, G_ASN_280	NE1, H_TRP_50	HE1, H_TRP_50	2.86	2.03	11.46
3SE9.PDB	O, G_ARG_456	ND2, H_ASN_57	HD22, H_ASN_57	2.82	1.98	10.42
3SE9.PDB	OG, G_SER_365	NH1, H_ARG_64	HH11, H_ARG_64	2.81	2.04	21.79
3SE9.PDB	OD2, G_ASP_368	NH1, H_ARG_71	HH12, H_ARG_71	2.77	1.92	7.25
3SE9.PDB	O, G_GLY_429	NH1, H_ARG_73	HH12, H_ARG_73	2.99	2.23	23.32
3SE9.PDB	OD1, G_ASN_279	NE1, H_TRP_100D	HE1, H_TRP_100D	2.86	2.13	26.83
3SE9.PDB	OH, L_TYR_36	N, H_PHE_100F	H, H_PHE_100F	2.88	2.05	11.59
3SE9.PDB	OD1, L_ASN_138	NE2, H_HIS_164	HE2, H_HIS_164	2.87	2.10	22.18
3SE9.PDB	O, H_PRO_167	OG, L_SER_162	HG, L_SER_162	2.60	1.89	25.20

Table 1800: Interfacial 3SE9-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
3THM.PDB	O, H.ALA.117	ND2, L.ASN.35	HD21, L.ASN.35	2.77	1.97	17.79
3THM.PDB	OE1, L.GLN.39	NE2, H.GLN.41	HE22, H.GLN.41	2.98	2.14	9.35
3THM.PDB	O, F.CYS.43	NH1, H.ARG.105	HH12, H.ARG.105	2.85	2.05	18.46
3THM.PDB	OG, L.SER.183	NZ, H.LYS.162	HZ1, H.LYS.162	2.77	1.97	21.34
3THM.PDB	OG1, L.THR.135	NZ, H.LYS.162	HZ2, H.LYS.162	2.85	2.02	17.75
3THM.PDB	OH, H.TYR.35	ND1, F.HIS.44	HD1, F.HIS.44	2.69	1.83	5.98
3THM.PDB	OG, H.SER.63	NE2, F.HIS.44	HE2, F.HIS.44	2.83	2.07	23.36
3THM.PDB	O, L.SER.51	NZ, F.LYS.78	HZ2, F.LYS.78	3.00	2.15	15.09

Table 1801: Interfacial 3THM-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
3TJE.PDB	O, H.ALA.117	ND2, L.ASN.35	HD21, L.ASN.35	2.81	2.01	17.88
3TJE.PDB	OE1, L.GLN.39	NE2, H.GLN.41	HE21, H.GLN.41	2.98	2.15	10.85
3TJE.PDB	O, F.CYS.43	NH1, H.ARG.105	HH12, H.ARG.105	2.85	2.08	23.11
3TJE.PDB	OH, L.TYR.37	N, H.PHE.119	H, H.PHE.119	2.96	2.10	4.74
3TJE.PDB	OH, H.TYR.35	ND1, F.HIS.44	HD1, F.HIS.44	2.56	1.70	3.69

Table 1802: Interfacial 3TJE-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
3U2S.PDB	OE1, L_GLN_38	NE2, H_GLN_39	HE22, H_GLN_39	2.89	2.04	8.55
3U2S.PDB	OH, L_TYR_36	N, H_MET_100T	H, H_MET_100T	2.95	2.15	18.41
3U2S.PDB	OG, L_SER_165	NE2, H_HIS_164	HE2, H_HIS_164	2.93	2.12	16.97
3U2S.PDB	OE1, H_GLN_39	NE2, L_GLN_38	HE22, L_GLN_38	2.91	2.09	13.75
3U2S.PDB	OD2, C_ASP_167	ND2, L_ASN_60	HD22, L_ASN_60	2.90	2.14	22.76
3U2S.PDB	OD1, H_ASP_61	NH2, L_ARG_95A	HH22, L_ARG_95A	2.34	1.58	22.53
3U2S.PDB	OE2, H_GLU_95	NH2, L_ARG_96	HH21, L_ARG_96	2.87	2.05	15.72
3U2S.PDB	O, H_ASN_100F	N, G_LYS_169	H, G_LYS_169	2.84	1.99	7.68
3U2S.PDB	OH, H_TYR_100K	ND2, G_ASN_173	HD21, G_ASN_173	2.97	2.13	8.87
3U2S.PDB	OE1, B_GLN_38	NE2, A_GLN_39	HE22, A_GLN_39	2.92	2.07	7.34
3U2S.PDB	O, C_ASP_167	N, A_ASN_100F	H, A_ASN_100F	2.97	2.14	14.21
3U2S.PDB	OG1, B_THR_131	NZ, A_LYS_143	HZ2, A_LYS_143	2.41	1.67	27.35
3U2S.PDB	OE1, A_GLN_39	NE2, B_GLN_38	HE22, B_GLN_38	2.92	2.08	10.61
3U2S.PDB	OG1, H_THR_160	N, B_ALA_80	H, B_ALA_80	2.90	2.08	14.44
3U2S.PDB	OD1, A_ASP_61	NH1, B_ARG_95A	HH12, B_ARG_95A	2.63	1.91	26.97
3U2S.PDB	OE2, A_GLU_95	NH2, B_ARG_96	HH21, B_ARG_96	2.98	2.16	13.77
3U2S.PDB	O, A_ASN_100F	N, C_LYS_169	H, C_LYS_169	2.91	2.08	13.24

Table 1803: Interfacial 3U2S-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
3UYR.PDB	OE1, P_GLN_48	N, H_ASN_101	H, H_ASN_101	2.90	2.08	14.57
3UYR.PDB	OH, L_TYR_41	N, H_LEU_104	H, H_LEU_104	2.91	2.05	4.02
3UYR.PDB	OE2, L_GLU_127	NZ, H_LYS_212	HZ3, H_LYS_212	2.87	2.08	23.12
3UYR.PDB	O, P_PRO_50	NE2, L_HIS_31	HE2, L_HIS_31	2.91	2.13	21.00
3UYR.PDB	O, H_PRO_171	OG, L_SER_166	HG, L_SER_166	2.72	1.97	20.46
3UYR.PDB	OD1, H_ASN_101	NE2, P_GLN_48	HE22, P_GLN_48	2.57	1.87	29.89

Table 1804: Interfacial 3UYR-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4F33.PDB	OE1, B_GLN_39	NE2, A_GLN_38	HE22, A_GLN_38	2.96	2.13	12.75
4F33.PDB	O, B_GLY_110	OG, A_SER_43	HG, A_SER_43	2.65	1.95	25.99
4F33.PDB	O, B_ARG_104	NH1, A_ARG_46	HH11, A_ARG_46	2.62	1.83	18.99
4F33.PDB	O, B_PRO_173	OG, A_SER_162	HG, A_SER_162	2.76	2.03	23.18
4F33.PDB	OE1, A_GLN_38	NE2, B_GLN_39	HE22, B_GLN_39	2.82	1.97	5.31
4F33.PDB	OH, A_TYR_36	N, B_PHE_106	H, B_PHE_106	2.97	2.12	7.79
4F33.PDB	OE2, G_GLU_123	N, B_GLY_124	H, B_GLY_124	2.73	1.87	2.75
4F33.PDB	O, H_ASP_214	N, B_LYS_212	H, B_LYS_212	2.81	2.00	15.02
4F33.PDB	O, H_LYS_212	N, B_ASP_214	H, B_ASP_214	2.84	2.02	15.98
4F33.PDB	OE1, A_GLU_123	NZ, B_LYS_215	HZ1, B_LYS_215	2.68	1.82	12.44
4F33.PDB	OG1, H_THR_211	NZ, B_LYS_215	HZ2, B_LYS_215	2.83	1.95	7.37
4F33.PDB	O, D_GLY_110	OG, C_SER_43	HG, C_SER_43	2.70	1.98	23.76
4F33.PDB	O, D_ARG_104	NH1, C_ARG_46	HH11, C_ARG_46	2.70	1.92	20.25
4F33.PDB	O, D_TYR_60	NE2, C_HIS_94	HE2, C_HIS_94	2.75	2.00	24.62
4F33.PDB	O, D_PRO_173	OG, C_SER_162	HG, C_SER_162	2.78	2.07	25.83
4F33.PDB	OE1, C_GLN_38	NE2, D_GLN_39	HE22, D_GLN_39	2.89	2.03	5.23
4F33.PDB	OE2, E_GLU_123	N, D_GLY_124	H, D_GLY_124	2.84	1.99	7.85
4F33.PDB	O, F_ASP_214	N, D_LYS_212	H, D_LYS_212	2.98	2.15	12.10
4F33.PDB	O, F_LYS_212	N, D_ASP_214	H, D_ASP_214	2.85	2.03	14.94
4F33.PDB	OE1, C_GLU_123	NZ, D_LYS_215	HZ1, D_LYS_215	2.79	1.99	22.47
4F33.PDB	OG1, F_THR_211	NZ, D_LYS_215	HZ2, D_LYS_215	2.86	1.99	10.67
4F33.PDB	O, F_ASN_210	N, D_LYS_216	H, D_LYS_216	2.98	2.16	15.42
4F33.PDB	O, F_GLY_110	OG, E_SER_43	HG, E_SER_43	2.52	1.83	27.97
4F33.PDB	O, F_ARG_104	NH1, E_ARG_46	HH11, E_ARG_46	2.85	2.03	15.38
4F33.PDB	O, F_LEU_176	NE2, E_GLN_160	HE22, E_GLN_160	2.93	2.08	4.21
4F33.PDB	O, F_PRO_173	OG, E_SER_162	HG, E_SER_162	2.63	1.89	21.98
4F33.PDB	O, A_GLY_60	N, F_PHE_29	H, F_PHE_29	2.97	2.18	20.00
4F33.PDB	OE1, E_GLN_38	NE2, F_GLN_39	HE22, F_GLN_39	2.92	2.06	5.53
4F33.PDB	OH, E_TYR_36	N, F_PHE_106	H, F_PHE_106	2.80	1.96	9.30
4F33.PDB	OE2, C_GLU_123	N, F_GLY_124	H, F_GLY_124	2.81	1.96	5.00
4F33.PDB	O, D_ASP_214	N, F_LYS_212	H, F_LYS_212	2.94	2.11	12.64
4F33.PDB	O, D_LYS_212	N, F_ASP_214	H, F_ASP_214	2.84	2.02	14.84
4F33.PDB	OE1, E_GLU_123	NZ, F_LYS_215	HZ1, F_LYS_215	2.61	1.84	24.34
4F33.PDB	OG1, D_THR_211	NZ, F_LYS_215	HZ2, F_LYS_215	2.92	2.04	7.71
4F33.PDB	O, H_TYR_60	NE2, G_HIS_94	HE2, G_HIS_94	2.97	2.17	17.68
4F33.PDB	O, H_LEU_176	NE2, G_GLN_160	HE22, G_GLN_160	2.89	2.04	8.42
4F33.PDB	O, H_PRO_173	OG, G_SER_162	HG, G_SER_162	2.65	1.94	25.59
4F33.PDB	O, C_GLY_60	N, H_PHE_29	H, H_PHE_29	2.96	2.15	17.00
4F33.PDB	OH, G_TYR_36	N, H_PHE_106	H, H_PHE_106	2.74	1.89	7.07
4F33.PDB	OE2, A_GLU_123	N, H_GLY_124	H, H_GLY_124	2.97	2.12	7.35
4F33.PDB	O, G_SER_208	NZ, H_LYS_135	HZ3, H_LYS_135	2.85	1.99	13.05
4F33.PDB	O, B_LYS_212	N, H_ASP_214	H, H_ASP_214	2.71	1.89	15.00
4F33.PDB	OE1, G_GLU_123	NZ, H_LYS_215	HZ1, H_LYS_215	2.97	2.19	24.10
4F33.PDB	OG1, B_THR_211	NZ, H_LYS_215	HZ2, H_LYS_215	2.80	1.95	14.49
4F33.PDB	O, B_ASN_210	N, H_LYS_216	H, H_LYS_216	2.82	2.01	16.40

Table 1805: Interfacial 4F33-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4F3F.PDB	OE1, B_GLN_39	NE2, A_GLN_38	HE22, A_GLN_38	2.88	2.04	8.75
4F3F.PDB	O, B_ARG_104	NH1, A_ARG_46	HH11, A_ARG_46	2.93	2.16	22.46
4F3F.PDB	OG, B_SER_59	NE2, A_HIS_94	HE2, A_HIS_94	2.82	2.03	19.68
4F3F.PDB	OE1, C_GLU_52	N, B_ASP_102	H, B_ASP_102	2.88	2.08	17.53
4F3F.PDB	OH, A_TYR_36	N, B_PHE_106	H, B_PHE_106	2.71	1.88	12.56
4F3F.PDB	OD1, A_ASN_138	NE2, B_HIS_170	HE2, B_HIS_170	2.82	2.05	21.56
4F3F.PDB	O, B_ASP_102	NZ, C_LYS_24	HZ2, C_LYS_24	2.85	2.03	18.08
4F3F.PDB	OD1, B_ASP_102	N, C_LYS_25	H, C_LYS_25	2.86	2.02	9.58
4F3F.PDB	OH, B_TYR_101	NZ, C_LYS_25	HZ3, C_LYS_25	2.87	2.11	26.18
4F3F.PDB	OH, A_TYR_32	NE1, C_TRP_26	HE1, C_TRP_26	2.97	2.17	18.16

Table 1806: Interfacial 4F3F-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4JAM.PDB	OH, L_TYR_36	N, H_PHE_100E	H, H_PHE_100E	2.85	2.03	15.20
4JAM.PDB	OD1, H_ASN_100B	ND2, L_ASN_32	HD21, L_ASN_32	2.96	2.21	25.94
4JAM.PDB	O, B_THR_201	N, L_THR_201	H, L_THR_201	2.84	2.04	18.18
4JAM.PDB	O, B_GLY_199	N, L_GLU_203	H, L_GLU_203	2.91	2.13	21.03
4JAM.PDB	OH, B_TYR_36	N, A_PHE_100E	H, A_PHE_100E	2.90	2.09	16.41
4JAM.PDB	O, L_THR_201	N, B_THR_201	H, B_THR_201	2.77	1.96	16.15
4JAM.PDB	O, L_GLY_199	N, B_GLU_203	H, B_GLU_203	2.79	1.99	17.96

Table 1807: Interfacial 4JAM-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4JAN.PDB	OH, L.TYR_36	N, H.PHE_100E	H, H.PHE_100E	2.91	2.16	24.28
4JAN.PDB	OD2, B.ASP_92	OG, H.SER_156	HG, H.SER_156	2.50	1.78	23.90
4JAN.PDB	OE1, L.GLU_123	NZ, H.LYS_209	HZ1, H.LYS_209	2.89	2.13	26.71
4JAN.PDB	OD1, H.ASN_100B	ND2, L.ASN_32	HD21, L.ASN_32	2.76	1.91	6.44
4JAN.PDB	OH, B.TYR_36	N, A.PHE_100E	H, A.PHE_100E	2.74	1.90	10.14
4JAN.PDB	O, L.GLY_458	ND2, B.ASN_32	HD22, B.ASN_32	2.86	2.11	24.85

Table 1808: Interfacial 4JAN-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4KRM.PDB	OE1, B_GLU_110	NH1, A_ARG_353	HH11, A_ARG_353	2.81	2.05	22.81
4KRM.PDB	O, B_GLU_110	NH1, A_ARG_353	HH12, A_ARG_353	2.55	1.85	29.89
4KRM.PDB	O, B_ALA_100	NH2, A_ARG_353	HH21, A_ARG_353	2.89	2.04	4.33
4KRM.PDB	O, B ASP_112	NE2, A_GLN_384	HE22, A_GLN_384	2.93	2.19	25.19
4KRM.PDB	O, C_LYS_310	N, B_THR_58	H, B_THR_58	2.99	2.17	13.91
4KRM.PDB	O, C_GLU_308	N, B_TYR_60	H, B_TYR_60	2.75	1.96	19.67
4KRM.PDB	O, B_TYR_60	N, C_GLU_308	H, C_GLU_308	2.91	2.19	28.33
4KRM.PDB	O, B_THR_58	N, C_LYS_310	H, C_LYS_310	2.88	2.06	14.23
4KRM.PDB	O, B ASP_56	N, C_VAL_312	H, C_VAL_312	2.73	1.89	9.64
4KRM.PDB	OE1, D_GLU_110	NH1, C_ARG_353	HH11, C_ARG_353	2.87	2.05	16.15
4KRM.PDB	O, D_ALA_100	NH2, C_ARG_353	HH21, C_ARG_353	2.80	2.00	16.96
4KRM.PDB	OD2, C ASP_355	NH1, D_ARG_30	HH12, D_ARG_30	2.45	1.63	13.53
4KRM.PDB	O, E_GLU_308	N, D_TYR_60	H, D_TYR_60	2.82	2.08	26.84
4KRM.PDB	O, D_THR_58	N, E_LYS_310	H, E_LYS_310	2.79	2.02	22.01
4KRM.PDB	OE1, F_GLU_110	NH1, E_ARG_353	HH11, E_ARG_353	2.85	2.03	14.34
4KRM.PDB	O, F_GLU_110	NH1, E_ARG_353	HH12, E_ARG_353	2.46	1.72	24.77
4KRM.PDB	O, F_ALA_100	NH2, E_ARG_353	HH21, E_ARG_353	2.81	1.99	15.85
4KRM.PDB	OD2, F ASP_112	NH2, E_ARG_353	HH22, E_ARG_353	2.96	2.18	20.33
4KRM.PDB	O, F ASP_112	NE2, E_GLN_384	HE22, E_GLN_384	2.82	2.10	28.13
4KRM.PDB	O, J_THR_58	N, G_LYS_310	H, G_LYS_310	2.73	1.87	4.39
4KRM.PDB	O, J ASP_56	N, G_VAL_312	H, G_VAL_312	2.86	2.02	9.25
4KRM.PDB	OD1, H ASP_112	N, G_VAL_350	H, G_VAL_350	2.96	2.25	28.54
4KRM.PDB	O, H_GLU_110	NH1, G_ARG_353	HH12, G_ARG_353	2.56	1.83	26.87
4KRM.PDB	O, H_ALA_100	NH2, G_ARG_353	HH21, G_ARG_353	2.51	1.75	22.59
4KRM.PDB	OE2, B_GLU_5	NZ, G_LYS_407	HZ1, G_LYS_407	2.98	2.17	20.60
4KRM.PDB	OD2, G ASP_355	NH1, H_ARG_30	HH12, H_ARG_30	2.45	1.69	23.45
4KRM.PDB	O, L_TYR_60	N, I_GLU_308	H, I_GLU_308	2.69	1.88	16.25
4KRM.PDB	O, L_THR_58	N, I_LYS_310	H, I_LYS_310	2.70	1.84	3.45
4KRM.PDB	O, L ASP_56	N, I_VAL_312	H, I_VAL_312	2.83	1.98	8.53
4KRM.PDB	OD1, J ASP_112	N, I_VAL_350	H, I_VAL_350	2.88	2.05	13.27
4KRM.PDB	OE1, J_GLU_110	NH1, I_ARG_353	HH11, I_ARG_353	2.86	2.07	18.90
4KRM.PDB	O, J_ALA_100	NH2, I_ARG_353	HH21, I_ARG_353	2.97	2.14	13.62
4KRM.PDB	OD2, J ASP_112	NH2, I_ARG_353	HH22, I_ARG_353	3.00	2.19	17.61
4KRM.PDB	O, G_GLU_308	N, J_TYR_60	H, J_TYR_60	2.74	1.97	22.05
4KRM.PDB	OD1, L ASP_112	N, K_VAL_350	H, K_VAL_350	2.89	2.07	15.44
4KRM.PDB	OE1, L_GLU_110	NH1, K_ARG_353	HH11, K_ARG_353	2.89	2.06	12.41
4KRM.PDB	O, L_GLU_110	NH1, K_ARG_353	HH12, K_ARG_353	2.54	1.80	24.42
4KRM.PDB	O, L_ALA_100	NH2, K_ARG_353	HH21, K_ARG_353	2.92	2.14	20.95
4KRM.PDB	OD2, L ASP_112	NH2, K_ARG_353	HH22, K_ARG_353	2.89	2.07	13.96
4KRM.PDB	OD2, K ASP_355	NH1, L_ARG_30	HH12, L_ARG_30	2.44	1.65	18.93
4KRM.PDB	O, I_LYS_310	N, L_THR_58	H, L_THR_58	2.98	2.15	12.69
4KRM.PDB	O, I_GLU_308	N, L_TYR_60	H, L_TYR_60	2.75	2.02	27.31

Table 1809: Interfacial 4KRM-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4KRO.PDB	O, D_GLY_54	NH1, A_ARG_353	HH12, A_ARG_353	2.81	1.97	9.47
4KRO.PDB	OG, B_SER_103	NZ, A_LYS_375	HZ2, A_LYS_375	2.61	1.76	15.34
4KRO.PDB	OH, D_TYR_102	NE2, A_GLN_384	HE21, A_GLN_384	2.87	2.16	29.24
4KRO.PDB	O, B_TYR_100	NH2, A_ARG_403	HH22, A_ARG_403	2.57	1.73	11.63
4KRO.PDB	OD1, B_ASP_118	NE, A_ARG_405	HE, A_ARG_405	2.72	1.93	19.48
4KRO.PDB	O, A_GLY_458	N, B_VAL_2	H, B_VAL_2	2.76	1.93	12.61
4KRO.PDB	OE1, D_GLN_39	NE2, C_GLN_38	HE22, C_GLN_38	2.85	2.00	7.50
4KRO.PDB	OD2, D_ASP_103	OH, C_TYR_50	HH, C_TYR_50	2.49	1.72	20.15
4KRO.PDB	O, D_TYR_104	NE2, C_GLN_89	HE22, C_GLN_89	3.00	2.19	16.80
4KRO.PDB	OD1, D_ASP_103	ND2, C_ASN_91	HD21, C_ASN_91	2.93	2.12	16.18
4KRO.PDB	O, A_ASN_469	N, C_TRP_94	H, C_TRP_94	2.75	1.95	19.24
4KRO.PDB	OD2, D_ASP_58	NE1, C_TRP_94	HE1, C_TRP_94	2.80	2.10	29.15
4KRO.PDB	O, D_LEU_176	NE2, C_GLN_160	HE22, C_GLN_160	2.74	1.92	15.89
4KRO.PDB	OE1, C_GLN_38	NE2, D_GLN_39	HE22, D_GLN_39	2.80	1.94	4.32
4KRO.PDB	OE1, A_GLN_408	OH, D_TYR_102	HH, D_TYR_102	2.75	1.97	18.39
4KRO.PDB	OH, C_TYR_36	N, D_PHE_106	H, D_PHE_106	2.93	2.08	9.34

Table 1810: Interfacial 4KRO-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4KRP.PDB	O, D_GLY_54	NH2, A_ARG_353	HH22, A_ARG_353	2.83	1.98	6.79
4KRP.PDB	OD1, B_ASP_115	NH2, A_ARG_405	HH21, A_ARG_405	2.63	1.81	15.48
4KRP.PDB	O, D_TYR_102	OG, A_SER_440	HG, A_SER_440	2.65	1.82	4.10
4KRP.PDB	OD1, D_ASP_58	NZ, A_LYS_443	HZ1, A_LYS_443	2.65	1.82	17.69
4KRP.PDB	OD2, D_ASP_103	NZ, A_LYS_465	HZ2, A_LYS_465	2.93	2.05	5.06
4KRP.PDB	OE1, D_GLN_39	NE2, C_GLN_38	HE22, C_GLN_38	2.70	1.84	6.09
4KRP.PDB	OD2, D_ASP_103	OH, C_TYR_50	HH, C_TYR_50	2.43	1.66	18.96
4KRP.PDB	OD1, D_ASP_103	ND2, C_ASN_91	HD21, C_ASN_91	2.77	1.91	6.24
4KRP.PDB	O, A_ASN_469	N, C_TRP_94	H, C_TRP_94	2.68	1.89	19.97
4KRP.PDB	OD2, D_ASP_58	NE1, C_TRP_94	HE1, C_TRP_94	2.98	2.17	17.26
4KRP.PDB	O, D_LEU_176	NE2, C_GLN_160	HE22, C_GLN_160	2.56	1.80	22.58
4KRP.PDB	O, D_PRO_173	OG, C_SER_162	HG, C_SER_162	2.80	2.10	28.74
4KRP.PDB	OE1, C_GLN_38	NE2, D_GLN_39	HE22, D_GLN_39	2.72	1.87	5.47
4KRP.PDB	OE1, A_GLN_408	OH, D_TYR_102	HH, D_TYR_102	2.56	1.74	10.00
4KRP.PDB	OG, A_SER_440	OH, D_TYR_104	HH, D_TYR_104	2.94	2.22	25.72
4KRP.PDB	OH, C_TYR_36	N, D_PHE_106	H, D_PHE_106	2.89	2.11	20.61
4KRP.PDB	OE1, A_GLU_431	OH, B_TYR_32	HH, B_TYR_32	2.59	1.78	7.49
4KRP.PDB	OE1, A_GLU_400	OH, B_TYR_100	HH, B_TYR_100	2.94	2.13	13.29
4KRP.PDB	OE2, A_GLU_431	OH, B_TYR_116	HH, B_TYR_116	2.43	1.75	29.09

Table 1811: Interfacial 4KRP-specific side chain and main chain hydrogen bonding analysis.

In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4NZR.PDB	OH, L_TYR_36	N, H_PHE_100J	H, H_PHE_100J	2.96	2.11	8.14
4NZR.PDB	OG, L_SER_176	OG, H_SER_188	HG, H_SER_188	2.88	2.16	24.46
4NZR.PDB	OE2, L_GLU_123	NZ, H_LYS_221	HZ2, H_LYS_221	2.99	2.10	2.00
4NZR.PDB	O, M_PRO_119	OG, L_SER_14	HG, L_SER_14	2.76	2.00	18.37
4NZR.PDB	OG1, M_THR_110	N, L_THR_18	H, L_THR_18	2.82	2.00	15.23
4NZR.PDB	OH, M_TYR_444	N, L_LYS_54	H, L_LYS_54	2.91	2.06	4.85
4NZR.PDB	O, M_ALA_391	NH2, L_ARG_61	HH21, L_ARG_61	2.90	2.11	19.46
4NZR.PDB	OG, M_SER_106	N, L_ASN_77	H, L_ASN_77	2.86	2.01	5.30
4NZR.PDB	O, H_ALA_100G	NE, L_ARG_96	HE, L_ARG_96	2.83	2.08	23.79
4NZR.PDB	O, H_ALA_100G	NH2, L_ARG_96	HH21, L_ARG_96	2.80	2.05	24.03
4NZR.PDB	O, M_ASN_177	NH2, L_ARG_108	HH22, L_ARG_108	2.82	2.05	22.21
4NZR.PDB	O, M_GLY_178	N, L_THR_109	H, L_THR_109	2.92	2.07	5.99
4NZR.PDB	O, M_GLY_178	OG1, L_THR_109	HG1, L_THR_109	2.88	2.17	26.23
4NZR.PDB	O, M_ASP_117	N, L_VAL_110	H, L_VAL_110	2.96	2.14	15.09
4NZR.PDB	O, H_LEU_178	NE2, L_GLN_160	HE22, L_GLN_160	2.86	2.01	7.83
4NZR.PDB	O, H_PRO_175	OG, L_SER_162	HG, L_SER_162	2.79	1.98	7.14
4NZR.PDB	OG, H_SER_188	OG, L_SER_176	HG, L_SER_176	2.88	2.09	13.66
4NZR.PDB	OE1, L_GLU_81	NE, M_ARG_384	HE, M_ARG_384	2.93	2.09	10.37
4NZR.PDB	OD1, H_ASP_31E	NH1, M_ARG_457	HH12, M_ARG_457	2.96	2.12	11.27
4NZR.PDB	OD2, H_ASP_31E	NH2, M_ARG_457	HH22, M_ARG_457	2.55	1.75	17.03

Table 1812: Interfacial 4NZR-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4NZU.PDB	OH, L_TYR_36	N, H_PHE_100H	H, H_PHE_100H	2.86	2.04	13.13

Table 1813: Interfacial 4NZU-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4WUU.PDB	OD2, B_ASP_53	NE, A_ARG_48	HE, A_ARG_48	2.84	2.13	29.12
4WUU.PDB	OH, E_TYR_104	NZ, A_LYS_66	HZ3, A_LYS_66	2.89	2.02	10.84
4WUU.PDB	OXT, C_LEU_9	OH, A_TYR_84	HH, A_TYR_84	2.64	1.82	12.17
4WUU.PDB	O, B_TRP_60	NE2, A_GLN_96	HE22, A_GLN_96	2.78	1.93	8.81
4WUU.PDB	O, C_LEU_9	NZ, A_LYS_146	HZ3, A_LYS_146	2.76	1.90	13.68
4WUU.PDB	O, C_TYR_8	NE1, A_TRP_147	HE1, A_TRP_147	2.81	1.99	15.97
4WUU.PDB	O, C_ARG_1	OH, A_TYR_159	HH, A_TYR_159	2.86	2.02	6.39
4WUU.PDB	OE1, B_GLN_8	NH1, A_ARG_234	HH11, A_ARG_234	2.79	2.07	27.49
4WUU.PDB	O, A_PRO_235	OH, B_TYR_10	HH, B_TYR_10	2.61	1.79	11.75
4WUU.PDB	O, A_ALA_236	ND2, B_ASN_24	HD21, B_ASN_24	2.81	2.05	22.96
4WUU.PDB	OE1, A_GLU_232	OH, B_TYR_26	HH, B_TYR_26	2.95	2.14	13.27
4WUU.PDB	OH, A_TYR_171	N, C_ARG_1	H1, C_ARG_1	2.79	2.03	25.96
4WUU.PDB	OE2, A_GLU_63	N, C_MET_2	H, C_MET_2	2.90	2.09	16.21
4WUU.PDB	OE1, E_GLN_39	NE2, D_GLN_39	HE22, D_GLN_39	2.94	2.18	23.53
4WUU.PDB	OD1, E_ASP_106	NE1, D_TRP_99	HE1, D_TRP_99	2.95	2.19	24.35
4WUU.PDB	OE1, D_GLN_39	NE2, E_GLN_39	HE22, E_GLN_39	2.55	1.73	14.29
4WUU.PDB	OE2, A_GLU_166	NH2, E_ARG_50	HH22, E_ARG_50	2.67	1.88	18.69
4WUU.PDB	OE1, A_GLU_63	OH, E_TYR_104	HH, E_TYR_104	2.59	1.76	7.82
4WUU.PDB	OE1, A_GLU_58	N, E_TYR_105	H, E_TYR_105	2.88	2.05	12.40
4WUU.PDB	OE1, A_GLU_55	OH, E_TYR_105	HH, E_TYR_105	2.47	1.79	29.86

Table 1814: Interfacial 4WUU-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4Z0X.PDB	OE1, B_GLN_64	NE2, A_GLN_37	HE22, A_GLN_37	2.75	1.99	23.41
4Z0X.PDB	O, B_GLY_129	NE2, A_GLN_88	HE22, A_GLN_88	2.63	1.87	22.97
4Z0X.PDB	O, B_GLY_129	NE1, A_TRP_90	HE1, A_TRP_90	2.96	2.14	15.73
4Z0X.PDB	OH, C_TYR_443	N, A_SER_93	H, A_SER_93	2.99	2.17	13.42
4Z0X.PDB	O, C_LEU_441	N, B_SER_127	H, B_SER_127	2.61	1.82	19.78
4Z0X.PDB	OH, A_TYR_35	N, B_TYR_131	H, B_TYR_131	2.85	2.09	23.16

Table 1815: Interfacial 4Z0X-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5I76.PDB	OE1, B_GLN_39	NE2, A_GLN_38	HE22, A_GLN_38	2.94	2.10	10.68
5I76.PDB	O, B_GLY_110	OG, A_SER_43	HG, A_SER_43	2.73	2.02	27.09
5I76.PDB	OD2, B_ASP_103	OH, A_TYR_50	HH, A_TYR_50	2.64	1.88	21.01
5I76.PDB	O, B_PRO_173	OG, A_SER_162	HG, A_SER_162	2.48	1.79	28.75
5I76.PDB	OE1, A_GLN_38	NE2, B_GLN_39	HE22, B_GLN_39	2.80	1.95	6.66
5I76.PDB	OG, A_SER_176	OG, B_SER_185	HG, B_SER_185	2.89	2.15	23.05
5I76.PDB	OE1, A_GLU_123	NZ, B_LYS_215	HZ1, B_LYS_215	2.73	1.96	24.68
5I76.PDB	OE2, A_GLU_123	NZ, B_LYS_215	HZ1, B_LYS_215	2.89	2.11	24.69
5I76.PDB	OD2, A_ASP_70	NH1, C_ARG_24	HH12, C_ARG_24	2.95	2.23	28.81
5I76.PDB	O, D_GLY_110	OG, C_SER_43	HG, C_SER_43	2.84	2.15	29.22
5I76.PDB	OD2, D_ASP_103	OH, C_TYR_50	HH, C_TYR_50	2.76	1.95	12.40
5I76.PDB	O, A_SER_202	NE2, C_GLN_147	HE22, C_GLN_147	2.78	1.96	13.33
5I76.PDB	OE1, C_GLN_38	NE2, D_GLN_39	HE22, D_GLN_39	2.85	2.01	10.98
5I76.PDB	OH, C_TYR_36	N, D_PHE_106	H, D_PHE_106	2.93	2.09	12.40
5I76.PDB	OE1, C_GLU_123	NZ, D_LYS_215	HZ1, D_LYS_215	2.60	1.73	11.40

Table 1816: Interfacial 5I76-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5JO5.PDB	OE1, L_GLN_38	NE2, H_GLN_39	HE22, H_GLN_39	2.84	2.00	9.38
5JO5.PDB	OH, L_TYR_36	N, H_PHE_100L	H, H_PHE_100L	2.79	1.96	12.88
5JO5.PDB	O, L_GLY_41	NH2, H_ARG_105	HH22, H_ARG_105	2.85	2.05	18.48
5JO5.PDB	OE2, L_GLU_124	NZ, H_LYS_143	HZ2, H_LYS_143	2.46	1.63	17.05
5JO5.PDB	OH, L_TYR_177	OG, H_SER_179	HG, H_SER_179	2.73	2.00	25.96
5JO5.PDB	OE1, D_GLN_24	OG, L_SER_30	HG, L_SER_30	2.84	2.07	18.45
5JO5.PDB	OE1, H_GLN_39	NE2, L_GLN_38	HE22, L_GLN_38	2.83	2.00	13.03
5JO5.PDB	OE2, H_GLU_100J	NH2, L_ARG_91	HH22, L_ARG_91	2.69	1.84	7.26
5JO5.PDB	OD1, H_ASP_58	NE, L_ARG_95B	HE, L_ARG_95B	2.95	2.13	14.76
5JO5.PDB	O, H_GLY_42	OG1, L_THR_163	HG1, L_THR_163	2.52	1.79	25.04
5JO5.PDB	OE1, B_GLN_38	NE2, A_GLN_39	HE22, A_GLN_39	2.87	2.02	8.31
5JO5.PDB	OH, B_TYR_36	N, A_PHE_100L	H, A_PHE_100L	2.86	2.06	18.12
5JO5.PDB	O, B_GLY_41	NH1, A_ARG_105	HH12, A_ARG_105	2.66	1.82	9.49
5JO5.PDB	OE2, B_GLU_124	NZ, A_LYS_143	HZ2, A_LYS_143	2.62	1.83	23.29
5JO5.PDB	OH, B_TYR_177	OG, A_SER_179	HG, A_SER_179	2.83	2.10	25.21
5JO5.PDB	OE2, B_GLU_123	NZ, A_LYS_209	HZ1, A_LYS_209	2.55	1.68	10.64
5JO5.PDB	OE1, A_GLN_39	NE2, B_GLN_38	HE22, B_GLN_38	2.90	2.07	12.43
5JO5.PDB	O, F_ARG_29	ND2, B_ASN_69	HD21, B_ASN_69	2.80	1.99	16.03
5JO5.PDB	O, A_GLY_100H	NE, B_ARG_91	HE, B_ARG_91	2.94	2.09	9.41
5JO5.PDB	O, A_GLY_42	OG1, B_THR_163	HG1, B_THR_163	2.48	1.73	21.87
5JO5.PDB	OE1, D_GLN_38	NE2, C_GLN_39	HE22, C_GLN_39	2.86	2.02	9.45
5JO5.PDB	OH, D_TYR_36	N, C_PHE_100L	H, C_PHE_100L	2.87	2.08	19.05
5JO5.PDB	OE2, D_GLU_124	NZ, C_LYS_143	HZ2, C_LYS_143	2.79	1.92	10.71
5JO5.PDB	OH, D_TYR_177	OG, C_SER_179	HG, C_SER_179	2.71	1.97	23.23
5JO5.PDB	OE2, D_GLU_123	NZ, C_LYS_209	HZ1, C_LYS_209	2.58	1.72	11.28
5JO5.PDB	OE1, C_GLN_39	NE2, D_GLN_38	HE22, D_GLN_38	2.92	2.09	12.72
5JO5.PDB	O, L_ARG_29	ND2, D_ASN_69	HD21, D_ASN_69	2.86	2.03	13.06
5JO5.PDB	OD1, C_ASP_58	NE, D_ARG_95B	HE, D_ARG_95B	2.94	2.10	11.64
5JO5.PDB	O, C_GLY_42	OG1, D_THR_163	HG1, D_THR_163	2.56	1.81	22.64
5JO5.PDB	OE1, F_GLN_38	NE2, E_GLN_39	HE22, E_GLN_39	2.90	2.06	10.70
5JO5.PDB	OH, F_TYR_36	N, E_PHE_100L	H, E_PHE_100L	2.79	1.96	13.04
5JO5.PDB	O, F_GLY_41	NH2, E_ARG_105	HH22, E_ARG_105	2.92	2.13	19.96
5JO5.PDB	OE2, F_GLU_124	NZ, E_LYS_143	HZ2, E_LYS_143	2.55	1.75	21.57
5JO5.PDB	OH, F_TYR_177	OG, E_SER_179	HG, E_SER_179	2.58	1.87	27.02
5JO5.PDB	OE2, F_GLU_123	NZ, E_LYS_209	HZ1, E_LYS_209	2.57	1.74	17.62
5JO5.PDB	OE1, B_GLN_24	OG, F_SER_30	HG, F_SER_30	2.88	2.11	20.15
5JO5.PDB	OE1, E_GLN_39	NE2, F_GLN_38	HE22, F_GLN_38	2.85	2.02	12.75
5JO5.PDB	OE2, E_GLU_100J	NH2, F_ARG_91	HH22, F_ARG_91	2.72	1.87	5.99
5JO5.PDB	OD1, E_ASP_58	NE, F_ARG_95B	HE, F_ARG_95B	2.92	2.09	12.47
5JO5.PDB	O, E_GLY_42	OG1, F_THR_163	HG1, F_THR_163	2.55	1.80	22.10

Table 1817: Interfacial 5JO5-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5JR1.PDB	OH, L-TYR_36	N, H-PHE_100L	H, H-PHE_100L	2.93	2.14	18.24
5JR1.PDB	O, L-GLY_41	NH1, H-ARG_105	HH11, H-ARG_105	2.58	1.82	23.25
5JR1.PDB	OH, L-TYR_178	OG, H-SER_179	HG, H-SER_179	2.83	2.03	15.88
5JR1.PDB	N, H-PHE_100L	OH, L-TYR_36	HH, L-TYR_36	2.93	2.21	26.41
5JR1.PDB	O, H-PRO_100F	NH1, L-ARG_91	HH12, L-ARG_91	2.89	2.18	29.36
5JR1.PDB	O, H-PRO_100F	NH2, L-ARG_91	HH22, L-ARG_91	2.82	2.09	26.91
5JR1.PDB	OD2, H-ASP_58	NH2, L-ARG_95B	HH22, L-ARG_95B	2.47	1.67	16.99

Table 1818: Interfacial 5JR1-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5JUE.PDB	O, H_MET_100E	OH, L_TYR_36	HH, L_TYR_36	2.57	1.73	1.94
5JUE.PDB	OH, H_TYR_91	NE2, L_GLN_38	HE22, L_GLN_38	2.57	1.77	17.09
5JUE.PDB	O, H_PRO_167	OG, L_SER_162	HG, L_SER_162	2.70	1.95	22.84
5JUE.PDB	OG, H_SER_178	OG, L_SER_176	HG, L_SER_176	2.78	1.94	3.13
5JUE.PDB	OE1, L_GLU_123	NZ, H_LYS_208	HZ1, H_LYS_208	2.81	1.98	17.66
5JUE.PDB	O, L_PRO_119	NH1, H_ARG_213	HH12, H_ARG_213	2.84	2.13	29.21
5JUE.PDB	O, L_PRO_120	NH2, H_ARG_213	HH22, H_ARG_213	2.94	2.13	15.93

Table 1819: Interfacial 5JUE-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5JXA.PDB	OD2, L_ASP_50	OH, H_TYR_100	HH, H_TYR_100	2.57	1.75	11.76
5JXA.PDB	OH, L_TYR_36	N, H_TRP_100F	H, H_TRP_100F	2.85	2.00	7.52
5JXA.PDB	OH, H_TYR_100	NH2, L_ARG_53	HH21, L_ARG_53	2.89	2.07	18.12
5JXA.PDB	O, H_LEU_170	NE2, L_GLN_160	HE22, L_GLN_160	2.84	1.99	4.55
5JXA.PDB	O, H_PRO_167	OG, L_SER_162	HG, L_SER_162	2.69	1.94	23.37

Table 1820: Interfacial 5JXA-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5M33.PDB	OE1, A_GLN_129	N, B_VAL_114	H, B_VAL_114	2.67	1.84	13.32

Table 1821: Interfacial 5M33-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5T6P.PDB	O, B_GLY_107	OG, A_SER_48	HG, A_SER_48	2.52	1.72	14.73
5T6P.PDB	O, B_PRO_170	OG, A_SER_167	HG, A_SER_167	2.98	2.14	3.80
5T6P.PDB	OE1, A_GLN_43	NE2, B_GLN_39	HE22, B_GLN_39	2.71	1.86	5.14
5T6P.PDB	O, F_PRO_8	ND2, B_ASN_57	HD21, B_ASN_57	2.91	2.07	9.74
5T6P.PDB	OE1, D_GLN_39	NE2, C_GLN_43	HE22, C_GLN_43	3.00	2.17	12.88
5T6P.PDB	O, D_GLY_107	OG, C_SER_48	HG, C_SER_48	2.66	1.94	25.38
5T6P.PDB	OE1, C_GLN_43	NE2, D_GLN_39	HE22, D_GLN_39	2.79	1.94	7.20
5T6P.PDB	OH, C_TYR_41	N, D_PHE_103	H, D_PHE_103	2.95	2.09	5.85
5T6P.PDB	OE1, C_GLU_39	NE, E_ARG_5	HE, E_ARG_5	2.86	2.02	10.72

Table 1822: Interfacial 5T6P-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5T78.PDB	OD1, C_ASN_150	N, A_ASP_1	H1, A_ASP_1	2.85	2.07	23.76
5T78.PDB	OE1, B_GLN_39	NE2, A_GLN_43	HE22, A_GLN_43	2.92	2.08	9.79
5T78.PDB	O, B_GLY_107	OG, A_SER_48	HG, A_SER_48	2.44	1.64	14.53
5T78.PDB	O, B_LYS_43	OH, A_TYR_92	HH, A_TYR_92	2.74	2.03	27.20
5T78.PDB	O, B_PRO_170	OG, A_SER_167	HG, A_SER_167	2.91	2.11	14.54
5T78.PDB	OE1, A_GLN_43	NE2, B_GLN_39	HE22, B_GLN_39	2.63	1.78	5.56
5T78.PDB	OH, A_TYR_41	N, B_PHE_103	H, B_PHE_103	2.85	2.00	5.24
5T78.PDB	OE1, A_GLU_39	NH1, F_ARG_5	HH11, F_ARG_5	2.68	1.83	9.33
5T78.PDB	O, D_GLY_107	OG, C_SER_48	HG, C_SER_48	2.59	1.80	15.22
5T78.PDB	O, D_LYS_43	OH, C_TYR_92	HH, C_TYR_92	2.90	2.21	29.37
5T78.PDB	O, A_SER_26	N, C_ASN_166	H, C_ASN_166	2.63	1.86	20.95
5T78.PDB	O, D_PRO_170	OG, C_SER_167	HG, C_SER_167	2.87	2.05	10.83
5T78.PDB	OE1, C_GLN_43	NE2, D_GLN_39	HE22, D_GLN_39	2.72	1.87	5.23
5T78.PDB	OH, C_TYR_41	N, D_PHE_103	H, D_PHE_103	2.85	2.00	7.54
5T78.PDB	OD1, C_ASN_142	NE2, D_HIS_167	HE2, D_HIS_167	2.85	2.00	9.68
5T78.PDB	OD2, A_ASP_75	N, D_SER_175	H, D_SER_175	2.84	2.00	10.93
5T78.PDB	OE1, C_GLU_39	NH1, E_ARG_5	HH11, E_ARG_5	2.69	1.87	13.16

Table 1823: Interfacial 5T78-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5U3J.PDB	OD1, L_ASP_31	OH, H_TYR_100K	HH, H_TYR_100K	2.88	2.04	5.22
5U3J.PDB	OH, L_TYR_36	N, H_MET_100N	H, H_MET_100N	2.75	1.92	13.09
5U3J.PDB	OE1, H_GLU_100F	OH, L_TYR_32	HH, L_TYR_32	2.62	1.91	27.84
5U3J.PDB	OE1, H_GLN_39	NE2, L_GLN_38	HE22, L_GLN_38	2.66	1.83	12.57
5U3J.PDB	O, H_PRO_167	OG, L_SER_162	HG, L_SER_162	2.90	2.16	24.21

Table 1824: Interfacial 5U3J-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5U3N.PDB	OD2, A_ASP_674	NH1, H_ARG_52A	HH12, H_ARG_52A	3.00	2.24	24.41
5U3N.PDB	OD1, L_ASP_31	NH2, H_ARG_100B	HH22, H_ARG_100B	2.97	2.15	14.50
5U3N.PDB	OD1, L_ASN_34	ND2, H_ASN_100J	HD21, H_ASN_100J	2.72	1.86	2.61
5U3N.PDB	OH, L_TYR_36	N, H_MET_100M	H, H_MET_100M	2.99	2.13	5.54
5U3N.PDB	OD1, L_ASN_138	NE2, H_HIS_164	HE2, H_HIS_164	2.92	2.21	29.54
5U3N.PDB	O, H_PRO_167	OG, L_SER_162	HG, L_SER_162	2.77	1.98	17.29

Table 1825: Interfacial 5U3N-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5UCB.PDB	OE1, L_GLN_38	NE2, H_GLN_39	HE22, H_GLN_39	2.96	2.12	9.92
5UCB.PDB	O, B_LEU_5	OH, H_TYR_53	HH, H_TYR_53	2.73	1.99	23.03
5UCB.PDB	O, B_VAL_145	N, H_GLY_97	H, H_GLY_97	2.90	2.05	8.98
5UCB.PDB	O, L_SER_208	NZ, H_LYS_129	HZ2, H_LYS_129	2.83	2.06	25.53
5UCB.PDB	OD2, B_ASP_51	OG, L_SER_30	HG, L_SER_30	2.58	1.81	20.19
5UCB.PDB	OE1, H_GLN_39	NE2, L_GLN_38	HE22, L_GLN_38	2.95	2.13	14.86
5UCB.PDB	O, B_SER_47	NH1, L_ARG_66	HH12, L_ARG_66	2.77	1.99	21.64
5UCB.PDB	O, B_SER_47	NH2, L_ARG_66	HH22, L_ARG_66	2.89	2.16	27.12
5UCB.PDB	O, B_ARG_48	N, L_GLY_68	H, L_GLY_68	2.79	1.95	9.02
5UCB.PDB	O, H_LEU_170	NE2, L_GLN_160	HE22, L_GLN_160	2.99	2.13	5.75
5UCB.PDB	O, H_PRO_167	OG, L_SER_162	HG, L_SER_162	2.68	1.94	24.13
5UCB.PDB	O, L_ASP_91	OH, B_TYR_111	HH, B_TYR_111	2.57	1.75	11.11
5UCB.PDB	OG, H_SER_58	NZ, B_LYS_142	HZ3, B_LYS_142	2.83	1.96	8.82
5UCB.PDB	OD1, L_ASP_91	NH2, B_ARG_144	HH21, B_ARG_144	2.84	2.03	16.18

Table 1826: Interfacial 5UCB-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5UK0.PDB	OD1, F_ASP_590	ND2, B_ASN_560	HD22, B_ASN_560	2.72	1.94	19.72
5UK0.PDB	O, F_LEU_502	ND2, B_ASN_617	HD22, B_ASN_617	2.60	1.80	16.74
5UK0.PDB	OD1, D_ASP_586	NH2, C_ARG_311	HH22, C_ARG_311	2.98	2.20	18.56
5UK0.PDB	OD1, B_ASP_590	ND2, D_ASN_560	HD22, D_ASN_560	2.73	1.95	20.06
5UK0.PDB	O, B_LEU_502	ND2, D_ASN_617	HD22, D_ASN_617	2.62	1.80	13.03
5UK0.PDB	O, D_LEU_502	ND2, F_ASN_617	HD22, F_ASN_617	2.71	1.89	14.40

Table 1827: Interfacial 5UK0-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5VXJ.PDB	OE1, I_GLU_200	NH1, B_ARG_50	HH12, B_ARG_50	2.92	2.07	7.25
5VXJ.PDB	OE1, I_GLU_201	OH, B_TYR_105	HH, B_TYR_105	2.51	1.70	12.69
5VXJ.PDB	O, D_GLY_56	NH2, C_ARG_132	HH22, C_ARG_132	2.97	2.20	22.55
5VXJ.PDB	OD1, C_ASN_140	NE, D_ARG_19	HE, D_ARG_19	2.55	1.80	23.66
5VXJ.PDB	OE1, E_GLU_201	OH, D_TYR_105	HH, D_TYR_105	2.53	1.70	8.84
5VXJ.PDB	OD2, F_ASP_73	NZ, E_LYS_137	HZ2, E_LYS_137	2.77	1.96	20.15
5VXJ.PDB	O, D_TYR_105	OG, E_SER_173	HG, E_SER_173	2.87	2.17	28.40
5VXJ.PDB	OD1, D_ASN_97	NZ, E_LYS_197	HZ1, E_LYS_197	2.80	1.95	14.72
5VXJ.PDB	O, F_GLY_112	ND2, E_ASN_216	HD21, E_ASN_216	2.68	1.91	21.74
5VXJ.PDB	OE1, G_GLU_200	NH2, F_ARG_50	HH22, F_ARG_50	2.70	1.89	15.49
5VXJ.PDB	OE1, G_GLU_201	OH, F_TYR_105	HH, F_TYR_105	2.57	1.75	11.97
5VXJ.PDB	O, E_THR_217	NE2, F_GLN_111	HE22, F_GLN_111	2.98	2.12	6.26
5VXJ.PDB	O, H_GLY_56	NH2, G_ARG_132	HH22, G_ARG_132	2.94	2.20	26.37
5VXJ.PDB	O, F_TYR_105	OG, G_SER_173	HG, G_SER_173	2.88	2.16	26.33
5VXJ.PDB	OD1, I_ASN_292	N, G_GLY_176	H, G_GLY_176	2.76	2.01	25.37
5VXJ.PDB	OE1, H_GLN_111	OG1, G_THR_217	HG1, G_THR_217	2.86	2.17	29.58
5VXJ.PDB	OD2, J_ASP_73	NZ, I_LYS_137	HZ3, I_LYS_137	2.90	2.17	29.52
5VXJ.PDB	OD1, B_ASN_97	NZ, I_LYS_197	HZ1, I_LYS_197	2.68	1.88	21.92
5VXJ.PDB	O, I_THR_217	NE2, J_GLN_111	HE22, J_GLN_111	2.92	2.11	16.33

Table 1828: Interfacial 5VXJ-specific side chain and main chain hydrogen bonding analysis.

In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5VXK.PDB	OD1, A_ASN_280	N, B_SER_103	H, B_SER_103	2.64	1.78	2.03
5VXK.PDB	OD1, A_ASN_280	N, B_VAL_104	H, B_VAL_104	2.84	2.01	12.48
5VXK.PDB	OG, A_SER_168	NE2, B_GLN_106	HE21, B_GLN_106	2.99	2.23	24.43
5VXK.PDB	OD2, A_ASP_287	NE2, B_GLN_106	HE22, B_GLN_106	2.77	1.94	12.81
5VXK.PDB	OG1, B_THR_102	OH, A_TYR_276	HH, A_TYR_276	2.57	1.73	6.50

Table 1829: Interfacial 5VXK-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5VXL.PDB	OD2, B_ASP_52	NZ, A_LYS_205	HZ1, A_LYS_205	3.00	2.13	10.69
5VXL.PDB	O, A_ALA_198	OH, B_TYR_54	HH, B_TYR_54	2.38	1.67	27.03
5VXL.PDB	OD1, A_ASP_166	N, B_SER_55	H, B_SER_55	2.91	2.18	28.04
5VXL.PDB	OD1, A_ASP_166	OG, B_SER_55	HG, B_SER_55	2.56	1.73	4.68
5VXL.PDB	OE2, A_GLU_201	NH2, B_ARG_102	HH22, B_ARG_102	2.87	2.08	20.03

Table 1830: Interfacial 5VXL-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5VXM.PDB	OE2, B.GLU_111	NE1, A.TRP_177	HE1, A.TRP_177	2.76	1.97	19.61
5VXM.PDB	O, A.ASP_166	NE1, B.TRP_102	HE1, B.TRP_102	2.92	2.09	13.88
5VXM.PDB	OE2, A.GLU_201	N, B.CYS_104	H, B.CYS_104	2.85	2.02	10.45
5VXM.PDB	OE1, A.GLU_201	N, B.SER_105	H, B.SER_105	2.58	1.74	9.22

Table 1831: Interfacial 5VXM-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5VXR.PDB	OE1, L_GLN_38	NZ, H_LYS_39	HZ2, H_LYS_39	2.72	1.76	14.94
5VXR.PDB	OD1, P_ASN_415	OH, H_TYR_50	HH, H_TYR_50	2.71	1.82	21.79
5VXR.PDB	OH, L_TYR_36	N, H_PHE_106	H, H_PHE_106	2.92	1.92	7.59
5VXR.PDB	OD1, L_ASN_138	NE2, H_HIS_170	HE2, H_HIS_170	2.89	1.98	20.57
5VXR.PDB	OE2, L_GLU_123	NZ, H_LYS_214	HZ1, H_LYS_214	2.93	1.98	15.97
5VXR.PDB	O, H_GLY_101	NZ, L_LYS_30	HZ1, L_LYS_30	2.83	1.85	13.06
5VXR.PDB	O, P_GLY_418	NE1, L_TRP_96	HE1, L_TRP_96	2.88	1.87	5.74
5VXR.PDB	OG, H_SER_184	OG, L_SER_176	HG, L_SER_176	2.79	1.86	17.30
5VXR.PDB	OH, H_TYR_33	N, P_ASN_415	H, P_ASN_415	2.82	1.94	24.20
5VXR.PDB	O, L_ASN_91	NE1, P_TRP_420	HE1, P_TRP_420	2.80	1.97	28.78

Table 1832: Interfacial 5VXR-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5WKQ.PDB	OG, B.SER_208	NH2, A.ARG_135	HH21, A.ARG_135	2.89	2.06	11.87
5WKQ.PDB	OE2, A.GLU_131	ND1, B.HIS_207	HD1, B.HIS_207	2.65	1.88	22.26
5WKQ.PDB	OE1, A.GLU_131	OG1, B.THR_211	HG1, B.THR_211	2.63	1.86	19.68

Table 1833: Interfacial 5WKQ-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5WN9.PDB	OD1, H_ASN_57	NE, A_ARG_188	HE, A_ARG_188	2.58	1.61	2.15

Table 1834: Interfacial 5WN9-specific side chain and main chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1A14.PDB	OE1, L_GLN_38	NE2, H_GLN_39	HE21, H_GLN_39	2.62	1.69	9.24

Table 1835: 1A14-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1E6J.PDB	OE1, H_GLN_39	NE2, L_GLN_37	HE22, L_GLN_37	2.69	1.84	23.98

Table 1836: 1E6J-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1F3R.PDB	NE1, A_TRP_67	OG, B_SER_61	HG, B_SER_61	2.86	1.89	6.31

Table 1837: 1F3R-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1HGD.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.80	1.78	9.95
1HGD.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.83	1.84	13.41
1HGD.PDB	OD2, F_ASP_79	OG, A_SER_110	HG, A_SER_110	2.92	1.96	11.03
1HGD.PDB	OD1, E_ASP_101	NE2, A_GLN_210	HE22, A_GLN_210	3.00	2.15	26.33
1HGD.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.78	1.86	19.99
1HGD.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.93	1.92	13.44
1HGD.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.77	1.80	12.79
1HGD.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ1, B_LYS_62	2.61	1.78	29.53
1HGD.PDB	OD2, F_ASP_90	NZ, B_LYS_62	HZ3, B_LYS_62	2.73	1.84	25.56
1HGD.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.96	2.01	12.34
1HGD.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.88	1.91	8.67
1HGD.PDB	OE2, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.84	1.82	2.51
1HGD.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.71	1.71	6.80
1HGD.PDB	OE1, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.75	1.75	3.21
1HGD.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.65	1.81	23.27
1HGD.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.76	1.72	5.59
1HGD.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.83	2.02	28.17
1HGD.PDB	OE2, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.88	2.01	22.00
1HGD.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.80	1.77	7.54
1HGD.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.87	1.88	13.44
1HGD.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.73	1.84	19.59
1HGD.PDB	OD1, A_ASP_101	NE2, C_GLN_210	HE22, C_GLN_210	2.97	2.13	27.21
1HGD.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.69	1.80	23.00
1HGD.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.80	1.83	17.68
1HGD.PDB	OE1, D_GLU_15	NZ, C_LYS_326	HZ1, C_LYS_326	2.78	1.77	11.96
1HGD.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.79	1.82	13.03
1HGD.PDB	OD2, B_ASP_90	NZ, D_LYS_62	HZ3, D_LYS_62	2.62	1.79	29.99
1HGD.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.96	1.98	5.65
1HGD.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.83	1.87	10.56
1HGD.PDB	OE2, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.78	1.77	3.14
1HGD.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.65	1.67	9.42
1HGD.PDB	OE1, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.69	1.70	6.24
1HGD.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.57	1.79	29.87
1HGD.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.76	1.72	5.75
1HGD.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.80	2.01	29.31
1HGD.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.82	1.95	21.73
1HGD.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.79	1.77	8.77
1HGD.PDB	OE2, F_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.82	1.85	14.73
1HGD.PDB	OD2, D_ASP_79	OG, E_SER_110	HG, E_SER_110	2.81	1.89	15.50
1HGD.PDB	OD1, C_ASP_101	NE2, E_GLN_210	HE22, E_GLN_210	2.98	2.14	27.07
1HGD.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.77	1.90	25.11
1HGD.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ3, E_LYS_238	2.87	1.86	13.40
1HGD.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.97	1.97	16.19
1HGD.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.72	1.75	12.85
1HGD.PDB	OD2, D_ASP_90	NZ, F_LYS_62	HZ3, F_LYS_62	2.71	1.86	28.09
1HGD.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.95	1.98	9.92
1HGD.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.86	1.90	10.66
1HGD.PDB	OE2, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.77	1.75	1.42
1HGD.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.64	1.65	5.37
1HGD.PDB	OE1, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.71	1.72	7.42
1HGD.PDB	OE1, B_GLU_85	OH, F_TYR_83	HH, F_TYR_83	2.53	1.75	27.84
1HGD.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.67	1.66	8.83
1HGD.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.96	2.14	28.71
1HGD.PDB	OE2, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.94	2.05	20.84

Table 1838: 1HGD-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1HGE.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.80	1.78	10.14
1HGE.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.74	1.75	12.19
1HGE.PDB	OD2, F_ASP_79	OG, A_SER_110	HG, A_SER_110	2.90	1.95	11.19
1HGE.PDB	OD1, E_ASP_101	NE2, A_GLN_210	HE22, A_GLN_210	2.91	2.05	24.48
1HGE.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.71	1.78	19.14
1HGE.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.91	1.89	11.73
1HGE.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.84	1.86	12.76
1HGE.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ1, B_LYS_62	2.60	1.76	28.82
1HGE.PDB	OD2, F_ASP_90	NZ, B_LYS_62	HZ3, B_LYS_62	2.69	1.82	26.81
1HGE.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.97	2.02	12.36
1HGE.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.87	1.91	11.56
1HGE.PDB	OE2, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.84	1.83	5.81
1HGE.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.70	1.70	6.45
1HGE.PDB	OE1, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.79	1.79	3.91
1HGE.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.65	1.81	24.86
1HGE.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.75	1.71	5.62
1HGE.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.80	1.98	27.36
1HGE.PDB	OE2, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.94	2.06	21.65
1HGE.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.79	1.77	8.74
1HGE.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.78	1.79	11.19
1HGE.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.78	1.86	15.09
1HGE.PDB	OD1, A_ASP_101	NE2, C_GLN_210	HE22, C_GLN_210	2.93	2.07	24.92
1HGE.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.64	1.76	23.09
1HGE.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.78	1.80	16.75
1HGE.PDB	OE1, D_GLU_15	NZ, C_LYS_326	HZ1, C_LYS_326	2.74	1.73	12.73
1HGE.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.87	1.89	12.82
1HGE.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.96	1.98	6.23
1HGE.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.79	1.85	14.06
1HGE.PDB	OE2, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.78	1.78	7.91
1HGE.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.63	1.67	11.36
1HGE.PDB	OE1, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.74	1.75	7.04
1HGE.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.58	1.80	29.40
1HGE.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.71	1.68	6.52
1HGE.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.78	1.98	28.90
1HGE.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.90	2.01	20.41
1HGE.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.79	1.77	9.75
1HGE.PDB	OE2, F_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.78	1.79	11.63
1HGE.PDB	OD2, D_ASP_79	OG, E_SER_110	HG, E_SER_110	2.82	1.89	14.19
1HGE.PDB	OD1, C_ASP_101	NE2, E_GLN_210	HE22, E_GLN_210	2.89	2.04	25.02
1HGE.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.74	1.87	25.04
1HGE.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ3, E_LYS_238	2.85	1.84	12.25
1HGE.PDB	OD1, F_ASP_86	NZ, E_LYS_310	HZ3, E_LYS_310	2.86	2.02	29.64
1HGE.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.99	2.00	17.08
1HGE.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.80	1.82	12.52
1HGE.PDB	OD2, D_ASP_90	NZ, F_LYS_62	HZ2, F_LYS_62	2.67	1.83	29.15
1HGE.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.94	1.97	9.11
1HGE.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.85	1.89	11.64
1HGE.PDB	OE2, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.73	1.73	6.19
1HGE.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.65	1.66	5.51
1HGE.PDB	OE1, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.70	1.73	9.07
1HGE.PDB	OE1, B_GLU_85	OH, F_TYR_83	HH, F_TYR_83	2.51	1.76	30.00
1HGE.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.67	1.65	8.34
1HGE.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.92	2.09	27.36

Table 1839: 1HGE-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1HGF.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.79	1.86	21.55
1HGF.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.92	1.92	10.51
1HGF.PDB	OD2, F_ASP_79	OG, A_SER_110	HG, A_SER_110	2.82	1.90	15.87
1HGF.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.64	1.76	23.62
1HGF.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ2, A_LYS_238	2.85	1.85	14.58
1HGF.PDB	OE2, A_GLU_325	NH2, B_ARG_25	HH22, B_ARG_25	2.99	2.04	16.52
1HGF.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.83	1.86	13.50
1HGF.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ2, B_LYS_62	2.71	1.70	11.44
1HGF.PDB	OD2, F_ASP_90	NZ, B_LYS_62	HZ3, B_LYS_62	2.77	1.82	20.37
1HGF.PDB	OG, A_SER_266	ND1, B_HIS_64	HD1, B_HIS_64	2.66	1.79	20.68
1HGF.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.89	1.92	10.70
1HGF.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.92	1.92	2.47
1HGF.PDB	OE1, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.86	1.84	3.80
1HGF.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.73	1.74	10.29
1HGF.PDB	OE2, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.75	1.74	3.91
1HGF.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.57	1.80	29.66
1HGF.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.72	1.70	9.91
1HGF.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.80	1.86	13.00
1HGF.PDB	OE1, F_GLU_131	NH2, B_ARG_163	HH21, B_ARG_163	2.74	1.86	24.20
1HGF.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.81	1.85	19.93
1HGF.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.91	1.92	11.49
1HGF.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.69	1.85	25.37
1HGF.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.56	1.72	26.72
1HGF.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ2, C_LYS_238	2.75	1.78	18.48
1HGF.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.84	1.86	12.74
1HGF.PDB	OD2, B_ASP_86	NZ, D_LYS_62	HZ2, D_LYS_62	2.69	1.69	13.49
1HGF.PDB	OD2, B_ASP_90	NZ, D_LYS_62	HZ3, D_LYS_62	2.68	1.77	22.81
1HGF.PDB	OG, C_SER_266	ND1, D_HIS_64	HD1, D_HIS_64	2.64	1.83	27.58
1HGF.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.90	1.92	7.33
1HGF.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.82	1.85	5.34
1HGF.PDB	OE1, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.79	1.78	3.81
1HGF.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.64	1.68	12.43
1HGF.PDB	OE2, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.70	1.71	7.38
1HGF.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.58	1.80	29.87
1HGF.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.68	1.69	13.85
1HGF.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.79	1.88	16.40
1HGF.PDB	OE1, B_GLU_131	NH2, D_ARG_163	HH21, D_ARG_163	2.70	1.83	24.43
1HGF.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.75	1.83	22.30
1HGF.PDB	OE2, F_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.88	1.88	11.28
1HGF.PDB	OD2, D_ASP_79	OG, E_SER_110	HG, E_SER_110	2.78	1.90	21.69
1HGF.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.65	1.79	25.97
1HGF.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ2, E_LYS_238	2.83	1.84	16.42
1HGF.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.79	1.81	11.74
1HGF.PDB	OD2, D_ASP_86	NZ, F_LYS_62	HZ2, F_LYS_62	2.67	1.68	13.64
1HGF.PDB	OD2, D_ASP_90	NZ, F_LYS_62	HZ3, F_LYS_62	2.75	1.81	20.23
1HGF.PDB	OG, E_SER_266	ND1, F_HIS_64	HD1, F_HIS_64	2.65	1.77	20.25
1HGF.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.89	1.92	9.46
1HGF.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.86	1.88	5.84
1HGF.PDB	OE1, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.78	1.77	1.59
1HGF.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.69	1.70	7.61
1HGF.PDB	OE2, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.71	1.73	8.88
1HGF.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.55	1.63	21.75
1HGF.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.90	1.96	15.73
1HGF.PDB	OE1, D_GLU_131	NH2, F_ARG_163	HH21, F_ARG_163	2.69	1.84	27.00

Table 1840: 1HGF-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1HGG.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.90	1.87	9.15
1HGG.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.84	1.86	14.43
1HGG.PDB	OD2, F_ASP_79	OG, A_SER_110	HG, A_SER_110	2.88	1.95	14.29
1HGG.PDB	OD1, E_ASP_101	NE2, A_GLN_210	HE22, A_GLN_210	2.99	2.07	17.95
1HGG.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.73	1.78	15.93
1HGG.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.93	1.93	14.31
1HGG.PDB	OE2, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.74	1.91	29.92
1HGG.PDB	OE1, B_GLU_67	NH1, A_ARG_269	HH12, A_ARG_269	2.69	1.86	28.34
1HGG.PDB	OD1, B_ASP_90	NZ, A_LYS_310	HZ2, A_LYS_310	2.70	1.74	18.08
1HGG.PDB	OE2, B_GLU_15	NZ, A_LYS_326	HZ1, A_LYS_326	2.83	1.89	21.04
1HGG.PDB	OE2, A_GLU_325	NH2, B_ARG_25	HH22, B_ARG_25	2.94	1.96	12.23
1HGG.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.75	1.76	9.96
1HGG.PDB	OD2, F_ASP_90	NZ, B_LYS_62	HZ2, B_LYS_62	2.65	1.82	29.87
1HGG.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ3, B_LYS_62	2.64	1.73	23.35
1HGG.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.90	1.96	14.63
1HGG.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.94	1.96	10.47
1HGG.PDB	OE1, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.88	1.89	10.69
1HGG.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.73	1.73	5.91
1HGG.PDB	OE2, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.82	1.82	7.26
1HGG.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.68	1.80	19.99
1HGG.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.77	1.73	5.14
1HGG.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.84	1.98	22.96
1HGG.PDB	OE2, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.81	1.98	25.54
1HGG.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.94	1.91	8.28
1HGG.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.85	1.88	14.56
1HGG.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.76	1.86	17.83
1HGG.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.61	1.71	21.26
1HGG.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.83	1.86	17.18
1HGG.PDB	OE2, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.70	1.87	29.85
1HGG.PDB	OE1, D_GLU_67	NH1, C_ARG_269	HH12, C_ARG_269	2.69	1.85	27.75
1HGG.PDB	OD1, D_ASP_90	NZ, C_LYS_310	HZ2, C_LYS_310	2.65	1.73	21.74
1HGG.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.76	1.78	10.56
1HGG.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.86	1.90	9.42
1HGG.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.86	1.89	9.57
1HGG.PDB	OE1, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.78	1.80	12.10
1HGG.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.67	1.68	6.66
1HGG.PDB	OE2, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.74	1.75	9.29
1HGG.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.59	1.78	26.83
1HGG.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.73	1.70	8.35
1HGG.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.86	2.00	22.57
1HGG.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.78	1.96	26.12
1HGG.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.91	1.88	8.89
1HGG.PDB	OE2, F_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.88	1.90	14.20
1HGG.PDB	OD2, D_ASP_79	OG, E_SER_110	HG, E_SER_110	2.79	1.88	16.48
1HGG.PDB	OD1, C_ASP_101	NE2, E_GLN_210	HE22, E_GLN_210	2.96	2.04	17.70
1HGG.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.72	1.80	20.26
1HGG.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ1, E_LYS_238	2.89	1.89	13.93
1HGG.PDB	OE1, F_GLU_67	NH1, E_ARG_269	HH12, E_ARG_269	2.69	1.85	27.32
1HGG.PDB	OD1, F_ASP_90	NZ, E_LYS_310	HZ2, E_LYS_310	2.64	1.72	22.12
1HGG.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.98	1.97	15.13
1HGG.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.73	1.74	10.16
1HGG.PDB	OD2, D_ASP_86	NZ, F_LYS_62	HZ3, F_LYS_62	2.58	1.75	29.01
1HGG.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.87	1.91	10.03
1HGG.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.88	1.92	11.44
1HGG.PDB	OE1, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.75	1.76	9.13
1HGG.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.67	1.68	1.99
1HGG.PDB	OE2, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.79	1.81	10.64

1HGG.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.68	1.67	10.46
1HGG.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.96	2.09	22.59
1HGG.PDB	OE2, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.87	2.01	24.00

Table 1841: 1HGG-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1HGH.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.78	1.76	9.03
1HGH.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.86	1.88	13.48
1HGH.PDB	OD2, F_ASP_79	OG, A_SER_110	HG, A_SER_110	2.97	2.01	11.65
1HGH.PDB	OD1, E_ASP_101	NE2, A_GLN_210	HE22, A_GLN_210	2.97	2.14	27.61
1HGH.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.66	1.73	18.15
1HGH.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.92	1.93	15.64
1HGH.PDB	OD1, B_ASP_86	NZ, A_LYS_310	HZ2, A_LYS_310	2.71	1.84	27.09
1HGH.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.82	1.86	15.60
1HGH.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ1, B_LYS_62	2.66	1.80	27.71
1HGH.PDB	OD2, F_ASP_90	NZ, B_LYS_62	HZ3, B_LYS_62	2.68	1.82	27.13
1HGH.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.87	1.91	11.96
1HGH.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.87	1.90	9.70
1HGH.PDB	OE2, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.91	1.90	8.45
1HGH.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.77	1.76	5.47
1HGH.PDB	OE1, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.89	1.87	2.83
1HGH.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.69	1.84	23.96
1HGH.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.74	1.71	7.44
1HGH.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.76	1.94	26.47
1HGH.PDB	OE2, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.83	1.98	23.62
1HGH.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.82	1.78	7.61
1HGH.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.86	1.88	13.66
1HGH.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.78	1.85	13.87
1HGH.PDB	OD1, A_ASP_101	NE2, C_GLN_210	HE22, C_GLN_210	2.93	2.07	24.87
1HGH.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.57	1.72	26.03
1HGH.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.71	1.80	22.72
1HGH.PDB	OD1, D_ASP_86	NZ, C_LYS_310	HZ2, C_LYS_310	2.73	1.85	26.20
1HGH.PDB	OE1, D_GLU_15	NZ, C_LYS_326	HZ1, C_LYS_326	2.77	1.75	11.00
1HGH.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.80	1.85	16.64
1HGH.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.84	1.88	10.18
1HGH.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.79	1.84	10.45
1HGH.PDB	OE2, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.77	1.77	10.38
1HGH.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.70	1.70	6.41
1HGH.PDB	OE1, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.75	1.75	5.88
1HGH.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.59	1.81	29.86
1HGH.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.66	1.64	7.83
1HGH.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.80	1.98	26.35
1HGH.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.84	1.99	23.38
1HGH.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.77	1.74	8.08
1HGH.PDB	OE2, F_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.88	1.90	13.56
1HGH.PDB	OD2, D_ASP_79	OG, E_SER_110	HG, E_SER_110	2.90	1.94	9.49
1HGH.PDB	OD1, C_ASP_101	NE2, E_GLN_210	HE22, E_GLN_210	2.95	2.09	25.33
1HGH.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.68	1.79	22.30
1HGH.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ3, E_LYS_238	2.87	1.88	15.42
1HGH.PDB	OE1, F_GLU_67	NH1, E_ARG_269	HH12, E_ARG_269	2.71	1.88	29.19
1HGH.PDB	OD1, F_ASP_86	NZ, E_LYS_310	HZ2, E_LYS_310	2.74	1.87	26.77
1HGH.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.90	1.89	12.96
1HGH.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.72	1.77	15.67
1HGH.PDB	OD2, D_ASP_90	NZ, F_LYS_62	HZ2, F_LYS_62	2.68	1.83	28.02
1HGH.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.87	1.91	9.23
1HGH.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.84	1.87	10.72
1HGH.PDB	OE2, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.73	1.73	5.34
1HGH.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.71	1.70	1.21
1HGH.PDB	OE1, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.78	1.78	7.19
1HGH.PDB	OE1, B_GLU_85	OH, F_TYR_83	HH, F_TYR_83	2.53	1.74	27.23
1HGH.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.65	1.63	9.88
1HGH.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.89	2.06	26.55
1HGH.PDB	OE2, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.92	2.03	21.52

Table 1842: 1HGH-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1HGI.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.90	1.86	7.66
1HGI.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.80	1.81	13.24
1HGI.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.65	1.73	18.55
1HGI.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.85	1.85	15.00
1HGI.PDB	OD1, B_ASP_86	NZ, A_LYS_310	HZ3, A_LYS_310	2.76	1.92	29.34
1HGI.PDB	OE2, B_GLU_15	NZ, A_LYS_326	HZ1, A_LYS_326	2.79	1.93	27.33
1HGI.PDB	OE2, A_GLU_325	NH2, B_ARG_25	HH22, B_ARG_25	2.93	1.95	13.46
1HGI.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.81	1.84	14.63
1HGI.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ1, B_LYS_62	2.67	1.78	25.75
1HGI.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.87	1.89	8.13
1HGI.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.86	1.89	7.04
1HGI.PDB	OE2, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.92	1.89	1.72
1HGI.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.71	1.72	8.42
1HGI.PDB	OE1, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.86	1.86	6.93
1HGI.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.78	1.84	13.46
1HGI.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.65	1.64	9.94
1HGI.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.81	1.96	23.50
1HGI.PDB	OE2, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.86	2.02	24.92
1HGI.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.88	1.83	6.58
1HGI.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.82	1.84	15.02
1HGI.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.85	1.90	11.29
1HGI.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.62	1.75	23.70
1HGI.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.67	1.77	23.68
1HGI.PDB	OD1, D_ASP_86	NZ, C_LYS_310	HZ3, C_LYS_310	2.77	1.93	29.51
1HGI.PDB	OE1, D_GLU_15	NZ, C_LYS_326	HZ1, C_LYS_326	2.83	1.84	16.25
1HGI.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.81	1.85	15.40
1HGI.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.83	1.85	2.78
1HGI.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.80	1.82	5.40
1HGI.PDB	OE2, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.78	1.76	4.18
1HGI.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.61	1.67	15.38
1HGI.PDB	OE1, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.76	1.77	8.75
1HGI.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.69	1.81	20.41
1HGI.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.66	1.64	7.30
1HGI.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.84	1.98	23.95
1HGI.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.88	2.03	24.96
1HGI.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.86	1.82	7.44
1HGI.PDB	OE2, F_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.78	1.80	14.37
1HGI.PDB	OD2, D_ASP_79	OG, E_SER_110	HG, E_SER_110	2.90	1.94	10.08
1HGI.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.69	1.80	23.03
1HGI.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ3, E_LYS_238	2.80	1.81	15.90
1HGI.PDB	OD1, F_ASP_86	NZ, E_LYS_310	HZ3, E_LYS_310	2.76	1.91	29.16
1HGI.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.88	1.86	11.05
1HGI.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.75	1.79	14.82
1HGI.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.84	1.87	3.62
1HGI.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.85	1.88	7.37
1HGI.PDB	OE2, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.77	1.76	3.93
1HGI.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.64	1.66	4.79
1HGI.PDB	OE1, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.76	1.78	10.40
1HGI.PDB	OE1, B_GLU_85	OH, F_TYR_83	HH, F_TYR_83	2.58	1.75	24.06
1HGI.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.61	1.62	12.49
1HGI.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.96	2.09	23.50
1HGI.PDB	OE2, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.96	2.09	23.34
1HGI.PDB	OE2, D_GLU_131	NH2, F_ARG_163	HH22, F_ARG_163	2.69	1.85	26.81

Table 1843: 1HGI-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1HGJ.PDB	OE2, B_GLU_97	NZ, A_LYS_27	HZ1, A_LYS_27	2.81	1.78	9.30
1HGJ.PDB	OE2, B_GLU_67	NH2, A_ARG_109	HH21, A_ARG_109	2.75	1.77	12.07
1HGJ.PDB	OD2, F_ASP_79	OG, A_SER_110	HG, A_SER_110	2.94	1.98	10.39
1HGJ.PDB	OE1, C_GLN_210	NH2, A_ARG_220	HH21, A_ARG_220	2.67	1.78	22.50
1HGJ.PDB	OE1, F_GLU_72	NZ, A_LYS_238	HZ3, A_LYS_238	2.90	1.90	13.91
1HGJ.PDB	OE2, A_GLU_325	NH2, B_ARG_25	HH22, B_ARG_25	2.97	2.01	15.94
1HGJ.PDB	OE2, F_GLU_97	NH2, B_ARG_54	HH22, B_ARG_54	2.77	1.81	15.09
1HGJ.PDB	OD2, F_ASP_86	NZ, B_LYS_62	HZ1, B_LYS_62	2.65	1.75	23.55
1HGJ.PDB	OD2, F_ASP_90	NZ, B_LYS_62	HZ3, B_LYS_62	2.74	1.89	28.52
1HGJ.PDB	OG, A_SER_110	NE2, B_HIS_64	HE2, B_HIS_64	2.89	1.93	11.21
1HGJ.PDB	OE2, D_GLU_81	NE, B_ARG_76	HE, B_ARG_76	2.90	1.93	10.80
1HGJ.PDB	OE2, D_GLU_74	NH1, B_ARG_76	HH12, B_ARG_76	2.88	1.87	5.28
1HGJ.PDB	OE1, D_GLU_81	NH2, B_ARG_76	HH21, B_ARG_76	2.72	1.72	3.64
1HGJ.PDB	OE1, D_GLU_74	NH2, B_ARG_76	HH22, B_ARG_76	2.85	1.84	3.19
1HGJ.PDB	OE1, D_GLU_85	OH, B_TYR_83	HH, B_TYR_83	2.67	1.83	24.12
1HGJ.PDB	OH, F_TYR_83	NZ, B_LYS_88	HZ1, B_LYS_88	2.78	1.75	7.42
1HGJ.PDB	OE1, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.82	2.00	27.29
1HGJ.PDB	OE2, F_GLU_132	NE, B_ARG_124	HE, B_ARG_124	2.91	2.02	20.91
1HGJ.PDB	OE2, D_GLU_97	NZ, C_LYS_27	HZ1, C_LYS_27	2.82	1.80	8.63
1HGJ.PDB	OE2, D_GLU_67	NH2, C_ARG_109	HH21, C_ARG_109	2.76	1.78	13.33
1HGJ.PDB	OD2, B_ASP_79	OG, C_SER_110	HG, C_SER_110	2.79	1.87	14.95
1HGJ.PDB	OE1, E_GLN_210	NH2, C_ARG_220	HH21, C_ARG_220	2.66	1.82	26.85
1HGJ.PDB	OE1, B_GLU_72	NZ, C_LYS_238	HZ1, C_LYS_238	2.75	1.79	18.67
1HGJ.PDB	OD1, D_ASP_86	NZ, C_LYS_310	HZ3, C_LYS_310	2.94	2.10	29.37
1HGJ.PDB	OE1, D_GLU_15	NZ, C_LYS_326	HZ1, C_LYS_326	2.91	1.86	5.48
1HGJ.PDB	OE2, B_GLU_97	NH2, D_ARG_54	HH22, D_ARG_54	2.84	1.88	15.58
1HGJ.PDB	OG, C_SER_110	NE2, D_HIS_64	HE2, D_HIS_64	2.89	1.91	5.59
1HGJ.PDB	OE2, F_GLU_81	NE, D_ARG_76	HE, D_ARG_76	2.85	1.89	10.87
1HGJ.PDB	OE2, F_GLU_74	NH1, D_ARG_76	HH12, D_ARG_76	2.76	1.76	7.89
1HGJ.PDB	OE1, F_GLU_81	NH2, D_ARG_76	HH21, D_ARG_76	2.68	1.69	5.65
1HGJ.PDB	OE1, F_GLU_74	NH2, D_ARG_76	HH22, D_ARG_76	2.71	1.72	5.59
1HGJ.PDB	OE1, F_GLU_85	OH, D_TYR_83	HH, D_TYR_83	2.63	1.81	25.72
1HGJ.PDB	OH, B_TYR_83	NZ, D_LYS_88	HZ1, D_LYS_88	2.75	1.72	7.31
1HGJ.PDB	OE1, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.80	1.98	27.33
1HGJ.PDB	OE2, B_GLU_132	NE, D_ARG_124	HE, D_ARG_124	2.87	2.00	21.99
1HGJ.PDB	OH, B_TYR_141	NH1, D_ARG_127	HH12, D_ARG_127	2.99	2.02	12.89
1HGJ.PDB	OE2, F_GLU_97	NZ, E_LYS_27	HZ1, E_LYS_27	2.81	1.79	8.50
1HGJ.PDB	OE2, F_GLU_67	NH2, E_ARG_109	HH21, E_ARG_109	2.76	1.77	12.82
1HGJ.PDB	OD2, D_ASP_79	OG, E_SER_110	HG, E_SER_110	2.79	1.87	15.96
1HGJ.PDB	OD1, C_ASP_101	NE2, E_GLN_210	HE22, E_GLN_210	2.94	2.10	26.45
1HGJ.PDB	OE1, A_GLN_210	NH2, E_ARG_220	HH21, E_ARG_220	2.69	1.86	28.41
1HGJ.PDB	OE1, D_GLU_72	NZ, E_LYS_238	HZ3, E_LYS_238	2.87	1.86	13.82
1HGJ.PDB	OD1, F_ASP_86	NZ, E_LYS_310	HZ3, E_LYS_310	2.93	2.08	29.22
1HGJ.PDB	OE1, F_GLU_15	NZ, E_LYS_326	HZ3, E_LYS_326	2.87	1.86	12.83
1HGJ.PDB	OE2, D_GLU_97	NH2, F_ARG_54	HH22, F_ARG_54	2.77	1.81	14.54
1HGJ.PDB	OG, E_SER_110	NE2, F_HIS_64	HE2, F_HIS_64	2.90	1.93	7.02
1HGJ.PDB	OE2, B_GLU_81	NE, F_ARG_76	HE, F_ARG_76	2.85	1.89	12.57
1HGJ.PDB	OE2, B_GLU_74	NH1, F_ARG_76	HH12, F_ARG_76	2.70	1.70	4.55
1HGJ.PDB	OE1, B_GLU_81	NH2, F_ARG_76	HH21, F_ARG_76	2.65	1.66	2.84
1HGJ.PDB	OE1, B_GLU_74	NH2, F_ARG_76	HH22, F_ARG_76	2.72	1.73	7.95
1HGJ.PDB	OE1, B_GLU_85	OH, F_TYR_83	HH, F_TYR_83	2.53	1.75	28.54
1HGJ.PDB	OH, D_TYR_83	NZ, F_LYS_88	HZ1, F_LYS_88	2.70	1.68	8.19
1HGJ.PDB	OE1, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.92	2.09	27.65
1HGJ.PDB	OE2, D_GLU_132	NE, F_ARG_124	HE, F_ARG_124	2.96	2.06	20.98

Table 1844: 1HGJ-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1OSP.PDB	OD2, L_ASP_1	OG, H_SER_62	HG, H_SER_62	2.98	2.17	26.53
1OSP.PDB	OG, L_SER_176	OG, H_SER_185	HG, H_SER_185	2.74	1.91	24.72
1OSP.PDB	OE1, L_GLU_123	NZ, H_LYS_215	HZ2, H_LYS_215	2.78	1.85	20.53

Table 1845: 1OSP-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
1VFB.PDB	OE1, B_GLU_98	NH1, A_ARG_96	HH12, A_ARG_96	2.82	1.84	8.38
1VFB.PDB	OE2, B_GLU_98	NH2, A_ARG_96	HH22, A_ARG_96	2.81	1.85	10.74
1VFB.PDB	OE1, A_GLN_38	NE2, B_GLN_39	HE21, B_GLN_39	2.95	1.98	8.04

Table 1846: 1VFB-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
3SE8.PDB	OD1, G_ASN_280	NE1, H_TRP_50	HE1, H_TRP_50	3.00	2.21	20.49
3SE8.PDB	OD1, G_ASP_457	NE2, H_GLN_64	HE22, H_GLN_64	2.94	2.12	14.23
3SE8.PDB	OD2, G_ASP_368	NH2, H_ARG_71	HH22, H_ARG_71	2.91	2.05	6.24

Table 1847: 3SE8-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
3SE9.PDB	OD1, G_ASN_280	NE1, H_TRP_50	HE1, H_TRP_50	2.86	2.03	11.46
3SE9.PDB	OG, G_SER_365	NH1, H_ARG_64	HH11, H_ARG_64	2.81	2.04	21.79
3SE9.PDB	OD2, G_ASP_368	NH1, H_ARG_71	HH12, H_ARG_71	2.77	1.92	7.25
3SE9.PDB	OD1, G_ASN_279	NE1, H_TRP_100D	HE1, H_TRP_100D	2.86	2.13	26.83
3SE9.PDB	OD1, L_ASN_138	NE2, H_HIS_164	HE2, H_HIS_164	2.87	2.10	22.18

Table 1848: 3SE9-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
3THM.PDB	OE1, L_GLN_39	NE2, H_GLN_41	HE22, H_GLN_41	2.98	2.14	9.35
3THM.PDB	OG, L_SER_183	NZ, H_LYS_162	HZ1, H_LYS_162	2.77	1.97	21.34
3THM.PDB	OG1, L_THR_135	NZ, H_LYS_162	HZ2, H_LYS_162	2.85	2.02	17.75
3THM.PDB	OH, H_TYR_35	ND1, F_HIS_44	HD1, F_HIS_44	2.69	1.83	5.98
3THM.PDB	OG, H_SER_63	NE2, F_HIS_44	HE2, F_HIS_44	2.83	2.07	23.36

Table 1849: 3THM-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
3TJE.PDB	OE1, L_GLN_39	NE2, H_GLN_41	HE21, H_GLN_41	2.98	2.15	10.85
3TJE.PDB	OH, H_TYR_35	ND1, F_HIS_44	HD1, F_HIS_44	2.56	1.70	3.69

Table 1850: 3TJE-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
3U2S.PDB	OE1, L_GLN_38	NE2, H_GLN_39	HE22, H_GLN_39	2.89	2.04	8.55
3U2S.PDB	OG, L_SER_165	NE2, H_HIS_164	HE2, H_HIS_164	2.93	2.12	16.97
3U2S.PDB	OE1, H_GLN_39	NE2, L_GLN_38	HE22, L_GLN_38	2.91	2.09	13.75
3U2S.PDB	OD2, C_ASP_167	ND2, L_ASN_60	HD22, L_ASN_60	2.90	2.14	22.76
3U2S.PDB	OD1, H_ASP_61	NH2, L_ARG_95A	HH22, L_ARG_95A	2.34	1.58	22.53
3U2S.PDB	OE2, H_GLU_95	NH2, L_ARG_96	HH21, L_ARG_96	2.87	2.05	15.72
3U2S.PDB	OH, H_TYR_100K	ND2, G_ASN_173	HD21, G_ASN_173	2.97	2.13	8.87
3U2S.PDB	OE1, B_GLN_38	NE2, A_GLN_39	HE22, A_GLN_39	2.92	2.07	7.34
3U2S.PDB	OG1, B_THR_131	NZ, A_LYS_143	HZ2, A_LYS_143	2.41	1.67	27.35
3U2S.PDB	OE1, A_GLN_39	NE2, B_GLN_38	HE22, B_GLN_38	2.92	2.08	10.61
3U2S.PDB	OD1, A_ASP_61	NH1, B_ARG_95A	HH12, B_ARG_95A	2.63	1.91	26.97
3U2S.PDB	OE2, A_GLU_95	NH2, B_ARG_96	HH21, B_ARG_96	2.98	2.16	13.77

Table 1851: 3U2S-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
3UYR.PDB	OE2, L_GLU_127	NZ, H_LYS_212	HZ3, H_LYS_212	2.87	2.08	23.12
3UYR.PDB	OD1, H_ASN_101	NE2, P_GLN_48	HE22, P_GLN_48	2.57	1.87	29.89

Table 1852: 3UYR-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4F33.PDB	OE1, B_GLN_39	NE2, A_GLN_38	HE22, A_GLN_38	2.96	2.13	12.75
4F33.PDB	OE1, A_GLN_38	NE2, B_GLN_39	HE22, B_GLN_39	2.82	1.97	5.31
4F33.PDB	OE1, A_GLU_123	NZ, B_LYS_215	HZ1, B_LYS_215	2.68	1.82	12.44
4F33.PDB	OG1, H_THR_211	NZ, B_LYS_215	HZ2, B_LYS_215	2.83	1.95	7.37
4F33.PDB	OE1, C_GLN_38	NE2, D_GLN_39	HE22, D_GLN_39	2.89	2.03	5.23
4F33.PDB	OE1, C_GLU_123	NZ, D_LYS_215	HZ1, D_LYS_215	2.79	1.99	22.47
4F33.PDB	OG1, F_THR_211	NZ, D_LYS_215	HZ2, D_LYS_215	2.86	1.99	10.67
4F33.PDB	OE1, E_GLN_38	NE2, F_GLN_39	HE22, F_GLN_39	2.92	2.06	5.53
4F33.PDB	OE1, E_GLU_123	NZ, F_LYS_215	HZ1, F_LYS_215	2.61	1.84	24.34
4F33.PDB	OG1, D_THR_211	NZ, F_LYS_215	HZ2, F_LYS_215	2.92	2.04	7.71
4F33.PDB	OE1, G_GLU_123	NZ, H_LYS_215	HZ1, H_LYS_215	2.97	2.19	24.10
4F33.PDB	OG1, B_THR_211	NZ, H_LYS_215	HZ2, H_LYS_215	2.80	1.95	14.49

Table 1853: 4F33-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4F3F.PDB	OE1, B_GLN_39	NE2, A_GLN_38	HE22, A_GLN_38	2.88	2.04	8.75
4F3F.PDB	OG, B_SER_59	NE2, A_HIS_94	HE2, A_HIS_94	2.82	2.03	19.68
4F3F.PDB	OD1, A_ASN_138	NE2, B_HIS_170	HE2, B_HIS_170	2.82	2.05	21.56
4F3F.PDB	OH, B_TYR_101	NZ, C_LYS_25	HZ3, C_LYS_25	2.87	2.11	26.18
4F3F.PDB	OH, A_TYR_32	NE1, C_TRP_26	HE1, C_TRP_26	2.97	2.17	18.16

Table 1854: 4F3F-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4JAM.PDB	OD1, H_ASN_100B	ND2, L_ASN_32	HD21, L_ASN_32	2.96	2.21	25.94

Table 1855: 4JAM-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4JAN.PDB	OD2, B_ASP_92	OG, H_SER_156	HG, H_SER_156	2.50	1.78	23.90
4JAN.PDB	OE1, L_GLU_123	NZ, H_LYS_209	HZ1, H_LYS_209	2.89	2.13	26.71
4JAN.PDB	OD1, H_ASN_100B	ND2, L_ASN_32	HD21, L_ASN_32	2.76	1.91	6.44

Table 1856: 4JAN-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4KRM.PDB	OE1, B_GLU_110	NH1, A_ARG_353	HH11, A_ARG_353	2.81	2.05	22.81
4KRM.PDB	OE1, D_GLU_110	NH1, C_ARG_353	HH11, C_ARG_353	2.87	2.05	16.15
4KRM.PDB	OD2, C_ASP_355	NH1, D_ARG_30	HH12, D_ARG_30	2.45	1.63	13.53
4KRM.PDB	OE1, F_GLU_110	NH1, E_ARG_353	HH11, E_ARG_353	2.85	2.03	14.34
4KRM.PDB	OD2, F_ASP_112	NH2, E_ARG_353	HH22, E_ARG_353	2.96	2.18	20.33
4KRM.PDB	OE2, B_GLU_5	NZ, G_LYS_407	HZ1, G_LYS_407	2.98	2.17	20.60
4KRM.PDB	OD2, G_ASP_355	NH1, H_ARG_30	HH12, H_ARG_30	2.45	1.69	23.45
4KRM.PDB	OE1, J_GLU_110	NH1, I_ARG_353	HH11, I_ARG_353	2.86	2.07	18.90
4KRM.PDB	OD2, J_ASP_112	NH2, I_ARG_353	HH22, I_ARG_353	3.00	2.19	17.61
4KRM.PDB	OE1, L_GLU_110	NH1, K_ARG_353	HH11, K_ARG_353	2.89	2.06	12.41
4KRM.PDB	OD2, L_ASP_112	NH2, K_ARG_353	HH22, K_ARG_353	2.89	2.07	13.96
4KRM.PDB	OD2, K_ASP_355	NH1, L_ARG_30	HH12, L_ARG_30	2.44	1.65	18.93

Table 1857: 4KRM-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4KRO.PDB	OG, B.SER_103	NZ, A.LYS_375	HZ2, A.LYS_375	2.61	1.76	15.34
4KRO.PDB	OH, D.TYR_102	NE2, A.GLN_384	HE21, A.GLN_384	2.87	2.16	29.24
4KRO.PDB	OD1, B.ASP_118	NE, A.ARG_405	HE, A.ARG_405	2.72	1.93	19.48
4KRO.PDB	OE1, D.GLN_39	NE2, C.GLN_38	HE22, C.GLN_38	2.85	2.00	7.50
4KRO.PDB	OD2, D.ASP_103	OH, C.TYR_50	HH, C.TYR_50	2.49	1.72	20.15
4KRO.PDB	OD1, D.ASP_103	ND2, C.ASN_91	HD21, C.ASN_91	2.93	2.12	16.18
4KRO.PDB	OD2, D.ASP_58	NE1, C.TRP_94	HE1, C.TRP_94	2.80	2.10	29.15
4KRO.PDB	OE1, C.GLN_38	NE2, D.GLN_39	HE22, D.GLN_39	2.80	1.94	4.32
4KRO.PDB	OE1, A.GLN_408	OH, D.TYR_102	HH, D.TYR_102	2.75	1.97	18.39

Table 1858: 4KRO-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4KRP.PDB	OD1, B_ASP_115	NH2, A_ARG_405	HH21, A_ARG_405	2.63	1.81	15.48
4KRP.PDB	OD1, D_ASP_58	NZ, A_LYS_443	HZ1, A_LYS_443	2.65	1.82	17.69
4KRP.PDB	OD2, D_ASP_103	NZ, A_LYS_465	HZ2, A_LYS_465	2.93	2.05	5.06
4KRP.PDB	OE1, D_GLN_39	NE2, C_GLN_38	HE22, C_GLN_38	2.70	1.84	6.09
4KRP.PDB	OD2, D_ASP_103	OH, C_TYR_50	HH, C_TYR_50	2.43	1.66	18.96
4KRP.PDB	OD1, D_ASP_103	ND2, C_ASN_91	HD21, C_ASN_91	2.77	1.91	6.24
4KRP.PDB	OD2, D_ASP_58	NE1, C_TRP_94	HE1, C_TRP_94	2.98	2.17	17.26
4KRP.PDB	OE1, C_GLN_38	NE2, D_GLN_39	HE22, D_GLN_39	2.72	1.87	5.47
4KRP.PDB	OE1, A_GLN_408	OH, D_TYR_102	HH, D_TYR_102	2.56	1.74	10.00
4KRP.PDB	OG, A_SER_440	OH, D_TYR_104	HH, D_TYR_104	2.94	2.22	25.72
4KRP.PDB	OE1, A_GLU_431	OH, B_TYR_32	HH, B_TYR_32	2.59	1.78	7.49
4KRP.PDB	OE1, A_GLU_400	OH, B_TYR_100	HH, B_TYR_100	2.94	2.13	13.29
4KRP.PDB	OE2, A_GLU_431	OH, B_TYR_116	HH, B_TYR_116	2.43	1.75	29.09

Table 1859: 4KRP-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4NZR.PDB	OG, L.SER_176	OG, H.SER_188	HG, H.SER_188	2.88	2.16	24.46
4NZR.PDB	OE2, L.GLU_123	NZ, H.LYS_221	HZ2, H.LYS_221	2.99	2.10	2.00
4NZR.PDB	OG, H.SER_188	OG, L.SER_176	HG, L.SER_176	2.88	2.09	13.66
4NZR.PDB	OE1, L.GLU_81	NE, M.ARG_384	HE, M.ARG_384	2.93	2.09	10.37
4NZR.PDB	OD1, H.ASP_31E	NH1, M.ARG_457	HH12, M.ARG_457	2.96	2.12	11.27
4NZR.PDB	OD2, H.ASP_31E	NH2, M.ARG_457	HH22, M.ARG_457	2.55	1.75	17.03

Table 1860: 4NZR-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4WUU.PDB	OD2, B_ASP_53	NE, A_ARG_48	HE, A_ARG_48	2.84	2.13	29.12
4WUU.PDB	OH, E_TYR_104	NZ, A_LYS_66	HZ3, A_LYS_66	2.89	2.02	10.84
4WUU.PDB	OXT, C_LEU_9	OH, A_TYR_84	HH, A_TYR_84	2.64	1.82	12.17
4WUU.PDB	OE1, B_GLN_8	NH1, A_ARG_234	HH11, A_ARG_234	2.79	2.07	27.49
4WUU.PDB	OE1, A_GLU_232	OH, B_TYR_26	HH, B_TYR_26	2.95	2.14	13.27
4WUU.PDB	OE1, E_GLN_39	NE2, D_GLN_39	HE22, D_GLN_39	2.94	2.18	23.53
4WUU.PDB	OD1, E_ASP_106	NE1, D_TRP_99	HE1, D_TRP_99	2.95	2.19	24.35
4WUU.PDB	OE1, D_GLN_39	NE2, E_GLN_39	HE22, E_GLN_39	2.55	1.73	14.29
4WUU.PDB	OE2, A_GLU_166	NH2, E_ARG_50	HH22, E_ARG_50	2.67	1.88	18.69
4WUU.PDB	OE1, A_GLU_63	OH, E_TYR_104	HH, E_TYR_104	2.59	1.76	7.82
4WUU.PDB	OE1, A_GLU_55	OH, E_TYR_105	HH, E_TYR_105	2.47	1.79	29.86

Table 1861: 4WUU-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
4Z0X.PDB	OE1, B_GLN_64	NE2, A_GLN_37	HE22, A_GLN_37	2.75	1.99	23.41

Table 1862: 4Z0X-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5I76.PDB	OE1, B_GLN_39	NE2, A_GLN_38	HE22, A_GLN_38	2.94	2.10	10.68
5I76.PDB	OD2, B_ASP_103	OH, A_TYR_50	HH, A_TYR_50	2.64	1.88	21.01
5I76.PDB	OE1, A_GLN_38	NE2, B_GLN_39	HE22, B_GLN_39	2.80	1.95	6.66
5I76.PDB	OG, A_SER_176	OG, B_SER_185	HG, B_SER_185	2.89	2.15	23.05
5I76.PDB	OE1, A_GLU_123	NZ, B_LYS_215	HZ1, B_LYS_215	2.73	1.96	24.68
5I76.PDB	OE2, A_GLU_123	NZ, B_LYS_215	HZ1, B_LYS_215	2.89	2.11	24.69
5I76.PDB	OD2, A_ASP_70	NH1, C_ARG_24	HH12, C_ARG_24	2.95	2.23	28.81
5I76.PDB	OD2, D_ASP_103	OH, C_TYR_50	HH, C_TYR_50	2.76	1.95	12.40
5I76.PDB	OE1, C_GLN_38	NE2, D_GLN_39	HE22, D_GLN_39	2.85	2.01	10.98
5I76.PDB	OE1, C_GLU_123	NZ, D_LYS_215	HZ1, D_LYS_215	2.60	1.73	11.40

Table 1863: 5I76-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5JO5.PDB	OE1, L_GLN_38	NE2, H_GLN_39	HE22, H_GLN_39	2.84	2.00	9.38
5JO5.PDB	OE2, L_GLU_124	NZ, H_LYS_143	HZ2, H_LYS_143	2.46	1.63	17.05
5JO5.PDB	OH, L_TYR_177	OG, H_SER_179	HG, H_SER_179	2.73	2.00	25.96
5JO5.PDB	OE1, D_GLN_24	OG, L_SER_30	HG, L_SER_30	2.84	2.07	18.45
5JO5.PDB	OE1, H_GLN_39	NE2, L_GLN_38	HE22, L_GLN_38	2.83	2.00	13.03
5JO5.PDB	OE2, H_GLU_100J	NH2, L_ARG_91	HH22, L_ARG_91	2.69	1.84	7.26
5JO5.PDB	OD1, H_ASP_58	NE, L_ARG_95B	HE, L_ARG_95B	2.95	2.13	14.76
5JO5.PDB	OE1, B_GLN_38	NE2, A_GLN_39	HE22, A_GLN_39	2.87	2.02	8.31
5JO5.PDB	OE2, B_GLU_124	NZ, A_LYS_143	HZ2, A_LYS_143	2.62	1.83	23.29
5JO5.PDB	OH, B_TYR_177	OG, A_SER_179	HG, A_SER_179	2.83	2.10	25.21
5JO5.PDB	OE2, B_GLU_123	NZ, A_LYS_209	HZ1, A_LYS_209	2.55	1.68	10.64
5JO5.PDB	OE1, A_GLN_39	NE2, B_GLN_38	HE22, B_GLN_38	2.90	2.07	12.43
5JO5.PDB	OE1, D_GLN_38	NE2, C_GLN_39	HE22, C_GLN_39	2.86	2.02	9.45
5JO5.PDB	OE2, D_GLU_124	NZ, C_LYS_143	HZ2, C_LYS_143	2.79	1.92	10.71
5JO5.PDB	OH, D_TYR_177	OG, C_SER_179	HG, C_SER_179	2.71	1.97	23.23
5JO5.PDB	OE2, D_GLU_123	NZ, C_LYS_209	HZ1, C_LYS_209	2.58	1.72	11.28
5JO5.PDB	OE1, C_GLN_39	NE2, D_GLN_38	HE22, D_GLN_38	2.92	2.09	12.72
5JO5.PDB	OD1, C_ASP_58	NE, D_ARG_95B	HE, D_ARG_95B	2.94	2.10	11.64
5JO5.PDB	OE1, F_GLN_38	NE2, E_GLN_39	HE22, E_GLN_39	2.90	2.06	10.70
5JO5.PDB	OE2, F_GLU_124	NZ, E_LYS_143	HZ2, E_LYS_143	2.55	1.75	21.57
5JO5.PDB	OH, F_TYR_177	OG, E_SER_179	HG, E_SER_179	2.58	1.87	27.02
5JO5.PDB	OE2, F_GLU_123	NZ, E_LYS_209	HZ1, E_LYS_209	2.57	1.74	17.62
5JO5.PDB	OE1, B_GLN_24	OG, F_SER_30	HG, F_SER_30	2.88	2.11	20.15
5JO5.PDB	OE1, E_GLN_39	NE2, F_GLN_38	HE22, F_GLN_38	2.85	2.02	12.75
5JO5.PDB	OE2, E_GLU_100J	NH2, F_ARG_91	HH22, F_ARG_91	2.72	1.87	5.99
5JO5.PDB	OD1, E_ASP_58	NE, F_ARG_95B	HE, F_ARG_95B	2.92	2.09	12.47

Table 1864: 5JO5-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5JR1.PDB	OH, L_TYR_178	OG, H_SER_179	HG, H_SER_179	2.83	2.03	15.88
5JR1.PDB	OD2, H_ASP_58	NH2, L_ARG_95B	HH22, L_ARG_95B	2.47	1.67	16.99

Table 1865: 5JR1-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5JUE.PDB	OH, H-TYR_91	NE2, L-GLN_38	HE22, L-GLN_38	2.57	1.77	17.09
5JUE.PDB	OG, H-SER_178	OG, L-SER_176	HG, L-SER_176	2.78	1.94	3.13
5JUE.PDB	OE1, L-GLU_123	NZ, H-LYS_208	HZ1, H-LYS_208	2.81	1.98	17.66

Table 1866: 5JUE-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5JXA.PDB	OD2, L_ASP_50	OH, H_TYR_100	HH, H_TYR_100	2.57	1.75	11.76
5JXA.PDB	OH, H_TYR_100	NH2, L_ARG_53	HH21, L_ARG_53	2.89	2.07	18.12

Table 1867: 5JXA-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5T6P.PDB	OE1, A_GLN_43	NE2, B_GLN_39	HE22, B_GLN_39	2.71	1.86	5.14
5T6P.PDB	OE1, D_GLN_39	NE2, C_GLN_43	HE22, C_GLN_43	3.00	2.17	12.88
5T6P.PDB	OE1, C_GLN_43	NE2, D_GLN_39	HE22, D_GLN_39	2.79	1.94	7.20
5T6P.PDB	OE1, C_GLU_39	NE, E_ARG_5	HE, E_ARG_5	2.86	2.02	10.72

Table 1868: 5T6P-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5T78.PDB	OE1, B_GLN_39	NE2, A_GLN_43	HE22, A_GLN_43	2.92	2.08	9.79
5T78.PDB	OE1, A_GLN_43	NE2, B_GLN_39	HE22, B_GLN_39	2.63	1.78	5.56
5T78.PDB	OE1, A_GLU_39	NH1, F_ARG_5	HH11, F_ARG_5	2.68	1.83	9.33
5T78.PDB	OE1, C_GLN_43	NE2, D_GLN_39	HE22, D_GLN_39	2.72	1.87	5.23
5T78.PDB	OD1, C_ASN_142	NE2, D_HIS_167	HE2, D_HIS_167	2.85	2.00	9.68
5T78.PDB	OE1, C_GLU_39	NH1, E_ARG_5	HH11, E_ARG_5	2.69	1.87	13.16

Table 1869: 5T78-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5U3J.PDB	OD1, L_ASP_31	OH, H_TYR_100K	HH, H_TYR_100K	2.88	2.04	5.22
5U3J.PDB	OE1, H_GLU_100F	OH, L_TYR_32	HH, L_TYR_32	2.62	1.91	27.84
5U3J.PDB	OE1, H_GLN_39	NE2, L_GLN_38	HE22, L_GLN_38	2.66	1.83	12.57

Table 1870: 5U3J-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5U3N.PDB	OD2, A_ASP_674	NH1, H_ARG_52A	HH12, H_ARG_52A	3.00	2.24	24.41
5U3N.PDB	OD1, L_ASP_31	NH2, H_ARG_100B	HH22, H_ARG_100B	2.97	2.15	14.50
5U3N.PDB	OD1, L_ASN_34	ND2, H_ASN_100J	HD21, H_ASN_100J	2.72	1.86	2.61
5U3N.PDB	OD1, L_ASN_138	NE2, H_HIS_164	HE2, H_HIS_164	2.92	2.21	29.54

Table 1871: 5U3N-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5UCB.PDB	OE1, L_GLN_38	NE2, H_GLN_39	HE22, H_GLN_39	2.96	2.12	9.92
5UCB.PDB	OD2, B_ASP_51	OG, L_SER_30	HG, L_SER_30	2.58	1.81	20.19
5UCB.PDB	OE1, H_GLN_39	NE2, L_GLN_38	HE22, L_GLN_38	2.95	2.13	14.86
5UCB.PDB	OG, H_SER_58	NZ, B_LYS_142	HZ3, B_LYS_142	2.83	1.96	8.82
5UCB.PDB	OD1, L_ASP_91	NH2, B_ARG_144	HH21, B_ARG_144	2.84	2.03	16.18

Table 1872: 5UCB-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5UK0.PDB	OD1, F_ASP_590	ND2, B_ASN_560	HD22, B_ASN_560	2.72	1.94	19.72
5UK0.PDB	OD1, D_ASP_586	NH2, C_ARG_311	HH22, C_ARG_311	2.98	2.20	18.56
5UK0.PDB	OD1, B_ASP_590	ND2, D_ASN_560	HD22, D_ASN_560	2.73	1.95	20.06

Table 1873: 5UK0-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5VXJ.PDB	OE1, I_GLU_200	NH1, B_ARG_50	HH12, B_ARG_50	2.92	2.07	7.25
5VXJ.PDB	OE1, I_GLU_201	OH, B_TYR_105	HH, B_TYR_105	2.51	1.70	12.69
5VXJ.PDB	OD1, C_ASN_140	NE, D_ARG_19	HE, D_ARG_19	2.55	1.80	23.66
5VXJ.PDB	OE1, E_GLU_201	OH, D_TYR_105	HH, D_TYR_105	2.53	1.70	8.84
5VXJ.PDB	OD2, F_ASP_73	NZ, E_LYS_137	HZ2, E_LYS_137	2.77	1.96	20.15
5VXJ.PDB	OD1, D_ASN_97	NZ, E_LYS_197	HZ1, E_LYS_197	2.80	1.95	14.72
5VXJ.PDB	OE1, G_GLU_200	NH2, F_ARG_50	HH22, F_ARG_50	2.70	1.89	15.49
5VXJ.PDB	OE1, G_GLU_201	OH, F_TYR_105	HH, F_TYR_105	2.57	1.75	11.97
5VXJ.PDB	OE1, H_GLN_111	OG1, G_THR_217	HG1, G_THR_217	2.86	2.17	29.58
5VXJ.PDB	OD2, J_ASP_73	NZ, I_LYS_137	HZ3, I_LYS_137	2.90	2.17	29.52
5VXJ.PDB	OD1, B_ASN_97	NZ, I_LYS_197	HZ1, I_LYS_197	2.68	1.88	21.92

Table 1874: 5VXJ-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5VXK.PDB	OG, A_SER_168	NE2, B_GLN_106	HE21, B_GLN_106	2.99	2.23	24.43
5VXK.PDB	OD2, A_ASP_287	NE2, B_GLN_106	HE22, B_GLN_106	2.77	1.94	12.81
5VXK.PDB	OG1, B_THR_102	OH, A_TYR_276	HH, A_TYR_276	2.57	1.73	6.50

Table 1875: 5VXK-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5VXL.PDB	OD2, B_ASP_52	NZ, A_LYS_205	HZ1, A_LYS_205	3.00	2.13	10.69
5VXL.PDB	OD1, A_ASP_166	OG, B_SER_55	HG, B_SER_55	2.56	1.73	4.68
5VXL.PDB	OE2, A_GLU_201	NH2, B_ARG_102	HH22, B_ARG_102	2.87	2.08	20.03

Table 1876: 5VXL-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5VXM.PDB	OE2, B.GLU_111	NE1, A.TRP_177	HE1, A.TRP_177	2.76	1.97	19.61

Table 1877: 5VXM-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5VXR.PDB	OE1, L_GLN_38	NZ, H_LYS_39	HZ2, H_LYS_39	2.72	1.76	14.94
5VXR.PDB	OD1, P_ASN_415	OH, H_TYR_50	HH, H_TYR_50	2.71	1.82	21.79
5VXR.PDB	OD1, L_ASN_138	NE2, H_HIS_170	HE2, H_HIS_170	2.89	1.98	20.57
5VXR.PDB	OE2, L_GLU_123	NZ, H_LYS_214	HZ1, H_LYS_214	2.93	1.98	15.97
5VXR.PDB	OG, H_SER_184	OG, L_SER_176	HG, L_SER_176	2.79	1.86	17.30

Table 1878: 5VXR-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5WKQ.PDB	OG, B.SER_208	NH2, A.ARG_135	HH21, A.ARG_135	2.89	2.06	11.87
5WKQ.PDB	OE2, A.GLU_131	ND1, B.HIS_207	HD1, B.HIS_207	2.65	1.88	22.26
5WKQ.PDB	OE1, A.GLU_131	OG1, B.THR_211	HG1, B.THR_211	2.63	1.86	19.68

Table 1879: 5WKQ-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(^{\circ})$
5WN9.PDB	OD1, H_ASN_57	NE, A_ARG_188	HE, A_ARG_188	2.58	1.61	2.15

Table 1880: 5WN9-specific interfacial side chain hydrogen bonding analysis. In this table, a PDB file is specified with a four-letter PDB ID, except that the names of the PDB files corresponding to the single NMR structural model split from the NMR ensemble is specified with a four-letter PDB ID in addition to a hyphen followed by the single NMR structural model numeric ID, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).